CTCF Site	Chromosome	Start	End	Score	Strand
CTACCAGCAGGGGGCGCAC	chr3	182910180	182910198	23.64346786	+
TGGCCTCTAGAGGGCAGAC	chr3	183911235	183911253	19.06235562	-
TCACCACAAGAGGGTGGTA	chr3	59741	59758	17.63876703	+
CTGCCACTGGGAGGCAGCA	chr3	224842	224860	17.06625782	-
GCACCAGCAGAGGGCAGAC	chr3	371222	371240	18.18163135	-
AATCCAGCAGAGGGCACTG	chr3	498550	498567	19.30318065	+
CCGCCAGCAGAGGGAGCTG	chr3	552843	552860	21.85385819	+
GTACCACCAGGTGGCGCTT	chr3	649451	649468	20.11814941	+
CTGCCAGCAGGTGACACAC	chr3	868314	868332	17.73336316	-
TCACCAGTAGAGGGCAGCT	chr3	919047	919064	19.04497884	+
TGTCCACCAGAGGGCACCC	chr3	1098882	1098899	23.81484235	+
CTGCCACTAGATGGTGCCA	chr3	1292332	1292349	19.90544365	+
TACCCACTAGATGGCGGAG	chr3	1365426	1365444	18.02727226	-
GGGCCACCAGAGGGAGCCT	chr3	1456275	1456292	19.82687043	+
CTGCCACACGGTGGCGCTG	chr3	2173113	2173131	18.23162084	-
TGGCCAACAGGGGGAGCCC	chr3	2730810	2730828	21.09442574	-
GGGCCGCCAGGGGGCGCTG	chr3	3196462	3196480	23.92643608	-
CGGCCACTAGGAGGAACCC	chr3	3213015	3213032	19.4535874	+
TAGCCACAAGATGGCGGGG	chr3	3217497	3217514	19.46321933	+
TCAACAGTAGAGGGCAGCA	chr3	4015028	4015046	17.42418273	-
TGGCCACTAGAGGGAGAAC	chr3	4367666	4367683	17.84055719	+
CAGCCACTAGATGTCACTC	chr3	4650256	4650274	17.89978464	-
TTACCAGCAGGTGTCACTA	chr3	4728243	4728260	19.1000558	+
TTGCCAGCAGAAGGCGATG	chr3	5043727	5043745	18.40677517	-
TGCCCACCAGGTGGCGATG	chr3	5138865	5138882	21.49356761	+
TGGCAAGGAGGGGGCACTC	chr3	5263569	5263586	17.14651591	+
CGGCCCCTAGAGGGCAACA	chr3	5322251	5322268	17.85785711	+
TGGCCTCTAGGGGACACAA	chr3	5493292	5493309	17.92369728	+
CCACCACTAGGGGGCAGGC	chr3	6816168	6816186	20.94182071	-
TTACCAACAGATGGCACTG	chr3	6952298	6952315	18.25904394	+
AGACCACCAGTGGGCAGTC	chr3	7647856	7647873	17.40665264	+
GAGCCAGCAGGTGGCGAGA	chr3	8112623	8112640	18.36381174	+
CAGCCACCAGGGGACATCC	chr3	8256595	8256613	17.33668681	-
TGTCCAGTAGAGGGAGCTC	chr3	8318857	8318875	19.62287913	-
TAGCCACAAGGTGGCACTG	chr3	8434252	8434270	22.18484429	-
CAACCACTAGATGTCACCA	chr3	8458882	8458899	17.49653377	+
TGGCCACAAGGTGGCGGTG	chr3	8639770	8639788	24.39654517	-
TGTCCACCAGGGGGTGCTA	chr3	8680333	8680350	22.5630618	+
GGTCCGCTAGGGGGCGGGC	chr3	8786215	8786232	17.74180135	+
TGACCACATGAGGGCAGCA	chr3	8987844	8987861	17.26407343	+
CTGCCACCAGATGGCTGTA	chr3	9241383	9241400	18.95801348	+
GAACCACTAGGTGGCAGGG	chr3	9370032	9370049	18.13690254	+
TAGCCAGCAGAGGGCTGGA	chr3	9421553	9421570	17.58163977	+
CCGCCAGGAGGGGGCGCTG	chr3	9517390	9517407	23.45469128	+
CTGCCGCCAGAGGGCAGGC	chr3	9520069	9520086	18.80728412	+
TGACCTGGAGGGGGCACAG	chr3	9712557	9712574	18.16083182	+
CAGCCAGCTGGGGGAGCCA	chr3	9713392	9713409	18.13025495	+
TGTCCTCTAGGGGACGCTA	chr3	9743831	9743848	18.3668998	+
GCGCCAGCAGGAGGCAGGG	chr3	9748111	9748128	17.59963305	+
GGGCCTGCAGGAGGCGCTG	chr3	9803699	9803716	19.58775658	+
TGGCCAGTAGAGGGCAACT	chr3	9817405	9817422	19.38964136	+

CGGCCGCCAGGGGCCGCGC	chr3	9949638	9949655	17.69867459	+
CGTCCAGCAGGCGGCGACG	chr3	9963979	9963996	18.16793564	+
TGGCCCGCAGGGGACGCGG	chr3	10027538	10027555	17.37971264	+
TCTCCACTAGAGGGCAATA	chr3	10339181	10339199	18.62291382	-
CCTCCAGTAGGAGGCGCGG	chr3	10351429	10351447	17.87083289	-
AGACCAGCAGGTGGCAAGA	chr3	10488946	10488964	17.59614581	-
TGGACACCAGGGGGCGCCA	chr3	10755741	10755759	24.74680019	-
TGGCCACATGAGGGCAGCA	chr3	10775427	10775444	18.49819964	+
CTGCCACCAGGTGGCAGCA	chr3	10900378	10900396	24.42208028	-
CTGCCACCTGGTGGCAGTG	chr3	10900382	10900399	19.15420167	+
CTGCCTCAAGGGGACGCTG	chr3	10951986	10952003	17.33670746	+
TGGCCAGCAGGGGTCACTA	chr3	10958915	10958933	23.1449727	-
CAGCCACCAGGTGGCGCTG	chr3	10962542	10962559	25.63003073	+
TGTCCAGCAGGTGGCGCCG	chr3	11077589	11077606	24.91635715	+
TCTCCTGTAGGGGGCGGTG	chr3	11178548	11178565	19.7569163	+
CAACCACCAGGTGGCAATC	chr3	11222769	11222787	19.83857488	-
TGACCAGCAGGTGGTGCTA	chr3	11253469	11253486	21.80299295	+
TTGCCAGGAGAGGGTGCTA	chr3	11351664	11351682	18.13893538	-
TCACCAGCAGAGGGCAGTT	chr3	11820650	11820668	19.74732817	-
GTGCCTCTAGGTGGCAGCA	chr3	11851699	11851717	18.67717292	-
TCTCCACTAGATGGCAGCC	chr3	12063090	12063108	19.58970791	-
TTGCCAGTGGGTGGCGGCC	chr3	12151717	12151734	19.41776346	+
TGACCACCAGGTGTCACTG	chr3	12192534	12192552	21.42394939	-
CTGACACAAGGGGGCACAG	chr3	12465516	12465534	17.50418998	-
GAACCAGTAGGTGGCAGAA	chr3	12617758	12617775	17.58296231	+
TTTCCACTAGAGGGCTCTC	chr3	12723146	12723163	17.01074087	+
CTTCCAGCAGGCGGCGGTA	chr3	12804026	12804043	18.57748151	+
GGACCACTAGAGGGCTCCC	chr3	12884617	12884634	18.06958382	+
TGGCCCCCTGGGGGCGCTG	chr3	12948155	12948172	18.98771406	+
GCACCAGGAGGGGGCACCG	chr3	12960104	12960122	19.6347131	-
CCACCAGAAGAGGGCGCCT	chr3	13000858	13000876	19.10952155	-
CGGGCACCAGGGGGCGCCT	chr3	13011632	13011650	21.41244413	-
GTTCCAGCAGAGGGCAGCG	chr3	13108827	13108844	19.45682649	+
CATCCAGCAGAGGGCAGGG	chr3	13318864	13318881	19.10514445	+
TGACCACCAGGGGGCGAGG	chr3	13408000	13408017	22.65984492	+
CTGCCACAAGAGGGCGCTG	chr3	13478264	13478282	23.0842255	-
CTCCCGCCAGGGGGCGGAG	chr3	13496572	13496589	18.7325152	+
TGGGCACAAGAGGGCAGCC	chr3	13512950	13512967	18.04056024	+
TGACCAGCAGAGGGTGCCC	chr3	13516807	13516824	21.33516558	+
TGCCCACCAGGCGGCGGCA	chr3	13587154	13587171	20.47400982	+
CTGCCACCAGGAGGAACAG	chr3	13649465	13649483	17.33064613	-
CAGCCACGAGGGGGCACTG	chr3	13664929	13664947	22.72763878	-
CCACCGCCAGGTGTCGCTG	chr3	13667128	13667146	18.07664836	-
CCGCCGCCAGGGGCCGCTG	chr3	13671985	13672002	18.53326926	+
TGGCCACTAGGAGGCTCAA	chr3	13689899	13689917	17.54524032	-
TATCCAGCAGGGGGCGACA	chr3	13902091	13902109	21.21220514	-
TAGACACGAGATGGCGCCA	chr3	13913235	13913252	17.43835323	+
TGTCCAGGAGGGGGCAGTG	chr3	14169345	14169362	21.09283498	+
TGGCCACTAGATGGCGGTG	chr3	14277824	14277841	24.58897525	+
TGAGCAGCAGGGGGAGCCG	chr3	14478435	14478453	18.88714875	-
TGTCCAGCAGGGGGCGCTC	chr3	14525584	14525601	25.22322718	+
CAGCCACAAGGGGGAGTCG	chr3	14564961	14564979	17.26275882	-
CAGCCAGCAGGTGGTAGAG	chr3	14618425	14618443	17.78223194	-
TGACCGCGAGGGGGCGGGA	chr3	14618741	14618759	19.20079578	-

TTGCCACACGGTGGCGCCA	chr3	14650514	14650531	18.59327056	+
AAGCCACCAGGGGGCAGCC	chr3	14930854	14930872	22.6337594	-
AAACCACTAGAGGGCAGCA	chr3	14942338	14942355	19.63997557	+
TTGCCACGGGGTGGCGGCG	chr3	14964527	14964544	18.5754528	+
CAGCCACCAGGGGGCGGCA	chr3	15124769	15124786	26.4084487	+
CCGCCAGCAGGGGGCGCCC	chr3	15135312	15135329	26.21200237	+
CGCCCACTAGGGGGCAGGA	chr3	15284624	15284641	21.15840317	+
AAACCAGCAGATGGCGACA	chr3	15394937	15394955	17.49501319	-
GTTCCTCCAGGTGGCACTG	chr3	15521695	15521713	17.75710006	-
GCTCCACCAGGTGGTGCCC	chr3	15566944	15566962	17.76870582	-
TCACCCCTAGGGGGCACAG	chr3	15970572	15970590	17.57743188	-
TGGCCACCAGAGGGGGGCA	chr3	16065378	16065395	20.95866577	+
GGGCCAGCAGAGGGCGCTG	chr3	16195018	16195036	24.76560393	-
CTGCCACTAGGTGGCGCAA	chr3	16263988	16264006	23.12993023	-
TGGGCAATAGGGGGCGCTA	chr3	16266033	16266051	18.78644075	-
TGAGCAGCAGAGGGCACTG	chr3	16307000	16307017	19.55682932	+
ACAACAGCAGAGGGCGCTA	chr3	16336021	16336039	17.49892401	-
CAGCCAGCAGGTGGCGCTC	chr3	16617943	16617960	24.43932792	+
TGGCCACAAGGGGTCCCTC	chr3	16845460	16845477	17.02415682	+
CGGCCTGTAGGGGGCAGCG	chr3	16900696	16900713	22.6799956	+
TGTCCACTAGATGGCACAC	chr3	17275520	17275537	19.74108381	+
TTGCCACTAGGTGGCACTA	chr3	17429611	17429629	23.86878584	-
TAACCAGCAGGGGGAGATA	chr3	17661766	17661783	18.65899263	+
CTGCCACTGGGGGGCAGTG	chr3	18311921	18311939	20.37080821	-
TTTCCACCAGGGGGCACTC	chr3	18405798	18405816	23.17715701	-
CAACCAGTAGGGGGAGACA	chr3	18774787	18774805	17.88601439	-
TAGCCACAAGAGGGAACCA	chr3	19005302	19005320	18.98639377	-
AGGCCACTAGATGGCAATG	chr3	19365616	19365633	18.93013838	+
CGCCCGCCAGGGGGCGAGG	chr3	20056459	20056477	17.96539869	-
CAGCCAGCAGAGGGCGGGA	chr3	20356993	20357010	22.38154916	+
CAGCCAGGAGGTGGCGCTT	chr3	21033868	21033885	19.38315155	+
TTGTCAGCAGGGGGCACTG	chr3	21500994	21501012	20.5806331	-
TAGCCACTGGAGGGAGCCC	chr3	21911151	21911169	17.06435796	-
TTGTCAGTAGAGGGCACTA	chr3	22105883	22105900	18.28112096	+
TGACCAGCAGAAGGCAGTG	chr3	23069230	23069248	20.20555257	-
CGGCCTGTCGGGGGCGCCC	chr3	23827490	23827507	18.74276408	+
TGCCCACCAGGTGGCAGAC	chr3	24202581	24202598	20.62147155	+
TGGTCACCAGAGGGCAGGC	chr3	24214522	24214539	18.63941291	+
TCTCCACCAGGTGTCAGTA	chr3	24254700	24254718	18.30140569	-
AGTCCACAAGAGGGCAGTC	chr3	24281339	24281356	18.11005993	+
TAGCCACCAGGGGGCCGCC	chr3	24513249	24513267	21.19572138	-
AAGCCACAAGAGGGCAGAA	chr3	24599674	24599692	17.39240907	-
AAGCCAGCAGAGGGCAGCA	chr3	24697164	24697181	21.20650425	+
GTACCACCAGATGGCAGGA	chr3	24700457	24700475	17.95890314	-
TGTCCTCCAGGGGGAGCTC	chr3	25050105	25050123	19.67470201	-
CCGCCAGTAGAGGGCGCAC	chr3	25457928	25457945	21.93948899	+
AGGCCAGTAGGGGTCACTA	chr3	25610620	25610638	19.88013139	-
AGACCAGAAGGTGGCAGAA	chr3	25920944	25920961	17.54436541	+
TGTCCTCCAGGGGGCGATA	chr3	26729107	26729125	20.51167104	-
TCACCAGTAGAGGGCCGTG	chr3	26980058	26980076	17.62421554	-
CAAACACCAGAGGGCAGTG	chr3	27150857	27150874	18.33248496	+
TGGCCAGCAGGGGGCTGTG	chr3	27675853	27675871	22.5048462	-
TGCCCACTAGAGGGCAGGC	chr3	27697859	27697877	19.35267733	-
TGGCCACCAGATGGCGAAG	chr3	27728724	27728741	21.52675299	+

CCGCCTGGAGGGGGCGGAA	chr3	27745096	27745114	18.23394452	-
CTTCCTCTAGGGGGCACAG	chr3	27843733	27843751	18.07249454	-
TGGCCAACAGATGGCGCTA	chr3	28684333	28684350	22.20020799	+
CTGCCACCAGAGGGGGCCA	chr3	28743540	28743558	19.84510094	-
TGGTCACCAGGTGGCGCTG	chr3	30029615	30029632	22.80077384	+
GTTCCACCAGAGGGCACCA	chr3	30058928	30058945	20.75802298	+
TGGCCACTAGGTGGAGAAA	chr3	30129576	30129593	18.58928597	+
TAGCCAACAGGTGGCGCTG	chr3	30215778	30215796	21.6782934	-
GTGCCACCAGGGGGCAGGC	chr3	30785399	30785416	21.09706218	+
CTGACAGAAGAGGGCGCTC	chr3	30944630	30944647	17.68284049	+
TGCCCAGCTGAGGGCACTC	chr3	30944951	30944968	17.11721986	+
AGGCCACTAGGTGGTGCTT	chr3	31465182	31465200	17.83324002	-
CTGCCACTAGATGGCAGGA	chr3	31567360	31567377	20.06277827	+
AGACCACAAGGGGGTGGTG	chr3	31711944	31711962	18.14746677	-
TTGTCAGCAGGGGGCAGCA	chr3	31785443	31785461	20.23142511	-
CAGCCACCAGGGGGTAATA	chr3	32035749	32035766	18.88931341	+
TTACCACAAGAGGGCACTG	chr3	32160790	32160808	20.90697449	-
TGCCCACTAGAGGTCGCTC	chr3	32192295	32192312	18.90842259	+
TGACCACTAGGGGATGCTC	chr3	32194563	32194580	17.88300061	+
TGGCCAGTAGAGGGCAGCA	chr3	32313382	32313399	24.34302005	+
CAGCCTGAAGATGGCACTA	chr3	32357654	32357671	17.23844877	+
TGACCACAAGGGGGAGCCA	chr3	32391733	32391750	21.93057806	+
TAACCCCTAGGGGGCGGTA	chr3	32415715	32415733	19.27890953	-
TGGCCGCCAGGGGGCGTGC	chr3	32484489	32484507	19.55841992	-
CCGCCGGTAGGTGGTGCTC	chr3	32798133	32798151	17.14283973	-
CTACCTCCAGGAGGCACTG	chr3	32890398	32890415	18.16055988	+
CTGCCTGCAGGTGGAGCTG	chr3	32919697	32919715	18.93482027	-
CTGCCAGCAGATGGCAGCA	chr3	32950822	32950840	22.4448512	-
GATGCACCAGGGGGCGCTG	chr3	32964379	32964396	17.76760217	+
CTGACAGGAGGTGGCGCTC	chr3	33022749	33022767	17.36739276	-
TATCCACCAGAGGGCAGTG	chr3	33091135	33091153	21.59539068	-
CAGCCACTGGGTGGCACAA	chr3	33148282	33148299	18.05653879	+
GGTTCAGTAGGGGGCGCTG	chr3	33161155	33161173	18.11814062	-
GAGCCACCAGAGGGTGGAG	chr3	33437668	33437686	17.39507941	-
TAGCCACAAGAGGGAACTA	chr3	33900120	33900137	18.70549237	+
TTGCCAGTAGGGGGCAGAA	chr3	34123463	34123480	22.02335431	+
GGGCCACCAGGTGGGGCTA	chr3	34277283	34277300	19.59311943	+
CGACCACGAGGTGGCAGTA	chr3	35925064	35925082	21.57395318	-
TCTCCACCAGGGGGAGATA	chr3	36148888	36148906	18.65558259	-
TTGTCACCAGGGGACACTG	chr3	36714297	36714315	17.06623948	-
TGGGCAGCAGGTGGTGCTC	chr3	36717640	36717658	17.60262196	-
CAGCCTCCAGGAGGCAGCC	chr3	36850144	36850161	18.34049291	+
CCACCACCAGATGGCAGCA	chr3	36885535	36885553	22.07070908	-
TGGCCTGTAGGGGGAACTC	chr3	36940113	36940130	19.27938088	+
TGGCCACAAGATGGCAGCA	chr3	37229667	37229685	22.34743147	-
CGGCCCGCAGGGGGCGCTG	chr3	37468526	37468543	23.24309468	+
AGGCCTGTAGGAGGCGGTA	chr3	37571051	37571068	17.61643444	+
CATCCAGCAGTGGGCACCC	chr3	37620402	37620420	17.03131488	-
TCGCCACCAGAGGGCATTC	chr3	37796231	37796249	20.32942247	-
CTGCCAGAAGGGGGCGATT	chr3	37820740	37820757	18.17626994	+
TGGCCACCAGGGGGCGGGC	chr3	37872052	37872069	25.71760919	+
CCTCCACTAGGGGGAAGCC	chr3	37928719	37928737	18.68236929	-
TAGCCACCAGGGGGAGGAG	chr3	37983966	37983984	21.21535989	-
GGACCTCTAGGGGGCAGTG	chr3	37991315	37991332	19.96281659	+

CTGCCAGCAGAGGTCGCCA	chr3	38020026	38020044	21.35945338	-
GGGCCAGAGGGTGGCAGCA	chr3	38134113	38134131	17.19470895	-
TGGCCAGTAGGAGGCACCA	chr3	38167856	38167873	22.71405846	+
CTCCCACAAGGTGGCAGTC	chr3	38385022	38385039	18.04759669	+
TGGCCATTAGAGGGCACCA	chr3	38496517	38496535	20.33244723	-
TGTCCACAAGGTGGCGCAA	chr3	38538070	38538087	21.11238137	+
TTTCCAGCAGATGGCAGTC	chr3	38672394	38672412	19.43207316	-
TGTCCAGCAGAGGGCAGTA	chr3	39117785	39117802	22.79283779	+
CCGCCGGCCGGGGGCGCCC	chr3	39169456	39169473	18.34424594	+
CTTCCACCAGGAGGCAGGA	chr3	39200997	39201015	17.65193299	-
CAGCCTGAAGGTGGCACCA	chr3	39225144	39225161	18.84573098	+
TTACCACAAGGGGGCGCCC	chr3	39308517	39308535	22.98815588	-
TGGCCACTAGAGGGAACAC	chr3	39394778	39394796	19.83052489	-
TTTTCACCAGGTGGCACTC	chr3	39399793	39399810	17.31146928	+
GGGCCACCAGAGGGCTCCT	chr3	39434024	39434041	18.24704862	+
TGGCCACAAGAGGGCAGTA	chr3	39464543	39464560	23.19415603	+
TGTCCGGCAGGGGGCAGCA	chr3	39515255	39515273	21.58372308	-
GTGCCTCCAGAGGGCACAA	chr3	39654487	39654504	18.13901581	+
AGTACACCAGGGGGCAGTA	chr3	39685101	39685118	18.2777941	+
TTGCCACATGGTGGCGCCA	chr3	39829224	39829241	18.66777226	+
AGTCCACTAGAGGGCAGCC	chr3	40007249	40007267	19.90977223	-
CGCCCAGCAGAGGGCACCA	chr3	40195634	40195652	22.8543241	-
CAACCAGCAGGTGGAAGCC	chr3	40197906	40197923	18.54140412	+
TGGCCACAAGGGGGTGATA	chr3	40333738	40333756	19.30981036	-
CTGCCACTAGGTGGAGCTC	chr3	40597189	40597206	20.97122021	+
TGGCCTGCAGGGGGCAGCA	chr3	40601210	40601227	23.74399466	+
TAGCCACCTGAGGGCAGTC	chr3	40605118	40605135	18.33120995	+
GGGCCACCAGAGGGCTCCT	chr3	41712468	41712485	18.24704862	+
ATGTCAGCAGGGGGCACCC	chr3	41910672	41910689	18.04008941	+
CTTCCAGCAGGTGGCAGTT	chr3	42133857	42133874	18.6479129	+
ATACCACTAGAGGGCGCCA	chr3	42207819	42207837	21.44896934	-
TAGCCAGCAGAGGGCACTT	chr3	42246527	42246544	21.25753612	+
TTTCCACTTGAGGGCGCTG	chr3	42264163	42264180	17.4442759	+
TCACCAGTAGGTGGCAGTG	chr3	42460502	42460520	21.54259896	-
GAGCCAGCAGGGGGCAGAG	chr3	42553092	42553110	20.91784583	-
CATCCACCAGGGGGCGATA	chr3	42556562	42556580	21.5115231	-
TGGCCACCAGGGGGCGCAG	chr3	42564101	42564119	26.98448117	-
TTACCACCAGATGTCACTG	chr3	42797499	42797516	18.41440386	+
TTATCAGCAGGGGGCGCTG	chr3	42847927	42847944	20.3602606	+
CGACCGCCAGAGGTCAGCA	chr3	42897644	42897662	17.98896073	-
TGGCCACTTGGTGGTGCTA	chr3	42978294	42978311	17.72785889	+
CCACCAATAGGGGGCAGCA	chr3	43087943	43087961	19.51909888	-
AAACCACTAGAGGGAGCCC	chr3	43519755	43519773	17.45326766	-
TGACCAGCAGGGGGCGGCT	chr3	43786107	43786124	23.842393	+
CCGTCACTAGATGGCGGTG	chr3	44215314	44215332	18.30625567	-
TATCCACTAGAGGGCCCCA	chr3	44252623	44252641	17.82376098	-
TGGCCACCAGGGGATGCTG	chr3	44440300	44440318	20.64023209	-
CAGCCTCCAGAGGGCAGTA	chr3	44546616	44546633	20.87875584	+
CATCCACTAGATGGCGCTT	chr3	44549464	44549481	18.48810089	+
TCGTCAGCAGGTGGCAGCA	chr3	44930569	44930587	19.31293496	-
TGCCCACAAGAGGGCACTC	chr3	45054317	45054334	20.24286429	+
CCAGCAGCAGGTGGCAGTA	chr3	45054412	45054429	17.58081695	+
TCTCCACTAGAAGGCACTG	chr3	45057391	45057408	18.02094461	+
TGACCTGAAGATGGCACCA	chr3	45072223	45072241	18.19402885	-

TGGCCAGCAGGAGGCTGAG	chr3	45095541	45095558	17.22729458	+
CCGCCACCAGGTGGTGCCC	chr3	45227224	45227242	21.87423708	-
CGGCCAGATGAGGGCGGCC	chr3	45241793	45241810	18.24050223	+
GCTCCAGAAGGGGGCGCTC	chr3	45563324	45563342	19.32350805	-
CCGCCACTAGGTGGTGCCA	chr3	45673447	45673465	21.44096028	-
TGGTCACTAGATGGCGGTG	chr3	45777795	45777812	19.85091348	+
GTGACACCAGGGGGCAGAA	chr3	45945725	45945743	17.52314255	-
TGACCACTAGAGGGCACCC	chr3	45955443	45955460	23.84999699	+
TAACCACCAGGTGGCACCA	chr3	46095472	46095490	23.74380053	-
GGACCTCCAGGTGGCAGTG	chr3	46411760	46411777	19.81844137	+
ACGCCTCCAGGGGGCAGCC	chr3	46461614	46461631	20.08924952	+
GGGCCACGGGAGGGCGGTC	chr3	46505397	46505414	17.31547818	+
CTATCTGCAGGGGGCGCTG	chr3	46513411	46513428	17.38097475	+
CGGCCACTGGGAGGCGCCG	chr3	46646631	46646649	20.39328566	-
TCACCACAAGGGGGAGGCT	chr3	46690845	46690862	17.22643424	+
TGGCCTCCAGGTGTCGCCA	chr3	46721676	46721693	21.05419317	+
TGGCCCCTGGGGGGCGCCA	chr3	46734449	46734467	19.36771545	-
TCCCCTGCAGGGGGCGCGA	chr3	46862529	46862546	18.8327312	+
AGTCCAACAGGGGGCAGCG	chr3	46865132	46865149	18.73689208	+
CAGCCAGCAGGGGGCGCAG	chr3	46883412	46883429	24.42482801	+
GCCCCACCAGGGGGCGCAC	chr3	46911858	46911876	20.00542255	-
TGGCCACTGGGGGGCAGCA	chr3	46926207	46926225	22.41562266	-
CCTCCACTAGAGGGTGCAA	chr3	46940158	46940175	17.02679202	+
CAGCAGCCAGGGGGCGCTC	chr3	47015220	47015238	17.10218029	-
CTGACAGCAGGTGGAGCTC	chr3	47103979	47103996	17.09294048	+
TGGCCAGCAGATGGCGCCA	chr3	47387845	47387863	25.85262735	-
TCTCCACCAGGGGGCAGAA	chr3	47437702	47437719	21.61405755	+
AGGCCTGCAGAGGGCAGCA	chr3	47439028	47439045	20.13602329	+
TGTCCACCAGAGGGCGAAC	chr3	47492540	47492558	19.86199283	-
CACCCACCAGAGGGCAGCA	chr3	47538763	47538780	21.02676759	+
AGGCCAGTAGGGGGCAAAA	chr3	47816436	47816454	19.06143588	-
CGGCCCGCAGGGGGCGCGC	chr3	47841440	47841457	20.9344711	+
GCGCCAGCAGGGGGAGCTG	chr3	47854354	47854371	21.32723933	+
TGGCCAGTAGAGGGCAGTG	chr3	48006626	48006644	24.05199924	-
TCACCCCCAGGAGGCGCTG	chr3	48174777	48174795	17.66084554	-
AGGCCACCGGAGGGCACTA	chr3	48211095	48211112	20.15022943	+
TCTCCAGCAGGTGGAGCTA	chr3	48290290	48290307	19.88082975	+
TGGCCAGAAGATGGCAGCA	chr3	48417460	48417477	21.6965832	+
TGGCCACCAGGTGTCGCTC	chr3	48452597	48452615	23.13197478	-
CAGCCACATGGTGGCACCA	chr3	48481972	48481989	17.4283784	+
CTGCCACGAGGGGGAAGCA	chr3	48520229	48520247	19.24272555	-
TGGCCACCAGGGGGCAGGA	chr3	48561346	48561364	25.25382942	-
GGGCCACAAGGGGGTGCTG	chr3	48749537	48749554	20.37978378	+
TGGCCAGCAGGGGCCGGGC	chr3	48752535	48752553	19.29462334	-
TTGCCAGTGGGGGGCACCA	chr3	48965132	48965150	20.72183846	-
TGGGCACCTGGGGGCGCTA	chr3	49124825	49124842	18.81519992	+
CAGCCACGAGGGGGCACTC	chr3	49137892	49137910	22.18778425	-
CTGCCTCTAGGTGGCACCA	chr3	49170718	49170736	21.17040139	-
TGGCCTCCAGGGGGCGCCG	chr3	49183621	49183638	26.03870604	+
CTTCCAGCAGATGGCGCTA	chr3	49461716	49461734	21.56540071	-
CTCCCAGGAGGTGGCGCCA	chr3	49552259	49552276	19.36740371	+
GCAGCACCAGGGGGCAGCA	chr3	49684311	49684329	17.78719293	-
GGGCCACCAGGTGGTGGGA	chr3	49714008	49714026	19.355341	-
TGGCCACCAGAGGGTGCCC	chr3	49716058	49716075	23.22014006	+

TCCCCACTAGAGGGCAGTC	chr3	49815167	49815184	19.64741747	+
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TGACCAGCAGAGGGAAGTG	chr3	49911644	49911661	20.51040729	+
GAGCCAGCAGGGGGCAGGA	chr3	49912426	49912444	20.84117659	-
CGGCCACACGGTGGCAGCG	chr3	49918909	49918927	18.54170446	-
TGGCCACCAGGTGGCAGCA	chr3	50134159	50134177	26.17587391	+
CAGCCACAAGGGGACGGAG	chr3	50135127	50135145	17.76814394	+
ACACCAGTAGAGGGCACAG	chr3	50158834	50158852	18.02050195	-
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AGGCCGCCAGGCGGCGCCC	chr3	50207107	50207125	18.5078238	+
AGACCTCTAGAGGGCAGCC	chr3	50234425	50234443	18.01952067	-
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GGCCCGCCAGGAGGCGCCG	chr3	50239929	50239947	17.57021968	+
CCACCACCAGGGGGCGCCC	chr3	50258794	50258812	25.62872443	-
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CGGCCGCCAGGGGGCGCCG	chr3	50272575	50272593	26.06033716	+
CAGCCGCGAGGGGGCAGCA	chr3	50285516	50285534	19.56203386	-
TGCCCACTGGGGGGCGCCC	chr3	50286899	50286917	20.47808463	+
TGGCCACTGGAGGGCACAT	chr3	50315585	50315603	17.17670274	+
TGGCCAGCAGGTGGCTGTG	chr3	50337171	50337189	21.37722023	-
TGCCCACCAGATGGCGATC	chr3	50359831	50359849	19.62733227	+
TAGCAGGCAGGGGGCGCTG	chr3	50388174	50388192	17.06181546	+
GCACCAGCAGGGGGCACTG	chr3	50448679	50448697	22.37007591	+
TGACCACCAGGGGGCAGGA	chr3	50532104	50532122	24.01970321	+
CAGCCACCAGGTGGCAGCA	chr3	50555049	50555067	24.26706903	-
TGAACACCAGGTGGCGGTG	chr3	50562714	50562732	21.45379839	-
CTTCCTCCAGGGGGCACTG	chr3	50584715	50584733	20.73772569	+
GCACCGCTAGGTGGCAGTG	chr3	50626687	50626705	17.45342174	-
TGACCAGCAGGTGGCCCCA	chr3	50665373	50665391	21.21149966	-
AGGGCGGCAGGGGGCGCTG	chr3	50687932	50687950	18.03310255	+
AGGCCAGTAGGTGGCGCTT	chr3	50984096	50984114	21.04337933	+
TGGCCACCAGAGGGAGTTC	chr3	51112904	51112922	19.5264886	+
TGATCAGCAGGGGGAGCTG	chr3	51384611	51384629	18.75270884	-
GTACCACTAGAGGGCAGCA	chr3	51401995	51402013	20.15294882	+
CTGCCACCAGATGGCACTG	chr3	51511273	51511291	23.44490747	+
TGGCCAGGAGGGGTCAGCA	chr3	51647143	51647161	19.76938109	-
TGGCCACCAGGAGGCAGCA	chr3	51678498	51678516	23.70792868	-
TGGCCAGGAGATGGCACTA	chr3	51685107	51685125	21.54170802	+
GGACCAGCAGAGGGTGCTC	chr3	51719792	51719810	19.1306356	+
TCACCAGCAGAGGGCACTA	chr3	51728342	51728360	22.97744308	+
AGGCCACAGGAGGGCAGCG	chr3	51728384	51728402	17.27872099	-
TGTCCCCCAGGTGGCGATG	chr3	51731572	51731590	17.5806929	+
TGGCCGCTGGGGGGCGCCA	chr3	51951272	51951290	21.25320825	+
CCACCAGCAGGGGGCTGCC	chr3	51967064	51967082	19.46710905	-
TGGCCAGGAGAGGGAGGTG	chr3	51975795	51975813	19.74202299	-
TGGCCACAAGAGGGCGCCC	chr3	51983148	51983166	24.57906601	-
CGTCCGCAAGGGGGCAGAG	chr3	52010725	52010743	17.68887959	+
CCGCCTCTAGGAGGCGCTT	chr3	52064389	52064407	17.05455817	-
CAGCCTCCAGGTGGAAGCA	chr3	52083794	52083812	18.06769559	-
CCTCCAGCAGGGAGCGCTC	chr3	52132356	52132374	17.69989188	-
GCACCACCAGGTGGCAGGG	chr3	52153511	52153529	19.48430035	-
TGGCCACCAGAGGGCGCAA	chr3	52229652	52229670	25.66821977	+
CCACCAGCAGGGGGAGCCC	chr3	52240746	52240764	21.68715967	+

ACGCCTGCAGGAGGCGCCA	chr3	52287939	52287957	18.04678649	-
CTGACAGAAGAGGGCGCCC	chr3	52348783	52348801	17.9637419	-
CAAACACCAGAGGGCACTG	chr3	52437761	52437779	18.97271377	+
TGGGCACCAGGGGGCGGTC	chr3	52481188	52481206	22.60185498	+
CTGCCTGAAGGGGGCGCTG	chr3	52491362	52491380	20.85110109	+
CAGCCTGCAGGTGGCCCTG	chr3	52503608	52503626	17.33714322	-
CAGCCACTAGAGGGCAGGA	chr3	53081888	53081906	21.03539299	-
CTACCACTAGGGGGCACTG	chr3	53123156	53123174	23.68153729	+
CAGCCACTAGGTGGCAGAT	chr3	53143935	53143953	18.73105036	+
TGGCCGCCAGAGGGCGCTG	chr3	53205146	53205164	24.52368385	-
GGGACAGCAGAGGGCAGCA	chr3	53207829	53207847	19.19196002	+
GTGCCAGGAGGTGGCAGTG	chr3	53209063	53209081	18.61094731	+
TGGCCAGTAGGTGGGGCCG	chr3	53239181	53239199	20.15343098	-
TTAACACCAGAGGGCAGTG	chr3	53241309	53241327	18.55812512	+
AAGCCAGCAGAGGGCAGCT	chr3	53496528	53496546	18.61661815	-
TGCCCAGCAGGTGGCAGGT	chr3	53540985	53541003	17.84392247	+
ATGCCACCAGGGGGAAGTC	chr3	53705982	53706000	19.21715275	+
CCAGCACCAGGTGGCAGTA	chr3	53738894	53738912	18.23166522	+
CGACCAGCAGAGGGAGGCT	chr3	53747154	53747172	19.15466681	+
CTCCCACTAGGTGTCACCA	chr3	53947891	53947909	17.17050543	+
CAGCCAGCAGGGAGAGCCA	chr3	54044187	54044205	17.12843527	-
CATCCACTAGATGTCGCTG	chr3	54437528	54437546	17.20086127	+
TGTCCTGCAGAGGGAGCTG	chr3	54543112	54543130	18.23732746	-
TGGCCACTAGATGGTGGCA	chr3	54839929	54839947	21.01900848	+
TGGGCACCAGATGGCAGTG	chr3	54847215	54847233	19.67394903	+
TGTCCAGTAGGTGGCGCGC	chr3	54863060	54863078	21.34358141	+
TGCCCAGCAGAGGGCTGTC	chr3	55022429	55022447	17.59706426	-
TGGCCACTAGGGGGCTTTC	chr3	55190200	55190218	18.28979685	-
TGCCCACTAGGGGGCAGCT	chr3	55444024	55444042	20.68881643	+
CGGCCAACAGGGGGCAGCC	chr3	55494325	55494343	22.66053081	+
TGCCCACTAGATGGCAGCC	chr3	56260601	56260619	20.27472182	-
TGGTCAGCAGGTGGAGCTG	chr3	56336118	56336136	18.85920908	-
TGCCCACAAGGTGGCACCA	chr3	56349742	56349760	21.27249448	+
CTGCCTATAGGGGGCGCTG	chr3	56356450	56356468	18.99839403	+
ATGCCACAAGGTGTCGCTG	chr3	56456352	56456370	17.20501237	-
ATTCCAGCAGAGGGCAGCA	chr3	56711750	56711768	19.10898391	+
CTGCCTCCAGGTGTCACTA	chr3	56811364	56811382	18.00574443	-
AGACCAGCAGGGGGCCCTG	chr3	56865112	56865130	19.76651424	+
CGGCCAGCAGAGGGCACTC	chr3	56998140	56998158	25.06499536	-
TTGACACTAGGGGGCAGCC	chr3	57109351	57109369	19.87642826	+
TAACCGCGAGGGGGCGCGC	chr3	57179391	57179409	17.45287467	+
TTGCCACCAGTGGGCACCA	chr3	57825783	57825801	20.71030884	+
CTGGCACCAGGGGGCACTC	chr3	57871950	57871968	20.47453645	-
TGACCGCTAGGGGTCGCCT	chr3	58138651	58138669	17.46681611	+
TGGACACCAGAGGGCGCTG	chr3	58266923	58266941	23.12939857	+
CAGCCTGCAGAGGGCAGTG	chr3	58268599	58268617	20.21778816	+
CTGCCGTTAGGGGGCGCCC	chr3	58452717	58452735	17.55241725	+
TGGCCACCAGGTGGCGGCC	chr3	58493690	58493708	26.63965368	-
CGGCCAGCAGAGGGCGCTC	chr3	58529519	58529537	26.07874906	+
TCACCAGTAGGTGGCGGCA	chr3	58591063	58591081	22.84737348	-
CCGCCGCTAGATGGAGGCG	chr3	58601563	58601581	17.21810543	+
TCTCCACCAGGGTGCACTG	chr3	58620252	58620270	17.64769715	-
GGGCCTGAAGATGGCACCA	chr3	58737197	58737215	17.50452648	+
CAGCCAGGAGGTGGCGCTT	chr3	59025224	59025242	19.38315155	+

TGGCCAGCAGATGGCGGAA	chr3	59536368	59536386	23.24951672	+
GGACCAGCAGGTGGCGCCC	chr3	59818695	59818713	23.47127943	-
TGGCCTCCAGGAGGAACCA	chr3	60216475	60216493	18.14878405	+
TGGCCAGCAGGGGCAGGCA	chr3	61133617	61133635	18.60355124	+
CCACCACCAGAGGGAGACC	chr3	61332028	61332046	18.00790574	-
TTGCCACTAGATGGCACTA	chr3	61342677	61342695	22.54240503	-
TGACCAGTAGGGGGCGGGT	chr3	61897241	61897259	20.8094718	-
TGGGCACTAGGTGGCGCCA	chr3	62149732	62149750	21.96208242	-
CAGCCACTAGGAGGCAGAA	chr3	62454298	62454316	18.85299123	+
TCGCCACCAGGTGGATCCA	chr3	62515176	62515194	18.19457273	+
GAGCCAACAGAGGGCAGCA	chr3	62519455	62519473	18.1929483	-
TAGCCACTAGATGGCAATC	chr3	62583475	62583493	18.83369844	+
GAGCCAGAAGGTGGCGGCG	chr3	62834488	62834506	20.26479375	+
TCGGCACCAGGGGGCACAG	chr3	62887490	62887508	19.61217529	-
CCGCCAGCAGGGGACACCT	chr3	62976382	62976400	18.9930946	+
TGCCCAGTAGGTGGCGAAA	chr3	63310490	63310508	18.18760758	+
CTACCAGAAGGTGGCAGAG	chr3	63366780	63366798	18.06204293	+
TCACCACAAGGTGGCAGCA	chr3	63779438	63779456	20.96565716	-
TGACCACCAGGTGGCTCAG	chr3	63954503	63954521	19.75219069	-
TGTCCAGCAGAGGACGCTG	chr3	63984262	63984280	20.271459	-
TGACCAGCAGAGGGCAGCA	chr3	63991552	63991570	24.09214459	+
TGGCCACCAGGTGGAACCA	chr3	64072779	64072797	23.52538623	-
CTGCCACTAGGAGGCACCA	chr3	64424446	64424464	21.6111131	-
TGACCAGCAGGTGGCATGC	chr3	64445300	64445318	18.34846269	-
CGGTCAGCAGAGGGCAGGG	chr3	64494509	64494527	18.45779026	+
GGGCCACCAGGGGGCGATG	chr3	65302988	65303006	23.7391116	+
AGGACACCAGGTGGCACAG	chr3	65373535	65373553	18.35082872	-
TGGCCACTAGATGCCAGTA	chr3	65397510	65397528	17.81320338	-
TGCCCAGCAGGGGGCAGGA	chr3	65712001	65712019	21.56143454	-
TAACCACAAGAGGGCGCTT	chr3	65745964	65745982	19.18595026	+
TGACCCCGAGAGGGCAGCA	chr3	66506051	66506069	17.02483894	-
CTGCCAGCAGAGGGCACCA	chr3	66541047	66541065	24.21270597	+
TTTCCAGTAGGTGGCACTA	chr3	66949446	66949464	20.96540597	-
TTGACAGTAGAGGGCAGCA	chr3	67071657	67071675	18.44917312	+
CTTCCACTAGGGGGCAGGG	chr3	67247123	67247141	20.25413404	+
CAGCCTCAAGGTGGCGCTC	chr3	67518073	67518091	19.67945761	+
CCTCCAGCAGGGGTCGACA	chr3	67673874	67673892	17.638717	+
TGTCCACAGGAGGGCACCA	chr3	69025666	69025684	17.95812817	-
GGACCACAAGGTGGCAGTC	chr3	69104402	69104420	19.68518215	-
TGACCAGAAGGGGGAGCCA	chr3	69252904	69252922	21.27972978	+
CGACCAGAAGGTGGTAGCC	chr3	69667694	69667712	17.30724736	-
AAGCCACAAGAGGGAGCCC	chr3	70080302	70080320	17.16858298	-
TGGCCAGAAGATGGTGCAG	chr3	70196209	70196227	17.51657689	+
TTGCCAACAGGTGTCACCG	chr3	70197707	70197725	17.23344605	+
CTGCCAGCAGGAGGAGCTC	chr3	70252399	70252417	18.83567745	+
ATTCCAGCAGAGGGCAGTC	chr3	70490997	70491015	18.27810856	-
GCCCCAGCAGGGGGCAGAG	chr3	70539651	70539669	18.24044629	+
TGTCCACAAGGCGGCAGTA	chr3	70663090	70663108	17.46630807	+
GCTCCACTAGGTGGCGCCC	chr3	70682762	70682780	20.64644266	+
TTGCCAGCAGAGGGCAGGC	chr3	71201877	71201895	21.04346167	-
TGGCCACTAGATGGCAGTC	chr3	71861862	71861880	23.03536702	+
GCCCCAGCAGATGGCAGCA	chr3	72007407	72007425	17.75944075	+
CTGCCACCAGGTGGAGACT	chr3	72058223	72058241	17.1917388	+
TGGCCACTTGAGGGCACTC	chr3	72087498	72087516	19.82636399	+

TGGACTGTAGAGGGCGCTA	chr3	73024890	73024908	18.59676201	-
TGGCCACAGGAGGGCACCA	chr3	73218022	73218040	20.21065977	-
TGTCCAGCAGAGGGAGCAC	chr3	73233088	73233106	18.92414947	+
AGGCCACCAGGGGGTGATA	chr3	73564461	73564479	19.53028143	-
GAGCCAGCAGGTGGTGCTC	chr3	73634708	73634726	18.72534067	-
GGACCACTAGGGGGCGATT	chr3	73640395	73640413	18.94196796	+
TTGCCACTGGAGGGCACCA	chr3	74000731	74000749	20.04630593	+
TTGTCAGTAGAGGGCGCCA	chr3	75324080	75324098	19.57577607	+
TCACCACAAGAGGGTGGTA	chr3	75390836	75390854	17.63876703	+
TGGCCACTGGGAGGCGCTG	chr3	75554066	75554084	20.18301315	-
CCACCAGGAGAGGGCAGCA	chr3	75561643	75561661	19.53122257	-
GCTCCACTAGGTGGTGCTG	chr3	75659694	75659712	17.0444082	+
TGTCCACTAGGTGGTGCTG	chr3	75684144	75684162	20.44206568	-
CGGCCAGCAGAGGGCGCCA	chr3	75712203	75712221	26.90962441	-
TGTCCAGAAGGGGGCAGAT	chr3	75736562	75736580	17.34529045	+
AGGGCTCCAGGGGGCGCCA	chr3	75790883	75790901	18.88271162	-
CAGCCACCAGAGGGCTCCC	chr3	75855525	75855543	20.30178447	+
CTGCCGATAGGGGGCACTA	chr3	76779199	76779217	18.08701975	-
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CCACCACAAGGTGGCAGTG	chr3	77387267	77387285	20.60400744	-
TTGCCACTAGAGGGAAGCT	chr3	77452575	77452593	17.43010101	-
AGGCCTGCAGGGGGCATTC	chr3	77625532	77625550	17.2887364	-
TGACCACTAGAGGGAGGAC	chr3	78777761	78777779	18.96992358	-
GGACCAGCAGATGGCGCCA	chr3	78791415	78791433	22.69487257	+
TGGCCACTAGATGGAAGCA	chr3	79110054	79110072	20.57552587	-
CAGCCAGCAGAGGGCAATA	chr3	79164737	79164755	20.77307192	-
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TTGCCACTAGATGGCACTA	chr3	79493793	79493811	22.54240503	-
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TAACCACAAGGTGGCAGAA	chr3	79653255	79653273	18.63862827	+
GGAACACCAGGGGGCAGCG	chr3	79856213	79856231	19.92494349	-
TCAACAGCAGGGGGCGCCT	chr3	79978580	79978598	18.79791069	-
TCGACAGCAGAGGGCACCC	chr3	80820872	80820890	19.73181455	-
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CCACCACTAGAGGGCGCCA	chr3	81622500	81622518	23.86906682	+
TGGGCACCAGAGGGCAGAA	chr3	81714037	81714055	19.12971399	+
CTTCCACTAGGTGGCGACA	chr3	82042281	82042299	19.83655905	+
TTGCCACTAGTTGGCAGTA	chr3	82144808	82144826	17.67830192	+
TGTCCAGCAGGGGCCGCAG	chr3	82265022	82265040	18.30896371	-
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CCACCGCGAGGGGGCGGGG	chr3	85090493	85090511	17.64601856	-
AAACCTGCAGGTGGCAGCA	chr3	85492793	85492811	17.26247594	-
TCGCCTACAGGGGGCGCTA	chr3	85699100	85699118	20.2715289	-
CTGCCACTAGATGGCAGCC	chr3	85708106	85708124	21.56247479	-
TGACCACTGGAGGGAGGTG	chr3	85933977	85933995	17.28713205	-
AGGCCACCAGAGGGCAGGG	chr3	85953164	85953182	21.63573864	+
TGACCAGTAGAGGGAGCCA	chr3	86695388	86695406	21.47215987	-
ATACCACTAGGTGGCAGAG	chr3	86906122	86906140	18.02074044	+
GTGCCACAAGAGGGCGCAA	chr3	87101828	87101846	19.55936483	+
TTGCCACCAGAGGTCACTC	chr3	87214824	87214842	20.2363015	-
CTGCCGACAGAGGGCACTG	chr3	87277554	87277572	17.73377028	-
TGACCAACAGATGGCAGTA	chr3	87299894	87299912	19.31209926	-
GTGCCACCAGAGGGCACTG	chr3	87392212	87392230	22.71953376	+
ACACCAGCAGGTGGCACTA	chr3	87430138	87430156	20.89460735	+

TTGCCACTAGATGGCACTG	chr3	87482631	87482649	22.53228562	+
CTTCCAGCAGGGGGAAGCA	chr3	87635921	87635939	19.35560988	-
CAGCCAGTAGGTGGCACTT	chr3	87903287	87903305	20.40241131	+
TCACCTGCAGAGGGCAGCA	chr3	88135177	88135195	19.70945874	-
TGGCCACAAGATGTCACCA	chr3	88312419	88312437	19.12065397	-
CCACCAGCAGGGGAAGCTC	chr3	89181130	89181148	17.24101636	-
TCTCCACTAGAGGGCTCTA	chr3	89231003	89231021	17.76985063	-
CAGCCAGGAGGTGGCGCTT	chr3	89831789	89831807	19.38315155	-
TGGCCACTTGGTGGCGATG	chr3	89984052	89984070	18.57500566	-
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TGTCCAATAGATGGCGCCC	chr3	95435908	95435926	18.69535311	+
AGACCACCAGGGGGCAGTG	chr3	95451233	95451251	23.49676229	+
TCACCTCCAGGTGGCAGGG	chr3	95918344	95918362	18.49927198	-
AGGCCAGTAGATGGCAATG	chr3	96064414	96064432	18.27929011	+
TGCCCAGCAGGGGTCGACA	chr3	96385717	96385735	18.39435981	-
CAGCCAGCAGGGGCCACTC	chr3	97902611	97902629	18.7810626	-
GCTCCACTAGGGGGCGCCC	chr3	97981524	97981542	21.77406863	-
TCACCACAAGAGGGCACAC	chr3	98860395	98860413	18.89427537	-
GCGCCACTAGATGGCGGAA	chr3	98920919	98920937	19.51945676	-
TAGCCACTAGGTGTCAGTA	chr3	98995141	98995159	19.20653948	+
CAGCCACCAGGAGACACCG	chr3	99169701	99169719	18.26399129	-
CGGCCACCAGGGGGCGCCA	chr3	99224945	99224963	28.88685349	-
CAGCCAGTAGGGGGCATTT	chr3	99241022	99241040	17.54701612	+
CCACCACTAGATGGAAGCA	chr3	99241314	99241332	17.79674185	+
GATCCAGCAGATGGCGCCT	chr3	99531248	99531266	17.2484051	-
TTGTCAGTAGAGGGCGCTG	chr3	99545624	99545642	19.28475526	-
TGACCACAAGAAGGCACTG	chr3	99659265	99659283	18.99456802	-
TGTACACTAGAGGGCACTC	chr3	99803785	99803803	18.34000799	+
CAGCCAGGAGGTGGCGCTT	chr3	99814349	99814367	19.38315155	+
TATCCAGTAGGTGGAGGTA	chr3	100014514	100014532	17.89320313	-
GATCCACTAGGTGGCGCTT	chr3	100374754	100374772	17.96148202	-
CATCCACCAGAGGGCAGAT	chr3	100700916	100700934	17.26301467	+
TAGCCAGTAGGGGGCACTG	chr3	100733987	100734005	24.18043287	-
TCACCAGTAGAGGGAGCCA	chr3	100847063	100847081	19.99813096	+
CTGCCGCTAGGTGGCTCCA	chr3	100888712	100888730	17.40587682	-
TGGCCACGAGAGGGAGACC	chr3	101009900	101009918	17.77042555	-
TTACCTCTAGATGGCAGCA	chr3	101033701	101033719	18.04029448	+
CAGCCACTAGAGGGTAGAA	chr3	101044962	101044980	17.26119404	+
CGCCCAGCAGGTGGCACTG	chr3	101270471	101270489	22.76205812	+
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TTGCCAGCAGGAGGCAGGG	chr3	102095309	102095327	19.31412581	+
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TGGGCAGTAGGGGGCGTTG	chr3	102837929	102837947	18.16481814	-
AGGCCAGCAGAGGGAGCAC	chr3	103004893	103004911	18.8950905	+
GGACCAGCAGGGGGCATTC	chr3	103010909	103010927	19.32122913	+
TGTCCACGAGATGGCGGTA	chr3	103430773	103430791	20.3135496	+
TGGCCACCAGATGGCTGTG	chr3	103437398	103437416	20.7016877	+
TGACCAATAGGTGGTGCTG	chr3	103672739	103672757	17.43810484	+
CAGCCACTAGATGGCAGTA	chr3	103875216	103875234	21.67653607	+
GGGCCCCTAGGTGGCGCCC	chr3	104611967	104611985	19.67111345	-
CAGCCAGCAGGGGACGCTC	chr3	105193168	105193186	21.40171199	+
GTGCCAGTAGGTGGCAGTA	chr3	105765775	105765793	20.65408018	+
AGGCCACTAGGGGGCTACA	chr3	105829909	105829927	17.81838138	+

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CAGACACTAGGGGGCACTG	chr3	107811425	107811443	20.54997004	-
AGGCCACAAGGTGTCACTG	chr3	108026500	108026518	17.87442339	+
AGGCCAGAGGGGGGCACCA	chr3	108319925	108319943	18.60460173	-
TTACCTCCAGGGGGCAGTA	chr3	108407840	108407858	21.19665059	+
TGAACAGCAGGGGGCAGTA	chr3	108437565	108437583	20.92694178	+
TGGCCAGCAGAGGGAGCAG	chr3	108892238	108892256	21.7165356	+
CGGCCGCCAGAGGGCGGGC	chr3	109129211	109129229	21.50420255	-
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TAACCACTAGGTGGCACTG	chr3	109863869	109863887	22.46952897	+
TGGACACAAGAGGGCAGTA	chr3	110116743	110116761	18.98347382	-
TGGCCAGCAGGTGGCACTT	chr3	110225393	110225411	23.29446694	+
TCGCCAGCAGAGGGCAGCC	chr3	110426093	110426111	23.30226795	-
GAACCAGCAGAGGGCAGAC	chr3	110571222	110571240	17.81748428	-
CCTCCAGTAGAGGGCGCAC	chr3	110611523	110611541	19.6869574	+
TGGCCACAAGGGGGAGATT	chr3	111516243	111516261	17.29019536	-
TGACCAGCAGAGGGCGCCT	chr3	112919251	112919269	23.15624101	+
CTGCCACCAGGGGGCAACC	chr3	113169392	113169410	22.63623971	-
TGAACAGGAGGTGGCAGCA	chr3	113215250	113215268	17.06395302	-
TAGCCACTAGGGGGCGAGT	chr3	113245355	113245373	18.49277771	-
TAGCCAGAAGAGGGAGCTC	chr3	113313520	113313538	18.51842386	+
CATCCAGCAGAGGGCAATG	chr3	113721117	113721135	18.51042091	-
AGACCAGCAGGTGGTGCTC	chr3	113783959	113783977	18.97142844	+
CAGTCACCAGATGGCGCAC	chr3	113844617	113844635	17.34375321	+
TGGCCTCTAGGGGGAGCTC	chr3	113936439	113936457	20.94398287	+
GGGCCACTAGAGGGAGGTT	chr3	114237105	114237123	17.92248947	+
TCTCCACCAGAGGGCAGCA	chr3	114252918	114252936	22.25055857	+
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CCACCACCAGATGGCATTC	chr3	114696742	114696760	17.89704139	+
CTGCCACTGGGTGGCAGTA	chr3	114779579	114779597	19.25330165	-
CGGCCGCCAGAGGGCGCAA	chr3	115040289	115040307	22.78119394	+
TGGCCATCGGAGGGCACTA	chr3	115354135	115354153	17.13017009	+
CAGCCAGGAGAGGGCGCCT	chr3	115357107	115357125	19.46529812	-
TGGCCAGAAGAGGGTGCTT	chr3	115357139	115357157	17.74641658	-
CTGCCACCAGGAGGCGCTG	chr3	115492558	115492576	23.31709674	+
CAGCCACTAGAGGGAGGAC	chr3	115501120	115501138	18.2952449	-
TGACCTGAAGGGGGCGGTA	chr3	115572515	115572533	20.74065911	-
CATCCACTAGAGGGCAGTA	chr3	115620413	115620431	20.55163044	-
TGGCCACTAGATGGCAGGT	chr3	115728760	115728778	19.2266858	+
TGGGCACTAGATGGCGGCA	chr3	116242405	116242423	19.99547281	+
GGGACACAAGGTGGCACTG	chr3	116293847	116293865	17.88870949	+
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ATCCCAGCAGAGGGCACCA	chr3	116894618	116894636	18.96019771	-
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CTGCCACGAGGGGGCAGCA	chr3	116986198	116986216	22.53344204	-
TGGACAGCAGGTGGCGCCA	chr3	117016498	117016516	22.96832594	-
TTACCACAAGATGGCAACA	chr3	117021462	117021480	17.06664794	-
TGTCCACGAGGTGGCAATA	chr3	117021525	117021543	18.2626841	+
TGACCTCAAGGTGGCAGTC	chr3	117719028	117719046	18.70015378	-
CAACCACTAGGGGGAAATG	chr3	117816516	117816534	17.23208814	+
TGTCCAGTAGAGGGAGCCT	chr3	117959922	117959940	17.86386838	-

TGGCCAGTTGAGGGCGGAA	chr3	117972523	117972541	18.41703414	+
ATTCCACCAGGGGGTGCTC	chr3	118728200	118728218	18.04833257	-
TGAGCACTAGATGGCAGTA	chr3	119199174	119199192	17.46669149	-
TTGCCACCAGGTGGCTGGC	chr3	119937820	119937838	18.03628019	+
TCACCACAAGGTGGTGCCA	chr3	120019404	120019422	18.75865208	-
GTGCCACAAGGGGGCAGTG	chr3	120084084	120084102	20.90362413	+
CCACCACCTGGGGGCAGCA	chr3	120086387	120086405	19.54785806	+
CTGCCACTAGGTGGCCCTC	chr3	120443190	120443208	19.52855441	-
AGCCCAGCAGAGGGCACCC	chr3	120524423	120524441	20.0933885	-
CGGCCAGAAGAGGGGGCTG	chr3	120630258	120630276	18.08433494	-
TGGGCAGTAGGTGGCAGCA	chr3	121032760	121032778	19.65725163	+
TAGCCAGCAGGTGGCAGAG	chr3	121274559	121274577	21.71384843	-
TAACCACCAGATGGCAGTC	chr3	121445971	121445989	20.94631558	+
TGGCCAGCAGGGGGCGCTC	chr3	121760604	121760622	27.47575877	-
TGACCAGCAGAGGGCAGAC	chr3	121762948	121762966	21.57928883	+
CCACCACAAGGGGGCGGGG	chr3	121824745	121824763	20.97661806	+
GGGTCAGCAGGGGGCGCTC	chr3	121996766	121996784	20.81406843	-
TCACCAGCAGGAGGCAGGA	chr3	123142388	123142406	18.29925482	-
TGGCCAGAAGAGGGAGCTA	chr3	123197253	123197271	20.90657378	-
TTTACAGTAGGGGGCACTC	chr3	123303286	123303304	17.33237579	+
TGGCCACCAGGAGGGGCTC	chr3	123440844	123440862	18.49882883	+
TGGCCACTTGGTGGCAATA	chr3	123507542	123507560	17.57137136	+
TGGCCAGCTGGGGGCACCC	chr3	123558156	123558174	21.76604867	-
TTTCCACTAGGTGGCACTG	chr3	123594610	123594628	21.60613483	+
TAGCCAGAAGAGGGCACTG	chr3	123660711	123660729	21.33524118	+
TTGCCTCCAGAGGGCACTG	chr3	123762366	123762384	21.73450539	+
CTACCTGCAGATGGCGCTC	chr3	123880843	123880861	19.12517521	-
TGGCCGGCAGGGGGCCCCT	chr3	124144595	124144613	18.16696881	+
TGGCCAACAGAGGGAGGAG	chr3	124154333	124154351	17.70478884	+
TGGCCAGCTGGGGTCGGCC	chr3	124184567	124184585	18.27256727	-
GTGCCAGCAGGAGGCGGTC	chr3	124362906	124362924	19.63316546	+
TGCCCAGTAGAGGGCTCTG	chr3	124487991	124488009	17.79389685	+
TGGCCACAAGGTGGCGCGG	chr3	124530550	124530568	23.26800492	+
TGGCCTGCAGGTGGCCCTG	chr3	124533155	124533173	19.2459481	-
CCGCCCGCAGGGGGCGCCC	chr3	124649680	124649698	21.51011265	+
TCACCACTAGATGGCACCC	chr3	124760775	124760793	21.24834211	-
TGGCCTGCAGGTGGCGCTC	chr3	124844129	124844147	23.43947586	+
AGAACACTAGAGGGCACCC	chr3	124854062	124854080	17.35772422	+
CTGCCACCAGGGGGTGATG	chr3	124858415	124858433	20.04795896	-
ATGCCAGCAGGTGGCAGCC	chr3	124903785	124903803	21.0102964	-
TGGCCACAAGGTGGCACCA	chr3	124920827	124920845	24.31404108	-
CAGCCACTGGAGGGCAGAG	chr3	124982863	124982881	17.20743574	-
TGGCCAGCAGAGGGTGCAT	chr3	125082878	125082896	18.56649781	-
TCACCACTAGATGGCAGCA	chr3	125181491	125181509	21.15808724	-
CTACCACCAGGTGGCAGTA	chr3	125281061	125281079	22.90705266	-
CTACCACTTGGTGGCAGCA	chr3	125448711	125448729	17.22784553	-
TGCCCAGCAGGTGGCACTC	chr3	125694509	125694527	22.2928325	+
TAGCCACTAGAGGGAAGCA	chr3	125752149	125752167	19.86497586	-
ACGCCACTAGATGGCAGTG	chr3	125761558	125761576	19.81960207	-
CCTCCACTAGATGGCAGCA	chr3	125766657	125766675	20.06905295	+
AGGGCAGCAGGTGGCAGCG	chr3	125890545	125890563	18.3487924	-
TGACCAGCAGAGGGCAGCA	chr3	125890555	125890573	24.09214459	-
CTTCCAGCAGGGGGCAGCA	chr3	125962951	125962969	22.64632637	+
GGGCCGGTAGGTGGCGCTG	chr3	126103025	126103043	21.16471109	-

ATGCCACAAGGTGGCGCAG	chr3	126130335	126130353	19.39003827	+
TGTCCAGCAGAGGGCAGAG	chr3	126188235	126188253	21.10073798	-
TGGCCAGAAGATGTCACTG	chr3	126197132	126197150	18.17878488	+
CTACCACCAGGTGGCGGTA	chr3	126639515	126639533	23.92080637	-
TGACCACCAGATGGCACAG	chr3	126787339	126787357	22.28259448	-
TGGCCACAAAGTGGCGCCA	chr3	126885882	126885900	18.75415769	+
CGGCCAGCAGAGGGCGCCA	chr3	126967953	126967971	26.90962441	+
TCTCCACTAGGTGGCGCTG	chr3	127011732	127011750	22.82902436	-
ACACCTCCAGGGGGCGCCA	chr3	127062275	127062293	21.05907976	-
CCACCAGGAGAGGGCAGCA	chr3	127123446	127123464	19.53122257	+
TGGCCACTGGGAGGCGCTG	chr3	127130866	127130884	20.18301315	+
TCACCACTAGATGGCAGCA	chr3	127174097	127174115	21.15808724	+
AGGCCAGCGGGTGGCAGCC	chr3	127252825	127252843	18.78883466	+
AAGCCACCAGATGGCAGCA	chr3	127335855	127335873	20.72972656	+
CAGCCAGCAGGGGTCGCTT	chr3	127447802	127447820	19.66003542	+
CAGCGAGCAGGGGGCGCCA	chr3	127448054	127448072	19.2237693	+
TGACCAGCGGGGGGCAGTG	chr3	127461162	127461180	21.22287811	+
CCTCCACCAGGTGGTGCCA	chr3	127553857	127553875	20.17167943	-
TGGCCACCAGGTGGCAGCA	chr3	127723988	127724006	26.17587391	+
GGGCCTGCAGGTGGCACAC	chr3	127727771	127727789	18.82011317	+
TGGCCTGCAGAGGGCACCG	chr3	127771939	127771957	23.04772325	+
GGCCCACGAGGTGGCGGCG	chr3	127856341	127856359	19.19806883	+
CGGCCGCGAGGTGGCACTG	chr3	127880944	127880962	20.62179187	+
AGCCCACTAGGTGGCAGGC	chr3	127953931	127953949	17.2698416	+
AGGCCTGTGGGGGGCGCCA	chr3	128146831	128146849	18.22850938	+
GGGCCTGCAGGGGGCGCCC	chr3	128184176	128184194	22.92437466	+
CGCCCGGGAGGTGGCGCCC	chr3	128206743	128206761	17.68419757	+
CGCCCACAAGGAGGCGGCC	chr3	128290415	128290433	18.5574713	-
TGGCCGGCAGGAGGCAGGA	chr3	128294450	128294468	18.19101302	-
TTCCCAGCAGGTGGAGCAA	chr3	128378950	128378968	17.20069851	-
CAACCACTAGGGGAAGCTG	chr3	128434259	128434277	17.08432135	-
CCACCGACAGGGGGCACCC	chr3	128575709	128575727	17.77620757	+
TCACCAGCAGGGGGCTGAA	chr3	128607948	128607966	18.12483007	+
GGGGCGGCAGGGGGCGCTG	chr3	128657250	128657268	18.39106454	-
TCTCCACCAGGTGGCACTC	chr3	128674917	128674935	22.25866686	-
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TGGGCACCAGGGGGCGGTG	chr3	128749457	128749475	23.14170951	-
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CTGCCACCAGAGGGCTCTC	chr3	128758289	128758307	20.17589431	-
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TAGCCTCCAGAGGGCAGGA	chr3	128793735	128793753	19.18061569	+
GAGCCACCAGGGGGGGCTG	chr3	128853875	128853893	18.87245001	+
CTGCCACCAGAGGTAGCTG	chr3	128892574	128892592	18.42856435	+
TGGCCACCAGAGGGCTCAG	chr3	128896097	128896115	20.78756206	-
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CTGCCACAAGGGGGCAGGG	chr3	129092716	129092734	20.98785474	-
CAGCCAGGAGGTGGCGCCG	chr3	129212915	129212933	22.24381965	+
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CGCCCACACGGGGGCGCTG	chr3	129277285	129277303	18.00086493	+
CTGCCTGGAGGTGGCAGTG	chr3	129295974	129295992	17.55529004	-
TCCCCAGCAGGGGGCACCA	chr3	129296844	129296862	22.7773049	+
TCTGCACTAGGGGGCACCC	chr3	129335217	129335235	17.79942023	-
CCTCCACCAGGGGGCCCCC	chr3	129428514	129428532	19.87693675	+
CAGCCAGCAGGTGGCAGAG	chr3	129523762	129523780	21.64321953	-

TAGCCTCTAGGGGGCTCTA	chr3	129640235	129640253	18.07595902	-
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CCGCCGCCAGGTGGCGCTC	chr3	129699540	129699558	22.63792634	-
TGCCCACAAGGTGGCAGGG	chr3	129704805	129704823	18.5724758	-
CGGCCGCCAGAGGGCGCCC	chr3	129810052	129810070	24.19410182	-
GGCCCAGCAGAGGGCGCCC	chr3	129819378	129819396	21.4651042	+
CTGCCGCCAGAGGGCGCGG	chr3	129882400	129882418	21.00112116	+
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CTTCCACCAGGGGGCACTG	chr3	129996747	129996765	23.64638264	-
GGACCTGCAGAGGGCGCCA	chr3	130047586	130047604	20.91384159	-
AGGCCACTAGAGGGTGACA	chr3	130077282	130077300	17.50155129	+
TGCCCAGCAGGGGCCAGTC	chr3	130109840	130109858	17.00809208	+
TAGCCAGGAGAGGGCGCAC	chr3	130171975	130171993	19.61295737	+
TGCCCACCAGGTGGCCCTC	chr3	130430642	130430660	19.22405219	+
TGCCCTCTAGGTGGCACCA	chr3	130447482	130447500	19.88264842	-
CAGCCCGTAGGGGGCGGGG	chr3	130546212	130546230	18.0126701	-
TCCCCACTAGATGGCAGAG	chr3	130584986	130585004	17.37766562	+
CAGCCAGCGGGTGGTGCTG	chr3	130612605	130612623	17.21356839	+
CAGCCAGTAGGTGGCAGGG	chr3	130623709	130623727	20.57318014	-
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TGACCACCAGGTGGTGCCC	chr3	131026656	131026674	22.18476869	-
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ATTCCACCAGAGGGCACTA	chr3	131901494	131901512	20.11915958	+
ATTCCACTAGAGGGCAGTG	chr3	131961440	131961458	18.48556062	+
TAACCACTAGAGGGCAGGG	chr3	132094600	132094618	19.86177628	-
CAGCCAGAAGGTGGCGCTT	chr3	132249292	132249310	19.89735412	+
TTACCACCAGGAGGCAGAA	chr3	132751055	132751073	18.82775592	+
CAACCCCCAGGGGGCGCTC	chr3	133236601	133236619	20.28178624	-
ATTCCAGCAGATGGCAGTA	chr3	133381958	133381976	17.70045653	-
TTGCCAGGAGGGGACAGCA	chr3	133412464	133412482	17.78798077	-
CGTCCAATAGATGGCACTA	chr3	133454982	133455000	17.88004303	+
TGGCCTACAGATGGCGCTA	chr3	133554272	133554290	19.29155104	+
TGGTCAGCAGATGGCGCTG	chr3	133737715	133737733	20.82354476	+
TTACCAGTAGATGGCACTG	chr3	134242939	134242957	20.64731114	+
CAGCCAGCAGGTGGCGCCA	chr3	134625281	134625299	25.27020327	-
AGACCTCTAGGGGGCAGTG	chr3	134689631	134689649	19.6048546	+
GGGCCAGCAGGTGGCAGTA	chr3	135020547	135020565	23.32049566	+
CCGCCACCAGGGGGCGCCG	chr3	135129257	135129275	27.40270517	-
TTAACAGTAGGTGGCACTC	chr3	135399383	135399401	17.22315521	+
CTGCCACCAGGGGGTGCTA	chr3	135414615	135414633	23.06179977	+
GGGCCACTAGAGGGCTCCT	chr3	135426263	135426281	17.26379787	-
GGGCCACCAGGGGACGCTG	chr3	135510082	135510100	22.57759111	+
TGGGCAGCAGGGGGAGCTG	chr3	135560201	135560219	19.84037355	+
TGGACAGCAGGGGGCAGGA	chr3	135650986	135651004	20.39229894	-
TACCCAGCAGGGGGCGCTC	chr3	135675651	135675669	22.59603619	-
CCACCACTAGAGGGAGGTC	chr3	135681248	135681266	19.10724618	-
TGGCCACCAGGTGGCAGCA	chr3	135694198	135694216	26.17587391	-
TCGCCAGCAGGGGTCCCCG	chr3	135728756	135728774	18.22209721	-

CGGACACCTGGGGGCGCCC	chr3	135802544	135802562	19.14933954	+
CTTCCAGCAGAGGGAGCAG	chr3	135842633	135842651	17.71021037	-
TGCCCGCCGGGGGGCGCCC	chr3	135852273	135852291	18.64493845	-
GCACCACGAGGGGGAGCCC	chr3	135996575	135996593	17.46874406	+
CTGCCACCAGGTGGCGGTG	chr3	136040317	136040335	25.14481317	-
CCGCCACCTGGTGGCAGTG	chr3	136040321	136040339	19.36333748	+
GGGCCAGTAGGTGCCGCCA	chr3	136417727	136417745	18.49999125	+
GGGCCAGCAGGAGGAGCTA	chr3	136447743	136447761	19.21581644	-
CGGCCTCTCGGGGGCACCA	chr3	136705563	136705581	18.92983259	-
TCAGCAGTAGAGGGCGCCC	chr3	136938469	136938487	17.85435025	+
AGCCCACCAGGAGGCACAA	chr3	136993891	136993909	17.06213849	-
TGGCCACGAGAGGGCACCA	chr3	137096828	137096846	23.60108367	-
GGGCCTGGAGGGGGCAGTA	chr3	137210764	137210782	18.52320047	+
TTTCCACTAGAGGGCACTC	chr3	137244337	137244355	20.86752546	-
TCACCACTAGATGGTGCTC	chr3	137276931	137276949	18.12020682	+
CCAGCACTAGGGGGCACTG	chr3	137593329	137593347	19.00614984	+
GGGGCAGCAGGGGGCACAC	chr3	137936115	137936133	17.97187282	+
ATGCCACCAGATGGCGGGT	chr3	137953876	137953894	17.25893496	-
CGGCCAGCAGAGGGCGGTC	chr3	137953934	137953952	25.43852026	-
TGACCACAAGGTGGCGCCA	chr3	138215589	138215607	24.09366858	-
TGACCATAAGAGGGCGCCA	chr3	138306988	138307006	18.59326384	+
CTGCCAGTAGGTGGTGCTT	chr3	138323435	138323453	17.71018868	+
AAACCACTAGAGGGCAGGG	chr3	138713392	138713410	17.58018571	-
TGACCACTAGAGGGCAGTA	chr3	139148086	139148104	23.47884071	-
CCGCCACAAGAGGGAGCCA	chr3	139172903	139172921	20.29366564	-
CTGCCACCAGAGGTCGCCG	chr3	139270288	139270306	22.00018224	+
TTGGCAGCAGAGGGCACTC	chr3	139320593	139320611	18.56793627	-
CTCCCAGCAGAGGGCATCA	chr3	139599638	139599656	17.18813822	-
CGTCCACCAGATGGCAGCA	chr3	139619232	139619250	22.52633261	+
CACCCAGCAGGTGGAGCTG	chr3	139652737	139652755	18.64691936	+
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GGGCCGCCAGGGGGCGCTG	chr3	140117094	140117112	23.92643608	-
CGGCCGCCAGGTGGCGCCC	chr3	140117660	140117678	24.39285666	-
CCTCCACAAGGGGGCAGTG	chr3	140125149	140125167	20.71322801	-
GTGCCAGCAGAGGGCAGCC	chr3	140137910	140137928	21.16950356	+
CCGCCGCCAGGGGGCTCCT	chr3	140142996	140143014	17.13600325	+
GGTCCTCCAGGGGGCGGAG	chr3	140222533	140222551	19.25943524	-
CTCCCACTAGATGGCACTG	chr3	140313542	140313560	19.42011012	+
CTGCCAAGAGGGGGCACTA	chr3	140521492	140521510	18.87040321	+
GGGCCGCTAGGTGGCGCTG	chr3	140531038	140531056	21.81555937	-
TAACCACTAGGAGGCGCCT	chr3	140629259	140629277	18.71647216	+
TGGCCTCCAGGAGGCAATG	chr3	140636562	140636580	18.14475832	+
CCAACAGCAGGGGGCAGTA	chr3	140721782	140721800	19.38228397	-
TGGCCACCAGAGGTCTCTC	chr3	140830781	140830799	18.06268164	-
ATACCAGCAGGGGGCAAAG	chr3	140946277	140946295	17.11727628	+
TAGCCGCGAGGAGGCGGCG	chr3	141136993	141137011	17.04072586	-
CAGCCAGCAGACGGCACTA	chr3	141253060	141253078	18.97509615	-
CAGCCAGGAGAGGGCAGGC	chr3	141330285	141330303	17.80155731	+
TCTCCACCAGGAGGCACTG	chr3	141421765	141421783	20.33057616	-
TGGCCTCTAGAGGTCAGCA	chr3	141478375	141478393	18.21820508	+
TGGCCACCGGGTGGTGCCA	chr3	141938796	141938814	20.06424236	-
TTGCCAGCAGGTGGCGACA	chr3	142065432	142065450	22.49212202	-
TGGCCACTTGGTGGCAGCA	chr3	142201748	142201766	20.21576537	+
TGTGCACGAGGGGGCGCTC	chr3	142213216	142213234	17.97328798	+

GTACCACCAGGTGGCGATG	chr3	142307488	142307506	19.6941947	-
CTACCACCAGGGGGCAGGC	chr3	142393944	142393962	21.71593564	-
GGGTCGGCAGGGGGCGCTG	chr3	142433296	142433314	18.53752604	+
CAGCCACGAGGAGGCACCC	chr3	142437285	142437303	18.87311445	+
TAGCCACCAGAGTGCAGTC	chr3	142481013	142481031	17.02961754	-
CAACCACTAGGGGGCAGCA	chr3	142505097	142505115	23.17731804	+
TGTCCACAAGATGGTGCTG	chr3	142623455	142623473	17.59687398	-
CTGCCAGCAGAGGTCACTG	chr3	142661823	142661841	20.05467885	+
TATCCAACAGGGGGCACTA	chr3	142675934	142675952	19.54975347	+
CTGCCAGAAGGGGGCGGAA	chr3	142995199	142995217	21.44766822	+
CAGACAGCAGGGGGTGCTG	chr3	143047131	143047149	18.03513863	-
TGGCCAGCATGGGGAGCCC	chr3	143147452	143147470	17.67527294	+
AGACCGGCAGGGGGCGCAA	chr3	143164254	143164272	20.0116386	+
CACCCACCAGATGGCACAC	chr3	143224035	143224053	18.02651467	+
AAGCCAGAAGGTGGCGACG	chr3	143327895	143327913	17.54333916	+
CTCCCAGTAGGGGGCGACA	chr3	143342324	143342342	19.52432174	-
TGACCACTGGGTGGCACAA	chr3	143382489	143382507	18.73121747	+
TGACCACCAGGTGGTACTA	chr3	143788525	143788543	21.44008752	+
CGAGCAGCAGAGGGCAGTG	chr3	144130843	144130861	18.84597161	+
TAACCACTAGAGGGCACAT	chr3	144188796	144188814	18.00902703	-
TTGCCACGTGGTGGCGCTG	chr3	144195698	144195716	17.86254887	-
TTCCCTGCAGGGGGCAGCG	chr3	144322979	144322997	19.00916392	+
CGGGCAGCGGGGGGCGCAA	chr3	144323059	144323077	17.48397366	+
CAACCAGAAGAGGGCGCTA	chr3	144850436	144850454	21.05435918	+
TCCCCACCAGGTGGTACTC	chr3	144872208	144872226	17.60866427	+
CCACCACCAGGTGGCATGC	chr3	145153093	145153111	17.45465315	-
CTGCCACCAGGTGGCTGGC	chr3	145707829	145707847	17.96565129	+
TGGCCACCAGGTGGAGGAT	chr3	147116458	147116476	19.34614321	-
TGGCCACCAGGAGGAGAAG	chr3	147221634	147221652	17.09447207	+
TGACCACAAGGTGGAGCTG	chr3	147266178	147266196	20.51193128	+
CAGCCACCAGGTGGCGATC	chr3	147419560	147419578	22.0864548	+
CCACCACAAGATGGCAGCA	chr3	147790575	147790593	19.56864745	+
CCTCCGCTAGGGGGCGCGA	chr3	148562488	148562506	19.31097485	+
CACCCACCAGATGGCAGCC	chr3	148913027	148913045	19.34916768	+
TTACCAGTAGGTGTCACTA	chr3	149277986	149278004	18.11680505	-
TACCCACTAGATGGCAGTA	chr3	149510067	149510085	18.70561837	+
TTTCCAGTAGAGGGCAGCA	chr3	150144220	150144238	20.40732373	-
GAACCAGAAGAGGGCACTG	chr3	150156133	150156151	18.1774864	+
TCTCCACTAGGGGGAGACA	chr3	150491846	150491864	17.95323325	-
TATCCACAAGGGGGTGCCA	chr3	150534975	150534993	18.50372559	-
CTACCACCAGGAGGTGCTC	chr3	150694837	150694855	17.68212842	+
CAGCCATTAGAGGGCAGCC	chr3	150712952	150712970	17.23343961	+
TTTCCACCAGAGGGCACTT	chr3	150769613	150769631	19.81086405	+
CCTCCACTAGGTGGCAGAG	chr3	151008885	151008903	19.42243253	-
GAGCCACAAGAGGGAGCCA	chr3	151421907	151421925	18.07651891	-
CAACCACCAGGTGGAGACA	chr3	151696233	151696251	18.39248744	-
CCACCACTAGGGGTCAGGC	chr3	151988426	151988444	17.07481441	+
TGTCCACAAGGTGGTGCTA	chr3	152065941	152065959	18.9333742	-
GGGCCAGCAGGGGGCCCCG	chr3	152126322	152126340	21.63950385	+
AGGGCTCCAGAGGGCGCTA	chr3	152285972	152285990	17.27542941	+
TGGTCACCAGAGGGTGCTG	chr3	152346663	152346681	18.74103142	-
GTGCCACCAGAGGGCGACG	chr3	152368940	152368958	21.01046748	+
TATCCACTAGGTGGCAGTT	chr3	152428379	152428397	18.23112808	+
CGCCCACCAGAGGGCTCTG	chr3	152613638	152613656	19.35736697	-

TAACCACCAGATGGCAGAT	chr3	152640270	152640288	17.224423	+
TCTCCACTAGAGGGAGCCT	chr3	152668965	152668983	17.04068774	+
AGACCACCAGATGGAGCCA	chr3	153384131	153384149	19.69704236	+
AGGCCAGTAGGTGGTGCTT	chr3	153740059	153740077	17.18239174	-
TGGCCACTGGGTGGCAGCG	chr3	153775126	153775144	21.27787728	-
CTACCACCAGGTGGTAGCA	chr3	154161886	154161904	19.32696648	-
TTGCCACTAGGGGGAACGT	chr3	154713903	154713921	17.34704016	+
TCTCCACTAGGTGACAGTA	chr3	154795869	154795887	17.01991935	-
AGGCCAGTAGGTGGTGCTT	chr3	154969533	154969551	17.18239174	-
TGTCCACCAGGGGTCACTG	chr3	155218755	155218773	21.53316997	-
CGTCCAGCAGGGGGCAGAG	chr3	155453709	155453727	22.35648988	-
TGCCCACCAGAGGGGGCCC	chr3	155817021	155817039	18.00737403	-
GAGCCAGTAGGTGGCACTG	chr3	155884690	155884708	21.12917833	+
CTTCCAGCAGGGGGAGATC	chr3	156105008	156105026	17.17499565	+
ATGCCACTAGATGGCACAA	chr3	156553574	156553592	18.57883405	+
CTGGCGGCAGGGGGCGCCC	chr3	157006775	157006793	18.30194636	+
CGGCCACTGGGAGGAGCCA	chr3	157071086	157071104	17.11268857	-
CTTCCAATAGGGGGCGGGG	chr3	157184509	157184527	17.24552152	-
TGGCCACTGGGAGGCGCTT	chr3	157244535	157244553	17.60324646	+
AGAACACTAGAGGGCAGCA	chr3	157710372	157710390	17.26746935	-
TTGCCACTAGATGGCAGTG	chr3	157741711	157741729	21.89205682	-
TGTCCACCAGGGGGCAGGC	chr3	158282372	158282390	22.45132388	-
TGGCCACAAGGGGGTAGCA	chr3	158331277	158331295	20.94045065	-
ACGCCACTAGAGGTCACTC	chr3	158338092	158338110	17.18059601	-
CTTCCAGCAGGCGGCGGTC	chr3	158363284	158363302	18.02750757	+
TGGCCACTAGATGGCATTT	chr3	158402328	158402346	17.65266251	-
CTTCCACTAGAGGTCACTA	chr3	158694302	158694320	17.47986419	-
CTTCCACAAGGGGGCACAC	chr3	158733255	158733273	18.92248606	+
CAACCACCAGGGGGCAGTA	chr3	158773222	158773240	23.87966738	-
CTGTCACCAGGGGGAGCCC	chr3	158807248	158807266	18.62493656	+
TGGCCACTGGATGGAGCTG	chr3	158814148	158814166	18.03386109	-
CCACCAGCAGGGGGCGTGC	chr3	159066008	159066026	18.94518454	+
CAGCCAATAGATGGCACTG	chr3	159514002	159514020	18.28427924	-
AAACCACCAGGTGGCAGCA	chr3	159740089	159740107	20.82198116	+
GCACCAGCAGGTGGAGGTG	chr3	159873264	159873282	18.32525835	+
TCACCACCAGAGGGCAACT	chr3	159928423	159928441	18.31558526	+
TGACCACTAGGTGGCAATT	chr3	160046421	160046439	18.72421686	+
TTTCCAGAAGGGGGCAGTT	chr3	160112895	160112913	17.34410613	+
GCTCCAGTAGGTGGCAGCG	chr3	160118568	160118586	18.8814664	+
TGAACACCAGAGGGCGGTG	chr3	160460730	160460748	21.25504355	-
CTATCACTAGAGGGCACTC	chr3	160464402	160464420	17.07724018	+
TGGCCTATAGGGGGCACTT	chr3	160467458	160467476	17.15866726	+
GGGTCGCCAGGGGGCGCAG	chr3	160523008	160523026	17.5063939	+
ATTCCAGCAGAGGGCAGCA	chr3	160787245	160787263	19.10898391	-
AGTCCACTAGAGGGCACCA	chr3	161029109	161029127	21.09997497	+
GGGCCACTGGGTGGCGCCA	chr3	161204194	161204212	21.01835063	-
AAGCCACTAGATGGCAGGA	chr3	161232870	161232888	17.69680536	+
ACGCCACTAGGGGGTAGCA	chr3	161614305	161614323	18.70364207	-
CTGCCACAAGGTGGCAGTG	chr3	161687053	161687071	21.62899783	-
CCACCAGCAGGTGGAGGGC	chr3	161764834	161764852	17.86963443	+
CCTCCACCAGATGGCACCC	chr3	162142563	162142581	21.14255856	-
CGAGCACCAGGTGGCAGTC	chr3	162297434	162297452	19.15572019	+
TGTCCCCTAGGGGGCGGTA	chr3	162475361	162475379	20.09868012	-
TTTCCACCAGAGGGCAATA	chr3	162624585	162624603	19.39702875	-

TTGCCAGCAGGTGGCGCTT	chr3	163054792	163054810	22.62505592	+
AGGCCACCAGGTGGCCCCT	chr3	164243755	164243773	18.22499747	-
TTTCCACTAGGTGGCGGTT	chr3	164257555	164257573	19.39989304	+
TCACCAGCAGAGGGCAGCC	chr3	164690894	164690912	22.06814174	-
TGCCCACCAGGTGGCAATT	chr3	165117483	165117501	17.90004721	+
CTACCAGCAGAGGGCATTA	chr3	165152069	165152087	18.71465721	-
CAGCCAGCAGGGGTTGCTC	chr3	165533466	165533484	17.83896	+
AGGCCATTAGAGGGCAGCA	chr3	166386382	166386400	17.41062786	-
CAGCCAGCAGGGGTCGGTC	chr3	166825429	166825447	21.05971878	+
TGAACACTAGAGGGCACTT	chr3	167055256	167055274	17.31850121	+
CTGCCAAGAGGTGGCGCTC	chr3	167075184	167075202	18.20655701	+
TGGGCACAAGAGGGCGCTT	chr3	167096576	167096594	17.37372918	+
TATCCAGCAGATGGCGGTT	chr3	167213747	167213765	18.25090346	+
TGTCCAGTAGGGGGCAATT	chr3	168038223	168038241	18.18258916	+
CCGCCGGCAGAGGGCGAAC	chr3	168580864	168580882	17.10262141	+
GAACCACCAGGGGGCAGTA	chr3	168885055	168885073	22.02666771	-
CAGCCACTAGATGGCAGAT	chr3	169082762	169082780	17.40466956	-
TTCCCACTAGGTGGCGACC	chr3	169366315	169366333	18.56819901	-
TAACCAGTAGATGGCAGCG	chr3	169668006	169668024	20.13297249	-
CTGCCACCAGGTGGTGGCA	chr3	170495800	170495818	21.5748464	-
CCACCACCTGGTGGCAGCC	chr3	170495804	170495822	17.87025815	+
CCGCCGGCAGGCGGCGCCC	chr3	171238392	171238410	18.59390828	+
CGGACTGCAGGGGGCGGCC	chr3	171239417	171239435	19.92646332	-
CCTTCAGCAGGGGGCAGTC	chr3	171247560	171247578	17.28652508	+
CCACCACCAGGGGCCAGTC	chr3	171510797	171510815	17.92170293	+
CCGCCACTAGGGGGAGCGG	chr3	171891041	171891059	21.07906747	-
GAACCACTAGGGGGCACTC	chr3	172012626	172012644	21.13367184	-
TTACCACCAGGAGGCAGCT	chr3	172363865	172363883	18.20075164	+
TGTCCTCTAGGTGGTGCTA	chr3	172767496	172767514	17.54352814	-
GAGCCAGCAGAGGCCGCTG	chr3	172815202	172815220	17.15529037	+
GGGCCACTAGGTGGCACAG	chr3	172904691	172904709	21.93622217	+
CTGCCTCCAGGTGGCCCTG	chr3	173030595	173030613	18.14300274	-
CTGCCTCCAGAGGGCAGAC	chr3	173235767	173235785	18.80181274	+
CAGCCACTAGAGGGAAGGC	chr3	173490264	173490282	17.19470256	+
TGGCCAGAAGAGGGCACTT	chr3	173533177	173533195	20.59365046	+
TTTCCAGCAGATGGCAGTA	chr3	173542149	173542167	19.9820471	-
CTGCCACCAGGTGGCGAGT	chr3	173677958	173677976	18.43278483	-
TCGCCACCTGGTGGCAGCT	chr3	173677962	173677980	17.1351011	+
CGTCCACCAGGGGGCACAC	chr3	173690797	173690815	23.10771243	+
TTGCCAGTAGAGGGCGCCT	chr3	173823897	173823915	21.72395174	-
TTTCCACTAGGCGGCGCTG	chr3	173867487	173867505	18.94581734	-
TAACCAGTAGAGGGCATTA	chr3	173918161	173918179	17.64702411	-
TGGCCAGGAGGTGGCGGTG	chr3	173951018	173951036	23.23149432	-
TCGCCAGTAGGGGGAGCAT	chr3	174037071	174037089	18.00587005	+
CTACCAGCAGAGGGAACCC	chr3	174187953	174187971	19.13788934	+
AGGTCAGCAGATGGCAGCA	chr3	174572527	174572545	17.1789925	+
CGGCCAGTAGGTGGCACTC	chr3	174729738	174729756	24.28049945	+
CAGCCAGCAGAGGGCTCAA	chr3	174754333	174754351	18.23802831	-
GAACCAGCAGGTGGTGCTG	chr3	174933703	174933721	18.03106899	+
CAGCCAGCAGGTGTCAGAC	chr3	175420413	175420431	17.23635869	+
GCTCCACTAGGTGGTGCCG	chr3	175729971	175729989	17.3253096	+
TGTCCAGAGGAGGGCGCCA	chr3	176321931	176321949	18.3210336	-
TAGCCAGTAGGTGGCACTT	chr3	177141610	177141628	20.47304021	-
AGGCCAGTAGGTGGCACTT	chr3	177142105	177142123	20.02962562	-

TTTCCACTAGGTGGCGCTT	chr3	177714897	177714915	20.04012185	+
TTGCCAGTAGGTGGCATCC	chr3	178139668	178139686	18.96584388	-
CTGACAGCAGGTGGAGCTC	chr3	178721889	178721907	17.09294048	+
CAGCCAGGAGGTGGTGCTC	chr3	178840994	178841012	17.56207613	+
TGGCCAGGAGAGGGTGACA	chr3	179038186	179038204	17.09928012	-
GCACCAGCAGAGGGCAGGA	chr3	179099928	179099946	18.64481665	-
GCTCCACTAGGTGGTGCCG	chr3	179946529	179946547	17.3253096	+
AGTCCACAAGGTGGCACTA	chr3	180216185	180216203	19.49901751	+
CCACCAGGAGGTGGCACCG	chr3	180473042	180473060	20.36008681	-
TGCCCACCAGGAGGTGGCA	chr3	180473045	180473063	17.81914819	-
CCTCCGGCAGGGGGCGCGC	chr3	180523368	180523386	19.09340338	+
CGTCCAGTAGAGGGCGCAC	chr3	180850251	180850269	21.16098631	+
TTACCAGGAGAGGGCACCT	chr3	180974707	180974725	17.44305836	+
CTGACAGCAGGGGGCAGCC	chr3	181129718	181129736	20.13820183	+
TAACCACCAGGTGGTGCCT	chr3	182304282	182304300	18.30668055	+
CAGCCAGGAGGTGGCGCTC	chr3	182430933	182430951	21.42306371	+
TATCCACTAGAGGGCACTT	chr3	182527299	182527317	18.67260205	+
TTGCCATTAGAGGGCGCCA	chr3	182901109	182901127	19.66303621	-
TGTCCAACAGGGGGCGCTG	chr3	182902743	182902761	22.39156375	-
TGGCCACCAGATGGCTCTT	chr3	183449014	183449032	18.76214981	+
ATGCCAGCAGAGGTCAGTG	chr3	184389561	184389579	17.20348838	-
CAACCAGTAGGTGGCTCCA	chr3	184586655	184586673	18.18228802	-
AGGCCACAAGATGGCAGGC	chr3	184761234	184761252	17.4661965	-
CAGCCACTGGAGGGCAGTC	chr3	184967675	184967693	18.34956162	-
CCGTCGCCAGGGGGCACCC	chr3	185026258	185026276	18.29463824	+
GGGCCACCAGAGGGCTCCG	chr3	185087331	185087349	20.82681531	+
CCTCCTCCAGGGGGCACTC	chr3	185105074	185105092	20.40700698	+
CGGCCGCCAGGGGGCGCTG	chr3	185218017	185218035	25.77943575	-
CAGCCACTAGGTGGTACTC	chr3	185345898	185345916	19.23218416	+
CCACCAGCAGGTGGGGCTC	chr3	185365405	185365423	17.53714177	+
CAAGCAGCAGGGGGCAGCC	chr3	185442521	185442539	18.07522332	-
CCACCTCAAGATGGCGCCC	chr3	185490037	185490055	17.76399908	-
CTGCCAGCAGGGGGCACCC	chr3	185554941	185554959	24.98911284	+
TGGCCACCAGGGGGAGGCT	chr3	185618502	185618520	22.436651	+
TGACCTGTAGGAGGCGCTC	chr3	185669047	185669065	18.75415367	-
TGGCCACCAGGTGGAGGCT	chr3	185670023	185670041	21.30902503	+
CGCCCACTAGAGGGCATTG	chr3	185714389	185714407	18.24787966	-
TCACCAGCAGGGGGCGGTG	chr3	185741749	185741767	24.66722938	-
AATCCACCAGAGGGCACTG	chr3	185744630	185744648	19.95402892	-
GGGCCACATGGGGGCGCCG	chr3	185761907	185761925	19.54481498	+
TGCCCAGCAGAGGGAGCTT	chr3	185786636	185786654	17.77720271	+
GTGCCTCTAGGGGGCAGCA	chr3	185928121	185928139	19.80479889	-
TGGCCACCAGGTGGCAATC	chr3	185978420	185978438	22.98150597	-
TGGCCACCAGATGGTGCTG	chr3	186003905	186003923	22.35146722	-
TGGCCACCAAGTGGCAGTG	chr3	186003952	186003970	19.311216	-
TTACCAGCAGGTGGCACCT	chr3	186075698	186075716	20.65807741	+
CAGCCACCAGGGGCAGCTC	chr3	186271168	186271186	17.1549481	+
TGGCCAGAAGATGGCACCG	chr3	186272062	186272080	22.32669259	-
TGCCCACCAGATGGTGCTG	chr3	186377428	186377446	19.30992061	-
TGACCACTAGATGGCAGGT	chr3	186481428	186481446	17.99255959	-
TCACCACCAGAGGGAGGTT	chr3	186661388	186661406	18.12121367	+
TGCCCACAAGAGGGCGCTT	chr3	186861088	186861106	19.21670584	+
CCACCACTAGAGGGCAGTG	chr3	186969146	186969164	21.92406349	-
CAACCAGCAGAGGGCAGCC	chr3	187144171	187144189	21.63336577	+

CAGCCTGTAGGTGGCAGAC	chr3	187154271	187154289	17.21145731	+
TGGCCACAAGGTGGCGCTT	chr3	187178078	187178096	22.45700728	+
CCACCACTAGATGGCAGTC	chr3	187184175	187184193	20.25658299	+
CCGACAGCAGAGGGCAGCA	chr3	187442477	187442495	19.57093078	-
CGGCCAGTAGAGGGCTCTC	chr3	187460186	187460204	20.22496002	+
CAGCCACAAGGTGGCGGCA	chr3	187741165	187741183	22.7787611	-
TCTCCAGGAGATGGCAGCA	chr3	187810131	187810149	17.45582012	-
TCGCCAGCAGGGGGAAGTT	chr3	187815517	187815535	19.0171187	+
GGGCCAGCAGGGGGCAGTC	chr3	187817701	187817719	23.89814769	-
CTTCCACTAGATGGCAGAA	chr3	188022108	188022126	17.89703531	-
ATGCCTCCAGGGGGCGCTA	chr3	188340313	188340331	21.80316874	+
CTGCCAGGAGGTGGCGCTT	chr3	188351282	188351300	19.5381628	-
AGACCAGTAGGAGGCGCTA	chr3	188631273	188631291	19.93119399	+
AAGCCAGCAGAGGGCAGGA	chr3	188879548	188879566	19.15683379	-
CAGCCACAAGAGGGAGCGC	chr3	188880278	188880296	17.32987418	-
TAGCCACAAGGTGGCAGGG	chr3	188915061	188915079	19.77584643	-
CTGCCGCTAGGGGCCGCCC	chr3	188940585	188940603	17.08192957	+
CTACCAGGAGATGGCGCCC	chr3	190031603	190031621	19.29846936	+
TCACCACCTGGTGGCGGAA	chr3	190035080	190035098	17.54173288	-
ATTCCAGCAGAGGGCGCTC	chr3	190155273	190155291	19.93209107	-
TGACCACTAGGGGTCAGAC	chr3	190157505	190157523	18.70626086	-
CTGCCACCAGAGGGCCCCA	chr3	190242161	190242179	21.14392567	-
GGGCCAGGAGGTGGCGCTT	chr3	190250144	190250162	19.36832786	-
TGCCCACCAGATGGCAGTG	chr3	190348673	190348691	21.51692569	-
GCTCCACTAGGTGGTGCCG	chr3	190381270	190381288	17.3253096	+
TCACCAGCAGAGGGCAACA	chr3	190433906	190433924	20.25462309	-
CCTCCTGCAGGGGGCAGTC	chr3	190541326	190541344	19.1159299	+
AAGCCACAAGGTGGAGCTA	chr3	190852722	190852740	17.63641034	+
GGGCCACTAGAGGGAAATG	chr3	190888131	190888149	17.12500986	+
TGTCCACTAGAGGGCAACT	chr3	191159155	191159173	17.78795804	+
CGGCCACTAGATGGAGGAC	chr3	191167934	191167952	19.00579492	+
AAACCGCCAGGGGGCGCTC	chr3	191522990	191523008	19.95631737	-
CCGCCGCCAGGAGGCGCGG	chr3	191714377	191714395	18.94106658	-
TCACCAGGAGATGGCGCTT	chr3	192012463	192012481	17.25742051	+
CTCCCTCCAGGGGGCGCCA	chr3	192078648	192078666	21.25348521	-
GTGCCAGCAGAGGGCACCG	chr3	192617660	192617678	22.3495869	+
TGGCCACTAGGTGGCACAT	chr3	193331197	193331215	21.28008405	+
CCGCCACTAGGTGGCGGGC	chr3	193388894	193388912	22.06207466	+
GTGCCAGCAGGGGGAGACG	chr3	193438936	193438954	18.39528352	+
GGCCCGGGAGGGGGCGCTG	chr3	193610413	193610431	17.21777699	+
TGTCCACGAGGTGGCGCTC	chr3	193645173	193645191	21.73018527	-
GCGCCGGCAGGGGGCGGGG	chr3	193715393	193715411	19.39256104	+
AGGCCTGCAGGTGGAGCTG	chr3	193989923	193989941	18.40702333	-
TGTCCAGAAGAGGGCGAGA	chr3	194330274	194330292	17.17226822	-
GTACCACTAGGAGGCAGCG	chr3	194496656	194496674	17.87363901	+
AGGCCTGTAGATGGCAGCC	chr3	194764688	194764706	17.47517264	-
TCACCACTAGAGGGAGCCC	chr3	194806560	194806578	20.0990053	-
CCGTCAGCAGATGGCGCCC	chr3	194981430	194981448	19.01993382	+
GGGCCTATAGGGGGCACTG	chr3	194988785	194988803	17.81480538	+
CCGCCGGGAGGGGGCGCCG	chr3	195338453	195338471	20.91919576	-
CGGCCACTAGGGCGCGCTG	chr3	195516319	195516337	20.45929673	-
GCACCAGCAGAGGGCAGCA	chr3	195546522	195546540	20.69448711	-
ATGCCATTAGGTGGCGCCA	chr3	195606845	195606863	17.58020048	-
TTCCCACTAGAGGGCGCTC	chr3	195796897	195796915	21.09226416	-

CCGCCGCTGGGGGGCGGCC	chr3	195835492	195835510	18.51834769	-
AAACCACTAGGGGGTGCTA	chr3	195873634	195873652	18.4784499	+
CAGCCAGCAGGTGGTGGGC	chr3	196204124	196204142	18.16934248	+
CCACCAGGAGGTGGCGATG	chr3	196429295	196429313	18.0892177	-
TGGCCACCAGGAGGTGGCG	chr3	196429298	196429316	20.85057539	-
CGGCCGCCTGGGGGCGCCG	chr3	196462220	196462238	21.08347936	-
TGGCCAGCAGGGGGCCCCT	chr3	196473687	196473705	20.98336573	+
CCGCCGGCAGGGGGCGCGC	chr3	197061121	197061139	21.34593498	+
CTGCCTCCAGGTGGTGCTC	chr3	197074512	197074530	18.47554291	+
CGACCGGCAGAGGGCAGTA	chr3	197106043	197106061	20.92421736	-
TGTCCACCAGGGGGCACCA	chr3	197126463	197126481	25.69119709	-
GGGCCACCAGAGGGCTCCG	chr3	197233496	197233514	20.82681531	+
CTGGCTGCAGGGGGCGCTC	chr3	197408058	197408076	17.92878493	-
CGGCCAGAAGGGGTCACTC	chr3	197465036	197465054	20.02230822	+
CTCCCAGCAGGTGGAGCTC	chr3	197697724	197697742	18.26207608	+
TTTCCACGAGGTGGCGCTG	chr3	197730602	197730620	20.58687508	-
CTTCCACCAGGGGGAGACA	chr3	197734098	197734116	18.65671927	-
CTCCCAGCAGGGGGCAGCC	chr3	197820719	197820737	21.30733743	+
TTACCACCAGGGGGCAGAA	chr3	197896323	197896341	22.42332712	-
CAGCCAGAAGGTGGAACCC	chr3	198159848	198159866	17.9136975	+
CTCCCGCCAGGGGGCAGCG	chr3	198181311	198181329	19.68164331	-
CCGCCAGCAGAGGCCGCTC	chr3	198214160	198214178	18.83258257	+
CCTCCAGCAGGGGGCGCGC	chr3	198241170	198241188	21.90980031	-
TGACCACTAGATGGTGCTC	chr3	198398427	198398445	19.59423573	-
TGGCCAGGAGGGGGCAGTC	chr3	198713396	198713414	22.80551205	-
CTGCCGCTAGAGGGCGCTC	chr3	198721580	198721598	21.24678494	-
AGACCAGCAGAGGGAGCAC	chr3	198737154	198737172	17.66096429	-
GTGTCAGTAGAGGGCGCTG	chr3	199117418	199117436	17.36112668	+
GGGCCACCAGAGGGCTCCG	chr3	199262235	199262253	20.82681531	+

Supplementary Table 1 – Statistically significant CTCF sites (weight score of 18 and above) detected in chromosome 3 of human (hg19 build), where *Sox2* is located. Syntenic CTCF sites conserved in human, chick and mouse harbouring the *Sox2* gene are highlighted in red.

>Sox2-Enhancer1 TTGTAGTAGAGATTTTTTTTTCTGCATTTTAGCTCTCCTAAAATGATCAGATCTGTCATTCAGCTTTAAAAGGGAATGTATATTCTTCCTCTCCTGGATTTTTTTTCCCCCAAGGGGTATAATGCTAATTTTACTTATTCAGAAATTAAAATAGCAAACAGTTTATGTGAGGTGTTGATAATTACCTATATTACTGTAACGCTGTGACAGATGTTGGCAAAAAGAAGCAGAAAATGCCTACAGCTGTGCACTCCATGACATCCAGTTTATACTCAGACAGAAGGCTAACAGATGTTCTGAACTGTCACTTTGCCTAAATGTTTTTAAAGTCTAAGGACCTGCTTTATAATTCACTGGGGCCTCATTTGGTTTCGCAGAGGTCCTCAGAATTCCCATCTGTGACAATTAATGTTGAAGACTTTTATAAATCAACCCTTGTCCTTATTAGCCCTCTGCAAATAGATATTGTGTATCTGTATACTCCCGAGACTTCTAT
>Sox2-N3-Enhancer AGTTGCCATTTCTTTTTAAAAGCTGGGTTCCTGTTGTACAGCAGTTTAATAGCTTTAACATTGCACTGCCGTAATCGGTGTTTGGCCTCTTCTGTTCCCCAATCCTGTATGGAAGCAGAACTCCAAATTGTACATCTTTCTGGGTTTGTTTCTAAATTACTCCCCACACTTAATTACGAGGATGAGAGGGATGCCTTATTCCTCTTTGTTATAGGCTAAGCTCTCAGTAATCCCAAACAAAAGAGCCAGTTCTGGAAGATATAGGATTTGCTAGCAGGATTATGGTCTCATAGATAATGATGTGCAGTCAGCAGAAGCGAAGCTTTATTTTAATTCAAATAAGCTAGTAAACAAACCACTGACAAGTCTGCTGGTGAGAGTAACTGGCTTCTGTTGCCACATTGGCAGCTAAATTATAGAAAATCTATTATACCCTGTTCACCATATGTTTAATTTAATACAGATACAAATTAAACTATCCACAGTGCCTATTAAAATAACAATACATATTTTTAAAATATATGAATGTTTTAAGATACATTCCCCTGACCTTAAGAAGGGCAAATGCTGATTTGGGAGACT
>Sox2-Enhancer4 CTGAGGGTGGGGGGAGGTGGGGGGAACCCTGCAGCTGCAAGTCAAAGAAATATATTGATAAAATATTTCAGTAGTAGTAAATACGCGGGGATCGGCTCGACCTTGCGAGGTCTTCATTTTAATTTTTTTTTTCCCCCTATATACAAAAATCTTTATCAAACCTCTATTCTATGGCTTCAATAAACAGAACCCATTACCTCACGGCAGCTTTTGTTGGCCTGTATACAAGCGAGAACAAAATGGTTATTCAGGAGAACGCTTTCGATTTTTATTGTGTGTAGTATGCACAAAGAGCAGTGTTATTGTATTAAAAAGAACCATCTGTAGCAGAAACAATGGCATCAAATTATCTTTGAATACCCACTGCAAAAATATAAAGCTTTTTTATTATTCTTCTGCTGTACGGTGGGGGACAGAGAAGTGACTTTTTTGTTGTCGCGGGTGCATTCTTATAACACACACAAAATCAGCCATTTGGATTTTTTAAGCCATAAACGATTTTTTCCCCTCTTGTTCCAGGGACCGCAGTTAAAAGCTAGGGCTAGGACTTGGAGGACGTGTAGGCAAACGGAAGGAGAGCCGGGGGAAGAAAAGCCGAAATGGATTCATTCTCCGTCCTGGCTGGAGGAGGAGAGGAGCGGGGACGTGCGGGCTGCCTGCAGCTGCCTCTGTCCGGTGAGAAGTGCTCCCAGCCCCGCGGCTGACTCGGGCTCGGGAGTCCGCGCGGACTTTCGCTCGAAGCTGCCAATCAAACCGCTAACCGCCACCACCCTGCGCTGGCACCGACATGTGAGTACTGCACCACAACTTTGACATTCACGGGTTTCCCCCTTCCTCCCCCGTGACCTTTAAAACGACGGAGAAATACCGCTGTC
>Sox2-NOP1-Enhancer GGGTAAGAATTTGGTAGATAAAGGTTAATCTTGGGCTGAATTATAGAGCTGTGATTGACAAGAGAAAAGGTGTTGAGGGCAGGTCGAGCTGTCTTATTTACAGCCCACTGCTTGCTATAGAGCCTTTGTTAGGACTGGAAAGCTAATTTAGTGCTGATCAAAAGCACCACGGAGTTAAAGGACTGGTAATGACTGCTAATTTCATTTCAGCCTCATACATCCCCAACCGCTGTAATTAAAGACGTGCTATTTAAATACAGGTGAAGAGTTTTTGTAGCAGGGGGAAAGTGGGCAGCCGGGTACCATTTTATTTCTGCTTAATG
>Sox2-Enhancer7 ATTCTGAAATCACAAGCCTAAGTTGTCACAATGAGCCCATGGTGTCAATAAACCATGGACGAGATGGAGAGATTGTCACTCCAGACCATAACAGTTCTGAAAGTGTCATTACCGTCTGTCCTGTCAATGAGCTCCAAATTAAGG
>Sox2-N2-Enhancer GAGGAAATTTCTCTGTACGTTTTCGTCTTCGGCTTTTTTTTTTTTTAACGTAATGAAATTAAAACTTTTGGAGCTCAGAGTTGACATTTTGCGGAAAATTGAGTTATCAAGGCAGTAATTATTTCACAGGGAGATAAAACTCTCATAGCCCTAACTGTCAAATAGGGCCCTTTTCAGATTTTAATTACAAAATAAAATTAGTCTGCTCTTCCTCGGAAGGGTTTGTGAGTGGCTAAACAGAGCTTTCCCCAATACTGGTGGTCGTCAAACTCTGCTAATTAGCAATGCTGAGAAATTCCAGTTAACAAGGACATTCTCTAAGTCTCTGCAGGTTCCCTGCCGTTCGCCTTCATTTCCATAAGAAGATTAAGAGTGGAGGGGAACACACTCAAATGCAGATGCAGAAAAGAAGCGTTTTTAACAAGCATCATAATAGTAAGATGCTTGGCTAGTTCTCACCTAATTACTGCAAGTTAAACCTCTATTTGCAGCTAAGGACAAAAAATGGAGCTGCAATCTTCCATCTCCACAAGAC
>Sox2-Enhancer9 CCCTTTCTCTCCCCTCCTTCCTTTGTCGTCAAGTGCGTTTTAGCAACAAAGATCCCAACAAGAGAGTGGAAGTAAACTTAGCCGGGGCTTTGTGCGGCCCCGTGTAGCGACAACAAGAGAAACAAAACTACCTATTTGTTCCTGCGG

G
>Sox2-Enhancer12 GCCGGGGTGTTAAAATATTTTGCGGAACTGGAGAGGTAGATTAGCGGGGTTTCTTGCCAAAGCCGGGAAGCTGGTATTACAGCTCGTCCCAGGGGGACATCGCTCACATTAACCACTAAATGAATATTTGACAAGGGCTCATTCGGGGGTATTATTACTACAAACGGGTCCCTACTGGACTTTCCGAGGGTCAAAGAGCAATGGTTCAATTAATTATTTAGACTGTTAGGAGATGCGATTGTAATAGCGGCGCTTATTTCTGCAACCGACGGTTCTCGAGGGGGGA
>Sox2-N5-Enhancer CGAATATCAAGTATTGTAAGATTTCTTCCCTGCCCCCCGGCACTGATTGGCAATACTCTTCGTTTTTTTTTTCTTCTTTTTTTTTTTTCTTGTGTGTTGGTTTGAAAAGCAGGAAGAAATGTAATGAATTGAGTGCTGTCAGAGATGTCTTCTGTGTTGATGTGGTGAATGGCAGTAGCTCCCTGATCCAGTGCAGGTGCAGTAGAGCTGGGGAATAAAAGAGGGGGGCTCTCTGTTCAGTGGAAAAAGCACATTCCCTACAATAGACCACACACTGCCAGCCAGCACGGCATCAGCTCACACACAGACTTTTTTCGCCTCTTTCCACAGTCCCGAGCTCACAAAATGGCTATACATTAGCCCTA
>Sox2-Enhancer15 TTTGTGTCCCGGCGCTGCGCACACCCGTAATTAATCCTCCTGCTTACCGCTTACATCCCGGACCCAAGGGGCAACTCAAACCTATTTAGATCGCCTTGGTTGGTTGCACAAATTTAAGTGGCAAATGAGTTATAAACCTAATAACCGCTTTAATAAAAATAATTATTTGATTATGGCGGAGTACGTT
>Sox2-Enhancer16 CGTCAAACGCTTCGTTGGATTGGCCCCGACAGAGAAGACCTTTTCTTTCTAGGCAGTGTTGTTGAGAAAGAACAATGCAGATCTAATTGTGGAGATTTCAGAAGTTGGCTCCTGTAAATGAACAGCTTAGATATGGAAGTTCCAGCAGATGTCTGCACTTTTCCCTGTGACAAACCTTGTAACCCCCCTTCCTCCCCCACTGCCCCGTCCTCCCCCCTCCCCGACTTATTGAAGATTTTTTGTTCTCACATCCTAGCAACAACCTAAATCTTCCCGCAGCAATACCCCCTCTCCCCTGGTTGCTACCCAGCCCTCAGCTGGCAGCCTCCGAGCTCCAAATTAG
>Sox2-N1-Enhancer AAGATGTATAAATATCAAAGTGAAGGAGCCCGAGTAAGTCTTTCTAGAAGCGAGGAGGAAGCTTAAGCAGCTTTCTTTAATGGTGATTTGTAGCTCTGTAAGGGGCACGGATAGCAAATACCCTGCAGGTGCATGTTGTAACACTGCCATCCGGACTTTAATGTAGATTACTCTCCAACTCGTTTGATCGGTCCTTTGAAACCCTTTACAATTGCCTGTGACGAACCGCCAGTCTCAGTTTTTTTTCTTTGAATAATGCCTTAAGGGTAAGTCCTCGGGGCTTTTAAAGATCTCCAGC
>Sox2-SC1-Enhancer TCTGAATTAAAGGCCCATTTGGGACACTCGAGACTACAAAGGGTTACACATAAATAAATGCCACATTTGCCTATTGCAAAAGTTTTCTCTGTCCTTTCTCAGTCGCAACAGGGGAGGAAAAAGCCGTCGTTTATTATCTCGCGCCGGGCAGGAGCAGCCCCTCCAGAATGTGCTCCGGCAGAAGAGGCACTCTTTTTCCCCCCCCTCAACAGCAGCTCCTTTTGTTCTCCAGATCTCTTTCCCAATTTCAAGCTTCACTTGCGGATCCGAAGTTTGTTTGTTAATGACGCTATTACCATCTGGCTCGTCCTACTTTCCAAAAGATATAAATCTCCCCGGTTTCATTGCCCACATTATCATTTAAGTGCCACCATCGCTGGAAGAAAAATACGCTTTCAAGGCAGCGGGTTCT
>Sox2-Enhancer19 GATCTTGTTTATAAATTTATATGACGACCTTTCCTTTGTGTCTGCTCTAAAGTTGATATGGACAAATTGCAGAGGTATACAATTTAAGTAGATGCACTTTTAATCACCGATCATTAAAATGGTTATGTTAAATATACTCAATTACATGCATGACTTCACCCTAACAGTACTTTCTATTCTCCCAGCTGCTCACGTATTCCTTAACTATAGTCAGCAGAAGAAACTCGATTATGCTGAATCCATACATTTCTATGGATTTCATCAGCCTAATTAATGCTTCAGTGTGGTCCATGTGTCTGAATGGTCCCTTTGCTATTACTTGGGTAAGGAGACAGTGCAGGAATGCAGAGGGGCTTTCTTT
>Sox2-SC2-Enhancer CACAGCCAGCACGTTCCCAAACTTTGAAATGCCAAATCACGTTATTGCTGCGGCGGGAGGCTGCTTTCGGATCTGTGACAGCTGAGTTTTTCCTATCGATTATGTGACACTGCCGTTCATTTACACAGCTCAAAAGCTTAAAGCCACGGGAGGAGCCCCCAGTTGAACCC
>Sox2-N4-Enhancer CCTGATAGACATCTCTACAAGGTAGGTTTTAACGTTTTGTTTTTTTTTTTTCCCTCTTAATTTTTTTTTTTCCTGTGGTAAGAAGGATAAGCTTGGAGTGCCCAGTCACCGTGGTAACTGCCAGAAAAATTCTCCTGAAGTTTGAAGGGGTCAGCGCGCGGGGTCAACAACTCTGGCCTCTCCCCGCGCCGGGGCTGCAGGCTCCGTCCCGTGGCCGGGCCTTAGCGCGGGCTCAGCCCTGGGAGGTGGGCCGCTCCCGCTCTGATATAAATTTTTTGAGTCAGTTCACGGCCTGGGCTCTCCAGGTGGCCTCCAAAATCGATCGTGACCTCATGACCCTGTCTAACGGAGGCATAGCATCCAAC

CTAAGTAAGGATTTAGGCAGGAGCGACAGCTTTCCGCTGAGTGTTATTGGGGACAGTGCAAACAGTTTTGGAAGCGAGGAGGTAGGTATGAGGAGCTGAGGTCATTAAAGGC
>Sox2-Enhancer25 CATGAGTTATGATAACATATAAGCAGCTTAGAGAATTCTTATCGGAATGAGTTGAACACAATGCGACGTTTAACTCTTAATGACAGCCACCTCTGACTGAGTGACACATTATAAATTATGTTTGAACTGGGTGTTTTTTTTCAGAGGCAGATATCCCCCTGCCACCCAGCCAGCCCTGCGAAGTTGCACTTGTGGCCTTAATCCCACTTGGATGTGTGCCCCGCTGCCTCCACTCTCCGTCACTCGGGTGCTTTAGTGTTCTTGAACAAGTGAACAATCTTTGTTTCTGTACCTTATTAGGCCAGAGACCATAGCAGCGAGCGATGGCATCAGCAGGCCCCGCAGGCAGGATTCTCTGCAGACACAGCCAACCTCCAACAAACCCCTTTTTATCCTCCTGTTTCTAGGAAGAATTATGATGGTGGTGCCCTGCTGTTGATCAGTCAAATCTGTGGTGGGCCTAGAGATAAGTCCTGTAAGTGTGGTGTACTGTAAAACAGCGGCTCCCATTCATTAGTGGCTTGTGTGTAATAAACCACCCAACAGAGGGGGTTGGGGAAGAGAGGGAAAGAGCAGCTGCAGTGTGCAGGAACAAACAACACAACTCATTCTTGGGAGCCAAAACTTTCTAATTTGCTGCTGGGCTGCTGGGAGCACTCAAATTCTTTCTGATAA
>ECR1-P1
AACTATTTAGGGGTGATTTAAATATTTAGGTCTCCTTTTTTTCTCCTTCAAATTAATAGAAAGGCCTTCGATATAGTTAAAAGTATTTGAAACTGGGGGCAAGGTTAACAGGCCAAAGGGATCAGTGTCAGCTTTTTAAGTACTTCTAAAAAGATCATGTGAACAGATGG
>ECR1-P2
AATCGGCGTCTTAACTATTTTGGTGGTGGTTACGGGTAGGGG
>ECR1-P3
AATTTGATAGATAAAGGTTAATCTTGGGCTGAATGATAGAGCTATGATTGACAAGAGAAAAGGTGTTGAGGGCAGGTCGCGCTGTCTTATTTACAGCCCACTGCTTGCTGTAGAGTCTTTGTTAGGACTGGAAAGCTAATTTAGTGCTGATCAAAAGCACCACAGAGTTAAAGGACTGGTAATGACTGCTAATTTCATTTCAGCCTCATGCATCCCCAACTGCTGTAATTAAAGACACGCTATTTAAATACAGGTGAAGGGTTTTTTTTTTTTAAGTTGGGTTGGGGGGGGGTGGGTGGGTGGATTACAATTTTATTTAGATCTTCTACTCTACTT
>ECR1-P4
ACTATAGCTGCAGTGTTGGCTCAGAAACCGTGTAATTTCTCATCCGATAGGAGTTTCTTTATGAGAACATCAAAGGATAAAAAGCTCTGCATTTTCGTAGTTGGTTAAAATTGATAACCACCCCCCCATGC
>ECR1-P5
CAGAATAAGCAGGAAATATTACCTGAGAGAAGGAATTACAG
>ECR1-P6
GAAACGGGATGCGAAAACAAATTTTTATATCCTTGAAAA
>ECR1-P7
GAGCCGCTCCTTGTCATTTATACCTGGCTTTGCAGAATCGGAAGTGTGAAATG
>ECR1-P8
GGCGATACTACAATTTTAATTCAATAAAAAATAAAGACTGTCC
>ECR1-P9
GGGGTGATGGGGCTTGCTCTTTGGCGCCCTCTAATGGCAACTTGAACCAATG
>ECR1-P10
TATCCCCAAAAAAGAATTTAGCCTTTAATCTCTTTTTATCCACGAAGACTAAAGCTCTGTACTCGACCCCGCGAGCGGCTCTCGCCTTCCGGGGCTGGAACCCGACTCAGATGTGAAGCGGCACTGAGCCGCTGCGCAGGTTCGTGCCCAGCGCCCCCTGTTGGACACAGTAGGAGCTGCGCAGCGCCAGTCCCAGAAATCGCTG
>ECR1-P11
TCACATAAAAGCCCCTGTTTAAAGAAAGGGTGGGACGGGGG
>ECR1-P12
TCCTAGGGAAGGGGGAGTATTTTTACACTTCCAAAAAACT
>ECR10-P1
AGGAACAGTGAAGACTTCCTGAACTTTTTTTTTCCTT
>ECR10-P2
GCTTGCCTTTAGCTTTAAAAATGATTTTGTTTTAACATATGTTAGCTGAAGCAAAAAATAATACAGTAGGAGCT

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>ECR10-P3
GGTTCTCCAATACTAGTCATTTTTTTTGGTTAAAACTTTG
>ECR10-P4
GTTTCTTTCTGTGAGATTTAAAACTAAAAATATATGAGTTACAAATTT
>ECR10-P5
TAAATACTGACAGAGTTCTTATTTCTTTTATATTGTCTGGAATAAAATTGATAAATGAAAAAAATCTGTAA
>ECR10-P6
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Supplementary Table 2 – A list of Conserved ECRs generated from DREiVe analysis of Sox2 insulator locus. These sequences are conserved in human, chick and mouse. Known *Sox2* enhancers identified by DREiVe are highlighted in red. For other potential enhancers, multiple conserved patterns located in the same ECR are annotated as P#

#seq_id	**ft_type**	**ft_name**	**Strand**	**sequence**	**weight**	**ln_Pval**
Sox2-Enhancer 1	site	TAL1::TCF3	R	AGAACATCTGTT	11.8	-14.538
Sox2-Enhancer 1	site	SRF	R	ACCAAATGAGGCCCCAGT	9.1	-11.141
Sox2-Enhancer 1	site	TAL1::TCF3	R	CCAACATCTGTC	9.3	-10.99
Sox2-Enhancer 1	site	EBF1	D	CCCCAAGGGG	8.9	-10.884
Sox2-Enhancer 1	site	Nkx2-1-Nkx2-1-isoform1	D	CCCCCAAGGGGT	7.6	-10.725
Sox2-Enhancer 1	site	TAL1::TCF3	D	CTAACAGATGTT	8.5	-10.306
Sox2-Enhancer 1	site	HNF1A	D	TGTTGATAATTACC	8.1	-10.178
Sox2-Enhancer 1	site	C-EBPgamma	R	TTGATTTATAAAA	8.1	-10.123
Sox2-Enhancer 1	site	IRF1	R	CAAAGTGACAGT	7.9	-10.07
Sox2-Enhancer 1	site	AIRE	R	GAGTATAAACTGGATGTCATGGAGT	1.8	-9.988
Sox2-Enhancer 1	site	Pax4	R	GAATAAGTAAAATTAGCATTATACCCCTTG	7.8	-9.933
Sox2-Enhancer 1	site	Dlx5	D	TTGATAATTACCTATA	8.2	-9.878
Sox2-Enhancer 1	site	Dbp	D	AGCAAAC	7.2	-9.853
Sox2-Enhancer 1	site	FOXA1	R	TGTTTGCTATT	8	-9.769

Sox2-Enhancer 1	site	SPIB	R	AGAGGAA	7.8	-9.758
Sox2-Enhancer 1	site	RXRA::VDR	R	ATGTCATGGAGTGCA	7.1	-9.727
Sox2-Enhancer 1	site	HNF1A	R	AGGTAATTATCAAC	7.5	-9.662
Sox2-Enhancer 1	site	PPARG	R	ATAGGTAATTATCAACACCT	6	-9.519
Sox2-Enhancer 1	site	Nkx2-5	R	TTAATTG	7	-9.519
Sox2-Enhancer 1	site	Meis2	D	TCAGATCTGTCATTCA	6.9	-9.48
Sox2-Enhancer 1	site	TBX5	D	TGAGGTGTTGAT	7.9	-9.418
Sox2-Enhancer 1	site	OCT4_01	D	TTTACTTATTCAGAA	7	-9.327
Sox2-Enhancer 1	site	Zic1_1	R	TACCCCTTGGGGGA	7.2	-9.29
Sox2-Enhancer 1	site	Dlx5	D	GTGACAATTAATGTTG	7.6	-9.169
Sox2-Enhancer 12	site	Msx1	D	TTCAATTAATTATTTA	10.4	-13.088
Sox2-Enhancer 12	site	HNF4A	D	GGGTCAAAGAGCA	9.1	-11.52
Sox2-Enhancer 12	site	Lhx3	D	CAATTAATTATTT	9.3	-11.303
Sox2-Enhancer 12	site	NR1H2::RXRA	D	GAGGGTCAAAGAGCAAT	5.3	-10.965
Sox2-Enhancer	site	HNF-4>HNF-4alpha>HNF-4alpha1>HNF-	D	GGGTCAAAGA	8.9	-10.873

12		4alpha2>HNF-4alpha3>HNF-4alpha4		GCAA		
Sox2-Enhancer 12	site	RELA	D	TGGACTTTCC	9.2	-10.821
Sox2-Enhancer 12	site	Pax4	R	AAATAAGCGCCGCTATTACAATCGCATCTC	8.5	-10.741
Sox2-Enhancer 12	site	PPARG::RXRA	D	GAGGGTCAAAGAGCA	8.7	-10.73
Sox2-Enhancer 12	site	Msx1	R	TCTAAATAATTAATTG	8.9	-10.698
Sox2-Enhancer 12	site	Lhx3	R	TAAATAATTAATT	8.6	-10.625
Sox2-Enhancer 12	site	REL	D	TGGACTTTCC	8.5	-10.484
Sox2-Enhancer 12	site	EBF1	R	CCCCCTGGGA	8.6	-10.479
Sox2-Enhancer 12	site	MZF1_5-13	D	CGAGGGGGGA	7.9	-10.346
Sox2-Enhancer 12	site	Isl2	D	TTCAATTAATTATTTA	8.2	-10.081
Sox2-Enhancer 12	site	Lhx3	R	TAATTAATTGAAC	7.8	-9.984
Sox2-Enhancer 12	site	HNF1B	D	TGAATATTTGAC	7.8	-9.874
Sox2-Enhancer 12	site	EBF	R	TCCCCCTGGGA	7.5	-9.664
Sox2-Enhancer 12	site	HNF1B	R	TTAGTGGTTAAT	7.5	-9.637
Sox2-Enhancer 12	site	Nkx2-5	R	TTAATTG	7	-9.519

Sox2-Enhancer 12	site	CTF-CTF-1-CTF-2-NF-1	D	GGGGTTTCTTGCCAAAG	7.5	-9.494
Sox2-Enhancer 12	site	HNF-6alpha-OC-2	D	CTAAATGAATAT	7.4	-9.475
Sox2-Enhancer 12	site	PLZF>PLZFB	R	CTCCTAACAGTCTAAATAATTAATTGAAC	5.1	-9.446
Sox2-Enhancer 12	site	HNF1B	R	TAAATAATTAAT	7.3	-9.423
Sox2-Enhancer 12	site	Zic1_1	R	GTCCCCCTGGGACG	7.3	-9.394
Sox2-Enhancer 12	site	Pitx3	D	AGGTAGATTAGCGGGG	6.8	-9.326
Sox2-Enhancer 15	site	Zfp628	D	CTTGGTTGGTTGC	12.6	-14.931
Sox2-Enhancer 15	site	Nkx3-2	D	TTAAGTGGC	7.8	-11.296
Sox2-Enhancer 15	site	Pitx1	R	GCAGGAGGATTAATTAC	9.4	-11.199
Sox2-Enhancer 15	site	EBF1	D	ACCCAAGGGG	9	-11.077
Sox2-Enhancer 15	site	Pitx3	R	AGGAGGATTAATTACG	9.1	-11.028
Sox2-Enhancer 15	site	Pitx2	R	CAGGAGGATTAATTACG	9.2	-10.984
Sox2-Enhancer 15	site	Lhx3	D	AAAATAATTATTT	8.6	-10.625
Sox2-Enhancer 15	site	Msx1	D	TAAAAATAATTATTTG	8.8	-10.569
Sox2-Enhancer	site	Msx1	R	ATCAAATAATT	8.7	-10.443

15				ATTTT		
Sox2-Enhancer 15	site	Isl2	R	ATCAAATAATTATTTT	8.3	-10.19
Sox2-Enhancer 15	site	Foxd3	D	AATTATTTGATT	8.4	-10.15
Sox2-Enhancer 15	site	Dlx5	D	CCCGTAATTAATCCTC	8.4	-10.147
Sox2-Enhancer 15	site	MTF-1	D	GCTGCGCACACCCG	7.9	-10.06
Sox2-Enhancer 15	site	Lhx3	D	TAATTAATCCTCC	7.9	-10.059
Sox2-Enhancer 15	site	Crx	D	TAATTAATCCTCC	7.7	-9.934
Sox2-Enhancer 15	site	CEBPA	R	TTGTGCAAC	7.3	-9.711
Sox2-Enhancer 15	site	Zfp423	D	CGGACCCAAGGGGCA	6.7	-9.621
Sox2-Enhancer 15	site	HOXA5	D	CACAAATT	7.2	-9.466
Sox2-Enhancer 15	site	Msx1	D	CACCCGTAATTAATCC	7.8	-9.435
Sox2-Enhancer 15	site	YY1	R	TCCGCCATAAT	7.3	-9.436
Sox2-Enhancer 15	site	Dlx5	R	GGATTAATTACGGGTG	7.7	-9.278
Sox2-Enhancer 15	site	KAISO_01	D	CTCCTGCTTA	7.1	-9.252
Sox2-Enhancer 15	site	MEF2A	R	TTATTTTTAT	6.6	-9.162

Sox2-Enhancer 16	site	ZNF219	D	CTCCCCCCTCCC	13.2	-14.981
Sox2-Enhancer 16	site	EWSR1-FLI1	R	GGCAGTGGGGGAGGAAGG	2.8	-12.376
Sox2-Enhancer 16	site	CKROX_Q2	D	CCCCTCCCC	10.3	-12.054
Sox2-Enhancer 16	site	Pax-2-Pax-5-Pax-8	R	CTGGAACTTCC	9.1	-11.215
Sox2-Enhancer 16	site	MAZ	R	GGGGAGGG	9.6	-11.08
Sox2-Enhancer 16	site	MZF1_5-13	R	GGAGGGGGGA	8.3	-11.072
Sox2-Enhancer 16	site	Pax4	D	TAAATCTTCCCGCAGCAATACCCCCTCTCC	8.7	-10.982
Sox2-Enhancer 16	site	SP1	D	CCCCTCCCCG	9	-10.838
Sox2-Enhancer 16	site	CAR>CAR:RXR-alpha>PXR-1A>PXR-1A:RXR-alpha>PXR-1A:RXR-beta>RXR-alpha>SXR:RXR-alpha>VDR	D	ACCCCCCTTCCTCCCCCACTG	8.8	-10.808
Sox2-Enhancer 16	site	SP1	D	CCCCTCTCCC	8.8	-10.736
Sox2-Enhancer 16	site	SP1	D	CCCCCTCCCC	8.7	-10.705
Sox2-Enhancer 16	site	CAR>CAR:RXR-alpha>PXR-1A>PXR-1A:RXR-alpha>PXR-1A:RXR-beta>RXR-alpha>SXR:RXR-alpha>VDR	D	AATACCCCCTCTCCCCTGGTT	8.6	-10.624
Sox2-Enhancer 16	site	RXRA::VDR	R	GGGTTACAAGGTTTG	8	-10.428
Sox2-Enhancer 16	site	PLAG1	R	GGGGAGGAAGGGGG	7.5	-10.221
Sox2-Enhancer	site	Egr-1>Egr-2>Egr-3>Egr-4	D	TCCTCCCCCAC	8.2	-10.198

16				TGC		
Sox2-Enhancer 16	site	WT1>WT1-del2	D	CCCCCCTCC	7.5	-10.117
Sox2-Enhancer 16	site	MAZ	R	GGGGAGAG	8.2	-9.995
Sox2-Enhancer 16	site	SP1	D	CCCTTCCTCC	8	-9.95
Sox2-Enhancer 16	site	SP1	D	CCCCCCTCCC	8	-9.95
Sox2-Enhancer 16	site	HNF4A	R	AGGGAAAAGTGCA	7.8	-9.913
Sox2-Enhancer 16	site	BRCA1	R	ACAACAC	6.4	-9.9
Sox2-Enhancer 16	site	Egr-1>Egr-2>Egr-3>Egr-4	D	TCCTCCCCCCTCCC	7.8	-9.843
Sox2-Enhancer 16	site	Pax5	R	GGGGTATTGCTGCGGGAAGA	7.8	-9.814
Sox2-Enhancer 16	site	PPARG::RXRA	R	ACAGGGAAAAGTGCA	7.8	-9.807
Sox2-Enhancer 16	site	SOX9	D	GAACAATGC	7.8	-9.805
Sox2-Enhancer 16	site	SP1	D	CCCCGTCCTC	7.9	-9.78
Sox2-Enhancer 16	site	HNF-4>HNF-4alpha>HNF-4alpha1>HNF-4alpha2>HNF-4alpha3>HNF-4alpha4	R	AGGGAAAAGTGCAG	7.8	-9.726
Sox2-Enhancer 16	site	CTCF	D	GTTCCAGCAGATGTCTGCA	6.5	-9.693
Sox2-Enhancer 16	site	SP1	D	CCCCTTCCTC	7.7	-9.608

Sox2-Enhancer 16	site	Myf	R	AGACATCTGCTG	7.5	-9.606
Sox2-Enhancer 16	site	SZF1-1	R	CCAGGGGAGAGGGGG	7.3	-9.53
Sox2-Enhancer 16	site	Pax4	D	CAAACCTTGTAACCCCCCTTCCTCCCCCAC	7.4	-9.494
Sox2-Enhancer 16	site	HSF1-L>HSF1-S	R	CTGCTGGAACTTCCATA	7	-9.469
Sox2-Enhancer 16	site	SP1	D	CCCCCTCTCC	7.6	-9.464
Sox2-Enhancer 16	site	SP1	D	CCCAGCCCTC	7.6	-9.464
Sox2-Enhancer 16	site	CTCF	R	CTGCCAGCTGAGGGCTGGG	6.1	-9.439
Sox2-Enhancer 16	site	Pou5f1	D	CTTAGATATGGAAGT	6.9	-9.378
Sox2-Enhancer 16	site	Foxd3	D	GATTTTTTGTTC	7.5	-9.33
Sox2-Enhancer 16	site	OCT4_01	D	CTTAGATATGGAAGT	7	-9.327
Sox2-Enhancer 16	site	Sp3	R	ATAAGTCGGGGAGG	7.3	-9.282
Sox2-Enhancer 16	site	HIC1_02	D	CCCCACTGCCCCGTC	7.3	-9.255
Sox2-Enhancer 16	site	HSF1-L>HSF1-S	D	ATTGTGGAGATTTCAGA	6.7	-9.241
Sox2-Enhancer 16	site	STAT1	R	CACTGCCTAGAAAGA	7	-9.208
Sox2-Enhancer	site	CAR>CAR:RXR-alpha>PXR-1A>PXR-1A:RXR-alpha>PXR-1A:RXR-beta>RXR-	D	GACAAACCTT	6.9	-9.178

16		alpha>SXR:RXR-alpha>VDR		GTAACCCCCCT		
Sox2-Enhancer 19	site	Pax6	D	TACATGCATGACTT	9.3	-11.358
Sox2-Enhancer 19	site	Pax6	D	TTAATGCTTCAGTG	9.3	-11.358
Sox2-Enhancer 19	site	NHLH1	D	TCCCAGCTGCTC	9.4	-11.158
Sox2-Enhancer 19	site	NHLH1	R	GAGCAGCTGGGA	8.8	-10.643
Sox2-Enhancer 19	site	Foxq1	D	TCTTGTTTATA	8.8	-10.527
Sox2-Enhancer 19	site	NR3C1	R	GAGAATAGAAAGTACTGT	8.1	-10.125
Sox2-Enhancer 19	site	HSF1-L>HSF1-S	R	ATTCCTGCACTGTCTCC	7.6	-9.938
Sox2-Enhancer 19	site	HNF-6alpha-OC-2	R	TGAAATCCATAG	7.8	-9.798
Sox2-Enhancer 19	site	IK_Q5	R	GCTGGGAGAA	7.7	-9.623
Sox2-Enhancer 19	site	Isl2	R	AAGCATTAATTAGGCT	7.6	-9.464
Sox2-Enhancer 19	site	Msx1	D	TCAGCCTAATTAATGC	7.7	-9.336
Sox2-Enhancer 19	site	Nkx3-2	D	TTAAGTAGA	7	-9.327
Sox2-Enhancer 19	site	NF-kappaB	D	GGGGCTTTCT	7.3	-9.265
Sox2-Enhancer 19	site	AhR>AhR:Arnt>Arnt>ARNT2>HIF-1>HIF-1alpha>HIF-1alpha-isoform1	R	TACGTGAGC	7.4	-9.194

Sox2-Enhancer 19	site	SRY	D	GTATACAAT	7.3	-9.177
Sox2-Enhancer 25	site	BCL6_Q3	D	GTTTCTAGGA	9.2	-12.624
Sox2-Enhancer 25	site	STAT1	R	TTCTTCCTAGAAACA	10.1	-11.906
Sox2-Enhancer 25	site	Myf	D	GAGCAGCTGCAG	10	-11.705
Sox2-Enhancer 25	site	AP-2alphaA-AP-2alphaB-AP-2beta-AP-2gamma	D	GGCCCCGCAGGCA	9.1	-11.51
Sox2-Enhancer 25	site	Stat3	D	TTCTAGGAAG	9.8	-11.474
Sox2-Enhancer 25	site	Zfx	R	GCCTGCGGGGCCTG	9.6	-11.211
Sox2-Enhancer 25	site	Tal1::Gata1	D	GGTGGGCCTAGAGATAAG	9	-10.864
Sox2-Enhancer 25	site	Pax-2-Pax-5-Pax-8	D	CAGGAACAAAC	8.7	-10.841
Sox2-Enhancer 25	site	HNF4A	D	AGGCCAGAGACCA	8.5	-10.758
Sox2-Enhancer 25	site	Myf	D	AAAGAGCAGCTG	8.4	-10.622
Sox2-Enhancer 25	site	SRF	R	GGCCTAATAAGG	8	-10.612
Sox2-Enhancer 25	site	MTF-1	R	CCTGCACACTGCAG	8.5	-10.55
Sox2-Enhancer 25	site	RREB1	D	CAGCCAACCTCCAACAAACC	7.5	-10.452
Sox2-Enhancer	site	Pax4	R	GAAAAAAAACACCCAGTTCA	8.2	-10.388

25				AACATAATTT		
Sox2-Enhancer 25	site	NHLH1	D	GAGCAGCTGCAG	8.4	-10.31
Sox2-Enhancer 25	site	SZF1-1	D	AGAGGGAAAGAGCAG	8.1	-10.24
Sox2-Enhancer 25	site	Ar	R	AAAAAAACACCCAGTTCAAACA	8	-10.17
Sox2-Enhancer 25	site	BRCA1:USF2	R	TTGTGTTG	6.9	-10.141
Sox2-Enhancer 25	site	Meis2	R	AGGTGGCTGTCATTAA	7.8	-10.126
Sox2-Enhancer 25	site	Nkx2-5	D	TCCCACTTGG	8.4	-10.089
Sox2-Enhancer 25	site	Pitx1	R	CAAGTGGGATTAAGGCC	8.1	-10.079
Sox2-Enhancer 25	site	Spz1	D	AGGGAAAGAGC	8	-10.045
Sox2-Enhancer 25	site	INSM1	R	TGGCAGGGGGAT	8.1	-10.029
Sox2-Enhancer 25	site	SRF	D	TACCTTATTAGG	7	-10.026
Sox2-Enhancer 25	site	RREB1	D	CCCCCTGCCACCCAGCCAGC	6.8	-9.96
Sox2-Enhancer 25	site	BRCA1	D	ACAACAC	6.4	-9.9
Sox2-Enhancer 25	site	TLX1::NFIC	D	TGCCACCCAGCCAG	6.9	-9.886
Sox2-Enhancer 25	site	HNF-4>HNF-4alpha>HNF-4alpha1>HNF-4alpha2>HNF-4alpha3>HNF-4alpha4	D	AGGCCAGAGACCAT	7.9	-9.825

Sox2-Enhancer 25	site	SRF	D	ACCTTATTAGGCCAGAGA	7.5	-9.77
Sox2-Enhancer 25	site	znf143	D	TGCCACCCAGCCAGCCCTGC	7.4	-9.638
Sox2-Enhancer 25	site	RFX1>RFX1:RFX2>RFX1:RFX3>RFX2>RFX3>RFX4>RFX5>RFX5:RFXAP:RFXANK>RFXANK>RFXAP	R	CTGATGCCA	7.2	-9.638
Sox2-Enhancer 25	site	HOXA5	R	CACTAATG	7.2	-9.466
Sox2-Enhancer 25	site	SP1	R	CCCAACCCCC	7.6	-9.464
Sox2-Enhancer 25	site	Pitx3	R	AGTGGGATTAAGGCCA	7	-9.46
Sox2-Enhancer 25	site	PPARG::RXRA	D	TTAGGCCAGAGACCA	7.3	-9.33
Sox2-Enhancer 25	site	Crx	D	GCCTTAATCCCAC	7.3	-9.327
Sox2-Enhancer 25	site	Foxq1	R	TGTTGTTTGTT	7.4	-9.328
Sox2-Enhancer 25	site	PLAG1	R	GGGTGGCAGGGGGA	6.2	-9.321
Sox2-Enhancer 25	site	Gfi	D	CAAATCTGTG	7.5	-9.314
Sox2-Enhancer 25	site	PBX1	D	TGATCAGTCAAA	7.2	-9.298
Sox2-Enhancer 25	site	NR4A2	R	AAGGCCAC	7.6	-9.232
Sox2-Enhancer 25	site	Pou5f1	D	TTTTCAGAGGCAGAT	6.7	-9.226
Sox2-Enhancer	site	Gata1	D	AGAGATAAGT	7.8	-9.208

25				C		
Sox2-Enhancer 25	site	CP2a	R	GCTGGGTGGCAGGGG	7.3	-9.199
Sox2-Enhancer 25	site	SRY	D	GTGAACAAT	7.3	-9.177
Sox2-Enhancer 4	site	RREB1	R	CCCCCCACCTCCCCCCACCC	13.8	-15.983
Sox2-Enhancer 4	site	ZNF219	R	CTCCCCCCACCC	12.8	-14.488
Sox2-Enhancer 4	site	HIF-1-HIF-1alpha-HIF-1alpha-isoform1	D	GGGGACGTGCGGGC	11.1	-14.116
Sox2-Enhancer 4	site	Myf	R	AGGCAGCTGCAG	11.6	-13.555
Sox2-Enhancer 4	site	IRF1	R	AAAATCGAAAGC	9.9	-11.843
Sox2-Enhancer 4	site	SOX9	D	AAACAATGG	9.4	-11.838
Sox2-Enhancer 4	site	RREB1	R	CCCCCACCTCCCCCCACCCT	9.1	-11.656
Sox2-Enhancer 4	site	NR2F1	D	TGACCTTTAAAACG	9.4	-11.403
Sox2-Enhancer 4	site	E12-E47-ITF-1-MyoD	D	GCAGCTGCCTCTGT	9.1	-11.349
Sox2-Enhancer 4	site	NR4A2	R	AAGGTCAC	9	-11.165
Sox2-Enhancer 4	site	HIF1A::ARNT	D	GGACGTGC	8.2	-11.125
Sox2-Enhancer 4	site	RORA_1	R	TTAAAGGTCA	9.4	-11.035

Sox2-Enhancer 4	site	MZF1_5-13	R	GAAGGGGGAA	8.1	-10.961
Sox2-Enhancer 4	site	MIZF	R	GAAAGTCCGC	8.9	-10.73
Sox2-Enhancer 4	site	TAL1::TCF3	D	GAACCATCTGTA	8.7	-10.493
Sox2-Enhancer 4	site	SP1	R	CCCCACCTCC	8.3	-10.333
Sox2-Enhancer 4	site	ZNF219	D	CTCCCCCGTGAC	7.7	-10.297
Sox2-Enhancer 4	site	PLAG1	R	GGGGAGGAAGGGGG	7.5	-10.221
Sox2-Enhancer 4	site	E12-E47-MyoD	R	CAGAGGCAGCTGCAGGCA	8.3	-10.217
Sox2-Enhancer 4	site	Klf4	D	AGGGTGGGGG	8.3	-10.183
Sox2-Enhancer 4	site	AhR>AhR:Arnt>Arnt>ARNT2>HIF-1>HIF-1alpha>HIF-1alpha-isoform1	D	GACGTGCGG	7.8	-10.178
Sox2-Enhancer 4	site	RREB1	R	CCCCACCTCCCCCCACCCTC	7.1	-10.169
Sox2-Enhancer 4	site	Esrrb	R	TTTTAAAGGTCA	8.2	-10.067
Sox2-Enhancer 4	site	CTF-CTF-1-CTF-2-NF-1	R	TTGTATACAGGCCAACA	7.9	-10.053
Sox2-Enhancer 4	site	CACD_01	R	CCCCACCC	8.1	-10.006
Sox2-Enhancer 4	site	Ar	D	AAAAGAACCATCTGTAGCAGAA	7.8	-10.005
Sox2-Enhancer	site	AP-2alphaA-AP-2alphaB-AP-2beta-AP-	D	CAGCCCCGCG	8	-10.004

4		2gamma		GCT		
Sox2-Enhancer 4	site	IRF2	R	GGAGAATGAATCCATTTC	7.1	-10.001
Sox2-Enhancer 4	site	SP1	D	CCCTTCCTCC	8	-9.95
Sox2-Enhancer 4	site	Pax4	R	GAATGAATCCATTTCGGCTTTTCTTCCCCC	7.8	-9.933
Sox2-Enhancer 4	site	MTF-1	D	AGTGCTCCCAGCCC	7.6	-9.813
Sox2-Enhancer 4	site	SP1	R	CTCCTCCTCC	7.9	-9.78
Sox2-Enhancer 4	site	Sox5	D	AAACAAT	8.3	-9.776
Sox2-Enhancer 4	site	RREB1	D	CCGCTAACCGCCACCACCCT	6.5	-9.754
Sox2-Enhancer 4	site	MZF1_5-13	R	ATAGGGGGAA	7.5	-9.675
Sox2-Enhancer 4	site	MITF>MITF-M1>TFE3>TFEB-isoform1	D	ACATGTGA	8	-9.631
Sox2-Enhancer 4	site	DMRT3_01	D	ATATTGATAAAATAT	7.2	-9.624
Sox2-Enhancer 4	site	SP1	D	CCCCTTCCTC	7.7	-9.608
Sox2-Enhancer 4	site	SREBP_Q6	R	CCCCCCACCTCCCCC	7.4	-9.605
Sox2-Enhancer 4	site	Pou5f1	R	CTTTGACTTGCAGCT	7.1	-9.533
Sox2-Enhancer 4	site	Mafb	D	GCTGACTC	6.8	-9.504

Sox2-Enhancer 4	site	SP1	R	CCCCACCCTC	7.6	-9.464
Sox2-Enhancer 4	site	Foxq1	R	TTCTGTTTATT	7.5	-9.422
Sox2-Enhancer 4	site	DMRT3_01	R	TTTTTAATACAATAA	6.9	-9.406
Sox2-Enhancer 4	site	HIF-1-HIF-1alpha-HIF-1alpha-isoform1	D	GAGGACGTGTAGGC	7.6	-9.404
Sox2-Enhancer 4	site	ZNF219	R	TTCCCCCCACCT	6.2	-9.377
Sox2-Enhancer 4	site	PR	R	CCTGAATAACCATTTTGTTCTCGCTTG	6.7	-9.354
Sox2-Enhancer 4	site	TFAP2A	R	GCCGCGGGG	7.1	-9.28
Sox2-Enhancer 4	site	NR2F1	D	GGAACCCTGCAGCT	7.1	-9.269
Sox2-Enhancer 4	site	Pax5	D	GGCAAACGGAAGGAGAGCCG	7.3	-9.267
Sox2-Enhancer 4	site	Egr-1>Egr-2>Egr-3>Egr-4	R	CCCACCTCCCCCCA	7.1	-9.247
Sox2-Enhancer 4	site	OCT4_02	R	TTTGACTTGCAGCTG	7	-9.233
Sox2-Enhancer 4	site	AP-2alphaA-AP-2alphaB-AP-2beta-AP-2gamma	R	TCTTCCCCCGGCT	7.3	-9.208
Sox2-Enhancer 4	site	SP1	D	CCCAGCCCCG	7.3	-9.182
Sox2-Enhancer 4	site	OCT4_01	R	CTTTGACTTGCAGCT	6.8	-9.173
Sox2-Enhancer	site	C-EBPgamma	R	GTGATTTCAG	8.4	-10.512

7				AAT		
Sox2-Enhancer 7	site	Sox17	R	CTCATTGTG	8.1	-10.009
Sox2-Enhancer 7	site	Meis2	D	TCTGTCCTGTCAATGA	7.3	-9.765
Sox2-Enhancer 7	site	RXR::RAR_DR5	R	AGCTCATTGACAGGACA	7.4	-9.707
Sox2-Enhancer 7	site	Hand1::Tcfe2a	R	GGTCTGGAGT	7.5	-9.23
Sox2-Enhancer 9	site	NR3C1	D	AGAAACAAAACTACCTAT	8.6	-10.666
Sox2-Enhancer 9	site	znf143	D	TCTCTCCCCTCCTTCCTTTG	8.2	-10.333
Sox2-Enhancer 9	site	SP1	D	CCCCTCCTTC	8.1	-10.081
Sox2-Enhancer 9	site	MAZ	R	GGGGAGAG	8.2	-9.995
Sox2-Enhancer 9	site	MZF1_5-13	R	GGAGGGGAGA	7.4	-9.51
Sox2-Enhancer 9	site	LEF-1>TCF-1>TCF-1A>TCF-1B>TCF-1C>TCF-1E>TCF-1F>TCF-1G	R	TCTTTGTTGCT	7.6	-9.305
Sox2-N1-Enhancer	site	LEF-1	D	TATCAAAGTG	8.5	-10.619
Sox2-N1-Enhancer	site	LEF-1>TCF-1>TCF-1A>TCF-1B>TCF-1C>TCF-1E>TCF-1F>TCF-1G	R	ACTTTGATATT	8.5	-10.195
Sox2-N1-Enhancer	site	TBP	R	CTTTAAAAGCCCCGA	8.2	-10.058
Sox2-N1-Enhancer	site	C-EBPgamma	R	ACCATTAAAGAAA	8	-10.002
Sox2-N1-Enhancer	site	c-Ets-1>c-Ets-2>ELF-1>ELFR>Elk-1>Elk-1-isoform1>Erg-1>Erg-2>Ets-1>Fli-1>GABP-alpha>GABP-alpha:GABP-beta>GABP-beta1>GABP-beta2>NERF-1a>NERF-	R	GCTTCCTC	7.7	-9.999

		1b>NERF-2>Net>p38erg>p49erg>p55>p55erg>PEA3>PU.1>SAP-1a>SAP-1b>Spi-B>Spi-B-isoform1>TCF>Tel-2a>Tel-2b>Tel-2c>Tel-2d>Tel-2e>Tel-2f>TEL1				
Sox2-N1-Enhancer	site	TBP	D	GTATAAATATCAAAG	7.9	-9.701
Sox2-N1-Enhancer	site	LEF-1>TCF-1>TCF-1A>TCF-1B>TCF-1C>TCF-1E>TCF-1F>TCF-1G	D	CCTTTGAAACC	8	-9.666
Sox2-N1-Enhancer	site	Gfi	R	CAAATCACCA	7.5	-9.314
Sox2-N1-Enhancer	site	TFAP2A	R	GCCCCGAGG	7.1	-9.28
Sox2-N1-Enhancer	site	LEF-1	R	TTTCAAAGGA	7.5	-9.183
Sox2-N1-Enhancer	site	OCT4_01	R	CTTTGATATTTATAC	6.8	-9.173
Sox2-N2-Enhancer	site	PLZF>PLZFB	R	TTATTTTGTAATTAAAATCTGAAAAGGGC	10.2	-12.802
Sox2-N2-Enhancer	site	Pou5f1	R	TCTTCTTATGGAAAT	9.5	-11.571
Sox2-N2-Enhancer	site	OCT4_01	R	TTTTGTAATTAAAAT	9.3	-11.286
Sox2-N2-Enhancer	site	Pou5f1	D	CACTCAAATGCAGAT	8.9	-11.028
Sox2-N2-Enhancer	site	POU2F1	D	TCATTTCCATA	8.7	-10.95
Sox2-N2-Enhancer	site	Dlx5	R	GCAGTAATTAGGTGAG	8.8	-10.743
Sox2-N2-Enhancer	site	Dlx5	D	GCAGTAATTATTTCAC	8.7	-10.586
Sox2-N2-Enhancer	site	OCT4_01	D	CACTCAAATGCAGAT	8.4	-10.469
Sox2-N2-Enhancer	site	OCT4_01	R	TCTTCTTATGGAAAT	8.2	-10.297
Sox2-N2-Enhancer	site	OCA-B-Oct-1-Oct-2-Oct-2.1-oct-B2-oct-B3-Octa-factor-octamer-binding-POU2F1-POU2F2B-POU3F1-POU3F2-POU4F1(l)-POU5F1A-POU5F1B-POU5F1C	D	TCATTTCCATA	8.1	-10.238

Sox2-N2-Enhancer	site	NR3C1	R	AAGACGAAAACGTACAGA	8.1	-10.125
Sox2-N2-Enhancer	site	OCT4_02	R	TTTGTAATTAAAATC	8.1	-10.124
Sox2-N2-Enhancer	site	NF-AT1-NF-AT1C-NF-AT2-NF-AT3-NF-AT4	D	GAGGAAATTT	8.1	-10.08
Sox2-N2-Enhancer	site	NF-AT1-NF-AT1C-NF-AT2-NF-AT3-NF-AT4	D	GCGGAAAATT	8.1	-10.08
Sox2-N2-Enhancer	site	LXR-alpha-LXR-alpha:RXR-alpha-LXR-beta-LXR-beta:RXR-alpha	D	CAGGTTCCCTGCCGTTCG	7.4	-9.896
Sox2-N2-Enhancer	site	OCT4_02	D	TTTCAGATTTTAATT	7.8	-9.871
Sox2-N2-Enhancer	site	Msx1	D	AGGCAGTAATTATTTC	8.2	-9.856
Sox2-N2-Enhancer	site	RORA_2	R	AGTAATTAGGTGAG	7	-9.804
Sox2-N2-Enhancer	site	Gata1	D	GGAGATAAAAC	8.2	-9.684
Sox2-N2-Enhancer	site	C-EBPgamma	D	TTAATTACAAAAT	7.6	-9.602
Sox2-N2-Enhancer	site	IRF1	D	GAAATTAAAACT	7.3	-9.579
Sox2-N2-Enhancer	site	Msx1	D	CTCACCTAATTACTGC	7.9	-9.537
Sox2-N2-Enhancer	site	T	R	TTAGGTGAGAA	6.3	-9.534
Sox2-N2-Enhancer	site	CTF-CTF-1-CTF-2-NF-1	R	GTGAGAACTAGCCAAGC	7.5	-9.494
Sox2-N2-Enhancer	site	Tal1::Gata1	D	ATTTCACAGGGAGATAAA	7.8	-9.487
Sox2-N2-Enhancer	site	HOXA5	D	CAGTAATT	7.2	-9.466
Sox2-N2-Enhancer	site	HOXA5	R	CAGTAATT	7.2	-9.466
Sox2-N2-Enhancer	site	Pou5f1	R	TTTTGTAATTAAAAT	7	-9.455
Sox2-N2-Enhancer	site	Msx1	R	GTGAAATAATTACTGC	7.8	-9.435
Sox2-N2-	site	OCT4_01	D	TTTTCAGATTT	7.1	-9.404

Enhancer				TAAT		
Sox2-N2-Enhancer	site	CAR>CAR:RXR-alpha>COUP-TF1>COUP-TF2>LXR-alpha>LXR-alpha:RXR-alpha>LXR-beta>LXR-beta:RXR-alpha>PXR-1A>PXR-1A:RXR-alpha>PXR-1A:RXR-beta>RAR-alpha>RAR-alpha:RXR-alpha>RAR-alpha:RXR-gamma>RAR-alpha1>RAR-beta>RAR-gamma>RXR-beta>SXR:RXR-alpha	R	CGAACGGCAGGGAACCT	7.3	-9.346
Sox2-N2-Enhancer	site	Dlx5	D	CTGCTAATTAGCAATG	7.7	-9.278
Sox2-N2-Enhancer	site	IRF2	R	CGAAGACGAAAACGTACA	6	-9.235
Sox2-N2-Enhancer	site	FOXO3	D	GCTAAACA	7.4	-9.204
Sox2-N2-Enhancer	site	Nobox	R	TAATTAGC	7.8	-9.179
Sox2-N2-Enhancer	site	Nobox	D	TAATTAGC	7.8	-9.179
Sox2-N2-Enhancer	site	Pax4	D	CAAAAAATGGAGCTGCAATCTTCCATCTCC	7.1	-9.175
Sox2-N3-Enhancer	site	RFX1>RFX1:RFX2>RFX1:RFX3>RFX2>RFX3>RFX4>RFX5>RFX5:RFXAP:RFXANK>RFXANK>RFXAP	D	CTGTTGCCA	7.9	-12.455
Sox2-N3-Enhancer	site	OCT4_01	D	TATTTTAATTCAAAT	10.4	-12.392
Sox2-N3-Enhancer	site	OCT4_01	R	TATTGTTATTTTAAT	9.9	-11.874
Sox2-N3-Enhancer	site	TAL1::TCF3	D	TCACCATATGTT	10	-11.65
Sox2-N3-Enhancer	site	KAISO_01	R	ATCCTGCTAG	10.2	-11.641
Sox2-N3-Enhancer	site	TAL1::TCF3	R	TAAACATATGGT	9.6	-11.282
Sox2-N3-Enhancer	site	Pou5f1	R	TATTGTTATTTTAAT	9	-11.115
Sox2-N3-Enhancer	site	OCT4_02	R	ATTGTTATTTTAATA	9.1	-11.017
Sox2-N3-Enhancer	site	BRCA1:USF2	D	TTCTGTTG	7	-10.859

Sox2-N3-Enhancer	site	Sox2	R	GTATTGTTATTTTAA	8.8	-10.828
Sox2-N3-Enhancer	site	Pou5f1	D	TATTTTAATTCAAAT	8.5	-10.675
Sox2-N3-Enhancer	site	IK_Q5	D	TTTGGGAGAC	8.7	-10.638
Sox2-N3-Enhancer	site	TEAD1	D	TACATTCCCCTG	8.4	-10.434
Sox2-N3-Enhancer	site	FOXD1	D	GTAAACAA	9.4	-10.43
Sox2-N3-Enhancer	site	NR3C1	D	CAAAAGAGCCAGTTCTGG	8.2	-10.231
Sox2-N3-Enhancer	site	SRY	D	GTAAACAAA	7.9	-10.186
Sox2-N3-Enhancer	site	Foxd3	D	ATATGTTTAATT	8.4	-10.15
Sox2-N3-Enhancer	site	FOXL1	R	TAAACATA	6.4	-9.98
Sox2-N3-Enhancer	site	CP2a	D	GCTGGGTTCCTGTTG	8	-9.928
Sox2-N3-Enhancer	site	Foxd3	R	TATTGTTATTTT	8.1	-9.863
Sox2-N3-Enhancer	site	PLZF>PLZFB	R	TTTGAATTAAAATAAAGCTTCGCTTCTGC	5.7	-9.795
Sox2-N3-Enhancer	site	Crx	D	TCAGTAATCCCAA	7.6	-9.772
Sox2-N3-Enhancer	site	SPIB	R	AGAGGAA	7.8	-9.758
Sox2-N3-Enhancer	site	Lhx3	D	AAATTAAACTATC	7.4	-9.667
Sox2-N3-Enhancer	site	NR4A2	R	AAGGTCAG	7.7	-9.541
Sox2-N3-Enhancer	site	Pitx3	D	AGCAGGATTATGGTCT	7.1	-9.527
Sox2-N3-Enhancer	site	Mafb	R	GCTGACTG	6.8	-9.504
Sox2-N3-Enhancer	site	CMAF_01	R	GCTTCTGCTGACTGCACAT	7.4	-9.4

Sox2-N3-Enhancer	site	Dlx5	R	CTCGTAATTAAGTGTG	7.8	-9.39
Sox2-N3-Enhancer	site	Lhx3	R	AAATTAAACATAT	6.9	-9.282
Sox2-N3-Enhancer	site	FOXL1	D	AATACATA	6.2	-9.249
Sox2-N3-Enhancer	site	SRY	D	AATAACAAT	7.3	-9.177
Sox2-N4-Enhancer	site	FOXP1_01	D	GTTTTTGTTTTTTTTTTTTT	5	-12.71
Sox2-N4-Enhancer	site	FOXA1	R	TGTTTGCACTG	10.5	-12.385
Sox2-N4-Enhancer	site	Pax4	R	AAAAAAAAACAAAAACGTTAAAACCTACCT	9.7	-12.257
Sox2-N4-Enhancer	site	FOXP1_01	D	ACGTTTTTGTTTTTTTTTTT	4	-12.178
Sox2-N4-Enhancer	site	Foxd3	D	TTTTGTTTTTTT	9.1	-10.925
Sox2-N4-Enhancer	site	Pax4	R	AAAAAAAAAACAAAAACGTTAAAACCTACC	8.6	-10.861
Sox2-N4-Enhancer	site	Zfp628	D	CAAGGTAGGTTTT	8.2	-10.672
Sox2-N4-Enhancer	site	Pax4	R	AAAAAAAAAAACAAAAACGTTAAAACCTAC	8.3	-10.505
Sox2-N4-Enhancer	site	E2	D	TTTAACGTTTTTGTTT	8.5	-10.388
Sox2-N4-Enhancer	site	PLZF>PLZFB	D	TTTTTTTCCCTCTTAATTTTTTTTTTTTC	6.4	-10.215
Sox2-N4-Enhancer	site	ESR2	R	CAGGGTCATGAGGTCACG	8.1	-10.135
Sox2-N4-Enhancer	site	NR2F1	R	TGACCTCAGCTCCT	8.1	-10.134
Sox2-N4-Enhancer	site	GLI1>GLI2alpha>GLI3	D	CCTGGGAGGTGG	8.1	-10.127
Sox2-N4-Enhancer	site	Foxa2	R	TGTTTGCACTGT	8.4	-10.064

Sox2-N4-Enhancer	site	NR4A2	R	GAGGTCAC	8.1	-10.051
Sox2-N4-Enhancer	site	MAZ	R	GGGGAGAG	8.2	-9.995
Sox2-N4-Enhancer	site	NFE2L2	R	GTGACTGGGCA	8	-9.993
Sox2-N4-Enhancer	site	AP-1-c-Fos-c-Jun-Fra-1-Fra-2-JunB-JunD	D	TGAGTCAG	7.8	-9.948
Sox2-N4-Enhancer	site	IK_Q5	D	CCTGGGAGGT	8.1	-9.901
Sox2-N4-Enhancer	site	Pax4	R	AAAAAAAACAAAAACGTTAAAACCTACCTT	7.7	-9.821
Sox2-N4-Enhancer	site	INSM1	D	TTGAAGGGGTCA	7.8	-9.806
Sox2-N4-Enhancer	site	Nr2e3	R	CAAGCTT	8.8	-9.713
Sox2-N4-Enhancer	site	AP1	R	TGACTCA	8.1	-9.713
Sox2-N4-Enhancer	site	Zfx	D	CGTGGCCGGGCCTT	8	-9.696
Sox2-N4-Enhancer	site	HNF-4-HNF-4alpha-HNF-4alpha1	D	CTGAAGTTTGAAG	7.6	-9.51
Sox2-N4-Enhancer	site	Zfp628	R	TTAGGTTGGATGC	6.4	-9.491
Sox2-N4-Enhancer	site	Egr1	R	AGCGGGAGCGG	7.5	-9.476
Sox2-N4-Enhancer	site	CREB1	R	TGAGGTCA	7.5	-9.475
Sox2-N4-Enhancer	site	CREB1	D	TGAGGTCA	7.5	-9.475
Sox2-N4-Enhancer	site	SREBP_Q6	R	CGGCCCACCTCCCAG	7.3	-9.455
Sox2-N4-Enhancer	site	IRF1	R	AAAAACAAAAAC	7.1	-9.433
Sox2-N4-Enhancer	site	Sp3	D	AGCCCTGGGAGGTG	7.4	-9.385
Sox2-N4-Enhancer	site	Pax4	R	AAAAAAAAAAAACAAAAACGTTAAAACCTA	7.2	-9.28

Sox2-N4-Enhancer	site	Bach1>Bach2>LCR-F1>Maf>MafB>MafF>MafG>MafG:MafG>MafK>NF-E2>Nrf1>Nrf1:MafG>Nrf1:MafK>Nrf2>Nrf2-isoform1>Nrf2:MafG>Nrf2:MafK>Nrf3:MafK	D	TTTTGAGTCAG	7.2	-9.254
Sox2-N4-Enhancer	site	HNF-4>HNF-4alpha>HNF-4alpha1>HNF-4alpha2>HNF-4alpha3>HNF-4alpha4	D	GGAGCTGAGGTCAT	7.3	-9.254
Sox2-N4-Enhancer	site	USF1-USF2-USF2a-USF2b	R	GGCCACGGGACG	7.3	-9.253
Sox2-N4-Enhancer	site	AP-2alphaA-AP-2alphaB-AP-2beta-AP-2gamma	D	CCGTCCCGTGGCC	7.3	-9.208
Sox2-N5-Enhancer	site	SP1	D	CCCTGCCCCC	9.4	-11.622
Sox2-N5-Enhancer	site	FOXP1_01	D	TTTTTTTTCTTCTTTTTTTT	2.2	-11.488
Sox2-N5-Enhancer	site	E12-E47-MyoD	D	CCAGTGCAGGTGCAGTAG	9.3	-11.474
Sox2-N5-Enhancer	site	FOXP1_01	D	TTTTTCTTCTTTTTTTTTT	1.2	-11.127
Sox2-N5-Enhancer	site	REST	R	CTCGGGACTGTGGAAAGAGGC	6	-10.799
Sox2-N5-Enhancer	site	Egr-1>Egr-2>Egr-3>Egr-4	D	CCTGCCCCCCCGGC	8.5	-10.478
Sox2-N5-Enhancer	site	Isl2	R	CTCAATTCATTACATT	8.5	-10.413
Sox2-N5-Enhancer	site	DMRT3_01	R	AATTCATTACATTTC	8.2	-10.377
Sox2-N5-Enhancer	site	FBI-1	R	AGAGCCCCC	7.6	-10.3
Sox2-N5-Enhancer	site	WT1>WT1-del2	D	CCCCCCGGC	7.5	-10.117
Sox2-N5-Enhancer	site	RREB1	R	CACCACATCAACACAGAAGA	7	-10.099
Sox2-N5-Enhancer	site	AP-2alphaA-AP-2alphaB-AP-2beta-AP-2gamma	D	TGCCCCCCCGGCA	8	-10.004
Sox2-N5-Enhancer	site	Gfi	R	CCAATCAGTG	7.9	-9.955

Sox2-N5-Enhancer	site	znf143	D	CTCTTTCCACAGTCCCGAGC	7.6	-9.808
Sox2-N5-Enhancer	site	core-binding_factor	R	TGTGGTCT	8	-9.767
Sox2-N5-Enhancer	site	RREB1	R	AACCAACACACAAGAAAAAA	6.5	-9.754
Sox2-N5-Enhancer	site	NF-AT1-NF-AT1C-NF-AT2-NF-AT3-NF-AT4	D	GTGGAAAAAG	7.9	-9.711
Sox2-N5-Enhancer	site	Tel-2a-Tel-2b-Tel-2c	R	TTTCTTCCTG	8.1	-9.661
Sox2-N5-Enhancer	site	YY1	R	ATAGCCATTTT	7.4	-9.6
Sox2-N5-Enhancer	site	NFATC2	R	TTTTCCA	8.4	-9.593
Sox2-N5-Enhancer	site	ZNF219	D	TGCCCCCCCGGC	6.5	-9.508
Sox2-N5-Enhancer	site	Ar	D	AAAAGCACATTCCCTACAATAG	7.1	-9.446
Sox2-N5-Enhancer	site	CKROX_Q2	D	TCCCTGCCC	7.5	-9.41
Sox2-N5-Enhancer	site	RUNX1	R	GTGTGTGGTCT	7.6	-9.339
Sox2-N5-Enhancer	site	TFAP2A	R	GCCGGGGGG	7.1	-9.28
Sox2-NOP1-Enhancer	site	PLZF>PLZFB	D	TTGTTAGGACTGGAAAGCTAATTTAGTGC	8.5	-11.574
Sox2-NOP1-Enhancer	site	Gfi	R	TCAATCACAG	8.5	-11.009
Sox2-NOP1-Enhancer	site	HIC1_02	R	CCCGGCTGCCCACTT	8.2	-10.632
Sox2-NOP1-Enhancer	site	ESR1	R	AAGACAGCTCGACCTGCCCT	8.2	-10.4
Sox2-NOP1-Enhancer	site	Pax-6	R	CAGTCCTTTAACTC	7.8	-10.393

Sox2-NOP1-Enhancer	site	TBX5	D	AAAGGTGTTGAG	8.7	-10.284
Sox2-NOP1-Enhancer	site	PLZF>PLZFB	D	GAATTTGGTAGATAAAGGTTAATCTTGGG	6.5	-10.276
Sox2-NOP1-Enhancer	site	Evi1	D	TTGACAAGAGAAAA	7.5	-10.14
Sox2-NOP1-Enhancer	site	OCT4_02	R	TTTCTCTTGTCAATC	7.3	-9.469
Sox2-NOP1-Enhancer	site	LEF-1	R	TAACAAAGGC	7.7	-9.425
Sox2-NOP1-Enhancer	site	HIF1A::ARNT	D	AGACGTGC	7.6	-9.359
Sox2-SC1-Enhancer	site	DEC1>DEC2	R	CCGCAAGTGAAGC	10	-13.181
Sox2-SC1-Enhancer	site	Pax6	D	TTCAAGCTTCACTT	10.9	-13.049
Sox2-SC1-Enhancer	site	Sox2	D	CTTTTGTTCTCCAGA	10.4	-12.576
Sox2-SC1-Enhancer	site	Myf	R	AAGGAGCTGCTG	9.7	-11.514
Sox2-SC1-Enhancer	site	LEF-1>TCF-1>TCF-1A>TCF-1B>TCF-1C>TCF-1E>TCF-1F>TCF-1G	R	CCTTTGTAGTC	9.2	-11.196
Sox2-SC1-Enhancer	site	RFX1>RFX1:RFX2>RFX1:RFX3>RFX2>RFX3>RFX4>RFX5>RFX5:RFXAP:RFXANK>RFXANK>RFXAP	R	CTGTTGCGA	7.7	-11.097
Sox2-SC1-Enhancer	site	CEBPA	R	TTTTGCAAT	7.8	-10.628
Sox2-SC1-Enhancer	site	SP1	D	CCCCCCCCTC	8.5	-10.582
Sox2-SC1-Enhancer	site	LEF-1	D	CTACAAAGGG	8.3	-10.368
Sox2-SC1-Enhancer	site	ZNF219	D	TTCCCCCCCCTC	7.5	-10.194
Sox2-SC1-Enhancer	site	RREB1	D	CCCCCCCTCAACAGCAGCTC	7	-10.099

Sox2-SC1-Enhancer	site	TAL1::TCF3	D	TTACCATCTGGC	8.2	-10.045
Sox2-SC1-Enhancer	site	FOXF2	D	TACACATAAATAAA	8.1	-10.031
Sox2-SC1-Enhancer	site	FXR	R	TAGCGTCATTAACA	7.9	-10.016
Sox2-SC1-Enhancer	site	PR	D	AACAGCAGCTCCTTTTGTTCTCCAGAT	7.4	-9.799
Sox2-SC1-Enhancer	site	Nkx3-2	D	TTAAGTGCC	7.2	-9.767
Sox2-SC1-Enhancer	site	Nr2e3	D	CAAGCTT	8.8	-9.713
Sox2-SC1-Enhancer	site	Nkx2-5	D	CTTCACTTGC	7.9	-9.488
Sox2-SC1-Enhancer	site	Spz1	D	AGGGTTACACA	7.5	-9.447
Sox2-SC1-Enhancer	site	HNF1B	R	TTTATGTGTAAC	7.3	-9.423
Sox2-SC1-Enhancer	site	OCT4_01	D	CATTATCATTTAAGT	7.1	-9.404
Sox2-SC1-Enhancer	site	FOXI1	D	GTTTGTTTGTTA	7.7	-9.296
Sox2-SC1-Enhancer	site	znf143	D	AATCTCCCCGGTTTCATTGC	6.9	-9.225
Sox2-SC2-Enhancer	site	OCT4_01	D	CTTTGAAATGCCAAA	8.9	-10.917
Sox2-SC2-Enhancer	site	Pou5f1	D	CTTTGAAATGCCAAA	8.4	-10.589
Sox2-SC2-Enhancer	site	E12-E47-ITF-1-MyoD	R	TCAGCTGTCACAGA	8.4	-10.378
Sox2-SC2-Enhancer	site	FBI-1	D	GGAGCCCCC	7.6	-10.3
Sox2-SC2-Enhancer	site	WT1>WT1-del2	R	GCCTCCCGC	7.5	-10.117
Sox2-SC2-Enhancer	site	Gfi1>Gfi1b	D	CCAAATCACGTTA	7.7	-9.985
Sox2-SC2-Enhancer	site	Meis2	R	ACTCAGCTGTCACAGA	7.4	-9.836

Sox2-SC2-Enhancer	site	HIF-1-HIF-1alpha-HIF-1alpha-isoform1	R	GGGAACGTGCTGGC	8	-9.782
Sox2-SC2-Enhancer	site	ETF	D	GCGGCGG	7.6	-9.772
Sox2-SC2-Enhancer	site	NFE2L2	D	GTGACACTGCC	7.7	-9.714
Sox2-SC2-Enhancer	site	NFKB1	R	GGGGCTCCTCC	7.2	-9.391
Sox2-SC2-Enhancer	site	PLAG1	R	GGGTTCAACTGGGG	6	-9.178

Supplementary Table 3 – Statistically significant Transcription Factor Binding Sites detected in known *Sox2* enhancers using RSAT