

Supplementary Table 2

chr	start	end	strand	gene	bindingsiteseq	on_other_strand of the gene
chr5	98032886	98032898	-	Antxr2	TTTCCAGGTGTGA	FALSE
chr5	98032645	98032657	-	Antxr2	ACCCATCTGGAAC	TRUE
chr5	98032886	98032898	-	Antxr2	TTTCCAGGTGTGA	FALSE
chr5	98032645	98032657	-	Antxr2	ACCCATCTGGAAC	TRUE
chr5	97995957	97995969	-	Antxr2	CTTACAGCTGTTC	FALSE
chr11	101553819	101553831	-	Brca1	CAACCAGCTGTTC	FALSE
chr11	101509714	101509726	-	Brca1	CATCGACATGTTT	FALSE
chr11	101508470	101508482	-	Brca1	ATTACAGATGGTT	FALSE
chr11	101522696	101522708	-	Brca1	CAAAATCTGGGAT	TRUE
chr11	101522327	101522339	-	Brca1	AAGCATCTGGGTG	TRUE
chr11	101553819	101553831	-	Brca1	CAACCAGCTGTTC	FALSE
chr11	101551639	101551651	-	Brca1	GTCCCAGACGTTT	FALSE
chr11	118427631	118427643	+	C1qtnf1	CCTCCAGATGCTG	FALSE
chr11	118428014	118428026	+	C1qtnf1	CGTCCAGAAGTAG	FALSE
chr11	118427938	118427950	+	C1qtnf1	TCACATCTGGAAA	TRUE
chr11	118428132	118428144	+	C1qtnf1	TCACATCTGGCTG	TRUE
chr11	118427631	118427643	+	C1qtnf1	CCTCCAGATGCTG	FALSE
chr11	118428014	118428026	+	C1qtnf1	CGTCCAGAAGTAG	FALSE
chr11	118427938	118427950	+	C1qtnf1	TCACATCTGGAAA	TRUE
chr11	118428132	118428144	+	C1qtnf1	TCACATCTGGCTG	TRUE
chr11	118433454	118433466	+	C1qtnf1	GTTCCAGCTGTCA	FALSE
chr11	118441657	118441669	+	C1qtnf1	TATGCATATGTGT	FALSE
chr11	118442258	118442270	+	C1qtnf1	TGTTCCAGATGTGT	FALSE
chrX	143827872	143827884	-	Capn6	TGGCCAAATGTTA	FALSE
chrX	143827475	143827487	-	Capn6	CTTCCAGATTTTC	FALSE
chrX	143827494	143827506	-	Capn6	GCACATCTGGCAG	TRUE
chrX	143827872	143827884	-	Capn6	TGGCCAAATGTTA	FALSE
chrX	143827475	143827487	-	Capn6	CTTCCAGATTTTC	FALSE
chrX	143827494	143827506	-	Capn6	GCACATCTGGCAG	TRUE
chr8	83725825	83725837	-	Adgre5	TAGCCAGGTGTGC	FALSE
chr8	83726496	83726508	-	Adgre5	CCATATCTGGGTC	TRUE
chr8	83730252	83730264	-	Adgre5	TTCCCAGATGTGA	FALSE
chr8	83729520	83729532	-	Adgre5	TCTGCAGATGTGG	FALSE
chr8	83729411	83729423	-	Adgre5	CAACTTCTGGGTC	TRUE
chr8	83730252	83730264	-	Adgre5	TTCCCAGATGTGA	FALSE
chr8	83729520	83729532	-	Adgre5	TCTGCAGATGTGG	FALSE
chr8	83729411	83729423	-	Adgre5	CAACTTCTGGGTC	TRUE
chr18	59173441	59173453	+	Chsy3	TAAGCAGATGTGG	FALSE
chr9	65264268	65264280	+	Cilp	CATACATATGTGT	FALSE
chr9	65265070	65265082	+	Cilp	TCAGATCTGGTTT	TRUE
chr9	65264268	65264280	+	Cilp	CATACATATGTGT	FALSE
chr9	65265070	65265082	+	Cilp	TCAGATCTGGTTT	TRUE
chr9	65265717	65265729	+	Cilp	AAACAACCTGGTAC	TRUE

chr9	65266002	65266014 +	Cilp	ACTCATCTGGAGA	TRUE
chr8	11212216	11212228 -	Col4a1	AATTCAGATGGGG	FALSE
chr8	11211676	11211688 -	Col4a1	TATTCAGATGCTG	FALSE
chr8	11211203	11211215 -	Col4a1	TCTGCAGATGTCT	FALSE
chr8	11218998	11219010 -	Col4a1	GAAGCAGATGTGG	FALSE
chr8	11218800	11218812 -	Col4a1	TCCGCAGATGTTT	FALSE
chr8	11242685	11242697 -	Col4a1	TACCCAGATATGG	FALSE
chr8	11241849	11241861 -	Col4a1	GAGGCAGATGTAG	FALSE
chr8	11241566	11241578 -	Col4a1	ATTCCAAATGTGC	FALSE
chr8	11241556	11241568 -	Col4a1	TGCCCAGCTGTTA	FALSE
chr8	11242857	11242869 -	Col4a1	TCACAGCTGGCTG	TRUE
chr8	11241785	11241797 -	Col4a1	GAACACCTGGTCC	TRUE
chr8	11280587	11280599 -	Col4a1	GAACAACCTGGGAA	TRUE
chr8	11280283	11280295 -	Col4a1	ACACAACCTGTATA	TRUE
chr2	27884571	27884583 +	Col5a1	AAGGCAGATGTTC	FALSE
chr2	27885711	27885723 +	Col5a1	TTTCCAGCTGTCA	FALSE
chr2	27884892	27884904 +	Col5a1	ACACATATGCATG	TRUE
chr2	28015457	28015469 +	Col5a1	GAGCCAGATGTGT	FALSE
chr2	28016036	28016048 +	Col5a1	ACACAGCTGGATG	TRUE
chr2	28016312	28016324 +	Col5a1	CAGCACCTGGATC	TRUE
chr2	28016515	28016527 +	Col5a1	TAACATCTGTGAC	TRUE
chr2	28020546	28020558 +	Col5a1	TGTCCAAATGTCC	FALSE
chr2	28020554	28020566 +	Col5a1	TGTCCAAATGTCC	FALSE
chr2	27884571	27884583 +	Col5a1	AAGGCAGATGTTC	FALSE
chr2	27885711	27885723 +	Col5a1	TTTCCAGCTGTCA	FALSE
chr2	27884892	27884904 +	Col5a1	ACACATATGCATG	TRUE
chr2	28015457	28015469 +	Col5a1	GAGCCAGATGTGT	FALSE
chr2	28016036	28016048 +	Col5a1	ACACAGCTGGATG	TRUE
chr2	28016312	28016324 +	Col5a1	CAGCACCTGGATC	TRUE
chr2	28016515	28016527 +	Col5a1	TAACATCTGTGAC	TRUE
chr2	28020546	28020558 +	Col5a1	TGTCCAAATGTCC	FALSE
chr2	28020554	28020566 +	Col5a1	TGTCCAAATGTCC	FALSE
chr3	137623923	137623935 +	Ddit4l	TTCCCAGTTGTGC	FALSE
chr1	184011474	184011486 +	Dusp10	CAGCCAGTTGTGA	FALSE
chr1	184033018	184033030 +	Dusp10	GGACATCTGAACC	TRUE
chr14	54926859	54926871 -	Efs	AAGACAGATGTGG	FALSE
chr14	54926859	54926871 -	Efs	AAGACAGATGTGG	FALSE
chr14	54928095	54928107 -	Efs	GAACATCTGGTTT	TRUE
chr14	54926859	54926871 -	Efs	AAGACAGATGTGG	FALSE
chr5	30913180	30913192 +	Emilin1	TATTCAGATTTGG	FALSE
chr5	30913301	30913313 +	Emilin1	GAAGCAGATGTGG	FALSE
chr5	30912459	30912471 +	Emilin1	CAACATCTCGTAG	TRUE
chr5	30913180	30913192 +	Emilin1	TATTCAGATTTGG	FALSE
chr5	30913301	30913313 +	Emilin1	GAAGCAGATGTGG	FALSE
chr5	30913836	30913848 +	Emilin1	GACCAAGATGTGC	FALSE
chr5	30912459	30912471 +	Emilin1	CAACATCTCGTAG	TRUE
chr5	30919866	30919878 +	Emilin1	AGAGCAGATGTTG	FALSE

chr5	30919608	30919620	+	Emilin1	AACCATCTGTAAT	TRUE
chr1	14232356	14232368	-	Eya1	AAGCCAGATGAGT	FALSE
chr1	14232565	14232577	-	Eya1	GGCCATCTGGACG	TRUE
chr1	14306594	14306606	-	Eya1	TCACATCTGTGTC	TRUE
chr1	14306594	14306606	-	Eya1	TCACATCTGTGTC	TRUE
chr3	52267763	52267775	+	Foxo1	CTTGCAGGTGTGC	FALSE
chr3	52266723	52266735	+	Foxo1	TCACAGCTGGATT	TRUE
chr3	52266951	52266963	+	Foxo1	GCACCTCTGGTTC	TRUE
chr13	114460315	114460327	-	Fst	AAACAACCTGTCTT	TRUE
chr13	114460315	114460327	-	Fst	AAACAACCTGTCTT	TRUE
chr13	114460315	114460327	-	Fst	AAACAACCTGTCTT	TRUE
chr10	56375783	56375795	+	Gja1	CTTCCAGAAGTCC	FALSE
chr10	56375812	56375824	+	Gja1	CAACCACATGTTG	FALSE
chr10	56375783	56375795	+	Gja1	CTTCCAGAAGTCC	FALSE
chr10	56375812	56375824	+	Gja1	CAACCACATGTTG	FALSE
chr10	56375783	56375795	+	Gja1	CTTCCAGAAGTCC	FALSE
chr10	56375812	56375824	+	Gja1	CAACCACATGTTG	FALSE
chr10	56375783	56375795	+	Gja1	CTTCCAGAAGTCC	FALSE
chr10	56375812	56375824	+	Gja1	CAACCACATGTTG	FALSE
chr10	56375783	56375795	+	Gja1	CTTCCAGAAGTCC	FALSE
chr10	56375812	56375824	+	Gja1	CAACCACATGTTG	FALSE
chr7	130935877	130935889	+	Htra1	ATTGCAGCTGTGG	FALSE
chr7	130935491	130935503	+	Htra1	AAACATCTTGTTT	TRUE
chr7	130935877	130935889	+	Htra1	ATTGCAGCTGTGG	FALSE
chr7	130935491	130935503	+	Htra1	AAACATCTTGTTT	TRUE
chr7	130980372	130980384	+	Htra1	CTCACAGATGTCT	FALSE
chr7	130981172	130981184	+	Htra1	CTACAGCTGGCTG	TRUE
chr7	130981542	130981554	+	Htra1	CCACACCTGGCAA	TRUE
chr7	130981172	130981184	+	Htra1	CTACAGCTGGCTG	TRUE
chr7	130981542	130981554	+	Htra1	CCACACCTGGCAA	TRUE
chr7	130982045	130982057	+	Htra1	GTAGATCTGGAAC	TRUE
chr7	130982287	130982299	+	Htra1	TCACATCTAGGTG	TRUE
chr9	65100299	65100311	+	Igdcc4	ATTACAGATGGTT	FALSE
chr9	65099631	65099643	+	Igdcc4	GAAGATCAGGATG	TRUE
chr9	65100299	65100311	+	Igdcc4	ATTACAGATGGTT	FALSE
chr9	65099631	65099643	+	Igdcc4	GAAGATCAGGATG	TRUE
chr9	65100299	65100311	+	Igdcc4	ATTACAGATGGTT	FALSE
chr9	65099631	65099643	+	Igdcc4	GAAGATCAGGATG	TRUE
chr9	65100299	65100311	+	Igdcc4	ATTACAGATGGTT	FALSE
chr9	65099631	65099643	+	Igdcc4	GAAGATCAGGATG	TRUE
chr9	65100299	65100311	+	Igdcc4	ATTACAGATGGTT	FALSE
chr9	65099631	65099643	+	Igdcc4	GAAGATCAGGATG	TRUE
chr9	65100299	65100311	+	Igdcc4	ATTACAGATGGTT	FALSE
chr9	65099631	65099643	+	Igdcc4	GAAGATCAGGATG	TRUE
chr9	65100299	65100311	+	Igdcc4	ATTACAGATGGTT	FALSE
chr9	65099631	65099643	+	Igdcc4	GAAGATCAGGATG	TRUE
chr11	7215637	7215649	-	Igfbp3	CCACATCTAGAAT	TRUE

chr11	7215471	7215483 -	Igfbp3	GAACAACCTGGGAC	TRUE
chr11	7215637	7215649 -	Igfbp3	CCACATCTAGAAT	TRUE
chr11	7215471	7215483 -	Igfbp3	GAACAACCTGGGAC	TRUE
chr11	99041068	99041080 +	Igfbp4	CTTTCAGATGTTG	FALSE
chr11	99040565	99040577 +	Igfbp4	CAACATCTAGGAA	TRUE
chr11	99041068	99041080 +	Igfbp4	CTTTCAGATGTTG	FALSE
chr11	99040565	99040577 +	Igfbp4	CAACATCTAGGAA	TRUE
chr11	99041068	99041080 +	Igfbp4	CTTTCAGATGTTG	FALSE
chr11	99042239	99042251 +	Igfbp4	CATGCACATGTGC	FALSE
chr11	99040565	99040577 +	Igfbp4	CAACATCTAGGAA	TRUE
chr11	99042242	99042254 +	Igfbp4	GCACATGTGCATA	TRUE
chr11	99042239	99042251 +	Igfbp4	CATGCACATGTGC	FALSE
chr11	99042800	99042812 +	Igfbp4	CAGACAGATCTTG	FALSE
chr11	99042242	99042254 +	Igfbp4	GCACATGTGCATA	TRUE
chr11	99042800	99042812 +	Igfbp4	CAGACAGATCTTG	FALSE
chr11	99043910	99043922 +	Igfbp4	ACACAACCTGTCTG	TRUE
chr11	99046157	99046169 +	Igfbp4	TATTCAGTTGTTC	FALSE
chr11	99046428	99046440 +	Igfbp4	GAGCCAGATGTGG	FALSE
chr11	99047226	99047238 +	Igfbp4	AAACCAGATGTAA	FALSE
chr11	99045825	99045837 +	Igfbp4	GCACACCTGGATG	TRUE
chr11	99047255	99047267 +	Igfbp4	CAACATCTGGAAT	TRUE
chr9	21799782	21799794 -	Kank2	ACACATGTGGAGT	TRUE
chr9	21799782	21799794 -	Kank2	ACACATGTGGAGT	TRUE
chr9	21798334	21798346 -	Kank2	TAACATCTGCGCC	TRUE
chr9	21799782	21799794 -	Kank2	ACACATGTGGAGT	TRUE
chr9	21798334	21798346 -	Kank2	TAACATCTGCGCC	TRUE
chrX	100632435	100632447 +	Kif4	GCTCCAGTTGTTT	FALSE
chrX	100632473	100632485 +	Kif4	GCACATCTGCTAC	TRUE
chrX	100711341	100711353 +	Kif4	AGTGCAGATGTTT	FALSE
chrX	100712224	100712236 +	Kif4	AATCCAGTTTTTC	FALSE
chrX	100711845	100711857 +	Kif4	CGACATCTGAATG	TRUE
chr1	153186248	153186260 -	Lamc2	GGGCCAGGTGTGC	FALSE
chr1	153186248	153186260 -	Lamc2	GGGCCAGGTGTGC	FALSE
chr1	153127254	153127266 -	Lamc2	GGCACAGATGTTT	FALSE
chr1	153128257	153128269 -	Lamc2	TTACATCTGCAAC	TRUE
chr1	153153669	153153681 -	Lamc2	ACACATCTGCCTG	TRUE
chr1	153153271	153153283 -	Lamc2	GAACATCTGATCC	TRUE
chr1	153152145	153152157 -	Lamc2	TATCATCTGGACC	TRUE
chr1	153186248	153186260 -	Lamc2	GGGCCAGGTGTGC	FALSE
chr6	17462644	17462656 +	Met	ATACCAGCTGTGT	FALSE
chr6	17462644	17462656 +	Met	ATACCAGCTGTGT	FALSE
chr6	17462644	17462656 +	Met	ATACCAGCTGTGT	FALSE
chr6	17464041	17464053 +	Met	GAGCCAGATGCTG	FALSE
chr6	17462644	17462656 +	Met	ATACCAGCTGTGT	FALSE
chr6	17464041	17464053 +	Met	GAGCCAGATGCTG	FALSE
chr6	17489531	17489543 +	Met	TAGCCAGATGTCA	FALSE
chr6	17489838	17489850 +	Met	CAGACAGATGTGC	FALSE

chr6	17490283	17490295	+	Met	AATTCACATGTTT	FALSE
chr6	17489419	17489431	+	Met	TAAAATCTGTATC	TRUE
chr6	17534340	17534352	+	Met	AATATAGATGTTT	FALSE
chr6	17534839	17534851	+	Met	CTTACAGATGTAA	FALSE
chr6	17534802	17534814	+	Met	CCACCTCTGGAAA	TRUE
chr6	17545924	17545936	+	Met	TATAAAGATGTGC	FALSE
chr14	54429896	54429908	+	Mmp14	CAGCCAGATCTTG	FALSE
chr14	54430427	54430439	+	Mmp14	GTTCCAGAGGTTA	FALSE
chr14	54429896	54429908	+	Mmp14	CAGCCAGATCTTG	FALSE
chr14	54430427	54430439	+	Mmp14	GTTCCAGAGGTTA	FALSE
chr14	54429896	54429908	+	Mmp14	CAGCCAGATCTTG	FALSE
chr14	54430427	54430439	+	Mmp14	GTTCCAGAGGTTA	FALSE
chr14	54429896	54429908	+	Mmp14	CAGCCAGATCTTG	FALSE
chr14	54430427	54430439	+	Mmp14	GTTCCAGAGGTTA	FALSE
chr14	54436601	54436613	+	Mmp14	TCACGTCTGGATG	TRUE
chr14	54438764	54438776	+	Mmp14	CAACATCTGTGAC	TRUE
chr8	92827139	92827151	+	Mmp2	GGTGCAGATGTGG	FALSE
chr8	92827409	92827421	+	Mmp2	CATCCAGGAGTTT	FALSE
chr8	92827338	92827350	+	Mmp2	CCACATCTGGCGT	TRUE
chr8	92841862	92841874	+	Mmp2	GTTCTGATGTAT	FALSE
chr8	92842235	92842247	+	Mmp2	CTGCCAGATGTGG	FALSE
chr8	92842900	92842912	+	Mmp2	TCTGCAGATGTCA	FALSE
chr8	92842235	92842247	+	Mmp2	CTGCCAGATGTGG	FALSE
chr8	92842900	92842912	+	Mmp2	TCTGCAGATGTCA	FALSE
chr15	25620692	25620704	+	Myo10	GCACATCTGTTTT	TRUE
chr15	25621274	25621286	+	Myo10	CAACATCTGGAAA	TRUE
chr15	25620692	25620704	+	Myo10	GCACATCTGTTTT	TRUE
chr15	25621274	25621286	+	Myo10	CAACATCTGGAAA	TRUE
chr15	25620692	25620704	+	Myo10	GCACATCTGTTTT	TRUE
chr15	25621274	25621286	+	Myo10	CAACATCTGGAAA	TRUE
chr15	25672913	25672925	+	Myo10	GGACCTCTGGAAG	TRUE
chr15	25673430	25673442	+	Myo10	TGACATCTGGGAC	TRUE
chr15	25712506	25712518	+	Myo10	TGTACAGATGTTC	FALSE
chr15	25712883	25712895	+	Myo10	TGTCCAGCTGTCC	FALSE
chr15	25713168	25713180	+	Myo10	GATGCAGAAGTGC	FALSE
chr15	25741349	25741361	+	Myo10	GTTACAGATGGTT	FALSE
chr15	25740923	25740935	+	Myo10	CCACATCTTCATT	TRUE
chr15	25751213	25751225	+	Myo10	TGTACAGATGTAA	FALSE
chr15	25751213	25751225	+	Myo10	TGTACAGATGTAA	FALSE
chr15	25756812	25756824	+	Myo10	CATCCAGATATGG	FALSE
chr15	25757303	25757315	+	Myo10	CATCCAGGTTTTTC	FALSE
chr15	25757548	25757560	+	Myo10	CTTCCAGATGTGC	FALSE
chr15	25758118	25758130	+	Myo10	GTGCCAGATGCTG	FALSE
chr15	25756812	25756824	+	Myo10	CATCCAGATATGG	FALSE
chr15	25757303	25757315	+	Myo10	CATCCAGGTTTTTC	FALSE
chr15	25757548	25757560	+	Myo10	CTTCCAGATGTGC	FALSE
chr15	25758118	25758130	+	Myo10	GTGCCAGATGCTG	FALSE

chr15	25767453	25767465 +	Myo10	TAAATCTGGCAA	TRUE
chr15	25773850	25773862 +	Myo10	CCTCCAGCTGTGA	FALSE
chr15	25779732	25779744 +	Myo10	CAGGCAGCTGTTG	FALSE
chr15	25780084	25780096 +	Myo10	ATTACAGGTGTGT	FALSE
chr15	25778550	25778562 +	Myo10	CAAGATCTGAATT	TRUE
chr15	25778865	25778877 +	Myo10	GAACATTTGTAAG	TRUE
chr6	5299875	5299887 -	Pon2	GTCACAGATGTGT	FALSE
chr6	5299768	5299780 -	Pon2	TGGCCTGATGTGC	FALSE
chr6	5299266	5299278 -	Pon2	CCACACCTGGCTA	TRUE
chr6	5299875	5299887 -	Pon2	GTCACAGATGTGT	FALSE
chr6	5299768	5299780 -	Pon2	TGGCCTGATGTGC	FALSE
chr6	5299266	5299278 -	Pon2	CCACACCTGGCTA	TRUE
chr6	5290483	5290495 -	Pon2	CGTCCAGCTGTTA	FALSE
chr13	92609287	92609299 +	Serinc5	ATGCCACATGTTT	FALSE
chr13	92609287	92609299 +	Serinc5	ATGCCACATGTTT	FALSE
chr7	99353179	99353191 -	Serpinh1	TTTCCAGAAGTTT	FALSE
chr7	99353179	99353191 -	Serpinh1	TTTCCAGAAGTTT	FALSE
chr7	99353179	99353191 -	Serpinh1	TTTCCAGAAGTTT	FALSE
chr7	99353179	99353191 -	Serpinh1	TTTCCAGAAGTTT	FALSE
chr7	99353179	99353191 -	Serpinh1	TTTCCAGAAGTTT	FALSE
chr7	99353179	99353191 -	Serpinh1	TTTCCAGAAGTTT	FALSE
chr7	99353179	99353191 -	Serpinh1	TTTCCAGAAGTTT	FALSE
chr7	99353179	99353191 -	Serpinh1	TTTCCAGAAGTTT	FALSE
chr7	99353179	99353191 -	Serpinh1	TTTCCAGAAGTTT	FALSE
chr7	99353179	99353191 -	Serpinh1	TTTCCAGAAGTTT	FALSE
chr7	99353179	99353191 -	Serpinh1	TTTCCAGAAGTTT	FALSE
chr7	99353179	99353191 -	Serpinh1	TTTCCAGAAGTTT	FALSE
chr7	99353179	99353191 -	Serpinh1	TTTCCAGAAGTTT	FALSE
chr7	99353179	99353191 -	Serpinh1	TTTCCAGAAGTTT	FALSE
chr7	99353179	99353191 -	Serpinh1	TTTCCAGAAGTTT	FALSE
chr7	99353179	99353191 -	Serpinh1	TTTCCAGAAGTTT	FALSE
chr17	85690151	85690163 -	Six2	TGACATCTGGATT	TRUE
chr17	85690151	85690163 -	Six2	TGACATCTGGATT	TRUE
chr5	88885787	88885799 +	Slc4a4	CAACCTCTGTATC	TRUE
chr5	88885787	88885799 +	Slc4a4	CAACCTCTGTATC	TRUE
chr5	88885787	88885799 +	Slc4a4	CAACCTCTGTATC	TRUE
chr5	88885787	88885799 +	Slc4a4	CAACCTCTGTATC	TRUE
chr5	88933577	88933589 +	Slc4a4	TAACCAGATGTCT	FALSE
chr5	88932535	88932547 +	Slc4a4	TAACAGCTGTATT	TRUE
chr5	88933602	88933614 +	Slc4a4	GAACATGTGGGTC	TRUE
chr5	88933577	88933589 +	Slc4a4	TAACCAGATGTCT	FALSE
chr5	88933602	88933614 +	Slc4a4	GAACATGTGGGTC	TRUE
chr5	89026659	89026671 +	Slc4a4	GTTACAGATGATG	FALSE
chr5	89026831	89026843 +	Slc4a4	CTACATCTGAGTC	TRUE
chr5	89027133	89027145 +	Slc4a4	CAACATCTGGAGA	TRUE
chr5	89026659	89026671 +	Slc4a4	GTTACAGATGATG	FALSE
chr5	89026831	89026843 +	Slc4a4	CTACATCTGAGTC	TRUE
chr5	89027133	89027145 +	Slc4a4	CAACATCTGGAGA	TRUE
chr5	89026659	89026671 +	Slc4a4	GTTACAGATGATG	FALSE

chr5	89026831	89026843	+	Slc4a4	CTACATCTGAGTC	TRUE
chr5	89027133	89027145	+	Slc4a4	CAACATCTGGAGA	TRUE
chr16	14705571	14705583	+	Snai2	CCACATCTGGAAG	TRUE
chr14	69028272	69028284	+	Stc1	GTGACAGATGTCT	FALSE
chr14	69029137	69029149	+	Stc1	AAGCCAGAGGTGC	FALSE
chr9	116177030	116177042	-	Tgfb2	CACTCAGATGTGC	FALSE
chr9	116175339	116175351	-	Tgfb2	TGCCCAGCTGTTG	FALSE
chr9	116175827	116175839	-	Tgfb2	AAACTCCTGGATT	TRUE
chr9	116175138	116175150	-	Tgfb2	CCACATCTGGCCC	TRUE
chr9	116177030	116177042	-	Tgfb2	CACTCAGATGTGC	FALSE
chr9	116175339	116175351	-	Tgfb2	TGCCCAGCTGTTG	FALSE
chr9	116175827	116175839	-	Tgfb2	AAACTCCTGGATT	TRUE
chr6	53822534	53822546	-	Tril	GGTCCAGAGGTGA	FALSE
chr6	53820969	53820981	-	Tril	CGTACAGCTGTTT	FALSE
chr6	53821136	53821148	-	Tril	CAACATCTTGCG	TRUE
chr6	42352650	42352662	+	Zyx	AGTACAGTTGTTG	FALSE
chr6	42352660	42352672	+	Zyx	TTGCCAGTTGTTA	FALSE
chr6	42353191	42353203	+	Zyx	GATGCAGATGAGT	FALSE
chr6	42353191	42353203	+	Zyx	GATGCAGATGAGT	FALSE
chr6	42353849	42353861	+	Zyx	CAACATTTGGCG	TRUE