

Supplementary Table 2:

#	Chr	±	Pos. 1	Pos. 2	ε	Box 1	Box 2
1	chr3R	+	24959215	24960667	0	AAACTAAACTC	GAGTTTAGTTT
2	chr3R	-	27043447	27042905	0	TGTATTGGTTT	GAACCAATACA
3	chr3R	-	18981470	18980780	0	TCCACAACCAG	TTGGTTGTGGA
4	chr3R	+	7026333	7030199	0	CACTTGCAAAGTGC	GCATTTTGCAAGTG
5	chrX	-	8536408	8534640	0	AATGTGCTGAAAGTTT	GAACTTTCAGCACATT
6	chr2R	+	12000497	12002198	0	TTGAACGGTTA	TAACCGTTCAA
7	chr3R	+	16983502	16999482	0	CTTTTGTGT	ACACAAAGG
8	chr2R	-	6419485	6371880	0	ATGAAAAAGCAA	TTGCTTTTTTCAT
9	chr3L	-	14746367	14744966	0	GAGGCGACA	TGTCGTCCCTC
10	chr2L	+	873612	874922	0	TTTTGCTTTTGT	AGCAAAAGCAAAA
11	chr3L	-	2156582	2154837	0	GGTGCGTGAGTGC	GCACTCACGCACT
12	chr2R	-	3213547	3212340	0	TTATTTCTGTTTT	AAAACAGAAGTAA
13	chr3L	+	7008415	7012637	0	TACACAAAATGGTTTGG	CCAAACCATTGTGTGTG
14	chr3R	+	20772084	20772486	0	GATACGTACATGA	TCAGTGTGGTGATC
15	chrX	-	8536408	8534640	0	AATGTGCTGAAAGTTT	GAACTTTCAGCACATT
16	chr3L	-	18790541	18757100	0	CTGTTGTTGCTG	CAGCAACAGCAG
17	chr2R	-	21074311	21072615	0	GGAACCACC	GGTGGTTCC
18	chr3R	-	27044616	27043733	0	GAGATAAAGT	ACTTTATCTC
19	chr2R	-	8061528	8055772	0	TCGATTTTGTAGTG	CGCTACAAAATCGA
20	chr2L	-	8252190	8245311	0	CTGGTGTTTGAATGGT	ACCATTCAAACACCAG
21	chrX	+	1803522	1804593	0	GTCCCTGTGTG	CACACAGGGGC
22	chr2R	-	9077000	9072790	0	ACACACATACACATG	CATGTGTGTATGTGTGT
23	chr2R	+	12020629	12023427	1	AAGCAGAAGC	GCTTTTGCTT
24	chr2R	-	10122147	10121893	0	ATCTCTCACTTTAAA	TTTAAAGTGAGAGAT
25	chr2L	+	18385021	18387151	0	CAACATCATCATCA	TGATGATGGTGTG
26	chr3L	+	8594542	8594666	0	ACAGCAACAAAT	ATTTGTTGCTGT
27	chrX	+	9647368	9647515	0	GCGCACAGCG	CGCTGTGCGC
28	chr3L	-	19903048	19881807	0	GTCATGTTCAAG	CTTGAACATGGC
29	chr3R	+	24939941	24940060	0	TATTATCTCATT	AATGGGATAATA
30	chr2R	-	14324930	14320346	0	ATCCGAGCA	TGTTCCGAT
31	chr3R	+	9583526	9584084	0	AGTTTTTGCATT	AATGCAAAAGACT
32	chr2R	-	18226234	18223350	0	TGTGTGTGTGTGTGTG	CACACACACACACGCA
33	chr3R	+	7203987	7217151	0	CAGCATTCA	TGAATGCTG
34	chr3R	-	23009510	23009116	0	TGGCAATTG	CAATTGTCA
35	chr3L	+	13995511	13996151	0	GGAGCGAGACGA	TCGTCTCGCTCT
36	chr2L	-	743287	741049	1	TGGCGACAAG	TTTGTCCGA
37	chr3R	+	20500661	20500794	0	TATGCATACAAATCGGT	ATCGATTTGTATGCATG
38	chr2L	-	6800627	6800368	0	CTGCTGTGGC	GCCACAGCAG
39	chr3R	+	11826594	11827392	0	TTGTGTGGAACAA	TTGTTCCACACGA
40	chr2L	+	9519535	9519629	0	TAAAAAGGCACAAAAT	ATTTTGTGTCTTTTAA
41	chrX	-	20103119	20101743	0	AATAGGAAC	GTTCCCTGTT
42	chr2R	-	10103358	10103308	0	CTCGCAGTATA	TATACTGTGAG
43	chr3L	+	21828360	21829003	0	GTGTGTGTGTTTGGC	CGCAAGCACACACAC
44	chr3R	+	20532082	20532169	0	CTGGCCAGGA	TCCTGGCCAG
45	chr3L	+	4580256	4586443	0	TTGTTGTTGTTG	CAACAATAACAA
46	chr4	+	261057	261196	0	AAAGGTGATACGTAAG	TTTACGTATCGCCTTT
47	chr3L	-	2564371	2564023	1	AAGAAGGGGC	GCCCCTTTTT
48	chr2R	-	3212053	3211554	0	AATTTCCAAT	ATTGAAAATT
49	chr3L	-	14750715	14750563	1	CGCGTGTGTGT	ACACACATGCG
50	chr2R	+	6175850	6179915	1	CGTTTTTCAG	CTGAAAATG
51	chrX	-	20103119	20101743	0	AATAGGAAC	GTTCCCTGTT
52	chr3R	+	15592464	15600243	0	CTTTTGTAT	ATCAAAAAG
53	chrX	-	20103119	20101743	0	AATAGGAAC	GTTCCCTGTT
54	chr3L	-	1723525	1718152	0	CGCCTTGGGT	ACCCAAGGCG
55	chr3L	-	2090953	2087259	0	CCAGAGTTCGA	TCGAACTCTGG
56	chr2R	-	2625347	2613992	0	GTTGCAGTTT	AAACTGCAGC
57	chrX	+	7126662	7131626	1	GCAGCAGCTG	CAGCTGCTGC

Supplementary Table 2: (continued)

58	chr2L	+	8655054	8655144	0	CAGCAAATGC	GCATTTGTTG
59	chr4	+	261057	261196	0	AAAGGTGATACGTAAG	TTTACGTATCGCCTTT
60	chr2L	-	250653	242863	0	TTGAGCGTATTTT	AAAATACGCTCAA
61	chrUextra	-	15909332	15868644	0	TGGATGTTGT	ATAACATCCA
62	chr3R	-	11740417	11740319	0	AAGCTATTGA	TCAATAGTTT
63	chr3R	-	14080994	14079245	0	TTACAAGTGAA	TTCACCTGTAA
64	chr3L	-	1668543	1668300	1	ATCGATCAGCAA	TTGCTGATCGAT
65	chr2R	+	12312204	12313150	0	TGTGTGTGT	ACACACATA
66	chr3L	-	15500516	15499518	0	GCTTATGCAAAC	GTTTGCATAAGT
67	chr3R	-	17644543	17644283	1	TGCGTTTGTTTTGG	CAAAACAAGCGCA
68	chr2L	+	9447078	9460432	1	AGAGAGAGA	TCTCTCTCT
69	chr3R	+	7048521	7048723	0	CACACACACAAAA	TTTTGTGTGTGTG
70	chr2R	+	4282194	4282418	0	TAACTAAAGTGC	GCACTTTAGTTA
71	chr3R	-	272059	271231	2	TGGCATCGT	ACGATGCCA
72	chr2L	-	6337974	6337347	0	ACAACAGCAAT	ATTGTTGTTGT
73	chr2L	-	17655592	17651558	0	TATGCGACAACAACCT	GAGTTGTTGTTGCATA
74	chr2L	+	17404869	17405282	1	ATGTACATTG	CAATGTACAT
75	chr2R	+	9714623	9717024	0	AGTGA AAAAGTGA	TCACTTTTTATT
76	chr3L	+	17427614	17429347	0	AACTGCACGCCG	TGGCGTGCAGTT
77	chr2R	-	10840548	10840181	2	GACTCAGC	GCTGAGTTC
78	chr2L	-	13171281	13170912	0	ATAATAGTGCGTAGA	TTTACGCACTGTTAT
79	chr2R	+	2698734	2699308	0	TGTGTGCGTGC	GCACGCACACA
80	chr3R	-	20870617	20870587	1	CCCATACATA	TATGTATGGG
81	chr2R	+	10853574	10859143	0	GGTGTGTGTGT	GCACACACATC
82	chrX	-	8990751	8989726	0	TATGTTGTTGT	ACAACAACATG
83	chr2L	-	11798589	11797860	0	GCGTCAGCATA	TGTGCTGACGC
84	chr3L	+	1331053	1331187	0	CGCTGGCAAA	TTTGCCAGTG
85	chr2R	+	17088230	17098717	0	GTGTGTGTATG	TATACACACAT
86	chr3R	+	17011350	17028080	0	GAACAGCAAGTACCAG	TTGGTACTTGCTGTTT
87	chr3L	+	8462837	8463182	0	TCAATCGTATTTG	CAGATACGATTGA
88	chr2L	-	3279210	3278660	1	CACATATAC	GTATATGTG
89	chrX	-	13306254	13305552	1	GCTTCTCCCG	CGGGAGAAAGC
90	chr2L	+	21121770	21122098	0	TAAACGAATTTTG	TAAAATTCGTTTA
91	chr2L	+	21237539	21238218	0	TGTATGGGT	ACCCATACA
92	chr3R	+	17868137	17868513	0	GTAGCAACAACAA	TTGTTGTTGCTGC
93	chr3R	-	5594045	5593689	1	TACACACATACAT	GTGTATGTGTGTG
94	chr3L	-	20229445	20228879	0	ACAACAACAA	TTGTTGTTGT
95	chr2R	+	19538692	19538814	2	AGGCCAAACA	TGTTTGCCCT
96	chr2R	+	14638861	14639055	0	CTGCAAATGA	TCATTTGCAG
97	chrX	+	18801946	18802215	1	GCAACAACA	TGTTGTTGC
98	chr2R	-	9072223	9067713	1	GTTGGTTGT	ACAACCAAT
99	chr2R	-	2618948	2614002	0	GTCAATCAA	TTGATTGAC
100	chr3L	-	5161291	5160249	1	TGTTTTTGT	ACAAAAACA
101	chr3R	-	2734099	2724372	0	GCATACAACAGC	GTTGTTGTATGC
102	chr3L	-	5161291	5160249	1	TGTTTTTGT	ACAAAAACA
103	chrX	-	13493398	13491507	0	GTTGGTTTTG	CAAAACCAAT
104	chr2R	-	6139384	6138791	0	CAGCGCACAAAAGCA	TGCTTTTGTGCGTTG
105	chr3R	-	4064413	4064117	2	GAAATCGAA	TTCGATTTT
106	chr2L	+	7773764	7774169	0	TGTAGTTAGT	GCTAACTACA
107	chrX	-	7428044	7427390	0	AGTCAAGTGC	GCATTTGACT
108	chr3R	-	27707408	27699892	1	CTCTCTCTCTT	AAGAGAGAGAG
109	chrX	-	18006527	18001090	1	ATCAAAATC	GATTTTGAT
110	chr2L	-	3708848	3708716	0	ATTTATGCAGG	CCTGCATAGAT
111	chrX	+	3982461	3983779	0	CAGACGATGGTCAC	GTGACCGTCGTCG
112	chr2R	-	9791220	9791135	0	GTGCATTTGGT	ACCAAGTGCAC
113	chrX	-	11922392	11922214	1	TGTATGTAC	GTACATGCA
114	chr2L	-	3362904	3361537	1	GCAACAAAG	TTTTGTTGC
115	chr3R	+	1450285	1450518	0	CAAATGTGTG	CACACATTTG

Supplementary Table 2: (continued)

116	chr3R	-	22790246	22790110	1	AGCAACAACAA	TTGTTGTTGCT
117	chrX	-	16394504	16393013	0	CACACACAC	GTGTGTGTG
118	chr3L	+	9576825	9579661	0	ATATTTCTGCC	GGCAGAAATAT
119	chr2R	-	20290031	20289416	0	TGCGTGTGTGT	ACACACACGCA
120	chr2L	+	13274428	13274635	0	GGCGCTTTC	GAAAGCGCC
121	chr2R	-	15517564	15516627	2	CAAAACAAA	TTTGTTTTG
122	chr3L	-	7688390	7659183	0	TGATGGGTATCGT	ACGATACCCATCA
123	chrX	-	19638244	19635296	2	GTAAGCCAA	TTGGTTTAC
124	chrX	-	19638244	19635296	2	GTAAGCCAA	TTGGTTTAC
125	chr3R	-	10650675	10650111	0	CCAGGGACCGCAA	TTGCGGTCCTGG
126	chr2R	-	8960020	8955841	0	CCCCTCCA	TGGAGTGGG
127	chr3L	-	8732212	8728026	0	GGAAGTAGCCC	GGGCTACTTCT
128	chr2L	+	5044799	5045733	0	GCAAACAGA	TTTGTTTGC
129	chr3L	+	9892594	9892744	1	TTGTTGTTG	CAACAGCAA
130	chr3R	-	8386080	8382902	2	GCTAATTAG	CTGATTAGC
131	chr3R	-	14258175	14257890	0	GGTTTTTTC	GAAAAAATC
132	chr3R	+	14100884	14107333	0	CTCTTTGTTTC	GAAACAAAGAG
133	chr3L	+	11925562	11926339	2	AATTGGCAA	TTGCTAATT
134	chr2R	+	8445327	8446301	1	TCCAGTATTT	AAATACTGGA
135	chr2L	-	12540431	12539606	1	TGTTGTTGG	CCAACAGCA
136	chr2R	-	19644874	19644177	2	TTGTTGTGT	ACACAACAA
137	chr3R	-	19070913	19062533	0	TTGCAATTGCC	GGCAATTGCAA
138	chr2R	-	6139419	6138700	2	GTGGTGGAA	TTCCGCCAC
139	chr3R	-	5933069	5931838	0	TGCAACGAT	ATTGTTGCA
140	chr2R	+	13360396	13360488	0	CAATGCAAT	ATTTGCATTG
141	chrX	-	19638244	19635296	2	GTAAGCCAA	TTGGTTTAC
142	chr3R	+	22543755	22543960	2	TCAGGCTAC	GTAGTTGA
143	chr3R	+	11126830	11128777	0	CAAAAAGTGGC	GCCACTTTTTG
144	chr3L	-	19000502	19000149	0	GCAAAAACAA	TTGTTTTTGT
145	chr2L	+	16990484	16991979	2	TGGCGACAT	GTGTCGCCA
146	chr2L	+	10459559	10459799	0	GAAAGCCCCT	AGGGCTTTTC
147	chr3R	+	27330936	27331341	0	AACCAGGGATG	CATCCCTGTT
148	chr3R	-	27434985	27428022	1	TGCAAAAAGAG	TTCTTTTTGCA
149	chrX	-	17520872	17519795	0	ATGTGTGTGTGTGTGT	ACACACACACACAT
150	chr3L	+	20821442	20822455	2	AGACAAACAA	TTGTTTGTTT
151	chr2R	-	18223060	18222584	1	TGAAGCTTT	AAAGTTTCA
152	chr3L	+	5668439	5669299	0	CTTAATTGA	TCAATTAGG
153	chr3R	-	5959581	5959418	0	GTGTGTGTGTGTGT	GCACACACACAC
154	chr2R	+	3008246	3012389	0	AAATTTGCA	TGCAGATTT
155	chr2R	-	5144886	5143343	2	CCTGGTTTG	CAGACCAGG
156	chr3R	-	19065369	19063205	1	CCAGAACCC	GGGTTCTGG
157	chr3R	+	22543755	22543960	2	TCAGGCTAC	GTAGTTGA
158	chr2R	-	9786904	9782555	0	ATCTTTGCGAGG	CCTCGCAAAGAT
159	chr3R	+	24167317	24167773	1	TGTTGTTGTT	ACAATAACA
160	chr3R	+	24694767	24694795	0	GATGGCGGC	GCTGCCATC
161	chr3R	-	2734099	2724373	0	CATACAACAGC	GTTGTTGTATG
162	chr3R	-	16409560	16409487	2	TAGTGGTGG	CTACCACTA
163	chr2L	+	12974789	12975495	0	TGTCAGCTGAC	GTCAGCTGACA
164	chr3R	+	19803913	19804570	0	GACATCGAG	CTCGATGTT
165	chr2R	+	18706520	18706845	2	CGATTTCCA	TGGAAATCG
166	chr2R	+	6181465	6181558	0	CTGAAGCATT	AATGCTTCAG
167	chr3L	-	14750544	14750515	0	TCTCGCTCTCGCGC	GTGCGAGAGCGGA
168	chr3R	+	22543755	22543960	2	TCAGGCTAC	GTAGCTTGA
169	chr3R	-	19440789	19440281	0	GCTTAATGCATTTGT	GCAAATGCATTAAGC
170	chr2L	+	8428132	8430169	0	AAGTACAACAACAACAA	TTGTTGTTGTTGTGCTT
171	chr3L	+	9252094	9259295	2	CAGATATAT	ATATATCTG
172	chr3R	-	17634217	17633544	0	ACGCACACACGCACA	TGTGCGTGTGTGTGT
173	chr3R	-	16679064	16679039	0	TTTGAGCCA	TGGTTCAAA

Supplementary Table 2: (continued)

174	chr3R	+	24535044	24535899	0	ATTGTGCAG	CTGCATAAT
175	chr2L	-	479391	478321	0	TGACCTACAA	TTGTGGGTCA
176	chr2R	-	14325622	14325505	1	ATTGCTTTG	CAAAGCAAT
177	chr2R	+	10851875	10859117	0	TTGCATAATTG	CAATTATGCAG
178	chr3L	+	8572406	8572504	0	GTGTGTGTT	AACGCACAC
179	chrX	+	16191303	16191580	1	TGCATATAT	ATATATGCA
180	chr2L	+	9519535	9519629	0	TAAAAAGGCACAAAAT	ATTTTGTGTCTTTTA
181	chr3R	+	24526743	24527050	0	AATGCAAGT	ATTTGCATT
182	chr3R	-	24973659	24973610	0	GACAAAGGA	TCCTTTGTC
183	chr2R	-	11887186	11885827	0	TTGAACTTG	CAAGTTCAA
184	chr2R	-	19090976	19079192	1	GTTTATGCA	TGCATAAAT
185	chrX	-	1113708	1113678	1	GCGGTGTGGA	TCCACATCGC
186	chr2R	-	9845353	9844918	1	GTTTGTGTG	CGCACAAAC
187	chr3L	-	22792989	22792643	1	AGATACAGA	TTTGTATCT
188	chr2L	-	11987635	11987573	1	CGATTGCCG	CGGCAATTG
189	chrX	+	8460178	8460261	0	TATGCTGGC	GCCAGCATG
190	chr3L	+	16045314	16046032	0	CGTGCGTGTGCG	CGCACACGCACG
191	chr3L	+	3645262	3645766	0	GTGAAATCTCGCA	TGCGAGATTTTCAT
192	chr3L	+	8462837	8463182	0	TCAATCGTATTTG	CAGATACGATTGA
193	chrX	-	13493398	13491507	0	GTTGGTTTTG	CAAACCAAT
194	chr3R	-	6013634	6004731	0	TTTCTGGAC	GTCCAGAAA
195	chr2R	+	15366421	15368535	0	AATGGAATAT	ATATTCCGTT
196	chr3L	-	2076837	2076773	0	AGTTGAAATGC	GCATTTCAACT
197	chr2R	-	9072175	9070768	1	CGTATTTGG	CCAAATATG
198	chr3R	+	11219258	11221993	0	TTTCGATTT	AAATGTGAA
199	chr3R	+	15592464	15593181	0	CTTTTGAT	ATCAAAAAG
200	chr2R	-	19583927	19583841	0	AATGAAACCGT	ACGGTTTCATT
201	chr2L	-	16724841	16724807	0	GAAATTGAA	TTCGATTTT
202	chr3R	+	6077769	6077814	1	CGCTGATAA	TTATCAGTG