

<i>Eco</i> RI primers				
Primer name	Alternative name	Sequence	Coordinates	Feature
O1	JD74	GGTTATGAGCCCTAGAGCAATGCTTCTG	Chr3:1430-1458	Left telomere
O2	AM53	ACCAGCTTGGGGATCAACATCCTAATTT	Chr3:6466-6493	
O3	AM34	GGATCAACACAGTATCTTATGAATGGGT	Chr3:11220-11247	
O4	JD75	CATGGTAGAGACAGTCTTTGACATGCTG	Chr3:16627-16654	<i>HML</i>
O5	AM54	GTTAGATCGGAATCTGTTGAGACAAGT	Chr3:17479-17506	
O6	AM55	GCGTCTGCGTGAATGAAGAAGAGACATT	Chr3:21731-21758	
O7	JD96	AATGCACCAGAAACAAGATGAAGCAGATTC	Chr3:33248-33277	Recombination enhancer
O8	JD98	GTCAAGAGTCTGAACACAAACTCACCGA	Chr3:42342-42369	
O9	JD77	GATCTCCTGTTTTTTACGTTCTCTGACCTG	Chr3:64759-64788	
O10	JD78	GGTGAGTTCTCAAGTAGTTCTTCCAGGG	Chr3:95300-95327	
O11	JD79	CGCCAATCCAGCAATACCTGTACCTCTA	Chr3:117225-117252	Centromere
O12	JD80	CTCGTTATTAGTAGGTCGTGCTCTTAAAAG	Chr3:132248-132277	
O13	JD81	TGGTTTGGCCATCTCTTCTTGGTTGCGA	Chr3:173262-173289	
O14	JD82	GGTGGCACTTCTTCCTCTTGTTCTTATAG	Chr3:192214-192242	
O15	JD123	CTTCCTCTTCATCGTGCTCAGGCGTATC	Chr3:204568-204595	Mating type locus
O16	JD83	AGCCATTGCGCCGGTTTGTTGACGCTAA	Chr3:222275-222302	
O17	JD125	GCCGAAGATCAATTTTACGTCTATGACTCA	Chr3:232314-232353	
O18	JD182	CACCGCTACCAGTAGCAAAAACGTTATATTCTG	Chr3:260355-260387	
O19	AM29	CTGGTCCTCACAGTTCGCAGGATAACTA	Chr3:290553-290580	
O20	AM36	AATGGCTATATACATCAAGTCTGGAGGC	Chr3:291233-291260	
O21	AM144	CATCACCAATCCTTGCATTTGTTTTCCA	Chr3:291482-291509*	
O22	AM31	CCAGAAGAATTATGGGCCACCCTCCATG	Chr3:301581-301608	<i>HMR</i>
O23	AM37	GTTATATCGTAGTTTCCATTCAGCCTGC	Chr3:303919-303946	
O24	AM32	GGCGGTTTCTCGAAACATTTACGATTT	Chr3:306606-306633	Right telomere
O25	JD277	AGCCCACTATTTATTGGCTAACAGTGGC	Chr6:150214-150241	
O26	JD279	GTTGCTGTGCAATATTTGGTTTTAATAACTC	Chr6:151664-151694	
O27	JD280	CCGCGTTGCCCATCGAACTGAACGAGTTAC	Chr6:156905-156934	
O28	JD281	CAAAAGATCGCAAAGAAAGTCGCCAAGAGA	Chr6:162920-162949	
O29	JD282	TTCGATGTCTTCTTTTGAAGTTGCAGCAAC	Chr6:177991-178020	
O30	JD283	AATAACAAGTCATCCTCTATTTCGATTGAGC	Chr6:183420-183449	
O31	JD290	ACGATTTCTTGAAGAACGAGCCCTTGACT	Chr6:202320-202348	
O32	JD286	CCCCTTTTAATTATCGTTTCAGCAGCACCA	Chr6:209230-209259	
O33	JD288	GACGCCAACATCCCATTACATGAAAATCAG	Chr6:235825-235854	
O34	JD292	AGCGAGGTTTAACTTTTCATACAATTTACGG	Chr6:237970-238000	
O35 □ □	JD153 □ □	GATCCTTACAGGTTTTAAGGTTGCAAAGGG □	Chr1:6761-6790 □ □	Left telomere
<i>Xba</i> I primers				
O36	Xba2	CCTAAGGCATAAAACCCTAGATCCATCCA	Chr3:10966-10994*	<i>HML-E</i>
O37	Xba3	AGTTGCAATTTCTCTTTGTCAATCAGCTGA	Chr3:20020-20049	<i>HML-I</i>
O38	Xba10	GCGCAGGTACTCCTGGTTTTTGTAAAAC	Chr3:292906-292934	<i>HMR-E</i>
O39	Xba29	CCTTACAGAGGACACCGGTTTACAAAAG	Chr3:293394-293421*	<i>HMR-I</i>

Acil primers

Primer name	Alternative name	Sequence	Coordinates	Feature
O40	Ac21	CTCCCCTAGATTTATGTTTCCTATTGCTCT	Chr3:4722-4751	<i>HML-E</i>
O41	Ac1	GTACCGGTTACAATGGGCAAATGATATAC	Chr3:10373-10401	
O42	Ac3	CGTCATTCAAAC TTGTATTAGACGAGGG	Chr3:11497-11524	
O43	Ac4	CCCATTACGAGCTGTAGTAGTGCTGTGA	Chr3:11759-11786	
O44	Ac5	GTGACTTATGAATTGTTGTAGAAGGACGTC	Chr3:12124-12153	
O45	Ac12	CACAGGATAGCGTCTGGAAGTCAAATAAC	Chr3:13480-13508	<i>HML-I</i>
O46	Ac31	GCTGGAAATGGCAAACGAAAATACTATGAC	Chr3:14722-14751	
O47	Ac10	GAAATTGTCAGCGACTTCTATTACAGGAG	Chr3:15840-15868	
O48	Ac16	GTTGCATGTTAACGTCTCTGATATCAGAGC	Chr3:290129-290158	<i>HMR-E</i>
O49	Ac17	CCGTCAC TTTTACCATTGGTTCTAGAATGG	Chr3:290398-290427*	
O50	Ac29	GTTCTTTCGGGGAAACTGTATAAACTTCC	Chr3:293744-293773	
O51	Ac33	CAAAGAAATGTGGCATTACTCCACTTCAAG	Chr3:294196-294225	<i>HMR-I</i>
O52	Ac35	GTCACTACATTATATAAACAATAGGAATTG	Chr3:294630-294659*	
O53	Ac20	CCTGGTAGTCTTGCAAAGGTGTGAGTAC	Chr3:296331-296358	

* Primer is designed on reverse strand