農業生物のゲノム情報解析研究

－国産品種ダイズのゲノム配列解析とカイコゲノムデータベースの開発－

別冊

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博士論文（本審査）

2018 年 12 月

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Chromosome	etic dist.	Marker name	Forward marker	Chr/Scaffold	Start position (bp)	End position (bp)	Reverse marker	Chr/Scaffold	Start position (bp)	End position (bp)	Forward marker sequence	Reverse marker sequence
Chr01	0	T000100040s	T000100040s_F	Chr01	39,711	39,733	T000100040s_R	Chr01	39,910	39,888	CTGGTTCTGTCAATTTCCTTCAG	GCAATCCACTCATTAAACTCAGC
Chr01	0.8	Sat_413	Sat_413_F	Chr01	354,524	354,548	Sat_413_R	Chr01	354,718	354,691	CTCCCTTCTTTTCCACTGAATTGA	TTTTCTCTCGGTTTCTCTCTTCTTATTA
Chr01	0.8	Sat_332	Sat_332_F	Chr01	355,622	355,649	Sat_332_R	Chr01	355,863	355,836	TAAAAACCTTTAGAAAGAACAATAAGAA	AGCAATCAATTCAAAAGAATAATGAAAA
Chr01	5.1	GMES4240	GMES4240_F	Chr01	882,790	882,811	GMES4240_R	Chr01	883,044	883,025	CATGATCCAATACCACATCACA	ACTTGCAGCAGAAGATGGCT
Chr01	10.3	Satt184-2	Satt184-2_F	Chr01	1,473,012	1,473,031	Satt184-2_R	Chr01	1,473,244	1,473,220	CCTAGCTTGCTGTGCATGAG	TGAAGCTCCATCATATATTCATGTC
Chr01	12.5	GMES3386	GMES3386_F	Chr01	1,689,828	1,689,809	GMES3386_R	Chr01	1,689,677	1,689,697	TGTTTCGACGTCGTTTCATC	CCTCTTCAGCCTTTTCCAGTT
Chr01	13.3	GMES3158	GMES3158_F	Chr01	1,734,839	1,734,820	GMES3158_R	Chr01	1,734,735	1,734,754	TTCCACAACACTTCACCGAA	GTATTACGAGCGGTTAGCGG
Chr01	13.3	GMES4052	GMES4052_F	Chr01	1,750,199	1,750,180	GMES4052_R	Chr01	1,749,928	1,749,947	AGCCATACATCTGTCACCCC	ACATCCTTGTCCTCACTGGC
Chr01	14	GMES1307	GMES1307_F	Chr01	1,773,051	1,773,070	GMES1307_R	Chr01	1,773,159	1,773,140	GTTCTCCGCGAACTCAACTC	TGGAGACCAGGAAGAACCAC
Chr01	16.7	s017000801-2	s017000801-2_F	Chr01	2,060,400	2,060,422	s017000801-2_R	Chr01	2,060,551	2,060,529	CGCATCATACTATGTCATCCACA	ATATCCGCAACATATCTTTGTCC
Chr01	17.6	C01-BARC-016475-02620	C01-BARC-016475-02620_F	Chr01	2,211,173	2,211,192	C01-BARC-016475-02620_R	Chr01	2,211,256	2,211,237	TCTTCTTCCCAAGAAGGCTG	CTTTGTGAACAGTGAATCCC
Chr01	19.1	T000102376s	T000102376s_F	Chr01	2,382,499	2,382,522	T000102376s_R	Chr01	2,382,707	2,382,685	GAACACTTCATATCCTTGCATGTT	GTGTTCACAGCATTGTTCTTAGG
Chr01	25.2	T000102848m	T000102848m_F	Chr01	2,863,354	2,863,375	T000102848m_R	Chr01	2,863,690	2,863,667	AACATGCATTCTGCGATACAAA	TTATTTGTTTCCTTAGCCTAATTT
Chr01	26.9	T000102921m	T000102921m_F	Chr01	2,936,496	2,936,518	T000102921m_R	Chr01	2,936,726	2,936,704	AAAGTTGAAGGATCAAATGTGGA	GGATCAGCTATCCTTTGCCTTAT
Chr01	30.5	T000103082m	T000103082m_F	Chr01	3,097,663	3,097,685	T000103082m_R	Chr01	3,097,988	3,097,968	TAACGAGCTTGATTGCTTAGTCC	CACAAAGTTTACATTGAGTGC
Chr01	35.6	T000103277l	T000103277l_F	Chr01	3,291,291	3,291,317	T000103277l_R	Chr01	3,291,663	3,291,641	TGTAGGTGTTTATGGTTAACTCACATT	TGCAAGTATGCACCACTTGTATC
Chr01	39	s031200036	s031200036_F	Chr01	3,549,417	3,549,439	s031200036_R	Chr01	3,549,781	3,549,757	TTGAGGGTGTCTTTGGTAAGTTG	GGCAATACTAATAAACCAGCTGAAA
Chr01	40.1	s031200132-2	s031200132-2_F	Chr01	3,644,893	3,644,914	s031200132-2_R	Chr01	3,645,092	3,645,070	AAATGGAAGATACTTTGGTTTC	ATTGACCGAACTTAAGGGTTTCT
Chr01	40.6	Satt531-2	Satt531-2_F	Chr01	3,779,492	3,779,516	Satt531-2_R	Chr01	3,779,880	3,779,861	GCAATTGCTATCTATTCCTATTCCT	GGATGTGAACGTGGATTGGT
Chr01	41.9	GMES2778.1	GMES2778_F	Chr01	3,896,545	3,896,526	GMES2778_R	Chr01	3,896,314	3,896,333	TGTGGTCCGATTGTTTGCTA	ACACCAAGCTCGAAAACCAC
Chr01	43.6	GMES0519	GMES0519_F	Chr01	3,947,413	3,947,394	GMES0519_R	Chr01	3,947,124	3,947,143	CATCAAACAACATCGGTTGG	ACGAGCCGAAACTGGTGTAG
Chr01	43.6	C01-BARC-021671-04176	C01-BARC-021671-04176_F	Chr01	3,957,599	3,957,613	C01-BARC-021671-04176_R	Chr01	3,957,694	3,957,675	AAGGGTGAAGTTCCGTAC	GATTTGTCTGTTATCCGTGA
Chr01	48.3	T000104165s	T000104165s_F	Chr01	4,185,728	4,185,755	T000104165s_R	Chr01	4,185,936	4,185,914	TGGTCTAAATTATTTCTTATCTTTACGA	CCTTTATGGGTTCTACAAGCAAA
Chr01	50.1	GMES0626	GMES0626_F	Chr01	4,457,136	4,457,117	GMES0626_R	Chr01	4,456,840	4,456,863	AGCAGGAACTGGAGTCCTCA	CAACATTTTTCCAAACACGTTAAT
Chr01	52.8	s029200170	s029200170_F	Chr01	5,238,278	5,238,301	s029200170_R				TTTAGGCTTTAACTGATCAACTTT	ATTTCTCGGTACAGATTAACCGC
Chr01	52.8	GMES4842	GMES4842_F	Chr01	5,549,496	5,549,516	GMES4842_R	Chr01	5,549,752	5,549,733	AAAACAAAACGCTTAACGCAA	CAAGTGATCGCTCATTGGAA
Chr01	53.1	C01-BARC-017943-02463	C01-BARC-017943-02463_F	Chr01	5,664,760	5,664,779	C01-BARC-017943-02463_R	Chr01	5,664,837	5,664,818	CCCTGCTTCTCCATTTTTAC	AGGGTGTGTTTGGAAAACCG
Chr01	53.6	Satt368	Satt368_F	Chr01	6,926,557	6,926,534	Satt368_R	Chr01	6,926,298	6,926,321	AGTGCAAGAAAAAGGGAGAAAATA	CTTTTCTTTCCTTTTTTTTCTCTT
Chr01	54.3	s029100034	s029100034_F	Chr01	7,253,897	7,253,872	s029100034_R	Chr01	7,253,613	7,253,635	CAGAATCTTAATATATCCGAAACAAA	CATTCCATCGTTTGGTTACAAGT
Chr01	54.7	GMES0899	GMES0899_F	Chr01	7,373,706	7,373,725	GMES0899_R	Chr01	7,373,940	7,373,921	GGCAACACTGTCATCACACC	GACGATACATCAGCTGGCAA
Chr01	55.5	Sat_353	Sat_353_F	Chr01	7,728,528	7,728,555	Sat_353_R	Chr01	7,728,766	7,728,740	GTCACTCGGCTAAGTAATTGTGTAGAAA	GGTAATGCTAGGTTTTGGAAAATGATT
Chr01	56.8	C01-BARC-015055-02546	C01-BARC-015055-02546_F	Chr01	10,812,268	10,812,287	C01-BARC-015055-02546_R	Chr01	10,812,346	10,812,327	TTCAGGGAATGAATGAAGGG	CAGCAGGTTTTTCTACGTTG
Chr01	57.9	Satt221	Satt221_F	Chr01	24,274,598	24,274,619	Satt221_R	Chr01	24,274,804	24,274,786	ATTGTACCACTAAAAACCATAG	GCAAACCATTATCTTCATT
Chr01	57.9	GMES4431	GMES4431_F	Chr01	25,843,651	25,843,632	GMES4431_R	Chr01	25,843,272	25,843,291	GGAACGGTAGCGGAGTACAA	AGCTCCACCGTTTCTCTTCA
Chr01	61.5	s011700279r	s011700279r_F	Chr01	29,050,396	29,050,380	s011700279r_R	Chr01	29,050,173	29,050,194	CCACCCTTTCTCGCACC	TGATTTGATCCACTAATACCAA
Chr01	61.7	Sat_346	Sat_346_F	Chr01	33,260,226	33,260,205	Sat_346_R	Chr01	33,260,084	33,260,103	GTACGGCATCTGCAATGACTTT	GAGCCAACCACCTCAGTATC
Chr01	64.7	C01-BARC-039815-07590	C01-BARC-039815-07590_F	Chr01	41,168,558	41,168,577	C01-BARC-039815-07590_R	Chr01	41,168,643	41,168,624	CTGAATCCGCTCACTTGTTG	TTGTATGTCTTCAGCCCTGC
Chr01	64.7	Sat_201	Sat_201_F	Chr01	42,510,477	42,510,460	Sat_201_R	Chr01	42,510,207	42,510,224	ATCGTTAACTCCTTACAC	GCCCAGAAGTAGTCAAAG
Chr01	65	C01-BARC-040871-07859	C01-BARC-040871-07859_F	Chr01	43,430,440	43,430,459	C01-BARC-040871-07859_R	Chr01	43,430,513	43,430,494	TGCAACCATTAACAATACCG	GCTATGTTGTTTTCACAAGG
Chr01	65.8	GMES1291	GMES1291_F	Chr01	43,934,610	43,934,629	GMES1291_R	Chr01	43,934,886	43,934,867	ACACTGCCTCAAGGAGGAAA	CCAAGCCTATACCACCACCA
Chr01	67.7	C01-BARC-043191-08551	C01-BARC-043191-08551_F	Chr01	44,790,270	44,790,289	C01-BARC-043191-08551_R	Chr01	44,790,349	44,790,330	TGCGTAATGAATCTTGTCCC	ATGACAGTGTGCACTTGACC
Chr01	70.1	Satt370	Satt370_F	Chr01	47,375,561	47,375,539	Satt370_R	Chr01	47,375,336	47,375,356	GTTAAGGGAATTTGTAACTTGAA	ATCATGCATTTATTTGAGATA
Chr01	71.7	s001302387	s001302387_F	Chr01	48,037,288	48,037,309	s001302387_R	Chr01	48,037,396	48,037,374	CCACCGACGTGTCGCACGATGAGAGGTAGGCACAACTCC	ATCAGATTCTCGATCAATTCTTT
Chr01	71.7	s001302706	s001302706_F	Chr01	48,357,272	48,357,295	s001302706_R	Chr01	48,357,408	48,357,389	AAGTTACTTCCATCCAACTATAAA	TTTCAACTGGCCAATATCAT
Chr01	75.1	T000147811l	T000147811l_F	Chr01	48,682,828	48,682,851	T000147811l_R	Chr01	48,683,134	48,683,114	TCAAATACTGATTCCTTGCATATT	GATCGGCTAGTTCTCCCAGTATAA
Chr01	79.6	s001303327-2	s001303327-2_F	Chr01	48,977,791	48,977,814	s001303327-2_R	Chr01	48,977,990	48,977,967	TGAGTCTATGAGTCGAGTTTATGA	TTGTACATTTGTTGCAGTTAAATA
Chr01	82	T000148451m	T000148451m_F	Chr01	49,328,092	49,328,115	T000148451m_R	Chr01	49,328,422	49,328,399	GTTCTCTCGAGAATACTAACTCAT	TTCACTTTAAATCTTTAACCAATG
Chr01	87.2	Satt436	Satt436_F	Chr01	49,567,977	49,568,000	Satt436_R	Chr01	49,568,192	49,568,168	TATAAAGAAAAACGAGCATATCAT	CTTATAAAGGCTTGTGAAAGACACT
Chr01	88.1	Satt468	Satt468_F	Chr01	49,731,987	49,731,963	Satt468_R	Chr01	49,731,775	49,731,799	TCTCTTATTTTGACCTTTTTAACTT	TTTTGTATTTGGTCTATCTGCTTAG
Chr01	88.3	Satt077	Satt077_F	Chr01	49,780,906	49,780,881	Satt077_R	Chr01	49,780,794	49,780,810	GATCTAAAGTCTGATATTTTTAACTA	AAAAGGAGAAGGAATGC
Chr01	89.4	T000149090l	T000149090l_F	Chr01	49,968,838	49,968,860	T000149090l_R	Chr01	49,969,181	49,969,159	AGATGTTGCCATTACTCAAATGC	GAAACTGAGGAGCTGAAAGGTGT
Chr01	92.6	s001304421	s001304421_F	Chr01	50,072,545	50,072,567	s001304421_R	Chr01	50,072,941	50,072,919	AGATTTGATGACACTAGCGGTCT	AGGTTGAATGCACAAATTAAAGC
Chr01	94.6	s001304710	s001304710_F	Chr01	50,362,863	50,362,886	s001304710_R	Chr01	50,363,218	50,363,197	AAATGATGGATGAGAATCCAAGTT	CCAGACCCACAATCCATATCAT
Chr01	95.9	s001305022	s001305022_F	Chr01	50,674,958	50,674,980	s001305022_R	Chr01	50,675,152	50,675,130	GGACAAATTCCATTGTTTAAGGG	CCCTCAACTTTAAATTCAATCAA
Chr01	99.6	s001305363	s001305363_F	Chr01	51,016,726	51,016,748	s001305363_R	Chr01	51,016,901	51,016,882	ACCTTGACACGGTAATGAGAAAT	TTTAAAGGACAAAGGGCAAA
Chr01	102.6	T000150333m	T000150333m_F	Chr01	51,215,869	51,215,893	T000150333m_R	Chr01	51,216,187	51,216,165	TTGCTAGATAACAAGCTAACAAATG	CATTCGTTGAAAGCTAGATTCGT
Chr01	105.1	s001305760	s001305760_F	Chr01	51,411,831	51,411,857	s001305760_R	Chr01	51,412,231	51,412,209	AAAGACTACAAATACAAATAAGTCTCA	TTCCTACCATGTATTAATGCCCA
Chr01	108.1	T000150800s	T000150800s_F	Chr01	51,683,230	51,683,253	T000150800s_R	Chr01	51,683,412	51,683,390	AATAGAATTATTTAAACACGCCTT	ATTCTATCTTGGAGAGATGACCG
Chr01	112	s001306372-2	s001306372-2_F	Chr01	52,022,983	52,023,009	s001306372-2_R	Chr01	52,023,115	52,023,093	AGATGTACTACTACTTAAACAGCAAGA	ATAAGATTCTTGAGGCACTGAGC
Chr01	113.6	Sat_414	Sat_414_F	Chr01	52,334,653	52,334,633	Sat_414_R	Chr01	52,334,438	52,334,458	TTGTGCTTAGGGAAAATAAAA	AAAAACACTGTCTGAAATACT
Chr01	113.6	Sat_305	Sat_305_F	Chr01	52,377,465	52,377,491	Sat_305_R	Chr01	52,377,796	52,377,772	ACAATGCAAAACACATTTGTATTACTT	CTATGCCCATGTGTTTAGTGATTAG
Chr01	114.4	C01-BARC-021569-04147	C01-BARC-021569-04147_F	Chr01	52,434,533	52,434,514	C01-BARC-021569-04147_R	Chr01	52,434,448	52,434,467	CGCAGCAGTCAAGTATCCAC	GCAAGTCTCAACACATTCCG
Chr01	114.4	GMES4584	GMES4584_F	Chr01	52,584,054	52,584,035	GMES4584_R	Chr01	52,583,820	52,583,839	GAGTCCATCGTCGAGGTCAT	CCCCCATTTCAGTTGTTCTT
Chr01	118.5	s001307253	s001307253_F	Chr01	52,907,362	52,907,385	s001307253_R	Chr01	52,907,714	52,907,692	AAGACTTTATTTAAGGAATCCAAA	TAATCAATTTCCGATCAACATCC
Chr01	120.7	T000152201s	T000152201s_F	Chr01	53,085,377	53,085,398	T000152201s_R	Chr01	53,085,585	53,085,563	AGGTACATCAAACAGCACCACA	AAAGCTTTATCGTTCCACACGTA
Chr01	123.7	s001307583	s001307583_F	Chr01	53,238,326	53,238,348	s001307583_R	Chr01	53,238,490	53,238,468	CCACGAATCTATTTGTTACCCAG	TTAAAGTCACATCAAGTTAACGG
Chr01	127.3	T000152766m	T000152766m_F	Chr01	53,648,534	53,648,556	T000152766m_R	Chr01	53,648,826	53,648,804	AAAGAATAGAGGGAATATGATGT	TTTAGGGATGACGAGTGACAACT
Chr01	130.6	s001308421	s001308421_F	Chr01	54,072,696	54,072,718	s001308421_R	Chr01	54,072,866	54,072,844	ATACACAGAGAGACGTGTGCATT	ACATTACAACCTCAGCTTCCAAA
Chr01	135	s001308859-2	s001308859-2_F	Chr01	54,533,994	54,534,015	s001308859-2_R	Chr01	54,534,417	54,534,395	AAACTACGGTGCATAACACAAA	ACTACGAAGACTACACCGTGGAC
Chr01	136.4	Satt147	Satt147_F	Chr01	54,826,429	54,826,448	Satt147_R	Chr01	54,826,598	54,826,574	CCATCCCTTCCTCCAAATAGAT	CTTCCACACCCTAGTTTAGTGACAA
Chr01	137.2	Satt129	Satt129_F	Chr01	55,164,063	55,164,090	Satt129_R	Chr01	55,164,211	55,164,188	TTCAGTACAAGTCGGGTGAATAATAATA	TCACATGTTCGGGACTTAAGGTAT
Chr01	137.2	C01-BARC-040447-07743	C01-BARC-040447-07743_F	Chr01	55,349,032	55,349,013	C01-BARC-040447-07743_R	Chr01	55,348,954	55,348,973	CGACTTATTTCCTTCTTTGG	GTTTGCAGATAACGAGGATG
Chr01	137.3	GMES0765.1	GMES0765_F	Chr01	55,521,842	55,521,823	GMES0765_R	Chr01	55,521,705	55,521,722	TGCTTGCTGCCTCTTATTCA	TGGCTATACGTGTGTGTGTGC
Chr01	138.5	GMES0281	GMES0281_F	Chr01	55,570,772	55,570,753	GMES0281_R	Chr01	55,570,577	55,570,596	TCACCACCAACCCTCTAACC	CAGTGTCGGGACTACAAGCA
Chr01	141.2	GMES4224	GMES4224_F	Chr01	56,379,566	56,379,585	GMES4224_R	Chr01	56,379,715	56,379,696	CCCAAGAGTTTGGAGCTCTG	TTCACGCGCTTTCCTACTTT
Chr01	142	T000155868l	T000155868l_F	Chr01	56,782,044	56,782,066	T000155868l_R	Chr01	56,782,414	56,782,392	CGATTATTTGCAACGTTAGAAGG	AGTAACATTATTGGCAGTGCTGA

Chr02	0	T000200100l	T000200100l_F	Chr02	98,978	99,000	T000200100l_R	Chr02	99,323	99,301	CCTCAACCCTGTCAAGTAACACA	AGAAACAAGACATGGTGATGGAT
Chr02	0	C02-BARC-013955-01283	C02-BARC-013955-01283_F	Chr02	133,052	133,071	C02-BARC-013955-01283_R	Chr02	133,115	133,096	GATTCTTCTCTTGCTGCCAC	GAGCATTTGATGTCATCGAG
Chr02	0.5	T000200458l	T000200458l F	Chr02	457,059	457,081	T000200458l R	Chr02	457,370	457,348	GTGCAAAGGCTATATTGGGAAGT	CATATGCAGTCACGATCAAGAAA
Chr02	0.7	alphaP-AT17.1										
Chr02	2.1	T000200778l	T000200778l_F	Chr02	776,747	776,769	T000200778l_R	Chr02	777,093	777,071	GGTAGAATAGAAGGAGGGAGCAC	ACTGTTCTTTGGTGGTGATGAAC
Chr02	6.6	T000201012s	T000201012s_F	Chr02	1,010,649	1,010,673	T000201012s_R	Chr02	1,010,849	1,010,827	TCTTTATTCTTTATTTGAGACCGGA	GAGAGTTATGTCTTCGTTCACGG
Chr02	9.3	s016800026	s016800026 F	Chr02	1,319,271	1,319,249	s016800026 R	Chr02	1,319,008	1,319,030	TGATCGAAAGCTCTAATCCTCAG	GCTCTTCGTAGAAACCAAGCATA
Chr02	10.4	s031800033	s031800033_F	Chr02	1,462,265	1,462,243	s031800033_R	Chr02	1,461,945	1,461,967	AATGGAGGGAAATTGAGATTGTT	GTACATGGCCCTGCAAACATAGT
Chr02	15.4	Sat_096	Sat_096_F	Chr02	1,783,743	1,783,769	Sat_096_R	Chr02	1,783,936	1,783,914	ATTATAGGGAGTAACCACAAAGAAAAA	GCTAGCTACCTGCCAGTGATTAT
Chr02	15.6	GMES0767	GMES0767 F	Chr02	1,902,422	1,902,403	GMES0767 R	Chr02	1,902,126	1,902,145	TTTCAAAATCAAACGCCAAA	CGAAACACCATGGAACACAG
Chr02	16.4	Sat_279	Sat_279_F	Chr02	2,004,612	2,004,638	Sat_279_R	Chr02	2,004,880	2,004,853	TTGCGTTGTTACGTGAAAGCACAGAAAC	ACTGGTTAATCTAGTCAGACTTAACAGA
Chr02	20.9	T000202368m	T000202368m_F	Chr02	2,398,219	2,398,241	T000202368m_R	Chr02	2,398,436	2,398,414	CACTAATCTTCCATTCTGGCAAT	ATCCATTACTGAACGTCTTGGAA
Chr02	21.9	GMES2778	GMES2778_F	Chr02	2,677,776	2,677,795	GMES2778_R	Chr02	2,678,015	2,677,996	TGTGGTCCGATTGTTTGCTA	ACACCAAGCTCGAAAACCAC
Chr02	23.6	GMES1360	GMES1360 F	Chr02	3,086,631	3,086,612	GMES1360 R	Chr02	3,086,402	3,086,421	TGCAGAAAAGATGCCACAAC	CCTTCTTCCCTTCCTGCTCT
Chr02	23.8	GMES0949	GMES0949_F	Chr02	3,144,990	3,144,971	GMES0949_R	Chr02	3,144,807	3,144,826	TCACAGAGAAAGATGGCTGC	CTGAGAACCAACCGGGAATA
Chr02	25.2	GMES2512	GMES2512_F	Chr02	3,571,818	3,571,837	GMES2512_R	Chr02	3,571,921	3,571,902	CCTATACCACCCATTCACCG	CATGTTGGGTGCTTCATCTG
Chr02	25.2	GMES3944	GMES3944_F	Chr02	3,687,825	3,687,806	GMES3944_R	Chr02	3,687,674	3,687,693	ACACCTTCTCTCCTCCAAGG	GCCCAAGTGGAACACTGAAT
Chr02	27.3	Satt216	Satt216_F	Chr02	4,104,630	4,104,611	Satt216_R	Chr02	4,104,448	4,104,470	TACCCTTAATCACCGGACAA	AGGGAACTAACACATTTAATCATCA
Chr02	28.4	GMES4519	GMES4519_F	Chr02	4,458,389	4,458,408	GMES4519_R	Chr02	4,458,485	4,458,466	TCACACTTTCAACCCCATCA	CGAGTTTGCATCATCATTGG
Chr02	29.2	C02-BARC-016063-02051	C02-BARC-016063-02051_F	Chr02	4,596,742	4,596,723	C02-BARC-016063-02051_R	Chr02	4,596,664	4,596,683	AAGAAGGGCCAACTCTTCAG	ATGTTGCTCTTCAGCCGTTC
Chr02	30.5	Sat_351	Sat_351 F	Chr02	4,904,884	4,904,865	Sat_351 R	Chr02	4,904,610	4,904,629	CCACCCAAGGGCATCTTTCG	GGCCGCAACTATGAAAAGAC
Chr02	33	GMES6916	GMES6916_F	Chr02	5,122,188	5,122,169	GMES6916_R	Chr02	5,121,897	5,121,916	CTCTCCGATTCAATTCCCAA	CCTTGGTCAGCCATCAAACT
Chr02	34.9	GMES0303	GMES0303_F	Chr02	5,362,546	5,362,527	GMES0303_R	Chr02	5,362,289	5,362,308	GCCTCCTGTATCTCTTTGCG	TGAGGAATTTCGGCTACACC
Chr02	35.1	GMES0671	GMES0671_F	Chr02	5,389,204	5,389,185	GMES0671_R	Chr02	5,389,066	5,389,084	GTTGAAGAGGGAATTTGCCA	AAAGAAGACGAAGGCGATGA
Chr02	35.1	GMES0637	GMES0637 F	Chr02	5,440,875	5,440,894	GMES0637 R	Chr02	5,441,152	5,441,133	GTCACTCACGCTAGGGCTTC	TGCAACTTTGAGAGGAGGAA
Chr02	36.4	C02-BARC-045259-08916	C02-BARC-045259-08916_F	Chr02	5,670,734	5,670,753	C02-BARC-045259-08916_R	Chr02	5,670,829	5,670,810	CAGTAGTTGCAAGACTATGG	GTGTTTGAATTTGACTTGTG
Chr02	39.1	T000206013m	T000206013m_F	Chr02	6,071,140	6,071,162	T000206013m_R	Chr02	6,071,470	6,071,447	CTTAAATGACACAGCTACTGGCG	AAAGGATTTGACTGATAATCGAAG
Chr02	41.8	GMES5577	GMES5577 F	Chr02	6,662,386	6,662,367	GMES5577 R	Chr02	6,662,156	6,662,181	GACTCTGCAGCTCAAAACCC	GATTTTGACCACAAATTAAGAGATTT
Chr02	43.9	T000206938m	T000206938m_F	Chr02	7,015,369	7,015,391	T000206938m_R	Chr02	7,015,692	7,015,670	GACACCTCTCTTCCACAAAGATT	TAGTTTGTCCTCTTATGCTGCCA
Chr02	47.9	s013000037-2	s013000037-2_F	Chr02	7,322,114	7,322,135	s013000037-2_R	Chr02	7,322,233	7,322,211	AATTAATTTGATTGGGCTGTTT	TTTAATTGTTATGTACGGTAAGC
Chr02	49.6	s013000204-2	s013000204-2_F	Chr02	7,488,875	7,488,894	s013000204-2_R	Chr02	7,489,024	7,488,998	GGGATTTCTAGTGGAGTTCA	TTAAAGTGCATACCTCTAGTTATTATT
Chr02	51.5	GMES1698	GMES1698 F	Chr02	7,827,002	7,826,983	GMES1698 R	Chr02	7,826,721	7,826,741	AACCTTCCAATGCTTGTTGC	TGCGATAAAGTGGTGAAATCC
Chr02	52.9	T000208383m	T000208383m_F	Chr02	8,471,689	8,471,710	T000208383m_R	Chr02	8,471,973	8,471,949	ATAAATCATGGGTGAGCGAGAG	AACATGATCATTAATAGTTGAACGG
Chr02	56.4	C02-BARC-040713-07825	C02-BARC-040713-07825_F	Chr02	8,774,729	8,774,710	C02-BARC-040713-07825_R	Chr02	8,774,663	8,774,682	GGGCATATAACAAGCTCAAG	GGCAATTTTTGGTGCTTAAC
Chr02	56.4	Satt701	Satt701_F	Chr02	8,792,920	8,792,901	Satt701_R	Chr02	8,792,686	8,792,707	CTCAGCGGAAAGCCTTCTCA	ATGTCGCACCTACACCCAAAAA
Chr02	56.4	Sat_211	Sat_211_F	Chr02	8,831,522	8,831,542	Sat_211_R	Chr02	8,831,777	8,831,752	ATCACCGGACTTAGAGAGTTA	GAGCTAATTAAAAAGTCATTCCAATA
Chr02	56.4	s022200063	s022200063_F	Chr02	9,415,299	9,415,320	s022200063_R	Chr02	9,415,658	9,415,636	ACAAGTTTGCGTCAAGGGTAAT	CCATAATGGGCGTACTTATACCA
Chr02	56.7	Sat_173	Sat_173_F	Chr02	9,481,942	9,481,923	Sat_173_R	Chr02	9,481,693	9,481,714	GGGATGGCCTTTTATTCTAC	TGTCTCCATTGCTACGACTAAG
Chr02	57	C02-BARC-025955-05182	C02-BARC-025955-05182 F	Chr02	9,688,781	9,688,762	C02-BARC-025955-05182 R	Chr02	9,688,693	9,688,712	GAACTCATCAATGCCTGCAC	TTGGTACCATGCCAAAGGAG
Chr02	58.3	GMES0884	GMES0884_F	Chr02	10,121,539	10,121,520	GMES0884_R	Chr02	10,121,339	10,121,358	CACTCATTTTCCTTCCCCTG	TGATTCCAGATCCACGTTCA
Chr02	61	Satt558	Satt558_F	Chr02	10,618,848	10,618,868	Satt558_R	Chr02	10,619,071	10,619,051	CTCACACCCTTTCATTATCTA	AAATCGCGCATCTAAATTTAC
Chr02	61	s026600230	s026600230_F	Chr02	10,698,496	10,698,518	s026600230_R	Chr02	10,698,754	10,698,732	GATGGATTCGACATTCAGACTTT	CAACTCATTCATACTCTTTCGGG
Chr02	61	s026600239	s026600239 F	Chr02	10,707,262	10,707,284	s026600239 R	Chr02	10,707,651	10,707,629	TACAACGTGTGAATATTGCCAAA	ATGCTTGCTCTCGTATGATTTCT
Chr02	61	s026600256	s026600256_F	Chr02	10,724,294	10,724,316	s026600256_R	Chr02	10,724,627	10,724,605	AAACCCTTCCATTGGAGTTAGAG	AGTGTCGAAGTGCTTGATCGAAT
Chr02	62.6	s026600345	s026600345_F	Chr02	10,814,234	10,814,252	s026600345_R	Chr02	10,814,543	10,814,522	TTTGCTCATGTATGGTGGG	CTTGAATACATATGTTGGGTTC
Chr02	62.6	s026600346	s026600346 F	Chr02	10,815,292	10,815,315	s026600346 R	Chr02	10,815,627	10,815,605	CGTCGATCTTATAAACAACTTCCA	GTTGTTGAGGGATGAGAAAGAAA
Chr02	63.2	s023400007	s023400007_F	Chr02	10,843,817	10,843,839	s023400007_R	Chr02	10,844,153	10,844,131	CGGCTCTTTCATTTCTTCTTCTT	CGTACGTGCTGAATAATGTTGAA
Chr02	63.2	s023400009	s023400009_F	Chr02	10,846,097	10,846,117	s023400009_R	Chr02	10,846,399	10,846,377	CCCAATGTGAAATTATGAACACC	ATAGAAACTGGAATTTGAAGCCC
Chr02	63.2	s023400019	s023400019_F	Chr02	10,855,895	10,855,917	s023400019_R	Chr02	10,856,205	10,856,183	ACTGACGATCAACCAGGTTAAGG	TCAATGTGCTAGAGTTATGCACG
Chr02	64.5	GMES0777	GMES0777 F	Chr02	11,300,972	11,300,989	GMES0777 R	Chr02	11,301,175	11,301,156	CGCACCTCTTGTCCAGAAAT	AGTGAGGGCAAGAAAAAGCA
Chr02	65	s023400577	s023400577_F	Chr02	11,415,619	11,415,641	s023400577_R	Chr02	11,415,940	11,415,921	TTGTTGTACATGGGACCTTTCTT	TTTGGACACACCAAAGGAGA
Chr02	65	s021200808	s021200808_F	Chr02	11,676,658	11,676,636	s021200808_R	Chr02	11,676,389	11,676,411	TTCTAACTTCTAACGCATGCTCC	TGAGAGAAGAAGGAGAAACCAAA
Chr02	65.3	s021200706	s021200706_F	Chr02	11,778,701	11,778,679	s021200706_R	Chr02	11,778,418	11,778,440	TCAGTAAGGTAGTCCCACTTTGG	TATTCTGGGAGGAAGCACCTTAT
Chr02	65.3	C02-BARC-040465-07747	C02-BARC-040465-07747_F	Chr02	11,825,569	11,825,550	C02-BARC-040465-07747_R	Chr02	11,825,473	11,825,492	GCATTTTTGTTTGACAATCC	CCTCGTGGAAGTGTTCATTT
Chr02	65.6	s021200597	s021200597_F	Chr02	11,885,168	11,885,146	s021200597_R	Chr02	11,884,881	11,884,903	TTGAATAACCAATGTGATGAGGC	TTAAAGGATAACAACAACAAACA
Chr02	65.8	s021200522-2	s021200522-2_F	Chr02	11,960,130	11,960,108	s021200522-2_R	Chr02	11,959,789	11,959,811	CACATTGACACTCTTGGAAGTGA	AAATTTACCTGCATAGTGCGAAA
Chr02	65.8	s021200446	s021200446 F	Chr02	12,035,802	12,035,780	s021200446 R	Chr02	12,035,700	12,035,718	TTGGTTCAATATCAACGATTCTG	GAGATCGATGCATCCCTTG
Chr02	66.1	s021200320	s021200320_F	Chr02	12,161,903	12,161,874	s021200320_R	Chr02	12,161,721	12,161,743	CATGAAAGTAATAAGTTGTTATTAGGAGAA	ACTCTGCTAATATGGTGGTGGTG
Chr02	66.4	s021200291-2	s021200291-2_F	Chr02	12,190,488	12,190,465	s021200291-2_R	Chr02	12,190,100	12,190,122	TTTCTGTCAGCATTCTAAGAGTTT	GAAGTACACATGTTTCGCACAGA
Chr02	66.6	s021200143-2	s021200143-2_F	Chr02	12,338,700	12,338,678	s021200143-2_R	Chr02	12,338,244	12,338,265	TGAATAGAAAGCGCACTTGTACC	AAATCGCAACCTTATTCATTGC
Chr02	66.9	s021200060-2	s021200060-2 F	Chr02	12,421,496	12,421,474	s021200060-2 R	Chr02	12,421,368	12,421,390	CTCTTGCCAAATCTCAACACTCT	TGACCTTGGATCAGTGACGTAAT
Chr02	66.9	s021200007	s021200007_F	Chr02	12,474,290	12,474,268	s021200007_R	Chr02	12,474,152	12,474,175	CATCAGCAATCCTCTCTCTCCTA	TGCTCAATCATTTCACACTAAACA
Chr02	69.6	s028700116r	s028700116r_F	Chr02	12,606,030	12,606,005	s028700116r_R	Chr02	12,605,796	12,605,817	GCTCCATTGTCATGTTTATCTTAATC	TTTGGAACATCAATTAGACAAT
Chr02	69.9	s019700968-2	s019700968-2 F	Chr02	12,761,430	12,761,408	s019700968-2 R	Chr02	12,761,225	12,761,243	TTTCCATGGTAAGAGGGACATAC	AAACAATAGTTGGGAATTTGAA
Chr02	70.1	s019700760	s019700760_F	Chr02	12,967,253	12,967,230	s019700760_R	Chr02	12,967,054	12,967,077	TCATCAATATATAATTGCACTCAA	CTTCATAGAATCACATCCAAATTA
Chr02	70.1	s019700759	s019700759_F	Chr02	12,967,915	12,967,893	s019700759_R	Chr02	12,967,724	12,967,747	GGCATGCCACAACTAAGAACTAA	AATCCCACTAATCAAATTTATCTC
Chr02	70.9	Satt542	Satt542 F	Chr02	13,315,810	13,315,789	Satt542 R	Chr02	13,315,607	13,315,628	CACCAGCACAGAACAATCATTT	CACGGTCTAACCTTTCCTTCTA
Chr02	70.9	Satt296	Satt296 F	Chr02	13,335,189	13,335,171	Satt296 R	Chr02	13,335,005	13,335,027	GCCCCACAACCAGAAACAC	GAAATTTGGCGACTAAAAACTGC
Chr02	70.9	s019700394-2	s019700394-2_F	Chr02	13,335,185	13,335,164	s019700394-2_R	Chr02	13,335,050	13,335,073	CACAACCAGAAACACCCAATTC	AAAGACAGCCCTAAACTTAAAGGA
Chr02	70.9	s019700302-2	s019700302-2_F	Chr02	13,426,424	13,426,402	s019700302-2_R	Chr02	13,426,290	13,426,314	AATACGGGTCCTGAAATGTAGGT	TTTGTCTTACAACATAATATTGAGC
Chr02	70.9	s019700026	s019700026_F	Chr02	11,439,495	11,439,471	s019700026_R	Chr02	11,439,112	11,439,136	TGACATAGAACTCTGCTAGCAACAC	ATTGTCAAAGTGCATTTGCTTTTAT
Chr02	73.7	T000213573m	T000213573m_F	Chr02	13,768,070	13,768,092	T000213573m_R	Chr02	13,768,359	13,768,341	AGTAATGACCCTTTAACCATGCC	TCTTAAATCAATGGTCGTTGGAC
Chr02	77.6	GMES1732	GMES1732_F	Chr02	14,218,111	14,218,130	GMES1732_R	Chr02	14,218,342	14,218,323	ATATCTGGGCCCCCATTAAG	AGGTGTGGGACAGCTTTTTG
Chr02	80.3	GMES0031	GMES0031_F	Chr02	14,485,421	14,485,402	GMES0031_R	Chr02	14,485,183	14,485,202	ATTCTTCCACAGCATACCCG	GAAGATGCAAGTCCTGCTCC
Chr02	81.1	GMES0271	GMES0271 F	Chr02	14,653,054	14,653,035	GMES0271 R	Chr02	14,652,903	14,652,922	GAACAATTGAGGTCGACGGT	GCAACACACATGCATTCTCC
Chr02	85.3	T000214752m	T000214752m_F	Chr02	14,952,948	14,952,970	T000214752m_R	Chr02	14,953,227	14,953,205	CCAATGACGATACATACAAAGCA	TTGGTTCATGTCTGACAAATAGG
Chr02	87.4	T000214950m	T000214950m_F	Chr02	15,151,305	15,151,328	T000214950m_R	Chr02	15,151,611	15,151,587	TTAGTTAATTTCATCAGCGTGTCA	GGCATAATTAAGAGATTATACGGAA

Chr02	91	T000215049s	T000215049s_F	Chr02	15,251,032	15,251,054	T000215049s_R	Chr02	15,251,204	15,251,182	ATTAGTCCCTTAGCGTGGAAACT	AAGTTAGGGTGAATCTCGTCAAA
Chr02	92.4	s004305162-2	s004305162-2_F	Chr02	15,342,289	15,342,267	s004305162-2_R	Chr02	15,341,992	15,342,014	GAGTGCAACTTGGTCCAGATATT	ATTTCTCATGTTGCTTTGACGTT
Chr02	95.8	s004304842-2	s004304842-2 F	Chr02	15,664,104	15,664,077	s004304842-2 R	Chr02	15,663,730	15,663,752	TGGTAAAGAATTTACTGTTACTCAATCA	TCCTCTAGTCAAGGATTCACCTG
Chr02	100.1	Satt537	Satt537_F	Chr02	15,992,899	15,992,878	Satt537_R	Chr02	15,992,748	15,992,769	TGTACATCAAAATGGTGTATTC	GGAGGAACTTTGTCTCAGTAAT
Chr02	100.1	s009401425	s009401425_F	Chr02	21,093,139	21,093,161	s009401425_R	Chr02	21,093,352	21,093,330	TGAACACAATTGTAAGGGACCAT	ATTGCGTTCAGAGCTTCAGAGTA
Chr02	100.1	s000600215-2	s000600215-2_F				s000600215-2_R				TCAATCCAACGATGAGTTCTAAG	GAATCATAGAAGCAATGGCAAA
Chr02	100.9	GMES4211	GMES4211 F	scaffold 2140	1	20	GMES4211 R	scaffold 2140	193	174	GAACTACCGCTACGGTTCCA	GGAGCCATTAGGGATTCTCC
Chr02	101.4	Satt611	Satt611_F	Chr02	28,902,329	28,902,349	Satt611_R	Chr02	28,902,538	28,902,516	GGGAATAATAAGAATATGGAC	CTTTCACTATGTGACCTGAATTA
Chr02	103	s001500012-2	s001500012-2_F	Chr02	37,722,715	37,722,735	s001500012-2_R	Chr02	37,723,069	37,723,044	TGAATCCCGGTGATCAATATG	CAACCAAGTTAAATGATAGAAGTTCA
Chr02	103.3	s001500409-2	s001500409-2 F	Chr02	38,119,282	38,119,305	s001500409-2 R	Chr02	38,119,649	38,119,627	AGAACTTAATAAACTTGCTTTCAA	CTAATTTCTTTGCAGGCATCCTA
Chr02	103.9	s001500947-2	s001500947-2_F	Chr02	38,656,545	38,656,568	s001500947-2_R	Chr02	38,656,731	38,656,709	TTTGTCATCACATCTTGGATTATG	CACAGCACTAATATGACAGGACC
Chr02	106	T000242057m	T000242057m_F	Chr02	38,984,421	38,984,443	T000242057m_R				TCTGATTTCAAAGGCTAACAAGG	TAACAATGACGGTAGTCCTTTGG
Chr02	107.9	T000242267l	T000242267l_F	Chr02	39,194,090	39,194,112	T000242267l_R	Chr02	39,194,470	39,194,447	AAATTCTGCAGCAAACTTCTTGT	GGAGAAGTATAGAGTCTCACGTCG
Chr02	111.2	T000242517s	T000242517s F	Chr02	39,444,288	39,444,310	T000242517s R	Chr02	39,444,464	39,444,442	TTCATCTTGCATCTCAAACTCTG	TGAGTCATCCATGCGAATATACA
Chr02	113.3	T000243113s	T000243113s_F				T000243113s_R	Chr02	40,034,894	40,034,872	TGTAAGTTTCGTATATTTCGATATCCC	TAAGAATTGAAGTCATCTTGGTT
Chr02	114.4	Satt546	Satt546_F	Chr02	40,698,078	40,698,098	Satt546_R	Chr02	40,698,317	40,698,297	TGAGCGATCAAGAAGCACTTA	TTTGGATCGCATAACACTTTA
Chr02	114.9	GMES4599	GMES4599_F	Chr02	40,991,956	40,991,978	GMES4599_R	Chr02	40,992,219	40,992,200	AACTGCTTGTAACCCTTATGCAG	GAGTTGAAGCAGTCCGATCC
Chr02	114.9	C02-BARC-018115-02528	C02-BARC-018115-02528_F	Chr02	40,997,808	40,997,789	C02-BARC-018115-02528_R	Chr02	40,997,723	40,997,742	GACTAGTGCGAGTAGGAATC	TCTGGGAAGAGTCAAACCAC
Chr02	116.8	T000244457l	T000244457l_F	Chr02	41,377,361	41,377,386	T000244457l_R	Chr02	41,377,703	41,377,677	GCTTATTTACTATGCTATAGAGCGGC	TTAATAGATTCACCCTTGAGTACAACC
Chr02	119.8	s001504057-2	s001504057-2_F	Chr02	41,758,020	41,758,042	s001504057-2_R	Chr02	41,758,382	41,758,360	GAGTTCGATTCTTAAGCTGATGC	CACATTGTCACCAACCAGTTAAA
Chr02	120.9	s001504461-2	s001504461-2 F	Chr02	42,162,054	42,162,077	s001504461-2 R	Chr02	42,162,193	42,162,171	AGCATCTAGCACAATACTTATACA	AAATAATATGTGCCGAGGTTGAC
Chr02	122.2	C02-BARC-030361-06860	C02-BARC-030361-06860_F	Chr02	42,735,897	42,735,878	C02-BARC-030361-06860_R	Chr02	42,735,816	42,735,835	CACCTTCATGAACATCATCC	GCAAACTGAATCTAGTCCTG
Chr02	123.3	s001505206-2	s001505206-2_F	Chr02	42,908,969	42,908,991	s001505206-2_R	Chr02	42,909,112	42,909,090	GAAAGGACGTAGTATCAAATGGC	AAATCACAGTTTGGATTCATCGT
Chr02	125.9	Sat_069	Sat_069_F	Chr02	43,277,640	43,277,655	Sat_069_R	Chr02	43,277,795	43,277,774	CGACCAGCTGAAGAAA	CTGAATACCCATCATTACTTAA
Chr02	128.5	s001505884-2	s001505884-2 F	Chr02	43,592,575	43,592,598	s001505884-2 R	Chr02	43,592,754	43,592,728	TCATTGATAACATGTGCATTGATT	AAAGTTAAGTAGATAATTCTAGCCTTT
Chr02	132.9	T000247139s	T000247139s_F	Chr02	44,049,390	44,049,414	T000247139s_R	Chr02	44,049,563	44,049,541	TGATTTGATATCTCTTGTTAAGGTC	TTTGTGTGGGAGACTTATGTTTG
Chr02	134.5	C02-BARC-026065-05239	C02-BARC-026065-05239_F	Chr02	44,225,255	44,225,274	C02-BARC-026065-05239_R	Chr02	44,225,352	44,225,333	ATCTGTTATGCCTTCACCCG	GAAGTGACATCAATACTGAC
Chr02	134.6	s001506608-2	s001506608-2 F	Chr02	44,315,937	44,315,964	s001506608-2 R	Chr02	44,316,124	44,316,102	GACATGTAGGAGATTAGTTTGATAGCAC	ACCCGATATCTAAACATATCAAA
Chr02	139.1	GMES0650	GMES0650_F	Chr02	44,791,370	44,791,390	GMES0650_R	Chr02	44,791,502	44,791,483	CGAGCACTTTAACATAAAATCACAA	GATGTATCGGTTGCTGGGTT
Chr02	140.9	C02-BARC-045013-08864	C02-BARC-045013-08864_F	Chr02	45,057,885	45,057,904	C02-BARC-045013-08864_R	Chr02	45,057,975	45,057,956	GTATCCTCTGATAGCTAGGG	GAGGAGGATAGCCGTAAAGG
Chr02	143	Satt274	Satt274_F	Chr02	45,265,479	45,265,501	Satt274_R	Chr02	45,265,661	45,265,640	GGGTCAATTAGTTTTCGTCAGTT	CACGGTATATAATCGAACCTAT
Chr02	143	Satt459	Satt459 F	Chr02	45,309,728	45,309,703	Satt459 R	Chr02	45,309,548	45,309,569	TCGTGTTAGATTTTTACTGTCACATT	AACTGCATACCCTTTGTTTGAA
Chr02	144.1	T000248469s	T000248469s_F	Chr02	45,387,750	45,387,773	T000248469s_R	Chr02	45,387,939	45,387,917	AAAGAGAGCAAAGAGTGGTTCATT	AGTTCGAGGCAACAAACTCTAAC
Chr02	144.6	T000248521l	T000248521l_F	Chr02	45,440,122	45,440,144	T000248521l_R	Chr02	45,440,477	45,440,455	GTGGAGCATACTCATATGAAGCC	CAACATTCGGATTTCCAAGTAAC
Chr02	144.6	T000248608l	T000248608l_F	Chr02	45,526,881	45,526,906	T000248608l_R	Chr02	45,527,225	45,527,203	TCTCATTCTTATCTTATCTTGCATGG	TTTCTGCCGTGTATTATTTGGTT
Chr02	144.6	T000248608l	T000248608l_F	Chr02	45,526,881	45,526,906	T000248608l_R	Chr02	45,527,225	45,527,203	TCTCATTCTTATCTTATCTTGCATGG	TTTCTGCCGTGTATTATTTGGTT
Chr02	147.9	T000248854s	T000248854s_F	Chr02	45,773,489	45,773,511	T000248854s_R	Chr02	45,773,635	45,773,614	AACAAAGGATCTAAAGGCCAAAC	TCCTAGCCTTCTGATCTTCAGC
Chr02	149.3	T000248976l	T000248976l_F	Chr02	45,896,048	45,896,070	T000248976l_R	Chr02	45,896,393	45,896,370	TGAGAGCTTACCACCAAAGATTC	AATATATGCCTATCCGAAGTGAGC
Chr02	153.4	s001508433-2	s001508433-2 F	Chr02	46,144,818	46,144,842	s001508433-2 R	Chr02	46,145,011	46,144,989	CGGGTATGTTGTTCATATGGATACT	GTTTCTTCCTCCTACGACCCTTA
Chr02	155.6	T000249764m	T000249764m_F	Chr02	46,683,655	46,683,677	T000249764m_R	Chr02	46,683,973	46,683,951	ATAAAGCCCAACAATTTGGAGAG	CATAATGCCAATCCAAAGTCCTA
Chr02	158.9	GMES2618	GMES2618_F	Chr02	47,279,826	47,279,849	GMES2618_R	Chr02	47,279,934	47,279,915	TCCTCAGTTCTGTTCTATTTTTCG	CAAATGTTGGTGGAGACACG
Chr02	159.7	C02-BARC-030511-06893	C02-BARC-030511-06893_F	Chr02	47,361,597	47,361,578	C02-BARC-030511-06893_R	Chr02	47,361,509	47,361,527	GCTACAGGTACCTAATCCAC	GACAAAGATGTAAAGTCTC
Chr02	161.3	T000250781m	T000250781m F	Chr02	47,699,747	47,699,769	T000250781m R	Chr02	47,700,010	47,699,988	GCTTCTCACCTTCGTTACACCTA	AACTGTCTTCATCTTCCCTCTCC
Chr02	161.3	GMES3942	GMES3942_F	Chr02	47,710,045	47,710,026	GMES3942_R	Chr02	47,709,757	47,709,776	CGGGTGCTGTATATGGGTTT	AGCTTCTGGGTTTTCAGCAA
Chr02	161.6	T000250903l	T000250903l_F	Chr02	47,821,550	47,821,573	T000250903l_R	Chr02	47,821,909	47,821,887	CCCTACTAGAGCTTCTTTCTGCAT	ATGGTCAAAGGATAACCAGGAAT
Chr02	162.5	T000251080s	T000251080s F	Chr02	47,999,319	47,999,341	T000251080s R	Chr02	47,999,516	47,999,494	CAACAGCTTGTTCAGAGTGTGAC	TGGCAATAGTTGATGAGTAGCAA
Chr02	162.6	T000251200l	T000251200l_F	Chr02	48,118,931	48,118,953	T000251200l_R	Chr02	48,119,278	48,119,256	TTAAGAAGAAGAAAGGACGGTGG	TTCTTCTATTGCGTTGAGAATCG
Chr02	162.9	C02-BARC-039653-07533	C02-BARC-039653-07533_F	Chr02	48,152,829	48,152,810	C02-BARC-039653-07533_R	Chr02	48,152,746	48,152,765	GATGCTGGCATTTCTCGAAG	ACGGGAAGGAAGACTACAAC
Chr02	165.6	Satg001	Satg001_F	Chr02	48,354,075	48,354,092	Satg001_R				GCACCTCGTATTCTACCT	TACGCCAAGCTTGTCCAG
Chr02	165.6	T000251579l	T000251579l F	Chr02	48,497,260	48,497,285	T000251579l R	Chr02	48,497,670	48,497,644	TTTATGTTATCTCCTTGTAAGAGTTT	TGTGATAACTACAAATCATACTTAATG
Chr03	0	GMES1173	GMES1173_F	Chr03	202,756	202,775	GMES1173_R	Chr03	202,967	202,948	TATGGGACATCAAAGCCACA	CGCACTGCCATATGAAGAGA
Chr03	0.5	Sct_195	Sct_195_F	Chr03	323,438	323,457	Sct_195_R	Chr03	323,583	323,564	CTATGCAAGGTCTAACTACA	AAACCGTCACACAGTCTCTG
Chr03	3	C03-BARC-044643-08744	C03-BARC-044643-08744_F	Chr03	459,434	459,452	C03-BARC-044643-08744_R	Chr03	459,514	459,494	CAAATTAGTCTCTCAATGC	CAAGTAGTTCTTAAAGTATTG
Chr03	3	Sat_379	Sat_379_F	Chr03	461,803	461,823	Sat_379_R	Chr03	462,042	462,020	TTTTGGCTCATCTTTCTTTTA	GCCCTAAGCACAACTGAACCTAT
Chr03	5.1	T000300555l	T000300555l_F	Chr03	553,673	553,695	T000300555l_R	Chr03	554,028	554,006	GCAATGCTTCAACTTAGGAGTTC	CGATGACGTGATACGTACCTCAC
Chr03	7.9	s029800007	s029800007_F	Chr03	745,904	745,929	s029800007_R	Chr03	746,183	746,161	CGGTCTAGTTTAGAGGTAGTTTCAGG	AGGGTGTGCCTAAAGACTGTGTA
Chr03	9.2	T000300796s	T000300796s F	Chr03	803,183	803,205	T000300796s R	Chr03	803,382	803,360	GCCATGGCACTAGTTAATGATAA	CGAGTATCGCCGTTGTTAATAGT
Chr03	10	T000300832s	T000300832s_F	Chr03	839,582	839,605	T000300832s_R	Chr03	839,749	839,727	CATCATATGAGCGCATCACTTATT	AAGATAAGGTGTAGCTTGACAAA
Chr03	10	T000300840l	T000300840l_F	Chr03	847,525	847,548	T000300840l_R	Chr03	847,862	847,841	TGATTGTTTGAAATTCTGATCATT	TGTCACAATCTGCAACTCATAAT
Chr03	12.7	T000301226l	T000301226l_F	Chr03	1,241,718	1,241,740	T000301226l_R	Chr03	1,242,059	1,242,037	GAAGCTGCATCCCTCATAAAGTA	TGACTGTGTGACGAACGAAATAC
Chr03	12.7	T000301272m	T000301272m F	Chr03	1,293,415	1,293,437	T000301272m R	Chr03	1,293,624	1,293,598	TGATATGGGATCAACATGTGTCT	TCTAGGTCAACGTCATTAGTTTGATAA
Chr03	13.8	GMES0925	GMES0925_F	Chr03	1,332,982	1,333,001	GMES0925_R	Chr03	1,333,271	1,333,252	TGCCAAACGCAACAAATAAA	TGGTTGCATTCCAAATTTCC
Chr03	16	T000301502s	T000301502s_F	Chr03	1,523,873	1,523,895	T000301502s_R	Chr03	1,524,080	1,524,059	TTTGTGAAATACAAGCGGAACTC	AGAATCACGGAACTAATCGGAA
Chr03	19	GMES6380	GMES6380 F	Chr03	1,780,800	1,780,819	GMES6380 R	scaffold 585	5,919	5,938	TCCTGAGTTCTCCACCAACC	TGAAAGGGTGATGATGACGA
Chr03	20.6	C03-BARC-042969-08483	C03-BARC-042969-08483_F	Chr03	2,009,155	2,009,174	C03-BARC-042969-08483_R	Chr03	2,009,236	2,009,217	GAGCTTGTTGTGGATGTATG	CTTAAAACTATTAGTGCTTG
Chr03	22.4	GMES3247	GMES3247_F	Chr03	2,493,838	2,493,857	GMES3247_R	Chr03	2,494,049	2,494,029	GGCGCACTCTCTATCCTCAA	CAGCATCTACCTAATCAGCCG
Chr03	23.1	C03-BARC-027728-06652	C03-BARC-027728-06652_F	Chr03	2,770,164	2,770,146	C03-BARC-027728-06652_R	Chr03	2,770,076	2,770,094	ACCAAACAGAAAGTTAGAC	CTTTGATGTGTTCCTTTAG
Chr03	23.9	T000302895l	T000302895l F	Chr03	2,923,168	2,923,188	T000302895l R	Chr03	2,923,520	2,923,498	AAACATTAGCAAGCGACCAAA	GATGATTGTGACCGTATGATGTG
Chr03	28.9	Satt152	Satt152_F	Chr03	3,366,475	3,366,493	Satt152_R	Chr03	3,366,722	3,366,698	CTATTCCTATCACAACACA	TAGGGTTGTCACTGTTTTGTTCTTA
Chr03	31.5	s026000076	s026000076_F	Chr03	3,934,182	3,934,160	s026000076_R				TTATATTTGATGCGACAATGGAA	CTAGGAGGACATGACTCGTGTTG
Chr03	32.1	C03-BARC-014709-01626	C03-BARC-014709-01626_F	Chr03	3,985,869	3,985,850	C03-BARC-014709-01626_R	Chr03	3,985,791	3,985,810	CACTGCATTTTCATATCCCC	GTACTTGAGATTTTCCTTCC
Chr03	32.8	T000304497m	T000304497m_F	Chr03	4,304,900	4,304,927	T000304497m_R	Chr03	4,305,136	4,305,114	TCATTGATGACAGTGATACTAATAGAGC	GTAAGAGCGTAGGGACCCATTAC
Chr03	37.3	T000305242m	T000305242m_F	Chr03	5,143,914	5,143,935	T000305242m_R	Chr03	5,144,202	5,144,184	GGTTACTCAAATTCGTTTACCA	AAGTATATCTCTCTTTGAGTTCGATT
Chr03	40.1	Satt530	Satt530_F	Chr03	5,669,546	5,669,525	Satt530_R	Chr03	5,669,335	5,669,354	CATGCATATTGACTTCATTATT	CCAAGCGGGTGAAGAGGTTTTT
Chr03	40.6	C03-BARC-045053-08869	C03-BARC-045053-08869 F	Chr03	6,539,973	6,539,954	C03-BARC-045053-08869 R	Chr03	6,539,894	6,539,913	ACTACTACTACCATTCTACC	AAGTGTTCCTCTCCTAGGTG
Chr03	40.9	Satt675	Satt675_F	Chr03	6,771,370	6,771,343	Satt675_R	Chr03	6,771,239	6,771,266	CTATTTCCGTCCTATTATCATTTTCGTC	TCTAACACGTATTTATTATTATTGGTCAATT
Chr03	42	s034100005	s034100005_F	Chr03	7,870,305	7,870,327	s034100005_R	Chr03	7,870,668	7,870,646	CCTAGTGATCTGGTCTTCAATGG	TGGAGGTTGGAGTAATGTTATGG

Chr03	42.2	Satt683	Satt683_F	Chr03	8,686,351	8,686,372	Satt683_R	Chr03	8,686,537	8,686,516	GGTGTGGGTCCTCAATTAAATA	GTTTTCCCTAAACTAACCTAAC
Chr03	42.8	s030300013-3	s030300013-3_F	scaffold_41	38,459	38,481	s030300013-3_R	scaffold_41	38,792	38,771	TTGGTAAAGGAGAATTGAGCGTA	GCCGAGCTCTGATACCAACTAA
Chr03	42.8	s030300013-2	s030300013-2_F	scaffold_41	38,459	38,481	s030300013-2_R	scaffold_41	38,792	38,771	TTGGTAAAGGAGAATTGAGCGTA	GCCGAGCTCTGATACCAACTAA
Chr03	42.8	s030300002-2	s030300002-2_F	scaffold_41	27,128	27,150	s030300002-2_R	scaffold_41	27,237	27,216	TCCACACCAACATACTTGAATTT	TGTTCCACATTAATTTCCTCCC
Chr03	44.4	GMES3814	GMES3814_F	Chr03	17,786,064	17,786,083	GMES3814_R	Chr03	17,786,257	17,786,238	CAGCAAGCCTTCCGATAAAC	CAACAAAATCCCAAGGGAAA
Chr03	48.2	GMES0610	GMES0610_F	Chr03	26,332,301	26,332,320	GMES0610_R	Chr03	26,332,441	26,332,421	GGGTGATGATGGAGGAGAGA	TCGTCATTCTTCTTCCCAATG
Chr03	48.5	C03-BARC-013579-01164	C03-BARC-013579-01164_F	Chr03	28,993,375	28,993,394	C03-BARC-013579-01164_R	Chr03	28,993,467	28,993,447	GAAAAGTTCCACAACAGTGC	CACAGCTTCAATAAAACCACC
Chr03	48.5	s011400371r	s011400371r_F	Chr03	29,003,521	29,003,494	s011400371r_R	Chr03	29,003,302	29,003,326	TGAGTGATATGAATGCTACTCTCTAATG	TCTCCTATACGTACTGAAGAGACAT
Chr03	48.5	C03-BARC-022187-04294	C03-BARC-022187-04294_F	Chr03	29,582,519	29,582,500	C03-BARC-022187-04294_R	Chr03	29,582,452	29,582,471	TCTATGGTAAGGGAACATGG	GGAATATCATCTTTCTCACC
Chr03	51.2	GMES1856	GMES1856_F	Chr03	32,635,269	32,635,250	GMES1856_R	Chr03	32,634,975	32,634,994	CCCTTCCTTTTTCTGGTTCC	AGGGTAGAAATGCACCATGC
Chr03	51.7	GMES6159	GMES6159_F	Chr03	32,735,414	32,735,395	GMES6159_R	Chr03	32,735,190	32,735,209	ATAGCAGAAAACCGTGCTGC	ACCTCCAACCAAGTTCAGGA
Chr03	52.6	Sat_033	Sat_033_F	Chr03	32,838,458	32,838,479	Sat_033_R	Chr03	32,838,629	32,838,608	GCAGATATTTAATCCCCTCACC	ATCTCGGAGAGAAAGAAATCGC
Chr03	52.8	C03-BARC-015309-02277	C03-BARC-015309-02277_F	Chr03	32,938,744	32,938,763	C03-BARC-015309-02277_R	Chr03	32,938,836	32,938,817	TACCAGGCATGGCAAAAACC	TGCCAACTTTTAGGGTGTCG
Chr03	53.2	GMES1738	GMES1738_F	Chr03	32,940,416	32,940,397	GMES1738_R	Chr03	32,940,194	32,940,213	CTCAAGCAGCAACAACCAAA	ATATCGGGATGTCGTCTTCG
Chr03	54.4	Satt080	Satt080_F	Chr03	33,419,564	33,419,543	Satt080_R	Chr03	33,419,412	33,419,433	CCATAAAATAATAAAGGTCAAT	TAATCAGTGGAAAAAAAGTTAT
Chr03	57.7	T000335805s	T000335805s_F	Chr03	33,775,202	33,775,226	T000335805s_R	Chr03	33,775,377	33,775,355	GAAATCAAGTTAAACACAATTCTCG	TAGAGATGAGGGAAAGGGTTAGC
Chr03	58.2	Sat_266	Sat_266_F	Chr03	34,017,521	34,017,544	Sat_266_R	Chr03	34,017,735	34,017,711	CTCCCACTAAAGAAATATTTTGGA	GCCATTTGTTTCAAACTTTGAGGTA
Chr03	60	Satt137-2_re	Satt137-2_re_F	scaffold_109	26,782	26,765	Satt137-2_re_R	Chr03	35,138,246	35,138,224	GGCCACAATGCACCTCTCTT	ATCATTGGAATGGATTATCAAGC
Chr03	61.8	T000336255m	T000336255m_F	Chr03	34,232,614	34,232,636	T000336255m_R	Chr03	34,232,884	34,232,862	TTCCTTCTATCCTCGGTAAGGTC	TTCAGTCAGTCACTTCAGTCGAA
Chr03	64	T000336692m	T000336692m_F	Chr03	34,669,980	34,670,002	T000336692m_R	Chr03	34,670,301	34,670,279	GGTTCCCGGTAGCTTAGAAGTAA	CTTGTTGATTCGGTGGTAGACTC
Chr03	64.5	T000337093s	T000337093s_F				T000337093s_R				CCAAGCTGCAATGAGAGAAA	CCAGGAAACTGGATTATGATTCT
Chr03	65.6	T000337264l	T000337264l_F	Chr03	35,237,108	35,237,130	T000337264l_R	Chr03	35,237,587	35,237,565	TTTGTCACCTACCTAACAAGCTG	GATCGTGATACTAATTGTGACAT
Chr03	68.9	Sat_236	Sat_236_F	Chr03	35,596,280	35,596,256	Sat_236_R	Chr03	35,596,063	35,596,090	GGTGCCTATGGTTCTACGTAGTTAC	TTTGGATTAGATCAATAAAAATCACATT
Chr03	71.4	C03-BARC-021465-04110	C03-BARC-021465-04110_F	Chr03	35,802,084	35,802,065	C03-BARC-021465-04110_R	Chr03	35,801,985	35,802,004	AGGGATACATTGAGGCACAC	CCCCTGTGGTGAAGGTATTT
Chr03	72.7	T000338004l	T000338004l_F	Chr03	35,977,425	35,977,447	T000338004l_R	Chr03	35,977,766	35,977,744	CAAGGTGCATACATACGACAAAG	ATGTTGTTAATGTGCTTCCATCC
Chr03	73	C03-BARC-013321-00482	C03-BARC-013321-00482_F	Chr03	35,991,083	35,991,064	C03-BARC-013321-00482_R	Chr03	35,990,996	35,991,015	ATTGGCACCAAAACTTGCGG	TGATCATCATGCCATGGGAC
Chr03	74.2	T000338134l	T000338134l_F	Chr03	36,107,444	36,107,466	T000338134l_R	Chr03	36,107,796	36,107,774	CCTTTGCTCAGTCCATGATTAAC	TCACTTTATGCAAGGAAGGAAAC
Chr03	75.6	C03-BARC-040277-07706	C03-BARC-040277-07706_F	Chr03	36,369,321	36,369,302	C03-BARC-040277-07706_R	Chr03	36,369,247	36,369,266	GAAGACCGAGATTGGATCTG	AAGGCAACCAACTACATACG
Chr03	75.9	GMES1399	GMES1399_F				GMES1399_R	Chr03	36,399,367	36,399,349	TTCTTGCCAAACAATGACCA	GGGATACAAAAGTGGGGGAG
Chr03	76.7	GMES4060	GMES4060_F	Chr03	36,456,701	36,456,720	GMES4060_R	Chr03	36,456,824	36,456,805	CATTACAAGCTCGACGCAAA	ACACCAGCCAGTGGAAAAAC
Chr03	76.7	GMES2817	GMES2817_F	Chr03	36,492,205	36,492,226	GMES2817_R	Chr03	36,492,435	36,492,416	TCCTATTCCACCTCACATTCCT	GCAACTGTGGAATGGAACCT
Chr03	81	T000338936m	T000338936m_F	Chr03	36,918,272	36,918,294	T000338936m_R	Chr03	36,918,605	36,918,580	CATTTGGTGTGGATGATTACTGA	AAATTACTTTATACACCACGATCTTT
Chr03	86.9	Satt549	Satt549_F	Chr03	37,343,230	37,343,209	Satt549_R	Chr03	37,342,993	37,343,011	GCAAAACTTTGGAGTATTGCAA	CGCAACAATCACTAGTACG
Chr03	89.1	C03-BARC-042245-08221	C03-BARC-042245-08221_F	Chr03	37,461,164	37,461,183	C03-BARC-042245-08221_R	Chr03	37,461,257	37,461,238	TAGGCACAACTGCTTTGTAG	AGTGGTGTGTTCAAATTCTG
Chr03	92.1	GMES1100	GMES1100_F	Chr03	37,940,052	37,940,071	GMES1100_R	Chr03	37,940,205	37,940,186	ATAAGCGTTCCATGGTGGAG	ATGCTTTCACTTGTGAGCCA
Chr03	94.8	T000340442s	T000340442s_F	Chr03	38,427,655	38,427,680	T000340442s_R	Chr03	38,427,858	38,427,836	TTGAAATGACTATACTGAGTGCTTCC	ATTAAGTGGAACCAAGTGACCAA
Chr03	98.5	C03-BARC-020101-04446	C03-BARC-020101-04446_F	Chr03	39,135,423	39,135,442	C03-BARC-020101-04446_R	Chr03	39,135,504	39,135,485	ATAAAACACGGCAGGAGCAC	CTCCTCCTTCCACGTTTTTC
Chr03	98.5	T000341165l	T000341165l_F	Chr03	39,152,857	39,152,879	T000341165l_R	Chr03	39,153,231	39,153,206	AGGCAAAGTTAAGAATTGGATCG	TTTCAGAATTAGTGTGCTAAGAGTTT
Chr03	101.8	GMES4212	GMES4212_F	Chr03	39,647,601	39,647,582	GMES4212_R	Chr03	39,647,404	39,647,423	CATTGAAATTCCCGCAGACT	TTGTTCTGCGATTCGATGAG
Chr03	102.5	GMES4109	GMES4109_F	Chr03	39,958,172	39,958,191	GMES4109_R	Chr03	39,958,424	39,958,405	CAGCCGTGCTCTCTCTCTCT	GGGGAAACGAAGTTGACGTA
Chr03	104.4	Satt234	Satt234_F	Chr03	40,168,795	40,168,812	Satt234_R	Chr03	40,169,007	40,168,991	TGAGAGCAGGACATTTTT	TCTGCGAGTGTTTTCTG
Chr03	107.8	T000342500m	T000342500m_F	Chr03	40,488,152	40,488,169	T000342500m_R	Chr03	40,488,366	40,488,344	AAATGGTATTACGCGTGCATTT	CTGCGTAAATTGCTCGTACTAAA
Chr03	111.1	s006300677	s006300677_F	Chr03	40,898,557	40,898,536	s006300677_R	Chr03	40,898,448	40,898,469	CATGACAACGCTGTCTTTGAAC	CAAGCTCCATATTAGAGGCCAA
Chr03	112.2	s006300367	s006300367_F	Chr03	41,209,104	41,209,082	s006300367_R	Chr03	41,208,718	41,208,740	TTCAAGCCACATTTATCAGTGAA	AAGCTCCAATCATGTGCTGTACT
Chr03	114.4	s006300056	s006300056_F	Chr03	41,520,078	41,520,055	s006300056_R	Chr03	41,519,929	41,519,952	AATCTTTATTAAATGCGTGACTTT	TTAAAGATGAAACTTTAGGTTTGT
Chr03	116.8	T000343683s	T000343683s_F	Chr03	41,679,812	41,679,834	T000343683s_R	Chr03	41,679,982	41,679,960	AGTCGAAATCCTATGTTGGACCT	GGCCCATCAATATTACATTTCAG
Chr03	118.7	T000343872m	T000343872m_F	Chr03	41,868,325	41,868,349	T000343872m_R	Chr03	41,868,623	41,868,598	TCACATCATTTATTGTTGACGATTT	TGTTATAGTGATAATTACATGTCCTG
Chr03	120	GMES4701	GMES4701_F	Chr03	42,091,500	42,091,519	GMES4701_R	Chr03	42,091,741	42,091,722	GCCACGATACAAACAAAGCA	ACATCGATCAGGAAGGCATC
Chr03	121.7	GMES0685	GMES0685_F	Chr03	42,409,601	42,409,582	GMES0685_R	Chr03	42,409,163	42,409,185	ATCTCAGAAGCAGCAGGAGC	CAACATCGTAAGGAACATTAGGC
Chr03	123.3	Satt022	Satt022_F	Chr03	42,676,603	42,676,582	Satt022_R	Chr03	42,676,404	42,676,427	GGGGGATCTGATTGTATTTTACCT	CGGGTTTCAAAAAACCATCCTTAC
Chr03	124.2	Sat_125-2	Sat_125-2_F	Chr03	42,764,964	42,764,945	Sat_125-2_R	Chr03	42,764,829	42,764,844	TTCTTTGGGCTTTGACTTGG	TGGTCCAAAATCAACTACCG
Chr03	127.9	GMES2723	GMES2723_F	Chr03	43,332,523	43,332,504	GMES2723_R	Chr03	43,332,227	43,332,246	CAGCCCAATGCACTTCACTA	CGCAGCCTCAGATCTCTACC
Chr03	128.2	C03-BARC-018125-02530	C03-BARC-018125-02530_F	Chr03	43,513,304	43,513,323	C03-BARC-018125-02530_R	Chr03	43,513,387	43,513,368	ACTACTCCCACCAACTACAC	TCCCCACAATTTCGGGTATC
Chr03	131.6	GMES0491	GMES0491_F	Chr03	44,247,260	44,247,241	GMES0491_R	Chr03	44,247,100	44,247,125	GTCATCCCAAGAAACCTGGA	AAAGGTAAGAAAAACATAGGGAAAAA
Chr03	131.7	GMES1187	GMES1187_F	Chr03	44,250,944	44,250,925	GMES1187_R	Chr03	44,250,749	44,250,768	CGCGTCGAACAGAGATCATA	TGCCATCAATTCCTTCAACA
Chr03	132.3	GMES2806	GMES2806_F	Chr03	44,282,054	44,282,035	GMES2806_R	Chr03	44,281,784	44,281,803	GTTTCAGCCAACCCAACACT	AGCTTGATTTTGCGCTTGTT
Chr03	134.7	GMES1265	GMES1265_F	Chr03	44,521,958	44,521,977	GMES1265_R	Chr03	44,522,056	44,522,037	AAGTGGGAACACACGGAAAG	AAACAAAGCTAGGCCTGCAA
Chr03	135.5	s004200019	s004200019_F	Chr03	44,648,275	44,648,253	s004200019_R				TGTGATCACTTTGTAGCTTTCCA	AAAGGCCTAGGTGCTCTAGTTG
Chr03	135.7	T000346856l	T000346856l_F				T000346856l_R	Chr03	44,855,211	44,855,193	AAATAGAGGGATGGATGGAGAGT	AAAGGGAGAGGGCTAATTT
Chr03	139.8	T000347318m	T000347318m_F	Chr03	45,315,628	45,315,648	T000347318m_R	Chr03	45,315,940	45,315,916	TTGAAACTAAAGCCTATGAAGGG	TGCTTGACAAATCTATTTGAGAGTG
Chr03	140.5	s004106980-2.1	s004106980-2_F	Chr03	45,743,401	45,743,378	s004106980-2_R	Chr03	45,743,243	45,743,264	TCTTTGAAGAAGATAAATCAACATGG	TTGAACGGTTTAACAAGCTGTAAC
Chr03	141.8	T000347670l	T000347670l_F	Chr03	45,668,267	45,668,289	T000347670l_R	Chr03	45,668,611	45,668,589	TTTCTCTCTAACACTGCTCAAAT	AGATTGCTCTACTGCATCATTGG
Chr04	0	GMES0624	GMES0624_F	Chr04	128,234	128,253	GMES0624_R	Chr04	128,535	128,516	GATCTCAAGGCCCAGTCAAA	CAGATGCACAAATCGGAGAC
Chr04	0.8	GMES0489	GMES0489_F	Chr04	317,800	317,781	GMES0489_R	Chr04	317,439	317,458	TGGATCTCCTCCTTTCCCTT	AGCTCGGCAGGAGTTAACAA
Chr04	1.1	C04-BARC-031911-07224	C04-BARC-031911-07224_F	Chr04	443,249	443,230	C04-BARC-031911-07224_R	Chr04	443,176	443,195	CCTCCCTCTCATTCATAGAC	GCAAAAACGCTAGAAAACGC
Chr04	1.1	Satt565	Satt565_F	Chr04	549,826	549,848	Satt565_R	Chr04	549,981	549,959	CCCGGAACTTGTAATAACCTAAT	CTCTCTTATGATGTTCATAATAA
Chr04	2.7	GMES0858	GMES0858_F	Chr04	1,109,047	1,109,066	GMES0858_R	Chr04	1,109,261	1,109,242	GTGCTAAATTCATGGCCACC	CGAGAACCACCGAGAGTAGC
Chr04	3	C04-BARC-031853-07222	C04-BARC-031853-07222_F	Chr04	1,202,354	1,202,336	C04-BARC-031853-07222_R	Chr04	1,202,262	1,202,280	CCTCTCATAATATTAGGAC	GTATCTTAAGAGTTAAGAC
Chr04	4.3	s023700293	s023700293_F	Chr04	1,595,581	1,595,559	s023700293_R	Chr04	1,595,290	1,595,312	AAATGTGCGTTTATTGAGATGCT	CTGCAAGTTATTTCAGTGCTTCC
Chr04	5.4	C04-BARC-016959-02166	C04-BARC-016959-02166_F	Chr04	1,757,966	1,757,947	C04-BARC-016959-02166_R	Chr04	1,757,886	1,757,905	GGAGAGTACGCTGTTTCATC	AAACTTCACCGGCAAAGCAG
Chr04	5.9	C04-BARC-025861-05129	C04-BARC-025861-05129_F	Chr04	1,947,795	1,947,775	C04-BARC-025861-05129_R	Chr04	1,947,707	1,947,726	CATCAAGTTCCCAATTAGTTC	AGTTTACGCATGGTGTGCTC
Chr04	6.7	T000402078s	T000402078s_F	Chr04	2,133,501	2,133,524	T000402078s_R	Chr04	2,133,699	2,133,677	TTGACTGTTACTTAAAGTTTCCAA	ATACGAGTAAGGCTAGGCAGGTT
Chr04	8.9	C04-BARC-019133-03313	C04-BARC-019133-03313_F	Chr04	2,753,256	2,753,237	C04-BARC-019133-03313_R	Chr04	2,753,157	2,753,176	CATGACAATCCTCGTACAGC	CGACGCAATAGCCTTTTTGG
Chr04	9.2	Satt396	Satt396_F	Chr04	2,776,344	2,776,364	Satt396_R	Chr04	2,776,520	2,776,503	AAAAGGGATAAGTTTAAAAAT	GGCCTGTAAAGGGATTCC
Chr04	11.4	GMES0757	GMES0757_F	Chr04	3,282,281	3,282,262	GMES0757_R	Chr04	3,282,037	3,282,056	TCCTCTCAACACCTTTGCCT	TCGCTCTTCCTCGTAATCGT
Chr04	12.4	C04-BARC-015529-01991	C04-BARC-015529-01991_F	Chr04	3,425,064	3,425,045	C04-BARC-015529-01991_R	Chr04	3,424,971	3,424,990	TTGTCCGTTACCCACATCAC	AAATGGTGACTGGAAGGAGC
Chr04	13.8	T000403565l	T000403565l_F	Chr04	3,618,980	3,619,004	T000403565l_R	Chr04	3,619,359	3,619,337	TGTTTAGAATAATACACTTCAGGGC	ATACATATACATGATTGGCGGCT

Chr04	15.7	s034200001	s034200001_F	Chr04	3,926,981	3,926,959	s034200001_R				CAAGGCAGAACTACCTTATTGCT	ATGCCAGAATGCCCAACTT
Chr04	17	GMES6334	GMES6334_F	Chr04	4,168,350	4,168,331	GMES6334_R	Chr04	4,168,121	4,168,140	TCAAGATGAAGGGGATTTCG	CGGTGTTGCAGAGGTAGACA
Chr04	18.3	C04-BARC-044273-08655	C04-BARC-044273-08655_F	Chr04	4,217,220	4,217,239	C04-BARC-044273-08655_R	Chr04	4,217,312	4,217,293	TTCAATGGGGTGTGATCGAC	TACAACCTCCCTCAACACTG
Chr04	18.5	Sat_337	Sat_337_F	Chr04	4,221,001	4,220,975	Sat_337_R	Chr04	4,220,742	4,220,769	CATGTTTTACAAATTTTGAAGCCTTAG	ATCAATCCATTTATGAGGTTAGTTTCTT
Chr04	18.6	T000404245l	T000404245l_F	Chr04	4,292,435	4,292,455	T000404245l_R	Chr04	4,292,814	4,292,792	ACGTGCTGCACTTTATTCCAA	TTTGTTTGGATATTTGTATCTGA
Chr04	22.5	T000404556l	T000404556l_F	Chr04	4,603,704	4,603,726	T000404556l_R	Chr04	4,604,120	4,604,098	AACAAGTTCAAAGGCAGTGCATA	CGTCTTCCATTATGGGTAAGTCA
Chr04	23	T000404649l	T000404649l_F	Chr04	4,701,565	4,701,588	T000404649l_R	Chr04	4,701,920	4,701,898	AAATTGTGCTCAACTTAAACACCT	AATTACTCCGAATGAACCCTTTC
Chr04	23	T000404663l	T000404663l_F	Chr04	4,715,490	4,715,513	T000404663l_R	Chr04	4,715,870	4,715,848	AACGTTGGTCCTACTATTCAAGTT	TTCTATATTGCTTCCACTGATTT
Chr04	26.9	s009300334-2	s009300334-2_F	Chr04	4,874,616	4,874,594	s009300334-2_R	Chr04	4,874,456	4,874,478	AATTTATGCAATGTTGGAGCACT	TGTCTGAGTTCCTCTTTACTGGG
Chr04	31.3	Sat_140	Sat_140_F	Chr04	5,285,911	5,285,888	Sat_140_R	Chr04	5,285,713	5,285,736	CCATGAAATTATTTGGCAAGTATT	GTTGAAGAATGGAAACTAAAAATG
Chr04	33.8	s019500613-2	s019500613-2_F	Chr04	5,615,379	5,615,359	s019500613-2_R	Chr04	5,615,013	5,615,035	CCGGTCAACCAATTTACCATT	CCACAGAACCAGGCACATTAGTA
Chr04	36.2	s019500336-2	s019500336-2_F	Chr04	5,892,249	5,892,227	s019500336-2_R	Chr04	5,892,064	5,892,086	ATACGAGCTCCAATGTTAAACGA	AGGTAATTAAATCCCTCCGACAG
Chr04	38.9	T000406042s	T000406042s_F	Chr04	6,106,115	6,106,137	T000406042s_R	Chr04	6,106,282	6,106,260	TTTCTAATCATGTCGAGCACTGT	AAATGTCAAGTATCTTCCCATAA
Chr04	41.9	T000406355l	T000406355l_F	Chr04	6,428,363	6,428,385	T000406355l_R	Chr04	6,428,714	6,428,692	GAGACGGAGAAGAAATTCTGGAT	AGTATTGTTCTCAACCAGCATGA
Chr04	44	C04-BARC-035457-07203	C04-BARC-035457-07203_F	Chr04	6,628,637	6,628,618	C04-BARC-035457-07203_R	Chr04	6,628,552	6,628,571	TGTCTAGCGATTAGTGCAGG	GCTGCTTCTAAATTCTAATC
Chr04	44.3	s025600001	s025600001_F				s025600001_R	Chr04	6,675,468	6,675,489	TTTCTTATTCATATTCTGTATGGGTC	AATTGCTGCAAAGCTCCTTTAG
Chr04	44.9	138ct25	138ct25_F	Chr04	6,687,210	6,687,193	138ct25_R				TAAGAGGGTCTTATCCAC	CTCGGTATTGACCATATC
Chr04	45.9	C04-BARC-025825-05110	C04-BARC-025825-05110_F	Chr04	6,757,416	6,757,398	C04-BARC-025825-05110_R	Chr04	6,757,321	6,757,340	CCTCTCACCTTTTCATATA	CCCACCTCAGGTGAGTTTTA
Chr04	48.4	T000406924s	T000406924s_F	Chr04	6,998,768	6,998,790	T000406924s_R	Chr04	6,998,927	6,998,905	AGTGGCCAATACTCCTCAATATG	CAGTTCATCGCTATTACAGCAAC
Chr04	52.8	GMES6071	GMES6071_F	Chr04	7,532,473	7,532,454	GMES6071_R	Chr04	7,532,366	7,532,385	CTCCCCTTAGACAACACCGA	ATACTCTCTCGCCTCACCGA
Chr04	56.9	GMES2745	GMES2745_F	Chr04	8,147,631	8,147,614	GMES2745_R	Chr04	8,147,426	8,147,445	GCGGAGGGCAACATACAC	GTGACAGACAGCGTTGGAGA
Chr04	57.5	C04-BARC-040731-07827	C04-BARC-040731-07827_F	Chr04	8,630,647	8,630,666	C04-BARC-040731-07827_R	Chr04	8,630,724	8,630,706	GACTTAGGAGTGGACTCTAC	TAGCGCAAAAGAACAAAAG
Chr04	59.6	T000409029l	T000409029l_F	Chr04	9,103,112	9,103,138	T000409029l_R	Chr04	9,103,503	9,103,477	GGATAGATATTAATGTTGTATTGAACT	TGTAGAAATTGTGTTTATTTACCCTTT
Chr04	61.5	T000409190s	T000409190s_F	Chr04	9,264,431	9,264,452	T000409190s_R	Chr04	9,264,632	9,264,610	GACAACCAAATGCCCAAATATC	CCAATTCCTTTAGGTGCTTGTAA
Chr04	64.5	T000409896s	T000409896s_F	Chr04	9,966,286	9,966,308	T000409896s_R	Chr04	9,966,506	9,966,484	CACAAAGCATTACCTGTCTCAAA	TACATATAGGCTGCACAACGAAA
Chr04	64.5	T000410781s	T000410781s_F	Chr04	10,956,350	10,956,372	T000410781s_R	Chr04	10,956,553	10,956,528	CTTCTTCCAACATCAATCTCTCC	CACAGTAAATTTATTATTCGTGATGA
Chr04	65.3	T000411607s	T000411607s_F	Chr04	12,654,313	12,654,337	T000411607s_R	Chr04	12,654,480	12,654,455	CCTTGTTTAAGGACTACATACCTTT	AAACTTCATCTAAAGTGTTATACGGA
Chr04	65.3	T000411967m	T000411967m_F	Chr04	12,993,192	12,993,215	T000411967m_R	Chr04	12,993,529	12,993,507	GAGAAATTATACAAATTCCTCCTT	GAGAGGTGAGAGATTAGTTTGGG
Chr04	65.3	T000413356s	T000413356s_F	Chr04	14,375,738	14,375,760	T000413356s_R	Chr04	14,375,844	14,375,822	TCCTTCAAAGGCCTAGAAATAGT	GCTAACTCATGATGGCTAAGTGG
Chr04	65.3	T000414734m	T000414734m_F	Chr04	15,759,846	15,759,868	T000414734m_R				CACTGCACACAGATACACCATCT	TTATCATGAACCCTCATGAATCC
Chr04	65.9	Satt190	Satt190_F	Chr04	16,737,067	16,737,048	Satt190_R	Chr04	16,736,887	16,736,905	GGGAGTGTGAACTTACATTGTCT	GGGCCTTGAATTTTGTGCTAT
Chr04	66.9	GMES6375	GMES6375_F	Chr04	19,192,278	19,192,292	GMES6375_R	Chr04	19,192,371	19,192,352	ACCAGCAGCGATAAGCAAAA	CCAATCGTCCCACACTTCTT
Chr04	67.2	GMES0002	GMES0002_F	Chr04	21,671,915	21,671,896	GMES0002_R	Chr04	21,671,643	21,671,662	TAGGTGACCATGGAGCATCA	CCCCGAAAGAAAGACAGAAA
Chr04	67.2	T000430002s	T000430002s_F	Chr04	24,469,636	24,469,614	T000430002s_R	Chr04	24,469,449	24,469,471	ACCCTAAGAACTCGTGACTTTCC	TGCGTAGAAGCTCACTACTCAAA
Chr04	68.8	T000428065s	T000428065s_F	Chr04	36,523,465	36,523,488	T000428065s_R	Chr04	36,523,641	36,523,619	TGATTTAAATACATTCCACTCACA	TGCTTTAGATGTGAACAAGAACA
Chr04	68.8	T000426917s	T000426917s_F	Chr04	35,399,280	35,399,302	T000426917s_R	Chr04	35,399,484	35,399,462	CGCCTTGTCATTAGATATCACCA	TCATGTATTCGGTTAAGTTTGGG
Chr04	68.8	Sat_357	Sat_357_F	Chr04	33,967,556	33,967,536	Sat_357_R	Chr04	33,967,283	33,967,303	AGGGTTTAAGGTGTAGGTTGT	CACCGCTTTTGTTTCTTTTTG
Chr04	70.4	GMES0628	GMES0628_F	Chr04	42,387,308	42,387,289	GMES0628_R	Chr04	42,387,131	42,387,150	TGTGTGCCCCTGCTACAATA	GTAGGTGCTGCCCAAAACAT
Chr04	70.4	GMES0782	GMES0782_F	Chr04	42,387,131	42,387,150	GMES0782_R	Chr04	42,387,308	42,387,289	GTAGGTGCTGCCCAAAACAT	TGTGTGCCCCTGCTACAATA
Chr04	71.2	Satt294	Satt294_F	Chr04	43,302,112	43,302,132	Satt294_R	Chr04	43,302,362	43,302,340	GGTCAAATGCAAATTATTTTT	CTCAGTGTGAAAGTTGTTTCTAT
Chr04	73.4	Sat_042	Sat_042_F	Chr04	44,367,916	44,367,890	Sat_042_R	Chr04	44,367,680	44,367,706	CCACGTATTAGGGAATGATATGAAATT	AACGGATACAAGTAAACTTGAATTTTA
Chr04	74.9	T000441843l	T000441843l_F	Chr04	44,986,140	44,986,162	T000441843l_R	Chr04	44,986,497	44,986,479	GAAACATAACATTTCCCATCCAA	CAGAGGCTCGATAGTGTAACTGG
Chr04	79.4	GMES0664	GMES0664_F	Chr04	45,660,600	45,660,619	GMES0664_R	Chr04	45,660,842	45,660,823	GAAATGACAATAATGCCGGG	CCCTACCTCCCTCCCTTGTA
Chr04	82.6	T000442866m	T000442866m_F	Chr04	46,007,013	46,007,035	T000442866m_R	Chr04	46,007,350	46,007,328	ACACCCGTCCTATACTCGTACCT	TCTTGTTCCTGTTCTCACTCTCC
Chr04	83.5	T000442938s	T000442938s_F	Chr04	46,079,125	46,079,147	T000442938s_R	Chr04	46,079,299	46,079,277	AGGCTAAATTTGGAGCCAATAAG	AACACCGCTTAGATAGCTTCTCC
Chr04	89.1	s004700076-2	s004700076-2_F	Chr04	46,689,369	46,689,347	s004700076-2_R	Chr04	46,689,178	46,689,200	AAATCGGTCCTGATTCTAAAGGT	CTCCATGGTATGAATTCTTGAGG
Chr04	92.2	GMES1044	GMES1044_F	Chr04	46,930,327	46,930,346	GMES1044_R	Chr04	46,930,805	46,930,786	GGAGAATAGCACCAATGGGA	ATTTGCAATCGGTGACAACA
Chr04	93	GMES1013	GMES1013_F	Chr04	47,000,018	47,000,033	GMES1013_R	Chr04	47,000,340	47,000,321	TTTGTCCGATATCCTCAGGC	CCACATGCCCCTAATTTCTG
Chr04	93.3	Sat_235	Sat_235_F	scaffold_21	3,141,999	3,141,985	Sat_235_R	Chr04	47,074,634	47,074,655	TTGGGATGGGTGTAAAACATT	GAAGGCAAGTCAAGTTGATGAG
Chr04	93.3	GMES0708	GMES0708_F	Chr04	47,085,344	47,085,325	GMES0708_R	Chr04	47,084,885	47,084,904	CCTTCAGACAAGGGACGAAA	CCAAAGCATTGCACTGAAGA
Chr04	93.3	C04-BARC-040387-07722	C04-BARC-040387-07722_F	Chr04	47,156,953	47,156,972	C04-BARC-040387-07722_R	Chr04	47,157,046	47,157,027	CCTCAACGTCATTCAGATTC	TCCTAAGCTATTAGTGCAAG
Chr04	93.8	Sct_191	Sct_191_F	Chr04	47,305,560	47,305,578	Sct_191_R	Chr04	47,305,683	47,305,663	TGAAATGCTTGAGAAGTAA	GCGCAGTTGAAACTATAACAC
Chr04	94.8	s006504377-2	s006504377-2_F	Chr04	47,391,437	47,391,414	s006504377-2_R	Chr04	47,391,288	47,391,313	GCCTAATCTGAGCTAGGTAGGAAA	AAGATCTTGATGAGAAATTGTTTGAA
Chr04	97.9	s006504009-2	s006504009-2_F	Chr04	47,764,166	47,764,146	s006504009-2_R	Chr04	47,763,976	47,763,998	AAATCTGTTGTCACACTTGGCTT	TCTGATTCTCTCGTTCCTTTCAA
Chr04	99.5	T000444782l	T000444782l_F	Chr04	47,907,583	47,907,605	T000444782l_R	Chr04	47,907,913	47,907,891	TGAAGGGAACAATGATTATGTCA	TATTATGACGATAGTCGCAGGGT
Chr04	100	T000444806l	T000444806l_F	Chr04	47,931,636	47,931,658	T000444806l_R	Chr04	47,931,991	47,931,969	GATCAGGTTAATCGTTTGACAAT	CAAATCTCCAATTGTTGATCCTT
Chr04	102.8	s006503597	s006503597_F	Chr04	48,176,564	48,176,542	s006503597_R	Chr04	48,176,228	48,176,250	AACGCTGGTAAAGGACTAAAGGT	GCAACACTATATTGTGCAGACCA
Chr04	103.9	s006503310-2	s006503310-2_F	Chr04	48,463,527	48,463,505	s006503310-2_R	Chr04	48,463,418	48,463,440	TTTCTTACCTTCAACTTTCCTTT	CATTTAGGCATGAGCAGACAGAC
Chr04	107.8	T000445584s	T000445584s_F	Chr04	48,709,831	48,709,855	T000445584s_R	Chr04	48,710,023	48,710,001	CCTTTATACCTTCAAGTCTCGATCA	ATGTTGCAGTTGTGGGAGTTAAA
Chr04	110.8	T000445723l	T000445723l_F	Chr04	48,848,283	48,848,305	T000445723l_R	Chr04	48,848,638	48,848,615	ATAGAGCATGTGGATTTGGAAGA	TCAATAACCTTCATATATACCCGA
Chr04	115	s006502610-2	s006502610-2_F	Chr04	49,162,849	49,162,827	s006502610-2_R	Chr04	49,162,690	49,162,713	TCATCTCATCCAATGCGTCTAAT	AAACCTTCTTTCATTGATACTGTT
Chr04	116.4	GMES1325	GMES1325_F	Chr04	49,580,658	49,580,639	GMES1325_R	Chr04	49,580,408	49,580,427	TGGAGATGGCATGGATATGA	AAAGCCTACTCAAATCCCCA
Chr04	117	GMES2627	GMES2627_F	Chr04	49,739,446	49,739,465	GMES2627_R	Chr04	49,739,685	49,739,666	GAAGAATACACCAACCGCGT	GCTGGTCTTGCTGTTGTTGA
Chr04	119.5	GMES1807	GMES1807_F	Chr04	50,333,224	50,333,205	GMES1807_R	Chr04	50,332,871	50,332,890	GTGCACCCTTCCACATTCTT	TTATTGACCATGTCCTCGCA
Chr04	121.6	Satt180	Satt180_F	Chr04	50,427,794	50,427,781	Satt180_R	Chr04	50,427,582	50,427,599	TCGCGTTTGTCAGC	TTGATTGAAACCCAACTA
Chr04	125.6	Satt164	Satt164_F	Chr04	50,805,530	50,805,508	Satt164_R	Chr04	50,805,300	50,805,327	CACCAATGGCTAAAGGTACATAT	AGGAGAAGAAAAAATCACATAAAATATC
Chr04	127.8	C04-BARC-028671-05985	C04-BARC-028671-05985_F	Chr04	51,249,456	51,249,475	C04-BARC-028671-05985_R	Chr04	51,249,535	51,249,516	CATCTCCGTCCAAGTCAAAC	GAACAAGGGAGAGAGCAAAG
Chr04	129.8	T000448538s	T000448538s_F	Chr04	51,665,820	51,665,842	T000448538s_R	Chr04	51,666,024	51,666,002	CGTATGACCTTATTGGAAGGGAT	ATTAATTGCTATTTGCCGAATCA
Chr04	132	C04-BARC-029125-06087	C04-BARC-029125-06087_F	Chr04	52,316,206	52,316,187	C04-BARC-029125-06087_R	Chr04	52,316,122	52,316,141	ATCTGCGGTATGCCTTTTTG	AATGAGGTACTAATCCCCCC
Chr04	132.1	s023100049	s023100049_F	Chr04	52,330,686	52,330,664	s023100049_R	Chr04	52,330,338	52,330,360	CTCAAACGCAACTTAGGGACTTA	AAATGGCCATATCAGACTCAAGA
Chr05	0	s003507308	s003507308_F	Chr05	83,109	83,086	s003507308_R	Chr05	82,968	82,990	TTGACGGAACAGAGCTACTACATT	ATTTGCTTCCGTAAATTCCTCTC
Chr05	0	GMES2497	GMES2497_F	Chr05	170,822	170,802	GMES2497_R	Chr05	170,587	170,606	TGAATTTCTTCGACACACACA	TTGCTAGCTCTTGTGGGGTT
Chr05	0.8	GMES5789	GMES5789_F	Chr05	497,775	497,756	GMES5789_R	Chr05	497,545	497,564	TGTGTTGTTGCATTGTCCCT	GCACGTCAGCTCAAATTCAA
Chr05	0.8	GMES5782	GMES5782_F	Chr05	497,775	497,756	GMES5782_R	Chr05	497,490	497,509	TGTGTTGTTGCATTGTCCCT	AGTCTGAGAAAGCAGGAGCG
Chr05	1.3	C05-BARC-029923-06753	C05-BARC-029923-06753_F	Chr05	590,280	590,299	C05-BARC-029923-06753_R	Chr05	590,367	590,348	GGAATTGAGGGCGATACAAA	GAGCAATTTCACTTAATGTC
Chr05	1.9	GMES0706	GMES0706_F	Chr05	1,043,794	1,043,775	GMES0706_R	Chr05	1,043,506	1,043,525	GTGTTTCCCTTGTGCCTGAT	GGCGCCGTAATTCACAGTAT
Chr05	3.8	GMES6481	GMES6481_F	Chr05	1,452,009	1,452,028	GMES6481_R	Chr05	1,452,208	1,452,189	AGTGCGTACCCTAGCAGGAA	ACGGAGCGAAAACAAGAAGA

Chr05	5.6	C05-BARC-028503-05925	C05-BARC-028503-05925_F	Chr05	1,607,588	1,607,569	C05-BARC-028503-05925_R	Chr05	1,607,491	1,607,511	ACTCAATCACCCCCCAAATT	CCAACGTTAGAAAAGAAAGAG
Chr05	8.1	s003505623	s003505623_F	Chr05	1,766,234	1,766,212	s003505623_R	Chr05	1,765,843	1,765,865	GAGAGTGCGATTTACTGTACGAA	GTTGTCAAGAATGGAAAGTGGTT
Chr05	9.7	s003505524-2	s003505524-2 F	Chr05	1,865,247	1,865,222	s003505524-2 R	Chr05	1,865,082	1,865,106	TTCCTTTACTAATTAGACCTTGTTGG	TTTAACAGAAGATACTGAGTCTGGG
Chr05	11.6	s003505358	s003505358_F	Chr05	2,031,595	2,031,572	s003505358_R	Chr05	2,031,214	2,031,236	GCATCAATGAGTTAAGTTGAAGCA	CCCGTATAATCAACAAATTGTGC
Chr05	13.2	GMES5019	GMES5019_F	Chr05	2,208,048	2,208,067	GMES5019_R	Chr05	2,208,153	2,208,134	AACCAAACAACGCCTACTCG	CAACGAGGGAGTGGAACATT
Chr05	14	C05-BARC-040651-07807	C05-BARC-040651-07807_F	Chr05	2,295,665	2,295,684	C05-BARC-040651-07807_R	Chr05	2,295,755	2,295,736	TCATAGAGGAAAGGGTGGTG	ATGCAGTCACCACTGTACTC
Chr05	16.8	Sat_137	Sat_137_F	Chr05	2,670,986	2,671,006	Sat_137_R	Chr05	2,671,248	2,671,228	GATGACGCCGCAGGTTTCTCC	GGTGCGGTTCCACAGTTTTTT
Chr05	18.5	s003504305	s003504305_F	Chr05	3,121,232	3,121,210	s003504305_R	Chr05	3,121,037	3,121,063	TTGGTGGATAAAGGTCAATTGTG	TTCCTTATATGGGTTATTAAGACCACT
Chr05	21.3	s003503982	s003503982_F	Chr05	3,450,562	3,450,540	s003503982_R	Chr05	3,450,416	3,450,437	TAGCCAACCTTATCGTTTGGTTC	TTTCATTCAAATGAGTAGCTTT
Chr05	24.8	T000501873I	T000501873I F	Chr05	3,595,189	3,595,214	T000501873I R	Chr05	3,595,551	3,595,526	AAGATGACAATCTATCTTTCAGAGAC	TTGAGTTTAATGAGCTTACAATGATG
Chr05	26.4	s003503672	s003503672_F	Chr05	3,760,214	3,760,192	s003503672_R	Chr05	3,760,098	3,760,121	AAATTGTTAGACGAAACACAAGT	GCTGAACTAAGTAAATGCGTTCTC
Chr05	30.9	T000502221m	T000502221m_F	Chr05	3,942,890	3,942,913	T000502221m_R				TGAAATAAAGAAGGGAGGATAGCA	AAATTTGTACACCCTGGTGTTTG
Chr05	32.7	s003503358	s003503358_F	Chr05	4,074,306	4,074,284	s003503358_R	Chr05	4,073,963	4,073,984	TTTCAAATAAATCAATCCCTTCA	GATCATTCTGGAGATGCAAGAG
Chr05	33.9	T000502439m	T000502439m F	Chr05	4,159,635	4,159,657	T000502439m R	Chr05	4,159,954	4,159,932	AAATGGAGCCAAACACAAATAGT	TAGCAACTACTTCTTGCGGATGT
Chr05	36.9	GMES4809	GMES4809_F	Chr05	4,401,138	4,401,157	GMES4809_R	Chr05	4,401,361	4,401,342	CCTCGTCCTCGTTTTCTCAG	TCTTTGGGCTAGGCAAATTC
Chr05	38	T000502682m	T000502682m_F	Chr05	4,402,329	4,402,351	T000502682m_R	Chr05	4,402,610	4,402,589	TGCTTATCTACCTCCCATTTGTT	CCTTAAAGGGTTACATCCCTGG
Chr05	38.3	T000502707s	T000502707s_F	Chr05	4,421,597	4,421,619	T000502707s_R	Chr05	4,421,799	4,421,777	TTTGGTTCTAAATTACTCCTGCG	AAGGGTTTCATGCAGACTTAACA
Chr05	38.6	GMES4350	GMES4350_F	Chr05	4,421,619	4,421,638	GMES4350_R	Chr05	4,421,739	4,421,718	GTTGGTTTCATGGTTCGTCC	TGAAATCCATATTGGCATGTTT
Chr05	38.8	T000502751m	T000502751m_F	Chr05	4,465,473	4,465,495	T000502751m_R	Chr05	4,465,761	4,465,740	AATGTACCAAGACCGAGACGATA	ACGTGTTTCTTTGCAAGACGTG
Chr05	39.1	T000502758m	T000502758m_F	Chr05	4,472,816	4,472,838	T000502758m_R	Chr05	4,473,088	4,473,065	AGTTACTTTGTCAGTGCCGTGAA	CAATTTCTCAATCGTTGAAAGTAA
Chr05	41.7	T000502901m	T000502901m F	Chr05	4,615,301	4,615,325	T000502901m R	Chr05	4,615,633	4,615,611	GAGTAGTTATTCTGATTTGGTTGGG	AGGAAATGTGGATAGGTGTCAGA
Chr05	42	T000502939m	T000502939m_F	Chr05	4,653,714	4,653,736	T000502939m_R	Chr05	4,654,040	4,654,011	ACGATACACTAGAAGCACGGTGT	TGAAGTGAATGTGAATATTAAATCTATGTG
Chr05	43.9	T000503104I	T000503104I_F	Chr05	4,817,685	4,817,711	T000503104I_R	Chr05	4,818,080	4,818,059	TTCTTGAAATAACTTTGATCACTTCTT	ACATGTGTGCATTAGTCATCCC
Chr05	43.9	T000503147I	T000503147I_F	Chr05	4,862,853	4,862,875	T000503147I_R	Chr05	4,863,193	4,863,171	TAGTCTCACGGGCCACTATTATG	AGTGATCCAATTGACCGAAATAA
Chr05	45.8	T000503229I	T000503229I F				T000503229I R	Chr05	4,944,494	4,944,467	ACTTGTGTGAGGTGGACCTTTAG	TGAATTTATTTAATTACAAGTTGATCCG
Chr05	49.5	Satt276-2	Satt276-2_F	Chr05	5,158,611	5,158,586	Satt276-2_R	Chr05	5,158,320	5,158,345	AACAGATATTATTGACGGTAAGGACT	GAATTTAAATCTCATAATCGTCATCA
Chr05	53.5	s003501972	s003501972_F	Chr05	5,459,796	5,459,774	s003501972_R	Chr05	5,459,406	5,459,428	CCCTCTCATCCTATTCAAACCTT	GGATTTGGATGTCTCATGTTAGC
Chr05	55.1	s003501708	s003501708 F	Chr05	5,724,167	5,724,143	s003501708 R	Chr05	5,723,974	5,723,994	CCTTTAGTGAATTACTATGCCATGA	ATGCCAAAGCACAGGAAGTTT
Chr05	57.6	s003501332	s003501332_F	Chr05	6,099,952	6,099,930	s003501332_R	Chr05	6,099,755	6,099,781	TCCTATCTGTCTGCTTGATCCAT	TTGAGAATGATATTTCTTAGGAATGAA
Chr05	59.2	s003500986	s003500986_F	Chr05	6,444,769	6,444,743	s003500986_R	Chr05	6,444,582	6,444,606	GAGAGTCAAATACTAACGAATAGTCAA	AACATCGTCAATCTTACTCTTTACA
Chr05	60	s003500647	s003500647_F	Chr05	6,784,014	6,783,989	s003500647_R	Chr05	6,783,849	6,783,871	TGGGTACAATTCGTAGAATTAACATT	AACTCCAAATAATTTAAGCGCAA
Chr05	61	s003500347	s003500347 F	Chr05	7,083,709	7,083,682	s003500347 R	Chr05	7,083,510	7,083,528	TATAACATCCTAGAGTTAAAGTCATTAT	CTAACGTGGGTTCGGCAGT
Chr05	61.4	s003500045	s003500045_F	Chr05	7,385,438	7,385,416	s003500045_R	Chr05	7,385,039	7,385,061	TCCTCTGTGAATCAGGCATATTT	AATTTGAACCGCATTATTAGCAT
Chr05	61.8	T000506202s	T000506202s_F	Chr05	7,584,041	7,584,060	T000506202s_R	Chr05	7,905,212	7,905,191	TTCTAAACCAAGTAATACTGCCCA	TGACAGCTAACGCCAACACTTA
Chr05	62	T000506451I	T000506451I_F	Chr05	8,161,203	8,161,225	T000506451I_R	Chr05	8,161,551	8,161,529	ATGGGCATTACCAGGTTGTTATT	TAAAGCACTATGTGGCTATGTGG
Chr05	62.1	T000506933s	T000506933s_F	Chr05	8,645,607	8,645,631	T000506933s_R	Chr05	8,645,814	8,645,792	GCTGATAGTTTAGCTCTTTATCCCA	TTCTTCAAGTTGGTTGTTGTGTG
Chr05	62.4	T000511990m	T000511990m_F	Chr05	8,645,915	8,645,937	T000511990m_R	Chr05	8,646,133	8,646,109	ATCTAACCCGCATATTTCTCTCC	AAACAATCAGTAGAGGATCCAGATG
Chr05	62.4	T000513220m	T000513220m_F	Chr05	9,895,984	9,896,003	T000513220m_R	Chr05	9,896,247	9,896,225	TTTGCACCCTACAAATGCTA	TTCGAATTATATGCAGGTCCACT
Chr05	63	T000513898I	T000513898I F	Chr05	10,563,657	10,563,679	T000513898I R	Chr05	10,564,036	10,564,014	TCTAAGGACACTTGAATTCGTTT	AGCCTAGGTGAATGATTGTTTGA
Chr05	63.4	T000515027I	T000515027I_F	Chr05	11,795,402	11,795,380	T000515027I_R	Chr05	11,795,029	11,795,051	CGGATGGGTTGATATACCAAGTT	CATGCATCTTATTGATACCCAAA
Chr05	63.4	T000515966m	T000515966m_F	Chr05	10,853,542	10,853,520	T000515966m_R	Chr05	10,853,311	10,853,333	GGAAGACATATACCAGGCAACTG	ACGTACGCACGTAACTGAGAATA
Chr05	63.7	T000509183s	T000509183s_F	Chr05	13,746,876	13,746,857	T000509183s_R	Chr05	13,746,699	13,746,722	GTGAGCCCAGAGCATTTGAT	AAGATGATTGGTTATATGTACGTG
Chr05	63.7	T000509488I	T000509488I F	Chr05	13,452,049	13,452,029	T000509488I R	Chr05	13,451,701	13,451,723	AAACAATTTAACCTTCCCAAA	CAATTTGTCTTGATGGAAGTTGA
Chr05	63.7	T000510174I	T000510174I_F	Chr05	12,754,731	12,754,709	T000510174I_R	Chr05	12,754,363	12,754,385	AACAACCACATTAACGATCATCC	AAACCTTGCAATTGTCTTCAGAG
Chr05	64	T000510747m	T000510747m_F	Chr05	14,232,329	14,232,351	T000510747m_R	Chr05	14,232,602	14,232,580	TGACTCACAGTATGTAGGGCAAC	TTTAAATTAACATCCGTACATGA
Chr05	64.2	T000511342s	T000511342s F	Chr05	14,837,977	14,837,999	T000511342s R	Chr05	14,838,129	14,838,107	TCTTACTTCCTTTCTGTCCGTTG	TCCTTCGTGCAAACCTATTTCTA
Chr05	64.5	T000517293s	T000517293s_F	Chr05	15,796,292	15,796,314	T000517293s_R	Chr05	15,796,501	15,796,478	TGATTCAACAAACAGAATGGAGA	CATTGCCAAATCTATTGTATGCAC
Chr05	64.8	s000318623-2	s000318623-2_F	Chr05	16,381,152	16,381,126	s000318623-2_R	Chr05	16,380,953	16,380,975	CATTGAGATCATTGTATGATGTAGTTT	AGCAGTCGAGGTAGTATGAATGA
Chr05	64.8	s000317639-2	s000317639-2_F	Chr05	17,367,157	17,367,135	s000317639-2_R	Chr05	17,366,793	17,366,815	CCCAACCTCTCGAGTTAAAGAAC	CTTAGACATGCATCCCAAATGTT
Chr05	64.8	s000314909-2	s000314909-2 F	Chr05	18,438,424	18,438,403	s000314909-2 R	Chr05	18,438,277	18,438,300	TCACTGGACCGAGGTTACTCTT	ACAGATACCATAACACCTGTATTT
Chr05	64.8	s000311101-2	s000311101-2_F	Chr05	22,220,451	22,220,429	s000311101-2_R	Chr05	22,220,250	22,220,273	TCTTATATGCACCCAAACAAACA	TGGTTGGATTAGAAGTGGATTACA
Chr05	65.6	s000310179-2	s000310179-2_F	Chr05	23,135,772	23,135,744	s000310179-2_R	Chr05	23,135,323	23,135,352	ATTATCTATTTAATTACAGACCGGAAATG	AGGTTACTCGTATTAGAAAGATTACACACA
Chr05	66.6	s000309231-2	s000309231-2_F	Chr05	24,100,881	24,100,857	s000309231-2_R	Chr05	24,100,610	24,100,632	TTTGTAAGTTGATTTCTAACGGTCA	GAACCTTCTGAACACCAATGAGA
Chr05	68.5	Satt591	Satt591_F	Chr05	25,343,778	25,343,791	Satt591_R	Chr05	25,343,942	25,343,922	CGACCTTAATGATA	CCCAAAGCTTAAAATTTAATA
Chr05	69.9	s000306883-2	s000306883-2_F	Chr05	26,431,902	26,431,880	s000306883-2_R	Chr05	26,431,506	26,431,528	AGAGAAGGTCCCTCATATTCACG	GATCGACATCTTCAGTCCATTCT
Chr05	69.9	s000307246-2	s000307246-2_F	Chr05	26,076,077	26,076,055	s000307246-2_R	Chr05	26,075,884	26,075,906	AAATTGTGTCTCTTCTCATCCTT	AGTCAATCAATCACATTTACGCA
Chr05	70.9	s000306482-2	s000306482-2 F	Chr05	26,833,458	26,833,436	s000306482-2 R	Chr05	26,833,059	26,833,082	GCTTGAAAGGGATGAACACTTCT	GGCTTTGTACCACCATAAATTAAA
Chr05	72	s000305748-2	s000305748-2_F	Chr05	27,568,315	27,568,293	s000305748-2_R	Chr05	27,568,167	27,568,189	GTGCGTTAAGTTCCTCTGTTCCT	TGGATTTCAATGACTTAATACAA
Chr05	72.3	GMES0477	GMES0477_F	Chr05	27,609,449	27,609,430	GMES0477_R	Chr05	27,609,155	27,609,174	ATTCCGACCTCGAAGATTCC	CGTCTCTCGAAGAAGGGTTG
Chr05	73.6	s000305464-2	s000305464-2_F	Chr05	27,853,453	27,853,435	s000305464-2_R	Chr05	27,853,282	27,853,304	CATGCATGTAATGCACGCT	CATACGTTTGTAACATTGGCTTC
Chr05	73.6	C05-BARC-044399-08697	C05-BARC-044399-08697 F	Chr05	27,882,796	27,882,815	C05-BARC-044399-08697 R	Chr05	27,882,895	27,882,876	GGCTATCATGGTCTGTGCTA	CAGAACAAGTGAATGAAAAC
Chr05	76.1	s000305125-2	s000305125-2_F	Chr05	28,187,258	28,187,236	s000305125-2_R	Chr05	28,186,887	28,186,909	CCGTGCAGTCCGTCAGCGAGGATACATATGACTTG	TGGTCTGGTTTAGTTTAACTGGC
Chr05	78.1	T000531672I	T000531672I_F	Chr05	28,419,776	28,419,792	T000531672I_R	Chr05	28,420,189	28,420,167	ATGCTGCATTCCCATTT	AATGTTAAGAACAGCTAAAGGTT
Chr05	82	T000531787I	T000531787I F	Chr05	28,534,205	28,534,227	T000531787I R	Chr05	28,534,564	28,534,542	TTAACTCGTGACAATACAAGCGA	TTATGGATTTAAGGCTCTGTTGG
Chr05	83	s000304457-2	s000304457-2_F	Chr05	28,854,607	28,854,585	s000304457-2_R	Chr05	28,854,409	28,854,432	CCGTGCAGTCCGTCAGCATGTACACACAAGTAGCC/	TCATGTTGTATGCTAGAGGTTCAA
Chr05	85.3	Sat_356	Sat_356_F	Chr05	29,134,738	29,134,763	Sat_356_R	Chr05	29,135,003	29,134,977	CCGGAAAAATGTGAGAAATCATAAAA	TTGCATGACTATCATTCAATCAAAAAT
Chr05	89.9	Satt050	Satt050_F	Chr05	29,578,039	29,578,054	Satt050_R	Chr05	29,578,232	29,578,214	GAACGTCCCAACAATG	GGCCTTGTAAACATATAGG
Chr05	94.4	T000533388m	T000533388m F	Chr05	30,133,667	30,133,691	T000533388m R	Chr05	30,134,004	30,133,982	AAATCGATTCTTAGACCGGTTAGTT	TCTAAATCAGTGACAGGGTCAAA
Chr05	95.1	C05-BARC-031361-07062	C05-BARC-031361-07062_F	Chr05	30,427,898	30,427,879	C05-BARC-031361-07062_R	Chr05	30,427,806	30,427,825	GAAGAGTACTGGTTTGAAGC	GCTCGAGTTGTCATTAATCC
Chr05	96.2	Sat_407	Sat_407_F	Chr05	30,466,000	30,465,976	Sat_407_R	Chr05	30,465,778	30,465,805	TCAAAGAACACAACTTAAATAATAAAT	ATGAATTACATTACATATGAAAAAGATA
Chr05	98.2	s000302553-2	s000302553-2_F	Chr05	30,764,713	30,764,691	s000302553-2_R	Chr05	30,764,531	30,764,553	AATTCAGATGTAACTGCACCGTC	GGATCTGACGCTCTCAGCTATTA
Chr05	101	s000302219-2	s000302219-2_F	Chr05	31,098,780	31,098,761	s000302219-2_R	Chr05	31,098,598	31,098,624	AAAGATCCAAACCATGCACC	GGAGATAATATAACAAGATGGTCAAGC
Chr05	103.8	C05-BARC-026129-05273	C05-BARC-026129-05273_F	Chr05	31,434,225	31,434,207	C05-BARC-026129-05273_R	Chr05	31,434,146	31,434,165	CCTCGTACATAGTATAAAC	CCCTAATCTGCTAGCTAGGT
Chr05	103.8	s000301875-2	s000301875-2_F	Chr05	31,441,044	31,441,024	s000301875-2_R	Chr05	31,440,887	31,440,913	CCTTTGCAGGTTGCATCTAAA	GATGGAACTTACTTAAGATATGAGAAA
Chr05	105.4	T000534921m	T000534921m F	Chr05	31,670,346	31,670,368	T000534921m R	Chr05	31,670,571	31,670,549	AGACCATATCAAATGCTGGACAT	CACAATCTAGTTTCGGCCTACAT
Chr05	106	SOYNOD26A	SOYNOD26A_F	Chr05	31,850,633	31,850,650	SOYNOD26A_R	Chr05	31,850,746	31,850,726	GAACAAAATGCCTGAGTT	CCATTCTCAATTCTTCTAGTT
Chr05	106	T000535184s	T000535184s_F	Chr05	31,933,425	31,933,444	T000535184s_R	Chr05	31,933,624	31,933,603	GATGCCGTGAATTCCACTTT	TAGAAGTCAAATTGGCAAGGGT

Chr05	107.3	T000535489l	T000535489l_F	Chr05	32,238,382	32,238,403	T000535489l_R	Chr05	32,238,727	32,238,705	TTTAGGTGGAAGTGTGTAACCT	AGTCATAACCGTGCATAGACATC
Chr05	108.1	C05-BARC-039495-07502	C05-BARC-039495-07502_F	Chr05	32,440,194	32,440,213	C05-BARC-039495-07502_R	Chr05	32,440,271	32,440,252	TTACAGGCCATTGTTTGAAG	GACACTTGTTGCAGTGTAGG
Chr05	108.4	T000535778m	T000535778m_F	Chr05	32,514,620	32,514,642	T000535778m_R	Chr05	32,514,900	32,514,878	ATGTAAGTGGAGTGTGCCTTGAT	CTTTGGGTACCTACAGAAATTCA
Chr05	110.8	T000536122m	T000536122m_F	Chr05	32,882,825	32,882,851	T000536122m_R	Chr05	32,883,156	32,883,136	TGAGATGAGATTAAGATTGATTATTGG	CAGATTCTGATGGTTTCGGAG
Chr05	111.9	T000536198l	T000536198l_F	Chr05	32,958,946	32,958,968	T000536198l_R	Chr05	32,959,314	32,959,291	GAAAGGTCGTTTCTATAAAGGTT	TGGTTTCACTATCTAAATTGGGTC
Chr05	113.2	T000536371s	T000536371s_F	Chr05	33,132,069	33,132,091	T000536371s_R	Chr05	33,132,267	33,132,245	TTCTATCTCCTCTTGATCCTCCC	CTCACGTGAATCAATCTGTGATG
Chr05	113.2	T000536435m	T000536435m_F	Chr05	33,196,051	33,196,076	T000536435m_R	Chr05	33,196,377	33,196,355	CATTTCATTATACATGATTGTCAAGG	ATGTTACGGGAAATTTGTTCTCA
Chr05	113.2	GMES3395	GMES3395_F	Chr05	33,198,378	33,198,359	GMES3395_R	Chr05	33,198,123	33,198,146	GTCACGGTCTTTCACAGGGT	GGATTGAATCAAATGAAAATGAAA
Chr05	114.3	GMES0965	GMES0965_F	scaffold_614	6,457	6,476	GMES0965_R	scaffold_614	6,549	6,530	TGGGTTGTGGTCAAACAAGA	CAAACCAATTTGCGAAGAAA
Chr05	114.8	T000536768m	T000536768m_F	Chr05	33,535,998	33,536,021	T000536768m_R	Chr05	33,536,281	33,536,259	CCCTTGTTTGTTAACTCTCACCTT	AATGCTCATGTCAGATTTCTGCT
Chr05	115.9	T000537010m	T000537010m_F	Chr05	33,777,646	33,777,668	T000537010m_R	Chr05	33,777,941	33,777,919	AACATGTAAAGAGCTAGCCATGC	ATGATATGGCTGAAGATTGAAGG
Chr05	117.5	T000537175l	T000537175l_F	Chr05	33,943,165	33,943,187	T000537175l_R	Chr05	33,943,519	33,943,497	CTCAATCATTTCAACCTACCTGA	TTTCCATCAAACGGAGATTATTG
Chr05	120.2	T000537309s	T000537309s_F	Chr05	34,077,161	34,077,183	T000537309s_R	Chr05	34,077,353	34,077,326	ACATGTTATCGCAGGCTAACTTT	GTATTAATTGTTAACACCTTCTAATTCT
Chr05	122.3	GMES0283	GMES0283_F	Chr05	34,274,748	34,274,767	GMES0283_R	Chr05	34,275,013	34,274,994	AGGGTACGGGGGAGAGAGTA	TTGGCACTCACCGAACCTAT
Chr05	123.2	T000537775l	T000537775l_F	Chr05	34,543,374	34,543,396	T000537775l_R	Chr05	34,543,750	34,543,728	TCTCGTCTTCACCTGTGGAATTA	ATCTTTACGTATCGACACCATCG
Chr05	123.5	C05-BARC-028171-05784	C05-BARC-028171-05784_F	Chr05	34,697,265	34,697,245	C05-BARC-028171-05784_R	Chr05	34,697,166	34,697,185	CGTCACATCTATTTTCACACC	GGGAAGATAGGAATATCTTG
Chr05	124.5	T000541937l	T000541937l_F	Chr05	34,880,702	34,880,680	T000541937l_R	Chr05	34,880,347	34,880,369	CCGTGTAATATGCGGTCTTTAAT	CAGAATCACAATTCGGATTTCAA
Chr05	124.8	T000541909s	T000541909s_F	Chr05	34,908,937	34,908,915	T000541909s_R	Chr05	34,908,741	34,908,763	CCACAACCATTCATCAATTTACC	ATATATTGTGTTCAAACGGTGCC
Chr05	124.8	T000541888s	T000541888s_F				T000541888s_R	Chr05	34,929,372	34,929,393	ATTGGATAAACCGATAACCCTGT	AAAGATCGTCCGCAACATTAAA
Chr05	125.6	T000541815m	T000541815m_F	Chr05	35,002,418	35,002,396	T000541815m_R	Chr05	35,002,209	35,002,231	ATGCAATGTGCATAGAAGAGTGT	ATGTTACATGAAGTCCACCTTGC
Chr05	125.9	Satt599	Satt599_F	Chr05	35,125,933	35,125,914	Satt599_R	Chr05	35,125,769	35,125,790	GTGTTTTTATTTGGTTTTTA	CCCTGCAGCTCAAAAATTAACT
Chr05	128	T000541110m	T000541110m_F	Chr05	35,708,376	35,708,354	T000541110m_R	Chr05	35,708,033	35,708,058	TCCTCTTACTGTATTTCCGCATT	TGACCAATTAAATAAATAGCTCCAAA
Chr05	129.7	GMES2489	GMES2489_F				GMES2489_R				CGGACATGGACGAGGTTACT	ACTCCTTGCCCTTGGAAACT
Chr05	132.4	Satt225	Satt225_F	Chr05	36,741,902	36,741,928	Satt225_R	Chr05	36,742,003	36,741,982	AAAAATGTGTTAGAGCTTGTGTTGTTA	GCCACACTATTCCAGCCACTAC
Chr05	135.5	T000539868l	T000539868l_F	Chr05	36,951,065	36,951,041	T000539868l_R	Chr05	36,950,719	36,950,741	TGTGTTGATAGGCTAAGTTGAAAGA	CAAGTCATAACCCGAAGGTTAAA
Chr05	136.9	C05-BARC-030735-06928	C05-BARC-030735-06928_F	Chr05	37,006,116	37,006,135	C05-BARC-030735-06928_R	Chr05	37,006,202	37,006,183	AGGAATCAGGACCAAATGGG	TGCTTCATGATAGGGATTGC
Chr05	137.9	s007803856-2	s007803856-2_F	Chr05	37,207,808	37,207,832	s007803856-2_R	Chr05	37,207,955	37,207,934	AAGGAAATTAATCACATGTAAACGG	GATCTTCCCGAGAAACAAACAC
Chr05	139.3	C05-BARC-028991-06048	C05-BARC-028991-06048_F	Chr05	37,544,498	37,544,517	C05-BARC-028991-06048_R	Chr05	37,544,591	37,544,572	TCCGATCGCCACAGAATATC	ACGATGATGTGGAAGGTGAC
Chr05	139.3	T000539254s	T000539254s_F	Chr05	37,573,429	37,573,408	T000539254s_R	Chr05	37,573,263	37,573,285	CGATCAAGTTAATTGGGTTTGAG	TTGTCAATATAACCTCCTCAGGG
Chr05	142.6	Sat_271	Sat_271_F	Chr05	37,994,273	37,994,246	Sat_271_R	Chr05	37,994,056	37,994,080	TCACTTTAATCATTACAATAAAACAACA	ACTTAGGCACACTCTAATATAACCA
Chr05	143.1	Sat_217	Sat_217_F	Chr05	38,157,094	38,157,067	Sat_217_R	Chr05	38,156,804	38,156,828	AAAAATTGTCAATGATATGATCAGTAAG	GTCCTAGATGAAAAATGCTTTGTAA
Chr05	144.2	T000538499s	T000538499s_F	Chr05	38,329,369	38,329,348	T000538499s_R	Chr05	38,329,202	38,329,224	AAAGTGTCAATCCACTGCACAA	CAGGTGACTTCTTCTAGGCCTTT
Chr05	144.7	T000538322l	T000538322l_F	Chr05	38,506,801	38,506,778	T000538322l_R	Chr05	38,506,437	38,506,462	AAAGAAAGTTGTAAGGTCAATGCC	TGTATCTTACAAATTGAGACATTCCA
Chr05	144.7	T000538317s	T000538317s_F	Chr05	38,512,083	38,512,061	T000538317s_R	Chr05	38,511,914	38,511,936	TATTTACAAGGCACCTGAACCAT	TTATACAGGTGCAATTTGATCCC
Chr05	144.7	T000538271s	T000538271s_F	Chr05	38,558,123	38,558,101	T000538271s_R	Chr05	38,557,922	38,557,944	CAATCTTAGACCATAATCCATTT	AAAGAGAATGATGCATGTGGAGT
Chr05	144.7	T000538238m	T000538238m_F	Chr05	38,590,841	38,590,819	T000538238m_R	Chr05	38,590,584	38,590,606	ACACAATAATGTTGCCTTTGTCA	ACCACTAGTGTCCAACGAACTGT
Chr05	144.7	s016401421-2	s016401421-2_F	Chr05	38,668,596	38,668,620	s016401421-2_R	Chr05	38,668,777	38,668,755	TGTGAAGTAAATAGGTTGAATTTGC	TCATAAACTTGTGAGTTTGCAGG
Chr05	144.7	T000538132s	T000538132s_F	Chr05	38,697,124	38,697,102	T000538132s_R	Chr05	38,696,919	38,696,941	CTAAACCCTAAATCCCATGAACC	TCATAGAAACGATGAAATCCACC
Chr06	0	T000600010s	T000600010s_F	Chr06	8,889	8,912	T000600010s_R	Chr06	9,026	9,004	CAATTTCTCAAAGCATAAGTTCCA	TTTGATATTGTTTCACCCTCAAT
Chr06	1.2	GMES6352	GMES6352_F				GMES6352_R	Chr06	458,940	458,959	CGTTCGTCACTCTCCCTCTC	AATTTGTAAGCAGCATGGCA
Chr06	1.4	Satt681	Satt681_F	Chr06	493,703	493,688	Satt681_R	Chr06	493,468	493,485	GTGCACTTGTCAATCTGTT	GTGAGGCATATGTCAGTC
Chr06	1.4	AW734043	AW734043_F	Chr06	525,705	525,727	AW734043_R	Chr06	525,811	525,788	CCACTTGTACCTAGATTGATATA	TTTTCAGATTAATTAGTACCTAGAT
Chr06	4.1	GMES1603	GMES1603_F	Chr06	1,098,134	1,098,153	GMES1603_R	Chr06	1,098,416	1,098,397	AGACACCGATTCATTCGACC	CTTAATTGGTTCGGGGGAGT
Chr06	7.9	Sat_130-2	Sat_130-2_F	Chr06	1,856,705	1,856,731	Sat_130-2_R	Chr06	1,857,143	1,857,118	TTCATTTGATACTTAAATCCAGAAATC	GTGGATTAATTACTTCAACATAAACG
Chr06	10.4	s002607789	s002607789_F	Chr06	2,141,614	2,141,592	s002607789_R	Chr06	2,141,440	2,141,464	TGAAGTTGTGAGATTTGTGCAAG	TTCTGACTTCTTGTCTAGCTACCCT
Chr06	13.5	s002607210-2	s002607210-2_F	Chr06	2,734,945	2,734,923	s002607210-2_R	Chr06	2,734,581	2,734,603	TCTGATTTGTTGGTTAAGTGGCT	ATTCAGTTCATGCGCTACAAAGT
Chr06	15.6	T000602951l	T000602951l_F	Chr06	2,976,783	2,976,806	T000602951l_R	Chr06	2,977,178	2,977,156	AACAATTTAGACAAACATGTCAGA	AGTTGTGATTGGTAAATTTGCTT
Chr06	16.1	T000603141s	T000603141s_F	Chr06	3,166,632	3,166,653	T000603141s_R	Chr06	3,166,829	3,166,806	GCGTTATACGTACACCCGGATA	CGAATCATATTTGAATGGTAACGA
Chr06	18.3	GMES5629	GMES5629_F	Chr06	3,405,251	3,405,232	GMES5629_R	Chr06	3,404,993	3,405,012	ATGATAAGCAACTCCACGGG	CGAACAAAGGAACCAGGAAA
Chr06	21.2	s002606194	s002606194_F	Chr06	3,754,707	3,754,685	s002606194_R	Chr06	3,754,312	3,754,336	TTAAAGAGGTGGATTGTCATCTG	GACTAGGCTCAAGTCTAATGTCTGC
Chr06	21.5	C06-BARC-016957-02165	C06-BARC-016957-02165_F	Chr06	3,822,862	3,822,843	C06-BARC-016957-02165_R	Chr06	3,822,793	3,822,812	GAGTTAACTATTTCGCGCAC	CTTCGGTCCTCAACTATTCG
Chr06	24.3	s002605873	s002605873_F	Chr06	4,075,342	4,075,320	s002605873_R	Chr06	4,074,981	4,075,003	ATAGCTTTGCAGCATCCTGATTA	TGTCTCAGATAATGGATTTGGCT
Chr06	27.6	s002605258	s002605258_F	Chr06	4,656,807	4,656,784	s002605258_R	Chr06	4,656,447	4,656,469	TGATCGATGATGTAAGTAAGGTGA	CATGTGCTTTGAGATGATGGTTA
Chr06	30.6	T000604871m	T000604871m_F	Chr06	4,875,129	4,875,151	T000604871m_R	Chr06	4,875,408	4,875,386	GGTTTACAGCTATGGTCGAATTG	ACAAACCATGGGAGGTTTAGATT
Chr06	31.4	T000604948s	T000604948s_F	Chr06	4,952,514	4,952,536	T000604948s_R	Chr06	4,952,713	4,952,690	AGGAGTGATGCAAACATTCCTTA	TTTAATCTCAACGGTCTATTATTT
Chr06	33.7	s002604620-2	s002604620-2_F	Chr06	5,293,261	5,293,238	s002604620-2_R	Chr06	5,292,783	5,292,804	AAACAAACACATCAAATACAATGA	GGCTTAATTTCCCTAATGGGAC
Chr06	35.5	C06-BARC-014949-01930	C06-BARC-014949-01930_F	Chr06	5,409,550	5,409,569	C06-BARC-014949-01930_R	Chr06	5,405,489	5,405,470	GTAGCATAAGCAGTAGCACG	CCTTCCTGACGATGATGATG
Chr06	36.8	s002603925	s002603925_F	Chr06	5,988,203	5,988,181	s002603925_R	Chr06	5,987,835	5,987,857	GATTAGACCGACCCTAATGCTCT	TTCGACGAGGGATAAAGTATCTG
Chr06	39	Satt432	Satt432_F	Chr06	6,293,038	6,293,017	Satt432_R	Chr06	6,292,764	6,292,786	GCCAGGTTGTGTTCTTGAGATA	TTCACCGAATATTCTTTTTAGGTC
Chr06	40.9	GMES4236	GMES4236_F	Chr06	6,865,412	6,865,431	GMES4236_R	Chr06	6,865,728	6,865,709	GAAGACGTTCCTCACTTCGC	CGTCCATGTGCACGAAATAC
Chr06	42.3	s002602817	s002602817_F	Chr06	7,094,714	7,094,690	s002602817_R				GAACGTACACTTATTAGTTAAGGGA	TCATCTCTCTTAATATATTCTCCCTCTTC
Chr06	47.2	C06-BARC-026151-05283	C06-BARC-026151-05283_F	Chr06	7,677,251	7,677,233	C06-BARC-026151-05283_R	Chr06	7,677,157	7,677,176	ATAAAATGACGTAGAAGAG	GGCGCTTTGAATTTTGGTTC
Chr06	47.4	s002602116	s002602116_F	Chr06	7,795,595	7,795,573	s002602116_R	Chr06	7,795,215	7,795,240	GGAGGATTAGGCGTTTGATACTT	AAGTCTAACATGATAAAGTTTGTTGC
Chr06	49	s002601715	s002601715_F	Chr06	8,197,718	8,197,696	s002601715_R	Chr06	8,197,357	8,197,381	CCTTCTTCCTTTATTAACGACCG	TCATGAATCAACTATTGAAGCAGAT
Chr06	50.7	s002601386-2	s002601386-2_F	Chr06	8,524,779	8,524,757	s002601386-2_R	Chr06	8,524,427	8,524,449	ATTCCTTTGGACACAGATCTTCA	AAGGAGTCATCCCTCCTCAATTA
Chr06	50.7	Satt457	Satt457_F	Chr06	8,787,745	8,787,764	Satt457_R	Chr06	8,788,006	8,787,985	GTCCGTGTATTTTGTTTTGC	TTATCCATTTTCCCTTTAGTCC
Chr06	56	T000609415s	T000609415s_F	Chr06	9,424,141	9,424,163	T000609415s_R	Chr06	9,424,326	9,424,303	ATAGCTTGAATCATGTCTGAGAA	TGCAGTTATTTATACGAGTTGCTC
Chr06	57.9	GMES4267	GMES4267_F	Chr06	10,058,807	10,058,788	GMES4267_R	Chr06	10,058,594	10,058,613	ACTGCAAAGGGATGGATGAC	GCGAAGGCATTGGAGTACAT
Chr06	58.9	GMES4771	GMES4771_F	Chr06	10,191,220	10,191,200	GMES4771_R	Chr06	10,191,033	10,191,052	CGCTCACAAGTTCTCAACTCA	GATTTTTGCTTCCGGTGGTA
Chr06	60.3	GMES0001	GMES0001_F				GMES0001_R	Chr06	10,639,163	10,639,144	CTTTGGTCGCTTGAGTCTCC	GAGTACAGGCTCAAGACGGG
Chr06	62.2	GMES4162	GMES4162_F	Chr06	10,964,393	10,964,374	GMES4162_R	Chr06	10,964,219	10,964,238	CCAGGCCCAGATTCAAAATA	GTCCCACTGGCGAAGTATGT
Chr06	63.2	GMES0468	GMES0468_F				GMES0468_R	Chr06	10,862,467	10,862,450	GCAAACACGAAACAAGGGTT	GGGAATTCACCTGAATAAAACA
Chr06	63.2	Satt170	Satt170_F	Chr06	11,293,431	11,293,454	Satt170_R	Chr06	11,293,546	11,293,524	GGGAAATCTAAATAAAATGATGGATAT	GGGGTAGTTAAAATTCATCCTTAAAA
Chr06	63.2	C06-BARC-029635-06268	C06-BARC-029635-06268_F	Chr06	11,338,533	11,338,552	C06-BARC-029635-06268_R	Chr06	11,338,615	11,338,598	CCCTCTTTATTGGAGGATTG	GCAAAAACTGGCAAAAAAAC
Chr06	67.1	T000612075s	T000612075s_F	Chr06	12,100,585	12,100,607	T000612075s_R	Chr06	12,100,785	12,100,763	GTAGGCACCTCCAACCAATTAAC	ACTAGTTCCAGAGCTTCTTTGCC
Chr06	67.4	C06-BARC-031571-07113	C06-BARC-031571-07113_F	Chr06	12,155,637	12,155,656	C06-BARC-031571-07113_R	Chr06	12,155,711	12,155,692	CTTGTCAGTTGAACCAATGC	AGTGCCCATCTGCTAGAAAC
Chr06	67.4	T000612251l	T000612251l_F	Chr06	12,276,625	12,276,647	T000612251l_R	Chr06	12,276,968	12,276,946	TAGGCACCAGTCCCTACAAGTTA	GATGCTATTATGAGGGTCACGTC

Chr06	67.4	C06-BARC-022299-04310	C06-BARC-022299-04310_F	Chr06	12,299,841	12,299,860	C06-BARC-022299-04310_R	Chr06	12,299,934	12,299,915	TCTCTAGCTCGCGTTTCTTC	ACCGCTTCGTCGCTTATATC
Chr06	67.4	T000612321m	T000612321m_F	Chr06	12,346,817	12,346,840	T000612321m_R	Chr06	12,347,124	12,347,101	AAATTGATCCAGTGTTGGTGTAAA	TGCCAAATTAACACATTCTCTGTC
Chr06	70.4	T000612567m	T000612567m_F	Chr06	12,593,211	12,593,233	T000612567m_R	Chr06	12,593,471	12,593,447	AACTGAAGCAAGGAGATAGATGC	TTTAACTAACGATATAGGTCCAGAA
Chr06	75.1	T000613046m	T000613046m_F	Chr06	13,071,888	13,071,910	T000613046m_R	Chr06	13,072,175	13,072,148	CATTTGCAATGTTTGAATGCTTA	AAAGTATTATCTATACACACAACACACG
Chr06	80.6	s025700041	s025700041_F	Chr06	13,817,027	13,817,049	s025700041_R	Chr06	13,817,296	13,817,273	AGATTATGATTTCATTAGCGCGT	TTTGATAAATTCATTGTAAGCTCG
Chr06	84.2	T000614183m	T000614183m_F	Chr06	14,228,089	14,228,112	T000614183m_R	Chr06	14,228,339	14,228,316	AAGTCCTGATTTACGTATACCCTC	AAAGAAAGGTGCTTTACTAAGAGT
Chr06	86.7	Sat_213	Sat_213_F	Chr06	14,643,508	14,643,529	Sat_213_R	Chr06	14,643,694	14,643,670	ATCCCTAATTGTTATCTAATAA	CAATATACTCCCCCATACCTTCGCA
Chr06	91.2	Satt363	Satt363_F	scaffold_345	5,789	5,762	Satt363_R	scaffold_345	5,551	5,578	TAGAGGGATCCAATTAGAATCCAAGAAA	TCTTCGATCTTCATATTCATTTTTGTAA
Chr06	93.7	C06-BARC-040023-07637	C06-BARC-040023-07637_F	Chr06	16,256,023	16,256,004	C06-BARC-040023-07637_R	Chr06	16,255,926	16,255,945	TTGACCCTTTGTGAATTGCG	CCCCCTTTCCTTCACCATTT
Chr06	97	T000616552l	T000616552l_F	Chr06	16,595,828	16,595,850	T000616552l_R	Chr06	16,596,168	16,596,146	GCAAGGAATTACTCCTATCAAGC	GTTTAGGGTTCGACGATCGATTA
Chr06	99.5	Satt277	Satt277_F	Chr06	17,217,951	17,217,929	Satt277_R	Chr06	17,217,717	17,217,739	GGTGGTGGCGGGTTACTATTACT	CCACGCTTCAGTTGATTCTTACA
Chr06	100.6	C06-BARC-014491-01562	C06-BARC-014491-01562_F	Chr06	17,477,978	17,477,961	C06-BARC-014491-01562_R	Chr06	17,477,883	17,477,902	GCGGGTTTTTCATTTTGTGTC	GGCAGGCCAAGAAACAAAAG
Chr06	102.8	sF3H	sF3H_F	Chr06	18,735,971	18,735,991	sF3H_R	Chr06	18,736,073	18,736,048	TGTGAGATATTTGGCTACCACCTCC	CTAAACTCCAATGGGTCATTCCACTC
Chr06	103.6	FT1SSR9	FT1SSR9_F	Chr06	20,073,350	20,073,369	FT1SSR9_R	scaffold_94	29,554	29,535	GCGCTACAGTTCAACCCTTC	TGTTGGCCTTTCAATCTTGT
Chr06	103.6	C06-BARC-042161-08189	C06-BARC-042161-08189_F	Chr06	20,279,486	20,279,505	C06-BARC-042161-08189_R	Chr06	20,279,585	20,279,565	AAAAAAGGATACTTTCAATG	GAGGTGAAGAACATGAATAGC
Chr06	104.3	s005700017	s005700017_F	Chr06	21,207,119	21,207,148	s005700017_R	Chr06	21,207,330	21,207,308	CTTATAAGATAAACTATATTAAGAGGTGAC	TGAACTTAGTGCTCTTTGAGCGT
Chr06	105.7	s007100484	s007100484_F	Chr06	27,748,821	27,748,843	s007100484_R	Chr06	27,749,184	27,749,162	TGATGTTATGTGCTTATCGTTGC	ACTCTCCACCATTTAAAGCATCA
Chr06	105.7	C06-BARC-031099-06997	C06-BARC-031099-06997_F	Chr06	26,236,063	26,236,044	C06-BARC-031099-06997_R	Chr06	26,235,984	26,236,003	ATCTGATATGTGGCTGCTGG	GGATTGTTAAGGTAGATGAG
Chr06	106	s004400457	s004400457_F	Chr06	32,797,099	32,797,122	s004400457_R	Chr06	32,797,301	32,797,279	CCAAATTAAGATTTACCCGATTTG	AAACCGTAGCATAAGAACCCTTC
Chr06	106	s004400621	s004400621_F	Chr06	32,962,820	32,962,842	s004400621_R	Chr06	32,963,188	32,963,166	TGTGCAGAATGGCTTTATAACTT	AAACTTCTTTCATTCCCGTGTAA
Chr06	107.8	C06-BARC-029025-06052	C06-BARC-029025-06052_F	Chr06	35,974,978	35,974,958	C06-BARC-029025-06052_R	Chr06	35,974,914	35,974,930	CATAGCAACTATTTTCCAAAG	GGGCACTAGCCAAATAAAAA
Chr06	107.9	Satt708	Satt708_F	Chr06	37,527,906	37,527,930	Satt708_R	Chr06	37,528,142	37,528,115	CAATTTTAAGAGATTTTCGGGATAA	ACTCGGTTGATTTTTTTTTCAATTTTTT
Chr06	108.4	s025900023	s025900023_F	Chr06	42,217,240	42,217,262	s025900023_R	Chr06	42,217,607	42,217,585	TTAGTCAATCAAATTATAGGCAA	ATCTTCTCCCTTTGGTAACTTGG
Chr06	108.4	GMES0696	GMES0696_F	Chr06	42,497,148	42,497,167	GMES0696_R	Chr06	42,497,542	42,497,523	AGCTTCAACGCTCGACACTT	CTCATGGCCTCATCAATCCT
Chr06	108.4	s027000323	s027000323_F	Chr06	42,918,616	42,918,638	s027000323_R	Chr06	42,918,904	42,918,888	GGACCACCATTATCATCATTCAT	GAGAGGAGCTATTCTCCACTGTA
Chr06	108.9	Satt460	Satt460_F	Chr06	44,049,493	44,049,513	Satt460_R	Chr06	44,049,642	44,049,618	CGATGGGCTGTTGGTTTTTAT	CATACGATTTGGCATTTTTCTATTG
Chr06	109.2	T000643603m	T000643603m_F				T000643603m_R				CAATTGTCATTGGTGATTCTTGA	ACATCCAGTCGAGCACAACTATT
Chr06	109.3	T000643835m	T000643835m_F	Chr06	44,386,952	44,386,974	T000643835m_R	Chr06	44,387,195	44,387,172	ATAACTTCTTATGATGGACCTTT	TTTCCTACTCAAATCACTTACCGA
Chr06	110.5	T000644173s	T000644173s_F	Chr06	44,722,033	44,722,055	T000644173s_R	Chr06	44,722,235	44,722,213	GCATACTATTGGCCGTGAGTAGA	CTGCCACTAATGACTTCTCAATG
Chr06	111.3	T000644478s	T000644478s_F	Chr06	45,037,309	45,037,331	T000644478s_R	Chr06	45,037,484	45,037,462	GCAAATACTTGAGTTCTGCATTG	TCCAATTTGTAGAGAAGGAACCA
Chr06	111.3	T000644825m	T000644825m_F	Chr06	45,391,787	45,391,810	T000644825m_R	Chr06	45,392,075	45,392,053	TCCTTTAATTTATGTTTGACTCGG	CACCACTAGGTGATTTGGAACAT
Chr06	111.6	C06-BARC-025467-06510	C06-BARC-025467-06510_F	Chr06	45,821,093	45,821,112	C06-BARC-025467-06510_R	Chr06	45,821,181	45,821,162	CGTATCAAGCCCATGATAAC	CTACGATCTATTATGATTTC
Chr06	111.6	C06-BARC-010457-00640	C06-BARC-010457-00640_F	Chr06	45,850,830	45,850,849	C06-BARC-010457-00640_R	Chr06	45,850,903	45,850,883	GAGATTGATGGTGCTCCAAG	CCTCAAAAAAGACAAGTGTCG
Chr06	111.8	T000645398s	T000645398s_F	Chr06	45,964,846	45,964,869	T000645398s_R				GATTTGCAGTAGAAGAACTTGACA	AATGTAATAATTGGTCAAGGATG
Chr06	114	Satt307	Satt307_F	Chr06	46,820,476	46,820,489	Satt307_R	Chr06	46,820,631	46,820,609	CTGGCCTTTAGAAC	TTGTAGGAAATTTGAGTAGTAAG
Chr06	115.7	T000646749l	T000646749l_F	Chr06	47,295,137	47,295,159	T000646749l_R	Chr06	47,295,514	47,295,492	ATCAAGTGGAGTCATAGCCATTG	TGATAATGGTTCTCAAACCCAAC
Chr06	118.7	GMES1191	GMES1191_F	Chr06	47,877,938	47,877,957	GMES1191_R	Chr06	47,878,221	47,878,202	AGAAGCCAAACAACAATGCC	CTGGCTGGGACTGTGAGATT
Chr06	119.1	GMES4738	GMES4738_F	Chr06	47,933,864	47,933,845	GMES4738_R	Chr06	47,933,693	47,933,712	CTCATCACACGCTGCTACAA	TGAGCAGCCATTGCTATTTG
Chr06	119.9	Satt316	Satt316_F	Chr06	48,015,726	48,015,704	Satt316_R	Chr06	48,015,563	48,015,583	GTGAGAAACTAGCCAAGAATAGA	CAATTGTTTCCAAATGACACT
Chr06	120.6	s027400052r	s027400052r_F				s027400052r_R				CACCATTAAGGATCCCATAGTCA	AAATACAGGTTAACTTCAAGGTTT
Chr06	120.6	s027400057	s027400057_F	Chr06	48,289,073	48,289,095	s027400057_R	Chr06	48,289,397	48,289,375	TTGGCTCCATTACTGTTTGACTT	AGTTAAGGGTAAGGGCTGTATGC
Chr06	123	T000647986m	T000647986m_F	Chr06	48,611,637	48,611,659	T000647986m_R	Chr06	48,611,910	48,611,888	CGCAACATCTTTAACTTATGCAA	TGAAGATCTGTGTCCAGATGAGA
Chr06	124.3	T000648254l	T000648254l_F	Chr06	48,862,620	48,862,644	T000648254l_R	Chr06	48,862,926	48,862,904	TTGCATAACTAAATTGTCTACACACTAA	CAATTCTATCCGTCCTCCCTATT
Chr06	127.5	s022800028	s022800028_F	Chr06	49,108,402	49,108,380	s022800028_R	Chr06	49,108,102	49,108,124	TGTTGGTTATCATAAATCTCCGA	CCCTCTGTCTAAGCTAGGTGGTT
Chr06	128.9	C06-BARC-038923-07399	C06-BARC-038923-07399_F	Chr06	49,188,021	49,188,040	C06-BARC-038923-07399_R	Chr06	49,188,106	49,188,087	CTAGTAATCACTCCCAACCC	GGCCTATGGTGTCTTGATAT
Chr06	129.8	T000648696l	T000648696l_F	Chr06	49,284,765	49,284,787	T000648696l_R	Chr06	49,285,105	49,285,083	TTCCCTTCAAGAACAAATTACCA	TTGATTGCACAGACTTGAAGAAA
Chr06	132	GMES4077	GMES4077_F	Chr06	49,645,029	49,645,010	GMES4077_R	Chr06	49,644,850	49,644,869	ATCCCCTTTCAAGTCAGCCT	ATGATCATTGTCGGGGAGAG
Chr06	133.7	GMES6551	GMES6551_F				GMES6551_R	Chr06	49,783,251	49,783,271	TTCTTTTGGGCATCATTTCC	CAACATCCAAAAGCACTGTGA
Chr06	135.5	T000649317s	T000649317s_F	Chr06	49,916,707	49,916,729	T000649317s_R	Chr06	49,916,877	49,916,855	AGCCAAAGGAGCTTTAGTCCTAC	TATACTCCTCTCTCCTTCCAGCC
Chr06	135.8	T000649400m	T000649400m_F	Chr06	49,999,334	49,999,357	T000649400m_R	Chr06	49,999,687	49,999,664	AATGAATTCGAAATAAAGTTAGAC	CCAAACAAACTAATGATTAAACGG
Chr06	137.9	T000649516l	T000649516l_F	Chr06	50,115,211	50,115,233	T000649516l_R	Chr06	50,115,587	50,115,565	AAGAAATGTTTCCAGGAAGTGAA	TCTTCATGACTTGTCCAAAGGTT
Chr06	139.5	T000649627l	T000649627l_F	Chr06	50,226,259	50,226,285	T000649627l_R	Chr06	50,226,687	50,226,665	CATATAAAGTACGTGTTATAGCAATTT	GTTGCTAGAATTTGTCCGGATTT
Chr06	139.5	T000649664l	T000649664l_F	Chr06	50,263,345	50,263,363	T000649664l_R	Chr06	50,263,673	50,263,651	TACTAGCTCGTGATTTGCCTTGT	TCATCCACCTAACCATCTGCTAC
Chr06	140.3	T000649756m	T000649756m_F	Chr06	50,356,173	50,356,195	T000649756m_R	Chr06	50,356,346	50,356,324	ACACACTAACCCTGTACTCGCAT	ATATTCGGAACTTGAGCAAACAA
Chr06	141.1	Satt357	Satt357_F	Chr06	50,508,668	50,508,686	Satt357_R	Chr06	50,508,882	50,508,862	CCTGAGCAATTCATACTCC	TAACCGATCCGATCCTTGACA
Chr06	141.4	C06-BARC-042781-08405	C06-BARC-042781-08405_F	Chr06	50,570,163	50,570,144	C06-BARC-042781-08405_R	Chr06	50,570,083	50,570,102	CTGGTAAGAGAAATGGTAGC	CTCAATGATTCTTGGCCAAT
Chr06	145.6	T000650068s	T000650068s_F	Chr06	50,739,627	50,739,649	T000650068s_R	Chr06	50,739,804	50,739,780	CACACTTTCTTTACGGTCTGAGG	TTTCCTTATTCAGTAAGAGCACTCC
Chr06	146.9	T000650178l	T000650178l_F	Chr06	50,851,370	50,851,392	T000650178l_R	Chr06	50,851,730	50,851,708	ACATTCTACACCAGTCCATTTGC	GACACACCAAACTTTCAGAAACC
Chr06	148.2	T000650186m	T000650186m_F	Chr06	50,859,638	50,859,660	T000650186m_R	Chr06	50,859,975	50,859,953	TTTATTGTTGATTTCGGGTGTTT	TCAGAATCTGCACCAATTAACCT
Chr06	149.3	T000650324m	T000650324m_F	Chr06	50,997,464	50,997,486	T000650324m_R	Chr06	50,997,792	50,997,769	TCCATCAATTGCCTCTTTACCTA	GATCCCAATCATCTAACTGACAAA
Chr06	149.5	T000650345s	T000650345s_F	Chr06	51,017,971	51,017,993	T000650345s_R	Chr06	51,018,168	51,018,146	TTCATTTATTTGACAAACCGCAT	AGTCAAATCAACAGGTATTTCGG
Chr06	149.6	T000650353m	T000650353m_F	Chr06	51,026,205	51,026,227	T000650353m_R	Chr06	51,026,468	51,026,446	GCAACTTCTTATGGTCAAGCCTA	TGCAGAGGTTGGTTATCAAGATT
Chr06	151.2	T000650496m	T000650496m_F	Chr06	51,169,322	51,169,344	T000650496m_R	Chr06	51,169,618	51,169,596	ATGCACAATAGTTAATCGATGTT	AACTGTGTGGCTGTAGCAAATCT
Chr06	154.4	T000650650m	T000650650m_F	Chr06	51,323,768	51,323,791	T000650650m_R	Chr06	51,324,032	51,324,010	GCATATAGATCAGATGTGTCGAGC	AGCTTCTTTCCTCATGTAACCCT
Chr07	0	T000700038m	T000700038m_F	Chr07	39,131	39,153	T000700038m_R	Chr07	39,453	39,428	TGATGAATGTTGTGAATTGAACG	CAATATATGCAAATTAAGTCGATCAG
Chr07	0	T000700095m	T000700095m_F	Chr07	98,869	98,888	T000700095m_R	Chr07	99,205	99,182	GCAACGACTCGATGTTGTAA	GGATCTTTATTCTGAGGAGGAATG
Chr07	0	Satt404	Satt404_F	Chr07	225,578	225,561	Satt404_R	Chr07	225,389	225,406	TCATCCGCCATTGATTTT	GCCCGGAACATACAAAAT
Chr07	1.1	C07-BARC-039701-07555	C07-BARC-039701-07555_F	Chr07	460,613	460,632	C07-BARC-039701-07555_R	Chr07	460,686	460,667	TACTCTCGAGTTCCTTGCAG	CATCCTGCAGCACTTGTTTC
Chr07	1.3	GMSC514-2	GMSC514-2_F	Chr07	509,298	509,324	GMSC514-2_R	Chr07	509,662	509,640	GGGACCATATTCTTGATATCACTTCTC	GTTTGGACGTTCCGGATTATCTT
Chr07	3.2	T000701267s	T000701267s_F	Chr07	1,268,000	1,268,025	T000701267s_R	Chr07	1,268,190	1,268,168	TGATGGTTATAACTCACTAGCATTCA	TCACTTGGCATAATTGTTCATTG
Chr07	6.5	GMES1479	GMES1479_F	Chr07	1,792,035	1,792,054	GMES1479_R	Chr07	1,792,329	1,792,309	TGTGGGTGACAAAGATGAGG	TGCCTTTCTTTCCACAAGTCT
Chr07	7	GMES4149	GMES4149_F	Chr07	1,949,434	1,949,455	GMES4149_R	Chr07	1,949,823	1,949,804	CATCCATGTTCCTCTTTTCTCA	CTGCGTCGATTTGGAATTTT
Chr07	7.8	C07-BARC-042621-08318	C07-BARC-042621-08318_F	Chr07	2,203,387	2,203,368	C07-BARC-042621-08318_R	Chr07	2,215,323	2,215,342	TGAACATTAGTAGACTGCTG	CATCTGTTATGCAGCCATCC
Chr07	7.9	C08-BARC-042621-08319	C08-BARC-042621-08319_F	Chr07	2,203,359	2,203,378	C08-BARC-042621-08319_R				CCACAGAATCAGCAGTCTAC	GAAGTCCGTTGTTGCTGATG
Chr07	8.4	Satt150	Satt150_F	Chr07	2,433,896	2,433,920	Satt150_R	Chr07	2,434,102	2,434,081	AAGCTTGAGGTTATTCGAAAATGAC	TGCCATCAGGTTGTGTAAGTGT
Chr07	10.8	GMES4783	GMES4783_F	Chr07	2,571,041	2,571,022	GMES4783_R	Chr07	2,570,909	2,570,928	AGATCAAAATGTTGCGGAGG	TAGAGGCAGGAGCGAGAGAG
Chr07	10.8	GMES2848	GMES2848_F	Chr07	2,571,198	2,571,179	GMES2848_R	Chr07	2,570,909	2,570,928	GACCAATCCATAGCCGAAGA	TAGAGGCAGGAGCGAGAGAG

Chr07	15.4	s010700655	s010700655_F	Chr07	2,782,895	2,782,873	s010700655_R	Chr07	2,782,755	2,782,777	TTCCTGCAGATCTTATCAAGAGG	ACAAAGAACTTGGTATCATCAAA
Chr07	16.2	s010700293	s010700293_F	Chr07	3,144,333	3,144,310	s010700293_R	Chr07	3,144,230	3,144,252	TTCTCGTAACCAAAGTGGATAATG	GATATGTCAGTAGTGCCCATTCC
Chr07	16.5	C07-BARC-042631-08334	C07-BARC-042631-08334_F	Chr07	3,203,719	3,203,701	C07-BARC-042631-08334_R	Chr07	3,203,650	3,203,669	AACCCATTATAGTTAGCTG	AGGTCAGAGTTCCATTCAGG
Chr07	20.7	s010700001	s010700001_F	Chr07	3,436,281	3,436,258	s010700001_R	Chr07	3,435,891	3,435,913	TCAAGAACGAGTTTATCGTAGCTC	AAATAGGCCCTGCATATACGAGT
Chr07	26.2	T000703965m	T000703965m_F	Chr07	3,991,608	3,991,630	T000703965m_R	Chr07	3,991,828	3,991,806	TTTAAAGAGGCTTGGTTACTTCG	AGGTCTTGGTAAGCAATCATCAC
Chr07	29.4	C07-BARC-031399-07089	C07-BARC-031399-07089_F	Chr07	4,246,437	4,246,418	C07-BARC-031399-07089_R	Chr07	4,246,361	4,246,379	TTGCACTCTCATCTAATCAC	GTAAGACTTTTAAGATAGC
Chr07	29.9	s020200030	s020200030_F	Chr07	4,323,059	4,323,037	s020200030_R	Chr07	4,322,691	4,322,715	TCCTTCTTAGGTCTTGACAAGTG	TTGACTCACACATAAGGAACTACAA
Chr07	30.2	C07-BARC-015945-02020	C07-BARC-015945-02020_F	Chr07	4,428,825	4,428,844	C07-BARC-015945-02020_R	Chr07	4,428,890	4,428,874	CCAAAGGACAAAAGGGCTTC	GCCCGTGCCAAAATTCTAAC
Chr07	31.8	Satt567	Satt567_F	Chr07	4,558,650	4,558,667	Satt567_R	Chr07	4,558,761	4,558,743	GGCTAACCCGCTCTATGT	GGGCCATGCACCTGCTACT
Chr07	35.7	T000704890s	T000704890s_F	Chr07	4,936,182	4,936,204	T000704890s_R	Chr07	4,936,363	4,936,342	GGAGGTACTAAATTCAGCCAACA	CCGAGACTGTTATCGTTGGATT
Chr07	40.4	T000705452m	T000705452m_F	Chr07	5,488,842	5,488,864	T000705452m_R	Chr07	5,489,116	5,489,094	TAGGCATAAGCCAAGTAAAGAGC	ACATCGATGAAGGAGCATGTATT
Chr07	40.8	s014900168-2	s014900168-2_F	Chr07	5,967,565	5,967,544	s014900168-2_R				AACCTGTGATTGATGACGAGTG	TCAATCACTGTTGGCTATAACATT
Chr07	40.8	s020300806-2	s020300806-2_F	Chr07	6,221,271	6,221,249	s020300806-2_R	Chr07	6,221,125	6,221,154	ATAGTAGCGTGTTGGATAGGCTT	CATTGTTCTATCCTCTTTAATATCATTCTG
Chr07	42.7	C07-BARC-042815-08424	C07-BARC-042815-08424_F	Chr07	6,442,366	6,442,347	C07-BARC-042815-08424_R				GGGAGGCATGTCTGTAATGA	TACAACCCCCTAGAGTGATG
Chr07	42.7	GMES1143	GMES1143_F	Chr07	6,611,636	6,611,660	GMES1143_R	Chr07	6,611,780	6,611,761	CCAACAAATATAAAAATCAACCCTC	GGAAATGGTTTCGGATTTGA
Chr07	45.3	T000707138m	T000707138m_F	Chr07	7,174,452	7,174,467	T000707138m_R	Chr07	7,174,669	7,174,649	TGATGGCGCCTCCAAA	GGTGTAGTCGATCGCAATCTC
Chr07	45.7	T000707199l	T000707199l_F	Chr07	7,235,530	7,235,553	T000707199l_R	Chr07	7,235,909	7,235,884	CGGTTGATTGATATTACTTTGAGG	CAATCAGTAAGTCCAACCCTAATACA
Chr07	48.7	T000707413m	T000707413m_F	Chr07	7,450,842	7,450,864	T000707413m_R	Chr07	7,451,147	7,451,120	TTGGGAAATCACTAAGCACTGTT	CGTTATCTTGTAAATAAGTCTAGTCTCC
Chr07	51.3	T000707720l	T000707720l_F	Chr07	7,757,957	7,757,980	T000707720l_R	Chr07	7,758,320	7,758,297	TTGAATCTCTAAGGCACTTCTTCA	CCATCTTCTTAGGACATTATCACG
Chr07	54.7	Satt463	Satt463_F	Chr07	8,282,338	8,282,313	Satt463_R	Chr07	8,282,118	8,282,143	TTGGATCTCATATTCAAACTTTCAAG	CTGCAAATTTGATGCACATGTGTCTA
Chr07	57.9	GMES0689	GMES0689_F	Chr07	9,065,622	9,065,603	GMES0689_R	Chr07	9,065,434	9,065,453	CTGGCCAGAGACCAGAGAGT	GAGCACACCATGGAACTGAA
Chr07	59.5	C07-BARC-016783-02329	C07-BARC-016783-02329_F	Chr07	9,664,500	9,664,481	C07-BARC-016783-02329_R	Chr07	9,664,417	9,664,436	ATTTCATCTGCCGCAGTTCC	TGATGCTGGAATAGCTGTGG
Chr07	60.6	T000709733s	T000709733s_F	Chr07	9,777,138	9,777,159	T000709733s_R	Chr07	9,777,343	9,777,323	GGACTGCATGACATGGCTTAAC	AAATCCTAATGGCATTGATAA
Chr07	63	s023200001	s023200001_F				s023200001_R	Chr07	10,265,035	10,265,062	TCACTTAGACTATAAAGGATAATAAACA	TTTGAATTAATTAACCTAGCTATGATGT
Chr07	64.4	Satt323	Satt323_F	Chr07	10,463,949	10,463,969	Satt323_R	Chr07	10,464,104	10,464,081	GTCGTCCTATCTAATGAAGAG	TGTGCGTTTAAATTGCAGCTAAAT
Chr07	64.7	T000714755s	T000714755s_F	Chr07	10,532,985	10,532,963	T000714755s_R	Chr07	10,532,787	10,532,809	TTTAAGCAACATGGAAGAGCATT	TTTAATTTGTTAGGTTTCCGGCT
Chr07	64.7	Sat_258	Sat_258_F	Chr07	10,654,981	10,654,955	Sat_258_R	Chr07	10,654,795	10,654,819	CAATAGATAATCGAAAAACATACAAGA	GGGAAAGTGAAAACAAGATCAAATA
Chr07	64.7	GMES0583	GMES0583_F	Chr07	10,675,259	10,675,278	GMES0583_R	Chr07	10,675,523	10,675,504	GCTTGCTTCCACGATTCTTC	TGTAGCGGTGTGTGTTTGGT
Chr07	65.8	C07-BARC-032007-07237	C07-BARC-032007-07237_F	Chr07	11,699,293	11,699,274	C07-BARC-032007-07237_R	Chr07	11,699,227	11,699,246	CTGAAAAACTCGAGTATATG	CATGATCCCTGACTACTTGG
Chr07	71.1	T000714935m	T000714935m_F	Chr07	15,020,115	15,020,137	T000714935m_R	Chr07	15,020,452	15,020,432	ATATAGAGACTACCCGCTACCCG	AGCCACTCTCGTGAAGTCATAAA
Chr07	72.7	T000714998l	T000714998l_F	Chr07	15,083,101	15,083,123	T000714998l_R	Chr07	15,083,481	15,083,459	CATTGATTTGGTTGAGACAGTGA	AACATAGCCGATTCAGGGTAAAT
Chr07	74.3	s003407198-2	s003407198-2_F	Chr07	15,209,390	15,209,373	s003407198-2_R	Chr07	15,209,193	15,209,212	GGGATGCTACGAAACCTT	ACGTCGCTGTCAAGGTCAAG
Chr07	76.4	s003406906-2	s003406906-2_F	Chr07	15,500,606	15,500,584	s003406906-2_R	Chr07	15,500,418	15,500,442	AATGTAGGTTCACTCAACCGATG	AAATAGATGGAATAGGCTTGTTAAA
Chr07	77.8	GMES4434	GMES4434_F	Chr07	15,747,496	15,747,515	GMES4434_R	Chr07	15,747,870	15,747,854	TGAAATCTCCCACAAGAAGC	AAGCCCATAGTCCTTGACGA
Chr07	79.2	C07-BARC-041817-08104	C07-BARC-041817-08104_F	Chr07	16,168,038	16,168,019	C07-BARC-041817-08104_R	Chr07	16,167,948	16,167,967	AGGGCGCTATAAATTAATGC	TTCCGCTTTCCTAGCTTTCC
Chr07	80.2	Satt230	Satt230_F	Chr07	16,342,304	16,342,327	Satt230_R	Chr07	16,342,523	16,342,500	CCGTCACCGTTAATAAAATAGCAT	CTCCCCCAAATTTAACCTTAAAGA
Chr07	80.5	Satt494	Satt494_F	Chr07	16,519,512	16,519,535	Satt494_R	Chr07	16,519,728	16,519,705	GGCCGGTTCTCATTACAGGTCTCT	GGATTTCCATCTTGAATTTTATTA
Chr07	82.9	Sct_147	Sct_147_F	Chr07	16,888,039	16,888,023	Sct_147_R	Chr07	16,887,913	16,887,929	TCTCGACTCACGACTCA	CCAAGGTCTCTCAGAGG
Chr07	87.2	GMES5158	GMES5158_F	Chr07	18,180,359	18,180,340	GMES5158_R	Chr07	18,180,113	18,180,132	CATTAGGCCTCACTCCCAAA	AACACCATGGTTCACCACCT
Chr07	87.5	C07-BARC-029795-06410	C07-BARC-029795-06410_F	Chr07	18,351,365	18,351,346	C07-BARC-029795-06410_R	Chr07	18,351,266	18,351,285	AGTTGAGGCTGTGAGTGTCT	GAGAAGCAAAAGAAACATTC
Chr07	89.6	C07-BARC-014319-01316	C07-BARC-014319-01316_F	Chr07	20,696,264	20,696,245	C07-BARC-014319-01316_R	Chr07	20,696,166	20,696,184	CGGCCACTCTGAAAAATTAG	CATGAGAACTACCATGTAT
Chr07	89.6	s014001830-2	s014001830-2_F	Chr07	24,837,228	24,837,205	s014001830-2_R	Chr07	24,837,029	24,837,051	AATATTACTGGAATACGCATAGTG	TCAACGAGATGCTGGTTATTACA
Chr07	89.6	s014001815-2	s014001815-2_F	Chr07	24,851,981	24,851,959	s014001815-2_R	Chr07	24,851,838	24,851,858	CATGTTTGCTTGTCATAGAATGG	TTTACAAGCACACCCATCAAA
Chr07	89.6	s017500010	s017500010_F	Chr07	33,814,553	33,814,575	s017500010_R	Chr07	33,814,900	33,814,878	CTAAGAAGGCTACTACCCAAGGC	CCGATATAATGGAAGCAATTGAA
Chr07	89.6	s015400132	s015400132_F	Chr07	34,091,876	34,091,901	s015400132_R	Chr07	34,092,242	34,092,220	AGATGAGATGAAGAGTAAATTAAAGA	TTTAGTCGCTAGATTGCACATGA
Chr07	89.6	T000734693l	T000734693l_F	Chr07	34,561,216	34,561,238	T000734693l_R	Chr07	34,561,586	34,561,564	TCACATCACACTTTAGCTGCTTC	GTGGGAAGAGTTGCAGATTCTAA
Chr07	95.8	s026300027	s026300027_F	Chr07	35,589,504	35,589,526	s026300027_R	Chr07	35,589,871	35,589,849	CAAGATGTTTACTTTGCCAGCTA	AAATGGTGACTGAATGATGGTTT
Chr07	99.4	s019100039	s019100039_F	Chr07	35,991,034	35,991,056	s019100039_R	Chr07	35,991,341	35,991,319	TTCCATAGACAATGCAGGAGAAT	TTTCAACCATTTCAGCTACACCT
Chr07	103.5	GMES0734.1										
Chr07	103.6	C07-BARC-028385-05857	C07-BARC-028385-05857_F	Chr07	36,707,835	36,707,854	C07-BARC-028385-05857_R	Chr07	36,707,916	36,707,897	TCGGTGTAGATGGTAAGTCC	ATGGGTCAGATGATGGCAAG
Chr07	103.8	Satt551	Satt551_F	Chr07	37,077,913	37,077,934	Satt551_R	Chr07	37,078,138	37,078,117	GAATATCACGCGAGAATTTTAC	TATATGCGAACCCTCTTACAAT
Chr07	104.9	C07-BARC-045287-08922	C07-BARC-045287-08922_F	Chr07	37,480,835	37,480,816	C07-BARC-045287-08922_R	Chr07	37,480,739	37,480,759	GAGTGTGGTATTAGTATTTC	GTGAGATTCACCCAATAATAG
Chr07	106.8	GMES4369	GMES4369_F	Chr07	38,015,149	38,015,168	GMES4369_R	Chr07	38,015,284	38,015,264	AGGTTGAATCGCAGAAATGC	TCGTTATCGTCCTTGTCATCA
Chr07	108.4	GMES0798	GMES0798_F	Chr07	38,179,723	38,179,704	GMES0798_R	Chr07	38,179,532	38,179,551	CTCTTTGTGTCGCCTGGTCT	GAACCTGACCCTGCTGGTTA
Chr07	110.8	GMES0642	GMES0642_F	Chr07	38,567,416	38,567,435	GMES0642_R	Chr07	38,567,550	38,567,531	CTACCCTTCACAAAGCCACC	GCAAAACAAGAGGGGTTTGA
Chr07	111.4	Sat_121	Sat_121_F	Chr07	38,575,762	38,575,733	Sat_121_R	Chr07	38,575,616	38,575,643	GACAAATGTAAAAAGTGACAGATAGAATGT	GTGTGGTGGTGGTACAGTTTTATACTAA
Chr07	115.4	Satt250	Satt250_F	Chr07	39,086,827	39,086,846	Satt250_R	Chr07	39,087,028	39,087,005	CGCCAGCTAGCTAGTCTCAT	AATTTGCTCCAGTGTTTTAAGTTT
Chr07	117.1	T000739974m	T000739974m_F	Chr07	39,928,836	39,928,858	T000739974m_R	Chr07	39,929,107	39,929,083	ACGCTTCTTTAGTATTCCATGTT	GATGAAATAGTTAGAAAGGGTATTT
Chr07	123.1	Satt210	Satt210_F	Chr07	40,918,405	40,918,381	Satt210_R	Chr07	40,918,161	40,918,185	AAAAACGTCAGGTCAATGACTGAAA	GGGCTTAGATATAAAAAAAAAGATG
Chr07	127.4	s006803086-2	s006803086-2_F	Chr07	41,526,853	41,526,833	s006803086-2_R	Chr07	41,526,704	41,526,727	TCATAACTGCTGGTCCGTGAT	TGTCCCAAACCCATTTACTACTTT
Chr07	129.4	T000741880s	T000741880s_F	Chr07	41,823,896	41,823,914	T000741880s_R	Chr07	41,824,104	41,824,082	GATGAACCGGAGGATGAAA	CTTCCAAACAAACCAGATAAACG
Chr07	135.4	s006802361-2	s006802361-2_F	Chr07	42,251,591	42,251,569	s006802361-2_R	Chr07	42,251,192	42,251,214	ACGAACCATGCATCTAGTCAAAC	TCCGGAGTGAGCTAGAATACAAA
Chr07	139	s006802107-2	s006802107-2_F	Chr07	42,505,055	42,505,033	s006802107-2_R	Chr07	42,504,878	42,504,900	GTGTTGTTATTATCCGGCACAGT	TGAAATGTTCTTTCATTGTGTGA
Chr07	140.1	Satt308	Satt308_F	Chr07	42,821,045	42,821,027	Satt308_R	Chr07	42,820,907	42,820,929	TTAAGGTTGGCAGGGTGGAAGTG	CAGCTTTATACAAAAATCAACAA
Chr07	140.1	GMES5903	GMES5903_F	Chr07	42,896,209	42,896,190	GMES5903_R	Chr07	42,895,948	42,895,967	TCCTTTGTGGTAGGGTCCAC	GCGAACATAGCAAACGTTGA
Chr07	143	GMES6390	GMES6390_F	Chr07	43,119,946	43,119,925	GMES6390_R	Chr07	43,119,849	43,119,868	CAAGAGTTTTAGGTTTGTGGGA	CAAGTGAAGAGGACAAGGGC
Chr07	146.4	T000743441m	T000743441m_F	Chr07	43,385,770	43,385,792	T000743441m_R	Chr07	43,386,093	43,386,071	AGATCCTTCATGACCAAGAGTGT	TTCCTACTTCGTACGTTGGATTT
Chr07	148.6	Sat_359	Sat_359_F	Chr07	43,600,215	43,600,188	Sat_359_R	Chr07	43,599,875	43,599,901	GGTCACGATTCTAGTCACTATAACTTCA	CAACGTAAGAAATGTAAATACAATGGA
Chr07	148.9	C07-BARC-028517-05936	C07-BARC-028517-05936_F	Chr07	43,654,605	43,654,624	C07-BARC-028517-05936_R	Chr07	43,654,687	43,654,668	ACTCGTTGGAAGTGGGAATG	ACAACCACGCAAGATGGTAG
Chr08	0	T000800090l	T000800090l_F	Chr08	89,878	89,906	T000800090l_R	Chr08	90,238	90,216	GGATACATGAATAGTAATGGTTATTGAAA	TTAATTAAAGTGGATCAGTCCCT
Chr08	1.1	T000800432m	T000800432m_F	Chr08	433,021	433,045	T000800432m_R	Chr08	433,268	433,246	AAATGTTATGTCAATTACAAGTGCT	TCTGTATTGCTTTATGTCTTCCC
Chr08	5	T000800981s	T000800981s_F	Chr08	982,117	982,137	T000800981s_R	Chr08	982,318	982,296	ATAAATGATGTAACATGGGTCGC	GATTGCAATGGACCTCTCTTATG
Chr08	7.2	T000801202m	T000801202m_F	Chr08	1,203,432	1,203,454	T000801202m_R	Chr08	1,203,757	1,203,735	ATTCACTCGCTCTGCATATAACG	ATTATCATATGAGGATTCGGATG
Chr08	9.4	C08-BARC-021937-04237	C08-BARC-021937-04237_F	Chr08	1,467,871	1,467,890	C08-BARC-021937-04237_R	Chr08	1,467,964	1,467,944	AGAGCTGGTGCATTTATTCG	CCAATCATGTAACAACATAGG
Chr08	9.4	T000801549l	T000801549l_F	Chr08	1,550,486	1,550,508	T000801549l_R	Chr08	1,550,796	1,550,774	CTTCCACTCTCCAAACAAGAATG	AGCGAGCACCAACTGAATAAGTA
Chr08	10.2	GMES1342	GMES1342_F	Chr08	1,802,247	1,802,266	GMES1342_R	Chr08	1,802,546	1,802,527	TTATCAGCTGGCAAAAGCCT	CTTCACTCCTTTCTGCTCCG
Chr08	12.2	Sct_067-2	Sct_067-2_F	Chr08	2,436,350	2,436,369	Sct_067-2_R	Chr08	2,436,723	2,436,700	TCTCCTCTCTGCATTCACCA	TTTGCCACATCATTTTACTTATGA

Chr08	15.3	C08-BARC-044051-08595	C08-BARC-044051-08595_F	Chr08	3,178,647	3,178,666	C08-BARC-044051-08595_R	Chr08	3,178,725	3,178,706	GTAATTCAAGGCGCTGAAAG	ACCTGGTGCCTGAAATCTTC
Chr08	15.9	C08-BARC-042199-08208	C08-BARC-042199-08208_F	Chr08	3,311,444	3,311,463	C08-BARC-042199-08208_R	Chr08	3,311,527	3,311,508	TCCTCAGAGCAGAAAAAAGG	CAAATTCCTACCCAGGTGAG
Chr08	15.9	GMES1112	GMES1112 F	Chr08	3,339,474	3,339,455	GMES1112 R	Chr08	3,339,198	3,339,217	TTCCTGCTTCAAGATGGGAG	ACGTTCCCATTTCTTCGTTG
Chr08	20.4	GMES3525	GMES3525_F	Chr08	3,603,475	3,603,494	GMES3525_R	Chr08	3,603,680	3,603,661	ACGACACCCTTTTCTGCAAC	TTCTTCACCCCATCGAAGTC
Chr08	23.5	Satt207	Satt207_F	Chr08	4,005,798	4,005,821	Satt207_R	Chr08	4,006,030	4,006,010	TTTTTCTCATTTTGATTCCTAAAC	ATTGTGATTGTAGTCCCTAAA
Chr08	29.7	T000804292l	T000804292l_F	Chr08	4,297,017	4,297,039	T000804292l_R	Chr08	4,297,372	4,297,350	TCATCATGTAGACTTGCCATTTG	AATTCTGAACCCATCTAATCCGT
Chr08	32.9	T000804554s	T000804554s F	Chr08	4,559,031	4,559,053	T000804554s R	Chr08	4,559,231	4,559,213	GCTGCAATTAATCATGACGGTAG	AAATCAGCCACACACATTT
Chr08	37.3	s002207765-2	s002207765-2_F	Chr08	4,901,293	4,901,272	s002207765-2_R	Chr08	4,901,094	4,901,116	GCATAATTGGCACACTGGAAAT	GGACGACTTCACCCTAATCATAA
Chr08	38.2	GMES0604	GMES0604_F	Chr08	5,170,931	5,170,950	GMES0604_R	Chr08	5,171,145	5,171,126	GCAGCTGCCAACTGATACAA	CAAATGGTGACACGAGGAGA
Chr08	38.7	Satt589	Satt589 F	Chr08	5,182,058	5,182,081	Satt589 R	Chr08	5,182,232	5,182,208	CAGACAATTTCAGTGGCAGATAGA	AAAAAGTAATATAAGTAGAAAAAGG
Chr08	38.7	C08-BARC-025925-05160	C08-BARC-025925-05160_F	Chr08	5,287,077	5,287,058	C08-BARC-025925-05160_R	Chr08	5,286,985	5,287,004	CTCGCAAATTGAATCCACCC	AAGCCTTCTCGATCACCAAG
Chr08	42.5	s002206987-2	s002206987-2_F	Chr08	5,680,100	5,680,079	s002206987-2_R	Chr08	5,679,965	5,679,990	AGGCCACATTACACATACAAAT	AAGCATTTGTTAATATAGTTTCAGCA
Chr08	43.3	s002206558-2	s002206558-2_F	Chr08	6,108,446	6,108,429	s002206558-2_R	Chr08	6,108,230	6,108,251	CGACGAGCTTTGGCATTT	ATGTTGGTTGAATCACATCGAG
Chr08	46.9	T000806399s	T000806399s F	Chr08	6,400,775	6,400,799	T000806399s R	Chr08	6,400,980	6,400,965	TCAAGAATAGTAATCCACCAAGTGA	AAAGTATTTGGAACTTGAAAGTGTA
Chr08	51.1	T000806826m	T000806826m_F	Chr08	6,829,468	6,829,490	T000806826m_R	Chr08	6,829,770	6,829,747	AAATCCATAAGAGGTGTCCTAAA	AATTCATTATTAAAGTGAGCATGA
Chr08	54.6	GMES1620	GMES1620_F	Chr08	7,122,226	7,122,207	GMES1620_R	Chr08	7,122,031	7,122,050	TTCTCTCATCCCCTTTTTGC	CAAGTTTCTGGAGGAGGCAG
Chr08	57.2	C08-BARC-025811-05086	C08-BARC-025811-05086_F	Chr08	7,470,081	7,470,061	C08-BARC-025811-05086_R	Chr08	7,469,992	7,470,012	CTTTAGTCTTAACAGAACACG	GGGAAAATGAAACAAAGGGTG
Chr08	58.6	Sat_400	Sat_400_F	Chr08	7,891,093	7,891,120	Sat_400_R	Chr08	7,891,368	7,891,345	TTGAGCCAATTAAAATTATATTTATGAT	CAAATGCCATTCAATTAGTAGTCA
Chr08	59.4	Satt632	Satt632_F	Chr08	8,222,541	8,222,564	Satt632_R	Chr08	8,222,803	8,222,780	GGGCTATGAAGGGAATGGAAAGGA	CCCATATTGAAGATTTGAAGTAAT
Chr08	59.4	Sat_162	Sat_162_F	Chr08	8,282,868	8,282,850	Sat_162_R				TGGTTTTTCGCTGGATATA	CATTTCGTAACATATTTTTCAC
Chr08	60	AY262686B	AY262686B F	Chr08	8,372,116	8,372,135	AY262686B R	Chr08	8,372,454	8,372,435	CTCACTAATAGCGTGATTGG	ACACTCTAGTAGTAAGCGGAC
Chr08	60.8	AY262686Z	AY262686Z_F	Chr08	8,591,700	8,591,677	AY262686Z_R	Chr08	8,591,423	8,591,446	GAAGCTGTCCTGTAATCTGTCACC	CACCTACAAGAGTCTGCTTGATCC
Chr08	62.2	s002203917	s002203917_F	Chr08	8,883,183	8,883,161	s002203917_R	Chr08	8,882,817	8,882,840	TGACACCACACACATCAATTACA	CACACATTAGTAACATTTGCATGG
Chr08	62.3	s002203914	s002203914_F	Chr08	8,886,575	8,886,553	s002203914_R	Chr08	8,886,314	8,886,336	TCTATGAGCTGGCTTACATTTGA	CCAGGTAGATCGCTTACAAAGTG
Chr08	62.6	C08-BARC-015419-01822	C08-BARC-015419-01822 F	Chr08	8,936,460	8,936,441	C08-BARC-015419-01822 R	Chr08	8,936,364	8,936,383	GACACTTATTTTGGAATGGG	CCAACCGCTTCCTATATATC
Chr08	64.8	Sat_215	Sat_215_F	Chr08	9,203,404	9,203,424	Sat_215_R	Chr08	9,203,654	9,203,629	TAGCAACAAAGCAATCTACAG	TCCCATTTTATTCCACACTATGTAAT
Chr08	68.6	C08-BARC-039145-07456	C08-BARC-039145-07456_F	Chr08	10,077,769	10,077,788	C08-BARC-039145-07456_R	Chr08	10,077,855	10,077,835	AGATCTAGTTACTCAAGAGC	CCCATTAAATCGTCTATCAGC
Chr08	68.6	alphaP-AT17.5										
Chr08	69.3	T000810277l	T000810277l_F				T000810277l_R	Chr08	10,188,374	10,188,351	ATCACAATTGAGACGGGTGAT	AAAGATAAATTCCCAATGTAAGCA
Chr08	74.6	GMES1626	GMES1626_F	Chr08	11,477,458	11,477,439	GMES1626_R	Chr08	11,477,188	11,477,207	TTATGCCTTGATGCCCTTTC	CGGAGACTGTTAAACCGGAA
Chr08	76.9	C08-BARC-040893-07862	C08-BARC-040893-07862_F	Chr08	11,761,612	11,761,593	C08-BARC-040893-07862_R	Chr08	11,761,515	11,761,534	AAACCCTTAAAATTAGTAAA	GCTGCATGTGAGCTTCCTTG
Chr08	76.9	GMES2791	GMES2791 F	Chr08	11,786,242	11,786,261	GMES2791 R	Chr08	11,786,426	11,786,407	GTTGCTGCTCTTGGTCCATT	AACATCCAACCATTTTCCCA
Chr08	76.9	GMES0759	GMES0759_F	Chr08	11,815,379	11,815,398	GMES0759_R	Chr08	11,815,583	11,815,564	CTCTCTCGCCCTCTCTCTCA	TAATCGTTTCGGGAACCTTG
Chr08	80.2	C08-BARC-040357-07717	C08-BARC-040357-07717_F	Chr08	12,898,248	12,898,267	C08-BARC-040357-07717_R	Chr08	12,898,343	12,898,324	AAAAGTAGCAGGTTCTGGAG	ATCCAACAAGGGGCAATTTG
Chr08	81	s023900448-2	s023900448-2_F	Chr08	13,168,884	13,168,906	s023900448-2_R	Chr08	13,169,033	13,169,005	TGCTTAAAGTTGACTGCCTTTGT	AAACAATTAAGCTATAGGTAGAATGAACA
Chr08	81.3	GMES2839	GMES2839_F				GMES2839_R				CACACTCGTTTGGTTTCATCTC	GTGCACGTTCTCACAGAGGA
Chr08	82.6	GMES4195	GMES4195_F	Chr08	13,575,937	13,575,918	GMES4195_R	Chr08	13,575,578	13,575,597	GCAAGAATCGCACAACAGAA	ATGGTTGTTGAAAACCGAGG
Chr08	83.1	GMES6325	GMES6325_F	Chr08	13,790,853	13,790,872	GMES6325_R	Chr08	13,791,062	13,791,043	GAAGGACAGTGAGGGTGAGG	CCCTTGGCAGTCAACTCATT
Chr08	84.5	GMES4207	GMES4207 F	Chr08	14,134,869	14,134,888	GMES4207 R	Chr08	14,135,145	14,135,126	TTTCTGAAATAGCGTGCCCT	TTGAGTCCATTTTGTTGGCA
Chr08	85	GMES3946	GMES3946_F	Chr08	14,212,772	14,212,791	GMES3946_R	Chr08	14,213,046	14,213,027	CCCTTTCTCAAAACCCCATT	AGTTTTGGTCACAACGGAGG
Chr08	86.1	C08-BARC-043207-08556	C08-BARC-043207-08556_F	Chr08	14,365,429	14,365,409	C08-BARC-043207-08556_R	Chr08	14,365,330	14,365,349	GACTCTTCTCTTCCATCTAAC	CAGATCAAGCTTATAACAAC
Chr08	87.2	C08-BARC-016119-02287	C08-BARC-016119-02287_F	Chr08	14,522,890	14,522,909	C08-BARC-016119-02287_R	Chr08	14,522,970	14,522,951	TTCTCTCTTAGAGCACTCCC	TGGGTCTTTTACTAGGGTCG
Chr08	88	Sat 129	Sat 129 F	Chr08	14,659,970	14,659,950	Sat 129 R	Chr08	14,659,734	14,659,758	GGGGACTCCCTCTCCAGAAGTAAT	GGGAGCAATTGATAAGTGTGAAAATAAT
Chr08	89.6	GMES6201	GMES6201_F	Chr08	14,792,218	14,792,199	GMES6201_R	Chr08	14,791,924	14,791,941	ATTCGGTAACCTCTCCCTCC	GCTGGAGAGTATGAAACGCC
Chr08	93	GMES0714	GMES0714_F	Chr08	15,071,661	15,071,642	GMES0714_R	Chr08	15,071,388	15,071,410	TGGAAACTGCTGGTGTTTTG	TTCAATGTTAAGGTTTAGGCACC
Chr08	95.7	s014601205-2	s014601205-2 F	Chr08	15,642,862	15,642,884	s014601205-2 R				TGCTCTGTTGTTGAATAAGGGAT	ATGAAGATCGAACTCATTAAGGC
Chr08	96.8	C08-BARC-028281-05811	C08-BARC-028281-05811_F	Chr08	15,848,413	15,848,432	C08-BARC-028281-05811_R	Chr08	15,848,495	15,848,475	CCTTGGAGGTTAGATTTGTG	CCAATGTCAAACTCTAAGAAG
Chr08	96.8	s014601595-2	s014601595-2_F	Chr08	16,033,570	16,033,548	s014601595-2_R	Chr08	16,033,183	16,033,205	GGTTGAAACAAGACCCATTATCA	TCCTACTGGGACTAATACAGCGA
Chr08	96.8	s011302441-2	s011302441-2_F	Chr08	16,177,660	16,177,638	s011302441-2_R	Chr08	16,177,301	16,177,328	AGTAATCTTCCGGACCACACAAT	ACTTGTAGAAATTAACTATCTTACCTTT
Chr08	97	s011302137-2	s011302137-2 F	Chr08	16,482,313	16,482,291	s011302137-2 R	Chr08	16,482,164	16,482,193	GAGAGTCTGAGACCGATGTGAAC	TTCTCCTTGTATAGTGATTATAGCTAGTGT
Chr08	97	C08-BARC-042491-08277	C08-BARC-042491-08277_F	Chr08	16,557,082	16,557,101	C08-BARC-042491-08277_R	Chr08	16,557,153	16,557,135	CTATGCTTTGTTTGAAACCC	CAAACAGTTGAAAAACACC
Chr08	98	s011301837-2	s011301837-2_F	Chr08	16,782,460	16,782,438	s011301837-2_R	Chr08	16,782,273	16,782,294	AATGGATCAAATTTAGCAAGTTA	ATGCATGGAACGATCATTGTAA
Chr08	102.5	GMES3930	GMES3930_F	Chr08	17,086,545	17,086,528	GMES3930_R	Chr08	17,086,459	17,086,478	CGAGAACACTCTATCCCTCGTT	GATTGCACCATGTTGGTCAG
Chr08	104.7	T000817572m	T000817572m_F	Chr08	17,504,572	17,504,595	T000817572m_R	Chr08	17,504,899	17,504,877	GGGTTCAATAACAAGGCTTAATTT	TAATATGGCAAATGTTAATCGGG
Chr08	109.5	GMES1495	GMES1495_F	Chr08	18,012,683	18,012,702	GMES1495_R	Chr08	18,012,901	18,012,882	CGTGGAGAAGAATTGAAGCC	TGTTTATCGGAATGCGAACA
Chr08	112	Satt437	Satt437_F	Chr08	18,870,205	18,870,178	Satt437_R	Chr08	18,869,836	18,869,860	ATCCCATTGTAGTGCATTTATAGTGACG	GGTAACCTATTTTTTATGCTTCTGT
Chr08	114	s001810280-2	s001810280-2 F	Chr08	19,211,817	19,211,797	s001810280-2 R	Chr08	19,211,619	19,211,643	CCTCTTTGGCAGTTAAAGGCT	TGTTAGTTAAGACACAAAGTGCGTG
Chr08	114.5	GMES1220	GMES1220_F	Chr08	19,299,852	19,299,832	GMES1220_R	Chr08	19,299,600	19,299,619	CCCAGATGAGATGAAGACCAA	ATCCCCTAAGCCTCCCACTA
Chr08	114.8	s001809965-2	s001809965-2_F	Chr08	19,529,672	19,529,650	s001809965-2_R	Chr08	19,529,487	19,529,507	TTTGTCTGTTTGAGGAACCATTT	CACTTGCATGCCACGATATTA
Chr08	114.8	GMES1463	GMES1463_F	Chr08	19,675,865	19,675,884	GMES1463_R	Chr08	19,676,078	19,676,059	TTGAACCCTCCTCCCTCTTT	CCGAAAATCTCGAATACCCA
Chr08	115	s001809561-2	s001809561-2 F	Chr08	19,935,031	19,935,009	s001809561-2 R	Chr08	19,934,832	19,934,854	TGGAGAGAGACATCTACGAAAGT	GGCCCATGAATCTATACCAATTA
Chr08	115.6	s001809121-2	s001809121-2_F	Chr08	20,375,977	20,375,955	s001809121-2_R	Chr08	20,375,835	20,375,862	TTTCTCATTATTTCCCAACTGAT	TCACCTATTAAATTTATGGATAACAGAA
Chr08	116.1	GMES0152	GMES0152_F	Chr08	20,402,006	20,402,025	GMES0152_R	Chr08	20,402,382	20,402,363	GCAAGGGCTTGACTCCTCTA	TTTTATTCTTTCCCGTCCCC
Chr08	117.2	C08-BARC-021629-04159	C08-BARC-021629-04159 F	Chr08	20,486,748	20,486,731	C08-BARC-021629-04159 R	Chr08	20,486,676	20,486,696	GAAGGAATGGTTAACAAT	CATCATTCTCAATGATGTTGG
Chr08	118.2	s001808569-2	s001808569-2_F	Chr08	20,927,974	20,927,952	s001808569-2_R	Chr08	20,927,591	20,927,617	TATTCAGCCGTTAACTTCAGTCC	TGCATAAGTACTAAACGAATAAGAGCA
Chr08	121	GMES5716	GMES5716_F	Chr08	21,801,686	21,801,710	GMES5716_R	Chr08	21,801,845	21,801,826	CACTCAGTTTCTGCCTCTTATTTTT	TGGCTGCAAGATGTTAGTGC
Chr08	125.6	T000822864l	T000822864l F				T000822864l R				CTGCTGATATCCTCACGATGAA	AAATACAGCATGGGTGTGATGA
Chr08	128.7	T000822923l	T000822923l F	Chr08	22,840,994	22,841,016	T000822923l R	Chr08	22,841,366	22,841,343	ATGTGATATGGGTGTCATGTTCA	CAAATTTAAATCCTTCCACTAACC
Chr08	132.7	T000823214l	T000823214l_F	Chr08	23,131,037	23,131,058	T000823214l_R	Chr08	23,131,415	23,131,392	CCCTATGGCCCTATCTGTAATA	CCCATGTAAATACTTCGATGTCAA
Chr08	134.9	T000823620l	T000823620l_F	Chr08	23,541,123	23,541,145	T000823620l_R	Chr08	23,541,491	23,541,469	TGATGTCCCATAACCCTGTTAAT	TTTATGGAACAGTTAACCCGATG
Chr08	136	T000825762l	T000825762l_F	Chr08	25,669,231	25,669,254	T000825762l_R				TGATATATGTTATCACGTACCACT	CAATTAAACAGAATGCACAACAG
Chr08	137	T000826069m	T000826069m_F	Chr08	25,977,322	25,977,344	T000826069m_R	Chr08	25,977,616	25,977,594	TAGGACACACCTAGTTGCTCACA	CATGCATTTCCAAGGTATCTTTC
Chr08	137	T000826836s	T000826836s_F	Chr08	26,726,088	26,726,110	T000826836s_R	Chr08	26,726,380	26,726,358	ATACCAGAGATCAGCGGAGTGAT	AAAGTGTTCTACCTGGATGGATG
Chr08	137.3	T000831023s	T000831023s_F	Chr08	31,677,587	31,677,609	T000831023s_R	Chr08	31,677,782	31,677,759	CACTCTTGTGCTGAACAACCTTA	GACCATATGATGTGCAGTTCTTTC
Chr08	138.7	s002900066	s002900066 F	Chr08	37,208,487	37,208,465	s002900066 R	Chr08	37,208,188	37,208,211	AGGGATGAGACTGTAGCTCTGTG	GGGAATATTGGTAAATATTTGTGC
Chr08	139.7	s014700009	s014700009_F	Chr08	38,802,852	38,802,831	s014700009_R	Chr08	38,802,582	38,802,604	AAGAGGTTGAAGAAACTGACGC	AACATCATTCAAGCACCCATATC
Chr08	141.6	GMES3015	GMES3015_F	Chr08	39,397,561	39,397,544	GMES3015_R	Chr08	39,397,290	39,397,309	TTGACACTGTTTCACAGGGC	TGTGTCCACCGCATACAAGT

Chr08	142.8	T000839074s	T000839074s_F	Chr08	39,705,950	39,705,974	T000839074s_R	Chr08	39,706,140	39,706,118	TTGTTTACAGTTTATTCACCAAGAA	TTGCTAGGAAATAGCTCTTGGAA
Chr08	143.5	C08-BARC-042889-08449	C08-BARC-042889-08449_F	Chr08	39,863,324	39,863,343	C08-BARC-042889-08449_R	Chr08	39,863,417	39,863,398	TGTCACTTGGATACCACTGC	AGATCCAATGGCACACTTCG
Chr08	143.7	T000839411s	T000839411s_F	Chr08	40,043,288	40,043,310	T000839411s_R	Chr08	40,043,445	40,043,423	TGAAACACATTTGACTGCACCTA	TGACTTGTCATGAACTAAATGCG
Chr08	145.6	T000840052s	T000840052s_F	Chr08	40,678,607	40,678,629	T000840052s_R	Chr08	40,678,796	40,678,773	TTATAATTTCACTACGCAATGGG	AATGCACTGACGAAGCTAGACTAA
Chr08	149.5	T000840473s	T000840473s_F	Chr08	41,107,697	41,107,719	T000840473s_R	Chr08	41,107,906	41,107,884	CAAATGTTCTGTTCCATTGGTTT	TTGAACATGAAGTGGTAACTTGG
Chr08	150	T000840975l	T000840975l_F	Chr08	41,609,114	41,609,136	T000840975l_R	Chr08	41,609,479	41,609,456	ATGTGACTTGTTCGTGTGAGAGA	GCAAGACGTTCTGACAAGGTACTA
Chr08	151.4	C08-BARC-028831-06024	C08-BARC-028831-06024_F	Chr08	42,173,880	42,173,899	C08-BARC-028831-06024_R	Chr08	42,173,969	42,173,950	CATGCTTAATTAATCCCCCC	GACCAGTTAACAGATCAACA
Chr08	151.4	Satt209	Satt209_F	Chr08	42,189,884	42,189,903	Satt209_R	Chr08	42,190,031	42,190,006	GTGGATAAAAGCCATCTCTA	TCCATAGGCTTAATTCTTATGATGTT
Chr08	154.4	s022700259	s022700259_F	Chr08	42,769,862	42,769,886	s022700259_R	Chr08	42,770,218	42,770,196	AAATAGGTCATCTACCTCTTGTTTG	CTTGAGTTATCTTTCTCAAGCCT
Chr08	159.2	GMES0681	GMES0681_F	Chr08	43,898,297	43,898,278	GMES0681_R	Chr08	43,898,105	43,898,124	CACAATATTTGGACCGAGGG	TCCATCGCGTCAATTACAAA
Chr08	161.1	s018600015	s018600015_F	Chr08	43,979,150	43,979,172	s018600015_R	Chr08	43,979,307	43,979,285	TTTGACTGATGATCCTAATCGCT	ATGTCAAGGGATTTCTGTCTCAA
Chr08	165.3	T000843805s	T000843805s_F	Chr08	44,638,754	44,638,776	T000843805s_R	Chr08	44,638,958	44,638,942	AATTAGCAATGTCGCTTGGATTA	GATTCATGCGTGCAGGG
Chr08	168.6	Satt409	Satt409_F	Chr08	45,105,010	45,105,036	Satt409_R	Chr08	45,105,191	45,105,166	CCTTAGACCATGAATGTCTCGAAGATA	CTTAAGGACACGTGGAAGATGACTAC
Chr08	169.2	GMES1684	GMES1684_F	Chr08	45,194,777	45,194,758	GMES1684_R	Chr08	45,194,554	45,194,573	TGACATCCACCTCTCAGCAG	TCTCTTGGGGATCATTCTCG
Chr08	172.9	GMES2829	GMES2829_F	Chr08	45,727,519	45,727,538	GMES2829_R	Chr08	45,727,788	45,727,769	GGCCTTGAAAAATCATGCAC	ACAATCACAGAAATCGTGCG
Chr08	175.2	T000845100m	T000845100m_F	Chr08	45,949,698	45,949,720	T000845100m_R	Chr08	45,949,924	45,949,902	TTTGCTTTAGATCCCATACCTCA	AGGGAGTAGTGAAGCCTGAGTTT
Chr08	180.1	T000845306s	T000845306s_F	Chr08	46,156,506	46,156,528	T000845306s_R	Chr08	46,156,714	46,156,693	TAGTTCTTTGCACGATCATTTCC	GGCTATCTTGGAGCCGTTACTA
Chr08	186.3	s011900983-2	s011900983-2_F	Chr08	46,913,930	46,913,908	s011900983-2_R	Chr08	46,913,730	46,913,751	CAACCTTAGCCAAAGTAGGTTCC	GTTAGCAATGCTCCCTAACCAC
Chr08	189.8	GMES1414	GMES1414_F	Chr08	47,210,744	47,210,724	GMES1414_R	Chr08	47,210,485	47,210,504	CAAGCAAGAATTGGAATTGGA	AGAAGGATGCAGTGTGGCTT
Chr08	190.1	Satt429	Satt429_F	Chr08	47,216,205	47,216,229	Satt429_R	Chr08	47,216,468	47,216,441	ACCATCATCTAATCACAATCTACTA	TCCCCATCATTTATCGAAAATAATAATT
Chr08	193.1	T000846583l	T000846583l_F	Chr08	47,432,316	47,432,337	T000846583l_R	Chr08	47,432,667	47,432,649	ATACTCAATCCGGGCCTACAAT	TTTGGGTGAAATTAACGAT
Chr08	195.1	Satt378	Satt378_F	Chr08	47,609,912	47,609,889	Satt378_R	Chr08	47,609,752	47,609,773	TACAATGACGAGAGGAGAAGAGAC	TGAAACCACAAACAACAACAAC
Chr09	0	GMES0319	GMES0319_F	Chr09	253,788	253,808	GMES0319_R	Chr09	254,051	254,032	CGAAACACACGAATAGACACG	TGACAAGCCACCATTCATGT
Chr09	0.8	Satt715-2	Satt715-2_F	Chr09	376,721	376,698	Satt715-2_R	Chr09	376,333	376,355	ACGTGACTAACTAAATGACAAATCA	CGTGACCCACCCATTTCTCTTAT
Chr09	6	T000900767m	T000900767m_F	Chr09	767,727	767,749	T000900767m_R	Chr09	768,059	768,037	TTGTCAATGTTCTCCGTTCTACA	TTCTTGTGGATCGCTTCTAATTT
Chr09	6.1	C09-BARC-028004-06715	C09-BARC-028004-06715_F	Chr09	775,250	775,269	C09-BARC-028004-06715_R	Chr09	775,315	775,296	TGGGAACAGTTCCCATGTTG	ATAGGTGGCGGCATTAAAGG
Chr09	8.5	GMES1035	GMES1035_F	Chr09	1,175,143	1,175,124	GMES1035_R	Chr09	1,174,904	1,174,923	CATTGATCAGATGTGCCACC	AAAAACAGTTCCTCCCCCTC
Chr09	11.8	T000901542s	T000901542s_F	Chr09	1,556,370	1,556,394	T000901542s_R	Chr09	1,556,560	1,556,538	CAAAGACATATGCAATCAAGTAGCA	CTTCGATGAGACCTAAACGTCAA
Chr09	14.2	T000901811s	T000901811s_F				T000901811s_R				GGCTTGACATCAATAGTTCACAAA	CCAAATCAAATTATTACGATTGTT
Chr09	15	T000901942s	T000901942s_F	Chr09	1,956,860	1,956,884	T000901942s_R	Chr09	1,957,049	1,957,027	TCCATATAGCACATGTACTTGACTT	GAACGAGAGAGAAATGTCAGACG
Chr09	15.8	Satt242	Satt242_F	Chr09	2,245,610	2,245,587	Satt242_R	Chr09	2,245,421	2,245,444	TTGATCAGGTCGATTTTTATTTGT	AGTGCCAACTAACTACTTTTATGA
Chr09	16.6	Sat_119	Sat_119_F				Sat_119_R	Chr09	2,399,376	2,399,397	TAGGCTTTCAATTTGCAGAACT	GTTAGGTGTCCCAAGCAACTTA
Chr09	20	C09-BARC-044791-08808	C09-BARC-044791-08808_F	Chr09	2,766,984	2,766,965	C09-BARC-044791-08808_R	Chr09	2,766,921	2,766,939	TTCCAGATTTGGGAGATGGG	CATGCGGGTGCATTTGACA
Chr09	21.6	GMES1693	GMES1693_F	Chr09	2,900,979	2,900,959	GMES1693_R	Chr09	2,900,773	2,900,792	AAAAATCATTCATTCCCAGCC	GGATTCAGATTCGGGTGAAA
Chr09	22.1	C09-BARC-010523-00698	C09-BARC-010523-00698_F	Chr09	2,967,138	2,967,157	C09-BARC-010523-00698_R	Chr09	2,967,234	2,967,215	CTACTACAGTTTACCATCGG	CAATAATGACATAGTTAACA
Chr09	23.8	T000903106s	T000903106s_F	Chr09	3,145,423	3,145,445	T000903106s_R	Chr09	3,145,586	3,145,564	ATATTCTCTTGTGTGTGGCTCGT	ATGCTTCATTCAGTCTAGAGGCA
Chr09	25.2	GMES2329	GMES2329_F	Chr09	3,356,138	3,356,157	GMES2329_R	Chr09	3,356,275	3,356,258	TCGTGCAAGGACTTCTGATG	ACCACTTCGTATCATTTTCCA
Chr09	30.2	T000903912s	T000903912s_F	Chr09	3,954,338	3,954,360	T000903912s_R	Chr09	3,954,501	3,954,479	TATACTGCAGGTCTTTGCATGTG	GAATCAAGGGCACTCTTATGAAA
Chr09	31.3	s008602030	s008602030_F	Chr09	4,205,080	4,205,058	s008602030_R	Chr09	4,204,720	4,204,744	AGCAAGTCACAGTCCATTGTTTA	AAAGAAGCAATTGATTGTAGAGAGA
Chr09	32.9	s008601784	s008601784_F	Chr09	4,453,376	4,453,355	s008601784_R	Chr09	4,453,225	4,453,245	CCATCAAACCACTCTCCAGAAG	GCGGTGAGAAGGAACAATACA
Chr09	33.4	C09-BARC-041991-08151	C09-BARC-041991-08151_F	Chr09	4,557,685	4,557,704	C09-BARC-041991-08151_R	Chr09	4,557,777	4,557,758	GGGTTTCGCTTTATTGGTTG	GGGACAAGGGAGAAAAAAGC
Chr09	35.5	s008601429	s008601429_F	Chr09	4,809,297	4,809,275	s008601429_R	Chr09	4,809,124	4,809,146	TTCGACCATAGCTTAGATTTGTG	GGATCGAATCCATAGCATCATTA
Chr09	36.2	s008601107-2	s008601107-2_F	Chr09	5,121,281	5,121,254	s008601107-2_R	Chr09	5,121,083	5,121,102	CAACTTGTTAATAGAAACTCTCTTTGGA	TCCCTCTAGGACAAGACATAGGA
Chr09	39.2	GMES4146	GMES4146_F	Chr09	5,675,176	5,675,157	GMES4146_R	Chr09	5,675,070	5,675,089	GCGATCTTTCGAAAAGCCTA	TGAAATTCATGCTGGAATCG
Chr09	44	GMES1010	GMES1010_F	Chr09	6,046,111	6,046,092	GMES1010_R	Chr09	6,045,995	6,046,014	GGAAGGGTTTGAAGGAAGGT	GGGACTTCCACTGCGTGTAT
Chr09	44.2	C09-BARC-026035-05233	C09-BARC-026035-05233_F	Chr09	6,074,953	6,074,972	C09-BARC-026035-05233_R	Chr09	6,075,042	6,075,023	AGATCGAAAGACCTGACCTG	ATGACCTGACTCGTTCCAGC
Chr09	44.4	s025200027	s025200027_F	Chr09	6,149,183	6,149,161	s025200027_R	Chr09	6,148,818	6,148,840	ATTAACCATTTGTTGGTGGTTCA	TTAATTTGCCCAATTTCTCTCTG
Chr09	46.2	C09-BARC-021491-04132	C09-BARC-021491-04132_F	Chr09	6,551,649	6,551,668	C09-BARC-021491-04132_R	Chr09	6,551,739	6,551,720	ATAAACACCAGACTGGCCAC	TCTAGCTCTATGTTGCTCTG
Chr09	47.6	Satt178	Satt178_F	Chr09	6,912,737	6,912,757	Satt178_R	Chr09	6,912,897	6,912,877	GGGAAAATTCTTTTCATATAGATG	GGGGTTGAGATATTTTGTTCATAC
Chr09	50.6	C09-BARC-015513-01990	C09-BARC-015513-01990_F	Chr09	7,391,650	7,391,669	C09-BARC-015513-01990_R	Chr09	7,391,748	7,391,729	GGTTACACCACTAAGGTGTC	GTCACTGTAGTAGAGACTCA
Chr09	51.4	C09-BARC-043033-08504	C09-BARC-043033-08504_F	Chr09	7,994,015	7,994,034	C09-BARC-043033-08504_R	Chr09	7,994,100	7,994,081	ACCATTTGCAGTTTTTTGGG	ATGCTAAAACCGATGGGCTG
Chr09	51.4	Satt555	Satt555_F	Chr09	8,020,600	8,020,584	Satt555_R	Chr09	8,020,334	8,020,354	GTTGGCTTTGATGATGT	TTACCGCATGTTCTTGGACTA
Chr09	52.5	C09-BARC-041083-07904	C09-BARC-041083-07904_F	Chr09	8,810,069	8,810,050	C09-BARC-041083-07904_R	Chr09	8,809,982	8,809,999	ACAAGAGGCCAATTTGTCCC	TGCTTGCTTGTGTAGAATGC
Chr09	53	C09-BARC-042003-08157	C09-BARC-042003-08157_F	Chr09	9,898,684	9,898,665	C09-BARC-042003-08157_R	Chr09	9,898,592	9,898,610	AGTTGTCTTGCACTAGTTGG	CTAGATCTCTCACAATGACC
Chr09	53.6	GMES1323	GMES1323_F	Chr09	10,568,065	10,568,046	GMES1323_R	Chr09	10,567,885	10,567,904	TCCATCTTCCCCATCATCTC	GGACTAAAATAGGGGGCAGC
Chr09	53.6	Satt441	Satt441_F	Chr09	11,224,401	11,224,379	Satt441_R	Chr09	11,224,120	11,224,139	AAACCCACCCTCAAAAATAAAAA	AAATGCACCCATCAATCACA
Chr09	54.6	C09-BARC-014761-01655	C09-BARC-014761-01655_F	Chr09	12,675,034	12,675,015	C09-BARC-014761-01655_R	Chr09	12,674,950	12,674,969	AATCAGGTGGGTGTCTTCAG	AAGCCCCCTGTTAAGAAACC
Chr09	54.9	Sct_196	Sct_196_F	Chr09	12,797,131	12,797,113	Sct_196_R	Chr09	12,796,877	12,796,895	GGTCGAAGGTAGGGATTTA	GATGGATCTATGTTCAGAA
Chr09	55.2	s032000015	s032000015_F				s032000015_R	Chr09	18,245,857	18,245,832	TGAGTGTGGGTAGTCCAAGAAAT	GAAAGGTATACAGGTAAACATATTGG
Chr09	55.2	s005900863-2	s005900863-2_F	Chr09	19,202,176	19,202,196	s005900863-2_R	Chr09	19,202,325	19,202,308	AGAATGGCTCAAGGAGGTGTT	CCCTTCCTTTCTGGGTCC
Chr09	55.2	C09-BARC-042823-08431	C09-BARC-042823-08431_F	Chr09	19,421,778	19,421,759	C09-BARC-042823-08431_R	Chr09	19,421,680	19,421,699	ACAAAAGCCAATGACATGAC	AGAGAACACAGGAGGTAAGG
Chr09	56	C09-BARC-029275-06135	C09-BARC-029275-06135_F	Chr09	22,065,774	22,065,756	C09-BARC-029275-06135_R	Chr09	22,065,691	22,065,710	GGCTACAATCATCTTAAAC	GTTCTGTTCCATAGAACTTC
Chr09	57.6	GMES0973	GMES0973_F	Chr09	29,228,525	29,228,544	GMES0973_R	Chr09	29,228,812	29,228,793	CAGCACCGTAATGTGGTGAG	TTTTTATGGGTGGCTTCTGG
Chr09	61.9	T000931476m	T000931476m_F	Chr09	34,101,334	34,101,356	T000931476m_R	Chr09	34,101,639	34,101,617	ATTTGTGCTTCAAGGCTAACTCA	CAAGCATATTACAGGGATCCAAA
Chr09	62.7	LFsoy1	LFsoy1_F				LFsoy1_R	Chr09	35,651,844	35,651,824	GTACTTCTGGATCTGTCACAG	CTCATTTCCCATCGAGCAACC
Chr09	65.6	GMES5601	GMES5601_F	Chr09	37,428,467	37,428,448	GMES5601_R	Chr09	37,428,109	37,428,128	CCAAATCAGCTTCAGTGCAA	AACCCGTTAAATACACGCCA
Chr09	67.3	Satt559	Satt559_F	Chr09	37,762,468	37,762,489	Satt559_R	Chr09	37,762,771	37,762,750	ATTCGAAATATTAGTCAAACAA	CGAGCATATAGTCGGTAAAGTT
Chr09	71.5	Satt273	Satt273_F	Chr09	38,799,180	38,799,161	Satt273_R	Chr09	38,798,908	38,798,931	CCTGATTACATTATCGCTTA	GCCTTTCGTTCTCAAACTGAGAGT
Chr09	72.9	C09-BARC-021551-04138	C09-BARC-021551-04138_F	Chr09	38,943,196	38,943,177	C09-BARC-021551-04138_R	Chr09	38,943,102	38,943,121	TGTCTCTGAACTTTTTGAGC	GCTGTAGTAAACTAACTTAG
Chr09	74.8	T000936837l	T000936837l_F	Chr09	39,409,517	39,409,539	T000936837l_R	Chr09	39,409,866	39,409,848	GTACAGGCTGCACAAACACAAAT	AAAGCACCTGGGAGCAGAG
Chr09	76.4	s000501043-2	s000501043-2_F	Chr09	39,879,363	39,879,340	s000501043-2_R	Chr09	39,879,176	39,879,198	CCACGTGCCAATAATATCTATCTC	ATAGCACAATAGGTAGGTGTGGG
Chr09	77.5	s000500658-2	s000500658-2_F	Chr09	40,292,169	40,292,147	s000500658-2_R	Chr09	40,291,855	40,291,874	TTGATGTGATATACAACGAGTTT	TGAGCTCAACATTAAGCCAT
Chr09	81.2	Satt499	Satt499_F	Chr09	40,583,101	40,583,081	Satt499_R				GCAGAGATAATTGTATTTTTG	CTGCCCACTAGGGAACGAAAGATGA
Chr09	81.8	s000500003-2	s000500003-2_F				s000500003-2_R				TGACTTATGCAATAACAACAGCG	CACATGTGTTTGGTTTACAATA
Chr09	85.6	s003005833-2	s003005833-2_F	Chr09	41,351,159	41,351,181	s003005833-2_R	Chr09	41,351,343	41,351,320	TCCATATAAAGTATAGCTCGGAA	TGGATGACATCTGTGTACATTTGA
Chr09	88.1	C13-BARC-044609-08740	C13-BARC-044609-08740_F	Chr09	41,745,058	41,745,039	C13-BARC-044609-08740_R	Chr09	41,744,963	41,744,982	GAGTGATGCACTAAAGTTTC	GGATTAAAATGATGGAACTG
Chr09	88.9	s001302387.1	s001302387_F	Chr09	41,791,652	41,791,669	s001302387_R	Chr09	41,791,753	41,791,731	CCACCGACGTGTCGCACGATGAGAGGTAGGCACAA	ATCAGATTCTCGATCAATTCTTT

Chr09	90.2	Satt260	Satt260_F	Chr09	42,407,488	42,407,466	Satt260_R	Chr09	42,407,266	42,407,288	CCAAATGTATACTTTAAATTCTT	GGTTTAGCTAAAATAGTTCGTGC
Chr09	90.5	GMES2537	GMES2537_F	Chr09	42,452,635	42,452,651	GMES2537_R	Chr09	42,452,907	42,452,888	CAAGTTCAAATGCAGAGGCA	TATCTGCTGCTGCTGCCTAA
Chr09	94	GMES2511	GMES2511 F	Chr09	42,934,203	42,934,222	GMES2511 R	Chr09	42,934,319	42,934,304	CACGAAAAATCATCCACCCT	GCACCCATGATTCTCCTGTT
Chr09	97.5	T000940539l	T000940539l_F	Chr09	43,215,354	43,215,376	T000940539l_R	Chr09	43,215,731	43,215,709	TCGCTTCTCTCGTATCTTTATCG	TCGTCACCTAACCGAACAGTAGT
Chr09	98.5	s013801912-2	s013801912-2_F	Chr09	43,386,811	43,386,789	s013801912-2_R	Chr09	43,386,693	43,386,718	TTACAATTATCAGACGCAAGCAA	TGACAGATCTCCATACATAATTGAAA
Chr09	100.4	T000941057s	T000941057s_F	Chr09	43,769,933	43,769,956	T000941057s_R	Chr09	43,770,043	43,770,021	AACTTTGTGCATCCTTCTTAATTT	CAACTATTAGGTGTCCTCACAAA
Chr09	105.2	GMES1553	GMES1553 F	Chr09	44,315,360	44,315,342	GMES1553 R	Chr09	44,315,155	44,315,174	TTGATAATGTCGTCGGCGT	AGCATCTTGAAAATCGGGTG
Chr09	109.3	T000941863l	T000941863l_F	Chr09	45,057,175	45,057,197	T000941863l_R	Chr09	45,057,521	45,057,499	TTAAGTGTTTAGATGGGTGCTTC	TAGTCTGGTTTGCTTGATATCGC
Chr09	112.3	s013800540-2	s013800540-2_F	Chr09	45,243,714	45,243,692	s013800540-2_R	Chr09	45,243,515	45,243,537	CAAATTAGTGTGATAAGGCATAA	TCTGGATATTGTAAAGGGATTCA
Chr09	113.1	GMES0221	GMES0221 F	Chr09	45,646,083	45,646,102	GMES0221 R	Chr09	45,646,250	45,646,231	TTTGAGCAGAGGAGGAGGAG	ACGAGGGAGTCCGGTACTTT
Chr09	113.4	C09-BARC-045189-08902	C09-BARC-045189-08902_F	Chr09	45,709,316	45,709,335	C09-BARC-045189-08902_R	Chr09	45,709,395	45,709,376	AATGGAATAGGAGGAGGAGG	TTGATGTCGACTTCGAGGAG
Chr09	116.7	Satt196	Satt196_F	Chr09	46,513,953	46,513,977	Satt196_R	Chr09	46,514,144	46,514,121	TTGGGAAATAGTGATTGAGGTAAAA	AAATCCCCATTGAATGAGAATAAG
Chr09	116.7	`4-8	`4-8_F	Chr09	46,519,265	46,519,287	`4-8_R	Chr09	46,519,331	46,519,309	GTGGTTTCACACCTTCTATGTGA	CCTCCACACTGCAAAACACTAAA
Chr09	118.6	GMES0633	GMES0633 F	Chr09	47,017,069	47,017,088	GMES0633 R	Chr09	47,017,238	47,017,219	GCCTGTGGTTGGTCTTCATT	AAAACCATATGCTTGCGGAC
Chr09	119.9	C09-BARC-042081-08175	C09-BARC-042081-08175_F	Chr09	47,193,795	47,193,815	C09-BARC-042081-08175_R	Chr09	47,193,885	47,193,867	CGTGAAAACATAAAAGATGAG	CATTTTCCTTTATGAGGAG
Chr09	121.8	GMES1280	GMES1280_F	Chr09	47,438,286	47,438,267	GMES1280_R	Chr09	47,438,032	47,438,051	TTGCAATGGAATCAATCAGG	CATGCAGGCAGCAACTTAAA
Chr09	126	C09-BARC-031123-07000	C09-BARC-031123-07000_F	Chr09	48,171,225	48,171,206	C09-BARC-031123-07000_R	Chr09	48,171,144	48,171,163	TGATGAAGTTTAGTGAGGGC	GGTCTTCTAGCCACTGTAAG
Chr09	126.2	GMES0083	GMES0083_F	Chr09	48,182,472	48,182,453	GMES0083_R	Chr09	48,182,248	48,182,267	TGTGGAGTTTACCTCTGGGG	AAGTGGCACTCATCCCAAAC
Chr09	127.6	Satt588	Satt588_F	Chr09	48,618,067	48,618,046	Satt588_R	Chr09	48,617,941	48,617,963	GCTGCATATCCACTCTCATTGACT	GAGCCAAAACCAAAGTGAAGAAC
Chr09	128.8	GMES6570	GMES6570_F	Chr09	48,843,470	48,843,489	GMES6570_R	Chr09	48,843,750	48,843,731	TTGCGTTTGTCACCACTCTC	CCGTTCAGAAAAAGACCCAA
Chr09	129.7	T000945908s	T000945908s F	Chr09	49,104,114	49,104,135	T000945908s R	Chr09	49,104,280	49,104,261	AATTCATATTGGGTGATGCAGAG	AATATATCAGAGTTGGCAAAGGG
Chr09	129.7	T000946473s	T000946473s_F	Chr09	49,675,948	49,675,970	T000946473s_R	Chr09	49,676,151	49,676,126	CGATTTGCATCGTATGAAGATTT	GAATGGATTAGAAAGATTATCACTGG
Chr09	131.3	T000946713s	T000946713s_F	Chr09	49,918,247	49,918,274	T000946713s_R	Chr09	49,918,448	49,918,428	CCAAATTATCACATTTATTTGTATCTTC	AGTCAAATTGAATGGCTTCAG
Chr09	131.6	C09-BARC-029231-06131	C09-BARC-029231-06131_F	Chr09	50,019,002	50,019,021	C09-BARC-029231-06131_R	Chr09	50,019,078	50,019,059	GGTAAATCTGGTGTAGGTGG	CTTGTGTGGATTCTCTTGGC
Chr09	131.6	T000946842l	T000946842l F	Chr09	50,047,159	50,047,183	T000946842l R	Chr09	50,047,583	50,047,560	GGAATACTATTGACTGGAATATAAA	GATGTTTGACTCATGGAATCTTGA
Chr09	131.9	s032300008	s032300008_F	Chr09	50,067,403	50,067,430	s032300008_R	Chr09	50,067,861	50,067,837	TCATTATTACAACATTACTAAAGTGAGA	GGTTATGTCTAGCATAGCTTTATTT
Chr10	0	Sat_196	Sat_196_F	Chr10	174,815	174,794	Sat_196_R	Chr10	174,595	174,619	AAACGAGATACTAGGATTTTGACTT	AGCCTTAGGAGTAGTTAATGATGAT
Chr10	2.8	T001000586m	T001000586m F	Chr10	580,259	580,285	T001000586m R	Chr10	580,552	580,530	TGATGAATTTGAATTAGCTTAAGTGAG	AGTATAGAGCCGTGAGATTGTTT
Chr10	4.1	s016700850-2	s016700850-2_F	Chr10	847,622	847,644	s016700850-2_R	Chr10	847,820	847,796	AAATTCCAACAACATGCAGATTC	GAAATAGTGTACAACATCAATCAAA
Chr10	5.8	C10-BARC-017663-03094	C10-BARC-017663-03094_F	Chr10	967,582	967,601	C10-BARC-017663-03094_R	Chr10	967,668	967,649	GCCACTGGTAAATATTGCTC	GTAGGTGAGAATGAGTGACG
Chr10	6.4	T001001023s	T001001023s_F	Chr10	1,018,560	1,018,582	T001001023s_R	Chr10	1,018,748	1,018,726	AAGCAGAGTGCGGAGTAATTAAA	TAGCTGTGCGCTTTATGTAACAA
Chr10	6.9	T001001120s	T001001120s F	Chr10	1,115,240	1,115,262	T001001120s R	Chr10	1,115,452	1,115,428	GGTAAACCACCATCCTAGGAGAC	TGATGATGATAGTGAAGCTATGCAG
Chr10	7.7	T001001269l	T001001269l_F	Chr10	1,264,436	1,264,458	T001001269l_R	Chr10	1,264,801	1,264,779	CCAGGTCAAACTGTATTCCACAT	CTTCCTCTCTAAGAGGCTGCAAT
Chr10	11.3	Satt487	Satt487_F	Chr10	1,395,586	1,395,606	Satt487_R	Chr10	1,395,789	1,395,767	ATCACGGACCAGTTCATTTGA	TGAACCGCGTATTCTTTTAATCT
Chr10	15.7	T001001797s	T001001797s_F	Chr10	1,801,391	1,801,408	T001001797s_R	Chr10	1,801,600	1,801,580	CGTTGACACGTGATTGAT	CTCATGAGGCCTAACAATAAT
Chr10	18.4	T001002109l	T001002109l_F	Chr10	2,115,862	2,115,884	T001002109l_R	Chr10	2,116,227	2,116,202	CAAGCTCGAAGAGACAAATGTTA	TTTGTTTATCTATCCATCCTATATGT
Chr10	21.1	C10-BARC-029811-06423	C10-BARC-029811-06423_F	Chr10	2,376,804	2,376,785	C10-BARC-029811-06423_R	Chr10	2,376,732	2,376,751	TTCAATCTTTCTGAGCAGCC	ATCATATGTTCTGGAGGCCC
Chr10	21.2	s012400988-2	s012400988-2_F	Chr10	2,379,362	2,379,384	s012400988-2_R	Chr10	2,379,553	2,379,532	AATTCAGAGATTATACGGAATTG	AAAGCATGACATTCTCAAACATA
Chr10	23	GMES0676	GMES0676 F	Chr10	2,563,033	2,563,014	GMES0676 R	Chr10	2,562,788	2,562,807	CGAGCCTCACGCTTAAACTC	TTACGAGCAACTGTATGGCG
Chr10	23.9	Satt445	Satt445_F	Chr10	2,662,346	2,662,363	Satt445_R	Chr10	2,662,545	2,662,527	CATTGCATCGAATTATTA	TTGGAATTTGTGATTGACA
Chr10	24.9	GMES2487	GMES2487_F	Chr10	2,814,424	2,814,405	GMES2487_R	Chr10	2,814,207	2,814,226	TATCCTGGGTTGTAGGGTGG	TCCATTTGCTAGGTATCGGC
Chr10	24.9	GMES6337	GMES6337_F	Chr10	3,019,080	3,019,099	GMES6337_R	Chr10	3,019,376	3,019,357	AGGCAAAGGGGTTTGAGTTT	CCTTCCTTGAAGAAGCCTCC
Chr10	29.3	T001003390s	T001003390s F	Chr10	3,397,765	3,397,786	T001003390s R	Chr10	3,397,971	3,397,948	GGTGAAGTTGAGGATTGGTTTC	TGTCTAACACTGTTGTAACTTTGG
Chr10	32.9	GMES4797	GMES4797_F	Chr10	3,838,856	3,838,875	GMES4797_R	Chr10	3,839,267	3,839,248	ACAAACACAAGAACCCCAGC	TTCTTTGAGACGGGAATTGG
Chr10	36.2	C10-BARC-040995-07876	C10-BARC-040995-07876_F				C10-BARC-040995-07876_R	Chr10	4,244,683	4,244,664	GGGTTTTGCTTAGGGCAATT	TTTAAGGTGTATCCCCTTAC
Chr10	36.7	GMES1066	GMES1066 F	Chr10	4,375,117	4,375,098	GMES1066 R	Chr10	4,374,837	4,374,856	GCCAAATTTACGTGCTTTGC	ACGCCTAAAACCAAGAGTCG
Chr10	37.8	T001004527s	T001004527s_F	Chr10	4,543,294	4,543,316	T001004527s_R	Chr10	4,543,479	4,543,454	AGGGAGATGATGATACGAAGAAA	CCTACTGTGTGTTATTTAAGGGATGA
Chr10	37.8	T001004548m	T001004548m_F	Chr10	4,563,478	4,563,500	T001004548m_R	Chr10	4,563,689	4,563,667	AAATCCATTATTTCCCTCCATTT	TTGCAACACATTAAGCAGTGAGT
Chr10	40.1	T001004836m	T001004836m_F	Chr10	4,853,956	4,853,980	T001004836m_R	Chr10	4,854,214	4,854,192	CATTTGAATATAACCCTTCGATCTC	CTATTCCTACTCATTTGGACGGA
Chr10	42.3	Satt347	Satt347 F	Chr10	5,059,709	5,059,692	Satt347 R				CGCTTCCATTTTAAAGTA	GTCACCGTTGTATACCTA
Chr10	46	s022500055-2	s022500055-2_F	Chr10	5,442,533	5,442,557	s022500055-2_R	Chr10	5,442,851	5,442,829	TTTCCTCCTTTGTTTATATGTGTTT	GTTATTGTTTCCTTCTGCATTCG
Chr10	47.2	s022500108-2	s022500108-2_F	Chr10	5,496,300	5,496,323	s022500108-2_R	Chr10	5,496,516	5,496,494	TTTAGTTCCTACTGCCATAACTCA	TTCTCAAACGTTCTTTGCTTAGG
Chr10	48.5	s022500586-2	s022500586-2_F	Chr10	5,972,913	5,972,935	s022500586-2_R	Chr10	5,973,311	5,973,288	AGTATGTCACTCCCACCTTGTTT	AAATTCACGGAAAGGTCATATCAT
Chr10	49.7	s029400110	s029400110_F	Chr10	6,163,955	6,163,977	s029400110_R	Chr10	6,164,137	6,164,115	CAAATATTTCAGCAACCATTTGA	ATGGAGTTGATCTTTGATGATGG
Chr10	50.5	s026100018	s026100018_F	Chr10	6,285,251	6,285,276	s026100018_R	Chr10	6,285,620	6,285,598	TCTTCTACAAGGATACCTATAATTCA	TATTCATTTCTAGCTAGGTGCGG
Chr10	52.1	T001006551s	T001006551s_F	Chr10	6,578,105	6,578,127	T001006551s_R	Chr10	6,578,314	6,578,292	CCATCCCTACTTACATGGCATAC	TGGAAAGTCTTGGCTAAACAATG
Chr10	56	GMES1523	GMES1523 F	Chr10	7,133,205	7,133,224	GMES1523 R	Chr10	7,133,468	7,133,449	CAAACGGAACCGTAATCGTT	CTTCTTGCTCCTTCAAACGG
Chr10	57.8	s032900010	s032900010_F	Chr10	7,236,243	7,236,265	s032900010_R	Chr10	7,236,690	7,236,665	TGGATTGTGATTAGATGATGCTG	CATGAAATGGTATGGAGTATTTCTTT
Chr10	58.5	s018300465r	s018300465r_F	Chr10	7,860,352	7,860,373	s018300465r_R	Chr10	7,860,746	7,860,726	TGGTCGACTCTTTAATTTCCTTG	AAACGATAGGAGAGAGAAGGTGT
Chr10	59.2	Sat_221	Sat_221_F	Chr10	9,817,808	9,817,832	Sat_221_R				CCCTAAAATGGAGTAAAATGGAAGA	AAAGGAGCTAACTCAGTTGATTGA
Chr10	59.3	C10-BARC-042707-08378	C10-BARC-042707-08378 F	Chr10	10,143,798	10,143,779	C10-BARC-042707-08378 R	Chr10	10,143,728	10,143,747	GATTTGAACATTCCACTCAC	CAACATACACTGAGTGAAGG
Chr10	59.6	s012201678-2	s012201678-2_F	Chr10	10,179,150	10,179,172	s012201678-2_R	Chr10	10,179,298	10,179,279	TAAATTTGGTCCACTGGCTAAGA	CAAGACCGGATTTCGATCAG
Chr10	59.6	s020900037-2	s020900037-2_F	Chr10	11,570,823	11,570,845	s020900037-2_R	Chr10	11,570,961	11,570,943	GACGTGACACACGAATAAGAACA	AAATTCACATGCGCCAATC
Chr10	59.6	s019800659-2	s019800659-2 F	Chr10	11,902,673	11,902,651	s019800659-2 R	Chr10	11,902,478	11,902,501	CTAGAGCCTGCAGAGGTATTACG	GGATAATTTCAGGGACAGACACTC
Chr10	60.4	s019800028	s019800028_F	Chr10	12,526,953	12,526,931	s019800028_R	Chr10	12,482,164	12,482,186	CATGCTAATTGAGGGCTAAACAC	TTTAGCAATTTGTTCATGTCCTG
Chr10	60.4	Sat_291	Sat_291_F	Chr10	12,724,545	12,724,518	Sat_291_R	Chr10	12,724,232	12,724,258	ATGTGTGCAGGAATTAAATATATCAATA	AAGCCACAAAAATTAAGAATATAAAGC
Chr10	61.2	Satt633	Satt633_F	Chr10	12,960,308	12,960,331	Satt633_R	Chr10	12,960,438	12,960,415	GGGACACTATCGGCCTAGAAAGTT	GGGTGATAAAGTTCCCCCTCTAAG
Chr10	61.4	C10-BARC-040251-07694	C10-BARC-040251-07694 F	Chr10	16,543,548	16,543,567	C10-BARC-040251-07694 R	Chr10	18,079,953	18,079,972	GGAAACAAAGAGGCAAAAGG	CAGTCTGGAGGTAGTATATG
Chr10	61.7	s007900046	s007900046_F	Chr10	19,052,129	19,052,153	s007900046_R	Chr10	19,052,486	19,052,468	TTTCACAATCATATTAATGCACGTT	TTAGCATTCCTAATTAAGGGCAA
Chr10	61.7	GMES0208	GMES0208_F	Chr10	23,948,733	23,948,714	GMES0208_R	Chr10	23,948,345	23,948,364	TTCTCTCGGAGCCGCTATTA	GGAACTCCAGGAGAGGGAAC
Chr10	62.2	GMES0587	GMES0587_F	Chr10	28,940,120	28,940,101	GMES0587_R	Chr10	28,939,888	28,939,907	TCATCAACATTTTCTGCCCA	GTCAACCTCGACCTCAGAGC
Chr10	62.3	s027000323.1										
Chr10	63	GMES0684	GMES0684_F	Chr10	32,584,837	32,584,814	GMES0684_R	Chr10	32,584,684	32,584,703	TGACTCACACACACACTCTCTCTC	GAGCTGGCTCACCTTCAGTC
Chr10	63	Satt241	Satt241_F	Chr10	33,310,335	33,310,357	Satt241_R	Chr10	33,310,577	33,310,555	CTTGGTCTAAGAAAACTTTTGGT	GGGGGTTTTATCTCTTAAATGTG
Chr10	63.8	Satt262	Satt262 F	Chr10	36,042,564	36,042,546	Satt262 R	Chr10	36,042,318	36,042,337	CCCCATTAATGTTAACACA	GAGTTCAACGCATTCACCTT
Chr10	63.8	Satt473	Satt473_F	Chr10	36,113,531	36,113,506	Satt473_R	Chr10	36,113,274	36,113,299	ATCTCGACCTAGTTGTCCATGTTCAA	CGAGAGTTGCTAACTTTAGGATAGTG
Chr10	63.8	T001036463s	T001036463s_F	Chr10	36,988,423	36,988,445	T001036463s_R	Chr10	36,988,615	36,988,593	TTTAAAGGATTAGTCTTCGATCA	ATGATTGATCAACGAGTACCAAA

Chr10	66.9	T001036990s	T001036990s_F	Chr10	37,515,880	37,515,900	T001036990s_R	Chr10	37,516,089	37,516,067	CTCAGCCCATGGGTTATTCTT	ACGGATGGACCTTACAGATTGTT
Chr10	70.6	T001037597l	T001037597l_F	Chr10	38,120,184	38,120,206	T001037597l_R	Chr10	38,120,560	38,120,538	GAATGGAATTAATCTGGTCAGCA	TCTTTACACAAGGAAGGGATGAG
Chr10	74.6	s020800013-2	s020800013-2 F	Chr10	38,648,445	38,648,468	s020800013-2 R	Chr10	38,648,627	38,648,605	TGTAAGTCACAATTGAATGACTAT	ATGGTGAATTGGTGAAACAAATG
Chr10	79	T001038587s	T001038587s_F	Chr10	39,133,706	39,133,728	T001038587s_R	Chr10	39,133,903	39,133,876	ACATTCATGCAGGAAATTGACTT	TTAGACTTATATTCGGTATAATTAGAAG
Chr10	81.1	GMES4351	GMES4351_F	Chr10	39,349,454	39,349,432	GMES4351_R	Chr10	39,349,262	39,349,281	TGGATGAAAGAAAGTAAAAGGGA	CGGGTGCAGAAATGAGAAAT
Chr10	81.2	GMES0051	GMES0051_F	Chr10	39,389,635	39,389,616	GMES0051_R	Chr10	39,389,462	39,389,481	CTTTCATGTGCCGAGTCAGA	AGCACTGGATGAGTCCAACC
Chr10	81.2	GMES4281	GMES4281 F	Chr10	39,423,407	39,423,388	GMES4281 R	Chr10	39,423,303	39,423,322	CTCCCATGGAATCCGATCTA	CGTCGTAGTCCTCTTCGTCC
Chr10	82.8	s014200002	s014200002_F	Chr10	39,469,090	39,469,112	s014200002_R	Chr10	39,469,403	39,469,381	CATTGCATGAGTTCTTACACTAA	ACATTCGCAGGAACTGATCTTTA
Chr10	87.3	T001039320l	T001039320l_F	Chr10	39,874,736	39,874,758	T001039320l_R	Chr10	39,875,102	39,875,080	CACATTGATGCATTCCGTATTTA	GGAGAGGGCCTACTGTCACTTAG
Chr10	89.5	T001039788m	T001039788m F	Chr10	40,343,799	40,343,821	T001039788m R	Chr10	40,344,123	40,344,101	CTCTCTCACACGTACATGCACTC	AAACCTGAGGCTCTGACAATAAT
Chr10	91.1	T001039931l	T001039931l_F	Chr10	40,488,860	40,488,882	T001039931l_R	Chr10	40,489,225	40,489,203	GCCGCTTCATCTCCTAAGATAAT	GTTTGTGTCGTGTCCGTATCAAT
Chr10	91.4	C10-BARC-040653-07810	C10-BARC-040653-07810_F	Chr10	40,541,834	40,541,853	C10-BARC-040653-07810_R	Chr10	40,541,911	40,541,893	ACCTCCACTGAATCAATGCC	TGGCACAAAATAACAATGG
Chr10	93.3	T001040053s	T001040053s_F	Chr10	40,610,943	40,610,966	T001040053s_R	Chr10	40,611,109	40,611,087	TTCAATGAATTGCGTTATCAATTT	CGAACGAAAGATAAACGTTACGA
Chr10	95.7	T001040189s	T001040189s F	Chr10	40,746,859	40,746,881	T001040189s R	Chr10	40,747,048	40,747,026	ATATCCTTATTCCAACCCAATCG	TTGGTTGACGTCTGTAACACAAC
Chr10	97.1	T001040621s	T001040621s_F	Chr10	41,152,794	41,152,816	T001040621s_R	Chr10	41,152,993	41,152,971	AAGTTGGTACTACTGGCACCTTA	AATCCTTGCGGTATTGTTTCATA
Chr10	98.4	GMES4216	GMES4216_F	Chr10	41,456,897	41,456,878	GMES4216_R	Chr10	41,456,652	41,456,671	CTCAACATTCCCAAAGCCAT	TCTGCTTGTTTCCCCATGAT
Chr10	99	s022600649-2	s022600649-2_F	Chr10	41,690,742	41,690,726	s022600649-2_R	Chr10	41,690,593	41,690,612	AAGATGCAGCCTTTGGG	TAATTTGTGTGGGAATTGAAA
Chr10	101.1	s022600099	s022600099_F	Chr10	42,244,715	42,244,693	s022600099_R	Chr10	42,244,392	42,244,415	TTGTTGTTATCCTCATCCTCGTC	CAAACTTAATATTGTTTACGGTTT
Chr10	101.1	C10-BARC-032641-09002	C10-BARC-032641-09002_F	Chr10	42,293,798	42,293,779	C10-BARC-032641-09002_R	Chr10	42,293,720	42,293,739	GGAACAAAGCATTGAACCAC	TCCTCGTAGCAGTTGAGTTG
Chr10	101.9	s021600511	s021600511_F	Chr10	42,631,602	42,631,580	s021600511_R	Chr10	42,631,258	42,631,280	TTAGGCGCGTAGAATGTGTTTAC	AGGCAGATGAAGCTTTAAGTCGT
Chr10	104.4	T001042474m	T001042474m F	Chr10	43,038,110	43,038,133	T001042474m R	Chr10	43,038,449	43,038,426	TTTAGTTCAGCGGCCTATTTATTT	GCTTTACCAAAGACTAACTCTTCA
Chr10	106.5	GMES1511	GMES1511_F	Chr10	43,382,903	43,382,922	GMES1511_R	Chr10	43,383,199	43,383,180	GGATGCTTACCCACCAGAGA	CGGACCAATTAAGAAGGCAA
Chr10	107.6	s030100085r	s030100085r_F	Chr10	43,513,779	43,513,801	s030100085r_R	Chr10	43,514,148	43,514,125	GACCGGAAAGAGTGCAATTACTA	AAAGTATTTCATAAATGGAGTGAT
Chr10	108.2	s030100090	s030100090_F	Chr10	43,519,190	43,519,212	s030100090_R	Chr10	43,519,357	43,519,334	TTGCACTCCAGTATTTGATGTTG	TGAATTCTCAAATTAAACTTTCCA
Chr10	110.3	Satt331	Satt331 F	Chr10	44,029,661	44,029,682	Satt331 R	Chr10	44,029,901	44,029,885	GCAGAGTCCCCCCTAAATATAG	CGGGAACAACCACACTCTCCATT
Chr10	112.2	C10-BARC-031677-07213	C10-BARC-031677-07213_F	Chr10	44,420,460	44,420,440	C10-BARC-031677-07213_R	Chr10	44,420,365	44,420,385	CACACATTTTAATGTGTCTTG	GGATTTTTTTTCCTCTTCCATC
Chr10	113.3	Satt581	Satt581_F	Chr10	44,712,637	44,712,615	Satt581_R	Chr10	44,712,503	44,712,527	CCAAAGCTGAGCAGCTGATAACT	CCCTCACTCCTAGATTATTTGTTGT
Chr10	115.5	T001044400l	T001044400l F	Chr10	44,975,706	44,975,728	T001044400l R	Chr10	44,976,048	44,976,025	GTTGAGGACATATTATTGCCGAT	CCATGCATATCCTATAGCTTGTTG
Chr10	118.4	C10-BARC-015925-02017	C10-BARC-015925-02017_F	Chr10	45,329,812	45,329,792	C10-BARC-015925-02017_R	Chr10	45,329,716	45,329,736	CAAGGTACAAATTTAAATGCC	GTTAAAATGCGTATGTCATCC
Chr10	119	FT2-300H01d	FT2-300H01d_F	Chr10	45,363,142	45,363,161	FT2-300H01d_R	Chr10	45,363,558	45,363,539	GTGGATGTGCGTGAGAAATG	GCCATATTGGGCTGGTGTAT
Chr10	122.6	s005205820-2	s005205820-2_F	Chr10	45,770,392	45,770,370	s005205820-2_R	Chr10	45,770,242	45,770,259	TGTCCTCAAATCCGTACATACAT	CCCATTTCCTTTCGACCC
Chr10	127.1	T001045537m	T001045537m F	Chr10	46,107,025	46,107,047	T001045537m R				ATATTGGCCGCCTAATCTTTAAT	CTCACCCTCTCTTATGTGGATTG
Chr10	127.4	s005205185-2	s005205185-2_F	Chr10	46,394,754	46,394,732	s005205185-2_R	Chr10	46,394,379	46,394,401	ACATCTCAAGCTGATTCCGATAA	TAGGATTCTAATTGTTCCCGGTT
Chr10	127.9	C10-BARC-028651-05984	C10-BARC-028651-05984_F	Chr10	46,490,778	46,490,759	C10-BARC-028651-05984_R	Chr10	46,490,697	46,490,717	CTACCTGTACACACTCTTGG	GGTTCATATGACTTTTCTGAG
Chr10	129	Satt243	Satt243_F	Chr10	46,656,439	46,656,417	Satt243_R	Chr10	46,656,244	46,656,267	CATTGCACATTAGGTTTTCTGTT	GTAAGATCACGCCATTATTTAAGA
Chr10	129.3	s005204843-2	s005204843-2_F	Chr10	46,734,516	46,734,498	s005204843-2_R	Chr10	46,734,367	46,734,390	CAAGAAGCAAGGAACCAAA	AGTATGTCCATCATTGTAAGATTT
Chr10	134	alphaP	alphaP_F	Chr10	47,494,035	47,494,054	alphaP_R	Chr10	47,494,230	47,494,211	CAACCACCCCAATTTTGTTC	ATAATGTTGCGCTCGCTCTT
Chr10	135.3	s005203925-2	s005203925-2_F	Chr10	47,639,391	47,639,375	s005203925-2_R	Chr10	47,639,243	47,639,269	TGAACATACTTTAATACTGACTCAACTTC	TGTATATAGAAGATAATGAATTGATGG
Chr10	136.4	Sat_231	Sat_231_F	Chr10	47,769,294	47,769,270	Sat_231_R	Chr10	47,769,006	47,769,033	GTATGTTTAGTGAATAAATGACTCG	AGACTCATCCAACTATAATTTATCATAT
Chr10	138	138ct58	138ct58_F	Chr10	48,248,523	48,248,503	138ct58_R	Chr10	48,248,383	48,248,400	AGCTATCAGTATCTTATAAAC	GAGGCACATTGTTCTGGG
Chr10	138	GMES1692	GMES1692_F	Chr10	48,319,637	48,319,656	GMES1692_R	Chr10	48,319,848	48,319,829	ACCCTCCACAGGGAGGATAC	ATCAATCGATCTGAGTCGCC
Chr10	139.1	s005203017-2	s005203017-2_F	Chr10	48,548,104	48,548,082	s005203017-2_R	Chr10	48,547,771	48,547,793	CTCGAACGAGGAAGTAGAAACAA	TGCATCCATGATCCAACTAATAA
Chr10	139.1	GMES0397	GMES0397 F	Chr10	48,624,302	48,624,283	GMES0397 R	Chr10	48,624,152	48,624,176	TAACCACCAAAAGAGGACGC	GCATTTGCTTAGTAATGGCTATTGT
Chr10	139.9	GMES1727	GMES1727_F	Chr10	48,784,978	48,784,959	GMES1727_R	Chr10	48,784,683	48,784,702	GTGACGAAGGAAAGTGGGAA	ACGACGAGGCTGAGAGAGAC
Chr10	140.7	s005202718-2	s005202718-2_F	Chr10	48,845,174	48,845,152	s005202718-2_R	Chr10	48,845,066	48,845,092	TCCCTTCCTCTTTAATTTGCTTT	GAAGAGAAGACAGAACAGAGTATTTGA
Chr10	140.9	GMES2784	GMES2784 F	Chr10	48,911,095	48,911,075	GMES2784 R	Chr10	48,910,684	48,910,703	CGCATGCAGTTTCTTCTAACA	CGAAAACTTTTGACAAACGCA
Chr10	140.9	GMES4774	GMES4774_F	Chr10	48,911,095	48,911,075	GMES4774_R	Chr10	48,910,838	48,910,857	CGCATGCAGTTTCTTCTAACA	AGGATCACATACCAGGCACC
Chr10	141.2	GMES1940	GMES1940_F	Chr10	49,140,497	49,140,516	GMES1940_R	Chr10	49,140,758	49,140,739	CCAATTCTTCCACCATCACC	CCAAGAGATGAGTTGCTGGC
Chr10	142.8	GMES4094	GMES4094_F	Chr10	49,417,614	49,417,633	GMES4094_R	Chr10	49,417,881	49,417,862	TCCTTGTCTGAAGATGCGTG	CTGACCCAGCAATGTCTTCA
Chr10	142.8	s005202072-2	s005202072-2 F	Chr10	49,495,942	49,495,920	s005202072-2 R	Chr10	49,495,551	49,495,578	ATTTATACTTCAAGGGTGCCTCA	GAATGTGTTAAAGTAAAGGATAAGATCG
Chr10	143.3	C10-BARC-024123-04768	C10-BARC-024123-04768_F	Chr10	49,666,014	49,665,994	C10-BARC-024123-04768_R	Chr10	49,665,915	49,665,934	CACAACCTTCGATCACAAATC	GGACAACTTACTTACCAAGG
Chr10	144.1	GMES4853	GMES4853_F				GMES4853_R	Chr10	49,716,083	49,716,102	CGAGTTCTCTTGAAAACGGC	TTCAGGGACCAAATGGAAAG
Chr10	144.1	GMES6346	GMES6346_F	Chr10	49,741,590	49,741,609	GMES6346_R	Chr10	49,741,689	49,741,665	TTAATCGTGCCGCTGAATTT	GAATATGATGTGCATGTATTCAAGT
Chr10	144.1	s005201780-2	s005201780-2_F	Chr10	49,788,416	49,788,393	s005201780-2_R	Chr10	49,788,031	49,788,053	AACTTTCACGTGATACATTATTTG	TAGTTTAAAGTGCATCATCGGGT
Chr10	146.3	s005201440-2	s005201440-2_F				s005201440-2_R	Chr10	50,125,455	50,125,481	GAGGGCGCATCCCTACT	TGAATCTTGTGTTTAGTCTCATGTCTT
Chr10	146.6	C10-BARC-017339-02269	C10-BARC-017339-02269_F	Chr10	50,313,537	50,313,556	C10-BARC-017339-02269_R	Chr10	50,313,625	50,313,606	GATAACTGTGTCACTAAGAG	GGCTGCATTCTTAGCTAGTC
Chr10	146.6	GMES0682	GMES0682 F	Chr10	50,357,214	50,357,233	GMES0682 R	Chr10	50,357,399	50,357,380	AGGGTTTCACACTTTGTCCG	ATCTGCGGATCCATCAAATC
Chr10	146.8	GMES5806	GMES5806_F	Chr10	50,481,805	50,481,786	GMES5806_R	Chr10	50,481,587	50,481,606	GTCGTTCGATGGTGATGATG	GATTGAAGTGAGCCCAAAGC
Chr10	146.8	s005201076-2	s005201076-2_F	Chr10	50,489,360	50,489,338	s005201076-2_R	Chr10	50,488,968	50,488,992	ATATCAGCCTTTGCACACTTGTT	TTCTCTCAATACTCTTGTCTTCTTT
Chr10	149.3	s005200757-2	s005200757-2_F	Chr10	50,807,814	50,807,792	s005200757-2_R	Chr10	50,807,674	50,807,698	CTTTCAGCTTTGAGGATTGTCAT	TCAACTTACATGTTGTACCAGTGTC
Chr10	152.3	s005200402-2	s005200402-2 F	Chr10	51,162,984	51,162,955	s005200402-2 R	Chr10	51,162,800	51,162,822	TGTACAACACTATTTATAGAATATACTCAG	AAGATAACTTAACAAACGCATAA
Chr10	154.2	s005200103-2	s005200103-2_F	Chr10	51,462,719	51,462,696	s005200103-2_R	Chr10	51,462,578	51,462,598	GGTTAGAGATATCCTCATCCTTGA	CTTTCTCACCCATGCTCTGTT
Chr10	154.7	GMES4153	GMES4153_F	Chr10	51,485,235	51,485,216	GMES4153_R	Chr10	51,484,950	51,484,969	TGTTCTGGAGTGGCAGTGAG	TGACACGATGGACGGTAGAA
Chr11	0	C11-BARC-017811-02392	C11-BARC-017811-02392 F	Chr11	29,893	29,874	C11-BARC-017811-02392 R	Chr11	29,802	29,821	GCAATGGAGCGAAGGTGTTG	AAACTGGCGCAAATGGCAAC
Chr11	0	GMES2425	GMES2425_F	Chr11	117,378	117,359	GMES2425_R	Chr11	117,065	117,084	AACAACAGGTCTTGGATGGC	AAGGTGCCATCAATCTGGAC
Chr11	0	GMES6342	GMES6342_F	Chr11	199,191	199,172	GMES6342_R	Chr11	198,910	198,929	ACGACCTATCTTGCGTGGTC	TGCAGAAATCCGCTCTCTTT
Chr11	0	BE806308	BE806308_F	Chr11	199,129	199,110	BE806308_R	Chr11	198,911	198,930	ATTTGACCCCGTTCATACAT	GCAGAAATCCGCTCTCTTTA
Chr11	0	C09-BARC-041591-08048	C09-BARC-041591-08048 F	Chr11	263,448	263,429	C09-BARC-041591-08048 R	Chr11	263,355	263,374	TCGTAAGCTAGGTCAAATCG	AGCAATAGTCTTCAATCGGG
Chr11	0.5	GMES3568.1										
Chr11	4.1	GMES2514	GMES2514_F	Chr11	716,352	716,371	GMES2514_R	Chr11	716,552	716,533	AGCGGTGGAAGAGAGATGAG	CAAATCCAGAGGTTTCCCAA
Chr11	4.1	GMES0979	GMES0979_F	Chr11	1,018,401	1,018,382	GMES0979_R	Chr11	1,018,133	1,018,153	GGAGCTCCTACACCTTTGGT	GCTCGAATCTCAGTACGTTCC
Chr11	4.7	GMES0765	GMES0765_F	Chr11	1,109,005	1,109,024	GMES0765_R	Chr11	1,109,163	1,109,143	TGCTTGCTGCCTCTTATTCA	TGGCTATACGTGTGTGTGTGC
Chr11	8.7	s001001756-2	s001001756-2_F	Chr11	2,012,973	2,012,995	s001001756-2_R	Chr11	2,013,150	2,013,128	AAAGCATCTTATCTCTTCGCTAT	TGACGCAGGAACCAATATCTTAT
Chr11	11	T001102190m	T001102190m_F	Chr11	2,197,768	2,197,790	T001102190m_R	Chr11	2,198,094	2,198,072	TGTTTCTTATCGCTGCTTTCATT	CGATCTAGATTAGACAACGTGGC
Chr11	15.4	T001102495s	T001102495s F	Chr11	2,502,535	2,502,557	T001102495s R	Chr11	2,502,699	2,502,677	ACGCCAGTGTCGTATCGTATTAT	TGACTCTACCAAAGATACACGGG
Chr11	17	Sat_272	Sat_272_F	Chr11	2,718,834	2,718,853	Sat_272_R	Chr11	2,719,065	2,719,040	ATGGCAATATGTTTTTGAGC	GCCTTGTAATTTTCCTTGTTAATGTG
Chr11	19	T001103032l	T001103032l_F	Chr11	3,038,649	3,038,671	T001103032l_R	Chr11	3,038,955	3,038,932	CTTTGAGCTAAGCCGAATGAAGT	TTTGACATGCAAGTATATCCCTTT

Chr11	23.2	s005305357-2	s005305357-2_F	Chr11	3,234,326	3,234,304	s005305357-2_R	Chr11	3,234,180	3,234,202	GCCAAACTGTTCAACTTTAATGC	TCCACCTGGTTACTGATTGATTT
Chr11	25.1	s005305067-2	s005305067-2_F	Chr11	3,524,867	3,524,845	s005305067-2_R	Chr11	3,524,501	3,524,523	ATCCACAAACTTTCTTAATGACT	TCACCATATGCAACTCCTTTACA
Chr11	28.8	T001103887l	T001103887l F	Chr11	3,895,547	3,895,569	T001103887l R	Chr11	3,895,898	3,895,876	TCATAGCCTGAGCATTACACTGA	TATAGCGGAAGTCTCTGTTCCAG
Chr11	32.3	Sat_270	Sat_270_F	Chr11	4,234,163	4,234,142	Sat_270_R	Chr11	4,233,940	4,233,960	AAAGCACTTGGATGACACATAA	AGGGGTAGAGACTGGAGAGTA
Chr11	35	T001104672m	T001104672m_F	Chr11	4,680,917	4,680,939	T001104672m_R	Chr11	4,681,207	4,681,185	GTCCATTCGTTGACTCAATAACC	TTTACCTGATGATACTTACGGGC
Chr11	36.9	GMES6228	GMES6228_F	Chr11	4,958,019	4,958,039	GMES6228_R	Chr11	4,958,221	4,958,202	AAGGAGGAACAAGGAGAAGGA	CAAAGCTGTTCCTGTGGCTT
Chr11	39.7	C11-BARC-030509-06888	C11-BARC-030509-06888 F	Chr11	5,376,621	5,376,640	C11-BARC-030509-06888 R	Chr11	5,376,698	5,376,679	TCTGTGGTGAGTTGAGGAAG	AAACACACAGCAACGCTATC
Chr11	41.7	GMES1998	GMES1998_F	Chr11	5,688,235	5,688,216	GMES1998_R	Chr11	5,688,056	5,688,075	TTGCTGCTAGGAGGACTGGT	TGGCAGAAATGGTGATCAAA
Chr11	42.2	GMES4577	GMES4577_F	Chr11	6,058,425	6,058,445	GMES4577_R	Chr11	6,058,681	6,058,662	TCCTCTCTCTTCTTCTGCTGC	TACTTTCCAAACTCGCCAGC
Chr11	42.2	GMES0823	GMES0823 F				GMES0823 R	Chr11	6,080,677	6,080,696	CAAACTGAAGACGCTGGTCA	GGAGTCTAGCCACAGCCTTG
Chr11	42.7	GMES0045	GMES0045_F	Chr11	6,203,264	6,203,283	GMES0045_R	Chr11	6,203,452	6,203,433	TGAGAACGCGCTAACTGCTA	TAAGAGCGAAAGGCGTTGTT
Chr11	42.7	Satt509	Satt509_F	Chr11	6,216,403	6,216,426	Satt509_R	Chr11	6,216,583	6,216,563	CTACCGTGTGGTGGTGTGCTACCT	CAAGTGGCCAGCTCATCTATT
Chr11	47.5	GMES0959	GMES0959_F				GMES0959_R	Chr11	7,264,371	7,264,371	TTCATTCACCAACACAACCC	GGCAGCCATATTGTGAGGAT
Chr11	49.8	GMES5234	GMES5234 F	Chr11	7,527,933	7,527,952	GMES5234 R	Chr11	7,528,217	7,528,198	TGGTTTCCGTCCCTTACTTG	GGTAAGTCCTTGGAGGAGGG
Chr11	52.1	GMES1708	GMES1708_F	Chr11	8,171,848	8,171,829	GMES1708_R				GTTTCGTTTGCAGTTTGGGT	TTTTCATGCCCAAGAAATCA
Chr11	54.5	s024800057-2	s024800057-2_F	Chr11	8,651,822	8,651,844	s024800057-2_R	Chr11	8,652,188	8,652,164	CAGGTGATCAAGATGACGAATAA	TCATATTATGTACTTCAGGATCAAG
Chr11	56.7	Satt197	Satt197_F	Chr11	8,898,592	8,898,573	Satt197_R	Chr11	8,898,420	8,898,444	CACTGCTTTTTCCCCTCTCT	AAGATACCCCCAACATTATTTGTAA
Chr11	57	s013700007-2	s013700007-2_F	Chr11	9,106,372	9,106,390	s013700007-2_R	Chr11	9,106,481	9,106,464	GTGTGCAGTGTGCTGTGAT	TCGCTGAAACTTCCTACG
Chr11	58.6	T001109308s	T001109308s_F	Chr11	9,335,167	9,335,189	T001109308s_R	Chr11	9,335,362	9,335,341	TCCAAATTGAGACTTGGAATCAT	CTCGCCTGCATACTGGTTTAAT
Chr11	61.1	T001109543l	T001109543l_F	Chr11	9,571,180	9,571,202	T001109543l_R	Chr11	9,571,487	9,571,465	TGACAAACGAACAAGCACTTAAC	TATTATTTGCGCGGTTTACAAGT
Chr11	62.1	T001109656s	T001109656s F	Chr11	9,683,464	9,683,486	T001109656s R	Chr11	9,683,650	9,683,628	TGCACTTTCATCATGGTTATGTC	TCAAGTCTTATGCATGTTGTTCC
Chr11	65.1	Sat_128	Sat_128_F	Chr11	10,010,722	10,010,698	Sat_128_R	Chr11	10,010,508	10,010,532	GGGGTTTTGTTAATCATTGTCCTTAGAT	GGGAGAAAATTTTTAATGCCAGTAGTTA
Chr11	65.7	GMES2543	GMES2543_F	Chr11	10,159,757	10,159,774	GMES2543_R	Chr11	10,160,069	10,160,050	ACCAGCTCCAGCGCAACT	GCAGAGGGAAAATGTACGGA
Chr11	65.7	C11-BARC-042767-08401	C11-BARC-042767-08401_F				C11-BARC-042767-08401_R	Chr11	10,211,921	10,211,902	AAACTGAGAGACGCTAGGAC	TTGGTGTGCAGACTAGCTAC
Chr11	69.4	GMES0766	GMES0766 F	Chr11	10,593,097	10,593,116	GMES0766 R	Chr11	10,593,262	10,593,240	GGGGTGCGTGAAGTTGTAGT	GTTAAATTCATGGAGCAAATTGT
Chr11	71.7	s013701958-2	s013701958-2_F	Chr11	11,055,924	11,055,946	s013701958-2_R	Chr11	11,056,099	11,056,077	TCCTTAACGAATTAGGTTGCACT	TCTCTATCAAAGCGCACAATATC
Chr11	71.9	s008000014-2	s008000014-2_F	scaffold_32	12,933	12,955	s008000014-2_R	scaffold_32	13,286	13,264	TACAACTTTGATGTTCCCATCTT	AAGCTCCTTCCTCTCAAGTTGTT
Chr11	74.9	T001111280m	T001111280m F	scaffold_32	244,735	244,757	T001111280m R	scaffold_32	244,945	244,923	GGTGCTCTTCCTCACATTAGAGA	TAGGTTGCAAGTATAGCGTGTTT
Chr11	77.4	GMES0027	GMES0027_F	scaffold_21	3,388,310	3,388,292	GMES0027_R	scaffold_21	3,388,081	3,388,100	GCAGATGCGGTTACGAATTT	AAACCGTCAACCTGGTCAAG
Chr11	79.6	s008000965-2	s008000965-2_F	scaffold_21	2,877,576	2,877,554	s008000965-2_R	scaffold_21	2,877,395	2,877,417	TGGGCTAAACCCACTATAATTCA	AAGCCCTCTATATTTCTTGACGC
Chr11	79.6	s008002161-2	s008002161-2_F	scaffold_21	1,675,562	1,675,544	s008002161-2_R	scaffold_21	1,546,311	1,546,332	CGTCGCCCTAGAAATTTGA	CATGGTCAAGGTAGTTAACATT
Chr11	79.6	Satt519 F	Satt519 F	scaffold_21	886,743	886,721	Satt519 R	scaffold_21	886,506	886,529	GGATTTCAAAGAATGAACACAGA	CCGCAAGGTTACGAACTGCTCGAA
Chr11	79.6	s008003458-2	s008003458-2_F	scaffold_21	407,129	407,110	s008003458-2_R	scaffold_21	406,930	406,949	AATGGGAATTTAGCTGGTAT	CATCATTCACAGAATGCAAA
Chr11	80.1	s008003841-2	s008003841-2_F				s008003841-2_R	scaffold_21	14,824	14,846	AAATAGGTTGTCAAGACCTCTGAA	GCCGAATCACCTCTAATTAAATC
Chr11	81.8	T001115342m	T001115342m_F	Chr11	13,354,878	13,354,900	T001115342m_R	Chr11	13,355,175	13,355,153	AAATTTAATTCAAACGTCCCGAG	TTGGTGATCTTTATGTTTCGAGG
Chr11	85	T001115835m	T001115835m_F	Chr11	13,853,711	13,853,733	T001115835m_R	Chr11	13,853,970	13,853,948	GGCATCAATGGCTGAAGATATAA	ACTAACATAAAGGCAAATGCCAC
Chr11	88.6	GMES0675	GMES0675_F	Chr11	14,367,562	14,367,540	GMES0675_R	Chr11	14,367,447	14,367,466	GCACCAATTCATTCTCATACATTC	TGCAGATCGTAAGTGGCTTG
Chr11	90.8	T001116639s	T001116639s_F	Chr11	14,697,985	14,698,005	T001116639s_R	Chr11	14,698,194	14,698,172	TTTGGATGTTCCCAACTGAAG	CTAAGACATGCATCATAAATGGG
Chr11	93.8	Sat_348	Sat_348_F	Chr11	14,953,240	14,953,218	Sat_348_R	Chr11	14,952,996	14,953,014	AAGCCGCACACTAAGATGAAGAT	TGAATAACCAAATGGAAAGAGATT
Chr11	94	Satt597	Satt597_F	Chr11	15,124,629	15,124,649	Satt597_R	Chr11	15,124,784	15,124,765	GCTGCAGCGTGTCTGTAGTAT	CGAGGCACAACCATCACCAC
Chr11	97.9	GMES2944	GMES2944_F	Chr11	16,086,354	16,086,335	GMES2944_R	Chr11	16,086,256	16,086,275	ATTCCAAACCCCTCTTTGCT	TGGTTGTGGTTTTGGTGAGA
Chr11	98.4	s019400004	s019400004_F	Chr11	18,158,793	18,158,771	s019400004_R	Chr11	18,158,431	18,158,453	GCGGAAGAAGAAAGTTTAACTCA	ACCCATGCACGTATAACAAAGAG
Chr11	98.4	s010300014	s010300014 F	Chr11	18,180,529	18,180,554	s010300014 R	Chr11	18,180,887	18,180,865	CCATAATCATAATAACAACAAACACA	GAAGCCAAGCCATGAGTAATACA
Chr11	98.7	s011500007	s011500007_F	Chr11	20,949,637	20,949,652	s011500007_R				ACCAGACGATTCATTCTTTGATG	CTTGGTATGAGGAGGTGAACTTG
Chr11	99.2	Satt332	Satt332_F	Chr11	24,261,882	24,261,862	Satt332_R	Chr11	24,261,641	24,261,661	CATCCAGGGCTTGCAACAAAG	GTCCTTATATATGGAAGATCA
Chr11	99.5	s004503530-2	s004503530-2 F	Chr11	25,683,170	25,683,193	s004503530-2 R	Chr11	25,683,310	25,683,288	TTGAGAAACAAAGAAATGGAGAAA	TCACAACAGAGACTCAACCTCAA
Chr11	99.5	s004504766-2	s004504766-2_F	Chr11	26,916,890	26,916,912	s004504766-2_R	Chr11	26,916,997	26,916,975	ATTGCTTCCATAAACACTTTCCT	TTTGGCGCTATTAATATGGAAGA
Chr11	99.5	s004505064-2	s004505064-2_F	Chr11	27,216,590	27,216,612	s004505064-2_R	Chr11	27,216,956	27,216,934	AAATGTTCAGTTCAAACTTTATG	ATATGTTGAGTTGTCCATCCCAT
Chr11	99.5	s004506014-2	s004506014-2_F	Chr11	28,146,514	28,146,536	s004506014-2_R	Chr11	28,146,926	28,146,904	AAGTGGGTGGGTTTGACTTATCT	CGAAATTCAAATGAACACTCACA
Chr11	100	s004507090-2	s004507090-2 F	Chr11	29,249,850	29,249,872	s004507090-2 R	Chr11	29,250,239	29,250,217	GAAACATATTTGGGCACGTTTAG	ACAGTTGCAATGACCAGCTATTT
Chr11	101.1	s008100306-2	s008100306-2_F	Chr11	29,584,107	29,584,128	s008100306-2_R	Chr11	29,584,256	29,584,234	CGCAGTTGACTGGTTGGTAGAT	AAATCCTAGTTAGCAAGACCCTG
Chr11	101.9	s008101679-2	s008101679-2_F	Chr11	30,907,002	30,907,024	s008101679-2_R	Chr11	30,907,192	30,907,168	CATATCCTAGTGATCTCCTTCCC	TGAGAGATGATTTGTTTCTTATACA
Chr11	102	s008102061-2	s008102061-2_F				s008102061-2_R				CATACTTGTCAGCCCGAGTATGT	GAGTTGGAGTTGCGATGAATAAC
Chr11	106.1	T001135274s	T001135274s_F	Chr11	32,036,419	32,036,441	T001135274s_R	Chr11	32,036,613	32,036,591	AGAATCAATTCCTCAGTGTCCAG	GATCAAGTTCAGGTACTTGTGGG
Chr11	109.4	s008102683-2	s008102683-2_F	Chr11	32,312,171	32,312,193	s008102683-2_R	Chr11	32,312,370	32,312,348	TTTGAAATAATAACATATGGGTG	TGGTCGTCTATCTCTTTATCTTT
Chr11	110.5	s008102932-2	s008102932-2_F	Chr11	32,559,252	32,559,274	s008102932-2_R	Chr11	32,559,436	32,559,414	TATTTATAATCAACGCCTGCTGC	ACGACCCAATTAGGACAAACTAA
Chr11	115.3	GMES1633	GMES1633 F	Chr11	32,882,552	32,882,533	GMES1633 R	Chr11	32,882,393	32,882,412	ATGAGAGGTTGCCACTGGAG	GGCATGTTCTGACCATTGTG
Chr11	118.4	Satt665	Satt665_F	Chr11	32,993,502	32,993,480	Satt665_R	Chr11	32,993,250	32,993,276	TTGAATTCGCTGGTTTAATCCTA	CATGACTTAATTTTACACCCTTTATTT
Chr11	122	s029700038	s029700038_F	Chr11	33,330,955	33,330,977	s029700038_R	Chr11	33,331,260	33,331,237	GCTTTGTCGTTCCTTTGTATGTT	GGATATATTCCTTTCATCCATCTG
Chr11	125.4	Satt359	Satt359_F	Chr11	33,650,518	33,650,499	Satt359_R	Chr11	33,650,345	33,650,368	AGAAAATAATCCTGCTCAAG	TTTAAGTCCAATAACAAAGATAAC
Chr11	129.6	s024000510	s024000510 F	Chr11	34,007,712	34,007,732	s024000510 R	Chr11	34,008,049	34,008,027	ATGCTTGAGGAGTGGATCCTT	GGCCATAAGTCTATGCCTTCTTT
Chr11	130.7	GMES4299	GMES4299_F	Chr11	34,195,668	34,195,694	GMES4299_R	Chr11	34,195,843	34,195,824	ACCATAATCCATAGATATTCTTATTGC	CCCTATTGGTGGGGTTTCTT
Chr11	133.8	GMES1793	GMES1793_F	Chr11	34,549,704	34,549,723	GMES1793_R	Chr11	34,549,975	34,549,956	GGAGGAAGAAGGGGAACAAG	ATATGAACCGTTGGCCTGAG
Chr11	136.4	GMES1076	GMES1076 F	Chr11	34,731,435	34,731,454	GMES1076 R	Chr11	34,731,639	34,731,620	ATCCACCGTTGTATCCGAAG	GCGCAGATCTCACAGAAGTG
Chr11	137.8	T001138898m	T001138898m_F	Chr11	34,874,929	34,874,907	T001138898m_R	Chr11	34,874,662	34,874,689	AACTAGCCAAGTCCTATCCAACC	TTGAAATTGAGAAAGTATTAACTTCACT
Chr11	141.1	GMES2517	GMES2517_F	Chr11	35,220,623	35,220,604	GMES2517_R	Chr11	35,220,494	35,220,513	TCCTCTCTCGAATTCACGCT	CACGAACACTTGATGACGCT
Chr11	143	Satt453	Satt453 F	Chr11	35,412,705	35,412,685	Satt453 R	Chr11	35,412,463	35,412,483	GAAAAAAAACAATAAACAACA	TAGTGGGGAAGGGAAGTTACC
Chr11	143.6	BE801538	BE801538 F	Chr11	35,567,221	35,567,239	BE801538 R	Chr11	35,567,422	35,567,408	TAGCTTTCTATTGTCTAAT	AACTCCACCACTCTG
Chr11	143.6	GMES0591	GMES0591_F	Chr11	35,567,269	35,567,290	GMES0591_R	Chr11	35,567,406	35,567,387	GCAAGAAGCAAGTAATCCCTCA	TCTTCCCTGGCAATTGAAAC
Chr11	143.6	GMES1589	GMES1589_F	Chr11	35,567,268	35,567,288	GMES1589_R	Chr11	35,567,420	35,567,401	TGCAAGAAGCAAGTAATCCCT	CTCCACCACTCTGCTCTTCC
Chr11	144.2	GMES2797	GMES2797_F	Chr11	35,602,613	35,602,632	GMES2797_R	Chr11	35,602,863	35,602,844	GGTTCTGATTCCGAGGTTGA	CTCAAGCTGTTCCTTGAGGG
Chr11	144.9	GMES1132	GMES1132_F	Chr11	35,759,045	35,759,064	GMES1132_R	Chr11	35,759,296	35,759,277	ACTCCCACTCCCACTTCCTC	CCTGGTGTTTCCAGAGCATT
Chr11	144.9	GMES6369	GMES6369_F	Chr11	35,769,687	35,769,706	GMES6369_R	Chr11	35,769,806	35,769,787	GCGTAGCACAGAGACACAGC	TGAAGGCGAAAGAATGGAGT
Chr12	0	T001200015l	T001200015l_F	Chr12	18,323	18,341	T001200015l_R	Chr12	18,688	18,670	GATGTGGTCACTCAGTTGGATTT	GTTCTGAGAGAGAGAATGACGGA
Chr12	0.8	Satt666	Satt666 F	Chr12	311,932	311,957	Satt666 R	Chr12	312,165	312,138	TGGCTTGTCATCTCTACTTTTATTAG	TCATGCATCTAATTTGTTTTATCTATCA
Chr12	6.1	T001200938m	T001200938m_F	Chr12	942,400	942,422	T001200938m_R	Chr12	942,631	942,609	GCAACTCAGCATTAGGTCCTTTA	GTTTATGTAACGATCGAGTTCGG
Chr12	6.4	C12-BARC-026101-05260	C12-BARC-026101-05260_F	Chr12	1,078,483	1,078,502	C12-BARC-026101-05260_R	Chr12	1,078,552	1,078,533	AGAACAGGAAACATACTCCG	CTGGCCTGATATCAAACCTC

Chr12	9.4	Satt353	Satt353_F	Chr12	1,687,063	1,687,086	Satt353_R	Chr12	1,687,229	1,687,207	CATACACGCATTGCCTTTCCTGAA	AATGGGAATGCCTTCTTATTCTA
Chr12	10.4	C12-BARC-016413-02582	C12-BARC-016413-02582_F	Chr12	2,101,055	2,101,074	C12-BARC-016413-02582_R	Chr12	2,101,138	2,101,120	ACCATCTACAATACTACCCC	GCTGTAAAAAGCTTGTACT
Chr12	13.2	C12-BARC-021905-04235	C12-BARC-021905-04235_F	Chr12	2,776,242	2,776,261	C12-BARC-021905-04235_R	Chr12	2,776,322	2,776,303	CTCTTCAAACGCACCATGAT	GGCAATAAAGGGTGATCAAC
Chr12	13.7	GMES4242	GMES4242_F	Chr12	2,969,338	2,969,358	GMES4242_R	Chr12	2,969,600	2,969,581	CACGCGCTCGTTTCTATATTC	ATCACTCCCGGAGAAACCTT
Chr12	13.7	C12-BARC-040509-07765	C12-BARC-040509-07765_F	Chr12	3,007,125	3,007,144	C12-BARC-040509-07765_R	Chr12	3,007,192	3,007,173	TGTTGTTGCTTTGACGCGTG	TCAAATAATGCGGTAGCCAG
Chr12	13.7	GMES0816	GMES0816_F	Chr12	3,122,039	3,122,058	GMES0816_R	Chr12	3,122,300	3,122,281	AGTTTCTCCAGCCTCCATCA	AATGGACAGAACTTGGACGG
Chr12	14	GMES1494	GMES1494_F	Chr12	3,122,368	3,122,349	GMES1494_R	Chr12	3,122,139	3,122,158	GATCCAGGGGTTTTGGATTT	ATAACCACCGTCACGGCTAC
Chr12	17.2	GMES3950	GMES3950_F	Chr12	3,463,289	3,463,308	GMES3950_R	Chr12	3,463,518	3,463,499	ATCTCCGTGGCTATTGCCTT	CTGCTTGATTTGAATCCCGT
Chr12	18.6	GMES0837	GMES0837_F	Chr12	3,704,626	3,704,645	GMES0837_R	Chr12	3,704,740	3,704,721	TCTCTGAACCCCATTTTTGC	TCTCACACACATCGCACTGA
Chr12	18.6	C12-BARC-014337-01324	C12-BARC-014337-01324_F	Chr12	3,709,922	3,709,941	C12-BARC-014337-01324_R	Chr12	3,710,003	3,709,984	CCCTTAACCTTGCTTCATCC	GTAAAGCCTTTTTCTAATCG
Chr12	21.2	T001203975l	T001203975l_F	Chr12	3,979,102	3,979,124	T001203975l_R	Chr12	3,979,465	3,979,443	TGGTGTTGATTTACCCACTTACA	AAACAAATATACCGATCCCAGGT
Chr12	25	Satt568	Satt568_F	Chr12	4,519,715	4,519,696	Satt568_R	Chr12	4,519,483	4,519,508	GAATAATCCAATTCAATTTA	CGGACACCGGTCTACTAGGAAAGTAA
Chr12	27.8	T001204926m	T001204926m_F	Chr12	4,926,915	4,926,937	T001204926m_R	Chr12	4,927,225	4,927,203	ACCTCACGAGCTAAGTACGTGTC	AGAGTGAATCAGCGCTACCTAAA
Chr12	30.3	s011202278	s011202278_F	Chr12	5,224,080	5,224,102	s011202278_R	Chr12	5,224,379	5,224,354	TGGAACTAGGAATTTCAAAGCAA	GGAGGTGTAAATCAAATGATAGATGA
Chr12	33.9	s024200450	s024200450_F	Chr12	5,542,211	5,542,187	s024200450_R	Chr12	5,542,028	5,542,048	TGCTAACAATATTCTCGTCAAAGAA	TTATCCAACATCCCAAATCCC
Chr12	36.1	s024200389	s024200389_F	Chr12	5,603,742	5,603,720	s024200389_R	Chr12	5,603,584	5,603,606	TGGTCACATCCATGATTCAAATA	CGTAAATCAGCATGGCTAGATAA
Chr12	40.3	s024200027	s024200027_F	Chr12	5,964,305	5,964,283	s024200027_R	Chr12	5,964,084	5,964,106	CAGAGTCACCGCTGATTAAGATT	ACTGACATGTTGCTTTGTCGTGT
Chr12	41.1	s023500372	s023500372_F	Chr12	6,207,815	6,207,793	s023500372_R	Chr12	6,207,471	6,207,493	TCAAATATAATGGGACGAAAGGA	TATCTGTAAGAGTGATCTGGCGG
Chr12	42.8	Satt442	Satt442_F	Chr12	6,390,238	6,390,259	Satt442_R	Chr12	6,390,494	6,390,473	CCTGGACTTGTTTGCTCATCAA	GTTCAAGGCTTCAAGTAGTCAC
Chr12	42.8	C12-BARC-041917-08135	C12-BARC-041917-08135_F	Chr12	6,399,270	6,399,289	C12-BARC-041917-08135_R	Chr12	6,399,345	6,399,325	CTCATTTAAAGAAGAGGAGG	GAGCCTTAAGAAACAAGTTAG
Chr12	43.3	s023500058	s023500058_F	Chr12	6,521,863	6,521,841	s023500058_R	Chr12	6,521,515	6,521,537	TAAATTGTGGCATCAGGTCTAGC	ACTGGAAATGTTCCCATTAGTCA
Chr12	44.1	s022000092-2	s022000092-2_F				s022000092-2_R	Chr12	6,671,044	6,671,022	CCCACTAAACCTTGTGTACCTATTT	CCTTATGCATAGGTTGAATTTGC
Chr12	45.8	C12-BARC-044091-08613	C12-BARC-044091-08613_F	Chr12	6,884,392	6,884,411	C12-BARC-044091-08613_R	Chr12	6,884,459	6,884,441	TGGGAGACCAAACAGCAAAC	CAGTAGGTTTCTAGCTTTG
Chr12	46.6	GMES0947	GMES0947_F	Chr12	7,168,302	7,168,283	GMES0947_R	Chr12	7,168,001	7,168,020	CCAAACCAAACGCTTTTCTC	TTCTGAGTGATGGCCTCCTT
Chr12	47.4	GMES1103	GMES1103_F	Chr12	7,175,878	7,175,895	GMES1103_R	Chr12	7,176,321	7,176,302	CACTCCAAGACCCTCACCAT	TCCACCCACGTACATGAGAA
Chr12	48.2	s011002118-2	s011002118-2_F	Chr12	7,755,322	7,755,304	s011002118-2_R	Chr12	7,755,129	7,755,151	AGTTGGCCAAATCGACCTT	TACCAAAGGCTATTAAACTTCCT
Chr12	52.1	C12-BARC-015305-02270	C12-BARC-015305-02270_F	Chr12	8,035,009	8,035,028	C12-BARC-015305-02270_R	Chr12	8,035,082	8,035,063	TGTGTGGAAGCTAGATTCAG	GCCACACACTACAGTTATGG
Chr12	53.8	T001208472m	T001208472m_F	Chr12	8,506,006	8,506,024	T001208472m_R	Chr12	8,506,333	8,506,311	CCCTTCGTGATGAATCTTT	TTTGTATGCAAATATGTAGGAAT
Chr12	55.7	C06-BARC-030173-06820	C06-BARC-030173-06820_F	Chr12	9,127,485	9,127,466	C06-BARC-030173-06820_R	Chr12	9,127,426	9,127,445	TTTTTACATTACAAGAACTC	ATAGACCCTATGTTTCTGTG
Chr12	55.7	Sat_334	Sat_334_F	Chr12	9,131,072	9,131,049	Sat_334_R	Chr12	9,130,854	9,130,875	TAACGTAGCAAATTGACTATAAGA	TGTGCAAAGACAATTTCAATGA
Chr12	56.8	s032700039-2	s032700039-2_F	Chr12	9,914,400	9,914,421	s032700039-2_R	Chr12	9,914,500	9,914,478	AATGTCCACCGTTCACAAATCT	TATATGACTCGGCATTTCCTGTT
Chr12	57.3	s032700098-2	s032700098-2_F	Chr12	9,973,491	9,973,513	s032700098-2_R	Chr12	9,973,625	9,973,603	GTCCCGTGGGTTAGAAATTAGAA	GCTGATATCTCCTTGTGCAGAGT
Chr12	57.3	s032700102-2	s032700102-2_F	Chr12	9,976,988	9,977,008	s032700102-2_R	Chr12	9,977,347	9,977,325	CCAAACCCGAATTCACACTTT	TTCAGACATCGTTTCCAAATCTT
Chr12	57.3	C15-BARC-018577-02980	C15-BARC-018577-02980_F	Chr12	10,406,910	10,406,929	C15-BARC-018577-02980_R	Chr12	10,406,989	10,406,970	TCCTTATGTGTGTACTTGTG	CCTTCCTTTCTCTTCTCGTG
Chr12	60.4	Satt541	Satt541_F	Chr12	12,319,253	12,319,237	Satt541_R	Chr12	12,319,087	12,319,108	AATCCATCACACATAAA	GTACTCCCTCCAGAAAATAACC
Chr12	62.2	C12-BARC-039961-07622	C12-BARC-039961-07622_F	Chr12	15,679,096	15,679,116	C12-BARC-039961-07622_R	Chr12	15,679,178	15,679,160	CTGTTCAAATACTGGACAGAC	TGTTGTACATTCAAAAGCG
Chr12	62.5	GMES1506	GMES1506_F	Chr12	17,231,914	17,231,895	GMES1506_R	Chr12	17,231,804	17,231,823	CAGCAAGAGCAACAGCAATC	GAGAGGGGGAGGAGAGAGAA
Chr12	63.3	T001222767s	T001222767s_F	Chr12	18,964,230	18,964,251	T001222767s_R	Chr12	18,964,427	18,964,405	TTCGTATACGCATGGCTTCTTT	ATCCAAATATTGGCCTTCTGTTT
Chr12	63.8	T001223395s	T001223395s_F	Chr12	19,594,528	19,594,550	T001223395s_R	Chr12	19,594,691	19,594,669	GGCACAAACGTATTCTATTCTCG	TGCAATAGTCAGAAACTGAACCA
Chr12	65.2	T001225156s	T001225156s_F	Chr12	21,353,602	21,353,624	T001225156s_R	Chr12	21,353,797	21,353,773	ATCTTACCTAGGTGCACACACAA	CCTCATATGTAGCCATGTTTATTGA
Chr12	66.5	Satt222	Satt222_F	Chr12	28,162,318	28,162,345	Satt222_R	Chr12	28,162,552	28,162,530	TGTTTTGTGAAAATAATAATTAAAGATG	CCACAAGTAACTAATGTAATAGGTGTT
Chr12	66.5	T001228018s	T001228018s_F	Chr12	24,394,664	24,394,686	T001228018s_R	Chr12	24,394,868	24,394,846	ACGAGGCTCTAATACCATTCGAT	ATTAAATTTGTATCCTCCTCAAA
Chr12	66.8	T001229478m	T001229478m_F	Chr12	30,270,362	30,270,384	T001229478m_R	Chr12	30,270,606	30,270,582	AGTTTCTAACTATCAGCGGAGGG	TTTAACTTAACAATGGTCATCCAAA
Chr12	67.1	T001231438s	T001231438s_F	Chr12	31,393,498	31,393,520	T001231438s_R	Chr12	31,393,643	31,393,621	AAGATGAGGAGTAACTTGGTCCC	TCTTCATGATGTTGATCGATTTG
Chr12	70.1	T001232591l	T001232591l_F	Chr12	32,547,942	32,547,964	T001232591l_R	Chr12	32,548,304	32,548,282	CATCTTCCAATTAGAAATCCGTG	TTATTTGACTCGAGAACAAGCGT
Chr12	74.2	GMES6353	GMES6353_F	Chr12	33,409,423	33,409,442	GMES6353_R	Chr12	33,409,661	33,409,642	ACTTGTTATGGCCAACCTGG	GCATCCTTGGAAGGAACACA
Chr12	77.8	T001234032l	T001234032l_F	Chr12	33,992,177	33,992,199	T001234032l_R	Chr12	33,992,525	33,992,502	ATGTCATAGCATTTGTGGGCTAT	AAAGAACTATGCTCTGTGCGTAAA
Chr12	80.5	GMES4202	GMES4202_F	Chr12	34,399,045	34,399,022	GMES4202_R	Chr12	34,398,954	34,398,973	CTTCTTTATCCTCTTCCTCTTCCT	GCTGCCATTTCTGTTGGATT
Chr12	80.8	LFsoy8	LFsoy8_F	Chr12	34,539,900	34,539,881	LFsoy8_R	Chr12	34,539,515	34,539,533	TGAGGGAACACTTACACTGG	CTTTCATTCAGGCTCAGACC
Chr12	83.4	Satt302	Satt302_F	Chr12	35,083,082	35,083,058	Satt302_R	Chr12	35,082,880	35,082,905	AACTGTAGTTTACTAAAAATAAGTG	GACTGAATTAATATTGGTGTTGAATT
Chr12	85.5	T001235266m	T001235266m_F	Chr12	35,240,248	35,240,270	T001235266m_R	Chr12	35,240,562	35,240,540	ATTAATGATAGCCGGTGTGCTAA	GTGGAAGCAAGAGTGACGTATTT
Chr12	88.7	Satt637	Satt637_F	Chr12	35,538,950	35,538,970	Satt637_R	Chr12	35,539,142	35,539,120	CCATAAGCGAAAGCGATGAAT	GAGAAAAATAAGAACATCACCCA
Chr12	91.2	T001235782s	T001235782s_F	Chr12	35,755,690	35,755,714	T001235782s_R	Chr12	35,755,848	35,755,824	TTTAGGGTTATAGTAGATTTGGAGA	GAATCAAGTAATGACTTCTGTCTCA
Chr12	92.8	Sat_216	Sat_216_F				Sat_216_R	Chr12	35,871,951	35,871,975	ACAAGATATTTGAATGTAGATGAGAC	CCGATCCTCTCGTAAATATAAGGAA
Chr12	93.3	Satt142	Satt142_F	Chr12	36,033,821	36,033,801	Satt142_R	Chr12	36,033,671	36,033,694	GGACAACAACAGCGTTTTTAC	TTTGCCACAAAGTTAATTAATGTC
Chr12	93.3	Satt293	Satt293_F	Chr12	36,036,612	36,036,590	Satt293_R	Chr12	36,036,414	36,036,436	CAGAAGGTTTGCATAAAAAGAAT	GGCTAAAAAGTTGATGTAATGTG
Chr12	98.6	T001236301l	T001236301l_F				T001236301l_R				CAAAGGTTACATATAGTCCATATTGTCG	AAAGGAAATTGAACCTCATGTTT
Chr12	98.6	Satt181	Satt181_F	Chr12	36,365,746	36,365,730	Satt181_R	Chr12	36,365,532	36,365,549	TGGCTAGCAGATTGACA	GGAGCATAGCTGTTAGGA
Chr12	99.7	GMES0183	GMES0183_F	Chr12	36,553,442	36,553,461	GMES0183_R	Chr12	36,553,647	36,553,628	AGTGATGTGGAAATGGAGCC	GAGCCTGAAATCGCCAAATA
Chr12	99.7	Sat_175	Sat_175_F	Chr12	36,556,063	36,556,090	Sat_175_R	Chr12	36,556,343	36,556,320	TCATTGTTAAAACTTAGTGTCTAATAAA	GTCAAAGTCAGTTAGTGAAAGAGA
Chr12	103.8	s015200524	s015200524_F	Chr12	36,951,018	36,950,997	s015200524_R	Chr12	36,950,772	36,950,795	TTAGATGAGGCACCATGTCATC	GTGATATTGCTTACCGTCATGTTG
Chr12	104.3	s015200498	s015200498_F	Chr12	36,977,012	36,976,989	s015200498_R	Chr12	36,976,707	36,976,730	ATTATACGGAGTTCCTTCACCAAC	TTAATATATGATGCAGCCATGTCG
Chr12	106.2	s015200299	s015200299_F	Chr12	37,175,119	37,175,095	s015200299_R	Chr12	37,174,821	37,174,842	TTGCTTGAATATATAGCAACTCTTG	TTGATCATTCTATCCGCCAGTT
Chr12	106.5	s015200130	s015200130_F	Chr12	37,344,419	37,344,397	s015200130_R	Chr12	37,343,998	37,344,021	TTATTCAATTTCGATGGAGCAAA	AAATAGAAGCAAAGAAATGGAAAC
Chr12	106.8	s015200071	s015200071_F	Chr12	37,403,272	37,403,249	s015200071_R	Chr12	37,402,905	37,402,929	TTCTATGTGACAATGGGTGATTAAA	AAGCCAAAGATAATTGCTAAATAAA
Chr12	107	GMES2597	GMES2597_F	Chr12	37,428,239	37,428,220	GMES2597_R	Chr12	37,427,998	37,428,017	TTGTGGTCACATCCGACACT	ATCAGCGGGTAATCGAACAG
Chr12	107	s015200037	s015200037_F	Chr12	37,436,907	37,436,885	s015200037_R	Chr12	37,436,550	37,436,572	CGTGTTCTACCGTTGAGATAACC	CTAAGCCAAATGGCCAAGTCTAT
Chr12	107.3	Sat_218	Sat_218_F	Chr12	37,557,103	37,557,080	Sat_218_R	Chr12	37,556,823	37,556,844	CACGTTAAATGAACTGGTATGATA	GGCCAAAGAGGAAGATTGTAAT
Chr12	107.6	C12-BARC-042997-08496	C12-BARC-042997-08496_F	Chr12	37,731,996	37,732,015	C12-BARC-042997-08496_R	Chr12	37,732,078	37,732,059	TCTAACAACCACCACCTCTC	GGAGTTAGGGCAGTTGAATT
Chr12	108.7	s025000125	s025000125_F	Chr12	37,843,061	37,843,039	s025000125_R	Chr12	37,842,620	37,842,642	TCTTAAGGGTATTGTTTGGCTGA	AATTGAAGGAACATTCCATTGTG
Chr12	112.6	GMES0893	GMES0893_F	Chr12	38,085,900	38,085,879	GMES0893_R	Chr12	38,085,743	38,085,762	AAAACATTTCCCTGCTACTTCA	GAGGCAAACTCAATTGGGAA
Chr12	113.7	C12-BARC-039237-07479	C12-BARC-039237-07479_F	Chr12	38,180,672	38,180,691	C12-BARC-039237-07479_R	Chr12	38,180,748	38,180,729	CCCATGTTGTTCTAGAGACC	AGGATGTTATCTATCCACTC
Chr12	114.7	Satt434	Satt434_F	Chr12	38,429,066	38,429,042	Satt434_R	Chr12	38,428,727	38,428,751	TTCCGATATACTATATAATCCTAAT	GGGTTAGTCTTTTTATTTAACTTAA
Chr12	115	GMES3677	GMES3677_F	Chr12	38,522,868	38,522,887	GMES3677_R	Chr12	38,523,043	38,523,024	GGAAGGCATCATAGCAGTGG	GTCAAAGAAACCAGGGTGGA
Chr12	119	T001239064s	T001239064s_F	Chr12	39,038,954	39,038,976	T001239064s_R	Chr12	39,039,118	39,039,095	TGCTAAATGTTACCTCGGTTTGT	CCTGAGAATACATAGAAGCAAACG
Chr12	122	GMES0862	GMES0862_F	Chr12	39,617,801	39,617,820	GMES0862_R	Chr12	39,618,070	39,618,051	TTTTCCCCTACGCACAAATC	ACCGAGGTCTCTCGAACTGA
Chr12	122	GMES4755	GMES4755_F	Chr12	39,662,710	39,662,691	GMES4755_R	Chr12	39,662,499	39,662,519	AGCATCAAGATGGCAAAAGG	TGCGACTCCATTAGGTTGTTT

Chr12	123.1	T001239885l	T001239885l_F	Chr12	39,862,981	39,863,003	T001239885l_R	Chr12	39,863,323	39,863,301	AATGAATTTGAATCACTCCCAGA	ACCTTAAACCTGGGTTGTTTGAT
Chr12	123.1	C12-BARC-025709-05012	C12-BARC-025709-05012_F				C12-BARC-025709-05012_R	Chr12	39,868,377	39,868,396	TGTTTTATTCAGGGTCACCG	GGGAGCATCTGTCTTTTGTT
Chr13	0	T001320046m	T001320046m_F	Chr13	215,642	215,620	T001320046m_R	Chr13	215,323	215,345	TTGAAGTGTAAACATGCTGATGG	TTTCATTGATCCCATGCTTTAAT
Chr13	0	T001319486m	T001319486m_F	Chr13	766,596	766,574	T001319486m_R	Chr13	766,283	766,304	CAATAATGACCCTCCCACACTTA	CCCATGCATTCATTATCAAATCT
Chr13	0	T001319133l	T001319133l_F	Chr13	1,121,553	1,121,531	T001319133l_R	Chr13	1,121,195	1,121,217	TTCAGAACTATTTCCGGTGAAGA	ACCATTGTTCATTGAGAGACGAC
Chr13	0.3	T001318664l	T001318664l_F	Chr13	1,473,860	1,473,836	T001318664l_R				TGTAGTAGTGATTCCAAATCAATGG	GGGAGCACTATAGCTTGCTTAAC
Chr13	0.5	T001317338m	T001317338m_F	Chr13	2,717,319	2,717,297	T001317338m_R	Chr13	2,717,003	2,717,025	CTGTTCATGTCAAGGATTAGGCT	GAGTGAGAGGAATAGAAGCCCAT
Chr13	0.5	T001316370s	T001316370s_F	Chr13	3,690,956	3,690,934	T001316370s_R	Chr13	3,690,835	3,690,857	AATTGAACTTGCTACGTCATGGT	GCACATCTCTAACACACATTGGT
Chr13	0.5	T001314272m	T001314272m_F	Chr13	6,025,753	6,025,731	T001314272m_R	Chr13	6,025,466	6,025,488	CTATGAGGCCCAAAGTCATCTAC	GGGTAACCCTTATGTATCATGTG
Chr13	0.5	T001314138m	T001314138m_F	Chr13	6,159,331	6,159,311	T001314138m_R	Chr13	6,159,084	6,159,106	TAGTTTCCTCGGTCACCATCTAA	TGTTCGTCAACTTTCCTGAGAAT
Chr13	0.5	T001313681l	T001313681l_F	Chr13	6,606,406	6,606,384	T001313681l_R	Chr13	6,606,028	6,606,052	CTCCCACATGAAGATATACCGAA	TGACATAGCATTGCATAAGGATAAA
Chr13	0.5	Satt325	Satt325_F	Chr13	6,720,127	6,720,107	Satt325_R	Chr13	6,719,884	6,719,904	GGGTATTAAGGGAAAACAAAA	TAAACGAACAATCACTTCATA
Chr13	0.5	T001313439l	T001313439l_F	Chr13	6,928,360	6,928,342	T001313439l_R	Chr13	6,927,938	6,927,960	CCTCCTCCCTTGGCAATTT	TTGTAACTGTTTGAATGCCTGAA
Chr13	0.5	Satt146	Satt146_F	Chr13	7,288,065	7,288,045	Satt146_R	Chr13	7,287,779	7,287,803	AAGGGATCCCTCAACTGACTG	GTGGTGGTGGTGAAAACTATTAGAA
Chr13	0.8	GMES1672	GMES1672_F	Chr13	7,757,434	7,757,415	GMES1672_R	Chr13	7,757,176	7,757,195	CACCAACACCACTTCCTCCT	GTTGTCCCCATGCTTCTTGT
Chr13	1.6	Satt343	Satt343_F	Chr13	10,392,211	10,392,229	Satt343_R	Chr13	10,392,340	10,392,323	CATGGCGGAAAGCGAAACA	TCCCAATTCACCTCTTCA
Chr13	2.3	GMES0321	GMES0321_F	Chr13	10,466,274	10,466,255	GMES0321_R	Chr13	10,466,046	10,466,065	TAAGCAAGCCTGGTTTCGAG	ATCCTCCTTGGTTGATGCTG
Chr13	2.9	Satt193	Satt193_F	Chr13	11,847,351	11,847,329	Satt193_R	Chr13	11,847,117	11,847,136	TTTCGATAAAAATGTTACACCTC	TGTTCGCATTATTGATCAAAAAT
Chr13	2.9	s000703340-2	s000703340-2_F	Chr13	12,944,643	12,944,621	s000703340-2_R	Chr13	12,944,425	12,944,447	CCGTGCAGTCCGTCAGCTGAATACACGAATGCTAAA	TTAGTTAGCCCTAGGACAAGTGG
Chr13	3.2	s000702833-2	s000702833-2_F	Chr13	13,446,571	13,446,549	s000702833-2_R	Chr13	13,446,422	13,446,445	TCACAATCTCGCAAGATCAAATA	AATTGCACCGAGTGTAAACTATAA
Chr13	6.2	s000702358-2	s000702358-2_F	Chr13	13,923,316	13,923,294	s000702358-2_R	Chr13	13,922,927	13,922,949	CTAGTGTAATACCTCGTGCCTGC	TAGTATAGTGCGGGTAACAAGCG
Chr13	7.1	s000701869-2	s000701869-2_F	Chr13	14,411,868	14,411,846	s000701869-2_R	Chr13	14,411,673	14,411,694	CAATTAGGCCAACTTTGAATGAG	CCTTGAACGAGAGATGCTTTGT
Chr13	8.7	s000701362-2	s000701362-2_F	Chr13	14,921,630	14,921,607	s000701362-2_R	Chr13	14,921,276	14,921,298	TGCAATTCACGTATGTTGAAATCT	CACTCATCTTTGTTTGACATTGC
Chr13	13.6	s000700355-2	s000700355-2_F	Chr13	15,914,965	15,914,943	s000700355-2_R	Chr13	15,914,708	15,914,730	CCACCGACGTGTCGCACTGCAAATATGGTCCTCCA1	TCGTCTATGTCTTTCATTTGCTT
Chr13	15.6	Satt252	Satt252_F	Chr13	16,454,076	16,454,098	Satt252_R	Chr13	44,343,869	44,343,853	AATTTGGATTAATTAAATTTATG	CTCGGTCCTCTCAAATAAGGTCTC
Chr13	20.3	T001304982m	T001304982m_F	Chr13	16,849,396	16,849,374	T001304982m_R	Chr13	16,849,159	16,849,182	TGAACCATATGCAACTGACTTTG	AAGTGAATCGTTAGCATTCTTTGA
Chr13	22.1	s017700544-2	s017700544-2_F	Chr13	17,033,970	17,033,948	s017700544-2_R	Chr13	17,033,772	17,033,794	TCAGGGACTAACATAACCAATGC	TTCTGTTACCTTGGTACTTCTGG
Chr13	25	s010002208-2	s010002208-2_F	Chr13	18,303,034	18,303,011	s010002208-2_R	Chr13	18,302,850	18,302,870	AAATGTAGAGGACTAGTGGTGGAG	TTTATCTCTCCCAAGATTTCG
Chr13	26.7	s010001660-2	s010001660-2_F	Chr13	18,852,758	18,852,736	s010001660-2_R	Chr13	18,852,599	18,852,623	GGATTATTCGGAGGTGACTCTTT	AACAAGGAGAAGAATAAACTCTCAG
Chr13	27.7	C13-BARC-032373-08957	C13-BARC-032373-08957_F	Chr13	19,157,559	19,157,540	C13-BARC-032373-08957_R	Chr13	19,157,469	19,157,489	CCACCTAACTTTCAAAATAC	GGTCTCTGTATTTCTATGTTG
Chr13	28.5	Satt206	Satt206_F	Chr13	19,577,977	19,578,001	Satt206_R	Chr13	19,578,176	19,578,154	CATGTGAAAAGAATGAGATTATGTA	TCCAAACTCATCCTTAAGGTATT
Chr13	28.8	Sat_298	Sat_298_F	Chr13	19,950,573	19,950,555	Sat_298_R	Chr13	19,950,299	19,950,317	CGTCGAAGCAAAAATTAAA	GCGAAACCCACAAAGCATA
Chr13	29.9	C13-BARC-025291-06469	C13-BARC-025291-06469_F	Chr13	20,409,667	20,409,686	C13-BARC-025291-06469_R	Chr13	20,409,755	20,409,736	AGCGATAGTGTTGCCAGAGC	TTTGATCCTCCATGGCCAAC
Chr13	30.1	s010000061	s010000061_F	Chr13	20,451,307	20,451,284	s010000061_R	Chr13	20,450,913	20,450,936	TGTTCTTGAGAATTTGTTCGGTAA	TGACTTTGTCTACACCAAACATCC
Chr13	30.5	s010000016	s010000016_F	Chr13	20,496,106	20,496,083	s010000016_R	Chr13	20,495,633	20,495,650	AATGCTCCTAAGTGTTGGTATCAC	CTTCCGGCCATGAGGATT
Chr13	30.9	Sat_240	Sat_240_F	Chr13	20,519,633	20,519,607	Sat_240_R	Chr13	20,519,410	20,519,437	GGCAGAAGTCTAATGAATGTGAAATGA	GTTGTGACCGAAATAGATGTTATTTAAT
Chr13	30.9	Satt659	Satt659_F	Chr13	20,572,260	20,572,279	Satt659_R	Chr13	20,572,422	20,572,398	GCTCAACTTCGTGTAACAAG	CATCGGTAACTATCTAATATTCGTA
Chr13	34.4	T001301136s	T001301136s_F	Chr13	20,728,204	20,728,182	T001301136s_R				TGGCCACTTTACCATCAGATATT	GATTGTGACTATCCCAGTGTGGT
Chr13	36.1	T001301019l	T001301019l_F	Chr13	20,845,650	20,845,628	T001301019l_R	Chr13	20,845,294	20,845,318	CTACAGACAAGAACCGCCATAAC	AAATGTGTTAGAGTGTACGTGTTCC
Chr13	37.5	s008400599	s008400599_F	Chr13	21,107,077	21,107,099	s008400599_R	Chr13	21,107,402	21,107,378	ATAAATGCGTCCCTGAAATATGA	GCAAAGATTAAAGTTTGACAAGGAA
Chr13	40.2	s008401007	s008401007_F	Chr13	21,516,809	21,516,831	s008401007_R				AAATAGCCTACATGACACGGAGA	AAACGAATCGGAGTAGCAAATTA
Chr13	44.6	T001300005s	T001300005s_F	Chr13	21,855,169	21,855,147	T001300005s_R	Chr13	21,854,960	21,854,982	TACTTAAGAGAGCAATCGGGAAA	ATCAAGAATTACAACGAGAGAAA
Chr13	45.6	T001320432s	T001320432s_F	Chr13	21,984,390	21,984,413	T001320432s_R	Chr13	21,984,482	21,984,460	TGACTTTGCTAAGTAGCTCTCCAA	TGACACTTACGTTGCAAGTCTTC
Chr13	47	s034100101r	s034100101r_F				s034100101r_R	Chr13	22,100,448	22,100,470	TCACAAATTCTGCTGTGTAGGAT	CGTAGCCTAAATAAAGCACTAAA
Chr13	47.5	s008401806	s008401806_F	Chr13	22,315,505	22,315,527	s008401806_R	Chr13	22,315,708	22,315,686	CGTGAGTCCATGCATTACAATTA	TAAGCGTGTGTTAGGAGGCTATC
Chr13	50	T001320982l	T001320982l_F	Chr13	22,536,002	22,536,024	T001320982l_R				TCCAAATTTATACTGCAACATGC	GCATATTTAATTTGAATGGTAATG
Chr13	50.8	T001321054m	T001321054m_F	Chr13	22,607,615	22,607,637	T001321054m_R	Chr13	22,607,922	22,607,900	ATGTTAACTGCTCCTAGTGCTGC	TAAACTCATCCTTCCAGCAATGT
Chr13	53.3	s008402420	s008402420_F	Chr13	22,928,615	22,928,637	s008402420_R	Chr13	22,928,900	22,928,878	CAGGACATGGCAACTACCTTAAA	TGCTTGCTTGTAGATTGCATAAA
Chr13	54.9	Sat_309	Sat_309_F	Chr13	23,682,568	23,682,595	Sat_309_R	Chr13	23,682,873	23,682,846	AACGGATATATACCCATAAATTTTCATG	TCATCCAATATAACAATTGTTAAAGTCA
Chr13	56.5	T001322331l	T001322331l_F	Chr13	23,815,699	23,815,721	T001322331l_R	Chr13	23,816,073	23,816,049	TCATTTCATCAGCCTTGAAACTT	TGCATTGAGATATCGTAATTGTCTC
Chr13	58.4	T001322429l	T001322429l_F	Chr13	23,912,461	23,912,483	T001322429l_R	Chr13	23,912,889	23,912,867	CAGGTTTGGTGGAAGTTAGTTCA	AAACGAGTTTGGCAATGCTACTA
Chr13	62	T001322733m	T001322733m_F	Chr13	24,218,395	24,218,417	T001322733m_R	Chr13	24,218,694	24,218,672	TGGCTTAAATGGACATAGGACTG	TTGACCAAACTTCTGTTGACCTT
Chr13	65.3	Satt595	Satt595_F	Chr13	24,602,095	24,602,076	Satt595_R	Chr13	24,601,881	24,601,897	GATGGGAAGCAAACAAGAAG	AACCCCCTCCCCTAAAT
Chr13	67.2	T001323280m	T001323280m_F	Chr13	24,765,478	24,765,500	T001323280m_R	Chr13	24,765,826	24,765,804	TTTCCTCATTATTCACCTGTTCG	CCGGCCTATGACTCAAATCTTAT
Chr13	70.5	s017600842	s017600842_F	Chr13	25,361,881	25,361,904	s017600842_R	Chr13	25,362,173	25,362,151	AAGCCTACCCTCTTTGTAAGAGTC	TGTGGTTCCCTATTCTTTCTTGA
Chr13	74.1	s017601243	s017601243_F	Chr13	25,763,570	25,763,592	s017601243_R	Chr13	25,763,909	25,763,887	AAATGATATTTGGATGAAGAGCG	CTAATAGCAACACCCAAACATGC
Chr13	74.9	s017601245	s017601245_F	Chr13	25,765,711	25,765,733	s017601245_R	Chr13	25,766,011	25,765,990	ATTGTGAACGTGTGTGATTTCTG	CACAATCATCGTGTGACGTAAA
Chr13	74.9	s020000942	s020000942_F	Chr13	25,784,318	25,784,295	s020000942_R	Chr13	25,783,989	25,784,014	AACACAATGGTTCCTAATAATGTAAA	GGTTTGATTCATAATAGAGTTTGTGA
Chr13	74.9	s020000912	s020000912_F	Chr13	25,814,257	25,814,235	s020000912_R	Chr13	25,814,095	25,814,117	AGATTCCGCGTCACTTGTATAAT	ACATAACATTGCAGCATCACACT
Chr13	75.7	s020000882	s020000882_F	Chr13	25,844,390	25,844,372	s020000882_R	Chr13	25,844,029	25,844,051	AATGCTCCAGCTTGGTGTC	TGCCAGAGAGGATAGCTAATACG
Chr13	75.7	Satt663	Satt663_F	Chr13	25,935,893	25,935,875	Satt663_R	Chr13	25,935,687	25,935,710	TCATGCAATGTTGTATAAT	ACTGCAGATAACTTGACTGGTAGT
Chr13	76.2	C13-BARC-045205-08910	C13-BARC-045205-08910_F	Chr13	26,195,300	26,195,319	C13-BARC-045205-08910_R	Chr13	26,195,395	26,195,374	TCCGTAATTATGGTCCCTTC	GTCTCTAATTTAAAATGAGAGG
Chr13	78.9	s020000149	s020000149_F	Chr13	26,577,982	26,577,960	s020000149_R	Chr13	26,577,668	26,577,691	AAATAGAGTGAACGGAGGAGGAG	TGTTCCCAACAAAGTGTTAGAGAG
Chr13	78.9	s020000125	s020000125_F	Chr13	26,601,337	26,601,316	s020000125_R	Chr13	26,601,015	26,601,037	TTGCAATCATTATCCACCCATA	CAACAAAGGAATGTTGGGTATGT
Chr13	79.4	s045000017	s045000017_F				s045000017_R				TTTGTTGGACTCAAATCAAGAGTG	GACCTAAATGCCATGACTCAAGA
Chr13	81.6	s026700161	s026700161_F				s026700161_R				TTCATGCTTTGTTTGAAGACGTA	CAATGATAACCCATTGAATCCAC
Chr13	84.3	Sat_229	Sat_229_F	Chr13	26,987,543	26,987,516	Sat_229_R	Chr13	26,987,290	26,987,317	TGTGCTACTTCACATCTTGAGAGAAAGA	AGGGTTTAGAAAAAGATTCACCAAATAT
Chr13	87.3	T001326098m	T001326098m_F				T001326098m_R	Chr13	27,283,021	27,283,003	TTTGTTGGTGAACGGTACCTAAT	CTGACAAGTGACAATTAGGCCAT
Chr13	87.6	C13-BARC-029167-06103	C13-BARC-029167-06103_F	Chr13	27,368,274	27,368,293	C13-BARC-029167-06103_R	Chr13	27,368,354	27,368,335	ACATAGATCGGCATGGAGTC	CTATCTGTGCAATCAATAGG
Chr13	89	Sat_234	Sat_234_F	Chr13	27,656,063	27,656,036	Sat_234_R	Chr13	27,655,729	27,655,756	ATGCGTTTAATAAGTTTTGAAAAATGCC	GAAACCATCCTTATATGTCAATTGCTCA
Chr13	91.9	GMES0895	GMES0895_F	Chr13	28,130,478	28,130,459	GMES0895_R	Chr13	28,130,129	28,130,148	CCTTCTCCTTCTCCGGTTCT	TAGCAGGCATTACTCCTCCG
Chr13	92.9	GMES0864	GMES0864_F	Chr13	28,323,875	28,323,856	GMES0864_R	Chr13	28,323,649	28,323,668	ACCACCTTCACTCGCAAAAC	GGCGAAACTGCCTAATGTGT
Chr13	96.2	GMES0039	GMES0039_F	Chr13	28,804,801	28,804,820	GMES0039_R	Chr13	28,805,014	28,804,995	CTCTCTTTCGCTTCATGGCT	AAATCGTGGAGGTGTTGCTC
Chr13	96.2	Satt114	Satt114_F	Chr13	28,911,931	28,911,948	Satt114_R	Chr13	28,912,038	28,912,018	GGGTTATCCTCCCCAATA	ATATGGGATGATAAGGTGAAA
Chr13	96.8	GMES3937	GMES3937_F	Chr13	29,166,228	29,166,209	GMES3937_R	Chr13	29,166,065	29,166,084	AGGTACTGGACACTCGGTGG	GGAGAAGGCCTCATCAACAG
Chr13	96.8	GMES0734	GMES0734_F	Chr13	29,235,262	29,235,243	GMES0734_R	Chr13	29,235,130	29,235,149	CTCTTCACCCACCAGCAAAT	AGTAGGAGGCTTAGCAGGGG
Chr13	97.4	Satt334-2	Satt334-2_F	Chr13	29,608,551	29,608,527	Satt334-2_R	Chr13	29,608,317	29,608,341	TGGATTGAATAATTTTTGTGTTTGA	TGCATTTATGTTTAGTCAATTCAGG

Chr13	98.2	s017200782	s017200782_F	Chr13	30,235,371	30,235,349	s017200782_R	Chr13	30,235,164	30,235,186	CGAAAGTTAGCTCAACAGACGTT	AAGACTAAACACTCTCTCGCTGC
Chr13	98.9	s017200718	s017200718_F	Chr13	30,300,056	30,300,031	s017200718_R	Chr13	30,299,823	30,299,845	CAAGACAATAATGCTGTAAACATAAA	CGTCGACACGTGTATCATTGTAT
Chr13	99.8	C13-BARC-029683-06320	C13-BARC-029683-06320_F	Chr13	30,831,004	30,830,985	C13-BARC-029683-06320_R	Chr13	30,830,910	30,830,929	GGTGCCTAAGGATGTTTTGG	GACCTAATCCGACATGATTG
Chr13	101	s017200003	s017200003_F	Chr13	31,008,772	31,008,750	s017200003_R	Chr13	31,008,489	31,008,511	TAGATGATTCACATGTTTGACGC	TTATTTGTATGGAGGCTGGCTTA
Chr13	101.6	s003000073-2	s003000073-2_F	Chr13	31,093,857	31,093,876	s003000073-2_R	Chr13	31,094,018	31,093,997	TACCTAGCTGATGCGTGATCATA	TTAATGCAATACCAAACACACAT
Chr13	101.6	C13-BARC-041141-07916	C13-BARC-041141-07916_F	Chr13	31,193,045	31,193,026	C13-BARC-041141-07916_R	Chr13	31,192,956	31,192,975	TTTCTACTCCCCTTGTCCAC	CAATGGACCAGAGAGAAATG
Chr13	101.8	C13-BARC-017917-02451	C13-BARC-017917-02451_F	Chr13	31,659,868	31,659,888	C13-BARC-017917-02451_R	Chr13	31,659,966	31,659,949	GAAGTTACCTGAAGGATATTC	AGAGCTTCTTCAACTCTC
Chr13	103.2	GMES1122	GMES1122_F	Chr13	31,886,475	31,886,456	GMES1122_R	Chr13	31,886,212	31,886,231	CCAAACCACACACCTCACAC	TCTTCACAGACTCAATGCGG
Chr13	105.3	C13-BARC-015903-02010	C13-BARC-015903-02010_F	scaffold_1223	1,309	1,291	C13-BARC-015903-02010_R	Chr13	32,176,405	32,176,386	GAAAAACTATGTGGTATGG	GAAGCATGCTACTTGCTCTC
Chr13	105.3	GMES2710	GMES2710_F	Chr13	32,230,960	32,230,942	GMES2710_R	Chr13	32,230,739	32,230,758	AGACGAGTTCGACGACGAGT	TCCTCCACTACCACCACCTC
Chr13	105.7	GMES4780	GMES4780_F	Chr13	32,232,328	32,232,310	GMES4780_R	Chr13	32,232,171	32,232,190	CTCATGCCTCTCCAGTCTCC	TGAGTGAGCAGAGAAAGCGA
Chr13	105.9	s003001318-2	s003001318-2_F	Chr13	32,348,695	32,348,717	s003001318-2_R	Chr13	32,348,860	32,348,838	AAACTACTTTGCTCTGTTTGTGA	CTGTATGACATCCACCTATGCAA
Chr13	108.3	GMES1566	GMES1566_F	Chr13	32,607,166	32,607,147	GMES1566_R	Chr13	32,606,956	32,606,975	ACCCCTCGTCTTTCCTTGTT	GCGTTGGGTGAAACAATCTT
Chr13	108.3	GMES5641	GMES5641_F	Chr13	32,633,019	32,633,038	GMES5641_R	Chr13	32,633,440	32,633,421	TTATTTTGCCCCTCTGCTTC	TGCAGAAACTGACCATCCAG
Chr13	108.6	Satt335	Satt335_F	Chr13	32,720,218	32,720,199	Satt335_R	Chr13	32,720,059	32,720,080	CAAGCTCAAGCCTCACACAT	TGACCAGAGTCCAAAGTTCATC
Chr13	110.5	GMES0250	GMES0250_F	Chr13	33,139,108	33,139,127	GMES0250_R	Chr13	33,139,336	33,139,317	TTTAAAACCCCCTACACCCC	CAGGCCTTCACTATGTGGGT
Chr13	110.5	C13-BARC-025765-05056	C13-BARC-025765-05056_F	Chr13	33,204,080	33,204,098	C13-BARC-025765-05056_R	Chr13	33,204,169	33,204,150	TCACTATGATGATGAAAAC	ATAAAGTGTGTGGAGACTTG
Chr13	114.3	GMES4664	GMES4664_F	Chr13	34,019,985	34,020,004	GMES4664_R				CTTTGTGTTTGTTTTGCAGC	TCTGAGGGTATGTGCCATGA
Chr13	114.3	GMES6737	GMES6737_F	Chr13	34,034,123	34,034,104	GMES6737_R	Chr13	34,033,895	34,033,912	CAAGCACGGGAGAGATTTTC	CCATCAGTGCCATCAACAAC
Chr13	114.6	Satt362	Satt362_F	Chr13	34,076,518	34,076,542	Satt362_R	Chr13	34,076,766	34,076,742	TTGTTGTTTCAAATGTATTTTTAGTT	GACGGATCATCAAACCAATCAAGAC
Chr13	115.1	C13-BARC-031493-07101	C13-BARC-031493-07101_F	Chr13	34,471,826	34,471,845	C13-BARC-031493-07101_R	Chr13	34,471,918	34,471,899	TATAGCAGCCAAGAGTGACC	GCTCTGAGATAAGTTGATAG
Chr13	116.2	GMES6605	GMES6605_F	Chr13	34,641,761	34,641,780	GMES6605_R	Chr13	34,642,010	34,641,991	AACCCCACTTCTTACCACCC	TGGCAGCATCGTTGTTGTAG
Chr13	117.3	Sct_188-2	Sct_188-2_F	Chr13	34,766,006	34,766,029	Sct_188-2_R	Chr13	34,766,370	34,766,347	CTCGACCTATTAATTCCCACTCAA	GAAGAGTGGGCTAAATTTCGTACT
Chr13	121.1	s003004189-2	s003004189-2_F	Chr13	35,203,852	35,203,873	s003004189-2_R	Chr13	35,204,055	35,204,033	AATAAAGCTTCTTGCGGATTGA	GTTACCCACGTCATTGGAAACTA
Chr13	121.6	C13-BARC-027502-06599	C13-BARC-027502-06599_F	Chr13	35,433,433	35,433,414	C13-BARC-027502-06599_R	Chr13	35,433,348	35,433,367	TGCATGTTAAGTGGAGACAG	ATCAAGAGGAACGGTGAAGG
Chr13	124.9	s003004926-2	s003004926-2_F	Chr13	35,936,646	35,936,668	s003004926-2_R	Chr13	35,937,006	35,936,984	ACCACTTGTAACGTTAGACCGAA	GCTCATTTAATGTTGAAGTTGCC
Chr13	125.9	GMES4860	GMES4860_F	Chr13	36,160,625	36,160,606	GMES4860_R	Chr13	36,160,378	36,160,397	TTTCAACCTTTTCAAACGCC	GGTTCACAAGGGAGATCACG
Chr13	126.5	GMES4020	GMES4020_F	Chr13	36,416,506	36,416,487	GMES4020_R	Chr13	36,416,288	36,416,309	CAATGCTGTCTTGCAGTGCT	CACAACCTGACATTCAAGGAAA
Chr13	126.5	C13-BARC-042673-08344	C13-BARC-042673-08344_F	Chr13	36,427,197	36,427,216	C13-BARC-042673-08344_R	Chr13	36,427,275	36,427,256	TTGATCACGGGTGAAACTCC	GGAACTTGAACCAGGAAACC
Chr13	127.3	C13-BARC-041127-07909	C13-BARC-041127-07909_F	Chr13	36,627,652	36,627,671	C13-BARC-041127-07909_R	Chr13	36,627,727	36,627,708	TACCCTTAAGTAGATGAGGT	CAGCAAAAGGCTCCACTTTC
Chr13	130.1	GMES0517	GMES0517_F	Chr13	37,271,394	37,271,413	GMES0517_R	Chr13	37,271,668	37,271,649	TTGCTGACTCACCCACTGAG	GGCAATTGATCCAACATGAA
Chr13	135	T001336798m	T001336798m_F	Chr13	37,936,714	37,936,736	T001336798m_R	Chr13	37,936,987	37,936,965	TATCCTTGTCAAACTGCAGTCAA	GTCTTCTCTGATCAACAAGGTGC
Chr13	137.8	s027600022	s027600022_F	Chr13	38,514,517	38,514,495	s027600022_R	Chr13	38,514,258	38,514,280	CTACATATGCATTCGGCATACAA	TAGGTGTTATCCATCTTTCACGG
Chr13	138.4	s033000025	s033000025_F	Chr13	38,642,569	38,642,547	s033000025_R	Chr13	38,642,218	38,642,239	AAAGTCAAGAGGGATGAAAGCAT	CCATACTATTTGATTCTGGGCAA
Chr13	142.2	Satt554	Satt554_F	Chr13	39,251,180	39,251,200	Satt554_R	Chr13	39,251,431	39,251,411	ATATGCTTTGTAAGAAAATTA	CAAGCCCAAATATTACAAATT
Chr13	144.6	Satt657	Satt657_F	Chr13	39,734,001	39,734,018	Satt657_R	Chr13	39,734,254	39,734,234	CATTTGGACTTTTACTTC	ACGATGTTAATTGGTAGAATC
Chr13	147.2	T001338938l	T001338938l_F	Chr13	40,112,176	40,112,198	T001338938l_R				AGATCCTTTCTCGAAGTGCAAAC	GATAGGAGATAACCACCACTTATTT
Chr13	147.2	T001338956s	T001338956s_F	Chr13	40,130,477	40,130,496	T001338956s_R	Chr13	40,130,655	40,130,633	GAGGAGGCAAGATGATCCAA	CGACGGATCGATCAAGTTAAAGT
Chr13	148.9	T001339285m	T001339285m_F	Chr13	40,462,054	40,462,076	T001339285m_R	Chr13	40,462,393	40,462,371	CAAAGCTTGCTCCCTACATTAAA	AAATAGTTCATGGACAGCAAATG
Chr13	152.7	T001339638m	T001339638m_F	Chr13	40,814,901	40,814,923	T001339638m_R	Chr13	40,815,230	40,815,206	CCAAGTGGATGTGACAGGTAAAG	TCCGTATTATCTATCGCATTAGTCA
Chr13	154	LFsoy7	LFsoy7_F	Chr13	41,160,054	41,160,035	LFsoy7_R	Chr13	41,159,675	41,159,694	GTTTCAGTCAGGCTCAGACC	ACAGATCCAGACGTTCCTGG
Chr13	158.1	AW756935	AW756935_F	Chr13	41,605,191	41,605,175	AW756935_R	Chr13	41,604,945	41,604,966	GCTGGTGATTGTGTAAT	TAATATAGTTTTGTATTGAAAT
Chr13	162.1	T001340717l	T001340717l_F	Chr13	42,161,148	42,161,170	T001340717l_R	Chr13	42,161,527	42,161,506	CGAACGTTTCATACAAGGATCTC	GTTGTTCAACGGCCATTTACTT
Chr13	163.8	T001340960m	T001340960m_F				T001340960m_R	Chr13	42,398,361	42,398,339	CGATATATACTCATCATGCCGAT	ACACCTCACTTTCGGTAAACTTG
Chr13	165.4	T001341102s	T001341102s_F	Chr13	42,539,891	42,539,913	T001341102s_R	Chr13	42,540,045	42,540,023	TCCATATAGGCAAATTAGCAAGC	CCCATCTAGGGTTATCAAATCAG
Chr13	167.4	T001341265l	T001341265l_F	Chr13	42,703,052	42,703,074	T001341265l_R	Chr13	42,703,430	42,703,408	TTCTTGATTCGTTCTGTGATTGA	TGCTCTTGTTGATTTGGACTATG
Chr13	170	s013400530-2	s013400530-2_F	Chr13	42,864,696	42,864,718	s013400530-2_R	Chr13	42,864,888	42,864,866	CGAAATAACCAAATTGAGCATTC	TAATTGCTCATAGTCGATTTCTA
Chr13	174.3	GMES3245	GMES3245_F	Chr13	43,287,818	43,287,837	GMES3245_R	Chr13	43,288,147	43,288,128	GGAAATTTGGAAATGCGAGA	ATCGCATCGAATGAGAATCC
Chr13	174.3	Satt656	Satt656_F	Chr13	43,323,493	43,323,517	Satt656_R	Chr13	43,323,641	43,323,617	TACTAAAAATGGCAATTATTTGTTG	TGTTTCAGTATTTGGATAATAGAAT
Chr13	174.5	GMES3230	GMES3230_F	Chr13	43,525,175	43,525,156	GMES3230_R	Chr13	43,524,934	43,524,953	GATTGTCATGGTTTCGGACC	AGTCTCCCGATTTCAAGGGT
Chr13	175.1	GMES6918	GMES6918_F	Chr13	43,796,737	43,796,763	GMES6918_R	Chr13	43,796,833	43,796,814	CCACAATCTAAGTAAGTGTTGAGAGAA	TTGTGACCCTTGTTTCCTCC
Chr13	177.3	s013401911-2	s013401911-2_F	Chr13	44,232,319	44,232,343	s013401911-2_R	Chr13	44,232,467	44,232,446	TGCGTGTTATTTCTCTCATCTTACA	AGAAAGACACAGGCTATCCACC
Chr13	182.1	Satt395	Satt395_F	Chr13	45,319,000	45,319,019	Satt395_R	Chr13	45,319,274	45,319,257	CGCGCTAGTTGAATGAATGT	CATTGAGGAATTTTTTAT
Chr13	182.1	GMES4587	GMES4587_F	Chr13	45,327,720	45,327,701	GMES4587_R	Chr13	45,327,471	45,327,490	TCCAAAATGTTGGGCAGAAT	TGCTGCTGTTGTTGTTGTTG
Chr13	183.7	s025500044	s025500044_F	Chr13	45,816,658	45,816,636	s025500044_R	Chr13	45,816,308	45,816,330	GCATCAAGTAGCATATCAAAGGG	GTGAGGTTTGATTGATGTCCTGT
Chr14	0	T001400036s	T001400036s_F	Chr14	41,834	41,857	T001400036s_R	Chr14	42,039	42,017	CAGCCTATCCTGTACACAACAATC	CTTGTGATGTTTGGAGACACTTG
Chr14	1.1	Satt577	Satt577_F	Chr14	675,325	675,348	Satt577_R	Chr14	675,436	675,411	CAAGCTTAAGTCTTGGTCTTCTCT	GGCCTGACCCAAAACTAAGGGAAGTG
Chr14	1.6	C14-BARC-014457-01379	C14-BARC-014457-01379_F	Chr14	809,365	809,346	C14-BARC-014457-01379_R	Chr14	809,270	809,288	GATGGATTATACAGGTATGG	GAAAATCGTCATCATGAAT
Chr14	4.4	GMES0963	GMES0963_F	Chr14	1,269,194	1,269,210	GMES0963_R	Chr14	1,269,334	1,269,315	AGAGAAGAGAGGAGAGGGGG	AGCGCCTTCACTTCAGACTC
Chr14	5.2	GMES2796	GMES2796_F	Chr14	1,327,650	1,327,631	GMES2796_R	Chr14	1,352,338	1,352,357	AATGCCAACGCTAAAACACC	GGTCCTGTTCTGTGCCAACT
Chr14	8.1	C14-BARC-024295-04829	C14-BARC-024295-04829_F	Chr14	1,872,662	1,872,643	C14-BARC-024295-04829_R	Chr14	1,872,595	1,872,614	CAACTGTCCAAGAGCTAGTA	GAGCCAATGTGTGAACTGTG
Chr14	8.5	T001401890m	T001401890m_F	Chr14	1,885,290	1,885,312	T001401890m_R	Chr14	1,885,511	1,885,489	CAAACCCTGGTCAACCACTATTA	AGTGTTTACGCCTAACTCGATCC
Chr14	12.8	T001402652s	T001402652s_F	Chr14	2,652,927	2,652,949	T001402652s_R	Chr14	2,653,074	2,653,052	AAATTCCAATCATAAAGCGAGTG	AATTGAAGGAAGGAATTATCCAC
Chr14	13.3	Sat_342	Sat_342_F	Chr14	2,958,099	2,958,078	Sat_342_R	Chr14	2,957,871	2,957,892	ACTCTGGGGAAAATTAGTTTAG	GAGTCGGGGAGCACTACTTGTC
Chr14	13.6	GMES1204	GMES1204_F	Chr14	3,061,344	3,061,363	GMES1204_R	Chr14	3,061,533	3,061,514	AGGACCAAGAGCCAGTTGAA	CGCTCCTCTTGTTGTTCCTC
Chr14	13.8	alphaP-AT17.4										
Chr14	14.9	GMES1617	GMES1617_F	Chr14	3,766,011	3,766,030	GMES1617_R	Chr14	3,766,393	3,766,374	TCCCAGAAACATCGTCAACA	CGGATAGTGCCCGTAACACT
Chr14	18.5	GMES2219	GMES2219_F	Chr14	4,542,749	4,542,768	GMES2219_R	Chr14	4,542,912	4,542,893	AGAAACCATGCTTCTCCGAA	ACGGTTCAAAAATCACTCCG
Chr14	20.2	T001404790l	T001404790l_F	Chr14	4,876,268	4,876,290	T001404790l_R	Chr14	4,876,632	4,876,611	AAAGAATTGTTGAGGAGAGAAGC	GTGTTTGGAAACTCGTTACGGA
Chr14	22.7	C09-BARC-039595-07510	C09-BARC-039595-07510_F	Chr14	5,114,890	5,114,909	C09-BARC-039595-07510_R	Chr14	5,114,979	5,114,960	AATCTGGATTAGGGAGGTGC	GTGCCGTGTATTGGATATTG
Chr14	24.9	Sat_287	Sat_287_F	Chr14	5,290,075	5,290,053	Sat_287_R	Chr14	5,289,821	5,289,848	CATTCCCTATTTTTTAGAATGAGTAAAT	CCATAATCAGCATGCACACCTTATATGG
Chr14	27.9	T001405527l	T001405527l_F	Chr14	5,638,988	5,639,010	T001405527l_R	Chr14	5,639,333	5,639,310	ACGCTGATATCTGTTGTCTTTCC	TGTACAGCATAGAAGACACAAAGG
Chr14	31.2	GMES1593	GMES1593_F	Chr14	6,173,820	6,173,839	GMES1593_R	Chr14	6,173,998	6,173,979	AGGAGATTGGAGAGGGCATT	CAATAGCAACTCAGGTGGCA
Chr14	33.4	s017901076-2	s017901076-2_F	Chr14	6,478,312	6,478,290	s017901076-2_R	Chr14	6,478,121	6,478,143	GCCAATCATTGTCTTTCAAACTC	AAGCCTAGCCTTCTCATGTTCTT
Chr14	36.4	T001406633m	T001406633m_F	Chr14	6,742,913	6,742,935	T001406633m_R				GCAGAGTGAAATGACTCAGGTCT	AGTACATTGAGTGTTCCAGCCAT
Chr14	38.6	T001407042m	T001407042m_F	Chr14	7,150,713	7,150,736	T001407042m_R	Chr14	7,151,038	7,151,016	TCTTCATAATTCTTCTTGTCGGAA	AGAACTGTCCACGTAACCCATTA
Chr14	43.1	s017900038	s017900038_F	Chr14	7,519,597	7,519,575	s017900038_R	Chr14	7,519,261	7,519,283	TGATTTCTGACCGATGAATACCT	TTAATGGACGTTCGTATCAACAA

Chr14	46.8	T001407710m	T001407710m_F	Chr14	7,815,499	7,815,521	T001407710m_R	Chr14	7,815,774	7,815,752	TCATACACGTATAAAGGTTTGCT	ATTCATTGAGAAGGAGTTGTGCT
Chr14	49.5	T001407954s	T001407954s_F	scaffold_28	297,018	296,998	T001407954s_R				GTTCACCTTACCACCACCAAA	AAGATGTAACTCTCACTAGTCTTGTGTAT
Chr14	50.6	s020700146	s020700146_F	scaffold_28	128,996	129,018	s020700146_R	scaffold_28	129,317	129,295	ATGCACAACGATTTCTGGTAAGT	CAAAGAATCGATTTGGAATTCAG
Chr14	53.3	Satt416	Satt416_F	Chr14	8,436,339	8,436,314	Satt416_R	Chr14	8,435,984	8,436,010	TATAGCCCAGCAAAAAAAAACAGAGAT	ATCAAAACCGACCAATGAACAAAAAAA
Chr14	59.2	T001409417m	T001409417m_F	Chr14	9,210,600	9,210,622	T001409417m_R	Chr14	9,210,923	9,210,901	CAAAGATTAGTCATCGGCAGAAC	AACAATTCCTGACAGACACTTGG
Chr14	60.4	T001409860m	T001409860m_F	Chr14	9,654,403	9,654,425	T001409860m_R	Chr14	9,654,613	9,654,592	AATTTAGGTCATTACGATCGGCT	CCAGCACGTAAACATTGCTAAA
Chr14	61.7	T001411151m	T001411151m_F	Chr14	10,945,604	10,945,629	T001411151m_R	Chr14	10,945,818	10,945,796	CATCAATTACTAGCTTAGCCTCTTCA	TTTATCAGCAGCTAGCACTCTGT
Chr14	61.7	s007403816-2	s007403816-2_F	Chr14	11,875,094	11,875,116	s007403816-2_R	Chr14	11,875,280	11,875,255	TGAGTCAGTTCAACGATGACTTT	TGTGAATAGAGCATCAATAATTTGAA
Chr14	63	Sat_355	Sat_355_F	Chr14	13,587,720	13,587,696	Sat_355_R	Chr14	13,587,514	13,587,538	ATAACACTAAATGACCAGCAGGATT	GAGCCAAGTATCAAACCAAAACAAC
Chr14	63.8	T001418240m	T001418240m_F	Chr14	22,373,532	22,373,554	T001418240m_R	Chr14	22,373,746	22,373,724	CCCTCAGGGACTAAATTCTCCTA	AATGGTGTAGCTTACTAGCGCAC
Chr14	64.9	GMES4127	GMES4127_F	Chr14	26,042,606	26,042,627	GMES4127_R	Chr14	26,042,808	26,042,789	CAGTGCTACATAGGAGGTGCAT	GGGCACAGCTCCATTCTAAG
Chr14	64.9	GMES0016	GMES0016_F	Chr14	28,514,619	28,514,600	GMES0016_R	Chr14	28,514,396	28,514,415	TCAACGAACACAGTACCCCA	ACCATTTCCACAACCTCAGC
Chr14	64.9	GMES5996	GMES5996_F	Chr14	28,987,983	28,987,964	GMES5996_R	Chr14	28,987,541	28,987,558	TGGATTTTACCCCAATGGAA	CAATGATCCACTGCCTTGTG
Chr14	65.2	T001425271l	T001425271l_F	Chr14	29,394,202	29,394,224	T001425271l_R	Chr14	29,394,547	29,394,525	ATATTAAGCTCGTAGTGTTGGCG	TTTGTCACACAACAATTATGCAC
Chr14	65.4	s004007100	s004007100_F	Chr14	30,238,512	30,238,490	s004007100_R	scaffold_522	5,466	5,444	TGAACATCAGTTGGATTCCATAG	TGTGCCCTTGATATCTGCTTTAC
Chr14	65.4	Satt601	Satt601_F	Chr14	31,286,161	31,286,186	Satt601_R	Chr14	31,286,339	31,286,318	CCTACGCAAGTAACATTGGTTGTCAT	GCTAAAACGTATTAAATTAAGA
Chr14	70.7	s004002046	s004002046_F	Chr14	35,345,277	35,345,255	s004002046_R	Chr14	35,344,964	35,344,986	ACATCATGGATTATGTCACGACC	GGCCAGGGTAGTAATAGGCTTAG
Chr14	70.7	T001435717m	T001435717m_F	Chr14	18,889,235	18,889,257	T001435717m_R	Chr14	18,889,522	18,889,500	GGTGATTTGTGAAGCAAACTGTA	CATCGTGAGGAGTTGTGGTTAAT
Chr14	70.7	Satt556	Satt556_F	Chr14	38,861,141	38,861,158	Satt556_R	Chr14	38,861,297	38,861,280	ATAAAACCCGATAAATAA	TTGTGCACCTTGTTTTCT
Chr14	70.7	s003600119	s003600119_F	Chr14	39,068,156	39,068,178	s003600119_R	Chr14	39,068,354	39,068,331	TGATTGGGCATGTAAGTCCTAGA	TTCATCAAACACTACACAAACACG
Chr14	70.7	s003600885	s003600885_F	scaffold_23	88,011	88,033	s003600885_R	Chr14	39,824,566	39,824,544	CGTTAATTAGTCTAACCCGCGTA	GATGTTGATGCTGTGACATCCTA
Chr14	71.8	s003601923	s003601923_F	Chr14	40,859,318	40,859,340	s003601923_R	Chr14	40,859,475	40,859,453	AAATTCAGTTGTACTTCACGCAT	TTGCAGGTGATTCGACTTATACC
Chr14	71.8	s003602279	s003602279_F	Chr14	41,216,038	41,216,060	s003602279_R	Chr14	41,216,428	41,216,406	AACTTATAGAGGATTGGGTCAAA	GCACAATTTGGAATGTTTCATTT
Chr14	72.1	s003602737	s003602737_F	Chr14	41,673,425	41,673,450	s003602737_R	Chr14	41,673,813	41,673,791	TTCAAATCTATGGGATATAAACATTC	TTCCCTTTGTTGCATTCTCTTTA
Chr14	73	s003603136	s003603136_F	Chr14	42,073,465	42,073,487	s003603136_R	Chr14	42,073,628	42,073,611	TCCAATCGGTCGTTTAGTGTTAT	GATGCTTAAGTAGTCAAGTTGTTGG
Chr14	75.9	s003604395-2	s003604395-2_F	Chr14	43,323,688	43,323,710	s003604395-2_R	Chr14	43,323,837	43,323,813	GTCCATGTGTTGACTTGTAAAGC	CCAGAATTCTTATTACACAATGCAA
Chr14	76.8	s003604717-2	s003604717-2_F	Chr14	43,645,880	43,645,902	s003604717-2_R	Chr14	43,646,059	43,646,038	GATGGAGGGATACCTTGATTCAT	ACCGCTTGATTTGACCAATAAT
Chr14	78.4	s003605092-2	s003605092-2_F				s003605092-2_R	Chr14	44,016,452	44,016,427	AAATCAATGTCAAGATAAGATGAGTG	AAACAAACAGACACATATTACTCCAA
Chr14	79.7	T001444884s	T001444884s_F	Chr14	44,158,530	44,158,554	T001444884s_R	Chr14	44,158,702	44,158,680	TTTATACAATCGTTCAATCTCAACA	GCGTTAACCGTATCCACAAGATA
Chr14	84.2	s003605440-2	s003605440-2_F	Chr14	44,366,904	44,366,929	s003605440-2_R	Chr14	44,367,102	44,367,080	AAACTTTGGAAGAAGATAAACTACAT	AAATTGAAACGAATGGGTAATTT
Chr14	89.8	T001445242s	T001445242s_F	Chr14	44,521,536	44,521,558	T001445242s_R	Chr14	44,521,745	44,521,724	CAATGGTGAGGATGAAAGGTAAT	AGGTGCTGATGCCTAATTGTCT
Chr14	92.8	s003605780-2	s003605780-2_F	Chr14	44,706,146	44,706,169	s003605780-2_R	Chr14	44,706,340	44,706,317	CAACAAACTCTATTCAATTCCGTG	TTTGTGACGTCTTATTCTGATAAA
Chr14	93.7	Satt534	Satt534_F	Chr14	45,043,431	45,043,452	Satt534_R	Chr14	45,043,615	45,043,597	CTCCTCCTGCGCAACAACAATA	GGGGGATCTAGGCCATGAC
Chr14	95.7	T001446170l	T001446170l_F	Chr14	45,449,514	45,449,536	T001446170l_R	Chr14	45,449,874	45,449,849	TTTATTGTGGAATCAGGGTGATA	TTTGATCTATGTTCAGTGTCTTATTT
Chr14	100.3	GMES4048	GMES4048_F	Chr14	45,886,163	45,886,182	GMES4048_R	Chr14	45,886,368	45,886,349	CACTCTGCTCCTCCCTCTTG	TAGGGGGAGAGGGGAAATAA
Chr14	101.9	GMES2363	GMES2363_F	Chr14	46,051,521	46,051,540	GMES2363_R	Chr14	46,051,668	46,051,649	TCGTCTTGTTCTTCGCCTTC	GTCGCTTCCTCTTCAAAACG
Chr14	106.5	Satt726	Satt726_F	Chr14	46,328,517	46,328,538	Satt726_R	Chr14	46,328,710	46,328,695	TTTTTAGTATGGATAATGTTTT	AAGGGACAAGAGTGAT
Chr14	108.3	C14-BARC-040821-07850	C14-BARC-040821-07850_F	Chr14	46,774,311	46,774,293	C14-BARC-040821-07850_R	Chr14	46,774,215	46,774,234	CTGAAATGTGCTTGTAAAG	TTGCCTTGATAAGCTAGAAG
Chr14	108.9	s015600642	s015600642_F	Chr14	46,893,640	46,893,661	s015600642_R	Chr14	46,893,890	46,893,868	ATAAATTTCCTTGTGATTCCCG	GCTACGTGATGTTTGGAAATGAT
Chr14	109	s015600675	s015600675_F	Chr14	46,923,909	46,923,931	s015600675_R	Chr14	46,924,218	46,924,196	AAGTTAGATCGGCTGTGTGAAAG	GCAGAATGCACTCAACTAACTTC
Chr14	109.1	s015600697	s015600697_F	Chr14	46,946,430	46,946,452	s015600697_R	Chr14	46,946,732	46,946,710	CCTCGCGGTTCGTTTATTATTAC	GAACAACGTGAATGACGTAAAGG
Chr14	110	s015600824	s015600824_F	Chr14	47,073,901	47,073,923	s015600824_R	Chr14	47,074,245	47,074,223	AACATCAATTGGAGTCCCTTAGC	GAGGTCACCTATGAAAGTCCCTT
Chr14	110.5	GMES2238	GMES2238_F	Chr14	47,093,360	47,093,341	GMES2238_R	Chr14	47,092,896	47,092,915	CGCTATCATCCAATGACCAA	TGCACTGCATGAGGTAGGAG
Chr14	110.5	s015600843	s015600843_F	Chr14	47,092,944	47,092,966	s015600843_R	Chr14	47,093,230	47,093,208	CAAGATGCGTTTAGAAGCCATAC	AAGTCCCTTTGGTCTTCATCTTC
Chr14	110.7	s015600857	s015600857_F	Chr14	47,106,906	47,106,928	s015600857_R	Chr14	47,107,196	47,107,176	AGTATGAGATGGGAGACCCAAAT	CCCTGGATTTGAAAGACTAAA
Chr14	111.8	s001505206-2.1										
Chr14	112.3	GMES1809	GMES1809_F	Chr14	47,592,441	47,592,460	GMES1809_R	Chr14	47,592,727	47,592,708	GCAGCCGCTGAAGAAGTTAG	TTGGGTGAAACCATTCTCAA
Chr14	113.9	T001448411s	T001448411s_F	Chr14	47,731,482	47,731,503	T001448411s_R	Chr14	47,731,690	47,731,665	ATATTTGCACCATTGCATGTGA	AAACTAAACATAGGTTATGAGGTTAG
Chr14	115.3	C14-BARC-012703-00380	C14-BARC-012703-00380_F	Chr14	47,835,746	47,835,726	C14-BARC-012703-00380_R	Chr14	47,835,649	47,835,667	CCTCTCACTATATATAGACAC	CCCCTCCAATAAACACTCTA
Chr14	116.9	T001448628m	T001448628m_F	Chr14	47,948,920	47,948,942	T001448628m_R	Chr14	47,949,238	47,949,216	GCTACGAGGAATCTACCTGGTTT	AAATGTCAAATTCAAACGTTGCT
Chr14	119.3	T001448722m	T001448722m_F	Chr14	48,042,509	48,042,531	T001448722m_R	Chr14	48,042,814	48,042,792	GGAGAGAGAGCTAGAACAGGGTC	TATTATGGCCAGTTTAATTTCCG
Chr14	120.4	T001449696l	T001449696l_F	Chr14	48,076,257	48,076,235	T001449696l_R	Chr14	48,075,878	48,075,900	ATAATTTCATCTACTCCGTGGCA	TAATGAGGAAGTCAGGATGAACG
Chr14	120.4	T001449699l	T001449699l_F	Chr14	48,073,032	48,073,010	T001449699l_R	Chr14	48,072,668	48,072,690	TGAAGGTACATCCTAAGAATCCG	ATGGTTAAGATCGTGAGTTGAGG
Chr14	120.8	T001449676m	T001449676m_F	Chr14	48,096,087	48,096,065	T001449676m_R	Chr14	48,095,862	48,095,883	ACGACAAGATGATGGTCAGATTT	ACGGGTACACACGAGCTTTAAT
Chr14	122	GMES0104	GMES0104_F	Chr14	48,218,169	48,218,148	GMES0104_R	Chr14	48,218,058	48,218,081	TGGGTTAGGTCAATTCAGATCA	AAAGGAGCTTCTTCTTTTAAGACC
Chr14	122	T001449533s	T001449533s_F	Chr14	48,239,370	48,239,348	T001449533s_R	Chr14	48,239,219	48,239,241	ACTTTCTCCGGTAATCATCCTCT	AAATCCAGTTAAACCTACAACACTTT
Chr14	124.4	T001449387m	T001449387m_F	Chr14	48,384,832	48,384,810	T001449387m_R	Chr14	48,384,574	48,384,600	AATATGCAAGGTCAGTCCAAGAA	GGGTTGACTTAATAATGAGTGAGACTT
Chr14	126.5	T001449159l	T001449159l_F	Chr14	48,612,951	48,612,929	T001449159l_R	Chr14	48,612,572	48,612,598	TTCGTAAGAATTTATCCATCTGT	CTTGTTGTATTATCTTTCTTATGATCT
Chr14	128.8	T001448885l	T001448885l_F	Chr14	48,886,827	48,886,805	T001448885l_R	Chr14	48,886,485	48,886,507	GGAGTCAATTGAATGGCAAATAC	AAATTAATTAACCCACATCCACA
Chr14	128.8	T001448893l	T001448893l_F	Chr14	48,879,337	48,879,315	T001448893l_R	Chr14	48,878,958	48,878,981	ATTGATAATGAACCTTGCCCAAT	CAAATTAACATCCTTACGTTCGAT
Chr14	128.8	s004000269	s004000269_F	Chr14	48,776,797	48,776,775	s004000269_R	Chr14	48,776,450	48,776,472	GTTTCCCTACCAACAAACCAAAT	ATGTACGTGCACCAGAAACAAAT
Chr15	0	T001500125s	T001500125s_F	Chr15	123,822	123,846	T001500125s_R	Chr15	124,009	123,985	TTTGGAAAGAGAGAAGACTATGAAA	CGAATTACTGCGTATAGCTTACTTT
Chr15	1.4	T001500358l	T001500358l_F	Chr15	356,718	356,742	T001500358l_R	Chr15	357,141	357,116	CTTTCAAGATCTAACTCACTAAGAA	GGAATGTAAATCTCAAATGTAAGAAG
Chr15	3.3	C15-BARC-030171-06819	C15-BARC-030171-06819_F	Chr15	754,929	754,948	C15-BARC-030171-06819_R	Chr15	755,009	754,990	AGAAGCTAAGTACTCCCTCG	ACTCTCAATCTCTAAGGAGG
Chr15	4.3	Satt575	Satt575_F	Chr15	876,299	876,319	Satt575_R	Chr15	876,494	876,474	GCTAATTTTGTTTATAGGAAT	CCGCTACCATCTCGGAGGACT
Chr15	5.3	GMES1424	GMES1424_F	Chr15	920,094	920,113	GMES1424_R	Chr15	920,286	920,267	TCTTCGGTGTTGCAATCAAG	ACAACCTTCAAACTGGCTGG
Chr15	9.9	GMES0357	GMES0357_F	Chr15	2,353,821	2,353,840	GMES0357_R	Chr15	2,353,990	2,353,971	CACACCCTTTTAGCTGCACA	GAGGTATTGTCTTTGGGGCA
Chr15	10.1	C15-BARC-013501-00503	C15-BARC-013501-00503_F	Chr15	2,400,580	2,400,561	C15-BARC-013501-00503_R	Chr15	2,400,490	2,400,509	CTGATACCTAGGTCAGCAAC	TTCCACTGGATGAAACATGC
Chr15	10.1	GMES0779	GMES0779_F	Chr15	2,420,459	2,420,478	GMES0779_R	Chr15	2,420,688	2,420,669	CCCATATGATCTCGTCGTCC	GTAGCAATACCAGGGCAAGG
Chr15	10.7	Satt411	Satt411_F	Chr15	2,516,746	2,516,769	Satt411_R	Chr15	2,516,840	2,516,818	TGGCCATGTCAAACCATAACAACA	TTGAAGCCGCCTACAAATATAAT
Chr15	11.6	GMES2824	GMES2824_F	Chr15	2,841,820	2,841,801	GMES2824_R	Chr15	2,841,547	2,841,566	TTAATTACTCGCATTCCGCC	GAAGAAGCTGCTAAGGGCAA
Chr15	12.9	C15-BARC-017893-02417	C15-BARC-017893-02417_F	Chr15	3,308,090	3,308,110	C15-BARC-017893-02417_R	Chr15	3,308,179	3,308,160	CAGAATGAGATATTTCTGGTC	GCTGTGTCTTCAATGAAGCC
Chr15	16.2	T001503496l	T001503496l_F	Chr15	3,514,794	3,514,813	T001503496l_R	Chr15	3,515,190	3,515,168	GCCGAATTTCGTAGATCCAGT	CTCCATTTATGCACGCTATTAGG
Chr15	17.6	Satt720	Satt720_F	Chr15	4,154,382	4,154,409	Satt720_R	Chr15	4,154,648	4,154,621	CATATACGAAACATATTGTCAAGTTACA	TCATGAGTGGTTTGTTCTATACTTCTAT
Chr15	18.8	C15-BARC-039433-07497	C15-BARC-039433-07497_F	Chr15	4,413,928	4,413,947	C15-BARC-039433-07497_R	Chr15	4,414,007	4,413,988	ACCAAGAGCTAAGAATCAAG	TGAACTTTCCTGGGAAAGGG
Chr15	20.9	s007003323-2	s007003323-2_F	Chr15	4,620,984	4,620,962	s007003323-2_R	Chr15	4,620,592	4,620,614	CCAAATCTGCTATCAGTCAATCC	AACGTTATTGTACTCCTTTGGCA
Chr15	24.5	s007002959-2	s007002959-2_F				s007002959-2_R				TGCATCCGGGTTAAATTAAATA	TGAGATGCGCGCAATAAATA

Chr15	29	s007002562-2	s007002562-2_F	Chr15	5,380,117	5,380,095	s007002562-2_R	Chr15	5,379,902	5,379,924	TTTCGGGAGTACTTCACATGATA	CTTCTCCTCCTTTCTTCTTGGAA
Chr15	30.4	GMES1163	GMES1163_F	Chr15	5,694,178	5,694,159	GMES1163_R	Chr15	5,693,911	5,693,930	AGGGTCTACTTCGAACGCAA	GGGAAGGCAAAATTCACAAC
Chr15	30.4	GMES1287	GMES1287 F	Chr15	5,891,796	5,891,777	GMES1287 R	Chr15	5,891,607	5,891,627	CCTTGGCAAGCTCAGAAAAC	TCCAAATTTTGTCCATTCCAA
Chr15	35.1	T001506329l	T001506329l_F	Chr15	6,347,581	6,347,604	T001506329l_R	Chr15	6,347,928	6,347,906	CCCTTTAACAATTCAAACTTGTGG	TATGGTGGGTTTGAAGAGACACT
Chr15	37.5	Satt651	Satt651_F	Chr15	6,823,804	6,823,828	Satt651_R	Chr15	6,823,960	6,823,938	TGCTGTCTTTATACGAAGTACACTA	TGGCAATAAATATTCTCACTGAA
Chr15	41.4	T001507357s	T001507357s_F	Chr15	7,370,747	7,370,769	T001507357s_R	Chr15	7,370,925	7,370,901	ATTTAGAGTGGATCGACCTTTCC	CCTACTCATGTCATGTACCTCAAAG
Chr15	44.7	GMES4794	GMES4794 F	Chr15	7,760,212	7,760,231	GMES4794 R	Chr15	7,760,378	7,760,359	AAGAAACCAAGCAAAGCCAA	TGATTGGAACACGAAGGTGA
Chr15	48.9	s027100030	s027100030_F	Chr15	8,257,681	8,257,659	s027100030_R	Chr15	8,257,380	8,257,402	AGAATTATCAATAGCCACCAGCA	TGGCTGCTGAGAAATTAAGAAAG
Chr15	52.5	C15-BARC-040755-07843	C15-BARC-040755-07843_F	Chr15	9,120,889	9,120,870	C15-BARC-040755-07843_R	Chr15	9,120,805	9,120,823	ATCAACTCTGACCCAGAATC	AATAACATGACTGTTAACC
Chr15	52.8	s018900012	s018900012 F	Chr15	9,350,498	9,350,476	s018900012 R	Chr15	9,350,133	9,350,155	TGCTAGTTCTTGCTGGTGTGTTA	GCATCGTGAAATTAAGCAATACC
Chr15	52.8	s029300038	s029300038_F	Chr15	9,501,363	9,501,386	s029300038_R	Chr15	9,501,689	9,501,664	AATACTCTCTCTTCCCTCCTCCTC	GCATATTAATAGTCATACTCAAATCG
Chr15	52.8	Sat_273	Sat_273_F	Chr15	9,396,602	9,396,626	Sat_273_R	Chr15	9,396,819	9,396,796	TTTCCTAGGGTAAGCACAGTGTATT	GGGTGGAGAGAAAAAGAAAGAACA
Chr15	52.8	C09-BARC-025663-04988	C09-BARC-025663-04988_F	Chr15	9,505,124	9,505,143	C09-BARC-025663-04988_R	Chr15	9,505,214	9,505,195	AGATCGACGACGACGTTTTG	AGAGAATGGAGAAGAGGTCG
Chr15	53.3	C15-BARC-039087-07438	C15-BARC-039087-07438 F	Chr15	9,710,601	9,710,582	C15-BARC-039087-07438 R	Chr15	9,710,512	9,710,531	TTAGGATACACATCCCCAGC	GCTACAAAGAGTTGCTTCTG
Chr15	53.3	GMES3926	GMES3926_F	Chr15	9,757,038	9,757,057	GMES3926_R	Chr15	9,757,314	9,757,295	AAAGTAACAGCAACGACGGC	TCCTTCTCCCATTCTCCCTT
Chr15	55.2	T001509940l	T001509940l_F	Chr15	10,092,730	10,092,752	T001509940l_R	Chr15	10,093,109	10,093,087	AATCACAGGAGTCAAGGACAGAC	AACAGAGGTATGGTGTCATGGAT
Chr15	55.2	T001510057l	T001510057l_F	Chr15	10,209,948	10,209,975	T001510057l_R	Chr15	10,210,291	10,210,267	TCCATATAAGTATGTCAATAAGCAGTCC	CAGATCTTATTAAATCCAAGGCAAA
Chr15	57.6	T001510237l	T001510237l_F	Chr15	10,387,739	10,387,761	T001510237l_R	Chr15	10,388,117	10,388,095	TAATTCCTTTGTGGGACTTGATG	CCATTTGCTTCAGTTCAAATCAT
Chr15	58.5	T001510448l	T001510448l_F	Chr15	10,525,130	10,525,152	T001510448l_R	Chr15	10,525,492	10,525,470	CCTTCAGGCTATAACAGAGGGTT	CAAATGCACGGTTCTTTCTTTAC
Chr15	59	T001510477s	T001510477s_F	Chr15	10,554,417	10,554,438	T001510477s_R	Chr15	10,554,626	10,554,606	AAACTGGCTATCAAGTTAAACA	AAGGGTACCATCTTCAGCCAG
Chr15	61.7	T001510617s	T001510617s F	Chr15	10,692,466	10,692,490	T001510617s R	Chr15	10,692,635	10,692,613	TGCTGACTCGAATAGTCAAATTAAA	TAAGGGAACAACCGAACAAGTTA
Chr15	62.9	GMES5916	GMES5916_F	Chr15	10,794,771	10,794,752	GMES5916_R				CCAGGGAAAGTTGTCCTCAC	TCCACCCACCTCCAAAACTA
Chr15	64.1	GMES4669	GMES4669_F	Chr15	10,999,818	10,999,799	GMES4669_R	Chr15	10,999,618	10,999,637	TCTCACTCAACTCGCCAATG	TCTCCGACAAATCCTGGAAG
Chr15	65.5	Satt512	Satt512_F	Chr15	11,239,651	11,239,669	Satt512_R	Chr15	11,239,782	11,239,759	GCGTGCTAAAGCTCATGAGGAG	GCGGGCGTAATAACTCAAAATTTGTTT
Chr15	69.3	s012000395-2	s012000395-2 F	Chr15	11,551,052	11,551,074	s012000395-2 R	Chr15	11,551,237	11,551,215	TGTTTATGCATTTGGTTATGATG	CACACTTCCTTACAAACACCACA
Chr15	69.6	C15-BARC-044707-08763	C15-BARC-044707-08763_F	Chr15	11,583,459	11,583,478	C15-BARC-044707-08763_R	Chr15	11,583,552	11,583,533	GCATAGGTGTGCATGCTTTG	CTTACAATACACAAGTCATC
Chr15	71.8	T001511840s	T001511840s_F	Chr15	11,858,778	11,858,803	T001511840s_R	Chr15	11,858,984	11,858,962	AAGTGAGTTAGAGATACCATAAGAGA	AATAACAATTACCATTTGCCTAA
Chr15	76.2	s012001055-2	s012001055-2 F	Chr15	12,212,767	12,212,789	s012001055-2 R				TGTGAGGAATTGTTGTGAAATGT	AAACACTTTGGGTGTGATCTCTG
Chr15	78.2	s012001347-2	s012001347-2_F	Chr15	12,504,649	12,504,672	s012001347-2_R	Chr15	12,505,142	12,505,120	GGTATGTTGCTAACCTACTCCTTC	AAATGGAAAGAATAGTAATTGGA
Chr15	82.1	GMES3928	GMES3928_F	Chr15	13,106,716	13,106,735	GMES3928_R	Chr15	13,106,988	13,106,969	CCACGCGTCCTTCTTCTTAC	ACAGAGCCAACGATGAATCC
Chr15	85.6	Satt573	Satt573_F	Chr15	13,653,601	13,653,623	Satt573_R	Chr15	13,653,757	13,653,732	GATTTCGATTTGAATATACTTAC	CCTGTGGCTGTTATACTATGCATATA
Chr15	86.6	GMES0025	GMES0025 F	Chr15	14,043,447	14,043,428	GMES0025 R	Chr15	14,043,317	14,043,331	ATGAGCACCGAAAAGGAGAA	GATACACCTCGGTGGAGGAA
Chr15	90.2	Satt606	Satt606_F	Chr15	14,942,604	14,942,623	Satt606_R	Chr15	14,942,875	14,942,855	TTCTAAATTAAGCAATTCTT	TGGGTAATAATATTGGTTCAG
Chr15	91.5	GMES3192	GMES3192_F	Chr15	15,222,808	15,222,827	GMES3192_R	Chr15	15,222,988	15,222,965	AGGGGAAGCAACTCACAGAA	TCAAAAATTTTAAAAGAGAGGGGA
Chr15	93.9	Sat_136	Sat_136_F	Chr15	16,631,537	16,631,556	Sat_136_R	Chr15	16,631,706	16,631,685	ATCATGCTTCAACACTCTTT	TCCTATTTTTGCCCTTGTATTT
Chr15	98.5	Satt204	Satt204_F	Chr15	17,701,447	17,701,425	Satt204_R	Chr15	17,701,219	17,701,243	GCCATCTTGTTACAATGCAGGTA	CCTTACTCACTCCATTGGCATAATA
Chr15	99.8	s009500028	s009500028_F	Chr15	19,721,111	19,721,133	s009500028_R	Chr15	19,721,479	19,721,456	ATATGACAGCTTGGGCATTATGT	CATTCATGTTAATCACGCTAGAAA
Chr15	100.7	C15-BARC-030059-06796	C15-BARC-030059-06796_F	Chr15	20,741,320	20,741,339	C15-BARC-030059-06796_R	Chr15	20,741,398	20,741,379	AGGATAAAGATCCAAGACTG	CTCTAGGTTGAGGTAAGTGC
Chr15	101.5	Sat_172	Sat_172_F	Chr15	22,890,174	22,890,154	Sat_172_R	Chr15	22,889,973	22,889,994	TTCTAATTTCCTGACACTGTT	GGACGTAAACGGATAATAAGGT
Chr15	101.5	Satt268	Satt268_F	Chr15	22,967,939	22,967,962	Satt268_R	Chr15	22,968,173	22,968,154	TCAGGGGTGGACCTATATAAAATA	CAGTGGTGGCAGATGTAGAA
Chr15	101.8	GMES4754	GMES4754_F	Chr15	24,136,302	24,136,283	GMES4754_R	Chr15	24,136,087	24,136,106	ATCACCACCATCCCGAAATA	GCATGGCATACTGGGGTTAC
Chr15	102.6	s005500687	s005500687_F	Chr15	39,638,846	39,638,868	s005500687_R	Chr15	39,639,179	39,639,156	CCATTGAGCCATTAGTTAACCTG	CGTCATTTGGTCATATAACACTTT
Chr15	103.4	T001541524l	T001541524l F	Chr15	42,280,300	42,280,323	T001541524l R	Chr15	42,280,651	42,280,629	CAACTAACATTGAGAACGCATACA	TGGAACTAATGTCGGTGCTTTAT
Chr15	108.7	s022900033	s022900033_F	Chr15	44,939,688	44,939,710	s022900033_R	Chr15	44,940,004	44,939,982	AATGAAGGACAATCACGTAATGC	GAAGGTGATAACAAGCAACAAGG
Chr15	110.6	T001546042l	T001546042l_F	Chr15	46,826,185	46,826,205	T001546042l_R	Chr15	46,826,546	46,826,524	AAGAGGAGGCATCATCGGTAT	GACCTTAGTGACGATCTCGTTTG
Chr15	115.9	C15-BARC-040087-07660	C15-BARC-040087-07660 F	Chr15	48,419,439	48,419,420	C15-BARC-040087-07660 R	Chr15	48,419,358	48,419,377	GCCCTCTCTTTTTCCTTTCC	GGGAGGGTAAAGAAAGGAAG
Chr15	115.9	GMES0712	GMES0712_F	Chr15	48,498,757	48,498,776	GMES0712_R	Chr15	48,499,019	48,499,000	AGGCCTTTGAGAGGAAGAGG	CAAACAAAAACGGAATGCCT
Chr15	119.8	Satt369	Satt369_F	Chr15	49,009,066	49,009,090	Satt369_R	Chr15	49,009,309	49,009,289	AACATCCAAAGAAATGTGTTCACAA	AGTTCGAATTTCTTTTCAAGT
Chr15	121.1	GMES0145	GMES0145_F	Chr15	49,755,417	49,755,398	GMES0145_R	Chr15	49,755,147	49,755,166	TGTCTCTTCCCCATCACTCC	GCCTTCCATTAAGGGTGTCA
Chr15	121.4	s023900002	s023900002 F	Chr15	49,905,232	49,905,207	s023900002 R	Chr15	49,904,964	49,904,990	GAGTTTCTGATGTTAGAGACTTGTCC	CCAGAATTAAAGTTCTAGAAGGATTTG
Chr15	122.2	T001549335m	T001549335m_F	Chr15	50,126,284	50,126,306	T001549335m_R	Chr15	50,126,607	50,126,585	GTGTAATGTCAATTTGAGCGGAT	AACCTCCTCATAGTGGTGCAATA
Chr15	122.5	C15-BARC-029659-06286	C15-BARC-029659-06286_F	Chr15	50,327,382	50,327,401	C15-BARC-029659-06286_R	Chr15	50,327,472	50,327,453	GTATCAGTTCAGATGGTTTC	CACTCGGAGAGGAAATTGGC
Chr15	124.6	T001549770l	T001549770l_F	Chr15	50,566,300	50,566,325	T001549770l_R	Chr15	50,566,640	50,566,616	TTCATGTTCTCCTTCTTATATGTTCC	AAAGATTGTTGCTAAAGATTCTACC
Chr15	128	T001549997s	T001549997s_F	Chr15	50,793,175	50,793,197	T001549997s_R	Chr15	50,793,366	50,793,344	CATTGCACTCTCATTCCTTGTTT	CTAGAGGAGGCGATAGAGAGAGG
Chr15	134.1	Satt231	Satt231_F	Chr15	51,293,482	51,293,462	Satt231_R	Chr15	51,293,246	51,293,267	TGTGCAAAATGTTCATCATCT	GGCACGAATCAACATCAAAACTTC
Chr15	134.1	C15-BARC-040647-07806	C15-BARC-040647-07806_F	Chr15	51,350,322	51,350,303	C15-BARC-040647-07806_R	Chr15	51,350,251	51,350,270	GCAATTTAATCAAGTTGCAG	GTACATTAACTACGTGACTG
Chr15	135.5	s024400161-2	s024400161-2 F	Chr15	51,593,512	51,593,487	s024400161-2 R	Chr15	51,593,130	51,593,152	AAGGAAGATGTATAATTGATCAACCC	TCCTCCTTGAACATGTTATTCGT
Chr16	0	C16-BARC-016027-02038	C16-BARC-016027-02038_F	Chr16	133,154	133,135	C16-BARC-016027-02038_R	Chr16	133,068	133,087	TCTGGTGTCATTCACTCCTG	GGGTCAGGGTTATAAAGCAA
Chr16	0.5	T001600185s	T001600185s_F	Chr16	184,380	184,402	T001600185s_R	Chr16	184,589	184,568	CTCTCTTCACAAGTCACCAGACC	TGGTTTGGTGAGAGAATCCAAT
Chr16	1.1	GMES1300	GMES1300_F	Chr16	417,988	417,969	GMES1300_R	Chr16	417,777	417,802	TGGGATTTCTCAGTTTTCGG	GACATGACTAAAGGTCAAAATAGTGG
Chr16	1.1	AW310961	AW310961 F	Chr16	417,826	417,850	AW310961 R	Chr16	417,999	417,979	CAACTTTTTAGTAAATATTGCATAA	CATACATCTTTTGGGATTTCT
Chr16	6.1	Satt249	Satt249_F	Chr16	1,149,218	1,149,202	Satt249_R	Chr16	1,149,006	1,149,027	GCAAATTGTTATTGTGAGAC	GGCCAGTGTTGAGGGATTTAGA
Chr16	8.3	GMES2461	GMES2461_F	Chr16	1,222,870	1,222,851	GMES2461_R	Chr16	1,222,639	1,222,658	GGCTCAACTGGGTTTCCTTT	TGTTCCAAAACCCAACCAAT
Chr16	10.8	T001601773m	T001601773m F				T001601773m R	Chr16	1,790,020	1,789,998	TACCGTACACGTGTGAAGAGAAA	GGGACGAGCTTTACTTAAGCATT
Chr16	15.8	C16-BARC-025277-06467	C16-BARC-025277-06467_F	Chr16	2,336,784	2,336,765	C16-BARC-025277-06467_R	Chr16	2,336,702	2,336,721	CCCAACAATAGACAACCCAC	CGAATTATCTCATTCCGGTG
Chr16	16.1	GMES0236	GMES0236_F	Chr16	2,391,198	2,391,179	GMES0236_R	Chr16	2,390,802	2,390,821	CCTCCTCCCTCTGAAACCTC	TTTCTTCTCTCCCTTGGGCT
Chr16	18.9	Satt285	Satt285_F	Chr16	2,827,791	2,827,814	Satt285_R	Chr16	2,827,985	2,827,960	ACATATTGCATTAAAAACATACTT	GACTAATTCTATTTTACACCAACAAC
Chr16	21.2	T001603161m	T001603161m F	Chr16	3,184,970	3,184,992	T001603161m R	Chr16	3,185,308	3,185,286	TTGAATTAGGATATCTTCGGCCT	TAAAGTCTTCACGTTTGGTGTCG
Chr16	26.5	T001603446m	T001603446m_F	Chr16	3,470,879	3,470,901	T001603446m_R	Chr16	3,471,093	3,471,071	AAACTACGTGGGAGTCAAACTCA	TCAGTAATCGACTCACAAGGACA
Chr16	27	C16-BARC-018661-03226	C16-BARC-018661-03226_F	Chr16	3,585,124	3,585,106	C16-BARC-018661-03226_R	Chr16	3,585,038	3,585,057	TGGAGAATTTGGATAGAGC	TTATCTCCCACTGCTGCATC
Chr16	28.4	T001603705l	T001603705l_F	Chr16	3,729,321	3,729,344	T001603705l_R	Chr16	3,729,662	3,729,637	AGAAATCTTCGTAAGACTCTCAAA	GAACATTATATAAGGATTGCCATCAA
Chr16	33.8	GMES0775	GMES0775_F	Chr16	4,032,164	4,032,145	GMES0775_R	Chr16	4,031,959	4,031,978	TCCCCTTCAACCACTCTCAC	GTGGTGGTTATGGGAAGGTG
Chr16	34.7	C16-BARC-016775-02320	C16-BARC-016775-02320_F	Chr16	4,273,239	4,273,221	C16-BARC-016775-02320_R	Chr16	4,273,148	4,273,167	CTAAAATGAGTTAGTGTTG	CGGAATGTCCTGCAAACAAC
Chr16	35.7	C16-BARC-013953-01276	C16-BARC-013953-01276_F	Chr16	4,427,935	4,427,955	C16-BARC-013953-01276_R	Chr16	4,428,026	4,428,007	CTCGAGCTATTTTATGTACAC	TTAAGTGCCAGGGTTGCTTC
Chr16	37.4	GMES6291	GMES6291 F	Chr16	4,527,244	4,527,225	GMES6291 R	Chr16	4,527,058	4,527,077	CAAAGCCAAGCTCAATTTCC	CAAGGGTTGTTGTTGTGGTG
Chr16	41.3	s016200713	s016200713_F	Chr16	5,037,245	5,037,267	s016200713_R	Chr16	5,037,543	5,037,521	TTCTCAATCTGCTTAATGGTTCC	TGGCCATAGAGGATGAGATTCTA
Chr16	44.7	s016201264	s016201264_F	Chr16	5,579,513	5,579,535	s016201264_R	Chr16	5,579,749	5,579,726	GCATCATTTGTTAAGTTCCATGA	CGATGTTAACAGAAGGAGGTAGAA

Chr16	45.4	s016201509	s016201509_F	Chr16	5,824,566	5,824,584	s016201509_R	Chr16	5,824,874	5,824,852	AGATTCAAACAGTATCAACCCGA	GTTGCGGTCTTAGACTCTCATGT
Chr16	46.6	s027500283-2	s027500283-2_F	Chr16	5,988,178	5,988,155	s027500283-2_R	Chr16	5,988,033	5,988,056	TTCATACACAACTCACATCTTTGG	CCGCAAATGACATCAAGAATATAA
Chr16	48.2	GMES2423	GMES2423 F	Chr16	6,234,535	6,234,554	GMES2423 R	Chr16	6,234,629	6,234,610	GCATTCTCACAGGCACTGAA	GTCTAAATGGGGCACATGCT
Chr16	48.2	s027500035	s027500035_F	Chr16	6,235,152	6,235,132	s027500035_R	Chr16	6,235,015	6,235,037	AAAGTGCTCAAAGATCCAACT	TCAAGTTGAATTTGCGTTGATTA
Chr16	48.2	Satt693	Satt693_F	Chr16	6,325,753	6,325,775	Satt693_R	Chr16	6,326,024	6,326,001	AGGCCACTCATGTCACTGTCATT	CCAAGAATAAGTTATTTGAAATAAT
Chr16	50.9	s027700214	s027700214_F	Chr16	6,761,744	6,761,761	s027700214_R	Chr16	6,761,911	6,761,889	AAATTTGTTTCCGCAACT	AATTCTGCTTTGGTTTGTTGAAA
Chr16	54.7	T001607665s	T001607665s F	Chr16	7,822,807	7,822,829	T001607665s R	Chr16	7,823,003	7,822,981	TTCAACCACAACATAAATCGAAA	CACATAGAGACGTAGGAAGAGGG
Chr16	57.8	Satt414	Satt414_F	Chr16	8,909,806	8,909,829	Satt414_R	Chr16	8,910,109	8,910,086	TATTCCTAGTCACATGCTATTTCA	TCATAATAATGCCTAGAACATAAA
Chr16	57.8	GMES0644	GMES0644_F	Chr16	9,958,304	9,958,285	GMES0644_R	Chr16	9,958,179	9,958,198	CGATTCTTGGCATTCCACTT	CCGGACATGTTCCACAAAAT
Chr16	57.8	Sct_065	Sct_065_F	Chr16	10,668,514	10,668,499	Sct_065_R	Chr16	10,668,355	10,668,376	CCCTGTGTTTCCCTCT	GAAAAGTTTTATGTTCTGAGTG
Chr16	57.8	C16-BARC-045065-08871	C16-BARC-045065-08871_F	Chr16	13,961,905	13,961,886	C16-BARC-045065-08871_R	Chr16	13,961,808	13,961,826	CTATGATGAGGTTTAGAAGC	GAAGCTACTTGACATCAAT
Chr16	57.8	Satt596	Satt596_F	Chr16	14,155,351	14,155,334	Satt596_R	Chr16	14,155,096	14,155,112	TCCCTTCGTCCACCAAAT	CCGTCGATTCCGTACAA
Chr16	57.8	C16-BARC-044047-08593	C16-BARC-044047-08593_F	Chr16	15,844,260	15,844,279	C16-BARC-044047-08593_R	Chr16	15,844,338	15,844,319	GATATACAGTGCTGTTTCCC	CTGACTTCTTCTCCCTAACC
Chr16	57.8	C16-BARC-017157-02225	C16-BARC-017157-02225 F	Chr16	16,723,864	16,723,845	C16-BARC-017157-02225 R	Chr16	16,723,792	16,723,811	CCACCTTAGTGTTTCTTTCC	CAAAATCATGTATCCCCCCC
Chr16	58.1	GMES0058	GMES0058_F	Chr16	20,761,946	20,761,927	GMES0058_R	Chr16	20,761,744	20,761,770	ATCAAACACAGGGCAACCTC	TCAAATAAGATAAAAGATGTGAACAAA
Chr16	58.1	C16-BARC-016205-02309	C16-BARC-016205-02309_F	Chr16	21,014,983	21,014,964	C16-BARC-016205-02309_R	Chr16	21,014,898	21,014,917	CCTCCAGAAGGCTTTCTTAC	TGAAGGCGATTTGGATTAGG
Chr16	58.9	Satt456	Satt456_F	Chr16	21,571,135	21,571,156	Satt456_R	Chr16	21,571,424	21,571,399	GGGCCTTCGTTTGAGTTCATAG	GGGATCATTGGTTAATTGTTGTAAGA
Chr16	59.4	C16-BARC-032295-08940	C16-BARC-032295-08940_F	Chr16	25,015,992	25,016,011	C16-BARC-032295-08940_R	Chr16	25,016,070	25,016,051	AGACATGACAATGGGCGATG	ATATAAAAACATATTTAAAG
Chr16	60.2	C16-BARC-010251-00569	C16-BARC-010251-00569_F	Chr16	26,626,521	26,626,540	C16-BARC-010251-00569_R	Chr16	26,626,614	26,626,596	AAAGGATGAAGTAGCGTAGC	ATATCCCTTAAGTGTAATC
Chr16	62.8	alphaP-AT17.6										
Chr16	63.4	GMES0824	GMES0824 F	Chr16	28,146,255	28,146,274	GMES0824 R	Chr16	28,146,417	28,146,398	GAATCATCAAACCCCACACC	CGCCATTCTGAAACATAGCA
Chr16	63.5	C16-BARC-043101-08533	C16-BARC-043101-08533_F	Chr16	28,463,709	28,463,728	C16-BARC-043101-08533_R	Chr16	28,463,798	28,463,779	CTGGATGCTACATATTTTGC	AGGATGCATGAAATCAGGTC
Chr16	66.5	T001629204m	T001629204m_F	Chr16	29,570,015	29,570,037	T001629204m_R	Chr16	29,570,215	29,570,193	TGAAGATCATGGGAACTCTTGAC	AGTCACTCACAAGATCCCTCCTT
Chr16	68.7	GMES5722	GMES5722_F	Chr16	30,203,439	30,203,458	GMES5722_R	Chr16	30,203,640	30,203,621	GTGTTGTGAATGCGTTGAGG	GCTGCTGACAAAGGAGGAAC
Chr16	68.7	s014800003	s014800003 F	Chr16	30,283,312	30,283,287	s014800003 R	Chr16	30,283,073	30,283,095	AAGACCACAAATATTATTGCTTCAAA	CTCGACATAAACATCAGCATCAA
Chr16	68.7	C16-BARC-018761-03243	C16-BARC-018761-03243_F	Chr16	26,685,590	26,685,576	C16-BARC-018761-03243_R	Chr16	30,369,894	30,369,875	ATGAGTTGAATAGGCCATCC	GGAGAGAAGCATGAGTGTAG
Chr16	68.7	GMES2804	GMES2804_F	Chr16	30,370,320	30,370,301	GMES2804_R	Chr16	30,370,133	30,370,152	TTGGGCCAAACAGTCTTTTC	TCATGAAATTTGGTGGAGCA
Chr16	69.2	Sat_366	Sat_366 F	Chr16	30,404,612	30,404,634	Sat_366 R	Chr16	30,404,814	30,404,787	GCACAAGAACAGAGGAAACTATT	GACATGGTACATCTATATTACGAGTATT
Chr16	69.2	s014300091-2	s014300091-2_F	Chr16	30,416,492	30,416,514	s014300091-2_R	Chr16	30,416,850	30,416,829	TCATTCAACAATCATAATCACCG	GCCGGAGAGGTTAGTTTGTCTT
Chr16	71.7	s014300472-2	s014300472-2_F	Chr16	30,797,741	30,797,765	s014300472-2_R	Chr16	30,797,887	30,797,865	TTGGTATCAACTTCAACTCAACTTC	AGACTGAGTCCAAGCCTTCAATA
Chr16	75.5	T001630709l	T001630709l_F	Chr16	31,076,321	31,076,343	T001630709l_R	Chr16	31,076,631	31,076,608	ATAAGATAGCTTTCCAATCAACA	TTCACACTGATTTATTTATGATGG
Chr16	76.9	GMES4751	GMES4751 F	Chr16	31,233,434	31,233,414	GMES4751 R	Chr16	31,233,242	31,233,261	TGTGATTTCAAAGGAGTTGCC	AGGGTGCAAAGTTTCCATGT
Chr16	77.2	GMES4395	GMES4395_F	Chr16	31,265,789	31,265,808	GMES4395_R	Chr16	31,266,033	31,266,014	CTTCTCTCCCACCTCTCGTG	ATCCACTTGACTGGTGGAGG
Chr16	80.7	GMES1619	GMES1619_F	Chr16	31,732,074	31,732,053	GMES1619_R	Chr16	31,731,794	31,731,813	GAAAACACATTCAGAAACCACG	AAAAGCTGAACGTAGGGGGT
Chr16	82.4	C16-BARC-012111-00333	C16-BARC-012111-00333_F	Chr16	31,890,946	31,890,966	C16-BARC-012111-00333_R	Chr16	31,891,045	31,891,026	CATGGATATGTTATGTGTTGC	CCTCTTTAACAATGTTGCCA
Chr16	84	GMES1798	GMES1798_F	Chr16	32,379,824	32,379,805	GMES1798_R	Chr16	32,379,534	32,379,553	GGGGTGATCCAGAGTTGAGA	GCACCATGAAGTCACCAATG
Chr16	84.5	s027900013	s027900013_F	Chr16	32,408,405	32,408,431	s027900013_R	Chr16	32,408,768	32,408,746	TTTCACTCTGTCTATCATTGTCTTACA	AGCAATGCCACTTTGTTGTCTAT
Chr16	86.4	C16-BARC-039625-07527	C16-BARC-039625-07527_F	Chr16	32,589,736	32,589,716	C16-BARC-039625-07527_R	Chr16	32,589,645	32,589,665	CAGTATAGTTACACACAGTGG	GTGATGCTTTAATAATTGTGG
Chr16	89.1	s026800043	s026800043 F	Chr16	32,718,773	32,718,795	s026800043 R	Chr16	32,719,059	32,719,037	ATAGAAGATTGGTTGGAATCCGT	TGTTATAAATGCGAAGTTATGCG
Chr16	91.7	s024700008	s024700008_F	Chr16	33,039,147	33,039,169	s024700008_R	Chr16	33,039,412	33,039,390	TTGTTGCACTATCAATCATCCAG	ATGCAAGTCATGTTTGATATCCC
Chr16	93.8	Satt244	Satt244_F	Chr16	33,483,624	33,483,600	Satt244_R	Chr16	33,818,814	33,818,790	CCCCATATGTTTAAATTATATGGAG	ATGGGGATATTTTCTTTATTATCAG
Chr16	94.6	GMES3739	GMES3739_F	Chr16	33,929,714	33,929,695	GMES3739_R	Chr16	33,929,420	33,929,438	AAGTGGAGCCAGCAAAAGAA	GTGTTGCTGGAAAAGCCAA
Chr16	94.7	GMES1616	GMES1616 F	Chr16	33,971,917	33,971,898	GMES1616 R	Chr16	31,574,532	31,574,516	CACCAACCTCACCTGAACCT	ACATGACAGCAGCAACAAGG
Chr16	95.4	Satt547	Satt547_F	Chr16	34,035,076	34,035,093	Satt547_R	Chr16	34,035,278	34,035,258	CTATCCGATCCATATGTG	TGATTTCGCTAGGTAAAATCA
Chr16	98.6	GMES2494	GMES2494_F	Chr16	35,634,296	35,634,315	GMES2494_R	Chr16	35,634,591	35,634,572	ACGCAAACACTGAACCACAC	CCTTGAGTTCTTCCTCGGTG
Chr16	99.8	GMES0830	GMES0830 F	Chr16	35,761,685	35,761,704	GMES0830 R	Chr16	35,761,820	35,761,801	GAGAGAGGGAGGAGGAGGAA	CAATCCAACGGCTCAGATTT
Chr16	101.1	LFsoy6	LFsoy6_F	Chr16	35,778,780	35,778,799	LFsoy6_R	Chr16	35,779,139	35,779,119	GCTTTTGGTTAGTCTCTCTCC	CTTCCTCTCTGCTTGAACAAG
Chr16	104.2	C16-BARC-044031-08587	C16-BARC-044031-08587_F	Chr16	36,090,685	36,090,704	C16-BARC-044031-08587_R	Chr16	36,090,774	36,090,755	CCAGGGTTTGTGAAATTGGG	TCCATCAGGACGGAATATTG
Chr16	104.7	Satt431	Satt431_F	Chr16	36,221,613	36,221,595	Satt431_R	Chr16	36,221,395	36,221,415	TGGCACCCTTGATAAATAA	CACGAAAGTTTTTCTGTAACA
Chr16	106.3	T001636111l	T001636111l F	Chr16	36,613,162	36,613,184	T001636111l R	Chr16	36,613,528	36,613,506	CCGATAGATTAAGCCATGAAATG	TTTCTTTGGCATGATATTTGGTA
Chr16	109.9	T001636573m	T001636573m_F	Chr16	37,075,516	37,075,538	T001636573m_R	Chr16	37,075,754	37,075,732	TAGGTCCTGTTATGTACGGCACT	GAATATTCCAGACCTCAAGTTGC
Chr16	112.1	Sat_395	Sat_395_F	Chr16	37,577,292	37,577,270	Sat_395_R	Chr16	37,577,074	37,577,100	TCTTAGTCGTGCTGACACTACTC	AGTTTGTTTAGCTCAATCTTTCACTCA
Chr16	113.2	GMES6308	GMES6308_F	Chr16	37,795,590	37,795,571	GMES6308_R	Chr16	37,795,380	37,795,399	CATGGCTCAATTCCGTTTCT	GTTCTTCTCGTTGTCGCCTC
Chr17	0	T001700092s	T001700092s_F	Chr17	87,592	87,614	T001700092s_R	Chr17	87,789	87,771	CCTTTCAAATCAATGTAAGGCTG	TTTCAATTAAGTCCGCATT
Chr17	1.6	T001700369m	T001700369m_F	Chr17	364,571	364,593	T001700369m_R	Chr17	364,785	364,763	CAACCTGACACTTGATCGTTAAT	TATTGCTACGGTGCCATCAGTAT
Chr17	1.9	Sctt008	Sctt008_F	Chr17	665,014	665,034	Sctt008_R	Chr17	665,103	665,087	ACGCAGAGATAGAGAAAGAGA	CCCCCAGACACAACATA
Chr17	4.4	s002501021-2	s002501021-2 F	Chr17	1,014,998	1,015,020	s002501021-2 R	Chr17	1,015,145	1,015,122	CACCTGAATGCATCATGGTTACT	TTCTCTTCTCTTACACCTTTCTGC
Chr17	9.4	s002501359-2	s002501359-2_F	Chr17	1,351,548	1,351,572	s002501359-2_R	Chr17	1,351,718	1,351,694	TCTCATTAACACCTAATCATTCATTCA	TCAGATTTCACAGTTATCACCAATC
Chr17	12.8	Sat_333	Sat_333_F	Chr17	1,746,730	1,746,703	Sat_333_R	Chr17	1,746,582	1,746,607	TCACAGCTAGGTATTCACGAAAGAGAAA	GCCACCTTATTACACACCTCAAAACA
Chr17	14.2	GMES0866	GMES0866_F	Chr17	1,896,833	1,896,852	GMES0866_R	Chr17	1,897,048	1,897,029	CTCCACCGTGCACCTTATTT	ACTGGACAGTAGCAGGGTGC
Chr17	16.5	GMES1769	GMES1769 F	Chr17	2,564,340	2,564,359	GMES1769 R	Chr17	2,564,601	2,564,582	CCATTCACCTTTCTCCTCCA	CTCTGGTCCTCTTGCCGTAG
Chr17	16.5	GMES0854	GMES0854_F	Chr17	2,627,529	2,627,548	GMES0854_R	Chr17	2,627,789	2,627,770	AAGCAACGTTTGGAGGAAGA	ATCACATCAGAAGCCGAACC
Chr17	16.5	C17-BARC-018767-03009	C17-BARC-018767-03009_F	Chr17	2,638,024	2,638,005	C17-BARC-018767-03009_R	Chr17	2,637,952	2,637,971	CCTTCTAGAGGGAACCAAAC	GCAGGTATTGACTTACAGAC
Chr17	18.6	GMES3215	GMES3215 F	Chr17	3,123,615	3,123,634	GMES3215 R	Chr17	3,123,780	3,123,761	TCATTCGCCTTTCTGATTCC	GCCTAATTAAGAACCGGGGA
Chr17	20	GMES1639	GMES1639_F	Chr17	3,577,683	3,577,707	GMES1639_R	Chr17	3,577,866	3,577,847	CCAACAACTCCTATTAAGTTTTCAG	TTTCTCTTTCGGACCCCTTT
Chr17	20.5	GMES3352	GMES3352_F	Chr17	3,730,736	3,730,755	GMES3352_R	Chr17	3,731,000	3,730,981	TTGTCACTGCTCATTTTCGC	ACCTCCTGTTGGTGGATCTG
Chr17	21.8	GMES0732	GMES0732_F	Chr17	4,063,804	4,063,823	GMES0732_R	Chr17	4,063,978	4,063,959	AAATCGTACGGTGACGGAAG	CCTTCTTGAACTTGGCTTCG
Chr17	25.6	GMES2822	GMES2822 F	Chr17	4,855,754	4,855,773	GMES2822 R	Chr17	4,856,030	4,856,011	TCCCCTCTGGATCTCATGTC	GGATGGTGACCTTCTTGGTG
Chr17	25.8	C17-BARC-014447-01372	C17-BARC-014447-01372_F	Chr17	4,872,073	4,872,054	C17-BARC-014447-01372_R	Chr17	4,871,977	4,871,996	CAGCTAAAGAACTATTGCAG	GCGGTTAGACAATTGGGGAT
Chr17	26.9	GMES0860	GMES0860_F	Chr17	5,042,218	5,042,237	GMES0860_R	Chr17	5,042,489	5,042,470	TCAAAAGGAGTTGCATTCCC	TGCACCCAACTCAGTCTGTC
Chr17	28	C17-BARC-044761-08805	C17-BARC-044761-08805_F	Chr17	5,400,150	5,400,169	C17-BARC-044761-08805_R	Chr17	5,400,229	5,400,210	ACCATGAATGAATCACTGTC	CTTTCAAGTCTGTGTATTAC
Chr17	29.4	Satt135	Satt135_F	Chr17	5,892,060	5,892,036	Satt135_R	Chr17	5,891,893	5,891,913	CACGGATTTTAAATCATTATTACAT	TTCCAATACCTCCCAACTAAC
Chr17	34.1	s002506120-2	s002506120-2_F	Chr17	6,107,339	6,107,363	s002506120-2_R	Chr17	6,107,538	6,107,516	GAAATTGAACTTAACAAGGAGGTTT	CATTCGTCCAAATTAAGGTCCTA
Chr17	36.2	s002506580-2	s002506580-2_F	Chr17	6,568,376	6,568,394	s002506580-2_R	Chr17	6,568,517	6,568,494	GAACGCTTAGCCTCCATCC	GGATAGATCGATAGAAGCAGATTG
Chr17	39.2	Satt486	Satt486 F	Chr17	6,831,598	6,831,621	Satt486 R	Chr17	6,831,839	6,831,812	CATGCATTACCATAGGCTATAATA	GGGGTCATGCATAATAGAGATAGAACCA
Chr17	41.7	C17-BARC-021191-03999	C17-BARC-021191-03999_F	Chr17	7,118,473	7,118,457	C17-BARC-021191-03999_R	Chr17	7,118,397	7,118,416	CTGGTCATTCGCTACTTCAC	GTTTGTGTTTGTTGCTCAAG
Chr17	42.2	s002507263-2	s002507263-2_F	Chr17	7,245,265	7,245,287	s002507263-2_R	Chr17	7,245,448	7,245,424	TAAATAATCAAGCATGCTCACGA	CGGAAATAATGTAATGACAATGAAA

Chr17	44.7	s002507558-2	s002507558-2_F	Chr17	7,542,020	7,542,039	s002507558-2_R	Chr17	7,542,156	7,542,129	ACGCACTAATTAAACGGCTT	GCTAGAAAGAAACATAATAAAGAGTAAA
Chr17	48	T001708138l	T001708138l_F	Chr17	7,868,021	7,868,045	T001708138l_R	Chr17	7,868,367	7,868,341	TGGTTTAATTATCAGTTGGTTCCTC	TTTCTACTCTTATCGAAATTAAACTGA
Chr17	51.1	GMES6395	GMES6395 F	Chr17	8,237,730	8,237,749	GMES6395 R	Chr17	8,237,990	8,237,971	CTCTCACTCCCCCACTCATC	ACTCTTGCTCCTCCGTGAAA
Chr17	52.5	GMES0580	GMES0580_F	Chr17	8,363,773	8,363,792	GMES0580_R	Chr17	8,364,022	8,364,003	CCAATTCATTGAAGGCCACT	AAGGGAAACAAGGGATTCCA
Chr17	53.5	C17-BARC-035383-07190	C17-BARC-035383-07190_F	Chr17	8,569,070	8,569,089	C17-BARC-035383-07190_R	Chr17	8,569,160	8,569,141	TTAAGTAAGTAGAAATGTAG	CGTGCATTAGATTTCAGTTC
Chr17	54.9	GMES4177	GMES4177_F	Chr17	8,683,093	8,683,112	GMES4177_R	Chr17	8,683,227	8,683,209	GCTTCAGCGAAATCCTGTTC	AAGAATTTTCCAGCAAGCGA
Chr17	56.1	Satt002	Satt002 F	Chr17	8,817,882	8,817,861	Satt002 R	Chr17	8,817,757	8,817,774	TGTGGGTAAAATAGATAAAAAT	TCATTTTGAATCGTTGAA
Chr17	58.9	T001709449l	T001709449l_F	Chr17	9,177,914	9,177,936	T001709449l_R	Chr17	9,178,260	9,178,238	ATGGAGTAACATATGCAGCAACC	GCTGAACAAGGAATCTCCATAAA
Chr17	62.6	Satt154	Satt154_F	Chr17	9,576,946	9,576,922	Satt154_R	Chr17	9,576,675	9,576,699	AGATACTAACAAGAGGCATAAAACT	AAAGAAACGGAACTAATACTACATT
Chr17	66.5	s017100534-2	s017100534-2 F	Chr17	9,892,807	9,892,829	s017100534-2 R	Chr17	9,893,167	9,893,144	AAGTGAGTTACAACCGTCGGATA	GGAGGTCATGTTTAAATGATCAAG
Chr17	70.1	GMES0256	GMES0256_F	Chr17	10,223,249	10,223,230	GMES0256_R	Chr17	10,222,967	10,222,986	GTGACTCTTCCGTTGCTTCC	TCAGTCTCCGTTCCTCGTCT
Chr17	74.1	T001710954m	T001710954m_F	Chr17	10,667,360	10,667,382	T001710954m_R	Chr17	10,285,360	10,285,374	TTACTAACATTGTGTTTGGCCGT	CCTAGAGGCCACATCTCCTTATT
Chr17	76.3	C17-BARC-025885-05138	C17-BARC-025885-05138_F	Chr17	10,880,499	10,880,480	C17-BARC-025885-05138_R	Chr17	10,880,402	10,880,419	GTTGACCGAACTGGATCGAA	CGGAACAGAACTGTTTTTTG
Chr17	77.4	GMES4191	GMES4191 F	Chr17	11,114,999	11,114,980	GMES4191 R	Chr17	11,114,744	11,114,763	GTGTCCGAGGATGAGGTTGT	CCAAGTAAACTGCAGCACGA
Chr17	78.5	Satt397	Satt397_F	Chr17	11,445,439	11,445,458	Satt397_R	Chr17	11,445,609	11,445,589	TCTCGGGATCCTTGTTAGAT	AAGAAGAAGAGAACATGTGAA
Chr17	78.7	C17-BARC-013637-01187	C17-BARC-013637-01187_F	Chr17	11,636,533	11,636,552	C17-BARC-013637-01187_R	Chr17	11,636,619	11,636,600	AGTGAAGCAAGGTGCAACTC	AAAATGTGACAGCTGCATGG
Chr17	78.7	s028100044	s028100044_F	Chr17	11,777,500	11,777,522	s028100044_R	Chr17	11,777,815	11,777,793	GTCTTCATATTACGGGAAATCCA	TTTCTCTTCTTCTCGTGCTTCTC
Chr17	81.4	Satt208	Satt208_F	Chr17	12,425,090	12,425,103	Satt208_R	Chr17	12,425,275	12,425,258	ATCGTATTGGGTCT	CCCGTTATTTTCGTATGA
Chr17	84.2	T001713396s	T001713396s_F	Chr17	13,132,958	13,132,979	T001713396s_R	Chr17	13,133,158	13,133,137	AGTAGTGCGCGCGTGTATATGT	ACAATTTGTATGGCGCTTCATT
Chr17	84.4	C17-BARC-025247-06464	C17-BARC-025247-06464_F	Chr17	13,181,403	13,181,384	C17-BARC-025247-06464_R	Chr17	13,181,308	13,181,327	TTCTCCCTTTCACATATGCC	GGGAAGAGATAGTGAAGGAG
Chr17	88.6	Satt389	Satt389 F	Chr17	13,771,928	13,771,909	Satt389 R	Chr17	13,771,706	13,771,725	GCTGGTGTATGGTGAAATCA	CCAAAACCAAAAGTTATATC
Chr17	93	GMES3721	GMES3721_F	Chr17	15,630,510	15,630,529	GMES3721_R	Chr17	15,630,785	15,630,766	AAGCCCACCATCAATTCAAC	GTTTCTCGGTTTTGGGGATT
Chr17	95.5	C17-BARC-030169-06817	C17-BARC-030169-06817_F	Chr17	20,208,121	20,208,102	C17-BARC-030169-06817_R	Chr17	20,208,051	20,208,070	AGACTTTTAGGCATGGGAGC	TTCCACACAAGGTTAGAAGC
Chr17	95.5	Sat_300	Sat_300_F	Chr17	20,378,904	20,378,926	Sat_300_R	Chr17	20,378,985	20,378,958	CGCATTCGCATGTGTGGTAACTA	ACAATCCCATGCAACTACATGATTAAGA
Chr17	95.5	Sat_338	Sat_338 F	Chr17	20,586,832	20,586,808	Sat_338 R	Chr17	20,586,625	20,586,648	GGGCATTAATAAACCTCCTCTAACT	CCATTTTGGTCATTCCTAACAACT
Chr17	96	C17-BARC-028773-06009	C17-BARC-028773-06009_F	Chr17	23,797,146	23,797,127	C17-BARC-028773-06009_R	Chr17	23,797,047	23,797,066	AGAAAAAGCCACAGAAGCAG	CCCTGATCAAGCCTATTGTG
Chr17	96	Satt662	Satt662_F	Chr17	23,947,783	23,947,806	Satt662_R	Chr17	23,947,937	23,947,915	TTGAAGGAAAGGGTAAACCTATAT	TCTTATCGTTCCGTGCTCCAGAT
Chr17	97.6	C17-BARC-029781-06338	C17-BARC-029781-06338 F	Chr17	34,621,126	34,621,106	C17-BARC-029781-06338 R	Chr17	34,621,040	34,621,059	GTCTGTTCATTTTGTGACCTC	ATGACCCTGTGCTTGGATAC
Chr17	98.7	Sat_001	Sat_001_F	Chr17	36,454,399	36,454,417	Sat_001_R	Chr17	36,454,649	36,454,631	GATACGACCAAAAATTGTT	AACTGCGAAGATACTACCC
Chr17	98.7	GMES0251	GMES0251_F	Chr17	36,523,504	36,523,490	GMES0251_R	Chr17	36,523,384	36,523,403	ACCAGTTGGAATTCAGGCAC	TGATCAATGATTGGCCTTGA
Chr17	101.2	s014100269-2	s014100269-2_F	Chr17	37,148,041	37,148,064	s014100269-2_R	Chr17	37,148,201	37,148,179	ATTAACCTATGTGTTTAATGGTTT	ACACTAATTCACCTTCTGCTGGA
Chr17	103.9	s014100777-2	s014100777-2 F	Chr17	37,655,856	37,655,878	s014100777-2 R	Chr17	37,656,162	37,656,140	GTTTGGATCCTCTTACGGTCAAT	CCCTACTTAAACCCATCACAAAT
Chr17	109.5	T001738317m	T001738317m_F	Chr17	38,023,751	38,023,777	T001738317m_R	Chr17	38,024,004	38,023,981	TGATTAGTTGTCTCTTACTGATGTGTG	AAGTCTACCTTTAAATGAGGTGGG
Chr17	110.9	GMES0909	GMES0909_F	Chr17	38,311,765	38,311,784	GMES0909_R	Chr17	38,311,972	38,311,953	AGACATTGCTTGCCCAAGTT	GATCCCACTGGAGCACTGTT
Chr17	111.7	T001738683s	T001738683s_F	Chr17	38,389,152	38,389,174	T001738683s_R	Chr17	38,389,338	38,389,316	TTTAACCAGAAAGGATGAGTGGA	TGTCATTATGCCACTTAACCAAA
Chr17	113.6	C17-BARC-017613-02631	C17-BARC-017613-02631_F	Chr17	38,549,705	38,549,724	C17-BARC-017613-02631_R	Chr17	38,549,782	38,549,763	GTTCAACAGGCTGCTAAAAC	CAGACAATTCAGAAAGATCC
Chr17	113.8	T001738877l	T001738877l_F	Chr17	38,582,234	38,582,254	T001738877l_R	Chr17	38,582,619	38,582,590	AAACCTACCCATCTTGCACAT	TCAATCCTACTATAAAGAACCTTACAAAGA
Chr17	115.1	s030800156	s030800156_F	scaffold_44	156,174	156,196	s030800156_R	scaffold_44	156,472	156,449	CCTGCAATAGCGATAACTCATTT	CCCTTCTCAAGAATATTTAATCCC
Chr17	115.2	s052400012	s052400012 F	scaffold_44	166,173	166,150	s052400012_R	scaffold_44	165,945	165,968	GGTCACTACATGGCTGATGGTCAC	TCAAGTACTCACACTGCACAAGCG
Chr17	115.2	s052400010	s052400010_F	scaffold_44	168,482	168,459	s052400010_R	scaffold_44	168,204	168,229	TAACCGGACACGATCATTCTTCAA	CAACAGACTGCCATATTCATGTAGCC
Chr17	121.3	s030600085	s030600085_F	Chr17	38,823,065	38,823,043	s030600085_R	Chr17	38,822,869	38,822,891	ATAGGCTGCAGATAATTCATCCC	CACTTAGTCGCCTCAAGTTAGGA
Chr17	124.1	s018700067-2	s018700067-2_F	Chr17	38,985,188	38,985,210	s018700067-2_R	Chr17	38,985,539	38,985,514	TAGGTTTGGAACCAAGATACCCT	TATCCTAGAGCATCTACAATAGATAA
Chr17	129.1	s018700334-2	s018700334-2 F	Chr17	39,253,401	39,253,418	s018700334-2 R	Chr17	39,253,597	39,253,575	TGCACACATATGCACAAA	ATTCCTGCTTAGATCTTAGGTTT
Chr17	129.8	C17-BARC-035371-07167	C17-BARC-035371-07167_F	Chr17	39,357,016	39,357,036	C17-BARC-035371-07167_R	Chr17	39,357,076	39,357,057	CCATATTTCCAAGTTCCAACC	TGCCTTTCTTCTCATTCGCC
Chr17	131.6	T001739751s	T001739751s_F	Chr17	39,474,241	39,474,265	T001739751s_R	Chr17	39,474,450	39,474,428	TTCCTGCCTATATATCTGCTCTAAA	TAAAGCAAATTCAATTCGTTGCT
Chr17	133.5	Satt031	Satt031 F	Chr17	39,658,444	39,658,463	Satt031 R	Chr17	39,658,565	39,658,544	TTCCACTTTGTATCACTTTC	TGACTGTAAAAGAACAGATAAA
Chr17	136	T001740270s	T001740270s_F	Chr17	40,000,926	40,000,946	T001740270s_R				AATAACCTTGACGCAAACACG	CAACTTCTAATAACATATCGGAAACA
Chr17	141.1	GMES0687	GMES0687_F	Chr17	40,222,893	40,222,874	GMES0687_R	Chr17	40,222,765	40,222,785	CTTCTCCCTTGGGTTCTTCC	CATCCTAACCGGTCAAAAACA
Chr17	142.9	Satt386	Satt386_F	Chr17	40,469,314	40,469,291	Satt386_R	Chr17	40,469,154	40,469,181	GATGATTTTTATAGAATAGATAAT	CTTCGTTGATACCTCAGTAGAGTACAAA
Chr17	147.3	T001740967m	T001740967m F	Chr17	40,698,433	40,698,455	T001740967m R	Chr17	40,698,766	40,698,744	AACTGAGTTTATCAGGGTAAGGG	TTAGCAGTTTACGCGCTCATTAT
Chr17	150.3	T001741151m	T001741151m_F	Chr17	40,882,534	40,882,557	T001741151m_R	Chr17	40,882,800	40,882,780	AAATGTTGCTCTATATTCATTCAA	AACCAACAGCGTAGCTTCAAA
Chr17	152	Sat_220	Sat_220_F	Chr17	41,065,942	41,065,966	Sat_220_R	Chr17	41,066,216	41,066,192	CACGCCTCACTATATTATTTTTGAA	ATGGAAATTAAACGCTATCATGCTA
Chr17	153.3	C17-BARC-039151-07458	C17-BARC-039151-07458_F	Chr17	41,222,164	41,222,183	C17-BARC-039151-07458_R	Chr17	41,222,263	41,222,244	ATCTGCTGAAGAAGAGACCC	CTTTTAACTAAGTTCTACTC
Chr17	155.8	GMES5401	GMES5401_F	Chr17	41,494,647	41,494,666	GMES5401_R	Chr17	41,494,944	41,494,925	ATGTCCATGCCTACTCCCAG	CACCACCAAGGGTAAGAGGA
Chr18	0	T001800107s	T001800107s_F	Chr18	106,473	106,495	T001800107s_R	Chr18	106,682	106,662	CAGGACAGGAGTTGAGATTTACG	GGATGGGATGATGGATACAAA
Chr18	1.3	T001800318s	T001800318s_F	Chr18	316,979	317,001	T001800318s_R	Chr18	317,188	317,168	ATACTCTCTCTCCTGACTGAAAT	CTCTCTGGCCAGTACAGTGAC
Chr18	3.8	T001800702s	T001800702s F	Chr18	702,093	702,115	T001800702s R	Chr18	702,295	702,273	GTTACCGAATTTCTCCGGTTATT	GCATACAGATACAAGGGAACAGG
Chr18	5.1	C18-BARC-028719-05996	C18-BARC-028719-05996_F	Chr18	977,333	977,352	C18-BARC-028719-05996_R	Chr18	977,413	977,394	AGGAAGAAGCAAGTGCAGAG	TTTCAGTGGACAGCAAAGGG
Chr18	6.1	GMES2435	GMES2435_F	Chr18	1,117,451	1,117,432	GMES2435_R	Chr18	1,117,173	1,117,192	GCACGGCACTAGTCGTTTTT	GCAAGTATCTGCGACTTCCC
Chr18	7	Satt038	Satt038_F	Chr18	1,344,022	1,344,042	Satt038_R	Chr18	1,344,188	1,344,169	GGGAATCTTTTTTTCTTTCTATTAAGTT	GGGCATTGAAATGGTTTTAGTCA
Chr18	10	Satt309-2	Satt309-2 F	Chr18	1,736,292	1,736,313	Satt309-2 R	Chr18	1,736,775	1,736,753	CCACACAGAACACCAATTGACT	GGCTAGATTCAAGAAACAAAAGG
Chr18	15.4	T001802291l	T001802291l_F	Chr18	2,299,204	2,299,226	T001802291l_R	Chr18	2,299,566	2,299,544	CTTTGAAGGATGGTATATGTGCT	GAAAGAGGTGCTCGCATTTAATA
Chr18	17.8	GMES1633.1	GMES1633_F	Chr18	2,831,682	2,831,701	GMES1633_R	Chr18	2,831,865	2,831,846	ATGAGAGGTTGCCACTGGAG	GGCATGTTCTGACCATTGTG
Chr18	17.8	GMES0791	GMES0791 F	Chr18	2,831,707	2,831,726	GMES0791 R	Chr18	2,831,865	2,831,846	TCAAGGTGAGGAGGAAATGC	GGCATGTTCTGACCATTGTG
Chr18	21.1	GMES4967	GMES4967_F	Chr18	3,191,977	3,191,996	GMES4967_R	Chr18	3,192,078	3,192,059	GAAGAAAGTCCTGGTGGTCG	GATGTCTTGGAACGAAGGGA
Chr18	21.6	GMES4241	GMES4241_F	Chr18	3,281,047	3,281,028	GMES4241_R	Chr18	3,280,800	3,280,819	ACAACCCCATTTTCCTTTCC	CACGAACCTTGTACCCCAAC
Chr18	23.9	T001803568m	T001803568m_F	Chr18	3,590,063	3,590,083	T001803568m_R	Chr18	3,590,329	3,590,307	TTTGCATTTAGGCAAGCATTA	TGATGATCGATCCAAGGTCTATT
Chr18	27.4	GMES4035	GMES4035 F	Chr18	3,881,191	3,881,211	GMES4035 R	Chr18	3,881,337	3,881,318	TCAATTTTCTCCCCCTCTCTC	TGCTGTGTAGTTTGCTTGGC
Chr18	27.9	T001803970s	T001803970s_F	Chr18	3,991,258	3,991,280	T001803970s_R	Chr18	3,991,430	3,991,408	CAACAGATTGAGGAGGATGATGT	TGCTTTGATTTGTTAGCATGTTC
Chr18	27.9	T001803988m	T001803988m_F	Chr18	4,009,203	4,009,225	T001803988m_R				AGAAATACAATCACAGTGAGCCC	GGCAAATTGAGACCAATTCTCTA
Chr18	28.7	T001804222s	T001804222s_F	Chr18	4,240,381	4,240,403	T001804222s_R	Chr18	4,240,591	4,240,569	TTTAGTCCTATGCCAGTTGATCC	TGTGTTTCATCTTTACAGAATTG
Chr18	29.6	T001804263m	T001804263m_F	Chr18	4,280,811	4,280,833	T001804263m_R	Chr18	4,281,069	4,281,047	TTTGCATGTCCAAAGCATATTAC	GTTCATCGGGCTCTCTTTAAATC
Chr18	30.8	T001804377m	T001804377m_F	Chr18	4,395,625	4,395,647	T001804377m_R				CCCATCAACACCTTGAGAATTAG	CACATGCAAGATTAAAGCATAGAA
Chr18	34	Satt130-2_re	Satt130-2_re_F				Satt130-2_re_R				CATTAGGGACAAAGATTGCTGA	CGTCTATATTGGATCTCCATGATCTC
Chr18	34.3	T001804644l	T001804644l F	Chr18	4,663,732	4,663,754	T001804644l R	Chr18	4,664,074	4,664,052	GAGTCATGGGTATTTCTTTCACG	TAGCACTCACTAGATGCAACCAA
Chr18	37.2	T001804817m	T001804817m_F	Chr18	4,832,921	4,832,945	T001804817m_R	Chr18	4,833,232	4,833,210	TGTGTTTCACTTCTCTTTAGCATGT	TCTTCATTTATCCTCGCAACATT
Chr18	38.1	T001804875l	T001804875l_F	Chr18	4,891,547	4,891,569	T001804875l_R	Chr18	4,891,898	4,891,876	CTTTGCCCGATCATATAATGCTT	ACAATATTTATGGGCACACTTGG

Chr18	40.2	GMES0033	GMES0033_F	Chr18	5,309,465	5,309,484	GMES0033_R	Chr18	5,309,757	5,309,738	TGCGTTTCTTCTGTCCCTCT	TGGTCGAAGAGGTCTCGTTT
Chr18	41	C18-BARC-013237-00459	C18-BARC-013237-00459_F	Chr18	5,543,441	5,543,460	C18-BARC-013237-00459_R	Chr18	5,543,536	5,543,517	TCCCTCAGGTAATTTTAGTC	CCAAATTAAGGGGCACAGAG
Chr18	41	GMES0794	GMES0794 F	Chr18	5,575,896	5,575,877	GMES0794 R	Chr18	5,575,658	5,575,677	GCCACCAATCTCATCCAGAC	ATCTTCTTGGGTCGGGTCTT
Chr18	44.6	Satt324	Satt324_F	Chr18	5,926,765	5,926,787	Satt324_R	Chr18	5,927,000	5,926,982	GTTCCCAGGTCCCACCATCTATG	TTTCTTTTATACCTTCAAG
Chr18	50	T001806170s	T001806170s_F	Chr18	6,206,988	6,207,010	T001806170s_R	Chr18	6,207,177	6,207,156	TTTGTAGTCCCATAAATAAGCCA	TTTCGTTGGTCCTTAACGTAGC
Chr18	51.8	T001806567l	T001806567l_F	Chr18	6,591,093	6,591,115	T001806567l_R	Chr18	6,591,436	6,591,411	AATTTGTTGACTTGTGTGGGAAT	GCGTAAACTATATTGTTCTTTGAACG
Chr18	55.1	s000401152-2	s000401152-2 F	Chr18	7,055,069	7,055,091	s000401152-2 R	Chr18	7,055,466	7,055,439	CGAGTAACTATCGAGTTCATGGG	TTCTGTTTACTTCTATATCCATTATTCA
Chr18	55.1	C18-BARC-042925-08463	C18-BARC-042925-08463_F	Chr18	7,057,261	7,057,280	C18-BARC-042925-08463_R	Chr18	7,057,337	7,057,318	ATGTCTGCAAGGTAAGTGAC	GTGTTATGTGTTTTTTGTCC
Chr18	56.6	s000401695-2	s000401695-2_F	Chr18	7,598,066	7,598,088	s000401695-2_R	Chr18	7,598,260	7,598,239	TCATGGTGTAGCAGTAGGATGAA	AATGTTGGTCGATATGGTTGTTC
Chr18	57.6	s000402585-2	s000402585-2 F	Chr18	8,487,716	8,487,740	s000402585-2 R	Chr18	8,487,915	8,487,894	TCTTATGAATTATGGAAACCCTTGA	AACGTGGCACCTAACCTTTAGA
Chr18	59.5	s000403406-2	s000403406-2_F	Chr18	9,335,021	9,335,041	s000403406-2_R	Chr18	9,335,167	9,335,146	TCTGGAGACTCTATGACCCAAGA	AGAAATATTCTTTGGCGGTGGT
Chr18	60	Satt394	Satt394_F	Chr18	9,765,839	9,765,863	Satt394_R	Chr18	9,766,137	9,766,113	TTTTTTCAATTTAAAGAGAATTGAC	TAACTTGCATGTGTATATCGAGATG
Chr18	60.3	GMES0241	GMES0241_F	Chr18	9,816,304	9,816,285	GMES0241_R	Chr18	9,816,086	9,816,105	CTTCAGAGCATTCCTGAGGC	ATAACCCTCAAACCCCAACC
Chr18	61.6	T001811100m	T001811100m F	Chr18	11,124,285	11,124,307	T001811100m R	Chr18	11,124,495	11,124,472	CCGTTAAGTGATGATGTGGAGTA	ATGATGAGTTGTTGGTCTCTATCC
Chr18	62.7	T001812033l	T001812033l_F	Chr18	12,057,382	12,057,404	T001812033l_R	Chr18	12,057,743	12,057,720	GTCCGCTGATCTAGAATCTTTCA	TGTTTATTTCCCAATCATTCTCAA
Chr18	63.2	GMES4022	GMES4022_F	Chr18	12,480,635	12,480,616	GMES4022_R	Chr18	12,480,538	12,480,557	CCAGTGATCAAAGGGGAAGA	ACATGAAAGGCGTAAGGGTG
Chr18	64.3	C18-BARC-017647-02644	C18-BARC-017647-02644_F	Chr18	14,984,114	14,984,095	C18-BARC-017647-02644_R	Chr18	14,984,015	14,984,033	CCAGTCAGACCACAAAGTAG	TTGACTTGGAATTACCTTC
Chr18	65.6	C18-BARC-020159-04489	C18-BARC-020159-04489_F	Chr18	17,683,382	17,683,401	C18-BARC-020159-04489_R	Chr18	17,683,462	17,683,443	TAATCCTATCCGCGGCATTC	ATTCGGTTTCTTCGGGTTGC
Chr18	65.6	GMES3568	GMES3568_F	Chr18	17,691,193	17,691,212	GMES3568_R	Chr18	17,691,465	17,691,446	AGTGGAGGGTGGTCATCAAC	AACCTGCAATTTCATTTGGC
Chr18	68.5	Satt352	Satt352_F	Chr18	21,086,521	21,086,498	Satt352_R	Chr18	21,086,335	21,086,360	AATGTATTTTTGTTTCTCCATCAA	TGATAAGCCAAAAAATGGAAGCATAG
Chr18	69.4	C18-BARC-013825-01251	C18-BARC-013825-01251 F	Chr18	28,657,678	28,657,697	C18-BARC-013825-01251 R	Chr18	28,657,760	28,657,741	TTTACCCAGTGTCCCAAAGG	GGATGGAAAACTGGAGAACC
Chr18	69.4	s003700176	s003700176_F	Chr18	25,272,188	25,272,211	s003700176_R	Chr18	25,272,407	25,272,385	GGGTTGAATAATGTGATAACCAAA	GTCATCCCTTTCATGCCTAGTAA
Chr18	69.4	s003902576	s003902576_F	Chr18	34,741,366	34,741,388	s003902576_R	Chr18	34,741,586	34,741,564	ATTCCTAGCTAGCCACATGCAAT	TGCATTGTCAAGTAAGACTCACC
Chr18	69.7	s003903175-2	s003903175-2_F	Chr18	35,317,047	35,317,069	s003903175-2_R	Chr18	35,317,396	35,317,374	TGACATATTCAGAGGGAAACACG	GGATGTTTGGACGGTACAGATTA
Chr18	70.7	s033800001	s033800001 F	scaffold_1831	2,540	2,518	s033800001 R	scaffold_128	2,380	2,402	TATATGTCCCAATGTTGCTAGGG	CGAAGCGTGATGAAACATTTAGT
Chr18	71.3	s003905552-2	s003905552-2_F	Chr18	38,694,626	38,694,604	s003905552-2_R	Chr18	38,694,467	38,694,489	GAAGCAACGTATCACTCTTGAAA	CTCTCCTATTCCTAAACGTACCC
Chr18	71.3	GMES4003	GMES4003_F	Chr18	38,954,916	38,954,897	GMES4003_R	Chr18	38,954,647	38,954,673	GCTTGAGACTGGACGTAGGC	TTTTTCCACTAATAAACTTTAACCTCA
Chr18	71.6	s015100043	s015100043 F	Chr18	41,112,867	41,112,845	s015100043 R	Chr18	41,112,499	41,112,523	ACAAGCCTTTAATCAAGACAGCA	CAAATTGTGATCTTTCTTTCATGTG
Chr18	72.4	s026400360-2	s026400360-2_F	Chr18	41,526,328	41,526,348	s026400360-2_R	Chr18	41,526,463	41,526,441	AAAGTTCCCAATTTAGACAAA	TTAGAATTTACAAAGCTTGAGCA
Chr18	72.4	s008900001	s008900001_F	Chr18	41,707,846	41,707,868	s008900001_R	Chr18	41,708,145	41,708,123	TTAAGTTGGACGTGTTCATACCC	CCTCTCACCCTCATCCTCTATTT
Chr18	74	C18-BARC-038795-07335	C18-BARC-038795-07335_F	Chr18	45,931,993	45,932,012	C18-BARC-038795-07335_R	Chr18	45,932,084	45,932,064	TAAGCAGAAAGGGGATCCTA	CAAACCAACCACTTGTTCATC
Chr18	75.3	C18-BARC-029289-06142	C18-BARC-029289-06142 F	Chr18	47,495,974	47,495,955	C18-BARC-029289-06142 R	Chr18	47,495,900	47,495,915	CTGTATTGGTGCCCAATGTG	TACCGGCCACAATGATCAG
Chr18	75.3	Sat_223	Sat_223_F	Chr18	47,632,035	47,632,056	Sat_223_R	Chr18	47,632,218	47,632,196	CGGTTTTAAGCTATAACACATC	CAAGCACACTACTATTTATCATT
Chr18	75.7	Sat_203	Sat_203_F				Sat_203_R	Chr18	47,927,267	47,927,240	TGTGGCAAGTTATAGTTGAGTAGTTGAA	GGCTATAATGTCCTTAATACTTATTTAT
Chr18	78	Satt505	Satt505_F	Chr18	48,198,854	48,198,871	Satt505_R	Chr18	48,199,084	48,199,064	CGCATCGGTGGTTGTTAA	TGACCCAAAAGTAATTTGGAG
Chr18	78	C18-BARC-031339-07055	C18-BARC-031339-07055_F	Chr18	48,469,742	48,469,723	C18-BARC-031339-07055_R	Chr18	48,469,664	48,469,683	GTAATGCATTTTTTGTGTTC	ACGGCTCCTTCCTACACATT
Chr18	78.1	s002100366	s002100366_F	Chr18	48,508,128	48,508,150	s002100366_R	Chr18	48,508,508	48,508,486	TTTACATTGGTTGCCTACGTCTC	TTACAACCTGTTTCCAAGGACTC
Chr18	78.8	s002100692	s002100692_F	Chr18	48,840,578	48,840,601	s002100692_R	Chr18	48,840,777	48,840,755	GCAGCAATATGGGAGTCTAGTAGT	AGATTGCTAACATCCTTCAATTA
Chr18	79.6	s002100995	s002100995 F	Chr18	49,143,521	49,143,543	s002100995 R	Chr18	49,143,920	49,143,898	CTGCTTACTTTCCAAGTGTCCTG	TGATGTGAACGGATTCTATTCCT
Chr18	79.6	C18-BARC-013627-01180	C18-BARC-013627-01180_F	Chr18	49,306,578	49,306,597	C18-BARC-013627-01180_R	Chr18	49,306,665	49,306,646	GTTTTCTTTAGCTCCCACTG	ATGGCCAATGTTTGCAGAGC
Chr18	79.9	s002101345	s002101345_F	Chr18	49,493,130	49,493,152	s002101345_R	Chr18	49,493,324	49,493,301	TCTCCTACTTCTCTTTCTCCCGT	TTCAAAGAAGAATTGCAACTTGAC
Chr18	82.9	T001854045l	T001854045l_F	Chr18	49,766,396	49,766,420	T001854045l_R	Chr18	49,766,774	49,766,753	GAACGTGTATAGTGATCAAGAAAGC	ATAAGTTGGGTTTGCGTTGAGT
Chr18	84.9	T001854127m	T001854127m F	Chr18	49,848,587	49,848,607	T001854127m R	Chr18	49,848,855	49,848,832	TTCAACGGTTCGGTGAATAAA	GGGTTTAATAGGCATTAGGTGTAA
Chr18	88.9	T001854293s	T001854293s_F	Chr18	50,014,183	50,014,205	T001854293s_R	Chr18	50,014,345	50,014,323	AGCAGAGTTATAGTGGAGATGCG	CGATGAACTATTTCAACCACGTT
Chr18	90.3	s002102138	s002102138_F	Chr18	50,282,130	50,282,152	s002102138_R	Chr18	50,282,329	50,282,304	AAAGTGTTAGGAAGTAAGATCCA	TCAAGTTATTGAATCCTATATCATCT
Chr18	95	T001854972m	T001854972m F	Chr18	50,693,518	50,693,541	T001854972m R	Chr18	50,693,750	50,693,728	CGTGATAATAATTTCATCGGATTT	TCAGTATCGCATAATCCAGACAA
Chr18	97.2	GMES4067	GMES4067_F	Chr18	50,937,390	50,937,370	GMES4067_R	Chr18	50,937,126	50,937,145	TTATCACGACACCAATTCTCC	AGTGATGTAGGACGGAACGG
Chr18	97.2	Satt288	Satt288_F	Chr18	51,123,892	51,123,870	Satt288_R	Chr18	51,123,677	51,123,699	GGGTGATTTAGTGTTTGACACCT	CTTATAATTAAGAGCAAAAGAAG
Chr18	99.4	s002103628	s002103628_F	Chr18	51,775,769	51,775,792	s002103628_R	Chr18	51,776,124	51,776,100	GACAGTCTCTACTCCTGCTCATCA	AAGAGTTTGACTGTGATGATTGATT
Chr18	100.8	C18-BARC-027488-06597	C18-BARC-027488-06597 F	Chr18	51,838,785	51,838,766	C18-BARC-027488-06597 R	Chr18	51,838,700	51,838,720	TTGAACAGTTCGCTATCCCC	CTGATTACTCACCGATAATAC
Chr18	102.9	s002104271	s002104271_F	Chr18	52,423,195	52,423,222	s002104271_R	Chr18	52,423,393	52,423,369	TGTTACATAATTGGGAGTAATTAACTTT	AAGGCTTCACGTGTTATATAGTTGC
Chr18	102.9	C18-BARC-042393-08251	C18-BARC-042393-08251_F	Chr18	52,439,978	52,439,997	C18-BARC-042393-08251_R	Chr18	52,440,062	52,440,043	TCTGCTGATGATGATCCTTC	CTAGTGCAGCTGTTCTTTGG
Chr18	104.4	s002104592	s002104592_F	Chr18	52,746,894	52,746,914	s002104592_R	Chr18	52,747,038	52,747,016	GTGTCCCGCATGCACTAATTT	GCAGCCATCACATACATACACAC
Chr18	106.9	s002104937	s002104937_F	Chr18	53,093,277	53,093,299	s002104937_R	Chr18	53,093,407	53,093,385	CACACAACTTCCTCAAATTATCG	TGTTGTTTCTCGTGTCTCCTAAA
Chr18	107.5	GMES0651	GMES0651_F	Chr18	53,155,533	53,155,514	GMES0651_R	Chr18	53,155,393	53,155,412	CCTCTATGCCAGTGGTTGGT	CTTTGTCCCTTGAGACAGGC
Chr18	108.3	T001857606l	T001857606l_F	Chr18	53,331,786	53,331,809	T001857606l_R	Chr18	53,332,143	53,332,120	TGAGCTTACATGCACAGTTAGACA	TCTTACACCTATCTCCATCACTCG
Chr18	112.6	GMES2625	GMES2625 F	Chr18	53,505,790	53,505,771	GMES2625 R	Chr18	53,505,618	53,505,637	CTCGTGGGTCCACTTCAAAT	TGTTGAGGCTTCTCGTGTTG
Chr18	114.7	T001857894m	T001857894m_F	Chr18	53,620,108	53,620,130	T001857894m_R	Chr18	53,620,438	53,620,416	TTTAAACATACACGTGAGAAGAA	TTTGGCAGAGCAGTATCATTAGT
Chr18	118.2	GMES5412	GMES5412_F	Chr18	53,857,805	53,857,790	GMES5412_R	Chr18	53,857,603	53,857,622	TCCTCTGATGATGATGGGGT	TCCACGATTTCCCTCAAGTC
Chr18	121.2	Satt191	Satt191_F	Chr18	54,447,567	54,447,552	Satt191_R	Chr18	42,169,523	42,169,506	CGCGATCATGTCTCTG	GGGAGTTGGTGTTTTCTTGTG
Chr18	122.3	GMES1017	GMES1017 F	Chr18	54,515,094	54,515,112	GMES1017 R	Chr18	54,515,247	54,515,228	GCAGCATCTCCTCAAACACA	GTGCCAAGATCATAGCAGCA
Chr18	124.1	GMES1232	GMES1232_F	Chr18	54,891,204	54,891,223	GMES1232_R	Chr18	54,891,491	54,891,472	AACGAACGGTGATCCTTCTG	CAGCAGCACAACCAACACTT
Chr18	127.6	C18-BARC-024251-04812	C18-BARC-024251-04812_F	Chr18	55,196,662	55,196,643	C18-BARC-024251-04812_R	Chr18	55,177,429	55,177,448	CAAGTGCAAAGTCTCATGCG	GCAGTGAGAGCATATGCTTC
Chr18	127.8	T001859611m	T001859611m F	Chr18	55,334,692	55,334,714	T001859611m R	Chr18	55,334,997	55,334,975	ACTTTAAGAGGCCTTTCATGGAC	AAGGTGCCAGGTCGTTTATTATT
Chr18	128.2	T001859843s	T001859843s_F	scaffold_3003	128,511	128,495	T001859843s_R				TATTTCTCAGCAGCTTCCTTCAG	TTTGATATTGAAAGTTGGTCAGGA
Chr18	130.1	s002107611	s002107611_F	Chr18	55,759,400	55,759,422	s002107611_R	Chr18	55,759,865	55,759,843	GTCCTATAAGACAATTCAACAAA	TTGTTGTGTATGTTTGTGTGTGC
Chr18	131.1	s002107925	s002107925_F	Chr18	56,064,028	56,064,048	s002107925_R	Chr18	56,064,188	56,064,166	TAGCTTCAGTACCACGTTCCTTC	GTTTACCTTCGGCCTTAGACTTT
Chr18	131.6	C18-BARC-031121-06998	C18-BARC-031121-06998 F	Chr18	56,185,068	56,185,049	C18-BARC-031121-06998 R	Chr18	56,184,984	56,185,003	ACTCCACCACTACAAAACCC	TGCTTTGGCCTTTGTAGTAG
Chr18	132.2	Sat_064	Sat_064_F	Chr18	56,329,880	56,329,856	Sat_064_R	Chr18	56,329,738	56,329,758	TAGCTTTATAATGAGTGTGATAGAT	GTATGCAAGGGATTAATTAAG
Chr18	135.4	GMES1110	GMES1110_F	Chr18	56,755,562	56,755,543	GMES1110_R	Chr18	56,755,429	56,755,448	GAAACAAAGCAGCACCCATT	ATCGGTGACTGACCACACAA
Chr18	137.1	T001861387s	T001861387s_F	Chr18	57,084,624	57,084,639	T001861387s_R	Chr18	57,084,852	57,084,831	GAGCGGAACCGCGTAA	GCAATGTAGGGATTCCGATAAA
Chr18	139.2	T001861839l	T001861839l_F	Chr18	57,536,221	57,536,243	T001861839l_R	Chr18	57,536,582	57,536,560	AAGACTGACTCCCTTTGGATACC	TAATGTGCTATAACCAGGCTTCC
Chr18	139.8	T001862276l	T001862276l_F	Chr18	57,981,721	57,981,743	T001862276l_R	Chr18	57,983,296	57,983,272	ATTGTCTATGGAACTGGTGCATT	CCTTAGTTTAAACGTCAAAGAATCG
Chr19	0	C19-BARC-043223-08561	C19-BARC-043223-08561_F	Chr19	20,076	20,095	C19-BARC-043223-08561_R	Chr19	20,160	20,141	ACCATCGACGATAGCCTGAG	CCCTTCTTCACTTCTACCTC
Chr19	0	GMES0701	GMES0701 F	Chr19	95,949	95,968	GMES0701 R	Chr19	96,180	96,164	CGAAACGACATCTTTCAGCA	CGTAACCTCTTCGAAGCCTG
Chr19	1.4	T001900352m	T001900352m_F				T001900352m_R	Chr19	249,898	249,919	GGTAGCTAACAATTTAACCGATTTG	CACGTATCTTCAATCTACCGAGG
Chr19	2.4	T001900267m	T001900267m_F	Chr19	335,443	335,421	T001900267m_R	Chr19	335,111	335,132	GACAAACAACAACAGAATCCACA	AGCCTACAAACGGACAGAGAAC

Chr19	3.5	T001900179l	T001900179l_F	Chr19	451,967	451,943	T001900179l_R	Chr19	451,603	451,625	TTGTACTATTATTCATGCTCAGCCA	ATCACAAATTTCCAAGGACTGAA
Chr19	5.4	T001900085l	T001900085l_F	Chr19	545,825	545,803	T001900085l_R	Chr19	545,450	545,475	CAAATATGAGGGTTCGTTTCCTT	GAAGAAATTGACTGAAATGTCTCTTT
Chr19	6.8	T001900602m	T001900602m_F	Chr19	641,601	641,623	T001900602m_R				ACAAGTGCACACACACTGATAGC	GCTTCATAATTGAATCAACGTCA
Chr19	8.4	Satt495	Satt495_F	Chr19	690,087	690,110	Satt495_R	Chr19	690,318	690,295	TGCCGCGAGATTAATATAATTTGT	GTGCGGCAAGAAGTTGAAATAAAG
Chr19	10	GMES0704	GMES0704_F	Chr19	880,270	880,251	GMES0704_R	Chr19	879,981	880,000	AAATTCACCTCCCCACAACA	GAGGAATCAGCTTGGGAACA
Chr19	13	T001901004l	T001901004l_F	Chr19	1,039,836	1,039,858	T001901004l_R	Chr19	1,040,196	1,040,174	ACAAGGTCTGAGACAAGCAGTTC	GACTTTATGGATTGCGAGTGAAA
Chr19	15.2	GMES0748	GMES0748_F	Chr19	1,228,633	1,228,652	GMES0748_R	Chr19	1,228,820	1,228,801	AGCGTGTGGGAAATCAAGAG	AAGCTGCAAAAGGCAAAGAA
Chr19	16.4	s019601002-2.1										
Chr19	17.6	s019601002-2	s019601002-2_F	Chr19	1,522,813	1,522,791	s019601002-2_R	Chr19	1,522,446	1,522,467	GCAGGTAACAGAGAATGGAGAGA	AAATTCCCGTAAATTATGCAGC
Chr19	19.3	T001901766l	T001901766l_F	Chr19	1,809,365	1,809,387	T001901766l_R	Chr19	1,809,744	1,809,721	TGAAATGTTATGTTCAACGATGG	AAATGTAATCCAACATCAACTCAA
Chr19	20.3	T001901796s	T001901796s_F	Chr19	1,839,721	1,839,743	T001901796s_R	Chr19	1,839,900	1,839,878	CCTTGATCGAATTGTCTCAGTTT	CCTTGACCCAATTTCATACTCAC
Chr19	22.5	Satt182	Satt182_F	Chr19	2,059,531	2,059,550	Satt182_R	Chr19	2,059,724	2,059,706	GGTCCACATGAAATGAAGGT	TCTCAGCCTGCAAAGAAAA
Chr19	24.6	T001902216s	T001902216s_F	Chr19	2,261,139	2,261,161	T001902216s_R	Chr19	2,261,318	2,261,296	TTGACTATGAGAAATGGGTTCGT	ATGTGAATGAGTGTGATCAATGC
Chr19	30.9	s000200001-2	s000200001-2_F	Chr19	2,534,674	2,534,696	s000200001-2_R	Chr19	2,534,855	2,534,833	GATCAAATTTAGCCTTTGTCTCG	CCATTAACCAAAGTGGAGTTCAG
Chr19	34.2	s000200296-2	s000200296-2_F	Chr19	2,827,467	2,827,487	s000200296-2_R	Chr19	2,827,612	2,827,588	AAAGTATCGCCCTTGGGATTA	TGATTGTAAGCACAACTTCTAGTTT
Chr19	37.7	GMES3204	GMES3204_F	Chr19	3,454,232	3,454,251	GMES3204_R	Chr19	3,454,390	3,454,371	CACTTCTTCCTCCGATCCAA	CCCAGCTCTTAGTCACTGGC
Chr19	38.4	GMES1705	GMES1705_F	Chr19	3,630,910	3,630,887	GMES1705_R	Chr19	3,630,637	3,630,656	GGACAAAAGTCACAAAACAAAACA	AACAACCCACGATGGAGAAG
Chr19	39.4	Satt388	Satt388_F	Chr19	4,244,193	4,244,217	Satt388_R	Chr19	4,244,476	4,244,452	TAACTGGTATTTTTAGAACAAAAGT	TCTGGGACTGGATTTATTGTTTGAA
Chr19	40.8	T001905375m	T001905375m_F	Chr19	5,361,277	5,361,299	T001905375m_R	Chr19	5,361,603	5,361,579	CATGATGCATGTGGAAACTAGAA	TCAAATTCATTCATATACGTCTGTT
Chr19	41.7	C19-BARC-038881-07382	C19-BARC-038881-07382_F	Chr19	7,376,306	7,376,286	C19-BARC-038881-07382_R				GTTTGTCAATAGGGAACACTC	GGGAAAACAAGTCTCCAAGG
Chr19	42.7	T001910235s	T001910235s_F	Chr19	10,170,805	10,170,825	T001910235s_R	Chr19	10,171,014	10,170,992	AAACTTACAAGCGAGTGCAGC	TAGTAGGCTGAGGATGATCTTGG
Chr19	42.7	T001915546l	T001915546l_F	Chr19	21,022,129	21,022,107	T001915546l_R	Chr19	21,021,757	21,021,779	TTTCACACTGTTCTTCGAGAATG	AACCAACATTTAGAGGTGGAATG
Chr19	42.7	T001920586s	T001920586s_F	Chr19	17,885,073	17,885,093	T001920586s_R	Chr19	17,885,280	17,885,253	CAAGATTGGCGATGATGTTCT	CAGATTAAATATGATGAATATAGCAGCAA
Chr19	42.7	T001921490l	T001921490l_F	Chr19	25,389,577	25,389,553	T001921490l_R	Chr19	25,389,206	25,389,228	TTTCTAATTAATTTAGGGACCACCA	ATCCTCTACAACCTGCAAGTCAA
Chr19	43.7	T001926877m	T001926877m_F	Chr19	27,028,693	27,028,717	T001926877m_R	Chr19	27,028,921	27,028,899	TTTCTTCTTTAGGCAATCTTTATCC	TTTCAGTCCACTCAAGAGACAAA
Chr19	43.7	T001930963s	T001930963s_F	Chr19	31,107,139	31,107,160	T001930963s_R	Chr19	31,107,342	31,107,322	AAAGAATGCGTTGAAATGGTTT	AGAGGTGGAAGGATGAAGGAA
Chr19	43.7	C19-BARC-042921-08457	C19-BARC-042921-08457_F	Chr19	31,110,203	31,110,222	C19-BARC-042921-08457_R	Chr19	31,110,293	31,110,274	GGTTCTCATAAAAAATTTCG	AATTAAATAGTCTATGATGG
Chr19	44	C19-BARC-018117-02529	C19-BARC-018117-02529_F	Chr19	32,334,107	32,334,126	C19-BARC-018117-02529_R	Chr19	32,334,186	32,334,167	GTCCAACTGACAAGATAGAG	CAACAACTCAGCCTTTACGG
Chr19	44.5	Satt497	Satt497_F	Chr19	33,863,897	33,863,917	Satt497_R	Chr19	33,864,161	33,864,138	GTTTTGGATTGACTTTGTTGA	GGCTCAATTAGAGCATGCAACATC
Chr19	48.4	T001934251m	T001934251m_F	Chr19	34,413,211	34,413,233	T001934251m_R	Chr19	34,413,482	34,413,459	CAATGAAGGACTATACCTGTGGC	TGATTATTTATAATAACGGTGTCA
Chr19	49	T001934360m	T001934360m_F	Chr19	34,522,375	34,522,391	T001934360m_R				GAAAGATTGGAGAGTGAAACAGC	AAAGTTAAATCGTTCAATTGATGT
Chr19	50.5	Satt313	Satt313_F	Chr19	34,751,890	34,751,912	Satt313_R	Chr19	34,752,130	34,752,108	GTAAGTCATGGCTTTTTAATCTT	CGAGGTATGGAACCTAACTCACA
Chr19	51.9	Satt613	Satt613_F	Chr19	35,279,793	35,279,771	Satt613_R	Chr19	35,279,645	35,279,666	GAATATGATCATTGGTAATGTAC	CGGCTTCAAACGGCAAATAATC
Chr19	51.9	C19-BARC-041465-08003	C19-BARC-041465-08003_F	Chr19	35,465,451	35,465,470	C19-BARC-041465-08003_R	Chr19	35,465,530	35,465,511	CTTAAATCACTAGTCACCGC	TCTAACCGTTGAGACCGTTG
Chr19	53	GMES1048	GMES1048_F	Chr19	35,787,418	35,787,437	GMES1048_R	Chr19	35,787,569	35,787,548	CTCAACTCTCCCCTGAGTGC	TGATAATGTGAATGTGACACGG
Chr19	54.7	s010901301	s010901301_F	Chr19	36,233,475	36,233,452	s010901301_R	Chr19	36,233,290	36,233,313	GTGTTGACATTATCGGCAACGAAT	GGCGCGTACCCATTTTAACTCTTT
Chr19	55	T001936293l	T001936293l_F	Chr19	36,472,316	36,472,338	T001936293l_R	Chr19	36,472,674	36,472,652	TAATTGACTAATTCGATCGGGAA	CCCTTTGCGAGTAAACCTCTAGT
Chr19	57.8	T001936630l	T001936630l_F	Chr19	36,807,012	36,807,034	T001936630l_R	Chr19	36,807,399	36,807,381	AAAGGACTTACCATCCAACAGTG	CCTAATCGCCATTAACATAGCAG
Chr19	61.4	T001936838m	T001936838m_F	Chr19	37,015,034	37,015,056	T001936838m_R	Chr19	37,015,316	37,015,294	TGAAGTATCAATGGCATCTGTTG	ACCCACATTGTATTGCTCTTACC
Chr19	61.6	T001936942s	T001936942s_F	Chr19	37,119,000	37,119,022	T001936942s_R	Chr19	37,119,195	37,119,178	GGGCTTTAGTGCTAGGGTACAGT	AATAAGGGCTTTGAGTTAGGTCG
Chr19	63.8	GMES5355	GMES5355_F	Chr19	37,941,241	37,941,260	GMES5355_R	Chr19	37,941,545	37,941,526	CCCTTTGGTCCACTCGTAAA	CTCTGCAACGCTGATACCAA
Chr19	65.8	C19-BARC-031623-07122	C19-BARC-031623-07122_F	Chr19	38,370,943	38,370,962	C19-BARC-031623-07122_R	Chr19	38,371,037	38,371,017	GGACTCTTGAAAACATCTGG	GTCAGATCTATTTTGCTTTGG
Chr19	68.1	GMES3285	GMES3285_F	Chr19	38,633,690	38,633,709	GMES3285_R	Chr19	38,633,976	38,633,957	AGTTCACGGCCATGTTTAGG	TTCTTCACGTTGGAGTGCAG
Chr19	70.3	T001938721m	T001938721m_F	Chr19	38,932,296	38,932,318	T001938721m_R	Chr19	38,932,598	38,932,576	CCAAATTACTGAGTTGCTTGTCC	CTTCCTTGTTCCCTGTTAACCTT
Chr19	73.6	T001939240l	T001939240l_F	Chr19	39,439,716	39,439,738	T001939240l_R	Chr19	39,440,094	39,440,072	CAACCACTCCCGTCTCTTACATA	AACATAAAGGACTCATACCGTTT
Chr19	74.2	s007701934-2	s007701934-2_F	Chr19	39,813,360	39,813,338	s007701934-2_R	Chr19	39,813,183	39,813,208	TCGTTTATAATACTCACACTTCTGC	AAGTAGATATCACACTTTCATTAAGC
Chr19	76.9	T001940085l	T001940085l_F	Chr19	40,275,676	40,275,698	T001940085l_R	Chr19	40,276,042	40,276,020	TGAACTTGCTATATACGGAGCGT	TCGATGCAATAGCTTACAGAACA
Chr19	79.4	Sat_340	Sat_340_F	Chr19	40,636,694	40,636,713	Sat_340_R	Chr19	40,636,922	40,636,901	ATGGAGCCGTGCTTATTCAC	GCTTTCCCCTTTTAACTCTGAG
Chr19	83.6	Sct_010	Sct_010_F	Chr19	41,378,951	41,378,936	Sct_010_R	Chr19	41,378,803	41,378,818	TCCCAAAAGCATTGAG	TATGCACGGAAGAGGA
Chr19	86	GMES6825	GMES6825_F	Chr19	42,028,489	42,028,510	GMES6825_R	Chr19	42,028,694	42,028,675	TTTCCTCCACGTTTCACTTTTT	CTTGATGGGTTAAGGTTGGG
Chr19	90.1	T001942220l	T001942220l_F	Chr19	42,419,411	42,419,433	T001942220l_R	Chr19	42,419,786	42,419,763	GGTATCTTTAGGCTGTAGCCACT	AAAGTATGATGCAAAGGGTATATT
Chr19	93.6	T001942475s	T001942475s_F	Chr19	42,674,218	42,674,241	T001942475s_R	Chr19	42,674,410	42,674,388	TGAAACTGAATATAAGCCTCCAGA	GTCGCTTTACACGTTACATGGAT
Chr19	95.8	Satt527	Satt527_F	Chr19	43,035,863	43,035,839	Satt527_R	Chr19	43,035,672	43,035,696	GTTACATCTTGCAAACTAAATTAAC	GAATTTTGCACATAAATTAATAACT
Chr19	96.3	GMES3292	GMES3292_F	Chr19	43,298,252	43,298,271	GMES3292_R	Chr19	43,298,555	43,298,536	CCGAACGAAAAAGAAAGACG	GCTATGGTGGAGTTGGTGCT
Chr19	99.4	s023300462-2	s023300462-2_F	Chr19	43,630,490	43,630,512	s023300462-2_R	Chr19	43,630,854	43,630,831	CTTATTAAGGCGTGTTTCAATCG	AAAGAGATGTTAAGAATGATCTGA
Chr19	103.5	T001943785l	T001943785l_F	Chr19	43,986,572	43,986,594	T001943785l_R	Chr19	43,986,934	43,986,912	AACCCAATCCTAGTGGCTAGAAA	TTATGTTGCACGAAGAGGTGAAT
Chr19	104.8	s004100370-2	s004100370-2_F	Chr19	44,115,711	44,115,733	s004100370-2_R	Chr19	44,115,899	44,115,874	TGCGAGTGAGTTTGATTCTTCAT	GGTGATAAGTGCATGTAGACTTGTTT
Chr19	105.9	GMES0259	GMES0259_F	Chr19	44,408,495	44,408,514	GMES0259_R	Chr19	44,416,420	44,416,401	ACCTAACTTGCGTGGGAGTG	TTTGTCTTGTTCCTCCGAGC
Chr19	109.5	GMES1723	GMES1723_F	Chr19	45,140,719	45,140,738	GMES1723_R	Chr19	45,140,805	45,140,786	CATCATCAACAACCTCACGC	GCCATGTCTGGATCTGTGTG
Chr19	109.5	Sat_286	Sat_286_F	Chr19	45,181,148	45,181,175	Sat_286_R	Chr19	45,181,298	45,181,280	TTGCTTGCTAAGTAGTGTTTTTAATCCT	TCTCCCATCATGCAACTTCAATA
Chr19	109.5	LFsoy3	LFsoy3_F	Chr19	45,183,524	45,183,505	LFsoy3_R	Chr19	45,183,252	45,183,271	CAAGGTTGAGATTGAGGGTG	GTCAGTCATGATCTGCACCG
Chr19	110	C19-BARC-013061-00434	C19-BARC-013061-00434_F	Chr19	45,438,272	45,438,253	C19-BARC-013061-00434_R	Chr19	595,476	595,491	TAAAGTGTTGCTTGCATGCG	TCCGGGGTCTCATGGCATAT
Chr19	111.1	GMES3931	GMES3931_F	Chr19	45,805,480	45,805,499	GMES3931_R	Chr19	45,805,715	45,805,696	TTCCGTTGTAAGGGGAAAAA	GTTGATCCTTGGCTCTCTGC
Chr19	113.8	Satt664	Satt664_F	Chr19	46,226,294	46,226,320	Satt664_R	Chr19	46,226,511	46,226,485	TAGATGCTCAACATCAACACTAATCTG	GACGATGAAGAAATATACTATTACGAA
Chr19	116.1	C19-BARC-030101-06809	C19-BARC-030101-06809_F	Chr19	46,632,846	46,632,828	C19-BARC-030101-06809_R				TGTCTTCTCTATAACACAC	CTCATTCTATACATTGTCTC
Chr19	116.5	Satt229	Satt229_F	Chr19	47,166,079	47,166,053	Satt229_R	Chr19	47,165,904	47,165,927	TGGCAGCACACCTGCTAAGGGAATAAA	AGGTGGTCTAAAATTATTACCTAT
Chr19	119	FT3-751	FT3-751_F	Chr19	47,632,584	47,632,565	FT3-751_R	Chr19	47,632,395	47,632,414	GAGACACTGCCATGCCATAA	GGCTGCAATCATCATCACAT
Chr19	119	FT3-190	FT3-190_F	Chr19	47,661,543	47,661,522	FT3-190_R	Chr19	47,661,245	47,661,266	CATTTCCATTTGTGCCTACCAC	TTTCTTCCTTCTCTCACCCACT
Chr19	122.8	C19-BARC-021827-04217	C19-BARC-021827-04217_F	Chr19	48,212,538	48,212,557	C19-BARC-021827-04217_R	Chr19	48,212,635	48,212,617	CTTACGTGGGTGCATAAATT	GGTACGCATAATATTATGG
Chr19	123.1	GMES4376	GMES4376_F	Chr19	48,224,525	48,224,506	GMES4376_R	Chr19	48,228,710	48,228,729	TTGGCACATCTTGCTTGAAC	TGACGGGATCCCAATAAAAA
Chr19	124.4	GMES1550	GMES1550_F	Chr19	48,382,071	48,382,090	GMES1550_R	Chr19	48,382,363	48,382,344	CCGGTTTTGTTGCCTAAGAA	ACGAATTGGCAACCCACTAC
Chr19	125.5	GMES4173	GMES4173_F	Chr19	48,608,682	48,608,701	GMES4173_R	Chr19	48,608,950	48,608,931	TCCATAAGGCACAATGCAGA	TGAATGTGCTGCTGGGTATG
Chr19	126.3	s021200706.1	s021200706_F	Chr19	48,871,958	48,871,944	s021200706_R	Chr19	48,871,714	48,871,736	TCAGTAAGGTAGTCCCACTTTGG	TATTCTGGGAGGAAGCACCTTAT
Chr19	129.3	GMES2731	GMES2731_F	Chr19	49,238,097	49,238,116	GMES2731_R	Chr19	49,238,375	49,238,356	CTGTGTTTGATTGTCACGGC	TGAGCAATAAGCACTCACGG
Chr19	129.7	Satt373	Satt373_F	Chr19	49,312,044	49,312,022	Satt373_R	Chr19	49,311,824	49,311,848	TCCGCGAGATAAATTCGTAAAAT	GGCCAGATACCCAAGTTGTACTTGT
Chr19	130.5	GMES0853	GMES0853_F	Chr19	49,440,990	49,441,009	GMES0853_R	Chr19	49,441,242	49,441,223	TCCCCCTCTCAATCTTTTCC	AGAAGGATCCATCGCTACCC
Chr19	131	GMES2377	GMES2377_F	Chr19	49,528,338	49,528,319	GMES2377_R	Chr19	49,528,189	49,528,208	CTCTTTCTTCCACCACCACC	ACCGAGTGAGGGTACAGCAT

Chr19	131.8	GMES0975	GMES0975_F	Chr19	49,631,616	49,631,635	GMES0975_R	Chr19	49,631,813	49,631,794	CGCACCTCTTTTGTGTCTCA	GAGAAGGAGAAGGAGGACGG
Chr19	136.7	Sat_245	Sat_245_F	Chr19	50,144,143	50,144,170	Sat_245_R	Chr19	50,144,311	50,144,284	AGCCTACTTTTACTAGAACGTCAACAAG	AAAAATTCAACTCCCCTTTAATAGATTC
Chr19	136.7	GMES6625	GMES6625 F	Chr19	50,342,555	50,342,574	GMES6625 R	Chr19	50,342,830	50,342,811	TTTGATAGCCAATGCAGCAG	CCCTAATCGAACAAGCCAAA
Chr19	137.9	s004106980-2	s004106980-2_F	Chr19	50,647,123	50,647,148	s004106980-2_R	Chr19	50,647,316	50,647,293	TCTTTGAAGAAGATAAATCAACATGG	TTGAACGGTTTAACAAGCTGTAAC
Chr20	0	T002000016s	T002000016s_F	Chr20	15,136	15,160	T002000016s_R	Chr20	15,345	15,326	CAGACATTATCATTGGTGTAACTTT	TTGTTGGGTCTCGACAGAAA
Chr20	0.5	T002000059s	T002000059s_F	Chr20	58,306	58,328	T002000059s_R	Chr20	58,471	58,449	GCAATGGTATGTGTAAGAAGCCT	CACCACTACTTTGTTGAGGAAGG
Chr20	1.6	T002000188l	T002000188l F	Chr20	187,552	187,573	T002000188l R	scaffold 21	377,481	377,460	AAACACCACATGCAATACCTTG	TAGGATGGGTAAGACTATTTGGG
Chr20	4.6	T002000300m	T002000300m_F	Chr20	298,951	298,973	T002000300m_R	Chr20	299,257	299,235	GAAGCCATAGTCATGTCCTCTGT	TGATGCTCAAATCTTACCCTAGC
Chr20	6	T002000417l	T002000417l_F	Chr20	412,178	412,200	T002000417l_R	Chr20	412,557	412,534	TGCTTGGAGATTTACATAGAGAA	TTAACACAAGGACAACATTGACTC
Chr20	11.6	T002000523l	T002000523l F	Chr20	518,643	518,665	T002000523l R	Chr20	518,988	518,966	TAGATGACAAGACCAAACTCACG	TCATTGCAATATCTTGCTTGTGT
Chr20	11.9	T002000573s	T002000573s_F	Chr20	567,151	567,173	T002000573s_R	Chr20	567,276	567,254	ACTGGGTTTGTTCTCACATGACT	TTGAAACCACGTACACGTAGAAA
Chr20	13.8	GMES3485	GMES3485_F	Chr20	657,246	657,266	GMES3485_R	Chr20	657,457	657,438	TTAGGGTTTCTGATTGGAGCA	ATGTTGGAGAGGAGGAGGGT
Chr20	14.6	C20-BARC-028335-05832	C20-BARC-028335-05832_F	Chr20	690,228	690,209	C20-BARC-028335-05832_R	Chr20	690,129	690,148	CACCATGTCAGCTATAACTC	AGAGTAGCAGATGGAAGTTG
Chr20	15.1	T002000730s	T002000730s F	Chr20	724,595	724,616	T002000730s R	Chr20	724,793	724,771	ATATATTGTCACGTGCCGACTG	TCTTTCTGGTATTTGGGATTGTG
Chr20	20.7	T002000983m	T002000983m_F	Chr20	978,617	978,639	T002000983m_R	Chr20	978,951	978,929	TGACTAACACTGCTGAAGCTCAT	ATCATTGTTGTACCCAGCTATGG
Chr20	22.3	GMES1618	GMES1618_F	Chr20	1,084,522	1,084,503	GMES1618_R	Chr20	1,084,245	1,084,264	ATGCTCTTGGGTGGTGGTAG	TCCAGCTTTGCGTGTAACAG
Chr20	25.9	Satt571-2	Satt571-2_F	Chr20	1,287,772	1,287,752	Satt571-2_R	Chr20	1,287,441	1,287,462	TTTCAACAGCTGAGAGATTGC	AGGAAAGACGACAAACGCAAAT
Chr20	26.8	C20-BARC-040123-07661	C20-BARC-040123-07661_F	Chr20	1,386,455	1,386,436	C20-BARC-040123-07661_R	Chr20	1,386,374	1,386,393	ATTCTGAGAGAAAATAATAG	CGCTGACAGCCTTAACATTC
Chr20	28	Satt419	Satt419_F	Chr20	1,885,401	1,885,423	Satt419_R	Chr20	1,885,636	1,885,613	CCATGACGCCAGCTTGCTTTTCC	CCATTATATACAAATTACGATCAT
Chr20	30.5	C20-BARC-042619-08314	C20-BARC-042619-08314_F	Chr20	2,072,979	2,072,998	C20-BARC-042619-08314_R	Chr20	2,073,054	2,073,036	TTGCAGTCCAGAAGACATCG	CCCAGTATTTAACAAGCAT
Chr20	31.3	T002002126s	T002002126s F	Chr20	2,119,071	2,119,093	T002002126s R	Chr20	2,119,257	2,119,235	GGCATTCCTTCAAATATATCCCT	GGCAATTCTACATGGTAGCCTCT
Chr20	35.1	Sat_368-2_re	Sat_368-2_re_F				Sat_368-2_re_R				GCGAGTGCAAGAAAAAGGGAGAAAATA	GCGCTTTTCTTTCCTTTTTTTTCTCTT
Chr20	35.4	T002002565m	T002002565m_F	Chr20	2,557,683	2,557,706	T002002565m_R	Chr20	2,558,006	2,557,984	TGATATGTCACTTCTCTTGTGACT	CTTCGTCCTCGTATCAGTCAATC
Chr20	39.7	Satt614	Satt614_F	Chr20	3,903,530	3,903,555	Satt614_R	Chr20	3,903,836	3,903,811	CTCCCCTTTAACCTTTCCTTTATTAG	CGGTAGGAATTAATTGTAGATAGGAT
Chr20	39.7	GMES6670	GMES6670 F	Chr20	4,285,101	4,285,082	GMES6670 R	Chr20	4,284,838	4,284,857	CACCGTCTTTCAGCACTTCA	TCCCACCCTATGAACTCGTC
Chr20	39.7	T002004816l	T002004816l_F	Chr20	4,798,294	4,798,316	T002004816l_R	Chr20	4,798,675	4,798,653	TACACATCATCAAGGCACTCATC	AAATCCAATGGTGAAGAATAAAC
Chr20	40.5	T002005440m	T002005440m_F	Chr20	5,406,453	5,406,475	T002005440m_R	Chr20	5,406,664	5,406,644	GTTGCAACAATAAGATTTACGGG	TCACATGTCGATCACCAGTCTTA
Chr20	41.8	T002011255l	T002011255l F	Chr20	7,253,544	7,253,566	T002011255l R	Chr20	7,253,891	7,253,869	AATTCAGAGTCAGTTGAAGCACC	GAAGCAAATGCATTGGAACTAAG
Chr20	43.4	Satt127	Satt127_F	Chr20	8,169,605	8,169,624	Satt127_R	Chr20	8,169,828	8,169,808	CGCTTGTGAACCCTGCTAAA	CCATCCTCTGAAACCGTTATCT
Chr20	44.2	s000119123-2	s000119123-2_F	Chr20	18,048,873	18,048,896	s000119123-2_R	Chr20	18,049,203	18,049,181	CAAGTCCCTATGGAGATGAACTCT	ACCGTTGGTTATGGGTTACTCTT
Chr20	44.2	T002006435l	T002006435l_F	Chr20	17,107,815	17,107,793	T002006435l_R	Chr20	17,107,471	17,107,493	AGTTTATTAGGTGACGGGTGTCG	TTTGAGGTAATCCAATAACGGCT
Chr20	44.2	s020400333	s020400333 F	Chr20	16,596,736	16,596,758	s020400333 R	scaffold 3002	301,099	301,077	CGAAGACTTTGAGTCCTACGAAA	TTTACCCGTGTGAATTTGGTTAC
Chr20	44.2	T002009756m	T002009756m_F				T002009756m_R	Chr20	18,656,915	18,656,937	TTGTATCTTTCCGCTGATCTCAT	GACATGAAGACTGTAACGACACG
Chr20	44.2	T002008955m	T002008955m_F	Chr20	19,456,436	19,456,414	T002008955m_R	Chr20	19,456,171	19,456,193	TGCTCATGTTTCATTACATGCTT	CACAAGTTAGGTCAAGGTTGGTC
Chr20	44.5	T002007942m	T002007942m_F	Chr20	20,456,170	20,456,148	T002007942m_R	Chr20	20,455,847	20,455,869	TGGTTGATAGTTATGTCCCGTTT	CGGTCTATAGCCACCCAAATAGT
Chr20	44.5	C20-BARC-029827-06444	C20-BARC-029827-06444_F	Chr20	24,177,948	24,177,967	C20-BARC-029827-06444_R	Chr20	24,178,041	24,178,021	TGCTTCCTGGATTCTTCATC	GGTAATTTTCTGCAGAAGCTC
Chr20	44.7	Satt239	Satt239_F	Chr20	25,275,420	25,275,438	Satt239_R	Chr20	25,275,605	25,275,584	CCAAAAAATGAATCACAAT	AACACAATCAACATCCTTGAAC
Chr20	45	Sat_219	Sat_219_F	Chr20	25,674,600	25,674,580	Sat_219_R	Chr20	25,674,346	25,674,365	TCATGCCACGTGATATTTTAT	TGTGTCCCAAATGTGATTCA
Chr20	45	Sat_174	Sat_174_F	Chr20	25,693,539	25,693,563	Sat_174_R	Chr20	25,693,761	25,693,738	TACGAAATATTGCAAGAGATACATT	GCCTTAGATCAATTGTGATAAAAA
Chr20	45	T002026426s	T002026426s_F	Chr20	27,586,772	27,586,798	T002026426s_R	Chr20	27,587,024	27,587,002	GAGACAAACTTATAACTCCGATTGTTC	TTTAAGCGTAACGCAACTCTTTC
Chr20	46.1	T002027923l	T002027923l_F	Chr20	29,085,333	29,085,355	T002027923l_R	Chr20	29,085,676	29,085,654	TTATGGTAATGTTTGTCTGGCTT	CACCATTTGTAGGGAAGTGACAT
Chr20	46.6	T002029541l	T002029541l_F	Chr20	30,691,118	30,691,140	T002029541l_R	Chr20	30,691,492	30,691,470	CAACAACACTGCAAACTTCTGTT	ATTCTCGCCTTATAAGCAGGTTT
Chr20	47.7	T002031490m	T002031490m F	Chr20	32,630,726	32,630,748	T002031490m R	Chr20	32,630,974	32,630,952	TAATTAATCCAACCCGAAGGTTT	AATGAATCTTGTGATCTCATCCG
Chr20	47.7	T002031881l	T002031881l_F	Chr20	33,029,245	33,029,267	T002031881l_R	Chr20	19,472,010	19,472,025	GGGAGGCAAATCTAATAAGTCCA	TCATATATACGGAGTGTGAATGGAA
Chr20	48.5	T002032140s	T002032140s_F	Chr20	33,288,062	33,288,084	T002032140s_R	Chr20	33,288,249	33,288,227	TTTGACCATCTCGTTTAACTTCG	CATGAAATGATGGCAATTGAACT
Chr20	49	T002032323s	T002032323s F	Chr20	33,463,908	33,463,930	T002032323s R	Chr20	33,464,112	33,464,090	ATAATGATATGCGCTTCCAAGAA	ATCTACGAGGCTCTAAGTTCAAA
Chr20	52.1	T002032584s	T002032584s_F	Chr20	33,725,180	33,725,202	T002032584s_R	Chr20	33,725,348	33,725,326	ATTTGCCATATGAACAACCACTG	TAAGTTCCGTAGGCTACTTGGTG
Chr20	55.8	T002032785s	T002032785s_F	Chr20	33,926,257	33,926,279	T002032785s_R	Chr20	33,926,454	33,926,431	CCACAAATTTGGAAACAGACTTC	AAGTAGATTTCTCCTATACCGTTT
Chr20	57.8	GMES5899	GMES5899_F	Chr20	34,243,284	34,243,305	GMES5899_R	Chr20	34,243,564	34,243,545	AAAACGTATGCCACTGTTGTTC	TGAAGGCAATAATTGGAGGG
Chr20	62.4	GMES4748	GMES4748 F	Chr20	34,574,638	34,574,654	GMES4748 R				GGGTCTAGCGGAAGACCTTT	TGACACACATGTTGCAATGG
Chr20	64.4	T002033603m	T002033603m_F	Chr20	34,742,227	34,742,249	T002033603m_R	Chr20	34,742,541	34,742,519	AAGGTTGTTACTTGGTATCATTC	GCTCGTTGAATACTCGGCTAATA
Chr20	68.2	T002033899s	T002033899s_F	Chr20	35,037,585	35,037,612	T002033899s_R	Chr20	35,037,794	35,037,772	TCAATAATAAGAAGAAATAAGAGTGAGA	TTTCTTTGGCTTACAAGAACGAT
Chr20	69	Satt270	Satt270_F	Chr20	35,362,781	35,362,765	Satt270_R	Chr20	35,362,590	35,362,607	TGTGATGCCCCTTTTCT	CAGTGCATGGTTTTCTCA
Chr20	70.6	C20-BARC-029461-06194	C20-BARC-029461-06194_F	Chr20	35,578,934	35,578,953	C20-BARC-029461-06194_R	Chr20	35,579,017	35,578,998	GGTCAATGACTGAAAAGCAC	AAGACGTCAGAAGAGATGGC
Chr20	71.2	GMES1628	GMES1628_F	Chr20	35,644,604	35,644,585	GMES1628_R	Chr20	35,644,365	35,644,385	CTGCTGATGGTGCTTGAAAA	TCAAACTTTCACCAAACGAGC
Chr20	76.2	GMES0205	GMES0205_F	Chr20	36,390,380	36,390,399	GMES0205_R	Chr20	36,390,677	36,390,658	GAGGATCGGGTAACGAATCA	TAATTCAGCGGAAAGAAGCC
Chr20	77.5	GMES1146	GMES1146 F	Chr20	36,740,656	36,740,638	GMES1146 R	Chr20	36,740,396	36,740,415	GGCGTTGTGTTGGTGGAAT	TAATGGGTGCTCGAAAAAGG
Chr20	77.5	s005202718-2.1	s005202718-2_F	Chr20	36,831,067	36,831,089	s005202718-2_R	Chr20	36,831,145	36,831,119	TCCCTTCCTCTTTAATTTGCTTT	GAAGAGAAGACAGAACAGAGTATTTGA
Chr20	77.5	C20-BARC-029803-06416	C20-BARC-029803-06416_F	Chr20	36,855,900	36,855,919	C20-BARC-029803-06416_R	Chr20	36,855,996	36,855,977	GGAGTATGTTGCTACTATTC	GTGTGCGTCTAAATTTCAAG
Chr20	81.4	s013301378-2	s013301378-2_F	Chr20	37,108,757	37,108,735	s013301378-2_R	Chr20	37,108,559	37,108,575	TTTCCTTTCTGTTTAGATTTCCT	TAGACCTCCAACGCGCC
Chr20	85	T002036224s	T002036224s F	Chr20	37,318,499	37,318,521	T002036224s R	Chr20	37,318,708	37,318,686	TACAGGATAAATGCTACCGAGGA	CTTGTAGACCGGCCTAACCTATT
Chr20	88.4	s013300975-2	s013300975-2_F	Chr20	37,510,270	37,510,245	s013300975-2_R	Chr20	37,510,126	37,510,149	AAAGCTATTATGGATCATGGTTAGTT	TTATGAAACTTCAGTGTTGAACGA
Chr20	92	Satt650	Satt650_F	Chr20	38,171,771	38,171,788	Satt650_R	Chr20	38,172,012	38,171,992	CAGTTGGCTGGTCAAATC	TCTGGGTTACTTTTATTGTCA
Chr20	95.8	alpha3UTRat	alpha3UTRat F	Chr20	38,680,442	38,680,463	alpha3UTRat R	Chr20	38,680,641	38,680,626	CTGTCTGCTTAGCTAATTTGAT	CTGACAGACTCAATAACAAGAT
Chr20	100.6	Sat_170	Sat_170_F	Chr20	39,770,195	39,770,171	Sat_170_R	Chr20	39,770,036	39,770,060	GATTGATTTAATTAAGTGTGATTAA	CCGATGATCATGAATTAGAATAACA
Chr20	102.5	Satt330	Satt330_F	Chr20	40,155,042	40,155,061	Satt330_R	Chr20	40,155,159	40,155,138	CCTCCATTCCACAACAAATA	GCATCCGTTTCTAAGATAGTTA
Chr20	104.4	C20-BARC-040751-07840	C20-BARC-040751-07840_F	Chr20	40,540,243	40,540,262	C20-BARC-040751-07840_R	Chr20	40,540,303	40,540,284	GTATCAAAAGAGAAATACAC	TAAACTCATTTACATATGAC
Chr20	106.1	GMES0743	GMES0743 F	Chr20	40,865,394	40,865,375	GMES0743 R	Chr20	40,865,021	40,865,040	AAACCCTCCCCTCACACTCT	TCCTTGTCGAACCGGTAAAG
Chr20	106.1	Sat_324	Sat_324_F	Chr20	40,998,720	40,998,694	Sat_324_R	Chr20	40,998,523	40,998,548	CAATGTCCCTCTTTCTTCCAATGATAA	TGCAGGGGAGATTAGCTAGAAATGTG
Chr20	106.1	C20-BARC-029151-06094	C20-BARC-029151-06094_F	Chr20	41,021,913	41,021,895	C20-BARC-029151-06094_R	Chr20	41,021,834	41,021,853	TAATATAAGCTGGTATTCC	AGTGCCTATAAATGGCTGGG
Chr20	110.6	Satt623	Satt623_F	Chr20	42,164,986	42,164,963	Satt623_R				GTGCAATGATTTTAATGATATGAT	CGTGTAAAAGGTTATAACGTGTAA
Chr20	114.3	T002041468m	T002041468m_F				T002041468m_R	Chr20	42,583,596	42,583,576	TTATGATCACTTGATCCCTCTTT	AGGTATTGCACATTTGCATCG
Chr20	115.7	Sat_155	Sat_155_F	Chr20	42,932,725	42,932,702	Sat_155_R	Chr20	42,932,556	42,932,573	GGGACAGCACCGTCAAGGAGGAGA	TGGGAAAGAAATTGTAGC
Chr20	116.2	Sat_420	Sat_420_F				Sat_420_R	Chr20	42,932,568	42,932,584	GATGGAGCCAACA	TGTAGCCCTAGAAAGTT
Chr20	121.4	T002042675s	T002042675s F	Chr20	43,789,864	43,789,886	T002042675s R	Chr20	43,790,061	43,790,039	TAATTGTGGACTTCAAAGAAGGG	TTGATTGGGAATTCGTTTCTACA
Chr20	122.3	s030900011	s030900011_F	Chr20	44,167,801	44,167,823	s030900011_R	Chr20	44,168,129	44,168,107	TCCTCGGAGAGTAATGTCAGAAA	TTGCAGCTGTAGTTGTGGTTACA
Chr20	127.4	Satt102	Satt102_F	Chr20	44,793,295	44,793,312	Satt102_R	Chr20	44,793,449	44,793,426	CACCTTGCTTCAAAATTC	AATAAGTGAGAGCATAGAAAATAC

Chr20	128	C20-BARC-008253-00130	C20-BARC-008253-00130_F	Chr20	45,013,486	45,013,467	C20-BARC-008253-00130_R	Chr20	45,013,406	45,013,425	CATCGCTTGCTTGAAGACAC	GATGTGGCAGACAATGATGG
Chr20	128.7	T002044011s	T002044011s_F	Chr20	45,136,975	45,136,997	T002044011s_R	Chr20	45,137,185	45,137,157	ATCATGATAGATTAGAGGTGGGA	TCAATAAGTCTGATTCTATTTACGATTTG
Chr20	129	C20-BARC-015569-02005	C20-BARC-015569-02005_F	Chr20	45,169,154	45,169,173	C20-BARC-015569-02005_R	Chr20	45,169,248	45,169,229	CACATAATGCCTAACACTTG	GGAAAATGAAGTAGCCGAGC
Chr20	132.1	GMES6273	GMES6273_F	Chr20	45,597,042	45,597,027	GMES6273_R	Chr20	45,596,843	45,596,862	TGATTCGGCTCTGATCTTCC	GTTCCTGCTTGACGGAGAAT
Chr20	134.5	GMES0425	GMES0425_F	Chr20	46,194,622	46,194,603	GMES0425_R	Chr20	46,194,442	46,194,461	GGGAAAGGAATGCAAACTGA	TTCTTCAGGCCACCAAGAAT
Chr20	135.4	GMES1641	GMES1641_F	Chr20	46,578,094	46,578,113	GMES1641_R	Chr20	46,578,374	46,578,355	GGGTCAGAGAGGTCCAATGA	GGTGTGGCCTTCCATACATC
Chr20	135.7	Sct_189	Sct_189_F	Chr20	46,676,804	46,676,820	Sct_189_R	Chr20	46,676,964	46,676,946	CTTTTCCTGGCAATGAT	AAAATCGCAAAACCTTAGT
Chr20	135.7	GMES1596	GMES1596_F	Chr20	46,783,599	46,783,580	GMES1596_R	Chr20	46,783,343	46,783,362	ACCAGTTTCTCCAAACCACG	AAGCAAGGCTTTGTCGAAGA
Chr20	135.9	C20-BARC-018065-02503	C20-BARC-018065-02503_F	Chr20	46,825,329	46,825,309	C20-BARC-018065-02503_R	Chr20	46,825,255	46,825,274	GCAGAGCATGACAAACTAAAG	ATACTAGGCATGGATGGCAG
Chr20	135.9	GMES2744	GMES2744_F	Chr20	46,871,195	46,871,214	GMES2744_R	Chr20	46,871,334	46,871,315	TGCAGGAGCTGAATTTTCCT	CAACCCGAAATGGATTACCA
Chr20	138.4	GMES3036	GMES3036_F	Chr20	47,356,838	47,356,857	GMES3036_R	Chr20	47,357,082	47,357,061	CAAGACTCCCTTGCCAAAAG	AACTTCTTCGTCCGATCTTACA
Chr20	139.2	GMES2783	GMES2783_F	Chr20	47,617,909	47,617,928	GMES2783_R	Chr20	47,618,295	47,618,276	GCCACACTGACACACCAAAC	AGAAAGAGCATTCGGGTGAA
Chr20	139.2	BE820889	BE820889_F	Chr20	47,836,136	47,836,162	BE820889_R	Chr20	47,836,521	47,836,501	ACAACATTCCATAGACACAAATAATAA	TTTGGTCTTGGCCTGTATTTG

別冊表 2-3 系統解析で使用したフィルタされたシングルコピー遺伝子

***G. max* cv. Enrei**	**Gmax275**	***A. lyrata***	***A. thaliana***	***O. sativa***	***M. truncatula***
Gmech0010G03752	Glyma.10G240400.1	918223|PACid:16042081	AT5G51880.1	Os03t0119000-01	Medtr1g101840.1|PACid:23045905
Gmech0010G03367	Glyma.10G195900.1	317863|PACid:16057405	AT3G10620.1	Os04t0685800-01	Medtr1g090550.1|PACid:23044306
Gmech0017G00678	Glyma.17G075900.1	488173|PACid:16050482	AT5G13510.1	Os03t0284400-01	Medtr4g131540.1|PACid:23051912
Gmech0009G02400	Glyma.09G124600.1	894884|PACid:16060776	AT1G70670.1	Os06t0254700-01	AC233676_19.1|PACid:23053850
Gmech0004G01407	Glyma.04G123100.1	484970|PACid:16040808	AT3G45900.1	Os03t0853600-01	Medtr5g026680.1|PACid:23032897
Gmech0007G00627	Glyma.07G075100.1	914207|PACid:16045354	AT4G23890.1	Os07t0196200-01	Medtr8g032260.1|PACid:23038658
Gmech0015G03542	Glyma.15G238400.1	482887|PACid:16046124	AT2G38750.1	Os05t0382600-02	Medtr8g038170.1|PACid:23040107
Gmech0015G01121	Glyma.15G125100.1	484158|PACid:16053857	AT2G02400.1	Os01t0978400-01	Medtr2g028620.1|PACid:23018641
Gmech0013G01754	Glyma.13G101400.1	474402|PACid:16054419	AT1G52760.1	Os02t0207900-01	Medtr4g127220.1|PACid:23049891
Gmech0002G00715	Glyma.02G081200.1	488450|PACid:16061910	AT5G16010.1	Os07t0162100-00	Medtr6g043740.1|PACid:23026238
Gmech0002G00498	Glyma.02G057000.1	495016|PACid:16057064	AT5G49560.1	Os07t0569500-01	Medtr8g077610.1|PACid:23039706
Gmech0002G00967	Glyma.02G103500.1	912997|PACid:16046371	AT4G34050.1	Os06t0165800-01	Medtr4g085590.1|PACid:23051314
Gmech0002G00099	Glyma.02G009700.1	470202|PACid:16037968	AT1G02420.1	Os03t0208600-01	Medtr1g086500.1|PACid:23041737
Gmech0002G03713	Glyma.02G245800.1	475745|PACid:16038726	AT1G66430.1	Os06t0232200-00	Medtr5g079460.1|PACid:23030763
Gmech0002G00462	Glyma.02G052600.1	490994|PACid:16055842	AT4G36420.1	Os03t0734400-01	Medtr8g076780.1|PACid:23037104
Gmech0019G01927	Glyma.19G079000.1	340279|PACid:16042385	AT3G01660.1	Os04t0481300-01	Medtr7g032900.1|PACid:23022343
Gmech0019G02086	Glyma.19G084400.1	861820|PACid:16039529	AT5G14280.1	Os05t0302600-01	Medtr8g088170.1|PACid:23038862
Gmech0019G00523	Glyma.19G044200.1	916464|PACid:16051880	AT5G38630.1	Os08t0384000-01	AC233140_79.1|PACid:23053583
Gmech0003G02625	Glyma.03G128800.1	897197|PACid:16052298	AT3G10210.1	Os01t0948300-01	Medtr7g090050.1|PACid:23023079
Gmech0003G02539	Glyma.03G119400.1	494675|PACid:16040108	AT5G43280.1	Os01t0925200-01	Medtr3g085700.1|PACid:23014006
Gmech0020G03931	Glyma.20G244100.1	909305|PACid:16036840	AT5G13520.1	Os03t0819100-01	Medtr1g116230.1|PACid:23043181
Gmech0011G00629	Glyma.11G075600.1	496977|PACid:16044663	AT5G66290.1	Os03t0727100-01	Medtr5g021750.1|PACid:23034887
Gmech0011G00684	Glyma.11G082400.1	491070|PACid:16054827	AT4G35760.1	Os03t0131500-01	Medtr5g023180.1|PACid:23032537
Gmech0011G00148	Glyma.11G018300.1	474917|PACid:16054018	AT1G64350.1	Os01t0620100-01	Medtr6g072020.1|PACid:23027443
Gmech0011G00030	Glyma.11G003800.1	477902|PACid:16044993	AT3G06035.1	Os07t0645000-01	Medtr5g005710.1|PACid:23034235
Gmech0014G03697	Glyma.14G193000.1	496002|PACid:16054459	AT5G58770.1	Os01t0857200-01	Medtr5g070210.1|PACid:23029504
Gmech0014G00150	Glyma.14G017000.1	314447|PACid:16047098	AT1G50590.1	Os09t0484800-01	Medtr5g094250.1|PACid:23032812
Gmech0014G00577	Glyma.14G067900.1	325857|PACid:16051108	AT5G13830.1	Os03t0822300-01	Medtr5g080020.1|PACid:23031161
Gmech0014G03948	Glyma.14G222500.1	895485|PACid:16057263	AT1G76080.1	Os07t0476900-01	Medtr1g026130.1|PACid:23045413
Gmech0008G01298	Glyma.08G152800.1	478619|PACid:16037132	AT3G12610.1	Os08t0505900-01	Medtr3g027940.1|PACid:23013913
Gmech0008G04290	Glyma.08G354800.1	478027|PACid:16037842	AT3G07080.1	Os06t0681700-01	Medtr7g058520.1|PACid:23024886
Gmech0008G01544	Glyma.08G180000.1	471781|PACid:16056597	AT1G15820.1	Os04t0457000-01	Medtr2g008610.1|PACid:23019252
Gmech0001G03206	Glyma.01G121700.1	478195|PACid:16047061	AT3G08920.1	Os03t0289400-00	AC235756_4.1|PACid:23053331
Gmech0001G00125	Glyma.01G013900.1	473398|PACid:16048931	AT1G32170.1	Os02t0127800-01	Medtr5g029100.1|PACid:23030494
Gmech0001G04597	Glyma.01G243100.1	479469|PACid:16038659	AT3G19553.1	Os12t0580400-01	Medtr5g005160.1|PACid:23033183
Gmech0012G02870	Glyma.12G188200.1	470906|PACid:16042415	AT1G08460.1	Os05t0440250-01	Medtr2g087270.1|PACid:23015846
Gmech0012G01021	Glyma.12G111000.1	480913|PACid:16061953	AT2G20770.1	Os04t0529600-01	Medtr6g007490.1|PACid:23027353
Gmech0012G00223	Glyma.12G026000.1	471936|PACid:16050494	AT1G17330.1	Os10t0486000-01	Medtr4g023480.1|PACid:23050274
Gmech0006G00389	Glyma.06G047700.1	890273|PACid:16043457	AT1G27480.1	Os03t0730000-01	Medtr2g075650.1|PACid:23015728
Gmech0018G00518	Glyma.18G057700.1	481930|PACid:16044064	AT2G30200.1	Os03t0297400-01	Medtr3g031380.1|PACid:23012364
Gmech0018G04200	Glyma.18G273900.1	494088|PACid:16053387	AT5G38900.1	Os03t0598900-01	Medtr7g016650.1|PACid:23024999
Gmech0016G00358	Glyma.16G042000.1	896421|PACid:16065872	AT3G03980.1	Os07t0561500-01	AC233662_54.1|PACid:23040635
Gmech0016G02477	Glyma.16G153000.1	883152|PACid:16049204	AT1G55370.2	Os03t0748300-01	Medtr6g032880.1|PACid:23027777
Gmech0009G03367	Glyma.09G196700.1	316562|PACid:16040039	AT1G76410.1	Os02t0686100-00	Medtr8g073120.1|PACid:23036729
Gmech0014G00228	Glyma.14G026500.1	490317|PACid:16045328	AT4G02485.1	Os11t0657200-01	Medtr5g091920.1|PACid:23031465

別冊表 2-4 子葉タンパクデータに対応する Gmax275 とエンレイの遺伝子モデル

Family	Member	Gmax189 gene model	Score	Mass	No. of matches	mol%	Description	Classification	Gmax275 gene model	Enrei gene model	Ortholog group
4	1	Glyma20g28550.1	1931	26156	40	7.87	AT3G22490.1|Seed maturation protein	Storage	Glyma.20G147600	Gmech0020G03098	my_prefix5715
6	1	Glyma10g03310.1	950	27496	30	6.06	AT3G22490.1|Seed maturation protein	Storage	Glyma.10G027600	Gmech0010G00247	my_prefix5715
1	2	Glyma03g32030.1	3920	56299	229	4.31	AT5G44120.3|RmlC-like cupins superfamily protein	Storage	Glyma.03G163500	Gmech0003G02931	my_prefix1539
4	2	Glyma10g39270.1	1316	26280	26	3.29	AT3G22490.1|Seed maturation protein	Storage	Glyma.10G247500	Gmech0010G03809	my_prefix38470
2	1	Glyma13g18450.1	4500	55793	134	3.06	AT1G03890.1|RmlC-like cupins superfamily protein	Storage	Glyma.13G123500	Gmech0013G01961	my_prefix1539
3	2	Glyma20g28640.1	2798	50468	185	2.38	AT3G22640.1|cupin family protein	Storage	Glyma.20G148200	Gmech0020G03089	my_prefix8093
3	4	Glyma20g28460.1	2373	50502	162	2.38	AT3G22640.1|cupin family protein	Storage	Glyma.20G146200		my_prefix8093
3	1	Glyma10g39150.1	3435	72469	180	2.2	AT3G22640.1|cupin family protein	Storage	Glyma.10G246300	Gmech0010G03798	my_prefix7644
1	1	Glyma04g32950.1	5050	44606	157	1.99	AT5G44120.3|RmlC-like cupins superfamily protein	Storage	Glyma.04G165500	Gmech0004G03229	my_prefix2432
3	3	Glyma20g28650.1	2621	70549	167	1.93	AT3G22640.1|cupin family protein	Storage	Glyma.20G148400	Gmech0020G03104	my_prefix7644
5	1	Glyma10g03390.1	1904	58353	84	1.92	AT3G22640.1|cupin family protein	Storage	Glyma.10G028300	Gmech0010G00251	my_prefix10537
1	3	Glyma19g34780.1	1406	54835	64	1.88	AT5G44120.3|RmlC-like cupins superfamily protein	Storage	Glyma.19G164900	Gmech0019G03127	my_prefix1539
11	1	Glyma13g36400.1	592	20652	27	1.88		Miscellaneous	Glyma.13G288100		
18	1	Glyma01g10900.1	290	22718	19	1.63	AT1G73260.1|kunitz trypsin inhibitor 1	Protease/inhibitor	Glyma.01G095000	Gmech0001G02291	my_prefix35353
19	1	Glyma08g45531.1	283	24346	11	1.49	AT1G73260.1|kunitz trypsin inhibitor 1	Protease/inhibitor	Glyma.08G341500	Gmech0008G04169	my_prefix37794
5	2	Glyma02g16440.1	767	58123	58	1.36	AT3G22640.1|cupin family protein	Storage	Glyma.02G145700	Gmech0002G01378	my_prefix10537
20	1	Glyma17g17860.1	282	10055	4	1.32	AT2G23110.1|Late embryogenesis abundant protein, group 6	LEA proteins	Glyma.17G164200		my_prefix17607
9	1	Glyma10g07410.1	633	48766	19	1.13	AT2G36640.1|embryonic cell protein 63	Miscellaneous	Glyma.10G064400	Gmech0010G00567	my_prefix15332
47	1	Glyma14g06900.1	110	17729	5	1.13	AT1G53540.1|HSP20-like chaperones superfamily protein	Sorting/folding	Glyma.14G063700	Gmech0014G00538	my_prefix39592
41	1	Glyma02g08400.1	125	17907	11	1.11	AT1G53540.1|HSP20-like chaperones superfamily protein	Sorting/folding	Glyma.02G076600	Gmech0002G00668	my_prefix35603
22	2	Glyma06g18110.1	246	36855	12	1.1	AT1G13440.1|glyceraldehyde-3-phosphate dehydrogenase C2	Glycolysis	Glyma.06G172600		my_prefix12337
22	3	Glyma04g36860.1	208	36861	13	1.1	AT1G13440.1|glyceraldehyde-3-phosphate dehydrogenase C2	Glycolysis	Glyma.04G193400		my_prefix12337
10	1	Glyma09g31740.1	622	26671	9	0.97		Miscellaneous	Glyma.09G185500	Gmech0009G03260	my_prefix38062
22	1	Glyma18g01330.1	259	37087	12	0.86	AT3G04120.1|glyceraldehyde-3-phosphate dehydrogenase C subunit 1	Glycolysis	Glyma.18G009700	Gmech0018G00077	my_prefix5472
34	1	Glyma10g05580.1	172	44721	12	0.86	AT3G09630.1|Ribosomal protein L4/L1 family	Miscellaneous	Glyma.10G048600	Gmech0010G00429	my_prefix2435
65	1	Glyma10g43770.1	70	14310	4	0.86	AT2G39390.1|Ribosomal L29 family protein	Miscellaneous	Glyma.10G291500		my_prefix3135
13	1	Glyma11g15870.1	391	53054	20	0.85	AT2G28490.1|RmlC-like cupins superfamily protein	Storage	Glyma.U020300	Gmesc0021G00124	my_prefix22886
7	1	Glyma03g39940.1	929	47105	43	0.81	AT1G03220.1|Eukaryotic aspartyl protease family protein	Protease/inhibitor	Glyma.03G239700	Gmech0003G03603	my_prefix14531
8	1	Glyma13g42320.1	764	78929	28	0.81	AT1G55020.1|lipoxygenase 1	Lipid	Glyma.13G347600	Gmech0013G03921	my_prefix1052
56	2	Glyma20g38440.1	83	23514	6	0.79	AT1G75270.1|dehydroascorbate reductase 2	Miscellaneous	Glyma.20G240300	Gmech0020G03905	my_prefix13352
16	1	Glyma10g29630.1	344	32150	12	0.78	AT1G54870.1|NAD(P)-binding Rossmann-fold superfamily protein	Miscellaneous	Glyma.10G155300		my_prefix9938
16	2	Glyma20g37670.1	242	32054	9	0.78	AT1G54870.1|NAD(P)-binding Rossmann-fold superfamily protein	Miscellaneous	Glyma.20G233000	Gmech0020G03848	my_prefix9938
17	1	Glyma13g09530.1	306	41925	25	0.74	AT1G77120.1|alcohol dehydrogenase 1	Miscellaneous	Glyma.13G035200	Gmech0013G00889	my_prefix16561
26	1	Glyma15g41550.1	216	42409	11	0.74	AT1G79550.1|phosphoglycerate kinase	Glycolysis	Glyma.15G262100	Gmech0015G03843	my_prefix2297
21	1	Glyma13g23790.1	267	43082	15	0.72	AT5G14780.1|formate dehydrogenase	Miscellaneous	Glyma.13G168700	Gmech0013G02394	my_prefix3865
81	1	Glyma16g03470.1	52	16735	6	0.72	AT1G01470.1|Late embryogenesis abundant protein	LEA proteins	Glyma.16G031300	Gmech0016G00258	my_prefix40109
32	1	Glyma07g10030.1	192	25644	5	0.71		Miscellaneous	Glyma.07G090400	Gmech0007G00775	my_prefix37174
31	1	Glyma04g01181.1	192	17310	5	0.7	AT2G21490.1|dehydrin LEA	LEA proteins	Glyma.04G009900	Gmech0004G00087	my_prefix22292

47	2	Glyma02g42000.1	97	17283	3	0.7	AT1G53540.1|HSP20-like chaperones superfamily protein	Sorting/folding	Glyma.02G252800	Gmech0002G03773	my_prefix35820
30	1	Glyma09g32540.1	205	17498	5	0.68	AT1G65980.1|thioredoxin-dependent peroxidase 1	Miscellaneous	Glyma.09G192800	Gmech0009G03327	my_prefix38068
34	2	Glyma13g19930.1	167	44691	11	0.68	AT3G09630.1|Ribosomal protein L4/L1 family	Miscellaneous	Glyma.13G136400	Gmech0013G02088	my_prefix2435
46	1	Glyma13g29550.1	111	27847	5	0.65	AT5G45690.1|Protein of unknown function (DUF1264)	Miscellaneous	Glyma.13G223700	Gmech0013G02882	my_prefix8566
35	1	Glyma12g34160.1	169	18393	17	0.64		Miscellaneous	Glyma.12G213600	Gmech0012G03096	my_prefix14951
69	1	Glyma11g29350.1	66	28317	6	0.64	AT1G07080.1|Thioredoxin superfamily protein	Miscellaneous	Glyma.11G165600	Gmech0011G01786	my_prefix8685
64	1	Glyma03g29801.1	71	9612	2	0.58	AT3G45030.1|Ribosomal protein S10p/S20e family protein	Miscellaneous			
2	2	Glyma10g04280.1	2039	64215	49	0.56	AT5G44120.3|RmlC-like cupins superfamily protein	Storage	Glyma.10G037100		my_prefix1539
8	2	Glyma15g03030.1	556	97107	30	0.56	AT1G55020.1|lipoxygenase 1	Lipid	Glyma.15G026300	Gmech0015G00243	my_prefix1052
33	1	Glyma07g38790.1	188	32097	13	0.56	AT1G54870.1|NAD(P)-binding Rossmann-fold superfamily protein	Miscellaneous	Glyma.07G258200	Gmech0007G03708	my_prefix18063
89	1	Glyma16g05090.1	45	9978	2	0.56	AT3G61110.1|ribosomal protein S27	Miscellaneous	Glyma.16G046500		
50	1	Glyma10g33350.1	105	21319	6	0.54	AT5G55240.1|ARABIDOPSIS THALIANA PEROXYGENASE 2	Lipid	Glyma.10G189900	Gmech0010G03312	my_prefix38408
39	2	Glyma04g42690.1	107	58963	12	0.5	AT1G77510.1|PDI-like 1-2	Sorting/folding	Glyma.04G247900	Gmech0004G04095	my_prefix2339
68	1	Glyma02g26840.1	66	22852	6	0.5	AT2G37270.1|ribosomal protein 5B	Miscellaneous	Glyma.02G167900	Gmech0002G02243	my_prefix3751
7	2	Glyma19g42490.1	408	47859	31	0.49	AT1G03220.1|Eukaryotic aspartyl protease family protein	Protease/inhibitor	Glyma.19G236600	Gmech0019G03768	my_prefix14531
36	1	Glyma02g00810.1	169	35787	5	0.49	AT5G43330.1|Lactate/malate dehydrogenase family protein	Miscellaneous	Glyma.02G005500	Gmech0002G00058	my_prefix6847
56	1	Glyma10g43730.1	89	23491	4	0.49	AT1G75270.1|dehydroascorbate reductase 2	Miscellaneous	Glyma.10G291100		my_prefix13352
126	1	Glyma0169s00200.1	18	11439	1	0.49	AT3G44590.1|60S acidic ribosomal protein family	Miscellaneous	Glyma.11G209200	Gmech0011G02896	my_prefix38763
9	2	Glyma13g21291.1	289	50613	10	0.46	AT2G36640.1|embryonic cell protein 63	Miscellaneous	Glyma.13G149000	Gmech0013G02207	my_prefix39275
27	1	Glyma08g09310.1	213	24542	7	0.46	AT1G48130.1|1-cysteine peroxiredoxin 1	Miscellaneous	Glyma.08G088000	Gmech0008G00739	my_prefix12121
82	1	Glyma06g01310.1	50	11987	2	0.46	AT4G39200.1|Ribosomal protein S25 family protein	Miscellaneous	Glyma.06G011000		my_prefix3211
94	1	Glyma01g31610.1	42	12051	1	0.46	AT5G01650.1|Tautomerase/MIF superfamily protein	Miscellaneous	Glyma.01G126000	Gmech0001G03341	my_prefix16915
15	1	Glyma05g36600.1	353	77821	13	0.44	AT5G42020.1|Heat shock protein 70 (Hsp 70) family protein	Sorting/folding	Glyma.05G219600	Gmech0005G03191	my_prefix1062
74	1	Glyma02g00490.1	61	12578	3	0.44	AT1G36240.1|Ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein	Miscellaneous	Glyma.02G002300		my_prefix4722
54	1	Glyma05g26290.1	98	12844	2	0.43	AT1G74270.1|Ribosomal protein L35Ae family protein	Miscellaneous	Glyma.05G132500	Gmech0005G02434	my_prefix18568
63	1	Glyma08g09200.1	71	12875	3	0.43	AT1G74270.1|Ribosomal protein L35Ae family protein	Miscellaneous	Glyma.08G087000		my_prefix25651
138	1	Glyma11g11290.1	15	12695	1	0.43	AT2G21060.1|glycine-rich protein 2B	Miscellaneous			
8	3	Glyma13g42310.1	390	97499	15	0.42	AT1G55020.1|lipoxygenase 1	Lipid	Glyma.13G347500	Gmech0013G03920	my_prefix1052
117	1	Glyma04g17670.1	22	13281	2	0.42	AT1G29040.1|	Miscellaneous	Glyma.04G136400	Gmech0004G01771	my_prefix36348
39	1	Glyma06g12090.1	144	56365	11	0.4	AT1G77510.1|PDI-like 1-2	Sorting/folding	Glyma.06G114800	Gmech0006G00970	my_prefix2339
93	1	Glyma13g25870.1	42	27708	5	0.4	AT3G12490.2|cystatin B	Protease/inhibitor	Glyma.13G189500	Gmech0013G02563	my_prefix6215
28	1	Glyma02g01590.1	210	30909	18	0.36	AT5G10530.1|Concanavalin A-like lectin protein kinase family protein	Miscellaneous	Glyma.02G012600	Gmech0002G00118	my_prefix35523
51	1	Glyma02g09370.1	102	30441	4	0.36	AT3G57490.1|Ribosomal protein S5 family protein	Miscellaneous	Glyma.02G085300	Gmech0002G00749	
57	1	Glyma03g32380.1	88	15174	2	0.36	AT1G04480.1|Ribosomal protein L14p/L23e family protein	Miscellaneous	Glyma.03G166700		my_prefix3147
106	1	Glyma13g44020.1	29	15145	2	0.36	AT1G52690.1|Late embryogenesis abundant protein (LEA) family protein	LEA proteins	Glyma.13G363300	Gmech0013G04054	my_prefix10368
80	1	Glyma03g33530.1	52	15834	2	0.35	AT5G02960.1|Ribosomal protein S12/S23 family protein	Miscellaneous	Glyma.03G178000	Gmech0003G03061	my_prefix3410
14	1	Glyma13g36780.1	376	67993	12	0.33	AT2G42560.1|late embryogenesis abundant domain-containing protein / LEA domain-containing protein	LEA proteins	Glyma.13G291800	Gmech0013G03451	my_prefix16932
88	1	Glyma03g21680.1	45	16093	1	0.33	AT5G48580.1|FK506- and rapamycin-binding protein 15 kD-2	Miscellaneous	Glyma.03G086100	Gmech0003G01903	my_prefix5970
113	1	Glyma03g25820.1	25	16308	2	0.33	AT4G09320.1|Nucleoside diphosphate kinase family protein	Miscellaneous	Glyma.03G109500		my_prefix12603
85	1	Glyma07g37270.1	48	16808	3	0.32	AT1G24020.1|MLP-like protein 423	Miscellaneous	Glyma.07G243600		my_prefix37374

87	1	Glyma02g44350.1	46	16908	1	0.32	AT2G27030.3|calmodulin 5	Miscellaneous	Glyma.02G275600	Gmech0002G03965	my_prefix2669
91	1	Glyma14g39140.1	43	51554	5	0.32	AT5G17310.2|UDP-glucose pyrophosphorylase 2	Miscellaneous	Glyma.14G210700		my_prefix4767
119	1	Glyma20g24500.1	21	16878	1	0.32	AT2G27510.1|ferredoxin 3	Miscellaneous	Glyma.20G110800	Gmech0020G02780	my_prefix41417
139	1	Glyma05g03850.1	15	17187	3	0.32	AT4G00100.1|ribosomal protein S13A	Miscellaneous	Glyma.05G052300	Gmech0005G00505	my_prefix5616
48	1	Glyma04g32950.1	107	17687	2	0.31	AT1G13950.1|eukaryotic elongation factor 5A-1	Miscellaneous	Glyma.04G165500	Gmech0004G03229	my_prefix2432
73	1	Glyma11g17920.1	62	17374	2	0.31	AT3G44100.1|MD-2-related lipid recognition domain-containing protein	Miscellaneous	Glyma.U012200		my_prefix14730
77	1	Glyma10g06040.1	57	17827	4	0.31	AT3G53430.1|Ribosomal protein L11 family protein	Miscellaneous	Glyma.10G053100		my_prefix4236
118	1	Glyma02g11540.1	22	17925	2	0.31	AT5G18380.1|Ribosomal protein S5 domain 2-like superfamily protein	Miscellaneous	Glyma.02G103600	Gmech0002G00968	my_prefix4368
121	1	Glyma07g32050.1	21	18500	1	0.29	AT1G53540.1|HSP20-like chaperones superfamily protein	Sorting/folding	Glyma.07G200200	Gmech0007G03063	my_prefix1939
52	1	Glyma02g38730.1	100	38469	5	0.28	AT2G36460.1|Aldolase superfamily protein	Glycolysis	Glyma.02G222400	Gmech0002G03502	my_prefix2290
110	1	Glyma12g03470.1	26	19150	2	0.28	AT2G21060.1|glycine-rich protein 2B	Miscellaneous	Glyma.12G030800	Gmech0012G00266	my_prefix38841
17	2	Glyma14g24860.1	159	41152	6	0.26	AT1G77120.1|alcohol dehydrogenase 1	Miscellaneous	Glyma.14G156400		my_prefix16561
79	1	Glyma08g42820.1	53	19954	5	0.26	AT3G20390.1|endoribonuclease L-PSP family protein	Miscellaneous	Glyma.08G316200	Gmech0008G03965	my_prefix5178
90	1	Glyma05g33880.1	44	20022	2	0.26	AT1G18210.1|Calcium-binding EF-hand family protein	Miscellaneous	Glyma.05G245600	Gmech0005G03400	my_prefix36735
95	1	Glyma13g07610.1	42	20234	3	0.26	AT5G38410.1|Ribulose bisphosphate carboxylase (small chain) family protein	Miscellaneous	Glyma.13G046200	Gmech0013G01147	my_prefix2059
108	1	Glyma01g43110.1	28	20047	6	0.26	AT4G25740.1|RNA binding Plectin/S10 domain-containing protein	Miscellaneous	Glyma.01G222100		my_prefix4202
29	1	Glyma08g12270.1	210	43130	5	0.25	AT1G09850.1|xylem bark cysteine peptidase 3	Protease/inhibitor	Glyma.08G116300	Gmech0008G00989	my_prefix37514
66	1	Glyma03g37340.1	69	20954	1	0.25	AT5G27850.1|Ribosomal protein L18e/L15 superfamily protein	Miscellaneous	Glyma.03G215300	Gmech0003G03389	my_prefix3827
70	1	Glyma08g44210.1	65	43837	4	0.25	AT5G55730.1|FASCICLIN-like arabinogalactan 1	Miscellaneous	Glyma.08G329900		my_prefix3203
124	1	Glyma04g40430.1	20	21417	3	0.25	AT1G33140.1|Ribosomal protein L6 family	Miscellaneous	Glyma.04G226500		
25	1	Glyma03g39860.1	220	22324	4	0.24	AT1G54860.1|Glycoprotein membrane precursor GPI-anchored	Miscellaneous	Glyma.03G238700	Gmech0003G03595	my_prefix18160
37	1	Glyma10g39170.1	168	68392	8	0.24	AT3G22640.1|cupin family protein	Storage	Glyma.10G246500	Gmech0010G03800	my_prefix38468
42	1	Glyma08g45480.1	119	22961	3	0.24	AT1G17860.1|Kunitz family trypsin and protease inhibitor protein	Protease/inhibitor	Glyma.08G341000	Gmech0008G04165	my_prefix37790
45	1	Glyma06g08290.1	117	22698	2	0.24	AT2G25890.1|Oleosin family protein	Lipid	Glyma.06G078700	Gmech0006G00646	my_prefix23045
120	1	Glyma03g27570.1	21	22117	1	0.24	AT3G12390.1|Nascent polypeptide-associated complex (NAC), alpha subunit family protein	Miscellaneous	Glyma.03G120800	Gmech0003G02552	my_prefix3129
12	1	Glyma16g07800.1	586	23378	15	0.22	AT3G01570.1|Oleosin family protein	Lipid	Glyma.16G071800		
23	1	Glyma16g31331.1	254	96970	12	0.22	AT4G25580.1|CAP160 protein	Miscellaneous	Glyma.16G189900	Gmech0016G02786	my_prefix10611
38	1	Glyma19g37520.1	156	47929	4	0.22	AT2G36530.1|Enolase	Glycolysis	Glyma.19G190900	Gmech0019G03368	my_prefix2552
38	2	Glyma03g34830.1	132	47914	3	0.22	AT2G36530.1|Enolase	Glycolysis	Glyma.03G190500	Gmech0003G03172	my_prefix2552
61	1	Glyma13g04050.1	75	24300	1	0.22	AT5G12110.1|Glutathione S-transferase, C-terminal-like;Translation elongation factor EF1B/ribosomal protein S6	Miscellaneous	Glyma.13G073200	Gmech0013G01432	my_prefix10094
134	1	Glyma08g03510.1	15	24338	2	0.22	AT2G19830.1|SNF7 family protein	Sorting/folding	Glyma.08G031200	Gmech0008G00275	my_prefix4634
24	1	Glyma09g25830.1	235	103327	10	0.21	AT4G25580.1|CAP160 protein	Miscellaneous	Glyma.09G139600	Gmech0009G02743	my_prefix10611
44	1	Glyma10g28890.1	118	50140	3	0.21	AT1G09210.1|calreticulin 1b	Miscellaneous	Glyma.10G147600		my_prefix3487
58	1	Glyma02g38450.1	87	25504	2	0.21	AT1G26910.1|Ribosomal protein L16p/L10e family protein	Miscellaneous	Glyma.02G220000	Gmech0002G03482	my_prefix16605
84	1	Glyma15g42620.1	48	25915	5	0.21	AT1G74060.1|Ribosomal protein L6 family protein	Miscellaneous	Glyma.15G271300	Gmech0015G03949	my_prefix40076
97	1	Glyma08g45610.1	39	26216	2	0.21	AT1G73260.1|kunitz trypsin inhibitor 1	Protease/inhibitor	Glyma.08G342300	Gmech0008G04176	my_prefix37799
116	1	Glyma04g07350.1	23	25505	1	0.21	AT5G55190.1|RAN GTPase 3	Miscellaneous	Glyma.04G069100		
62	1	Glyma06g45700.1	74	56378	7	0.19	AT4G15210.1|beta-amylase 5	Miscellaneous	Glyma.06G301500	Gmech0006G03971	my_prefix2829
78	1	Glyma19g36080.1	54	27049	2	0.19	AT5G02790.1|Glutathione S-transferase family protein	Miscellaneous	Glyma.19G177200		my_prefix2725
105	1	Glyma11g36840.1	30	27277	2	0.19	AT1G05510.1|Protein of unknown function (DUF1264)	Miscellaneous	Glyma.11G252800		my_prefix11126

141	1	Glyma16g33240.1	14	26337	2	0.19	AT5G35530.1|Ribosomal protein S3 family protein	Miscellaneous	Glyma.16G207400	Gmech0016G02929	my_prefix3922
143	1	Glyma12g06950.1	14	27212	1	0.19	AT2G28790.1|Pathogenesis-related thaumatin superfamily protein	Miscellaneous	Glyma.12G064300	Gmech0012G00551	my_prefix11959
40	1	Glyma07g02270.1	143	28392	3	0.18	AT3G13580.1|Ribosomal protein L30/L7 family protein	Miscellaneous	Glyma.07G020000	Gmech0007G00156	my_prefix37107
60	1	Glyma10g39050.1	75	29828	6	0.18	AT3G04840.1|Ribosomal protein S3Ae	Miscellaneous	Glyma.10G245200		my_prefix4776
71	1	Glyma20g32454.1	64	28212	3	0.18	AT3G54940.2|Papain family cysteine protease	Protease/inhibitor			
72	1	Glyma01g37250.1	64	28297	3	0.18	AT4G36130.1|Ribosomal protein L2 family	Miscellaneous	Glyma.01G167300	Gmech0001G03917	my_prefix35448
107	1	Glyma02g35780.1	29	28665	2	0.18	AT5G06290.1|2-cysteine peroxiredoxin B	Miscellaneous	Glyma.02G198400	Gmech0002G03218	my_prefix11778
109	1	Glyma18g16260.1	28	29771	1	0.18	AT3G01280.1|voltage dependent anion channel 1	Miscellaneous	Glyma.18G125500	Gmech0018G01389	my_prefix40748
123	1	Glyma08g47900.1	20	29537	2	0.18	AT3G02520.1|general regulatory factor 7	Miscellaneous	Glyma.08G363800		my_prefix1884
133	1	Glyma01g03700.1	16	28515	5	0.18	AT1G70420.1|Protein of unknown function (DUF1645)	Miscellaneous	Glyma.01G030300	Gmech0001G00277	my_prefix23263
53	1	Glyma08g08970.1	100	31561	2	0.17	AT2G34470.2|urease accessory protein G	Miscellaneous	Glyma.08G084800	Gmech0008G00717	my_prefix7055
55	1	Glyma13g24720.1	93	31646	2	0.17	AT2G34700.1|Pollen Ole e 1 allergen and extensin family protein	Miscellaneous	Glyma.13G178700	Gmech0013G02483	my_prefix13109
115	1	Glyma03g37080.1	24	31609	7	0.17	AT3G12290.1|Amino acid dehydrogenase family protein	Miscellaneous	Glyma.03G212700		my_prefix9429
122	1	Glyma09g00660.1	21	32504	3	0.17	AT1G11840.6|glyoxalase I homolog	Miscellaneous	Glyma.09G004300	Gmech0009G00039	my_prefix2334
135	1	Glyma19g30520.1	15	30336	2	0.17	AT5G19750.1|Peroxisomal membrane 22 kDa (Mpv17/PMP22) family protein	Miscellaneous	Glyma.19G125200	Gmech0019G02753	my_prefix8856
59	1	Glyma14g06630.1	83	34225	2	0.15	AT2G40010.1|Ribosomal protein L10 family protein	Miscellaneous	Glyma.14G061100	Gmech0014G00516	my_prefix3525
129	1	Glyma10g03241.1	17	33015	2	0.15	AT3G63190.1|ribosome recycling factor, chloroplast precursor	Miscellaneous	Glyma.10G026900	Gmech0010G00240	my_prefix5911
76	1	Glyma13g34290.1	58	38697	5	0.14	AT1G78660.2|gamma-glutamyl hydrolase 1	Miscellaneous			
100	1	Glyma06g34190.1	32	36192	3	0.14	AT1G53240.1|Lactate/malate dehydrogenase family protein	Miscellaneous	Glyma.06G231500	Gmech0006G03400	my_prefix7271
86	1	Glyma14g27940.1	47	41548	3	0.13	AT1G77120.1|alcohol dehydrogenase 1	Miscellaneous	Glyma.14G121200	Gmech0014G01505	my_prefix1841
104	1	Glyma08g19420.1	30	41767	2	0.13	AT3G12110.1|actin-11	Miscellaneous	Glyma.08G182200	Gmech0008G01564	my_prefix1098
111	1	Glyma01g43540.1	25	43236	1	0.13	AT4G10960.1|UDP-D-glucose/UDP-D-galactose 4-epimerase 5	Miscellaneous	Glyma.01G225800	Gmech0001G04433	my_prefix4925
125	1	Glyma13g16500.1	19	43355	2	0.13	AT2G19480.1|nucleosome assembly protein 1;2	Miscellaneous	Glyma.13G105600		my_prefix2461
132	1	Glyma09g40420.1	16	42536	2	0.13	AT3G60900.1|FASCICLIN-like arabinogalactan-protein 10	Miscellaneous	Glyma.09G267700		
49	1	Glyma09g40990.1	107	46068	3	0.11	AT5G08380.1|alpha-galactosidase 1	Miscellaneous	Glyma.09G273400	Gmech0009G04022	my_prefix8991
75	1	Glyma15g01000.1	58	45623	4	0.11	AT1G15330.1|Cystathionine beta-synthase (CBS) protein	Miscellaneous	Glyma.15G007300	Gmech0015G00080	my_prefix13499
92	1	Glyma05g04520.1	43	45119	1	0.11	AT4G17260.1|Lactate/malate dehydrogenase family protein	Miscellaneous	Glyma.05G058100	Gmech0005G00567	my_prefix12237
98	1	Glyma10g24590.1	38	49213	2	0.11	AT2G33150.1|peroxisomal 3-ketoacyl-CoA thiolase 3	Lipid	Glyma.10G124700	Gmech0010G02508	my_prefix2771
103	1	Glyma06g19000.1	30	91685	8	0.11	AT5G03340.1|ATPase, AAA-type, CDC48 protein	Miscellaneous	Glyma.06G180000	Gmech0006G01558	my_prefix1548
114	1	Glyma13g27820.1	24	52185	1	0.1	AT1G03220.1|Eukaryotic aspartyl protease family protein	Protease/inhibitor	Glyma.13G208000	Gmech0013G02738	my_prefix39355
127	1	Glyma06g47780.1	18	54311	2	0.1	AT1G33590.1|Leucine-rich repeat (LRR) family protein	Miscellaneous	Glyma.06G319700	Gmech0006G04155	my_prefix9798
128	1	Glyma05g28400.1	17	54616	1	0.1	AT4G14030.1|selenium-binding protein 1	Miscellaneous	Glyma.05G151300	Gmech0005G02617	my_prefix3065
137	1	Glyma08g22560.1	15	50390	7	0.1	AT1G52630.1|O-fucosyltransferase family protein	Miscellaneous	Glyma.08G211300	Gmech0008G01811	my_prefix4491
140	1	Glyma10g29600.1	14	51789	2	0.1	AT5G27470.1|seryl-tRNA synthetase / serine--tRNA ligase	Miscellaneous	Glyma.10G155000	Gmech0010G03003	my_prefix2104
43	1	Glyma17g08150.1	118	60177	3	0.08	AT4G30920.1|Cytosol aminopeptidase family protein	Miscellaneous	Glyma.17G073800	Gmech0017G00662	my_prefix2781
67	1	Glyma10g41330.1	67	59913	4	0.08	AT5G08680.1|ATP synthase alpha/beta family protein	Miscellaneous	Glyma.10G267200	Gmech0010G03979	my_prefix3770
96	1	Glyma06g43641.1	39	116570	8	0.08	AT2G42560.1|late embryogenesis abundant domain-containing protein / LEA domain-containing protein	LEA proteins	Glyma.06G283900	Gmech0006G03817	my_prefix37047
99	1	Glyma19g22730.1	34	61196	4	0.08	AT2G24200.1|Cytosol aminopeptidase family protein	Miscellaneous	Glyma.19G077800	Gmech0019G01881	my_prefix2781
142	1	Glyma17g14660.1	14	64480	3	0.08	AT1G62740.1|stress-inducible protein, putative	Miscellaneous	Glyma.17G137700	Gmech0017G01210	my_prefix2546
83	1	Glyma10g40340.1	48	71723	3	0.07	AT2G14740.1|vacuolar sorting receptor 3	sorting/folding	Glyma.10G257300	Gmech0010G03897	my_prefix1232

101	1	Glyma01g38340.1	32	71984	1	0.07	AT2G18540.1|RmlC-like cupins superfamily protein	Storage	Glyma.01G177000	Gmech0001G03998	my_prefix8289
112	1	Glyma20g38740.1	25	67965	3	0.07	AT1G50480.1|10-formyltetrahydrofolate synthetase	Miscellaneous	Glyma.20G243700	Gmech0020G03928	my_prefix6493
130	1	Glyma03g08017.1	17	75904	3	0.07		Miscellaneous			
131	1	Glyma11g19070.1	17	92178	3	0.06	AT5G22470.1|NAD+ ADP-ribosyltransferases;NAD+ ADP-ribosyltransferases	Miscellaneous	Glyma.11G184100	Gmech0011G01440	my_prefix6990
102	1	Glyma16g05240.1	31	117546	4	0.04	AT5G13980.1|Glycosyl hydrolase family 38 protein	Miscellaneous	Glyma.16G048100	Gmech0016G00417	my_prefix1442
136	1	Glyma16g30190.1	15	148773	2	0.03	AT4G20850.1|tripeptidyl peptidase ii	Protease/inhibitor	Glyma.16G182500	Gmech0016G02734	my_prefix3440

別冊表 3-1 ライブラリ由来のカイコ cDNA ライブラリと EST のアクセッション番号

Library ID	Number of clones	Strain/Race	Organ/Tissue	Developmental stage	Sex	Vector	Cloning site	Sequence direction
F1mg	2611	F1 (J150 x J203)	Midgut	4th-instar larva day-2	mixed	pBluescript SK-	EcoR1 for 5' Xho1for 3'	sequenced from T3 primer (5' -> 3')
FJsb	1261	F1-J150	Midgut	4th-instar larva day-2	mixed	pBluescript SK-	EcoR1 for 5' Xho1for 3'	sequenced from T3 primer (5' -> 3')
JFsb	567	J150-F1	Midgut	4th-instar larva day-3	mixed	pBluescript SK-	EcoR1 for 5' Xho1for 3'	sequenced from T3 primer (5' -> 3')
n	806	Unknown; BmN cultured cell	Cultured cell (derived from ovary)	Unknown		pBluescript SK-	EcoR1 for 5' Xho1for 3'	sequenced from T3 primer (5' -> 3')
NV06	313	Unknown; BmN cultured cell	Cultured cell (derived from ovary)	BmNPV infected; 6 hr postinfection		pBluescript SK-	EcoR1 for 5' Xho1for 3'	sequenced from T3 primer (5' -> 3')
NV12	300	Unknown; BmN cultured cell	Cultured cell (derived from ovary)	BmNPV infected; 12 hr postinfection		pBluescript SK-	EcoR1 for 5' Xho1for 3'	sequenced from T3 primer (5' -> 3')
Nnor	223	BmN normalized library	Cultured cell (derived from ovary)	Unknown		pBluescript SK-	EcoR1 for 5' Xho1for 3'	sequenced from T3 primer (5' -> 3')
an--	632	Shuko x Ryuhaku	Antenna	Adult moth		pBluescript SK-	EcoR1 for 5' Xho1for 3'	sequenced from T3 primer (5' -> 3')
br--	623	p50	Brain	Pupation stege day-0	mixed	pBluescript SK-	EcoR1 for 5' Xho1for 3'	sequenced from T3 primer (5' -> 3')
brS-	14	p50	Brain	Spinning stage day-0 - day-4	mixed	pBluescript SK-	EcoR1 for 5' Xho1for 3'	sequenced from T3 primer (5' -> 5')
ceN-	2106	same as ce-- (diff. preparation)	Compound eyes	5th-instar larva - Pupation stage	mixed	pBluescript SK-	EcoR1 for 5' Xho1for 3'	sequenced from T3 primer (5' -> 3')
e100	7839	p50T	Embryo	100hr after oviposition	mixed	pGCAPI, G-capping		from 5' with M(-21)
e4	728	p50	Diapause-destined embryo	40 hr after oviposition	mixed	pBluescript SK-	EcoR1 for 5' Xho1for 3'	sequenced from T3 primer (5' -> 3')
e96h	661	p50	Diapause-cancelled embryo	96 hr after oviposition	mixed	pBluescript SK-	EcoR1 for 5' Xho1for 3'	sequenced from T3 primer (5' -> 3')
epV3	815	p50	Epidermis	5th-instar larva day-3	mixed	pBluescript SK-	EcoR1 for 5' Xho1for 3'	sequenced from T3 primer (5' -> 3')
fbS2	425	C202 x J201	Fat body	Spinning stage day-2	male	pBluescript SK-	EcoR1 for 5' Xho1for 3'	sequenced from T3 primer (5' -> 3')
fbf	213	p50	Fat body	5th-instar larva day-3	female	cloned into pUC18 Sma!	Sma!-Blunt-end	sequenced from M4 primer (direction unknown)
fbm	348	p50	Fat body	5th-instar larva day-3	male	cloned into pUC18 Sma!	Sma!-Blunt-end	sequenced from M4 primer (direction unknown)
fbpv	622	Shuko x Ryuhaku	Fat body	Spinning stage day-2, BmNPV infected 2hr	mixed	pBluescript SK-	EcoR1 for 5' Xho1for 3'	sequenced from T3 primer (5' -> 3')
fcP8	3357	p50T	Follicle cells	Pupation stege day-8	female	pBluescript SK-	EcoR1 for 5' Xho1for 3'	sequenced from T3 primer (5' -> 3')
heS0	718	C108	Hemocyte	Spinning stage day-0	mixed	pBluescript SK-	EcoR1 for 5' Xho1for 3'	sequenced from T3 primer (5' -> 3')
heS3	557	C108	Hemocyte	Spinning stage day-3	mixed	pBluescript SK-	EcoR1 for 5' Xho1for 3'	sequenced from T3 primer (5' -> 3')
maV3	775	p50	Malpighian tubule	5th-instar larva day-3	mixed	pBluescript SK-	EcoR1 for 5' Xho1for 3'	sequenced from T3 primer (5' -> 3')
mg	778	p50	Midgut	5th-instar larva day-3	mixed	pBluescript SK-	EcoR1 for 5' Xho1for 3'	sequenced from T3 primer (5' -> 3')
ovS0	4727	p50T	Ovary	Spinning stage day-0	female	pBluescript SK-	EcoR1 for 5' Xho1for 3'	sequenced from T3 primer (5' -> 3')
ovS3	4860	p50	Ovary	Spinning stage day-3	female	pBluescript SK-	EcoR1 for 5' Xho1for 3'	sequenced from T3 primer (5' -> 3')
pg--	446	Shuko x Ryuhaku	Pheromone gland	Newly-eclosed adult	female	pBluescript SK-	EcoR1 for 5' Xho1for 3'	sequenced from T3 primer (5' -> 3')
prW-	2791	p50T	Prothoracic gland	Spinning stage	mixed	pGCAPI, G-capping		sequenced from 5' with T7 primer
prgv	842	p50	Prothoracic gland	5th-instar larva day-4	mixed	pBluescript SK-	EcoR1 for 5' Xho1for 3'	sequenced from T3 primer (5' -> 3')
vg4M	4618	p50T	Verson's gland	4th molting stage day-2	male	pBluescript SK-	EcoR1 for 5' Xho1for 3'	sequenced from T3 primer (5' -> 3')
ws0	864	C108	Wing disc	Spinning stage day-0	mixed	pBluescript SK-	EcoR1 for 5' Xho1for 3'	sequenced from T3 primer (5' -> 3')
ws2	814	C108	Wing disc	Spinning stage day-2	mixed	pBluescript SK-	EcoR1 for 5' Xho1for 3'	sequenced from T3 primer (5' -> 3')
wdV1	281	C108	Wing disc	5th-instar larva day-1	mixed	pBluescript SK-	EcoR1 for 5' Xho1for 3'	sequenced from T3 primer (5' -> 3')
wdV3	672	C108	Wing disc	5th-instar larva day-3	mixed	pBluescript SK-	EcoR1 for 5' Xho1for 3'	sequenced from T3 primer (5' -> 3')
wv4	823	C108	Wing disc	5th-instar larva day-4	mixed	pBluescript SK-	EcoR1 for 5' Xho1for 3'	sequenced from T3 primer (5' -> 3')
MSV3	4361	p50T	Middle silkgland	5th-instar larva day-3	mixed	pGADT7		sequenced from 5' with T7, from 3' with RV
mxg-	3724	p50T	Maxillary galea	5th-instar larva day-3	mixed	pGCAPI, G-capping		sequenced from 5' with T7 primer
psgV	4740	p50T	Posterior silkgland	5th-instar larva day-3	mixed	pGADT7		sequenced from 5' with T7, from 3' with RV
BmN-	6391	Unknown; BmN cultured cell	Cultured cell (derived from ovary)	Undefined		Oligo-cap		sequenced from 5'
swa	9479	P50	silk gland	5th-instar larva day-3	mixed	pBluescript II SK+	EcoR1 for 5' Xho1for 3'	sequenced from T7 primer (5' -> 3')
swb	7255	P50	midgut	5th-instar larva day-3	mixed	pBluescript II SK+	EcoR1 for 5' Xho1for 3'	sequenced from T7 primer (5' -> 3')
swc	6105	P50	Fat body	5th-instar larva day-3	female	pBluescript II SK+	EcoR1 for 5' Xho1for 3'	sequenced from T7 primer (5' -> 3')
swd	6532	P50	Fat body	5th-instar larva day-3	male	pBluescript II SK+	EcoR1 for 5' Xho1for 3'	sequenced from T7 primer (5' -> 3')
swj	4490	P50	testis	Embryo (72 hours)	mixed	pBluescript II SK+	EcoR1 for 5' Xho1for 3'	sequenced from T7 primer (5' -> 3')
swe	6424	P50	Hemocyte	5th-instar larva day-3	female	pBluescript II SK+	EcoR1 for 5' Xho1for 3'	sequenced from T7 primer (5' -> 3')
swf	4993	P50	Hemocyte	5th-instar larva day-3	male	pBluescript II SK+	EcoR1 for 5' Xho1for 3'	sequenced from T7 primer (5' -> 3')
swg	8407	P50	testis	5th-instar larva day-3	male	pBluescript II SK+	EcoR1 for 5' Xho1for 3'	sequenced from T7 primer (5' -> 3')
swh	8330	P50	ovary	5th-instar larva day-3	female	pBluescript II SK+	EcoR1 for 5' Xho1for 3'	sequenced from T7 primer (5' -> 3')
swk	4527	P50		Embryo (nondiapause)	mixed	pBluescript II SK+	EcoR1 for 5' Xho1for 3'	sequenced from T7 primer (5' -> 3')
swl	6179	P50	Fat body (pupa)	P0	mixed	pBluescript II SK+	EcoR1 for 5' Xho1for 3'	sequenced from T7 primer (5' -> 3')
swp	7754	P50		Embryo (unfertilized)	mixed	pBluescript II SK+	EcoR1 for 5' Xho1for 3'	sequenced from T7 primer (5' -> 3')
BmP	1003	Qingsong-Haoyue	whole pupae body excluding skin	metaphase	mixed	pHelix	Site_1 Hind II	M13 Forward