Non-LTR retrotransposons revealed in the Celera release 1 sequence

Chr – chromosome (for some elements from "small" sequences chromosomal location might be determined but indicated as unknown (?) in the tables)

Cyt – cytological localization interpolated from GenBank annotations

Acc – accession number preceded by a chunk part (sequences were processed in chunks of 3000000 nucleotides)

S – strand of Acc matching to element

Coordinates – coordinates of sequence from Acc chunk matching to element. Actual coordinates of the sequence in accession are calculated as (coordinates in chunk)+3000000*(chunk part)

Element – part of full-length element matching to Acc chunk

Len – length of match

Type – type of element truncation: **F** – full-length element; **5'.** – 5' truncated; **.3'** – 3' truncated; **5'3'** – truncated at both ends; **?** – unfinished

D – length of target site duplication

5' flank – 10 nucleotides of 5' flank of the element

TSD – sequence of target site duplication

Start - 5' flank – 10 nucleotides of the element start

End – 20 nucleotides of the element end

3' flank – 10 nucleotides of 3' flank of the element

BS

Chr	Cyt	Acc	S	Coordinates		Element	Len	Type	D	5' flank	TSD	Start	End	3' flank
2L	34A-34A	2_AE002690	+	2277439	2279766	2796-5122	2327	5'.	6	ACTTGAACTT	AGTAGG	CCATATGCCC	AAATAAATATATAAAAAAAA	AAATATTTTA
3L	73A-73A3	1_AE002602	-	751038	756169	3-5124	5122	F	14	CAATTGAACT	AAACGTTTTGCCGA	GTCGCAAATC	AAATATATAAAAAAAAAAA	CTCATGCACA
2R	42A10-42A10	0_AE002769	-	154863	155438	4550-5124	575	?.	0	NNNNNNNNNN		CTGAAAGCTA	AAAAAAAAAAAAAAAAAAA	CGGCCCACCA
2R	42A10-42A10	0_AE002769	-	159119	159782	1-659	659	.?	0	ACGGCCCACC		GAAGTCGCAA	AGAAGATAATCTCAGCGATG	NNNNNNNNNN
?	?	0_AE002909	-	6393	7593	3-1196	1194	.3'	0	CAAGCGGCAG		AGTCGCAAAT	CACTTATCAAATGCTGACAG	GCATTTTGTT
3L	75C2-75C1	0_AE002602	-	1772676	1777752	2-5122	5121	F	12	ATTTCCATTT	AGTTAATTGCAA	ATAAGTCGCA	AAATAAATATAAAAAAAAA	TCAGGAATGT
?	?	0_AE003029	+	6345	7952	3261-5122	1862	5'.	0	TTTCCCCTGG		TCAAACATCA	AACAAAGAAATATAAAAATA	GTGACAGATT
2L	38B5-38C	5_AE002690	-	84431	85579	3447-4592	1146	5'3'	0	AGCATCAGCC		ATCATCCAGA	GTTTCCCACGCTACACCACC	GGAAGCAGGG
2L	38B5-38C	5_AE002690	+	87326	87563	2538-2774	237	5'3'	0	ATTGAGCGCT		TCGCAACTGA	CTTGCAGACGTGCGATTCGA	TCTCAAGACC
2L	39C3-?	5_AE002690	-	1283543	1283943	4722-5122	401	5'.	12	TTACTCGTAG	AGTAAAAGGGTT	ACCGCATTCA	AAATAAATATATAAACAAAA	TACTAAATTC
3R	92E-92E2	4_AE002708	+	732410	733157	4373-5124	752	5'.	13	AACGACTTGT	AATACTTGTAATA	TATGGAATTT	TAAATAAATATATAAAAAAA	AAATGCCTTG
3R	87A10-87A7	1_AE002708	-	1109009	1109251	4882-5124	243	?.	0	NNNNNNNNNN		CAGTATACAT	TAAATATATAAAAAAAAAA	AATCTTTTGA
3R	87A10-87A7	1_AE002708	-	1113374	1113878	3-502	500	.?	0	TCTTTTGATG		AGTCGCAAAT	TAACTCAAAGCAGTAGCGTC	NNNNNNNNNN
3L	65E-65D4	4_AE002602	+	1249072	1249627	4566-5121	556	5'.	0	GGGTTTTAGT		GAAGACTTTT	AAATAAATATATATAAAAA	GTGAAGACTT
X	16F5-16F7	2_AE002593	-	1366405	1366875	4653-5123	471	5'.	12	ATTTACATTT	AGAATACAAGGC	TCCACTGCGT	AATAAATATATAAAAAAAA	AAACCATAAT
3R	90A-90A	3_AE002708	+	528000	528459	4736-5124	389	5'.	0	AAACTACTGT		TTTCTAAGTT	AAAAAAAATAAAAAAAAAA	GTCACTGAAT
X	7E2-7F	2_AE002566	+	2160628	2160950	4802-5124	323	5'.	11	CTCTAAATGC	ATTGTTTAATT	TTTCGTGATC	ATAGTAAAAAAAAAAAAAA	GATTCTCTGG
?	?	0_AE003078	-	301	635	7-662	656	.?	0	TAACCGTTGT		GCAAATCTGC	AAGATAATCTCAGCGATGCT	Gnnnnnnnnn
?	?	0_AE003132	-	12855	13083	4612-4838	227	5'3'	0	GGAGCAATGC		AATAAGCAAT	CACTGTGGAAGAACAGATGT	GTAGAAGTTA

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Full-length elements:  2/0
5' truncated elements:  5/3
3' truncated elements:  0/1
5'3' truncated elements: 0/3
Unfinished elements:  5
Total number of elements: 19
Total length of elements: 22761
TSD lengths (min/max):  6/14
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Doc

Chr	Cyt	Acc	S	Coordinates		Element	Len	Type	D	5' flank	TSD	Start	End	3' flank
3L	76C-76C	0_AE002602	+	549830	554566	1-4719	4719	F	11	AAATATAAGT	AGCTTTTTGTC	ACATTCGGCA	AAAAAAAAAAAAAAAAAAA	TTCCCGCCAG
3L	76C-76C1	0_AE002602	+	581258	585990	1-4715	4715	F	8	TATTGGTCAA	GAAATTTG	TATTCGGCAT	AAAAAAAAAAAAAAAAAAA	CACTTTACTC
3L	76A-76A	0_AE002602	+	1083265	1084589	3404-4719	1316	5'.	5	TTTGACGCTC	AACTT	AAAGATAAAA	AAAAAAAAAAAAAAAAAAA	GGTAGCAGCA
3L	75C2-75C1	0_AE002602	-	1696967	1698890	2801-4719	1919	5'.	11	AATCTGTTTT	AAAAATGATAG	AGCGGCTGGT	ATTAAAAAAAAAAAAAAAA	GTTTTTCAGA
2R	51A2-50E4	2_AE002787	+	329967	334693	1-4719	4719	F	13	TTCAAATGCC	AGAAGCTCTTATG	GTTCGGCATT	AAAAATTAAAAAAAAAAAA	CATTTGGTTT
2R	31F2-49E6	2_AE002787	+	1582112	1586841	1-4719	4719	F	7	TAAAGACTGT	GACTGTG	CCACATTCGG	AAAAAAAAAAAAAAAAAAA	GTTGTCTGCC
2L	33F1-33F1	2_AE002690	-	1774021	1778841	1-4715	4715	F	13	AATTCAGTCC	ATTTATAGCAATT	CGGCATTGCT	ATTAAAAAAAAAAAAAAAA	AAAATGTATA
2L	34E-34C	2_AE002690	+	2441010	2445744	1-4719	4719	F	6	AAAAAGCGTT	GGGAAG	CGTTCGGCAT	AAAAAAAAAAAAAAAAAAA	TAAGTAAATG
2L	34D4-34D1	2_AE002690	-	2789082	2790133	3671-4719	1049	5'.	13	ACCGCGACAC	AAATCAAACCACC	ATGGACTTTT	AAAAAAAAAAAAAAAAAAA	TCAATAAACG
3L	79A-79A4	0_AE002647	+	1407868	1412601	1-4717	4717	F	11	TGATCAACGC	ACTGTTACCCA	CGTTCGGCAT	TAAAATAAAAAAAAAAAAA	TGCGGCAACT
3L	79E4-79E	0_AE002647	+	2235719	2240455	1-4719	4719	F	13	AGAAGGAGCC	AACTTGGTGAGCA	CGGCATTCCA	AAAAAAAAAAAAAAAAAAA	GGATGGGAGG
3L	79E-79F3	0_AE002647	-	2516855	2517932	3651-4719	1069	5'.	11	TTACAATTTT	AATTACAAAGG	CATTTGACAG	ATAAAAAAAAAAAAAAAAA	TCGCTCTATG
3R	93A-93B2	4_AE002708	+	1080708	1085448	1-4719	4719	F	14	GGTTTGATCC	ACAAAACAACGGC	ATTGATTCGG	TAAAAAAAAAAAAAAAAAA	GGTCTTCCAA
3R	100D2-100D3	7_AE002708	+	2879265	2883994	5-4718	4714	F	7	GATGAAACAC	AGATATC	ACAGTCTTCG	AATTAAAAAAAAAAAAAAA	CAATCAAGAG
3R	96A21-96A21	5_AE002708	-	1945604	1947916	2411-4719	2309	5'.	10	ATTATGGACT	GAGAACGGTA	TCCCCGGGTA	AAAAAAAAAAAAAAAAAAA	GTGAAAAATT
3R	96B5-96B1	5_AE002708	+	2142683	2147420	1-4718	4718	F	11	ATGTGAATTC	GAGAAGTCACA	CACATTCGGC	AAAAAAAAAAAAAAAAAAA	GATTAGGATA
X	6A2-6A	2_AE002566	+	201267	206001	1-4719	4719	F	13	CAGTCCAGTC	AAGATGATGCTGC	ATTCGGCATT	AAAAAAAAAAAAAAAAAAA	TCGGTTTGCT
?	?	0_AE002841	-	5908	10645	1-4719	4719	F	14	TTTGCATCCC	AATATAGGCGCCGC	ATTCGGCATT	AAAAAAAAAAAAAAAAAAA	AAGGCAAAGA
?	?	0_AE003091	-	4105	8836	1-4719	4719	F	11	ATAAGTCGTT	AAGTACCATCA	TATATTCGGC	AAAAAAAAAAAAAAAAAATA	CTACTGAATC
X	12F1-12F5	1_AE002593	-	957289	962120	1-4719	4719	F	12	TTAAAACATT	AAGTCCAGAAAA	AAAATTCGGC	AAAAAAAAAAAAAAAAAAA	GACAATTACG
3R	87E4-87F1	1_AE002708	-	2544540	2549361	1-4711	4711	F	14	ATTCCTCGTC	ACCTATCCCTTCTT	TTTCGGCATT	AAAAAAAAAAAAAAAAAAA	AAAAAATATT
3L	65D3-65D1	4_AE002602	+	1461444	1463407	2758-4719	1962	5'.	3	CACTAAAGTT	ATG	AAATTATGTT	AAAAAAAAAAAAAAAAAAA	TTGCAGTTAA
3L	65A-64F	4_AE002602	+	2194672	2196987	2403-4715	2313	5'.	5	GTTCATCTGC	TTGTG	AACTTTTTAG	TTAATAAAAAAAAAAAAAA	TCGCTTGGCA
2L	25D6-25E1	0_AE002690	-	400547	402868	2399-4719	2321	5'.	11	TTATCACATT	AAGAGAGCGAA	TTATCCCCGG	AAAAAAAAAAAAAAAAAAA	CATTTCTGGG
?	?	0_AE003003	-	22500	24423	26-1944	1919	5'3'	6	AACCGTAAGC	TGCGCG	GACGTGTTTC	TCTGTGGAACGCAAATGGCG	TCGCCACTTG
3R	84A5-84A5	0_AE002699	+	958757	960485	2991-4718	1728	5'.	8	AACTCTCATT	AATCACGA	GCTCACAGAA	TAAAAAAAAAAAAAAAAAA	AATCAATGCA
3L	67E4-67D5	3_AE002602	+	843856	846123	2416-4715	2300	5'.	11	TTAGTGGTCC	AAGAAGGAGAG	AAGGTCCCGG	AAAAAAAAAAAAAAAAAAA	CAAACAGTGG
3L	67B10-67B1	3_AE002602	-	1865065	1867903	1886-4719	2834	5'.	11	TTTAGAGTTC	AGTTCAGGCAG	AGCTCACACA	AAAAAAAAAAAAAAAAAAA	TCAGTGCGTG
3R	88E-88E8	2_AE002708	-	1272754	1276563	1012-4712	3701	5'.	12	AATGGGTATT	AGAGGTGTTTTG	TTTCAGACCA	AAAAAATTAAAAAAAAAAA	CTTTCTTGTG
3L	73A3-72F2	1_AE002602	-	833314	835608	2439-4719	2281	5'.	7	TGCAATTCAC	TTTTTCA	ACATCAACAG	AAAAAAAAAAAAAAAAAAA	TGTTTTCCAT
3L	70F2-70E1	1_AE002602	-	2554795	2558211	867-4719	3853	5'.	13	AATTTGTGTT	AGTTAGTAGTTAG	GCCTCCACCA	AAAAAAAAAAAAAAAAAAA	ACCTTCAAGC
2L	30A-30A7	1_AE002690	-	1264622	1269448	1-4719	4719	F	12	TGAAGTTAAC	ATCTACAATGAC	CGGCATTCCA	AAAAAAAAAAAAAAAAAAA	GAAAGAACTT
?	?	0_AE003176	-	15000	18710	1118-4718	3601	5'.	12	AATCTGAAAC	ACATCAATTCCC	CCAGCAACAG	AAAAAAAAAAAAAAAAAAA	TATGCTCCAT
3L	68D3-68C8	2_AE002602	-	2535017	2539839	4-4718	4715	F	11	AATTTGATTT	GATTTGAAGAA	TCAAATCTTC	ATAAAAAAAAAAAAAAAAA	CACTGTATTT
3L	63B8-63C6	1_AE002584	+	255932	256361	4290-4719	430	5'.	12	CATGGCGAAC	AATTAGCAAGG	AAACGGCTCC	AAAAAAAAAAAAAAAAAAA	CGAGGCAACA
?	?	0_AE003403	+	5907	7116	3506-4718	1213	5'.	11	TTTAGGCGAC	AAAAATATTGC	GATCGAACAG	AATAAGTTAAAAAAAAAAA	TGCGCCTTGC
3R	84F2-84F6	0_AE002708	+	493188	493972	3938-4714	777	5'.	5	TTGGGTTGGC	AGGGC	TGTATCCAAG	AAGTAAAATAAAAAAAAAA	CGTTGTGGCA
?	?	0_AE003267	-	688	866	3712-4045	334	5'3'	10	ATGTTTAAAA	TAATCAAACA	TACATAAGCT	CAAACAGGTAACATTTACCC	AAGCTGCCCG
3L	76B6-76B	0_AE002602	+	893176	893784	4119-4719	601	5'.	0	AACGGTACCT		TAGGAGTACA	TAAAAAAAAAAAAAAAAAA	TGGGCGGTGG
3L	75B5-75A	0_AE002602	-	2417395	2417672	6-283	278	.?	0	ATTAATTTAT		TTCCACAGTC	TCTTTACAACCGCACAATGC	NNNNNNNNNN
2L	32E-32E1	2_AE002690	-	254296	254772	1-477	477	.?	0	AACCTAAATT		CGGCATTCCA	GCGCCAAACGACCGTCCCGG	NNNNNNNNNN
2L	33F1-33F1	2_AE002690	+	1824790	1825216	3269-3695	427	5'?	0	CCAATATGCT		ACACCGGAAA	CGGCCTAATGTTTAAAATTA	AAACANNNNN
2L	33F1-33F1	2_AE002690	-	1828001	1828568	4157-4718	562	?.	0	NNNNNNNNNN		CACATTGAAG	AAATAAAAATAAAAAAAAA	TCTTTCTTCA
3L	33F1-77B3	0_AE002647	+	7202	8444	3211-4708	1498	5'.	6	GTAGAGATAT	TGAAGG	GAGTGGCAGG	TAAGCAAAACATGAAAAAAA	CTAGTTTTCC
3R	92D1-92E	4_AE002708	-	474298	474662	1227-1591	365	5'3'	5	AAATTTAAAA	AAGGA	CAACTTGAAC	GAACACGGCGCGGGCACACC	TCAGCTACCC
X	3D5-3D	1_AE002566	+	362539	362833	1113-1408	296	5'3'	0	AAAGCGCAAG		ATTGATGCAA	GCGTACTATACACTGAAATC	TAATCTAGGA
X	3D5-3D	1_AE002566	-	377038	377468	4183-4617	435	5'3'	3	GAGTGTTCGC	GGG	TAGACTAAAA	TGTTAGTCTCTTAAGTAAAA	CAAATTCAAA
3R	94C8-94D1	5_AE002708	+	96451	96996	1-546	546	.?	0	AGTTGGCATT		CGGCATTCCA	CACAACATCAACTTCGTCAG	NNNNNNNNNN
3R	96C1-96C	5_AE002708	-	2540093	2540680	4136-4719	584	?.	0	NNNNNNNNNN		AGGCGGCTCA	AAAAAAAAAAAAAAAAAAA	CAACATCTTC
3R	96C1-96C	5_AE002708	-	2543999	2544528	201-722	522	5'?	0	GAAATCAACA		AGGAAATGAT	AGCTCAGCCCTCAAAACAAT	NNNNNNNNNN
2L	36E1-36E1	4_AE002690	+	1377269	1377845	1-576	576	.?	0	AACCTAAAGA		CGGCATTCCA	ATTATTCGCTGGGCCAGCTG	NNNNNNNNNN
2L	36E1-36E1	4_AE002690	+	1381950	1382273	4397-4719	323	?.	0	NNNNNNNNNG		AACGAAACA	AAAAAAAAAAAAAAAAAAA	CCCTAAAGAC
2L	37D2-37D2	4_AE002690	+	2313484	2313896	1-413	413	.?	0	TTTGTCAGTT		CGGCATTCCA	TGCCTGCTTCGGCTCACAAG	NNNNNNNNNN
2L	37D2-37D2	4_AE002690	+	2322671	2323265	4129-4719	591	?.	0	NNNNNNNNNN		TCTGGACAGG	AAAAAAAAAAAAAAAAAAA	ATTTTTTGTC
2L	38A1-38A1	4_AE002690	+	2644838	2645303	4253-4719	467	?.	0	NNNNNNNNNN		CTTCTATCAA	AAAAAAAAAAAAAAAAAAA	AAATTTTTTC
3L	67C-69	3_AE002602	+	1732182	1733805	3100-4719	1620	5'.	11	TTTGATGAGT	AAAAGTACTTT	ACAAAATGTA	TAAAAAAAAAAAAAAAAAA	TAAACTGAAG
2R	42A2-41F9	0_AE002769	+	352937	353465	1707-2237	531	5'3'	0	AAGTCGACTT		CTACTCGGGA	GCCGTATACTTGCCCCCCCC	CACCACCACC
?	?	0_AE002910	-	29055	29944	1729-2608	880	5'3'	0	TCGGGAAGAA		CAGAAAATAA	AGCAGCCCTACAGGCTGACA	GGCAACAGGT
2R	43F2-43E6	4_AE002787	+	807223	807768	1-546	546	.?	0	ATTCGGCATT		CGGCATTCCA	CACAACATCAACTTCGTCAG	NNNNNNNNNN
2R	43F2-43E6	4_AE002787	+	811253	811693	4274-4714	441	?.	0	NNNNNNNNNN		AAACCTATCT	ATTAAAAAAAAAAAAAAAA	GTCTGAAAAT
?	?	0_AE003322	+	35912	36973	3658-4716	1059	5'.	0	AATCAGCGGG		TGACCGAGTC	TAAAAAAATAAAAAAAAAA	CTAGGTTCCT
2L	28D5-28D	1_AE002690	+	62407	62891	4236-4719	484	?.	0	NNNNNNNNNN		GTCTGGAGTT	AAAAAAAAAAAAAAAAAAA	CCAAAACTAA
?	?	0_AE002751	+	31980	32257	4435-4713	279	5'.	0	TTTTTTGTCA		AATCGATAGA	AAAAACAAACAAAAAAAAA	CTCCTTTGTA
?	?	0_AE002751	-	75672	76877	3515-4716	1202	5'.	0	AAAAAGGCGA		AATACAATAC	TTAACAAAAAAAAAAAAAAA	TTGTGCTAAT
?	?	0_AE003029	-	21073	21799	842-1567	726	5'3'	0	TTGAGATTTG		ACCGGCAAAG	AAGACCCCCCTTAACAAACG	CGGAGAATCA
3R	90C-90D1	3_AE002708	+	1272591	1273199	4119-4719	601	5'.	0	TAACGTACCT		TAGGAGTACA	AAAAAAAAAAAAAAAAAAA	GTAGGTTTTT
3L	64C5-?	1_AE002584	+	2017804	2018356	1-554	554	.?	0	AACTTAGATT		CGGCATTCCA	TCAACTTCGCAGCGGCCCAA	NNNNNNNNNN
3L	64C5-?	1_AE002584	-	2022388	2022900	4207-4719	513	?.	0	NNNNNNNNNC		CTGGCTCATA	AAAAAAAAAAAAAAAAAAA	CTTAGATTTA
2L	35A3-35B1	3_AE002690	-	491717	492160	4272-4719	448	5'.	0	TTAATTTTTG		TAAAAAAAAC	AACAAAAAAAAAAAAAAAAA	GTTAAAGACT
2L	35A3-35B1	3_AE002690	-	494597	495190	2732-3327	596	5'?	0	TACGAAGAAA		TCTGGTTTAA	CTTCACATCTGCCTGTTGTT	NNNNNNNNNN
2L	36B2-36C2	3_AE002690	+	2928594	2929053	1-460	460	.?	0	TTTTTATCATT		CGGCATTTCA	ACCCCGCTCCTCTCGCAGCG	NNNNNNNNNN
?	?	0_AE002992	-	9063	9393	3749-4081	333	5'3'	0	TTCAGCACTT		AGATCAATTC	CTGCCCGCCCTTGGCTCAAT	GCCCTTCAGC
?	?	0_AE002992	-	10841	11078	1821-2055	235	5'3'	0	CACACAAAAC		ACCATCATTC	AACTTCCAAATACCAGGATA	TAAAGGCCCA
?	?	0_AE002693	+	2003	2989	2846-3983	1138	5'3'	0	GGGTGCACTA		CAGTCCAATA	CCGACACTTAACTGTAGAAC	CTTAATCTGT

Chr	Cyt	Acc	S	Coordinates		Element	Len	Type	D	5' flank	TSD	Start	End	3' flank
2R	46A-46B1	3_AE002787	+	1960099	1961439	3365-4708	1344	5'.	0	CTCATCTGTT		TGGATGTGGT	CAAAAATGTGGAAAAAAAAA	CTTTGTTAGC
?	?	0_AE003027	-	301	647	1-647	647	.?	0	AAGTCGCATT		CGGCATTCCA	GAAGAATCAAAACAAAAGCA	Gnnnnnnnnn
?	?	0_AE003048	-	15565	16095	3111-3647	537	5'3'	0	CTGATCATCT		TATTTCAACC	AGACGTTGCACAAGCATTCG	ATAGAGTATG
2L	22A4-22A3	1_AE002638	+	203048	203770	1776-2487	712	5'?	0	AACAAAAACT		GAAGCTATGA	ATCGACTTCGCAGTTACGAA	NNNNNNNNNN
2L	22A4-22A3	1_AE002638	-	312719	312990	1923-2193	271	5'?	0	TCTGAACTTG		CTACGTGGAA	ACATCTATCAACATTCAGCT	GGATNNNNNN
?	?	0_AE003090	-	26902	27487	2-585	584	.?	0	CCTCAATTAT		GGCAATTCCA	TGTGCCAGCTGTAAATAATT	NNNNNNNNNN
?	?	0_AE003064	-	21480	21716	4188-4718	531	?.	0	nnnnnnnnnn		TTAAAGCAAG	AAAAAAAAAAAAAAAAAAAA	GTAAAGATCT
?	?	0_AE002962	+	372	870	26-524	499	5'?	0	GAGATTCGCG		GACGTGTTTC	CAGTGACCTCACTGGCAACT	NNNNNNNNNN
?	?	0_AE002743	-	34346	34612	3400-3665	266	5'3'	0	AGAGCAACTG		AAGCAAAGAT	CGCTCAGGCATTTGACAGAG	CAGACACTAA
?	?	0_AE002743	-	82056	83119	3653-4716	1064	5'.	0	AATGAAATCA		GCATTTGACC	TAAGTTAAAAAAAAAAAAAA	TAAAACTTAA
?	?	0_AE002639	-	10294	11013	126-853	728	5'?	0	TCTTATTTTT		TTTCTGACTA	CAACGAAAAAACGGAGGGGA	NNNNNNNNNN
?	?	0_AE002782	+	3920	4361	1-442	442	.?	0	AATTATTATT		CGGCATTCCA	GAAGAGACCGCCTCTCCTAC	NNNNNNNNNN
?	?	0_AE003173	-	10559	11125	2999-3571	573	5'3'	0	CTCGTTGTGG		AAAGACCACA	AACATGGAGCGAGTATACAG	CGAGCACAGT
?	?	0_AE002770	+	301	334	4387-4719	333	?.	0	nnnnnnnnnG		TACCTTCGAA	AAAAAAAAAAAAAAAAAAAA	AAATTGCAAT
?	?	0_AE002873	-	1372	1466	4174-4570	397	?3'	0	nnnnnnnnnn		GACGCACCTC	ACCAACCAGCCCAGCGTTAA	TTTGCAGGCG
?	?	0_AE002687	-	8213	8519	3280-3589	310	5'3'	0	ACTTGAGCCG		GCTCGTTAAA	AGGCCAATCGAATAACGTCA	TTTTTGGATT
?	?	0_AE003032	+	29549	29694	3515-3950	436	5'?	0	AAAAAGGCGA		AATACAATAC	ATGCCCAGCAAAGGCAACAG	AGCAACTTGn
2R	54C-54B	1_AE002787	-	252102	252621	4205-4718	514	?.	0	NNNNNNNNNN		CACTGGCTCA	AAATAAAAAAAAAAACAAAA	TTGTTTAGAC
?	?	0_AE003351	-	301	378	4257-4637	381	?3'	0	nnnnnnnCTT		ATATAACTCC	TTAGTTAGTTTATAATAAGA	AAAATGCCAA
?	?	0_AE003253	+	23803	23716	26-239	214	5'?	0	GAGATTCGCG		GACGTGTTTC	ACATACGTTCTCAGCGACAA	nnnnnnnnnn
?	?	0_AE002952	-	14500	14408	4510-4717	208	?.	0	nnnnnnnnnn		ACTAATCCGA	AAAAAAAAAAAAAAAAAAA	TTCAAACTCA
?	?	0_AE002832	+	743	1081	4373-4706	334	5'.	0	CAGATACGGA		ACTGGAGCTC	AGCAAAACATGAAAAAAAA	GTGTGGGCAT
X	5A6-5C3	1_AE002566	+	2535884	2540620	1-4718	4718	F	0	CACGTAATTT		CGGCATTCCA	AAAAAAAAAAAAAAAAAAA	TATATTGTAT
2L	36E4-36F	4_AE002690	+	1550895	1553697	1924-4715	2792	5'.	0	AAAAGTACAA		TCTGTGGAAC	AAAAAAAAAAAAAAAAAAAA	TGATTTCAAG
?	?	0_AE002781	+	7219	9577	2335-4714	2380	5'.	0	TGTGTGAACA		GGGATCTCGA	AAAAAAAAAAAAAAAAAAAA	TTTTTTGGCG
2R	41F11-41C	0_AE002769	+	991680	993667	2944-4080	1137	5'3'	0	CACTACTAAG		ATACATCGAG	TTCCCGCCCTTGGTTATGAA	GGTATTCATC
2R	41C-?	0_AE002769	-	1285880	1287085	3329-4588	1260	5'3'	0	GCCCTTCCAG		AACTCTCATC	AAATTTGTTAGGCATATAAT	CTTTTACTAT
?	?	0_AE003322	+	38378	39058	3963-4719	757	5'.	0	CAGTGGAAGA		GCCACACAAA	AAAAAACAAAAAACAAAAAA	CATTTTGTGG
3L	71A2-70F1	1_AE002602	-	2457086	2457987	2784-4607	1824	5'?	0	GCATTTTCTT		TCAAAACTAA	TGAAAAAAAAAAACTATCAC	NNNNNNNNNN
?	?	0_AE003029	-	18007	19374	3261-4687	1427	5'3'	0	CCAAAAAATC		ACCTGGGTGA	AAAGAGAAGATCCAATAAAT	TTGGATCTTT
2L	38B5-38C	5_AE002690	-	261707	263044	2461-4718	2258	5'.	0	TTGGTTTATT		ACACCTGATC	AAAAAAAAAAAAAAAAAAAA	GTTATCTCTT
?	?	0_AE002734	+	13164	14953	1298-3665	2368	?3'	0	NNNNNNNNNN		CTTGCTCATC	CGCGCAGGCATTTGACAGAG	CTAAGACCCT
?	?	0_AE002734	-	16185	16415	4096-4333	238	5'3'	0	GAATAACATA		ACAAACCGAC	CGTCCATCAGTCAACAACAC	TGAGAACCAT
?	?	0_AE002612	-	33794	34123	4390-4719	330	5'.	0	NNNNNNNNGT		CCTTCGGAAC	AAAAAAAAAAAAAAAAAAAA	AAAATATAAT
?	?	0_AE002612	-	34176	34813	1-638	638	.?	0	AATCGGGATT		CGGCATTCCA	CACGTAAAGAAGAATCAAAA	NNNNNNNNNN
?	?	0_AE002903	+	7161	8578	3129-4577	1449	5'3'	0	CTTAAAAAAG		CCACTAGCTC	GCCCAGCATTAAATTTTATT	TTTCAATATT
?	?	0_AE003217	-	12829	13180	3186-3536	351	5'3'	0	TACTCTCCCG		CCTTTTAACT	CGCCTTTGAACACCGTGAAT	ACTGCACAGC
2L	36F-36F7	4_AE002690	-	1603146	1607969	1-4719	4719	F	0	TTCGGTCATT		CGGCATTCCA	AAAAAAAAAAAAAAAAAAAA	CAAATTGGGT
X	17E9-18C1	2_AE002593	-	2232808	2237626	3-4719	4717	F	0	TTTAATAGTA		GCATTCCACA	AAAAAAAAAAAAAAAAAAAA	TTGGTAATAT
3L	65D5-65D2	4_AE002602	-	1383785	1388611	1-4718	4718	F	0	CTGTTACATT		CGGCATTCCA	AAAAAAAAAAAAAAAAAAAA	CTGGTATTCT
3R	65D5-84D4	0_AE002699	-	133292	138102	10-4719	4710	F	0	GGATAACATA		ACAGTCTTCG	AAAAAAAAGTTGTTAAAAAA	CTATTTGTTA
2R	41F11-41C	0_AE002769	-	990835	991314	3600-4080	481	5'3'	0	GCAGGGCAC		CTGCTTTGAA	TTCCCGCCCTTGGTTATGAA	GGTATTCATC
2R	41F11-41C	0_AE002769	+	1209234	1210389	3520-4705	1186	5'.	0	GATGTCGCTA		ACTCCCATCG	AATTAAAACATGGAAAAAAA	CCGCCGGCGT
2R	44D-44C1	4_AE002787	-	278860	283682	1-4713	4713	F	11	GCAGGCGGTC	ATTTATTTCGG	CATTCGGCAT	AAATTAAAAAAAAAAAAAAA	GGACCAAGGC
?	?	0_AE003119	+	3069	5455	829-3994	3166	5'3'	0	CGGATTCTGG		AACCGAACAA	CTGTAGAACGAGGGCTTGCC	TTAAACAAAC
?	?	0_AE003083	+	928	1481	1016-1749	734	5'3'	0	ACACCAAATT		CCAAATTATC	CCGAACAAATACCAAATACA	AATACATCGT
?	?	0_AE003083	+	2258	3659	3085-4709	1625	5'.	0	CTCTGGCACC		TGGTTTCGCC	AAAAATCTTAACTATAACAA	GTATTTTTTG
?	?	0_AE002894	+	6230	8748	1729-4698	2970	5'3'	0	ATTTACTGCA		CCGAAGAATA	GCAAATAATAATTGTAGTTA	TTGTTATTAT
?	?	0_AE002989	+	11310	11563	414-660	247	5'3'	0	GCTTTTGCTC		TCGCGGAGCG	AAAGCAGAAGGCGATTGCCA	AGAATACGGC
?	?	0_AE002989	+	11607	11912	1575-1873	299	5'3'	0	GGTTTAACGT		ATAGCAAATA	ATCTTCAAAATCCCCATGCT	GGCTTCCCTA
?	?	0_AE002989	+	12459	12777	3219-3536	318	5'3'	0	ATTATGTGAA		TTAGCAAAGG	GAACCATCGAACAGGCCAAT	CGAATCACGT
?	?	0_AE002872	-	13501	14692	3357-4645	1289	5'3'	5	GTCATTAAAG	AGCAA	CTCAAAACTG	AAGACTAAGACTAATAAATA	AACATGCAAA
2L	39F3-39E	0_AE002725	-	95163	95766	94-1131	1038	5'3'	0	CAGTGCAGTG		AAAGTTGAAC	CATTGTAGCAACAGTGGCAC	TTCTTCAGAC
?	?	0_AE002754	+	301	545	4157-4715	559	5'.	0	CTCGGCGTTC		ACCTAGAATC	TTAAAAAAAAAAAAAAAAGA	TTTTTCTAGA

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Full-length elements:  19/5
5' truncated elements:  20/16
3' truncated elements:  0/0
5'3' truncated elements: 5/25
Unfinished elements:  38
Total number of elements: 128
Total length of elements: 218491
TSD lengths (min/max):  3/14
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F

Chr	Cyt	Acc	S	Coordinates		Element	Len	Type	D	5' flank	TSD	Start	End	3' flank
2R	42A2-41F9	0_AE002769	+	353493	355114	2610-4242	1633	5'.	0	GCAGTATTAG		AGCTCACAAA	AATTAAAAAAAAAAAAAAAA	TTGCTTATCC
2R	41F11-41C	0_AE002769	+	695417	698155	1-2732	2732	.3'	0	CTCGTCATCG		CTGCACCCGC	CTAAAGAAATAACCTCTATAA	CTTCCTCGGA
2R	41F11-41C	0_AE002769	+	700272	704510	1-4242	4242	F	0	CTCGTCATCG		CTGCACCCGC	AAAAAAAAAAAAAAAAAAAA	TTACTATTTC
2R	41F11-41C	0_AE002769	+	716685	718889	1-4240	4240	F	0	CTCGTCATCG		CTGCACCCGC	AAAAAAAAAAAAAAAAAAAA	GGAACTTTAT
2R	41F11-41C	0_AE002769	-	725757	727557	2439-4233	1795	?.	0	NNNNNNNNNN		ACGATCAGCG	GTAAAATAAAAAAAAAAAAA	GTGTGGGAAC
2R	41F11-41C	0_AE002769	+	929298	929684	329-724	396	5'3'	0	TGCCACTGAA		TCAGTCGATA	AAAACAAGTATCTAAAAAAA	ATCCACCTTC
2R	41F11-41C	0_AE002769	+	946401	948791	799-3885	3087	5'3'	0	GTCGCCTCTA		ACGCTTTTGT	ACAGATTCTGACAACCATCAC	GAAAAGATCA

3

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2R     41C-?        0_AE002769   +   1334187   1334651   3766-4239   474    ?.    0    NNNNNNNNNN                            GCTCATCAAC   AAAAAAAAAAAAAAAAAAAAA   TCGCGTGCTA
X      12E5-12F1    1_AE002593   -   596108    600356    1-4242      4242   F     0    CTCGTCATCG                            CTGCACCCGC   AAAAAAAAAAAAAAAAAAAAA   TTTAAAACAT
X      20A5-20      0_AE002629   -   152742    156987    1-4236      4236   F     0    CTCGTCATCG                            CTGCACCCGC   AAAAAAAAAAAAAAAAAAAAA   TTATTATTAC
2R     43B2-42D1    4_AE002787   +   1473469   1477718   1-4241      4241   F     0    CTCGTCATCG                            CTGCACCCGC   ATAAAAAAAAAAAAAAAAAAA   CTTTTAAAGT
2L     33F1-33F1    2_AE002690   +   1766365   1770610   1-4242      4242   F     0    CTCGTCATCG                            CTGCACCCGC   TAAAATAAAAAAAAAAAAAAA   TTTTTTCTTT
2L     33F1-33F1    2_AE002690   +   1824790   1825221   2780-3211   432    5'?   0    TCCAATATGC                            ACACCGGAAA   CTAATGTTTAAAATTAAAACA   NNNNNNNNNN
2L     33F1-33F1    2_AE002690   -   1828001   1832187   623-4235    3613   5'.   13   TTATTCAATT   ATCTTTCTTCATT            TTACGCCAAA   TAAAATAAAAATAAAAAAAAA   ATTGCCAATT
2L     34D4-34D4    2_AE002690   +   2597230   2601484   1-4238      4238   F     0    CTCGTCATCG                            CTGCACCCGC   AAAAAAAAAAAAAAAAAAAAA   TTTCTCTTTA
?      ?            0_AE003098   -   5107      9359      1-4241      4241   F     0    CTCGTCATCG                            CTGCACCCGC   TAAAAAAAAAAAAAAAAAAAA   GATTATGGTC
3L     76B6-76B     0_AE002602   +   889533    893785    1-4241      4241   F     0    CTCGTCATCG                            CTGCACCCGC   ATAAAAAAAAAAAAAAAAAAA   TGGGCGGTGG
3L     75C2-75C1    0_AE002602   -   1786169   1786521   831-1183    353    5'?   0    GAAAACGACG                            TAAGTGCACA   TTTAAAATCAGGTATGACGCC   NNNNNNNNNN
3R     35E-35F      2_AE002708   +   412636    416892    1-4242      4242   F     0    CTCGTCATCG                            CTGCACCCGC   AAAAAAAAAAAAAAAAAAAAA   GGATAAGAGT
3R     88E-88E8     2_AE002708   +   1394323   1398571   1-4242      4242   F     3    GCCTCGTCAT   GGC                     TGCACCGCT    AAAAAAAAAAAAAAAAAAAAA   GATGGAAACG
3R     88F-89A5     2_AE002708   -   1967778   1969981   1-4237      4237   F     0    TCGTCATCGG                            CTGCACCCGC   AATAAAAAAAAAAAAAAAAAA   CTTGAGAAGA
3R     88F-89A5     2_AE002708   -   1972392   1972881   1-486       486    .3'   0    CTCGTCATCG                            CTGCACCCGC   AGGACGACTACAGAAAAGTCA   TGTGTCCCGT
3L     62F-63A1     0_AE002584   +   2726046   2730281   19-4242     4224   5'.   35   CAACCAAGAG   ATGTATCTTTTTCATAAT      GCAATAAACG   AAAAAAAAAAAAAAAAAAAAA   CGCCTTATGT
                                                                                                   TACTTAACTGATTGTTA
2L     36B2-36C2    4_AE002690   -   243645    247893    1-4242      4242   F     0    CTCGTCATCG                            CTGCACCCGC   AAAAAAAAAAAAAAAAAAAAA   TTTCTCTTTG
2L     36D1-36D3    4_AE002690   +   659237    663495    1-4241      4241   F     0    CTCGTCATCG                            CTGCACCCGC   AAAAAAAAAAAAAAAAAAAAA   TTTGCAGTCG
2L     37D2-37D2    4_AE002690   +   2322672   2323266   3641-4237   597    ?.    0    NNNNNNNNNN                            CTGGACAGGC   AAAAAAAAAAAAAAAAAAAAA   TTTTTTGTCA
2R     37D2-57A4    0_AE002787   -   36684     37120     3805-4242   438    ?.    0    NNNNNNNNNN                            CTCCAGTTAT   AAAAAAAAAAAAAAAAAAAAA   TTAACCAATT
2R     55A4-54F3    0_AE002787   -   2626718   2630659   295-4240    3946   5'.   0    AAAAGAGCAA                            GATACATTTC   AAAAAAAAAAAAAAAAAAAAA   TTATTGTCTA
3R     90A-90A      3_AE002708   -   580119    581791    2632-4233   1602   5'.   11   AACGTAGTCG   ACTATACTCAC             TCCTATACTC   AGTAAAATAAAAAAAAAAAAA   ATCACTTGAA
3R     90B2-90B3    3_AE002708   +   824831    825197    3875-4241   367    5'.   11   CATATATACA   ATATATCCCCC             ATCCCCCCAG   ATAAAAAAAAAAAAAAAAAAA   GACTCGGCGA
3R     90C-90D1     3_AE002708   +   1269456   1273201   503-4239    3737   5'.   0    ATTATATATA                            ATATAAAATA   TAAAAAAAAAAAAAAAAAAAA   GTAGGTTTTT
3R     90D6-90E1    3_AE002708   -   1296039   1297562   2718-4242   1525   5'.   0    AAAGACATGT                            AATTGAATTG   AAAAAAAAAAAAAAAAAAAAA   TCCTTAGGTT
3R     91B2-91C7    3_AE002708   -   1844526   1845001   88-562      475    5'?   0    ATACTAACTT                            AAATGGTAAA   CAAGGGCCTGCAAGTAGTCCT   NNNNNNNNNN
3R     91F11-92A1   3_AE002708   +   2428825   2433081   1-4241      4241   F     10   AATTCCATTT   AATAATGCGG              CTGCACCCGC   AAAAAAAAAAAAAAAAAAAAA   TGACAGTGGG
2L     22B-22C1     0_AE002638   +   2825781   2829535   503-4242    3740   5'.   0    ATTATATATA                            ATATAAAATA   TTTAAAAAAAAAAAAAAAAAA   TTCAAACCAT
2L     22A4-22A3    1_AE002638   +   197798    198167    3875-4240   366    5'.   0    CCCATCCCCC                            AGAACCATCA   AAAAAAAAAAAAAAAAAAAAA   TGTCCTTGTC
2L     22A4-22A3    1_AE002638   +   201768    203619    1-1845      1845   .3'   0    CTCGTCATCG                            CTGCACCCGC   CGCTAAACATACTCACTTGGG   GATCGCGACT
2L     22A4-22A3    1_AE002638   -   309929    310275    3890-4236   347    ?.    0    NNNNNNNNNN                            GCACCGTGGT   AAATAAAAAAAAAAAAAAAAA   TCTGAACTTG
2L     22A4-22A3    1_AE002638   -   312715    313017    1403-1702   300    5'?   0    TTGTTTCTTT                            TGAATAATAT   TCTATCAACATTCAGCTGGAT   NNNNNNNNNN
?      ?            0_AE003090   -   2916      5118      1-4236      4236   F     0    TCGTCATCGG                            CTGCACCCGG   AAATAAAAAAAAAAAAAAAAA   TTTATGAACA
3R     92D1-92E     4_AE002708   -   471099    474655    691-4242    3552   5'.   13   AATGTAAATT   AAAAAAGGACAAC           TTGAACCAGA   ATAAAAAAAAAAAAAAAAAAA   AGTAATTTGA
3L     79A-79A4     0_AE002647   -   1296061   1296335   3964-4238   275    5'.   12   GTATTCTTCT   ATAAGAATGATT            AACTTAAGGA   AAAAAAAAAAAAAAAAAAAAA   GTGTCGCCGA
3L     71A2-71A1    1_AE002602   -   2310696   2310942   3985-4231   247    5'3'  11   CTTTTCATAT   ATATTATGGTT             CACACGCTTC   GCAAAGTAAAATAAAAAAAAA   AAAAAAAAATT
3L     71A2-70F1    1_AE002602   +   2454831   2456256   1469-3245   1777   5'3'  0    TCAAATGGTC                            CTAGCTCAAT   GCACACACAAACTTCTAAAGT   GGGGGGCCAG
3L     71A2-70F1    1_AE002602   -   2456244   2457136   867-1757    891    5'3'  0    CCAATCCCTT                            GTAGGCGTCG   GGCCCCCCACTTTAGAAGTTT   GTGTGTGCTT
3L     70E2-70D5    1_AE002602   -   2754664   2754889   4011-4234   224    ?.    0    NNNNNNNNNN                            TAGCGCGAGG   AAAAATAAAAAAAAAAAAAAA   CTATATCCTT
?      ?            0_AE003217   -   3057      4778      371-2350    1980   5'3'  0    CCAAAGAGCA                            AAACGGTTTG   AGAGGAACAATACGCTCAGAA   CCGATGTATA
2R     60F1-60F1    1_AE002575   -   1384285   1387090   1-2793      2793   .3'   0    CTCGTCATCG                            CTGCACCCGC   ACCTTATAACACCGGTGTGAT   AGGTTCAACA
?      ?            0_AE003083   -   3561      5956      1854-4242   2389   5'.   0    AGTTTGTTTG                            TTGTTGTTCC   AAAAAAAAAAAAAAAAAAAAA   CCTAAGTGAT
?      ?            0_AE003083   -   6239      7731      2377-4240   1864   5'.   0    CCCTTTGTTT                            AAGAGACTAA   AAAAAAAAAAAAAAAAAAAAA   TTCGGTTCAG
3L     70D6-70D3    2_AE002602   -   11779     16027     1-4242      4242   F     0    CTCGTCATCG                            CTGCACCCGC   AAAAAAAAAAAAAAAAAAAAA   TATCTGCACT
3R     96C1-96C     5_AE002708   -   2540088   2540680   3647-4241   595    ?.    0    NNNNNNNNNN                            AGGCGGCTCA   AAAAAAAAAAAAAAAACAACA   TCTTCGAAAT
3L     66A4-2E1     4_AE002602   -   742104    742557    3789-4242   454    ?.    0    NNNNNNNNNN                            CAATCTGGAC   AAAAAAAAAAAAAAAAAAAAA   ATTGCTTCAA
2L     28D5-28D     1_AE002690   +   62413     62899     3751-4241   491    ?.    0    NNNNNGTCTG                            AGTTCAAAGC   AAAAAAAAAAAAAAACCAAAA   CTAAAAACAT
?      ?            0_AE002751   +   65332     66771     163-2565    2403   5'3'  0    AGACTGGAAT                            GACCGCTACA   CATAAGGAATTCCTTAAGCGG   TAGACAGAGC
?      ?            0_AE002700   -   8437      10687     1-2901      2901   .3'   0    TTCGCCGTTG                            CTGCACCCGC   AAGAGATCGATCTTTAACGAT   CTTAATATCA
?      ?            0_AE002909   +   8345      9394      1-1043      1043   .3'   0    CTCGTCATCG                            CTGCACCCGC   AGAATGAACACGGCGCCGGGA   GTTACAATCC
?      ?            0_AE003350   -   11424     11683     3333-3591   259    5'3'  0    TATAAACACT                            GAGTACTTGG   TGCCCTTCGATCACATCTGAA   GCTTAAGGCT
3R     84F2-84F6    0_AE002708   +   493187    493972    3448-4231   784    5'3'  0    TGGCAGGGCT                            TATCCAAGCT   AAGTAAAATAAAAAAAAAAAA   GGGCCGTTGT
2L     35B-35B4     3_AE002690   +   1014543   1014955   1-411       411    .3'   0    CTCGTCATCG                            CTGCACCCGC   ATTGGGAAAGATAGTGTAATA   ATTGTAATGC
?      ?            0_AE002666   +   19436     19803     618-985     368    5'3'  0    AAGTAGAACT                            AAGGGCATTG   CACAGCAAACTACAGAGGCTG   CTTGCTTCTG
?      ?            0_AE002666   +   23774     23853     2882-3246   365    5'3'  0    TACTTTCCAC                            ACGATGGAAG   AAACCCCAGACTTCTAAAGTC   AGAAAGTTTG
?      ?            0_AE002837   +   29153     29441     1315-1599   285    5'3'  0    CGCTCCTCTA                            AATGTATAAA   TCACCGCGATGGTAGAGCACA   TATATCATTA
?      ?            0_AE003199   +   19139     20460     2772-4231   1460   5'3'  6    CTGGAGTCAA   CGATCG                  ATTCACCTTA   AATTAAACCAAAAAAAAAAAA   TCTGTGCAAG
2L     38B5-38C     5_AE002690   +   257134    257503    3875-4240   366    5'.   0    CCCATCCCCC                            AGAACCATCA   AAAAAAAAAAAAAAAAAAAAA   TGTCCTTGTC
2L     38B5-38C     5_AE002690   +   261104    261707    1-602       602    .3'   0    CTCGTCATCG                            CTGCACCCGC   GTTACGCCCGAAGAGATAACT   TTTTTTTTTTT
2R     54C-54B      1_AE002787   +   252102    252621    3716-4235   520    ?.    0    NNNNNNNNNN                            CACTGGCTCA   AAATAAAAAAAAAAAAAAAAA   TTGTTTAGAC
?      ?            0_AE003149   -   301       785       2587-3723   1137   5'?   0    TTTTATTCTA                            CACCGCCACC   AAGCCAACTACTTACACTGGC   Tnnnnnnnnn
?      ?            0_AE002786   +   27120     27932     2874-3689   816    5'3'  0    CCGGAGAGAG                            GATGGAAAAA   ACATCGAAGTCAAAAGAACAC   GTGGAAAAAC
?      ?            0_AE002992   +   8546      8788      1-244       244    .3'   0    TTCGCCGTTG                            CTGCACTCTC   CAACAATGAAGCGCCCGCAAA   GGACGTGCCA
4      102C2-102B   0_AE002796   -   312513    312848    3904-4242   339    5'.   0    AGAACTATCA                            TGGGAACGAA   ATAAAATCAAAGTTTAAAAAA   AGGTTCGGAA
4      102B2-101F   0_AE002796   +   570822    571161    3516-3856   341    5'3'  0    TTCCTAGCAT                            TAAAAGAAAA   CGTAGCGAGCACACTCAAAGA   TTTTGAGAAT
4      101F1-101F1  0_AE002796   +   688508    688761    2713-2976   264    5'3'  0    CTAAATTTTT                            TATTGGAATA   CTAAGATCTGCATACGAAAAT   CGTGAGTACT
?      ?            0_AE002770   +   301       758       900-1361    462    5'?   0    AAGATTCAAT                            AATAATAAAA   ATTCAAGACATGATGCGTAAT   NNNNNNNNNN
?      ?            0_AE002983   -   301       439       3804-4242   439    ?.    0    nnnnnnnnnn                            CTACAGTTAT   AAAAAAAAATAAAAAAAAAAA   AAACTTATAC
?      ?            0_AE003354   +   1832      2536      2984-3724   741    5'3'  0    GTAGAGAATG                            AAATCTTCCA   GTCAACAACTAACACTGGCTC   GCACGACTTG
?      ?            0_AE003035   +   301       368       3873-4240   368    ?.    0    nnnnnnnnnn                            GAGAACCATC   AAAAAAAAAAAAAAAAAAAAA   TTTCGAAGAA
?      ?            0_AE002760   -   43780     44706     1708-2655   948    5'3'  0    ACAAGCGCAT                            CAACCGCCTG   CGAGGCTACTAGCACATTCGC   AAAAAAATAAT
?      ?            0_AE002743   +   5740      6066      1938-2265   328    5'?   0    CATTCGCTTG                            CATACTGGCC   CAGCTCTTACTCAACACCAAA   NNNNNNNNNN
?      ?            0_AE002743   +   81458     82065     1864-3462   1599   5'3'  0    TTAAAAAAAA                            AAAAATAAAA   ATCCCCAATCCAAGCCAGATC   CAACCCAGAT
?      ?            0_AE003183   +   56390     56747     503-861     359    5'3'  0    GAAGGAAAAC                            ACAGAAAGTT   CGGGTAGTATGTGGAGACCTC   CACAACTCCA
?      ?            0_AE003163   +   12867     13300     3105-3535   431    5'3'  0    TTGGGCTTTG                            TAGGACCGGC   ATAAAAGTAAACGAGAAAACA   GACGTTAAAC
?      ?            0_AE003026   +   301       1164      219-1398    1180   5'3'  0    GGGGACCCAT                            TGATCGACAA   CATACTGCGAGCACAATCAAT   GGTACGTTCG
?      ?            0_AE003171   -   6674      7230      1489-4222   2734   ?3'   0    nCACACACAC                            GAAGCATATC   TAAAAGCAATGGTAAAAAAAA   GTCAATCAGC
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Chr	Cyt	Acc	S	Coordinates		Element	Len	Type	D	5' flank	TSD	Start	End	3' flank
?	?	0_AE002709	+	31996	32453	2534-3001	468	5'3'	0	GGAATGCGCT		AGCGTTTTGT	GAAACATGTCTACTAATTCGA	GAGAGAGAGA
?	?	0_AE002927	+	10745	11012	3013-3273	261	5'3'	0	AAAGTCTGCT		TCTTATTCTA	CTATGACAGCAAGCTTGCAGT	CACTTCCACT
2R	101F1-42B	0_AE002778	-	4528	4798	3972-4242	271	?.	0	NNNNNNNNNN		AAAAATACCA	AAAAAAAAAAAAAAAAAAAA	TTCAAATTTA
?	?	0_AE002642	+	12711	13013	3731-4070	340	?3'	0	NNNNNNNNNN		TCTGGTTCTC	TCCGGCGAAAGGACCTACCTA	AATAATACAA
?	?	0_AE003037	+	725	1041	3907-4224	318	5'3'	0	GGATTAAAAA		GAAAGAAAAC	AAAAGAAAATTAAAAAAAAAA	CTTCTGCTCA
?	?	0_AE002736	+	2020	1941	1-222	222	.?	0	CTCGTCATCG		CTGCACCCGC	CACGCGACAACTCTACCTTGA	nnnnnnnnnn
?	?	0_AE002692	+	301	217	4012-4228	217	?3'	0	nnnnnnnnnn		GCGCGAGGTC	GCAAAGTAAAAAAAAAAAAA	CCGCCATTCC
3L	63B8-63C6	1_AE002584	+	255932	256370	3801-4242	442	5'.	12	GCATGGCGAA	AATTAGCAAAGG	AAACGGCTCC	AAAAAAAAAAAAAAAAAAA	CGAGGCAACA
?	?	0_AE002691	+	29366	29619	3970-4220	251	?3'	0	NNNNNNNNNN		GGAAAAATAC	GTAAAAAAAAAAAAAAAAAA	TATCTCTGTA
?	?	0_AE003242	-	13139	13371	3321-3549	229	5'3'	0	GCCGCCCCTT		TCCATCAAAG	GCAAAAATGAGAGCATGTAAC	TGCAACAACA

Full-length elements: 2/15
5' truncated elements: 7/10
3' truncated elements: 0/9
5'3' truncated elements: 2/24
Unfinished elements: 25
Total number of elements: 94
Total length of elements: 155644
TSD lengths (min/max): 0/35

G

Chr	Cyt	Acc	S	Coordinates		Element	Len	Type	D	5' flank	TSD	Start	End	3' flank
2R	60D16-100C	1_AE002575	+	976898	978814	2456-4346	1891	5'.	9	TTCGCACCAG	AGCGAGGGA	AAAAAGGCGC	CACAAAAAAAAAAAAAAAAAA	TTACCCCATT
2R	60F1-60F1	1_AE002575	+	1362746	1366567	633-4346	3714	5'.	0	CAGCACCCCC		ATCACCCCAA	CGCTAAAAAAAAAAAAAAAAA	CTAAATTGAT
2R	60F1-60F1	1_AE002575	+	1366945	1371041	1-4343	4343	F	8	ATATGCGTCA	CTAAATTG	ACAGTCGCGA	TCGCTAAAAAAAAAAAAAAA	ATGACGAGGT
2R	60F1-60F1	1_AE002575	+	1371143	1374812	1-3622	3622	.3'	0	CACTAAATTG		ACAGTCGCGA	CATCATTCAAAGCCAGCTGCA	CTTATCGAGG
2R	60F1-60F1	1_AE002575	+	1374999	1375640	1-650	650	.3'	0	CACTAAATTG		ACAGTCGCGA	GGAATCGCTCCAAAAACCAT	TGTTCGAGTT
3R	84E-84E8	0_AE002708	-	387456	390424	1334-4345	3012	5'.	7	TTTTATTTGT	ACTACAG	AGATGCGCTC	GGCTACACAAAAAAAAAAAA	CTAGTCATCC
?	?	0_AE003204	+	6277	9451	885-4281	3397	5'3'	0	GACACGGCCA		ACTGTAAGGG	ATGTCCTCAATCCAAACACTT	GTCGAAAATG
2L	38B5-38C	5_AE002690	-	79489	79806	3088-3412	325	5'3'	0	GGCTTTTATC		TGCTGGAAAT	TAAAGAGTTTCAAGTCAGATG	TTCAGATAAT
2L	38B5-38C	5_AE002690	-	85508	85995	3187-3674	488	5'3'	0	GGGAGGATTT		TCAGGCGATT	ATCGTGATCAACGCTGATAAA	AAAAATAGTG
2L	38B5-38C	5_AE002690	-	86152	86691	3805-4346	542	5'.	0	AGGAAGCGTA		CCAGGCCAAC	CTACACAAAAAAAAAAAAAAA	CAATTTTTTG
2L	38B5-38C	5_AE002690	-	124800	127295	888-4273	3386	5'3'	0	TGGGGCATAA		GTCAGGAACT	AAGTTAATGCAACCACCCCCC	CCCCCCCCCC
X	3D5-3D	1_AE002566	-	363223	363454	888-1120	233	5'3'	0	TGGGGCATAA		GTCAGAGACC	TCTAGAACACCGCTGTGTAAA	AGAAGTGACA
X	3D5-3D	1_AE002566	+	365430	365624	2432-2633	202	5'3'	0	TTGAATGTAT		CCAGCAAATT	AACATAATCTGTTGCAAGTCA	TATCAGGAGG
X	3D5-3D	1_AE002566	-	365658	368318	377-4186	3810	5'3'	0	CCCGCACCAA		AGGCCCTACA	GCCTGCAGATAACGCACCCGC	ACCGGCGACG
X	3D5-3D	1_AE002566	-	368925	371275	377-2726	2350	5'3'	0	CCCGCACCAA		AGGCCCTACA	AAGCCGAAAGAGCTGAAGCGT	TTTTTTTGGA
X	3D5-3D	1_AE002566	-	371876	373848	377-2726	2350	5'3'	0	CCCGCACCAA		AGGCCCTACA	AAGCCGAAAGAGCTGAAGCGT	TTTTTTGGAG
X	3D5-3D	1_AE002566	-	374207	374726	888-1409	522	5'3'	0	TGGGGCATAA		GTCAGAGACC	GAATCCCGAGCTCCTCGTGGA	TGGCGGAATA
2L	32F2-33A1	2_AE002690	-	351325	353688	2011-4346	2336	5'.	0	AAACAGCGCC		CCAGCAGAGC	AAAAAAAAAAAAAAAAAAAAA	TTTTTTCCCG
2L	34D4-34D4	2_AE002690	-	2635507	2636637	3237-4346	1110	5'.	0	TCCCCATCTC		ATTTTGAGAT	AAAAAAAAAAAAAAAAAAAAA	CATACATATA
?	?	0_AE002837	-	50563	52096	2838-4346	1509	5'.	0	GAGTCCATGT		CTCCTAGCCC	AAAAAAAAAAAAAAAAAAAAA	CCAATATTTT
?	?	0_AE002837	-	57520	57991	1658-2161	504	5'3'	0	GCTTTTGGAA		CCGAGATCCA	AGCGCAGTAAGCATGCTCTTA	AACATCCCCG
?	?	0_AE003213	-	3502	3923	1298-1722	425	5'3'	0	GGACATGTTA		CTCCCGCGAC	AAACCACCCTTCCGGCAGAGC	AGCAATCCTC
?	?	0_AE003213	-	10650	12528	1823-4339	2517	5'.	0	TTATTTTTCC		ATCCTTCAGG	ATGAACGTTACAACAAAAAAA	TTTATATATG
?	?	0_AE002938	-	301	480	2093-2498	406	5'3'	0	GACTTCAACG		CTGGATTTTG	ATCTGGTTCTTCTCGCGGAAA	CGTGCAGAAG
?	?	0_AE002938	+	4560	4930	3969-4341	373	5'.	0	TTTGTGTAGC		AGCGATTTCA	AAAGGCTACACAAAAAAAAAA	CCCCATTTGT
?	?	0_AE002938	+	6177	6544	3969-4340	372	5'.	0	TTTGTGTAGC		AGCGATTTCA	AAAGGCTACACAAAAAAAAAA	CCCCATTTGT
?	?	0_AE002938	-	9703	9936	888-1120	233	5'3'	0	GTGGGCATAA		GTCAGAGACC	TCTAGAACACCGCTGTGTAAA	ACACACGAGC
?	?	0_AE002772	+	7084	8632	1152-3396	2245	5'3'	0	GACCATAAAA		GAAAAAAAGG	AATCCTTTAAGGAGGGTAGAG	CTTCTTCGGC
3L	78C9-78A	0_AE002647	+	1020493	1021392	3468-4346	879	5'.	0	AAATACTTTT		GTCCTTGGTC	CAAAAAAAAAAAAAAAAAAAA	TTCTAAAACT
2L	38A1-38A1	4_AE002690	+	2648729	2649219	3855-4346	492	5'.	0	TCCACTGGCT		CCAAGCTGCG	CTACACAAAAAAAAAAAAAAA	CAATTTTTTG
2R	38A1-42B	0_AE002778	+	301	625	1357-4346	2990	?.	0	nnnnnnnGTG		ACGCAGCACC	AAAAAAAAAAAAAAAAAAAA	CTGTTACTGT
2R	41F11-41C	0_AE002769	-	1123417	1123627	4037-4248	212	5'3'	0	CTTATAACCA		AGAAAGAACT	AAAATACAGTACTTCTTATTC	TTATTATTAT
?	?	0_AE003021	+	21336	22057	934-1753	820	5'3'	0	TTGGCAGGAA		TAGGGATATT	GCAGCCATGCTCATCAGGAGC	AAGTGGCAAG
?	?	0_AE002712	+	2049	2361	4013-4337	325	5'.	0	CAACAGCAAG		CATGCAATTA	AAACGCACGCTACAAAAAAAA	GTAGTATAGG
?	?	0_AE003024	-	58479	58755	1450-4346	2897	5'.	0	GGAAGGAATG		TGGAAAGGAT	CAAAAAAAAAAAAAAAAAAAA	ATTTTTGTCCG
?	?	0_AE003383	+	2982	2926	2040-2283	244	5'?	0	AGAATGGATT		CAATTGGGAG	ACTCTGGACGCTGTCCTCTCT	Gnnnnnnnnn
?	?	0_AE003092	+	301	296	4048-4346	299	?.	0	nnnnnnnnnC		GGATTCATGG	GGCTACACAAAAAAAAAAAAA	GAACAGAAAA

Full-length elements: 1/0
5' truncated elements: 2/12
3' truncated elements: 0/2
5'3' truncated elements: 0/17
Unfinished elements: 3
Total number of elements: 37
Total length of elements: 56025
TSD lengths (min/max): 7/9

Idm

Chr	Cyt	Acc	S	Coordinates		Element	Len	Type	D	5' flank	TSD	Start	End	3' flank
3R	98B8-98B	6_AE002708	+	1937821	1943206	1-5374	5374	F	13	TCTGTATTAT	ATATTCTATTTAT	CAGTACCACT	TCATAATAATAATAATAATA	GGGCAAAATA

Chr	Cyt	Acc	S	Coordinates		Element	Len	Type	D	5' flank	TSD	Start	End	3' flank
3R	98B-98C	6_AE002708	-	2277574	2282959	1-5374	5374	F	12	TTTTAAAAAC	ACAAACCAAACG	TCAGTACCAC	TCATAATAATAATAATAATA	AGTAAATCTC
X	11A4-11A6	0_AE002593	+	1371575	1376962	1-5374	5374	F	17	GGGCAATGGA	AATATTTCTAATGTACA	GTACCACTTC	ATCATAATAATAATAATAAT	AAGTCTGTTG
X	19F-19E3	0_AE002620	+	544610	549995	1-5374	5374	F	16	AATCATGATA	AATAATACAAGGGCTG	GCAGTACCAC	TCTATCATAATAATAATAAT	TGAATCTATA
X	4F10-5A6	1_AE002566	+	2290140	2294096	1424-5374	3951	5'.	13	TTGTTGAGCA	ATCTTAGTAATGA	CCTAACCGTT	AATAAATAAAAAAAAAAAAA	ATATATGGGC
2L	23A2-22A1	0_AE002638	-	2279164	2280940	3604-5374	1771	5'.	11	TTTATTTGCT	ATATTTCATGC	ATCGACGATA	TCATAATAATAATAATAATA	CTGCCTGCAC
X	2B-2B6	1_AE002566	-	1322872	1324609	3641-5374	1734	5'.	11	GCGTCAATTT	ATATTAAATAT	CCTATCCCTA	TCATAATAATAATAATAATA	ATGTATTTTC
4	101F1-101F1	0_AE002796	-	708395	708687	5082-5374	293	?.	0	NNNNNNNNNN		CAAGATATAT	CATAATAATAATAATAATAA	TCAGTGATCA
4	101F1-101F1	0_AE002796	+	713552	714000	1-449	449	.?	0	GTGATCAATT		CAGTACCACT	CTAACAAAAATTGCAGATGA	NNNNNNNNNN
3L	78C9-78A	0_AE002647	-	1024609	1029997	1-5374	5374	F	14	TAACTCTTAC	ATTTGCTTGCATTC	ATTCAGTACC	TCATAATAATAATAATAATA	TAATTATTCA
X	12C1-12D1	1_AE002593	-	134666	137893	2159-5374	3216	5'.	9	AGCCAGAATT	ATAAATAAC	AACACTATTC	TCATAATAATAATAATAATA	TGAATGGTTT
X	12F1-12F1	1_AE002593	-	815649	821037	1-5374	5374	F	14	AGTTTCCATT	TAGTTTGTGTTATT	CAGTACCACT	TATCATAATAATAATAATAA	GCCATGCTCA
?	?	0_AE003041	-	7817	9675	3505-5374	1870	5'.	0	TTGACATTTA		TTCAAAATTC	CATAATAAATAAATAAATAA	AAACAGAGGA
?	?	0_AE003172	+	301	1983	708-2385	1678	?3'	0	nnnnnnnnnA		ACAGTCCGAG	GAACAACTTGCCTGGATAAA	ATTAAGCCGC
?	?	0_AE003173	-	3282	3966	4687-5374	688	5'.	0	TGCACCTAAA		ATTAAGGAAT	CATAATAAATAAATAAATAA	ATCTTCAACG
?	?	0_AE002862	-	301	1011	1376-2445	1070	??	0	nnnnnnGAAG		ATAATCTATC	AACAAAAACAACTTGCCTGG	Annnnnnnnn
3L	66E2-66D14	3_AE002602	-	2462695	2463202	4867-5374	508	?.	0	NNNNNNNNNN		CGAACACCTC	TATCATAATAATAATAATAA	TTAACCCATT
3L	66E2-66D14	3_AE002602	-	2467763	2468082	1-320	320	.?	0	AACCCATTCT		CAGTACCACT	TCACCATTCATCATAAAAAA	TNNNNNNNNN
?	?	0_AE002809	-	20213	20409	3423-3624	202	5'3'	0	TGAAGTTGGG		TTCAGCTAAC	TACAATATGCAAGAATATGT	AAGAAATGTA
3R	86A-86B1	0_AE002708	-	2525553	2526062	1487-2000	514	?3'	0	NNNNNNNNCT		ACCGTTACAC	AAAAGACTCAAAAATTGAAT	CTAAAGCTAA
3R	86A-86B1	0_AE002708	+	2530283	2530563	5096-5374	279	?.	0	NNNNNNNNNN		CAACACCAAC	TCATAATAAATAATAAATAA	AATAAACATA
2R	42A2-41F9	0_AE002769	+	289211	289417	5167-5373	207	5'.	6	TATAAAGTAT	ATAAAT	TAAAAAATTA	TATTCTATCTATCATAATAA	ATTCCTGATC
2R	42A2-41F9	0_AE002769	+	305400	305955	4810-5372	563	5'.	0	TTTCGGCGGC		CGAACAATAT	TATACAGCAAAGAACCAAAT	CTAAAATACT
2R	41F11-41C	0_AE002769	-	978283	978658	1-383	383	.3'	0	TGCAAAACAA		CAGTACCACT	CGAACAAGAGACGGCAACCT	AAGACCGTCT
?	?	0_AE003402	+	301	554	2807-3358	552	?3'	0	nnnnnnnnnA		ATAGCCCAAA	ACTAAAGCCACCTCTAAAAA	GAGGCTTGTA
2R	44D-44C1	4_AE002787	-	264761	265492	4642-5373	732	5'.	0	AAAAAAAGGG		TAACAAACTA	ACGAGAATTTTATGAAAGTA	TTAAACTTAA
3L	64C11-64C9	5_AE002602	+	67546	67916	5004-5374	371	?.	0	NNNNNNNNNN		CCAACTTGCC	TATCATAATAATAATAATAA	TAATTTCTTT
2L	39C3-?	5_AE002690	-	1341063	1341421	1544-1908	365	5'3'	0	GTTGTATTAC		AACGATGGAC	CATTTAATATACAACAAACA	TGTAGGGGTA
?	?	0_AE003036	-	2667	3082	1555-1970	416	?3'	0	NNNNNNNNAT		AATCCAATTT	AGGGCTCACCAACAACAATT	TTTTTAAACA
?	?	0_AE003307	+	12927	13016	33-398	366	5'3'	0	TCTCGGTTCA		GTACTACCCA	TGACCATCAACACAGCCCAA	TTGACCGCAA
?	?	0_AE003055	-	1713	2027	2548-2865	318	5'3'	0	TCCAAATATG		GCGCTTTATT	TTATTGCCATATACCACAAA	ACAAGGCCAA
?	?	0_AE002736	+	301	326	5052-5374	323	?.	0	nnnnnnnnnA		ACTCATGCCC	CATAATAAATAATTAAATAA	AACGCAATAA
?	?	0_AE003023	-	301	248	4917-5165	249	5'?	0	GAATCCCTCA		ACCACATGCG	CAAAAACTCATACTTTTCCT	Cnnnnnnnnn
?	?	0_AE002631	-	1699	1702	5077-5374	298	?.	0	nnnnnnnnnn		CCAAACAAGA	TATAAAAAAAAAAAAAAAAA	TTATAAAATT
?	?	0_AE003220	-	301	320	4789-5104	316	5'?	0	AATTCACTGT		AACAGTTAGG	AGACATATTTAACAACACTA	Annnnnnnnn
3R	87F2-50D	1_AE002708	+	2606054	2606376	853-1175	323	5'3'	0	CTAATTGTAA		ACAAACGAAA	CAAATCCGGAGACTACACAC	CACCATAGGT
2L	21B7-21B3	1_AE002638	+	1689760	1689981	5153-5374	222	5'.	0	TTCTCAGTTA		CATACATTAT	CATAATAAATAATAAATAAA	ATAATTAAAC
4	102A-101F	0_AE002796	-	642597	643877	4059-5374	1316	5'.	0	ACATATTTTA		AATACTCCCT	TATTCTATCTATCATAATAA	ATAAATAACT
4	102A-101F	0_AE002796	-	645198	646803	2017-3720	1704	5'3'	0	TAGTTGGAGT		TCCTCAAAAC	CAAGATAAGCTGCAACAACT	GGAACGAACT
3L	102A-77B3	0_AE002647	-	3408	4510	36-1176	1141	5'3'	0	TCCGAAAGCC		CCACCCAGTT	TTCGAGCCGATCAAAACTCT	GTATAGTTAG
?	?	0_AE002918	-	14117	16217	1-2169	2169	.3'	0	ACATTTACAT		CAGTACCACT	CTCCTCGCCCATTGTCCTAA	TTGTGGCAAC
?	?	0_AE003173	-	5427	6586	61-1286	1226	5'3'	0	AGTCTATCTA		CGTGGCACAC	TAGAAGACATGGATAAACGA	AAAACGCAAA
?	?	0_AE002931	-	11437	14039	1422-4261	2840	5'3'	0	ACCAACATTT		CTACAAACCT	GAACTCCTTTTCCCCTAACC	TTTTCCTTCC
?	?	0_AE002809	-	11236	12713	3501-5374	1874	5'.	0	TAACGCTGCC		TGCGTGCAGC	TTGTCATAATAAATAAATAA	ATATTTATTT
?	?	0_AE003063	+	6436	7529	4241-5371	1131	5'.	0	ACTTGGAACC		AAAACTTCAT	CTATCATAATTAATAAATAA	ATCTCACATA
2R	46A-46B1	3_AE002787	-	1958743	1959845	36-1176	1141	5'3'	0	TCCGAAAGCC		CCACCCAGTT	TTCGAGCCGATCAAAACTCT	GTATAGTTAG
?	?	0_AE003181	+	12276	13376	4830-5369	540	5'.	8	ATTATATTAT	AATAAACA	GCAGTCCATG	TCTATCTATCATAATAAATA	TTGTCATCTC
?	?	0_AE002603	+	43577	44184	3056-3698	643	5'3'	0	AACAATCTGA		ACACCAAACC	GTTCCTATCGTTACTTCAAA	AAATTTTAGG

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Full-length elements:  6/0
5' truncated elements:  6/8
3' truncated elements:  0/2
5'3' truncated elements: 0/11
Unfinished elements:  15
Total number of elements: 48
Total length of elements: 72516
TSD lengths (min/max):  6/17
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Jockey

Chr	Cyt	Acc	S	Coordinates		Element	Len	Type	D	5' flank	TSD	Start	End	3' flank
2L	25A8-25A5	0_AE002638	+	15360	20359	1-5049	5049	F	12	AAGAGCAAGT	AAGATTTGCATT	CATTCGCATG	AATAAAAACATCATCGTAAAT	GCATACTTTT
X	20A5-20	0_AE002620	-	399726	404726	1-5049	5049	F	15	CTAGACTCCT	ATACAGAGGTGGTCA	CATTCGCATG	ATAAAAAAAAAAAAAAAAAA	AAAGTATTTA
2R	43B2-43B1	4_AE002787	-	1434026	1439023	1-5047	5047	F	13	TTTTGCCATG	TCTTCCGAGCCAG	TCGCATGGGA	AAAAAAAAAAAAAAAAAAAA	AGCAGGAAAT
3L	65A-64F	4_AE002602	+	2233035	2235616	1-5048	5048	F	10	TTACGTATTA	AAGGAAATAC	ACAGTCGCAT	AAAAAAAAAAAAAAAAAAAA	GACTTATTCC
3L	64E-64D	4_AE002602	+	2698807	2699057	4791-5049	259	5'.	11	TTAATGTTTT	ACTGTTATGGT	ACACCACCCT	AAATCTAAAAAAAAAAAAAA	TACTGTACAA
2L	30A8-30B	1_AE002690	-	1440270	1443165	2114-5049	2936	5'.	3	TTTACTTGTT	ACA	GGATATTCCT	TCGAAATAAATGTAAAAAAA	GTGCTAATGA
3R	87F2-50D	1_AE002708	-	2747838	2751352	2286-5049	2764	5'.	12	AAAAGCGATC	ATACTTGTGATT	CTGACACCTA	GAGAAAAAAAAAAAAAAAAA	ATGCTTTTTT
3L	69F6-69D	2_AE002602	+	1387337	1389607	2746-5049	2304	5'.	0	TTCTAATAAA		ACATACCAAA	AAAAAAAAAAAAAAAAAAAA	TGCTTTAAGT
3L	68C5-68A8	2_AE002602	-	2928345	2931504	1852-5049	3198	5'.	13	TGTGGTTTAT	AATCATTAAGAGT	AACATTAACA	AAAAAAAAAAAAAAAAAAAA	GACCGTCGGT
2R	56F9-56E	0_AE002787	-	1000761	1003994	1777-5049	3273	5'.	12	TCGCTCAGTA	AGAAATCATGAT	CATACCAGCT	AAAAAAAAAAAAAAAAAAAA	GACGAAATGG
2R	55E4-55C	0_AE002787	+	2381230	2381775	1-554	554	.?	0	AATAGTTCCA		GGGAGATGAG	AATGCAAGTGTTACCTGCACT	NNNNNNNNNN
2R	55E4-55C	0_AE002787	+	2383635	2383854	4821-5049	229	?.	0	NNNNNNNNNN		TTTGCCTAGA	AAAAAAAAAAAAAAAAAAAA	GGACAACATG
2R	55A4-54F3	0_AE002787	-	2696250	2696501	4790-5049	260	5'.	13	TCAGGCAATC	ATATAAAGTTAGC	CACCACCCTC	AAAAAAAAAAAAAAAAAAAA	AGTTGTAATC
2R	58D1-58D6	0_AE002575	-	1569356	1571075	3291-5049	1759	5'.	10	GCCACAGACG	ACACACATGG	ATACTTGGAA	GTAAAAAAAAAAAAAAAAAA	GACCCCAATA
2R	58D1-58D6	0_AE002575	+	1580018	1580360	4694-5049	356	5'.	8	CTCAGTGTGG	AATTTACA	TTTTACACCC	AAAAAAAAAAAAAAAAAAAA	TCCGTTTCGG
2R	58E4-58E4	0_AE002575	-	1745421	1748885	1546-5049	3504	5'.	11	GAATCGTGTT	ACCCTTATGTC	TGCGCCCAGG	AAAAAAAAAAAAAAAAAAAA	GACTCGGGTT

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2R   59A-59B1      0_AE002575   +   1994639   1994979   4696-5049   354    5'.    14   TTTCCTAGCT   TTAAGAGCTGAGCA     CCCCAACAGC   CATCAAAGAAAAAAAAAAAA    TATCGATTTA
3R   85A11-85B9    0_AE002708   -   995194    997370    1-2190      2190   .3'    0    CATGGTCGCA                      GGGAGATGAG   TTACTATGTTATATCAACTAT   TATAATTCTC
3R   85D2-85D10    0_AE002708   +   1601649   1601987   4696-5047   352    5'.    11   TCTGGCTTTC   ATTATGACCGT        GTACACCCCA   AAAAAAAAAAAAAAAAAAAA    AATACTGTCA
2L   22A4-22A3     1_AE002638   +   264926    265175    4792-5049   258    5'.    13   TTGCCTTGGC   TTGCTTTTCCTTT      CACCACCCTC   CATCATCGTAATCGTAAAAA    TCGGGTTTGT
2L   21B5-21A3     1_AE002638   -   1813836   1818834   1-5049      5049   F      12   AAAACGAACA   ATATTGAAAAGC       ATTCGCATGG   AAAAAAAAAAAAAAAAAAAA    GAAAACAGGA
2R   50C2-50A12    2_AE002787   +   1138779   1139028   4792-5049   258    5'.    12   TCAACGATCG   ATTGATAATATT       CACCACCCTC   AAAAAAAAAAAAAAAAAAAA    GCCTAGGCTT
2R   49D6-49D1     2_AE002787   -   1900367   1905364   1-5049      5049   F      13   AATCCTTTGG   AGACACACACACA      TTCGCATGGG   ATAAAAACATCATCATAAAAA   CGCACACAAA
3R   84A2-?        0_AE002699   -   1182956   1187957   1-5049      5049   F      11   AAAGCCGGCT   GTGGTTACACT        CATTCGCATG   ATCATCGAAAAAAAAAAAAA    GCTAAGTGCA
X    4D3-4E1       1_AE002566   -   1510089   1510348   4782-5049   268    5'.    10   TTTGTTTTAT   ACTGCTTGCA         CACCACCCTC   AAAAAAAAAAAAAAAAAAAA    GTTTCTACAA
X    4D3-4E1       1_AE002566   -   1541460   1546459   1-5049      5049   F      12   TTTATCTAGT   GTACATTTATTT       TTCATTCGCA   AAAAAAAAAAAAAAAAAAAA    GGCTAACTGC
X    4D3-4E1       1_AE002566   -   1601547   1601894   4691-5049   359    5'.    13   CTTTCCGTCC   CTTAAATGTGAAT      CCCCAACAGC   AAAAAAAAAAAAAAAAAAAA    GCAAATATAT
X    4F10-5A6      1_AE002566   -   2148304   2149457   3863-5049   1187   5'.    13   GTTTCGGTTG   TTGATTGGAAGCG      GCTGTTCCCG   AAAAAAAAAAAAAAAAAAAA    AAGAACCCCT
X    7A-7B3        2_AE002566   -   1284674   1286092   3598-5049   1452   5'.    10   TTTTGTCTGT   ACATTAGCGA         TGCCCATCAG   GACAAAAAAAAAAAAAAAAA    CGCATCGCAG
X    7A-7B3        2_AE002566   +   1506150   1506489   4696-5048   353    5'.    14   CAATCGCGAT   ATCAGTTTGTAACT     TGTACACCCC   AAAAAAAAAAAAAAAAAAAA    GCTAGAAATC
X    7B3-7C3       2_AE002566   -   1587519   1587768   4786-5044   259    5'.    11   ACTCCATCTT   ATGGAATATGC        TTTGACCTAG   AAAAAAAAAAAAAAAAAAAA    AGCAGTTTGC
X    8B-8A5        2_AE002566   +   2716702   2717041   4697-5049   353    5'.    9    GCTATTGTCG   ATCAATTGG          AGTACACCCC   AAAAAAAAAAAAAAAAAAAA    TAGCATTTAC
3R   97B-97D1      6_AE002708   +   853770    854071    4737-5049   313    5'.    12   GCGTATACGC   ATGTTGTCAACT       TGGTCAATGC   AAAAAAAAAAAAAAAAAAAA    GGTTGGGCAG
3R   98B-98C       6_AE002708   +   2462170   2465119   1-5049      5049   F      12   CATCTGGCTT   AAAATATTTACG       ATTCGCATGG   CAAAAAAAAAAAAAAAAAAA    GTCTCTTCGG
3R   98C-98D       6_AE002708   +   2511503   2511842   4697-5049   353    5'.    15   ATGTACACGT   AGGTAAAAAGAAGTC    GTACACCCCA   AAAAAAAAAAAAAAAAAAAA    ATTTTGTTGT
3R   98E2-98E      6_AE002708   +   2989759   2990342   1-594       594    .?     0    ACCGCAAATA                      GGGAGATGAG   CAACATGATCTGACTCCTACA   ANNNNNNNNN
3R   98E2-98E      6_AE002708   +   2994173   2994423   4791-5049   259    ?.     0    NNNNNNNNNN                      ACACCACCCT   AAAAAAAAAAAAAAAAAAAA    CCCGCAAATA
3R   35F-88B1      2_AE002708   +   477783    479194    3606-5049   1444   5'.    11   GCTGTGGTTT   CCAGCTGTGCC        CCCATCTCTG   TAAAAAAAAAAAAAAAAAAA    GACAGACGCC
3R   99A6-99B5     7_AE002708   +   516094    516344    4791-5049   259    5'.    0    TTGTTACCTT                      AAACCACCCT   TCAAATAATAAAAACATCATC   GTAATCGTTA
3R   99A6-99B5     7_AE002708   +   603004    604199    3821-5049   1229   5'.    13   TATCATATTG   ACGCTGCGTGGGA      TTGACAGAGT   GCCAGGCGGCGCTGCAAAGTA   ACCACAAAGC
3R   99B5-99B9     7_AE002708   -   849523    850001    1861-5049   3189   ?.     0    NNNNNNNNNN                      TGTGCAGGCT   TAAAAAAAAAAAAAAAAAAA    CAGAGCCTTT
3R   99B5-99B9     7_AE002708   -   851043    851635    1-601       601    .?     0    TTGAGTCGCA                      GGGAGATGAG   TCTGGACTCCTACATACACTG   NNNNNNNNNN
3R   99F11-99F6    7_AE002708   -   1669332   1669663   4704-5048   345    ?.     0    NNNNNNNNNN                      CCAACAGCCT   AAAAAAAAAAAAAAAAAAAA    TGAATTTCTT
3R   99F11-99F6    7_AE002708   -   1671104   1671637   1-540       540    .?     0    TTCATTCGCA                      GGGAGATGAG   CAGCAGCAACACCAATGCAAG   NNNNNNNNNN
3L   67C-69        3_AE002602   -   1679238   1679701   1-470       470    .?     0    TATAGTCGCA                      GGGAGATGAG   GTGCAGTTGTTTCCCCTAACC   NNNNNNNNNN
3L   67C-69        3_AE002602   +   1684039   1684340   4737-5047   311    ?.     0    NNNNNNNNNN                      CAGCTGTGGT   ACATCAAAAAAAAAAAAAAAA   TGTACATATA
3L   67C-69        3_AE002602   +   1688080   1688328   4793-5049   257    5'.    14   TTATTTACTT   ACACTATACCTTAC     CACCCTCATG   AAAAAAAAAAAAAAAAAAAA    ATTTGCGGAT
3L   67A-66F5      3_AE002602   +   2040451   2041057   4428-5049   622    5'.    15   TGCAGCTGCC   ACTATGCTATTCCCT    GTCCATATTG   AAAAAAAAAAAAAAAAAAAA    AGTTTTTCCC
X    12A-12A3      0_AE002593   +   2625065   2626133   3946-5049   1104   5'.    0    GTCATTGCCA                      AGAAATCTGC   AAAAAAAAAAAAAAAAAAAA    GGGATGAAAA
X    12A-12A3      0_AE002593   +   2626347   2626925   4454-5048   595    5'.    0    ACCTGAATAT                      TCCAAGGTCA   CTAAAAAAAAAAAAAAAAAAA   GCGTCTTAAC
2L   38A1-38A1     4_AE002690   +   2586207   2587103   4121-5048   928    5'.    11   TTTCCCTGCG   TAGACCATGGC        AGTAAAAGTA   AAAAAAAAAAAAAAAAAAAA    GACCACTGCT
3L   61D2-61E      0_AE002584   -   919237    920285    3951-5049   1099   5'.    13   CTGAAATTTT   ATGCTTCAACTTT      TGCAGCTGGA   AATAAAAACATCATCGTAATA   CTTGCTGTTG
?    ?             0_AE002818   -   652       1015      2746-3413   668    5'?    0    TCACTCATTG                      ACTTGCCCAT   AAGCTGCCACTTAAGAAAGCT   nnnnnnnnnn
?    ?             0_AE003183   +   23192     23935     1438-2216   779    5'3'   0    AAAGCAAGCC                      AAATAACTCA   AGGATATCGTGTGCATCATGC   AGTGGTAACA
X    19F-19E3      0_AE002620   +   419801    420795    4019-5049   1031   5'.    11   ATACGTATTT   AGCCCAAAAGC        CACCTACGCT   AAAAAAAAAAAAAAAAAAAA    AGTAAGCATT
2R   47F18-47D1    3_AE002787   +   690985    691573    21-616      596    5'?    0    AGCAAATTCA                      GACGTGTTCA   ACACTGATTGCACAACCGTGA   NNNNNNNNNN
2L   38E6-39A      5_AE002690   -   842721    843185    1-471       471    .?     0    TACATTCGCA                      GGGAGATGAG   TGCAGTTGTTTCCCCTAACCT   NNNNNNNNNN
X    8D9-8E4       3_AE002566   +   302101    302642    3595-4140   546    5'?    0    TACTCATTAT                      TGCAGGCCCA   AAGTAAAAGTATCCTGGCTGC   NNNNNNNNNN
2R   54B1-54B2     1_AE002787   -   465053    465403    4686-5049   364    5'.    11   TTTGTGACAG   ATAAAAAATTA        TTGTACACCC   AAATAATAAAAACATCATCGT   CGTTTTTGAA
2R   54B2-54A1     1_AE002787   +   590026    590409    1-389       389    .?     0    CACATTCGCA                      GGGAGATGAG   TGGGTGCGATAAATTTGAGAA   NNNNNNNNNN
2R   51E-51C       1_AE002787   +   2732683   2732918   4807-5049   243    5'.    11   ATCTTAGTTT   TCTGGTTTTTC        CCCCTAACCT   AAAAAAAAAAAAAAAAAAAA    TCCAATTTAA
2R   42A2-41F9     0_AE002769   -   333319    333942    2973-3613   641    5'3'   0    AGAGAGTTCC                      GAAGACTTTG   CTTACAGGTCTACTCCCTTCC   CTGGGAAAAA
2R   42A2-41F9     0_AE002769   +   333880    334113    2603-2842   240    5'3'   0    CAGTTGGCAA                      TCATCCCTTG   GACGCGGTGCATATTGATAAT   AAATAAATTA
2R   41F11-41C     0_AE002769   -   853426    853701    2992-3268   277    5'3'   0    GCTGCTCTTC                      TGCTGCACCG   CAACGGCCTTGTACACCCTAT   ACCTATGCAT
2R   41C-?         0_AE002769   +   1276505   1276761   3729-3983   255    5'3'   0    CCCCTCCTTT                      ACCCCTAAGC   AATTGCAGCTGGAAGTGTCCT   AGGCCCTACC
?    ?             0_AE002837   -   53916     56726     2777-4712   1936   5'3'   0    TGGCGTGAAC                      AAAACCAATC   TTAATGCACACCCAAACAGCC   TTTTCAGAAA
?    ?             0_AE002931   +   15143     15395     2785-3039   255    5'3'   0    ATGTCATTGA                      TTTTGAATTA   CGGATTCACTGTTGCAGTGGC   GCTGCAAAAA
3L   73A3-73A3     1_AE002602   +   784974    785438    4570-5049   480    5'.    0    AGCATCTATT                      CTTAAAACGA   AACATCATCGAAATAAAAAAA   GAGAAAAAAA
3L   72A3-71E3     1_AE002602   -   1379462   1379910   4586-5049   464    5'.    15   CTCCGTGTCG   TGGAGACGCGGCGGC    TCGGGGGCTC   AAAAAAAAAAAAAAAAAAAA    AAGTGACGTA
4    102D1-102D6   0_AE002796   -   76872     77077     3997-4202   206    5'3'   0    GTTCTGATAA                      TAGGCCCCAT   GCTGAAAAGTGTGCCAATGTG   ACAGGTAGTT
4    102B8-102B1   0_AE002796   +   373898    374193    4454-4755   302    5'?    0    ACCTGAATAT                      TCCAAGGTCA   TGCAGCTGTGGTCAATGCTGA   NNNNNNNNNN
?    ?             0_AE002830   -   743       1530      3759-4657   899    5'3'   0    GTGCACGGTG                      TTTGCTGTAG   ACCAAAGCTCAGAGCATCGCT   GAAAAGTACA
?    ?             0_AE002673   +   3168      3747      1532-2130   599    5'3'   0    CAAATCTGTG                      ACACTAATAA   CTTCGGTTATTCCTTAGCGAT   AGACTTGTCA
2L   34C-34C7      2_AE002690   -   2517774   2518303   4504-5049   546    5'.    13   AAAAATATAC   ATGAAAATTAATT      CTGCAGGTAT   AACATCATCGTAATAAAAAAA   TGTGCACCAT
X    15B-15D6      2_AE002593   -   112151    112491    4696-5049   354    5'.    12   TCTAGACTTT   CTTAAGAAACCC       TTGTACACCC   AAACATCATCGTATTATTAAA   CACCTCGAAT
X    16A1-16D1     2_AE002593   -   607216    607465    4792-5049   258    5'.    12   GCTGATGCGG   ATCCGAGGAAAT       TCACCACCCT   TAAAAAAAAAAAAAAAAAAA    CAGAGAACTC
X    17E9-18C1     2_AE002593   -   2645065   2645772   4541-5049   509    5'.    16   GCTGTCCTTT   ACACACAAACTCGCAC   TAAGATCCGG   AAAACATCATCGTAAAAAAA    ACACAGACAC
3R   95D9-95E1     5_AE002708   -   1287700   1288041   4696-5049   354    5'.    13   CCATTCTGCT   ACTCCTTCGCTGT      ACACCCCAAC   AAAAAAAAAAAAAAAAAAAA    CACTTAACCA
3L   63D3-63E1     1_AE002584   -   449460    449800    4696-5049   354    5'.    11   CCGTGTGCGC   ATTTTGTCAGT        TGTACACCCC   AAAAAAAAAAAAAAAAAAAA    GCATAAATTA
3L   79A-79A4      0_AE002647   -   1412601   1412907   4702-5019   318    5'3'   0    ATCACACTTT                      CCCCAACAGC   AGTTGCCGCATGGGTAACAGT   TTTTTTTTTT
2L   35B2-35B      3_AE002690   -   645078    645427    4666-5049   384    5'.    0    TCAACATTCG                      TCGCCCAAAA   AAAAAAAAAAAAAAAAAAAA    GAATATCTAT
2L   35B-35B4      3_AE002690   +   913609    913949    4696-5049   354    5'.    9    TGCTTTGTCA   AAGTTCTCT          GTACACCCCA   AAAAAAAAAAAAAAAAAAAA    AACCTTTGGC
3L   76A-75D       0_AE002602   -   1283670   1283926   4786-5049   264    5'.    13   AACTTTCGGG   ATAAAAATCGCAC      ACCACCCTCA   AATAAAAAAAAAAAAAAAAA    TGCAAATTTA
3R   82C5-82A4     0_AE002681   +   1825548   1825741   4520-4720   201    5'3'   0    AACAAGAGCA                      ATTCGCTCCC   TCATCCTAATAGTCTAGCTAG   ACGACTAAGT
?    ?             0_AE002781   -   2893      3098      2305-2508   204    5'3'   0    AATAGTGTTG                      AATGACAGAC   CAATGATCCTGCATCCTAAGG   ATGCTTTTAT
?    ?             0_AE003314   +   301       435       4502-4720   219    5'3'   0    GCATATCACT                      CTATACAGCG   TCATCCTAATAGTCTAGCTAG   ACGACTAAGT
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Full-length elements: 9/0
5' truncated elements: 40/6
3' truncated elements: 0/1
5'3' truncated elements: 0/14
Unfinished elements: 16
Total number of elements: 86
Total length of elements: 104949

JuanDm

Chr	Cyt	Acc	S	Coordinates		Element	Len	Type	D	5' flank	TSD	Start	End	3' flank
2R	43C7-43C1	4_AE002787	+	1235891	1240123	1-4243	4243	F	12	AAATTATATT	TAAATTCATTAC	ACAGTCTTCG	CAAATAAATAAATAAATAAAA	TTACCAGGAG
X	7D2-7D5	2_AE002566	-	1828981	1833212	1-4243	4243	F	12	TATTTGAATC	TTAAATATTATG	TCAGTCTTCG	TTAATTAAAAAAAAAATTAA	CAGATACGTA
X	13B-13C1	1_AE002593	+	1591855	1596087	1-4243	4243	F	13	TGTGAGCCAC	ATTGCGATGACTA	CAGTCTTCGA	AAATAAATAATAATAATAAAA	TTCTCGTGCG
X	20A5-20	0_AE002629	+	268307	272538	1-4242	4242	F	13	AATATGCACA	TAATGTTGTTTCG	GTGTCTTCGA	GCACAAATAAATTAAATTAAT	TTCGTTGGCA
2L	24D-24D1	0_AE002638	+	874492	877244	1482-4242	2761	5'.	14	ATGCAATTTT	AAAAGCAAAACAAA	CCGTTTTAAT	AAATTAATTAATTAATTAATT	CACTTGTTGA
3R	88E-88E8	2_AE002708	-	1363833	1366823	1-4243	4243	F	15	AAGACGTTAA	ATTACTGCTTATTAC	AGTCTTCGAC	AATAAATTAAATTAAAATTAA	CTTTTCGGGA
3R	82C5-82A4	0_AE002681	+	1923410	1923933	3712-4242	531	?.	0	NNNNNNNNNN		TTATAAATTA	CAAATAAATTAATTAAATTAA	TTAATAAAAA
3L	75A7-74F1	0_AE002602	+	2582603	2583169	3724-4243	520	5'.	13	AAATTTAATT	ATTTAGTGTTTTC	CACTGTACCC	AATTAAATTAAATTAAATTAA	AGCTAAAAAG

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Full-length elements:  5/0
5' truncated elements:  2/0
3' truncated elements:  0/0
5'3' truncated elements: 0/0
Unfinished elements:  1
Total number of elements: 8
Total length of elements: 25026
TSD lengths (min/max):  12/15
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Waldo-A

Chr	Cyt	Acc	S	Coordinates		Element	Len	Type	D	5' flank	TSD	Start	End	3' flank
2L	31A-31B3	1_AE002690	-	2182875	2188091	217-5408	5192	5'.	5	CACACACACT	AGATA	TAAAGCAGCT	ATAATAAAAAAAAAAAAAAAA	GCACTCTATG
2L	32B-32C	1_AE002690	-	2907119	2908673	3850-5407	1558	5'.	15	TGCACGGGCC	AAGGGCACAGGACGA	TACGGAATGG	ATAATAAAAAAAAAAAAAAA	ACAAGGTTCA
3R	98B-98A	6_AE002708	+	2003321	2006599	2087-5409	3323	5'.	0	CTAACCCACC		CCACCTCCAC	TAAGTCAAATAATAAAAAAA	CACACACACA
3R	83A6-82E4	0_AE002681	+	989371	994362	372-5401	5030	5'.	14	TACATACATG	ATGCAAGCGAAAG	TAGTTGTGTC	GTCAAATAATAAAAAAAAAA	GACTATGGAA
3R	84A2-?	0_AE002699	-	1278982	1281244	3146-5409	2264	5'.	26	CACACACACA	ACACACACACACACACAC ACACACACG	TGTTACCAAA	AAAAAAAAAAAAAAAAAAAA	AAAGTCAAAC
3L	70F2-70E1	1_AE002602	-	2560842	2562637	3606-5403	1798	5'.	10	GTCGGGCCCC	CATTAGCAGC	CTAGCCTAAC	TCAAATAATAAAAAAAAAAA	TTGTAAAAAC
3R	88A4-88B1	2_AE002708	+	210091	212167	3278-5409	2132	5'.	14	TACATTCGTA	ATATATGCACATAT	GCACAGAACT	TCAAATAATAAAAAAAAAAA	AGCCAGCGAT
3L	65C-65B5	4_AE002602	+	1623583	1623949	5042-5408	367	5'.	15	CACACATATC	ACACGTACACTTGGC	ACATCCAACA	AATAAAAAAAAAAAAAAAAA	TCACACATGG
?	?	0_AE003116	-	399	3588	411-5176	4766	5'3'	0	AAACAGAACC		AATAAAAATA	GCCCTCATGGACTCACCAAAG	TCATACCTTG
?	?	0_AE002665	-	105237	108002	1-5409	5409	F	11	CACACACACA	ACCCGTTGGAG	ACCAAGTCTA	AAATAATAAAAAAAAAAAAA	CGCGAGAGTG
2R	44D4-44D	4_AE002787	-	189616	191230	3743-5409	1667	5'.	15	CAATACACAA	ACACACACACACACA	CGTCCAATTG	GTCAAATAATAAAAAAAAAA	TAGTGAGCAG
?	?	0_AE002751	-	57160	61158	1112-5303	4192	5'3'	13	TTGTTGACCC	TTCTAACGCCCAC	GGAAGACCAA	AAAAAAAAAATATAAAAAAA	AACCCGCACA
?	?	0_AE002751	-	64862	65166	776-1080	305	5'3'	0	AATCTCGGTT		CGCCGTTGGC	GCTCCTTAACTCTCAGCCGTT	ATTTTACATG
?	?	0_AE002805	+	3007	6264	4-5260	5257	.3'	16	GCGGTTAATA	AAGATTAGATTCTAAG	GAAGACCAAG	GTCGAATAATAATAAAAAAA	CTATCAAGTA
?	?	0_AE002700	-	23296	25687	1683-5310	3628	5'3'	0	CGGCCGCTTT		TTGAGACGTA	AGGCATAACTCCAATAGGGCT	GTCCATTATT
?	?	0_AE002777	+	12782	15629	1989-5409	3421	5'.	0	GGTGAGCGTG		CCACAATGCC	AAAAAAAAAAAAACAAAAGA	CAAACAATAA
?	?	0_AE003166	-	843	4391	696-5408	4713	5'.	14	GATCTGATTT	AGACAAACATGGAA	GACAAAGTCT	TCGAATAACAAAATAAAAAAA	ACAGTAAATG
X	20A5-20	0_AE002629	+	258229	260985	1-4959	4959	.3'	4	CCTTTGCTTC	GGAG	ACCAAGTCTA	CCTAGTGAATAGCGTGGCATG	CTGGGACACA
2R	41F11-41C	0_AE002769	-	598287	598956	3955-5150	1196	5'3'	7	GGTTTTTCCC	AAGGATC	TGGGGAACAT	AAAAGGCTAAAAGTAGGGGAA	GGATCTGTTA
2R	41F11-41C	0_AE002769	-	649497	650000	4802-5303	502	5'3'	0	AGGTTTAAGA		TCCTCACAAG	AGTACGTAGGCATAATCCCTA	CCTACGGACA
2R	41F11-41C	0_AE002769	-	655047	659167	69-4448	4380	5'3'	4	CGATCCTATT	AACT	GATATAGGGT	TCCCGCCTGGCAACATCGCCG	CTTGTTATCG
2R	41F11-41C	0_AE002769	-	704697	705459	3349-4111	763	5'3'	0	AGATACTAAT		GGACAAGATG	CGATTGGTACTGTCATCCACT	ACACTGTGGT
2R	41F11-41C	0_AE002769	+	708966	711310	27-2813	2787	5'3'	7	GTGTTTTTTA	ACAAGCA	TGGACGAAAT	CTATATATATATTCATAACAA	CATTGTAGCA
2R	41F11-41C	0_AE002769	-	751906	756299	929-5409	4481	5'.	0	ACACACACAT		CTTCGGACCT	TGTCCCATGGTACGATAAGGA	CAGGGGCTCC
2R	41F11-41C	0_AE002769	-	866975	868868	679-3841	3163	5'3'	0	TGAGACGTGA		CATACGTGTG	TGTCCCATGGTACGATAAGGA	AGCTGGGCCA
2R	41F11-41C	0_AE002769	-	989689	990632	324-1283	960	5'3'	5	TCTTAAGTAA	AGAGA	AGATTCAATA	GGAGAAGGAAAGGCGAAAGGC	CGGGTGAGAG
2R	41F11-41C	0_AE002769	-	991273	991477	324-529	206	5'3'	0	TCTCTTAAGT		AAAGAGAAGA	CTGCACAGCTCTATTCATAGA	CATTGCACAG
2R	41F11-41C	0_AE002769	-	992120	992324	324-529	206	5'3'	0	TCTCTTAAGT		AAAGAGAAGA	CTGCACAGCTCTATTCATAGA	CATTGCACAG
2R	41F11-41C	0_AE002769	-	995474	996688	2324-3573	1250	5'3'	0	AGGAACTGGC		GAATCACCTA	TCGGAGCCATAAACTGTATGG	AAAAGCCTTG
2R	41F11-41C	0_AE002769	-	1013090	1014952	703-3820	3118	5'3'	0	AAGGGAAACC		GTCGGGAACC	TCGGAGCCATAAACTGTATGG	TACCTGAGGA
2R	41F11-41C	0_AE002769	+	1108778	1109160	5024-5406	383	5'.	0	CATTAGTTGG		GAGCAGCACG	TAAAATAAAAAATACACCTAAA	CCGGAGCATT
2R	41F11-41C	0_AE002769	-	1139890	1140817	3387-4394	1008	5'3'	0	TCGTAATTTA		GGAGTTGAGT	CACGAAACCAATGATACCAAT	GATTGATGGT
2R	41C-?	0_AE002769	-	1336802	1339555	611-5394	4784	5'3'	0	CCGTAGGCCG		AATTGATGGA	CGTAAGTCGAATAAATAAAAA	TCCAATCGCA
2L	41C-39E3	0_AE002725	+	36156	38036	1934-5176	3243	5'3'	0	AGCGTCAAAA		CAGCAGCTTA	AGCACGTGGAGATTTTTGTTT	TCATACCTTC
2L	40A4-?	0_AE002725	-	705501	705660	4972-5281	310	5'3'	0	TTGTTATTCT		GTGTCTTTGG	AGCACGTGGAGATTTTTGTTT	CGGCAGTCAC
?	?	0_AE002590	-	301	2002	1212-4352	3141	??	0	NNNNNNAAAA		CCCAAAGTTC	TAGCTAGACTCATGCCCAACG	Tnnnnnnnnn
3R	86D-86D1	1_AE002708	+	225812	226441	84-714	631	5'?	0	CACACACACA		GTCCGTGGAG	ACCAGAGGAGTCGGTAACCCG	NNNNNNNNNN
3R	86D-86D1	1_AE002708	+	230478	230927	4957-5409	453	?.	0	NNNNNNNNNN		ATGATGGCGA	TAAAAAAAAAAAAAAAACACA	TGTGCGTGTG
?	?	0_AE002705	+	1576	3674	1970-5403	3434	5'.	0	AGATGTCTTC		ATACGGTTAG	AAAAAAAAAAAAAACACCTAAA	TTCACAATAC
?	?	0_AE002752	+	964	2988	3-4114	4112	.3'	0	AAATTTTTTT		GGACAAAGTC	TTGGAGCTGCCATCCACTGGC	AGCACTACTA
?	?	0_AE002740	-	301	1646	103-3876	3774	?3'	0	nnnnnnnnnA		TGGCAGAACC	TAAACAACGGAAGCCGGCCCA	AAAAAATACC
3L	70C5-70A	2_AE002602	-	690654	691133	2-481	480	.?	0	CATATGTATG		GGGACGAAGT	TCACCGGGCTGGTGCCTAAGC	NNNNNNNNNN
3L	69F6-69D	2_AE002602	+	1340272	1345294	1-5409	5409	F	14	CAGAAGCCTG	AGGACATTCCCACA	GGGGACGAAG	ATAAAAAAAAAAAAAAAAAA	TTACTCCATC
2R	49B12-48F5	2_AE002787	-	2212941	2213353	4996-5409	414	?.	0	NNNNNNNNNN		ATTATCATTA	TAAAAAAAAAAAAAAAAAAA	AAAAAAAAAA
2R	49B12-48F5	2_AE002787	-	2214863	2215285	3325-3747	423	5'?	0	CTCCACTTTT		CGCATCAAAC	AGGAAGGAATACTGCGCAATT	NNNNNNNNNN
?	?	0_AE003091	-	11380	12809	2555-4359	1805	5'3'	0	GCCTGAGGCA		TAATGCTGAA	TATGTTGGCGAACAGCGAGGC	ATGGGAGCTG
?	?	0_AE002896	-	14931	16487	1171-4273	3103	5'3'	0	GACTGAGGAA		AAAAGCCTAC	TGTAATGATAGTGTACAATAT	TAATTTATTT

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Chr	Cyt	Acc	S	Coordinates		Element	Len	Type	D	5' flank	TSD	Start	End	3' flank
?	?	0_AE002760	+	5251	5592	21-363	343	5'3'	0	TTCCATCCAT		CGTGAAGACA	AAATCTTTAAATTTAATTTCA	TACTGGTTCC
X	17E-17E	2_AE002593	-	1956702	1958663	811-5232	4422	5'3'	4	ATCAGCGCCT	GTCC	GTGGACATCT	CATCGAAGTCATACAATGGCA	CGGTGAGCGT
?	?	0_AE002902	+	301	672	1660-2337	678	?3'	0	nnnnnnnnnn		AGCAGAGGAG	TTGCGGGGTATCGCTTTTGCG	CCAGAGGCCG
?	?	0_AE002586	-	369	1106	3878-5006	1129	?3'	0	nnnnnnTGGC		GCTACAAAGC	CCTTATCATTAATATGATGAA	GCGAGTCCGA
?	?	0_AE003100	-	301	392	5141-5409	269	5'.	0	TACGCTTAGT		GGCCGTAAAA	AAAAAGACAAACATGGAAACA	ATAAATGTTG
?	?	0_AE003100	-	34010	34785	2528-3396	869	5'3'	0	GGGAATCAGA		TAGACGCTAT	TTGTTAAAGCAGTCGGTGGAT	TAAGATATCC
?	?	0_AE002943	-	1561	2242	3733-4427	695	5'3'	0	TCGTATATAC		GAATACTGCG	GGTAGCAAAGGCTTCGCCACT	AGCAGGGGTT
?	?	0_AE003230	-	301	543	1-543	543	.?	0	AATGTTCGGG		GGGGACGAAG	TCCGTAAAAGCCAGGGGGAAA	Tnnnnnnnnn
?	?	0_AE003151	+	658	908	684-1233	550	5'?	0	TGCATGTGCA		GTGATCCCCC	CAAAAGTCCAGTCGCCCAAGC	nnnnnnnnnn
?	?	0_AE002808	+	2631	2982	4600-5212	613	5'3'	0	GCAATGCCAC		AGCAGGGCTT	TGGCCTCACATCCTGCTCATC	CTGTTCAATC
?	?	0_AE002688	-	14380	15021	4418-5291	874	5'3'	0	CGGCCAGGAA		CTGCTGGTGG	GGTTTTTGTTTTAGTACGCAG	TTTATGAATC
3L	17E-77B1	0_AE002602	-	3215	4504	452-3669	3218	5'3'	0	TATTTAATTT		ATCATCCTCT	AATAGTGCCCTGGACGCTCCT	GGACGCAATT
X	19F-19E3	0_AE002620	+	343445	343899	4954-5406	453	5'.	0	CTCTTAGGTT		GCCATGATGT	TAATAAATGATAATAATAATA	TGATAGCAGA
X	5E8-5E	2_AE002566	-	89028	89818	293-5388	5096	5'3'	7	CACACACACA	ACACACA	CGACAAGTGT	TTCCTGCCGTATATAAAAAAA	GATGCATGGA
X	6A2-6A	2_AE002566	-	238651	243433	16-5409	5394	5'.	19	CACATACACA	ACACACACACACACACACA	GACGACAGGA	TAATAAAAAAAAAAAAAAAAA	AGCAAACAGA
?	?	0_AE002918	-	28782	29233	4953-5409	457	5'.	0	GCTATGGCTA		GGCTATGTTG	TCGAGTTATAATAAAAAAAAA	CACACACACC
?	?	0_AE002580	+	301	618	4752-5409	658	?.	0	nnnnnnnnnn		ACCCAGTTTC	TAATAATAAAAAAAAAACATA	CAGAAAAGGG
?	?	0_AE002806	-	3006	3303	2364-3038	675	?3'	0	nnnnnnnnnn		CTGCTATGCT	CCACGCGGAGGTCTTGGAGGC	CAAAGCCATA
?	?	0_AE002644	+	301	515	3352-3657	306	5'3'	0	CCAAGCAAAG		CAGATGGTAT	TTCCGGAAAGGAAAGAGTAGT	GACCTGCAAT
?	?	0_AE003085	+	301	442	4718-5111	394	5'3'	0	CAGCTCATCC		AGAGATGACG	GCGAAGAATTCTATCTCAGCG	CTTTTAATTA
?	?	0_AE002703	+	301	386	5011-5409	399	?.	0	nnnnnnnnnn		TGAAGCGCGT	CAAATAATAAAAAAAAAAAAA	TCATTCGCTG
?	?	0_AE002837	+	10364	10968	1157-2323	1167	5'3'	0	TAAACACATA		AAAAAGGCCT	TGGCAGCCTAACTTATGCGGG	TAAGTAAGAG
?	?	0_AE002653	+	2172	2500	2493-2821	329	5'?	0	CACACTAACA		CACCACACAC	ATCATATCAATTCCCTGGAAA	NNNNNNNNNN
?	?	0_AE003040	+	12802	13087	2050-2343	294	5'3'	4	TTACGAAAGA	GTTA	GCTCAACCTA	GCGGGTACGTCATTTGTTGAC	CCTTTATCAG
?	?	0_AE002960	-	19200	19647	4229-5272	1044	??	0	nnnnnnnnCC		AAGACTCCCC	GGACTAAAGAGCACACGGAGG	NNNNNNNNNN
?	?	0_AE002919	-	2273	2495	3757-3987	231	5'3'	0	GATGGCTAAA		GACAGAAGAA	ATGTACGATGCATTGTTTTGC	TGACGATGTG
?	?	0_AE003098	+	301	287	4746-5032	287	?3'	0	nnnnnnnnnn		CACCTAACCC	GTGGACGTGTAAGTCCAAAGA	GTCGTCCTGG
?	?	0_AE003048	+	28233	28555	5087-5409	323	5'.	0	CTTTAGAGTT		GCGGGCGAAG	AAAAAAAACAATAAAAAAAAA	TGGGTCGTCA
?	?	0_AE003278	+	2969	3299	1975-2301	327	5'3'	0	GATCACAGCC		GGTGAGCTGT	CAGCAGTGCCAGATGGAGCAA	TACGGTAGCC
?	?	0_AE002761	+	3912	4116	1945-2497	553	5'?	0	ACCCCTTTTC		GATAAGGAGA	GGGCACTGGAATGGGGCAGCA	AAGTAnnnnn
?	?	0_AE003118	+	39973	40169	2540-2739	200	5'3'	0	CCCCAGAGGC		GAATGCTGGA	AGTGGCTGCTGAGAGAGGTGG	TCTTACCAGC
?	?	0_AE003109	+	2394	2428	4-338	335	.?	0	CCCTGTATGA		GACGAAGTCT	GGCGCGCAATTCAAAATTAAA	nnnnnnnnnn
?	?	0_AE003017	-	17684	17927	3733-3983	251	5'?	0	TCGTATATAC		GAATACTGCG	CATCATTTACGATGGGATCTT	NNNNNNNNNN
?	?	0_AE003243	-	633	920	4976-5355	380	5'3'	0	TTCAAGACGC		CTTTGTAGCG	CGGTATTTGATCTGCAATTAG	GTCTCCTTTA
?	?	0_AE003183	+	46763	46957	5207-5408	202	5'.	0	GACTTCAAAA		CTCATAGAAG	ATAAAAAAATAAAAACCATAA	TACCCCATAA

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Full-length elements:  2/0
5' truncated elements:  10/10
3' truncated elements:  2/1
5'3' truncated elements:  8/29
Unfinished elements:  20
Total number of elements:  82
Total length of elements: 153858
TSD lengths (min/max):  4/26
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Waldo-B

Chr	Cyt	Acc	S	Coordinates		Element	Len	Type	D	5' flank	TSD	Start	End	3' flank
3L	61F-62A1	0_AE002584	+	1404029	1409224	1-5179	5179	F	12	CACACACACA	ACATCCATTGTC	CCGCGTATTT	AAAAAAAAAAAAAAAAAAAA	GGGCGCAGTC
3R	92A14-92B2	3_AE002708	+	2971807	2976993	1-5179	5179	F	16	CACGGAAACA	ACAGGGTCCTAAATGG	AGTTCCCGCG	ATAAAAAAAAAAAAAAAAAA	CAAAATGCTA
3R	85D2-85D10	0_AE002708	-	1561293	1566460	1-5179	5175	F	15	AGCACGACAC	TCCAGCAGAGCGATG	AGAGGTGTGT	AAAAAAAAAAAAAAAAAAAA	GCCGAATAAA
?	?	0_AE002870	+	1266	6282	164-5175	5012	5'.	0	CGCGTCACGGT		TCGTAATAAA	GCCATCACAAAATCATGAAA	TGCCTTAGGA
3L	66C-66B10	4_AE002602	+	19315	24509	1-5179	5179	F	13	CACACACACG	ACACAAAGAACTG	TGAGGAGACG	AAAAAAAAAAAAAAAAAAAA	CACACAGACA
3L	65C-65B5	4_AE002602	+	1623683	1623951	4906-5180	275	5'.	0	GGCGACTAAA		GGTGGAAGGA	AAAAAAAAAAAAAAAAAAAA	CGTACACTTG
?	?	0_AE003116	+	15395	20439	4440-4752	313	5'3'	5	CGTGAACACA	CACAA	CACAGCACAA	AGAGGCTTGGTTGCTGCTATG	AGTAAGACGG
2R	50C3-50C4	2_AE002787	-	812315	814233	3266-5180	1915	5'.	16	TTTTATTCCC	AGATCAGTTTTTACCT	TGTCCTTCTG	AAAAAAAAAAAAAAAAAAAA	CTCTGCGCTG
2R	49B12-48F5	2_AE002787	-	2212934	2213210	4906-5180	275	5'.	0	GGCGACTAAA		GGTGGAAGGA	AAAAAAAAAAAAAAAAAAAA	CCTCCACTTT
2L	31A-31B3	1_AE002690	-	2182873	2183141	4906-5177	272	5'.	0	GGCGACTAAA		GGTGGAAGGA	TAATAAAAAAAAAAAAAAAA	GATAGCACTC
?	?	0_AE002751	-	1304	3588	1902-4881	2980	5'3'	0	CCCCCTTCTG		CATCATTCAG	CCGTATGTTGGCGGGGCAAGA	TACGTAGGGC
?	?	0_AE002600	+	3908	8862	1-5177	5177	F	0	CGTTCGAGTT		CCGCGTATTT	AAAAAAAAAACAAAAAAAAA	TCACAAGTAC
2R	41F11-41C	0_AE002769	-	628652	630187	2785-5172	2388	5'.	0	GGTACTATAT		CAGTGATCTA	AGAGCGGAGGCTTTTTTAGT	CCGTAAATGT
2R	41F11-41C	0_AE002769	-	645872	648121	1682-4521	2840	5'3'	0	TCCAGGACAT		CGACCGGGCT	ACTACATGGGCTGAGTGTGAG	TGGACTACCA
2R	41F11-41C	0_AE002769	-	751900	752173	4906-5179	274	5'.	0	GGCGACTAAA		GGTGGAAGGA	AAAAAAAAAAAAAAAAAAAA	CAGGGGCTCC
2R	41F11-41C	0_AE002769	+	821448	823244	2111-5049	2939	5'3'	0	GGCCATTAAA		GCGGCCTAGC	AGAGCGGAGGCTTTTTTAATT	CTCTAAAATA
2R	41F11-41C	0_AE002769	-	1090465	1091325	3266-4230	965	5'3'	0	GTTTCTTTCT		AACTGGTCAT	GCTGCCCCTATCTGGAGCTGC	AAAATCGTTT
2R	41F11-41C	0_AE002769	-	1184036	1184844	3448-4363	916	5'3'	0	GCAACCCGCA		ACGCTCGGCG	GGCATTACACACCCATTGACC	CCCATGGACG
3R	98B-98A	6_AE002708	+	2006331	2006603	4906-5180	275	5'.	0	GGCGACTAAA		GGTGGAAGGG	TAAGTCAAATAATAAAAAAA	CACACACACA
3L	68C5-68A8	2_AE002602	+	2982758	2983699	4230-5180	951	5'.	15	ATAAACAGAA	ACACTTATCCATAAG	AAAACCTATC	ATAATAAAAAAAAAAAAAAA	TAATGGCAAA
3R	84A2-?	0_AE002699	-	1278978	1279249	4906-5180	275	5'.	0	GGCGACTAAA		GGTGGAAGGA	AAAAAAAAAAAAAAAAAAAA	CACACACACA
?	?	0_AE003166	-	835	1113	4902-5180	279	5'.	8	CCCGGCTTTT	GTAAATGT	CGACTAGAGG	AAAAAGACAAACATGGAAACA	TGTCTGCTTT
?	?	0_AE002760	+	45656	47380	3326-5180	1810	5'3'	0	GGACAGCAT		TGTATCTGTT	ATCTTTAGAAGATTTTACTTT	TATTTTTGTC
3R	88A4-88B1	2_AE002708	-	211906	212171	4906-5173	268	5'.	0	GGCGACTAAA		GGTGGAAGGG	CAAATAATAAAAAAAAAAAA	TATATGCACA
?	?	0_AE002665	-	105232	105505	4906-5180	275	5'.	0	GGCGTATAAA		GGTGGAAGGA	AATAATAAAAAAAAAAAAAA	CCCGTTGGAG
?	?	0_AE002777	+	15415	15633	4958-5179	222	5'.	0	AGGGAGTGGG		GCCTCACATC	AAAAAAAAACAAAAGACAAA	CAATAAAACG
3L	64C2-64C1	1_AE002584	-	1747372	1748152	4397-5180	784	5'.	0	GAAGGGCTGC		GCTGCACTCA	AATAATAATAAAAAAAAAAA	CACATATATA

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Chr	Cyt	Acc	S	Coordinates		Element	Len	Type	D	5' flank	TSD	Start	End	3' flank
2R	44D4-44D	4_AE002787	+	190962	191234	4906-5180	275	5'.	0	GGCGACTAAA		GGTGGAAGGG	TCAAATAATAAAAAAAAAAA	CACACACACA
?	?	0_AE003100	-	301	614	4683-5120	438	5'3'	0	GTATGCCATT		CGAGGAGAGG	GGTATCTTTAGAAGATTTCAT	TTTCCTGCCG
?	?	0_AE003159	+	11060	11772	1776-2425	650	5'3'	0	GGCTACGACG		CCAAGATGCT	ATGTCACCTTTGTTAGCAGAG	AGTGGCTAAT
?	?	0_AE003010	+	1476	2451	4116-5166	1051	5'3'	0	TCGTTCAAAA		AGCGGCAATG	GCGATATAAAATAAAAAAAAA	GATATTGTTT
?	?	0_AE002902	-	9450	10549	1648-3124	1477	5'3'	0	GGTGTCGCAT		GTCCAACAAT	TCGAAGCTGCAAAGAGAATCA	AGGGTGTCGG
?	?	0_AE002705	+	3441	3685	4932-5180	249	5'.	0	TTTCGGCTTG		CGTTAAAGGC	AACACCTAAATTCACAATACA	CTGAGCGATT
?	?	0_AE003344	-	608	1577	3043-4594	1552	5'3'	0	TTTTGCCGCC		TGGCCAACAT	TTCGAGGGTACCTATCTATGT	GTATTTAAAT
?	?	0_AE003394	+	2303	4014	2432-3454	1023	5'3'	0	CTATACCTTT		TGGCGTGGAA	GAAAGGGCAAATGCACGGTAG	TTAGCAACCG
2L	44D4-39E3	0_AE002725	+	37984	38222	4932-5166	235	5'3'	0	TCCCGGCTTG		CGTAAAAGTC	CGAATAATAAAAAAAAAAAAA	CTGCCGATGAA
?	?	0_AE003262	+	301	388	4766-5154	389	?3'	0	nnnnnnnnnn		CGTTTGGGAT	TTCCTGCCGTATATAATAAAA	CCTCCTCATA
?	?	0_AE002911	+	7497	7906	3759-4165	407	5'3'	0	GCGTGCTATG		TATGTAACAG	TTGAAGGACCCAGAATGCCGG	GAGTCTTCCG
?	?	0_AE002662	+	4450	4811	1838-2196	359	5'3'	0	AAGGTCTGCG		CCTGACCTAC	AGCCCGGAGCAATTCGAGGAC	CAGGAGTCCT
?	?	0_AE003279	-	301	648	89-454	366	5'3'	0	CCATAATTAA		AATCCACACT	AGTTGTGGGGGGGGGGGGGGG	GTGGCGGCTC
?	?	0_AE003243	-	589	838	4919-5170	252	5'.	0	GAGGTGCGTC		CGATGCTGTA	GTTTAGAAAACTTAAATAACA	CTCCTTAGAA
X	19D-19D	0_AE002620	+	1108795	1109036	4920-5164	245	5'3'	0	GCCACGAATC		GCTGGTGGCG	AAGTTCAATAATAAAAAAAAA	TACGCTGAAA
?	?	0_AE002761	+	3917	4116	1737-2290	554	5'?	0	TTTTCTGATA		GGAGAACATA	GCACTGGAAGTGGGCAGCAAA	GTAnnnnnnn
X	5E8-5E	2_AE002566	+	89445	89827	552-5163	4612	5'3'	0	TCCAATTCAC		GAGCGAGGGG	TCCTGCCGTATATAAAAAAAA	CACACAGAGC
X	6A2-6A	2_AE002566	-	238647	238881	4943-5180	238	?.	0	NNNNNNNNNG		AGGGAGTGCG	AATAAAAAAAAAAAAAAAAAA	CACACACACA
?	?	0_AE003048	+	28301	28558	4918-5176	259	5'.	0	TGGAAGGCGG		GCCCTCATAT	AAAAAAAACAATAAAAAAAAA	TGGGTCGTCA
?	?	0_AE003322	-	43487	43418	4949-5180	232	?.	0	nnnnnnnnnn		TACGACGTGG	AAAAAAAGACAAACATGGAAA	CAGTAAATGT
?	?	0_AE002918	-	28778	29049	4906-5177	272	5'.	0	GGCGACTAAA		GGTGGAAGGA	TCGAGTTATAATAAAAAAAAA	CACACACACC

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Full-length elements:  4/1
5' truncated elements:  3/17
3' truncated elements:  0/0
5'3' truncated elements: 1/18
Unfinished elements:  4
Total number of elements: 48
Total length of elements: 67527
TSD lengths (min/max):  5/16
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Chr	Cyt	Acc	S	Coordinates		Element	Len	Type	D	5' flank	TSD	Start	End	3' flank
3L	79E-79F3	0_AE002647	+	2419411	2424785	5-5373	5369	F	10	GTACTGGTGT	ATATTTGCAA	CGTCACCGAC	GTTAAATAAAATAAATAAAA	TTGACCAGCA
X	79E-19F6	0_AE002620	+	56440	61816	2-5373	5372	F	13	TCCTGATTTT	TAAGATGATGTGC	AGTCACCGAC	TGTTAAATAAATAAATAAAA	TCAAAACAAG
X	1F-1F	0_AE002566	-	1119136	1124111	1-5373	5373	F	11	TATCATTTTT	AATTTAGGATA	CGCAGTCACC	TGTTAAATAAAATAAATAAA	GTCATACTTT
?	?	0_AE003194	-	3969	8196	14-5373	5360	F	0	AAATCTGTGG		TATATCTCTT	TTTGTTAAATAAATAATAAA	TAGTTCCTAA
?	?	0_AE002635	-	2894	6936	284-5103	4820	5'3'	0	TCTCTTCGAG		TACCAGACCT	CCAACTAGGCGGGGACGAGC	ATTTGAATAA
?	?	0_AE002569	-	308	4611	194-5194	5001	5'3'	6	TGCAAATCCA	AAAACA	TTCAATATCC	ATTCTTTAGGCTTATTATAT	ATTAACCCAT
?	?	0_AE003172	+	3125	6529	35-5371	5337	5'.	0	CTTTCCAATT		GTGTGCGCTT	TTTGTTAAATAAAATAAACA	TTTATTGCAA
2L	1F-39E3	0_AE002725	+	53283	55586	1366-5350	3985	5'3'	0	GGCGGAAGCA		AATGCTCTAA	TAATTTTGTTAAATAAGTAA	ACTCATCCGT
2L	40A4-?	0_AE002725	+	562247	566169	263-4778	4516	5'3'	7	TCAATTTAAC	AAAAAATA	AGTGGAATAA	GGGTGCTCTAATAGACTCCA	TTTTGGGAAC
?	?	0_AE002816	-	1547	2160	4745-5373	629	5'.	0	TTCTAAGTTC		AAAAATCATC	TATTAAATAAAAAAAAAATA	AACATGATTA
?	?	0_AE002816	-	3085	3527	3149-3654	506	5'3'	0	AAAAACGCT		AACCCTAGAA	AATAATATAAATATTAGAAA	TTAACTTTTG
?	?	0_AE002601	-	5105	6524	3853-5373	1521	5'.	12	GCTGCTAAAT	ATATATTTAAGA	AACTAGATTT	CTAATTTGGTTAATTAAAAA	GAAGGAACAA
?	?	0_AE002975	+	1964	2524	35-904	870	5'?	0	CTTTCCAATT		GTGTGCGATT	ATGCACTAGCATTTTCTGTG	nnnnnnnnnn
2R	60F1-60F1	1_AE002575	-	1415337	1416329	3214-4224	1011	5'3'	0	GTCTTTAAAT		ATATTCGTGT	GCTAACCAAAGACTTCGGAG	AGCTCAAAGA
?	?	0_AE002743	-	16097	16307	5024-5231	208	5'3'	0	GCGCGACCTT		CATCCGCCTA	ATATCCCAAAAATTAACCAA	AACCCTGTAG
?	?	0_AE002743	-	19501	20697	3438-4990	1553	5'3'	0	CCCTGGACGG		CGGAACTACC	AAGCCACTACCGAACGTACA	AGTTATTGCC
?	?	0_AE003394	-	12422	12869	4493-4940	448	5'3'	0	TAACATTTTA		CACCGACTCA	CACTCTTCATGCACAGGTAC	ATGATTTGGC
?	?	0_AE002955	+	2383	2481	115-518	404	5'?	0	GTTACATTGA		TATTTATCAT	ACCTCTTTACCTGGCTTATG	nnnnnnnnnn
?	?	0_AE002840	+	10667	10634	194-466	273	5'?	0	AATCCAAAAA		CATTCAATAT	CCTTCTCTTGCTGGTTAACT	nnnnnnnnnn

```
Full-length elements:  3/1
5' truncated elements:  1/2
3' truncated elements:  0/0
5'3' truncated elements: 2/7
Unfinished elements:  3
Total number of elements: 19
Total length of elements: 52556
TSD lengths (min/max):  6/13
```