

chr9	21968178	21968217	CDKN2A_1	-	GTGACCTATGCACCAGACGTGAGGCTCTGAGAAACCTCGGGAAACTTAGATCATCAGTCAAGATCGGAAGAGCGGTTTCAG
chr9	21970851	21970890	CDKN2A_2	-	GTGACCTATGCACCAGACGTGATCTGAGAAATTTGTACCCTGAGAGCTTCCAAAGCTCAAGATCGGAAGAGCGGTTTCAG
chr9	21970952	21970991	CDKN2A_3	-	GTGACCTATGCACCAGACGTGCATCGCGATGTCGCACGGTACCTGCGCGCGGCTGCGGGGGAGATCGGAAGAGCGGTTTCAG
chr9	21974426	21974465	CDKN2A_4	-	GTGACCTATGCACCAGACGTGCGTACAGATCTCTCGAATGCTGAGAAGATCTGAAGGGGGAGATCGGAAGAGCGGTTTCAG
chr9	21974627	21974666	CDKN2A_5	-	GTGACCTATGCACCAGACGTGGTCTGCAGCGGGAGCAGGGGATGGCGGGCGACTCTGGAGAGATCGGAAGAGCGGTTTCAG
chr9	21994088	21994127	CDKN2A_6	-	GTGACCTATGCACCAGACGTCCCTCGAAAAGTCCGGGGCGCATTCCGCACTTGTGTTTTGTTAGATCGGAAGAGCGGTTTCAG
chr7	55086921	55086960	EGFR_7	-	GTGACCTATGCACCAGACGTGAAAGAGCTGCTCCGGCTCTCCCGATCAATACTGGACCGGATCGGAAGAGCGGTTTCAG
chr7	55209929	55209968	EGFR_8	-	GTGACCTATGCACCAGACGTAAAGACAGATATCACATGAAATACTGAGAAATGCAGAAAAAAGATCGGAAGAGCGGTTTCAG
chr7	55210948	55210987	EGFR_9	-	GTGACCTATGCACCAGACGTAAAAACATAAATGCGTGATTTCTCTTTTGAGGAAGTCAAGAAGATCGGAAGAGCGGTTTCAG
chr7	55214249	55214288	EGFR_10	-	GTGACCTATGCACCAGACGTATGGAAGTGCAGGAGCAGTCTTTCCAGCTCCTTTAAATAGATCGGAAGAGCGGTTTCAG
chr7	55218937	55218976	EGFR_11	-	GTGACCTATGCACCAGACGTAAAGTAATAGATGCATATCTCAGTGAATGATGAGAACTAGATCGGAAGAGCGGTTTCAG
chr7	55220189	55220228	EGFR_12	-	GTGACCTATGCACCAGACGTGCAAAGGTTCCCTGTGAGCTGAAGAGTGAGGGTAGGATCAAGATCGGAAGAGCGGTTTCAG
chr7	55221654	55221693	EGFR_13	-	GTGACCTATGCACCAGACGTGAGAGGACACCTGGCAAGTGAGGTAAAGTACACTACGCCAGATCGGAAGAGCGGTTTCAG
chr7	55223473	55223512	EGFR_14	-	GTGACCTATGCACCAGACGTGAGCATGAAAGGAAGGTGATGACGGTGGCACCAGGTGCTCAGATCGGAAGAGCGGTTTCAG
chr7	55224176	55224215	EGFR_15	-	GTGACCTATGCACCAGACGTAAAGAGAGACGTGATTCCGTTCCACATTTGTTGGATTAAGAAGATCGGAAGAGCGGTTTCAG
chr7	55224402	55224441	EGFR_16	-	GTGACCTATGCACCAGACGTCAACAGGGTGATTATGATCACCATCTCTACCAGTTAAAGATCGGAAGAGCGGTTTCAG
chr7	55225306	55225345	EGFR_17	-	GTGACCTATGCACCAGACGTGATGAAAGACTTCAGACACACCACGTTAGGAGTTTCTTTAGATCGGAAGAGCGGTTTCAG
chr7	55227782	55227821	EGFR_18	-	GTGACCTATGCACCAGACGTGAGAAAGAAATCATGTGGTGAATAATAAAAAAATGAGATCGGAAGAGCGGTTTCAG
chr7	55229142	55229181	EGFR_19	-	GTGACCTATGCACCAGACGTAGAGTGGGTACAGCAGTCAAGTACAGAGCAGGGACCCGAAGATCGGAAGAGCGGTTTCAG
chr7	55231376	55231415	EGFR_20	-	GTGACCTATGCACCAGACGTGAAGAGGAAACCCGTCAGCCCACCCCTGAGACATTATGAGATCGGAAGAGCGGTTTCAG
chr7	55232923	55232962	EGFR_21	-	GTGACCTATGCACCAGACGTGTTGAGAAAAATGTTTCATGCATGCTCTTTCTTTCTCTTAGATCGGAAGAGCGGTTTCAG
chr7	55236166	55236205	EGFR_22	-	GTGACCTATGCACCAGACGTATAGAAAAGACATTAGAAAAATGACCATAACATTTTAAATAGATCGGAAGAGCGGTTTCAG
chr7	55237950	55237989	EGFR_23	-	GTGACCTATGCACCAGACGTATGGACAAGTACATTTCAATATGTAGAGGCCCTGGGGAGCAGATCGGAAGAGCGGTTTCAG
chr7	55238818	55238857	EGFR_24	-	GTGACCTATGCACCAGACGTGAAAGAAATATACATTTTCTCATTCTACTTCTTTGAGATCGGAAGAGCGGTTTCAG
chr7	55240626	55240665	EGFR_25	-	GTGACCTATGCACCAGACGTGTTGAGGAACAAGGAAGGGTGAAGTTGCTGACAGATCCAAGATCGGAAGAGCGGTTTCAG
chr7	55241564	55241603	EGFR_26	-	GTGACCTATGCACCAGACGTCAAGAACACAGAGACAAGGGTCACTCAGCCCTCACCATGAGATCGGAAGAGCGGTTTCAG
chr7	55242365	55242404	EGFR_27	-	GTGACCTATGCACCAGACGTGAGAGAAGGAAGACGTTAACTGGCAATTGTGAGATGGTGCAGATCGGAAGAGCGGTTTCAG
chr7	55248936	55248975	EGFR_28	-	GTGACCTATGCACCAGACGTGGAGAGGCCAGTCAAGTGGCTTCGCATGGTGGCCAGAAGAGATCGGAAGAGCGGTTTCAG
chr7	55259362	55259401	EGFR_29	-	GTGACCTATGCACCAGACGTGAAGACCCTGCTGTGAGGGACAGATCATGGGAAGAAGAGATCGGAAGAGCGGTTTCAG
chr7	55260409	55260448	EGFR_30	-	GTGACCTATGCACCAGACGTGAGAGATGAGGCAATGAGGCAACTATTAGTTTCCCTCTGAGATCGGAAGAGCGGTTTCAG
chr7	55266360	55266399	EGFR_31	-	GTGACCTATGCACCAGACGTGAAGCAAGAAAAGAAGGCAGTGGGATCATGAATGAACAATAGATCGGAAGAGCGGTTTCAG
chr7	55267959	55267998	EGFR_32	-	GTGACCTATGCACCAGACGTAAAGAAAAACAGTGCATTAAGAACAAGTGAAGAATGAGATCGGAAGAGCGGTTTCAG
chr7	55268831	55268870	EGFR_33	-	GTGACCTATGCACCAGACGTGATTTTGAAGGCTATTAGAATGGCCCTGAGAGATGCTATTCAAGATCGGAAGAGCGGTTTCAG
chr7	55269378	55269417	EGFR_34	-	GTGACCTATGCACCAGACGTAAAGAAAGTGGCCATGGAATGCTTTGACCATCTCAAGATCGGAAGAGCGGTTTCAG
chr17	7572877	7572916	TP53_35	-	GTGACCTATGCACCAGACGTCTTCTGTTCCCTACTGACAGCCTCCCAACCCCATCTCCAGATCGGAAGAGCGGTTTCAG
chr17	7573877	7573916	TP53_36	-	GTGACCTATGCACCAGACGTTCAGCCCTTCTGCCCCTACTCCCTGCCTTCTAGGTTAGATCGGAAGAGCGGTTTCAG
chr17	7576803	7576842	TP53_37	-	GTGACCTATGCACCAGACGTGGGACCTCTTATCAAGTGGAAAGTTTCCAGTCTAACACAGATCGGAAGAGCGGTTTCAG
chr17	7576969	7577008	TP53_38	-	GTGACCTATGCACCAGACGTAGGACAAGAAGCGGTTGGAGGAGACCAAGGGTGCAGTTATGAGATCGGAAGAGCGGTTTCAG
chr17	7577449	7577488	TP53_39	-	GTGACCTATGCACCAGACGTACTTGCCACCCTGCACACTGGCCTGCTGTGCCCCAGCCTCAGATCGGAAGAGCGGTTTCAG
chr17	7578127	7578166	TP53_40	-	GTGACCTATGCACCAGACGTCAACTGGGCTCTGAGGAGGAGGGTTAAGGGTGGTTGTCAGATCGGAAGAGCGGTTTCAG
chr17	7578321	7578360	TP53_41	-	GTGACCTATGCACCAGACGTGGGGCTGGAGAGACGACAGGCGTGGTTGCCAGGGTCCCCAGGGTCCCCAGATCGGAAGAGCGGTTTCAG
chr17	7579262	7579301	TP53_42	-	GTGACCTATGCACCAGACGTCTGAGGGGCTGGCTTCCATGAGACTTCAATGCCTGGCCGTAGATCGGAAGAGCGGTTTCAG
chr17	7579789	7579828	TP53_43	-	GTGACCTATGCACCAGACGTCCATTGGAAGGGCAGGCCACCACCCCAACCCCAAGATCGGAAGAGCGGTTTCAG
chr3	178916564	178916603	PIK3CA_44	-	GTGACCTATGCACCAGACGTCTTTGCAAGTTTACATATAAACTACTTTAAGGAATTAGATCGGAAGAGCGGTTTCAG
chr3	178917428	178917467	PIK3CA_45	-	GTGACCTATGCACCAGACGTATTACATAAAGAATATAAATCTTATTACATACACAGATAGATCGGAAGAGCGGTTTCAG
chr3	178919028	178919067	PIK3CA_46	-	GTGACCTATGCACCAGACGTAAAAACATTAGATGCAATCACCATCTCTCTTTTCAATTTTCCAGATCGGAAGAGCGGTTTCAG
chr3	178921282	178921321	PIK3CA_47	-	GTGACCTATGCACCAGACGTAAAGGGGGCGAGCCATTTCTGTAAGGTTTTTCAATTTTAAAGATCGGAAGAGCGGTTTCAG
chr3	178922241	178922280	PIK3CA_48	-	GTGACCTATGCACCAGACGTAAAGTAGGTATATACTAATGTATACACTCAACATACACATAGATCGGAAGAGCGGTTTCAG
chr3	178927924	178927963	PIK3CA_49	-	GTGACCTATGCACCAGACGTAAAGAAAAATATCTACTAGTCTAAATATAAAAAACATTTAGATCGGAAGAGCGGTTTCAG
chr3	178928169	178928208	PIK3CA_50	-	GTGACCTATGCACCAGACGTGAAGAAAAGCTATTATATATACATAAGAGAGAAGGTTTGAAGATCGGAAGAGCGGTTTCAG
chr3	178935948	178935987	PIK3CA_51	-	GTGACCTATGCACCAGACGTAAATAATATCTTATATAGCTTTCTTTGTCATATTTTCCAGATCGGAAGAGCGGTTTCAG
chr3	178936934	178936973	PIK3CA_52	-	GTGACCTATGCACCAGACGTGAAAGAAAAATAAACATAAACATTTGCTGTTCCAAAAGATCGGAAGAGCGGTTTCAG
chr3	178937309	178937348	PIK3CA_53	-	GTGACCTATGCACCAGACGTGAAAGACAATAAATCATATTTAAAGGGGAAAGATGTTGTAGATCGGAAGAGCGGTTTCAG
chr3	178937687	178937726	PIK3CA_54	-	GTGACCTATGCACCAGACGTCCAAAAAAACAATCAGGGTCAGTTTCTGCATGGCCGATCAGATCGGAAGAGCGGTTTCAG
chr3	178941819	178941858	PIK3CA_55	-	GTGACCTATGCACCAGACGTAAAAAGGATAGTACAGTAAGAAACTGACTTAATAAAAAGAAAGATCGGAAGAGCGGTTTCAG
chr3	178942438	178942477	PIK3CA_56	-	GTGACCTATGCACCAGACGTGTTAAAAACTTTACTAGGTAACCTTTGCTTTATTATTATTAGATCGGAAGAGCGGTTTCAG
chr3	178943700	178943739	PIK3CA_57	-	GTGACCTATGCACCAGACGTAAATAATATGATCACCATTTAATGCCAGATGCAAATTTAGATCGGAAGAGCGGTTTCAG
chr3	178947010	178947049	PIK3CA_58	-	GTGACCTATGCACCAGACGTAGTAAACAGCTTTACAATTTAATGATGGAATTTTAAATAGATCGGAAGAGCGGTTTCAG

chr3	178947742	178947781	PIK3CA_59	-	GTGACCTATGCACCAGACGTTAAACACCTCATGAGTAGTATGAAATATAGTGATTACAGGAGATCGGAAGAGCGGTTTCAG
chr3	178947963	178948002	PIK3CA_60	-	GTGACCTATGCACCAGACGTTAAGAAATTATGTTATAGTTTGTATATCGCAGATACAAAAAGATCGGAAGAGCGGTTTCAG
chr3	178951832	178951871	PIK3CA_61	-	GTGACCTATGCACCAGACGTTAAGAACAGTTTGGTCAGTTTGGAGCAAATGATGTTAATAAGATCGGAAGAGCGGTTTCAG
chr13	48877999	48878038	RB1_62	-	GTGACCTATGCACCAGACGTCGCGGGGGGAGCCAGCGAGCTGTGGAGGAGCGCGGGGAGAGATCGGAAGAGCGGTTTCAG
chr13	48881366	48881405	RB1_63	-	GTGACCTATGCACCAGACGTTAAATAATCATATAATTGGCATATACTTATAAATCAAATTAGATCGGAAGAGCGGTTTCAG
chr13	48916685	48916724	RB1_64	-	GTGACCTATGCACCAGACGTTAAATAAAGATCAAATTTTCATTAATAATCACACACTAGATCGGAAGAGCGGTTTCAG
chr13	48919166	48919205	RB1_65	-	GTGACCTATGCACCAGACGTTAAGAATAGAAAAAGTAAATCAGTAACCTTAAAAATTTGTAGATCGGAAGAGCGGTTTCAG
chr13	48921911	48921950	RB1_66	-	GTGACCTATGCACCAGACGTTAAACATTATGACTTTTTTAACATTTTTTTCGTAATTTAGAAGAGATCGGAAGAGCGGTTTCAG
chr13	48923042	48923081	RB1_67	-	GTGACCTATGCACCAGACGTTAATGAAAGCAGAAAAAACAGGAAAAATGTATCACTGAAGATCGGAAGAGCGGTTTCAG
chr13	48934103	48934142	RB1_68	-	GTGACCTATGCACCAGACGTTAATGTACATTTTTAAAGAAAGTTAGAGATTCAGATCTTTGAGATCGGAAGAGCGGTTTCAG
chr13	48936901	48936940	RB1_69	-	GTGACCTATGCACCAGACGTTGTAATTTAGATAAGAACAATTTGATACATCCATCATATAAAAGATCGGAAGAGCGGTTTCAG
chr13	48938980	48939019	RB1_70	-	GTGACCTATGCACCAGACGTTGAAGTTACAACATGATCATTAAAAATTTAAACAAAAATCTAGATCGGAAGAGCGGTTTCAG
chr13	48941580	48941619	RB1_71	-	GTGACCTATGCACCAGACGTTAAAGTCAACTGACAATTTACTCTTTACATGTCTATTACATCTAGATCGGAAGAGCGGTTTCAG
chr13	48942613	48942652	RB1_72	-	GTGACCTATGCACCAGACGTATAAGTGAAGTCATTCACATACTGAAAAATTTACAATTTGTAGATCGGAAGAGCGGTTTCAG
chr13	48947491	48947530	RB1_73	-	GTGACCTATGCACCAGACGTTAAAAATAGGAAAAATGTGTTAAGCAATGAAGGGAGAAAAAGATCGGAAGAGCGGTTTCAG
chr13	48951004	48951043	RB1_74	-	GTGACCTATGCACCAGACGTTAAAAACAGAAATCAATGTCGAGGATACTGTGTAATCAGAAGATCGGAAGAGCGGTTTCAG
chr13	48953719	48953758	RB1_75	-	GTGACCTATGCACCAGACGTACAAAAAATAAAGAGCCTGCTATTTTAGAAAAATCACAGATCGGAAGAGCGGTTTCAG
chr13	48954139	48954178	RB1_76	-	GTGACCTATGCACCAGACGTTAATTTAAAAAATAAAGAAAGTTGTTTAAATTTGAAACCTAGATCGGAAGAGCGGTTTCAG
chr13	48955333	48955372	RB1_77	-	GTGACCTATGCACCAGACGTTAAAAAAGTAACATTTTATGAAATTTAACCTTTGAGCAGATCGGAAGAGCGGTTTCAG
chr13	49027079	49027118	RB1_78	-	GTGACCTATGCACCAGACGTCATGATGAAATTTAAACCACATTAGTAAGCATAATTTCCAGATCGGAAGAGCGGTTTCAG
chr13	49030290	49030329	RB1_79	-	GTGACCTATGCACCAGACGTTTAAAGGAAAAGCTTTCATTTCAAGTTGGCTAAGAATCACAGATCGGAAGAGCGGTTTCAG
chr13	49033774	49033813	RB1_80	-	GTGACCTATGCACCAGACGTTAAGAAAAATTAGTCATTTTTACTGTTTCATTTTGAATTTACAAGATCGGAAGAGCGGTTTCAG
chr13	49037817	49037856	RB1_81	-	GTGACCTATGCACCAGACGTTAATTTGATGTAAGTAGTCAGAATTTTATTACATGGTTTATAGATCGGAAGAGCGGTTTCAG
chr13	49039291	49039330	RB1_82	-	GTGACCTATGCACCAGACGTTAACAAAAAGTAGATTTATTTAATGTTTTGGTGGACAGATCGGAAGAGCGGTTTCAG
chr13	49047446	49047485	RB1_83	-	GTGACCTATGCACCAGACGTTAAGATGAAATACCAATTAGTAATAAAAAACCATATACAATAGATCGGAAGAGCGGTTTCAG
chr13	49050787	49050826	RB1_84	-	GTGACCTATGCACCAGACGTCAGAATCTTTACTTTAAATCATTAAATGCCAGTGTTCAGATCGGAAGAGCGGTTTCAG
chr13	49051441	49051480	RB1_85	-	GTGACCTATGCACCAGACGTTAAAAATGCAAAACATTTTCATGTGTTATATAAATGAAAGATCGGAAGAGCGGTTTCAG
chr13	49054084	49054123	RB1_86	-	GTGACCTATGCACCAGACGTTGATGAAGAATGTTAACAGCATTGATGGTACTGGGTAAGTAGATCGGAAGAGCGGTTTCAG
chr17	29482951	29482990	NF1_87	-	GTGACCTATGCACCAGACGTTAAGAAAAAACACGTTAACAGCTTATCTTAAAAACAGATCGGAAGAGCGGTTTCAG
chr17	29485978	29486017	NF1_88	-	GTGACCTATGCACCAGACGTTAGATTTAGAACATTAAGATTTAGTTTACTTTCTGCTACAGATCGGAAGAGCGGTTTCAG
chr17	29508390	29508429	NF1_89	-	GTGACCTATGCACCAGACGTCACAATTTTTAAAAATTAACCTCTAGAATAAGTTAACACAAGATCGGAAGAGCGGTTTCAG
chr17	29508678	29508717	NF1_90	-	GTGACCTATGCACCAGACGTAGAACCACATGTCTTTACAGTGATTTTTTGTAAATACAGTAAGATCGGAAGAGCGGTTTCAG
chr17	29509476	29509515	NF1_91	-	GTGACCTATGCACCAGACGTTAATATATAAATGACATTATTAGATAGGAACAAAATCCCTAGATCGGAAGAGCGGTTTCAG
chr17	29527390	29527429	NF1_92	-	GTGACCTATGCACCAGACGTTCAATATAGCGATAAGATAATATAGAAATTTCTTCTATTAGATCGGAAGAGCGGTTTCAG
chr17	29528005	29528044	NF1_93	-	GTGACCTATGCACCAGACGTTCCAAACAGAAACAAAAGCTTTAAATACCCATGCAGTATAGATCGGAAGAGCGGTTTCAG
chr17	29528379	29528418	NF1_94	-	GTGACCTATGCACCAGACGTAGAAAAAAGCAGATTATTTCTATGAGAAAAATACTCAGATCGGAAGAGCGGTTTCAG
chr17	29533208	29533247	NF1_95	-	GTGACCTATGCACCAGACGTACAAAGACCAATAGGAAGAAAAAGTACAAAATTACGTGAGAGATCGGAAGAGCGGTTTCAG
chr17	29541419	29541458	NF1_96	-	GTGACCTATGCACCAGACGTTAACAAAAACATGGTATCAGACATAAGACTCAGGATAATAGAGATCGGAAGAGCGGTTTCAG
chr17	29548818	29548857	NF1_97	-	GTGACCTATGCACCAGACGTTAAAAAGAGAAAGACAAAAGAGACTCACTCAAACATTAGATCGGAAGAGCGGTTTCAG
chr17	29550412	29550451	NF1_98	-	GTGACCTATGCACCAGACGTATAAAGTTTCATTGTTACTAGCATCATCAATACCTAATGCAGATCGGAAGAGCGGTTTCAG
chr17	29552063	29552102	NF1_99	-	GTGACCTATGCACCAGACGTATAAATAAATGAAAGCTTTTAAAGCACTGACAACCAAGAGATCGGAAGAGCGGTTTCAG
chr17	29553403	29553442	NF1_100	-	GTGACCTATGCACCAGACGTAGGGTGAAGACATATATTTGCAACTTTGGGTAATTTTATGAGATCGGAAGAGCGGTTTCAG
chr17	29554186	29554225	NF1_101	-	GTGACCTATGCACCAGACGTACAAACAGCAAAATCAAGTTACTGCACCTTAGAGCCCTGCCTGAGATCGGAAGAGCGGTTTCAG
chr17	29554491	29554530	NF1_102	-	GTGACCTATGCACCAGACGTTGGCAATTTACTTTGAAAGCAACTTAGTCTAGAGCTAAACAGATCGGAAGAGCGGTTTCAG
chr17	29555993	29556032	NF1_103	-	GTGACCTATGCACCAGACGTTAATTTGTGCAAAAGCATGAATTTAAACCTTAAATAGTTGAAGATCGGAAGAGCGGTTTCAG
chr17	29556803	29556842	NF1_104	-	GTGACCTATGCACCAGACGTAAACAAATGATTAATGATTTGCCATCAATGCCAGAAGACAGATCGGAAGAGCGGTTTCAG
chr17	29557228	29557267	NF1_105	-	GTGACCTATGCACCAGACGTATAGAAACAATAAAAAATTTATCAGATATAGACAAAAGAGATCGGAAGAGCGGTTTCAG
chr17	29557810	29557849	NF1_106	-	GTGACCTATGCACCAGACGTTGGAGAAAAAGAGAAACAGCAAAATGTTTTTGAAGCCAAGATCGGAAGAGCGGTTTCAG
chr17	29559668	29559707	NF1_107	-	GTGACCTATGCACCAGACGTTAAAGACTGACCTTTACATAGTGAAGGCCGTATCAACTAGAGATCGGAAGAGCGGTTTCAG
chr17	29559970	29560009	NF1_108	-	GTGACCTATGCACCAGACGTTCAACAGATGCAAAATTTACTAACATGGCCTTGCTGAAGTAAGATCGGAAGAGCGGTTTCAG
chr17	29562579	29562618	NF1_109	-	GTGACCTATGCACCAGACGTTAAACAAATCAGTTAGTGCAAAACATCCCATTTTATTTTATGATCGGAAGAGCGGTTTCAG
chr17	29562886	29562925	NF1_110	-	GTGACCTATGCACCAGACGTTGACGCAATAGGAGTTTATATACCTGCTCCATATATTTTAAAGATCGGAAGAGCGGTTTCAG
chr17	29575952	29575991	NF1_111	-	GTGACCTATGCACCAGACGTATAAAAAATAAATCCTAACACTTTTTGTTTAAAAACAATAAAGATCGGAAGAGCGGTTTCAG
chr17	29579906	29579945	NF1_112	-	GTGACCTATGCACCAGACGTGAGATGAGCACAACAAGTCACAGCACCGACTACATACAGATCGGAAGAGCGGTTTCAG
chr17	29585312	29585351	NF1_113	-	GTGACCTATGCACCAGACGTTGGAGTTGAGAATTGAGTATAAGGTTTTGAATTAATAAAGAGATCGGAAGAGCGGTTTCAG
chr17	29586000	29586039	NF1_114	-	GTGACCTATGCACCAGACGTTAAACAGGGTTATAAATAATCAGATTATTTATTGTATGAAGAGATCGGAAGAGCGGTTTCAG
chr17	29587337	29587376	NF1_115	-	GTGACCTATGCACCAGACGTTCAAAAGCTAGAAATTTCAACACAGATACCCAGACAGATCGGAAGAGCGGTTTCAG
chr17	29588679	29588718	NF1_116	-	GTGACCTATGCACCAGACGTTCAAACTACTTTAGAAAAAATTTAGCAGTTTCACATTTAGCAAGATCGGAAGAGCGGTTTCAG

chr17	29592197	29592236	NF1_117	-	GTGACCTATGCACCAGACGTAATAACAGAGTAATTATGAGGCTTTATGTTGTCTACTGAGAGATCGGAAGAGCGGTTTCAG
chr17	29652788	29652827	NF1_118	-	GTGACCTATGCACCAGACGTTGACAAAAAAGACAAGGATTTATAGCAGTGTTTAAAATAAAGATCGGAAGAGCGGTTTCAG
chr17	29654467	29654506	NF1_119	-	GTGACCTATGCACCAGACGTGTGGTGACGGGGTGAAGTGGAGAAGAATAAACTCTTTTAAAGATCGGAAGAGCGGTTTCAG
chr17	29657264	29657303	NF1_120	-	GTGACCTATGCACCAGACGTACACAAATGAAGTTGTTTTAAAACGTATTTTTCTTATAGAGATCGGAAGAGCGGTTTCAG
chr17	29661806	29661845	NF1_121	-	GTGACCTATGCACCAGACGTATACACTATTAGCATGTGATGGTCAATGAAAATCACATCAAGATCGGAAGAGCGGTTTCAG
chr17	29664336	29664375	NF1_122	-	GTGACCTATGCACCAGACGTATAAAGGAACAAGTAAAGACAGAAAATATTACTTTTTTAATAGATCGGAAGAGCGGTTTCAG
chr17	29664787	29664826	NF1_123	-	GTGACCTATGCACCAGACGTGGATACTGTAATACATTTGTACATAAATGTTTTAGAAAAGATCGGAAGAGCGGTTTCAG
chr17	29665672	29665711	NF1_124	-	GTGACCTATGCACCAGACGTAACAGAATTTTTTATTTTACTTTTCATTGAAATAAAACATTAGATCGGAAGAGCGGTTTCAG
chr17	29667473	29667512	NF1_125	-	GTGACCTATGCACCAGACGTAGATATGTTTGGGCTAGTAAGATGAATCATGACATAGTCAGATCGGAAGAGCGGTTTCAG
chr17	29669977	29670016	NF1_126	-	GTGACCTATGCACCAGACGTTAATCATGAGATGGTTGATGAGGTTACACAGTAGCTTTTCAGATCGGAAGAGCGGTTTCAG
chr17	29677151	29677190	NF1_127	-	GTGACCTATGCACCAGACGTAACGGTGGCAGGTTAAAAAATTTAACAAATCACAAGTGTGAGATCGGAAGAGCGGTTTCAG
chr17	29679225	29679264	NF1_128	-	GTGACCTATGCACCAGACGTAAAAATAAGAGAAAAATCAATTAATATGTGTGACAAATACAGATCGGAAGAGCGGTTTCAG
chr17	29683428	29683467	NF1_129	-	GTGACCTATGCACCAGACGTAAGTTAAGAATTCGCAAGTTCACTTAACACTACAGTGCTATAAGATCGGAAGAGCGGTTTCAG
chr17	29683928	29683967	NF1_130	-	GTGACCTATGCACCAGACGTATAGGGAATTAACGTGATCAAAACCTGGATAATCACTTCAGATCGGAAGAGCGGTTTCAG
chr17	29684237	29684276	NF1_131	-	GTGACCTATGCACCAGACGTGCAAAAAAGTAAACACACAACATTTTACTTTTGTGGCTGAAGATCGGAAGAGCGGTTTCAG
chr17	29685448	29685487	NF1_132	-	GTGACCTATGCACCAGACGTAAAAAAGTCAACACAGGAAACATTTTAGAGGAAAAATTAATAGATCGGAAGAGCGGTTTCAG
chr17	29685937	29685976	NF1_133	-	GTGACCTATGCACCAGACGTTCAAATTTTACTCTTATAACAAGCAAGGTATCTTTAATTAGATCGGAAGAGCGGTTTCAG
chr17	29687455	29687494	NF1_134	-	GTGACCTATGCACCAGACGTAAGTAAAGGAAATTTTACTTCTTTTTTAAAGTAAATCAGATCGGAAGAGCGGTTTCAG
chr17	29700981	29701020	NF1_135	-	GTGACCTATGCACCAGACGTTAGAGAAGCCAGTTACTTCTTCTTTTCTTCCAGGACTGAGATCGGAAGAGCGGTTTCAG
chr7	116339089	116339128	MET_136	-	GTGACCTATGCACCAGACGTTTATCTGCCAAAACAGGTTCAAGGCGAGAGCAGTTTCAGTTAGATCGGAAGAGCGGTTTCAG
chr7	116371672	116371711	MET_137	-	GTGACCTATGCACCAGACGTATATGGTCATAGAGTTAATGTGAATCCAGACATGAACAAGAGATCGGAAGAGCGGTTTCAG
chr7	116379954	116379993	MET_138	-	GTGACCTATGCACCAGACGTTAAAAAGTTATAACATCCTTATTCCAACAAGCTCAGTTTAAAGATCGGAAGAGCGGTTTCAG
chr7	116380856	116380895	MET_139	-	GTGACCTATGCACCAGACGTAAGGGGTGGAAGAGCTCCAGAGGGGTATCTAGTTTGTAGATCGGAAGAGCGGTTTCAG
chr7	116395359	116395398	MET_140	-	GTGACCTATGCACCAGACGTAAACATAGAACTTTTAAAAAACCCAAATATATAATTTAGATCGGAAGAGCGGTTTCAG
chr7	116397441	116397480	MET_141	-	GTGACCTATGCACCAGACGTAACCCAAAGTTTAAATACATGACAAATCCAAGGAATTTTCTAGATCGGAAGAGCGGTTTCAG
chr7	116397642	116397681	MET_142	-	GTGACCTATGCACCAGACGTGATAAAAAACAAAACAAAGTAACTTGTTCATCTTATAATTTAGATCGGAAGAGCGGTTTCAG
chr7	116398463	116398502	MET_143	-	GTGACCTATGCACCAGACGTAAAAATTAAGGAAGTGAATTTTAGCTATTAGAGATACACATTAGATCGGAAGAGCGGTTTCAG
chr7	116399341	116399380	MET_144	-	GTGACCTATGCACCAGACGTGGGATTCAAATTTAATCACCTGCACTGATTACAGGTCAGAGAGATCGGAAGAGCGGTTTCAG
chr7	116399395	116399434	MET_145	-	GTGACCTATGCACCAGACGTAAGATGAAACTGACATGTTGAGAGGTTCTTCCACCAAGATCGGAAGAGCGGTTTCAG
chr7	116403054	116403093	MET_146	-	GTGACCTATGCACCAGACGTACACAATTTCCACTGTAAACACAGAATACAGCTTGGCAACAAGATCGGAAGAGCGGTTTCAG
chr7	116409649	116409688	MET_147	-	GTGACCTATGCACCAGACGTAAAAAAAAAAAGGTTGTTAACACTTCACAGTTCTGCAGAGATCGGAAGAGCGGTTTCAG
chr7	116411502	116411541	MET_148	-	GTGACCTATGCACCAGACGTCAAATAAAGAAAAGTCAAGCATTAGCCATGATAGATTTAGATCGGAAGAGCGGTTTCAG
chr7	116411853	116411892	MET_149	-	GTGACCTATGCACCAGACGTAGAGAAAAGAAAGGCTTGTAAAGACGGCTATCATGGCCAGATCGGAAGAGCGGTTTCAG
chr7	116414885	116414924	MET_150	-	GTGACCTATGCACCAGACGTAAGGAAATTTAAAGAACACACAGTAAACCTCATTTAAAGATCGGAAGAGCGGTTTCAG
chr7	116417393	116417432	MET_151	-	GTGACCTATGCACCAGACGTGAAAAGAACTTGGTTGACTCGCTGAACATTTAATTGAAAAGATCGGAAGAGCGGTTTCAG
chr7	116418780	116418819	MET_152	-	GTGACCTATGCACCAGACGTCAAGTGGTGGAGACATTAACCTCATTATGGAACAGTGAATAAGATCGGAAGAGCGGTTTCAG
chr7	116421992	116422031	MET_153	-	GTGACCTATGCACCAGACGTAGAGAGTTAGAAAAGCATAAACTAAGCATCTACTGTTCTAAGATCGGAAGAGCGGTTTCAG
chr7	116423308	116423347	MET_154	-	GTGACCTATGCACCAGACGTGACAAAAATTTACCCGTTGGCTGAAATAGAATAATTTACAGATCGGAAGAGCGGTTTCAG
chr7	116435659	116435698	MET_155	-	GTGACCTATGCACCAGACGTAAGAAACAGGACAGATGAGGTGAGAGATGTACCATACATAGATCGGAAGAGCGGTTTCAG
chr7	116435891	116435930	MET_156	-	GTGACCTATGCACCAGACGTAAGAAAGACATGCTGTAAGAGACCTTTGAAGGCAGGCATAGATCGGAAGAGCGGTTTCAG
chr7	116339489	116339528	MET_157	-	GTGACCTATGCACCAGACGTGAAGTTGATCATAGTAGTGTGTCGACAACATAGAGCCATGATCGGAAGAGCGGTTTCAG
chr7	116339889	116339928	MET_158	-	GTGACCTATGCACCAGACGTCCGTCAAGAAGTAAATAAAATTTGTTGCTTCAAAGGCATGAGATCGGAAGAGCGGTTTCAG
chr12	58142258	58142297	CDK4_159	-	GTGACCTATGCACCAGACGTGGCTGCCATGGAAGGAAAGAAAGCTGCCATTTCCCTTCTGAGATCGGAAGAGCGGTTTCAG
chr12	58142915	58142954	CDK4_160	-	GTGACCTATGCACCAGACGTTGGCTGTGGGCGACAGGGAAAAGAAATAGAGACTGGGGAAAAGAGATCGGAAGAGCGGTTTCAG
chr12	58143187	58143226	CDK4_161	-	GTGACCTATGCACCAGACGTAACATGGGAGAAAAGATTTTCTATTCTGAGTCCCTCTTTCAGATCGGAAGAGCGGTTTCAG
chr12	58144389	58144428	CDK4_162	-	GTGACCTATGCACCAGACGTACATACCTGGACTACCTTGAATCCCAAATCGCTTTGATAGATCGGAAGAGCGGTTTCAG
chr12	58144656	58144695	CDK4_163	-	GTGACCTATGCACCAGACGTAGATGGTACCAAATGGGTTCTGGTTGGGAGTAGGAGATAGATCGGAAGAGCGGTTTCAG
chr12	58144940	58144979	CDK4_164	-	GTGACCTATGCACCAGACGTTTGGTAGGCATTGAGAGGTGGATTGGGACCTTTGTAGTAGATCGGAAGAGCGGTTTCAG
chr12	58145233	58145272	CDK4_165	-	GTGACCTATGCACCAGACGTGGTGAGGGTTGGGCGTGGGGAGTAAAGGAAAAGACAGCAGATCGGAAGAGCGGTTTCAG
chr11	108098453	108098492	ATM_166	-	GTGACCTATGCACCAGACGTAAGGAAATAATAATGGGTTACTAATCACACTTATTTCAAAGATCGGAAGAGCGGTTTCAG
chr11	108099855	108099894	ATM_167	-	GTGACCTATGCACCAGACGTACAAAATGCAATTTCCAGAACTCGTTGAATACTTAAATTAAGATCGGAAGAGCGGTTTCAG
chr11	108106347	108106386	ATM_168	-	GTGACCTATGCACCAGACGTAAACAAATTAAGAAAACATAAAATTTGAACAAAAATAAAGATCGGAAGAGCGGTTTCAG
chr11	108115465	108115504	ATM_169	-	GTGACCTATGCACCAGACGTACAAACAAGCTCAACTGGGTATAACAGGGGAAACAAACTGAGATCGGAAGAGCGGTTTCAG
chr11	108117641	108117680	ATM_170	-	GTGACCTATGCACCAGACGTA AAAAT TAAATGTAATTTTATGTATGACTCTGTTTACAGATCGGAAGAGCGGTTTCAG
chr11	108121378	108121417	ATM_171	-	GTGACCTATGCACCAGACGTAAAAAAGGATAATTTGAAAACATTTCCATCACATTAACAAGATCGGAAGAGCGGTTTCAG
chr11	108122514	108122553	ATM_172	-	GTGACCTATGCACCAGACGTACAAAGGACAATTTGTAAAAGCAAGCTATTGGAGGGGCAAAGATCGGAAGAGCGGTTTCAG
chr11	108123494	108123533	ATM_173	-	GTGACCTATGCACCAGACGTAACAAAAGCTTCACTTGAAGAACCAAGCCATGTA AAAAGATCGGAAGAGCGGTTTCAG
chr11	108124491	108124530	ATM_174	-	GTGACCTATGCACCAGACGTTAAGATCTTTAATATATAAACCAAGTCACTAATGCTTTGAGATCGGAAGAGCGGTTTCAG

chr11	108128158	108128197	ATM_175	-	GTGACCTATGCACCAGACGTTAGAAGGAAAAATGCAAAATCCAGTTAAAATTATAGTTTAAAGATCGGAAGAGCGGTTTCAG
chr11	108129663	108129702	ATM_176	-	GTGACCTATGCACCAGACGTGACAACCAAGAACCAAGCAACAAGAAATAAAAAACAATTAGATCGGAAGAGCGGTTTCAG
chr11	108137848	108137887	ATM_177	-	GTGACCTATGCACCAGACGTGAGAAAACAAAGATGTTCAAGATGGCTTCTGCAGGAGCATAGATCGGAAGAGCGGTTTCAG
chr11	108139087	108139126	ATM_178	-	GTGACCTATGCACCAGACGTAAAGCACTCATTAACTAAGAGAAGGGCACAAACAGCCATAGATCGGAAGAGCGGTTTCAG
chr11	108141741	108141780	ATM_179	-	GTGACCTATGCACCAGACGTAGGAGGGAAAAAATCAGGTTTATCCACAAATCATTACTAGATCGGAAGAGCGGTTTCAG
chr11	108141928	108141967	ATM_180	-	GTGACCTATGCACCAGACGTAAAAAAGTTCAACTTTATAAGCTTAACAGAACACAGATCGGAAGAGCGGTTTCAG
chr11	108143209	108143248	ATM_181	-	GTGACCTATGCACCAGACGTAAAGTTTTCCAAAGTTAAATAATCATTCTGATAAAAGCAAGATCGGAAGAGCGGTTTCAG
chr11	108143399	108143438	ATM_182	-	GTGACCTATGCACCAGACGTAGAAGTGTGGTTAAATGAAATAGAGAAAAATTACTIONATAGATCGGAAGAGCGGTTTCAG
chr11	108151672	108151711	ATM_183	-	GTGACCTATGCACCAGACGTAAATAAAAAAGTAAATGTAATGTAATGTAATGTTTAAACAGATCGGAAGAGCGGTTTCAG
chr11	108153387	108153426	ATM_184	-	GTGACCTATGCACCAGACGTCAAAAAGTCAATGTGTTAAGAAAAATGAAAAAATAAATCAGATCGGAAGAGCGGTTTCAG
chr11	108154904	108154943	ATM_185	-	GTGACCTATGCACCAGACGTAAAAATTTAAATACAGGTTATATATAACTTTTCCAAGTAAGATCGGAAGAGCGGTTTCAG
chr11	108158328	108158367	ATM_186	-	GTGACCTATGCACCAGACGTACCAACTCTCTGGTAATTAATAAGTATCAATAAGTATCAAGATCGGAAGAGCGGTTTCAG
chr11	108159654	108159693	ATM_187	-	GTGACCTATGCACCAGACGTAAAGGAAAAAATCAGTCATCGTTTTAAAAAGTTTTGTAGATCGGAAGAGCGGTTTCAG
chr11	108160279	108160318	ATM_188	-	GTGACCTATGCACCAGACGTAAACAGATTTAGTAAAAACTGTTTAAATAGATACTCGGCTAGATCGGAAGAGCGGTTTCAG
chr11	108163296	108163335	ATM_189	-	GTGACCTATGCACCAGACGTGAGAAAAAACAACAACAACAGTAAGTTCTGGAAAAATAGATCGGAAGAGCGGTTTCAG
chr11	108165604	108165643	ATM_190	-	GTGACCTATGCACCAGACGTAAATGTAACCTTGCTTTTAAACACGTATTGGTTAAGCCTGTGAGATCGGAAGAGCGGTTTCAG
chr11	108167964	108168003	ATM_191	-	GTGACCTATGCACCAGACGTTTTTTAAAAATAGTTTAACTAGCATGAAGACAACACTAGATCGGAAGAGCGGTTTCAG
chr11	108170391	108170430	ATM_192	-	GTGACCTATGCACCAGACGTAAATCTTATTTAGTAGATCATAGGTAAAGAGATCATACAAGATCGGAAGAGCGGTTTCAG
chr11	108172325	108172364	ATM_193	-	GTGACCTATGCACCAGACGTCAATTCAAATGCCTATCAAGTACACCAGTTATTAATCTTGAGATCGGAAGAGCGGTTTCAG
chr11	108173530	108173569	ATM_194	-	GTGACCTATGCACCAGACGTAGGGATTAGAAAATGTAATAAGAGAAGTGGAAATCATTGAGATCGGAAGAGCGGTTTCAG
chr11	108175352	108175391	ATM_195	-	GTGACCTATGCACCAGACGTCAACAATCCACCATAAGTGTGAGTAAAAATGAGTAAAGATCGGAAGAGCGGTTTCAG
chr11	108178574	108178613	ATM_196	-	GTGACCTATGCACCAGACGTAAAAATCTCCCTCAGTCCAGGCATTCTTGCTTACACAAGATCGGAAGAGCGGTTTCAG
chr11	108180837	108180876	ATM_197	-	GTGACCTATGCACCAGACGTATGAGATATAATGTCATTCATTTTTTAACTTCAATATCAGATCGGAAGAGCGGTTTCAG
chr11	108183088	108183127	ATM_198	-	GTGACCTATGCACCAGACGTAAAGAACCTCTTTTTAATGAGAACATACTATTTGGAAGCAGATCGGAAGAGCGGTTTCAG
chr11	108186500	108186539	ATM_199	-	GTGACCTATGCACCAGACGTGAAACAACAATAAATTGAAGAAGGAAAAAATCGGCTAAGATCGGAAGAGCGGTTTCAG
chr11	108186688	108186727	ATM_200	-	GTGACCTATGCACCAGACGTAGATTGTAAAAATGCTTTGGGTTTTACACACACATACTAGATCGGAAGAGCGGTTTCAG
chr11	108188050	108188089	ATM_201	-	GTGACCTATGCACCAGACGTGTTATTTGTTTTAAGTTAAGTAATCAAGATATCAACAAGATCGGAAGAGCGGTTTCAG
chr11	108190631	108190670	ATM_202	-	GTGACCTATGCACCAGACGTAGTCAAAGAAAAAATATACTTAAAAACAGAACCTAAGAAGATCGGAAGAGCGGTTTCAG
chr11	108191978	108192017	ATM_203	-	GTGACCTATGCACCAGACGTAAAGAAAAAGCACTCTGAAATAAAGAAGGTTTTTCAGAGATCGGAAGAGCGGTTTCAG
chr11	108195987	108196026	ATM_204	-	GTGACCTATGCACCAGACGTGCATAGAGTTCAATGTAAGCAAGAGAATGAAAAAATAAAGATCGGAAGAGCGGTTTCAG
chr11	108196735	108196774	ATM_205	-	GTGACCTATGCACCAGACGTAAATGACATATGGGAATAAATACTTTTACTACTGATACTACAGATCGGAAGAGCGGTTTCAG
chr11	108198322	108198361	ATM_206	-	GTGACCTATGCACCAGACGTAAAGGCAAAATCTTAAATATAATGCATTACCATGACTGTAAGATCGGAAGAGCGGTTTCAG
chr11	108199698	108199737	ATM_207	-	GTGACCTATGCACCAGACGTACACAACCAATTTAAATTTATTTTACAAATACTAAATACAAGATCGGAAGAGCGGTTTCAG
chr11	108200891	108200930	ATM_208	-	GTGACCTATGCACCAGACGTATAATTAAGTAAAAACAAAAAGCCATGAACTTTAAACAGAAGATCGGAAGAGCGGTTTCAG
chr11	108202121	108202160	ATM_209	-	GTGACCTATGCACCAGACGTAAAAAAGACACAATAAATAAGAAACAAAGTATTTTCAAATATAGATCGGAAGAGCGGTTTCAG
chr11	108202556	108202595	ATM_210	-	GTGACCTATGCACCAGACGTAGAAGTATTAGATTTATGCAAATAAACAAAAAATAAATAGATCGGAAGAGCGGTTTCAG
chr11	108203439	108203478	ATM_211	-	GTGACCTATGCACCAGACGTAAAAAACAACATTACATAAGGAACCTACCAACATTTAAAGATCGGAAGAGCGGTTTCAG
chr11	108204563	108204602	ATM_212	-	GTGACCTATGCACCAGACGTAAATGAAGAGATTTTGTAGTACAAACTGAGGAACAGCATTGAGATCGGAAGAGCGGTTTCAG
chr11	108205646	108205685	ATM_213	-	GTGACCTATGCACCAGACGTTATAACATGATTGATAATAGGTCAGATACACTATTTGCAAGATCGGAAGAGCGGTTTCAG
chr11	108206522	108206561	ATM_214	-	GTGACCTATGCACCAGACGTAAAGCATGAATAAACAGTACAGTTATTTTATTATAAGATCGGAAGAGCGGTTTCAG
chr11	108213899	108213938	ATM_215	-	GTGACCTATGCACCAGACGTAGATTAATAACCTTTTAAATTTTAAAGGCCATTAAAGAGCAGATCGGAAGAGCGGTTTCAG
chr11	108216420	108216459	ATM_216	-	GTGACCTATGCACCAGACGTAGAATATATAATTTTTCATATTTGTTTCAATTAAGATCGGAAGAGCGGTTTCAG
chr11	108217956	108217995	ATM_217	-	GTGACCTATGCACCAGACGTAAAGAAACAACAATCTGAAATCACTGATTCCATCTCTTTCAGATCGGAAGAGCGGTTTCAG
chr11	108224443	108224482	ATM_218	-	GTGACCTATGCACCAGACGTGAATACAGTGAAGTTAGGAGGTTTTGACAGCTAATTTACTTAGATCGGAAGAGCGGTTTCAG
chr11	108225488	108225527	ATM_219	-	GTGACCTATGCACCAGACGTACACATATAAATACGGATTTGTTTACACCAATGTTGTAGATCGGAAGAGCGGTTTCAG
chr11	108235759	108235798	ATM_220	-	GTGACCTATGCACCAGACGTAGAACATATGTTAAAGAACAATGATACATTTTAAATCAGATCGGAAGAGCGGTTTCAG
chr11	108236002	108236041	ATM_221	-	GTGACCTATGCACCAGACGTAAACACAAGGTTTTCAGTGAGGTGAACAGTTTAAAGGCCATAGATCGGAAGAGCGGTTTCAG
chr4	55124886	55124925	PDGFRA_222	-	GTGACCTATGCACCAGACGTAACTAGAAAAGTCAAAAGTCAACAGAAACAGCATTAGCAAAGATCGGAAGAGCGGTTTCAG
chr4	55127212	55127251	PDGFRA_223	-	GTGACCTATGCACCAGACGTAAAGCACGCTCTGAATAGGATGCAGTCAGAAAGGACAGTCTAGATCGGAAGAGCGGTTTCAG
chr4	55129784	55129823	PDGFRA_224	-	GTGACCTATGCACCAGACGTAAAAAGAATGAAGACTCTATTAGACATTAATTTACCTTTAGATCGGAAGAGCGGTTTCAG
chr4	55131036	55131075	PDGFRA_225	-	GTGACCTATGCACCAGACGTGAACAAATCAAGGGCCTAAAAATCCACAGGATGCCAGGATCGGAAGAGCGGTTTCAG
chr4	55133669	55133708	PDGFRA_226	-	GTGACCTATGCACCAGACGTAAAGTTTTCCATTAAATAATGATTACCACATATGGATCCGAGATCGGAAGAGCGGTTTCAG
chr4	55136750	55136789	PDGFRA_227	-	GTGACCTATGCACCAGACGTAAAGTTTTGTTTCAACAAGCAGTAGCTAAGTAAGTTCCAAGATCGGAAGAGCGGTTTCAG
chr4	55138511	55138550	PDGFRA_228	-	GTGACCTATGCACCAGACGTGAGAAAGAAGTCAGAAATGGAATAGCTCGTGTCCAGAACAAGATCGGAAGAGCGGTTTCAG
chr4	55139654	55139693	PDGFRA_229	-	GTGACCTATGCACCAGACGTAAAGGGCCTAAGTATAGGGCAATTCCTGAGAGTCATGGCAGATCGGAAGAGCGGTTTCAG
chr4	55140648	55140687	PDGFRA_230	-	GTGACCTATGCACCAGACGTAGAGAGAGGGCAATGAAAAGTTTCTGGCAGACATGCAGATCGGAAGAGCGGTTTCAG
chr4	55140958	55140997	PDGFRA_231	-	GTGACCTATGCACCAGACGTCCAGACAGTAACTGGTGAATACCAAGTCCAGATCGGAAGAGCGGTTTCAG
chr4	55143505	55143544	PDGFRA_232	-	GTGACCTATGCACCAGACGTGCAAGATCATTAAACACCAAAATCCAGACGCTCCTCAAGATCGGAAGAGCGGTTTCAG

chr4	55144013	55144052	PDGFRA_233	-	GTGACCTATGCACCAGACGTAATAAATCACATATCAGTCCAGCTGAGCTACCAACTTCCTAGATCGGAAGAGCGGTTTCAG
chr4	55144479	55144518	PDGFRA_234	-	GTGACCTATGCACCAGACGTA AAAAGCCGTTAGGAGATGGGTATGAAAATGAAGAACAGAAAGATCGGAAGAGCGGTTTCAG
chr4	55146433	55146472	PDGFRA_235	-	GTGACCTATGCACCAGACGTAGAAAGAGAAATCTTACCCAGGGTGCCCTTCTGAAGTGGTAGATCGGAAGAGCGGTTTCAG
chr4	55151488	55151527	PDGFRA_236	-	GTGACCTATGCACCAGACGTGAAATTAATGTATTGGTGTGGCAGGCAGCAGGAAATCAAGATCGGAAGAGCGGTTTCAG
chr4	55151958	55151997	PDGFRA_237	-	GTGACCTATGCACCAGACGTAAAGGAAGAAATGACTCAGGATCAAGCCATCTGTAGCTGAAAGATCGGAAGAGCGGTTTCAG
chr4	55153547	55153586	PDGFRA_238	-	GTGACCTATGCACCAGACGTGGAGGGGACAGTTAAACCCATGTCTACTCACTGATGATCAGATCGGAAGAGCGGTTTCAG
chr4	55154956	55154955	PDGFRA_239	-	GTGACCTATGCACCAGACGTAAACAAATAAACACACAGGACTAAACAAACGCTCAGTGCATTGAGATCGGAAGAGCGGTTTCAG
chr4	55155126	55155165	PDGFRA_240	-	GTGACCTATGCACCAGACGTAGAACTCAAGAGTGGGCACAGGGGGAAGTCTCAGGGCCCCAGATCGGAAGAGCGGTTTCAG
chr4	55156430	55156469	PDGFRA_241	-	GTGACCTATGCACCAGACGTTCAATGAACATATTTAATCAAGTGTAAACAACCAACCTCAGATCGGAAGAGCGGTTTCAG
chr4	55161242	55161281	PDGFRA_242	-	GTGACCTATGCACCAGACGTGAGAGAAGAGCAAATATTACAACCTCCTGCACAGAAC TAGAAGATCGGAAGAGCGGTTTCAG
chr12	69202208	69202247	MDM2_243	-	GTGACCTATGCACCAGACGTGCGCGCTTGGAGTGGGGGTCCCTCAAGACTCCCCAGTTTCAGATCGGAAGAGCGGTTTCAG
chr12	69202938	69202977	MDM2_244	-	GTGACCTATGCACCAGACGTAAAAAAGACACGATGAAAATCGGAAATCATGAAACATCTGAGATCGGAAGAGCGGTTTCAG
chr12	69202942	69202981	MDM2_245	-	GTGACCTATGCACCAGACGTGGA AAAAAGACACGATGAAAATCTGAAAATCATGAAACAAGATCGGAAGAGCGGTTTCAG
chr12	69207284	69207323	MDM2_246	-	GTGACCTATGCACCAGACGTAAAAGAAGTCTATTATACTTCCAAAATTATCCAGAACTAGATCGGAAGAGCGGTTTCAG
chr12	69210542	69210581	MDM2_247	-	GTGACCTATGCACCAGACGTAATATGATTTCTGAGCATTAAGAAAAC TAAATGTTAGTTAGATCGGAAGAGCGGTTTCAG
chr12	69214055	69214094	MDM2_248	-	GTGACCTATGCACCAGACGTGAAAAAATAAACAAGAGATGTACATTTTAGAATAAAGATCGGAAGAGCGGTTTCAG
chr12	69218285	69218324	MDM2_249	-	GTGACCTATGCACCAGACGTAGGAAAAAATAAACAACAACCTTAAACATAACCAGTAAGATCGGAAGAGCGGTTTCAG
chr12	69222501	69222540	MDM2_250	-	GTGACCTATGCACCAGACGTAAAGGAAAAAATAAATGCTGTACTGTGATTTAGAAAATAGATCGGAAGAGCGGTTTCAG
chr12	69229559	69229598	MDM2_251	-	GTGACCTATGCACCAGACGTAAAAAATATATAACTTAATAAACATCACCTCTTGACCTCAGATCGGAAGAGCGGTTTCAG
chr12	69230402	69230441	MDM2_252	-	GTGACCTATGCACCAGACGTACATTCATTAGCATCAATTCATCGCCCTATTTCCTTCAATAGATCGGAAGAGCGGTTTCAG
chr12	69233004	69233043	MDM2_253	-	GTGACCTATGCACCAGACGTATAAGACACACAGTCAGTTTCTGTAACCCTTTAACTGCTCAGATCGGAAGAGCGGTTTCAG
chr12	69233292	69233331	MDM2_254	-	GTGACCTATGCACCAGACGTTCTTCACTTTCTTGTGATTGTGAAGCTTGTGTAATTTTATAGATCGGAAGAGCGGTTTCAG
chr5	112090538	112090577	APC_255	-	GTGACCTATGCACCAGACGTCTTGGACCTATAAGGTTAAAAAGGATTTTGAATTCAGTACTAGATCGGAAGAGCGGTTTCAG
chr5	112101973	112102012	APC_256	-	GTGACCTATGCACCAGACGTGAACAATATTAACATTAAGTGAANTCTAAATAACTTCAAGAGATCGGAAGAGCGGTTTCAG
chr5	112102836	112102875	APC_257	-	GTGACCTATGCACCAGACGTTAGAAAACAAGTTTTTATACAACAATTGCTTTAAGCAGTCTAGATCGGAAGAGCGGTTTCAG
chr5	112116437	112116476	APC_258	-	GTGACCTATGCACCAGACGTAATAATAAAAAAGTATCAATATCTGTATTTACGTTAATAGATCGGAAGAGCGGTTTCAG
chr5	112136926	112136965	APC_259	-	GTGACCTATGCACCAGACGTGGAGTTAACATCAGTACATGCAAAAATGGTGTAGGCTTTCAGATCGGAAGAGCGGTTTCAG
chr5	112151142	112151181	APC_260	-	GTGACCTATGCACCAGACGTAGCACATTTATAGATGGTATAATTTAGACTATAGGTAAATAAGATCGGAAGAGCGGTTTCAG
chr5	112154613	112154652	APC_261	-	GTGACCTATGCACCAGACGTAATGATTTAGAAAACAAAATACGACTTTAATATCCAAAAGATCGGAAGAGCGGTTTCAG
chr5	112157543	112157582	APC_262	-	GTGACCTATGCACCAGACGTA AATCAACATAAACCAATGCTTTGTTATTTGAAGAGCAAGATCGGAAGAGCGGTTTCAG
chr5	112162755	112162794	APC_263	-	GTGACCTATGCACCAGACGTAAGGGCAAGAGGAAAAAGACAATCATCTAAAATAAAAACAAGATCGGAAGAGCGGTTTCAG
chr5	112163576	112163615	APC_264	-	GTGACCTATGCACCAGACGTAATACAGAATAGAGGATCATTAAAAAGACAACCTTGAAGCCAGATCGGAAGAGCGGTTTCAG
chr5	112164503	112164542	APC_265	-	GTGACCTATGCACCAGACGTATCAATTTTATAGTTAATTTATACATAAATCATACTAGTTAGATCGGAAGAGCGGTTTCAG
chr5	112170598	112170637	APC_266	-	GTGACCTATGCACCAGACGTACAGAATAGGTCATCTAATAGATTTGGAATTTGCTCAGATCGGAAGAGCGGTTTCAG
chr5	112173200	112173239	APC_267	-	GTGACCTATGCACCAGACGTAACTGATACAGATACAAAATTAAGGTCAATGTGTATCGAGATCGGAAGAGCGGTTTCAG
chr5	112173670	112173709	APC_268	-	GTGACCTATGCACCAGACGTATGTCGATTGGTGTCAAAAACATAATCACCATAGAGACTTAGATCGGAAGAGCGGTTTCAG
chr5	112174140	112174179	APC_269	-	GTGACCTATGCACCAGACGTCTATCATTGAAGATCTCTTGTATTCTAATTTGGCATAAGAGATCGGAAGAGCGGTTTCAG
chr5	112174610	112174649	APC_270	-	GTGACCTATGCACCAGACGTCATGATTAGAACCCTCGATTTGTTTCTGAACCATTTGGCAGATCGGAAGAGCGGTTTCAG
chr5	112175080	112175119	APC_271	-	GTGACCTATGCACCAGACGTTGAACATCATCTTGA AAAACATATTGGAGTATCTTCTACAAGATCGGAAGAGCGGTTTCAG
chr5	112175550	112175589	APC_272	-	GTGACCTATGCACCAGACGTGGTGGCATGTTTGTCCAGGCTATCGGAAGATCACTGGAGATCGGAAGAGCGGTTTCAG
chr5	112176020	112176059	APC_273	-	GTGACCTATGCACCAGACGTTAAGTATGACTTTTGTGGCAGTGGCAAAAATAATACATTCAGATCGGAAGAGCGGTTTCAG
chr5	112176490	112176529	APC_274	-	GTGACCTATGCACCAGACGTTATCTTTTTACACGGAAAGGCTTGTGACTTTTCCCTTTGAGATCGGAAGAGCGGTTTCAG
chr5	112176960	112176999	APC_275	-	GTGACCTATGCACCAGACGTTTGGAGGTTAGTTCTGTGTGGCTGGTAACTTTAGCCCTGAGATCGGAAGAGCGGTTTCAG
chr5	112177430	112177469	APC_276	-	GTGACCTATGCACCAGACGTTATCACCCCTTGAGTCTTGAAGGCTTTTTCTTTTTTGGCATAAGATCGGAAGAGCGGTTTCAG
chr5	112177900	112177939	APC_277	-	GTGACCTATGCACCAGACGTGGGCTGTTCTACTTGGCCTGAAATTTCTGAATTAGATCGAAGATCGGAAGAGCGGTTTCAG
chr5	112178370	112178409	APC_278	-	GTGACCTATGCACCAGACGTACTGTCTGTCTGAGATGTATGACATTTTTCCGAACAGATCGGAAGAGCGGTTTCAG
chr5	112178840	112178879	APC_279	-	GTGACCTATGCACCAGACGTGTGCAATATCATGGCGCTTGTGCTTCCATCATTATAAGATCGGAAGAGCGGTTTCAG
chr5	112179310	112179349	APC_280	-	GTGACCTATGCACCAGACGTAACACTGTCAATCACCGGGGGAGTATTACCTGTGGGAGATAGATCGGAAGAGCGGTTTCAG
chr22	41488959	41488998	EP300_281	-	GTGACCTATGCACCAGACGTTTCGGAGATACAAGCGAGGAAAACCAAGAATCCTCAGGAAAAGATCGGAAGAGCGGTTTCAG
chr22	41513141	41513180	EP300_282	-	GTGACCTATGCACCAGACGTAGGGAAAAGACAAAAGTCAAAAGTATGACAAAACCAAAAATAAGATCGGAAGAGCGGTTTCAG
chr22	41521818	41521857	EP300_283	-	GTGACCTATGCACCAGACGTGAAAACAAAAGAAAACAAAATAAGCAATAAAATTAAGCAAGATCGGAAGAGCGGTTTCAG
chr22	41523441	41523480	EP300_284	-	GTGACCTATGCACCAGACGTTAAACAATATTTAATGGATGAGTCAATAATGTGCTATTTAGATCGGAAGAGCGGTTTCAG
chr22	41525844	41525883	EP300_285	-	GTGACCTATGCACCAGACGTGAAAACATATTTTTCAAGAGCAGGTTAATGTTTTACATAGATCGGAAGAGCGGTTTCAG
chr22	41527342	41527381	EP300_286	-	GTGACCTATGCACCAGACGTCAAAAAGATATAGTATTACAAATTAATGCTGGTGAGAAAAAAGATCGGAAGAGCGGTTTCAG
chr22	41531767	41531806	EP300_287	-	GTGACCTATGCACCAGACGTATGAAAATAACAGGAGACAAAATAAATACAACAGCCCAAGATCGGAAGAGCGGTTTCAG
chr22	41533607	41533646	EP300_288	-	GTGACCTATGCACCAGACGTGGGTCAACAAATAGTTTTAGTGAAGAAAGTAGGAGAAGAGATCGGAAGAGCGGTTTCAG
chr22	41536094	41536133	EP300_289	-	GTGACCTATGCACCAGACGTA AACTCAACTGTAAATCATGTACAGATTTAATTAAGATCGGAAGAGCGGTTTCAG
chr22	41537002	41537041	EP300_290	-	GTGACCTATGCACCAGACGTTGTAAGTAAAATAAGGAGATGAGGAAAAAGAACTACAGATCGGAAGAGCGGTTTCAG

chr22	41542693	41542732	EP300_291	-	GTGACCTATGCACCAGACGTAAAGAGAAATAAGTATCTTTGCACCATCTTCCCTTAACCAAGATCGGAAGAGCGGTTTCAG
chr22	41543791	41543830	EP300_292	-	GTGACCTATGCACCAGACGTGAGCAAAAATGTTAGATCTGAATGCCTTTGTGAAATTGAATAGATCGGAAGAGCGGTTTCAG
chr22	41544992	41545031	EP300_293	-	GTGACCTATGCACCAGACGTAAAAAACACAAATCACCAAATGCTTCATTATAGTTATTAGATCGGAAGAGCGGTTTCAG
chr22	41545715	41545754	EP300_294	-	GTGACCTATGCACCAGACGTAAAAACATAACAAGACAGCAATTCAGAACAGAATTAAGGAGATCGGAAGAGCGGTTTCAG
chr22	41547787	41547826	EP300_295	-	GTGACCTATGCACCAGACGTAAAAAGGGGAAGTAGGTGAGACACACGCAGAGTCTGCCAAAGATCGGAAGAGCGGTTTCAG
chr22	41548160	41548199	EP300_296	-	GTGACCTATGCACCAGACGTACGTAAGAATTTTTAGTATTCCAAGATATCTAGTTGGGAAGATCGGAAGAGCGGTTTCAG
chr22	41550949	41550988	EP300_297	-	GTGACCTATGCACCAGACGTAAAAAGTGCAATTTGAAATTAGTTACCAATTAAAGCAGAAGAAAGATCGGAAGAGCGGTTTCAG
chr22	41553123	41553162	EP300_298	-	GTGACCTATGCACCAGACGTAAGTGACATCAAACTACTCAAGTCTCACTATTTTTACGAGATCGGAAGAGCGGTTTCAG
chr22	41554366	41554405	EP300_299	-	GTGACCTATGCACCAGACGTAACCATTTGTTAAAAAGCACAGAGGCCTTAAGGACAAGCTAGATCGGAAGAGCGGTTTCAG
chr22	41556596	41556635	EP300_300	-	GTGACCTATGCACCAGACGTGAAGGCCATACTGGGGTGAACGTGCCGTTCACACAACACAGATCGGAAGAGCGGTTTCAG
chr22	41558677	41558716	EP300_301	-	GTGACCTATGCACCAGACGTAAAAAGGGACACAATGAGAAAAAGTGATAGAGATGAGCAATAGATCGGAAGAGCGGTTTCAG
chr22	41560007	41560046	EP300_302	-	GTGACCTATGCACCAGACGTAGAGCCAATTCAAAATTAACCCAAACCTTAACCAAATGAGATCGGAAGAGCGGTTTCAG
chr22	41562553	41562592	EP300_303	-	GTGACCTATGCACCAGACGTACCAAAAATTTGCTTACACAACCTTAGATAAACCCGTTGAATAGATCGGAAGAGCGGTTTCAG
chr22	41564403	41564442	EP300_304	-	GTGACCTATGCACCAGACGTAAAAAGTTAAAAGTTACTGAGGTGCAAAATTTACTGTTGTTAAGATCGGAAGAGCGGTTTCAG
chr22	41564675	41564714	EP300_305	-	GTGACCTATGCACCAGACGTGAGATGGTGGGGGAACCAACAATAACTCATTAGACTGGAGATCGGAAGAGCGGTTTCAG
chr22	41565457	41565496	EP300_306	-	GTGACCTATGCACCAGACGTTGAAGAGAAATGAAGAGGAAAAAAAAGTCAGGTCACATAAGATCGGAAGAGCGGTTTCAG
chr22	41566360	41566399	EP300_307	-	GTGACCTATGCACCAGACGTAAAGAGAAAGAACATTAAGGAAAAAGAGATAATCTATTCTAAGATCGGAAGAGCGGTTTCAG
chr22	41568453	41568492	EP300_308	-	GTGACCTATGCACCAGACGTGCATGTACATATAGAAATTTCTATGTTCTTTTAAAGCAAGATCGGAAGAGCGGTTTCAG
chr22	41569577	41569616	EP300_309	-	GTGACCTATGCACCAGACGTGCACAAAAGGAGACAAGAAAAAAGGTTTTTGTTAAGTAATAGATCGGAAGAGCGGTTTCAG
chr22	41572727	41572766	EP300_310	-	GTGACCTATGCACCAGACGTAACAGGAGGTGCACGTAAACTCTCCAAGATTTAAGTCATTAGATCGGAAGAGCGGTTTCAG
chr22	41513458	41513497	EP300_311	-	GTGACCTATGCACCAGACGTGGAGAGTCAAGCCTGCCTGTGTCATTGGGCTTTTGACCAAGATCGGAAGAGCGGTTTCAG
chr22	41573164	41573203	EP300_312	-	GTGACCTATGCACCAGACGTTGCGAAGCATTTGGGCCTGCTGTAGTCCGGTCTGCAGCTGAGATCGGAAGAGCGGTTTCAG
chr22	41573601	41573640	EP300_313	-	GTGACCTATGCACCAGACGTACTCTGGTCATGGGAGTGGGTTTCATACCCATGGGGCCAGATCGGAAGAGCGGTTTCAG
chr22	41574038	41574077	EP300_314	-	GTGACCTATGCACCAGACGTTGACCTGGCATGGTAGGTGCTGTAGCCCTGGCTGCCCTCGAAGAGCGGTTTCAG
chr22	41574475	41574514	EP300_315	-	GTGACCTATGCACCAGACGTGCTGAAGGAGTCTGCTGCTGATAGGCCCTGTAGACTGGCACCAGATCGGAAGAGCGGTTTCAG
chr19	45854837	45854876	ERCC2_316	-	GTGACCTATGCACCAGACGTTGGGGCCATAAACGGTTCTCTGGTACTCCTGAGTCTTGCCAGATCGGAAGAGCGGTTTCAG
chr19	45855417	45855456	ERCC2_317	-	GTGACCTATGCACCAGACGTGCTCCCCCTCCCGGCACCCTCCAGGCTGAGCTTCTCCTCAGATCGGAAGAGCGGTTTCAG
chr19	45855714	45855753	ERCC2_318	-	GTGACCTATGCACCAGACGTAGGGGTGCCCTTGCTCCTCCATCCAGGCTCCAAGAACAAGATCGGAAGAGCGGTTTCAG
chr19	45855954	45855993	ERCC2_319	-	GTGACCTATGCACCAGACGTCTGTCTCCAGGGAGTCCCACAGTGTAGGATCAAGGCAGATCGGAAGAGCGGTTTCAG
chr19	45856291	45856330	ERCC2_320	-	GTGACCTATGCACCAGACGTTGGGCTTCTCTCCAGGTTCTTCCACAGACTCTCTGGAGATCGGAAGAGCGGTTTCAG
chr19	45856450	45856489	ERCC2_321	-	GTGACCTATGCACCAGACGTGAGGCCAGCGTGGAGAGGGGTGGGAGGTTGGCTCTGAGGAGATCGGAAGAGCGGTTTCAG
chr19	45857938	45857977	ERCC2_322	-	GTGACCTATGCACCAGACGTCCACCCCTCCCTGCACCTGCTCTCCTCAGTCCCTGGCACAGATCGGAAGAGCGGTTTCAG
chr19	45860478	45860517	ERCC2_323	-	GTGACCTATGCACCAGACGTGAGGCTAGGGCTGGGGCCGGGAGGGGAGATGGGGGCAAGGAGATCGGAAGAGCGGTTTCAG
chr19	45860682	45860721	ERCC2_324	-	GTGACCTATGCACCAGACGTTTTCCCGTCCCTCTAGTCCCTGACTCCCTCCATCCGATCGGAAGAGCGGTTTCAG
chr19	45860838	45860877	ERCC2_325	-	GTGACCTATGCACCAGACGTGCCCGTGGCCGCTGTGAATGCTGTGGTGGTGGGGCCAAAGATCGGAAGAGCGGTTTCAG
chr19	45864732	45864771	ERCC2_326	-	GTGACCTATGCACCAGACGTCTTTTTCTCTCTGCTGCTGGCCTCCTAGCAGCTGGAATCAAGATCGGAAGAGCGGTTTCAG
chr19	45866951	45866990	ERCC2_327	-	GTGACCTATGCACCAGACGTAGACAGCGCGGGTGGGGGCCCGGCAGGTCCTGGTTATAGATCGGAAGAGCGGTTTCAG
chr19	45867194	45867233	ERCC2_328	-	GTGACCTATGCACCAGACGTACCCCCCGCTGCCCCCGAGTCCCTTTCCCGCTCCCGTCCAGATCGGAAGAGCGGTTTCAG
chr19	45867443	45867482	ERCC2_329	-	GTGACCTATGCACCAGACGTGGACGCTGGCGGTGGTGGCCCGCTGCCCTGGGACCCTAGATCGGAAGAGCGGTTTCAG
chr19	45867632	45867671	ERCC2_330	-	GTGACCTATGCACCAGACGTGCCAGGGGCCAAGGGATGCCAGCCCTCTGATGAGGCAGATCGGAAGAGCGGTTTCAG
chr19	45868250	45868289	ERCC2_331	-	GTGACCTATGCACCAGACGTGGCAGGGCTGAGGGAGGGAGGACAGGATGCTAGCTGGGGAGATCGGAAGAGCGGTTTCAG
chr19	45871838	45871877	ERCC2_332	-	GTGACCTATGCACCAGACGTGTTCTTCTCTCTGCTGCTGGCCTCCTAGCAGCTGGAATCAAGATCGGAAGAGCGGTTTCAG
chr19	45872138	45872177	ERCC2_333	-	GTGACCTATGCACCAGACGTACTCATCTGGTGTCCAGCCCACTGTTCCCTAGGCCCTAGATCGGAAGAGCGGTTTCAG
chr19	45872278	45872317	ERCC2_334	-	GTGACCTATGCACCAGACGTGCTGAACCCGTAAGGCAGACAAAGGAAGGGGCGGGACAAGATCGGAAGAGCGGTTTCAG
chr19	45873341	45873380	ERCC2_335	-	GTGACCTATGCACCAGACGTGGTGGGGCCAGCCGCCCACTGACCCGTTGGGGTGGCCACAGATCGGAAGAGCGGTTTCAG
chr19	45873744	45873783	ERCC2_336	-	GTGACCTATGCACCAGACGTGGTGGGGTCCGCTGCTAGCGGGCGCGGGGGTCTTGATCGGAAGAGCGGTTTCAG
chr12	25362679	25362718	KRAS_337	-	GTGACCTATGCACCAGACGTTACTTTTTCTTAAGGCATACTAGTACAAGTGGTAATTTTATAGATCGGAAGAGCGGTTTCAG
chr12	25368325	25368364	KRAS_338	-	GTGACCTATGCACCAGACGTTTAAGTTCAGCACATTAATTTTGGCAGAAAGCAGATGTCTAGATCGGAAGAGCGGTTTCAG
chr12	25378498	25378537	KRAS_339	-	GTGACCTATGCACCAGACGTCTGAAATAAATACAGATCTGTTTTCTGCAAAATCATAACTAGATCGGAAGAGCGGTTTCAG
chr12	25380118	25380157	KRAS_340	-	GTGACCTATGCACCAGACGTATTGAATATAAAGCTGACATTAAGGAGTAATTTATAGTTAGATCGGAAGAGCGGTTTCAG
chr12	25398158	25398197	KRAS_341	-	GTGACCTATGCACCAGACGTTTTAATATGCATTAAGTGGTCAGGACCATCTTTGATAGATCGGAAGAGCGGTTTCAG
chr7	106507957	106507996	PIK3CG_342	-	GTGACCTATGCACCAGACGTACCTGGAGCGGAGGACAGGATTTGTCAAGAAGAGATCGGAAGAGCGGTTTCAG
chr7	106512932	106512971	PIK3CG_343	-	GTGACCTATGCACCAGACGTAACACATTGGCATTTGAGGACTGTACTCTATGCTGTTGAAGATCGGAAGAGCGGTTTCAG
chr7	106513108	106513147	PIK3CG_344	-	GTGACCTATGCACCAGACGTGTACAAGAAAGTTGAAATTATTGACTAATGCTTTAGGTAGATCGGAAGAGCGGTTTCAG
chr7	106515095	106515134	PIK3CG_345	-	GTGACCTATGCACCAGACGTCAAAGTACACAAGAGTTATGTGAGTTCCAGAAATCATCAAGATCGGAAGAGCGGTTTCAG
chr7	106519914	106519953	PIK3CG_346	-	GTGACCTATGCACCAGACGTGCAGTCACATATCCCCACACACAATGAATAACGAATATAAGATCGGAAGAGCGGTTTCAG
chr7	106523428	106523467	PIK3CG_347	-	GTGACCTATGCACCAGACGTGCACAGAGTCTGATGGAGATTTGGGGCCAGACTCGGAGATCGGAAGAGCGGTTTCAG
chr7	106524550	106524589	PIK3CG_348	-	GTGACCTATGCACCAGACGTGCATTTGAAATATTAGTTGCTTCTTAACACAAAAAGCATAGATCGGAAGAGCGGTTTCAG

chr7	106526530	106526569	PIK3CG_349	-	GTGACCTATGCACCAGACGTGAAAGTATCTGACATCATTACAGTGGCACAGCACTTTGTTAGATCGGAAGAGCGGTTTCAG
chr7	106545504	106545543	PIK3CG_350	-	GTGACCTATGCACCAGACGTAAAGAAGAAAATGCTGTTACTGTTGTTATGGTAACTAACAAAGATCGGAAGAGCGGTTTCAG
chr7	106508456	106508495	PIK3CG_351	-	GTGACCTATGCACCAGACGTAGTGACGTCATAGCCAATCAGCGCCGTGAGCTGCCGCTGGAGATCGGAAGAGCGGTTTCAG
chr7	106508955	106508994	PIK3CG_352	-	GTGACCTATGCACCAGACGTTGCAGTCATCCACCAGTGGCCACTCTTCCTTCCCTCACCTCAGATCGGAAGAGCGGTTTCAG
chr7	106509454	106509493	PIK3CG_353	-	GTGACCTATGCACCAGACGCTTCCCTTGGTCTTCTCCCTTCCAGATATCTGCCACATGTAGATCGGAAGAGCGGTTTCAG
chr17	41197645	41197684	BRCA1_354	-	GTGACCTATGCACCAGACGTCCACAGGTACAGGCCACAGGACCCCAAGAATGAGCTTACAGATCGGAAGAGCGGTTTCAG
chr17	41201088	41201127	BRCA1_355	-	GTGACCTATGCACCAGACGTGGTGCCTGTGCAGAGGCGAGGACACAATATTCTCTCCTGAGATCGGAAGAGCGGTTTCAG
chr17	41203030	41203069	BRCA1_356	-	GTGACCTATGCACCAGACGTGGGAGAACCCAGAGTTCAGACCAGCCTTTGTCTTACAAGATCGGAAGAGCGGTTTCAG
chr17	41209019	41209058	BRCA1_357	-	GTGACCTATGCACCAGACGTCTCCCTCAAGTTGACAAAAATCTACCCACCACCTCTGTAAGATCGGAAGAGCGGTTTCAG
chr17	41215300	41215339	BRCA1_358	-	GTGACCTATGCACCAGACGTGATGTTACAAACTAACCCAGAGATATTCATTAGTATATAAGATCGGAAGAGCGGTTTCAG
chr17	41215841	41215880	BRCA1_359	-	GTGACCTATGCACCAGACGTACTATTTCTCCCCTCTCCCTTTAACACCTCAGAATTCAGATCGGAAGAGCGGTTTCAG
chr17	41219575	41219614	BRCA1_360	-	GTGACCTATGCACCAGACGTAACTTTACGAATACTTGCATCTGCTGCATAAAACCCAGATCGGAAGAGCGGTTTCAG
chr17	41222895	41222934	BRCA1_361	-	GTGACCTATGCACCAGACGTCCATATGTATCTCCCTAATGACTAAGACTTAAACAACATTCAGATCGGAAGAGCGGTTTCAG
chr17	41226298	41226337	BRCA1_362	-	GTGACCTATGCACCAGACGTATCTGCTGTATTGGAACAAACACTTTGATTTTACTCTGAAAGATCGGAAGAGCGGTTTCAG
chr17	41228455	41228494	BRCA1_363	-	GTGACCTATGCACCAGACGTTCAATGTAAGATGCTGTGGTATCTGACATCTTTATTTATAGATCGGAAGAGCGGTTTCAG
chr17	41234371	41234410	BRCA1_364	-	GTGACCTATGCACCAGACGTTTGGCCAAACACTGATATCTTAAGCAAAATTTCTTCCCTTCCAGATCGGAAGAGCGGTTTCAG
chr17	41242911	41242950	BRCA1_365	-	GTGACCTATGCACCAGACGTTGTGTGTGTGCACATCGCGTGTGTGTGTGTCCTTTGCAAGATCGGAAGAGCGGTTTCAG
chr17	41243402	41243441	BRCA1_366	-	GTGACCTATGCACCAGACGTGAGGTTTTTGTGTTTGGCCAGCTATTATAGAAGTAGAGATCGGAAGAGCGGTTTCAG
chr17	41247813	41247852	BRCA1_367	-	GTGACCTATGCACCAGACGTAGTTTGCCAACTTAACAGGCACTGAAAAGAGAGTGGGTAGAGATCGGAAGAGCGGTTTCAG
chr17	41249211	41249250	BRCA1_368	-	GTGACCTATGCACCAGACGTGAGAACCTTTGCTATGAAGCTGGTATTTTCTATTTAGTAGATCGGAAGAGCGGTTTCAG
chr17	41251742	41251781	BRCA1_369	-	GTGACCTATGCACCAGACGTGAGTTTTTAAAGTATTTAATAAATTGCTGGATTCCCTTAGATCGGAAGAGCGGTTTCAG
chr17	41256835	41256874	BRCA1_370	-	GTGACCTATGCACCAGACGTAATATCCCAAGAATGACACTCAAGTGTCTGCCATGAAAACAGATCGGAAGAGCGGTTTCAG
chr17	41258423	41258462	BRCA1_371	-	GTGACCTATGCACCAGACGTTGTAATGATGCTAGTGTGAAGCAACACAGTAGGAAGAAAGATCGGAAGAGCGGTTTCAG
chr17	41267693	41267732	BRCA1_372	-	GTGACCTATGCACCAGACGTAGTGTGCTGTGCTGCTTATTAGCTTTTGTGTTTGTCCAGATCGGAAGAGCGGTTTCAG
chr17	41275984	41276023	BRCA1_373	-	GTGACCTATGCACCAGACGTACAAGAGTGATTAATTTGGGATTCCTATGATTATCTCCTAGATCGGAAGAGCGGTTTCAG
chr17	41243860	41243899	BRCA1_374	-	GTGACCTATGCACCAGACGTTCTAGTGAGGATGAAGAGCTTCCCTGCTTCCAACACTGTAGATCGGAAGAGCGGTTTCAG
chr17	41243891	41243930	BRCA1_375	-	GTGACCTATGCACCAGACGTCAAGAAATTAGAGTCCCTCAGAAGAGAACTTATCTAGTGAGAGATCGGAAGAGCGGTTTCAG
chr17	41244318	41244357	BRCA1_376	-	GTGACCTATGCACCAGACGTGTGATGAAAACATTCAAGCAGAAGTAGGTAGAAAACAGAGGATCGGAAGAGCGGTTTCAG
chr17	41244380	41244419	BRCA1_377	-	GTGACCTATGCACCAGACGTTATTAATGAAGTAGTTCAGACTAATGAAGTGGGCTCCAGATCGGAAGAGCGGTTTCAG
chr17	41244776	41244815	BRCA1_378	-	GTGACCTATGCACCAGACGTAAAGAATGAGTCTAATATCAAGCCTGTACAGACAGTTAATAGATCGGAAGAGCGGTTTCAG
chr17	41244869	41244908	BRCA1_379	-	GTGACCTATGCACCAGACGTGGAATGTGCAACATTCTCTGCCCACTCTGGTCCTTAAAGAGATCGGAAGAGCGGTTTCAG
chr17	41245234	41245273	BRCA1_380	-	GTGACCTATGCACCAGACGTCAAACCTGAAAGATCTGTAGAGAGTAGCAGTATTTTATTGGAGATCGGAAGAGCGGTTTCAG
chr17	41245358	41245397	BRCA1_381	-	GTGACCTATGCACCAGACGTACTTAAAGAATTTGCAATCCTAGCCTTCCAAGAGAAGAAAGATCGGAAGAGCGGTTTCAG
chr17	41245692	41245731	BRCA1_382	-	GTGACCTATGCACCAGACGTTAAAAAGAATAGGCTGAGGAGGAAGCTTCTACCAGGCAAGATCGGAAGAGCGGTTTCAG
chr17	41245847	41245886	BRCA1_383	-	GTGACCTATGCACCAGACGTGAATAAAACAAAAGGTGATTCTATTAGAATGAGAAAATAGATCGGAAGAGCGGTTTCAG
chr17	41246150	41246189	BRCA1_384	-	GTGACCTATGCACCAGACGTGAGTAATATTGAAGACAAAATTTTGGGAAAACCTATCGGAGATCGGAAGAGCGGTTTCAG
chr17	41246336	41246375	BRCA1_385	-	GTGACCTATGCACCAGACGTACTGTTAGGTTCTGATGACTCACATGATGGGGAGTCTGAAAGATCGGAAGAGCGGTTTCAG
chr19	1206863	1206902	STK11_386	-	GTGACCTATGCACCAGACGTGGGTCTGGAGTCCCAGCCGCCAGCCCTGAGTCCGCGGGTGAATCGGAAGAGCGGTTTCAG
chr19	1218366	1218405	STK11_387	-	GTGACCTATGCACCAGACGTGAGGACAGGGGTGTATCAGCCGACCCAACTCAGGATGATAGATCGGAAGAGCGGTTTCAG
chr19	1219273	1219312	STK11_388	-	GTGACCTATGCACCAGACGTAAAGACACACAGCTCAGGGGCGGCCCCACTCACAGCCAGATCGGAAGAGCGGTTTCAG
chr19	1220322	1220361	STK11_389	-	GTGACCTATGCACCAGACGTCAACACCCGCTCCTGGGCGGAGGCCTCCCTGCCCTCACAGATCGGAAGAGCGGTTTCAG
chr19	1220530	1220569	STK11_390	-	GTGACCTATGCACCAGACGTGCCGTGCGCCCTCAGGGAGTGCCTGGGAGGGGGCGCCAGATCGGAAGAGCGGTTTCAG
chr19	1221162	1221201	STK11_391	-	GTGACCTATGCACCAGACGTAGGGGAGGGAAGAAAGGCGTGGTCAAGGTGGTTGACAGATCGGAAGAGCGGTTTCAG
chr19	1221898	1221937	STK11_392	-	GTGACCTATGCACCAGACGTGCCGCGGAGGAGCCTGTGAGTGGGCACAGGCCTGAGACCAGATCGGAAGAGCGGTTTCAG
chr19	1222934	1222973	STK11_393	-	GTGACCTATGCACCAGACGTCCAGAAGCAGTGGCCGCTGTGAGGCTGCAGGTCGCCACCAGGGCGGTAGATCGGAAGAGCGGTTTCAG
chr19	1226403	1226442	STK11_394	-	GTGACCTATGCACCAGACGTGACCGCAAGTGTGGCCTGAGCTGAGGGGCGCAACCCAGAAAGATCGGAAGAGCGGTTTCAG
chr13	32890548	32890587	BRCA2_395	-	GTGACCTATGCACCAGACGTGATATTCCTCCAATGCTTGGTAAATAAGTCTGCAAAAACAGAGATCGGAAGAGCGGTTTCAG
chr13	32893164	32893203	BRCA2_396	-	GTGACCTATGCACCAGACGTAAAAAATCCCACCTTAGTTTTAAACAGTGACAGACAAATTAGATCGGAAGAGCGGTTTCAG
chr13	32900188	32900227	BRCA2_397	-	GTGACCTATGCACCAGACGTACAAAGCAAATCCCTTAGGTTATTTAAAAAACTGGCAAAAGATCGGAAGAGCGGTTTCAG
chr13	32900329	32900368	BRCA2_398	-	GTGACCTATGCACCAGACGTAAAAAGGGGAAAATTTGTTAAGTTTTATTTTATTAACATTAGATCGGAAGAGCGGTTTCAG
chr13	32900586	32900625	BRCA2_399	-	GTGACCTATGCACCAGACGTAGAAAATAGTTTATTTTATAGAAATCCCTGATCATAAGATCGGAAGAGCGGTTTCAG
chr13	32903530	32903569	BRCA2_400	-	GTGACCTATGCACCAGACGTAAAATTTATGTGATTGTATATATCACTAGAATGCAAAAAGATCGGAAGAGCGGTTTCAG
chr13	32905006	32905045	BRCA2_401	-	GTGACCTATGCACCAGACGTTATAGTTTAAATCACTAGTATAAAAACCTCAATGCACAAGATCGGAAGAGCGGTTTCAG
chr13	32906359	32906398	BRCA2_402	-	GTGACCTATGCACCAGACGTATAAAACAGAAGCACATTAATTTTTATAAGCCATATAATAGATCGGAAGAGCGGTTTCAG
chr13	32910352	32910391	BRCA2_403	-	GTGACCTATGCACCAGACGTAAACCAAAGTGACAAAATTAAGTACCATCAATCACATTAGATCGGAAGAGCGGTTTCAG
chr13	32918645	32918684	BRCA2_404	-	GTGACCTATGCACCAGACGTATATTCATATATGTTTTAAGGCAATAATACAGTTTTAGATCGGAAGAGCGGTTTCAG
chr13	32920914	32920953	BRCA2_405	-	GTGACCTATGCACCAGACGTATATTTATATTACATATTAGTTAAAATCAAGAGAATAAGATCGGAAGAGCGGTTTCAG
chr13	32928948	32928987	BRCA2_406	-	GTGACCTATGCACCAGACGTGAGAAAAATATAAGTTTATTGACTAGTACACATATAAATAGATCGGAAGAGCGGTTTCAG

chr13	32930515	32930554	BRCA2_407	-	GTGACCTATGCACCAGACGTATAAATACTTAGCAAAAATAAAATTGAAATTTAAAAAGCAAGATCGGAAGAGCGGTTTCAG
chr13	32931829	32931868	BRCA2_408	-	GTGACCTATGCACCAGACGTTAAACACACACAAAAAGAAAAACAATTTAAAGTAAACATAGATCGGAAGAGCGGTTTCAG
chr13	32936610	32936649	BRCA2_409	-	GTGACCTATGCACCAGACGTAAAAAGTAGAATATTATCATAAAAAACCACATAGGATGATACAGATCGGAAGAGCGGTTTCAG
chr13	32937266	32937305	BRCA2_410	-	GTGACCTATGCACCAGACGTAAACAAAAATGCATATTTTAGGAAGTGTGACTCTAGAATTAGATCGGAAGAGCGGTTTCAG
chr13	32944489	32944528	BRCA2_411	-	GTGACCTATGCACCAGACGTTAATAAATATATTGATTTAGTAGTTAAATATGTATTCAATAGATCGGAAGAGCGGTTTCAG
chr13	32945043	32945082	BRCA2_412	-	GTGACCTATGCACCAGACGTGTGTACACACACAAAAAAGTCACATATAACATTTCAAAGATCGGAAGAGCGGTTTCAG
chr13	32950757	32950796	BRCA2_413	-	GTGACCTATGCACCAGACGTAAAAAGTATTATAATTCACATAAACTGAAATTTCAAAGCAAGATCGGAAGAGCGGTTTCAG
chr13	32953404	32953443	BRCA2_414	-	GTGACCTATGCACCAGACGTTTAAAGATTTGGAATAAAAAAGCAATCAGAACAAAAAGTTAGATCGGAAGAGCGGTTTCAG
chr13	32953837	32953876	BRCA2_415	-	GTGACCTATGCACCAGACGTAAAGATGAGAAAGATGCAATGGAAGAAGTATTATCATTAGATCGGAAGAGCGGTTTCAG
chr13	32954094	32954133	BRCA2_416	-	GTGACCTATGCACCAGACGTCAAAACAAAAATTTCAACATATGGAGATTCATAAACTAACAGATCGGAAGAGCGGTTTCAG
chr13	32968776	32968815	BRCA2_417	-	GTGACCTATGCACCAGACGTAAAAAAAGAAAAAAGATGTTATTATAGATGTGTTAGATGAAAGATCGGAAGAGCGGTTTCAG
chr13	32970985	32971024	BRCA2_418	-	GTGACCTATGCACCAGACGTAAAGTGGAAAAGTGCCTTTATAAATTCGAAACCCACATATTAGATCGGAAGAGCGGTTTCAG
chr13	32972249	32972288	BRCA2_419	-	GTGACCTATGCACCAGACGTAAAGTGAACAGTATGCCTATCATAATTTAGTAGTAAACATAAAAGATCGGAAGAGCGGTTTCAG
chr13	32972553	32972592	BRCA2_420	-	GTGACCTATGCACCAGACGTTTTCTTTATGGGTGTTTCGTATTTGGTGCCACAACCTCCTTAGATCGGAAGAGCGGTTTCAG
chr13	32906731	32906770	BRCA2_421	-	GTGACCTATGCACCAGACGTCTGGAGATTTTGTCACTTCCACTCTCAAAGGGCTTCTGAAGATCGGAAGAGCGGTTTCAG
chr13	32907103	32907142	BRCA2_422	-	GTGACCTATGCACCAGACGTTCTTATTCTGAATATAGACTTTTTGATACCTGAAATGAAAGATCGGAAGAGCGGTTTCAG
chr13	32910845	32910884	BRCA2_423	-	GTGACCTATGCACCAGACGTGCTGTGCTGACTGATTTTGTATGATTTTGCCTCTAGAATAGATCGGAAGAGCGGTTTCAG
chr13	32911338	32911377	BRCA2_424	-	GTGACCTATGCACCAGACGTGCTGTGCTTACACTTTTGTCTTCTCGCAAGAACATAGATCGGAAGAGCGGTTTCAG
chr13	32911831	32911870	BRCA2_425	-	GTGACCTATGCACCAGACGTTTCAAACACTGACTTCTGATTCTTCTAATATAGTAGAAAGTATAGATCGGAAGAGCGGTTTCAG
chr13	32912324	32912363	BRCA2_426	-	GTGACCTATGCACCAGACGTGGCATTATTATTTTTTCACTTACAGTTTTATCATTATGAGATCGGAAGAGCGGTTTCAG
chr13	32912817	32912856	BRCA2_427	-	GTGACCTATGCACCAGACGTTCTGGTTTCTGATCAAAGAAATTTACAATTTTATTAAATGAGATCGGAAGAGCGGTTTCAG
chr13	32913310	32913349	BRCA2_428	-	GTGACCTATGCACCAGACGTATTATCACTTAAGAGCTTAGGTGGCACCACAGTCTCAATAAGATCGGAAGAGCGGTTTCAG
chr13	32913803	32913842	BRCA2_429	-	GTGACCTATGCACCAGACGTTTTTTGATCTTCAACTTCTCAATCTGGCTCAATACCAGATCGGAAGAGCGGTTTCAG
chr13	32914296	32914335	BRCA2_430	-	GTGACCTATGCACCAGACGTCAAGGTGATTTTTGAAAACCTTTCTCAATCCAGACATATAGATCGGAAGAGCGGTTTCAG
chr13	32914789	32914828	BRCA2_431	-	GTGACCTATGCACCAGACGTTCTCTTATCAACACGAGGAAGTATTTTTGATACATTTTGTAGATCGGAAGAGCGGTTTCAG
chr17	37856442	37856481	ERBB2_432	-	GTGACCTATGCACCAGACGTGCGGCTCCGGCCCATGGCTCCGGCTGGACCCGGCTGGGAAGATCGGAAGAGCGGTTTCAG
chr17	37863193	37863232	ERBB2_433	-	GTGACCTATGCACCAGACGTAGACAGATGGGTACAGAGGACTGGCGGGGGACCTTCTCAGATCGGAAGAGCGGTTTCAG
chr17	37863210	37863249	ERBB2_434	-	GTGACCTATGCACCAGACGTGTGCACACTGGCAGGAGAGCAGCATGGGTGAGAGGACACAGATCGGAAGAGCGGTTTCAG
chr17	37864524	37864563	ERBB2_435	-	GTGACCTATGCACCAGACGTGAAGCAGAGTGGGGCTGAAATGAGAACACTGCCACCCAGATCGGAAGAGCGGTTTCAG
chr17	37865521	37865560	ERBB2_436	-	GTGACCTATGCACCAGACGTAGCAATGATCAGAGGACCCCTTCCCTTCTGTCACCTTCTAGATCGGAAGAGCGGTTTCAG
chr17	37866016	37866055	ERBB2_437	-	GTGACCTATGCACCAGACGTAACCAGAGACAGGCAGTGAGAGAGATGTCTAACAGCGAGAAGATCGGAAGAGCGGTTTCAG
chr17	37866289	37866328	ERBB2_438	-	GTGACCTATGCACCAGACGTAAGGGCAGGATGAGGGCTGAGTGGCGCCCTGGGCACCAGAAGATCGGAAGAGCGGTTTCAG
chr17	37866543	37866582	ERBB2_439	-	GTGACCTATGCACCAGACGTAGGTGGCTGGCTTCACTGTGCTGTTTTGCCCTGGTGTGCAGATCGGAAGAGCGGTTTCAG
chr17	37868131	37868170	ERBB2_440	-	GTGACCTATGCACCAGACGTGAGGAACATGTAGCCACATACCCCTGCCCTTCTGCAACAGATCGGAAGAGCGGTTTCAG
chr17	37868525	37868564	ERBB2_441	-	GTGACCTATGCACCAGACGTGGGGGTGGGTGGGCAAGGGCCGCTGCTCAGCCTTCAACAGATCGGAAGAGCGGTTTCAG
chr17	37871489	37871528	ERBB2_442	-	GTGACCTATGCACCAGACGTACAGGAGAGGATCAGCAGGGCCAGGAACAGGGTGGACATCAGATCGGAAGAGCGGTTTCAG
chr17	37871649	37871688	ERBB2_443	-	GTGACCTATGCACCAGACGTAGGGTGAGATTAAGGAGTGGGGACAGGACAAGGACTCCAGATCGGAAGAGCGGTTTCAG
chr17	37871943	37871982	ERBB2_444	-	GTGACCTATGCACCAGACGTAAGTGGGGACCTTACCACGGACCCCTTCCCGGTACAGCAAAGATCGGAAGAGCGGTTTCAG
chr17	37872504	37872543	ERBB2_445	-	GTGACCTATGCACCAGACGTGAGGAAGGGACCCGAGGGGACTTTTAGGGGAGGGCCAGGAGATCGGAAGAGCGGTTTCAG
chr17	37872718	37872757	ERBB2_446	-	GTGACCTATGCACCAGACGTGGACAGTGGTGAAGGGCTGAGAGGAGCCCATGCACCCAGATCGGAAGAGCGGTTTCAG
chr17	37873523	37873562	ERBB2_447	-	GTGACCTATGCACCAGACGTGAAAAGATTTGTGGGGGCTGGCCTGACACCCCAAGATCGGAAGAGCGGTTTCAG
chr17	37875990	37876029	ERBB2_448	-	GTGACCTATGCACCAGACGTAACAGTCTCATCAACAATCTGGGAACCCCTTGGGAAGATCGGAAGAGCGGTTTCAG
chr17	37879522	37879561	ERBB2_449	-	GTGACCTATGCACCAGACGTAAGCCAGGGTCAGGGATTGAGGGCTAGTTTGGGGTGGGAGAGATCGGAAGAGCGGTTTCAG
chr17	37879741	37879780	ERBB2_450	-	GTGACCTATGCACCAGACGTGGGGTGGTGGGTGAGTGCAGGGGGCCGGTGCAGACCCCAAGATCGGAAGAGCGGTTTCAG
chr17	37880115	37880154	ERBB2_451	-	GTGACCTATGCACCAGACGTAGAGGAGGATAGTGAAGAGCGTGGGCTGGATCTTAAGATCGGAAGAGCGGTTTCAG
chr17	37880929	37880968	ERBB2_452	-	GTGACCTATGCACCAGACGTGGGTACGCTGAGAGGGTATGGGAGACCACACACCCCAAGATCGGAAGAGCGGTTTCAG
chr17	37881252	37881291	ERBB2_453	-	GTGACCTATGCACCAGACGTAAGCACCCATGTAGACCTTCTGGGAGGGCCCTGGGCCTGGCAGATCGGAAGAGCGGTTTCAG
chr17	37881530	37881569	ERBB2_454	-	GTGACCTATGCACCAGACGTAGAAGAGGAAGTCCCTCAACTGTGTGTTGTTGGGAGGTTGGAGATCGGAAGAGCGGTTTCAG
chr17	37881910	37881949	ERBB2_455	-	GTGACCTATGCACCAGACGTGACAGGGTCAGGAGTGGGAGGGCCAGAGGGAGCTTTAGTGAATCGGAAGAGCGGTTTCAG
chr17	37882765	37882804	ERBB2_456	-	GTGACCTATGCACCAGACGTAGGGAGGTCAGCATGCTAGTCCCAGGCCCTGTGTGCTTGCAGATCGGAAGAGCGGTTTCAG
chr17	37883018	37883057	ERBB2_457	-	GTGACCTATGCACCAGACGTAGGAGGACGATGGTGGCCCTCCCAAGCCAGATCGAGATCGGAAGAGCGGTTTCAG
chr17	37883498	37883537	ERBB2_458	-	GTGACCTATGCACCAGACGTGAAAAGAAAGTTCATGATGGGGTCACTACCGATCTGGGATAGATCGGAAGAGCGGTTTCAG
chr17	37883892	37883931	ERBB2_459	-	GTGACCTATGCACCAGACGTAAGAGAAGGTGACCCATTAGGGGAAGGAACCCCGGTGTCTAGATCGGAAGAGCGGTTTCAG
chr7	140434347	140434386	BRAF_460	-	GTGACCTATGCACCAGACGTTGAGAGAGTTCAGGAGAGTAGCAACAAAAGAAAATAAATAGATCGGAAGAGCGGTTTCAG
chr7	140439562	140439601	BRAF_461	-	GTGACCTATGCACCAGACGTGCTTCATGCTATCCAAAGAACAGACTAACATTATAGACAGATCGGAAGAGCGGTTTCAG
chr7	140449037	140449076	BRAF_462	-	GTGACCTATGCACCAGACGTACCACGCTTTGGTGTATTATTTACCCTCTATATACAAGGCAGATCGGAAGAGCGGTTTCAG
chr7	140453025	140453064	BRAF_463	-	GTGACCTATGCACCAGACGTAGGCTATTTTCCACTGATTTAAATTTTGGCCCTGAGATGAGATCGGAAGAGCGGTTTCAG
chr7	140453937	140453976	BRAF_464	-	GTGACCTATGCACCAGACGTTGAAATTTGTCTGCGAAGTTGAAAACATCCTGACTTTTTAGATCGGAAGAGCGGTTTCAG



chr7	140476662	140476701	BRAF_465	-	GTGACCTATGCACCAGACGTTTCGTAAATGTCTTGTAATATTTTTGAAGACCATTGAAGATCGGAAGAGCGGTTTCAG
chr7	140477741	140477780	BRAF_466	-	GTGACCTATGCACCAGACGTTGTAATCTCTTTCCAGAGAAAGAGTTATTTTTATTAAGATCGGAAGAGCGGTTTCAG
chr7	140481326	140481365	BRAF_467	-	GTGACCTATGCACCAGACGTAATGTGGTGACATTGTGACAAGTCATAATAGGATATGTTTAGATCGGAAGAGCGGTTTCAG
chr7	140482771	140482810	BRAF_468	-	GTGACCTATGCACCAGACGTATGATATCTTTTTCTCTGAATCTTTCTTCTTAGAAGTAGATCGGAAGAGCGGTTTCAG
chr7	140487298	140487337	BRAF_469	-	GTGACCTATGCACCAGACGTATTTTCAGGTTTTTTAAAAAAGCAAGGAAACTGCAATTTGCAGATCGGAAGAGCGGTTTCAG
chr7	140494058	140494097	BRAF_470	-	GTGACCTATGCACCAGACGTAGCATTGCTAGAAGTAAAAAACCACAGTATGTATCTTTAGATCGGAAGAGCGGTTTCAG
chr7	140500112	140500151	BRAF_471	-	GTGACCTATGCACCAGACGTTCTGCTCTTTGGCGACATGCTACTTTGAACCGCTTTCTAGATCGGAAGAGCGGTTTCAG
chr7	140501162	140501201	BRAF_472	-	GTGACCTATGCACCAGACGTCAAAAATATCTCTTTTCTACCTACCATTTTACACTTAATAGATCGGAAGAGCGGTTTCAG
chr7	140507710	140507749	BRAF_473	-	GTGACCTATGCACCAGACGTTTACATTTTTTTTTGAAATGTCAAAAATGTTTAGATTTAAGATCGGAAGAGCGGTTTCAG
chr7	140508642	140508681	BRAF_474	-	GTGACCTATGCACCAGACGTTATGTGACGTGAAATTTTGTAAAAAGAAAATCACACATAGATCGGAAGAGCGGTTTCAG
chr7	140534359	140534398	BRAF_475	-	GTGACCTATGCACCAGACGTTTAATATCACCATTTTGTCTTTTCTTTGTATTTTTCAGAAGATCGGAAGAGCGGTTTCAG
chr7	140549861	140549900	BRAF_476	-	GTGACCTATGCACCAGACGTGAGTATCATCTAGTAAATTTTAAAAAGAAAAAATGAAAGATCGGAAGAGCGGTTTCAG
chr7	140624316	140624355	BRAF_477	-	GTGACCTATGCACCAGACGTGCGCCACCCTGCGCCTCCCGACTCCGGCTCGCGGCTAGATCGGAAGAGCGGTTTCAG
chr4	153243983	153244022	FBXW7_478	-	GTGACCTATGCACCAGACGTAGATGAATTTGTCCAATTGTGTAGACGATATACTCCCTGCAGATCGGAAGAGCGGTTTCAG
chr4	153245286	153245325	FBXW7_479	-	GTGACCTATGCACCAGACGTCTCACCTTTTCGTTTTGTTTCATTAATAAGATGAGATCATTATAGATCGGAAGAGCGGTTTCAG
chr4	153247108	153247147	FBXW7_480	-	GTGACCTATGCACCAGACGTTTATCTCTCCCTTAATGCTCTCCTGATGAATCATAAGGTAGATCGGAAGAGCGGTTTCAG
chr4	153249310	153249349	FBXW7_481	-	GTGACCTATGCACCAGACGTATCTCTCATGGTGGGACTTCTTCTCTTATTATTGGTGAAGATCGGAAGAGCGGTTTCAG
chr4	153250774	153250813	FBXW7_482	-	GTGACCTATGCACCAGACGTTCTTCTCATCTTCAAAAGTCAATAATTTGTGATATCAAGATCGGAAGAGCGGTTTCAG
chr4	153251834	153251873	FBXW7_483	-	GTGACCTATGCACCAGACGTTCTGCACAATGTAACAGAAACCCTTAATCAGTGTTAGTACAGATCGGAAGAGCGGTTTCAG
chr4	153253698	153253737	FBXW7_484	-	GTGACCTATGCACCAGACGTAATTCATAGAGAATATGTTTATCTTTGAAAAGCAGAGAGATCGGAAGAGCGGTTTCAG
chr4	153258904	153258943	FBXW7_485	-	GTGACCTATGCACCAGACGTTCAATTACATCTTTCATTGGGTGTTATTGAAATATATAACAGATCGGAAGAGCGGTTTCAG
chr4	153268032	153268071	FBXW7_486	-	GTGACCTATGCACCAGACGTTAAACATAGTACTTGAATGCCTCACTTAATTGCTGCAAAAAGATCGGAAGAGCGGTTTCAG
chr4	153271144	153271183	FBXW7_487	-	GTGACCTATGCACCAGACGTATAATGATTATCTCATGATCTCAGTTTTTTAGAGTTGAGATCGGAAGAGCGGTTTCAG
chr4	153273572	153273611	FBXW7_488	-	GTGACCTATGCACCAGACGTTGTTTTCTTCTATGCTATGTGATTGTGTGTGATGCTGAGATCGGAAGAGCGGTTTCAG
chr4	153303291	153303330	FBXW7_489	-	GTGACCTATGCACCAGACGTACATTTGAAAATATGAATGTTTATTAAAGTGAAGTACCAGATCGGAAGAGCGGTTTCAG
chr4	153332405	153332444	FBXW7_490	-	GTGACCTATGCACCAGACGTTCAATATATTGTTAACCTGAGAAACTTTACATATCTATTAGATCGGAAGAGCGGTTTCAG
chr3	37034989	37035028	MLH1_491	-	GTGACCTATGCACCAGACGTGAAGAGCCAAGGAAACGCTTAGATGCTCAACGGAAGTGCCAGATCGGAAGAGCGGTTTCAG
chr3	37038060	37038099	MLH1_492	-	GTGACCTATGCACCAGACGTAACAGAAAATAATTTATCAGTCTGCAACTACTCTAATGTAGATCGGAAGAGCGGTTTCAG
chr3	37042396	37042435	MLH1_493	-	GTGACCTATGCACCAGACGTCCAAAAGATGAGTAAATAATCATGTTACTATTTTTCCAAGATCGGAAGAGCGGTTTCAG
chr3	37045842	37045881	MLH1_494	-	GTGACCTATGCACCAGACGTAAAGAAAATAGACTAAAGAAAAAAGTACTGCTGGGTACAGATCGGAAGAGCGGTTTCAG
chr3	37048432	37048471	MLH1_495	-	GTGACCTATGCACCAGACGTAATAACAAATTAATATCCAGTAGAGAGATAGATACTAAAGATCGGAAGAGCGGTTTCAG
chr3	37050255	37050294	MLH1_496	-	GTGACCTATGCACCAGACGTGATTGATTTTTCTTGTAATTCATAGAAGTACTTGAATAAGATCGGAAGAGCGGTTTCAG
chr3	37053261	37053300	MLH1_497	-	GTGACCTATGCACCAGACGTAAAAAAGAGTAAGAAAAGATTTGCCAAAAACACACAGATCGGAAGAGCGGTTTCAG
chr3	37053491	37053491	MLH1_498	-	GTGACCTATGCACCAGACGTAACAGCAGAGACACAAGGATTTATTGTTCTCATGGCTGAGAGATCGGAAGAGCGGTTTCAG
chr3	37055873	37055912	MLH1_499	-	GTGACCTATGCACCAGACGTGAGGATTTGAAAGCTTTTTGAAAATACTCAAAACTCAAAACAGATCGGAAGAGCGGTTTCAG
chr3	37058947	37058986	MLH1_500	-	GTGACCTATGCACCAGACGTA AAAAGCAACCAAGTTCAAAACTGTCTGAGGGTGAGAGATCGGAAGAGCGGTTTCAG
chr3	37061751	37061790	MLH1_501	-	GTGACCTATGCACCAGACGTAATAAGAGAGAACAATTACCTTAGATAGTGGGAGGGGAGAGATCGGAAGAGCGGTTTCAG
chr3	37070225	37070264	MLH1_502	-	GTGACCTATGCACCAGACGTGAAAAGGAAGTGCAGATCATTATTATCTTGTTTTTAAACAGATCGGAAGAGCGGTTTCAG
chr3	37081627	37081666	MLH1_503	-	GTGACCTATGCACCAGACGTA AAAAATAAAACCAAAAACAGGTAAGTAATAGAATCCTACAGATCGGAAGAGCGGTTTCAG
chr3	37083709	37083748	MLH1_504	-	GTGACCTATGCACCAGACGTA AATGAAGTGACTTTAAGGAAAAGTGAATTCATGCTTGAAGATCGGAAGAGCGGTTTCAG
chr3	37088960	37088999	MLH1_505	-	GTGACCTATGCACCAGACGTGAAAGAAACATGAAAGCAAGCTTTAACGGAGCATCCAAAAGATCGGAAGAGCGGTTTCAG
chr3	37089958	37089997	MLH1_506	-	GTGACCTATGCACCAGACGTGAAAAGGACAAGGGAACAAGAAATAATGCTGTCATAGTTAGATCGGAAGAGCGGTTTCAG
chr3	37090345	37090384	MLH1_507	-	GTGACCTATGCACCAGACGTGAAATTC AATACCTCAAAATAGGTACGAATTTAAACATTCAGATCGGAAGAGCGGTTTCAG
chr3	37091927	37091966	MLH1_508	-	GTGACCTATGCACCAGACGT CATTAGATGTCATAAGCCTCCCTGTTTGCATCCCAACATAAGATCGGAAGAGCGGTTTCAG
chr2	47630281	47630320	MSH2_509	-	GTGACCTATGCACCAGACGTTCTCCTCGTTGTAAGAAAATGCGCGACCCACCCAGATCGGAAGAGCGGTTTCAG
chr2	47635529	47635529	MSH2_510	-	GTGACCTATGCACCAGACGTAAAAAAGTACATTACAGATTTGAGATTTACATGTTCAAGAGATCGGAAGAGCGGTTTCAG
chr2	47639503	47639542	MSH2_511	-	GTGACCTATGCACCAGACGTAGAAATAGTTTAAACTACTATGAGAAAAGGAATAAGAAAAGATCGGAAGAGCGGTTTCAG
chr2	47641358	47641397	MSH2_512	-	GTGACCTATGCACCAGACGTGAATTTAAAAATCGAAGATTTCTATACCACTGGATCCAGTAGATCGGAAGAGCGGTTTCAG
chr2	47643385	47643424	MSH2_513	-	GTGACCTATGCACCAGACGTAAAAATAAAATAGAAAAGATGGCAAGCTCATTAGTGA AAAAGATCGGAAGAGCGGTTTCAG
chr2	47672637	47672676	MSH2_514	-	GTGACCTATGCACCAGACGTG TAGTAAAAAACAATAAAAAGATCTCATTTTACAGAAAAGATCGGAAGAGCGGTTTCAG
chr2	47690120	47690159	MSH2_515	-	GTGACCTATGCACCAGACGTAACAAAGTGACAAAATCCTATAAATGGGTAAAGACAGAGATCGGAAGAGCGGTTTCAG
chr2	47693747	47693786	MSH2_516	-	GTGACCTATGCACCAGACGTGAAAGAAAAGATTTCCATAAATACCTACTACCAAGATCGGAAGAGCGGTTTCAG
chr2	47702114	47702153	MSH2_517	-	GTGACCTATGCACCAGACGTATAAAAAACAGAAAATGTACACAGGAATACTGAATAATAAAAAGATCGGAAGAGCGGTTTCAG
chr2	47703456	47703495	MSH2_518	-	GTGACCTATGCACCAGACGTAATTATATCAGAAAAGCAAGATTTTAAACTTCTTTCTGCTAAGATCGGAAGAGCGGTTTCAG
chr2	47705361	47705400	MSH2_519	-	GTGACCTATGCACCAGACGTTAATTACATGAAATTTCCCATCACATAAAATGTGGTAACAAAGATCGGAAGAGCGGTTTCAG
chr2	47707785	47707824	MSH2_520	-	GTGACCTATGCACCAGACGTTTTGGGGAAGCGTGAGGGGACAGCATGAGAAGAGACAGCAAGATCGGAAGAGCGGTTTCAG
chr2	47709868	47709907	MSH2_521	-	GTGACCTATGCACCAGACGTTTGAATGTTCCCATGATTAATAACTTTTTCTAAAAAGATCGGAAGAGCGGTTTCAG
chr18	48573367	48573406	SMAD4_522	-	GTGACCTATGCACCAGACGTTTTCCTTTTAAATCAAATGTCTCCAATTTCTGAAGCAAGATCGGAAGAGCGGTTTCAG

chr18	48575615	48575654	SMAD4_523	-	GTGACCTATGCACCAGACGTTAAAGGGGAAAACAATGAAACATTAATCATTACAATGAAAGATCGGAAGAGCGGTTTCAG
chr18	48584445	48584484	SMAD4_524	-	GTGACCTATGCACCAGACGTAAGAAGACATTAACATGGTACATTCATAGATGCATCTTAAGATCGGAAGAGCGGTTTCAG
chr18	48584660	48584699	SMAD4_525	-	GTGACCTATGCACCAGACGTAGGCCACATGGGTTAATTTGCTTTTATAAAGGCTGCCTAAGATCGGAAGAGCGGTTTCAG
chr18	48586186	48586225	SMAD4_526	-	GTGACCTATGCACCAGACGTGACAACAAAATTCATTTTTATTACTAAAAGTTGTCTAAGATCGGAAGAGCGGTTTCAG
chr18	48591743	48591782	SMAD4_527	-	GTGACCTATGCACCAGACGTTAAATGGGAAAGAACATCCTCCATGAGAAAGATATAAGGAGATCGGAAGAGCGGTTTCAG
chr18	48593339	48593378	SMAD4_528	-	GTGACCTATGCACCAGACGTA AAAAGAAAATTCATTTTTATCTTGATAAGTATTTAAATAGATCGGAAGAGCGGTTTCAG
chr18	48602958	48602997	SMAD4_529	-	GTGACCTATGCACCAGACGTA AAAACATTTACACTATGAGTTCATAAAGAAAAATTCATAGATCGGAAGAGCGGTTTCAG
chr18	48604576	48604615	SMAD4_530	-	GTGACCTATGCACCAGACGTAGATTTGGAAGACATCAGAGGGACAGGGTATCTCTCCAGATCGGAAGAGCGGTTTCAG
chr9	22005936	22005975	CDKN2B_531	-	GTGACCTATGCACCAGACGTCCCAGCCGCCACAACGACTTTATTTTCTTACCCAATTCAGATCGGAAGAGCGGTTTCAG
chr9	22008666	22008705	CDKN2B_532	-	GTGACCTATGCACCAGACGTTAGATTTGTACAGGAGTCTCCGTTGGCCGGAGGTGTGCATAGATCGGAAGAGCGGTTTCAG
chr9	22008747	22008786	CDKN2B_533	-	GTGACCTATGCACCAGACGTCCCCAGGCCCTCGCCGGCAGGGGGCCGCGCAACGCGGGGCGAGATCGGAAGAGCGGTTTCAG
chr4	1800931	1800970	FGFR3_534	-	GTGACCTATGCACCAGACGTGATGGCAACCATGAGGCAGGCACCCCAACCCCGGCACAGATCGGAAGAGCGGTTTCAG
chr4	1801424	1801463	FGFR3_535	-	GTGACCTATGCACCAGACGTGAGATGGCCGCAACCAATGCCCAACCTGCCCCAGGAGGCAGATCGGAAGAGCGGTTTCAG
chr4	1803044	1803083	FGFR3_536	-	GTGACCTATGCACCAGACGTAGGTGCGTGTGAAGGCCATGACCCGAGTGGGAGCAGAGGCAGATCGGAAGAGCGGTTTCAG
chr4	1803297	1803336	FGFR3_537	-	GTGACCTATGCACCAGACGTACCGGGGGCGGTGAGTGAGCGGAGGCAGCAACCACCCGCGCAGATCGGAAGAGCGGTTTCAG
chr4	1805369	1805408	FGFR3_538	-	GTGACCTATGCACCAGACGTAGACGAGAGCGATAGGCGAGCCAGCACCGCCCTCGCGGAGATCGGAAGAGCGGTTTCAG
chr4	1806007	1806046	FGFR3_539	-	GTGACCTATGCACCAGACGTATGGGCGTTGAGGCTGGCCTGGCCGCCCCCCACCGGGGAGATCGGAAGAGCGGTTTCAG
chr4	1806501	1806540	FGFR3_540	-	GTGACCTATGCACCAGACGTGACGAGGGCCAGGTTGGCGCCGCGTGGCGCAGAGGGCGTGAGATCGGAAGAGCGGTTTCAG
chr4	1807032	1807071	FGFR3_541	-	GTGACCTATGCACCAGACGTAGGCAGAGGGACCATGAGTGTGCAAACCTCGCCACTCTCAAGATCGGAAGAGCGGTTTCAG
chr4	1807236	1807275	FGFR3_542	-	GTGACCTATGCACCAGACGTAGCGGGGGGCTGTGTGACGGCGGCGGGCGGCCCCAGCCAGATCGGAAGAGCGGTTTCAG
chr4	1807427	1807466	FGFR3_543	-	GTGACCTATGCACCAGACGTGGGCTCCTCAGACGGGCTGCCAGGCCAGGAGGGCCGCCAGATCGGAAGAGCGGTTTCAG
chr4	1807728	1807767	FGFR3_544	-	GTGACCTATGCACCAGACGTGGTGGGAGGCAGGGCTGAAGCCTCTCCACCTCTCCCGCTAGATCGGAAGAGCGGTTTCAG
chr4	1807934	1807973	FGFR3_545	-	GTGACCTATGCACCAGACGTGTTGGGAGGCGGCTGTTGGCGCCAGGCGTCTACTGGCATGAGATCGGAAGAGCGGTTTCAG
chr4	1808223	1808262	FGFR3_546	-	GTGACCTATGCACCAGACGTAGGTGAGGTGAGGCTGTCTGAGACTCCAGGACAGACAGATCGGAAGAGCGGTTTCAG
chr4	1808506	1808545	FGFR3_547	-	GTGACCTATGCACCAGACGTGGCGCTCAGGAGTGAGCCCGCCGCTTCCCGCTTATTTCGAGATCGGAAGAGCGGTTTCAG
chr4	1808793	1808832	FGFR3_548	-	GTGACCTATGCACCAGACGTGAGGCGGGGTGAGCGCTGTGCCACCGAGCCCTCTTCGCAAGATCGGAAGAGCGGTTTCAG
chr2	48010323	48010362	MSH6_549	-	GTGACCTATGCACCAGACGTGGCAAGGCCAACCGTTCTGTGCGACGGAGCTCCTAAAAGAGATCGGAAGAGCGGTTTCAG
chr2	48018016	48018055	MSH6_550	-	GTGACCTATGCACCAGACGTAAGGAAATACATAACTAGTTAATTTGGTCAAGTTTCCAGATCGGAAGAGCGGTTTCAG
chr2	48025700	48025739	MSH6_551	-	GTGACCTATGCACCAGACGTAGGAAAGAGTATTTAAAAACAATCAAATTTGGAAAACAGATCGGAAGAGCGGTTTCAG
chr2	48030509	48030548	MSH6_552	-	GTGACCTATGCACCAGACGTAGCGGGTACAGGCTGAGGCTTATGAGCCCTCATCGTTTTGGGGTTTTATCAGATCGGAAGAGCGGTTTCAG
chr2	48031999	48032038	MSH6_553	-	GTGACCTATGCACCAGACGTGGGAGGAAAAGGTCCTTTTATGACTGGTAGTAACAGTTTCAAGATCGGAAGAGCGGTTTCAG
chr2	48032707	48032746	MSH6_554	-	GTGACCTATGCACCAGACGTAAAAAATCACAAATGAATACTCATTTTGCAAATCATATTAAGATCGGAAGAGCGGTTTCAG
chr2	48033293	48033332	MSH6_555	-	GTGACCTATGCACCAGACGTAAAAATATGCATAAGGAAGTAACCAAAGGAATTA AAAACAAAGATCGGAAGAGCGGTTTCAG
chr2	48033541	48033580	MSH6_556	-	GTGACCTATGCACCAGACGTAAAAATATTGAGTACATGTGCTAGCAAGAGAAGTGCCCAAGATCGGAAGAGCGGTTTCAG
chr2	48026124	48026163	MSH6_557	-	GTGACCTATGCACCAGACGTTTTAGAATTTTGAGGGGCAAGAAAGCTCTCAAAGTATTCAGATCGGAAGAGCGGTTTCAG
chr2	48026548	48026587	MSH6_558	-	GTGACCTATGCACCAGACGTGAGTCTCAGTCTGTTCCACTCGTCTACTTTTATAGCCCTTAGATCGGAAGAGCGGTTTCAG
chr2	48026972	48027011	MSH6_559	-	GTGACCTATGCACCAGACGTGCATCCCAAACCTGGGAGCCGGGTATCAGACCTTCTGAAAGATCGGAAGAGCGGTTTCAG
chr2	48027396	48027435	MSH6_560	-	GTGACCTATGCACCAGACGTCTTACAAAAGGAGTATGGCAAGTATCAACCCCTCTCTAGTAGATCGGAAGAGCGGTTTCAG
chr2	48027820	48027859	MSH6_561	-	GTGACCTATGCACCAGACGTCCCTCGGTTCAATTCTACAGTCAAATCAGGAAAACGACCAGATCGGAAGAGCGGTTTCAG
chr3	138374181	138374220	PIK3CB_562	-	GTGACCTATGCACCAGACGTTCCGCTCAATGATTTTGGTTCATTTTCATTTAGATCGGAAGAGCGGTTTCAG
chr3	138374934	138374973	PIK3CB_563	-	GTGACCTATGCACCAGACGTACTTTTTCTCTCTGGACTTTGGCCATTGAGCTCAAAGATCGGAAGAGCGGTTTCAG
chr3	138376482	138376521	PIK3CB_564	-	GTGACCTATGCACCAGACGTCCCTTGTGCCAAGGCTGAACACTTCTAACATTTTCTTATCAGATCGGAAGAGCGGTTTCAG
chr3	138382698	138382737	PIK3CB_565	-	GTGACCTATGCACCAGACGTCTCAGGATCTGCCAAGGGCCTAGTAATGCTATTTCTTAAAGATCGGAAGAGCGGTTTCAG
chr3	138383828	138383867	PIK3CB_566	-	GTGACCTATGCACCAGACGTTCTGTTAATTTATCATTTTTCTGTACAACAGCCAAACAAGATCGGAAGAGCGGTTTCAG
chr3	138400759	138400798	PIK3CB_567	-	GTGACCTATGCACCAGACGTGCTTTTTTTTTTTTTCAGTCTAATGCTTTCCATAGCAAAGATCGGAAGAGCGGTTTCAG
chr3	138402470	138402509	PIK3CB_568	-	GTGACCTATGCACCAGACGTAGATTTTTAACATCAAATTTTACATTTTTCATTTTGTATAGATCGGAAGAGCGGTTTCAG
chr3	138403417	138403456	PIK3CB_569	-	GTGACCTATGCACCAGACGTGTGCTTTGCGCAGTAATCTCCTATGAATAGCAAGCAGAAAGATCGGAAGAGCGGTTTCAG
chr3	138407667	138407706	PIK3CB_570	-	GTGACCTATGCACCAGACGTGTTTTATTTATTCATTTTTCTTTTTTTGACAGACAACGTAGATCGGAAGAGCGGTTTCAG
chr3	138409792	138409831	PIK3CB_571	-	GTGACCTATGCACCAGACGTTATATTTTACTTTGAGCCACCAGGTGCTTTAGTAACATAGATCGGAAGAGCGGTTTCAG
chr3	138413578	138413617	PIK3CB_572	-	GTGACCTATGCACCAGACGTCAAGTGGTTTTCTTTGGGGCAAGGAATAACTTGGGTGGGTAGATCGGAAGAGCGGTTTCAG
chr3	138417699	138417738	PIK3CB_573	-	GTGACCTATGCACCAGACGTATCGTTCTATAACTTTTTGGGTGATGGTACTTTGGTTAGATCGGAAGAGCGGTTTCAG
chr3	138423235	138423274	PIK3CB_574	-	GTGACCTATGCACCAGACGTAGATTTTTAAATGGCCCTTTCTTATGAGTTGTGCACATTAGATCGGAAGAGCGGTTTCAG
chr3	138425951	138425990	PIK3CB_575	-	GTGACCTATGCACCAGACGTTATTTAAAGGACCTCTATGCATGAAATGATTGAATGATCAAGATCGGAAGAGCGGTTTCAG
chr3	138431000	138431039	PIK3CB_576	-	GTGACCTATGCACCAGACGTCAATCTTATCCTTAGTGTTAAAGCATAACTAACTTTGGCAGATCGGAAGAGCGGTTTCAG
chr3	138433260	138433299	PIK3CB_577	-	GTGACCTATGCACCAGACGTACCAACTCTGAGGATGTTTTATATAACGGAATAATTTAGATCGGAAGAGCGGTTTCAG
chr3	138452153	138452192	PIK3CB_578	-	GTGACCTATGCACCAGACGTAAAGATTTGAAATTTGCCATCCGCTCCAGTATTTGAATAAGATCGGAAGAGCGGTTTCAG
chr3	138453426	138453465	PIK3CB_579	-	GTGACCTATGCACCAGACGTTTTCTGAACCTTTAGTAAACCCCAAAAGCATGTGATTTGTAGATCGGAAGAGCGGTTTCAG
chr3	138477965	138478004	PIK3CB_580	-	GTGACCTATGCACCAGACGTAGGTATAATTTCTATGTGTTTAGCATACTGTGTCACTTGGAGATCGGAAGAGCGGTTTCAG

chr5	67522454	67522493	PIK3R1_581	-	GTGACCTATGCACCAGACGCTGTGCTACCATGCAACAGTTGAGCCTGGTTGTACAGAGCAGAGATCGGAAGAGCGGTTTCAG
chr5	67569168	67569207	PIK3R1_582	-	GTGACCTATGCACCAGACGCTCAAATCCCACCATTGTATTTAATTTGGATAGTTGAATGCAGATCGGAAGAGCGGTTTCAG
chr5	67569717	67569756	PIK3R1_583	-	GTGACCTATGCACCAGACGTAACAGACCACAGACCATGTATGCAAAACACAGCTCTCTGAGATCGGAAGAGCGGTTTCAG
chr5	67575380	67575419	PIK3R1_584	-	GTGACCTATGCACCAGACGTATTTAAGAAATATTTCCAGACATTTATTTATAGAATACATAGATCGGAAGAGCGGTTTCAG
chr5	67576306	67576345	PIK3R1_585	-	GTGACCTATGCACCAGACGTAAAAAAGAAAGAAATGAGTAAGCGACTACTTCCAGATCGGAAGAGCGGTTTCAG
chr5	67576705	67576744	PIK3R1_586	-	GTGACCTATGCACCAGACGTGAGAGTTTATTAGAAACCTTTTCCCTAAAAGCAAACATCATAGATCGGAAGAGCGGTTTCAG
chr5	67584514	67584553	PIK3R1_587	-	GTGACCTATGCACCAGACGTCCCTTTGAAATGCCTGTATCCGCACAAATGAAAAAAGATCGGAAGAGCGGTTTCAG
chr5	67586507	67586546	PIK3R1_588	-	GTGACCTATGCACCAGACGTGTTTCTTGGCTGAGCTCAGTTATAAGAAAAGAGTCCGGCAGATCGGAAGAGCGGTTTCAG
chr5	67588037	67588076	PIK3R1_589	-	GTGACCTATGCACCAGACGTAAAAGAAAAAGTTGTTCCGCAATCCCACTACATTAGAAGTATAGATCGGAAGAGCGGTTTCAG
chr5	67588879	67588918	PIK3R1_590	-	GTGACCTATGCACCAGACGTAAACAAAAAATGCTCATCTTAAGGTTTGTAGTACCACAGAGATCGGAAGAGCGGTTTCAG
chr5	67589081	67589120	PIK3R1_591	-	GTGACCTATGCACCAGACGTAATATAAAAAATAAGGTATTAACATTTTGAATAAGGAAAAGATCGGAAGAGCGGTTTCAG
chr5	67589487	67589526	PIK3R1_592	-	GTGACCTATGCACCAGACGTTAAAATAAATTCATGGATAAGTATTTAATCAAATAACAAGATCGGAAGAGCGGTTTCAG
chr5	67590314	67590353	PIK3R1_593	-	GTGACCTATGCACCAGACGTATTTTAAAAAGATAATGTCATCTTATGAACAATCTAGATCGGAAGAGCGGTTTCAG
chr5	67590926	67590965	PIK3R1_594	-	GTGACCTATGCACCAGACGTAAGAAACGTATTTGTTATTATCTGGGTACATCAGGAACGGAGATCGGAAGAGCGGTTTCAG
chr5	67591198	67591237	PIK3R1_595	-	GTGACCTATGCACCAGACGTGTTTGAAGAGAACGCATTAACCTCATCCTGAATTGTAGAGATCGGAAGAGCGGTTTCAG
chr5	67591949	67591988	PIK3R1_596	-	GTGACCTATGCACCAGACGTAGGACAGAAAGTTTCTAAATGAAGAGTGCAGGAGCCATCAAGATCGGAAGAGCGGTTTCAG
chr5	67593190	67593229	PIK3R1_597	-	GTGACCTATGCACCAGACGTGAGAAAGAAACCTGCTTTTGGCTTGTCCAAGCAATTCAGATCGGAAGAGCGGTTTCAG
chr2	128015122	128015161	ERCC3_598	-	GTGACCTATGCACCAGACGTGGGTACTTCGTTCAAGCCGGCGCTTGGCACCTTGTGGAGATCGGAAGAGCGGTTTCAG
chr2	128016822	128016861	ERCC3_599	-	GTGACCTATGCACCAGACGTGGGTGAGGAGTTCCAGGTGCTAGTCTCACAGGGCAGAGATCGGAAGAGCGGTTTCAG
chr2	128018754	128018793	ERCC3_600	-	GTGACCTATGCACCAGACGTATTTGGCTTCTGGTTAGACTAGGACCAAGGCCTTCTTGATAGATCGGAAGAGCGGTTTCAG
chr2	128028862	128028901	ERCC3_601	-	GTGACCTATGCACCAGACGTCTTTCATCTTCTGTTGCAGGAGTCACTCCTCTTAAACCAAGATCGGAAGAGCGGTTTCAG
chr2	128030391	128030430	ERCC3_602	-	GTGACCTATGCACCAGACGTATATGGGTGGAGGTGAGGCCCTAGCACTCTGGGGACCAGATCGGAAGAGCGGTTTCAG
chr2	128036699	128036738	ERCC3_603	-	GTGACCTATGCACCAGACGTAACCTGGAGCTTCTCCAGGCCAGTTTCTCTCCCATAGATCGGAAGAGCGGTTTCAG
chr2	128037973	128038012	ERCC3_604	-	GTGACCTATGCACCAGACGTCTGGCTGGGGCGCTGCGGAAAGGGCCCTCTCCTTAGGAGATCGGAAGAGCGGTTTCAG
chr2	128044229	128044268	ERCC3_605	-	GTGACCTATGCACCAGACGTTGGAGCTGAGCTGTCCACTTGTGAACAGACAAACCAATTAGATCGGAAGAGCGGTTTCAG
chr2	128046186	128046225	ERCC3_606	-	GTGACCTATGCACCAGACGTCCAGAGTTAAGAAGGTGGTCAGGCTGTTGTGTCTGGATCTAGATCGGAAGAGCGGTTTCAG
chr2	128046863	128046902	ERCC3_607	-	GTGACCTATGCACCAGACGTGTACCTTCTCCTGGTTCTTCACTGACTGCTGTTAGAAAGATCGGAAGAGCGGTTTCAG
chr2	128047215	128047254	ERCC3_608	-	GTGACCTATGCACCAGACGTTCTTGGCCACCCTTGGGTGGGGCAGGCATTTAGGATTTAGATCGGAAGAGCGGTTTCAG
chr2	128047750	128047789	ERCC3_609	-	GTGACCTATGCACCAGACGTCCATGACAGGCCTGCCCCAGGCCTGTCACTTTCTCGCAGATCGGAAGAGCGGTTTCAG
chr2	128050136	128050175	ERCC3_610	-	GTGACCTATGCACCAGACGTGCTGAGACCAGCAATTCACCTGCCCTGCTAATGTAACAAAGATCGGAAGAGCGGTTTCAG
chr2	128051039	128051078	ERCC3_611	-	GTGACCTATGCACCAGACGTCTTAGCTTGGGCAGGGCCAGGAGTGTGCGGAGCGGCAGAGATCGGAAGAGCGGTTTCAG
chr2	128051580	128051619	ERCC3_612	-	GTGACCTATGCACCAGACGTGCGCGGCACGCTCAGCCACGACTGCCCTTGGCCGGCCTGAGATCGGAAGAGCGGTTTCAG
chr9	5021938	5021977	JAK2_613	-	GTGACCTATGCACCAGACGTTTTCAGAAACATTTGCCCTGTAAGAGAAAACAATAAAGTTACAGATCGGAAGAGCGGTTTCAG
chr9	5029733	5029772	JAK2_614	-	GTGACCTATGCACCAGACGTGACAGAGAAAGGAATTTAAAGGTACACAACAGAATATTAGATCGGAAGAGCGGTTTCAG
chr9	5044353	5044392	JAK2_615	-	GTGACCTATGCACCAGACGTATAAAACATTTGGTCAGCTTCCAATAGTTCAAATACAAAGATCGGAAGAGCGGTTTCAG
chr9	5050636	5050675	JAK2_616	-	GTGACCTATGCACCAGACGTAATTTGAAGGAAATATCTCATCGTAAGTTTCATTATCATAGATCGGAAGAGCGGTTTCAG
chr9	5054513	5054552	JAK2_617	-	GTGACCTATGCACCAGACGTAAGACACATACAGAAAACAAAACAAAACAAAATTTGAAAGATCGGAAGAGCGGTTTCAG
chr9	5055619	5055658	JAK2_618	-	GTGACCTATGCACCAGACGTAAAGCATGTAATAAATAAAACCGGTGAGAATTTACAGAGCCAAGATCGGAAGAGCGGTTTCAG
chr9	5064833	5064872	JAK2_619	-	GTGACCTATGCACCAGACGTAAGAAAGAAAGAAATAGCACCTTTTAGAAAGTCAACTCCAAGATCGGAAGAGCGGTTTCAG
chr9	5066628	5066667	JAK2_620	-	GTGACCTATGCACCAGACGTAGAAGAAGCAATTTGAATAATATCAAGACCATAATATAGATCGGAAGAGCGGTTTCAG
chr9	5068972	5069011	JAK2_621	-	GTGACCTATGCACCAGACGTTAATATAAAAGAAAGGGAGGATGACATCACAATGGACATCAGATCGGAAGAGCGGTTTCAG
chr9	5069875	5069914	JAK2_622	-	GTGACCTATGCACCAGACGTAATAATACATATATCACTTCAAATACACTGAAAGTATGAGATCGGAAGAGCGGTTTCAG
chr9	5072442	5072481	JAK2_623	-	GTGACCTATGCACCAGACGTAAGAGTAAAGAAAAGAAATGAGTAAAGATGGAGAACGAAAGATCGGAAGAGCGGTTTCAG
chr9	5073648	5073687	JAK2_624	-	GTGACCTATGCACCAGACGTAAAAAAGTACAAAGAATTTGTTGTTGACTGTTGTCATAAAGATCGGAAGAGCGGTTTCAG
chr9	5078256	5078295	JAK2_625	-	GTGACCTATGCACCAGACGTTAAACGCACATATTTCAAATATCAGTCCACAAGTACTGGAGATCGGAAGAGCGGTTTCAG
chr9	5080179	5080218	JAK2_626	-	GTGACCTATGCACCAGACGTATACGAACAGTAGTGGTTAAATATCCAAGTAAACCAAGATCGGAAGAGCGGTTTCAG
chr9	5080483	5080522	JAK2_627	-	GTGACCTATGCACCAGACGTAGAACCACAACTGAGAATAAATTTGTAATGCCACACCAAGATCGGAAGAGCGGTTTCAG
chr9	5081675	5081714	JAK2_628	-	GTGACCTATGCACCAGACGTAAGAATATTATCACCTTAAATTAGCAAATAACATTTCTAGATCGGAAGAGCGGTTTCAG
chr9	5089624	5089663	JAK2_629	-	GTGACCTATGCACCAGACGTATCACATTAGGATGGAATAACCAAGTTTCAAGGCAAATAGATCGGAAGAGCGGTTTCAG
chr9	5090396	5090435	JAK2_630	-	GTGACCTATGCACCAGACGTAAGGTGGAATAATGTTTACTCTGCCATATTACTGAAAGATCGGAAGAGCGGTTTCAG
chr9	5090689	5090728	JAK2_631	-	GTGACCTATGCACCAGACGTAACATTTTCTTTCAGCTAGTTTATAAATAAAACAATTAGATCGGAAGAGCGGTTTCAG
chr9	5122954	5122993	JAK2_632	-	GTGACCTATGCACCAGACGTGAATAAACATTTAAAGACAGTTACTTTGATATGTTGAGATCGGAAGAGCGGTTTCAG
chr9	5126283	5126322	JAK2_633	-	GTGACCTATGCACCAGACGTCCCCTTTCAATATTTTTGTACATTTAATTTGTAGCAAAGATCGGAAGAGCGGTTTCAG
chr9	5126634	5126673	JAK2_634	-	GTGACCTATGCACCAGACGTGAAAATAAACCAAAAATTAATGAACACTAAGGGCCATCTTAGATCGGAAGAGCGGTTTCAG
chr4	55524132	55524171	KIT_635	-	GTGACCTATGCACCAGACGTGCGATGGGATCCGAGCTCTGTGCCAGTTCCAGCTCTCGCAGATCGGAAGAGCGGTTTCAG
chr4	55561628	55561667	KIT_636	-	GTGACCTATGCACCAGACGTAACAGAAATCGTGTGAGTATGATCTTCTTCCCTGGCGAAAGATCGGAAGAGCGGTTTCAG
chr4	55564400	55564439	KIT_637	-	GTGACCTATGCACCAGACGTATACAAAATCAGTAGTTGAAATGGCTGGTCACAGACAGATCGGAAGAGCGGTTTCAG
chr4	55565746	55565785	KIT_638	-	GTGACCTATGCACCAGACGTGAAGAAATGTGGCCCTCAAATAATTTGTATTATAGCATGAAGATCGGAAGAGCGGTTTCAG

chr4	55569840	55569879	KIT_639	-	GTGACCTATGCACCAGACGTGAGAAAAGGAGAAAAAATGAAGATTACCATATAATTTAGATCGGAAGAGCGGTTTCAG
chr4	55573214	55573253	KIT_640	-	GTGACCTATGCACCAGACGTTGAAATAAGACAGAAAGAACCTTATCTACAACACTGAGATCGGAAGAGCGGTTTCAG
chr4	55575540	55575579	KIT_641	-	GTGACCTATGCACCAGACGTAAGACAACCTAGTCAATCACCTGTGGATAGCATGCCTTGAAGATCGGAAGAGCGGTTTCAG
chr4	55589700	55589739	KIT_642	-	GTGACCTATGCACCAGACGTACAGAAATGGCCATATGTCAGAGTGCCTGGAAAACCTCAGCAGATCGGAAGAGCGGTTTCAG
chr4	55591973	55592012	KIT_643	-	GTGACCTATGCACCAGACGTGAAAAACAAAGCCCTGGCTTACTCTAGGAAAAATAAATAAAGATCGGAAGAGCGGTTTCAG
chr4	55593334	55593373	KIT_644	-	GTGACCTATGCACCAGACGTAGAGAAATGTGGAATCACAACTTTTGGCAGGATGGGATCTAGATCGGAAGAGCGGTTTCAG
chr4	55593532	55593571	KIT_645	-	GTGACCTATGCACCAGACGTAAAAGGAAAAAATGATCACCTTTTAATAATTATTGTCTCAAGATCGGAAGAGCGGTTTCAG
chr4	55593939	55593978	KIT_646	-	GTGACCTATGCACCAGACGTGAAGACAACAAGGTAAGTGGTGTGCTGGTGGTGGAAAGATCGGAAGAGCGGTTTCAG
chr4	55594127	55594166	KIT_647	-	GTGACCTATGCACCAGACGTAAACATGCATTTTAGCAAAAAGCACAACCTGGCAAACCTGATAGATCGGAAGAGCGGTTTCAG
chr4	55595451	55595490	KIT_648	-	GTGACCTATGCACCAGACGTATAAGAAAAGGTTAGAAGAAGGTTGAGATATATAGATTAAGATCGGAAGAGCGGTTTCAG
chr4	55597444	55597483	KIT_649	-	GTGACCTATGCACCAGACGTTGAAACAAGTCATGACTGAATCAAGTGGGACATGTAGAAGAGATCGGAAGAGCGGTTTCAG
chr4	55597987	55598026	KIT_650	-	GTGACCTATGCACCAGACGTGAGAGGATTTTTCTTAGCAATTACAACCATAAAGTTCAGGATCGGAAGAGCGGTTTCAG
chr4	55599186	55599225	KIT_651	-	GTGACCTATGCACCAGACGTGGAGGAGAAAAGAACCTTTAAATTCATTTTAACTTGTAGATCGGAAGAGCGGTTTCAG
chr4	55602614	55602653	KIT_652	-	GTGACCTATGCACCAGACGTAGCACAACAGAGTCAATAATGTTAATTCAGAAGCTCAACAAGATCGGAAGAGCGGTTTCAG
chr4	55602837	55602876	KIT_653	-	GTGACCTATGCACCAGACGTGTTTGCAAAGCAGTGTAAATCACAAAGGAGCAGGACACCAAGATCGGAAGAGCGGTTTCAG
chr4	55603291	55603330	KIT_654	-	GTGACCTATGCACCAGACGTAGGGGCCATTACTATCCCTCCTCAATGCCCTCAGCTTGTAGATCGGAAGAGCGGTTTCAG
chr4	55604545	55604584	KIT_655	-	GTGACCTATGCACCAGACGTCAAGCCCATGCAATACAGCAGTCCCTACAACGAACATAAGATCGGAAGAGCGGTTTCAG
chr10	43572657	43572696	RET_656	-	GTGACCTATGCACCAGACGTGCTGGGGCCAGGCTGGAGGAGCTGCGGGTACGGCCGAGATCGGAAGAGCGGTTTCAG
chr10	43595857	43595896	RET_657	-	GTGACCTATGCACCAGACGTTAGGGAAGTGAAGTGAAGGATGGTGAAGATAAGGCTTCTTCAAGATCGGAAGAGCGGTTTCAG
chr10	43597740	43597779	RET_658	-	GTGACCTATGCACCAGACGTAAGTCAGGTCTGTGGGGGCATCGGCCACATCTGCCAGGCAAGATCGGAAGAGCGGTTTCAG
chr10	43600350	43600389	RET_659	-	GTGACCTATGCACCAGACGTAGCAGACAGGGGCCCGCGTGATCACCAGCCGGGACCGGGAGATCGGAAGAGCGGTTTCAG
chr10	43601774	43601813	RET_660	-	GTGACCTATGCACCAGACGTGAGAGGGCGTTGGTCAAGTGCAGGCGAGATGGGCCCTCAGAGATCGGAAGAGCGGTTTCAG
chr10	43604429	43604468	RET_661	-	GTGACCTATGCACCAGACGTGGGCACAACAATGACCACCAAGCTGCTGTGGCTGCTTCTCAGATCGGAAGAGCGGTTTCAG
chr10	43606605	43606644	RET_662	-	GTGACCTATGCACCAGACGTACAGGGAACACCTTAGCCAGGCAAGCTGGACCGGCTGAAGATCGGAAGAGCGGTTTCAG
chr10	43607497	43607536	RET_663	-	GTGACCTATGCACCAGACGTGAGACAAGCAGGGTACAGGGGGCTGGCCCTGGGCCACGAGATCGGAAGAGCGGTTTCAG
chr10	43608251	43608290	RET_664	-	GTGACCTATGCACCAGACGTACACAGCAGGCTGTACCCATGTGGGAGCCCCGCCACACAGATCGGAAGAGCGGTTTCAG
chr10	43608954	43608993	RET_665	-	GTGACCTATGCACCAGACGTACGTAGCCCACTACGCCTCCTGGGGCCCTGACCACCCCAAGATCGGAAGAGCGGTTTCAG
chr10	43609878	43609917	RET_666	-	GTGACCTATGCACCAGACGTGGGTGGTGTGAGGCTTGGCACCCGAGGCTCGGCACCAAGATCGGAAGAGCGGTTTCAG
chr10	43611982	43612021	RET_667	-	GTGACCTATGCACCAGACGTAATGAGGGAAGGGGGAAGAGGGGGAAAAGTGTGAGGAAGATCGGAAGAGCGGTTTCAG
chr10	43613771	43613810	RET_668	-	GTGACCTATGCACCAGACGTGCACAGAGCAGGTTGCAAAACGATCGCTCCTGGAAGCCCTAGATCGGAAGAGCGGTTTCAG
chr10	43614929	43614968	RET_669	-	GTGACCTATGCACCAGACGTAGAGAGGGGGCCCTGGGCGTGGGGTCAAGGCTGGGCTAGATCGGAAGAGCGGTTTCAG
chr10	43615479	43615518	RET_670	-	GTGACCTATGCACCAGACGTAATAGCACAGTGTGTCAGGCCATGGCCAGGCAGCAGCGGAGATCGGAAGAGCGGTTTCAG
chr10	43617344	43617383	RET_671	-	GTGACCTATGCACCAGACGTGATGGAATAAAGACATTTGAAGTTACTCTAACTCTCTAGGAAGATCGGAAGAGCGGTTTCAG
chr10	43619069	43619108	RET_672	-	GTGACCTATGCACCAGACGTTGAAAGGACCAGTGAAGTGGCTCCACCTGGCCCTCAGAGAGATCGGAAGAGCGGTTTCAG
chr10	43620281	43620320	RET_673	-	GTGACCTATGCACCAGACGTGAAAGAGGCCAATATGATGCAACAGGAGGCCAGGTTCTAGATCGGAAGAGCGGTTTCAG
chr10	43621973	43622012	RET_674	-	GTGACCTATGCACCAGACGTGAGATGGCCGGTCACTCCAAGCCATGTGCCACAACCTAGATAGATCGGAAGAGCGGTTTCAG
chr10	43623510	43623549	RET_675	-	GTGACCTATGCACCAGACGTAACAGATCATTTGTTCTGCACTGAAGAACCAAACTTCAAGATCGGAAGAGCGGTTTCAG
chr14	105236628	105236667	AKT1_676	-	GTGACCTATGCACCAGACGTGACTGCGCTGGACGATAGCTTGGAGGATGGAGAGGGCCGAGATCGGAAGAGCGGTTTCAG
chr14	105237032	105237071	AKT1_677	-	GTGACCTATGCACCAGACGTACTGCCTGCCCCGCCCACTCCCTTTTCTCTCCACACTCAAGATCGGAAGAGCGGTTTCAG
chr14	105238652	105238691	AKT1_678	-	GTGACCTATGCACCAGACGTTCCCGCATATTCACGCGCAGCATCTCCCCACATCTCAGATCGGAAGAGCGGTTTCAG
chr14	105239165	105239204	AKT1_679	-	GTGACCTATGCACCAGACGTCCCATCCAGCTACAGCTACACCTCCATCCCTCATCCAGATCGGAAGAGCGGTTTCAG
chr14	105239538	105239577	AKT1_680	-	GTGACCTATGCACCAGACGTCACTGCGTGCATACGCGTTGCTGCGTCCCCACGTCTGAAGATCGGAAGAGCGGTTTCAG
chr14	105239742	105239781	AKT1_681	-	GTGACCTATGCACCAGACGTGGGCAGCAGGGGGGAGGGCCCTGGGGGCTGGCGGCACAGATCGGAAGAGCGGTTTCAG
chr14	105240199	105240238	AKT1_682	-	GTGACCTATGCACCAGACGTGGGCTGCGGGGGATGACTTCGCGGCCCTGTGGGCCGCCAAGATCGGAAGAGCGGTTTCAG
chr14	105241225	105241264	AKT1_683	-	GTGACCTATGCACCAGACGTGCCAGATGGGGCTGAAGGGCTGGGGCCAGGTAGCGACTCAGATCGGAAGAGCGGTTTCAG
chr14	105241363	105241402	AKT1_684	-	GTGACCTATGCACCAGACGTGGCCAGTGGGGGAGGGTGGAGATGAGGGTGGGGGAGGATCGGAAGAGCGGTTTCAG
chr14	105241939	105241978	AKT1_685	-	GTGACCTATGCACCAGACGTTCCCACTTCTGCCTGTGCCTGGGGTGCCTTGGACTGTGAGATCGGAAGAGCGGTTTCAG
chr14	105242946	105242985	AKT1_686	-	GTGACCTATGCACCAGACGTTGTGGCGCCAGGCCAGGCACTTGGGCAGCCCCAGCGCTTAGATCGGAAGAGCGGTTTCAG
chr14	105246375	105246414	AKT1_687	-	GTGACCTATGCACCAGACGTCTTGGCCCTCGGGATTACAGATTTGGGGGTTGGCTGGAAGATCGGAAGAGCGGTTTCAG
chr14	105258885	105258924	AKT1_688	-	GTGACCTATGCACCAGACGTGCTGCCAGGGCTGGGCCCTGGGGAGGGAGAGATGGGGGTAGAGATCGGAAGAGCGGTTTCAG
chr20	39766232	39766271	PLCG1_689	-	GTGACCTATGCACCAGACGTGGGGGCGGGCCAGGCGGCACAGGCAAGCCCGGGAGCAGATCGGAAGAGCGGTTTCAG
chr20	39788196	39788235	PLCG1_690	-	GTGACCTATGCACCAGACGTAGCAAAGAGGCCAAGATCAAGCTGGGGTCTCCAGATCGGAAGAGCGGTTTCAG
chr20	39788460	39788499	PLCG1_691	-	GTGACCTATGCACCAGACGTGGTATCAATAGCTGCCCCGAGGGCACATACTCCCACTGGAGATCGGAAGAGCGGTTTCAG
chr20	39788696	39788735	PLCG1_692	-	GTGACCTATGCACCAGACGTAAGCCTGAGGTGAGGGCCACTTCTCCATCTACAGTCAGGCAGATCGGAAGAGCGGTTTCAG
chr20	39791042	39791081	PLCG1_693	-	GTGACCTATGCACCAGACGTAGGGACATCCCAAGTGGTCTCATCCAGCTTCTCATGACCTAGATCGGAAGAGCGGTTTCAG
chr20	39791232	39791271	PLCG1_694	-	GTGACCTATGCACCAGACGTTAGAGCAGGAGTGCAGCTCAGGCAGCTCAGGCCCCAGCTGAGATCGGAAGAGCGGTTTCAG
chr20	39791548	39791587	PLCG1_695	-	GTGACCTATGCACCAGACGTGACAACCTGGTCAGGGCAAGACCTGGGAGGCCATGTGGAGATCGGAAGAGCGGTTTCAG
chr20	39791793	39791832	PLCG1_696	-	GTGACCTATGCACCAGACGTGAAGGTAAGCTAGCTAGTATGCTCAACAGACAACAAGGTAGATCGGAAGAGCGGTTTCAG

chr20	39791968	39792007	PLCG1_697	-	GTGACCTATGCACCAGACGTAGGGAGGGCAGGGGATGAGAGAAGCCTCCAGTCAGGGATGAGATCGGAAGAGCGGTTTCAG
chr20	39792305	39792344	PLCG1_698	-	GTGACCTATGCACCAGACGTACATGTGGAAGGGAAGAGACAGTGAGTCCCTGCCCTGTCCAGATCGGAAGAGCGGTTTCAG
chr20	39792511	39792550	PLCG1_699	-	GTGACCTATGCACCAGACGTAAGGAGAGGACAGGTAGGTATGGTCAGATGGGCCCTCCTGGAGATCGGAAGAGCGGTTTCAG
chr20	39792671	39792710	PLCG1_700	-	GTGACCTATGCACCAGACGTACATCACCATGGTCAAGCGGGCAGGCCTCCCATCTCCCTAGATCGGAAGAGCGGTTTCAG
chr20	39793523	39793562	PLCG1_701	-	GTGACCTATGCACCAGACGTGGGGACAAGCAGATGAACAGATTCTGCAATCTCTGGGAGATCGGAAGAGCGGTTTCAG
chr20	39793835	39793874	PLCG1_702	-	GTGACCTATGCACCAGACGTAACCAAGAAGCGGCAATGCAGACCCGATCCTCACCCACAGATCGGAAGAGCGGTTTCAG
chr20	39794040	39794079	PLCG1_703	-	GTGACCTATGCACCAGACGTCCAAGAGGGGACTGTGAGCCAGGGCTCTCACACCCACTGAGATCGGAAGAGCGGTTTCAG
chr20	39794229	39794268	PLCG1_704	-	GTGACCTATGCACCAGACGTAAGGCAACAGCAAAGATACTGTGACCCTGGCCAGGCCCTGAGATCGGAAGAGCGGTTTCAG
chr20	39794784	39794823	PLCG1_705	-	GTGACCTATGCACCAGACGTACAGAGTGAGGGAGGCTGGGAAAACAGGCCAGGGCCCCAGATCGGAAGAGCGGTTTCAG
chr20	39795066	39795105	PLCG1_706	-	GTGACCTATGCACCAGACGTGCAGAGTCAGGCCCGGCCAGCACCCCATGGCCCTGCCAGATCGGAAGAGCGGTTTCAG
chr20	39795269	39795308	PLCG1_707	-	GTGACCTATGCACCAGACGTACAAAACAGTCACACAGGGTCAGGGCAGCTCAGACCCAAGAGATCGGAAGAGCGGTTTCAG
chr20	39796442	39796481	PLCG1_708	-	GTGACCTATGCACCAGACGTGACACAATGGGATGTTAATGCCCCAGGCCAGAGCTAAGATCGGAAGAGCGGTTTCAG
chr20	39797357	39797396	PLCG1_709	-	GTGACCTATGCACCAGACGTGAGAAGCACCAGTCAGAGCAGAAAGGGCTCTCCCTGCCACTAGATCGGAAGAGCGGTTTCAG
chr20	39797669	39797708	PLCG1_710	-	GTGACCTATGCACCAGACGTACAGGGTGTGACCTCCAGCAACACCCCGAAGTCCCATAGATCGGAAGAGCGGTTTCAG
chr20	39798047	39798086	PLCG1_711	-	GTGACCTATGCACCAGACGTCAAAGCCCACCAATGGTCAGCATGGCTACTGCATATGTGTAGATCGGAAGAGCGGTTTCAG
chr20	39798702	39798741	PLCG1_712	-	GTGACCTATGCACCAGACGTGAGAGCAGATAACAGCTGGGAATAGACATCTCACCCCTCAGATCGGAAGAGCGGTTTCAG
chr20	39800783	39800822	PLCG1_713	-	GTGACCTATGCACCAGACGTACACAAGGCCCTGTAGCCCCAGGCTACAGCCCTGCCAGGAGATCGGAAGAGCGGTTTCAG
chr20	39801011	39801050	PLCG1_714	-	GTGACCTATGCACCAGACGTGAGGAAAACACTTACAGAGCCGCCACCCAGGAAGTGTAGATCGGAAGAGCGGTTTCAG
chr20	39801319	39801358	PLCG1_715	-	GTGACCTATGCACCAGACGTGAGATTATGGTGTATTCCAGTCCAGCTGCCCCACAGTCCAGATCGGAAGAGCGGTTTCAG
chr20	39802010	39802049	PLCG1_716	-	GTGACCTATGCACCAGACGTACAAAGAAGGGCCTGGGATGTCTTCTGCTCCCTCAAAGATCGGAAGAGCGGTTTCAG
chr20	39802242	39802281	PLCG1_717	-	GTGACCTATGCACCAGACGTAAAGCAAAAGGCTTCAGGTACCCTGGGAGAGGATGGGAAGATCGGAAGAGCGGTTTCAG
chr20	39802513	39802552	PLCG1_718	-	GTGACCTATGCACCAGACGTGAAAAGCCTGGCCCTCAGCCCACGAGGGACAGCAAGGGAGATCGGAAGAGCGGTTTCAG
chr20	39802714	39802753	PLCG1_719	-	GTGACCTATGCACCAGACGTGCCAGGTGCACAAGAGGGTCAATGACTCCTCTGCATCTTAGATCGGAAGAGCGGTTTCAG
chr20	39802717	39802756	PLCG1_720	-	GTGACCTATGCACCAGACGTGAAGCCAGGTGACAAGAGGGTCAAGTACTCCTCTGCATCTAGATCGGAAGAGCGGTTTCAG
chr20	39803057	39803096	PLCG1_721	-	GTGACCTATGCACCAGACGTGGGAAGAGTGTCTTACTGGCAGGCAGGGCCTTGCAGCCAGATCGGAAGAGCGGTTTCAG
chr19	11094778	11094817	SMARCA4_722	-	GTGACCTATGCACCAGACGTGCTGCAGACAGTGGCCTCCTGCTGGAAGACAGTCTGGTCAGATCGGAAGAGCGGTTTCAG
chr19	11095899	11095938	SMARCA4_723	-	GTGACCTATGCACCAGACGTGACCATGGCAAGGCAGGGTCAGCATGTGGAACGTGAGGTGAGATCGGAAGAGCGGTTTCAG
chr19	11096815	11096854	SMARCA4_724	-	GTGACCTATGCACCAGACGTAGGTGAGCCCACTGGTCACTCGGCAGCATATGCTGTGTAGATCGGAAGAGCGGTTTCAG
chr19	11097531	11097570	SMARCA4_725	-	GTGACCTATGCACCAGACGTGGAGAACAAGAGAAACAGTGCCTCCAGGTTTATGCAGATCGGAAGAGCGGTTTCAG
chr19	11098292	11098331	SMARCA4_726	-	GTGACCTATGCACCAGACGTGCAAGGGGCCAGGGCTCATGTTGAGCTCTGGGGCCCATCAGATCGGAAGAGCGGTTTCAG
chr19	11099943	11099982	SMARCA4_727	-	GTGACCTATGCACCAGACGTAGACAAGGAGCAAAGGCGGTGAGAGGGTTGCCAGGGCACCAGATCGGAAGAGCGGTTTCAG
chr19	11101776	11101815	SMARCA4_728	-	GTGACCTATGCACCAGACGTGAAGAGGACAAGCCCGCAGCTGCACAGCTCTGTGGCAGATCGGAAGAGCGGTTTCAG
chr19	11105454	11105493	SMARCA4_729	-	GTGACCTATGCACCAGACGTGCACAAAAGAGAAGGCTGACCCTTACAGCAGCATGGTGGACAGATCGGAAGAGCGGTTTCAG
chr19	11106839	11106878	SMARCA4_730	-	GTGACCTATGCACCAGACGTATGGGGTTACTGCAATGTGGTGGCACAATGTGCATGTCTAGATCGGAAGAGCGGTTTCAG
chr19	11107120	11107159	SMARCA4_731	-	GTGACCTATGCACCAGACGTAGAGAGACAGCTGACGGGTCAGCCACAAGGCTGAGCCAGATCGGAAGAGCGGTTTCAG
chr19	11113655	11113694	SMARCA4_732	-	GTGACCTATGCACCAGACGTGTCAATCGTGTGACACTGAGGTTGCAGGGCCTCCAGACCAAGATCGGAAGAGCGGTTTCAG
chr19	11113966	11114005	SMARCA4_733	-	GTGACCTATGCACCAGACGTTGTAAGGGCTTTCATACAAATCTGCTCAGAGCCAGCAGAAAGATCGGAAGAGCGGTTTCAG
chr19	11118528	11118567	SMARCA4_734	-	GTGACCTATGCACCAGACGTACAAAGCCATGTCACTCAGTTTATCCCCAGAGAGGGGAGATCGGAAGAGCGGTTTCAG
chr19	11121007	11121046	SMARCA4_735	-	GTGACCTATGCACCAGACGTGATGGAGGTGCCGGTAAGGACACACATTCTATCTGTGAAGATCGGAAGAGCGGTTTCAG
chr19	11123575	11123614	SMARCA4_736	-	GTGACCTATGCACCAGACGTAGATGCGCCACGCCAGGACTGAAGGCCGGTCGGACACCAGATCGGAAGAGCGGTTTCAG
chr19	11129583	11129622	SMARCA4_737	-	GTGACCTATGCACCAGACGTAAGGAAATGAGAGTCAAGTGCAGGCTCTCATCAATGGCTAGATCGGAAGAGCGGTTTCAG
chr19	11130217	11130256	SMARCA4_738	-	GTGACCTATGCACCAGACGTAGCAGGATGCACAGCTCGGCTTTTGGAGCCGGTGGCCAGAGATCGGAAGAGCGGTTTCAG
chr19	11132351	11132390	SMARCA4_739	-	GTGACCTATGCACCAGACGTGAGAGTGGGCAATCAGGGCAGGGGGCAGCAGGTGGCCCGGAGATCGGAAGAGCGGTTTCAG
chr19	11134144	11134183	SMARCA4_740	-	GTGACCTATGCACCAGACGTCCAAGACAGGAGAAGCAAGCGTTACCTCAAAGGAGGGCGAGATCGGAAGAGCGGTTTCAG
chr19	11134957	11134996	SMARCA4_741	-	GTGACCTATGCACCAGACGTACATAATGCTCACAGAGGGCCAAAGTGGCTTGGAGCCCTGAGATCGGAAGAGCGGTTTCAG
chr19	11136048	11136087	SMARCA4_742	-	GTGACCTATGCACCAGACGTGATGAGAGGCAACCAAGTGGGTCTTGCCTCCTGGGTGAGATCGGAAGAGCGGTTTCAG
chr19	11136926	11136965	SMARCA4_743	-	GTGACCTATGCACCAGACGTAGGAGAGAGGGTCAAGTGCAGGCGAGGAGCAGGCCACCGGAGATCGGAAGAGCGGTTTCAG
chr19	11138410	11138449	SMARCA4_744	-	GTGACCTATGCACCAGACGTGAGGAGGCAGGAGAGAAGGCGCAGGATGTTAACTGGAAGATCGGAAGAGCGGTTTCAG
chr19	11141356	11141395	SMARCA4_745	-	GTGACCTATGCACCAGACGTGAGAGGAGAAGAGGGTCAAGCGGGTGCACCTCAGGGGTAGAAGATCGGAAGAGCGGTTTCAG
chr19	11143916	11143955	SMARCA4_746	-	GTGACCTATGCACCAGACGTAGGTGCCAGTCAAGTCCCAAAGGAGCCAGGAGTGCATAAAAGATCGGAAGAGCGGTTTCAG
chr19	11144749	11144788	SMARCA4_747	-	GTGACCTATGCACCAGACGTGCAAAGTCAAGTCCGCTGAGGAGGGCCGGGTGGCCAGATCGGAAGAGCGGTTTCAG
chr19	11145540	11145579	SMARCA4_748	-	GTGACCTATGCACCAGACGTGGGAGCAACGGGACAGGATCAGCATGCAGGCACAGGGAGATCGGAAGAGCGGTTTCAG
chr19	11151924	11151963	SMARCA4_749	-	GTGACCTATGCACCAGACGTAAAATAGGACAGCCAGCACCCAGGTCGACAAGCAGAGGCCAGATCGGAAGAGCGGTTTCAG
chr19	11151933	11151972	SMARCA4_750	-	GTGACCTATGCACCAGACGTAATAGTAGTAAATAGGACAGCCAGCACCCAGGTCGACAAGATCGGAAGAGCGGTTTCAG
chr19	11168881	11168920	SMARCA4_751	-	GTGACCTATGCACCAGACGTGAACCGGCGGCTATCACCCCGAGTCCGCCACCCGGGAGATCGGAAGAGCGGTTTCAG
chr19	11168884	11168923	SMARCA4_752	-	GTGACCTATGCACCAGACGTGCAAGACCGGCGGCTATCACCCCGAGTCCGCCACCCGGGAGATCGGAAGAGCGGTTTCAG
chr19	11169414	11169453	SMARCA4_753	-	GTGACCTATGCACCAGACGTGCGGAGGAGCGTTCACCTCAGGCCCGCCCTGCCTGAGATCGGAAGAGCGGTTTCAG
chr19	11170379	11170418	SMARCA4_754	-	GTGACCTATGCACCAGACGTACACAGGGGCTTGAAGTGGATGGGCCCGACTGGAGGGCTGAGATCGGAAGAGCGGTTTCAG

chr19	11170671	11170710	SMARCA4_755	-	GTGACCTATGCACCAGACGTCGGGGAGGAAAGACAGCCTTGAGCTCTGGGAATGCAGCAAGATCGGAAGAGCGGTTTCAG
chr19	11172410	11172449	SMARCA4_756	-	GTGACCTATGCACCAGACGTCGACAGGAGGAGAGAGTGTGCGTTGGCCACCCTGCCAGGGAGATCGGAAGAGCGGTTTCAG
chr16	68772150	68772189	CDH1_757	-	GTGACCTATGCACCAGACGTGGAAGGTAGATGGAACCGGGTGACTCGGAGGGTTCCTCAGATCGGAAGAGCGGTTTCAG
chr16	68835523	68835562	CDH1_758	-	GTGACCTATGCACCAGACGTGAAATCACAGAGATTAGGAAATGGACAGATTAAGACAAAGATCGGAAGAGCGGTTTCAG
chr16	68842277	68842316	CDH1_759	-	GTGACCTATGCACCAGACGTAGAGATGAGGAACAAGATAAGACAATTCAGACGGATACAGATCGGAAGAGCGGTTTCAG
chr16	68842546	68842585	CDH1_760	-	GTGACCTATGCACCAGACGTAAATGAAAGAAAAAGAAATAGTAAAGAAAGGATCCCAACACTAGATCGGAAGAGCGGTTTCAG
chr16	68844050	68844089	CDH1_761	-	GTGACCTATGCACCAGACGTCAAGTGAGGGTGACTTGAGCCTGTGATGAGGAAGAAAAACATAGATCGGAAGAGCGGTTTCAG
chr16	68845537	68845576	CDH1_762	-	GTGACCTATGCACCAGACGTTCAAGGAGATGAAGGTTTGTAGACAAGCTGCACTTTGGGACTAGATCGGAAGAGCGGTTTCAG
chr16	68845988	68846027	CDH1_763	-	GTGACCTATGCACCAGACGTATCGACACAACCAAGTCAGGACCAGGAACACTAGCCACCTAGATCGGAAGAGCGGTTTCAG
chr16	68847166	68847205	CDH1_764	-	GTGACCTATGCACCAGACGTAAAGAGATGTGTCAATTCACAAAGTACCAAGACTGCTAGCAGAGATCGGAAGAGCGGTTTCAG
chr16	68849368	68849407	CDH1_765	-	GTGACCTATGCACCAGACGTGAAACAATGAAGTTAAAAACAAAACGAAACATTTTGTGTTAGATCGGAAGAGCGGTTTCAG
chr16	68853133	68853172	CDH1_766	-	GTGACCTATGCACCAGACGTACAAGCTCTGGCTTTTGAATAGGACCAGCAAAACAACATGAGATCGGAAGAGCGGTTTCAG
chr16	68855854	68855893	CDH1_767	-	GTGACCTATGCACCAGACGTATACACAGAAAATGTGGCAGCTTGGCAACAGTAATGAATCAGATCGGAAGAGCGGTTTCAG
chr16	68857252	68857291	CDH1_768	-	GTGACCTATGCACCAGACGTCAATAAAAAAGAAATGATGAGACCAGGGGAGGAAAATAAAAAAGATCGGAAGAGCGGTTTCAG
chr16	68862027	68862066	CDH1_769	-	GTGACCTATGCACCAGACGTGGGGGAGACAGAGCAAGTGTGAGAGCCAAAGATAAAGAAAGATCGGAAGAGCGGTTTCAG
chr16	68863507	68863546	CDH1_770	-	GTGACCTATGCACCAGACGTAAAAGGTTGAAGTACAATGAAGAGTAGGAAAGAAATAGTCAGATCGGAAGAGCGGTTTCAG
chr16	68867143	68867182	CDH1_771	-	GTGACCTATGCACCAGACGTAGGGACAAAAGCATCTTTAGTGAAGGAAGGGCACACCTAGATCGGAAGAGCGGTTTCAG
chr6	36651829	36651868	CDKN1A_772	-	GTGACCTATGCACCAGACGTGACAGATAACAGGAAGGCCCTGGTACGGCGGAGATAGAGCTCGGAAGAGCGGTTTCAG
chr6	36653478	36653517	CDKN1A_773	-	GTGACCTATGCACCAGACGTACACGATAAGTCAGCCAGGCCAAGAAGAAGAGAGCGGGCAGATCGGAAGAGCGGTTTCAG
chr19	10244293	10244332	DNMT1_774	-	GTGACCTATGCACCAGACGTCCGTCACCCCTGTTTCTGGCACCAGGAATCCCAACATGCAGATCGGAAGAGCGGTTTCAG
chr19	10244843	10244882	DNMT1_775	-	GTGACCTATGCACCAGACGTGTGGGGCAGGCTTCCTCTGGGGCCTGACTGCCCTCTGGGGAGATCGGAAGAGCGGTTTCAG
chr19	10246362	10246401	DNMT1_776	-	GTGACCTATGCACCAGACGTGGCGCCCGCTGGGTCTGGACAGGAAGGAGGCTTCTGTGCAGATCGGAAGAGCGGTTTCAG
chr19	10246747	10246786	DNMT1_777	-	GTGACCTATGCACCAGACGTAGGGGGCAGCCGAGGGCCTGGTTCAGGCCCTGTACTTGGCAGATCGGAAGAGCGGTTTCAG
chr19	10247711	10247750	DNMT1_778	-	GTGACCTATGCACCAGACGTAAAGTTGTGGTTCCTCCGGTGGGCTGAGGGGAAGGAAGGCAGATCGGAAGAGCGGTTTCAG
chr19	10248458	10248497	DNMT1_779	-	GTGACCTATGCACCAGACGTCTGACAGAGCGGCTCCTCCTCGAGGCCAGCCAGCAGCAGATCGGAAGAGCGGTTTCAG
chr19	10249065	10249104	DNMT1_780	-	GTGACCTATGCACCAGACGTCCCCTGCTCCTCCACACACTGCCGAGCAGGCCTCAGTAGAGATCGGAAGAGCGGTTTCAG
chr19	10250302	10250341	DNMT1_781	-	GTGACCTATGCACCAGACGTGGGCTGGGGCGGGCAGACAGATGTGGCCAGCACGTGACCCAGATCGGAAGAGCGGTTTCAG
chr19	10250672	10250711	DNMT1_782	-	GTGACCTATGCACCAGACGTAGAAGCCCCCAGTGTGTCACAGCCGCCCGGGGCTGTGCCAGATCGGAAGAGCGGTTTCAG
chr19	10251407	10251446	DNMT1_783	-	GTGACCTATGCACCAGACGTGTAGGCTCCTCTGTAACACTGGTGAGCCAGCCGAGATCGGAAGAGCGGTTTCAG
chr19	10251731	10251770	DNMT1_784	-	GTGACCTATGCACCAGACGTGATGAGTTTCTTCAAGTTATTCTCTGTAACCTGGAGAGATCGGAAGAGCGGTTTCAG
chr19	10252654	10252693	DNMT1_785	-	GTGACCTATGCACCAGACGTTGCTTGCTAGAGGGAAGGCTTCGGGGTCAAAGTTGGCCAGAGATCGGAAGAGCGGTTTCAG
chr19	10254392	10254431	DNMT1_786	-	GTGACCTATGCACCAGACGTGCCTCTGTTCTTCCACGAGGCCACAGACTCTTCTAGAAGGAGATCGGAAGAGCGGTTTCAG
chr19	10256977	10257016	DNMT1_787	-	GTGACCTATGCACCAGACGTCTCGGAGCAGCCGGGGCCAGGGCGCTCCAGGCTGAGCCAAGATCGGAAGAGCGGTTTCAG
chr19	10259510	10259549	DNMT1_788	-	GTGACCTATGCACCAGACGTGGGCTGGGCTCGGGTCCAGCGACTTTTCAGCCACATCAGATCGGAAGAGCGGTTTCAG
chr19	10260079	10260118	DNMT1_789	-	GTGACCTATGCACCAGACGTGGTGCCTCTGCTGAGCCCTCAGCCTTATCTGAGGGTACACAGATCGGAAGAGCGGTTTCAG
chr19	10260479	10260518	DNMT1_790	-	GTGACCTATGCACCAGACGTTTTCTTTTGTGCTTACTGCTGATGCACTTTCTCATCAAGTAGATCGGAAGAGCGGTTTCAG
chr19	10262024	10262063	DNMT1_791	-	GTGACCTATGCACCAGACGTGAGCCCTTGGTCACTGCTACTGCCATGTTCCAATAAGCAAGATCGGAAGAGCGGTTTCAG
chr19	10262376	10262415	DNMT1_792	-	GTGACCTATGCACCAGACGTCCGAGTCTTCTCCTCTGTGGCAGAGGACTTGGCAGCTGGTGAGATCGGAAGAGCGGTTTCAG
chr19	10264919	10264958	DNMT1_793	-	GTGACCTATGCACCAGACGTCTGTGGTGCTCCCGCTCCCTAAGTGGCCAGCCTCTGAGATCGGAAGAGCGGTTTCAG
chr19	10265212	10265251	DNMT1_794	-	GTGACCTATGCACCAGACGTGGCAGGACAGATGAAGACTGGAGCCGGGAGGTAGATCGGAAGAGCGGTTTCAG
chr19	10265531	10265570	DNMT1_795	-	GTGACCTATGCACCAGACGTGAGGGTCTCAGACTCCGGGATTCGCTGAAACTGGAAACTTGCAGATCGGAAGAGCGGTTTCAG
chr19	10266479	10266518	DNMT1_796	-	GTGACCTATGCACCAGACGTGGCCCATCATAGGCTGGCCGGGGTCTGAAAGGGGCCTCAAGATCGGAAGAGCGGTTTCAG
chr19	10270284	10270323	DNMT1_797	-	GTGACCTATGCACCAGACGTTTTCTGTTGTCATGTTTGTCTGTTGGAAGGAGGCACATCCAGATCGGAAGAGCGGTTTCAG
chr19	10270468	10270507	DNMT1_798	-	GTGACCTATGCACCAGACGTCTCTCTTCCAGCCTCCTCTGCTGTCCCTGTCCACTAGATCGGAAGAGCGGTTTCAG
chr19	10270644	10270683	DNMT1_799	-	GTGACCTATGCACCAGACGTGCCGGGAATAAAGCCGGTGGCGGGCTCACGAGGCGGCTGAGATCGGAAGAGCGGTTTCAG
chr19	10271010	10271049	DNMT1_800	-	GTGACCTATGCACCAGACGTATTCTTGAAGTATCGAAAGCAGATGGTAATGTTAAATGAGATCGGAAGAGCGGTTTCAG
chr19	10273952	10273991	DNMT1_801	-	GTGACCTATGCACCAGACGTAAATGCTTGTGCTTTTGTGTCATCTGGATCAGTAGAAAGAGATCGGAAGAGCGGTTTCAG
chr19	10277224	10277263	DNMT1_802	-	GTGACCTATGCACCAGACGTGTTATTTGTTTCTGAACTCCCCCTCATTCTTCTGCTCCTGAGATCGGAAGAGCGGTTTCAG
chr19	10278956	10278995	DNMT1_803	-	GTGACCTATGCACCAGACGTGCAACCTGCCTTTGTGCTTTGTTGTAAGTGAATTGCTAAGATCGGAAGAGCGGTTTCAG
chr19	10283716	10283755	DNMT1_804	-	GTGACCTATGCACCAGACGTATCACCTCAAGTTTGTAAATCTCCCTTAATCCTATATGAGATCGGAAGAGCGGTTTCAG
chr19	10284497	10284536	DNMT1_805	-	GTGACCTATGCACCAGACGTTTACTATACCTTTCTTTTGTCTACGAGTGTGTAATAGATCGGAAGAGCGGTTTCAG
chr19	10286166	10286205	DNMT1_806	-	GTGACCTATGCACCAGACGTGGCTTTCATTTCTGACTCTACCTTACCTAAGTTGTTGATTTGATCGGAAGAGCGGTTTCAG
chr19	10287918	10287957	DNMT1_807	-	GTGACCTATGCACCAGACGTGATAAATGGCGGCTGCCTTTTTAGGGGCCGGCTGTTTTAGATCGGAAGAGCGGTTTCAG
chr19	10291404	10291443	DNMT1_808	-	GTGACCTATGCACCAGACGTTCTCAGCATCCTAGCCTCTAGAAAAATGCTCCTCCTAGTAGATCGGAAGAGCGGTTTCAG
chr19	10292667	10292706	DNMT1_809	-	GTGACCTATGCACCAGACGTCTTAAATTTTTCTTATTACCAATCTGACTGACACACTAGATCGGAAGAGCGGTTTCAG
chr19	10305446	10305485	DNMT1_810	-	GTGACCTATGCACCAGACGTTGGGGGGAAACACGGACTCAGGGGACAGGCGGCTGAGATCGGAAGAGCGGTTTCAG
chr12	56474035	56474074	ERBB3_811	-	GTGACCTATGCACCAGACGTAGGGTGAAGGGAGCCAGCCAGCTCCGGCCGGGGCCAGATCGGAAGAGCGGTTTCAG
chr12	56477485	56477524	ERBB3_812	-	GTGACCTATGCACCAGACGTAGAGGGAAGAGTGGCTGAGGGTGGACACAAATTTCTCAGAGATCGGAAGAGCGGTTTCAG

chr12	56478729	56478768	ERBB3_813	-	GTGACCTATGCACCAGACGTGCAGATTATGTAATGAGAGAGACAACAGGGCAAATAATAGATCGGAAGAGCGGTTTCAG
chr12	56480265	56480304	ERBB3_814	-	GTGACCTATGCACCAGACGTGAAAAGAAGTGACAGGGTTAAGGGCCGACGCGGAACGCCTCAGATCGGAAGAGCGGTTTCAG
chr12	56481311	56481350	ERBB3_815	-	GTGACCTATGCACCAGACGTAGGAAGGCAACACAAGGGGCCATCAGGGCTAAGAAAGGCTAGATCGGAAGAGCGGTTTCAG
chr12	56481529	56481568	ERBB3_816	-	GTGACCTATGCACCAGACGTAGAGAAAGCATGGCTGTTAGGGCTCCTAGGACTGAATCTAGATCGGAAGAGCGGTTTCAG
chr12	56481755	56481794	ERBB3_817	-	GTGACCTATGCACCAGACGTAGGAGGCTCATCAGATTATGTTACGTGTGACCCTACCAGATCGGAAGAGCGGTTTCAG
chr12	56482277	56482316	ERBB3_818	-	GTGACCTATGCACCAGACGTGGAGGAGGACACATTAGAGATGAGGGAGGAACATCACCAAGATCGGAAGAGCGGTTTCAG
chr12	56482482	56482521	ERBB3_819	-	GTGACCTATGCACCAGACGTAAAGAGAGGTTACGTGGGGTGTGCTGCGCAGGCTCAGAGGAGATCGGAAGAGCGGTTTCAG
chr12	56486720	56486759	ERBB3_820	-	GTGACCTATGCACCAGACGTGGAGAGAGGCATATGGGCAGGGAGCCTTCTTCTTTCTTGGAGATCGGAAGAGCGGTTTCAG
chr12	56487079	56487118	ERBB3_821	-	GTGACCTATGCACCAGACGTGGAGACAGGATGAGAGGAGAGACTACTAAGGGAACATTAAGATCGGAAGAGCGGTTTCAG
chr12	56487498	56487537	ERBB3_822	-	GTGACCTATGCACCAGACGTAGGGGTGGGTTAGGAGAGGAGTCTGAGGACTCCAGCAAGAGATCGGAAGAGCGGTTTCAG
chr12	56487833	56487872	ERBB3_823	-	GTGACCTATGCACCAGACGTGAATAAAGGGAGGGGGGGGTCACCTCCAAGTCTGACCTTAGATCGGAAGAGCGGTTTCAG
chr12	56488136	56488175	ERBB3_824	-	GTGACCTATGCACCAGACGTGAGAGAAGGTCAGGAAGAATCAGATCCCAAGGTCAATCCAGATCGGAAGAGCGGTTTCAG
chr12	56488991	56489030	ERBB3_825	-	GTGACCTATGCACCAGACGTAAAGTACCACCTTAAATGAGAGCTGGACAGCAGAGGCTCAGATCGGAAGAGCGGTTTCAG
chr12	56489399	56489438	ERBB3_826	-	GTGACCTATGCACCAGACGTTATAGAAACCCAACATTATCCTGGGTTTGCATCTTCTTAAGATCGGAAGAGCGGTTTCAG
chr12	56490237	56490276	ERBB3_827	-	GTGACCTATGCACCAGACGTAATGGGAAGGATTAAGTACTCAGGAAAGGCCATCCCATGTCAGATCGGAAGAGCGGTTTCAG
chr12	56490482	56490521	ERBB3_828	-	GTGACCTATGCACCAGACGTTGGGGCAGGAGTTGGCATAAGGTCATTCTCCCTAGGTCAAAGATCGGAAGAGCGGTTTCAG
chr12	56490779	56490818	ERBB3_829	-	GTGACCTATGCACCAGACGTCAAAGGTTATTCTAGGAAACCAACAGGTTACATACACAGATCGGAAGAGCGGTTTCAG
chr12	56491519	56491558	ERBB3_830	-	GTGACCTATGCACCAGACGTAGGGGAAGAAAGTATTTCTTAAGGTTGGGGAAATCAGTACAGATCGGAAGAGCGGTTTCAG
chr12	56492234	56492273	ERBB3_831	-	GTGACCTATGCACCAGACGTAAGATAGAGGTATCACAAAGTTTATTTCCACAAATTTCTTAGATCGGAAGAGCGGTTTCAG
chr12	56492493	56492532	ERBB3_832	-	GTGACCTATGCACCAGACGTAAGACATGGACTAGTCACTGGCAAATAGTAGACATGGGCAGATCGGAAGAGCGGTTTCAG
chr12	56493572	56493611	ERBB3_833	-	GTGACCTATGCACCAGACGTAGGTTGATTGTTAGGGGAATCCTGGTTCAGCCAACTCCTAGATCGGAAGAGCGGTTTCAG
chr12	56493908	56493947	ERBB3_834	-	GTGACCTATGCACCAGACGTAAATAAGGAAAAGGTTAAGATGAAGGGAGAAATCTACATAGATCGGAAGAGCGGTTTCAG
chr12	56494795	56494834	ERBB3_835	-	GTGACCTATGCACCAGACGTAATAAACAGAAAATATGCAAGGAAATTTACATGATGAGAGATCGGAAGAGCGGTTTCAG
chr12	56495263	56495302	ERBB3_836	-	GTGACCTATGCACCAGACGTAGAAGAAAGGCTAGGTATGTGAAGAACTTCATGAGGTTAGAGATCGGAAGAGCGGTTTCAG
chr12	56495526	56495565	ERBB3_837	-	GTGACCTATGCACCAGACGTGCAGTGGGCATGATGGGTACAGGGTGGAGTGGGCAACTCTAGATCGGAAGAGCGGTTTCAG
chr9	139390473	139390512	NOTCH1_838	-	GTGACCTATGCACCAGACGTCCACGAGACCCCGGCTTCTTTCCCAAGCCTTCGGGCGTCAGATCGGAAGAGCGGTTTCAG
chr9	139393301	139393340	NOTCH1_839	-	GTGACCTATGCACCAGACGTGGCTGGGATGCCAGGGGAGACGTGAGGGCTGAATCCACAGAGATCGGAAGAGCGGTTTCAG
chr9	139393514	139393553	NOTCH1_840	-	GTGACCTATGCACCAGACGTGGGGGCCAGGGCTGCTCTGTCTGGGGCGGGACCGCCACAGAGATCGGAAGAGCGGTTTCAG
chr9	139394954	139394993	NOTCH1_841	-	GTGACCTATGCACCAGACGTGCTGCTGCTGCTGCCACTGCCCTCCTCAGGGCCGCTGGAGATCGGAAGAGCGGTTTCAG
chr9	139396150	139396189	NOTCH1_842	-	GTGACCTATGCACCAGACGTGCAGCAGCCAGGGCTTCCCTAGCCCGCTGGCCACCTGCCTAGATCGGAAGAGCGGTTTCAG
chr9	139396403	139396442	NOTCH1_843	-	GTGACCTATGCACCAGACGTAGGCTCCCGGGCTCCTGGGCTCCCGGCCACCTGCTGCCGGAGATCGGAAGAGCGGTTTCAG
chr9	139396674	139396713	NOTCH1_844	-	GTGACCTATGCACCAGACGTGCCCGCCCTGCTTCTGGGTCCCGGTGGGAGGTGGACCTAGATCGGAAGAGCGGTTTCAG
chr9	139397584	139397623	NOTCH1_845	-	GTGACCTATGCACCAGACGTCCCCATCCCGGGAACAGGCTCTGCTGCAGGGGTGCCATAGATCGGAAGAGCGGTTTCAG
chr9	139399075	139399114	NOTCH1_846	-	GTGACCTATGCACCAGACGTCCCGCGCCACGGTCAATCCCCGCAACTCTCCTGGGCCAGATCGGAAGAGCGGTTTCAG
chr9	139399712	139399751	NOTCH1_847	-	GTGACCTATGCACCAGACGTGGGGCTCATGGGCTGAGGGAGGACCTGAACTGGATGTGAGATCGGAAGAGCGGTTTCAG
chr9	139400929	139400968	NOTCH1_848	-	GTGACCTATGCACCAGACGTGGGTGCAGGGAGGCAGGGGCCCGCCAGGGGAGACACCTGGAGATCGGAAGAGCGGTTTCAG
chr9	139401118	139401157	NOTCH1_849	-	GTGACCTATGCACCAGACGTGCCAGGCGGGTGGGGCGTGTGGGGCAGCAGGGTGAGCCAGATCGGAAGAGCGGTTTCAG
chr9	139401707	139401746	NOTCH1_850	-	GTGACCTATGCACCAGACGTCTGCACGGAGGGCTGGTGTGGCCATCCATGCCAGGGCAAGATCGGAAGAGCGGTTTCAG
chr9	139402357	139402396	NOTCH1_851	-	GTGACCTATGCACCAGACGTCTCCTAGGGTAAGGGTTGTGGCCGGCACGAGTGTGCCACAGATCGGAAGAGCGGTTTCAG
chr9	139402634	139402673	NOTCH1_852	-	GTGACCTATGCACCAGACGTGTGCCACAGGCTCGGGTCCCAGCCATCAAGTCTCTAGATCGGAAGAGCGGTTTCAG
chr9	139403272	139403311	NOTCH1_853	-	GTGACCTATGCACCAGACGTGCGCCACAGAGGTGCCGGAAGGAGGGGCCCTGGGTGGGTGAGATCGGAAGAGCGGTTTCAG
chr9	139404135	139404174	NOTCH1_854	-	GTGACCTATGCACCAGACGTCTCAGTGAGGCGGTGGAAGGGAACGGGCGGTGCGGGCCAAGATCGGAAGAGCGGTTTCAG
chr9	139405055	139405094	NOTCH1_855	-	GTGACCTATGCACCAGACGTCCCGCGCTCTGGCCTCTCCAGGAAGCTCTCAGGCCTCAGAGATCGGAAGAGCGGTTTCAG
chr9	139405554	139405593	NOTCH1_856	-	GTGACCTATGCACCAGACGTCCAGGGCCCGTGGGGCTGGGATGGGAGGTCAGGATGTCAGATCGGAAGAGCGGTTTCAG
chr9	139407462	139407462	NOTCH1_857	-	GTGACCTATGCACCAGACGTGGTGGGGCTGTGCTGGAGGGGGGGGCTATGTGGGAGAGATCGGAAGAGCGGTTTCAG
chr9	139407794	139407833	NOTCH1_858	-	GTGACCTATGCACCAGACGTTCGCGGTTTCTCAGTGTGCGAGTGGAGGGCCCTCGAGTCTGGGAGATCGGAAGAGCGGTTTCAG
chr9	139408912	139408951	NOTCH1_859	-	GTGACCTATGCACCAGACGTGGGCCGATCATGGGACACATCAGTCTAAACCCTGGGAGAGATCGGAAGAGCGGTTTCAG
chr9	139409692	139409731	NOTCH1_860	-	GTGACCTATGCACCAGACGTCTGCACGTGGGGGCTGACTGCACTGTGCTCAGAGGTCAGAGATCGGAAGAGCGGTTTCAG
chr9	139409885	139409924	NOTCH1_861	-	GTGACCTATGCACCAGACGTAGGCGGGTGGCCGGCGGGGGCCAGTGGGCAGGGCGGGCCAGATCGGAAGAGCGGTTTCAG
chr9	139410383	139410422	NOTCH1_862	-	GTGACCTATGCACCAGACGTGCGCCACCACGCGGGAGGGACTGGGACGGGACAGGGCAAGATCGGAAGAGCGGTTTCAG
chr9	139411674	139411713	NOTCH1_863	-	GTGACCTATGCACCAGACGTCCCCCGCCCTCCTCCCGGGTCTGTCACCTCGGCCTCAGATCGGAAGAGCGGTTTCAG
chr9	139412154	139412193	NOTCH1_864	-	GTGACCTATGCACCAGACGTGGGGCAGGGCGGAAAGCCAGTGCAGGCTGGGCAGCTGATCGGAAGAGCGGTTTCAG
chr9	139412539	139412578	NOTCH1_865	-	GTGACCTATGCACCAGACGTGCACAGGGGTGCGGCCAGGTGGGGTGGCAGCCTGGCCAGATCGGAAGAGCGGTTTCAG
chr9	139412993	139413032	NOTCH1_866	-	GTGACCTATGCACCAGACGTTGAGGCCAGGTGGGGCAGGGGGCTCACATGGGCCAGGCAGATCGGAAGAGCGGTTTCAG
chr9	139413845	139413884	NOTCH1_867	-	GTGACCTATGCACCAGACGTGGGTGCGCCGACGGCGGGGTAGCCGGGGCGGGGCTGCTACAGATCGGAAGAGCGGTTTCAG
chr9	139417252	139417291	NOTCH1_868	-	GTGACCTATGCACCAGACGTCCCGTGGCGGGGTGCACGAGCCCTCCCGGCTGCCAGGAGATCGGAAGAGCGGTTTCAG
chr9	139418119	139418158	NOTCH1_869	-	GTGACCTATGCACCAGACGTACCCACAGCTGAGGGTGGGCAGACCCAGCCCGCCAGATCGGAAGAGCGGTTTCAG
chr9	139438426	139438465	NOTCH1_870	-	GTGACCTATGCACCAGACGTCCCTGCGGGACCTGTTCTTGTGAGGGCAGAGCCCTAGATCGGAAGAGCGGTTTCAG

chr9	139440128	139440167	NOTCH1_871	-	GTGACCTATGCACCAGACGTACCCACCCGCGAGCCCCACTTTCCGCGCCCTTTGGAACAGATCGGAAGAGCGGTTTCAG
chr9	139399998	139400037	NOTCH1_872	-	GTGACCTATGCACCAGACGTGCGCGACATCCCCCGCCGCTGATCGAGGAGCGTGCAGAGATCGGAAGAGCGGTTTCAG
chr9	139390969	139391008	NOTCH1_873	-	GTGACCTATGCACCAGACGTGAGAACCTGCAGCCAGCAAACATCCAGCAGCAGCAAAGCCAGATCGGAAGAGCGGTTTCAG
chr9	139391465	139391504	NOTCH1_874	-	GTGACCTATGCACCAGACGTGCCCTCAACCACCTGCTGGGATGCCGACACCCACCTGAGATCGGAAGAGCGGTTTCAG
chr12	4383157	4383196	CCND2_875	-	GTGACCTATGCACCAGACGTGCGGCCCTCTCCCTCTGCTTTCCCGCGCCTGGAAAAAGAGATCGGAAGAGCGGTTTCAG
chr12	4385121	4385160	CCND2_876	-	GTGACCTATGCACCAGACGTAGTGGGAAAGGGTGGGGGGCGGGGGTGGAGAGCATAGCAAGATCGGAAGAGCGGTTTCAG
chr12	4387876	4387915	CCND2_877	-	GTGACCTATGCACCAGACGTAGGCAAGGAAAGAGGAGAACTAAATTCACAGGCTGAGATCGGAAGAGCGGTTTCAG
chr12	4397958	4397997	CCND2_878	-	GTGACCTATGCACCAGACGTGAGAGGAGGAGGAGGTCAGGGCACAGAACGAATTTGGATCCAGATCGGAAGAGCGGTTTCAG
chr12	4408976	4409015	CCND2_879	-	GTGACCTATGCACCAGACGTGGTCCAGACCAGAGTTGTTAGTAAGGAAACAGGACATAGAGATCGGAAGAGCGGTTTCAG
chr8	128748790	128748829	MYC_880	-	GTGACCTATGCACCAGACGTGCTGCAAGGAGAGCCTTTCAGAGAAGCGGGTCTGGCAGCAGATCGGAAGAGCGGTTTCAG
chr8	128750444	128750483	MYC_881	-	GTGACCTATGCACCAGACGTGCACACAAAGCGGGAGGCAGTCTTGAGTTAAAGGGGCTTAGATCGGAAGAGCGGTTTCAG
chr8	128752592	128752631	MYC_882	-	GTGACCTATGCACCAGACGTGGAATAAGAACTACTCTTTAGCAAGGTTACATTAATAATAGATCGGAAGAGCGGTTTCAG
chr8	128750830	128750869	MYC_883	-	GTGACCTATGCACCAGACGTGCTCGCGGTCCAGATGAAACTCTGGTTCACCATGTCTCCAGATGCTCCAGATCGGAAGAGCGGTTTCAG
chr8	128752873	128752912	MYC_884	-	GTGACCTATGCACCAGACGTGTCATTTTCGGTGTGTTGCTGATCTGTCTCAGGACTCTGAAGATCGGAAGAGCGGTTTCAG
chr1	115251106	115251145	NRAS_885	-	GTGACCTATGCACCAGACGTATATGGTTTCTTGGCATAATTACAAATCTTAGTATATAGTAGATCGGAAGAGCGGTTTCAG
chr1	115252140	115252179	NRAS_886	-	GTGACCTATGCACCAGACGTGCTTTCAGCATTTGTGCAAGAGTTGTCATCAGTTGATTAAGATCGGAAGAGCGGTTTCAG
chr1	115256371	115256410	NRAS_887	-	GTGACCTATGCACCAGACGTATTATTTCTGAAAGGATGATCTTTGTGTTCTGAATCAGATCGGAAGAGCGGTTTCAG
chr1	115258621	115258660	NRAS_888	-	GTGACCTATGCACCAGACGTGGTGTGGTCCCGCTGACCTGATCTCTCCTCCTGCTGAGATCGGAAGAGCGGTTTCAG
chr19	40739729	40739768	AKT2_889	-	GTGACCTATGCACCAGACGTACGCGAGAGGACGACGCTCGCTGCCATCACCGCTGGGTGAGATCGGAAGAGCGGTTTCAG
chr19	40740902	40740941	AKT2_890	-	GTGACCTATGCACCAGACGTGGGGCCCCCGCGTGGTGTGCTGCCCCAGGGGTGGAGGGAGATCGGAAGAGCGGTTTCAG
chr19	40741120	40741159	AKT2_891	-	GTGACCTATGCACCAGACGTCTGCTTGGCCAGCAGGACCCCTCAGGGACCTGGCCACTCAGATCGGAAGAGCGGTTTCAG
chr19	40741747	40741786	AKT2_892	-	GTGACCTATGCACCAGACGTGCGTCCGGCCCCACCCAGCCAGCCAGCTGCTGCCACTGAGATCGGAAGAGCGGTTTCAG
chr19	40742114	40742153	AKT2_893	-	GTGACCTATGCACCAGACGTGGTGGGGTAGGAACGTTGAGGCCAAGGGTAGGGGAAGATCGGAAGAGCGGTTTCAG
chr19	40743826	40743865	AKT2_894	-	GTGACCTATGCACCAGACGTGGGTGTCGCGCAGGCTGACCTGAGCTGGCATGCACACCACATGAGATCGGAAGAGCGGTTTCAG
chr19	40744762	40744801	AKT2_895	-	GTGACCTATGCACCAGACGTGCTGCCCTTGACTTTGCCCTCTGGGGCCTCCTTCTTAGGGAGATCGGAAGAGCGGTTTCAG
chr19	40745902	40745941	AKT2_896	-	GTGACCTATGCACCAGACGTCTCCCTTCCAGACAGTGTGAGGCCAGCCTTTGGACAGAAGATCGGAAGAGCGGTTTCAG
chr19	40747795	40747834	AKT2_897	-	GTGACCTATGCACCAGACGTGCGGAATTGCGCTCGCGAGCCTCTGTGGGGGCTCGGTTAGATCGGAAGAGCGGTTTCAG
chr19	40748391	40748430	AKT2_898	-	GTGACCTATGCACCAGACGTGGAGCAGGGGTGGGGTGGCCAGCCTGCGGTGCCCCACCCAGATCGGAAGAGCGGTTTCAG
chr19	40761015	40761054	AKT2_899	-	GTGACCTATGCACCAGACGTGCCTGTGTGCTGCCCTGAGAGGGAGCAAGCCTGGTGAGATCGGAAGAGCGGTTTCAG
chr19	40762783	40762822	AKT2_900	-	GTGACCTATGCACCAGACGTGGATGAGTGGTCAAGTGTCTGTTGCTCACAGATGCTGAGATCGGAAGAGCGGTTTCAG
chr19	40771079	40771118	AKT2_901	-	GTGACCTATGCACCAGACGTGCTTTTCCCGCCAGATTTCTTCCACGCTGGCTCCTCAGATCGGAAGAGCGGTTTCAG
chr16	3777669	3777708	CREBBP_902	-	GTGACCTATGCACCAGACGTGCATCACCTTTTCCCTTTCATGTTCTTGGACCTTTTGTACAGATCGGAAGAGCGGTTTCAG
chr16	3781143	3781182	CREBBP_903	-	GTGACCTATGCACCAGACGTCCCCACCCCCACCCCCACAGCGCCGCTGGGGTCTGACGAAGATCGGAAGAGCGGTTTCAG
chr16	3781727	3781766	CREBBP_904	-	GTGACCTATGCACCAGACGTGCTCGGCTGCTGAGGCTGACCCGCTGCCCTGGCCGGGAGGAGGGAAGATCGGAAGAGCGGTTTCAG
chr16	3785987	3786026	CREBBP_905	-	GTGACCTATGCACCAGACGTCTCTGCTGCTCATTGCCATTCAGCTGCTCCGCTGGAGCTGACATCGGAAGAGCGGTTTCAG
chr16	3786601	3786640	CREBBP_906	-	GTGACCTATGCACCAGACGTCTGAAGGAAGGTGGTGGCTTTTGTACAACCTGAGGGGAGGAGATCGGAAGAGCGGTTTCAG
chr16	3788510	3788549	CREBBP_907	-	GTGACCTATGCACCAGACGTATTAATTTTGAACCTAGTAAGAACCCTTTATTTTTAGATCGGAAGAGCGGTTTCAG
chr16	3789529	3789568	CREBBP_908	-	GTGACCTATGCACCAGACGTAGCTCCTCCAGGGCGTGTCACTCAGTGAGCCGTGTTAGGAGATCGGAAGAGCGGTTTCAG
chr16	3790350	3790389	CREBBP_909	-	GTGACCTATGCACCAGACGTCTGCTCTACAGTGTCTGCGAGCAGTCCCACGCCCCGAGATCGGAAGAGCGGTTTCAG
chr16	3794845	3794884	CREBBP_910	-	GTGACCTATGCACCAGACGTGGAAGCTTTCTGTTTCTGGACTGCACATTTAGAAACTTAGATCGGAAGAGCGGTTTCAG
chr16	3795228	3795267	CREBBP_911	-	GTGACCTATGCACCAGACGTCTCCCTGGCCGTGAGGCGAGTTCGCACAGAGCCAGTGGCAGATCGGAAGAGCGGTTTCAG
chr16	3799578	3799617	CREBBP_912	-	GTGACCTATGCACCAGACGTAGCTATTTCTTTTTACTTTTCAGTTTTGGTTTTGAAATCGGAGATCGGAAGAGCGGTTTCAG
chr16	3801677	3801716	CREBBP_913	-	GTGACCTATGCACCAGACGTTCCTGTCTTTCTCTGGGGTGAAGGAGGGTACCTTAAAGATCGGAAGAGCGGTTTCAG
chr16	3807239	3807278	CREBBP_914	-	GTGACCTATGCACCAGACGTAGCAGCATCTGCATTATGCTTAGGGCAAGGCACGTTCAAGATCGGAAGAGCGGTTTCAG
chr16	3807760	3807799	CREBBP_915	-	GTGACCTATGCACCAGACGTAAAGTTTTCCGGAAGTGAATTTCTGGTTAATCCAGCCAGATCGGAAGAGCGGTTTCAG
chr16	3808805	3808844	CREBBP_916	-	GTGACCTATGCACCAGACGTTCATAAAAATAGATTAACCTTTGCTGGTGAATCTTCAAGATCGGAAGAGCGGTTTCAG
chr16	3817671	3817710	CREBBP_917	-	GTGACCTATGCACCAGACGTATTCTATTACCTTATTAAGCATGCTGCTTTTCCACGGTGAAGATCGGAAGAGCGGTTTCAG
chr16	3819125	3819164	CREBBP_918	-	GTGACCTATGCACCAGACGTCTCCCTAGGAATGCATTGACTGCGTATCGCAACTTTACCCAGATCGGAAGAGCGGTTTCAG
chr16	3820521	3820560	CREBBP_919	-	GTGACCTATGCACCAGACGTCTGTCTGCTGTTTTGGGCCAAGACTCTTAGAAGATAAAGATCGGAAGAGCGGTTTCAG
chr16	3823702	3823741	CREBBP_920	-	GTGACCTATGCACCAGACGTCCACTGGGACCGTGGCTCCCTAGGCAAAATAAATCTTTGTGAGATCGGAAGAGCGGTTTCAG
chr16	3824520	3824559	CREBBP_921	-	GTGACCTATGCACCAGACGTCTTCCGCTGCTGCTGCAGATGACCCCTCCTCAGATCGGAAGATCGGAAGAGCGGTTTCAG
chr16	3827564	3827603	CREBBP_922	-	GTGACCTATGCACCAGACGTGTTTGGTGGTGAATCATATTTTAGTTTTACATTCACAGCCAGATCGGAAGAGCGGTTTCAG
chr16	3827962	3828001	CREBBP_923	-	GTGACCTATGCACCAGACGTATTCTTCTACTGCCATCCCTTAGCCTGTTTCTTGGTTTTAGATCGGAAGAGCGGTTTCAG
chr16	3828651	3828690	CREBBP_924	-	GTGACCTATGCACCAGACGTGTTTACCCTGCTCTGGCCTTACAGCATCTGTAGTAGACAAGATCGGAAGAGCGGTTTCAG
chr16	3830683	3830722	CREBBP_925	-	GTGACCTATGCACCAGACGTGTTTGCAGTTTCATAGATGTTTGAATTTTCTGTTAGATCGGAAGAGCGGTTTCAG
chr16	3831155	3831194	CREBBP_926	-	GTGACCTATGCACCAGACGTGTTTCAGATCTGAGTGACAGTCCAACAGGAGCATGGACTGAGATCGGAAGAGCGGTTTCAG
chr16	3832635	3832674	CREBBP_927	-	GTGACCTATGCACCAGACGTGAACTCAACTCTGTTCTTACTTGTCCACATGCAGCAAAAGATCGGAAGAGCGGTTTCAG
chr16	3841932	3841971	CREBBP_928	-	GTGACCTATGCACCAGACGTACGGGGCCAGAGAAGCTTTGGAGATGAGAATAGAAGTTGTTAGATCGGAAGAGCGGTTTCAG



chr16	3843337	3843376	CREBBP_929	-	GTGACCTATGCACCAGACGTTTTTTTGGAACTCCTAGTGGTAGAGGTCAGGAAGAATTTGCAGATCGGAAGAGCGGTTTCAG
chr16	3860554	3860593	CREBBP_930	-	GTGACCTATGCACCAGACGCTTTGGCCCTCAGTGTATGGCTCTCCGGTGGGTGCTGTGGAGATCGGAAGAGCGGTTTCAG
chr16	3900248	3900287	CREBBP_931	-	GTGACCTATGCACCAGACGTTGAAGCACTTTCAATACTTCTACCTAACCCGCGGGCTTTCAGATCGGAAGAGCGGTTTCAG
chr16	3900604	3900643	CREBBP_932	-	GTGACCTATGCACCAGACGTGAATCCGCAAGCACAAAAGCAAGTGGGGCTGGCGACTAGCAGATCGGAAGAGCGGTTTCAG
chr16	3778100	3778139	CREBBP_933	-	GTGACCTATGCACCAGACGTGCAGATTTGGGTCCCCAGGCCAGCCGAACCCCATGAGCCCCAGATCGGAAGAGCGGTTTCAG
chr16	3778531	3778570	CREBBP_934	-	GTGACCTATGCACCAGACGTGCGATGGGAGGCCGTGAACCCAGGGGCCAGGCCTTGAACAAGATCGGAAGAGCGGTTTCAG
chr16	3778962	3779001	CREBBP_935	-	GTGACCTATGCACCAGACGTGGCTTGCCTCCCGGCGAGTGGCAGCAGCGGCCCTTCCCGCAAGATCGGAAGAGCGGTTTCAG
chr16	3779393	3779432	CREBBP_936	-	GTGACCTATGCACCAGACGTGAACACCCGCAACGTGCCTCAGCAGAGTCTGCCTTCTCCTAGATCGGAAGAGCGGTTTCAG
chr22	29999938	29999977	NF2_937	-	GTGACCTATGCACCAGACGTTCAGGCCCGGGACCCTCGCGCCCCAGGCCTGCACCTCTGAAGATCGGAAGAGCGGTTTCAG
chr22	30032690	30032729	NF2_938	-	GTGACCTATGCACCAGACGTAAACCAATGGGGAAAGGACACTGTGAGCAAAAATCATTAAATAGATCGGAAGAGCGGTTTCAG
chr22	30035029	30035068	NF2_939	-	GTGACCTATGCACCAGACGTGCAGAGCAAAAAGACAAACACACTATATTGGCACTTCTCCAGATCGGAAGAGCGGTTTCAG
chr22	30038141	30038180	NF2_940	-	GTGACCTATGCACCAGACGTCAACAAGGGAGACACTGATACTGTGTAGTGAAGTGAGGTAGATCGGAAGAGCGGTTTCAG
chr22	30050596	30050635	NF2_941	-	GTGACCTATGCACCAGACGTGAAAGGGAGGACAGGCCGATTGAGATTCATAAGATAACTGCAGATCGGAAGAGCGGTTTCAG
chr22	30051533	30051572	NF2_942	-	GTGACCTATGCACCAGACGTATAGAGCAAAAATAAAAAACCTACACATGAAGTAAATTTGGAGATCGGAAGAGCGGTTTCAG
chr22	30054128	30054167	NF2_943	-	GTGACCTATGCACCAGACGTAAACGAAGACACTGTCATTGGAGCTAAGTGAGATGGGTGGAGATCGGAAGAGCGGTTTCAG
chr22	30057144	30057183	NF2_944	-	GTGACCTATGCACCAGACGTAAATAAGAACAGCTACTGTAAGCGCCAGCTGAGGCTCAAAAAGATCGGAAGAGCGGTTTCAG
chr22	30060929	30060968	NF2_945	-	GTGACCTATGCACCAGACGTGAAGCAGAACACAGTTTCAGTCCGACAGCCTGGAATGTTAAGATCGGAAGAGCGGTTTCAG
chr22	30064272	30064311	NF2_946	-	GTGACCTATGCACCAGACGTGAAAGGCAGACAAAAGGTTAATATCCACAAAATTTTCAAGATCGGAAGAGCGGTTTCAG
chr22	30067765	30067804	NF2_947	-	GTGACCTATGCACCAGACGTTGAAGAAAAACAGTCAATGAATCACAGGGCTCGAGACCTAAGATCGGAAGAGCGGTTTCAG
chr22	30069208	30069247	NF2_948	-	GTGACCTATGCACCAGACGTCAAGTCTTAGCTGAAGTGGGATCATGTGCTGTTCTCCAGATCGGAAGAGCGGTTTCAG
chr22	30070775	30070814	NF2_949	-	GTGACCTATGCACCAGACGTAGGATGAGATGTACGCTTACAGAAAGAGGGCAGGTAGCAGAGATCGGAAGAGCGGTTTCAG
chr22	30074135	30074174	NF2_950	-	GTGACCTATGCACCAGACGTGAAATTTTCGATTAGGAGCTTGGGTCTACAAAGCACAGAAAGATCGGAAGAGCGGTTTCAG
chr22	30077378	30077417	NF2_951	-	GTGACCTATGCACCAGACGTGAGGGTATCATGCATCAGGGCTTGGGCAGACAGTGAAGACAGATCGGAAGAGCGGTTTCAG
chr22	30078959	30078998	NF2_952	-	GTGACCTATGCACCAGACGTAAATAAGTAAAGCAAAAACAAAACCTTGTGATATAGATCGGAAGAGCGGTTTCAG
chr22	30090691	30090730	NF2_953	-	GTGACCTATGCACCAGACGTGCAGAGAAGAAGCTGAGAGGGCACAAAGACCTCCGCTCTGTAGATCGGAAGAGCGGTTTCAG
chr1	156785572	156785611	NTRK1_954	-	GTGACCTATGCACCAGACGTGCCACTCACTCCCTTACTGCTCTTAGGCCCTCTGGAAGCAGATCGGAAGAGCGGTTTCAG
chr1	156830677	156830716	NTRK1_955	-	GTGACCTATGCACCAGACGTCCCGCTCGCTCAGGCCGGGCAGCCGTCTGTGCGCTCCCAAGATCGGAAGAGCGGTTTCAG
chr1	156834096	156834135	NTRK1_956	-	GTGACCTATGCACCAGACGTAGCGATGGGAGTCAAGCGGGCTCAGGCCACACTTGAGTTAGATCGGAAGAGCGGTTTCAG
chr1	156834470	156834509	NTRK1_957	-	GTGACCTATGCACCAGACGTGTGCGAGGAGTACCTCCCGCTCAGCTACTTGGGCAGATCGGAAGAGCGGTTTCAG
chr1	156836652	156836691	NTRK1_958	-	GTGACCTATGCACCAGACGTGGAGACAGCAAGACAGACCCCTTGAGTGACCCGACCTCAGATCGGAAGAGCGGTTTCAG
chr1	156837846	156837885	NTRK1_959	-	GTGACCTATGCACCAGACGTTGGGGGACACCAACAGAGTCAAGGAAAGGGCCTGAGGGATAGATCGGAAGAGCGGTTTCAG
chr1	156838247	156838286	NTRK1_960	-	GTGACCTATGCACCAGACGTAGGACGCCCCAGGGCCAAAGGGTGTAGAGCTGGGAGTGGAGATCGGAAGAGCGGTTTCAG
chr1	156841365	156841404	NTRK1_961	-	GTGACCTATGCACCAGACGTAAAGAGAGGGGGGAATAAGAAGGAGCTTTAGCCAGCTTGGAGATCGGAAGAGCGGTTTCAG
chr1	156843375	156843414	NTRK1_962	-	GTGACCTATGCACCAGACGTGAAAGAGCAACAGCAGGAGGTCAAGGGCCGACCTGGAGGGAAAGATCGGAAGAGCGGTTTCAG
chr1	156844125	156844164	NTRK1_963	-	GTGACCTATGCACCAGACGTAGGGAGGAGAGAAAGAGTCAAGGAGGAGAGAAAGCAGAGATCGGAAGAGCGGTTTCAG
chr1	156844313	156844352	NTRK1_964	-	GTGACCTATGCACCAGACGTACAGGGCAGGAGGGTGAAGCTTACACACACTGTAGCCTAGATCGGAAGAGCGGTTTCAG
chr1	156844648	156844687	NTRK1_965	-	GTGACCTATGCACCAGACGTACAGGGGTAGTTAGATCCAGGGGCTCCTCTGTACTCTCAAGATCGGAAGAGCGGTTTCAG
chr1	156845262	156845301	NTRK1_966	-	GTGACCTATGCACCAGACGTGACACAGCCGATGGAGGGGTTTGCACACCTTGGCCCTAGATCGGAAGAGCGGTTTCAG
chr1	156845822	156845861	NTRK1_967	-	GTGACCTATGCACCAGACGTTTGCAGGGTCAAGCAGTACGCCCCAGTCTTGGGAGGGCTGGAGATCGGAAGAGCGGTTTCAG
chr1	156846142	156846181	NTRK1_968	-	GTGACCTATGCACCAGACGTGCGGCAGGGACAGGACTGAGTTGGGGCCGAGCCCTCACTAGATCGGAAGAGCGGTTTCAG
chr1	156848864	156848903	NTRK1_969	-	GTGACCTATGCACCAGACGTGAAAAGAGAGGGGATAGGCTGGGAGGATAGAATCCCAAGATCGGAAGAGCGGTTTCAG
chr1	156849741	156849780	NTRK1_970	-	GTGACCTATGCACCAGACGTGCGACACTGCATCAATTCAGGGGCGCCTGGGACAGCCGAGATCGGAAGAGCGGTTTCAG
chr5	149495276	149495315	PDGFRB_971	-	GTGACCTATGCACCAGACGTCTACCCTGCCCTGCCTGAAGCTCCCCCCTGCCAGACAGATCGGAAGAGCGGTTTCAG
chr5	149498260	149498299	PDGFRB_972	-	GTGACCTATGCACCAGACGTGCAGGGTAGGGGTGGAGCACGGAGAGCTCTGGTGCAGAAGAGATCGGAAGAGCGGTTTCAG
chr5	149499525	149499564	PDGFRB_973	-	GTGACCTATGCACCAGACGTTTTCTCCTCCAGCCCTCAGCATCTGGCCTGGTGTCTACCAGATCGGAAGAGCGGTTTCAG
chr5	149500401	149500440	PDGFRB_974	-	GTGACCTATGCACCAGACGTTCCTCGCCCTGCAGGGCAGTACAGTGCCTGTGACCAGATCGGAAGAGCGGTTTCAG
chr5	149500717	149500756	PDGFRB_975	-	GTGACCTATGCACCAGACGTTGTTGGTGGGGCAGAGTGGGGGCTGTGGGGAGGTGGGTCAAGATCGGAAGAGCGGTTTCAG
chr5	149501393	149501432	PDGFRB_976	-	GTGACCTATGCACCAGACGTATAGTGACATAGTACCCACATCCAACAGGCTGATGCTCAGATCGGAAGAGCGGTTTCAG
chr5	149502555	149502594	PDGFRB_977	-	GTGACCTATGCACCAGACGTGGAGGCCAGGGACTGAATCTTTGGGATACCTGAGGACACAGATCGGAAGAGCGGTTTCAG
chr5	149503763	149503802	PDGFRB_978	-	GTGACCTATGCACCAGACGTCACTGCCCCAGAGGCCCTCAGGGAAAGTGCACCACCAAGAGATCGGAAGAGCGGTTTCAG
chr5	149504240	149504279	PDGFRB_979	-	GTGACCTATGCACCAGACGTCTTGGAGCCCTCCACCTTGGGCCCTCACTTCCCTGCCAGATCGGAAGAGCGGTTTCAG
chr5	149506033	149506072	PDGFRB_980	-	GTGACCTATGCACCAGACGTCCCTGCCAGTGGGTGAAGACTGACACATCAATTTTGAATCGGAAGAGCGGTTTCAG
chr5	149509270	149509309	PDGFRB_981	-	GTGACCTATGCACCAGACGTAGCCTCAGTGGCCCTGACGATCCCAATCCCTACCTTAATAGATCGGAAGAGCGGTTTCAG
chr5	149510052	149510091	PDGFRB_982	-	GTGACCTATGCACCAGACGTCTGGGCCTCAGTCTCCAGTGTCCCAAGTGGCTAGAAAAAGATCGGAAGAGCGGTTTCAG
chr5	149512263	149512302	PDGFRB_983	-	GTGACCTATGCACCAGACGTGCTCTCCATCCCATCTTGAAGTATTTTTCTTTCAGAGATCGGAAGAGCGGTTTCAG
chr5	149513099	149513138	PDGFRB_984	-	GTGACCTATGCACCAGACGTTGGGCTCAGCCCAATCCCAATCCTTCAACGCTCCCAACAGATCGGAAGAGCGGTTTCAG
chr5	149513394	149513433	PDGFRB_985	-	GTGACCTATGCACCAGACGTGCCAGGCTCGAGGCTGGAGGGCCAGGAACGGTGGATAGATCGGAAGAGCGGTTTCAG
chr5	149515068	149515107	PDGFRB_986	-	GTGACCTATGCACCAGACGTCCAGCCTGTGTGCCCACTCTTACCCCTTGTCAACTGGAGATCGGAAGAGCGGTTTCAG

chr5	149516521	149516560	PDGFRB_987	-	GTGACCTATGCACCAGACGTGGGAGATAAGGTAGGGGACCCGGGGGCTGCGGAGTGGAAGATCGGAAGAGCGGTTTCAG
chr9	133589657	133589696	ABL1_988	-	GTGACCTATGCACCAGACGTTAGGTACCCCTTTCCAGAAAGGGTTCAAGATCTTCCAGAAGATCGGAAGAGCGGTTTCAG
chr9	133729401	133729440	ABL1_989	-	GTGACCTATGCACCAGACGTAAGGGGGGAACAGAAAAAAGAAAAAGGAAGAGAAAATTGGAGATCGGAAGAGCGGTTTCAG
chr9	133730138	133730177	ABL1_990	-	GTGACCTATGCACCAGACGTAGGAACCAAATCAGACATATCAGCTTTGGAAACCAGCTTCAGATCGGAAGAGCGGTTTCAG
chr9	133738100	133738139	ABL1_991	-	GTGACCTATGCACCAGACGTCAGGGAACAGCCTTCAGCCCACAGAGACAGGCAAGCTCAAAGATCGGAAGAGCGGTTTCAG
chr9	133747466	133747505	ABL1_992	-	GTGACCTATGCACCAGACGTAAAAAACGAAGGTGAAATTTATTCAGGAAGTGCTTTTCAAGATCGGAAGAGCGGTTTCAG
chr9	133748197	133748236	ABL1_993	-	GTGACCTATGCACCAGACGTGACAACCGGACTTCAACAGCTGGCTCCGCTCCCACTGAAGATCGGAAGAGCGGTTTCAG
chr9	133750205	133750244	ABL1_994	-	GTGACCTATGCACCAGACGTAAATGTTACCCATGAGAGCTCCTGGCCAACCTTCCACTAGATCGGAAGAGCGGTTTCAG
chr9	133753752	133753791	ABL1_995	-	GTGACCTATGCACCAGACGTACCGAAAGAGAAAGGCTGTCAAGATGTGTAGCATTTTACAGATCGGAAGAGCGGTTTCAG
chr9	133755405	133755444	ABL1_996	-	GTGACCTATGCACCAGACGTGAAACCCAAGTCAGATCATCCATGAGATCTGGCTAGCAATAGATCGGAAGAGCGGTTTCAG
chr9	133755837	133755876	ABL1_997	-	GTGACCTATGCACCAGACGTTACAGGGGACAGAAACAAAATCCAGCAGCCATCAGTACTGAGATCGGAAGAGCGGTTTCAG
chr9	133759735	133759774	ABL1_998	-	GTGACCTATGCACCAGACGTGGCTAGGCGGCTGTGGTCAGCTGCTGGACTTCTTCCACAGATCGGAAGAGCGGTTTCAG
chr9	133760164	133760203	ABL1_999	-	GTGACCTATGCACCAGACGTAAAGGCACTGCCCTTCCAGCTTCTTCCCTTGTGGGGAGGAGATCGGAAGAGCGGTTTCAG
chr9	133760593	133760632	ABL1_1000	-	GTGACCTATGCACCAGACGTCAACGTGGAGGGAACGGGGGCTGGGCTGATGGGGTCCCCAGATCGGAAGAGCGGTTTCAG
chr11	69456032	69456071	CCND1_1001	-	GTGACCTATGCACCAGACGTCTTCTGGGACGCTGGGAGGGCTGTGGGTCCTGGCTGGGAGATCGGAAGAGCGGTTTCAG
chr11	69457749	69457788	CCND1_1002	-	GTGACCTATGCACCAGACGTACGGGGCCCGTGACCGCCGCGCCAGGTGCGCGCCGCCCCAGATCGGAAGAGCGGTTTCAG
chr11	69458550	69458589	CCND1_1003	-	GTGACCTATGCACCAGACGTAGGGTGAGCGGGCCATCAGGGGAGGTCGGGGCCAGCCCGGGAGATCGGAAGAGCGGTTTCAG
chr11	69462712	69462751	CCND1_1004	-	GTGACCTATGCACCAGACGTAGGAGAGGAGAGGCTGTGAGCAGGGGACCCTCTCAAGATCGGAAGAGCGGTTTCAG
chr11	69465836	69465875	CCND1_1005	-	GTGACCTATGCACCAGACGTGAGGGTGGGGAGAGGTGGGAAGAGGGGCTCCTTAGAAGGGAGATCGGAAGAGCGGTTTCAG
chr7	92244404	92244443	CDK6_1006	-	GTGACCTATGCACCAGACGTGCCGCCTTAAGCTGATCCTGCGGAGAACACCCTTGGTGGCAGATCGGAAGAGCGGTTTCAG
chr7	92247336	92247375	CDK6_1007	-	GTGACCTATGCACCAGACGTCTGATGTCAAGCTCGTCTGCACTGTGCCAGTGAGACACCTAGATCGGAAGAGCGGTTTCAG
chr7	92252300	92252339	CDK6_1008	-	GTGACCTATGCACCAGACGTATTATAATTTTACACCAGTGTCCATAGCATTAAACATTTAGATCGGAAGAGCGGTTTCAG
chr7	92300690	92300729	CDK6_1009	-	GTGACCTATGCACCAGACGTCAATTTTCTACTCTGCTTTTCCCTTGAAAGAGACTGTGGAGATCGGAAGAGCGGTTTCAG
chr7	92354890	92354929	CDK6_1010	-	GTGACCTATGCACCAGACGTGAGTCTGCTCTTTTAACTTATTAACATTTTCCCTATTTTGAAAGTCGGAAGAGCGGTTTCAG
chr7	92403960	92403999	CDK6_1011	-	GTGACCTATGCACCAGACGTTTCATCTTTCATGTCTTATCAGGCAGTCGACTATTATAGTCTAGATCGGAAGAGCGGTTTCAG
chr7	92462355	92462394	CDK6_1012	-	GTGACCTATGCACCAGACGTGAGCTGCGCCCTGCCATCTGGGCTCGCGCGCGGGGAGATCGGAAGAGCGGTTTCAG
chr14	102547999	102548038	HSP90AA1_1013	-	GTGACCTATGCACCAGACGTAGGGATGACTTACTGTTTCAGTACTCTACAATTCCTCTGAAGATCGGAAGAGCGGTTTCAG
chr14	102548398	102548437	HSP90AA1_1014	-	GTGACCTATGCACCAGACGTTACTATGTAATGTAAAAAGAAAATAAACACACAGCTGATCATAGATCGGAAGAGCGGTTTCAG
chr14	102549321	102549360	HSP90AA1_1015	-	GTGACCTATGCACCAGACGTACACTGATTTCTGATCATTGATCTCTAAGTGTCTTCAAGATCGGAAGAGCGGTTTCAG
chr14	102549833	102549872	HSP90AA1_1016	-	GTGACCTATGCACCAGACGTACTGTTTACAGTCAACAGCTCGTCTTACAATCTTGAAGATCGGAAGAGCGGTTTCAG
chr14	102550686	102550725	HSP90AA1_1017	-	GTGACCTATGCACCAGACGTATAGGAAAAATAACTACTGTCACTGATTAAGAAGTACTTAGATCGGAAGAGCGGTTTCAG
chr14	102550968	102551007	HSP90AA1_1018	-	GTGACCTATGCACCAGACGTGATGGGTGCTTCAAGCTTGTCTTAGATTATCATCTTTCTAGATCGGAAGAGCGGTTTCAG
chr14	102551585	102551624	HSP90AA1_1019	-	GTGACCTATGCACCAGACGTATGTAATTCAGAGTGAATTTCTGTCTGTAGGTGATTGGGAGATCGGAAGAGCGGTTTCAG
chr14	102552045	102552084	HSP90AA1_1020	-	GTGACCTATGCACCAGACGTGAACACTGATTTAAGTGAGCGGTGGAAGGGTGGGGTGGAGATCGGAAGAGCGGTTTCAG
chr14	102552504	102552543	HSP90AA1_1021	-	GTGACCTATGCACCAGACGTATTAATCCAGAACTGGATTGGGTTTCAGTGTGAACCTGAGATCGGAAGAGCGGTTTCAG
chr14	102568162	102568201	HSP90AA1_1022	-	GTGACCTATGCACCAGACGTTAAGGTTTAAATTAATCTATCCTAAACATTTCTAGCTAATGAGATCGGAAGAGCGGTTTCAG
chr14	102605537	102605576	HSP90AA1_1023	-	GTGACCTATGCACCAGACGTACTCAAGATTTACGCTTCACTATGTTTTATTTTCAGGCGGGAGATCGGAAGAGCGGTTTCAG
chr19	1611656	1611695	TCF3_1024	-	GTGACCTATGCACCAGACGTTCCGTGGGACGAGCCACCCGCTTTCAGCCCTGTGCTCTGGAGATCGGAAGAGCGGTTTCAG
chr19	1612156	1612195	TCF3_1025	-	GTGACCTATGCACCAGACGTGGCCAGGGGCTGCCACAGCACCCCTCTCCCTTCCCCACACCAGATCGGAAGAGCGGTTTCAG
chr19	1615234	1615273	TCF3_1026	-	GTGACCTATGCACCAGACGTGCGCGGGGCCACACAGCTCCCTGCAGCGCCACCCTCCCTCGAGATCGGAAGAGCGGTTTCAG
chr19	1615635	1615674	TCF3_1027	-	GTGACCTATGCACCAGACGTACCCCTCGGCATCCCCACCCTCACCCATCAGGACACAGATCGGAAGAGCGGTTTCAG
chr19	1619060	1619099	TCF3_1028	-	GTGACCTATGCACCAGACGTGAGCTTGGGACTGTCCGACTCCTGGTTCCAGTTGGGGAAAAGATCGGAAGAGCGGTTTCAG
chr19	1619265	1619304	TCF3_1029	-	GTGACCTATGCACCAGACGTGGCGAGGGTGGAGCTGGGCAAGTGGGCGGGGACCCTCGGCTCCAGATCGGAAGAGCGGTTTCAG
chr19	1619729	1619768	TCF3_1030	-	GTGACCTATGCACCAGACGTGCCCGGCCACCCACCCCTTCCCCGACAGAATTTGCAAGGAGATCGGAAGAGCGGTTTCAG
chr19	1620917	1620956	TCF3_1031	-	GTGACCTATGCACCAGACGTGTTTTGGGGGAGGGGAGGCTGAGGCTGTGAGGGTTTGGAGATCGGAAGAGCGGTTTCAG
chr19	1621082	1621121	TCF3_1032	-	GTGACCTATGCACCAGACGTGGCCATGGGGGCTGGCCAGGCAAGTGACCTGAGAGGCCGAGATCGGAAGAGCGGTTTCAG
chr19	1621787	1621826	TCF3_1033	-	GTGACCTATGCACCAGACGTTCCCTGGGATGCGGCCCTCCTCCAGGGGACACTGGGCTCCAAGATCGGAAGAGCGGTTTCAG
chr19	1622003	1622042	TCF3_1034	-	GTGACCTATGCACCAGACGTGGGCAGGGGCGAGGGGTGGGCGGAGGGTGGCAGTCCCAAGATCGGAAGAGCGGTTTCAG
chr19	1622262	1622301	TCF3_1035	-	GTGACCTATGCACCAGACGTGGGCGGGGCTCGCCAGGGACGGTAGGGCAGGGCTGGGGTAGATCGGAAGAGCGGTTTCAG
chr19	1623900	1623939	TCF3_1036	-	GTGACCTATGCACCAGACGTGAGGGGAGAGGGACCCACAGCTCGTCAAGTGGCAGTGCCAGATCGGAAGAGCGGTTTCAG
chr19	1625525	1625564	TCF3_1037	-	GTGACCTATGCACCAGACGTTCTGGCCGGGATCGGGGGCTTCTGGGAGGGAGCCTCAAGATCGGAAGAGCGGTTTCAG
chr19	1627308	1627347	TCF3_1038	-	GTGACCTATGCACCAGACGTGCGGCGGGCTGGGTTGATTTTATTAAACAAATCTGAGATCGGAAGAGCGGTTTCAG
chr19	1631987	1632026	TCF3_1039	-	GTGACCTATGCACCAGACGTGGCCTGGTGCGGTCCCTCTGTGTGCACAGATGTGCAGACAGATCGGAAGAGCGGTTTCAG
chr19	1632281	1632320	TCF3_1040	-	GTGACCTATGCACCAGACGTCCGTGAGGCCTGAGACCTGAGTTTCTGTCCCCAGAGTTAGATCGGAAGAGCGGTTTCAG
chr19	1646304	1646343	TCF3_1041	-	GTGACCTATGCACCAGACGTGCCCTTCTGCCAGCGCTCGTGAGTGAAGGATCAAGGGTAGATCGGAAGAGCGGTTTCAG
chr19	1650126	1650165	TCF3_1042	-	GTGACCTATGCACCAGACGTACCCCGGCCACCCCGACACCCCTTGCCTCCACAGTTAGATCGGAAGAGCGGTTTCAG
chr3	41265510	41265549	CTNNB1_1043	-	GTGACCTATGCACCAGACGTGGATTTTCAAACAGCTTGTATGGTACTTCAAATACCCTAGATCGGAAGAGCGGTTTCAG
chr3	41265967	41266006	CTNNB1_1044	-	GTGACCTATGCACCAGACGTGAAACAGATTAGCATTAGATTGAAATGTTACTTTAAGATCGGAAGAGCGGTTTCAG

chr3	41266395	41266434	CTNNB1_1045	-	GTGACCTATGCACCAGACGTTTAATTCACACTCACTATCCACAGTTCAGCATTACCTAAGATCGGAAGAGCGGTTTCAG
chr3	41266775	41266814	CTNNB1_1046	-	GTGACCTATGCACCAGACGTTGAAATTCAGAAAACATCGTTAGTTTTCAAGTACTGGTATTGAGATCGGAAGAGCGGTTTCAG
chr3	41267101	41267140	CTNNB1_1047	-	GTGACCTATGCACCAGACGTTGAAAAAGCCTCATCAGAAATATTGTGAGTATACTCTTCTAGATCGGAAGAGCGGTTTCAG
chr3	41268649	41268688	CTNNB1_1048	-	GTGACCTATGCACCAGACGTATATATATATATCTTGTAGTCAAGGAATCTTGATCAGATAGATCGGAAGAGCGGTTTCAG
chr3	41274782	41274821	CTNNB1_1049	-	GTGACCTATGCACCAGACGTTAAAAAGGATATAAGGCCCTAGTTCATTAGCTAGAAAGTGCCTAGATCGGAAGAGCGGTTTCAG
chr3	41274970	41275009	CTNNB1_1050	-	GTGACCTATGCACCAGACGTTAAAAACAGTGGTCAAGTACAAGCACATACTCATCTTGACTAGATCGGAAGAGCGGTTTCAG
chr3	41275580	41275619	CTNNB1_1051	-	GTGACCTATGCACCAGACGTTGAAGGAAGAATGGCATAACAACAAATCAATTTCTAGATCGGAAGAGCGGTTTCAG
chr3	41277165	41277204	CTNNB1_1052	-	GTGACCTATGCACCAGACGTTAAACATGGTTAAACAAACAGGGCATTCTCCTCTGTAAGGTTAGATCGGAAGAGCGGTTTCAG
chr3	41277790	41277829	CTNNB1_1053	-	GTGACCTATGCACCAGACGTTAACAAAAACAACTAATTAATCTAAAGCTAAAACATGAGATCGGAAGAGCGGTTTCAG
chr3	41278029	41278068	CTNNB1_1054	-	GTGACCTATGCACCAGACGTAGGAGAAAAAGGCCCTTGAGGAAAAACTGAGACTTCAATGAGATCGGAAGAGCGGTTTCAG
chr3	41279457	41279496	CTNNB1_1055	-	GTGACCTATGCACCAGACGTATGCACAAAAGGAAGAATAGAAAAGCAAAATGAAAATTAGATCGGAAGAGCGGTTTCAG
chr3	41280575	41280614	CTNNB1_1056	-	GTGACCTATGCACCAGACGTGAGGTTGTCAACAAAATAGGCAAGAAGGAAGGCAAAAAGAGAGATCGGAAGAGCGGTTTCAG
chr8	38271096	38271135	FGFR1_1057	-	GTGACCTATGCACCAGACGTACAGCCCTCCCCAGACTCCACCGTCAAGCTGTAACCCCTCACAGATCGGAAGAGCGGTTTCAG
chr8	38271386	38271425	FGFR1_1058	-	GTGACCTATGCACCAGACGTCCCGTCCAGAGCCAGAGCTCAGGCCCTCCCACTGCGTGCAGATCGGAAGAGCGGTTTCAG
chr8	38271620	38271659	FGFR1_1059	-	GTGACCTATGCACCAGACGTGGAGATGTCGGAGGCCCTGAGCCAGGCCCTGGGGCAAGAGAGATCGGAAGAGCGGTTTCAG
chr8	38272027	38272066	FGFR1_1060	-	GTGACCTATGCACCAGACGTAAATAGCAATTGCCAGGGAGGTGTGGGATAGAGAGCTTCAAGATCGGAAGAGCGGTTTCAG
chr8	38272247	38272286	FGFR1_1061	-	GTGACCTATGCACCAGACGTACAAGGCCCGCCTGTGCTGGTGGTTTCATCTGAGAAGCAAAAGATCGGAAGAGCGGTTTCAG
chr8	38273338	38273377	FGFR1_1062	-	GTGACCTATGCACCAGACGTGAAGGCTCCCTGGTGTAGTCCAGGTTGGGAACAGATCGGAAGAGCGGTTTCAG
chr8	38274774	38274813	FGFR1_1063	-	GTGACCTATGCACCAGACGTGCCAGACTGGCTTTCCCTGCCAGCGGGGAGAAGATCTGAAGATCGGAAGAGCGGTTTCAG
chr8	38275338	38275377	FGFR1_1064	-	GTGACCTATGCACCAGACGTCTTCTGTCTTGCAAAAGAAAATCTTGCCATTCCAAGCAAGATCGGAAGAGCGGTTTCAG
chr8	38275696	38275735	FGFR1_1065	-	GTGACCTATGCACCAGACGTTTTGACTCCCAACTTTTTGAAGGCATTCTTCTGCTTATAGATCGGAAGAGCGGTTTCAG
chr8	38277001	38277040	FGFR1_1066	-	GTGACCTATGCACCAGACGTGGGGGATTTGCACACTCAGCACCCCTCTCTCTGGGCCAGATCGGAAGAGCGGTTTCAG
chr8	38279265	38279304	FGFR1_1067	-	GTGACCTATGCACCAGACGTTAACTTCTCCTCTCGATGTCCTGCCCTGCCACGGGCACAGATCGGAAGAGCGGTTTCAG
chr8	38281737	38281776	FGFR1_1068	-	GTGACCTATGCACCAGACGTGACGACCTACTGGCCCTTGGGGTCACTACACAAGGAAGATCGGAAGAGCGGTTTCAG
chr8	38281977	38282016	FGFR1_1069	-	GTGACCTATGCACCAGACGTACCAGTCTTCGTGGGCCAGTCTACTGGGAAGGAGACCACAGATCGGAAGAGCGGTTTCAG
chr8	38283590	38283629	FGFR1_1070	-	GTGACCTATGCACCAGACGTAGAGGCAGCAGGGAATGAGTTAGTGGGAAGAGCCAGGAGATCGGAAGAGCGGTTTCAG
chr8	38285389	38285428	FGFR1_1071	-	GTGACCTATGCACCAGACGTGTGCATGCGAAAGTTAGAGTAATGGGAACAGGGGAGGCCGAGATCGGAAGAGCGGTTTCAG
chr8	38285814	38285853	FGFR1_1072	-	GTGACCTATGCACCAGACGTGTTTCTTACTGCCCCTTTGGGTTGCGGCATTGGGTTAGATCGGAAGAGCGGTTTCAG
chr8	38285820	38285859	FGFR1_1073	-	GTGACCTATGCACCAGACGTGACACTGTTCTTCTTACTGCCCCTTTGGGTTGCGGCATTGGGTTAGATCGGAAGAGCGGTTTCAG
chr8	38287150	38287189	FGFR1_1074	-	GTGACCTATGCACCAGACGTAAAGCCCTGCCCTTCCCTCCCTACACCCACCCCTCCAGAGATCGGAAGAGCGGTTTCAG
chr8	38314824	38314863	FGFR1_1075	-	GTGACCTATGCACCAGACGTGGCTGGGGCAGCCTGGACTCCTGGGCTTGGGAACAGGAAGATCGGAAGAGCGGTTTCAG
chrX	15364205	15364244	FIGF_1076	-	GTGACCTATGCACCAGACGTCAAGTCCCCATCCTGTGATTTTTAACAGCATGCTGCTTAGATCGGAAGAGCGGTTTCAG
chrX	15365236	15365275	FIGF_1077	-	GTGACCTATGCACCAGACGTTGAGTTGTCTTGCCTTTACTCATGACATTTAACGTAGATGAGATCGGAAGAGCGGTTTCAG
chrX	15373222	15373261	FIGF_1078	-	GTGACCTATGCACCAGACGTTGTTTTTTTTTATACTGGATTATGCTTATTTTTGCCTAGATCGGAAGAGCGGTTTCAG
chrX	15376075	15376114	FIGF_1079	-	GTGACCTATGCACCAGACGTGATTCGGCAAGCCTGCGCTCTCTAAAGCCTGATGATAATAGATCGGAAGAGCGGTTTCAG
chrX	15381181	15381220	FIGF_1080	-	GTGACCTATGCACCAGACGTGGATGTGGAGACAAATCTTTCTTTTATTAGATAGTGACAGATCGGAAGAGCGGTTTCAG
chrX	15401929	15401968	FIGF_1081	-	GTGACCTATGCACCAGACGTTCAATTTTTAATGTGATGAAGTCTTTTTATTGGCTCATAAGATCGGAAGAGCGGTTTCAG
chr11	532586	532625	HRAS_1082	-	GTGACCTATGCACCAGACGTGGGGACTCCCAGGGCGGCCACGCCACCGGATGACCCAGATCGGAAGAGCGGTTTCAG
chr11	533246	533285	HRAS_1083	-	GTGACCTATGCACCAGACGTCCCTCGCGCTGTAAGTCTCCCGGACGGCAGGGCAGTGAGGAGATCGGAAGAGCGGTTTCAG
chr11	533403	533442	HRAS_1084	-	GTGACCTATGCACCAGACGTTTCCACCCACAGCTAGCCAGGGACCCGCCCGCCCGCAGATCGGAAGAGCGGTTTCAG
chr11	533716	533755	HRAS_1085	-	GTGACCTATGCACCAGACGTTGAGGCTGGCCCGGACGCCACGCCACAGGTGGGGCCAAGATCGGAAGAGCGGTTTCAG
chr11	534162	534201	HRAS_1086	-	GTGACCTATGCACCAGACGTGCCCGCCTCCAGGTGCCAGCAGCTGCTGCGGGCAGCCAGATCGGAAGAGCGGTTTCAG
chr15	88420116	88420155	NTRK3_1087	-	GTGACCTATGCACCAGACGTTGGTCATGAATTCATACTCTGTTGCCCTCCTCTCCTCCAGATCGGAAGAGCGGTTTCAG
chr15	88423451	88423490	NTRK3_1088	-	GTGACCTATGCACCAGACGTGGTGCAGTGAATCTTATTGGGGGAGGGCTCATAAGAGCAGATCGGAAGAGCGGTTTCAG
chr15	88472372	88472411	NTRK3_1089	-	GTGACCTATGCACCAGACGTTTTCCAGCTGCAGGACTCAGCCACAGCTAGCGCCTTGAGATCGGAAGAGCGGTTTCAG
chr15	88476193	88476232	NTRK3_1090	-	GTGACCTATGCACCAGACGTATTGTCTTCCCTGCTCAGCTGACCCAGTCCACAGCACCAGATCGGAAGAGCGGTTTCAG
chr15	88483804	88483843	NTRK3_1091	-	GTGACCTATGCACCAGACGTGAGGCATGCCGGCACCAGGAGGAGGGCTGGCTGAGGGCCAGATCGGAAGAGCGGTTTCAG
chr15	88522526	88522565	NTRK3_1092	-	GTGACCTATGCACCAGACGTTAAGCCTCCTGTTTTGATGTCACCTTGGTAGGCTGGGCCAGATCGGAAGAGCGGTTTCAG
chr15	88524407	88524446	NTRK3_1093	-	GTGACCTATGCACCAGACGTTCCCTTGTGAGCTTTGTATGAGTAAGATCCCTCCCTAAGATCGGAAGAGCGGTTTCAG
chr15	88576038	88576077	NTRK3_1094	-	GTGACCTATGCACCAGACGTGGATGGAATGCTCTCCCTCCTGGGAGGGGAGGGTGGTTGAGATCGGAAGAGCGGTTTCAG
chr15	88669452	88669491	NTRK3_1095	-	GTGACCTATGCACCAGACGTGTTTTCATTTCAAGGGCCTCATGGGGGAAACATTACTGAGATCGGAAGAGCGGTTTCAG
chr15	88670343	88670382	NTRK3_1096	-	GTGACCTATGCACCAGACGTTTGGTCAAGAGGAGTGTGTGACTGGCATAGTCAATTTAGATCGGAAGAGCGGTTTCAG
chr15	88671892	88671931	NTRK3_1097	-	GTGACCTATGCACCAGACGTTTTACCTGTTGCTTTGAAACTGATTATTCTGATACTATCAGATCGGAAGAGCGGTTTCAG
chr15	88678282	88678321	NTRK3_1098	-	GTGACCTATGCACCAGACGTCGTAGCTGGATCGGAGGTGTATGGATTCTTTTCAAGCTAGATCGGAAGAGCGGTTTCAG
chr15	88679080	88679119	NTRK3_1099	-	GTGACCTATGCACCAGACGTGTTATTGTGGGGATGGCTGTGTGTGAGGGCAACTGGCAAGATCGGAAGAGCGGTTTCAG
chr15	88679648	88679687	NTRK3_1100	-	GTGACCTATGCACCAGACGTTGGGCTTACGCCCATCAGGAGGCTAGGGAGTATCACACAGATCGGAAGAGCGGTTTCAG
chr15	88680585	88680624	NTRK3_1101	-	GTGACCTATGCACCAGACGTTGGCCAGTGGCCAGCTGACTCCAGGAGGATCCCTCAGATCGGAAGAGCGGTTTCAG
chr15	88690516	88690555	NTRK3_1102	-	GTGACCTATGCACCAGACGTTTTTGAAGACTGTCAGGTAAGTGGTGAATGGCTAGATCGGAAGAGCGGTTTCAG

chr15	88726599	88726638	NTRK3_1103	-	GTGACCTATGCACCAGACGCTCGGGCTGCAGGGATTGGGGGCACATGGCAGGTACTCTTGAGATCGGAAGAGCGGTTTCAG
chr15	88727406	88727445	NTRK3_1104	-	GTGACCTATGCACCAGACGTCGGGCCACAGAGAGGCCCTTCCCTGTGGAAGGGGTGGATGAGATCGGAAGAGCGGTTTCAG
chr15	88799087	88799126	NTRK3_1105	-	GTGACCTATGCACCAGACGTCGGCCGCTCCCCAGCCTGCCTCCCCCGCTCTGCGTCTCAGATCGGAAGAGCGGTTTCAG
chr11	32410554	32410593	WT1_1106	-	GTGACCTATGCACCAGACGTTCCGGGACCGTTCAGTGTCCCAGGCAGCACAGTGTGTGAAAGATCGGAAGAGCGGTTTCAG
chr11	32413468	32413507	WT1_1107	-	GTGACCTATGCACCAGACGTTTTTCTCACATTTATTTTTCAATTTTTTTAAACTATTAGATCGGAAGAGCGGTTTCAG
chr11	32413477	32413516	WT1_1108	-	GTGACCTATGCACCAGACGTTGCGTAAACTTTCTTCCACATTTATTTTTCAATTTTTTTAGATCGGAAGAGCGGTTTCAG
chr11	32414162	32414201	WT1_1109	-	GTGACCTATGCACCAGACGTTCACTTCTCATTGCTCCAGCTGTGTCCCTTGGCTAGGAGATCGGAAGAGCGGTTTCAG
chr11	32417753	32417792	WT1_1110	-	GTGACCTATGCACCAGACGTCGCTGTCCAGTCTTGGGCAAACATGGTTCAAGAGCTCCTAGATCGGAAGAGCGGTTTCAG
chr11	32421444	32421483	WT1_1111	-	GTGACCTATGCACCAGACGTAGACAGGCCAGCGGGAAGGGGGCCGCACTGCCTCTTCCAGATCGGAAGAGCGGTTTCAG
chr11	32437986	32438025	WT1_1112	-	GTGACCTATGCACCAGACGTAATGCGGAGATGGCAAAGCAAATGGCGTAGGCCCTTGCTGAAGATCGGAAGAGCGGTTTCAG
chr11	32439073	32439112	WT1_1113	-	GTGACCTATGCACCAGACGTCCTATTCCATTGCCTTTCCACAGTAACCTTATACCTGTTTATAGATCGGAAGAGCGGTTTCAG
chr11	32449452	32449491	WT1_1114	-	GTGACCTATGCACCAGACGTGCTGGGCTGCGTCTGGGCTTGGACCCCGGAGGGGAAGATCGGAAGAGCGGTTTCAG
chr11	32449993	32450032	WT1_1115	-	GTGACCTATGCACCAGACGTGGAACCAAAGTGGAGTCCCTTCCCTTCTCCGCTGCTATCAGATCGGAAGAGCGGTTTCAG
chr11	32456196	32456235	WT1_1116	-	GTGACCTATGCACCAGACGTCGGGGAGCGCCCCCTACGCGCGGGGCACTGGCGCCAGGGGAAGATCGGAAGAGCGGTTTCAG
chr1	22404922	22404961	CDC42_1117	-	GTGACCTATGCACCAGACGTGTTTTGATCCACTTTAAATATTTCAAATCTGATGATGACAGATCGGAAGAGCGGTTTCAG
chr1	22408165	22408204	CDC42_1118	-	GTGACCTATGCACCAGACGTAAAAATACAACACTGTAGTGTGCAAGGAGAGAGTAAAAAGATCGGAAGAGCGGTTTCAG
chr1	22412882	22412921	CDC42_1119	-	GTGACCTATGCACCAGACGTGAAAAATTTGGAGAGAATTCAGCAACTGAATCTTGGTGTAGATCGGAAGAGCGGTTTCAG
chr1	22413112	22413151	CDC42_1120	-	GTGACCTATGCACCAGACGTGATTTTAAATACACTTTTGTTAATCAACAAGCCCTAAAGATCGGAAGAGCGGTTTCAG
chr1	22416386	22416425	CDC42_1121	-	GTGACCTATGCACCAGACGTGAGGGGAGGAGAGAATAGCAGCCAGGTTAGAGGATTAGATCGGAAGAGCGGTTTCAG
chr1	22417871	22417910	CDC42_1122	-	GTGACCTATGCACCAGACGTGAGAAAGAAAAATGGCGGCTGATTTTCAGTATAATAAGATCGGAAGAGCGGTTTCAG
chr8	118811901	118811940	EXT1_1123	-	GTGACCTATGCACCAGACGTTGAGTGGGGGAGGGGAAGCAAGAAGGGATGGGGGTCAAGCAGATCGGAAGAGCGGTTTCAG
chr8	118816911	118816950	EXT1_1124	-	GTGACCTATGCACCAGACGTAAGAGCCCTTCCCTTGCTTCACTCACTGGTGGTTCAGCAGATCGGAAGAGCGGTTTCAG
chr8	118819406	118819445	EXT1_1125	-	GTGACCTATGCACCAGACGTTGGACATGCTCTACAGACTTTACATAGCTTTTTATATAGATCGGAAGAGCGGTTTCAG
chr8	118825061	118825100	EXT1_1126	-	GTGACCTATGCACCAGACGTGACCTGACGAGCAGCAGGTTGCGCTGTTCCAGGAGCTACCAGATCGGAAGAGCGGTTTCAG
chr8	118830624	118830663	EXT1_1127	-	GTGACCTATGCACCAGACGTAAGGGGACCTATATGTGGAACCACTGTGGAGCCTTGGTTAGATCGGAAGAGCGGTTTCAG
chr8	118831865	118831904	EXT1_1128	-	GTGACCTATGCACCAGACGTAGTTGACAGAGAAGCCCTGCCTGCTCCAGCTCCAGACCAAGATCGGAAGAGCGGTTTCAG
chr8	118834654	118834693	EXT1_1129	-	GTGACCTATGCACCAGACGTTTCCCTCCAGGGAGTTGCCCTTGTTTACCTGAAGATGCAAGATCGGAAGAGCGGTTTCAG
chr8	118842419	118842458	EXT1_1130	-	GTGACCTATGCACCAGACGTCCACTTGGCTCTTGGGCTTGAATAATGGTCCCTTTATACACAGATCGGAAGAGCGGTTTCAG
chr8	118847633	118847672	EXT1_1131	-	GTGACCTATGCACCAGACGTGGCTGTGGCTTCAACACATCAGCAGATATTGCTGCCCAAGATCGGAAGAGCGGTTTCAG
chr8	118849297	118849336	EXT1_1132	-	GTGACCTATGCACCAGACGCTGGAAGCCTTCCCAAGATAGGCTGAGGACCCGAAGCAGAAGATCGGAAGAGCGGTTTCAG
chr8	119122274	119122313	EXT1_1133	-	GTGACCTATGCACCAGACGTGGGCTGGCGTGTCTTTGGGAGTCAGCCTTGGGCTGCTGCCGAGATCGGAAGAGCGGTTTCAG
chr8	119122755	119122794	EXT1_1134	-	GTGACCTATGCACCAGACGTCCAGTTGTACCTCAGTATGTGCAACAATTTGAGATCCAAAAGATCGGAAGAGCGGTTTCAG
chr6	108984608	108984647	FOXO3_1135	-	GTGACCTATGCACCAGACGTAAAAAGAAATACAGAGTATGAACCAGAATGGTCCAAAACAGATCGGAAGAGCGGTTTCAG
chr6	108882672	108882711	FOXO3_1136	-	GTGACCTATGCACCAGACGTCAACCCGGCCGAGTCCCAAGGACCGCCCGGAGCCAGCAGATCGGAAGAGCGGTTTCAG
chr6	108985075	108985114	FOXO3_1137	-	GTGACCTATGCACCAGACGTTGCTTACTGAAAGTACAGCTGGCTGAGCTGCTGTAGAGAGATCGGAAGAGCGGTTTCAG
chr6	108985542	108985581	FOXO3_1138	-	GTGACCTATGCACCAGACGTCGGATCATTGCGAAGCATCACGTTCCGGCGGGAATTCTGGAGATCGGAAGAGCGGTTTCAG
chr1	204494597	204494636	MDM4_1139	-	GTGACCTATGCACCAGACGTAAGAAATGCAGTCTGTTGGTAAACTAAATGAAAAAAGATCGGAAGAGCGGTTTCAG
chr1	204495438	204495477	MDM4_1140	-	GTGACCTATGCACCAGACGTCAAAAATAAATGTGCTATTTACATTTCAAGTAGGTTTCTAGATCGGAAGAGCGGTTTCAG
chr1	204499762	204499801	MDM4_1141	-	GTGACCTATGCACCAGACGTTAAAATACCATGTTGTGATCTGTCCAGCTGCTACCAAAAAGATCGGAAGAGCGGTTTCAG
chr1	204501269	204501308	MDM4_1142	-	GTGACCTATGCACCAGACGTGAGAAGATAAAAATTAACAACCCCAATGCCACTATGAAGATCGGAAGAGCGGTTTCAG
chr1	204506508	204506547	MDM4_1143	-	GTGACCTATGCACCAGACGTGATAAAAACAAAAGGAAAACCTTCCCTGGTAATAACCATTACAGATCGGAAGAGCGGTTTCAG
chr1	204507287	204507326	MDM4_1144	-	GTGACCTATGCACCAGACGTGGAAGGTTGCCATCAGTGCAGTAGAAATAACTGAGACCAAGATCGGAAGAGCGGTTTCAG
chr1	204511862	204511901	MDM4_1145	-	GTGACCTATGCACCAGACGTCAAATGAAAAGAATGATAACTATGCACAATACGTAATAACAGATCGGAAGAGCGGTTTCAG
chr1	204513613	204513652	MDM4_1146	-	GTGACCTATGCACCAGACGTAAAAACAACATGAGTTTCTGTATTACAGAGTTTATCAGAAGATCGGAAGAGCGGTTTCAG
chr1	204515875	204515914	MDM4_1147	-	GTGACCTATGCACCAGACGTAAAAACTCTCATTGAATGTTTACTTGTTTTTAGATGAGATCGGAAGAGCGGTTTCAG
chr1	204518191	204518230	MDM4_1148	-	GTGACCTATGCACCAGACGTAAAGTGAAGCAATTAATACTGAGGGGTTAATATGATGATCGGAAGAGCGGTTTCAG
chr1	204518476	204518515	MDM4_1149	-	GTGACCTATGCACCAGACGTTCCACTGAGTTGCAGGGATCAAAAAGTTTGGAGTTTTCTTAGATCGGAAGAGCGGTTTCAG
chr7	538151	538190	PDGFA_1150	-	GTGACCTATGCACCAGACGTCAGCCCTTCTGGGACATGGATGACATGGCGTGTACAAGATCGGAAGAGCGGTTTCAG
chr7	540031	540070	PDGFA_1151	-	GTGACCTATGCACCAGACGTCAGGTAGGACTGTCTGCCGGACACACTGAGTCCCTGCAGGGAGATCGGAAGAGCGGTTTCAG
chr7	540703	540742	PDGFA_1152	-	GTGACCTATGCACCAGACGTGCCCTTCGTCCGATCGGTGTTGGAGAACAGGTTCTCAGAGAGATCGGAAGAGCGGTTTCAG
chr7	558526	558565	PDGFA_1153	-	GTGACCTATGCACCAGACGTCGCCCGCCCGCTCCCTCGCCGGCTCCTCCGGCCACAAGATCGGAAGAGCGGTTTCAG
chr7	6012980	6013019	PMS2_1154	-	GTGACCTATGCACCAGACGTTGATGAAATAAGTTTATGCTCCAGATTTTTATGTTTTAGATCGGAAGAGCGGTTTCAG
chr7	6017169	6017208	PMS2_1155	-	GTGACCTATGCACCAGACGTAAAGCCTGGCTGTCAGCTCAGCTGCTCAAGCTTGCAGTTCAGATCGGAAGAGCGGTTTCAG
chr7	6022405	6022444	PMS2_1156	-	GTGACCTATGCACCAGACGTTTAGTGTTCATTTCCAGACTCCCTCAAATGAAGATCTAGATCGGAAGAGCGGTTTCAG
chr7	6029381	6029420	PMS2_1157	-	GTGACCTATGCACCAGACGTTACAGTGTACAACAGCTTCTAAAGCTTTTAGCTAATGTGAGATCGGAAGAGCGGTTTCAG
chr7	6031554	6031593	PMS2_1158	-	GTGACCTATGCACCAGACGTTTGGCATTTCAGTACAACAGTGTACTAATGCCTCAAAGAAAGATCGGAAGAGCGGTTTCAG
chr7	6035115	6035154	PMS2_1159	-	GTGACCTATGCACCAGACGTTTTTGTGTTGTTGTTGTTTGTGCTTTGACTTTTAAGATCGGAAGAGCGGTTTCAG
chr7	6036907	6036946	PMS2_1160	-	GTGACCTATGCACCAGACGTTGCTGGCAAGAACTACAATTGAACATTTTATCCTGAGAAGATCGGAAGAGCGGTTTCAG

chr7	6038689	6038728	PMS2_1161	-	GTGACCTATGCACCAGACGTCGGGTTACTTCAACGCCTCTTATTGCTCTAGTGATTATAGAGATCGGAAGAGCGGTTTCAG
chr7	6042034	6042073	PMS2_1162	-	GTGACCTATGCACCAGACGTTTAACTCTGGTTTTCAAGAGTATTGGTTAATGCACATGAGAGATCGGAAGAGCGGTTTCAG
chr7	6043271	6043310	PMS2_1163	-	GTGACCTATGCACCAGACGTATTTTTTACTCACTCACTTGACCCCTTAGAGAACTCTCTAGATCGGAAGAGCGGTTTCAG
chr7	6043553	6043592	PMS2_1164	-	GTGACCTATGCACCAGACGTTTTTTTCTAATCTATTATAAAATAATTGGGTCACATGTCTAGATCGGAAGAGCGGTTTCAG
chr7	6045473	6045512	PMS2_1165	-	GTGACCTATGCACCAGACGTGAGAGTTTTAAAGCCACAAGAAATGATCTGTGAATGTTGTTAGATCGGAAGAGCGGTTTCAG
chr7	6048578	6048617	PMS2_1166	-	GTGACCTATGCACCAGACGTCCTCGCAGTCTCCGGTCTCCCTCTCGCGCCCTCTTTGATCGGAAGAGCGGTTTCAG
chr7	6026771	6026810	PMS2_1167	-	GTGACCTATGCACCAGACGTCGCAGGAACATGTGGACTCTCAGGATAAAGCGCTTAAACAGATCGGAAGAGCGGTTTCAG
chr21	36171548	36171587	RUNX1_1168	-	GTGACCTATGCACCAGACGTTGAAAACACATTCTTTGCGAGCTGAGCTGGGGTGGAGGTCAGATCGGAAGAGCGGTTTCAG
chr21	36193915	36193954	RUNX1_1169	-	GTGACCTATGCACCAGACGTAGTCTTCTGTCCATCCCTCTCCCAGCCAGGATAGAGCTAGATCGGAAGAGCGGTTTCAG
chr21	36206657	36206696	RUNX1_1170	-	GTGACCTATGCACCAGACGTGATGGAGCCACTGCCCGCCTCTCCTGCACCTGGGCCACCAGATCGGAAGAGCGGTTTCAG
chr21	36231721	36231760	RUNX1_1171	-	GTGACCTATGCACCAGACGTCCACTTGGGGCTGGTACACCCCTCCAGGCTGGTACACCCCTCAGATCGGAAGAGCGGTTTCAG
chr21	36252804	36252843	RUNX1_1172	-	GTGACCTATGCACCAGACGTTGTCAAACCTATGCTTGAACACGTTTCATGGCAACAACAGATCGGAAGAGCGGTTTCAG
chr21	36259090	36259129	RUNX1_1173	-	GTGACCTATGCACCAGACGTGGAGAGGGTGGTGGGAGGACAGGCCGGAGGCCGCGAGGATCGGAAGAGCGGTTTCAG
chr21	36265172	36265211	RUNX1_1174	-	GTGACCTATGCACCAGACGTTTTCCAAGTTATATTTTTAAATAAAGTACACACCTTCATAGAGATCGGAAGAGCGGTTTCAG
chr21	36421089	36421128	RUNX1_1175	-	GTGACCTATGCACCAGACGTGCTGGTCTTGTAAATATCTACTTTTTGCTCAGCTTTGCCTGTAGATCGGAAGAGCGGTTTCAG
chr3	10183482	10183521	VHL_1176	-	GTGACCTATGCACCAGACGTATCCAGACCACCCGGCCGGACGCCGCGGATCCGCGGGTAGATCGGAAGAGCGGTTTCAG
chr3	10191421	10191460	VHL_1177	-	GTGACCTATGCACCAGACGTAAACACCACTCAGTGGCAGACTAGGGTCTCAGTACAAGATCGGAAGAGCGGTTTCAG
chr8	30915914	30915953	WRN_1178	-	GTGACCTATGCACCAGACGTTCTTATGTCAGACTCCAAACAAATGCTTTCATGGTATCGGAAGAGCGGTTTCAG
chr8	30916619	30916658	WRN_1179	-	GTGACCTATGCACCAGACGTGTAATTTCAAACAGCCAAAGTTCACATCAAATAACAAGATCGGAAGAGCGGTTTCAG
chr8	30922381	30922420	WRN_1180	-	GTGACCTATGCACCAGACGTTTCTTGTATTTCCATAAGTCTGTCAAGTATGATGGATTAGATCGGAAGAGCGGTTTCAG
chr8	30924499	30924538	WRN_1181	-	GTGACCTATGCACCAGACGTTGAAAAGCAACACAGTAAATCAGTTCCTGTTTTAGGTTAGATCGGAAGAGCGGTTTCAG
chr8	30925724	30925763	WRN_1182	-	GTGACCTATGCACCAGACGTACAGAAAATTTAAAGTATGCTAAAGATCACCGAAATAAGATCGGAAGAGCGGTTTCAG
chr8	30933639	30933678	WRN_1183	-	GTGACCTATGCACCAGACGTAAATAATCAATATTAATTTCAAACCAAAAGCAGAGATAAGATCGGAAGAGCGGTTTCAG
chr8	30938333	30938372	WRN_1184	-	GTGACCTATGCACCAGACGTAAATAAGAAATTAATTTCAACTTCATTTGCAATTAACACTACAGATCGGAAGAGCGGTTTCAG
chr8	30941165	30941204	WRN_1185	-	GTGACCTATGCACCAGACGTAGTATTAAGCATTAAATTTCCAATATAATTGACTTCATATCAGATCGGAAGAGCGGTTTCAG
chr8	30942632	30942671	WRN_1186	-	GTGACCTATGCACCAGACGTAAGTATTAAGCATTAAATTTCAAATATAATTGACTTCATATAGATCGGAAGAGCGGTTTCAG
chr8	30945242	30945281	WRN_1187	-	GTGACCTATGCACCAGACGTAAAGAAATCTTAAAGCAAACCACTGACAGTGTCTATAGATCGGAAGAGCGGTTTCAG
chr8	30946356	30946395	WRN_1188	-	GTGACCTATGCACCAGACGTAATAAAATGTGCATTATGTTCAAGTAGAAAAACACCACAAGATCGGAAGAGCGGTTTCAG
chr8	30947931	30947970	WRN_1189	-	GTGACCTATGCACCAGACGTAAAGCAAAAGTATGTTTCTTTATTAATAAGAAACCCCAAGATCGGAAGAGCGGTTTCAG
chr8	30949296	30949335	WRN_1190	-	GTGACCTATGCACCAGACGTAAACAAATAATCTGGCCATGTACACATTAACATATAGATCGGAAGAGCGGTTTCAG
chr8	30958315	30958354	WRN_1191	-	GTGACCTATGCACCAGACGTAGAAAAACATAAAGGAAAAGATAAAGCTCGAAAGGAAAAGATCGGAAGAGCGGTTTCAG
chr8	30969081	30969120	WRN_1192	-	GTGACCTATGCACCAGACGTTAAACTGATATTTAAAGGAAAAGAGCTCATTATTCCAGATCGGAAGAGCGGTTTCAG
chr8	30973820	30973859	WRN_1193	-	GTGACCTATGCACCAGACGTAGAAGAACAAAAGAGCAAACATATATACTTTATACATGCTAGATCGGAAGAGCGGTTTCAG
chr8	30977709	30977748	WRN_1194	-	GTGACCTATGCACCAGACGTATCACAAACAGTTTGACAACATATTTAGCAGAATGAAAAGATCGGAAGAGCGGTTTCAG
chr8	30981988	30982027	WRN_1195	-	GTGACCTATGCACCAGACGTAAACATCACAGGAATATGTAACCTGTATTGGCAACTTTAGATCGGAAGAGCGGTTTCAG
chr8	30989831	30989870	WRN_1196	-	GTGACCTATGCACCAGACGTATAATAACATTTGAAGAAAGCTTAGCAAAGGCATGTATCTAGATCGGAAGAGCGGTTTCAG
chr8	30988896	30988935	WRN_1197	-	GTGACCTATGCACCAGACGTGAATAAAATCAGTATCTAAAAATGCTAATTTAAACATATAAGATCGGAAGAGCGGTTTCAG
chr8	30999147	30999186	WRN_1198	-	GTGACCTATGCACCAGACGTCAAAAAGGATCTTTTAAATGTGGAGTGGGAAAACAAAATTAAGATCGGAAGAGCGGTTTCAG
chr8	31001016	31001055	WRN_1199	-	GTGACCTATGCACCAGACGTACATATAAAGGTCATTTAAAAAAGTTTCAAAAACCTTTTATAGATCGGAAGAGCGGTTTCAG
chr8	31004830	31004869	WRN_1200	-	GTGACCTATGCACCAGACGTAAACAAAGAAACAACACTTTTTAAAGTGTACTTTAAAGATCAGATCGGAAGAGCGGTTTCAG
chr8	31012090	31012129	WRN_1201	-	GTGACCTATGCACCAGACGTTTAAATGATGACCAAAATGATCAATTAATCAATACAATAAAGATCGGAAGAGCGGTTTCAG
chr8	31014834	31014873	WRN_1202	-	GTGACCTATGCACCAGACGTATCAGCAAAGAACCCAGTGAAGTTGAAAAGTGTCCACTCCAGATCGGAAGAGCGGTTTCAG
chr8	31024488	31024527	WRN_1203	-	GTGACCTATGCACCAGACGTTAAAAAATCCATTTCAAATAAATACAGAGAATATTAGATCGGAAGAGCGGTTTCAG
chr8	31030461	31030500	WRN_1204	-	GTGACCTATGCACCAGACGTTAGAAAAGAAAAGAAATCAAATCTTTGACTACTGAGAAGAGATCGGAAGAGCGGTTTCAG
chr2	29416040	29416079	ALK_1205	-	GTGACCTATGCACCAGACGTACTCACTCTCTTCTTCCCTTGGGATCCCTAAGACCGTGGAGATCGGAAGAGCGGTTTCAG
chr2	29419586	29419625	ALK_1206	-	GTGACCTATGCACCAGACGTTTCTCCCTTTGGTCAACTTTACTCTATGAAACAGTCTAGATCGGAAGAGCGGTTTCAG
chr2	29420358	29420397	ALK_1207	-	GTGACCTATGCACCAGACGTTTTAGGAACACTTCTGCTAGTTACTAAGCAGTTTTTCTTTAGATCGGAAGAGCGGTTTCAG
chr2	29429987	29430026	ALK_1208	-	GTGACCTATGCACCAGACGTCATCATCTCCAGGTATCCCTGCAGCCATAAGGTGGTCTAGATCGGAAGAGCGGTTTCAG
chr2	29432602	29432641	ALK_1209	-	GTGACCTATGCACCAGACGTACTGCCTCACCCCTCCGGGCCTGTCTCTTCCACCTCAGCCAGATCGGAAGAGCGGTTTCAG
chr2	29436800	29436839	ALK_1210	-	GTGACCTATGCACCAGACGTGTGACTGTGCTCTTCTGTCTATCTGCTGCTGATCTGTGTAGATCGGAAGAGCGGTTTCAG
chr2	29443522	29443561	ALK_1211	-	GTGACCTATGCACCAGACGTAGCAGTTTGTGCTGAGTTGTGTGCCAAGGACAGGACAGATCGGAAGAGCGGTTTCAG
chr2	29445160	29445199	ALK_1212	-	GTGACCTATGCACCAGACGTAGAGAGACACCCCTCACCCCACTGCCCCCAAGAGATCGGAAGAGCGGTTTCAG
chr2	29445333	29445372	ALK_1213	-	GTGACCTATGCACCAGACGTGCTCACTCTTGAAGCCTGCCCTTGGCTTGGGACTCTGTAGATCGGAAGAGCGGTTTCAG
chr2	29446158	29446197	ALK_1214	-	GTGACCTATGCACCAGACGTTGCTGCCGTCTGGGAGGAGAGGGTGCAGTGTAGGGGCTAGATCGGAAGAGCGGTTTCAG
chr2	29448277	29448316	ALK_1215	-	GTGACCTATGCACCAGACGTAGAGCCCCAGGGACTCCCAAGGGGGCAGGAAGGCACGATAGATCGGAAGAGCGGTTTCAG
chr2	29449738	29449777	ALK_1216	-	GTGACCTATGCACCAGACGTAGGGCCAGGGGAGGCGCCATAGCCTGAGATTTGAGATCGGAAGAGCGGTTTCAG
chr2	29450390	29450429	ALK_1217	-	GTGACCTATGCACCAGACGTTGCCAGCAGCAAGAACTTGTCTAGGTCAGTCTCCAGATCGGAAGAGCGGTTTCAG
chr2	29451700	29451739	ALK_1218	-	GTGACCTATGCACCAGACGTTTCGTGTTCAAGGTGCTACTCCCTCCCTGCTTAGTCTAGATCGGAAGAGCGGTTTCAG

chr2	29455120	29455159	ALK_1219	-	GTGACCTATGCACCAGACGTGCAAGCGTGCCCTCTCCAGAACCTCTCCAGGCCCTCAGAGATCGGAAGAGCGGTTTCAG
chr2	29456381	29456420	ALK_1220	-	GTGACCTATGCACCAGACGTGCTGCCAGATTTCCACCAGGTTCTGTGCATCTGCAATGAGATCGGAAGAGCGGTTTCAG
chr2	29462496	29462535	ALK_1221	-	GTGACCTATGCACCAGACGTAGAGCAGGGGTTTCTCGTCTGCACTCTGTCAGGCCCCGGGAGATCGGAAGAGCGGTTTCAG
chr2	29473921	29473960	ALK_1222	-	GTGACCTATGCACCAGACGTAAGAGGGGGAGGGGAGGGGCAGACCACCCCTCCGAAGAAAGATCGGAAGAGCGGTTTCAG
chr2	29497915	29497954	ALK_1223	-	GTGACCTATGCACCAGACGTAGCTCACAATGTGAGCAGTAACCTCTTGTGTCAAAAGAGATCGGAAGAGCGGTTTCAG
chr2	29498218	29498257	ALK_1224	-	GTGACCTATGCACCAGACGTTCTGACCCAGCACTCTGTCGCCAACCCCATGGCCCATAGATCGGAAGAGCGGTTTCAG
chr2	29519704	29519743	ALK_1225	-	GTGACCTATGCACCAGACGTGTCATCTCCCCAATACCTTCTCCCTATCAGCTAAAATAGATCGGAAGAGCGGTTTCAG
chr2	29541120	29541159	ALK_1226	-	GTGACCTATGCACCAGACGTTTGTCTCTAGTTCTCTAATTTCTCCCTCCACCTCTTGTAGATCGGAAGAGCGGTTTCAG
chr2	29543567	29543606	ALK_1227	-	GTGACCTATGCACCAGACGTTCTCCTGCCTTCTCTGGTGCCATCTTCATGCCACATAGATCGGAAGAGCGGTTTCAG
chr2	29551166	29551205	ALK_1228	-	GTGACCTATGCACCAGACGTGGGGCTGCCACCCTGCCTGAGCCAGCCATGCTCATAAGATCGGAAGAGCGGTTTCAG
chr2	29606548	29606587	ALK_1229	-	GTGACCTATGCACCAGACGTCTGGCTTTCCACGCCTCTTGGTAGCCTATTGTGTTAGATAGATCGGAAGAGCGGTTTCAG
chr2	29754731	29754770	ALK_1230	-	GTGACCTATGCACCAGACGTCCATGTCCAAAATGATTTTATACACAGGTGATTTGGCTAGATCGGAAGAGCGGTTTCAG
chr2	29917766	29917705	ALK_1231	-	GTGACCTATGCACCAGACGTGGCTGCTGGTGTGATGTCTGGTGGGTGAGGTCAGGGCCAGGCTGGAGATCGGAAGAGCGGTTTCAG
chr2	29940394	29940433	ALK_1232	-	GTGACCTATGCACCAGACGTGTTAATATTTACTTGAGATACACTGTCACTATCTCATAAAGATCGGAAGAGCGGTTTCAG
chr2	30142809	30142848	ALK_1233	-	GTGACCTATGCACCAGACGTCCCGCTGAGTGTGCCGGGATTTAGTGTTTTATGTCACATAGATCGGAAGAGCGGTTTCAG
chr2	29416389	29416428	ALK_1234	-	GTGACCTATGCACCAGACGTTCCCTGGTTTACAGAGAAAACCCACCAAAAAGAATAATCCTAAGATCGGAAGAGCGGTTTCAG
chr2	30143142	30143181	ALK_1235	-	GTGACCTATGCACCAGACGTAGCCCGCGCAGAGGCCCGCCAGCGCTGTCCAGGGTGTCTGAAGAGATCGGAAGAGCGGTTTCAG
chrX	66764939	66764978	AR_1236	-	GTGACCTATGCACCAGACGTGGCTGAATCTCCACCTACTTCCCTTACCCCGCTCCCTCAGATCGGAAGAGCGGTTTCAG
chrX	66788795	66788834	AR_1237	-	GTGACCTATGCACCAGACGTGACAGGCAATGTACAGGACACTCTGCATTCTTTCCCTGGAGATCGGAAGAGCGGTTTCAG
chrX	66863048	66863087	AR_1238	-	GTGACCTATGCACCAGACGTACAAAAACCAATGCAACACATGTCACTGAATGGCAGAAAAGATCGGAAGAGCGGTTTCAG
chrX	66905802	66905841	AR_1239	-	GTGACCTATGCACCAGACGTAAATACAGAGTTGATAGACCTGATAATGAGTTTCCAGAGAGATCGGAAGAGCGGTTTCAG
chrX	66931194	66931233	AR_1240	-	GTGACCTATGCACCAGACGTGGAAGAGAGACTTGAATTTATCATCAGTGGTCAAAAACACAGATCGGAAGAGCGGTTTCAG
chrX	66937270	66937309	AR_1241	-	GTGACCTATGCACCAGACGTAGAGGCAGAGGCAGTGGTCACTGTTGGTACTGACGGTTGAGATCGGAAGAGCGGTTTCAG
chrX	66941625	66941664	AR_1242	-	GTGACCTATGCACCAGACGTGATACAGAGGAAAAGGAATGGGGAAGTTTACAATAAGATCGGAAGAGCGGTTTCAG
chrX	66942619	66942658	AR_1243	-	GTGACCTATGCACCAGACGTATGAAGACAGAATGGGAGGGGAAGCATGCCACGAAGGAAGATCGGAAGAGCGGTTTCAG
chrX	66943478	66943517	AR_1244	-	GTGACCTATGCACCAGACGTCAATAAGAGGGAGAAAACAGGGTTGACAAGGAGGTGGCCAGATCGGAAGAGCGGTTTCAG
chrX	66765343	66765382	AR_1245	-	GTGACCTATGCACCAGACGTGCAACCTCTCTCGGGGTGGCACTCCAGGGCCGACTGCGGAGATCGGAAGAGCGGTTTCAG
chrX	66765747	66765786	AR_1246	-	GTGACCTATGCACCAGACGTATCCCCCGAAGCTGTTCCCTGGACTCAGATGCTCCAACAGATCGGAAGAGCGGTTTCAG
chrX	66766151	66766190	AR_1247	-	GTGACCTATGCACCAGACGTGCCGCCAGCGCTGCCGTAGCTCCAGCGGGTTCTCCAGCTAGATCGGAAGAGCGGTTTCAG
chr1	51435991	51436030	CDKN2C_1248	-	GTGACCTATGCACCAGACGTCCTGACGATCAGGAAAAGATGAATTAGTCTGTTTTCTTTTATAGATCGGAAGAGCGGTTTCAG
chr1	51439515	51439554	CDKN2C_1249	-	GTGACCTATGCACCAGACGTAGTAAATGGTGAATCCTCAAGTGCATATGCTACAGAAGATCGGAAGAGCGGTTTCAG
chr11	125496614	125496653	CHEK1_1250	-	GTGACCTATGCACCAGACGTAGCACCCTGGCTGTAAAAGGCAGGAATCCAGAAAAGATGTAGATCGGAAGAGCGGTTTCAG
chr11	125497452	125497491	CHEK1_1251	-	GTGACCTATGCACCAGACGTAAAGAGTTTTAATACATCAGAATTCATTTCTTTAAAACAGATCGGAAGAGCGGTTTCAG
chr11	125499077	125499116	CHEK1_1252	-	GTGACCTATGCACCAGACGTTATGAAAGTAAGTTTATTGACTAAATATAATCAGGTAGCAAGATCGGAAGAGCGGTTTCAG
chr11	125499236	125499275	CHEK1_1253	-	GTGACCTATGCACCAGACGTGACAGAGAAAACACACTGAATAATGGTAAATGTAATGTAGATCGGAAGAGCGGTTTCAG
chr11	125503008	125503047	CHEK1_1254	-	GTGACCTATGCACCAGACGTAGAAAAAAGATGACACTGAATAAAAAATGTTTTGCAAATAAGATCGGAAGAGCGGTTTCAG
chr11	125505274	125505313	CHEK1_1255	-	GTGACCTATGCACCAGACGTAGCAAGTCCAGTTTTTAAATGTTCTTATTATAAAGATAGATCGGAAGAGCGGTTTCAG
chr11	125507294	125507333	CHEK1_1256	-	GTGACCTATGCACCAGACGTACATTACGACAACATTCACGAAAGAATCATGTTAGAGAAGAGATCGGAAGAGCGGTTTCAG
chr11	125513637	125513676	CHEK1_1257	-	GTGACCTATGCACCAGACGTAACAAATACAAATGCTTCAAGTCTTCTATGCAAGATGAGATCGGAAGAGCGGTTTCAG
chr11	125513936	125513975	CHEK1_1258	-	GTGACCTATGCACCAGACGTAAGACAGAAGAAAACATACATTTAATAAAAAATCTATAGATCGGAAGAGCGGTTTCAG
chr11	125514357	125514396	CHEK1_1259	-	GTGACCTATGCACCAGACGTAACAGAAGACAAATGAATAAAATCCATTAGGACTAAAGACAAGATCGGAAGAGCGGTTTCAG
chr22	29083835	29083874	CHEK2_1260	-	GTGACCTATGCACCAGACGTTTGAACACGAAAGAAATGTACCTTCTTCACTCTGTCATCAGATCGGAAGAGCGGTTTCAG
chr22	29085073	29085112	CHEK2_1261	-	GTGACCTATGCACCAGACGTTCCCTGATGATCAATAATGTAGTCTGGGCTTAAGGAGCTGAGATCGGAAGAGCGGTTTCAG
chr22	29089970	29090009	CHEK2_1262	-	GTGACCTATGCACCAGACGTGCAAGTGCCTGCTAGCATAAAATACATGGGAAGCCCTGCTAGATCGGAAGAGCGGTTTCAG
chr22	29091065	29091104	CHEK2_1263	-	GTGACCTATGCACCAGACGTGAAAGGGTTAAGAATTTGTGGTATGCTAAAATGTGTATGTAGATCGGAAGAGCGGTTTCAG
chr22	29091648	29091687	CHEK2_1264	-	GTGACCTATGCACCAGACGTTTTTCTGCTGACAGACTGGTAGGAGGTGATTAGATGAAGATCGGAAGAGCGGTTTCAG
chr22	29092839	29092878	CHEK2_1265	-	GTGACCTATGCACCAGACGTGGCATTCTGTATGTGGCTATTCTGTAGATTCTTGTTCAGAGATCGGAAGAGCGGTTTCAG
chr22	29095776	29095815	CHEK2_1266	-	GTGACCTATGCACCAGACGTCCCTCAATTTCTTTGACAGCTGCCTTTCTTTAGTTGAATAGATCGGAAGAGCGGTTTCAG
chr22	29099443	29099482	CHEK2_1267	-	GTGACCTATGCACCAGACGTAACCTTTTTAAAATTTCTGTTTTCCATTCAAATGCTTTATAAGATCGGAAGAGCGGTTTCAG
chr22	29105944	29105983	CHEK2_1268	-	GTGACCTATGCACCAGACGTTTATAGACTCATACTTAGATTTATCTATCTCAAATATGAGATCGGAAGAGCGGTTTCAG
chr22	29107847	29107886	CHEK2_1269	-	GTGACCTATGCACCAGACGTATAAAGGCTGATCACTTTTTATTAACACGCTTCATAACAGATCGGAAGAGCGGTTTCAG
chr22	29115333	29115372	CHEK2_1270	-	GTGACCTATGCACCAGACGTTTCTTATATAAATGACTCACTTAATTTTTTCACTATACATTTGAGATCGGAAGAGCGGTTTCAG
chr22	29120915	29120954	CHEK2_1271	-	GTGACCTATGCACCAGACGTTATCTTATGGTTACTGGAATTTTTTTTTTCACTCTCTCAAGATCGGAAGAGCGGTTTCAG
chr22	29121181	29121220	CHEK2_1272	-	GTGACCTATGCACCAGACGTAATACCCATGTATCTAGGAGAGCTGGTAATTTGGTCATTGAGATCGGAAGAGCGGTTTCAG
chr22	29130341	29130380	CHEK2_1273	-	GTGACCTATGCACCAGACGTTTGTGTATAGTATCACGTTTTGTTCAGAAAACACTTACAGATCGGAAGAGCGGTTTCAG
chr13	103498567	103498606	ERCC5_1274	-	GTGACCTATGCACCAGACGTGCTCCTAAGAGCCGACCCGCAACTCTACTCTAATTTAGATCGGAAGAGCGGTTTCAG
chr13	103504418	103504457	ERCC5_1275	-	GTGACCTATGCACCAGACGTTGTTAATGGAAAACACTCCCGGATTTTTCTCTCATCCTCAGATCGGAAGAGCGGTTTCAG
chr13	103506057	103506096	ERCC5_1276	-	GTGACCTATGCACCAGACGTAAGAGATGAAGATCTCACTTCAGGATATTAGACCACTAGAGATCGGAAGAGCGGTTTCAG

chr13	103506588	103506627	ERCC5_1277	-	GTGACCTATGCACCAGACGTACAAAATCTTTAAACAGATTATGCAGACCCCTGCTCAGGATAGATCGGAAGAGCGGTTTCAG
chr13	103508352	103508391	ERCC5_1278	-	GTGACCTATGCACCAGACGTAAACATACATCTTTACGATATCTATGATTTTTAAGGACCCCTTAGATCGGAAGAGCGGTTTCAG
chr13	103510575	103510614	ERCC5_1279	-	GTGACCTATGCACCAGACGTAAATACACAGCACCATGAAATTTACATTTACATACCTTAGAGATCGGAAGAGCGGTTTCAG
chr13	103513807	103513846	ERCC5_1280	-	GTGACCTATGCACCAGACGTAAATAAAACAAAATAAATTTACTGTTTTATATTAATACAGATAGATCGGAAGAGCGGTTTCAG
chr13	103514330	103514369	ERCC5_1281	-	GTGACCTATGCACCAGACGTATTAACACACTTCTACCATTTCAGTTTTACAGTGTGACAAAGATCGGAAGAGCGGTTTCAG
chr13	103517967	103518006	ERCC5_1282	-	GTGACCTATGCACCAGACGTATTAAGAGTCACTTCACTACAATCAAACATTAATAGATCGGAAGAGCGGTTTCAG
chr13	103518562	103518601	ERCC5_1283	-	GTGACCTATGCACCAGACGTTTTTTCACTTTATAGTTTATATTAATAATCCAATGAGTAGATCGGAAGAGCGGTTTCAG
chr13	103518932	103518971	ERCC5_1284	-	GTGACCTATGCACCAGACGTAGGGGTACACAGTGACGCCAGGGAAGGGCACCGCCAGGCAGATCGGAAGAGCGGTTTCAG
chr13	103524498	103524537	ERCC5_1285	-	GTGACCTATGCACCAGACGTAAAGAAACAATTACTTACACAGCAATGAGACATTATAGTTAGATCGGAAGAGCGGTTTCAG
chr13	103525559	103525598	ERCC5_1286	-	GTGACCTATGCACCAGACGTAAAGACTTATAAATATTTTGAAGATATTAACAAGTGAAGATCGGAAGAGCGGTTTCAG
chr13	103527607	103527646	ERCC5_1287	-	GTGACCTATGCACCAGACGTAAACAAAAGAATAATAATAATAATACAGACAAGTAAGTCAAAGATCGGAAGAGCGGTTTCAG
chr13	103527905	103527944	ERCC5_1288	-	GTGACCTATGCACCAGACGTGCATGTATCTTTCCCTTTAGAATCTGAAAGCCTCTTTCTTAGATCGGAAGAGCGGTTTCAG
chr13	103514688	103514727	ERCC5_1289	-	GTGACCTATGCACCAGACGTGCACATCATCCCCAGCACACAGCTTTTACATCTTCGTCATCAGATCGGAAGAGCGGTTTCAG
chr13	103515046	103515085	ERCC5_1290	-	GTGACCTATGCACCAGACGTCAAGTTGGAGATGCCGGTGTGAGTTCCCTTCCATTCCGGGAAGATCGGAAGAGCGGTTTCAG
chr10	90750584	90750623	FAS_1291	-	GTGACCTATGCACCAGACGTCAATCCTCCGAAGTGAAGAGCTTCCCCAACTCCGTAAGTACTGAGATCGGAAGAGCGGTTTCAG
chr10	90762736	90762775	FAS_1292	-	GTGACCTATGCACCAGACGTAAAGCATGAAGAGAATTTATTGATTTCTGAAGTAAGCAAAGATCGGAAGAGCGGTTTCAG
chr10	90767407	90767446	FAS_1293	-	GTGACCTATGCACCAGACGTAAAAAGGAGCAAGTGTGTTGAACAGGACACGGGCAGGTAAGAGATCGGAAGAGCGGTTTCAG
chr10	90768596	90768635	FAS_1294	-	GTGACCTATGCACCAGACGTGAAATTTGGAAACTATTAGTTAGCGGCTAATATAAGCAGATCGGAAGAGCGGTTTCAG
chr10	90770246	90770285	FAS_1295	-	GTGACCTATGCACCAGACGTAAATACAGGAGAAATCAAAGCCTGCGAGAATAATTCTAGATCGGAAGAGCGGTTTCAG
chr10	90770460	90770499	FAS_1296	-	GTGACCTATGCACCAGACGTGAACATTGGACATTTTATATGAAAATAAGCAATCTTAAAGATCGGAAGAGCGGTTTCAG
chr10	90771706	90771745	FAS_1297	-	GTGACCTATGCACCAGACGTAAAGAAATTTTATCAACTCAGGTCCTCAGCCTTGTAAGATGAGATCGGAAGAGCGGTTTCAG
chr10	90773050	90773089	FAS_1298	-	GTGACCTATGCACCAGACGTAAAAATGGAAGCAGAGAAAGACAAATAAAAAATATATCTTTAGATCGGAAGAGCGGTTTCAG
chr10	90773826	90773865	FAS_1299	-	GTGACCTATGCACCAGACGTGAAATAGTCTGAAAATTTGTTTTCTAAATGAAATCCCAGATCGGAAGAGCGGTTTCAG
chr10	123239321	123239360	FGFR2_1300	-	GTGACCTATGCACCAGACGTCTGCCTGTCCCCAAACAGGACAGCACTGGGAACCTAGCTAAGATCGGAAGAGCGGTTTCAG
chr10	123243162	123243201	FGFR2_1301	-	GTGACCTATGCACCAGACGTCTTCTAGAAAGCCCTTGCTCTTGGTTGTCTTGTGAGACAAGATCGGAAGAGCGGTTTCAG
chr10	123244859	123244898	FGFR2_1302	-	GTGACCTATGCACCAGACGTGTTGTCTTCTGCGGGTCCCCAGTGACCTGCCACACCAAGATCGGAAGAGCGGTTTCAG
chr10	123246818	123246857	FGFR2_1303	-	GTGACCTATGCACCAGACGTCTCTTTCTCTGGCTTTTTCTGGGCTTGAGCTGCAAAAAAGATCGGAAGAGCGGTTTCAG
chr10	123247455	123247494	FGFR2_1304	-	GTGACCTATGCACCAGACGTGGCAGTAACACAGTGGGCAGGGGGGGGTGAGGCTCAGAAGATCGGAAGAGCGGTTTCAG
chr10	123255996	123256035	FGFR2_1305	-	GTGACCTATGCACCAGACGTACACTTACTTGCTGGTGGTGGAACTCAAATGTCAGATCGGAAGAGCGGTTTCAG
chr10	123257959	123257998	FGFR2_1306	-	GTGACCTATGCACCAGACGTGGAATAACTGCATTTCGCCAAATACTCTGCAGTTTGTATGAGATCGGAAGAGCGGTTTCAG
chr10	123260290	123260329	FGFR2_1307	-	GTGACCTATGCACCAGACGTAGGCCGGGAGGCTCGGGGAGGGGCTGGTGGAGAGTCTTATAGATCGGAAGAGCGGTTTCAG
chr10	123263254	123263293	FGFR2_1308	-	GTGACCTATGCACCAGACGTCTCTTGCCATGTCCCAGGATGGAGACTCAGCTATAAATGAGATCGGAAGAGCGGTTTCAG
chr10	123274581	123274620	FGFR2_1309	-	GTGACCTATGCACCAGACGTAAAGAGTTTAAAGAAATTTACTCTCCCCATGACCCAGCAGATCGGAAGAGCGGTTTCAG
chr10	123274587	123274626	FGFR2_1310	-	GTGACCTATGCACCAGACGTGTAGATAAAGAGTTTAAAGAAATTTACTCTCCCCATGAAAGATCGGAAGAGCGGTTTCAG
chr10	123276783	123276822	FGFR2_1311	-	GTGACCTATGCACCAGACGTCTCTTTCTGTTCTGGGTTTTTTCCCTTCTTGGTGTACTAGATCGGAAGAGCGGTTTCAG
chr10	123278146	123278185	FGFR2_1312	-	GTGACCTATGCACCAGACGTCTTTCATTTTTGTCTTTTTTAAAAAGAAAGCTGGATATAGATCGGAAGAGCGGTTTCAG
chr10	123279443	123279482	FGFR2_1313	-	GTGACCTATGCACCAGACGTCTGAATCTAAAGGTACCCACAACCTGGGGTCTCTTTCATGAGATCGGAAGAGCGGTTTCAG
chr10	123298056	123298095	FGFR2_1314	-	GTGACCTATGCACCAGACGTCTCTCTCTGTTGGCAGGCTGCATACCAGCCATTCTTGCTAGATCGGAAGAGCGGTTTCAG
chr10	123323966	123324005	FGFR2_1315	-	GTGACCTATGCACCAGACGTGCCCGCTCCGATGGTCCCCGAGAGAGGAGCATGGAGGGAAGATCGGAAGAGCGGTTTCAG
chr10	123324902	123324941	FGFR2_1316	-	GTGACCTATGCACCAGACGTCCGCCAGCATGCTCTCTCTCTGTAGCCATTACATAGATCGGAAGAGCGGTTTCAG
chr10	123353173	123353212	FGFR2_1317	-	GTGACCTATGCACCAGACGTAAATTTCACTTTTCACTTTTGGATTTTGGATTTGTCTGGGAGATCGGAAGAGCGGTTTCAG
chr1	32757721	32757760	HDAC1_1318	-	GTGACCTATGCACCAGACGTCCCGTCCCTACCCTCAGTCCGTCGCTCCGCTCCGCCAGATCGGAAGAGCGGTTTCAG
chr1	32768172	32768211	HDAC1_1319	-	GTGACCTATGCACCAGACGTGAGAGTGACAGCTTCACTAACACAGTTAGGCATACACTACAGATCGGAAGAGCGGTTTCAG
chr1	32782216	32782255	HDAC1_1320	-	GTGACCTATGCACCAGACGTGAAGGGGAGAAGGGCAAGTTATTTTTGACCACGGCCAGTCAGATCGGAAGAGCGGTTTCAG
chr1	32790030	32790069	HDAC1_1321	-	GTGACCTATGCACCAGACGTATAAGCAAAAAGTTAGTTTTCCACAATTTCCCTTTAGTTTACAGATCGGAAGAGCGGTTTCAG
chr1	32792490	32792529	HDAC1_1322	-	GTGACCTATGCACCAGACGTGAAAAGAGAACAATAGCCCTGTACTAACACTCTCCCAGATCGGAAGAGCGGTTTCAG
chr1	32793087	32793126	HDAC1_1323	-	GTGACCTATGCACCAGACGTAAAGGGGTACAGGGTCTGGGGGCTCTTTGGGATGGGACGAGATCGGAAGAGCGGTTTCAG
chr1	32794619	32794658	HDAC1_1324	-	GTGACCTATGCACCAGACGTAGGCCATTAAGTAAAAGTAAAGGATGAAGCTTGAAGGAAAGATCGGAAGAGCGGTTTCAG
chr1	32796129	32796168	HDAC1_1325	-	GTGACCTATGCACCAGACGTACATCTGGTCAACCAACCTCAAGAAAGCAATACGAGGAGATCGGAAGAGCGGTTTCAG
chr1	32796319	32796358	HDAC1_1326	-	GTGACCTATGCACCAGACGTAGAAGGGGTGCTGAGTTACAGGAGCACAAGCAGGACCCAGATCGGAAGAGCGGTTTCAG
chr1	32797025	32797064	HDAC1_1327	-	GTGACCTATGCACCAGACGTGAGGAGAGAAGACCGTCAAGAGACTGGCCACCCAGCCATGATCGGAAGAGCGGTTTCAG
chr1	32797227	32797266	HDAC1_1328	-	GTGACCTATGCACCAGACGTGGGAGAGATAGCAGGGCTGCTGCTCAGGGACAACAAAGATCGGAAGAGCGGTTTCAG
chr1	32797641	32797680	HDAC1_1329	-	GTGACCTATGCACCAGACGTGTTGGAAAGCATGGGTGAGAGGGCAGGGGGTCTGATTTAAGATCGGAAGAGCGGTTTCAG
chr1	32798252	32798291	HDAC1_1330	-	GTGACCTATGCACCAGACGTAGAGTACAGGGATGGCCAAGGGCAGCACCTCTGGGAAGACAGATCGGAAGAGCGGTTTCAG
chr1	32798568	32798607	HDAC1_1331	-	GTGACCTATGCACCAGACGTAGCAGAGACTGGCATGAGATGACCCAGCCAGAGCCTCAGAGATCGGAAGAGCGGTTTCAG
chr4	55946058	55946097	KDR_1332	-	GTGACCTATGCACCAGACGTCCACACCCCAACTCTGGACATCACATGAGAGGTGCTGCAGATCGGAAGAGCGGTTTCAG
chr4	55948073	55948112	KDR_1333	-	GTGACCTATGCACCAGACGTGCCATATTAATAAAGCAAATTTCAATGAAATTTTTGGAAGATCGGAAGAGCGGTTTCAG
chr4	55948653	55948692	KDR_1334	-	GTGACCTATGCACCAGACGTCTTTTAAAAATAGTCTTGAATAATAACAAGGATGAAACAGATCGGAAGAGCGGTTTCAG

chr4	55953724	55953763	KDR_1335	-	GTGACCTATGCACCAGACGTTGGCCTAACATCCCCCGGGGGAGGGTGACTTCAAGGCCATAGATCGGAAGAGCGGTTTCAG
chr4	55954985	55955024	KDR_1336	-	GTGACCTATGCACCAGACGTTCCATCCAAGAAGCACCTACAAAGAGTACTTAGATGTCAAAGATCGGAAGAGCGGTTTCAG
chr4	55955491	55955530	KDR_1337	-	GTGACCTATGCACCAGACGTAAGAAGTATTCTGTGTTCTCTTTCTTTGCTCGCAAATTCAGATCGGAAGAGCGGTTTCAG
chr4	55955808	55955847	KDR_1338	-	GTGACCTATGCACCAGACGTTCTTTTTGTCCTTCCATCCAGACTCCAAGAGGAAGACAAAGATCGGAAGAGCGGTTTCAG
chr4	55956073	55956112	KDR_1339	-	GTGACCTATGCACCAGACGTAATATGAACCCAGTGCTTGGTTAAGTAACAGAATTAACAGATCGGAAGAGCGGTTTCAG
chr4	55958734	55958773	KDR_1340	-	GTGACCTATGCACCAGACGTTTGAGGGGAAATCAGCTATCTTTTCAGATCACAGGTTTGGAGATCGGAAGAGCGGTTTCAG
chr4	55960919	55960958	KDR_1341	-	GTGACCTATGCACCAGACGTGGCTTCCGTGCATGCTATGGCATGCTCTTGTACAGACAGAAGATCGGAAGAGCGGTTTCAG
chr4	55961694	55961733	KDR_1342	-	GTGACCTATGCACCAGACGTTCCATACTGCTGCTGGCCATGTTATAAAATGAAGGGAAAAGATCGGAAGAGCGGTTTCAG
chr4	55962346	55962385	KDR_1343	-	GTGACCTATGCACCAGACGTGGGGTGGTTTTGGTCACCAATTTAAACATGCCTCTCTGAGATCGGAAGAGCGGTTTCAG
chr4	55963779	55963818	KDR_1344	-	GTGACCTATGCACCAGACGTAATTATGTGGTGATCTATCTTTCTGTTTATCTAGTCTTTAGATCGGAAGAGCGGTTTCAG
chr4	55964254	55964293	KDR_1345	-	GTGACCTATGCACCAGACGTAATTGCTATTAATTTGATATTGTGTTTACCAGGCCATCTCAGATCGGAAGAGCGGTTTCAG
chr4	55964814	55964853	KDR_1346	-	GTGACCTATGCACCAGACGTAATTTCCCTTCTGCCATGCACATGGTTTTTCATGATTAAGATCGGAAGAGCGGTTTCAG
chr4	55968479	55968518	KDR_1347	-	GTGACCTATGCACCAGACGTTAATGGCTATCACTTTGGGTTGCAGAACCTTTCCAGGATAGATCGGAAGAGCGGTTTCAG
chr4	55970760	55970799	KDR_1348	-	GTGACCTATGCACCAGACGTAATTCTGGATCATTGTGCAGAGGCAGTTGGAATGCCTTAAAGATCGGAAGAGCGGTTTCAG
chr4	55971949	55971988	KDR_1349	-	GTGACCTATGCACCAGACGTTTCTCTGGAGGTTGGGTTGGATCACTCACACAGTGGGTAAGATCGGAAGAGCGGTTTCAG
chr4	55972804	55972843	KDR_1350	-	GTGACCTATGCACCAGACGTAGTTTTAAAAATTTGAAAATCTCTCTCTCTTAATGGAAGGAGATCGGAAGAGCGGTTTCAG
chr4	55973854	55973893	KDR_1351	-	GTGACCTATGCACCAGACGTTCCACATCTCTTTGCTTTCCCTCCCATCTTGCATTTCTTACAGATCGGAAGAGCGGTTTCAG
chr4	55976520	55976559	KDR_1352	-	GTGACCTATGCACCAGACGTTCAATTTGCTCTCTGCCCAGATTTATATGATACATTGAGATCGGAAGAGCGGTTTCAG
chr4	55976771	55976810	KDR_1353	-	GTGACCTATGCACCAGACGTGAAATAATGCAAAGCATCATTTCGTGTGAGAGCAAATCCAGATCGGAAGAGCGGTTTCAG
chr4	55979421	55979460	KDR_1354	-	GTGACCTATGCACCAGACGTGCTTGGAAATATTCTGTGCCTTGACAAGTGAGATAATTAGATCGGAAGAGCGGTTTCAG
chr4	55980243	55980282	KDR_1355	-	GTGACCTATGCACCAGACGTTGATTCAAAGCCAGACCTCCAATACTTAGATAATAAGCCAGATCGGAAGAGCGGTTTCAG
chr4	55980991	55981030	KDR_1356	-	GTGACCTATGCACCAGACGTATTTCCCTTCCATATCATTAAATAACATATCCTTGTATTAAAGATCGGAAGAGCGGTTTCAG
chr4	55981398	55981437	KDR_1357	-	GTGACCTATGCACCAGACGTTCTCCCAATCGTCTCTTAAGTTTTATAATTTAAGCTAGATCGGAAGAGCGGTTTCAG
chr4	55984721	55984760	KDR_1358	-	GTGACCTATGCACCAGACGTAAATAAAATTCATTTCCACGTTCTTTTACCAGTTATAAAAGATCGGAAGAGCGGTTTCAG
chr4	55987214	55987253	KDR_1359	-	GTGACCTATGCACCAGACGTATTCTAGATCTAGATTTCTGTGTTAAGTAAGTATTGTTAGATCGGAAGAGCGGTTTCAG
chr4	55991344	55991383	KDR_1360	-	GTGACCTATGCACCAGACGTCACTCTGGAGGAGGAAGGCAGACAGGTCGGGTGAGGGCGGAGATCGGAAGAGCGGTTTCAG
chr7	150690842	150690881	NOS3_1361	-	GTGACCTATGCACCAGACGTGTCCACTCTGCTGCCTGCTCCAGCAGAGCCCTGGCCTTTTATAGATCGGAAGAGCGGTTTCAG
chr7	150692241	150692280	NOS3_1362	-	GTGACCTATGCACCAGACGTCCAGGGATAGGGTGCATCAGGAAGGGTTGTTTCCCTTTACAGATCGGAAGAGCGGTTTCAG
chr7	150693801	150693840	NOS3_1363	-	GTGACCTATGCACCAGACGTGGGGGTGGGAAGGGCAAGCAGGAAGTTGTGTGGACAAGATCGGAAGAGCGGTTTCAG
chr7	150695395	150695434	NOS3_1364	-	GTGACCTATGCACCAGACGTGAGGCAGCGGAGAGAGGGTGCAGGAGACAGACGGGGGAGATCGGAAGAGCGGTTTCAG
chr7	150695577	150695616	NOS3_1365	-	GTGACCTATGCACCAGACGTTGGGAAAGAGCTGGTGCAGAGCCCCGCTTCCCTGCCTTGAGATCGGAAGAGCGGTTTCAG
chr7	150695984	150696023	NOS3_1366	-	GTGACCTATGCACCAGACGTTGGGCCAGAGGGGTTCTGGGGCTGAGCCCTCATGCCCTCCAGATCGGAAGAGCGGTTTCAG
chr7	150696228	150696267	NOS3_1367	-	GTGACCTATGCACCAGACGTTGGGGTGTGGGATCAGCACCCCTTGCAAGGCCCTTTGAAGATCGGAAGAGCGGTTTCAG
chr7	150697536	150697575	NOS3_1368	-	GTGACCTATGCACCAGACGTAGGGTGTGTGGCATCGGTAGGCAGAGGTTGATCACGGGGAGATCGGAAGAGCGGTTTCAG
chr7	150698269	150698308	NOS3_1369	-	GTGACCTATGCACCAGACGTGAGAGAGGGGGAGGCTCAAACAGACCACAGCCCTCGAGATCGGAAGAGCGGTTTCAG
chr7	150698582	150698621	NOS3_1370	-	GTGACCTATGCACCAGACGTATGATGGGTTGGGAGGGGAGGTAAGAAAAGGAAAGTTAGATCGGAAGAGCGGTTTCAG
chr7	150698859	150698898	NOS3_1371	-	GTGACCTATGCACCAGACGTGGAAGGTGTGAGGGTGTCTGGTGCACAGAGGCAGGGCCAGATCGGAAGAGCGGTTTCAG
chr7	150699238	150699277	NOS3_1372	-	GTGACCTATGCACCAGACGTGAAGACAGATGTCCCTGGGTGCTGTGGCCCCGAGGCCCTAGATCGGAAGAGCGGTTTCAG
chr7	150703465	150703504	NOS3_1373	-	GTGACCTATGCACCAGACGTGAGTGTTCATCAGGGTTAGTTTTGTTTCATTTCAAAGTATCGGAAGAGCGGTTTCAG
chr7	150703927	150703966	NOS3_1374	-	GTGACCTATGCACCAGACGTAGGACAAAGACAAGTTGTCAACAGGCCCTGGGGATACAGATCGGAAGAGCGGTTTCAG
chr7	150704140	150704179	NOS3_1375	-	GTGACCTATGCACCAGACGTGGGGTCCGTCAGTGCAGCTCCCTTTGCAGGCCACGTTTGCAGATCGGAAGAGCGGTTTCAG
chr7	150705968	150706007	NOS3_1376	-	GTGACCTATGCACCAGACGTGGCCGGTGGGGCTGAGGACCTCCCGCCACCAGGGGTGCAGATCGGAAGAGCGGTTTCAG
chr7	150706227	150706266	NOS3_1377	-	GTGACCTATGCACCAGACGTGGAGGGCAAATGAGGCAGCCTGAGCTAGGGAGCAGGGCCAGATCGGAAGAGCGGTTTCAG
chr7	150706436	150706475	NOS3_1378	-	GTGACCTATGCACCAGACGTGGAGAGGGGCACTTATGGGGAGTCAGAGAGGGGTGGGGCCAGATCGGAAGAGCGGTTTCAG
chr7	150707153	150707192	NOS3_1379	-	GTGACCTATGCACCAGACGTTGCACAGGGAGCTCTGAGGACAGGCCCCAGCAGGATGCAAGATCGGAAGAGCGGTTTCAG
chr7	150707635	150707674	NOS3_1380	-	GTGACCTATGCACCAGACGTAGGATGCAGTGGTTGGAGCCCCATAGACCCTTCTAGTAGATCGGAAGAGCGGTTTCAG
chr7	150707937	150707976	NOS3_1381	-	GTGACCTATGCACCAGACGTGAAGGAGAGGCCGGTGGAGGGCCAGAGAGGGGCCGTTCCAGATCGGAAGAGCGGTTTCAG
chr7	150709389	150709428	NOS3_1382	-	GTGACCTATGCACCAGACGTAGACACTCCATCAGGTCCCCTTTGCCTTTCTGCTCCACCAGATCGGAAGAGCGGTTTCAG
chr7	150710269	150710308	NOS3_1383	-	GTGACCTATGCACCAGACGTCCCCGCGCTTGGGAAGGCTCTTCTCCGGGCACAGTGCTAAGATCGGAAGAGCGGTTTCAG
chr7	150710762	150710801	NOS3_1384	-	GTGACCTATGCACCAGACGTGCGGGTTAGGGCGGGCCCTGGTGGGGTGGGCGCGGGGAGATCGGAAGAGCGGTTTCAG
chr7	150711046	150711085	NOS3_1385	-	GTGACCTATGCACCAGACGTAGACACAGTGGATCAGAACCAGCTCGGAGACCTTAGCAAGATCGGAAGAGCGGTTTCAG
chr9	98209144	98209183	PTCH1_1386	-	GTGACCTATGCACCAGACGTGAGCAACTGACCCAGCCAGCCAGCCAGCCAGCCAAAGAAGATCGGAAGAGCGGTTTCAG
chr9	98211301	98211340	PTCH1_1387	-	GTGACCTATGCACCAGACGTCTGCAGAACCAGGGGGAGGGTCTTCCACCCTGGTAGTGAGATCGGAAGAGCGGTTTCAG
chr9	98212073	98212112	PTCH1_1388	-	GTGACCTATGCACCAGACGTACACGGGGATGTCACAGTGTAGGCCGGCTGAATGCTGTGAGATCGGAAGAGCGGTTTCAG
chr9	98218508	98218547	PTCH1_1389	-	GTGACCTATGCACCAGACGTCAATTTGAAGCAAAAATTTGTGAAAAACAACCCATTTCCAGATCGGAAGAGCGGTTTCAG
chr9	98220245	98220284	PTCH1_1390	-	GTGACCTATGCACCAGACGTTATAAGGGCTTTGTGGAAGTCAAATTCCTTTTCAGATAGAGATCGGAAGAGCGGTTTCAG
chr9	98221832	98221871	PTCH1_1391	-	GTGACCTATGCACCAGACGTTTTATCGGGAGTGTGGGAACTACAGAGGTGCTTCCAGATCGGAAGAGCGGTTTCAG
chr9	98224088	98224127	PTCH1_1392	-	GTGACCTATGCACCAGACGTGCTGGGCATGAGGGGCTCCAGGGTCTCGGGCCGCTGATCGGAAGAGCGGTTTCAG



chr9	98229348	98229387	PTCH1_1393	-	GTGACCTATGCACCAGACGCTGTGGGAGGCTCTCGTCTTTTCGGTCTTTTTCGGTGTTCAGCAGATCGGAAGAGCGGTTTCAG
chr9	98230983	98231022	PTCH1_1394	-	GTGACCTATGCACCAGACGTACAACCTTAAGGCTCTTCTGTCTTCAAATAAACAGAAAGATCGGAAGAGCGGTTTCAG
chr9	98232045	98232084	PTCH1_1395	-	GTGACCTATGCACCAGACGTAGACTGCTGTGGCCTTTTGATTGGGTGCAGAATGGTGTGAGATCGGAAGAGCGGTTTCAG
chr9	98238266	98238305	PTCH1_1396	-	GTGACCTATGCACCAGACGTGGTGATGAAGGCTGTGGTGATCCTGAACGGGGGACTGACTAGATCGGAAGAGCGGTTTCAG
chr9	98238991	98239030	PTCH1_1397	-	GTGACCTATGCACCAGACGTAAACAAAAGAGAGCTTTGGGGACATCACAGCTTCTCTAGATCGGAAGAGCGGTTTCAG
chr9	98239779	98239818	PTCH1_1398	-	GTGACCTATGCACCAGACGTAGCCATTTATCTGCTGTCCGTTGCAGAAATGCCACCCGGCCAGATCGGAAGAGCGGTTTCAG
chr9	98240287	98240326	PTCH1_1399	-	GTGACCTATGCACCAGACGTGACCTGCTCTGGGGCTGGAGTTTGGTTTGGTTTGGTTAGATCGGAAGAGCGGTTTCAG
chr9	98241232	98241271	PTCH1_1400	-	GTGACCTATGCACCAGACGTCTTGAATCGGCGTGCAGACTCGCTGGTTATGCAATTTAGATCGGAAGAGCGGTTTCAG
chr9	98242201	98242240	PTCH1_1401	-	GTGACCTATGCACCAGACGTTCCCAGGACAATCTATGCCCTGTAGTCTTCTTCCCTTCCAGATCGGAAGAGCGGTTTCAG
chr9	98242622	98242661	PTCH1_1402	-	GTGACCTATGCACCAGACGTGCAGTGAGCGCTCTCAGAAGGTGGAGAGCAAAACACTTTAGATCGGAAGAGCGGTTTCAG
chr9	98244181	98244220	PTCH1_1403	-	GTGACCTATGCACCAGACGTGATCATGCTTTCTGTATGCTGTGACTTCTCTAGGACTCAGAGATCGGAAGAGCGGTTTCAG
chr9	98244366	98244405	PTCH1_1404	-	GTGACCTATGCACCAGACGTTTCTGTTGGCAAAAATTTCTCAGGAACACCCCACTAGTGTGAGATCGGAAGAGCGGTTTCAG
chr9	98247917	98247956	PTCH1_1405	-	GTGACCTATGCACCAGACGTCCCGCTCCACTAATGAGCAGCAGGTAAGGGCGTGGGAGATCGGAAGAGCGGTTTCAG
chr9	98270393	98270432	PTCH1_1406	-	GTGACCTATGCACCAGACGTGACTCTCTCCCTCCACTTTCTCTCCCTCTCTAACTCTTAGATCGGAAGAGCGGTTTCAG
chr9	98278701	98278740	PTCH1_1407	-	GTGACCTATGCACCAGACGTCCAGCGCGCGCGCCGACGCCACCTCGCTCGCGCCAGATCGGAAGAGCGGTTTCAG
chr9	98278855	98278894	PTCH1_1408	-	GTGACCTATGCACCAGACGTGACGAGGGAAGACTGGGAGAAGACGGAGGACGGAGGACGAGATCGGAAGAGCGGTTTCAG
chr9	98209414	98209453	PTCH1_1409	-	GTGACCTATGCACCAGACGTCCGGCTACTGCCAGCCATCACACTGTGACGGCTTCTGCAGATCGGAAGAGCGGTTTCAG
chr5	1253793	1253832	TERT_1410	-	GTGACCTATGCACCAGACGTCCACAGCGCGCCGAGCAGACAGCAGCCCTGTCAAGATCGGAAGAGCGGTTTCAG
chr5	1254433	1254472	TERT_1411	-	GTGACCTATGCACCAGACGTGTGGAGGCCAGTGCGGGCCCCACCTGCCAGGGGTATCCAGATCGGAAGAGCGGTTTCAG
chr5	1255352	1255391	TERT_1412	-	GTGACCTATGCACCAGACGTGTGCTTGGCCTCAGTGGCAGCAGTGCCTGCCTGCTGGTGTAGATCGGAAGAGCGGTTTCAG
chr5	1258663	1258702	TERT_1413	-	GTGACCTATGCACCAGACGTACCAGGGGTGCAGGCCAGCCCTCCAGGGACCCTCCGCGCAGATCGGAAGAGCGGTTTCAG
chr5	1264469	1264508	TERT_1414	-	GTGACCTATGCACCAGACGTGTGGCCGGAAGTGGAGCCTGTGCCCGGCTGGGGCAGGTGCAGATCGGAAGAGCGGTTTCAG
chr5	1266529	1266568	TERT_1415	-	GTGACCTATGCACCAGACGTGGCGTGTCTGTGGGACCTCCACAGCCTGTGGCTTTAGATCGGAAGAGCGGTTTCAG
chr5	1268585	1268624	TERT_1416	-	GTGACCTATGCACCAGACGTCTCTCCCGAGGGGCTTGGGTGGGGGTTGATTTGCTTTAGATCGGAAGAGCGGTTTCAG
chr5	1271184	1271223	TERT_1417	-	GTGACCTATGCACCAGACGTTGGCCAGGTGCCATTGCCCTGCGGGTGGCTGGGCGGGCTGAGATCGGAAGAGCGGTTTCAG
chr5	1272250	1272289	TERT_1418	-	GTGACCTATGCACCAGACGTTGCCCTGCAGGTTGGGACGGACTCCCAGCAGTGGGTCCAGATCGGAAGAGCGGTTTCAG
chr5	1278706	1278745	TERT_1419	-	GTGACCTATGCACCAGACGTGCTGTGATAGTCTGTCCAGGATGTGTGCTCTGGGATATAGATCGGAAGAGCGGTTTCAG
chr5	1279356	1279395	TERT_1420	-	GTGACCTATGCACCAGACGTGGGACCCCGTGAGCAGCCCTGCTGACCTTGGGAGTGGCAGATCGGAAGAGCGGTTTCAG
chr5	1280223	1280262	TERT_1421	-	GTGACCTATGCACCAGACGTTTTGGTTAACTTCTTTTAAACAGAAGTGCGTTGAGCAGATCGGAAGAGCGGTTTCAG
chr5	1282494	1282533	TERT_1422	-	GTGACCTATGCACCAGACGTCCCACGCGAGCCCTCTGCTTCTCGAAGTCTGGAACCAAGATCGGAAGAGCGGTTTCAG
chr5	1293378	1293417	TERT_1423	-	GTGACCTATGCACCAGACGTGGTGGCCGTGAGGGGCCAGGCCAGAGCTGAATGCAGTATAGATCGGAAGAGCGGTTTCAG
chr5	1294836	1294875	TERT_1424	-	GTGACCTATGCACCAGACGTCCGGGGTCCGGCTCCGGCTGGGGTTGAGGGCGGCCGGGGAGATCGGAAGAGCGGTTTCAG
chr5	1293829	1293868	TERT_1425	-	GTGACCTATGCACCAGACGTGGTTGCCCGCCTGCCACAGCGCTACTGGCAATGCGGCCAGATCGGAAGAGCGGTTTCAG
chr5	1294280	1294319	TERT_1426	-	GTGACCTATGCACCAGACGTGCCAGCCGAAGTGTGCCCTGGCCCAAGAGGCCAGGCGTGAGATCGGAAGAGCGGTTTCAG
chr16	2098567	2098606	TSC2_1427	-	GTGACCTATGCACCAGACGTGACGACAGCAAAAAACCCTCTGTGCAAAACGAAACGAAATAGATCGGAAGAGCGGTTTCAG
chr16	2100351	2100390	TSC2_1428	-	GTGACCTATGCACCAGACGTATGAAAGAAGAAAAAGGGGCCAGTGTCTCAGGCCACGGTCTAGATCGGAAGAGCGGTTTCAG
chr16	2103293	2103332	TSC2_1429	-	GTGACCTATGCACCAGACGTGACAGGGGACAGCGGTGAGGATGTGCTCTCCAAGAACCCTAGATCGGAAGAGCGGTTTCAG
chr16	2104247	2104286	TSC2_1430	-	GTGACCTATGCACCAGACGTAAAGCCACAGGATCAGCAGAGCCTGCCAGCGTCCGCCACACAGATCGGAAGAGCGGTTTCAG
chr16	2105353	2105392	TSC2_1431	-	GTGACCTATGCACCAGACGTAGCGGGCCAGTTTGCAGGAGCAGCCGAATCTACATCTCCAGATCGGAAGAGCGGTTTCAG
chr16	2106147	2106186	TSC2_1432	-	GTGACCTATGCACCAGACGTGACGAGCTCAGTCCCGGCAGCAGCTCCCTGGATGGCCGAGATCGGAAGAGCGGTTTCAG
chr16	2106595	2106634	TSC2_1433	-	GTGACCTATGCACCAGACGTGGGAGACGGCTCACGCCCTCCTACCCAGCTCTCCCAAGATCGGAAGAGCGGTTTCAG
chr16	2107056	2107095	TSC2_1434	-	GTGACCTATGCACCAGACGTCAATGCGTGTGAGGGGCTGGCAGGCATAAGCCCTGCCCCAGATCGGAAGAGCGGTTTCAG
chr16	2108698	2108737	TSC2_1435	-	GTGACCTATGCACCAGACGTTCCCGAGAGAGCGGAATGTGAGCAGGGCCCTGTCCAGGAGATCGGAAGAGCGGTTTCAG
chr16	2110621	2110660	TSC2_1436	-	GTGACCTATGCACCAGACGTAGCCCGCCAGCACACAGGGTTCAGAGCTGCTTCTGCTGAGATCGGAAGAGCGGTTTCAG
chr16	2111822	2111861	TSC2_1437	-	GTGACCTATGCACCAGACGTAGGCAGATGACACAGGCTGACTTCCACTCCCCACATCGGAAGAGCGGTTTCAG
chr16	2112448	2112487	TSC2_1438	-	GTGACCTATGCACCAGACGTAAAGAGCGGTGTGCCCTCTGCCCTCCGGCTCTCTAGATCGGAAGAGCGGTTTCAG
chr16	2112923	2112962	TSC2_1439	-	GTGACCTATGCACCAGACGTGACGCTGTGGGGCGGTTGGGGAGTGCCCGGCCACAGCCAGATCGGAAGAGCGGTTTCAG
chr16	2114223	2114262	TSC2_1440	-	GTGACCTATGCACCAGACGTACAAGGGAGGCCAATGAGCGCCAGCCCAACGAGGGCCACAAGATCGGAAGAGCGGTTTCAG
chr16	2115470	2115509	TSC2_1441	-	GTGACCTATGCACCAGACGTAAAGGCCAGGACTTACACACAGGCTCATGTTCTGAGTCAGAGATCGGAAGAGCGGTTTCAG
chr16	2120407	2120446	TSC2_1442	-	GTGACCTATGCACCAGACGTAGGACGCGACTCACACCGCGCAGGAGGTGAAAACGCACTAGATCGGAAGAGCGGTTTCAG
chr16	2121461	2121500	TSC2_1443	-	GTGACCTATGCACCAGACGTGAGGATGGTGAAGCCAGAGCCAACTCGTGCAGGCCAGATCGGAAGAGCGGTTTCAG
chr16	2121735	2121774	TSC2_1444	-	GTGACCTATGCACCAGACGTAAAGAGAGAGCTGAGGCCAAGTCCCGCAGCAGGAACGAGATCGGAAGAGCGGTTTCAG
chr16	2122192	2122231	TSC2_1445	-	GTGACCTATGCACCAGACGTAGGAGGCGTACAGACAGGGCCTTCTGGACCCTAGAGACAGAGATCGGAAGAGCGGTTTCAG
chr16	2122800	2122839	TSC2_1446	-	GTGACCTATGCACCAGACGTAATCCAGGCATGAAACCTCTCCCGAGCGGCCAGGTACGGAGATCGGAAGAGCGGTTTCAG
chr16	2124151	2124190	TSC2_1447	-	GTGACCTATGCACCAGACGTGAGGACACCTCAGGCCACCCGCTTCAGCAGAGGCAGCAGATCGGAAGAGCGGTTTCAG
chr16	2125750	2125789	TSC2_1448	-	GTGACCTATGCACCAGACGTGGAGAGGGTGGTCAAGGGAGCCGGGTTCCCGTGCAGCGCCAGATCGGAAGAGCGGTTTCAG
chr16	2126019	2126058	TSC2_1449	-	GTGACCTATGCACCAGACGTAAGGGGCTGGACTGCTGACAGCAGGGAACACTCCAGATCGGAAGAGCGGTTTCAG
chr16	2126442	2126481	TSC2_1450	-	GTGACCTATGCACCAGACGTGAGCACACCCAGACAGTGTAGGGTGGCAATGGGGCTGGAAGATCGGAAGAGCGGTTTCAG

chr16	2127549	2127588	TSC2_1451	-	GTGACCTATGCACCAGACGTAGGAAGGAGCCCCAACGCCCCAGAGAGCCAGCTCCCGGGAGATCGGAAGAGCGGTTTCAG
chr16	2128983	2129022	TSC2_1452	-	GTGACCTATGCACCAGACGTAGGCCGTGACCAGGGTCAGGGTGCCAGGTAGGGCGGGCCGAGATCGGAAGAGCGGTTTCAG
chr16	2129227	2129266	TSC2_1453	-	GTGACCTATGCACCAGACGTGGGAGCGTGAAACCCAGCTTGCCCGTGGAGCTCCCGCAGGAGATCGGAAGAGCGGTTTCAG
chr16	2129508	2129547	TSC2_1454	-	GTGACCTATGCACCAGACGTAATCCCACGCACAGGGTGGACTTAGTCCCAGGCTGGTACAGATCGGAAGAGCGGTTTCAG
chr16	2130116	2130155	TSC2_1455	-	GTGACCTATGCACCAGACGTGGGCAGAGGACTGGTGACCACCACTTACCTGATGCAAAACAGATCGGAAGAGCGGTTTCAG
chr16	2131546	2131585	TSC2_1456	-	GTGACCTATGCACCAGACGTGGCAGCAGCTTTGGCCTGAGGCCAGTACCTCCCCTTACCAGATCGGAAGAGCGGTTTCAG
chr16	2132387	2132426	TSC2_1457	-	GTGACCTATGCACCAGACGTGAGCCGTGTGCCGCGTGTCCGGCAGTCAGCAGAGGAGGGGCTACACAGATCGGAAGAGCGGTTTCAG
chr16	2133646	2133685	TSC2_1458	-	GTGACCTATGCACCAGACGTACAGACGGGGCTGCTGGATGTGGGGCTGGGCCAGGCCCTGAGATCGGAAGAGCGGTTTCAG
chr16	2134179	2134218	TSC2_1459	-	GTGACCTATGCACCAGACGTCCATCCCAAAGAGAACCCCTGTCAGCAGGCCACCCTCGAGCAGATCGGAAGAGCGGTTTCAG
chr16	2134902	2134941	TSC2_1460	-	GTGACCTATGCACCAGACGTAGGGGATGGTGGGCACCAGGTGAGGGCCTGGCCAGGGCAAGATCGGAAGAGCGGTTTCAG
chr16	2135181	2135220	TSC2_1461	-	GTGACCTATGCACCAGACGTACAGAGCCCTGCCTGAGCCCCAGACGCCCGTCCACAGGAGGAGATCGGAAGAGCGGTTTCAG
chr16	2136144	2136183	TSC2_1462	-	GTGACCTATGCACCAGACGTAGGGGAGAGGCCAGGGTGGCATCTCCCGGGCCGGGCCCTAGATCGGAAGAGCGGTTTCAG
chr16	2136683	2136722	TSC2_1463	-	GTGACCTATGCACCAGACGTGACAGGCCGGATGGGTTTGTGGGGCCAGTGTCTGAGGCCCTAGATCGGAAGAGCGGTTTCAG
chr16	2137814	2137853	TSC2_1464	-	GTGACCTATGCACCAGACGTAAGAGAAAGGGTTCATCCCCGCACACAGCGTGTGCTGAAGGAGATCGGAAGAGCGGTTTCAG
chr16	2137999	2138038	TSC2_1465	-	GTGACCTATGCACCAGACGTTTGGTGGTACGCCAGGCCAGGGCTCTTGGCCGCACACTAGATCGGAAGAGCGGTTTCAG
chr16	2138178	2138217	TSC2_1466	-	GTGACCTATGCACCAGACGTAGGCAGGGGGTGTAGCTACTATCAGGTGGCAGCTGGGCCCTAGATCGGAAGAGCGGTTTCAG
chr16	2138397	2138436	TSC2_1467	-	GTGACCTATGCACCAGACGTAGGCCGGCTTGGGCAGTAAAGTCTGGGAGGGCGTGGCAACCCGAGATCGGAAGAGCGGTTTCAG
chr15	91290573	91290612	BLM_1468	-	GTGACCTATGCACCAGACGTAGTGAGGAAAAAGAAATCAGTGGAGTTAGGTACTTTTCAAGATCGGAAGAGCGGTTTCAG
chr15	91292547	91292586	BLM_1469	-	GTGACCTATGCACCAGACGTATGGAAAACTAGATTAGATGGATCCATTTTAAAGAAACCCAGATCGGAAGAGCGGTTTCAG
chr15	91294967	91295006	BLM_1470	-	GTGACCTATGCACCAGACGTACAGTTGATAAACATAGATTTGTTAACCACTAATGAGACAAGATCGGAAGAGCGGTTTCAG
chr15	91297991	91298030	BLM_1471	-	GTGACCTATGCACCAGACGTAAAAAATGTTAAGCCAAATCATACTATAGGCTAGACTCAATAGATCGGAAGAGCGGTTTCAG
chr15	91303327	91303366	BLM_1472	-	GTGACCTATGCACCAGACGTATTATGTTGTTAATATTTTCTTTGAGGGAAAAAAGATCGGAAGAGCGGTTTCAG
chr15	91303774	91303813	BLM_1473	-	GTGACCTATGCACCAGACGTAAAAAGAGAACACCTAATAAATAAGTAGTTACTCTGGAGATCGGAAGAGCGGTTTCAG
chr15	91306146	91306185	BLM_1474	-	GTGACCTATGCACCAGACGTAATCAACGTTAAGAAAACTAGTACATGAATACAGTGAAGAAAGATCGGAAGAGCGGTTTCAG
chr15	91308476	91308515	BLM_1475	-	GTGACCTATGCACCAGACGTACAAATGAAAAATATCTGTGAGGTTCTGTCTTACAGAGCATAGATCGGAAGAGCGGTTTCAG
chr15	91310090	91310129	BLM_1476	-	GTGACCTATGCACCAGACGTAAGTAGTAAACAATTTCAATTTTATACATTAACCTGACAAGATCGGAAGAGCGGTTTCAG
chr15	91312313	91312352	BLM_1477	-	GTGACCTATGCACCAGACGTAATACATTAGACATGTAAAAAACTGAAACACATCACCTCAGATCGGAAGAGCGGTTTCAG
chr15	91312618	91312657	BLM_1478	-	GTGACCTATGCACCAGACGTAAAAAATACTGCTTTTACAGTACTTGGAGCTTCTTCTAGATCGGAAGAGCGGTTTCAG
chr15	91326002	91326041	BLM_1479	-	GTGACCTATGCACCAGACGTCCCAAGATAAATTTAGTTATTAGAAAAATATGACATAGATCGGAAGAGCGGTTTCAG
chr15	91328101	91328140	BLM_1480	-	GTGACCTATGCACCAGACGTACCAAGACTGACAAACAGAAATTTTAAACATAAACAAAGATCGGAAGAGCGGTTTCAG
chr15	91333829	91333868	BLM_1481	-	GTGACCTATGCACCAGACGTAGCAAAAGCTTATTAGATTATAAGGCACAGACTTGAAGGAGATCGGAAGAGCGGTTTCAG
chr15	91337347	91337386	BLM_1482	-	GTGACCTATGCACCAGACGTTGAAGACTATAGTAAGACATACTTATAGGGGAAAAATAGAAGATCGGAAGAGCGGTTTCAG
chr15	91341370	91341409	BLM_1483	-	GTGACCTATGCACCAGACGTAAGAGAAATACTTTCTGCTATAATTAAGGTAACAATGCCTAGATCGGAAGAGCGGTTTCAG
chr15	91346701	91346740	BLM_1484	-	GTGACCTATGCACCAGACGTGATACAGGAAGTAAGATGAGTAAATGTACGTATATCATAGATCGGAAGAGCGGTTTCAG
chr15	91347347	91347386	BLM_1485	-	GTGACCTATGCACCAGACGTAGCAAAACAAATCATAGGAGTGGGTATATGTGCACTTGTACAGATCGGAAGAGCGGTTTCAG
chr15	91352317	91352356	BLM_1486	-	GTGACCTATGCACCAGACGTGCATAAAATTAAGAAATTTAAATTTACCCATAGAAAAACCAGATCGGAAGAGCGGTTTCAG
chr15	91354385	91354424	BLM_1487	-	GTGACCTATGCACCAGACGTAAAAATGCAGATGTTTACAGGTGATGTGCACTGGTCCACGAGATCGGAAGAGCGGTTTCAG
chr15	91358282	91358321	BLM_1488	-	GTGACCTATGCACCAGACGTACAAAGAAAAAATCAAATGTTAATGAAACCAAAAATGAGATCGGAAGAGCGGTTTCAG
chr15	91292897	91292936	BLM_1489	-	GTGACCTATGCACCAGACGTATCTGGTGAAGAATAAATTTCTAATTTCTTGGAGCAGTAAGATCGGAAGAGCGGTTTCAG
chr15	91304105	91304144	BLM_1490	-	GTGACCTATGCACCAGACGTTTTTTCCTAGTCTTGGTGTTCAGCCAGTTGCTACTTAAGATCGGAAGAGCGGTTTCAG
chr11	119077078	119077117	CBL_1491	-	GTGACCTATGCACCAGACGTGGGTCCGAGCCGAGCGGGTCCCGGCTCGGCTCGACTGAGATCGGAAGAGCGGTTTCAG
chr11	119103108	119103147	CBL_1492	-	GTGACCTATGCACCAGACGTTGAAAAAGAAGGGCTATTACTTGGAGAATTTTAAAGACAGAGATCGGAAGAGCGGTTTCAG
chr11	119144528	119144567	CBL_1493	-	GTGACCTATGCACCAGACGTGGTGGAGAGGAGGCATAAAGTAAATAACAGAGATAATTCAGATCGGAAGAGCGGTTTCAG
chr11	119145492	119145531	CBL_1494	-	GTGACCTATGCACCAGACGTAAGATCAATCACAGACTATTAGGTCAGATGTACAACCAAGATCGGAAGAGCGGTTTCAG
chr11	119146657	119146696	CBL_1495	-	GTGACCTATGCACCAGACGTACATAAACCAAGCGTTTGTAGATTAGTCTGGTATTACGGAGATCGGAAGAGCGGTTTCAG
chr11	119148417	119148456	CBL_1496	-	GTGACCTATGCACCAGACGTTAACCAACCTGGGTTTTTAAAGCAATTTGCCAGTGCAGATCGGAAGAGCGGTTTCAG
chr11	119148826	119148865	CBL_1497	-	GTGACCTATGCACCAGACGTAAAAAATTAAGAGACTATTAGTTGAATAAATACTGCAATAGATCGGAAGAGCGGTTTCAG
chr11	119149170	119149209	CBL_1498	-	GTGACCTATGCACCAGACGTAGCAAAAGATAGTAACAGATGCATCTGAAAATACTTAAAAAGATCGGAAGAGCGGTTTCAG
chr11	119155629	119155668	CBL_1499	-	GTGACCTATGCACCAGACGTTAAAAATTTAACAGATTACTTTCTGTTTGGGAAATGGCAAGATCGGAAGAGCGGTTTCAG
chr11	119155849	119155888	CBL_1500	-	GTGACCTATGCACCAGACGTAGGGTGAAGCAAAATCAGTAAAAACCCACTAGTACACAGCAGATCGGAAGAGCGGTTTCAG
chr11	119158512	119158551	CBL_1501	-	GTGACCTATGCACCAGACGTAAGAAAAGTGTGAAAAACAATTTCTTACCACAGCTGAGAGATCGGAAGAGCGGTTTCAG
chr11	119167578	119167617	CBL_1502	-	GTGACCTATGCACCAGACGTAAAGATAAAAAATGAAAAAGAAAGTAAACAACCAAGTAAACAGATCGGAAGAGCGGTTTCAG
chr11	119168044	119168083	CBL_1503	-	GTGACCTATGCACCAGACGTAGGAAAAGTGCATAATGATCTTTGAAATAGAAGTGTATAGATCGGAAGAGCGGTTTCAG
chr11	119169018	119169057	CBL_1504	-	GTGACCTATGCACCAGACGTATGAGTGATGTTATCTTCTTGTGACGCACCTCATCTTCTAAGATCGGAAGAGCGGTTTCAG
chr11	119170155	119170194	CBL_1505	-	GTGACCTATGCACCAGACGTTAGGAAAGAAAATTTTGAATCTGGGAAATCCTCATTAGATCGGAAGAGCGGTTTCAG
chr17	48262813	48262852	COL1A1_1506	-	GTGACCTATGCACCAGACGTTCCCAACCTGGCTCCCTCCCACCAACCACTTTCCCCAGATCGGAAGAGCGGTTTCAG
chr17	48263089	48263128	COL1A1_1507	-	GTGACCTATGCACCAGACGTAGATACCCAGGCAGGGCCACCTCCGGCCTTGGGCTAGATCGGAAGAGCGGTTTCAG
chr17	48263628	48263667	COL1A1_1508	-	GTGACCTATGCACCAGACGTTGGACCTCAGGCCAGTGTAGGAGATGGGCTAGCCAGTATAGATCGGAAGAGCGGTTTCAG

chr17	48263951	48263990	COL1A1_1509	-	GTGACCTATGCACCAGACGTGCCCTAGCCTCTCCCTCCCTCCTACTCCTGCCATGCCAGGAGATCGGAAGAGCGGTTTCAG
chr17	48264326	48264365	COL1A1_1510	-	GTGACCTATGCACCAGACGTCTCATCCCTCTGCTCATGGCCCTCCAGCCCCAAAGCAAGATCGGAAGAGCGGTTTCAG
chr17	48264795	48264834	COL1A1_1511	-	GTGACCTATGCACCAGACGTCTTCTCTCTCCTCTTCTGAGCCCCAAGCCCAGGCTCACAGATCGGAAGAGCGGTTTCAG
chr17	48265187	48265226	COL1A1_1512	-	GTGACCTATGCACCAGACGTTCAGCCCCCTCCCAGTCCCATGCTGTGCTGTGGGATAGGAGATCGGAAGAGCGGTTTCAG
chr17	48265407	48265446	COL1A1_1513	-	GTGACCTATGCACCAGACGTGTGCTGTGCCCTATGCCTTTAGAAGCTACAGATGCAGAAGATCGGAAGAGCGGTTTCAG
chr17	48265841	48265880	COL1A1_1514	-	GTGACCTATGCACCAGACGTGGGCTCCAGTTCCCTGTACCTGGTGCAGGCTCCGACTCTTAGATCGGAAGAGCGGTTTCAG
chr17	48266053	48266092	COL1A1_1515	-	GTGACCTATGCACCAGACGTAACACTCCATGACCACAGCCTTGTCTGCTGCTTCCCTGCCAGATCGGAAGAGCGGTTTCAG
chr17	48266214	48266253	COL1A1_1516	-	GTGACCTATGCACCAGACGTCCCAGCCCCATGCCAGTACCCTCAGCATGGCCATTGTGGAGATCGGAAGAGCGGTTTCAG
chr17	48266479	48266518	COL1A1_1517	-	GTGACCTATGCACCAGACGTCCCTCACCTTGGGGGGCCCTGAGAAAACCATCACAGGACAGATCGGAAGAGCGGTTTCAG
chr17	48266688	48266727	COL1A1_1518	-	GTGACCTATGCACCAGACGTGCTCAGATCTCTGCAGCTCCGGAGGTGTGCAGAGCTGGGGAGATCGGAAGAGCGGTTTCAG
chr17	48266990	48267029	COL1A1_1519	-	GTGACCTATGCACCAGACGTGCAGCAGACTCCACTGCTCTAGGTTGGGGGTGCTGGGTGGAGATCGGAAGAGCGGTTTCAG
chr17	48267170	48267209	COL1A1_1520	-	GTGACCTATGCACCAGACGTCCCAGCTCTCTGTGAGCCTCCTCCCTCCTCCCAGGCACAGATCGGAAGAGCGGTTTCAG
chr17	48267312	48267351	COL1A1_1521	-	GTGACCTATGCACCAGACGTGGCCCTCTGTGCCACAGAGGCTGTGGGCTGGGACCCAGAGATCGGAAGAGCGGTTTCAG
chr17	48267638	48267677	COL1A1_1522	-	GTGACCTATGCACCAGACGTAGACCCCCATCATTTTTTTCATCACCAGCTGGGACCTGGGACAGATCGGAAGAGCGGTTTCAG
chr17	48267854	48267893	COL1A1_1523	-	GTGACCTATGCACCAGACGTAAGACCTGTTAAGACCCATACTTGGCCCTCCCTCCCTTAGATCGGAAGAGCGGTTTCAG
chr17	48268128	48268167	COL1A1_1524	-	GTGACCTATGCACCAGACGTGCCTCCCCACCTTCTGCCCTAACACATAGCCTCCTCAGCAGATCGGAAGAGCGGTTTCAG
chr17	48268694	48268733	COL1A1_1525	-	GTGACCTATGCACCAGACGTCTTCCCCTCCCCTGAGCCCTACATGGCTCCCCTCTCTAGATCGGAAGAGCGGTTTCAG
chr17	48269099	48269138	COL1A1_1526	-	GTGACCTATGCACCAGACGTCTGGAAAGGGGCTGTGCCAAGTGGCCAGGACAGGCTAGATCGGAAGAGCGGTTTCAG
chr17	48269291	48269330	COL1A1_1527	-	GTGACCTATGCACCAGACGTCTCTCGCTGCATCCGTCAGAGTGGCTGCTGCTACTTGGCCAGATCGGAAGAGCGGTTTCAG
chr17	48269786	48269825	COL1A1_1528	-	GTGACCTATGCACCAGACGTGCAGCCGGCCAGAGGGGTGGGAGATGCAGGGAATCCAGAGAGATCGGAAGAGCGGTTTCAG
chr17	48269951	48269990	COL1A1_1529	-	GTGACCTATGCACCAGACGTATGGCTGTCAGGATGCTGGGAGGTAGGGGTAGGAAACACCAGATCGGAAGAGCGGTTTCAG
chr17	48270108	48270147	COL1A1_1530	-	GTGACCTATGCACCAGACGTCTGATGGGGAGATCGGGGAGCAGAAAAGGGGAGACACCAGATCGGAAGAGCGGTTTCAG
chr17	48270305	48270344	COL1A1_1531	-	GTGACCTATGCACCAGACGTCTTCCATCCCTACCTCCTTCCCATTGCTGCCCGGCACAGATCGGAAGAGCGGTTTCAG
chr17	48271441	48271480	COL1A1_1532	-	GTGACCTATGCACCAGACGTCTCCCTGCAACCCCTGCCATTTGCTGCTGCCTCCCTAGATCGGAAGAGCGGTTTCAG
chr17	48271660	48271699	COL1A1_1533	-	GTGACCTATGCACCAGACGTAGGCTTTTTCAGCCTGGCTGGCCAGGCCCTGACCATCCCGTAGATCGGAAGAGCGGTTTCAG
chr17	48271884	48271923	COL1A1_1534	-	GTGACCTATGCACCAGACGTCTTGGCGCCGGGGGCTGACCCTGCCGCTCCCTGGGCATCAGATCGGAAGAGCGGTTTCAG
chr17	48272032	48272071	COL1A1_1535	-	GTGACCTATGCACCAGACGTCTGCCCGCCCCCTCCCGCTCCACCCTATTGCCCTGGCTGGAGATCGGAAGAGCGGTTTCAG
chr17	48272358	48272397	COL1A1_1536	-	GTGACCTATGCACCAGACGTCCGCCACTTCTTCTGAGCCACAGCCACCCTGCCCTAGGAAGATCGGAAGAGCGGTTTCAG
chr17	48272543	48272582	COL1A1_1537	-	GTGACCTATGCACCAGACGTAACCTCCTTCTGCCACCCACTGCTGCTCCAGTGCAGATCGGAAGAGCGGTTTCAG
chr17	48272745	48272784	COL1A1_1538	-	GTGACCTATGCACCAGACGTGGCCAGCTTCCAGTCCCACTCCTGCCCGCTGCAGCCCTGCCAGATCGGAAGAGCGGTTTCAG
chr17	48272878	48272917	COL1A1_1539	-	GTGACCTATGCACCAGACGTCCGACTCAGTGTCCCTTTGCCACTTTCTAACCTCAGAGTAGATCGGAAGAGCGGTTTCAG
chr17	48273234	48273273	COL1A1_1540	-	GTGACCTATGCACCAGACGTCCACTCTCCTCTAAGCATGACCCTCATGGGCCAAGGGGTAGATCGGAAGAGCGGTTTCAG
chr17	48273466	48273505	COL1A1_1541	-	GTGACCTATGCACCAGACGTCTGTAGGCCCTCAGGGCCTGGGAGTGGGGAGGGGTCTCAGAGATCGGAAGAGCGGTTTCAG
chr17	48273625	48273664	COL1A1_1542	-	GTGACCTATGCACCAGACGTGTGCCCTTTGGGGGATCCCTGAGCTCTGGAAGGGGCTCCAGATCGGAAGAGCGGTTTCAG
chr17	48273795	48273834	COL1A1_1543	-	GTGACCTATGCACCAGACGTCCAGTTCCAGTAGGGCAGGATGGGACAGGAGGCAGGGCCAAAGATCGGAAGAGCGGTTTCAG
chr17	48273928	48273967	COL1A1_1544	-	GTGACCTATGCACCAGACGTGTCTGAACATCATGGTCTCCACATCCCAGAGTCCCACCAGATCGGAAGAGCGGTTTCAG
chr17	48274321	48274360	COL1A1_1545	-	GTGACCTATGCACCAGACGTTTTGAGTCATTTAAGCTCCCCAAGTCCCTAGCATACCCCCAGATCGGAAGAGCGGTTTCAG
chr17	48274491	48274530	COL1A1_1546	-	GTGACCTATGCACCAGACGTGGCTGTGGCTGAACCTGGGCTTCACTGCACCTTGGGCTTCAAGATCGGAAGAGCGGTTTCAG
chr17	48275043	48275082	COL1A1_1547	-	GTGACCTATGCACCAGACGTCCAGCAAGAAGATACCATCTGACCCCATGGCCTCCATGGGAGATCGGAAGAGCGGTTTCAG
chr17	48275260	48275299	COL1A1_1548	-	GTGACCTATGCACCAGACGTTCTATACAGATTACTACTCCTTCTACAACACACAGACTCAGATCGGAAGAGCGGTTTCAG
chr17	48275472	48275511	COL1A1_1549	-	GTGACCTATGCACCAGACGTATGACAGCTTTCATAGCCTCCTTGGGCTTTGGTCTTTTGGAGATCGGAAGAGCGGTTTCAG
chr17	48275744	48275783	COL1A1_1550	-	GTGACCTATGCACCAGACGTAGGGGGAGCATGGATGACAGAAGAGAGAATGGGTATCCAGAGATCGGAAGAGCGGTTTCAG
chr17	48276537	48276576	COL1A1_1551	-	GTGACCTATGCACCAGACGTAGGCCCTTGTGTGCCACTCTCCCCTGTTTTGTTTTTTGTTTAGATCGGAAGAGCGGTTTCAG
chr17	48276729	48276768	COL1A1_1552	-	GTGACCTATGCACCAGACGTCACTCTGGGCTGTGGGGGGCTGCAGGTGGGCATGGCTCTCAGATCGGAAGAGCGGTTTCAG
chr17	48276867	48276906	COL1A1_1553	-	GTGACCTATGCACCAGACGTGCCCTCGAATTTTGGCCCTGCGCGGCCCGTGACTCCTCACAGATCGGAAGAGCGGTTTCAG
chr17	48278722	48278761	COL1A1_1554	-	GTGACCTATGCACCAGACGTAACCTTTTGGAGTGGCAAGATACTATATCGCGCCTTTCAGATCGGAAGAGCGGTTTCAG
chr3	168802647	168802686	MECOM_1555	-	GTGACCTATGCACCAGACGTGTTGACCAGAGTGGGACCAAGTCCAACAGTAGCATGGCTCAGATCGGAAGAGCGGTTTCAG
chr3	168806738	168806777	MECOM_1556	-	GTGACCTATGCACCAGACGTTCCCATAGTACAGCATCATGGTTACATTATGCATGAAACGAGATCGGAAGAGCGGTTTCAG
chr3	168807738	168807777	MECOM_1557	-	GTGACCTATGCACCAGACGTTGGGTGACTTTAGAAAATAAGCTAGAGTAGATCCATGTACAGATCGGAAGAGCGGTTTCAG
chr3	168810696	168810735	MECOM_1558	-	GTGACCTATGCACCAGACGTCTTTTACTTTTTAAACTCTGTGACGACTGAAATGAACATGAGATCGGAAGAGCGGTTTCAG
chr3	168812814	168812853	MECOM_1559	-	GTGACCTATGCACCAGACGTAATTGTGTTATAAGTCAAAAGTACTTCTTTTTCGTTTATAGATCGGAAGAGCGGTTTCAG
chr3	168819798	168819837	MECOM_1560	-	GTGACCTATGCACCAGACGTTAATTATGCTGACTTTCCAGAAATCTCCCCTCTAGATCGGAAGAGCGGTTTCAG
chr3	168825664	168825703	MECOM_1561	-	GTGACCTATGCACCAGACGTTACTTTATATTTTTGACTAAAGTGATGTAGCATTAAAAAGAAGATCGGAAGAGCGGTTTCAG
chr3	168830525	168830564	MECOM_1562	-	GTGACCTATGCACCAGACGTTGGATTGAGATTTCCAGCTTGTAAACTAACTTGTGATCAGATCGGAAGAGCGGTTTCAG
chr3	168833121	168833160	MECOM_1563	-	GTGACCTATGCACCAGACGTATGGAAGATGACGAAATATGACAGATGTATGAAAGGCGGAGATCGGAAGAGCGGTTTCAG
chr3	168838794	168838833	MECOM_1564	-	GTGACCTATGCACCAGACGTAACACTCCAGCCCTCCTTCCCACATCTGTCTCTTCCCAGATCGGAAGAGCGGTTTCAG
chr3	168840318	168840357	MECOM_1565	-	GTGACCTATGCACCAGACGTTTTGTAGGCTACTTGGCCCTCTGTATGTCATCTAGATCGGAAGAGCGGTTTCAG
chr3	168845582	168845621	MECOM_1566	-	GTGACCTATGCACCAGACGTGCATGTTGTACCATAACAATCTGTATTTTTTCTGCAATGAGATCGGAAGAGCGGTTTCAG

chr3	168849167	168849206	MECOM_1567	-	GTGACCTATGCACCAGACGCTCTCAGCCACCTCCTTATCACCTTATCATCGCGACTATAAGATCGGAAGAGCGGTTTCAG
chr3	168833573	168833612	MECOM_1568	-	GTGACCTATGCACCAGACGTACAAAAAAGTTGGAGCTTTACCTTACCCTTCCATGTTTCCAGATCGGAAGAGCGGTTTCAG
chr3	168834025	168834064	MECOM_1569	-	GTGACCTATGCACCAGACGTTCCAGATACTGCCAGCTACACAGGATATTTTGAAGGCACTAAGATCGGAAGAGCGGTTTCAG
chr17	11924154	11924193	MAP2K4_1570	-	GTGACCTATGCACCAGACGTGAAGAGCCGAGCGGCGCCGCGGCGCTGCAATGCAGCAAGAGATCGGAAGAGCGGTTTCAG
chr17	11958156	11958195	MAP2K4_1571	-	GTGACCTATGCACCAGACGTACAAATAAAAAGTAAAGTTTCAAGTACTACAAAACAGCTAGATCGGAAGAGCGGTTTCAG
chr17	11984623	11984662	MAP2K4_1572	-	GTGACCTATGCACCAGACGTATTGGGAAGCAATTTTTCCACATTTAAATAGGTTTTAACAGATCGGAAGAGCGGTTTCAG
chr17	11998842	11998881	MAP2K4_1573	-	GTGACCTATGCACCAGACGTGACAAAAGATGTCAAAAAACACAATAATTTGTCAAAGATCGGAAGAGCGGTTTCAG
chr17	12011057	12011096	MAP2K4_1574	-	GTGACCTATGCACCAGACGTACAAATATCTGTTATTCTTATACATCTTAAATATCACCTTAGATCGGAAGAGCGGTTTCAG
chr17	12013642	12013681	MAP2K4_1575	-	GTGACCTATGCACCAGACGTAAAGGAGAGATGGGATAAAACAAC TTGTTTCTTTTATTCAAGATCGGAAGAGCGGTTTCAG
chr17	12016500	12016539	MAP2K4_1576	-	GTGACCTATGCACCAGACGTAGATATCATT CAGTATACAATTAGCTTCTTCTTAAGTTAAGATCGGAAGAGCGGTTTCAG
chr17	12028561	12028600	MAP2K4_1577	-	GTGACCTATGCACCAGACGTAAAGACAAGTGTAAAGTTATTAATGCCTTACACTCAAGGAAAGATCGGAAGAGCGGTTTCAG
chr17	12032406	12032445	MAP2K4_1578	-	GTGACCTATGCACCAGACGTCAAAGGAAAGGACAAAATACACCAGGCATCATTACTAAGATCGGAAGAGCGGTTTCAG
chr17	12043106	12043145	MAP2K4_1579	-	GTGACCTATGCACCAGACGTATAAAAAATAACATTATAAAGTGTAGATTCAATTTGCCTAAAAGATCGGAAGAGCGGTTTCAG
chr17	12044414	12044453	MAP2K4_1580	-	GTGACCTATGCACCAGACGTATTGAAAACAAAAAAGTCAAAGTTTGTATGACAGCCCAAAGATCGGAAGAGCGGTTTCAG
chr22	39621678	39621717	PDGFB_1581	-	GTGACCTATGCACCAGACGTAGGAGAGTGTGTGGGCAGGTGAGGGCCAGGCGGGGCAACTAGATCGGAAGAGCGGTTTCAG
chr22	39626039	39626078	PDGFB_1582	-	GTGACCTATGCACCAGACGTTTCCAGGCTCAGCCCTCAGCCCTTCCCTGCAGCAGCTAGATCGGAAGAGCGGTTTCAG
chr22	39627577	39627616	PDGFB_1583	-	GTGACCTATGCACCAGACGTCCGCGGCCCCCGAGGCTGGTCCCGGTTGGTGGGTTGGAGAAGATCGGAAGAGCGGTTTCAG
chr22	39629429	39629468	PDGFB_1584	-	GTGACCTATGCACCAGACGTGACGCCCAACAGGTCCTTCAAATAGCATGGGGCCAGAGATCGGAAGAGCGGTTTCAG
chr22	39631733	39631772	PDGFB_1585	-	GTGACCTATGCACCAGACGTTCTCCGCCCCGCGCTCCGCCCCCTCCGAGGAGACTTTAAGAAGATCGGAAGAGCGGTTTCAG
chr22	39636810	39636849	PDGFB_1586	-	GTGACCTATGCACCAGACGTCTCCACGCTTGTCTTCCCTCCCCACATTGAGGAGCCTCAGATCGGAAGAGCGGTTTCAG
chr22	39639856	39639895	PDGFB_1587	-	GTGACCTATGCACCAGACGTACGGCGGCTGGGGCTGGTTCTTCAATCATTACCTTCCGCCAGATCGGAAGAGCGGTTTCAG
chr3	30648326	30648365	TGFBR2_1588	-	GTGACCTATGCACCAGACGTGCTGCTCGTATAGACCGAGCCCCAGCGCAGCGGACGGCAGATCGGAAGAGCGGTTTCAG
chr3	30686189	30686228	TGFBR2_1589	-	GTGACCTATGCACCAGACGTAGAAAATATATAATTAATGATTCCAAGTCCAGGCCAGCCAGATCGGAAGAGCGGTTTCAG
chr3	30691712	30691751	TGFBR2_1590	-	GTGACCTATGCACCAGACGTAGAAATCTTGAAGCGGAGGGGAGGAGAGAGAAAAGATCGGAAGAGCGGTTTCAG
chr3	30713080	30713119	TGFBR2_1591	-	GTGACCTATGCACCAGACGTACAAAAACAAGGAGAGAAGGAGTTGGATGTGGTAGGTAAGAGATCGGAAGAGCGGTTTCAG
chr3	30715547	30715586	TGFBR2_1592	-	GTGACCTATGCACCAGACGTAAACAGACAGTGAGGCCCATCATTTAATCCAGCTGCCTTTAGATCGGAAGAGCGGTTTCAG
chr3	30729826	30729865	TGFBR2_1593	-	GTGACCTATGCACCAGACGTAGCCAGCAAACACAGGGTCACTGAGAATGGCATGTGCAGCAGATCGGAAGAGCGGTTTCAG
chr3	30732862	30732901	TGFBR2_1594	-	GTGACCTATGCACCAGACGTAAAGATAAAAGGCCACCATGAGTTGGTGGGCTCCGCGAGATCGGAAGAGCGGTTTCAG
chr3	30713480	30713519	TGFBR2_1595	-	GTGACCTATGCACCAGACGTATAGGAAAGATCTTGACTGCCACTGTCTCAAACCTCAGATCGGAAGAGCGGTTTCAG
chr7	98478724	98478763	TRRAP_1596	-	GTGACCTATGCACCAGACGTGGCTGGTTTGCCTTCTCAAGAGAAAAGTATCAGGTTCCATGAAGATCGGAAGAGCGGTTTCAG
chr7	98479548	98479587	TRRAP_1597	-	GTGACCTATGCACCAGACGTCAAAAACAAGCATCAGGTAATTGAAATTATGTTAAGGAAATAGATCGGAAGAGCGGTTTCAG
chr7	98487908	98487947	TRRAP_1598	-	GTGACCTATGCACCAGACGTAAAAATAAAGACCCCATTCAGTTATGTGTATGTTATTTTCAGATCGGAAGAGCGGTTTCAG
chr7	98489997	98490036	TRRAP_1599	-	GTGACCTATGCACCAGACGTAAAAATAAATGAATGATAAAAAATACTTCCAAGGGTTAGATCGGAAGAGCGGTTTCAG
chr7	98491371	98491410	TRRAP_1600	-	GTGACCTATGCACCAGACGTCTAATTAAGTAAATCTGAAAGTCTGAAGACTCACTTTAAAAGATCGGAAGAGCGGTTTCAG
chr7	98493337	98493376	TRRAP_1601	-	GTGACCTATGCACCAGACGTGCAGACACTTTTCTGTTATAGGAAGATTCATAAAACAGAAAAGATCGGAAGAGCGGTTTCAG
chr7	98495314	98495353	TRRAP_1602	-	GTGACCTATGCACCAGACGTGCATAAAAAATATTTTTCTTAAAGTCAAACCCAATATTAGATCGGAAGAGCGGTTTCAG
chr7	98496995	98497034	TRRAP_1603	-	GTGACCTATGCACCAGACGTGAAATGGTAGGACCCGGTTACCATTGTGGCATTAAAAAGATCGGAAGAGCGGTTTCAG
chr7	98497252	98497291	TRRAP_1604	-	GTGACCTATGCACCAGACGTACATACCAGATTTTTCATACATTGACACTCTGCTATGGCGAAGATCGGAAGAGCGGTTTCAG
chr7	98498197	98498236	TRRAP_1605	-	GTGACCTATGCACCAGACGTAGAGAACAATAATACCTCTCAATTATGAGTGATGTTAAGATCGGAAGAGCGGTTTCAG
chr7	98500952	98500991	TRRAP_1606	-	GTGACCTATGCACCAGACGTAGAGTGAGATGACACAGTACAGGGATAGGAGAGTGTTAAAGATCGGAAGAGCGGTTTCAG
chr7	98503750	98503789	TRRAP_1607	-	GTGACCTATGCACCAGACGTAAACATCCATTGCACAGATCACTAAACAAAACCAATTACACAAGATCGGAAGAGCGGTTTCAG
chr7	98506301	98506340	TRRAP_1608	-	GTGACCTATGCACCAGACGTAGACCTCGACTAGTGCTCATTCCCACGTGGCCATGCCTGCAGATCGGAAGAGCGGTTTCAG
chr7	98507629	98507668	TRRAP_1609	-	GTGACCTATGCACCAGACGTGAGAAATCAAGAGGGAAGACAGAATTATCTTCTTCAACAGATCGGAAGAGCGGTTTCAG
chr7	98508083	98508122	TRRAP_1610	-	GTGACCTATGCACCAGACGTGAAAGTATATTAAGTTAACTTGAATAAAAACCTCACTTTATGAGATCGGAAGAGCGGTTTCAG
chr7	98508650	98508689	TRRAP_1611	-	GTGACCTATGCACCAGACGTGGAAAAAGCCGCCACAGGCATAAAAACCTCACTCTCTAGATCGGAAGAGCGGTTTCAG
chr7	98509595	98509634	TRRAP_1612	-	GTGACCTATGCACCAGACGTAGAAAACACATGTGAAAATAATCCCTTCCCAAAGCAGAGATCGGAAGAGCGGTTTCAG
chr7	98513296	98513335	TRRAP_1613	-	GTGACCTATGCACCAGACGTGAGAAGACGCAGATTAAGTGGCATCTAAATGAGGAGGGTCTAGATCGGAAGAGCGGTTTCAG
chr7	98514996	98515035	TRRAP_1614	-	GTGACCTATGCACCAGACGTGGGTGCAGCTATCAGAGAGGGAAGACGCTCCCCAGACTCGAGATCGGAAGAGCGGTTTCAG
chr7	98519326	98519365	TRRAP_1615	-	GTGACCTATGCACCAGACGTGCGTGCTTTTCAATTAAGTCTCTTAAAGTAAATGCCTTACAGATCGGAAGAGCGGTTTCAG
chr7	98522685	98522724	TRRAP_1616	-	GTGACCTATGCACCAGACGTGACACAAAAGAACTACAGTTTGTGCTGAAATTACATGATTAGATCGGAAGAGCGGTTTCAG
chr7	98524740	98524779	TRRAP_1617	-	GTGACCTATGCACCAGACGTAAATCAGATCTGGTGTACAGACACCCACTCTCTGAGCTGAAGATCGGAAGAGCGGTTTCAG
chr7	98527562	98527601	TRRAP_1618	-	GTGACCTATGCACCAGACGTAGATGGGAAGGCAGTGCAGACACTCTTCCCTCAAACATGATCGGAAGAGCGGTTTCAG
chr7	98528978	98529017	TRRAP_1619	-	GTGACCTATGCACCAGACGTGGGATGTCTTAGAATGAAAGCAGGGCGATGCCACCCACTGAGATCGGAAGAGCGGTTTCAG
chr7	98530814	98530853	TRRAP_1620	-	GTGACCTATGCACCAGACGTCAAGGAGGAGGCCACTCACCAGCTGCCCTTGTAGACACAGATCGGAAGAGCGGTTTCAG
chr7	98533152	98533191	TRRAP_1621	-	GTGACCTATGCACCAGACGTAAAAACAATTTCAATTTAGCCACTCTTCTGTGAAGACATAGATCGGAAGAGCGGTTTCAG
chr7	98534729	98534768	TRRAP_1622	-	GTGACCTATGCACCAGACGTAGAAATCAAGACAATTCATTTAACTGGAAGATGCCAGATCGGAAGAGCGGTTTCAG
chr7	98535223	98535262	TRRAP_1623	-	GTGACCTATGCACCAGACGTAGAAAAGTTGTAAGAAAATAAGCAACTGAGGACATTCAGATCGGAAGAGCGGTTTCAG
chr7	98540522	98540561	TRRAP_1624	-	GTGACCTATGCACCAGACGTACACATCTCTGAGACACAACTTCAAGTAGGTCATTCCAAGATCGGAAGAGCGGTTTCAG

chr7	98545794	98545833	TRRAP_1625	-	GTGACCTATGCACCAGACGTAAACCAGAAATTATAAACAGGTCGATTAATTTTGAAGTGAGATCGGAAGAGCGGTTTCAG
chr7	98546139	98546178	TRRAP_1626	-	GTGACCTATGCACCAGACGTTGTGGGAATGCTGCATCTCACAACTTCCTCTTCTCAGAGCAGATCGGAAGAGCGGTTTCAG
chr7	98546990	98547029	TRRAP_1627	-	GTGACCTATGCACCAGACGTAAACAAATAGAAAAGCCGTTTTAAGCTAATCAAACCTCACAGAGATCGGAAGAGCGGTTTCAG
chr7	98547233	98547272	TRRAP_1628	-	GTGACCTATGCACCAGACGTAGAGATAATTAGGGAACCGTGTCTCGATTAACCCCTGGGAGATCGGAAGAGCGGTTTCAG
chr7	98547637	98547676	TRRAP_1629	-	GTGACCTATGCACCAGACGTAAAAGAAAGACAGGTTAACTTAGAGCAAATTTCAATAAAGATCGGAAGAGCGGTTTCAG
chr7	98548449	98548488	TRRAP_1630	-	GTGACCTATGCACCAGACGTAATTTAAATAAAGAAAGGAGAAAACAAAGCCATGCTGTTTAGATCGGAAGAGCGGTTTCAG
chr7	98550740	98550779	TRRAP_1631	-	GTGACCTATGCACCAGACGTACAGCAGGAAGGACTCATTTCCAGTTGTGAACCTGGGTTACAGATCGGAAGAGCGGTTTCAG
chr7	98552671	98552710	TRRAP_1632	-	GTGACCTATGCACCAGACGTGAAGAGACGTTTATGGAGGATGAGAAGGAAGGCTTTAAGAAGATCGGAAGAGCGGTTTCAG
chr7	98553719	98553758	TRRAP_1633	-	GTGACCTATGCACCAGACGTAGGGCCAGCATCACGCCGGAACATGGGAGCTTGGTCCCACAGATCGGAAGAGCGGTTTCAG
chr7	98553972	98554011	TRRAP_1634	-	GTGACCTATGCACCAGACGTACAGGGCGCTTGGTTTTACTGACTGATTTCTAGGGAGAAGAGATCGGAAGAGCGGTTTCAG
chr7	98555554	98555593	TRRAP_1635	-	GTGACCTATGCACCAGACGTACCTCCTTTTCAGGCAGGAAGAGAATCGCAACACTAATTTTCAGATCGGAAGAGCGGTTTCAG
chr7	98556917	98556956	TRRAP_1636	-	GTGACCTATGCACCAGACGTATCCGAGTTACAGCCGGCCTTTCACTGCATCCGAGTTTACAGATCGGAAGAGCGGTTTCAG
chr7	98558834	98558873	TRRAP_1637	-	GTGACCTATGCACCAGACGTCAAACACAGGCCACTCACAGAGGAAACAAACACTCAATGACAGATCGGAAGAGCGGTTTCAG
chr7	98559875	98559914	TRRAP_1638	-	GTGACCTATGCACCAGACGTGCAGGGACCCAGGCACTGTGGTTATGGCTCTTGGGCCACAGATCGGAAGAGCGGTTTCAG
chr7	98562202	98562241	TRRAP_1639	-	GTGACCTATGCACCAGACGTGAAATTGCCAAGTGTTCACAGAAAAGTAACAACCACGAAAGATCGGAAGAGCGGTTTCAG
chr7	98563269	98563308	TRRAP_1640	-	GTGACCTATGCACCAGACGTCAATTAAGAACAACCCACGGGCTCTAAACGTTGATTTAAGATCGGAAGAGCGGTTTCAG
chr7	98564614	98564653	TRRAP_1641	-	GTGACCTATGCACCAGACGTTTTTGAAAAAGACGCAGTTAAAGTATTTCAACCATCTGCAGATCGGAAGAGCGGTTTCAG
chr7	98565058	98565097	TRRAP_1642	-	GTGACCTATGCACCAGACGTAAAGTACAGACAGGCAAGAGGACTGCCACTCCCAAGTCAAGATCGGAAGAGCGGTTTCAG
chr7	98567685	98567724	TRRAP_1643	-	GTGACCTATGCACCAGACGTTGCGGAAAGGAGACAGACCCAAGGCATGCGCGTGGCATTTCAGATCGGAAGAGCGGTTTCAG
chr7	98569372	98569411	TRRAP_1644	-	GTGACCTATGCACCAGACGTAAAGCAGCAAGCAAAACCAAAGGTCAAAGGCTTCAAGAAAAGATCGGAAGAGCGGTTTCAG
chr7	98573722	98573761	TRRAP_1645	-	GTGACCTATGCACCAGACGTAAAGACAACAGGCTGAGATGGCCACGGGCTGGGGGTGCCTAGATCGGAAGAGCGGTTTCAG
chr7	98574056	98574095	TRRAP_1646	-	GTGACCTATGCACCAGACGTAGCAATGTCTTTAGCCCTTCAATCAAATAATCGGCAAGTAGATCGGAAGAGCGGTTTCAG
chr7	98574512	98574551	TRRAP_1647	-	GTGACCTATGCACCAGACGTAAAGTAAGTCTCTGAGTGTCTTGAGACAGAGACTTTTTTTAGATCGGAAGAGCGGTTTCAG
chr7	98575784	98575823	TRRAP_1648	-	GTGACCTATGCACCAGACGTTAATGTTTTTAAATGACTGTTTAACTAGAACAACACCTTAGATCGGAAGAGCGGTTTCAG
chr7	98576342	98576381	TRRAP_1649	-	GTGACCTATGCACCAGACGTACAGATCCAGAGCAAAAGCTCAATCACCAGCACACTCATAGATCGGAAGAGCGGTTTCAG
chr7	98579342	98579381	TRRAP_1650	-	GTGACCTATGCACCAGACGTAAAGACGTGACACAGGACGTGAGGGGCTTCTTTCCCTCAAGATCGGAAGAGCGGTTTCAG
chr7	98580837	98580876	TRRAP_1651	-	GTGACCTATGCACCAGACGTGAGCATAAGAGACTCTGCGGTAATGTGAGTAAGATCAAAGATCGGAAGAGCGGTTTCAG
chr7	98581666	98581705	TRRAP_1652	-	GTGACCTATGCACCAGACGTAAAGAAAGGAATCATTAGCCCAACCCGATCCTCTTTCAAAGAGATCGGAAGAGCGGTTTCAG
chr7	98582517	98582556	TRRAP_1653	-	GTGACCTATGCACCAGACGTAAATGAGCAGAAAAAAGTTCTTGAATTTCTAAACAATAGATCGGAAGAGCGGTTTCAG
chr7	98588028	98588067	TRRAP_1654	-	GTGACCTATGCACCAGACGTAGGAGAAATCTAGAGTAGAATGACAATTTCTGAAGCCCTAGATCGGAAGAGCGGTTTCAG
chr7	98589710	98589749	TRRAP_1655	-	GTGACCTATGCACCAGACGTACAAGATGTTATAACAGTGTCTGCTCTGCTGAGCTCTGAGATCGGAAGAGCGGTTTCAG
chr7	98591165	98591204	TRRAP_1656	-	GTGACCTATGCACCAGACGTATGGGACTGGTTACCCACTGAACCTTGGCTGCTGCTGCTCAAGATCGGAAGAGCGGTTTCAG
chr7	98592160	98592199	TRRAP_1657	-	GTGACCTATGCACCAGACGTAGAGCCAGACAACTGACAAACACAGCCCTCCACTCCAGATCGGAAGAGCGGTTTCAG
chr7	98601763	98601802	TRRAP_1658	-	GTGACCTATGCACCAGACGTAAACATGATTAACAAAGCTTTTATGTCATCTGGGCCAGTTTCAGATCGGAAGAGCGGTTTCAG
chr7	98602704	98602743	TRRAP_1659	-	GTGACCTATGCACCAGACGTGAGAAGCCATGAGGACATGCCCTGACATCTCTGCTAGCATTAGATCGGAAGAGCGGTTTCAG
chr7	98605950	98605989	TRRAP_1660	-	GTGACCTATGCACCAGACGTAGGAAGAGAAACGGGGCAGGCTGAGGGTGACCGCGGGCCAAGATCGGAAGAGCGGTTTCAG
chr7	98608625	98608664	TRRAP_1661	-	GTGACCTATGCACCAGACGTGCGCTCCGTGACACTCCCATCTCACTCACTGATTTTTTTTAGATCGGAAGAGCGGTTTCAG
chr7	98608914	98608953	TRRAP_1662	-	GTGACCTATGCACCAGACGTGAAGGAGACACTTTAGGAACCTCAGCAGAAAGGCGATGTCAGATCGGAAGAGCGGTTTCAG
chr7	98609644	98609683	TRRAP_1663	-	GTGACCTATGCACCAGACGTGAGAGAACGAGACGACTTGTGTTTAAACCAAGAACAGCCCAAGATCGGAAGAGCGGTTTCAG
chr4	110834442	110834481	EGF_1664	-	GTGACCTATGCACCAGACGTAGTTTGAACTTTCAAAGAAAACAGCTTGATTTTGTGGAAGATCGGAAGAGCGGTTTCAG
chr4	110862052	110862091	EGF_1665	-	GTGACCTATGCACCAGACGTGAAAGAGACCAAACCTGATATACTTTAATATTTTATCTCAAGATCGGAAGAGCGGTTTCAG
chr4	110864360	110864399	EGF_1666	-	GTGACCTATGCACCAGACGTAAATTTTAAATTTGTTATTAATACCTCCCCATTCAACAACAGATCGGAAGAGCGGTTTCAG
chr4	110864948	110864987	EGF_1667	-	GTGACCTATGCACCAGACGTACACATTACATAGACCCAAAATGAATGTATAGTGCCTTAAGATCGGAAGAGCGGTTTCAG
chr4	110866179	110866218	EGF_1668	-	GTGACCTATGCACCAGACGTACCACAAAAGAAAAGAAACAAGAACATTTGTTCCCTTGAAGATCGGAAGAGCGGTTTCAG
chr4	110880418	110880457	EGF_1669	-	GTGACCTATGCACCAGACGTAGATGCTTTATTTGGAGTGGGGCCGCTTTTTGACAGAGGAAGATCGGAAGAGCGGTTTCAG
chr4	110881973	110882012	EGF_1670	-	GTGACCTATGCACCAGACGTACAAACAGCAATACATTCAAATGGCTATTTTTTGAATAAAGATCGGAAGAGCGGTTTCAG
chr4	110882969	110883008	EGF_1671	-	GTGACCTATGCACCAGACGTAAAGAAACAGGTCAGATGATGTTAAATCGGGTTTGCAAAAGATCGGAAGAGCGGTTTCAG
chr4	110884279	110884318	EGF_1672	-	GTGACCTATGCACCAGACGTAAATGCTTAGTAATGATGCTACGTCATCCAAAATAAATAGATCGGAAGAGCGGTTTCAG
chr4	110885507	110885546	EGF_1673	-	GTGACCTATGCACCAGACGTAAATTTCAAATATGGCTGAATTTAAAACGTGCTTAGAAACAGATCGGAAGAGCGGTTTCAG
chr4	110890077	110890116	EGF_1674	-	GTGACCTATGCACCAGACGTGAACACAGGCAATTTCTGATTTTTTTTTAAAACATATGTGGAGATCGGAAGAGCGGTTTCAG
chr4	110895809	110895848	EGF_1675	-	GTGACCTATGCACCAGACGTTGCAAAAATAGGGAGTTTGTATAACACCTTTACTTTTCAAGATCGGAAGAGCGGTTTCAG
chr4	110897118	110897157	EGF_1676	-	GTGACCTATGCACCAGACGTGAAAGCACACAAAATAATATCTGCATGAAATAAATATAGATCGGAAGAGCGGTTTCAG
chr4	110901078	110901117	EGF_1677	-	GTGACCTATGCACCAGACGTTTTCAAGTTTGTAAATACACCTTCTTTGCTTTTGAATGAAGATCGGAAGAGCGGTTTCAG
chr4	110901932	110901971	EGF_1678	-	GTGACCTATGCACCAGACGTAAAGAAAACAAATTCACAAGTGGGTTTGAAGATGAAAAGGAAGATCGGAAGAGCGGTTTCAG
chr4	110904528	110904567	EGF_1679	-	GTGACCTATGCACCAGACGTTCAATAGATGCAATTAATTTAGCTTTTTCTGTTTCAAAAAGATCGGAAGAGCGGTTTCAG
chr4	110908850	110908889	EGF_1680	-	GTGACCTATGCACCAGACGTCAAGAATCCCGTGCAGTTATTTCTAGACCTTAGAGAAGAAAGATCGGAAGAGCGGTTTCAG
chr4	110909690	110909729	EGF_1681	-	GTGACCTATGCACCAGACGTAAATGAACTAGTGCATATTTAGGCACTTATGATATAAAGATCGGAAGAGCGGTTTCAG
chr4	110914353	110914392	EGF_1682	-	GTGACCTATGCACCAGACGTAGACAGAGTACGGGAGAGAAAAGTGGGGTACAGAAAAGAAAGATCGGAAGAGCGGTTTCAG

chr4	110915839	110915878	EGF_1683	-	GTGACCTATGCACCAGACGTCCAAGACATTACTTTTACTTTCTGAATGGATTAGTGTCTTAGATCGGAAGAGCGGTTTCAG
chr4	110920785	110920824	EGF_1684	-	GTGACCTATGCACCAGACGTACACAAAACAGAGGTCATCAGAGATGCCTGGCCAAAAACGCAGATCGGAAGAGCGGTTTCAG
chr4	110925611	110925650	EGF_1685	-	GTGACCTATGCACCAGACGTGCCAAAATTTGAGACAATCTCACAAAACAAAATACTCAGATCGGAAGAGCGGTTTCAG
chr4	110929258	110929297	EGF_1686	-	GTGACCTATGCACCAGACGTCAAAAAGGAGGGAGAGAGGATATTGTTAAAATTCACAATAGATCGGAAGAGCGGTTTCAG
chr4	110932308	110932347	EGF_1687	-	GTGACCTATGCACCAGACGTGACAAAAGAAATTTCAATATTTCATATCATTAAACAATAGATAGATCGGAAGAGCGGTTTCAG
chr13	28578139	28578178	FLT3_1688	-	GTGACCTATGCACCAGCGTTAGTTTTAAGGACTTACCTCCACCTATCCCTAACAGGAGATCGGAAGAGCGGTTTCAG
chr13	28588578	28588578	FLT3_1689	-	GTGACCTATGCACCAGACGTGCCAGACTTTATAAAGAGCTTTACAAAAGAAATTTGGTAAATAGATCGGAAGAGCGGTTTCAG
chr13	28589244	28589283	FLT3_1690	-	GTGACCTATGCACCAGACGTGTCAGACTGTAATTTGGTTGAAATCAGAAAAGGTACAGTCTAGATCGGAAGAGCGGTTTCAG
chr13	28589677	28589716	FLT3_1691	-	GTGACCTATGCACCAGACGTGCTGCTGGCCTCCCTGGCTCTGGCTTTGCATCCTCTAGATCGGAAGAGCGGTTTCAG
chr13	28592554	28592593	FLT3_1692	-	GTGACCTATGCACCAGACGTATTTTCTACTTATTTTTATACGGCTATTTTGTGTTGTGTAGATCGGAAGAGCGGTTTCAG
chr13	28597437	28597476	FLT3_1693	-	GTGACCTATGCACCAGACGTTTTAAAGAAAACAAAACAAAAGATTTGAAAAGATAGATCGGAAGAGCGGTTTCAG
chr13	28598948	28598987	FLT3_1694	-	GTGACCTATGCACCAGACGTATTCTAAGTAGTAGCACTTTAAAATGAAATGAATGCAAAAAGATCGGAAGAGCGGTTTCAG
chr13	28601175	28601214	FLT3_1695	-	GTGACCTATGCACCAGACGTGGGTACAGGTTTCGTAATTACACATCATAGAACGTAGGCAAGATCGGAAGAGCGGTTTCAG
chr13	28602265	28602304	FLT3_1696	-	GTGACCTATGCACCAGACGTTCACGAAAATCACCTCATCAAAAAGACTGTAGCTTGATGAGATCGGAAGAGCGGTTTCAG
chr13	28607974	28608013	FLT3_1697	-	GTGACCTATGCACCAGACGTGTTGGAAGGACAGCAACAAAGATGCACAAAATGGGAGGCAAGATCGGAAGAGCGGTTTCAG
chr13	28608169	28608208	FLT3_1698	-	GTGACCTATGCACCAGACGTAAATGTGCCAAATGTTTCTGCAGCATTCTTTTCCATTGGAAGATCGGAAGAGCGGTTTCAG
chr13	28608388	28608427	FLT3_1699	-	GTGACCTATGCACCAGACGTAGGTAAAATTCATTATTTCTTCTCTATCTGCCAAGTCTGAGATCGGAAGAGCGGTTTCAG
chr13	28609582	28609621	FLT3_1700	-	GTGACCTATGCACCAGACGTGTTCTTGATATTCACCATCAGAAATCCCCACTAGAAAGATCGGAAGAGCGGTTTCAG
chr13	28610022	28610061	FLT3_1701	-	GTGACCTATGCACCAGACGTCAATGATGCCTCTTATAATGGAAGAACATAAACTCTCTGAGATCGGAAGAGCGGTTTCAG
chr13	28611272	28611311	FLT3_1702	-	GTGACCTATGCACCAGACGTGGCCGAGAATTTGATTTTTATTTTTAATTTCTTAATTTAGATCGGAAGAGCGGTTTCAG
chr13	28622362	28622401	FLT3_1703	-	GTGACCTATGCACCAGACGTAAAGGACTCTAAGATACCATTTTTAGCATAATTTCTCTTGAGATCGGAAGAGCGGTTTCAG
chr13	28623471	28623510	FLT3_1704	-	GTGACCTATGCACCAGACGTCTGCTCACACAATCTTTATTTCTTATTTAGTCGCTGTAGAGATCGGAAGAGCGGTTTCAG
chr13	28623722	28623761	FLT3_1705	-	GTGACCTATGCACCAGACGTAAGTTTGATTTCTGAAAATCGAGAAACAATACTAATAGAGATCGGAAGAGCGGTTTCAG
chr13	28624182	28624221	FLT3_1706	-	GTGACCTATGCACCAGACGTGAATATCACTACTTTTCAATTTAGTACCGGTTCTTAGCAAGATCGGAAGAGCGGTTTCAG
chr13	28626632	28626671	FLT3_1707	-	GTGACCTATGCACCAGACGTTCATGTTGAGTCTATTCTCATAATTTCTTTTGGCCTTAGATCGGAAGAGCGGTTTCAG
chr13	28631434	28631473	FLT3_1708	-	GTGACCTATGCACCAGACGTCTGCTACTAGTATTCCAGCCTGGAATACCACAATTTTCAGATCGGAAGAGCGGTTTCAG
chr13	28635954	28635993	FLT3_1709	-	GTGACCTATGCACCAGACGTGAATACCTTCTTGACATAAAATGTGGTTCATTTGGAATTTAGATCGGAAGAGCGGTTTCAG
chr13	28644578	28644617	FLT3_1710	-	GTGACCTATGCACCAGACGTATTAATAATACCTTTAGCTGTTTTTCTCTAGAGAAGTCTAGATCGGAAGAGCGGTTTCAG
chr13	28674555	28674594	FLT3_1711	-	GTGACCTATGCACCAGACGTGCTGCTCGCTCGCAGCCCTCGCGTCCCTCAGCCCCAAGATCGGAAGAGCGGTTTCAG
chr17	73316399	73316438	GRB2_1712	-	GTGACCTATGCACCAGACGTGCAATTTAAAGAAAAGTAAAATGTAATAACACATACAAGATCGGAAGAGCGGTTTCAG
chr17	73317690	73317729	GRB2_1713	-	GTGACCTATGCACCAGACGTTCAAGGTTGAGATGGGATCATTTTTAGTTAAGAATAGCTCCAGATCGGAAGAGCGGTTTCAG
chr17	73321929	73321968	GRB2_1714	-	GTGACCTATGCACCAGACGTCTGCTGTCAGTTGCCGTGGAATCCTGTCTCTGACTGATCCAAGATCGGAAGAGCGGTTTCAG
chr17	73328731	73328770	GRB2_1715	-	GTGACCTATGCACCAGACGTCTCCATTAGTCTTGAAGGGTTGGACCCACCTCTGTTTAGATCGGAAGAGCGGTTTCAG
chr17	73389582	73389621	GRB2_1716	-	GTGACCTATGCACCAGACGTATGCCGAGCAATGCTGAGATCGCTCTCCCTGTGCTCACAGATCGGAAGAGCGGTTTCAG
chr17	26084222	26084261	NOS2_1717	-	GTGACCTATGCACCAGACGTGAGGGTTAAAGCTGCCGCGCACGAACATAAGGATGGAGATCGGAAGAGCGGTTTCAG
chr17	26085857	26085896	NOS2_1718	-	GTGACCTATGCACCAGACGTGGGTGTGTGGGCTGAAGGTGCCGGCCAAGGGCACAGGCCGAGATCGGAAGAGCGGTTTCAG
chr17	26087006	26087045	NOS2_1719	-	GTGACCTATGCACCAGACGTCTCAAAGCAGGTGAAGCATTACACACAAGCTCCACTGAGATCGGAAGAGCGGTTTCAG
chr17	26087599	26087638	NOS2_1720	-	GTGACCTATGCACCAGACGTAGGGTCTCCAGGTGGGAGGGGCCACCAGGGGCCAGCCCTAGATCGGAAGAGCGGTTTCAG
chr17	26088120	26088159	NOS2_1721	-	GTGACCTATGCACCAGACGTCTCCACTCTGTCCCCTGTGGGGCCGCCACCCTGGGAGAGATCGGAAGAGCGGTTTCAG
chr17	26089774	26089813	NOS2_1722	-	GTGACCTATGCACCAGACGTGGCAGAGGCTTGAACAGCCCCGCTCCGCCATTTAGGATCGGAAGAGCGGTTTCAG
chr17	26090957	26090996	NOS2_1723	-	GTGACCTATGCACCAGACGTGGGCTGGTGGGCTGAGGGGATGTTGGGGGTCCCAGCATAGATCGGAAGAGCGGTTTCAG
chr17	26092511	26092550	NOS2_1724	-	GTGACCTATGCACCAGACGTGGCTAGAAAAGCCAGTGTGCTGCCGTTGCCACCCTCTGGCCGCCAGATCGGAAGAGCGGTTTCAG
chr17	26093486	26093525	NOS2_1725	-	GTGACCTATGCACCAGACGTGTGCAGGGCTTCGTGGGTGATACTCTGTCGATTTTATTTTAGATCGGAAGAGCGGTTTCAG
chr17	26094681	26094720	NOS2_1726	-	GTGACCTATGCACCAGACGTCTCTGCAGCACATGGGGCTTGTGTTGTTGGGGTCTGAGCAGATCGGAAGAGCGGTTTCAG
chr17	26095953	26095992	NOS2_1727	-	GTGACCTATGCACCAGACGTAGCCAGAGCTGCCCCACAGCAGGGGACATGACAGGGTGCATAGATCGGAAGAGCGGTTTCAG
chr17	26096511	26096550	NOS2_1728	-	GTGACCTATGCACCAGACGTTCCGTTGCTACTCTGACCTGCCCCTGTGGACCCAAAAGATCGGAAGAGCGGTTTCAG
chr17	26097889	26097928	NOS2_1729	-	GTGACCTATGCACCAGACGTTGAGGTGTGGCTGGTCTAGGGGGTGGTAGGGCACGGGAGGAGATCGGAAGAGCGGTTTCAG
chr17	26099284	26099323	NOS2_1730	-	GTGACCTATGCACCAGACGTAGTGGGATGGCTGTTGTTTTTCTGCTTGTGTGCAGGGGAAGATCGGAAGAGCGGTTTCAG
chr17	26100137	26100176	NOS2_1731	-	GTGACCTATGCACCAGACGTGTGGCAGTGGCTAGTAGTGATGTGTGAACATATCTCTCCAGATCGGAAGAGCGGTTTCAG
chr17	26101233	26101272	NOS2_1732	-	GTGACCTATGCACCAGACGTTTCTCTCTCTCTCTCCCTGGGGGCTCAGATGTGGCTGTAAGATCGGAAGAGCGGTTTCAG
chr17	26105666	26105705	NOS2_1733	-	GTGACCTATGCACCAGACGTAGTTTTGTAGTCTGAAGACTTTTTGGTGAGAAGCTTAACAGATCGGAAGAGCGGTTTCAG
chr17	26105858	26105897	NOS2_1734	-	GTGACCTATGCACCAGACGTGCTTCCAGCTGGCCAGTGAAGATGAAGGTGTGGGCTGGGGTGGAGATCGGAAGAGCGGTTTCAG
chr17	26107743	26107782	NOS2_1735	-	GTGACCTATGCACCAGACGTTGAGGGTGTGGGGGCAAGGGCAGTCAACACACAGCCCTAGATCGGAAGAGCGGTTTCAG
chr17	26108012	26108051	NOS2_1736	-	GTGACCTATGCACCAGACGTGAGCCTCAGCCACCGGCCATTTGGGGCGGGAGCCCCGTGGAGATCGGAAGAGCGGTTTCAG
chr17	26108991	26109030	NOS2_1737	-	GTGACCTATGCACCAGACGTATTTCCAGGGCTGCAGAGGGCTTGCCTTGCCTGAGAATAGATCGGAAGAGCGGTTTCAG
chr17	26109920	26109959	NOS2_1738	-	GTGACCTATGCACCAGACGTTTAGACTTGAGCGGGAGAGAGCTGGAGGGCGGCCAGCCCTAGATCGGAAGAGCGGTTTCAG
chr17	26114654	26114693	NOS2_1739	-	GTGACCTATGCACCAGACGTCTCCAGGGTGCCTGACCTGACCTGCTCCCTCTCTGCTCAGATCGGAAGAGCGGTTTCAG
chr17	26115785	26115824	NOS2_1740	-	GTGACCTATGCACCAGACGTGCTTCCAGGGAGAACCACCTTTGTCCAAAGCTGGTGAAGCAGATCGGAAGAGCGGTTTCAG

chr17	26116580	26116619	NOS2_1741	-	GTGACCTATGCACCAGACGTACATGGGTGTGGGAAGCCCCCTTCTCCTGGTCCAGGCAAGATCGGAAGAGCGGTTTCAG
chr17	26125676	26125715	NOS2_1742	-	GTGACCTATGCACCAGACGTCTGGGGGAACCTCCTGCTTGTCTCCTGGGCACCCATGCAGATCGGAAGAGCGGTTTCAG
chr15	40453372	40453411	BUB1B_1743	-	GTGACCTATGCACCAGACGTTGGCTCAGGTCCTCGTCTGCTGCAGGCCTTCTCCTGGGAGATCGGAAGAGCGGTTTCAG
chr15	40457204	40457243	BUB1B_1744	-	GTGACCTATGCACCAGACGTGGAAACAAATGTAATCTCATACCAACATTGACTATTATAAGATCGGAAGAGCGGTTTCAG
chr15	40462213	40462252	BUB1B_1745	-	GTGACCTATGCACCAGACGTAAACAGAAAAAGTTAGCATATGCAATAGTGACAACAGCCAAAGATCGGAAGAGCGGTTTCAG
chr15	40462688	40462727	BUB1B_1746	-	GTGACCTATGCACCAGACGTGGAAAAAGATAAGAACACATTTAAATTTAAACATGTACTTAGATCGGAAGAGCGGTTTCAG
chr15	40468667	40468667	BUB1B_1747	-	GTGACCTATGCACCAGACGTAGTGTAAACAGTTAACCTTTCTACTACGTATTGAATGAGATCGGAAGAGCGGTTTCAG
chr15	40475865	40475904	BUB1B_1748	-	GTGACCTATGCACCAGACGTAGAATGCACAACCTTTTGTAGTGGTGCACACTATTTTACCAAGATCGGAAGAGCGGTTTCAG
chr15	40477316	40477355	BUB1B_1749	-	GTGACCTATGCACCAGACGTAAATATTTAAACCTCATGTAATGTTTCATTATTAACCTTAGATCGGAAGAGCGGTTTCAG
chr15	40477702	40477741	BUB1B_1750	-	GTGACCTATGCACCAGACGTAGAAGAAAACTAAAATTTACCATAGTTTTATGTTCTCAGACAGATCGGAAGAGCGGTTTCAG
chr15	40488696	40488735	BUB1B_1751	-	GTGACCTATGCACCAGACGTAAAATTTACTATTATTCATATGGGTCAAAAATAAAAAAATCAGATCGGAAGAGCGGTTTCAG
chr15	40491766	40491805	BUB1B_1752	-	GTGACCTATGCACCAGACGTAAAAGTTGCTTGGAGTATTCTCTCATAGTAACCTATTTCAGATCGGAAGAGCGGTTTCAG
chr15	40492395	40492434	BUB1B_1753	-	GTGACCTATGCACCAGACGTAAATAAACAAAAATCAATGTCCTCCATCCAGAAAATGCAGATCGGAAGAGCGGTTTCAG
chr15	40493082	40493121	BUB1B_1754	-	GTGACCTATGCACCAGACGTACTTGTTTTAAATCATGTGCTCAATACCCACAGAAAGAACAGATCGGAAGAGCGGTTTCAG
chr15	40494556	40494595	BUB1B_1755	-	GTGACCTATGCACCAGACGTAGAGACTAGATACATACTCTAGGAGTAAATGCTTTACTCTAGATCGGAAGAGCGGTTTCAG
chr15	40494740	40494779	BUB1B_1756	-	GTGACCTATGCACCAGACGTACATACCTCACTTAGCAATTTTTTTCATAACAGTAACCCAGATCGGAAGAGCGGTTTCAG
chr15	40498335	40498374	BUB1B_1757	-	GTGACCTATGCACCAGACGTGACCATATAAAGTTTAAAGTAAATTTTCAATACATGAAGAGATCGGAAGAGCGGTTTCAG
chr15	40500788	40500827	BUB1B_1758	-	GTGACCTATGCACCAGACGTCAAAAATAAAGTTAATTTCTATAGGAATAATATATATCAACAGATCGGAAGAGCGGTTTCAG
chr15	40501786	40501825	BUB1B_1759	-	GTGACCTATGCACCAGACGTGAGGGAAAGGTGAAAATATATACCAAAAAAACCTAATGAGATCGGAAGAGCGGTTTCAG
chr15	40502261	40502300	BUB1B_1760	-	GTGACCTATGCACCAGACGTAGTTTGATTCCATTTAAAAATCACTGTGAACATATACAGCAGATCGGAAGAGCGGTTTCAG
chr15	40505483	40505522	BUB1B_1761	-	GTGACCTATGCACCAGACGTAAAGGACAGAAAACCTCACTATTTTCTCAAGTTTGGCAGATCGAGATCGGAAGAGCGGTTTCAG
chr15	40509647	40509686	BUB1B_1762	-	GTGACCTATGCACCAGACGTATTTAAGAGAAGGAGATAATAAAAAATAGGCCATGAAAGAAAGATCGGAAGAGCGGTTTCAG
chr15	40510607	40510646	BUB1B_1763	-	GTGACCTATGCACCAGACGTAAAAAGCACCATCAGCTAAAATAATCTCTGCCTTACCAAGATCGGAAGAGCGGTTTCAG
chr15	40512715	40512754	BUB1B_1764	-	GTGACCTATGCACCAGACGTAAACCCATTTCCATCAAGATTAGCCATATGAAAATTTAGATCGGAAGAGCGGTTTCAG
chr12	12870724	12870763	CDKN1B_1765	-	GTGACCTATGCACCAGACGTGGTCTGCACGACCCCTCTCTCGCACTCTCAAAAAAACAAAGATCGGAAGAGCGGTTTCAG
chr12	12871709	12871748	CDKN1B_1766	-	GTGACCTATGCACCAGACGTGGGAAATTTTTAAAAAGAACACACAATCTTTATAGAAAAGATCGGAAGAGCGGTTTCAG
chr1	68512241	68512280	DIRAS3_1767	-	GTGACCTATGCACCAGACGTAAAGAGCCAGCTCTTCTATCCTGTAGCGTGTAGAAAACAGATCGGAAGAGCGGTTTCAG
chr1	68512586	68512625	DIRAS3_1768	-	GTGACCTATGCACCAGACGTCCAAGAAGGAAACCCCTGGAAGAGCTGAAGGCCCTTCTATGAAGATCGGAAGAGCGGTTTCAG
chr19	2180662	2180701	DOT1L_1769	-	GTGACCTATGCACCAGACGTGAGAGAAAGTTTGAAGCAGGACCCATCTCCACCCCGTGAAGATCGGAAGAGCGGTTTCAG
chr19	2189681	2189720	DOT1L_1770	-	GTGACCTATGCACCAGACGTCAAGGGAAGGCCCTGGTCTCGGGCAGGAGCCACCCGCAAGATCGGAAGAGCGGTTTCAG
chr19	2190961	2191000	DOT1L_1771	-	GTGACCTATGCACCAGACGTAGGGTGGCCCGGCCATGTCACATAAACCTCACGGCCAGCAGATCGGAAGAGCGGTTTCAG
chr19	2193638	2193677	DOT1L_1772	-	GTGACCTATGCACCAGACGTAGAGATCCATCAGATACCACACAGCGCTCAGATGCCACCAGATCGGAAGAGCGGTTTCAG
chr19	2199833	2199872	DOT1L_1773	-	GTGACCTATGCACCAGACGTAAACAGGTTGAGCGCGGCCACCCCGGCCCTCCTGGCACTCAGATCGGAAGAGCGGTTTCAG
chr19	2202648	2202688	DOT1L_1774	-	GTGACCTATGCACCAGACGTATACCTCAGTCCATGAGGCTCGTCTCACGGGCAAGATCGGAAGAGCGGTTTCAG
chr19	2206679	2206717	DOT1L_1775	-	GTGACCTATGCACCAGACGTGACACTGCTTACTGCCACAGAGGAGGAAACAGAAAGATCGGAAGAGCGGTTTCAG
chr19	2207523	2207562	DOT1L_1776	-	GTGACCTATGCACCAGACGTACAGGTTGAGGCCGGGCCCTGCGCCTGCCACAGCCCTCAGATCGGAAGAGCGGTTTCAG
chr19	2208884	2208923	DOT1L_1777	-	GTGACCTATGCACCAGACGTGAAAGAGAACCCTGATTAGAAGGGAGTCCCAATCTCTGTTAGATCGGAAGAGCGGTTTCAG
chr19	2210349	2210388	DOT1L_1778	-	GTGACCTATGCACCAGACGTAGCAGGTTGAGCCACAGGAAGCCACGCGCTGCCACCGGAGATCGGAAGAGCGGTTTCAG
chr19	2210570	2210609	DOT1L_1779	-	GTGACCTATGCACCAGACGTCAAGGGAAGAACAGGGATGGGCACAGAGCCTCCACCCATAGATCGGAAGAGCGGTTTCAG
chr19	2211048	2211087	DOT1L_1780	-	GTGACCTATGCACCAGACGTGGAGGGCAGGCTCAGCACAGGGCGGTCGGGAGAGCGGTAGATCGGAAGAGCGGTTTCAG
chr19	2211700	2211739	DOT1L_1781	-	GTGACCTATGCACCAGACGTGAGCCGAACACAGGTGAGAAGAGAGCAGCTGAGACTGAGAAGATCGGAAGAGCGGTTTCAG
chr19	2213488	2213527	DOT1L_1782	-	GTGACCTATGCACCAGACGTAAACAGGTCAGTACTAAGGGCCAGGGCAGGTGACTGAGGAGATCGGAAGAGCGGTTTCAG
chr19	2213798	2213837	DOT1L_1783	-	GTGACCTATGCACCAGACGTGGGGCGGGGAGAGGTCATGCTGGTGGCCCTCAAGGTGAAAGATCGGAAGAGCGGTTTCAG
chr19	2214420	2214459	DOT1L_1784	-	GTGACCTATGCACCAGACGTAGGGATGGGACAGTTGCGACTGGCTGGCTGCCCTGCCACAGCAGATCGGAAGAGCGGTTTCAG
chr19	2216230	2216269	DOT1L_1785	-	GTGACCTATGCACCAGACGTAGAGATGGTGTGTCAGGCCCGCCACCGGGGACCACTCAAGATCGGAAGAGCGGTTTCAG
chr19	2216904	2216943	DOT1L_1786	-	GTGACCTATGCACCAGACGTAAAGCTGACGTCACTCTCGAGGCGGTGGCTGGCACTGAGATCGGAAGAGCGGTTTCAG
chr19	2217721	2217760	DOT1L_1787	-	GTGACCTATGCACCAGACGTAGGCCCGACCCCACTGCTGGGTCAACAAACCCCTCCAGGAGATCGGAAGAGCGGTTTCAG
chr19	2220057	2220096	DOT1L_1788	-	GTGACCTATGCACCAGACGTAAAACCTGTGTGTGTCAGGGGCAGCAGGTGCCACAGGAGACAGATCGGAAGAGCGGTTTCAG
chr19	2221925	2221964	DOT1L_1789	-	GTGACCTATGCACCAGACGTGGACATGGGGTCTCAGGGGACACAGGATGGCCAAAGAGAAAGATCGGAAGAGCGGTTTCAG
chr19	2223230	2223269	DOT1L_1790	-	GTGACCTATGCACCAGACGTACAGACACAATGGATGCACATACCACAGACCCGGGACCCAGATCGGAAGAGCGGTTTCAG
chr19	2225337	2225376	DOT1L_1791	-	GTGACCTATGCACCAGACGTAAAAGGTCATTAATGCTTGAACCCAGCTGCATACTAAGAGATCGGAAGAGCGGTTTCAG
chr19	2226132	2226171	DOT1L_1792	-	GTGACCTATGCACCAGACGTGAAAGGCAGGACCGTGAAGCCGAGGCCACAGCAGCTGCCCGGAGATCGGAAGAGCGGTTTCAG
chr19	2229734	2229773	DOT1L_1793	-	GTGACCTATGCACCAGACGTGCACAGCGGGAAGAGCGGCTGAGGTTACCATCGCGCCTGAGATCGGAAGAGCGGTTTCAG
chr19	2222217	2222256	DOT1L_1794	-	GTGACCTATGCACCAGACGTAGGGCAGGTTCTCCCTTGTGGCTCGGGCAACGGGCCCTGAGATCGGAAGAGCGGTTTCAG
chr19	2226604	2226643	DOT1L_1795	-	GTGACCTATGCACCAGACGTGTCAGGCTGCTCTTGTCTCAGGAAAGGTTGGCGTCCGAAGATCGGAAGAGCGGTTTCAG
chr3	134514424	134514463	EPHB1_1796	-	GTGACCTATGCACCAGACGTGCGCCCGCAGCCGAGCAAGCCGAGGCAGCAGCGCCGAGATCGGAAGAGCGGTTTCAG
chr3	134644608	134644647	EPHB1_1797	-	GTGACCTATGCACCAGACGTAAAAGAAAAACGAATAAACAAAAACAAATGAGTCAGAAGGAGATCGGAAGAGCGGTTTCAG
chr3	134670163	134670202	EPHB1_1798	-	GTGACCTATGCACCAGACGTGAGGCCACAGGCACACACATGCAAAAACACAAAATAGAGAAGATCGGAAGAGCGGTTTCAG

chr3	134825240	134825279	EPHB1_1799	-	GTGACCTATGCACCAGACGTAAGAGACCATGTGATAATTAATGGAAGTGTGGCAGCCAGAAGATCGGAAGAGCGGTTTCAG
chr3	134851506	134851545	EPHB1_1800	-	GTGACCTATGCACCAGACGTACAAGAAGGTCAGTGTAGGCTAGACATAAGCTTCCCTTTAGATCGGAAGAGCGGTTTCAG
chr3	134872944	134872983	EPHB1_1801	-	GTGACCTATGCACCAGACGTAGAAAGAAACAGGGTAGCTGAACAGACACTCAATTATAGGAGATCGGAAGAGCGGTTTCAG
chr3	134880810	134880849	EPHB1_1802	-	GTGACCTATGCACCAGACGTGCAAGGGAAGGGTCACTATCCCATTCTGAAGGCTACACAGATCGGAAGAGCGGTTTCAG
chr3	134884760	134884799	EPHB1_1803	-	GTGACCTATGCACCAGACGTAAAGAGGCATTAGAAATCCTCCCATGTGCCCTTTGCATACAAGATCGGAAGAGCGGTTTCAG
chr3	134885734	134885773	EPHB1_1804	-	GTGACCTATGCACCAGACGTAAAGAGGGGCTCTCTCAGCCACAGGGCACCCACCCAGTTCAGATCGGAAGAGCGGTTTCAG
chr3	134898652	134898691	EPHB1_1805	-	GTGACCTATGCACCAGACGTGAGATAAGCAGGGTTAACAATCCCAAGAGGACATGTTGTAGATCGGAAGAGCGGTTTCAG
chr3	134911368	134911407	EPHB1_1806	-	GTGACCTATGCACCAGACGTAAAAATGCCATTAATATCCTCTTCTCTCAGTCTGTGGAAGATCGGAAGAGCGGTTTCAG
chr3	134920266	134920305	EPHB1_1807	-	GTGACCTATGCACCAGACGTACATAGAGGGCATTGGGATCAAGACGGGCTTCAATGGTTAAGATCGGAAGAGCGGTTTCAG
chr3	134959940	134959979	EPHB1_1808	-	GTGACCTATGCACCAGACGTGAGAACCCTGGTCAGCCCAACAATCAGGTTTCTGATTGAAGATCGGAAGAGCGGTTTCAG
chr3	134967108	134967147	EPHB1_1809	-	GTGACCTATGCACCAGACGTATACAGGGAAACAGGTGTGATTGAGTGACTGCCACCAGCCAAGATCGGAAGAGCGGTTTCAG
chr3	134968128	134968167	EPHB1_1810	-	GTGACCTATGCACCAGACGTAGAGATGGGCAGGTGACCACACTGCAGAGATGCATGGAAGATCGGAAGAGCGGTTTCAG
chr3	134977804	134977843	EPHB1_1811	-	GTGACCTATGCACCAGACGTAGAGGCCAGAAAAGAGTCACTTTAGTGTAGGTTAGCTTTAGATCGGAAGAGCGGTTTCAG
chr3	134670504	134670543	EPHB1_1812	-	GTGACCTATGCACCAGACGTCAAAGTCCACCTGGGAGAAGCTCTCATCTGCAGCAATGGTAGATCGGAAGAGCGGTTTCAG
chr7	142560936	142560975	EPHB6_1813	-	GTGACCTATGCACCAGACGTGAGGGGCTCCACCATCGCCCCAGCCACCACCTGCTCCTGAGATCGGAAGAGCGGTTTCAG
chr7	142561339	142561378	EPHB6_1814	-	GTGACCTATGCACCAGACGTATAAGAGGGGCACACAGTGGCCAAGCCTCCAGCCAGACTAGATCGGAAGAGCGGTTTCAG
chr7	142561674	142561713	EPHB6_1815	-	GTGACCTATGCACCAGACGTGGCCAGGAGAAGCTTTAGGGGCTCCGGGCTTAAGCAAGGCAGATCGGAAGAGCGGTTTCAG
chr7	142563180	142563219	EPHB6_1816	-	GTGACCTATGCACCAGACGTGAGAGAGTGGGGGCTGCACCTCGCTGTCCACCCACAGATCGGAAGAGCGGTTTCAG
chr7	142563665	142563704	EPHB6_1817	-	GTGACCTATGCACCAGACGTGAGGATATGGCAGTCCAAGGGCCAAGAGGGCAGTGGAGATCGGAAGAGCGGTTTCAG
chr7	142564186	142564225	EPHB6_1818	-	GTGACCTATGCACCAGACGTAAAGGAAAATTATTATGGGGATAGGAGTCCCTGGGAGCAGAGATCGGAAGAGCGGTTTCAG
chr7	142564611	142564650	EPHB6_1819	-	GTGACCTATGCACCAGACGTGAGCCACTCACTCCCTGCCTGGCCCCCTCTTGCCCCCTGCTAGATCGGAAGAGCGGTTTCAG
chr7	142565313	142565352	EPHB6_1820	-	GTGACCTATGCACCAGACGTAGCCGACAGGGTCCACAGTGGGGCAGGCTCTCTCACAGGTGAGATCGGAAGAGCGGTTTCAG
chr7	142565702	142565741	EPHB6_1821	-	GTGACCTATGCACCAGACGTAAACGGTACTGGGGATGACGCTCCCATTTCCACCCCTTAGATCGGAAGAGCGGTTTCAG
chr7	142565946	142565985	EPHB6_1822	-	GTGACCTATGCACCAGACGTGGAGGATGTTGATGAGCGTGTGTGAAGGCAGGGCTGCAGATCGGAAGAGCGGTTTCAG
chr7	142566197	142566236	EPHB6_1823	-	GTGACCTATGCACCAGACGTAGGTGTAGGTTGGGGTGGGGATCAAGGCTCACAGCGTCTAGATCGGAAGAGCGGTTTCAG
chr7	142566677	142566716	EPHB6_1824	-	GTGACCTATGCACCAGACGTGGGGCAGGGGCAGAGTCACTGATCGGAGACGGGGAGACAGATCGGAAGAGCGGTTTCAG
chr7	142567917	142567956	EPHB6_1825	-	GTGACCTATGCACCAGACGTGAGGAAGACTATGATGATGGGAAGTTTTGTTAGTAGAGGGAGATCGGAAGAGCGGTTTCAG
chr7	142568233	142568272	EPHB6_1826	-	GTGACCTATGCACCAGACGTAGGGGCAAGCAGGGTCAAGGCTCCTCTTCTTACCTTAGCCAGATCGGAAGAGCGGTTTCAG
chr7	142568499	142568538	EPHB6_1827	-	GTGACCTATGCACCAGACGTGGGAAGGACTCAAATCGGGCCAGCTTCTCCGAGATCCCAGATCGGAAGAGCGGTTTCAG
chr20	57415112	57415151	GNAS_1828	-	GTGACCTATGCACCAGACGTACACCCAGAGAAGCCGGCCCTCGCTTGTGCTGCAGAGAAGATCGGAAGAGCGGTTTCAG
chr20	57428271	57428310	GNAS_1829	-	GTGACCTATGCACCAGACGTGGCCCTCTCAAATAAGTTTGGGGCTCCGTAAGATGGAGCAGATCGGAAGAGCGGTTTCAG
chr20	57470617	57470656	GNAS_1830	-	GTGACCTATGCACCAGACGTAAAGTAAGTCTCAGGTTATGAAGGAGGCATTTAACACTTAGATCGGAAGAGCGGTTTCAG
chr20	57473946	57473985	GNAS_1831	-	GTGACCTATGCACCAGACGTGAGATTGAAAGCTCACCTAATCTGCAAGGCACCCGAGTGTAGATCGGAAGAGCGGTTTCAG
chr20	57478533	57478572	GNAS_1832	-	GTGACCTATGCACCAGACGTGAAAAGAAAAGAAATCATATTGCACCATGCAGTTAGGAAGATCGGAAGAGCGGTTTCAG
chr20	57478536	57478575	GNAS_1833	-	GTGACCTATGCACCAGACGTATTGAAAAGAAAAGAAAATCATATTGCACCATGTCAGTTAAGATCGGAAGAGCGGTTTCAG
chr20	57478677	57478716	GNAS_1834	-	GTGACCTATGCACCAGACGTTTTAGCAAAGCGGTGAGGGAAACGACTGGCTGGGAGGGCAGATCGGAAGAGCGGTTTCAG
chr20	57480388	57480427	GNAS_1835	-	GTGACCTATGCACCAGACGTACACAAGAAAGTTTAGAGAAAAGCAAGAGCTTGAACATAATAGATCGGAAGAGCGGTTTCAG
chr20	57484167	57484206	GNAS_1836	-	GTGACCTATGCACCAGACGTAAAGAAAGACACGTGGGGTGTTCACAGCGCTCACATCAATTAGATCGGAAGAGCGGTTTCAG
chr20	57484355	57484394	GNAS_1837	-	GTGACCTATGCACCAGACGTATTGAGGTCAATGGATCTCACCAAAGCCAACCGAAACAGTAGATCGGAAGAGCGGTTTCAG
chr20	57484526	57484565	GNAS_1838	-	GTGACCTATGCACCAGACGTGGAGGACGCTGGTTATTCAGAGGGACTGGGGTGAATGTAGATCGGAAGAGCGGTTTCAG
chr20	57484689	57484728	GNAS_1839	-	GTGACCTATGCACCAGACGTGAGAGCAAAGGCCAAGAGCGTGAGCAGCCACTGATCCCTAGATCGGAAGAGCGGTTTCAG
chr20	57484956	57484995	GNAS_1840	-	GTGACCTATGCACCAGACGTGGAGGCCGTGTGAATGCTTGGGAGAAGCGCGCTTTCCGCCAGATCGGAAGAGCGGTTTCAG
chr20	57485339	57485378	GNAS_1841	-	GTGACCTATGCACCAGACGTAGGGAAATACATATTAAATGTAATTTAAATTAAGCAGAGCAGATCGGAAGAGCGGTTTCAG
chr20	57485688	57485727	GNAS_1842	-	GTGACCTATGCACCAGACGTAAACAAGGGGACTTGTCACTGACACCCCTGCCAGGAACCAAGATCGGAAGAGCGGTTTCAG
chr20	57415481	57415520	GNAS_1843	-	GTGACCTATGCACCAGACGTTCGATTTCCGGACTCGGCTCGCTCTCGGCTCGTGTAGTGAAGATCGGAAGAGCGGTTTCAG
chr20	57428684	57428723	GNAS_1844	-	GTGACCTATGCACCAGACGTGCAAGGCCTCAAGGCCTGCACTGGCCCACTGGGGAATCCAGATCGGAAGAGCGGTTTCAG
chr20	57429097	57429136	GNAS_1845	-	GTGACCTATGCACCAGACGTGCGGTTGCGCGCGGGAGTGAGGGCGGACCGCACTCGAGGCCAGATCGGAAGAGCGGTTTCAG
chr20	57429510	57429549	GNAS_1846	-	GTGACCTATGCACCAGACGTTCTTCTGGGGTTGCCCCGGAGTCAGGATCGGCTGGGGCTGAGATCGGAAGAGCGGTTTCAG
chr20	57429923	57429962	GNAS_1847	-	GTGACCTATGCACCAGACGTGCGAGTAGGCCGCGGAGTAGGCCGATCGGCAGCCTGGATAGATCGGAAGAGCGGTTTCAG
chr14	62162473	62162512	HIF1A_1848	-	GTGACCTATGCACCAGACGTTCCCCCGATGTCTTACGGCGGGCGGCCCCAGGCTCGCAGATCGGAAGAGCGGTTTCAG
chr14	62187050	62187089	HIF1A_1849	-	GTGACCTATGCACCAGACGTACAACAAGAAAACAGAGATGGAAGTGTATACAAGTTAAGATCGGAAGAGCGGTTTCAG
chr14	62188177	62188216	HIF1A_1850	-	GTGACCTATGCACCAGACGTACAAGAAAGGAAAATAATAGTTAAAAAGTTGACTTAAGATCGGAAGAGCGGTTTCAG
chr14	62188407	62188446	HIF1A_1851	-	GTGACCTATGCACCAGACGTATTTTTAAAAAATTAGGGCTAGATCATAAAATCATAAAAAACAGATCGGAAGAGCGGTTTCAG
chr14	62193374	62193413	HIF1A_1852	-	GTGACCTATGCACCAGACGTCATGAAATAAAGTTTAAAGCAACTAAATATACAAATTTGAGATCGGAAGAGCGGTTTCAG
chr14	62194121	62194160	HIF1A_1853	-	GTGACCTATGCACCAGACGTAGAACAAAGCAGTTAAAAAAAATATTTACAATGCTAGGGAAGATCGGAAGAGCGGTTTCAG
chr14	62199086	62199125	HIF1A_1854	-	GTGACCTATGCACCAGACGTAAATAACAAGATTTAAGAAAAAAAAGGGAGACACTGATAAAGATCGGAAGAGCGGTTTCAG
chr14	62200806	62200845	HIF1A_1855	-	GTGACCTATGCACCAGACGTAAAGAAAATAATCATGACAGAAAATAATTTAACTTTGAGATCGGAAGAGCGGTTTCAG
chr14	62203557	62203596	HIF1A_1856	-	GTGACCTATGCACCAGACGTAAAGAAAATTGTAATTCACAATAATGACACTTGATACAGTAGATCGGAAGAGCGGTTTCAG



chr14	62207173	62207212	HIF1A_1857	-	GTGACCTATGCACCAGACGTAAATATGTTTACTATTTCTGAAGAAGCTTCCATATACTTAGATCGGAAGAGCGGTTTCAG
chr14	62207423	62207462	HIF1A_1858	-	GTGACCTATGCACCAGACGTGCAAATACATGAGTTTTTACAATGCCACACCTTATAAATAGATCGGAAGAGCGGTTTCAG
chr14	62211373	62211412	HIF1A_1859	-	GTGACCTATGCACCAGACGTAAAAATCTAAATGAAAATATAGCGTTTTTAAAAAAAATAAGATCGGAAGAGCGGTTTCAG
chr14	62212359	62212398	HIF1A_1860	-	GTGACCTATGCACCAGACGTAAAGTTATTTCAAGTTTAGTTTGTGAATTTTTTTTTAAGATCGGAAGAGCGGTTTCAG
chr11	94153241	94153280	MRE11A_1861	-	GTGACCTATGCACCAGACGTGGCATTGAGAAACATGCAAGATACAGGAAAAATGAAAATGAGATCGGAAGAGCGGTTTCAG
chr11	94168948	94168987	MRE11A_1862	-	GTGACCTATGCACCAGACGTGATTTCTGCAAAAAGAACATCTGAAAAAAATAAAAATAGATCGGAAGAGCGGTTTCAG
chr11	94170293	94170332	MRE11A_1863	-	GTGACCTATGCACCAGACGTAAAGTTTTTCTGAGTTGTGATTAATAATTTATGTTTTCTGCAAGATCGGAAGAGCGGTTTCAG
chr11	94178926	94178965	MRE11A_1864	-	GTGACCTATGCACCAGACGTACTGCAAGTGATTATTTATAAATTTCCAACTTAGAAAGACAGATCGGAAGAGCGGTTTCAG
chr11	94180335	94180374	MRE11A_1865	-	GTGACCTATGCACCAGACGTAGTTCAGTCTGTGCACATTCACACTTGGCAGTTGAGTGAGATCGGAAGAGCGGTTTCAG
chr11	94189392	94189431	MRE11A_1866	-	GTGACCTATGCACCAGACGTGCTGCAAAATCTGTGTTTATATATCACTTTCTTAAACTAGATCGGAAGAGCGGTTTCAG
chr11	94192524	94192563	MRE11A_1867	-	GTGACCTATGCACCAGACGTAAATTTGAGTGTCTAGGTCTATTTAAATAGCTGTCTTTAAAGATCGGAAGAGCGGTTTCAG
chr11	94194052	94194091	MRE11A_1868	-	GTGACCTATGCACCAGACGTACAGTTACATTTGAAATAAGTCTTATAGTAAACAGATCGGAAGAGCGGTTTCAG
chr11	94197229	94197268	MRE11A_1869	-	GTGACCTATGCACCAGACGTATTTTTATGAGGTAATAAAAAATGTTCTTATAGGATTTGTGAGATCGGAAGAGCGGTTTCAG
chr11	94200929	94200968	MRE11A_1870	-	GTGACCTATGCACCAGACGTTTTATATAGATTGAATATTATAATTTTCAAAGCATAGTAAGATCGGAAGAGCGGTTTCAG
chr11	94203587	94203626	MRE11A_1871	-	GTGACCTATGCACCAGACGTGATAAAGTCAATGAGATCTACTTTAGTTGAAGAATTATAGATCGGAAGAGCGGTTTCAG
chr11	94204690	94204729	MRE11A_1872	-	GTGACCTATGCACCAGACGTATATTTTTGAGCCAAATTTTAAAGAAATCTTTGCTATAATAAGATCGGAAGAGCGGTTTCAG
chr11	94209405	94209444	MRE11A_1873	-	GTGACCTATGCACCAGACGTCTCTGAAAAAGTTTGACCAAGTGTGAGGCTTCCCAAAAGATCGGAAGAGCGGTTTCAG
chr11	94211851	94211890	MRE11A_1874	-	GTGACCTATGCACCAGACGTTTTTTACTGTTTATGACCATGTGTGATTTTAAACAAGATCGGAAGAGCGGTTTCAG
chr11	94212790	94212829	MRE11A_1875	-	GTGACCTATGCACCAGACGTTTTTCTTAGAGTTTGTGGAATTTTGGAAATGATCAGTTTATAGATCGGAAGAGCGGTTTCAG
chr11	94219040	94219079	MRE11A_1876	-	GTGACCTATGCACCAGACGTATTACTTGTAGTGAGTGATTACTTTGTGTATGGTATTTGAGATCGGAAGAGCGGTTTCAG
chr11	94223949	94223988	MRE11A_1877	-	GTGACCTATGCACCAGACGTTTGTATTTGTGCATATCTACCATATTCCTTGGTTAACAGATCGGAAGAGCGGTTTCAG
chr11	94225898	94225937	MRE11A_1878	-	GTGACCTATGCACCAGACGTGACTTCTGGAATCCCTTGTATTTGGGGTTTCTAAAGCTCAGATCGGAAGAGCGGTTTCAG
chr16	81819545	81819584	PLCG2_1879	-	GTGACCTATGCACCAGACGTCCAGGGGAAAGGAAGAAATCGGGAGAATCAGGAAGCTGAGATCGGAAGAGCGGTTTCAG
chr16	81887999	81888038	PLCG2_1880	-	GTGACCTATGCACCAGACGTATTAACATGAGCCAATTAGAAGCTGGATGCTCCCTCCACCTAGATCGGAAGAGCGGTTTCAG
chr16	81891818	81891857	PLCG2_1881	-	GTGACCTATGCACCAGACGTGAAAGGGAACAGAAATGCTGTGTTAATCTCTGGGAAGACGAGATCGGAAGAGCGGTTTCAG
chr16	81892671	81892710	PLCG2_1882	-	GTGACCTATGCACCAGACGTATATGAGACAAAAGAAAGAGAGAAAGAGAAAATTAGAAAAAGATCGGAAGAGCGGTTTCAG
chr16	81902769	81902808	PLCG2_1883	-	GTGACCTATGCACCAGACGTGGGAGACCCAGTTCTGTCACTTGAGGGTTTTCAACAGCAAGATCGGAAGAGCGGTTTCAG
chr16	81904407	81904446	PLCG2_1884	-	GTGACCTATGCACCAGACGTGAAAAAAGTGACCACATGATTTTTGATGTCCACCCTAAGAAGATCGGAAGAGCGGTTTCAG
chr16	81914465	81914504	PLCG2_1885	-	GTGACCTATGCACCAGACGTGAGCACACAAAAAAGAACCTTAGACAAGTCACTTAAAGATCGGAAGAGCGGTTTCAG
chr16	81916824	81916863	PLCG2_1886	-	GTGACCTATGCACCAGACGTGAAAGGGGTCAGTTAGACACAGACACATTCAACAGAGAGATCGGAAGAGCGGTTTCAG
chr16	81922727	81922766	PLCG2_1887	-	GTGACCTATGCACCAGACGTCAAAGAGAACGAGAGATCAGCAAAGTGAGAACTGATAAAAAGATCGGAAGAGCGGTTTCAG
chr16	81925027	81925066	PLCG2_1888	-	GTGACCTATGCACCAGACGTCAAACACGAAGACCGAATCATCAGTTGACGGGCAGGATGAGATCGGAAGAGCGGTTTCAG
chr16	81927264	81927303	PLCG2_1889	-	GTGACCTATGCACCAGACGTGAAGGCAGGTGGCCGTGTGAGAGTGGCAGCCACAGGGTTAGATCGGAAGAGCGGTTTCAG
chr16	81929362	81929401	PLCG2_1890	-	GTGACCTATGCACCAGACGTAAACGGGCGCCTCAATACCAGTGTGTTCACTGACAGCAGATCGGAAGAGCGGTTTCAG
chr16	81934167	81934206	PLCG2_1891	-	GTGACCTATGCACCAGACGTAAAGAGGCTAGAGGCTCGGCAGGAGGACACACACTCTGAGATCGGAAGAGCGGTTTCAG
chr16	81938958	81938997	PLCG2_1892	-	GTGACCTATGCACCAGACGTAAACATATACATAGGCTGTCTCCATGGAGACCCAAGTTTAGAGATCGGAAGAGCGGTTTCAG
chr16	81941240	81941279	PLCG2_1893	-	GTGACCTATGCACCAGACGTAAACTGGTATTAGTGCCCCCAAGTCTCTACCTCATCAAAGATCGGAAGAGCGGTTTCAG
chr16	81941971	81942010	PLCG2_1894	-	GTGACCTATGCACCAGACGTAAAGAGAGGAGGGTTTTCTGAAAGCCTTGGACCAAACCCCAAGATCGGAAGAGCGGTTTCAG
chr16	81944075	81944114	PLCG2_1895	-	GTGACCTATGCACCAGACGTAGGACGCCATCAGTGTGGGAGAACGCAGGCCAGGCCATTAGATCGGAAGAGCGGTTTCAG
chr16	81946152	81946191	PLCG2_1896	-	GTGACCTATGCACCAGACGTGGGCCAGGGAAAAACAGCCAGGTGAGCCGTCTCCAGGCTGATAGATCGGAAGAGCGGTTTCAG
chr16	81953039	81953078	PLCG2_1897	-	GTGACCTATGCACCAGACGTAAAGAACACAGGGTTGACATGCAAGATCCTGGTGGCCAAAAGATCGGAAGAGCGGTTTCAG
chr16	81954753	81954792	PLCG2_1898	-	GTGACCTATGCACCAGACGTAAAGAAAAGAAAGAAATGGAATAATCCATGCTCCTGGAATAAGATCGGAAGAGCGGTTTCAG
chr16	81957040	81957079	PLCG2_1899	-	GTGACCTATGCACCAGACGTAAACAAGAAAGAAAAGGTGAGCCAGGGACAGGAGGGGAGAGATCGGAAGAGCGGTTTCAG
chr16	81960637	81960676	PLCG2_1900	-	GTGACCTATGCACCAGACGTAGAGAGGACATGGGGGCGCTGTCAACAGGTGGCATGAATTAGATCGGAAGAGCGGTTTCAG
chr16	81962113	81962152	PLCG2_1901	-	GTGACCTATGCACCAGACGTACAAGACATAACTCACGTTAGTTGTAACGGGAATAATAAAAAGATCGGAAGAGCGGTTTCAG
chr16	81965052	81965091	PLCG2_1902	-	GTGACCTATGCACCAGACGTGAGAATGAGAAATGCTCCAATCAGCAATCAGATCGGAAGAGCGGTTTCAG
chr16	81967984	81968023	PLCG2_1903	-	GTGACCTATGCACCAGACGTCTTACTGTCTTTAGTGCCCGCCCCGAGAAATCCCATCTTAGATCGGAAGAGCGGTTTCAG
chr16	81969724	81969763	PLCG2_1904	-	GTGACCTATGCACCAGACGTAGAAAAAGTTCATCAGTACTTCTGTGCTCATCTGTGCATAGATCGGAAGAGCGGTTTCAG
chr16	81971313	81971352	PLCG2_1905	-	GTGACCTATGCACCAGACGTAAAGTGAACGCCTGTGTAAGTCAAGCATGAGCACGCTGGCAGATCGGAAGAGCGGTTTCAG
chr16	81972356	81972395	PLCG2_1906	-	GTGACCTATGCACCAGACGTAAAGGGAAGCATTGGAACCCCCCTGGGGTCTGAAACAGGCAGATCGGAAGAGCGGTTTCAG
chr16	81979730	81979769	PLCG2_1907	-	GTGACCTATGCACCAGACGTACAAGGAGGAAAATGCAAAGGCAGGTAAATTAATGTCAGACAGATCGGAAGAGCGGTTTCAG
chr16	81991511	81991550	PLCG2_1908	-	GTGACCTATGCACCAGACGTACAGATTTACCATCAGCAGTGGGCCATGAGAAATGGGCTAGATCGGAAGAGCGGTTTCAG
chr12	112856866	112856905	PTPN11_1909	-	GTGACCTATGCACCAGACGTCCCTCCGGCTCCGCGACGGACCCGCTCCTTGTCTCAGGCTCAGATCGGAAGAGCGGTTTCAG
chr12	112884030	112884069	PTPN11_1910	-	GTGACCTATGCACCAGACGTAAAGACAAAGTAAGTAATAAAAAAACAAGACACTGTGACGAAGATCGGAAGAGCGGTTTCAG
chr12	112888072	112888111	PTPN11_1911	-	GTGACCTATGCACCAGACGTCCATTGGAAGGGAGCAAGGGGACAATAAAGAGTTACAGATCGGAAGAGCGGTTTCAG
chr12	112890949	112890988	PTPN11_1912	-	GTGACCTATGCACCAGACGTAAAAATAAAAAAAGAAATTTAGCTCTACTATGGGTTTATGAGATCGGAAGAGCGGTTTCAG
chr12	112892318	112892357	PTPN11_1913	-	GTGACCTATGCACCAGACGTAAACACATGACATTTATAATTTGTACTTTATGTTACATAGATCGGAAGAGCGGTTTCAG
chr12	112893704	112893743	PTPN11_1914	-	GTGACCTATGCACCAGACGTACACAGTTGATGTGATAAAGAAAATATTACAGAAAACAGATCGGAAGAGCGGTTTCAG

chr12	112910698	112910737	PTPN11_1915	-	GTGACCTATGCACCAGACGTAGAAAAAGTCAATATTATTACGTGTCAAAGAGTCACAGAAAAGATCGGAAGAGCGGTTTCAG
chr12	112915405	112915444	PTPN11_1916	-	GTGACCTATGCACCAGACGTAAAGAGACCAGGTCACATAAGTCTCGACTGCTTCAGGAAAAGATCGGAAGAGCGGTTTCAG
chr12	112915611	112915650	PTPN11_1917	-	GTGACCTATGCACCAGACGTAGGAAGAAAATCCTTCAAACACCTTAAAGTTACTTTTCAGGAGATCGGAAGAGCGGTTTCAG
chr12	112919828	112919867	PTPN11_1918	-	GTGACCTATGCACCAGACGTTCAGAAAAAAGAAAGTAAATCTGTGAACCTCTGAAATAAAGATCGGAAGAGCGGTTTCAG
chr12	112924229	112924268	PTPN11_1919	-	GTGACCTATGCACCAGACGTGCCAAGAAAACCAGAAAAGAAATTAATAAATCAAGAGGTAGATCGGAAGAGCGGTTTCAG
chr12	112926197	112926236	PTPN11_1920	-	GTGACCTATGCACCAGACGTAAAGGACAAAAGCAGGGACAACAGAATCATTTCATGGGGGTAGATCGGAAGAGCGGTTTCAG
chr12	112926778	112926817	PTPN11_1921	-	GTGACCTATGCACCAGACGTAAACATCATGAAGATAAAGGAAAACCTGCAGAGCCAGGATGAGATCGGAAGAGCGGTTTCAG
chr12	112939898	112939937	PTPN11_1922	-	GTGACCTATGCACCAGACGTGAAGAGTGCACATGTGAGGGACAATGGTTATTTTAAAGGGAGATCGGAAGAGCGGTTTCAG
chr12	112942449	112942488	PTPN11_1923	-	GTGACCTATGCACCAGACGTAAAGAAAAAGAAAGACATTTACAAAATGTAGACCACGCTGAGATCGGAAGAGCGGTTTCAG
chr5	131892967	131893006	RAD50_1924	-	GTGACCTATGCACCAGACGTGTTTCTAATCTCACCAGGGACCTGGAGCCCAAAAGGCTTAGATCGGAAGAGCGGTTTCAG
chr5	131894926	131894965	RAD50_1925	-	GTGACCTATGCACCAGACGTAGAAAATTACATTATTTCTGTTATAAGAGAACCACAGAAAGTAGATCGGAAGAGCGGTTTCAG
chr5	131911419	131911458	RAD50_1926	-	GTGACCTATGCACCAGACGTAAACACAGAAAAAATCTATGTTACTTTAATAAGCACCAAGTAGATCGGAAGAGCGGTTTCAG
chr5	131914959	131914998	RAD50_1927	-	GTGACCTATGCACCAGACGTGAAAATCAAGAATATATGAAAATAACCTTCAGTGTATCAGATCGGAAGAGCGGTTTCAG
chr5	131915011	131915050	RAD50_1928	-	GTGACCTATGCACCAGACGTATTTCTGCACACTTAGAGCTCAGACTGACCTTTTCACCATAGATCGGAAGAGCGGTTTCAG
chr5	131923204	131923243	RAD50_1929	-	GTGACCTATGCACCAGACGTAGAAAACATTACATAAATAAACTCCTATAGCTTACATGGAGATCGGAAGAGCGGTTTCAG
chr5	131923566	131923605	RAD50_1930	-	GTGACCTATGCACCAGACGTCCAAAATAAAAAGCTTTAATGTACAACATAAGAAAATATAGATCGGAAGAGCGGTTTCAG
chr5	131924329	131924368	RAD50_1931	-	GTGACCTATGCACCAGACGTAAAAATCTCAATAATTTTTTTTCACTGGTGTCTAAAAAGAGATCGGAAGAGCGGTTTCAG
chr5	131925273	131925312	RAD50_1932	-	GTGACCTATGCACCAGACGTGTAAGAATGAGCATTAATAAATTTACTAAACAATTTAAAGATCGGAAGAGCGGTTTCAG
chr5	131926866	131926905	RAD50_1933	-	GTGACCTATGCACCAGACGTATTCATACAAATGCAAAAGGTGTTATATATTTTGTCAAGAAGATCGGAAGAGCGGTTTCAG
chr5	131927519	131927558	RAD50_1934	-	GTGACCTATGCACCAGACGTAAAAAAAATCTTTAAAAATAAAGTCTATATCTCCACATTAGATCGGAAGAGCGGTTTCAG
chr5	131930511	131930550	RAD50_1935	-	GTGACCTATGCACCAGACGTAGCAAAATGGATTTTCATTTTAAAAATAGGAGAAATAGTAGATCGGAAGAGCGGTTTCAG
chr5	131931215	131931254	RAD50_1936	-	GTGACCTATGCACCAGACGTAAAAATAAATATATACCAATGAGAAAAAACATAAAAATAAGATCGGAAGAGCGGTTTCAG
chr5	131939562	131939601	RAD50_1937	-	GTGACCTATGCACCAGACGTAAACAAAATGATTTCTTAAATAAATCTACTGCATTATTCAGATCGGAAGAGCGGTTTCAG
chr5	131940448	131940487	RAD50_1938	-	GTGACCTATGCACCAGACGTACATAATTTACAGATAATTAAGTAAAGGCTATAGAAAATAAAGATCGGAAGAGCGGTTTCAG
chr5	131944759	131944798	RAD50_1939	-	GTGACCTATGCACCAGACGTATATTCATTAATTTTACACTGGTGTACTTAAAGGGCACATAGATCGGAAGAGCGGTTTCAG
chr5	131951645	131951684	RAD50_1940	-	GTGACCTATGCACCAGACGTACATTAATTAGTTAACAAAAATAACCAAGTTACTAACATAGATCGGAAGAGCGGTTTCAG
chr5	131953712	131953751	RAD50_1941	-	GTGACCTATGCACCAGACGTGAAAAATGACAAATGAGGACCATTTTTTAGCTTTTAAACAAGATCGGAAGAGCGGTTTCAG
chr5	131973723	131973762	RAD50_1942	-	GTGACCTATGCACCAGACGTAGAAAGAATATTTTAGAGGAACCTATGCTCTGTAGCCTTTAGATCGGAAGAGCGGTTTCAG
chr5	131976314	131976353	RAD50_1943	-	GTGACCTATGCACCAGACGTGCCCTATGTGAGAAGCCAGCACAGACCTTCTCATCTCAAGATCGGAAGAGCGGTTTCAG
chr5	131977820	131977859	RAD50_1944	-	GTGACCTATGCACCAGACGTATATTGAGCATATATTATGATAAAGAGCAACTAACCCCTTCAGATCGGAAGAGCGGTTTCAG
chr15	40990907	40990946	RAD51_1945	-	GTGACCTATGCACCAGACGTACAAAATGCTTATCAGTATAAACACTAGAGAAATAAGGTGAGATCGGAAGAGCGGTTTCAG
chr15	40998325	40998364	RAD51_1946	-	GTGACCTATGCACCAGACGTAAAGAAATATAAATCAACAAAATAATTTCTTACCACAAGATCGGAAGAGCGGTTTCAG
chr15	41001173	41001212	RAD51_1947	-	GTGACCTATGCACCAGACGTGATAAGAAATAACTTTAGCATATAACAACATGTAGAAAAGATCGGAAGAGCGGTTTCAG
chr15	41010953	41010992	RAD51_1948	-	GTGACCTATGCACCAGACGTCAAAAACAACAGTAAAGATGAACATTGTATTTCTGATACAAGATCGGAAGAGCGGTTTCAG
chr15	41020859	41020898	RAD51_1949	-	GTGACCTATGCACCAGACGTGAAAGACACTTTTTAGGCTGCACAGAACTCAGGCAGAAAGATCGGAAGAGCGGTTTCAG
chr15	41021653	41021692	RAD51_1950	-	GTGACCTATGCACCAGACGTCAAGGATTCTCTGAAGCCTATTTCTAGCCTGTGTAGATTAGATCGGAAGAGCGGTTTCAG
chr15	41022001	41022040	RAD51_1951	-	GTGACCTATGCACCAGACGTAAAGATAAATGTCAATTTTGTGCCATAGACACTCCAAAAGATCGGAAGAGCGGTTTCAG
chr15	41023203	41023242	RAD51_1952	-	GTGACCTATGCACCAGACGTGACACAGACCAAAGACCAATTTATATAATTAACAATAGATCGGAAGAGCGGTTTCAG
chr13	80910843	80910882	SPRY2_1953	-	GTGACCTATGCACCAGACGTGAGGAAATTTACAGTAAATGAGGATTTTTTCTTTCTTTTATAGATCGGAAGAGCGGTTTCAG
chr13	80911317	80911356	SPRY2_1954	-	GTGACCTATGCACCAGACGTAGCTTAAGCCACTGAGCAAGGAAGATTTGGGCCCTGCACGCAGATCGGAAGAGCGGTTTCAG
chr16	89804959	89804998	FANCA_1955	-	GTGACCTATGCACCAGACGTCACTGCACACCAGCCAGCTCCCGTGTAAATAATTTATTAAGATCGGAAGAGCGGTTTCAG
chr16	89805240	89805279	FANCA_1956	-	GTGACCTATGCACCAGACGTGATGCCACCTTGGGCCATGTGGGGGACATGAGAATTGACAGATCGGAAGAGCGGTTTCAG
chr16	89805491	89805530	FANCA_1957	-	GTGACCTATGCACCAGACGTGGGCCAGTCCACCTCAGGGGAGCTCCCCAGCCGGAGAGATCGGAAGAGCGGTTTCAG
chr16	89805836	89805875	FANCA_1958	-	GTGACCTATGCACCAGACGTCCACAGGGCTGGTCAGGGCTGGGAGTGTTCACAGACCAGATCGGAAGAGCGGTTTCAG
chr16	89806352	89806391	FANCA_1959	-	GTGACCTATGCACCAGACGTGCTGCTGAGGCCAAATGCGGAGGGCCGCTCTTTTCAAGAAGATCGGAAGAGCGGTTTCAG
chr16	89807162	89807201	FANCA_1960	-	GTGACCTATGCACCAGACGTCTTACCAGCCAGGTGCTCTCCACTGTGGGCCAGCAGATCGGAAGAGCGGTTTCAG
chr16	89809158	89809197	FANCA_1961	-	GTGACCTATGCACCAGACGTAAATTTCTTTACTGATTTATTTTCTCGCAAGCTTGGTTTCAGATCGGAAGAGCGGTTTCAG
chr16	89811317	89811356	FANCA_1962	-	GTGACCTATGCACCAGACGTGGTGAGATGGGGTGTGCCCGCCAGATGCACCTCGGAAGATCGGAAGAGCGGTTTCAG
chr16	89812942	89812981	FANCA_1963	-	GTGACCTATGCACCAGACGTGTCTTGTGTTGGTGTGTTTGTGTTGGGGATGAGTGGGACACAGATCGGAAGAGCGGTTTCAG
chr16	89813189	89813228	FANCA_1964	-	GTGACCTATGCACCAGACGTCCCTCAGCCCTCTCGTGGCCTTCTCAGAACGCCGTGGGTAGATCGGAAGAGCGGTTTCAG
chr16	89815017	89815056	FANCA_1965	-	GTGACCTATGCACCAGACGTGCTGTGCACGTGCTCGTCCGATGCTGCATGCTGCTGCTGGCCGAGATCGGAAGAGCGGTTTCAG
chr16	89816088	89816127	FANCA_1966	-	GTGACCTATGCACCAGACGTCTACCACCTGGGCAGGCCAGCCAGCTGGGCAGGCAGATCGGAAGAGCGGTTTCAG
chr16	89818496	89818535	FANCA_1967	-	GTGACCTATGCACCAGACGTGGGTGCCACAACCTCAGTGCATTCACTTCAATTTAAGCCGCGAGATCGGAAGAGCGGTTTCAG
chr16	89831248	89831287	FANCA_1968	-	GTGACCTATGCACCAGACGTGTTCTTCTCTGCATCATGCCAGTCTGAGTCTAGGGTAGATCGGAAGAGCGGTTTCAG
chr16	89833499	89833538	FANCA_1969	-	GTGACCTATGCACCAGACGTCTTTTCTATTTTCCATTCTGCCATACGTTTCAGGTTTAGATCGGAAGAGCGGTTTCAG
chr16	89836524	89836563	FANCA_1970	-	GTGACCTATGCACCAGACGTCTTCATGGGGGCCACCTTGGGGGCCACTCTGAGGCCAGATCGGAAGAGCGGTTTCAG
chr16	89836922	89836961	FANCA_1971	-	GTGACCTATGCACCAGACGTGGGCAGCTCCCTGAGTGGTGGGGCTCTGGGTGCCACCAGATCGGAAGAGCGGTTTCAG
chr16	89838036	89838075	FANCA_1972	-	GTGACCTATGCACCAGACGTGGGCTCAGAACAAGCAGGGGGTCTTACCATTTCATTAGATCGGAAGAGCGGTTTCAG

chr16	89839629	89839668	FANCA_1973	-	GTGACCTATGCACCAGACGTATGGGAGCTCATGCTGTGTCTCATGTGTGCAGCCTGTGGTAGATCGGAAGAGCGGTTTCAG
chr16	89842100	89842139	FANCA_1974	-	GTGACCTATGCACCAGACGTGGGCCCTGTGCCACTCTGGGACTTGTGCTTTTCCATTTTAGATCGGAAGAGCGGTTTCAG
chr16	89845159	89845198	FANCA_1975	-	GTGACCTATGCACCAGACGTACGGTTAGAAGGGGATGACTACTTCCAGGTTTCTTCTGACAGATCGGAAGAGCGGTTTCAG
chr16	89845301	89845340	FANCA_1976	-	GTGACCTATGCACCAGACGTGTCTCCATGAGTTTGTGACCAGTTGTGTAGAAAAGCAAGGAAGATCGGAAGAGCGGTTTCAG
chr16	89846227	89846266	FANCA_1977	-	GTGACCTATGCACCAGACGTCTGCCGAAAAGGCCTCTAGCAGCTGCAGTGTGTGCAGACCAGATCGGAAGAGCGGTTTCAG
chr16	89849217	89849256	FANCA_1978	-	GTGACCTATGCACCAGACGTTTGAGCCCTGCAGGGTCTCAGCCAGTCAAGCCACCATGCAGATCGGAAGAGCGGTTTCAG
chr16	89849365	89849404	FANCA_1979	-	GTGACCTATGCACCAGACGTCTCCATGCCACTCTCACACCTGTCCACAGCAAACCTGAGATCGGAAGAGCGGTTTCAG
chr16	89851212	89851251	FANCA_1980	-	GTGACCTATGCACCAGACGTGGCTGCCACATCCATGATTTCTGGTGCTTCGCTCACCTGCAGATCGGAAGAGCGGTTTCAG
chr16	89857761	89857800	FANCA_1981	-	GTGACCTATGCACCAGACGTTGCCAATCGGCTACCTAATACCTGATCTTCCAGAAGGCCAGATCGGAAGAGCGGTTTCAG
chr16	89858285	89858324	FANCA_1982	-	GTGACCTATGCACCAGACGTACGCGAGCCCGTGGTGTCTGGTCAAGAGTGTGTGTAGGGGAGATCGGAAGAGCGGTTTCAG
chr16	89858829	89858868	FANCA_1983	-	GTGACCTATGCACCAGACGTGGTATTATACCTGCTTCTGAGCTCGTGGCGGGGGGATTAGATCGGAAGAGCGGTTTCAG
chr16	89862264	89862303	FANCA_1984	-	GTGACCTATGCACCAGACGTTGTGGAGGCTGCTCAGTTCTACCTACCTTTTGGGATGCTAGATCGGAAGAGCGGTTTCAG
chr16	89865437	89865476	FANCA_1985	-	GTGACCTATGCACCAGACGTCCCGCTCCTGAGCACACTTCTCTGCCAGTTACGATAACGAGATCGGAAGAGCGGTTTCAG
chr16	89865524	89865563	FANCA_1986	-	GTGACCTATGCACCAGACGTGAGGGTGGCCTGCCTGAGTGTGCAGCAGGGAGGTGTCTGCAGATCGGAAGAGCGGTTTCAG
chr16	89865963	89866002	FANCA_1987	-	GTGACCTATGCACCAGACGTTGCACTGCAGCCAGACTGTAATGACTTAGTTTGTCTATAGATCGGAAGAGCGGTTTCAG
chr16	89869617	89869656	FANCA_1988	-	GTGACCTATGCACCAGACGTAAGTCAAGTGAAGAGTTTAGCGGAAGGAGCCGCTCTATTAGATCGGAAGAGCGGTTTCAG
chr16	89871638	89871677	FANCA_1989	-	GTGACCTATGCACCAGACGTGCAAGATGCGGGTCTTGGGTAACACTATTGATCTGAGATCGGAAGAGCGGTTTCAG
chr16	89874652	89874691	FANCA_1990	-	GTGACCTATGCACCAGACGTAATGATGATTGACTGTTACTGTCTTTCAGTCTAGTCTAGAGATCGGAAGAGCGGTTTCAG
chr16	89877065	89877104	FANCA_1991	-	GTGACCTATGCACCAGACGTGATTGCAAACTGACTCTCCAGTGTCCAGGCAATGTTCTAGATCGGAAGAGCGGTTTCAG
chr16	89877287	89877326	FANCA_1992	-	GTGACCTATGCACCAGACGTAGCAAAGATGAGGAAACCTGCCGTTGTTACTTTAAAGCTAGATCGGAAGAGCGGTTTCAG
chr16	89880878	89880917	FANCA_1993	-	GTGACCTATGCACCAGACGTGCTTCATTTTCTCTATTTTGAATTGCAGAAGGGTTTTTATAGATCGGAAGAGCGGTTTCAG
chr16	89882235	89882274	FANCA_1994	-	GTGACCTATGCACCAGACGTGCTGGTGTCCGCTGCGGGCAGATTTAGGTTTCGGGGTTTTAGATCGGAAGAGCGGTTTCAG
chr16	89882895	89882934	FANCA_1995	-	GTGACCTATGCACCAGACGTGCGGAGCCCGGGAGTGGCGGCTCCGGCCCGGACGATCGGAAGAGCGGTTTCAG
chr11	22646182	22646221	FANCF_1996	-	GTGACCTATGCACCAGACGTGTTATTACTTGAATATAGAATATAGTTTACAAAATGAAAGATCGGAAGAGCGGTTTCAG
chr11	22646557	22646596	FANCF_1997	-	GTGACCTATGCACCAGACGTCCCTCCCAGCCGGCTTTTACTTTAGTACTAGCCGCAAGATCGGAAGAGCGGTTTCAG
chr11	22646932	22646971	FANCF_1998	-	GTGACCTATGCACCAGACGTTCCAAGAGAGCCTGGCCCGCTTGGCCCGCGGCTGTCAGATCGGAAGAGCGGTTTCAG
chr5	176516554	176516593	FGFR4_1999	-	GTGACCTATGCACCAGACGTCACTCTCAGGGACCCAAAGCTGGACTTCCCACCAACTGCCAGATCGGAAGAGCGGTTTCAG
chr5	176517341	176517380	FGFR4_2000	-	GTGACCTATGCACCAGACGTAGGGCAGAGGTCAGCAGACCCCGCAGCCCATCTGAGGCAAGATCGGAAGAGCGGTTTCAG
chr5	176517696	176517735	FGFR4_2001	-	GTGACCTATGCACCAGACGTGACAGAGGGAAGCATTAAGTCCAAGAGGGCAGGCTGAGATCGGAAGAGCGGTTTCAG
chr5	176517889	176517928	FGFR4_2002	-	GTGACCTATGCACCAGACGTGGGGAAGGCCCTAGAAATGACCGTGTGTCCACACAGGCAGATCGGAAGAGCGGTTTCAG
chr5	176518636	176518675	FGFR4_2003	-	GTGACCTATGCACCAGACGTAGAGAGTGTCCGGGACCACCGGACCATGTCCACCAAGGGGAGATCGGAAGAGCGGTTTCAG
chr5	176519272	176519311	FGFR4_2004	-	GTGACCTATGCACCAGACGTGGCGAGACAGTCAACCCTGACCACCGGCACCCATAGAAAGCAGATCGGAAGAGCGGTTTCAG
chr5	176519597	176519636	FGFR4_2005	-	GTGACCTATGCACCAGACGTGGACATGCTCTGGGGTTCACAGCAGGGCCTGGGGCCACACTAGATCGGAAGAGCGGTTTCAG
chr5	176520089	176520128	FGFR4_2006	-	GTGACCTATGCACCAGACGTACATGGACACACAGACAGCAAACCTGGTCAAGTGGAGAGATCGGAAGAGCGGTTTCAG
chr5	176520283	176520322	FGFR4_2007	-	GTGACCTATGCACCAGACGTAGAGGGAAGCGGAGAGCTTCTGCACAGTGGCGGGCGGACAGATCGGAAGAGCGGTTTCAG
chr5	176520357	176520396	FGFR4_2008	-	GTGACCTATGCACCAGACGTGGAGACTTGGTCTGCCTGCTGGAGTCAAGGCTGTCACATGAGATCGGAAGAGCGGTTTCAG
chr5	176520605	176520644	FGFR4_2009	-	GTGACCTATGCACCAGACGTAGAAAGTCCAGCCTCAGACCTCCGAGTCACTCTGCGGAGAGATCGGAAGAGCGGTTTCAG
chr5	176522281	176522320	FGFR4_2010	-	GTGACCTATGCACCAGACGTAGCAGACGGGTTGAAGAGGCTGCCCTCAACTGCACGAGGAGATCGGAAGAGCGGTTTCAG
chr5	176522484	176522523	FGFR4_2011	-	GTGACCTATGCACCAGACGTAGTGGAGGGAGCGTGGAGAGGCTGCCAAAGCTTTGGCTCTAGATCGGAAGAGCGGTTTCAG
chr5	176523008	176523047	FGFR4_2012	-	GTGACCTATGCACCAGACGTGGGGGCTTGGTGCCTCAGCAGCACCTGGCCTGGAGTTGAAGATCGGAAGAGCGGTTTCAG
chr5	176523238	176523277	FGFR4_2013	-	GTGACCTATGCACCAGACGTGAGGAGGGCCTCAGTGCAGATCCACAGGTCCTCGCTAGATCGGAAGAGCGGTTTCAG
chr5	176523555	176523594	FGFR4_2014	-	GTGACCTATGCACCAGACGTGGCCAGGGCTCAGTGTGGCTCAGCGCCCTCCCAGCAGCCGAGATCGGAAGAGCGGTTTCAG
chr5	176524243	176524282	FGFR4_2015	-	GTGACCTATGCACCAGACGTTGGGGCGGAGGTTACAGGGAGCCCTCAGGCCTCAGGAGGAGATCGGAAGAGCGGTTTCAG
chr5	176524478	176524517	FGFR4_2016	-	GTGACCTATGCACCAGACGTCCGAGCTGGTCAAGCTCTGCAGCGCCCGGATGGGACGGGAGATCGGAAGAGCGGTTTCAG
chr13	28877254	28877293	FLT1_2017	-	GTGACCTATGCACCAGACGTGAAGCCTTATTTCTAGAAGCACATGTGTATTTATACCCCAAGATCGGAAGAGCGGTTTCAG
chr13	28880765	28880804	FLT1_2018	-	GTGACCTATGCACCAGACGTGGTATCTTTCTGTGATCAGTTGATGGAGGGGTACGAGGGAGATCGGAAGAGCGGTTTCAG
chr13	28882930	28882969	FLT1_2019	-	GTGACCTATGCACCAGACGTAAGTTAAGGTACCTAGTGCACCCCGATAGACCCCTTCTTTCAGATCGGAAGAGCGGTTTCAG
chr13	28886080	28886119	FLT1_2020	-	GTGACCTATGCACCAGACGTATTTATTTACATCAAATGCCCTTGAATGTACGTCAAGGGAGATCGGAAGAGCGGTTTCAG
chr13	28891585	28891624	FLT1_2021	-	GTGACCTATGCACCAGACGTGGTGCCTCTGCTCCCATCTGACAGCTCGCTTTTACCAGATCGGAAGAGCGGTTTCAG
chr13	28893510	28893549	FLT1_2022	-	GTGACCTATGCACCAGACGTGAGAAGGAAGAAATCAAACAGCCCAAGAAATAATGTCTGCAGATCGGAAGAGCGGTTTCAG
chr13	28895550	28895589	FLT1_2023	-	GTGACCTATGCACCAGACGTTTGTATTTTATTTGACTCATGTGTCTTACATCTTTAAAGATCGGAAGAGCGGTTTCAG
chr13	28896349	28896388	FLT1_2024	-	GTGACCTATGCACCAGACGTGTTTACTGTTTTCTCTCTGCGGAGGCTGGACACACAAGATCGGAAGAGCGGTTTCAG
chr13	28896877	28896916	FLT1_2025	-	GTGACCTATGCACCAGACGTATTCCTTCTGTCTACGCGCTGAGATTTTTTACAACATAGATCGGAAGAGCGGTTTCAG
chr13	28901549	28901588	FLT1_2026	-	GTGACCTATGCACCAGACGTCAAAGTTGGAGGTTTTTAAAGATAGCAATGAGTTTTTATAGATCGGAAGAGCGGTTTCAG
chr13	28903702	28903741	FLT1_2027	-	GTGACCTATGCACCAGACGTAGGGGAGGGCCGCTCCGCTCTCCCTGCACAGGCTGGGAAGATCGGAAGAGCGGTTTCAG
chr13	28908112	28908151	FLT1_2028	-	GTGACCTATGCACCAGACGTTGATTTTGGCTTTCAACTGACCCATCACCATTTTGCATTAGATCGGAAGAGCGGTTTCAG
chr13	28919532	28919571	FLT1_2029	-	GTGACCTATGCACCAGACGTAGGTGATGTTCTGCTCCTTTTACATATATCTAAAAGATCGGAAGAGCGGTTTCAG
chr13	28931641	28931680	FLT1_2030	-	GTGACCTATGCACCAGACGTGCTTAAAGAAACAAGAAATTTGGTCAGACATCTATTTTCAGATCGGAAGAGCGGTTTCAG

chr13	28958972	28959011	FLT1_2031	-	GTGACCTATGCACCAGACGTTTTTTTTCTCCATTATTATTTCTCATCTTTTCATCAGCCAGATCGGAAGAGCGGTTTCAG
chr13	28963883	28963922	FLT1_2032	-	GTGACCTATGCACCAGACGCTCAACAAAAAGGCTGTTTTCTCTCGATCTCCAAATTTAAAGATCGGAAGAGCGGTTTCAG
chr13	28971047	28971086	FLT1_2033	-	GTGACCTATGCACCAGACGTCATCCTATAACCAGAGACAGCCTGGTGACTTCATTCTCTCAGATCGGAAGAGCGGTTTCAG
chr13	28979867	28979906	FLT1_2034	-	GTGACCTATGCACCAGACGTTAAAAATGCGCACTGGGATATTATCCACAAATACACTCAGATCGGAAGAGCGGTTTCAG
chr13	29001246	29001285	FLT1_2035	-	GTGACCTATGCACCAGACGTTCACTTTTTTACTAATCTTTCAAATACTTTTTGACACCTGAGATCGGAAGAGCGGTTTCAG
chr13	29001839	29001878	FLT1_2036	-	GTGACCTATGCACCAGACGTTGTTCTATCTTTCTCTGGTTCTGGTAGGCAACAAATTAGAGATCGGAAGAGCGGTTTCAG
chr13	29004137	29004176	FLT1_2037	-	GTGACCTATGCACCAGACGTCCTTATTTCCATAACAGTTTAAAGACATACTTTGTAAGTGAGATCGGAAGAGCGGTTTCAG
chr13	29005223	29005262	FLT1_2038	-	GTGACCTATGCACCAGACGTTTTCAGCGTTGCCAATCATGCTATGCTTTCTAATCATTGTAGATCGGAAGAGCGGTTTCAG
chr13	29007906	29007945	FLT1_2039	-	GTGACCTATGCACCAGACGTCATTTTTCTATTTCTTCTGCAGGACAGTATTTAAGCAAGAGATCGGAAGAGCGGTTTCAG
chr13	29008145	29008184	FLT1_2040	-	GTGACCTATGCACCAGACGCTTCAAAGGCATGAACATAAGCCGAAGTGCTCTGTATTTAGATCGGAAGAGCGGTTTCAG
chr13	29012308	29012347	FLT1_2041	-	GTGACCTATGCACCAGACGTACACCGCTATTCTCAGCATACTTTCACTGCAAATAAGCATAGATCGGAAGAGCGGTTTCAG
chr13	29040990	29041029	FLT1_2042	-	GTGACCTATGCACCAGACGTCATTTTTCTACATTTGTTTGGCTTTTGCTTTGCAAATGAGTAGATCGGAAGAGCGGTTTCAG
chr13	29041608	29041647	FLT1_2043	-	GTGACCTATGCACCAGACGTTGTTGGTTGGTAAATCTAGTTGCCATGCCCTAAGGCAAGATCGGAAGAGCGGTTTCAG
chr13	29068867	29068906	FLT1_2044	-	GTGACCTATGCACCAGACGTGCTGGGGGCCGGGGCCTGAGGCGGGCTGCGATGGGGCGGCAGATCGGAAGAGCGGTTTCAG
chr13	41133610	41133649	FOXO1_2045	-	GTGACCTATGCACCAGACGTGCAGGTAAGTTCACCCCAATATCAAAGACCTTTTGAAAAAGATCGGAAGAGCGGTTTCAG
chr13	41239670	41239709	FOXO1_2046	-	GTGACCTATGCACCAGACGTTCCGGCGCGCGGCCGGACCTTTGGGGCGCGGTTGGTCCAGCAGATCGGAAGAGCGGTTTCAG
chr13	41134056	41134095	FOXO1_2047	-	GTGACCTATGCACCAGACGTATCTCATAACAAAATGATGAATCCAGCTCCCATACCACAGATCGGAAGAGCGGTTTCAG
chr13	41134502	41134541	FOXO1_2048	-	GTGACCTATGCACCAGACGTTCTGAGATAAGCAATCCGAAAAAATCGAAAAATCTTTTGAGATCGGAAGAGCGGTTTCAG
chr15	66679636	66679675	MAP2K1_2049	-	GTGACCTATGCACCAGACGTGTTAAGCGCTTCCAACCTCCGGGGGAGGGCAGCACCTCTAGATCGGAAGAGCGGTTTCAG
chr15	66727315	66727354	MAP2K1_2050	-	GTGACCTATGCACCAGACGTGTTGGGGAGCACAAGTCAATACTGTCACCAGAGAAGTCAACAGATCGGAAGAGCGGTTTCAG
chr15	66729034	66729073	MAP2K1_2051	-	GTGACCTATGCACCAGACGTGTGGGAAGAAAGAGAGGTTTTATGAAAGAAAGAGGGAGGAAAGATCGGAAGAGCGGTTTCAG
chr15	66735568	66735607	MAP2K1_2052	-	GTGACCTATGCACCAGACGTGAATACCAGACCAGTTAGTGACAATGTTCTAATACTTCTAGATCGGAAGAGCGGTTTCAG
chr15	66736944	66736983	MAP2K1_2053	-	GTGACCTATGCACCAGACGTGGGAATGTAAGAAAGAAAGAAATACTGGTGATAAGAAAAAGATCGGAAGAGCGGTTTCAG
chr15	66774043	66774082	MAP2K1_2054	-	GTGACCTATGCACCAGACGTGAGAAAATGAAAAGAGGGAAGTACACAGGTAGATTGAGATCGGAAGAGCGGTTTCAG
chr15	66777278	66777317	MAP2K1_2055	-	GTGACCTATGCACCAGACGTGACAGACAGTGATAATCACCTAACCTAAGTTGGACCCCTGAGATCGGAAGAGCGGTTTCAG
chr15	66779516	66779555	MAP2K1_2056	-	GTGACCTATGCACCAGACGTTATAAAAAGAAAAAATCTTCTCAGAAACAGATTACTTGATAGATCGGAAGAGCGGTTTCAG
chr15	66781503	66781542	MAP2K1_2057	-	GTGACCTATGCACCAGACGTGTTGAGATAAGAAAAATGCCCTGGCTCCTTGCTCCAGCCAGATCGGAAGAGCGGTTTCAG
chr15	66782006	66782045	MAP2K1_2058	-	GTGACCTATGCACCAGACGTGAAAGACAAGGTAAGAGCTGTTGCCCTGGCACTGGTTCTAGAGATCGGAAGAGCGGTTTCAG
chr15	66782790	66782829	MAP2K1_2059	-	GTGACCTATGCACCAGACGTGGAAAGCAGGAGAGCTGGTGTGTAAGAAAGAAAAACAAACAGATCGGAAGAGCGGTTTCAG
chr19	52693300	52693339	PPP2R1A_2060	-	GTGACCTATGCACCAGACGTTCCCTTTCTGTCAAGCTGCGGGCAGCGCTGTGCTGAAACAGATCGGAAGAGCGGTTTCAG
chr19	52705147	52705186	PPP2R1A_2061	-	GTGACCTATGCACCAGACGTAACAAGAAGAGGAGGGGAGAATGTTAGAATCCCAGACACAGATCGGAAGAGCGGTTTCAG
chr19	52709166	52709205	PPP2R1A_2062	-	GTGACCTATGCACCAGACGTAAGACAGACTTCGTGACTATCCATCTCAACTCTGACCCAGATCGGAAGAGCGGTTTCAG
chr19	52714463	52714502	PPP2R1A_2063	-	GTGACCTATGCACCAGACGTAACAACAAAGTCACTGGACAGCTCCCTCTCCACCATCCGCAAGATCGGAAGAGCGGTTTCAG
chr19	52716158	52716197	PPP2R1A_2064	-	GTGACCTATGCACCAGACGTGAGAGGAACAGTGGGAGGGCAGCAGAGGCCCTGCTGAGCTAGATCGGAAGAGCGGTTTCAG
chr19	52718982	52719021	PPP2R1A_2065	-	GTGACCTATGCACCAGACGTGAGAGGAGGAGGAGGAGTGAGAGGGCTGGCAGTTACTAGATCGGAAGAGCGGTTTCAG
chr19	52719207	52719246	PPP2R1A_2066	-	GTGACCTATGCACCAGACGTGAGAGGGAGGGCAAGGGGAAGTGAGACCTGATGTGCTAGTAGATCGGAAGAGCGGTTTCAG
chr19	52719732	52719771	PPP2R1A_2067	-	GTGACCTATGCACCAGACGTGAAGAGGCAGGCACAGGGGTGAGTGAACCCCTGCAGCAGAGATCGGAAGAGCGGTTTCAG
chr19	52722894	52722933	PPP2R1A_2068	-	GTGACCTATGCACCAGACGTGAAAGAAGGATTCTGAGAGAAATGCAATGCACACAGCAACCAGATCGGAAGAGCGGTTTCAG
chr19	52723392	52723431	PPP2R1A_2069	-	GTGACCTATGCACCAGACGTAACCAAGGGTTCCAAGGTAAGCGTTCCAGGAGAGCAAAACAAGATCGGAAGAGCGGTTTCAG
chr19	52724182	52724221	PPP2R1A_2070	-	GTGACCTATGCACCAGACGTGTGAGGGTGAGAGAGACAGGGATTGGAGTGAAAGACTGAGATCGGAAGAGCGGTTTCAG
chr19	52725302	52725341	PPP2R1A_2071	-	GTGACCTATGCACCAGACGTGTGAGTGGCAGGGGTGAGTATGCCAAAGCTCCTGGCTCCTGCTAATACTAGATCGGAAGAGCGGTTTCAG
chr19	52728920	52728959	PPP2R1A_2072	-	GTGACCTATGCACCAGACGTAAGGAGACAGGGAGAGAGGGTGAGCCAGGATGGACTGAGATCGGAAGAGCGGTTTCAG
chr19	52729168	52729207	PPP2R1A_2073	-	GTGACCTATGCACCAGACGTAGGAACAGGCAAGAATCAGAACAGACCCCTCTCTGCCAGATCGGAAGAGCGGTTTCAG
chr1	186644980	186645019	PTGS2_2074	-	GTGACCTATGCACCAGACGTTTATTGAAAACCAAAACAAAAGACTAGTCAGTAACCTTTAGAGATCGGAAGAGCGGTTTCAG
chr1	186645549	186645588	PTGS2_2075	-	GTGACCTATGCACCAGACGTAATGATTATATAAAACCCTCTCCCAAGGGAAAAATTAGAGATCGGAAGAGCGGTTTCAG
chr1	186645915	186645954	PTGS2_2076	-	GTGACCTATGCACCAGACGTTTATGACTTAAAGACTTAGTTATACCCTTATACCATAACCATAAGATCGGAAGAGCGGTTTCAG
chr1	186646731	186646770	PTGS2_2077	-	GTGACCTATGCACCAGACGTGTTAATATCTTAGAGTTAGTAAATATAACCAATCATAGAGATCGGAAGAGCGGTTTCAG
chr1	186647343	186647382	PTGS2_2078	-	GTGACCTATGCACCAGACGTAGAATCCATTAGAGATGTATTAATAAGACGGGCTGCAAGATCGGAAGAGCGGTTTCAG
chr1	186648140	186648179	PTGS2_2079	-	GTGACCTATGCACCAGACGTGTGTCTTTCTAAGGTTTTAGCCTTCTCAAAGAAAAATATAGATCGGAAGAGCGGTTTCAG
chr1	186648404	186648443	PTGS2_2080	-	GTGACCTATGCACCAGACGTCTTTGGTTGCCTCATTAGGAGTGGGGCTGGATACAGTTAAGATCGGAAGAGCGGTTTCAG
chr1	186649321	186649360	PTGS2_2081	-	GTGACCTATGCACCAGACGTGGCGCCGCGCACCGGGACTCCGGTCCACGACCCGGGCAGATCGGAAGAGCGGTTTCAG
chr1	154936229	154936268	SHC1_2082	-	GTGACCTATGCACCAGACGTGCTCTCTCCAGAGATGCCCTCCAATCTTTCCACCTAGATCGGAAGAGCGGTTTCAG
chr1	154937969	154938008	SHC1_2083	-	GTGACCTATGCACCAGACGTGAGAGGTGTGGGTGAGGGGTGGCAAAAAGGAAGGTACAGTAGATCGGAAGAGCGGTTTCAG
chr1	154938372	154938411	SHC1_2084	-	GTGACCTATGCACCAGACGTGCTCTCTCTCTCTGTCATCCCCACCTTTCTACTTGGTTTCAGATCGGAAGAGCGGTTTCAG
chr1	154938588	154938627	SHC1_2085	-	GTGACCTATGCACCAGACGTAGCCGAGATAGGCAGAGCTGGGGAGTGTGGAGGCAGGGCAGATCGGAAGAGCGGTTTCAG
chr1	154938745	154938784	SHC1_2086	-	GTGACCTATGCACCAGACGTTGGATGGAGGCGGGCTGGGGCTAGGTTGGAGTGGTTGGTAGATCGGAAGAGCGGTTTCAG
chr1	154940097	154940136	SHC1_2087	-	GTGACCTATGCACCAGACGTGGGGAGAGTGGGAGGCTCTTGATTAGGATTAGGAAAAAGATCGGAAGAGCGGTTTCAG
chr1	154940406	154940445	SHC1_2088	-	GTGACCTATGCACCAGACGTGGGGGACACTGGGTGGCTGGCTGTTTGGAGAGGTGAAGATCGGAAGAGCGGTTTCAG

chr1	154940630	154940669	SHC1_2089	-	GTGACCTATGCACCAGACGTGAACAGAGCAAAGGCGGTGGGAGAAGAGCAAGGGGCTAGGAGATCGGAAGAGCGGTTTCAG
chr1	154940921	154940960	SHC1_2090	-	GTGACCTATGCACCAGACGTGTGGGCAGACGACCAGAAACTGATGGGGTCTAAGGAGATCGGAAGAGCGGTTTCAG
chr1	154941197	154941236	SHC1_2091	-	GTGACCTATGCACCAGACGTTCCTTGGGGATAGGGATGCTGCTGGGAAATGTGGAGGGGCAGATCGGAAGAGCGGTTTCAG
chr1	154941804	154941843	SHC1_2092	-	GTGACCTATGCACCAGACGTAGGGAGTGGATTGTGGGAGTCTGGGATTAGTGAGGCCATAGATCGGAAGAGCGGTTTCAG
chr1	154942458	154942497	SHC1_2093	-	GTGACCTATGCACCAGACGTATCCTCCTCTCCATTCCCCCGCAGACCCCTCCAGTTCTAAGATCGGAAGAGCGGTTTCAG
chr2	1418131	1418170	TPO_2094	-	GTGACCTATGCACCAGACGTACGGAAGGAGACAGATGTAATCAAGCACTGACAAGGCAGATCGGAAGAGCGGTTTCAG
chr2	1426767	1426806	TPO_2095	-	GTGACCTATGCACCAGACGTGAATGTCCACACAGTCAAAGCGCAATGACAGTTACAGGATTAGATCGGAAGAGCGGTTTCAG
chr2	1437160	1437199	TPO_2096	-	GTGACCTATGCACCAGACGTAAAGAAGATATAAAATAGATTATTTGTCTATGTTATCTTAGATCGGAAGAGCGGTTTCAG
chr2	1439974	1440013	TPO_2097	-	GTGACCTATGCACCAGACGTTAGGAAACCATGAATCTGTGCTTGTAAACCACAAATCCACAGATCGGAAGAGCGGTTTCAG
chr2	1457416	1457455	TPO_2098	-	GTGACCTATGCACCAGACGTAAATGCAAGGATGTGTTTGAGATGGGGGAGAAGAACACAGAGATCGGAAGAGCGGTTTCAG
chr2	1459798	1459837	TPO_2099	-	GTGACCTATGCACCAGACGTAGAGACCATTGGTCAGGACATAGGAGGACCCCTGTGGTAGCAGATCGGAAGAGCGGTTTCAG
chr2	1480808	1480847	TPO_2100	-	GTGACCTATGCACCAGACGTAGGGGAGTTCAAGTCAACCCAGGGCCCCCGTGCACCTTTAGATCGGAAGAGCGGTTTCAG
chr2	1488318	1488357	TPO_2101	-	GTGACCTATGCACCAGACGTAGGAAAAGCATCTCAGTAGGGCCAGGATACCAGAGGAGAGATCGGAAGAGCGGTTTCAG
chr2	1491543	1491582	TPO_2102	-	GTGACCTATGCACCAGACGTCCATGCACAAGGCAAGGACAGCTCTTGGCTCAGTTCTAGAAGATCGGAAGAGCGGTTTCAG
chr2	1497524	1497563	TPO_2103	-	GTGACCTATGCACCAGACGTGAGAGGCTGCAGGGTTTCTCTCACAGAACTGAATTTTGTAGATCGGAAGAGCGGTTTCAG
chr2	1499711	1499750	TPO_2104	-	GTGACCTATGCACCAGACGTGGAGACAGTGAAGTAAAGTCAAGTGCATGGAGAACCCTCAAGATCGGAAGAGCGGTTTCAG
chr2	1500317	1500356	TPO_2105	-	GTGACCTATGCACCAGACGTTGGCAGCGTTGACATGTAGTCAAATACGAGAAAAAGAAAAGATCGGAAGAGCGGTTTCAG
chr2	1507670	1507709	TPO_2106	-	GTGACCTATGCACCAGACGTGCAAGGCCACACAGCTGAGAGGAAGCGGCTGCACCCCAAGATCGGAAGAGCGGTTTCAG
chr2	1520605	1520644	TPO_2107	-	GTGACCTATGCACCAGACGTGAAAAGAGCCCTGGTTAGAAGAACCCTCCAGGGCCTGGGCAAGATCGGAAGAGCGGTTTCAG
chr2	1544316	1544355	TPO_2108	-	GTGACCTATGCACCAGACGTACGTGTCAGTTATCGGGAGAGGGTCCGGCACCGTGACTAGATCGGAAGAGCGGTTTCAG
chr2	1546143	1546182	TPO_2109	-	GTGACCTATGCACCAGACGTGCAGAAACAACATTAATAACGTCTGAATCTGACTGCTCCAGATCGGAAGAGCGGTTTCAG
chr2	1481067	1481106	TPO_2110	-	GTGACCTATGCACCAGACGTGAGGCGCGCTGGACGCGGAGCAGCCCTCCGGCACTGGTCAGATCGGAAGAGCGGTTTCAG
chr9	100437671	100437710	XPA_2111	-	GTGACCTATGCACCAGACGTGAGTGCCTGTTTATAGAAATTTATATTTAAATAAAGGAAGATCGGAAGAGCGGTTTCAG
chr9	100447155	100447194	XPA_2112	-	GTGACCTATGCACCAGACGTACATTTTATATGCTGAAGGATGTGTTTACCATTGCAAGATCGGAAGAGCGGTTTCAG
chr9	100449328	100449367	XPA_2113	-	GTGACCTATGCACCAGACGTAGTTGTATTTATTTTACTCTGGTAAATCTTAATAAGATCGGAAGAGCGGTTTCAG
chr9	100451766	100451805	XPA_2114	-	GTGACCTATGCACCAGACGTTAGATGGTGTCTTAATTGCTAATGTTTATGTAGGTTTATAGATCGGAAGAGCGGTTTCAG
chr9	100455881	100455920	XPA_2115	-	GTGACCTATGCACCAGACGTTTTTCCAAAAATAAGTATCTAGATTGGTTATTTTGTAGTAAAGATCGGAAGAGCGGTTTCAG
chr9	100459353	100459392	XPA_2116	-	GTGACCTATGCACCAGACGTGCTCCGCGCTTCCCTTCCCTCTCCCGCCTCCCGGTCAGATCGGAAGAGCGGTTTCAG
chr3	14187391	14187430	XPC_2117	-	GTGACCTATGCACCAGACGTACTAGAGGGCACCACCACTGCTGCTGCCCACTACAAGATCGGAAGAGCGGTTTCAG
chr3	14188740	14188779	XPC_2118	-	GTGACCTATGCACCAGACGTGTTTGCAGAGAAGCAAGCTCAGGGTCAAGTTCTTGAGATCGGAAGAGCGGTTTCAG
chr3	14189358	14189397	XPC_2119	-	GTGACCTATGCACCAGACGTATGACAGGACTGAGGGACAGCAGAAGCGGGAAGCAACACTCAGATCGGAAGAGCGGTTTCAG
chr3	14190012	14190051	XPC_2120	-	GTGACCTATGCACCAGACGTGGCCTTCGATGGAGGCTAAACACAGGGATGGGGAGGGGTGAGATCGGAAGAGCGGTTTCAG
chr3	14190264	14190303	XPC_2121	-	GTGACCTATGCACCAGACGTATCAGAAAGGGCTCAGGACCAGGCCCTGTTCCCTGCAGATCGGAAGAGCGGTTTCAG
chr3	14193785	14193824	XPC_2122	-	GTGACCTATGCACCAGACGTCTGGGGGCTCCCTGTGGGAGTGGTGACACAGGCCCTGTAGATCGGAAGAGCGGTTTCAG
chr3	14197785	14197824	XPC_2123	-	GTGACCTATGCACCAGACGTGACGCTGGTTGGCTCAGGGGCTTCTGATGGCATGGATAGATCGGAAGAGCGGTTTCAG
chr3	14201191	14201230	XPC_2124	-	GTGACCTATGCACCAGACGTGAGGGCTGCCAGAGAAGAGGAGCAATTGACAGGAAATTTAGATCGGAAGAGCGGTTTCAG
chr3	14206263	14206302	XPC_2125	-	GTGACCTATGCACCAGACGTCTCCCGGATCACTGTTTTTATCAGTACTGTTAACTAATGAGATCGGAAGAGCGGTTTCAG
chr3	14206878	14206917	XPC_2126	-	GTGACCTATGCACCAGACGTCCGCTGTCTGCTGCAGAGCTGGGGAGTGTAGGATTTGTGTTAGATCGGAAGAGCGGTTTCAG
chr3	14208619	14208658	XPC_2127	-	GTGACCTATGCACCAGACGTGGAATGATGGGGAAGGACTTTTCTTGTGCGGTGCAAGAGAGATCGGAAGAGCGGTTTCAG
chr3	14209707	14209746	XPC_2128	-	GTGACCTATGCACCAGACGTGCCCTTGCCTTAGGCTCCTGTACATGCAGTAGGCAACAAGATCGGAAGAGCGGTTTCAG
chr3	14211888	14211927	XPC_2129	-	GTGACCTATGCACCAGACGTTTTCTTTCTTTTCCAGAACTGTTTGGTCTGTTTTGTTTTTGTAGATCGGAAGAGCGGTTTCAG
chr3	14211895	14211934	XPC_2130	-	GTGACCTATGCACCAGACGTAAACATCTTTCTTTGTTTTCCAGAACTGTTTGGTCTGTTTGTAGATCGGAAGAGCGGTTTCAG
chr3	14214317	14214356	XPC_2131	-	GTGACCTATGCACCAGACGTTGCAAAAGCTTGTCTCGGGTCTTGATTTTTCTCATCAGAGAGATCGGAAGAGCGGTTTCAG
chr3	14219916	14219955	XPC_2132	-	GTGACCTATGCACCAGACGTGGCCAGCGGGCTTCGCGGGAGACGCCCGGTTGGGCGGAAGATCGGAAGAGCGGTTTCAG
chr3	14199902	14199941	XPC_2133	-	GTGACCTATGCACCAGACGTAGATGGCTCCAGGACCCATCGGGAGCCATCGTAAGGAAGATCGGAAGAGCGGTTTCAG
chr6	69348518	69348557	BAI3_2134	-	GTGACCTATGCACCAGACGTTTGGCTGTAAAATGGCAATGAAAGTAAATGCAAGTAGAGATCGGAAGAGCGGTTTCAG
chr6	69640401	69640440	BAI3_2135	-	GTGACCTATGCACCAGACGTAATAAAGGTATATGAAAGCTTGTGTGTAGACATTTCTCACAGATCGGAAGAGCGGTTTCAG
chr6	69646361	69646400	BAI3_2136	-	GTGACCTATGCACCAGACGTGACAACAATAAACATGAAACTGTCTTAAGTATTATCATCAGATCGGAAGAGCGGTTTCAG
chr6	69653672	69653711	BAI3_2137	-	GTGACCTATGCACCAGACGTGCAAAAGAAGCTTCAACAACAAAACAGAGCAGTAAATCAAGATCGGAAGAGCGGTTTCAG
chr6	69665866	69665905	BAI3_2138	-	GTGACCTATGCACCAGACGTAGAAAAAGAGACAGCATGAGGATATCTTCCAATAGGACAAAGATCGGAAGAGCGGTTTCAG
chr6	69666487	69666526	BAI3_2139	-	GTGACCTATGCACCAGACGTTGTTCTGATGTCATGTCACTATCCACACACTCCTTAGATCGGAAGAGCGGTTTCAG
chr6	69684605	69684644	BAI3_2140	-	GTGACCTATGCACCAGACGTAACAAGGGACCTGAAATGTGACGTAGTGTGTTTTAAAAAATTTAGATCGGAAGAGCGGTTTCAG
chr6	69685076	69685115	BAI3_2141	-	GTGACCTATGCACCAGACGTCAAAGAACAGAGAGAAGCTTTATAATAGGGATGTTTGAAGAGATCGGAAGAGCGGTTTCAG
chr6	69703610	69703649	BAI3_2142	-	GTGACCTATGCACCAGACGTCAAAGAACAGAGCAAACATCAGAATCTTCTTACCATTAGATCGGAAGAGCGGTTTCAG
chr6	69723880	69723919	BAI3_2143	-	GTGACCTATGCACCAGACGTAATTAGATAAAAGATTAAATATACATGAGAGAATTATACAGATCGGAAGAGCGGTTTCAG
chr6	69728233	69728272	BAI3_2144	-	GTGACCTATGCACCAGACGTAAGCAAAGTTAGAAGGAATAAAAAATCTATACATAAATAGATCGGAAGAGCGGTTTCAG
chr6	69758027	69758066	BAI3_2145	-	GTGACCTATGCACCAGACGTTAAATTTGAAGTATTGACAAACAGCAAGAAAATACTATGAGATCGGAAGAGCGGTTTCAG
chr6	69759113	69759152	BAI3_2146	-	GTGACCTATGCACCAGACGTTAAATTTGAAGTATTGACAAACAGCAAGAAAATACTATGAGATCGGAAGAGCGGTTTCAG

chr6	69772776	69772815	BAI3_2147	-	GTGACCTATGCACCAGACGTGTAATTATAATTAAGGAGAAATGAGTGCTGAAAAGTATAGATCGGAAGAGCGGTTTCAG
chr6	69785837	69785876	BAI3_2148	-	GTGACCTATGCACCAGACGTAGCAGAGAAAGAATGCATATATCTTGAGTACATATATAAAAAGATCGGAAGAGCGGTTTCAG
chr6	69943132	69943171	BAI3_2149	-	GTGACCTATGCACCAGACGTGAGTGAGGGGGGAGGAAATCGGGATAAATACGCCTGATAGAGATCGGAAGAGCGGTTTCAG
chr6	69944874	69944913	BAI3_2150	-	GTGACCTATGCACCAGACGTAAACAAAAACAAAAAGAAACAAATTGGTTTTTAATAAATTAAGATCGGAAGAGCGGTTTCAG
chr6	69948966	69949005	BAI3_2151	-	GTGACCTATGCACCAGACGTAGAGAAAAGTTACCCAACCTTTAAAAATCCAACAGAAAGATGAGATCGGAAGAGCGGTTTCAG
chr6	70034714	70034753	BAI3_2152	-	GTGACCTATGCACCAGACGTAAACAAAAACAAAAAGACTCACACTGAACCTGGGAGAGGGAAAAGATCGGAAGAGCGGTTTCAG
chr6	70037662	70037701	BAI3_2153	-	GTGACCTATGCACCAGACGTAGCAATGTACGCATCATATTAGCTATAACCACACTATGCAGATCGGAAGAGCGGTTTCAG
chr6	70040348	70040387	BAI3_2154	-	GTGACCTATGCACCAGACGTATTAGATAAGAACAACAAAAATTAAGTGACAAGTATTAGAGATCGGAAGAGCGGTTTCAG
chr6	70042765	70042804	BAI3_2155	-	GTGACCTATGCACCAGACGTGAAACAAAGTTGACCTTTCAATGATATTGAAGGGAATCAGAGATCGGAAGAGCGGTTTCAG
chr6	70048758	70048797	BAI3_2156	-	GTGACCTATGCACCAGACGTACAGAACACCCACAAAAAGAACAAAAATTTGAATTTGCACAGATCGGAAGAGCGGTTTCAG
chr6	70049175	70049214	BAI3_2157	-	GTGACCTATGCACCAGACGTCAAGAAAAGTAACATTACGTAGCTATACATCACACCCCAGGAGATCGGAAGAGCGGTTTCAG
chr6	70064075	70064114	BAI3_2158	-	GTGACCTATGCACCAGACGTGGGGAACACATTAATTTCTTCTCTCTTAATAATGACAAGAGATCGGAAGAGCGGTTTCAG
chr6	70065663	70065702	BAI3_2159	-	GTGACCTATGCACCAGACGTAAATAATAAGACATAGAACCCATCATTTAATTGAAGACCTCAAGATCGGAAGAGCGGTTTCAG
chr6	70070711	70070750	BAI3_2160	-	GTGACCTATGCACCAGACGTGAATGTAAGGTTGAAGAAAGAGAGTTAATGTGTGTTTATTAGATCGGAAGAGCGGTTTCAG
chr6	70082248	70082287	BAI3_2161	-	GTGACCTATGCACCAGACGTTATTTTTAAAAAGAAAGGAGAAAAACCAATAAAGTTATGTTAGATCGGAAGAGCGGTTTCAG
chr6	70092673	70092712	BAI3_2162	-	GTGACCTATGCACCAGACGTGAACAAGATAGCTCTCATCCCCAACCTTGATGTATGTTTTAGATCGGAAGAGCGGTTTCAG
chr6	70098545	70098584	BAI3_2163	-	GTGACCTATGCACCAGACGTGAGAGGAAAGAGAGTCAATTTGTGATGACCAGGATCACAGATCGGAAGAGCGGTTTCAG
chr6	69348896	69348935	BAI3_2164	-	GTGACCTATGCACCAGACGTGAGCTGTAGAAAACGAAAGACTTCTTGAATTGCAGAGTTAGATCGGAAGAGCGGTTTCAG
chr6	70071033	70071072	BAI3_2165	-	GTGACCTATGCACCAGACGTTTTCTTTCTTGAGGATGGACTATGTCATGTCAGCCCCCTAGATCGGAAGAGCGGTTTCAG
chr2	215593350	215593389	BARD1_2166	-	GTGACCTATGCACCAGACGTAGATGAACATTTCAAATTTGAATTTGCACGGTTTGTGAGAGAGATCGGAAGAGCGGTTTCAG
chr2	215595085	215595124	BARD1_2167	-	GTGACCTATGCACCAGACGTTTTAATACAACCTTTCAATTTCTTCTTATTATGACATACTATTAGATCGGAAGAGCGGTTTCAG
chr2	215609741	215609780	BARD1_2168	-	GTGACCTATGCACCAGACGTGATTTGAGAGAAATTAAGAAATGAATTAGACTAGTTTTGTTAGATCGGAAGAGCGGTTTCAG
chr2	215610396	215610435	BARD1_2169	-	GTGACCTATGCACCAGACGTGAATTTTGGGAGGTGGGCTGAGAAAATGTTAAATAGATAGATCGGAAGAGCGGTTTCAG
chr2	215632156	215632195	BARD1_2170	-	GTGACCTATGCACCAGACGTCAACGTAATAATTTTTAAAAATGGACCTATATTCTTGAAGATCGGAAGAGCGGTTTCAG
chr2	215633906	215633945	BARD1_2171	-	GTGACCTATGCACCAGACGTGTTTTTATTCTCATTCTTTCTGTGTTTTACAGTCTTATAGATCGGAAGAGCGGTTTCAG
chr2	215645234	215645273	BARD1_2172	-	GTGACCTATGCACCAGACGTTACTCTGAAATACCATCTCAGAATGAGGCCAACTATAAAGAGATCGGAAGAGCGGTTTCAG
chr2	215656971	215657010	BARD1_2173	-	GTGACCTATGCACCAGACGTTCCCTATCTCTTCTAGTTAAATTCATAGTTAAAAACTGAAGATCGGAAGAGCGGTTTCAG
chr2	215661735	215661774	BARD1_2174	-	GTGACCTATGCACCAGACGTACGGTTTGATGTATATAGTACAACCTGATTTTTTACTAGAAGATCGGAAGAGCGGTTTCAG
chr2	215674086	215674125	BARD1_2175	-	GTGACCTATGCACCAGACGTAGCTTCTTGGGGTGCTGCGAGGGCACGGGTCGCACAGTAGATCGGAAGAGCGGTTTCAG
chr2	215645709	215645748	BARD1_2176	-	GTGACCTATGCACCAGACGTGAGCAAAATAGAGTCTCCAGACACTAAGACAGGAATGAAGAGATCGGAAGAGCGGTTTCAG
chr18	60795808	60795847	BCL2_2177	-	GTGACCTATGCACCAGACGTCTGCCCAAACAATATGCAAAAGGTTCACTAAAGCAGTAGATCGGAAGAGCGGTTTCAG
chr18	60985232	60985271	BCL2_2178	-	GTGACCTATGCACCAGACGTCCGAGATGCGGGGGTGGAGTGCGGGTGGGCTCCTGGGGCAGATCGGAAGAGCGGTTTCAG
chr18	60985265	60985304	BCL2_2179	-	GTGACCTATGCACCAGACGTTTGGTGATGTGAGTCTGGGCTGAGGCCACAGGTCAGATAGATCGGAAGAGCGGTTTCAG
chr18	60985541	60985580	BCL2_2180	-	GTGACCTATGCACCAGACGTGTACCCTCCGACCTTCCGCGAGATGTCAGCCAGTCAAGATCGGAAGAGCGGTTTCAG
chr18	60985557	60985596	BCL2_2181	-	GTGACCTATGCACCAGACGTGACGACTTCTCCCGCTTCCGCGCAGCTTCCGCGAGACTTCCGCGAGAAAGATCGGAAGAGCGGTTTCAG
chr19	11015577	11015616	CARM1_2182	-	GTGACCTATGCACCAGACGTAGACAGGCTGGCGTGAGCGGTGCAGCCCTGTCAGCTGCCTAGATCGGAAGAGCGGTTTCAG
chr19	11018665	11018704	CARM1_2183	-	GTGACCTATGCACCAGACGTGAAGCCAAGTACCCTGGGGGGCGGTGAGCAACCCAGCATGTAGATCGGAAGAGCGGTTTCAG
chr19	11019729	11019768	CARM1_2184	-	GTGACCTATGCACCAGACGTGACATACCGATGGCACGGGGCACATGGTGGCACGAGGCAGAGATCGGAAGAGCGGTTTCAG
chr19	11022810	11022849	CARM1_2185	-	GTGACCTATGCACCAGACGTAGTGGGAGGTGAGAGCGAGACATAGGAGGCGACGGTGATGAGATCGGAAGAGCGGTTTCAG
chr19	11024503	11024542	CARM1_2186	-	GTGACCTATGCACCAGACGTGCAGGGCCATGTGGCTTCCCTGCGTCTTCCATGCCATGGAGATCGGAAGAGCGGTTTCAG
chr19	11027033	11027072	CARM1_2187	-	GTGACCTATGCACCAGACGTGGCAGGAGGGTGGCTGGCGTGACACATCCACACAGATCGGAAGAGCGGTTTCAG
chr19	11027322	11027361	CARM1_2188	-	GTGACCTATGCACCAGACGTGCCCCACCCCCACAGCAAGGTCAGGGCTGCAGAAGAGGCAAGATCGGAAGAGCGGTTTCAG
chr19	11030221	11030260	CARM1_2189	-	GTGACCTATGCACCAGACGTCCACAGGTGTGACGTGGCATCTGACGCCAGGGCCAGCATGAGATCGGAAGAGCGGTTTCAG
chr19	11030503	11030542	CARM1_2190	-	GTGACCTATGCACCAGACGTAAGGGCAGTGGCTGCTGGGGAAGCCAGACAGGCGCTGCCGAGATCGGAAGAGCGGTTTCAG
chr19	11031062	11031101	CARM1_2191	-	GTGACCTATGCACCAGACGTGGGACAGGCACATCTTACTGGCCGGCGCCACCCTGGAGATCGGAAGAGCGGTTTCAG
chr19	11031285	11031324	CARM1_2192	-	GTGACCTATGCACCAGACGTGGTGACGGCCGTGGCATGAGCTGCTGGCAGCTGCTGGCAGATGGACCCAGATCGGAAGAGCGGTTTCAG
chr19	11031460	11031499	CARM1_2193	-	GTGACCTATGCACCAGACGTGACAGAGCCATGGGCAGGGGCAAGGGGTTGCAGGGCCGGAGATCGGAAGAGCGGTTTCAG
chr19	11031676	11031715	CARM1_2194	-	GTGACCTATGCACCAGACGTAGAGGGAGACGTGAGGGCTGGAGGCAGAGGGGCCAGGCTAGATCGGAAGAGCGGTTTCAG
chr19	11032001	11032040	CARM1_2195	-	GTGACCTATGCACCAGACGTAGAGGGAGGAAAGAAGGAAGGGAGACGGCGTCAACC GCCCAGATCGGAAGAGCGGTTTCAG
chr19	11032241	11032280	CARM1_2196	-	GTGACCTATGCACCAGACGTGGCAATGGCAGTGAGGGGCTGCCCTGGCCCCGCCAGCCAGATCGGAAGAGCGGTTTCAG
chr12	56360743	56360782	CDK2_2197	-	GTGACCTATGCACCAGACGTGAGTGGGTGACGGCCCTGGAGCGGGGCTGGGAAAGATCGGAAGAGCGGTTTCAG
chr12	56361591	56361630	CDK2_2198	-	GTGACCTATGCACCAGACGTTTGGGAAAGCAGATGGAAATGAGTTACAAATATCTTAGATCGGAAGAGCGGTTTCAG
chr12	56361783	56361822	CDK2_2199	-	GTGACCTATGCACCAGACGTAAAGTTTGGGAAATGGAGGTGTGTGAGAGAGAGAAATGCAGATCGGAAGAGCGGTTTCAG
chr12	56362512	56362551	CDK2_2200	-	GTGACCTATGCACCAGACGTAGAAAGAGAGGACTGTGTTTCTCCATTACAGTGAGCAGACAGATCGGAAGAGCGGTTTCAG
chr12	56363209	56363248	CDK2_2201	-	GTGACCTATGCACCAGACGTGGAATAGGGAGGGGCGGGGTGGTTTATAGGGTATGGAATAGATCGGAAGAGCGGTTTCAG
chr12	56364778	56364817	CDK2_2202	-	GTGACCTATGCACCAGACGTGGAAGAGGAAATACCAAGACCACGTTGACGTGAGTCAAGATCGGAAGAGCGGTTTCAG
chr12	56365255	56365294	CDK2_2203	-	GTGACCTATGCACCAGACGTAGATGCTGTTGACTTCAATGATGTATAGTGGACTAAATAGATCGGAAGAGCGGTTTCAG
chr22	47082981	47083020	CERK_2204	-	GTGACCTATGCACCAGACGTTCTCTCACAAAACCTGGGAAAGTGTGAAAACATTTAAGAAGATCGGAAGAGCGGTTTCAG

chr22	47085839	47085878	CERK_2205	-	GTGACCTATGCACCAGACGTGGGTCCTCCAGCCACCAGCGCCATCCCCTTGAGCCCTGAGAGATCGGAAGAGCGGTTTCAG
chr22	47087419	47087458	CERK_2206	-	GTGACCTATGCACCAGACGTGCTCTTGCATGGAGCCTCCACTGCGGAGTAATTTATGTTAGATCGGAAGAGCGGTTTCAG
chr22	47089274	47089313	CERK_2207	-	GTGACCTATGCACCAGACGTAAACACAGGCTCAGTGTGTCCTGTTGTGCTGGAGTGCAGATCGGAAGAGCGGTTTCAG
chr22	47091057	47091096	CERK_2208	-	GTGACCTATGCACCAGACGTGCTTTGTGTGTTCTCTTGCAAATGACGGGAAATGAAAGCAGATCGGAAGAGCGGTTTCAG
chr22	47095160	47095199	CERK_2209	-	GTGACCTATGCACCAGACGTATAATGCAGACTCGCTCCCGCTGGTCTGTCGCCCGACTGCAGATCGGAAGAGCGGTTTCAG
chr22	47097483	47097522	CERK_2210	-	GTGACCTATGCACCAGACGTCTCTGCGCATGCGCAGCGTGGCAGCCGCGGCTCCTGCGCAGATCGGAAGAGCGGTTTCAG
chr22	47103690	47103729	CERK_2211	-	GTGACCTATGCACCAGACGTGGCCTGGCCTGCTCTGTTCTCTGTTCCCGTCTTAGGAAGATCGGAAGAGCGGTTTCAG
chr22	47106933	47106972	CERK_2212	-	GTGACCTATGCACCAGACGTGCTCTTTTCATCGCCATCAAGTCCATTGTTAATGAAAAAGTAGATCGGAAGAGCGGTTTCAG
chr22	47108015	47108054	CERK_2213	-	GTGACCTATGCACCAGACGTCTATGTTAATATGTAGAAGTAAGTTTGAAGATGATCAAAGATCGGAAGAGCGGTTTCAG
chr22	47115933	47115972	CERK_2214	-	GTGACCTATGCACCAGACGTGTTTGGACTGAGAGACAGGATGGCCGTGGTGGCATGCCAAGATCGGAAGAGCGGTTTCAG
chr22	47116749	47116788	CERK_2215	-	GTGACCTATGCACCAGACGTAAATGTCTTCTCCACATTCTTCAATTTCTATGTAGAAGATCGGAAGAGCGGTTTCAG
chr11	46354776	46354815	DGKZ_2216	-	GTGACCTATGCACCAGACGTCTTCCGCCCGCGCTCCTGCGCCCTTTCGGCCACCCGCTAGATCGGAAGAGCGGTTTCAG
chr11	46367027	46367066	DGKZ_2217	-	GTGACCTATGCACCAGACGTGACCCCGGCCCTCCCCTTCTCCGTCGCCAGCGCTCCAAGATCGGAAGAGCGGTTTCAG
chr11	46387757	46387796	DGKZ_2218	-	GTGACCTATGCACCAGACGTTGGCTGTTGGGCACAGAGACCAGGAGCATCAGGAGCTGGAAGATCGGAAGAGCGGTTTCAG
chr11	46388791	46388830	DGKZ_2219	-	GTGACCTATGCACCAGACGTGAAGACAGCTGAGGAGGGGCTGAGCATTGCTGACCCTAAGATCGGAAGAGCGGTTTCAG
chr11	46389152	46389191	DGKZ_2220	-	GTGACCTATGCACCAGACGTGATGGGCTTGTCTCAGCACAGCTGGCCGCCACGCCCTCCAGATCGGAAGAGCGGTTTCAG
chr11	46389502	46389541	DGKZ_2221	-	GTGACCTATGCACCAGACGTGGAAGAGAGGGCCCTGAGGCCAGCTAAGTCTATCTCGAGATCGGAAGAGCGGTTTCAG
chr11	46389505	46389544	DGKZ_2222	-	GTGACCTATGCACCAGACGTACAGGAAGAGAGGGCCCTGAGGCAGCTAAGTCTATCAGATCGGAAGAGCGGTTTCAG
chr11	46390994	46391033	DGKZ_2223	-	GTGACCTATGCACCAGACGTTGGCAGTGACCACCAAAATGTCAGAACCTCCCTTCGGGTGATCGGAAGAGCGGTTTCAG
chr11	46391441	46391480	DGKZ_2224	-	GTGACCTATGCACCAGACGTAGGGGAAAAATTTCACTGGGTGAGGGGTGGGCAGGGGCACAGATCGGAAGAGCGGTTTCAG
chr11	46392813	46392852	DGKZ_2225	-	GTGACCTATGCACCAGACGTACAGGATGATGGGAACCAGGCAGGCTGGAGCAGCAGAAAGATCGGAAGAGCGGTTTCAG
chr11	46392987	46393026	DGKZ_2226	-	GTGACCTATGCACCAGACGTGAGGGGCCGGGCTCAGCGGGACCGTGTTCAGACTCGGGGAGATCGGAAGAGCGGTTTCAG
chr11	46393204	46393243	DGKZ_2227	-	GTGACCTATGCACCAGACGTAGCAGGGGTGTTGGTGACGAGGTGGCAGGCTGGGTAGCAGATCGGAAGAGCGGTTTCAG
chr11	46393575	46393614	DGKZ_2228	-	GTGACCTATGCACCAGACGTAGGTGAGAGGCTGTAAGCTCTCCGTCACAGCACCTTAGATCGGAAGAGCGGTTTCAG
chr11	46393928	46393967	DGKZ_2229	-	GTGACCTATGCACCAGACGTTGGGGAGCCAAGAGACAGTCAGGCAGTGGTGGGACGAAGTAGATCGGAAGAGCGGTTTCAG
chr11	46394117	46394156	DGKZ_2230	-	GTGACCTATGCACCAGACGTGGGAAGATGGCAGTGGGGTCAGGGGATGTGTGCTGTACCCAGATCGGAAGAGCGGTTTCAG
chr11	46394271	46394310	DGKZ_2231	-	GTGACCTATGCACCAGACGTAAAGAACAGAGGCAATCAGGCCACAGGGACCCCGGTTTCAGATCGGAAGAGCGGTTTCAG
chr11	46394461	46394500	DGKZ_2232	-	GTGACCTATGCACCAGACGTAGGAGGGACTGAGCCCTCTGTGGTGGAGAGGCCCCAGCAGATCGGAAGAGCGGTTTCAG
chr11	46395657	46395696	DGKZ_2233	-	GTGACCTATGCACCAGACGTGTCAAGGGACCAAAATGAGGCTGGCCCTCACAAATGTCAGATCGGAAGAGCGGTTTCAG
chr11	46395899	46395938	DGKZ_2234	-	GTGACCTATGCACCAGACGTACAAAGCAGTGGGGGCCAGTGAGTACCCACAGCCTGCCACAGATCGGAAGAGCGGTTTCAG
chr11	46396104	46396143	DGKZ_2235	-	GTGACCTATGCACCAGACGTACAGAGGGCGTACCATCTGCTGACAGAGATCTTCTCACAGATCGGAAGAGCGGTTTCAG
chr11	46396266	46396305	DGKZ_2236	-	GTGACCTATGCACCAGACGTGCGGGGAGGGTGTGAGGTGCATGTGCCAGGTGGCCTCCGAGATCGGAAGAGCGGTTTCAG
chr11	46396434	46396473	DGKZ_2237	-	GTGACCTATGCACCAGACGTGGGCGATGACATGGGCTCAAACACAGTCTCTGCAGGACAGATCGGAAGAGCGGTTTCAG
chr11	46396932	46396971	DGKZ_2238	-	GTGACCTATGCACCAGACGTAGGAAGCTGGGTGATGTCAGTGGCAGGCTGGGGGAGGATCGGAAGAGCGGTTTCAG
chr11	46397351	46397390	DGKZ_2239	-	GTGACCTATGCACCAGACGTGGGCCGGAAGCGGGGCTCAGCAAGGGCCCTGCCTTGGTAGATCGGAAGAGCGGTTTCAG
chr11	46397566	46397605	DGKZ_2240	-	GTGACCTATGCACCAGACGTGAGCACCTGTGACGAGCTGGCTGACCCACAGCCCTGCCAGATCGGAAGAGCGGTTTCAG
chr11	46397828	46397867	DGKZ_2241	-	GTGACCTATGCACCAGACGTAAAGCAAAGGCCAGGCTGGGATAGAGTGGGGGCCAGGGAGGATCGGAAGAGCGGTTTCAG
chr11	46398024	46398063	DGKZ_2242	-	GTGACCTATGCACCAGACGTGAGGGCAGCTGAGGATCAGGGAGTGCCATGTCCAGGCCCAAGATCGGAAGAGCGGTTTCAG
chr11	46398573	46398612	DGKZ_2243	-	GTGACCTATGCACCAGACGTAGGTGAGGGCGGGAGGTGAGGGCACCTGACGGTGGGGGCCAGATCGGAAGAGCGGTTTCAG
chr11	46399698	46399737	DGKZ_2244	-	GTGACCTATGCACCAGACGTGCATGATGCTGTGACCGCTACGGCAGGCCAGCTGGAGATCGGAAGAGCGGTTTCAG
chr11	46399957	46399996	DGKZ_2245	-	GTGACCTATGCACCAGACGTACTGCTGTCTGCACTGCGAGTGGAGGCCCTGGGCTTGGGAGATCGGAAGAGCGGTTTCAG
chr11	46400491	46400530	DGKZ_2246	-	GTGACCTATGCACCAGACGTGAGGCATGGCAGGGCTGGACCTCCTGGGGCCACCCCTCCTAGATCGGAAGAGCGGTTTCAG
chr11	46400703	46400742	DGKZ_2247	-	GTGACCTATGCACCAGACGTGGAGGTGGTGGTCAGAGAGCCCTGGCAGCCCTCCTCCTCAGATCGGAAGAGCGGTTTCAG
chr11	46400969	46401008	DGKZ_2248	-	GTGACCTATGCACCAGACGTAGGGGCTGGCTGTGTACCCCATCCGCTCCCTGTATCCACAGATCGGAAGAGCGGTTTCAG
chr11	46401331	46401370	DGKZ_2249	-	GTGACCTATGCACCAGACGTGCGGAGCTGCGATCAGCAGGGCCAGAGGCAGGCTAACCCAGATCGGAAGAGCGGTTTCAG
chr11	46388121	46388160	DGKZ_2250	-	GTGACCTATGCACCAGACGTCTATTCTATGCCCCACAGCCCGGTCAACAGCAGGGGTGCAAGATCGGAAGAGCGGTTTCAG
chr20	32264488	32264527	E2F1_2251	-	GTGACCTATGCACCAGACGTAGGGACAGGGTTTCCAGAGATGCTCACCTTGTCTCTGCAAGATCGGAAGAGCGGTTTCAG
chr20	32264861	32264900	E2F1_2252	-	GTGACCTATGCACCAGACGTGGTAGGTGGTGGTGGGTCAGAGAGCCCTGGCAGCCCTCCTCCTCAGATCGGAAGAGCGGTTTCAG
chr20	32265957	32265996	E2F1_2253	-	GTGACCTATGCACCAGACGTATTGGCCGTAGGGTGTGGAAGGCAGGCTTAGCAGGCAGGGAGATCGGAAGAGCGGTTTCAG
chr20	32267511	32267550	E2F1_2254	-	GTGACCTATGCACCAGACGTGCCACACAGGAGGGCAGGCACACCTGCCATGCCAGCCTGAGATCGGAAGAGCGGTTTCAG
chr20	32268082	32268121	E2F1_2255	-	GTGACCTATGCACCAGACGTAGCTTGGGCTGGGCAGACCCCTGTGACCAGGCCAGTTAGATCGGAAGAGCGGTTTCAG
chr20	32273760	32273799	E2F1_2256	-	GTGACCTATGCACCAGACGTGAGGACGCCGCCGACAGCCGCGCTGTGCCCCCGCGAGATCGGAAGAGCGGTTTCAG
chr3	89156849	89156888	EPHA3_2257	-	GTGACCTATGCACCAGACGTACAGAGGGCAGTGAAGAGCAGATATCTCCATGAAGCATGCCAGATCGGAAGAGCGGTTTCAG
chr3	89176309	89176348	EPHA3_2258	-	GTGACCTATGCACCAGACGTACATAATACAAAACACAGTTAATAACAGTGAATTTTTCAGATCGGAAGAGCGGTTTCAG
chr3	89258960	89258999	EPHA3_2259	-	GTGACCTATGCACCAGACGTAAAGAGAAACAGAGAGTGAAGCAGAAATTAATGATAATAACAGATCGGAAGAGCGGTTTCAG
chr3	89390016	89390055	EPHA3_2260	-	GTGACCTATGCACCAGACGTAATGACTCTCTTTAAAAGTCTGTGATAATTTTTTGAAGAGATCGGAAGAGCGGTTTCAG
chr3	89390855	89390894	EPHA3_2261	-	GTGACCTATGCACCAGACGTGTTCAACAAGATTAATGAGTACTTCTGTTTCTCTACTAGATCGGAAGAGCGGTTTCAG
chr3	89444937	89444976	EPHA3_2262	-	GTGACCTATGCACCAGACGTAGGATGGGAGGGAAAGTGAAGCAGAAATTAATGGGTAGATCGGAAGAGCGGTTTCAG

chr3	89448418	89448457	EPHA3_2263	-	GTGACCTATGCACCAGACGTGAGAAAAAAATTCATGTAAAAATCAAATCTTCATAATGCAGATCGGAAGAGCGGTTTCAG
chr3	89456369	89456408	EPHA3_2264	-	GTGACCTATGCACCAGACGTGAAGAGAAAAAATAAGAACAGGTATTATAATCATGACTAAAGATCGGAAGAGCGGTTTCAG
chr3	89457167	89457206	EPHA3_2265	-	GTGACCTATGCACCAGACGTATCAAGGAAAGCGAACACATAAGAGGAATATATTTAAATAGATCGGAAGAGCGGTTTCAG
chr3	89462241	89462280	EPHA3_2266	-	GTGACCTATGCACCAGACGTAAAGAAAGAAAGGCGCAATTGTAGCTAGATTTGTACAACAGATCGGAAGAGCGGTTTCAG
chr3	89468305	89468344	EPHA3_2267	-	GTGACCTATGCACCAGACGTGCAGAAACAGCAACAAAATGTAAGGAATTCATAATAAAAAAGATCGGAAGAGCGGTTTCAG
chr3	89478206	89478245	EPHA3_2268	-	GTGACCTATGCACCAGACGTAGTAAATAATAATAATCAGTACAGTTCAAGTATTATAGATCGGAAGAGCGGTTTCAG
chr3	89480250	89480289	EPHA3_2269	-	GTGACCTATGCACCAGACGTTTTCAAATGTACAATTAAGATACGTTTCTATTTCCTAAAGATCGGAAGAGCGGTTTCAG
chr3	89498325	89498364	EPHA3_2270	-	GTGACCTATGCACCAGACGTAAAAATCATGTCTACATAATCAGCAATGCATAGAACATATAGATCGGAAGAGCGGTTTCAG
chr3	89499277	89499316	EPHA3_2271	-	GTGACCTATGCACCAGACGTAGCAAAGTTTTTCAGGAACCAGGAAGTTTTTCAGGAAGTGCAGATCGGAAGAGCGGTTTCAG
chr3	89521564	89521603	EPHA3_2272	-	GTGACCTATGCACCAGACGTAAAAACACCAAAGGGAGACAGATCAGGAGTCAGCAGAGTTAGATCGGAAGAGCGGTTTCAG
chr3	89528497	89528536	EPHA3_2273	-	GTGACCTATGCACCAGACGTAGAAAACAAATAAGAATCGGTTTCTCGATAGTGATAAAGATCGGAAGAGCGGTTTCAG
chr3	89259290	89259329	EPHA3_2274	-	GTGACCTATGCACCAGACGTCCAAGATCCATTTGAGTGAACCTTTTCATCAGCTGCAATGGAGATCGGAAGAGCGGTTTCAG
chr7	100318554	100318593	EPO_2275	-	GTGACCTATGCACCAGACGTGGCCGGGTCCTCAGCCAGCTGGGGCGCCCGGTTGACAGATCGGAAGAGCGGTTTCAG
chr7	100319131	100319170	EPO_2276	-	GTGACCTATGCACCAGACGTTAGCCAGGCTGAGAGTCAGGCCGGGGAGGGAGAAGGGTGGCAGATCGGAAGAGCGGTTTCAG
chr7	100319535	100319574	EPO_2277	-	GTGACCTATGCACCAGACGTCACAGCCCGGGGAGTCAAGGGTCCCTGAAGGCTCTGGCCAGATCGGAAGAGCGGTTTCAG
chr7	100320237	100320276	EPO_2278	-	GTGACCTATGCACCAGACGTTGGACTCTGGGAGTCAAGTCAACCTCTCCCTAGATCGGAAGAGCGGTTTCAG
chr7	100320551	100320590	EPO_2279	-	GTGACCTATGCACCAGACGTGAAAACAGGAGGTCGCTGCAGTGCACAGAAAGGAAGGAAAGATCGGAAGAGCGGTTTCAG
chr2	212248290	212248329	ERBB4_2280	-	GTGACCTATGCACCAGACGTGGTTTTTGGTGGAGGACACACTGCTCCAATTTCCCCAGATCGGAAGAGCGGTTTCAG
chr2	212251528	212251567	ERBB4_2281	-	GTGACCTATGCACCAGACGTATTATTTCAGAAACGATCGCCATTGCAAGTTCACCTCCATCAGATCGGAAGAGCGGTTTCAG
chr2	212252620	212252659	ERBB4_2282	-	GTGACCTATGCACCAGACGTCACAATCAACCTTCATCTTTTAGGATTTTCGGTCTTTGCTAGATCGGAAGAGCGGTTTCAG
chr2	212285116	212285155	ERBB4_2283	-	GTGACCTATGCACCAGACGTATTATATACATATCATATTCTTTCTGAGATATAAAATCAGATCGGAAGAGCGGTTTCAG
chr2	212286682	212286721	ERBB4_2284	-	GTGACCTATGCACCAGACGTTTGACTTATGCTTTTAAAGACTAGGCCAATGGCAAACCTCACAGATCGGAAGAGCGGTTTCAG
chr2	212288830	212288869	ERBB4_2285	-	GTGACCTATGCACCAGACGTAAAATATGTTTACCATCATCATCTTAGTAAAGTAAATAGATCGGAAGAGCGGTTTCAG
chr2	212293083	212293122	ERBB4_2286	-	GTGACCTATGCACCAGACGTCTTTTTCGCAATTAAGCTGTGAAAGCAAAAATACATATAGATCGGAAGAGCGGTTTCAG
chr2	212295620	212295659	ERBB4_2287	-	GTGACCTATGCACCAGACGTTTTTGGAGCAATCTTGCTTGAATAATAGTATAATATCCAGATCGGAAGAGCGGTTTCAG
chr2	212426578	212426617	ERBB4_2288	-	GTGACCTATGCACCAGACGTGCAATTTCTATGAAATACATTTTTAGGTTAATATTTAGATCGGAAGAGCGGTTTCAG
chr2	212483852	212483891	ERBB4_2289	-	GTGACCTATGCACCAGACGTACACCCAGGCAATCACATTTTTCTCCATTATCAAATAGCCAGATCGGAAGAGCGGTTTCAG
chr2	212488597	212488636	ERBB4_2290	-	GTGACCTATGCACCAGACGTAACAACCGCATATCGTTAGTTAAGTTTTGTTTTAGATGTTTAGATCGGAAGAGCGGTTTCAG
chr2	212495137	212495176	ERBB4_2291	-	GTGACCTATGCACCAGACGTTCTTCTCCTCTCATGTGTTGGGATTTTCATCAGGTTAGATCGGAAGAGCGGTTTCAG
chr2	212522429	212522468	ERBB4_2292	-	GTGACCTATGCACCAGACGTCCATGTTTCCATTTTTCTGCTTCAAATCCTTTCCAGTATAGATCGGAAGAGCGGTTTCAG
chr2	212529998	212530037	ERBB4_2293	-	GTGACCTATGCACCAGACGTTTCTGGCCAAAGGGCTCACCTGGTATGTTTATCCACATGAGATCGGAAGAGCGGTTTCAG
chr2	212537839	212537878	ERBB4_2294	-	GTGACCTATGCACCAGACGTAGACATCTGTGGTGTGTTGGCTTATTAGTATCATGTATGAGATCGGAAGAGCGGTTTCAG
chr2	212543727	212543766	ERBB4_2295	-	GTGACCTATGCACCAGACGTTTCTAGGTTGCTTCCACCTCATGAGCTTTGAAGGACTGAAGATCGGAAGAGCGGTTTCAG
chr2	212566642	212566681	ERBB4_2296	-	GTGACCTATGCACCAGACGTTACTCAGCATTTTAAACATAGAAACTTAAATTTTTCCAGATCGGAAGAGCGGTTTCAG
chr2	212568779	212568818	ERBB4_2297	-	GTGACCTATGCACCAGACGTATGTTTAAAGCTGCAAGGCTCACAGATTTCAAAGAGCAAGATCGGAAGAGCGGTTTCAG
chr2	212576725	212576764	ERBB4_2298	-	GTGACCTATGCACCAGACGTAATTTTTGTGCAAGTATTTTTACAAAGTGTAGACAAAACACTAGATCGGAAGAGCGGTTTCAG
chr2	212578210	212578249	ERBB4_2299	-	GTGACCTATGCACCAGACGTGCTCAGATTATTTAGTTAGAAGTGGCCTATATAACAAGGAGATCGGAAGAGCGGTTTCAG
chr2	212587068	212587107	ERBB4_2300	-	GTGACCTATGCACCAGACGTGAATAAGAAATAACAAATTAATAGGTCATTATTTGAAATAGATCGGAAGAGCGGTTTCAG
chr2	212589751	212589790	ERBB4_2301	-	GTGACCTATGCACCAGACGTGATTTCTCTTTTTATTATCCTGCTCTCCTTTCCCTTAGATCGGAAGAGCGGTTTCAG
chr2	212615314	212615353	ERBB4_2302	-	GTGACCTATGCACCAGACGTATCAGTACAGACACACAGTTTGTATGGTCAAGGAATTTAGATCGGAAGAGCGGTTTCAG
chr2	212652700	212652739	ERBB4_2303	-	GTGACCTATGCACCAGACGTTTTATTCTTTTTTAATTTCTCAAATGTTCTACCCATGTGAGATCGGAAGAGCGGTTTCAG
chr2	212812105	212812144	ERBB4_2304	-	GTGACCTATGCACCAGACGTTATCCAAAATGGCAAATATGCTTTTATTATCAATATAAGGAGATCGGAAGAGCGGTTTCAG
chr2	212989427	212989466	ERBB4_2305	-	GTGACCTATGCACCAGACGTGGCTTTCTTTCTTTTGTGAATGGACAGTGGCGTCATAGATCGGAAGAGCGGTTTCAG
chr2	213403123	213403162	ERBB4_2306	-	GTGACCTATGCACCAGACGTTCTGGCACTCCGGTCCGCCAACTGCAGCCGCCGGGGAGATCGGAAGAGCGGTTTCAG
chr6	35420273	35420312	FANCE_2307	-	GTGACCTATGCACCAGACGTGGGTGCCCGCCGCCCTACTCTGGTGTGGGGCTCAGCAGATCGGAAGAGCGGTTTCAG
chr6	35423474	35423513	FANCE_2308	-	GTGACCTATGCACCAGACGTGAGGAGCAGCAAGCAAGCTTAAAGTGTGGCTGAAGGGAGCAAGATCGGAAGAGCGGTTTCAG
chr6	35425283	35425322	FANCE_2309	-	GTGACCTATGCACCAGACGTGAGCCAGTCACTGCTACGTCCTCCCTCCCTGCAGCATGACAGATCGGAAGAGCGGTTTCAG
chr6	35425643	35425682	FANCE_2310	-	GTGACCTATGCACCAGACGTAATCTCATGTTAGGGCTGGCAGAGCCCTCAGTGACAAGTAGATCGGAAGAGCGGTTTCAG
chr6	35426024	35426063	FANCE_2311	-	GTGACCTATGCACCAGACGTAGTGGGGGGGAGAGAGACACCCGGACATGCACTCTGCCAGATCGGAAGAGCGGTTTCAG
chr6	35427058	35427097	FANCE_2312	-	GTGACCTATGCACCAGACGTGAGGGAGAAAAAATAATTTTCTTCTTCAACAGATCGGAAGAGCGGTTTCAG
chr6	35427409	35427448	FANCE_2313	-	GTGACCTATGCACCAGACGTGACAGCAGAAAGGGAAGTCTGGGGGAAATGGCAGAAGACAGATCGGAAGAGCGGTTTCAG
chr6	35428279	35428318	FANCE_2314	-	GTGACCTATGCACCAGACGTGAGGCCCTAGTGAAAAATGCTGGCCCTCCACCCAAAGCTAGATCGGAAGAGCGGTTTCAG
chr6	35433971	35434010	FANCE_2315	-	GTGACCTATGCACCAGACGTGAAAAATCATGTCAAGACTCCAGCAACTGATCCCTCCCGAGATCGGAAGAGCGGTTTCAG
chr6	35423777	35423816	FANCE_2316	-	GTGACCTATGCACCAGACGTGGGATTTCAACCTCCTGCCCCAGGCCAGCCCTACAAGATCGGAAGAGCGGTTTCAG
chr1	241663687	241663726	FH_2317	-	GTGACCTATGCACCAGACGTAAAGAAATAATATCATTTTTGAATGCAAAAATAAAAACAGATCGGAAGAGCGGTTTCAG
chr1	241665693	241665732	FH_2318	-	GTGACCTATGCACCAGACGTAATCTGATTTTTAATGTTTTTGACCAAGGCTTATTATCAGATCGGAAGAGCGGTTTCAG
chr1	241669253	241669292	FH_2319	-	GTGACCTATGCACCAGACGTACGTGAATTTTCTCAITTTCTATTATACGTTGGAGATCGGAAGAGCGGTTTCAG
chr1	241671853	241671892	FH_2320	-	GTGACCTATGCACCAGACGTTTGACTAATTTGATTCAAATTTAGAGCTTGGTACAAATGGCAGATCGGAAGAGCGGTTTCAG



chr1	241675217	241675256	FH_2321	-	GTGACCTATGCACCAGACGTGAGCTTTGCTGTTTTTTGGTTATAAATTGAAAAGCATACCAGATCGGAAGAGCGGTTTCAG
chr1	241676853	241676892	FH_2322	-	GTGACCTATGCACCAGACGTATAAGTGTGTTTTGCTTAATAACCTCAGACCATGCCATACAGATCGGAAGAGCGGTTTCAG
chr1	241680432	241680471	FH_2323	-	GTGACCTATGCACCAGACGTGTTTGTGGAATGTTGGCTATTTTGGATGAAGTAGGCTGTAAGATCGGAAGAGCGGTTTCAG
chr1	241682841	241682880	FH_2324	-	GTGACCTATGCACCAGACGTGCCGCCATCCCCGGCCTCCCCGCAGTGACCTTCAGCCCTAGATCGGAAGAGCGGTTTCAG
chr5	180030142	180030181	FLT4_2325	-	GTGACCTATGCACCAGACGTACAGACCCCCAGCACTTGGGGGTTCAAGCCCCGGCAGGGCAGATCGGAAGAGCGGTTTCAG
chr5	180035918	180035957	FLT4_2326	-	GTGACCTATGCACCAGACGTGCTGAGCCCTGCCTGCAGTGCAGGTATCGATGTTGCCCTCCCAGATCGGAAGAGCGGTTTCAG
chr5	180036855	180036894	FLT4_2327	-	GTGACCTATGCACCAGACGTGAAGGTGGGGCTGCGCTCTCGCTCAGGGCTGGGCGAGATCGGAAGAGCGGTTTCAG
chr5	180038281	180038320	FLT4_2328	-	GTGACCTATGCACCAGACGTCTGCAGGTCCAGGAGTAGGGTGGGAGAAAAGCCATGTGGACAGATCGGAAGAGCGGTTTCAG
chr5	180039456	180039495	FLT4_2329	-	GTGACCTATGCACCAGACGTTCCCAACCTGTTCTACTATGGCCTTTGGCCCTGCCCTGAGATCGGAAGAGCGGTTTCAG
chr5	180039961	180040000	FLT4_2330	-	GTGACCTATGCACCAGACGTCCATGGCCCTGCAGGTTTTGGGGACAGCAAGCGTCGGGGGAGATCGGAAGAGCGGTTTCAG
chr5	180041018	180041057	FLT4_2331	-	GTGACCTATGCACCAGACGTGATGGGGTGCCGGTGGGGAGAGGAGGCGAGGTCACCTGGCGAGATCGGAAGAGCGGTTTCAG
chr5	180043317	180043356	FLT4_2332	-	GTGACCTATGCACCAGACGTGCCATTGAGGAGGGGAACCTGGGGCGGAACAGGTGAAGGAGATCGGAAGAGCGGTTTCAG
chr5	180043850	180043889	FLT4_2333	-	GTGACCTATGCACCAGACGTGCCGGAAGGCCCTCAGACGGGAAAAGGGTGCATCCCCACAGATCGGAAGAGCGGTTTCAG
chr5	180045720	180045759	FLT4_2334	-	GTGACCTATGCACCAGACGTGGCCTCTTCCCTTTTCTAGTGCTGCACGGGCCCGGTTATAGATCGGAAGAGCGGTTTCAG
chr5	180046615	180046654	FLT4_2335	-	GTGACCTATGCACCAGACGTAGCGGGCGGAAGGGCAGCCTAGCTGGTGAGGAGCAGCAGAGATCGGAAGAGCGGTTTCAG
chr5	180047123	180047162	FLT4_2336	-	GTGACCTATGCACCAGACGTACCAGCCTGCCAACCCACACCTCCTGCCCGACCCACTAGATCGGAAGAGCGGTTTCAG
chr5	180047559	180047598	FLT4_2337	-	GTGACCTATGCACCAGACGTCTCCCCGCTCTGATGGAGTCTCTCTCAGGCCTTCCCACAGATCGGAAGAGCGGTTTCAG
chr5	180047826	180047865	FLT4_2338	-	GTGACCTATGCACCAGACGTAGGCTGCACCCTCAACTCCCTCCCGTCCCGAGTTAACGAGATCGGAAGAGCGGTTTCAG
chr5	180048056	180048095	FLT4_2339	-	GTGACCTATGCACCAGACGTGGCCCTGGCGAAGGGCAGCTCCGGAGGCCCGCAGGCGGAGATCGGAAGAGCGGTTTCAG
chr5	180048492	180048531	FLT4_2340	-	GTGACCTATGCACCAGACGTCCGCGGGGAGGGCGGGGACGCGCTCTCTTAGCAGTAGCAGATCGGAAGAGCGGTTTCAG
chr5	180049681	180049720	FLT4_2341	-	GTGACCTATGCACCAGACGTAGACCAGGGCGGGGAGGCCTGGGTACAGGGTCAGGAGGGGAGATCGGAAGAGCGGTTTCAG
chr5	180050885	180050924	FLT4_2342	-	GTGACCTATGCACCAGACGTGCCGCGCTGCTGAGTGCCAGGGAGAAAGGAGAAGGGAGGAAGATCGGAAGAGCGGTTTCAG
chr5	180052819	180052858	FLT4_2343	-	GTGACCTATGCACCAGACGTCTCCAGCCTCAGGTCCTGCACAGCCACAGCCCCAGCCAGATCGGAAGAGCGGTTTCAG
chr5	180053061	180053100	FLT4_2344	-	GTGACCTATGCACCAGACGTGACGGGAGAGCGCAGGGTGGCGCGCTGGCATTTGAGGGCAGATCGGAAGAGCGGTTTCAG
chr5	180055832	180055871	FLT4_2345	-	GTGACCTATGCACCAGACGTGGCTCCCCACCGACCCCGCGGATACCCCTTCCAAGTCCAGAGATCGGAAGAGCGGTTTCAG
chr5	180056209	180056248	FLT4_2346	-	GTGACCTATGCACCAGACGTGAAACCAGGGTCTTGTGCCCTGTGGGCTGGGCCAGAAAGATCGGAAGAGCGGTTTCAG
chr5	180056646	180056685	FLT4_2347	-	GTGACCTATGCACCAGACGTGACGCTGCCAGGCTGTCTGTCCCCAGGAGTCCCTGTGAAGATCGGAAGAGCGGTTTCAG
chr5	180056893	180056932	FLT4_2348	-	GTGACCTATGCACCAGACGTTGTGCCCGTTCCCAGTAAACGGGGGCTGTCACCTGCCTACTAGATCGGAAGAGCGGTTTCAG
chr5	180057175	180057214	FLT4_2349	-	GTGACCTATGCACCAGACGTACCCCAACCCAGCCTCCAGCCTCCCATCCACCCCTGGAGATCGGAAGAGCGGTTTCAG
chr5	180057505	180057544	FLT4_2350	-	GTGACCTATGCACCAGACGTGAGCGGGCCAGCCTGGAGCAGGGTCCCGGGCAGCTGGGGAGATCGGAAGAGCGGTTTCAG
chr5	180058632	180058671	FLT4_2351	-	GTGACCTATGCACCAGACGTCTCTCCACTGGCAGGCCAGAGAGGCTGCACAAGCCCAAGATCGGAAGAGCGGTTTCAG
chr5	180076438	180076477	FLT4_2352	-	GTGACCTATGCACCAGACGTGCAACGGGCCACCCGCCGAGCGTGGGGCTGGCCGGGGAGAGATCGGAAGAGCGGTTTCAG
chr2	227659676	227659715	IRS1_2353	-	GTGACCTATGCACCAGACGTATCACAGCAGGTGCGTTTTATGTTGACAAAGTCAAGAAAGATCGGAAGAGCGGTTTCAG
chr2	227660142	227660181	IRS1_2354	-	GTGACCTATGCACCAGACGTCCACAAGGGTGGCCGGGAGGCATAGCTCCGAGACTTTCTAGATCGGAAGAGCGGTTTCAG
chr2	227660608	227660647	IRS1_2355	-	GTGACCTATGCACCAGACGTGGCACTGGAGCAGTACATGAAGATGGACCTGGGGCCGGCAGATCGGAAGAGCGGTTTCAG
chr2	227661074	227661113	IRS1_2356	-	GTGACCTATGCACCAGACGTAGGAGGGTGCCCGGCATCAGCACCTCCGCCCTTCCACTAGAGATCGGAAGAGCGGTTTCAG
chr2	227661540	227661579	IRS1_2357	-	GTGACCTATGCACCAGACGTGAAAGGGCAGTGAGACTATATGCCCATGAGCCCCAAGAAGATCGGAAGAGCGGTTTCAG
chr2	227662006	227662045	IRS1_2358	-	GTGACCTATGCACCAGACGTCAAGGGGCCCTCCACCCTGACCGCCCCAACGGTCACTACAGATCGGAAGAGCGGTTTCAG
chr2	227662472	227662511	IRS1_2359	-	GTGACCTATGCACCAGACGTGCATGGTGGGCGGGAAGCCAGGCTCCTTCCGTGTCCGCGCAGATCGGAAGAGCGGTTTCAG
chr2	227662938	227662977	IRS1_2360	-	GTGACCTATGCACCAGACGTTTCAAAGGGTCTGGCAAGTGATCCTGAAGCCAAAGGGCCAGATCGGAAGAGCGGTTTCAG
chr22	22123443	22123482	MAPK1_2361	-	GTGACCTATGCACCAGACGTGACTGGAGTTTTAATACAGTGAGCTTAGCAAGGGAGGCGAGATCGGAAGAGCGGTTTCAG
chr22	22127112	22127151	MAPK1_2362	-	GTGACCTATGCACCAGACGTATGTTCTGGCTGCTGCTTACGGACATAGATCAGCCAGCAGATCGGAAGAGCGGTTTCAG
chr22	22142496	22142535	MAPK1_2363	-	GTGACCTATGCACCAGACGTTTTCTGTTGATTAGTTTTTCTTAGGCTTAGCTTCGCGTTAGATCGGAAGAGCGGTTTCAG
chr22	22142933	22142972	MAPK1_2364	-	GTGACCTATGCACCAGACGTGAGCCCTCAGGAGCTAGATTTACTCAAGTTTTGTACAGCAGATCGGAAGAGCGGTTTCAG
chr22	22153251	22153290	MAPK1_2365	-	GTGACCTATGCACCAGACGTAGTTTTGCATAAAAAGAAATCCAGTAAGTAAAGAACTTTTCAGATCGGAAGAGCGGTTTCAG
chr22	22160089	22160128	MAPK1_2366	-	GTGACCTATGCACCAGACGTTTTACTATTAAAGGTATATATATGAAACCCCTTTCAGATCGGAAGAGCGGTTTCAG
chr22	22161903	22161942	MAPK1_2367	-	GTGACCTATGCACCAGACGTTAGGCAACTGGCCAATTCACCTGCTTGGTAACCTTGTGAAGATCGGAAGAGCGGTTTCAG
chr8	90947760	90947799	NBN_2368	-	GTGACCTATGCACCAGACGTAAAAAGAGCCATGAAAAAATCTCCTAGTAAGCATCTACAGATCGGAAGAGCGGTTTCAG
chr8	90949204	90949243	NBN_2369	-	GTGACCTATGCACCAGACGTATTACCTTTCTCATGTACCTTTGAGAGATGTATATAAAAAGATCGGAAGAGCGGTTTCAG
chr8	90955431	90955470	NBN_2370	-	GTGACCTATGCACCAGACGTAGTGAGGCCAGAAAGTTGCTTAAATTTGCACCTTTGGTCCAAGATCGGAAGAGCGGTTTCAG
chr8	90958318	90958357	NBN_2371	-	GTGACCTATGCACCAGACGTCAACTGTATCACAGAGGTCAGTGTGTTGAAATGTTTTAGAGATCGGAAGAGCGGTTTCAG
chr8	90960002	90960041	NBN_2372	-	GTGACCTATGCACCAGACGTTTTATTAATTTTTATACAGATTGCTTACGAGTTTGGCTTACGGGACTGATCGGAAGAGCGGTTTCAG
chr8	90965422	90965461	NBN_2373	-	GTGACCTATGCACCAGACGTTTTTAAATGAGAGGTATAGTACATAGAAGCTTGAATGCTAGATCGGAAGAGCGGTTTCAG
chr8	90967461	90967500	NBN_2374	-	GTGACCTATGCACCAGACGTGATAACTTCTCTCATGTCTCTGAAAAAAAATGAAAGTTTAGATCGGAAGAGCGGTTTCAG
chr8	90970903	90970942	NBN_2375	-	GTGACCTATGCACCAGACGTTTCATTACCGTACTATTGTTATTCTATCAATAAATTAAGATCGGAAGAGCGGTTTCAG
chr8	90976588	90976627	NBN_2376	-	GTGACCTATGCACCAGACGTCAATTTTTATTGATTGTTAGCAACTTTATTATGTAATAGATCGGAAGAGCGGTTTCAG
chr8	90982542	90982581	NBN_2377	-	GTGACCTATGCACCAGACGTTATCTTTTACTTAAAGTAAAAAGTCAAGTAGGAGATTTTATGAGATCGGAAGAGCGGTTTCAG
chr8	90983351	90983390	NBN_2378	-	GTGACCTATGCACCAGACGTATAAGCTAAATTTTTCTAAAGAATACATTACAAACTAGGAGATCGGAAGAGCGGTTTCAG

chr8	90990398	90990437	NBN_2379	-	GTGACCTATGCACCAGACGTTATTTTAAATATAACAAGATGTCACCTTATATGATAGCATTAGATCGGAAGAGCGGTTACG
chr8	90992912	90992951	NBN_2380	-	GTGACCTATGCACCAGACGTTGCTTGTCTTATGTTAAAAATAAGTTATTTGAATTTAAAGATCGGAAGAGCGGTTACG
chr8	90993553	90993592	NBN_2381	-	GTGACCTATGCACCAGACGTTTAAAATTGATTTTAAAATGGACAGCTTTGTTTCAGCCAAAGATCGGAAGAGCGGTTACG
chr8	90994900	90994939	NBN_2382	-	GTGACCTATGCACCAGACGTAATTTTATTTTCACTAGTTTCCAGTAAGGGGGTTGAAATCAAGATCGGAAGAGCGGTTACG
chr8	90996703	90996742	NBN_2383	-	GTGACCTATGCACCAGACGTAAGGGAAGCCCTCGGGGCCATTTTTCCCGGTAGCGACTGCCAGATCGGAAGAGCGGTTACG
chr20	8113249	8113288	PLCB1_2384	-	GTGACCTATGCACCAGACGTTCCGGCTCCGGGCCCGCCGGCGAGCGCGGACTGGAGATCGGAAGAGCGGTTACG
chr20	8130891	8130930	PLCB1_2385	-	GTGACCTATGCACCAGACGTTAAGAAAGAAACATGAATATCAACATATACACTGTAGAAAAAAGATCGGAAGAGCGGTTACG
chr20	8351979	8352018	PLCB1_2386	-	GTGACCTATGCACCAGACGTTAAAACGTGAAATCGTTAAGCAACGACACAGACCTTTCTCAGATCGGAAGAGCGGTTACG
chr20	8608891	8608930	PLCB1_2387	-	GTGACCTATGCACCAGACGTAATATTGAAAATAATTAGTCTATAACTAGAGATCCAACGAGATCGGAAGAGCGGTTACG
chr20	8626699	8626738	PLCB1_2388	-	GTGACCTATGCACCAGACGTTAAATAACACTTGCATTAGCTTAAATACTGCACAGTATTAGATCGGAAGAGCGGTTACG
chr20	8629971	8630010	PLCB1_2389	-	GTGACCTATGCACCAGACGTAACAACAACAAGGAGAGAGGTTTAAATGGCACATGGATCAAGATCGGAAGAGCGGTTACG
chr20	8639135	8639174	PLCB1_2390	-	GTGACCTATGCACCAGACGTTGAAAACCAAGCAATAAGAATTTTTAAACTAAGTTTTCAAGATCGGAAGAGCGGTTACG
chr20	8665529	8665568	PLCB1_2391	-	GTGACCTATGCACCAGACGTTGAAGTTAGAAAGGATGTAATGCATTTCTTTATGGGTGTAGATCGGAAGAGCGGTTACG
chr20	8678223	8678262	PLCB1_2392	-	GTGACCTATGCACCAGACGTTCAAACAACAAACCCAGATTCCCATGAAGCAAGGATGAAGATCGGAAGAGCGGTTACG
chr20	8689267	8689306	PLCB1_2393	-	GTGACCTATGCACCAGACGTTGAACACATGTATATTCAGTATGCCAGAATTTTCATCTGTAGATCGGAAGAGCGGTTACG
chr20	8696861	8696900	PLCB1_2394	-	GTGACCTATGCACCAGACGTACAGAACAAGAAAGGAAAGTAGGGAGGCTTATCCAAAGAGATCGGAAGAGCGGTTACG
chr20	8698268	8698307	PLCB1_2395	-	GTGACCTATGCACCAGACGTTGAAAGGCATATTTTAAAAAATACTGCTCCCTCTTTTCCAGAGATCGGAAGAGCGGTTACG
chr20	8702951	8702990	PLCB1_2396	-	GTGACCTATGCACCAGACGTTAATAACAGATCATCTTCAACATTTTCAACATTTAGCTAGATCGGAAGAGCGGTTACG
chr20	8705253	8705292	PLCB1_2397	-	GTGACCTATGCACCAGACGTTGAATAAAAAAGAAAAACATTTCCAGAGTCAGCATTATATTAAGATCGGAAGAGCGGTTACG
chr20	8707906	8707945	PLCB1_2398	-	GTGACCTATGCACCAGACGTTACAACAACAAAAAGGGGAAGGTGAGAATACAATTAGATCGGAAGAGCGGTTACG
chr20	8709647	8709686	PLCB1_2399	-	GTGACCTATGCACCAGACGTATGTTAAGTAGTGAATACAATTATAAAAAATTTAGTCAAAGATCGGAAGAGCGGTTACG
chr20	8713835	8713874	PLCB1_2400	-	GTGACCTATGCACCAGACGTTAAAACACAAGCCTTATTGTGAGTTTATCTATACTTTGGGGTAGATCGGAAGAGCGGTTACG
chr20	8717625	8717664	PLCB1_2401	-	GTGACCTATGCACCAGACGTTAATAAATCAATCCATAAGGAATTTTGATATGCAAAATAGATCGGAAGAGCGGTTACG
chr20	8719858	8719897	PLCB1_2402	-	GTGACCTATGCACCAGACGTTAATAAGTACACACTGGTTAAGAATGAACAATTTCAAAGATCGGAAGAGCGGTTACG
chr20	8720941	8720980	PLCB1_2403	-	GTGACCTATGCACCAGACGTAGAATAATGCTGTGTAGCACATATTTCTTTCCAATGTTAAGATCGGAAGAGCGGTTACG
chr20	8737643	8737682	PLCB1_2404	-	GTGACCTATGCACCAGACGTTAAATATCCTTTTCTTTCCACATTTCTTTTATTCTTTTCCAGATCGGAAGAGCGGTTACG
chr20	8741004	8741043	PLCB1_2405	-	GTGACCTATGCACCAGACGTTAAAGATAAAAAATAAGCCTCTTCAACTTTTTTAAATTTTAAAGATCGGAAGAGCGGTTACG
chr20	8745736	8745775	PLCB1_2406	-	GTGACCTATGCACCAGACGTTGAATATGAAAGCTAAGGGAATGGGAGGGCTGAACATCCAAGATCGGAAGAGCGGTTACG
chr20	8755136	8755175	PLCB1_2407	-	GTGACCTATGCACCAGACGTACAGAGTTGACTCACAAAAACAGACAGCCATAACAAGGTAGATCGGAAGAGCGGTTACG
chr20	8769046	8769085	PLCB1_2408	-	GTGACCTATGCACCAGACGTTAAAGTGTCTTGTGCTATTTCAAATGATTGCAAAACAGACAGATCGGAAGAGCGGTTACG
chr20	8769230	8769269	PLCB1_2409	-	GTGACCTATGCACCAGACGTTAATGGAAGTAAAAGAGAAAAAGAGGCAATCAGATGGGAAGATCGGAAGAGCGGTTACG
chr20	8770115	8770154	PLCB1_2410	-	GTGACCTATGCACCAGACGTATGATGAATACATCATTATACCAATTCATCCAGAATTGACAGATCGGAAGAGCGGTTACG
chr20	8770772	8770811	PLCB1_2411	-	GTGACCTATGCACCAGACGTGTTACAAGAAACATACTTTTCTTCACTAAACATTTAAAGTGAAGATCGGAAGAGCGGTTACG
chr20	8782653	8782692	PLCB1_2412	-	GTGACCTATGCACCAGACGTTAAAAGGGAGGCTGTCAATTTTTGTGGCAATGAAATTTGATAGATCGGAAGAGCGGTTACG
chr20	8862219	8862258	PLCB1_2413	-	GTGACCTATGCACCAGACGTTAAGAGGGGAGATGACTTGAAGTTGTTTATGTTTCTATAAGATCGGAAGAGCGGTTACG
chr1	1982020	1982059	PRKCZ_2414	-	GTGACCTATGCACCAGACGTCCCCGCCCGCTCAGCGCTGCGCCCCGGGAGCTCCGGCCAAGATCGGAAGAGCGGTTACG
chr1	1986830	1986869	PRKCZ_2415	-	GTGACCTATGCACCAGACGTGGGGACATGGGCATCTGTTACCGTGGGGCATATTTGAATCAGATCGGAAGAGCGGTTACG
chr1	1987873	1987912	PRKCZ_2416	-	GTGACCTATGCACCAGACGTCAAGAGACGGTGCTGACGTCCGCCAAGGGCCGAGGCAAAGATCGGAAGAGCGGTTACG
chr1	1990930	1990969	PRKCZ_2417	-	GTGACCTATGCACCAGACGTGAGAGAAAGAGACAGCGTCAAGACCCTGCGGCTGCCACTCAGATCGGAAGAGCGGTTACG
chr1	2066651	2066690	PRKCZ_2418	-	GTGACCTATGCACCAGACGTTATGAGAAGGTGTAAGAAACAGCCTGGCAGCCACGAGCAGATCGGAAGAGCGGTTACG
chr1	2075599	2075638	PRKCZ_2419	-	GTGACCTATGCACCAGACGTGAAATGACAGGCTGAAAGCCACAGCCACACTGAGGGGCCAGCAGATCGGAAGAGCGGTTACG
chr1	2075728	2075767	PRKCZ_2420	-	GTGACCTATGCACCAGACGTCAAGTCAAGGACGAGGCGGTCAGCGCTTATGGACCAAGATCGGAAGAGCGGTTACG
chr1	2077416	2077455	PRKCZ_2421	-	GTGACCTATGCACCAGACGTGACACAGAGATGGCAGCATGACCAAGTGCTAGAGCAGGTGAGATCGGAAGAGCGGTTACG
chr1	2080261	2080300	PRKCZ_2422	-	GTGACCTATGCACCAGACGTAGGGAGGAAGGAAGGGGGCTTACGGTGTGGTCAGGAACGCAGATCGGAAGAGCGGTTACG
chr1	2082179	2082218	PRKCZ_2423	-	GTGACCTATGCACCAGACGTAGAACAAGACCCGAAAGTGAAGAGGGGGTTCCCGGGAGAGATCGGAAGAGCGGTTACG
chr1	2087384	2087423	PRKCZ_2424	-	GTGACCTATGCACCAGACGTCAACAGGGAGTGTAATGAGGCTCCCGCAATGCTCCTCACAAAGATCGGAAGAGCGGTTACG
chr1	2100907	2100946	PRKCZ_2425	-	GTGACCTATGCACCAGACGTAGAGGCGCCGGAGGCTGCAGTCACTCGGCAGACGCGGCAGATCGGAAGAGCGGTTACG
chr1	2103444	2103483	PRKCZ_2426	-	GTGACCTATGCACCAGACGTGGATGCCGTATGGGGCAGTGCCTGTGCCAGAGGCTGCGAGATCGGAAGAGCGGTTACG
chr1	2103690	2103729	PRKCZ_2427	-	GTGACCTATGCACCAGACGTAAAGTTACTGGGAGAGGGTTCTTGTAGACACTACCCCGCAGATCGGAAGAGCGGTTACG
chr1	2105286	2105325	PRKCZ_2428	-	GTGACCTATGCACCAGACGTGCACACAGCATCACCGAGTGGGGCCACATGGGCCGCGAGATCGGAAGAGCGGTTACG
chr1	2106143	2106182	PRKCZ_2429	-	GTGACCTATGCACCAGACGTGGAGCCTGGTGAAGACTTGCCTGTGTTGTGCCATTTGCAGATCGGAAGAGCGGTTACG
chr1	2106613	2106652	PRKCZ_2430	-	GTGACCTATGCACCAGACGTGAGTTCAAACAAGGACCAAGTCAAGCCCATCCCGGAAGCCAGATCGGAAGAGCGGTTACG
chr1	2115972	2116011	PRKCZ_2431	-	GTGACCTATGCACCAGACGTCAATAGGAGAAGGGTCAGCTCCGCGCGGGCATCATCCCTAAGATCGGAAGAGCGGTTACG
chr1	2116311	2116350	PRKCZ_2432	-	GTGACCTATGCACCAGACGTAGGTGGCAGGGGGGAGGGGGGTGACCGTGTGTTTCTCCAGATCGGAAGAGCGGTTACG
chr22	24129307	24129346	SMARCB1_2433	-	GTGACCTATGCACCAGACGTGAGGGCGGGCGGCCGAGCCGGGCTGCGAGGGATCAGGAGGATCGGAAGAGCGGTTACG
chr22	24133893	24133932	SMARCB1_2434	-	GTGACCTATGCACCAGACGTAGCAAGAAGGCTCATTATAAGGGTCCGAGCACCACAGGGAAGATCGGAAGAGCGGTTACG
chr22	24135696	24135735	SMARCB1_2435	-	GTGACCTATGCACCAGACGTCAACACTAGGCTCACTGCTGTTGGCGGTGGCACAGATCGGAAGAGCGGTTACG
chr22	24143081	24143120	SMARCB1_2436	-	GTGACCTATGCACCAGACGTACAAGAAAGTCTCCAGTCACTAGTATAGGACCTGATCGGAAGAGCGGTTACG

chr22	24145432	24145471	SMARCB1_2437	-	GTGACCTATGCACCAGACGTAATGGAAGCAACAGTCAAGCGAGGGGGCCGAGCCCTAGGTAGATCGGAAGAGCGGTTTCAG
chr22	24158907	24158946	SMARCB1_2438	-	GTGACCTATGCACCAGACGTTGAGAGGGAAGGGATGCCAAGAGATTGCACCATGCTTTGGGCAGATCGGAAGAGCGGTTTCAG
chr22	24167362	24167401	SMARCB1_2439	-	GTGACCTATGCACCAGACGTAACCAAAGGACACAAGTTAGAGCTTTTGCAGCCCAGGGAGAGATCGGAAGAGCGGTTTCAG
chr22	24175709	24175748	SMARCB1_2440	-	GTGACCTATGCACCAGACGTTGGGAGGCGAGTGAAGAGGAATGACTTTTCCAGCTATAGATGGAGATCGGAAGAGCGGTTTCAG
chr22	24176278	24176317	SMARCB1_2441	-	GTGACCTATGCACCAGACGTTAGTGGGGAGGGCAATGAGTCGGGGCCAGCTCCCAGCCCTGGAGATCGGAAGAGCGGTTTCAG
chr15	57212062	57212101	TCF12_2442	-	GTGACCTATGCACCAGACGTTTCTAGCAGGTCCTAGGGCAGAGGAAACGGGCTCAGCGAGAGATCGGAAGAGCGGTTTCAG
chr15	57213174	57213213	TCF12_2443	-	GTGACCTATGCACCAGACGTTACCCAAATATATCTGTAGTCTGAAATTTCTTAGATTACAGATCGGAAGAGCGGTTTCAG
chr15	57355898	57355937	TCF12_2444	-	GTGACCTATGCACCAGACGTTAAGAAAATAAAGATATATCTAAAAACATACTTTTGTGGAAGATCGGAAGAGCGGTTTCAG
chr15	57383937	57383976	TCF12_2445	-	GTGACCTATGCACCAGACGTTAAAAAGATCAGAGTATTAAGAGATTATTTGGCAGTCCCAGATCGGAAGAGCGGTTTCAG
chr15	57458550	57458589	TCF12_2446	-	GTGACCTATGCACCAGACGTTAAGAAAATAAAGTATATAAAAACCCCTTCATTATTGACAGAGATCGGAAGAGCGGTTTCAG
chr15	57484306	57484345	TCF12_2447	-	GTGACCTATGCACCAGACGTTAGGCCAAGGAAACAAGTTATTTTCTGCTGATACTGACCCAGATCGGAAGAGCGGTTTCAG
chr15	57489921	57489960	TCF12_2448	-	GTGACCTATGCACCAGACGTTAAAAACAATACATTTCTTCCAGCATAATATACCAGAAAAAAGATCGGAAGAGCGGTTTCAG
chr15	57511670	57511709	TCF12_2449	-	GTGACCTATGCACCAGACGTTAAATGTTACTATTTTGTAGCTATGCACACAGCCCTCTCTCAGATCGGAAGAGCGGTTTCAG
chr15	57523300	57523339	TCF12_2450	-	GTGACCTATGCACCAGACGTTAACAGCACAATTTAATTAATAATGTAAGTACTATCATATTAAGATCGGAAGAGCGGTTTCAG
chr15	57524439	57524478	TCF12_2451	-	GTGACCTATGCACCAGACGTTAAGAAAATAAATAATTTTCTTGTAGCTAAAAATTTCTTGTAGATCGGAAGAGCGGTTTCAG
chr15	57524860	57524899	TCF12_2452	-	GTGACCTATGCACCAGACGTTAGAGATATGATCTATTAATATATTTTTCTGAATAATATTCAGATCGGAAGAGCGGTTTCAG
chr15	57526191	57526230	TCF12_2453	-	GTGACCTATGCACCAGACGTTACAGAGAAAATAAATCAAGAATTTTACAAGCAAGTATTATAGATCGGAAGAGCGGTTTCAG
chr15	57535620	57535659	TCF12_2454	-	GTGACCTATGCACCAGACGTTAACAAGAAATAACATGATCAACATGTGACAACAGCACAAAGATCGGAAGAGCGGTTTCAG
chr15	57543498	57543537	TCF12_2455	-	GTGACCTATGCACCAGACGTTCAAAGTAGCCACACACCTGGGTTAACTCAGTGATCTTGTAGATCGGAAGAGCGGTTTCAG
chr15	57544569	57544608	TCF12_2456	-	GTGACCTATGCACCAGACGTTCAAGACAGAACAGGAGGCCAAGCACAGGTTAAGATTAAC TAGATCGGAAGAGCGGTTTCAG
chr15	57545410	57545449	TCF12_2457	-	GTGACCTATGCACCAGACGTTAAAAAAAACATGGTGGTTATTGCTGGCATCTGTTAGAAGATCGGAAGAGCGGTTTCAG
chr15	57554242	57554281	TCF12_2458	-	GTGACCTATGCACCAGACGTTGGAAAACCCAAAAATAAAAAAGATTAAGATAGTTTCAGAGAGATCGGAAGAGCGGTTTCAG
chr15	57555260	57555299	TCF12_2459	-	GTGACCTATGCACCAGACGTTGGCAAAGGAAAATAAAAAAGACGACTCATATAGATCGGAAGAGCGGTTTCAG
chr15	57565178	57565217	TCF12_2460	-	GTGACCTATGCACCAGACGTTAAGTAGCCAAAGGTCATTAGGTTTCTATAAAGTAAGAAGATCGGAAGAGCGGTTTCAG
chr15	57574593	57574632	TCF12_2461	-	GTGACCTATGCACCAGACGTTGGGAAAAGATTTTATCACTATGGTTTTAAGTTATGAATTAGATCGGAAGAGCGGTTTCAG
chr1	186283053	186283092	TPR_2462	-	GTGACCTATGCACCAGACGTTACAATAAACAACCTGTGAATAAGATTATCAAATCTGTTTTAAGATCGGAAGAGCGGTTTCAG
chr1	186283711	186283750	TPR_2463	-	GTGACCTATGCACCAGACGTTGACATAACTGGATTACATGATAGAATGTGGAATAGTAATAAGATCGGAAGAGCGGTTTCAG
chr1	186286564	186286603	TPR_2464	-	GTGACCTATGCACCAGACGTTGCCCTTGACTGCAATACAGTTTTTATACATCAAACCTGTTAGATCGGAAGAGCGGTTTCAG
chr1	186287529	186287568	TPR_2465	-	GTGACCTATGCACCAGACGTTATTTGTTGTTTGGCTTGTAGCTCAACAGACTGTAGATCGGAAGAGCGGTTTCAG
chr1	186287815	186287854	TPR_2466	-	GTGACCTATGCACCAGACGTTAAGCGCAGATAGTAGGTTCTGTTTTATTGGTAAAAATGAAAAGATCGGAAGAGCGGTTTCAG
chr1	186289394	186289433	TPR_2467	-	GTGACCTATGCACCAGACGTTAAACCTTTAGATCCCCTGAATTTGTATGATTTTGGTAATAAGATCGGAAGAGCGGTTTCAG
chr1	186291400	186291439	TPR_2468	-	GTGACCTATGCACCAGACGTTGAAAGAGAAACATACTTTATAACTAATCAAACCTTTTAGTACAGATCGGAAGAGCGGTTTCAG
chr1	186291600	186291639	TPR_2469	-	GTGACCTATGCACCAGACGTTACCCATTATGTAAGAGTAATTCATTTCTTGAGCAGATATTAGATCGGAAGAGCGGTTTCAG
chr1	186292768	186292807	TPR_2470	-	GTGACCTATGCACCAGACGTTACTGGTCAATTAAGAAATGAACTTTGAAAAAAATCTTGGAGATCGGAAGAGCGGTTTCAG
chr1	186294846	186294885	TPR_2471	-	GTGACCTATGCACCAGACGTTAATAGCCTTTTTTGTAGCCTTTTGAATTAATCTGAGTATTCTTAAAGATCGGAAGAGCGGTTTCAG
chr1	186295186	186295225	TPR_2472	-	GTGACCTATGCACCAGACGTTAGAATTTTAAACCATTATAGTTCTTTCTATGAGCTTTCTTAGATCGGAAGAGCGGTTTCAG
chr1	186296542	186296581	TPR_2473	-	GTGACCTATGCACCAGACGTTTTGAAATCATCTAGTGTTTTTAACTATTGGATGAAAGTAGATCGGAAGAGCGGTTTCAG
chr1	186300580	186300619	TPR_2474	-	GTGACCTATGCACCAGACGTTACATACCTAAAGTACCACACCGTTGCTTTTTCTGTAATGAAAGATCGGAAGAGCGGTTTCAG
chr1	186301277	186301316	TPR_2475	-	GTGACCTATGCACCAGACGTTTCTTTCTGTGATTTTAACTTTTACCAGTAGAGTTAAGGAGATCGGAAGAGCGGTTTCAG
chr1	186302204	186302243	TPR_2476	-	GTGACCTATGCACCAGACGTTTTTAAAAAGAGTCAGAGTAGACCTATGCATTATAAAGAGATCGGAAGAGCGGTTTCAG
chr1	186303407	186303446	TPR_2477	-	GTGACCTATGCACCAGACGTTAATACAGATCTGATGAGACTGCTTATTAGATTATATAGATCGGAAGAGCGGTTTCAG
chr1	186304150	186304189	TPR_2478	-	GTGACCTATGCACCAGACGTTGTTATTTTATAGTCTGTTATTTTTCTTTTAAAGCTCAGGGAGATCGGAAGAGCGGTTTCAG
chr1	186304420	186304459	TPR_2479	-	GTGACCTATGCACCAGACGTAATTCTGCTTAAAGTAACAAATGTTTTTCTTTGTACATTAGATCGGAAGAGCGGTTTCAG
chr1	186305578	186305617	TPR_2480	-	GTGACCTATGCACCAGACGTTGTTTAAAGTTTGAACCTTGGTAGTGAAGGTTGATTATGTGATAGATCGGAAGAGCGGTTTCAG
chr1	186306095	186306134	TPR_2481	-	GTGACCTATGCACCAGACGTTGAGAACAGTCTGTTCTTAATCTTTCTGTTTATACACCTAAGATCGGAAGAGCGGTTTCAG
chr1	186307115	186307154	TPR_2482	-	GTGACCTATGCACCAGACGTTGAAACTTCTTACAAAAAAAAAC TAGGATGAATGTTATAGATCGGAAGAGCGGTTTCAG
chr1	186308724	186308763	TPR_2483	-	GTGACCTATGCACCAGACGTTAGAAGCCTTAAATCATATATAATATAAAAAGAAGTTATTTAGATCGGAAGAGCGGTTTCAG
chr1	186310110	186310149	TPR_2484	-	GTGACCTATGCACCAGACGTTTAAACTCTTCCAAAACATGGAACACAGTGTTTTTAATAAGATCGGAAGAGCGGTTTCAG
chr1	186310334	186310373	TPR_2485	-	GTGACCTATGCACCAGACGTTAGTTATCAAGAGTGGAAAGCATGTTGTTTTAATAATAAAAAGATCGGAAGAGCGGTTTCAG
chr1	186312408	186312447	TPR_2486	-	GTGACCTATGCACCAGACGTTAAGCTTTAAGAAAGCACTGTTAAATCAAAGAGAAGCAAGATCGGAAGAGCGGTTTCAG
chr1	186312988	186313027	TPR_2487	-	GTGACCTATGCACCAGACGTTTCTTACTGCTTCACTTTCTGTGTATAACAACATGAAATAGATCGGAAGAGCGGTTTCAG
chr1	186314662	186314701	TPR_2488	-	GTGACCTATGCACCAGACGTTCAATTTATGAGAAATGAGCTCGATCCTAGAGAATGATTAGATCGGAAGAGCGGTTTCAG
chr1	186315217	186315256	TPR_2489	-	GTGACCTATGCACCAGACGTTAAACCGTATAATTTTTTTTTTAACTTGAAGGATTTGAAAGATCGGAAGAGCGGTTTCAG
chr1	186316374	186316413	TPR_2490	-	GTGACCTATGCACCAGACGTTTCTGAATTCAGAATCAATCTCAACACATTTGTTAACTTAGATCGGAAGAGCGGTTTCAG
chr1	186319305	186319344	TPR_2491	-	GTGACCTATGCACCAGACGTTAAGTAGACCAATATAAATGTAATAAACAAGTACTTCTTAGATCGGAAGAGCGGTTTCAG
chr1	186320412	186320451	TPR_2492	-	GTGACCTATGCACCAGACGTTACAGAGTCTGAAATTTCTGTAGGGTGTATTGTTTCAAGTAATAGATCGGAAGAGCGGTTTCAG
chr1	186321058	186321097	TPR_2493	-	GTGACCTATGCACCAGACGTTAAGAAAGCTATGATAAAAAATGATAAAAAAGTTAAATTTAAGATCGGAAGAGCGGTTTCAG
chr1	186322770	186322809	TPR_2494	-	GTGACCTATGCACCAGACGTTATCCCTTGCCAACCTTGCAATTAAGTTGCATTTGACATAGATCGGAAGAGCGGTTTCAG

chr1 186324492 186324531 TPR\_2495 - GTGACCTATGCACCAGACGTTTTTTGTTTCAAATTAATTAAGTCTAAATGTTATACTTTACAGATCGGAAGAGCGGTTTCAG

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chr1 186325368 186325407 TPR\_2497 - GTGACCTATGCACCAGACGTATAAAGTTATTTTTAAGGAATAATTTAGAAATGTATATAAAGATCGGAAGAGCGGTTTCAG

chr1 186326479 186326518 TPR\_2498 - GTGACCTATGCACCAGACGTACATACCTCAGCTTGTGAGCAAACATTTATGAAAACCTCAGATCGGAAGAGCGGTTTCAG

chr1 186327625 186327664 TPR\_2499 - GTGACCTATGCACCAGACGTTTTTTGTTTGTTCCTACTTTTTAAAAACCTGACTGCCAGAGATCGGAAGAGCGGTTTCAG

chr1 186328881 186328920 TPR\_2500 - GTGACCTATGCACCAGACGTTTCCTAAAATTTAGCCGTGGTGAACAATACAAATGAGAAATAGATCGGAAGAGCGGTTTCAG

chr1 186329355 186329394 TPR\_2501 - GTGACCTATGCACCAGACGTTATAAAGTTGTGTTAAATTCITTTTTCTTCAGCAAATGTATAGATCGGAAGAGCGGTTTCAG

chr1 186329847 186329886 TPR\_2502 - GTGACCTATGCACCAGACGTTAGATGCTTGTAGTGAGTTGAAATACTACAGCTTTCTAAGATCGGAAGAGCGGTTTCAG

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chr1 186331919 186331958 TPR\_2506 - GTGACCTATGCACCAGACGTTAAAATGTGTTTTCTTCATGTTGAGTATACTTACATTTAGATCGGAAGAGCGGTTTCAG

chr1 186332424 186332463 TPR\_2507 - GTGACCTATGCACCAGACGTTGATAAAGTTAATCCTAAATGCATAAATAGCTTTTTTATAAAAACAGATCGGAAGAGCGGTTTCAG

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chr1 186340052 186340091 TPR\_2509 - GTGACCTATGCACCAGACGTTTTCTTAGAATAAGCTCATTGTAGACATTTTACTTGAAGGAGATCGGAAGAGCGGTTTCAG

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chr6 43749643 43749682 VEGFA\_2518 - GTGACCTATGCACCAGACGTGCAAAAGGAAAGACACTAAGCTAGAGCATCAGCAGAGAGATCGGAAGAGCGGTTTCAG

chr6 43752228 43752267 VEGFA\_2519 - GTGACCTATGCACCAGACGTTGGAAAACAAAGGCTGGGGTTAGGGCCAAGTGAGGAGGCCAGATCGGAAGAGCGGTTTCAG

chr6 43752294 43752333 VEGFA\_2520 - GTGACCTATGCACCAGACGTTAAACCTGAGGGAGGCTCTTCTCTCTGCCGCTCACCAGATCGGAAGAGCGGTTTCAG

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chr17 48735746 48735785 ABCC3\_2526 - GTGACCTATGCACCAGACGTAGAGAATAGGACGGGGGAATCAGGAGTGCCACCACCCTCAGATCGGAAGAGCGGTTTCAG

chr17 48736548 48736587 ABCC3\_2527 - GTGACCTATGCACCAGACGTGTAAGCCCGCAGGCGACCCCGCAGAGGGTCAAGGTTAAGATCGGAAGAGCGGTTTCAG

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chr17 48750780 48750819 ABCC3\_2539 - GTGACCTATGCACCAGACGTGGCAGCAGGCTCACCCTCACCCTCCAGCACACCCCAGATCGGAAGAGCGGTTTCAG

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chr17 48757109 48757148 ABCC3\_2546 - GTGACCTATGCACCAGACGTGAGCTGGGTTATAGCTGGCATGCTCCCTCCCACTGAGATCGGAAGAGCGGTTTCAG

chr17 48760921 48760960 ABCC3\_2547 - GTGACCTATGCACCAGACGTGGGCAGATGGGTCACATCAGCTGCCAGTGAAGCCCTCTAGATCGGAAGAGCGGTTTCAG

chr17 48761260 48761299 ABCC3\_2548 - GTGACCTATGCACCAGACGTAAAGGAAGGGCTCTGAGGGGAAAGCTGAGAGGTCAAAGGAGATCGGAAGAGCGGTTTCAG

chr17 48762020 48762059 ABCC3\_2549 - GTGACCTATGCACCAGACGTAACGTGGCCTCAGAGGGAGGCAGCTTAGGCCCTAGGAAGATCGGAAGAGCGGTTTCAG

chr17 48764847 48764886 ABCC3\_2550 - GTGACCTATGCACCAGACGTAGAAGGACGATTTCCAGCTGGGGCTCCCACTGCCTAGATCGGAAGAGCGGTTTCAG

chr17 48768403 48768442 ABCC3\_2551 - GTGACCTATGCACCAGACGTAAAGAGAGAGTGGTCAAGTTTTCCATGACCCTGACCTAGATCGGAAGAGCGGTTTCAG

chr11 35160801 35160840 CD44\_2552 - GTGACCTATGCACCAGACGTGCGAAGCGAGGGCGGGCGAAAGGAGCTGGAGGTCCCTAGATCGGAAGAGCGGTTTCAG

chr11	35198072	35198111	CD44_2553	-	GTGACCTATGCACCAGACGTAAATAGAAATGTTAGATTCTTTTGCATAAATAATTTGGAGAGATCGGAAGAGCGGTTTCAG
chr11	35201771	35201810	CD44_2554	-	GTGACCTATGCACCAGACGTAAAAACAACAGGATATTGACCTAAATGGCTAAGATGGGAATAGATCGGAAGAGCGGTTTCAG
chr11	35208329	35208368	CD44_2555	-	GTGACCTATGCACCAGACGTGGAAAAAAGGATGAGAACCCTTTAAAAACATGAGGAAAAAGATCGGAAGAGCGGTTTCAG
chr11	35211332	35211371	CD44_2556	-	GTGACCTATGCACCAGACGTGAAAAGGTACTTACAGAACTTACAGCTCATATTTGAGTAGATCGGAAGAGCGGTTTCAG
chr11	35218243	35218282	CD44_2557	-	GTGACCTATGCACCAGACGTCATGATTGAATTTGATTGTTGAAAGATTAATTAACGGTTCAGATCGGAAGAGCGGTTTCAG
chr11	35219618	35219657	CD44_2558	-	GTGACCTATGCACCAGACGTGACTTGCTATTGAGTGGCTGAGCTGGACGCAAGCAACCCACAGATCGGAAGAGCGGTTTCAG
chr11	35222579	35222618	CD44_2559	-	GTGACCTATGCACCAGACGTGATGATTAAGCAATTAGAAAAATGTTATTTCTTGAGCTAGATCGGAAGAGCGGTTTCAG
chr11	35223168	35223207	CD44_2560	-	GTGACCTATGCACCAGACGTGATGGTTAAATACACTGTGACTTGTATCAACCAATCTTTAGATCGGAAGAGCGGTTTCAG
chr11	35226009	35226048	CD44_2561	-	GTGACCTATGCACCAGACGTAAATATCAGTTGGGAGACATAATTGTCTATTTTCTCACCAGATCGGAAGAGCGGTTTCAG
chr11	35227609	35227648	CD44_2562	-	GTGACCTATGCACCAGACGTGCAGTTTGAGCAATTGTCAAAGTGTAAATGGACGCTTGGTAGATCGGAAGAGCGGTTTCAG
chr11	35229602	35229641	CD44_2563	-	GTGACCTATGCACCAGACGTCAATATTAGTGTATTGCTTGTATTTCCCAAACCACTACCTAGATCGGAAGAGCGGTTTCAG
chr11	35231462	35231501	CD44_2564	-	GTGACCTATGCACCAGACGTGAGGAATGAATCCAGTGTAATTTGAAAGCTACGGTACAAAAGATCGGAAGAGCGGTTTCAG
chr11	35232743	35232782	CD44_2565	-	GTGACCTATGCACCAGACGTGTGGAAATCAGTGTGAACCCGATTTTGTAAAGATCACCCACAGATCGGAAGAGCGGTTTCAG
chr11	35236349	35236388	CD44_2566	-	GTGACCTATGCACCAGACGTCAATCAGGAAGGTCAGTACTGCATGTTTTACTTACACTCAGATCGGAAGAGCGGTTTCAG
chr11	35240813	35240852	CD44_2567	-	GTGACCTATGCACCAGACGTAAACAACATCTCTCAACCAAGTTTGAATGTGTAAACATAGATCGGAAGAGCGGTTTCAG
chr11	35243151	35243190	CD44_2568	-	GTGACCTATGCACCAGACGTAAATTAATGACATGCGTGAGCTTCAGAGACACACTTTGAGATCGGAAGAGCGGTTTCAG
chr11	35243202	35243241	CD44_2569	-	GTGACCTATGCACCAGACGTCAAAGCCAAGGCAAGGGATGCCAAGATGATCAGCCATAGATCGGAAGAGCGGTTTCAG
chr11	35250626	35250665	CD44_2570	-	GTGACCTATGCACCAGACGTGAAAATGTACCATATCAGAAAGATTGCAGTACTCAGCCAGATCGGAAGAGCGGTTTCAG
chr19	10677684	10677723	CDKN2D_2571	-	GTGACCTATGCACCAGACGTCCCTCTCCAGCAAGAGAACCCTGGGGTTATGTATCAGAAGATCGGAAGAGCGGTTTCAG
chr19	10679139	10679178	CDKN2D_2572	-	GTGACCTATGCACCAGACGTGCCGGTCCAGGTTGGGGCGGGCGGCTAAGCGGGATGAGGAGATCGGAAGAGCGGTTTCAG
chr5	149433582	149433621	CSF1R_2573	-	GTGACCTATGCACCAGACGTACAGGGAGTACCACTCTCCCTCCCAAACTTCAACTCCAGATCGGAAGAGCGGTTTCAG
chr5	149433835	149433874	CSF1R_2574	-	GTGACCTATGCACCAGACGTTGAGGCTTGGGGTGGGTGGCCGGTAAAGCACGTTGGGCTGAGATCGGAAGAGCGGTTTCAG
chr5	149434750	149434789	CSF1R_2575	-	GTGACCTATGCACCAGACGTGGATCCCAGGGAGGAAAAGGCAACCCAGGCTTTCCGTGAGATCGGAAGAGCGGTTTCAG
chr5	149435539	149435578	CSF1R_2576	-	GTGACCTATGCACCAGACGTGGGCCACTCGAGCCAGCCAGCTGGGCTGGCTCCCTCTGGTAGATCGGAAGAGCGGTTTCAG
chr5	149435732	149435771	CSF1R_2577	-	GTGACCTATGCACCAGACGTGAGGGCTTGGGCCAGGCTGGGGAGGGGTGAAGAGTCCGAGATCGGAAGAGCGGTTTCAG
chr5	149436800	149436839	CSF1R_2578	-	GTGACCTATGCACCAGACGTACCTGGCCCTGGCTCATAGCCACCAGGCTGTGCTCCGGAGATCGGAAGAGCGGTTTCAG
chr5	149437017	149437056	CSF1R_2579	-	GTGACCTATGCACCAGACGTCCCAGGGCCAGCCCCATTTGCTTGATAACAAGGAAAAAGAGATCGGAAGAGCGGTTTCAG
chr5	149439213	149439252	CSF1R_2580	-	GTGACCTATGCACCAGACGTGCAAAGGACAAGAAAAAGGCCAGGCTCTGGGAGGCAAGGATCAGATCGGAAGAGCGGTTTCAG
chr5	149440375	149440414	CSF1R_2581	-	GTGACCTATGCACCAGACGTTGGGTTCTCTGGGCCAAGGCTTTGGGGCTCTGGGCAATAGATCGGAAGAGCGGTTTCAG
chr5	149441004	149441043	CSF1R_2582	-	GTGACCTATGCACCAGACGTGGAGGGGATGAGGGAAGGGATGGGGGTTGAGATGCTGGAGATCGGAAGAGCGGTTTCAG
chr5	149441236	149441275	CSF1R_2583	-	GTGACCTATGCACCAGACGTAGCTCATCACTCCACAGCTTCCATACAGGGCCTGTGGGAGATCGGAAGAGCGGTTTCAG
chr5	149447728	149447767	CSF1R_2584	-	GTGACCTATGCACCAGACGTGCGGAGTGGGGCTGCCAGGTGCCTGAGTGAGCCAGATTTGAGATCGGAAGAGCGGTTTCAG
chr5	149449695	149449734	CSF1R_2585	-	GTGACCTATGCACCAGACGTTCCACTCACCTCCCTCAGCTGGGCTCAGGGGCTGGGCACCAGATCGGAAGAGCGGTTTCAG
chr5	149449969	149450008	CSF1R_2586	-	GTGACCTATGCACCAGACGTGGGCCGAGCCCACTGGGGCGGAGGCCCTGGGACTGCCTAGATCGGAAGAGCGGTTTCAG
chr5	149452814	149452853	CSF1R_2587	-	GTGACCTATGCACCAGACGTTCAAGCTCCGCTCTACAGCCGACACCAGATGGGGTATAGATCGGAAGAGCGGTTTCAG
chr5	149456789	149456828	CSF1R_2588	-	GTGACCTATGCACCAGACGTGGGTGGTGGTGACAGTCCGATAGGATCCTGCAGGAGTGTAGATCGGAAGAGCGGTTTCAG
chr5	149457625	149457664	CSF1R_2589	-	GTGACCTATGCACCAGACGTGCAGATCACAAGGTGAAGTCTGGCCATCTCCAGCACACAGATCGGAAGAGCGGTTTCAG
chr5	149459565	149459604	CSF1R_2590	-	GTGACCTATGCACCAGACGTCATGGGGACCCGACAGCCAGCCGTAAGAGTGGGGACAGAGATCGGAAGAGCGGTTTCAG
chr5	149460280	149460319	CSF1R_2591	-	GTGACCTATGCACCAGACGTTGAGCCTCCTCCAAAGAGGCTGACCCGGCAGGGCCCCACTAGATCGGAAGAGCGGTTTCAG
chr5	149465892	149465931	CSF1R_2592	-	GTGACCTATGCACCAGACGTAACGGGGGGTGGGGACTTTGTTGGGTGTGATGGAGAAGAGATCGGAAGAGCGGTTTCAG
chr1	97544482	97544521	DPYD_2593	-	GTGACCTATGCACCAGACGTGAAACAGTGTCTGTGAACCTTTCTACCTACATATAGATCGGAAGAGCGGTTTCAG
chr1	97547836	97547875	DPYD_2594	-	GTGACCTATGCACCAGACGTTGCTGGAATTAGAATGCTATGAGACATGTTTCTTCTTGTAGATCGGAAGAGCGGTTTCAG
chr1	97563995	97564034	DPYD_2595	-	GTGACCTATGCACCAGACGTTGCCAACTATAAGTATGCTACTTTACTGGTTAAATATAGATCGGAAGAGCGGTTTCAG
chr1	97658575	97658614	DPYD_2596	-	GTGACCTATGCACCAGACGTAAATCTCCTGTGTATTCTTGAGAACTCAGCCTTGGTTTCAGATCGGAAGAGCGGTTTCAG
chr1	97700358	97700397	DPYD_2597	-	GTGACCTATGCACCAGACGTTGTTGTCTGCTCCCTTTAAAAATCTCCATCTCACAATGAGATCGGAAGAGCGGTTTCAG
chr1	97770765	97770804	DPYD_2598	-	GTGACCTATGCACCAGACGTCCCCTCTTGCATTTGCTTTCTTGAGGTTGCTGAAAAAGATCGGAAGAGCGGTTTCAG
chr1	97771683	97771722	DPYD_2599	-	GTGACCTATGCACCAGACGTGACTTGAATCAGTTGCCGCTATTGTAATATTGGCCACAGATCGGAAGAGCGGTTTCAG
chr1	97839067	97839106	DPYD_2600	-	GTGACCTATGCACCAGACGTTGACAGCTGCCACTAAGTATGTCAGTGTACATAACAGGCAGATCGGAAGAGCGGTTTCAG
chr1	97847899	97847938	DPYD_2601	-	GTGACCTATGCACCAGACGCTTTAGTATATATTTATTTTCTTCTCTCTATTTTAGATCGGAAGAGCGGTTTCAG
chr1	97915565	97915604	DPYD_2602	-	GTGACCTATGCACCAGACGTTTTAACATCTAAAACAAGAGAATGGCATAAGTTGGTGAAGATCGGAAGAGCGGTTTCAG
chr1	97981232	97981271	DPYD_2603	-	GTGACCTATGCACCAGACGTATTATTGAAGTCATATAGAAATGCTCTCATATATTTAAAGATCGGAAGAGCGGTTTCAG
chr1	98015066	98015105	DPYD_2604	-	GTGACCTATGCACCAGACGTGCCATTTCCACTTAATTTCTTCAATGGATAAGTGCAGATCGGAAGAGCGGTTTCAG
chr1	98039266	98039305	DPYD_2605	-	GTGACCTATGCACCAGACGTGGGAGCTGAAATGTGTGATGCAATTGTCTGTTATTTAGTAGATCGGAAGAGCGGTTTCAG
chr1	98058724	98058763	DPYD_2606	-	GTGACCTATGCACCAGACGTACCATCAGAAAAATGGAGTTGTACTCCAACAGATTTTAGAGATCGGAAGAGCGGTTTCAG
chr1	98060565	98060604	DPYD_2607	-	GTGACCTATGCACCAGACGTTGTCTTTATGCTTAATAGTGAATGATGCTATTTTATTAAGATCGGAAGAGCGGTTTCAG
chr1	98157223	98157262	DPYD_2608	-	GTGACCTATGCACCAGACGTAAACACCTATCTGTGTACTGCTCAAAAAGAAAGGAGTAAAGATCGGAAGAGCGGTTTCAG
chr1	98164857	98164896	DPYD_2609	-	GTGACCTATGCACCAGACGTTATTTATGTTATAGTTTATAGTTCAGAAATGATGGAGACAAAGATCGGAAGAGCGGTTTCAG
chr1	98187016	98187055	DPYD_2610	-	GTGACCTATGCACCAGACGTATACAGCTGACATCCCCCACTACCATGCACAAGATCGGAAGAGCGGTTTCAG

chr1	98205898	98205937	DPYD_2611	-	GTGACCTATGCACCAGACGTATTTAACTCTGCAAATGAAAATAACAGTATTTGATCTTGTAGATCGGAAGAGCGGTTTCAG
chr1	98293620	98293659	DPYD_2612	-	GTGACCTATGCACCAGACGTGTACCATTAGCAACAGTACACAGATGTGGTAAAGAAAAAGTAGATCGGAAGAGCGGTTTCAG
chr1	98348770	98348809	DPYD_2613	-	GTGACCTATGCACCAGACGTCTGATACACTATTTTCATGCTGAAAATTACCTCACTCCACAAGATCGGAAGAGCGGTTTCAG
chr1	98386390	98386429	DPYD_2614	-	GTGACCTATGCACCAGACGTGCGCGCGGCTCGTGGTGGTGGCGGGTGGTGGGGAGTGCAGATCGGAAGAGCGGTTTCAG
chr14	64694201	64694240	ESR2_2615	-	GTGACCTATGCACCAGACGTAACCTCGGTGGCCTAAAGAAAAATCTTGGGTAACATTTTCAAGATCGGAAGAGCGGTTTCAG
chr14	64699805	64699844	ESR2_2616	-	GTGACCTATGCACCAGACGTTGAGGTGAACCTGGCCACAGAGGTCACAGGCTGAAGCGTGAGATCGGAAGAGCGGTTTCAG
chr14	64701638	64701677	ESR2_2617	-	GTGACCTATGCACCAGACGTTAAAGGAGCTGCTCTGCTGGGATGGGATGTATGTGAGATCGGAAGAGCGGTTTCAG
chr14	64716214	64716253	ESR2_2618	-	GTGACCTATGCACCAGACGTACACAGCTGGGCCATGTTTTATCGGGGAGAGATGCTGTTTTAGATCGGAAGAGCGGTTTCAG
chr14	64723894	64723933	ESR2_2619	-	GTGACCTATGCACCAGACGTATACATTGTGTTTCTCTGACTTGTTTGAGTAAGGTGCAGATCGGAAGAGCGGTTTCAG
chr14	64735463	64735502	ESR2_2620	-	GTGACCTATGCACCAGACGTGCTTCCCTTCTTATTGAATATGGGCCCTTGCTAAAAGCCCTAGATCGGAAGAGCGGTTTCAG
chr14	64746649	64746688	ESR2_2621	-	GTGACCTATGCACCAGACGTATTGTTAACTGCTTCTTTAGTTTCTACTTTTGATTTCAAAGATCGGAAGAGCGGTTTCAG
chr14	64749292	64749331	ESR2_2622	-	GTGACCTATGCACCAGACGTTCTTCACTTGAATATAGTTGCTAGCCATTCTCAAATCAGATCGGAAGAGCGGTTTCAG
chr22	29668155	29668194	EWSR1_2623	-	GTGACCTATGCACCAGACGTAAACAGGAGAAATAGTGTAAAGTTAGCAGAAACAAGGAAGATCGGAAGAGCGGTTTCAG
chr22	29668319	29668358	EWSR1_2624	-	GTGACCTATGCACCAGACGTATTAATGCAATAACTTGAATAGAGAACATCAAATACCAAGATCGGAAGAGCGGTTTCAG
chr22	29669680	29669719	EWSR1_2625	-	GTGACCTATGCACCAGACGTAAAAACGAATGCAAGAACTTCATACATGAACTTTTGATAGATCGGAAGAGCGGTTTCAG
chr22	29673969	29674008	EWSR1_2626	-	GTGACCTATGCACCAGACGTGGAGAGCTGCATCAGATTTTCAGGTCCTCAGAGATCTGCAGATCGGAAGAGCGGTTTCAG
chr22	29682862	29682901	EWSR1_2627	-	GTGACCTATGCACCAGACGTGAGAAGAGAAAAAAAAGGCTTTTGAAGAGGCGTTAGATCGGAAGAGCGGTTTCAG
chr22	29684545	29684584	EWSR1_2628	-	GTGACCTATGCACCAGACGTAGTCACATGTAAAGCCATGGCCAGCATTTACACCATGAGATCGGAAGAGCGGTTTCAG
chr22	29687501	29687540	EWSR1_2629	-	GTGACCTATGCACCAGACGTAAACGAGAAGAAATGAAGGCCCTTCCCTTTAAAAGCCAGTACAGATCGGAAGAGCGGTTTCAG
chr22	29688076	29688115	EWSR1_2630	-	GTGACCTATGCACCAGACGTGGAAGATCATATAAATATTATTAGTGCACGCTTGCAAAGATCGGAAGAGCGGTTTCAG
chr22	29688427	29688466	EWSR1_2631	-	GTGACCTATGCACCAGACGTCAACAAGACAGGAGAAATTATTATCATGTATCTATAGGGGTAGATCGGAAGAGCGGTTTCAG
chr22	29692179	29692218	EWSR1_2632	-	GTGACCTATGCACCAGACGTAATAGCATAGTTAGGGCATGACTAGAATATACTAATTTGGGAGATCGGAAGAGCGGTTTCAG
chr22	29693767	29693806	EWSR1_2633	-	GTGACCTATGCACCAGACGTACAACAGAACATCAATTAATCCCCTGACTCCCCTGTTACAGATCGGAAGAGCGGTTTCAG
chr22	29694673	29694712	EWSR1_2634	-	GTGACCTATGCACCAGACGTAAACAAGAAACAGCAAACTATTTCTCTGTAGCACAAGAGATCGGAAGAGCGGTTTCAG
chr22	29695174	29695213	EWSR1_2635	-	GTGACCTATGCACCAGACGTTTACATCACAGCAGAAATCACAATTTGAACTAAGGAAGATAGATCGGAAGAGCGGTTTCAG
chr22	29695539	29695578	EWSR1_2636	-	GTGACCTATGCACCAGACGTAATAGCAGGGCGAAAGCAGTCAAGTGGTGGCTGCAGAGGCAGATCGGAAGAGCGGTTTCAG
chr22	29696062	29696101	EWSR1_2637	-	GTGACCTATGCACCAGACGTAAAGAGGGCCCTTCGGTTAGAAATGGGAAGGGGTGAGGAAGCAGATCGGAAGAGCGGTTTCAG
chr3	10070292	10070331	FANCD2_2638	-	GTGACCTATGCACCAGACGTGCTTTGTGCACTTAAATTAATCTTCTAGAGCAAAATCGGGAAGATCGGAAGAGCGGTTTCAG
chr3	10074466	10074505	FANCD2_2639	-	GTGACCTATGCACCAGACGTAAAAATTTTCAAGAATGTGCAAAATGAAAAGAAAAATAGATCGGAAGAGCGGTTTCAG
chr3	10076103	10076142	FANCD2_2640	-	GTGACCTATGCACCAGACGTAAACAAGAGACTGGTACCAGTTTTCTACCATAGTTTTCCAGATCGGAAGAGCGGTTTCAG
chr3	10076807	10076846	FANCD2_2641	-	GTGACCTATGCACCAGACGTAAAAAAATCTGTTTTCCACTTTGCTTTCTTGTTTTAAATAGATCGGAAGAGCGGTTTCAG
chr3	10077921	10077960	FANCD2_2642	-	GTGACCTATGCACCAGACGTAGACATAGGGAGTTAGGAGATGATCTCAAATACACAATAAGATCGGAAGAGCGGTTTCAG
chr3	10080913	10080952	FANCD2_2643	-	GTGACCTATGCACCAGACGTAGGAAGAGAAAAACAGGAACTGAGCCTTTCTGGTCAAAAATAGATCGGAAGAGCGGTTTCAG
chr3	10081355	10081394	FANCD2_2644	-	GTGACCTATGCACCAGACGTAGACACTATTAGAACTGCAGCAGATCCCAAGAAAGAAAGATCGGAAGAGCGGTTTCAG
chr3	10083257	10083296	FANCD2_2645	-	GTGACCTATGCACCAGACGTGAAAGAAAGAAAAAGTTGATAATTGGTTTTGAACAGAGTAGATCGGAAGAGCGGTTTCAG
chr3	10084193	10084232	FANCD2_2646	-	GTGACCTATGCACCAGACGTAAAGCACAGAACTTAATAGGTTTTCATGTCACTACCTCAAGATCGGAAGAGCGGTTTCAG
chr3	10084684	10084723	FANCD2_2647	-	GTGACCTATGCACCAGACGTAAATATTAGCTATGTTTTCTGCTCATTATAGTTGGTAAAGATCGGAAGAGCGGTTTCAG
chr3	10085118	10085157	FANCD2_2648	-	GTGACCTATGCACCAGACGTGAGAGAGAAAAAATTAATCTTCTACGTACCAGAAAAAGAAAGATCGGAAGAGCGGTTTCAG
chr3	10085463	10085502	FANCD2_2649	-	GTGACCTATGCACCAGACGTAGGAGAGAGTCAAAAAATATTATGACACATCAGCGAAACAGATCGGAAGAGCGGTTTCAG
chr3	10088214	10088253	FANCD2_2650	-	GTGACCTATGCACCAGACGTAAATATGCAACAACAGAAAAACAGTTAACAAATCAGTACAGATCGGAAGAGCGGTTTCAG
chr3	10089551	10089590	FANCD2_2651	-	GTGACCTATGCACCAGACGTGAAGAGTAGAGAGAGAAAAAGACTGTAGGAACAGTTAGATCGGAAGAGCGGTTTCAG
chr3	10091008	10091047	FANCD2_2652	-	GTGACCTATGCACCAGACGTGAGAGTCAACAGAACAGTGTAAAAACAAATATGGATGGCCAGATCGGAAGAGCGGTTTCAG
chr3	10094021	10094060	FANCD2_2653	-	GTGACCTATGCACCAGACGTAATGATGCCAACATGAGGCTAGCAGTAACATTTTTCCAGATCGGAAGAGCGGTTTCAG
chr3	10101928	10101967	FANCD2_2654	-	GTGACCTATGCACCAGACGTATGATGAAGAAAGATGAAAATGCTGGAATGGCACAGCAAAAGATCGGAAGAGCGGTTTCAG
chr3	10105426	10105465	FANCD2_2655	-	GTGACCTATGCACCAGACGTGAGGAAGAATGGTTTTAAACCTTTGGGCTGCCAATCTTTCCAGATCGGAAGAGCGGTTTCAG
chr3	10106363	10106402	FANCD2_2656	-	GTGACCTATGCACCAGACGTAAACCAGACTGATGTTGCTGAGCTCAGGAATACGCAAGGCAGATCGGAAGAGCGGTTTCAG
chr3	10107028	10107067	FANCD2_2657	-	GTGACCTATGCACCAGACGTGAAATAAATTTCTAGACCACACTTCATAGGTGTATTACTCAGATCGGAAGAGCGGTTTCAG
chr3	10107498	10107537	FANCD2_2658	-	GTGACCTATGCACCAGACGTACAACATTTCCAACACTCTTAGTGCAAGCCAATAAAAACAGATCGGAAGAGCGGTTTCAG
chr3	10108843	10108882	FANCD2_2659	-	GTGACCTATGCACCAGACGTCAAATACATTTCTACACTTCCAATGTTTCAGATTTAACAGATCGGAAGAGCGGTTTCAG
chr3	10114505	10114544	FANCD2_2660	-	GTGACCTATGCACCAGACGTGACGAGGCTGAAGCTCAATGTGTACCAATTACACACCACAGATCGGAAGAGCGGTTTCAG
chr3	10114887	10114926	FANCD2_2661	-	GTGACCTATGCACCAGACGTAAAAAGAGAAAAAGTACTCAAGTAATTAATAATCATGTTTATGATCGGAAGAGCGGTTTCAG
chr3	10116164	10116203	FANCD2_2662	-	GTGACCTATGCACCAGACGTGTACAGACGAAACAAGAAATATAAATCTTCTATATTAAGATCGGAAGAGCGGTTTCAG
chr3	10119715	10119754	FANCD2_2663	-	GTGACCTATGCACCAGACGTGAGGAAGGATTAGTTCAGGAATGTCCTAGTCAATTTTATAGATCGGAAGAGCGGTTTCAG
chr3	10122734	10122773	FANCD2_2664	-	GTGACCTATGCACCAGACGTTGCAGAGTTATGAGTGAAGAAACTGCTGGATAGCGTCTCAAGATCGGAAGAGCGGTTTCAG
chr3	10122980	10123019	FANCD2_2665	-	GTGACCTATGCACCAGACGTAATGATTTTTAGGACAGTTGCTTACAGTAATTGCTCTATTAGATCGGAAGAGCGGTTTCAG
chr3	10127446	10127485	FANCD2_2666	-	GTGACCTATGCACCAGACGTCAAGGTAAGAGGGTTAGCTTAGTTTCTGAAAACACTTATAGATCGGAAGAGCGGTTTCAG
chr3	10128768	10128807	FANCD2_2667	-	GTGACCTATGCACCAGACGTAAACAGAAAAACAATAAGTAAATGCTATGTGTCAGATCGGAAGAGCGGTTTCAG
chr3	10130083	10130122	FANCD2_2668	-	GTGACCTATGCACCAGACGTAGAAGACAAAGAAATCTTACATATGGAACTTGACCTCATAGATCGGAAGAGCGGTTTCAG

chr3	10130462	10130501	FANCD2_2669	-	GTGACCTATGCACCAGACGTAGTCAAATATTTGACCCACTAATTAACAAAGTAGAATACAAGATCGGAAGAGCGGTTTCAG
chr3	10131926	10131965	FANCD2_2670	-	GTGACCTATGCACCAGACGTGAAAGCATGCGTGCCACACCATGATGCACTGCTTAGAAGATCGGAAGAGCGGTTTCAG
chr3	10133815	10133854	FANCD2_2671	-	GTGACCTATGCACCAGACGTCAAATATATGGGCACCTCTGAGTACACGCCAAATACTTCCAGATCGGAAGAGCGGTTTCAG
chr3	10134919	10134958	FANCD2_2672	-	GTGACCTATGCACCAGACGTGAAAGACAAGAAACCAAGGCTGAGATCTGCTCCTTTGAGCAGATCGGAAGAGCGGTTTCAG
chr3	10135923	10135962	FANCD2_2673	-	GTGACCTATGCACCAGACGTGAGACACACTGTTACCTCTAGCTGAGGTATCTCACTGAAAAGATCGGAAGAGCGGTTTCAG
chr3	10136834	10136873	FANCD2_2674	-	GTGACCTATGCACCAGACGTTAAGTTTATAAATGCTCTATGAAATGTCTGATTTTCATTAGATCGGAAGAGCGGTTTCAG
chr3	10137960	10137999	FANCD2_2675	-	GTGACCTATGCACCAGACGTATAAATAACATCCCTTTTTGTGAGTTTATCATCATGCCCTAGATCGGAAGAGCGGTTTCAG
chr3	10140354	10140393	FANCD2_2676	-	GTGACCTATGCACCAGACGTATGGACCAAGAAAATGGTGGGTTATAATGATCACATTTAGAGATCGGAAGAGCGGTTTCAG
chr3	10142822	10142861	FANCD2_2677	-	GTGACCTATGCACCAGACGTAAAGATAAATAAATAAGCATTATAGTACTGCTCTGGGTAGATCGGAAGAGCGGTTTCAG
chr14	75745636	75745675	FOS_2678	-	GTGACCTATGCACCAGACGTAGGCAAGCCGCGGAGGGGCCGAGGGCCGAGACAGGTTGAGATCGGAAGAGCGGTTTCAG
chr14	75746530	75746569	FOS_2679	-	GTGACCTATGCACCAGACGTACAGAAGGGGAAAGCCGACCTGAGCGAGCAGGTTCCGGACAGATCGGAAGAGCGGTTTCAG
chr14	75747213	75747252	FOS_2680	-	GTGACCTATGCACCAGACGTACAAAAAAGACCCGACATTAGTAAAGTGTCTGCCATCAGATCGGAAGAGCGGTTTCAG
chr14	75747436	75747475	FOS_2681	-	GTGACCTATGCACCAGACGTAGGGATAAAGGAAAGCATTAAAGACACAGTCTTACTCAAGGGAGATCGGAAGAGCGGTTTCAG
chr14	75747757	75747796	FOS_2682	-	GTGACCTATGCACCAGACGTTCATCAAAGGGCTCGGTCTTACGCTCCATGCTGCTGATGCAGATCGGAAGAGCGGTTTCAG
chr11	33880852	33880891	LMO2_2683	-	GTGACCTATGCACCAGACGTCCGGGCATCTTTGGGGAGGTGTTCACTGAAGACGCCGCTAGATCGGAAGAGCGGTTTCAG
chr11	33886098	33886137	LMO2_2684	-	GTGACCTATGCACCAGACGTCCGGCCTCCACTGGGCCCTCGGAAGGGAGGCTGGGTGGTCAGATCGGAAGAGCGGTTTCAG
chr11	33890842	33890881	LMO2_2685	-	GTGACCTATGCACCAGACGTCCCCCTGCCCTGCCACCCCGGTTGCCACCGCTCGCGAGATCGGAAGAGCGGTTTCAG
chr19	15276129	15276168	NOTCH3_2686	-	GTGACCTATGCACCAGACGTAGAGGAATCAAGTCAAGTGGTGTGGTGTACCTGGCCAGATCGGAAGAGCGGTTTCAG
chr19	15276548	15276587	NOTCH3_2687	-	GTGACCTATGCACCAGACGTACACACTTTGGACCTCAGAGCTGGGGCAGGCATTAGACTAGATCGGAAGAGCGGTTTCAG
chr19	15278010	15278049	NOTCH3_2688	-	GTGACCTATGCACCAGACGTGTCGCCCTCCCAAAGGGATGCCCTCACCCATCCTACCTGAGATCGGAAGAGCGGTTTCAG
chr19	15280847	15280886	NOTCH3_2689	-	GTGACCTATGCACCAGACGTCCCTCTGACCTTTGCCCTCCTCTGACCCTCCCTCAGAGATCGGAAGAGCGGTTTCAG
chr19	15281092	15281131	NOTCH3_2690	-	GTGACCTATGCACCAGACGTGGCTCGCTCCCTGTCCCTGACTACGGGGACCTTGTGAACCAGATCGGAAGAGCGGTTTCAG
chr19	15281432	15281471	NOTCH3_2691	-	GTGACCTATGCACCAGACGTGCTTGGGAGGGGTGGCGGGGCGGAGCTGGGGCGGCAGATCGGAAGAGCGGTTTCAG
chr19	15284829	15284868	NOTCH3_2692	-	GTGACCTATGCACCAGACGTCCACTGGGATAAAGCCGTGGTGGCTGGGGAGAGGAGATGAGATCGGAAGAGCGGTTTCAG
chr19	15289584	15289623	NOTCH3_2693	-	GTGACCTATGCACCAGACGTGTGGCGGCCTTTGGAGGAGGAGTAGGGGCGTGGCCTCTGGAGATCGGAAGAGCGGTTTCAG
chr19	15289786	15289825	NOTCH3_2694	-	GTGACCTATGCACCAGACGTGCGAAGGGGCTGGCCTGGGACCCCGCTGTCAATCCCCAAGATCGGAAGAGCGGTTTCAG
chr19	15290125	15290164	NOTCH3_2695	-	GTGACCTATGCACCAGACGTGCCAGGGTGGGGGACAGGATGAGAGGCTGTCTTCATTAGATCGGAAGAGCGGTTTCAG
chr19	15290833	15290872	NOTCH3_2696	-	GTGACCTATGCACCAGACGTGCTCCCCAGGAGGGGAAGGAGGAGGTTGGGCATGCTTGGGTAGATCGGAAGAGCGGTTTCAG
chr19	15291442	15291481	NOTCH3_2697	-	GTGACCTATGCACCAGACGTGCATGTGGCGGGCTGGCGGGGCGGAGCTGGGGCGGCAGATCGGAAGAGCGGTTTCAG
chr19	15291722	15291761	NOTCH3_2698	-	GTGACCTATGCACCAGACGTCTTACTGGGGACCTGGGGAGGAGCCTGCCTGGGATCCTAGAGATCGGAAGAGCGGTTTCAG
chr19	15292337	15292376	NOTCH3_2699	-	GTGACCTATGCACCAGACGTCTCTGCTTGGAGAGCAGGGACTCTGGCTTGGGATGGGGCAGATCGGAAGAGCGGTTTCAG
chr19	15295667	15295706	NOTCH3_2700	-	GTGACCTATGCACCAGACGTGCTTCTCTTCCCTCCTCCTCCTCCATCCTCTGCCCTTAGATCGGAAGAGCGGTTTCAG
chr19	15296018	15296057	NOTCH3_2701	-	GTGACCTATGCACCAGACGTACCTTCCCTCTGCAGCCCCAACACCATGGGCCTTAGATCGGAAGAGCGGTTTCAG
chr19	15296248	15296287	NOTCH3_2702	-	GTGACCTATGCACCAGACGTCTTCTCAGCCTCAGACACTGCCCTCCTCCTGCCCTAGATCGGAAGAGCGGTTTCAG
chr19	15297639	15297678	NOTCH3_2703	-	GTGACCTATGCACCAGACGTGGCTGCTCAGAGGGGCTCCTTAGATCGAGGGTGAAGTTCAGATCGGAAGAGCGGTTTCAG
chr19	15297866	15297905	NOTCH3_2704	-	GTGACCTATGCACCAGACGTGGGCTGGGGCAGAAACAGCACACCTGGAGGGGCACAGAGGATCGGAAGAGCGGTTTCAG
chr19	15298642	15298681	NOTCH3_2705	-	GTGACCTATGCACCAGACGTCCAATGACAGTCCGACAAGAATCAGGAGGCGGGCTTGTGAGATCGGAAGAGCGGTTTCAG
chr19	15298996	15299035	NOTCH3_2706	-	GTGACCTATGCACCAGACGTGAGGAGAGGGAGCCGAAAGACATGCTGGGAAGGGGCAAGATCGGAAGAGCGGTTTCAG
chr19	15299750	15299789	NOTCH3_2707	-	GTGACCTATGCACCAGACGTGGCGTGGCCTGGCGGGTCTGAGGCAAGGGGCGGGGACAAGATCGGAAGAGCGGTTTCAG
chr19	15300034	15300073	NOTCH3_2708	-	GTGACCTATGCACCAGACGTCTCCATGCTGTGAATGGCTGGAAAGAGGGGAGAGGAAGATCGGAAGAGCGGTTTCAG
chr19	15302185	15302224	NOTCH3_2709	-	GTGACCTATGCACCAGACGTGTTTTCTCGCAGGGACCATGGATGGATGGTTTTTGTAGGGAGATCGGAAGAGCGGTTTCAG
chr19	15302506	15302545	NOTCH3_2710	-	GTGACCTATGCACCAGACGTGGCCAGAGGGAGCGGGGAGGCAGGCCCTCGGGTGGACATGAGATCGGAAGAGCGGTTTCAG
chr19	15302721	15302760	NOTCH3_2711	-	GTGACCTATGCACCAGACGTCTACTCAGGAGAGTCAAGAGGGTGGGCTGGGGCAGCAAGATCGGAAGAGCGGTTTCAG
chr19	15303138	15303177	NOTCH3_2712	-	GTGACCTATGCACCAGACGTAAAGAGTCTGGAGGGGAGGTAGTGGGGGTGTGGTCACTCAGATCGGAAGAGCGGTTTCAG
chr19	15308261	15308300	NOTCH3_2713	-	GTGACCTATGCACCAGACGTGGCTCAGAGCCACAGTGGGCGCTGTGTGGGGCGGGGAGATCGGAAGAGCGGTTTCAG
chr19	15311549	15311588	NOTCH3_2714	-	GTGACCTATGCACCAGACGTGGGACCTGGGACCTGGGAGCCGAGGGGCGCAGAGGGGAGTGCAGATCGGAAGAGCGGTTTCAG
chr19	15271774	15271813	NOTCH3_2715	-	GTGACCTATGCACCAGACGTGCCTTACCTGGCAGTCCCAGGACATGGCGAGGAGTACCCAGATCGGAAGAGCGGTTTCAG
chr19	15272125	15272164	NOTCH3_2716	-	GTGACCTATGCACCAGACGTGGCTGACAGCTCGGTACCGTGTGCGCCGTGGACTCGCTAGATCGGAAGAGCGGTTTCAG
chr1	226549111	226549150	PARP1_2717	-	GTGACCTATGCACCAGACGTAGCCGAGTACACCCGGTGGCTCTGGTATGAATTCACCAGATCGGAAGAGCGGTTTCAG
chr1	226549620	226549659	PARP1_2718	-	GTGACCTATGCACCAGACGTGGAGTATGCTGTGTGAGCACAAAGGATGTTCTCGAGCTAGATCGGAAGAGCGGTTTCAG
chr1	226550750	226550789	PARP1_2719	-	GTGACCTATGCACCAGACGTCCAAAGCTGTTGCTACAGCCGAGGACCCCTGGACAGCAAGATCGGAAGAGCGGTTTCAG
chr1	226551594	226551633	PARP1_2720	-	GTGACCTATGCACCAGACGTCTGGCTCGGACTGATGCCATTTTCATGGGGACAGGTGGAAGATCGGAAGAGCGGTTTCAG
chr1	226552653	226552692	PARP1_2721	-	GTGACCTATGCACCAGACGTGGCCTGGCGAGGGGTGGGCAATGCCTGTCTGCAAGTGTAGATCGGAAGAGCGGTTTCAG
chr1	226553605	226553644	PARP1_2722	-	GTGACCTATGCACCAGACGTCTTCTCCCCACTTCTTCTGTGCTCCTGCCAGCTCTCCAGATCGGAAGAGCGGTTTCAG
chr1	226555850	226555889	PARP1_2723	-	GTGACCTATGCACCAGACGTGGTTCAGAAAGGACTCAGAGTCTGCTGGCTGGGTGTGAAGATCGGAAGAGCGGTTTCAG
chr1	226558085	226558124	PARP1_2724	-	GTGACCTATGCACCAGACGTGGCTACCAGGGCCCTCCTGGAACCTCCTCTGGCCGACTTAGATCGGAAGAGCGGTTTCAG
chr1	226561877	226561916	PARP1_2725	-	GTGACCTATGCACCAGACGTTTATACCTTTTATCTGTGAGCATTTGCTGGATGATTAGATCGGAAGAGCGGTTTCAG
chr1	226564759	226564798	PARP1_2726	-	GTGACCTATGCACCAGACGTAAATGCCCTTTACACTGTCTTCTAGGAAAAGGAAGGACAGATCGGAAGAGCGGTTTCAG

chr1	226566793	226566832	PARP1_2727	-	GTGACCTATGCACCAGACGTGAGGTTAGCTGTTGTGCAGAGACATGGGCCGTCCTGAGATCGGAAGAGCGGTTTCAG
chr1	226567224	226567263	PARP1_2728	-	GTGACCTATGCACCAGACGTAGGACTGCCAGCAAAGTGGGCTGTGCCGCCCCCAACCCAGATCGGAAGAGCGGTTTCAG
chr1	226567573	226567612	PARP1_2729	-	GTGACCTATGCACCAGACGTCAAGCTGCCCCCTCCAGGGCCAAAAGCCAGGGACATTGGTAGATCGGAAGAGCGGTTTCAG
chr1	226568719	226568758	PARP1_2730	-	GTGACCTATGCACCAGACGTTCTGAATTTGTGCAACAGGGACAATGCTTCTGTATCTTATAGATCGGAAGAGCGGTTTCAG
chr1	226570687	226570726	PARP1_2731	-	GTGACCTATGCACCAGACGTTGGGACCCCGGCTTTAGAGCTGCTTTGCAGGAATGTTTTGAGATCGGAAGAGCGGTTTCAG
chr1	226573155	226573194	PARP1_2732	-	GTGACCTATGCACCAGACGTGGGGGAAGACTCTGGGATCTGTTGGGAGAAAAACCTGGCCAGATCGGAAGAGCGGTTTCAG
chr1	226573977	226574016	PARP1_2733	-	GTGACCTATGCACCAGACGTTTTGTGTTAAGTGGGACACGCTGTAGGCGGACCCGTCAGATCGGAAGAGCGGTTTCAG
chr1	226576307	226576346	PARP1_2734	-	GTGACCTATGCACCAGACGTAGCTCTGTGTCTCCTTTTCGACATTCTGCTGTCTGGATTCTAGATCGGAAGAGCGGTTTCAG
chr1	226578061	226578100	PARP1_2735	-	GTGACCTATGCACCAGACGTCACTGCGGGGTTGCCCTGGGGGTTCAAGAGATCGGAAGAGCGGTTTCAG
chr1	226579850	226579889	PARP1_2736	-	GTGACCTATGCACCAGACGTGGGGGCCAGATCCCTGAACTTTATGATTGCTTGAATGAGATCGGAAGAGCGGTTTCAG
chr1	226589865	226589904	PARP1_2737	-	GTGACCTATGCACCAGACGTACTGGGGCAGCATGGGCATTGACCCCAACCCCTGAAGCTCAGATCGGAAGAGCGGTTTCAG
chr17	64302164	64302203	PRKCA_2738	-	GTGACCTATGCACCAGACGTAACCAAGAACAAATATCTTAACATATTTCTGTTGGATAGATCGGAAGAGCGGTTTCAG
chr17	64492269	64492308	PRKCA_2739	-	GTGACCTATGCACCAGACGTTAAAAGCAAATAAAATTAGAATAGACATGATTTAACATACAGATCGGAAGAGCGGTTTCAG
chr17	64637423	64637462	PRKCA_2740	-	GTGACCTATGCACCAGACGTAAGAAGCACAAATGCTCATTTTTAGTCATGAAAGGACCACGTAGATCGGAAGAGCGGTTTCAG
chr17	64641451	64641490	PRKCA_2741	-	GTGACCTATGCACCAGACGTAGAAGGAGAGGGTGAGCTGGGCATATGGACTCCAACCACAGATCGGAAGAGCGGTTTCAG
chr17	64683179	64683218	PRKCA_2742	-	GTGACCTATGCACCAGACGTAGAAGGAAAGAAAATATTACAAAAAGAGAACAGACCTATATAGATCGGAAGAGCGGTTTCAG
chr17	64684370	64684409	PRKCA_2743	-	GTGACCTATGCACCAGACGTACACACATGCAAACTAGGTTATCTGATCATGGTTTCAGATCGGAAGAGCGGTTTCAG
chr17	64685019	64685058	PRKCA_2744	-	GTGACCTATGCACCAGACGTCGGGAGAAAGAGTTACCACCGCAAGTTTAAACAAGCTTAGATCGGAAGAGCGGTTTCAG
chr17	64728756	64728795	PRKCA_2745	-	GTGACCTATGCACCAGACGTAGCACAAATGGGAAACACGTGGGTCATTTTTCTGGGAAAAGATCGGAAGAGCGGTTTCAG
chr17	64731557	64731596	PRKCA_2746	-	GTGACCTATGCACCAGACGTGTCAAGAACAACCTGAACACTTGAAGCACATATCTGGGAGATCGGAAGAGCGGTTTCAG
chr17	64734832	64734871	PRKCA_2747	-	GTGACCTATGCACCAGACGTAGGTTCAACACATGAGCAGGGCTCCTCCCAAGCCAAAGTGGAGATCGGAAGAGCGGTTTCAG
chr17	64737727	64737766	PRKCA_2748	-	GTGACCTATGCACCAGACGTAACCGGGCTTCAGGTTTCTCACTTGTCTTCTTAGATGCCTAGATCGGAAGAGCGGTTTCAG
chr17	64738690	64738729	PRKCA_2749	-	GTGACCTATGCACCAGACGTCGGGTTAAACATCAGATCCTTCCCATGACATAACATGGTAGATCGGAAGAGCGGTTTCAG
chr17	64770055	64770094	PRKCA_2750	-	GTGACCTATGCACCAGACGTACAAAACATCAATTAATTGATGTTGTAAGTCCAATAGCCAGATCGGAAGAGCGGTTTCAG
chr17	64782935	64782974	PRKCA_2751	-	GTGACCTATGCACCAGACGTAAGAAAGAAAGATGGGAAAGTATTTAGGCAGAGTAATTCAAGATCGGAAGAGCGGTTTCAG
chr17	64784907	64784946	PRKCA_2752	-	GTGACCTATGCACCAGACGTAAGGAGAAAAGGAGAACAATGGATGCAAGGGCTTCCCAAGATCGGAAGAGCGGTTTCAG
chr17	64799941	64799980	PRKCA_2753	-	GTGACCTATGCACCAGACGTAAGACAAAAGAAAGGAAAGGTGAGTCAACATGACAATGCGAGATCGGAAGAGCGGTTTCAG
chr18	45368148	45368187	SMAD2_2754	-	GTGACCTATGCACCAGACGTATCAAGTCCCATGAAAAGACTTAATGTAACAACCTTCTGAGATCGGAAGAGCGGTTTCAG
chr18	45371661	45371700	SMAD2_2755	-	GTGACCTATGCACCAGACGTATATTTGGTTCTTAAATTTCCACAGTGTAATTATGTTTCAGATCGGAAGAGCGGTTTCAG
chr18	45371984	45372023	SMAD2_2756	-	GTGACCTATGCACCAGACGTAATAATGTACATAAACCTATCATGTCAACTTGCCTTAGATCGGAAGAGCGGTTTCAG
chr18	45374796	45374835	SMAD2_2757	-	GTGACCTATGCACCAGACGTTTTTCTTGTGTGAAAATAAATGCTGTATACTCATAATAGATCGGAAGAGCGGTTTCAG
chr18	45377595	45377634	SMAD2_2758	-	GTGACCTATGCACCAGACGTATATGTTCCCTCATCATTTTTATACTGTATCACCTACTAGATCGGAAGAGCGGTTTCAG
chr18	45391380	45391419	SMAD2_2759	-	GTGACCTATGCACCAGACGTTGCTTTGAAAATCTCCAGTTATTAGATATACATTTCTTAGATCGGAAGAGCGGTTTCAG
chr18	45394644	45394683	SMAD2_2760	-	GTGACCTATGCACCAGACGTTCTTGAATCTCCATAAACCTGGATAGATACAAAATTTGTAGATCGGAAGAGCGGTTTCAG
chr18	45395564	45395603	SMAD2_2761	-	GTGACCTATGCACCAGACGTTGCAAGTTTTTTTTCTGTGTTTTGAAATTAATGCTTGAACATGATCGGAAGAGCGGTTTCAG
chr18	45396796	45396835	SMAD2_2762	-	GTGACCTATGCACCAGACGTTGCCCTCTGTGCAATCTTAGAGATCTTGTGGGAGGGGGTATGATCGGAAGAGCGGTTTCAG
chr18	45422842	45422881	SMAD2_2763	-	GTGACCTATGCACCAGACGTTTAGATCCAGGTTTGTATCAAATATGTCAAGGAATCTGAAGATCGGAAGAGCGGTTTCAG
chr15	67430315	67430354	SMAD3_2764	-	GTGACCTATGCACCAGACGTTTGGGAGGTCACAGGGACGGGAGGGAGGGATTCTGATGATAGATCGGAAGAGCGGTTTCAG
chr15	67457183	67457222	SMAD3_2765	-	GTGACCTATGCACCAGACGTGGGGAGGGGCAGAAAGAGAGGGAATGTGGATTGTGCTTGAGATCGGAAGAGCGGTTTCAG
chr15	67457541	67457580	SMAD3_2766	-	GTGACCTATGCACCAGACGTGAGACAGAGCAGAGGTGGCTCAGTGTGATGCCAGACCCAGATCGGAAGAGCGGTTTCAG
chr15	67459067	67459106	SMAD3_2767	-	GTGACCTATGCACCAGACGTGAAGGAAGGTGGTCTGTGTTAAAGGCCCTCACAGCTTGGCTAGATCGGAAGAGCGGTTTCAG
chr15	67462842	67462881	SMAD3_2768	-	GTGACCTATGCACCAGACGTAGACAAGTTGTGAGACTTCACAAAAGATTCTTGGCCTGGAAGATCGGAAGAGCGGTTTCAG
chr15	67473529	67473568	SMAD3_2769	-	GTGACCTATGCACCAGACGTAGGGTGGGCTACTGGGTCATTGGGTGTCCCAAGCCCATGAGATCGGAAGAGCGGTTTCAG
chr15	67477015	67477054	SMAD3_2770	-	GTGACCTATGCACCAGACGTTCAAGTTAGACTGGACAGGGTGCCTTTGCTCACACACAATAGATCGGAAGAGCGGTTTCAG
chr15	67479653	67479692	SMAD3_2771	-	GTGACCTATGCACCAGACGTCACAGAAAACGGGCTGTGGGGATGGAAGTGGCCAGGTCGAGATCGGAAGAGCGGTTTCAG
chr15	67482701	67482740	SMAD3_2772	-	GTGACCTATGCACCAGACGTTAGGCTAGGACAGGGGTTGGGTTGGGGACTTAAAAAATCTCCAGATCGGAAGAGCGGTTTCAG
chr9	135771572	135771611	TSC1_2773	-	GTGACCTATGCACCAGACGTTCAATCAGTGTTAACTTGCATATTTGTTGCCACAGAACAGGAGATCGGAAGAGCGGTTTCAG
chr9	135772521	135772560	TSC1_2774	-	GTGACCTATGCACCAGACGTAGAAGTATTGATGACCTTGGGACTAAGCTGCCAATTCAGATCGGAAGAGCGGTTTCAG
chr9	135772760	135772799	TSC1_2775	-	GTGACCTATGCACCAGACGTTACAGAAAGGCTTTTGTGTTTTTATAAGTGAACCTCCTAGATCGGAAGAGCGGTTTCAG
chr9	135776052	135776091	TSC1_2776	-	GTGACCTATGCACCAGACGTGCTCGGGAGCCAGACCTTAGTGGGAAAAGCGTTTCAGACCAGATCGGAAGAGCGGTTTCAG
chr9	135776926	135776965	TSC1_2777	-	GTGACCTATGCACCAGACGTAGGCGAGACCTGAATCTGCTGAAACCAATTTGCTAACAGATCGGAAGAGCGGTTTCAG
chr9	135777942	135777981	TSC1_2778	-	GTGACCTATGCACCAGACGTTAGGACCAGGCAAGGCAACTGCCAGAACTCCGAGATCGGAAGAGCGGTTTCAG
chr9	135778988	135779027	TSC1_2779	-	GTGACCTATGCACCAGACGTGGGAGGGGACAGGTGGAGCTTGCTTTTTGTTTTGTTTTGGAGATCGGAAGAGCGGTTTCAG
chr9	135779748	135779787	TSC1_2780	-	GTGACCTATGCACCAGACGTTACTTTAGCTCCAAATCCAGCCACATGGTTCTGCTTGCAGATCGGAAGAGCGGTTTCAG
chr9	135780918	135780957	TSC1_2781	-	GTGACCTATGCACCAGACGTGGGGCACTCTCTTCTGTGTTAAATGGTCAATTTTATGTGAGATCGGAAGAGCGGTTTCAG
chr9	135782068	135782107	TSC1_2782	-	GTGACCTATGCACCAGACGTTGGGATTGCTATGAGTTGATAAAAACCTGACCTCGCTCTGAGATCGGAAGAGCGGTTTCAG
chr9	135782638	135782677	TSC1_2783	-	GTGACCTATGCACCAGACGTTGCGTTACTACAGGCTTGGCTTCTTAATTGGGTTAGATCGGAAGAGCGGTTTCAG
chr9	135785908	135785947	TSC1_2784	-	GTGACCTATGCACCAGACGTGCTGCTGCTATCCCTCTGCCAGGCACAGTGACTCACTAGATCGGAAGAGCGGTTTCAG



chr9	135786339	135786378	TSC1_2785	-	GTGACCTATGCACCAGACGCTTAGTGGATTGATTAGTTGGTTTTGCCTGCCTTTAAGATCGGAAGAGCGGTTTCAG
chr9	135786790	135786829	TSC1_2786	-	GTGACCTATGCACCAGACGTAACCTAGTGTGCCTGCTCTCCTCTGCTTTCTGGTGAAGCAGATCGGAAGAGCGGTTTCAG
chr9	135787619	135787658	TSC1_2787	-	GTGACCTATGCACCAGACGTTCTTTGGTACTTATCTGTTTTGCAACTTTGTCTCTGGAAGAGATCGGAAGAGCGGTTTCAG
chr9	135796700	135796739	TSC1_2788	-	GTGACCTATGCACCAGACGTTAGTGTCAAATTTAAAGAATCTTTCGAGAGATTGAAAAGATCGGAAGAGCGGTTTCAG
chr9	135797156	135797195	TSC1_2789	-	GTGACCTATGCACCAGACGTTACTGCTTGTGTTGCTACTTAGTATACTGTTTAGATAGAGATCGGAAGAGCGGTTTCAG
chr9	135798685	135798724	TSC1_2790	-	GTGACCTATGCACCAGACGTTCTCATATACCTGTTGGGCCCTGTGAGGTGAATGCTTTCAAGATCGGAAGAGCGGTTTCAG
chr9	135800924	135800963	TSC1_2791	-	GTGACCTATGCACCAGACGTTGAAGGTTTGAATGAAATGGTTTTATGAGTATGTTTTCAGATCGGAAGAGCGGTTTCAG
chr9	135802538	135802577	TSC1_2792	-	GTGACCTATGCACCAGACGTTAAATATCATAGGCTTTCATATGTTCTTCATGAGTACAACAGATCGGAAGAGCGGTTTCAG
chr9	135804104	135804143	TSC1_2793	-	GTGACCTATGCACCAGACGTTAATATCCTTTTTAGCTTATCTTCTAGAAAAGAGAGATTGAGATCGGAAGAGCGGTTTCAG
chr9	135771832	135771871	TSC1_2794	-	GTGACCTATGCACCAGACGTCAGTTCAAAGGCTTCCCTGGGTATGAAGGCTCGAGAGTTAAGATCGGAAGAGCGGTTTCAG
chr9	135781197	135781236	TSC1_2795	-	GTGACCTATGCACCAGACGTGAGACCAGTATCTTCACTCCCAGTCTTTGTAATAATCCACAGATCGGAAGAGCGGTTTCAG
chr16	4015726	4015765	ADCY9_2796	-	GTGACCTATGCACCAGACGTACCCGCTGCCCGGCTGCTCTGTTTGTGCAACACAGTAAAGATCGGAAGAGCGGTTTCAG
chr16	4024620	4024659	ADCY9_2797	-	GTGACCTATGCACCAGACGTAATATTGCACTTCTGTCTGAATAACAGAGAGTGAATGATAGATCGGAAGAGCGGTTTCAG
chr16	4027433	4027472	ADCY9_2798	-	GTGACCTATGCACCAGACGTAGCACTGCTTGCGGGCACCAGGGTGCCTGGCCACCTTGCCAGATCGGAAGAGCGGTTTCAG
chr16	4029067	4029106	ADCY9_2799	-	GTGACCTATGCACCAGACGTGCTCAGCCGTTTTATTTCCACGCTCTCCTGGACTCCCTAAAGATCGGAAGAGCGGTTTCAG
chr16	4033183	4033222	ADCY9_2800	-	GTGACCTATGCACCAGACGTCGTGGACTGGGTCTCCAGCTCTGAGCCGTTAGCTCCCTCTAGATCGGAAGAGCGGTTTCAG
chr16	4038945	4038984	ADCY9_2801	-	GTGACCTATGCACCAGACGTTTTCTCTTCCGCTTTTTACTAAAGATGTGTTTTGTTGTTCTAGATCGGAAGAGCGGTTTCAG
chr16	4042097	4042136	ADCY9_2802	-	GTGACCTATGCACCAGACGTGGCTGTCTGGGAAAAAGTTCAGGCAGGAAGCCCTCAGATCGGAAGAGCGGTTTCAG
chr16	4043357	4043396	ADCY9_2803	-	GTGACCTATGCACCAGACGTCATGGCTGTTGTTCTGTCAGTTCTCTCCTGGCGCATCCAGATCGGAAGAGCGGTTTCAG
chr16	4057319	4057358	ADCY9_2804	-	GTGACCTATGCACCAGACGTTTTGTTTTTTTTTCTACTTCTAAAACCTTCTATTAAATTCAGATCGGAAGAGCGGTTTCAG
chr16	4163701	4163740	ADCY9_2805	-	GTGACCTATGCACCAGACGTTGCTTTACCTCGGCATCCCCCTCCCTGATCCTGATTGTAAGATCGGAAGAGCGGTTTCAG
chr16	4016123	4016162	ADCY9_2806	-	GTGACCTATGCACCAGACGTAGAGGGACCGTGAATGTCAAAGGGGAAAGGCCAGATGAAGAAGATCGGAAGAGCGGTTTCAG
chr16	4016520	4016559	ADCY9_2807	-	GTGACCTATGCACCAGACGTGAGCTCTAAGCAAAGCCGGACTACAGCAGCATCGGAAGAGATCGGAAGAGCGGTTTCAG
chr16	4164124	4164163	ADCY9_2808	-	GTGACCTATGCACCAGACGTCCGCTGTGTGAGGACCAAGTGTGAGAAAATCAGCACCATCGGAAGAGCGGTTTCAG
chr16	4164547	4164586	ADCY9_2809	-	GTGACCTATGCACCAGACGTGCTCCACGGCTGCATCCACGCCATCGGGTCCACCTGTTTCAGATCGGAAGAGCGGTTTCAG
chr16	4164970	4165009	ADCY9_2810	-	GTGACCTATGCACCAGACGTGGTCGCCCGCGCTGTGCTTCTCCTGGTGTGTGTGGGCAGATCGGAAGAGCGGTTTCAG
chr12	58120285	58120324	AGAP2_2811	-	GTGACCTATGCACCAGACGTGGAGAGACACCCCATCCCCACGCGGGCCGGGCACGACCAAGATCGGAAGAGCGGTTTCAG
chr12	58120707	58120746	AGAP2_2812	-	GTGACCTATGCACCAGACGTTGGGGGGAGAAAAGGGGGTCTTTGAGCTTTCATCTCGGAAAGATCGGAAGAGCGGTTTCAG
chr12	58121093	58121132	AGAP2_2813	-	GTGACCTATGCACCAGACGTGGGAACAGAGCGGGGGAGGGTGTGCTGAGGGTGTGCGAACAGATCGGAAGAGCGGTTTCAG
chr12	58121414	58121453	AGAP2_2814	-	GTGACCTATGCACCAGACGTGGAGGACGCGGAGGGGGTAGGGAGTGTATGTAAGTCCGGGAGATCGGAAGAGCGGTTTCAG
chr12	58121670	58121709	AGAP2_2815	-	GTGACCTATGCACCAGACGTGAGGTGGAGTGGAGGACTGGCCGCAGGAACGACCCTGGTAGATCGGAAGAGCGGTTTCAG
chr12	58122051	58122090	AGAP2_2816	-	GTGACCTATGCACCAGACGTGGGAGCCGGAGGGGCGCTCAGCTGGGTGCAGAAGGGTGTGATCGGAAGAGCGGTTTCAG
chr12	58123372	58123411	AGAP2_2817	-	GTGACCTATGCACCAGACGTGGCAGGCACCTTCCACTCCCACCCAGAACCTCATCCCCAAGATCGGAAGAGCGGTTTCAG
chr12	58124228	58124267	AGAP2_2818	-	GTGACCTATGCACCAGACGTGACCTTCCATCTGCTGTCTTCCACACCCAAATAGGATGAGATCGGAAGAGCGGTTTCAG
chr12	58124524	58124563	AGAP2_2819	-	GTGACCTATGCACCAGACGTTTTATGACATAGGAGACGAAGAGGGCCAGGGCTGGGAAAGATCGGAAGAGCGGTTTCAG
chr12	58125099	58125138	AGAP2_2820	-	GTGACCTATGCACCAGACGTGAGACTGGGCCACATTGGCCAGCTTTGGATTTCCTCAAGATCGGAAGAGCGGTTTCAG
chr12	58125289	58125328	AGAP2_2821	-	GTGACCTATGCACCAGACGTGAGGGCTGGGACAGGCTAGGGGCAGCTGGTCTTGTAGTTGAGATCGGAAGAGCGGTTTCAG
chr12	58125542	58125581	AGAP2_2822	-	GTGACCTATGCACCAGACGTTGGACATGCTGACCCCATCCTCCTGTCGCCCATGACCTGAGATCGGAAGAGCGGTTTCAG
chr12	58126136	58126175	AGAP2_2823	-	GTGACCTATGCACCAGACGTGTTTCAGAGTCTGCAGAGGGGGCCGTAAGATGCAGAGGGGAGATCGGAAGAGCGGTTTCAG
chr12	58126578	58126617	AGAP2_2824	-	GTGACCTATGCACCAGACGTTGATCTCCAGCATATGTGGGAAGCCAGAGCAAGGGCCCTGAGATCGGAAGAGCGGTTTCAG
chr12	58127759	58127798	AGAP2_2825	-	GTGACCTATGCACCAGACGTTGTTAGGAAAGCACTGCTTTAAGGGAGGCCCTAAGGAGGCAGATCGGAAGAGCGGTTTCAG
chr12	58128052	58128091	AGAP2_2826	-	GTGACCTATGCACCAGACGTAGGTGGTGGGGACAGGCTGGCTGGGGTCAAGACTGGCCAAGATCGGAAGAGCGGTTTCAG
chr12	58128325	58128364	AGAP2_2827	-	GTGACCTATGCACCAGACGTAAGAGCCATAGTAAGCTAACCATTTGGGGTTCAGGGATCCAGAGATCGGAAGAGCGGTTTCAG
chr12	58129102	58129141	AGAP2_2828	-	GTGACCTATGCACCAGACGTCAGTCCCCTTGCTATAGGGAAGGCTGACCTCCCACCCACAGATCGGAAGAGCGGTTTCAG
chr12	58130812	58130851	AGAP2_2829	-	GTGACCTATGCACCAGACGTTCAAGGGCTTGAACAAGAGGGAGGGTACCTGGAATGCAGATCGGAAGAGCGGTTTCAG
chr12	58135645	58135684	AGAP2_2830	-	GTGACCTATGCACCAGACGTGGTCAAGCTTCAACTTGGGTGTATCAGGGACTAGCAGGTGAGATCGGAAGAGCGGTTTCAG
chr12	58131201	58131240	AGAP2_2831	-	GTGACCTATGCACCAGACGTGGGAAGTTGTCCTCGGAAAGGCAAGAGTAAGACCTTGGAGATCGGAAGAGCGGTTTCAG
chr12	58131590	58131629	AGAP2_2832	-	GTGACCTATGCACCAGACGTGGGGCGCCCCACCTCCTCCCGCGCCCCCTGCTCAGCAGAGATCGGAAGAGCGGTTTCAG
chr19	49458755	49458794	BAX_2833	-	GTGACCTATGCACCAGACGTAAGGAAGGGAAAGAGGTACCTGGACTCTGGGTTCTAGGGGAGATCGGAAGAGCGGTTTCAG
chr19	49458894	49458933	BAX_2834	-	GTGACCTATGCACCAGACGTGATGGAGTGAGGGTGCAGAATCAGAACGGGGTGTCACTCCAGATCGGAAGAGCGGTTTCAG
chr19	49459405	49459444	BAX_2835	-	GTGACCTATGCACCAGACGTGAGGAGAAGCCGTGCCGGGAGCAGCATCAGGCTGATGGAGATCGGAAGAGCGGTTTCAG
chr19	49464017	49464056	BAX_2836	-	GTGACCTATGCACCAGACGTTGGAGTGGCGTGTAGGCATGACACCTTGTCCCCTGCTCCAGATCGGAAGAGCGGTTTCAG
chr19	49464739	49464778	BAX_2837	-	GTGACCTATGCACCAGACGTGGACATCAGTCTGTTGACTGCTCGGCCAGGGGCAGCCCCAGATCGGAAGAGCGGTTTCAG
chr2	60679650	60679689	BCL11A_2838	-	GTGACCTATGCACCAGACGTGGTGGGGTGGACGCTGCCGCCAGTGCAGCTCAGCTGGAGATCGGAAGAGCGGTTTCAG
chr2	60679660	60679699	BCL11A_2839	-	GTGACCTATGCACCAGACGTAGCCCCAGGGGTGGGGTGGACGCTGCCGCCAGTGCAGATCGGAAGAGCGGTTTCAG
chr2	60687489	60687528	BCL11A_2840	-	GTGACCTATGCACCAGACGTATACCCCTCCCTCACTCCCACCTGACACCCCTTTTTACAGATCGGAAGAGCGGTTTCAG
chr2	60687767	60687806	BCL11A_2841	-	GTGACCTATGCACCAGACGTTGGGAAAGTCTCAAGAAGTGTAGCAATCTCCTCAGATCGGAAGAGCGGTTTCAG
chr2	60689367	60689406	BCL11A_2842	-	GTGACCTATGCACCAGACGTTCTTAGGACTGAGTGCAAGATGTCTTCAAGCCACCTTAGATCGGAAGAGCGGTTTCAG

chr2	60695817	60695856	BCL11A_2843	-	GTGACCTATGCACCAGACGTCTTATTTCTTCTACAAATGTCCATGTGTATAGAGATGAGAGATCGGAAGAGCGGTTTCAG
chr2	60773056	60773095	BCL11A_2844	-	GTGACCTATGCACCAGACGTAGCAAGGAGAAAAGCTGTTTTGCATGTTTTCTTTTCATTTTAGATCGGAAGAGCGGTTTCAG
chr2	60688203	60688242	BCL11A_2845	-	GTGACCTATGCACCAGACGTTTAATGGCCGCGGCTGCTCCCCGGGCGAGTCGGCCTCGGGAGATCGGAAGAGCGGTTTCAG
chr2	60688639	60688678	BCL11A_2846	-	GTGACCTATGCACCAGACGTGGCAGCGCCAGCAGCGCGCTCAAGTCCGTGGTGGCCAAGTAGATCGGAAGAGCGGTTTCAG
chr2	60689075	60689114	BCL11A_2847	-	GTGACCTATGCACCAGACGTGCCATGGATTTCTCTAGGAGACTTAGAGAGCTGGCAGGGAGATCGGAAGAGCGGTTTCAG
chr2	60687893	60687932	BCL11A_2848	-	GTGACCTATGCACCAGACGTGTGGACGGGAGGATCTCGGGGCGCAGCGGCACGGGAAGTAGATCGGAAGAGCGGTTTCAG
chr2	60688297	60688336	BCL11A_2849	-	GTGACCTATGCACCAGACGTAAAGCGGCCAACCTGGCCGAGGCGCCAGGGACAGAGATCGGAAGAGCGGTTTCAG
chr2	60688701	60688740	BCL11A_2850	-	GTGACCTATGCACCAGACGTCAAGTCCGACGACGGTCTCTCCACCGCCAGCTCCCCGGAAGATCGGAAGAGCGGTTTCAG
chr2	60689105	60689144	BCL11A_2851	-	GTGACCTATGCACCAGACGTGCGGTTGAATCCAATGGCTATGGAGCCTCCGCCATGGATAGATCGGAAGAGCGGTTTCAG
chr22	23595936	23595975	BCR_2852	-	GTGACCTATGCACCAGACGTAAAGAAGCATCCTGTGTAGAGACAGAGAAGGGAGCATCCAGATCGGAAGAGCGGTTTCAG
chr22	23603087	23603126	BCR_2853	-	GTGACCTATGCACCAGACGTAATAGACAGAAGTCAGCCTGGAAGGGTGGTAGGGGGATTTCAGATCGGAAGAGCGGTTTCAG
chr22	23603492	23603531	BCR_2854	-	GTGACCTATGCACCAGACGTGCACAAGTGAAGTACAGAGTGGAGAGGGCTGCCATCCGAGATCGGAAGAGCGGTTTCAG
chr22	23610545	23610584	BCR_2855	-	GTGACCTATGCACCAGACGTGGAAGGGAAGAGAGTGGGACAGGTGCTGCTCTCCCCAAAGATCGGAAGAGCGGTTTCAG
chr22	23613669	23613708	BCR_2856	-	GTGACCTATGCACCAGACGTAAAGCGCATGTTACACAGATGACAGAAGCAGCTTTGATAGATCGGAAGAGCGGTTTCAG
chr22	23615218	23615257	BCR_2857	-	GTGACCTATGCACCAGACGTAGAGGGGAGGTGAGAGAGTTGCACATGGAGAAGCACACCAGATCGGAAGAGCGGTTTCAG
chr22	23615771	23615810	BCR_2858	-	GTGACCTATGCACCAGACGTAAAGAAAGACTTGAGTTAGACACAGAGGAGCACTGGCACCTAGATCGGAAGAGCGGTTTCAG
chr22	23626114	23626153	BCR_2859	-	GTGACCTATGCACCAGACGTAGGGTAAGGCTGGGGTCAAGGGCAGCCTGGGGTGGGTGAGATCGGAAGAGCGGTTTCAG
chr22	23627170	23627209	BCR_2860	-	GTGACCTATGCACCAGACGTGGAGGGAAGAAGCTTACATGTGACCCACTGCTTCTATGGAGATCGGAAGAGCGGTTTCAG
chr22	23629296	23629335	BCR_2861	-	GTGACCTATGCACCAGACGTATGCCACAGCCTACCTTCCCATTCCAGCGCTCCACACAAAGATCGGAAGAGCGGTTTCAG
chr22	23630234	23630273	BCR_2862	-	GTGACCTATGCACCAGACGTCAAGAAGAACACACCCAGTTATCTCCGCCCTGGCTACGCAAGATCGGAAGAGCGGTTTCAG
chr22	23631654	23631693	BCR_2863	-	GTGACCTATGCACCAGACGTGGAAGAGAGTGCACCAATTGGTCAATCTGCTCCTTGGCCAGATCGGAAGAGCGGTTTCAG
chr22	23632476	23632515	BCR_2864	-	GTGACCTATGCACCAGACGTGATCAAAGAGTCACTTCTGTTGTCCCGGAAAGGGAGGAGATCGGAAGAGCGGTTTCAG
chr22	23634678	23634717	BCR_2865	-	GTGACCTATGCACCAGACGTAAGTGGACATGGAGAAGTCAACAGTCTTTTTCCACATCACAGATCGGAAGAGCGGTTTCAG
chr22	23637161	23637200	BCR_2866	-	GTGACCTATGCACCAGACGTGGAAGGGAAGTGGAGTCCAGTGTGAAACAAACGGGTCAATCGAGATCGGAAGAGCGGTTTCAG
chr22	23651561	23651600	BCR_2867	-	GTGACCTATGCACCAGACGTGGAGTCATGATTGGCAGAGGCCCTGGGGTCTGTTTCAGAGGAGATCGGAAGAGCGGTTTCAG
chr22	23652461	23652500	BCR_2868	-	GTGACCTATGCACCAGACGTGAGAAGGGGCACAGTCTCTAATCCTTCTGGTCCATAGAGATCGGAAGAGCGGTTTCAG
chr22	23653834	23653873	BCR_2869	-	GTGACCTATGCACCAGACGTAGGGAAATGTTCTCAGTGTCTAACAGCCCTGCTTGGGCCAAGATCGGAAGAGCGGTTTCAG
chr22	23655024	23655063	BCR_2870	-	GTGACCTATGCACCAGACGTACGGAAATGCAGCGCCCTCTTGGAGATCCCGAGTGAAGTAGATCGGAAGAGCGGTTTCAG
chr22	23656105	23656144	BCR_2871	-	GTGACCTATGCACCAGACGTCCGTGGTACTCCTTGGGTCCACAACGAGCCAGACTAGATCGGAAGAGCGGTTTCAG
chr22	23656689	23656728	BCR_2872	-	GTGACCTATGCACCAGACGTCAAAGAGTCCAGCGGGTCTGCTTTTTCAACGCCACCCAGGAAAGATCGGAAGAGCGGTTTCAG
chr22	23657570	23657609	BCR_2873	-	GTGACCTATGCACCAGACGTAGAGTAGGGAAGAGAAGAGTGGCTCAGAGCGGGGCTCACAAAGATCGGAAGAGCGGTTTCAG
chr22	23523524	23523563	BCR_2874	-	GTGACCTATGCACCAGACGTGACGCGGCTGCCCGGGCCTGCGGGCGGTCGGGGCCTGGAGATCGGAAGAGCGGTTTCAG
chr22	23523950	23523989	BCR_2875	-	GTGACCTATGCACCAGACGTCTCTGGTAGGGCTGGTACTCCAGGGCGGCCAAGGGGGCCAGATCGGAAGAGCGGTTTCAG
chr17	76210348	76210387	BIRC5_2876	-	GTGACCTATGCACCAGACGTCCACCTCTGCCAACGGGTCCCGGATTCAAATCTGGCGGTAGATCGGAAGAGCGGTTTCAG
chr17	76210711	76210750	BIRC5_2877	-	GTGACCTATGCACCAGACGTGACACAGCTGCTGAGTGGACGTGGCAGCCTGAGCAAGAAAGAGAAAGATCGGAAGAGCGGTTTCAG
chr17	76211997	76212036	BIRC5_2878	-	GTGACCTATGCACCAGACGTAAAGGGCAGAGAAGGGCATTATTGCCCGGGTCCCAAGAGATCGGAAGAGCGGTTTCAG
chr17	76212695	76212734	BIRC5_2879	-	GTGACCTATGCACCAGACGTCAAACAACAGCGGAAAGGCAGCTGAAGGGATTAAAGCGGAGATCGGAAGAGCGGTTTCAG
chr17	76219496	76219535	BIRC5_2880	-	GTGACCTATGCACCAGACGTAGAATAGACACATGACACTGAAACAGAGCTTCCCAGTCAAGATCGGAAGAGCGGTTTCAG
chr7	116165067	116165106	CAV1_2881	-	GTGACCTATGCACCAGACGTGGCTGGATGAAACTGTGAGGAGGTTTTCCCTGGGCTGTGCAGATCGGAAGAGCGGTTTCAG
chr7	116166529	116166568	CAV1_2882	-	GTGACCTATGCACCAGACGTGGAGGGCGGACGGCCAGGAGGGGAGGGCGGCAACGGCGAGATCGGAAGAGCGGTTTCAG
chr7	116198950	116198989	CAV1_2883	-	GTGACCTATGCACCAGACGTGAAGTGCACAACATGAGCAGACAAGTAAAGAAAAGAGAAAGATCGGAAGAGCGGTTTCAG
chr19	30303413	30303452	CCNE1_2884	-	GTGACCTATGCACCAGACGTCTCCGGCCTGAGGCCTGCGGGGCGGCGGGGTGAGGCGGAGATCGGAAGAGCGGTTTCAG
chr19	30303546	30303585	CCNE1_2885	-	GTGACCTATGCACCAGACGTGGGTGGCACC GGCCGGGTGAGCACCCGCGGCCGCCCTCAGATCGGAAGAGCGGTTTCAG
chr19	30303568	30303607	CCNE1_2886	-	GTGACCTATGCACCAGACGTTCCTTCGCATCCCTGTGGACCCGGGTGGCACCCGGCCGGGAGATCGGAAGAGCGGTTTCAG
chr19	30303826	30303865	CCNE1_2887	-	GTGACCTATGCACCAGACGTGCCACCCCATGACCCCAAGGAAACACACCAAAACAGACAAGATCGGAAGAGCGGTTTCAG
chr19	30307994	30308033	CCNE1_2888	-	GTGACCTATGCACCAGACGTGAAATACACAGAGAGGTGAGATGACAAAGCTTAGATCGGAAGAGCGGTTTCAG
chr19	30308263	30308302	CCNE1_2889	-	GTGACCTATGCACCAGACGTACACACAACAAAATGAGGCCACAAAGGGGTAAGAATGCAGATCGGAAGAGCGGTTTCAG
chr19	30311559	30311598	CCNE1_2890	-	GTGACCTATGCACCAGACGTATTTAGTAAGTTTTAGCACAAAGTAAATTTACTTGGAGGAAGATCGGAAGAGCGGTTTCAG
chr19	30312579	30312618	CCNE1_2891	-	GTGACCTATGCACCAGACGTATAAAAGATGGCACTAGCACCAAGGCCAATCTCTAACAGTAGATCGGAAGAGCGGTTTCAG
chr19	30312853	30312892	CCNE1_2892	-	GTGACCTATGCACCAGACGTACAGAGAGAAAAGACCGATGATTGAGAAAAGAAGTTCAAGATCGGAAGAGCGGTTTCAG
chr19	30313097	30313136	CCNE1_2893	-	GTGACCTATGCACCAGACGTGAAAAGAACGCTGAGATGGATGCCACCACGCTATTCTAGATCGGAAGAGCGGTTTCAG
chr19	30313303	30313342	CCNE1_2894	-	GTGACCTATGCACCAGACGTGACATCGTGGGCTTAATCTGAGGCTGACAACCTGGATGTAAGATCGGAAGAGCGGTTTCAG
chr19	30314512	30314551	CCNE1_2895	-	GTGACCTATGCACCAGACGTGAATAAAAGGGACAACACATTAGAGTAGAACATATCCTTGGAGATCGGAAGAGCGGTTTCAG
chr7	14188706	14188745	DGKB_2896	-	GTGACCTATGCACCAGACGTTTTCACTCTTAGAAAATTGAATTAGCATAATTTGGCCATGGAGATCGGAAGAGCGGTTTCAG
chr7	14216399	14216438	DGKB_2897	-	GTGACCTATGCACCAGACGTATGTCAATCTCAGTTTTGCTTTCCTTTTGACTAAATAACAGATCGGAAGAGCGGTTTCAG
chr7	14216414	14216453	DGKB_2898	-	GTGACCTATGCACCAGACGTAGTAGTTGATGCTATGTCAATCTCAGTTTTGCTTTCTAGATCGGAAGAGCGGTTTCAG
chr7	14217606	14217645	DGKB_2899	-	GTGACCTATGCACCAGACGTTTCACTGAACTGACAAAGCGGTTTTGATATGGCATAGCCTCAAGATCGGAAGAGCGGTTTCAG
chr7	14378090	14378129	DGKB_2900	-	GTGACCTATGCACCAGACGTTTCAATAATTAGTTGTTAAATGCTTTGTTAACCTGTTTTCAAAGATCGGAAGAGCGGTTTCAG

chr7	14384876	14384915	DGKB_2901	-	GTGACCTATGCACCAGACGTAATGAATCTCTTTTGTAAATATGATGAAATGGCTTGAGCTAGATCGGAAGAGCGGTTTCAG
chr7	14517736	14517775	DGKB_2902	-	GTGACCTATGCACCAGACGTAAAGAGATGAAATATAGATATAGTTGCTGAATTTTGCCAGATCGGAAGAGCGGTTTCAG
chr7	14613787	14613826	DGKB_2903	-	GTGACCTATGCACCAGACGTCCACTAAATTTTACCTTTGTACCTGTACTGTATAATCACAAAGATCGGAAGAGCGGTTTCAG
chr7	14620437	14620476	DGKB_2904	-	GTGACCTATGCACCAGACGTTGCAACAACAAAAGCAGAAACAGTACACAACACCCTTTTCAGATCGGAAGAGCGGTTTCAG
chr7	14622627	14622666	DGKB_2905	-	GTGACCTATGCACCAGACGTCACATACTTAATATGGCTGGGAGAGAGCAATAGCTTTAAAGATCGGAAGAGCGGTTTCAG
chr7	14647009	14647048	DGKB_2906	-	GTGACCTATGCACCAGACGTGGATAATATTACCATTAACTCAGTTAATGTTAATTAAGATCGGAAGAGCGGTTTCAG
chr7	14652915	14652954	DGKB_2907	-	GTGACCTATGCACCAGACGTGATTGATTTAGTGTCTATGTCATGTATGTAAAAAAGATCGGAAGAGCGGTTTCAG
chr7	14660953	14660992	DGKB_2908	-	GTGACCTATGCACCAGACGTTTAAATCAAATTTTGTAGGTTTTTATATTTGATACTTCTAGATCGGAAGAGCGGTTTCAG
chr7	14669811	14669850	DGKB_2909	-	GTGACCTATGCACCAGACGTAAAAACAGGTTTTTACACTTAAATTTATAGGTCATTATACAGATCGGAAGAGCGGTTTCAG
chr7	14712504	14712543	DGKB_2910	-	GTGACCTATGCACCAGACGTCCTTATCATTCTACTATAACTTAGGATTGCTGTGACTTATAGATCGGAAGAGCGGTTTCAG
chr7	14722128	14722167	DGKB_2911	-	GTGACCTATGCACCAGACGTATTGGAAAAAAATCCAGCATTACCCCACTGAAGACGAGATCGGAAGAGCGGTTTCAG
chr7	14722328	14722367	DGKB_2912	-	GTGACCTATGCACCAGACGTGTGCATCTGCTTCTGAAAGTGCCATTATGTAGTGTGAGATCGGAAGAGCGGTTTCAG
chr7	14724820	14724859	DGKB_2913	-	GTGACCTATGCACCAGACGTTTGCTGCTGGACATCATCTCCTCAAGTGAGGAAAGGTAGATCGGAAGAGCGGTTTCAG
chr7	14733650	14733689	DGKB_2914	-	GTGACCTATGCACCAGACGTCCACAGAGGGTGGCCTGGTGGTGAGTCAGTGGGGCTCAGATCGGAAGAGCGGTTTCAG
chr7	14741256	14741295	DGKB_2915	-	GTGACCTATGCACCAGACGTTCTCAAAGTTTCTGTGAAAACTTCAAAGATTTTCTTCTGAGATCGGAAGAGCGGTTTCAG
chr7	14758117	14758156	DGKB_2916	-	GTGACCTATGCACCAGACGTCCTCATTTTGTACTTATCGTGATTGGGGCAGGAGAAAAGATCGGAAGAGCGGTTTCAG
chr7	14775616	14775655	DGKB_2917	-	GTGACCTATGCACCAGACGTTTACTTTAAACATTTATAGTACAATTTCAAAGGCTAAAGATCGGAAGAGCGGTTTCAG
chr7	14793503	14793542	DGKB_2918	-	GTGACCTATGCACCAGACGTTCTTTTCTATTAAGCTGTGCTTTTCTTCTTTTATCTGAGATCGGAAGAGCGGTTTCAG
chr7	14797230	14797269	DGKB_2919	-	GTGACCTATGCACCAGACGTTTCTTTTATATCAGTTTTCTATATATGCTTGGAAAGAGAGATCGGAAGAGCGGTTTCAG
chr7	14880769	14880808	DGKB_2920	-	GTGACCTATGCACCAGACGTATATTGATATTATGAGATTATTTGACATTTGTCTAGACAAGATCGGAAGAGCGGTTTCAG
chr7	100401033	100401072	EPHB4_2921	-	GTGACCTATGCACCAGACGTCCTCCCACCCAGGGACACCCGCTCCCATTTCGGGGCAGATCGGAAGAGCGGTTTCAG
chr7	100402738	100402777	EPHB4_2922	-	GTGACCTATGCACCAGACGTGCAGGAGCTGGAGTGGGGCTGGGAGAGCGGGGACGCTGGAAGATCGGAAGAGCGGTTTCAG
chr7	100403073	100403112	EPHB4_2923	-	GTGACCTATGCACCAGACGTGAGAAATGGCCCTCCTTCCCGCTCTGCCCCACTCCAGATCGGAAGAGCGGTTTCAG
chr7	100403992	100404031	EPHB4_2924	-	GTGACCTATGCACCAGACGTCGTGCTCTACCAAGCTTCTCCGAGTTCCTCAGATGTTCTCTCACCTCGGAAGAGCGGTTTCAG
chr7	100404937	100404976	EPHB4_2925	-	GTGACCTATGCACCAGACGTGGGTAATACTGGGTGTGAGCTTCTTAGGGCCAGGTGGGCAAGATCGGAAGAGCGGTTTCAG
chr7	100410319	100410358	EPHB4_2926	-	GTGACCTATGCACCAGACGTTCCCTGGCTTCTGCGGCCACCCGGAGTTCCACTTACACCAGATCGGAAGAGCGGTTTCAG
chr7	100410667	100410706	EPHB4_2927	-	GTGACCTATGCACCAGACGTAAGGCTGCCCGGGCACCTGGGAACGAAGCGGGGTGGCAAGATCGGAAGAGCGGTTTCAG
chr7	100411491	100411530	EPHB4_2928	-	GTGACCTATGCACCAGACGTTGACACCCAGAGGCCCTCGGAAGCCCTCAGTTGATGGCCAAGATCGGAAGAGCGGTTTCAG
chr7	100414764	100414803	EPHB4_2929	-	GTGACCTATGCACCAGACGTGGAAGGGGTGAGGGTGGGGTGGAAAGACCCCAAGTAGATCGGAAGAGCGGTTTCAG
chr7	100416092	100416131	EPHB4_2930	-	GTGACCTATGCACCAGACGTCCTCCACGCCCTGGGGTGGGTGGGCAATGGTTGTGCTCTCAGATCGGAAGAGCGGTTTCAG
chr7	100417129	100417168	EPHB4_2931	-	GTGACCTATGCACCAGACGTGGGGCTGGGGCGGCTGGTGGTCTGGCGGGAGAGATGTACAGATCGGAAGAGCGGTTTCAG
chr7	100417713	100417752	EPHB4_2932	-	GTGACCTATGCACCAGACGTAGCACCCAGGTGCAGTTCCTGCGGGAGGGTCCAGACCTAGATCGGAAGAGCGGTTTCAG
chr7	100419843	100419882	EPHB4_2933	-	GTGACCTATGCACCAGACGTGAGCTTCCCCTGCGACTGCTGCTCATCCGGGGAGAGTCCAGATCGGAAGAGCGGTTTCAG
chr7	100421216	100421255	EPHB4_2934	-	GTGACCTATGCACCAGACGTGCCCCAGGGCTCAGCCACGCCAAGGTGGGATTCCAGCCAGATCGGAAGAGCGGTTTCAG
chr7	100421775	100421814	EPHB4_2935	-	GTGACCTATGCACCAGACGTACCCAGGACTGGAGCTCTGAGGAAACTGAGGGAGGAAGATCGGAAGAGCGGTTTCAG
chr7	100424551	100424590	EPHB4_2936	-	GTGACCTATGCACCAGACGTTTGCGGGGGGGGCGCACCCCGTCACTCCTGGACCTCCCAGATCGGAAGAGCGGTTTCAG
chr10	50666811	50666850	ERCC6_2937	-	GTGACCTATGCACCAGACGTTTCTAAACTTTCAAGTCCCTTTTTCTAACGGGCATTTCTAGATCGGAAGAGCGGTTTCAG
chr10	50668369	50668408	ERCC6_2938	-	GTGACCTATGCACCAGACGTTAACTTTTTGCTTTCCAGGGTGAGACTTGCTTGATTGAAAGATCGGAAGAGCGGTTTCAG
chr10	50669348	50669387	ERCC6_2939	-	GTGACCTATGCACCAGACGTGCTGCATGCCATACTTGAAGGAGTCCAAACAATAAGGCAGATCGGAAGAGCGGTTTCAG
chr10	50678178	50678217	ERCC6_2940	-	GTGACCTATGCACCAGACGTTGATACGTTTGCACAGGGATGCTAGGATTAGAAAATGAGAGATCGGAAGAGCGGTTTCAG
chr10	50678971	50679010	ERCC6_2941	-	GTGACCTATGCACCAGACGTTAACTTTAAATTTAAAGTAATCAATTGCACAAGATGATAAGATCGGAAGAGCGGTTTCAG
chr10	50680372	50680411	ERCC6_2942	-	GTGACCTATGCACCAGACGTACAGTGGCCACTCTGGCTGTGCGTTCCCAGAGTCTTGAGAGATCGGAAGAGCGGTTTCAG
chr10	50680905	50680944	ERCC6_2943	-	GTGACCTATGCACCAGACGTATTTTTTTTTTAAAGAAATGATTAAGTAGAAAATAGTTTATAGATCGGAAGAGCGGTTTCAG
chr10	50681473	50681512	ERCC6_2944	-	GTGACCTATGCACCAGACGTAATGTAACAGGGAGATTGAGTGGTGTGCTGTACGTGGAGAGATCGGAAGAGCGGTTTCAG
chr10	50682023	50682062	ERCC6_2945	-	GTGACCTATGCACCAGACGTAGACTTTCAGCGGGAAACAGGCTGGTTCTTTATGACAGCCAGATCGGAAGAGCGGTTTCAG
chr10	50684211	50684250	ERCC6_2946	-	GTGACCTATGCACCAGACGTTAAAGACTGGAGAACTGGAGAAATGAATTGTGGACCAAGAGATAGATCGGAAGAGCGGTTTCAG
chr10	50686350	50686389	ERCC6_2947	-	GTGACCTATGCACCAGACGTCCAGGAGTTAACGAAGCATTCTTAAAGACAAGTGTGCTAGATCGGAAGAGCGGTTTCAG
chr10	50690683	50690722	ERCC6_2948	-	GTGACCTATGCACCAGACGTAGGATGATAACTTTTTGGCATTTAATATTTAAAGTGTAGATCGGAAGAGCGGTTTCAG
chr10	50691342	50691381	ERCC6_2949	-	GTGACCTATGCACCAGACGTTTTTAACAAGGGAGATTTCCAAGTGGAGAAGAATAATTAAGATCGGAAGAGCGGTTTCAG
chr10	50701113	50701152	ERCC6_2950	-	GTGACCTATGCACCAGACGTATTTTCAGTACCTTTTTGTTTTGTTTTAATGCCCTCCATTAGATCGGAAGAGCGGTTTCAG
chr10	50708534	50708573	ERCC6_2951	-	GTGACCTATGCACCAGACGTCTCTGCAGCTGTCTGAGCTCAATTAATATTTTCAGATCGGAAGAGCGGTTTCAG
chr10	50713880	50713919	ERCC6_2952	-	GTGACCTATGCACCAGACGTATGTTCTTTCTTTCTTATTGCTATCAAGCCATTATGTAAGATCGGAAGAGCGGTTTCAG
chr10	50732029	50732068	ERCC6_2953	-	GTGACCTATGCACCAGACGTGGGGATTATAAATACATTGTACTGTTTGCTTTATCTTAGGAGATCGGAAGAGCGGTTTCAG
chr10	50736413	50736452	ERCC6_2954	-	GTGACCTATGCACCAGACGTTAGGAGCAGTTTCTCTGTGTTCTTGAATTGATGCCTGATGAGATCGGAAGAGCGGTTTCAG
chr10	50738716	50738755	ERCC6_2955	-	GTGACCTATGCACCAGACGTATAACATTACAGTATTGCATTTTTGAAAAAGTCATCATTTAAGATCGGAAGAGCGGTTTCAG
chr10	50740539	50740578	ERCC6_2956	-	GTGACCTATGCACCAGACGTCCCATCTTCTTCTTCAAAGTGGTGGTAAAAACATGACAGAGATCGGAAGAGCGGTTTCAG
chr10	50678532	50678571	ERCC6_2957	-	GTGACCTATGCACCAGACGTAAGCATTGATGAAAAGTATAGGTTCTTTCTTACAAAAGAAAAGATCGGAAGAGCGGTTTCAG
chr10	50732401	50732440	ERCC6_2958	-	GTGACCTATGCACCAGACGTGGGATTGCCAAAAGGCAAGGAGACCTTGGGAGTCAGACAAGATCGGAAGAGCGGTTTCAG

chr6	152128998	152129037	ESR1_2959	-	GTGACCTATGCACCAGACGTGCGGGGACAGGGTGCAGACCGTGTCCCCGACAGGGCAGAAGGAGATCGGAAGAGCGGTTTCAG
chr6	152163682	152163721	ESR1_2960	-	GTGACCTATGCACCAGACGTAAAAACAGTAAATCCATTAAACATTAGAAAAGCAAACATGAGATCGGAAGAGCGGTTTCAG
chr6	152201740	152201779	ESR1_2961	-	GTGACCTATGCACCAGACGTCAAGAGGACAGAATTAATATTTTTCAGGAAACTTAGCCAAGATCGGAAGAGCGGTTTCAG
chr6	152265258	152265297	ESR1_2962	-	GTGACCTATGCACCAGACGTAGGTGGAAAAAATAATAGTTTATTTTTTCCCGTGTAAAAGATCGGAAGAGCGGTTTCAG
chr6	152332741	152332780	ESR1_2963	-	GTGACCTATGCACCAGACGTGCAAGAAAAACCCTGCTGACTCAAATGAAAAAGACTCATTAGATCGGAAGAGCGGTTTCAG
chr6	152415470	152415509	ESR1_2964	-	GTGACCTATGCACCAGACGTAGAGAGAGAGTGTAGAGAGAGAGTAAAGACTCAAAGAGGATGAGGTAGATCGGAAGAGCGGTTTCAG
chr6	152419817	152419856	ESR1_2965	-	GTGACCTATGCACCAGACGTGAAGACACAGAAAGGACTTTAGAGCCAACCCGAGCCAGATCGGAAGAGCGGTTTCAG
chr7	128475330	128475369	FLNC_2966	-	GTGACCTATGCACCAGACGTGAGGGGACAGACGGGCTCAGGGGGCCCCACCCTCCACTGAGATCGGAAGAGCGGTTTCAG
chr7	128477164	128477203	FLNC_2967	-	GTGACCTATGCACCAGACGTGATGGAGGGAGACGATGGTGGGGGACAGCCAGCCGGCCAGAGATCGGAAGAGCGGTTTCAG
chr7	128477402	128477441	FLNC_2968	-	GTGACCTATGCACCAGACGTAAAGGAGTGATGTACATGGCGCCCTCTTTTCCAGCAGCCAGATCGGAAGAGCGGTTTCAG
chr7	128477641	128477680	FLNC_2969	-	GTGACCTATGCACCAGACGTGGAGCAGAGCCAGGTTACTCAGGGAGAGCCTACATGTGCAGATCGGAAGAGCGGTTTCAG
chr7	128477991	128478030	FLNC_2970	-	GTGACCTATGCACCAGACGTGGAAAAAGATTGGAAGCCTCCCAATGACCATAGCCCTCAGATCGGAAGAGCGGTTTCAG
chr7	128478271	128478310	FLNC_2971	-	GTGACCTATGCACCAGACGTGAGGTCAAAGGTTAGCTTCTAGGGGAGAGCCAGTCTGAGAAGATCGGAAGAGCGGTTTCAG
chr7	128478607	128478646	FLNC_2972	-	GTGACCTATGCACCAGACGTGAGGGCTGTGAGCCACTCTGGACACACAGCTGCCAGATCGGAAGAGCGGTTTCAG
chr7	128480027	128480066	FLNC_2973	-	GTGACCTATGCACCAGACGTAAAGAAAAGAGGTTGGGGTGTGAGGGGCTTGGACCAAGATCGGAAGAGCGGTTTCAG
chr7	128480552	128480591	FLNC_2974	-	GTGACCTATGCACCAGACGTGGGGGACAGGGTGGGGGAAGAAGGCAGATCAATATCCTTGAAAGATCGGAAGAGCGGTTTCAG
chr7	128480838	128480877	FLNC_2975	-	GTGACCTATGCACCAGACGTAGGGAGTGGTGTCCATGCCAGGAAGTGCCCCCAAAGTCAGATCGGAAGAGCGGTTTCAG
chr7	128481174	128481213	FLNC_2976	-	GTGACCTATGCACCAGACGTGTGGGGGAGGTCGGGGTCCAGCATCGGAAGACCCCTGATGTCAGGAAGAGCGGTTTCAG
chr7	128481458	128481497	FLNC_2977	-	GTGACCTATGCACCAGACGTGGAAGAAGGCTGAGTTGGGGAGGGAGGAGAACCAGCTTGAGATCGGAAGAGCGGTTTCAG
chr7	128482235	128482274	FLNC_2978	-	GTGACCTATGCACCAGACGTCAACCAAGCAAAGTTCATAGCTGTGGCCTCTGCAGAGCGCAGATCGGAAGAGCGGTTTCAG
chr7	128482579	128482618	FLNC_2979	-	GTGACCTATGCACCAGACGTGGTGCAGCTCAGCGTGGTGCCCTCCCTCAAGGCTCATCCAGATCGGAAGAGCGGTTTCAG
chr7	128482798	128482837	FLNC_2980	-	GTGACCTATGCACCAGACGTGCGGGACTGCTGTGAGTTGGGCTCAGCCCCGACTCGACAGATCGGAAGAGCGGTTTCAG
chr7	128483233	128483272	FLNC_2981	-	GTGACCTATGCACCAGACGTAGGAGGCTCAGTCAGGGCTCAGGGGAACACACCCCTGAGATCGGAAGAGCGGTTTCAG
chr7	128483412	128483451	FLNC_2982	-	GTGACCTATGCACCAGACGTACCCAGAGATGTGTGTAGGGCTGCGCAGCCACCTAACCCAGATCGGAAGAGCGGTTTCAG
chr7	128483800	128483839	FLNC_2983	-	GTGACCTATGCACCAGACGTCAATGGTAGGTCAGAACTGGATATAAGGCAAGGTCCTACAAGATCGGAAGAGCGGTTTCAG
chr7	128484008	128484047	FLNC_2984	-	GTGACCTATGCACCAGACGTGGCAAGTGACACCATGAGGAGACTCCGGTCCACCCTACCCAGATCGGAAGAGCGGTTTCAG
chr7	128484662	128484701	FLNC_2985	-	GTGACCTATGCACCAGACGTAGGACAGTTGTGGGTTCCCTGCACCTGGCCTCCTATCCAGATCGGAAGAGCGGTTTCAG
chr7	128485994	128486033	FLNC_2986	-	GTGACCTATGCACCAGACGTGGGGTGGGCTGTTTCAGCAGGGGTGGGGGCAGCCTTACACAGATCGGAAGAGCGGTTTCAG
chr7	128486305	128486344	FLNC_2987	-	GTGACCTATGCACCAGACGTGCCACAGGGGCATCAATCAGGGCTGTGCGCCCCACCCAGATCGGAAGAGCGGTTTCAG
chr7	128486749	128486788	FLNC_2988	-	GTGACCTATGCACCAGACGTACATCCCCCATTAGCTTTCATAAGACCAGTGAAGTGAAGATCGGAAGAGCGGTTTCAG
chr7	128487701	128487740	FLNC_2989	-	GTGACCTATGCACCAGACGTAAAGACATTAGACCCTGCCACCAGCCCTGATGGTCCCCAGATCGGAAGAGCGGTTTCAG
chr7	128487949	128487988	FLNC_2990	-	GTGACCTATGCACCAGACGTGGCACAGGGTCAAGAGAGCCTCCGGGCGTCCCGCCCACCCAGATCGGAAGAGCGGTTTCAG
chr7	128488565	128488604	FLNC_2991	-	GTGACCTATGCACCAGACGTAGAAGGGATAAACAGTTGGCTGGGTGGCATGGACGGGGCCAGATCGGAAGAGCGGTTTCAG
chr7	128488797	128488836	FLNC_2992	-	GTGACCTATGCACCAGACGTAGCAGAGGTCAGGGCCCGCTGTGCTTGGAGATGACCTGAGATCGGAAGAGCGGTTTCAG
chr7	128489185	128489224	FLNC_2993	-	GTGACCTATGCACCAGACGTAGAAAGAGTGTGAGGGCCGCTGTCTCAACGTGGGCTGGGAGATCGGAAGAGCGGTTTCAG
chr7	128489335	128489374	FLNC_2994	-	GTGACCTATGCACCAGACGTGGAGATCCTGCTCAGGGAGCTGGTGGGCTGGAGCCAGCCAGATCGGAAGAGCGGTTTCAG
chr7	128489980	128490019	FLNC_2995	-	GTGACCTATGCACCAGACGTAAAGGCACGGGGCACAGGGTGTGGCAGCCTCACAGGCCTAAGATCGGAAGAGCGGTTTCAG
chr7	128490388	128490427	FLNC_2996	-	GTGACCTATGCACCAGACGTTGAGAGGGAACAGTCAAGTACTGGGGAAGGCCAGGAGTTAGATCGGAAGAGCGGTTTCAG
chr7	128490807	128490846	FLNC_2997	-	GTGACCTATGCACCAGACGTGACACAGTTACGTGGAGACCCTGGTTTCCCCACTGCAACAGATCGGAAGAGCGGTTTCAG
chr7	128491236	128491275	FLNC_2998	-	GTGACCTATGCACCAGACGTAGAGAAAAAGGGGCTGGGTGAGCAGCATCGGATTATCTGAAGATCGGAAGAGCGGTTTCAG
chr7	128491459	128491498	FLNC_2999	-	GTGACCTATGCACCAGACGTAGGTGAGGGCAAGATCAGAGGCTCCTGCCCTCACCCCTGCCAGATCGGAAGAGCGGTTTCAG
chr7	128492595	128492634	FLNC_3000	-	GTGACCTATGCACCAGACGTAGTTGGGGCATCAGGCTGCTATGACTCCAGGCAGGCCCTGAGATCGGAAGAGCGGTTTCAG
chr7	128492832	128492871	FLNC_3001	-	GTGACCTATGCACCAGACGTTGGGTGTTAGGCAGAGCATCCTGTGGGCCCCACCCCTGAAGATCGGAAGAGCGGTTTCAG
chr7	128493473	128493512	FLNC_3002	-	GTGACCTATGCACCAGACGTGCAAGGAACACATCTCCCTCAGTCTAGGCTGGCCAAGCCAGATCGGAAGAGCGGTTTCAG
chr7	128493719	128493758	FLNC_3003	-	GTGACCTATGCACCAGACGTGACAAGGGTGGGTGAGCAACCTCAGAGCCCCAGCCCTAGATCGGAAGAGCGGTTTCAG
chr7	128493978	128494017	FLNC_3004	-	GTGACCTATGCACCAGACGTAAAGGAGCCAGGGGTGAGGGAGGGAAGCGAGGGGTGAGGAAAGATCGGAAGAGCGGTTTCAG
chr7	128494417	128494456	FLNC_3005	-	GTGACCTATGCACCAGACGTTGGGGGATGTCAGGGCAACACTGGGATTCTCTAGCCCTAGATCGGAAGAGCGGTTTCAG
chr7	128494779	128494818	FLNC_3006	-	GTGACCTATGCACCAGACGTGCAAGGTAGTGGACTTCAGCATCATCGCCCTCACACTGGAGATCGGAAGAGCGGTTTCAG
chr7	128495203	128495242	FLNC_3007	-	GTGACCTATGCACCAGACGTAGACCAGTCAAGCAGAGGTTCCGGGATGGAGGTTGGCAGGGAGATCGGAAGAGCGGTTTCAG
chr7	128496522	128496561	FLNC_3008	-	GTGACCTATGCACCAGACGTACGGAGGATGCTCAGACTCCTGGGAGGCCGGGGCTGGAGAGATCGGAAGAGCGGTTTCAG
chr7	128496749	128496788	FLNC_3009	-	GTGACCTATGCACCAGACGTAGGTTGGTGGCTTAGCCTCCATCTCCCTCCCCAAGATCGGAAGAGCGGTTTCAG
chr7	128497122	128497161	FLNC_3010	-	GTGACCTATGCACCAGACGTAGGTTAGCAAGGCTGAGGGCAGGAGGGCTTGTGCCCAAAGATCGGAAGAGCGGTTTCAG
chr7	128498012	128498051	FLNC_3011	-	GTGACCTATGCACCAGACGTGGTGGAGGGGGCACAAACCTAGTCAGAAGGGCTTCTGTTAGATCGGAAGAGCGGTTTCAG
chr7	128498340	128498379	FLNC_3012	-	GTGACCTATGCACCAGACGTAGGCAGAGGGACAGGCTCACACCAGGGAGTCCCCTACTGTAGATCGGAAGAGCGGTTTCAG
chr7	128484961	128485000	FLNC_3013	-	GTGACCTATGCACCAGACGTTGGCCCGCACCTGCTCGGGTCAAACACAGGCCGAATGGTAGATCGGAAGAGCGGTTTCAG
chr2	216226228	216226267	FN1_3014	-	GTGACCTATGCACCAGACGTCAATCCAGAGAAACAAGCATGTCTCTGCAAGATCCATAGATCGGAAGAGCGGTTTCAG
chr2	216226642	216226681	FN1_3015	-	GTGACCTATGCACCAGACGTATGACGACAGGTTGTGACCTATAAGATGACAGACTCTCTTAGATCGGAAGAGCGGTTTCAG
chr2	216229552	216229591	FN1_3016	-	GTGACCTATGCACCAGACGTGTGCCAGGCTCCCTACAACTAGATAAGATAAAGGGTGTAGATCGGAAGAGCGGTTTCAG

chr2	216230178	216230217	FN1_3017	-	GTGACCTATGCACCAGACGTACAGATCATTTTAGTGCCTTATTAAGCATTCTCACTTTCAGATCGGAAGAGCGGTTTCAG
chr2	216232536	216232575	FN1_3018	-	GTGACCTATGCACCAGACGTGCTTTTGCATCCACTTCCGTGTTTGTCTCCCTCAAGTCCAGATCGGAAGAGCGGTTTCAG
chr2	216234967	216235006	FN1_3019	-	GTGACCTATGCACCAGACGTACGTACTATTTAGACACAGGCTCCCTCTGCTGTACACCAAGATCGGAAGAGCGGTTTCAG
chr2	216236582	216236621	FN1_3020	-	GTGACCTATGCACCAGACGTGTTCTCTTCACTTCTCATGGGGCAGCACAGAAAGGAATAAAGATCGGAAGAGCGGTTTCAG
chr2	216236782	216236821	FN1_3021	-	GTGACCTATGCACCAGACGTCCAAATTTGGTACATCCCCAGGGAAGATGTAGACTATCACAGATCGGAAGAGCGGTTTCAG
chr2	216237995	216238034	FN1_3022	-	GTGACCTATGCACCAGACGTCTTTCAGGTAACAGGAAAGATAGGACAAAACATAAAGATCGGAAGAGCGGTTTCAG
chr2	216239887	216239926	FN1_3023	-	GTGACCTATGCACCAGACGTCTCCATGCTGTCAATTTCCCTTCTTACTACTAGCACATAGATCGGAAGAGCGGTTTCAG
chr2	216240302	216240341	FN1_3024	-	GTGACCTATGCACCAGACGTCTTCTACTGAGGAAATGCCATTGACTTGTATGCAATCAGTAGATCGGAAGAGCGGTTTCAG
chr2	216241171	216241210	FN1_3025	-	GTGACCTATGCACCAGACGTTCATTGCTACTAACCACATTTGTTAAACAATACCCACAATGAGATCGGAAGAGCGGTTTCAG
chr2	216242848	216242887	FN1_3026	-	GTGACCTATGCACCAGACGTAAATGTCTTTCATATGGACAAAACCTTCTGTATAGACAAAAAGATCGGAAGAGCGGTTTCAG
chr2	216243803	216243842	FN1_3027	-	GTGACCTATGCACCAGACGTACCGTTGTTTCATTGGAATAAAGATGGAGATCATCTCTAACAGATCGGAAGAGCGGTTTCAG
chr2	216245484	216245523	FN1_3028	-	GTGACCTATGCACCAGACGTAATTGCACCACAGGTCGCCATGGGAGCAGCGGCTTTATGAGATCGGAAGAGCGGTTTCAG
chr2	216246885	216246924	FN1_3029	-	GTGACCTATGCACCAGACGTACTGTTGGTTTCCATTTTCAAAGTCAAATTTTGTCTTTCAGATCGGAAGAGCGGTTTCAG
chr2	216248693	216248732	FN1_3030	-	GTGACCTATGCACCAGACGTCTACTCTGGGGTGACACCAGCTTTTACTTATTAGATACTAGATCGGAAGAGCGGTTTCAG
chr2	216249533	216249572	FN1_3031	-	GTGACCTATGCACCAGACGTAAATGTCTTTTCACTCTGATTAAATCAGATTCTGTTGAGATCGGAAGAGCGGTTTCAG
chr2	216251362	216251401	FN1_3032	-	GTGACCTATGCACCAGACGTTTGTCTGCAAAGAAACTCAGAAGACTTTCCTACCCAGTTGAGATCGGAAGAGCGGTTTCAG
chr2	216252885	216252924	FN1_3033	-	GTGACCTATGCACCAGACGTTTGGCAGTATGCTTCCATCCAGTAGCTTTTGCCTATCAATTTCAGATCGGAAGAGCGGTTTCAG
chr2	216256305	216256344	FN1_3034	-	GTGACCTATGCACCAGACGTGAATGTATCTGTTCCATAATATTAACCTAGAGCATAGCAAGATCGGAAGAGCGGTTTCAG
chr2	216257604	216257643	FN1_3035	-	GTGACCTATGCACCAGACGTAAAACTTCTGCGTTTGAGACATAGATGGTGTTCATGCTGAGATCGGAAGAGCGGTTTCAG
chr2	216259201	216259240	FN1_3036	-	GTGACCTATGCACCAGACGTAATAAGCTGCTATCCTGAGAGTGACACTTCCAATAAGAGTAGATCGGAAGAGCGGTTTCAG
chr2	216261810	216261849	FN1_3037	-	GTGACCTATGCACCAGACGTGATGGATCAGAGGGCAAGTATACACCATACCTTCCCAAGAAGATCGGAAGAGCGGTTTCAG
chr2	216262353	216262392	FN1_3038	-	GTGACCTATGCACCAGACGTTTTTTTTCCCTTTTCTATTAGTTTTTAAAACCTGTTCTACTTAGATCGGAAGAGCGGTTTCAG
chr2	216263930	216263969	FN1_3039	-	GTGACCTATGCACCAGACGTGATGTTCCCTAATCTGTGATACAGCCCTGAGCTGCTTTCAGATCGGAAGAGCGGTTTCAG
chr2	216269062	216269101	FN1_3040	-	GTGACCTATGCACCAGACGTAAATGCTTCTTAACTATATTTACATTTCTTATTAGATCGGAAGAGCGGTTTCAG
chr2	216270911	216270950	FN1_3041	-	GTGACCTATGCACCAGACGTTCCCTATCTCTATCTCCCCTCAAATTTCTCCACCCTCACTTAGATCGGAAGAGCGGTTTCAG
chr2	216271800	216271839	FN1_3042	-	GTGACCTATGCACCAGACGTTAAGAAGACACTTCTATGTTATCTTATCAGGATTGTTCCAGATCGGAAGAGCGGTTTCAG
chr2	216272781	216272820	FN1_3043	-	GTGACCTATGCACCAGACGTGCTCCCTCTTTGGCTGCTATGTTAATCTTAATGACATCAGATCGGAAGAGCGGTTTCAG
chr2	216272971	216273010	FN1_3044	-	GTGACCTATGCACCAGACGTGCTACTAGTGTAAAAGAACTCTTTTCTGTAAAACACAGAGATCGGAAGAGCGGTTTCAG
chr2	216274236	216274275	FN1_3045	-	GTGACCTATGCACCAGACGTTATCTCGCTCAAGACAGTTTCAGGCGACTGCTGGAAACAGATCGGAAGAGCGGTTTCAG
chr2	216274607	216274646	FN1_3046	-	GTGACCTATGCACCAGACGTAAACACCCTCATGCTCCCTACCCTCAGGTTTCTAGAGACTAGATCGGAAGAGCGGTTTCAG
chr2	216279477	216279516	FN1_3047	-	GTGACCTATGCACCAGACGTCTTATCAATTTCTGATGGTTTTTTTTTTTCCAGCTTTTGAAGATCGGAAGAGCGGTTTCAG
chr2	216279510	216279549	FN1_3048	-	GTGACCTATGCACCAGACGTCAACCAGAAACCTTGATACTGAGTCTCCTAATCTTATCAAGATCGGAAGAGCGGTTTCAG
chr2	216283915	216283954	FN1_3049	-	GTGACCTATGCACCAGACGTCTATTACTCGAAGTTGAGAACTGCCAATTTGGGTTATAACAAGATCGGAAGAGCGGTTTCAG
chr2	216285346	216285385	FN1_3050	-	GTGACCTATGCACCAGACGTCTATTTCCCTAGATGAGTTTGACACAGGGGGAATGGTTAGCAGATCGGAAGAGCGGTTTCAG
chr2	216286764	216286803	FN1_3051	-	GTGACCTATGCACCAGACGTGTTAATAACAAAATATTTGAGATGGCAAAGGTACAGAAAAGATCGGAAGAGCGGTTTCAG
chr2	216288023	216288062	FN1_3052	-	GTGACCTATGCACCAGACGTGCCCTTGTGGGTTGTCTTGTTTGACAACAATTTAGGGAGTAGATCGGAAGAGCGGTTTCAG
chr2	216288819	216288858	FN1_3053	-	GTGACCTATGCACCAGACGTCAAGGGGAGCCACAGAAAGTGAAGAAAACCTCACTTTTCATGAGATCGGAAGAGCGGTTTCAG
chr2	216289767	216289806	FN1_3054	-	GTGACCTATGCACCAGACGTTCTTTTTGAAGAATAGGACTGATGACTTTTATTATTAGTTAGATCGGAAGAGCGGTTTCAG
chr2	216292853	216292892	FN1_3055	-	GTGACCTATGCACCAGACGTGGACGAGCAGGGGCGGGAATGGGAAGCAGGTCAAGAAAAGATCGGAAGAGCGGTTTCAG
chr2	216295388	216295427	FN1_3056	-	GTGACCTATGCACCAGACGTCACTTTATGTTAAAGATTAAGCCAGGTATTGTTTTCTGGAGATCGGAAGAGCGGTTTCAG
chr2	216296506	216296545	FN1_3057	-	GTGACCTATGCACCAGACGTCTTAGGGCTGAGCAAGAGTGGGATGCTTACTGTTCTAATGTAGATCGGAAGAGCGGTTTCAG
chr2	216297997	216298036	FN1_3058	-	GTGACCTATGCACCAGACGTGATTGTGTTAAAATGATGCCAAAATATCAATATGAATTTTCAGATCGGAAGAGCGGTTTCAG
chr2	216299369	216299408	FN1_3059	-	GTGACCTATGCACCAGACGTACAAGCCCCATAGTTAGTATCTTTTAAATACATGAAGTGGTAGATCGGAAGAGCGGTTTCAG
chr2	216300328	216300367	FN1_3060	-	GTGACCTATGCACCAGACGTACCCTGGGGCTGAAACAGGCTGCCTCAGGGATGGGACCTAAGATCGGAAGAGCGGTTTCAG
chr3	119545585	119545624	GSK3B_3061	-	GTGACCTATGCACCAGACGTGACGCCAGCTGCACAGGAAAAACCCAGTTACTTGTAGTGATCGGAAGAGCGGTTTCAG
chr3	119582216	119582255	GSK3B_3062	-	GTGACCTATGCACCAGACGTACACTGACCTTCCAGCTTCTAGGAAAGCTACACCCTAGATCGGAAGAGCGGTTTCAG
chr3	119585387	119585426	GSK3B_3063	-	GTGACCTATGCACCAGACGTAATTTTTTTTTTCCAAAAATTTTCAGGGCAGGTTCTATAAAAACAGATCGGAAGAGCGGTTTCAG
chr3	119595210	119595249	GSK3B_3064	-	GTGACCTATGCACCAGACGTTTTTTTTTAAAGTATATTAATCAGTAGTTAACTAAAACAGAGATCGGAAGAGCGGTTTCAG
chr3	119631501	119631540	GSK3B_3065	-	GTGACCTATGCACCAGACGTATCTGAATATAATGCTCATAATTATTAATTGCTTCTTGATAGATCGGAAGAGCGGTTTCAG
chr3	119634841	119634880	GSK3B_3066	-	GTGACCTATGCACCAGACGTGTCCTCTCCCTGCCCTTCCCTTTTCCCTCCTCCCTTAGATCGGAAGAGCGGTTTCAG
chr3	119642170	119642209	GSK3B_3067	-	GTGACCTATGCACCAGACGTACATAACAATTTTCCATTTAGAAAACATTTTTATGAACAGATCGGAAGAGCGGTTTCAG
chr3	119666065	119666104	GSK3B_3068	-	GTGACCTATGCACCAGACGTACAAAAGTGTACTGAATATTGTGATAAATTTGTTATTAGATCGGAAGAGCGGTTTCAG
chr3	119720843	119720882	GSK3B_3069	-	GTGACCTATGCACCAGACGTCAATTTTTCATATTTTTGTTGCTGTCGTAATACATATACAGATCGGAAGAGCGGTTTCAG
chr3	119812144	119812183	GSK3B_3070	-	GTGACCTATGCACCAGACGTGTTTTATTTTACACCCTTTTCCACCTCGCCTTAAAATAAGATCGGAAGAGCGGTTTCAG
chr6	114262172	114262211	HDAC2_3071	-	GTGACCTATGCACCAGACGTCTACCAATTTTCAGAAAATCATAAAAAGAAAATTTGAAAGATCGGAAGAGCGGTTTCAG
chr6	114262822	114262861	HDAC2_3072	-	GTGACCTATGCACCAGACGTTTTCTTCAAGTACTTTTTACATACATAAAAACTAAAGATCGGAAGAGCGGTTTCAG
chr6	114264465	114264504	HDAC2_3073	-	GTGACCTATGCACCAGACGTTTTTCTTGGTAATTTGTTTTAAATTTGAAAATTTAAAATTTAGATCGGAAGAGCGGTTTCAG
chr6	114265394	114265433	HDAC2_3074	-	GTGACCTATGCACCAGACGTGCCTTTATTTTTCCAATTTGTCAAAATGATAATTGAAATGAGATCGGAAGAGCGGTTTCAG

chr6	114266476	114266515	HDAC2_3075	-	GTGACCTATGCACCAGACGTATTGAATTGTTTTGATAAACATTTTATCTTGACAAGATTAGATCGGAAGAGCGGTTTCAG
chr6	114270093	114270132	HDAC2_3076	-	GTGACCTATGCACCAGACGCTCAAAGGGTGGTATTTCCAGAAAAAATGGTTTTCTTCCAAGATCGGAAGAGCGGTTTCAG
chr6	114270282	114270321	HDAC2_3077	-	GTGACCTATGCACCAGACGTTTTGTTTTCACAATTGGAATGGAATTTCCAGAATGTTATTGGAGATCGGAAGAGCGGTTTCAG
chr6	114274391	114274430	HDAC2_3078	-	GTGACCTATGCACCAGACGTATTCTGTCTGAAAAAATATTGTGAGATGAACTAGGAGATAGATCGGAAGAGCGGTTTCAG
chr6	114277127	114277166	HDAC2_3079	-	GTGACCTATGCACCAGACGTTTATATTGATACTCTTTTCAGTGATAAAGTGTTCATTAAAGATCGGAAGAGCGGTTTCAG
chr6	114277733	114277772	HDAC2_3080	-	GTGACCTATGCACCAGACGTGAACTCAGATTTAAAAGTTGATCTGAACTTGGTGTTAGATCGGAAGAGCGGTTTCAG
chr6	114279763	114279802	HDAC2_3081	-	GTGACCTATGCACCAGACGCTAAGTAAAAGTAGTTTTGCTTTGATAAATGTAATAGTAGAATCGGAAGAGCGGTTTCAG
chr6	114281020	114281059	HDAC2_3082	-	GTGACCTATGCACCAGACGCTTTTTAATACATATTCCAGCACTGATCTTTTTTATTTTTTTAGATCGGAAGAGCGGTTTCAG
chr7	27203172	27203211	HOXA9_3083	-	GTGACCTATGCACCAGACGTGCTTATTAGAAAAAAGGGTAAGCTAGAGAGAAAAAGAAAGATCGGAAGAGCGGTTTCAG
chr7	27204447	27204486	HOXA9_3084	-	GTGACCTATGCACCAGACGTCCTCCCTTCAAATCCGCCGCCGCCTCCACGCCGGCCTCCAGATCGGAAGAGCGGTTTCAG
chr7	27204737	27204776	HOXA9_3085	-	GTGACCTATGCACCAGACGTGCGGCCGCCGGACGGCAGGTACATGCGCTCCTGGCTGGAGCAGATCGGAAGAGCGGTTTCAG
chr11	64571756	64571795	MEN1_3086	-	GTGACCTATGCACCAGACGTACTTCGGACCGCTGTGGGGACCCAGGCTCCGCCCTTAGTAGATCGGAAGAGCGGTTTCAG
chr11	64572456	64572495	MEN1_3087	-	GTGACCTATGCACCAGACGCTGCTGCACAGAGGTCTGGGCACCTACAGGTGGTGACAGCAGCAGATCGGAAGAGCGGTTTCAG
chr11	64573057	64573096	MEN1_3088	-	GTGACCTATGCACCAGACGTGGAGCTCCAGCCTGTGTCCAGCCTCCACCTGGACAGGGCAGATCGGAAGAGCGGTTTCAG
chr11	64573654	64573693	MEN1_3089	-	GTGACCTATGCACCAGACGTCCTACTAGGGCCTGCAGCCTGTCTTTCTCCCTCCATAGATCGGAAGAGCGGTTTCAG
chr11	64574433	64574472	MEN1_3090	-	GTGACCTATGCACCAGACGCTAAGAGGGTGCAGAAAGGGAGACCTAACAGTGGCTGAGAGATCGGAAGAGCGGTTTCAG
chr11	64574601	64574640	MEN1_3091	-	GTGACCTATGCACCAGACGTGGAGTGCCACAGGCTGCCCTGTGAGGCCGGGGGGTGGAGATCGGAAGAGCGGTTTCAG
chr11	64575313	64575352	MEN1_3092	-	GTGACCTATGCACCAGACGTCCTCCCGCCAGCTTGTCGCCCTTCACTAGTAGTACGCCAAAGATCGGAAGAGCGGTTTCAG
chr11	64577072	64577111	MEN1_3093	-	GTGACCTATGCACCAGACGTTATCCATGACCCACTTCTTCAAACCTCCATGGTTTACAAGATCGGAAGAGCGGTTTCAG
chr11	64577087	64577126	MEN1_3094	-	GTGACCTATGCACCAGACGTAGTAGGGGAATCTTATCCATGACCCACTTCTTCAAACAGATCGGAAGAGCGGTTTCAG
chr22	36678664	36678703	MYH9_3095	-	GTGACCTATGCACCAGACGCTGACAGCCTGAGATGGATGGACAGACAGACACCACGCCATAGATCGGAAGAGCGGTTTCAG
chr22	36680089	36680128	MYH9_3096	-	GTGACCTATGCACCAGACGTCGCCCACCCGCCCTTTGCCTCGGCCACTTCTCTCAAAGATCGGAAGAGCGGTTTCAG
chr22	36680399	36680438	MYH9_3097	-	GTGACCTATGCACCAGACGTGGTGGGGCAGTGAGAAGGGCAGCGGGCTGGGCAGCAGAAGATCGGAAGAGCGGTTTCAG
chr22	36681117	36681156	MYH9_3098	-	GTGACCTATGCACCAGACGCTGCTGCCCCGCCCAACCCAGCTGTCTGGAAAAAATCTGAGATCGGAAGAGCGGTTTCAG
chr22	36681654	36681693	MYH9_3099	-	GTGACCTATGCACCAGACGTGGACTTCTCCCACCTCTGGGCTGTGGCTGGAGCCACCACGGAGATCGGAAGAGCGGTTTCAG
chr22	36681861	36681900	MYH9_3100	-	GTGACCTATGCACCAGACGTTGAGGGGGCAGAGTTGGGGGGGACCAGGTGTGTCCCAGGAGATCGGAAGAGCGGTTTCAG
chr22	36682714	36682753	MYH9_3101	-	GTGACCTATGCACCAGACGTCGCAATGGAGAGCGGCACCCGCTGCCCTGCGGCCAGCAGGAGATCGGAAGAGCGGTTTCAG
chr22	36684248	36684287	MYH9_3102	-	GTGACCTATGCACCAGACGTGCGGGGGCCAGGTGAGGGTGGGGCGGCCACCCGACTGAGCCAAGATCGGAAGAGCGGTTTCAG
chr22	36684723	36684762	MYH9_3103	-	GTGACCTATGCACCAGACGTCCTCCTGCTACCCATGGGTGCCCAAGGCTGCCCTTAGATCGGAAGAGCGGTTTCAG
chr22	36685081	36685120	MYH9_3104	-	GTGACCTATGCACCAGACGCTGGCCTGGCAGCCAGGTTGGAAAGGGGCCAGGTGCCCTGCTGAGATCGGAAGAGCGGTTTCAG
chr22	36687982	36688021	MYH9_3105	-	GTGACCTATGCACCAGACGTGTTGGCCCCATCCTTGCATTTCTCTCCTTCAAGCACTGAGATCGGAAGAGCGGTTTCAG
chr22	36689325	36689364	MYH9_3106	-	GTGACCTATGCACCAGACGTCGTTGGGGACCGGCCGACTCTGCAGGCTGGGGAGCTGCTGAGATCGGAAGAGCGGTTTCAG
chr22	36689755	36689794	MYH9_3107	-	GTGACCTATGCACCAGACGTCGCCAGGTTCCAGAAAGTGGACCCCTCCAGAAAGGCCCTCAGATCGGAAGAGCGGTTTCAG
chr22	36690088	36690127	MYH9_3108	-	GTGACCTATGCACCAGACGTGCCCCAGGACCCCTGGCGGGCAGCTGGGCCCTAGCAGCAGATAGATCGGAAGAGCGGTTTCAG
chr22	36690928	36690967	MYH9_3109	-	GTGACCTATGCACCAGACGTCCTCCTGAGACCCGAGGGGGAGGGCAGGGTTCGCCCTGCTGAGATCGGAAGAGCGGTTTCAG
chr22	36691501	36691540	MYH9_3110	-	GTGACCTATGCACCAGACGTGGACCAAGTCCCTCGGGATGGGGAGGGCAGCCAGGGGGCAGATCGGAAGAGCGGTTTCAG
chr22	36692839	36692878	MYH9_3111	-	GTGACCTATGCACCAGACGTCGCCTGCCCGCTGAGGCCAGGTGGCCTGGGCCAGCCCTTAGATCGGAAGAGCGGTTTCAG
chr22	36694915	36694954	MYH9_3112	-	GTGACCTATGCACCAGACGTGACGAGCAGGAGGTGATGGGCAGGGGCTGGCGGGCAAGGGAGATCGGAAGAGCGGTTTCAG
chr22	36696123	36696162	MYH9_3113	-	GTGACCTATGCACCAGACGTTGGCTGTGCGCTGCCGCTGCTCCAGGGGGCGCCGTGGATGGAGATCGGAAGAGCGGTTTCAG
chr22	36696847	36696886	MYH9_3114	-	GTGACCTATGCACCAGACGTCCTGCCCAGGCGGTGGCCAGGGGCTGGCCAGGGCGGAGATCGGAAGAGCGGTTTCAG
chr22	36697530	36697569	MYH9_3115	-	GTGACCTATGCACCAGACGTTGTCAGCCCTCAGCTCAGCTCAGCAGCAGCTGCCTGCCTGAGATCGGAAGAGCGGTTTCAG
chr22	36699991	36700030	MYH9_3116	-	GTGACCTATGCACCAGACGTGGAGATACTCCTGCCCGCATGCCAGGCCTTGCACGCCAGATCGGAAGAGCGGTTTCAG
chr22	36701029	36701068	MYH9_3117	-	GTGACCTATGCACCAGACGCTGCTGTGCCCTGCCTCTCTGGATGGCAGCCCTTGTCTGAGATCGGAAGAGCGGTTTCAG
chr22	36701926	36701965	MYH9_3118	-	GTGACCTATGCACCAGACGTGCCCGGAGCCCGCTTCTCCTGGGCCCTGCTGTGCGTGCAGAGATCGGAAGAGCGGTTTCAG
chr22	36702410	36702449	MYH9_3119	-	GTGACCTATGCACCAGACGTTGGTGGGGTGCCCGGCGCCGCACTGTGGTGTGGTGGATCGGAAGAGCGGTTTCAG
chr22	36705277	36705316	MYH9_3120	-	GTGACCTATGCACCAGACGTCCTCCTGCCCCCTGCCCTCTTGCTGGCTGGCTGGTCAAGATCGGAAGAGCGGTTTCAG
chr22	36708044	36708083	MYH9_3121	-	GTGACCTATGCACCAGACGTCACAGGGGAGGTGCTGGCCAGATCTTCACAGGAGAGGTGAGATCGGAAGAGCGGTTTCAG
chr22	36710140	36710179	MYH9_3122	-	GTGACCTATGCACCAGACGTGGCTTGCTTTGACCTCACACCTGCCTCTGGCTTTTCCCTTAGATCGGAAGAGCGGTTTCAG
chr22	36712512	36712551	MYH9_3123	-	GTGACCTATGCACCAGACGTCCTTCCATTACCACCCCTGCTGCCCTCCTTGGCCCTGTTGGTAGATCGGAAGAGCGGTTTCAG
chr22	36714202	36714241	MYH9_3124	-	GTGACCTATGCACCAGACGTTGGGGCCAGGGCAGCTGGCTGCCTCCTGGGTGAATGTCCAGATCGGAAGAGCGGTTTCAG
chr22	36715535	36715574	MYH9_3125	-	GTGACCTATGCACCAGACGTGGCCCTCCTGGAATAATGGGGCAGGTTGGCTGGCCATAGATCGGAAGAGCGGTTTCAG
chr22	36716215	36716254	MYH9_3126	-	GTGACCTATGCACCAGACGTGGCCCTCCTATGGTGTGAGTGTGGGCAGAGAAAGGCTGGTAGATCGGAAGAGCGGTTTCAG
chr22	36716793	36716832	MYH9_3127	-	GTGACCTATGCACCAGACGTGGCCTGCAGCCTGACACCGGGGCTGCCGGCTCTGGCCCTAGATCGGAAGAGCGGTTTCAG
chr22	36717753	36717792	MYH9_3128	-	GTGACCTATGCACCAGACGTGGTTCGTTGGGATAAGAGTCTGGATCCGGAGGGGAGGCAAGATCGGAAGAGCGGTTTCAG
chr22	36718424	36718463	MYH9_3129	-	GTGACCTATGCACCAGACGTCGGCGCGCCCCGCTCTGGGGACAGAGGGCCTTGCCCGGAGATCGGAAGAGCGGTTTCAG
chr22	36722563	36722602	MYH9_3130	-	GTGACCTATGCACCAGACGTCAGCCCTTGCTCCTGTGCCCGCCTGCTTGGCCCTTGGTGGAGATCGGAAGAGCGGTTTCAG
chr22	36723456	36723495	MYH9_3131	-	GTGACCTATGCACCAGACGTCCTGCTGGGATGTGGTGTTCACCCAGCTGTTCTGAGATCGGAAGAGCGGTTTCAG
chr22	36737365	36737404	MYH9_3132	-	GTGACCTATGCACCAGACGTTAGTGTGTCGCCACTGGGGCTGAATCTCACCTTCCAGTGGGCCAGATCGGAAGAGCGGTTTCAG

chr22	36744899	36744938	MYH9_3133	-	GTGACCTATGCACCAGACGTGCCGTGGCACCCCGCAGGCTGGGTCTGAGGGCTCCGAGGTAGATCGGAAGAGCGGTTTCAG
chr8	71025817	71025856	NCOA2_3134	-	GTGACCTATGCACCAGACGTGCCAGTTGCTTCTTCAGCTGACCGGGCTCACTTGCTCAAAGATCGGAAGAGCGGTTTCAG
chr8	71033487	71033526	NCOA2_3135	-	GTGACCTATGCACCAGACGTACAGTGAATATATGAATATGGAAGTAAAGCAAACATGAAAGATCGGAAGAGCGGTTTCAG
chr8	71036069	71036108	NCOA2_3136	-	GTGACCTATGCACCAGACGTAAAGGAGAAGCAACCCAGTGGCTTCATATCACGGCTTTTTTAGATCGGAAGAGCGGTTTCAG
chr8	71036873	71036912	NCOA2_3137	-	GTGACCTATGCACCAGACGTATCCTTCTCTTTTCATACCGCCACTGTGACAGCTGAAGGAGATCGGAAGAGCGGTTTCAG
chr8	71038998	71039037	NCOA2_3138	-	GTGACCTATGCACCAGACGTAGATCCCCACCACCTTTCCACCAGTCTTTTCTCCCCAGTGGACCGGAAGAGCGGTTTCAG
chr8	71040618	71040657	NCOA2_3139	-	GTGACCTATGCACCAGACGTATACCAGCCATTACCTTTGATGATGCACGACTGCTTAGATCGGAAGAGCGGTTTCAG
chr8	71040887	71040926	NCOA2_3140	-	GTGACCTATGCACCAGACGTGATGGCACCTGGGAAGTCAGGGGTGCTGGGTGGAGGACAAGATCGGAAGAGCGGTTTCAG
chr8	71044022	71044061	NCOA2_3141	-	GTGACCTATGCACCAGACGTAAAGGCAGCAGGTGGGGGCCAAGCGCTCTCATGGGCGCAGAGATCGGAAGAGCGGTTTCAG
chr8	71050388	71050427	NCOA2_3142	-	GTGACCTATGCACCAGACGTAGCACTAGGGTAGCCAGTATTTTTATACCTGTCCAGAAAAGATCGGAAGAGCGGTTTCAG
chr8	71053369	71053408	NCOA2_3143	-	GTGACCTATGCACCAGACGTTCTAGTGTCTTTTGTCTTTAACTTTTATGCTCTCTTAGAAAAGATCGGAAGAGCGGTTTCAG
chr8	71056827	71056866	NCOA2_3144	-	GTGACCTATGCACCAGACGTAATGCATGTTACTTTATTGGTGGTTTATTTAATTTAATAGATCGGAAGAGCGGTTTCAG
chr8	71060458	71060497	NCOA2_3145	-	GTGACCTATGCACCAGACGTGAAATGGCTGGTGTGCAAGAAATTTCCATATAACTACTAGATCGGAAGAGCGGTTTCAG
chr8	71068156	71068195	NCOA2_3146	-	GTGACCTATGCACCAGACGTTACATCTTCTCGCAGGTGACTAATCTGTATCCATCAAGAGATCGGAAGAGCGGTTTCAG
chr8	71071690	71071729	NCOA2_3147	-	GTGACCTATGCACCAGACGTTTCTAAGAAGTCATTTTCCATTTCCAAGTTAAGAGGAGATAGATCGGAAGAGCGGTTTCAG
chr8	71074896	71074935	NCOA2_3148	-	GTGACCTATGCACCAGACGTTCAAATGATTTTTCTTAAATATTGCTTCTGTGGGAGCTAGATCGGAAGAGCGGTTTCAG
chr8	71075650	71075689	NCOA2_3149	-	GTGACCTATGCACCAGACGTTCTCCAAAGAACCAAGGAATCATTTTGAATACTTACAGATCGGAAGAGCGGTTTCAG
chr8	71078751	71078790	NCOA2_3150	-	GTGACCTATGCACCAGACGTATCCCTAGGGTGTCTGTGTGTGTATTTATTCTGTAGATCGGAAGAGCGGTTTCAG
chr8	71082387	71082426	NCOA2_3151	-	GTGACCTATGCACCAGACGTGCTGGGTCTCCCTCCCTACCTCCCGTCACCCCCACCTGCCAGATCGGAAGAGCGGTTTCAG
chr8	71086941	71086980	NCOA2_3152	-	GTGACCTATGCACCAGACGTTTCACTTTTAGTGTCTATTTTAAATCTTGTGATCTTCAAGATCGGAAGAGCGGTTTCAG
chr8	71126088	71126127	NCOA2_3153	-	GTGACCTATGCACCAGACGTTGAATTAGTATTTTGAAGAGTTGAATTGGTTTCTGTTTTAGATCGGAAGAGCGGTTTCAG
chr8	71128845	71128884	NCOA2_3154	-	GTGACCTATGCACCAGACGTTGCTGAGAAAAGGAATCAGTATTGCTGTAAAGCCACATAGATCGGAAGAGCGGTTTCAG
chr8	71068579	71068618	NCOA2_3155	-	GTGACCTATGCACCAGACGTTGCTGGATACAAACAAGACTCCACAGGTAGCTTGCCTGGAGATCGGAAGAGCGGTTTCAG
chr8	71069002	71069041	NCOA2_3156	-	GTGACCTATGCACCAGACGTGCAGCAGCAAGAAATAGCCATAGTTATACCAACAGCTCAGATCGGAAGAGCGGTTTCAG
chr20	5095879	5095918	PCNA_3157	-	GTGACCTATGCACCAGACGTAATTCAGAAAATAAAAATAAGCTCTTTGAGAAGTCTTCAGATCGGAAGAGCGGTTTCAG
chr20	5096045	5096084	PCNA_3158	-	GTGACCTATGCACCAGACGTAATTTGAACCTTGTTTTGTAGGTAGTCATATGTGATACAAGATCGGAAGAGCGGTTTCAG
chr20	5098066	5098105	PCNA_3159	-	GTGACCTATGCACCAGACGTTTAAAGTAAAAGAAAATAGTTTGAAGAGAATTATAATACAGATCGGAAGAGCGGTTTCAG
chr20	5099206	5099245	PCNA_3160	-	GTGACCTATGCACCAGACGTGTTCTCTATTGTAGAGAGTGTGTACACAGGCACGATAGTAGATCGGAAGAGCGGTTTCAG
chr20	5099365	5099404	PCNA_3161	-	GTGACCTATGCACCAGACGTCTTTTACCGAGTACGAAAGCTACAGAAAATCAAACACTCAGATCGGAAGAGCGGTTTCAG
chr20	5100174	5100213	PCNA_3162	-	GTGACCTATGCACCAGACGTCTGGCCCCGGGAGCCGCCCCCGCCCTGCCACCTCCGAGATCGGAAGAGCGGTTTCAG
chr15	74287104	74287143	PML_3163	-	GTGACCTATGCACCAGACGTTTAGTTTTCGATTCTCGGTTTAGATCTTGGAGTGCCTGAAGAGATCGGAAGAGCGGTTTCAG
chr15	74290295	74290334	PML_3164	-	GTGACCTATGCACCAGACGTAGAGAGGCAGGTGAGGGCTGGAGAAGTCCCAAAGCCCCAGATCGGAAGAGCGGTTTCAG
chr15	74315119	74315158	PML_3165	-	GTGACCTATGCACCAGACGTACAAGGTTGGCCTGGGTTAGGACTCTCTGACTTTTTCTAGATCGGAAGAGCGGTTTCAG
chr15	74317148	74317187	PML_3166	-	GTGACCTATGCACCAGACGTTCAAAGAAGTTCACAGGCAGGTCAAGGACATGCTGGTAAGGAGATCGGAAGAGCGGTTTCAG
chr15	74324863	74324902	PML_3167	-	GTGACCTATGCACCAGACGTGGGAAAATAGTGTAGCAAAATGACTAGGCAGCAGCCAGGATCGGAAGAGCGGTTTCAG
chr15	74325447	74325486	PML_3168	-	GTGACCTATGCACCAGACGTGGAGTCAACAGGCCAGGTGAGGTGCCTGCAGGGGTGAGTGAAGATCGGAAGAGCGGTTTCAG
chr15	74326769	74326808	PML_3169	-	GTGACCTATGCACCAGACGTGAAGGGGAGATGCATTATGAATGCCTAGGATGCATGCTGAGATCGGAAGAGCGGTTTCAG
chr15	74328298	74328337	PML_3170	-	GTGACCTATGCACCAGACGTGGGCAGGGGTGTTGGCTGCAAGGTTACAAGAGAAGGGTAGAGATCGGAAGAGCGGTTTCAG
chr15	74335280	74335319	PML_3171	-	GTGACCTATGCACCAGACGTGAAAAACCAAGCGTCAGGGATTGAGAGGGCCAAAGCAGATCGGAAGAGCGGTTTCAG
chr15	74336512	74336551	PML_3172	-	GTGACCTATGCACCAGACGTGAGAAGGGCAGGGTGAGGACCCAGGTCACAGAGAGCTTAGATCGGAAGAGCGGTTTCAG
chr15	74315409	74315448	PML_3173	-	GTGACCTATGCACCAGACGTCTCCTGAGCCCGCACGTGACCTACCACCTGGCGCACGCGCAGATCGGAAGAGCGGTTTCAG
chr15	74327853	74327892	PML_3174	-	GTGACCTATGCACCAGACGTGCAGGAGTGTGGCTTGGACCACATGGGGAGACCAAGTCCAGATCGGAAGAGCGGTTTCAG
chr15	74336906	74336945	PML_3175	-	GTGACCTATGCACCAGACGTCCAGCACGGCAGCCATGGCGCTGCGCTCGCTCATGTTTCTAGATCGGAAGAGCGGTTTCAG
chr3	12393042	12393081	PPARG_3176	-	GTGACCTATGCACCAGACGTAATAGGGGTTTGTCTGTAATTCACACTGATATTTTGTCTTAGATCGGAAGAGCGGTTTCAG
chr3	12421153	12421192	PPARG_3177	-	GTGACCTATGCACCAGACGTAATAGACTAGCTGTGAAGTTAAGTCTAGAGAACACAGCAGATCGGAAGAGCGGTTTCAG
chr3	12421155	12421194	PPARG_3178	-	GTGACCTATGCACCAGACGTAAAATAGACTAGCTGTGAAGTTAAGTCTAGAGAACACAGCAGATCGGAAGAGCGGTTTCAG
chr3	12422771	12422810	PPARG_3179	-	GTGACCTATGCACCAGACGTAGACATGTGAGAGGATAATTATCCCATGAAAACAGTCTTAAGATCGGAAGAGCGGTTTCAG
chr3	12447331	12447370	PPARG_3180	-	GTGACCTATGCACCAGACGTAGAGGAATGACAGGATGAATCATTGGATTACTACTGCTCTAGATCGGAAGAGCGGTTTCAG
chr3	12458153	12458192	PPARG_3181	-	GTGACCTATGCACCAGACGTAAACAGGGAAAACGTGGATGACTTGGAGATTTTAACTCACAGATCGGAAGAGCGGTTTCAG
chr3	12475347	12475386	PPARG_3182	-	GTGACCTATGCACCAGACGTACATATGAAAACACAAACAGGGGGTTTCAGTCAAAAAATCCAGATCGGAAGAGCGGTTTCAG
chr4	23797395	23797434	PPARGC1A_3183	-	GTGACCTATGCACCAGACGTAGCTGAGGATGACAGAGGGATGGCGAATACCTCATGGGACAGATCGGAAGAGCGGTTTCAG
chr4	23803303	23803342	PPARGC1A_3184	-	GTGACCTATGCACCAGACGTTATTGTACTGTGAAATGAGGAATCCATAATGTAGAGCTCAAAGATCGGAAGAGCGGTTTCAG
chr4	23803797	23803836	PPARGC1A_3185	-	GTGACCTATGCACCAGACGTTCAAAGTATTTTCTGTTTGAAGTGCAGTATGTA AAAAAGATCGGAAGAGCGGTTTCAG
chr4	23814320	23814359	PPARGC1A_3186	-	GTGACCTATGCACCAGACGTTGGAGCTCACTTTTATTTTAAAGTAGGGTTTCTTCTTTTATAGATCGGAAGAGCGGTTTCAG
chr4	23814594	23814633	PPARGC1A_3187	-	GTGACCTATGCACCAGACGTATGTCTTTTCTTTAGCTCCCTTTATCCCTCTTGTAGAAGATCGGAAGAGCGGTTTCAG
chr4	23826036	23826075	PPARGC1A_3188	-	GTGACCTATGCACCAGACGTAGA AATGAACATTTTCTGAAAGGGAAGGGGGTCTAATAGATCGGAAGAGCGGTTTCAG
chr4	23829973	23830012	PPARGC1A_3189	-	GTGACCTATGCACCAGACGTGACCAAACAGCTGGTGTGAGGGCACTGGAAGCAAAGAAGATCGGAAGAGCGGTTTCAG
chr4	23831036	23831075	PPARGC1A_3190	-	GTGACCTATGCACCAGACGTA AATTTTTTAAATCAGTGGGGGATGTACCAAAGATTTTGTAGATCGGAAGAGCGGTTTCAG

chr4	23833130	23833169	PPARGC1A_3191	-	GTGACCTATGCACCAGACGTTTCCCTACTGTTTAGCAGGAATTGGAGTTGCCCTGGCTACAGATCGGAAGAGCGGTTTCAG
chr4	23886325	23886364	PPARGC1A_3192	-	GTGACCTATGCACCAGACGTCCTTTGAAACATTAATTTTTTCATTGAGTTTGGCTTGGCAGATCGGAAGAGCGGTTTCAG
chr4	23891477	23891516	PPARGC1A_3193	-	GTGACCTATGCACCAGACGTGCAGGGCTCGGCGCTGCAGCCAACTGACGCTTCCCTCAAGATCGGAAGAGCGGTTTCAG
chr4	23815721	23815760	PPARGC1A_3194	-	GTGACCTATGCACCAGACGTCAAGAAAACAGCTCCAAGACCAGGAATCCGAGCCGAGCTAGATCGGAAGAGCGGTTTCAG
chr17	38487421	38487460	RARA_3195	-	GTGACCTATGCACCAGACGTACAGTCAAGGGGAGGCAGACAGTCTGGCAGGGGGCTCTAGATCGGAAGAGCGGTTTCAG
chr17	38498907	38498946	RARA_3196	-	GTGACCTATGCACCAGACGTGAAGGCAAGAGGTCCGAGTGGGAAGTCTGCGCGCCGCCAGATCGGAAGAGCGGTTTCAG
chr17	38504518	38504557	RARA_3197	-	GTGACCTATGCACCAGACGTAAAGAGGGGAGGGCAGTTAGAGCACTAGGTCGCCATCCTTAGATCGGAAGAGCGGTTTCAG
chr17	38505986	38506025	RARA_3198	-	GTGACCTATGCACCAGACGTAGGGGAGGGAGTCAAGTTGTCCACACCCACAGTGGGAGCAAGATCGGAAGAGCGGTTTCAG
chr17	38508112	38508151	RARA_3199	-	GTGACCTATGCACCAGACGTCAAGGGGGTTAAGAGGGCAGCTGCAGGCTGCTCAGGGCCAGATCGGAAGAGCGGTTTCAG
chr17	38508533	38508572	RARA_3200	-	GTGACCTATGCACCAGACGTAGGGAGAGTGAAGGCTTCTTCTCCATGGCACCCCTTCTCAGATCGGAAGAGCGGTTTCAG
chr17	38510504	38510543	RARA_3201	-	GTGACCTATGCACCAGACGTAGGATGCTTGGGTTTCAAGGGACTGGAACCCGAACCCACTCTGAGATCGGAAGAGCGGTTTCAG
chr17	38511465	38511504	RARA_3202	-	GTGACCTATGCACCAGACGTAGAACCACCCCTGAGCAGCTGGGAACACAGCTGCACCCAGATCGGAAGAGCGGTTTCAG
chr17	38512211	38512250	RARA_3203	-	GTGACCTATGCACCAGACGTGGAGGGGGCAGGTCAGCACGCTGGGCCAGCCCTCCACAGATCGGAAGAGCGGTTTCAG
chr5	36152315	36152354	SKP2_3204	-	GTGACCTATGCACCAGACGTGGCCCGGGAGTTAAATACGTGCATTAACCTGACAGAGCTGAGATCGGAAGAGCGGTTTCAG
chr5	36152823	36152862	SKP2_3205	-	GTGACCTATGCACCAGACGTGCACATAACCCCGGTTCTTTTGGAAAACACACCCATAAAAGATCGGAAGAGCGGTTTCAG
chr5	36163697	36163736	SKP2_3206	-	GTGACCTATGCACCAGACGTAAAACAAGTGTGGTCCATCACCATTCTTTCACCCATCAAAGATCGGAAGAGCGGTTTCAG
chr5	36166571	36166610	SKP2_3207	-	GTGACCTATGCACCAGACGTGGAGATACTTAATTTGGCCAGTCGGTCCACACTAAATGCTGAGATCGGAAGAGCGGTTTCAG
chr5	36168365	36168404	SKP2_3208	-	GTGACCTATGCACCAGACGTGAGAAAAAGAGTCCATAGTGGCTCTCACGGGTACAAAGATCGGAAGAGCGGTTTCAG
chr5	36170396	36170435	SKP2_3209	-	GTGACCTATGCACCAGACGTAGAAAAACGTCAAGAAAAAGACCAGTAAGACACTATTAGATCGGAAGAGCGGTTTCAG
chr5	36171655	36171694	SKP2_3210	-	GTGACCTATGCACCAGACGTGAGGGGTAAATAACAAAATATGAAACCATCACACGGGAATAGATCGGAAGAGCGGTTTCAG
chr5	36177237	36177276	SKP2_3211	-	GTGACCTATGCACCAGACGTGGCAGAAGAAAAGATATTGAAAATCACACATTGATCCTAGAGATCGGAAGAGCGGTTTCAG
chr5	36181870	36181909	SKP2_3212	-	GTGACCTATGCACCAGACGTAGAAAAAGACTTTCAGAATAGCAGTATCTATGGAACCTGATAGATCGGAAGAGCGGTTTCAG
chr5	36183892	36183931	SKP2_3213	-	GTGACCTATGCACCAGACGTAAATTTCAAGTAGTATTAGCATTTTTAATCTATTAAAGAAAGATCGGAAGAGCGGTTTCAG
chr16	11348650	11348689	SOCS1_3214	-	GTGACCTATGCACCAGACGTGCCCGGTGCAGCAGCATTAACCTGGATGCCGTGTTATTTAGATCGGAAGAGCGGTTTCAG
chr16	11348968	11349007	SOCS1_3215	-	GTGACCTATGCACCAGACGTACTGCTTTTTCGCCCTTAGCGTGAAGATGGCCTCGGGACCAGATCGGAAGAGCGGTTTCAG
chr2	39212915	39212954	SOS1_3216	-	GTGACCTATGCACCAGACGTACTGGGATGTATTTTTCTAGCCCAAATCCATTGCTGGAGATCGGAAGAGCGGTTTCAG
chr2	39214564	39214603	SOS1_3217	-	GTGACCTATGCACCAGACGTAAATCTTGTGTGAGAAATGGAATCATTACAGTTTATTAGATCGGAAGAGCGGTTTCAG
chr2	39216361	39216400	SOS1_3218	-	GTGACCTATGCACCAGACGTGGTGGTTAAGACTCATAATTTCTGCTTTGGCTTTAAAAATAGATCGGAAGAGCGGTTTCAG
chr2	39222214	39222253	SOS1_3219	-	GTGACCTATGCACCAGACGTAAATTTAAGTGCATTAAGTATTGTTAGTACTATACATAGATCGGAAGAGCGGTTTCAG
chr2	39224013	39224052	SOS1_3220	-	GTGACCTATGCACCAGACGTGTATATTTGCTGGTATGATCTACTACCATATGTGTTAAGATCGGAAGAGCGGTTTCAG
chr2	39224344	39224383	SOS1_3221	-	GTGACCTATGCACCAGACGTATTTAAAGATTCACTCTTGATTAAGTTTCTAAACTAAGATCGGAAGAGCGGTTTCAG
chr2	39233503	39233542	SOS1_3222	-	GTGACCTATGCACCAGACGTCTTCTGAATTTTTATTGCATTTCTGGATAAAACAAAACAGATCGGAAGAGCGGTTTCAG
chr2	39237675	39237714	SOS1_3223	-	GTGACCTATGCACCAGACGTCTAGCATTTCTATATTTATAGCTGCAGCTATGTTATGAAGATCGGAAGAGCGGTTTCAG
chr2	39239217	39239256	SOS1_3224	-	GTGACCTATGCACCAGACGTAAACATTCAAGTTGAAAAGCTATTTCAAAGAGTTAACTTAGATCGGAAGAGCGGTTTCAG
chr2	39240551	39240590	SOS1_3225	-	GTGACCTATGCACCAGACGTATTTTTAGTGGCTGCTATTTTTATATGTAATAAAAGTACCAAAGATCGGAAGAGCGGTTTCAG
chr2	39240958	39240997	SOS1_3226	-	GTGACCTATGCACCAGACGTAAATAATGAAGTAAATAAGTCTTTATCAAACCTTTCGTTTCAGATCGGAAGAGCGGTTTCAG
chr2	39249661	39249700	SOS1_3227	-	GTGACCTATGCACCAGACGTTGCAGTTGCCCTGTCACCTTTGTTTTCTGCTTCAAACCTGAAGATCGGAAGAGCGGTTTCAG
chr2	39251101	39251140	SOS1_3228	-	GTGACCTATGCACCAGACGTTTACTTTTTAAAAATATCCTTTTTTCCCTGAATATTGGTAGATCGGAAGAGCGGTTTCAG
chr2	39262303	39262342	SOS1_3229	-	GTGACCTATGCACCAGACGTTCTTTATTGTTATTTGTAACATATTCAAGTGTGAATTTTTAGATCGGAAGAGCGGTTTCAG
chr2	39262481	39262520	SOS1_3230	-	GTGACCTATGCACCAGACGTTTTAAATGAAGATGACAATGCTGAAAAGTAAACTTAAAGATCGGAAGAGCGGTTTCAG
chr2	39278235	39278274	SOS1_3231	-	GTGACCTATGCACCAGACGTGAATATATACCCGAAAAAGTCTGCATAAAAGCCTACATTTAGATCGGAAGAGCGGTTTCAG
chr2	39281705	39281744	SOS1_3232	-	GTGACCTATGCACCAGACGTTTGTATATATGCCTCTCATTGAATGTGTTGTGAAATTTGCAGATCGGAAGAGCGGTTTCAG
chr2	39283793	39283832	SOS1_3233	-	GTGACCTATGCACCAGACGTGAGCTTTTTCTATTTTTTCTTAAAGTTTCTTTTTATGACTTAGATCGGAAGAGCGGTTTCAG
chr2	39285764	39285803	SOS1_3234	-	GTGACCTATGCACCAGACGTACTACTGCCTTCTGCTTTTTAAGGGAAAAATAAAACCCAAAGATCGGAAGAGCGGTTTCAG
chr2	39294719	39294758	SOS1_3235	-	GTGACCTATGCACCAGACGTTGTGCTTGTATTTACTTTATATCTAATTTGTGTTGGAGATCGGAAGAGCGGTTTCAG
chr2	39347427	39347466	SOS1_3236	-	GTGACCTATGCACCAGACGTGCGGGACCCCGCTCCGCGCCGACGCCCCAGCGGAGATCGGAAGAGCGGTTTCAG
chr2	39249989	39250028	SOS1_3237	-	GTGACCTATGCACCAGACGTTTGAAATAATTTAAAAGATGAAAATAGTGTATATTTTCAGATCGGAAGAGCGGTTTCAG
chr20	36012507	36012546	SRC_3238	-	GTGACCTATGCACCAGACGTGGAGAGAGAGAAGACACTGGAACAGGCAGGGCTGCCGGGGAGATCGGAAGAGCGGTTTCAG
chr20	36014428	36014467	SRC_3239	-	GTGACCTATGCACCAGACGTGGGTGGGGTGTGTGAGAACAGTGGGGCCACAGCCAGGGAAGATCGGAAGAGCGGTTTCAG
chr20	36022248	36022287	SRC_3240	-	GTGACCTATGCACCAGACGTACAGAAGGAGGGAGGAAAGGAGAAGGGAGCCGTCAGCCACAGATCGGAAGAGCGGTTTCAG
chr20	36022527	36022566	SRC_3241	-	GTGACCTATGCACCAGACGTGAGGACGGAGGATGGTGTGCTGACTGTCCAGGCTTCTGCCAAGATCGGAAGAGCGGTTTCAG
chr20	36024515	36024554	SRC_3242	-	GTGACCTATGCACCAGACGTCCGAGGGGAGCCGTCCAGGCCATTGCCCTCTCCCCCTCCAGAGATCGGAAGAGCGGTTTCAG
chr20	36026052	36026091	SRC_3243	-	GTGACCTATGCACCAGACGTGGCAGGAGGAGCAGTTAGGCGGGTCTTCTGCCCTGGGGCCAGATCGGAAGAGCGGTTTCAG
chr20	36028468	36028507	SRC_3244	-	GTGACCTATGCACCAGACGTGGGATGCAGGCTGACTCAGTGGAGCCCCCAACTCCTACCAGATCGGAAGAGCGGTTTCAG
chr20	36029955	36029994	SRC_3245	-	GTGACCTATGCACCAGACGTAGAGACCCAGCTCCAGCTCCTGCCCTGTCCCTCTGCCAGGAGATCGGAAGAGCGGTTTCAG
chr20	36030788	36030827	SRC_3246	-	GTGACCTATGCACCAGACGTAACCGTGGGAGCCTGGCTCAGGTGCCACCCATGCCCTCCAGATCGGAAGAGCGGTTTCAG
chr20	36031524	36031563	SRC_3247	-	GTGACCTATGCACCAGACGTAGCGAGCTGGGAGCCCGGCTCCGCTGAGGAAAGTGGGAGATCGGAAGAGCGGTTTCAG
chr9	27109539	27109578	TEK_3248	-	GTGACCTATGCACCAGACGTACTCTCCATCCAGTTTCCACAAATGTGCATGAGTCCCAAGATCGGAAGAGCGGTTTCAG



chr9	27157779	27157818	TEK_3249	-	GTGACCTATGCACCAGACGTAGAGAGACAATAATGTATGACTAAGGTTATTAACATGACCAGATCGGAAGAGCGGTTTCAG
chr9	27168443	27168482	TEK_3250	-	GTGACCTATGCACCAGACGTAGAGAAAACAAATACCAAAAATGGGATCACACATTTTCTCAGATCGGAAGAGCGGTTTCAG
chr9	27169425	27169464	TEK_3251	-	GTGACCTATGCACCAGACGTGGAAGAGTGAAGAACCGTAGGTCACACTGAAACATACCTGAGATCGGAAGAGCGGTTTCAG
chr9	27173170	27173209	TEK_3252	-	GTGACCTATGCACCAGACGTAAAAGAAAAGATGATTCAGAGTCAAATATGCAACCCCTTGAGATCGGAAGAGCGGTTTCAG
chr9	27180188	27180227	TEK_3253	-	GTGACCTATGCACCAGACGTAGACATCAAAAAACAGTATTAATCCAGGGGAAGAGAGGAAGATCGGAAGAGCGGTTTCAG
chr9	27183407	27183446	TEK_3254	-	GTGACCTATGCACCAGACGTAAAACAGCACTGTAAATCTAATATTTAACAGAGCCAGCAAGATCGGAAGAGCGGTTTCAG
chr9	27185433	27185472	TEK_3255	-	GTGACCTATGCACCAGACGTCAAATCAAAAAATAAAAACTTCAGGGAGGCATAAAACAGATCGGAAGAGCGGTTTCAG
chr9	27190477	27190516	TEK_3256	-	GTGACCTATGCACCAGACGTTCAGAAAGGCAGATTAGTCCCTTCGGCTTTGAGGTTTTGTAGATCGGAAGAGCGGTTTCAG
chr9	27192437	27192476	TEK_3257	-	GTGACCTATGCACCAGACGTAAAACGTCCAGGAACTTAAGTTGGCATTCTCTTACATTAGATCGGAAGAGCGGTTTCAG
chr9	27202768	27202807	TEK_3258	-	GTGACCTATGCACCAGACGTAAAAGAAAAAAGATTCACTTAAGATATACTACCATGGCCTAGATCGGAAGAGCGGTTTCAG
chr9	27204859	27204898	TEK_3259	-	GTGACCTATGCACCAGACGTAGACAGAGGTTGAAGCAGGTGATCTTTAGTTTACATAGAGAAAAGATCGGAAGAGCGGTTTCAG
chr9	27206530	27206569	TEK_3260	-	GTGACCTATGCACCAGACGTAAATATTTTCATCATTTTGTGTCAGGATTTTTCATAATTCTAGATCGGAAGAGCGGTTTCAG
chr9	27209069	27209108	TEK_3261	-	GTGACCTATGCACCAGACGTAGTCAAGGGTTGTGATTCCTTTGTTTACACCTTTTCAGAAAGTCGGAAGAGCGGTTTCAG
chr9	27212655	27212694	TEK_3262	-	GTGACCTATGCACCAGACGTGGAAGAGAGCATCGACTCATCAGTGGCCCTGAACAGCTATAGATCGGAAGAGCGGTTTCAG
chr9	27213432	27213471	TEK_3263	-	GTGACCTATGCACCAGACGTTGAAAACATTATGTATTTTCAGCCTAATGAAAGCCCCAGGAGATCGGAAGAGCGGTTTCAG
chr9	27217636	27217675	TEK_3264	-	GTGACCTATGCACCAGACGTCAAAGTGAGATTTCACTTAACCTGGGACAGGGTCTTTAAGAAGATCGGAAGAGCGGTTTCAG
chr9	27218725	27218764	TEK_3265	-	GTGACCTATGCACCAGACGTGACAAGTGTAAACCAACAATCAGCAACAGAGTCAACCCAGATCGGAAGAGCGGTTTCAG
chr9	27219997	27220036	TEK_3266	-	GTGACCTATGCACCAGACGTAAACAGTGCCACTTAAGTCCCTCTGCGCATGAAAAGCAATAGATCGGAAGAGCGGTTTCAG
chr9	27228154	27228193	TEK_3267	-	GTGACCTATGCACCAGACGTAAAAGAATTAAGGGTTAATTCTATAACTGTGCTTCAGTCCAGATCGGAAGAGCGGTTTCAG
chr9	27229106	27229145	TEK_3268	-	GTGACCTATGCACCAGACGTGAAAATGGTTCAGAGACATAGGCTGCTTTGATTCCACCTCAGATCGGAAGAGCGGTTTCAG
chr17	38545721	38545760	TOP2A_3269	-	GTGACCTATGCACCAGACGTGATTATTTAAGTAATATCTTACCAGCCCAAGACTGGTAGATCGGAAGAGCGGTTTCAG
chr17	38546167	38546206	TOP2A_3270	-	GTGACCTATGCACCAGACGTATCCTAGTCACTCTTTGCTGTAGATGTTCTGAAACACGAGATCGGAAGAGCGGTTTCAG
chr17	38547708	38547747	TOP2A_3271	-	GTGACCTATGCACCAGACGTATCTTTGAGATGGTGAATGTTGCAATACCTAAGTGGTTAGATCGGAAGAGCGGTTTCAG
chr17	38548270	38548309	TOP2A_3272	-	GTGACCTATGCACCAGACGTAAAGTAGTAGACTGTCCTTACTGGACACTCAAGATCGGAAGAGCGGTTTCAG
chr17	38548420	38548459	TOP2A_3273	-	GTGACCTATGCACCAGACGTATCTAATATGGGTTTTGTCATGATTGTTCTAATATATTAGATCGGAAGAGCGGTTTCAG
chr17	38548787	38548826	TOP2A_3274	-	GTGACCTATGCACCAGACGTCTAAAGAACATTATAGATAAACTGTAAGAGTGGAAATGGCCAGATCGGAAGAGCGGTTTCAG
chr17	38551651	38551690	TOP2A_3275	-	GTGACCTATGCACCAGACGTATTTTGAAGAAAATGGTATAAAGTGAAGATTAATTTGTGTAGATCGGAAGAGCGGTTTCAG
chr17	38554760	38554799	TOP2A_3276	-	GTGACCTATGCACCAGACGTATAATGCCCTGTAGAATTTTATTAATGAAATAATAGATCGGAAGAGCGGTTTCAG
chr17	38554975	38555014	TOP2A_3277	-	GTGACCTATGCACCAGACGTAGTAGGATGACACTGCTTAGTCTTTGTTCTATTCTAAAGATCGGAAGAGCGGTTTCAG
chr17	38555242	38555281	TOP2A_3278	-	GTGACCTATGCACCAGACGTGTGGCACTTTTCTATATTGTTAAAGACTGATTTGTACAAAGATCGGAAGAGCGGTTTCAG
chr17	38556074	38556113	TOP2A_3279	-	GTGACCTATGCACCAGACGTGGAATAATAACTGCTTACTAAAACCTAGTTACGCCAAACAGATCGGAAGAGCGGTTTCAG
chr17	38556411	38556450	TOP2A_3280	-	GTGACCTATGCACCAGACGTGTTTTGTAGATGTACAGTTCATTTATATTAAGATAGATCGGAAGAGCGGTTTCAG
chr17	38556731	38556770	TOP2A_3281	-	GTGACCTATGCACCAGACGTATGGATTTCTTTTTAGGTTTTGTGATCAAAAAGAAATACCTAGATCGGAAGAGCGGTTTCAG
chr17	38557052	38557091	TOP2A_3282	-	GTGACCTATGCACCAGACGTGTGTGTGTTAAGAGCCTTAACTTTTCCCTGGGTTTTGATAGATCGGAAGAGCGGTTTCAG
chr17	38559108	38559147	TOP2A_3283	-	GTGACCTATGCACCAGACGTTCCTAAGTACCATTGATGACTTCCATTTCCAGTTTTGAAAACAGATCGGAAGAGCGGTTTCAG
chr17	38560354	38560393	TOP2A_3284	-	GTGACCTATGCACCAGACGTAAATCCATGTTCCAGAAAGCATTATATCAGAAATCCCTGCAGATCGGAAGAGCGGTTTCAG
chr17	38560579	38560618	TOP2A_3285	-	GTGACCTATGCACCAGACGTATTTGTTAGTCTGTTTTTCATTGTAAGATGGAATCAAATAGATCGGAAGAGCGGTTTCAG
chr17	38560993	38561032	TOP2A_3286	-	GTGACCTATGCACCAGACGTAAATATATGCCACAAAATGGATTTGTTAGACTGACCTTTTATAGATCGGAAGAGCGGTTTCAG
chr17	38562586	38562625	TOP2A_3287	-	GTGACCTATGCACCAGACGTGTTGATTTTTATATACATTCTAATTTTAGAAATCACTACTAGATCGGAAGAGCGGTTTCAG
chr17	38562786	38562825	TOP2A_3288	-	GTGACCTATGCACCAGACGTAAACCCATATAGAACTTCTCATTTTATATACACCCTGTAAGATCGGAAGAGCGGTTTCAG
chr17	38563034	38563073	TOP2A_3289	-	GTGACCTATGCACCAGACGTTCCTAAGTACCATTGATGATTTTAAAGCCCTACTCCTCAGATCGGAAGAGCGGTTTCAG
chr17	38563751	38563790	TOP2A_3290	-	GTGACCTATGCACCAGACGTTTATTAATTTTTAGATTGTTCAACTAAATTAAGCATGTCAGATCGGAAGAGCGGTTTCAG
chr17	38564169	38564208	TOP2A_3291	-	GTGACCTATGCACCAGACGTAGACGATTTTCAAGATCAAATCTAATTTATAATACAAGAAGATCGGAAGAGCGGTTTCAG
chr17	38564694	38564733	TOP2A_3292	-	GTGACCTATGCACCAGACGTAAATATGTTTTCCAACTTTTAAAGTCTTATAGTTGTTATTTAGATCGGAAGAGCGGTTTCAG
chr17	38567311	38567350	TOP2A_3293	-	GTGACCTATGCACCAGACGTAGAGGAAAATAAAAAATGAAACACCTGACTTTATTTTCCAAGATCGGAAGAGCGGTTTCAG
chr17	38567556	38567595	TOP2A_3294	-	GTGACCTATGCACCAGACGTTCAGAGTTTTCTTTTCTGAAAGTCAAGGAAGAAGAGAAAGATCGGAAGAGCGGTTTCAG
chr17	38567847	38567886	TOP2A_3295	-	GTGACCTATGCACCAGACGTCTTAAATTTAATCATGATTTATCTTTACATATATGTAGATCGGAAGAGCGGTTTCAG
chr17	38568961	38569000	TOP2A_3296	-	GTGACCTATGCACCAGACGTTCTGGATGTTAAGGATAATAAGGGATTTTGAATCATTGAGATCGGAAGAGCGGTTTCAG
chr17	38569397	38569436	TOP2A_3297	-	GTGACCTATGCACCAGACGTAAAGTGTCTTTGATCTTAATGATAAATGGTAGTAGTATAGCAGATCGGAAGAGCGGTTTCAG
chr17	38572207	38572246	TOP2A_3298	-	GTGACCTATGCACCAGACGTGCTTAGTTTTGTTATGTAGCTGCTTGTCTATTGTTAGCTAGATCGGAAGAGCGGTTTCAG
chr17	38572624	38572663	TOP2A_3299	-	GTGACCTATGCACCAGACGTCTTTAATATAAAGATCTGGTCAAATCTTTCATAAGAAGTAGATCGGAAGAGCGGTTTCAG
chr17	38572942	38572981	TOP2A_3300	-	GTGACCTATGCACCAGACGTGCTCAAGTAAAGGCAGTTAACTTAGTAGTTGAAATGGATAGATCGGAAGAGCGGTTTCAG
chr17	38573973	38574012	TOP2A_3301	-	GTGACCTATGCACCAGACGTGCGGGGGGACTGGCGGTGGAGCCTCCGCGCGGCCCGGGCAAGATCGGAAGAGCGGTTTCAG
chr1	154130065	154130104	TPM3_3302	-	GTGACCTATGCACCAGACGTTCCACCCTGCTGCTGCTCCTCCCTCGACCAGACTCCGAGATCGGAAGAGCGGTTTCAG
chr1	154131395	154131434	TPM3_3303	-	GTGACCTATGCACCAGACGTTCAATGATGCCATTAAACTGAGCTTACTGCTCACACCACAGATCGGAAGAGCGGTTTCAG
chr1	154140363	154140402	TPM3_3304	-	GTGACCTATGCACCAGACGTTTCTGCTGTTCTGGATCGCCCTTTACTCTCGGGGAGATCGGAAGAGCGGTTTCAG
chr1	154141731	154141770	TPM3_3305	-	GTGACCTATGCACCAGACGTGACAGTAGAGTGGGGCTGGGATCTTGGCTTTGGTGGATAGATCGGAAGAGCGGTTTCAG
chr1	154142826	154142865	TPM3_3306	-	GTGACCTATGCACCAGACGTGGAGTAGGGATTGAAATAGAGAAATAGAGGAAGACTGAGATCGGAAGAGCGGTTTCAG

chr1	154143075	154143114	TPM3_3307	-	GTGACCTATGCACCAGACGTGGGATTTATAGGGCAGAACCACAAACATTTAGAGGTATATAGATCGGAAGAGCGGTTTCAG
chr1	154143839	154143878	TPM3_3308	-	GTGACCTATGCACCAGACGTGTTTTGTGAAAGTGACAGGCTTTGGGGCCTGGGCCAGCCAGATCGGAAGAGCGGTTTCAG
chr1	154145334	154145373	TPM3_3309	-	GTGACCTATGCACCAGACGTAGCTCCCCAAATCTGTGATTACCAATTTATCCCTTCCCCAGATCGGAAGAGCGGTTTCAG
chr1	154145510	154145549	TPM3_3310	-	GTGACCTATGCACCAGACGTTTCTGTAGTCCCTCTCGTATCGGCCTTTTACAAAGCATAAGATCGGAAGAGCGGTTTCAG
chr1	154148541	154148580	TPM3_3311	-	GTGACCTATGCACCAGACGTAAGCCTGATGGAGTGTGGATTTTAAAAAGTTATAATAGTTAGATCGGAAGAGCGGTTTCAG
chr1	154155414	154155453	TPM3_3312	-	GTGACCTATGCACCAGACGTGGTGGAGGCTCATGAGGGAGGGGCAAGCGGCTGGAGTATCCGAGATCGGAAGAGCGGTTTCAG
chr1	154163612	154163651	TPM3_3313	-	GTGACCTATGCACCAGACGTGAGAGATGGAGTGGTAACTACACATATAGATCTTAGATCGGAAGAGCGGTTTCAG
chr1	154164328	154164367	TPM3_3314	-	GTGACCTATGCACCAGACGTGCATTGATCTCTCATCTGCTAGTGAACAAAGACTGTGAAAGATCGGAAGAGCGGTTTCAG
chr9	107546546	107546585	ABCA1_3315	-	GTGACCTATGCACCAGACGTTCCATACGGGGTGGCTGAAAGTAAAGAGGAACTAGACTTTTCAGATCGGAAGAGCGGTTTCAG
chr9	107547627	107547666	ABCA1_3316	-	GTGACCTATGCACCAGACGTAGTGTCAAACAGATTTACTTCTCAGGGTGTGGATTCTGAGATCGGAAGAGCGGTTTCAG
chr9	107548529	107548568	ABCA1_3317	-	GTGACCTATGCACCAGACGTTAATTTCTTTGGGATAGTCCCTAGTGAGAAGGCTTGATATAGATCGGAAGAGCGGTTTCAG
chr9	107549104	107549143	ABCA1_3318	-	GTGACCTATGCACCAGACGTAAGTCTTTGGGTTCCCTACTGTGGGATGTTTTAACTTTTCCAAGATCGGAAGAGCGGTTTCAG
chr9	107550151	107550190	ABCA1_3319	-	GTGACCTATGCACCAGACGTCTGGATGGAAACTGTTGTTCTGCGCTGAGTGGAAACAGATCGGAAGAGCGGTTTCAG
chr9	107550657	107550696	ABCA1_3320	-	GTGACCTATGCACCAGACGTCACTGAAAGCCAGCCTGTCTCCTTTGGCATCCTGACAATAGATCGGAAGAGCGGTTTCAG
chr9	107553153	107553192	ABCA1_3321	-	GTGACCTATGCACCAGACGTAAGTGGCTTGATTTTGTCTGCAAAGACTTTGTTTTAATTAGATCGGAAGAGCGGTTTCAG
chr9	107554167	107554206	ABCA1_3322	-	GTGACCTATGCACCAGACGTTTTGTCTATATTGCCGTTTGTCCCTATTAGTTCAGACTATCAGATCGGAAGAGCGGTTTCAG
chr9	107555017	107555056	ABCA1_3323	-	GTGACCTATGCACCAGACGTACAGGTTACAATAGCTCATCTCAGTTTTTTTTTTCAGCTTTAAGATCGGAAGAGCGGTTTCAG
chr9	107555402	107555441	ABCA1_3324	-	GTGACCTATGCACCAGACGTTCTGTAGAACCTGTGGAGCCCTGGAGCCTGGTTGAGGGTCCACAGAGAGATCGGAAGAGCGGTTTCAG
chr9	107556618	107556657	ABCA1_3325	-	GTGACCTATGCACCAGACGTCACTGGCTGTAGGATGCTTTAATGGAGATGGCACTCTGCAAGATCGGAAGAGCGGTTTCAG
chr9	107558540	107558579	ABCA1_3326	-	GTGACCTATGCACCAGACGTTCTGAGTGAGGGAGCTGCACAGTGGATAAGGCATTTGGTGAGATCGGAAGAGCGGTTTCAG
chr9	107560652	107560691	ABCA1_3327	-	GTGACCTATGCACCAGACGTAGGCCCTGCTGTATCTTTCTGATGTCTGTCAGGGCCATGGAAGATCGGAAGAGCGGTTTCAG
chr9	107562050	107562089	ABCA1_3328	-	GTGACCTATGCACCAGACGTCTGTGTCTGTATAGATGGAGTGGGGCAAGGGAGAGGGTTAAGATCGGAAGAGCGGTTTCAG
chr9	107562741	107562780	ABCA1_3329	-	GTGACCTATGCACCAGACGTGCTCTTTGCTTAGTAGCTTTTTGATGAACAATAATCCTTAAGATCGGAAGAGCGGTTTCAG
chr9	107564285	107564324	ABCA1_3330	-	GTGACCTATGCACCAGACGTATCTGGATGGAAACTGTATCAGAAAAATGGGCATGTAGCTGTAGATCGGAAGAGCGGTTTCAG
chr9	107565515	107565554	ABCA1_3331	-	GTGACCTATGCACCAGACGTGCTTTCTGGCACGTTTAGCTCAGGGGGAGGATGGTGTGAGATCGGAAGAGCGGTTTCAG
chr9	107566857	107566896	ABCA1_3332	-	GTGACCTATGCACCAGACGTACTAAACTTGGCCCTGCCGTATTACTAATAGAGGAAGATCGGAAGAGCGGTTTCAG
chr9	107568472	107568511	ABCA1_3333	-	GTGACCTATGCACCAGACGTTTCAGGGGGTGATTGGGCAGAAAGGGTGCAGGATGGGCTGAGATCGGAAGAGCGGTTTCAG
chr9	107571697	107571736	ABCA1_3334	-	GTGACCTATGCACCAGACGTCTTAGCCATAAGCAGGCTTCTTGTGCTTGTGCCTGGTTAGATCGGAAGAGCGGTTTCAG
chr9	107573031	107573070	ABCA1_3335	-	GTGACCTATGCACCAGACGTCTTACACTCCAGAGGGGTGAAGATCGAGCAGACCAAGATCGGAAGAGCGGTTTCAG
chr9	107574805	107574844	ABCA1_3336	-	GTGACCTATGCACCAGACGCTGTTTTGCGCACAGACTCGGCTTTCATGGGTGGGCTGCAAGATCGGAAGAGCGGTTTCAG
chr9	107576349	107576388	ABCA1_3337	-	GTGACCTATGCACCAGACGTGCAAGATCAAACAGTGTCTACTGTTTGAATGTGAAATTCAGATCGGAAGAGCGGTTTCAG
chr9	107576658	107576697	ABCA1_3338	-	GTGACCTATGCACCAGACGTTGAGGGAGAATGGCACACTTAAGATAGTGCCCTCTGCTGGAGATCGGAAGAGCGGTTTCAG
chr9	107578374	107578413	ABCA1_3339	-	GTGACCTATGCACCAGACGTTGGCTGACTGTCCGAATATATAGCAAAGGCCAAATGTCTTAAGATCGGAAGAGCGGTTTCAG
chr9	107579563	107579602	ABCA1_3340	-	GTGACCTATGCACCAGACGTTGGGTTCTTATCCAGTGGTGGCTGAGCTTCCCCCAGCAGATCGGAAGAGCGGTTTCAG
chr9	107580894	107580933	ABCA1_3341	-	GTGACCTATGCACCAGACGTGTCTTGGTCTGTTGCTGGGCTGGGCTGGGCTGGGCAAGATCGGAAGAGCGGTTTCAG
chr9	107581817	107581856	ABCA1_3342	-	GTGACCTATGCACCAGACGTTGTATTTATTCTGAGTAAATGGACTGAGAGAGAGCGGGGAGATCGGAAGAGCGGTTTCAG
chr9	107582158	107582197	ABCA1_3343	-	GTGACCTATGCACCAGACGTGAGCTACCTTCCCTATCCCTCTCCCTCCTCCTCCGGCTAAGATCGGAAGAGCGGTTTCAG
chr9	107583606	107583645	ABCA1_3344	-	GTGACCTATGCACCAGACGTGCAGCACGTTAAGAAATAGGCCTTTTCTGGATGTGTGTGAGATCGGAAGAGCGGTTTCAG
chr9	107584727	107584766	ABCA1_3345	-	GTGACCTATGCACCAGACGTGGTGTGGTTCCCGCAGAATCAGCCACAGGAGGGTCTGCAAGATCGGAAGAGCGGTTTCAG
chr9	107586696	107586735	ABCA1_3346	-	GTGACCTATGCACCAGACGTTTGACCTCTGCTTTCTTTAACCTAGTGTCTGCTGCCTCAGATCGGAAGAGCGGTTTCAG
chr9	107587914	107587953	ABCA1_3347	-	GTGACCTATGCACCAGACGTTGGGCTGCTGTTTTGGAAAATGACTTCTAGCTGATCGGATCGGAAGAGCGGTTTCAG
chr9	107589179	107589218	ABCA1_3348	-	GTGACCTATGCACCAGACGTCTGGCCTTTCTTCACTGGCTGTAGGCATTTGACCTTCTTAGATCGGAAGAGCGGTTTCAG
chr9	107591147	107591186	ABCA1_3349	-	GTGACCTATGCACCAGACGTCTCACTCGCTCTTCCCTGCCAGGAAACTCCGAAATAGCTCAGATCGGAAGAGCGGTTTCAG
chr9	107593156	107593195	ABCA1_3350	-	GTGACCTATGCACCAGACGTTGCAAGCCACTGTTTTTAAACCAGTTTATACTGTGCCAGATAGATCGGAAGAGCGGTTTCAG
chr9	107593853	107593892	ABCA1_3351	-	GTGACCTATGCACCAGACGTTCCCATCACACCAGCCTGGTCTTTGGGAGGTCCAGAGCACAGATCGGAAGAGCGGTTTCAG
chr9	107594805	107594844	ABCA1_3352	-	GTGACCTATGCACCAGACGTTGCTGGATCTTAGAAAGACTTAACCGGTTCTTTCTCAGATCGGAAGAGCGGTTTCAG
chr9	107599211	107599250	ABCA1_3353	-	GTGACCTATGCACCAGACGTCTCCCATTTATACCATGTGCTGCTTGATACTGGAGAGGTAGATCGGAAGAGCGGTTTCAG
chr9	107599659	107599698	ABCA1_3354	-	GTGACCTATGCACCAGACGTCCCAGCCAAAGACTCCCTCCCAGAATCTCCCAGAACTGAGATCGGAAGAGCGGTTTCAG
chr9	107602510	107602549	ABCA1_3355	-	GTGACCTATGCACCAGACGTATGCAGACCCAGCCCTGTCCCAACCCCATCCCTCCCTTAGATCGGAAGAGCGGTTTCAG
chr9	107607708	107607747	ABCA1_3356	-	GTGACCTATGCACCAGACGTTCTTCCAGTACCAGGAAAGCGGATCATCCACTGTATCAGTAGATCGGAAGAGCGGTTTCAG
chr9	107620753	107620792	ABCA1_3357	-	GTGACCTATGCACCAGACGTTTGCCTACTGGAGAACTCAAGCATAATGCTTTTCGAAAGATCGGAAGAGCGGTTTCAG
chr9	107623910	107623949	ABCA1_3358	-	GTGACCTATGCACCAGACGTGCTCCAGCTTCCCTCAGTAAAGCTGATGGCAATTGAGATCGGAAGAGCGGTTTCAG
chr9	107645270	107645309	ABCA1_3359	-	GTGACCTATGCACCAGACGTACCTTCTGCTCCGTTTATAATTGGAATTTGACCTGCAAGATCGGAAGAGCGGTTTCAG
chr9	107646658	107646697	ABCA1_3360	-	GTGACCTATGCACCAGACGTGATCAGGTTTTCTTTCCAAACTTGTGACTTAATCTTTTCAGATCGGAAGAGCGGTTTCAG
chr9	107651333	107651372	ABCA1_3361	-	GTGACCTATGCACCAGACGTGTGGATGTTGCCTGAGACTACCAATGGCAGGAAAATCCAGATCGGAAGAGCGGTTTCAG
chr9	107665845	107665884	ABCA1_3362	-	GTGACCTATGCACCAGACGTGTTTTTCAGCAGCGGGGGTCTCTCATTTTTTCTTTGTGAGATCGGAAGAGCGGTTTCAG
chr19	1452951	1452990	APC2_3363	-	GTGACCTATGCACCAGACGTTGGAGCTGGGATCAGAGGTTCCAGAGGTTCCAGTATAGATCGGAAGAGCGGTTTCAG
chr19	1453196	1453235	APC2_3364	-	GTGACCTATGCACCAGACGTGGGAAAAGGGCGGGAAGCCATGACGACTGCATGGGCTAGATCGGAAGAGCGGTTTCAG

chr19	1453380	1453419	APC2_3365	-	GTGACCTATGCACCAGACGTGGGGACAGGGCGGAGGTCAGCGGCCCTGCCTGCCTTTCCAGATCGGAAGAGCGGTTTCAG
chr19	1455098	1455137	APC2_3366	-	GTGACCTATGCACCAGACGTAGTCAGCGGGGGCGGGCTCAGAGGGCGCGCCGTGTGTGTAGATCGGAAGAGCGGTTTCAG
chr19	1455333	1455372	APC2_3367	-	GTGACCTATGCACCAGACGTGACGGCGGGCGGGCCACGGTGAGGGGGCGCCGGGGCCAGGCCAGATCGGAAGAGCGGTTTCAG
chr19	1456255	1456294	APC2_3368	-	GTGACCTATGCACCAGACGTAGCACCAGGGTCGGGGGTACAGTCCCAGAGCACCCAGTCTAGATCGGAAGAGCGGTTTCAG
chr19	1456802	1456841	APC2_3369	-	GTGACCTATGCACCAGACGTGGCAGGGTCAGGGTGGGGTCCCTCACCTGCCCCCGCACAAAGATCGGAAGAGCGGTTTCAG
chr19	1457914	1457953	APC2_3370	-	GTGACCTATGCACCAGACGTAGGGACCATGATCAGAGCCCCATCCCAGGAAATGTCCCAAGATCGGAAGAGCGGTTTCAG
chr19	1460130	1460169	APC2_3371	-	GTGACCTATGCACCAGACGTCAAACAAGTTGGTGGGTGCCAGGGATGACCCTGCCTGTAGATCGGAAGAGCGGTTTCAG
chr19	1460729	1460768	APC2_3372	-	GTGACCTATGCACCAGACGTATATGCAGCGGGGTACAGGGGTTGGGACACAAAGGGAGACAGATCGGAAGAGCGGTTTCAG
chr19	1460986	1461025	APC2_3373	-	GTGACCTATGCACCAGACGTTGAGGGGCAAGTGTGGTGGGACTAGGGTCCAGGCCCCCAAGATCGGAAGAGCGGTTTCAG
chr19	1461912	1461951	APC2_3374	-	GTGACCTATGCACCAGACGTGGCGGGAGAGGGGGCGGGTACAGGGCCTGAGTGGCCCGGAGGAGATCGGAAGAGCGGTTTCAG
chr19	1465104	1465143	APC2_3375	-	GTGACCTATGCACCAGACGTAGGGCGGGTTAGCCTGGGCGACCCCCACCCTCCCCTGCCAGATCGGAAGAGCGGTTTCAG
chr19	1465564	1465603	APC2_3376	-	GTGACCTATGCACCAGACGTGCCAGGCCCTCAGGTGTCGACGGGGCGGCAGCGGCTTCTAGATCGGAAGAGCGGTTTCAG
chr19	1466024	1466063	APC2_3377	-	GTGACCTATGCACCAGACGTGCTGCGGTGGGGCCGCTTGAGCCGACGACGCGGGTGGCGCCAGATCGGAAGAGCGGTTTCAG
chr19	1466484	1466523	APC2_3378	-	GTGACCTATGCACCAGACGTAGGAAAGGGAGCTGCATCGGGACAGCGAGAGTGGCCCTCAGATCGGAAGAGCGGTTTCAG
chr19	1466944	1466983	APC2_3379	-	GTGACCTATGCACCAGACGTTGGGTGGCCTCGGGGGGACCCTGTGGCGGGGGCGCCAGCGAGATCGGAAGAGCGGTTTCAG
chr19	1467404	1467443	APC2_3380	-	GTGACCTATGCACCAGACGTGGCCGGGGCGGGACCAACATGTAGACGGGCACGGGGAGTAGATCGGAAGAGCGGTTTCAG
chr19	1467864	1467903	APC2_3381	-	GTGACCTATGCACCAGACGTGAGGGATGGCCGATGTGCGCCGGTGGGTTGGCGTGGGCGCAGATCGGAAGAGCGGTTTCAG
chr19	1468324	1468363	APC2_3382	-	GTGACCTATGCACCAGACGTGCGCGCCACTCCACGCTATCCAGGTCGGAGGCCGTCGAGATCGGAAGAGCGGTTTCAG
chr19	1468784	1468823	APC2_3383	-	GTGACCTATGCACCAGACGTCCGCGACCGCTGCTGCCCGGGGCTCGGGACTTTGGCTGGAAGATCGGAAGAGCGGTTTCAG
chr19	1469244	1469283	APC2_3384	-	GTGACCTATGCACCAGACGTGCTGTGCCGGAAGCCGAGCGGTCGGAGGACTCGCTGCCAGATCGGAAGAGCGGTTTCAG
chr19	1469704	1469743	APC2_3385	-	GTGACCTATGCACCAGACGTGCCGCCAGGTCGTGCCCGGGCGCGCCACCCTGGGGAGCGAGATCGGAAGAGCGGTTTCAG
chr20	54945164	54945203	AURKA_3386	-	GTGACCTATGCACCAGACGTGGGGGAGAAATCCTTGACACAGGCTGCCATATAACCTGAAGATCGGAAGAGCGGTTTCAG
chr20	54945491	54945530	AURKA_3387	-	GTGACCTATGCACCAGACGTGAAAGGACCCAGCACATGCTGGAATTTCTTCTAGATCGGAAGAGCGGTTTCAG
chr20	54948414	54948453	AURKA_3388	-	GTGACCTATGCACCAGACGTTAGAGGTTGGAAGTGTGTTGTTTACCAGCCCTGGGAGATCGGAAGAGCGGTTTCAG
chr20	54956439	54956478	AURKA_3389	-	GTGACCTATGCACCAGACGTATTTATTGTCCAGGCTAATTGTGTTTCTTTATACCTGTAGATCGGAAGAGCGGTTTCAG
chr20	54957991	54958030	AURKA_3390	-	GTGACCTATGCACCAGACGTAGGTTTCATGTTCAAAGAAATGTTCCACCAATGCTGCACCCAGATCGGAAGAGCGGTTTCAG
chr20	54959276	54959315	AURKA_3391	-	GTGACCTATGCACCAGACGTATTTATTAACAAGTCTGTACTGTTCTACTAGAATATATAAGATCGGAAGAGCGGTTTCAG
chr20	54961263	54961302	AURKA_3392	-	GTGACCTATGCACCAGACGTGTTTGTAGACTATTGGATAGTCTTCTTTGTGCTGTTGAGATCGGAAGAGCGGTTTCAG
chr20	54963162	54963201	AURKA_3393	-	GTGACCTATGCACCAGACGTAACTCTGTAATCTCATTACATTTATAAACCCACATGGAGAGATCGGAAGAGCGGTTTCAG
chr6	41903628	41903667	CCND3_3394	-	GTGACCTATGCACCAGACGTGCCCTGTGAGTGGCCATAAGCAGAGAGGGGGCGCTGCAGATCGGAAGAGCGGTTTCAG
chr6	41904247	41904286	CCND3_3395	-	GTGACCTATGCACCAGACGTGGTAGCTGGGCAGCAGCCTCTCCATTATAAAGTAGTGTAGATCGGAAGAGCGGTTTCAG
chr6	41904923	41904962	CCND3_3396	-	GTGACCTATGCACCAGACGTTATGCACATTTTGGCAAATTTGGAATAATCAGAAAGACTTAAGATCGGAAGAGCGGTTTCAG
chr6	41908058	41908097	CCND3_3397	-	GTGACCTATGCACCAGACGTAATCCCCCCACCCCGACACGATTTGTCTCCCACTTTTCAGATCGGAAGAGCGGTTTCAG
chr6	41909140	41909179	CCND3_3398	-	GTGACCTATGCACCAGACGTGACGCGTCCCCCTCCCCACCGCTCCCGGGTCTGGACACAAGATCGGAAGAGCGGTTTCAG
chrX	135730358	135730397	CD40LG_3399	-	GTGACCTATGCACCAGACGTAGTTGAAATGGTATCTTCTGCGCAGAGAAGGTTGGCAGAGGATCGGAAGAGCGGTTTCAG
chrX	135732375	135732414	CD40LG_3400	-	GTGACCTATGCACCAGACGTATAACAAGGATATGATAAATGTCATTGCGAAGGAGAATACAGATCGGAAGAGCGGTTTCAG
chrX	135736482	135736521	CD40LG_3401	-	GTGACCTATGCACCAGACGTAAAGCATTGCAAGAGGTCATTTTACAGGGGCTCTGCTGTAGATCGGAAGAGCGGTTTCAG
chrX	135738465	135738504	CD40LG_3402	-	GTGACCTATGCACCAGACGTACCAAAACTGTAGGCTAAAATAATGCAAAAACTGCCAAAGATCGGAAGAGCGGTTTCAG
chrX	135741148	135741187	CD40LG_3403	-	GTGACCTATGCACCAGACGTGAAAGGGAAAGTTTGTGGTGGAGGTAAGCAGAGCATGGTTAGATCGGAAGAGCGGTTTCAG
chr13	28537202	28537241	CDX2_3404	-	GTGACCTATGCACCAGACGTTCTGCAGCGCCAGGCAATTCAGGCTGAGCCATGAGGAGAGATCGGAAGAGCGGTTTCAG
chr13	28538957	28538996	CDX2_3405	-	GTGACCTATGCACCAGACGTCCTAGCTCCCGGCAAGCCGCACTGCCCTGGCAGAGACAGATCGGAAGAGCGGTTTCAG
chr13	28542553	28542592	CDX2_3406	-	GTGACCTATGCACCAGACGTGCTGCGCCCTTCGGAGGGTGTCTGGGAAGGCGCGGGTTCAGATCGGAAGAGCGGTTTCAG
chr13	28542823	28542862	CDX2_3407	-	GTGACCTATGCACCAGACGTGGCCCTCAACGGTGGCTCCCCGGCCGACGATGGCTACAGATCGGAAGAGCGGTTTCAG
chr15	51502955	51502994	CYP19A1_3408	-	GTGACCTATGCACCAGACGTTACGTAACCACTTGGAGCATTCTCATCAGTAGTTCACAAGATCGGAAGAGCGGTTTCAG
chr15	51504467	51504506	CYP19A1_3409	-	GTGACCTATGCACCAGACGTTTCCATAAACTGATGTGCCACTCTTGAAGATGCAACTAGATCGGAAGAGCGGTTTCAG
chr15	51507217	51507256	CYP19A1_3410	-	GTGACCTATGCACCAGACGTAACTAAATAATACATCTTAAAAACAATTTCTTCTGAAAGATCGGAAGAGCGGTTTCAG
chr15	51507850	51507889	CYP19A1_3411	-	GTGACCTATGCACCAGACGTGAACAACTGTAATTTCCCTGCCACATATGTTATGACTGTAGATCGGAAGAGCGGTTTCAG
chr15	51510688	51510727	CYP19A1_3412	-	GTGACCTATGCACCAGACGTCAACTTTGGAAGATTTATGAGTACAATTTGATTGGTTTTTATAGATCGGAAGAGCGGTTTCAG
chr15	51514496	51514535	CYP19A1_3413	-	GTGACCTATGCACCAGACGTTTCACTCTCACATCTTGACCATCTGTCCCTTACTGAACAAGATCGGAAGAGCGGTTTCAG
chr15	51519926	51519965	CYP19A1_3414	-	GTGACCTATGCACCAGACGTACTTAGTTAGCTACAATCTTTTTTGTCTATGAATGTGCTAGATCGGAAGAGCGGTTTCAG
chr15	51529006	51529045	CYP19A1_3415	-	GTGACCTATGCACCAGACGTTCAATCTGAAGACATACTTTTAACTCGAGGCTGGAGTTAGATCGGAAGAGCGGTTTCAG
chr15	51534915	51534954	CYP19A1_3416	-	GTGACCTATGCACCAGACGTCATTATTTCTGTATCTAAGGAGATTAATTTACTTGGGATTAGATCGGAAGAGCGGTTTCAG
chr20	31367872	31367911	DNMT3B_3417	-	GTGACCTATGCACCAGACGTTGTCCGAAGGCTCAGACGCCAGCACCCAGGACAGAGTGGAGATCGGAAGAGCGGTTTCAG
chr20	31368074	31368113	DNMT3B_3418	-	GTGACCTATGCACCAGACGTAGCCAGAATGGGTGGGGTGAAGGGAAGCAGGGACATGAGAGATCGGAAGAGCGGTTTCAG
chr20	31368080	31368119	DNMT3B_3419	-	GTGACCTATGCACCAGACGTGGGAGAAAGCCAGAATGGGTGGGGTGAAGGGAAGCAGGGAAGATCGGAAGAGCGGTTTCAG
chr20	31369109	31369148	DNMT3B_3420	-	GTGACCTATGCACCAGACGTAACAGCCAGGAGTCTGTTTTGGGGGCGAGCCAGCTAGATCGGAAGAGCGGTTTCAG
chr20	31372514	31372553	DNMT3B_3421	-	GTGACCTATGCACCAGACGTAACAGATGATGAACATGATGAAGCCAGGCTATCAGCAAGATCGGAAGAGCGGTTTCAG
chr20	31374258	31374297	DNMT3B_3422	-	GTGACCTATGCACCAGACGTGAGAGGACACTGAGGCTTGGGCTTAGGTTGACTGGAGGCTGGAGATCGGAAGAGCGGTTTCAG

chr20	31374986	31375025	DNMT3B_3423	-	GTGACCTATGCACCAGACGTAAGGACACATAGTTTGGGCCAGAGCAAAGGATGTCGGTGAAGATCGGAAGAGCGGTTTCAG
chr20	31376610	31376649	DNMT3B_3424	-	GTGACCTATGCACCAGACGTTACCCACATGAAGAAATCCCAGTGAGGAGAGGCCATCCTGGAGATCGGAAGAGCGGTTTCAG
chr20	31379357	31379396	DNMT3B_3425	-	GTGACCTATGCACCAGACGTAAGACATCATCAACATCCACCTACAGGTGTGTCCCAGGTGAGATCGGAAGAGCGGTTTCAG
chr20	31380382	31380421	DNMT3B_3426	-	GTGACCTATGCACCAGACGTAGAGTCTGTGATGAATGGGGGGTGGGGAGGAGGTGCTCGAGATCGGAAGAGCGGTTTCAG
chr20	31383165	31383204	DNMT3B_3427	-	GTGACCTATGCACCAGACGTTAATTAGACTGCAGCCGTGGCTTGGTAGGAGGGTCCAGAGAGATCGGAAGAGCGGTTTCAG
chr20	31383406	31383445	DNMT3B_3428	-	GTGACCTATGCACCAGACGTAAGAAGAAGGCATGAGATGAGGTGAGGTCAGGAGCCGGGTACAGAGATCGGAAGAGCGGTTTCAG
chr20	31384585	31384586	DNMT3B_3429	-	GTGACCTATGCACCAGACGTTAAAGATGACAGCCGAGGGTTGTGGCTTTTGGCAGTTGAGGCCCTGACACCAAGATCGGAAGAGCGGTTTCAG
chr20	31384943	31384982	DNMT3B_3430	-	GTGACCTATGCACCAGACGTGAGAGAAACACCAAGTGAATCGGAGACCAGAGAAGGGCAGAGATCGGAAGAGCGGTTTCAG
chr20	31386216	31386255	DNMT3B_3431	-	GTGACCTATGCACCAGACGTTGGCAGGGAGAAGGGATGCCTTTGTCAGAGCTGGTCTCCTAGATCGGAAGAGCGGTTTCAG
chr20	31387000	31387039	DNMT3B_3432	-	GTGACCTATGCACCAGACGTAGGAAGGAGGTCATGGTGGTGAAGGCACAGGGCAAAGACTAGATCGGAAGAGCGGTTTCAG
chr20	31387909	31387948	DNMT3B_3433	-	GTGACCTATGCACCAGACGTGACAGAGACACAGAAGCATAAATGATGCTGAGCACACAGCAGATCGGAAGAGCGGTTTCAG
chr20	31388591	31388630	DNMT3B_3434	-	GTGACCTATGCACCAGACGTGAGACAGAGTCAGGATGAGGGTGTGGACAGAGGGAAAGAGAGATCGGAAGAGCGGTTTCAG
chr20	31389034	31389073	DNMT3B_3435	-	GTGACCTATGCACCAGACGTTAAAGATGACAGCCGAGGGTTCATTTGAAACCTCCAGCCAGATCGGAAGAGCGGTTTCAG
chr20	31390141	31390180	DNMT3B_3436	-	GTGACCTATGCACCAGACGTTAAAGAAGGTTACTGTTAGGAGCCTATTATTAGAGTTTCAGAGATCGGAAGAGCGGTTTCAG
chr20	31393094	31393133	DNMT3B_3437	-	GTGACCTATGCACCAGACGTCCAAAACCCATTACTTCTTACTAGCTATAGAGGGTCCCTAGATCGGAAGAGCGGTTTCAG
chr20	31393965	31394004	DNMT3B_3438	-	GTGACCTATGCACCAGACGTTAAATGACATCATGGAGTGAGCACAGAATGAAGGGACCTGGAGATCGGAAGAGCGGTTTCAG
chr20	31395518	31395557	DNMT3B_3439	-	GTGACCTATGCACCAGACGTCGGAGTGAAAGACAGCAAGTCAAGATGCCTCCAGGATGAGATCGGAAGAGCGGTTTCAG
chr19	45912883	45912922	ERCC1_3440	-	GTGACCTATGCACCAGACGTTGCCAAGGAAACCCAGTGAATAAATAATCGTCCTCCAGATCGGAAGAGCGGTTTCAG
chr19	45916885	45916924	ERCC1_3441	-	GTGACCTATGCACCAGACGTTGGGAAAGAACCAGAGGTTGGGGAAAGGAGAGAGCCCCAGATCGGAAGAGCGGTTTCAG
chr19	45917171	45917210	ERCC1_3442	-	GTGACCTATGCACCAGACGTGCTCCCCTGCCCATAGGCATTTCTGTCCCCTTGCCCTTTAGATCGGAAGAGCGGTTTCAG
chr19	45918069	45918108	ERCC1_3443	-	GTGACCTATGCACCAGACGTCTCACTCCCATCCTGCCTGGGCCCTCCCGCAGCTCCTGAGATCGGAAGAGCGGTTTCAG
chr19	45920029	45920068	ERCC1_3444	-	GTGACCTATGCACCAGACGTGGCTTCCCTGCCTCATTAGGCTCCACCTGGGATTGGTCCAGATCGGAAGAGCGGTTTCAG
chr19	45922345	45922384	ERCC1_3445	-	GTGACCTATGCACCAGACGTGCTGCTCCCTGCCAGCCCTACCCGGCTTTGAGGTTGTGCAGATCGGAAGAGCGGTTTCAG
chr19	45923532	45923571	ERCC1_3446	-	GTGACCTATGCACCAGACGTCGGCGCCACCCAGACTTCAGGAAGGGCACCCCTGGCCAGATCGGAAGAGCGGTTTCAG
chr19	45924386	45924425	ERCC1_3447	-	GTGACCTATGCACCAGACGTAGACGGAGAAGTGAGGCCCTTGGAGTTTTCAGTGGGAAACGAGATCGGAAGAGCGGTTTCAG
chr19	45926478	45926517	ERCC1_3448	-	GTGACCTATGCACCAGACGTGAGATGCGGGGCCCTGGGAGGCTGGGGGCTGTTAGACGAGATCGGAAGAGCGGTTTCAG
chr16	14013973	14014012	ERCC4_3449	-	GTGACCTATGCACCAGACGTCGGGTCGCAGCCGAACGCAGCCGAAGGAAGCCGACTCCTAGATCGGAAGAGCGGTTTCAG
chr16	14015838	14015877	ERCC4_3450	-	GTGACCTATGCACCAGACGTTCAAACCTTGATTAGTAGGCTATTTAATACAGGGCAGTTTTAGATCGGAAGAGCGGTTTCAG
chr16	14021835	14021874	ERCC4_3451	-	GTGACCTATGCACCAGACGTTAAATATTTTCAACAATTTTCTAGAGTTTTCAGCAGCTATGAGATCGGAAGAGCGGTTTCAG
chr16	14024517	14024556	ERCC4_3452	-	GTGACCTATGCACCAGACGTTAAATAATTTGCTATTTGCTAAATATGTTAAGTATAGTTAAGATCGGAAGAGCGGTTTCAG
chr16	14025964	14026003	ERCC4_3453	-	GTGACCTATGCACCAGACGTAAGTTAAAGAAAAAGTGCCATCAATTTATGGTTAATTTAAGATCGGAAGAGCGGTTTCAG
chr16	14027999	14028038	ERCC4_3454	-	GTGACCTATGCACCAGACGTATAAAAATATCTCATTCTATGTGATAAATTTACCCATAAAGATCGGAAGAGCGGTTTCAG
chr16	14028953	14028992	ERCC4_3455	-	GTGACCTATGCACCAGACGTTAAACAACATTATGTTACTATTACCTCACTTGTCCCTCTAAGATCGGAAGAGCGGTTTCAG
chr16	14031573	14031612	ERCC4_3456	-	GTGACCTATGCACCAGACGTAGACAGAATTTTAGGTTGGAAAAACAGCATTTTAATCCAGATCGGAAGAGCGGTTTCAG
chr16	14038530	14038569	ERCC4_3457	-	GTGACCTATGCACCAGACGTTAAACACTTCTCAACACTTCTGAAACAAATTTCAAATTTAAGATCGGAAGAGCGGTTTCAG
chr16	14041421	14041460	ERCC4_3458	-	GTGACCTATGCACCAGACGTTAAAGTAAGTAATGTCCTACTGGGGAAGAACTCTCAAAGAAGGAGATCGGAAGAGCGGTTTCAG
chr16	14029252	14029291	ERCC4_3459	-	GTGACCTATGCACCAGACGTGGTTTTCTACCATTGAGTTAAGGTCAACTTCCGTTTTTAGATCGGAAGAGCGGTTTCAG
chr16	14041788	14041827	ERCC4_3460	-	GTGACCTATGCACCAGACGTTAAGAAGAGTGAGTTTGGAACTAATGTCATTGCTGGAGATAGATCGGAAGAGCGGTTTCAG
chr17	41605837	41605876	ETV4_3461	-	GTGACCTATGCACCAGACGTCGTGTTCCCTGCTCCGCGAGGTGGTGCTGCCCTGTGTACATAGATCGGAAGAGCGGTTTCAG
chr17	41606453	41606492	ETV4_3462	-	GTGACCTATGCACCAGACGTTGGGTCACGGCAAGGTGGTGGGGGGCAGTGGCTGTGAGAGATCGGAAGAGCGGTTTCAG
chr17	41606822	41606861	ETV4_3463	-	GTGACCTATGCACCAGACGTCGGATGTTCCAGCCCTCCTTTCCAAAGTTTACAGCTGGAGATCGGAAGAGCGGTTTCAG
chr17	41607202	41607241	ETV4_3464	-	GTGACCTATGCACCAGACGTTGACTGTTGATGGGAGGGTCAAGGCTTTATCACGCTGTGTAGATCGGAAGAGCGGTTTCAG
chr17	41607425	41607464	ETV4_3465	-	GTGACCTATGCACCAGACGTCCTCCCTTCCCTGCCAAGCCCTCCATGTTGGGGAGGGAGAGATCGGAAGAGCGGTTTCAG
chr17	41609992	41610031	ETV4_3466	-	GTGACCTATGCACCAGACGTTGGGGTGGGGCAGGGTGGCATGTGATCAAGTGTTCAGTTAAAGATCGGAAGAGCGGTTTCAG
chr17	41610505	41610544	ETV4_3467	-	GTGACCTATGCACCAGACGTAGGGAAACCCACTGCTCATGGGCCAGGTGTTTTTTCAATAGATCGGAAGAGCGGTTTCAG
chr17	41611177	41611216	ETV4_3468	-	GTGACCTATGCACCAGACGTGCCCTGGACCTGGTGAAGGTAGGAGGGTCCAGAGGAAGATCGGAAGAGCGGTTTCAG
chr17	41613744	41613783	ETV4_3469	-	GTGACCTATGCACCAGACGTGTCCTGGGGAGAGGGTATAGGGAGTGGAGGATGGCAGGAAGATCGGAAGAGCGGTTTCAG
chr17	41622293	41622332	ETV4_3470	-	GTGACCTATGCACCAGACGTTTGTGACCTTTTCTATTTTGGGAGGCTGGACAGGGGGACAAGATCGGAAGAGCGGTTTCAG
chr15	91428226	91428265	FES_3471	-	GTGACCTATGCACCAGACGTTGGGGACAGAAAAGGGGCCATCCTGGAGGCAAGGCAGCAAGATCGGAAGAGCGGTTTCAG
chr15	91428592	91428631	FES_3472	-	GTGACCTATGCACCAGACGTGAGATGGGGAGGCGAGGGGGGGCAATGGCTCCCAAAGATCGGAAGAGCGGTTTCAG
chr15	91430141	91430180	FES_3473	-	GTGACCTATGCACCAGACGTAGGAGAGGGCCAGTGTGGGGCAGCAGGTCCCAAGTTGGAAGATCGGAAGAGCGGTTTCAG
chr15	91430367	91430406	FES_3474	-	GTGACCTATGCACCAGACGTTGGGGCAGGGGTATAGATGACAGCATGGAGGCCAGGCAAGATCGGAAGAGCGGTTTCAG
chr15	91432697	91432736	FES_3475	-	GTGACCTATGCACCAGACGTCAGCGCCCCGTGAGTGACAGGCCAGCAGCCCTGGGCCAAAGATCGGAAGAGCGGTTTCAG
chr15	91433020	91433059	FES_3476	-	GTGACCTATGCACCAGACGTGAGAAGGGCAGCATTAGAACCAGCCCTCCTGCCCTCAAGATCGGAAGAGCGGTTTCAG
chr15	91433272	91433311	FES_3477	-	GTGACCTATGCACCAGACGTTGGCGGGTGGGAGGGTGGATGAGAATAAGGGCTCGGCTGAGATCGGAAGAGCGGTTTCAG
chr15	91433581	91433620	FES_3478	-	GTGACCTATGCACCAGACGTGGACAGACGTCAGCGGGTGGCCAGGCTTAGGGAGGGGGAGAGATCGGAAGAGCGGTTTCAG
chr15	91434162	91434201	FES_3479	-	GTGACCTATGCACCAGACGTGAGGATCGAGGAGGACCTTAAACCTTTGTTGAAGAGATCGGAAGAGCGGTTTCAG
chr15	91434734	91434773	FES_3480	-	GTGACCTATGCACCAGACGTTGGGACCCGGGTCAGCAGCCTCCTTCTGAGGGGCGTGAGATCGGAAGAGCGGTTTCAG

chr15	91435238	91435277	FES_3481	-	GTGACCTATGCACCAGACGTGAGGAGACAGGGGATCAGAAGTCTGAAGAAAAGGGGTGCTAGATCGGAAGAGCGGTTTCAG
chr15	91435887	91435926	FES_3482	-	GTGACCTATGCACCAGACGCTTTGGGCTCCTACCACGGCCTCCAGTCCCGCAGTTCTCAGATCGGAAGAGCGGTTTCAG
chr15	91436280	91436319	FES_3483	-	GTGACCTATGCACCAGACGCTGTGCTCAGGATCTACGTGGCCAGGCCCGCTCCCCAGAGATCGGAAGAGCGGTTTCAG
chr15	91436471	91436510	FES_3484	-	GTGACCTATGCACCAGACGTGGAGGACCCCTGCTGAGCCTCCTGAGGTAAGGCTGCCACCAGATCGGAAGAGCGGTTTCAG
chr15	91436834	91436873	FES_3485	-	GTGACCTATGCACCAGACGTCAGGGCAGGGGCTCATTGGCCAACAGTCCGCTGCCACAGATCGGAAGAGCGGTTTCAG
chr15	91437116	91437155	FES_3486	-	GTGACCTATGCACCAGACGTGGCGAGGAGGTGAGGCAGCGTGTAGTGCACCCTCCCTGGGGAGATCGGAAGAGCGGTTTCAG
chr15	91438596	91438635	FES_3487	-	GTGACCTATGCACCAGACGTAAAGCACAGCACAGCAGCAGGATGAGGGAGTGTGAGGGTGCATCGGAAGAGCGGTTTCAG
chr4	144258292	144258331	GAB1_3488	-	GTGACCTATGCACCAGACGTTCTCGGGCTCCGGGCCGGGCAGCTGAGGGGGCGGGCGCAGATCGGAAGAGCGGTTTCAG
chr4	144336580	144336619	GAB1_3489	-	GTGACCTATGCACCAGACGTAACAAAATATCCATTCACTATTAACCTTGTAGATAATGTTTAGATCGGAAGAGCGGTTTCAG
chr4	144354594	144354633	GAB1_3490	-	GTGACCTATGCACCAGACGTAAAGTTTAACTATCACGCTATCACAGTTAAACAATTTTATAGATCGGAAGAGCGGTTTCAG
chr4	144359102	144359141	GAB1_3491	-	GTGACCTATGCACCAGACGTATTGTTAATGACACAATAAAAGGTGGAGACTAAGAATAAGATCGGAAGAGCGGTTTCAG
chr4	144360905	144360944	GAB1_3492	-	GTGACCTATGCACCAGACGTGAACAAAATCAACATTTATCCCATCTTTGCCAGCTCTAGATCGGAAGAGCGGTTTCAG
chr4	144361182	144361221	GAB1_3493	-	GTGACCTATGCACCAGACGTATATATTTCTTTAATAAACAACAACTCTTGTACACATAGATCGGAAGAGCGGTTTCAG
chr4	144378783	144378822	GAB1_3494	-	GTGACCTATGCACCAGACGTAAAGAAGACTCTCTTAATATAATGTTATTTAATTTGGAGATCGGAAGAGCGGTTTCAG
chr4	144380488	144380527	GAB1_3495	-	GTGACCTATGCACCAGACGTAAAGAGAAAAGAGATTTTATGATACAGAACTTTGGAAAAGATCGGAAGAGCGGTTTCAG
chr4	144381467	144381506	GAB1_3496	-	GTGACCTATGCACCAGACGTAAATATCATCACAAACATAAGCCTTGACAAAATATCTAAGATCGGAAGAGCGGTTTCAG
chr4	144387206	144387245	GAB1_3497	-	GTGACCTATGCACCAGACGTTAGACAACAAAATCAACGGTCAGACATTCCACAGACATACAGATCGGAAGAGCGGTTTCAG
chr4	144390134	144390173	GAB1_3498	-	GTGACCTATGCACCAGACGTAAAGAAAACAACAAAGCTCAACATATAAAGGAGTGTCTAGATCGGAAGAGCGGTTTCAG
chr4	144359403	144359442	GAB1_3499	-	GTGACCTATGCACCAGACGTTCTCGATGCCAGATGGGGTATAAAAACATAGAGTTCTCAGATCGGAAGAGCGGTTTCAG
chr7	81331847	81331886	HGF_3500	-	GTGACCTATGCACCAGACGTTGTGTCTGAAGCACCCACCAATAACAACGTCTTTTACATGAGATCGGAAGAGCGGTTTCAG
chr7	81334656	81334695	HGF_3501	-	GTGACCTATGCACCAGACGTAGTTCTTTAATAAGGAGTATGTGATTCATAGCTTAGTGTAGATCGGAAGAGCGGTTTCAG
chr7	81335553	81335592	HGF_3502	-	GTGACCTATGCACCAGACGTTTGAAGATTTTGTATTTTTCACCTGGACAAGAATTGTTGAGATCGGAAGAGCGGTTTCAG
chr7	81336556	81336595	HGF_3503	-	GTGACCTATGCACCAGACGTTTAAAATAGTATATTTTGTAGCCTTTAAAATGTGTATGAGATCGGAAGAGCGGTTTCAG
chr7	81339413	81339452	HGF_3504	-	GTGACCTATGCACCAGACGTATAGTGAAGTCAAGTCAATCATGATCCAGAATATGTACAAGAGAAGATCGGAAGAGCGGTTTCAG
chr7	81340747	81340786	HGF_3505	-	GTGACCTATGCACCAGACGTTTTCACAATAAAGTATATTCTGAGTCTCTCTGTGTGAGATCGGAAGAGCGGTTTCAG
chr7	81346498	81346537	HGF_3506	-	GTGACCTATGCACCAGACGTTTAGGGATTGGTGTCTGTGAAATATTTAAAATGTACTACAGATCGGAAGAGCGGTTTCAG
chr7	81350011	81350050	HGF_3507	-	GTGACCTATGCACCAGACGTTTCTCCTTTCAATATATAGAATGTAGTGATACCAACAGAAAGATCGGAAGAGCGGTTTCAG
chr7	81355156	81355195	HGF_3508	-	GTGACCTATGCACCAGACGTACATTCTGCAGGGTGGGCATGATTAATTCAGGGGAAATGAGATCGGAAGAGCGGTTTCAG
chr7	81358871	81358910	HGF_3509	-	GTGACCTATGCACCAGACGTTAGGCAATTTATACATTTTTCAGTAGCCCTGGGGAAAATGAGATCGGAAGAGCGGTTTCAG
chr7	81372208	81372247	HGF_3510	-	GTGACCTATGCACCAGACGTCAACTGATGGTGAACCTTCTTGTGTGAGTGACAGAGGCTGAGATCGGAAGAGCGGTTTCAG
chr7	81372619	81372658	HGF_3511	-	GTGACCTATGCACCAGACGTGCAAAATTTATGCTTCTTTTCTCTCACAGACTGGATCAGATCGGAAGAGCGGTTTCAG
chr7	81374266	81374305	HGF_3512	-	GTGACCTATGCACCAGACGTAATGAATCATGCTTTTTCAGTATTCTTTTACAACATATATAGATCGGAAGAGCGGTTTCAG
chr7	81381378	81381417	HGF_3513	-	GTGACCTATGCACCAGACGTCATGTGGGCCATCTATTCCCCCTATGTGTAGAATGTAAAGATCGGAAGAGCGGTTTCAG
chr7	81381386	81381425	HGF_3514	-	GTGACCTATGCACCAGACGTCATGTAATGCCATGTGGGCCATCTATTCCCCCTATGTGTAGATCGGAAGAGCGGTTTCAG
chr7	81386455	81386494	HGF_3515	-	GTGACCTATGCACCAGACGTTTGAAGAAAAGAGATGAAGCCCTCTGTCTTTTTTACATGTAGATCGGAAGAGCGGTTTCAG
chr7	81387958	81387997	HGF_3516	-	GTGACCTATGCACCAGACGTTCTCCCTAAATATTGCATAATGAAATAAAGTATAATGAAAAGATCGGAAGAGCGGTTTCAG
chr7	81391973	81392012	HGF_3517	-	GTGACCTATGCACCAGACGTTTCATTTTCTTCTTGAATAATTTTCCAAATATAGCATGCAAGATCGGAAGAGCGGTTTCAG
chr7	81399150	81399189	HGF_3518	-	GTGACCTATGCACCAGACGTTTCTTCTTCTTCAATATAGTATTAGTATTTAACTCTCTAGATCGGAAGAGCGGTTTCAG
chr12	68551643	68551682	IFNG_3519	-	GTGACCTATGCACCAGACGTTTAAATCTTTTCTTTGGTTTCATTGCCGAGGGTCTTGCAAAGATCGGAAGAGCGGTTTCAG
chr12	68551921	68551960	IFNG_3520	-	GTGACCTATGCACCAGACGTTATCCCATTTGGCTAAATTTCTGTGCTTCTTCTGAAGATCGGAAGAGCGGTTTCAG
chr12	68553232	68553271	IFNG_3521	-	GTGACCTATGCACCAGACGTTTCTTTAATAGTACTTGTGTTGTGTTGAAAATGACTGAATAGATCGGAAGAGCGGTTTCAG
chr6	160412166	160412205	IGF2R_3522	-	GTGACCTATGCACCAGACGTAGAAAAACAACCTGTCAATGTCACCTGATTTATCAAAAATTAGATCGGAAGAGCGGTTTCAG
chr6	160429992	160430031	IGF2R_3523	-	GTGACCTATGCACCAGACGTAGAAAAGAGAGTGAACAGGCTATAAAAACATACATAACCAAGATCGGAAGAGCGGTTTCAG
chr6	160431669	160431708	IGF2R_3524	-	GTGACCTATGCACCAGACGTAAATAGTAATTATAATGTTACCATACCACACATTTGTAAGATCGGAAGAGCGGTTTCAG
chr6	160445554	160445593	IGF2R_3525	-	GTGACCTATGCACCAGACGTGGAAGAAAAGTGTAGTCTTTCAGTATACCTTTGGTCAATAGATCGGAAGAGCGGTTTCAG
chr6	160448167	160448206	IGF2R_3526	-	GTGACCTATGCACCAGACGTTGATTAATCACTTAACTAGATTAGGTTAGGAGTGATAATAGATCGGAAGAGCGGTTTCAG
chr6	160450532	160450571	IGF2R_3527	-	GTGACCTATGCACCAGACGTCACATTGAGAAAAGAGTATTACAAAAGTATAAAGTACATCAGATCGGAAGAGCGGTTTCAG
chr6	160453533	160453572	IGF2R_3528	-	GTGACCTATGCACCAGACGTCATGTGAAAGAAGCAAAAATAAATGTTTCATGCAGCTAGATCGGAAGAGCGGTTTCAG
chr6	160453924	160453963	IGF2R_3529	-	GTGACCTATGCACCAGACGTGGAATTAACAAGAAGAGGCTTGTGTTTATATGAATAGGTAAGATCGGAAGAGCGGTTTCAG
chr6	160455401	160455440	IGF2R_3530	-	GTGACCTATGCACCAGACGTGTGAATACACAGACAAATGTGTTTGGGAGAACCAAGAAAAGATCGGAAGAGCGGTTTCAG
chr6	160461542	160461581	IGF2R_3531	-	GTGACCTATGCACCAGACGTCAAGAGGAGAAATTTAACTCCATACGTCACCAAAATTTGAAGATCGGAAGAGCGGTTTCAG
chr6	160464130	160464169	IGF2R_3532	-	GTGACCTATGCACCAGACGTACAAAAGTATTTTATGCCAAAAGCAATGCTGATTTCTAGATCGGAAGAGCGGTTTCAG
chr6	160465496	160465535	IGF2R_3533	-	GTGACCTATGCACCAGACGTAAGGGGGAGAAAACAGAAGATGTGGTTAAAATGATCATCAGATCGGAAGAGCGGTTTCAG
chr6	160466727	160466766	IGF2R_3534	-	GTGACCTATGCACCAGACGTGGAAGAGAGATGGGGATCACTAATCCGTTTCTTCTAAAAGATCGGAAGAGCGGTTTCAG
chr6	160467480	160467519	IGF2R_3535	-	GTGACCTATGCACCAGACGTATAAAAACAATAAAGTATGGAAGGTCAGTCCGACAGTTAAGATCGGAAGAGCGGTTTCAG
chr6	160468141	160468180	IGF2R_3536	-	GTGACCTATGCACCAGACGTCACAGTTCTCTCAGCAAAGCCTGAGGGGCGAAGACACAGATCGGAAGAGCGGTTTCAG
chr6	160468774	160468813	IGF2R_3537	-	GTGACCTATGCACCAGACGTTGACATGCCGCGGAGGGATGGCAAAAAGCAACAGTGTAGATCGGAAGAGCGGTTTCAG
chr6	160469357	160469396	IGF2R_3538	-	GTGACCTATGCACCAGACGTTAAAGCAAAAATGTATATGCTTTTAAAGAGCTTACACATTTTCAGATCGGAAGAGCGGTTTCAG

chr6	160477406	160477445	IGF2R_3539	-	GTGACCTATGCACCAGACGTAAATCCAGGGTAAAAGTCAATACAGTAACATGGAACCTGAAGATCGGAAGAGCGGTTTCAG
chr6	160479005	160479044	IGF2R_3540	-	GTGACCTATGCACCAGACGTCAAAATGGGGAAAAAGGGGCGCATTCAAACCAATTCACAAGATCGGAAGAGCGGTTTCAG
chr6	160479888	160479927	IGF2R_3541	-	GTGACCTATGCACCAGACGTGACGGTAAGAGCCATACAAAACAAATTTATGCCTCGTATCTAGATCGGAAGAGCGGTTTCAG
chr6	160481529	160481568	IGF2R_3542	-	GTGACCTATGCACCAGACGTAGAAGGCCAGATTTAAGAGACAGAACAGTATTCATGGCAGATCGGAAGAGCGGTTTCAG
chr6	160482485	160482524	IGF2R_3543	-	GTGACCTATGCACCAGACGTACAAAAAACACCGCTGGAGAATCTGCCTCCTTGTGAGCAAGATCGGAAGAGCGGTTTCAG
chr6	160482735	160482774	IGF2R_3544	-	GTGACCTATGCACCAGACGTAGAATAAGTGGTTTGGGCATGAGGAAGCCGATGACCTTGAAGATCGGAAGAGCGGTTTCAG
chr6	160483514	160483553	IGF2R_3545	-	GTGACCTATGCACCAGACGTAAATCAGACGCTGATTTGTTTCTGATTTTAAATAATAGATCGGAAGAGCGGTTTCAG
chr6	160484397	160484436	IGF2R_3546	-	GTGACCTATGCACCAGACGTATGGAAGAAGTGAAGGGCAACTGCAACCACACACGCATTAGATCGGAAGAGCGGTTTCAG
chr6	160485383	160485422	IGF2R_3547	-	GTGACCTATGCACCAGACGTGGAGAACATTAACAAGGTTTGGTTCCGGTCCCTAGGCTGAGATCGGAAGAGCGGTTTCAG
chr6	160485786	160485825	IGF2R_3548	-	GTGACCTATGCACCAGACGTAAAGAGGCACATATATAAAAGTGAAGATGCAAAACTTTAGAGATCGGAAGAGCGGTTTCAG
chr6	160489231	160489270	IGF2R_3549	-	GTGACCTATGCACCAGACGTGAAAACCCGCGAGTTAGTTAGGCTTGGTCTGTTTCTCTTAAAGATCGGAAGAGCGGTTTCAG
chr6	160490850	160490889	IGF2R_3550	-	GTGACCTATGCACCAGACGTAGACACAAGAAAGATGGCTTTAGTACTCCCAGGCTAAGATCGGAAGAGCGGTTTCAG
chr6	160492892	160492931	IGF2R_3551	-	GTGACCTATGCACCAGACGTGCACACAGACGCTGGAAGGGATCACGCAAAAACCTCAGATGAGATCGGAAGAGCGGTTTCAG
chr6	160493747	160493786	IGF2R_3552	-	GTGACCTATGCACCAGACGTGAAGAAGATGGGGACACAGTACTCCAGGGAGCTGAGACTAGATCGGAAGAGCGGTTTCAG
chr6	160494195	160494234	IGF2R_3553	-	GTGACCTATGCACCAGACGTAGGGAAAGGGCGGAGAAAACACATACAGACTCGATGGCCAGATCGGAAGAGCGGTTTCAG
chr6	160494739	160494778	IGF2R_3554	-	GTGACCTATGCACCAGACGTGGAAGACTGCTTTGAGTCTACAAAAAATTTTCCATATCAGATCGGAAGAGCGGTTTCAG
chr6	160496829	160496868	IGF2R_3555	-	GTGACCTATGCACCAGACGTAGCGAGGGCAAACAGTATTTTCAGAAATTAACCATTCCCAAGATCGGAAGAGCGGTTTCAG
chr6	160499183	160499222	IGF2R_3556	-	GTGACCTATGCACCAGACGTGAAGAGCACGGTGCTTAAAACCCATGGCATAGGGATGAGATCGGAAGAGCGGTTTCAG
chr6	160500562	160500601	IGF2R_3557	-	GTGACCTATGCACCAGACGTACCATGCGTGGCCGTCAGCAGAGTGGCAGCACCCAGGCTAGATCGGAAGAGCGGTTTCAG
chr6	160501111	160501150	IGF2R_3558	-	GTGACCTATGCACCAGACGTGAAGAACATTATCAGTGTGGCAGCTGTGCCTCGCCAGGCAAGATCGGAAGAGCGGTTTCAG
chr6	160505977	160506016	IGF2R_3559	-	GTGACCTATGCACCAGACGTACACAAAGGGCAGGTAAGAGGCATGCAAGTGACGCTCTAGATCGGAAGAGCGGTTTCAG
chr6	160509015	160509054	IGF2R_3560	-	GTGACCTATGCACCAGACGTCAAATGATTGAACTGACATTATTTCTAGTGCATTATAAAAAGATCGGAAGAGCGGTTTCAG
chr6	160510089	160510128	IGF2R_3561	-	GTGACCTATGCACCAGACGTGGAAGCACAGGCTACAGTCACTCCCAGCCAGACATAAGAGATCGGAAGAGCGGTTTCAG
chr6	160510898	160510937	IGF2R_3562	-	GTGACCTATGCACCAGACGTAGAAGAAGATCAGATGACATGGAAGCTTCAAGAAGGCATCGGAAGAGCGGTTTCAG
chr6	160517421	160517460	IGF2R_3563	-	GTGACCTATGCACCAGACGTGGAAGGGCACACATGGCATGTACCATCATTTTTTACGAGAGATCGGAAGAGCGGTTTCAG
chr6	160523501	160523540	IGF2R_3564	-	GTGACCTATGCACCAGACGTGCACAGAAAAGGAGCCGTGTACAGGGTGGTCTGCTGCAGATCGGAAGAGCGGTTTCAG
chr6	160524728	160524767	IGF2R_3565	-	GTGACCTATGCACCAGACGTAAAGGAGACAATAATTACTCCAGTGTAGAGAGGGCATGGGAGATCGGAAGAGCGGTTTCAG
chr6	160525656	160525695	IGF2R_3566	-	GTGACCTATGCACCAGACGTTCAACAGCAGAGACCACGTCAGCCCCCTAAGAGACCCCATAGATCGGAAGAGCGGTTTCAG
chr19	7117017	7117056	INSR_3567	-	GTGACCTATGCACCAGACGTGTGGCGGGGGCGGCGAGGGTCCCATTTTCGTTTCTAGATCGGAAGAGCGGTTTCAG
chr19	7119410	7119449	INSR_3568	-	GTGACCTATGCACCAGACGTAAAGGGTTTAAAGTGTGTGAGGTGTTGTTGTTGAAAGGGTATAGATCGGAAGAGCGGTTTCAG
chr19	7120581	7120620	INSR_3569	-	GTGACCTATGCACCAGACGTTGTGGATGGGTGGATGGACGCTGGGCTTGAATTCAGGTGAGATCGGAAGAGCGGTTTCAG
chr19	7122575	7122614	INSR_3570	-	GTGACCTATGCACCAGACGCTTTTCTGCTTTGAAAACATAACGACCAGGCCAGGTTTGAAGATCGGAAGAGCGGTTTCAG
chr19	7122840	7122879	INSR_3571	-	GTGACCTATGCACCAGACGTTCCGGGGACCCAGCGGGGTACTCGGTGGAGCACCCGCTCCAGATCGGAAGAGCGGTTTCAG
chr19	7125244	7125283	INSR_3572	-	GTGACCTATGCACCAGACGTTGGGGTGGGACATGGGCTGGCTTCCCTGACCTTCCCTTAGATCGGAAGAGCGGTTTCAG
chr19	7126545	7126584	INSR_3573	-	GTGACCTATGCACCAGACGTTCCCTTCCCTGTGGTGGCCAGAACCCCTACTCATCAGCTTAGATCGGAAGAGCGGTTTCAG
chr19	7132119	7132158	INSR_3574	-	GTGACCTATGCACCAGACGTATGGCAGCCTCAGCTGACTGGGGCTGTGCTTAGCACTGAGAGATCGGAAGAGCGGTTTCAG
chr19	7141638	7141677	INSR_3575	-	GTGACCTATGCACCAGACGTTGACTCTTGGGCATGCCCTGCACACTTACAGATGCCCTAGATCGGAAGAGCGGTTTCAG
chr19	7142777	7142816	INSR_3576	-	GTGACCTATGCACCAGACGTTGCTCCGGGGTCCGAGTGTGATGGTGGGACATCAAGGCTAGATCGGAAGAGCGGTTTCAG
chr19	7150458	7150497	INSR_3577	-	GTGACCTATGCACCAGACGTCCTGTGCGACCCCTGGTGCCTGCTCCGCGCAGGGCCGGCAGATCGGAAGAGCGGTTTCAG
chr19	7152687	7152726	INSR_3578	-	GTGACCTATGCACCAGACGTGGCGCTGGGCTCTTGTGGTGGCAATTGGCTTGGTGTAGATCGGAAGAGCGGTTTCAG
chr19	7162993	7163032	INSR_3579	-	GTGACCTATGCACCAGACGTGACGCTGGCTAGGATCGGTGGGGTTTGCACACGTGTGATCGGAAGAGCGGTTTCAG
chr19	7166115	7166154	INSR_3580	-	GTGACCTATGCACCAGACGTTTGGGAATGTGAATTCGATGTGAATCAGACCTCTTGTAGATCGGAAGAGCGGTTTCAG
chr19	7167929	7167968	INSR_3581	-	GTGACCTATGCACCAGACGTGAGTTAGAGAGACGCTGAGGAGGCGAGGGCTGGCTGGCTCAGATCGGAAGAGCGGTTTCAG
chr19	7172251	7172290	INSR_3582	-	GTGACCTATGCACCAGACGCTGATTGTGTGATGGCCTGAGTGCTAACTAGGAAGTTTCAGATCGGAAGAGCGGTTTCAG
chr19	7174544	7174583	INSR_3583	-	GTGACCTATGCACCAGACGTTCTGTGGCGGCTGGGGGTCCTGTTGGGCTCCATGCCCAGATCGGAAGAGCGGTTTCAG
chr19	7184277	7184316	INSR_3584	-	GTGACCTATGCACCAGACGTGATGTGGTCTGGGGGCGAGGAGGAGAGGAACTGAGATCGGAAGAGCGGTTTCAG
chr19	7267306	7267345	INSR_3585	-	GTGACCTATGCACCAGACGTGATACAGGGTTCTAAGCAGTGTCTCGTGCCTTGTCTAGAAGATCGGAAGAGCGGTTTCAG
chr19	7293753	7293792	INSR_3586	-	GTGACCTATGCACCAGACGTGGGCGCGGGCGTGGGCGGGGAGCGCCGCGATGGGAGAGGAGATCGGAAGAGCGGTTTCAG
chr19	7267582	7267621	INSR_3587	-	GTGACCTATGCACCAGACGTGGAACCTCGGCCTCTACAACCTGATGAACATCACCCGGGGTAGATCGGAAGAGCGGTTTCAG
chr10	3821681	3821720	KLF6_3588	-	GTGACCTATGCACCAGACGTAGGTGGATCCTGTAGGCTAAAAGGCTTCCAGGCTGAGAGCAGATCGGAAGAGCGGTTTCAG
chr10	3822248	3822287	KLF6_3589	-	GTGACCTATGCACCAGACGTGAGGACAATGCTGGGCAAGGAGCGTGGGGCTTGGGAATGAGATCGGAAGAGCGGTTTCAG
chr10	3823783	3823822	KLF6_3590	-	GTGACCTATGCACCAGACGTACGCGCCGCGGAGGAGGCGGCTGGTGGGCGCCACTCGAGATCGGAAGAGCGGTTTCAG
chr10	3824070	3824109	KLF6_3591	-	GTGACCTATGCACCAGACGTTTGGTCACTCGGGAAAATTGAGCTCCTCTGTACCTCCAAGATCGGAAGAGCGGTTTCAG
chr1	43803470	43803509	MPL_3592	-	GTGACCTATGCACCAGACGTACTGTGTGCTGCCTTAGCCCATCTCCCTTCCAGGAAGCTAGATCGGAAGAGCGGTTTCAG
chr1	43803720	43803759	MPL_3593	-	GTGACCTATGCACCAGACGTGCTGTGTGAGTTGGCCCTGGGCTCCAGGCATGTTTATGAGATCGGAAGAGCGGTTTCAG
chr1	43804163	43804202	MPL_3594	-	GTGACCTATGCACCAGACGTAGAAGAGGTTCCCTCTACACAGCCACCATGCGGAGCCCTGAGATCGGAAGAGCGGTTTCAG
chr1	43804892	43804931	MPL_3595	-	GTGACCTATGCACCAGACGTGACAGGGCACATCGAACTGAGTACCACAGTCTAGGACATCGGAAGAGCGGTTTCAG
chr1	43805585	43805624	MPL_3596	-	GTGACCTATGCACCAGACGTTAAATCCCAGCTTCAACTAGGTTCTGCCTGTGAGATCGGAAGAGCGGTTTCAG

chr1	43806008	43806047	MPL_3597	-	GTGACCTATGCACCAGACGTAGAAGTAAGTCCCATCAGGGCCCGTGTGCCCTACTGTATAGATCGGAAGAGCGGTTTCAG
chr1	43812066	43812105	MPL_3598	-	GTGACCTATGCACCAGACGTGCCCCACAGAGTCATTGAATCAGGCCTGCCCCAGAGACTAAGATCGGAAGAGCGGTTTCAG
chr1	43812413	43812452	MPL_3599	-	GTGACCTATGCACCAGACGTGTCAGCAGGGAGCAGCTTAAGTCCTTCTGTGCACAAGGCAAGATCGGAAGAGCGGTTTCAG
chr1	43814464	43814503	MPL_3600	-	GTGACCTATGCACCAGACGTAAGCGTGCGGTGGCCCGCGTGGGGCTTCGATAGCCCAGAGATCGGAAGAGCGGTTTCAG
chr1	43814884	43814923	MPL_3601	-	GTGACCTATGCACCAGACGTAAAGGGTCAGACTTCGGCCACCCTGGCCGGAGCCCCGAGATCGGAAGAGCGGTTTCAG
chr1	43817837	43817876	MPL_3602	-	GTGACCTATGCACCAGACGTAGGAAGAGAGCAGACTGAGCCATGGCAGTGGATTGGCAGAGATCGGAAGAGCGGTTTCAG
chr1	43818139	43818178	MPL_3603	-	GTGACCTATGCACCAGACGTGAGGAGAGGGCTGGATTAAGCAGATCCTGTGGGAGGAAGATCGGAAGAGCGGTTTCAG
chr1	45794928	45794967	MUTYH_3604	-	GTGACCTATGCACCAGACGTAGCCCCATTCCCTGAGAATCCTGTTGTTAGTAAAGTGCTAGATCGGAAGAGCGGTTTCAG
chr1	45796138	45796177	MUTYH_3605	-	GTGACCTATGCACCAGACGTTAGGCCCTCTCCCAACCGTGTCTCCCAGGCCTGAGTCCATAGATCGGAAGAGCGGTTTCAG
chr1	45796804	45796843	MUTYH_3606	-	GTGACCTATGCACCAGACGTTGTTGTCTTTGTTGACTTCTTGTGTTTTCTACATGTTCCAGATCGGAAGAGCGGTTTCAG
chr1	45797042	45797081	MUTYH_3607	-	GTGACCTATGCACCAGACGTAGCCGAATAGCCAAGGATGTTGGCTTTTGAGGCTATATCCAGATCGGAAGAGCGGTTTCAG
chr1	45797283	45797322	MUTYH_3608	-	GTGACCTATGCACCAGACGTACTGGCGTGGAGGGCAGTGGCATGAGTAAACAAGAGAGAAAGATCGGAAGAGCGGTTTCAG
chr1	45797645	45797684	MUTYH_3609	-	GTGACCTATGCACCAGACGTAACTAGCCCCACCCCAACCCCTTCTGGCCCGAGTCAGAAAAGATCGGAAGAGCGGTTTCAG
chr1	45797788	45797827	MUTYH_3610	-	GTGACCTATGCACCAGACGTTGGGGAAGGGGACAGTGAGAAGTCTAAGGAGTGACTCTGCAGATCGGAAGAGCGGTTTCAG
chr1	45798013	45798052	MUTYH_3611	-	GTGACCTATGCACCAGACGTGGGGTAACAAGGGTGTCTCAGGGGTGTCTGCAAAGGAGCTAGATCGGAAGAGCGGTTTCAG
chr1	45798196	45798235	MUTYH_3612	-	GTGACCTATGCACCAGACGTAGCCCAACCCCACTTTGTGCGTGCCAGCCTCCTTCTCCAGATCGGAAGAGCGGTTTCAG
chr1	45798385	45798424	MUTYH_3613	-	GTGACCTATGCACCAGACGTGGCAGGAGGGTAGGAACCCAGGAGTCTTGGGTGTCTTATAAGATCGGAAGAGCGGTTTCAG
chr1	45798540	45798579	MUTYH_3614	-	GTGACCTATGCACCAGACGTCCCTAGGGTAGGGGAATAGGAACAAATAGAGGGACTGACGAGATCGGAAGAGCGGTTTCAG
chr1	45798719	45798758	MUTYH_3615	-	GTGACCTATGCACCAGACGTGGGAGGAAGGGGAGGTCATGGGTCAGACCCAGATGAGAAGATCGGAAGAGCGGTTTCAG
chr1	45798907	45798946	MUTYH_3616	-	GTGACCTATGCACCAGACGTCTCCTGAGAGCAGGGCCACTTTGCCTCGAGGCCCTTGGGTAGATCGGAAGAGCGGTTTCAG
chr1	45799035	45799074	MUTYH_3617	-	GTGACCTATGCACCAGACGTGAGGAGCAGGGACAGTGGGTGGGAGGCAGGCACCCAGCCAGATCGGAAGAGCGGTTTCAG
chr1	45800013	45800052	MUTYH_3618	-	GTGACCTATGCACCAGACGTAGGTTGTGGCCCAAGGCTCATTGGCCATGAAAGGCAGATTAGATCGGAAGAGCGGTTTCAG
chr1	45805841	45805880	MUTYH_3619	-	GTGACCTATGCACCAGACGTTTGGGTCCTCTCGCCCGGTTCCAGGCAGTCGGGAAGATCGGAAGAGCGGTTTCAG
chr1	40362994	40363033	MYCL1_3620	-	GTGACCTATGCACCAGACGTGACGTTCTGCTTACGAAGACCAAGTTTATTTAGATCGGAAGAGCGGTTTCAG
chr1	40366436	40366475	MYCL1_3621	-	GTGACCTATGCACCAGACGTGTAGTCCCCAACCGTGTCTGTCTGGCACGTGGGTGTGTTGAGATCGGAAGAGCGGTTTCAG
chr1	40366561	40366600	MYCL1_3622	-	GTGACCTATGCACCAGACGTCCCCGAGCCATCCAAGAGGGGGCCACCCATGGGTGGCCAAGATCGGAAGAGCGGTTTCAG
chr1	40363293	40363332	MYCL1_3623	-	GTGACCTATGCACCAGACGTCCCCAACCTGTGACTTCTGATACTGAGGATGTGACCAAGAGATCGGAAGAGCGGTTTCAG
chr1	40366746	40366785	MYCL1_3624	-	GTGACCTATGCACCAGACGTGCTGTGAGGCACCGGCTCGCTCCTGGCGCGCCCGGGGAAGATCGGAAGAGCGGTTTCAG
chr5	142658879	142658918	NR3C1_3625	-	GTGACCTATGCACCAGACGTAACAATTTGGCGCTCAAAAAATAGAAGTCAATGAGAAAAAGATCGGAAGAGCGGTTTCAG
chr5	142661404	142661443	NR3C1_3626	-	GTGACCTATGCACCAGACGTAAGAATGGTTGCCTTAAAGAACTCGAATTAATAGCTTTTAGATCGGAAGAGCGGTTTCAG
chr5	142662083	142662122	NR3C1_3627	-	GTGACCTATGCACCAGACGTAACATAAAGCCAATATAAGAGTTTTCTGGGACAAAGTATAGATCGGAAGAGCGGTTTCAG
chr5	142674975	142675014	NR3C1_3628	-	GTGACCTATGCACCAGACGTACCTTTTACCTTATGTCAAAAGCATGAAATATGAAGGCAGATCGGAAGAGCGGTTTCAG
chr5	142678183	142678222	NR3C1_3629	-	GTGACCTATGCACCAGACGTTGTGTGTCATTTTCCCTGTATTCTATAGGGTATCTTTAACCCAGATCGGAAGAGCGGTTTCAG
chr5	142680000	142680039	NR3C1_3630	-	GTGACCTATGCACCAGACGTAACATAAAGAGCAACTATAAACCCTTTGTGTTTTCTTAGATCGGAAGAGCGGTTTCAG
chr5	142689612	142689651	NR3C1_3631	-	GTGACCTATGCACCAGACGTTATCTGAAAGCAATTGTTTGTCTGTAGCTTATAAAAAATAGATCGGAAGAGCGGTTTCAG
chr5	142693514	142693553	NR3C1_3632	-	GTGACCTATGCACCAGACGTTGAAGAGTTTTTTTTCTCTACTTGGTTTTCTATTCTCAAGATCGGAAGAGCGGTTTCAG
chr5	142693517	142693556	NR3C1_3633	-	GTGACCTATGCACCAGACGTTTTTGAAGAGTTTTTTTTCTCTACTTGGTTTTCTATTCTAGATCGGAAGAGCGGTTTCAG
chr5	142779171	142779210	NR3C1_3634	-	GTGACCTATGCACCAGACGTTGTTTTTCTGTTTTCTTAAAGAAATGGTACATTTAAGGTAGATAGATCGGAAGAGCGGTTTCAG
chr5	142779565	142779604	NR3C1_3635	-	GTGACCTATGCACCAGACGTCCCCAGTAATGTAACACTGCCCAAGTGAACACAGAAAAAGATCGGAAGAGCGGTTTCAG
chr5	142779959	142779998	NR3C1_3636	-	GTGACCTATGCACCAGACGTGAGAAACCCCAAGATTCAGCATCCACTGCTGTCTGCAGATCGGAAGAGCGGTTTCAG
chr18	39535207	39535246	PIK3C3_3637	-	GTGACCTATGCACCAGACGTGCAAAGTACCACCTAAGCGGGAACCTTAGGTACAGGAAAAAGATCGGAAGAGCGGTTTCAG
chr18	39537485	39537524	PIK3C3_3638	-	GTGACCTATGCACCAGACGTAAGACCAACAATGTTTCAGACATGAATTTTTAAGCATGTAGATCGGAAGAGCGGTTTCAG
chr18	39542404	39542443	PIK3C3_3639	-	GTGACCTATGCACCAGACGTGAAGTTAACATAAATCAGAAATACATATATATATCTTTAGATCGGAAGAGCGGTTTCAG
chr18	39550241	39550280	PIK3C3_3640	-	GTGACCTATGCACCAGACGTAGAGAATGTTCCAGGGTAGAAGTAAATTAATACAGTTTCATTAGATCGGAAGAGCGGTTTCAG
chr18	39567726	39567765	PIK3C3_3641	-	GTGACCTATGCACCAGACGTAATACAATCAGCAAAATTTAATATACATCTAGTAGAAAAGATCGGAAGAGCGGTTTCAG
chr18	39570373	39570412	PIK3C3_3642	-	GTGACCTATGCACCAGACGTAAGATTTTCTGAAAAATGATTATTTTCAACATTTCTAGATCGGAAGAGCGGTTTCAG
chr18	39575804	39575843	PIK3C3_3643	-	GTGACCTATGCACCAGACGTTTTTAAATATTGACAATGTAACACTTCAACAAAAGGAAATAGATCGGAAGAGCGGTTTCAG
chr18	39576552	39576591	PIK3C3_3644	-	GTGACCTATGCACCAGACGTAAGAAAAAGAACTAATTTTGTCAACAATACATGTCTAAGATCGGAAGAGCGGTTTCAG
chr18	39584270	39584309	PIK3C3_3645	-	GTGACCTATGCACCAGACGTAAATATTTAAAAATAGAAACAGCCTATTTCTGGGATAAGATCGGAAGAGCGGTTTCAG
chr18	39593356	39593395	PIK3C3_3646	-	GTGACCTATGCACCAGACGTAAAAAAGTAAAGTAATATTAGGAAAAGAAATGCAAAATTAAGATCGGAAGAGCGGTTTCAG
chr18	39595390	39595429	PIK3C3_3647	-	GTGACCTATGCACCAGACGTAATAAAGAGATCACTGAGATGTAATAACTCTGTCCATAAGATCGGAAGAGCGGTTTCAG
chr18	39600552	39600591	PIK3C3_3648	-	GTGACCTATGCACCAGACGTAAAGAAATGTATTATATATCATCTACTAGTAATGATAAGATCGGAAGAGCGGTTTCAG
chr18	39607357	39607396	PIK3C3_3649	-	GTGACCTATGCACCAGACGTGTTTGGCCATTGATGTGATGTGAAATGAACTTAGATTAGATCGGAAGAGCGGTTTCAG
chr18	39609239	39609278	PIK3C3_3650	-	GTGACCTATGCACCAGACGTCAAAGTGAGAAAAAATAGTTCTATGTTGCGTAAATGATCTAGATCGGAAGAGCGGTTTCAG
chr18	39613740	39613779	PIK3C3_3651	-	GTGACCTATGCACCAGACGTTCAAAAAGGATTAAAGAGTTAAAATAGAAAGATAGTTTAAAGATCGGAAGAGCGGTTTCAG
chr18	39617606	39617645	PIK3C3_3652	-	GTGACCTATGCACCAGACGTAATAATTGATTTCAAATTTGGCCATGAATTAATGCATAAAGATCGGAAGAGCGGTTTCAG
chr18	39618695	39618734	PIK3C3_3653	-	GTGACCTATGCACCAGACGTAAAGTAAACATATATAAGCACTGTAAAGACTGTTAAAAAGATCGGAAGAGCGGTTTCAG
chr18	39620591	39620630	PIK3C3_3654	-	GTGACCTATGCACCAGACGTATGATGCATGCAATTAAGCATAGCTACTGGTTAAGAAATAGATCGGAAGAGCGGTTTCAG

chr18	39623647	39623686	PIK3C3_3655	-	GTGACCTATGCACCAGACGTATTATTACATGTTTTAGAATTAAGTACAACAACAAACAGATCGGAAGAGCGGTTTCAG
chr18	39629445	39629484	PIK3C3_3656	-	GTGACCTATGCACCAGACGTAGTTAAAAAAAATATGTGAAAAACAATGCAAAACCAGGTTAAGATCGGAAGAGCGGTTTCAG
chr18	39637797	39637836	PIK3C3_3657	-	GTGACCTATGCACCAGACGTACAAGAACTCATTTGTTTCCAGAATTATCTTAAAGAACTAGATCGGAAGAGCGGTTTCAG
chr18	39644654	39644693	PIK3C3_3658	-	GTGACCTATGCACCAGACGTGCAGAAAAGAAAAAATAGCAACGATTAAGAATTCTGCATAGATCGGAAGAGCGGTTTCAG
chr18	39647302	39647341	PIK3C3_3659	-	GTGACCTATGCACCAGACGTACTCTTAGTCTTTACAACGAAGAAAAATAGGGCACATTAGATCGGAAGAGCGGTTTCAG
chr18	39661037	39661076	PIK3C3_3660	-	GTGACCTATGCACCAGACGTAAAAAAGAAATAAACAGAAAATTTACTTAATTATTCAAGATCGGAAGAGCGGTTTCAG
chr1	9770464	9770503	PIK3CD_3661	-	GTGACCTATGCACCAGACGTACTTCCAGATGACAGTTGTCCATAAAATGAAGAAATGGAGATCGGAAGAGCGGTTTCAG
chr1	9775549	9775588	PIK3CD_3662	-	GTGACCTATGCACCAGACGTAGTACCCTGTCAGCCCTCCACCAAGGCAGCCACTGGGAAGATCGGAAGAGCGGTTTCAG
chr1	9775857	9775896	PIK3CD_3663	-	GTGACCTATGCACCAGACGTGGGAGGGCTGGGTGAGCGGGTGGGGCAGGCAGGGCCAGCCAGATCGGAAGAGCGGTTTCAG
chr1	9776448	9776487	PIK3CD_3664	-	GTGACCTATGCACCAGACGTGAGGGAGGTACGTCTCTGCCCTCGAGGCCCCCGGGGTTAGATCGGAAGAGCGGTTTCAG
chr1	9776967	9777006	PIK3CD_3665	-	GTGACCTATGCACCAGACGTGTGCAGGGTGAAGCGGCTGGTGGGGCGGCCCAACCACTCCAGATCGGAAGAGCGGTTTCAG
chr1	9777545	9777584	PIK3CD_3666	-	GTGACCTATGCACCAGACGTGGGAAGCAGGGCTGTTAACACGGCTCAAAGTGCAGCTTGATAGATCGGAAGAGCGGTTTCAG
chr1	9778702	9778741	PIK3CD_3667	-	GTGACCTATGCACCAGACGTGGCCGGATGATGGGTGAGGAGGCAGAGGCCAGCCCTCAGATCGGAAGAGCGGTTTCAG
chr1	9779929	9779968	PIK3CD_3668	-	GTGACCTATGCACCAGACGTACAGGGCAGGTGAGGACAGCCACTCAGGGGCTCCAGACCAGATCGGAAGAGCGGTTTCAG
chr1	9780120	9780159	PIK3CD_3669	-	GTGACCTATGCACCAGACGTGGGCAGATGAAGTTGTAGAGGGTGAACAGCATCTCTGGGAGATCGGAAGAGCGGTTTCAG
chr1	9780619	9780658	PIK3CD_3670	-	GTGACCTATGCACCAGACGTGGCTGCACCTCAGCGTCCCCAGGGGCTGGACCAGCCCGGAGATCGGAAGAGCGGTTTCAG
chr1	9780750	9780789	PIK3CD_3671	-	GTGACCTATGCACCAGACGTGGGCAGGAGTGAAGGGCTCTGGTTCACGCGGGCTCCATGAGATCGGAAGAGCGGTTTCAG
chr1	9781452	9781491	PIK3CD_3672	-	GTGACCTATGCACCAGACGTGGAGGGCTGGGGCTCCGACTCCCGCAGGCAGGACAGATCGGAAGAGCGGTTTCAG
chr1	9781769	9781808	PIK3CD_3673	-	GTGACCTATGCACCAGACGTAAAGGAGGGCTGAGCCTCAGCAGGCAGCACCCAGATCGGAAGAGCGGTTTCAG
chr1	9781983	9782022	PIK3CD_3674	-	GTGACCTATGCACCAGACGTGATGGGAGGGCGGGTGGGCAGGTCCCAGCCTCGACCAAGATCGGAAGAGCGGTTTCAG
chr1	9782252	9782291	PIK3CD_3675	-	GTGACCTATGCACCAGACGTAGAGAGCGGGCAGTACAGAGGGGCTCCTTACCAGCCCTCAGATCGGAAGAGCGGTTTCAG
chr1	9782536	9782575	PIK3CD_3676	-	GTGACCTATGCACCAGACGTGGCCGGTGGGAGGAGAAGCGTGAGTTTCTGGTAGGTTCTCAGATCGGAAGAGCGGTTTCAG
chr1	9783133	9783172	PIK3CD_3677	-	GTGACCTATGCACCAGACGTGGGAAGAGGGCAGGGCAAATGGCATGGTCAAGGGCTGCCAGATCGGAAGAGCGGTTTCAG
chr1	9784284	9784323	PIK3CD_3678	-	GTGACCTATGCACCAGACGTGGGAGAGGGAGGGGAGATTGAGAAGGTGCAGACAGGAGAGATCGGAAGAGCGGTTTCAG
chr1	9784812	9784851	PIK3CD_3679	-	GTGACCTATGCACCAGACGTGGGACAGAGGAAGTGAGGCTCTGGGAACTCCCAGCCACAGAGATCGGAAGAGCGGTTTCAG
chr1	9786917	9786956	PIK3CD_3680	-	GTGACCTATGCACCAGACGTATCACAGCGGTGTCCACGTTAAGGGGGCCCGACCTTGCTAGATCGGAAGAGCGGTTTCAG
chr19	18266640	18266679	PIK3R2_3681	-	GTGACCTATGCACCAGACGTGTGGGGTGGGGTCTGGATGGTTAGGTGGCTGCTTGGAGCCAGATCGGAAGAGCGGTTTCAG
chr19	18271231	18271270	PIK3R2_3682	-	GTGACCTATGCACCAGACGTAAACAGGGGGGTTGCATGTTGGTGGGGTCTTGGAAAGGAGAGATCGGAAGAGCGGTTTCAG
chr19	18271679	18271718	PIK3R2_3683	-	GTGACCTATGCACCAGACGTAGGGGACAGCGGAGTCAAGCTTCAAATGCTGCCCCAGCTAGATCGGAAGAGCGGTTTCAG
chr19	18271814	18271853	PIK3R2_3684	-	GTGACCTATGCACCAGACGTAGGGGGGCACAGCTCCAACTCATGTACTGGGGCCCAAGATCGGAAGAGCGGTTTCAG
chr19	18272039	18272078	PIK3R2_3685	-	GTGACCTATGCACCAGACGTATGGCCAGGGCAGGGTGAAGCAGGCTGGGGCTCCACCAAGATCGGAAGAGCGGTTTCAG
chr19	18272726	18272765	PIK3R2_3686	-	GTGACCTATGCACCAGACGTAGGGGAGTGTGGTGAAGGCTGGGTAGGGCTGTCCGCCAAGATCGGAAGAGCGGTTTCAG
chr19	18272962	18273001	PIK3R2_3687	-	GTGACCTATGCACCAGACGTGAAACAAATGCATCCTGAGCACCGACTGTATACTGTGGAGATCGGAAGAGCGGTTTCAG
chr19	18273168	18273207	PIK3R2_3688	-	GTGACCTATGCACCAGACGTATCCAACATGGGACTGCCGACCCACCTGGAGACCCCGCTAGATCGGAAGAGCGGTTTCAG
chr19	18273727	18273766	PIK3R2_3689	-	GTGACCTATGCACCAGACGTAGAGGGGTGTCCGACCTGTCGGCAGCCAGTGGACCCCGCACCTGACCCAGATCGGAAGAGCGGTTTCAG
chr19	18274023	18274062	PIK3R2_3690	-	GTGACCTATGCACCAGACGTGTGGCGGAATGAGGGGAGATGCATAGCCTGGTGGGTCTAAGATCGGAAGAGCGGTTTCAG
chr19	18276920	18276959	PIK3R2_3691	-	GTGACCTATGCACCAGACGTGGGCAGCTCAGCACCTCTGGGACTCCCCAAAAGGCCAGATCGGAAGAGCGGTTTCAG
chr19	18279486	18279525	PIK3R2_3692	-	GTGACCTATGCACCAGACGTGGGCGTGGCGGGGAGGGCCCTGTACTCACTGACCTGCCAGCAGATCGGAAGAGCGGTTTCAG
chr19	18279847	18279886	PIK3R2_3693	-	GTGACCTATGCACCAGACGTAGACGAGAGGGGGAGTGGAAAGGCTGGCCCTCCCGCCAAGATCGGAAGAGCGGTTTCAG
chr7	113517728	113517767	PPP1R3A_3694	-	GTGACCTATGCACCAGACGTACTATTCTCTTAAAAGATAAGCTATTTAAACCCAAACAAGATCGGAAGAGCGGTTTCAG
chr7	113522044	113522083	PPP1R3A_3695	-	GTGACCTATGCACCAGACGTGGTTGGTGGCCAGGTATAGAGAAGATGAATCCATTTCTGTAGATCGGAAGAGCGGTTTCAG
chr7	113522267	113522306	PPP1R3A_3696	-	GTGACCTATGCACCAGACGTTCATTAATTTTAAAACAAATTTGTCTCTTTTGTGAAAGTAGATCGGAAGAGCGGTTTCAG
chr7	113558220	113558259	PPP1R3A_3697	-	GTGACCTATGCACCAGACGTATCTACATATTTATTATTACAAATCTTAAAGTTTTATAGATCGGAAGAGCGGTTTCAG
chr7	113558611	113558650	PPP1R3A_3698	-	GTGACCTATGCACCAGACGTGTCTCTTCTGGGTCTACAAGTATCAAGGGTATTATTCGAAGATCGGAAGAGCGGTTTCAG
chr7	113518208	113518247	PPP1R3A_3699	-	GTGACCTATGCACCAGACGTCTTATCTGAGTCTAAACCTGAAGAAGTTCCAGAAGTTTCAGATCGGAAGAGCGGTTTCAG
chr7	113518688	113518727	PPP1R3A_3700	-	GTGACCTATGCACCAGACGTGTTGTAATGTACTGTGATGAATGAAGAAGGAGGAAATCGGAAGAGCGGTTTCAG
chr7	113519168	113519207	PPP1R3A_3701	-	GTGACCTATGCACCAGACGTATAATAGCCACAGCATAAAACAAAGTTGGAATGTTCTGGAAGATCGGAAGAGCGGTTTCAG
chr7	113519648	113519687	PPP1R3A_3702	-	GTGACCTATGCACCAGACGTGAGATTTCCATTAGATACGTGGCATGTCTCAAAGAATCAGATCGGAAGAGCGGTTTCAG
chr11	111597639	111597678	PPP2R1B_3703	-	GTGACCTATGCACCAGACGTAAAAAAGAAACATAAAAAATAAAGTACCACACATATTGAGATCGGAAGAGCGGTTTCAG
chr11	111608122	111608161	PPP2R1B_3704	-	GTGACCTATGCACCAGACGTGAAAGCCTGGGGTCAAGTCTGCCCTCAGGGCTGCGGGCAAGATCGGAAGAGCGGTTTCAG
chr11	111612270	111612309	PPP2R1B_3705	-	GTGACCTATGCACCAGACGTGAGGAAAAGCCCTTACTAGATTCTTGACAAAATTTAGATCGGAAGAGCGGTTTCAG
chr11	111612727	111612766	PPP2R1B_3706	-	GTGACCTATGCACCAGACGTCTTTTGGCTTTGCTTGGCTTACTGCTTGGTTAACTGGGAAGATCGGAAGAGCGGTTTCAG
chr11	111613197	111613236	PPP2R1B_3707	-	GTGACCTATGCACCAGACGTAGTGTGTTAGTCTGTTTTAAAAGTGTACTTTAAATTTTACAGATCGGAAGAGCGGTTTCAG
chr11	111614050	111614089	PPP2R1B_3708	-	GTGACCTATGCACCAGACGTACAACTGTTATTGCTAAGCTTAATCATTAAAGCAAATTAGATCGGAAGAGCGGTTTCAG
chr11	111618628	111618667	PPP2R1B_3709	-	GTGACCTATGCACCAGACGTAAAAACAGATTATGAAAGCCCATATATCCATGATTTTCAAGATCGGAAGAGCGGTTTCAG
chr11	111622833	111622872	PPP2R1B_3710	-	GTGACCTATGCACCAGACGTGTTGCTCCATGAACTGCAGGGTAGTGTGCAGATAGTGACAAAGATCGGAAGAGCGGTTTCAG
chr11	111624117	111624156	PPP2R1B_3711	-	GTGACCTATGCACCAGACGTCTTTATGTTTCTGGCTTTGATGATAATTTGATTTTATAGATCGGAAGAGCGGTTTCAG
chr11	111625173	111625212	PPP2R1B_3712	-	GTGACCTATGCACCAGACGTCTTTATGTTTCTTACTCTCTTTTATATGAAGGTAACCTAGATCGGAAGAGCGGTTTCAG



chr11	111625654	111625693	PPP2R1B_3713	-	GTGACCTATGCACCAGACGTTCAATTTATGTTGGAACATGTGTCATTCAATTTTGGTGCATAGATCGGAAGAGCGGTTTCAG
chr11	111625969	111626008	PPP2R1B_3714	-	GTGACCTATGCACCAGACGTCATTTTTAAAGTACTAAGGAAATAAACCTGAAAAACATAGAGATCGGAAGAGCGGTTTCAG
chr11	111630478	111630517	PPP2R1B_3715	-	GTGACCTATGCACCAGACGTTCTTAGTATTTAAGGGACACAGATATGCTCCTTCTCTAAGATCGGAAGAGCGGTTTCAG
chr11	111631493	111631532	PPP2R1B_3716	-	GTGACCTATGCACCAGACGTTGATTTTTTGCCTTGTAAAGCAGAAAATCAGGTAGTAAGAGATCGGAAGAGCGGTTTCAG
chr11	111635479	111635518	PPP2R1B_3717	-	GTGACCTATGCACCAGACGTATAAGCTGCCTACCCTCCTTACAACTTTTGCAGTATAAAGATCGGAAGAGCGGTTTCAG
chr11	111635968	111636007	PPP2R1B_3718	-	GTGACCTATGCACCAGACGTTCTTTGTTAAAGAAAGTAGGGACATTCATTTCCAGTAAGATCGGAAGAGCGGTTTCAG
chr11	111636922	111636961	PPP2R1B_3719	-	GTGACCTATGCACCAGACGTGAGGCCGGGGACCCGAGCCGAGACCCGGTGGTCCGCTGGTAGATCGGAAGAGCGGTTTCAG
chr12	70915219	70915258	PTPRB_3720	-	GTGACCTATGCACCAGACGTGAAGAGCTCCTGGATAAAAATTATTCACTGTGTGATTTGTAGATCGGAAGAGCGGTTTCAG
chr12	70918201	70918240	PTPRB_3721	-	GTGACCTATGCACCAGACGTACTTCACTTACTTCCCAAGTTTCTTCATCAAGATATGGTAGATCGGAAGAGCGGTTTCAG
chr12	70925765	70925804	PTPRB_3722	-	GTGACCTATGCACCAGACGTAGACTGAAAGTTACAGGCCACCCTCCTCCCCACTGTATTAGATCGGAAGAGCGGTTTCAG
chr12	70928218	70928257	PTPRB_3723	-	GTGACCTATGCACCAGACGTACCTAGCAGCCAATAAAATGGCAGCCATAAGGGGGTTGTGAGATCGGAAGAGCGGTTTCAG
chr12	70928563	70928602	PTPRB_3724	-	GTGACCTATGCACCAGACGTTTGCTTGACTTAAACAACCGAGCTGGGAGATGAATGAGAAGATCGGAAGAGCGGTTTCAG
chr12	70929755	70929794	PTPRB_3725	-	GTGACCTATGCACCAGACGTAGCCCTTCCTGGCATCAAAGCTTTTGACTTTCTGCCACCTGGAAGATCGGAAGAGCGGTTTCAG
chr12	70931885	70931924	PTPRB_3726	-	GTGACCTATGCACCAGACGTCACTAGGCCATAGTGTTCAGGATGAGGCTTTGGTGGGTGGAGATCGGAAGAGCGGTTTCAG
chr12	70932654	70932693	PTPRB_3727	-	GTGACCTATGCACCAGACGTTGTCAAATTTGTAATACTGTCTTCTCTAGCCATTTCTGAGATCGGAAGAGCGGTTTCAG
chr12	70933355	70933394	PTPRB_3728	-	GTGACCTATGCACCAGACGTGGCAGAATGAAGCTTCAGCATCCCTAGTTCTTAGCAGAAATAGATCGGAAGAGCGGTTTCAG
chr12	70933557	70933596	PTPRB_3729	-	GTGACCTATGCACCAGACGTGAACACATTAATCTATATTTACTGCTTTGAAATATGAAGATCGGAAGAGCGGTTTCAG
chr12	70933669	70933708	PTPRB_3730	-	GTGACCTATGCACCAGACGTGACCTTCTGATAATTTGTTGAAAGATGGTATTATGTAGATCGGAAGAGCGGTTTCAG
chr12	70934588	70934627	PTPRB_3731	-	GTGACCTATGCACCAGACGTAGATCCTTTTGTTGGTAGTGACCACAACCTTTAAAAATGCAAGATCGGAAGAGCGGTTTCAG
chr12	70938287	70938326	PTPRB_3732	-	GTGACCTATGCACCAGACGTCTTTACATCATGTTCTACCAACTGCCATGTCACCTACAAAGATCGGAAGAGCGGTTTCAG
chr12	70946507	70946546	PTPRB_3733	-	GTGACCTATGCACCAGACGTTTACCACGTGTTTTGCTAGAAGGGACATGCTACATTACTAAAGATCGGAAGAGCGGTTTCAG
chr12	70948890	70948929	PTPRB_3734	-	GTGACCTATGCACCAGACGTATGAGTTAACTCCACTCTGAGACACAGAATGCTTCTCAAGATCGGAAGAGCGGTTTCAG
chr12	70949600	70949639	PTPRB_3735	-	GTGACCTATGCACCAGACGTGAGGCTGCGCACAGACAGCCCTCTGCACTGGAGTGAAGGAGATCGGAAGAGCGGTTTCAG
chr12	70953073	70953112	PTPRB_3736	-	GTGACCTATGCACCAGACGTTTTTGCTACTCTTATTTCTCAAATGGAGTAGAGGAAGTATAGCTCGGAAGAGCGGTTTCAG
chr12	70954401	70954440	PTPRB_3737	-	GTGACCTATGCACCAGACGTGAGGTGCCAATGGCCAAGGGATGGTGGGAAGTAGCTTCCAAGATCGGAAGAGCGGTTTCAG
chr12	70956574	70956613	PTPRB_3738	-	GTGACCTATGCACCAGACGTGACCCAAGCAGTAATGAATCGTGGGGGAATGTCCCGGTAAAGATCGGAAGAGCGGTTTCAG
chr12	70960165	70960204	PTPRB_3739	-	GTGACCTATGCACCAGACGTGAGCATAATGTTTTGTAGCACAATTTGCCAATGTCTGTGTAAGATCGGAAGAGCGGTTTCAG
chr12	70963405	70963444	PTPRB_3740	-	GTGACCTATGCACCAGACGTACCTGGAGAAGGCTAGATTGTAGAATGCCCTCATGGTTCTAGATCGGAAGAGCGGTTTCAG
chr12	70964756	70964795	PTPRB_3741	-	GTGACCTATGCACCAGACGTATACTGTTCTTGAACCTGAATAGATGCAGTGGTGCATTTAAGATCGGAAGAGCGGTTTCAG
chr12	70965554	70965593	PTPRB_3742	-	GTGACCTATGCACCAGACGTGATTTGCAAATCTGACAGTTGGTTGGACTTGAAGTCTCAGATCGGAAGAGCGGTTTCAG
chr12	70970112	70970151	PTPRB_3743	-	GTGACCTATGCACCAGACGTATGAAGTTTCAGGGCTCCGTAAGAACCAATTCACATGTGGAGATCGGAAGAGCGGTTTCAG
chr12	70974766	70974805	PTPRB_3744	-	GTGACCTATGCACCAGACGTGAGATATGTGTCTGTGACTTAACTAAGATCTGAGTACATGAGATCGGAAGAGCGGTTTCAG
chr12	70980737	70980776	PTPRB_3745	-	GTGACCTATGCACCAGACGTTTATAAATTTTACATTTTAAAGTGTCTGTCTGTGTAATTAGATCGGAAGAGCGGTTTCAG
chr12	70983694	70983733	PTPRB_3746	-	GTGACCTATGCACCAGACGTGAAGATGTTAATCCCAATGGAAGAGTAATTTGTTCCCTAGATCGGAAGAGCGGTTTCAG
chr12	70986012	70986051	PTPRB_3747	-	GTGACCTATGCACCAGACGTGGCTCCAGAATGTTCTTGGTTGCTGCAACTCACTCTCTGAAGATCGGAAGAGCGGTTTCAG
chr12	70988197	70988236	PTPRB_3748	-	GTGACCTATGCACCAGACGTCTAGCTAGCTGAAGAAGAATAAAGTGAATCAAGGGAAATAGATCGGAAGAGCGGTTTCAG
chr12	70989779	70989818	PTPRB_3749	-	GTGACCTATGCACCAGACGTTTTATTTTATAGCTGAGTAGTTAATAGGATACTTTTCAAGAGATCGGAAGAGCGGTTTCAG
chr12	71002799	71002838	PTPRB_3750	-	GTGACCTATGCACCAGACGTACAGGTGCAATGGATGGCCAAGCCACACGGGGTTGGCCAGATCGGAAGAGCGGTTTCAG
chr12	71003491	71003530	PTPRB_3751	-	GTGACCTATGCACCAGACGTGAGAAGGGGTCAGAGCTGATGCGCCCCCTCCCCGCCAAAGATCGGAAGAGCGGTTTCAG
chr12	71016120	71016159	PTPRB_3752	-	GTGACCTATGCACCAGACGTGGGGTGTGGAGTGTGGTCTGTCACGCTCAGGAGGCTAGATCGGAAGAGCGGTTTCAG
chr12	71029401	71029440	PTPRB_3753	-	GTGACCTATGCACCAGACGTCTTTTCTAGTACAATAATCCTGAAATGCTTCTACTAAATATCAGATCGGAAGAGCGGTTTCAG
chr12	71031071	71031110	PTPRB_3754	-	GTGACCTATGCACCAGACGTCTGCCTCAGTGTCTGAGGCAATTTCTTCAAGATCTAGCCAAGATCGGAAGAGCGGTTTCAG
chr6	117609605	117609644	ROS1_3755	-	GTGACCTATGCACCAGACGTTGGGAAATAGAGAGTTGAGATAAACACTCTCATTCACTAGATCGGAAGAGCGGTTTCAG
chr6	117622087	117622126	ROS1_3756	-	GTGACCTATGCACCAGACGTTTCTTCAAGATTTTCTAGTTTTCTGCTGCACTGTGAACTGAAGATCGGAAGAGCGGTTTCAG
chr6	117629907	117629946	ROS1_3757	-	GTGACCTATGCACCAGACGTTATGTTAACATATGTAATCCCCAACAAAAACATGTGCACAGATCGGAAGAGCGGTTTCAG
chr6	117632133	117632172	ROS1_3758	-	GTGACCTATGCACCAGACGTTCTTGGATACGGGTTATTACGGATATTGGCACAATAATAGATCGGAAGAGCGGTTTCAG
chr6	117638256	117638295	ROS1_3759	-	GTGACCTATGCACCAGACGTGGGATCCATAATATTGGTTTCTAATGCAAATGCCCTATAAGATCGGAAGAGCGGTTTCAG
chr6	117639301	117639340	ROS1_3760	-	GTGACCTATGCACCAGACGTAAATAATTTCTCCTGGTATGGGTAAGAAGTTTTAAGTCCGAGATCGGAAGAGCGGTTTCAG
chr6	117640981	117641020	ROS1_3761	-	GTGACCTATGCACCAGACGTCTTTCGAACCTCTGACACATTATATCACCATATCTACAAAGATCGGAAGAGCGGTTTCAG
chr6	117642372	117642411	ROS1_3762	-	GTGACCTATGCACCAGACGTTTGCCATCATTATGGAGCACCTAGGCAAAAGGTTGGCAAAGATCGGAAGAGCGGTTTCAG
chr6	117645445	117645484	ROS1_3763	-	GTGACCTATGCACCAGACGTGAGATTTTTAAATAGGCAACAAACTGTTTACTTAAATCAAGATCGGAAGAGCGGTTTCAG
chr6	117647337	117647376	ROS1_3764	-	GTGACCTATGCACCAGACGTAGTCTGTCTGACACACTGACTTATTACCTAAAAGTTTCACTAGATCGGAAGAGCGGTTTCAG
chr6	117650442	117650481	ROS1_3765	-	GTGACCTATGCACCAGACGTTTGCAAAGTACTTTGAAATGACAAAGAACTAAGAAGATAAAGATCGGAAGAGCGGTTTCAG
chr6	117658285	117658324	ROS1_3766	-	GTGACCTATGCACCAGACGTACATACTCAATACTCAGAAAACCTGTGTTTCAGTTTTTATAGATCGGAAGAGCGGTTTCAG
chr6	117662248	117662287	ROS1_3767	-	GTGACCTATGCACCAGACGTTAATGCAAGTCTTTATTTTATGATAGAATAAATGGAAAAGATCGGAAGAGCGGTTTCAG
chr6	117662513	117662552	ROS1_3768	-	GTGACCTATGCACCAGACGTTTACTAGGCACTTTTATTGTCTATTCTCAAGTGAAGGCAGATCGGAAGAGCGGTTTCAG
chr6	117663513	117663552	ROS1_3769	-	GTGACCTATGCACCAGACGTTGGCTTTGTTGGTTCTTCAAGCAGAATATTGTGATATAGATCGGAAGAGCGGTTTCAG
chr6	117665173	117665212	ROS1_3770	-	GTGACCTATGCACCAGACGTTAAGTGTGGTCTTTGCTTTTCCACAAGATGTTCTTTTTGAGATCGGAAGAGCGGTTTCAG

chr6	117674103	117674142	ROS1_3771	-	GTGACCTATGCACCAGACGTACATTGCGTAACTAGCTTTGTTCTCCCAATTAGGGTCCAGAAGATCGGAAGAGCGGTTTCAG
chr6	117677742	117677781	ROS1_3772	-	GTGACCTATGCACCAGACGTGATGATGTGCACAGATATTTGTTAATAAGAGCAGCCCTAGATCGGAAGAGCGGTTTCAG
chr6	117678917	117678956	ROS1_3773	-	GTGACCTATGCACCAGACGTGCAAGTATTTTTTATATTGTGATGAAATAGATATAGACAAGATCGGAAGAGCGGTTTCAG
chr6	117680922	117680961	ROS1_3774	-	GTGACCTATGCACCAGACGTATGTAATTCTCCGAAATAAAGGAAGTGAAGTATTGTCATAGATCGGAAGAGCGGTTTCAG
chr6	117683716	117683755	ROS1_3775	-	GTGACCTATGCACCAGACGTGAAAACAGAAAGATAGAGAGTCTTAATAGCCGCATTGTGGAGATCGGAAGAGCGGTTTCAG
chr6	117686173	117686212	ROS1_3776	-	GTGACCTATGCACCAGACGTAAAATCTGTCTTTTTCTTAAAAAAGCAGAATCTCACTTAGATCGGAAGAGCGGTTTCAG
chr6	117686694	117686733	ROS1_3777	-	GTGACCTATGCACCAGACGTGGTTCTAGTAGTACCTTTTCAATTTCCCAAACAGACTGTACCTCAGATCGGAAGAGCGGTTTCAG
chr6	117687189	117687228	ROS1_3778	-	GTGACCTATGCACCAGACGTTCATTCTGCTTACCCTACTCCACTATACCTTCAGTTAAAAGATCGGAAGAGCGGTTTCAG
chr6	117700172	117700211	ROS1_3779	-	GTGACCTATGCACCAGACGTTCCCTCAAAGGCAATTGATTGAGAAGAAAACCTTGCAGTCAGATCGGAAGAGCGGTTTCAG
chr6	117704430	117704469	ROS1_3780	-	GTGACCTATGCACCAGACGTAAAAGATCTGATCATTAGTAATACTGAATAGCTCTATATAGATCGGAAGAGCGGTTTCAG
chr6	117708002	117708041	ROS1_3781	-	GTGACCTATGCACCAGACGTAGTCTCTGTTCCTCACTTGAATGACAGATTTTCTACTATAAGAGATCGGAAGAGCGGTTTCAG
chr6	117708893	117708932	ROS1_3782	-	GTGACCTATGCACCAGACGTGTTCTGGATTTAGGGAGTGACTCTACAAAAAGAGGACTAAGATCGGAAGAGCGGTTTCAG
chr6	117710463	117710502	ROS1_3783	-	GTGACCTATGCACCAGACGTGTGCCACAGCTGCCCTGCGCTTACTGCGCTTGTGGAATAAGAGGAAGATCGGAAGAGCGGTTTCAG
chr6	117714337	117714376	ROS1_3784	-	GTGACCTATGCACCAGACGTGCGCTTGTAAAGATGAATCTCTTCCATTGGGAATAAATAAAGATCGGAAGAGCGGTTTCAG
chr6	117715275	117715314	ROS1_3785	-	GTGACCTATGCACCAGACGTGAAGTAAAGAGGAATAGTGATAGACAGTGATACTGATATAGATCGGAAGAGCGGTTTCAG
chr6	117715729	117715768	ROS1_3786	-	GTGACCTATGCACCAGACGTAAAGGATAAATGATTCTTATGTTGTAAGAAAGATTTCAAAGATCGGAAGAGCGGTTTCAG
chr6	117717301	117717340	ROS1_3787	-	GTGACCTATGCACCAGACGTGGCTTCTTCCCTTAGCTACACAGGAATGAGGGTGGCAAGGATCGGAAGAGCGGTTTCAG
chr6	117718028	117718067	ROS1_3788	-	GTGACCTATGCACCAGACGTAGTGATACAGGAAAATGTAAACAGCATGGCTGCAGGCAAGATCGGAAGAGCGGTTTCAG
chr6	117724252	117724291	ROS1_3789	-	GTGACCTATGCACCAGACGTACACACTTCTTATAAGAGGACATTATTTCAAAGCTTTGGAAGATCGGAAGAGCGGTTTCAG
chr6	117730695	117730734	ROS1_3790	-	GTGACCTATGCACCAGACGTACACACGACTTTTTAAAAATAGGCTGCACCCTCTAGTGAAGATCGGAAGAGCGGTTTCAG
chr6	117737371	117737410	ROS1_3791	-	GTGACCTATGCACCAGACGTATTAGATTCTTATTTTATGACTGATGTTTCTTTCAAAGAGGAGATCGGAAGAGCGGTTTCAG
chr6	117739575	117739614	ROS1_3792	-	GTGACCTATGCACCAGACGTCTTCTCAGTTGTCAAGAATTTACATGTTTGTGTTGATAAAGATCGGAAGAGCGGTTTCAG
chr6	117746647	117746686	ROS1_3793	-	GTGACCTATGCACCAGACGTCAATCTAATATTTGTCTTTGAGAGACTAGAACCTGTAGCAGATCGGAAGAGCGGTTTCAG
chr6	166826200	166826239	RPS6KA2_3794	-	GTGACCTATGCACCAGACGTCTGCCCCAGCTGCCCTGCCAGCTCCCTCGTCCAGTCAAGATCGGAAGAGCGGTTTCAG
chr6	166827232	166827271	RPS6KA2_3795	-	GTGACCTATGCACCAGACGTGCGACAGTGAGGACAGAGTGGTGGGAATGGGAAACCCAGAAGATCGGAAGAGCGGTTTCAG
chr6	166831663	166831702	RPS6KA2_3796	-	GTGACCTATGCACCAGACGTGCCACAGCTTGTCTTTAAATATTCAGATTCTGAATAGCAGATCGGAAGAGCGGTTTCAG
chr6	166833320	166833359	RPS6KA2_3797	-	GTGACCTATGCACCAGACGTACCTCAAACAGGTGTCCAGGAGGAGACACAGGGCAGCAGCCAGATCGGAAGAGCGGTTTCAG
chr6	166836694	166836733	RPS6KA2_3798	-	GTGACCTATGCACCAGACGTCCCGACTGCCAGACCCCGCTCTATATGCCCAAAGCAGGAGATCGGAAGAGCGGTTTCAG
chr6	166843891	166843930	RPS6KA2_3799	-	GTGACCTATGCACCAGACGTGGCTGGCGAGCCTTCCGGGAGGAGCGGCTTCAGGGCAAGATCGGAAGAGCGGTTTCAG
chr6	166845839	166845878	RPS6KA2_3800	-	GTGACCTATGCACCAGACGTCCCGTGCAACAGCATCTCCACTTCTGTTCTTCAACAGATCGGAAGAGCGGTTTCAG
chr6	166862162	166862201	RPS6KA2_3801	-	GTGACCTATGCACCAGACGTCTGCTGAGTGAGCAGGGCCCTGTGTGAGTGACGCGCTGAGATCGGAAGAGCGGTTTCAG
chr6	166864541	166864580	RPS6KA2_3802	-	GTGACCTATGCACCAGACGTGGCTGACGTGGGTTGGGGGTAAGAGGGCACTTGGATGAAGATCGGAAGAGCGGTTTCAG
chr6	166872887	166872926	RPS6KA2_3803	-	GTGACCTATGCACCAGACGTGACGTGGTCCCTCTATCGTGGCTTCTCCACCTGACCCAGATCGGAAGAGCGGTTTCAG
chr6	166883279	166883318	RPS6KA2_3804	-	GTGACCTATGCACCAGACGTGCCACAGTCCCACCTGCACACGCTGACACAGAAGTGGAGATCGGAAGAGCGGTTTCAG
chr6	166902271	166902310	RPS6KA2_3805	-	GTGACCTATGCACCAGACGTCCCGGACACCCACCCAGGAGCTGACAGGGCTGCCCCAGATCGGAAGAGCGGTTTCAG
chr6	166904109	166904148	RPS6KA2_3806	-	GTGACCTATGCACCAGACGTGGGAGCCACCCAGAGACTGCGAGCACCTTCTGATATCAGATCGGAAGAGCGGTTTCAG
chr6	166911946	166911985	RPS6KA2_3807	-	GTGACCTATGCACCAGACGTCCCGACCTCTTCTGTGCCATGGCGCTGTTCCCCACGTGAGATCGGAAGAGCGGTTTCAG
chr6	166914325	166914364	RPS6KA2_3808	-	GTGACCTATGCACCAGACGTGACGCGCAGGCCCTCCATGGCTTCATCTCAGCCCTGGTAAGATCGGAAGAGCGGTTTCAG
chr6	166917944	166917983	RPS6KA2_3809	-	GTGACCTATGCACCAGACGTAAAACACTAGGGCTGACTTCCCCACGCCATCAGCTCCATGAGATCGGAAGAGCGGTTTCAG
chr6	166921641	166921680	RPS6KA2_3810	-	GTGACCTATGCACCAGACGTGCCACATCACACAGGAGGGCGGGCAGGAGCTTCTGTGAGATCGGAAGAGCGGTTTCAG
chr6	166923715	166923754	RPS6KA2_3811	-	GTGACCTATGCACCAGACGTTCAAATGACACTTTAAAGAGGACCCAGGCAACCTTCTCAGATCGGAAGAGCGGTTTCAG
chr6	166944670	166944709	RPS6KA2_3812	-	GTGACCTATGCACCAGACGTGCGAAGGGCCGGCTGCTTCAGAGACAGGTAACCTGCAATTTAGATCGGAAGAGCGGTTTCAG
chr6	166952106	166952145	RPS6KA2_3813	-	GTGACCTATGCACCAGACGTCCCTGGCTGTCTTGGAGTCTATTCTTCAACACAAAGGAAGATCGGAAGAGCGGTTTCAG
chr6	167040359	167040398	RPS6KA2_3814	-	GTGACCTATGCACCAGACGTGCCCTCGGGGCGCGCAGTGTCCGGCCTGAGCGGGCCGAGATCGGAAGAGCGGTTTCAG
chr6	167271638	167271677	RPS6KA2_3815	-	GTGACCTATGCACCAGACGTACTGTTTTATTACACTGCTGTTTTGGGAGATTGGCCAGATCGGAAGAGCGGTTTCAG
chr6	167275546	167275585	RPS6KA2_3816	-	GTGACCTATGCACCAGACGTGAGAGAACGCATTTTACAGACTCTCAAGATCCGAAACAGATCGGAAGAGCGGTTTCAG
chr1	17345326	17345365	SDHB_3817	-	GTGACCTATGCACCAGACGTGCTAAACATGATTTATAACCAGCTCAGAGCTGAACATAATAGATCGGAAGAGCGGTTTCAG
chr1	17349053	17349092	SDHB_3818	-	GTGACCTATGCACCAGACGTCTGGTGACCCTCAGCTCTGCCCTCAGAGCTGACACGCCAGAAGATCGGAAGAGCGGTTTCAG
chr1	17350418	17350457	SDHB_3819	-	GTGACCTATGCACCAGACGTCTTAATTGCTTTAAGAGAAATTGAAACTCAAGCATCCAGAGATCGGAAGAGCGGTTTCAG
chr1	17354194	17354233	SDHB_3820	-	GTGACCTATGCACCAGACGTCTATTTATTGTTTCAATCTGAAGAATTTATGCAAAGATAGATCGGAAGAGCGGTTTCAG
chr1	17355045	17355084	SDHB_3821	-	GTGACCTATGCACCAGACGTGCATCTCTGTTTTGTTTTATTGTCATGGGGGCGAGTAGATCGGAAGAGCGGTTTCAG
chr1	17359505	17359544	SDHB_3822	-	GTGACCTATGCACCAGACGTCTTCTCTGGCTCCAGATCTGTGGCTTTCCAAAGAAAGATCGGAAGAGCGGTTTCAG
chr1	17371206	17371245	SDHB_3823	-	GTGACCTATGCACCAGACGTCTGTGAAAGCCAGCTATTGAAGGAGAGTTCTTGTATTGATAGATCGGAAGAGCGGTTTCAG
chr1	17380393	17380432	SDHB_3824	-	GTGACCTATGCACCAGACGTGAGCCTCAGAGAGGGAAAAGTCAAGAAAACCCAGAGACTAGATCGGAAGAGCGGTTTCAG
chr12	53774026	53774065	SP1_3825	-	GTGACCTATGCACCAGACGTGAGGGAACAAGCTCAAGGGGCTCCTGTCGGGGGGGTTGGGAGATCGGAAGAGCGGTTTCAG
chr12	53775393	53775432	SP1_3826	-	GTGACCTATGCACCAGACGTAAAAAACAACAACGTAAACTTGAGGGAAGAAAAGAAATAGATCGGAAGAGCGGTTTCAG
chr12	53775407	53775446	SP1_3827	-	GTGACCTATGCACCAGACGTGAGTAAAGATAAATAACAACAACGTAAACTTGAGAGATCGGAAGAGCGGTTTCAG
chr12	53775844	53775883	SP1_3828	-	GTGACCTATGCACCAGACGTTAGGAAAGAGAAAAGAGTTAGTGACACCCAGCTGCAGAGATCGGAAGAGCGGTTTCAG

chr12	53800319	53800358	SP1_3829	-	GTGACCTATGCACCAGACGTGAGAGAAAAGGTCACACATGTGACATGGGCAGGTTATCACAGATCGGAAGAGCGGTTTCAG
chr12	53803096	53803135	SP1_3830	-	GTGACCTATGCACCAGACGTGGACACAACGTGTAATCATTACTTCTAGAGAAAACAAAGAGATCGGAAGAGCGGTTTCAG
chr12	53804661	53804700	SP1_3831	-	GTGACCTATGCACCAGACGTGAAGAAAAGATAAGAAGCTGACATGTTAGGAAGTGAGGTTAGATCGGAAGAGCGGTTTCAG
chr12	53776222	53776261	SP1_3832	-	GTGACCTATGCACCAGACGTGGGATTACTTGATACTGAATATTAGGCATCACTCCAGGTAAGATCGGAAGAGCGGTTTCAG
chr12	53776600	53776639	SP1_3833	-	GTGACCTATGCACCAGACGTGTCCCTGAGGTGACAGGCTGTGAGCCACTCTCTGGGACCAGATCGGAAGAGCGGTTTCAG
chr12	53776978	53777017	SP1_3834	-	GTGACCTATGCACCAGACGTGTTGTAGTTGTAAGGTCGCCCTGCAAAATGGTGTCTGCTTAGATCGGAAGAGCGGTTTCAG
chr15	39874009	39874048	THBS1_3835	-	GTGACCTATGCACCAGACGTGTTGGTGCCACAGGACTCCCTGTAGCAGGAAGCACAAGAGATCGGAAGAGCGGTTTCAG
chr15	39874344	39874383	THBS1_3836	-	GTGACCTATGCACCAGACGTGGAGAGAACAAGTGAGCTTTCTAGGCTGGGACCAGCAAGATCGGAAGAGCGGTTTCAG
chr15	39875768	39875807	THBS1_3837	-	GTGACCTATGCACCAGACGTAGGACACACATTACTTGTAGAATGCAGAGCGGGTGGGGAAGATCGGAAGAGCGGTTTCAG
chr15	39876139	39876178	THBS1_3838	-	GTGACCTATGCACCAGACGTACAAAATGAAAACCTTCAAATAGATACTTACCAACCAAGCAGATCGGAAGAGCGGTTTCAG
chr15	39876451	39876490	THBS1_3839	-	GTGACCTATGCACCAGACGTGAGAATATCATAGTTGCCCCCGCATTTCAGTCATTGAGATCGGAAGAGCGGTTTCAG
chr15	39877621	39877660	THBS1_3840	-	GTGACCTATGCACCAGACGTAGAGAGTGAGAGGGGAACAGGCTGCTGAGCATGTTGCATAAGATCGGAAGAGCGGTTTCAG
chr15	39879498	39879537	THBS1_3841	-	GTGACCTATGCACCAGACGTAAACAGAGGTTTCATCAGGTCAGTGTGATGATTAGGACAAGCTGAGATCGGAAGAGCGGTTTCAG
chr15	39880193	39880232	THBS1_3842	-	GTGACCTATGCACCAGACGTGAGTTGATGGTCACAAATGGTTTTGGCTTAGAGACAGCCAAGATCGGAAGAGCGGTTTCAG
chr15	39880677	39880716	THBS1_3843	-	GTGACCTATGCACCAGACGTATGAACACAGGCAACAATTAAGATCAACTTCAAATCCCAGATCGGAAGAGCGGTTTCAG
chr15	39881110	39881149	THBS1_3844	-	GTGACCTATGCACCAGACGTGAGAGAGAGCAGTCACAGTAAATGGTTGGTCTAAGCTGCAGATCGGAAGAGCGGTTTCAG
chr15	39881353	39881392	THBS1_3845	-	GTGACCTATGCACCAGACGTAATAAGAGCGTGCATCATGTTAGAAGTCACTGCCATAAGAGATCGGAAGAGCGGTTTCAG
chr15	39881956	39881995	THBS1_3846	-	GTGACCTATGCACCAGACGTACCATGCTGCTGTTACACAGGCTTTTGTAGAAATCCCTCAGAAGATCGGAAGAGCGGTTTCAG
chr15	39882667	39882706	THBS1_3847	-	GTGACCTATGCACCAGACGTGAAGATATATCACTGCTTCAGTTGCCTTCTCATGCTGAGATCGGAAGAGCGGTTTCAG
chr15	39883342	39883381	THBS1_3848	-	GTGACCTATGCACCAGACGTAGAANAATGGAGCACTTAAACAATGTTGTCCTTGAAAACAGCAGATCGGAAGAGCGGTTTCAG
chr15	39883656	39883695	THBS1_3849	-	GTGACCTATGCACCAGACGTCAAGGGACAATAAGAGCTGGGCTCTCCAGCCTTGATGTAGATCGGAAGAGCGGTTTCAG
chr15	39884719	39884758	THBS1_3850	-	GTGACCTATGCACCAGACGTGATGTAATGGAGGGTAAATTCAGATATAAACCTTATGAGATCGGAAGAGCGGTTTCAG
chr15	39885151	39885190	THBS1_3851	-	GTGACCTATGCACCAGACGTAAAAGCAAAGAGTTTCAGAAAATCTCAAAGTCTATTATTAAGATCGGAAGAGCGGTTTCAG
chr15	39885548	39885587	THBS1_3852	-	GTGACCTATGCACCAGACGTGAGAGGAAAGAGGCTGAGTAAACCTCAGCCCTTCAGAAGGTTAGATCGGAAGAGCGGTTTCAG
chr15	39886250	39886289	THBS1_3853	-	GTGACCTATGCACCAGACGTAGGAAAAGGAAAGGTTGAAACACAGCTCCTTCAGGTAAGAGATCGGAAGAGCGGTTTCAG
chr15	39886452	39886491	THBS1_3854	-	GTGACCTATGCACCAGACGTAAAAAATCTTTGTTTGTAGTACAATGCTATTTAATACTTTTGTAGATCGGAAGAGCGGTTTCAG
chr15	39887513	39887552	THBS1_3855	-	GTGACCTATGCACCAGACGTAAACAATAATAAATAATAACAAATGAAAACATAATTCAAGATCGGAAGAGCGGTTTCAG
chr15	39874624	39874663	THBS1_3856	-	GTGACCTATGCACCAGACGTAGTGGTCTTCCGCTCCAGGGCCAGCAGCTGCCCGGGTAGATCGGAAGAGCGGTTTCAG
chr1	3598880	3598919	TP73_3857	-	GTGACCTATGCACCAGACGTCCGGCTCCGAGGGCAGCTGCTGTCAGGAAGGAAGAAAGATCGGAAGAGCGGTTTCAG
chr1	3599574	3599613	TP73_3858	-	GTGACCTATGCACCAGACGTGAGAGGAAAATGAAAGCAGTCCAGCTCCAGTTTTGGGTTCAAGATCGGAAGAGCGGTTTCAG
chr1	3607420	3607459	TP73_3859	-	GTGACCTATGCACCAGACGTGGGGGGTCTGCACACGCCAGGGAAGCTGGTGTCCCGTGGAAGATCGGAAGAGCGGTTTCAG
chr1	3624063	3624102	TP73_3860	-	GTGACCTATGCACCAGACGTAAAGGGGAGGAGGGAGGGGAAACACACAGTCAAGTCTAGATCGGAAGAGCGGTTTCAG
chr1	3638535	3638574	TP73_3861	-	GTGACCTATGCACCAGACGTGGAGAGGGAGCGGGTGAGACCAGTGGTCCCAACTGCACCCAGATCGGAAGAGCGGTTTCAG
chr1	3639868	3639907	TP73_3862	-	GTGACCTATGCACCAGACGTGGGTCGACATTCAGAGAGGTGCATAGAGGTGCCACCCCAAGATCGGAAGAGCGGTTTCAG
chr1	3643629	3643668	TP73_3863	-	GTGACCTATGCACCAGACGTGGGAGCAGGGAGAGGGCTAGCATCAGCAGCCAGCCACCCAGATCGGAAGAGCGGTTTCAG
chr1	3644142	3644181	TP73_3864	-	GTGACCTATGCACCAGACGTGGCAGACCCAGAATTGTGAGCTCAACCCTGCCACCCTCAAGATCGGAAGAGCGGTTTCAG
chr1	3644643	3644682	TP73_3865	-	GTGACCTATGCACCAGACGTAGGCAGGGCAGGGGGTGAGCAGGCAGGACCAGAGGGTGAGATCGGAAGAGCGGTTTCAG
chr1	3645841	3645880	TP73_3866	-	GTGACCTATGCACCAGACGTAGGAGCAGATCTCTGCCACGTGCCCCAGACCCCACGGGAGATCGGAAGAGCGGTTTCAG
chr1	3646514	3646553	TP73_3867	-	GTGACCTATGCACCAGACGTGCAACGGCTCGCATGGGTGGGAAGCAAGGCAGCCCTCGTGCAGATCGGAAGAGCGGTTTCAG
chr1	3647441	3647480	TP73_3868	-	GTGACCTATGCACCAGACGTGGCAGGTGGGGCCATCAGGGCAGCCAGGCTGGGCATCCAGATCGGAAGAGCGGTTTCAG
chr1	3647977	3648016	TP73_3869	-	GTGACCTATGCACCAGACGTAATTGTGAGAAAAGAAAGCAGCATTAGCTTCCGAGCACAGGGAGATCGGAAGAGCGGTTTCAG
chr1	3649261	3649300	TP73_3870	-	GTGACCTATGCACCAGACGTCCGGCGCATTAGGGGCGAGGGGCGAGTGAGCAGGGAGAGCAGATCGGAAGAGCGGTTTCAG
chr12	121746233	121746272	ANAPC5_3871	-	GTGACCTATGCACCAGACGTCTGCTGGGCTGCTGTGCAGAGTATAAGATTTTGACCTTGTAGATCGGAAGAGCGGTTTCAG
chr12	121747454	121747493	ANAPC5_3872	-	GTGACCTATGCACCAGACGTGTACGAAGACTGTTAGGCAATGCTATTCCAGAAGAAGCATTGAGATCGGAAGAGCGGTTTCAG
chr12	121756030	121756069	ANAPC5_3873	-	GTGACCTATGCACCAGACGTCTCTGTTTTATGACACATATTTGTGCTCAAGAGCTGGTGAGATCGGAAGAGCGGTTTCAG
chr12	121756254	121756293	ANAPC5_3874	-	GTGACCTATGCACCAGACGTCTTGTACATCTAGCAGATAGTGGTGTTGATCTTTCAAGATCGGAAGAGCGGTTTCAG
chr12	121757450	121757489	ANAPC5_3875	-	GTGACCTATGCACCAGACGTTTTGAAAACCTTAACCCCAAGAATAAAATAATTGTTAAATGGAGATCGGAAGAGCGGTTTCAG
chr12	121758138	121758177	ANAPC5_3876	-	GTGACCTATGCACCAGACGTTTTGTCATGGCAATAGATTTATTTCTGATAAAAATAGCTTAGATCGGAAGAGCGGTTTCAG
chr12	121764849	121764888	ANAPC5_3877	-	GTGACCTATGCACCAGACGTGGCCGGGCCACGTGCTTCTGGAGCAATGGAGGCTCTACCAGATCGGAAGAGCGGTTTCAG
chr12	121766069	121766108	ANAPC5_3878	-	GTGACCTATGCACCAGACGTCAAGCCCTGGGGGTGTGAATTTCTTAGAGAGAAGCAGGAAGATCGGAAGAGCGGTTTCAG
chr12	121768336	121768375	ANAPC5_3879	-	GTGACCTATGCACCAGACGTCTTTCTGTGATAGTTTCCATAAATGGTCAGGCTTTGAGATCGGAAGAGCGGTTTCAG
chr12	121769100	121769139	ANAPC5_3880	-	GTGACCTATGCACCAGACGTCCTCTGCTGTTGGGAGTTTTGTACAGGGTGAATTTGGCCAGATCGGAAGAGCGGTTTCAG
chr12	121773286	121773325	ANAPC5_3881	-	GTGACCTATGCACCAGACGTAGACCTTTGTCTTGCGCAAAATGAAGGAACCGATGACAAGATCGGAAGAGCGGTTTCAG
chr12	121775044	121775083	ANAPC5_3882	-	GTGACCTATGCACCAGACGTCCCAGAATTTGTTGCTGTGTTGAAAGGAATGACAAGGCAAGATCGGAAGAGCGGTTTCAG
chr12	121779756	121779795	ANAPC5_3883	-	GTGACCTATGCACCAGACGTTCTGTAATTTATCATGAACCTTCTGTTCTAGTCTGTGATGAGATCGGAAGAGCGGTTTCAG
chr12	121783592	121783631	ANAPC5_3884	-	GTGACCTATGCACCAGACGTTTTTCTGACAGGGACTTTTTCTGTAATAGTATAATTAGATCGGAAGAGCGGTTTCAG
chr12	121784649	121784688	ANAPC5_3885	-	GTGACCTATGCACCAGACGTTTTCTTCAAGAGCAGAGATTTTTCATGAAGTGACAGATCGGAAGAGCGGTTTCAG
chr12	121785555	121785594	ANAPC5_3886	-	GTGACCTATGCACCAGACGTTTCTTCTTTATATATGAAAAGGTGTGAAGGTAGATGAAAGATCGGAAGAGCGGTTTCAG

chr3	142168221	142168260	ATR_3887	-	GTGACCTATGCACCAGACGTTGTAAGAATATGTTAATAATCTAAAAGTAATGCATTTGAGATCGGAAGAGCGGTTTCAG
chr3	142171920	142171959	ATR_3888	-	GTGACCTATGCACCAGACGTTGGTATAGCTTGATATGGGCTGTAGTCCATCTCTACAAAAGATCGGAAGAGCGGTTTCAG
chr3	142176396	142176435	ATR_3889	-	GTGACCTATGCACCAGACGTATACTTTGTAATAATTTAACAGTAACTCGAATATAATTAGATCGGAAGAGCGGTTTCAG
chr3	142177750	142177789	ATR_3890	-	GTGACCTATGCACCAGACGTTGAGTTACTCTTACTAATTTGTGTTTCTCTCAATTTCTTAGATCGGAAGAGCGGTTTCAG
chr3	142180732	142180771	ATR_3891	-	GTGACCTATGCACCAGACGTTAATCTTATACATATACAGTGTGGGTAAGTTATATAAGATCGGAAGAGCGGTTTCAG
chr3	142185116	142185155	ATR_3892	-	GTGACCTATGCACCAGACGTTTATATGACTATGATTTTAAATTTAGTTGTTAAAAAGATCGGAAGAGCGGTTTCAG
chr3	142186726	142186765	ATR_3893	-	GTGACCTATGCACCAGACGTTAATCTTAGCTGTATAAAGTATGTTGGTAAATTATGTATAGATCGGAAGAGCGGTTTCAG
chr3	142188129	142188168	ATR_3894	-	GTGACCTATGCACCAGACGTTCTTTTACCTTTTATATGAAAAGATCTTTTACCATTTTATAGATCGGAAGAGCGGTTTCAG
chr3	142188878	142188917	ATR_3895	-	GTGACCTATGCACCAGACGTTACGTAAGTGTAAAGGACTAGGAATTATAACTTTGGAGATCGGAAGAGCGGTTTCAG
chr3	142203932	142203971	ATR_3896	-	GTGACCTATGCACCAGACGTTGAATGTCATGTTTGCAGATTAATATGAAGGATGACTATAGATCGGAAGAGCGGTTTCAG
chr3	142211924	142211963	ATR_3897	-	GTGACCTATGCACCAGACGTTGATAATGCAGTTTCAGTTAACTCTGTTGACTACGTAAAAAGATCGGAAGAGCGGTTTCAG
chr3	142215805	142215844	ATR_3898	-	GTGACCTATGCACCAGACGTTACTTTTTTAAAAATGTCATTTACTTGAATTTGGTATAGATCGGAAGAGCGGTTTCAG
chr3	142217389	142217428	ATR_3899	-	GTGACCTATGCACCAGACGTTATTTCCATTTTATATTTTCCGCTATAAATGTCACCTGAAGATCGGAAGAGCGGTTTCAG
chr3	142222154	142222193	ATR_3900	-	GTGACCTATGCACCAGACGTATAAAATGATTTTCTTTGTTATTGCATCTGAATGGAGAAGATCGGAAGAGCGGTTTCAG
chr3	142223931	142223970	ATR_3901	-	GTGACCTATGCACCAGACGTAAATGAAAGGCAACTGTAATGAAAATAGCCCTGAATGGAAGATCGGAAGAGCGGTTTCAG
chr3	142226723	142226762	ATR_3902	-	GTGACCTATGCACCAGACGTAATATAGTGAATTTAATAATGAAAATTAATGTGCCAGTCAGATCGGAAGAGCGGTTTCAG
chr3	142231052	142231091	ATR_3903	-	GTGACCTATGCACCAGACGTACTTCTGTTTTTTTTTTTTTTTTTTAGCTATTCACCAGATCGGAAGAGCGGTTTCAG
chr3	142232293	142232332	ATR_3904	-	GTGACCTATGCACCAGACGTTTCATCTTACTTGTGTTTTGAACATGGAACCTACTTTCTAGATCGGAAGAGCGGTTTCAG
chr3	142234187	142234226	ATR_3905	-	GTGACCTATGCACCAGACGTTCTGTTAGTTTGTAACTGAAATGAAAATCTAAAGGAAACAGATCGGAAGAGCGGTTTCAG
chr3	142241520	142241559	ATR_3906	-	GTGACCTATGCACCAGACGTATATAGTCATTACTGGCTTTAAATTGTTAATCAAATAAAGATCGGAAGAGCGGTTTCAG
chr3	142242785	142242824	ATR_3907	-	GTGACCTATGCACCAGACGTTGAAATTTGGAATGACAAAAGAGTTCTCTGTCCCTATTGAGGAGATCGGAAGAGCGGTTTCAG
chr3	142253872	142253911	ATR_3908	-	GTGACCTATGCACCAGACGTATGATATAATAAAAATGATAACAAAGAAAGATTGGAGGAGATCGGAAGAGCGGTTTCAG
chr3	142254900	142254939	ATR_3909	-	GTGACCTATGCACCAGACGTTTAATTTGTGGTTTAGGAGATCATAACAGCAATTGTTAGATCGGAAGAGCGGTTTCAG
chr3	142257274	142257313	ATR_3910	-	GTGACCTATGCACCAGACGTTGAATTAATAGTAAATTAATAACTTTTTAAACTGTATTTAGATCGGAAGAGCGGTTTCAG
chr3	142261457	142261496	ATR_3911	-	GTGACCTATGCACCAGACGTATAGTCCAGAGTGCTAAGATAGAATTTCATACAGAATAAAGATCGGAAGAGCGGTTTCAG
chr3	142266517	142266556	ATR_3912	-	GTGACCTATGCACCAGACGTTGTTCTATGAGGTTTTTTGTTGTTTCTTCTTTTCAGATCGGAAGAGCGGTTTCAG
chr3	142268924	142268963	ATR_3913	-	GTGACCTATGCACCAGACGTACATATAGTTCACCTTGAAGTTTGAACCTAGATTTTTGTTAGATCGGAAGAGCGGTTTCAG
chr3	142272019	142272058	ATR_3914	-	GTGACCTATGCACCAGACGTGCGTTTTGTCTGGACTATAGGCAACAGCAGTACTTTTTAAGAGATCGGAAGAGCGGTTTCAG
chr3	142272432	142272471	ATR_3915	-	GTGACCTATGCACCAGACGTGAGCTTGTCTTCTTATTTTGGCCATTCTCCAGATCGGAAGAGCGGTTTCAG
chr3	142272617	142272656	ATR_3916	-	GTGACCTATGCACCAGACGTTTTGTTTTTAACTTTGAGTTTTACGTTCAACCTAGCTCTAAAGATCGGAAGAGCGGTTTCAG
chr3	142274669	142274708	ATR_3917	-	GTGACCTATGCACCAGACGTATGACTTATTAATACTTTAAACCTATTTAAGCTCTGCTAGATCGGAAGAGCGGTTTCAG
chr3	142275175	142275214	ATR_3918	-	GTGACCTATGCACCAGACGTAGATTTTAATTTGAATATATCACTCTATTGGAAGATCATAGATCGGAAGAGCGGTTTCAG
chr3	142278043	142278082	ATR_3919	-	GTGACCTATGCACCAGACGTATTAGCAACAGATCAGAATAAGCTTTAAAGATAATCAGTAAGATCGGAAGAGCGGTTTCAG
chr3	142279055	142279094	ATR_3920	-	GTGACCTATGCACCAGACGTTCTTCTGTTTCTGGGTTGGGTTTCTGTAAATGAATTTGAGATCGGAAGAGCGGTTTCAG
chr3	142280035	142280074	ATR_3921	-	GTGACCTATGCACCAGACGTTCTTCTTCACTGTTTTGATTTAGCCATTAAATAAACTTTGTTAGATCGGAAGAGCGGTTTCAG
chr3	142281024	142281063	ATR_3922	-	GTGACCTATGCACCAGACGTTTTAGGTTACTAGTTAAGTATGATTTTTGTTTCATCATTTAGATCGGAAGAGCGGTTTCAG
chr3	142284913	142284952	ATR_3923	-	GTGACCTATGCACCAGACGTTTATTCATGCATTCCTTGGCCATCTGTTCTATAAAATCCTAGATCGGAAGAGCGGTTTCAG
chr3	142286855	142286894	ATR_3924	-	GTGACCTATGCACCAGACGTAATTTTCTTATATAAATTTATAAATTAAGATTTTTCTTAGATCGGAAGAGCGGTTTCAG
chr3	142297438	142297477	ATR_3925	-	GTGACCTATGCACCAGACGTGCCCAGCCTGGGTCTGCATCCTCCTCCGCTGATTCGGCAGATCGGAAGAGCGGTTTCAG
chr3	142281463	142281502	ATR_3926	-	GTGACCTATGCACCAGACGTTGCAATTGCTTTTTAACAGAAGTTTTCAGCTGGAGGACATCGGAAGAGCGGTTTCAG
chr19	45251998	45252037	BCL3_3927	-	GTGACCTATGCACCAGACGTGGGACGCGGCGGCGGACCGCTGGGCTCGGCTGCACGGGAGATCGGAAGAGCGGTTTCAG
chr19	45254434	45254473	BCL3_3928	-	GTGACCTATGCACCAGACGTGAGGACAGAGAAGGGACATGGGTGAGGCCACACCCACAGAAGATCGGAAGAGCGGTTTCAG
chr19	45259439	45259478	BCL3_3929	-	GTGACCTATGCACCAGACGTGGGAGTGAAGGAATCACAGGCATTAGGGGTTGTTACCTCAGATCGGAAGAGCGGTTTCAG
chr19	45260224	45260263	BCL3_3930	-	GTGACCTATGCACCAGACGTGTGACTGTGAGGGACCTGTGTCCAGCCCTGCTCTCTAGTCAGATCGGAAGAGCGGTTTCAG
chr19	45260534	45260573	BCL3_3931	-	GTGACCTATGCACCAGACGTGGAGGGCTCGGTGAAACCTAGGCCCGGGCTTTGCGGCCGAGATCGGAAGAGCGGTTTCAG
chr19	45260853	45260892	BCL3_3932	-	GTGACCTATGCACCAGACGTGAGGGAGGCTTAGTTTTCTCCAAGCTGCTCCAGCAGATCGGAAGAGCGGTTTCAG
chr19	45261453	45261492	BCL3_3933	-	GTGACCTATGCACCAGACGTGGAGGGCCGGGTGAGGAGGCGCGCGGCCACCCGGGTAAGATCGGAAGAGCGGTTTCAG
chr19	45261931	45261970	BCL3_3934	-	GTGACCTATGCACCAGACGTATGGCGTGACCATAGAGCCACCCATGCCTCACAGTCTCAGATCGGAAGAGCGGTTTCAG
chr2	32582180	32582219	BIRC6_3935	-	GTGACCTATGCACCAGACGTGGGGCAAGCCGAGCGCTTAGCCGGAAGTGAAGTCAGCGCAGATCGGAAGAGCGGTTTCAG
chr2	32602606	32602645	BIRC6_3936	-	GTGACCTATGCACCAGACGTAACAAAATTAACACTTAAGATTTTCAGGCCAATGGTCTAGATCGGAAGAGCGGTTTCAG
chr2	32613768	32613807	BIRC6_3937	-	GTGACCTATGCACCAGACGTATGGGATTAAGCAAAAGGAAAATGACTCAACAGTTTTAAGATCGGAAGAGCGGTTTCAG
chr2	32617057	32617096	BIRC6_3938	-	GTGACCTATGCACCAGACGTACATCTTATGTAATTAAGTTAGGCATCAAATCACAGTAGATCGGAAGAGCGGTTTCAG
chr2	32620529	32620568	BIRC6_3939	-	GTGACCTATGCACCAGACGTATAAAGAAAAGAGACAGAAAAGGTAATCATTATTAATAAGATCGGAAGAGCGGTTTCAG
chr2	32626181	32626220	BIRC6_3940	-	GTGACCTATGCACCAGACGTATTTAGAAAAGAAAAGTTTACTAAAATAAAGCAATTCAGAGATCGGAAGAGCGGTTTCAG
chr2	32626481	32626520	BIRC6_3941	-	GTGACCTATGCACCAGACGTGAAAAGCCTAAGTTTACAACCTGATCTTTTTCAATTAAGATCGGAAGAGCGGTTTCAG
chr2	32631517	32631556	BIRC6_3942	-	GTGACCTATGCACCAGACGTAAAACAAAGTAAACAATTTGAATTTCAAAAAAGTATACAGATCGGAAGAGCGGTTTCAG
chr2	32639787	32639826	BIRC6_3943	-	GTGACCTATGCACCAGACGTGAACAATTTCATAGATGTTTTCTACTCATCCAGTCAGAGATCGGAAGAGCGGTTTCAG
chr2	32654164	32654203	BIRC6_3944	-	GTGACCTATGCACCAGACGTTGAAATTTATAGATACATGAAAATAAGGTAACATTCAAAGATCGGAAGAGCGGTTTCAG

chr2	32658662	32658701	BIRC6_3945	-	GTGACCTATGCACCAGACGTAGGGGAAAAATGCTAAATAAGCAAAAATCTTTCTTTCAGCAGATCGGAAGAGCGGTTTCAG
chr2	32660514	32660553	BIRC6_3946	-	GTGACCTATGCACCAGACGTAGGAAAGGTGATCTGCCTATCTACTGCTGTTTCTAGAGGAAGATCGGAAGAGCGGTTTCAG
chr2	32661071	32661110	BIRC6_3947	-	GTGACCTATGCACCAGACGTAAATACATATTTTTCTTTTAAATTCATTCATTTAAATGTAGATCGGAAGAGCGGTTTCAG
chr2	32664526	32664565	BIRC6_3948	-	GTGACCTATGCACCAGACGTGGAGTAGAATGGGGAAAAATAACTGAATCACCAATAAAATTCAGATCGGAAGAGCGGTTTCAG
chr2	32666347	32666386	BIRC6_3949	-	GTGACCTATGCACCAGACGTCAAATAATAATGAATTTTAAAAAATAAACTAAACTAAAAAAGATCGGAAGAGCGGTTTCAG
chr2	32667083	32667122	BIRC6_3950	-	GTGACCTATGCACCAGACGTGAAAAATATAAACCACTTACCAAAAAACAAAACAACAACATAGATCGGAAGAGCGGTTTCAG
chr2	32667342	32667381	BIRC6_3951	-	GTGACCTATGCACCAGACGTATAGCAGACATTTAGACTCATCTGAACITTCATCATAAAGATCGGAAGAGCGGTTTCAG
chr2	32668509	32668548	BIRC6_3952	-	GTGACCTATGCACCAGACGTTTTTAAAAAGAAAAATTTGTAAGACATTTACTCAAGGTCTAAAGATCGGAAGAGCGGTTTCAG
chr2	32670539	32670578	BIRC6_3953	-	GTGACCTATGCACCAGACGTAAAAACAAAATAAATGTTTCTTTTCTCTCTTTCTCTCTAGATCGGAAGAGCGGTTTCAG
chr2	32673813	32673852	BIRC6_3954	-	GTGACCTATGCACCAGACGTAAATAATGACTAACAATTTTCTCTTTCAGCCATCTAATTAAGATCGGAAGAGCGGTTTCAG
chr2	32678826	32678865	BIRC6_3955	-	GTGACCTATGCACCAGACGTAAAGACAAGTTTTATAACACGTGAAGATAATTTTTAAAAAGAGATCGGAAGAGCGGTTTCAG
chr2	32688212	32688251	BIRC6_3956	-	GTGACCTATGCACCAGACGTACAAGGGTAAAAACAAAAACAAAAACACCAGGATGAAGAGATCGGAAGAGCGGTTTCAG
chr2	32689527	32689566	BIRC6_3957	-	GTGACCTATGCACCAGACGTAGTAAAAACAACATATATAGACTAATCTGCCTACCTAAAAAGATCGGAAGAGCGGTTTCAG
chr2	32690083	32690122	BIRC6_3958	-	GTGACCTATGCACCAGACGTGAAAAAATAAATACTAATCTTATATTGATATTACTATAGAGATCGGAAGAGCGGTTTCAG
chr2	32692543	32692582	BIRC6_3959	-	GTGACCTATGCACCAGACGTAAAGAGAAACAGTTGACCAAAAATATATCAATTAACAAAAGATCGGAAGAGCGGTTTCAG
chr2	32692921	32692960	BIRC6_3960	-	GTGACCTATGCACCAGACGTAAATATAATATACATATATACACACTCTGCCACAATAAAAGATCGGAAGAGCGGTTTCAG
chr2	32693455	32693494	BIRC6_3961	-	GTGACCTATGCACCAGACGTAAAAGATTGAACAAAAATAATCTTGTAATGTCTCTTTATAGATCGGAAGAGCGGTTTCAG
chr2	32694413	32694452	BIRC6_3962	-	GTGACCTATGCACCAGACGTAAAGAAAAACAACTTTCTTATTAATGTATTGTATAAGATCGGAAGAGCGGTTTCAG
chr2	32695186	32695225	BIRC6_3963	-	GTGACCTATGCACCAGACGTAAACAAAAAAGAAAAGAATAAGAATCAATTCGATTGTAGATCGGAAGAGCGGTTTCAG
chr2	32696032	32696071	BIRC6_3964	-	GTGACCTATGCACCAGACGTATGACAGCAAAGGAAAAACATCCAGATGACTTTAGGATTCAGATCGGAAGAGCGGTTTCAG
chr2	32698130	32698169	BIRC6_3965	-	GTGACCTATGCACCAGACGTAGGAAAACTTGTATTAAATTCCTGTTAAATGTGATTTTAAAGATCGGAAGAGCGGTTTCAG
chr2	32701231	32701270	BIRC6_3966	-	GTGACCTATGCACCAGACGTCAAATAAAACAATTAATCTTTAAACAAGTTAAAAACAAAAAGATCGGAAGAGCGGTTTCAG
chr2	32702386	32702425	BIRC6_3967	-	GTGACCTATGCACCAGACGTAAATGTATAGTGTAAAATCAATGTTTACTTAATGAAAATAGATCGGAAGAGCGGTTTCAG
chr2	32703653	32703692	BIRC6_3968	-	GTGACCTATGCACCAGACGTTTTTATAAAATCATACACTTAAATAGCAATTAACATGTTTTAGATCGGAAGAGCGGTTTCAG
chr2	32704480	32704519	BIRC6_3969	-	GTGACCTATGCACCAGACGTGGGGATAGTCTGTTTTAATAATTTATACAGATTTGAAAAGATCGGAAGAGCGGTTTCAG
chr2	32706338	32706377	BIRC6_3970	-	GTGACCTATGCACCAGACGTAAAAAGTATCTTATTGGTGGAGTGATCACATAAAATAGATCGGAAGAGCGGTTTCAG
chr2	32707447	32707486	BIRC6_3971	-	GTGACCTATGCACCAGACGTGGAAAAAAACTGTGGTTTTATTTTTGCCTCTTGCTGAAAGATCGGAAGAGCGGTTTCAG
chr2	32710660	32710699	BIRC6_3972	-	GTGACCTATGCACCAGACGTCAATTGAAAGAAAAAGAAAACATTGACAATTTACTCATAGATCGGAAGAGCGGTTTCAG
chr2	32712664	32712703	BIRC6_3973	-	GTGACCTATGCACCAGACGTAAACAAGTATAATTTATACATAAAGATCAGGATATGTAGATCGGAAGAGCGGTTTCAG
chr2	32713605	32713644	BIRC6_3974	-	GTGACCTATGCACCAGACGTAAAAATCAACAGGAGAAAAATGTACCTATTATAATATGAGATCGGAAGAGCGGTTTCAG
chr2	32715058	32715097	BIRC6_3975	-	GTGACCTATGCACCAGACGTAAAGAAAAGGGAAAAATTTTTTCAGAAAAACAATGTTTTATAGATCGGAAGAGCGGTTTCAG
chr2	32716442	32716481	BIRC6_3976	-	GTGACCTATGCACCAGACGTTTTTTTAAAAACCTCTTAAGAAATGGACCATGAAATATGAGATCGGAAGAGCGGTTTCAG
chr2	32718557	32718596	BIRC6_3977	-	GTGACCTATGCACCAGACGTATGTATTTCACTGAAAACCTGCTTACTGGTAACATGTTAAAGATCGGAAGAGCGGTTTCAG
chr2	32727812	32727851	BIRC6_3978	-	GTGACCTATGCACCAGACGTAAATATGCATATTTATGACTTTATATATCTGTGTAATAAGATCGGAAGAGCGGTTTCAG
chr2	32728059	32728098	BIRC6_3979	-	GTGACCTATGCACCAGACGTAAAGAAATGAAATGAAATGCATCTCAGGACAGATGGTTTCAGATCGGAAGAGCGGTTTCAG
chr2	32730022	32730061	BIRC6_3980	-	GTGACCTATGCACCAGACGTATTTTTTACATAAATTTATAAGAACTTGCAAAAAGAAACATAAAGATCGGAAGAGCGGTTTCAG
chr2	32732997	32733036	BIRC6_3981	-	GTGACCTATGCACCAGACGTAGAAAACGAATCATCACAAAAAGACAAAAGTATACATAGATTAGATCGGAAGAGCGGTTTCAG
chr2	32734755	32734794	BIRC6_3982	-	GTGACCTATGCACCAGACGTAAAAATGACTTGTATGATCAATATAAGTCGCTCAAATCACTAGATCGGAAGAGCGGTTTCAG
chr2	32735543	32735582	BIRC6_3983	-	GTGACCTATGCACCAGACGTAGAAATCCAAAGAAAAGTTTGCTAAATAAGCAAGTTAACCCAGATCGGAAGAGCGGTTTCAG
chr2	32737950	32737989	BIRC6_3984	-	GTGACCTATGCACCAGACGTGAAAAAGAAATCATATAACCAACTATATAGTGAATTTGCGAGATCGGAAGAGCGGTTTCAG
chr2	32740007	32740046	BIRC6_3985	-	GTGACCTATGCACCAGACGTAAAGATATCATATTAATGATACAAAGTATATTTTTAGAAAGAAAGATCGGAAGAGCGGTTTCAG
chr2	32743271	32743310	BIRC6_3986	-	GTGACCTATGCACCAGACGTAAAAATTTTTAAAAAGTTAAATGCAAGATTTATATGCAGCTAGATCGGAAGAGCGGTTTCAG
chr2	32743834	32743873	BIRC6_3987	-	GTGACCTATGCACCAGACGTAGAAATCAAGAATCAGGAAGTAACTTTTTGAATACATAGATCGGAAGAGCGGTTTCAG
chr2	32749905	32749944	BIRC6_3988	-	GTGACCTATGCACCAGACGTATATTATCTAAAATACACTGCTTTTTCCAATCATTAAAGAAAGATCGGAAGAGCGGTTTCAG
chr2	32750481	32750520	BIRC6_3989	-	GTGACCTATGCACCAGACGTAGGATCAGTAAGATTCTACATAGTCAACACTAATATGAAGATCGGAAGAGCGGTTTCAG
chr2	32754668	32754707	BIRC6_3990	-	GTGACCTATGCACCAGACGTATAACTAAGTTAAATCTGGAACCCGAGAAAGAAAACATTTAAGATCGGAAGAGCGGTTTCAG
chr2	32756372	32756411	BIRC6_3991	-	GTGACCTATGCACCAGACGTAAATACAAAATAACTGAATAGGTAAGAAAAGGGTATTTTTAGATCGGAAGAGCGGTTTCAG
chr2	32768258	32768297	BIRC6_3992	-	GTGACCTATGCACCAGACGTAGAAAAGTGTGGCTTGGCCATTACATTTTCAACATCAGAGATCGGAAGAGCGGTTTCAG
chr2	32770660	32770699	BIRC6_3993	-	GTGACCTATGCACCAGACGTGAAAGAAAGAGGACTCAAGATTAATAAAGATGAAAACACAAGATCGGAAGAGCGGTTTCAG
chr2	32772867	32772906	BIRC6_3994	-	GTGACCTATGCACCAGACGTCAAAAAATGAAAATCCATTACAATTTGTTTTGCTTATCTAGATCGGAAGAGCGGTTTCAG
chr2	32774330	32774369	BIRC6_3995	-	GTGACCTATGCACCAGACGTGTTGAAATTAATTTGGATTTTCAGTTTCACATACTTCAAAGAGATCGGAAGAGCGGTTTCAG
chr2	32800173	32800212	BIRC6_3996	-	GTGACCTATGCACCAGACGTAAAGAAAGCAAAAAGCAAAAATGAGCAATGATAAATAAAGATCGGAAGAGCGGTTTCAG
chr2	32818932	32818971	BIRC6_3997	-	GTGACCTATGCACCAGACGTAAATATGGAAGAAAAGCAAGGAAAATTAAGATTTTAGGAGATCGGAAGAGCGGTTTCAG
chr2	32822768	32822807	BIRC6_3998	-	GTGACCTATGCACCAGACGTAAAGAAAAATAAACCAGAACTGCAAAAATTTGTTATAAAGATCGGAAGAGCGGTTTCAG
chr2	32824756	32824795	BIRC6_3999	-	GTGACCTATGCACCAGACGTATAAACAATAAAAAGTCTATGTTAACATTCCTAAACACTGAGATCGGAAGAGCGGTTTCAG
chr2	32828023	32828062	BIRC6_4000	-	GTGACCTATGCACCAGACGTAAAAAGCATAAACAGAATGAAAAAGAGTGCTTAAAAAGATCGGAAGAGCGGTTTCAG
chr2	32832472	32832511	BIRC6_4001	-	GTGACCTATGCACCAGACGTAAAGAAAAGAACACTATGAGGGACATTTTTACTGTGGAGATCGGAAGAGCGGTTTCAG
chr2	32836465	32836504	BIRC6_4002	-	GTGACCTATGCACCAGACGTAGTAAAACAGGAAACAAGCAGTGTTTACAGTCAAATTTAAAGATCGGAAGAGCGGTTTCAG

chr2	32842742	32842781	BIRC6_4003	-	GTGACCTATGCACCAGACGTGAAAAGGACTAATGTTAGAAGTCAAACCCCTCTAGCACAAGATCGGAAGAGCGGTTTCAG
chr2	32724845	32724884	BIRC6_4004	-	GTGACCTATGCACCAGACGTCATTTCGCCACAAAAGTCTTTTGCATCACCCGACGAATAAGATCGGAAGAGCGGTTTCAG
chr2	32740397	32740436	BIRC6_4005	-	GTGACCTATGCACCAGACGTAGCTAGAAAATGTGGCTAAAGCAGAAAAGTCCCTAGATCGGAAGAGCGGTTTCAG
chr2	32640252	32640291	BIRC6_4006	-	GTGACCTATGCACCAGACGCTTTCTCTGCTTTCTCATCAGATTCCCTTGATGCTATAAAGAAGATCGGAAGAGCGGTTTCAG
chr2	32640717	32640756	BIRC6_4007	-	GTGACCTATGCACCAGACGTGATTACATAATATTTGCACCATTCACTACACGAAGATTTAGATCGGAAGAGCGGTTTCAG
chr17	59760607	59760646	BRIP1_4008	-	GTGACCTATGCACCAGACGTTCTCAAGTCAAGTAAAATATGTCATCATGCTTATGTTAAAGATCGGAAGAGCGGTTTCAG
chr17	59763147	59763186	BRIP1_4009	-	GTGACCTATGCACCAGACGTCTTCCCTTTACCTTTGATAGAGAAGTCTTTTCATTATAAGATCGGAAGAGCGGTTTCAG
chr17	59793262	59793301	BRIP1_4010	-	GTGACCTATGCACCAGACGTTGAAATTTAATAATAATTATCTGTGACAGGGCTATATATAGATCGGAAGAGCGGTTTCAG
chr17	59820324	59820363	BRIP1_4011	-	GTGACCTATGCACCAGACGTAAAACCTTAAGTTTTATTATTACAGGAGTCAATGGTTTTGAGATCGGAAGAGCGGTTTCAG
chr17	59821743	59821782	BRIP1_4012	-	GTGACCTATGCACCAGACGTATTATTTTCATGGTCCGTGAAAAAATATTTTTTATTACAAAAGATCGGAAGAGCGGTTTCAG
chr17	59853712	59853751	BRIP1_4013	-	GTGACCTATGCACCAGACGTATTTATTGTTTTCTTTTGCCTTTAAATAATCATTTCATTTAGATCGGAAGAGCGGTTTCAG
chr17	59857572	59857611	BRIP1_4014	-	GTGACCTATGCACCAGACGTGTTTTTTTTTGGAAAGCCCTTCAGTGTCTTCTACTTCAATAGATCGGAAGAGCGGTTTCAG
chr17	59858151	59858190	BRIP1_4015	-	GTGACCTATGCACCAGACGTGATGTAATGGAAATTTTGTCTTCTTGCATACCAGCAAGATCGGAAGAGCGGTTTCAG
chr17	59861581	59861620	BRIP1_4016	-	GTGACCTATGCACCAGACGTATAACTAGTATGATTTTTCTTTTAAAAATAGCCTAATTTAGATCGGAAGAGCGGTTTCAG
chr17	59870908	59870947	BRIP1_4017	-	GTGACCTATGCACCAGACGTTTTTCTACCTGTGAAACGTATTAGTGAATTAGAAGTGATAGATCGGAAGAGCGGTTTCAG
chr17	59876411	59876450	BRIP1_4018	-	GTGACCTATGCACCAGACGTTTGTCTATAGTGTATTTGTGCTGCCTTTATATGAAAAATAGATCGGAAGAGCGGTTTCAG
chr17	59878564	59878603	BRIP1_4019	-	GTGACCTATGCACCAGACGTGTGTAATAAGAACCTTCTTCTACTCATGGAGATGTAAGATCGGAAGAGCGGTTTCAG
chr17	59885778	59885817	BRIP1_4020	-	GTGACCTATGCACCAGACGTTATTTTGTGTAGAGAAAAATAGGCTGAAAAATTTAAGATCGGAAGAGCGGTTTCAG
chr17	59924412	59924451	BRIP1_4021	-	GTGACCTATGCACCAGACGTATGCCATTGTTTCAGTTTTAAAGAAAGGAAGATGGAATTTAGATCGGAAGAGCGGTTTCAG
chr17	59926440	59926479	BRIP1_4022	-	GTGACCTATGCACCAGACGTTTTATTGGCAGTAAATAACCCAGTATAGTACAGCTGAACAAGATCGGAAGAGCGGTTTCAG
chr17	59934369	59934408	BRIP1_4023	-	GTGACCTATGCACCAGACGTTTTTGCCTGGGTGAGTTGATATCTGTAATAAGAGTCTTAAAGATCGGAAGAGCGGTTTCAG
chr17	59937107	59937146	BRIP1_4024	-	GTGACCTATGCACCAGACGTGCTTGATATCTTCAGGTTACTTACTGGGATCTGAGAAAATAGATCGGAAGAGCGGTTTCAG
chr17	59938758	59938797	BRIP1_4025	-	GTGACCTATGCACCAGACGTTTTCAGCAGTAAAGTTTTTAAATAGATAGATACTTATGAAGATCGGAAGAGCGGTTTCAG
chr17	59761029	59761068	BRIP1_4026	-	GTGACCTATGCACCAGACGTACAGTCCACTTCAAAATAGAGATTTTGAACAAGAAGATCGGAAGAGCGGTTTCAG
chr16	88943334	88943373	CBFA2T3_4027	-	GTGACCTATGCACCAGACGTCCCTGGCCTGCCGGACACAGCACCGTGCCAACCCACCCCAAGATCGGAAGAGCGGTTTCAG
chr16	88945628	88945667	CBFA2T3_4028	-	GTGACCTATGCACCAGACGTCCGGCCACGCTGACACCCATCCCTGCCTCGGCTCCCCTGAGATCGGAAGAGCGGTTTCAG
chr16	88947078	88947117	CBFA2T3_4029	-	GTGACCTATGCACCAGACGTGTGCAGGGGCTGGCCACGAGAGCTGTGGGAGGCCAGGGCAGATCGGAAGAGCGGTTTCAG
chr16	88947649	88947688	CBFA2T3_4030	-	GTGACCTATGCACCAGACGTGGTGTGGGGGGAGGGAGCAGACACGGGGTGCTCTGGTGGGAGATCGGAAGAGCGGTTTCAG
chr16	88951404	88951443	CBFA2T3_4031	-	GTGACCTATGCACCAGACGTGGTGGGGGGGAGCGTGGACCGGTTACAGAGCACACAGATCGGAAGAGCGGTTTCAG
chr16	88952319	88952358	CBFA2T3_4032	-	GTGACCTATGCACCAGACGTGCTCCGGGATCTCGGGCTGGGGTGGCCGTGGACCGGCAGATCGGAAGAGCGGTTTCAG
chr16	88958240	88958279	CBFA2T3_4033	-	GTGACCTATGCACCAGACGTACCCGTCCCGCTGCTGCGGGAGCCTCCCTAGAAGGCCCAGATCGGAAGAGCGGTTTCAG
chr16	88958602	88958641	CBFA2T3_4034	-	GTGACCTATGCACCAGACGTACGGGACAGCCGGGGCCTTGGGACATGCATATCCCTCCGAGATCGGAAGAGCGGTTTCAG
chr16	88964436	88964475	CBFA2T3_4035	-	GTGACCTATGCACCAGACGTAAACAAAACCCGAGCCCTCCCACAGAGTCTTACCAGAGATCGGAAGAGCGGTTTCAG
chr16	88967862	88967901	CBFA2T3_4036	-	GTGACCTATGCACCAGACGTCCCACCTCCAGCAGCCGGGGCAGTGTTCAGGGGAGGCCAGATCGGAAGAGCGGTTTCAG
chr16	89043015	89043054	CBFA2T3_4037	-	GTGACCTATGCACCAGACGTCCBAGGGGAGGTTGGTGGGTTGGGGGACAGAGCGGAGCCAGATCGGAAGAGCGGTTTCAG
chr1	193094192	193094231	CDC73_4038	-	GTGACCTATGCACCAGACGTAAAGCAAGATTTTTTTTACTGACAATTCTAATTCAACTCAGATCGGAAGAGCGGTTTCAG
chr1	193099254	193099293	CDC73_4039	-	GTGACCTATGCACCAGACGTAAATTTAAATGAGATATGAAATGAATAACAATGATACACAAGATCGGAAGAGCGGTTTCAG
chr1	193104471	193104510	CDC73_4040	-	GTGACCTATGCACCAGACGTAAAAAGATTCACGTAAGGATTAATTTTCAACATATATATAGATCGGAAGAGCGGTTTCAG
chr1	193104617	193104656	CDC73_4041	-	GTGACCTATGCACCAGACGTAAAGAGAAGTAAATAAATGTGTAGTTTTGGAATGGGCTTCTAGATCGGAAGAGCGGTTTCAG
chr1	193107165	193107204	CDC73_4042	-	GTGACCTATGCACCAGACGTCCACTGGTAAATGCATTTAAATTTTTTATGAACTTTTAGAGATCGGAAGAGCGGTTTCAG
chr1	193110930	193110969	CDC73_4043	-	GTGACCTATGCACCAGACGTTTTCTTTTTTAAATTTTACACGAAAGGCATTCCCTGGAGTGTAGATCGGAAGAGCGGTTTCAG
chr1	193116947	193116986	CDC73_4044	-	GTGACCTATGCACCAGACGTAAATGGATTTTAAATTAAGCCCACTTTAAATATACAATAGTAAAGATCGGAAGAGCGGTTTCAG
chr1	193119384	193119423	CDC73_4045	-	GTGACCTATGCACCAGACGTATTAATTTAGTACTTGTTAATATTTTTAAATGTCACATAGATCGGAAGAGCGGTTTCAG
chr1	193121460	193121499	CDC73_4046	-	GTGACCTATGCACCAGACGTAAAGAGGCTTATTTGTTAAGATTTTATAGATCATGTATCTTAGATCGGAAGAGCGGTTTCAG
chr1	193172875	193172914	CDC73_4047	-	GTGACCTATGCACCAGACGTATAAGAATTGATATATAAGATCAAAGTTTTCTTACATAATAGATCGGAAGAGCGGTTTCAG
chr1	193181145	193181184	CDC73_4048	-	GTGACCTATGCACCAGACGTGAAAAAATCACAACCTCTGTGCATAAAAAACCATATTTCTAGATCGGAAGAGCGGTTTCAG
chr1	193181470	193181509	CDC73_4049	-	GTGACCTATGCACCAGACGTAAAAATTTACAGGTAGAAAATATATTATTAGAATTATACTAGATCGGAAGAGCGGTTTCAG
chr1	193202073	193202112	CDC73_4050	-	GTGACCTATGCACCAGACGTACAGAGATGAGAAAAAGTCAATGTATTCCACGTGATGAAAAGATCGGAAGAGCGGTTTCAG
chr1	193205336	193205375	CDC73_4051	-	GTGACCTATGCACCAGACGTAAAAAGTGGGTGGGGGGAGGTAGGGGACAGCAGGAGATTATAGATCGGAAGAGCGGTTTCAG
chr1	193218810	193218849	CDC73_4052	-	GTGACCTATGCACCAGACGTGGTGGAGAGAAGTTATCATTTTTACTCAAATAAAAAAAGATCGGAAGAGCGGTTTCAG
chr1	193219756	193219795	CDC73_4053	-	GTGACCTATGCACCAGACGTATTATGTTAGTAGTTATAAGTACTATAGGAATTTTGAATTTAGATCGGAAGAGCGGTTTCAG
chr5	68530753	68530792	CDK7_4054	-	GTGACCTATGCACCAGACGTAAAGCCGACTCCAGCCGAAAGGGCAGCTCCAGGACAGATCGGAAGAGCGGTTTCAG
chr5	68531171	68531210	CDK7_4055	-	GTGACCTATGCACCAGACGTAAATAGAATAACATAAGTTTTATGGGAGTTTTTGTGTTTGGAGATCGGAAGAGCGGTTTCAG
chr5	68548195	68548234	CDK7_4056	-	GTGACCTATGCACCAGACGTGGAAAAAACCCAAATATATTTAAATGTGTTAAATTATAGATCGGAAGAGCGGTTTCAG
chr5	68550379	68550418	CDK7_4057	-	GTGACCTATGCACCAGACGTAGGCAAGCAAAAAGTGAATAATTTCTGAAATCTCAAACCTAGATCGGAAGAGCGGTTTCAG
chr5	68551237	68551276	CDK7_4058	-	GTGACCTATGCACCAGACGTAAAAATTTAAATGTGATTCACTATTTAATACCTGACAGTAGATCGGAAGAGCGGTTTCAG
chr5	68553820	68553859	CDK7_4059	-	GTGACCTATGCACCAGACGTAGTATACATAATACAGGTACCCCTTATTTCAAATAAAAAAGATCGGAAGAGCGGTTTCAG
chr5	68555595	68555634	CDK7_4060	-	GTGACCTATGCACCAGACGTGAAGTTTTTAAACAAAACAAATGAAGCAGGTTAGGGGAGAACAAAGATCGGAAGAGCGGTTTCAG

chr5	68557982	68558021	CDK7_4061	-	GTGACCTATGCACCAGACGTA AAAAGAATTAGTATCATTTTAGCATGAAATATCAAAGCAAGATCGGAAGAGCGGTTCCAG
chr5	68572320	68572359	CDK7_4062	-	GTGACCTATGCACCAGACGTA AAAAGATACCAAAGTAAAGGTAGGTGAGTATCTGAAATGTAGATCGGAAGAGCGGTTCCAG
chr5	68572884	68572923	CDK7_4063	-	GTGACCTATGCACCAGACGTA AAAAGAACAAGAAAAAAGTTGTTCCACATTTAACAAAAGATCGGAAGAGCGGTTCCAG
chr17	57724709	57724748	CLTC_4064	-	GTGACCTATGCACCAGACGTAATCAAGAAATTATAATCATTTAAAGAGTAAAGTTTAGAAAAGATCGGAAGAGCGGTTCCAG
chr17	57725551	57725590	CLTC_4065	-	GTGACCTATGCACCAGACGTTCAAAGGAGAATAACGTTTGAAGACCCATAAATCAAAACTAGATCGGAAGAGCGGTTCCAG
chr17	57733165	57733204	CLTC_4066	-	GTGACCTATGCACCAGACGTA AAAACTCAACACTTTAGTAAAAAATGAATCTACAAAACAGAAGATCGGAAGAGCGGTTCCAG
chr17	57737702	57737741	CLTC_4067	-	GTGACCTATGCACCAGACGTTAAGAATAAAATGTAGCTGCAATGTGTTCATTTGGATACAAAAGATCGGAAGAGCGGTTCCAG
chr17	57738754	57738793	CLTC_4068	-	GTGACCTATGCACCAGACGTGAGA AATGTTAAAGCTCTTCGAAAAGTGAAGAAGGAGAAAAGATCGGAAGAGCGGTTCCAG
chr17	57741153	57741192	CLTC_4069	-	GTGACCTATGCACCAGACGTG AAAAGAGATTGTTTAGTGATCCATGAACGTGTTTAGAAAAGATCGGAAGAGCGGTTCCAG
chr17	57742098	57742137	CLTC_4070	-	GTGACCTATGCACCAGACGTACA AAGACTTAAACGCTGCTCCTAAGTTTCAATTTATAGAGATCGGAAGAGCGGTTCCAG
chr17	57743414	57743453	CLTC_4071	-	GTGACCTATGCACCAGACGTAG ATTTAAAAGAAATTTGTTTTAAGATACTATGGAGAGTATAGATCGGAAGAGCGGTTCCAG
chr17	57743791	57743830	CLTC_4072	-	GTGACCTATGCACCAGACGTACA AAACAAGGCAAGTTATTGTCCACTCCACTACATGAGAGATCGGAAGAGCGGTTCCAG
chr17	57746088	57746127	CLTC_4073	-	GTGACCTATGCACCAGACGTCAA GATTTACA AATTAAGCATAGGCACACTTTTGAAATGAGATCGGAAGAGCGGTTCCAG
chr17	57750958	57750997	CLTC_4074	-	GTGACCTATGCACCAGACGTGACA AAACAAAAGGAAAACCTTAAATTTCTTCTATGAGGTATAGATCGGAAGAGCGGTTCCAG
chr17	57752012	57752051	CLTC_4075	-	GTGACCTATGCACCAGACGTAAA GAAGTAGAAGAATGTTATTATGTTATTTAAAAGCAAAGATCGGAAGAGCGGTTCCAG
chr17	57754265	57754304	CLTC_4076	-	GTGACCTATGCACCAGACGTAG GAAAAAAACCTCACACACACATACTGTATTATAAATAAAGATCGGAAGAGCGGTTCCAG
chr17	57756708	57756747	CLTC_4077	-	GTGACCTATGCACCAGACGTTAT GATAGATTAATTTCAAGTAAAAAGTAAAGGACTTTTATAGATCGGAAGAGCGGTTCCAG
chr17	57758223	57758262	CLTC_4078	-	GTGACCTATGCACCAGACGTTAT ATGGGACATAAGTACTGAAATCAAGTTGTTTAAAAGATCGGAAGAGCGGTTCCAG
chr17	57758606	57758645	CLTC_4079	-	GTGACCTATGCACCAGACGTAAA AAGAATATTTTTAAATGCAATATTTTAAAGTTTATCCGAAGATCGGAAGAGCGGTTCCAG
chr17	57758958	57758997	CLTC_4080	-	GTGACCTATGCACCAGACGTAAG TTTGAAATTAGGGTTAGAGTAAATCAATCCTACCCAAGATCGGAAGAGCGGTTCCAG
chr17	57759582	57759621	CLTC_4081	-	GTGACCTATGCACCAGACGTAAA AAGAAAAAATATATCCAAAACACTAACATCCTAGTTTAAAGATCGGAAGAGCGGTTCCAG
chr17	57759940	57759979	CLTC_4082	-	GTGACCTATGCACCAGACGTAAA GGTAACCCACATTCAGCAAGATATTAGTGTGAGCTTAAAGATCGGAAGAGCGGTTCCAG
chr17	57760218	57760257	CLTC_4083	-	GTGACCTATGCACCAGACGTCA TTTCCCTTGCTGTGAACCTCAATGTAAAACATGGCTAGTAGATCGGAAGAGCGGTTCCAG
chr17	57760406	57760445	CLTC_4084	-	GTGACCTATGCACCAGACGTGAA GATGTTAGATGAAGAATCTATGTTGAAAAGAAAGATCGGAAGAGCGGTTCCAG
chr17	57760698	57760737	CLTC_4085	-	GTGACCTATGCACCAGACGTAAG ACTTAATTGCTTTAGATATGAGTCTAGCTAACAGCCTAGATCGGAAGAGCGGTTCCAG
chr17	57760936	57760975	CLTC_4086	-	GTGACCTATGCACCAGACGTAAA ATCCATACATAAGTCAAGTTACTTCCTAATGAGCTTTCAGATCGGAAGAGCGGTTCCAG
chr17	57761186	57761225	CLTC_4087	-	GTGACCTATGCACCAGACGTAA GAGTTTGTACAAATATAGCACATTATTGAAGTCCCAGAGATCGGAAGAGCGGTTCCAG
chr17	57762367	57762406	CLTC_4088	-	GTGACCTATGCACCAGACGTAAA AAGCCATCCAATGCCAGTCAATTTTGTTTAACATAGATCGGAAGAGCGGTTCCAG
chr17	57762898	57762937	CLTC_4089	-	GTGACCTATGCACCAGACGTA AATAGTGAAGCTCAAAAACATTAGACCCACATACTGAAAGATCGGAAGAGCGGTTCCAG
chr17	57767947	57767986	CLTC_4090	-	GTGACCTATGCACCAGACGTACA CATCATGTTAATTAGCACCCCAAAGTATTATAAACCAGATCGGAAGAGCGGTTCCAG
chr17	57771039	57771078	CLTC_4091	-	GTGACCTATGCACCAGACGTAGA AAAACAAAAGAGCAGGGGGCAGGGGCAAGGAGGCAGAGATCGGAAGAGCGGTTCCAG
chr8	113236950	113236989	CSMD3_4092	-	GTGACCTATGCACCAGACGTTTT GCCTTCTTCCAGAAGCTTGGAAATCGACACACAAAACAAGATCGGAAGAGCGGTTCCAG
chr8	113240935	113240974	CSMD3_4093	-	GTGACCTATGCACCAGACGTTG ATTTTTAACTACAAAATGTTTCCCAAATCTGTTTTTCAAGATCGGAAGAGCGGTTCCAG
chr8	113243724	113243763	CSMD3_4094	-	GTGACCTATGCACCAGACGTCAT TTTGATTTTTCACGAACCTGTTTATTATCCAGACATAGATCGGAAGAGCGGTTCCAG
chr8	113246544	113246583	CSMD3_4095	-	GTGACCTATGCACCAGACGTTT ATTTTTAACTTCTGCTGCTGATTTTTAATGATAAATTTGATAGATCGGAAGAGCGGTTCCAG
chr8	113249369	113249408	CSMD3_4096	-	GTGACCTATGCACCAGACGTA AAAACAGCAGCGAAATATACCTTCATGACTTTATTCTAAGATCGGAAGAGCGGTTCCAG
chr8	113253899	113253938	CSMD3_4097	-	GTGACCTATGCACCAGACGTTCA TTTGTTTTCTAGAGTTCATTATTTCTAAAATGGTCAGATCGGAAGAGCGGTTCCAG
chr8	113256573	113256612	CSMD3_4098	-	GTGACCTATGCACCAGACGTTCT ATAGAATCTTTTAAACACAAGAGATTGCACATTGCTAGATCGGAAGAGCGGTTCCAG
chr8	113259199	113259238	CSMD3_4099	-	GTGACCTATGCACCAGACGTTGG ATAAGAAAATGCTATCATGGGTAAAGAAATTTATAGATCGGAAGAGCGGTTCCAG
chr8	113266432	113266471	CSMD3_4100	-	GTGACCTATGCACCAGACGTTAG CTATGCTCATTAGCATCATACTAGGTGAGAATGCGTAGATCGGAAGAGCGGTTCCAG
chr8	113267433	113267472	CSMD3_4101	-	GTGACCTATGCACCAGACGTTT AAAGGCTGATTTGCACAGTAACGTGTGAATTAATAGAGATCGGAAGAGCGGTTCCAG
chr8	113275818	113275857	CSMD3_4102	-	GTGACCTATGCACCAGACGTTTT CTACTAACAACTGTTACTTAAAATTTTCAAATTTTTCAGATCGGAAGAGCGGTTCCAG
chr8	113293353	113293392	CSMD3_4103	-	GTGACCTATGCACCAGACGTTCT CAATATTTAAAAATCAGTAATTATAGAAATGTTGAAGATCGGAAGAGCGGTTCCAG
chr8	113299243	113299282	CSMD3_4104	-	GTGACCTATGCACCAGACGTGC AAAAAATTAATATATTGCAACTACTGGATTTTAGTGTGAGATCGGAAGAGCGGTTCCAG
chr8	113301544	113301583	CSMD3_4105	-	GTGACCTATGCACCAGACGTA AATTTGGACAATGTGTTGGAAATACATTATTTGTTAAAGATCGGAAGAGCGGTTCCAG
chr8	113303689	113303728	CSMD3_4106	-	GTGACCTATGCACCAGACGTAAT GTGAATGTTTCTTGAGAACATGTCAATGGAACATAAGATCGGAAGAGCGGTTCCAG
chr8	113304716	113304755	CSMD3_4107	-	GTGACCTATGCACCAGACGTAAG TATATTTCCCAATTTGGTGGCATGATAATAATATTACAAGATCGGAAGAGCGGTTCCAG
chr8	113308012	113308051	CSMD3_4108	-	GTGACCTATGCACCAGACGTAT GGCAAAAGCAATTAGAGACCTCTGATCTTTGGAATAATAGATCGGAAGAGCGGTTCCAG
chr8	113313972	113314011	CSMD3_4109	-	GTGACCTATGCACCAGACGTTT AAATTTGTTTTGTCAAACCTCCCTGCCCTCACCCTAGATCGGAAGAGCGGTTCCAG
chr8	113316900	113316939	CSMD3_4110	-	GTGACCTATGCACCAGACGTACT CTGCTAACTTATTTCATAAGCTATGTTTGGTTATCGAGATCGGAAGAGCGGTTCCAG
chr8	113318186	113318225	CSMD3_4111	-	GTGACCTATGCACCAGACGTAAG GAAATTTCACTGTTTCTCTGGTATTATTATAGATCGGAAGAGCGGTTCCAG
chr8	113323157	113323196	CSMD3_4112	-	GTGACCTATGCACCAGACGTTT ATGGCAAAATGAAACAAAACATGAATGTGAGATTAGCAAGATCGGAAGAGCGGTTCCAG
chr8	113326085	113326124	CSMD3_4113	-	GTGACCTATGCACCAGACGTTCT TATAACTCAGGACAGATCTCACTATCATCTCGGTATAGATCGGAAGAGCGGTTCCAG
chr8	113326608	113326647	CSMD3_4114	-	GTGACCTATGCACCAGACGTGTT ATATTTATTGGATATTCATCAATTAAGTACA AATGTTAGATCGGAAGAGCGGTTCCAG
chr8	113331016	113331055	CSMD3_4115	-	GTGACCTATGCACCAGACGTGTT CCTATGATTATTTATTCTTAAATATTTGCTTTATGTAGATCGGAAGAGCGGTTCCAG
chr8	113332080	113332119	CSMD3_4116	-	GTGACCTATGCACCAGACGTTAA ATTTATTTTCAAAGAAAACATACTGCTGGCAACTATAGATCGGAAGAGCGGTTCCAG
chr8	113347508	113347547	CSMD3_4117	-	GTGACCTATGCACCAGACGTTCT GAGAGTTCTTATTTCACTGTTTAAATTTGTCAGATCGGAAGAGCGGTTCCAG
chr8	113348831	113348870	CSMD3_4118	-	GTGACCTATGCACCAGACGTACT ATTTGTTATTGATTTTCAATTTATATACAGATAAAAAGATCGGAAGAGCGGTTCCAG

chr8	113349722	113349761	CSMD3_4119	-	GTGACCTATGCACCAGACGTAACCTGAAGCTATCTTTTAGGTGATGTCATCTGTTTTTAAAGATCGGAAGAGCGGTTCCAG
chr8	113358276	113358315	CSMD3_4120	-	GTGACCTATGCACCAGACGTTAAAAACACGTGAAGAGCTTTCAATATTTATTAATGTAGAGATCGGAAGAGCGGTTCCAG
chr8	113363354	113363393	CSMD3_4121	-	GTGACCTATGCACCAGACGTAGACTATAAAGTATTTACCCTAGAACCTAAAGTGTAATAAAGATCGGAAGAGCGGTTCCAG
chr8	113364595	113364634	CSMD3_4122	-	GTGACCTATGCACCAGACGTTTTAAAGTTGTGGTTTTGATTTTTCATGGCCCTTTCAGAAATAGATCGGAAGAGCGGTTCCAG
chr8	113395746	113395785	CSMD3_4123	-	GTGACCTATGCACCAGACGTGAGCTGAGCTTAATTAATAACAGATATAATAGGAATATAGATCGGAAGAGCGGTTCCAG
chr8	113402843	113402882	CSMD3_4124	-	GTGACCTATGCACCAGACGTTAAAGTTTTCTCTTTTCATTGTGTGTTAGTAAATCAGATCGGAAGAGCGGTTCCAG
chr8	113418703	113418742	CSMD3_4125	-	GTGACCTATGCACCAGACGTAAATTTGTATGATCTGTGATATACATAGTTTATATAAAGATCGGAAGAGCGGTTCCAG
chr8	113420497	113420536	CSMD3_4126	-	GTGACCTATGCACCAGACGTCTGTAGTCTAGAAACACACTAAGGAATGATATAATTTTCCAGATCGGAAGAGCGGTTCCAG
chr8	113421098	113421137	CSMD3_4127	-	GTGACCTATGCACCAGACGTATAGAAGTCCATGCATCAGTTACTGATTAAGACTGACTAGATCGGAAGAGCGGTTCCAG
chr8	113484770	113484809	CSMD3_4128	-	GTGACCTATGCACCAGACGTTTTGACTCATTATGTAGTATTTTCATCCAGACATGCTTTATAGATCGGAAGAGCGGTTCCAG
chr8	113504668	113504707	CSMD3_4129	-	GTGACCTATGCACCAGACGTTATTTTTGGCTGAATTTTCATGATTAGAAAAAATCAAAAAGATCGGAAGAGCGGTTCCAG
chr8	113515969	113516008	CSMD3_4130	-	GTGACCTATGCACCAGACGTACATCCATGTTAGTATCATGATTTAAATATAGATTTAGATCGGAAGAGCGGTTCCAG
chr8	113518870	113518909	CSMD3_4131	-	GTGACCTATGCACCAGACGTATATATTTATTTCCACGTAAAAAATATATTTGTTAGCCAGATCGGAAGAGCGGTTCCAG
chr8	113529213	113529252	CSMD3_4132	-	GTGACCTATGCACCAGACGTAAAGAACAAATTAATTTTATATAAACATAAAAAAATGGTTAGATCGGAAGAGCGGTTCCAG
chr8	113562850	113562889	CSMD3_4133	-	GTGACCTATGCACCAGACGTTCAAAAAATTTCTCAATGCAAAATAGGAAGGTGATGTAAGATCGGAAGAGCGGTTCCAG
chr8	113564773	113564812	CSMD3_4134	-	GTGACCTATGCACCAGACGTTTTCATTTTCTCAACATTACTAGGGAATCTGAAGTGCCTAAAGATCGGAAGAGCGGTTCCAG
chr8	113568942	113568981	CSMD3_4135	-	GTGACCTATGCACCAGACGTGTCATAGATTTTCATTGAAATTTCTGTGAAAACTTTATCAGATCGGAAGAGCGGTTCCAG
chr8	113585680	113585719	CSMD3_4136	-	GTGACCTATGCACCAGACGTAGAAGAGTAAATGCCCACAAACACTGGGGTCTGCTCATGTAAGATCGGAAGAGCGGTTCCAG
chr8	113648996	113649035	CSMD3_4137	-	GTGACCTATGCACCAGACGTAGCTGCTTTTCATTGCTTGTATGTGTAGTCACTGTCCATGAGATCGGAAGAGCGGTTCCAG
chr8	113650875	113650914	CSMD3_4138	-	GTGACCTATGCACCAGACGTAAAAACAAAAGGGCTCATTCAAGTAACTTTTAAAAAAGCAAGATCGGAAGAGCGGTTCCAG
chr8	113657288	113657327	CSMD3_4139	-	GTGACCTATGCACCAGACGTTCATGAAATAATAATGGACTATCTTCTGAATTTTTCATTGAGATCGGAAGAGCGGTTCCAG
chr8	113662340	113662379	CSMD3_4140	-	GTGACCTATGCACCAGACGTATTTGACATGCAAAAATGCTGATTTATAACAGAAAAATAGATCGGAAGAGCGGTTCCAG
chr8	113668333	113668372	CSMD3_4141	-	GTGACCTATGCACCAGACGTATAAACTTTTTGATTTCTCATTCTGTTTTGCCCTACTTTAGATCGGAAGAGCGGTTCCAG
chr8	113678456	113678495	CSMD3_4142	-	GTGACCTATGCACCAGACGTATATTTTTTCTACTTTTTAAAGAAAAATATCTAAAAAGATTAGATCGGAAGAGCGGTTCCAG
chr8	113694621	113694660	CSMD3_4143	-	GTGACCTATGCACCAGACGTAGTGTAGTGAGAAATAGAACCTCATCATATTATGTACAAAGATCGGAAGAGCGGTTCCAG
chr8	113697585	113697624	CSMD3_4144	-	GTGACCTATGCACCAGACGTGTTTCTGTTTTTTCCCATATAATATTTCTATAAATTTAGATCGGAAGAGCGGTTCCAG
chr8	113702047	113702086	CSMD3_4145	-	GTGACCTATGCACCAGACGTAATGCTTTTCTTCCAGATAGCATATGTTACCCTGTCCTTGAGATCGGAAGAGCGGTTCCAG
chr8	113812341	113812380	CSMD3_4146	-	GTGACCTATGCACCAGACGTATTTCTACATAGGAAATGTTATCTTAATACCACCAGAGAAAGATCGGAAGAGCGGTTCCAG
chr8	113841865	113841904	CSMD3_4147	-	GTGACCTATGCACCAGACGTAATGTTTTCATTTGCTTAGCCCTACGGGTACTAATAAAGATCGGAAGAGCGGTTCCAG
chr8	113871324	113871363	CSMD3_4148	-	GTGACCTATGCACCAGACGTACCATCTGTGATTTAAAAAAGCAATTAATCATAAAGACAGATCGGAAGAGCGGTTCCAG
chr8	113933806	113933845	CSMD3_4149	-	GTGACCTATGCACCAGACGTATAATAATGCCCTCTGAACACATTTTAAATAGTTAACTTAGATCGGAAGAGCGGTTCCAG
chr8	113959969	113960008	CSMD3_4150	-	GTGACCTATGCACCAGACGTAAATATTGACTTCATTATTTATCTTGTCAAGGTTTATTAGATCGGAAGAGCGGTTCCAG
chr8	113966863	113966902	CSMD3_4151	-	GTGACCTATGCACCAGACGTTTTCTTTTTTGTACTTTCTCTAGTGCAGAGTGAAGTTTGTAGATCGGAAGAGCGGTTCCAG
chr8	113988055	113988055	CSMD3_4152	-	GTGACCTATGCACCAGACGTTTATTTTCTTTGCCCCATTTAGTTACAGCCAAAGCTATAAGATCGGAAGAGCGGTTCCAG
chr8	114031246	114031285	CSMD3_4153	-	GTGACCTATGCACCAGACGTGGAATTAACCTTTTCCCTTTTGGATGTAAAAATAATTTGGAGATCGGAAGAGCGGTTCCAG
chr8	114110935	114110974	CSMD3_4154	-	GTGACCTATGCACCAGACGTAGCTTCTATTAACCTTGCATTGATGTTGTTGAAGCAAAGTAGATCGGAAGAGCGGTTCCAG
chr8	114185901	114185940	CSMD3_4155	-	GTGACCTATGCACCAGACGTAACTTTAAAAATGAGAGTTGTTATCAGCCAGTGTATTTAGATCGGAAGAGCGGTTCCAG
chr8	114290771	114290810	CSMD3_4156	-	GTGACCTATGCACCAGACGTGTAGTGGCAAACAAACACTGCCCTTAATGTAATTAACAAGATCGGAAGAGCGGTTCCAG
chr8	114326750	114326789	CSMD3_4157	-	GTGACCTATGCACCAGACGTTTTGAATGGAAGACTGGAGAGAAAAATTTCTGGGTAAAAGATCGGAAGAGCGGTTCCAG
chr8	114388917	114388956	CSMD3_4158	-	GTGACCTATGCACCAGACGTTGGCTCTTAGCTCCTTGGCCCCAACCTTCGGTCTTGTAGATCGGAAGAGCGGTTCCAG
chr8	114448856	114448895	CSMD3_4159	-	GTGACCTATGCACCAGACGTTTTGGGGTCCCTCCGCTTTGGATGGAGTGGGTGGCTGACTAGATCGGAAGAGCGGTTCCAG
chr19	1969722	1969761	CSNK1G2_4160	-	GTGACCTATGCACCAGACGTTACCCTGGCTCTCCACGGTGACTCTGCTGCCGTGCAAAATAGATCGGAAGAGCGGTTCCAG
chr19	1978254	1978293	CSNK1G2_4161	-	GTGACCTATGCACCAGACGTAGAGACCATCAGCACCGCCAGCGCAGGGCCACCTAGCCAGATCGGAAGAGCGGTTCCAG
chr19	1978391	1978430	CSNK1G2_4162	-	GTGACCTATGCACCAGACGTAAGAGCGAGTCACCAGGGGACCGGGTCCGCTGCCCTGAAATAGATCGGAAGAGCGGTTCCAG
chr19	1978551	1978590	CSNK1G2_4163	-	GTGACCTATGCACCAGACGTGGACAGACGCAGCCGGGCTGCGGGCGGCAGCCCTCCCTGCAGATCGGAAGAGCGGTTCCAG
chr19	1979268	1979307	CSNK1G2_4164	-	GTGACCTATGCACCAGACGTCTGTGGTCAAGCTTGTCTCCGCCCTCGCTCCCGCCAGATCGGAAGAGCGGTTCCAG
chr19	1979701	1979740	CSNK1G2_4165	-	GTGACCTATGCACCAGACGTGGGAGCAGGGGTCAGGATGGGCTGCAGCGCCGGTTCATAGATCGGAAGAGCGGTTCCAG
chr19	1979860	1979899	CSNK1G2_4166	-	GTGACCTATGCACCAGACGTCAGTAGGGGTACGCTGGCCGCCCATGCCCTCCCTGGGAGATCGGAAGAGCGGTTCCAG
chr19	1980098	1980137	CSNK1G2_4167	-	GTGACCTATGCACCAGACGTGCAAGTGGCTCAGGTAGGAGACCGGGTGCAGGGCGGGGCAGATCGGAAGAGCGGTTCCAG
chr5	138117564	138117603	CTNNA1_4168	-	GTGACCTATGCACCAGACGTGAACAACAAAGTCAAGTCAAGCAACACAAACATAGATCGGAAGAGCGGTTCCAG
chr5	138118816	138118855	CTNNA1_4169	-	GTGACCTATGCACCAGACGTCAATTTTAACTAAACTGGAGTCAATAAATGACAACAGATCGGAAGAGCGGTTCCAG
chr5	138145677	138145716	CTNNA1_4170	-	GTGACCTATGCACCAGACGTGAATGAAAACAAACTCAGCAAGAATGAACCTCAAAATACTAGATCGGAAGAGCGGTTCCAG
chr5	138147822	138147861	CTNNA1_4171	-	GTGACCTATGCACCAGACGTAGAAAGACCCCAAAACCAAAATCTGAATGTAGGTTCTGAGATCGGAAGAGCGGTTCCAG
chr5	138160169	138160208	CTNNA1_4172	-	GTGACCTATGCACCAGACGTAAATAAAACAAGAAATTTGGAGCACTTTTATATGGGCTTTAGATCGGAAGAGCGGTTCCAG
chr5	138163154	138163193	CTNNA1_4173	-	GTGACCTATGCACCAGACGTAGTATACCAGATTTAGTACTCATCTCTGTTCCCTTCTAGATCGGAAGAGCGGTTCCAG
chr5	138221851	138221890	CTNNA1_4174	-	GTGACCTATGCACCAGACGTGAAAGAGATGAGCATTTTATTTATCAAAAGAACTAGATCGGAAGAGCGGTTCCAG
chr5	138223129	138223168	CTNNA1_4175	-	GTGACCTATGCACCAGACGTAATTTGAATAATTTGATTTTTTTTCCAAAAAGGTATTAGATCGGAAGAGCGGTTCCAG
chr5	138239988	138240027	CTNNA1_4176	-	GTGACCTATGCACCAGACGTAATAAATCTTTAAAGATTTTTCTTTTTGACTGCTAAAGATCGGAAGAGCGGTTCCAG



chr5	138253381	138253420	CTNNA1_4177	-	GTGACCTATGCACCAGACGTTATAAACTTCACTGTTTACTCTTTTCAGAGTCATGGCTAGATCGGAAGAGCGGTTTCAG
chr5	138260149	138260188	CTNNA1_4178	-	GTGACCTATGCACCAGACGTAGCAAAAAGTTGAATGAGGAAGGAGGCTTTCTATGAAAAGAGATCGGAAGAGCGGTTTCAG
chr5	138260895	138260934	CTNNA1_4179	-	GTGACCTATGCACCAGACGTAGAGGCACAGTAGATACCCTGGTCAGCAGGCAGCATCATTAGATCGGAAGAGCGGTTTCAG
chr5	138264885	138264924	CTNNA1_4180	-	GTGACCTATGCACCAGACGTGACAAGATCACAGGTCAGACACATCTCTGGGCCACCAGCAGATCGGAAGAGCGGTTTCAG
chr5	138266112	138266151	CTNNA1_4181	-	GTGACCTATGCACCAGACGTAAAGCACAAGAGACTCTTACATAAAAAAATATGAAGTTCTAGATCGGAAGAGCGGTTTCAG
chr5	138266469	138266508	CTNNA1_4182	-	GTGACCTATGCACCAGACGTGGAAGAGAACAAGGATTATTGTATGTGAAGCCCCTCACAGAGATCGGAAGAGCGGTTTCAG
chr5	138268217	138268256	CTNNA1_4183	-	GTGACCTATGCACCAGACGTGACAGGCTTAAACACCAAGTACTCTGGCCCTGCCCCAAGCACAGATCGGAAGAGCGGTTTCAG
chr5	138269441	138269480	CTNNA1_4184	-	GTGACCTATGCACCAGACGTGACAGGGGTGTAAGAAGCACCGGCCTGACCTCCAGCCTCAGATCGGAAGAGCGGTTTCAG
chr2	38297815	38297854	CYP1B1_4185	-	GTGACCTATGCACCAGACGTGCAAGCTGAAATTTTAGAAATATTCACATCTTCGGAGATGAGATCGGAAGAGCGGTTTCAG
chr2	38301439	38301478	CYP1B1_4186	-	GTGACCTATGCACCAGACGTTGGGAGGCGTGGGCCAGGCTTTTTCTCCTCTGAAAAGGCAGATCGGAAGAGCGGTTTCAG
chr2	38298109	38298148	CYP1B1_4187	-	GTGACCTATGCACCAGACGTGCCTCATCAACAAGGACCTGACCAGCAGAGTGATGATTTTAGATCGGAAGAGCGGTTTCAG
chr2	38301786	38301825	CYP1B1_4188	-	GTGACCTATGCACCAGACGTGCGCGGCCAGCCTGGTGGACGTGATGCCCTGGCTGCAGTAAGATCGGAAGAGCGGTTTCAG
chr2	38302133	38302172	CYP1B1_4189	-	GTGACCTATGCACCAGACGTGCGCTTCCGCTGCTGGTGTCCGGCCGCGCAGCATCGGCTAGATCGGAAGAGCGGTTTCAG
chr11	47236638	47236677	DDB2_4190	-	GTGACCTATGCACCAGACGTGTGTGAAGGGTACTGTGCTCTATGCGAAGATCATGGAGGAGATCGGAAGAGCGGTTTCAG
chr11	47237837	47237876	DDB2_4191	-	GTGACCTATGCACCAGACGTGAACAGACATATTTCTCCTCCAATCTCACGAAAGGTTTTAGATCGGAAGAGCGGTTTCAG
chr11	47238359	47238398	DDB2_4192	-	GTGACCTATGCACCAGACGTGAGAATGAATTAGGTTGAATTAACCCAAAGTTCTGGGTAGATCGGAAGAGCGGTTTCAG
chr11	47254315	47254354	DDB2_4193	-	GTGACCTATGCACCAGACGTGAAGGAAAAGCCAGTGAGTGATGATGGGCCCTGGCCGTGAAGATCGGAAGAGCGGTTTCAG
chr11	47256258	47256297	DDB2_4194	-	GTGACCTATGCACCAGACGTGAGCTGAGTTCCAGTGGGACACAGAACCAGAGTTGGGGTAGATCGGAAGAGCGGTTTCAG
chr11	47256771	47256810	DDB2_4195	-	GTGACCTATGCACCAGACGTGAAAAGCCCCTGAGCTGAAGGAACCAAGCCCTCTGTGGAGATCGGAAGAGCGGTTTCAG
chr11	47259338	47259377	DDB2_4196	-	GTGACCTATGCACCAGACGTGAGAGGCCGGCCATGAGGGTAAACACAGAACATGATCAAGAGATCGGAAGAGCGGTTTCAG
chr11	47259639	47259678	DDB2_4197	-	GTGACCTATGCACCAGACGTAAAGAGTGTCAACATGAGGAGAGGGTGAAGGTATTAGCAGAAGATCGGAAGAGCGGTTTCAG
chr11	47260301	47260340	DDB2_4198	-	GTGACCTATGCACCAGACGTTGAGACCAGTCTGACTTACACTTTCTGTTACCAATCTCTCAGATCGGAAGAGCGGTTTCAG
chr7	137075916	137075955	DGKI_4199	-	GTGACCTATGCACCAGACGTGGGCAAAGAGGACATGAGCAAGCGTATCACATCGCCCTAGATCGGAAGAGCGGTTTCAG
chr7	137080294	137080333	DGKI_4200	-	GTGACCTATGCACCAGACGTGAGTGAGTGCAACATCTCCCGCTGGGCGAGATCGAGATCGGAAGAGCGGTTTCAG
chr7	137082073	137082112	DGKI_4201	-	GTGACCTATGCACCAGACGTCTTTTTATTACATAGTCTAGGTTATTTCTTCCAGAACATAAGATCGGAAGAGCGGTTTCAG
chr7	137092571	137092610	DGKI_4202	-	GTGACCTATGCACCAGACGTATAGTGAACCTACCAAGGATCACTTACCTGTGAAATCCATAGATCGGAAGAGCGGTTTCAG
chr7	137096866	137096905	DGKI_4203	-	GTGACCTATGCACCAGACGTTTCTACCAAATCTTTGGCGATGCTTTAAGAACTTTAATAGATCGGAAGAGCGGTTTCAG
chr7	137128773	137128812	DGKI_4204	-	GTGACCTATGCACCAGACGTTCTGTCTTATTTATACCAATTCAGGATTGAAACTTGACCAGATCGGAAGAGCGGTTTCAG
chr7	137148185	137148224	DGKI_4205	-	GTGACCTATGCACCAGACGTTCTGTCTTTCTTTCTCTGTGCCACTGTATTGCTGGGAGATCGGAAGAGCGGTTTCAG
chr7	137150604	137150643	DGKI_4206	-	GTGACCTATGCACCAGACGTTTCTCCTGGCCTGTGAGGCTGGCCCTTAGGGTGACATCCATAGATCGGAAGAGCGGTTTCAG
chr7	137151598	137151637	DGKI_4207	-	GTGACCTATGCACCAGACGTTTCCAGCCTGCTTGTGAAAGTGA AAAATTC CCAAGTTAATAGATCGGAAGAGCGGTTTCAG
chr7	137154246	137154285	DGKI_4208	-	GTGACCTATGCACCAGACGTCCTTTCTTGGGGATCGTGGGAGTTGGGGAAGTTGAAGAAGATCGGAAGAGCGGTTTCAG
chr7	137170070	137170109	DGKI_4209	-	GTGACCTATGCACCAGACGTATTGACTCTCCTTTGTTTCTTACCTTCTGGCCAAATGAAGTAGATCGGAAGAGCGGTTTCAG
chr7	137172306	137172345	DGKI_4210	-	GTGACCTATGCACCAGACGTTTAGCCAAATTTTTATTCTCTCAACTTTCCATTTTTGTAAGATCGGAAGAGCGGTTTCAG
chr7	137206562	137206601	DGKI_4211	-	GTGACCTATGCACCAGACGTAGTGCCCTATTGATTTTACATCGCATAGCCTATCTTCCAGTATCGGAAGAGCGGTTTCAG
chr7	137237065	137237104	DGKI_4212	-	GTGACCTATGCACCAGACGTTTCATGGCCTACCTTCTTAAACATGAAGACCTTGGAGAGGAAGATCGGAAGAGCGGTTTCAG
chr7	137255871	137255910	DGKI_4213	-	GTGACCTATGCACCAGACGTTAACTGTTTTATTAATAAGAAATGTATTTAGTACAGAGAGATCGGAAGAGCGGTTTCAG
chr7	137257461	137257500	DGKI_4214	-	GTGACCTATGCACCAGACGTTTTGATTGTTTCCCTTTGGTTTGAGCTGAACTCTGACTTGAAGATCGGAAGAGCGGTTTCAG
chr7	137261918	137261957	DGKI_4215	-	GTGACCTATGCACCAGACGTAATATGTTGATTTATTAATTTGAATATGATGACTGCCAGATCGGAAGAGCGGTTTCAG
chr7	137262966	137263005	DGKI_4216	-	GTGACCTATGCACCAGACGTATTTTATTCATAATTACTACATATTACTTATTGCCAATTAGATCGGAAGAGCGGTTTCAG
chr7	137266546	137266585	DGKI_4217	-	GTGACCTATGCACCAGACGTCTCCCTTTCCATTTCCACAGGAGGAAGTTTCTAGCAGGAGATCGGAAGAGCGGTTTCAG
chr7	137269905	137269944	DGKI_4218	-	GTGACCTATGCACCAGACGTTTTTTGTTCTGCAGAAAGGAGCCCTGGAGCATCTGCCTGAAGATCGGAAGAGCGGTTTCAG
chr7	137271793	137271832	DGKI_4219	-	GTGACCTATGCACCAGACGTCCTCTCGGGACTGCCCATATCATCAAACAACAACCCGGATAGATCGGAAGAGCGGTTTCAG
chr7	137282543	137282582	DGKI_4220	-	GTGACCTATGCACCAGACGTGAGAGAGAATCCAGTTCTCTGCCAATCTATCTTTCTTATAGATCGGAAGAGCGGTTTCAG
chr7	137284519	137284558	DGKI_4221	-	GTGACCTATGCACCAGACGTAATATTCTCCATGGTCCATATGATTTTTAGGCAAGTGAGAGATCGGAAGAGCGGTTTCAG
chr7	137293662	137293701	DGKI_4222	-	GTGACCTATGCACCAGACGTTTTTATCATTTTCAACTTTGCAAGTTTTGATAATTTCTGAAATCGGAAGAGCGGTTTCAG
chr7	137304520	137304559	DGKI_4223	-	GTGACCTATGCACCAGACGTGGACTCTGGTCTGCTGGGCCAGTGCAGAGAAAATGAACAGATCGGAAGAGCGGTTTCAG
chr7	137308179	137308218	DGKI_4224	-	GTGACCTATGCACCAGACGTGATGAAATAAAGCAATGTGGGCTCATGTTTTGCGAAATAAGATCGGAAGAGCGGTTTCAG
chr7	137330168	137330207	DGKI_4225	-	GTGACCTATGCACCAGACGTAGCCACCTCATGGCCTCGCAGGAGGCTCCCCAGGCCTCTGAGATCGGAAGAGCGGTTTCAG
chr7	137339428	137339467	DGKI_4226	-	GTGACCTATGCACCAGACGTGACAGCTTGATTCAAGTATCACCTTTGATTTCTCATTGAAGATCGGAAGAGCGGTTTCAG
chr7	137341162	137341201	DGKI_4227	-	GTGACCTATGCACCAGACGTGCCCTTGTGCAGTTTTGTACATTTGCAAGTATTTGGTCAGATCGGAAGAGCGGTTTCAG
chr7	137363253	137363292	DGKI_4228	-	GTGACCTATGCACCAGACGTGCTCCGCTTCTGGTGGGGAAGGCCCTGTGGATCTGAATGAAAAGATCGGAAGAGCGGTTTCAG
chr7	137374590	137374629	DGKI_4229	-	GTGACCTATGCACCAGACGTGCCTTTTTCATTTAAACATCACTTTCAGTGATGTTTTGTGTAGATCGGAAGAGCGGTTTCAG
chr7	137531158	137531197	DGKI_4230	-	GTGACCTATGCACCAGACGTGGAGCCGGCAGCCGAGACAGGTGCGCCGCGGCGGGAGACCAGATCGGAAGAGCGGTTTCAG
chr6	10983964	10984003	ELOVL2_4231	-	GTGACCTATGCACCAGACGTGAGAAAAGCACATATACTAGCCTAACAGATTGGCTTGTTAGATCGGAAGAGCGGTTTCAG
chr6	10990501	10990540	ELOVL2_4232	-	GTGACCTATGCACCAGACGTCTCTTTTACTTTTTCTCCATGTGGCTTATGGATGGGGAAGATCGGAAGAGCGGTTTCAG
chr6	10995190	10995229	ELOVL2_4233	-	GTGACCTATGCACCAGACGTTTGTAAATTTCCGTTTTGAGGAATGGCTTTAGAGACCAAGATCGGAAGAGCGGTTTCAG
chr6	11000270	11000309	ELOVL2_4234	-	GTGACCTATGCACCAGACGTAGAAGCAATCAACCAACTATAACCAGTTCCTTACATGACAAAGATCGGAAGAGCGGTTTCAG

chr6	11005555	11005594	ELOVL2_4235	-	GTGACCTATGCACCAGACGTGTAGCCAAAGCTGAAGTCCAGTAACTAGCAGTTTTTATAGATCGGAAGAGCGGTTTCAG
chr6	11010929	11010968	ELOVL2_4236	-	GTGACCTATGCACCAGACGTTACTTGAGAACCTAATGTGGAAAGAACACAGGAAGAACACAGATCGGAAGAGCGGTTTCAG
chr6	11044411	11044450	ELOVL2_4237	-	GTGACCTATGCACCAGACGTCCGCGCGCCGCCACCCGACCCGCCGCGCTTTCTTCTCTCAGATCGGAAGAGCGGTTTCAG
chr12	132445115	132445154	EP400_4238	-	GTGACCTATGCACCAGACGTCTTCTGTATCCAATGTGTGCTTCTCTCTAAAATATAAATTAGATCGGAAGAGCGGTTTCAG
chr12	132464192	132464231	EP400_4239	-	GTGACCTATGCACCAGACGTAAAAGATTGAAAAAATGAGATTTTGATCACTGAAGGCCATTAGATCGGAAGAGCGGTTTCAG
chr12	132466588	132466627	EP400_4240	-	GTGACCTATGCACCAGACGTAGAAAAGTGCACAAAGCATTGATTTCCAAAGTGTGGCAGCTAGATCGGAAGAGCGGTTTCAG
chr12	132471009	132471048	EP400_4241	-	GTGACCTATGCACCAGACGTGAGGGCACAAGTGGAGCAAGTGAAGAAAAGATGTCGGGGCAGATCGGAAGAGCGGTTTCAG
chr12	132472200	132472239	EP400_4242	-	GTGACCTATGCACCAGACGTTACATGGGGGATGGTGGGGTCCGCATGTGATGAGTGTGTTAGATCGGAAGAGCGGTTTCAG
chr12	132474459	132474498	EP400_4243	-	GTGACCTATGCACCAGACGTAAAGTGAAGAATTGTATGTTGTACTCTATGTCATGCTGGAGATCGGAAGAGCGGTTTCAG
chr12	132475131	132475170	EP400_4244	-	GTGACCTATGCACCAGACGTAGGATTAATGAATAAGCACATTAAGGATGGGAATTAAGATCGGAAGAGCGGTTTCAG
chr12	132475902	132475941	EP400_4245	-	GTGACCTATGCACCAGACGTAAGGAGCACAGTTCGTTCCCAAGGCCCCCATGCTTGGCGGAGATCGGAAGAGCGGTTTCAG
chr12	132476668	132476707	EP400_4246	-	GTGACCTATGCACCAGACGTAGAAAAGAAAACCAAGCATGAGATCCAAACACTCGAAAGATCGGAAGAGCGGTTTCAG
chr12	132479362	132479401	EP400_4247	-	GTGACCTATGCACCAGACGTTATCAGCAAGTGTCACTGAGAGGCAACACCATTGAGTGTAGATCGGAAGAGCGGTTTCAG
chr12	132489572	132489611	EP400_4248	-	GTGACCTATGCACCAGACGTTTGGCGGCAGAAGGGCTGTTACTTTATAACAACAAGTGAAGATCGGAAGAGCGGTTTCAG
chr12	132490607	132490646	EP400_4249	-	GTGACCTATGCACCAGACGTAATAAACACAGAGAAGTGAAGGGCCACTGAGAAAGCTTTATAAGATCGGAAGAGCGGTTTCAG
chr12	132491195	132491234	EP400_4250	-	GTGACCTATGCACCAGACGTGAACAAATAAAGAATTGACAGCTCGTCAAATAATCACCCAGATCGGAAGAGCGGTTTCAG
chr12	132495993	132496032	EP400_4251	-	GTGACCTATGCACCAGACGTAAAACAGAAATTTCCAGCTCAAAGTATCTGTCATGTCCTCAAGATCGGAAGAGCGGTTTCAG
chr12	132497504	132497543	EP400_4252	-	GTGACCTATGCACCAGACGTGAGAGACAGTCAAGTGCCTTCAACCTCCACTGTCTTTCAAGATCGGAAGAGCGGTTTCAG
chr12	132497985	132498024	EP400_4253	-	GTGACCTATGCACCAGACGTGACAAGAGCAACAAGTGGAGTTCACAGCCACGGGGCTGGAGATCGGAAGAGCGGTTTCAG
chr12	132498272	132498311	EP400_4254	-	GTGACCTATGCACCAGACGTAAGTGTACTGTTTTCTTTCCAAAATGCTGCTGTAAACAGATCGGAAGAGCGGTTTCAG
chr12	132502030	132502069	EP400_4255	-	GTGACCTATGCACCAGACGTAGAAAGAAACACGAAGCATTCAATCCAAACGGCCATCGGAAGATCGGAAGAGCGGTTTCAG
chr12	132502705	132502744	EP400_4256	-	GTGACCTATGCACCAGACGTAAGAAAAAAGTCTTGTCTGCATGAAGAGGGCAAAAAAAGCAGATCGGAAGAGCGGTTTCAG
chr12	132504544	132504583	EP400_4257	-	GTGACCTATGCACCAGACGTATTGGTCCAGCAAGAATACAGATCAGACCCAGAAAGATCGGAAGAGCGGTTTCAG
chr12	132505574	132505613	EP400_4258	-	GTGACCTATGCACCAGACGTTAAGGTTTGTGCAAGAGTGTGATAGGTTCTTAATAAAGATCGGAAGAGCGGTTTCAG
chr12	132508272	132508311	EP400_4259	-	GTGACCTATGCACCAGACGTGAGAGGAAAAGTGAATTCAGATCATTGGAAAAATAGATCGGAAGAGCGGTTTCAG
chr12	132510141	132510180	EP400_4260	-	GTGACCTATGCACCAGACGTAGGTCCACTAGGTGTCAATGACAGGCATGTGTACATACAAGATCGGAAGAGCGGTTTCAG
chr12	132511932	132511971	EP400_4261	-	GTGACCTATGCACCAGACGTATAAAGGAAGAGGTGAAAAGGAAGCCCAAGTTCACAGGATAGATCGGAAGAGCGGTTTCAG
chr12	132512512	132512551	EP400_4262	-	GTGACCTATGCACCAGACGTAAGTGTGATAAACAAGTACTTGAAGAACAGAAATGACAAGAGATCGGAAGAGCGGTTTCAG
chr12	132514196	132514235	EP400_4263	-	GTGACCTATGCACCAGACGTGAAGCTGTTTTGTCCACCACGAGCCACACCTTCAAGATCGGAAGAGCGGTTTCAG
chr12	132514484	132514523	EP400_4264	-	GTGACCTATGCACCAGACGTAATCACATCAAGAGCGCTCATTCCAGGCGCGTGCAGAGATCGGAAGAGCGGTTTCAG
chr12	132516448	132516487	EP400_4265	-	GTGACCTATGCACCAGACGTACAAAACACAGGAGTTAGTATTCTGGAAAATGTTGGAAAGATCGGAAGAGCGGTTTCAG
chr12	132522177	132522216	EP400_4266	-	GTGACCTATGCACCAGACGTAAGATGTAAGATGCTAAGTCAGTCACCAGGAAACACAGTGTAGATCGGAAGAGCGGTTTCAG
chr12	132522448	132522487	EP400_4267	-	GTGACCTATGCACCAGACGTAGATGTGTGTTACTCCCCAGTACAAGTCCAAAGTGTGCATAGATCGGAAGAGCGGTTTCAG
chr12	132527799	132527838	EP400_4268	-	GTGACCTATGCACCAGACGTTCTATGTTTAGTTCGCTTATAGATCTTTTAAATGAGGGAGATCGGAAGAGCGGTTTCAG
chr12	132528140	132528179	EP400_4269	-	GTGACCTATGCACCAGACGTAGTATATTTTTGAATAGGGTTAATAGCAAGTAAATAAAAAGATCGGAAGAGCGGTTTCAG
chr12	132528672	132528711	EP400_4270	-	GTGACCTATGCACCAGACGTGAGCAGCAAGAAGTTCAGGATCAGGAGTGCAGCTCAGAGAGATCGGAAGAGCGGTTTCAG
chr12	132529166	132529205	EP400_4271	-	GTGACCTATGCACCAGACGTACGGCAAGCTCTGACTTCCACCAAGTCTCAGTGTATGATCGGAAGAGCGGTTTCAG
chr12	132529295	132529334	EP400_4272	-	GTGACCTATGCACCAGACGTAAGGGAAGGCCATGAGATGTGGAACCTCACAGGAAGCTGCAGATCGGAAGAGCGGTTTCAG
chr12	132529814	132529853	EP400_4273	-	GTGACCTATGCACCAGACGTAGGCAGTCTTCCAGCAAGAGAGTAAACCAGGAGATTCACAAAGATCGGAAGAGCGGTTTCAG
chr12	132530222	132530261	EP400_4274	-	GTGACCTATGCACCAGACGTAGATTTCAAGTAAAACAGGTGAATACACTAAGTCAGAAAGATCGGAAGAGCGGTTTCAG
chr12	132534818	132534857	EP400_4275	-	GTGACCTATGCACCAGACGTATTGACGAGAGTGCATCTGAATTAAGGCAGCATGGACAGACAGATCGGAAGAGCGGTTTCAG
chr12	132535094	132535133	EP400_4276	-	GTGACCTATGCACCAGACGTGACAGTGTGACAGCAATTATAAATAAAGGAAATCTGAAGATCGGAAGAGCGGTTTCAG
chr12	132537641	132537680	EP400_4277	-	GTGACCTATGCACCAGACGTGACGCAAGGTTAAAACATACAGGCAAGTTTAAGACAGAGATCGGAAGAGCGGTTTCAG
chr12	132537838	132537877	EP400_4278	-	GTGACCTATGCACCAGACGTAGGAAGGAAGAGGAGCCACTGGAGGGGCAGACTCGGCCTGAGATCGGAAGAGCGGTTTCAG
chr12	132539594	132539633	EP400_4279	-	GTGACCTATGCACCAGACGTAGGCGGGCATAAGGCAACAGCGCCAGGAAATGGGGTCCAGATCGGAAGAGCGGTTTCAG
chr12	132546605	132546644	EP400_4280	-	GTGACCTATGCACCAGACGTCAAACAGGACCTCAAATAATTTTACACAGACACTCAGAGATCGGAAGAGCGGTTTCAG
chr12	132546961	132547000	EP400_4281	-	GTGACCTATGCACCAGACGTGTTTGTCTATTAGTCTGGACAGGGATACTCGCCACCTTAGATCGGAAGAGCGGTTTCAG
chr12	132549163	132549202	EP400_4282	-	GTGACCTATGCACCAGACGTAGCAAAGTATCTTCTTCAACATTAAGTGTGCTCCATTAGATCGGAAGAGCGGTTTCAG
chr12	132551269	132551308	EP400_4283	-	GTGACCTATGCACCAGACGTGAAAATAATGGGAGAGTCCAGAGAAATTCAGGACACGGTATAGATCGGAAGAGCGGTTTCAG
chr12	132551857	132551896	EP400_4284	-	GTGACCTATGCACCAGACGTCAAAAGCCCTTAGTCAAGCAGACTGGGAAAAGAGCTTGAAGATCGGAAGAGCGGTTTCAG
chr12	132553990	132554029	EP400_4285	-	GTGACCTATGCACCAGACGTACTGCGAAATTAGGGCCGACAGACACTCCGCGCTCAAGAGATCGGAAGAGCGGTTTCAG
chr12	132561011	132561050	EP400_4286	-	GTGACCTATGCACCAGACGTACAAAAGGCCAAAACATACAGATTCAAAGGAGTATGTGCAAGATCGGAAGAGCGGTTTCAG
chr12	132561896	132561935	EP400_4287	-	GTGACCTATGCACCAGACGTAGAGTACAGAAAACACACTTGCACAGGAAACTCAGTCCAGAGATCGGAAGAGCGGTTTCAG
chr12	132445560	132445599	EP400_4288	-	GTGACCTATGCACCAGACGTCTGCCCGGGCCGGACTGGGCTGCGTGGGACTCTGGGTGAGATCGGAAGAGCGGTTTCAG
chr12	132446005	132446044	EP400_4289	-	GTGACCTATGCACCAGACGTAGCCAGGGGCCGGGGCAGCGGGCCGCTGCAGCACCTGAGATCGGAAGAGCGGTTTCAG
chr1	22895732	22895771	EPHA8_4290	-	GTGACCTATGCACCAGACGTGGAGACAAGAGGGCATCAGGCCCTCTGACTTCTCCCAGAGATCGGAAGAGCGGTTTCAG
chr1	22902660	22902699	EPHA8_4291	-	GTGACCTATGCACCAGACGTGAGGAACACAGCTACAGCAGACCCACCTCACCTAGATCGGAAGAGCGGTTTCAG
chr1	22912923	22912962	EPHA8_4292	-	GTGACCTATGCACCAGACGTGAAGGCGGCTGCACATGAGCCAGAGCCACCCCTGGCTGAGATCGGAAGAGCGGTTTCAG

chr1	22915314	22915353	EPHA8_4293	-	GTGACCTATGCACCAGACGTAGGATGACAGATGGGGCAGTGGTTATTTATTTGGGCTGTGAGATCGGAAGAGCGGTTTCAG
chr1	22919769	22919808	EPHA8_4294	-	GTGACCTATGCACCAGACGCTAATCCCCTGATGAGGCGGAGGAGACAAGGCGTGGCCAGATCGGAAGAGCGGTTTCAG
chr1	22919967	22920006	EPHA8_4295	-	GTGACCTATGCACCAGACGTACGGTGGTCACTGGGCGCTGCTGGCCAGCCCCTCAGATCGGAAGAGCGGTTTCAG
chr1	22921673	22921712	EPHA8_4296	-	GTGACCTATGCACCAGACGTAAGCCAGGGTTGGGGGACCAGGCTCTCAGCCCTGGCCTTGAGATCGGAAGAGCGGTTTCAG
chr1	22922549	22922588	EPHA8_4297	-	GTGACCTATGCACCAGACGTGGGCACCGCCCTGCTGAGGCCAGGCCACCCCTAGCCCGGAGATCGGAAGAGCGGTTTCAG
chr1	22923755	22923794	EPHA8_4298	-	GTGACCTATGCACCAGACGTGGAGGAGGGCCCTTCACTGGGGCCAGGAGAGATTGCTTTTAGATCGGAAGAGCGGTTTCAG
chr1	22924119	22924158	EPHA8_4299	-	GTGACCTATGCACCAGACGTGAGAGAGGGTGTGGAGGGCCAGTGGGACCCCTGAAGATCGGAAGAGCGGTTTCAG
chr1	22924594	22924633	EPHA8_4300	-	GTGACCTATGCACCAGACGTAGTAGGGAGAGGGTGGCTCTTGTTGGTGGGGCTCAGGGCTGAGATCGGAAGAGCGGTTTCAG
chr1	22925281	22925320	EPHA8_4301	-	GTGACCTATGCACCAGACGTACATGGCTTGGACTTCAGGAAAGCCCGGGAGGCGCCTGGAGATCGGAAGAGCGGTTTCAG
chr1	22927104	22927143	EPHA8_4302	-	GTGACCTATGCACCAGACGTACACAAGAGTTGAGGGGGCTGCCAGGCCTGGCAGGGTGTAGATCGGAAGAGCGGTTTCAG
chr1	22927341	22927380	EPHA8_4303	-	GTGACCTATGCACCAGACGTTCAGCGCTGGGCTCAGCCCTCCCTCCCTGCACCTGAGGCAGATCGGAAGAGCGGTTTCAG
chr1	22927743	22927782	EPHA8_4304	-	GTGACCTATGCACCAGACGTGGGGCTCTGGTAAGTGGCCAGAGGGTTCCGGAGGCTGGAAGATCGGAAGAGCGGTTTCAG
chr1	22928070	22928109	EPHA8_4305	-	GTGACCTATGCACCAGACGTAGGGTGTCTGGCTGGCCAGCTGGGAGCTGGGAGGCTGGGAGCAGATCGGAAGAGCGGTTTCAG
chr1	22902992	22903031	EPHA8_4306	-	GTGACCTATGCACCAGACGTACCAAGGTGCGCACCTGTGAAGCTCTCGTGGCCGCAATAGATCGGAAGAGCGGTTTCAG
chr1	22915568	22915607	EPHA8_4307	-	GTGACCTATGCACCAGACGTTAGTTCATGTGGCCAGCAGGTTGGCCACCAGCAGGCTGGAGATCGGAAGAGCGGTTTCAG
chr1	23107864	23107903	EPHB2_4308	-	GTGACCTATGCACCAGACGTAGCAAAAGATCACCACCCCGCCCACTACCAGGCGCTGTAGATCGGAAGAGCGGTTTCAG
chr1	23110835	23110874	EPHB2_4309	-	GTGACCTATGCACCAGACGTAATGCTGTCAGTGGGGAGTAAAGGCTCAGCCCCAGCAAGATCGGAAGAGCGGTTTCAG
chr1	23189480	23189519	EPHB2_4310	-	GTGACCTATGCACCAGACGTAGCAAGGAGTCAACGAAACTGAGATGAAGACTCAGAAGATCGGAAGAGCGGTTTCAG
chr1	23191320	23191359	EPHB2_4311	-	GTGACCTATGCACCAGACGTGAGAGGTTGTTGGTCACTGGGGGGCTCAGGGGTACTATTAGATCGGAAGAGCGGTTTCAG
chr1	23208802	23208841	EPHB2_4312	-	GTGACCTATGCACCAGACGTGGCCAGAGGTCAGGGATCAGGGAGGCATGAGAAGTGCAGAGATCGGAAGAGCGGTTTCAG
chr1	23219327	23219366	EPHB2_4313	-	GTGACCTATGCACCAGACGTACAGAGAAGAAAATTAGTGAGGTTGTGGCTCATAGTGGTAGATCGGAAGAGCGGTTTCAG
chr1	23221915	23221954	EPHB2_4314	-	GTGACCTATGCACCAGACGTAGCATGGTAGGGCATTCTCAGCCTGGCTGTGGGAGTCGTAAGATCGGAAGAGCGGTTTCAG
chr1	23222854	23222893	EPHB2_4315	-	GTGACCTATGCACCAGACGTAGCAAAAGGCTGGAGCCACTGAAGCGCCAGGGAGCTGAGATCGGAAGAGCGGTTTCAG
chr1	23222857	23222896	EPHB2_4316	-	GTGACCTATGCACCAGACGTAAAGGCAAAAGGCTGAGCCACTGAAGCGCCAGGGAGAGCTCGGAAGAGCGGTTTCAG
chr1	23232430	23232469	EPHB2_4317	-	GTGACCTATGCACCAGACGTAGACCAGGCTCTGTATATGGACTGACTCAAGATGCACACAGATCGGAAGAGCGGTTTCAG
chr1	23233153	23233192	EPHB2_4318	-	GTGACCTATGCACCAGACGTAACACCAAGACAGACAGGATGTCACTTCCAGGTTGGAAGGAGATCGGAAGAGCGGTTTCAG
chr1	23234396	23234435	EPHB2_4319	-	GTGACCTATGCACCAGACGTAGTGGGGAAAAACACAGAGTAAACAGAAGAGCAGGCATCAGAGATCGGAAGAGCGGTTTCAG
chr1	23236825	23236864	EPHB2_4320	-	GTGACCTATGCACCAGACGTGACAGAGTGCAGTGGGGTGGGTGGATGGGCTGAGGGCGTAGATCGGAAGAGCGGTTTCAG
chr1	23238887	23238926	EPHB2_4321	-	GTGACCTATGCACCAGACGTGGTGGGCGACAGATGGTCAGGCGACCTGTTTCAGGGAGATCGGAAGAGCGGTTTCAG
chr1	23239905	23239944	EPHB2_4322	-	GTGACCTATGCACCAGACGTGAAGCAGCTGTGTTGGAAGAAATGCGGGTGAAGGGTCCAGATCGGAAGAGCGGTTTCAG
chr1	23111177	23111216	EPHB2_4323	-	GTGACCTATGCACCAGACGTCCCAGTCCACCTGGGAGAAGCTCTCGTGGCTGCAATGGAGATCGGAAGAGCGGTTTCAG
chr21	39755275	39755314	ERG_4324	-	GTGACCTATGCACCAGACGTGAGGCTTTTCCCATCAGCGTGCATTACCAGCCCATCGCCAGATCGGAAGAGCGGTTTCAG
chr21	39762867	39762906	ERG_4325	-	GTGACCTATGCACCAGACGTGCTGATGTTTCTTCTTACAAAATTACTTTTTGGCAGTGAAGATCGGAAGAGCGGTTTCAG
chr21	39763531	39763570	ERG_4326	-	GTGACCTATGCACCAGACGTGGGGCGCTGGGATAAACATAAGACAAGATTAGGCTCAGAGATCGGAAGAGCGGTTTCAG
chr21	39764248	39764287	ERG_4327	-	GTGACCTATGCACCAGACGTGGCTCCCATGACCTGAGTTTTCATGTACAGGCATGGATGATCGGAAGAGCGGTTTCAG
chr21	39772446	39772485	ERG_4328	-	GTGACCTATGCACCAGACGTACCCCTGTGTGATCTTCTTATTGAGAGACATCCCAGATGTAGATCGGAAGAGCGGTTTCAG
chr21	39774429	39774468	ERG_4329	-	GTGACCTATGCACCAGACGTCCCCGCCCTGCTCCAGCAAGAGCGTAGGGTCTTACGTAGATCGGAAGAGCGGTTTCAG
chr21	39775378	39775417	ERG_4330	-	GTGACCTATGCACCAGACGTCTTCTTCTCAAGGATAGATGGCTGTGGCTATGGTCTTATAGATCGGAAGAGCGGTTTCAG
chr21	39795282	39795321	ERG_4331	-	GTGACCTATGCACCAGACGTACAGCTTCACTGCCCTCGGCAGATCGCAACTTCCCAGAGATCGGAAGAGCGGTTTCAG
chr21	39817277	39817316	ERG_4332	-	GTGACCTATGCACCAGACGTGTTCCGCCCTTCTCCTCCCTGACCTCCCATTTCTATCCAGATCGGAAGAGCGGTTTCAG
chr21	39870237	39870276	ERG_4333	-	GTGACCTATGCACCAGACGTGGTTTCTTCTTAAATTTGACAAAATCTTGTCTTACTTAGATCGGAAGAGCGGTTTCAG
chr21	39947536	39947575	ERG_4334	-	GTGACCTATGCACCAGACGTCTTGGCTGGGAAGCCAGCTCTGCCCTTCTCTGTGCCTAGAGATCGGAAGAGCGGTTTCAG
chr21	39755535	39755574	ERG_4335	-	GTGACCTATGCACCAGACGTGGCCCTCCAGCCCAACCCCGGAGTATCTCTGTACAAGAGATCGGAAGAGCGGTTTCAG
chr11	44129213	44129252	EXT2_4336	-	GTGACCTATGCACCAGACGTACAGCCTTCTCCTCACACTCCTGGTACCAGGGAGAGAAAAGATCGGAAGAGCGGTTTCAG
chr11	44130694	44130733	EXT2_4337	-	GTGACCTATGCACCAGACGTATTTAAATGTAGGAGAATTAAGTGTCAACTATGAAAAGAGATCGGAAGAGCGGTTTCAG
chr11	44135685	44135724	EXT2_4338	-	GTGACCTATGCACCAGACGTAGTATTTTGTAAACAGATGAAAGAAAGGACTTTTATTCTAGATCGGAAGAGCGGTTTCAG
chr11	44146289	44146328	EXT2_4339	-	GTGACCTATGCACCAGACGTAAAAAACAGGTGATTGGAAAATTGCAGCTGGTATGTTAGTAGATCGGAAGAGCGGTTTCAG
chr11	44148316	44148355	EXT2_4340	-	GTGACCTATGCACCAGACGTACAAAGAGGCAAGAGATTACAACTAGTTTTGCTGATCCAAGATCGGAAGAGCGGTTTCAG
chr11	44151545	44151584	EXT2_4341	-	GTGACCTATGCACCAGACGTACAGAAAACAGTTTACATACACACAGCCCTTACAGAAAAGAGATCGGAAGAGCGGTTTCAG
chr11	44193111	44193150	EXT2_4342	-	GTGACCTATGCACCAGACGTAATAATGCTGTTTTAAGTAGCAAGCGACAGAGTGGGAAGATCGGAAGAGCGGTTTCAG
chr11	44219329	44219368	EXT2_4343	-	GTGACCTATGCACCAGACGTACAGATTAACACGGGTCAGAAAAGCAGCTGTAACAATATGAGATCGGAAGAGCGGTTTCAG
chr11	44228293	44228332	EXT2_4344	-	GTGACCTATGCACCAGACGTAGAAAAGGTTATTACTTATCTTCTTAACTTTTGTGAGGAGAAGATCGGAAGAGCGGTTTCAG
chr11	44253853	44253892	EXT2_4345	-	GTGACCTATGCACCAGACGTACACATAATAAACAATCAAGTCCCAATTGACAGCAACCAAGATCGGAAGAGCGGTTTCAG
chr11	44255615	44255654	EXT2_4346	-	GTGACCTATGCACCAGACGTAGACAGAAAAGAAGAAATATTCAAAAATAGCAGTTCCCTTTAGATCGGAAGAGCGGTTTCAG
chr11	44257793	44257832	EXT2_4347	-	GTGACCTATGCACCAGACGTAGGACAAAACATACCTGGCTGTCAAGTGTCAAGGACAATAAGATCGGAAGAGCGGTTTCAG
chr11	44265649	44265688	EXT2_4348	-	GTGACCTATGCACCAGACGTTGGAGAGGAGTGGGGAGGAGGGGTTTGGAGCAATGAGAAGATCGGAAGAGCGGTTTCAG
chr11	44129481	44129520	EXT2_4349	-	GTGACCTATGCACCAGACGTGCTGCAACTGAGATCCCCCGCTGCGGATGGGACTGTGAGATCGGAAGAGCGGTTTCAG
chr9	97863939	97863978	FANCC_4350	-	GTGACCTATGCACCAGACGTGGCCGTGTGGGTGCCCGGCTGAGGGATCAGGCTCCAGAGATCGGAAGAGCGGTTTCAG

chr9	97869328	97869337	FANCC_4351	-	GTGACCTATGCACCAGACGTCTGTGGTCCAGCATCCTAGTACTCATTCTTCTGCCAGGCGAGATCGGAAGAGCGGTTTCAG
chr9	97873695	97873734	FANCC_4352	-	GTGACCTATGCACCAGACGTGGCCCCACTGCATGTGTTTTGGGGTGGGCTCTGGGGGGCTGAGATCGGAAGAGCGGTTTCAG
chr9	97876861	97876900	FANCC_4353	-	GTGACCTATGCACCAGACGTACTGACCACTCCCAAACTACTTCACACATGGTTTTCCCTAAGATCGGAAGAGCGGTTTCAG
chr9	97879547	97879586	FANCC_4354	-	GTGACCTATGCACCAGACGTGTTGACTTTGCCACATCAGAATGATTTCTGGGAAGAGCAGATCGGAAGAGCGGTTTCAG
chr9	97887318	97887357	FANCC_4355	-	GTGACCTATGCACCAGACGTTCACATATATTACTATTCCAGAAATAAGACGCTGAGATCGGAAGAGCGGTTTCAG
chr9	97888761	97888800	FANCC_4356	-	GTGACCTATGCACCAGACGTCACTGTTTTCTTAGTAATTGATGAAAAAGGTTCCATTAGATCGGAAGAGCGGTTTCAG
chr9	97897578	97897617	FANCC_4357	-	GTGACCTATGCACCAGACGTGGTTTTGATGAAGGGAAAACTTGAAGGAGATGCTTGGAGATCGGAAGAGCGGTTTCAG
chr9	97912155	97912194	FANCC_4358	-	GTGACCTATGCACCAGACGTAATGTTTTCTGTCTCCTGCGTCTGTTTTCTTTTTCTTAGAGATCGGAAGAGCGGTTTCAG
chr9	97933311	97933350	FANCC_4359	-	GTGACCTATGCACCAGACGTAACATAACATCTTCTTCTCAGGTTTTCAAATGTATCAGTAGATCGGAAGAGCGGTTTCAG
chr9	97934269	97934308	FANCC_4360	-	GTGACCTATGCACCAGACGTAAAATTTATCACTTTTGAATGTTAATGCTGAATGTGCCAGATCGGAAGAGCGGTTTCAG
chr9	98002881	98002920	FANCC_4361	-	GTGACCTATGCACCAGACGTAAATCTTGCTCTGCACCTCTTTGAATTAATGATTATTTAGATCGGAAGAGCGGTTTCAG
chr9	98009664	98009703	FANCC_4362	-	GTGACCTATGCACCAGACGTAAAACGTGCTCTCAAATGGCTATTTAATCTTTGCATAGATCGGAAGAGCGGTTTCAG
chr9	98011359	98011398	FANCC_4363	-	GTGACCTATGCACCAGACGTGACCAAGATAAATAAATTTTTCTGACCTCAGGGACTCTAGATCGGAAGAGCGGTTTCAG
chr9	35074055	35074094	FANCC_4364	-	GTGACCTATGCACCAGACGTTTTGAAGAGCTTGAGCTGGGTCCCCAGTGGGCTGTCTCTAGATCGGAAGAGCGGTTTCAG
chr9	35074318	35074357	FANCC_4365	-	GTGACCTATGCACCAGACGTGGCCTGCTGGCTTGGGGCTGAGGGGCAGTTGGTGTCTAGAGATCGGAAGAGCGGTTTCAG
chr9	35074874	35074913	FANCC_4366	-	GTGACCTATGCACCAGACGTTTGCATGACGTGCGCTATGCATAGATGTGCAAGGACAGAGATCGGAAGAGCGGTTTCAG
chr9	35075226	35075265	FANCC_4367	-	GTGACCTATGCACCAGACGTCTTTCAAGTTTTCTTACCTCTGGAAGTGGTAGTGGTGGATCGGAAGAGCGGTTTCAG
chr9	35075412	35075451	FANCC_4368	-	GTGACCTATGCACCAGACGTGGCTCCTAGAGGGGGTGGAGGATGATTTTTCTGATTGGAGATCGGAAGAGCGGTTTCAG
chr9	35075909	35075948	FANCC_4369	-	GTGACCTATGCACCAGACGTTCAAGCTTCTGCAATGGGGTAGACGGGTTGGTGTCCAGATCGGAAGAGCGGTTTCAG
chr9	35076379	35076418	FANCC_4370	-	GTGACCTATGCACCAGACGTCTTGTCTCACCTGAGCTTCTTCCCCTTCTGATGCTCAGATCGGAAGAGCGGTTTCAG
chr9	35076671	35076710	FANCC_4371	-	GTGACCTATGCACCAGACGTGCCAGTGAAGATGTGGGGTGGAGGATTCTGAGGTGCTTAGATCGGAAGAGCGGTTTCAG
chr9	35076918	35076957	FANCC_4372	-	GTGACCTATGCACCAGACGTTCTAGGGTGGATTGGGAAACCAGAAGCATTATGTATAGATCGGAAGAGCGGTTTCAG
chr9	35077211	35077250	FANCC_4373	-	GTGACCTATGCACCAGACGTAACCTGACTCATCTTCTACCTTTAAGTGGTCTCCAGAAGATCGGAAGAGCGGTTTCAG
chr9	35078088	35078127	FANCC_4374	-	GTGACCTATGCACCAGACGTAAAGTGACCTGAAGCTGAGGGTCTCCCTCTCCATAGATCGGAAGAGCGGTTTCAG
chr9	35078552	35078591	FANCC_4375	-	GTGACCTATGCACCAGACGTGAGATTGTCCCTGATTCCCCTGCCATCTTCACTCTGGGTTAGATCGGAAGAGCGGTTTCAG
chr9	35079098	35079137	FANCC_4376	-	GTGACCTATGCACCAGACGTCTCCCCAGGATGGTCAGTCCCCTTCCATAGCCAGAGATCGGAAGAGCGGTTTCAG
chr9	35079388	35079427	FANCC_4377	-	GTGACCTATGCACCAGACGTTGCTGGCACCTCGGTTTGCAGCCTCAAGATCCCTGAAAGAGATCGGAAGAGCGGTTTCAG
chr1	11167492	11167531	MTOR_4378	-	GTGACCTATGCACCAGACGTAGATGTGCCCATCACTGTTTTTCTGAGGCTTTTGTACTTTAGATCGGAAGAGCGGTTTCAG
chr1	11168188	11168227	MTOR_4379	-	GTGACCTATGCACCAGACGTCTCTCAAAGTACTTTTAAATAAGCAATCAGTCCCAGATCGGAAGAGCGGTTTCAG
chr1	11169297	11169336	MTOR_4380	-	GTGACCTATGCACCAGACGTATGTGTTTTACTTAAAGGGACATAAAATCTGACACACTAGATCGGAAGAGCGGTTTCAG
chr1	11169656	11169695	MTOR_4381	-	GTGACCTATGCACCAGACGTCTCTGAGGAACCCGACCAAGTACTAGCTCATTAAAGAAAAGATCGGAAGAGCGGTTTCAG
chr1	11172859	11172898	MTOR_4382	-	GTGACCTATGCACCAGACGTCCACGGGAGGTGCAAAAGGCTCTCCCCTTGTGCAGAGTGAGATCGGAAGAGCGGTTTCAG
chr1	11174820	11174859	MTOR_4383	-	GTGACCTATGCACCAGACGTATCGGAACGAGTCTCTCAAATGGGATCAGGACAGTTAAGATCGGAAGAGCGGTTTCAG
chr1	11175403	11175442	MTOR_4384	-	GTGACCTATGCACCAGACGTGTTCTAGAACCCCACTCATCTCCCGGGTATCATTAGATCGGAAGAGCGGTTTCAG
chr1	11177011	11177050	MTOR_4385	-	GTGACCTATGCACCAGACGTTAATTTGGTTTTTGTAGTCTTCTTCTCCATTGTAGTTTTAGATCGGAAGAGCGGTTTCAG
chr1	11181253	11181292	MTOR_4386	-	GTGACCTATGCACCAGACGTGGGCCCTGCAGACCTGCGCTCTCTGGAACCCCACTCGCAGATCGGAAGAGCGGTTTCAG
chr1	11181986	11182025	MTOR_4387	-	GTGACCTATGCACCAGACGTGGCCACGAGAGCTAGTGCCCTTCCGTGGCAGGAATCTAGATCGGAAGAGCGGTTTCAG
chr1	11184505	11184544	MTOR_4388	-	GTGACCTATGCACCAGACGTACCCTGAAATGGCAACAATTTGAGAAGTCTTCTGGTTTTAGATCGGAAGAGCGGTTTCAG
chr1	11186629	11186668	MTOR_4389	-	GTGACCTATGCACCAGACGTTTGTGCACTTCTGTCAACCACTTCTCCCTCTACACTGGCAGATCGGAAGAGCGGTTTCAG
chr1	11187017	11187056	MTOR_4390	-	GTGACCTATGCACCAGACGTGAGGCTCCTGGCAGGGTAACTGTCAATTAGTCTTTCTAGATCGGAAGAGCGGTTTCAG
chr1	11187631	11187670	MTOR_4391	-	GTGACCTATGCACCAGACGTAAAACAGCAAAAGGACATAAACCCCTGTAGAAATATTCTGCCAGATCGGAAGAGCGGTTTCAG
chr1	11188011	11188050	MTOR_4392	-	GTGACCTATGCACCAGACGTGCCACTGTGGGGCTTCATAGACCCTGGTCCCTTAGCTGGTATAGATCGGAAGAGCGGTTTCAG
chr1	11188461	11188500	MTOR_4393	-	GTGACCTATGCACCAGACGTACTCTGGGCAGTTTCTCATCTAACCACTGGTTTGGTGGTTCAGATCGGAAGAGCGGTTTCAG
chr1	11188862	11188901	MTOR_4394	-	GTGACCTATGCACCAGACGTTTGGTTACAGGTAAGGTGGCTCCAAGTCTCTTCTGTGAGATCGGAAGAGCGGTTTCAG
chr1	11189745	11189784	MTOR_4395	-	GTGACCTATGCACCAGACGTAGGGAAGGATGCAACTCTGGTAGGCCATGTTAATGGCAAGAGATCGGAAGAGCGGTTTCAG
chr1	11190536	11190575	MTOR_4396	-	GTGACCTATGCACCAGACGTCTTCTTCTTATAACCAACCAAGGTCAGAGGCTCAGATCGGAAGAGCGGTTTCAG
chr1	11193087	11193126	MTOR_4397	-	GTGACCTATGCACCAGACGTGCAGGCCACCTGTGAGACCAACCAACCTGGCTGGCTCGTGGATCGGAAGAGCGGTTTCAG
chr1	11194358	11194397	MTOR_4398	-	GTGACCTATGCACCAGACGTCACTGACCTGGGGCAAGTCATATCCAGCCCTGTCCAGATCGGAAGAGCGGTTTCAG
chr1	11199311	11199350	MTOR_4399	-	GTGACCTATGCACCAGACGTCAATGCATCCAGAACAGACCACCTTCTCCAGAATGCTCGCAGATCGGAAGAGCGGTTTCAG
chr1	11199540	11199579	MTOR_4400	-	GTGACCTATGCACCAGACGTACCACCCACACATGGGCAGGTAGGCCCCATGGTGTCCAGATCGGAAGAGCGGTTTCAG
chr1	11204655	11204694	MTOR_4401	-	GTGACCTATGCACCAGACGTTAGAAAGCCCAAGTTCACCACTTACCCTTCCCAAGATCGGAAGAGCGGTTTCAG
chr1	11204975	11205014	MTOR_4402	-	GTGACCTATGCACCAGACGTACTATTCTGACAGCTTATTCTTTGAGGCTTATTTCCATAGATCGGAAGAGCGGTTTCAG
chr1	11206683	11206722	MTOR_4403	-	GTGACCTATGCACCAGACGTACATGCACCCAGATCTCTCAGTGAGGAAAAGATTGTAGTGAGATCGGAAGAGCGGTTTCAG
chr1	11210133	11210172	MTOR_4404	-	GTGACCTATGCACCAGACGTCTCACAGGCACCTGTGAAGGATGGGGTAGTGAGGCTAAGATCGGAAGAGCGGTTTCAG
chr1	11217159	11217198	MTOR_4405	-	GTGACCTATGCACCAGACGTTAGAATGATGGCATGTGTGGCTCAAGAGACTTGTCTCTAGATCGGAAGAGCGGTTTCAG
chr1	11227449	11227488	MTOR_4406	-	GTGACCTATGCACCAGACGTACTTCTTTGGAAAAGCAGGAGGTAGAGACTTGGCTAGGAGATCGGAAGAGCGGTTTCAG
chr1	11259265	11259304	MTOR_4407	-	GTGACCTATGCACCAGACGTAACCTTTTTAATTGCTGCTCATGCAAAATGACCTCAGATCGGAAGAGCGGTTTCAG
chr1	11259548	11259587	MTOR_4408	-	GTGACCTATGCACCAGACGTTCCCAATTGCTCCAGATGGAGGACAGGGAACCACTGGAGATCGGAAGAGCGGTTTCAG

chr1	11264568	11264607	MTOR_4409	-	GTGACCTATGCACCAGACGTTTCAGGGCGGGTGGAGAAGATCAGCACATAGAAAACGATATAGATCGGAAGAGCGGTTTCAG
chr1	11269319	11269358	MTOR_4410	-	GTGACCTATGCACCAGACGTTGTTTCAGGTGACTGGGAAAGGAGAGCTCTGCTCTTCTCAAGATCGGAAGAGCGGTTTCAG
chr1	11270821	11270860	MTOR_4411	-	GTGACCTATGCACCAGACGTTCTTTCTTTCTGTTCTGAAGTCCCTGTTGTCTTTACTACTTAGATCGGAAGAGCGGTTTCAG
chr1	11272319	11272358	MTOR_4412	-	GTGACCTATGCACCAGACGTAGTCTGGACAGACAGGTGCTCTTCTGCCTTATTGGAAAGAGATCGGAAGAGCGGTTTCAG
chr1	11272803	11272842	MTOR_4413	-	GTGACCTATGCACCAGACGTCCTCTTTGGGACTAGCAATCTTTAAGCTTTAATGTTTTGTAGATCGGAAGAGCGGTTTCAG
chr1	11273406	11273445	MTOR_4414	-	GTGACCTATGCACCAGACGTTACGTCACTCCAGAGAGATTTTCTGATTTCTCTGAGTAGATCGGAAGAGCGGTTTCAG
chr1	11276155	11276194	MTOR_4415	-	GTGACCTATGCACCAGACGTTGTAATGCTTTGGCCCTTTCCATCTTCCGTTTGGGTCAAGGAAGAGATCGGAAGAGCGGTTTCAG
chr1	11288675	11288714	MTOR_4416	-	GTGACCTATGCACCAGACGTCAAAACCCCAATCCTTCTCTTCTCCTCTGCACCACACATGAGATCGGAAGAGCGGTTTCAG
chr1	11290932	11290971	MTOR_4417	-	GTGACCTATGCACCAGACGTTGGTAGCCATGAAAGACTTGCCAAGTTCTCACTCACAGAGCAGATCGGAAGAGCGGTTTCAG
chr1	11291307	11291346	MTOR_4418	-	GTGACCTATGCACCAGACGTTGGCAAACCTTGGTCTTTAAAGACTTTGCTGGGACGATGGCAGATCGGAAGAGCGGTTTCAG
chr1	11293405	11293444	MTOR_4419	-	GTGACCTATGCACCAGACGTAGCTACTTTTTCCATAGCGGAGATAGGGTGGAAAAGAAAACAGATCGGAAGAGCGGTTTCAG
chr1	11294150	11294189	MTOR_4420	-	GTGACCTATGCACCAGACGTTCCGAGAGGCTGGTCTTCTGTGCGTGTGCATCAGCTCAGATCGGAAGAGCGGTTTCAG
chr1	11297850	11297889	MTOR_4421	-	GTGACCTATGCACCAGACGTTGATGGCCAGACCCACAGGCAAGGGAAGACAGGACTCTCGCAGATCGGAAGAGCGGTTTCAG
chr1	11298409	11298448	MTOR_4422	-	GTGACCTATGCACCAGACGTTCCAGACAGAAGAACTAGGGGAGTTAAGGAGCTTAGGACAGATCGGAAGAGCGGTTTCAG
chr1	11300310	11300349	MTOR_4423	-	GTGACCTATGCACCAGACGTACAACGGCTCTTGCCAAGATAGTGAGAGATGCTGAAAACATAGATCGGAAGAGCGGTTTCAG
chr1	11301560	11301599	MTOR_4424	-	GTGACCTATGCACCAGACGTTGAAACCTGAGCTTGCCCTGTATCAGCGTAGGCTTGGCCAGATCGGAAGAGCGGTTTCAG
chr1	11303121	11303160	MTOR_4425	-	GTGACCTATGCACCAGACGTTCTGTTATGATTTACCTTCCACTCCATTTGGTTGGAGAGGATCGGAAGAGCGGTTTCAG
chr1	11307632	11307671	MTOR_4426	-	GTGACCTATGCACCAGACGTTGATGGAGATTCATTACCCTCAGGGTAAACAGGGAAGATCGGAAGAGCGGTTTCAG
chr1	11307826	11307865	MTOR_4427	-	GTGACCTATGCACCAGACGTAGAGGCCCTTTCCCTCTTTTCTTAAGCTCCACACCTCACTAGATCGGAAGAGCGGTTTCAG
chr1	11315999	11316038	MTOR_4428	-	GTGACCTATGCACCAGACGTGGCTCCATTCCCACCCTAGCAAAGCACATCTGCGTAGAGAGATCGGAAGAGCGGTTTCAG
chr1	11316940	11316979	MTOR_4429	-	GTGACCTATGCACCAGACGTACAGGGAGGACACAGCCAGGCTTGGGGAACGATGGTGTGATCGGAAGAGCGGTTTCAG
chr1	11318492	11318531	MTOR_4430	-	GTGACCTATGCACCAGACGTAGTCTCTGGTCAAAAAACAACACACTCACCTTTGTGCCAGATCGGAAGAGCGGTTTCAG
chr1	11319255	11319294	MTOR_4431	-	GTGACCTATGCACCAGACGTGATCTGGGCGGCTATTGTGGGATGTGGGCTAAATGATAGATCGGAAGAGCGGTTTCAG
chrX	48649467	48649506	GATA1_4432	-	GTGACCTATGCACCAGACGTGGGATTAAGCTGACAGCAGGAGGGTCTCTCAGACACAGATCGGAAGAGCGGTTTCAG
chrX	48650201	48650240	GATA1_4433	-	GTGACCTATGCACCAGACGTCAAGGTAGGGATGGAGGAAAGAAGAGGCAAAATCAGTCTAGAGATCGGAAGAGCGGTTTCAG
chrX	48650680	48650719	GATA1_4434	-	GTGACCTATGCACCAGACGTGGAGAGGAGAAGAGGGAGCTAGGCTCAGCTCAGCTTTACTAGATCGGAAGAGCGGTTTCAG
chrX	48651529	48651568	GATA1_4435	-	GTGACCTATGCACCAGACGTACAGGATGTGAGATCAGTCCCTGGGGATGTGGAAGTGGGAGATCGGAAGAGCGGTTTCAG
chrX	48652150	48652189	GATA1_4436	-	GTGACCTATGCACCAGACGTGGAGGCTGCGGGTGTCCCAACTCCAGACCTTTGCCTCTCAGATCGGAAGAGCGGTTTCAG
chr3	155588610	155588649	GMPS_4437	-	GTGACCTATGCACCAGACGTGCCGGAGCCGGCGGCTCAGCGCCAGATCAGGAGGGGAGATCGGAAGAGCGGTTTCAG
chr3	155611257	155611296	GMPS_4438	-	GTGACCTATGCACCAGACGTCAATACAATAACAAGCTTAATTTATGAAAATTAAGCTAAGATCGGAAGAGCGGTTTCAG
chr3	155615666	155615705	GMPS_4439	-	GTGACCTATGCACCAGACGTAGGAACAATCAGTGAAGAACTCTGTAAATTTTTATACAAGATCGGAAGAGCGGTTTCAG
chr3	155621602	155621641	GMPS_4440	-	GTGACCTATGCACCAGACGTAAAAAATTAATGTTAATAGAAATCAAAAGAAAAATACCAGATCGGAAGAGCGGTTTCAG
chr3	155623899	155623938	GMPS_4441	-	GTGACCTATGCACCAGACGTAAAAAATAAAACACAAAATATCTTAATTAATAACATGATAGATCGGAAGAGCGGTTTCAG
chr3	155628431	155628470	GMPS_4442	-	GTGACCTATGCACCAGACGTAAAAATGACAAAATTTTATGCTGAAAAGACAGATCGGAAGAGCGGTTTCAG
chr3	155628853	155628892	GMPS_4443	-	GTGACCTATGCACCAGACGTAAATGAAAAATAAAATGAGCAAAACAAGCAAAAAAGAAAAAGATCGGAAGAGCGGTTTCAG
chr3	155632158	155632197	GMPS_4444	-	GTGACCTATGCACCAGACGTGGGGAGAAGCGTTTTAAATTTGGTATAACATGTTTTTAAATAGATCGGAAGAGCGGTTTCAG
chr3	155633758	155633797	GMPS_4445	-	GTGACCTATGCACCAGACGTCAAGGATAAAACAGCCTTGTAAAGATAAATTTTTTAAAGATCGGAAGAGCGGTTTCAG
chr3	155636972	155637011	GMPS_4446	-	GTGACCTATGCACCAGACGTGAAAAGAAGCCAACCAATAAACTAGTAACCAAGATGACAAGATCGGAAGAGCGGTTTCAG
chr3	155642980	155643019	GMPS_4447	-	GTGACCTATGCACCAGACGTCCAAAGAGGCACTTTTTTTCAGTTTTAAGAAATAAGGTATTGATCGGAAGAGCGGTTTCAG
chr3	155649504	155649543	GMPS_4448	-	GTGACCTATGCACCAGACGTAAAGATAATCAATAATTTTTAATAGTCAAAAGATACACAAGATCGGAAGAGCGGTTTCAG
chr3	155652655	155652694	GMPS_4449	-	GTGACCTATGCACCAGACGTAAAGGTAGAGGTAATAAATAACAGCAATTTCAATTTCAAAATGTAGAAGATCGGAAGAGCGGTTTCAG
chr3	155654077	155654116	GMPS_4450	-	GTGACCTATGCACCAGACGTGTATATGTAGAACAATCACACACCATAGAAAAGCACTCAGATCGGAAGAGCGGTTTCAG
chr3	155655330	155655369	GMPS_4451	-	GTGACCTATGCACCAGACGTAAATATAGAAAAAGTCAAGATCCACTGCATGTCAGCAAGATCGGAAGAGCGGTTTCAG
chrX	132670102	132670141	GPC3_4452	-	GTGACCTATGCACCAGACGTCCCAGCACATGTGCTGCCCTACAGCACCTGTGGTCTTCCAGATCGGAAGAGCGGTTTCAG
chrX	132730418	132730457	GPC3_4453	-	GTGACCTATGCACCAGACGTAGTGTACCCAAATGTAATCAAAAATGGTGTGCTCAGAGATCGGAAGAGCGGTTTCAG
chrX	132826347	132826386	GPC3_4454	-	GTGACCTATGCACCAGACGTTTGAAGTTACATATAGCAATTTGAGGAATAATTGTCAAGATCGGAAGAGCGGTTTCAG
chrX	132833873	132833912	GPC3_4455	-	GTGACCTATGCACCAGACGTTCTTTTTTTTATTCCACAATAACAATTAACAATTGTATTAGATCGGAAGAGCGGTTTCAG
chrX	132887459	132887498	GPC3_4456	-	GTGACCTATGCACCAGACGTGTCTACAGTTGTACAGGATTTGGCCCTATTGGGGTGAAGATCGGAAGAGCGGTTTCAG
chrX	133087027	133087066	GPC3_4457	-	GTGACCTATGCACCAGACGTGGGATTATTTTAGATGTGCTGCTTAGTGGCATCATTATTAGATCGGAAGAGCGGTTTCAG
chrX	133119252	133119291	GPC3_4458	-	GTGACCTATGCACCAGACGTGCCCTTGAGCGTGCCTAGCGCCACCGGGAGCAAGGCGAGATCGGAAGAGCGGTTTCAG
chrX	132887806	132887845	GPC3_4459	-	GTGACCTATGCACCAGACGTTCTGAATTTGAATTTGAATGATCAACCAACTGATCAGATCGGAAGAGCGGTTTCAG
chr2	239974743	239974782	HDAC4_4460	-	GTGACCTATGCACCAGACGTAAAGCTGCTGTTCTTTGCTGTCTGTCTGTCTGTTGAAGCAGATCGGAAGAGCGGTTTCAG
chr2	239975106	239975145	HDAC4_4461	-	GTGACCTATGCACCAGACGTGCCCTGCCGCCCGCTGCAGGCTCACCCAGCCCCACTGTGAGATCGGAAGAGCGGTTTCAG
chr2	239976395	239976434	HDAC4_4462	-	GTGACCTATGCACCAGACGTTGGCTGGGTGCTCACAGGGGACACGCCCTGGGGTGGGAAGATCGGAAGAGCGGTTTCAG
chr2	239988368	239988407	HDAC4_4463	-	GTGACCTATGCACCAGACGTCCCAGAGACCCACAGGATGCTCCACTGACAGGCTCGGAGATCGGAAGAGCGGTTTCAG
chr2	239990135	239990174	HDAC4_4464	-	GTGACCTATGCACCAGACGTTCCGATGACTGAGGAGCCGGTCTGCTCATGTCCATGAAGATCGGAAGAGCGGTTTCAG
chr2	240002741	240002780	HDAC4_4465	-	GTGACCTATGCACCAGACGTTCCGCTTCCATGACACCTGAAGTAGCAGCTTTTCTCTGTAGATCGGAAGAGCGGTTTCAG
chr2	240003748	240003787	HDAC4_4466	-	GTGACCTATGCACCAGACGTTATATAAGGGCTCTGGGGGAAAGGGGACTGCGGGAGAGATCGGAAGAGCGGTTTCAG

chr2	240005801	240005840	HDAC4_4467	-	GTGACCTATGCACCAGACGTCCGCCCTTGCCACGCGCAGCTCAGGTTGCTCCTTTGCCGTAGATCGGAAGAGCGGTTTCAG
chr2	240009205	240009244	HDAC4_4468	-	GTGACCTATGCACCAGACGTGCCGACGCCCCGCACAGCAGGGGAACCCAGGTCTTCTTCAGATCGGAAGAGCGGTTTCAG
chr2	240011655	240011694	HDAC4_4469	-	GTGACCTATGCACCAGACGTGCCTGGACAGTGGTGGCCCTCCAGGAGGCTGCCATAGATAGATCGGAAGAGCGGTTTCAG
chr2	240016656	240016695	HDAC4_4470	-	GTGACCTATGCACCAGACGTCTTAATGTGTAATAATGTCCTGTTTTCTTCAGATCCCAGATCGGAAGAGCGGTTTCAG
chr2	240024422	240024461	HDAC4_4471	-	GTGACCTATGCACCAGACGTACCTTCCCTTCCCTCCATATTTGGGTTTGAAGTCCCCTGAGAGATCGGAAGAGCGGTTTCAG
chr2	240029696	240029735	HDAC4_4472	-	GTGACCTATGCACCAGACGTCCGGGGCAGGTGGGCAGCTGCGGCTTTGGGACCATTAGAAGATCGGAAGAGCGGTTTCAG
chr2	2400332172	240033211	HDAC4_4473	-	GTGACCTATGCACCAGACGTGCGGTTGTGACGCTGAGGGTGAACGCGGGCCACAGTGGAGATCGGAAGAGCGGTTTCAG
chr2	240036699	240036738	HDAC4_4474	-	GTGACCTATGCACCAGACGTGCGGGGAGGGCACCAGAAAGGCTGGCACGCACAGCCACCTAGATCGGAAGAGCGGTTTCAG
chr2	240048102	240048141	HDAC4_4475	-	GTGACCTATGCACCAGACGTGGCTCAGCGCTCCCAGGCCCCAGGGCGGCTGTGTGCTGTAGATCGGAAGAGCGGTTTCAG
chr2	240055891	240055930	HDAC4_4476	-	GTGACCTATGCACCAGACGTATGGGCTGGGTGCAGCCAGGCTCTGAGGCTGCCACCGCTAGATCGGAAGAGCGGTTTCAG
chr2	240056173	240056212	HDAC4_4477	-	GTGACCTATGCACCAGACGTCCCCGTGGGTCCGTGTGGTGTGGGGTGGTGGTGTGGGTGATCGGAAGAGCGGTTTCAG
chr2	240061330	240061369	HDAC4_4478	-	GTGACCTATGCACCAGACGTAGCGTTTTGTCCTGTGTCCTACGGCTAGATCGGACTCGGGAGATCGGAAGAGCGGTTTCAG
chr2	240066229	240066268	HDAC4_4479	-	GTGACCTATGCACCAGACGTTAGAGCAGGTAGCCAGCCCGCCGCTGCCCTCTCTGCCAGGCCAGATCGGAAGAGCGGTTTCAG
chr2	240078298	240078337	HDAC4_4480	-	GTGACCTATGCACCAGACGTAGGCATGCTGTGGGCCGGGAGGTCTCCTGCACGGGCACCTAGATCGGAAGAGCGGTTTCAG
chr2	240085449	240085488	HDAC4_4481	-	GTGACCTATGCACCAGACGTGTGTGGGGAGCACCCCGGCTCCTCTCTGGGGGCCAGAGAGATCGGAAGAGCGGTTTCAG
chr2	240111479	240111518	HDAC4_4482	-	GTGACCTATGCACCAGACGTGTGCCGGGGCTGCGGGTGGGCCAGGCCCTCCGGCACCTCAAAGATCGGAAGAGCGGTTTCAG
chr2	240158239	240158278	HDAC4_4483	-	GTGACCTATGCACCAGACGTCCACCCCTGCCCTGTCCGGCCGGCCCTGCCTGAGCCAAAAGATCGGAAGAGCGGTTTCAG
chr2	240274323	240274362	HDAC4_4484	-	GTGACCTATGCACCAGACGTGCTAATTTCTCTGTGGCCACACAGCGGGGCTTTCTTTGGCAGATCGGAAGAGCGGTTTCAG
chr6	34208508	34208547	HMGA1_4485	-	GTGACCTATGCACCAGACGTCTAAGGAGCAGGTGGAAGAGTGATGGCTGGGATGCTGGGAAGATCGGAAGAGCGGTTTCAG
chr6	34210439	34210478	HMGA1_4486	-	GTGACCTATGCACCAGACGTAGAGGGGTAGTACAGGGACAGTCATCACCTGTTTCCACCCAGATCGGAAGAGCGGTTTCAG
chr6	34211195	34211234	HMGA1_4487	-	GTGACCTATGCACCAGACGTAGAGAAAATATCTCCTAAGTCCAAAATGCTCATAGTGTAGATCGGAAGAGCGGTTTCAG
chr6	34212558	34212597	HMGA1_4488	-	GTGACCTATGCACCAGACGTGGCAGTTGTTGGTGTGAGCTCTGGCCGGTCCCCTCTTCAGATCGGAAGAGCGGTTTCAG
chr2	176972034	176972073	HOXD11_4489	-	GTGACCTATGCACCAGACGTGTGCGCGCCAGCGAGCCTGTGGCCCTCCCGCCGACCCAGATCGGAAGAGCGGTTTCAG
chr2	176973585	176973624	HOXD11_4490	-	GTGACCTATGCACCAGACGTGTAAGCAGGTAGAGGGGTGAGAGCGCCGCTGCCTGACAGCCAGATCGGAAGAGCGGTTTCAG
chr2	209101753	209101792	IDH1_4491	-	GTGACCTATGCACCAGACGTGAGCTAAGAAGGATAATTGTCTTTTGGTAAGTGTCTACAGATCGGAAGAGCGGTTTCAG
chr2	209103745	209103784	IDH1_4492	-	GTGACCTATGCACCAGACGTGATGCCCTAGTTTCTATGGTCAAATTAACACTTATCCTCAAGATCGGAAGAGCGGTTTCAG
chr2	209104537	209104576	IDH1_4493	-	GTGACCTATGCACCAGACGTGTTTACATTGATTTCTCACAGAGAGTGTCTCCTCAAAGCAAGATCGGAAGAGCGGTTTCAG
chr2	209106668	209106707	IDH1_4494	-	GTGACCTATGCACCAGACGTGGAGCCTGGCCGTGTAGGAACAGGGTCAATCCAGGTAAGTGTAGATCGGAAGAGCGGTTTCAG
chr2	209108101	209108140	IDH1_4495	-	GTGACCTATGCACCAGACGTCTTTTTTAACTTTTTCTTATTCTCAAGTAAGTGTACAAGATCGGAAGAGCGGTTTCAG
chr2	209109993	209110032	IDH1_4496	-	GTGACCTATGCACCAGACGTCTGTAGCAATAAGCTCTTTTTTTTTTAAACAAATGATTTAAGATCGGAAGAGCGGTTTCAG
chr2	209113043	209113082	IDH1_4497	-	GTGACCTATGCACCAGACGTGGCAATAATGTGATTTTGCATGTTTTTTTTTTCATGGCAGATCGGAAGAGCGGTTTCAG
chr15	99250741	99250780	IGF1R_4498	-	GTGACCTATGCACCAGACGTACAAGAGGGTAAAGTCTCAGTTAGAAGGAAATAATTTTAGATCGGAAGAGCGGTTTCAG
chr15	99434504	99434543	IGF1R_4499	-	GTGACCTATGCACCAGACGTAGAGGAGAGACGGAGATGAGACCCGGGCAGGGGAGGCCACCGAGATCGGAAGAGCGGTTTCAG
chr15	99439936	99439975	IGF1R_4500	-	GTGACCTATGCACCAGACGTAGAAAAAAATCAAAACACACATAATTTAGTCTGTCTAGATCGGAAGAGCGGTTTCAG
chr15	99442656	99442695	IGF1R_4501	-	GTGACCTATGCACCAGACGTGAGGGAATGTGCTACTGTGTCTCACTTGTGTAAGGTTGAGATCGGAAGAGCGGTTTCAG
chr15	99451864	99451903	IGF1R_4502	-	GTGACCTATGCACCAGACGTAGAAATCGATGTTAGCGCACCTGCCCTTGGCCACAGTCCAGATCGGAAGAGCGGTTTCAG
chr15	99454494	99454533	IGF1R_4503	-	GTGACCTATGCACCAGACGTGAGTACATCCGTGAGTGACAGAGATTCATGTGTCTCTGAAAGATCGGAAGAGCGGTTTCAG
chr15	99456223	99456262	IGF1R_4504	-	GTGACCTATGCACCAGACGTATTAAGTTACAGAAAAGTTCGGGGCTCTGACATCAAAACAGATCGGAAGAGCGGTTTCAG
chr15	99459143	99459182	IGF1R_4505	-	GTGACCTATGCACCAGACGTGAACAAAGAACATTCTAGAAAATGAAATGAACTTAAAGATAGATCGGAAGAGCGGTTTCAG
chr15	99459851	99459890	IGF1R_4506	-	GTGACCTATGCACCAGACGTAGAAAAACCAAAACAAGTGGGAATGAAAGCCGTTATAAGATCGGAAGAGCGGTTTCAG
chr15	99465327	99465366	IGF1R_4507	-	GTGACCTATGCACCAGACGTGAGAGAAATGGGCTTTTTTAAAGTACTTTTACCTCTTTTTCAGATCGGAAGAGCGGTTTCAG
chr15	99467055	99467094	IGF1R_4508	-	GTGACCTATGCACCAGACGTAAACAGGTGACAAAGTTGGATTTGGGTTCCAGGGAGGGAGATCGGAAGAGCGGTTTCAG
chr15	99467704	99467743	IGF1R_4509	-	GTGACCTATGCACCAGACGTAAAACATACATGTCAATTTCCCATGAATGCAGGAGAAATCAGATCGGAAGAGCGGTTTCAG
chr15	99472737	99472776	IGF1R_4510	-	GTGACCTATGCACCAGACGTGAGGAGGAAATGATAAAATATCACCAAGGTGAACAATTTGCAGATCGGAAGAGCGGTTTCAG
chr15	99473414	99473453	IGF1R_4511	-	GTGACCTATGCACCAGACGTGATTAATTTACGTTAAACAAAACCCACCTCCATACATTAGATCGGAAGAGCGGTTTCAG
chr15	99478003	99478042	IGF1R_4512	-	GTGACCTATGCACCAGACGTAAACGTAATTAAGCAGGTACAGAAACCAAGCCCTTAGACAAGATCGGAAGAGCGGTTTCAG
chr15	99478495	99478534	IGF1R_4513	-	GTGACCTATGCACCAGACGTTCAAAAAGAGAAAGACTCAGAGGGTCAGGTGCCCTTGTAGATCGGAAGAGCGGTTTCAG
chr15	99482380	99482419	IGF1R_4514	-	GTGACCTATGCACCAGACGTAAAAAAATTCACATGAGAAATTTGGATTTTTTTTTTTCAGATCGGAAGAGCGGTTTCAG
chr15	99486102	99486141	IGF1R_4515	-	GTGACCTATGCACCAGACGTAGAGAGGGCGCAGAGTCAACAGCTGGAGCAGGCACCACTGAGATCGGAAGAGCGGTTTCAG
chr15	99491753	99491792	IGF1R_4516	-	GTGACCTATGCACCAGACGTAAAAAACTGTGAGGAGCTTGGAAAGGGATGGACTGAACAAGATCGGAAGAGCGGTTTCAG
chr15	99500240	99500279	IGF1R_4517	-	GTGACCTATGCACCAGACGTGACACACGGGAGGGGCTCAAACCCGGCCACATGGAGATCGGAAGAGCGGTTTCAG
chr15	99251014	99251053	IGF1R_4518	-	GTGACCTATGCACCAGACGTGATGACCAAGGCGTGTGTAAGAGTTCAGAGCCGGAGATCGGAAGAGCGGTTTCAG
chr7	45954369	45954408	IGFBP3_4519	-	GTGACCTATGCACCAGACGTCAAGGGTGTACTCAGGAGGGGCAGCCTGGGGCTCCAGGAGATCGGAAGAGCGGTTTCAG
chr7	45956097	45956136	IGFBP3_4520	-	GTGACCTATGCACCAGACGTTCCTCAGTGTGTTTTCTTCTCTTCTGTTGACACAGAGGAAGATCGGAAGAGCGGTTTCAG
chr7	45956762	45956801	IGFBP3_4521	-	GTGACCTATGCACCAGACGTTCCTCTTGTAAAGGAGGAGGGCAAGACTGCCAAGCCTAGATCGGAAGAGCGGTTTCAG
chr7	45960269	45960308	IGFBP3_4522	-	GTGACCTATGCACCAGACGTTCAGCACCCGGCGCACTGGCCGGAAGGGCTGGGGTTAGATCGGAAGAGCGGTTTCAG
chr7	45960287	45960326	IGFBP3_4523	-	GTGACCTATGCACCAGACGTGCGCCAGTGCCTGCTGTCAGCACCCGCGCACTGGCGAGATCGGAAGAGCGGTTTCAG
chr3	123813635	123813674	KALRN_4524	-	GTGACCTATGCACCAGACGTACTCATCTTACAGCCAGTCCCTCGGCAGAGCCTCATCAGATCGGAAGAGCGGTTTCAG

chr3	123946787	123946826	KALRN_4525	-	GTGACCTATGCACCAGACGTACA AAC CAGAAGGAATCAGGGTGAGAGGAGCCAGCTGGCTAGATCGGAAGAGCGGTTCCAG
chr3	123953626	123953665	KALRN_4526	-	GTGACCTATGCACCAGACGTGAGGAAAGAGAGAGTGTTTAAGAAAACCACTCAGAAAGGAAGATCGGAAGAGCGGTTCCAG
chr3	123983295	123983334	KALRN_4527	-	GTGACCTATGCACCAGACGTGTCAGAGGTCGGTATGGTCACTCTGGGTAGCTGAGACTTTAGATCGGAAGAGCGGTTCCAG
chr3	123987540	123987579	KALRN_4528	-	GTGACCTATGCACCAGACGTGACAGACAGACAAGGATACTCAGTGATGTCAGGGGAAGAAAAGATCGGAAGAGCGGTTCCAG
chr3	124017588	124017627	KALRN_4529	-	GTGACCTATGCACCAGACGTCAAGAAGGCACAGCATAATCAGAAATGGTCATGGTCTGAATAGATCGGAAGAGCGGTTCCAG
chr3	124044777	124044816	KALRN_4530	-	GTGACCTATGCACCAGACGTAAAGGAGAGTGTCTAGTGGGGCAGGCTCAAAGACATCCACAGATCGGAAGAGCGGTTCCAG
chr3	124048658	124048697	KALRN_4531	-	GTGACCTATGCACCAGACGTAGCAGGTTGGATGTGGGGGAGCACTGGGGGTGAGGAGAGATCGGAAGAGCGGTTCCAG
chr3	124053062	124053101	KALRN_4532	-	GTGACCTATGCACCAGACGTGAGAGAAAGTTAAAGTTAAGGGAAAAGGGTGATAGGCAGGGAGATCGGAAGAGCGGTTCCAG
chr3	124065940	124065979	KALRN_4533	-	GTGACCTATGCACCAGACGTAAAGATAACAGCAACAATGACTTTCTAGCAGAAGGAAAGAGATCGGAAGAGCGGTTCCAG
chr3	124103642	124103681	KALRN_4534	-	GTGACCTATGCACCAGACGTCAACAGTGAGGGCAAAGTCAAGTTGACAGTCGCGCCTTCCAGAGATCGGAAGAGCGGTTCCAG
chr3	124113932	124113971	KALRN_4535	-	GTGACCTATGCACCAGACGTAGAGCAGAGATTCACCTCAGGGAAGATGGGAGAGGCCAGGAGATCGGAAGAGCGGTTCCAG
chr3	124117494	124117533	KALRN_4536	-	GTGACCTATGCACCAGACGTGTTGGGGAGAAAAAGGGAGGGAGAGGCCTTTCCATGTTAAAGATCGGAAGAGCGGTTCCAG
chr3	124132267	124132306	KALRN_4537	-	GTGACCTATGCACCAGACGTACCACCTGCATCAGCACAGGCTCACCAGGTCCACGAGAGAAAGATCGGAAGAGCGGTTCCAG
chr3	124141609	124141648	KALRN_4538	-	GTGACCTATGCACCAGACGTAAAAATGAAACAATAAAAACCAGCTAGTACTGTGAAGGAGATCGGAAGAGCGGTTCCAG
chr3	124149453	124149492	KALRN_4539	-	GTGACCTATGCACCAGACGTGGGACAGCACACAGGTGAATGGCCTTCCGCAGTTTCCCAGATCGGAAGAGCGGTTCCAG
chr3	124153104	124153143	KALRN_4540	-	GTGACCTATGCACCAGACGTGGAGAGGAGAGAAAGTCCGTGGGAACAACCCAGCGCTGGAGATCGGAAGAGCGGTTCCAG
chr3	124157685	124157724	KALRN_4541	-	GTGACCTATGCACCAGACGTGAGAAAGAAAGACTCAGTAAATTAATTATTTCAGGAATTAAGATCGGAAGAGCGGTTCCAG
chr3	124160742	124160781	KALRN_4542	-	GTGACCTATGCACCAGACGTCAAAGCTGTGAGGCCCTGTCGCCAGGTGTATGGAATCAGATCGGAAGAGCGGTTCCAG
chr3	124164958	124164997	KALRN_4543	-	GTGACCTATGCACCAGACGTAGGAGATGCATGATGGTCAACAAGGGGCTCTGAGCAATCCAGATCGGAAGAGCGGTTCCAG
chr3	124165560	124165599	KALRN_4544	-	GTGACCTATGCACCAGACGTAAACAACCTCATCCAGTCCCCAAAAGGCAGCTGTCAGTAGAGATCGGAAGAGCGGTTCCAG
chr3	124173974	124174013	KALRN_4545	-	GTGACCTATGCACCAGACGTAGATGGCCTTAAGTTACTGGATTACATTTATTCTCCTGCCAGATCGGAAGAGCGGTTCCAG
chr3	124175407	124175446	KALRN_4546	-	GTGACCTATGCACCAGACGTAGGGATCACAAGGTCACCTTGTGATGCTTTGGGAAAGCAAGATCGGAAGAGCGGTTCCAG
chr3	124180687	124180726	KALRN_4547	-	GTGACCTATGCACCAGACGTACAATGGGCTTTTACTTTGGATATAGATAATGTCTCTCAGATCGGAAGAGCGGTTCCAG
chr3	124181321	124181360	KALRN_4548	-	GTGACCTATGCACCAGACGTGTAACAGTTTCACTGGCACTGGCAGGCCATATAAAAGATCGGAAGAGCGGTTCCAG
chr3	124193460	124193499	KALRN_4549	-	GTGACCTATGCACCAGACGTAGAAAAAGACTGAATCAGACACCTCTGTGCAGCTGACCCAGATCGGAAGAGCGGTTCCAG
chr3	124196042	124196081	KALRN_4550	-	GTGACCTATGCACCAGACGTCAAAGATAATAAGATAAGCATTATTAGTTGTTCCCTTAGATCGGAAGAGCGGTTCCAG
chr3	124201605	124201644	KALRN_4551	-	GTGACCTATGCACCAGACGTGAGAAACAATGTGCAATTAGACACAGAGGGGTGTGTGCATGAGATCGGAAGAGCGGTTCCAG
chr3	124207001	124207040	KALRN_4552	-	GTGACCTATGCACCAGACGTAAAGTCCCGACATAATTAGGGCCATCTCCCCAGCTTCCAGATCGGAAGAGCGGTTCCAG
chr3	124209491	124209530	KALRN_4553	-	GTGACCTATGCACCAGACGTCCATTTCCACCTGTGGAGTTTCTACTGCCACGTCAAGATCGGAAGAGCGGTTCCAG
chr3	124210120	124210159	KALRN_4554	-	GTGACCTATGCACCAGACGTGAAATGCCTATGACAGGGCGGGAAGGGAGGGCAGTGGGGAGATCGGAAGAGCGGTTCCAG
chr3	124211537	124211576	KALRN_4555	-	GTGACCTATGCACCAGACGTACAGGGAGAAAAGACTGAGAACCCCAACTCCCATCACCTTAAGATCGGAAGAGCGGTTCCAG
chr3	124215108	124215147	KALRN_4556	-	GTGACCTATGCACCAGACGTAAAGAGAAAAAACAGGGGTGGGGGTGGGGGAACCACTGAGATCGGAAGAGCGGTTCCAG
chr3	124237197	124237236	KALRN_4557	-	GTGACCTATGCACCAGACGTAAAGGGCCGGGCTCTGTGATTTGCATATAACTTTGCAAAAAGATCGGAAGAGCGGTTCCAG
chr3	124303619	124303658	KALRN_4558	-	GTGACCTATGCACCAGACGTGCCCCAGCGCTCCCGCATGCCACAGCGGGGCCAGCCGGGAGATCGGAAGAGCGGTTCCAG
chr3	124351217	124351256	KALRN_4559	-	GTGACCTATGCACCAGACGTGCGGACAGACAGCCATGTACAGAGTGGTGAAGGCAGCCAGATCGGAAGAGCGGTTCCAG
chr3	124352646	124352685	KALRN_4560	-	GTGACCTATGCACCAGACGTAGAGCAGCATTAGTTACTGTGTACAAACATGCCAGTGGTAGATCGGAAGAGCGGTTCCAG
chr3	124356005	124356044	KALRN_4561	-	GTGACCTATGCACCAGACGTTCCGGCAGCAGAGGAAAAGCAGATTAGCAAAGAATAAGGAAGATCGGAAGAGCGGTTCCAG
chr3	124369605	124369644	KALRN_4562	-	GTGACCTATGCACCAGACGTAGAAAAACAGGCTTAGAGAAAGTGTACTTTGAAAAGTCAATTAGATCGGAAGAGCGGTTCCAG
chr3	124374398	124374437	KALRN_4563	-	GTGACCTATGCACCAGACGTGATTAAGAACAGTGAGTGTTCCTTTCATTGTTAAGCCAAAGATCGGAAGAGCGGTTCCAG
chr3	124376245	124376284	KALRN_4564	-	GTGACCTATGCACCAGACGTAAAGGCAATGGTTAGTAGCATATTTACAGGAAAAGCTTTAGATCGGAAGAGCGGTTCCAG
chr3	124376531	124376570	KALRN_4565	-	GTGACCTATGCACCAGACGTAAAAGGGGATAGAGAAGGAAGCAACTTATTCAGAAGTGTAGATCGGAAGAGCGGTTCCAG
chr3	124377228	124377267	KALRN_4566	-	GTGACCTATGCACCAGACGTAGAGAGAGACATGTGGACAGTCAGGCATCTTGTGTCTTTTAGATCGGAAGAGCGGTTCCAG
chr3	124378162	124378201	KALRN_4567	-	GTGACCTATGCACCAGACGTGGCAGCAATATTAGAAGAAAAGGAAGTGAAGAACTGGGGAGATCGGAAGAGCGGTTCCAG
chr3	124379720	124379759	KALRN_4568	-	GTGACCTATGCACCAGACGTGGGGAAAGCAGGCAAGAGTGTGGGAAGGGGTAATAATTAGTAAGATCGGAAGAGCGGTTCCAG
chr3	124380648	124380687	KALRN_4569	-	GTGACCTATGCACCAGACGTGAACAACCTGTTACTCAGGAGGGGGAACAGCACTCAGGCAGAGATCGGAAGAGCGGTTCCAG
chr3	124385246	124385285	KALRN_4570	-	GTGACCTATGCACCAGACGTGACCGCTGGGGTGAAGTGAATGAAAATGGGGAGCGAGCATCGGAAGAGCGGTTCCAG
chr3	124385809	124385848	KALRN_4571	-	GTGACCTATGCACCAGACGTACGAGTTGATCCTTTTTACATTTAAAAGATTTTTTAAAAAAGATCGGAAGAGCGGTTCCAG
chr3	124390457	124390496	KALRN_4572	-	GTGACCTATGCACCAGACGTAGAGCAGGTGGTTACTCTAAGCTTTGGGAATCCACAAGGAGATCGGAAGAGCGGTTCCAG
chr3	124393158	124393197	KALRN_4573	-	GTGACCTATGCACCAGACGTAGGGTGAGAGGGGCACAACAAGGAGCGCTAGTTCACATAGATCGGAAGAGCGGTTCCAG
chr3	124396987	124397026	KALRN_4574	-	GTGACCTATGCACCAGACGTAAAAATGCACCAATCAAAATGGCAGGTCAGGGACAGCGAAGATCGGAAGAGCGGTTCCAG
chr3	124398255	124398294	KALRN_4575	-	GTGACCTATGCACCAGACGTAGCATGAGGAAGGGGAAGAAAAGCAACACAGTTAGAACAAGATCGGAAGAGCGGTTCCAG
chr3	124412601	124412640	KALRN_4576	-	GTGACCTATGCACCAGACGTAAAAGAGACAGAAAATGCTTGAAGTAACTTAACCTAAAAGATCGGAAGAGCGGTTCCAG
chr3	124413129	124413168	KALRN_4577	-	GTGACCTATGCACCAGACGTATCAACATACATTAACATCATTAGAGCAAATTTAGAATAAGATCGGAAGAGCGGTTCCAG
chr3	124414931	124414970	KALRN_4578	-	GTGACCTATGCACCAGACGTCAAAGGATGCTCTTCAGACTCCAGTAATGAGACACTTGAAGATCGGAAGAGCGGTTCCAG
chr3	124416390	124416429	KALRN_4579	-	GTGACCTATGCACCAGACGTAGAAATCAGGATCAGGTGCTATTTCTGCAGAACTTGCATAGATCGGAAGAGCGGTTCCAG
chr3	124418666	124418705	KALRN_4580	-	GTGACCTATGCACCAGACGTGTTTCCCAGGAGGGGAAAAGAGAAAAGCCAAAGGGATATTAGATCGGAAGAGCGGTTCCAG
chr3	124420835	124420874	KALRN_4581	-	GTGACCTATGCACCAGACGTAAAAGAAATCCATTTACAATCAGAGGATGTCATATAAGAAGATCGGAAGAGCGGTTCCAG
chr3	124431732	124431771	KALRN_4582	-	GTGACCTATGCACCAGACGTAAAGAGGGAGAGTTTGCCAACATTCATTAATTAAC TAGATAAGATCGGAAGAGCGGTTCCAG

chr3	124436044	124436083	KALRN_4583	-	GTGACCTATGCACCAGACGTGCAGGGAAAGGCAAAGGAAATATGTTTGAATGAAGAAATAGATCGGAAGAGCGGTTTCAG
chr3	124437722	124437761	KALRN_4584	-	GTGACCTATGCACCAGACGTCCAAGGAAGCAGGGAGAAAAGAGGGAAAGTTTGTAGCCCTCAGATCGGAAGAGCGGTTTCAG
chr3	123987796	123987835	KALRN_4585	-	GTGACCTATGCACCAGACGTCTGTGTGTTCGTCATGAGCCGCCGAGAGCCCTCCACAAGATCGGAAGAGCGGTTTCAG
chr3	124437995	124438034	KALRN_4586	-	GTGACCTATGCACCAGACGTGATACGTTGATACATGTCTCCTCTTTGCTCTCATCCAAGAAGATCGGAAGAGCGGTTTCAG
chr3	20081920	20081959	KAT2B_4587	-	GTGACCTATGCACCAGACGTAGCACGGCAGGAGCGGCCGAGTGTGACGGCCGCCGCCGCGCAGATCGGAAGAGCGGTTTCAG
chr3	20113775	20113814	KAT2B_4588	-	GTGACCTATGCACCAGACGTAATAAAGAAAGAGACAAAATATTTAACAGGCAGCCGTTGGAGATCGGAAGAGCGGTTTCAG
chr3	20136705	20136744	KAT2B_4589	-	GTGACCTATGCACCAGACGTGATCAAAGAAACATATGTAAGACCTCAATTGGAAACCAAAGATCGGAAGAGCGGTTTCAG
chr3	20142729	20142768	KAT2B_4590	-	GTGACCTATGCACCAGACGTGGGAAGGCAATTTCTTCATGCAGCTATGCAATCATACTAAAGATCGGAAGAGCGGTTTCAG
chr3	20153038	20153077	KAT2B_4591	-	GTGACCTATGCACCAGACGTAGAAGTCAAGCACCATCAATATCCATAAACCCCCAGGTCAGATCGGAAGAGCGGTTTCAG
chr3	20156324	20156363	KAT2B_4592	-	GTGACCTATGCACCAGACGTGAGTAATAGCAATAAGATTAATAAAAAAACTACTGTAAGGAAGATCGGAAGAGCGGTTTCAG
chr3	20161040	20161079	KAT2B_4593	-	GTGACCTATGCACCAGACGTAAAAAGGAGAAGAAGGTGTAGATGACTGACTCCTTTCTTAAGATCGGAAGAGCGGTTTCAG
chr3	20164110	20164149	KAT2B_4594	-	GTGACCTATGCACCAGACGTCAAAATAAAAGGCAACAATGGGTGGTTCTAAACACAAAAGATCGGAAGAGCGGTTTCAG
chr3	20167347	20167386	KAT2B_4595	-	GTGACCTATGCACCAGACGTGAGACAGGAAAAATACACAGAGCTATTCTCTCAAGACAGATCGGAAGAGCGGTTTCAG
chr3	20168865	20168904	KAT2B_4596	-	GTGACCTATGCACCAGACGTAAGATTATGTCAAAGTTTTACCTATCCTAGTTATATAAATAGATCGGAAGAGCGGTTTCAG
chr3	20178384	20178423	KAT2B_4597	-	GTGACCTATGCACCAGACGTGTTAGTATACAAACAATACATTAGACTGGGGAGAAAATAGATCGGAAGAGCGGTTTCAG
chr3	20187758	20187797	KAT2B_4598	-	GTGACCTATGCACCAGACGTGAGGAAGGAAATGTGTTTAGGGAAGAAGTCTATGGATACAGATCGGAAGAGCGGTTTCAG
chr3	20189405	20189444	KAT2B_4599	-	GTGACCTATGCACCAGACGTACAAGGTAAACACTGAATGAGAAGTCTTTGGTCAAGAAGATCGGAAGAGCGGTTTCAG
chr3	20189685	20189724	KAT2B_4600	-	GTGACCTATGCACCAGACGTAAAAAGGAAACAGGAAAGCAATGATTAGAGTTTTACCCATAGATCGGAAGAGCGGTTTCAG
chr3	20189845	20189884	KAT2B_4601	-	GTGACCTATGCACCAGACGTGAAAAAGTAAGGTATCTAATATGAAATTCATGTGGGAAGATCGGAAGAGCGGTTTCAG
chr3	20193774	20193813	KAT2B_4602	-	GTGACCTATGCACCAGACGTAAAAAAATATTAGCAATCTTTGACTCCCTTTAAACACCAAGATCGGAAGAGCGGTTTCAG
chr18	6942028	6942067	LAMA1_4603	-	GTGACCTATGCACCAGACGTGAATCCTCAGTTGGAATCATTGCTAATATTTGAGGAGAAAGATCGGAAGAGCGGTTTCAG
chr18	6943129	6943168	LAMA1_4604	-	GTGACCTATGCACCAGACGTGTACCTGCTCTTCCACTCAAAGCGGCAGCTGTCCCTGGAGAGATCGGAAGAGCGGTTTCAG
chr18	6947112	6947151	LAMA1_4605	-	GTGACCTATGCACCAGACGTCTCTCCTCAGTTGAGGCTCTTCTCCCGCCAGTGTGAGAGACAAGATCGGAAGAGCGGTTTCAG
chr18	6948352	6948391	LAMA1_4606	-	GTGACCTATGCACCAGACGTGCAACACTCTGAAAGCCAGGCACTCCCCAGATGAGTCTGTACTCAGATCGGAAGAGCGGTTTCAG
chr18	6949050	6949089	LAMA1_4607	-	GTGACCTATGCACCAGACGTTTTTCCATACTGACATTTTACCTTCGTTGTGTTGTTAGATCGGAAGAGCGGTTTCAG
chr18	6950731	6950770	LAMA1_4608	-	GTGACCTATGCACCAGACGTAGGAGGCTTGTGGTGGCTGCTTCTGAGTTCTGTTCCATCTAGATCGGAAGAGCGGTTTCAG
chr18	6955302	6955341	LAMA1_4609	-	GTGACCTATGCACCAGACGTTTCTAACATCCTTATGCGGCGTCTCATTGCTAGATGTATGAGATCGGAAGAGCGGTTTCAG
chr18	6956585	6956624	LAMA1_4610	-	GTGACCTATGCACCAGACGTCTCCTTTACTATCAGTCCAGTCCAGTCAGCAAAGGAGGGAGATCGGAAGAGCGGTTTCAG
chr18	6958426	6958465	LAMA1_4611	-	GTGACCTATGCACCAGACGTCTGCTCTGCTGATTTCTGCATTTCTGACCTTTTCATGAGATCGGAAGAGCGGTTTCAG
chr18	6959290	6959329	LAMA1_4612	-	GTGACCTATGCACCAGACGTGCGGCCAGGCAGTGTGTAATGAAGTTGTGGTGAAGTCAAGATCGGAAGAGCGGTTTCAG
chr18	6961535	6961574	LAMA1_4613	-	GTGACCTATGCACCAGACGTCCAGTGCTCCTGAGCCCCAAGCTCAGGAAATTAATTCGGGAGATCGGAAGAGCGGTTTCAG
chr18	6961894	6961933	LAMA1_4614	-	GTGACCTATGCACCAGACGTTTGTATTAAATGTTCAAATGAGTTCCATAAGTGTCCATTAGATCGGAAGAGCGGTTTCAG
chr18	6965237	6965276	LAMA1_4615	-	GTGACCTATGCACCAGACGTAGATGGACTCACCAGATGTCGGTCCACCTCATAAGAATAGATCGGAAGAGCGGTTTCAG
chr18	6966096	6966135	LAMA1_4616	-	GTGACCTATGCACCAGACGTTTGTGCGGCCCTGACCCCTACTGTATCACACATTTAGATAGATCGGAAGAGCGGTTTCAG
chr18	6971806	6971845	LAMA1_4617	-	GTGACCTATGCACCAGACGTGTCACGGTTTAGCACATGTATGTTATTCTGTTAACATCTAGATCGGAAGAGCGGTTTCAG
chr18	6973006	6973045	LAMA1_4618	-	GTGACCTATGCACCAGACGTGAAAGTCTTCTGAACAGGACTGATTGACTGATTTTACCTAGATCGGAAGAGCGGTTTCAG
chr18	6974852	6974891	LAMA1_4619	-	GTGACCTATGCACCAGACGTATGTTCTCTCAAAGCAGCTCTCTTTTTAAAGTGTGTCTCAGATCGGAAGAGCGGTTTCAG
chr18	6975886	6975925	LAMA1_4620	-	GTGACCTATGCACCAGACGTGACCTTTGGAAAGCGACACTGAATCTTTTATGCATTTCTAAGATCGGAAGAGCGGTTTCAG
chr18	6977676	6977715	LAMA1_4621	-	GTGACCTATGCACCAGACGTGGCCCCGTGGCTTTCTGTAAGTGGGCTCTCAGTCTGTTGGGAGATCGGAAGAGCGGTTTCAG
chr18	6978145	6978184	LAMA1_4622	-	GTGACCTATGCACCAGACGTGCCCTTCTCCAGTCTGCTGCTGCTGCTGATGCAGACGAGATCGGAAGAGCGGTTTCAG
chr18	6980470	6980509	LAMA1_4623	-	GTGACCTATGCACCAGACGTAGGACTTTCTTCTGTAATAACGTTCTTCTCATTGTAAGAAGATCGGAAGAGCGGTTTCAG
chr18	6982446	6982485	LAMA1_4624	-	GTGACCTATGCACCAGACGTGGCTCGGACGGTGTAGACAGGCAGAGTGAAGCGTGAAGCGTCAAGATCGGAAGAGCGGTTTCAG
chr18	6983048	6983087	LAMA1_4625	-	GTGACCTATGCACCAGACGTACGTTGGCTTCTTTTTCTGGGCTCTGTGGGAGATTTTTCTGAGATCGGAAGAGCGGTTTCAG
chr18	6985186	6985225	LAMA1_4626	-	GTGACCTATGCACCAGACGTGCCCTTTGTGGGAACCTAAGAGCTTGCAGTCTATTGATCGGAGATCGGAAGAGCGGTTTCAG
chr18	6985476	6985515	LAMA1_4627	-	GTGACCTATGCACCAGACGTTCTGACACAGCCACAGTACAGTTTTTAAAGAATCTTACAGATCGGAAGAGCGGTTTCAG
chr18	6986086	6986125	LAMA1_4628	-	GTGACCTATGCACCAGACGTCTTGCTCTCCTCTCTCAATAGAACAGGTAACAAAATACAGATCGGAAGAGCGGTTTCAG
chr18	6992510	6992549	LAMA1_4629	-	GTGACCTATGCACCAGACGTAATTACTGTGTGCAATGCAACCAAGTAGAGAGAGAAAATCTAGATCGGAAGAGCGGTTTCAG
chr18	6993590	6993629	LAMA1_4630	-	GTGACCTATGCACCAGACGTGCTGCTAGTTTGAAGTATCTGTGCTTATCTAGTAAGAAAGATCGGAAGAGCGGTTTCAG
chr18	6995306	6995345	LAMA1_4631	-	GTGACCTATGCACCAGACGTTCCATAACCAACCAACCTTCTCCTGGTCCCTCCCATCAGAGATCGGAAGAGCGGTTTCAG
chr18	6997691	6997730	LAMA1_4632	-	GTGACCTATGCACCAGACGTGAAATACAGAGATGAACAGACACTTGTATCATTAAAGGATAGATCGGAAGAGCGGTTTCAG
chr18	6999394	6999433	LAMA1_4633	-	GTGACCTATGCACCAGACGTCTCCTCTAAATGTGTAAGATGTTTTTCTCCCAAATGTAGATCGGAAGAGCGGTTTCAG
chr18	6999860	6999899	LAMA1_4634	-	GTGACCTATGCACCAGACGTGATGTTGTCTGATGTGAAATCCCTGGGCACTCTGTTTTTGTAGATCGGAAGAGCGGTTTCAG
chr18	7002213	7002252	LAMA1_4635	-	GTGACCTATGCACCAGACGTACAGGGCAGCTGGCATGCTGGGCTGCCAGGGCTGCTTCAGATCGGAAGAGCGGTTTCAG
chr18	7007088	7007127	LAMA1_4636	-	GTGACCTATGCACCAGACGTTTGTGGGGTCTTGGCTGAGTTTGAAGTAAAGTGGACGAGATCGGAAGAGCGGTTTCAG
chr18	7008437	7008476	LAMA1_4637	-	GTGACCTATGCACCAGACGTTCTAGTCCAAATCTATTTCTGGGTTTGTAGTTGAAATGTGAGATCGGAAGAGCGGTTTCAG
chr18	7009188	7009227	LAMA1_4638	-	GTGACCTATGCACCAGACGTCTTAGAATTTGACCGTTATTTTATATTTGAAAGCAAAGATCGGAAGAGCGGTTTCAG
chr18	7010149	7010188	LAMA1_4639	-	GTGACCTATGCACCAGACGTGATCTTTTCATAGATCCCTTAAAGACATTGACTTTTGTAGATCGGAAGAGCGGTTTCAG
chr18	7011249	7011288	LAMA1_4640	-	GTGACCTATGCACCAGACGTGCGCCCTCCGAGGCCAGTCCGTTGCTTCTTAGGATATACAAGATCGGAAGAGCGGTTTCAG



chr18	7011944	7011983	LAMA1_4641	-	GTGACCTATGCACCAGACGTACACAGCGAAAGTGTCTGCTTCTAACCCCACTCCCCTGGGAGATCGGAAGAGCGGTTTCAG
chr18	7013764	7013803	LAMA1_4642	-	GTGACCTATGCACCAGACGTTCCATCCTCTCTTTCATCCTGTCTCTGGCTCCTCATCATAGATCGGAAGAGCGGTTTCAG
chr18	7015671	7015710	LAMA1_4643	-	GTGACCTATGCACCAGACGTTCCATCCACGCTCTTGCTTAACTGAGAGTTGCTTTGCTGTAAGATCGGAAGAGCGGTTTCAG
chr18	7016440	7016479	LAMA1_4644	-	GTGACCTATGCACCAGACGTATTTCCCTGTTTGTAGACTTTGTAGTCATTCCCAGAGCTTTAGATCGGAAGAGCGGTTTCAG
chr18	7017227	7017266	LAMA1_4645	-	GTGACCTATGCACCAGACGTTGTGACTAATTGACACCTTAGCCTTGGTACAGAGGCGATTAGATCGGAAGAGCGGTTTCAG
chr18	7023113	7023152	LAMA1_4646	-	GTGACCTATGCACCAGACGTGACCGTGAAGTCAGGTCAGCTGTTTATTGCCATAGGAAGTAGATCGGAAGAGCGGTTTCAG
chr18	7024329	7024368	LAMA1_4647	-	GTGACCTATGCACCAGACGTTCCACTGGCTTCAACACATTTTTCGAAATTAATAATAATAGATCGGAAGAGCGGTTTCAG
chr18	7025928	7025967	LAMA1_4648	-	GTGACCTATGCACCAGACGTGACCTCATCAGCGGTTCTGCCAGCATGGCCAGGATTCCCAGATCGGAAGAGCGGTTTCAG
chr18	7032015	7032054	LAMA1_4649	-	GTGACCTATGCACCAGACGTCACTGTAGTTCAGGTGCCCTCTCCTCAATTCCAGAGCCAGATCGGAAGAGCGGTTTCAG
chr18	7032933	7032972	LAMA1_4650	-	GTGACCTATGCACCAGACGTTCTCTTCTGTCTTTTTCCCTTCCTTCCGTTCCCTTAAGGGGAAGATCGGAAGAGCGGTTTCAG
chr18	7034428	7034467	LAMA1_4651	-	GTGACCTATGCACCAGACGTAAAAATGGAGGAAAAAATTACGGTGAAGGTACTTCCATTTTAGATCGGAAGAGCGGTTTCAG
chr18	7035936	7035975	LAMA1_4652	-	GTGACCTATGCACCAGACGTTTGCTTTGATTCTGCTATAGACTTAGGGCTTAGTGGCTAGATCGGAAGAGCGGTTTCAG
chr18	7037527	7037566	LAMA1_4653	-	GTGACCTATGCACCAGACGTCCGTAGCGATGTCTCAGATGAAGATCTCAGGGAAGATCGGAAGAGCGGTTTCAG
chr18	7038759	7038798	LAMA1_4654	-	GTGACCTATGCACCAGACGTCCATCTGCGCGCGGGATTAAATGAGCAGGTCGTATTGCAAGATCGGAAGAGCGGTTTCAG
chr18	7040025	7040064	LAMA1_4655	-	GTGACCTATGCACCAGACGTAGGTGAGAGACACCCCTGAGCTTCCCTTGGAGCTTCTCTGGAGATCGGAAGAGCGGTTTCAG
chr18	7042094	7042133	LAMA1_4656	-	GTGACCTATGCACCAGACGTGATTCACTTTTGTGCTTGAATTGATTTGTGTGTGTGAGATCGGAAGAGCGGTTTCAG
chr18	7043176	7043215	LAMA1_4657	-	GTGACCTATGCACCAGACGTTTTCTTTGCCATTGCTGATCTTCATCATCTCCCCAGGTGGAGATCGGAAGAGCGGTTTCAG
chr18	7044671	7044710	LAMA1_4658	-	GTGACCTATGCACCAGACGTTTAGAATCTGAAAGTCAGTACGTTTTCTCTTAATACGTAGATCGGAAGAGCGGTTTCAG
chr18	7046227	7046266	LAMA1_4659	-	GTGACCTATGCACCAGACGTGATTTTACATTTTTACTAAAACCTTCAAAAACGAAATTTGAAGATCGGAAGAGCGGTTTCAG
chr18	7049027	7049066	LAMA1_4660	-	GTGACCTATGCACCAGACGTGACGGCAGTCTGCCAAATAAAAATAAAAAGATTTCATTTAAGATCGGAAGAGCGGTTTCAG
chr18	7050643	7050682	LAMA1_4661	-	GTGACCTATGCACCAGACGTTGCCCGCTGCAGCAAGATCTGTTTCTCATCAGAGTCTCCAGATCGGAAGAGCGGTTTCAG
chr18	7079924	7079963	LAMA1_4662	-	GTGACCTATGCACCAGACGTCCAGAACCATTGAAGAGTGTCTACAGGCTGCTGAGCTGTGAGATCGGAAGAGCGGTTTCAG
chr18	7080236	7080275	LAMA1_4663	-	GTGACCTATGCACCAGACGTGCGCTTTATTTCTGAAATCCCATTGGGAATGTACACTTTGAGATCGGAAGAGCGGTTTCAG
chr13	113960750	113960789	LAMP1_4664	-	GTGACCTATGCACCAGACGTCCGTGAGGCAAGCAGGACCATCAAAAACCTGTCAGAAAATACAGATCGGAAGAGCGGTTTCAG
chr13	113963908	113963947	LAMP1_4665	-	GTGACCTATGCACCAGACGTACACAATTAATGTAACCCAATTGGGATGCAGGTTATTAAGATCGGAAGAGCGGTTTCAG
chr13	113964974	113965013	LAMP1_4666	-	GTGACCTATGCACCAGACGTAAAAAATAAATCACAATTGCAAACTACTTGCAGTACTTAAGATCGGAAGAGCGGTTTCAG
chr13	113973734	113973773	LAMP1_4667	-	GTGACCTATGCACCAGACGTAGTGAGGGGAGATTAGGTTCTGGGTTTCTATAACCATCAAGATCGGAAGAGCGGTTTCAG
chr13	113974610	113974649	LAMP1_4668	-	GTGACCTATGCACCAGACGTCAAGCAAGCAAGTCAACCCCTAGCTCAGGTTCTCCACACAGATCGGAAGAGCGGTTTCAG
chr13	113975669	113975708	LAMP1_4669	-	GTGACCTATGCACCAGACGTAAAATGATCTTAACTCAGGACAGATTCATAGAAAGATGAGATCGGAAGAGCGGTTTCAG
chr13	113976547	113976586	LAMP1_4670	-	GTGACCTATGCACCAGACGTAGACCGGATGTTGTCAAGGCTCTGCTCACACAGGGCCCTGCAGATCGGAAGAGCGGTTTCAG
chr11	18418340	18418379	LDHA_4671	-	GTGACCTATGCACCAGACGTGAACCAAAAGGAATCTATAGGAGGAAAAACATTTAGTGTGATCGGAAGAGCGGTTTCAG
chr11	18420928	18420967	LDHA_4672	-	GTGACCTATGCACCAGACGTTCAAATCTTTAGTTAAATGGAAAATGCCACTTCTAGATTAGATCGGAAGAGCGGTTTCAG
chr11	18422334	18422373	LDHA_4673	-	GTGACCTATGCACCAGACGTGGGGAATAATGACCAGATTAAGGCCTTTAGAATAAATTTAGATCGGAAGAGCGGTTTCAG
chr11	18424337	18424376	LDHA_4674	-	GTGACCTATGCACCAGACGTGGAGAAAAATAAATCACCATTATCTCTCCCTACACACAGATCGGAAGAGCGGTTTCAG
chr11	18425191	18425230	LDHA_4675	-	GTGACCTATGCACCAGACGTAGTACAGACTATTATTTTATGTTACCAACAGATTAGATCGGAAGAGCGGTTTCAG
chr11	18426946	18426985	LDHA_4676	-	GTGACCTATGCACCAGACGTGAAACCATAGGTAAGGAGCAAAAAAGCAGGGTGGGAGAAAGATCGGAAGAGCGGTTTCAG
chr11	18428614	18428653	LDHA_4677	-	GTGACCTATGCACCAGACGTAATGAAAAAATAAATCTCACATTTTGTCTATGCATTCCAGATCGGAAGAGCGGTTTCAG
chr2	33173892	33173931	LTBP1_4678	-	GTGACCTATGCACCAGACGTGCAAGATCGCTGAGTCCAGCAGCAGAAAGACCCCTTCCCAGATCGGAAGAGCGGTTTCAG
chr2	33245926	33245965	LTBP1_4679	-	GTGACCTATGCACCAGACGTAAAAACAGAAAGGCACAGCTTTGAAGAACAACATTGTAGACTAGATCGGAAGAGCGGTTTCAG
chr2	33335599	33335638	LTBP1_4680	-	GTGACCTATGCACCAGACGTACAAAATAAAGAGAAGGAATTAATAATGGGCTTTAAAAAGATCGGAAGAGCGGTTTCAG
chr2	33359810	33359849	LTBP1_4681	-	GTGACCTATGCACCAGACGTAGGCAGGGAGAAAAAACAACACACATCAGCTTAGTAAGATCGGAAGAGCGGTTTCAG
chr2	33411873	33411912	LTBP1_4682	-	GTGACCTATGCACCAGACGTAAAGAGAAAAACATGGAGAGTTGGTTAGTCTCTCAGAGGCTAGATCGGAAGAGCGGTTTCAG
chr2	33413594	33413633	LTBP1_4683	-	GTGACCTATGCACCAGACGTTTGGGAGGAAAACTTGTGATGCTGAATAACTAACAGGCAAGATCGGAAGAGCGGTTTCAG
chr2	33442569	33442608	LTBP1_4684	-	GTGACCTATGCACCAGACGTTAGTGTGAAATATGAAGGTTAATTGAGTGCAGGATGCCAGATCGGAAGAGCGGTTTCAG
chr2	33447097	33447136	LTBP1_4685	-	GTGACCTATGCACCAGACGTAGAAATGCTTTGTACATCTTAAATCTTCAACTCTTAGAGATCGGAAGAGCGGTTTCAG
chr2	33468679	33468718	LTBP1_4686	-	GTGACCTATGCACCAGACGTACACAATCTTTAGAAAGGAGCAGTCAAGCCCATGAGCAAGATCGGAAGAGCGGTTTCAG
chr2	33477694	33477733	LTBP1_4687	-	GTGACCTATGCACCAGACGTGAGATAAAGCCGACATTACATGAGAAACCAAACTACATAGATCGGAAGAGCGGTTTCAG
chr2	33482301	33482340	LTBP1_4688	-	GTGACCTATGCACCAGACGTGATGGGAAATATCTCTTTAAAAATCTAACAGTCAAAACAGATCGGAAGAGCGGTTTCAG
chr2	33484605	33484644	LTBP1_4689	-	GTGACCTATGCACCAGACGTAAAAAGAAAAGGGTATTAGTACCATTAAAGACAATTAGTAGATCGGAAGAGCGGTTTCAG
chr2	33487739	33487778	LTBP1_4690	-	GTGACCTATGCACCAGACGTGATTTAAAAAGAGAATAAGAAAAAAGAAATGAAAGAGATCGGAAGAGCGGTTTCAG
chr2	33488311	33488350	LTBP1_4691	-	GTGACCTATGCACCAGACGTAAGCAGAGGATAAAAAAGAAAATTAAGCCCTTATGTGCAAGATCGGAAGAGCGGTTTCAG
chr2	33498673	33498712	LTBP1_4692	-	GTGACCTATGCACCAGACGTAAAATAAATGTTGAAAAAACCCACAGAAATGAACAGATAGATCGGAAGAGCGGTTTCAG
chr2	33499982	33500021	LTBP1_4693	-	GTGACCTATGCACCAGACGTAAATACATATAAAAAATATTAGTTCTGTGTAGCAAGAACTTAGATCGGAAGAGCGGTTTCAG
chr2	33500818	33500857	LTBP1_4694	-	GTGACCTATGCACCAGACGTGATAGCATTGTTGAGTTTTGTGTTCAAATACTGTTTCAGATCGGAAGAGCGGTTTCAG
chr2	33505056	33505095	LTBP1_4695	-	GTGACCTATGCACCAGACGTAAAAACCTAGGTCGTGAACATTTTATCAGAAATACCAAAACAGATCGGAAGAGCGGTTTCAG
chr2	33518177	33518216	LTBP1_4696	-	GTGACCTATGCACCAGACGTGTTGCGTAATGAAAGAAACAAAAAAGAAAGAAAAAGATCGGAAGAGCGGTTTCAG
chr2	33525468	33525507	LTBP1_4697	-	GTGACCTATGCACCAGACGTAAACAGGCAATTTTTCTGAAAAAGAGACTACCAGGAGAAAGATCGGAAGAGCGGTTTCAG
chr2	33526539	33526578	LTBP1_4698	-	GTGACCTATGCACCAGACGTGAGAATACAAAAGAACTGTGGAAGTGGTCTTCAAAAACAGATCGGAAGAGCGGTTTCAG

chr2	33534451	33534490	LTBP1_4699	-	GTGACCTATGCACCAGACGTATTTAAAAATTTTTAAAGACTAAATAAATCACATATCGGAAGATCGGAAGAGCGGTTCCAG
chr2	33540161	33540200	LTBP1_4700	-	GTGACCTATGCACCAGACGTAAATAGAGTCTTAAAAAATTGAAAAAATCGGTTTCATTAGATCGGAAGAGCGGTTCCAG
chr2	33567855	33567894	LTBP1_4701	-	GTGACCTATGCACCAGACGTGACATGGAACATCAGACACAAAACAAACACAGGCTGACAAAGATCGGAAGAGCGGTTCCAG
chr2	33572384	33572423	LTBP1_4702	-	GTGACCTATGCACCAGACGTGAGCACAGACCAAGTGAATGTGTGCCTCATTACAGACAGAGATCGGAAGAGCGGTTCCAG
chr2	33585614	33585653	LTBP1_4703	-	GTGACCTATGCACCAGACGTAGAGAAAGTAGAGTGACAATAGGCACATCAGAACTACCAGATCGGAAGAGCGGTTCCAG
chr2	33586446	33586485	LTBP1_4704	-	GTGACCTATGCACCAGACGTAAGAGACAAAAAAGATTTCAACATCTTCCATGAAGATCGGAAGAGCGGTTCCAG
chr2	33588407	33588446	LTBP1_4705	-	GTGACCTATGCACCAGACGTAAAAAATTGAGAAATCAAAAAAGAGTTAGGTTTGATCTTTAGATCGGAAGAGCGGTTCCAG
chr2	33589233	33589272	LTBP1_4706	-	GTGACCTATGCACCAGACGTAAAAAAGTATTACTAAAGAAAATCAGCCATCAGTTGTACAGATCGGAAGAGCGGTTCCAG
chr2	33590350	33590389	LTBP1_4707	-	GTGACCTATGCACCAGACGTAGACATAGTTCCATGAAAATCGCACAGTTATTCATTTAAGATCGGAAGAGCGGTTCCAG
chr2	33614201	33614240	LTBP1_4708	-	GTGACCTATGCACCAGACGTGACAAGCAGCATGAGGCCCCACCAGTGTAGCTCGACCTAGATCGGAAGAGCGGTTCCAG
chr2	33622150	33622189	LTBP1_4709	-	GTGACCTATGCACCAGACGTAAGGGCAGAAGCTAAGTTAGAGCTTCTCAACTTCTATATAGATCGGAAGAGCGGTTCCAG
chr2	33623381	33623420	LTBP1_4710	-	GTGACCTATGCACCAGACGTTCAAGCCAGTCAAGGTAACAATCTGGATATTATCTGTGAGATCGGAAGAGCGGTTCCAG
chr16	30127939	30127978	MAPK3_4711	-	GTGACCTATGCACCAGACGTCATCTCTGCACCCTGGGGCCTGTTGAGTGTCTCCATGGCCAGATCGGAAGAGCGGTTCCAG
chr16	30128108	30128147	MAPK3_4712	-	GTGACCTATGCACCAGACGTTGCCAGGCCTGAGCCTTGCTGTCTTACCACCCAGCCAGAGATCGGAAGAGCGGTTCCAG
chr16	30128165	30128204	MAPK3_4713	-	GTGACCTATGCACCAGACGTCCCCAGCAGCAGTGGGGCTGGGGGCAGGGGAGCAGGGGGGAGATCGGAAGAGCGGTTCCAG
chr16	30128425	30128464	MAPK3_4714	-	GTGACCTATGCACCAGACGTCATGAGGGTGGGTGTGGGATAAACCTTGGGTGTCTGGAGAGATCGGAAGAGCGGTTCCAG
chr16	30128941	30128980	MAPK3_4715	-	GTGACCTATGCACCAGACGTCGCCGCTGGCTGAGTTGGGGATGATTAGCTTTTCCGAGGTAGATCGGAAGAGCGGTTCCAG
chr16	30129318	30129357	MAPK3_4716	-	GTGACCTATGCACCAGACGTCGCCACTCTGAAAGAACCGACAGTCCAGGAAGCAGATCGGAAGAGCGGTTCCAG
chr16	30129620	30129659	MAPK3_4717	-	GTGACCTATGCACCAGACGTTGGGCACCTGTCCCTCTCCCCAGGCTCTGGGGCTCCAGATCGGAAGAGCGGTTCCAG
chr16	30133095	30133134	MAPK3_4718	-	GTGACCTATGCACCAGACGTCCTTGCCAGTCCGGCTGGTCAAGGCACGGCTCGCAGCTGGAGATCGGAAGAGCGGTTCCAG
chr16	30134311	30134350	MAPK3_4719	-	GTGACCTATGCACCAGACGTGTTCCGGGGGAGGGGTGCCCTCAGGGGAGGGGGCTTCGAGATCGGAAGAGCGGTTCCAG
chr10	89264623	89264662	MINPP1_4720	-	GTGACCTATGCACCAGACGTGTCAGTGGAGTGCGCCGAGCCAGCTGCAGATGCCCGTTAGATCGGAAGAGCGGTTCCAG
chr10	89268043	89268082	MINPP1_4721	-	GTGACCTATGCACCAGACGTAAAAAATTATATGTTATTGTAATCACTGACATAAATGAAGATCGGAAGAGCGGTTCCAG
chr10	89272831	89272870	MINPP1_4722	-	GTGACCTATGCACCAGACGTGCAAAAGGTAAAAATTTGGGGTTCATTATTTTCTGCAATTTAGATCGGAAGAGCGGTTCCAG
chr10	89311789	89311828	MINPP1_4723	-	GTGACCTATGCACCAGACGTAAATTAAGAGAAAATAAGGTATATATTAATGTCATAGAAGATCGGAAGAGCGGTTCCAG
chr10	89264941	89264980	MINPP1_4724	-	GTGACCTATGCACCAGACGTCTCAGCTTGCAGTCTGTTTGACCGTGGGGTAGCGGTTGCAGATCGGAAGAGCGGTTCCAG
chr11	118307178	118307217	MLL_4725	-	GTGACCTATGCACCAGACGTTGAAGTGAAGCAGCGAGAGGGAGAGGCGACAACACAGGGGAGATCGGAAGAGCGGTTCCAG
chr11	118339440	118339479	MLL_4726	-	GTGACCTATGCACCAGACGTGAAAAATTTTAAAAATCAGAAGCAAAAACGTCATACAAGATCGGAAGAGCGGTTCCAG
chr11	118342327	118342366	MLL_4727	-	GTGACCTATGCACCAGACGTAAATTAACAAATGAAGACCATATATTAGCTGTGTAGTTAGATCGGAAGAGCGGTTCCAG
chr11	118347470	118347509	MLL_4728	-	GTGACCTATGCACCAGACGTGGCAATCCAAAAACAATAACAACATCATCATGTTGAAATTAAGATCGGAAGAGCGGTTCCAG
chr11	118348632	118348671	MLL_4729	-	GTGACCTATGCACCAGACGTAATGTGGCATTAGTTCCAAGGGAGTACTGAATTCAAACCTAGATCGGAAGAGCGGTTCCAG
chr11	118350839	118350878	MLL_4730	-	GTGACCTATGCACCAGACGTAACGAATAAACCATGAAACAATAAATTTAGAAGAAAAGAGATCGGAAGAGCGGTTCCAG
chr11	118352380	118352419	MLL_4731	-	GTGACCTATGCACCAGACGTAACACAACAACATCATCTGTCTATAGTGAATAAATTTAAGATCGGAAGAGCGGTTCCAG
chr11	118353087	118353126	MLL_4732	-	GTGACCTATGCACCAGACGTCAGAATAAATTCGAGTCAGATGCTGGCAACGACTACTTTAAGATCGGAAGAGCGGTTCCAG
chr11	118354848	118354887	MLL_4733	-	GTGACCTATGCACCAGACGTAAAAAGGTAAATATAAGAAAACAAACACACCTATTGCTTTAGATCGGAAGAGCGGTTCCAG
chr11	118355527	118355566	MLL_4734	-	GTGACCTATGCACCAGACGTAGAAAGGTCACTTAGGAAAAGTTTTACAATACACAACCTTTAGATCGGAAGAGCGGTTCCAG
chr11	118359279	118359318	MLL_4735	-	GTGACCTATGCACCAGACGTAACATGGGAAGATAGAAGTATGTCAAATAATATGTAGAAAAGATCGGAAGAGCGGTTCCAG
chr11	118360457	118360496	MLL_4736	-	GTGACCTATGCACCAGACGTATATAATGGCAAAAAGATAAGCATCATATTACCTTCACCAGATCGGAAGAGCGGTTCCAG
chr11	118360794	118360833	MLL_4737	-	GTGACCTATGCACCAGACGTAGAAAAGAAATCAATAGGAATTTCTTGTTTTAAATATCTAGATCGGAAGAGCGGTTCCAG
chr11	118361861	118361900	MLL_4738	-	GTGACCTATGCACCAGACGTAGCAAAGTTTACAGCAGTCTTTGGCTCACATACCCGTGTAGATCGGAAGAGCGGTTCCAG
chr11	118362409	118362448	MLL_4739	-	GTGACCTATGCACCAGACGTAAAAACCTACCATGATGAGGCTCTGAAAGAATGAGAGAGATCGGAAGAGCGGTTCCAG
chr11	118363722	118363761	MLL_4740	-	GTGACCTATGCACCAGACGTGAAAGATATGTTGCTTTTCTAACACTAAAACCAAGGTGAGATCGGAAGAGCGGTTCCAG
chr11	118364953	118364992	MLL_4741	-	GTGACCTATGCACCAGACGTAAACAAAATGTTAATTTCTTAAAACAGTGTGCTCTGAAAGATCGGAAGAGCGGTTCCAG
chr11	118365359	118365398	MLL_4742	-	GTGACCTATGCACCAGACGTACACAAAACAAAATGTAATATGTAACACTCATTTAGATAAGATCGGAAGAGCGGTTCCAG
chr11	118366926	118366965	MLL_4743	-	GTGACCTATGCACCAGACGTAAAAAGACTCCCATCAATACCTTTGAGATCCAGTTAAAATGAGATCGGAAGAGCGGTTCCAG
chr11	118368601	118368640	MLL_4744	-	GTGACCTATGCACCAGACGTAAAGAGTCTTTTTTCTTAAAGAAATAATGCCAAAGAAAGATCGGAAGAGCGGTTCCAG
chr11	118369035	118369074	MLL_4745	-	GTGACCTATGCACCAGACGTAAAAAGAACAGAGTCTTATTAGACATTTTATATGTTTTAAAGATCGGAAGAGCGGTTCCAG
chr11	118369968	118370007	MLL_4746	-	GTGACCTATGCACCAGACGTACCCATGGTAGCTGTTAATAGGCTGTCCCTTGCACATTAAGATCGGAAGAGCGGTTCCAG
chr11	118371652	118371691	MLL_4747	-	GTGACCTATGCACCAGACGTAGATTTGGGAAAATCATCATAAGGGAGAGGATAGAAGCAGAGATCGGAAGAGCGGTTCCAG
chr11	118372337	118372376	MLL_4748	-	GTGACCTATGCACCAGACGTAAATAAAAACTCTTAACTAAAAAGGCCAATTAATAATCAGATCGGAAGAGCGGTTCCAG
chr11	118373063	118373102	MLL_4749	-	GTGACCTATGCACCAGACGTGAGAAAAGTAAATAATGCTATTGTAGATAAACAATGTAGATCGGAAGAGCGGTTCCAG
chr11	118378194	118378233	MLL_4750	-	GTGACCTATGCACCAGACGTGGCATTGTATCTTTTCAAGACAACCCAGTAATATGAGATCGGAAGAGCGGTTCCAG
chr11	118379801	118379840	MLL_4751	-	GTGACCTATGCACCAGACGTACCAAAATGTAAGATAAATATCAGCTAGTCTTCAATTCAGATCGGAAGAGCGGTTCCAG
chr11	118382616	118382655	MLL_4752	-	GTGACCTATGCACCAGACGTATAAAGAAAACCCGTAAGCCAGAAAATATGCACGTAACCCAGATCGGAAGAGCGGTTCCAG
chr11	118390283	118390322	MLL_4753	-	GTGACCTATGCACCAGACGTGAGAAAGCAGAGGAAAGTGAAGAGCGCAGTCAACAGGAAAAGATCGGAAGAGCGGTTCCAG
chr11	118390622	118390661	MLL_4754	-	GTGACCTATGCACCAGACGTAAGATTAACACATATTTAGAGAAAATGCTTTAATAAAGCAGAGATCGGAAGAGCGGTTCCAG
chr11	118391467	118391506	MLL_4755	-	GTGACCTATGCACCAGACGTAGACACTATTAAAGCAATTTTTTCAAGAAAATGTTTGTAGATCGGAAGAGCGGTTCCAG
chr11	118391953	118391992	MLL_4756	-	GTGACCTATGCACCAGACGTGAGAAAAGGTCAGACACAAAATTTTGAAGTAAAGTTAGATCGGAAGAGCGGTTCCAG

chr11	118392562	118392601	MLL_4757	-	GTGACCTATGCACCAGACGTAGAAGAAGGGAGAAGAACTTGTCACTTTCTATAAACTCAGAGATCGGAAGAGCGGTTTCAG
chr11	118342769	118342808	MLL_4758	-	GTGACCTATGCACCAGACGTTCCCTTCTGTTGATGGAGGCCCTTCTCCTCCGTCGTACAATAGATCGGAAGAGCGGTTTCAG
chr11	118343211	118343250	MLL_4759	-	GTGACCTATGCACCAGACGTGAAGATCCACAGGACGGGGCACTGAATCTACTATTCCGGTGAAGATCGGAAGAGCGGTTTCAG
chr11	118343653	118343692	MLL_4760	-	GTGACCTATGCACCAGACGTCCTTGCATAGGAGCAGTGAAGCAGGCAAAAATGGTGATAGATCGGAAGAGCGGTTTCAG
chr11	118344095	118344134	MLL_4761	-	GTGACCTATGCACCAGACGTAGTGAAGAAGGATCTTGGTTTCAGATCGAATAGGACTAAAAGATCGGAAGAGCGGTTTCAG
chr11	118373535	118373574	MLL_4762	-	GTGACCTATGCACCAGACGTGACGCTCCCTCTGAGCTCTGGAACCTCAGCACTTTGGTCTTAGATCGGAAGAGCGGTTTCAG
chr11	118374007	118374046	MLL_4763	-	GTGACCTATGCACCAGACGTGGTTGGCCCATACTCAGGAGTCAAACCTCATCCATAAAGATCGGAAGAGCGGTTTCAG
chr11	118374479	118374518	MLL_4764	-	GTGACCTATGCACCAGACGTGAGTGGGGTAAAGCCAAAAACATGTTAGAACGTGCACGGAGATCGGAAGAGCGGTTTCAG
chr11	118374951	118374990	MLL_4765	-	GTGACCTATGCACCAGACGTGTTTTAACTCTGCTTACAGAATGGCAGTTATCCATCTTAGATCGGAAGAGCGGTTTCAG
chr11	118375423	118375462	MLL_4766	-	GTGACCTATGCACCAGACGTAGTCTACTGGGATTCTGGCTGGGGACAGTGGGACTCCGGGAGATCGGAAGAGCGGTTTCAG
chr11	118375895	118375934	MLL_4767	-	GTGACCTATGCACCAGACGTAGAGGTCAATTGGATTTTTGGGTCACTCCATTTGGAAGAAGATCGGAAGAGCGGTTTCAG
chr11	118376367	118376406	MLL_4768	-	GTGACCTATGCACCAGACGTAGGAAGCTGGGAGGGTGAAGTTAATCAATGTCATATTAGATCGGAAGAGCGGTTTCAG
chr11	118376839	118376878	MLL_4769	-	GTGACCTATGCACCAGACGTGTTATTGCAGCAGTAGAGGGGGTGTGTGATGTCCCAGATTAGATCGGAAGAGCGGTTTCAG
chr7	151833867	151833906	MLL3_4770	-	GTGACCTATGCACCAGACGTTTCTAGCTCAGCGGGCGGCTTGTCCCTAGGAAGAGGCGAAGATCGGAAGAGCGGTTTCAG
chr7	151835831	151835870	MLL3_4771	-	GTGACCTATGCACCAGACGTGAGAGATTGCATCTGCCATGTTGTTTCAGATCCTGGGCGAAAGATCGGAAGAGCGGTTTCAG
chr7	151836221	151836260	MLL3_4772	-	GTGACCTATGCACCAGACGTGAGGAACCTGACGGGGAGTGCTTTTGTCTGTGGGGCCAGTAGATCGGAAGAGCGGTTTCAG
chr7	151836710	151836749	MLL3_4773	-	GTGACCTATGCACCAGACGTGGTCCCGAGATTGATACACAGCACCATCATCTCCAGATCGGAAGAGCGGTTTCAG
chr7	151841748	151841787	MLL3_4774	-	GTGACCTATGCACCAGACGTACTTTGCTAGCAGGAAGTGGAGAGCGGGTGTGAGTGTCCCAGATTAGATCGGAAGAGCGGTTTCAG
chr7	151842188	151842227	MLL3_4775	-	GTGACCTATGCACCAGACGTTTAACTTACATAGTACAGCCAGGGTTTCTAGGCGTATTAGATCGGAAGAGCGGTTTCAG
chr7	151843634	151843673	MLL3_4776	-	GTGACCTATGCACCAGACGTTGGTCAGGCTTTGAGATTGGAATTGCTTTTCTGATTGATAGATCGGAAGAGCGGTTTCAG
chr7	151845068	151845107	MLL3_4777	-	GTGACCTATGCACCAGACGTCCGTTACATGCTGTGCAGTGTCTACTTACTCTGATGTCAGAGATCGGAAGAGCGGTTTCAG
chr7	151848477	151848516	MLL3_4778	-	GTGACCTATGCACCAGACGTACTCCTTTTATGACCCACCTCCTACCTCCAGCGAAAATGAGATCGGAAGAGCGGTTTCAG
chr7	151849740	151849779	MLL3_4779	-	GTGACCTATGCACCAGACGTGAGCTTTTTGTTAACCCCAAATCCATTCTGATTCAAAGAGATCGGAAGAGCGGTTTCAG
chr7	151851045	151851084	MLL3_4780	-	GTGACCTATGCACCAGACGTGTTAATGACTTCTTAATGTTAAACGATGTTGCTCCCAATTTTTCAGATCGGAAGAGCGGTTTCAG
chr7	151851302	151851341	MLL3_4781	-	GTGACCTATGCACCAGACGTCACTTAACTTATTATTTCCCTTTTACTACTACGCCAATTTAAGATCGGAAGAGCGGTTTCAG
chr7	151852945	151852984	MLL3_4782	-	GTGACCTATGCACCAGACGTTTTTTTTCTCAAATAATCTTAGTATTCTTCTTTTAAAGATCGGAAGAGCGGTTTCAG
chr7	151853240	151853279	MLL3_4783	-	GTGACCTATGCACCAGACGTAGCCTCAAATTTACACCTCGGAGAAATGTGCCTCTGCCAGATCGGAAGAGCGGTTTCAG
chr7	151859152	151859191	MLL3_4784	-	GTGACCTATGCACCAGACGTATCAAAAAACGACAACCTTTTTTCTTTTGTTTAAATATAGATCGGAAGAGCGGTTTCAG
chr7	151864181	151864220	MLL3_4785	-	GTGACCTATGCACCAGACGTGGTTTGCAAAATGAAACTCAACCAATTAATGAGTAGAAAGATCGGAAGAGCGGTTTCAG
chr7	151866221	151866260	MLL3_4786	-	GTGACCTATGCACCAGACGTGTTCTAATAAGTAAATGTTTCTGGGGATTGCTTGTCTGCAAGATCGGAAGAGCGGTTTCAG
chr7	151868299	151868338	MLL3_4787	-	GTGACCTATGCACCAGACGTCTGTAATGAGTCCCTCTAGAATGCACGCTTTTCTGTTTCCAGATCGGAAGAGCGGTTTCAG
chr7	151871166	151871205	MLL3_4788	-	GTGACCTATGCACCAGACGTTGGCTGCTTGTCTTACTGGGCATCTAGACATTCATGAAAAGATCGGAAGAGCGGTTTCAG
chr7	151873226	151873265	MLL3_4789	-	GTGACCTATGCACCAGACGTTCTTGAGTCTCAACGTATATTACTATGGGTATTAGAGTGGAGATCGGAAGAGCGGTTTCAG
chr7	151876869	151876908	MLL3_4790	-	GTGACCTATGCACCAGACGTTAATTTCTGCCGAATTTAAATGCTATTAGAAGAGGGAAAGATCGGAAGAGCGGTTTCAG
chr7	151877746	151877785	MLL3_4791	-	GTGACCTATGCACCAGACGTGATGTTCTCAAGTTTTAAATGATTATTGAGGAAGCTGAGATCGGAAGAGCGGTTTCAG
chr7	151880009	151880048	MLL3_4792	-	GTGACCTATGCACCAGACGTTTTGGATAATCTACTTTTTGAAGTTGCATTTTTGTTTTGAAGATCGGAAGAGCGGTTTCAG
chr7	151882593	151882632	MLL3_4793	-	GTGACCTATGCACCAGACGTAACTCCTCTATCTTTAAATATTTAAATACAGTGTGTAAGATCGGAAGAGCGGTTTCAG
chr7	151884297	151884336	MLL3_4794	-	GTGACCTATGCACCAGACGTAATATATATTTCTGTTTTACCAACATTTTCACATGTGCAAGATCGGAAGAGCGGTTTCAG
chr7	151884750	151884789	MLL3_4795	-	GTGACCTATGCACCAGACGTTATTTCTATGGAACCTAAATGCACTAATTTCTGTTTGAAGATCGGAAGAGCGGTTTCAG
chr7	151891044	151891083	MLL3_4796	-	GTGACCTATGCACCAGACGTACTTTATAATCTACATTATATCACACACATGTGATATAGATCGGAAGAGCGGTTTCAG
chr7	151891264	151891303	MLL3_4797	-	GTGACCTATGCACCAGACGTTTTGATTTTCTAGTTTTCTAATGAAAATGGCGTTCCCATACCAAGATCGGAAGAGCGGTTTCAG
chr7	151891475	151891514	MLL3_4798	-	GTGACCTATGCACCAGACGTTGCCCTACATCTAGGCTTTCTAAAAGACCTGAGTAAATATAGATCGGAAGAGCGGTTTCAG
chr7	151892942	151892981	MLL3_4799	-	GTGACCTATGCACCAGACGTATACTGTTTACCCTTTTTCTGGTTTCTGATGTGAGCGAGAAGATCGGAAGAGCGGTTTCAG
chr7	151896314	151896353	MLL3_4800	-	GTGACCTATGCACCAGACGTTTATTACAGATATTTCTTTATATCATATAACATACATCAGATCGGAAGAGCGGTTTCAG
chr7	151899969	151900008	MLL3_4801	-	GTGACCTATGCACCAGACGTGCTTTACATATTTTACATGGTTTGTAAATGAGGAAATAAGATCGGAAGAGCGGTTTCAG
chr7	151904335	151904374	MLL3_4802	-	GTGACCTATGCACCAGACGTGAGGTAGACATTTCAATATCATCAACACTTGGTTAATTAAGATCGGAAGAGCGGTTTCAG
chr7	151917558	151917597	MLL3_4803	-	GTGACCTATGCACCAGACGTTTTATTTTCCATGAAATATGTGTGCAAGAATTAAGCATAAGATCGGAAGAGCGGTTTCAG
chr7	151919036	151919075	MLL3_4804	-	GTGACCTATGCACCAGACGTAATGCTTTACTTGATTTAATTAATTTACTTTGCTTAATTAGATCGGAAGAGCGGTTTCAG
chr7	151919608	151919647	MLL3_4805	-	GTGACCTATGCACCAGACGTAATTTAAACTGTGAGTCTGCACTCTTGATCCACTCACTTGAGATCGGAAGAGCGGTTTCAG
chr7	151921050	151921089	MLL3_4806	-	GTGACCTATGCACCAGACGTATTTTTTCTATCTTTTTAAAGCTTTTCTCTTTGAAATGTAGAGATCGGAAGAGCGGTTTCAG
chr7	151921470	151921509	MLL3_4807	-	GTGACCTATGCACCAGACGTGTTTGGCTTGTGCTTAGTCTTTCAAGTTCAGAGCTTTCTAGATCGGAAGAGCGGTTTCAG
chr7	151926958	151926997	MLL3_4808	-	GTGACCTATGCACCAGACGTTTTAATTTGAGTTAACAATAATGATTGAATTTTTTGGAGATCGGAAGAGCGGTTTCAG
chr7	151927255	151927294	MLL3_4809	-	GTGACCTATGCACCAGACGTGACAATTTACTGTCTTCTCATTGAATTCCTCCTTGCACAAGATCGGAAGAGCGGTTTCAG
chr7	151932852	151932891	MLL3_4810	-	GTGACCTATGCACCAGACGTTCTCATGTATTTTTCTCTAATCTAAATGTCAGTTAATGAAGATCGGAAGAGCGGTTTCAG
chr7	151935742	151935781	MLL3_4811	-	GTGACCTATGCACCAGACGTTTGCATTTACATTCATATATCATTTCTGTCTGATTTGTTTAGATCGGAAGAGCGGTTTCAG
chr7	151944937	151944976	MLL3_4812	-	GTGACCTATGCACCAGACGTTTTAATGATATTGACAGAAAAGATTTGGAACAATTCATAGATCGGAAGAGCGGTTTCAG
chr7	151946911	151946950	MLL3_4813	-	GTGACCTATGCACCAGACGTTTTCATATTGCTAAATTTGATTGAGTTACAAGATAATGATCGGAAGAGCGGTTTCAG
chr7	151947888	151947927	MLL3_4814	-	GTGACCTATGCACCAGACGTTTTAATGGATATACTGTTTTTGAAGAAAATGTGTATATAAGATCGGAAGAGCGGTTTCAG

chr7	151948974	151949013	MLL3_4815	-	GTGACCTATGCACCAGACGTGAATGATTTTTTTTTAAATTTTTTGTGTTTGTGTAATGTTGTAGATCGGAAGAGCGGTTTCAG
chr7	151949581	151949620	MLL3_4816	-	GTGACCTATGCACCAGACGTAGTTATTCTATTCAAGTTGTTTTGTCGATTGTTTTATTATAGATCGGAAGAGCGGTTTCAG
chr7	151962073	151962112	MLL3_4817	-	GTGACCTATGCACCAGACGTATTTCAATTCAAAGCTGTGTATTGGGTTAAGAGGGACCCAGATCGGAAGAGCGGTTTCAG
chr7	151970740	151970779	MLL3_4818	-	GTGACCTATGCACCAGACGTTACGGATAGACTTTAAACTTCAACCAATGTATTTACTGAAGATCGGAAGAGCGGTTTCAG
chr7	152007001	152007040	MLL3_4819	-	GTGACCTATGCACCAGACGTAAAGCAAATATTTAAATCATAGTTTTATAACATTCACTTTAGATCGGAAGAGCGGTTTCAG
chr7	152008833	152008872	MLL3_4820	-	GTGACCTATGCACCAGACGTGTTTTCAATAATGACTGCCTCTTAATCTGGAAGCATTTTTAGATCGGAAGAGCGGTTTCAG
chr7	152012173	152012212	MLL3_4821	-	GTGACCTATGCACCAGACGTTCGACTTTAAATGTGGAAATGATTAAGACTGCATATAATAGATCGGAAGAGCGGTTTCAG
chr7	152027636	152027675	MLL3_4822	-	GTGACCTATGCACCAGACGTGAATGCAGCTGGATTGGATATTAGTGACAGGAATAAAGCAAGATCGGAAGAGCGGTTTCAG
chr7	152055622	152055661	MLL3_4823	-	GTGACCTATGCACCAGACGTTCAAGAATTTATAAGAAATGTATAATGATGCTTTGCATATGAGATCGGAAGAGCGGTTTCAG
chr7	152132661	152132700	MLL3_4824	-	GTGACCTATGCACCAGACGTTGCGAGGGAGCCAGGCCGGGAGCCAGCGCGCGGCCGGGCAGATCGGAAGAGCGGTTTCAG
chr7	151945296	151945335	MLL3_4825	-	GTGACCTATGCACCAGACGTAAATTCTGAACCTTTCTACTGGATTGATGGACTCTGAAATGAGATCGGAAGAGCGGTTTCAG
chr7	151845441	151845480	MLL3_4826	-	GTGACCTATGCACCAGACGTTTCATGAGCAAGAATAAGTTACTTTGCAGTCTTCAGGAGATCGGAAGAGCGGTTTCAG
chr7	151845814	151845853	MLL3_4827	-	GTGACCTATGCACCAGACGTGGCACTTCCCTTAAACCTGATGCTTGCCCAAAGACTATCAGATCGGAAGAGCGGTTTCAG
chr7	151859579	151859618	MLL3_4828	-	GTGACCTATGCACCAGACGTAACAAACTGCCCAATAGTGATTTCTACAAGCAACTCAAAGATCGGAAGAGCGGTTTCAG
chr7	151873681	151873720	MLL3_4829	-	GTGACCTATGCACCAGACGTCCACCAACTCTGCCGGCTCCCATCCAATCATGTGTCAAAGATCGGAAGAGCGGTTTCAG
chr7	151878217	151878256	MLL3_4830	-	GTGACCTATGCACCAGACGTGAGGGGTTTTACTAGGTCCCTCAATGACAAGACCAGTCTAGATCGGAAGAGCGGTTTCAG
chr7	151860006	151860045	MLL3_4831	-	GTGACCTATGCACCAGACGTTTTCTGGGACCAGCTCCAGCAGTCCCAGTGAGGCGCTTCTAGATCGGAAGAGCGGTTTCAG
chr7	151874136	151874175	MLL3_4832	-	GTGACCTATGCACCAGACGTAGTGTCTGTTGACCAAAAAAGGAACAAGAAAGATCGGAAGAGCGGTTTCAG
chr7	151878688	151878727	MLL3_4833	-	GTGACCTATGCACCAGACGTAAAGGCCTGCTTTGACACCAAGACCTATAGATAATTTTTTCAGATCGGAAGAGCGGTTTCAG
chr7	151860433	151860472	MLL3_4834	-	GTGACCTATGCACCAGACGTAACGGGAACGTAAGGAACGTTTACGAGAACAGCAAGAGAGATCGGAAGAGCGGTTTCAG
chr7	151874591	151874630	MLL3_4835	-	GTGACCTATGCACCAGACGTTTCTTGTCCATTCTCTATGGTCAATGAGGACTCTGAGATCGGAAGAGCGGTTTCAG
chr7	151879159	151879198	MLL3_4836	-	GTGACCTATGCACCAGACGTGAAGAAATCTGCTGCACCAGTGGAAAATGTACACCTTTAGATCGGAAGAGCGGTTTCAG
chr3	49924690	49924729	MST1R_4837	-	GTGACCTATGCACCAGACGTGGGCTGGACCTGCTTAGCTGCCTTGAGCTAACCCCAAGCTAGATCGGAAGAGCGGTTTCAG
chr3	49927868	49927907	MST1R_4838	-	GTGACCTATGCACCAGACGTGGCCTGCCCTACAGTCCACATGCTTGTGGCACCACAAGAACAGATCGGAAGAGCGGTTTCAG
chr3	49928580	49928619	MST1R_4839	-	GTGACCTATGCACCAGACGTAGAGTAGCTGGGGTGAAGCAAAGGACAGGGCATGAGGGTAGATCGGAAGAGCGGTTTCAG
chr3	49928782	49928821	MST1R_4840	-	GTGACCTATGCACCAGACGTATCTGGCTCTGGGTTGGGGCTGGGCAGCAGCTGGAGAAGAGATCGGAAGAGCGGTTTCAG
chr3	49929141	49929180	MST1R_4841	-	GTGACCTATGCACCAGACGTGAGAGATGGGAAGGACAGAGGGAGGGCCCTCAGGCTGGGAAGATCGGAAGAGCGGTTTCAG
chr3	49932550	49932589	MST1R_4842	-	GTGACCTATGCACCAGACGTGAGGTGGGGCTGGGGCAGAGATGGAGTCTCAAGATGACATAGATCGGAAGAGCGGTTTCAG
chr3	49932830	49932869	MST1R_4843	-	GTGACCTATGCACCAGACGTGGAGGCATGAGAAGCTAAAGCCACCCCTGCCCTACAAGATCGGAAGAGCGGTTTCAG
chr3	49933098	49933137	MST1R_4844	-	GTGACCTATGCACCAGACGTGCTCCTACCTTTAATCAGCCCTACCCCCAACCAATGGCAGATCGGAAGAGCGGTTTCAG
chr3	49933344	49933383	MST1R_4845	-	GTGACCTATGCACCAGACGTGAGTGGACCTCCCTGGGAAACACGGGCAGAGGGCCTACAAGATCGGAAGAGCGGTTTCAG
chr3	49933578	49933617	MST1R_4846	-	GTGACCTATGCACCAGACGTGGGATAGGGGCAGGGACAGTTGGGGATCTGAAAGTAGGGGAGATCGGAAGAGCGGTTTCAG
chr3	49933923	49933962	MST1R_4847	-	GTGACCTATGCACCAGACGTGCTGGCCAGGAGGGAGGAAGGCTGGATGAGTCCCTGAGCAGATCGGAAGAGCGGTTTCAG
chr3	49934112	49934151	MST1R_4848	-	GTGACCTATGCACCAGACGTCTCTTTGCCACTCTGGCCCTGGGGAATGAGAGCCCAAGATCGGAAGAGCGGTTTCAG
chr3	49934663	49934702	MST1R_4849	-	GTGACCTATGCACCAGACGTCCAGCCAGCATGGGAGGCCCGCAGGGTCTTATCCAGGTGGAGATCGGAAGAGCGGTTTCAG
chr3	49934903	49934942	MST1R_4850	-	GTGACCTATGCACCAGACGTCTTGCCCTGTCTGTGCCCTTGCCAGTGCATGGTACGGGAAGATCGGAAGAGCGGTTTCAG
chr3	49935434	49935473	MST1R_4851	-	GTGACCTATGCACCAGACGTGCCCTCCCTCCCTTTCCCTGAAGGGGAAACCAAGCAGAGATCGGAAGAGCGGTTTCAG
chr3	49935901	49935940	MST1R_4852	-	GTGACCTATGCACCAGACGTCCCTGGCAGGGCACAGGTAAGAGTGGGACAGGCTGGGCCTGAGATCGGAAGAGCGGTTTCAG
chr3	49936250	49936289	MST1R_4853	-	GTGACCTATGCACCAGACGTGAGGGGAGGGCCCTGGGGCCAGGGTGTGGGATCACAGACAGATCGGAAGAGCGGTTTCAG
chr3	49936458	49936497	MST1R_4854	-	GTGACCTATGCACCAGACGTATCCCAAGTCCCTAGCCCTGGGTCCTTGTCTCCATCCAGATCGGAAGAGCGGTTTCAG
chr3	49939763	49939802	MST1R_4855	-	GTGACCTATGCACCAGACGTAGAAGGGCCCTACTTGTGAGTGCATGCATGGCTGAAGATCGGAAGAGCGGTTTCAG
chr3	49940173	49940212	MST1R_4856	-	GTGACCTATGCACCAGACGTACACGCCTGGCACGGCTTAGCGCCACTGAGCCAGAGTTGAGATCGGAAGAGCGGTTTCAG
chr3	49940583	49940622	MST1R_4857	-	GTGACCTATGCACCAGACGTGGCCGCTGCTTCTGATGAGCTAGAGCCCAAGGGACAGAGATCGGAAGAGCGGTTTCAG
chr1	155158561	155158600	MUC1_4858	-	GTGACCTATGCACCAGACGTCCCGCTGAGCTGAGTGGCCAGCCAGTGCCATTCCACTCCAAGATCGGAAGAGCGGTTTCAG
chr1	155159651	155159690	MUC1_4859	-	GTGACCTATGCACCAGACGTGCCCCACAGCCAGGGGAAGCAGAGGGTTTGGCTGGGCAAGATCGGAAGAGCGGTTTCAG
chr1	155159881	155159920	MUC1_4860	-	GTGACCTATGCACCAGACGTTCCTGGCCCTGATCAGAGCCCCCGGTGAGAAAGCCTCCAGATCGGAAGAGCGGTTTCAG
chr1	155160148	155160187	MUC1_4861	-	GTGACCTATGCACCAGACGTTTTCCCTGGCTGACAGCCAGCACCATGCCGGGGCCCTCTCAGATCGGAAGAGCGGTTTCAG
chr1	155160434	155160473	MUC1_4862	-	GTGACCTATGCACCAGACGTGGGTGTGGACCAAGTGTGGTGGTTGGAGGGTGGTGGTGGAGATCGGAAGAGCGGTTTCAG
chr1	155160589	155160628	MUC1_4863	-	GTGACCTATGCACCAGACGTGCCCTTCCCTTCCCATGCTCCCTGAAGCAGCCATCAGAAGATCGGAAGAGCGGTTTCAG
chr1	155161924	155161963	MUC1_4864	-	GTGACCTATGCACCAGACGTCCAGCAGCTACTCTCCAGCCACAGCCCCGGTTCCAGGCTCAGATCGGAAGAGCGGTTTCAG
chr1	155162527	155162566	MUC1_4865	-	GTGACCTATGCACCAGACGTGAGGTGGGAGTGGGCTGCCCTGCTTAGTGGTCTTCGATAGATCGGAAGAGCGGTTTCAG
chr10	76602566	76602605	MYST4_4866	-	GTGACCTATGCACCAGACGTGACTTCTTCAACAAAAGTTACCATAGAGGTTCTCTTAGATCGGAAGAGCGGTTTCAG
chr10	76719678	76719717	MYST4_4867	-	GTGACCTATGCACCAGACGTATTAATAAAAAAATACTGTCACTTTTCCATTTCAAAGTAGATCGGAAGAGCGGTTTCAG
chr10	76729368	76729407	MYST4_4868	-	GTGACCTATGCACCAGACGTAAAAAGCAAATGCTTGTGAGGGAAATGGTGCCTTTGACTTTAGATCGGAAGAGCGGTTTCAG
chr10	76729728	76729767	MYST4_4869	-	GTGACCTATGCACCAGACGTACATATTAGAGACTAATTGAGACTGAAACCAACTGTAAAAGATCGGAAGAGCGGTTTCAG
chr10	76732215	76732254	MYST4_4870	-	GTGACCTATGCACCAGACGTATATATGAGAAAAATTTAATGTTTTATTATTTAAGAGAGATCGGAAGAGCGGTTTCAG
chr10	76735107	76735146	MYST4_4871	-	GTGACCTATGCACCAGACGTATTATAGAGAAATGATCAGCATTTAATAAATAGAATTATAAGATCGGAAGAGCGGTTTCAG
chr10	76737024	76737063	MYST4_4872	-	GTGACCTATGCACCAGACGTAAACCAGCAAGAAATGATTACTGACTTGAATCATGATAGATCGGAAGAGCGGTTTCAG

chr10	76738932	76738971	MYST4_4873	-	GTGACCTATGCACCAGACGTGAAAGAAAAGAAAATAATAATATATATACTTCACTTACAAGATCGGAAGAGCGGTTTCAG
chr10	76741495	76741534	MYST4_4874	-	GTGACCTATGCACCAGACGTTTAAAAATCATAGAATCTATCAGATAGATTATACTGTTGGAGATCGGAAGAGCGGTTTCAG
chr10	76744788	76744827	MYST4_4875	-	GTGACCTATGCACCAGACGTGAAACAGACAACATTATTTAACATAAAAAATACTGCACCATAGATCGGAAGAGCGGTTTCAG
chr10	76748727	76748766	MYST4_4876	-	GTGACCTATGCACCAGACGTGAGAAAACAGATCAAGTATGTCAGAGCCCTGCTGAAGTGGGAGATCGGAAGAGCGGTTTCAG
chr10	76780290	76780329	MYST4_4877	-	GTGACCTATGCACCAGACGTAAAAATAAATGGGCATTCTCCTACTGTGGCATTCCCAGAGCAGATCGGAAGAGCGGTTTCAG
chr10	76780834	76780873	MYST4_4878	-	GTGACCTATGCACCAGACGTATAAGGCGAGAACAAGATGTAATCACAAGCTGAAATTTACAGATCGGAAGAGCGGTTTCAG
chr10	76781589	76781628	MYST4_4879	-	GTGACCTATGCACCAGACGTAGGGTAAAATGTGGCCAGTGAGAGGGCAGTTACACAGCAGATCGGAAGAGCGGTTTCAG
chr10	76784666	76784705	MYST4_4880	-	GTGACCTATGCACCAGACGTTTCCAAACATAACACATAAGAGCTCATGAGAAATTAATGAGATCGGAAGAGCGGTTTCAG
chr10	76788197	76788236	MYST4_4881	-	GTGACCTATGCACCAGACGTAGACAAAAACGGGAAGGAAAAAAAACAGTCTTAGAAAGCAGATCGGAAGAGCGGTTTCAG
chr10	76602876	76602915	MYST4_4882	-	GTGACCTATGCACCAGACGTATTACATGATCCTCTAGACCCTTGGCTGACTTAGGAAAAAGATCGGAAGAGCGGTTTCAG
chr10	76735573	76735612	MYST4_4883	-	GTGACCTATGCACCAGACGTCTGGGGCTCTGACCGGAGATGGGGGTTGGGGGTGGAAGTGAGATCGGAAGAGCGGTTTCAG
chr10	76789049	76789088	MYST4_4884	-	GTGACCTATGCACCAGACGTAGATTCGGGTACAGCTTCAGGGTCCCCAGCAAGCTCCTTGAGATCGGAAGAGCGGTTTCAG
chr10	76789475	76789514	MYST4_4885	-	GTGACCTATGCACCAGACGTGATGTTCTGCGAGATGGCAGTGCAGATGGCACTTTGATCTAGATCGGAAGAGCGGTTTCAG
chr10	76789901	76789940	MYST4_4886	-	GTGACCTATGCACCAGACGTCTCGGGGATTTTCAGCCAGCTGCATGGGTGGGGTGAAGTTAAGATCGGAAGAGCGGTTTCAG
chr10	76790327	76790366	MYST4_4887	-	GTGACCTATGCACCAGACGTCTGGTTCATGGAGATGTGGCCCTTGCTGGCAATCTGGAGATCGGAAGAGCGGTTTCAG
chr12	78225192	78225231	NAV3_4888	-	GTGACCTATGCACCAGACGTAAATATCTTCTTCTGCTGCCAAAGAAAATGCTTCTAACCTCAGATCGGAAGAGCGGTTTCAG
chr12	78334049	78334088	NAV3_4889	-	GTGACCTATGCACCAGACGTGAGAGAAGGAAAAAGTGAGATGGGGTGGGGGAAAAACAGAGAGATCGGAAGAGCGGTTTCAG
chr12	78334811	78334850	NAV3_4890	-	GTGACCTATGCACCAGACGTGAGATAAAAAGAGAAAAAGAAAAAAGAACGCAGATCTTAAGATCGGAAGAGCGGTTTCAG
chr12	78359959	78359998	NAV3_4891	-	GTGACCTATGCACCAGACGTAAAAGCAGTGAAAAAGCAACTTAGAGGATTATATTTTTAACAGATCGGAAGAGCGGTTTCAG
chr12	78362249	78362288	NAV3_4892	-	GTGACCTATGCACCAGACGTTGAAAAATACAAAAAAGAATCATATGTATTTAATGTCTTAGATCGGAAGAGCGGTTTCAG
chr12	78388533	78388572	NAV3_4893	-	GTGACCTATGCACCAGACGTAGAAACAGAGAAATTAAGTAAAGAGATTCTTTGAACATGAGATCGGAAGAGCGGTTTCAG
chr12	78392067	78392106	NAV3_4894	-	GTGACCTATGCACCAGACGTATAAGAAAAATTACATCATTATTGTACATTACAAAAAGTAGATCGGAAGAGCGGTTTCAG
chr12	78400149	78400188	NAV3_4895	-	GTGACCTATGCACCAGACGTTTAGAGAAAAATAAGAAAAAGCCGATTAACTTTGATCAAGATCGGAAGAGCGGTTTCAG
chr12	78415477	78415516	NAV3_4896	-	GTGACCTATGCACCAGACGTCTTGAATAAAGAAAGAAATAGCAGTTATAGTCTACTAGATCGGAAGAGCGGTTTCAG
chr12	78443723	78443762	NAV3_4897	-	GTGACCTATGCACCAGACGTAAATGATAAATTTGCTATTTCATGACATTTAGTATCCTCAAGATCGGAAGAGCGGTTTCAG
chr12	78444494	78444533	NAV3_4898	-	GTGACCTATGCACCAGACGTAAATGGAGAAATAACTATACTCTGGTTCACTTAGGGCCATAGATCGGAAGAGCGGTTTCAG
chr12	78452726	78452765	NAV3_4899	-	GTGACCTATGCACCAGACGTATGTCTAATTAATTCACAGAAAACTAAATCAACTCAACTGAGATCGGAAGAGCGGTTTCAG
chr12	78510502	78510541	NAV3_4900	-	GTGACCTATGCACCAGACGTGACATGCAAGAGCAGTGAATCAAACACAGGATGCACAATGAGATCGGAAGAGCGGTTTCAG
chr12	78511757	78511796	NAV3_4901	-	GTGACCTATGCACCAGACGTAAATATTACAGAAAAACTTTATGTAGAAAAATTTATAAGAGATCGGAAGAGCGGTTTCAG
chr12	78512967	78513006	NAV3_4902	-	GTGACCTATGCACCAGACGTGAAATAACACAATAATATGTGCCTGTAGAGTTTGATATCAAGATCGGAAGAGCGGTTTCAG
chr12	78515670	78515709	NAV3_4903	-	GTGACCTATGCACCAGACGTAAACAATAACAACCTCAGTTGTTCCAAGAAGCTAATATCCAGATCGGAAGAGCGGTTTCAG
chr12	78520897	78520936	NAV3_4904	-	GTGACCTATGCACCAGACGTAAAGAAAACCCCTAAGGACATAATGTAACAAAACCTTCAAGATCGGAAGAGCGGTTTCAG
chr12	78522436	78522475	NAV3_4905	-	GTGACCTATGCACCAGACGTGCACAGCTATGACACTTAAGCACATCTACAAGGGCAAGGCAGATCGGAAGAGCGGTTTCAG
chr12	78530907	78530946	NAV3_4906	-	GTGACCTATGCACCAGACGTAAACACACAGAGCCTTACTTCTTAAGCTTGAAGATGAAAGATCGGAAGAGCGGTTTCAG
chr12	78534012	78534051	NAV3_4907	-	GTGACCTATGCACCAGACGTCAAAACAGACAATAAGATGTTAAACAATAAGGTCTACTCAAGATCGGAAGAGCGGTTTCAG
chr12	78540099	78540138	NAV3_4908	-	GTGACCTATGCACCAGACGTATAAAAAAGAAAGACTTTAACTATAAAAACTATTTTCAATTAGATCGGAAGAGCGGTTTCAG
chr12	78542572	78542611	NAV3_4909	-	GTGACCTATGCACCAGACGTTTAAAAAATCAATGGAATAGGCAAGTAGATTTTTACTTAAAGATCGGAAGAGCGGTTTCAG
chr12	78552933	78552972	NAV3_4910	-	GTGACCTATGCACCAGACGTAAATGGAAGAAACATAGTTTAAATGTCAGAATCTTATGTGGAGATCGGAAGAGCGGTTTCAG
chr12	78562485	78562524	NAV3_4911	-	GTGACCTATGCACCAGACGTAAACAGAGTTTGAAGCTTTAGTACCCGAAAGAAAAATAAAGATCGGAAGAGCGGTTTCAG
chr12	78569036	78569075	NAV3_4912	-	GTGACCTATGCACCAGACGTAGGGAGAGTATCATCCGGCTCATGAAGAGTCTCGATCTGAGATCGGAAGAGCGGTTTCAG
chr12	78570169	78570208	NAV3_4913	-	GTGACCTATGCACCAGACGTGTAAGAAAGAGTGTGAATTAACAATCAAGGGAATGAAGGCAGATCGGAAGAGCGGTTTCAG
chr12	78570871	78570910	NAV3_4914	-	GTGACCTATGCACCAGACGTGACAGAAATTACCCTTCTTGTCTATTTGCACTTGGAGAGCAGATCGGAAGAGCGGTTTCAG
chr12	78573259	78573298	NAV3_4915	-	GTGACCTATGCACCAGACGTAAACAAAACAGAATCAGTGGCCTGGGGAAGCCAGAGGATTAAGATCGGAAGAGCGGTTTCAG
chr12	78574601	78574640	NAV3_4916	-	GTGACCTATGCACCAGACGTGATGGAAAAACGAAAAAACTGAGTTGGTTTGATTGAGAAGATCGGAAGAGCGGTTTCAG
chr12	78579331	78579370	NAV3_4917	-	GTGACCTATGCACCAGACGTTTAAAAGAAAGACATACACAACAGTATAACATTAGCTCAGAGATCGGAAGAGCGGTTTCAG
chr12	78581978	78582017	NAV3_4918	-	GTGACCTATGCACCAGACGTACAAAATAAAAGTAAGATAAAAATCAAACCTGATCTTTTGAATCGGAAGAGCGGTTTCAG
chr12	78582339	78582378	NAV3_4919	-	GTGACCTATGCACCAGACGTACACAAAAAATAAATCAAACAGAGGTTCAACTCATCAGATCGGAAGAGCGGTTTCAG
chr12	78583714	78583753	NAV3_4920	-	GTGACCTATGCACCAGACGTAAACAAAAAATAGCATGATTTATTGTTCTACATAAGCTAAGATCGGAAGAGCGGTTTCAG
chr12	78590977	78591016	NAV3_4921	-	GTGACCTATGCACCAGACGTATGAAGAAAAACAGATACGTCAAGTATAAATTTATACTAATAGATCGGAAGAGCGGTTTCAG
chr12	78594203	78594242	NAV3_4922	-	GTGACCTATGCACCAGACGTATAAATAACAAAATTTTTAAGAGTTATATTAATAATCTAGATCGGAAGAGCGGTTTCAG
chr12	78598665	78598704	NAV3_4923	-	GTGACCTATGCACCAGACGTACCACGCGTTTAGGATATATAAAATGCATTTCTATTCAAGATCGGAAGAGCGGTTTCAG
chr12	78604128	78604167	NAV3_4924	-	GTGACCTATGCACCAGACGTGAAAAAGACATCGATGATGGCAATGATGCATTGAGTAAGCAGATCGGAAGAGCGGTTTCAG
chr12	78513321	78513360	NAV3_4925	-	GTGACCTATGCACCAGACGTGCTAACATGCAGCAACAACATCCTGATTCTGTGAACCGAGATCGGAAGAGCGGTTTCAG
chr12	78400491	78400530	NAV3_4926	-	GTGACCTATGCACCAGACGTACTGGGAGGCTGCGGGGGGCGTAAAGCAGTCCGGGCATTGAGATCGGAAGAGCGGTTTCAG
chr12	78400833	78400872	NAV3_4927	-	GTGACCTATGCACCAGACGTTTCTTCTAGCTGCTGTTGTCTTGGCTGCCCTTAGGGATCAGATCGGAAGAGCGGTTTCAG
chr1	120457879	120457918	NOTCH2_4928	-	GTGACCTATGCACCAGACGTCTCCAGTGTAGAGACATAACTGACTTTTTGTAATGCTGCTAGATCGGAAGAGCGGTTTCAG
chr1	120460238	120460277	NOTCH2_4929	-	GTGACCTATGCACCAGACGTTGGGCTCTGAGTCTGAGAGGCTCATAGCAGTGCCTCAGTAGATCGGAAGAGCGGTTTCAG
chr1	120460979	120461018	NOTCH2_4930	-	GTGACCTATGCACCAGACGTAAAGCAGGATTTGGATTCTTAACTGCAAGCATGCCTCTAGATCGGAAGAGCGGTTTCAG



chr5	176721597	176721636	NSD1_4989	-	GTGACCTATGCACCAGACGTTCTCAGGAGGTGGGAGTCTCTGGACAAAGAGGCATGGGGAGATCGGAAGAGCGGTTTCAG
chr5	176722004	176722043	NSD1_4990	-	GTGACCTATGCACCAGACGTTCTTCTGAGGCCTGAGTTGTTGGCTCATATAAAAAGGCCAGATCGGAAGAGCGGTTTCAG
chr5	176637014	176637053	NSD1_4991	-	GTGACCTATGCACCAGACGTAAGTTTCATTAGAGGCCTGCGTATCAGATATATCCCCAGAGAGATCGGAAGAGCGGTTTCAG
chr5	176637441	176637480	NSD1_4992	-	GTGACCTATGCACCAGACGTTGTTTGGCAGCAAACCTAGAATACTTTATCTTTTCATTAGATCGGAAGAGCGGTTTCAG
chr5	176637868	176637907	NSD1_4993	-	GTGACCTATGCACCAGACGTAGACCATCCACTTTCCCACCTTTAGAAATCGCTGGCCAAGAGATCGGAAGAGCGGTTTCAG
chr5	176638295	176638334	NSD1_4994	-	GTGACCTATGCACCAGACGTAGGATTGGCGAGTTCTGAGTGCCATCTCCCTTTTTCTCTAGATCGGAAGAGCGGTTTCAG
chr5	176638722	176638761	NSD1_4995	-	GTGACCTATGCACCAGACGTTACCAGGATCAGATTGCTTAACTTGGCTATCGAAATGCACAGATCGGAAGAGCGGTTTCAG
chr11	117023114	117023153	PAFAH1B2_4996	-	GTGACCTATGCACCAGACGTAGAAAAAACGTCTATGTCATGTTTCATTTGTTAACAGGAAAGATCGGAAGAGCGGTTTCAG
chr11	117031811	117031850	PAFAH1B2_4997	-	GTGACCTATGCACCAGACGTAAAAACTTGATTAGTGTACCTAAAACCTAGGGGAAAGTTTAGATCGGAAGAGCGGTTTCAG
chr11	117034436	117034475	PAFAH1B2_4998	-	GTGACCTATGCACCAGACGTAGAAAAAAGGGGGGAAAGGAGAAGATAAATACCCAGGAACAGATCGGAAGAGCGGTTTCAG
chr11	117038087	117038126	PAFAH1B2_4999	-	GTGACCTATGCACCAGACGTGTTGGAAAACATTAATTAGAAAGATTCACTTATTTTTCTCTAGATCGGAAGAGCGGTTTCAG
chr20	9520059	9520098	PAK7_5000	-	GTGACCTATGCACCAGACGTCGTGTAGGTGGCAAAGCTAGATGAGGCATGAGAATAATTAGATCGGAAGAGCGGTTTCAG
chr20	9523183	9523222	PAK7_5001	-	GTGACCTATGCACCAGACGTGACAGCTGTTGCTAAAGTTGCTAAAGTTTGGATTTTTGATTTCAGATCGGAAGAGCGGTTTCAG
chr20	9524966	9525005	PAK7_5002	-	GTGACCTATGCACCAGACGTACAGTCATAGGCGTGGCAGGACTGGGGACAGGCTCAGGGAGATCGGAAGAGCGGTTTCAG
chr20	9538205	9538244	PAK7_5003	-	GTGACCTATGCACCAGACGTGATGTTTGGCCCGTTCGTAGTTTTTCTTGTCACTCTGCTAGATCGGAAGAGCGGTTTCAG
chr20	9543488	9543527	PAK7_5004	-	GTGACCTATGCACCAGACGTTTATTATCCAGAGAATTCAGAGTGCCTTCTTATCTCTCCAGATCGGAAGAGCGGTTTCAG
chr20	9546490	9546529	PAK7_5005	-	GTGACCTATGCACCAGACGTTGTTGGGTCATCCTTTCTCTCTGTTGAACATTTATTTTTCAGATCGGAAGAGCGGTTTCAG
chr20	9560742	9560781	PAK7_5006	-	GTGACCTATGCACCAGACGTCTACCTCCTTTCCCTCAGTGTGCTGCAAAAACCTCCACAGGGAGATCGGAAGAGCGGTTTCAG
chr20	9624723	9624762	PAK7_5007	-	GTGACCTATGCACCAGACGTGGCTCCATCTTTGGCTGGGCTTAAAGAATCATGCTCTTATTAGATCGGAAGAGCGGTTTCAG
chr20	9561135	9561174	PAK7_5008	-	GTGACCTATGCACCAGACGTTGGACTCACTGAGCAAACCAAGTGAATACAGTGACCTCAAAGATCGGAAGAGCGGTTTCAG
chr14	20811751	20811790	PARP2_5009	-	GTGACCTATGCACCAGACGTGCTGACGTCATCAACCCGCTCCAAGGAATCGCGGGCCAAGATCGGAAGAGCGGTTTCAG
chr14	20813041	20813080	PARP2_5010	-	GTGACCTATGCACCAGACGTTGGAAATTAGCAAAAGAAATGAGTACACACCCGAATACGTTAGATCGGAAGAGCGGTTTCAG
chr14	20813503	20813542	PARP2_5011	-	GTGACCTATGCACCAGACGTACAGATAGGTACTATTTATGGGAATCAAAAACAGCTGTTAGATCGGAAGAGCGGTTTCAG
chr14	20814972	20815011	PARP2_5012	-	GTGACCTATGCACCAGACGTGAGAGAGGAAAAAACAATGATGATAGTTGTTTCAGCCCTGAGATCGGAAGAGCGGTTTCAG
chr14	20818635	20818674	PARP2_5013	-	GTGACCTATGCACCAGACGTTGAAAACAAAAAACAAGGAGTTTTGCAAAATGGAAAAGATCGGAAGAGCGGTTTCAG
chr14	20819156	20819195	PARP2_5014	-	GTGACCTATGCACCAGACGTAATGCCACACATAAGATAGTTCCCTAAGAGTACAGGCCAAAGATCGGAAGAGCGGTTTCAG
chr14	20820354	20820393	PARP2_5015	-	GTGACCTATGCACCAGACGTCAAGGTGTAAGAAAACTTTACAAATAAAGGTCCTACTATGAAGATCGGAAGAGCGGTTTCAG
chr14	20822918	20822957	PARP2_5016	-	GTGACCTATGCACCAGACGTACCAGAGATCAGACTCCAACCTAGGATCCCCTCTAGTGAAGATCGGAAGAGCGGTTTCAG
chr14	20823861	20823900	PARP2_5017	-	GTGACCTATGCACCAGACGTAGATATAACCATAATGAGCTTTCTGACATGTGGCTAAAAGATCGGAAGAGCGGTTTCAG
chr14	20824006	20824045	PARP2_5018	-	GTGACCTATGCACCAGACGTGAGATATAGAATCAATGTCAGGAGACACTGGTATAAGGGAAGATCGGAAGAGCGGTTTCAG
chr14	20824416	20824455	PARP2_5019	-	GTGACCTATGCACCAGACGTTAAGACAAAAAGGCTGATGTAGACTCTACAAGAGACTGAGAGATCGGAAGAGCGGTTTCAG
chr14	20824699	20824738	PARP2_5020	-	GTGACCTATGCACCAGACGTGCCAATATTATTGTACTCTGTTGTTCTGCACAGATAGGCCAGATCGGAAGAGCGGTTTCAG
chr14	20825160	20825199	PARP2_5021	-	GTGACCTATGCACCAGACGTTACATGAATACCAAGGTCAGCTTTCTAACCCACTGTGTTAGATCGGAAGAGCGGTTTCAG
chr14	20825505	20825544	PARP2_5022	-	GTGACCTATGCACCAGACGTAAAAACCTTTGAAATCCCATCTACTAAGAATTAGATGAGATCGGAAGAGCGGTTTCAG
chr14	20825747	20825786	PARP2_5023	-	GTGACCTATGCACCAGACGTGAAAAAAAGTTGTGTCAACATCACTGCTCTGGTTCAAGAGCTAGATCGGAAGAGCGGTTTCAG
chr17	26881188	26881227	PIGS_5024	-	GTGACCTATGCACCAGACGTACCTCCATAGGAAGCCTTCTTCTTGGCCAAGGTTGGCGGAGATCGGAAGAGCGGTTTCAG
chr17	26881819	26881858	PIGS_5025	-	GTGACCTATGCACCAGACGTAGGGGATGGATTCTGCAGCTTGGGACTGGAGTAGCCAGAGAGATCGGAAGAGCGGTTTCAG
chr17	26883134	26883173	PIGS_5026	-	GTGACCTATGCACCAGACGTGGATGATCCACTTTGGGACATAGTCTCCTTGGCTGTAGAGAGATCGGAAGAGCGGTTTCAG
chr17	26883795	26883834	PIGS_5027	-	GTGACCTATGCACCAGACGTCACTACGACAGCCCCAGAGCCCATGCTTCTGGGACAGGCAAGATCGGAAGAGCGGTTTCAG
chr17	26885444	26885483	PIGS_5028	-	GTGACCTATGCACCAGACGTAAGGATGAGGGCTTTCTTTCTGCCAGGCTAGGGGAAAGATCGGAAGAGCGGTTTCAG
chr17	26887017	26887056	PIGS_5029	-	GTGACCTATGCACCAGACGTGAGCAAGTTGAGGAGTCCTTTTCAATGTCTATACATATTAGATCGGAAGAGCGGTTTCAG
chr17	26888390	26888429	PIGS_5030	-	GTGACCTATGCACCAGACGTAGGCTCTGCCACATGAAGGGAGAGGAAATGAATTACATGGAGATCGGAAGAGCGGTTTCAG
chr17	26890399	26890438	PIGS_5031	-	GTGACCTATGCACCAGACGTAGAGAGGCTGCGACTTTGCTTTCTGCCAGGCTAGGGGAAAGATCGGAAGAGCGGTTTCAG
chr17	26890786	26890825	PIGS_5032	-	GTGACCTATGCACCAGACGTGGATGAGCACACCAATTTAATGTGAAGCCCTCTTTTTCTAGATCGGAAGAGCGGTTTCAG
chr17	26897820	26897859	PIGS_5033	-	GTGACCTATGCACCAGACGTGGGGATCAGGGCTGCTTTTCGCTCTGAGCTCAGTTCAAGAGATCGGAAGAGCGGTTTCAG
chr17	26898017	26898056	PIGS_5034	-	GTGACCTATGCACCAGACGTTGTGCGGAGGGTGTGGCGGACAGCCGCCCCGCAAGGTGGAGATCGGAAGAGCGGTTTCAG
chr17	26898431	26898470	PIGS_5035	-	GTGACCTATGCACCAGACGTCTTCGGGTGGGGGCGCTGCAGCTAGCTGATGGCAAGGGAGAGATCGGAAGAGCGGTTTCAG
chr12	133201233	133201272	POLE_5036	-	GTGACCTATGCACCAGACGTGCCCGGGTGCCTCTGCGTCCGTGCCAGGCCCTCTGATGCAGATCGGAAGAGCGGTTTCAG
chr12	133201441	133201480	POLE_5037	-	GTGACCTATGCACCAGACGTCCCTCATCTGCTCCTGGCTCAGCCTGGCCTCCTTGGCCTCCTAGATCGGAAGAGCGGTTTCAG
chr12	133202181	133202220	POLE_5038	-	GTGACCTATGCACCAGACGTACGCGCCTGCCCCGTGTCGCTGGAGTCCACAGGGGGGTAGATCGGAAGAGCGGTTTCAG
chr12	133202653	133202692	POLE_5039	-	GTGACCTATGCACCAGACGTGCTCCAGCGGCCCTCACTGTGGAGCAGAACATCCGAGGAGATCGGAAGAGCGGTTTCAG
chr12	133208851	133208890	POLE_5040	-	GTGACCTATGCACCAGACGTACGCTGCGTGTGAGGAGAGGACACTAACGTACATGTGTAAGATCGGAAGAGCGGTTTCAG
chr12	133209200	133209239	POLE_5041	-	GTGACCTATGCACCAGACGTTTTTGTCTTTGAGGCCACTGCCATGTGCCAGTGACCTAAAAGATCGGAAGAGCGGTTTCAG
chr12	133210722	133210761	POLE_5042	-	GTGACCTATGCACCAGACGTAGCCAGGGCTGCGCAGCCCCACTGAAGGGACTCATGGTAGATCGGAAGAGCGGTTTCAG
chr12	133212428	133212467	POLE_5043	-	GTGACCTATGCACCAGACGTTGCAGTGTGCCACCCGAGCCAGCTTTGGGGGTCCGCTTCAAGATCGGAAGAGCGGTTTCAG
chr12	133214550	133214589	POLE_5044	-	GTGACCTATGCACCAGACGTCGGTCTGGTGACGACGACTGTGGCTTTGAGAGGGATGAGATCGGAAGAGCGGTTTCAG
chr12	133215661	133215700	POLE_5045	-	GTGACCTATGCACCAGACGTCCTCCTCGTGGCTGCTCCAGCTGCGCTGAGATCGGAAGAGCGGTTTCAG
chr12	133218183	133218222	POLE_5046	-	GTGACCTATGCACCAGACGTCTCTGGGAAGGAGTGTACTAATAGAAGGGTCTTATCTTAGATCGGAAGAGCGGTTTCAG

chr12	133218713	133218752	POLE_5047	-	GTGACCTATGCACCAGACGTGGGAGGACGAGGCCCATGAGACCTGGCTGGTGTCTTCTGCCAGATCGGAAGAGCGGTTTCAG
chr12	133219042	133219081	POLE_5048	-	GTGACCTATGCACCAGACGTTACTGTCTGTGGGCCAGTGGTCCCCAGGCAGAGCCGGCAGATCGGAAGAGCGGTTTCAG
chr12	133219356	133219395	POLE_5049	-	GTGACCTATGCACCAGACGTTTGGGGTCTTGTCTGTGTGAGCCCCATCTTCTTTGAGGCTGAGATCGGAAGAGCGGTTTCAG
chr12	133219760	133219799	POLE_5050	-	GTGACCTATGCACCAGACGTGGCCCTCCATGGCAGCACATTGGCTGGGGCAGGGTTTGGGAGATCGGAAGAGCGGTTTCAG
chr12	133219943	133219982	POLE_5051	-	GTGACCTATGCACCAGACGTCACCAGCCGCCATCATGTGCCTGCCTCCCACACATCTGGAGATCGGAAGAGCGGTTTCAG
chr12	133220373	133220412	POLE_5052	-	GTGACCTATGCACCAGACGTAGCCCTCGACTGAACGGGGAGGCTCCAGCAGGGTGAGATCGGAAGAGCGGTTTCAG
chr12	133225465	133225504	POLE_5053	-	GTGACCTATGCACCAGACGTTCCGCTGGTGTCTGTGGCAGCTATGGCAGCCTGAGGTGAGATCGGAAGAGCGGTTTCAG
chr12	133225842	133225881	POLE_5054	-	GTGACCTATGCACCAGACGTTGATCCAAGGGGAGGGCAGTGGCTCTGCTGATGGCCCAGGAGATCGGAAGAGCGGTTTCAG
chr12	133226213	133226252	POLE_5055	-	GTGACCTATGCACCAGACGTCAGCTGTGATACTGTCTGTCTGTGAGGGTCTGCACAGCCAGATCGGAAGAGCGGTTTCAG
chr12	133233672	133233711	POLE_5056	-	GTGACCTATGCACCAGACGTGGCCCCAAGGCTGGGCTGGGCAGGATCCTTGTGACACACAAGATCGGAAGAGCGGTTTCAG
chr12	133233885	133233924	POLE_5057	-	GTGACCTATGCACCAGACGTGGTCACTGAGTGGCAGCGGGCTGTGGGGCTAAAACTGTGCAGTTAGATCGGAAGAGCGGTTTCAG
chr12	133234404	133234443	POLE_5058	-	GTGACCTATGCACCAGACGTGTTCGCTTCTACTCTTAAAGTTTACAAGGAAAGCTAGAGATCGGAAGAGCGGTTTCAG
chr12	133235831	133235870	POLE_5059	-	GTGACCTATGCACCAGACGTCCCCATCACGGAGAGGTTGAGGGCTCCTCCCATCACGGACAGATCGGAAGAGCGGTTTCAG
chr12	133237505	133237544	POLE_5060	-	GTGACCTATGCACCAGACGTACCCTCCACCCTCACCTGCTCTGAGGGATGAAGGATGAAGAGATCGGAAGAGCGGTTTCAG
chr12	133238063	133238102	POLE_5061	-	GTGACCTATGCACCAGACGTCATAGCTTTTGTGCTTTAGAAAGGACATGGATTGAGATAGAGATCGGAAGAGCGGTTTCAG
chr12	133240540	133240579	POLE_5062	-	GTGACCTATGCACCAGACGTGGCCTCTGGTCTGAGACTCTGGCTGGCCTGGCCTCAGTGAGATCGGAAGAGCGGTTTCAG
chr12	133240906	133240945	POLE_5063	-	GTGACCTATGCACCAGACGTAAGGGGAGCCGTGGGGCTGGGAGCAGGCTCTGGGGCAAGAGATCGGAAGAGCGGTTTCAG
chr12	133241838	133241877	POLE_5064	-	GTGACCTATGCACCAGACGTCCGGGCCGGGAGAGGCTTATGGAGGAATGGATGAGTCCAGATCGGAAGAGCGGTTTCAG
chr12	133244039	133244078	POLE_5065	-	GTGACCTATGCACCAGACGTAGGGGCTGCAAGCTTTGGCCTCTGTGAGGGCAGTTTCAGTATAGATCGGAAGAGCGGTTTCAG
chr12	133244892	133244931	POLE_5066	-	GTGACCTATGCACCAGACGTGGGCATGGTCAAGGCTGTAAAGATGTGGCTCCTGCTCCCAAGATCGGAAGAGCGGTTTCAG
chr12	133245171	133245210	POLE_5067	-	GTGACCTATGCACCAGACGTGCCGCTGGGTGGGCACCTCGGTGGGAAACGGGTGGGTGAGAGATCGGAAGAGCGGTTTCAG
chr12	133245347	133245386	POLE_5068	-	GTGACCTATGCACCAGACGTACTTCCCGTGTCAAGTCTGGAGCTCTCTCTGCCAGCCCTAGATCGGAAGAGCGGTTTCAG
chr12	133248751	133248790	POLE_5069	-	GTGACCTATGCACCAGACGTGGGAGCGAGGAAGGCCAGTCTGTGTTGGCGCTTCTTCAGATCGGAAGAGCGGTTTCAG
chr12	133249163	133249202	POLE_5070	-	GTGACCTATGCACCAGACGTTCCTGGGTTCCAGATTCTCCCACTTTGTGCTGTGCTAAAGATCGGAAGAGCGGTTTCAG
chr12	133249700	133249739	POLE_5071	-	GTGACCTATGCACCAGACGTTCTGTCTGTGGCACCCTGGCCTCCTCAGCCCTTCCCCAGATCGGAAGAGCGGTTTCAG
chr12	133250111	133250150	POLE_5072	-	GTGACCTATGCACCAGACGTCACATCCCGCTGCCCTGCTGCCGTGTGCACGCATCCAGAGATCGGAAGAGCGGTTTCAG
chr12	133251934	133251973	POLE_5073	-	GTGACCTATGCACCAGACGTCAGAGCAGCATGGCTCCTCACTGCTGCCGTGAGCGAGATAGATCGGAAGAGCGGTTTCAG
chr12	133252271	133252310	POLE_5074	-	GTGACCTATGCACCAGACGTGCTTCTATGAGTAACTGGGACGATTTGAGAGGGAGGAGATCGGAAGAGCGGTTTCAG
chr12	133252630	133252669	POLE_5075	-	GTGACCTATGCACCAGACGTACCTTGGAACTACCCGCTATTGTGGGAAGAACGGACAGATCGGAAGAGCGGTTTCAG
chr12	133253082	133253121	POLE_5076	-	GTGACCTATGCACCAGACGTTCCCTGGGTTTCCATAGACTCAGGTCAGACGACCTGTGTGCTATTCTGTGAGATCGGAAGAGCGGTTTCAG
chr12	133253899	133253938	POLE_5077	-	GTGACCTATGCACCAGACGTTGTGTTACCTTCATCCTAAAATTTCCAGTTTTCTGGAGAGATCGGAAGAGCGGTTTCAG
chr12	133254114	133254153	POLE_5078	-	GTGACCTATGCACCAGACGTCAGGGTTGGGTGCTGCTCACATGAATTTCCTAACAGCCAAGATCGGAAGAGCGGTTTCAG
chr12	133256033	133256072	POLE_5079	-	GTGACCTATGCACCAGACGTGCTTGTGAGCAAAGCATCAGCGGTTTCAGAACGACAAGATAGATCGGAAGAGCGGTTTCAG
chr12	133256490	133256529	POLE_5080	-	GTGACCTATGCACCAGACGTCACGACTTCCAGGGGTAATGAGGCGCAGATCTACATTAGATCGGAAGAGCGGTTTCAG
chr12	133256714	133256753	POLE_5081	-	GTGACCTATGCACCAGACGTTTCCATAGACTCAGGTCAGACGACCTGTGTGCTATTCTGTGAGATCGGAAGAGCGGTTTCAG
chr12	133257143	133257182	POLE_5082	-	GTGACCTATGCACCAGACGTGACTGCGACAAGCTAAAACCCACTTTTATGGGTGTTTCATGAGATCGGAAGAGCGGTTTCAG
chr12	133257674	133257713	POLE_5083	-	GTGACCTATGCACCAGACGTGGTCTTCTCCACCCAGGAATATGGCTGCAACCCTTCTGAGATCGGAAGAGCGGTTTCAG
chr12	133263790	133263829	POLE_5084	-	GTGACCTATGCACCAGACGTCCCTCCTGAGGCTCTCGGGCCGGCCCTCCGGAGGGTGCCAAGATCGGAAGAGCGGTTTCAG
chr19	45883398	45883437	PPP1R13L_5085	-	GTGACCTATGCACCAGACGTGGAGGTTTCTGAGGCTGACAGAAACAAGCATTCTGCTTAGATCGGAAGAGCGGTTTCAG
chr19	45885735	45885774	PPP1R13L_5086	-	GTGACCTATGCACCAGACGTGGGAGAAGTCAATGGGGACCTCCCGACAGTTGGGGTTGGGAGATCGGAAGAGCGGTTTCAG
chr19	45888770	45888809	PPP1R13L_5087	-	GTGACCTATGCACCAGACGTGGGCTGCTGGCCCTGGGTACCTGCGGGGTGCGCAGGAGCAGATCGGAAGAGCGGTTTCAG
chr19	45889032	45889071	PPP1R13L_5088	-	GTGACCTATGCACCAGACGTACCCGCGCGGTGGGCTGGGTCCCGCTGGGCGGACGCGCAAGATCGGAAGAGCGGTTTCAG
chr19	45889257	45889296	PPP1R13L_5089	-	GTGACCTATGCACCAGACGTCAGAGCGGAGGTGGGCACGGCGGGGATCGCAGATGCCAGATCGGAAGAGCGGTTTCAG
chr19	45895088	45895127	PPP1R13L_5090	-	GTGACCTATGCACCAGACGTCAGGAGGAAACCGGGGTATGTTGCTACATGAATCCAGGAAGATCGGAAGAGCGGTTTCAG
chr19	45898684	45898683	PPP1R13L_5091	-	GTGACCTATGCACCAGACGTAATGAGGGCCCTAGAGGACTGGGTGAAGGGAGGACAAATGAGATCGGAAGAGCGGTTTCAG
chr19	45899376	45899415	PPP1R13L_5092	-	GTGACCTATGCACCAGACGTGACGCTGGGAGGAGGAGCTGGGAGGTCGAGAGTCCGAGATCGGAAGAGCGGTTTCAG
chr19	45899546	45899585	PPP1R13L_5093	-	GTGACCTATGCACCAGACGTGAGGCCCCGGGAATGGAGGACCCGAGGAGAGGCAGCCCCAGATCGGAAGAGCGGTTTCAG
chr19	45899753	45899792	PPP1R13L_5094	-	GTGACCTATGCACCAGACGTGGGCCCTCGCGGGCCTTTGACTCGCGGGGTCAAAGCGGAGATCGGAAGAGCGGTTTCAG
chr19	45901213	45901252	PPP1R13L_5095	-	GTGACCTATGCACCAGACGTTTCCACCTTGATCTCAAAGCCAGCCTCTCGCCACAGTCAGATCGGAAGAGCGGTTTCAG
chr19	45901472	45901511	PPP1R13L_5096	-	GTGACCTATGCACCAGACGTGATGGGGGCGGGCTGGCGAGGCGGGGACCTCGGCAGCGGAGATCGGAAGAGCGGTTTCAG
chr19	45900010	45900049	PPP1R13L_5097	-	GTGACCTATGCACCAGACGTGCGCCCTCCCGCCCGGCGCCAGCCCGCTCCGCCAGCAGATCGGAAGAGCGGTTTCAG
chr8	30643701	30643740	PPP2CB_5098	-	GTGACCTATGCACCAGACGTGGAAACCTGCTTTGTATGTGGAAGTATACCTGCTTTTTAGATCGGAAGAGCGGTTTCAG
chr8	30648663	30648702	PPP2CB_5099	-	GTGACCTATGCACCAGACGTGAAATTTAATTGTATATACTTTCAGAAGGAAATTTAAGATCGGAAGAGCGGTTTCAG
chr8	30651383	30651422	PPP2CB_5100	-	GTGACCTATGCACCAGACGTTCTGACAGAATGATCTTTATTTAGATAGTATATACTTAGATCGGAAGAGCGGTTTCAG
chr8	30651658	30651697	PPP2CB_5101	-	GTGACCTATGCACCAGACGTTTAAAAAAGAGAAGAAAGAAAAGAAAATATAACCACAAGATCGGAAGAGCGGTTTCAG
chr8	30655047	30655086	PPP2CB_5102	-	GTGACCTATGCACCAGACGTGTGTCTTACATCTGGGAGGAGGTAATGGAAGCAGAGAAGATCGGAAGAGCGGTTTCAG
chr8	30657012	30657051	PPP2CB_5103	-	GTGACCTATGCACCAGACGTTGAAATTTTTTTTCAAGATTTAAACCAGGCAAAAAGATCGGAAGAGCGGTTTCAG
chr8	30669786	30669825	PPP2CB_5104	-	GTGACCTATGCACCAGACGTTGGCGGGGCGAGTGGCGGAGCGGGGCTGGGACGGCCGAGATCGGAAGAGCGGTTTCAG



chr5	145969460	145969499	PPP2R2B_5105	-	GTGACCTATGCACCAGACGTTATTACTTAATAATCTCACATACTGAATACTAGTCAAACAAGATCGGAAGAGCGGTTCCAG
chr5	145972484	145972523	PPP2R2B_5106	-	GTGACCTATGCACCAGACGCTCTGTGGCTGAAGAACCTTCCAAGATTGTCTTGAAGAGAGATCGGAAGAGCGGTTCCAG
chr5	145979804	145979843	PPP2R2B_5107	-	GTGACCTATGCACCAGACGTCACAGGCACCCATAGGTATATTGAACATTCCCTTCATGAGCAGATCGGAAGAGCGGTTCCAG
chr5	146017764	146017803	PPP2R2B_5108	-	GTGACCTATGCACCAGACGCTACTGAAGGGAGGTGGGGGGCATGCCACTGGCCCCAATGTAGATCGGAAGAGCGGTTCCAG
chr5	146030060	146030099	PPP2R2B_5109	-	GTGACCTATGCACCAGACGTTTTGTGATCAAGAATCAACTGCCCTGAATTAAGAGTATTCAGATCGGAAGAGCGGTTCCAG
chr5	146070641	146070680	PPP2R2B_5110	-	GTGACCTATGCACCAGACGTACAGCTGCCCTGCCACCACAGTCAGGGGCAGGTCTCCTAAGATCGGAAGAGCGGTTCCAG
chr5	146077492	146077531	PPP2R2B_5111	-	GTGACCTATGCACCAGACGTTTTCTGTGTTGGTATTTTCCAGATACAGTCGGGCAAACATAGATCGGAAGAGCGGTTCCAG
chr5	146080558	146080597	PPP2R2B_5112	-	GTGACCTATGCACCAGACGTGTGAATGCAAAATGCCATTCTTCACTTTTTAAAGGAGAGATCGGAAGAGCGGTTCCAG
chr5	146236012	146236051	PPP2R2B_5113	-	GTGACCTATGCACCAGACGTTATTATTATACCTACTCTTCTTGATAAAGTAGCAGTATAAGATCGGAAGAGCGGTTCCAG
chr5	146257515	146257554	PPP2R2B_5114	-	GTGACCTATGCACCAGACGTCCCCGCCGATTCCGCCGTTGGGGCCGGCGCAAGTTGCGAGATCGGAAGAGCGGTTCCAG
chr5	146435178	146435217	PPP2R2B_5115	-	GTGACCTATGCACCAGACGTGAGAGGGAGAGTGTCTGGTGGGTGGGAAAAGTGGGCTGGAGATCGGAAGAGCGGTTCCAG
chr1	45288037	45288076	PTCH2_5116	-	GTGACCTATGCACCAGACGTGAAGCACAGACCATGTGTGGGGCGTGTGGGTCACCTGGAGATCGGAAGAGCGGTTCCAG
chr1	45288691	45288730	PTCH2_5117	-	GTGACCTATGCACCAGACGTCCTCGGCACCATCCCTCTACTCCCAGCCCAAGGGACGGGGAGATCGGAAGAGCGGTTCCAG
chr1	45288865	45288904	PTCH2_5118	-	GTGACCTATGCACCAGACGTCCTCGGGCAGGGAGGCAGGGCTCAGGACAGGCCTGGGCTGAGATCGGAAGAGCGGTTCCAG
chr1	45292110	45292149	PTCH2_5119	-	GTGACCTATGCACCAGACGTGCAGGAGTGGGGACAGAGACACCCCACCCTTCCCTGCCCAAGATCGGAAGAGCGGTTCCAG
chr1	45292524	45292563	PTCH2_5120	-	GTGACCTATGCACCAGACGTGGGGGAGCTCGGCAAGAGCCTCACCTCGCCACACAAGCAGATCGGAAGAGCGGTTCCAG
chr1	45292789	45292828	PTCH2_5121	-	GTGACCTATGCACCAGACGTGGCTGGAGGGTCCACTAGTACAGGGGCTGCAGGCCTCCTAGATCGGAAGAGCGGTTCCAG
chr1	45293024	45293063	PTCH2_5122	-	GTGACCTATGCACCAGACGTGAGGACGGGCGAGAGGTGTCTGCAGGGAGAAACGCCAGATCGGAAGAGCGGTTCCAG
chr1	45293465	45293504	PTCH2_5123	-	GTGACCTATGCACCAGACGTGCAGAGCAGGGCAGAGACTTAGCATCTCTGGGCCAGAAAGATCGGAAGAGCGGTTCCAG
chr1	45293918	45293957	PTCH2_5124	-	GTGACCTATGCACCAGACGTGCCCCAGCCCTTCTCCCTGGTACCACGCCAGCCTGTCAGATCGGAAGAGCGGTTCCAG
chr1	45294128	45294167	PTCH2_5125	-	GTGACCTATGCACCAGACGTTACACGGGGCAGCTCAGGGTGGTGTGGGGCTGAGGCCAAGATCGGAAGAGCGGTTCCAG
chr1	45294604	45294643	PTCH2_5126	-	GTGACCTATGCACCAGACGTGTCCCCAGGGCTCATCTGAGGCAGCTCAGCTTACTGGTTAGATCGGAAGAGCGGTTCCAG
chr1	45294779	45294818	PTCH2_5127	-	GTGACCTATGCACCAGACGTACTGCAGGGCAGACTCAGTCCAGTACCAGGCTTCCAGGAGATCGGAAGAGCGGTTCCAG
chr1	45295024	45295063	PTCH2_5128	-	GTGACCTATGCACCAGACGTCACCTGCACCTTGCCCCACCCTCCAAACCAGTCCAGATCGGAAGAGCGGTTCCAG
chr1	45295236	45295275	PTCH2_5129	-	GTGACCTATGCACCAGACGTACAAGGACAAGGGGGTGCCCTGAGGCCATTCCCTCCTCCAGATCGGAAGAGCGGTTCCAG
chr1	45295531	45295570	PTCH2_5130	-	GTGACCTATGCACCAGACGTCTCTGGGAGTTGGTGAAGGGACTCTGTTTCATGAGAACCCAAGATCGGAAGAGCGGTTCCAG
chr1	45296470	45296509	PTCH2_5131	-	GTGACCTATGCACCAGACGTACCAGGTCTGCCAGGGAAAGGCTGTTTTCTCCCTTCCAGATCGGAAGAGCGGTTCCAG
chr1	45297328	45297367	PTCH2_5132	-	GTGACCTATGCACCAGACGTCTCCTGGGGCTGCTTCTATCCCGCTGGGGACTCTCCAGATCGGAAGAGCGGTTCCAG
chr1	45297597	45297636	PTCH2_5133	-	GTGACCTATGCACCAGACGTTGAGAGGGAGTAGGGCAGCACTTTTCTGTAGCTGGGAAGATCGGAAGAGCGGTTCCAG
chr1	45297774	45297813	PTCH2_5134	-	GTGACCTATGCACCAGACGCTGACGCCCTGAGCAGCTGGGGCCGAGGCCGCTGTGGGGAGATCGGAAGAGCGGTTCCAG
chr1	45307469	45307508	PTCH2_5135	-	GTGACCTATGCACCAGACGTGACACTGGCCATAGCTGCTCAGGTATGGTGAAGCCCAAGACAGATCGGAAGAGCGGTTCCAG
chr1	45308483	45308522	PTCH2_5136	-	GTGACCTATGCACCAGACGTGGGGAGCTGGAAGAAGGAAGAGAGCGGAGCCAGGTCTGTCAGATCGGAAGAGCGGTTCCAG
chr8	141669515	141669554	PTK2_5137	-	GTGACCTATGCACCAGACGTGGAGCAGCTTGTACTACCTCTTTTTGAAGATGTTCTCTAGAGATCGGAAGAGCGGTTCCAG
chr8	141674966	141675005	PTK2_5138	-	GTGACCTATGCACCAGACGTATCTCCCCCTTGACGCCCTGTGACAGCACTGGGCAGAGATCGGAAGAGCGGTTCCAG
chr8	141678318	141678357	PTK2_5139	-	GTGACCTATGCACCAGACGTGTCAATTTTTGTACTGGCAAAATGTTCTTTGTTTCTGTAAGATCGGAAGAGCGGTTCCAG
chr8	141684347	141684386	PTK2_5140	-	GTGACCTATGCACCAGACGTGAGCCTGTGACACCTTCTGCTTGCAGGATTTGTGGTGTAGATCGGAAGAGCGGTTCCAG
chr8	141685509	141685548	PTK2_5141	-	GTGACCTATGCACCAGACGTAAGAATTGGGCGGAAAGAAGTTAGTTTAATTTGATGAAAAGATCGGAAGAGCGGTTCCAG
chr8	141696681	141696720	PTK2_5142	-	GTGACCTATGCACCAGACGTGTTTTACAGCAGGATTTGATTTCCAGTCTCCTGTGCGTGGAGATCGGAAGAGCGGTTCCAG
chr8	141710940	141710979	PTK2_5143	-	GTGACCTATGCACCAGACGTTTTCTGAAAGGCTTCTTTGACTTTTTAAGCCCTGTTAGAGTAGATCGGAAGAGCGGTTCCAG
chr8	141712619	141712658	PTK2_5144	-	GTGACCTATGCACCAGACGTTGCTTTGGGCTTCACTTTGTAACCTATAAAGCATGGCAAGATCGGAAGAGCGGTTCCAG
chr8	141716168	141716207	PTK2_5145	-	GTGACCTATGCACCAGACGTCATTACAGATAAATCTGTGTATTATTATTAGCCTAGATCGGAAGAGCGGTTCCAG
chr8	141727647	141727686	PTK2_5146	-	GTGACCTATGCACCAGACGTTCCCCACCCCAACTTTGGGGTTACTCTTACTAACTTTCAAAGATCGGAAGAGCGGTTCCAG
chr8	141745300	141745339	PTK2_5147	-	GTGACCTATGCACCAGACGTGCGGGAGAGAGGGCCTGGGGGTGGGGGCAGATTATGCTGCAGATCGGAAGAGCGGTTCCAG
chr8	141749067	141749106	PTK2_5148	-	GTGACCTATGCACCAGACGTTTAAAAGTTTTGATTCTTTAAAATTTATATTTTCATATGTAGATCGGAAGAGCGGTTCCAG
chr8	141753279	141753318	PTK2_5149	-	GTGACCTATGCACCAGACGTAGAGTAGTACTCAAGAATAAGGCTTGAATCTTAACTTAAAGTAAAGATCGGAAGAGCGGTTCCAG
chr8	141754701	141754740	PTK2_5150	-	GTGACCTATGCACCAGACGTGTCAATAAAGTGTAAAGTCCCTTCTGAAAAGTAGTGATCAGATCGGAAGAGCGGTTCCAG
chr8	141756809	141756848	PTK2_5151	-	GTGACCTATGCACCAGACGTCCCCAAATCTTACCCTCTGGACTCAGCGTTTGATATCTTTAGATCGGAAGAGCGGTTCCAG
chr8	141762281	141762320	PTK2_5152	-	GTGACCTATGCACCAGACGTAGAAATTTCTGTGGAATCCATTGACTTTCTATCTGTGAAGATCGGAAGAGCGGTTCCAG
chr8	141771214	141771253	PTK2_5153	-	GTGACCTATGCACCAGACGTTAAGACTACCAAACAATAGACTAATTTTGACTATTTAAGAGATCGGAAGAGCGGTTCCAG
chr8	141774283	141774322	PTK2_5154	-	GTGACCTATGCACCAGACGTTTCTGATTTTGTCTTGTCTCAGACTTGACAGATGCCTCCTAGATCGGAAGAGCGGTTCCAG
chr8	141799523	141799562	PTK2_5155	-	GTGACCTATGCACCAGACGTTAGTAGACACTGAAAAGCACTCTCATGGGTAAGAAGATCGGAAGAGCGGTTCCAG
chr8	141803403	141803442	PTK2_5156	-	GTGACCTATGCACCAGACGTTTTTTTTGTACTGTTTATTTGTTTTGTTTGGAAAGTTTAAAGATCGGAAGAGCGGTTCCAG
chr8	141810508	141810547	PTK2_5157	-	GTGACCTATGCACCAGACGTGTTTTCTGAGCATTCCCAATTGCGCTTCTACCAAAATTTAAGATCGGAAGAGCGGTTCCAG
chr8	141813592	141813631	PTK2_5158	-	GTGACCTATGCACCAGACGTGTACGTTTCATCATTAAAGGAAAATGGTAAATAGGGATGAGATCGGAAGAGCGGTTCCAG
chr8	141828326	141828365	PTK2_5159	-	GTGACCTATGCACCAGACGTTCTGACCTTTCCGGAACTTGGCGTTACACAAAGAAGAATCAGATCGGAAGAGCGGTTCCAG
chr8	141828929	141828968	PTK2_5160	-	GTGACCTATGCACCAGACGTGAATAGGGAAATAGTGGGTAGTTTATTACTTTTTTCAGATCGGAAGAGCGGTTCCAG
chr8	141840521	141840560	PTK2_5161	-	GTGACCTATGCACCAGACGTTCTCCTTTATCATATAAATAAACAATAAGTATGCCAAGACATCGGAAGAGCGGTTCCAG
chr8	141856309	141856348	PTK2_5162	-	GTGACCTATGCACCAGACGTTACTTACAATCTATACCTGAAATAATGCAGAACTAAATCAGATCGGAAGAGCGGTTCCAG

chr8	141874361	141874400	PTK2_5163	-	GTGACCTATGCACCAGACGCTGCTTTTCATATACTTTTTGTTTGTTCCTTTGAATCCTAAGATCGGAAGAGCGGTTTCAG
chr8	141889520	141889559	PTK2_5164	-	GTGACCTATGCACCAGACGTAACCTGCTTTGGTGTGATGCACACTTGATTTCTTTTCTTTAGATCGGAAGAGCGGTTTCAG
chr8	141900592	141900631	PTK2_5165	-	GTGACCTATGCACCAGACGTTTTTCCATGAGACATCTTTAATGTTTTATTAGGTTAAAAATAGATCGGAAGAGCGGTTTCAG
chr9	8317824	8317863	PTPRD_5166	-	GTGACCTATGCACCAGACGTCCTTCTGGATTTTTACTACAGGCCCTTCATATCCATGAGATCGGAAGAGCGGTTTCAG
chr9	8319781	8319820	PTPRD_5167	-	GTGACCTATGCACCAGACGTCCTTTCGATTTTTTCCGATCTCAAGAGCCTACGTTTTGCTAAGATCGGAAGAGCGGTTTCAG
chr9	8331532	8331571	PTPRD_5168	-	GTGACCTATGCACCAGACGTATTGTGAATAAAGCAGTGATAAGTGGTGGTGTTCCTTCAAGATCGGAAGAGCGGTTTCAG
chr9	8338872	8338911	PTPRD_5169	-	GTGACCTATGCACCAGACGTACAGCTTCAACTTTAACCATTAGCTGAAAAGTAGCTAAGATCGGAAGAGCGGTTTCAG
chr9	8340293	8340332	PTPRD_5170	-	GTGACCTATGCACCAGACGTGGCCCTTGTGTCTCTCCTCATAAGACATTTACTCTGTGGAAGATCGGAAGAGCGGTTTCAG
chr9	8341040	8341079	PTPRD_5171	-	GTGACCTATGCACCAGACGTTTGTCTCCCTGACTATCCAAGCCTTGATATTTACATGTGAGATCGGAAGAGCGGTTTCAG
chr9	8341643	8341682	PTPRD_5172	-	GTGACCTATGCACCAGACGTGGATGTGATGTGGTTATTCAGGAGCAAGTCATTCTGGGTAGATCGGAAGAGCGGTTTCAG
chr9	8375886	8375925	PTPRD_5173	-	GTGACCTATGCACCAGACGTTTTGTTCACCTGCAGTCAGGAAACAGAAAAGCTAAATTGACAGATCGGAAGAGCGGTTTCAG
chr9	8376557	8376596	PTPRD_5174	-	GTGACCTATGCACCAGACGTCATCTTTTTCTCCCTCCCTTCTCTATTGTTTAAAGATCGGAAGAGCGGTTTCAG
chr9	8389182	8389221	PTPRD_5175	-	GTGACCTATGCACCAGACGTGTATCCACTCTTTCCCTTTTAAAAATTTCCCTCAGAGTCAGATCGGAAGAGCGGTTTCAG
chr9	8404487	8404526	PTPRD_5176	-	GTGACCTATGCACCAGACGTGCAGACATCACTGATACCTTTATTTTTCATGGATTTGAGTAAGATCGGAAGAGCGGTTTCAG
chr9	8436542	8436581	PTPRD_5177	-	GTGACCTATGCACCAGACGTGTGTTTTATTCTTTACAGTAATTTCAAGAGTTACTCTTCTCAGATCGGAAGAGCGGTTTCAG
chr9	8449675	8449714	PTPRD_5178	-	GTGACCTATGCACCAGACGTTACACATCTAATCCACACACAGCTTTCCTCAGAAAGTTGATAGATCGGAAGAGCGGTTTCAG
chr9	8460361	8460400	PTPRD_5179	-	GTGACCTATGCACCAGACGTCCAATATTTCTGTGTAATTTGGAGGCTGCCTTATTTTAGATCGGAAGAGCGGTTTCAG
chr9	8465416	8465455	PTPRD_5180	-	GTGACCTATGCACCAGACGTTATGATGGCTTGTTCCTATGGTACCGTTATACATTTTAGATCGGAAGAGCGGTTTCAG
chr9	8470945	8470984	PTPRD_5181	-	GTGACCTATGCACCAGACGTCAATTGTTGGCCATGCTTTTTATTGTTTAAATCTGCTGAGATCGGAAGAGCGGTTTCAG
chr9	8484069	8484108	PTPRD_5182	-	GTGACCTATGCACCAGACGTTGAAGGCTTAGGGCTGAAGGAAAGAATTATAGGTAATAGAGATCGGAAGAGCGGTTTCAG
chr9	8485177	8485216	PTPRD_5183	-	GTGACCTATGCACCAGACGTTTCTAATTTGTAAGAAATCACAGATAAAAGTAGAGGGACAGATCGGAAGAGCGGTTTCAG
chr9	8485712	8485751	PTPRD_5184	-	GTGACCTATGCACCAGACGTTCTGCTTACGGCCCTTCCCTTTAAAGGATTGTCAGTCTTAGATCGGAAGAGCGGTTTCAG
chr9	8492812	8492851	PTPRD_5185	-	GTGACCTATGCACCAGACGTTGTGCATGTATGTCCCTGAACAGTAATACTAATTTTAGATCGGAAGAGCGGTTTCAG
chr9	8497192	8497231	PTPRD_5186	-	GTGACCTATGCACCAGACGTTTTGACTTGTGTCAAAAGCAGACTATATGCTTGTTTAGATCGGAAGAGCGGTTTCAG
chr9	8499597	8499636	PTPRD_5187	-	GTGACCTATGCACCAGACGTGAAATTATGTACCTCTGTTTTATATAATAAGTTTATCTTAGATCGGAAGAGCGGTTTCAG
chr9	8500704	8500743	PTPRD_5188	-	GTGACCTATGCACCAGACGTTCCGCTACGTCTGTTGCACCTTCTGACACAGTCTTATAGATCGGAAGAGCGGTTTCAG
chr9	8504211	8504250	PTPRD_5189	-	GTGACCTATGCACCAGACGTCCTTTGCTTACTTTCTGCCTTTTTATTTCCTCGGGGAGAAAGATCGGAAGAGCGGTTTCAG
chr9	8507251	8507290	PTPRD_5190	-	GTGACCTATGCACCAGACGTAGTCTTCTCACCTTGGGAATTATTCATTACGTTGGGCAAGATCGGAAGAGCGGTTTCAG
chr9	8517798	8517837	PTPRD_5191	-	GTGACCTATGCACCAGACGTTTGAGGAGGAAATAGGGCAGGAGGGCTGGTCAAAAGATCGGAAGAGCGGTTTCAG
chr9	8521227	8521266	PTPRD_5192	-	GTGACCTATGCACCAGACGTTGGATTGCTTTGAGGATCTGGGTACACTCAAGCCAAGTAGATCGGAAGAGCGGTTTCAG
chr9	8523463	8523502	PTPRD_5193	-	GTGACCTATGCACCAGACGTTTTTACTTTTTACCACCTTACAAAATTAATAAACAGATCGGAAGAGCGGTTTCAG
chr9	8526577	8526616	PTPRD_5194	-	GTGACCTATGCACCAGACGTTGAACTAACGTTACAGAAATGATCTTACTATTCTTCTGAGATCGGAAGAGCGGTTTCAG
chr9	8527295	8527334	PTPRD_5195	-	GTGACCTATGCACCAGACGTAGTTCTGAAGCGCACTTCAACCCCACTAATTTCCATATCCAGATCGGAAGAGCGGTTTCAG
chr9	8633267	8633306	PTPRD_5196	-	GTGACCTATGCACCAGACGTAAGTGAAGGTTGCTCTTGTGCTATTGTTACAATTTGTAAGATCGGAAGAGCGGTTTCAG
chr9	8636649	8636688	PTPRD_5197	-	GTGACCTATGCACCAGACGTCATTGTTCTGTTTTCTGTTTTGAGGGAAGAAATGTATCTGCTGAGATCGGAAGAGCGGTTTCAG
chr9	8733730	8733769	PTPRD_5198	-	GTGACCTATGCACCAGACGTCTCCCTTCTCTAGGGGCTGTGACCATAATGAGTGGTTTAGATCGGAAGAGCGGTTTCAG
chr9	8486006	8486045	PTPRD_5199	-	GTGACCTATGCACCAGACGTCCTTCACTCAGAAGGCACCCTTCAACCTCCGTCAGTTAAGATCGGAAGAGCGGTTTCAG
chr9	8518089	8518128	PTPRD_5200	-	GTGACCTATGCACCAGACGTGAGGGATGTCCAGGCAGAAATGTTGAGTTCGACCACATTAGATCGGAAGAGCGGTTTCAG
chr14	68290211	68290250	RAD51L1_5201	-	GTGACCTATGCACCAGACGTCCAGCAAAGAAAAGAAACCATGAAAAAACACAGAATAGATCGGAAGAGCGGTTTCAG
chr14	68292131	68292170	RAD51L1_5202	-	GTGACCTATGCACCAGACGTATAAAGAGAGATTTTAAACATATATGTGTAACAAAGATAAGATCGGAAGAGCGGTTTCAG
chr14	68301747	68301786	RAD51L1_5203	-	GTGACCTATGCACCAGACGTTAAAGTATTAAGTTTTTTTTCAACCTTATATATAATTCAAAAGATCGGAAGAGCGGTTTCAG
chr14	68352536	68352575	RAD51L1_5204	-	GTGACCTATGCACCAGACGTAAAAATAGCACAAACGAAACAGTCAATTTACTTAAAGAGATCGGAAGAGCGGTTTCAG
chr14	68758551	68758590	RAD51L1_5205	-	GTGACCTATGCACCAGACGTACAGGGAGAAGGGGTAGGGGGCAAGGGAGAAGAAAGACAGATCGGAAGAGCGGTTTCAG
chr14	68878091	68878130	RAD51L1_5206	-	GTGACCTATGCACCAGACGTATGGTAAAGCAGCCTTTCAGATGCCCTTCTTGGATGGAGATCGGAAGAGCGGTTTCAG
chr14	68934839	68934878	RAD51L1_5207	-	GTGACCTATGCACCAGACGTAGCACATTTTTCTAGGGTTAGTCAAAGGATCAGGGATGGGAGATCGGAAGAGCGGTTTCAG
chr7	151164155	151164194	RHEB_5208	-	GTGACCTATGCACCAGACGTAAGCCTGAGACCTGGAAGATATTTCTACCTGAAGACAGATCGGAAGAGCGGTTTCAG
chr7	151167607	151167646	RHEB_5209	-	GTGACCTATGCACCAGACGTCTATAAACCCTCAATTTGCAATGCGTCTCATCAGTCGAGAGATCGGAAGAGCGGTTTCAG
chr7	151168430	151168469	RHEB_5210	-	GTGACCTATGCACCAGACGTTTTATAAAGTCAAATCTAAGATGATTTAGTCACTGAAGTAAGATCGGAAGAGCGGTTTCAG
chr7	151168585	151168624	RHEB_5211	-	GTGACCTATGCACCAGACGTCCATTTTTATCTGCTTGTAGAGAAACTCTTTTAAATAGTAAGATCGGAAGAGCGGTTTCAG
chr7	151174369	151174408	RHEB_5212	-	GTGACCTATGCACCAGACGTTGCTGCCTGCTTGAGTTGATTTGCTACTCATAGATAACATAGATCGGAAGAGCGGTTTCAG
chr7	151181773	151181812	RHEB_5213	-	GTGACCTATGCACCAGACGTTTGGATCTCAGAACTTATACAGCATATCAGACGTCTAGATCGGAAGAGCGGTTTCAG
chr7	151187979	151188018	RHEB_5214	-	GTGACCTATGCACCAGACGTTTTTCCATGTAAAAAAGTGAAGAACTTCCATTTTGTGTAAGATCGGAAGAGCGGTTTCAG
chr7	151216496	151216535	RHEB_5215	-	GTGACCTATGCACCAGACGTGGTGGCCGCGCGCTTCCGCGCCGCGGGGCTCGCTAGATCGGAAGAGCGGTTTCAG
chr3	49397592	49397631	RHOA_5216	-	GTGACCTATGCACCAGACGTCAAGCACAGCCCTTATGCGGTTAATTTGAAGTGTCTTTTAGATCGGAAGAGCGGTTTCAG
chr3	49399879	49399918	RHOA_5217	-	GTGACCTATGCACCAGACGTGGGCAGGACTGTCTGTAGATTCTTGAAGTGGGCCCAAGATCGGAAGAGCGGTTTCAG
chr3	49405811	49405850	RHOA_5218	-	GTGACCTATGCACCAGACGTCTGCCACCTGATTTTGCCTGCCTGTGTAGCTAGTTGGAGATCGGAAGAGCGGTTTCAG
chr3	49412817	49412856	RHOA_5219	-	GTGACCTATGCACCAGACGTTTTTCAACCACTGATGCCATTTTCCATTTGTAAGATTTAGATCGGAAGAGCGGTTTCAG
chr1	26856362	26856401	RPS6KA1_5220	-	GTGACCTATGCACCAGACGTCCAGCTCACCCGCTCTCTCCGGCGGCCCGGCTCGCAGATCGGAAGAGCGGTTTCAG

chr1	26863366	26863405	RPS6KA1_5221	-	GTGACCTATGCACCAGACGTGAAAGGAGATTGGGGGAGCACTGTGCAGAACTTACACGCTTAGATCGGAAGAGCGGTTTCAG
chr1	26872342	26872381	RPS6KA1_5222	-	GTGACCTATGCACCAGACGTGGGCCACGGCACCATGGCAGGAGCAGGCAGAGTCCGGGGCAGATCGGAAGAGCGGTTTCAG
chr1	26873308	26873347	RPS6KA1_5223	-	GTGACCTATGCACCAGACGTGACAGAGCTGGTGGGCATGGTGGGCCCCATCCAGGCAGCAAGATCGGAAGAGCGGTTTCAG
chr1	26873630	26873669	RPS6KA1_5224	-	GTGACCTATGCACCAGACGTAGAGCAGGAAGCAGGGCAGAAGATGGGAGAGGTCTGAGTCAGATCGGAAGAGCGGTTTCAG
chr1	26877838	26877877	RPS6KA1_5225	-	GTGACCTATGCACCAGACGTGAGAAGGAATCACCAGTAGCCTAGACACTCAACACAGCAGATCGGAAGAGCGGTTTCAG
chr1	26878085	26878124	RPS6KA1_5226	-	GTGACCTATGCACCAGACGTGGGAAAAGCCAAAGTGAGAGTCGGCGCGGCCTTATGATCTAGATCGGAAGAGCGGTTTCAG
chr1	26879832	26879871	RPS6KA1_5227	-	GTGACCTATGCACCAGACGTGAGGAGGGGCCTTCAGCAGAGGCACTCCTTCCTTAAGAGATCGGAAGAGCGGTTTCAG
chr1	26880655	26880694	RPS6KA1_5228	-	GTGACCTATGCACCAGACGTGAAATAGTGGTCAGGGCCCCCTCAGCTGTGGCCGTGTGGGTAGATCGGAAGAGCGGTTTCAG
chr1	26881037	26881076	RPS6KA1_5229	-	GTGACCTATGCACCAGACGTGAGGGCAGGAGGACACACTTAGGACCCCTGCCCTTCCTTGAGATCGGAAGAGCGGTTTCAG
chr1	26881592	26881631	RPS6KA1_5230	-	GTGACCTATGCACCAGACGTCAAGGATCTATTCAGGCTCTGATCCCTGTCTCCGACACACAGATCGGAAGAGCGGTTTCAG
chr1	26881978	26882017	RPS6KA1_5231	-	GTGACCTATGCACCAGACGTCCCCGGGACTCATCAAGGCTGAGCCCTGCCCCAGAGGCCCATCGGAAGAGCGGTTTCAG
chr1	26883095	26883134	RPS6KA1_5232	-	GTGACCTATGCACCAGACGTCCAAATGAAGGGTCTGTCCCTGGCTGGCACAAGTCCCAAGATCGGAAGAGCGGTTTCAG
chr1	26883439	26883478	RPS6KA1_5233	-	GTGACCTATGCACCAGACGTGGGTGGGCACCTGTGGTCACTATGCCATCCTCAACAGCCCAAGATCGGAAGAGCGGTTTCAG
chr1	26885248	26885287	RPS6KA1_5234	-	GTGACCTATGCACCAGACGTGGAAGGAGAATGTGAGGGTACCTGAGGAGGTCCCTCGACAGATCGGAAGAGCGGTTTCAG
chr1	26887167	26887206	RPS6KA1_5235	-	GTGACCTATGCACCAGACGTCCAAAATTGTGGCTGACCCTGGCTCTAGAGTGTAGGGAGATCGGAAGAGCGGTTTCAG
chr1	26887486	26887525	RPS6KA1_5236	-	GTGACCTATGCACCAGACGTGGGGTGCATGTGGCAGTGTCAGGGTGACAGGGTCCAGGGTAGATCGGAAGAGCGGTTTCAG
chr1	26887946	26887985	RPS6KA1_5237	-	GTGACCTATGCACCAGACGTCTCCACTCACCATCAGGCTCTCTCCCAAGTGTGAGGCTGAGCAGATCGGAAGAGCGGTTTCAG
chr1	26897890	26897929	RPS6KA1_5238	-	GTGACCTATGCACCAGACGTGGGGTGGGGCTAGTTCAGTGTGGGAGGTGGTGGTGTGAGATCGGAAGAGCGGTTTCAG
chr1	26898290	26898329	RPS6KA1_5239	-	GTGACCTATGCACCAGACGTGGCAGGGGAGGTGGTCACTGTGGGGGGCAGTAGAAAGTCAGATCGGAAGAGCGGTTTCAG
chr1	26898617	26898656	RPS6KA1_5240	-	GTGACCTATGCACCAGACGTGCCCGCACGGTCTGGGTACAGACTCTGGCTCCACTGTGGAGATCGGAAGAGCGGTTTCAG
chr1	26899665	26899704	RPS6KA1_5241	-	GTGACCTATGCACCAGACGTAGTGGGCAAGGGGTTGGGGAGGGCTGCAGGGGAGCAGGAGATCGGAAGAGCGGTTTCAG
chr1	26900520	26900559	RPS6KA1_5242	-	GTGACCTATGCACCAGACGTAGTGGCGGAGGTCAGGTCACAAATGGTGGGAGATGTAGCGGGAGATCGGAAGAGCGGTTTCAG
chr17	57970496	57970535	RPS6KB1_5243	-	GTGACCTATGCACCAGACGTCCGGCGCAGCCACACAGCCGCTGCCGCCATCACCGGTGTAGATCGGAAGAGCGGTTTCAG
chr17	57987873	57987912	RPS6KB1_5244	-	GTGACCTATGCACCAGACGTGGTGTAAAAGTTTCAGAATAATCTAATAAACATAAAATTTAGATCGGAAGAGCGGTTTCAG
chr17	57989995	57990034	RPS6KB1_5245	-	GTGACCTATGCACCAGACGTAAGCAAACCAAAATAAATTTGCAAAAAGTTAAATTAAGATCGGAAGAGCGGTTTCAG
chr17	57991946	57991985	RPS6KB1_5246	-	GTGACCTATGCACCAGACGTAAAAAGTGTGTGTATTTCAAAGGCAAACTATGTCAGGCATAGATCGGAAGAGCGGTTTCAG
chr17	58003746	58003785	RPS6KB1_5247	-	GTGACCTATGCACCAGACGTAGAGATCATCTAAGAACAATAAGTAGAACATTTTATTAGATCGGAAGAGCGGTTTCAG
chr17	58007428	58007467	RPS6KB1_5248	-	GTGACCTATGCACCAGACGTAAAGGAAAAAACATTAATAAAACAAGTATTTATTTCCAAAGATCGGAAGAGCGGTTTCAG
chr17	58008933	58008972	RPS6KB1_5249	-	GTGACCTATGCACCAGACGTAAAGTATTAAATAAAATTAAGAGGTAATCTATCCAAGATCGGAAGAGCGGTTTCAG
chr17	58011481	58011520	RPS6KB1_5250	-	GTGACCTATGCACCAGACGTGATTACAGCATGATTATTCTCCGAATTAAGTATGTGCAGATCGGAAGAGCGGTTTCAG
chr17	58011745	58011784	RPS6KB1_5251	-	GTGACCTATGCACCAGACGTGAAATAATATGCTTAAAAATTACCCATTTGCATATCATAGATCGGAAGAGCGGTTTCAG
chr17	58012504	58012543	RPS6KB1_5252	-	GTGACCTATGCACCAGACGTGAAACAAGTAAATAATATAGCAGGGAGAGAAAAATAAAGATCGGAAGAGCGGTTTCAG
chr17	58013526	58013565	RPS6KB1_5253	-	GTGACCTATGCACCAGACGTGAAAAAAGCTTGGATAAAGAACCTTAGTCAAACATGATTAGATCGGAAGAGCGGTTTCAG
chr17	58013775	58013814	RPS6KB1_5254	-	GTGACCTATGCACCAGACGTAAAAGCAGGAAGAAAAGTTGAGGGGACTAGACCTTTTCTGGAGATCGGAAGAGCGGTTTCAG
chr17	58018147	58018186	RPS6KB1_5255	-	GTGACCTATGCACCAGACGTGAAAAATAATTAGAAAATAAATAAATAGTCCATGTTACATAGATCGGAAGAGCGGTTTCAG
chr17	58022717	58022756	RPS6KB1_5256	-	GTGACCTATGCACCAGACGTGAACAGTGGACTACAGAATGGCATTTTGTATGTATCTCAGATCGGAAGAGCGGTTTCAG
chr17	58023862	58023901	RPS6KB1_5257	-	GTGACCTATGCACCAGACGTAGGAAGAGCTATCATTCACTTTGCTTAAAGGGTCATCTCAACAGATCGGAAGAGCGGTTTCAG
chr8	92972420	92972459	RUNX1T1_5258	-	GTGACCTATGCACCAGACGTGAAACTGTCGGAGGAAGACAACACAACCAACGCGAAACCAGATCGGAAGAGCGGTTTCAG
chr8	92982836	92982875	RUNX1T1_5259	-	GTGACCTATGCACCAGACGTGGGAAGCTCAAATAAAACAAGATAGTTTTTCACTCATTAAAGATCGGAAGAGCGGTTTCAG
chr8	92988083	92988122	RUNX1T1_5260	-	GTGACCTATGCACCAGACGTTTTAAAAATGAGTTTTCTGTTCTGGCAGCTGTGTCGACAGATCGGAAGAGCGGTTTCAG
chr8	92998302	92998341	RUNX1T1_5261	-	GTGACCTATGCACCAGACGTTCCAGATGAGTATCTCGAAAACCAATATTTCTTAGCTGTAGATCGGAAGAGCGGTTTCAG
chr8	92999065	92999104	RUNX1T1_5262	-	GTGACCTATGCACCAGACGTAGTAATCATTGGGATTAATAAATGTTTGGAAAACAACGATCGGAAGAGCGGTTTCAG
chr8	93003817	93003856	RUNX1T1_5263	-	GTGACCTATGCACCAGACGTGAGGACCTGTTCACTTCTTACGGGATGGTGTCTGAAGACAGATCGGAAGAGCGGTTTCAG
chr8	93017294	93017333	RUNX1T1_5264	-	GTGACCTATGCACCAGACGTGAGGAGCCTGGATGAACCATGACCTTTTTCCATACCTGAGATCGGAAGAGCGGTTTCAG
chr8	93023180	93023219	RUNX1T1_5265	-	GTGACCTATGCACCAGACGTGTTCACTGGTCTGTAAGATTTTAAACCATATTTGTTGATCGGAAGAGCGGTTTCAG
chr8	93026757	93026796	RUNX1T1_5266	-	GTGACCTATGCACCAGACGTGGAACCCAGTTTCTGTTGTAAAGGATAGTGGAATCGGAAGAGCGGTTTCAG
chr8	93029404	93029443	RUNX1T1_5267	-	GTGACCTATGCACCAGACGTATTTCAAGGCTTTTGGATTTTAAAGTTTAAATTAAGATCGGAAGAGCGGTTTCAG
chr8	93074724	93074763	RUNX1T1_5268	-	GTGACCTATGCACCAGACGTCTCTGTCTGTCTCTCTGTCTTCCAAATGAAGAAAGCTAGATCGGAAGAGCGGTTTCAG
chr8	93088143	93088182	RUNX1T1_5269	-	GTGACCTATGCACCAGACGTGACAATAATTTTGAATTTTGAATTTACTTACGTACCAGAAGATCGGAAGAGCGGTTTCAG
chr1	161284146	161284185	SDHC_5270	-	GTGACCTATGCACCAGACGTGGTCTGGACGGAAGTGACGCCAGGCGGCCCGCCACCCGAAGATCGGAAGAGCGGTTTCAG
chr1	161293354	161293393	SDHC_5271	-	GTGACCTATGCACCAGACGTAGAGAACTAAAACCAATACACATTTAGAGATCAACTTTAAGATCGGAAGAGCGGTTTCAG
chr1	161298136	161298175	SDHC_5272	-	GTGACCTATGCACCAGACGTGACAGACCTTTGAAAAATAACATAAATTTGTTTAAAGATAAATTTGTTTAAAGATCGGAAGAGCGGTTTCAG
chr1	161310334	161310373	SDHC_5273	-	GTGACCTATGCACCAGACGTACACACAAGACAATTTTAAAAGGAAAAGATGACACCATAGATCGGAAGAGCGGTTTCAG
chr1	161326417	161326456	SDHC_5274	-	GTGACCTATGCACCAGACGTAAACAAAGTAGTCTGTACAGCTGCTCATAAGTTACAATAAGATCGGAAGAGCGGTTTCAG
chr1	161332069	161332108	SDHC_5275	-	GTGACCTATGCACCAGACGTGCAAAAAAAGGAATTTCCAGTAAATAGGACATTAGATCGGAAGAGCGGTTTCAG
chr11	111957582	111957621	SDHD_5276	-	GTGACCTATGCACCAGACGTAGGCTCAAGGTCATCCACCAACCCGGAACCACTTAGGCAGATCGGAAGAGCGGTTTCAG
chr11	111958531	111958570	SDHD_5277	-	GTGACCTATGCACCAGACGTAGTCAATGATGATCATAAAGCAACCTCTCCTTAAACAGGAAGATCGGAAGAGCGGTTTCAG
chr11	111959541	111959580	SDHD_5278	-	GTGACCTATGCACCAGACGTGACCAAGATTCAATAAGGTTGATGTGAGAACACATCTTAGATCGGAAGAGCGGTTTCAG

chr11	111965479	111965518	SDHD_5279	-	GTGACCTATGCACCAGACGTGAGAAAAATCATAACATCAATAAAAAACCACAGTGAAATTAGATCGGAAGAGCGGTTTCAG
chr10	88718405	88718444	SNCG_5280	-	GTGACCTATGCACCAGACGTCAGGGTTGTCTGCTGCGAGCCAGGACGGAGCTGGATCTCCAGATCGGAAGAGCGGTTTCAG
chr10	88719340	88719379	SNCG_5281	-	GTGACCTATGCACCAGACGTAATGGAGCTGTGACCCAGACCTCCCTCGAGGTTGTGGGAGATCGGAAGAGCGGTTTCAG
chr10	88719708	88719747	SNCG_5282	-	GTGACCTATGCACCAGACGTACTGCTGGCTGGCCCTCACCAGCCAGCCCAAGGCAGAGATCGGAAGAGCGGTTTCAG
chr10	88722311	88722350	SNCG_5283	-	GTGACCTATGCACCAGACGTCAAAGGGGGCATGAGACCATGTGGAGAATCGAGAGACCAGATCGGAAGAGCGGTTTCAG
chr10	88722672	88722711	SNCG_5284	-	GTGACCTATGCACCAGACGTTAATGACCTGCACACCCAGCTCCAGCCCGCCAGCTTATGATCGGAAGAGCGGTTTCAG
chr12	93966624	93966663	SOCS2_5285	-	GTGACCTATGCACCAGACGTTACCCGCGGCAAGAGACAGGTGGCCGCCAGCTCAAGATCGGAAGAGCGGTTTCAG
chr12	93968448	93968487	SOCS2_5286	-	GTGACCTATGCACCAGACGTTGTTCAAAGAAAAGAAAAGAGGGTAAAACAGTTATTAAGATCGGAAGAGCGGTTTCAG
chr1	16174513	16174552	SPEN_5287	-	GTGACCTATGCACCAGACGTGTGCCGGCGACCGCCGCTGCTGGCTCCCCCTCGCCGGCTTAGATCGGAAGAGCGGTTTCAG
chr1	16199261	16199300	SPEN_5288	-	GTGACCTATGCACCAGACGTTAAAGTCAACGTTATTGCTGCATATCAATAATTTTCAAAGATCGGAAGAGCGGTTTCAG
chr1	16202647	16202686	SPEN_5289	-	GTGACCTATGCACCAGACGTGAGGGGGAAAAATATTTAATCAGAAAGGAGCAAGCAAAACAGATCGGAAGAGCGGTTTCAG
chr1	16235766	16235805	SPEN_5290	-	GTGACCTATGCACCAGACGTGCAACAACAACAACCTTAGTGAAAGACAACAAGATAAGATCGGAAGAGCGGTTTCAG
chr1	16237546	16237585	SPEN_5291	-	GTGACCTATGCACCAGACGTAAAAAAAACCAAGTTATTAACTTCTAATTTAATTTAAGATCGGAAGAGCGGTTTCAG
chr1	16242573	16242612	SPEN_5292	-	GTGACCTATGCACCAGACGTAATGGGGCCGAGTAAAAAGAGAAGACAGATTTTAAATGCAGATCGGAAGAGCGGTTTCAG
chr1	16245371	16245410	SPEN_5293	-	GTGACCTATGCACCAGACGTCAATGAATACAACCTTAGCAATATGCCCAAGAAAATAAATAGATCGGAAGAGCGGTTTCAG
chr1	16245849	16245888	SPEN_5294	-	GTGACCTATGCACCAGACGTAAGGCAAAAATTTCTATTAGTAAAGTTCACAATTTACTATTAGATCGGAAGAGCGGTTTCAG
chr1	16247315	16247354	SPEN_5295	-	GTGACCTATGCACCAGACGTAAACAAAAGAAAACAGTAAGAGCCCTCACTCCAGCTTAGATCGGAAGAGCGGTTTCAG
chr1	16248694	16248733	SPEN_5296	-	GTGACCTATGCACCAGACGTTAAAGAGGTGTTTGGCAAGTTCAAATTTTAAATGATGAGATCGGAAGAGCGGTTTCAG
chr1	16254536	16254575	SPEN_5297	-	GTGACCTATGCACCAGACGTATAACAAAGATATTAGTCTTTTTGTTTCTCATCACTTATAGATCGGAAGAGCGGTTTCAG
chr1	16263608	16263647	SPEN_5298	-	GTGACCTATGCACCAGACGTGAAGGAAGGCAAGGGACAGAGTCAAGTCTGTTGTGCACAAAGATCGGAAGAGCGGTTTCAG
chr1	16264257	16264296	SPEN_5299	-	GTGACCTATGCACCAGACGTGGAACAACAGGAAGTGAGCTCATGGCCCCCTCGCTGAGCAGATCGGAAGAGCGGTTTCAG
chr1	16265163	16265202	SPEN_5300	-	GTGACCTATGCACCAGACGTGGCCAGCTGCCAGTGAGCAGGGGGCCTCCTAGTCAAACAGCAGATCGGAAGAGCGGTTTCAG
chr1	16265741	16265780	SPEN_5301	-	GTGACCTATGCACCAGACGTGATAGAGAGCAAGTGGACCGCTGCTCTTCAACCCCAAGATCGGAAGAGCGGTTTCAG
chr1	16255017	16255056	SPEN_5302	-	GTGACCTATGCACCAGACGTATCTGGAGGGGAGAGTGAAGCTCAGCTCAGACTTCCAGCTGATCGGAAGAGCGGTTTCAG
chr1	16255498	16255537	SPEN_5303	-	GTGACCTATGCACCAGACGTTGATTCCAGTTTAGACAAGTCAAGATTTGACAGGCTCCGTCAGATCGGAAGAGCGGTTTCAG
chr1	16255979	16256018	SPEN_5304	-	GTGACCTATGCACCAGACGTATTACCTGCTAGTTCTCCAGTCTTGCTTGTAGGCTGAAGATCGGAAGAGCGGTTTCAG
chr1	16256460	16256499	SPEN_5305	-	GTGACCTATGCACCAGACGTGAATCTTCGCTGATTTGGCGTGAACCTCTGTAATTCGGTTAGATCGGAAGAGCGGTTTCAG
chr1	16256941	16256980	SPEN_5306	-	GTGACCTATGCACCAGACGTTAGCTTGTCTTCTGTCCTCAATAAAAAAGACAATCGAAGATCGGAAGAGCGGTTTCAG
chr1	16257422	16257461	SPEN_5307	-	GTGACCTATGCACCAGACGTTGGAATCGTTGTGCTGTTTCTCCCTCAGATGCTGCTTAGATCGGAAGAGCGGTTTCAG
chr1	16257903	16257942	SPEN_5308	-	GTGACCTATGCACCAGACGTGGAGGCTTGGCATTCCAGATTAAGCGGCTGGTCACTGATGAGATCGGAAGAGCGGTTTCAG
chr1	16258384	16258423	SPEN_5309	-	GTGACCTATGCACCAGACGTGAGAGGCAAACTTGGTTCCGGATGTTCAAGGCTGCAGCAAGATCGGAAGAGCGGTTTCAG
chr1	16258865	16258904	SPEN_5310	-	GTGACCTATGCACCAGACGTTTTAGGGGGTTTTTGTCTGTGCCAGCATCTTTTCTGTCAGATCGGAAGAGCGGTTTCAG
chr1	16259346	16259385	SPEN_5311	-	GTGACCTATGCACCAGACGTGCAGCCAGCTCTGTTTCACTTGCTTGGTGTGCAGGCTTGTAGATCGGAAGAGCGGTTTCAG
chr1	16259827	16259866	SPEN_5312	-	GTGACCTATGCACCAGACGTGTGCTGTACTGTTGTCCTCCTATTGCAAGCAGGACTCTCAAGATCGGAAGAGCGGTTTCAG
chr1	16260308	16260347	SPEN_5313	-	GTGACCTATGCACCAGACGTGAATCTTCTCAGGGTGCTGGAGCTGGTGTCAACATCAGAATCGGAAGAGCGGTTTCAG
chr1	16260789	16260828	SPEN_5314	-	GTGACCTATGCACCAGACGTTTTACAGGCCCTTTCAGGACGTTACGGGCCAGCAGGGGAGATCGGAAGAGCGGTTTCAG
chr1	16261270	16261309	SPEN_5315	-	GTGACCTATGCACCAGACGTAGTTTACCTGGGACTTGGACACTGACTGCTGAAATCAAGATCGGAAGAGCGGTTTCAG
chr1	16261751	16261790	SPEN_5316	-	GTGACCTATGCACCAGACGTCAGCTGCCAAATGGGAGACAGTTTCATGCTGGGATGCTAGATCGGAAGAGCGGTTTCAG
chr1	16262232	16262271	SPEN_5317	-	GTGACCTATGCACCAGACGTACTAGTACTCTGACTGCACAGGGGCTGTGGCTCGAGCGAAGATCGGAAGAGCGGTTTCAG
chrX	48887619	48887658	TFE3_5318	-	GTGACCTATGCACCAGACGTCCCCCTCCCTGGGACTTCCACCCAGGAAAGGAGGACCAAGATCGGAAGAGCGGTTTCAG
chrX	48888862	48888901	TFE3_5319	-	GTGACCTATGCACCAGACGTAGGAGATGGTGTGGGGGAGGAGGGGAGAGCTTCTCTGCAAGATCGGAAGAGCGGTTTCAG
chrX	48890930	48890969	TFE3_5320	-	GTGACCTATGCACCAGACGTGCTGGGACCCCTCAGGCCAGCGGGAGGTGGGGCAGGCGTCCAGATCGGAAGAGCGGTTTCAG
chrX	48891191	48891230	TFE3_5321	-	GTGACCTATGCACCAGACGTGAGCGTGTGCATTGCCCGGGTGTGTCAGGCTGCTCAAGATCGGAAGAGCGGTTTCAG
chrX	48891599	48891638	TFE3_5322	-	GTGACCTATGCACCAGACGTGGGTCTTGGCCCATGGCCCTACACTTTACCCAGGTGAGAGATCGGAAGAGCGGTTTCAG
chrX	48895485	48895524	TFE3_5323	-	GTGACCTATGCACCAGACGTGAGATGGGAGGTTGGTCTGAAAATTAGGGCACTTTCTGTATAGATCGGAAGAGCGGTTTCAG
chrX	48895672	48895711	TFE3_5324	-	GTGACCTATGCACCAGACGTACAGCCAACTCCCTCCCAACTCCCTCCCAATTTCTCAGATCGGAAGAGCGGTTTCAG
chrX	48896582	48896621	TFE3_5325	-	GTGACCTATGCACCAGACGTATCCAGAGGCCCTGGGAGGGGGCTCCTGGTACTGAGGAGAGATCGGAAGAGCGGTTTCAG
chrX	48897932	48897971	TFE3_5326	-	GTGACCTATGCACCAGACGTTGCTATCTGATCCCCTCCCAATTCCTCAGCCCTCCTAGATCGGAAGAGCGGTTTCAG
chrX	48900587	48900626	TFE3_5327	-	GTGACCTATGCACCAGACGTGCCTGGGGCTGGGAGTGCAGGACTGGGGCTCCAGGGGCTAGATCGGAAGAGCGGTTTCAG
chr9	101891087	101891126	TGFBR1_5328	-	GTGACCTATGCACCAGACGTAGAAAGATTCTTAGAAAAATCTCAAGGTTAACAGTTTGAAGATCGGAAGAGCGGTTTCAG
chr9	101894741	101894780	TGFBR1_5329	-	GTGACCTATGCACCAGACGTGCCCTGAGTGAATAACATCAACAACAGCAAAAACATGAGATCGGAAGAGCGGTTTCAG
chr9	101900091	101900130	TGFBR1_5330	-	GTGACCTATGCACCAGACGTAAATAAATAGTACTCAACAACATCAACAATATTACATGTTAGATCGGAAGAGCGGTTTCAG
chr9	101904768	101904807	TGFBR1_5331	-	GTGACCTATGCACCAGACGTGAATTAACATTTGCGTTGGGCTGCAGACCATTATGATTTAGATCGGAAGAGCGGTTTCAG
chr9	101906964	101907003	TGFBR1_5332	-	GTGACCTATGCACCAGACGTAAAAATTAACATGACTGCTTAAAAGTAAATCAACATCACAGATCGGAAGAGCGGTTTCAG
chr9	101908717	101908756	TGFBR1_5333	-	GTGACCTATGCACCAGACGTTTTGCAAAAAGAACTTTGAAAATCATCCCCTACTGCCATAGATCGGAAGAGCGGTTTCAG
chr9	101909886	101909925	TGFBR1_5334	-	GTGACCTATGCACCAGACGTTTAAAAAAATTAATTTTATGATTAATTTTACAGTAATGAGATCGGAAGAGCGGTTTCAG
chr10	102893882	102893921	TLX1_5335	-	GTGACCTATGCACCAGACGTTGTTAACAGTGAAGGGTGAGAGGCCACTGGAGCGGACAGATCGGAAGAGCGGTTTCAG
chr10	102896398	102896437	TLX1_5336	-	GTGACCTATGCACCAGACGTAAACAGCGTTACTGCCAGAGGCCAGCCAGCTCCCGAGATCGGAAGAGCGGTTTCAG

chr3	195591002	195591041	TNK2_5337	-	GTGACCTATGCACCAGACGTGAGAGCCAGAGGGCCTGCCTGAAGGAATCACCTGAGCCTGAGATCGGAAGAGCGGTTTCAG
chr3	195593710	195593749	TNK2_5338	-	GTGACCTATGCACCAGACGTCCACAGTCTGCCCGCTCCGTGCCCCAGGAGGGCTGTCAGATCGGAAGAGCGGTTTCAG
chr3	195593990	195594029	TNK2_5339	-	GTGACCTATGCACCAGACGTCTCCTGCTCACTCTGGCTCTCAGGGACCCTGAAGCCTGGTAGATCGGAAGAGCGGTTTCAG
chr3	195594182	195594221	TNK2_5340	-	GTGACCTATGCACCAGACGTAGCCTGGCTGTGGGCGAAGCGGGGCAGGGCCCAAGGGCCAGATCGGAAGAGCGGTTTCAG
chr3	195596318	195596357	TNK2_5341	-	GTGACCTATGCACCAGACGTCTGCTCCGATGCCTTGGCCCCGCCCCCGCCCTCTCTAGATCGGAAGAGCGGTTTCAG
chr3	195596935	195596974	TNK2_5342	-	GTGACCTATGCACCAGACGTCTCCTGGCTCCCTGGTGTCCCTAATCATCCGGCTACTCAGGAAGATCGGAAGAGCGGTTTCAG
chr3	195599097	195599136	TNK2_5343	-	GTGACCTATGCACCAGACGTGGCGGGTAGGATGCTGACCTGGCCCGCTCGGGACTCCAAGATCGGAAGAGCGGTTTCAG
chr3	195605074	195605113	TNK2_5344	-	GTGACCTATGCACCAGACGTGAGGGCTGGGCCGCCCTGGGATCGCTTGAAGGGCACAGAGATCGGAAGAGCGGTTTCAG
chr3	195605267	195605306	TNK2_5345	-	GTGACCTATGCACCAGACGTGGTCAGCCCAGGAGAGCTGGGGTGTTCAGCTGAGGGGCTAGATCGGAAGAGCGGTTTCAG
chr3	195605870	195605909	TNK2_5346	-	GTGACCTATGCACCAGACGTGGAGACGGGCCCCATAGGGCTGGTGGGGTGAATTCCATTAGATCGGAAGAGCGGTTTCAG
chr3	195608872	195608911	TNK2_5347	-	GTGACCTATGCACCAGACGTGGTGCCTGCCAGCTCACAGAGTCCCTGCAGACCCAGGCCTCAGATCGGAAGAGCGGTTTCAG
chr3	195609978	195610017	TNK2_5348	-	GTGACCTATGCACCAGACGTGGCGGGAGGGGGCGGGCAGGGAGAGGGCTCCGGTCCCAAGATCGGAAGAGCGGTTTCAG
chr3	195611633	195611672	TNK2_5349	-	GTGACCTATGCACCAGACGTGTGTCTGCCAGCCAGCAGAGGCGATGGGACCCGGGGCTAGATCGGAAGAGCGGTTTCAG
chr3	195615247	195615286	TNK2_5350	-	GTGACCTATGCACCAGACGTGTTGGCCTGGCTTGTCTTGCCTTACCCTTTCCGTCTTAGATCGGAAGAGCGGTTTCAG
chr3	195622067	195622106	TNK2_5351	-	GTGACCTATGCACCAGACGTAGGCTAGGGATAGCCAGATACCTGGGCCCCAGACCCCTTAGATCGGAAGAGCGGTTTCAG
chr3	195594631	195594670	TNK2_5352	-	GTGACCTATGCACCAGACGTCCAGAGCTTTGCCTCAGACCCCAAGTACGCCACCCCCAGAGATCGGAAGAGCGGTTTCAG
chr3	195595080	195595119	TNK2_5353	-	GTGACCTATGCACCAGACGTAACTACGCCTTTGTCCCTGAGCAGGGCGCCGCCCTCAGATCGGAAGAGCGGTTTCAG
chr19	54072581	54072620	ZNF331_5354	-	GTGACCTATGCACCAGACGTGTAAGAACTGTAGCTTCTCGGGTTTCCACTGAAGAAGATCGGAAGAGCGGTTTCAG
chr19	54074808	54074847	ZNF331_5355	-	GTGACCTATGCACCAGACGTAAACCACACGTGCATGAAATGAAAGGAAACAGCTTCCAGATCGGAAGAGCGGTTTCAG
chr19	54079901	54079940	ZNF331_5356	-	GTGACCTATGCACCAGACGTAGAACATATTTCTTTCTTTAGAGGGACACAAGTACAAAAGATCGGAAGAGCGGTTTCAG
chr19	54080319	54080358	ZNF331_5357	-	GTGACCTATGCACCAGACGTATGAATTTTTGATGTTGAGTAAGCTGATTGCCCAACGAGATCGGAAGAGCGGTTTCAG
chr19	54080737	54080776	ZNF331_5358	-	GTGACCTATGCACCAGACGTGGATCTTCTGTAGTGTAGTAAGGTAATTGACTCGAGTAAAGATCGGAAGAGCGGTTTCAG
chr11	10327198	10327237	ADM_5359	-	GTGACCTATGCACCAGACGTAAAGCGACCCCTGAAAAGAAGAAGAGAGTCGAGCGTGAGATCGGAAGAGCGGTTTCAG
chr11	10327446	10327485	ADM_5360	-	GTGACCTATGCACCAGACGTCAAGCAGCCGATTCGCGTCCAGTCAAGTACGCCACGGAGATCGGAAGAGCGGTTTCAG
chr11	10327829	10327868	ADM_5361	-	GTGACCTATGCACCAGACGTGGGGAGGGGAAGAAAGGCAACTTGAGACCCCATCAAGCAAGATCGGAAGAGCGGTTTCAG
chr14	20923755	20923794	APEX1_5362	-	GTGACCTATGCACCAGACGTAAAGCCCTTGGGCAGCTGTACCGCTCACCCACCGAAGCAAGATCGGAAGAGCGGTTTCAG
chr14	20924023	20924062	APEX1_5363	-	GTGACCTATGCACCAGACGTAGTAATATATACTGACAAAAAGCTGGTGGTTTTCCAACCTCAGATCGGAAGAGCGGTTTCAG
chr14	20924777	20924816	APEX1_5364	-	GTGACCTATGCACCAGACGTAAAGAAAGTGGGAAAACGTATTATCAATTCAGCAGAACATAGATCGGAAGAGCGGTTTCAG
chr14	20925100	20925139	APEX1_5365	-	GTGACCTATGCACCAGACGTGAAAAGAGATTAGCATAAAAAATAAGAAAAGGAAAGATCGGAAGAGCGGTTTCAG
chr14	20925359	20925398	APEX1_5366	-	GTGACCTATGCACCAGACGTACTTCTTTTTTTCCCTTGGGGTTCGAAGGTCAATTTTTCAGATCGGAAGAGCGGTTTCAG
chr19	41725248	41725287	AXL_5367	-	GTGACCTATGCACCAGACGTCTTCTCAGAAGTGTGGGGCTCCCAGCGGGGAGGGGGAGATCGGAAGAGCGGTTTCAG
chr19	41726491	41726530	AXL_5368	-	GTGACCTATGCACCAGACGTGATGGGAAGAGTTAGCTTAGGAACCCCCAGCTCCTTCCGAGATCGGAAGAGCGGTTTCAG
chr19	41727001	41727040	AXL_5369	-	GTGACCTATGCACCAGACGTAAAGAGGAGACAGAGAGGTTTCAGGGTTCAGAGCTGGACACAGATCGGAAGAGCGGTTTCAG
chr19	41727735	41727774	AXL_5370	-	GTGACCTATGCACCAGACGTGGGCAGTGGTAGAGGCTGGGGTCCCTCTGAGGCCCAAGAAGATCGGAAGAGCGGTTTCAG
chr19	41736822	41736861	AXL_5371	-	GTGACCTATGCACCAGACGTATATGAGGGGAAGGTTCCAATATCAGAGAGGGGCAGGAAGGATCGGAAGAGCGGTTTCAG
chr19	41737038	41737077	AXL_5372	-	GTGACCTATGCACCAGACGTACGGGAGAGATTGACCCTGGGGAGCCTTTGCTCAAAGCTCAGATCGGAAGAGCGGTTTCAG
chr19	41743799	41743838	AXL_5373	-	GTGACCTATGCACCAGACGTGCAAGGGTGTGAGGACGGGACAGCAAGCAATCACACGAGATCGGAAGAGCGGTTTCAG
chr19	41744325	41744364	AXL_5374	-	GTGACCTATGCACCAGACGTGGGAAGAGGGGAGCTGGCACCCCCACCTTCCCTGACCCAGATCGGAAGAGCGGTTTCAG
chr19	41745019	41745058	AXL_5375	-	GTGACCTATGCACCAGACGTCAAGAAGTGGATCAGGGTAGAACCTTACCCCCAGCTGTTAGATCGGAAGAGCGGTTTCAG
chr19	41745549	41745588	AXL_5376	-	GTGACCTATGCACCAGACGTAAAGGACAGAGGAGATGTGCTCAGAGAGGACAAGATGAGATCGGAAGAGCGGTTTCAG
chr19	41748738	41748777	AXL_5377	-	GTGACCTATGCACCAGACGTGTATGAGGAACAGGTGATGAGGCTTGGATCCAGCTAGATCGGAAGAGCGGTTTCAG
chr19	41749471	41749510	AXL_5378	-	GTGACCTATGCACCAGACGTGGGGGAGTAGGTGAGGGCAGGGAAAACCATGTGGAACCCAGATCGGAAGAGCGGTTTCAG
chr19	41754598	41754637	AXL_5379	-	GTGACCTATGCACCAGACGTCCAGAGGGAGACACTGACCTCAGAGGGCCCGTGGGGACTGAGATCGGAAGAGCGGTTTCAG
chr19	41758206	41758245	AXL_5380	-	GTGACCTATGCACCAGACGTAGAGAAAGTTCGTGAGGAGGAGGGGAGGAGGGGAGGACTAGATCGGAAGAGCGGTTTCAG
chr19	41758701	41758740	AXL_5381	-	GTGACCTATGCACCAGACGTGAGTAGCCCTGTCACTCTGTCTGGGCAGAAAGGCCAGATCGGAAGAGCGGTTTCAG
chr19	41759454	41759493	AXL_5382	-	GTGACCTATGCACCAGACGTGAAGCAGGTGAGGAGGAGGACTAACAGAGTCCCTTGTAGCGAGATCGGAAGAGCGGTTTCAG
chr19	41762307	41762346	AXL_5383	-	GTGACCTATGCACCAGACGTGGGGAAAAGGAACAGGGTCAGGGCATCAGTACCTCCACCAGATCGGAAGAGCGGTTTCAG
chr19	41763348	41763387	AXL_5384	-	GTGACCTATGCACCAGACGTGAGAGGAATTAGACAGTCTCTCTGCACAGAATCACCCAGATCGGAAGAGCGGTTTCAG
chr19	41765408	41765447	AXL_5385	-	GTGACCTATGCACCAGACGTAAAATGAGGGGTGGGAGATTGAGCAGGGACTCAGAAGGGGAGATCGGAAGAGCGGTTTCAG
chr11	102195191	102195230	BIRC3_5386	-	GTGACCTATGCACCAGACGTATGGGGAAGAAAAGGGACTAGCCTTTCTTAGGGAGGTAGATCGGAAGAGCGGTTTCAG
chr11	102196147	102196186	BIRC3_5387	-	GTGACCTATGCACCAGACGTGTTTATGACAAAACTATGAAATACATAATTTGCCCACTAGATCGGAAGAGCGGTTTCAG
chr11	102198733	102198772	BIRC3_5388	-	GTGACCTATGCACCAGACGTGAAAAGAAATAAAATTTAGGGATATTATACAAGTGAATAAGATCGGAAGAGCGGTTTCAG
chr11	102201680	102201719	BIRC3_5389	-	GTGACCTATGCACCAGACGTCAAAGAATTTAACACATATTAGGATAGCCTTATATTTCTTAGATCGGAAGAGCGGTTTCAG
chr11	102206647	102206686	BIRC3_5390	-	GTGACCTATGCACCAGACGTAAAGAAAACAGCATAAACATGTTCAAACCTCTGCTCACAAAAGATCGGAAGAGCGGTTTCAG
chr11	102207441	102207480	BIRC3_5391	-	GTGACCTATGCACCAGACGTAAAAGAAAAGCATTACTATGACAAATAAGGTTAATATTAGATCGGAAGAGCGGTTTCAG
chr11	102207590	102207629	BIRC3_5392	-	GTGACCTATGCACCAGACGTGAAAGAATTTTAAATAAAAGGCAGTTTGTCTTTCAGTGAAGATCGGAAGAGCGGTTTCAG
chr11	102195617	102195656	BIRC3_5393	-	GTGACCTATGCACCAGACGTGAAGAAAGCTCAGCCACGAAATTAACCTGTTTTCTGTACCCGAGATCGGAAGAGCGGTTTCAG
chr14	54418521	54418560	BMP4_5394	-	GTGACCTATGCACCAGACGTTCACCCAGCTGCGTGGGGAGGGCTGGTGGGACTGGCTAAGATCGGAAGAGCGGTTTCAG

chr14	54417128	54417167	BMP4_5395	-	GTGACCTATGCACCAGACGTCCTCCTGGTACACCTTTGGCCATGATGGCCGGGGCCATGCCAGATCGGAAGAGCGGTTTCAG
chr10	88635726	88635765	BMPR1A_5396	-	GTGACCTATGCACCAGACGTTAATGTTTCTGTACTGTACCTTTAATAATTGGTCTTAGATCGGAAGAGCGGTTTCAG
chr10	88649769	88649808	BMPR1A_5397	-	GTGACCTATGCACCAGACGTATATGGAATTTGTAAGTAAATCATTTCTGAAAAGCTCATTAGATCGGAAGAGCGGTTTCAG
chr10	88659501	88659540	BMPR1A_5398	-	GTGACCTATGCACCAGACGTAGTAATGATAAAATAGAAATGGTTGGTATTTAAACTGAGATCGGAAGAGCGGTTTCAG
chr10	88659734	88659773	BMPR1A_5399	-	GTGACCTATGCACCAGACGTAAGTAAACAATGTAAACAATTTGAAATGAAAAAATAATCTGAGATCGGAAGAGCGGTTTCAG
chr10	88671947	88671986	BMPR1A_5400	-	GTGACCTATGCACCAGACGTAGCAGAAAACAATCTACATTTAAAAATGAAAAACTATAAAAAAGATCGGAAGAGCGGTTTCAG
chr10	88676841	88676880	BMPR1A_5401	-	GTGACCTATGCACCAGACGTTAAAAGTAAAAGGTTTGAGCTTTGATGAAAGAAAACCCATTAGATCGGAAGAGCGGTTTCAG
chr10	88678879	88678918	BMPR1A_5402	-	GTGACCTATGCACCAGACGTGATGAGTTTAAAAGGTTAGTTATCATCAGAGATAGGCTAGAGATCGGAAGAGCGGTTTCAG
chr10	88681227	88681266	BMPR1A_5403	-	GTGACCTATGCACCAGACGTAGAAAAGCAAGGTCCAAGTTGAGGGCCAAAATAAAATAGAGATCGGAAGAGCGGTTTCAG
chr10	88683083	88683122	BMPR1A_5404	-	GTGACCTATGCACCAGACGTATGAGAAAACATGGGCACAAAATGGTTGCTGGACAAGATAGATCGGAAGAGCGGTTTCAG
chr10	88683301	88683340	BMPR1A_5405	-	GTGACCTATGCACCAGACGTAAGAGATGTTCACTGAGCAGAGAATATATTTGGTGGCATTAGATCGGAAGAGCGGTTTCAG
chr3	48200385	48200424	CDC25A_5406	-	GTGACCTATGCACCAGACGTACCAGCCAGCAGCCCAAGCTTCCCTCCATCCCCCTTTAGATCGGAAGAGCGGTTTCAG
chr3	48200784	48200823	CDC25A_5407	-	GTGACCTATGCACCAGACGTGGTGTGGAGAGCATCTCTCCCTGCCCCAGTGGTAAGATCGGAAGAGCGGTTTCAG
chr3	48205747	48205786	CDC25A_5408	-	GTGACCTATGCACCAGACGTACGGAACTGGGTTCTGGGGCACAGGCTCCATGATGCTTTAGATCGGAAGAGCGGTTTCAG
chr3	48207076	48207115	CDC25A_5409	-	GTGACCTATGCACCAGACGTCTGAGACTTGCTGTAGAAGGAGCCCTAACAGGATCTGTGAGATCGGAAGAGCGGTTTCAG
chr3	48207271	48207310	CDC25A_5410	-	GTGACCTATGCACCAGACGTCTTTTGAACCCACCACACATCGGGTACTTGAATCTAGTAGATCGGAAGAGCGGTTTCAG
chr3	48209286	48209325	CDC25A_5411	-	GTGACCTATGCACCAGACGTGCAGAGCTGCTCTGGCAAGTGTAGGAGGGAGTGGGTTATAGATCGGAAGAGCGGTTTCAG
chr3	48218811	48218850	CDC25A_5412	-	GTGACCTATGCACCAGACGTCTAGTGCTGTGGAGAACGCTCGTGATTGGGGCACTGAGATCGGAAGAGCGGTTTCAG
chr3	48219294	48219333	CDC25A_5413	-	GTGACCTATGCACCAGACGTTGTGTGTGTGTTTCTATTGTTCTACTAATTAATACCAGATCGGAAGAGCGGTTTCAG
chr3	48222161	48222200	CDC25A_5414	-	GTGACCTATGCACCAGACGTTGGCTTTTATAGGGGAATTCCTGACAGGAAGAAAGGATTAAGATCGGAAGAGCGGTTTCAG
chr3	48224369	48224408	CDC25A_5415	-	GTGACCTATGCACCAGACGTCTCAATGTACTAACCTGAGGCAGAGGTGAAACCCACAGGAGATCGGAAGAGCGGTTTCAG
chr3	48225240	48225279	CDC25A_5416	-	GTGACCTATGCACCAGACGTTCCCTTGTATTTTATTTGAGCTAATACCTGTTATCTGTTCTTAGATCGGAAGAGCGGTTTCAG
chr3	48226093	48226132	CDC25A_5417	-	GTGACCTATGCACCAGACGTACTGCTTTCAAATGTTTATATGTAAGAAAACGTGTCTAAAGATCGGAAGAGCGGTTTCAG
chr3	48228143	48228182	CDC25A_5418	-	GTGACCTATGCACCAGACGTCTGTGTTGGGGCAATACTTGAATTTCTGAAACATAGATCGGAAGAGCGGTTTCAG
chr3	48229218	48229257	CDC25A_5419	-	GTGACCTATGCACCAGACGTACCGGCGGGCGGTGCTCCGGGCCCTGGCCTCGGTGTGCGGATCGGAAGAGCGGTTTCAG
chr2	175666385	175666424	CHN1_5420	-	GTGACCTATGCACCAGACGTGACTTTGAGTCTTACACTTGTATTGCATCCAAATTTAAGAGATCGGAAGAGCGGTTTCAG
chr2	175673583	175673622	CHN1_5421	-	GTGACCTATGCACCAGACGTATGCATGATTTCAAATAACCTGACAACGTCTCTTGGTAAGATCGGAAGAGCGGTTTCAG
chr2	175676189	175676228	CHN1_5422	-	GTGACCTATGCACCAGACGTACAGATGTTCCATACTTAGGACAATAACTCTTTTCTAAGATCGGAAGAGCGGTTTCAG
chr2	175676987	175677026	CHN1_5423	-	GTGACCTATGCACCAGACGTTGCAGTCGGGGTTCGAGTGGTCTCCGTCTACTACCAGTACAGATCGGAAGAGCGGTTTCAG
chr2	175689112	175689151	CHN1_5424	-	GTGACCTATGCACCAGACGTTTGCTTTGTCTCTGATTGAGTCAAGTTGTGAAGTTATAAGATCGGAAGAGCGGTTTCAG
chr2	175711558	175711597	CHN1_5425	-	GTGACCTATGCACCAGACGTTTGCTTTTGTCTTTAAGAAATGCATATTACTTGAATAAGATCGGAAGAGCGGTTTCAG
chr2	175742518	175742557	CHN1_5426	-	GTGACCTATGCACCAGACGTATGAAACCACACTTATCTTTTTCTGTTTGGGGTCTTTTAGATCGGAAGAGCGGTTTCAG
chr2	175779736	175779775	CHN1_5427	-	GTGACCTATGCACCAGACGTGGCCTGCAATTACTACTGTGCTTTATTTAAACTCTCTAAGATCGGAAGAGCGGTTTCAG
chr2	175783212	175783251	CHN1_5428	-	GTGACCTATGCACCAGACGTATTTAGAAAACCTTTTATAGATTGGCATATGAAGCAAGATCGGAAGAGCGGTTTCAG
chr2	175809566	175809605	CHN1_5429	-	GTGACCTATGCACCAGACGTTGAAACTGCTACCAAAATAATGCTCTCAACATCTGTTTTCAGATCGGAAGAGCGGTTTCAG
chr2	175816842	175816881	CHN1_5430	-	GTGACCTATGCACCAGACGTAAATAATTGTGTGGTTATAGTGCTTTATAAGTAATATAAGATCGGAAGAGCGGTTTCAG
chr2	175869572	175869611	CHN1_5431	-	GTGACCTATGCACCAGACGTCCGCTCCCCCGCGCCGCCAGGTGGGCCCGCTCCCGGGGAGATCGGAAGAGCGGTTTCAG
chr12	57910542	57910581	DDIT3_5432	-	GTGACCTATGCACCAGACGTGCATCAGTCCCCACTTGGGCCACACTACCACCTTTCCAGATCGGAAGAGCGGTTTCAG
chr12	57911002	57911041	DDIT3_5433	-	GTGACCTATGCACCAGACGTTAGCCCTAAAGCTAAAGGGGGATGTTACCTTTCCCTTCTCAGATCGGAAGAGCGGTTTCAG
chr3	185867829	185867868	DGKG_5434	-	GTGACCTATGCACCAGACGTTAAACACCAGCTAAACCAAGAGAGAAAGCAAGAAACTATAAGATCGGAAGAGCGGTTTCAG
chr3	185879342	185879381	DGKG_5435	-	GTGACCTATGCACCAGACGTTCCAATCTTGTAGATGGGATGAGAAGCCTTATTTTTGAGCAGATCGGAAGAGCGGTTTCAG
chr3	185882637	185882676	DGKG_5436	-	GTGACCTATGCACCAGACGTTTGTACCCAACAGCCTCTGCATCTCCCCGCTGCGTACAAGATCGGAAGAGCGGTTTCAG
chr3	185905941	185905980	DGKG_5437	-	GTGACCTATGCACCAGACGTAATGAGGATAATTGTTTTAGGTCAATGCCAGTAGTAGGTAGATCGGAAGAGCGGTTTCAG
chr3	185929534	185929573	DGKG_5438	-	GTGACCTATGCACCAGACGTAAGTGGGGAGAAGGCTTCTGGATCTTGGTTCTGCTCTCAGATCGGAAGAGCGGTTTCAG
chr3	185960243	185960282	DGKG_5439	-	GTGACCTATGCACCAGACGTGGCCCCGGTGGCTGCCACCCACCCAGTGTGGCCCTGGCGAGATCGGAAGAGCGGTTTCAG
chr3	185969498	185969537	DGKG_5440	-	GTGACCTATGCACCAGACGTCAAAGCTCAACCTTCTGTATGAAAGGGAACCGCCAGAAAGATCGGAAGAGCGGTTTCAG
chr3	185970832	185970871	DGKG_5441	-	GTGACCTATGCACCAGACGTATGCTAATGGTGGTACCCTGGGAACAGGTGTTCTGTTAAGATCGGAAGAGCGGTTTCAG
chr3	185975593	185975632	DGKG_5442	-	GTGACCTATGCACCAGACGTGCTGAGAGGGCGTTTGTGCTTATTTATAGTAAGCGTATTAGATCGGAAGAGCGGTTTCAG
chr3	185978178	185978217	DGKG_5443	-	GTGACCTATGCACCAGACGTACAACTTTTACCTTATTTCTCCCTCCCTTTTAAACAGATCGGAAGAGCGGTTTCAG
chr3	185979438	185979477	DGKG_5444	-	GTGACCTATGCACCAGACGTTTCTGTTTCAAAGTGGAGCAACTAGGGCGACACGACTCAGAGATCGGAAGAGCGGTTTCAG
chr3	185982986	185983025	DGKG_5445	-	GTGACCTATGCACCAGACGTAGCTCAAATCCGATGCACCTTCTAAGTTGTTCCAGGGCAGATCGGAAGAGCGGTTTCAG
chr3	185985424	185985463	DGKG_5446	-	GTGACCTATGCACCAGACGTGCCCCGGCAGGGCTGTAGCTTCTCCGGTTCTGGTTTTCAGATCGGAAGAGCGGTTTCAG
chr3	185986540	185986579	DGKG_5447	-	GTGACCTATGCACCAGACGTGCCCCAGGGCGGCCCTGCTTCTTTTCAACGTTTTTTTTGCCAGATCGGAAGAGCGGTTTCAG
chr3	185989994	185990033	DGKG_5448	-	GTGACCTATGCACCAGACGTTCTACTGCCTTGTCTACTGCATGCCTCATCCAGAAACAAGATCGGAAGAGCGGTTTCAG
chr3	185993286	185993325	DGKG_5449	-	GTGACCTATGCACCAGACGTTTCTTCAAACCTCTTCCCCCGGCACTATCTTGTCTGCAGATCGGAAGAGCGGTTTCAG
chr3	185997590	185997629	DGKG_5450	-	GTGACCTATGCACCAGACGTTAAGCTGGAGTTTCAGAGATCTTGCCATTTCAGGAACATTGAGATCGGAAGAGCGGTTTCAG
chr3	185998409	185998448	DGKG_5451	-	GTGACCTATGCACCAGACGTATAAGGATGGGGTGCTTTGAGTGGAGCTTCTAAGACAGATCGGAAGAGCGGTTTCAG
chr3	186002399	186002438	DGKG_5452	-	GTGACCTATGCACCAGACGTACTCTAAATATCCCTCATGGAGCTGAGAAAGGCTGGGGGAAGATCGGAAGAGCGGTTTCAG

chr3	186006449	186006488	DGKG_5453	-	GTGACCTATGCACCAGACGTACCTGTCAAGGGGCTTCAGCTTTTTCTAGAGAAGGATCAGATCGGAAGAGCGGTTTCAG
chr3	186015160	186015199	DGKG_5454	-	GTGACCTATGCACCAGACGTGGAATATAAGACTTGTGGGAAAAGTAGGGAATACCTCATCAGATCGGAAGAGCGGTTTCAG
chr3	186015803	186015842	DGKG_5455	-	GTGACCTATGCACCAGACGTCTTTCCCAAGATGGGAAGACCTTGCGCAGCTCTCATCCCAGATCGGAAGAGCGGTTTCAG
chr3	186024640	186024679	DGKG_5456	-	GTGACCTATGCACCAGACGTTCATTTTAAAGCCTTAAAAACCCTGTGTTTTTTAGCCAGATCGGAAGAGCGGTTTCAG
chr3	186038132	186038171	DGKG_5457	-	GTGACCTATGCACCAGACGTGCATTGACAGCCCTGGGACGGGATTTCTTCTGGCTGGAGAGATCGGAAGAGCGGTTTCAG
chr8	120569711	120569750	ENPP2_5458	-	GTGACCTATGCACCAGACGTATCTGCAGTACAGTCTTATCACTGGTTGTATATTTTTATAGATCGGAAGAGCGGTTTCAG
chr8	120575047	120575086	ENPP2_5459	-	GTGACCTATGCACCAGACGTAGAGAGTCCCTTTAGGATTGTCCATAGTTTCCACTTCAGATCGGAAGAGCGGTTTCAG
chr8	120577013	120577052	ENPP2_5460	-	GTGACCTATGCACCAGACGTCACTTCTACTCAGTGTGTGATTTTTAAGTCCCAAGATCTCAGATCGGAAGAGCGGTTTCAG
chr8	120580365	120580404	ENPP2_5461	-	GTGACCTATGCACCAGACGTATTTACCTAATACTGTTATTTATGAAAATAAACATTTAGATCGGAAGAGCGGTTTCAG
chr8	120581425	120581464	ENPP2_5462	-	GTGACCTATGCACCAGACGTAAATCAAGATCTGATGCCTTCAGAGGGATGTCACATTGTAGATCGGAAGAGCGGTTTCAG
chr8	120584366	120584405	ENPP2_5463	-	GTGACCTATGCACCAGACGTAGTTTTGAAGGAAAAGCTGGGTTGTTTTACTGCCCTTAAGAGATCGGAAGAGCGGTTTCAG
chr8	120592306	120592345	ENPP2_5464	-	GTGACCTATGCACCAGACGTGTGCAAAAATACAGATAAGGTTTTCTCGTTTTCGAAAAGATCGGAAGAGCGGTTTCAG
chr8	120595907	120595946	ENPP2_5465	-	GTGACCTATGCACCAGACGTCAATTAATCAGAACCATTGAACAACATCTTAGTTAGTATAAGATCGGAAGAGCGGTTTCAG
chr8	120596152	120596191	ENPP2_5466	-	GTGACCTATGCACCAGACGTAGAAGTGTGAATTGTGTTTTAGTGGTCTTCGAAAAGATCGGAAGAGCGGTTTCAG
chr8	120598376	120598415	ENPP2_5467	-	GTGACCTATGCACCAGACGTTATGGGCTATTTCTGTTTTCTCATTTCCACAACCACCCCTTAGATCGGAAGAGCGGTTTCAG
chr8	120599234	120599273	ENPP2_5468	-	GTGACCTATGCACCAGACGTCCAGTTGTCCCGCCTCGCCCTGCCACAGCCCTCGCCCTAGATCGGAAGAGCGGTTTCAG
chr8	120605942	120605981	ENPP2_5469	-	GTGACCTATGCACCAGACGTGTTTTTTCTTGCTAATAGGATAGATGGATAATGTTTTCTGAGATCGGAAGAGCGGTTTCAG
chr8	120608037	120608076	ENPP2_5470	-	GTGACCTATGCACCAGACGTCTATTGTCTTCAAGCTTTGTGGCGGGCAGGTCTGAGTTGAAGATCGGAAGAGCGGTTTCAG
chr8	120612868	120612907	ENPP2_5471	-	GTGACCTATGCACCAGACGTTAGCATCTGCCTGAGAAGAATCTGTGGCCTGGGCTACCTAGATCGGAAGAGCGGTTTCAG
chr8	120613587	120613626	ENPP2_5472	-	GTGACCTATGCACCAGACGTCTCTCTTTCTCTTTCTTCAGTACATTTCTATCTTAGATCGGAAGAGCGGTTTCAG
chr8	120620112	120620151	ENPP2_5473	-	GTGACCTATGCACCAGACGTTTTTATTTTGCAATGTTTATAAAATGACAGCTATGATCAAGATCGGAAGAGCGGTTTCAG
chr8	120628455	120628494	ENPP2_5474	-	GTGACCTATGCACCAGACGTCACTTATTGTGTCTATGTGTTTTGTGTGTTTATGATTAGATCGGAAGAGCGGTTTCAG
chr8	120629354	120629393	ENPP2_5475	-	GTGACCTATGCACCAGACGTGTTTGAATGATACACATTCAAAAGGCTGATTTTCATCCGGAGATCGGAAGAGCGGTTTCAG
chr8	120629656	120629695	ENPP2_5476	-	GTGACCTATGCACCAGACGTCCATCTCTGTCTTATCTGTAATCTGCATCTCCACAGATCGGAAGAGCGGTTTCAG
chr8	120631434	120631473	ENPP2_5477	-	GTGACCTATGCACCAGACGTTTTATGACTATTTTGAAGTTTTATGATTAGCTGATAAACAGATCGGAAGAGCGGTTTCAG
chr8	120633584	120633623	ENPP2_5478	-	GTGACCTATGCACCAGACGTCTTTGGATTGGCCTGAGCTTTAAAAGAATAAAAACGGAGATCGGAAGAGCGGTTTCAG
chr8	120638755	120638794	ENPP2_5479	-	GTGACCTATGCACCAGACGTTATGAGTCCCTCTACTTCAAGTAGATGGCTTAAAGACTAGATCGGAAGAGCGGTTTCAG
chr8	120650615	120650654	ENPP2_5480	-	GTGACCTATGCACCAGACGTAAGTATTTGCATTTTCAATTTTTAAAAATATACATACAGATCGGAAGAGCGGTTTCAG
chr8	120650938	120650977	ENPP2_5481	-	GTGACCTATGCACCAGACGTGGAGGATACGGGGGACCTGTTGATCTTCAGAATCAGTAGATCGGAAGAGCGGTTTCAG
chr1	16451660	16451699	EPHA2_5482	-	GTGACCTATGCACCAGACGTGGCCTGTGAGGCCCCCAGCCAAAGATACTTGAAGAAAACAGATCGGAAGAGCGGTTTCAG
chr1	16455879	16455918	EPHA2_5483	-	GTGACCTATGCACCAGACGTCCCTTTCCGTCCCCCTCGCCTCCCGCCTCCCACTCCAGATCGGAAGAGCGGTTTCAG
chr1	16456671	16456710	EPHA2_5484	-	GTGACCTATGCACCAGACGTGGCCTCTGCCCATGATGACCTCAATTTTCTTCTGCAGAAGATCGGAAGAGCGGTTTCAG
chr1	16458166	16458205	EPHA2_5485	-	GTGACCTATGCACCAGACGTTTGCCTCCCAAGCCCTGCTCCGACCTGAACCTAAGCCCTAGATCGGAAGAGCGGTTTCAG
chr1	16458509	16458548	EPHA2_5486	-	GTGACCTATGCACCAGACGTGAAGGGGACCTCAAGGGAGAAGCGCCCTCCGCCCTGCATGAGATCGGAAGAGCGGTTTCAG
chr1	16458823	16458862	EPHA2_5487	-	GTGACCTATGCACCAGACGTGAGGGTGTAGGGGGGGGATGCCTGACCATTGAGCCCGGGAGATCGGAAGAGCGGTTTCAG
chr1	16459625	16459664	EPHA2_5488	-	GTGACCTATGCACCAGACGTGGGCCTGCCACACTGGGTGGAGAGGGGCCACTTAGCAGGAGATCGGAAGAGCGGTTTCAG
chr1	16459926	16459965	EPHA2_5489	-	GTGACCTATGCACCAGACGTCCCTGCCAAGGGGCCCTGAGGAGGCAGCGGTGGTGACAAGATCGGAAGAGCGGTTTCAG
chr1	16460305	16460344	EPHA2_5490	-	GTGACCTATGCACCAGACGTGCCCTCCAGGCCAGCCCTGCCCGCACCCTCCAGAGATCGGAAGAGCGGTTTCAG
chr1	16460913	16460952	EPHA2_5491	-	GTGACCTATGCACCAGACGTGCCATACCCTGGCTCCACATGGGCTGGGTGGGAAAATGAGATCGGAAGAGCGGTTTCAG
chr1	16461481	16461520	EPHA2_5492	-	GTGACCTATGCACCAGACGTGGACCTGGGCTGGACAGCCAGGCCACAGCCAGAACGACATCGGAAGAGCGGTTTCAG
chr1	16462100	16462139	EPHA2_5493	-	GTGACCTATGCACCAGACGTGAGGGGGGGGCTGGCTTAGCTGGGCCGACAGCAAGGGGAAGATCGGAAGAGCGGTTTCAG
chr1	16464298	16464337	EPHA2_5494	-	GTGACCTATGCACCAGACGTGGGGTGGCAGCTGTGCCCTATGGGGCTGCCAGGTGGGGAGATCGGAAGAGCGGTTTCAG
chr1	16464720	16464759	EPHA2_5495	-	GTGACCTATGCACCAGACGTGAGTGGGTGAGGGTGGCCTGACTGAGGGTGACGTGTCAGATCGGAAGAGCGGTTTCAG
chr1	16474823	16474862	EPHA2_5496	-	GTGACCTATGCACCAGACGTGTTCTGGGTTGACGGGAAGGGGTTCTGCATTTCCAGGTTAGATCGGAAGAGCGGTTTCAG
chr1	16482293	16482332	EPHA2_5497	-	GTGACCTATGCACCAGACGTGGCGGCTGGACCCCTGGCCCGCCCGCCCGCCAGATGCCCCAGATCGGAAGAGCGGTTTCAG
chr1	16475158	16475197	EPHA2_5498	-	GTGACCTATGCACCAGACGTGAGCGCTCCGTTGGGGCCCTCCAGCAAGGCTTACCAGATCGGAAGAGCGGTTTCAG
chr21	40181909	40181948	ETS2_5499	-	GTGACCTATGCACCAGACGTAAAAAAGTCAAAGAGGCCAAAAGATTAAGTACACTAAGATCGGAAGAGCGGTTTCAG
chr21	40184877	40184916	ETS2_5500	-	GTGACCTATGCACCAGACGTAGATGAAAAAATGAAATACAATTTAAACTGATTGAGATCGGAAGAGCGGTTTCAG
chr21	40186147	40186186	ETS2_5501	-	GTGACCTATGCACCAGACGTACCCTCCATGGGACATTAGGACTTCAAGTTGGTGATATCAGATCGGAAGAGCGGTTTCAG
chr21	40186655	40186694	ETS2_5502	-	GTGACCTATGCACCAGACGTAGAAGAAAAATGAAACACATGAGGTAACAAACAGTGGAAAAGATCGGAAGAGCGGTTTCAG
chr21	40188882	40188921	ETS2_5503	-	GTGACCTATGCACCAGACGTGACACAGGAGACGTAAGATGCCAGATGAGTGAAGTAAAACTAAGATCGGAAGAGCGGTTTCAG
chr21	40190299	40190338	ETS2_5504	-	GTGACCTATGCACCAGACGTACAATCGAGCCAGGACGCTCTTAAAGTCAAGTGTACCCTAGATCGGAAGAGCGGTTTCAG
chr21	40191377	40191416	ETS2_5505	-	GTGACCTATGCACCAGACGTCAACCAACACATACTTTGATTCCTCCAGGACACAGTTGGAGATCGGAAGAGCGGTTTCAG
chr21	40193460	40193499	ETS2_5506	-	GTGACCTATGCACCAGACGTAGGGAGGGAGACGGATCATACCCTTTCACAGATGTAATAATAGATCGGAAGAGCGGTTTCAG
chr21	40194548	40194587	ETS2_5507	-	GTGACCTATGCACCAGACGTGATGGTGAAGAAAGTAAACTCAATTTGTAATGAAGAAGATCGGAAGAGCGGTTTCAG
chr3	59737902	59737941	FHIT_5508	-	GTGACCTATGCACCAGACGTGATGCACTTTCGTCAATACCAGACCCCTCCGTTGGGCTCAGATCGGAAGAGCGGTTTCAG
chr3	59908022	59908061	FHIT_5509	-	GTGACCTATGCACCAGACGTCTCTGTATCTTTGTTTTGATCAGCGGACTGTCGGTGAAGAGCGGTTTCAG
chr3	59997047	59997086	FHIT_5510	-	GTGACCTATGCACCAGACGTTATTTGTGCATACAATAAATGAGAGCGGATTATGAGAACAGATCGGAAGAGCGGTTTCAG

chr3	59999683	59999722	FHIT_5511	-	GTGACCTATGCACCAGACGTAGATTTCTCAGAAATGATTTTTCTCCCTTTCATATCCCGAGATCGGAAGAGCGGTTTCAG
chr3	60522543	60522582	FHIT_5512	-	GTGACCTATGCACCAGACGTTTTTTTTTTTTTTGGAGAGGGAAAATAAAAAGTCTTCTGAGCCAGATCGGAAGAGCGGTTTCAG
chr15	91418921	91418960	FURIN_5513	-	GTGACCTATGCACCAGACGTGGTGGCTGGGACCCTGGAGCGCCGCTCCTTGGCCTGGTAGATCGGAAGAGCGGTTTCAG
chr15	91419435	91419474	FURIN_5514	-	GTGACCTATGCACCAGACGTGCAGGGAGACTGAGCTGGGCTTCCATCTGTGAGTCCCGAGATCGGAAGAGCGGTTTCAG
chr15	91419642	91419681	FURIN_5515	-	GTGACCTATGCACCAGACGTGTGAGGGAGAGATGGTGTGGGTGGAGCAGGAGGCGAGAGATCGGAAGAGCGGTTTCAG
chr15	91420076	91420115	FURIN_5516	-	GTGACCTATGCACCAGACGTACCCACCCACTTATGAGACATGATTGGTTTTGTGAGAGATCGGAAGAGCGGTTTCAG
chr15	91420315	91420354	FURIN_5517	-	GTGACCTATGCACCAGACGTTTTGGCCACCATCAGGAGAAGGTGACCTACTGATAGAAGATCGGAAGAGCGGTTTCAG
chr15	91420707	91420746	FURIN_5518	-	GTGACCTATGCACCAGACGTCAAGCACGTAGCATGAGTAGAACAATAAGGGTGAACAGGGAGATCGGAAGAGCGGTTTCAG
chr15	91421312	91421351	FURIN_5519	-	GTGACCTATGCACCAGACGTAGGGGGGGCAGGAAGAGGGATGCTGCATGGTCCAGCTGTAGATCGGAAGAGCGGTTTCAG
chr15	91421944	91421983	FURIN_5520	-	GTGACCTATGCACCAGACGTAGTGGGCTGGGTCTATTCAAGATTGGGACTTGAGGGAGGGAGATCGGAAGAGCGGTTTCAG
chr15	91422624	91422663	FURIN_5521	-	GTGACCTATGCACCAGACGTGAGAATCATATTGGGGCCCTGTGATGGGTGGAGGGGGCTAGAGATCGGAAGAGCGGTTTCAG
chr15	91422851	91422890	FURIN_5522	-	GTGACCTATGCACCAGACGTGGAAGGGAGAGGCTGGGGTCACTTTTTGGGAGCAGCAGATCGGAAGAGCGGTTTCAG
chr15	91423047	91423086	FURIN_5523	-	GTGACCTATGCACCAGACGTAGGGAGGTTAGGGTCACTGTGAGGTCAGGTCAGGTCAGGTCAGAGTGCCTTCTAGATCGGAAGAGCGGTTTCAG
chr15	91423274	91423313	FURIN_5524	-	GTGACCTATGCACCAGACGTGAGCACCATGATGGTCACTGGCCAGAGGGACCAGCGGAGATCGGAAGAGCGGTTTCAG
chr15	91423871	91423910	FURIN_5525	-	GTGACCTATGCACCAGACGTGAGTGCACACAGCCCTGAGGCCCTGCGGGACCCCAAGCCAGATCGGAAGAGCGGTTTCAG
chr15	91424110	91424149	FURIN_5526	-	GTGACCTATGCACCAGACGTGCGGGAGGAGGGCAAGAGTTAAGACAGTGTCTGGCACCAAGATCGGAAGAGCGGTTTCAG
chr15	91424466	91424505	FURIN_5527	-	GTGACCTATGCACCAGACGTGGGAGAGAGGGCAAGTGTGTGTGAGTCAAAACAGACTGTAGAGATCGGAAGAGCGGTTTCAG
chr15	91424762	91424801	FURIN_5528	-	GTGACCTATGCACCAGACGTGAGTGGCTGCTGTGGGGGACTCTGGCTGTCTAGATCGGAAGAGCGGTTTCAG
chr22	24376373	24376412	GSTT1_5529	-	GTGACCTATGCACCAGACGTCTCACCCCTTGCACGCTCCTCAGCAGTCCACAAGCATTTTATAGATCGGAAGAGCGGTTTCAG
chr22	24376772	24376811	GSTT1_5530	-	GTGACCTATGCACCAGACGTTGGGCAGGTGAACCCACTAGGCAGGGGGCCCTGGCTAGTTAGATCGGAAGAGCGGTTTCAG
chr22	24379311	24379350	GSTT1_5531	-	GTGACCTATGCACCAGACGTGAATGTGGGGGGCCGACGAGAGCATTCCCAAGGTGTAGATCGGAAGAGCGGTTTCAG
chr22	24384070	24384109	GSTT1_5532	-	GTGACCTATGCACCAGACGTCTCGGGTTTGGGGAACCGAAAAGTCAAGGAAGGGACAGGAGATCGGAAGAGCGGTTTCAG
chr5	14100985	141001024	HDAC3_5533	-	GTGACCTATGCACCAGACGTGGATGCTGTGCCAAAGAAATTTCTTTTCACTCTTGGTTAGATCGGAAGAGCGGTTTCAG
chr5	141004725	141004764	HDAC3_5534	-	GTGACCTATGCACCAGACGTAGGGTCACTGCTCCCTCAGGCTACCTTTCAATAGGCTTGGTGGAGGTAGATCGGAAGAGCGGTTTCAG
chr5	141005202	141005241	HDAC3_5535	-	GTGACCTATGCACCAGACGTACAGAAAAGCTGAGCACAAACTTCTCCTGAAAGGTGGAGCCAGATCGGAAGAGCGGTTTCAG
chr5	141005530	141005569	HDAC3_5536	-	GTGACCTATGCACCAGACGTCCCCACAACACCCCAATAACAGGAAGGCCATTCTCACAGAGATCGGAAGAGCGGTTTCAG
chr5	141005711	141005750	HDAC3_5537	-	GTGACCTATGCACCAGACGTCTCCTGATTTCTCCCTGTTGTCCAGTGTGAGCTAGGGTGTAGATCGGAAGAGCGGTTTCAG
chr5	141007410	141007449	HDAC3_5538	-	GTGACCTATGCACCAGACGTCTCCTTCTTCTCCCAAGGTTTTTAAGTGGCCTTGGACAGATCGGAAGAGCGGTTTCAG
chr5	141007631	141007670	HDAC3_5539	-	GTGACCTATGCACCAGACGTCACTTCTCCTCAGGATGTTCTGCTGGGCTTGGGAAAAGATCGGAAGAGCGGTTTCAG
chr5	141008076	141008115	HDAC3_5540	-	GTGACCTATGCACCAGACGTAAAGTCTTCCCTCTGTTCCCTTAGCCCTTCTTTTCTCCTAGATCGGAAGAGCGGTTTCAG
chr5	141009201	141009240	HDAC3_5541	-	GTGACCTATGCACCAGACGTGAGGAGGATGGGGGCGATTACGGGATTTTGGCTGAGGAGATCGGAAGAGCGGTTTCAG
chr5	141009377	141009416	HDAC3_5542	-	GTGACCTATGCACCAGACGTAGGTGATGGAAAGACAGTGGCCATCCTAGGGTAGGTGTAGATCGGAAGAGCGGTTTCAG
chr5	141009561	141009600	HDAC3_5543	-	GTGACCTATGCACCAGACGTCCCAGTCTGTTCTTCTCCTCTGGATCCCTGGACTCAGATCGGAAGAGCGGTTTCAG
chr5	141014328	141014367	HDAC3_5544	-	GTGACCTATGCACCAGACGTACTGGGATTTTTGATGTTCAACAGTTAATGCCAAGCCCTAGATCGGAAGAGCGGTTTCAG
chr5	141016065	141016104	HDAC3_5545	-	GTGACCTATGCACCAGACGTCCCGCTCGGGGCTGGGGGTTGGGGGTGGGGCGAGCTGTGGCAGATCGGAAGAGCGGTTTCAG
chr5	141016253	141016292	HDAC3_5546	-	GTGACCTATGCACCAGACGTAGGGATATGCATGAGGAGTTGGGACAGGAGTTTTTGGGAGATCGGAAGAGCGGTTTCAG
chr19	10381786	10381825	ICAM1_5547	-	GTGACCTATGCACCAGACGTAGGTTGCAACTCTGAGTAGCAGAGGAGCTCAGCGTCGACTAGATCGGAAGAGCGGTTTCAG
chr19	10394107	10394146	ICAM1_5548	-	GTGACCTATGCACCAGACGTACAGAGGTGGGGGTCTGGTGAAGTGGACCTTGTCTAGATCGGAAGAGCGGTTTCAG
chr19	10394659	10394698	ICAM1_5549	-	GTGACCTATGCACCAGACGTAAGAAAGGTGTGAGCAGACAGGGATGGACGTCCCGAAGCCAGATCGGAAGAGCGGTTTCAG
chr19	10395029	10395068	ICAM1_5550	-	GTGACCTATGCACCAGACGTACACAGTAGGCCCCCGGGTTTCAAGTCAACCCCAAGATCGGAAGAGCGGTTTCAG
chr19	10395409	10395448	ICAM1_5551	-	GTGACCTATGCACCAGACGTACGATGAGATGACATGGAGTGGGTGGGGGACGAGCTTGGAGATCGGAAGAGCGGTTTCAG
chr19	10395741	10395780	ICAM1_5552	-	GTGACCTATGCACCAGACGTGATACAACAGGCGGTGAGGATTGCATTAGGTCCATGGCCAGATCGGAAGAGCGGTTTCAG
chr4	123374815	123374854	IL2_5553	-	GTGACCTATGCACCAGACGTACTTTATTTGCTCTCCTGGAATAAAAAAAAAAAAGTAGAGATCGGAAGAGCGGTTTCAG
chr4	123377249	123377288	IL2_5554	-	GTGACCTATGCACCAGACGTTATTTTATGTTCAATTTCTGTTTTAATAAAATTTCAAAGTATAGATCGGAAGAGCGGTTTCAG
chr4	123377399	123377438	IL2_5555	-	GTGACCTATGCACCAGACGTTTTCTTTCTTAAATTTTACTAAATTTATACATTTAGTAATCTAGCTAGATCGGAAGAGCGGTTTCAG
chr10	6054785	6054824	IL2RA_5556	-	GTGACCTATGCACCAGACGTGAACAAAGAATTTCTTGGTAAGAGCCGGGAACAGACAACAGATCGGAAGAGCGGTTTCAG
chr10	6059966	6060005	IL2RA_5557	-	GTGACCTATGCACCAGACGTACACCAAGGCACCCCTTGGTCAAGTCAAACTGTACAGATCGGAAGAGCGGTTTCAG
chr10	6061341	6061380	IL2RA_5558	-	GTGACCTATGCACCAGACGTCACTGGCTTTGGGACAAAATGTACACAGGCTGAGATATAGATCGGAAGAGCGGTTTCAG
chr10	6061783	6061822	IL2RA_5559	-	GTGACCTATGCACCAGACGTAGACAAACGCTGGACACAGAGCCCTAGTCCAAAAGGGCAAGATCGGAAGAGCGGTTTCAG
chr10	6066157	6066196	IL2RA_5560	-	GTGACCTATGCACCAGACGTAATCTGTCTCCAGCTAACTCTGCTAGCGCACCCCTTCTCAGATCGGAAGAGCGGTTTCAG
chr10	6067747	6067786	IL2RA_5561	-	GTGACCTATGCACCAGACGTCTTCTGTACTACCAAGAATAAAAGAACTGCAGCAAGAGATCGGAAGAGCGGTTTCAG
chr10	6104001	6104040	IL2RA_5562	-	GTGACCTATGCACCAGACGTGTGGGTGGCCCCGGAAATTCGGGGAAGGCTGATGGCATTCCAGATCGGAAGAGCGGTTTCAG
chr17	45351735	45351774	ITGB3_5563	-	GTGACCTATGCACCAGACGTGAGCAAAAGGCATTAGCACCAGATTTGGCTCAGTGAAGGTAGATCGGAAGAGCGGTTTCAG
chr17	45360670	45360709	ITGB3_5564	-	GTGACCTATGCACCAGACGTGGAGCCAAAGAGAAGTCCAGCAATCAGAGCTATGGCAGAGATCGGAAGAGCGGTTTCAG
chr17	45361759	45361798	ITGB3_5565	-	GTGACCTATGCACCAGACGTGAAAAGATGTTAGTTTTATCTTCTCTCCACCAAGATTGAGATCGGAAGAGCGGTTTCAG
chr17	45363576	45363615	ITGB3_5566	-	GTGACCTATGCACCAGACGTATGGGATAATTTAAGCAGACACCTTCATGGAAAAGGCAAGATCGGAAGAGCGGTTTCAG
chr17	45364386	45364425	ITGB3_5567	-	GTGACCTATGCACCAGACGTAAAACAATAAAAGCAAGAGAGGACAAAACAATTCAGAGATCGGAAGAGCGGTTTCAG
chr17	45366997	45367036	ITGB3_5568	-	GTGACCTATGCACCAGACGTGAAGGATGTAGAGGTTAATGACGTTCTCATGTACATCTTAAGATCGGAAGAGCGGTTTCAG



chr17	45367501	45367540	ITGB3_5569	-	GTGACCTATGCACCAGACGTAAACAAAGATGTCCAGAGCTTACCAAAGGAAGCTGGTGGTAGATCGGAAGAGCGGTTTCAG
chr17	45368270	45368309	ITGB3_5570	-	GTGACCTATGCACCAGACGTAGGGGCACAAGAAGACAAGAAATGAACTGAAAGGAAACGAGATCGGAAGAGCGGTTTCAG
chr17	45369455	45369494	ITGB3_5571	-	GTGACCTATGCACCAGACGTAGAAAGATTGTATTTAGACACAGTTGGGCCAGTTAACACAGATCGGAAGAGCGGTTTCAG
chr17	45376624	45376663	ITGB3_5572	-	GTGACCTATGCACCAGACGTACAGCCCAGGAAGGTGGACCCGCTGGCGAGAGCTCCACTCAGATCGGAAGAGCGGTTTCAG
chr17	45377794	45377833	ITGB3_5573	-	GTGACCTATGCACCAGACGTGAGGACACAGTGATTAAGGCAAAGAGGAGCAAGCCTAAGAGATCGGAAGAGCGGTTTCAG
chr17	45380037	45380076	ITGB3_5574	-	GTGACCTATGCACCAGACGTGGAAATGGAGGAATAAAAAGTGAGACAACACTACTGGAAGAAGATCGGAAGAGCGGTTTCAG
chr17	45384787	45384826	ITGB3_5575	-	GTGACCTATGCACCAGACGTGAAACAGTAGGAGCAGGGCGGTTGTGAATGAAGCAGGAGTCAAGATCGGAAGAGCGGTTTCAG
chr17	45387455	45387494	ITGB3_5576	-	GTGACCTATGCACCAGACGTAAACAGAATAGCATCTTACAGTGACTTCTTAAAGTCTTCCAGATCGGAAGAGCGGTTTCAG
chr19	17940867	17940906	JAK3_5577	-	GTGACCTATGCACCAGACGTGAGGGCTAGCCTCAGTTTCCAGTCTGTAGATTGGGCCGGAGATCGGAAGAGCGGTTTCAG
chr19	17941262	17941301	JAK3_5578	-	GTGACCTATGCACCAGACGTTCACAGAGCCCCAGCCTTCTTCCCTCCACGCCCTCAGATCGGAAGAGCGGTTTCAG
chr19	17942433	17942472	JAK3_5579	-	GTGACCTATGCACCAGACGTGCGCCCCGGGACTTGTGGGGATTTCAGCTGGCACGGCCTGGAGATCGGAAGAGCGGTTTCAG
chr19	17943278	17943317	JAK3_5580	-	GTGACCTATGCACCAGACGTTCGCGGATGAGTGAACCAAGCATGGTGGTCTTTTCAAAGATCGGAAGAGCGGTTTCAG
chr19	17943549	17943588	JAK3_5581	-	GTGACCTATGCACCAGACGTGAGGGCCAGGTTGGGTTGGAGAGGCGAGGCGCATCCAGAGATCGGAAGAGCGGTTTCAG
chr19	17945330	17945369	JAK3_5582	-	GTGACCTATGCACCAGACGTGGACGGGTTGGGTGGGGAGGGCTGTGATGTCATATTGGGCAGATCGGAAGAGCGGTTTCAG
chr19	17945611	17945650	JAK3_5583	-	GTGACCTATGCACCAGACGTCTCACCCGGCATCGGTCTCCGAACCCCACTTTGACAGAAAGATCGGAAGAGCGGTTTCAG
chr19	17945842	17945881	JAK3_5584	-	GTGACCTATGCACCAGACGTGGAGGTGGAGGAGGGAGGGGCTGAGCAGGGCAAGGAAGTGAGATCGGAAGAGCGGTTTCAG
chr19	17946683	17946722	JAK3_5585	-	GTGACCTATGCACCAGACGTCTGCCCTGCTCCACCCCTCCTTCCAGGGAAAGGCTTTCTAGATCGGAAGAGCGGTTTCAG
chr19	17947888	17947927	JAK3_5586	-	GTGACCTATGCACCAGACGTCCACCCAGCCACCCACCCCTGCCTCACCCAAGCTAGGAGATCGGAAGAGCGGTTTCAG
chr19	17948691	17948730	JAK3_5587	-	GTGACCTATGCACCAGACGTTGTGGACCAGACTTTTGGAGTCGGGGCTGGCTGGAGAGGGAGATCGGAAGAGCGGTTTCAG
chr19	17949022	17949061	JAK3_5588	-	GTGACCTATGCACCAGACGTCTGGGAAATGAGGCGATACCTCAGTCTGGGGTCCAGAGACAGATCGGAAGAGCGGTTTCAG
chr19	17950236	17950275	JAK3_5589	-	GTGACCTATGCACCAGACGTTCTCCCTGGAATGAGTGCTGATCTGGACCCTGGCTTAGATCGGAAGAGCGGTTTCAG
chr19	17952148	17952187	JAK3_5590	-	GTGACCTATGCACCAGACGTGTCCTTCCCTCCCGCCTCTGTGGCCACTCAGGGCCCTCAGATCGGAAGAGCGGTTTCAG
chr19	17952399	17952438	JAK3_5591	-	GTGACCTATGCACCAGACGTGATTCCTTCCCTCCCTCAGCCTTACCCCGAGGGCGGGCCAGATCGGAAGAGCGGTTTCAG
chr19	17953075	17953114	JAK3_5592	-	GTGACCTATGCACCAGACGTACTCCCCGCTGGCGGGCCAGCCCACTGGGGCGGGGCTCGAGATCGGAAGAGCGGTTTCAG
chr19	17953786	17953825	JAK3_5593	-	GTGACCTATGCACCAGACGTCCAGGCTGTGGGACGGCCTCTGCTTGGGAGTGAGCAACGAGATCGGAAGAGCGGTTTCAG
chr19	17954139	17954178	JAK3_5594	-	GTGACCTATGCACCAGACGTGCCTGGGGTTTGACCCAGGGGTTGGGGTCCAAGGGCAAGATCGGAAGAGCGGTTTCAG
chr19	17954536	17954575	JAK3_5595	-	GTGACCTATGCACCAGACGTCCCCCAGCCCCAGGGATTGTACAATTTTATCATCTCTAGATCGGAAGAGCGGTTTCAG
chr19	17954993	17955032	JAK3_5596	-	GTGACCTATGCACCAGACGTCCCTAGTGGGCGCCAGAGGGAAGGATGGGGCTGTGTGAGATCGGAAGAGCGGTTTCAG
chr5	56111351	56111390	MAP3K1_5597	-	GTGACCTATGCACCAGACGTGGGCTAGATTGCTGCGGCCCTGCCAGGGAGGGGAGGGGCAGATCGGAAGAGCGGTTTCAG
chr5	56152377	56152416	MAP3K1_5598	-	GTGACCTATGCACCAGACGTGGCAGAAACAATAAATGAGAATGTATATATGAAAAATAGATCGGAAGAGCGGTTTCAG
chr5	56155492	56155531	MAP3K1_5599	-	GTGACCTATGCACCAGACGTGATTTCCAATATTTTATTACTTAAAAATATAAAAGGTAAAGATCGGAAGAGCGGTTTCAG
chr5	56160511	56160550	MAP3K1_5600	-	GTGACCTATGCACCAGACGTTTTTTTTTATTAGGTAGCTTTCTCATTTCTTAATTAAGAAGATCGGAAGAGCGGTTTCAG
chr5	56161117	56161156	MAP3K1_5601	-	GTGACCTATGCACCAGACGTAAAAAGAAAACCTATAGGTTAATACATCTGTGGTTTCAAAAGATCGGAAGAGCGGTTTCAG
chr5	56161606	56161645	MAP3K1_5602	-	GTGACCTATGCACCAGACGTAAAAAGACAGTAACAATGATATTTTGCCATAATTATACAAGATCGGAAGAGCGGTTTCAG
chr5	56167687	56167726	MAP3K1_5603	-	GTGACCTATGCACCAGACGTGGGGAAGAAATTAAGCATAAAAGAAATATAAAGTAGATCGGAAGAGCGGTTTCAG
chr5	56168418	56168457	MAP3K1_5604	-	GTGACCTATGCACCAGACGTACAGAAACAAAATCTTACAAAAATGTAATGTTTAAACATTAGATCGGAAGAGCGGTTTCAG
chr5	56168602	56168641	MAP3K1_5605	-	GTGACCTATGCACCAGACGTAAATAACAAAATCTGCTTTAAAAAATAAGACAAACCACAGATCGGAAGAGCGGTTTCAG
chr5	56170809	56170848	MAP3K1_5606	-	GTGACCTATGCACCAGACGTACACACAGATGAATTCATGTAAGAAAAGCTTATGGACCAGATCGGAAGAGCGGTTTCAG
chr5	56174757	56174796	MAP3K1_5607	-	GTGACCTATGCACCAGACGTAAATCTGAAGGTCAGTTTATGTACACTTAAAAAGCATCAGAGATCGGAAGAGCGGTTTCAG
chr5	56176488	56176527	MAP3K1_5608	-	GTGACCTATGCACCAGACGTAGGAAAAGCAACATCAATCTGGATCTTGGCTAAAACACTAGATCGGAAGAGCGGTTTCAG
chr5	56176860	56176899	MAP3K1_5609	-	GTGACCTATGCACCAGACGTGAAAAGTAAAAATAAATGATTAATAAAATAGTATATTAATAAAGATCGGAAGAGCGGTTTCAG
chr5	56177347	56177386	MAP3K1_5610	-	GTGACCTATGCACCAGACGTAAAAACATTCATTACCATATAAGTTCCAATTACTGAAAAATAGATCGGAAGAGCGGTTTCAG
chr5	56179304	56179343	MAP3K1_5611	-	GTGACCTATGCACCAGACGTAAAGAAAGCAATCTTTTACTGTTAAAGGAGTAAGATTTTAGATCGGAAGAGCGGTTTCAG
chr5	56180441	56180480	MAP3K1_5612	-	GTGACCTATGCACCAGACGTAAACACGTTCAAAAAGTTTTGCATATTTTCACTAGCAATAGATCGGAAGAGCGGTTTCAG
chr5	56181709	56181748	MAP3K1_5613	-	GTGACCTATGCACCAGACGTATAAGAAATATCATAAATTAAGACAGAATTAAGATAGATCGGAAGAGCGGTTTCAG
chr5	56183155	56183194	MAP3K1_5614	-	GTGACCTATGCACCAGACGTACAGCAAAATGACTTGTATGTTAAAAACAAAATAAGAGATCGGAAGAGCGGTTTCAG
chr5	56184003	56184042	MAP3K1_5615	-	GTGACCTATGCACCAGACGTTCCAGAGTTAATTTGAAATAGGACTCATTTGAAAAAGAGAAGATCGGAAGAGCGGTTTCAG
chr5	56189308	56189347	MAP3K1_5616	-	GTGACCTATGCACCAGACGTAAAGCCAGTGTGAAGCTTTGCACAACTGTAACCTCTGATAGATCGGAAGAGCGGTTTCAG
chr5	56177779	56177818	MAP3K1_5617	-	GTGACCTATGCACCAGACGTGCTCTCAGAAATGTCCCTGTAAGTGGCACTCAATTTTGTAGATCGGAAGAGCGGTTTCAG
chr5	56178211	56178250	MAP3K1_5618	-	GTGACCTATGCACCAGACGTCTCCCTGTTTACTTGTATTACGGGGTAGGTCTAGATGGAGATCGGAAGAGCGGTTTCAG
chr5	179663334	179663373	MAPK9_5619	-	GTGACCTATGCACCAGACGTATAGCAAACCTGTCAAGTGAAGCAACTCTCACCTCCGATCGGAAGAGCGGTTTCAG
chr5	179663465	179663504	MAPK9_5620	-	GTGACCTATGCACCAGACGTCACCTCTCAGTCTTATCATGCAATGACATTTTCATCCAGATCGGAAGAGCGGTTTCAG
chr5	179665282	179665321	MAPK9_5621	-	GTGACCTATGCACCAGACGTGCTTAAATTGATTGTATGATATTTTTCTTCCCTATTCAAAGATCGGAAGAGCGGTTTCAG
chr5	179666874	179666913	MAPK9_5622	-	GTGACCTATGCACCAGACGTAGCTTATTTTATGCTTCTTTTGTACATTTCTTCCAATCCAGATCGGAAGAGCGGTTTCAG
chr5	179667981	179668020	MAPK9_5623	-	GTGACCTATGCACCAGACGTGTTTTGAAAAGATTTATATAGAGAGCCAGGCTTATTTAGATCGGAAGAGCGGTTTCAG
chr5	179669523	179669562	MAPK9_5624	-	GTGACCTATGCACCAGACGTCTTTTTTCTTACTTGTGTTTTGTAATTCAGTGGTGCAGATCGGAAGAGCGGTTTCAG
chr5	179674348	179674387	MAPK9_5625	-	GTGACCTATGCACCAGACGTACCTGACCCACTCTTACACGAGCGCTCACAGGCAAAAAGATCGGAAGAGCGGTTTCAG
chr5	179674389	179674428	MAPK9_5626	-	GTGACCTATGCACCAGACGTCCGCGACCTTGGCCGCCCATGCTTCTTAAATGCCTCAGGAGATCGGAAGAGCGGTTTCAG

chr5	179674805	179674844	MAPK9_5627	-	GTGACCTATGCACCAGACGTGACGGGGACCCGGTACTTGGCCATGGAGGCTGGGGTGGGCGAGATCGGAAGAGCGGTTTCAG
chr5	179675923	179675962	MAPK9_5628	-	GTGACCTATGCACCAGACGTCCGGGGCTGGAAGAGGCTGGGATGTTTGAATAATGCCTCAAGATCGGAAGAGCGGTTTCAG
chr5	179691731	179691770	MAPK9_5629	-	GTGACCTATGCACCAGACGTTTTTTATTTCAGTAATGCACTGTACATCAAAGAATGAACATAGATCGGAAGAGCGGTTTCAG
chr5	179696230	179696269	MAPK9_5630	-	GTGACCTATGCACCAGACGTATTATGTTTTGTCTGTGTCTCCATATTGTCAATAATGTAGATCGGAAGAGCGGTTTCAG
chr5	179707390	179707429	MAPK9_5631	-	GTGACCTATGCACCAGACGTCTGTTTTAATAGCGTGGATTGAGTTTTTGCTGTAATAAAAAGATCGGAAGAGCGGTTTCAG
chr2	16082137	16082176	MYCN_5632	-	GTGACCTATGCACCAGACGTCCCGGCCGCTGACTGAGGGCTTCTTCCGCCCGTTCGTTAGATCGGAAGAGCGGTTTCAG
chr2	16085565	16085604	MYCN_5633	-	GTGACCTATGCACCAGACGTGATGTGATGTGAGAACCATTTGAATGAAATAGATCGGAAGAGCGGTTTCAG
chr2	16082532	16082571	MYCN_5634	-	GTGACCTATGCACCAGACGTGCGCGTCCAGCTTCTCGCGGGCGGAGAAAGCCGCTCCACATAGATCGGAAGAGCGGTTTCAG
chr2	16085867	16085906	MYCN_5635	-	GTGACCTATGCACCAGACGTCTCTTGAGCGGACGTGGGACGCTCGCTCTTTATCTTCTAGATCGGAAGAGCGGTTTCAG
chr9	134001042	134001081	NUP214_5636	-	GTGACCTATGCACCAGACGTTCAGTGTGTGGAAGCAGCCAAAGCTGCCTCCACCGCCTTAGATCGGAAGAGCGGTTTCAG
chr9	134002861	134002900	NUP214_5637	-	GTGACCTATGCACCAGACGTGAATCAAACAGAGATCAATTCATAAAGAAAGAAATTAAGATCGGAAGAGCGGTTTCAG
chr9	134003669	134003708	NUP214_5638	-	GTGACCTATGCACCAGACGTAAAAAATACAAAGCAGAAAACGGTATGTTCTAAGCATAAAGATCGGAAGAGCGGTTTCAG
chr9	134004616	134004655	NUP214_5639	-	GTGACCTATGCACCAGACGTAAATATGCAAAAAGTAAATAGTTAACAAATAGTAAATCGAATCGGAAGAGCGGTTTCAG
chr9	134006103	134006142	NUP214_5640	-	GTGACCTATGCACCAGACGTACAGTATTACCAAATGAAAACAAGAAAATGGAGCAAACCAAGATCGGAAGAGCGGTTTCAG
chr9	134007933	134007972	NUP214_5641	-	GTGACCTATGCACCAGACGTGGAGGGGAAAAATAAGTATCAAATGAAACAAATCCTAAGATCGGAAGAGCGGTTTCAG
chr9	134008443	134008482	NUP214_5642	-	GTGACCTATGCACCAGACGTATCTTAATCAGTAGCTCATAAAAATGACAGCAACCAGATAGATCGGAAGAGCGGTTTCAG
chr9	134010235	134010274	NUP214_5643	-	GTGACCTATGCACCAGACGTCAAAGCAGAAAAAATTTCTCATGTGCAATTTTTCTCAGAGATCGGAAGAGCGGTTTCAG
chr9	134011277	134011316	NUP214_5644	-	GTGACCTATGCACCAGACGTAAAAACGAGACCATACGTTCAAATACAGCAATAGTTCTAGATCGGAAGAGCGGTTTCAG
chr9	134015886	134015925	NUP214_5645	-	GTGACCTATGCACCAGACGTAGAAAAACAATAAAAAAACCAAGTGAATTTAAGGGCCTAGATCGGAAGAGCGGTTTCAG
chr9	134019617	134019656	NUP214_5646	-	GTGACCTATGCACCAGACGTAAAAAAGGAAGGAAAATGTTAACACTGTAACAGTGGAGGAGATCGGAAGAGCGGTTTCAG
chr9	134021466	134021505	NUP214_5647	-	GTGACCTATGCACCAGACGTGCAGCCTGAAGGCCTCAGAAGAGCCTGCTAGAAGATTTCTAGATCGGAAGAGCGGTTTCAG
chr9	134022827	134022866	NUP214_5648	-	GTGACCTATGCACCAGACGTAGAAGTCAAGTAAAATAGATGGCATTATTACCTTTATTAGATCGGAAGAGCGGTTTCAG
chr9	134025661	134025700	NUP214_5649	-	GTGACCTATGCACCAGACGTAGGAAAAGTTTAAAACTGCAAGTCAATGCTTCTACAAGAGATCGGAAGAGCGGTTTCAG
chr9	134025953	134025992	NUP214_5650	-	GTGACCTATGCACCAGACGTACAAAGTACGAAACTACTAGTCTGAAGGACAAAACAGTAAAGATCGGAAGAGCGGTTTCAG
chr9	134027073	134027112	NUP214_5651	-	GTGACCTATGCACCAGACGTACAATAATGTGTTGGTACAAAAGTTGTTACGTTCAAATAGATCGGAAGAGCGGTTTCAG
chr9	134034720	134034759	NUP214_5652	-	GTGACCTATGCACCAGACGTAAAATAAAAGGCAAATAACTTGTTTTTCTGATAGTTGGAGATCGGAAGAGCGGTTTCAG
chr9	134038328	134038367	NUP214_5653	-	GTGACCTATGCACCAGACGTCAATGAGAAAAGAATTAACATGAATGGTTCAAGTAAAGGAGATCGGAAGAGCGGTTTCAG
chr9	134039207	134039246	NUP214_5654	-	GTGACCTATGCACCAGACGTACAGCTGTAGATACAGACCACTAGGAGCTGAAAGATCGGAGATCGGAAGAGCGGTTTCAG
chr9	134039398	134039437	NUP214_5655	-	GTGACCTATGCACCAGACGTCCATAAACCCATAAATGATTAAGACTAGTTTTTAAAGATAGATCGGAAGAGCGGTTTCAG
chr9	134049392	134049431	NUP214_5656	-	GTGACCTATGCACCAGACGTCCCAAAACAAAACAAATTTAGACAACCTCAAAGCAAGCCAAAGATCGGAAGAGCGGTTTCAG
chr9	134050797	134050836	NUP214_5657	-	GTGACCTATGCACCAGACGTAAAGAAAATTAAGTGTGAGTGGGTGAGAGAACAGGAAAATAGATCGGAAGAGCGGTTTCAG
chr9	134053648	134053687	NUP214_5658	-	GTGACCTATGCACCAGACGTGAGAGAAGAGAGAACCATATTAATTCAGCAAAGGATAAGATCGGAAGAGCGGTTTCAG
chr9	134062626	134062665	NUP214_5659	-	GTGACCTATGCACCAGACGTACAAAAGCATACTACAGAAAAGGCATGACTAGGTA AAAAGATCGGAAGAGCGGTTTCAG
chr9	134064390	134064429	NUP214_5660	-	GTGACCTATGCACCAGACGTGAAAAGCAAAATGTTTTATGTTAAACCTAACCATTTAGATCGGAAGAGCGGTTTCAG
chr9	134070570	134070609	NUP214_5661	-	GTGACCTATGCACCAGACGTGAAAGAAAGAAAATTA AAAAGGAAACAAAGCCAAATAAGATCGGAAGAGCGGTTTCAG
chr9	134072553	134072592	NUP214_5662	-	GTGACCTATGCACCAGACGTAAAGAAATCAGAAAATGGGTTGGATTTAGCAAAGATGACAGATCGGAAGAGCGGTTTCAG
chr9	134076984	134077023	NUP214_5663	-	GTGACCTATGCACCAGACGTCAAAGAAAACAAAATTAATTTGGATTGGATGAGTCTTTAGATCGGAAGAGCGGTTTCAG
chr9	134090549	134090588	NUP214_5664	-	GTGACCTATGCACCAGACGTAAAGGGTCAAGGAAAGGATAAGGATGAGAGTCTATCGTGAAGATCGGAAGAGCGGTTTCAG
chr9	134098115	134098154	NUP214_5665	-	GTGACCTATGCACCAGACGTGAAGATGTGAGGGAGGTCAGAGGGAGACAAATGTCTTACAGATCGGAAGAGCGGTTTCAG
chr9	134103497	134103536	NUP214_5666	-	GTGACCTATGCACCAGACGTGAGAGGCAAAACAGAAATAGGAGAAAAGGAGGAGGATCGGAAGAGCGGTTTCAG
chr9	134105967	134106006	NUP214_5667	-	GTGACCTATGCACCAGACGTGTGAAAACAGACTGAGGTCAAGTGGGGCCTCTACCCTTAGATCGGAAGAGCGGTTTCAG
chr9	134107621	134107660	NUP214_5668	-	GTGACCTATGCACCAGACGTGAATAAGAGTGAAGTTAAAGCACGCATCCACTCGAAAGACAGATCGGAAGAGCGGTTTCAG
chr9	134108791	134108830	NUP214_5669	-	GTGACCTATGCACCAGACGTGCACAGGACAGTGGTGGAGTCACTGCTCTGTACAGAGCAGATCGGAAGAGCGGTTTCAG
chr9	134073003	134073042	NUP214_5670	-	GTGACCTATGCACCAGACGTAGGGGGCTCCGTGTGCTTCCCTAACCCGGGGGGCGAGTAAAGATCGGAAGAGCGGTTTCAG
chr9	134073453	134073492	NUP214_5671	-	GTGACCTATGCACCAGACGTAAACAGACTCAGAAGTTTGCGGAGGACCGCTGGGAAAGCTGGAGATCGGAAGAGCGGTTTCAG
chr9	134073903	134073942	NUP214_5672	-	GTGACCTATGCACCAGACGTGCCAAAGCAGACTGCTGCGGTCTGGCTGCCACTTGCCCAAGATCGGAAGAGCGGTTTCAG
chr11	100909797	100909836	PGR_5673	-	GTGACCTATGCACCAGACGTTTTTCTTTAAAGAATTAATTTTTGTGGTATGCTTTTTGTAGATCGGAAGAGCGGTTTCAG
chr11	100912626	100912665	PGR_5674	-	GTGACCTATGCACCAGACGTGGTTGATCCAGAATATCAATGATTATTCTCTGAATTTCTAGATCGGAAGAGCGGTTTCAG
chr11	100920610	100920649	PGR_5675	-	GTGACCTATGCACCAGACGTCCAAGTAACTAATGCAAGATATCTAGTTTTCTAATTCATAGATCGGAAGAGCGGTTTCAG
chr11	100922105	100922144	PGR_5676	-	GTGACCTATGCACCAGACGTACTTTTTGTTGTTTTGTTATTTAAGTGTACATGTAGGATAGATCGGAAGAGCGGTTTCAG
chr11	100933128	100933167	PGR_5677	-	GTGACCTATGCACCAGACGTTTTTTATATCAGCATGTAATAAAAAATATACTATGTTTGAAGATCGGAAGAGCGGTTTCAG
chr11	100962441	100962480	PGR_5678	-	GTGACCTATGCACCAGACGTGTTTATCATCAATAATACTGTGTAATCTTTATACTATAAGATCGGAAGAGCGGTTTCAG
chr11	100996688	100996727	PGR_5679	-	GTGACCTATGCACCAGACGTTCCTGATCTTTATTATTGGTTTAATTGTAATGGAGAGATCGGAAGAGCGGTTTCAG
chr11	100998115	100998154	PGR_5680	-	GTGACCTATGCACCAGACGTGGGACGGGCACGCCAGCGCTCCGGGAGTAGCGGTTCCAGATCGGAAGAGCGGTTTCAG
chr11	100998524	100998563	PGR_5681	-	GTGACCTATGCACCAGACGTCTCCCGGATTTCCCGTTGGGGCCACC GCCCGCTGCCGAGATCGGAAGAGCGGTTTCAG
chr11	100998933	100998972	PGR_5682	-	GTGACCTATGCACCAGACGTGCGCCAGTCCGCCCTGGTGGAGCAGCGCCGATGGCAGATCGGAAGAGCGGTTTCAG
chr11	100999342	100999381	PGR_5683	-	GTGACCTATGCACCAGACGTTGCCTGTTTTGCCCCGAACCTTCCCGAAGATCCACC GGCTGAGATCGGAAGAGCGGTTTCAG
chr22	46594231	46594270	PPARA_5684	-	GTGACCTATGCACCAGACGTGTTGGTGTGTTGTGCCCGCAGCTCCAAGCTACTGGGAGGAGATCGGAAGAGCGGTTTCAG

chr22	46611020	46611059	PPARA_5685	-	GTGACCTATGCACCAGACGTAGAGGAGAGACGGATGAATAGTCCAGGCATCACTATCCTGAGATCGGAAGAGCGGTTTCAG
chr22	46614110	46614149	PPARA_5686	-	GTGACCTATGCACCAGACGTAAATACACAGTGGATTTAAAGACCTGGGCCACTGAGAAACCAGATCGGAAGAGCGGTTTCAG
chr22	46615659	46615698	PPARA_5687	-	GTGACCTATGCACCAGACGTGAGGGGGAAACACAGGCATGAGCAGTGAGGTCATGACTGCAGATCGGAAGAGCGGTTTCAG
chr22	46627639	46627678	PPARA_5688	-	GTGACCTATGCACCAGACGTGGACACCAAGTAAGTCAGGTGATGTGGGATGCGCTATGCAGATCGGAAGAGCGGTTTCAG
chr22	46630980	46631019	PPARA_5689	-	GTGACCTATGCACCAGACGTAAAGAAGAGAGAGAGGTTTGTAGTGTATAATCACCCAAGAAAGATCGGAAGAGCGGTTTCAG
chr19	54385699	54385738	PRKCG_5690	-	GTGACCTATGCACCAGACGTAGCTAGCAGGGACAGGATCCTGCCTTTCTTGGGGGAAACAGATCGGAAGAGCGGTTTCAG
chr19	54386367	54386406	PRKCG_5691	-	GTGACCTATGCACCAGACGTGAGGATCCTAGGTCAGTGCAGAAAGGGGTACCTGGACCCAGATCGGAAGAGCGGTTTCAG
chr19	54387365	54387404	PRKCG_5692	-	GTGACCTATGCACCAGACGTAAATCATAGACACACAGCAGCGGAGGCATGGATTAGTCCAGCAGATCGGAAGAGCGGTTTCAG
chr19	54392842	54392881	PRKCG_5693	-	GTGACCTATGCACCAGACGTAGAAGACTGGCTTAGGGGGCGTTGGGAGGGTCCAAAACCAGATCGGAAGAGCGGTTTCAG
chr19	54393090	54393129	PRKCG_5694	-	GTGACCTATGCACCAGACGTAAAGCTGCGGGTAGCACCTCAGGCCCGCCCAAGCCAAGAGATCGGAAGAGCGGTTTCAG
chr19	54394878	54394917	PRKCG_5695	-	GTGACCTATGCACCAGACGTAGTGAGGAAGAGTGTGACGGGTTAGAGATCCAGGAAGGGGAGATCGGAAGAGCGGTTTCAG
chr19	54395713	54395752	PRKCG_5696	-	GTGACCTATGCACCAGACGTGTGGGGTGGATGGGGTGCAGAGCCGAGCTCATGGCTCCCCAGATCGGAAGAGCGGTTTCAG
chr19	54396192	54396231	PRKCG_5697	-	GTGACCTATGCACCAGACGTGACCGAGACCAAGCGGCGAGCGGGGATGGGGCACCCATAGATCGGAAGAGCGGTTTCAG
chr19	54396566	54396605	PRKCG_5698	-	GTGACCTATGCACCAGACGTAGAAGAGAGAGTCAAGGTTCCCAAGAGATGCAGGGGATCGAGATCGGAAGAGCGGTTTCAG
chr19	54401163	54401202	PRKCG_5699	-	GTGACCTATGCACCAGACGTGAGAAAGAAAGAGCCAGAGGCAGTTAGACCTTACACAGCGAGATCGGAAGAGCGGTTTCAG
chr19	54401644	54401683	PRKCG_5700	-	GTGACCTATGCACCAGACGTAGTTCCAAAAGGGCCAGTCCATGTTGGGAACCCAGTGGTAAGATCGGAAGAGCGGTTTCAG
chr19	54403437	54403476	PRKCG_5701	-	GTGACCTATGCACCAGACGTGTGCATGGGCTTAGAGGGCGGGATCCATCTACCCAGATAGAGATCGGAAGAGCGGTTTCAG
chr19	54403623	54403662	PRKCG_5702	-	GTGACCTATGCACCAGACGTGGGTGGTGGGGACGTCAAGAGGTCAGTGGCTGGATCTGAGATCGGAAGAGCGGTTTCAG
chr19	54403815	54403854	PRKCG_5703	-	GTGACCTATGCACCAGACGTCAAGGGTGTGGGGCAGGAATTGCAAGAAGTGTGAGTTCAAGATCGGAAGAGCGGTTTCAG
chr19	54406277	54406316	PRKCG_5704	-	GTGACCTATGCACCAGACGTTGGAAGGCAGGAATCATGATGCGTTCCTTAGGAAGCCTAAGATCGGAAGAGCGGTTTCAG
chr19	54407839	54407878	PRKCG_5705	-	GTGACCTATGCACCAGACGTGAGGGGATAGAGAGTCAAGGACATGCCCAACTGCCTTTCAGATCGGAAGAGCGGTTTCAG
chr19	54409911	54409950	PRKCG_5706	-	GTGACCTATGCACCAGACGTGCTGGGGGAGGGAAAGTTAAGCAGCTCCGAGGGCTCCTCGAGATCGGAAGAGCGGTTTCAG
chr1	198608355	198608394	PTPRC_5707	-	GTGACCTATGCACCAGACGTGGAAGTCAGCGTGCCTTAAAGAACAGCATGCGTCCCTTCAGATCGGAAGAGCGGTTTCAG
chr1	198661426	198661465	PTPRC_5708	-	GTGACCTATGCACCAGACGTGAAACAAAATCTCTTAGAAAATTTCAAATTTCCATATAAGATCGGAAGAGCGGTTTCAG
chr1	198665791	198665830	PTPRC_5709	-	GTGACCTATGCACCAGACGTATGGAATAATGGGAGAAGGACAAAATAAATATGTGAATCATAGATCGGAAGAGCGGTTTCAG
chr1	198668643	198668682	PTPRC_5710	-	GTGACCTATGCACCAGACGTAAAGTGAGATCATTACATCAGTCTTCCCCACTGGAGATGAGATCGGAAGAGCGGTTTCAG
chr1	198671466	198671505	PTPRC_5711	-	GTGACCTATGCACCAGACGTAAAGGGCCATCAGCACTGTCACTTGTGTCTGTACGCAAGGAGATCGGAAGAGCGGTTTCAG
chr1	198672377	198672416	PTPRC_5712	-	GTGACCTATGCACCAGACGTATGAATAGAAGAATAAAAGCTAATTAATTCGTTATATTAAGATCGGAAGAGCGGTTTCAG
chr1	198673551	198673590	PTPRC_5713	-	GTGACCTATGCACCAGACGTGAAAAAAAATGAAATATTTAAATTTTGCCTTGAATATAGATCGGAAGAGCGGTTTCAG
chr1	198675813	198675852	PTPRC_5714	-	GTGACCTATGCACCAGACGTATAGAACAATTCAGTGTATTTTTCCAGAATAAATAAACTAGATCGGAAGAGCGGTTTCAG
chr1	198677212	198677251	PTPRC_5715	-	GTGACCTATGCACCAGACGTGATACAGAAATAAACTTGATTAGTATTTCAATGTGTATAGATCGGAAGAGCGGTTTCAG
chr1	198678766	198678805	PTPRC_5716	-	GTGACCTATGCACCAGACGTGAAATATTTTCAATGAATATATCGATGCAATATTCACGCGAGATCGGAAGAGCGGTTTCAG
chr1	198682032	198682071	PTPRC_5717	-	GTGACCTATGCACCAGACGTAAATAAGAATGTTATGTAATATGAAAAATAAGACATGGATAAGATCGGAAGAGCGGTTTCAG
chr1	198685761	198685800	PTPRC_5718	-	GTGACCTATGCACCAGACGTATGTAAAAAAAATAGTAAGTCGTTAAAGTCAGTACTAAGATCGGAAGAGCGGTTTCAG
chr1	198687173	198687212	PTPRC_5719	-	GTGACCTATGCACCAGACGTGAAGAAAGATTTTGTATAAATAAATTAATAGATGCATATGAGATCGGAAGAGCGGTTTCAG
chr1	198697419	198697458	PTPRC_5720	-	GTGACCTATGCACCAGACGTAAATAATACATTAGAGAACGATTGTCAAATAACTTGCTAGATCGGAAGAGCGGTTTCAG
chr1	198698216	198698255	PTPRC_5721	-	GTGACCTATGCACCAGACGTAGGAAAAATAAGTTTCTATATTCTCAAGAAGCACAAAATTAGATCGGAAGAGCGGTTTCAG
chr1	198700696	198700735	PTPRC_5722	-	GTGACCTATGCACCAGACGTATTAAGATTCAACTACTAGTTACATGTGTCTTTCAGGTGGAGATCGGAAGAGCGGTTTCAG
chr1	198701379	198701418	PTPRC_5723	-	GTGACCTATGCACCAGACGTCAACGATTTCTTGGATCACAGCAGATTCAGGAAAAATAATAGATCGGAAGAGCGGTTTCAG
chr1	198701559	198701598	PTPRC_5724	-	GTGACCTATGCACCAGACGTAAAAGAAAAATAAACAGTGAATAATGAAATATCAAGTAAGATCGGAAGAGCGGTTTCAG
chr1	198703275	198703314	PTPRC_5725	-	GTGACCTATGCACCAGACGTACATGCAGAGATATGCTATTTGCTGAACATTCAATTAAGATCGGAAGAGCGGTTTCAG
chr1	198703407	198703446	PTPRC_5726	-	GTGACCTATGCACCAGACGTAAACAAAAGCTGATAAGAAAAATTTCTTAAAAGTGCAGATCGGAAGAGCGGTTTCAG
chr1	198710948	198710987	PTPRC_5727	-	GTGACCTATGCACCAGACGTGATAATATTTCTTTGAGATGATTTTTTAAAGCAAACTAAGATCGGAAGAGCGGTTTCAG
chr1	198711311	198711350	PTPRC_5728	-	GTGACCTATGCACCAGACGTAAAGCAAAAAAAGCAGAGGGCATGATCATGGAAAAAGCTGCAGATCGGAAGAGCGGTTTCAG
chr1	198713133	198713172	PTPRC_5729	-	GTGACCTATGCACCAGACGTAAAGAAACAAATACAGATGTTAACTGATAATCTAGAGTCTAGATCGGAAGAGCGGTTTCAG
chr1	198717188	198717227	PTPRC_5730	-	GTGACCTATGCACCAGACGTAAAACAAAACAGAAAACCTCTTAAATGTAATATTGGAGATCGGAAGAGCGGTTTCAG
chr1	198718495	198718534	PTPRC_5731	-	GTGACCTATGCACCAGACGTAAATCAGTAGTAAGTCTTCTTAAAAAATAAATTTCTAGATCGGAAGAGCGGTTTCAG
chr1	198719571	198719610	PTPRC_5732	-	GTGACCTATGCACCAGACGTAAAAAAGGGTGGGACTTCGTTACTACAGAAGAGAGCTCAAGATCGGAAGAGCGGTTTCAG
chr1	198721328	198721367	PTPRC_5733	-	GTGACCTATGCACCAGACGTGAAGACAATTAACAATTTGTTTCCATTTTGAATATGCAAGATCGGAAGAGCGGTTTCAG
chr1	198721673	198721712	PTPRC_5734	-	GTGACCTATGCACCAGACGTAAATGAAGAGAGCATTAACTGGAGTGAAGTTCAGCTTATTAGATCGGAAGAGCGGTTTCAG
chr1	198723348	198723387	PTPRC_5735	-	GTGACCTATGCACCAGACGTAAAGAAAGATAAAAAATCTTACTTACCAAAAAGGAGATCGGAAGAGCGGTTTCAG
chr1	198724985	198725024	PTPRC_5736	-	GTGACCTATGCACCAGACGTAAATTAAGTGGGAATTAACATGAAGAAATTTGATGTCATTAAAGATCGGAAGAGCGGTTTCAG
chr1	44010697	44010736	PTPRF_5737	-	GTGACCTATGCACCAGACGTAGCTCCACAGCCAGCCACAGCCAGGACAATCAACCTGTAAGATCGGAAGAGCGGTTTCAG
chr1	44019113	44019152	PTPRF_5738	-	GTGACCTATGCACCAGACGTTGGAGACCAAGTACCACAGCACAGTCACTATAGGAATAGATCGGAAGAGCGGTTTCAG
chr1	44019421	44019460	PTPRF_5739	-	GTGACCTATGCACCAGACGTACAGACATGGGGTACAGCCCTACTCAGGACACAGGAGCCTAGATCGGAAGAGCGGTTTCAG
chr1	44035211	44035250	PTPRF_5740	-	GTGACCTATGCACCAGACGTACAGCAATGTGTATTAGGGCTGGCTTGCCTGCCCTAGATCGGAAGAGCGGTTTCAG
chr1	44044431	44044470	PTPRF_5741	-	GTGACCTATGCACCAGACGTACGAAGAGGAGGCTCAGGACCGGCCCTGTCAGTGTGGCAGATCGGAAGAGCGGTTTCAG
chr1	44054352	44054391	PTPRF_5742	-	GTGACCTATGCACCAGACGTAGGGAGAGGCACTACAGGCCGGCAGGACACACAGCTAGATCGGAAGAGCGGTTTCAG

chr1	44056593	44056632	PTPRF_5743	-	GTGACCTATGCACCAGACGTAGTGGGAAGGCTCAAAGCTGCCCGAGGTCAAGATCCTTAGGAGATCGGAAGAGCGGTTTCAG
chr1	44057433	44057472	PTPRF_5744	-	GTGACCTATGCACCAGACGTCCACACCAGGCAGGTGAGCCTCATCTGCGTGAGGTCAGGGAGATCGGAAGAGCGGTTTCAG
chr1	44058078	44058117	PTPRF_5745	-	GTGACCTATGCACCAGACGTACAGGGAGCACTCACTGACAGCTCTGAGCTCAAAGTCACTCAGATCGGAAGAGCGGTTTCAG
chr1	44063369	44063408	PTPRF_5746	-	GTGACCTATGCACCAGACGTCAAATGGGGGGGAAGCAAGCAGATGGAGGGTGGGGATCACAGATCGGAAGAGCGGTTTCAG
chr1	44064341	44064380	PTPRF_5747	-	GTGACCTATGCACCAGACGTAGGTAGAGAAGGAAGTCAGGCCTGGAGGTATCAACCTAGAGATCGGAAGAGCGGTTTCAG
chr1	44067692	44067731	PTPRF_5748	-	GTGACCTATGCACCAGACGTGAGAGGGGAGAAAGGGAGACAGGATGGTGAAGGACTCTGAGATCGGAAGAGCGGTTTCAG
chr1	44069037	44069076	PTPRF_5749	-	GTGACCTATGCACCAGACGTGAGGGGTTCCGTTCCCATACAAGAAATGCAGGGAGAGGCAGATCGGAAGAGCGGTTTCAG
chr1	44069232	44069271	PTPRF_5750	-	GTGACCTATGCACCAGACGTACGGGCTGGGCTCTGGCGCTGCCTCCTGCTGCCCCACCCAGATCGGAAGAGCGGTTTCAG
chr1	44070524	44070563	PTPRF_5751	-	GTGACCTATGCACCAGACGTATAGAGAGAGTCAGCTCTGCTGGGTATATGAGGTGGGGTGGATCGGAAGAGCGGTTTCAG
chr1	44070811	44070850	PTPRF_5752	-	GTGACCTATGCACCAGACGTCTGGGAGGGGCAATCAATGCCTTTGGGTGAGGTTCCCTACCAGATCGGAAGAGCGGTTTCAG
chr1	44071150	44071189	PTPRF_5753	-	GTGACCTATGCACCAGACGTAGGGCAGGAATCAGGACTGTCACTGCTGTTACCTCCAGCAGATCGGAAGAGCGGTTTCAG
chr1	44071861	44071900	PTPRF_5754	-	GTGACCTATGCACCAGACGTAGACATGGGGTCCATGAGGGCCTTGGAGCATGCCGCCAGATCGGAAGAGCGGTTTCAG
chr1	44072435	44072474	PTPRF_5755	-	GTGACCTATGCACCAGACGTGTGGAGAACAGCAGGCTGTGAGCTCAGCGTGAGAACCCCCAGATCGGAAGAGCGGTTTCAG
chr1	44075004	44075043	PTPRF_5756	-	GTGACCTATGCACCAGACGTAGAAGGGAGGCTGGTGAACCTGAGGTCCAGGCTGAGACAGATCGGAAGAGCGGTTTCAG
chr1	44079239	44079278	PTPRF_5757	-	GTGACCTATGCACCAGACGTTAGGGCATAACAGGCAGCATTAGTGTGAGGCTTGGAGCAGATCGGAAGAGCGGTTTCAG
chr1	44083066	44083105	PTPRF_5758	-	GTGACCTATGCACCAGACGTTGGAGAAAGCGGGTGGGGTGGGGTAAAGGCCAAGTTGACAGATCGGAAGAGCGGTTTCAG
chr1	44083357	44083396	PTPRF_5759	-	GTGACCTATGCACCAGACGTGAAAGGAGGTGGGAGGGCACTTACTACAGGGTCCCCAGCCAGATCGGAAGAGCGGTTTCAG
chr1	44084251	44084290	PTPRF_5760	-	GTGACCTATGCACCAGACGTATGAGCAGGGCAGGCTGAGGAAAGCCACAGGCTCAGACGAGATCGGAAGAGCGGTTTCAG
chr1	44084669	44084708	PTPRF_5761	-	GTGACCTATGCACCAGACGTAAGTGGGGACATACTGGCGACTAGGAGCCTACCTGCCATAAGATCGGAAGAGCGGTTTCAG
chr1	44084909	44084948	PTPRF_5762	-	GTGACCTATGCACCAGACGTGGGGCTCAGCTTGGGACAGGGCAGCCCCACCTCCACCCAGATCGGAAGAGCGGTTTCAG
chr1	44085301	44085340	PTPRF_5763	-	GTGACCTATGCACCAGACGTGACAGGATTGGTCAGGCCAGGCTTCCTGTGGGGTGGGGGAGATCGGAAGAGCGGTTTCAG
chr1	44085716	44085755	PTPRF_5764	-	GTGACCTATGCACCAGACGTATAAGACTGGACATGCTGGAGGTGCTGCCCTTAGAGAGATCGGAAGAGCGGTTTCAG
chr1	44086075	44086114	PTPRF_5765	-	GTGACCTATGCACCAGACGTAGGGTCGGGCCCCATAATCAGTGAGAGGAATAGGGGAGAGATCGGAAGAGCGGTTTCAG
chr1	44086459	44086498	PTPRF_5766	-	GTGACCTATGCACCAGACGTGGGTGGGGTACATTAGAATTGCTGCCCTTAGCCAGCCAGATCGGAAGAGCGGTTTCAG
chr1	44086718	44086757	PTPRF_5767	-	GTGACCTATGCACCAGACGTACACAGTTGGGTGACAGGCTCTGCTTGCCTCATGAGTGGAGATCGGAAGAGCGGTTTCAG
chr1	44087556	44087595	PTPRF_5768	-	GTGACCTATGCACCAGACGTAGGGGGCTGGTCAGTGTGGTGCGCCAGTGGACACCCCCAGATCGGAAGAGCGGTTTCAG
chr1	44056884	44056923	PTPRF_5769	-	GTGACCTATGCACCAGACGTTTCTCCCGTGCCTGCCCGACTGCCTGCTGGCGGCCCTTAGATCGGAAGAGCGGTTTCAG
chr1	44069521	44069560	PTPRF_5770	-	GTGACCTATGCACCAGACGTCCCTCGGGGCTCCTGATCTCCTTCTCGAACTCCTCACCCAAAGATCGGAAGAGCGGTTTCAG
chr3	12625963	12626002	RAF1_5771	-	GTGACCTATGCACCAGACGTACTCTGCTTCCAGTCCAGGGGAGGAGAAGCCAAAGATCGGAAGAGCGGTTTCAG
chr3	12626296	12626335	RAF1_5772	-	GTGACCTATGCACCAGACGTGGGCTGCTAGAATTGTGATTAAGCATTGGGTTGGTTCTGTAAGATCGGAAGAGCGGTTTCAG
chr3	12626571	12626610	RAF1_5773	-	GTGACCTATGCACCAGACGTGCTGGTGCGAAAGGACCCAACTCGTGGGAGCCCCTGGGCCAGATCGGAAGAGCGGTTTCAG
chr3	12627130	12627169	RAF1_5774	-	GTGACCTATGCACCAGACGTGGGCTCCCACACAGCAGTCTCTGGTATAGGGCAAAGGAATAGATCGGAAGAGCGGTTTCAG
chr3	12629040	12629079	RAF1_5775	-	GTGACCTATGCACCAGACGTGTTGTTGAGTTCAATTTGACTGCTCGGTTCTAAATTTAGGGAGATCGGAAGAGCGGTTTCAG
chr3	12632247	12632286	RAF1_5776	-	GTGACCTATGCACCAGACGTGGTCTGATGCCTCTCTGGACCCAGGCATCAAATTTGCCAGATCGGAAGAGCGGTTTCAG
chr3	12633157	12633196	RAF1_5777	-	GTGACCTATGCACCAGACGTAGCTGGCGTCCAGTCCCTCTGGAGTCTGGAGTGGGGAGAGATCGGAAGAGCGGTTTCAG
chr3	12641140	12641179	RAF1_5778	-	GTGACCTATGCACCAGACGTGGCCCTCCCTTTACTAACTGCAGGGCTTTGGTGTGAAGTCAAGATCGGAAGAGCGGTTTCAG
chr3	12641601	12641640	RAF1_5779	-	GTGACCTATGCACCAGACGTACAACAGTACCTCCTGCCAATTAGGGTTCAGTAAGAAAAAAGATCGGAAGAGCGGTTTCAG
chr3	12641837	12641876	RAF1_5780	-	GTGACCTATGCACCAGACGTATAGTCATTTAGCCAAATAATGGGCTTTTTTTCTTTATAGATCGGAAGAGCGGTTTCAG
chr3	12645585	12645624	RAF1_5781	-	GTGACCTATGCACCAGACGTACCTTGGGGGTGGTAAATGTCAAGTCAATTAATGGGGTGGAGAGATCGGAAGAGCGGTTTCAG
chr3	12647650	12647689	RAF1_5782	-	GTGACCTATGCACCAGACGTACCTATAGCTTTTTCTTTAGAAAGTATTTGGGGTGGTGGAGATCGGAAGAGCGGTTTCAG
chr3	12650215	12650254	RAF1_5783	-	GTGACCTATGCACCAGACGTGTTCTTTTTCTAAAGGAAGATAGGGATGAGGAGTATACATAGATCGGAAGAGCGGTTTCAG
chr3	12650682	12650721	RAF1_5784	-	GTGACCTATGCACCAGACGTGATCTCTTCTTTCTGGCATGTTGAGGGCTTTGCCAGGCAGATCGGAAGAGCGGTTTCAG
chr3	12653399	12653438	RAF1_5785	-	GTGACCTATGCACCAGACGTAAAGTCAATTGACTTCTTACAGACTAGTAAGGATCTTCAAGATCGGAAGAGCGGTTTCAG
chr3	12659964	12660003	RAF1_5786	-	GTGACCTATGCACCAGACGTATTCTACTTAGGAAATTTAGCTATTTATCTGCTGTGGAGAGATCGGAAGAGCGGTTTCAG
chr7	128828943	128828982	SMO_5787	-	GTGACCTATGCACCAGACGTGCCAACTCAGCAAAAGCCCGGCCGCCCCCGCTGCTCCTCAGATCGGAAGAGCGGTTTCAG
chr7	128843175	128843214	SMO_5788	-	GTGACCTATGCACCAGACGTCAACAGCATTGCAAGTGAAGGCCCTCCTACTCTGACCCAAAGATCGGAAGAGCGGTTTCAG
chr7	128844994	128845033	SMO_5789	-	GTGACCTATGCACCAGACGTGGATGGGAAAAGACGGTGTCAAGGCAGCTCAGGGACGAGCAGATCGGAAGAGCGGTTTCAG
chr7	128845401	128845440	SMO_5790	-	GTGACCTATGCACCAGACGTGAAGTGGGCCATTCTGTGAGGTTAGGGTTATTCTGCTGACAGATCGGAAGAGCGGTTTCAG
chr7	128845941	128845980	SMO_5791	-	GTGACCTATGCACCAGACGTAGGTGAGGTGTCACTTGGAGCGGCTACTCTGTACTCCCTCAGATCGGAAGAGCGGTTTCAG
chr7	128846255	128846294	SMO_5792	-	GTGACCTATGCACCAGACGTAAGGGGTGGGACAGAAGGTGGGTTACTGGCCCCCTCCCTCAGATCGGAAGAGCGGTTTCAG
chr7	128848550	128848589	SMO_5793	-	GTGACCTATGCACCAGACGTGGGGACCTCAGACATTAGCAGGCTGAGGCTGCCCTGCTAGATCGGAAGAGCGGTTTCAG
chr7	128849080	128849119	SMO_5794	-	GTGACCTATGCACCAGACGTGAGGGCAGGACAGGACTTACCAAGCCAGTCCCCGACAGCATCGGAAGAGCGGTTTCAG
chr7	128850756	128850795	SMO_5795	-	GTGACCTATGCACCAGACGTAAGGGATAGGGAAGGAGCGTGAAGAAGCTGCCACTTCCCAAGATCGGAAGAGCGGTTTCAG
chr7	128851427	128851466	SMO_5796	-	GTGACCTATGCACCAGACGTGGAAGGAAGGAAAGGAGAAGGAATAGTACTTCCCGGTTCCAGATCGGAAGAGCGGTTTCAG
chr7	128851815	128851854	SMO_5797	-	GTGACCTATGCACCAGACGTGAGAGACAACACAGCCTGGGGCCTGGCTGTGCCATGACAGATCGGAAGAGCGGTTTCAG
chr10	104263860	104263899	SUFU_5798	-	GTGACCTATGCACCAGACGTAGGGCAGGCCTGGGGAACTGGAGAGGGCAAACGACGGAGATCGGAAGAGCGGTTTCAG
chr10	104268876	104268915	SUFU_5799	-	GTGACCTATGCACCAGACGTAAAAACAGGGGTTAGTGTAAGCCTGAAATCAGACAAAGATCGGAAGAGCGGTTTCAG
chr10	104309677	104309716	SUFU_5800	-	GTGACCTATGCACCAGACGTTAAAAAGCAAGTGTTTAAGCTCAATTACCTTAGGAAAAAAGATCGGAAGAGCGGTTTCAG

chr10	104352289	104352328	SUFU_5801	-	GTGACCTATGCACCAGACGTGATACAAGGATCCTCATTGTTCAAGGCCCCAGATCCAGGCAGATCGGAAGAGCGGTTTCAG
chr10	104353343	104353382	SUFU_5802	-	GTGACCTATGCACCAGACGTGGATAGAAAGCCATTGTGTGTTAATGGCCACCCCCACCAGATCGGAAGAGCGGTTTCAG
chr10	104353700	104353739	SUFU_5803	-	GTGACCTATGCACCAGACGTGGAAAGGGGATACAATGGTAACTGAGGGTCTGGGGCTGATAGATCGGAAGAGCGGTTTCAG
chr10	104356847	104356886	SUFU_5804	-	GTGACCTATGCACCAGACGTAGAACCAAAGGCCAGAGTCTTTTCAGAGAACTGGTGACCAGATCGGAAGAGCGGTTTCAG
chr10	104359140	104359179	SUFU_5805	-	GTGACCTATGCACCAGACGTACCATAAGTTGCCAGTGGCCCACTGGGCTCCAGCAATAGATCGGAAGAGCGGTTTCAG
chr10	104374975	104375014	SUFU_5806	-	GTGACCTATGCACCAGACGTAGCACAGGAAAGGTTCCGGACAAGGTGAAAGCTCAGGGAGATCGGAAGAGCGGTTTCAG
chr10	104376997	104377036	SUFU_5807	-	GTGACCTATGCACCAGACGTGAACATGGAGACAGTGAGGAGCTGGGCTTGGAAACACTTCAGATCGGAAGAGCGGTTTCAG
chr10	104386882	104386921	SUFU_5808	-	GTGACCTATGCACCAGACGTACAAGGCAGGCTTTTATTATTATTTTAAATGTATGATCTAGATCGGAAGAGCGGTTTCAG
chr10	104389773	104389812	SUFU_5809	-	GTGACCTATGCACCAGACGTAGCAAGCACAGACCAGGAGTGTGAGTGGTTAGCAGAATACAGATCGGAAGAGCGGTTTCAG
chr1	47685342	47685381	TAL1_5810	-	GTGACCTATGCACCAGACGTCCACCAGGATCAGCCAGGAGGGCGTCTTAGGCTGCTGGGAGATCGGAAGAGCGGTTTCAG
chr1	47689626	47689665	TAL1_5811	-	GTGACCTATGCACCAGACGTCCCACCCACCCTGTGTACCTGCCCTCACGCTGGTTAGAGAGATCGGAAGAGCGGTTTCAG
chr14	76425480	76425519	TGFB3_5812	-	GTGACCTATGCACCAGACGTGGCAGAGAGAGGGGAGAGAGAACCCACTGCCTGACTAGATCGGAAGAGCGGTTTCAG
chr14	76427216	76427255	TGFB3_5813	-	GTGACCTATGCACCAGACGTGGCTGGCTGATGCTGAGGCATGGGGCTGACCGACACAGATCGGAAGAGCGGTTTCAG
chr14	76429609	76429648	TGFB3_5814	-	GTGACCTATGCACCAGACGTGCCACATGGGAACCAACTCTACTGCCTGCCTACTGCCAGATCGGAAGAGCGGTTTCAG
chr14	76431881	76431920	TGFB3_5815	-	GTGACCTATGCACCAGACGTGAATGTGTATGGTAGGATGGGTGAGTGGGGGGGAAGTTAAAGATCGGAAGAGCGGTTTCAG
chr14	76437419	76437458	TGFB3_5816	-	GTGACCTATGCACCAGACGTCTTCAGATAAGCATTTTCAGAAATGAACCTCAGGTCCTTAAAGATCGGAAGAGCGGTTTCAG
chr14	76437848	76437887	TGFB3_5817	-	GTGACCTATGCACCAGACGTCTCAGAGCAAAACCCAGCGGAAAGCTGGTTCCTAGATCGGAAGAGCGGTTTCAG
chr14	76446835	76446874	TGFB3_5818	-	GTGACCTATGCACCAGACGTATTCTCGCTGGGGTGTCTGCTCTGGAGGGTCTGAAGTGGAAAGATCGGAAGAGCGGTTTCAG
chr17	76170790	76170829	TK1_5819	-	GTGACCTATGCACCAGACGTAGGGCCGCCCGCTCCCTTCTGCCACTGCCCTACTGGAAGATCGGAAGAGCGGTTTCAG
chr17	76171081	76171120	TK1_5820	-	GTGACCTATGCACCAGACGTCTGCCTTCCTGCAGGCCGGCGGGGTGGGGGTATGGCTCTAGATCGGAAGAGCGGTTTCAG
chr17	76171560	76171599	TK1_5821	-	GTGACCTATGCACCAGACGTGTATCCAGTCTGAGACTGGGATTGAGGAGGGCAAGAGGCAGATCGGAAGAGCGGTTTCAG
chr17	76178620	76178659	TK1_5822	-	GTGACCTATGCACCAGACGTGTGTCTTGGCATCACTTCTCCTGCCAGTTCCTCGCTCTGTGATCGGAAGAGCGGTTTCAG
chr17	76181086	76181125	TK1_5823	-	GTGACCTATGCACCAGACGTGCCCCCTGCAGTCTTCCAGTGCCAGTGAAATCACAAAGGCACAGATCGGAAGAGCGGTTTCAG
chr17	76182818	76182857	TK1_5824	-	GTGACCTATGCACCAGACGTGCCCGGCTGGGGTGGAGTCTCCTCTTCTCCGGGACAGATCGGAAGAGCGGTTTCAG
chr17	76182960	76182999	TK1_5825	-	GTGACCTATGCACCAGACGTGAGCCCTGCCGCTGGGCTGGGGATGAGGTGGTCTGGTATAGATCGGAAGAGCGGTTTCAG
chr12	48238479	48238518	VDR_5826	-	GTGACCTATGCACCAGACGTCTGTGGCGGTGCCTGGGTGGGGCTGCTCCTCCAGGGCCACAGATCGGAAGAGCGGTTTCAG
chr12	48240068	48240107	VDR_5827	-	GTGACCTATGCACCAGACGTAGGCAGGGAGGAGCTCAGGGACCTGGGGAGCGGGGAGATAGATCGGAAGAGCGGTTTCAG
chr12	48240390	48240429	VDR_5828	-	GTGACCTATGCACCAGACGTACTCCACCTCCTGGGGAGCTTTTTTCAGTCCCAGATTCAGATCGGAAGAGCGGTTTCAG
chr12	48249363	48249402	VDR_5829	-	GTGACCTATGCACCAGACGTTCGCAATCTCTGGGGAAGCAGATCAGATCTCAGATCGGAAGAGCGGTTTCAG
chr12	48250862	48250901	VDR_5830	-	GTGACCTATGCACCAGACGTCTTCAGTCTCCATAGATAAGTAGAGCGGGGCGCAGGAGTAGATCGGAAGAGCGGTTTCAG
chr12	48251237	48251276	VDR_5831	-	GTGACCTATGCACCAGACGTCTGCTGGGAGGATGAGCCGGTCCAGAGGAGAAGCACTAGTAGATCGGAAGAGCGGTTTCAG
chr12	48258780	48258819	VDR_5832	-	GTGACCTATGCACCAGACGTAGGGGCTGGGCAGGGTTTTGGGCCTGAAGTGGAGTCAAGGAGATCGGAAGAGCGGTTTCAG
chr12	48272701	48272740	VDR_5833	-	GTGACCTATGCACCAGACGTCTCCAGGCTCTCCCAAGTGGAAAGGGAGGGAGAAGAAGCAGATCGGAAGAGCGGTTTCAG
chr4	89013336	89013375	ABCG2_5834	-	GTGACCTATGCACCAGACGTAAATTCAGTATTATTCCTCACATAAAAAAGAAGCACTTAGATCGGAAGAGCGGTTTCAG
chr4	89015679	89015718	ABCG2_5835	-	GTGACCTATGCACCAGACGTAAATGGTGTTCGAAATACTCAAATGGCTTTTTGTACTACCATGGTGTGAAGATCGGAAGAGCGGTTTCAG
chr4	89016622	89016661	ABCG2_5836	-	GTGACCTATGCACCAGACGTCTTGTCTGTCACTGTGACTGCATTCCCAAGCTAGGAACAAGATCGGAAGAGCGGTTTCAG
chr4	89018555	89018594	ABCG2_5837	-	GTGACCTATGCACCAGACGTACTGTGTTTGTCTGATAAGGAATGTTTTTTTCTTCATAGATCGGAAGAGCGGTTTCAG
chr4	89020426	89020465	ABCG2_5838	-	GTGACCTATGCACCAGACGTAAACAAAACAAAAGGACATGCTTTTGTAGTCTTGCCTATGGAGATCGGAAGAGCGGTTTCAG
chr4	89022332	89022371	ABCG2_5839	-	GTGACCTATGCACCAGACGTCTTTGTTCTGGGAACGGGGCTGTCCAGCAGCAGGGGCTATAGATCGGAAGAGCGGTTTCAG
chr4	89028286	89028325	ABCG2_5840	-	GTGACCTATGCACCAGACGTGGATCTTGATTTTCAGAAAATGCTGTACTTTCTTCAAAGATCGGAAGAGCGGTTTCAG
chr4	89034405	89034444	ABCG2_5841	-	GTGACCTATGCACCAGACGTGTTCTTTTGTGAAATCTCAAATGGGAACAATGTGGTCTGAGATCGGAAGAGCGGTTTCAG
chr4	89036059	89036098	ABCG2_5842	-	GTGACCTATGCACCAGACGTCTGTACAGTCCCAGATTTTTGCCTAATTGAATTGGCTGAAGATCGGAAGAGCGGTTTCAG
chr4	89039211	89039250	ABCG2_5843	-	GTGACCTATGCACCAGACGTCTTTTTATGCTGTAAAATGCTTCATTAATAGAATCCTGAAGATCGGAAGAGCGGTTTCAG
chr4	89052163	89052202	ABCG2_5844	-	GTGACCTATGCACCAGACGTAAAACCTGAAAGCATCATGATCAGCATAAGTAGGACTTTCAGATCGGAAGAGCGGTTTCAG
chr4	89052905	89052944	ABCG2_5845	-	GTGACCTATGCACCAGACGTGGGGTTTGCATTTTCTGTTTCTGTTTCTATATGGGTAGATCGGAAGAGCGGTTTCAG
chr4	89053678	89053717	ABCG2_5846	-	GTGACCTATGCACCAGACGTGAGAGTATAAGTAAGCGTTTTCTGTGACTTTTAAATGTCAGATCGGAAGAGCGGTTTCAG
chr4	89060895	89060934	ABCG2_5847	-	GTGACCTATGCACCAGACGTGAACCTGTAAAAAGACAGCTTTTTAATTTACCTACAGTGAAGATCGGAAGAGCGGTTTCAG
chr5	131289877	131289916	ACSL6_5848	-	GTGACCTATGCACCAGACGTAAAGTCTTCTCAGTGAATGAAGTGTCTAGCAATATTATAAGATCGGAAGAGCGGTTTCAG
chr5	131295179	131295218	ACSL6_5849	-	GTGACCTATGCACCAGACGTCTTCCCACTACTCTGTACAACCTTCAGGCAGTGTGAAAGATCGGAAGAGCGGTTTCAG
chr5	131296163	131296202	ACSL6_5850	-	GTGACCTATGCACCAGACGTGGGGCTGTCTCCTGAAAGTTACTGAATGTTTTATGGTAAGATCGGAAGAGCGGTTTCAG
chr5	131298178	131298217	ACSL6_5851	-	GTGACCTATGCACCAGACGTTAGGCTTAGCCCTCCCACTATCTGGGCATGCTGAAAAGATCGGAAGAGCGGTTTCAG
chr5	131302059	131302098	ACSL6_5852	-	GTGACCTATGCACCAGACGTTTGGAAACCGAGCTCCAAACATTTGGCAGTGGGAGGTAGATCGGAAGAGCGGTTTCAG
chr5	131303583	131303622	ACSL6_5853	-	GTGACCTATGCACCAGACGTATTTAGCCATTCTGCTGTGGCTGTCTACATGTAGTGAGTAGATCGGAAGAGCGGTTTCAG
chr5	131305771	131305810	ACSL6_5854	-	GTGACCTATGCACCAGACGTCTAGAGATATAGGACTGGCTCGCGAGGCAGTGTGGAGTAAAGATCGGAAGAGCGGTTTCAG
chr5	131307193	131307232	ACSL6_5855	-	GTGACCTATGCACCAGACGTGTGTGTCTCCCTTGGAAACAGCAGGAAGTTCTGTAGGGAGATCGGAAGAGCGGTTTCAG
chr5	131308367	131308406	ACSL6_5856	-	GTGACCTATGCACCAGACGTGAACAAGTGATTATAGATGACACCTAAGTATCCAACGGGAGATCGGAAGAGCGGTTTCAG
chr5	131308909	131308948	ACSL6_5857	-	GTGACCTATGCACCAGACGTCCAGGAGTCTCAGCCAGGCTGAGGGGCTGCATATTTGCTAGATCGGAAGAGCGGTTTCAG
chr5	131310401	131310440	ACSL6_5858	-	GTGACCTATGCACCAGACGTGGCATCAGGGAGCCACTCTGTGCCTAGAACCATAACCAGATCGGAAGAGCGGTTTCAG

chr5	131310536	131310575	ACSL6_5859	-	GTGACCTATGCACCAGACGTACCTGACTGACCGGGCCTTGCTGGGCTCCTCTTTTTAGATCGGAAGAGCGGTTTCAG
chr5	131312291	131312330	ACSL6_5860	-	GTGACCTATGCACCAGACGTTAGCATTACTGTTGCAGGTGTCTCTTGAGGACAACCTCAAAGATCGGAAGAGCGGTTTCAG
chr5	131321050	131321089	ACSL6_5861	-	GTGACCTATGCACCAGACGTGCACGCAGATCCCCAGCCATGGCTACCTGCACCCTTCCTAGATCGGAAGAGCGGTTTCAG
chr5	131322465	131322504	ACSL6_5862	-	GTGACCTATGCACCAGACGTTACCTGCAGGTCTTTATTGAGCGAGATGGCGTGCAGGGCAGATCGGAAGAGCGGTTTCAG
chr5	131323691	131323730	ACSL6_5863	-	GTGACCTATGCACCAGACGTGCTTCTGGGCGGTTTGCTGGGCTACTGCTGGCTGGTACCAGATCGGAAGAGCGGTTTCAG
chr5	131324448	131324487	ACSL6_5864	-	GTGACCTATGCACCAGACGTTGCCACCCACCTTGCCACTGGCAACTGGTCCCCAGCCTCAGATCGGAAGAGCGGTTTCAG
chr5	131325050	131325089	ACSL6_5865	-	GTGACCTATGCACCAGACGTGTCTGACTGTTAGCTGGTTTTAGAGGGATTCTGGGGTAGGGTTGAGATCGGAAGAGCGGTTTCAG
chr5	131325743	131325782	ACSL6_5866	-	GTGACCTATGCACCAGACGTACAGGACAGGCCACCCTGGCCACCATTAGATCTGGCAAGATCGGAAGAGCGGTTTCAG
chr5	131326496	131326535	ACSL6_5867	-	GTGACCTATGCACCAGACGTTTGTGGGGGGGGTGTGGAGGGGCTGTGTGGCAGGGTGGAGATCGGAAGAGCGGTTTCAG
chr5	131329674	131329713	ACSL6_5868	-	GTGACCTATGCACCAGACGTAGGAGACGTTCCACTGCGGAAAGTAGGGGGCAGAGGACAAGATCGGAAGAGCGGTTTCAG
chr5	131347148	131347187	ACSL6_5869	-	GTGACCTATGCACCAGACGTGTCTGTCCGCTCCCGGACTCCCATCTCCCGCAGGCTATAGATCGGAAGAGCGGTTTCAG
chr20	43248425	43248464	ADA_5870	-	GTGACCTATGCACCAGACGTCTCCAAGCTTCACTGTGGAGTCAACCCAACTCTGTGATCGGAAGAGCGGTTTCAG
chr20	43248890	43248929	ADA_5871	-	GTGACCTATGCACCAGACGTGTCTGGGCTTCTGGGCTTCTGGGCTGCTGCTGGCCCTGCTGCCCCAGTGAGATCGGAAGAGCGGTTTCAG
chr20	43249609	43249648	ADA_5872	-	GTGACCTATGCACCAGACGTGTGAGCCATACTGGCCTTGACTCGGGTTTGGGAGTATGGTAGATCGGAAGAGCGGTTTCAG
chr20	43251179	43251218	ADA_5873	-	GTGACCTATGCACCAGACGTTTCCCTGGGCTGTTCAATTTTGTCCAGGAAGGCCAAAAGATCGGAAGAGCGGTTTCAG
chr20	43251420	43251459	ADA_5874	-	GTGACCTATGCACCAGACGTACGGGAGTGGGGAGGAACCATCCCCGGCTGTCCAACCTCAGATCGGAAGAGCGGTTTCAG
chr20	43251598	43251637	ADA_5875	-	GTGACCTATGCACCAGACGTGGGCTGGCCATGGGGTCCCTCCTCCTGCTCCTCCATAAGATCGGAAGAGCGGTTTCAG
chr20	43252793	43252832	ADA_5876	-	GTGACCTATGCACCAGACGTGTGAGAAGGAATGGAGAGGCTGGCCCTGGGTGAGCTGTCTAGATCGGAAGAGCGGTTTCAG
chr20	43254160	43254199	ADA_5877	-	GTGACCTATGCACCAGACGTTACCGCCCTGCCAGGGCCGGCTCTCACCTGGCCCTAGATCGGAAGAGCGGTTTCAG
chr20	43255047	43255086	ADA_5878	-	GTGACCTATGCACCAGACGTGGCCTGGAAGGGGCCATGCTGAGGGTGTGGCTGGGAGGCTAGATCGGAAGAGCGGTTTCAG
chr20	43257638	43257677	ADA_5879	-	GTGACCTATGCACCAGACGTCCCAACCCACAGGTCTTAGGGCAGCATTGATCCCTATGACAGATCGGAAGAGCGGTTTCAG
chr20	43264818	43264857	ADA_5880	-	GTGACCTATGCACCAGACGTACAGAAGAGCCCTCTCCTCCTGGGATTTGAGTGGGGTCCCAGATCGGAAGAGCGGTTTCAG
chr20	43280166	43280205	ADA_5881	-	GTGACCTATGCACCAGACGTGCGGGGCTCCGGGAGCGGGGTCGGGCGCTGGGCGCCAGATCGGAAGAGCGGTTTCAG
chr9	21968252	21968291	CDKN2A_5882	+	GTGACCTATGCACCAGACGTGACAGAAGAACAGGCGTTAGAAACCTGAGTCAAAGATGAGATCGGAAGAGCGGTTTCAG
chr9	21971218	21971257	CDKN2A_5883	+	GTGACCTATGCACCAGACGTGAACAGAATGGTCAGAGCCAGGGTGGGGCCGGCATGACGAGATCGGAAGAGCGGTTTCAG
chr9	21974837	21974876	CDKN2A_5884	+	GTGACCTATGCACCAGACGTGCCGCCGCTGCCTGCTCCTCCCTCCTCCGACCCGCCAAGATCGGAAGAGCGGTTTCAG
chr7	55210141	55210180	EGFR_5885	+	GTGACCTATGCACCAGACGTTTGAATTTTCTACACAAATAAAATTGGAGAAAATCTAAGTAGATCGGAAGAGCGGTTTCAG
chr7	55211192	55211231	EGFR_5886	+	GTGACCTATGCACCAGACGTGGGATGCCAAGGCTGGGGGTTTATAAATGCAGACAGCAGTAGATCGGAAGAGCGGTTTCAG
chr7	55214444	55214483	EGFR_5887	+	GTGACCTATGCACCAGACGTATACACACTATCTCTGCTCCCTCCTATGGGGACAGATCGGAAGAGCGGTTTCAG
chr7	55219066	55219105	EGFR_5888	+	GTGACCTATGCACCAGACGTGAACAGCCTACAGCCATGTGTGACCCCTCTCTTCTTCTAGATCGGAAGAGCGGTTTCAG
chr7	55220368	55220407	EGFR_5889	+	GTGACCTATGCACCAGACGTCTCCAGCAGCCTCCCTGGAGCAGGCTGGGGTGCACCCGAGATCGGAAGAGCGGTTTCAG
chr7	55221856	55221895	EGFR_5890	+	GTGACCTATGCACCAGACGTCTGTGGGCTCTAACTGGTACAGCATCCTTGTCCCGCAGATCGGAAGAGCGGTTTCAG
chr7	55223650	55223689	EGFR_5891	+	GTGACCTATGCACCAGACGTGCGCCGTGTGCGGAGCAGGCTGTTCTCGGCTGCTGAGGCAGATCGGAAGAGCGGTTTCAG
chr7	55224363	55224402	EGFR_5892	+	GTGACCTATGCACCAGACGTGGTTGCTGTTGTTATAAAGAAAAAATACTGCCTTTAGATCGGAAGAGCGGTTTCAG
chr7	55224536	55224575	EGFR_5893	+	GTGACCTATGCACCAGACGTAATATACATGAAATGGAATAACAGTGTGTTTAGAAGATCGGAAGAGCGGTTTCAG
chr7	55224547	55224586	EGFR_5894	+	GTGACCTATGCACCAGACGTGAATATAAATGGAAATCAGTGTGTTTAGAGAGAGAATTTAGATCGGAAGAGCGGTTTCAG
chr7	55228042	55228081	EGFR_5895	+	GTGACCTATGCACCAGACGTGCTTCTGTTTAGTTTAGTTAGTTGGTCTAATGGTCTAGATCGGAAGAGCGGTTTCAG
chr7	55229335	55229374	EGFR_5896	+	GTGACCTATGCACCAGACGTTATTTCTTAATCCCTTGGCTTGATCAAAAATAAGGCTCCAGATCGGAAGAGCGGTTTCAG
chr7	55231527	55231566	EGFR_5897	+	GTGACCTATGCACCAGACGTCTTGTCTATCCACGTCATTTTATGGGAAGGGCTTCAAGATCGGAAGAGCGGTTTCAG
chr7	55233141	55233180	EGFR_5898	+	GTGACCTATGCACCAGACGTAGTGAAGGAGAACAGAACATTTCTCCTTGCATAATCAGAGATCGGAAGAGCGGTTTCAG
chr7	55236233	55236272	EGFR_5899	+	GTGACCTATGCACCAGACGTCTGTCTGACTTTAGTCTCCACTCAAACTGCATTTCTTTAGATCGGAAGAGCGGTTTCAG
chr7	55238248	55238287	EGFR_5900	+	GTGACCTATGCACCAGACGTTTACGTTGTTTCCCCCGCTTTTCTTTCTGCCACCCAGATCGGAAGAGCGGTTTCAG
chr7	55238917	55238956	EGFR_5901	+	GTGACCTATGCACCAGACGTACAGCTCTGTGTACATGGACCTCGTCAAAGATGACCACAAGATCGGAAGAGCGGTTTCAG
chr7	55240828	55240867	EGFR_5902	+	GTGACCTATGCACCAGACGTGTCTGCTGGGCTCAGGAGCCCTCGCACCCCGACAGAAAGATCGGAAGAGCGGTTTCAG
chr7	55241747	55241786	EGFR_5903	+	GTGACCTATGCACCAGACGTTGCCACGCTCTGGGCTGGGCGCAGGGCTCTCATGGAGATCGGAAGAGCGGTTTCAG
chr7	55242524	55242563	EGFR_5904	+	GTGACCTATGCACCAGACGTGCTTGTGCTGTGGGGTCCATGGCTCTGAACCTCAGGCCAGATCGGAAGAGCGGTTTCAG
chr7	55249182	55249221	EGFR_5905	+	GTGACCTATGCACCAGACGTAAGGGAGATACGGGGAGGGAGATAAGGAGCCAGGATCTAGATCGGAAGAGCGGTTTCAG
chr7	55259578	55259617	EGFR_5906	+	GTGACCTATGCACCAGACGTGGCTTTAGGTACGCCAGCATTTTCTGACACCAGGGACCAAGATCGGAAGAGCGGTTTCAG
chr7	55260545	55260584	EGFR_5907	+	GTGACCTATGCACCAGACGTATCCTGATGCTAATGAGTTTGTACTGAGGCCAAGCTGGCTAGATCGGAAGAGCGGTTTCAG
chr7	55266567	55266606	EGFR_5908	+	GTGACCTATGCACCAGACGTGGTGGGCTGTGTCCACTGCCTAGCTGAGCCCTGGTGGCTAGATCGGAAGAGCGGTTTCAG
chr7	55268117	55268156	EGFR_5909	+	GTGACCTATGCACCAGACGTGACTGTGCTTCCATTGGGAAGATCCCTTAATGAGCAAGATCGGAAGAGCGGTTTCAG
chr7	55269059	55269098	EGFR_5910	+	GTGACCTATGCACCAGACGTGCTGTCTCTCTTCTCAAGCTGTGTCTACTCATTTGAGATCGGAAGAGCGGTTTCAG
chr7	55269486	55269525	EGFR_5911	+	GTGACCTATGCACCAGACGTACACCTTATAAGCCAGAATTTACAGCTCTCCACTATGGCTAGATCGGAAGAGCGGTTTCAG
chr7	55270329	55270368	EGFR_5912	+	GTGACCTATGCACCAGACGTTGTCTGGAACAGTCTGCTCCTCAACCTCCTGACCCACAGATCGGAAGAGCGGTTTCAG
chr7	55273321	55273360	EGFR_5913	+	GTGACCTATGCACCAGACGTTAGTATGAGCCCTAAAATCCAGACTTTTCTGATACCCAGAGATCGGAAGAGCGGTTTCAG
chr17	7573019	7573058	TP53_5914	+	GTGACCTATGCACCAGACGTACAGAAGCAGGGAGGAGATGACATCAGATGAGTGGAGGAGATCGGAAGAGCGGTTTCAG
chr17	7576595	7576634	TP53_5915	+	GTGACCTATGCACCAGACGTTCAAAGCATGAAACATTTTCTGCTCTTTAAACAATTTAGATCGGAAGAGCGGTTTCAG
chr17	7576668	7576707	TP53_5916	+	GTGACCTATGCACCAGACGTTATATTGGTATAAGTTGGTGTCTCAAGTTAGTTAGTATGATCGGAAGAGCGGTTTCAG

chr17	7576937	7576976	TP53_5917	+	GTGACCTATGCACCAGACGTGGCAAGGAAAGGTGATAAAAGTAATCTGAGGCATAACTGAGATCGGAAGAGCGGTTTCAG
chr17	7577166	7577205	TP53_5918	+	GTGACCTATGCACCAGACGTTAGGAAAAGAGAAGCAAGAGCGCAGTAAGGAAATCAGGTCCAGATCGGAAGAGCGGTTTCAG
chr17	7577619	7577658	TP53_5919	+	GTGACCTATGCACCAGACGTACACAGGCCCAAGATGAGGCCAGTGCGCCTTGGGGAGACCAGATCGGAAGAGCGGTTTCAG
chr17	7578300	7578339	TP53_5920	+	GTGACCTATGCACCAGACGTTGAGGAAATCAGAGGCCCTGGGGACCCTGGGCAACCAGAGATCGGAAGAGCGGTTTCAG
chr17	7578565	7578604	TP53_5921	+	GTGACCTATGCACCAGACGTAGGAAGGAGACAGAGTTGAAAGTCAAGGGCACAAAGTGAACAAGATCGGAAGAGCGGTTTCAG
chr17	7579732	7579771	TP53_5922	+	GTGACCTATGCACCAGACGTAGACAGCAAAGTCAAGTCCCATTGGAATTTTCGCTTCCCACAAGATCGGAAGAGCGGTTTCAG
chr17	7579923	7579962	TP53_5923	+	GTGACCTATGCACCAGACGTCGGAAGGAGCGTGGCTGCTGCAAGAGGAAAAGTGGGGATAGATCGGAAGAGCGGTTTCAG
chr3	178916976	178917015	PIK3CA_5924	+	GTGACCTATGCACCAGACGTATATCCTATTCTAAAATGCAAATAACCATAAAGCTTAACTAGATCGGAAGAGCGGTTTCAG
chr3	178917698	178917737	PIK3CA_5925	+	GTGACCTATGCACCAGACGTGACTAATCTACTCTAATCATTACTATAGTGCAGTCTTCTAAGATCGGAAGAGCGGTTTCAG
chr3	178921588	178921627	PIK3CA_5926	+	GTGACCTATGCACCAGACGTATGCTGATGCTTATTATTTATAGAAATTTATTTAGATAAAGATCGGAAGAGCGGTTTCAG
chr3	178922387	178922426	PIK3CA_5927	+	GTGACCTATGCACCAGACGTATATGATTTATATTTCCAAAGGTTATATTAGTGTGTTAGCAGATCGGAAGAGCGGTTTCAG
chr3	178927499	178927538	PIK3CA_5928	+	GTGACCTATGCACCAGACGTTCCAGAAACAATTATGTTTACCTTTAAAAAACCCTGATAGATCGGAAGAGCGGTTTCAG
chr3	178928137	178928176	PIK3CA_5929	+	GTGACCTATGCACCAGACGTTATTGTGATAAAATAGATATTTTTTATGGCAGTCAAACCTAGATCGGAAGAGCGGTTTCAG
chr3	178928364	178928403	PIK3CA_5930	+	GTGACCTATGCACCAGACGTTCACTGAGTTTTATTAAGTATCAATTATACTGTGGATTAGATCGGAAGAGCGGTTTCAG
chr3	178936133	178936172	PIK3CA_5931	+	GTGACCTATGCACCAGACGTAAATGGAGATTCTCTGTTTCTTTTCTTTATACAGAAAAGATCGGAAGAGCGGTTTCAG
chr3	178937076	178937115	PIK3CA_5932	+	GTGACCTATGCACCAGACGTGTTTGAGATTACTAGATAACTGTTGTACAAATTTGGTATGTAGATCGGAAGAGCGGTTTCAG
chr3	178937851	178937890	PIK3CA_5933	+	GTGACCTATGCACCAGACGTTTATTTCCCAATTAATCTTAAAGTACATATTACTTGGCTAGATCGGAAGAGCGGTTTCAG
chr3	178938956	178938995	PIK3CA_5934	+	GTGACCTATGCACCAGACGTCAGTTGTGTTTTGAGACTCTTTTCACTGCAGTGGGGCAGAGATCGGAAGAGCGGTTTCAG
chr3	178941986	178942025	PIK3CA_5935	+	GTGACCTATGCACCAGACGTGGGGGTTTCTATTGATATTTAAATAAATACCTTTTCTGGAGATCGGAAGAGCGGTTTCAG
chr3	178942620	178942659	PIK3CA_5936	+	GTGACCTATGCACCAGACGTGATTAATGAGCTTATGATGCATGAATTTAGCTATCTTTTAGATCGGAAGAGCGGTTTCAG
chr3	178943839	178943878	PIK3CA_5937	+	GTGACCTATGCACCAGACGTAGTAAGGCAACCTGTATGTTGAAAGTTATCCTGAAAAAGTAGATCGGAAGAGCGGTTTCAG
chr3	178947241	178947280	PIK3CA_5938	+	GTGACCTATGCACCAGACGTTTATTCTTTCTTCTCTATGTTAATCTAAGTTTTTGTGATAGATCGGAAGAGCGGTTTCAG
chr3	178947920	178947959	PIK3CA_5939	+	GTGACCTATGCACCAGACGTTCTGTTTTAAATTTTGGTGTCTTAAATTTATTCAAGATCGGAAGAGCGGTTTCAG
chr3	178948175	178948214	PIK3CA_5940	+	GTGACCTATGCACCAGACGTGCAATTAATAAACACAAAAAAGAGTTTCTGGCTGCTATAGATCGGAAGAGCGGTTTCAG
chr3	178952163	178952202	PIK3CA_5941	+	GTGACCTATGCACCAGACGTGAGAAAATGAAAGCTCACTCTGGATTCCACACTGCACTGTAGATCGGAAGAGCGGTTTCAG
chr13	48878196	48878235	RB1_5942	+	GTGACCTATGCACCAGACGTAGAGCCGCCCTGCGCTCACGCGGGAAGGGCGCCCCGGGTGAGATCGGAAGAGCGGTTTCAG
chr13	48916861	48916900	RB1_5943	+	GTGACCTATGCACCAGACGTTTGTATAAATATAAGCCTCTGCCATAAAGGAAACGAATTAGATCGGAAGAGCGGTTTCAG
chr13	48919346	48919385	RB1_5944	+	GTGACCTATGCACCAGACGTCAATTTATTAGGTTTACACTCTGATTTTTTATGTATTGTAGATCGGAAGAGCGGTTTCAG
chr13	48922010	48922049	RB1_5945	+	GTGACCTATGCACCAGACGTACAGAATTTATTTTTCACTTAAAAAAAAGATTTTTATAGATCGGAAGAGCGGTTTCAG
chr13	48923170	48923209	RB1_5946	+	GTGACCTATGCACCAGACGTTATTTTAAATGTAATAATTTCAAATGTAATAAATAAAGATCGGAAGAGCGGTTTCAG
chr13	48937104	48937143	RB1_5947	+	GTGACCTATGCACCAGACGTTTCATGATTTCTTTAAAACAGTTAAAGTAGATTTAGATGTAGATCGGAAGAGCGGTTTCAG
chr13	48939118	48939157	RB1_5948	+	GTGACCTATGCACCAGACGTAGGAAATTAATAAAATATTAATGTTTTGAGACTGTGGAGAGATCGGAAGAGCGGTTTCAG
chr13	48941750	48941789	RB1_5949	+	GTGACCTATGCACCAGACGTTGGTATATTTGATTGTTTCTTTAGATATAGTTGATACAGATCGGAAGAGCGGTTTCAG
chr13	48947639	48947678	RB1_5950	+	GTGACCTATGCACCAGACGTTGAAACATTTATTGTAATATCTTGGCAAAGAAACATAGATCGGAAGAGCGGTTTCAG
chr13	48951181	48951220	RB1_5951	+	GTGACCTATGCACCAGACGTTTATGTAATTTCTGGTACTATAGAGTAATAATATTAAAGATCGGAAGAGCGGTTTCAG
chr13	48954388	48954427	RB1_5952	+	GTGACCTATGCACCAGACGTTTTTTCATAAATAAACACTTTTTGTTCAATTTAAAGTTAAAAAGATCGGAAGAGCGGTTTCAG
chr13	48955590	48955629	RB1_5953	+	GTGACCTATGCACCAGACGTAATAATTGAAGAAATTCATTCATGTGCATATGGCTAACAAAGATCGGAAGAGCGGTTTCAG
chr13	49027258	49027297	RB1_5954	+	GTGACCTATGCACCAGACGTTATATGTTATGTTGACCATTCAAACCTGCAAATAGATTTTAAAGATCGGAAGAGCGGTTTCAG
chr13	49033980	49034019	RB1_5955	+	GTGACCTATGCACCAGACGTCAAGCACTTCACTTCTCTCCTCCTACTTACTTGTTAACAGATCGGAAGAGCGGTTTCAG
chr13	49037982	49038021	RB1_5956	+	GTGACCTATGCACCAGACGTTCCATAGTAAGTTTTTTGATAAATCCATATCCATAACAAGATCGGAAGAGCGGTTTCAG
chr13	49039258	49039297	RB1_5957	+	GTGACCTATGCACCAGACGTAGTATCTTGTATTGAAAAAATCTAATGTAATGGGTCCACAGATCGGAAGAGCGGTTTCAG
chr13	49039515	49039554	RB1_5958	+	GTGACCTATGCACCAGACGTTCTCTTAGGGAAGTAGTAAAGAATGAGAGGGGGATTATTAGATCGGAAGAGCGGTTTCAG
chr13	49047537	49047576	RB1_5959	+	GTGACCTATGCACCAGACGTTCTTCTATGAAATATAATAGTATGCATTGTAAGTATAAAAGATCGGAAGAGCGGTTTCAG
chr13	49050990	49051029	RB1_5960	+	GTGACCTATGCACCAGACGTGTTTTGAATGTTTTCCAGTACCGGAGATGGTCATCTGGGGAGATCGGAAGAGCGGTTTCAG
chr13	49051551	49051590	RB1_5961	+	GTGACCTATGCACCAGACGTTTTTTCACCTTGTTGTAATGAAATAAACAAATTTTACACTAGATCGGAAGAGCGGTTTCAG
chr13	49054218	49054257	RB1_5962	+	GTGACCTATGCACCAGACGTACCTTGGTGGACACTGTGTACACTCTGGATTCAATGTTCTAGATCGGAAGAGCGGTTTCAG
chr17	29422398	29422437	NF1_5963	+	GTGACCTATGCACCAGACGTGCTGGCGGGCGGGAGGTGGGAGCGGAGTGGGGGTGGGGACAGATCGGAAGAGCGGTTTCAG
chr17	29483155	29483194	NF1_5964	+	GTGACCTATGCACCAGACGTGGGTTACTGTGTTTTGGGGAATTTGCTTTCTTTTCTTTTATAGATCGGAAGAGCGGTTTCAG
chr17	29486122	29486161	NF1_5965	+	GTGACCTATGCACCAGACGTTGATCTTAAGTAGGCAGGCTTTGTGAATTTGATCTTGAGAAGATCGGAAGAGCGGTTTCAG
chr17	29490405	29490444	NF1_5966	+	GTGACCTATGCACCAGACGTTAAATCCACATGGGACTCAAGTAATATGAATATTAGAAAGATCGGAAGAGCGGTTTCAG
chr17	29497026	29497065	NF1_5967	+	GTGACCTATGCACCAGACGTATGTAATATATCTGAAAAAATCACTGGGTCAAAAACATAGATCGGAAGAGCGGTTTCAG
chr17	29508518	29508557	NF1_5968	+	GTGACCTATGCACCAGACGTACCTCTCTGGTATGAAATTTGTTTTTGTGTTGATAAATTTAGATCGGAAGAGCGGTTTCAG
chr17	29508814	29508853	NF1_5969	+	GTGACCTATGCACCAGACGTGATTGATTTTTTTTTTTTTTTTGTCTTTTAAATGCCTACTAGATCGGAAGAGCGGTTTCAG
chr17	29509694	29509733	NF1_5970	+	GTGACCTATGCACCAGACGTCAAATATTTCATTATATCTAGATGTGAAGCAGTTTATAGATCGGAAGAGCGGTTTCAG
chr17	29527624	29527663	NF1_5971	+	GTGACCTATGCACCAGACGTTATCTTCTCTACTACAACCTTAAAGAAAATTAATGAAAGATCGGAAGAGCGGTTTCAG
chr17	29528188	29528227	NF1_5972	+	GTGACCTATGCACCAGACGTTGGTTTTATCTAACTATATTACTGATGCTGTTATCTTTAGATCGGAAGAGCGGTTTCAG
chr17	29528514	29528553	NF1_5973	+	GTGACCTATGCACCAGACGTTAAGTATTGCTAAATTAACAAAAAATTTTTTTCTTTTCTTTAGATCGGAAGAGCGGTTTCAG
chr17	29533400	29533439	NF1_5974	+	GTGACCTATGCACCAGACGTTCAAGTAAATCTCACCTCTTCTATTGCAATTTTAGATCGGAAGAGCGGTTTCAG

chr17	29541614	29541653	NF1_5975	+	GTGACCTATGCACCAGACGTTTTTATGAAATGTCTCAAAATTATCACACTAAGTTAATTGAGATCGGAAGAGCGGTTTCAG
chr17	29546147	29546186	NF1_5976	+	GTGACCTATGCACCAGACGTAATGAATCCATGTTCTTGAAGGAAAGATTGTAACATATGTAGATCGGAAGAGCGGTTTCAG
chr17	29549019	29549058	NF1_5977	+	GTGACCTATGCACCAGACGTTCTGTAGTACTTAGTACATTGTA AAACTTACACTTCCAAAGAGATCGGAAGAGCGGTTTCAG
chr17	29550596	29550635	NF1_5978	+	GTGACCTATGCACCAGACGTTGACATATTTAAAAAATGGAAGAATATTTGGAATGGTAATAGATCGGAAGAGCGGTTTCAG
chr17	29552279	29552318	NF1_5979	+	GTGACCTATGCACCAGACGTTCTGTACTTTTTCTGTATCATTTTATGTGCTCTGTTTGTAGATCGGAAGAGCGGTTTCAG
chr17	29553713	29553752	NF1_5980	+	GTGACCTATGCACCAGACGTATAGTGGTTTTTTTTACTCAGTCTGCCTCAAAGCACATGGAGATCGGAAGAGCGGTTTCAG
chr17	29554320	29554359	NF1_5981	+	GTGACCTATGCACCAGACGTAGCAACGAACACCCCTCCAGCGCCACCCTCAATTTAGATCGGAAGAGCGGTTTCAG
chr17	29554635	29554674	NF1_5982	+	GTGACCTATGCACCAGACGTAAGTTGACTTTTTGTCTGTAACTGATCTGCTAAATATATAGATCGGAAGAGCGGTTTCAG
chr17	29556494	29556533	NF1_5983	+	GTGACCTATGCACCAGACGTTCTTATTTTTACCTTTCTCTATGAATAGAGTGACTTGTAGATCGGAAGAGCGGTTTCAG
chr17	29557003	29557042	NF1_5984	+	GTGACCTATGCACCAGACGTTACTGAAATGTAGCAGAACATTTTAAAGAGATAAGAAAAAGATCGGAAGAGCGGTTTCAG
chr17	29557411	29557450	NF1_5985	+	GTGACCTATGCACCAGACGTA AAAAGCAATGTAGGGTCTTGTAATCTTAATATGTCCAAGATCGGAAGAGCGGTTTCAG
chr17	29557954	29557993	NF1_5986	+	GTGACCTATGCACCAGACGTAATGACCTTCAAGTATTAGTGGGTTTTACTGTGAGAGTTAAGATCGGAAGAGCGGTTTCAG
chr17	29559218	29559257	NF1_5987	+	GTGACCTATGCACCAGACGTTGTCACCAAAAACATAAAGCAAAAAGCAAAATAAAGCCCAAGATCGGAAGAGCGGTTTCAG
chr17	29559910	29559949	NF1_5988	+	GTGACCTATGCACCAGACGTATGAAAGTTTTCATATAGAATAACAAAACCTAGAGAAGTGGAGATCGGAAGAGCGGTTTCAG
chr17	29562801	29562840	NF1_5989	+	GTGACCTATGCACCAGACGTTTTCATTTTGTGTGTATGTGTGCTGAGGATGTCAAGTAAGATCGGAAGAGCGGTTTCAG
chr17	29563050	29563089	NF1_5990	+	GTGACCTATGCACCAGACGTTTTTTCATAGAACCGCTGTTTTTGTTTTTTTTTTTTGTAGATCGGAAGAGCGGTTTCAG
chr17	29576148	29576187	NF1_5991	+	GTGACCTATGCACCAGACGTAGTTAGAGATTACCATTATTAATCTAAAGTTAAATTTAGAGATCGGAAGAGCGGTTTCAG
chr17	29580029	29580068	NF1_5992	+	GTGACCTATGCACCAGACGTGAGACTTTTTATGACTGTTTTCTTCAAAGCAAAAACAAAAAGATCGGAAGAGCGGTTTCAG
chr17	29585531	29585570	NF1_5993	+	GTGACCTATGCACCAGACGTTTGATAATCTAGCTACTTTAAATTCCTTCCAACATAAAGATCGGAAGAGCGGTTTCAG
chr17	29586158	29586197	NF1_5994	+	GTGACCTATGCACCAGACGTTGCCACTTACTCAGTTGCTCTGTTTGAATCAAATATTTTCAGATCGGAAGAGCGGTTTCAG
chr17	29587544	29587583	NF1_5995	+	GTGACCTATGCACCAGACGTCCAGTCATGGGGATAGTGAACACTCTCCGTTTTAAATTTAGAGATCGGAAGAGCGGTTTCAG
chr17	29588886	29588925	NF1_5996	+	GTGACCTATGCACCAGACGTACCTTGAATAGTTGATTGCTTTCTTTTTGGTTGAGAAGGAGATCGGAAGAGCGGTTTCAG
chr17	29592368	29592407	NF1_5997	+	GTGACCTATGCACCAGACGTTCTATGTTTTGGGTCCTTAAACAGAAATTTTTAAATTTATAGAGATCGGAAGAGCGGTTTCAG
chr17	29653281	29653320	NF1_5998	+	GTGACCTATGCACCAGACGTGTCTGTGTTTTGTAACAGTTCATTGCTTTTTCTTACTAAAGATCGGAAGAGCGGTTTCAG
chr17	29654868	29654907	NF1_5999	+	GTGACCTATGCACCAGACGTTAAAATTTCTCTTTCAGTTTGAATTTGGGGTTTGTGCTTTTAAAGATCGGAAGAGCGGTTTCAG
chr17	29657527	29657566	NF1_6000	+	GTGACCTATGCACCAGACGTATAATTTCTTTAATACTAACAAATTTCTAAGAGAATTAGATCGGAAGAGCGGTTTCAG
chr17	29663502	29663541	NF1_6001	+	GTGACCTATGCACCAGACGTTTCTTTTGCCTTCTGTACTATAGCATATCTGTTTTATCATAGATCGGAAGAGCGGTTTCAG
chr17	29663943	29663982	NF1_6002	+	GTGACCTATGCACCAGACGTGGAAGGAATTTGTGTTTACCAGTTCTCTTCCATTTTAAAGATCGGAAGAGCGGTTTCAG
chr17	29664611	29664650	NF1_6003	+	GTGACCTATGCACCAGACGTCAAAATGATAAGAACTAAGTTAAAATCTTTTTTAAAAAAGATCGGAAGAGCGGTTTCAG
chr17	29664909	29664948	NF1_6004	+	GTGACCTATGCACCAGACGTAATTAATAAAGTTGTAAGAAATATGCATATTGTTGAAAAAGATCGGAAGAGCGGTTTCAG
chr17	29665168	29665207	NF1_6005	+	GTGACCTATGCACCAGACGTGCCCTCAGTTCTCCCAAATTTTATGGTTCTCAAGTTGTAGATCGGAAGAGCGGTTTCAG
chr17	29665834	29665873	NF1_6006	+	GTGACCTATGCACCAGACGTTATAGAAAATGAGTGCATTCATTTTGGGTATCAGTGTGGAAGATCGGAAGAGCGGTTTCAG
chr17	29667674	29667713	NF1_6007	+	GTGACCTATGCACCAGACGTTTTGCCTTGAGGTTCTAGATTACTCAAATTTAGTACTCTAGATCGGAAGAGCGGTTTCAG
chr17	29670164	29670203	NF1_6008	+	GTGACCTATGCACCAGACGTTCTTATTTAGAAATTTTCTGAAAGTACTATTAAGAAAACAGATCGGAAGAGCGGTTTCAG
chr17	29676280	29676319	NF1_6009	+	GTGACCTATGCACCAGACGTAAAATAACAAAATTAATCTTGCTACATCTATATATAAGGATCGGAAGAGCGGTTTCAG
chr17	29677347	29677386	NF1_6010	+	GTGACCTATGCACCAGACGTTTACTCTCTATAATTACATAATCATAATCAAGTTTCAATAGATCGGAAGAGCGGTTTCAG
chr17	29683611	29683650	NF1_6011	+	GTGACCTATGCACCAGACGTAAGTATTGATCTAGATCATTGAAAATAAGGTGGGAGAGTAAGATCGGAAGAGCGGTTTCAG
chr17	29684119	29684158	NF1_6012	+	GTGACCTATGCACCAGACGTCCCTTTTTGAGTCCCCACCCTCAAATTTTTTATCCAGTAGATCGGAAGAGCGGTTTCAG
chr17	29684398	29684437	NF1_6013	+	GTGACCTATGCACCAGACGTTCTTTGATTTTAAATTCACCTTCGTGCCTGTCTTTAAGTTAGATCGGAAGAGCGGTTTCAG
chr17	29685651	29685690	NF1_6014	+	GTGACCTATGCACCAGACGTTGATCTGGAGAAGGATGGTGTGATGAACCTGCTAACATGCTAGATCGGAAGAGCGGTTTCAG
chr17	29686044	29686083	NF1_6015	+	GTGACCTATGCACCAGACGTATATTTTTTCTAACTTTTGCAAAATGAAGGTTTTCTGTAGATCGGAAGAGCGGTTTCAG
chr17	29687732	29687771	NF1_6016	+	GTGACCTATGCACCAGACGTTGATCTTTATAGACTTTGAGCAACAATAAGACACCAAGATCGGAAGAGCGGTTTCAG
chr17	29701184	29701223	NF1_6017	+	GTGACCTATGCACCAGACGTTCTTTTTTAAAATCAACTTAAACATGGGCTTCTCAAGATCGGAAGAGCGGTTTCAG
chr7	116340349	116340388	MET_6018	+	GTGACCTATGCACCAGACGTTTCAGTTCCCACTTATAAACTGTGAGGTATAAATTAGAAAAGATCGGAAGAGCGGTTTCAG
chr7	116371924	116371963	MET_6019	+	GTGACCTATGCACCAGACGTTCTGAGAGTAGCTGTGCTGTCTGTTCTATCTGGTATTGTGCAAAAGATCGGAAGAGCGGTTTCAG
chr7	116380149	116380188	MET_6020	+	GTGACCTATGCACCAGACGTTCCACAGGGAATTTGCTATAGACGTGTGTTTTTCCCAAATGCAGATCGGAAGAGCGGTTTCAG
chr7	116395580	116395619	MET_6021	+	GTGACCTATGCACCAGACGTTAAAATGCTTTTGTGGGGTGTGCTTGGAAAATAGTTTTGAGATCGGAAGAGCGGTTTCAG
chr7	116397604	116397643	MET_6022	+	GTGACCTATGCACCAGACGTTTCTATCCTATCATGTTTGTATTTTACTTAATCTATTTAAAGATCGGAAGAGCGGTTTCAG
chr7	116397839	116397878	MET_6023	+	GTGACCTATGCACCAGACGTTTTATTTTTTGTGCATCTGTCAATTTGAATTAATATCTGAGATCGGAAGAGCGGTTTCAG
chr7	116398685	116398724	MET_6024	+	GTGACCTATGCACCAGACGTGCTTCTGATGGGTAAAGAAAACAAATGAATACAAGGATGAAGATCGGAAGAGCGGTTTCAG
chr7	116399555	116399594	MET_6025	+	GTGACCTATGCACCAGACGTTGAGCAATGGTTCTACTCAGAGCTGCATCTTTGCCCTAGATCGGAAGAGCGGTTTCAG
chr7	116403333	116403372	MET_6026	+	GTGACCTATGCACCAGACGTTTAAAACCTTTCTAAATCATTGCTCAAACTTAATTTAGATCGGAAGAGCGGTTTCAG
chr7	116409856	116409895	MET_6027	+	GTGACCTATGCACCAGACGTTGCATTCCTCTCATGATGTAATAAGGAAGCCAGTGAATAGATCGGAAGAGCGGTTTCAG
chr7	116411719	116411758	MET_6028	+	GTGACCTATGCACCAGACGTTACTGTTTCAATTTTAGAAGTTACTTAAAGAACACAGTCAAGATCGGAAGAGCGGTTTCAG
chr7	116412054	116412093	MET_6029	+	GTGACCTATGCACCAGACGTTTATTTGTTCTGAGAAATACCTATACATATACCTCAGTGAAGATCGGAAGAGCGGTTTCAG
chr7	116415176	116415215	MET_6030	+	GTGACCTATGCACCAGACGTTCACTCAGCTTTTTGTAAATACGATTTTCCAGTAAGCATAGATCGGAAGAGCGGTTTCAG
chr7	116417534	116417573	MET_6031	+	GTGACCTATGCACCAGACGTTTTTATTTAAACCTGGAGTATACCTTTGTGGTTTGAACACAGATCGGAAGAGCGGTTTCAG
chr7	116419022	116419061	MET_6032	+	GTGACCTATGCACCAGACGTTGCCAAGCTTAACTGGCAAACACTGCTGTAAGCCAGCCAGATCGGAAGAGCGGTTTCAG



chr7	116422162	116422201	MET_6033	+	GTGACCTATGCACCAGACGTGAATCTCTGTGCCACAATCCAAATTAAGTGACAAGGAGGAAGATCGGAAGAGCGGTTTCAG
chr7	116423534	116423573	MET_6034	+	GTGACCTATGCACCAGACGTGGTTATCTCTGAGTTTCTCCTCTTTTACTTTTCATATCCAAAGATCGGAAGAGCGGTTTCAG
chr7	116435856	116435895	MET_6035	+	GTGACCTATGCACCAGACGTTTTCTGTACCTCTTACGTTCTTTACTTTTACAGAAATGCCAGATCGGAAGAGCGGTTTCAG
chr7	116436189	116436228	MET_6036	+	GTGACCTATGCACCAGACGTATGTCAAAGCAACAGTCCACACTTTGTCCAATGGTTTTTAGATCGGAAGAGCGGTTTCAG
chr7	116339549	116339588	MET_6037	+	GTGACCTATGCACCAGACGTGAGGGACCTGCCAGCGACATGTCTTTCCCCACAATCATAGATCGGAAGAGCGGTTTCAG
chr7	116339949	116339988	MET_6038	+	GTGACCTATGCACCAGACGTGCTCAGACTTTTCCACACAAGAAATAACAGTTCTGTTCCAAGATCGGAAGAGCGGTTTCAG
chr12	58142411	58142451	CDK4_6039	+	GTGACCTATGCACCAGACGTAGGCAAGAGTGCAGAAAAGGTCAGAAAACCATGAAGAAAACAGACTTCTGCAGATCGGAAGAGCGGTTTCAG
chr12	58143111	58143150	CDK4_6040	+	GTGACCTATGCACCAGACGTGAGGAGAACTCTGGTTCAGGAGGGTCTCCAGTTCCCATCCAGATCGGAAGAGCGGTTTCAG
chr12	58143298	58143337	CDK4_6041	+	GTGACCTATGCACCAGACGTAAAGGATATAAGGTAGCAGTCATTTTCAAAGATATCTTAGAGATCGGAAGAGCGGTTTCAG
chr12	58144559	58144598	CDK4_6042	+	GTGACCTATGCACCAGACGTAGGAAAGATGGATGGGGACCCCATGGGTACCATGAAACAGATCGGAAGAGCGGTTTCAG
chr12	58144884	58144923	CDK4_6043	+	GTGACCTATGCACCAGACGTAGGGGAGGTACAGATGCACTGGAAACTAGGCACCATACCTAGATCGGAAGAGCGGTTTCAG
chr12	58145136	58145175	CDK4_6044	+	GTGACCTATGCACCAGACGTAAATGCTCACTTTTCAATCCCCTTAAACCAACATGCCAGATCGGAAGAGCGGTTTCAG
chr12	58145511	58145550	CDK4_6045	+	GTGACCTATGCACCAGACGTAGGAGAACCTACAACTACAGACTCCTATCACCAAAGTCAGATCGGAAGAGCGGTTTCAG
chr11	108098434	108098473	ATM_6046	+	GTGACCTATGCACCAGACGTACTTAAATTCATTTTCTTCTGAAATAAGTGTGATTAGTAAGATCGGAAGAGCGGTTTCAG
chr11	108098626	108098665	ATM_6047	+	GTGACCTATGCACCAGACGTCAAATTTATTTACTGTCTTTATTTTCTCTTTTCATATTTAGATCGGAAGAGCGGTTTCAG
chr11	108100061	108100100	ATM_6048	+	GTGACCTATGCACCAGACGTTTATAAATATAAATAAATGGCTTAACAGATTAAGTGTGCGAGATCGGAAGAGCGGTTTCAG
chr11	108106572	108106611	ATM_6049	+	GTGACCTATGCACCAGACGTAAAGTGTGTTGTTGTTGTAATTTTCTCTCATGAAATGAACTAGATCGGAAGAGCGGTTTCAG
chr11	108114856	108114895	ATM_6050	+	GTGACCTATGCACCAGACGTCTCTTTTCTTTTGTGTTTGTGTTTGTGTTTAAATATGTTTGTATCGGAAGAGCGGTTTCAG
chr11	108115764	108115803	ATM_6051	+	GTGACCTATGCACCAGACGTAAAGTGTGTTTACTGTTTTGAAATTTGCTTCTTATTCAAACATAAGATCGGAAGAGCGGTTTCAG
chr11	108117865	108117904	ATM_6052	+	GTGACCTATGCACCAGACGTTAGGTCATGTCCACATTTAGAAATTTCTGTTAATTTTTTATAGATCGGAAGAGCGGTTTCAG
chr11	108119840	108119879	ATM_6053	+	GTGACCTATGCACCAGACGTACCATTTTCTCATTAGTGTCAATTTAATCTCTTGTATGTAGATCGGAAGAGCGGTTTCAG
chr11	108122769	108122808	ATM_6054	+	GTGACCTATGCACCAGACGTTTCATTAGCATGCTGCTGTTTTTTTTGTTTGTATATAGATCGGAAGAGCGGTTTCAG
chr11	108123650	108123689	ATM_6055	+	GTGACCTATGCACCAGACGTTAATAATGCTCTTTATCATTTAAGCTATAGCTTTAATTAAGATCGGAAGAGCGGTTTCAG
chr11	108124777	108124816	ATM_6056	+	GTGACCTATGCACCAGACGTTAAAGAAAGCAACTATATATGATTCAACTTTGGTAGATCGGAAGAGCGGTTTCAG
chr11	108127078	108127117	ATM_6057	+	GTGACCTATGCACCAGACGTTTATACTAATAAAGTTTCGGATAAATTTGAATGAAATGTAAGATCGGAAGAGCGGTTTCAG
chr11	108138080	108138119	ATM_6058	+	GTGACCTATGCACCAGACGTATTTACTACTTGGGATTTCTTTACTTCTTTATATTGATTAGATCGGAAGAGCGGTTTCAG
chr11	108139347	108139386	ATM_6059	+	GTGACCTATGCACCAGACGTTTAAATGAAGAAGCTCTTGATTTTTATCTGATGTTGCTGAAGATCGGAAGAGCGGTTTCAG
chr11	108141884	108141923	ATM_6060	+	GTGACCTATGCACCAGACGTAAACCTTATGTTATGTTCACTTTAAAGTTATAAATAACAGATCGGAAGAGCGGTTTCAG
chr11	108142144	108142183	ATM_6061	+	GTGACCTATGCACCAGACGTTCTATTTTGGTCTATTTTCTTTTGTCTATCTGTGGATGATCGGAAGAGCGGTTTCAG
chr11	108143345	108143384	ATM_6062	+	GTGACCTATGCACCAGACGTGCTATTTTTTGTAGTAAGATCTCCATTGAAAATTTTAAAGCAAGATCGGAAGAGCGGTTTCAG
chr11	108143590	108143629	ATM_6063	+	GTGACCTATGCACCAGACGTTAATATTCATGAAGTATTTGGAATGCTGCAGATGGCAGTAAGATCGGAAGAGCGGTTTCAG
chr11	108150346	108150385	ATM_6064	+	GTGACCTATGCACCAGACGTGTAACATGTATTGCTGTTATCATATGCTTGTCTATGAATAAGATCGGAAGAGCGGTTTCAG
chr11	108151906	108151945	ATM_6065	+	GTGACCTATGCACCAGACGTATGAGTATTTTATAGAAGCTTCTTAGGTCACCTGTGAAAAGATCGGAAGAGCGGTTTCAG
chr11	108153617	108153656	ATM_6066	+	GTGACCTATGCACCAGACGTACATGACATGTGAAATTTGTTTAAATTTAAATTTAAGATCGGAAGAGCGGTTTCAG
chr11	108155211	108155250	ATM_6067	+	GTGACCTATGCACCAGACGTTAATTTTATGACTTTTCTTACTTTTCAATTTTAAATTTAAGATCGGAAGAGCGGTTTCAG
chr11	108158453	108158492	ATM_6068	+	GTGACCTATGCACCAGACGTTTAAACTTAGAGAAGTACTCTAACTTCAAGTTTTTAAAGATCGGAAGAGCGGTTTCAG
chr11	108159841	108159880	ATM_6069	+	GTGACCTATGCACCAGACGTATGATGAGTTTAAATAATAGAACATCTCTTCTTTTTTATAGATCGGAAGAGCGGTTTCAG
chr11	108160539	108160578	ATM_6070	+	GTGACCTATGCACCAGACGTTATTTAGACCAATATATAAGCAGTCTTTCTATCCTGTTCTAGATCGGAAGAGCGGTTTCAG
chr11	108163531	108163570	ATM_6071	+	GTGACCTATGCACCAGACGTGACTCATCTTCAAATGGTATTTAAATATATAAAGTATTAGATCGGAAGAGCGGTTTCAG
chr11	108164215	108164254	ATM_6072	+	GTGACCTATGCACCAGACGTTTTCATCATCTACTATTTTTTATAGAACATAGTAGTAAGATCGGAAGAGCGGTTTCAG
chr11	108165797	108165836	ATM_6073	+	GTGACCTATGCACCAGACGTTAAATGACATGGGCTATTCTACCTGTTTTCTTTTTGAAAGATCGGAAGAGCGGTTTCAG
chr11	108170623	108170662	ATM_6074	+	GTGACCTATGCACCAGACGTATTGATACCTTATATGTAATCTCAATATGACATTCATGGAAGATCGGAAGAGCGGTTTCAG
chr11	108172527	108172566	ATM_6075	+	GTGACCTATGCACCAGACGTTAATAAATGTTTATTGAATACCAGCATATCTAAACAGTAGATCGGAAGAGCGGTTTCAG
chr11	108173767	108173806	ATM_6076	+	GTGACCTATGCACCAGACGTTAATTAGTCTGATATAATCTTGTTTTATGACCTGTTTATAGATCGGAAGAGCGGTTTCAG
chr11	108175590	108175629	ATM_6077	+	GTGACCTATGCACCAGACGTTAATTTTTAACTAATACTGTAACCTCAGTTCTAGAGAAAAGATCGGAAGAGCGGTTTCAG
chr11	108178722	108178761	ATM_6078	+	GTGACCTATGCACCAGACGTGAGTGTGCTTCTACGTTTAGAGTGTAACTTAGATCGGAAGAGCGGTTTCAG
chr11	108181053	108181092	ATM_6079	+	GTGACCTATGCACCAGACGTTTAGAATTTTTGGTTTTTAAATTAATGTTGGCATTGTCTAGATCGGAAGAGCGGTTTCAG
chr11	108183236	108183275	ATM_6080	+	GTGACCTATGCACCAGACGTGAGGCTCTATTATTTATGACAGTATTTATCTCATACTTTGAGATCGGAAGAGCGGTTTCAG
chr11	108186649	108186688	ATM_6081	+	GTGACCTATGCACCAGACGTTTTTCTAAACAACGGTATAGTAATCTGTTTATGAAGGAAGATCGGAAGAGCGGTTTCAG
chr11	108186851	108186890	ATM_6082	+	GTGACCTATGCACCAGACGTTCCAGATTTGGTAAAGCCATCACTAGTGTAGTGTGAGGAGATCGGAAGAGCGGTTTCAG
chr11	108188259	108188298	ATM_6083	+	GTGACCTATGCACCAGACGTTGACTGATTTTTTTTTTGCCTCTCTCATTCTAAAGATCGGAAGAGCGGTTTCAG
chr11	108190796	108190835	ATM_6084	+	GTGACCTATGCACCAGACGTTAAGCAAAAGTACTGTTTTTAACTTTAATGTCATGGCTAGATCGGAAGAGCGGTTTCAG
chr11	108192158	108192197	ATM_6085	+	GTGACCTATGCACCAGACGTGATGACTTTGTTATCCTAAAGTGCAGCTTTTCTGTTACAGATCGGAAGAGCGGTTTCAG
chr11	108196282	108196321	ATM_6086	+	GTGACCTATGCACCAGACGTTTTAAACTATGTCATCTTACCTTTGACTTTCTTTTATAGATCGGAAGAGCGGTTTCAG
chr11	108196963	108197002	ATM_6087	+	GTGACCTATGCACCAGACGTTTTATTGGCTGGATTAGTGTTTTACTGTTATTTAAAAAAGATCGGAAGAGCGGTTTCAG
chr11	108198496	108198535	ATM_6088	+	GTGACCTATGCACCAGACGTTGGAGCAACCTTAAGATGTTACTTAGCATGAATATGCTAGATCGGAAGAGCGGTTTCAG
chr11	108199976	108200015	ATM_6089	+	GTGACCTATGCACCAGACGTTTACAAAGTGACAAATTTTACTTCCACAGTTAACTGATGATCGGAAGAGCGGTTTCAG
chr11	108202775	108202814	ATM_6090	+	GTGACCTATGCACCAGACGTTAAACATGACCTTTTTAGAAGTGTGATTTACAGTCTTTAGATCGGAAGAGCGGTTTCAG

chr11	108203638	108203677	ATM_6091	+	GTGACCTATGCACCAGACGTTTTAAAGAAGAAACGTTACTTTCTTGCTGTGTTACTCTCTAGATCGGAAGAGCGGTTTCAG
chr11	108205847	108205886	ATM_6092	+	GTGACCTATGCACCAGACGCTCTTCTCTGGCTTAGCCCTTAGAGTTTTAGTGATGAAAATAGATCGGAAGAGCGGTTTCAG
chr11	108206699	108206738	ATM_6093	+	GTGACCTATGCACCAGACGTGACTTCTGTGATTCCACAAAAACATATAAAAGATGCCAAGATCGGAAGAGCGGTTTCAG
chr11	108214109	108214148	ATM_6094	+	GTGACCTATGCACCAGACGTCCCAAAATTAAGGTTATTGTAAGATTATTTAATGGCTTAAGATCGGAAGAGCGGTTTCAG
chr11	108216646	108216685	ATM_6095	+	GTGACCTATGCACCAGACGTTGTACATATAGTAGATTGACACCTTTGTTGTTTGGCAGGTAGATCGGAAGAGCGGTTTCAG
chr11	108218103	108218142	ATM_6096	+	GTGACCTATGCACCAGACGTAATCTATGTATCTATTCTTTTGTAGAAATTTGGTCATAGATCGGAAGAGCGGTTTCAG
chr11	108224618	108224657	ATM_6097	+	GTGACCTATGCACCAGACGTTGAAGTAAAGGAAAGAAAATTTTTGATGTCAAATTCACAGATCGGAAGAGCGGTTTCAG
chr11	108225612	108225651	ATM_6098	+	GTGACCTATGCACCAGACGTTTATAAGGAAGACTTTATTTTTTTCTTACCAGGTAGACTAGATCGGAAGAGCGGTTTCAG
chr11	108235956	108235995	ATM_6099	+	GTGACCTATGCACCAGACGTTTTTAAGAAGGTCCTGTTGTCAGTTTTTCAGATTTTCTTAAGATCGGAAGAGCGGTTTCAG
chr11	108236246	108236285	ATM_6100	+	GTGACCTATGCACCAGACGTATGAATTACCCTTTCATTAGCCCTTAGAAAATATATTTAGATCGGAAGAGCGGTTTCAG
chr4	55124995	55125034	PDGFRA_6101	+	GTGACCTATGCACCAGACGTGAGTCCCTCTGAGTTCCTTGTGGGTGCTTGTGTTTTTGTAGATCGGAAGAGCGGTTTCAG
chr4	55127590	55127629	PDGFRA_6102	+	GTGACCTATGCACCAGACGTTGGGTCTCCAGGACCAACTTCTCTCTTCTCCAGATCGGAAGAGCGGTTTCAG
chr4	55130105	55130144	PDGFRA_6103	+	GTGACCTATGCACCAGACGTCATCTCCTTCTTCTTAAAGTAAAGAGTAACAGGCAAAATCAGATCGGAAGAGCGGTTTCAG
chr4	55133638	55133677	PDGFRA_6104	+	GTGACCTATGCACCAGACGCTTTTCTAAAATGTCAGTTGTCCATGCTGCTCGGGATCCATAGATCGGAAGAGCGGTTTCAG
chr4	55133919	55133958	PDGFRA_6105	+	GTGACCTATGCACCAGACGTTCTCTGCCAAGATGCCTTTTTTAGTGTGCATCAGAGGAGATCGGAAGAGCGGTTTCAG
chr4	55136926	55136965	PDGFRA_6106	+	GTGACCTATGCACCAGACGTGGAGTATAAAGATAATGCTAGCTCTGTAGATGAGTGTCTTAGATCGGAAGAGCGGTTTCAG
chr4	55138698	55138737	PDGFRA_6107	+	GTGACCTATGCACCAGACGTCAGATGTGCTTCTTCTTTCCTGGTCAGAAATTTCTCCAGATCGGAAGAGCGGTTTCAG
chr4	55139908	55139947	PDGFRA_6108	+	GTGACCTATGCACCAGACGTTGAAACAGTCAAGCACTGAGCCGATCAGCTGCCCCAGATCGGAAGAGCGGTTTCAG
chr4	55140803	55140842	PDGFRA_6109	+	GTGACCTATGCACCAGACGTTCTCATAAACTAAAAGATCTTTGAAGCCAATGAGAACAAGAGATCGGAAGAGCGGTTTCAG
chr4	55141151	55141190	PDGFRA_6110	+	GTGACCTATGCACCAGACGTTGGGGTAACTCCCAAGACTCCCTTTTCCCTTGCACACAAGATCGGAAGAGCGGTTTCAG
chr4	55143670	55143709	PDGFRA_6111	+	GTGACCTATGCACCAGACGTTCTCTGGGGATTTTTGAGCAGGGGATTTTTGAGCATAGATCGGAAGAGCGGTTTCAG
chr4	55144184	55144223	PDGFRA_6112	+	GTGACCTATGCACCAGACGTTGACCTGGAGTGAGGATTTTCACTGGACACATGTGGTTGTAGATCGGAAGAGCGGTTTCAG
chr4	55144693	55144732	PDGFRA_6113	+	GTGACCTATGCACCAGACGTAGAGAGATGTTGCTGTCTATCATTATCTACAGGCATCAGATCGGAAGAGCGGTTTCAG
chr4	55151664	55151703	PDGFRA_6114	+	GTGACCTATGCACCAGACGTGGAAACAGACCTTTTTAAGACCAAGATTTTCACTGAGTGGAAAGATCGGAAGAGCGGTTTCAG
chr4	55152141	55152180	PDGFRA_6115	+	GTGACCTATGCACCAGACGTACTTCCCTCACTGGTCAAGCTCATCTCTTCACTTTAATAGATCGGAAGAGCGGTTTCAG
chr4	55153719	55153758	PDGFRA_6116	+	GTGACCTATGCACCAGACGTGACATTGCTGCTTATTTGGGCTGTTCTGAAACACCACTGGAGATCGGAAGAGCGGTTTCAG
chr4	55155076	55155115	PDGFRA_6117	+	GTGACCTATGCACCAGACGTTCCCATCCCGGGGGCTGTGTTTACAGTCTGTGGGTCTAAGATCGGAAGAGCGGTTTCAG
chr4	55155292	55155331	PDGFRA_6118	+	GTGACCTATGCACCAGACGTATCTGTGGGTGAAAGCTCTGGATAAAGCTGGAAGTTATAAGATCGGAAGAGCGGTTTCAG
chr4	55156732	55156771	PDGFRA_6119	+	GTGACCTATGCACCAGACGTGGGCAGCTCGGTGCTCACCCTTCCCTCCCTTAGGCAGATCGGAAGAGCGGTTTCAG
chr4	55161450	55161489	PDGFRA_6120	+	GTGACCTATGCACCAGACGTCGAGGGTTTCCCTTCCACTCTGGGGCCACCTCTGGATCCAGATCGGAAGAGCGGTTTCAG
chr12	69202282	69202321	MDM2_6121	+	GTGACCTATGCACCAGACGTGGCAGCGAGCGGTCACTTTTGGGTCTGGGCTGTGACGGTGAGATCGGAAGAGCGGTTTCAG
chr12	69203083	69203122	MDM2_6122	+	GTGACCTATGCACCAGACGTTTGTCTCGTGAACTTTTAAGAATAATTTATTTTATGAAGAGATCGGAAGAGCGGTTTCAG
chr12	69207419	69207458	MDM2_6123	+	GTGACCTATGCACCAGACGTTCAAGAGATAAGTAGTATCTCACTAGTTACATGTAGCCATAGATCGGAAGAGCGGTTTCAG
chr12	69210736	69210775	MDM2_6124	+	GTGACCTATGCACCAGACGTAGTTTAGTCCATTGTA AAAAGCCATCTGGGCTAACATTTTCAGATCGGAAGAGCGGTTTCAG
chr12	69214165	69214204	MDM2_6125	+	GTGACCTATGCACCAGACGTTTGGAGCATCTGGATAAATACCATAAAAACGTTTTAAAGAGATCGGAAGAGCGGTTTCAG
chr12	69218221	69218260	MDM2_6126	+	GTGACCTATGCACCAGACGTTAAATTTCTCATTCTAATGTAATATTTATTTGCAAATTTGGAAGATCGGAAGAGCGGTTTCAG
chr12	69218442	69218481	MDM2_6127	+	GTGACCTATGCACCAGACGTATATTTATTTGACGCATTCACACAGCTTTTTGATATTCTTAGATCGGAAGAGCGGTTTCAG
chr12	69222722	69222761	MDM2_6128	+	GTGACCTATGCACCAGACGTCATTTTAAAGTAAAGGCAAGACTCTTACTGTTCAAAGTCTAGAGATCGGAAGAGCGGTTTCAG
chr12	69222975	69222914	MDM2_6129	+	GTGACCTATGCACCAGACGTTTTTCCCTCTAATATATTGAAAAATTTATAAATTTTATAGATCGGAAGAGCGGTTTCAG
chr12	69230540	69230579	MDM2_6130	+	GTGACCTATGCACCAGACGTATCTACTTTTTAAGAAATAAAAATTTTATTAAGTCAAGAGATCGGAAGAGCGGTTTCAG
chr12	69233640	69233679	MDM2_6131	+	GTGACCTATGCACCAGACGTTAAGAGAATTTATATTTTTCTAACTATATAAACCTTAGGAAGATCGGAAGAGCGGTTTCAG
chr12	69233352	69233391	MDM2_6132	+	GTGACCTATGCACCAGACGTTAGTAGCATTATTTATAGCAGCCAAGAAGATGTGAAAGAAGATCGGAAGAGCGGTTTCAG
chr5	112090733	112090772	APC_6133	+	GTGACCTATGCACCAGACGTTGTGACTTTAATTGTAGTTATCCATTTTTATTTCAGTATAGATCGGAAGAGCGGTTTCAG
chr5	112102118	112102157	APC_6134	+	GTGACCTATGCACCAGACGTAAAAGTGTTTTAAAATAATTTTTTAAAGCTCAAATTTGCAAGATCGGAAGAGCGGTTTCAG
chr5	112103098	112103137	APC_6135	+	GTGACCTATGCACCAGACGTTTCATATAGTAAACATGCTTGTGACTCCAGTTTATTGAGATCGGAAGAGCGGTTTCAG
chr5	112114445	112114484	APC_6136	+	GTGACCTATGCACCAGACGTTGGCAGTACAACTTTTAAACTTTAAACTTTGATATTAGATCGGAAGAGCGGTTTCAG
chr5	112116611	112116650	APC_6137	+	GTGACCTATGCACCAGACGTTGTTTCTAAGTGATAAAAACAGCGAAGAGCTATTAGGAATAAGATCGGAAGAGCGGTTTCAG
chr5	112128237	112128276	APC_6138	+	GTGACCTATGCACCAGACGTTGCCTTTCTGTTTGTGGGTATAAAAATAGGTAGTTATTTCAGATCGGAAGAGCGGTTTCAG
chr5	112151301	112151340	APC_6139	+	GTGACCTATGCACCAGACGTATTACAACCCCTGGTCACTAATGCCATGACTACTTTGCTAAGATCGGAAGAGCGGTTTCAG
chr5	112155052	112155091	APC_6140	+	GTGACCTATGCACCAGACGTTATAGTGTACATCGTAGTGCATGTTTCAAAGCAAATGTGAAGATCGGAAGAGCGGTTTCAG
chr5	112157699	112157738	APC_6141	+	GTGACCTATGCACCAGACGTAATGTTTTTAAATGACATAGACAATTACTGGTGGATTTTATAGATCGGAAGAGCGGTTTCAG
chr5	112162955	112162994	APC_6142	+	GTGACCTATGCACCAGACGTATAACATGTATTTCTTAAAGATAGCTCAGGTATGAGTTAATAGATCGGAAGAGCGGTTTCAG
chr5	112164680	112164719	APC_6143	+	GTGACCTATGCACCAGACGTTAAACATTTAGTACTATAATGAATTTTCATGTTTGGCTTTAGATCGGAAGAGCGGTTTCAG
chr5	112170873	112170912	APC_6144	+	GTGACCTATGCACCAGACGTAGTTTTATATTACTTTTAAAGTACAGAATTCATACTCTCAAGATCGGAAGAGCGGTTTCAG
chr5	112179834	112179873	APC_6145	+	GTGACCTATGCACCAGACGTGAATGAAACTAAGAAAATTTCTATGTTAATTAACAAGTCTAAGATCGGAAGAGCGGTTTCAG
chr5	112173730	112173769	APC_6146	+	GTGACCTATGCACCAGACGTTTTAATACTGGCAACATGACTGCTCTTACCATATTTAGATCGGAAGAGCGGTTTCAG
chr5	112174200	112174239	APC_6147	+	GTGACCTATGCACCAGACGTTGATGGTTTAAAGAGGTTCAAATGAAACCCCTGATCGGAAGAGCGGTTTCAG
chr5	112174670	112174709	APC_6148	+	GTGACCTATGCACCAGACGTCAGTCTTTGTGTGAAAAGATGACTATGAAGATGATAAGCAGATCGGAAGAGCGGTTTCAG

chr5	112175140	112175179	APC_6149	+	GTGACCTATGCACCAGACGTTGAAGATGAAATAGGATGTAATCAGACGCACACAGGAAGCAAGATCGGAAGAGCGGTTTCAG
chr5	112175610	112175649	APC_6150	+	GTGACCTATGCACCAGACGTCACCACCTCCTCAAACAGCTCAAACCAAGCGAGAAGTACCAGATCGGAAGAGCGGTTTCAG
chr5	112176080	112176119	APC_6151	+	GTGACCTATGCACCAGACGTTACTGCTTCAAATACCTCCACCTGTGGCAAGGAAACCAAGATCGGAAGAGCGGTTTCAG
chr5	112176550	112176589	APC_6152	+	GTGACCTATGCACCAGACGTATCTGCGTCTTTCTTCTGCACCAACAAAAATCAGTTAGATAGATCGGAAGAGCGGTTTCAG
chr5	112177020	112177059	APC_6153	+	GTGACCTATGCACCAGACGTCACAAGCTATTGCAAAGCAGCCAAATAATCGAGGTACGCCAGATCGGAAGAGCGGTTTCAG
chr5	112177490	112177529	APC_6154	+	GTGACCTATGCACCAGACGTAATATGGTGGCATATTAGGTGAAGATCTGACACTTGATTAGATCGGAAGAGCGGTTTCAG
chr5	112177960	112177999	APC_6155	+	GTGACCTATGCACCAGACGTAATCTCTCGAGCCAGCAATGTTTCATATTCAGGAGTTAGATCGGAAGAGCGGTTTCAG
chr5	112178430	112178469	APC_6156	+	GTGACCTATGCACCAGACGTAACAACAGGTTTATCCAAGAATGCCAGTAGTATTCCAAGAGATCGGAAGAGCGGTTTCAG
chr5	112178900	112178939	APC_6157	+	GTGACCTATGCACCAGACGTTCTAGACTTCCAATCAATAGGTCAGGAACCTGAAAACGTGAGATCGGAAGAGCGGTTTCAG
chr5	112179370	112179409	APC_6158	+	GTGACCTATGCACCAGACGTCATTAAGATTCAAAAGATAATCAGGCAAACAAAAATGTGAGATCGGAAGAGCGGTTTCAG
chr22	41489113	41489152	EP300_6159	+	GTGACCTATGCACCAGACGTCGACGCCCGGCCCTCCACGTTCCCTTTAATCTTTTCTACTAGATCGGAAGAGCGGTTTCAG
chr22	41513836	41513875	EP300_6160	+	GTGACCTATGCACCAGACGTTTTGGTTGTGTGCACAATCCGCATGCATGTGAGTATTGAGATCGGAAGAGCGGTTTCAG
chr22	41522055	41522094	EP300_6161	+	GTGACCTATGCACCAGACGTATCCATTACAGACTGTTTTCAAATGGCATTMTTTCACAAAAGATCGGAAGAGCGGTTTCAG
chr22	41523763	41523802	EP300_6162	+	GTGACCTATGCACCAGACGTCACAGGGTTACTGTACTTAGCAATTTTTACAGCCAGGGAAGATCGGAAGAGCGGTTTCAG
chr22	41526018	41526057	EP300_6163	+	GTGACCTATGCACCAGACGTAATCTTTTGAAGGTTTATATGAAAAGTTTTAAAGTCTCAAGATCGGAAGAGCGGTTTCAG
chr22	41527648	41527687	EP300_6164	+	GTGACCTATGCACCAGACGTGTCACTCAATAACATGGTATTGGTTGTGTGTCAGTAAATGAAGATCGGAAGAGCGGTTTCAG
chr22	41531921	41531960	EP300_6165	+	GTGACCTATGCACCAGACGTACTGTGTTATACCTCGGGTACATTAACAATACTACTGGAGATCGGAAGAGCGGTTTCAG
chr22	41533805	41533844	EP300_6166	+	GTGACCTATGCACCAGACGTTGTGGACAGCTCATTCTGTAAGAGATGTTACGTCGAACAGATCGGAAGAGCGGTTTCAG
chr22	41536272	41536311	EP300_6167	+	GTGACCTATGCACCAGACGTGTTTTTTTCTATTAATAGCCAAGATTGAACCTGTTGTGGAGATCGGAAGAGCGGTTTCAG
chr22	41537237	41537276	EP300_6168	+	GTGACCTATGCACCAGACGTTTTGTTATATTTCTGTTTGGAGAAAATTGATAATAAAATAAGATCGGAAGAGCGGTTTCAG
chr22	41543961	41544000	EP300_6169	+	GTGACCTATGCACCAGACGTCGTCTTTGGTAATCTCTTTGGCCTTTACCTGGTATTTTGAAGATCGGAAGAGCGGTTTCAG
chr22	41545190	41545229	EP300_6170	+	GTGACCTATGCACCAGACGTTAAGTGGATTTTTCACTTATTTTTGATTCTTGAAACTTCTAGATCGGAAGAGCGGTTTCAG
chr22	41546213	41546252	EP300_6171	+	GTGACCTATGCACCAGACGTTATTTGGATTAGGCAGAACTTAGAGCTATACTGTAGTAAGATCGGAAGAGCGGTTTCAG
chr22	41548027	41548066	EP300_6172	+	GTGACCTATGCACCAGACGTGGAATGCTGTTTTGTTTTGTTAGGACTCAGTATAGGAAGATCGGAAGAGCGGTTTCAG
chr22	41548365	41548404	EP300_6173	+	GTGACCTATGCACCAGACGTGAAGCCATTGTTCTGGAGGTAGCTGAAGAAACCAAGACAGATCGGAAGAGCGGTTTCAG
chr22	41553423	41553462	EP300_6174	+	GTGACCTATGCACCAGACGTTGTTTCAGATTTGACTTTAACTTTTCTGGGATACCTAGAAAAGATCGGAAGAGCGGTTTCAG
chr22	41554515	41554554	EP300_6175	+	GTGACCTATGCACCAGACGTCAGGTGTGGACCATTGGTCCATGTGTCCACATGTCCAGGGAGATCGGAAGAGCGGTTTCAG
chr22	41556737	41556776	EP300_6176	+	GTGACCTATGCACCAGACGTGCATTATTTTGAAGAGTCTAATAGTTTGTGTTCCAGTGAAGATCGGAAGAGCGGTTTCAG
chr22	41558794	41558833	EP300_6177	+	GTGACCTATGCACCAGACGTTCCCTTTGAAATGTCAGTACGCTTTGGCTTTTCTTTTCCAGATCGGAAGAGCGGTTTCAG
chr22	41560145	41560184	EP300_6178	+	GTGACCTATGCACCAGACGTACGTTGTAATCTTCTGGAATTTTTCTTTATCGTAATAAGATCGGAAGAGCGGTTTCAG
chr22	41562681	41562720	EP300_6179	+	GTGACCTATGCACCAGACGTTTCTAAAGGTAATTTTGGCAAACCTATCTGAAGCCTAAGATCGGAAGAGCGGTTTCAG
chr22	41564614	41564653	EP300_6180	+	GTGACCTATGCACCAGACGTATTTCACTTTTCTCTCCTCGTGGATCCAAAATGCTCATAGATCGGAAGAGCGGTTTCAG
chr22	41564882	41564921	EP300_6181	+	GTGACCTATGCACCAGACGTCACAGTGGCTAGCTCCGGATTTGTGTGGGAGTTCCAACAGATCGGAAGAGCGGTTTCAG
chr22	41565631	41565670	EP300_6182	+	GTGACCTATGCACCAGACGTTTGTATAATGGCTTTTTTTCTTTAATAGCATGGCATTCTAGATCGGAAGAGCGGTTTCAG
chr22	41566586	41566625	EP300_6183	+	GTGACCTATGCACCAGACGTACATAGGGCCAGGTGCTGACAATAGATCTGGAATCTGGAATGACACAGATCGGAAGAGCGGTTTCAG
chr22	41568678	41568717	EP300_6184	+	GTGACCTATGCACCAGACGTTGAGTTTCTTTGAAACTTCTATCATGATTCTAATATTTAAGATCGGAAGAGCGGTTTCAG
chr22	41572543	41572582	EP300_6185	+	GTGACCTATGCACCAGACGTGGTTGTGGGAAGGAGGAGGTGAGCTCCGCAGGGTTGTTCTAGATCGGAAGAGCGGTTTCAG
chr22	41574971	41575010	EP300_6186	+	GTGACCTATGCACCAGACGTTAGTATTTTGGGAGCAAAAAATATTTTCTCTTAAACAAGATCGGAAGAGCGGTTTCAG
chr22	41513518	41513557	EP300_6187	+	GTGACCTATGCACCAGACGTGTGGACCAATCAGGGTCTACGCAGTCAACAGGTATGATAGATCGGAAGAGCGGTTTCAG
chr22	41573224	41573263	EP300_6188	+	GTGACCTATGCACCAGACGTCGGACTGGTGTGGTTGGGCAGCAACAGGGCCTCCCTCCAGATCGGAAGAGCGGTTTCAG
chr22	41573661	41573700	EP300_6189	+	GTGACCTATGCACCAGACGTAGGGATGGGACCGAGGATGCAGCAACAGCCACCCTGGAGATCGGAAGAGCGGTTTCAG
chr22	41574098	41574137	EP300_6190	+	GTGACCTATGCACCAGACGTCAGCCATGCAGAACATGAATCCAATGCAGGCGGGGCTTCAAGATCGGAAGAGCGGTTTCAG
chr22	41574535	41574574	EP300_6191	+	GTGACCTATGCACCAGACGTCAGCCCAACCCCATGAGCCCCAGCAGCATATGCTCCAAAGATCGGAAGAGCGGTTTCAG
chr19	45854990	45855029	ERCC2_6192	+	GTGACCTATGCACCAGACGTCAGAGGAAAGGGAGAGGGGGGCACTGTTGGCAGGGGCCAGATCGGAAGAGCGGTTTCAG
chr19	45855621	45855660	ERCC2_6193	+	GTGACCTATGCACCAGACGTAAGCGCAGGGCAGGGACAGAAGGTCATTGCGGGGAGCCTGGAGATCGGAAGAGCGGTTTCAG
chr19	45855918	45855957	ERCC2_6194	+	GTGACCTATGCACCAGACGTTGAGAGTGAAGCTGAGAGCTGGGAGGACTCCCTCCAGATCGGAAGAGCGGTTTCAG
chr19	45856085	45856124	ERCC2_6195	+	GTGACCTATGCACCAGACGTTGAGGAGAGGGGGCGAGGGGGTTTACAAGTGTGGCTGGTGGAGATCGGAAGAGCGGTTTCAG
chr19	45856424	45856463	ERCC2_6196	+	GTGACCTATGCACCAGACGTTGAGACCGAGACGCAAGTTAGTCACTCCTCAGAGCCACCTAGATCGGAAGAGCGGTTTCAG
chr19	45856603	45856642	ERCC2_6197	+	GTGACCTATGCACCAGACGTTACCAGGGAGGTGAGGGTGGGTTTCAAGGACAGCCATCCTAGATCGGAAGAGCGGTTTCAG
chr19	45858120	45858159	ERCC2_6198	+	GTGACCTATGCACCAGACGTTTCAAGGTTGGGCCCTCTCCTGGCCAGGTCCTCCTCCTAGATCGGAAGAGCGGTTTCAG
chr19	45858997	45859036	ERCC2_6199	+	GTGACCTATGCACCAGACGTACAGAGTACAGATGAGGAGGCGAGCAGCAACTGCTCCAGAGATCGGAAGAGCGGTTTCAG
chr19	45860640	45860679	ERCC2_6200	+	GTGACCTATGCACCAGACGTACAGTGGGAGGATCTCAGCAGGACTGGCAGGACAGGAGATCGGAAGAGCGGTTTCAG
chr19	45860812	45860851	ERCC2_6201	+	GTGACCTATGCACCAGACGTTAGGGCAGTGGGGCCCGGGGGCTGGGCCCCGACCCAGATCGGAAGAGCGGTTTCAG
chr19	45860968	45861007	ERCC2_6202	+	GTGACCTATGCACCAGACGTCAGGCAAGGAGGGGTGAGATTACCCACTACAGCCACAGCAGATCGGAAGAGCGGTTTCAG
chr19	45864911	45864950	ERCC2_6203	+	GTGACCTATGCACCAGACGTTGAGAGACGGGGTTCGGGGGGCAGACGGAAGCATGAGCAGGAGATCGGAAGAGCGGTTTCAG
chr19	45867180	45867219	ERCC2_6204	+	GTGACCTATGCACCAGACGTACGCTATCAGCGGCGAGCGGGGAGGCGGAAAGGGACTGGGAGATCGGAAGAGCGGTTTCAG
chr19	45867388	45867427	ERCC2_6205	+	GTGACCTATGCACCAGACGTTGAGCTGGGGCTGGAGGGGGCTGGCAACCTGGGGCAGCAAGATCGGAAGAGCGGTTTCAG
chr19	45867600	45867639	ERCC2_6206	+	GTGACCTATGCACCAGACGTTGGAGAGAGCCGGCTCAGGCAGGCCCTCAGAGGGCCTACTAGATCGGAAGAGCGGTTTCAG

chr19	45867816	45867855	ERCC2_6207	+	GTGACCTATGCACCAGACGTGGGGAGCAGGGTTACCAGGGCCCTGCCACCCCAACCCTAAGATCGGAAGAGCGGTTTCAG
chr19	45868223	45868262	ERCC2_6208	+	GTGACCTATGCACCAGACGTAGTGCCAGGGGTGACGGAGGCTGCCGCCAGGCTACCTAGATCGGAAGAGCGGTTTCAG
chr19	45868427	45868466	ERCC2_6209	+	GTGACCTATGCACCAGACGTGGGGCATCTTAGCACCCAGACAGGGTGGAAACCCAACCACAGATCGGAAGAGCGGTTTCAG
chr19	45872012	45872051	ERCC2_6210	+	GTGACCTATGCACCAGACGTGTTGGGGGGCAGGGGAGCTTGTGCTCATTGGAGGCACAAAGATCGGAAGAGCGGTTTCAG
chr19	45872261	45872300	ERCC2_6211	+	GTGACCTATGCACCAGACGTCAAGCGGACTCAGTCCCTGTCCCGCCCTTCTTTGTCTGAGATCGGAAGAGCGGTTTCAG
chr19	45872416	45872455	ERCC2_6212	+	GTGACCTATGCACCAGACGTGGGACCAGAGGGGCAACACAGGGTCTCAGAACCTTGGGAGATCGGAAGAGCGGTTTCAG
chr19	45873434	45873473	ERCC2_6213	+	GTGACCTATGCACCAGACGTGTGCTCGGGGTAGATGTAGCTACGCGGAAGTAGACCAGGAAGATCGGAAGAGCGGTTTCAG
chr19	45873501	45873540	ERCC2_6214	+	GTGACCTATGCACCAGACGTGGGGCTGCTGGGTGAGTTCCCGTCCCCTCAGCCCTCTCCAGATCGGAAGAGCGGTTTCAG
chr19	45873809	45873848	ERCC2_6215	+	GTGACCTATGCACCAGACGTGGACTGTGCAGCGGGTGCACCCGCTCCCTCATGAATATAGATCGGAAGAGCGGTTTCAG
chr12	25362856	25362895	KRAS_6216	+	GTGACCTATGCACCAGACGTAAAAAGTATAAAAATGTGAATATATACGATGGCTTCATGAGATCGGAAGAGCGGTTTCAG
chr12	25368505	25368544	KRAS_6217	+	GTGACCTATGCACCAGACGTAAACACAACCTCTTTAAAGTCTGTTGCATTGGTAAAGTAAGATCGGAAGAGCGGTTTCAG
chr12	25378718	25378757	KRAS_6218	+	GTGACCTATGCACCAGACGTAAAAAAGTTATAGCACAGCTATTAGTAACACAATATCTAGATCGGAAGAGCGGTTTCAG
chr12	25380357	25380396	KRAS_6219	+	GTGACCTATGCACCAGACGTGAGAACACAGTCTGGATTATACAGTGCACCTTTTACTTCAGATCGGAAGAGCGGTTTCAG
chr12	25398329	25398368	KRAS_6220	+	GTGACCTATGCACCAGACGTCTTATAATAAAAAATAATGAAATGTGACTATATTAGAACAGATCGGAAGAGCGGTTTCAG
chr7	106510012	106510051	PIK3CG_6221	+	GTGACCTATGCACCAGACGTGGTGTATCAATGGAAGCCTTCTCAAAGGAATGATTAGATCGGAAGAGCGGTTTCAG
chr7	106513058	106513097	PIK3CG_6222	+	GTGACCTATGCACCAGACGTCCATTTTGATAATAGCGTGAATTTTAAAGTTGCCAAGAATAGATCGGAAGAGCGGTTTCAG
chr7	106513394	106513433	PIK3CG_6223	+	GTGACCTATGCACCAGACGTATATTTTCTGTGTTCTTTCCAAATGCCTTCATCTCCAAGATCGGAAGAGCGGTTTCAG
chr7	106515259	106515298	PIK3CG_6224	+	GTGACCTATGCACCAGACGTCTGGATGCTCCATGGTCTTTTATGTCTTGAAGATGCAGATCGGAAGAGCGGTTTCAG
chr7	106520121	106520160	PIK3CG_6225	+	GTGACCTATGCACCAGACGTTTAAGATTGTTTTCAATTTACTGAAACAATTCTATATTAGATCGGAAGAGCGGTTTCAG
chr7	106522663	106522702	PIK3CG_6226	+	GTGACCTATGCACCAGACGTACCTCAGGAGATGAATAGACCTCTCAGCTCGTTTGAAAAGAGATCGGAAGAGCGGTTTCAG
chr7	106523619	106523658	PIK3CG_6227	+	GTGACCTATGCACCAGACGTGCTTTTTCCAGTCTAATGGCTCCTTACAAGTTGCATTAGATCGGAAGAGCGGTTTCAG
chr7	106526748	106526787	PIK3CG_6228	+	GTGACCTATGCACCAGACGTTCCTTCATCGCCTGCTGAGAATAGCACCAGAGCAGATGTAGATCGGAAGAGCGGTTTCAG
chr7	106545843	106545882	PIK3CG_6229	+	GTGACCTATGCACCAGACGTAGAATAAAAAAAGTTAGTGTCTATGGTTTAAATTAGATCGGAAGAGCGGTTTCAG
chr7	106508516	106508555	PIK3CG_6230	+	GTGACCTATGCACCAGACGTGATGAGCTGGAGTGGAGTGGCTGGCTGGTGACCCGAGATCGGAAGAGCGGTTTCAG
chr7	106509015	106509054	PIK3CG_6231	+	GTGACCTATGCACCAGACGTGAGCAGCTTACCATCCACGGCAAGGACCACGAGAGTGTGTAGATCGGAAGAGCGGTTTCAG
chr7	106509514	106509553	PIK3CG_6232	+	GTGACCTATGCACCAGACGTGCTCTGCACTAACCCAGACAAGGAGAATCAATGTCCATAGATCGGAAGAGCGGTTTCAG
chr17	41197830	41197869	BRCA1_6233	+	GTGACCTATGCACCAGACGTAGAACACAGCAGAGATTAGTGAATTCATTCTCTGGAAGATCGGAAGAGCGGTTTCAG
chr17	41201222	41201261	BRCA1_6234	+	GTGACCTATGCACCAGACGTATTAGATGTAATAACTGACGTAATCTGCATACTTAAAGATCGGAAGAGCGGTTTCAG
chr17	41203145	41203184	BRCA1_6235	+	GTGACCTATGCACCAGACGTAGAGGAAGAGAGGGGAGGGAATGGAGAGAAGAAAAGATCGGAAGAGCGGTTTCAG
chr17	41209163	41209202	BRCA1_6236	+	GTGACCTATGCACCAGACGTCCAAACACAACCCATCAGGATAAGAGAAGAGAAGCTTCCAGATCGGAAGAGCGGTTTCAG
chr17	41215401	41215440	BRCA1_6237	+	GTGACCTATGCACCAGACGTATAGAAAAGACAGGTTACATACAGCAGAAGAACGTGCTCAGATCGGAAGAGCGGTTTCAG
chr17	41215979	41216018	BRCA1_6238	+	GTGACCTATGCACCAGACGTAAAAACACTCAAAGATTAGAAGTTGAAAACAAAATCAGGAGATCGGAAGAGCGGTTTCAG
chr17	41219723	41219762	BRCA1_6239	+	GTGACCTATGCACCAGACGTATCAAATATTCATTATCATGAGTTACCTTAGCACACAGAGATCGGAAGAGCGGTTTCAG
chr17	41223266	41223305	BRCA1_6240	+	GTGACCTATGCACCAGACGTGGGGAAGTTAATTTACACAACGATGAATGTTGAATTAAGATCGGAAGAGCGGTTTCAG
chr17	41226549	41226588	BRCA1_6241	+	GTGACCTATGCACCAGACGTAAATGGAAGGAAAACCACTCCGCAACCAATTTGAAAAGGAAGATCGGAAGAGCGGTTTCAG
chr17	41228642	41228681	BRCA1_6242	+	GTGACCTATGCACCAGACGTAATGAGAAAACAATCTACTTTACTGCTTTGTTCTGATAGAGATCGGAAGAGCGGTTTCAG
chr17	41234603	41234642	BRCA1_6243	+	GTGACCTATGCACCAGACGTGATAAATGGCACCAAGAAAATGAAATACTTTGAGAAGCTTAGATCGGAAGAGCGGTTTCAG
chr17	41243060	41243099	BRCA1_6244	+	GTGACCTATGCACCAGACGTAAAAACAGAGTTTCAGATGTAAGAGCAGACTATAACGCTAGATCGGAAGAGCGGTTTCAG
chr17	41246670	41246709	BRCA1_6245	+	GTGACCTATGCACCAGACGTGTGAGTAATAAACTGCTGTTCTCATGCTGTAATGAGCTGGAGATCGGAAGAGCGGTTTCAG
chr17	41246888	41246927	BRCA1_6246	+	GTGACCTATGCACCAGACGTACAAAAATAACAAGTACTCAAACCTGAATGTCATTAAGATCGGAAGAGCGGTTTCAG
chr17	41247950	41247989	BRCA1_6247	+	GTGACCTATGCACCAGACGTAAGACAGAGTCTTAATAAGAAAACACTAGTTACATGATGCAGATCGGAAGAGCGGTTTCAG
chr17	41249317	41249356	BRCA1_6248	+	GTGACCTATGCACCAGACGTTCCCCCAAAAAATAAATCAATAAAAGTTTTCTTAATTAAGATCGGAAGAGCGGTTTCAG
chr17	41251908	41251947	BRCA1_6249	+	GTGACCTATGCACCAGACGTGGTAAAGAACAGTCAAGCAATTGTTGGCCAGTTCTGTGCAGATCGGAAGAGCGGTTTCAG
chr17	41256289	41256328	BRCA1_6250	+	GTGACCTATGCACCAGACGTCAAGGGAAAACATTATGTTTGCAGTTAGAGAAAATGTATAGATCGGAAGAGCGGTTTCAG
chr17	41256984	41257023	BRCA1_6251	+	GTGACCTATGCACCAGACGTATTGTTTGAGAAAACACACTCAGCAAGTGATTATCAACCTTAGATCGGAAGAGCGGTTTCAG
chr17	41258561	41258600	BRCA1_6252	+	GTGACCTATGCACCAGACGTAAAGAGAAAAGAACAACTTAAATTTACTTCTTTGTAGAGATCGGAAGAGCGGTTTCAG
chr17	41276124	41276163	BRCA1_6253	+	GTGACCTATGCACCAGACGTTCCAATGAACCTTAAACACATTAGAAAACATATATATAAGATCGGAAGAGCGGTTTCAG
chr17	41243920	41243959	BRCA1_6254	+	GTGACCTATGCACCAGACGTCTAATTTCTTGGCCCTCTTCGGTAACCTGAGCCAAATGAGATCGGAAGAGCGGTTTCAG
chr17	41243951	41243990	BRCA1_6255	+	GTGACCTATGCACCAGACGTAGCCAAATGTGTATGGGTGAAAAGGGCTAGGACTCCTGCTAAGATCGGAAGAGCGGTTTCAG
chr17	41244378	41244417	BRCA1_6256	+	GTGACCTATGCACCAGACGTCTGGAGCCCCTCTCATTAGTACTGGAACCTACTTCATTAAGATCGGAAGAGCGGTTTCAG
chr17	41244440	41244479	BRCA1_6257	+	GTGACCTATGCACCAGACGTAAAAACATTTCTCTAATGTTATTACGGCTAATTTGCTCAGATCGGAAGAGCGGTTTCAG
chr17	41244836	41244875	BRCA1_6258	+	GTGACCTATGCACCAGACGTTTACATTTCAAAGTACTTTTGGACTTTGTTTCTTAAAGAGATCGGAAGAGCGGTTTCAG
chr17	41244929	41244968	BRCA1_6259	+	GTGACCTATGCACCAGACGTTGAAAACGGAGCAAATGACTGGCGCTTTGAAACCTTGAATAGATCGGAAGAGCGGTTTCAG
chr17	41245294	41245333	BRCA1_6260	+	GTGACCTATGCACCAGACGTACATGAGATCTTTGGGGTCTTACGATTATTAGACTTTAGATCGGAAGAGCGGTTTCAG
chr17	41245418	41245457	BRCA1_6261	+	GTGACCTATGCACCAGACGTAGTAAAAGAACAGGTGCATTTGTTAACTTCAGCTCTGGGAGATCGGAAGAGCGGTTTCAG
chr17	41245752	41245791	BRCA1_6262	+	GTGACCTATGCACCAGACGTTTAAATTCGAGTTCATATTTGCTTATACTGCTGCTTATAGATCGGAAGAGCGGTTTCAG
chr17	41245907	41245946	BRCA1_6263	+	GTGACCTATGCACCAGACGTTTACCTACTTACCATTCTGCTCGTTTGGTTAGTCCGAGATCGGAAGAGCGGTTTCAG
chr17	41246210	41246249	BRCA1_6264	+	GTGACCTATGCACCAGACGTTCTTTTACTTTTACATTTAAAGCCTCATGAGGATCACTGAGATCGGAAGAGCGGTTTCAG

chr17	41246396	41246435	BRCA1_6265	+	GTGACCTATGCACCAGACGCTCATTAACTTTCTGAATGCTGCTATTTAGTGTATCCAAAGATCGGAAGAGCGGTTTCAG
chr19	1207213	1207252	STK11_6266	+	GTGACCTATGCACCAGACGCTTGTCTGGGGTCTGGGGCCGGGGCCGGCCAGTACAGGTCAGATCGGAAGAGCGGTTTCAG
chr19	1218510	1218549	STK11_6267	+	GTGACCTATGCACCAGACGCTCGGTGTTGGGACCGGGGGCCCTCCGTGGGAGGGGCTGGGGAGATCGGAAGAGCGGTTTCAG
chr19	1219423	1219462	STK11_6268	+	GTGACCTATGCACCAGACGTTGGGGCAGGGGCCAGGGTGGGGCCGGGGCCGGGGCCAGGCAGATCGGAAGAGCGGTTTCAG
chr19	1220515	1220554	STK11_6269	+	GTGACCTATGCACCAGACGTGCTAGGGGGGGCCCTGGGGCCGGCCCTCCCGGGCACTCCAGATCGGAAGAGCGGTTTCAG
chr19	1220727	1220766	STK11_6270	+	GTGACCTATGCACCAGACGTCGCCCCCGGGCACTACCCACAGCCACACTCCGAGGGGCAGATCGGAAGAGCGGTTTCAG
chr19	1221350	1221389	STK11_6271	+	GTGACCTATGCACCAGACGTCATCCCTCTGCCCGCAGCCAGGGAGGGCGGGGCTTTGTAGATCGGAAGAGCGGTTTCAG
chr19	1222016	1222055	STK11_6272	+	GTGACCTATGCACCAGACGTCCTGGGGCAGTGGGGCCGAGGCTGCAGGGAGGCCGGCCAAAGATCGGAAGAGCGGTTTCAG
chr19	1223182	1223221	STK11_6273	+	GTGACCTATGCACCAGACGTCGGGGGGCCCTGCCCGGCTCTGCTGACTCGGCCAGGATGTAGATCGGAAGAGCGGTTTCAG
chr19	1226657	1226696	STK11_6274	+	GTGACCTATGCACCAGACGCTGCAAGTGGGGCCGGCCGGGGCCGGGTGGGGCATGTGGAGATCGGAAGAGCGGTTTCAG
chr13	32890675	32890714	BRCA2_6275	+	GTGACCTATGCACCAGACGTATTTTATAAATTTATAAATTACACCCGAGAAAGTGTTTTAGATCGGAAGAGCGGTTTCAG
chr13	32900298	32900337	BRCA2_6276	+	GTGACCTATGCACCAGACGTAACAATGCTTTTTATTCTTAGAATACTAGAAATGTTAATAGATCGGAAGAGCGGTTTCAG
chr13	32900430	32900469	BRCA2_6277	+	GTGACCTATGCACCAGACGTTACCTGGTTATTTTTATGACTTAGTAATGAGAATTTGAAGATCGGAAGAGCGGTTTCAG
chr13	32900761	32900800	BRCA2_6278	+	GTGACCTATGCACCAGACGTCAAATGTGATTTTACAAGAAAGAGCAGATGAGGTTGATAAAGATCGGAAGAGCGGTTTCAG
chr13	32903640	32903679	BRCA2_6279	+	GTGACCTATGCACCAGACGTATGACATTGATTAGACTGTTGAAATGCTAACAATTTGGAGATCGGAAGAGCGGTTTCAG
chr13	32905178	32905217	BRCA2_6280	+	GTGACCTATGCACCAGACGTTGTTTAGTTGAACACAGGTTTTTTTTGTTGTTGTTGTTTATAGATCGGAAGAGCGGTTTCAG
chr13	32907535	32907574	BRCA2_6281	+	GTGACCTATGCACCAGACGCTTTTTTTTTTTGTAATAAGTACATATAGTTTTATAGATGAGATCGGAAGAGCGGTTTCAG
chr13	32915344	32915383	BRCA2_6282	+	GTGACCTATGCACCAGACGTATTTTTTACCTTTCGTGTGGCAACTCACTATTTTTAAAGTGAGATCGGAAGAGCGGTTTCAG
chr13	32918801	32918840	BRCA2_6283	+	GTGACCTATGCACCAGACGCTTTTTTATTTATCTGTTCTCCCTATAGGTATGGTATAGATCGGAAGAGCGGTTTCAG
chr13	32921044	32921083	BRCA2_6284	+	GTGACCTATGCACCAGACGTTTTAAATTTTTCTAAATTTCTAATACAGTATGAGAAAAGTCAGATCGGAAGAGCGGTTTCAG
chr13	32929436	32929475	BRCA2_6285	+	GTGACCTATGCACCAGACGTACAATTTGTGTGATGAATTTTTGCCTTTTAGATGATGATCGGAAGAGCGGTTTCAG
chr13	32930757	32930796	BRCA2_6286	+	GTGACCTATGCACCAGACGTGCTACAATACTGATGGCTTTTATGACAGAGTGAATTTTATAGATCGGAAGAGCGGTTTCAG
chr13	32932077	32932116	BRCA2_6287	+	GTGACCTATGCACCAGACGTCAAAAGATTGTGTGTTAACTTTTATGCTATCCCTCATCGATCGGAAGAGCGGTTTCAG
chr13	32936841	32936880	BRCA2_6288	+	GTGACCTATGCACCAGACGTAGCATGATTTACGTAACTATACGCAATGAGTTAAGAGATCGGAAGAGCGGTTTCAG
chr13	32937681	32937720	BRCA2_6289	+	GTGACCTATGCACCAGACGTTTGCACCTCTGGTAAAATCAGTCATTGATTGATTAAATAGATCGGAAGAGCGGTTTCAG
chr13	32944705	32944744	BRCA2_6290	+	GTGACCTATGCACCAGACGTTTCTTGAACCTTACCATATATTTCTTTCTTTGATACAATAGATCGGAAGAGCGGTTTCAG
chr13	32945248	32945287	BRCA2_6291	+	GTGACCTATGCACCAGACGTTTATATGGTACACATTGTTATTTCTAATATGAGAACAAAGAGATCGGAAGAGCGGTTTCAG
chr13	32950939	32950978	BRCA2_6292	+	GTGACCTATGCACCAGACGTAAGAGACATATAATGAGGCTTGATGATTATCAAGGTGAAGATCGGAAGAGCGGTTTCAG
chr13	32953663	32953702	BRCA2_6293	+	GTGACCTATGCACCAGACGTAATGCTTTTGTATTTTATGCTTTTATTAACCTAAAAAATGAGATCGGAAGAGCGGTTTCAG
chr13	32954061	32954100	BRCA2_6294	+	GTGACCTATGCACCAGACGTTTTCATTGTAATTTTTTTCAGTTTTGATAAGTGCTTGTGTTAGTATCGGAAGAGCGGTTTCAG
chr13	32954293	32954332	BRCA2_6295	+	GTGACCTATGCACCAGACGTATATAGTTAAATTTTTTTTATTGATTCTTTTAAAAAACATTAGATCGGAAGAGCGGTTTCAG
chr13	32969081	32969120	BRCA2_6296	+	GTGACCTATGCACCAGACGTTTTTTCAGCATACCACACATTTTGGTATTTTTCTATTTTGGATCGGAAGAGCGGTTTCAG
chr13	32971192	32971231	BRCA2_6297	+	GTGACCTATGCACCAGACGTGTAACCTCAAGGAATATTATAAAGATATATGAGAGCCAGATCGGAAGAGCGGTTTCAG
chr13	32972918	32972957	BRCA2_6298	+	GTGACCTATGCACCAGACGTAGGCAGCAATAAATTTTACGCTTAACTTTCCAGTTTAAAGATCGGAAGAGCGGTTTCAG
chr13	32972613	32972652	BRCA2_6299	+	GTGACCTATGCACCAGACGTGACTGCTCAATTTTAAAAAATTTCAATGAAATTTTCTCTTTTGGATCGGAAGAGCGGTTTCAG
chr13	32906791	32906830	BRCA2_6300	+	GTGACCTATGCACCAGACGTCGTGAATGGTCTCAACTAACCCTTTTTCAGGTCTAAATGGAAGATCGGAAGAGCGGTTTCAG
chr13	32907163	32907202	BRCA2_6301	+	GTGACCTATGCACCAGACGTCGAATGCAAGTTTTTTCAGGTCTATGACTGATCCAACTTTTATAGATCGGAAGAGCGGTTTCAG
chr13	32910905	32910944	BRCA2_6302	+	GTGACCTATGCACCAGACGTTCTGATGTTGAATTAACCAAAAATATTTCCATGGAAAAGAAGATCGGAAGAGCGGTTTCAG
chr13	32911398	32911437	BRCA2_6303	+	GTGACCTATGCACCAGACGTAAGATTTAAATCGGACATCTCCTTGAATATAGATAAAATAGATCGGAAGAGCGGTTTCAG
chr13	32911891	32911930	BRCA2_6304	+	GTGACCTATGCACCAGACGTAAGCTACATATTGCAGAAGACTACATTTGAAGTGCTGAAAGATCGGAAGAGCGGTTTCAG
chr13	32912384	32912423	BRCA2_6305	+	GTGACCTATGCACCAGACGTTTGAATGACTCTGGCCTTTTTGTTGAAGAAATTAAGTATCGGAAGAGCGGTTTCAG
chr13	32912877	32912916	BRCA2_6306	+	GTGACCTATGCACCAGACGTTAAATCTGAATTACATTCTGACATAAGAAAGAACAAAATAGATCGGAAGAGCGGTTTCAG
chr13	32913370	32913409	BRCA2_6307	+	GTGACCTATGCACCAGACGTTCTCAAAACATCAAAAAGTATCTTTTTGAAAGTTAAAGTAAGATCGGAAGAGCGGTTTCAG
chr13	32913863	32913902	BRCA2_6308	+	GTGACCTATGCACCAGACGTATATCCAATGTAAGAATGCAAAATGCATACCCACAAAATGAGATCGGAAGAGCGGTTTCAG
chr13	32914356	32914395	BRCA2_6309	+	GTGACCTATGCACCAGACGTCAGATATGTAATGTAGTATGGGAAGCTTCATAAGTCAGATCGGAAGAGCGGTTTCAG
chr13	32914849	32914888	BRCA2_6310	+	GTGACCTATGCACCAGACGTCAGATAATGGAAAAACCTGCAGTAAAGAATTTAAATTAAGATCGGAAGAGCGGTTTCAG
chr17	37856575	37856614	ERBB2_6311	+	GTGACCTATGCACCAGACGTTGTGGGGAGGGGACGGAGCAGCGGGCCGGACCCCTGCCCTGTAGATCGGAAGAGCGGTTTCAG
chr17	37863405	37863444	ERBB2_6312	+	GTGACCTATGCACCAGACGTTGGGCAACCCAGCCAGGCCCTGCCTCCAGCTGGGCTGAGCAGATCGGAAGAGCGGTTTCAG
chr17	37865716	37865755	ERBB2_6313	+	GTGACCTATGCACCAGACGTCCTCCCTGCTGCCTCTTCTCTCAGACAGCCTGACCCCAAGATCGGAAGAGCGGTTTCAG
chr17	37866145	37866184	ERBB2_6314	+	GTGACCTATGCACCAGACGTTGGGAGGGCTGGAGTCAGGGAAGGGGAGGGCTGGGGCCGGGAGATCGGAAGAGCGGTTTCAG
chr17	37866465	37866504	ERBB2_6315	+	GTGACCTATGCACCAGACGTCGTGTTTGTGCCAATTTGCTCTACCCCCAGGATGCAAGATCGGAAGAGCGGTTTCAG
chr17	37866745	37866784	ERBB2_6316	+	GTGACCTATGCACCAGACGTTGGGAAGAACACAGTTTCTCATTTTGGTGGGAGGTTTTGTAGATCGGAAGAGCGGTTTCAG
chr17	37868311	37868350	ERBB2_6317	+	GTGACCTATGCACCAGACGTAAGTCTGCCCCGAGGCCAGCTGCAGTTCCTGTCCCTCTGCGCAGATCGGAAGAGCGGTTTCAG
chr17	37868712	37868751	ERBB2_6318	+	GTGACCTATGCACCAGACGTCACAGTACCTGAGACAGTGTGAGGCAGACAGAGTCTAGATCGGAAGAGCGGTTTCAG
chr17	37871623	37871662	ERBB2_6319	+	GTGACCTATGCACCAGACGTTCTCTGCATCCTGTTCTGACAGGGGCTGGGAGTCTTGTCCAGATCGGAAGAGCGGTTTCAG
chr17	37871800	37871839	ERBB2_6320	+	GTGACCTATGCACCAGACGTAGAAAGAGGGGGCTGATGGGGAGGATCCCAGGGAGGAGATCGGAAGAGCGGTTTCAG
chr17	37872203	37872242	ERBB2_6321	+	GTGACCTATGCACCAGACGTTGGCCAGGTGCGCATCCCTATGCCAGCACACAGATCGGAAGAGCGGTTTCAG
chr17	37872697	37872736	ERBB2_6322	+	GTGACCTATGCACCAGACGTCGAGGAGGGTGGCTGGAGGGTGCATGGGGCTCCTCTAGATCGGAAGAGCGGTTTCAG

chr17	37872869	37872908	ERBB2_6323	+	GTGACCTATGCACCAGACGTGGCGGGCTCAGAGCTGGGTGGAGGGGGGCAGCGAGGGGGAAGATCGGAAGAGCGGTTTCAG
chr17	37873744	37873783	ERBB2_6324	+	GTGACCTATGCACCAGACGTCGGTCTTTTCTGCAGAAAGGAGGACTTTCTTTTCAGGGGTAGATCGGAAGAGCGGTTTCAG
chr17	37876098	37876137	ERBB2_6325	+	GTGACCTATGCACCAGACGTACCCAGGATGTACCCCTTCACTGCCCTTCACTCCCCACTAGATCGGAAGAGCGGTTTCAG
chr17	37879721	37879760	ERBB2_6326	+	GTGACCTATGCACCAGACGTGTGAAGTCTCCAGCCCGCGTGGGGTCTGCACCGGCCCCAGATCGGAAGAGCGGTTTCAG
chr17	37879924	37879963	ERBB2_6327	+	GTGACCTATGCACCAGACGTGGTCTCTGGGGTGGCGGGCCAGAGGATGGGGGCGGTGCCAGATCGGAAGAGCGGTTTCAG
chr17	37880274	37880313	ERBB2_6328	+	GTGACCTATGCACCAGACGTCCACCCTCTCTGCTAGGAGGACAGGAAGGCCCTATGCCAGATCGGAAGAGCGGTTTCAG
chr17	37881175	37881214	ERBB2_6329	+	GTGACCTATGCACCAGACGTGGGCTTTTGCAGGTCCTCCGGCAAACCCCTATGTCCAGATCGGAAGAGCGGTTTCAG
chr17	37881468	37881507	ERBB2_6330	+	GTGACCTATGCACCAGACGTGGACCAAGGAGCAGAGGAGGCTGGTGGAGTGGTGTCTAGAGATCGGAAGAGCGGTTTCAG
chr17	37881666	37881705	ERBB2_6331	+	GTGACCTATGCACCAGACGTGGGGGTGTTGGGAGGGTGGGTGAGGAGCCATGGCTGGAGAGATCGGAAGAGCGGTTTCAG
chr17	37882117	37882156	ERBB2_6332	+	GTGACCTATGCACCAGACGTGAGCTGTGCTGGCTGCTGGAGGAGGGTGGGAGGTCTGGAGATCGGAAGAGCGGTTTCAG
chr17	37882923	37882962	ERBB2_6333	+	GTGACCTATGCACCAGACGTTCTGTGCCCATCCTGCCTGTGGCTAAGAGCACCCCTCCTAGATCGGAAGAGCGGTTTCAG
chr17	37883267	37883306	ERBB2_6334	+	GTGACCTATGCACCAGACGTTCCGTACACTGTGTGGCTGTCTGCTTACCTCCCCAACCCAGATCGGAAGAGCGGTTTCAG
chr17	37883811	37883850	ERBB2_6335	+	GTGACCTATGCACCAGACGTGAAGTCAACAGCAGAGACTGATGGCAGGGGAGGTGGGACAGATCGGAAGAGCGGTTTCAG
chr17	37884308	37884347	ERBB2_6336	+	GTGACCTATGCACCAGACGTCAAGTCCGCAAGCCCTGATGTGTCTCAGGGAGCAGGGAGATCGGAAGAGCGGTTTCAG
chr7	140439757	140439796	BRAF_6337	+	GTGACCTATGCACCAGACGTAAAAAAGGGAATAATTCAACCTTGTAGATAAGTTGAAAGATCGGAAGAGCGGTTTCAG
chr7	140449229	140449268	BRAF_6338	+	GTGACCTATGCACCAGACGTATACAAAGAAAATATCTTCACTTCAATTGAATAAAGACAGATCGGAAGAGCGGTTTCAG
chr7	140453204	140453243	BRAF_6339	+	GTGACCTATGCACCAGACGTGAAGTAAAGGAAAAACAGTAGATCTCAATTTTCTATCAGAAGATCGGAAGAGCGGTTTCAG
chr7	140454044	140454083	BRAF_6340	+	GTGACCTATGCACCAGACGTGAAGTCAATTTAACTGAGTAGGGCTAAAGGACTCTGGACAGATCGGAAGAGCGGTTTCAG
chr7	140476899	140476938	BRAF_6341	+	GTGACCTATGCACCAGACGTAAATGTGACAGTAAACATTAATATGTCGACAAACTTTAGCAAGATCGGAAGAGCGGTTTCAG
chr7	140477886	140477925	BRAF_6342	+	GTGACCTATGCACCAGACGTATTGTTACTCCAAGTGTCAATTTCAATTTTTAAAATTTAAAAGATCGGAAGAGCGGTTTCAG
chr7	140481504	140481543	BRAF_6343	+	GTGACCTATGCACCAGACGTACAGTAAAAAAGTCAAGTCAAGCCAAACAGAAAAAGAAAAAGATCGGAAGAGCGGTTTCAG
chr7	140482968	140483007	BRAF_6344	+	GTGACCTATGCACCAGACGTGAAAAGAAAAATGTATACATTAAGGAGGAGCAAGTATGTTAGATCGGAAGAGCGGTTTCAG
chr7	140487395	140487434	BRAF_6345	+	GTGACCTATGCACCAGACGTATAGTAATGTATATTTATCCAAGCAAGCATATAATCAGAAGATCGGAAGAGCGGTTTCAG
chr7	140494278	140494317	BRAF_6346	+	GTGACCTATGCACCAGACGTGAAGTCAATTTGGAAGATGAAGTCAAGTAAACGATATAAAGAGATCGGAAGAGCGGTTTCAG
chr7	140500292	140500331	BRAF_6347	+	GTGACCTATGCACCAGACGTAAACAAAACAACTTAACCTTGTGCAAAACCCAGAAGCTTCAGATCGGAAGAGCGGTTTCAG
chr7	140501371	140501410	BRAF_6348	+	GTGACCTATGCACCAGACGTAAAAATCACAGAGATTTCAAAAACCTACAAGAAAACCTTCAGATCGGAAGAGCGGTTTCAG
chr7	140507873	140507912	BRAF_6349	+	GTGACCTATGCACCAGACGTGACACACAGCCTTTCTTGGTTATTACACCTAAAAATATTAGATCGGAAGAGCGGTTTCAG
chr7	140508806	140508845	BRAF_6350	+	GTGACCTATGCACCAGACGTATAAATATATGATAAGGTAAGGGAGCAAATACATTAGATCGGAAGAGCGGTTTCAG
chr7	140534683	140534722	BRAF_6351	+	GTGACCTATGCACCAGACGTAAAGCATTATATTAAGTCCGGACTTTGTCTGACATTAAGATCGGAAGAGCGGTTTCAG
chr7	140550023	140550062	BRAF_6352	+	GTGACCTATGCACCAGACGTAAACAAAAGATTTAAATAAAAATCACTTAGTATGAATAGATCGGAAGAGCGGTTTCAG
chr4	153244312	153244351	FBXW7_6353	+	GTGACCTATGCACCAGACGTACCAAAAAGATTTAATTACTGGTTAGAATAATGGCTATGAGATCGGAAGAGCGGTTTCAG
chr4	153245557	153245596	FBXW7_6354	+	GTGACCTATGCACCAGACGTACAGTATTATAGAATAGAAGTATGGACTCTTCTATCAGATCGGAAGAGCGGTTTCAG
chr4	153247394	153247433	FBXW7_6355	+	GTGACCTATGCACCAGACGTAGAAACAGAAAAACAAAACAAAACAAAACCCACGTTTAGATCGGAAGAGCGGTTTCAG
chr4	153249552	153249591	FBXW7_6356	+	GTGACCTATGCACCAGACGTACTAAGATGATTACTTTTGGGTAGAAAGGAAAAGTATTAGATCGGAAGAGCGGTTTCAG
chr4	153250948	153250987	FBXW7_6357	+	GTGACCTATGCACCAGACGTGATGTGCAGATAGAAATGTTAATTAATTTATGTTCTTAGATCGGAAGAGCGGTTTCAG
chr4	153252031	153252070	FBXW7_6358	+	GTGACCTATGCACCAGACGTACAGTTCAAGAGTAAATTCCTTACCATAATAACAGTTAGATCGGAAGAGCGGTTTCAG
chr4	153259099	153259138	FBXW7_6359	+	GTGACCTATGCACCAGACGTGAATTAGAAATTTTTATTGTTTTAACAGATGTCCCAAATTAGATCGGAAGAGCGGTTTCAG
chr4	153271287	153271326	FBXW7_6360	+	GTGACCTATGCACCAGACGTAAACAAAACAGATATGTTTTTAAAAATCGTCTAATCATTAGATCGGAAGAGCGGTTTCAG
chr4	153273893	153273932	FBXW7_6361	+	GTGACCTATGCACCAGACGTAGCTTGACTGAGAAGAAGCTCGAGGGAATAATGAGAGAGAAAGATCGGAAGAGCGGTTTCAG
chr4	153303498	153303537	FBXW7_6362	+	GTGACCTATGCACCAGACGTCTCTGGTTGACGAATACTCTACATGTAATACAGGCACAGATCGGAAGAGCGGTTTCAG
chr4	153332966	153333005	FBXW7_6363	+	GTGACCTATGCACCAGACGTGACTTGTACTTCTTGACACTTCTGGCTAGACTATCAGAAGAGATCGGAAGAGCGGTTTCAG
chr3	37035165	37035204	MLH1_6364	+	GTGACCTATGCACCAGACGTAGTCGAGCCGGGCTCACTTAAAGGGCTACGACTTAAAGGGCAGATCGGAAGAGCGGTTTCAG
chr3	37038211	37038250	MLH1_6365	+	GTGACCTATGCACCAGACGTCTCAAAGTAGCAGGATGTTGTGCGCTTCATGGAAGAGTAGATCGGAAGAGCGGTTTCAG
chr3	37042555	37042594	MLH1_6366	+	GTGACCTATGCACCAGACGTGATTCAAGAAATGTGTAATAATCTCCTGTGATGACATTAGATCGGAAGAGCGGTTTCAG
chr3	37045976	37046015	MLH1_6367	+	GTGACCTATGCACCAGACGTGACTTCTTTACTCATATATATTCATTTCAAATGTATTTAGATCGGAAGAGCGGTTTCAG
chr3	37048565	37048604	MLH1_6368	+	GTGACCTATGCACCAGACGTACTAGCAGAGTAAATTTGGAAGCTTTGTTGTATAAAGATCGGAAGAGCGGTTTCAG
chr3	37050407	37050446	MLH1_6369	+	GTGACCTATGCACCAGACGTAAATCTGGGAGTGGGTCTCTGAGATTTGTCATCAAAGTAAAGATCGGAAGAGCGGTTTCAG
chr3	37053364	37053403	MLH1_6370	+	GTGACCTATGCACCAGACGTGGTTTATGGGGATGGTTTTGTTTTATGAAAAGAAAAAGAGATCGGAAGAGCGGTTTCAG
chr3	37053601	37053640	MLH1_6371	+	GTGACCTATGCACCAGACGTAACTTATATAAAAAATCTTTTACATTTATTATCTTGGTTAGATCGGAAGAGCGGTTTCAG
chr3	37056046	37056085	MLH1_6372	+	GTGACCTATGCACCAGACGTAAAGAACACATGGGAAATCCACTCACAGGAAACACCCACAAGATCGGAAGAGCGGTTTCAG
chr3	37059101	37059140	MLH1_6373	+	GTGACCTATGCACCAGACGTAACTTCTCAACCAAGACTACAAGGAAACAGATGTTAGATCGGAAGAGCGGTTTCAG
chr3	37061965	37062004	MLH1_6374	+	GTGACCTATGCACCAGACGTCTTCTCATCAGTACTTCTCTGCGGCTTTGAAATGTGCCAGATCGGAAGAGCGGTTTCAG
chr3	37067509	37067548	MLH1_6375	+	GTGACCTATGCACCAGACGTTTTGGGAAAAGTACAGCCTACCTCTTTATTCTGTAATAAAGATCGGAAGAGCGGTTTCAG
chr3	37070434	37070473	MLH1_6376	+	GTGACCTATGCACCAGACGTGCTGTGGCCTGCCTGGGATGCATAGGGCCTCAACTGCCAAAGATCGGAAGAGCGGTTTCAG
chr3	37081796	37081835	MLH1_6377	+	GTGACCTATGCACCAGACGTTGAGTGTGTAACAGCAGAGCTACTACAACAATGGTCCAAGATCGGAAGAGCGGTTTCAG
chr3	37083833	37083872	MLH1_6378	+	GTGACCTATGCACCAGACGTACTTTTCACTTCTGAAATTTCAACTGATCGTTTCTGAAAGATCGGAAGAGCGGTTTCAG
chr3	37089185	37089224	MLH1_6379	+	GTGACCTATGCACCAGACGTCATTTTACTCTTGTGTTTCTTCAAATAAATTTCCAGATCGGAAGAGCGGTTTCAG
chr3	37090111	37090150	MLH1_6380	+	GTGACCTATGCACCAGACGTAAAGCAGTAACTAAGCATTTCGGTACATGCATGTGTCTGGAGATCGGAAGAGCGGTTTCAG

chr3	37090519	37090558	MLH1_6381	+	GTGACCTATGCACCAGACGTGATGCACACTGGCACCCAGGACTAGGACAGGACCTCATAAGATCGGAAGAGCGGTTTCAG
chr3	37092155	37092194	MLH1_6382	+	GTGACCTATGCACCAGACGTTTATGCACTGTGGGATGTGTTCTTCTTCTCTGATTCCGAGATCGGAAGAGCGGTTTCAG
chr2	47630552	47630591	MSH2_6383	+	GTGACCTATGCACCAGACGTGGACGGCGCGTCTGGGGAGGGACCCGGGGCCTTGTTGGCGAGATCGGAAGAGCGGTTTCAG
chr2	47635705	47635744	MSH2_6384	+	GTGACCTATGCACCAGACGTTCCTTTTTAATTTACTTATTTTTTTAAGAGTAGAAAAATAAGATCGGAAGAGCGGTTTCAG
chr2	47637522	47637561	MSH2_6385	+	GTGACCTATGCACCAGACGTTGAGTCTAGTGATAGAGGAGATCCAGGCCCTAGGAAAGGCAGATCGGAAGAGCGGTTTCAG
chr2	47643579	47643618	MSH2_6386	+	GTGACCTATGCACCAGACGTAGTTTTATACTTTCTGTTAGTTTTTGAACCTGCAGTTACCAGATCGGAAGAGCGGTTTCAG
chr2	47657091	47657130	MSH2_6387	+	GTGACCTATGCACCAGACGTTATTTTTGTTTTTTTTGTTTTTCCCTCAACTACATAATATATAAGATCGGAAGAGCGGTTTCAG
chr2	47672807	47672846	MSH2_6388	+	GTGACCTATGCACCAGACGTTACTTTTTTAATTTAAGCAGTAGTTATTTTTAAAAAGCAAAGATCGGAAGAGCGGTTTCAG
chr2	47690304	47690343	MSH2_6389	+	GTGACCTATGCACCAGACGTGCATTGGAGGTTGGAATAATCTTTTGTCTATACACTGTAGATCGGAAGAGCGGTTTCAG
chr2	47693958	47693997	MSH2_6390	+	GTGACCTATGCACCAGACGTCGTTATATATTTTTAACCCTTTATTAATCCCTAAATGCAGATCGGAAGAGCGGTTTCAG
chr2	47698212	47698251	MSH2_6391	+	GTGACCTATGCACCAGACGTTAGAACTAATAATGTTCTGAATGTCACCTGGCTTTTGGTAAGATCGGAAGAGCGGTTTCAG
chr2	47703721	47703760	MSH2_6392	+	GTGACCTATGCACCAGACGTCCTAGTCCCTTGAAGATGAAATGTATGTCTGTCTGTCTAGATCGGAAGAGCGGTTTCAG
chr2	47705669	47705708	MSH2_6393	+	GTGACCTATGCACCAGACGTTTGGAGTCTCTAAATTCAGAACTTGGTAATGGGAAACTTAGATCGGAAGAGCGGTTTCAG
chr2	47708021	47708060	MSH2_6394	+	GTGACCTATGCACCAGACGTTTGTTCATAGTTAACTTAGCTTCTCTATTATTACATAAGATCGGAAGAGCGGTTTCAG
chr2	47710099	47710138	MSH2_6395	+	GTGACCTATGCACCAGACGTTAATGGAATGAAGGTAATATTGATAAGCTATTGTCTGTAAGATCGGAAGAGCGGTTTCAG
chr18	48573676	48573715	SMAD4_6396	+	GTGACCTATGCACCAGACGTTAAGAGTTTTCTATACCCTCTATGGTGGCAGATTTAAAAAGATCGGAAGAGCGGTTTCAG
chr18	48575241	48575280	SMAD4_6397	+	GTGACCTATGCACCAGACGTTTTGTCTTCACTTCACTAAAGAACATAAAGGGAAAAAGGATCTCAGATCGGAAGAGCGGTTTCAG
chr18	48575705	48575744	SMAD4_6398	+	GTGACCTATGCACCAGACGTTGTTCTTACTACTTTCTCTTTGTTTTGTCTATCCTCTCAGATCGGAAGAGCGGTTTCAG
chr18	48581374	48581413	SMAD4_6399	+	GTGACCTATGCACCAGACGTGAATCAGATGTAGTCAGCAAGTTGAGTTTTCCATAATCATTAGATCGGAAGAGCGGTTTCAG
chr18	48584625	48584664	SMAD4_6400	+	GTGACCTATGCACCAGACGTACTTTAAAAAATCTTTAAATAGTTGAGAAAAAGTAGGCAGATCGGAAGAGCGGTTTCAG
chr18	48584837	48584876	SMAD4_6401	+	GTGACCTATGCACCAGACGTGTTTTGTTGTAAGGGCTATTTTTTTTTTTTTTTTGGTAGAGATCGGAAGAGCGGTTTCAG
chr18	48586297	48586336	SMAD4_6402	+	GTGACCTATGCACCAGACGTTTCAAATGATTTCTGTATTTAGATTGATTTAGTGGTGGATCGGAAGAGCGGTTTCAG
chr18	48591987	48592026	SMAD4_6403	+	GTGACCTATGCACCAGACGTTATAGTCAGATGTTACTTTAAAAAATGAGCATAGTCAAGATCGGAAGAGCGGTTTCAG
chr18	48593607	48593646	SMAD4_6404	+	GTGACCTATGCACCAGACGTATTTTTGAAATTTTTAGAACTTTAGACTTAAAGCTCTATTTGTTGAGATCGGAAGAGCGGTTTCAG
chr18	48603157	48603196	SMAD4_6405	+	GTGACCTATGCACCAGACGTTTTTTCATTCTTTTTTAAAGGTATAATAGTTGATATTTTTAAGATCGGAAGAGCGGTTTCAG
chr18	48604848	48604887	SMAD4_6406	+	GTGACCTATGCACCAGACGTGTTGGGGCCCTTAACCTTATCAGGATGGTGGACTACAAAAGATCGGAAGAGCGGTTTCAG
chr9	22006257	22006296	CDKN2B_6407	+	GTGACCTATGCACCAGACGTGAGCAGAGTGGTCAGAGCCAGGGTGGGGCCAGGTATGGGAAGATCGGAAGAGCGGTTTCAG
chr9	22008963	22009002	CDKN2B_6408	+	GTGACCTATGCACCAGACGTCCAGACCGCAGCGCCCGGATAATCCACCGTTGGCCGTAAGATCGGAAGAGCGGTTTCAG
chr4	1795781	1795820	FGFR3_6409	+	GTGACCTATGCACCAGACGTACCCACTAGCCAGCGGAGAGCCGGCTGCGGGCAGAGATCGGAAGAGCGGTTTCAG
chr4	1801261	1801300	FGFR3_6410	+	GTGACCTATGCACCAGACGTGGGCCAGCCAGCTTACAGAAAGGAGCCGAGTCCCGGCTCAGATCGGAAGAGCGGTTTCAG
chr4	1801550	1801589	FGFR3_6411	+	GTGACCTATGCACCAGACGTGGTCCAGGGTTTCAGGCCAGCCGGGGTGGGGCCCGCTGCCAAGATCGGAAGAGCGGTTTCAG
chr4	1803274	1803313	FGFR3_6412	+	GTGACCTATGCACCAGACGTGCGGGTGGCTCTGGCCCTGGCAGGCGCGGTGGTTGCTGCCAGATCGGAAGAGCGGTTTCAG
chr4	1803763	1803802	FGFR3_6413	+	GTGACCTATGCACCAGACGTGTGTGCACGTGGCTGCCCGCTGGGGCTCCTGGGCTGGCAGATCGGAAGAGCGGTTTCAG
chr4	1805574	1805613	FGFR3_6414	+	GTGACCTATGCACCAGACGTGCTGCTGCTGCTGCCCTCCGCACTGTCTGGGGGAGCGTGGAGATCGGAAGAGCGGTTTCAG
chr4	1806258	1806297	FGFR3_6415	+	GTGACCTATGCACCAGACGTGTAGTACCAGGTTCTGAGCTTCCAGGCTGCCGCCAGGCTCCAGATCGGAAGAGCGGTTTCAG
chr4	1806707	1806746	FGFR3_6416	+	GTGACCTATGCACCAGACGTCTGAGGGCCAGCGTTGGCTGTAGGGGGCTTGGTGGTGGGGAGATCGGAAGAGCGGTTTCAG
chr4	1807214	1807253	FGFR3_6417	+	GTGACCTATGCACCAGACGTGGCGGCCAGGGTGCAGAGCAGGGCTGGGGCCGCCGCCAGATCGGAAGAGCGGTTTCAG
chr4	1807407	1807446	FGFR3_6418	+	GTGACCTATGCACCAGACGTTAGCGCGGTGGTGGCCGCTGGGGCCGCCCTCCTGGGCTGAGATCGGAAGAGCGGTTTCAG
chr4	1807678	1807717	FGFR3_6419	+	GTGACCTATGCACCAGACGTGGCCAGGTGTGGTGGAGTAGGCTGGGCCCTGCCCTGAGAAGATCGGAAGAGCGGTTTCAG
chr4	1807911	1807950	FGFR3_6420	+	GTGACCTATGCACCAGACGTCCCTGGGGTGGGGGTGGGGGTGATGCCAGTAGGACGCGGATCGGAAGAGCGGTTTCAG
chr4	1808065	1808104	FGFR3_6421	+	GTGACCTATGCACCAGACGTGGCAGAGCTCAGGCTTTCAGGGGTGGAGCCGGAACTGGGCAGATCGGAAGAGCGGTTTCAG
chr4	1808421	1808460	FGFR3_6422	+	GTGACCTATGCACCAGACGTTCCCTGGCCCTCCACTGGGTCTCAGGGGTGGGGTCCCTAGATCGGAAGAGCGGTTTCAG
chr4	1808672	1808711	FGFR3_6423	+	GTGACCTATGCACCAGACGTGCTCTGGCCTGGTGCCACCCGCTATGCCCTCCCCCTGCAGATCGGAAGAGCGGTTTCAG
chr4	1809000	1809039	FGFR3_6424	+	GTGACCTATGCACCAGACGTGCCCAACAATGTGAGGGGTCCCTAGCAGCCACCCTGCAGATCGGAAGAGCGGTTTCAG
chr2	48010643	48010682	MSH6_6425	+	GTGACCTATGCACCAGACGTGGGGGTGGGGTGGAGCGGGGGCATAGCGGGCGGGGCTAGATCGGAAGAGCGGTTTCAG
chr2	48023213	48023252	MSH6_6426	+	GTGACCTATGCACCAGACGTGCAAGCATTGATTTGTTAGGGTATGGGGAAAGATCGGAAGAGCGGTTTCAG
chr2	48028305	48028344	MSH6_6427	+	GTGACCTATGCACCAGACGTGAACAAGCTTGTCTCAGGCTTTGATAAGTAGTGTGTTTATAGATCGGAAGAGCGGTTTCAG
chr2	48030835	48030874	MSH6_6428	+	GTGACCTATGCACCAGACGTCTTAAAGTTTTGTTATCAGAAAGTCAATTTGTGACATTAGGAGATCGGAAGAGCGGTTTCAG
chr2	48032177	48032216	MSH6_6429	+	GTGACCTATGCACCAGACGTTGTTCCCACTTAAAGTTCTCATTAGTCAATTTAGATGTGAAGATCGGAAGAGCGGTTTCAG
chr2	48032857	48032896	MSH6_6430	+	GTGACCTATGCACCAGACGTAAACTTCTCATTTGAAGACTTATCTTAAAAACATTTGAGATCGGAAGAGCGGTTTCAG
chr2	48033508	48033547	MSH6_6431	+	GTGACCTATGCACCAGACGTATTTGTTTTTCCCAAATTCGGTTTTTGGAGGGCACTAGATCGGAAGAGCGGTTTCAG
chr2	48033801	48033840	MSH6_6432	+	GTGACCTATGCACCAGACGTTAACTATAAGTAATTAATACTAACTTAACTTAAAGTTTCAAAGATCGGAAGAGCGGTTTCAG
chr2	48034010	48034049	MSH6_6433	+	GTGACCTATGCACCAGACGTTTGAAGCTTTGAGTTGACTTCTGACAAAGGTGGTAAATTAGATCGGAAGAGCGGTTTCAG
chr2	48026184	48026223	MSH6_6434	+	GTGACCTATGCACCAGACGTAGGTGGTGTGATGACAGTAGTCGCCCTACTGTTTGGTATCATAGATCGGAAGAGCGGTTTCAG
chr2	48026608	48026647	MSH6_6435	+	GTGACCTATGCACCAGACGTTGTAGAAAGATGGCACATATCCAAGTATGATAGAGTGGAGATCGGAAGAGCGGTTTCAG
chr2	48027032	48027071	MSH6_6436	+	GTGACCTATGCACCAGACGTTCCCTGAGGAAGAATTTTTAGGGAAAGCTAAGTGTAGGATCGGAAGAGCGGTTTCAG
chr2	48027456	48027495	MSH6_6437	+	GTGACCTATGCACCAGACGTTTGGCCCACTTGTAACTTGTAACTTATTAATGATCGGAAGAGCGGTTTCAG
chr2	48027880	48027919	MSH6_6438	+	GTGACCTATGCACCAGACGTGAGGCTCGAAAGACTGACCTTATTACTCCAAAGCAGGCTAGATCGGAAGAGCGGTTTCAG

chr3	138374379	138374418	PIK3CB_6439	+	GTGACCTATGCACCAGACGTAGGGGGGAAAATATGATTTTATATAACTTTAGTAGAGATGTAGATCGGAAGAGCGGTTTCAG
chr3	138375127	138375166	PIK3CB_6440	+	GTGACCTATGCACCAGACGTTGCAGCAAACCACATGAGCACAGTGTAGAGGGGAGAGAGAGATCGGAAGAGCGGTTTCAG
chr3	138376688	138376727	PIK3CB_6441	+	GTGACCTATGCACCAGACGTAATGGGATTTAATTTCCCTTCATTTTTCTGGTGGGTTCCAAAGATCGGAAGAGCGGTTTCAG
chr3	138382882	138382921	PIK3CB_6442	+	GTGACCTATGCACCAGACGTGAAAAGAACAAGCAAAAAGGTTTTCAGCCTCCAAGCGAGATCGGAAGAGCGGTTTCAG
chr3	138384056	138384095	PIK3CB_6443	+	GTGACCTATGCACCAGACGTAAAAATGGGCATAGAGTCATATTTTCTTAAAAATGAAACAAGATCGGAAGAGCGGTTTCAG
chr3	138400898	138400937	PIK3CB_6444	+	GTGACCTATGCACCAGACGTACAACTGCTTCATTACAAGTGCCTTTTCTTTTATGCCCTAGATCGGAAGAGCGGTTTCAG
chr3	138402640	138402679	PIK3CB_6445	+	GTGACCTATGCACCAGACGTGGGGGAAAATAGTCAAGTGTCAATGATACAGAAAGATCGGAAGAGCGGTTTCAG
chr3	138403656	138403695	PIK3CB_6446	+	GTGACCTATGCACCAGACGTAGTTCCCCACACAAAAATTCATTTGACTAAAAGTAATATAGATCGGAAGAGCGGTTTCAG
chr3	138407827	138407866	PIK3CB_6447	+	GTGACCTATGCACCAGACGTTTATGATATCTGAACAGTTTGTATCAACACTTCAGAAGATCGGAAGAGCGGTTTCAG
chr3	138409996	138410035	PIK3CB_6448	+	GTGACCTATGCACCAGACGTCAAAAGACACAGTGAAGTAAACAAACACCTGTGCCAGAAAAGATCGGAAGAGCGGTTTCAG
chr3	138413760	138413799	PIK3CB_6449	+	GTGACCTATGCACCAGACGTAATGAAACTGGTTCAGAATAATGGGGGACAAAAGTAATCAGATCGGAAGAGCGGTTTCAG
chr3	138417948	138417987	PIK3CB_6450	+	GTGACCTATGCACCAGACGTAATGCTCATTATAGAATTTAATGTGCAAAACCCACAGAGATCGGAAGAGCGGTTTCAG
chr3	138423346	138423385	PIK3CB_6451	+	GTGACCTATGCACCAGACGTAAAATTAAGAAAATGAATTTGGCTCTCATATTTGTGAAAAGATCGGAAGAGCGGTTTCAG
chr3	138426142	138426181	PIK3CB_6452	+	GTGACCTATGCACCAGACGTCAATAATTTTGGTCTTAAAAAATGCTTTAAACTAGGAGATCGGAAGAGCGGTTTCAG
chr3	138431157	138431196	PIK3CB_6453	+	GTGACCTATGCACCAGACGTAGATACCATTGCATAAATATGCTAAGAATAACTTTAAGGTAGATCGGAAGAGCGGTTTCAG
chr3	138433572	138433611	PIK3CB_6454	+	GTGACCTATGCACCAGACGTGCAGACAAAACAAAACAAAGTCATGAATACTGTACCACAGATCGGAAGAGCGGTTTCAG
chr3	138452291	138452330	PIK3CB_6455	+	GTGACCTATGCACCAGACGTATAAAAATAAATCAAAATTTTAAATGAAGAAAATGAATAAAGATCGGAAGAGCGGTTTCAG
chr3	138453657	138453696	PIK3CB_6456	+	GTGACCTATGCACCAGACGTAAAAGGAAAGGATGATTTTTCATGCCAACACCTAAAAGATCGGAAGAGCGGTTTCAG
chr3	138456739	138456778	PIK3CB_6457	+	GTGACCTATGCACCAGACGTAGGGAGATGGGAAAAAAGCAGTAATGTTATATTATGCAGATCGGAAGAGCGGTTTCAG
chr3	138461634	138461673	PIK3CB_6458	+	GTGACCTATGCACCAGACGTTTTTAAAGGTGTCATTTTCAGTAACTAACAAATAAAAAAGATCGGAAGAGCGGTTTCAG
chr3	138478196	138478235	PIK3CB_6459	+	GTGACCTATGCACCAGACGTGGGGCCCTAGAAAATCAGTAATTAACAACATAGCAAAAACACAGATCGGAAGAGCGGTTTCAG
chr5	67522848	67522887	PIK3R1_6460	+	GTGACCTATGCACCAGACGTATAAGTGGTGTCTAATGACTCCCTTTCTTTTTCTTTTTAAGATCGGAAGAGCGGTTTCAG
chr5	67569321	67569360	PIK3R1_6461	+	GTGACCTATGCACCAGACGTTGCTAGAGGGCATCGTTCCTTTGTTCTACCCCTATTTCAAGATCGGAAGAGCGGTTTCAG
chr5	67569852	67569891	PIK3R1_6462	+	GTGACCTATGCACCAGACGTGCAGATGAGAAATGCAAAATGGGAAAGACAGGCTTTGGCTTAGATCGGAAGAGCGGTTTCAG
chr5	67575572	67575611	PIK3R1_6463	+	GTGACCTATGCACCAGACGTTCTCTTCTGGGAACCTCATTGAACATACATGGAGATGTAGAGATCGGAAGAGCGGTTTCAG
chr5	67576568	67576607	PIK3R1_6464	+	GTGACCTATGCACCAGACGTGGAGACAAACATGTATTTGGGGTGATGAGGGTAGTCCCTAAGATCGGAAGAGCGGTTTCAG
chr5	67576845	67576884	PIK3R1_6465	+	GTGACCTATGCACCAGACGTTTGAGCATTTAACATTCTCTCATTTGTTCATTTTTAGAGCAGATCGGAAGAGCGGTTTCAG
chr5	67584629	67584668	PIK3R1_6466	+	GTGACCTATGCACCAGACGTTTGAATTTGTGACCTCTCTGTTCTTATCTGAGCGGTGCAGATCGGAAGAGCGGTTTCAG
chr5	67586673	67586712	PIK3R1_6467	+	GTGACCTATGCACCAGACGTAGTATTATTGTAGAGAGTAGTAAATTTCTGGCTTTTTAAGATCGGAAGAGCGGTTTCAG
chr5	67588200	67588239	PIK3R1_6468	+	GTGACCTATGCACCAGACGTAGAACAATTCATTTTCAGAGATTTTAGATTTAAAGAAAGAAAGATCGGAAGAGCGGTTTCAG
chr5	67589038	67589077	PIK3R1_6469	+	GTGACCTATGCACCAGACGTGAATATAGCTGAAATAGGGTTTTGGGCTGATATTAACAAGATCGGAAGAGCGGTTTCAG
chr5	67589322	67589361	PIK3R1_6470	+	GTGACCTATGCACCAGACGTCGAATGAATTACAGTTACGATGTTTAGACAAGATCCTAGATCGGAAGAGCGGTTTCAG
chr5	67589673	67589712	PIK3R1_6471	+	GTGACCTATGCACCAGACGTTATGAAAATCAGATTAAAAAATAAGAGTTCTAAACTTTTAAAGATCGGAAGAGCGGTTTCAG
chr5	67590517	67590556	PIK3R1_6472	+	GTGACCTATGCACCAGACGTCCTCTGTTCTGTGTAGAGTAACCAAAATCCTCTAAAAGATCGGAAGAGCGGTTTCAG
chr5	67591163	67591202	PIK3R1_6473	+	GTGACCTATGCACCAGACGTGAAATGAAATCCTATACATGAATAATGGTATTGCTACAAGATCGGAAGAGCGGTTTCAG
chr5	67591327	67591366	PIK3R1_6474	+	GTGACCTATGCACCAGACGTACTAAAGATGGTATAGCAGAAGATTTTTCTCATTTTAGGAGATCGGAAGAGCGGTTTCAG
chr5	67592180	67592219	PIK3R1_6475	+	GTGACCTATGCACCAGACGTCCAGCAAATTTTTTACAACATCTCATGAAGAGATGTTAGATCGGAAGAGCGGTTTCAG
chr5	67593440	67593479	PIK3R1_6476	+	GTGACCTATGCACCAGACGCTTTTGATCCTTCTCCTGAAGTTCAGCCACCCTGAGGCCTCAGATCGGAAGAGCGGTTTCAG
chr2	128015314	128015353	ERCC3_6477	+	GTGACCTATGCACCAGACGTGGGGGAAACCAGCCCATGTTAGTCTCCAGAAGAAAAGATACAGATCGGAAGAGCGGTTTCAG
chr2	128017035	128017074	ERCC3_6478	+	GTGACCTATGCACCAGACGTCAGCCAGCAGACATGCCCTTTCTGCTCTCTCCCCAGATCGGAAGAGCGGTTTCAG
chr2	128018933	128018972	ERCC3_6479	+	GTGACCTATGCACCAGACGTAAGTGAAGAGGTTTTATATATAGGAAAAAAGATCAGATCGGAAGAGCGGTTTCAG
chr2	128029040	128029079	ERCC3_6480	+	GTGACCTATGCACCAGACGTAAGTGAAGAGGTTTTATATATAGGAAAAAAGATCAGATCGGAAGAGCGGTTTCAG
chr2	128030548	128030587	ERCC3_6481	+	GTGACCTATGCACCAGACGTATGAAGCTGTGTTAGACCACAGAATAATGCCTCAGTTATCAGATCGGAAGAGCGGTTTCAG
chr2	128036962	128037001	ERCC3_6482	+	GTGACCTATGCACCAGACGTGAAGAACCAGGGGTCATTTTACAAGTTTAAACACCACAGATCGGAAGAGCGGTTTCAG
chr2	128044604	128044643	ERCC3_6483	+	GTGACCTATGCACCAGACGTCAGAGTGAATGCCAATCCCAACAGGAGGTTGAAATGAAGGAGATCGGAAGAGCGGTTTCAG
chr2	128046451	128046490	ERCC3_6484	+	GTGACCTATGCACCAGACGTGGCACAAGGGGTTTTAAATCTGTTACTGTCTCAAAAGATCGGAAGAGCGGTTTCAG
chr2	128047088	128047127	ERCC3_6485	+	GTGACCTATGCACCAGACGTGGTAGGTGCTGAACGTGCACACAACATTTAATCTGCTGTAGATCGGAAGAGCGGTTTCAG
chr2	128047411	128047450	ERCC3_6486	+	GTGACCTATGCACCAGACGTGGGAGGAAGAAGGGGCTACTGACCAGCAGGTACCTCTGAGATCGGAAGAGCGGTTTCAG
chr2	128047860	128047899	ERCC3_6487	+	GTGACCTATGCACCAGACGTAGATAACATCCAACAGGTAAATGTGCAGCTAACTCAGAACAGATCGGAAGAGCGGTTTCAG
chr2	128050433	128050472	ERCC3_6488	+	GTGACCTATGCACCAGACGTCCAATGGACAAAACAGACAAGGAAACATGAGTTGCAGAGAGATCGGAAGAGCGGTTTCAG
chr2	128051305	128051344	ERCC3_6489	+	GTGACCTATGCACCAGACGTCACAACAGAAGTAAGCCAGCAGGACCTTCAGGGTTCCAGATCGGAAGAGCGGTTTCAG
chr2	128051668	128051707	ERCC3_6490	+	GTGACCTATGCACCAGACGTGCAGACAGAAGATGACCCCGCTCCACAGCCCGCCAGATCGGAAGAGCGGTTTCAG
chr9	5022224	5022263	JAK2_6491	+	GTGACCTATGCACCAGACGTAAAAACAGCATTTTCTTTTTATGCATGGATTGTTTTAATAGATCGGAAGAGCGGTTTCAG
chr9	5029917	5029956	JAK2_6492	+	GTGACCTATGCACCAGACGTCAGTAAAGTAACTCACTTAATGCTAAAAGGCAAAATGGGAAGATCGGAAGAGCGGTTTCAG
chr9	5044531	5044570	JAK2_6493	+	GTGACCTATGCACCAGACGTATTATCTTACTTGATCATGATTAATGATAAATATCTTGAGATCGGAAGAGCGGTTTCAG
chr9	5050842	5050881	JAK2_6494	+	GTGACCTATGCACCAGACGTTTTGCAATCCTTACACATAAGTGTGAGTAGAGATTTATAGATCGGAAGAGCGGTTTCAG
chr9	5054895	5054934	JAK2_6495	+	GTGACCTATGCACCAGACGTATGATGTTCTGTTCTTTGTTATTTAAGTACAATGGAAGATCGGAAGAGCGGTTTCAG
chr9	5055799	5055838	JAK2_6496	+	GTGACCTATGCACCAGACGTTTTATGATTGAATAAGTTCATTTTATAGTCTCAGAAAAGATCGGAAGAGCGGTTTCAG



chr9	5065051	5065090	JAK2_6497	+	GTGACCTATGCACCAGACGTCAGACTTAAAAGTAAATTTTTAGAAAAGTAAATGCTGTATAGATCGGAAGAGCGGTTTCAG
chr9	5066800	5066839	JAK2_6498	+	GTGACCTATGCACCAGACGTCACACTTATTAGTGGTAACACTTTTATTAGTTTCATTTAATAGATCGGAAGAGCGGTTTCAG
chr9	5069219	5069258	JAK2_6499	+	GTGACCTATGCACCAGACGTTTTCTAGTTATTTTTAAATTACTGGTCATGGATTGTTTTATAGATCGGAAGAGCGGTTTCAG
chr9	5070063	5070102	JAK2_6500	+	GTGACCTATGCACCAGACGTAGATACTCATTACTGTCTTTTTGTCCTTTTAAAACAACAAGATCGGAAGAGCGGTTTCAG
chr9	5072637	5072676	JAK2_6501	+	GTGACCTATGCACCAGACGTTCTTTATATTGTTTCATGTAGTTTATGCTGTTTAAAGATGTAGATCGGAAGAGCGGTTTCAG
chr9	5073796	5073835	JAK2_6502	+	GTGACCTATGCACCAGACGTCACAGGCTTTCTAATGCCTTTCTCAGAGCATCTGTTTTTAGATCGGAAGAGCGGTTTCAG
chr9	5077630	5077591	JAK2_6503	+	GTGACCTATGCACCAGACGTCACACTTTTTATCAAAGTACTATTTTTATTTTTATAAAAACAGATCGGAAGAGCGGTTTCAG
chr9	5078455	5078494	JAK2_6504	+	GTGACCTATGCACCAGACGTGAAGGATTATATAATGTTACTAAGCTTTACTTGGGCAGAGATCGGAAGAGCGGTTTCAG
chr9	5080391	5080430	JAK2_6505	+	GTGACCTATGCACCAGACGTATAGACTAAGTTAGAATTACTCTATCTCGAACTTTTCATAAGATCGGAAGAGCGGTTTCAG
chr9	5080694	5080733	JAK2_6506	+	GTGACCTATGCACCAGACGTGAATGATCTTATTGATTTTTCCAGCTTTCTATCTTTATTGTAGATCGGAAGAGCGGTTTCAG
chr9	5081872	5081911	JAK2_6507	+	GTGACCTATGCACCAGACGTAGAAATTTTTCAAATAGAGTATAATCATTTCATTTAGGAAAGATCGGAAGAGCGGTTTCAG
chr9	5089874	5089913	JAK2_6508	+	GTGACCTATGCACCAGACGTCATTGAAACCTATTTAAATTCAGGTAATGTGTTTGGCATAAGATCGGAAGAGCGGTTTCAG
chr9	5090581	5090620	JAK2_6509	+	GTGACCTATGCACCAGACGTTCCGTGATTATTTGCTGTAGATGAAGCAACCGTGTTGAAGTAGATCGGAAGAGCGGTTTCAG
chr9	5090922	5090961	JAK2_6510	+	GTGACCTATGCACCAGACGTTTTCCAGTATGATAAATGAAATTTTAGAGCACAGACTTCAAAGATCGGAAGAGCGGTTTCAG
chr9	5126457	5126496	JAK2_6511	+	GTGACCTATGCACCAGACGTTTTTTTTAATCCAGGGTAGTCATGCATTTCTTTTACTTTTAGATCGGAAGAGCGGTTTCAG
chr9	5126802	5126841	JAK2_6512	+	GTGACCTATGCACCAGACGTTCTTCACTCTGAGACCAAGTAGATTTACAGAAACAAAGTTTAGATCGGAAGAGCGGTTTCAG
chr4	55524259	55524298	KIT_6513	+	GTGACCTATGCACCAGACGTGGCGCTGGCACCCCGCCGCTGCCACTACTCGGCGAAGCTAGATCGGAAGAGCGGTTTCAG
chr4	55561958	55561997	KIT_6514	+	GTGACCTATGCACCAGACGTTCCGTCTTCTGCAGTGTGTGTTTTCAAGAATTTAATATCTAGATCGGAAGAGCGGTTTCAG
chr4	55564742	55564781	KIT_6515	+	GTGACCTATGCACCAGACGTTTTCTTACTGCTCTGGGAGTTGAGAACTCACTTATCTAAGATCGGAAGAGCGGTTTCAG
chr4	55565943	55565982	KIT_6516	+	GTGACCTATGCACCAGACGTGCGTTCATTCTTCTCATGTTCTGTCTGTGGGAGATGATAGATCGGAAGAGCGGTTTCAG
chr4	55570069	55570108	KIT_6517	+	GTGACCTATGCACCAGACGTCATGGGAATGTTAAATTACTGGCAGTAGTGAAGAAGAAGATCGGAAGAGCGGTTTCAG
chr4	55573464	55573503	KIT_6518	+	GTGACCTATGCACCAGACGTGACCTTGCCCTGGGGGATTACACATTACCCCTTTTCCAGAGATCGGAAGAGCGGTTTCAG
chr4	55575716	55575755	KIT_6519	+	GTGACCTATGCACCAGACGTTGAAGGGCTCTTTAATTTTTATTCTTTTAAAGTTGTAGATCGGAAGAGCGGTTTCAG
chr4	55589875	55589914	KIT_6520	+	GTGACCTATGCACCAGACGTTATTTTTGGCAGCTGTTAATATGCAGAGGGGAAGGACTGCAGATCGGAAGAGCGGTTTCAG
chr4	55592215	55592254	KIT_6521	+	GTGACCTATGCACCAGACGTAGGTATATTTCTTTTTAATCCAATTAAGGGGATGTTTAGAGATCGGAAGAGCGGTTTCAG
chr4	55592227	55592266	KIT_6522	+	GTGACCTATGCACCAGACGTTTTTAATCCAATTAAGGGGATGTTTAGGCTGTCTACCAGATCGGAAGAGCGGTTTCAG
chr4	55593501	55593540	KIT_6523	+	GTGACCTATGCACCAGACGTTTTTGTCTCTCCAGAGTCTCTAATGACTGAGACAATAGATCGGAAGAGCGGTTTCAG
chr4	55593719	55593758	KIT_6524	+	GTGACCTATGCACCAGACGTAACAGGGGCTTCCATGTCACCTTTTTGGGTACACATAACAGATCGGAAGAGCGGTTTCAG
chr4	55594104	55594143	KIT_6525	+	GTGACCTATGCACCAGACGTGTATGGTACTGCTCATCGCTTGACATAGTTTGGCAGTTGCGAGTTGATCGGAAGAGCGGTTTCAG
chr4	55594298	55594337	KIT_6526	+	GTGACCTATGCACCAGACGTGTCCAAGCTGCCTTTTTATTGTCTGTACAGTTATCAAACAAGATCGGAAGAGCGGTTTCAG
chr4	55595662	55595701	KIT_6527	+	GTGACCTATGCACCAGACGTTTTACATAAATAGTTAGCTGTTGACAGGCAGTTTCATGGGGAGATCGGAAGAGCGGTTTCAG
chr4	55597596	55597635	KIT_6528	+	GTGACCTATGCACCAGACGTACCTATCAAGCAACCAAGAGTAACTTTACAGAGAGATGTAGATCGGAAGAGCGGTTTCAG
chr4	55599369	55599408	KIT_6529	+	GTGACCTATGCACCAGACGTATTCTCTGCTTGACAGCTCTGCAAAGGATTTTTAGTTTTCAAGATCGGAAGAGCGGTTTCAG
chr4	55602786	55602825	KIT_6530	+	GTGACCTATGCACCAGACGTTAACTGCCCAGCAACTTCATTAGCTCAGAGCATCTTCTAGATCGGAAGAGCGGTTTCAG
chr4	55602997	55603036	KIT_6531	+	GTGACCTATGCACCAGACGTAAAATTTTTCTTTAGTGTCCAGCTTTTTCCCTTTTTATTTTTAGATCGGAAGAGCGGTTTCAG
chr4	55603457	55603496	KIT_6532	+	GTGACCTATGCACCAGACGTCTGGCCAGGCATAGAATCCCCCTTCTCCAGTTCAGGTAGATCGGAAGAGCGGTTTCAG
chr4	55604734	55604773	KIT_6533	+	GTGACCTATGCACCAGACGTTGTTGGTCCACCCTCCAGGAATGATCTTCTTTTGGCAGATCGGAAGAGCGGTTTCAG
chr10	43572790	43572829	RET_6534	+	GTGACCTATGCACCAGACGTCCGGCCGCGCGGCTCCCGCAGGGGCCAGGGCGAAGTTGGCGAGATCGGAAGAGCGGTTTCAG
chr10	43596181	43596220	RET_6535	+	GTGACCTATGCACCAGACGTGCCCCAACACCCACCCCGTGGCCCCACCCACCCCTTCTAGATCGGAAGAGCGGTTTCAG
chr10	43598088	43598127	RET_6536	+	GTGACCTATGCACCAGACGTACCTGTGGGGCCGCCACAGTGCCTGCTACTGCTGTGCAGATCGGAAGAGCGGTTTCAG
chr10	43600652	43600691	RET_6537	+	GTGACCTATGCACCAGACGTGCGCGTGTGGTGGCTACCCAGTGTCTGTCTCCGGCCACAAGATCGGAAGAGCGGTTTCAG
chr10	43602030	43602069	RET_6538	+	GTGACCTATGCACCAGACGTCTGGTGGCACGGCCTGGCTAGGCCCCAGGAAATGAGGTGAGATCGGAAGAGCGGTTTCAG
chr10	43604689	43604728	RET_6539	+	GTGACCTATGCACCAGACGTACCTATTGCCTGTCTGGGGAAGATTGAAGGGCAAGGGACAGATCGGAAGAGCGGTTTCAG
chr10	43606924	43606963	RET_6540	+	GTGACCTATGCACCAGACGTGCTCCAGGGAGGGAGGGTTCGGGGCTTCTGGGGGCTTCTGGAAGATCGGAAGAGCGGTTTCAG
chr10	43607683	43607722	RET_6541	+	GTGACCTATGCACCAGACGTGAAACGCCAAAGGGAGGCCTCAGGGGCGATGGCACCGGTAGATCGGAAGAGCGGTTTCAG
chr10	43608422	43608461	RET_6542	+	GTGACCTATGCACCAGACGTTTTAATCAGGGCATGGGAACAGGTAGGAGATAGTAGGGGAAGATCGGAAGAGCGGTTTCAG
chr10	43609134	43609173	RET_6543	+	GTGACCTATGCACCAGACGTGGCGGGCCGGGACCACCACCTCCCAGCCCCACAGAGGTAGATCGGAAGAGCGGTTTCAG
chr10	43610195	43610234	RET_6544	+	GTGACCTATGCACCAGACGTCTGCGGGGCAGGGAAGATCCCCTGCCCTCCCAGCTGCCATAGATCGGAAGAGCGGTTTCAG
chr10	43612190	43612229	RET_6545	+	GTGACCTATGCACCAGACGTGGCACAGGCACAGTGCCTCCGTTGGGGAGTCTCCGGGGCGGGAGATCGGAAGAGCGGTTTCAG
chr10	43613939	43613978	RET_6546	+	GTGACCTATGCACCAGACGTCTGCAGGGTAGGTTGGGCAGCCACTGCACCCAGGCTGGGGAGATCGGAAGAGCGGTTTCAG
chr10	43615662	43615701	RET_6547	+	GTGACCTATGCACCAGACGTCCGGGGATGAGCGGGGCTCCAGGATCCCAGGTGCACCCAGATCGGAAGAGCGGTTTCAG
chr10	43617475	43617514	RET_6548	+	GTGACCTATGCACCAGACGTGTGTTGCTCTTTGGGGTGAGGTTACAGAACAACCCCTTAAGATCGGAAGAGCGGTTTCAG
chr10	43619267	43619306	RET_6549	+	GTGACCTATGCACCAGACGTACTGGCTTTGGCCAGCCTCACTTGGGAAGGGAGGGGACAAGATCGGAAGAGCGGTTTCAG
chr10	43620441	43620480	RET_6550	+	GTGACCTATGCACCAGACGTGGGTCCAATCCCACAAGCTGAAAGTGGCTTGGGGAGACTAGATCGGAAGAGCGGTTTCAG
chr10	43622181	43622220	RET_6551	+	GTGACCTATGCACCAGACGTCCATGCATTTACTAGATTCTAGCACCGCTGTCCCTTTGCAGATCGGAAGAGCGGTTTCAG
chr10	43623728	43623767	RET_6552	+	GTGACCTATGCACCAGACGTTGAAAGGTAATGGACTCACAAGGGGAAGAAACATGCTGAGAGATCGGAAGAGCGGTTTCAG
chr14	105236768	105236807	AKT1_6553	+	GTGACCTATGCACCAGACGTAGACAGCTCAGACCCGCTGCCCTCCCTCCCTCAGATCGGAAGAGCGGTTTCAG
chr14	105237195	105237234	AKT1_6554	+	GTGACCTATGCACCAGACGTGGGCAGCGGACGATGATGCTTCCCTCCCTCCCAAGATCGGAAGAGCGGTTTCAG

chr14	105238800	105238839	AKT1_6555	+	GTGACCTATGCACCAGACGTGAAACAAGGCCACAGTGTCCGGTACC GCCACCTGCCAGGCAGATCGGAAGAGCGGTTTCAG
chr14	105239440	105239479	AKT1_6556	+	GTGACCTATGCACCAGACGTGGCAGATGGGCAGGACTCGGCATCAAGGGGTGTCCGGGACAGATCGGAAGAGCGGTTTCAG
chr14	105239727	105239766	AKT1_6557	+	GTGACCTATGCACCAGACGTGGTGGCCTCAGGTGAGTGCAGGCGCCAGGCCCCAGGGCCCTGAGATCGGAAGAGCGGTTTCAG
chr14	105239928	105239967	AKT1_6558	+	GTGACCTATGCACCAGACGTGCGAACCTGAGGCACAGCCGTGGCTCGGGCCTCTGCCCCAGATCGGAAGAGCGGTTTCAG
chr14	105240328	105240367	AKT1_6559	+	GTGACCTATGCACCAGACGTGGGGAGCTGGAAGTGCAGCCACAGGCAGGACGGCAGCCAGATCGGAAGAGCGGTTTCAG
chr14	105241351	105241390	AKT1_6560	+	GTGACCTATGCACCAGACGTGGGCTGGTGGAGTGCACCCGCCACCTCATCTCCACCCAGATCGGAAGAGCGGTTTCAG
chr14	105241555	105241594	AKT1_6561	+	GTGACCTATGCACCAGACGTGACCAGGGTCAGCAAGCGGCGCTGCCAACAGTGCACAGATCGGAAGAGCGGTTTCAG
chr14	105242147	105242186	AKT1_6562	+	GTGACCTATGCACCAGACGTTCAGGTGAGGCTGCAGGCCTGTACCAGATCAGGAGCTCCAAGATCGGAAGAGCGGTTTCAG
chr14	105243118	105243157	AKT1_6563	+	GTGACCTATGCACCAGACGTGCAGAGCCTCTGTCTGCGTGCATCCCCCTGCCCTCCAGAGATCGGAAGAGCGGTTTCAG
chr14	105246564	105246603	AKT1_6564	+	GTGACCTATGCACCAGACGTGCGGGTGGTGAGAGCCACGCACACTCTACCCGTGAGACCCAGATCGGAAGAGCGGTTTCAG
chr14	105258991	105259030	AKT1_6565	+	GTGACCTATGCACCAGACGTGCTCCCGCAGCGCTCACGCGCTCCTCTCAGGCTGGCGCTCAGATCGGAAGAGCGGTTTCAG
chr20	39766509	39766548	PLCG1_6566	+	GTGACCTATGCACCAGACGTCCACTTCTGCCTGGGCCCGCCCGGGGCTCGTGGGAGATCGGAAGAGCGGTTTCAG
chr20	39788409	39788448	PLCG1_6567	+	GTGACCTATGCACCAGACGTAGGGGTAGAGGAGTAGAGGATAGTTAGGGGAATGCCTGAGATCGGAAGAGCGGTTTCAG
chr20	39788614	39788653	PLCG1_6568	+	GTGACCTATGCACCAGACGTCTCCTGAAGGGGTTAGGGCTGGGAGCATTAGGGACCAGGGAGATCGGAAGAGCGGTTTCAG
chr20	39788804	39788843	PLCG1_6569	+	GTGACCTATGCACCAGACGTAGCTGTGGCTGTAGCCAGCAGGGTGGGGATGGGCATCCAAGATCGGAAGAGCGGTTTCAG
chr20	39791187	39791226	PLCG1_6570	+	GTGACCTATGCACCAGACGTCCCAGGGCTGTCTGTAGATGGGGGCAGGGGAAGCCAAGAGAGATCGGAAGAGCGGTTTCAG
chr20	39791376	39791415	PLCG1_6571	+	GTGACCTATGCACCAGACGTACCTGCCCTCCCTCAACCCCTGCCCTGCTCTTCCACCCAGATCGGAAGAGCGGTTTCAG
chr20	39791643	39791682	PLCG1_6572	+	GTGACCTATGCACCAGACGTGAGTGGGGAGGTGGGGTTTCCCTGGGCCCCCTTCATCTCAGATCGGAAGAGCGGTTTCAG
chr20	39791926	39791965	PLCG1_6573	+	GTGACCTATGCACCAGACGTGCTGACATTGGCCAGGCTGGTAGGTTGTGGGGGGCTGGGAGATCGGAAGAGCGGTTTCAG
chr20	39792130	39792169	PLCG1_6574	+	GTGACCTATGCACCAGACGTGTTTACCATTTTTTGTCAAGAGAATGAGTAGGGGTGAAGATCGGAAGAGCGGTTTCAG
chr20	39792484	39792523	PLCG1_6575	+	GTGACCTATGCACCAGACGTCTCCTTACAGGCCACCCAGCTTCTCCCCAGGAGGGCCCAAGATCGGAAGAGCGGTTTCAG
chr20	39792657	39792696	PLCG1_6576	+	GTGACCTATGCACCAGACGTTCAGGGCTGGGGGAGGGGAAGTGGGAGGCCCTGCCCGCTTAGATCGGAAGAGCGGTTTCAG
chr20	39792852	39792891	PLCG1_6577	+	GTGACCTATGCACCAGACGTGGCTGAGTACCAGGGGTTAACTTGGCTCCAGTCTCAGATCGGAAGAGCGGTTTCAG
chr20	39793752	39793791	PLCG1_6578	+	GTGACCTATGCACCAGACGTGGGCTATTGCGGAAGGCCACACTTCTCAGTGCCTGCCAGATCGGAAGAGCGGTTTCAG
chr20	39794018	39794057	PLCG1_6579	+	GTGACCTATGCACCAGACGTGGCCAGGCTGGGGGTGGTAGGCCAGTGGGTGTGAGGACCAGATCGGAAGAGCGGTTTCAG
chr20	39794202	39794241	PLCG1_6580	+	GTGACCTATGCACCAGACGTAGCTCAGGTCTGGGGGCTGGGCCAGTCCAGGCCTGGGCCAAGATCGGAAGAGCGGTTTCAG
chr20	39794477	39794516	PLCG1_6581	+	GTGACCTATGCACCAGACGTCCATGCAGATGCGTATGTTCACTCAGCGTGTGTACACAGAAGATCGGAAGAGCGGTTTCAG
chr20	39795045	39795084	PLCG1_6582	+	GTGACCTATGCACCAGACGTGGCGGCGGCAAGGCAGGGCCAGGGCCATGGTGGTAGATCGGAAGAGCGGTTTCAG
chr20	39795246	39795285	PLCG1_6583	+	GTGACCTATGCACCAGACGTGGCTGGGCTGGGCTGGGGCTGGGCTGGGCTGAGCTGCCAGATCGGAAGAGCGGTTTCAG
chr20	39795510	39795549	PLCG1_6584	+	GTGACCTATGCACCAGACGTGGTGTAGAGCGGGCTAGGCAGGGGAGGAGAGAGACCCAGATCGGAAGAGCGGTTTCAG
chr20	39796580	39796619	PLCG1_6585	+	GTGACCTATGCACCAGACGTGGCCTCTGGGCATAGGAAGCTGGGGAGGGTCCCAGCTGCAGATCGGAAGAGCGGTTTCAG
chr20	39797521	39797560	PLCG1_6586	+	GTGACCTATGCACCAGACGTGGTGTGGTAGGCCAGAGTCCAAGGGCCCAAGTGGAGCTGAGATCGGAAGAGCGGTTTCAG
chr20	39797826	39797865	PLCG1_6587	+	GTGACCTATGCACCAGACGTAACCACCTGAGTAACAGCATTCCCTATCCAGATTCTCCAGATCGGAAGAGCGGTTTCAG
chr20	39798177	39798216	PLCG1_6588	+	GTGACCTATGCACCAGACGTATCTGTTTCTTCCCACTGTTCCCTAGGGTGAAGTCTAGATCGGAAGAGCGGTTTCAG
chr20	39798920	39798959	PLCG1_6589	+	GTGACCTATGCACCAGACGTGCTGGCAACCTCTGGGGGAGGCTGTGTGGGCCAGATCGGAAGAGCGGTTTCAG
chr20	39800940	39800979	PLCG1_6590	+	GTGACCTATGCACCAGACGTGGGCCAGGCGGGGTGTGCATGTGCCTGGAGGGCCTGGTGGATCGGAAGAGCGGTTTCAG
chr20	39801296	39801335	PLCG1_6591	+	GTGACCTATGCACCAGACGTCCCCTGTGAGGAGGGTGGAGGGGGCACTGTGGGCAGCTAGATCGGAAGAGCGGTTTCAG
chr20	39801528	39801567	PLCG1_6592	+	GTGACCTATGCACCAGACGTCTCATCTGGGCTTCAAGGTAGGAAAGGGGCTGCTTGCCGTAGATCGGAAGAGCGGTTTCAG
chr20	39802185	39802224	PLCG1_6593	+	GTGACCTATGCACCAGACGTCTCCAGTTCATCTCCTCATCTGCTGGGGCACTGCAAGAGATCGGAAGAGCGGTTTCAG
chr20	39802464	39802503	PLCG1_6594	+	GTGACCTATGCACCAGACGTTCCTGGAGGCAGTCCCTGCAATCTTGGCTGGCAGGGTGGATCGGAAGAGCGGTTTCAG
chr20	39802662	39802701	PLCG1_6595	+	GTGACCTATGCACCAGACGTCCAGGTGGGCTGGCCTGGGCTAGGTGGGAGGAGGCCAGATCGGAAGAGCGGTTTCAG
chr20	39802962	39803001	PLCG1_6596	+	GTGACCTATGCACCAGACGTTGGAGGGGTGTAGAGCCAGGAAGGCAGTGGCTAGGTCTAGATCGGAAGAGCGGTTTCAG
chr20	39803160	39803199	PLCG1_6597	+	GTGACCTATGCACCAGACGTGCCTCGTTGGAGAGCAGCAGGTGCTGTGCGCCTTGTAGAAAGATCGGAAGAGCGGTTTCAG
chr19	11095060	11095099	SMARCA4_6598	+	GTGACCTATGCACCAGACGTCTGTGCCCGCCTCGCACCTCGCGGCTCTGCCCACTAGGGCAGATCGGAAGAGCGGTTTCAG
chr19	11096092	11096131	SMARCA4_6599	+	GTGACCTATGCACCAGACGTGCTTCTCTCTGCTTGTGTTTGTCTACTACAGTCCAGATCCAGATCGGAAGAGCGGTTTCAG
chr19	11097280	11097319	SMARCA4_6600	+	GTGACCTATGCACCAGACGTCTGCCCTGCGCCCTCAGGTGTCTCAGAGCGAATGGCTGGGAGATCGGAAGAGCGGTTTCAG
chr19	11097690	11097729	SMARCA4_6601	+	GTGACCTATGCACCAGACGTTCTTCTATGGTGGTGCACCCGTGCCCTTACTCCCCATCTCAGATCGGAAGAGCGGTTTCAG
chr19	11098611	11098650	SMARCA4_6602	+	GTGACCTATGCACCAGACGTGGCCAGTTGCCAAGGTCACTGCCCTGTGTCCCCATGTAGATCGGAAGAGCGGTTTCAG
chr19	11100130	11100169	SMARCA4_6603	+	GTGACCTATGCACCAGACGTGCATGGCCGACGCTTCCGAAAAGGGGCTTTGTACCAACAGATCGGAAGAGCGGTTTCAG
chr19	11102010	11102049	SMARCA4_6604	+	GTGACCTATGCACCAGACGTGTGGCCCAAGGCCCTGCAGCCCCCACTGGCTGCCTGAGATCGGAAGAGCGGTTTCAG
chr19	11105688	11105727	SMARCA4_6605	+	GTGACCTATGCACCAGACGTGCCTTTGACGTGCGCTCTTACATGTGATGCTGTACAGATCGGAAGAGCGGTTTCAG
chr19	11107067	11107106	SMARCA4_6606	+	GTGACCTATGCACCAGACGCTCTGGCATGTGCCCGCCGCGGGTGGATGGGAGCAGCCAGATCGGAAGAGCGGTTTCAG
chr19	11107231	11107270	SMARCA4_6607	+	GTGACCTATGCACCAGACGTAGGGTTTCTTGTGGAAGTCAAGCTAGCCCTAAGGCGTTAGATCGGAAGAGCGGTTTCAG
chr19	11113846	11113885	SMARCA4_6608	+	GTGACCTATGCACCAGACGTCTTGCATTCCAGATGCAGTGGGGATCCAAGTCTCGGTGAGATCGGAAGAGCGGTTTCAG
chr19	11114084	11114123	SMARCA4_6609	+	GTGACCTATGCACCAGACGTATTTCCCTGGCTTCAAGGCTCTCAGTGCCTAGTGGCAGTGGATCGGAAGAGCGGTTTCAG
chr19	11118710	11118749	SMARCA4_6610	+	GTGACCTATGCACCAGACGTCCGACACAGGTTGTCTGTGCCAGTCTCCTGTGAGGTGGCAGATCGGAAGAGCGGTTTCAG
chr19	11121218	11121257	SMARCA4_6611	+	GTGACCTATGCACCAGACGTGGGTGGGAGGTCACCGCCACTAGCTGCCTCGGTGGCAGATCGGAAGAGCGGTTTCAG
chr19	11129710	11129749	SMARCA4_6612	+	GTGACCTATGCACCAGACGTGCCACTGAGGTTCTCTCTTGTCTACGGAGTGCAGGCGGAGATCGGAAGAGCGGTTTCAG

chr19	11130388	11130427	SMARCA4_6613	+	GTGACCTATGCACCAGACGTCTGTGGGAAATGCCAGGCCATGGGCCGAGTGCTCACACGAGATCGGAAGAGCGGTTTCAG
chr19	11132654	11132693	SMARCA4_6614	+	GTGACCTATGCACCAGACGTCCAGCTGTGCCATGCTGACGGTTCAGGTGCGGCTGGCTAGATCGGAAGAGCGGTTTCAG
chr19	11134318	11134357	SMARCA4_6615	+	GTGACCTATGCACCAGACGTTTTGAGGGGAGCCACCAGTGAAGCAGCCTCACGTGGGGCAGATCGGAAGAGCGGTTTCAG
chr19	11135125	11135164	SMARCA4_6616	+	GTGACCTATGCACCAGACGTGAGTCCCCAACTGCATCCCCACTGGGTGTCCAAGGCCGAGATCGGAAGAGCGGTTTCAG
chr19	11136195	11136234	SMARCA4_6617	+	GTGACCTATGCACCAGACGTGCGGGCTGGGACGGCTCAGGCCCTGCTGTCTGCTGAGCTCAGATCGGAAGAGCGGTTTCAG
chr19	11137033	11137072	SMARCA4_6618	+	GTGACCTATGCACCAGACGTTCCCACTGGATGGGGTGGCCAGGTGCTCCACCCAGGATAGATCGGAAGAGCGGTTTCAG
chr19	11138637	11138676	SMARCA4_6619	+	GTGACCTATGCACCAGACGTGCCAGTGGAGGTTTCTTACAGGGTTTTGTGTTGTGGCTAGATCGGAAGAGCGGTTTCAG
chr19	11141580	11141619	SMARCA4_6620	+	GTGACCTATGCACCAGACGTGCCGGGCCAGGTGCGAGGAGAAGGAGGGGTGCTGCAAGATCGGAAGAGCGGTTTCAG
chr19	11144204	11144243	SMARCA4_6621	+	GTGACCTATGCACCAGACGTACCAGGCCGACCCCTCCACAGCTGAATGGTGGACGCGAGATCGGAAGAGCGGTTTCAG
chr19	11144887	11144926	SMARCA4_6622	+	GTGACCTATGCACCAGACGTGAGGCTGGATGGGGCAGTTACAGGCATCCCACTCTGCTGCCAGATCGGAAGAGCGGTTTCAG
chr19	11145819	11145858	SMARCA4_6623	+	GTGACCTATGCACCAGACGTGAGAGGCCACAGCTGCCCGAGGCCAGCCAGGCAGGGAGATCGGAAGAGCGGTTTCAG
chr19	11152247	11152286	SMARCA4_6624	+	GTGACCTATGCACCAGACGTAGCGGGGAGGGCGGGGGCTGTAGGGTCCCCGTGGGACAGATCGGAAGAGCGGTTTCAG
chr19	11169050	11169089	SMARCA4_6625	+	GTGACCTATGCACCAGACGTGTTGTACTGCGCCCGCATGTGCCCGGAGGGAGTCTGAGATCGGAAGAGCGGTTTCAG
chr19	11169576	11169615	SMARCA4_6626	+	GTGACCTATGCACCAGACGTGCTGGGGTGGGGATGGGCCACTCCACAGCTGGGCTTAGATCGGAAGAGCGGTTTCAG
chr19	11170572	11170611	SMARCA4_6627	+	GTGACCTATGCACCAGACGTGGGGGTTTCCAGACGCCGGGTTACGCTGGCCCGAGAGCAGATCGGAAGAGCGGTTTCAG
chr19	11170874	11170913	SMARCA4_6628	+	GTGACCTATGCACCAGACGTGCCCGGAGCAGCCAGAGCTGGCATGTGCCAGGAGGCATCAGATCGGAAGAGCGGTTTCAG
chr19	11172503	11172542	SMARCA4_6629	+	GTGACCTATGCACCAGACGTTCCAGCTCTCGACCCGAGCCCTCGTTCAGAGCTGAGATCGGAAGAGCGGTTTCAG
chr16	68771377	68771416	CDH1_6630	+	GTGACCTATGCACCAGACGTCCCTACTTCCGAGGGCATTCCGGCCGCAAGCTCCAGATCGGAAGAGCGGTTTCAG
chr16	68772325	68772364	CDH1_6631	+	GTGACCTATGCACCAGACGTGCTGCCGTTGCCCTGGGCGGAGTAGGGAGGGGTTGAAAAGATCGGAAGAGCGGTTTCAG
chr16	68835807	68835846	CDH1_6632	+	GTGACCTATGCACCAGACGTATTTTTCTGAGAAGTTCGCTGTTGTTTTAGTGCCTGCTAGATCGGAAGAGCGGTTTCAG
chr16	68842481	68842520	CDH1_6633	+	GTGACCTATGCACCAGACGTAAAGTCTCTGTTTTCTCTGGGAGGATTTGGCAGAGAAGTAAGATCGGAAGAGCGGTTTCAG
chr16	68842762	68842801	CDH1_6634	+	GTGACCTATGCACCAGACGTCTTAGAAGCTTGTGGACACCGGGTAACATCCACCCAGGAAGATCGGAAGAGCGGTTTCAG
chr16	68844255	68844294	CDH1_6635	+	GTGACCTATGCACCAGACGTAAATGAGAATCTGAATACTCAGAAGACTCTTAGTCTTAGATCGGAAGAGCGGTTTCAG
chr16	68845773	68845812	CDH1_6636	+	GTGACCTATGCACCAGACGTGAGGAGTCCAGAGGGTGTGGAGGACAATGTGATTAGCAGATCGGAAGAGCGGTTTCAG
chr16	68846177	68846216	CDH1_6637	+	GTGACCTATGCACCAGACGTAACTCCTTAGAGGGTTTCCAAAGAAAGTCTTTTGTGTTAGATCGGAAGAGCGGTTTCAG
chr16	68847409	68847448	CDH1_6638	+	GTGACCTATGCACCAGACGTTACCTGGCAAGATGCAGAACTGGCATCCTCACAGCTGTTAGATCGGAAGAGCGGTTTCAG
chr16	68849673	68849712	CDH1_6639	+	GTGACCTATGCACCAGACGTGGATTTTTCAACTGACTTGCAGCAACTGGTATTTTATATAGATCGGAAGAGCGGTTTCAG
chr16	68853339	68853378	CDH1_6640	+	GTGACCTATGCACCAGACGTCTCATCTGAGCCTTTGCTGCTGACCTCCTAGCTAGTTCAGATCGGAAGAGCGGTTTCAG
chr16	68856139	68856178	CDH1_6641	+	GTGACCTATGCACCAGACGTGAGTTTTATTTTGGCAACTTTGCTCCAATGCCATGCTTACAGATCGGAAGAGCGGTTTCAG
chr16	68857540	68857579	CDH1_6642	+	GTGACCTATGCACCAGACGTGCGCAAGTGACTACGCTTTGACTTAAAAAAATGGCAGGAAGATCGGAAGAGCGGTTTCAG
chr16	68862218	68862257	CDH1_6643	+	GTGACCTATGCACCAGACGTAAAACCTTGGTAGCTCAGTGGTGATCTCTTTATTTCGAAGAGATCGGAAGAGCGGTTTCAG
chr16	68863711	68863750	CDH1_6644	+	GTGACCTATGCACCAGACGTACGTGGAAAGCCAAAGCATGGCTCATCTCTAAGCTCAGGAGATCGGAAGAGCGGTTTCAG
chr16	68867413	68867452	CDH1_6645	+	GTGACCTATGCACCAGACGTAGAGGCGGGGCCACAGCCATGTGCTGGGAAATGCAGAAAAGATCGGAAGAGCGGTTTCAG
chr6	36652334	36652373	CDKN1A_6646	+	GTGACCTATGCACCAGACGTGTGCACGGAAAGACTTTGTAAAGGACCAAGGATTCTCAGAAAAGATCGGAAGAGCGGTTTCAG
chr6	36653588	36653627	CDKN1A_6647	+	GTGACCTATGCACCAGACGTGGAAGGCTGACTCCTGGAAGGCGCAGGGCTCAAAGGCCAGATCGGAAGAGCGGTTTCAG
chr19	10244388	10244427	DNMT1_6648	+	GTGACCTATGCACCAGACGTATAAAAGGAAAAGTCACTCTGGGGAACACGCCCGGTGTCAAGATCGGAAGAGCGGTTTCAG
chr19	10244994	10245033	DNMT1_6649	+	GTGACCTATGCACCAGACGTGGAGAAGGGCAATGCCTGATGTGGACACCCAGGCCAAGGAGATCGGAAGAGCGGTTTCAG
chr19	10246539	10246578	DNMT1_6650	+	GTGACCTATGCACCAGACGTGAGGCGCGGTGGGCGAGGGCAGTAGCACCCAGGCCGGTTCAGATCGGAAGAGCGGTTTCAG
chr19	10246974	10247013	DNMT1_6651	+	GTGACCTATGCACCAGACGTGGACAGTGTGAGGCTGCAGTTGTGGGATGGGGTATAGGCAGATCGGAAGAGCGGTTTCAG
chr19	10247967	10248006	DNMT1_6652	+	GTGACCTATGCACCAGACGTGTGGGGGCCCCAGCTGCACCTCATGTGAGCAGCATCGGAAGATCGGAAGAGCGGTTTCAG
chr19	10248696	10248735	DNMT1_6653	+	GTGACCTATGCACCAGACGTGGAGGAGTCAACACCTCTGGAGATGCACGACGAGTGTAGATCGGAAGAGCGGTTTCAG
chr19	10249292	10249331	DNMT1_6654	+	GTGACCTATGCACCAGACGTGAAGGACGGACAACCCACCCTCAGTGGGACACTCCCAACAGATCGGAAGAGCGGTTTCAG
chr19	10250504	10250543	DNMT1_6655	+	GTGACCTATGCACCAGACGTGAGGAGACTGCAGGAGTCACTCCACAGACAGAGGGAAGATCGGAAGAGCGGTTTCAG
chr19	10251596	10251635	DNMT1_6656	+	GTGACCTATGCACCAGACGTGAGGGCAGAGGCTAAACCCGATCTCAGAGTCCAAGTCCAAGATCGGAAGAGCGGTTTCAG
chr19	10251876	10251915	DNMT1_6657	+	GTGACCTATGCACCAGACGTGAGAAGTCAATCGTGGGAGAGAAACGCAGTGTCCCCTAGATCGGAAGAGCGGTTTCAG
chr19	10252907	10252946	DNMT1_6658	+	GTGACCTATGCACCAGACGTGAGGAGCTCGTGGAGCCTCTGTTAGGACTCTCTTTGTGTTAGATCGGAAGAGCGGTTTCAG
chr19	10254674	10254713	DNMT1_6659	+	GTGACCTATGCACCAGACGTGCACCCACTTGACATCAATGAACCTTCCACCTTGCAGTGGAGATCGGAAGAGCGGTTTCAG
chr19	10257211	10257250	DNMT1_6660	+	GTGACCTATGCACCAGACGTCAAAGGGACAGAAACATAAGGCCCTGAGGTGGCCGGCAGTAGATCGGAAGAGCGGTTTCAG
chr19	10260344	10260383	DNMT1_6661	+	GTGACCTATGCACCAGACGTAAAGACGGGCATGGGGAGAAAGTTCTGACTTGCCAGCAGAAGATCGGAAGAGCGGTTTCAG
chr19	10260655	10260694	DNMT1_6662	+	GTGACCTATGCACCAGACGTGAGCATAAGTTCATGGAGGATCATTCTGAGGGTCTTTGCTAGATCGGAAGAGCGGTTTCAG
chr19	10262232	10262271	DNMT1_6663	+	GTGACCTATGCACCAGACGTACTGGTTTAACTAAGGCCCTTTTCTAAGTAAGACCAACAGATCGGAAGAGCGGTTTCAG
chr19	10265166	10265205	DNMT1_6664	+	GTGACCTATGCACCAGACGTGGTTCAGCATCTCAGAGGACTGGGACGAGGATGTGGGCAGATCGGAAGAGCGGTTTCAG
chr19	10265460	10265499	DNMT1_6665	+	GTGACCTATGCACCAGACGTAAACAGGTTTCTCTCATGCTTAAAGCCAAACTGGCTAAATCAGATCGGAAGAGCGGTTTCAG
chr19	10265743	10265782	DNMT1_6666	+	GTGACCTATGCACCAGACGTGAGGAGGTTGTGAAAAGGGGCTGGAATCTGATGGCCAGATCGGAAGAGCGGTTTCAG
chr19	10266632	10266671	DNMT1_6667	+	GTGACCTATGCACCAGACGTAAAGGAAATGACTAAAGGCTCTGACTCACATCCAAACAGATCGGAAGAGCGGTTTCAG
chr19	10267196	10267235	DNMT1_6668	+	GTGACCTATGCACCAGACGTAAACAAAGCACATGCTTACCAGTAAGCCGTGAAGGCGGGTAGATCGGAAGAGCGGTTTCAG
chr19	10270454	10270493	DNMT1_6669	+	GTGACCTATGCACCAGACGTGCGGGCTGGTGGAGCTGGGACGAGGATCGGACGAGGAGATCGGAAGAGCGGTTTCAG
chr19	10270609	10270648	DNMT1_6670	+	GTGACCTATGCACCAGACGTAGGAACACAGATGATGGCATCAGAGGACGACTCCACAGCCAGATCGGAAGAGCGGTTTCAG

chr19	10270750	10270789	DNMT1_6671	+	GTGACCTATGCACCAGACGTAATAAAGGGGAGGATTAAAGGCTAAGAGAGTGTTCACAGATCGGAAGAGCGGTTTCAG
chr19	10271105	10271144	DNMT1_6672	+	GTGACCTATGCACCAGACGTAACAGATACACAGCAAGTAGCAGCTTAGAAACACTAACCAAGATCGGAAGAGCGGTTTCAG
chr19	10273435	10273474	DNMT1_6673	+	GTGACCTATGCACCAGACGTAATAAAGGGGAGGTTAGAGAGATAAAGAAGGGAAAAAATTAAGATCGGAAGAGCGGTTTCAG
chr19	10274047	10274086	DNMT1_6674	+	GTGACCTATGCACCAGACGTTAGACAACACACACAGGCTGGTCAGCTCGGGGGGGCCAGATCGGAAGAGCGGTTTCAG
chr19	10277372	10277411	DNMT1_6675	+	GTGACCTATGCACCAGACGTTGGAAAAAACAAGTAAATTTTCCATTTGGTTTGGATAGATCGGAAGAGCGGTTTCAG
chr19	10279051	10279090	DNMT1_6676	+	GTGACCTATGCACCAGACGTTAAATAACACAGACCCCAAGTGTGAGTCCAGAGAGCTTCCAGATCGGAAGAGCGGTTTCAG
chr19	10283861	10283900	DNMT1_6677	+	GTGACCTATGCACCAGACGTTGAAAGGAAGAACAATAAAGATTAGAATACTGGTTTCAAGGAGATCGGAAGAGCGGTTTCAG
chr19	10284592	10284631	DNMT1_6678	+	GTGACCTATGCACCAGACGTCAGTGAGGCCAACCTTAGTGAACAAGACCCTAGGCCCTCAGATCGGAAGAGCGGTTTCAG
chr19	10286305	10286344	DNMT1_6679	+	GTGACCTATGCACCAGACGTTAAGAAAAAGCATTAAAAAGAAAAAAGCCACTATCAAGATCGGAAGAGCGGTTTCAG
chr19	10288054	10288093	DNMT1_6680	+	GTGACCTATGCACCAGACGTTAAAGGATAATTAAGTAGCAGTGAATGTAAACAAGTGTCAAGATCGGAAGAGCGGTTTCAG
chr19	10291256	10291295	DNMT1_6681	+	GTGACCTATGCACCAGACGTTAGATAGTTTAGCAGTACCCACATTTCCCAAGCTATTACAGATCGGAAGAGCGGTTTCAG
chr19	10291572	10291611	DNMT1_6682	+	GTGACCTATGCACCAGACGTTGAAATAGGGGAGAAAATACAAACACTTGTAAAGCACTTCAAGATCGGAAGAGCGGTTTCAG
chr19	10292764	10292803	DNMT1_6683	+	GTGACCTATGCACCAGACGTTCCAGCAGACGCGCGCGCGCAGCGCAGCGCCCGGCTTTAGATCGGAAGAGCGGTTTCAG
chr19	10305586	10305625	DNMT1_6684	+	GTGACCTATGCACCAGACGTTGAGAGCACCAGGCTCGGCACCTGGGAGCGGAAACCAGATCGGAAGAGCGGTTTCAG
chr12	56474177	56474216	ERBB3_6685	+	GTGACCTATGCACCAGACGTTCCACTCATAACGCTTTCCATATCCAGATCGGAAGAGCGGTTTCAG
chr12	56477697	56477736	ERBB3_6686	+	GTGACCTATGCACCAGACGTTCCCTCCTTCTCAACCTGCTCCTCTTTATCTCCCTAGATCGGAAGAGCGGTTTCAG
chr12	56478976	56479015	ERBB3_6687	+	GTGACCTATGCACCAGACGTTGATGGTTCTTCCCTTCCCTCAGCCCTCAGCCAGCCCAAGACAGATCGGAAGAGCGGTTTCAG
chr12	56479107	56479146	ERBB3_6688	+	GTGACCTATGCACCAGACGTTCCCTAAGCAATAGAGGGGAGCTAGGATCGGAAGAGCGGTTTCAG
chr12	56480451	56480490	ERBB3_6689	+	GTGACCTATGCACCAGACGTTGATCAAGATTGCTCCCAAGTCCCAACCAACAGATGAAGATCGGAAGAGCGGTTTCAG
chr12	56481437	56481476	ERBB3_6690	+	GTGACCTATGCACCAGACGTTCCCTCCTCAAACTTCACTCATAACGCTTTCCATATCCAGATCGGAAGAGCGGTTTCAG
chr12	56481708	56481747	ERBB3_6691	+	GTGACCTATGCACCAGACGTTTCCATTTGCCTGGGTTCTGAAATTGGGATGTGCCCTTTGAGATCGGAAGAGCGGTTTCAG
chr12	56481957	56481996	ERBB3_6692	+	GTGACCTATGCACCAGACGTTGAGGGGAAGAAACATGATCAACAATAGTAGATCCAAGATAGATCGGAAGAGCGGTTTCAG
chr12	56482451	56482490	ERBB3_6693	+	GTGACCTATGCACCAGACGTTGTAAGAAGTTGTAAGAGACAGCCTTTCCCTCAGCAGATCGGAAGAGCGGTTTCAG
chr12	56482663	56482702	ERBB3_6694	+	GTGACCTATGCACCAGACGTTCCCTCCTTCCCTTAGACCCACGCCACCCCTCAGATCGGAAGAGCGGTTTCAG
chr12	56486615	56486654	ERBB3_6695	+	GTGACCTATGCACCAGACGTTGAGAGTTTCCCTTCTAGAAGAATAGGTGAACCACTGGCAGATCGGAAGAGCGGTTTCAG
chr12	56486871	56486910	ERBB3_6696	+	GTGACCTATGCACCAGACGTTGGTATGAGGAAATGGCATCTTACAGCAATGAAGCCTGTGAGATCGGAAGAGCGGTTTCAG
chr12	56487345	56487384	ERBB3_6697	+	GTGACCTATGCACCAGACGTTGGTCTGCTAGGTGGTGAGAATAGGAGTCAAGGAGGAGAAGATCGGAAGAGCGGTTTCAG
chr12	56487691	56487730	ERBB3_6698	+	GTGACCTATGCACCAGACGTTGGGAGCAGTCAAGGATGGTGGGGTGGGGCCCTGCAATAGATCGGAAGAGCGGTTTCAG
chr12	56487984	56488023	ERBB3_6699	+	GTGACCTATGCACCAGACGTTAGCAGCAGGATCTCAAGGGAGACAGAAGGGGCAATACAGATCGGAAGAGCGGTTTCAG
chr12	56488351	56488390	ERBB3_6700	+	GTGACCTATGCACCAGACGTTGATAAAGGAGAGGGGTCAGGTGGAAGGGTAGGACCAAGATCGGAAGAGCGGTTTCAG
chr12	56489105	56489144	ERBB3_6701	+	GTGACCTATGCACCAGACGTTGGAGATTCTGGAACTGGGGATATTTGGGAGTTGGGAAGATCGGAAGAGCGGTTTCAG
chr12	56489601	56489640	ERBB3_6702	+	GTGACCTATGCACCAGACGTTAGCTTACTTTTTGTTTTTCTTTTTCTTTTTTGCATGTCCTAGATCGGAAGAGCGGTTTCAG
chr12	56490417	56490456	ERBB3_6703	+	GTGACCTATGCACCAGACGTTATAGGAATTTCTGGAGAGTGGGGAAAGGCATCTAGGGCAAAGATCGGAAGAGCGGTTTCAG
chr12	56490641	56490680	ERBB3_6704	+	GTGACCTATGCACCAGACGTTGAATTTCTGTATGCCGTAGGAGAGGACAATATAGATAGATCGGAAGAGCGGTTTCAG
chr12	56491025	56491064	ERBB3_6705	+	GTGACCTATGCACCAGACGTTCTCTAGGGCTTCTCAATTTTCTCGAATTTCTCGGGGAGATCGGAAGAGCGGTTTCAG
chr12	56491735	56491774	ERBB3_6706	+	GTGACCTATGCACCAGACGTTACAAGGGTAAGGAGGCGGGGGTGGAGTGAAGCATGGGAAGATCGGAAGAGCGGTTTCAG
chr12	56492370	56492409	ERBB3_6707	+	GTGACCTATGCACCAGACGTTGGATGCCCTCTCTACCATCACTGGCCCAAGTTTCAAATAGATCGGAAGAGCGGTTTCAG
chr12	56493540	56493579	ERBB3_6708	+	GTGACCTATGCACCAGACGTTAGTAGGAGTGTCTAAGGAAATTTAGAAAAGGAGGAGTTGAGATCGGAAGAGCGGTTTCAG
chr12	56493824	56493863	ERBB3_6709	+	GTGACCTATGCACCAGACGTTTCTAATTACCAACACTTTGCACCCTGAGCCCTCACAAAAGATCGGAAGAGCGGTTTCAG
chr12	56494040	56494079	ERBB3_6710	+	GTGACCTATGCACCAGACGTTTCTGAGAGGCTGGTTTATAGGATGATACGATAGATCGGAAGAGCGGTTTCAG
chr12	56495156	56495195	ERBB3_6711	+	GTGACCTATGCACCAGACGTTCTCCTAGGGCTTCTCAATTTTCTCGAATTTCTCGAGATCGGAAGAGCGGTTTCAG
chr12	56495850	56495889	ERBB3_6712	+	GTGACCTATGCACCAGACGTTCTGTGGCACTCAGGGAGCATTTAATGGCAGCTAGTGCCTTAGATCGGAAGAGCGGTTTCAG
chr12	56495856	56495895	ERBB3_6713	+	GTGACCTATGCACCAGACGTTACTATGAATATATGAATCGGCAACGAGATGGAGGTGGTCCAGATCGGAAGAGCGGTTTCAG
chr9	139392021	139392060	NOTCH1_6714	+	GTGACCTATGCACCAGACGTTAGGGCGGGGGCCGGTGGGGGGGCCAGGCCAGGCGTGGGGAGATCGGAAGAGCGGTTTCAG
chr9	139393459	139393498	NOTCH1_6715	+	GTGACCTATGCACCAGACGTTGAAGCAGATGGGCTAGGTTGGAGCCAGCTGGAGCAACCAGATCGGAAGAGCGGTTTCAG
chr9	139393722	139393761	NOTCH1_6716	+	GTGACCTATGCACCAGACGTTGGAGAGGCTCAGCGGGTGTGCTGGCAGACGTTACAGATCGGAAGAGCGGTTTCAG
chr9	139395310	139395349	NOTCH1_6717	+	GTGACCTATGCACCAGACGTTAGAGACGGGTGCTCAGTCTGGAGGGCCGGTCCCAAGCTGCAGATCGGAAGAGCGGTTTCAG
chr9	139396376	139396415	NOTCH1_6718	+	GTGACCTATGCACCAGACGTTGAGTGAGCAGAGCCTGTGAGGGCAGCCCGGCAGCAGGTGAGATCGGAAGAGCGGTTTCAG
chr9	139396551	139396590	NOTCH1_6719	+	GTGACCTATGCACCAGACGTTAGGGGTGAGAAAGTAGAGGCTGAGCGAGCTCCCTAGGAAGCAGATCGGAAGAGCGGTTTCAG
chr9	139396951	139396990	NOTCH1_6720	+	GTGACCTATGCACCAGACGTTGGGGCCAGGGGCGAGTGGCCGGACATCAGGCAGCGGCTAAGATCGGAAGAGCGGTTTCAG
chr9	139397793	139397832	NOTCH1_6721	+	GTGACCTATGCACCAGACGTTATCAGAGAGGGGCTGGGACCCGAGGCTTCTCCTCCCAAGATCGGAAGAGCGGTTTCAG
chr9	139399567	139399606	NOTCH1_6722	+	GTGACCTATGCACCAGACGTTCCGACACGCTCAGGCCCTTCTCGGGGGCCCTCGCAGATCGGAAGAGCGGTTTCAG
chr9	139400344	139400383	NOTCH1_6723	+	GTGACCTATGCACCAGACGTTGGGAAGACAGGACGGTGTGGGGTGGGCCACCCCGCCAGATCGGAAGAGCGGTTTCAG
chr9	139401102	139401141	NOTCH1_6724	+	GTGACCTATGCACCAGACGTTGAGCAGGGCAGTGAGAGGCTCACCTGCTGCCACACGCAGATCGGAAGAGCGGTTTCAG
chr9	139401436	139401475	NOTCH1_6725	+	GTGACCTATGCACCAGACGTTAGTTTCTGTCAGTGGCCAAAGCCCGCCACACCCCGCCCTAGATCGGAAGAGCGGTTTCAG
chr9	139401900	139401939	NOTCH1_6726	+	GTGACCTATGCACCAGACGTTGAGCAAGAGGGGCGCTTCCGCTCAGCCGGCCAGGATAGATCGGAAGAGCGGTTTCAG
chr9	139402602	139402641	NOTCH1_6727	+	GTGACCTATGCACCAGACGTTGGGTGGTAGCAGGTGAGGCCAGCCACAGAGACCAGATCGGAAGAGCGGTTTCAG
chr9	139402848	139402887	NOTCH1_6728	+	GTGACCTATGCACCAGACGTTATGGGGTACAGTGGTGGCCGCGCCCGGCTTTCCCAAGATCGGAAGAGCGGTTTCAG

chr9	139403534	139403573	NOTCH1_6729	+	GTGACCTATGCACCAGACGTGTGGGCAGCGGGGGCTGAGTGGAGGGCATTGGTGGGTCCAGATCGGAAGAGCGGTTTCAG
chr9	139404424	139404463	NOTCH1_6730	+	GTGACCTATGCACCAGACGTACGGAAGGGTGTAGTGTGAGGGGACAGGCACAAACCCACACCAGATCGGAAGAGCGGTTTCAG
chr9	139405268	139405307	NOTCH1_6731	+	GTGACCTATGCACCAGACGTGGAGGAGGCCGGTTGGTACCAGCGGCCCTGGCCCTCCAAGATCGGAAGAGCGGTTTCAG
chr9	139405734	139405773	NOTCH1_6732	+	GTGACCTATGCACCAGACGTGAGACACACGTGACCCCGGGAGCCTCACCCAGAGGGATCTAGATCGGAAGAGCGGTTTCAG
chr9	139407597	139407636	NOTCH1_6733	+	GTGACCTATGCACCAGACGTGGGGACAGCACTCGGCATGTCCAGCACTCCCAGGCACCTTAGATCGGAAGAGCGGTTTCAG
chr9	139408000	139408309	NOTCH1_6734	+	GTGACCTATGCACCAGACGTGACCACACTGCAGGTGCAGGGAGGCCGAGCAGCAGCCAGATCGGAAGAGCGGTTTCAG
chr9	139409165	139409204	NOTCH1_6735	+	GTGACCTATGCACCAGACGTGGCGGGTGCAGACTCCGAGGCCAGCCAGCCGAGGGGTCCCAAGATCGGAAGAGCGGTTTCAG
chr9	139409863	139409902	NOTCH1_6736	+	GTGACCTATGCACCAGACGTGGCAGCTGTGGTCTCAGGCCCCGCCCTGCCACTGAGATCGGAAGAGCGGTTTCAG
chr9	139410179	139410218	NOTCH1_6737	+	GTGACCTATGCACCAGACGTGGAGGGGGCGGCACAGGAAGACTTAGGACTGGCGGCCCCAGATCGGAAGAGCGGTTTCAG
chr9	139410557	139410596	NOTCH1_6738	+	GTGACCTATGCACCAGACGTGGAGGGGAGGGGAGGGAGTCAATGTGCAACAGCACTATGGCAGATCGGAAGAGCGGTTTCAG
chr9	139411848	139411887	NOTCH1_6739	+	GTGACCTATGCACCAGACGTGGGCAACAGTGTAGGGGGGACCGCGGCCCCAGTGGCCCCAAGATCGGAAGAGCGGTTTCAG
chr9	139412400	139412439	NOTCH1_6740	+	GTGACCTATGCACCAGACGTACACCGGTTGAGAGGCTGCTCCAGCCACCTGGCCCTGCAGATCGGAAGAGCGGTTTCAG
chr9	139412755	139412794	NOTCH1_6741	+	GTGACCTATGCACCAGACGTAGCCGGCTCAGTGGGACCGGCCCTGGGCCAGGCATGGCAGATCGGAAGAGCGGTTTCAG
chr9	139413287	139413326	NOTCH1_6742	+	GTGACCTATGCACCAGACGTGAGGAGCTGTGGCCCCGGGAGCTGCCACTCCCTGAGCTAGATCGGAAGAGCGGTTTCAG
chr9	139414028	139414067	NOTCH1_6743	+	GTGACCTATGCACCAGACGTAGGGGGCGGGTACGCCTCTCCCTGAGGTCCAGTCCGGCTAGATCGGAAGAGCGGTTTCAG
chr9	139417651	139417690	NOTCH1_6744	+	GTGACCTATGCACCAGACGTGGGGACAAGAGGGTCTGCTGCCCTCACTGCTCCCCGAGGAGATCGGAAGAGCGGTTTCAG
chr9	139418442	139418481	NOTCH1_6745	+	GTGACCTATGCACCAGACGTATGTGCCAGGGCAGTTAGTCTCCCACTGCTTCCCAGCGCAGATCGGAAGAGCGGTTTCAG
chr9	139438565	139438604	NOTCH1_6746	+	GTGACCTATGCACCAGACGTGACGGAGAAGAGGTTAGTCACTCCCGCACCACCACAGATCGGAAGAGCGGTTTCAG
chr9	139440249	139440288	NOTCH1_6747	+	GTGACCTATGCACCAGACGTGGCTGCCCTCTCGCCCCGGGCGCGCCCTCTGCGTGGAGATCGGAAGAGCGGTTTCAG
chr9	139400058	139400097	NOTCH1_6748	+	GTGACCTATGCACCAGACGTGTAGTCCAGGATGTGGCACAAGAGCCGTTGAATTTGGCGAGATCGGAAGAGCGGTTTCAG
chr9	139391029	139391068	NOTCH1_6749	+	GTGACCTATGCACCAGACGTGTGGCTGCACCTGCTGGGTCTGCACCAGGTGAGGCTGGGTAGATCGGAAGAGCGGTTTCAG
chr9	139391525	139391564	NOTCH1_6750	+	GTGACCTATGCACCAGACGTGGGGAGGGCAGGTGGCGGGCAGGGCCACGCTGTGACAGGAGATCGGAAGAGCGGTTTCAG
chr12	4383412	4383451	CCND2_6751	+	GTGACCTATGCACCAGACGTGGTGGCGCTCCAGGAGCCAGGACCCCTCCGGATCTCAGATCGGAAGAGCGGTTTCAG
chr12	4385397	4385436	CCND2_6752	+	GTGACCTATGCACCAGACGTGCCCTCTCCCTCTCTTCTTCCGATTCCCGCTTTCCCAGATCGGAAGAGCGGTTTCAG
chr12	4388096	4388135	CCND2_6753	+	GTGACCTATGCACCAGACGTGCTTGGAGCCGGGAGGGAGATGGGGAGGCTCTTTTGGGAGAGATCGGAAGAGCGGTTTCAG
chr12	4398167	4398206	CCND2_6754	+	GTGACCTATGCACCAGACGTACCACCTTCTTGGCTAAGTCCAGATGTCTCTTCTCAGCTCAGATCGGAAGAGCGGTTTCAG
chr12	4409186	4409225	CCND2_6755	+	GTGACCTATGCACCAGACGTGGGGCGAAAGAGAGAGACGCGTCCATAATCTGGTCTCTTAGATCGGAAGAGCGGTTTCAG
chr8	128748880	128748919	MYC_6756	+	GTGACCTATGCACCAGACGTAAGTCCACTGGCCTTTAATTTATTTTTTATCACTTTAAAGATCGGAAGAGCGGTTTCAG
chr8	128751276	128751315	MYC_6757	+	GTGACCTATGCACCAGACGTCCCGCCAGCCGTGTCAAAGTGGCGGCTGGATACCTTTAGATCGGAAGAGCGGTTTCAG
chr8	128753215	128753254	MYC_6758	+	GTGACCTATGCACCAGACGTGAAACAGATTCTCTTAAAGATAAATGCTCCTGAGCAATCAAGATCGGAAGAGCGGTTTCAG
chr8	128750890	128750929	MYC_6759	+	GTGACCTATGCACCAGACGTATCATCATCCAGGACTGTATGTGGAGCGGCTTCTCGGCCGAGATCGGAAGAGCGGTTTCAG
chr8	128752933	128752972	MYC_6760	+	GTGACCTATGCACCAGACGTCCGAGGAGAATGTCAAAGGGCAACACACAAGTCTTGAAGATCGGAAGAGCGGTTTCAG
chr1	115251286	115251325	NRAS_6761	+	GTGACCTATGCACCAGACGTAAAAAATGAAAAAATGAGAGAGGCTAGCTCAACGGACACAGATCGGAAGAGCGGTTTCAG
chr1	115256610	115256649	NRAS_6762	+	GTGACCTATGCACCAGACGTGGAGGGTAAGGGGACGGGAGGGAGGGAAAGTTCAATTTTAGATCGGAAGAGCGGTTTCAG
chr1	115258792	115258831	NRAS_6763	+	GTGACCTATGCACCAGACGTAAAGGCTGGTGGAAACAGTAATCAGGGTTAATTTGGCGAGATCGGAAGAGCGGTTTCAG
chr19	40739869	40739908	AKT2_6764	+	GTGACCTATGCACCAGACGTGAGAGGTGGATGGGGAGGACCAGTCAAGGAGAGGGCCTGGGAGATCGGAAGAGCGGTTTCAG
chr19	40741065	40741104	AKT2_6765	+	GTGACCTATGCACCAGACGTGAGGAGCTCAGGCTCAGGGACCCTGAGGCCAGGAGCCTCAGATCGGAAGAGCGGTTTCAG
chr19	40741268	40741307	AKT2_6766	+	GTGACCTATGCACCAGACGTACGGCCGTCAGCACCTGCCTCCCGAGCAGCTGGTTCGGAGATCGGAAGAGCGGTTTCAG
chr19	40742022	40742061	AKT2_6767	+	GTGACCTATGCACCAGACGTAGGAGAAATGAGGGCTGGGCCCTGGCCCTGAGGCTGGCAAGATCGGAAGAGCGGTTTCAG
chr19	40742303	40742342	AKT2_6768	+	GTGACCTATGCACCAGACGTAGTCAACGGATCTCAGGTGCATCTCCCAAGCTTCTCGAGATCGGAAGAGCGGTTTCAG
chr19	40744009	40744048	AKT2_6769	+	GTGACCTATGCACCAGACGTAAAGGGTGGGGAGGAGGAGGCTCAGGCCCCAGCCACCACAGATCGGAAGAGCGGTTTCAG
chr19	40744891	40744930	AKT2_6770	+	GTGACCTATGCACCAGACGTAAGGCAGCAGGGTGGGAGGTGGGAGGGAGGAGGGCTCTGCAGATCGGAAGAGCGGTTTCAG
chr19	40746028	40746067	AKT2_6771	+	GTGACCTATGCACCAGACGTACTGCGGGTGAAGGGCTGGTGGGCAACACCACACCTGCCAGATCGGAAGAGCGGTTTCAG
chr19	40747987	40748026	AKT2_6772	+	GTGACCTATGCACCAGACGTGAGGGAGTGGGGCAGTCAAGCCCTGGCTCATGGCCCCAGATCGGAAGAGCGGTTTCAG
chr19	40748605	40748644	AKT2_6773	+	GTGACCTATGCACCAGACGTACACAGTGTAGTCCCAGACGCCAGGAGTCTGGGCCCTCAGAGATCGGAAGAGCGGTTTCAG
chr19	40761187	40761226	AKT2_6774	+	GTGACCTATGCACCAGACGTAGGAAACAGACAGCAGGAGGGGATAGCCCTGCTAAGATCGGAAGAGCGGTTTCAG
chr19	40762972	40763011	AKT2_6775	+	GTGACCTATGCACCAGACGTGAGGAAAGGGAGGGAGAGAGGTTAGGACAAGGTTGAGTGAAGATCGGAAGAGCGGTTTCAG
chr19	40771185	40771224	AKT2_6776	+	GTGACCTATGCACCAGACGTTGGTACGCTGTCACTAGCTCGGGACAGCTCAGGGCAGCAAGATCGGAAGAGCGGTTTCAG
chr16	3779886	3779925	CREBBP_6777	+	GTGACCTATGCACCAGACGTGAAAGGGGACAGGCCGGTGTCAAGCATGGACCCAGTACCAGATCGGAAGAGCGGTTTCAG
chr16	3781485	3781524	CREBBP_6778	+	GTGACCTATGCACCAGACGTGGAGGGGCTTGTAGTCCCACACAAGGGACATGGCACCTCCAAGATCGGAAGAGCGGTTTCAG
chr16	3781949	3781988	CREBBP_6779	+	GTGACCTATGCACCAGACGTACGCAAGGCTGTGAGACAGGCAAGTGGCCCTCCACCTTAGATCGGAAGAGCGGTTTCAG
chr16	3786215	3786254	CREBBP_6780	+	GTGACCTATGCACCAGACGTAAGCAGCAACAGTGAAGATGAGGGCCATGACGCGCTCCCTCAGATCGGAAGAGCGGTTTCAG
chr16	3786827	3786866	CREBBP_6781	+	GTGACCTATGCACCAGACGTACGCACACACGTGATGAACGTGCCAGTGAATCGGCCAGATCGGAAGAGCGGTTTCAG
chr16	3788684	3788723	CREBBP_6782	+	GTGACCTATGCACCAGACGTGAGGCACATGTTAACTCAGGGTATCCCTCAAATCTGAAAAGATCGGAAGAGCGGTTTCAG
chr16	3789736	3789775	CREBBP_6783	+	GTGACCTATGCACCAGACGTAGCCAGAGCCGACATTTACAAAAGCTGTTGCTGACAAGGAGATCGGAAGAGCGGTTTCAG
chr16	3790561	3790600	CREBBP_6784	+	GTGACCTATGCACCAGACGTGAGAAGGAGCAGGTGAGAGGGCTTCAACAGCACTGTGAGAGATCGGAAGAGCGGTTTCAG
chr16	3794973	3795012	CREBBP_6785	+	GTGACCTATGCACCAGACGTATAGGGTATGATGAGACTGTATAATGATGATAAATGTAGATCGGAAGAGCGGTTTCAG
chr16	3795366	3795405	CREBBP_6786	+	GTGACCTATGCACCAGACGTAAGAAGGCCACTGTTAAAGCACACCGAACCCACAAGACCAAGATCGGAAGAGCGGTTTCAG

chr16	3799695	3799734	CREBBP_6787	+	GTGACCTATGCACCAGACGTAATAAGAAAACATGTTTTATTAATAAAATTTATCTGTTGAGATCGGAAGAGCGGTTCCAG
chr16	3801818	3801857	CREBBP_6788	+	GTGACCTATGCACCAGACGTAAGGCCATACTTGGGTGAAGTCCATCATAACACACAAGATCGGAAGAGCGGTTCCAG
chr16	3807388	3807427	CREBBP_6789	+	GTGACCTATGCACCAGACGTAAGGAGAAATACTTTTATATAAAAAATACATTCCATTTCAGATCGGAAGAGCGGTTCCAG
chr16	3808060	3808099	CREBBP_6790	+	GTGACCTATGCACCAGACGTAATAAATGGTCTCAGTATAGGGAATCCCCAATATCCAAAAGATCGGAAGAGCGGTTCCAG
chr16	3808984	3809023	CREBBP_6791	+	GTGACCTATGCACCAGACGTAACATCAAGAAAAGACACTTTGTAAAAGGTGCTCAGATCCAGATCGGAAGAGCGGTTCCAG
chr16	3817921	3817960	CREBBP_6792	+	GTGACCTATGCACCAGACGTACATTACAGATAACATATGAATATCAAAACCTTTATGTTAGATCGGAAGAGCGGTTCCAG
chr16	3819365	3819404	CREBBP_6793	+	GTGACCTATGCACCAGACGTACCAGAAAGCACTGCTCAGTAAAGCAAGGTAAACATAAATAGATCGGAAGAGCGGTTCCAG
chr16	3820998	3821037	CREBBP_6794	+	GTGACCTATGCACCAGACGTTGGACAGAGTATGGTAAAATTTATTTCCCGCTTTGAAAATAGATCGGAAGAGCGGTTCCAG
chr16	3823942	3823981	CREBBP_6795	+	GTGACCTATGCACCAGACGTACAAGCACCACCAGAGCTGTAGTTGGAAGCTGACGGCCAAGATCGGAAGAGCGGTTCCAG
chr16	3824705	3824744	CREBBP_6796	+	GTGACCTATGCACCAGACGTACCACAACCGGTTCAATAGAAAAGCACCACAGGAAAACAGATCGGAAGAGCGGTTCCAG
chr16	3828194	3828233	CREBBP_6797	+	GTGACCTATGCACCAGACGTATAATATTCAATATGAAACAGTTAAAACGTAAAAGCAAAAGATCGGAAGAGCGGTTCCAG
chr16	3828829	3828868	CREBBP_6798	+	GTGACCTATGCACCAGACGTAACACATCTATCAACTACTTTTTTTTTTTCTTTTITTTAGATCGGAAGAGCGGTTCCAG
chr16	3830890	3830929	CREBBP_6799	+	GTGACCTATGCACCAGACGTAATAAGACACTTTCATCCTACTGAAAGTGACTCAAAACAAGATCGGAAGAGCGGTTCCAG
chr16	3831318	3831357	CREBBP_6800	+	GTGACCTATGCACCAGACGTAGAAAAGAAATCAATCAACAGTTAAATTTAATATATACTAGATCGGAAGAGCGGTTCCAG
chr16	3832938	3832977	CREBBP_6801	+	GTGACCTATGCACCAGACGTAACAGACAGACAGACAAAACGAGAGGTAAGTAAAAGGGAGATCGGAAGAGCGGTTCCAG
chr16	3842106	3842145	CREBBP_6802	+	GTGACCTATGCACCAGACGTAATAAACAACGAGATGTTATTTTTCTATCCAATCGTCAAAAGATCGGAAGAGCGGTTCCAG
chr16	3843638	3843677	CREBBP_6803	+	GTGACCTATGCACCAGACGTGCAAAAATAAAAAACTTTAACCTCTCAGAGTTCCAAGAGATCGGAAGAGCGGTTCCAG
chr16	3860791	3860830	CREBBP_6804	+	GTGACCTATGCACCAGACGTAAGAGGTAACACTCAGCTGTGGTACGCGAGTCAATATAAAAAGATCGGAAGAGCGGTTCCAG
chr16	3901021	3901060	CREBBP_6805	+	GTGACCTATGCACCAGACGTAACAGAATAAGAAATGAGAAAAGTAAAGCAACCTTTACAGCTAGATCGGAAGAGCGGTTCCAG
chr16	3900664	3900703	CREBBP_6806	+	GTGACCTATGCACCAGACGTGGTGGGCCAGAGGTGCTGGCTGCCTGTTTAGCGAGGCTGAGATCGGAAGAGCGGTTCCAG
chr16	3778160	3778199	CREBBP_6807	+	GTGACCTATGCACCAGACGTCAGAATCCGCTGCTGCAGGGCTTGGTGGATGTTGGGGGTGAGATCGGAAGAGCGGTTCCAG
chr16	3778591	3778630	CREBBP_6808	+	GTGACCTATGCACCAGACGTCGGGGCCGCGGCACGCCAGCTGCATGGCATTAGGTTCTGAGATCGGAAGAGCGGTTCCAG
chr16	3779022	3779061	CREBBP_6809	+	GTGACCTATGCACCAGACGTCACCTGGTTGGTGGTGGGCACATTCAGGCTCACGGGGAGATCGGAAGAGCGGTTCCAG
chr16	3779453	3779492	CREBBP_6810	+	GTGACCTATGCACCAGACGTCATGAGCTGGGCTGCTGCAGCGGTGCTGGATCTGCTGCAGATCGGAAGAGCGGTTCCAG
chr22	30000112	30000151	NF2_6811	+	GTGACCTATGCACCAGACGTTGGCAGCCCCGACTGCTGCGGTGACAGTGCAGGTGGAAGCTAGATCGGAAGAGCGGTTCCAG
chr22	30032876	30032915	NF2_6812	+	GTGACCTATGCACCAGACGTAACCTCGATGAACTGGTGGGGCTGACGTGAGCTTTCCAGTAGATCGGAAGAGCGGTTCCAG
chr22	30035212	30035251	NF2_6813	+	GTGACCTATGCACCAGACGTCAGGCTACCCCCAGTTCTGAGAGAAGTTCGCCAGGAGTATCGGAAGAGCGGTTCCAG
chr22	30038285	30038324	NF2_6814	+	GTGACCTATGCACCAGACGTAGAAGAAAAATGATTTTTCTAGGCGGTTAATTTGGGTCAAGATCGGAAGAGCGGTTCCAG
chr22	30050725	30050764	NF2_6815	+	GTGACCTATGCACCAGACGTAATTCCTTTTTCAGGAAGACATGACAGATATGGTCTAAGATCGGAAGAGCGGTTCCAG
chr22	30051676	30051715	NF2_6816	+	GTGACCTATGCACCAGACGTTTCATTGTTGGTTTACATTCCTTTATGGGCTTTTTTTTTTAGATCGGAAGAGCGGTTCCAG
chr22	30054264	30054303	NF2_6817	+	GTGACCTATGCACCAGACGTACCTCTCTGAGCTCCTTGTTAGTAGACAGAGACTGAGTGCAGATCGGAAGAGCGGTTCCAG
chr22	30057339	30057378	NF2_6818	+	GTGACCTATGCACCAGACGTTGTGTACTGCAGATGGGTCCAGCAGATCTTCCCTGTCTGAGATCGGAAGAGCGGTTCCAG
chr22	30061064	30061103	NF2_6819	+	GTGACCTATGCACCAGACGTATCCTGGTTTTCTACTGATAATGGTAGCTTTTCTGAGAAGATCGGAAGAGCGGTTCCAG
chr22	30064446	30064485	NF2_6820	+	GTGACCTATGCACCAGACGTCCTTGGTTTAACTGATGATGTCAGTGTGGTGCAGTCTGAGATCGGAAGAGCGGTTCCAG
chr22	30067948	30067987	NF2_6821	+	GTGACCTATGCACCAGACGTTAGGGCTGAGGGTCCAGGACTGCTTGGGGACTTCTTGGAGATCGGAAGAGCGGTTCCAG
chr22	30069486	30069525	NF2_6822	+	GTGACCTATGCACCAGACGTACCGGGCACCAGACTGGCAGGAGGCTGGCGAAGGGCCGAGATCGGAAGAGCGGTTCCAG
chr22	30070941	30070980	NF2_6823	+	GTGACCTATGCACCAGACGTTGGGCCACCAGCTGGGGCTGCCTTAGTCTGGTGATGTTCTAGATCGGAAGAGCGGTTCCAG
chr22	30074323	30074362	NF2_6824	+	GTGACCTATGCACCAGACGTCCTGTGCCCTGCTGTGGGCAGCTGTGAAGTACTGAGTGCAGATCGGAAGAGCGGTTCCAG
chr22	30077601	30077640	NF2_6825	+	GTGACCTATGCACCAGACGTTCTCTTTCTTGTATTTTGTCTGATCAGGACCATCATAATGAGATCGGAAGAGCGGTTCCAG
chr22	30079055	30079094	NF2_6826	+	GTGACCTATGCACCAGACGTTAGGTTGTTCACAGTACTCTATGTGGTATGGTGCAGATCGGAAGAGCGGTTCCAG
chr22	30090802	30090841	NF2_6827	+	GTGACCTATGCACCAGACGTTAGGCTGAGGCCACCCCAAGTCCACTCTCTCTGCTACCAGGACAGATCGGAAGAGCGGTTCCAG
chr1	156785641	156785680	NTRK1_6828	+	GTGACCTATGCACCAGACGTTTTTCTCTCTCTCTCTGTCGCCAGCCCGTTGGCAGACAGATCGGAAGAGCGGTTCCAG
chr1	156811996	156812035	NTRK1_6829	+	GTGACCTATGCACCAGACGTCCTGTGCAATCTCACCAGCCATTGGATCATTCCCCCAAGATCGGAAGAGCGGTTCCAG
chr1	156830949	156830988	NTRK1_6830	+	GTGACCTATGCACCAGACGTTGGCGGGCGGTGGGGGGCGCGGGACAGGCAGGCATTGCAAGATCGGAAGAGCGGTTCCAG
chr1	156834231	156834270	NTRK1_6831	+	GTGACCTATGCACCAGACGTCGGGGACTGTGGGTGTGGAGTCCAGATGGGCTGGGGGAAGATCGGAAGAGCGGTTCCAG
chr1	156834602	156834641	NTRK1_6832	+	GTGACCTATGCACCAGACGTCAGTGTGGCAGTGGAGTTGGGAGGACACCAAGACTAGATCGGAAGAGCGGTTCCAG
chr1	156836781	156836820	NTRK1_6833	+	GTGACCTATGCACCAGACGTTGCGCTTCCAGGGGCAAGAGCACCAAGTGTGTGTGCCTGAGATCGGAAGAGCGGTTCCAG
chr1	156838052	156838091	NTRK1_6834	+	GTGACCTATGCACCAGACGTTGGTGGGGAGTGGTGTAAAGGGGCTGGGGAAGAGACCTAAGATCGGAAGAGCGGTTCCAG
chr1	156838450	156838489	NTRK1_6835	+	GTGACCTATGCACCAGACGTTCTGCTGGCAGCCCCAAGAGGTCCAGGCAGACAGGAGATCGGAAGAGCGGTTCCAG
chr1	156841558	156841597	NTRK1_6836	+	GTGACCTATGCACCAGACGTTGGCAGCTCCGGCACCACCCCTACTCATCTCTTCTCAGATCGGAAGAGCGGTTCCAG
chr1	156843762	156843801	NTRK1_6837	+	GTGACCTATGCACCAGACGTCATCCTGAACCTGCCCCACTCGGGCTCCTCCTGGTAGATCGGAAGAGCGGTTCCAG
chr1	156844203	156844242	NTRK1_6838	+	GTGACCTATGCACCAGACGTTCAAGTGGAGGGCAGGCTGCTGCTGGTCTCTGGAGTGCAGATCGGAAGAGCGGTTCCAG
chr1	156844429	156844468	NTRK1_6839	+	GTGACCTATGCACCAGACGTAAGTAGAAGCTTGTGCAGACTTTGGACCGGGAGGCTGGGAGATCGGAAGAGCGGTTCCAG
chr1	156844811	156844850	NTRK1_6840	+	GTGACCTATGCACCAGACGTTGCTGCAGAGGGCTGTCTGTCTGTCTGTTCTCCTGGCTTTGAGATCGGAAGAGCGGTTCCAG
chr1	156846013	156846052	NTRK1_6841	+	GTGACCTATGCACCAGACGTTGCCCGGGGGTACTGCTGECCTGGGTCCACCCCAAGATCGGAAGAGCGGTTCCAG
chr1	156846375	156846414	NTRK1_6842	+	GTGACCTATGCACCAGACGTTGGCTCAGCGCTGGCCCGGGCCCTGGCTGCTGGCCCCAGATCGGAAGAGCGGTTCCAG
chr1	156849165	156849204	NTRK1_6843	+	GTGACCTATGCACCAGACGTTTTGTCCCAACGCTTCCCTGCCATCCAAACTGTAGACAAGATCGGAAGAGCGGTTCCAG
chr1	156849960	156849999	NTRK1_6844	+	GTGACCTATGCACCAGACGTTGCCATGGTACCCTTGGCTGCCTCCCGTCCCATGCCAGATCGGAAGAGCGGTTCCAG

chr1	156851445	156851484	NTRK1_6845	+	GTGACCTATGCACCAGACGTGAGGGGCTGGGAGTGGTTAGCCGGAATACTGGGGCCTGCCAGATCGGAAGAGCGGTTTCAG
chr5	149495520	149495559	PDGFRB_6846	+	GTGACCTATGCACCAGACGTGAGGCAGTGAGTGAGGGGCTAGGAAGGAGCCAGGAGGATAGATCGGAAGAGCGGTTTCAG
chr5	149498426	149498465	PDGFRB_6847	+	GTGACCTATGCACCAGACGTGGAGAAGGGTCAGGGCCTCTGGCCAGGGTTTCAGGGGACAAGATCGGAAGAGCGGTTTCAG
chr5	149499140	149499179	PDGFRB_6848	+	GTGACCTATGCACCAGACGTGCAGAGACAAGAGATACACAGGCTCAGGGGTGAAAAGTGAGATCGGAAGAGCGGTTTCAG
chr5	149499697	149499736	PDGFRB_6849	+	GTGACCTATGCACCAGACGTGTCAGGACAGGTGCTGAGTGCAAGGAAGGACCTCAGCCCCAGATCGGAAGAGCGGTTTCAG
chr5	149500584	149500623	PDGFRB_6850	+	GTGACCTATGCACCAGACGTGGAGAGGGAGCTGAGGCCTTGGGACAATTGTGGGAAAAGATCGGAAGAGCGGTTTCAG
chr5	149500896	149500935	PDGFRB_6851	+	GTGACCTATGCACCAGACGTAGACAGAGGGTCACTGCTCTTATATCTCTTCTGGCCAGATCGGAAGAGCGGTTTCAG
chr5	149501614	149501653	PDGFRB_6852	+	GTGACCTATGCACCAGACGTAGGAGCATCACAGGAGAGCCCTGCAGGCTTTGCCTTCCCCTAGATCGGAAGAGCGGTTTCAG
chr5	149502775	149502814	PDGFRB_6853	+	GTGACCTATGCACCAGACGTACAGGCTCAGGGACAGTCCCTATGGAGGCCCTCAGGCGTCCAGATCGGAAGAGCGGTTTCAG
chr5	149503934	149503973	PDGFRB_6854	+	GTGACCTATGCACCAGACGTTGGGGGCCCCAGGCCAGGCCAGTTCATGGAGGCTCCATGGAGATCGGAAGAGCGGTTTCAG
chr5	149504405	149504444	PDGFRB_6855	+	GTGACCTATGCACCAGACGTGATGATCCATTAGTCTCTGGCCTACCAGGAAGCTGCACCAGATCGGAAGAGCGGTTTCAG
chr5	149505151	149505190	PDGFRB_6856	+	GTGACCTATGCACCAGACGTAACCCAGGAATAGTTATCAGAGGGAGTCTCAGGCCCTGAGATCGGAAGAGCGGTTTCAG
chr5	149506188	149506227	PDGFRB_6857	+	GTGACCTATGCACCAGACGTAGATGAGAGAGGCCATGAGCAAACCTCAGCCAGCTACCCTCAGATCGGAAGAGCGGTTTCAG
chr5	149509542	149509581	PDGFRB_6858	+	GTGACCTATGCACCAGACGTAGCCGGTAGGGTTGGCTGCCAGCCCCTTCCCCTTGCAGACAGATCGGAAGAGCGGTTTCAG
chr5	149510236	149510275	PDGFRB_6859	+	GTGACCTATGCACCAGACGTAGAGCACTGAGTTAGGAGGCGGGAGGGTCAGGACAGTTAAAGATCGGAAGAGCGGTTTCAG
chr5	149512516	149512555	PDGFRB_6860	+	GTGACCTATGCACCAGACGTTGACCGTCAAGGGCGGGGCCCTGGGGGCAGGGCACCACCTAGATCGGAAGAGCGGTTTCAG
chr5	149513334	149513373	PDGFRB_6861	+	GTGACCTATGCACCAGACGTAGGTTGGGCGAGGCCCTCCAAATCAGGAGGGGGCCGGGAGAAGATCGGAAGAGCGGTTTCAG
chr5	149513582	149513621	PDGFRB_6862	+	GTGACCTATGCACCAGACGTGAGATTGGCTTAGGTTAGGTTGGGAAAGTCAACCAGCCATAGATCGGAAGAGCGGTTTCAG
chr5	149515452	149515491	PDGFRB_6863	+	GTGACCTATGCACCAGACGTGGAGGTATCAGACATCAGGAAACAGGGGCTTCAGCACTCAGATCGGAAGAGCGGTTTCAG
chr5	149516621	149516660	PDGFRB_6864	+	GTGACCTATGCACCAGACGTAGAGTTAAACAGGAGTCAAGGGCCAGGGCAGGTGGAGGCAAGATCGGAAGAGCGGTTTCAG
chr9	133589853	133589892	ABL1_6865	+	GTGACCTATGCACCAGACGTTTCAAAATTTCTGCTCATGGTTTTCTCATGCATTCTATAGATCGGAAGAGCGGTTTCAG
chr9	133710923	133710962	ABL1_6866	+	GTGACCTATGCACCAGACGTGCCGCACGGGTTGGGCTGAGTAGCCGCGGCCCTCCCCTAGATCGGAAGAGCGGTTTCAG
chr9	133729635	133729674	ABL1_6867	+	GTGACCTATGCACCAGACGTTGGGCGAGCTAGTGGTGGTTGCAGGAGATAGAAATCTGGAGATCGGAAGAGCGGTTTCAG
chr9	133730494	133730533	ABL1_6868	+	GTGACCTATGCACCAGACGTTCTGGCAGGGGCGCTAGTGGCCAGGGCAGGGCAACCAAGATCGGAAGAGCGGTTTCAG
chr9	133738433	133738472	ABL1_6869	+	GTGACCTATGCACCAGACGTACTGCCGGGGTGCCAGGGTACGTGGGGCAAGGCGTCTGAGATCGGAAGAGCGGTTTCAG
chr9	133747611	133747650	ABL1_6870	+	GTGACCTATGCACCAGACGTCCGGGGCTCTGAAGAGAGGGTCTCGCGCCGACCCCCAGGAGATCGGAAGAGCGGTTTCAG
chr9	133748435	133748474	ABL1_6871	+	GTGACCTATGCACCAGACGTGGCCAGGCAGCCCTGCGCCATGGAGTCAAGGGCGTGGAGCAGATCGGAAGAGCGGTTTCAG
chr9	133750450	133750489	ABL1_6872	+	GTGACCTATGCACCAGACGTCTGCTGCACTGAAGTGGCTTCTCTGACTACAGGAGGGTTAGATCGGAAGAGCGGTTTCAG
chr9	133753965	133754004	ABL1_6873	+	GTGACCTATGCACCAGACGTTCTCAGCCTTCTCAGGATATATGGGGCATTCCAGGAAAGATCGGAAGAGCGGTTTCAG
chr9	133755555	133755594	ABL1_6874	+	GTGACCTATGCACCAGACGTCATCCCGGGGTACCTGCAAGTGGGTTGAAAGGGCAGCCATGAGATCGGAAGAGCGGTTTCAG
chr9	133756062	133756101	ABL1_6875	+	GTGACCTATGCACCAGACGTGCTTCCCCAACCCCACTGCTTCCCTTCCCCTGCCAGAAGATCGGAAGAGCGGTTTCAG
chr9	133761081	133761120	ABL1_6876	+	GTGACCTATGCACCAGACGTGGGTGAGGTGTGAGGCCGTGCGAGCTGCCTGCAGCACATAGATCGGAAGAGCGGTTTCAG
chr9	133759795	133759834	ABL1_6877	+	GTGACCTATGCACCAGACGTTGGCAGTCCAGCAAGCGCTTCTGCGCTTCTGCTCCGCCAGATCGGAAGAGCGGTTTCAG
chr9	133760224	133760263	ABL1_6878	+	GTGACCTATGCACCAGACGTGCCAGTGACCCCAAGGCAAGGCGTCCAGGTCAGCCAGATCGGAAGAGCGGTTTCAG
chr9	133760653	133760692	ABL1_6879	+	GTGACCTATGCACCAGACGTGCCAGGGGACCGCCGTCTCCACCTTCCATCCCTCAGATCGGAAGAGCGGTTTCAG
chr11	69456290	69456329	CCND1_6880	+	GTGACCTATGCACCAGACGTTCCGGCGGCTCTCTTAAGACTTCCCTGCAACTTGTGCCAGATCGGAAGAGCGGTTTCAG
chr11	69458770	69458809	CCND1_6881	+	GTGACCTATGCACCAGACGTCCCGGCAGCCCCGGCCTCCCCTTGAGAGCCGGCTCCTTAAGATCGGAAGAGCGGTTTCAG
chr11	69462921	69462960	CCND1_6882	+	GTGACCTATGCACCAGACGTGTGATGTCCAGGCGAGCCTTGGCCGGGGTTACAGGGGGAGAGATCGGAAGAGCGGTTTCAG
chr11	69466061	69466100	CCND1_6883	+	GTGACCTATGCACCAGACGTGAGGCGGGCGCCACCGCCACCCGACGAGGGCGGAGCCGAGATCGGAAGAGCGGTTTCAG
chr7	92244611	92244650	CDK6_6884	+	GTGACCTATGCACCAGACGTGAAAAAATAATTGGTTGATATACAATACATCAATGTAAGATCGGAAGAGCGGTTTCAG
chr7	92247532	92247571	CDK6_6885	+	GTGACCTATGCACCAGACGTACCAACATGGACATAAGCACTTAGCTACTATGCAGAAGCTAGATCGGAAGAGCGGTTTCAG
chr7	92252411	92252450	CDK6_6886	+	GTGACCTATGCACCAGACGTAAAGATACATTTAAATAAAGAAATGTTCTCAGATTACATTAGATCGGAAGAGCGGTTTCAG
chr7	92300860	92300899	CDK6_6887	+	GTGACCTATGCACCAGACGTAAAGCGGATCCAAGTGTACTGAGAAGGTGGCTGTTGGCTTAGATCGGAAGAGCGGTTTCAG
chr7	92355118	92355157	CDK6_6888	+	GTGACCTATGCACCAGACGTTAAAAAAGAAAATCAGTAAACACTCAAACGGAAGTTGAAGATCGGAAGAGCGGTTTCAG
chr7	92404156	92404195	CDK6_6889	+	GTGACCTATGCACCAGACGTAAACAAAGAGGTTAAGTAGGTGCAATTAAGCAAAAGAAAGTAAAGATCGGAAGAGCGGTTTCAG
chr14	102548169	102548208	HSP90AA1_6890	+	GTGACCTATGCACCAGACGTAAACAAATCCTCATATTAACAAGATTTCTTAAAGCCAGTATCGGAAGAGCGGTTTCAG
chr14	102548792	102548831	HSP90AA1_6891	+	GTGACCTATGCACCAGACGTAAAGTGATGACTAGAACCTAGAAAGATTAATTCCTAAACAGATCGGAAGAGCGGTTTCAG
chr14	102549650	102549689	HSP90AA1_6892	+	GTGACCTATGCACCAGACGTACAAAGTTACTTTTTAGACCTTTTAAACAGTTAAGAATGGTTAGATCGGAAGAGCGGTTTCAG
chr14	102550331	102550370	HSP90AA1_6893	+	GTGACCTATGCACCAGACGTTATAAACCAATGCACTGAGTCATTCCAAGGACAAAACCTGAGATCGGAAGAGCGGTTTCAG
chr14	102550912	102550951	HSP90AA1_6894	+	GTGACCTATGCACCAGACGTACAGATACACTAAGTACCAATGAACAATGCATTATAGAAGAGATCGGAAGAGCGGTTTCAG
chr14	102551346	102551385	HSP90AA1_6895	+	GTGACCTATGCACCAGACGTAAACAGGAAATACATCACTGCTCACTCAGAACTAAGCAGATCGGAAGAGCGGTTTCAG
chr14	102551779	102551818	HSP90AA1_6896	+	GTGACCTATGCACCAGACGTAGAAAAGAAAATGACTTAAATACATTCAATTTAGTCTCAAGATCGGAAGAGCGGTTTCAG
chr14	102552472	102552511	HSP90AA1_6897	+	GTGACCTATGCACCAGACGTAAAAATTAATTTAAGCATACAGCACCCCAAGAAGTTCAAGATCGGAAGAGCGGTTTCAG
chr14	102552726	102552765	HSP90AA1_6898	+	GTGACCTATGCACCAGACGTACCGCGCCGGTTAAAACCTTGCAGGACGTCTACAGAGGCAGATCGGAAGAGCGGTTTCAG
chr14	102568433	102568472	HSP90AA1_6899	+	GTGACCTATGCACCAGACGTAAACACAATCTTCTGGACTTCAAACCAAACATAACAGAGATCGGAAGAGCGGTTTCAG
chr14	102605752	102605791	HSP90AA1_6900	+	GTGACCTATGCACCAGACGTGAGGGTACCCCGGCTGGCTCCGAAGCGGTGGCCGTAGATCGGAAGAGCGGTTTCAG
chr19	1611859	1611898	TCF3_6901	+	GTGACCTATGCACCAGACGTGGGGGAGAGCTGTGGGAGAGCCGTTCCAGGGAGGGAAGATCGGAAGAGCGGTTTCAG
chr19	1612443	1612482	TCF3_6902	+	GTGACCTATGCACCAGACGTGCACCAGGCCCTGTTAGTGATGCGCCAAGGCTGGAGTGGAGATCGGAAGAGCGGTTTCAG

chr19	1615530	1615569	TCF3_6903	+	GTGACCTATGCACCAGACGTGGCCCGGGAGGGGGCCAGAGGGAGACAGTGAAGTTGGGGAGATCGGAAGAGCGGTTTCAG
chr19	1615831	1615870	TCF3_6904	+	GTGACCTATGCACCAGACGCTCCTAGGGTCAGGGGCTCGCTCGGCCTCCAGGGCCAAGTGAAGATCGGAAGAGCGGTTTCAG
chr19	1619244	1619283	TCF3_6905	+	GTGACCTATGCACCAGACGTGGGGAGACGGGTGCATCAGGGGGAGCCGGGTCCCGCCCAAGATCGGAAGAGCGGTTTCAG
chr19	1619484	1619523	TCF3_6906	+	GTGACCTATGCACCAGACGTGGGGGATGGTGTGAGGGGCCAAGCCGAGGGACCCACAGATCGGAAGAGCGGTTTCAG
chr19	1619863	1619902	TCF3_6907	+	GTGACCTATGCACCAGACGTGTGGGGACGTGAATGGGGTGCAGAGGGCGGGGTGTGAGCAAGATCGGAAGAGCGGTTTCAG
chr19	1621056	1621095	TCF3_6908	+	GTGACCTATGCACCAGACGTGACCAGGAGAGATGCGGGCTCAGGGGCCGCTCTCAGGTAGATCGGAAGAGCGGTTTCAG
chr19	1621201	1621240	TCF3_6909	+	GTGACCTATGCACCAGACGTAGAGAGGTGAGGCCACCGCCAGCCGCTGGGTGCTGCCGAGATCGGAAGAGCGGTTTCAG
chr19	1621980	1622019	TCF3_6910	+	GTGACCTATGCACCAGACGTAGGCAAGGAGGGTGGGTTAGATGGGACTGCCACCCTCAGATCGGAAGAGCGGTTTCAG
chr19	1622233	1622272	TCF3_6911	+	GTGACCTATGCACCAGACGTGAGCTGGTAAGTGGGGGCCGAGTGGGGAACCCAGCCCTAGATCGGAAGAGCGGTTTCAG
chr19	1622425	1622464	TCF3_6912	+	GTGACCTATGCACCAGACGTGTGGGCGGTGGGGGGTGCAGTCAAGACGGAGGGACCACGAAGATCGGAAGAGCGGTTTCAG
chr19	1624010	1624049	TCF3_6913	+	GTGACCTATGCACCAGACGTCAAAGGGGTGAGAACCAGCCACCGGCCATGAGAACAACCCAGATCGGAAGAGCGGTTTCAG
chr19	1625718	1625757	TCF3_6914	+	GTGACCTATGCACCAGACGTGCGGATGGTCAGAAAGCCAGCTGCCATCCAGACCCCAAGATCGGAAGAGCGGTTTCAG
chr19	1627436	1627475	TCF3_6915	+	GTGACCTATGCACCAGACGTAGAAGGAAGTTAGTGGGAGGCCAGCCCAAGGAACATCCTAGATCGGAAGAGCGGTTTCAG
chr19	1632126	1632165	TCF3_6916	+	GTGACCTATGCACCAGACGTTGGGGTGGGGATGAGAGGTGCTGGGGCTTACAGGCCCCAGATCGGAAGAGCGGTTTCAG
chr19	1632415	1632454	TCF3_6917	+	GTGACCTATGCACCAGACGTGACAGAGAGTATGGGTCAACCCTCACGCCTGCCAGCTAGATCGGAAGAGCGGTTTCAG
chr19	1646437	1646476	TCF3_6918	+	GTGACCTATGCACCAGACGTGGGAGGGGAGACGTGAGCCGGGGCGGGTGGCAAACCAACCCAGATCGGAAGAGCGGTTTCAG
chr19	1650258	1650297	TCF3_6919	+	GTGACCTATGCACCAGACGTCCAGGGCGCCACCTCAGGCCCTGGAAACCCCTGCTTGGTGGAGATCGGAAGAGCGGTTTCAG
chr3	41265622	41265622	CTNNB1_6920	+	GTGACCTATGCACCAGACGTTAAATCTTTAGTTACTGAATGGGGCTCGCTTTCGTTGCAGATCGGAAGAGCGGTTTCAG
chr3	41266255	41266294	CTNNB1_6921	+	GTGACCTATGCACCAGACGTTATTTTTTTCATTGCCTTACTGAAAGTCAGAAATGCAGTTTTGAGATCGGAAGAGCGGTTTCAG
chr3	41266709	41266748	CTNNB1_6922	+	GTGACCTATGCACCAGACGTACATAGCTAGCTTTTTAGTCTGCTTTGAGTAAATGCTCAAGATCGGAAGAGCGGTTTCAG
chr3	41267074	41267113	CTNNB1_6923	+	GTGACCTATGCACCAGACGTATGTCAGAAATGCTTGAAGCTAAAAGTAGAAGAGTATACTAGATCGGAAGAGCGGTTTCAG
chr3	41267363	41267402	CTNNB1_6924	+	GTGACCTATGCACCAGACGTTATTTCTTTATGTGGTTTTTTCATGGAGCATTGGACACCTCCAAGATCGGAAGAGCGGTTTCAG
chr3	41268854	41268893	CTNNB1_6925	+	GTGACCTATGCACCAGACGTGTATCTATTCTGAGTCTTGTGTATAGCATCTGCAGTTCTAAGATCGGAAGAGCGGTTTCAG
chr3	41274946	41274985	CTNNB1_6926	+	GTGACCTATGCACCAGACGTAGTAACTGGTGGCAATGAAAGTCAAGATGAGATCGGAAGAGCGGTTTCAG
chr3	41275369	41275408	CTNNB1_6927	+	GTGACCTATGCACCAGACGTAAAGTAGAATTTACCTTTGTTGCAGAATGAAAATGAAGCAGATCGGAAGAGCGGTTTCAG
chr3	41275799	41275838	CTNNB1_6928	+	GTGACCTATGCACCAGACGTTCTTACAGTGATACCTGGCTATCTAAAAGGAATGCATAAAAGATCGGAAGAGCGGTTTCAG
chr3	41277345	41277384	CTNNB1_6929	+	GTGACCTATGCACCAGACGTAGTGAAGTGTTCAGGTTTTATGTCATAAAATTTCCAGAAGATCGGAAGAGCGGTTTCAG
chr3	41278001	41278040	CTNNB1_6930	+	GTGACCTATGCACCAGACGTAGGAACCAAGCTTTAGCAGATGTGTACATTGAAGTCTCAGATCGGAAGAGCGGTTTCAG
chr3	41278211	41278250	CTNNB1_6931	+	GTGACCTATGCACCAGACGTGTGAGCAGTATTTATCTCGGTAGTTTCCCTAGACAGGTATAGATCGGAAGAGCGGTTTCAG
chr3	41279578	41279617	CTNNB1_6932	+	GTGACCTATGCACCAGACGTATATTTCTCGATTAACCTCAGATCAAGATCAAAAGTTCTAAAAGATCGGAAGAGCGGTTTCAG
chr3	41280844	41280883	CTNNB1_6933	+	GTGACCTATGCACCAGACGTAGGTAAGAAGTTTTAAAAGCCAGTTTGGGTAATAACTTAGATCGGAAGAGCGGTTTCAG
chr8	38271333	38271372	FGFR1_6934	+	GTGACCTATGCACCAGACGTGAGAGGAAGCAGCGATGGGCCGGGCCCTCCTCCCTGCTAGATCGGAAGAGCGGTTTCAG
chr8	38271552	38271591	FGFR1_6935	+	GTGACCTATGCACCAGACGTACTGTAAGGTCAGGGACGTCTCCCTGGAGATGGATACTCTCAGATCGGAAGAGCGGTTTCAG
chr8	38271818	38271857	FGFR1_6936	+	GTGACCTATGCACCAGACGTGCCGAGAGCCAGGGTGTAGAGCTTCCCGCTCCCTAGATCGGAAGAGCGGTTTCAG
chr8	38272158	38272197	FGFR1_6937	+	GTGACCTATGCACCAGACGTCAACGGAAGCAAAATGGACAGCACAGGCATGAGACCTCAGATCGGAAGAGCGGTTTCAG
chr8	38273589	38273628	FGFR1_6938	+	GTGACCTATGCACCAGACGTAGGAGAAGAGGCCATGGGGCCAGCAGCAGGTGAGCAGGTTAGATCGGAAGAGCGGTTTCAG
chr8	38274945	38274984	FGFR1_6939	+	GTGACCTATGCACCAGACGTACGTTGAGACTCATTTACTTGGGAAGGGAGGAGGGCAGGAGATCGGAAGAGCGGTTTCAG
chr8	38275520	38275559	FGFR1_6940	+	GTGACCTATGCACCAGACGTAAACAGAGAGTGGCATAAGTTGGGGCTGGTGAAGTTCAAAGATCGGAAGAGCGGTTTCAG
chr8	38275902	38275941	FGFR1_6941	+	GTGACCTATGCACCAGACGTGAGTGGGGTCAACCCTAGAGCAAGGAGGGGGGACCGGGTGAAGATCGGAAGAGCGGTTTCAG
chr8	38277264	38277303	FGFR1_6942	+	GTGACCTATGCACCAGACGTGCGAACAGGGTGTAGCAGCCTTGGAGGCCCCGTCCATGAGATCGGAAGAGCGGTTTCAG
chr8	38279470	38279509	FGFR1_6943	+	GTGACCTATGCACCAGACGTCAACGGAAGCAAAATGGACAGCACAGGCACATGAGACCTCAGATCGGAAGAGCGGTTTCAG
chr8	38282228	38282267	FGFR1_6944	+	GTGACCTATGCACCAGACGTTGGGAGAGGAGGCACTTGTTCATGGGGACCTTGGCATGGCTAGATCGGAAGAGCGGTTTCAG
chr8	38283774	38283813	FGFR1_6945	+	GTGACCTATGCACCAGACGTATGCCAAAGGATACATTGAGGGTCCAGAGGAAAATGCAGAGATCGGAAGAGCGGTTTCAG
chr8	38285622	38285661	FGFR1_6946	+	GTGACCTATGCACCAGACGTAAAGCCAAGAGAGAGAGCCAGGGTGGAGAGGAGCAGCTGGAGATCGGAAGAGCGGTTTCAG
chr8	38285964	38286003	FGFR1_6947	+	GTGACCTATGCACCAGACGTAAAGAAAGGGGCACTGAGGTTCTCTCAGGGACCCCTAGATTAGATCGGAAGAGCGGTTTCAG
chr8	38314975	38315014	FGFR1_6948	+	GTGACCTATGCACCAGACGTGAGTTAGAGTGTGTGACAAAGTCCACATCTCCATGGATCGGAAGAGCGGTTTCAG
chrX	15364392	15364431	FIGF_6949	+	GTGACCTATGCACCAGACGTAGAAAATAAAGATGAGAATTCAGAATCAATGACTGGATTGAGATCGGAAGAGCGGTTTCAG
chrX	15365492	15365531	FIGF_6950	+	GTGACCTATGCACCAGACGTACAGAAACGTGTTGGTCAGATAGTTGTAGTGTGGCAATTGAGATCGGAAGAGCGGTTTCAG
chrX	15371301	15371340	FIGF_6951	+	GTGACCTATGCACCAGACGTAAAACAATGAACCAGATTAAAAGCTTTCAAGGATAATCAAGATCGGAAGAGCGGTTTCAG
chrX	15376326	15376365	FIGF_6952	+	GTGACCTATGCACCAGACGTAAAGAAAGCTCACTGGGGCTAGCAGGTGGAATGGTCTGGAGATCGGAAGAGCGGTTTCAG
chrX	15381452	15381491	FIGF_6953	+	GTGACCTATGCACCAGACGTCAAAAATACCAGTTGAAAACAAGTTACTAAAATTTAAATAGATCGGAAGAGCGGTTTCAG
chrX	15402079	15402118	FIGF_6954	+	GTGACCTATGCACCAGACGTTCAATATCCACTGATTACTAAAGCAGTTGACATCAGGCAGCAGATCGGAAGAGCGGTTTCAG
chr11	532766	532805	HRAS_6955	+	GTGACCTATGCACCAGACGTAGGGATGGGATCAGGAGGGACCCGGCCTGTGGCCGCTGCCAGATCGGAAGAGCGGTTTCAG
chr11	533369	533408	HRAS_6956	+	GTGACCTATGCACCAGACGTGGAGAGGGTCAGTGAAGTGTGCTGCTCCCTGGCTGGGGCGGGGAGATCGGAAGAGCGGTTTCAG
chr11	533623	533662	HRAS_6957	+	GTGACCTATGCACCAGACGTGAAAGCGAGAGCTGGCTACGGGGGCTGCAGGCACCGGCAGATCGGAAGAGCGGTTTCAG
chr11	533955	533994	HRAS_6958	+	GTGACCTATGCACCAGACGTACAGGGCTCAGGGACCCCTCAGGACCTTCCGTGGGGGGAAGATCGGAAGAGCGGTTTCAG
chr11	534333	534372	HRAS_6959	+	GTGACCTATGCACCAGACGTGGGCTGGCCCGCCGCTCCCTCAGGGTCTCCTGCCAGATCGGAAGAGCGGTTTCAG
chr15	88420362	88420401	NTRK3_6960	+	GTGACCTATGCACCAGACGTGAGAAGAACAGGATTAACCCAAAGCTCAGCCTTGGTATCGGAAGAGCGGTTTCAG



chr15	88423670	88423709	NTRK3_6961	+	GTGACCTATGCACCAGACGTTTGAGATAGAGGCCACACAGAGTGACCAGATGCCAGAAATGAGATCGGAAGAGCGGTTTCAG
chr15	88472676	88472715	NTRK3_6962	+	GTGACCTATGCACCAGACGTTGGGGAGAAGAGAGGGGGCAGAGAGAAATCAGGAGATCAAGATCGGAAGAGCGGTTTCAG
chr15	88476426	88476465	NTRK3_6963	+	GTGACCTATGCACCAGACGTTGCAGGACACAGGTGTTTAAACAACACAGGGCAGGGGGCTAGATCGGAAGAGCGGTTTCAG
chr15	88483995	88484034	NTRK3_6964	+	GTGACCTATGCACCAGACGTTGGGACAAGAGAGGGGCAGCAAATCAGTCTCGTTTGGTGAGATCGGAAGAGCGGTTTCAG
chr15	88524602	88524641	NTRK3_6965	+	GTGACCTATGCACCAGACGTAGGCAGACATGGGGGAATTAATGGTCAGTATTAACCCCAAGATCGGAAGAGCGGTTTCAG
chr15	88576287	88576326	NTRK3_6966	+	GTGACCTATGCACCAGACGTCAAGAGAGACAGGACCTGGTGACGTACATCCGGCCAGAGATCGGAAGAGCGGTTTCAG
chr15	88669615	88669654	NTRK3_6967	+	GTGACCTATGCACCAGACGTGACAAACAGAGAGTACGAAACAATCACAGAAAACCCAATAGATCGGAAGAGCGGTTTCAG
chr15	88670468	88670507	NTRK3_6968	+	GTGACCTATGCACCAGACGTAACACAAAAAGGAGGAGGACAGTTAGCTTCCCAGGCTGGGGAGATCGGAAGAGCGGTTTCAG
chr15	88671976	88672015	NTRK3_6969	+	GTGACCTATGCACCAGACGTAGGACAAAGAGATAATTAACAAATTTAATAAAAACCAAGATCGGAAGAGCGGTTTCAG
chr15	88678639	88678678	NTRK3_6970	+	GTGACCTATGCACCAGACGTAGAAACCTGCTGAAATCCAGGACACAGAGTCTACCACCTCAGATCGGAAGAGCGGTTTCAG
chr15	88679282	88679321	NTRK3_6971	+	GTGACCTATGCACCAGACGTCAATAAAAAAGATAACAAATCAGATAGCTTCTACAAGGATGGAGATCGGAAGAGCGGTTTCAG
chr15	88679851	88679890	NTRK3_6972	+	GTGACCTATGCACCAGACGTGACAAAGTGGGTGAAAAGACAGGCCAAACCTTACTACCCAAAGATCGGAAGAGCGGTTTCAG
chr15	88680803	88680842	NTRK3_6973	+	GTGACCTATGCACCAGACGTAGAGAGAGGGGAAAGGGAACCTCTGAACCCGAAGATGCCCAAGATCGGAAGAGCGGTTTCAG
chr15	88690645	88690684	NTRK3_6974	+	GTGACCTATGCACCAGACGTGACAAATAAGGGAAATTTTAAACAAGTCTGGCACAAATAGATCGGAAGAGCGGTTTCAG
chr15	88726731	88726770	NTRK3_6975	+	GTGACCTATGCACCAGACGTAGAAAAAGAGGATCAGCAGAGCTCAAGTGGCAGAGGGGATAAGATCGGAAGAGCGGTTTCAG
chr11	32410736	32410775	WT1_6976	+	GTGACCTATGCACCAGACGTAATTTGCCAGTCAGACACTTGCAACAAGAGACAGGCACAGATCGGAAGAGCGGTTTCAG
chr11	32413621	32413660	WT1_6977	+	GTGACCTATGCACCAGACGTAGAAAGAGGTCTAGCCTCGGCCCTAAACATGTGGCCACAGTAGATCGGAAGAGCGGTTTCAG
chr11	32414312	32414351	WT1_6978	+	GTGACCTATGCACCAGACGTACACATATTTCTTAAATGATACTGTGAAAAGGGGATCAGATCGGAAGAGCGGTTTCAG
chr11	32417964	32418003	WT1_6979	+	GTGACCTATGCACCAGACGTAGAGTAAGAGGAAGGGAGGCTTTAAGCCACATGTGAACATAGATCGGAAGAGCGGTTTCAG
chr11	32421601	32421640	WT1_6980	+	GTGACCTATGCACCAGACGTAAGAAGGGAAAAAGGCTCAGTGTGGCTCACAGTCGCCATAGATCGGAAGAGCGGTTTCAG
chr11	32438097	32438136	WT1_6981	+	GTGACCTATGCACCAGACGTAGAAAGAGGTGGGGAGTGGGGAATGGAGCATGCATGGATCTAGATCGGAAGAGCGGTTTCAG
chr11	32439211	32439250	WT1_6982	+	GTGACCTATGCACCAGACGTAACATCTAGAGTTAGAAACATAACCCAAAAATAACAAGATCGGAAGAGCGGTTTCAG
chr11	32449615	32449654	WT1_6983	+	GTGACCTATGCACCAGACGTAACCGAAGACGCTGACGAGTGCGCCCCAAAGGCTCGGGAGATCGGAAGAGCGGTTTCAG
chr11	32450176	32450215	WT1_6984	+	GTGACCTATGCACCAGACGTAGCGGAGAGAGGAGCGAGTGCACGCTGCTCTCCGAAGACAGATCGGAAGAGCGGTTTCAG
chr11	32456902	32456941	WT1_6985	+	GTGACCTATGCACCAGACGTTCCAGGATCGCGGCGAGGAGACGGCGGGGCCCGGCCCTAGATCGGAAGAGCGGTTTCAG
chr11	32456579	32456618	WT1_6986	+	GTGACCTATGCACCAGACGTCCGGCGCCCACTGCGCCGCGCCGCTCACAGGCAGGGCACAAAGATCGGAAGAGCGGTTTCAG
chr1	22405087	22405126	CDC42_6987	+	GTGACCTATGCACCAGACGTAGGCTTCTCTGTAGTAAATGTTGTAATTTTGATATAGATCGGAAGAGCGGTTTCAG
chr1	22408298	22408337	CDC42_6988	+	GTGACCTATGCACCAGACGTAATGCTTTTTATACTGTTTTGATCTTTAACAGTTGCTAGTAGATCGGAAGAGCGGTTTCAG
chr1	22413052	22413091	CDC42_6989	+	GTGACCTATGCACCAGACGTAGATCTTCCCTAAGAAGATCATCTCAGAATTTAAGATCGGAAGAGCGGTTTCAG
chr1	22413370	22413409	CDC42_6990	+	GTGACCTATGCACCAGACGTCATGAAACCCCATGTGTATTATTTAGTCTCAGTCAATTTAAGATCGGAAGAGCGGTTTCAG
chr1	22416536	22416575	CDC42_6991	+	GTGACCTATGCACCAGACGTCCTTCCCTTCTTTGCTGCTGCTTCTGTCCTTCTGTCCTTCTGTAAGATCGGAAGAGCGGTTTCAG
chr1	22418021	22418060	CDC42_6992	+	GTGACCTATGCACCAGACGTAGAGCCCTTCTGTCACAGCTGGTGTGGCCTCATACTAAAAGATCGGAAGAGCGGTTTCAG
chr8	118812147	118812186	EXT1_6993	+	GTGACCTATGCACCAGACGTGGAGAGAAACAAGGATAATGATGAGAGAAAGTGAAGGTGAAGATCGGAAGAGCGGTTTCAG
chr8	118817143	118817182	EXT1_6994	+	GTGACCTATGCACCAGACGTCAAAAGTGGGTTTTCACAGGGGGCCATTATCACATGATGACAGATCGGAAGAGCGGTTTCAG
chr8	118819627	118819666	EXT1_6995	+	GTGACCTATGCACCAGACGTAACCAACAAGCCAAACGAAAGTGTAAACAATGTAGATCGGAAGAGCGGTTTCAG
chr8	118825211	118825250	EXT1_6996	+	GTGACCTATGCACCAGACGTGTAAGAGTAGGACGTTGGGAGGGAATGAGGGAAAGAGGTAAGATCGGAAGAGCGGTTTCAG
chr8	118830780	118830819	EXT1_6997	+	GTGACCTATGCACCAGACGTTGGGCTCATTAGATGGCTGGGGTAGGATGTATTTATGAAGATCGGAAGAGCGGTTTCAG
chr8	118832044	118832083	EXT1_6998	+	GTGACCTATGCACCAGACGTAAGGAGAGTAGAGCCCTAATGAAGCGCTGGAAGCAAGACTAGATCGGAAGAGCGGTTTCAG
chr8	118834847	118834886	EXT1_6999	+	GTGACCTATGCACCAGACGTAACATAGCACACAGTGAAGGATGAGATCCTGATGATATTTAGATCGGAAGAGCGGTTTCAG
chr8	118842599	118842638	EXT1_7000	+	GTGACCTATGCACCAGACGTAGGTGAACACATAGGAATATAACTGTAAAAACAAGAGATAGATCGGAAGAGCGGTTTCAG
chr8	118847801	118847840	EXT1_7001	+	GTGACCTATGCACCAGACGTAAGGGGACTTCTGTAATGTGAGAAAGCGACAGACAGATCGGAAGAGCGGTTTCAG
chr8	118849451	118849490	EXT1_7002	+	GTGACCTATGCACCAGACGTAAGAGGAGTAAACAGCAAATGAAGACTCATTGCGAATGTGAGATCGGAAGAGCGGTTTCAG
chr8	119123296	119123335	EXT1_7003	+	GTGACCTATGCACCAGACGTTGGGTCAAGAGGATTGTAATAAACACAAGAATCACCCAAAGATCGGAAGAGCGGTTTCAG
chr8	119122815	119122854	EXT1_7004	+	GTGACCTATGCACCAGACGTACTCAGGACAAAGAGGCACGCTGGCTGGGGTCCGAGGTGAGATCGGAAGAGCGGTTTCAG
chr6	108883043	108883082	FOXO3_7005	+	GTGACCTATGCACCAGACGTAACCCGGGCTGGCAGCAGGACCCCGGGCCTCCGCGCAAGATCGGAAGAGCGGTTTCAG
chr6	108986069	108986108	FOXO3_7006	+	GTGACCTATGCACCAGACGTAGGAAAGGGGAAGTGGGCAAGAGCGTCAAGTCCGGAATGCTAGATCGGAAGAGCGGTTTCAG
chr6	108882732	108882771	FOXO3_7007	+	GTGACCTATGCACCAGACGTCCCCGGGTCTGGGCCAGCCACCAGCCGGCGGGCGGGCTGAGCAGATCGGAAGAGCGGTTTCAG
chr6	108985135	108985174	FOXO3_7008	+	GTGACCTATGCACCAGACGTTCCACGGCTGACTGATATGGCAGGCACCATGAATCTGAATGAGATCGGAAGAGCGGTTTCAG
chr6	108985602	108985641	FOXO3_7009	+	GTGACCTATGCACCAGACGTGCCAACCAGGGAAGTTTGGTCAATCAGAACTTCTCCACAGATCGGAAGAGCGGTTTCAG
chr1	204499956	204499995	MDM4_7010	+	GTGACCTATGCACCAGACGTTGATGGGCTTGCATCTTTTTGGTGGCTTATACCTAACCAAGATCGGAAGAGCGGTTTCAG
chr1	204501385	204501424	MDM4_7011	+	GTGACCTATGCACCAGACGTTTCATTTCTCAGTCTGATCACAGCTTTGAGTTCAAGGAGATCGGAAGAGCGGTTTCAG
chr1	204506636	204506675	MDM4_7012	+	GTGACCTATGCACCAGACGTCACAGCGTGATCTCTTTTGTGTTACAGATGGCCCTTCTAGATCGGAAGAGCGGTTTCAG
chr1	204507447	204507486	MDM4_7013	+	GTGACCTATGCACCAGACGTGATTAAGGCTATATAGACTTTTTGTTCTTCTTCTTCCAAAGATCGGAAGAGCGGTTTCAG
chr1	204512083	204512122	MDM4_7014	+	GTGACCTATGCACCAGACGTCATTTGAAGGGAAGTGGTTTTTTTTCTTTTGAAGGGTAAAGATCGGAAGAGCGGTTTCAG
chr1	204513823	204513862	MDM4_7015	+	GTGACCTATGCACCAGACGTGAAAAATCCATGTTGATTCTGTTGTGTGCTCATAGTATAGATCGGAAGAGCGGTTTCAG
chr1	204516016	204516055	MDM4_7016	+	GTGACCTATGCACCAGACGTTTAGCAAGAACTTTTGCACCAGCCCATCTTCAGATGAAGATCGGAAGAGCGGTTTCAG
chr1	204518821	204518860	MDM4_7017	+	GTGACCTATGCACCAGACGTAACATAAAAAATCATTTTTCCGTTTCACTTACCACATATAGATCGGAAGAGCGGTTTCAG
chr1	204518536	204518575	MDM4_7018	+	GTGACCTATGCACCAGACGTTCTGAAAAGCCAAAGACCATCTCAAGCATGGGAGAACAAGATCGGAAGAGCGGTTTCAG

chr7	538222	538261	PDGFA_7019	+	GTGACCTATGCACCAGACGTAAGGGAAAGACAGACACTGAGACCACCGACCAAGTGAACCAGATCGGAAGAGCGGTTTCAG
chr7	540147	540186	PDGFA_7020	+	GTGACCTATGCACCAGACGTAAGGGCAGGGCCGTGAGTGGGCCGAGGGACGGCCGTCGGGAGATCGGAAGAGCGGTTTCAG
chr7	540890	540929	PDGFA_7021	+	GTGACCTATGCACCAGACGTAACAGAGCCCGCCATGAATGCCTGCATGGAGCTTCGGAAGATCGGAAGAGCGGTTTCAG
chr7	550644	550683	PDGFA_7022	+	GTGACCTATGCACCAGACGTGGGGGCACAGTGAGCGGGGACCGCCCTCTGCGACCACGGCAGATCGGAAGAGCGGTTTCAG
chr7	552103	552142	PDGFA_7023	+	GTGACCTATGCACCAGACGTAAGGAGAACCCTGTAATGCCCCAGCCCGTGCCTGTGCAGATCGGAAGAGCGGTTTCAG
chr7	558649	558688	PDGFA_7024	+	GTGACCTATGCACCAGACGTGGCGCTGGCTGCTCGGAGGAGAGCGGCGGGCGGGAGATCGGAAGAGCGGTTTCAG
chr7	6013184	6013223	PMS2_7025	+	GTGACCTATGCACCAGACGTGACACCAATGGTTCACCGTTTTAGTACTTTTTGACGTCAGAGATCGGAAGAGCGGTTTCAG
chr7	6017439	6017438	PMS2_7026	+	GTGACCTATGCACCAGACGTACAAATTTTTGAGAAAAATCCATGACTTGACAAAACGTTTTTCAGATCGGAAGAGCGGTTTCAG
chr7	6018338	6018377	PMS2_7027	+	GTGACCTATGCACCAGACGTCAAAAATGATTCACAAACCATATCCTGAAGTCAAACATTTAGAGATCGGAAGAGCGGTTTCAG
chr7	6022633	6022672	PMS2_7028	+	GTGACCTATGCACCAGACGTAAAATGTTAATTATCAGACATTTTACAAGATTATTTTTCTAGATCGGAAGAGCGGTTTCAG
chr7	6027262	6027301	PMS2_7029	+	GTGACCTATGCACCAGACGTGTGGACCGGAGAGAGGGTCAGGGACTATCCTGAAATGGTGAGATCGGAAGAGCGGTTTCAG
chr7	6031699	6031738	PMS2_7030	+	GTGACCTATGCACCAGACGTTACAAGGAGTAGAAAAGATAAATGACAAATGTTCCAGCAGATCGGAAGAGCGGTTTCAG
chr7	6035275	6035314	PMS2_7031	+	GTGACCTATGCACCAGACGTTTAAATGTTAAGGGCAGGATTCAGAGTGAAAGGGATTAGATCGGAAGAGCGGTTTCAG
chr7	6037065	6037104	PMS2_7032	+	GTGACCTATGCACCAGACGTAAAAAAAATTACAGTTACTTCTAATAAAGACAGAGTAGATCGGAAGAGCGGTTTCAG
chr7	6038917	6038956	PMS2_7033	+	GTGACCTATGCACCAGACGTAAACAAAAACAATATCTACATTACTTTAATATATAGGAGATCGGAAGAGCGGTTTCAG
chr7	6042278	6042317	PMS2_7034	+	GTGACCTATGCACCAGACGTATACCAGCATGGTGTGTTCAGTGAGAGACCCATGATGTTAGATCGGAAGAGCGGTTTCAG
chr7	6043473	6043473	PMS2_7035	+	GTGACCTATGCACCAGACGTGTAAAGTAAGGACTAAGATATCTCAAGTGTCTATAACAAAGATCGGAAGAGCGGTTTCAG
chr7	6045673	6045712	PMS2_7036	+	GTGACCTATGCACCAGACGTCAGTTTAAAGAAAACAATCAAGTATTCAGCTATATATTTAGATCGGAAGAGCGGTTTCAG
chr7	6048661	6048700	PMS2_7037	+	GTGACCTATGCACCAGACGTCCCAGTCCGCCTCGGGGACTGGGAAAGTTCCTCCAGGGCAGATCGGAAGAGCGGTTTCAG
chr7	6026831	6026870	PMS2_7038	+	GTGACCTATGCACCAGACGTCTGGCCGATACTCGTGTGCTGCACTGACTGCCCGTGTCTGAGATCGGAAGAGCGGTTTCAG
chr21	36164918	36164957	RUNX1_7039	+	GTGACCTATGCACCAGACGTGGCAAGAGAACGGAGCGGAAGTGAGTAGGAGGTTGCGGAGAGATCGGAAGAGCGGTTTCAG
chr21	36171770	36171809	RUNX1_7040	+	GTGACCTATGCACCAGACGTTCAAAAAGTCAATTATATGTAAGTGGGGTGGGATTTAAAGATCGGAAGAGCGGTTTCAG
chr21	36194004	36194043	RUNX1_7041	+	GTGACCTATGCACCAGACGTGATGTGACCAGGGGAAAAGTTCGAAAATAAGGACAATTAGATCGGAAGAGCGGTTTCAG
chr21	36231886	36231925	RUNX1_7042	+	GTGACCTATGCACCAGACGTACGTATGGTAAGAACAAAACAGAAATGAGTTGGTGGCTGAACAGATCGGAAGAGCGGTTTCAG
chr21	36253021	36253060	RUNX1_7043	+	GTGACCTATGCACCAGACGTGTCAAAGGACAAAATGCAGACATCAGGGATGTTATACATACAGATCGGAAGAGCGGTTTCAG
chr21	36259404	36259443	RUNX1_7044	+	GTGACCTATGCACCAGACGTACGCATCACAACAAGCCGATTGAGTTAGGACCTGCAACAGATCGGAAGAGCGGTTTCAG
chr21	36259420	36259459	RUNX1_7045	+	GTGACCTATGCACCAGACGTGATTTAGTTAGTACCCTGCAAAACAGCTCCTACCAGACGGAGATCGGAAGAGCGGTTTCAG
chr21	36265271	36265310	RUNX1_7046	+	GTGACCTATGCACCAGACGTAGAAAAGTAGAAAATAAAGTAATGCAAGTTTAAAAATTAAGATCGGAAGAGCGGTTTCAG
chr21	36421207	36421246	RUNX1_7047	+	GTGACCTATGCACCAGACGTTGAAAATGCACCCTCTTCTGAAGCGGGGACTCAATGATAGATCGGAAGAGCGGTTTCAG
chr3	10183882	10183921	VHL_7048	+	GTGACCTATGCACCAGACGTGGCGCTTACGCCCTGAGCCGAGCAGCGATAGCACGGTCTAGATCGGAAGAGCGGTTTCAG
chr3	10188331	10188370	VHL_7049	+	GTGACCTATGCACCAGACGTTTACTTTTTAAAAAGATAAGTTGTTGTGGTAAGTACAGAGATCGGAAGAGCGGTTTCAG
chr3	10191660	10191699	VHL_7050	+	GTGACCTATGCACCAGACGTTGAAACTTACACTGTTTCATCTCAGCTTTTGATGGTACTGAGATCGGAAGAGCGGTTTCAG
chr8	30916070	30916109	WRN_7051	+	GTGACCTATGCACCAGACGTCAATTGACTATTTCTTTGGGTGAGAAATTAATTTATATTTAGATCGGAAGAGCGGTTTCAG
chr8	30916792	30916831	WRN_7052	+	GTGACCTATGCACCAGACGTTGAATTTCTGATTTATTTGAAATTTGGACCCTTAGAAGGAGATCGGAAGAGCGGTTTCAG
chr8	30921961	30922000	WRN_7053	+	GTGACCTATGCACCAGACGTTCACTTACTTTTATTTATGTTGATGTAATTTGTAATATGTCAGATCGGAAGAGCGGTTTCAG
chr8	30922590	30922629	WRN_7054	+	GTGACCTATGCACCAGACGTTATATATATAATTTTCATGATGAAGATTATTTTGTGTTACAGATCGGAAGAGCGGTTTCAG
chr8	30924709	30924748	WRN_7055	+	GTGACCTATGCACCAGACGTAAGATCTTTAGAAATTTGATGTGTTTTAAAAACATTATAGATCGGAAGAGCGGTTTCAG
chr8	30925854	30925893	WRN_7056	+	GTGACCTATGCACCAGACGTATCCATAAATAAAATGTGAATTCACCTTTTTGTGAGGTTTAGATCGGAAGAGCGGTTTCAG
chr8	30933814	30933853	WRN_7057	+	GTGACCTATGCACCAGACGTACCTTTTTTTTTTAACTTAAATCAATCTGTTTATTTAGATCGGAAGAGCGGTTTCAG
chr8	30941306	30941345	WRN_7058	+	GTGACCTATGCACCAGACGTAATATAAAAAATTAATCTCAAGTCTTTTCAAAGGACATAGATCGGAAGAGCGGTTTCAG
chr8	30942773	30942812	WRN_7059	+	GTGACCTATGCACCAGACGTAATTATAAAAAACATTACTTCAAGTCTTTTCAAAGGACATAGATCGGAAGAGCGGTTTCAG
chr8	30945447	30945486	WRN_7060	+	GTGACCTATGCACCAGACGTAAGTATGTTTTGAAATGACTCACCTGTGATACCTACCCTGAGATCGGAAGAGCGGTTTCAG
chr8	30946492	30946531	WRN_7061	+	GTGACCTATGCACCAGACGTTCTCATTTAATCAAATCACATATTTAGTATCTCTTTAAAAGATCGGAAGAGCGGTTTCAG
chr8	30948059	30948098	WRN_7062	+	GTGACCTATGCACCAGACGTTTAAAGCAAACCTAATCCTTTAAAAAATAAAAACATAAAAGATCGGAAGAGCGGTTTCAG
chr8	30948469	30948508	WRN_7063	+	GTGACCTATGCACCAGACGTTTATCTTGGCACAATATCACCTCTTTTTTCTCTGTGAGATCGGAAGAGCGGTTTCAG
chr8	30954377	30954416	WRN_7064	+	GTGACCTATGCACCAGACGTTAAGAAAGTCTCTGTAATACTTACTGATTAATATTAAAGATCGGAAGAGCGGTTTCAG
chr8	30958482	30958521	WRN_7065	+	GTGACCTATGCACCAGACGTCAAAGTCTGATGTCCCGAAATTAATCTTAATAAAGGAGAAGATCGGAAGAGCGGTTTCAG
chr8	30969326	30969365	WRN_7066	+	GTGACCTATGCACCAGACGTAATGGTGTGATGAAATTTGGTAAATGATTTCTTTTTTTTTTAGATCGGAAGAGCGGTTTCAG
chr8	30974055	30974094	WRN_7067	+	GTGACCTATGCACCAGACGTCAATCATCATTTGCTCTCCGTTGCTCATAGTGAAGTGATAGATCGGAAGAGCGGTTTCAG
chr8	30977951	30977990	WRN_7068	+	GTGACCTATGCACCAGACGTTTTATTGTTTTACTCTTGACAGATTTCTTTCTTTCCAGATCGGAAGAGCGGTTTCAG
chr8	30982150	30982189	WRN_7069	+	GTGACCTATGCACCAGACGTTTATTTATGCCAATAGTATGGATTTATGGATGATCTCAGATCGGAAGAGCGGTTTCAG
chr8	30982527	30982566	WRN_7070	+	GTGACCTATGCACCAGACGTTTATTTATAGATGGACATTCGTAAGAATCTTTCTTTCTTTCTTAGATCGGAAGAGCGGTTTCAG
chr8	30990033	30990072	WRN_7071	+	GTGACCTATGCACCAGACGTATCTGTGAATCCCTTCATAGATCTTCTTTTACTTCTATTAGATCGGAAGAGCGGTTTCAG
chr8	30999127	30999166	WRN_7072	+	GTGACCTATGCACCAGACGTTAGGAGTCTGCCTGTTGACTTAAATTTGTTTCCCCTCCAGATCGGAAGAGCGGTTTCAG
chr8	30999302	30999341	WRN_7073	+	GTGACCTATGCACCAGACGTCAAGTTTTTTTCTTTGAACTTCTGCATTTTTTTGTTGCTATTAGATCGGAAGAGCGGTTTCAG
chr8	31000228	31000267	WRN_7074	+	GTGACCTATGCACCAGACGTAAGAAATTTGTTCTGATTTATTTCACTTTTATTGATTCAAAGATCGGAAGAGCGGTTTCAG
chr8	31001150	31001189	WRN_7075	+	GTGACCTATGCACCAGACGTCTAATTTCTATTCTTACTTGTATAGACTTTTTAGATCGGAAGAGCGGTTTCAG
chr8	31004655	31004694	WRN_7076	+	GTGACCTATGCACCAGACGTTGAAAAAGGTAATTAGTTTATGATAGGATGTTATGATTAGATCGGAAGAGCGGTTTCAG

chr8	31005003	31005042	WRN_7077	+	GTGACCTATGCACCAGACGTTTTTTGCATGTGTTCTATTTATTTCCCTCTAACAAAAATAAGAATCGGAAGAGCGGTTTCAG
chr8	31007982	31008021	WRN_7078	+	GTGACCTATGCACCAGACGTTGGTTTTGCAGGAGCTCTTAGAGAATAAGCATTTTTTGTAAAGATCGGAAGAGCGGTTTCAG
chr8	31012282	31012321	WRN_7079	+	GTGACCTATGCACCAGACGTTTTCATGTTTACAGGGAATTTTTTTAGTTTACTTAAACTTAGATCGGAAGAGCGGTTTCAG
chr8	31015057	31015096	WRN_7080	+	GTGACCTATGCACCAGACGTTGGCCTAGCTCTGCACCCTAATGACTTGATGAAGTAAACAGATCGGAAGAGCGGTTTCAG
chr8	31024757	31024796	WRN_7081	+	GTGACCTATGCACCAGACGTTATATAGAATTTTCATAAAGTGCAGTGTGTTCAATTTGCAGATCGGAAGAGCGGTTTCAG
chr8	31030629	31030668	WRN_7082	+	GTGACCTATGCACCAGACGTACCAACAATATGTTTCTTGCTGTATTATAAGAGGATAAGATCGGAAGAGCGGTTTCAG
chr2	29419737	29419776	ALK_7083	+	GTGACCTATGCACCAGACGTTAATTAATAAATAAGGAGAAGCAACAATGATGAAAAGATCGGAAGAGCGGTTTCAG
chr2	29430149	29430188	ALK_7084	+	GTGACCTATGCACCAGACGTTGGAGAGGAAAACAACTAGGATCTGGAGATGGCATTAAAGATCGGAAGAGCGGTTTCAG
chr2	29432755	29432794	ALK_7085	+	GTGACCTATGCACCAGACGTAGGAAATGCATTTCTAATTTTTATCCCTAGGAAGATGAGTAGATCGGAAGAGCGGTTTCAG
chr2	29436958	29436997	ALK_7086	+	GTGACCTATGCACCAGACGTACAGAAGCGGGCCACTGACGAGGAGCTTGTCACTGAGAGGAGATCGGAAGAGCGGTTTCAG
chr2	29443712	29443751	ALK_7087	+	GTGACCTATGCACCAGACGTGAGAGGGATGTAACCAAAATTAAGTACTGAGCTGAGTCTGGGCAGATCGGAAGAGCGGTTTCAG
chr2	29445285	29445324	ALK_7088	+	GTGACCTATGCACCAGACGTAAGGGGAGGGTGGGGAGGAGGAGGCTGTGAGCTGAGAAGATCGGAAGAGCGGTTTCAG
chr2	29445484	29445523	ALK_7089	+	GTGACCTATGCACCAGACGTGAGAAGACAAGAGGAGACAGAGTCAAACAGGCCACAATAAAGATCGGAAGAGCGGTTTCAG
chr2	29446405	29446444	ALK_7090	+	GTGACCTATGCACCAGACGTGTTGTCAGCTGCAACATGGCCTGGCAGCCTGGCCCTTGAAAGATCGGAAGAGCGGTTTCAG
chr2	29448442	29448481	ALK_7091	+	GTGACCTATGCACCAGACGTGGTCCCCTGGGGTATTGACAACCACACAGGTTCTCTTTAGATCGGAAGAGCGGTTTCAG
chr2	29449951	29449990	ALK_7092	+	GTGACCTATGCACCAGACGTGGAGGGAGGGTAGCTTTGGGCCAGCCTGCCTCCCCACTAGATCGGAAGAGCGGTTTCAG
chr2	29450549	29450588	ALK_7093	+	GTGACCTATGCACCAGACGTAAACAGACAGAGTTAATACGTGGGGGGTGGGTGCCAAAATAGATCGGAAGAGCGGTTTCAG
chr2	29451943	29451982	ALK_7094	+	GTGACCTATGCACCAGACGTAGTAGGGCAACCTGCGTGAGGATCTGGCAAAGTTCAATTAGATCGGAAGAGCGGTTTCAG
chr2	29455325	29455364	ALK_7095	+	GTGACCTATGCACCAGACGTGAGACATTCAGACATTGAGAAACCAGCTGTGCTTCCCCAGATCGGAAGAGCGGTTTCAG
chr2	29456573	29456612	ALK_7096	+	GTGACCTATGCACCAGACGTAAAAAGCACGTTAGGTTTGTGGCCAAACCAGAGTTTCCAAAGATCGGAAGAGCGGTTTCAG
chr2	29462707	29462746	ALK_7097	+	GTGACCTATGCACCAGACGTACAAGAAGCCTTGGCTCCCCTGTGTATGAAGACTGTCCAGATCGGAAGAGCGGTTTCAG
chr2	29474144	29474183	ALK_7098	+	GTGACCTATGCACCAGACGTAGAGGAGAGGCAGTCACTCATGTGGCCAGGCCCTCCCTCCAGATCGGAAGAGCGGTTTCAG
chr2	29498104	29498143	ALK_7099	+	GTGACCTATGCACCAGACGTGAAGACCCACGGGCTGAGTTAGGTGAGGGTTGATTTAGATCGGAAGAGCGGTTTCAG
chr2	29498373	29498412	ALK_7100	+	GTGACCTATGCACCAGACGTGAGAAGGAATGTTGTGAGGAGCAAACCTGGGGGCTTGTGATCGGAAGAGCGGTTTCAG
chr2	29519934	29519973	ALK_7101	+	GTGACCTATGCACCAGACGTGAGAAGAGTCAAGAGGACAAGGTATGATTGCTGAAAGGTCCAGATCGGAAGAGCGGTTTCAG
chr2	29541281	29541320	ALK_7102	+	GTGACCTATGCACCAGACGTGGAAAAGAATCACAAAGCACGCCATTATCAGGAACCTGGGGGAGATCGGAAGAGCGGTTTCAG
chr2	29543759	29543798	ALK_7103	+	GTGACCTATGCACCAGACGTAGCAGAGAGGCACCATCATTTTTCAGGACCACTAAAGGCCAAAGATCGGAAGAGCGGTTTCAG
chr2	29551358	29551397	ALK_7104	+	GTGACCTATGCACCAGACGTACAGACACACACCAATGGTAAGTTTGCATGGCCCCAGGCAGATCGGAAGAGCGGTTTCAG
chr2	29606736	29606775	ALK_7105	+	GTGACCTATGCACCAGACGTGGAAAACAGAGGAGAAACATAGAAACAGATGAGAGATCGGAAGAGCGGTTTCAG
chr2	29754993	29755032	ALK_7106	+	GTGACCTATGCACCAGACGTACAGGGAAAACGAATCCAGATGTGTTCCAGGTAAGACCAAGATCGGAAGAGCGGTTTCAG
chr2	29917891	29917930	ALK_7107	+	GTGACCTATGCACCAGACGTAGCCAAGGGTCAATGGAAAACCATTTCCAAACGTGACAGATCGGAAGAGCGGTTTCAG
chr2	29940574	29940613	ALK_7108	+	GTGACCTATGCACCAGACGTAAATAAAGAAAACACTGATCCATGTGCTTGGGGTGTGTCTAGATCGGAAGAGCGGTTTCAG
chr2	30143536	30143575	ALK_7109	+	GTGACCTATGCACCAGACGTGAGGGCCGTTTACACTGCTCTCCGGGCCAGCCCTCACCTTAGATCGGAAGAGCGGTTTCAG
chr2	29416449	29416488	ALK_7110	+	GTGACCTATGCACCAGACGTAGCTGGTGGCTTGTTCCTGGATCCGTTGACCTTTGTGCAAAAGATCGGAAGAGCGGTTTCAG
chr2	30143202	30143241	ALK_7111	+	GTGACCTATGCACCAGACGTGACCCCGGGCTGACCAGCAACTGAGCAGCGGGGCGAGATCGGAAGAGCGGTTTCAG
chrX	66766615	66766654	AR_7112	+	GTGACCTATGCACCAGACGTCTTCCAGAAATGTCGCCCTTTCGGCCCAGGGCAGAGTACAGATCGGAAGAGCGGTTTCAG
chrX	66788875	66788914	AR_7113	+	GTGACCTATGCACCAGACGTCTTCAATTGAAAACCTAGAAGTCAAGTTCTAGGGTAGTGAAGATCGGAAGAGCGGTTTCAG
chrX	66863260	66863299	AR_7114	+	GTGACCTATGCACCAGACGTTTGCACATGCACCTCTCTTTCCCTTTCTCCTTTACCTTCCAGATCGGAAGAGCGGTTTCAG
chrX	66937475	66937514	AR_7115	+	GTGACCTATGCACCAGACGTTCTGGGGCCAGACCTCACTAAATACAGCAGCTTGGCCAGAGATCGGAAGAGCGGTTTCAG
chrX	66941816	66941855	AR_7116	+	GTGACCTATGCACCAGACGTAGAAGTGCAGGGAAATCCCCCCTGAGGCACAGAGATTCAGAGATCGGAAGAGCGGTTTCAG
chrX	66942837	66942876	AR_7117	+	GTGACCTATGCACCAGACGTGATGGAGGCTTCTATACAGGGAGAACAAGCCTGATAGAGCAGATCGGAAGAGCGGTTTCAG
chrX	66943694	66943733	AR_7118	+	GTGACCTATGCACCAGACGTACCCTATTTCCACCCACAGCTCATGCCCTTTCAGATGAGATCGGAAGAGCGGTTTCAG
chrX	66765403	66765442	AR_7119	+	GTGACCTATGCACCAGACGTGTGGCCGCCAGCAAGGGGCTGCCGACAGCTGCCAGCACAGATCGGAAGAGCGGTTTCAG
chrX	66765807	66765846	AR_7120	+	GTGACCTATGCACCAGACGTGGGAGTTCACCCCGCTGTGCGTCCCACCTTGTGCCCAAGATCGGAAGAGCGGTTTCAG
chrX	66766211	66766250	AR_7121	+	GTGACCTATGCACCAGACGTTGGGACCTGGCGAGCCTGCATGCGCGGGTGCAGCGGGAGATCGGAAGAGCGGTTTCAG
chr1	51436180	51436219	CDKN2C_7122	+	GTGACCTATGCACCAGACGTAGAGAGTGGGGAGCACTGATCAATAATGTTGCCATCGTGAGATCGGAAGAGCGGTTTCAG
chr1	51439953	51439992	CDKN2C_7123	+	GTGACCTATGCACCAGACGTGGCTCCCCACGTTGCTCTACTTTATCAATTAAGTATGATCGGAAGAGCGGTTTCAG
chr11	125496739	125496778	CHEK1_7124	+	GTGACCTATGCACCAGACGTTTAAGCTTGCCTTCTGTTTTCTGAGTGCATATTCATTGTTTAGATCGGAAGAGCGGTTTCAG
chr11	125499202	125499241	CHEK1_7125	+	GTGACCTATGCACCAGACGTTTGTCTATTTCCCTTTACTTAAATTAGAGTGAATACATAGATCGGAAGAGCGGTTTCAG
chr11	125503257	125503296	CHEK1_7126	+	GTGACCTATGCACCAGACGTTTAAATCATGGTAAACTCCTATAAAAAGTCAGATTAGTTAGATCGGAAGAGCGGTTTCAG
chr11	125505439	125505478	CHEK1_7127	+	GTGACCTATGCACCAGACGTTATCTTGTGAGTGAAGAGTACCAATTTCTTGGATGAAAGTATGATCGGAAGAGCGGTTTCAG
chr11	125507450	125507489	CHEK1_7128	+	GTGACCTATGCACCAGACGTTAAACTCAAGTTTGTGTTTTTCTGTGGAAGAAAAGTATGATCGGAAGAGCGGTTTCAG
chr11	125513806	125513845	CHEK1_7129	+	GTGACCTATGCACCAGACGTTAAAGATTGAGTAGTTTTGATTGTAGTATCCCCATGAAAGATCGGAAGAGCGGTTTCAG
chr11	125514174	125514213	CHEK1_7130	+	GTGACCTATGCACCAGACGTTAATTTTTTAAAGTAATGGCAGCTCTTATTTTTTATTAGATCGGAAGAGCGGTTTCAG
chr11	125514549	125514588	CHEK1_7131	+	GTGACCTATGCACCAGACGTTTGAATTTTCATTATACCTTTTCTGAAGAAGAAATTAATAGATCGGAAGAGCGGTTTCAG
chr11	125523753	125523792	CHEK1_7132	+	GTGACCTATGCACCAGACGTTGTTTTATTGATTCTTTCTATGGAAATATTTCTATGAAAGATCGGAAGAGCGGTTTCAG
chr11	125525226	125525265	CHEK1_7133	+	GTGACCTATGCACCAGACGTGGCTGGGGAATCTGTGAAATATAGTGTCTGCTATGTTAGATCGGAAGAGCGGTTTCAG
chr22	29083985	29084024	CHEK2_7134	+	GTGACCTATGCACCAGACGTAGGAAAATGGAGAAATGTTCAAAGAAAATCACTGGCTTCAGATCGGAAGAGCGGTTTCAG

chr22	29085214	29085253	CHEK2_7135	+	GTGACCTATGCACCAGACGTATTAATAAACATAAGTAGCTGTGTCTGAAGGATAATAAACTAGATCGGAAGAGCGGTTTCAG
chr22	29090116	29090155	CHEK2_7136	+	GTGACCTATGCACCAGACGTAATTGGGCAAAATCACAGTGAAAAGGATAAAATATATTATCAAGATCGGAAGAGCGGTTTCAG
chr22	29091241	29091280	CHEK2_7137	+	GTGACCTATGCACCAGACGTGTAGAGAGAGAAGGAAAAGAAATCAAGTGGCATTCTCAGAGATCGGAAGAGCGGTTTCAG
chr22	29091872	29091911	CHEK2_7138	+	GTGACCTATGCACCAGACGTGTACAAAAGGGGAATAATGTTGAACCTGCCATAAAAATAAAAAGATCGGAAGAGCGGTTTCAG
chr22	29092986	29093025	CHEK2_7139	+	GTGACCTATGCACCAGACGTAGGCAGGCATGACCCTCAGATTTCATGCAGTAGATACTTAAAGATCGGAAGAGCGGTTTCAG
chr22	29095936	29095975	CHEK2_7140	+	GTGACCTATGCACCAGACGTAAAGCAAGGCAAGGGGTTTCATTCCTGGGGGAAAACCGCACTAGATCGGAAGAGCGGTTTCAG
chr22	29099565	29099604	CHEK2_7141	+	GTGACCTATGCACCAGACGTGGGGAGAAAAGGGGAAAGTAGTGAGAAAACCTCCAAGAGGAGATCGGAAGAGCGGTTTCAG
chr22	29106058	29106097	CHEK2_7142	+	GTGACCTATGCACCAGACGTGAGAATAACAGAGTTTTATTAGTAATAATAATTGCCAATATAGATCGGAAGAGCGGTTTCAG
chr22	29108016	29108055	CHEK2_7143	+	GTGACCTATGCACCAGACGTAAACAAAGATAGTGATTGTCTGAATGTTTTTAATTATGAGAGATCGGAAGAGCGGTTTCAG
chr22	29115484	29115523	CHEK2_7144	+	GTGACCTATGCACCAGACGTAAAGAGTAGAAAATGGGTTTTATTAAATTTATTACAAGAGGAGATCGGAAGAGCGGTTTCAG
chr22	29121123	29121162	CHEK2_7145	+	GTGACCTATGCACCAGACGTGAACATTTTTGTTTCAGACTTTGAATAGCAGAGATTTATAGAGATCGGAAGAGCGGTTTCAG
chr22	29121366	29121405	CHEK2_7146	+	GTGACCTATGCACCAGACGTAAAGCATGCATCAGAGGGCTGTTGAATTTTCATGTATCAAAAGATCGGAAGAGCGGTTTCAG
chr22	29130720	29130759	CHEK2_7147	+	GTGACCTATGCACCAGACGTAAAAGAAAATGTCCAACAACAAGGGTGAGTTTTCAAGGCACAGATCGGAAGAGCGGTTTCAG
chr13	103498715	103498754	ERCC5_7148	+	GTGACCTATGCACCAGACGTGCGCCGCGTTGGGACTTGGGGTGCAGGGATTTCGGGGCTGGAAGATCGGAAGAGCGGTTTCAG
chr13	103504654	103504693	ERCC5_7149	+	GTGACCTATGCACCAGACGTTATAGTTTTTGTAGTAAAGTGTCAAATAATTTTTTTCTTCTGAGATCGGAAGAGCGGTTTCAG
chr13	103506233	103506272	ERCC5_7150	+	GTGACCTATGCACCAGACGTAATTATAGTCGTGTTAGAGATGAAGTTTTAAAAAAGTGATAGATCGGAAGAGCGGTTTCAG
chr13	103506735	103506774	ERCC5_7151	+	GTGACCTATGCACCAGACGTAACATTTTAAAGATATTTTGTACTTTGCTACATTCAGAGATCGGAAGAGCGGTTTCAG
chr13	103508473	103508512	ERCC5_7152	+	GTGACCTATGCACCAGACGTCATTTTTAGTATGTAATGTAATTCGTTTTGAATTTGAAGATCGGAAGAGCGGTTTCAG
chr13	103510779	103510818	ERCC5_7153	+	GTGACCTATGCACCAGACGTCAACAGTACATTCATGCTTAGAATTAAGAACTTCAGCAAAAAGATCGGAAGAGCGGTTTCAG
chr13	103514075	103514114	ERCC5_7154	+	GTGACCTATGCACCAGACGTCCATCATTATATATTACATTAATAAATAAAGATATAGATCGGAAGAGCGGTTTCAG
chr13	103515464	103515503	ERCC5_7155	+	GTGACCTATGCACCAGACGTGTGCTTTTTGTAGAAATCTGGAACGGTAGGATTTCCCCTCTAGATCGGAAGAGCGGTTTCAG
chr13	103518272	103518311	ERCC5_7156	+	GTGACCTATGCACCAGACGTAACATTTGTGTTTCGACTCTTCTGCTGAGGAAGCCAGGTTAAAGATCGGAAGAGCGGTTTCAG
chr13	103518742	103518781	ERCC5_7157	+	GTGACCTATGCACCAGACGTGCAGCTTGGGTTCTTTTACCACTTCTTCAGACCCCTGGAGATCGGAAGAGCGGTTTCAG
chr13	103519206	103519245	ERCC5_7158	+	GTGACCTATGCACCAGACGTAGAGTCTTTTTGATTACTTTCTGACATTTACCTTCAGAGTAGATCGGAAGAGCGGTTTCAG
chr13	103520618	103520657	ERCC5_7159	+	GTGACCTATGCACCAGACGTTTTATTTCTTAATTTGGATAATTGTGTAATACCCAAATAAGATCGGAAGAGCGGTTTCAG
chr13	103524759	103524798	ERCC5_7160	+	GTGACCTATGCACCAGACGTCCTTTAAAAGAGAAGGAAACACCTTGTCAAATATGTTAGATCGGAAGAGCGGTTTCAG
chr13	103525704	103525743	ERCC5_7161	+	GTGACCTATGCACCAGACGTTGGACCCCTCTCCTAAGTTCAGGATGAAGGGTAGGCTGTGAGATCGGAAGAGCGGTTTCAG
chr13	103528264	103528303	ERCC5_7162	+	GTGACCTATGCACCAGACGTTGTATCTCTATAATTAGTTATGACAGCCATTTGTAATGAAGATCGGAAGAGCGGTTTCAG
chr13	103527965	103528004	ERCC5_7163	+	GTGACCTATGCACCAGACGTCGCCCTCAGCAATCATCTGATGGATCTTCAAGTGAAGATAGATCGGAAGAGCGGTTTCAG
chr13	103514748	103514787	ERCC5_7164	+	GTGACCTATGCACCAGACGTGAAGAAATGCGTATAAACAGCTCCACCAGAACAGTATGATGAGATCGGAAGAGCGGTTTCAG
chr13	103515106	103515145	ERCC5_7165	+	GTGACCTATGCACCAGACGTATGAAACACATGCTGAAGTGTGAGCAGCAGAACGAACTAGATCGGAAGAGCGGTTTCAG
chr10	90750674	90750713	FAS_7166	+	GTGACCTATGCACCAGACGTTCTGCCCCTGGTGGAGGCTTACCCCGCTTATGTCGGGGAGATCGGAAGAGCGGTTTCAG
chr10	90762962	90763001	FAS_7167	+	GTGACCTATGCACCAGACGTCAAACATCCAGAGATTACAGTGAAAGTACAGTATAGGAGAGATCGGAAGAGCGGTTTCAG
chr10	90767605	90767644	FAS_7168	+	GTGACCTATGCACCAGACGTTAAAATGCAATGAAAGAGGCCAATCTTGAATTTTCATGTAGATCGGAAGAGCGGTTTCAG
chr10	90768765	90768804	FAS_7169	+	GTGACCTATGCACCAGACGTGTCTTTCTGATTAAAACACTAGATATAACATGAGAGTTAGATCGGAAGAGCGGTTTCAG
chr10	90770368	90770407	FAS_7170	+	GTGACCTATGCACCAGACGTTTTTACGGTTTATTTCTCCTTTCCCCAACCCTCATGAAAAGATCGGAAGAGCGGTTTCAG
chr10	90770574	90770613	FAS_7171	+	GTGACCTATGCACCAGACGTTAAGTTCTTGTCTTTGTTCAAACCTGCAGATTGAAATAACTTAGATCGGAAGAGCGGTTTCAG
chr10	90770583	90770622	FAS_7172	+	GTGACCTATGCACCAGACGTGCTTTGTTCAAACCTGCAGATTGAAATAACTTTGGGAAGTAGAGATCGGAAGAGCGGTTTCAG
chr10	90771769	90771808	FAS_7173	+	GTGACCTATGCACCAGACGTAGTACAGAAAACATGCAGAAAAGCACAGAAAAGGAAAACCAAAAGATCGGAAGAGCGGTTTCAG
chr10	90771849	90771888	FAS_7174	+	GTGACCTATGCACCAGACGTAATAGTTATCAGCTTTCCTTAAAAGAAAATAGAGAAAAGATCGGAAGAGCGGTTTCAG
chr10	90773135	90773174	FAS_7175	+	GTGACCTATGCACCAGACGTATCATTTTTATTTTCATAGAGATTGCCATCCTTTAGAGTAATAGATCGGAAGAGCGGTTTCAG
chr10	90773898	90773937	FAS_7176	+	GTGACCTATGCACCAGACGTCAACACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAAGATCGGAAGAGCGGTTTCAG
chr10	90774218	90774257	FAS_7177	+	GTGACCTATGCACCAGACGTAACAAATTCAGTTCTGAGTATATGCAATTAGTGTGAAAAGATCGGAAGAGCGGTTTCAG
chr10	123239546	123239585	FGFR2_7178	+	GTGACCTATGCACCAGACGTGGAAGAGAGAGCGTTTTTATTTCATCTTGGTCCAGGATAACAAGATCGGAAGAGCGGTTTCAG
chr10	123241702	123241741	FGFR2_7179	+	GTGACCTATGCACCAGACGTTAAAACAGGGATATCAGTAGATTCCAAGTCTACAGTTAAAAGATCGGAAGAGCGGTTTCAG
chr10	123243328	123243367	FGFR2_7180	+	GTGACCTATGCACCAGACGTGGATTTCCCTTGAAATTAATTTTCATGCACTGGGTAGCTGAGATCGGAAGAGCGGTTTCAG
chr10	123245057	123245096	FGFR2_7181	+	GTGACCTATGCACCAGACGTAGGAGAAAAGCACGGCATTACTAACCCATCCACGTTGCCAAAGATCGGAAGAGCGGTTTCAG
chr10	123246949	123246988	FGFR2_7182	+	GTGACCTATGCACCAGACGTAGAGAAAATGCAAAAATAAATATATTTAAAAGAATTTAAGATCGGAAGAGCGGTTTCAG
chr10	123247638	123247677	FGFR2_7183	+	GTGACCTATGCACCAGACGTGAAAAGAAAGCAGAGAAATAAATAATTTCAAACACCCGCAAGATCGGAAGAGCGGTTTCAG
chr10	123256247	123256286	FGFR2_7184	+	GTGACCTATGCACCAGACGTAGAAGAGAAGCTCCCTAAAGAGAGAAATCCAGGGTCTCCCCAGATCGGAAGAGCGGTTTCAG
chr10	123258130	123258169	FGFR2_7185	+	GTGACCTATGCACCAGACGTTAGGCATATTCACAAATCAGTTTCTTCCCTAATCTAGATCGGAAGAGCGGTTTCAG
chr10	123260472	123260511	FGFR2_7186	+	GTGACCTATGCACCAGACGTAAATAGGATGATTAGACATGCATCTGCTGTGATGGGTTGTAAGATCGGAAGAGCGGTTTCAG
chr10	123263466	123263505	FGFR2_7187	+	GTGACCTATGCACCAGACGTAATGCAAAGACACAGATGTAATCCTGGCTCCATCTGAGAAAAGATCGGAAGAGCGGTTTCAG
chr10	123274844	123274883	FGFR2_7188	+	GTGACCTATGCACCAGACGTGATCACAGGAGGAGGAACAGATAAGCAGGCCATAGAGTTAAGATCGGAAGAGCGGTTTCAG
chr10	123276988	123277027	FGFR2_7189	+	GTGACCTATGCACCAGACGTAGGGAAAGCAAAGAAAAGGCTAGACGACACAGGAATGATTAGATCGGAAGAGCGGTTTCAG
chr10	123278354	123278393	FGFR2_7190	+	GTGACCTATGCACCAGACGTACAGGAGAACAATAAACGGCCAACCCAGGAAGTCTTAGAGATCGGAAGAGCGGTTTCAG
chr10	123279694	123279733	FGFR2_7191	+	GTGACCTATGCACCAGACGTGAGGGAAAGGAGGAGTGGGGATGGGGAATGAGAGACAGATCGGAAGAGCGGTTTCAG
chr10	123298240	123298279	FGFR2_7192	+	GTGACCTATGCACCAGACGTCAAAGCAAAGGCGGTTTATTAACAATCCTAGCACAGATAAAGATCGGAAGAGCGGTTTCAG

chr10	123310984	123311023	FGFR2_7193	+	GTGACCTATGCACCAGACGTAAACAGTATTAGAATGTACTGATGGACAGCTTCCCCTCAGATCGGAAGAGCGGTTTCAG
chr10	123324104	123324143	FGFR2_7194	+	GTGACCTATGCACCAGACGTAAAGAACATATTTCCATGGATGTGTTTTTTCAAAAGCAAAAAAGATCGGAAGAGCGGTTTCAG
chr10	123325229	123325268	FGFR2_7195	+	GTGACCTATGCACCAGACGTGTGGGAGAGAGAAGACGGAGACAGATGGGAAGGAGGGAGAAGATCGGAAGAGCGGTTTCAG
chr10	123353342	123353381	FGFR2_7196	+	GTGACCTATGCACCAGACGTCCAATCCCCGGTCTCTCCATATCTCCATGTGGACGTTAAGATCGGAAGAGCGGTTTCAG
chr1	32768345	32768384	HDAC1_7197	+	GTGACCTATGCACCAGACGTAGAGGTGCTACCGTCCCTAACCTCATCTGCTCTGGTTCAGATCGGAAGAGCGGTTTCAG
chr1	32782394	32782433	HDAC1_7198	+	GTGACCTATGCACCAGACGTCTGTTCCCTCACACTGGAAGCCGCAGTTGCATCTCCAGATCGGAAGAGCGGTTTCAG
chr1	32790165	32790204	HDAC1_7199	+	GTGACCTATGCACCAGACGTTCATCTCTCCAGGCTAGACTGGGTTGTCTAGTGAAGATCGGAAGAGCGGTTTCAG
chr1	32792689	32792728	HDAC1_7200	+	GTGACCTATGCACCAGACGTCTGGCCTGTCTCTTGGAAAGACACCTTAGGCCAGTTCCAGATCGGAAGAGCGGTTTCAG
chr1	32793289	32793328	HDAC1_7201	+	GTGACCTATGCACCAGACGTCTTTAGGAGCCAACCGGCTTACCCTCAGCTGGCAGCTCTAGATCGGAAGAGCGGTTTCAG
chr1	32794772	32794811	HDAC1_7202	+	GTGACCTATGCACCAGACGTTATCCACCCTTTGGGCTACAAACAGGGGATTGGTTGGCGAGATCGGAAGAGCGGTTTCAG
chr1	32796298	32796337	HDAC1_7203	+	GTGACCTATGCACCAGACGTGTAGCACAAGGATGGTGGGCGGGCTCTGCTTGGTGCTCAGATCGGAAGAGCGGTTTCAG
chr1	32796520	32796559	HDAC1_7204	+	GTGACCTATGCACCAGACGTGAGGCGCAGGTTCCGGCTGGCTGGTGGGAGCTGGAGCTCAGATCGGAAGAGCGGTTTCAG
chr1	32797194	32797233	HDAC1_7205	+	GTGACCTATGCACCAGACGTCTCCAGCACCCCTTGTTGTAACATTCCCTGACTTTGGTTAGATCGGAAGAGCGGTTTCAG
chr1	32797418	32797457	HDAC1_7206	+	GTGACCTATGCACCAGACGTGACCTAGAGCCCTATGCCTTCCATTCAATAGGCAGCTCACAGATCGGAAGAGCGGTTTCAG
chr1	32797854	32797893	HDAC1_7207	+	GTGACCTATGCACCAGACGTGTTGACTGGGACTTGGGCTCGAGCCTGAGAGGATGAATAGATCGGAAGAGCGGTTTCAG
chr1	32798361	32798400	HDAC1_7208	+	GTGACCTATGCACCAGACGTAGCTGCCTGTGGCCATCTCCCTGGCATTGGAGCACCAGCCAGATCGGAAGAGCGGTTTCAG
chr1	32798656	32798695	HDAC1_7209	+	GTGACCTATGCACCAGACGTCCAGCTCGGCTTCCGTGCTGAGTCCCTCACGTTTCTTCCAGATCGGAAGAGCGGTTTCAG
chr4	55946341	55946380	KDR_7210	+	GTGACCTATGCACCAGACGTAAAGTGGCAACAAGGATGTTGGCAGAGAGAAGACAATTCTAGATCGGAAGAGCGGTTTCAG
chr4	55948219	55948258	KDR_7211	+	GTGACCTATGCACCAGACGTGACAATGAGATGGCACAGTTAATTGAGCATATAAATGACAGATCGGAAGAGCGGTTTCAG
chr4	55948813	55948852	KDR_7212	+	GTGACCTATGCACCAGACGTACAATATTTATATTTAGTGGTGGTATATTTGACTGCAGAGATCGGAAGAGCGGTTTCAG
chr4	55953936	55953975	KDR_7213	+	GTGACCTATGCACCAGACGTAAACACAGAAAGACTGTTGTTATGGCTTCAGTTCTTCAAGTAGATCGGAAGAGCGGTTTCAG
chr4	55955151	55955190	KDR_7214	+	GTGACCTATGCACCAGACGTAAAAACTGATTTTCAATTAATGCCTCTTTCTTCTTCTGAATGAGATCGGAAGAGCGGTTTCAG
chr4	55955651	55955690	KDR_7215	+	GTGACCTATGCACCAGACGTACAGGAGGAGACATCTTTGATTTGATTTTCTTATAGATCGGAAGAGCGGTTTCAG
chr4	55955980	55956019	KDR_7216	+	GTGACCTATGCACCAGACGTAGAAAGCAGAAAGATTAGCAACCAATAGCAAAATCTGAAGATCGGAAGAGCGGTTTCAG
chr4	55956256	55956295	KDR_7217	+	GTGACCTATGCACCAGACGTAATCATGTGTGCATTAGGTCTCGGCACAGCTGATCTCTTATAGATCGGAAGAGCGGTTTCAG
chr4	55958892	55958931	KDR_7218	+	GTGACCTATGCACCAGACGTAGGCAGGAGGATGGAGATCAGTATTTCCATGAGTTAGTGTAGATCGGAAGAGCGGTTTCAG
chr4	55961133	55961172	KDR_7219	+	GTGACCTATGCACCAGACGTGCAAAAGAAACAAACAACTCCTTGAAACAAAATGAGTCTAGATCGGAAGAGCGGTTTCAG
chr4	55961843	55961882	KDR_7220	+	GTGACCTATGCACCAGACGTGATGTCAGGAAGGAAAATGGGTTTTCACTCATATTTCCCTCAGATCGGAAGAGCGGTTTCAG
chr4	55962520	55962559	KDR_7221	+	GTGACCTATGCACCAGACGTAGTACAAGAGGAAATCATAGTATGGACATTTCTTCAAGATCGGAAGAGCGGTTTCAG
chr4	55963944	55963983	KDR_7222	+	GTGACCTATGCACCAGACGTCAACAACAGCAACAACAAACAGACTGGATTACTATACAAAGATCGGAAGAGCGGTTTCAG
chr4	55964450	55964489	KDR_7223	+	GTGACCTATGCACCAGACGTTCAATCCTTCCAGTCATAAACACACTGTTGTTGGCTGTTAGATCGGAAGAGCGGTTTCAG
chr4	55964981	55965020	KDR_7224	+	GTGACCTATGCACCAGACGTACAATTGAATGAGTATCAACAGTTGAAACTTATACTTTATAGATCGGAAGAGCGGTTTCAG
chr4	55968206	55968245	KDR_7225	+	GTGACCTATGCACCAGACGTAAAGAAAACGATCATTCTCATTATGATGATGATGCTGTGAGATCGGAAGAGCGGTTTCAG
chr4	55968686	55968725	KDR_7226	+	GTGACCTATGCACCAGACGTAAAAAGAAAATCACAGAACATGGAATTATAACTTTTGAAGATCGGAAGAGCGGTTTCAG
chr4	55971162	55971201	KDR_7227	+	GTGACCTATGCACCAGACGTGAGGCTAGTATTGAAATGGTGAATTAACCTGGTACAGCAGATCGGAAGAGCGGTTTCAG
chr4	55972118	55972157	KDR_7228	+	GTGACCTATGCACCAGACGTAAAAACAAATCCCAGGCCATAAACACCGCGGCTGTTTGTAGATCGGAAGAGCGGTTTCAG
chr4	55972988	55973027	KDR_7229	+	GTGACCTATGCACCAGACGTGAGATAACAGCGCATATATGATTTAATTTTTCTTTAATTAGATCGGAAGAGCGGTTTCAG
chr4	55974071	55974110	KDR_7230	+	GTGACCTATGCACCAGACGTGAAAAACAACCTTTTGAATTTGCAGTACGCTTTGAAGAATGAGATCGGAAGAGCGGTTTCAG
chr4	55976744	55976783	KDR_7231	+	GTGACCTATGCACCAGACGTAAATTTCTCAGGAATTAGTATAGTCAAAGGATTTGCTCTCAAGATCGGAAGAGCGGTTTCAG
chr4	55976946	55976985	KDR_7232	+	GTGACCTATGCACCAGACGTAAAAAAGAAAAAGGTCAACTTACTGTAATGGTCTATTAGATCGGAAGAGCGGTTTCAG
chr4	55979659	55979698	KDR_7233	+	GTGACCTATGCACCAGACGTGAGTTGACTGAACTTCAAAGACAGCAGCATATAACATTACCAGATCGGAAGAGCGGTTTCAG
chr4	55980443	55980482	KDR_7234	+	GTGACCTATGCACCAGACGTAAATTTGAAAAACAGAAACATGAGAGAGCAAATAAGCCTAAGATCGGAAGAGCGGTTTCAG
chr4	55981220	55981259	KDR_7235	+	GTGACCTATGCACCAGACGTAAAAAGACATATCAAATATTAATCCAGTACCAAAAATGAGAGATCGGAAGAGCGGTTTCAG
chr4	55981589	55981628	KDR_7236	+	GTGACCTATGCACCAGACGTATTTAGTTTTATTAATGAGTTAATGATTTTACTAGAAAAAGATCGGAAGAGCGGTTTCAG
chr4	55984978	55985017	KDR_7237	+	GTGACCTATGCACCAGACGTAAATTTCCAGGGAGGTATTAATAGATGACCTGACCTGAGAGATCGGAAGAGCGGTTTCAG
chr4	55987368	55987407	KDR_7238	+	GTGACCTATGCACCAGACGTAAATAAATGAATGTATGGCCTGACTGATTAAGCTTAAGATCGGAAGAGCGGTTTCAG
chr4	55991471	55991510	KDR_7239	+	GTGACCTATGCACCAGACGTGAGCCGGGGCAAATGCCAGAAGCTCGGGAGCCGGTCTTTAGATCGGAAGAGCGGTTTCAG
chr7	150691060	150691099	NOS3_7240	+	GTGACCTATGCACCAGACGTGGCAGCTAGGAGCAGGTGGGCAACAAGGGTGGTGTCAAGGAGATCGGAAGAGCGGTTTCAG
chr7	150692413	150692452	NOS3_7241	+	GTGACCTATGCACCAGACGTGTCGCTGTCCTGTCCTCCAGGAAAGGGTGGGTAAAGATCGGAAGAGCGGTTTCAG
chr7	150693651	150693690	NOS3_7242	+	GTGACCTATGCACCAGACGTCCCGGACGCCACAGCCTCCCTTGTCCTCAGGCCCCAGAGATCGGAAGAGCGGTTTCAG
chr7	150694024	150694063	NOS3_7243	+	GTGACCTATGCACCAGACGTCCAGCAGCTGAGAGCCCGGGCGCTACCAAAAAGGGAGCGGATCGGAAGAGCGGTTTCAG
chr7	150695547	150695586	NOS3_7244	+	GTGACCTATGCACCAGACGTCCCAAGCCAGCCAGCCTTCTTCCCAAGGCAGGAGATCGGAAGAGCGGTTTCAG
chr7	150695779	150695818	NOS3_7245	+	GTGACCTATGCACCAGACGTAGGGCCACCCATGAGGGTGTCCCAAGGTGGAGAATGAGGAGATCGGAAGAGCGGTTTCAG
chr7	150696184	150696223	NOS3_7246	+	GTGACCTATGCACCAGACGTAAAGGATGACTGGGTGGGATGGAGGGGCCATCCCTGAGAGATCGGAAGAGCGGTTTCAG
chr7	150696463	150696502	NOS3_7247	+	GTGACCTATGCACCAGACGTGGATGGGGCTCGGGCACGAATGCACCTGTCCAAGGCAGGAGATCGGAAGAGCGGTTTCAG
chr7	150697698	150697737	NOS3_7248	+	GTGACCTATGCACCAGACGTCCAGACTGCCAGGAAAGGCAAGGGTTGCATACGGGGCAGATCGGAAGAGCGGTTTCAG
chr7	150698524	150698563	NOS3_7249	+	GTGACCTATGCACCAGACGTAACTGGCTCTGCCAGCTCCGCGCCAGCTCTAAATTCGAAGATCGGAAGAGCGGTTTCAG
chr7	150698716	150698755	NOS3_7250	+	GTGACCTATGCACCAGACGTGGAGCCCGGCTCTCCACACACACCTGGGGGCCACAGATCGGAAGAGCGGTTTCAG

chr7	150699064	150699103	NOS3_7251	+	GTGACCTATGCACCAGACGTGCCAGGGGAGCAGGGAGCTAGAAGAGGGGGCTCTATCAAGATCGGAAGAGCGGTTTCAG
chr7	150699403	150699442	NOS3_7252	+	GTGACCTATGCACCAGACGTCCAGGAAAGGGGCTGCTGGGAATGAGGAGAGACTCAGAATAGATCGGAAGAGCGGTTTCAG
chr7	150703593	150703632	NOS3_7253	+	GTGACCTATGCACCAGACGTTGAGAGTTTGGGGGAGCTGGGGGAGCTGATGCATTTGGAGAGATCGGAAGAGCGGTTTCAG
chr7	150704104	150704143	NOS3_7254	+	GTGACCTATGCACCAGACGTCCACCAAGAGGGGTGCAACGGGTGGCAAGCTGCCCTGGGCAAGATCGGAAGAGCGGTTTCAG
chr7	150704375	150704414	NOS3_7255	+	GTGACCTATGCACCAGACGTCCCAGCCCTGCTCTGACTCCTGCCCCCTGGGATGCCCTCCAGATCGGAAGAGCGGTTTCAG
chr7	150706161	150706200	NOS3_7256	+	GTGACCTATGCACCAGACGTCCCTCACCTAACCCTGGTTCCTCTGAGGCCCCACACAGATCGGAAGAGCGGTTTCAG
chr7	150706366	150706405	NOS3_7257	+	GTGACCTATGCACCAGACGTGGCTTTACCGCCCCCCACCCCTGTCTGAACACCTGAAGATCGGAAGAGCGGTTTCAG
chr7	150707386	150707425	NOS3_7258	+	GTGACCTATGCACCAGACGTACCCCAATGAGGCACAGGGGCTAGAGAGACGGGATGAGCTAGATCGGAAGAGCGGTTTCAG
chr7	150707906	150707945	NOS3_7259	+	GTGACCTATGCACCAGACGTAAAGCAGGAGCAGGCCTGGCCACAGCAGGGTTGGGACCGGCAGATCGGAAGAGCGGTTTCAG
chr7	150708085	150708124	NOS3_7260	+	GTGACCTATGCACCAGACGTTGGAAGACTTGGTGGGGAGCTGCCAGGGTCAGGGTGGCAAGATCGGAAGAGCGGTTTCAG
chr7	150709571	150709610	NOS3_7261	+	GTGACCTATGCACCAGACGTGGACTAAAGGACTGCCCTGAAGGGAGTCAACCAATCTAGGGAGATCGGAAGAGCGGTTTCAG
chr7	150710478	150710517	NOS3_7262	+	GTGACCTATGCACCAGACGTCTGAGGGCGCAATGGTAACCTGAAGATGGGAGAGAGGGGAGATCGGAAGAGCGGTTTCAG
chr7	150711017	150711056	NOS3_7263	+	GTGACCTATGCACCAGACGTGCGGGCCGGGCTGAGCCTGAGCTGCGGGTTCCTGCTAAGGTCTAGATCGGAAGAGCGGTTTCAG
chr7	150711268	150711307	NOS3_7264	+	GTGACCTATGCACCAGACGTGCTTTCCCTCCAGTTCGGGGAGAGCGGCTGCCCGACTCAAGATCGGAAGAGCGGTTTCAG
chr9	98209744	98209783	PTCH1_7265	+	GTGACCTATGCACCAGACGTTGAGGGTGGGTAGAAGGGTGGTATCCCAGGCTGGGCATGAGATCGGAAGAGCGGTTTCAG
chr9	98211616	98211655	PTCH1_7266	+	GTGACCTATGCACCAGACGTGGATTCCATGTTAAAAGTGTCTTGTCCATTACCTGCTGAGATCGGAAGAGCGGTTTCAG
chr9	98212233	98212272	PTCH1_7267	+	GTGACCTATGCACCAGACGTAAGAGGAAACGGGAACACCGGCTGTGACAGGGTGGATCGCAGATCGGAAGAGCGGTTTCAG
chr9	98215913	98215952	PTCH1_7268	+	GTGACCTATGCACCAGACGTGCCAAGATGTTCAACAGTGGTTCGACTTCACCTGGTAAGATCGGAAGAGCGGTTTCAG
chr9	98218706	98218745	PTCH1_7269	+	GTGACCTATGCACCAGACGTGCACACAGTGGTCACTGCGGGGAGAGGTACCCTCTGGGGAGATCGGAAGAGCGGTTTCAG
chr9	98220586	98220625	PTCH1_7270	+	GTGACCTATGCACCAGACGTAAGGGCACAGGTTAGGAGCAGCCAGGGTAGAAGAGCATCAGATCGGAAGAGCGGTTTCAG
chr9	98222076	98222115	PTCH1_7271	+	GTGACCTATGCACCAGACGTGGGAAGAACAGAGGCCTTTGAGAATGGGGTTGGGGTAAAAGATCGGAAGAGCGGTTTCAG
chr9	98224291	98224330	PTCH1_7272	+	GTGACCTATGCACCAGACGTCAATGATTGTAACACATTATACTGCAGCCAGAAGGACAGATCGGAAGAGCGGTTTCAG
chr9	98229718	98229757	PTCH1_7273	+	GTGACCTATGCACCAGACGTAGAGGCACAAGGTACAGCCACAGGAGCAGCCTGACTTAGATCGGAAGAGCGGTTTCAG
chr9	98231446	98231485	PTCH1_7274	+	GTGACCTATGCACCAGACGTGGGAAACATGTTGCAATGTTACTGAAACAGGGAAATGGAGATCGGAAGAGCGGTTTCAG
chr9	98232224	98232263	PTCH1_7275	+	GTGACCTATGCACCAGACGTAAAAAATTCAGAGGTCACCAACATGCCTCCGCCAATCAGATCGGAAGAGCGGTTTCAG
chr9	98238452	98238491	PTCH1_7276	+	GTGACCTATGCACCAGACGTAAAAACACAGCGCTGAGAGCTGCACTGGACATGGTCCCCTAGATCGGAAGAGCGGTTTCAG
chr9	98239150	98239189	PTCH1_7277	+	GTGACCTATGCACCAGACGTAAACAGAGGATGGTGGCATTAGACATGCGAGATGCAATTAAGATCGGAAGAGCGGTTTCAG
chr9	98239995	98240034	PTCH1_7278	+	GTGACCTATGCACCAGACGTAACAATGGGGGCACAGAACAAGCCGAACATTAGAATGTAGATCGGAAGAGCGGTTTCAG
chr9	98240479	98240518	PTCH1_7279	+	GTGACCTATGCACCAGACGTAACAGAATCGGAAATGCCAAATGCAATGAACACTCCACAGATCGGAAGAGCGGTTTCAG
chr9	98241440	98241479	PTCH1_7280	+	GTGACCTATGCACCAGACGTGTCCAAGGGGAAGGCACATCAGTATTCCAGGAAGCAGAGATCGGAAGAGCGGTTTCAG
chr9	98242881	98242920	PTCH1_7281	+	GTGACCTATGCACCAGACGTAATTAGGAGACGAGACCATGAAAAGAGCCTTCTAAACGCAAGATCGGAAGAGCGGTTTCAG
chr9	98244333	98244372	PTCH1_7282	+	GTGACCTATGCACCAGACGTTAAAAAGAGAGGCCATGGTTAGGTTAAGGCACACTACTAGATCGGAAGAGCGGTTTCAG
chr9	98248108	98248147	PTCH1_7283	+	GTGACCTATGCACCAGACGTCCAATCTTCTGGCGAGTATAATTTAATTCACGACTTACTCAGATCGGAAGAGCGGTTTCAG
chr9	98248167	98248206	PTCH1_7284	+	GTGACCTATGCACCAGACGTTGTACAGGTTAATTAAGAATAGCAAAAACACTGCAAACTCAGATCGGAAGAGCGGTTTCAG
chr9	98268892	98268931	PTCH1_7285	+	GTGACCTATGCACCAGACGTGGGAGGAGGAGGTGACAGGAAAGGCCCTCCTAATCAGACGTAGATCGGAAGAGCGGTTTCAG
chr9	98278764	98278803	PTCH1_7286	+	GTGACCTATGCACCAGACGTCAACCCCTGCTCGGAGCGCGGTTGCCGATGGCGCGGACGAGATCGGAAGAGCGGTTTCAG
chr9	98279113	98279152	PTCH1_7287	+	GTGACCTATGCACCAGACGTGGGGTGGTCTGCCGCGCCATAGGCAGGACCTGTCAGGGTAGATCGGAAGAGCGGTTTCAG
chr9	98209474	98209513	PTCH1_7288	+	GTGACCTATGCACCAGACGTGTGGACGCTGGGTTCGAGGGTGTGAGAACGGGCCCGCCAGATCGGAAGAGCGGTTTCAG
chr5	1253957	1253996	TERT_7289	+	GTGACCTATGCACCAGACGTAAAAATCAGACTCCGTTCCAGAAGAGGCCAGAGGTGGCATCAGATCGGAAGAGCGGTTTCAG
chr5	1254631	1254670	TERT_7290	+	GTGACCTATGCACCAGACGTACAGAGGCTGAGGAGTCAAGGCCAGCCAGCCAGCTCCCTCAGATCGGAAGAGCGGTTTCAG
chr5	1255537	1255576	TERT_7291	+	GTGACCTATGCACCAGACGTGGGAGGACAGCTGAGGAAAGGCCCTCCTAATCAGACGTAGATCGGAAGAGCGGTTTCAG
chr5	1258785	1258824	TERT_7292	+	GTGACCTATGCACCAGACGTCAAGAAAGAGTGAGAAACGGTAGAAACCTCTCTGGGATTAGATCGGAAGAGCGGTTTCAG
chr5	1260726	1260765	TERT_7293	+	GTGACCTATGCACCAGACGTGGGGGGAATGTCAGACACAGGTGCCCTGCCCCACACCCAGCAGATCGGAAGAGCGGTTTCAG
chr5	1264718	1264757	TERT_7294	+	GTGACCTATGCACCAGACGTGGGGCAATGTCAGCCCCAGGATGCGGGGCGCTCACCCAGGAGATCGGAAGAGCGGTTTCAG
chr5	1266661	1266700	TERT_7295	+	GTGACCTATGCACCAGACGTGGAAAATACACAGCAAGGTTAATCTTACGTTTACGTAAGATCGGAAGAGCGGTTTCAG
chr5	1268759	1268798	TERT_7296	+	GTGACCTATGCACCAGACGTAAGACAGCTGAGACAGGTCAGGACGCGGATGTGCTGACATAGATCGGAAGAGCGGTTTCAG
chr5	1271330	1271369	TERT_7297	+	GTGACCTATGCACCAGACGTAGACGGGAGACACATGGGAGTGAGCCGGTGGGTGCTGAGAAGATCGGAAGAGCGGTTTCAG
chr5	1272406	1272445	TERT_7298	+	GTGACCTATGCACCAGACGTAGGAGAGGGCATGAGCCAAATGTGGCCTGCCCGGCCAAGATCGGAAGAGCGGTTTCAG
chr5	1278886	1278925	TERT_7299	+	GTGACCTATGCACCAGACGTGTGTGCTAGCGCCCGTCCACATCCACTGTGTGAGTGGAGAGATCGGAAGAGCGGTTTCAG
chr5	1278922	1278961	TERT_7300	+	GTGACCTATGCACCAGACGTGGAGGCCGAGGAGACTGACAGTGCCACGCAGAACTCAGAAGATCGGAAGAGCGGTTTCAG
chr5	1279596	1279635	TERT_7301	+	GTGACCTATGCACCAGACGTGACATGGGACAGACTCAGGAAAGTGATCCGGCCAAGTGGATCGGAAGAGCGGTTTCAG
chr5	1280464	1280503	TERT_7302	+	GTGACCTATGCACCAGACGTGAGCCCTCAGGAGGCTTCTCAGCCAGACAACAGACTAGAGATCGGAAGAGCGGTTTCAG
chr5	1282750	1282789	TERT_7303	+	GTGACCTATGCACCAGACGTAAGGACATGCCACATCCAGATCACCGAGGGCCTGGTGACCAGATCGGAAGAGCGGTTTCAG
chr5	1294792	1294831	TERT_7304	+	GTGACCTATGCACCAGACGTAGCGCCCTGAGTCGCCTGCGCTGCTCTCCGATGTCGCTGAGATCGGAAGAGCGGTTTCAG
chr5	1295115	1295154	TERT_7305	+	GTGACCTATGCACCAGACGTGCCGGGGCCAGGGCTCCACAGTCCGCAGCAGGACGCAGCAGATCGGAAGAGCGGTTTCAG
chr5	1293889	1293928	TERT_7306	+	GTGACCTATGCACCAGACGTGAGGCCCTGGAACCCAGAAAGATGGTCTCCACGAGCCCTCAGATCGGAAGAGCGGTTTCAG
chr5	1294340	1294379	TERT_7307	+	GTGACCTATGCACCAGACGTTACCCTGTGTCTTGGTAGGCTAGAGGGAAATGCAGAGAAGATCGGAAGAGCGGTTTCAG
chr16	2098765	2098804	TSC2_7308	+	GTGACCTATGCACCAGACGTTACCTGTGTCTTGGTAGGCTAGAGGGAAATGCAGAGAAGATCGGAAGAGCGGTTTCAG

chr16	2100498	2100537	TSC2_7309	+	GTGACCTATGCACCAGACGTCCTTGTAGCTACTAGAGAGAGGCACGCTAGACTATTTCAGAAGATCGGAAGAGCGGTTTCAG
chr16	2103464	2103503	TSC2_7310	+	GTGACCTATGCACCAGACGTTGGGCGACGCTGGGATGGGTGACGTCAGGCTGCCACTGACAGATCGGAAGAGCGGTTTCAG
chr16	2104452	2104491	TSC2_7311	+	GTGACCTATGCACCAGACGTCCTTGGGTTGGAGGTTTCTCTGGCCCTTGACGATCAAGTGTAGATCGGAAGAGCGGTTTCAG
chr16	2105531	2105570	TSC2_7312	+	GTGACCTATGCACCAGACGTAATTGAGATCCTGTTCTGATAATGGTCTTAAGTTCAGCTCAGATCGGAAGAGCGGTTTCAG
chr16	2106781	2106820	TSC2_7313	+	GTGACCTATGCACCAGACGTTGAAACTGCCTGGAAGGTTCTGAGAGCACATGGATGGGAGATCGGAAGAGCGGTTTCAG
chr16	2107190	2107229	TSC2_7314	+	GTGACCTATGCACCAGACGTTGGTGGGGCCGAGGCGAGTGAGGCCCAGCACAGCCCCTCGAGATCGGAAGAGCGGTTTCAG
chr16	2108885	2108924	TSC2_7315	+	GTGACCTATGCACCAGACGTTTCTGTGTGCAGTGGCAGGAAACCGGAGAGCTCCCAGATCGGAAGAGCGGTTTCAG
chr16	2110825	2110864	TSC2_7316	+	GTGACCTATGCACCAGACGTTGGCAGGAGCTCCGGGAGCACCGGGAACCCAGACAGGCAGAGATCGGAAGAGCGGTTTCAG
chr16	2112020	2112059	TSC2_7317	+	GTGACCTATGCACCAGACGTTCCCTGGGTGGGGCCTTTGGGCTTTGGCTGGTGGGAGGGAGATCGGAAGAGCGGTTTCAG
chr16	2112612	2112651	TSC2_7318	+	GTGACCTATGCACCAGACGTTCTGTAGCCTTGCCTGGCACCTGGAGCCTGGCCCTGTCTAGATCGGAAGAGCGGTTTCAG
chr16	2113065	2113104	TSC2_7319	+	GTGACCTATGCACCAGACGTAGGCGGCCGACGCTGGGGGCTCAGGGCTATTTCTCCGTGGAGATCGGAAGAGCGGTTTCAG
chr16	2114439	2114478	TSC2_7320	+	GTGACCTATGCACCAGACGTTTGTACCCGGGGCCGGGTGCATGCGTCCAGAGCTCCGTGAGATCGGAAGAGCGGTTTCAG
chr16	2115647	2115686	TSC2_7321	+	GTGACCTATGCACCAGACGTTGACGAGGCCTCTGCTCCCGGGGCGCGCATGGCTAGCGTAGATCGGAAGAGCGGTTTCAG
chr16	2120590	2120629	TSC2_7322	+	GTGACCTATGCACCAGACGTTGGGGTTGCGCAGCCAGTTCCTGGGGGCCAGCCAGGTATAGATCGGAAGAGCGGTTTCAG
chr16	2121628	2121667	TSC2_7323	+	GTGACCTATGCACCAGACGTTCCCGCCACGGCCCATGAGGCTCAGGGCGTCAGAGGCGCAGATCGGAAGAGCGGTTTCAG
chr16	2121946	2121985	TSC2_7324	+	GTGACCTATGCACCAGACGTTCCGGGCGAGGGACCATCGTCCACGTTGGGCCAGGAGACAGATCGGAAGAGCGGTTTCAG
chr16	2122375	2122414	TSC2_7325	+	GTGACCTATGCACCAGACGTTGGCCCTGGGGTGGGGTGGGGGACCAGTAGGGTTTTTCCAGATCGGAAGAGCGGTTTCAG
chr16	2122995	2123034	TSC2_7326	+	GTGACCTATGCACCAGACGTAGAGCAGGACGGGCGAGCTGTGATGGGGCTGGGATTCGAGAGATCGGAAGAGCGGTTTCAG
chr16	2124401	2124440	TSC2_7327	+	GTGACCTATGCACCAGACGTTGCCCTGCGCATGCACCCGAGAGGTTCCGGCTGTGTAAGATCGGAAGAGCGGTTTCAG
chr16	2125904	2125943	TSC2_7328	+	GTGACCTATGCACCAGACGTGCCCCAGGCCCTGTGCCTCCCAGCCGTGGCCCGCCGCTAGGAGATCGGAAGAGCGGTTTCAG
chr16	2126182	2126221	TSC2_7329	+	GTGACCTATGCACCAGACGTTGGCCGTTGAAGGCTGTGTCTCCTGGTAGGCCAGGGCTTGAGATCGGAAGAGCGGTTTCAG
chr16	2126597	2126636	TSC2_7330	+	GTGACCTATGCACCAGACGTTCCGGGGTGTGCCTGGAGTCCGGTGTGGGGTGGGGAAGGACAAGATCGGAAGAGCGGTTTCAG
chr16	2127738	2127777	TSC2_7331	+	GTGACCTATGCACCAGACGTTGTCGGTGGGGGGCACGGACCCTGGAGCTTGCCCGCTGAGATCGGAAGAGCGGTTTCAG
chr16	2129208	2129247	TSC2_7332	+	GTGACCTATGCACCAGACGTTCACTACAGGCTGGCGGGCTCCGGAGCTCCACGGCAAGTCCAGGAGCGGTTTCAG
chr16	2129440	2129479	TSC2_7333	+	GTGACCTATGCACCAGACGTTCTCCTTCCCTCCGCGCCTGCCAGCCTCGACACCGGCTGTAGATCGGAAGAGCGGTTTCAG
chr16	2129681	2129720	TSC2_7334	+	GTGACCTATGCACCAGACGTTGCCACAGCCACCTCCACACAGGCACCGGGCTCCCTCAGTAGATCGGAAGAGCGGTTTCAG
chr16	2130389	2130428	TSC2_7335	+	GTGACCTATGCACCAGACGTTGGGCTGGCCTGAGCGCCATCTTCTGCCAGTACCCACAGAGATCGGAAGAGCGGTTTCAG
chr16	2131810	2131849	TSC2_7336	+	GTGACCTATGCACCAGACGTTGGCGGGCCTTGGCACGGGCTCTGCTCCCCTGGCCTGGTAGATCGGAAGAGCGGTTTCAG
chr16	2132516	2132555	TSC2_7337	+	GTGACCTATGCACCAGACGTTGAGAGGGAAGCGTTGGCTGCAGAGCGCCACTCGCTCAGATCGGAAGAGCGGTTTCAG
chr16	2133828	2133867	TSC2_7338	+	GTGACCTATGCACCAGACGTTCTCAGAGCCTGACCCCTGACTGCTGACCTCGGGGGCTCCTTAGAGATCGGAAGAGCGGTTTCAG
chr16	2134727	2134766	TSC2_7339	+	GTGACCTATGCACCAGACGTTGCTTCCGGGCGGGGCTCCTGACACCTCTCCTGCGGGAACAGATCGGAAGAGCGGTTTCAG
chr16	2135038	2135077	TSC2_7340	+	GTGACCTATGCACCAGACGTTCCCTCCTCCTGATCCGCTGGAGCTGTGTGGCTCGGGTGTAGATCGGAAGAGCGGTTTCAG
chr16	2135334	2135373	TSC2_7341	+	GTGACCTATGCACCAGACGTTGGGGCCGGCCCTAGTGCCTGGACAGGGCCAGCTGGGCCTCAGATCGGAAGAGCGGTTTCAG
chr16	2136391	2136430	TSC2_7342	+	GTGACCTATGCACCAGACGTTGCCCTACCCTCCTGCTGCCCCAGGCCCTCAGGGCACGGAGATCGGAAGAGCGGTTTCAG
chr16	2136883	2136922	TSC2_7343	+	GTGACCTATGCACCAGACGTTGCCCTGAGGCTGAGGCTGGCCCAAGCCAGGTCAGGATCGGAAGAGCGGTTTCAG
chr16	2137953	2137992	TSC2_7344	+	GTGACCTATGCACCAGACGTTGGGGCCCTGCAGTGCAGGAAAGTAGGGCCGGGTGGGAGATCGGAAGAGCGGTTTCAG
chr16	2138151	2138190	TSC2_7345	+	GTGACCTATGCACCAGACGTTGGGTCCAGGCGTGAGCTGGTGGGACAGGCCAGGTGCCAGATCGGAAGAGCGGTTTCAG
chr16	2138337	2138376	TSC2_7346	+	GTGACCTATGCACCAGACGTTGGGGCTCCCTCAGCGGGGTGTGCTGGCTGCCAAGCTGTAGATCGGAAGAGCGGTTTCAG
chr16	2138622	2138661	TSC2_7347	+	GTGACCTATGCACCAGACGTTCCCTCCTGCACCTGGCCCTGGACGGTATTGCCTGTCTAGATCGGAAGAGCGGTTTCAG
chr15	91290731	91290770	BLM_7348	+	GTGACCTATGCACCAGACGTTGACTGGTTTCTGTGTCACATAGGCACTAACTACCACATAGATCGGAAGAGCGGTTTCAG
chr15	91293308	91293347	BLM_7349	+	GTGACCTATGCACCAGACGTTTATCTTATTCTATTGTAGTATGCTCATTTGACTTTTTTATTAGATCGGAAGAGCGGTTTCAG
chr15	91295187	91295226	BLM_7350	+	GTGACCTATGCACCAGACGTTAAATAATTAGCATTATTATTGTTTCTGGGATACTTTAAAGATCGGAAGAGCGGTTTCAG
chr15	91298179	91298218	BLM_7351	+	GTGACCTATGCACCAGACGTTATTTTAGACATACCATGTATTTCAACTACTTACTTTTGAAGATCGGAAGAGCGGTTTCAG
chr15	91303520	91303559	BLM_7352	+	GTGACCTATGCACCAGACGTTTCCCCCTTCTGGAATATATCTGATTATATTTACCACAGATCGGAAGAGCGGTTTCAG
chr15	91304496	91304535	BLM_7353	+	GTGACCTATGCACCAGACGTTAAATAAATGAATGCTTATATAAAAACAAAAGTGTCCCAAAGATCGGAAGAGCGGTTTCAG
chr15	91306398	91306437	BLM_7354	+	GTGACCTATGCACCAGACGTTTAGAAGTGAATTTGCGAGATGCAATCCATTGGCAGATGTTAAAGATCGGAAGAGCGGTTTCAG
chr15	91308655	91308694	BLM_7355	+	GTGACCTATGCACCAGACGTTAAATACTAATAAAAAACACGCCCTTAGAAACAATTAATTTAGATCGGAAGAGCGGTTTCAG
chr15	91312472	91312511	BLM_7356	+	GTGACCTATGCACCAGACGTTTTTTTATATCCGGAAATACCGATAAATACATACTACCAAAGATCGGAAGAGCGGTTTCAG
chr15	91312827	91312866	BLM_7357	+	GTGACCTATGCACCAGACGTTGCACGTCACGTATTTGAGAACCCCTGGGGCAGTGACTGCCAAGATCGGAAGAGCGGTTTCAG
chr15	91326169	91326208	BLM_7358	+	GTGACCTATGCACCAGACGTTCCATGTGATTAGCTGTCTAGAAGTAACAAATGCTTTTTAAGATCGGAAGAGCGGTTTCAG
chr15	91328322	91328361	BLM_7359	+	GTGACCTATGCACCAGACGTTAAAGATAAAACAATAATAGAAATACTTTTATAGCATAAGATCGGAAGAGCGGTTTCAG
chr15	91334085	91334124	BLM_7360	+	GTGACCTATGCACCAGACGTTCCATTGTAGAGACATCTGCATCTCACCTCAGCCTCAGATAGATCGGAAGAGCGGTTTCAG
chr15	91341578	91341617	BLM_7361	+	GTGACCTATGCACCAGACGTTGTTTTGAATGTTTGTAGTTACTTCAATTGAAATTGAACATAGATCGGAAGAGCGGTTTCAG
chr15	91346961	91347000	BLM_7362	+	GTGACCTATGCACCAGACGTTTTTCATGTTTATTTTATCTCACAAATGAGTGAACCAAAGATCGGAAGAGCGGTTTCAG
chr15	91347600	91347639	BLM_7363	+	GTGACCTATGCACCAGACGTTGATTCCTTTGTTACTGTGCACAGATTAATAGGCCGAAAAGATCGGAAGAGCGGTTTCAG
chr15	91352500	91352539	BLM_7364	+	GTGACCTATGCACCAGACGTAGCCATGTGTCTCTAAAAGCCTGTTTAATGTGAAGCGAGATCGGAAGAGCGGTTTCAG
chr15	91354647	91354686	BLM_7365	+	GTGACCTATGCACCAGACGTTTTCATGATCTTTTTCTAATATAGGAAAGGAAAGAACAGACAGATCGGAAGAGCGGTTTCAG
chr15	91358520	91358559	BLM_7366	+	GTGACCTATGCACCAGACGTTCAATGTACATAGACCCCTTTTCTTTGTTGTCAGCATCTGAGATCGGAAGAGCGGTTTCAG

chr15	91292957	91292996	BLM_7367	+	GTGACCTATGCACCAGACGTTTGGGATGATATGGATGACTTTGATACTTCTGAGACTTCAAGATCGGAAGAGCGGTTTCAG
chr15	91304165	91304204	BLM_7368	+	GTGACCTATGCACCAGACGTCAGGAAATGTTCTCACAAAGCACTGCTGTGAAAGATCAGAAAGATCGGAAGAGCGGTTTCAG
chr11	119103416	119103455	CBL_7369	+	GTGACCTATGCACCAGACGTAATACTACACAAATAAATATGCAGGTCGTGACTGCCTGAAGATCGGAAGAGCGGTTTCAG
chr11	119142602	119142641	CBL_7370	+	GTGACCTATGCACCAGACGTGAATAATGAATTTGAACTATGAAAACTAAAGCTTACGAGAGATCGGAAGAGCGGTTTCAG
chr11	119144745	119144784	CBL_7371	+	GTGACCTATGCACCAGACGTAAAAAAGTTGACTAAACTGGTTACTCTACTTCGGTGAAGAGATCGGAAGAGCGGTTTCAG
chr11	119145674	119145713	CBL_7372	+	GTGACCTATGCACCAGACGTTGACGCCAAAGACTGTTTATTCTTCTGAATTTCTGTTATCTTGAAGATCGGAAGAGCGGTTTCAG
chr11	119146855	119146894	CBL_7373	+	GTGACCTATGCACCAGACGTACTGCATACCATCTGTTAGGACTGCGGAACCTTAGGGCTGAGATCGGAAGAGCGGTTTCAG
chr11	119148565	119148604	CBL_7374	+	GTGACCTATGCACCAGACGTTTTTCACATGATAACCATATCACTGGACACAAGCTTTAGTAAGATCGGAAGAGCGGTTTCAG
chr11	119149018	119149057	CBL_7375	+	GTGACCTATGCACCAGACGTAACAGCGACTTTTTTCAGCTATGTAATAACCTTGGAAAAAGATCGGAAGAGCGGTTTCAG
chr11	119149434	119149473	CBL_7376	+	GTGACCTATGCACCAGACGTAGTTTAGGAGACTGGCAAATCCATTGTGAGTTGCTTCTAGATCGGAAGAGCGGTTTCAG
chr11	119155821	119155860	CBL_7377	+	GTGACCTATGCACCAGACGTTTCCATTACGTGCAGTTTTTTGGGATCTTTGCTGTGTACTAGAGATCGGAAGAGCGGTTTCAG
chr11	119158667	119158706	CBL_7378	+	GTGACCTATGCACCAGACGTTAAAGCTATATTTGTACAGTGGAGTTGTACTTGTAAAAAGATCGGAAGAGCGGTTTCAG
chr11	119167755	119167794	CBL_7379	+	GTGACCTATGCACCAGACGTAAACAACCCCTTTTTGGCCCTATACCTTTATGTGGGTAATTAGATCGGAAGAGCGGTTTCAG
chr11	119168202	119168241	CBL_7380	+	GTGACCTATGCACCAGACGTATTCTGCTACTTTAAAAATCATTGATATGTCATAGGAATGAGATCGGAAGAGCGGTTTCAG
chr11	119169261	119169300	CBL_7381	+	GTGACCTATGCACCAGACGTAGACTACTTTGGGTTTGTCTGAATGCGAGTGTCGCTGTAGATCGGAAGAGCGGTTTCAG
chr11	119170502	119170541	CBL_7382	+	GTGACCTATGCACCAGACGTCCCTGCTGCAAGTTTAGAGGACCAGTGAGTTGGGAGTTATAGATCGGAAGAGCGGTTTCAG
chr17	48263020	48263059	COL1A1_7383	+	GTGACCTATGCACCAGACGTGCGGAGACAACGGGAGGGGACCTTACCACGTGGGAGTGATAGATCGGAAGAGCGGTTTCAG
chr17	48263392	48263431	COL1A1_7384	+	GTGACCTATGCACCAGACGTGGGGAGAGAGGGGAGGTCAGCCCTATGCGGGAACCTTAGATCGGAAGAGCGGTTTCAG
chr17	48263879	48263918	COL1A1_7385	+	GTGACCTATGCACCAGACGTGCAGGGCAAGATGGAGTCAGGGAAGGGAGCAGCCAGCACAGATCGGAAGAGCGGTTTCAG
chr17	48264294	48264333	COL1A1_7386	+	GTGACCTATGCACCAGACGTAGGGAGAGAGTGGGGATTACCGGCATCCAAGTGTCTTTGGAGATCGGAAGAGCGGTTTCAG
chr17	48264494	48264533	COL1A1_7387	+	GTGACCTATGCACCAGACGTGGAATGGTTTGAGAAAGGCTGCCAGAAGCCGAACACCAGATCGGAAGAGCGGTTTCAG
chr17	48264909	48264948	COL1A1_7388	+	GTGACCTATGCACCAGACGTGATAAAAAGGCGAGTTCAGGCCAGTGAGCGTCAAATGTAAGATCGGAAGAGCGGTTTCAG
chr17	48265355	48265394	COL1A1_7389	+	GTGACCTATGCACCAGACGTGAAAGGGCAACAACGTCAGCCGGAAGTTCCATTGGCCTGAGATCGGAAGAGCGGTTTCAG
chr17	48265521	48265560	COL1A1_7390	+	GTGACCTATGCACCAGACGTCAAGGAAAGCATGAGCTCTTGGCCAGTGGGAAAGGCTGAGGCTAGATCGGAAGAGCGGTTTCAG
chr17	48266009	48266048	COL1A1_7391	+	GTGACCTATGCACCAGACGTGAGCAGGGGAATATGGGTGAGCCCGGGTGAAGGGCCAGGAGATCGGAAGAGCGGTTTCAG
chr17	48266167	48266206	COL1A1_7392	+	GTGACCTATGCACCAGACGTAGAGAGAGAGAAGTGAGAGTCAGCCGGGAAGAGGGCTTAAAGATCGGAAGAGCGGTTTCAG
chr17	48266382	48266421	COL1A1_7393	+	GTGACCTATGCACCAGACGTAGAAAGAGTCAAGCCAGAGATAGGGTCTGGGAGGACCCTTAGATCGGAAGAGCGGTTTCAG
chr17	48266647	48266686	COL1A1_7394	+	GTGACCTATGCACCAGACGTCAAACAGGGGTGAGGTGCCAGAGCAGCAGCAGGGACCCAGATCGGAAGAGCGGTTTCAG
chr17	48266910	48266949	COL1A1_7395	+	GTGACCTATGCACCAGACGTATAGGAGGGGCTGACAGTCCAGGGGCTCTGGTGCATCAGATCGGAAGAGCGGTTTCAG
chr17	48267104	48267143	COL1A1_7396	+	GTGACCTATGCACCAGACGTAGAACATAGGAACAGTCAGAGGGAGAACAGCCAACCTCATCAGATCGGAAGAGCGGTTTCAG
chr17	48267284	48267323	COL1A1_7397	+	GTGACCTATGCACCAGACGTGCACAGAGGCATCAAGCCTGGACCCGCTCTGGGTCCCAGCAGATCGGAAGAGCGGTTTCAG
chr17	48267480	48267519	COL1A1_7398	+	GTGACCTATGCACCAGACGTAAAGCAGGGCGTGAATGGAGGGAAGGAGGCAGGAGTTCCAGATCGGAAGAGCGGTTTCAG
chr17	48267752	48267791	COL1A1_7399	+	GTGACCTATGCACCAGACGTAGGAGTCAGATGGAGAGTGCCTGACAGAGGGGAAGGCAGATCGGAAGAGCGGTTTCAG
chr17	48267968	48268007	COL1A1_7400	+	GTGACCTATGCACCAGACGTGGGACAAGAGGCTCAGGCTCAGGGCTCCCTGAACTCAGATCGGAAGAGCGGTTTCAG
chr17	48268296	48268335	COL1A1_7401	+	GTGACCTATGCACCAGACGTGGATAAGCTTGAATTTCCAGTGTGGGCAAGGAGTGCACAGATCGGAAGAGCGGTTTCAG
chr17	48268862	48268901	COL1A1_7402	+	GTGACCTATGCACCAGACGTACCAAGAAGACTGGAGTGAGGCCCTGGGGCCCAAGAGTGAGATCGGAAGAGCGGTTTCAG
chr17	48269258	48269297	COL1A1_7403	+	GTGACCTATGCACCAGACGTAGGACAGGGCATGTGAAGGCTGCTCTGGAGATAGGGCCAAAGATCGGAAGAGCGGTTTCAG
chr17	48269396	48269435	COL1A1_7404	+	GTGACCTATGCACCAGACGTGGGAGAGAGGAACAGACAGTGAGCAAAACCCACCTGGGGCAGATCGGAAGAGCGGTTTCAG
chr17	48269900	48269939	COL1A1_7405	+	GTGACCTATGCACCAGACGTGAAATGGGGGAAGAAGGGAGGGAAAGGTTTGAATCTGGAAAGATCGGAAGAGCGGTTTCAG
chr17	48270065	48270104	COL1A1_7406	+	GTGACCTATGCACCAGACGTAGAACACTACAGTCAAGGGGAGGCCGAGGAGCAGGGCCAGATCGGAAGAGCGGTTTCAG
chr17	48270222	48270261	COL1A1_7407	+	GTGACCTATGCACCAGACGTATAGCAAAGGGGCAAGCTAGGGTTAGGAGGCCCCGAGCAGCAGATCGGAAGAGCGGTTTCAG
chr17	48270419	48270458	COL1A1_7408	+	GTGACCTATGCACCAGACGTAGGGAGTTAGGGTTGAGGGGGCTGAAGTGAGAAAGCCAGGGAGATCGGAAGAGCGGTTTCAG
chr17	48271413	48271452	COL1A1_7409	+	GTGACCTATGCACCAGACGTGAGGCACGAAAGCAGCAGTGGAGACAGCAGGGAGGCAGACAGATCGGAAGAGCGGTTTCAG
chr17	48271555	48271594	COL1A1_7410	+	GTGACCTATGCACCAGACGTAGAGAGGTATGAGTGGGACTTTGGGGAAGAGCATGATGGAGAGATCGGAAGAGCGGTTTCAG
chr17	48271819	48271858	COL1A1_7411	+	GTGACCTATGCACCAGACGTGAAGTCAACAGGAACAGTTAGGGCTCAAGTTTGTGGCTTAGATCGGAAGAGCGGTTTCAG
chr17	48271998	48272037	COL1A1_7412	+	GTGACCTATGCACCAGACGTAGAGGAGGCCAGTGAAGCTCGGACAGGCACAGCCACCGATCGGAAGAGCGGTTTCAG
chr17	48272200	48272239	COL1A1_7413	+	GTGACCTATGCACCAGACGTCCGAGAGGAGGAGGCGCCCTGTGGTGAGGGGCCATCTGATAGATCGGAAGAGCGGTTTCAG
chr17	48272472	48272511	COL1A1_7414	+	GTGACCTATGCACCAGACGTGGAGAAGAGGATGAGCTGAGAGTCGGGGGCGCTCAGTTGGAGATCGGAAGAGCGGTTTCAG
chr17	48272702	48272741	COL1A1_7415	+	GTGACCTATGCACCAGACGTGAGACAGCCAGGGCGTGAGCCTAGGAGCAGAGGGAAAGGGAGATCGGAAGAGCGGTTTCAG
chr17	48272850	48272889	COL1A1_7416	+	GTGACCTATGCACCAGACGTGAGAAAGGAGTGTCAAGCAACAGGCAAGGACTCTGAGGTTAAGATCGGAAGAGCGGTTTCAG
chr17	48273037	48273076	COL1A1_7417	+	GTGACCTATGCACCAGACGTAGAAGAGCATATCAGAAGCCACCCTGGGAAACCACTTAGATCGGAAGAGCGGTTTCAG
chr17	48273348	48273387	COL1A1_7418	+	GTGACCTATGCACCAGACGTAAATGGAGATGTCAGCGAGAAAGAGATGGCAGTGCAAAAGATCGGAAGAGCGGTTTCAG
chr17	48273571	48273610	COL1A1_7419	+	GTGACCTATGCACCAGACGTGAGGGGAAGCCCGTTAAGTCCACTGAGCACTGGCCAGTCAGATCGGAAGAGCGGTTTCAG
chr17	48273739	48273778	COL1A1_7420	+	GTGACCTATGCACCAGACGTAAACAAAGAGAAGTCAGATGAGATGGAGACAGCCTTGTTCAGATCGGAAGAGCGGTTTCAG
chr17	48273900	48273939	COL1A1_7421	+	GTGACCTATGCACCAGACGTGAGAAATAATGAGTGAGAAATTCATTCATGGTGGGACTCTGAGATCGGAAGAGCGGTTTCAG
chr17	48274042	48274081	COL1A1_7422	+	GTGACCTATGCACCAGACGTAAAGAGGTAGAAGTGAAGAACCTGTGGAGGGGGTGAACAAGATCGGAAGAGCGGTTTCAG
chr17	48274435	48274474	COL1A1_7423	+	GTGACCTATGCACCAGACGTATGAAAGAAGACAAGGAAAGGCCCTAGTAACACATCAGCTAGATCGGAAGAGCGGTTTCAG
chr17	48274605	48274644	COL1A1_7424	+	GTGACCTATGCACCAGACGTGAGAAAAAGCATCATGCCTTGCTCCACCACCCTAGATCGGAAGAGCGGTTTCAG



chr17	48275157	48275196	COL1A1_7425	+	GTGACCTATGCACCAGACGTTAGAAGAGGTGGTTAGAATATGGATAAGAAAAAGAAGGAGATCGGAAGAGCGGTTTCAG
chr17	48275374	48275413	COL1A1_7426	+	GTGACCTATGCACCAGACGTAGGAAAAAGATGGGTAGAAGACAAGTCCTGTCAACCTTAGATCGGAAGAGCGGTTTCAG
chr17	48275577	48275616	COL1A1_7427	+	GTGACCTATGCACCAGACGTAGAAGAAAGGGGGTTCATGGTATCCCTCTGTAGGAAAGCAGATCGGAAGAGCGGTTTCAG
chr17	48275876	48275915	COL1A1_7428	+	GTGACCTATGCACCAGACGTCAAGAGAAGTCAGAGTGAGGACAGTGAATTGAAAGGCAGAAGATCGGAAGAGCGGTTTCAG
chr17	48276699	48276738	COL1A1_7429	+	GTGACCTATGCACCAGACGTAGAGGGCGGGCCGGGGTGAAGCGTGGGCGCCGAGAGCCATGAGATCGGAAGAGCGGTTTCAG
chr17	48276825	48276864	COL1A1_7430	+	GTGACCTATGCACCAGACGTGGGGGAGAAGAAACAAGAGCCACAGTTAGAGAAGGGGGAAGATCGGAAGAGCGGTTTCAG
chr17	48276962	48277001	COL1A1_7431	+	GTGACCTATGCACCAGACGTAAAGACAGCCGCTTAGAGCCAAAGTTTTGCTAATGCTCAGATCGGAAGAGCGGTTTCAG
chr17	48277319	48277358	COL1A1_7432	+	GTGACCTATGCACCAGACGTGGAAGAGGGGCGCTTGTGACTAGTACTGCAACCCCCAGCAGATCGGAAGAGCGGTTTCAG
chr17	48278885	48278924	COL1A1_7433	+	GTGACCTATGCACCAGACGTTAGACATGTAGACTCTTTGTTGGCTGGGGAGGGGTTAGCGAGATCGGAAGAGCGGTTTCAG
chr3	168802842	168802881	MECOM_7434	+	GTGACCTATGCACCAGACGTAAAGGAGAGACTCAGTAAATGGCATTGAAAAACATCACAGATCGGAAGAGCGGTTTCAG
chr3	168806982	168807021	MECOM_7435	+	GTGACCTATGCACCAGACGTCCAACGAAAAACACAGAAATTTCTTTTTCATTTGTTATCTAGATCGGAAGAGCGGTTTCAG
chr3	168808035	168808074	MECOM_7436	+	GTGACCTATGCACCAGACGTCAAAAAAAAGTCCAAATTTGTTGGTTTCATTTTAAAAAGATCGGAAGAGCGGTTTCAG
chr3	168810901	168810940	MECOM_7437	+	GTGACCTATGCACCAGACGTGCAAAAGCCCTTTATGACAAAAGATTATTGTTTTATCTAGCAAGATCGGAAGAGCGGTTTCAG
chr3	168813044	168813083	MECOM_7438	+	GTGACCTATGCACCAGACGTAAACAAGAGAAAAATATTAGCAAGCACATTAAGAGTTTATGATCGGAAGAGCGGTTTCAG
chr3	168818761	168818800	MECOM_7439	+	GTGACCTATGCACCAGACGTAAAGATGTTATAAGAGAAAAGTCAGCACAGTTGACTATATTAGATCGGAAGAGCGGTTTCAG
chr3	168820025	168820064	MECOM_7440	+	GTGACCTATGCACCAGACGTAAAGCACAAAGCCATGAAGCGTTTGGCATTCTTCTTAAGATCGGAAGAGCGGTTTCAG
chr3	168825751	168825790	MECOM_7441	+	GTGACCTATGCACCAGACGTAATTAACAAAAACAAAAATTTACTTCTGTGTTGGTATCAGATCGGAAGAGCGGTTTCAG
chr3	168830673	168830712	MECOM_7442	+	GTGACCTATGCACCAGACGTAAAATATAGATTTGGAGATGAAGCAGTCTCACATATCAATAGATCGGAAGAGCGGTTTCAG
chr3	168834538	168834577	MECOM_7443	+	GTGACCTATGCACCAGACGTACAACAAAAAAGATCTCAGGCTTATGTCAAATTGCTTCTAGATCGGAAGAGCGGTTTCAG
chr3	168839008	168839047	MECOM_7444	+	GTGACCTATGCACCAGACGTATGAGTACTGATTAAATCAAGAACTTAACTCAAGGGCACAAAGATCGGAAGAGCGGTTTCAG
chr3	168840526	168840565	MECOM_7445	+	GTGACCTATGCACCAGACGTAAACAATAGATTTAAAAAGACAAAGATGCATTATAAAGAGATCGGAAGAGCGGTTTCAG
chr3	168845859	168845898	MECOM_7446	+	GTGACCTATGCACCAGACGTAATTCAGGTGTTAGGATTGGGTGGTCAGGAATTGCCATCAAGATCGGAAGAGCGGTTTCAG
chr3	168849276	168849315	MECOM_7447	+	GTGACCTATGCACCAGACGTAGCTCTCTCCGGCCCAATGCTGCAACTACTCTATAGAAGATCGGAAGAGCGGTTTCAG
chr3	168833633	168833672	MECOM_7448	+	GTGACCTATGCACCAGACGTGTTGAACCAAGTCTTTCAGCAATAAGCAATAGCTAGATCGGAAGAGCGGTTTCAG
chr3	168834085	168834124	MECOM_7449	+	GTGACCTATGCACCAGACGTTTGACTTTTGTCTGTTTCTGTTGACTACTGATAGTCTTTAAGATCGGAAGAGCGGTTTCAG
chr17	11924329	11924368	MAP2K4_7450	+	GTGACCTATGCACCAGACGTGCGCCGCGCCGAGATCCCAGCCCCCTAGCGCGCAACCCGAGATCGGAAGAGCGGTTTCAG
chr17	11958319	11958358	MAP2K4_7451	+	GTGACCTATGCACCAGACGTTTGGTAATCAAAGGCTCAACTCAAGCAAGATTTTAAAGTAGATCGGAAGAGCGGTTTCAG
chr17	11984858	11984897	MAP2K4_7452	+	GTGACCTATGCACCAGACGTCCATGATTATTTTTGGTACTTTAATCCATTAGGATGAAATTAGATCGGAAGAGCGGTTTCAG
chr17	11999022	11999061	MAP2K4_7453	+	GTGACCTATGCACCAGACGTACTGGTTTTAGCTGACTAATGAATTAATTTGGACAAAGATCGGAAGAGCGGTTTCAG
chr17	12011237	12011276	MAP2K4_7454	+	GTGACCTATGCACCAGACGTGGTCTTTAAATTTATCTGTTGTATATAGTTATATAGAGAAGATCGGAAGAGCGGTTTCAG
chr17	12013754	12013793	MAP2K4_7455	+	GTGACCTATGCACCAGACGTATTTGGTATTTTTGTAATAGAAATTAACTTTTTTCTCCTAAGATCGGAAGAGCGGTTTCAG
chr17	12016688	12016727	MAP2K4_7456	+	GTGACCTATGCACCAGACGTAGTCCAGGCCCTTTGCTTGTATAGTATTGCACAGAGAGCAGATCGGAAGAGCGGTTTCAG
chr17	12028699	12028738	MAP2K4_7457	+	GTGACCTATGCACCAGACGTGCTGATTCAACCTTGCCACAGTAGCGTAACAATAAGAAATAGATCGGAAGAGCGGTTTCAG
chr17	12032615	12032654	MAP2K4_7458	+	GTGACCTATGCACCAGACGTGATTATGATGGTGGCAACAGCATGCGGCAAGAATAGTGAAGATCGGAAGAGCGGTTTCAG
chr17	12043212	12043251	MAP2K4_7459	+	GTGACCTATGCACCAGACGTGACTGTGGGATTGTAGGTACTCCTAACCAGGACTGATCGGAAGAGCGGTTTCAG
chr17	12044588	12044627	MAP2K4_7460	+	GTGACCTATGCACCAGACGTACATCAGACTCTAGAAAAAGGGCTGAGAGGAAGCAAGACAGATCGGAAGAGCGGTTTCAG
chr22	39621863	39621902	PDGFB_7461	+	GTGACCTATGCACCAGACGTAAAAAGAACCTCGTCAGCATGTGGACCATTGGGGAGGTAGATCGGAAGAGCGGTTTCAG
chr22	39626244	39626283	PDGFB_7462	+	GTGACCTATGCACCAGACGTGAGCCACAATAATGCCTCTGTAGAGACCACACAGCCAGGAGAGATCGGAAGAGCGGTTTCAG
chr22	39627843	39627882	PDGFB_7463	+	GTGACCTATGCACCAGACGTACGAAACCTGGGTCAGGAGCGTAGGCCCTGCCAGATCGGAAGAGCGGTTTCAG
chr22	39629540	39629579	PDGFB_7464	+	GTGACCTATGCACCAGACGTAGTACAGTCAGACACAGCCAGCCACCTTGGGCAGGAGATCGGAAGAGCGGTTTCAG
chr22	39631890	39631929	PDGFB_7465	+	GTGACCTATGCACCAGACGTGACACAAAAAGGCTGAGTGGAGTGGGAGTGGGGCTTTCCAGATCGGAAGAGCGGTTTCAG
chr3	30648480	30648519	TGFBR2_7466	+	GTGACCTATGCACCAGACGTCCCAGCCGGGCTCGGCCGGGGCGCCGGGGTCTTCTGGGAGATCGGAAGAGCGGTTTCAG
chr3	30664776	30664815	TGFBR2_7467	+	GTGACCTATGCACCAGACGTATTAATTAATCTTTTCATCATTTTTCTATTTTGTATGATCGGAAGAGCGGTTTCAG
chr3	30686418	30686457	TGFBR2_7468	+	GTGACCTATGCACCAGACGTCTTTAAGAAGTTATCTTTCTTTTCCCTTTTTACATAAAGATCGGAAGAGCGGTTTCAG
chr3	30691963	30692002	TGFBR2_7469	+	GTGACCTATGCACCAGACGTTTTCTCTTAAGGGTGTGGGACCTGAGATCTGTGCCAATTTAGATCGGAAGAGCGGTTTCAG
chr3	30713940	30713979	TGFBR2_7470	+	GTGACCTATGCACCAGACGTGCTAGTGTAGTCCCTTACCTTGAAGCTGACCACAGATCGGAAGAGCGGTTTCAG
chr3	30715749	30715788	TGFBR2_7471	+	GTGACCTATGCACCAGACGTACCAGCATCATTGTGTAGTGGTAAACTTGTCTTCAAAATAAGATCGGAAGAGCGGTTTCAG
chr3	30730014	30730053	TGFBR2_7472	+	GTGACCTATGCACCAGACGTAGTGTTTACAAAGGTGAGTAAAGATTCAACCAAGTTGCCTCAGATCGGAAGAGCGGTTTCAG
chr3	30733102	30733141	TGFBR2_7473	+	GTGACCTATGCACCAGACGTGCAGGCTGGGCCATGTCCAAAGAGGCTGCCCTCTCACAAGATCGGAAGAGCGGTTTCAG
chr3	30713540	30713579	TGFBR2_7474	+	GTGACCTATGCACCAGACGTACAGAGAAGGACATCTTCTCAGACATCAATCTGAAGCATGAGATCGGAAGAGCGGTTTCAG
chr7	98479658	98479697	TRRAP_7475	+	GTGACCTATGCACCAGACGTTATATTTTTCTATTTTCTATTTTGTAGGTAATATTCTATTAGATCGGAAGAGCGGTTTCAG
chr7	98488079	98488118	TRRAP_7476	+	GTGACCTATGCACCAGACGTAAAATAACATGAAAGACAAGGCTGCTGGGATTTGACAGATCGGAAGAGCGGTTTCAG
chr7	98490162	98490201	TRRAP_7477	+	GTGACCTATGCACCAGACGTAGAATTAATCTTGTGCTATAGCCGATGTAAAACTTTCAAGATCGGAAGAGCGGTTTCAG
chr7	98491515	98491554	TRRAP_7478	+	GTGACCTATGCACCAGACGTTAAAATCCTTATAGCATTATAAAGTGTGTCACATGTTTCAGATCGGAAGAGCGGTTTCAG
chr7	98493454	98493493	TRRAP_7479	+	GTGACCTATGCACCAGACGTACTTGGTTTTAATTAGTTACATTTGTTTATACTCCTTAAGATCGGAAGAGCGGTTTCAG
chr7	98495500	98495539	TRRAP_7480	+	GTGACCTATGCACCAGACGTCGCTGAGTTATTTACCCTGGCTCCTGCTAGTTTCGGATAGATCGGAAGAGCGGTTTCAG
chr7	98497133	98497172	TRRAP_7481	+	GTGACCTATGCACCAGACGTGCTCATTAGTCTCTTGGGTTTTGGGCTTCTATAAGAAAAGATCGGAAGAGCGGTTTCAG
chr7	98497401	98497440	TRRAP_7482	+	GTGACCTATGCACCAGACGTACTGATCCGGCTGCCACAGTGCCTGGATTCCAAGTAAAAGATCGGAAGAGCGGTTTCAG

chr7	98501151	98501190	TRRAP_7483	+	GTGACCTATGCACCAGACGTCCTGTCTTGTCTTGAATGCTGATGCTAGTCCCTGTGGCCATAGATCGGAAGAGCGGTTTCAG
chr7	98503889	98503928	TRRAP_7484	+	GTGACCTATGCACCAGACGTTAAACCAGTGATATCTGGTTGGTTAAATGCCAGGAGCATCAAGATCGGAAGAGCGGTTTCAG
chr7	98506596	98506635	TRRAP_7485	+	GTGACCTATGCACCAGACGTTTCTGAGAGTATCATCCATCCTGCACCTCTATCCTGTTTGATAGATCGGAAGAGCGGTTTCAG
chr7	98508053	98508092	TRRAP_7486	+	GTGACCTATGCACCAGACGTTCTCAGTTATGTAGACAAACAATAGTTTTCATAAAGTGAAGATCGGAAGAGCGGTTTCAG
chr7	98508241	98508280	TRRAP_7487	+	GTGACCTATGCACCAGACGTGCCCTCCAGCCAGGCTTTCGCATATGAAAGTACTCTTAAGATCGGAAGAGCGGTTTCAG
chr7	98508905	98508944	TRRAP_7488	+	GTGACCTATGCACCAGACGTCCTTTTTATGTGTTGTTGAACATTACAATCTTTTGTTAAGATCGGAAGAGCGGTTTCAG
chr7	98513522	98513561	TRRAP_7489	+	GTGACCTATGCACCAGACGTTGACTTTGGTTGCTTTTGTAGTCTTGTGTCTATGTAGTCCGGAAGAGCGGTTTCAG
chr7	98515313	98515352	TRRAP_7490	+	GTGACCTATGCACCAGACGTAGTGAGGTTGTTAGCTGGCTGCTTCCCTGGAAGCAGTGGGAGATCGGAAGAGCGGTTTCAG
chr7	98519587	98519626	TRRAP_7491	+	GTGACCTATGCACCAGACGTTGACAATGTCGTTTCGTTTAAAGCCTTGTGAAGATACTATAGATCGGAAGAGCGGTTTCAG
chr7	98522897	98522936	TRRAP_7492	+	GTGACCTATGCACCAGACGTCACCTTCCTTCTGTGTGGTTGGGTGGATCCTGTTTTAGAAAGATCGGAAGAGCGGTTTCAG
chr7	98525000	98525039	TRRAP_7493	+	GTGACCTATGCACCAGACGTGGGCACGGTGGGGCACGGGATTGGTTCTTTGACTTTTATAAGATCGGAAGAGCGGTTTCAG
chr7	98527840	98527879	TRRAP_7494	+	GTGACCTATGCACCAGACGTTGTTGAGGAGTGTCTTCTGATTTGGAGGGTGTCTGTACCTGAGATCGGAAGAGCGGTTTCAG
chr7	98528464	98528503	TRRAP_7495	+	GTGACCTATGCACCAGACGTGGTGGCCCCAAACCTTAACCATGCTGTTTTTAAATGGTTGGAGATCGGAAGAGCGGTTTCAG
chr7	98529299	98529338	TRRAP_7496	+	GTGACCTATGCACCAGACGTTGTACCAGAACCAAGGTAATTTCAACAAAACCTTTTGAGCAGATCGGAAGAGCGGTTTCAG
chr7	98531036	98531075	TRRAP_7497	+	GTGACCTATGCACCAGACGTGGTGGTGGGAGTGGTGTGGATGGTGTGATGACGTGTGTCTGAGATCGGAAGAGCGGTTTCAG
chr7	98533309	98533348	TRRAP_7498	+	GTGACCTATGCACCAGACGTGAAAATCTACGGGGTATAAAAGTGAAGAGGAGACTGACCACAGATCGGAAGAGCGGTTTCAG
chr7	98540651	98540690	TRRAP_7499	+	GTGACCTATGCACCAGACGTTGTTGTGTTCTGGGAAGGGCACCCAGCCCATGCTGGTCCAGATCGGAAGAGCGGTTTCAG
chr7	98545974	98546013	TRRAP_7500	+	GTGACCTATGCACCAGACGTTAGTGAAGGCTGCTTCCGCTTCCGCTGTCACCTGCCAGTCTTAGATCGGAAGAGCGGTTTCAG
chr7	98546319	98546358	TRRAP_7501	+	GTGACCTATGCACCAGACGTTGACGAGCTGGAGTACAGGGTCCCTTCAAATGCTTGTGAGAGATCGGAAGAGCGGTTTCAG
chr7	98547215	98547254	TRRAP_7502	+	GTGACCTATGCACCAGACGTTTCTCCAGCCCCAATGCCAGGGGTTAATCGAGACACAGATCGGAAGAGCGGTTTCAG
chr7	98547475	98547514	TRRAP_7503	+	GTGACCTATGCACCAGACGTCCTCCCGCCCTGCCCGCGGGACTGGCTCTGTCCAAAAGAGATCGGAAGAGCGGTTTCAG
chr7	98547896	98547935	TRRAP_7504	+	GTGACCTATGCACCAGACGTCCTTATGCTGTAGAAGGGTATGGGATTTGGTCTGGTTAGATCGGAAGAGCGGTTTCAG
chr7	98548638	98548677	TRRAP_7505	+	GTGACCTATGCACCAGACGTTATGTGTGGTGTGAGAAGTAGCCGTCGATGGATGAAGATCGGAAGAGCGGTTTCAG
chr7	98551067	98551106	TRRAP_7506	+	GTGACCTATGCACCAGACGTGGCTCCCTGCTGTCCGCCACATCAGCGTGAATCTCACATGAGATCGGAAGAGCGGTTTCAG
chr7	98552938	98552977	TRRAP_7507	+	GTGACCTATGCACCAGACGTGGGACGGTGGGCTGCCGGCGCGCGTCTTACGGCATTACAGATCGGAAGAGCGGTTTCAG
chr7	98553938	98553977	TRRAP_7508	+	GTGACCTATGCACCAGACGTCAGCCTCAGGGGTGCCCGGATGCTTCTCTTACTTCTCAGATCGGAAGAGCGGTTTCAG
chr7	98554167	98554206	TRRAP_7509	+	GTGACCTATGCACCAGACGTGTGCCCTCTGTATGGGTGCTGCGCATTCTGCTGGGAGTTGGAGATCGGAAGAGCGGTTTCAG
chr7	98555725	98555764	TRRAP_7510	+	GTGACCTATGCACCAGACGTCAAGTCCCTGCGTTAGGCTTCTGACAGCCAGAGGCTACAGATCGGAAGAGCGGTTTCAG
chr7	98557124	98557163	TRRAP_7511	+	GTGACCTATGCACCAGACGTTGTCTGAAGGGCCAGGGCAGCCAGCCAGATCGGAAGAGCGGTTTCAG
chr7	98559108	98559147	TRRAP_7512	+	GTGACCTATGCACCAGACGTTTTCCACGGGTGCTTTTCTTCAAAGTGGACGGTGGCCGAGATCGGAAGAGCGGTTTCAG
chr7	98560061	98560100	TRRAP_7513	+	GTGACCTATGCACCAGACGTGTCTGTCTGCTGGTGTGCTGGTGGCTCAGTTTGGCCTCTTATAGATCGGAAGAGCGGTTTCAG
chr7	98562409	98562448	TRRAP_7514	+	GTGACCTATGCACCAGACGTGGCCACCGGGGGCTTTCTCAGACTCTGTTGAACAGAGAAGATCGGAAGAGCGGTTTCAG
chr7	98563529	98563568	TRRAP_7515	+	GTGACCTATGCACCAGACGTACGGTGTGCCATGTGATCTCCCTTTCAATAAAAGAAAATTAGATCGGAAGAGCGGTTTCAG
chr7	98564796	98564835	TRRAP_7516	+	GTGACCTATGCACCAGACGTTCAATTAATCAAGTACTACATATATGGTCTTAAATGTGCTATAGATCGGAAGAGCGGTTTCAG
chr7	98565332	98565371	TRRAP_7517	+	GTGACCTATGCACCAGACGTTCCGGCTCACATCTGTCCCGGGGGCAGCTGTGGGTTTCTAGATCGGAAGAGCGGTTTCAG
chr7	98567925	98567964	TRRAP_7518	+	GTGACCTATGCACCAGACGTGCACCCACAGGCAGAATCCCAGAGAGGAGGTGAGGCCCCAGATCGGAAGAGCGGTTTCAG
chr7	98569579	98569618	TRRAP_7519	+	GTGACCTATGCACCAGACGTAGCTTGAAGAGGATTGCTTCTTCCATGGACAGTTAGATCGGAAGAGCGGTTTCAG
chr7	98573902	98573941	TRRAP_7520	+	GTGACCTATGCACCAGACGCTTTTAAATCCTGTTTTGGAAAATTTGATGTTTGTAGCTTTTAGATCGGAAGAGCGGTTTCAG
chr7	98574404	98574443	TRRAP_7521	+	GTGACCTATGCACCAGACGTGCCCTCAGTTTGTAAATACCTCTTCCCTGCCAGTGACTTCCAGATCGGAAGAGCGGTTTCAG
chr7	98574710	98574749	TRRAP_7522	+	GTGACCTATGCACCAGACGTGACCACTGACGGTCTGGGTGTGTAATGAGAGGTCATTAAGATCGGAAGAGCGGTTTCAG
chr7	98575957	98575996	TRRAP_7523	+	GTGACCTATGCACCAGACGTCACAGTGCTTGACGTGTCATGAATCAGTTAAGGGAAACCAAGATCGGAAGAGCGGTTTCAG
chr7	98576538	98576577	TRRAP_7524	+	GTGACCTATGCACCAGACGTCGGGGGGCATCCCTGCCGCTGCCTGGTCCCTTTCTGAAGATCGGAAGAGCGGTTTCAG
chr7	98579594	98579633	TRRAP_7525	+	GTGACCTATGCACCAGACGTTGCCCCATGCGAGCACAGGCTGTGGCCTGTGCGAGCCAAGATCGGAAGAGCGGTTTCAG
chr7	98581992	98582031	TRRAP_7526	+	GTGACCTATGCACCAGACGTGACACTTGAAGAATGAGGCCAGGTGGAGATTGAGGCCAGGAGATCGGAAGAGCGGTTTCAG
chr7	98582678	98582717	TRRAP_7527	+	GTGACCTATGCACCAGACGTTATATGAAAGGATAAGAGAAAAAATGCATCAGATTATTAGATCGGAAGAGCGGTTTCAG
chr7	98586600	98586639	TRRAP_7528	+	GTGACCTATGCACCAGACGTTAAACAGCCTTTGACGAGGAAACCACTGTACCTTCAAGAAATCGGAAGAGCGGTTTCAG
chr7	98588253	98588292	TRRAP_7529	+	GTGACCTATGCACCAGACGTGAGGGTGGCCTTGTTCACGTGCACAAAACATTGTGTCTTCCAGATCGGAAGAGCGGTTTCAG
chr7	98589861	98589900	TRRAP_7530	+	GTGACCTATGCACCAGACGTTGGTGGGCGGTAGGCCAGGCCGGGAAGGGCTCATTCCAGAGATCGGAAGAGCGGTTTCAG
chr7	98591371	98591410	TRRAP_7531	+	GTGACCTATGCACCAGACGTCGTATCTTGACATGGTGGCTCCTTGTAGAGGGGACGTGGAGATCGGAAGAGCGGTTTCAG
chr7	98592482	98592521	TRRAP_7532	+	GTGACCTATGCACCAGACGTATTTTCTTCCCTTCCATAGGGAGAATGTGCACGCTGATAGATCGGAAGAGCGGTTTCAG
chr7	98602049	98602088	TRRAP_7533	+	GTGACCTATGCACCAGACGTGACCTGGCAGTGGAACTAACCCAGCCGCCCCATGGACAAGATCGGAAGAGCGGTTTCAG
chr7	98602982	98603021	TRRAP_7534	+	GTGACCTATGCACCAGACGTGAGCCACAGCTCGTGGGTACACAGGCAGCTTACAGGTGAGATCGGAAGAGCGGTTTCAG
chr7	98606195	98606234	TRRAP_7535	+	GTGACCTATGCACCAGACGTGGCCGGCCGGGGCCGAGCTGCCGCTGCAGCCCTCTGAGATCGGAAGAGCGGTTTCAG
chr7	98608889	98608928	TRRAP_7536	+	GTGACCTATGCACCAGACGTTTGAACAGCCAGATCCTCTCCTGTGACATCGCCTTTCTGAGATCGGAAGAGCGGTTTCAG
chr7	98609169	98609208	TRRAP_7537	+	GTGACCTATGCACCAGACGTACGTCGTCCTATCACAGCGCAGGCTAGAGCCACTCAGATAGATCGGAAGAGCGGTTTCAG
chr7	98609989	98610028	TRRAP_7538	+	GTGACCTATGCACCAGACGTACCGCCACCCGGAATGTGAAGGGCGCTCCGGGCTCTGAGATCGGAAGAGCGGTTTCAG
chr4	110834629	110834668	EGF_7539	+	GTGACCTATGCACCAGACGTTCAATGAAAAGTGCTTCCGAGGCTCCGCGAAAAGCTGCCCAAGATCGGAAGAGCGGTTTCAG
chr4	110862312	110862351	EGF_7540	+	GTGACCTATGCACCAGACGTTTACACTAGTGTGTTGAGCTGTTTTGTACAGGCTGACAAAGATCGGAAGAGCGGTTTCAG

chr4	110864602	110864641	EGF_7541	+	GTGACCTATGCACCAGACGTCTGTATTAGACATTGAAATATATTTACAAATCTAGTGAAGATCGGAAGAGCGGTTTCAG
chr4	110865236	110865275	EGF_7542	+	GTGACCTATGCACCAGACGTCTCTTGGTATAAAAAATAAAACAATTGTCAATTTGAAGTCCACAGATCGGAAGAGCGGTTTCAG
chr4	110866442	110866481	EGF_7543	+	GTGACCTATGCACCAGACGTGTTGACCTTGCAGCGGCTGACACATAGTTCACCCATAGATCGGAAGAGCGGTTTCAG
chr4	110880604	110880643	EGF_7544	+	GTGACCTATGCACCAGACGTGAAGTACTGTGAAGGTAATGGAAGAGTCGCTGCTTGAGGGAGATCGGAAGAGCGGTTTCAG
chr4	110882156	110882195	EGF_7545	+	GTGACCTATGCACCAGACGTGCAACAAGTATTATTGTCATTAGTTTTCTTCATTTTCAATAGATCGGAAGAGCGGTTTCAG
chr4	110883152	110883191	EGF_7546	+	GTGACCTATGCACCAGACGTGGTTGCTTATTACCTTTTGTGTTTGAACAATACATTAGATCGGAAGAGCGGTTTCAG
chr4	110884465	110884504	EGF_7547	+	GTGACCTATGCACCAGACGTGGTTGCTGTGCAACTGTGTCCCTGAAAAAAATTCATGAAAAGATCGGAAGAGCGGTTTCAG
chr4	110885704	110885743	EGF_7548	+	GTGACCTATGCACCAGACGTGTTACTTGAACAGATGTGGACATGCTTTAAGGACAGAGTAAGATCGGAAGAGCGGTTTCAG
chr4	110890286	110890325	EGF_7549	+	GTGACCTATGCACCAGACGTGCTTCAGTTTTAAAGTGTGTGAGATGGGAGTATGATGGGATAGATCGGAAGAGCGGTTTCAG
chr4	110895974	110896013	EGF_7550	+	GTGACCTATGCACCAGACGTGAAAAATAAGGCACTGCTCTGCAGAGGTCATGTGACAGTAGATCGGAAGAGCGGTTTCAG
chr4	110897402	110897441	EGF_7551	+	GTGACCTATGCACCAGACGTGGGATGGGCGATTTTTCTTTGACTGAGTGTTTATGAGAGATCGGAAGAGCGGTTTCAG
chr4	110901306	110901345	EGF_7552	+	GTGACCTATGCACCAGACGTGAGATGTACACAGTCTTTCTTGGCTGGAATCTGCAACTAGATCGGAAGAGCGGTTTCAG
chr4	110902142	110902181	EGF_7553	+	GTGACCTATGCACCAGACGTAAATATGTGCAAAATTAACCTAACGTTGGCTCGAAAAACAGATCGGAAGAGCGGTTTCAG
chr4	110904708	110904747	EGF_7554	+	GTGACCTATGCACCAGACGTCTAGTTCCTCAATATACCTTTGGTTCACACAGTTTCCATCAGATCGGAAGAGCGGTTTCAG
chr4	110909027	110909066	EGF_7555	+	GTGACCTATGCACCAGACGTAGGGCAAAATCACATATTTGACAATACTGAACCAGAAACAGATCGGAAGAGCGGTTTCAG
chr4	110909876	110909915	EGF_7556	+	GTGACCTATGCACCAGACGTACATGTGCTGGGGAGGAGGGCAGAGGCAGGCCCTCAGAAATAGATCGGAAGAGCGGTTTCAG
chr4	110914536	110914575	EGF_7557	+	GTGACCTATGCACCAGACGTGGGTGGTCTACAGTGAAGGGAGGGGACTGGCTCGGGATAGATCGGAAGAGCGGTTTCAG
chr4	110916047	110916086	EGF_7558	+	GTGACCTATGCACCAGACGTGCTGCTGTGACTGTGCACAGGAGAGATGCTATTGATCCATAGATCGGAAGAGCGGTTTCAG
chr4	110921013	110921052	EGF_7559	+	GTGACCTATGCACCAGACGTCTTTCTTTGGTACTGAAACCTCTTTCTAAGACCTCCCAAGATCGGAAGAGCGGTTTCAG
chr4	110925789	110925828	EGF_7560	+	GTGACCTATGCACCAGACGTCAAAGCAGATGAAGCAAGGAATTGGCTTGATATTAACCCAGATCGGAAGAGCGGTTTCAG
chr4	110929397	110929436	EGF_7561	+	GTGACCTATGCACCAGACGTATCCCTGGCTCCTGGTGAATGGTATTTTTACTTAGATCCAGATCGGAAGAGCGGTTTCAG
chr4	110932622	110932661	EGF_7562	+	GTGACCTATGCACCAGACGTAAAAGGAAAGTCAAGAAGAATGAACATGTGCGATGCACAAGATCGGAAGAGCGGTTTCAG
chr13	28578322	28578361	FLT3_7563	+	GTGACCTATGCACCAGACGTGAAAGAGACAGAACAATGATTACCATCTGATGTAGATGCAAGATCGGAAGAGCGGTTTCAG
chr13	28588705	28588744	FLT3_7564	+	GTGACCTATGCACCAGACGTAAATGAAACAAGGAACAAGATCTGAAATGAAGCAAGATCGGAAGAGCGGTTTCAG
chr13	28589404	28589443	FLT3_7565	+	GTGACCTATGCACCAGACGTCAATGACAATTGCAGCCATTATCCATTTCTTTCATTTGTAGATCGGAAGAGCGGTTTCAG
chr13	28589849	28589888	FLT3_7566	+	GTGACCTATGCACCAGACGTCCCAGAGGAGATAAGATGGTGAATTTCCACATACAGACAAGATCGGAAGAGCGGTTTCAG
chr13	28592737	28592776	FLT3_7567	+	GTGACCTATGCACCAGACGTGACACCAGAGTGTATTACTGTGATGTGATTATCTGAGATCGGAAGAGCGGTTTCAG
chr13	28597625	28597664	FLT3_7568	+	GTGACCTATGCACCAGACGTGAGCCAGTCTTCACTTTTGCAAAAACTCAAGAAGTTGCCAGATCGGAAGAGCGGTTTCAG
chr13	28599091	28599130	FLT3_7569	+	GTGACCTATGCACCAGACGTATTTGTTTTTCAATTTTACATTTCTTCTCAGCAGAAGATCGGAAGAGCGGTTTCAG
chr13	28601389	28601428	FLT3_7570	+	GTGACCTATGCACCAGACGTACAGTTCAATTAATAGGCATACACAAAACCAACTGTTATAGATCGGAAGAGCGGTTTCAG
chr13	28602436	28602475	FLT3_7571	+	GTGACCTATGCACCAGACGTAAAGAGCATTAAAAATGAAAACTCAAGTAAAATACGAATAGATCGGAAGAGCGGTTTCAG
chr13	28608139	28608178	FLT3_7572	+	GTGACCTATGCACCAGACGTAAATGGTGAAGTACGTGCATTTAAAGATTTTCCAAATGGAAGATCGGAAGAGCGGTTTCAG
chr13	28608362	28608401	FLT3_7573	+	GTGACCTATGCACCAGACGTGAAATGATGACTCAGTTAGGAATAGGCAGTTCTGCAGATAAGATCGGAAGAGCGGTTTCAG
chr13	28608555	28608594	FLT3_7574	+	GTGACCTATGCACCAGACGTAGAGTGTCACTCAGCGATGAAACAGAATTCTGTGTGACAAGATCGGAAGAGCGGTTTCAG
chr13	28609821	28609860	FLT3_7575	+	GTGACCTATGCACCAGACGTAAATAGTCAAAAGATTAGACAAGTGTGACTGTCATCAGATTAGATCGGAAGAGCGGTTTCAG
chr13	28611436	28611475	FLT3_7576	+	GTGACCTATGCACCAGACGTAAAGAAATAAAGACAGATTTAGCCAAATGCTACAGGAGATAGATCGGAAGAGCGGTTTCAG
chr13	28622591	28622630	FLT3_7577	+	GTGACCTATGCACCAGACGTAAATAGGCATTTATGAGTTAGTTAATAATTCATAGGGAAGATCGGAAGAGCGGTTTCAG
chr13	28623685	28623724	FLT3_7578	+	GTGACCTATGCACCAGACGTATAAAACAGAGTTGCAATTAATGTTTTCAATCCAGACTAAGATCGGAAGAGCGGTTTCAG
chr13	28623922	28623961	FLT3_7579	+	GTGACCTATGCACCAGACGTAAAAAGTCCCAAGTGAGAAAAAAAAGTATTTTTGCCTCAGATCGGAAGAGCGGTTTCAG
chr13	28624370	28624409	FLT3_7580	+	GTGACCTATGCACCAGACGTAAAAAGATACCATTGGCTAAACAAGTTTAAAAATTAACAAGATCGGAAGAGCGGTTTCAG
chr13	28626822	28626861	FLT3_7581	+	GTGACCTATGCACCAGACGTAAAGTTAATTAACATTTTACTATTTTAAAAATAATTCTCAGATCGGAAGAGCGGTTTCAG
chr13	28631610	28631649	FLT3_7582	+	GTGACCTATGCACCAGACGTGGAAGAGAACTAGTTATTTTGGAAAAATGTGTGAAACTAAAGATCGGAAGAGCGGTTTCAG
chr13	28636217	28636256	FLT3_7583	+	GTGACCTATGCACCAGACGTGATAGAACAAAGTGAATTCATGAAAACTGCAGGTCCTAAGGAGATCGGAAGAGCGGTTTCAG
chr13	28644760	28644799	FLT3_7584	+	GTGACCTATGCACCAGACGTAAATAAAAAATGATAATGTTGATACATGCACACTTAAAAAAGATCGGAAGAGCGGTTTCAG
chr13	28674658	28674697	FLT3_7585	+	GTGACCTATGCACCAGACGTGCCCCGGGTCCCCAGGCCCGCGCCGCGCCCTGCGATGAGATCGGAAGAGCGGTTTCAG
chr17	73316645	73316684	GRB2_7586	+	GTGACCTATGCACCAGACGTGGAGCAGGAAAAACCCACATTCATTCTGGCTGTGACTAGATCGGAAGAGCGGTTTCAG
chr17	73317919	73317958	GRB2_7587	+	GTGACCTATGCACCAGACGTGAGAAGACACATGTGACCCGCTAAAGGCTCTAATTGGCAGATCGGAAGAGCGGTTTCAG
chr17	73322112	73322151	GRB2_7588	+	GTGACCTATGCACCAGACGTAAAGCAAGCTGGTCAACATCTGCTTCCCCACAAAGAAACAGATCGGAAGAGCGGTTTCAG
chr17	73328889	73328928	GRB2_7589	+	GTGACCTATGCACCAGACGTATAAGACAACAAAAAACCATATTTTCTTTTCCCTTTAGATCGGAAGAGCGGTTTCAG
chr17	73389720	73389759	GRB2_7590	+	GTGACCTATGCACCAGACGTGCTCAGTGTCTCAGCAGCTGAAGCAGGGGAAGGGAGTCTAGATCGGAAGAGCGGTTTCAG
chr17	26084390	26084429	NOS2_7591	+	GTGACCTATGCACCAGACGTAAAAACAGAGCAGTCAAGTCCAGGCTGGGATGAGCAGATCGGAAGAGCGGTTTCAG
chr17	26086112	26086151	NOS2_7592	+	GTGACCTATGCACCAGACGTAGGAACAAGTGGTGTGCTCAGCTCAGCTGCTCAGGACAAGGAGATCGGAAGAGCGGTTTCAG
chr17	26087215	26087254	NOS2_7593	+	GTGACCTATGCACCAGACGTCCCCGGGCTGTTGTTACCATGTTGGCCACCAGAGGGCCCAAGATCGGAAGAGCGGTTTCAG
chr17	26087781	26087820	NOS2_7594	+	GTGACCTATGCACCAGACGTGAGGAGAAGAGGGGCCAGTCTCAGACACCCAGGCCCAAGATCGGAAGAGCGGTTTCAG
chr17	26088268	26088307	NOS2_7595	+	GTGACCTATGCACCAGACGTACCACAAAGTGACCAACGTCACCCCACTGCCATCGCAGCAAGATCGGAAGAGCGGTTTCAG
chr17	26090042	26090081	NOS2_7596	+	GTGACCTATGCACCAGACGTAGGTTGATGTCAGTGACTCAGGGCCGCTGTCCCGCTTTGGAGATCGGAAGAGCGGTTTCAG
chr17	26091181	26091220	NOS2_7597	+	GTGACCTATGCACCAGACGTAAAGGAAGTTCAGGATGAGAAAAGAGGCCCACTCAGGATAGATCGGAAGAGCGGTTTCAG
chr17	26092753	26092792	NOS2_7598	+	GTGACCTATGCACCAGACGTAAAGCAAGCTCAGGTCAGGTCAGATTGACAGGATTTCTCCAGGAGATCGGAAGAGCGGTTTCAG

chr17	26093625	26093664	NOS2_7599	+	GTGACCTATGCACCAGACGTACACAGACGGTGAATGGCAAAGTGGTTCTTGAGCGTAGAGATCGGAAGAGCGGTTCCAG
chr17	26094874	26094913	NOS2_7600	+	GTGACCTATGCACCAGACGTGTGGAGCAGACTGCGGTTAATGGTGACAGCAGCAGCATCAGATCGGAAGAGCGGTTCCAG
chr17	26096188	26096227	NOS2_7601	+	GTGACCTATGCACCAGACGTACACACACAGACACATGTCCCATGCAAGCAGCACCTGGAGATCGGAAGAGCGGTTCCAG
chr17	26096621	26096660	NOS2_7602	+	GTGACCTATGCACCAGACGTAGGGGATGACAGAGTTCTCAAGCCAGGATGAATAAAAACAAGATCGGAAGAGCGGTTCCAG
chr17	26098054	26098093	NOS2_7603	+	GTGACCTATGCACCAGACGTCCCAAGTGGACATAGCCCTCGGCTCCAGTAGGGCCCTCAGATCGGAAGAGCGGTTCCAG
chr17	26099489	26099528	NOS2_7604	+	GTGACCTATGCACCAGACGTAGACAGCAGGCGCGCTGTGTGCTGAGTCAGCCTTCCAAGATCGGAAGAGCGGTTCCAG
chr17	26100280	26100319	NOS2_7605	+	GTGACCTATGCACCAGACGTGAAAGGAGATGTGAGGCGGGCTGGCTTGGCTAGATCGGAAGAGCGGTTCCAG
chr17	26101488	26101527	NOS2_7606	+	GTGACCTATGCACCAGACGTAGGCAAGATAGGGAGTGGAGATAAGGGTGGGGGAATCAGGAGATCGGAAGAGCGGTTCCAG
chr17	26105828	26105867	NOS2_7607	+	GTGACCTATGCACCAGACGTAGAGTGATAGCGGGCAGTCCGTCCCTGAAGCCACCCAGAGATCGGAAGAGCGGTTCCAG
chr17	26107943	26107982	NOS2_7608	+	GTGACCTATGCACCAGACGTAGACGGGCCCTGTGAGTCTGTAAGCCGGGGCTCGGTGTCTAGATCGGAAGAGCGGTTCCAG
chr17	26108214	26108253	NOS2_7609	+	GTGACCTATGCACCAGACGTCAAGAACAGTACTGTTTACCACCTAGCCCTGGTGGGGGCCAGATCGGAAGAGCGGTTCCAG
chr17	26109143	26109182	NOS2_7610	+	GTGACCTATGCACCAGACGTCCATCCAGACCATGCCATCAAAGACTGGGTAGACAGAGGATCGGAAGAGCGGTTCCAG
chr17	26110143	26110182	NOS2_7611	+	GTGACCTATGCACCAGACGTGGAAAGCAGCAGGAAGATGAACAATGAGATGGCCTTACATAGATCGGAAGAGCGGTTCCAG
chr17	26114863	26114902	NOS2_7612	+	GTGACCTATGCACCAGACGTAGAGGCAGGTGGTGGGGTGGGCCATTCGGCTCTTGCCAAAGATCGGAAGAGCGGTTCCAG
chr17	26115968	26116007	NOS2_7613	+	GTGACCTATGCACCAGACGTAAAAACAGGGTTTTCTCTCAGGTCTCTCTAGACCCAGAGATCGGAAGAGCGGTTCCAG
chr17	26125846	26125885	NOS2_7614	+	GTGACCTATGCACCAGACGTTACAAAGCAGGTCACTTATGTCACCTATCTGGATTTGAGAGATCGGAAGAGCGGTTCCAG
chr15	40453467	40453506	BUB1B_7615	+	GTGACCTATGCACCAGACGTGAAAGAGCTGCTGGGGCTGGCCCTGAGAGGCACGCGCTAGATCGGAAGAGCGGTTCCAG
chr15	40457408	40457447	BUB1B_7616	+	GTGACCTATGCACCAGACGTGGCTGAGTCTCAACTGCTGCTTCACTTAAATGTTGAGATCGGAAGAGCGGTTCCAG
chr15	40462333	40462372	BUB1B_7617	+	GTGACCTATGCACCAGACGTATTATTCACAAGACAATAGAAACATTAACAGATAAGTCCAGATCGGAAGAGCGGTTCCAG
chr15	40462893	40462932	BUB1B_7618	+	GTGACCTATGCACCAGACGTCTCAAGTGCATCTGAGTTTTAAATATTAAC TAAGAGATAGATCGGAAGAGCGGTTCCAG
chr15	40468885	40468924	BUB1B_7619	+	GTGACCTATGCACCAGACGTTTTGGAGCTTGTCTAACTCTAAAATAATAGAAATAATAGATCGGAAGAGCGGTTCCAG
chr15	40476095	40476134	BUB1B_7620	+	GTGACCTATGCACCAGACGTAAACGTTATTTTCGGAAAAGCTGGATTCTTAGTGTTAAAAGATCGGAAGAGCGGTTCCAG
chr15	40477591	40477630	BUB1B_7621	+	GTGACCTATGCACCAGACGTTTTAGATCCAGTCTTGTGCTGACACAACAAGACTTTCATATAGATCGGAAGAGCGGTTCCAG
chr15	40477854	40477893	BUB1B_7622	+	GTGACCTATGCACCAGACGTTTTTGGATATTTTGAAGTGGAAATTTAAGGGTGGGCAAGATCGGAAGAGCGGTTCCAG
chr15	40488986	40489025	BUB1B_7623	+	GTGACCTATGCACCAGACGTTCACAGTTTGTGAAAGGACTTAACTTAGTTGTGTAAGGAGATCGGAAGAGCGGTTCCAG
chr15	40491939	40491978	BUB1B_7624	+	GTGACCTATGCACCAGACGTTTTTTTTCATACAAAACAGATAATTTATTGAAACAAATTTAGATCGGAAGAGCGGTTCCAG
chr15	40492571	40492610	BUB1B_7625	+	GTGACCTATGCACCAGACGTATAGGTGGAAGGGACAATGCATATAGGAGGGCATTTGAAAGATCGGAAGAGCGGTTCCAG
chr15	40493192	40493231	BUB1B_7626	+	GTGACCTATGCACCAGACGTTTTGACAGCCTTTGAGAAGAAGCTTGTCTGATAACAAATGTATAGATCGGAAGAGCGGTTCCAG
chr15	40494677	40494716	BUB1B_7627	+	GTGACCTATGCACCAGACGTTTTTTTGTCTTTTGGTTTTTACTTAAAGATTTCTGAGATCGGAAGAGCGGTTCCAG
chr15	40494906	40494945	BUB1B_7628	+	GTGACCTATGCACCAGACGTGTATCCTTAAAGTTAATGTAATGGGCTAGTGGATTGTTAAGATCGGAAGAGCGGTTCCAG
chr15	40498670	40498709	BUB1B_7629	+	GTGACCTATGCACCAGACGTATTTACAGGTTTTTACAACACAGATTGTTTACTCTCTTATTAGATCGGAAGAGCGGTTCCAG
chr15	40500982	40501021	BUB1B_7630	+	GTGACCTATGCACCAGACGTCAACCACATATCCATGCCCTAGTGAACACTTGTTTATCTAGATCGGAAGAGCGGTTCCAG
chr15	40501987	40502026	BUB1B_7631	+	GTGACCTATGCACCAGACGTTTGAACCTATGCTCTGGTTCATGACAGTATACAAATAAAGATCGGAAGAGCGGTTCCAG
chr15	40502461	40502461	BUB1B_7632	+	GTGACCTATGCACCAGACGTTTCTTATAATTTCACTTACTTTGTAATAATACGGATTGAGATCGGAAGAGCGGTTCCAG
chr15	40504860	40504899	BUB1B_7633	+	GTGACCTATGCACCAGACGTCTAAAAAACATAATTTAAAGCTTCTGAAATAGAGAGATTTGATAGATCGGAAGAGCGGTTCCAG
chr15	40505686	40505725	BUB1B_7634	+	GTGACCTATGCACCAGACGTTTTATTCTTATAATTTCTGCCAGCTGTCTCTTAAACATGGAGATCGGAAGAGCGGTTCCAG
chr15	40509879	40509918	BUB1B_7635	+	GTGACCTATGCACCAGACGTAAACAAGCCTGAGCAATATGGAGAGGGTTTTCTTAATCTCTAGATCGGAAGAGCGGTTCCAG
chr15	40510774	40510813	BUB1B_7636	+	GTGACCTATGCACCAGACGTGTAATGTCAGGGTCTCTGCCTGTCCCAATAATTTCTGTAGATCGGAAGAGCGGTTCCAG
chr15	40512971	40513010	BUB1B_7637	+	GTGACCTATGCACCAGACGTCAAGTCTCACAGATTGCTGCCTCAGAGCAATGGTTGATTAGATCGGAAGAGCGGTTCCAG
chr12	12871259	12871298	CDKN1B_7638	+	GTGACCTATGCACCAGACGTTTTCCAAACATAGAATGTGTTTGGGCCCCGCTTGGCTAGATCGGAAGAGCGGTTCCAG
chr12	12871891	12871930	CDKN1B_7639	+	GTGACCTATGCACCAGACGTGGGTTGATCACTAAAGAGCAGCAGCATGGAACCCGGGCCAGATCGGAAGAGCGGTTCCAG
chr1	68512991	68513030	DIRAS3_7640	+	GTGACCTATGCACCAGACGTCCGAGGGGAGATACGTGCACAAGTCTCCACACTTAGCTAGATCGGAAGAGCGGTTCCAG
chr1	68512646	68512685	DIRAS3_7641	+	GTGACCTATGCACCAGACGTAAAGCGGTGGCCCCGGGCTATAACGTGGCGCTGCAGAGCGCAGATCGGAAGAGCGGTTCCAG
chr19	2164275	2164314	DOT1L_7642	+	GTGACCTATGCACCAGACGTCCCTCCACCGTCCCTACCTCCCGGCTCCCTCTCCGCCAGATCGGAAGAGCGGTTCCAG
chr19	2180766	2180805	DOT1L_7643	+	GTGACCTATGCACCAGACGTGGCCCTGACGTGTGTCTTCCACAGCCCTGAGCCACTTCCAGATCGGAAGAGCGGTTCCAG
chr19	2185939	2185978	DOT1L_7644	+	GTGACCTATGCACCAGACGTTCTCCTGTCAGCGCTCCGCTCCGAGCAGACTCGGCTCTAGATCGGAAGAGCGGTTCCAG
chr19	2189805	2189844	DOT1L_7645	+	GTGACCTATGCACCAGACGTTGCCCTGCCAGAGGGGTTAGTAGTGCCAGGCTCCCGAGATCGGAAGAGCGGTTCCAG
chr19	2191250	2191289	DOT1L_7646	+	GTGACCTATGCACCAGACGTCCCGCCATGCCCGGCTCTGTGCCTCAGGCCACACGCAGATCGGAAGAGCGGTTCCAG
chr19	2193793	2193832	DOT1L_7647	+	GTGACCTATGCACCAGACGTCTGAGGGCCAGGGTGTGTTGGAGGCAGGGACCATCAGAGAGATCGGAAGAGCGGTTCCAG
chr19	2199949	2199988	DOT1L_7648	+	GTGACCTATGCACCAGACGTCTGGGGCCAGCGGCATGTGGGGTGTGCGCTCACAGGCAGATCGGAAGAGCGGTTCCAG
chr19	2202789	2202828	DOT1L_7649	+	GTGACCTATGCACCAGACGTCTCCCTGCCGTCTGTGTGGTGTGATGATTGAGGAAGATCGGAAGAGCGGTTCCAG
chr19	2206807	2206846	DOT1L_7650	+	GTGACCTATGCACCAGACGTCATGTTGTTAATGATGAACAGCGGTAATTTAAACATCAGATCGGAAGAGCGGTTCCAG
chr19	2207690	2207729	DOT1L_7651	+	GTGACCTATGCACCAGACGTGCTGCGCCTCAGCCGCAGGGCCGCTCGTGGTCTTCCACCCAGATCGGAAGAGCGGTTCCAG
chr19	2208986	2209025	DOT1L_7652	+	GTGACCTATGCACCAGACGTGTGTTTTTCTCTGGGTTAATAACACGCATGCACCTGATGAGATCGGAAGAGCGGTTCCAG
chr19	2210520	2210559	DOT1L_7653	+	GTGACCTATGCACCAGACGTAGCCTGGCTCTGTGCTGGAGGGCACCCTCCCTCCAGATCGGAAGAGCGGTTCCAG
chr19	2210865	2210904	DOT1L_7654	+	GTGACCTATGCACCAGACGTCCACGCCCAGGGCCCCGCTCTCCCGAGTGCCGATGCCATAGATCGGAAGAGCGGTTCCAG
chr19	2211222	2211261	DOT1L_7655	+	GTGACCTATGCACCAGACGTGTGAGGCGTCCGGCTCTGGGCTTGGGTCATCCAGATCGGAAGAGCGGTTCCAG
chr19	2211852	2211891	DOT1L_7656	+	GTGACCTATGCACCAGACGTGCCCTTGGCATTCCGCTCCCGCACAGAGGCAGTTTCAGATCGGAAGAGCGGTTCCAG

chr19	2213650	2213689	DOT1L_7657	+	GTGACCTATGCACCAGACGTCCAGAGGGCAGGTGGCAGGTGGCAGCTGGGGCGCAGGCTGAGATCGGAAGAGCGGTTTCAG
chr19	2213996	2214035	DOT1L_7658	+	GTGACCTATGCACCAGACGTGCGGCCAAGGACAGGGACGTGGAACCAGAGGGGCCCTGCCAGATCGGAAGAGCGGTTTCAG
chr19	2214606	2214645	DOT1L_7659	+	GTGACCTATGCACCAGACGTGCGGAGGCTGCACTCCGTGGTGTCCGAGCCTCTCCATCAAGATCGGAAGAGCGGTTTCAG
chr19	2216775	2216814	DOT1L_7660	+	GTGACCTATGCACCAGACGTTGGTGGGGCTGGGGTCTGCAGCTGGTACTGCCACTCTAGATCGGAAGAGCGGTTTCAG
chr19	2217100	2217139	DOT1L_7661	+	GTGACCTATGCACCAGACGTGACCCCTGCCCGGGCTCAGGGAGGTGCTCAGCAGAGGCAGATCGGAAGAGCGGTTTCAG
chr19	2217928	2217967	DOT1L_7662	+	GTGACCTATGCACCAGACGTCCCAGGTGGCTGTCCCCAAGGGCCACGTTGAGGCAAAACAAGATCGGAAGAGCGGTTTCAG
chr19	2220232	2220271	DOT1L_7663	+	GTGACCTATGCACCAGACGTTCCTGTGCCCTACCTCAGACTCTGCTGCTGTCTGTAGATCGGAAGAGCGGTTTCAG
chr19	2222569	2222608	DOT1L_7664	+	GTGACCTATGCACCAGACGTGGACCCGACGGGCTGGGGAGCGCGGCCTGTGAAAGAAAGAAGATCGGAAGAGCGGTTTCAG
chr19	2223496	2223535	DOT1L_7665	+	GTGACCTATGCACCAGACGTGGGCCCGAGGGGGCGGGCCTGGCAGCAGGGGCAGGAGATCGGAAGAGCGGTTTCAG
chr19	2225462	2225501	DOT1L_7666	+	GTGACCTATGCACCAGACGTAGTGTTTTCGGCGCTGGCCAGGCCTGTCCGTGTGGCCGTGAGATCGGAAGAGCGGTTTCAG
chr19	2229802	2229841	DOT1L_7667	+	GTGACCTATGCACCAGACGTTCAACCCGCGACTATGCAAGGACGGTGTGGACCAACTCAGATCGGAAGAGCGGTTTCAG
chr19	2222277	2222316	DOT1L_7668	+	GTGACCTATGCACCAGACGTCTGAGAGTGAAGCCAAAGGAGGATTGTGTTCCACTCAAGATCGGAAGAGCGGTTTCAG
chr19	2226664	2226703	DOT1L_7669	+	GTGACCTATGCACCAGACGTGAGGGCAGCCGCCAAGGAGCAGGGGAGGGCGCCCTACAGATCGGAAGAGCGGTTTCAG
chr3	134514542	134514581	EPHB1_7670	+	GTGACCTATGCACCAGACGTCTCCACGGAGCAAGTTGGCTGCTGGTGGCCGGCCGCTTGGAGATCGGAAGAGCGGTTTCAG
chr3	134644733	134644772	EPHB1_7671	+	GTGACCTATGCACCAGACGTAAACCATTGCTCTTCAGTCCCTGCTATGAGGTCTGGATCCAGATCGGAAGAGCGGTTTCAG
chr3	134670905	134670944	EPHB1_7672	+	GTGACCTATGCACCAGACGTGAGCCTCTGCTTCCTGCCACTCTATGGCAGGGCCAGATCTAGATCGGAAGAGCGGTTTCAG
chr3	134825456	134825495	EPHB1_7673	+	GTGACCTATGCACCAGACGTAGTAATGGCTCTGGCTGGGGAGTTGGTTCCCTGTAGATCGGAAGAGCGGTTTCAG
chr3	134851902	134851941	EPHB1_7674	+	GTGACCTATGCACCAGACGTAGGCTCTGTGCTGCTGTGGTGTGGCTGGTGTGGATCGGAAGAGCGGTTTCAG
chr3	134873129	134873168	EPHB1_7675	+	GTGACCTATGCACCAGACGTTTACTGCAAGCTTGCAAGCCAAAGGCCAGCCACTGTAGATCGGAAGAGCGGTTTCAG
chr3	134881033	134881072	EPHB1_7676	+	GTGACCTATGCACCAGACGTGGGAGGGCAGTGGCATAATCACAGGGCAGGCAGTGTGGGAAGATCGGAAGAGCGGTTTCAG
chr3	134884929	134884968	EPHB1_7677	+	GTGACCTATGCACCAGACGTCACTCTCACTTGTCTCTCTGGACCAGGAAGCCCTCTCAGATCGGAAGAGCGGTTTCAG
chr3	134885859	134885898	EPHB1_7678	+	GTGACCTATGCACCAGACGTAGCAGAGACCCTGGTGTCTGACCCCCACAGGCCACTGAGTACAGATCGGAAGAGCGGTTTCAG
chr3	134898835	134898874	EPHB1_7679	+	GTGACCTATGCACCAGACGTTCCCTGCTCTTGTTCCTTGTCTCTGCTGTTCCCAACACTTAGATCGGAAGAGCGGTTTCAG
chr3	134911676	134911715	EPHB1_7680	+	GTGACCTATGCACCAGACGCTCAAGGGTGTGGTGGTTCAGATCGAGTGAATGATAGATCGGAAGAGCGGTTTCAG
chr3	134920542	134920581	EPHB1_7681	+	GTGACCTATGCACCAGACGTTTGGCATTCTCAAGTAGAAGCATGGCATGAGTTAAAGGGAGATCGGAAGAGCGGTTTCAG
chr3	134960150	134960189	EPHB1_7682	+	GTGACCTATGCACCAGACGTGCAGCACTTGGTCCACAAAACCCCCATTGAAGGGATCCCAGATCGGAAGAGCGGTTTCAG
chr3	134967362	134967401	EPHB1_7683	+	GTGACCTATGCACCAGACGTTGAACCGGTGATCCCTAAATATGGCTGGTTTCATGGTTCAGAGATCGGAAGAGCGGTTTCAG
chr3	134968344	134968383	EPHB1_7684	+	GTGACCTATGCACCAGACGTAGAATCTCTGTCCAGACCACACTAGGGGTCAGTGCTCAGATCGGAAGAGCGGTTTCAG
chr3	134977973	134978012	EPHB1_7685	+	GTGACCTATGCACCAGACGTTTCTGGGAAGGAGAGAGGACCAGGGTCAAGAGATCGGAAGAGCGGTTTCAG
chr3	134670564	134670603	EPHB1_7686	+	GTGACCTATGCACCAGACGTAAACACAGAACTCAGGACTTTGGCCCTTACTCGGAATGAGATCGGAAGAGCGGTTTCAG
chr7	142561096	142561135	EPHB6_7687	+	GTGACCTATGCACCAGACGTGGGGAGACAGGAGAACCAGACCTGCCATAGAGACCCAGTATAGATCGGAAGAGCGGTTTCAG
chr7	142561464	142561503	EPHB6_7688	+	GTGACCTATGCACCAGACGTCCTAATTCTGAACCTGAATCCCTTGGCCCTGCCCTCCCAGATCGGAAGAGCGGTTTCAG
chr7	142562515	142562554	EPHB6_7689	+	GTGACCTATGCACCAGACGTACTCGTCTTGCCTTGGCCGACACTCCACCCACCCCCAAGATCGGAAGAGCGGTTTCAG
chr7	142563396	142563435	EPHB6_7690	+	GTGACCTATGCACCAGACGTCAACCCAGCCCTGCAATGGGAAGAGACTTGGAGAGGGCCAGATCGGAAGAGCGGTTTCAG
chr7	142564082	142564121	EPHB6_7691	+	GTGACCTATGCACCAGACGTTTCCCTTGGCTTCAAGATCCCCTGCCTCCGCTCTTTGAGAGATCGGAAGAGCGGTTTCAG
chr7	142564371	142564410	EPHB6_7692	+	GTGACCTATGCACCAGACGTGGAGTGGGGTTCGCGCAGTAGGGCTGGTAGGAGCTCATAGAGATCGGAAGAGCGGTTTCAG
chr7	142564834	142564873	EPHB6_7693	+	GTGACCTATGCACCAGACGTGCAAGGGCCAGATGGGCAGGTGAAGGCCCAAGTGGGTAGAGATCGGAAGAGCGGTTTCAG
chr7	142565488	142565527	EPHB6_7694	+	GTGACCTATGCACCAGACGTACCCTGCCAACCTCTGCCAGCACCATTAACTCCACAGCAGATCGGAAGAGCGGTTTCAG
chr7	142565815	142565854	EPHB6_7695	+	GTGACCTATGCACCAGACGTGGAGAGGAAATGGGTGGGGCTGGGGAACACATGGTGGGGAGATCGGAAGAGCGGTTTCAG
chr7	142566126	142566165	EPHB6_7696	+	GTGACCTATGCACCAGACGTGCCAAAGCAGGGATCAGAGCAGCGGGCTCCCTTGTGCCAGATCGGAAGAGCGGTTTCAG
chr7	142566505	142566544	EPHB6_7697	+	GTGACCTATGCACCAGACGTCCTGGGTGAAGGAGGAGGGTCCCTTGGGTCAGGAAGCTTAGATCGGAAGAGCGGTTTCAG
chr7	142566911	142566950	EPHB6_7698	+	GTGACCTATGCACCAGACGTAGCCTTGGGGACACAGCCTGGGGCCTTGTGGCATGCCCAAGATCGGAAGAGCGGTTTCAG
chr7	142567730	142567769	EPHB6_7699	+	GTGACCTATGCACCAGACGTACCTAGACTGCTGATTCCCACCCCGATCCCTCCCAGGAGATCGGAAGAGCGGTTTCAG
chr7	142568171	142568210	EPHB6_7700	+	GTGACCTATGCACCAGACGTTGGGGCTAGAGCCTGGGAAAGCCAGGGAGGGTATAGTCAAAGATCGGAAGAGCGGTTTCAG
chr7	142568449	142568488	EPHB6_7701	+	GTGACCTATGCACCAGACGTAGTGGTGGGGTGGGGGCGAATGCTCCAGGCCCTGGCTGGAGATCGGAAGAGCGGTTTCAG
chr7	142568668	142568707	EPHB6_7702	+	GTGACCTATGCACCAGACGTACCCTGACTCAGCCTAGCAGCTGTCCGAGAAGGACAAAGATCGGAAGAGCGGTTTCAG
chr7	142562124	142562163	EPHB6_7703	+	GTGACCTATGCACCAGACGTGGGGCTGGACTGCAACTGAACGTCAAAGAGCGGAGCTTTGGAGATCGGAAGAGCGGTTTCAG
chr20	57415910	57415949	GNAS_7704	+	GTGACCTATGCACCAGACGTGCTCCAGATTCTCCTTGTTCATGGATTAGGTTAGTGTAGATCGGAAGAGCGGTTTCAG
chr20	57430399	57430438	GNAS_7705	+	GTGACCTATGCACCAGACGTGGACTCTGCCTGCGGGCAGCAGGGCCCGCCGGGAACCGGGAGATCGGAAGAGCGGTTTCAG
chr20	57470750	57470789	GNAS_7706	+	GTGACCTATGCACCAGACGTAATCTGTGCAGGGGGCCCAAGTAAAGGAACAGACTTTAGATCGGAAGAGCGGTTTCAG
chr20	57474051	57474090	GNAS_7707	+	GTGACCTATGCACCAGACGTTCAAACAGAAAAATTTGAACAACAAACAACAAATGAGATCGGAAGAGCGGTTTCAG
chr20	57478651	57478690	GNAS_7708	+	GTGACCTATGCACCAGACGTGCTCCTTGTGCTGTCTGTCTGTAGCGCCCTCCAGCCAGAGATCGGAAGAGCGGTTTCAG
chr20	57478857	57478896	GNAS_7709	+	GTGACCTATGCACCAGACGTCCCCGACTTGTGTGGCCTTAGCCCGCCACCTGAGCACAAAGATCGGAAGAGCGGTTTCAG
chr20	57480546	57480585	GNAS_7710	+	GTGACCTATGCACCAGACGTGCCACCAACCCATCAGCACATAAACAGACAAAAACAAGAGATCGGAAGAGCGGTTTCAG
chr20	57484282	57484321	GNAS_7711	+	GTGACCTATGCACCAGACGTCCCCCTCCACCAGAGACTCTGAGCCCTCTTTCCAAACTAGATCGGAAGAGCGGTTTCAG
chr20	57484489	57484528	GNAS_7712	+	GTGACCTATGCACCAGACGTTGTACCTTTTTATATAACAGAGATCATGGTTTCTTGACAAGATCGGAAGAGCGGTTTCAG
chr20	57484645	57484684	GNAS_7713	+	GTGACCTATGCACCAGACGTGTGGGCTGGCTTGTGTAAGAAGCCCTTGTCTGTAGATCGGAAGAGCGGTTTCAG
chr20	57484870	57484909	GNAS_7714	+	GTGACCTATGCACCAGACGTTGACGCCCCACCCCTGCGCTTGGCCAGGAGGCCCTGGTTCAGATCGGAAGAGCGGTTTCAG

chr20	57485147	57485186	GNAS_7715	+	GTGACCTATGCACCAGACGTCCTCCACTCTTGCTGGCTGTTTCATTGCGGTGGTTCTTTTATAGATCGGAAGAGCGGTTTCCAG
chr20	57485467	57485506	GNAS_7716	+	GTGACCTATGCACCAGACGTCCTGTCTTTAGTTTCCTCTCTTGTCTCCTCTTTTCTCAGATCGGAAGAGCGGTTTCCAG
chr20	57485895	57485934	GNAS_7717	+	GTGACCTATGCACCAGACGTCCTCCAAATTTAATTAAGCCTTAAGCACAATTAATAAAGAGATCGGAAGAGCGGTTTCCAG
chr20	57415541	57415580	GNAS_7718	+	GTGACCTATGCACCAGACGTCGGAGCCTGAGACCGCCCCACCCTGAGCCCCGAGACCGAAGATCGGAAGAGCGGTTTCCAG
chr20	57428744	57428783	GNAS_7719	+	GTGACCTATGCACCAGACGTTGAGCCTCAGTGGTCCAGACAGGCCTGGGAGGATACAAGATCGGAAGAGCGGTTTCCAG
chr20	57429157	57429196	GNAS_7720	+	GTGACCTATGCACCAGACGTCGCCATCGGCAGCCCAAGAGGCTGTGACACCTCTAGATCGGAAGAGCGGTTTCCAG
chr20	57429609	GNAS_7721		+	GTGACCTATGCACCAGACGTCAGCCGCTGACTCCGGGCACTTCGCAGCCGATCCCGAAGATCGGCAGAGCGGTTTCCAG
chr20	57429983	57430022	GNAS_7722	+	GTGACCTATGCACCAGACGTTCCGAGAGCAGCCGCGCGCGCTGTACTACGATGAAGAGATCGGAAGAGCGGTTTCCAG
chr14	62162568	62162607	HIF1A_7723	+	GTGACCTATGCACCAGACGTTCCCTCGGCCCGCCGCTTCTCCCCGGCGACCCCGCCGAGATCGGAAGAGCGGTTTCCAG
chr14	62187301	62187340	HIF1A_7724	+	GTGACCTATGCACCAGACGTTTACAAGGTTATAAATAGGCCTGAAAATTAGAAGTTAGAAAGATCGGAAGAGCGGTTTCCAG
chr14	62188383	62188422	HIF1A_7725	+	GTGACCTATGCACCAGACGTCACATATTAAGAGCTCTTCTATATGTTTTTATGATTTTATAGATCGGAAGAGCGGTTTCCAG
chr14	62188552	62188591	HIF1A_7726	+	GTGACCTATGCACCAGACGTTCTGTTGTTGATTTAATGTGACAGGTGGTTTTACATAATAGATCGGAAGAGCGGTTTCCAG
chr14	62193547	62193586	HIF1A_7727	+	GTGACCTATGCACCAGACGTATTATTTGATTGATTATACACTTTTATATACATAGACAGATCGGAAGAGCGGTTTCCAG
chr14	62194384	62194423	HIF1A_7728	+	GTGACCTATGCACCAGACGTTCTAAAATGTGAATTTGAAATTTTTAATAGTCTACAGCAAGATCGGAAGAGCGGTTTCCAG
chr14	62199253	62199292	HIF1A_7729	+	GTGACCTATGCACCAGACGTTGGAAGAACTCAGAGATATTCTAATTACTTAAGTGTGCAAGATCGGAAGAGCGGTTTCCAG
chr14	62201014	62201053	HIF1A_7730	+	GTGACCTATGCACCAGACGTTTGAGAAATAAACATTTTTGGGGAACAATAAGTAATTTTATAGATCGGAAGAGCGGTTTCCAG
chr14	62203838	62203877	HIF1A_7731	+	GTGACCTATGCACCAGACGTTATTTTTGTTAATCCCCTAAATTTGTGCTGTGTCTACAAGCAGATCGGAAGAGCGGTTTCCAG
chr14	62205102	62205141	HIF1A_7732	+	GTGACCTATGCACCAGACGTTGATATAATGAAAAGGGACAATTTTCAGATTTTAAACATTTAGATCGGAAGAGCGGTTTCCAG
chr14	62207356	62207395	HIF1A_7733	+	GTGACCTATGCACCAGACGTTTATTTGTTTATATAAATTTTCAATTTTTATGTTTGAAGATCGGAAGAGCGGTTTCCAG
chr14	62207917	62207956	HIF1A_7734	+	GTGACCTATGCACCAGACGTGTAACATTCAAGTTATAGTTCTTTTATTATTTTTGAGATAAGATCGGAAGAGCGGTTTCCAG
chr14	62212546	62212585	HIF1A_7735	+	GTGACCTATGCACCAGACGTTCTTTTTGACCTTGAACATCACAAAAGACAAAATACATGAAGATCGGAAGAGCGGTTTCCAG
chr14	62213668	62213707	HIF1A_7736	+	GTGACCTATGCACCAGACGTGCTGGGGCAATCAATGGATGAAAGTGATTACCACAGCTGAGATCGGAAGAGCGGTTTCCAG
chr14	62213814	62213853	HIF1A_7737	+	GTGACCTATGCACCAGACGTAATTTCACTTCTTTTTTGACACTGGTGGCTCATTACATAGATCGGAAGAGCGGTTTCCAG
chr11	94153358	94153397	MRE11A_7738	+	GTGACCTATGCACCAGACGTATACAATGTTGATTGATTGACTTCCCTGCTTCACTGAAGATCGGAAGAGCGGTTTCCAG
chr11	94169076	94169115	MRE11A_7739	+	GTGACCTATGCACCAGACGTAACAAGCAACAACACAGTTTTTTGTGAGAATAGACTCTGAAAGATCGGAAGAGCGGTTTCCAG
chr11	94170412	94170451	MRE11A_7740	+	GTGACCTATGCACCAGACGTAAGATGAAATGTGCATTATGTTATTCTAAAATAACTTAAGATCGGAAGAGCGGTTTCCAG
chr11	94179070	94179109	MRE11A_7741	+	GTGACCTATGCACCAGACGTAATGAACAGTCAATGTACAAGCCTATCAGCAGCTAAGGTTAGATCGGAAGAGCGGTTTCCAG
chr11	94180615	94180654	MRE11A_7742	+	GTGACCTATGCACCAGACGTGAAGAAGGAGAAAAGTACACAACATGAGATAACGTACCATAGATCGGAAGAGCGGTTTCCAG
chr11	94189515	94189554	MRE11A_7743	+	GTGACCTATGCACCAGACGTACAGATAAATCACAAAATTTGCATTTCCAGTTATGTAGATCGGAAGAGCGGTTTCCAG
chr11	94192758	94192797	MRE11A_7744	+	GTGACCTATGCACCAGACGTTCAATCACTGGATGCAGAAATGTTTTTATTCCTTAAAAAGATCGGAAGAGCGGTTTCCAG
chr11	94194213	94194252	MRE11A_7745	+	GTGACCTATGCACCAGACGTAGAAGTATATCAAAAAATAGCTTCTATCATAATGTTAAAAAGATCGGAAGAGCGGTTTCCAG
chr11	94197416	94197455	MRE11A_7746	+	GTGACCTATGCACCAGACGTAGAATAATCTATGAACGCTAGGAAACAACAATTTGCCAATAGATCGGAAGAGCGGTTTCCAG
chr11	94201070	94201109	MRE11A_7747	+	GTGACCTATGCACCAGACGTTTAAAAAGATAAAAAACAACCTAGTAACTGAGTTTAAACAGATCGGAAGAGCGGTTTCCAG
chr11	94203819	94203858	MRE11A_7748	+	GTGACCTATGCACCAGACGTGAAAAATGAACACCGACTACAGGTTAAATTTCTCAGGGAGATCGGAAGAGCGGTTTCCAG
chr11	94204936	94204975	MRE11A_7749	+	GTGACCTATGCACCAGACGTTATTTGAAAAATATAAATTTTCGTTGATTGAAAAAATTTTCATAGATCGGAAGAGCGGTTTCCAG
chr11	94209580	94209619	MRE11A_7750	+	GTGACCTATGCACCAGACGTCATTACATTATTTTTAAATTTGTTTTCTTACTTCGCTTAAAGATCGGAAGAGCGGTTTCCAG
chr11	94212053	94212092	MRE11A_7751	+	GTGACCTATGCACCAGACGTTAATTTCAAAGAATGTTAGTGTGTATGTAAGTAGGTATAGATCGGAAGAGCGGTTTCCAG
chr11	94212938	94212977	MRE11A_7752	+	GTGACCTATGCACCAGACGTTAAAAGTTACTTAAAATTTCCATACGGGACAAAAGCTGTTTAGATCGGAAGAGCGGTTTCCAG
chr11	94219261	94219300	MRE11A_7753	+	GTGACCTATGCACCAGACGTTAAAAAGGTGTTAAAATTTAGTATGTTTTACAGGTAAAATTAGATCGGAAGAGCGGTTTCCAG
chr11	94224142	94224181	MRE11A_7754	+	GTGACCTATGCACCAGACGTTAAGAAGAAACATTTCAATATATAAATTTTCAATTAAGAGATCGGAAGAGCGGTTTCCAG
chr11	94225978	94226017	MRE11A_7755	+	GTGACCTATGCACCAGACGTTAAGCTCCTCTGAGGACCACTTCTTCTTCCAAAGAACCCAGATCGGAAGAGCGGTTTCCAG
chr16	81819798	81819837	PLCG2_7756	+	GTGACCTATGCACCAGACGTGCTGGGTGGGGCAGTGTGGCCGCTCTCTGGGCCCCGGCAGATCGGAAGAGCGGTTTCCAG
chr16	81888203	81888242	PLCG2_7757	+	GTGACCTATGCACCAGACGTTTCTGTGCCCTTCTCCTTCCCTGTGCCCTTGTGCTTCCAGATCGGAAGAGCGGTTTCCAG
chr16	81891972	81892011	PLCG2_7758	+	GTGACCTATGCACCAGACGTTTTGCTGTGATTGCGTAGTTGCTGATTCTTTTATCTAGATCGGAAGAGCGGTTTCCAG
chr16	81892779	81892818	PLCG2_7759	+	GTGACCTATGCACCAGACGTTTTCAGTTTTTTCTGATCACTTTGGATTTCGATCCTCATTAGATCGGAAGAGCGGTTTCCAG
chr16	81902914	81902953	PLCG2_7760	+	GTGACCTATGCACCAGACGTTGGCTGAGCCTGGGAATTTTATGATTCGAGCTAGATCGGAAGAGCGGTTTCCAG
chr16	81904551	81904590	PLCG2_7761	+	GTGACCTATGCACCAGACGTTCTTGGCAAGTATCAAGTATGTTTCTGTTTTCCATGTAGATCGGAAGAGCGGTTTCCAG
chr16	81914569	81914608	PLCG2_7762	+	GTGACCTATGCACCAGACGTTCTGTGTGCTGTTGGGGCGGCTGTGCCGGACCTCGGTGAGATCGGAAGAGCGGTTTCCAG
chr16	81916957	81916996	PLCG2_7763	+	GTGACCTATGCACCAGACGTTAAGTGTGTGGTGCCTGAGGAGCTGGCGGGATGCTGCTAGATCGGAAGAGCGGTTTCCAG
chr16	81922889	81922928	PLCG2_7764	+	GTGACCTATGCACCAGACGTTGGGCTTGTGTGCTTGGGGGTGACTTTTTGATTGATGTAGATCGGAAGAGCGGTTTCCAG
chr16	81925206	81925245	PLCG2_7765	+	GTGACCTATGCACCAGACGTGATGCTGTGATGGTGTGGGCACACAGACGCTGAGAGATCGGAAGAGCGGTTTCCAG
chr16	81927410	81927449	PLCG2_7766	+	GTGACCTATGCACCAGACGTCCTTCTGTTGAGGTGAGGCTCGCAGCAAAATAGAGATAAGATCGGAAGAGCGGTTTCCAG
chr16	81929543	81929582	PLCG2_7767	+	GTGACCTATGCACCAGACGTTGATTTCTGGGTGGTGTGACTTAAAGGGGAAGGCAGCTAGAGATCGGAAGAGCGGTTTCCAG
chr16	81934396	81934435	PLCG2_7768	+	GTGACCTATGCACCAGACGTCGGGTGCTGCTGTTGGCTGTCCAGGGAGCCCAGTGGCTCGAGATCGGAAGAGCGGTTTCCAG
chr16	81939123	81939162	PLCG2_7769	+	GTGACCTATGCACCAGACGTTGCCCTTCCGTAGCCACTGCGGCCACGCCCTTGCAGCTAGATCGGAAGAGCGGTTTCCAG
chr16	81941390	81941429	PLCG2_7770	+	GTGACCTATGCACCAGACGTACCCTAGCCACATAGGGAGGAGCTCCCAAGAACCCGAGAGATCGGAAGAGCGGTTTCCAG
chr16	81942207	81942246	PLCG2_7771	+	GTGACCTATGCACCAGACGTCGACCCAGGGAACCGTACTTCTTCCATGCCAACCCGAAGATCGGAAGAGCGGTTTCCAG
chr16	81944336	81944375	PLCG2_7772	+	GTGACCTATGCACCAGACGTGAGGGTGGAGGAGGAGGCCAGGCCGTTGCTGGGTTAGTCTCAGATCGGAAGAGCGGTTTCCAG

chr16	81946332	81946371	PLCG2_7773	+	GTGACCTATGCACCAGACGTGGTGAGGGAGCCACATGCTCTACAGAGGGGCTTGCAAGGAAGATCGGAAGAGCGGTTTCAG
chr16	81953280	81953319	PLCG2_7774	+	GTGACCTATGCACCAGACGTGACTCCCTTGTGATTTGGTGGGATTTCTGTCTGAGGTTGAGATCGGAAGAGCGGTTTCAG
chr16	81954885	81954924	PLCG2_7775	+	GTGACCTATGCACCAGACGTGAACCTCCAATTCACATGATTTTGGAGTCACGAGGCTGATAGATCGGAAGAGCGGTTTCAG
chr16	81957210	81957249	PLCG2_7776	+	GTGACCTATGCACCAGACGTGTTGGAGGCTGGGCTGCTCGGCAGGTGGGCTTGACTTGTCCAGATCGGAAGAGCGGTTTCAG
chr16	81960794	81960833	PLCG2_7777	+	GTGACCTATGCACCAGACGTCTCTTCGATCCTCTACAGGAAGAAGGGATCTGCAGGTCAGATCGGAAGAGCGGTTTCAG
chr16	81962240	81962279	PLCG2_7778	+	GTGACCTATGCACCAGACGTACATCATCTTAGCCTGGATTTCACCCCTATCCCCATGGAGATCGGAAGAGCGGTTTCAG
chr16	81965270	81965309	PLCG2_7779	+	GTGACCTATGCACCAGACGTGCTCACCCGGTGCCAGTTGGGCTGGCATTCTGAGGGCTTAGATCGGAAGAGCGGTTTCAG
chr16	81968147	81968186	PLCG2_7780	+	GTGACCTATGCACCAGACGTCCCAAGAACATGCCCTATAACTCCAATGAAAACCTTAAGTATAGATCGGAAGAGCGGTTTCAG
chr16	81969994	81970033	PLCG2_7781	+	GTGACCTATGCACCAGACGTACTGAAGGTAGTCCCGTCCCTGCAAGGTGGCGGTTGCAGTAGATCGGAAGAGCGGTTTCAG
chr16	81971519	81971558	PLCG2_7782	+	GTGACCTATGCACCAGACGTCCCTCCCTTCTGCTGCCAGGGGAGCCAGCCGCCCTCCCTGGGAGATCGGAAGAGCGGTTTCAG
chr16	81972531	81972570	PLCG2_7783	+	GTGACCTATGCACCAGACGTACCTTGGGCCCTCTGCTTTTAAACGTCCGGCCAGTGAATAGATCGGAAGAGCGGTTTCAG
chr16	81973675	81973714	PLCG2_7784	+	GTGACCTATGCACCAGACGTTTTTAATTAAGATTTTCGATTTGGGCTGGCGTTGTACTTTAGATCGGAAGAGCGGTTTCAG
chr16	81979879	81979918	PLCG2_7785	+	GTGACCTATGCACCAGACGTAAACACCGATTAAGGGTTCCCTGAGCTATGCCTGCTGTTGAGATCGGAAGAGCGGTTTCAG
chr16	81990495	81990534	PLCG2_7786	+	GTGACCTATGCACCAGACGTCCCTCCACCTGCAAAAACCTTTTGGGGGTCTCTAGGCACAGATCGGAAGAGCGGTTTCAG
chr16	81991614	81991653	PLCG2_7787	+	GTGACCTATGCACCAGACGTATGTGTGAAGGGTATTGTGTGTGTGCGCATGTGTGTTGAGATCGGAAGAGCGGTTTCAG
chr12	112884213	112884252	PTPN11_7788	+	GTGACCTATGCACCAGACGTATGAAAAGAGAGGATCCTGAGAGTGTTTTCTAGGTAGGAAAAGATCGGAAGAGCGGTTTCAG
chr12	112888327	112888366	PTPN11_7789	+	GTGACCTATGCACCAGACGTTTTTAGTGACCACAAAGTCTGCTCCCTTGTCGCCCTGAAGATCGGAAGAGCGGTTTCAG
chr12	112891202	112891241	PTPN11_7790	+	GTGACCTATGCACCAGACGTAGTTGAAAACAGGTCGCAAGATGTACCTTTGGGTCGAAAGAGCGGTTTCAG
chr12	112892495	112892534	PTPN11_7791	+	GTGACCTATGCACCAGACGTGGAAAGCTCAAGCTTCTCTCTTAAAACCTTAAAACAAATAGATCGGAAGAGCGGTTTCAG
chr12	112893878	112893917	PTPN11_7792	+	GTGACCTATGCACCAGACGTAAAAACTGTTTTACGTGAGTTGTTATATCCTATTTTTAAGATCGGAAGAGCGGTTTCAG
chr12	112910855	112910894	PTPN11_7793	+	GTGACCTATGCACCAGACGTATATCCGCTCAGTAATAGTCACCTTGGAGATTTTGGATTAGATCGGAAGAGCGGTTTCAG
chr12	112915545	112915584	PTPN11_7794	+	GTGACCTATGCACCAGACGTCTTTTCCAGTGTTTTCTGACCATACATTTCTAGCCTATTAGATCGGAAGAGCGGTTTCAG
chr12	112915830	112915869	PTPN11_7795	+	GTGACCTATGCACCAGACGTGAACTCTTTTTCTGCTAACTGTTTTAAAGTATCAGACAGATCGGAAGAGCGGTTTCAG
chr12	112920020	112920059	PTPN11_7796	+	GTGACCTATGCACCAGACGTGGTCTGATTTCTAGACGTTGGGAAGTGGGATGTTGATGTTAGATCGGAAGAGCGGTTTCAG
chr12	112924444	112924483	PTPN11_7797	+	GTGACCTATGCACCAGACGTCTGCTGCCCTCTAGGCCACAGCCTGCTCCCTGTCTCTAGATCGGAAGAGCGGTTTCAG
chr12	112926325	112926364	PTPN11_7798	+	GTGACCTATGCACCAGACGTTGGTGGCAAGAAGCGACAGTTTCTGTTTTAGTTTATGGAGATCGGAAGAGCGGTTTCAG
chr12	112926990	112927029	PTPN11_7799	+	GTGACCTATGCACCAGACGTGAGGGCTGGCATGCGGATTCATCTCTTGTAGGCCTCAGATCGGAAGAGCGGTTTCAG
chr12	112940071	112940110	PTPN11_7800	+	GTGACCTATGCACCAGACGTCTGAAGGAAATCTTTTTACCTGGTCATGGTGGTTTTAAAAGATCGGAAGAGCGGTTTCAG
chr12	112942579	112942618	PTPN11_7801	+	GTGACCTATGCACCAGACGTGAAACTCTCAGCACAGAAATAGTATTAATGCAAGTCAGATCGGAAGAGCGGTTTCAG
chr5	131893156	131893195	RAD50_7802	+	GTGACCTATGCACCAGACGTAGTAGCCGCTTCAAGTTACAGGTCGCTACATCTTTGCGAAGATCGGAAGAGCGGTTTCAG
chr5	131911631	131911670	RAD50_7803	+	GTGACCTATGCACCAGACGTATATGATATTTGAATTTCTGTTTCATTTTCAGTCTTTTAGGAGATCGGAAGAGCGGTTTCAG
chr5	131915205	131915244	RAD50_7804	+	GTGACCTATGCACCAGACGTCTTAAATAGACTTTGTAGTCCATTAAGTTATTGAATCTGAGATCGGAAGAGCGGTTTCAG
chr5	131923393	131923432	RAD50_7805	+	GTGACCTATGCACCAGACGTGTAAGATTTTGTCTGCTCAAATTTTGGGATTTTGAAGATCGGAAGAGCGGTTTCAG
chr5	131923792	131923831	RAD50_7806	+	GTGACCTATGCACCAGACGTATTTATTTGGTCGTTTTTCTACTATGATGTTATACATAGATCGGAAGAGCGGTTTCAG
chr5	131924583	131924622	RAD50_7807	+	GTGACCTATGCACCAGACGTGAAATAACAGTATTTGTTATTTTGTTCATCATTTCTCAGATCGGAAGAGCGGTTTCAG
chr5	131925540	131925579	RAD50_7808	+	GTGACCTATGCACCAGACGTGTTTGAATAATCTAATAATTTAAGATATAACTTTTTAGAGATCGGAAGAGCGGTTTCAG
chr5	131927109	131927148	RAD50_7809	+	GTGACCTATGCACCAGACGTCTTTTTGTCTAATTATACTGTCTGGTACTTAAAATAGCAGATCGGAAGAGCGGTTTCAG
chr5	131927737	131927776	RAD50_7810	+	GTGACCTATGCACCAGACGTACATTTGGAGATGTAATAGAAATCTCTTATTTTCATGCTTAAGATCGGAAGAGCGGTTTCAG
chr5	131930747	131930786	RAD50_7811	+	GTGACCTATGCACCAGACGTACTTTATATATCAGGATCTTTGACACCTTTGAATTTTAGATCGGAAGAGCGGTTTCAG
chr5	131931513	131931552	RAD50_7812	+	GTGACCTATGCACCAGACGTGATTTACCTTCACTGTACATGTAGCAGCACATTGAAAAGAGATCGGAAGAGCGGTTTCAG
chr5	131939192	131939231	RAD50_7813	+	GTGACCTATGCACCAGACGTGTAGTTTAAAGGCAAGTAAACTTGTCCATAGGTTGCTTAGATCGGAAGAGCGGTTTCAG
chr5	131939749	131939788	RAD50_7814	+	GTGACCTATGCACCAGACGTCTGTGCTCTGTACTCATAGAGACTTTGACATTGCGAGAGATCGGAAGAGCGGTTTCAG
chr5	131944428	131944467	RAD50_7815	+	GTGACCTATGCACCAGACGTATTATATATTTACTTATCAAATATCTGTATAAACTTATAGATCGGAAGAGCGGTTTCAG
chr5	131945099	131945138	RAD50_7816	+	GTGACCTATGCACCAGACGTTTTGCTTATGATATCACTTACACATTGACATTTCTTTCTAGATCGGAAGAGCGGTTTCAG
chr5	131951833	131951872	RAD50_7817	+	GTGACCTATGCACCAGACGTAAATAACTCTTCAAGTTTAAATAACCTCTTTTACTGGAAGATCGGAAGAGCGGTTTCAG
chr5	131953997	131954036	RAD50_7818	+	GTGACCTATGCACCAGACGTGACTGGGGATTTTCTTATGCAAGTTAATAATTAACATACATAGATCGGAAGAGCGGTTTCAG
chr5	131972903	131972942	RAD50_7819	+	GTGACCTATGCACCAGACGTGGTGTATCACAATGCTCTTTCCAAAAGCCCTCTCCGCAGAGATCGGAAGAGCGGTTTCAG
chr5	131973926	131973965	RAD50_7820	+	GTGACCTATGCACCAGACGTCAAAGCCCTGGGGAGCCAACCTACCCAAAGTAACTGAAAGAGATCGGAAGAGCGGTTTCAG
chr5	131976508	131976547	RAD50_7821	+	GTGACCTATGCACCAGACGTCTTGACATGCTCTGGTTGAGTAAATCTCACCATTGGGAGATCGGAAGAGCGGTTTCAG
chr5	131978067	131978106	RAD50_7822	+	GTGACCTATGCACCAGACGTGATTTAAATGCCATAGAAATGTAGGTCCTCAGAAAAGTGAAGATCGGAAGAGCGGTTTCAG
chr15	40991054	40991093	RAD51_7823	+	GTGACCTATGCACCAGACGTAGTTGCTAAATTTGGAATATATACATAGATCTTCTACCTAGATCGGAAGAGCGGTTTCAG
chr15	40993410	40993449	RAD51_7824	+	GTGACCTATGCACCAGACGTCTTACTTAACTTAGGGAGGCCATTAGTGGAAATGACAAAAGATCGGAAGAGCGGTTTCAG
chr15	40998503	40998542	RAD51_7825	+	GTGACCTATGCACCAGACGTCTTTATCCTGTGTTGTAACCTCTAGTTAGGAAAGCTTCCAGATCGGAAGAGCGGTTTCAG
chr15	41001325	41001364	RAD51_7826	+	GTGACCTATGCACCAGACGTGGGGCTATAGCTAAATCAAATAAGCAAGCATTACTTCATTCAGATCGGAAGAGCGGTTTCAG
chr15	41011108	41011147	RAD51_7827	+	GTGACCTATGCACCAGACGTGGTTTAGATAAGAGAGACTATGGCTACACTTATCAATGTAAGATCGGAAGAGCGGTTTCAG
chr15	41021033	41021072	RAD51_7828	+	GTGACCTATGCACCAGACGTAGTATAAGACACCAAATGTTCTTAAGAGTCCCTCCCTGAGATCGGAAGAGCGGTTTCAG
chr15	41021843	41021882	RAD51_7829	+	GTGACCTATGCACCAGACGTGGATGGGCACAGAAATGCTACTTTTCAGTGGCTGTAAATAGATCGGAAGAGCGGTTTCAG
chr15	41022183	41022222	RAD51_7830	+	GTGACCTATGCACCAGACGTGATGGGATCGATTCCTTTTCCGGAATGTCATATTAAGTATAGATCGGAAGAGCGGTTTCAG

chr15	41023387	41023426	RAD51_7831	+	GTGACCTATGCACCAGACGTTTTTCTCTGTAAAAACCTTAAGTGCTGCAGCCTAATGAAGATCGGAAGAGCGGTTTCAG
chr13	80911851	80911890	SPRY2_7832	+	GTGACCTATGCACCAGACGTAAGTGTGGTCACTCCAGCAGCGCTTAGAACACATCTGAACTAGATCGGAAGAGCGGTTTCAG
chr13	80911377	80911416	SPRY2_7833	+	GTGACCTATGCACCAGACGTTTGGGTTGCACCCGGATTATGCCATCAGCAACAGGCCCGGAGATCGGAAGAGCGGTTTCAG
chr16	89805127	89805166	FANCA_7834	+	GTGACCTATGCACCAGACGTGGAGCAGGTCCTCAGCCCATGCCGCCACTAGGCCTCAGAAGATCGGAAGAGCGGTTTCAG
chr16	89805393	89805432	FANCA_7835	+	GTGACCTATGCACCAGACGTAACAGGCAAACCTACAGGTTAGAAGACATACAGAAACAGGAGATCGGAAGAGCGGTTTCAG
chr16	89805708	89805747	FANCA_7836	+	GTGACCTATGCACCAGACGTAGACAGTGTGACAATGGCTACAGACTGCTGGAAAGGTAGAGATCGGAAGAGCGGTTTCAG
chr16	89805972	89806011	FANCA_7837	+	GTGACCTATGCACCAGACGTAAGAAGTGGCTCAGGCAACTCTGGACATCTCTGCCTATTAAAGATCGGAAGAGCGGTTTCAG
chr16	89806518	89806557	FANCA_7838	+	GTGACCTATGCACCAGACGTCAGGAGACCAACCCTGAGAATGGCCGACCTGGTGTCTCCAAGATCGGAAGAGCGGTTTCAG
chr16	89807285	89807324	FANCA_7839	+	GTGACCTATGCACCAGACGTAAACGTGCACCTATTATTACATTAATAATACCTGTGCTGTAGATCGGAAGAGCGGTTTCAG
chr16	89809357	89809396	FANCA_7840	+	GTGACCTATGCACCAGACGTGAGAACGGGGTCATTGCGAGGGCCTTACAACCATAACAACCAGATCGGAAGAGCGGTTTCAG
chr16	89811490	89811529	FANCA_7841	+	GTGACCTATGCACCAGACGTAGCACCAGCACACAGATGAGGGTGGCTGAGATGGACACACAGATCGGAAGAGCGGTTTCAG
chr16	89813107	89813146	FANCA_7842	+	GTGACCTATGCACCAGACGTGAACGCAGCAGGAGGTGACGGTTTTGTGAGGACCCACAACAGATCGGAAGAGCGGTTTCAG
chr16	89813309	89813348	FANCA_7843	+	GTGACCTATGCACCAGACGTGTTCAAGGCAGGTAAGAAAAGCAACCCAGGAAAGAGAGGGGAAGATCGGAAGAGCGGTTTCAG
chr16	89815186	89815225	FANCA_7844	+	GTGACCTATGCACCAGACGTGGGGCTGTATTGGTGGCGACAGCACAGCGTACACTCTGCTAGATCGGAAGAGCGGTTTCAG
chr16	89816321	89816360	FANCA_7845	+	GTGACCTATGCACCAGACGTGCAGTATGCTGGCAGAGGAAGGCCTCGGGGCTCACTGCCAGATCGGAAGAGCGGTTTCAG
chr16	89818641	89818680	FANCA_7846	+	GTGACCTATGCACCAGACGTAATACATAAAATCCTCCTCAGTATCGCTAATAGTGCTGAGATCGGAAGAGCGGTTTCAG
chr16	89825124	89825163	FANCA_7847	+	GTGACCTATGCACCAGACGTAAACACTGCTATCAATCTGAGAAATGCTTCGTGGCCAGCAGATCGGAAGAGCGGTTTCAG
chr16	89828441	89828480	FANCA_7848	+	GTGACCTATGCACCAGACGTGAGCAAGCAATCAATCAATGAGACAGCACACAATCAGATCGGAAGAGCGGTTTCAG
chr16	89831485	89831524	FANCA_7849	+	GTGACCTATGCACCAGACGTGAGTGACCCGGCTTTCTTCAATGCGCAAGTTTCACTGTAGATCGGAAGAGCGGTTTCAG
chr16	89833656	89833695	FANCA_7850	+	GTGACCTATGCACCAGACGTAAATTATAACATATAAATGTAATCCATACAAAATAAGGGAAGATCGGAAGAGCGGTTTCAG
chr16	89836443	89836482	FANCA_7851	+	GTGACCTATGCACCAGACGTAATGAGGGTGGCAGAGCAGACTGCCCTCTTCCAAGCTGGAAGATCGGAAGAGCGGTTTCAG
chr16	89836678	89836717	FANCA_7852	+	GTGACCTATGCACCAGACGTAGCCGTGAAACCATCAGTACTAGCCATTCACTCCTGCACAAGATCGGAAGAGCGGTTTCAG
chr16	89837053	89837092	FANCA_7853	+	GTGACCTATGCACCAGACGTACAGTCTCATGAGCGTGGTGTCTCTGGGACGGGAGCAGCAGATCGGAAGAGCGGTTTCAG
chr16	89838233	89838272	FANCA_7854	+	GTGACCTATGCACCAGACGTGAAACTGATTAGGGATGACAAGAACCCGAAAGAGGGAAGATCGGAAGAGCGGTTTCAG
chr16	89839803	89839842	FANCA_7855	+	GTGACCTATGCACCAGACGTAAGGAAGAAACCAGATGGAAGACACTCAACAGGACTCTTAGATCGGAAGAGCGGTTTCAG
chr16	89842234	89842273	FANCA_7856	+	GTGACCTATGCACCAGACGTGGAACAATAACAATTAAGTCAGCTATGGCTTAAATTAATAGATCGGAAGAGCGGTTTCAG
chr16	89845269	89845308	FANCA_7857	+	GTGACCTATGCACCAGACGTAGAAGAGACCTGTGAGAGACTGACAGGAAAGTCCCTTGCTAGATCGGAAGAGCGGTTTCAG
chr16	89845422	89845461	FANCA_7858	+	GTGACCTATGCACCAGACGTGAGAAGCAGACAGTGTCATCAGTCAGAGCAGCGAGAAGGCAAGATCGGAAGAGCGGTTTCAG
chr16	89846376	89846415	FANCA_7859	+	GTGACCTATGCACCAGACGTACAGGGAGGAAAAGGAAAAGAACAGAGGACTTTAAAGAAAGATCGGAAGAGCGGTTTCAG
chr16	89849337	89849376	FANCA_7860	+	GTGACCTATGCACCAGACGTGACAGAGAATGAGAACAAGAAAACAAAGCAAGTTTCTGCTGAGATCGGAAGAGCGGTTTCAG
chr16	89849521	89849560	FANCA_7861	+	GTGACCTATGCACCAGACGTATAGCAGAGCGCAGCACCGTTAGTCTGGAACTGCCTGGGAGATCGGAAGAGCGGTTTCAG
chr16	89851383	89851422	FANCA_7862	+	GTGACCTATGCACCAGACGTAGAAGAGCGTGAAGCCAGGACAGCCAGGCGCGGCTGCACAGATCGGAAGAGCGGTTTCAG
chr16	89857955	89857994	FANCA_7863	+	GTGACCTATGCACCAGACGTACCATGACATATCACAGCAAGGCAAGGGGAGCCAGCAGAGATCGGAAGAGCGGTTTCAG
chr16	89858487	89858526	FANCA_7864	+	GTGACCTATGCACCAGACGTAGCATCCGCTCCTTCAATATCCAAGCAAACCAATGTGCGAGATCGGAAGAGCGGTTTCAG
chr16	89858966	89859005	FANCA_7865	+	GTGACCTATGCACCAGACGTGAGAAACAGCAAAAAAATCTCAAGTCAGAGATCAAAAAGTGTGATCGGAAGAGCGGTTTCAG
chr16	89862437	89862476	FANCA_7866	+	GTGACCTATGCACCAGACGTAGCAGAAAGAGGGTGCAGAAAGGGAGGGTGCCTTGCACGAGATCGGAAGAGCGGTTTCAG
chr16	89865498	89865537	FANCA_7867	+	GTGACCTATGCACCAGACGTTTTAAAATATCTTGGCTCTTTAATTTGGCAGACACTCCCTAGATCGGAAGAGCGGTTTCAG
chr16	89865651	89865690	FANCA_7868	+	GTGACCTATGCACCAGACGTAGCCAGGAACAGAAAACAGATGTACAGCACGCGCGGAGCAGATCGGAAGAGCGGTTTCAG
chr16	89866057	89866096	FANCA_7869	+	GTGACCTATGCACCAGACGTAGAATGTGAGTTACCATCTTGGTAATCTCTGTAATTTGTAGATCGGAAGAGCGGTTTCAG
chr16	89869760	89869799	FANCA_7870	+	GTGACCTATGCACCAGACGTATAAAACAAAGTATTATGACATCATGGTCTCCAAGCAGATCGGAAGAGCGGTTTCAG
chr16	89871811	89871850	FANCA_7871	+	GTGACCTATGCACCAGACGTACACAGAGGACAGCAAGGCTCAACTAATCCCATCATAGATCGGAAGAGCGGTTTCAG
chr16	89877221	89877260	FANCA_7872	+	GTGACCTATGCACCAGACGTAGATTACATTTTTAAAAAACAATAATACCTGAAACAATACAGATCGGAAGAGCGGTTTCAG
chr16	89877490	89877529	FANCA_7873	+	GTGACCTATGCACCAGACGTAAACAAAACCATAGCTTCTCTTAACACATGAGACAAAATAGATCGGAAGAGCGGTTTCAG
chr16	89882405	89882444	FANCA_7874	+	GTGACCTATGCACCAGACGTAAGTCGGTTTCAAACCATCACAGCAATTCACACACGGGAGATCGGAAGAGCGGTTTCAG
chr16	89883034	89883073	FANCA_7875	+	GTGACCTATGCACCAGACGTCCTACAGCCCGCGGGCTCCCTGCGCCCAGCCCGCGAGATCGGAAGAGCGGTTTCAG
chr11	22647367	22647406	FANCF_7876	+	GTGACCTATGCACCAGACGTAAAGGCGCTAAGGCTTCCGCTTCCACTTGAGAGCGGACTCTAGATCGGAAGAGCGGTTTCAG
chr11	22646617	22646656	FANCF_7877	+	GTGACCTATGCACCAGACGTACTTCCGAATTCGCCAGAAAGCCAGTGGACTAGCACTTGGCAGATCGGAAGAGCGGTTTCAG
chr11	22646992	22647031	FANCF_7878	+	GTGACCTATGCACCAGACGTGGAGCAGCCCGGCGGGAAAAGAGTTGCTGCACCAGGTGGTAGATCGGAAGAGCGGTTTCAG
chr5	176516705	176516744	FGFR4_7879	+	GTGACCTATGCACCAGACGTTGAGGTGGGAGAGGGTGGCAGGGGTGGGAAGAGTGGGACAGATCGGAAGAGCGGTTTCAG
chr5	176517665	176517704	FGFR4_7880	+	GTGACCTATGCACCAGACGTCTAGCAGGGAGTGAAGGATGCCTGGGGAGCAGACATGCAGATCGGAAGAGCGGTTTCAG
chr5	176517837	176517876	FGFR4_7881	+	GTGACCTATGCACCAGACGTCCTCAAGGACTTGTGCCCCTGCTGCTCATCATCACAGATCGGAAGAGCGGTTTCAG
chr5	176518116	176518155	FGFR4_7882	+	GTGACCTATGCACCAGACGTGGGTTCCAAAGACCCTGCTGCTCCCAATTTTCACTTCAAGATCGGAAGAGCGGTTTCAG
chr5	176518820	176518859	FGFR4_7883	+	GTGACCTATGCACCAGACGTGGCTGGGAACAGGGGAGGGCTGACCCATTTTGGGCTCAGTAGATCGGAAGAGCGGTTTCAG
chr5	176519523	176519562	FGFR4_7884	+	GTGACCTATGCACCAGACGTCACCTGCTGCAGCCTGGGCCCATCTTCTCCCACCTTGAGATCGGAAGAGCGGTTTCAG
chr5	176519796	176519835	FGFR4_7885	+	GTGACCTATGCACCAGACGTGAAGGGCCAGGAGATGCTGCGAGATGCCCTCTGGGCCAGAGATCGGAAGAGCGGTTTCAG
chr5	176520343	176520382	FGFR4_7886	+	GTGACCTATGCACCAGACGTCATCCCCACCTCACATGTGACAGCCTGACTCCAGCAGGCGATCGGAAGAGCGGTTTCAG
chr5	176520563	176520602	FGFR4_7887	+	GTGACCTATGCACCAGACGCTGTGTGGGGCCAGGGACGGCGGGTTGACAGCCGAGATCGGAAGAGCGGTTTCAG
chr5	176522452	176522491	FGFR4_7888	+	GTGACCTATGCACCAGACGTGGCGGGGCTGGCTGCACGGCCGTGAGGTGCAGGCCAAAAGATCGGAAGAGCGGTTTCAG



chr5	176522735	176522774	FGFR4_7889	+	GTGACCTATGCACCAGACGTTAGGGCTCTGAGCCCTCTCAGTCTCTCCAGCTCCACTCTAGATCGGAAGAGCGGTTTCAG
chr5	176523191	176523230	FGFR4_7890	+	GTGACCTATGCACCAGACGTTGGGGCAGAACTGGATGGGGGTGGAGGGGCACTGGGCCCGAGATCGGAAGAGCGGTTTCAG
chr5	176523369	176523408	FGFR4_7891	+	GTGACCTATGCACCAGACGTCGCGCGGTCACCTGTCTACCCACAAAAAGGCAAGGCACAGATCGGAAGAGCGGTTTCAG
chr5	176523753	176523792	FGFR4_7892	+	GTGACCTATGCACCAGACGTACCTGCCCCTGACCCCACTTCCAGTCTCTCTCTCCTCAGATCGGAAGAGCGGTTTCAG
chr5	176524409	176524448	FGFR4_7893	+	GTGACCTATGCACCAGACGTTCCACCCACCACCTCCCTCTGCCTGCTCCCTCCAGGCCAGATCGGAAGAGCGGTTTCAG
chr5	176524688	176524727	FGFR4_7894	+	GTGACCTATGCACCAGACGTAGGCTGTGCAGGCACATAGGCTGGTGGCCTTGGCCCTTGGAGATCGGAAGAGCGGTTTCAG
chr13	28877516	28877555	FLT1_7895	+	GTGACCTATGCACCAGACGTAAGGAGAAATCAAATATTCAAATTTGGTTTTTTAGAAAAGATCGGAAGAGCGGTTTCAG
chr13	28880920	28880959	FLT1_7896	+	GTGACCTATGCACCAGACGTAAGGAGAAAGTTATACTTTCCTGGCCAGCGGGGGTTCAGATCGGAAGAGCGGTTTCAG
chr13	28883075	28883114	FLT1_7897	+	GTGACCTATGCACCAGACGTAACAGAAAGAAATATCAAGACAGGAAAAGGCATCCAGCTCAGATCGGAAGAGCGGTTTCAG
chr13	28885880	28885919	FLT1_7898	+	GTGACCTATGCACCAGACGTAAGGTAAGAGCTCTCGTTGCACCAATTCTGACTTCAACAAAGATCGGAAGAGCGGTTTCAG
chr13	28886246	28886285	FLT1_7899	+	GTGACCTATGCACCAGACGTAACAGCAACAGAAATAGTTGGAGAGCAGTGATCATCTTAAGATCGGAAGAGCGGTTTCAG
chr13	28891745	28891784	FLT1_7900	+	GTGACCTATGCACCAGACGTCATGTGGAAAAACAGGGCCTGTTATGGCTTAAGGGTACAGATCGGAAGAGCGGTTTCAG
chr13	28893682	28893721	FLT1_7901	+	GTGACCTATGCACCAGACGTGCAAGGGGGCCTTGAGCAGAAAGGCATGAAAACAAAGCACAGATCGGAAGAGCGGTTTCAG
chr13	28895733	28895772	FLT1_7902	+	GTGACCTATGCACCAGACGTACAGTTGCATAATCAATGCATTTCTTAACCTAACCAACTAGATCGGAAGAGCGGTTTCAG
chr13	28896507	28896546	FLT1_7903	+	GTGACCTATGCACCAGACGTTTAGAACCGTAAGTGTGTTGTAATGGCTCTTGTATCCACAGATCGGAAGAGCGGTTTCAG
chr13	28897094	28897133	FLT1_7904	+	GTGACCTATGCACCAGACGTACCGAAAAAGACCCAGGTGAAAAGGAGCTCCAGCACACAGATCGGAAGAGCGGTTTCAG
chr13	28901698	28901737	FLT1_7905	+	GTGACCTATGCACCAGACGTAACAGCACATGCTCATGGCTCAGCCACACCAAGCCAGTCAGATCGGAAGAGCGGTTTCAG
chr13	28903876	28903915	FLT1_7906	+	GTGACCTATGCACCAGACGTGACAAGGAGACTGAGCCGCACAGCAATGGGGCTCTTAGATCGGAAGAGCGGTTTCAG
chr13	28908277	28908316	FLT1_7907	+	GTGACCTATGCACCAGACGTGAGAAGACACTGGTTTTGTTTCCGAGGCAATAGGGTGAAGATCGGAAGAGCGGTTTCAG
chr13	28913448	28913487	FLT1_7908	+	GTGACCTATGCACCAGACGTAAGAGATCTCAAAGTCATCGAGAAGAAAACAACCTTTACAAGATCGGAAGAGCGGTTTCAG
chr13	28919699	28919738	FLT1_7909	+	GTGACCTATGCACCAGACGTAAGAAATCACAAATAGTGGTGCAACAAAGAAATCCCAAACAGATCGGAAGAGCGGTTTCAG
chr13	28931833	28931872	FLT1_7910	+	GTGACCTATGCACCAGACGTAGAGATGTTTAGATTAGTGGGCTGGATGACAAAACAAAAAGATCGGAAGAGCGGTTTCAG
chr13	28959179	28959218	FLT1_7911	+	GTGACCTATGCACCAGACGTAAGAAAGGGAGCTGTGATTACTCGTCAACTTTATTCTTTAGATCGGAAGAGCGGTTTCAG
chr13	28964252	28964291	FLT1_7912	+	GTGACCTATGCACCAGACGTAGAATAAGAACTGATGTTACAGAAAATCAGTGTCTTTAGATCGGAAGAGCGGTTTCAG
chr13	28971216	28971255	FLT1_7913	+	GTGACCTATGCACCAGACGTAAGGAAACTTTAGCTAGCAACAGGACAAATAACTAATTGAGATCGGAAGAGCGGTTTCAG
chr13	28980042	28980081	FLT1_7914	+	GTGACCTATGCACCAGACGTAAGAAAGTTGTCACAATGTGGCTTTACAGCATGGTTTCAGTCAGATCGGAAGAGCGGTTTCAG
chr13	29001466	29001505	FLT1_7915	+	GTGACCTATGCACCAGACGTGATGAAGAACGGGACAGAAGTCAAGAGCAGTTCTAATGACAGATCGGAAGAGCGGTTTCAG
chr13	29002069	29002108	FLT1_7916	+	GTGACCTATGCACCAGACGTAACATGATCAGTAAGTCATTTACACGGCCCTCTCAATATAGATCGGAAGAGCGGTTTCAG
chr13	29004315	29004354	FLT1_7917	+	GTGACCTATGCACCAGACGTAGAAGTGATACATACATTAGAAAAGAAATTTCCATAAAGATCGGAAGAGCGGTTTCAG
chr13	29005458	29005497	FLT1_7918	+	GTGACCTATGCACCAGACGTAAGTATAACAAATGATTAGAAGGAGTGTTCATGCTTAAGATCGGAAGAGCGGTTTCAG
chr13	29008103	29008142	FLT1_7919	+	GTGACCTATGCACCAGACGTAAGAGAGAAATTTTTAAAATTAAGATTTTACATACAGAAAGATCGGAAGAGCGGTTTCAG
chr13	29008368	29008407	FLT1_7920	+	GTGACCTATGCACCAGACGTAGAGGCATGCATTAACAAGGTCCTATTAGCACTGGTTGGCAGATCGGAAGAGCGGTTTCAG
chr13	29012493	29012532	FLT1_7921	+	GTGACCTATGCACCAGACGTAGAAAATGAAAAAATATATACATAAATGATTGACATGCAAGATCGGAAGAGCGGTTTCAG
chr13	29041277	29041316	FLT1_7922	+	GTGACCTATGCACCAGACGTAGATAAGAAAACAAAATATTTATGGCTGGGCCCTAGGCAGATCGGAAGAGCGGTTTCAG
chr13	29041765	29041804	FLT1_7923	+	GTGACCTATGCACCAGACGTAATTTTTAAAATGTAATTTGTAATTTGTAATTTGCTCTTACCTAGATCGGAAGAGCGGTTTCAG
chr13	29068991	29069030	FLT1_7924	+	GTGACCTATGCACCAGACGTACGCGGCTGCTCGCCGGTGCCCGCGCTCCCCGCGCCAAGATCGGAAGAGCGGTTTCAG
chr13	41135008	41135047	FOXO1_7925	+	GTGACCTATGCACCAGACGTAACATCTTATTAGAAGTACAATACTTCTCTGCTTGCAAAAAGATCGGAAGAGCGGTTTCAG
chr13	41240360	41240399	FOXO1_7926	+	GTGACCTATGCACCAGACGTGCCCCCTCCCCAGCCGACGAGAGCCAAAGAGGGGAGAACAGATCGGAAGAGCGGTTTCAG
chr13	41134116	41134155	FOXO1_7927	+	GTGACCTATGCACCAGACGTACGACCAATAGGGCCCATCATGACGTTCTGGCCAGAAAGATCGGAAGAGCGGTTTCAG
chr13	41134562	41134601	FOXO1_7928	+	GTGACCTATGCACCAGACGTCATCTTTCGCGCAGATGGCGGGTACACCATGAAGATGACAGATCGGAAGAGCGGTTTCAG
chr15	66679776	66679815	MAP2K1_7929	+	GTGACCTATGCACCAGACGTGCGGGCGGTGAACTCGGGGCCGCTGGGAGGCTGGGAGGCTGGGAGATCGGAAGAGCGGTTTCAG
chr15	66727586	66727625	MAP2K1_7930	+	GTGACCTATGCACCAGACGTCCTGATTAACAGGTAATGGATTATTTCTCAGGGTACTTAAGATCGGAAGAGCGGTTTCAG
chr15	66729241	66729280	MAP2K1_7931	+	GTGACCTATGCACCAGACGTCCTCTCAGCCTCTGGAGCAATGGCCTTAAGAGTTGGGTGAGATCGGAAGAGCGGTTTCAG
chr15	66735706	66735745	MAP2K1_7932	+	GTGACCTATGCACCAGACGTTATGAAGTTTTTCTTCTAAGTCTCTCATTGATAAGTTAATAGATCGGAAGAGCGGTTTCAG
chr15	66737056	66737095	MAP2K1_7933	+	GTGACCTATGCACCAGACGTAATTTGCTAGTTATTTGCTTTGAAATTTAGATAATCCAAGATCGGAAGAGCGGTTTCAG
chr15	66774228	66774267	MAP2K1_7934	+	GTGACCTATGCACCAGACGTAAGTTTCTTCCATGCTTACGCTCTTGTACGGTCAGGGAGAGAGATCGGAAGAGCGGTTTCAG
chr15	66777540	66777579	MAP2K1_7935	+	GTGACCTATGCACCAGACGTTGGTGTGTCCCTCTTGGACTGTTGGAGGGGAGGGTCCCAGATCGGAAGAGCGGTTTCAG
chr15	66779641	66779680	MAP2K1_7936	+	GTGACCTATGCACCAGACGTCCTGGTTTCTTCACTTGGAAATTTACTTGTCTCATCTTAAAGATCGGAAGAGCGGTTTCAG
chr15	66781625	66781664	MAP2K1_7937	+	GTGACCTATGCACCAGACGTTCTTGTCTGGAAGCGTATACTCTGGATTGTGAGGCAGATCGGAAGAGCGGTTTCAG
chr15	66782112	66782151	MAP2K1_7938	+	GTGACCTATGCACCAGACGTTTATCCGGATTCTTACAGTACCTGTTTATTCATTTGTTTCAGATCGGAAGAGCGGTTTCAG
chr15	66782964	66783003	MAP2K1_7939	+	GTGACCTATGCACCAGACGTAGCAACAAAGAGCGGATCCCCCTGCGGGTGGTTTCCATGAGATCGGAAGAGCGGTTTCAG
chr19	52693438	52693477	PPP2R1A_7940	+	GTGACCTATGCACCAGACGTGAGCGGGACTTGGGGAAGACGCGGGGTACCTGGGGAGATCGGAAGAGCGGTTTCAG
chr19	52705298	52705337	PPP2R1A_7941	+	GTGACCTATGCACCAGACGTGGACCCCTGGGGCCAGATGTGGGGACTCTTGGGAGGTGGAGATCGGAAGAGCGGTTTCAG
chr19	52709327	52709366	PPP2R1A_7942	+	GTGACCTATGCACCAGACGTGGCAGGAAGTCTCTTGGCCACCCCTTAGGGTGGGCCATAGATCGGAAGAGCGGTTTCAG
chr19	52714756	52714795	PPP2R1A_7943	+	GTGACCTATGCACCAGACGTGCTCTGGAAGCTCCAAGCTCCCATCTCAGCTCCAACAGATCGGAAGAGCGGTTTCAG
chr19	52716097	52716136	PPP2R1A_7944	+	GTGACCTATGCACCAGACGTCCTTCCGTCCTGCTCTCCCTCTCTCTGGTGGTTTCTTAGATCGGAAGAGCGGTTTCAG
chr19	52716374	52716413	PPP2R1A_7945	+	GTGACCTATGCACCAGACGTGACCTGACCTGCTCCACTGGTGGGACACTGACACTCAGATCGGAAGAGCGGTTTCAG
chr19	52719157	52719196	PPP2R1A_7946	+	GTGACCTATGCACCAGACGTGACGCGGCAACACAGCAAGTGGGGTGGGTATCCAAGGGCAGATCGGAAGAGCGGTTTCAG

chr19	52719338	52719377	PPP2R1A_7947	+	GTGACCTATGCACCAGACGTGTTTGTATGGGAGGAACCAAGTGGATCCGAGCCTGCCAAAAAGATCGGAAGAGCGGTTTCAG
chr19	52719927	52719966	PPP2R1A_7948	+	GTGACCTATGCACCAGACGTCAGGATCTCAGCTCTGGGTTTGTGGAGGGGACAGGCGGGTAGATCGGAAGAGCGGTTTCAG
chr19	52723128	52723167	PPP2R1A_7949	+	GTGACCTATGCACCAGACGTAGGCCTGGGGGCCAGGCAGTGTCTGCCTCAGGGGAGGTGCAAGATCGGAAGAGCGGTTTCAG
chr19	52723513	52723552	PPP2R1A_7950	+	GTGACCTATGCACCAGACGTTACAGGAGCAGCAAGAGGAGATGGGAGCTCCAGAAAGGCAGATCGGAAGAGCGGTTTCAG
chr19	52724397	52724436	PPP2R1A_7951	+	GTGACCTATGCACCAGACGTCACCTGCCTGCTGGCCATCCCTAGGGAAGTGGAGCGCGTAGATCGGAAGAGCGGTTTCAG
chr19	52725505	52725544	PPP2R1A_7952	+	GTGACCTATGCACCAGACGTGATACTCCCCACACACTGGCAGGGCTTCTTGTGGGCACAGATCGGAAGAGCGGTTTCAG
chr19	52729072	52729111	PPP2R1A_7953	+	GTGACCTATGCACCAGACGTGAAAAGCAGCCAGCCCTAGCAGGAGGGTGGACTTTGAGGACAGATCGGAAGAGCGGTTTCAG
chr19	52729245	52729284	PPP2R1A_7954	+	GTGACCTATGCACCAGACGTGGAGCAAACACTGGCCTCTGGTGTCCACCCTCAACCCCCAGATCGGAAGAGCGGTTTCAG
chr1	186643905	186643944	PTGS2_7955	+	GTGACCTATGCACCAGACGTGATGAAGACAGAGATACAACCAATGTCAAACCTCACAAAAAGATCGGAAGAGCGGTTTCAG
chr1	186644539	186644578	PTGS2_7956	+	GTGACCTATGCACCAGACGTTAAAATTAGTTGTAAAACAAGAATTTTAGGCATATTTACTAGATCGGAAGAGCGGTTTCAG
chr1	186645327	186645366	PTGS2_7957	+	GTGACCTATGCACCAGACGTAAAATAAATAAAAAACATTTATTGTCATCTGATCACAAGAGATCGGAAGAGCGGTTTCAG
chr1	186646059	186646098	PTGS2_7958	+	GTGACCTATGCACCAGACGTGAAAAATTTAATTTTGTGGTCTGTGAAGTTTTCTTAAGATCGGAAGAGCGGTTTCAG
chr1	186646973	186647012	PTGS2_7959	+	GTGACCTATGCACCAGACGTAGAAGCTAAGGTAAAGATCCATCTATGTATTCAAGAAAGAGATCGGAAGAGCGGTTTCAG
chr1	186647547	186647586	PTGS2_7960	+	GTGACCTATGCACCAGACGTCAAAGAAAAAATGTTTTATTTATTCTCATTTGTTAAGTAAGATCGGAAGAGCGGTTTCAG
chr1	186648344	186648383	PTGS2_7961	+	GTGACCTATGCACCAGACGTACGAAGAAAGGGAGGGAGAAATTAATGGGACTCATTATAAGATCGGAAGAGCGGTTTCAG
chr1	186648581	186648620	PTGS2_7962	+	GTGACCTATGCACCAGACGTAGGACAGCAATAAATCATTCTCTAGTGTCTTAATCTTAAAGATCGGAAGAGCGGTTTCAG
chr1	186649433	186649472	PTGS2_7963	+	GTGACCTATGCACCAGACGTGGCAGGGCGCGCGGGGTAGGCTTTGCTGTCTGAGGGAGATCGGAAGAGCGGTTTCAG
chr1	154936418	154936457	SHC1_7964	+	GTGACCTATGCACCAGACGTGGGAAGGAGGCTCAATTCAGGTGAAGAGTCAAATAAGAGATCGGAAGAGCGGTTTCAG
chr1	154938268	154938307	SHC1_7965	+	GTGACCTATGCACCAGACGTAGAGGGAGGGTGGAGGGGAAGTAGCAGGCAACAACACACACACAGATCGGAAGAGCGGTTTCAG
chr1	154938564	154938603	SHC1_7966	+	GTGACCTATGCACCAGACGTAAAGGGAGGCTCTACAGTGTCCAGCCCTGCCTCCAACACAGATCGGAAGAGCGGTTTCAG
chr1	154938567	154938606	SHC1_7967	+	GTGACCTATGCACCAGACGTGGAGGCTCTACAGTGTCCAGCCCTGCCTCCAACACTCCAGATCGGAAGAGCGGTTTCAG
chr1	154938718	154938757	SHC1_7968	+	GTGACCTATGCACCAGACGTAAAATAAAGGTGAGACCAGAAGCCCTAACCAACCACTCCAGATCGGAAGAGCGGTTTCAG
chr1	154939004	154939043	SHC1_7969	+	GTGACCTATGCACCAGACGTGGACAGTGAAGCTGTGGCTGTAATGTGTGGTGGCAGGAAGATCGGAAGAGCGGTTTCAG
chr1	154940284	154940323	SHC1_7970	+	GTGACCTATGCACCAGACGTGAGGAGGCTGTGAGTGTGAGCTCAGGCCACTGGGAGGAGGATCGGAAGAGCGGTTTCAG
chr1	154940518	154940557	SHC1_7971	+	GTGACCTATGCACCAGACGTAGGTCAAATAAATTTTACAGTTCTACTTTACTCTGACCCAGATCGGAAGAGCGGTTTCAG
chr1	154940744	154940783	SHC1_7972	+	GTGACCTATGCACCAGACGTGGGCAGGGGATGAAGAAGGAAGGAATGCCATGTGTCAGGAGATCGGAAGAGCGGTTTCAG
chr1	154941101	154941140	SHC1_7973	+	GTGACCTATGCACCAGACGTGCCAGGGTCTCAGAAGGTGAGGGTTCACAGCAGAGGCAAGATCGGAAGAGCGGTTTCAG
chr1	154941321	154941360	SHC1_7974	+	GTGACCTATGCACCAGACGTAGGGGTACTCAGACCCAGCGCTGCCTGCCTGCCACAGATCGGAAGAGCGGTTTCAG
chr1	154941935	154941974	SHC1_7975	+	GTGACCTATGCACCAGACGTGGAGAAGGACAGCAGTCCAGCCCTCCCCACCCAGATCGGAAGAGCGGTTTCAG
chr1	154942683	154942722	SHC1_7976	+	GTGACCTATGCACCAGACGTAGGGGTAGGGGCGCTGAGTCTGCGAAGTGGATCTGAACAAGATCGGAAGAGCGGTTTCAG
chr1	154943013	154943052	SHC1_7977	+	GTGACCTATGCACCAGACGTAAAGAGGGGCTGCTGCCAGCCTGGCCCCCTGCCAGTTTAGATCGGAAGAGCGGTTTCAG
chr2	1418285	1418324	TPO_7978	+	GTGACCTATGCACCAGACGTAAACACATTTGCGGCTTCTGGCCTTATAAAGTTATTTTTCAAGATCGGAAGAGCGGTTTCAG
chr2	1426912	1426951	TPO_7979	+	GTGACCTATGCACCAGACGTGGGAGGGCGCCGCCAAATGCCACCGACAGGCGCATCAGATCGGAAGAGCGGTTTCAG
chr2	1437390	1437429	TPO_7980	+	GTGACCTATGCACCAGACGTCCCTCTCCCACTGAGGACGGCAACTCCGAAGGAGGAAGATCGGAAGAGCGGTTTCAG
chr2	1440167	1440206	TPO_7981	+	GTGACCTATGCACCAGACGTGGATTTTTCTTAATCTTCTGTCGTAAGTGGATCTGAACAAGATCGGAAGAGCGGTTTCAG
chr2	1457606	1457645	TPO_7982	+	GTGACCTATGCACCAGACGTAGAACGCTACTATCCTGGACTAAGATTGGGTCTGTGATGAGATCGGAAGAGCGGTTTCAG
chr2	1460065	1460104	TPO_7983	+	GTGACCTATGCACCAGACGTGAAAACGTTTCTATGTTTGTATGAAACTAAGTGTCTATTAGATCGGAAGAGCGGTTTCAG
chr2	1481387	1481426	TPO_7984	+	GTGACCTATGCACCAGACGTTGGTCTGGGCGCCCTGGGTGGCTGCGGGCAAAGCGGGGAGATCGGAAGAGCGGTTTCAG
chr2	1491774	1491813	TPO_7985	+	GTGACCTATGCACCAGACGTTCCCTTCCCTTGCACACCTCATGCAGCTGCTGCGGGATTTGAGATCGGAAGAGCGGTTTCAG
chr2	1497822	1497861	TPO_7986	+	GTGACCTATGCACCAGACGTATCCAGAGCGTCTTCTTACGTTCTGCACAGAGGCAGGTAGATCGGAAGAGCGGTTTCAG
chr2	1499980	1500019	TPO_7987	+	GTGACCTATGCACCAGACGTGTCTCCTCTCACACCAGTTACAGCATGTCATCTCATCAAGATCGGAAGAGCGGTTTCAG
chr2	1500548	1500587	TPO_7988	+	GTGACCTATGCACCAGACGTTCTTCAATGACAATTACAAAACATCTGAATGTTTCCGATAAGATCGGAAGAGCGGTTTCAG
chr2	1507862	1507901	TPO_7989	+	GTGACCTATGCACCAGACGTTCCCTCTCTCTGTCCGTCCATTTGCGAGTTTTTGAAGATCGGAAGAGCGGTTTCAG
chr2	1520765	1520804	TPO_7990	+	GTGACCTATGCACCAGACGTCACTTTTGACTGTTACTTAGACACAAGCAATCTCCTTTAGATCGGAAGAGCGGTTTCAG
chr2	1544506	1544545	TPO_7991	+	GTGACCTATGCACCAGACGTCCATGCCGCATGTTTCCAGCTGCCACCCGAGTGGTTGGACAGATCGGAAGAGCGGTTTCAG
chr2	1546257	1546296	TPO_7992	+	GTGACCTATGCACCAGACGTGCAGGACCTGCAGAACCTGCAGAACGTTTCATGTTCCAAAATCACCAGATCGGAAGAGCGGTTTCAG
chr2	1481127	1481166	TPO_7993	+	GTGACCTATGCACCAGACGTCTGCCCTTCTGTCGCCACCGCGCCCTGCGGCCTGTGCGAGATCGGAAGAGCGGTTTCAG
chr9	100437880	100437919	XPA_7994	+	GTGACCTATGCACCAGACGTAATTTTAAAGTCATCTTTTTCAGTGGTGTCTATTAGGTGAAAGATCGGAAGAGCGGTTTCAG
chr9	100447333	100447372	XPA_7995	+	GTGACCTATGCACCAGACGTAAATCCATATTTAAATAAGTTGTGATTAGACTTGCAAAAAGATCGGAAGAGCGGTTTCAG
chr9	100449554	100449593	XPA_7996	+	GTGACCTATGCACCAGACGTATTAAGTCCATTATATAAATTAGTTATTTTAAATAAGCTAAGATCGGAAGAGCGGTTTCAG
chr9	100451932	100451971	XPA_7997	+	GTGACCTATGCACCAGACGTGAAAATGAACCTAGTTTCTTTTTTATGACTAGAACATATAGATCGGAAGAGCGGTTTCAG
chr9	100456052	100456091	XPA_7998	+	GTGACCTATGCACCAGACGTGAGTAAAGCAGTCAACAATTAAGTAGTAAAGCCTGTATAGATCGGAAGAGCGGTTTCAG
chr9	100459585	100459624	XPA_7999	+	GTGACCTATGCACCAGACGTCTCCGAGGACCTAGCTCCCAGCTCCACGCACGCGCACTGCAGATCGGAAGAGCGGTTTCAG
chr3	14187670	14187709	XPC_8000	+	GTGACCTATGCACCAGACGTGGCAGTGGTGGGAGGACACAGGCGAGGGTTAGTAATCAGAAGATCGGAAGAGCGGTTTCAG
chr3	14188890	14188929	XPC_8001	+	GTGACCTATGCACCAGACGTAAATGAAGTGGGAGAAAAGTGTAAAGCACTGACATTTTCAAGATCGGAAGAGCGGTTTCAG
chr3	14189512	14189551	XPC_8002	+	GTGACCTATGCACCAGACGTACAACGCGATGTCAACCCCTCGAACCTGCTGCCTGCTGCAGATCGGAAGAGCGGTTTCAG
chr3	14190242	14190281	XPC_8003	+	GTGACCTATGCACCAGACGTTGACCAAGTCAAGTATGGCCAGCAGGGGAACAAGGCGGACATCGGAAGAGCGGTTTCAG
chr3	14190459	14190498	XPC_8004	+	GTGACCTATGCACCAGACGTTGACACGGCCACTGTTTACAACAAGGCATCCAGTTCTCAGATCGGAAGAGCGGTTTCAG

chr3	14193927	14193966	XPC_8005	+	GTGACCTATGCACCAGACGTAACACAGGACACAAAGGTAAGTCTAGTCCACAGCCCCACTGAGATCGGAAGAGCGGTTTCAG
chr3	14198006	14198045	XPC_8006	+	GTGACCTATGCACCAGACGTCAGACAGACAAAGTTGAGCATGTTATTAGAAAGAGGAAATAGATCGGAAGAGCGGTTTCAG
chr3	14200403	14200442	XPC_8007	+	GTGACCTATGCACCAGACGTATAAGAAATTTTGCTTTTTTTTCTCCCCCTCTTTTGCTAAGATCGGAAGAGCGGTTTCAG
chr3	14206444	14206483	XPC_8008	+	GTGACCTATGCACCAGACGTAGCAGGCATTCTTGTTGTGTCAGAGGTCAGGGCAAAGGGGAAAGATCGGAAGAGCGGTTTCAG
chr3	14207096	14207135	XPC_8009	+	GTGACCTATGCACCAGACGTGAAAAGGAAAGGGGCAGCATGGAAGGAAAGGCCGGACACCAGATCGGAAGAGCGGTTTCAG
chr3	14208764	14208803	XPC_8010	+	GTGACCTATGCACCAGACGTGTAGTGAATAATCTGGAAATGAAGGGGGGAAGTCAAACAGAGATCGGAAGAGCGGTTTCAG
chr3	14209787	14209826	XPC_8011	+	GTGACCTATGCACCAGACGTTGTTCAACTCTATCTCCACTGGCTTCCAGGTCAGGTCAGGAGAGATCGGAAGAGCGGTTTCAG
chr3	14209891	14209930	XPC_8012	+	GTGACCTATGCACCAGACGTGCATTTTTAAAAATCAGTAATAGTAATAACAATAATAAAGATCGGAAGAGCGGTTTCAG
chr3	14212061	14212100	XPC_8013	+	GTGACCTATGCACCAGACGTACCACAGGAAGGAAGATGAAGAAGACTCAGACATCTAGTAGATCGGAAGAGCGGTTTCAG
chr3	14214573	14214612	XPC_8014	+	GTGACCTATGCACCAGACGTACACAGAACATAAGGTGAGGGGTGGAAGGAAAGGTGGAAGGAGATCGGAAGAGCGGTTTCAG
chr3	14220079	14220118	XPC_8015	+	GTGACCTATGCACCAGACGTTGGGGCAAATTCACCTTCGCGAGTGACGCACCCGGCCGCGAAGATCGGAAGAGCGGTTTCAG
chr3	14199962	14200001	XPC_8016	+	GTGACCTATGCACCAGACGTTGAGGAGCGGGGGCTTCCCTCTGCTTTGGAGGGCCAGGTTAGATCGGAAGAGCGGTTTCAG
chr6	69349335	69349374	BAI3_8017	+	GTGACCTATGCACCAGACGTGAAGAGAGGGGAGGTGACGCGGGGAGCACTTTTGGGGATAGATCGGAAGAGCGGTTTCAG
chr6	69640572	69640611	BAI3_8018	+	GTGACCTATGCACCAGACGTAGTTACATTTTTCTATTATTGTTGTTAATTAATGAAACAGATCGGAAGAGCGGTTTCAG
chr6	69646583	69646622	BAI3_8019	+	GTGACCTATGCACCAGACGTCAGCAACTACAACGTGGATGTTATTGAATTGTGTCATGCAGATCGGAAGAGCGGTTTCAG
chr6	69653897	69653936	BAI3_8020	+	GTGACCTATGCACCAGACGTTCTGCATTTGGTTATGTTTGCATTATGTCTTTTTATATGAGATCGGAAGAGCGGTTTCAG
chr6	69666091	69666130	BAI3_8021	+	GTGACCTATGCACCAGACGTATTCCTGCATATCTGGGCATCTGATCCATGTAAGGGCAAGATCGGAAGAGCGGTTTCAG
chr6	69666712	69666751	BAI3_8022	+	GTGACCTATGCACCAGACGTACCCAAATTTCCAAAGAACATTTCCATAACGTGAAAAGATCGGAAGAGCGGTTTCAG
chr6	69684767	69684806	BAI3_8023	+	GTGACCTATGCACCAGACGTATGACCACCCCAACCCTAGTGATAATCCCATCCAAAGAAAGATCGGAAGAGCGGTTTCAG
chr6	69685243	69685282	BAI3_8024	+	GTGACCTATGCACCAGACGTAGCCAGCTTTAGTACTTGCTCTGTTTATTTTTGCTAATGAGATCGGAAGAGCGGTTTCAG
chr6	69703865	69703904	BAI3_8025	+	GTGACCTATGCACCAGACGTCAAGTTCGTGAAGGAAAGGGCTAGTGAAGATGCAATCAGTAGATCGGAAGAGCGGTTTCAG
chr6	69724009	69724048	BAI3_8026	+	GTGACCTATGCACCAGACGTGGTTATTTGAGAACTTGAAGTTGGCAAACAAAGTGTAAAAGATCGGAAGAGCGGTTTCAG
chr6	69728402	69728441	BAI3_8027	+	GTGACCTATGCACCAGACGTGGATTTTCCCCAAAATCTTTGAAATGAAAAAATTTGAGATCGGAAGAGCGGTTTCAG
chr6	69758237	69758276	BAI3_8028	+	GTGACCTATGCACCAGACGTGAAATGATGAGCTTGAACAAAGACATTTTTGATAAGTTCAGATCGGAAGAGCGGTTTCAG
chr6	69759249	69759288	BAI3_8029	+	GTGACCTATGCACCAGACGTAAAGTAATAAACTGTTGTAATTTGTAATTTTCCAAAATAGATCGGAAGAGCGGTTTCAG
chr6	69772939	69772978	BAI3_8030	+	GTGACCTATGCACCAGACGTTCCACTGGGCACTGACTTGCTTATGGAATTACCTTTCAAAGATCGGAAGAGCGGTTTCAG
chr6	69785941	69785980	BAI3_8031	+	GTGACCTATGCACCAGACGTGATGTTTTCTACATTACTTTGGGCTAAATTTCAAAGCAAGATCGGAAGAGCGGTTTCAG
chr6	69943319	69943358	BAI3_8032	+	GTGACCTATGCACCAGACGTAAAGGAAAAACCGGCTTTAACGCAAGACAGGGATATTGTAGATCGGAAGAGCGGTTTCAG
chr6	69945038	69945077	BAI3_8033	+	GTGACCTATGCACCAGACGTAATTGATAGACTGAAATGCAATGCTTAGTTGTTTCATAGATCGGAAGAGCGGTTTCAG
chr6	69949129	69949168	BAI3_8034	+	GTGACCTATGCACCAGACGTTAATTACTGATTTCTTTTTTGTTTATATTTTGGCATTAGATCGGAAGAGCGGTTTCAG
chr6	70034925	70034964	BAI3_8035	+	GTGACCTATGCACCAGACGTTGATATACCGTTTCATGCTCTTCTCAAATGACGTTGAACAGATCGGAAGAGCGGTTTCAG
chr6	70037792	70037831	BAI3_8036	+	GTGACCTATGCACCAGACGTCACAGAGATAAATCATGTTTATAATTTAACAAATCATCAAGATCGGAAGAGCGGTTTCAG
chr6	70040475	70040514	BAI3_8037	+	GTGACCTATGCACCAGACGTTAAATCAACGATTTTTGTTTTCTTAGGAAAAAAGAAAGATCGGAAGAGCGGTTTCAG
chr6	70042911	70042950	BAI3_8038	+	GTGACCTATGCACCAGACGTTGGTGGATTTTGAAGTTTATTTATCAGTGAATCCCATAGATCGGAAGAGCGGTTTCAG
chr6	70048917	70048956	BAI3_8039	+	GTGACCTATGCACCAGACGTATTCATTACATCTTCTGTTTACAATCTTTACAGTGCATAGATCGGAAGAGCGGTTTCAG
chr6	70049407	70049446	BAI3_8040	+	GTGACCTATGCACCAGACGTTTCTGTGATAGAGAACAGTGATGTTGGAATGGTATTTTCAGATCGGAAGAGCGGTTTCAG
chr6	70064231	70064270	BAI3_8041	+	GTGACCTATGCACCAGACGTTATTTTTCCCGATTGTTAATTAACCTCATGTTTCTCAAGGAGATCGGAAGAGCGGTTTCAG
chr6	70065763	70065802	BAI3_8042	+	GTGACCTATGCACCAGACGTTTAGATTTTGAATCTAATCAGTAGGGATGTTCAATCATTAGATCGGAAGAGCGGTTTCAG
chr6	70071415	70071454	BAI3_8043	+	GTGACCTATGCACCAGACGTGAAGATTAATTTTTCTTGATAGTTGAAATATGAATAGAAGATCGGAAGAGCGGTTTCAG
chr6	70082344	70082383	BAI3_8044	+	GTGACCTATGCACCAGACGTGAATTTTGAATGTAATTAAGTGAATCAAATAAGATCGGAAGAGCGGTTTCAG
chr6	70092838	70092877	BAI3_8045	+	GTGACCTATGCACCAGACGTTTGTCTTCAATGCCTGAGTAGAAGATGCATCATGTCAGATAGATCGGAAGAGCGGTTTCAG
chr6	70098794	70098833	BAI3_8046	+	GTGACCTATGCACCAGACGTATGGACTAAGGTAGAGACAAAACCTTTATTGCACTGACACTAGATCGGAAGAGCGGTTTCAG
chr6	69348956	69348995	BAI3_8047	+	GTGACCTATGCACCAGACGTTAGTCTGATGATTTCCAACATAATTTCCAGGATACAGAAAGATCGGAAGAGCGGTTTCAG
chr6	70071093	70071132	BAI3_8048	+	GTGACCTATGCACCAGACGTGTGATGCCAGAAAGTTCTGTAAATAACCAGCCTTCAATGAAGATCGGAAGAGCGGTTTCAG
chr2	215593743	215593782	BARD1_8049	+	GTGACCTATGCACCAGACGTGAGAAAAATTTGTTAAAGGCAGATCAAATACTGTATTTCAGATCGGAAGAGCGGTTTCAG
chr2	215595243	215595282	BARD1_8050	+	GTGACCTATGCACCAGACGTCACAAAGAAATTAAGCAAACTAAGTATCAAGTGAAGATAGATCGGAAGAGCGGTTTCAG
chr2	215609894	215609933	BARD1_8051	+	GTGACCTATGCACCAGACGTAAAAAGCAGTAAGAGAAAAGAAAGATACAAGCCAAAGTATAGATCGGAAGAGCGGTTTCAG
chr2	215610589	215610628	BARD1_8052	+	GTGACCTATGCACCAGACGTAAAAAGGAGATACCAGTGTAAAAACATTAGACGACTAGACAGATCGGAAGAGCGGTTTCAG
chr2	215617290	215617329	BARD1_8053	+	GTGACCTATGCACCAGACGTAAAGTGCAGATGTGTTAAGTAAGTCAAATGTGTGACTCGAAGATCGGAAGAGCGGTTTCAG
chr2	215632389	215632428	BARD1_8054	+	GTGACCTATGCACCAGACGTTTTTTGAAAAAGAGTGAAGAAGTGATAAGAAAGAGCAAAGATCGGAAGAGCGGTTTCAG
chr2	215634047	215634086	BARD1_8055	+	GTGACCTATGCACCAGACGTGAACAAAACGAAATTAAGCAATTAAGGAAAGAAAGAGATCGGAAGAGCGGTTTCAG
chr2	215646244	215646283	BARD1_8056	+	GTGACCTATGCACCAGACGTAAAGAAAAAAGAAATCTGTATCATGAAATTTATTGCTCCAGATCGGAAGAGCGGTTTCAG
chr2	215661852	215661891	BARD1_8057	+	GTGACCTATGCACCAGACGTAAATTAACAATCAAGATTTGAGTCATTGTTAGATAAACAGATCGGAAGAGCGGTTTCAG
chr2	215674304	215674343	BARD1_8058	+	GTGACCTATGCACCAGACGTTCCGATGAAAGGCTCCTCGCAGAGCGGGAAGCAAGGAAGCAGATCGGAAGAGCGGTTTCAG
chr2	215645769	215645808	BARD1_8059	+	GTGACCTATGCACCAGACGTGATTAACCTCCAAAACATTAGATTTCTGTCAGGAGCCAGATCGGAAGAGCGGTTTCAG
chr18	60796003	60796042	BCL2_8060	+	GTGACCTATGCACCAGACGTGGGAGAGGAGGGAAGAAAAGAAAGAGTATTAGAGAGAAAGATCGGAAGAGCGGTTTCAG
chr18	60985910	60985949	BCL2_8061	+	GTGACCTATGCACCAGACGTGGAAGCAACGGGGCCACCGCCACTCTCGCCCCAGCTAGATCGGAAGAGCGGTTTCAG
chr18	60985601	60985640	BCL2_8062	+	GTGACCTATGCACCAGACGTGCCTGGCGAGGGTCAAGTGCAGCCACAGGTGGCACCGGGCAGATCGGAAGAGCGGTTTCAG

chr19	11015763	11015802	CARM1_8063	+	GTGACCTATGCACCAGACGTCTCCTTCCATTCCGGTGACACCAGCCAAAGCGCCCAGAGAGATCGGAAGAGCGGTTTCAG
chr19	11018832	11018871	CARM1_8064	+	GTGACCTATGCACCAGACGTCTCCCCCTCAGCCAGGCCGCCTCCCCCGGCAGCCCCCTAGATCGGAAGAGCGGTTTCAG
chr19	11019894	11019933	CARM1_8065	+	GTGACCTATGCACCAGACGTGCGCGCATGTGCCACCTCTCTGCTTCTGTCTCGGTTTTTTAGATCGGAAGAGCGGTTTCAG
chr19	11022981	11023020	CARM1_8066	+	GTGACCTATGCACCAGACGTGCGTGGTGCCACCCAGCCTCGTCTCGCCATGAGTGCCAGATCGGAAGAGCGGTTTCAG
chr19	11024741	11024780	CARM1_8067	+	GTGACCTATGCACCAGACGTGGGGGTACACAGGCCAGCCCCCTCGGTGGAGGCCCTGGCTAGATCGGAAGAGCGGTTTCAG
chr19	11027184	11027223	CARM1_8068	+	GTGACCTATGCACCAGACGTCTGGGTGTCCCGCTGGCCGCCACAGCCTGCCTTCTCAGAGATCGGAAGAGCGGTTTCAG
chr19	11030653	11030692	CARM1_8069	+	GTGACCTATGCACCAGACGTGACAGCAGCCATGCTGGCTCCCTCCCACTCCAGGGCTTAGATCGGAAGAGCGGTTTCAG
chr19	11031260	11031299	CARM1_8070	+	GTGACCTATGCACCAGACGTCCCTGGGGCTGGTGGTGGTGGGAGGGGTCATCTGCCAGATCGGAAGAGCGGTTTCAG
chr19	11031435	11031474	CARM1_8071	+	GTGACCTATGCACCAGACGTCCCTTGCTGCACAGGGGGCGCCCGGCCCTGCAACCCAGATCGGAAGAGCGGTTTCAG
chr19	11031633	11031672	CARM1_8072	+	GTGACCTATGCACCAGACGTCCCACCCCAATGCCAGCCAAACCCGGGAGGCCGCCCTCGCAGATCGGAAGAGCGGTTTCAG
chr19	11031814	11031853	CARM1_8073	+	GTGACCTATGCACCAGACGTCCCAGGGCCAGGGGAGCCAGTGCACAGGACTGCCAGGACTGCAGATCGGAAGAGCGGTTTCAG
chr19	11032130	11032169	CARM1_8074	+	GTGACCTATGCACCAGACGTGGCGGGGGCAGGGGCCCTGGGGCGCAGCTAGCGTGTGAAGATCGGAAGAGCGGTTTCAG
chr12	56360919	56360958	CDK2_8075	+	GTGACCTATGCACCAGACGTGTGACCCGGGACTCCTAACTGGGGACTCCTTGATTGTAGATCGGAAGAGCGGTTTCAG
chr12	56361729	56361768	CDK2_8076	+	GTGACCTATGCACCAGACGTGCTGAGAGGTGATCCAGCTGGAAGGAGGATAAGTTCTGAGATCGGAAGAGCGGTTTCAG
chr12	56361964	56362003	CDK2_8077	+	GTGACCTATGCACCAGACGTTCATCAGTCTCTCATCATGGCATGTCTTGGGGACTGAGATCGGAAGAGCGGTTTCAG
chr12	56362743	56362782	CDK2_8078	+	GTGACCTATGCACCAGACGTTCATGCTTTTTCTCTGAGCTTCCAAGAGGTGTTAACTAGATCGGAAGAGCGGTTTCAG
chr12	56363371	56363410	CDK2_8079	+	GTGACCTATGCACCAGACGTTCGCCCCAAGTTCCACCCAGCCCTCCCTCTCTCCACAGATCGGAAGAGCGGTTTCAG
chr12	56365042	56365081	CDK2_8080	+	GTGACCTATGCACCAGACGTGACCTGTTCCTCATTCTTCTCCAGGGGAGCTAGATCGGAAGAGCGGTTTCAG
chr12	56365420	56365459	CDK2_8081	+	GTGACCTATGCACCAGACGTGAAGCCCCAGCCCTAATCTACCCTCTCTCCAGTGTGGAGATCGGAAGAGCGGTTTCAG
chr22	47083114	47083153	CERK_8082	+	GTGACCTATGCACCAGACGTAAAGCGCCACGTGTAACCCACAGTGTCCCTCACTCAAAGAGATCGGAAGAGCGGTTTCAG
chr22	47086108	47086147	CERK_8083	+	GTGACCTATGCACCAGACGTACAGTGAGAGGGACCATTACAGCTCAAAGCTCATCGTCTGAGATCGGAAGAGCGGTTTCAG
chr22	47087685	47087724	CERK_8084	+	GTGACCTATGCACCAGACGTAAAGAACCACGGAGATGTCACAGTTACAATGGCGCCGGGCAAGATCGGAAGAGCGGTTTCAG
chr22	47089411	47089450	CERK_8085	+	GTGACCTATGCACCAGACGTAGAATATCATCACTTTTTAAATATGGAGCTGCAGGTGCAGATCGGAAGAGCGGTTTCAG
chr22	47091223	47091262	CERK_8086	+	GTGACCTATGCACCAGACGTAGTCAGTGAAGAAATAACATCCAAAGGGTCACTTGATTGAGATCGGAAGAGCGGTTTCAG
chr22	47095373	47095412	CERK_8087	+	GTGACCTATGCACCAGACGTGAACGGCCGTGAGGGAAGGCAGCCCCCTCCAGCCCCCAGATCGGAAGAGCGGTTTCAG
chr22	47097618	47097657	CERK_8088	+	GTGACCTATGCACCAGACGTAAAAGAAGGTCCCAAATAGCATCAGAATAACAGAATTGTAGATCGGAAGAGCGGTTTCAG
chr22	47103896	47103935	CERK_8089	+	GTGACCTATGCACCAGACGTAAACACAGCCGGTCAAGGGCTCCTGCAGGTGCGGCCCTCTGAAGATCGGAAGAGCGGTTTCAG
chr22	47107057	47107096	CERK_8090	+	GTGACCTATGCACCAGACGTAAATACATCACACATTTTATTTACATCTGTGAGTCTAGATCGGAAGAGCGGTTTCAG
chr22	47108201	47108240	CERK_8091	+	GTGACCTATGCACCAGACGTACAACATGTAATAACAAACAAATAACAAAATCAAACAGATCGGAAGAGCGGTTTCAG
chr22	47116116	47116155	CERK_8092	+	GTGACCTATGCACCAGACGTGCAACGATCTCGTTAGTGCAAAAGTTTTGCAGGGTCACTGAAGATCGGAAGAGCGGTTTCAG
chr22	47116923	47116962	CERK_8093	+	GTGACCTATGCACCAGACGTACCACGTCTTCTGTCAAAGAATTCGTGAGAATCCACACAAGATCGGAAGAGCGGTTTCAG
chr22	47134056	47134095	CERK_8094	+	GTGACCTATGCACCAGACGTGGGCTCGTCCGCCAGGCTGGGGGCGCGGAGCCGAGGAGATCGGAAGAGCGGTTTCAG
chr11	46355048	46355087	DGKZ_8095	+	GTGACCTATGCACCAGACGTGCTGGGCGAGGGGAGCGCGGGCGCTTGGGACCACCCCTCTAGATCGGAAGAGCGGTTTCAG
chr11	46367146	46367185	DGKZ_8096	+	GTGACCTATGCACCAGACGTGGGGTGGCTGGGAGTGGGATGGGACCTCTGTCCCTCAAGATCGGAAGAGCGGTTTCAG
chr11	46369381	46369420	DGKZ_8097	+	GTGACCTATGCACCAGACGTGCGGCGCGGGGACGCCAGCCAGGCAAGGTTACCGCAGATCGGAAGAGCGGTTTCAG
chr11	46388545	46388584	DGKZ_8098	+	GTGACCTATGCACCAGACGTCTGTGGCCAGCAGGGCGAGTGGTGTGACCTCTGTGGGTGAGATCGGAAGAGCGGTTTCAG
chr11	46388960	46388999	DGKZ_8099	+	GTGACCTATGCACCAGACGTGAACACCCCTGGGTCCAGACCCTCTGGGCTCTTGCCAAAGATCGGAAGAGCGGTTTCAG
chr11	46389308	46389347	DGKZ_8100	+	GTGACCTATGCACCAGACGTGTAGGGGCACGCCGCCCTGCTGGTGGAGCCAGTAGCCGAGATCGGAAGAGCGGTTTCAG
chr11	46389640	46389679	DGKZ_8101	+	GTGACCTATGCACCAGACGTAGCTCAGCTTTGCCCGCCCCCTGCCCTTTGGGTGCTGAGGCAGATCGGAAGAGCGGTTTCAG
chr11	46391111	46391150	DGKZ_8102	+	GTGACCTATGCACCAGACGTAGGTTGGTCCAGGATGGGGCCACCCTAAGATTCTGCATGAGATCGGAAGAGCGGTTTCAG
chr11	46391570	46391609	DGKZ_8103	+	GTGACCTATGCACCAGACGTCTGCCCGGACATCGCCACCTGCACCTGCGGTCTGAGCAGATCGGAAGAGCGGTTTCAG
chr11	46392945	46392984	DGKZ_8104	+	GTGACCTATGCACCAGACGTCCCCCGCCCCAGGGCCAGGCCCTGCACTGCTGGGTTTGGAGATCGGAAGAGCGGTTTCAG
chr11	46393164	46393203	DGKZ_8105	+	GTGACCTATGCACCAGACGTCTGCACCCCTTGATGCCCGTACGCACCTTGGGTTCTGCCAAGATCGGAAGAGCGGTTTCAG
chr11	46393336	46393375	DGKZ_8106	+	GTGACCTATGCACCAGACGTGGCTGGGCAGAGGCTGCAGGGGAGCAGGAGAGAGGGGTTCTAGATCGGAAGAGCGGTTTCAG
chr11	46393731	46393770	DGKZ_8107	+	GTGACCTATGCACCAGACGTCTTGCCCTCAGCTAAGGGCTCGGGCGGGGGTTGGGTTGAGATCGGAAGAGCGGTTTCAG
chr11	46394071	46394110	DGKZ_8108	+	GTGACCTATGCACCAGACGTGCCAAGTTTTGTGGGACAGTGGGGGGAACCTTGCCCTAAGATCGGAAGAGCGGTTTCAG
chr11	46394238	46394277	DGKZ_8109	+	GTGACCTATGCACCAGACGTGCGATGGGCCAGCCGAGCAGGCTGGGCTGAAGCCGAGATCGGAAGAGCGGTTTCAG
chr11	46394445	46394484	DGKZ_8110	+	GTGACCTATGCACCAGACGTATAGGAGGGGGTGCAGCTGGGGCTCTCCAGCCACAGAGATCGGAAGAGCGGTTTCAG
chr11	46395796	46395835	DGKZ_8111	+	GTGACCTATGCACCAGACGTTCCTCACTGAGGCCAGGGCAGGGTGGGCACAGGAGTGTCCAGATCGGAAGAGCGGTTTCAG
chr11	46396015	46396054	DGKZ_8112	+	GTGACCTATGCACCAGACGTCTGCACCCCGCCTGTGCCACCTCTTCTACCACCCGTGAGATCGGAAGAGCGGTTTCAG
chr11	46396227	46396266	DGKZ_8113	+	GTGACCTATGCACCAGACGTCCAGCTGCCGTGGTGGTGGGCGGAGGGAGGAGGAGATCGGAAGAGCGGTTTCAG
chr11	46396400	46396439	DGKZ_8114	+	GTGACCTATGCACCAGACGTGCTGACCGAGCTGGGGGAGGCCCTGCTGCTCTGCTGAGATCGGAAGAGCGGTTTCAG
chr11	46396606	46396645	DGKZ_8115	+	GTGACCTATGCACCAGACGTCTGGGCCATGGTGCCTGGGAGCACAGCCAAAGGTGGAAGATCGGAAGAGCGGTTTCAG
chr11	46397512	46397551	DGKZ_8116	+	GTGACCTATGCACCAGACGTGGGGCGCCCTGGCAGGGTGGCCAGAGGGGTGAAGCAGAGATCGGAAGAGCGGTTTCAG
chr11	46397706	46397745	DGKZ_8117	+	GTGACCTATGCACCAGACGTGGGGCTCCCCAGGTGCCACCAGAGGGTGGTGGGAAGTAGATCGGAAGAGCGGTTTCAG
chr11	46397958	46397997	DGKZ_8118	+	GTGACCTATGCACCAGACGTCCAGGGTGCCTGTTCTGTTCTCCCTCCCTAGGGGAGATCGGAAGAGCGGTTTCAG
chr11	46398125	46398164	DGKZ_8119	+	GTGACCTATGCACCAGACGTGCCAGCTGCCAGCCAGCTGCTTCCGGCCCAAGGAGATCGGAAGAGCGGTTTCAG
chr11	46399790	46399829	DGKZ_8120	+	GTGACCTATGCACCAGACGTCCCTCTGGGGCCCTCTTTCTGCTGGTGGGGGAGGATCGGAAGAGCGGTTTCAG

chr11	46400061	46400100	DGKZ_8121	+	GTGACCTATGCACCAGACGTGAGGCTCCAGTTCCTTCCCCAGCAGCTCCCTCGGGCCCTAGATCGGAAGAGCGGTTTCAG
chr11	46400672	46400711	DGKZ_8122	+	GTGACCTATGCACCAGACGTGAGGAGCCAGGGCCCTGGGGCCAAGGTGGGAGGAGAGATCGGAAGAGCGGTTTCAG
chr11	46400797	46400836	DGKZ_8123	+	GTGACCTATGCACCAGACGTGGGCGAGTGCAGAACCGTGGTACCCCGGAAACCACCTTTAGATCGGAAGAGCGGTTTCAG
chr11	46401129	46401168	DGKZ_8124	+	GTGACCTATGCACCAGACGTGGCAGGCGAGGGAGCCACGAGGGCCACCAACCAACCTTTTCAGATCGGAAGAGCGGTTTCAG
chr11	46401508	46401547	DGKZ_8125	+	GTGACCTATGCACCAGACGTACGGGCAGCAGGAGGGACAATCGCGCCAGGGGACGAGCGCAGATCGGAAGAGCGGTTTCAG
chr11	46388181	46388220	DGKZ_8126	+	GTGACCTATGCACCAGACGTTGGTGGTAGCCGAGGCAATCGAGCGCCATCCAGCCAGGCCACCAAGATCGGAAGAGCGGTTTCAG
chr20	32264796	32264835	E2F1_8127	+	GTGACCTATGCACCAGACGTGGGGACCATCACAGCCGGGGATGCCCCAGCAGGGAAGATCGGAAGAGCGGTTTCAG
chr20	32265357	32265396	E2F1_8128	+	GTGACCTATGCACCAGACGTTCAAGGACCACATGACCTTTGACTTCTAGGGGGTCACTCAAGATCGGAAGAGCGGTTTCAG
chr20	32266170	32266209	E2F1_8129	+	GTGACCTATGCACCAGACGTGACCAGGGAGGGTAGGGTTAACAGCGATTGGCCCTCTGAGATCGGAAGAGCGGTTTCAG
chr20	32267791	32267830	E2F1_8130	+	GTGACCTATGCACCAGACGTGTGGTCAAGGACAGGGCCCTTCAGCATCCACCCACAGATCGGAAGAGCGGTTTCAG
chr20	32268233	32268272	E2F1_8131	+	GTGACCTATGCACCAGACGTAACGGGAGGATGCCAGTAACCCAGGAGTGAGGCCAGGAAGAAGATCGGAAGAGCGGTTTCAG
chr3	89156997	89157036	EPHA3_8132	+	GTGACCTATGCACCAGACGTTACCGGCAGCAGCGGAGCTCTGCCCCGCGGGCTCACGCTAGATCGGAAGAGCGGTTTCAG
chr3	89176434	89176473	EPHA3_8133	+	GTGACCTATGCACCAGACGTTAAACTATCACAAAGAAACATTTTCTCTATTACTGTCTTAGATCGGAAGAGCGGTTTCAG
chr3	89259681	89259720	EPHA3_8134	+	GTGACCTATGCACCAGACGTTCTCTATTTTTCTTTGAGCAATATTTCTCACCTATGAGTTAGATCGGAAGAGCGGTTTCAG
chr3	89390232	89390271	EPHA3_8135	+	GTGACCTATGCACCAGACGTTTGTGCAACCCATGCCTCCATGTTTGTGTTTTCTTCAGATCGGAAGAGCGGTTTCAG
chr3	89391251	89391290	EPHA3_8136	+	GTGACCTATGCACCAGACGTACTAGATGCTTCTTACTTATCATATCACGCTCTGAGTAAAGATCGGAAGAGCGGTTTCAG
chr3	89445122	89445161	EPHA3_8137	+	GTGACCTATGCACCAGACGTAATGTTTAAAGGTTGGGCTGTGTAGGCAAGAGCTGTTTCAGATCGGAAGAGCGGTTTCAG
chr3	89448641	89448680	EPHA3_8138	+	GTGACCTATGCACCAGACGTTTTCAATGCAGTCTAGAGGGGGCAGGGATCTTGCAAAAGATCGGAAGAGCGGTTTCAG
chr3	89448667	89448706	EPHA3_8139	+	GTGACCTATGCACCAGACGTAGGGATCTTGCAAAAGATGCTGATCGTTTATTCTCACTGAGATCGGAAGAGCGGTTTCAG
chr3	89456532	89456571	EPHA3_8140	+	GTGACCTATGCACCAGACGTAGTCTGTTTCACTATTCACTTTCTTTGTTGCTTTGTTTGCAGATCGGAAGAGCGGTTTCAG
chr3	89457292	89457331	EPHA3_8141	+	GTGACCTATGCACCAGACGTAAACTTGGCTTTTTGTTTTGCTTCCCGTTTAGCTTTAGAGATCGGAAGAGCGGTTTCAG
chr3	89462427	89462466	EPHA3_8142	+	GTGACCTATGCACCAGACGTTGACCCTACTGCCAACTTAGTACTGTATGTGAATCACGATAGATCGGAAGAGCGGTTTCAG
chr3	89468551	89468590	EPHA3_8143	+	GTGACCTATGCACCAGACGTTAGTCATAAGACCTGTGTTCCGATGTTGAGCAAAGTTAGATCGGAAGAGCGGTTTCAG
chr3	89478328	89478367	EPHA3_8144	+	GTGACCTATGCACCAGACGTGACCATACATATATGAATAAATGCTGAAAACAAGATCGGAAGAGCGGTTTCAG
chr3	89480520	89480559	EPHA3_8145	+	GTGACCTATGCACCAGACGTTAGATTTTTCTCTTTTTTATCATTGTTTTCCATCTTGTATAGATCGGAAGAGCGGTTTCAG
chr3	89498535	89498574	EPHA3_8146	+	GTGACCTATGCACCAGACGTGTGGTCTATGAGTTATGAGTTCAGATGAAAAGATCAAGCTAGATCGGAAGAGCGGTTTCAG
chr3	89499531	89499570	EPHA3_8147	+	GTGACCTATGCACCAGACGTCAATTTGTTATCTGGCATTCACTCTGAAATTTGTGTTTGCAGATCGGAAGAGCGGTTTCAG
chr3	89521780	89521819	EPHA3_8148	+	GTGACCTATGCACCAGACGTAATAAGAAATGAAAGGATGAAAGGATCTTTTGAACCTTCAGATCGGAAGAGCGGTTTCAG
chr3	89528663	89528702	EPHA3_8149	+	GTGACCTATGCACCAGACGTGGAAGTGTCTTGGACGGAAGTGGTGGCTGTGGAAGCGTAGATCGGAAGAGCGGTTTCAG
chr3	89259350	89259389	EPHA3_8150	+	GTGACCTATGCACCAGACGTGACACTGAGATAGAGAATGAGGCTCTGTCAACAAGAAGCGGAGATCGGAAGAGCGGTTTCAG
chr7	100318627	100318666	EPO_8151	+	GTGACCTATGCACCAGACGTGCGGGCTGGGCGCTCCCGCCCGCCGGGTCCTGTTTGGAGATCGGAAGAGCGGTTTCAG
chr7	100319337	100319376	EPO_8152	+	GTGACCTATGCACCAGACGTTTTCCCAGCACATTCACAGAACTCACGCTCAGGGCTTCAAGATCGGAAGAGCGGTTTCAG
chr7	100319682	100319721	EPO_8153	+	GTGACCTATGCACCAGACGTTTTTTTTTTTTTTTCTTTCTTTTGGAGAATCTCATTTCGAGATCGGAAGAGCGGTTTCAG
chr7	100320477	100320516	EPO_8154	+	GTGACCTATGCACCAGACGTGGCGACACTCTGCTTGCCTTTCTGTAAGAAGGGGAGAAAAGATCGGAAGAGCGGTTTCAG
chr7	100320767	100320806	EPO_8155	+	GTGACCTATGCACCAGACGTGCCACTGGGCATATCCACCACCTCCCTCACCAACATGCTAGATCGGAAGAGCGGTTTCAG
chr2	212248796	212248835	ERBB4_8156	+	GTGACCTATGCACCAGACGTAAAAAATATCAGCTAACCTCTAGTTTCTGAAAATATTAAGATCGGAAGAGCGGTTTCAG
chr2	212251886	212251925	ERBB4_8157	+	GTGACCTATGCACCAGACGTGAGAAAATATGTGGAGAGAAGGCGTTGTTAGAATAGTTAGATCGGAAGAGCGGTTTCAG
chr2	212252728	212252767	ERBB4_8158	+	GTGACCTATGCACCAGACGTAGAAAAATGGAATGATGGATATAATAAGAGGCAATATGAAAAGATCGGAAGAGCGGTTTCAG
chr2	212285347	212285386	ERBB4_8159	+	GTGACCTATGCACCAGACGTGATTGCCATCAGACAAAATATGATTCTTTCTTATCTTAAGATCGGAAGAGCGGTTTCAG
chr2	212286840	212286879	ERBB4_8160	+	GTGACCTATGCACCAGACGTACACAGTAAATGTCACATATTCGTAAGTAAAGGAGAGATCGGAAGAGCGGTTTCAG
chr2	212289037	212289076	ERBB4_8161	+	GTGACCTATGCACCAGACGTGAAAAAATCTTACTTCAAGCATATTAACAACATATGTTGAAGATCGGAAGAGCGGTTTCAG
chr2	212293219	212293258	ERBB4_8162	+	GTGACCTATGCACCAGACGTGTAAGAAGTAAAGTTTTAAATTAACATTAATAATCATTAGATCGGAAGAGCGGTTTCAG
chr2	212295836	212295875	ERBB4_8163	+	GTGACCTATGCACCAGACGTTCAAGTTCCCTTAATGATATTCAGTTAATGCCAGGTTTTTCAGATCGGAAGAGCGGTTTCAG
chr2	212426824	212426863	ERBB4_8164	+	GTGACCTATGCACCAGACGTAAAAATGCAATACCATTGATTTCAACTCAAATTTTTCTTAGATAGATCGGAAGAGCGGTTTCAG
chr2	212484011	212484050	ERBB4_8165	+	GTGACCTATGCACCAGACGTAAAAATTTACATTAATATGACATCTCAACTTATTAAGTTAGATCGGAAGAGCGGTTTCAG
chr2	212495330	212495369	ERBB4_8166	+	GTGACCTATGCACCAGACGTGAATGAGAAAAAATAAATAAAGATGAAAGATGAGAGAGAAAAGATCGGAAGAGCGGTTTCAG
chr2	212522564	212522603	ERBB4_8167	+	GTGACCTATGCACCAGACGTTTACAGAACAGAAAACATCATTCTCCATCCACAGTGACATAGATCGGAAGAGCGGTTTCAG
chr2	212530213	212530252	ERBB4_8168	+	GTGACCTATGCACCAGACGTAAAAAGAAAAAAGAAAAAGAAAAAGTGGTGTCTTTTCAGATCGGAAGAGCGGTTTCAG
chr2	212537993	212538032	ERBB4_8169	+	GTGACCTATGCACCAGACGTATCAGCCACATGAGGAGGTGTAAGCAAAACAAGCGTCAACTAGATCGGAAGAGCGGTTTCAG
chr2	212543920	212543959	ERBB4_8170	+	GTGACCTATGCACCAGACGTCCAAATCAAGGGGAAATAAACAGAGGATTGTGTCAAAAAGATCGGAAGAGCGGTTTCAG
chr2	212566902	212566941	ERBB4_8171	+	GTGACCTATGCACCAGACGTGGAAGTGAAGAAACGGAACCATGAAACGCTCCGAGTAAGATCGGAAGAGCGGTTTCAG
chr2	212568930	212568969	ERBB4_8172	+	GTGACCTATGCACCAGACGTAGAGTAGAAAAATAAATCAGAAATATCATTGCTCTAGATAGATCGGAAGAGCGGTTTCAG
chr2	212570127	212570166	ERBB4_8173	+	GTGACCTATGCACCAGACGTAAAGAAGAGATGTAGCCAAATTTAAATTTTACTAAAGGATTAGATCGGAAGAGCGGTTTCAG
chr2	212576912	212576951	ERBB4_8174	+	GTGACCTATGCACCAGACGTAAAGACTCAGAGTTAGGGGATTGAGAACTTATTTTTGGCCAGATCGGAAGAGCGGTTTCAG
chr2	212578384	212578423	ERBB4_8175	+	GTGACCTATGCACCAGACGTAAAAAAGGGTAAATAAGCATTAATGTTAACATTTCAGATCGGAAGAGCGGTTTCAG
chr2	212587270	212587309	ERBB4_8176	+	GTGACCTATGCACCAGACGTGCAAAATATTACTTTTCAATTAACAATAAATCATAATACTTAGATCGGAAGAGCGGTTTCAG
chr2	212589930	212589969	ERBB4_8177	+	GTGACCTATGCACCAGACGTGAGAGTAGGACCATGATGAAATGCTGCCACCAGGAAAGATCGGAAGAGCGGTTTCAG
chr2	212615440	212615479	ERBB4_8178	+	GTGACCTATGCACCAGACGTGAAAAGGGAAAAAGGACATGACCTTATAATCTTCACTAGATCGGAAGAGCGGTTTCAG

chr2	212652895	212652934	ERBB4_8179	+	GTGACCTATGCACCAGACGTAACAAATAACAAATTTTTTGTCAAACCTGCTTGTGATGAGATCGGAAGAGCGGTTTCAG
chr2	212812352	212812391	ERBB4_8180	+	GTGACCTATGCACCAGACGTACAACAGTTGCCCTGTGTTATAAAAACGAATTTGCTACTCTAGATCGGAAGAGCGGTTTCAG
chr2	212989639	212989678	ERBB4_8181	+	GTGACCTATGCACCAGACGTAAGAAGATACACGTGAAATTACATAACCTTTATATGATATAGATCGGAAGAGCGGTTTCAG
chr2	213403265	213403304	ERBB4_8182	+	GTGACCTATGCACCAGACGTTCTCAGATCCCCTGCTGACAATTACATGTCCAATGGCATAGATCGGAAGAGCGGTTTCAG
chr6	35420581	35420620	FANCE_8183	+	GTGACCTATGCACCAGACGTGCCCGCGGCCCTTAGCAGGTATGGGAGGCGGGGGCTGTAGATCGGAAGAGCGGTTTCAG
chr6	35424141	35424180	FANCE_8184	+	GTGACCTATGCACCAGACGTAGGGAGACTGGGTTTAGAGTGATCTTTCCAGCAGTGGTGGCAGATCGGAAGAGCGGTTTCAG
chr6	35425388	35425427	FANCE_8185	+	GTGACCTATGCACCAGACGTGCCACAGTCTACCATAGCCCTTTCTCCATCTTCTACCCAAGATCGGAAGAGCGGTTTCAG
chr6	35425772	35425811	FANCE_8186	+	GTGACCTATGCACCAGACGTATGACTGCCTGGCTCTGAGGTTACATTCTCTGTCCCTTATAGATCGGAAGAGCGGTTTCAG
chr6	35426228	35426267	FANCE_8187	+	GTGACCTATGCACCAGACGTTGGGAGGTAAGTCTCAGAGTGCCAAGGACAATGGGAAGAGCAAGATCGGAAGAGCGGTTTCAG
chr6	35427242	35427281	FANCE_8188	+	GTGACCTATGCACCAGACGTAAACCAGCCCCAGGCCAGTAGCTCTGCCCTCAGTGTCTCAGATCGGAAGAGCGGTTTCAG
chr6	35427548	35427587	FANCE_8189	+	GTGACCTATGCACCAGACGTAGGCCTCCGTGCTGTCCCCACTGCCACTGTTCCCCCAGGAGATCGGAAGAGCGGTTTCAG
chr6	35428406	35428445	FANCE_8190	+	GTGACCTATGCACCAGACGTTGCCCTGGGGAAGAGTGGACAAGAAGTGTGCAGTCTAGATCGGAAGAGCGGTTTCAG
chr6	35430702	35430741	FANCE_8191	+	GTGACCTATGCACCAGACGTATAGGGCCTTGGGCTTGGCTCTGCTGGCAGGGCTGCCCTGAGATCGGAAGAGCGGTTTCAG
chr6	35434133	35434172	FANCE_8192	+	GTGACCTATGCACCAGACGTAGGGACCACCTCTTGGTGTCCATCACCAGCTTCTGAAAGATCGGAAGAGCGGTTTCAG
chr6	35423837	35423876	FANCE_8193	+	GTGACCTATGCACCAGACGTGAAGAGGAGAACAGGGACTCCCAGCAGCTGGGAAACGCAAGATCGGAAGAGCGGTTTCAG
chr1	241661281	241661320	FH_8194	+	GTGACCTATGCACCAGACGTATAAAAAGACGACATATGGGTAGCAGTGATATTTGGTTAGATCGGAAGAGCGGTTTCAG
chr1	241665881	241665920	FH_8195	+	GTGACCTATGCACCAGACGTACCACCAATGACAGAGTAAAGACTAAATTTATGCAAATAAAGATCGGAAGAGCGGTTTCAG
chr1	241667556	241667595	FH_8196	+	GTGACCTATGCACCAGACGTGAAAACATGCTAGATGGGTGAACAAGTAAACTAAACATAGATCGGAAGAGCGGTTTCAG
chr1	241669479	241669518	FH_8197	+	GTGACCTATGCACCAGACGTAAAGAAAATTAAGGTAAGAATAAGTAATTCCTAATAGCTTAAGATCGGAAGAGCGGTTTCAG
chr1	241672096	241672135	FH_8198	+	GTGACCTATGCACCAGACGTTTTTTCAAAGAAATATAAAATGTTAAATCAGAGGCAACAAGATCGGAAGAGCGGTTTCAG
chr1	241675454	241675493	FH_8199	+	GTGACCTATGCACCAGACGTAAATGTTAAAAATGATTTTAAAAAAGGAAATAATAATGCTAGATCGGAAGAGCGGTTTCAG
chr1	241677024	241677063	FH_8200	+	GTGACCTATGCACCAGACGTTCCAGAAAAATATTTCAAATTTACAATTTTACTTAAGCATGAGATCGGAAGAGCGGTTTCAG
chr1	241680627	241680666	FH_8201	+	GTGACCTATGCACCAGACGTGAATACAACTATTACAAGTTGAAAAGAAACCCAGGATCAGATCGGAAGAGCGGTTTCAG
chr1	241683033	241683072	FH_8202	+	GTGACCTATGCACCAGACGTGAGCTTGGGTAGAATTTCTGGCGGCTGTGGCCACGCCTCAGATCGGAAGAGCGGTTTCAG
chr5	180036064	180036103	FLT4_8203	+	GTGACCTATGCACCAGACGTAGGACAAGCCAGGCTGTGGGTCCCGCCTGAGGCCCTCCTGAGATCGGAAGAGCGGTTTCAG
chr5	180037036	180037075	FLT4_8204	+	GTGACCTATGCACCAGACGTAAATCAGAAGGTGCTGAGGAACCGCTGCAGCAACCCTCCAGATCGGAAGAGCGGTTTCAG
chr5	180038490	180038529	FLT4_8205	+	GTGACCTATGCACCAGACGTGAGGAGAGGCCAGCCAGGCCAGAAACCACAGCCACTGCCAGATCGGAAGAGCGGTTTCAG
chr5	180039622	180039661	FLT4_8206	+	GTGACCTATGCACCAGACGTACGTGGGCTGCTGGACTGCATGCAACCCACCCCGTCCAAGATCGGAAGAGCGGTTTCAG
chr5	180040121	180040160	FLT4_8207	+	GTGACCTATGCACCAGACGTGAAGGGAGTGGTGGGAGCAACGCCCTCTGCGGCTCAGAGATCGGAAGAGCGGTTTCAG
chr5	180041190	180041229	FLT4_8208	+	GTGACCTATGCACCAGACGTAGAGGGAAGCTTGTCCCGTGGTGGATGGGGAGACGGAGGGAGATCGGAAGAGCGGTTTCAG
chr5	180043500	180043539	FLT4_8209	+	GTGACCTATGCACCAGACGTGGGAGGCGGCAGGGGGCTGTCAAGTGCAGGCCCTGGGGTAGATCGGAAGAGCGGTTTCAG
chr5	180044005	180044044	FLT4_8210	+	GTGACCTATGCACCAGACGTGAGCCAGGTGGGCTCAGGAGGCCCTCCTCCGCGGCTCCAGATCGGAAGAGCGGTTTCAG
chr5	180045931	180045970	FLT4_8211	+	GTGACCTATGCACCAGACGTACGAAGCTGGCTCGAGGGCGCCAGCTGCTCCGCCGACAGATCGGAAGAGCGGTTTCAG
chr5	180046120	180046159	FLT4_8212	+	GTGACCTATGCACCAGACGTACCGGGCGCGGCTCGGTTCCGAACCCGGGGCGGCTGAGATCGGAAGAGCGGTTTCAG
chr5	180046377	180046416	FLT4_8213	+	GTGACCTATGCACCAGACGTACGGGCCCTCACACGGCCCGACCCCTGGCAGTCCCCGTAGATCGGAAGAGCGGTTTCAG
chr5	180046780	180046819	FLT4_8214	+	GTGACCTATGCACCAGACGTAGGGGGCCAGTTGCAGGTGAGCTGTACGGGTGAGCGTGGAGATCGGAAGAGCGGTTTCAG
chr5	180047319	180047358	FLT4_8215	+	GTGACCTATGCACCAGACGTGGGACAGGGAGGAGTGGGGCAGCTCACTGATTTGGCCATAAGATCGGAAGAGCGGTTTCAG
chr5	180047726	180047765	FLT4_8216	+	GTGACCTATGCACCAGACGTAGAAGGGGGCGCGTGTGTGTGTGTGTGTAAGAGCGTAGATCGGAAGAGCGGTTTCAG
chr5	180048018	180048057	FLT4_8217	+	GTGACCTATGCACCAGACGTTGGGGTGGAGGTGCGGGTCCACCTGGGTTTGGGATCGTTCGAGATCGGAAGAGCGGTTTCAG
chr5	180048263	180048302	FLT4_8218	+	GTGACCTATGCACCAGACGTGGGTGAGAGGGAGCTAAGTGGAGCTGCACCTTAGCAGGAGATCGGAAGAGCGGTTTCAG
chr5	180048915	180048954	FLT4_8219	+	GTGACCTATGCACCAGACGTAGGAAGAAGCCCTGTGGCAGCTGCCCTGGGAGTTTGTCCAGATCGGAAGAGCGGTTTCAG
chr5	180049850	180049889	FLT4_8220	+	GTGACCTATGCACCAGACGTACAGGCACAAGGATCCATTTCTGCCAAGTTCTCCCAACAGATCGGAAGAGCGGTTTCAG
chr5	180051072	180051111	FLT4_8221	+	GTGACCTATGCACCAGACGTGAGAAGAGGCAAGGGCAGGTCAGGGATACAGGCAGGAAGGAGATCGGAAGAGCGGTTTCAG
chr5	180053042	180053081	FLT4_8222	+	GTGACCTATGCACCAGACGTACAGATGGCCGGTCACTGGCCTCCAATGCCAGGCCCCAGATCGGAAGAGCGGTTTCAG
chr5	180053276	180053315	FLT4_8223	+	GTGACCTATGCACCAGACGTAAAGGAGGTCAAGGCCATACAGATCCCACCACAGCCCAAGATCGGAAGAGCGGTTTCAG
chr5	180056010	180056049	FLT4_8224	+	GTGACCTATGCACCAGACGTGGAGAGCTGAGAGCTGTAATCCAGGACTGCCCTGTCGACAGATCGGAAGAGCGGTTTCAG
chr5	180056438	180056477	FLT4_8225	+	GTGACCTATGCACCAGACGTCCAGGGAAGCCCCGCTCAGCAGCGGGCTCCTGCACAGCAGATCGGAAGAGCGGTTTCAG
chr5	180056846	180056885	FLT4_8226	+	GTGACCTATGCACCAGACGTGCACACAGTACTCCCACGCCCTCACAGGACGACACCCACAGATCGGAAGAGCGGTTTCAG
chr5	180057116	180057155	FLT4_8227	+	GTGACCTATGCACCAGACGTAAAGGCCACCATATTGCCAGCTGCCCTTGTCTCTGGCCAGATCGGAAGAGCGGTTTCAG
chr5	180057348	180057387	FLT4_8228	+	GTGACCTATGCACCAGACGTGGAGCAAGCTGTTGGGGAAGGGACGTGGCGGCCAGGCTGGAGATCGGAAGAGCGGTTTCAG
chr5	180057810	180057849	FLT4_8229	+	GTGACCTATGCACCAGACGTACAGGAGTGGTCAAGTGGGCCACGGCCATGGGGAAGATCGGAAGAGCGGTTTCAG
chr5	180058789	180058828	FLT4_8230	+	GTGACCTATGCACCAGACGTAGCAGAGGTCAGGCTGGCTGGCTGTGACTTGGCACGAGATCGGAAGAGCGGTTTCAG
chr5	180076556	180076595	FLT4_8231	+	GTGACCTATGCACCAGACGTTGCGCGTGGGTCCGACCCGAGCGGCCGCGGCTCGGGGCTGAGATCGGAAGAGCGGTTTCAG
chr2	227663465	227663504	IRS1_8232	+	GTGACCTATGCACCAGACGTCCACCACCAACGCTGAGCAGAGGGAGGCTCCGAAAAACAAAGATCGGAAGAGCGGTTTCAG
chr2	227660202	227660241	IRS1_8233	+	GTGACCTATGCACCAGACGTCACTCTGGTTGCGGTTAGGACTGAGGTTACCCGGGTGAAAGATCGGAAGAGCGGTTTCAG
chr2	227660668	227660707	IRS1_8234	+	GTGACCTATGCACCAGACGTTGGCTGGACTGGGATGGACACCTGACAGAGGTGAGCTGAGATCGGAAGAGCGGTTTCAG
chr2	227661134	227661173	IRS1_8235	+	GTGACCTATGCACCAGACGTGTGGTGTAAAGATCTTGGCAATGAGTAGTAGGAGGAAGATCGGAAGAGCGGTTTCAG
chr2	227661600	227661639	IRS1_8236	+	GTGACCTATGCACCAGACGTCCCCGTTGGGACATGGGCATGTAGCCATCATCCGTGTGGAGAGATCGGAAGAGCGGTTTCAG

chr2	227662066	227662105	IRS1_8237	+	GTGACCTATGCACCAGACGTGCTTAGCTCCTCCTCACCGCGGGCTGGTGGGGTGTGGCCAGATCGGAAGAGCGGTTTCAG
chr2	227662532	227662571	IRS1_8238	+	GTGACCTATGCACCAGACGTATGCTCTCAGTGCCTGATCGCGGGTTCAGCCCCACCTGGCAGATCGGAAGAGCGGTTTCAG
chr2	227662998	227663037	IRS1_8239	+	GTGACCTATGCACCAGACGTACCCGTAGCTCAAGTCTCCCCAGCCTCACCAAGGCCGGAAGATCGGAAGAGCGGTTTCAG
chr22	22123620	22123659	MAPK1_8240	+	GTGACCTATGCACCAGACGTAAACAAAACATTTAACAGTCAAAGTTGTTATGGGTAAGGCAGATCGGAAGAGCGGTTTCAG
chr22	22127282	22127321	MAPK1_8241	+	GTGACCTATGCACCAGACGTAAAGGTTTTGCAGTAGTGAGAGCAGAAGTAGTCACAGAAAAGATCGGAAGAGCGGTTTCAG
chr22	22142688	22142727	MAPK1_8242	+	GTGACCTATGCACCAGACGTAAAAATTAGCTATTAGTTATCAGGACCAAGGTAATGACAGATCGGAAGAGCGGTTTCAG
chr22	22143108	22143147	MAPK1_8243	+	GTGACCTATGCACCAGACGTAAAAAGAGAGAAAAGACTGAAATGGTATCTGGTGTACAGAAAGATCGGAAGAGCGGTTTCAG
chr22	22153428	22153467	MAPK1_8244	+	GTGACCTATGCACCAGACGTAAAAAACAAGGATAACTTCTTGAATACTTAACCTTTCATAGATCGGAAGAGCGGTTTCAG
chr22	22160339	22160378	MAPK1_8245	+	GTGACCTATGCACCAGACGTAGGTTAAGGTAACAACCAATTAGCTGGTCACATTTAGCAAGATCGGAAGAGCGGTTTCAG
chr22	22162146	22162185	MAPK1_8246	+	GTGACCTATGCACCAGACGTAGAGAGAGAGATGGCATTAAAAACAGCCCTCAGAATATTTAGATCGGAAGAGCGGTTTCAG
chr8	90947851	90947890	NBN_8247	+	GTGACCTATGCACCAGACGTAGAAATGGGGTTAAATGATATTTAGATAAGGGATGGTATTAGATCGGAAGAGCGGTTTCAG
chr8	90949314	90949353	NBN_8248	+	GTGACCTATGCACCAGACGTAAACATAATTTCAAACATTTGCTCAGTGGTGAATATATAGATCGGAAGAGCGGTTTCAG
chr8	90955605	90955644	NBN_8249	+	GTGACCTATGCACCAGACGTATAAAGTAGTACAGTAAATCATATTAACAACAATAAAGATCGGAAGAGCGGTTTCAG
chr8	90958534	90958573	NBN_8250	+	GTGACCTATGCACCAGACGTGTTAAGATGGATAGGTAAGAAAGAGAAGAAATAACAAGAAGATCGGAAGAGCGGTTTCAG
chr8	90960131	90960170	NBN_8251	+	GTGACCTATGCACCAGACGTAAAAATAAAAAACTGTTTCATAGAGTATAAAAATGGTATAGATCGGAAGAGCGGTTTCAG
chr8	90965930	90965969	NBN_8252	+	GTGACCTATGCACCAGACGTAAAAAAGAAGAAAACAAAACAAGAAATGAACACAGCTAGATCGGAAGAGCGGTTTCAG
chr8	90967794	90967833	NBN_8253	+	GTGACCTATGCACCAGACGTAGAAAGAAGTCAAAGTAAATAAATCAAGTTTACAGCACTAGATCGGAAGAGCGGTTTCAG
chr8	90971093	90971132	NBN_8254	+	GTGACCTATGCACCAGACGTACAAAGTAGAAAGAAAGAACTACAACCTGCTAGATAGAAAGATCGGAAGAGCGGTTTCAG
chr8	90976746	90976785	NBN_8255	+	GTGACCTATGCACCAGACGTAAAAATAGTTTAAAGTATGATAATATATAAAGTAGCAACTAGATCGGAAGAGCGGTTTCAG
chr8	90982796	90982835	NBN_8256	+	GTGACCTATGCACCAGACGTAAAGAAACATTTTTTAAAGTAAATGTAGTAAATTTTTTGAAGATCGGAAGAGCGGTTTCAG
chr8	90983529	90983568	NBN_8257	+	GTGACCTATGCACCAGACGTAAATAAGTATATCTAATATATACTACTATGTTGCTAAGATCGGAAGAGCGGTTTCAG
chr8	90990562	90990601	NBN_8258	+	GTGACCTATGCACCAGACGTGAAAAATGTGAATATATATATTTACATGCTAGCATTTTTAGATCGGAAGAGCGGTTTCAG
chr8	90993132	90993171	NBN_8259	+	GTGACCTATGCACCAGACGTGAATAAGTTAAATAAGTCATAGTATCAGAGTTGCAGAGAAGATCGGAAGAGCGGTTTCAG
chr8	90993762	90993801	NBN_8260	+	GTGACCTATGCACCAGACGTGAAATAAATTTAAAGTCTTTTTACCACCTAGTACATTACAGATCGGAAGAGCGGTTTCAG
chr8	90996800	90996839	NBN_8261	+	GTGACCTATGCACCAGACGTCTCAGGGCTGGGCGCAGCTGCAACCCGCTAACCCGGGCAGATCGGAAGAGCGGTTTCAG
chr20	8113408	8113447	PLCB1_8262	+	GTGACCTATGCACCAGACGTGGGCGGCCGAGTCGGGGCGCTGGCTCGGGCACCCGGCAGATCGGAAGAGCGGTTTCAG
chr20	8131029	8131068	PLCB1_8263	+	GTGACCTATGCACCAGACGTAGGTATGCCTTTCTTACATTTTTTCAGTCGTTTACTACTTTAGATCGGAAGAGCGGTTTCAG
chr20	8352108	8352147	PLCB1_8264	+	GTGACCTATGCACCAGACGTGAGTGTGTTGTGCATGCACCAGATGCTGCTGATTGTTTGGAGATCGGAAGAGCGGTTTCAG
chr20	8609089	8609128	PLCB1_8265	+	GTGACCTATGCACCAGACGTGTAAGATTTGCTAAAGCTTATCATCATGATGCTGAATCCTTGAAGATCGGAAGAGCGGTTTCAG
chr20	8626839	8626878	PLCB1_8266	+	GTGACCTATGCACCAGACGTCTAATTTATTGCTAAGGGCTTGCTTCTTCTGAGTCAGTAGATCGGAAGAGCGGTTTCAG
chr20	8628611	8628650	PLCB1_8267	+	GTGACCTATGCACCAGACGTTGAGCATTCTCATTATTTATTTTTCTCAAGATCAGATCGGAAGAGCGGTTTCAG
chr20	8637942	8637981	PLCB1_8268	+	GTGACCTATGCACCAGACGTACATTTTAAAGCCATATCTTTTTCAGCTTGCATTGATTCTCAGATCGGAAGAGCGGTTTCAG
chr20	8639362	8639401	PLCB1_8269	+	GTGACCTATGCACCAGACGTTCTTTCACACAAAGGGGAAGCTCTTGTCTGATTGGGGGAGATCGGAAGAGCGGTTTCAG
chr20	8665736	8665775	PLCB1_8270	+	GTGACCTATGCACCAGACGTTCTAGTCTTTGTTACTTTAGCCAGTCTCACCAAAATTTCAAGATCGGAAGAGCGGTTTCAG
chr20	8678441	8678480	PLCB1_8271	+	GTGACCTATGCACCAGACGTTGAATGTTACTAAGAGAGCAGCTGGAGACACCTGATCCAGATCGGAAGAGCGGTTTCAG
chr20	8689410	8689449	PLCB1_8272	+	GTGACCTATGCACCAGACGTAAACACATTCAGGAATGAGTCTTTTTCCGAATAGGGCATAAGATCGGAAGAGCGGTTTCAG
chr20	8697006	8697045	PLCB1_8273	+	GTGACCTATGCACCAGACGTCTGATGTTTGTCTTGAAGGAATGATGCATTATTGATGAAGATCGGAAGAGCGGTTTCAG
chr20	8698506	8698545	PLCB1_8274	+	GTGACCTATGCACCAGACGTGGTGGGCTCTCCCCGTCATGTTTTGTGTTGGTTAAGAAATAGATCGGAAGAGCGGTTTCAG
chr20	8703079	8703118	PLCB1_8275	+	GTGACCTATGCACCAGACGTAGGGCTTCTGGTCCCTAAGGCATTCACCACCCTGTACTCAGATCGGAAGAGCGGTTTCAG
chr20	8705410	8705449	PLCB1_8276	+	GTGACCTATGCACCAGACGTCTGGAGAAAACCCCTCTTGACAGATATAATGATTATATAGATCGGAAGAGCGGTTTCAG
chr20	8708051	8708090	PLCB1_8277	+	GTGACCTATGCACCAGACGTTTTGACGAATGACTGAGAATGACACACAGCTGAAGCTTGGATCGGAAGAGCGGTTTCAG
chr20	8709832	8709871	PLCB1_8278	+	GTGACCTATGCACCAGACGTGCTTGTCCCATCTGCTATGAACTCACATTGCCAAGTGTAGATCGGAAGAGCGGTTTCAG
chr20	8714050	8714089	PLCB1_8279	+	GTGACCTATGCACCAGACGTCCCATCACAAAATTTGTTCTTAAACAATAGTTGAATTTATAGATCGGAAGAGCGGTTTCAG
chr20	8717850	8717889	PLCB1_8280	+	GTGACCTATGCACCAGACGTTGTTCTTGATATGAGTTAACTGCATTTTTTCAGGTGTTTAGATCGGAAGAGCGGTTTCAG
chr20	8720018	8720057	PLCB1_8281	+	GTGACCTATGCACCAGACGTTGTGCTGAGAAACCTTTTATCAAAGTTGCAAAAGAAATCAAGATCGGAAGAGCGGTTTCAG
chr20	8721106	8721145	PLCB1_8282	+	GTGACCTATGCACCAGACGTTAACTGAAATACCCTTTACTCAAAGGGGTTATTTCTGTCTAGATCGGAAGAGCGGTTTCAG
chr20	8722231	8722270	PLCB1_8283	+	GTGACCTATGCACCAGACGTGTTTTAATTTTACATATAGCATTAAGCATGATCACACACAGATCGGAAGAGCGGTTTCAG
chr20	8737836	8737875	PLCB1_8284	+	GTGACCTATGCACCAGACGTTGGAAGAGCTGGACAACATGAGCAAGATCCTCCAGTTCAAGATCGGAAGAGCGGTTTCAG
chr20	8741118	8741157	PLCB1_8285	+	GTGACCTATGCACCAGACGTCCCTTTCCCCCATGGAATTAAGCAGCTCAGTGTACACAAGATCGGAAGAGCGGTTTCAG
chr20	8746016	8746055	PLCB1_8286	+	GTGACCTATGCACCAGACGTTGAATATTTTAGTTGGTTTCATAGCATGAAGAGTTGTTAAGATCGGAAGAGCGGTTTCAG
chr20	8755377	8755416	PLCB1_8287	+	GTGACCTATGCACCAGACGTGAACATGATTATGTTGTGCAACTGGAACCTCCCTTATAAGATCGGAAGAGCGGTTTCAG
chr20	8769183	8769222	PLCB1_8288	+	GTGACCTATGCACCAGACGTTTCCCATTAACAATTTGACATGCTGATCTGAATTTATCAAAGATCGGAAGAGCGGTTTCAG
chr20	8769380	8769419	PLCB1_8289	+	GTGACCTATGCACCAGACGTAGTGTCCCTCTCCCAAACAGTTCATCTGGGAATTTTTAGATCGGAAGAGCGGTTTCAG
chr20	8770233	8770272	PLCB1_8290	+	GTGACCTATGCACCAGACGTTTCATCACGCTCTCTCTTTGCAAAACATGTGTGAACATTTAGATCGGAAGAGCGGTTTCAG
chr20	8770919	8770958	PLCB1_8291	+	GTGACCTATGCACCAGACGTTGAAATTAATAAATGAACAATTTATTTGATTTCCATTTAGATCGGAAGAGCGGTTTCAG
chr20	8782812	8782851	PLCB1_8292	+	GTGACCTATGCACCAGACGTTCCGGCCAGGTAGGACTGGATGGGAGGGGTCGCTTTTGGAGATCGGAAGAGCGGTTTCAG
chr20	8862507	8862546	PLCB1_8293	+	GTGACCTATGCACCAGACGTACGGCTCAGAAATGTCATGGCCACTCCAGCTCAGGATCGGAAGAGCGGTTTCAG
chr1	1982151	1982190	PRKCZ_8294	+	GTGACCTATGCACCAGACGTGAGAGGGCGGGAGCGCGGGTTCAGGCAGGGAGGGCGGAGATCGGAAGAGCGGTTTCAG

chr1	1987012	1987051	PRKCZ_8295	+	GTGACCTATGCACCAGACGTTCCCATGTTGGCCAGAATCCTCAGCCTCAGGGGACTTCGCAGATCGGAAGAGCGGTTTCAG
chr1	1988023	1988062	PRKCZ_8296	+	GTGACCTATGCACCAGACGTGGGTCTGTGGTGGGCAGCTCTGGGGGCTGTTCTGGCTGAGATCGGAAGAGCGGTTTCAG
chr1	1991041	1991080	PRKCZ_8297	+	GTGACCTATGCACCAGACGTGGGTTTCTACGCCGGTCTCGCATGTTACGGGGTTGAACAGATCGGAAGAGCGGTTTCAG
chr1	2066797	2066836	PRKCZ_8298	+	GTGACCTATGCACCAGACGTCCCTGGGACTAGTCCCTCAAGGGGCTTTTGTACTTTTAGATCGGAAGAGCGGTTTCAG
chr1	2075791	2075830	PRKCZ_8299	+	GTGACCTATGCACCAGACGTGGGCTGGGGAGGCCCGGGGGGCACGGGCGGGGTCGGGGCGAGATCGGAAGAGCGGTTTCAG
chr1	2077558	2077597	PRKCZ_8300	+	GTGACCTATGCACCAGACGTCTTTCTCCGGCCGGGTAGAGCTCGGCATCACCTACCCAGATCGGAAGAGCGGTTTCAG
chr1	2080374	2080413	PRKCZ_8301	+	GTGACCTATGCACCAGACGTGGAGCAGCTCGCTGCCATTTCCAGATCCTCTGGAAAGTCAGATCGGAAGAGCGGTTTCAG
chr1	2082428	2082467	PRKCZ_8302	+	GTGACCTATGCACCAGACGTCTTCTCATGGGGCCCGGGGGCCCGGAACGCGCTGCCCTGAGATCGGAAGAGCGGTTTCAG
chr1	2087542	2087581	PRKCZ_8303	+	GTGACCTATGCACCAGACGTGAAGGGTATTTCTGATATTCTGCAGATTTAGATGTGAACAGATCGGAAGAGCGGTTTCAG
chr1	2103640	2103679	PRKCZ_8304	+	GTGACCTATGCACCAGACGTGGACCACCCTCCCTGACCATCCCGCATGTGCGTCTCGGGAGATCGGAAGAGCGGTTTCAG
chr1	2103838	2103877	PRKCZ_8305	+	GTGACCTATGCACCAGACGTCTGCCCTGGCCCTCTCGGAGCACACAGGGCCAGAGATGGAGATCGGAAGAGCGGTTTCAG
chr1	2105466	2105505	PRKCZ_8306	+	GTGACCTATGCACCAGACGTGCGTGTGCTTCCCTCACCCCTCACCTGCAGACTGTCTCCAGATCGGAAGAGCGGTTTCAG
chr1	2106283	2106322	PRKCZ_8307	+	GTGACCTATGCACCAGACGTGGCCATGCTGACAAATCTGTTTTGTGGCTCGGTGTTGGAGATCGGAAGAGCGGTTTCAG
chr1	2106763	2106802	PRKCZ_8308	+	GTGACCTATGCACCAGACGTACAAAGCCTATTTGCACCCCATCCCATCCCAACCCCAAAGATCGGAAGAGCGGTTTCAG
chr1	2116148	2116187	PRKCZ_8309	+	GTGACCTATGCACCAGACGTCTGGGTGCGGGTCCCTGGAGCACCCCTCGGGCAGCCCATAGATCGGAAGAGCGGTTTCAG
chr1	2116459	2116498	PRKCZ_8310	+	GTGACCTATGCACCAGACGTGCTCTGTCTGCTGGACAGCGGTGATTGACCCTTTAACTGTAAGATCGGAAGAGCGGTTTCAG
chr22	24134065	24134104	SMARCB1_8311	+	GTGACCTATGCACCAGACGTAAACGCTAAACATAAGGGTGCCTTTCACGAGGGTTTTGTAAGATCGGAAGAGCGGTTTCAG
chr22	24134092	24134131	SMARCB1_8312	+	GTGACCTATGCACCAGACGTACGAGGGTTTTGTAACCTGTTTTCAAACCACTCGCTTAGATGATCGGAAGAGCGGTTTCAG
chr22	24135886	24135925	SMARCB1_8313	+	GTGACCTATGCACCAGACGTCTCGCCAGGGCATCTCTGGGGACACCTGTGGGGTCTTTTAGATCGGAAGAGCGGTTTCAG
chr22	24143279	24143318	SMARCB1_8314	+	GTGACCTATGCACCAGACGTATCGCTGCACCTCACCCCTCCGTGCTGATTCGCTTAGTTTCAGATCGGAAGAGCGGTTTCAG
chr22	24145620	24145659	SMARCB1_8315	+	GTGACCTATGCACCAGACGTGTGCGGCTTGGCTGGGCCGTCGCCCAACCCCTGTGTGTTAAGATCGGAAGAGCGGTTTCAG
chr22	24159134	24159173	SMARCB1_8316	+	GTGACCTATGCACCAGACGTCTCACCCAGCCTGGAGCCTTCCCTGGCCCTCAGGGTGGGAGATCGGAAGAGCGGTTTCAG
chr22	24167613	24167652	SMARCB1_8317	+	GTGACCTATGCACCAGACGTGACTGAGTCTCCCTCCCTCATCTCCCTGCAAACTGTTAGATCGGAAGAGCGGTTTCAG
chr22	24175901	24175940	SMARCB1_8318	+	GTGACCTATGCACCAGACGTCCCTGTGGTCTGGGCTCTGCCACAGGCACCTGGCTTTCAGATCGGAAGAGCGGTTTCAG
chr22	24176378	24176417	SMARCB1_8319	+	GTGACCTATGCACCAGACGTAGCACACGGCTCCACGAGCATCTCAGAAGATTGGGCCGAGATCGGAAGAGCGGTTTCAG
chr15	57213307	57213346	TCF12_8320	+	GTGACCTATGCACCAGACGTGCTTAACTAAAGACTCATATTTGGTGGTGTGATACATAGATCGGAAGAGCGGTTTCAG
chr15	57356032	57356071	TCF12_8321	+	GTGACCTATGCACCAGACGTGATCAACCTTGATTAAGCTGTAATTTGGCAGACTACGAGATCGGAAGAGCGGTTTCAG
chr15	57384100	57384139	TCF12_8322	+	GTGACCTATGCACCAGACGTAATTTCTCTGCAAGTAGTCTTCTCAAAGCTTCTTTGGTCAGAGATCGGAAGAGCGGTTTCAG
chr15	57458675	57458714	TCF12_8323	+	GTGACCTATGCACCAGACGTGATTAATAAAAGCAATGAGATGGTTTTAAACACATAAAAGATCGGAAGAGCGGTTTCAG
chr15	57484502	57484541	TCF12_8324	+	GTGACCTATGCACCAGACGTACACAACAAATCCCATCCCATATGTTGTTGTTGTTTGTAGATCGGAAGAGCGGTTTCAG
chr15	57490034	57490073	TCF12_8325	+	GTGACCTATGCACCAGACGTATCTTTTTAACTTGATGGTAAACAACTGATTTCAAGTAGATCGGAAGAGCGGTTTCAG
chr15	57511799	57511838	TCF12_8326	+	GTGACCTATGCACCAGACGTTTTCTTTGATAGCTTCTAACTACTTGTTTAAAGGAAAGCAGATCGGAAGAGCGGTTTCAG
chr15	57523466	57523505	TCF12_8327	+	GTGACCTATGCACCAGACGTCCAAACAATTGCCAAATACTACTCGAGCTCATCTGTATATCAGATCGGAAGAGCGGTTTCAG
chr15	57524639	57524678	TCF12_8328	+	GTGACCTATGCACCAGACGTACACGTGACTAGGGTACAGCAACACTTTGTCTCACTTGTAGATCGGAAGAGCGGTTTCAG
chr15	57525065	57525104	TCF12_8329	+	GTGACCTATGCACCAGACGTGAGTGGCAAAAATCTCCATAAAGTTTTGTGGACTTTTCAGTAGATCGGAAGAGCGGTTTCAG
chr15	57526316	57526355	TCF12_8330	+	GTGACCTATGCACCAGACGTATTTTACACATTCTACTGAATGAATTTTACTACTACTGAATAGATCGGAAGAGCGGTTTCAG
chr15	57535759	57535798	TCF12_8331	+	GTGACCTATGCACCAGACGTGTTTTATCTACTTCTAACTGGTGGGACTACTTGGAAATATAGATCGGAAGAGCGGTTTCAG
chr15	57543632	57543671	TCF12_8332	+	GTGACCTATGCACCAGACGTCTTATACATCAGTTTTATCTGATAGCTTAGAGTTTTGTTTGTAGATCGGAAGAGCGGTTTCAG
chr15	57544701	57544740	TCF12_8333	+	GTGACCTATGCACCAGACGTTTTTAGATGGTGCCTTTTTGTGTTTCAATTAATATACTAGATCGGAAGAGCGGTTTCAG
chr15	57545677	57545716	TCF12_8334	+	GTGACCTATGCACCAGACGTGCTCATCTTTTTGTAGTAAACCTAAAGATTTCTGCTAGATCGGAAGAGCGGTTTCAG
chr15	57554417	57554456	TCF12_8335	+	GTGACCTATGCACCAGACGTGTTGTTTTTCAGAAATACTCAGACAGAGATATCATTTGAGATCGGAAGAGCGGTTTCAG
chr15	57555483	57555522	TCF12_8336	+	GTGACCTATGCACCAGACGTGCATCCAGGTTTTAAATTTTATTCATTTCCATAGGTAAAGATCGGAAGAGCGGTTTCAG
chr15	57565471	57565510	TCF12_8337	+	GTGACCTATGCACCAGACGTTACGCCGAGATGTATACTGTTCTGCTTCAGATGGGCAAGATCGGAAGAGCGGTTTCAG
chr15	57574796	57574835	TCF12_8338	+	GTGACCTATGCACCAGACGTGGTAAGTACGGGTTTTGAAAAGAAACAGCAAGGAAATAACCAGATCGGAAGAGCGGTTTCAG
chr1	186283169	186283208	TPR_8339	+	GTGACCTATGCACCAGACGTAAAGAAATCAAATGAAATATCTTTTAAAGAAATCAAAGATCGGAAGAGCGGTTTCAG
chr1	186283867	186283906	TPR_8340	+	GTGACCTATGCACCAGACGTGCTAATAAGATAAAGAAAAGCAAGTGAATAAATGAGAAAGCAGATCGGAAGAGCGGTTTCAG
chr1	186286743	186286782	TPR_8341	+	GTGACCTATGCACCAGACGTGAAAAATGAGAAAAACAAAACCTGATCCTACAGTCAATCAAGATCGGAAGAGCGGTTTCAG
chr1	186287746	186287785	TPR_8342	+	GTGACCTATGCACCAGACGTACAACACAAGAAAAAGAACTTTAAACTTTGTGGTTTATCAGATCGGAAGAGCGGTTTCAG
chr1	186287971	186288010	TPR_8343	+	GTGACCTATGCACCAGACGTTTCTGAATATTAATGAATGACTGAAAAAACATAAAATTAAGATCGGAAGAGCGGTTTCAG
chr1	186289561	186289600	TPR_8344	+	GTGACCTATGCACCAGACGTAAAAACTAATTTAAGATGAAATTTAAAGTTAACCTATTTAAGATCGGAAGAGCGGTTTCAG
chr1	186291555	186291594	TPR_8345	+	GTGACCTATGCACCAGACGTGAAAAAGATTAACAAACAAACACACATATGACTAGATCGGAAGAGCGGTTTCAG
chr1	186291729	186291768	TPR_8346	+	GTGACCTATGCACCAGACGTAGATAAAGCAATTTGCTTTAAGAAATGAGGCAATGAGATCGGAAGAGCGGTTTCAG
chr1	186293013	186293052	TPR_8347	+	GTGACCTATGCACCAGACGTAGAGAAATTTACTTTTTGAAGTCTAAATTTACCACAAAAAAGATCGGAAGAGCGGTTTCAG
chr1	186295378	186295417	TPR_8348	+	GTGACCTATGCACCAGACGTGTTCCCCAGGCATAAATAAAAGTTTGAATATGGCCACAAGATCGGAAGAGCGGTTTCAG
chr1	186296803	186296842	TPR_8349	+	GTGACCTATGCACCAGACGTAAAAAGTTAAAAAGAAATTAAGAGCCCTATAACATACCAGATCGGAAGAGCGGTTTCAG
chr1	186300724	186300763	TPR_8350	+	GTGACCTATGCACCAGACGTATACATAATATTAACCATATCAGTGTAGTAGATGAAGAGATCGGAAGAGCGGTTTCAG
chr1	186301486	186301525	TPR_8351	+	GTGACCTATGCACCAGACGTATATAAATCTGAAATTAAGCCTAGATAAATCAATTAAGATCGGAAGAGCGGTTTCAG
chr1	186302537	186302576	TPR_8352	+	GTGACCTATGCACCAGACGTATATAATGCTGAATATAAGCCTTCTACTTTTATCAAAGCAGATCGGAAGAGCGGTTTCAG



chr1	186303676	186303715	TPR_8353	+	GTGACCTATGCACCAGACGTGAAAAATGGAAGAATAATTATAACAAATTATTATGCAAAAGATCGGAAGAGCGGTTTCAG
chr1	186304272	186304311	TPR_8354	+	GTGACCTATGCACCAGACGTAAAGCTCTTGATTGTTGTTCCCTAGCCACAAAGAGTCCACTAGATCGGAAGAGCGGTTTCAG
chr1	186304686	186304725	TPR_8355	+	GTGACCTATGCACCAGACGTAAACCAGGCGATTATATTAATATTATAATCAAACATTTAAAAGATCGGAAGAGCGGTTTCAG
chr1	186305837	186305876	TPR_8356	+	GTGACCTATGCACCAGACGTAAACAAAGTATTCACCATGGAATTCATCATTTCATATAAGATCGGAAGAGCGGTTTCAG
chr1	186307386	186307425	TPR_8357	+	GTGACCTATGCACCAGACGTGGAGGAAAGAAAGATTAATATATGAGACATTTTTTCAGATCGGAAGAGCGGTTTCAG
chr1	186308915	186308954	TPR_8358	+	GTGACCTATGCACCAGACGTAAAAATGCGATCTTGATTTTTTAGGTTTTATGAAACAAAAGATCGGAAGAGCGGTTTCAG
chr1	186310302	186310341	TPR_8359	+	GTGACCTATGCACCAGACGTGGCAATATTTAAACAACAATGTAAAAATTCATTTATTATAGATCGGAAGAGCGGTTTCAG
chr1	186310532	186310571	TPR_8360	+	GTGACCTATGCACCAGACGTCAAATAAATATACATACCAACATCTACAATAAGTTGAAAGAGATCGGAAGAGCGGTTTCAG
chr1	186312616	186312655	TPR_8361	+	GTGACCTATGCACCAGACGTACAGATATAAAATTTTTATGTGAATTTTAAAAAGCCAACAAGATCGGAAGAGCGGTTTCAG
chr1	186313233	186313272	TPR_8362	+	GTGACCTATGCACCAGACGTAGAGTCTATCAGAATAACAGATTTTCCAATGCATATTTAAAAGATCGGAAGAGCGGTTTCAG
chr1	186313721	186313760	TPR_8363	+	GTGACCTATGCACCAGACGTTTATTACCAATTGATACCAAAGATTAATAAAATCCATAAAAAGATCGGAAGAGCGGTTTCAG
chr1	186314839	186314878	TPR_8364	+	GTGACCTATGCACCAGACGTAGAACAAGATTAACCAAAATTAATTGCAAACTTACTTGAGATCGGAAGAGCGGTTTCAG
chr1	186315430	186315469	TPR_8365	+	GTGACCTATGCACCAGACGTTTACAAACAGTAGGATATAAAAATTACACACATTTAAAGTAGATCGGAAGAGCGGTTTCAG
chr1	186316601	186316640	TPR_8366	+	GTGACCTATGCACCAGACGTTAACAGCTCTGTTAAAATTAACATTTTCAATAGTATTAGAAGATCGGAAGAGCGGTTTCAG
chr1	186319531	186319570	TPR_8367	+	GTGACCTATGCACCAGACGTCATTAATCTTATAACATCTTTAGGTTCCCTAAGTAACTAAAGATCGGAAGAGCGGTTTCAG
chr1	186320613	186320652	TPR_8368	+	GTGACCTATGCACCAGACGTGAAAAGATTTTTGGTTATGCTTAAGAAAAGGCAATACAAAGATCGGAAGAGCGGTTTCAG
chr1	186321253	186321292	TPR_8369	+	GTGACCTATGCACCAGACGTGTAGAAATGAAATAAAAATGCTGAAAAACATGGTGCAAAAGATCGGAAGAGCGGTTTCAG
chr1	186322993	186323032	TPR_8370	+	GTGACCTATGCACCAGACGTGAAAAGTAATTTACAAGTAACCTGAAATGATCTCTAGCTTAGATCGGAAGAGCGGTTTCAG
chr1	186324701	186324740	TPR_8371	+	GTGACCTATGCACCAGACGTGAGATTATGAGAAGGTAACACTGTGTTCTCTAAAAACCTAAGATCGGAAGAGCGGTTTCAG
chr1	186324911	186324950	TPR_8372	+	GTGACCTATGCACCAGACGTGAAAGACTATAAAAATGCTTTGTTGGCTTTCATAAATCAAGATCGGAAGAGCGGTTTCAG
chr1	186325592	186325631	TPR_8373	+	GTGACCTATGCACCAGACGTAGTCGGCCTAATTCACAGGACTGAACTGAGAGTTAAGTGAAGATCGGAAGAGCGGTTTCAG
chr1	186326766	186326805	TPR_8374	+	GTGACCTATGCACCAGACGTAGTTTTAATATGTTATAAAAATAGTATTAGTTACAATTTCTGAGATCGGAAGAGCGGTTTCAG
chr1	186327793	186327832	TPR_8375	+	GTGACCTATGCACCAGACGTTAAATCAAGTGAATAATTTGTACTTCTCTAGGATTTAAGATCGGAAGAGCGGTTTCAG
chr1	186329139	186329178	TPR_8376	+	GTGACCTATGCACCAGACGTACAAGGGTGTGTTTCAAATCTAACCCATAACACCGCAAAATAAGATCGGAAGAGCGGTTTCAG
chr1	186329507	186329546	TPR_8377	+	GTGACCTATGCACCAGACGTAAATACACATCTAGTATAATTTGTAATAATTTCAAACCTAAAAGATCGGAAGAGCGGTTTCAG
chr1	186330048	186330087	TPR_8378	+	GTGACCTATGCACCAGACGTATTTAAAGACCAAATATTCAAACATACAGTTAAAATTTTAGATCGGAAGAGCGGTTTCAG
chr1	186330852	186330891	TPR_8379	+	GTGACCTATGCACCAGACGTATCTTAAAAAGTTACCTAACAGTCAACAATGCAACATTTAAGATCGGAAGAGCGGTTTCAG
chr1	186331012	186331051	TPR_8380	+	GTGACCTATGCACCAGACGTTAGCCCAATTTATAGCAGTCTACTTTGAACTAAATTTAGAAAAGATCGGAAGAGCGGTTTCAG
chr1	186331523	186331562	TPR_8381	+	GTGACCTATGCACCAGACGTAAAATAGACAGGGGGAAAGGATGTCATATTAACATGAAATAGATCGGAAGAGCGGTTTCAG
chr1	186332144	186332183	TPR_8382	+	GTGACCTATGCACCAGACGTCCAAGAGAAATAACACGTAACGTTAAAGATGATATATGATTAGATCGGAAGAGCGGTTTCAG
chr1	186332588	186332627	TPR_8383	+	GTGACCTATGCACCAGACGTGAAGAGAATAAAAAATAAATAACTAATTAACACTCAGGGGAGATCGGAAGAGCGGTTTCAG
chr1	186337125	186337164	TPR_8384	+	GTGACCTATGCACCAGACGTGAAGAGTAAAGTAAGAAAATCAAGTAGAGCAATACAGGAGATCGGAAGAGCGGTTTCAG
chr1	186340186	186340225	TPR_8385	+	GTGACCTATGCACCAGACGTGGAATTTTTATGAATACATACACATTTGCTTAAAACCTGCAAGATCGGAAGAGCGGTTTCAG
chr1	186342606	186342645	TPR_8386	+	GTGACCTATGCACCAGACGTCAAGCAAAAAACAAAAACAATAACCAACACATGTACATAAGATCGGAAGAGCGGTTTCAG
chr1	186344171	186344210	TPR_8387	+	GTGACCTATGCACCAGACGTCCAGGGCCACAGGGCCGCGCCGCTGCGAGCGCCTCTCCAGATCGGAAGAGCGGTTTCAG
chr6	43739060	43739099	VEGFA_8388	+	GTGACCTATGCACCAGACGTGTGCCCTGCTGGCGCCGCGGGCCGCTGCGAGCGCCTCTCCAGATCGGAAGAGCGGTTTCAG
chr6	43742140	43742179	VEGFA_8389	+	GTGACCTATGCACCAGACGTCTGGCTGTTGGATGGGGTTCCCTGTCTCTCAGGGGATGGAGATCGGAAGAGCGGTTTCAG
chr6	43745413	43745452	VEGFA_8390	+	GTGACCTATGCACCAGACGTTTGGGAAGTGGGGCAAGGGGGGGATAGGGAGGGGGTAAACAGATCGGAAGAGCGGTTTCAG
chr6	43746284	43746323	VEGFA_8391	+	GTGACCTATGCACCAGACGTAGTCACGGATTCTATTATCAGCAAGTGGCTGCAGGGTGCCTAGATCGGAAGAGCGGTTTCAG
chr6	43746666	43746705	VEGFA_8392	+	GTGACCTATGCACCAGACGTCTGACTTTAGCACTTCTCCCTCCATGCCCCTGTTGCTTTAGATCGGAAGAGCGGTTTCAG
chr6	43748533	43748572	VEGFA_8393	+	GTGACCTATGCACCAGACGTGGAGCGGTGAGCGCTGCTGCTTAATGCCCTGGAGCCTCCCTGGCCCCAGATCGGAAGAGCGGTTTCAG
chr6	43748551	43748590	VEGFA_8394	+	GTGACCTATGCACCAGACGTGCCCGCTGCTGCTAATGCCCTGGAGCCTCCCTGGCCCCAGATCGGAAGAGCGGTTTCAG
chr6	43749800	43749839	VEGFA_8395	+	GTGACCTATGCACCAGACGTTTGAGTTAAACGAACGTAACCTTGCAGGTTGGTTCAGAGGAGATCGGAAGAGCGGTTTCAG
chr6	43752294	43752333	VEGFA_8396	+	GTGACCTATGCACCAGACGTGGTGAGCCGGGCAGGAGGAAGGACCTCCCTCAGGGTTTATAGATCGGAAGAGCGGTTTCAG
chr6	43752310	43752349	VEGFA_8397	+	GTGACCTATGCACCAGACGTAGGAAGGAGCCTCCCTCAGGGTTTCGGGAACCATCTAGATCGGAAGAGCGGTTTCAG
chr6	43752376	43752415	VEGFA_8398	+	GTGACCTATGCACCAGACGTTCCGATACAGAAACACAGCTGCGCCGCCACCAACCATCACCAAGAGCGGTTTCAG
chr6	43738757	43738796	VEGFA_8399	+	GTGACCTATGCACCAGACGTGGGGGGCCGAGTGGCGACTCGGCGCTCGGAAGCCGGGCTCAGATCGGAAGAGCGGTTTCAG
chr17	48712353	48712392	ABCC3_8400	+	GTGACCTATGCACCAGACGTGGGCTCCGGGGTCACTGCGCGGGGGCCAGGGTTCGGCCGGCAGATCGGAAGAGCGGTTTCAG
chr17	48733380	48733419	ABCC3_8401	+	GTGACCTATGCACCAGACGTGAGGATCTCCTACCAGATGGGGCTGGGCCCTGGGGATTCTAGATCGGAAGAGCGGTTTCAG
chr17	48734199	48734238	ABCC3_8402	+	GTGACCTATGCACCAGACGTGGCCCTGGGAAAGTGGATGGGGGAGGTCTCCATTGGGTTGAGATCGGAAGAGCGGTTTCAG
chr17	48734555	48734594	ABCC3_8403	+	GTGACCTATGCACCAGACGTGGAGAGGGGAACCTGCCAGTTTAGCCCTGATAGGAGGGAGATCGGAAGAGCGGTTTCAG
chr17	48735579	48735618	ABCC3_8404	+	GTGACCTATGCACCAGACGTGAGGGGTGCGGGGGCTCCACAGTGGAGCTGAGCTCAGCCAGATCGGAAGAGCGGTTTCAG
chr17	48735868	48735907	ABCC3_8405	+	GTGACCTATGCACCAGACGTTCTCCACCAGCCAGGCCAGAGGGAGGGGATGGAAGAGATCGGAAGAGCGGTTTCAG
chr17	48736740	48736779	ABCC3_8406	+	GTGACCTATGCACCAGACGTCCCCTTGCCCCAACACCCAGCCCTTCGCTTACCCAGATAGATCGGAAGAGCGGTTTCAG
chr17	48738486	48738525	ABCC3_8407	+	GTGACCTATGCACCAGACGTACTCCGGCTCACTATAGCCCTGCCCTGGGCAGCAGGGCTGABATCGGAAGAGCGGTTTCAG
chr17	48741230	48741269	ABCC3_8408	+	GTGACCTATGCACCAGACGTGCAGGGCCAGGGGAAAGGCTGCCCTGGCCAGCTTGCAAAAGATCGGAAGAGCGGTTTCAG
chr17	48741483	48741522	ABCC3_8409	+	GTGACCTATGCACCAGACGTACCCCTGACCTCTGCCCTCTGACATGCTGCAGAAAGATCGGAAGAGCGGTTTCAG
chr17	48742617	48742656	ABCC3_8410	+	GTGACCTATGCACCAGACGTTACAGAGTGCATCTCCTGCTGAGCACCAGGGCTGAGATCGGAAGAGCGGTTTCAG

chr17	48745129	48745168	ABCC3_8411	+	GTGACCTATGCACCAGACGTGCACAGGGCTGGGTCCCTGCCTCCAGGGCTCTGGGTGCCAGATCGGAAGAGCGGTTTCAG
chr17	48745213	48745252	ABCC3_8412	+	GTGACCTATGCACCAGACGTACGCTGCTCAGGTGACCCCTGATCACCCCTCTGGGTGTACGTAGATCGGAAGAGCGGTTTCAG
chr17	48745381	48745420	ABCC3_8413	+	GTGACCTATGCACCAGACGTGTAGGGCTGGGGGCTCTACTGGAGTTGGAACAGGTTGTTGAGATCGGAAGAGCGGTTTCAG
chr17	48745889	48745928	ABCC3_8414	+	GTGACCTATGCACCAGACGTCCCCTACCTGGGCTGCCTGCCCCAGTCCCTTGTCCAGAAAAGATCGGAAGAGCGGTTTCAG
chr17	48746291	48746330	ABCC3_8415	+	GTGACCTATGCACCAGACGTCTCCCACTCCCTCCACAGCTGCCACGGTGGGCTGGAAGTAGATCGGAAGAGCGGTTTCAG
chr17	48746638	48746677	ABCC3_8416	+	GTGACCTATGCACCAGACGTGACGGGCTCCCTGGGCAGGGTGTGGGGCTCAGCCAGGCCTTAGATCGGAAGAGCGGTTTCAG
chr17	48746900	48746939	ABCC3_8417	+	GTGACCTATGCACCAGACGTCTTCCATCTTAAGAGGCTAGGACATAGAGCTGCCACAGATCGGAAGAGCGGTTTCAG
chr17	48750510	48750549	ABCC3_8418	+	GTGACCTATGCACCAGACGTCCAGAGGCTAAGGGGGCTAAGGTGAGATCTGAGGCCGAAAGATCGGAAGAGCGGTTTCAG
chr17	48751030	48751069	ABCC3_8419	+	GTGACCTATGCACCAGACGTTCTGGGCCCTCTGATTCCCATGCCTCCAGCATTCCCCAGATCGGAAGAGCGGTTTCAG
chr17	48752848	48752887	ABCC3_8420	+	GTGACCTATGCACCAGACGTGAGAGCTCCAGCCCTCCCGAGGCTGTATCAGGCCTCCAGATCGGAAGAGCGGTTTCAG
chr17	48753147	48753186	ABCC3_8421	+	GTGACCTATGCACCAGACGTGGGGCAAGAGGGGCTGGAGGGGATGGACAGGCAGGCCCAAGATCGGAAGAGCGGTTTCAG
chr17	48753462	48753501	ABCC3_8422	+	GTGACCTATGCACCAGACGTGGGGGTGCCAGAAAGGGCTCCAATATCCCTTCTCTGAGATCGGAAGAGCGGTTTCAG
chr17	48753960	48753999	ABCC3_8423	+	GTGACCTATGCACCAGACGTGGCGGTGATCCAGTGTGGCGTGTGGTTATTGGGGCGGGGAGATCGGAAGAGCGGTTTCAG
chr17	48755315	48755354	ABCC3_8424	+	GTGACCTATGCACCAGACGTGCCTCCCTCGCTCCCTGCTCCTCCAGGAATTCCAGCAGGAGATCGGAAGAGCGGTTTCAG
chr17	48755591	48755630	ABCC3_8425	+	GTGACCTATGCACCAGACGTCTGGACCCAGGGCAGGGCCACCCTGGGACAGAAAACCAAGATCGGAAGAGCGGTTTCAG
chr17	48757271	48757310	ABCC3_8426	+	GTGACCTATGCACCAGACGTGCATGAGCCCGGGACAGGGGGAATCTGAAGTAGCTGGGGAAGATCGGAAGAGCGGTTTCAG
chr17	48761128	48761167	ABCC3_8427	+	GTGACCTATGCACCAGACGTGGTAGGGCGGGCTGCGTGTGTGTTTCATGCCTGCAGACATGAGATCGGAAGAGCGGTTTCAG
chr17	48761479	48761518	ABCC3_8428	+	GTGACCTATGCACCAGACGTGGCATGGGCTGCCACTCACCAAGGCCTGGAGGCAGATCGGAAGAGCGGTTTCAG
chr17	48762247	48762286	ABCC3_8429	+	GTGACCTATGCACCAGACGTGGAGTGCAGAGGTCAGAACTGCAACCCCTCCCTGGGAAACAGATCGGAAGAGCGGTTTCAG
chr17	48765102	48765141	ABCC3_8430	+	GTGACCTATGCACCAGACGTGAAACCTGAGCAATGGGGAACCTGGTGGGGCCACTGGGGAGATCGGAAGAGCGGTTTCAG
chr17	48768572	48768611	ABCC3_8431	+	GTGACCTATGCACCAGACGTTGAGATTTCTCCTGGCCCTTCTGGTTTTTATCAGGAAGAGATCGGAAGAGCGGTTTCAG
chr11	35160928	35160967	CD44_8432	+	GTGACCTATGCACCAGACGTGCCGACGCTGGGCAGCAAGATGGTGCGGGGTGCTCAGCAGATCGGAAGAGCGGTTTCAG
chr11	35198298	35198337	CD44_8433	+	GTGACCTATGCACCAGACGTAGCACCCGACCCTGGGAAAGCTGGCGGCCTGGGACCCAGAGATCGGAAGAGCGGTTTCAG
chr11	35201965	35202004	CD44_8434	+	GTGACCTATGCACCAGACGTAGGGGGGTGCTGTTGGCTGAAAGGCTGTGGGACCTGGAGATCGGAAGAGCGGTTTCAG
chr11	35208458	35208497	CD44_8435	+	GTGACCTATGCACCAGACGTCTCTAATCTTAATTAATTTTTCTATTTTGGGGAAGGGAGATCGGAAGAGCGGTTTCAG
chr11	35211623	35211662	CD44_8436	+	GTGACCTATGCACCAGACGTTAAATCACTGTGCTTCCCAATGCAATTCCTGGCAAAATAGATCGGAAGAGCGGTTTCAG
chr11	35218432	35218471	CD44_8437	+	GTGACCTATGCACCAGACGTATTATTATCTCATAGCGTATGTTTTCTTGACAGCCTTGAAGATCGGAAGAGCGGTTTCAG
chr11	35219804	35219843	CD44_8438	+	GTGACCTATGCACCAGACGTTCAATTACAGTACAGCATTATGCAAGGCTTATTGATTAGATCGGAAGAGCGGTTTCAG
chr11	35222753	35222792	CD44_8439	+	GTGACCTATGCACCAGACGTGCGATTTAATGAAAGATTTTTCCCCTCAAAGCCCAAGATCGGAAGAGCGGTTTCAG
chr11	35223345	35223384	CD44_8440	+	GTGACCTATGCACCAGACGTGGCGATCGCGAGTCTGGTGTAGATGAATTAAGTAAAGACAGATCGGAAGAGCGGTTTCAG
chr11	35226198	35226237	CD44_8441	+	GTGACCTATGCACCAGACGTGTTAACAAGTAAATTTGGATGGAACTTCTTTTTGGGTTAGATCGGAAGAGCGGTTTCAG
chr11	35227801	35227840	CD44_8442	+	GTGACCTATGCACCAGACGTCTGAGATTTTATATATTATGTTTTTGAATCCACTGAGAGATCGGAAGAGCGGTTTCAG
chr11	35229764	35229803	CD44_8443	+	GTGACCTATGCACCAGACGTGATGCTCAGCCACTTTATTGACTGTATTCTGCTTCATAGATCGGAAGAGCGGTTTCAG
chr11	35231612	35231651	CD44_8444	+	GTGACCTATGCACCAGACGTTAAAACCTAGTTGGCTTCAGCTATTGATAAGAAATCAATCAAGATCGGAAGAGCGGTTTCAG
chr11	35233007	35233046	CD44_8445	+	GTGACCTATGCACCAGACGTATTATTATCTAGTTTTGCTTCTCTATATAGAAAACCAATAGATCGGAAGAGCGGTTTCAG
chr11	35236472	35236511	CD44_8446	+	GTGACCTATGCACCAGACGTAACCTGCTTTAGTCATTTACTGTTATAATCATTGAGCCTAAAGATCGGAAGAGCGGTTTCAG
chr11	35240945	35240984	CD44_8447	+	GTGACCTATGCACCAGACGTAACCTTGGAGGCAGAAAACACACTGAAAGCAGCTTTCTCAAGATCGGAAGAGCGGTTTCAG
chr11	35243290	35243329	CD44_8448	+	GTGACCTATGCACCAGACGTGTCCTGGGGCTTTCAACTTGGAAAGGGCATTCAATTAACAGATCGGAAGAGCGGTTTCAG
chr11	35250845	35250884	CD44_8449	+	GTGACCTATGCACCAGACGTAACCTGCAGAATGTGGACATGAAGATTGGGGTGTAAACCCAGATCGGAAGAGCGGTTTCAG
chr11	35250891	35250930	CD44_8450	+	GTGACCTATGCACCAGACGTTATCTGGAAAGAAAACCCCTTGGAAACATAACCATTAGATCGGAAGAGCGGTTTCAG
chr19	10678104	10678143	CDKN2D_8451	+	GTGACCTATGCACCAGACGTGACAGAGATCAGGAGGCTCCCAAGGGAGGTTCCACAAGATCGGAAGAGCGGTTTCAG
chr19	10679340	10679379	CDKN2D_8452	+	GTGACCTATGCACCAGACGTGCGGCCTGCAAGGCCCGCCCGCCCGCCCGCCCGCCTAGATCGGAAGAGCGGTTTCAG
chr5	149433798	149433837	CSF1R_8453	+	GTGACCTATGCACCAGACGTGAGGGACCAGAACTGTCAGTCCAGATCCATCAGGCCAGAGATCGGAAGAGCGGTTTCAG
chr5	149434004	149434043	CSF1R_8454	+	GTGACCTATGCACCAGACGTGGACAGAGGATGCCCATGGGCAGCTCCCTAGGGTCCAGGGAGATCGGAAGAGCGGTTTCAG
chr5	149434910	149434949	CSF1R_8455	+	GTGACCTATGCACCAGACGTCAAGATCAGGTAGAGGCCATGCCACTTGTCTTCCCCAAGATCGGAAGAGCGGTTTCAG
chr5	149435711	149435750	CSF1R_8456	+	GTGACCTATGCACCAGACGTAGTCCCCAGTTATTTGGCCCCGACTTCCACCCCTCCAGATCGGAAGAGCGGTTTCAG
chr5	149435915	149435954	CSF1R_8457	+	GTGACCTATGCACCAGACGTGCACTGCAGGGTTAGTCTTGGGCTTCTCCTACCTGAGCCAGATCGGAAGAGCGGTTTCAG
chr5	149436958	149436997	CSF1R_8458	+	GTGACCTATGCACCAGACGTAAGAGGCGTCAGGGCAGCCCTGCCACTCCCCACCCCTCAGATCGGAAGAGCGGTTTCAG
chr5	149437166	149437205	CSF1R_8459	+	GTGACCTATGCACCAGACGTGAGAGGGTTGGGGGCGAGAGTCACTCATCACTGCACAGATCGGAAGAGCGGTTTCAG
chr5	149439436	149439475	CSF1R_8460	+	GTGACCTATGCACCAGACGTCAAGGGTGTGGGGTAGGGAGGTTGCTGAGTGTCTCCCTCCAGATCGGAAGAGCGGTTTCAG
chr5	149440546	149440585	CSF1R_8461	+	GTGACCTATGCACCAGACGTGAACCACAGTCCAAAGCAGGGGAGAGGGCAGGACAGAAAGATCGGAAGAGCGGTTTCAG
chr5	149441169	149441208	CSF1R_8462	+	GTGACCTATGCACCAGACGTGACAGGCTCCCTAAGTCCCTGGGCACCAAGGGCCTCTGTAGATCGGAAGAGCGGTTTCAG
chr5	149441423	149441462	CSF1R_8463	+	GTGACCTATGCACCAGACGTGGAAGGGAGCAGTGGCAGTGGGGCTGGCAGGCAGTTCCAGATCGGAAGAGCGGTTTCAG
chr5	149447904	149447943	CSF1R_8464	+	GTGACCTATGCACCAGACGTTGAAGCAAAGCAGTGAAGCAGGGAGGGTGCCTCCGAGCCAGATCGGAAGAGCGGTTTCAG
chr5	149449637	149449676	CSF1R_8465	+	GTGACCTATGCACCAGACGTGAGAAATGTGGCTCAGAGCTTCCAGGGTCCAGCAGCCAGCAAGATCGGAAGAGCGGTTTCAG
chr5	149449876	149449915	CSF1R_8466	+	GTGACCTATGCACCAGACGTAAGGAGGAGGCCCAAGTCACACTTTCCCGCCACCTCCAGATCGGAAGAGCGGTTTCAG
chr5	149450145	149450184	CSF1R_8467	+	GTGACCTATGCACCAGACGTGAACAGTGGTGTGGTGGAGCCCGACTAGTATGGCCAGATCGGAAGAGCGGTTTCAG
chr5	149453067	149453106	CSF1R_8468	+	GTGACCTATGCACCAGACGTGAAACACACAAGCATCTGGCATTTAGTGGAAAGATGCTCTTGTAGATCGGAAGAGCGGTTTCAG

chr5	149457822	149457861	CSF1R_8469	+	GTGACCTATGCACCAGACGTGGGAGAGACCCCTGAACACCCAGGCTCCCTGAACATGATAAGATCGGAAGAGCGGTTTCAG
chr5	149459910	149459949	CSF1R_8470	+	GTGACCTATGCACCAGACGTGGAGGGCACAGGGTTACAACCTGCCCTCCCTCCACTGGGCCAGATCGGAAGAGCGGTTTCAG
chr5	149460598	149460637	CSF1R_8471	+	GTGACCTATGCACCAGACGTAGAGGGACAGCAGACAGAAGTGGGTCTAGGATGCGCCCCAGATCGGAAGAGCGGTTTCAG
chr5	149466001	149466040	CSF1R_8472	+	GTGACCTATGCACCAGACGTGGGAAGTGGCAGGCAGGTGCAGGGCTGCAAGGTGCCCAGGAGATCGGAAGAGCGGTTTCAG
chr1	97544713	97544752	DPYD_8473	+	GTGACCTATGCACCAGACGTAAATAGAGGGTATTGATGTCCTACTGACCACAAAAGGTCAACAAGATCGGAAGAGCGGTTTCAG
chr1	97548037	97548076	DPYD_8474	+	GTGACCTATGCACCAGACGTCCACTGAATTACTTAGCAAGCTCATTTTAAAACATTTTCAAGATCGGAAGAGCGGTTTCAG
chr1	97564239	97564238	DPYD_8475	+	GTGACCTATGCACCAGACGTAAACACAAAATGAAGGAGCATTTTGTCTCAGAGAAGAGAAAGATCGGAAGAGCGGTTTCAG
chr1	97658815	97658854	DPYD_8476	+	GTGACCTATGCACCAGACGTGACAGCAGTCAACCAAGTGTCAAACCAAGAGATAAATTCTCAGATCGGAAGAGCGGTTTCAG
chr1	97700561	97700600	DPYD_8477	+	GTGACCTATGCACCAGACGTTCAGAATAATCAATGGTTAGCACACTGACCCTTGTAGTATAGATCGGAAGAGCGGTTTCAG
chr1	97770945	97770984	DPYD_8478	+	GTGACCTATGCACCAGACGTGACATCAACATTTTCATGACGCTCTTATAAGACACGATAGAGATCGGAAGAGCGGTTTCAG
chr1	97771864	97771903	DPYD_8479	+	GTGACCTATGCACCAGACGTAGGTCGGTTAAATATAGAAAATAAAGAATTGTGATCAGATCGGAAGAGCGGTTTCAG
chr1	97839211	97839250	DPYD_8480	+	GTGACCTATGCACCAGACGTGAAAGGAAAATGAAAGAAAAGGCAAAAGCTTTATTTATATAAGATCGGAAGAGCGGTTTCAG
chr1	97848028	97848067	DPYD_8481	+	GTGACCTATGCACCAGACGTAAAAACAAAAGAATATAAGTCCAAGTAGTTATCCAGTTGATAGATCGGAAGAGCGGTTTCAG
chr1	97915790	97915829	DPYD_8482	+	GTGACCTATGCACCAGACGTAGTAAAGATATTGAGTCTCCTTTTGACAAAAGAAAAGCTATAGATCGGAAGAGCGGTTTCAG
chr1	97981508	97981547	DPYD_8483	+	GTGACCTATGCACCAGACGTCAAACCAATACTTGGTTTCATATTACATCTAAATTTGTCAGATCGGAAGAGCGGTTTCAG
chr1	98015311	98015350	DPYD_8484	+	GTGACCTATGCACCAGACGTAAAGTGA AAAACAATAGACAATCACTAGTCAACAGACAATTAGATCGGAAGAGCGGTTTCAG
chr1	98039537	98039576	DPYD_8485	+	GTGACCTATGCACCAGACGTACAGAACAAGAAAAGTAAATTTGAAATTTTCTTATTTCCACAGATCGGAAGAGCGGTTTCAG
chr1	98058954	98058993	DPYD_8486	+	GTGACCTATGCACCAGACGTAAAAGGAAAACCCCAATTTTCAAGTAGAGAAAACCAATTTCTGCAGATCGGAAGAGCGGTTTCAG
chr1	98060733	98060772	DPYD_8487	+	GTGACCTATGCACCAGACGTAAAATTTATAAAATATCATTAGCAGGAGGAGGGGCTTTTCCAGATCGGAAGAGCGGTTTCAG
chr1	98144749	98144788	DPYD_8488	+	GTGACCTATGCACCAGACGTCAATATTTTGCATAAAGAAAATTTGGCATATGATTAATTAAGATCGGAAGAGCGGTTTCAG
chr1	98157365	98157404	DPYD_8489	+	GTGACCTATGCACCAGACGTAGGAGAAAAGAAAACAGGCATCAGTAGAAAATGACCAATAGATCGGAAGAGCGGTTTCAG
chr1	98165114	98165153	DPYD_8490	+	GTGACCTATGCACCAGACGTATCAATTTGTCATGGTTAAAATTTTGAAGTACTTACATCAGATCGGAAGAGCGGTTTCAG
chr1	98187238	98187277	DPYD_8491	+	GTGACCTATGCACCAGACGTAAATAAAAATAAAAATTTTACTACTTAAAAATATACTTTAAAGATCGGAAGAGCGGTTTCAG
chr1	98206046	98206085	DPYD_8492	+	GTGACCTATGCACCAGACGTAAAATAACTATGTTAAGAACTACAAGATAAGTGAGATAATAGATCGGAAGAGCGGTTTCAG
chr1	98293763	98293802	DPYD_8493	+	GTGACCTATGCACCAGACGTAAAAATAATGCATTAATTCTCTAAGATCCTGAGAAAATAGATCGGAAGAGCGGTTTCAG
chr1	98348941	98348980	DPYD_8494	+	GTGACCTATGCACCAGACGTCAATAAACAATGTGTAATATATGAAAATATGTTGGCATTAGATCGGAAGAGCGGTTTCAG
chr1	98386489	98386528	DPYD_8495	+	GTGACCTATGCACCAGACGTACAGTCTCGAGTCTGCCAGTGACAACCCCTCCTTGCCTCCAGATCGGAAGAGCGGTTTCAG
chr14	64694343	64694382	ESR2_8496	+	GTGACCTATGCACCAGACGTGATGCGGGACAAGTCAAAGTTGCAGTGAAAGGAAGTGTGGAGATCGGAAGAGCGGTTTCAG
chr14	64700052	64700091	ESR2_8497	+	GTGACCTATGCACCAGACGTAAAAGGGTCTGAGATTCCCTCTCCGAGGCACAGGATCGGAAGAGCGGTTTCAG
chr14	64701879	64701918	ESR2_8498	+	GTGACCTATGCACCAGACGTAAATAAAAGCCAGAAGTCAATGCTCTGAGCAAAAGGACGAGAAGATCGGAAGAGCGGTTTCAG
chr14	64716408	64716447	ESR2_8499	+	GTGACCTATGCACCAGACGTTCGTTTGGAAAATTAAGGAACATAGCTTCAGGAAACCATCAGATCGGAAGAGCGGTTTCAG
chr14	64724093	64724132	ESR2_8500	+	GTGACCTATGCACCAGACGTCAAGAGGCGGTGAGACACCCCAACCCCTCCTCCTCAGCTCAGATCGGAAGAGCGGTTTCAG
chr14	64727477	64727516	ESR2_8501	+	GTGACCTATGCACCAGACGTAAAGCAGAGTCAATTCGAATTTGCCAGGGTAAAACCCGAGTCAAGATCGGAAGAGCGGTTTCAG
chr14	64735640	64735679	ESR2_8502	+	GTGACCTATGCACCAGACGTGGGGAGGGAAAAAGATTTGCTATGATCTTTAGTTAGATCGGAAGAGCGGTTTCAG
chr14	64746882	64746921	ESR2_8503	+	GTGACCTATGCACCAGACGTAAAGAAAATACATTGAACAGAGCATAAAAGGGAAAAGATAAGATCGGAAGAGCGGTTTCAG
chr14	64749714	64749753	ESR2_8504	+	GTGACCTATGCACCAGACGTAAACAGCTGAGAAAAACCTTGCAAGAAGAGGCACAAAGGTAGATCGGAAGAGCGGTTTCAG
chr22	29664349	29664388	EWSR1_8505	+	GTGACCTATGCACCAGACGTTGAACTGCGGTGCGCGCCGGGTAGCCGGAACGCCCAAAAGATCGGAAGAGCGGTTTCAG
chr22	29668252	29668291	EWSR1_8506	+	GTGACCTATGCACCAGACGTCTTTTATAACCGTATTTTGTGTGTGATTAATATTTTTTGAAGATCGGAAGAGCGGTTTCAG
chr22	29668431	29668470	EWSR1_8507	+	GTGACCTATGCACCAGACGTAAATAATTACATGTAGCTGCACCTCAAAGTAAATCAGTAAGATCGGAAGAGCGGTTTCAG
chr22	29669864	29669903	EWSR1_8508	+	GTGACCTATGCACCAGACGTCTTGGAGAGATTTTGGTGGTCTTGGCTAGGGCATTGGAGATCGGAAGAGCGGTTTCAG
chr22	29674216	29674255	EWSR1_8509	+	GTGACCTATGCACCAGACGTGGTGCCTTAAATGCGTCACTTCTATGTTGGAGGGAAAAGATAAGATCGGAAGAGCGGTTTCAG
chr22	29678557	29678596	EWSR1_8510	+	GTGACCTATGCACCAGACGTTTTTTGTGGCAAAAACAAAACAGTGACAAAACAGTTTTTTAGATCGGAAGAGCGGTTTCAG
chr22	29683134	29683173	EWSR1_8511	+	GTGACCTATGCACCAGACGTAAAGAGAGAAAACAAAATAAGAATGAATGTGTTTAGAGTTAGATCGGAAGAGCGGTTTCAG
chr22	29684786	29684825	EWSR1_8512	+	GTGACCTATGCACCAGACGTACCTTTTTCTCCTTTTACCTAATTTTGTTCATCCATAGGAAGATCGGAAGAGCGGTTTCAG
chr22	29687599	29687638	EWSR1_8513	+	GTGACCTATGCACCAGACGTGAGTATTACCATAGATAGTGTTTAAAAAAAATGCAGTCAAGATCGGAAGAGCGGTTTCAG
chr22	29688169	29688208	EWSR1_8514	+	GTGACCTATGCACCAGACGTATTCTAGTTGCTGCTTATGCTGCTTGTGTAATTAATAGATCGGAAGAGCGGTTTCAG
chr22	29688606	29688645	EWSR1_8515	+	GTGACCTATGCACCAGACGTGCATAACCAGGTCATCTGGCAGAACTTTAAACCACAGAGCAGATCGGAAGAGCGGTTTCAG
chr22	29692369	29692408	EWSR1_8516	+	GTGACCTATGCACCAGACGTCTCACTGGCATTCTTAATCTCCCTGGCTATAGAATATGGCAGATCGGAAGAGCGGTTTCAG
chr22	29693950	29693989	EWSR1_8517	+	GTGACCTATGCACCAGACGTGAGCTCCTATGTTGCATTAAGAGGTTTTTCAGTACACTTCAGATCGGAAGAGCGGTTTCAG
chr22	29694896	29694935	EWSR1_8518	+	GTGACCTATGCACCAGACGTGCTTTGGCAAATGATACCTACGAGTGAAGCCACCCTTCAGATCGGAAGAGCGGTTTCAG
chr22	29695332	29695371	EWSR1_8519	+	GTGACCTATGCACCAGACGTGTTTCATGAGTGTCCCTCAGCTCCTGGTGCTAAACCTCAGATCGGAAGAGCGGTTTCAG
chr22	29695852	29695891	EWSR1_8520	+	GTGACCTATGCACCAGACGTGTGAAAAGACAGCTGTGGCGCCGACAGTAAAGGACAGATCGGAAGAGCGGTTTCAG
chr22	29696162	29696201	EWSR1_8521	+	GTGACCTATGCACCAGACGTCCCGCAGAGCTGCATTGACTACCAGATTTATTTTTTAAACAGATCGGAAGAGCGGTTTCAG
chr3	10070416	10070455	FANCD2_8522	+	GTGACCTATGCACCAGACGTAGTCAATTTGTTGCTTTATTTCTGTAGCAATGTGTGAGGCAGATCGGAAGAGCGGTTTCAG
chr3	10074667	10074706	FANCD2_8523	+	GTGACCTATGCACCAGACGTAAATCTAATTTTATTCTCTGGGTTTAAATGAAATAGTTTCAGGATCGGAAGAGCGGTTTCAG
chr3	10076231	10076270	FANCD2_8524	+	GTGACCTATGCACCAGACGTTCCTGGTATTTTGGCTTGTGCCAGCATAACTTAGAAAAGATCGGAAGAGCGGTTTCAG
chr3	10076493	10076532	FANCD2_8525	+	GTGACCTATGCACCAGACGTGAGGCATGAAATCTTCTGTAATCTGCTGTTTGGCAAAGATCGGAAGAGCGGTTTCAG
chr3	10076928	10076967	FANCD2_8526	+	GTGACCTATGCACCAGACGTCACTTTTTCTGTGAACATTTGATGGAAGAGGTTTGTGTGAGATCGGAAGAGCGGTTTCAG

chr3	10078034	10078073	FANCD2_8527	+	GTGACCTATGCACCAGACGTTTATTATGGAATGTTCAAAGTACCTGTAGTACTTAAGTTAGATCGGAAGAGCGGTTTCAG
chr3	10081052	10081091	FANCD2_8528	+	GTGACCTATGCACCAGACGTTGACCTTTATCTCTTGAATTTAAAGAGTATGTTTCTCATATAGATCGGAAGAGCGGTTTCAG
chr3	10081540	10081579	FANCD2_8529	+	GTGACCTATGCACCAGACGTCCTCTGTGCATCATCTAAGTGAGGCTCAGCTATGGGGTTTCAGATCGGAAGAGCGGTTTCAG
chr3	10083405	10083444	FANCD2_8530	+	GTGACCTATGCACCAGACGTCCTCAGCTTTCCAGAAACAGAGCCAGCTTTCCAACCTCCCAGATCGGAAGAGCGGTTTCAG
chr3	10084358	10084397	FANCD2_8531	+	GTGACCTATGCACCAGACGTATATCCCATCACACCTAGATAAAAGCAACTTAAGTGCCAATAGATCGGAAGAGCGGTTTCAG
chr3	10084845	10084884	FANCD2_8532	+	GTGACCTATGCACCAGACGTCCTCCTCACACGATGTACAATTTTCTGACATCCCACATAGATCGGAAGAGCGGTTTCAG
chr3	10085287	10085326	FANCD2_8533	+	GTGACCTATGCACCAGACGTTGGAACCTTTGATTATCAAGGAGCAAATGAGTGGCAATTAGAGATCGGAAGAGCGGTTTCAG
chr3	10085559	10085598	FANCD2_8534	+	GTGACCTATGCACCAGACGTTGTACTATGCATTTTTCAGTATTGCAGACTTAAAGTAAATGAGATCGGAAGAGCGGTTTCAG
chr3	10089746	10089785	FANCD2_8535	+	GTGACCTATGCACCAGACGTACATTTATTTTGGCAAGGAGGGAACACAGAAAGGAAATAGATCGGAAGAGCGGTTTCAG
chr3	10091200	10091239	FANCD2_8536	+	GTGACCTATGCACCAGACGTGGCTTCTGTACTTTAGATATTGAATACTATAATTGGTGAGATCGGAAGAGCGGTTTCAG
chr3	10102098	10102137	FANCD2_8537	+	GTGACCTATGCACCAGACGTAGATTCTGACTTCTGTGGTTTAAAGATCAGTTAATCTTCTGCTAGATCGGAAGAGCGGTTTCAG
chr3	10105606	10105645	FANCD2_8538	+	GTGACCTATGCACCAGACGTTTGTCTTTTCTTAAAGCAATAAAGCATGAGAGCTGCTTTAAGATCGGAAGAGCGGTTTCAG
chr3	10106124	10106163	FANCD2_8539	+	GTGACCTATGCACCAGACGTTTACCTGTGGCTGGCTTGGTTGCACCTGGTGAAGTTACATCAAAGATCGGAAGAGCGGTTTCAG
chr3	10106570	10106609	FANCD2_8540	+	GTGACCTATGCACCAGACGTTTTTCTTTCTAAACCTGTTAGTGTGTTTGAATGTTTCATGAGATCGGAAGAGCGGTTTCAG
chr3	10107189	10107228	FANCD2_8541	+	GTGACCTATGCACCAGACGTAAGTCATCAGATCCTTCTCTTTATACTCTTCTTTGGTATAGATCGGAAGAGCGGTTTCAG
chr3	10107674	10107713	FANCD2_8542	+	GTGACCTATGCACCAGACGTTTAAATAGGATGTTTCAGCTTATTGTGCATAGTTTTCTCAAAGATCGGAAGAGCGGTTTCAG
chr3	10109012	10109051	FANCD2_8543	+	GTGACCTATGCACCAGACGTTGCTTACTACTGGTAGTACTACTAGGCCAGTAGTGAGGCAAGATCGGAAGAGCGGTTTCAG
chr3	10114676	10114715	FANCD2_8544	+	GTGACCTATGCACCAGACGTTTCTTCCCTCTGTCTGTCTGTCTCTGCTCCAAAGCTTCAATGAGATCGGAAGAGCGGTTTCAG
chr3	10115057	10115096	FANCD2_8545	+	GTGACCTATGCACCAGACGTGATGGGTATCCGTGAAGGTTTGTGACATCCCAGTGAGATTAGATCGGAAGAGCGGTTTCAG
chr3	10116368	10116407	FANCD2_8546	+	GTGACCTATGCACCAGACGTGGCTAGGATCTCAGAATTTAATCTTCTTTAGAAAAGTTCCAGATCGGAAGAGCGGTTTCAG
chr3	10119892	10119931	FANCD2_8547	+	GTGACCTATGCACCAGACGTGCAGAACATAGGACTTGGGCATAGTGGATTGGGAACAAGATCGGAAGAGCGGTTTCAG
chr3	10122923	10122962	FANCD2_8548	+	GTGACCTATGCACCAGACGTTAGACTTAGAAGCTGCTAAGCAAAATAGAGTTTCATTTTAGATCGGAAGAGCGGTTTCAG
chr3	10123159	10123198	FANCD2_8549	+	GTGACCTATGCACCAGACGTGGGAAGTGGGAGAGAAGATGATATATACTGCTTTTATAGATCGGAAGAGCGGTTTCAG
chr3	10127617	10127656	FANCD2_8550	+	GTGACCTATGCACCAGACGTTTACATAGCCAAAGATTTGTTGCCAAAGAACTCCTAGGAAGATCGGAAGAGCGGTTTCAG
chr3	10130237	10130276	FANCD2_8551	+	GTGACCTATGCACCAGACGTTGGTCTTCTTCCAATGAGCCAAATAGCTTTTTTCTATTTTGGATCGGAAGAGCGGTTTCAG
chr3	10130645	10130684	FANCD2_8552	+	GTGACCTATGCACCAGACGTTCTTCTCCAGTTTTTCCCTTAAAGATAGAATCATCATCAAGATCGGAAGAGCGGTTTCAG
chr3	10132080	10132119	FANCD2_8553	+	GTGACCTATGCACCAGACGTTAATAGTCACCTCAAGAAAGTGACTTTGGATTACTTGAAGATCGGAAGAGCGGTTTCAG
chr3	10133947	10133986	FANCD2_8554	+	GTGACCTATGCACCAGACGTAGACTGCTTGACACATCTCACCAAATAACTGCAGAAACCAAGATCGGAAGAGCGGTTTCAG
chr3	10135018	10135057	FANCD2_8555	+	GTGACCTATGCACCAGACGTTACTGGCCCTGTTTATATTTATCTTCTGTTGATCAGATCGGAAGAGCGGTTTCAG
chr3	10136058	10136097	FANCD2_8556	+	GTGACCTATGCACCAGACGTAGACGACAGACAACAAGATATGCACTGAAGAGTTGCTCAGAAGATCGGAAGAGCGGTTTCAG
chr3	10136969	10137008	FANCD2_8557	+	GTGACCTATGCACCAGACGTGAGCAGGTTCTATCAGCAGCCTGCCTGTTGGCTTAACTGAGATCGGAAGAGCGGTTTCAG
chr3	10138167	10138206	FANCD2_8558	+	GTGACCTATGCACCAGACGTGATCCTGCTAGTGATAATCCCCTACTCTTATTCTTTGTGAAGATCGGAAGAGCGGTTTCAG
chr3	10140510	10140549	FANCD2_8559	+	GTGACCTATGCACCAGACGTAAAACCCACCAAGCTGGCCACTGATGGTTGCATTTTGTAGATCGGAAGAGCGGTTTCAG
chr3	10140645	10140684	FANCD2_8560	+	GTGACCTATGCACCAGACGTGCTTATATATTTTTGGGACCAGAAACAACAGACACAAGATCGGAAGAGCGGTTTCAG
chr3	10142957	10142996	FANCD2_8561	+	GTGACCTATGCACCAGACGTAATTGTTCCTGCTTGTGCTCTGCGACCCCTGTGATCAAAGATCGGAAGAGCGGTTTCAG
chr14	75745837	75745876	FOS_8562	+	GTGACCTATGCACCAGACGTTCTCCGCTCGCCGCGGGGCGGGGGCTTGGGGTCCGCGGAGAGATCGGAAGAGCGGTTTCAG
chr14	75746842	75746881	FOS_8563	+	GTGACCTATGCACCAGACGTTAGCGTACTTCTCTGGGAATGTGGGGCTGGGTGGGAAGATCGGAAGAGCGGTTTCAG
chr14	75747381	75747420	FOS_8564	+	GTGACCTATGCACCAGACGTTGTGGGTTGCTCCTTTTTTAAACTTAAGGGGAAAGTTGGAAGATCGGAAGAGCGGTTTCAG
chr14	75748138	75748177	FOS_8565	+	GTGACCTATGCACCAGACGTAAGGGGAGGCAGCCGGCACCACAAGTGCCACTGCCCGAGAGATCGGAAGAGCGGTTTCAG
chr14	75747817	75747856	FOS_8566	+	GTGACCTATGCACCAGACGTTCCAGGCCAGTGGCTGTGAGACGCCGCTCCGTGCCAGAAGATCGGAAGAGCGGTTTCAG
chr11	33881132	33881171	LMO2_8567	+	GTGACCTATGCACCAGACGTAGAAGAAAAGCTAAGAAGACAGTCAAAGGGACAACCTCGTGAAGATCGGAAGAGCGGTTTCAG
chr11	33886374	33886413	LMO2_8568	+	GTGACCTATGCACCAGACGTGGCCAAAGCATCAGGGACAGCCTCACCAGAGTGAGACCAGCAGATCGGAAGAGCGGTTTCAG
chr11	33890943	33890982	LMO2_8569	+	GTGACCTATGCACCAGACGTGGCGGGTGTCCGGCGCGGGGGCGCTCCCTTTGTGGCCGAGATCGGAAGAGCGGTTTCAG
chr11	33891273	33891312	LMO2_8570	+	GTGACCTATGCACCAGACGTCCGCCGCCACCGCCCGTCCCTCTCGCGCGCTGTGCGCGGAGATCGGAAGAGCGGTTTCAG
chr19	15272536	15272575	NOTCH3_8571	+	GTGACCTATGCACCAGACGTAGAACCACAGAGGTCAGCGAAACCCAGCTAACAGTAGCAGATCGGAAGAGCGGTTTCAG
chr19	15273384	15273423	NOTCH3_8572	+	GTGACCTATGCACCAGACGTAAGGGAGGAGAGGTCAGGACCAGCCCTGTCTGGGCCAGATCGGAAGAGCGGTTTCAG
chr19	15276337	15276376	NOTCH3_8573	+	GTGACCTATGCACCAGACGTGAGTGGATGCAGCAGGAGGGGTCATGGCAGGAACAGAGGAAGATCGGAAGAGCGGTTTCAG
chr19	15276913	15276952	NOTCH3_8574	+	GTGACCTATGCACCAGACGTAGGAGTGTGTCAGCAGGAAGGTAACACAGGGCCTTTTCCAGATCGGAAGAGCGGTTTCAG
chr19	15278233	15278272	NOTCH3_8575	+	GTGACCTATGCACCAGACGTAGGACCCCTGGATCTCAGATCTCACCTTTGGTGCTGGGAGATCGGAAGAGCGGTTTCAG
chr19	15280992	15281031	NOTCH3_8576	+	GTGACCTATGCACCAGACGTATGGGAAGAGGGATGTGAGGGGGACACTAGAGGTGTCCAAGATCGGAAGAGCGGTTTCAG
chr19	15281375	15281414	NOTCH3_8577	+	GTGACCTATGCACCAGACGTGAAGCAGAGGGCGGGCTTCAGCCGAGGGCGGGCTTTGGAGATCGGAAGAGCGGTTTCAG
chr19	15281647	15281686	NOTCH3_8578	+	GTGACCTATGCACCAGACGTAGCAGAGGGGACAGAGGCTCAAATAATGCCGATCGGAAGATCGGAAGAGCGGTTTCAG
chr19	15285222	15285261	NOTCH3_8579	+	GTGACCTATGCACCAGACGTAGGGTGAGGCAGAGAGGGCGGAGTCAGGGGTTCAGAGGAGAGATCGGAAGAGCGGTTTCAG
chr19	15289763	15289802	NOTCH3_8580	+	GTGACCTATGCACCAGACGTGGGAGCATGTAGATCAGCCACAATGGGGAAATGACAGGCGAGATCGGAAGAGCGGTTTCAG
chr19	15290104	15290143	NOTCH3_8581	+	GTGACCTATGCACCAGACGTAAACAGGGGTTGTTCAAGAGGGAATGAAGACAGCCTCTCAAAGATCGGAAGAGCGGTTTCAG
chr19	15290318	15290357	NOTCH3_8582	+	GTGACCTATGCACCAGACGTGAAGAGAGGGGACCCACTCAGCTTAGTGGGACACAGACCAGATCGGAAGAGCGGTTTCAG
chr19	15291078	15291117	NOTCH3_8583	+	GTGACCTATGCACCAGACGTGAGAGTGGCAGCAGGAACACTGAGTAAACCCATACATCCCCAGATCGGAAGAGCGGTTTCAG
chr19	15291650	15291689	NOTCH3_8584	+	GTGACCTATGCACCAGACGTAGCATCAGACTCAGTACTGTGGGGTGGGGGTAGTCTGGAGATCGGAAGAGCGGTTTCAG

chr19	15292623	15292662	NOTCH3_8585	+	GTGACCTATGCACCAGACGTGAGGAAGCGGTTCTGGTACCTACCTTGCCCCATTAGCCAGATCGGAAGAGCGGTTTCAG
chr19	15295272	15295311	NOTCH3_8586	+	GTGACCTATGCACCAGACGTGAGCAAGGTTACACCTAGGGTTACAGGGTACAGAGCAGGATCGGAAGAGCGGTTTCAG
chr19	15295841	15295880	NOTCH3_8587	+	GTGACCTATGCACCAGACGTTGGAAGAGAGGGAAGCAGAGATAGCCTTGAGGGACTCCCTAGATCGGAAGAGCGGTTTCAG
chr19	15296230	15296269	NOTCH3_8588	+	GTGACCTATGCACCAGACGTAAAGTAGTCAGGCCAGGGAGGTGGGCCAGGGAGAGGGGCAGATCGGAAGAGCGGTTTCAG
chr19	15296501	15296540	NOTCH3_8589	+	GTGACCTATGCACCAGACGTCACAAGCAATCTCATCTCAGAACAAGTCAGCAGGGACAAAGATCGGAAGAGCGGTTTCAG
chr19	15297810	15297849	NOTCH3_8590	+	GTGACCTATGCACCAGACGTGGAACATGGCATGGAGTGGCCACCACCTGTGCCCACTAGAAAGATCGGAAGAGCGGTTTCAG
chr19	15298160	15298199	NOTCH3_8591	+	GTGACCTATGCACCAGACGTAAAGAGGTCAGGCTCCGCCACTTGCCAGGGGCCTGCCCAAGATCGGAAGAGCGGTTTCAG
chr19	15298816	15298855	NOTCH3_8592	+	GTGACCTATGCACCAGACGTGAGTGGGATGAGCAGAGGCCCAAAGGGTGAGAGCAGTAAGATCGGAAGAGCGGTTTCAG
chr19	15299170	15299209	NOTCH3_8593	+	GTGACCTATGCACCAGACGTGAATAGGGCTTAGGAAAGCGGGGCTACCCTATGGTGTGAAGATCGGAAGAGCGGTTTCAG
chr19	15299996	15300035	NOTCH3_8594	+	GTGACCTATGCACCAGACGTGAGTGGGATCGGTGTGGGCGTGGCTGGCCGGGACCCCTCAGATCGGAAGAGCGGTTTCAG
chr19	15300250	15300289	NOTCH3_8595	+	GTGACCTATGCACCAGACGTGTAAGCAGAAGTCATAGGCAGATCTTCTGCTCTGCCAAAGATCGGAAGAGCGGTTTCAG
chr19	15302479	15302518	NOTCH3_8596	+	GTGACCTATGCACCAGACGTGATGTCAGCAGCTCCAGCCACTGGCGCATGTCCACCCGAAGATCGGAAGAGCGGTTTCAG
chr19	15302689	15302728	NOTCH3_8597	+	GTGACCTATGCACCAGACGTAGGGGCAAGGATGGTCACCCGCGGGTGGCCTGCTGTCCAGATCGGAAGAGCGGTTTCAG
chr19	15303120	15303159	NOTCH3_8598	+	GTGACCTATGCACCAGACGTGAGGACAGGGTGAGTTTAGGACTGACCACACCCCGACTAAGATCGGAAGAGCGGTTTCAG
chr19	15303341	15303380	NOTCH3_8599	+	GTGACCTATGCACCAGACGTAGATGGCTTGGTTGGGCAGCACAGGGCAGGATGGCCCCAGAGATCGGAAGAGCGGTTTCAG
chr19	15308400	15308439	NOTCH3_8600	+	GTGACCTATGCACCAGACGTGTAAGGAAGGTGGAGGATCAGCCAGGTGCCAGGAACCCAGATCGGAAGAGCGGTTTCAG
chr19	15311727	15311766	NOTCH3_8601	+	GTGACCTATGCACCAGACGTGCGGACCCCTCCCTCTCCCTCCTCCCTGGGCTCCGGGCAGATCGGAAGAGCGGTTTCAG
chr19	15271834	15271873	NOTCH3_8602	+	GTGACCTATGCACCAGACGTACGGGGTCCCTGGGTTGAGCAGTGGGTCGGGTCGCCGGCAGATCGGAAGAGCGGTTTCAG
chr1	226549253	226549292	PARP1_8603	+	GTGACCTATGCACCAGACGTGCTTGTAAAGGACCAACAGCCATACAACAGAGGGTATGTAGATCGGAAGAGCGGTTTCAG
chr1	226549795	226549834	PARP1_8604	+	GTGACCTATGCACCAGACGTGAAGTCACAAGTGACATGAACTGTGAGTACAGATGTGGCAAGATCGGAAGAGCGGTTTCAG
chr1	226550872	226550911	PARP1_8605	+	GTGACCTATGCACCAGACGTGAGGACAGTCTCAGAAGAGGCCCTTACACTGGGCTCTCGAAGATCGGAAGAGCGGTTTCAG
chr1	226552866	226552905	PARP1_8606	+	GTGACCTATGCACCAGACGTTAGTAAACAAAGGGAAGGACAAAAGAAGCCATTTGTTACTAGATCGGAAGAGCGGTTTCAG
chr1	226553764	226553803	PARP1_8607	+	GTGACCTATGCACCAGACGTAGAATCTTGGATAGCACAAAAGATACCCAGGAGAGCTAAGATCGGAAGAGCGGTTTCAG
chr1	226555320	226555359	PARP1_8608	+	GTGACCTATGCACCAGACGTAAAAGAAAGCCCGGCTAGGTATCATGGTGAATGAGACAGATCGGAAGAGCGGTTTCAG
chr1	226556033	226556072	PARP1_8609	+	GTGACCTATGCACCAGACGTGGGGACAGAAGGAATGCAAGACTGAGGGAGCAGCTCCAAGAGATCGGAAGAGCGGTTTCAG
chr1	226558229	226558268	PARP1_8610	+	GTGACCTATGCACCAGACGTAGGGGATTTGCTCTGAAAGCTGGGCACTGTGCAGTGTGAAGATCGGAAGAGCGGTTTCAG
chr1	226562066	226562105	PARP1_8611	+	GTGACCTATGCACCAGACGTAAAGCACATTGCTAAGAGACCCAAATCAACAACCTCAAGCAAGATCGGAAGAGCGGTTTCAG
chr1	226565015	226565054	PARP1_8612	+	GTGACCTATGCACCAGACGTAAAGGAGGGTGTGAGTACACATCTGTGGGTCAGCTGTCCCAGATCGGAAGAGCGGTTTCAG
chr1	226566986	226567025	PARP1_8613	+	GTGACCTATGCACCAGACGTGGAAGAACCTACAGTTTTTCCCTTGGAGTGTCTAGATAGATCGGAAGAGCGGTTTCAG
chr1	226567353	226567392	PARP1_8614	+	GTGACCTATGCACCAGACGTAAACAAAAATGTAACATGAAGTTAAATGTAACATAAAAAAGATCGGAAGAGCGGTTTCAG
chr1	226567876	226567915	PARP1_8615	+	GTGACCTATGCACCAGACGTTGAAAGGAAAAAACCAAAATACAAGTTTAAACAAAACAGATCGGAAGAGCGGTTTCAG
chr1	226568920	226568959	PARP1_8616	+	GTGACCTATGCACCAGACGTAGGAGAGAATCATTGAGCAAGGCCAGCTCTGGTGTCTCAGATCGGAAGAGCGGTTTCAG
chr1	226570895	226570934	PARP1_8617	+	GTGACCTATGCACCAGACGTTTAAAGTTTTAGTTAAGAGCCAGCTCTCCCTTGGGTAACAGATCGGAAGAGCGGTTTCAG
chr1	226573392	226573431	PARP1_8618	+	GTGACCTATGCACCAGACGTTGGAGAACATGTCAGAGGGCAAATCGGGGACTACAAAAAGATCGGAAGAGCGGTTTCAG
chr1	226574154	226574193	PARP1_8619	+	GTGACCTATGCACCAGACGTGAGCCAGTGGCTGAGAGGCTAGCTCTTTTCAAAGGAAGAAAAGATCGGAAGAGCGGTTTCAG
chr1	226576467	226576506	PARP1_8620	+	GTGACCTATGCACCAGACGTACAGGATATGAGAGACAGCCAGACCCATTAAGTCTGAAGATCGGAAGAGCGGTTTCAG
chr1	226578336	226578375	PARP1_8621	+	GTGACCTATGCACCAGACGTAAACATATGTGGTACCAAGGGAGCGACAAGCAAGGATAGTAGATCGGAAGAGCGGTTTCAG
chr1	226580026	226580065	PARP1_8622	+	GTGACCTATGCACCAGACGTAAACAGACAGCAATGCTCATCTCAACAGCCCAAAATGCAAGATCGGAAGAGCGGTTTCAG
chr1	226590091	226590130	PARP1_8623	+	GTGACCTATGCACCAGACGTGAGAAACAGAGGGAAGTAAGTAAGCAGTTAACTTTTACTAGATCGGAAGAGCGGTTTCAG
chr1	226595641	226595680	PARP1_8624	+	GTGACCTATGCACCAGACGTCTCCGCCAAAGCTCCGGAAGCCCTCCAGCCACGACCTAGAAGATCGGAAGAGCGGTTTCAG
chr17	64299153	64299192	PRKCA_8625	+	GTGACCTATGCACCAGACGTGCGCCGGCACTCTGCCGCTCCCTCCCGCTCCGGTTCAGATCGGAAGAGCGGTTTCAG
chr17	64302256	64302295	PRKCA_8626	+	GTGACCTATGCACCAGACGTACTTTTTGGTTTTATTTTCAAGCACAAATGAAATAAGCATAGATCGGAAGAGCGGTTTCAG
chr17	64492412	64492451	PRKCA_8627	+	GTGACCTATGCACCAGACGTCTGAAATCATGATTTGATGTCAATGTGGATTTCTGAGCTTAGATCGGAAGAGCGGTTTCAG
chr17	64637595	64637634	PRKCA_8628	+	GTGACCTATGCACCAGACGTTTTCTTTCCAGTTCATAGCGAGGCTCTGTAGCTCATGCTAGATCGGAAGAGCGGTTTCAG
chr17	64641640	64641679	PRKCA_8629	+	GTGACCTATGCACCAGACGTCTCATCCCGGACAGCATCGTGGCGAGGCATTTGGATGAAAGATCGGAAGAGCGGTTTCAG
chr17	64683396	64683435	PRKCA_8630	+	GTGACCTATGCACCAGACGTTCTCCTTGCATAAATTTTCTTCTATACACCATCGAGTTGAGATCGGAAGAGCGGTTTCAG
chr17	64684565	64684604	PRKCA_8631	+	GTGACCTATGCACCAGACGTGCTTAGGTTGAGTATGTCTCAAAGCATCAGACCATTAGAGATCGGAAGAGCGGTTTCAG
chr17	64685176	64685215	PRKCA_8632	+	GTGACCTATGCACCAGACGTCAAATGCCCGGAAACACCTTTCTTTAGAAAGCCCAACTAGATCGGAAGAGCGGTTTCAG
chr17	64728954	64728993	PRKCA_8633	+	GTGACCTATGCACCAGACGTAGTCTGCTGCAAAATGCAAGGGGCTTCTGCAGAGAATGTCAGATCGGAAGAGCGGTTTCAG
chr17	64731791	64731830	PRKCA_8634	+	GTGACCTATGCACCAGACGTTGGGAATCCCTGCGATGCAAGTACCCAGCTCTCAGAGCTACAGATCGGAAGAGCGGTTTCAG
chr17	64734984	64735023	PRKCA_8635	+	GTGACCTATGCACCAGACGTTTTTTAAGTCTTTAATTTGAACAACCAAGTCTCAACCAAGATCGGAAGAGCGGTTTCAG
chr17	64737850	64737889	PRKCA_8636	+	GTGACCTATGCACCAGACGTGAAGCCCTCCTACAGCTCAGCAGAGAGGTTAGCTGGGATCGGAAGAGCGGTTTCAG
chr17	64738889	64738928	PRKCA_8637	+	GTGACCTATGCACCAGACGTGATGATGTTTTCTCAACCAGGACTCCCAAACCTGTAACACAGATCGGAAGAGCGGTTTCAG
chr17	64770196	64770235	PRKCA_8638	+	GTGACCTATGCACCAGACGTGCTACATTTTATGTTTGTGTTTATGCTGTGTATGTGAATAGATCGGAAGAGCGGTTTCAG
chr17	64783103	64783142	PRKCA_8639	+	GTGACCTATGCACCAGACGTTTGATACCTTTTGTATCATGAGCAAGAGCTTTGGTAGAGATCGGAAGAGCGGTTTCAG
chr17	64785108	64785147	PRKCA_8640	+	GTGACCTATGCACCAGACGTAAAGCAGCCTGTTTTCCGAAACCCCATGTCCCAAAATCTAGATCGGAAGAGCGGTTTCAG
chr17	64800166	64800205	PRKCA_8641	+	GTGACCTATGCACCAGACGTGAGAAACAACACTTTCCGACCCCAAGCCCTCCCGCAGAGATCGGAAGAGCGGTTTCAG
chr18	45368332	45368371	SMAD2_8642	+	GTGACCTATGCACCAGACGTGATACAGGAAAATGATTATGAAATTAAGTCCACAGGCAAGATCGGAAGAGCGGTTTCAG

chr18	45371866	45371905	SMAD2_8643	+	GTGACCTATGCACCAGACGTAAAAGGTAAAAGAAATGTCAAAGAGTATCATTATAAAAGATCGGAAGAGCGGTTTCAG
chr18	45372182	45372221	SMAD2_8644	+	GTGACCTATGCACCAGACGTATACAAATGAGATTAGTTTTGTAACATTTACTATTTCAGTAGATCGGAAGAGCGGTTTCAG
chr18	45377709	45377748	SMAD2_8645	+	GTGACCTATGCACCAGACGTAGGATTTAAAAATAAATGAAGTATTTCCAGAACTTCTGATAGATCGGAAGAGCGGTTTCAG
chr18	45391515	45391554	SMAD2_8646	+	GTGACCTATGCACCAGACGTTTAAAAACAAATCAAGCACAGCTGCAACATAATCTCACTACAGATCGGAAGAGCGGTTTCAG
chr18	45394839	45394878	SMAD2_8647	+	GTGACCTATGCACCAGACGTTCAAGAAATCCAAGTTAATGGCAAAGAGCAAAGGGGAGTGAGATCGGAAGAGCGGTTTCAG
chr18	45396946	45396985	SMAD2_8648	+	GTGACCTATGCACCAGACGTATTGAAAAACAAAAAATGATGTGAACATGGAAGCATGGTAGATCGGAAGAGCGGTTTCAG
chr18	45423138	45423177	SMAD2_8649	+	GTGACCTATGCACCAGACGTAAAGGCACAAAGCCAGCTAGGAAAAACGCCTCTTGATCGAGATCGGAAGAGCGGTTTCAG
chr15	67358709	67358748	SMAD3_8650	+	GTGACCTATGCACCAGACGTGCCCGGGGGGACCCGGGGTACGCGCGCCAGCCCTGAGATCGGAAGAGCGGTTTCAG
chr15	67430449	67430488	SMAD3_8651	+	GTGACCTATGCACCAGACGTGTCGCCGGGACATGCTTTTTCTTTCTTGAAGTCTGCTCAGATCGGAAGAGCGGTTTCAG
chr15	67457437	67457476	SMAD3_8652	+	GTGACCTATGCACCAGACGTTGGCCCTGCCTGTGGGGACAGCAGGTGCCAGGGGTATCACAGATCGGAAGAGCGGTTTCAG
chr15	67457733	67457772	SMAD3_8653	+	GTGACCTATGCACCAGACGTGGCGGGCACAGGCTGGCCTGGGAGGCGAGGGGCAGCGGTCAAGATCGGAAGAGCGGTTTCAG
chr15	67459202	67459241	SMAD3_8654	+	GTGACCTATGCACCAGACGTGAGGTCAGGCTGCTCTTATTCTTAAGTATTAGCAGCTGGTGAGATCGGAAGAGCGGTTTCAG
chr15	67462953	67462992	SMAD3_8655	+	GTGACCTATGCACCAGACGTCCCTGTGCACACAACTGGAAACCCCTAGCTGCAAGCCCTAGATCGGAAGAGCGGTTTCAG
chr15	67473802	67473841	SMAD3_8656	+	GTGACCTATGCACCAGACGTGCTCCATTCCCGCCCCCCCCACCCTGCCCTGCCACTCTAAGATCGGAAGAGCGGTTTCAG
chr15	67477213	67477252	SMAD3_8657	+	GTGACCTATGCACCAGACGTGCGCACAGCCACCCTGCCTTGAAGTCCCTCTCCGAGTCAAGATCGGAAGAGCGGTTTCAG
chr15	67479858	67479897	SMAD3_8658	+	GTGACCTATGCACCAGACGTGGTGTGCTGCCTACATCAGGGGACCCAACTCCAGGTGACTCTAGATCGGAAGAGCGGTTTCAG
chr15	67482885	67482924	SMAD3_8659	+	GTGACCTATGCACCAGACGTGTTGGTAGGGGAGGGCAGGCTGGGGAAAATGGCCATGCAAGATCGGAAGAGCGGTTTCAG
chr9	135772152	135772191	TSC1_8660	+	GTGACCTATGCACCAGACGTGCCGGGAGGAAAAAGAGCTGGTGATTGGACTGTCCACAGATCGGAAGAGCGGTTTCAG
chr9	135772743	135772782	TSC1_8661	+	GTGACCTATGCACCAGACGTGACAGCCAGCCAGAATATAGGAAGTTCCACTTAATAAAAAACAGATCGGAAGAGCGGTTTCAG
chr9	135773008	135773047	TSC1_8662	+	GTGACCTATGCACCAGACGTAAAAAAGACTGGAATTAGTACTTTATAAAAAATAAAAGATCGGAAGAGCGGTTTCAG
chr9	135776235	135776274	TSC1_8663	+	GTGACCTATGCACCAGACGTAAACATGAGCAAAGTGAAAAATCCGACGACATAAACTAGCAGATCGGAAGAGCGGTTTCAG
chr9	135777097	135777136	TSC1_8664	+	GTGACCTATGCACCAGACGTAGACGTGGACATGAAGTTTGAGGAACACCAACAGGCCAGAAGATCGGAAGAGCGGTTTCAG
chr9	135778185	135778224	TSC1_8665	+	GTGACCTATGCACCAGACGTCCAGAAATGTCACTTTTAGCTGTCTTCCAACACAGGCAAGATCGGAAGAGCGGTTTCAG
chr9	135779215	135779254	TSC1_8666	+	GTGACCTATGCACCAGACGTGACAGAGGGGAGGCTGGCAAGAAATGCCTTTTACAGATGGTTAGATCGGAAGAGCGGTTTCAG
chr9	135779852	135779891	TSC1_8667	+	GTGACCTATGCACCAGACGTAGTTTTGAGTAACAAAGTTACCGATCTTACCAAGAAAAAGATCGGAAGAGCGGTTTCAG
chr9	135781537	135781576	TSC1_8668	+	GTGACCTATGCACCAGACGTGAGAGGAAACAAAAGAAATGGCAGTCCGTTTCCACCTGGAGATCGGAAGAGCGGTTTCAG
chr9	135782233	135782272	TSC1_8669	+	GTGACCTATGCACCAGACGTACAAGACAACCTGAAGTCAAAGAAATACAGTGTAAATCCCTAGATCGGAAGAGCGGTTTCAG
chr9	135782768	135782807	TSC1_8670	+	GTGACCTATGCACCAGACGTAAAGTATCATTATATACAAGACGAAAAATGTTGCACATGAGATCGGAAGAGCGGTTTCAG
chr9	135786090	135786129	TSC1_8671	+	GTGACCTATGCACCAGACGTAGGGCAGAACATATGAACACTGAGCCCACTATTAGAAGATCGGAAGAGCGGTTTCAG
chr9	135786511	135786550	TSC1_8672	+	GTGACCTATGCACCAGACGTAAATAAAGTACATCAGCAGTGCCCAAAGGAATGCTAAGTCTATAGATCGGAAGAGCGGTTTCAG
chr9	135786966	135787005	TSC1_8673	+	GTGACCTATGCACCAGACGTAGAGAAGAACACAGGGGTTAGTGTGTGGTTTTAGGTTATAGATCGGAAGAGCGGTTTCAG
chr9	135787855	135787894	TSC1_8674	+	GTGACCTATGCACCAGACGTCAATGAAAGTCAAGAAATGCAAACCTGTAATCAACTGAATTAGATCGGAAGAGCGGTTTCAG
chr9	135797371	135797410	TSC1_8675	+	GTGACCTATGCACCAGACGTAAACCCGTTGAGAAGAGCCTCTTAGTTGGAGACAGATTGAGAGATCGGAAGAGCGGTTTCAG
chr9	135798890	135798929	TSC1_8676	+	GTGACCTATGCACCAGACGTAAAGGTCAAACAGGAAACGCTCTGACGGCACTGGCACCAGAGATCGGAAGAGCGGTTTCAG
chr9	135801137	135801176	TSC1_8677	+	GTGACCTATGCACCAGACGTAAAGAACAAGGGCAGCTCTACATGAATGTATGAAGTTAAGATCGGAAGAGCGGTTTCAG
chr9	135802702	135802741	TSC1_8678	+	GTGACCTATGCACCAGACGTAAAAAGGCAATGGATGATACTTATCCCCTTAACATCCTAAGATCGGAAGAGCGGTTTCAG
chr9	135804270	135804309	TSC1_8679	+	GTGACCTATGCACCAGACGTGAAGGCGCTGTGCTGGCTCCAGGACGTGTGCTACAGTTTCAGATCGGAAGAGCGGTTTCAG
chr9	135771892	135771931	TSC1_8680	+	GTGACCTATGCACCAGACGTGGGGATGCTGGCAGACGCTTCTCCATAGTCTGCTCTCCACAGATCGGAAGAGCGGTTTCAG
chr9	135781257	135781296	TSC1_8681	+	GTGACCTATGCACCAGACGTGTCTCCCGCAGGGCTTTCATCAGCACTGCCGACGGGCAGAGATCGGAAGAGCGGTTTCAG
chr16	4016978	4017017	ADCY9_8682	+	GTGACCTATGCACCAGACGTAAAGACCGGAAAGGGAGAGGTTACTGCTCGGCGCTCCAAGATCGGAAGAGCGGTTTCAG
chr16	4024722	4024761	ADCY9_8683	+	GTGACCTATGCACCAGACGTAAAGACAGAAATATTATCAAAGAGCAAAAGAGCATTAGATCGGAAGAGCGGTTTCAG
chr16	4027642	4027681	ADCY9_8684	+	GTGACCTATGCACCAGACGTGGAAGGGTTAGGACAGCCGCCAGGGCCACCCCGCCACCCAGATCGGAAGAGCGGTTTCAG
chr16	4029287	4029326	ADCY9_8685	+	GTGACCTATGCACCAGACGTGATGGGGTTAGCAGGACGACGGGGCCCGGGTGGGTCAAGATCGGAAGAGCGGTTTCAG
chr16	4033452	4033491	ADCY9_8686	+	GTGACCTATGCACCAGACGTGAGGAGTGGAGCAGAATGACTGGGAGGCCATGGGCGCCAAAGATCGGAAGAGCGGTTTCAG
chr16	4039108	4039147	ADCY9_8687	+	GTGACCTATGCACCAGACGTCAACAAATGCAGTCGATCAATACCCAGCACCATAACTGTGAGATCGGAAGAGCGGTTTCAG
chr16	4042375	4042414	ADCY9_8688	+	GTGACCTATGCACCAGACGTACAAGAGAGACGACGACAGCAGGAAAGTGAAGTGGACGGAGATCGGAAGAGCGGTTTCAG
chr16	4043522	4043561	ADCY9_8689	+	GTGACCTATGCACCAGACGTAAACACAGACTGTGGGGACACACCCAGAAACCAGACTGCCAGATCGGAAGAGCGGTTTCAG
chr16	4057570	4057609	ADCY9_8690	+	GTGACCTATGCACCAGACGTTAAAAGTTACAGTCAGCACAGATTGAAAGCACCGTCTGTTAGATCGGAAGAGCGGTTTCAG
chr16	4165454	4165493	ADCY9_8691	+	GTGACCTATGCACCAGACGTCCCGGGCCCTGCCCGGGCCGGGTACCAGTACCTGCCAGAGATCGGAAGAGCGGTTTCAG
chr16	4016183	4016222	ADCY9_8692	+	GTGACCTATGCACCAGACGTTCTTGCTCAAGACGCGGTAGTCTCTTCCGCTCACCTGGATAGATCGGAAGAGCGGTTTCAG
chr16	4016580	4016619	ADCY9_8693	+	GTGACCTATGCACCAGACGTGTTGAGGACCCGGTAGCACTCTTGGCGCCCTCGTAGTTCCAGATCGGAAGAGCGGTTTCAG
chr16	4164184	4164223	ADCY9_8694	+	GTGACCTATGCACCAGACGTGTTGAGGACCCACAGGGCCGTGGCAGACTTGTGGCAAGATCGGAAGAGCGGTTTCAG
chr16	4164607	4164646	ADCY9_8695	+	GTGACCTATGCACCAGACGTCCAGTGCAGGGCCCCGGCTCCGGCGAGGGGAAGCAGGCTAGATCGGAAGAGCGGTTTCAG
chr16	4165030	4165069	ADCY9_8696	+	GTGACCTATGCACCAGACGTGATGAGCCGCAAAATAGATGCTCCACAGAAGGCAGGCGAGATCGGAAGAGCGGTTTCAG
chr12	58120588	58120627	AGAP2_8697	+	GTGACCTATGCACCAGACGTGAAACGCGCCGCTGACCGCGCTCCACAGGGCCGCCACACAGATCGGAAGAGCGGTTTCAG
chr12	58121023	58121062	AGAP2_8698	+	GTGACCTATGCACCAGACGTAGGGATCAACGGAAAAGGCTCAGGGACCCCCAGCCAGGAAGATCGGAAGAGCGGTTTCAG
chr12	58121376	58121415	AGAP2_8699	+	GTGACCTATGCACCAGACGTAGAGGTGCGGCTCCGAGCCGGCAGCAGCAGCCACCCAGATCGGAAGAGCGGTTTCAG
chr12	58121565	58121604	AGAP2_8700	+	GTGACCTATGCACCAGACGTGGTTTTGGTTGGCACTGACTCTGCCTCACAAGCCCACTCAGATCGGAAGAGCGGTTTCAG

chr12	58121879	58121918	AGAP2_8701	+	GTGACCTATGCACCAGACGTGATGGGATGGGGTCATTAAGGGACAGAGTTCAAGCAGGGGAGATCGGAAGAGCGGTTTCAG
chr12	58123561	58123600	AGAP2_8702	+	GTGACCTATGCACCAGACGTAAGACACAGCTGCCTCAGTAGCCCCCTCCACAGATTTCCCTAGATCGGAAGAGCGGTTTCAG
chr12	58124408	58124447	AGAP2_8703	+	GTGACCTATGCACCAGACGTAAGATGAAACCTCAGTGAGCCTCTTTCTTCTGGCCCCATTAGATCGGAAGAGCGGTTTCAG
chr12	58124747	58124786	AGAP2_8704	+	GTGACCTATGCACCAGACGTACAGGGCCGAGAGTGTAGGGAAGGTTGGGGTCCTTGGTATAGATCGGAAGAGCGGTTTCAG
chr12	58125264	58125303	AGAP2_8705	+	GTGACCTATGCACCAGACGTGGGAAAGACACATGTGGGAAAAAAGCCAACCTAAGACCAGCAGATCGGAAGAGCGGTTTCAG
chr12	58125436	58125475	AGAP2_8706	+	GTGACCTATGCACCAGACGTTATTGGAATCAGTTTGAGGATGGATAGAGGGGATACACTGAAGATCGGAAGAGCGGTTTCAG
chr12	58125761	58125800	AGAP2_8707	+	GTGACCTATGCACCAGACGTATGGAAGAGTCAGCCAGGATGAGATGCCCCCTACTCCACCAGATCGGAAGAGCGGTTTCAG
chr12	58126306	58126345	AGAP2_8708	+	GTGACCTATGCACCAGACGTTTACCGAAAGGAGGTGTGAGCAGGCCAGATACCCAAGACCAGATCGGAAGAGCGGTTTCAG
chr12	58126773	58126812	AGAP2_8709	+	GTGACCTATGCACCAGACGTAGGAAAGGGGCAGGATTGAACAAGGAGCCCCACCTTGTTTCAGATCGGAAGAGCGGTTTCAG
chr12	58127967	58128006	AGAP2_8710	+	GTGACCTATGCACCAGACGTGTGAGGGGAGCAAATGAAAGTCAGACAGGTCTACTCCTCTAGATCGGAAGAGCGGTTTCAG
chr12	58128198	58128237	AGAP2_8711	+	GTGACCTATGCACCAGACGTGAGTTGGAAGGGGTAACAGGTCAGAGGTGACAGGTCACCAAGATCGGAAGAGCGGTTTCAG
chr12	58128473	58128512	AGAP2_8712	+	GTGACCTATGCACCAGACGTGGTTGTGGAGCAGAATTTGGGGATATAAGAAAGGCAGGAGATCGGAAGAGCGGTTTCAG
chr12	58129221	58129260	AGAP2_8713	+	GTGACCTATGCACCAGACGTAGAAGGGCAGTAAGAGGGGAGGTCCTGGCTCAGAAGGACAGATCGGAAGAGCGGTTTCAG
chr12	58132040	58132079	AGAP2_8714	+	GTGACCTATGCACCAGACGTGACCCCCGAGCTGGGGAGGGGAGGGGACTCCCCCGGACTGAGATCGGAAGAGCGGTTTCAG
chr12	58135865	58135904	AGAP2_8715	+	GTGACCTATGCACCAGACGTCTGTCTTGGCAGGCTAACACCACCTCTGGCCCTGAGGCAGATCGGAAGAGCGGTTTCAG
chr12	58131650	58131689	AGAP2_8716	+	GTGACCTATGCACCAGACGTAGTCCCCGGAGAGCGGGGTCGCCGGAGGGACGGCCAGAAGATCGGAAGAGCGGTTTCAG
chr19	49458867	49458906	BAX_8717	+	GTGACCTATGCACCAGACGTGGTCTGATTATTGTGGCACAGATTTGAGGAGTGACACCCAGATCGGAAGAGCGGTTTCAG
chr19	49459101	49459140	BAX_8718	+	GTGACCTATGCACCAGACGTCTGAGGACCAGACAGTCCAGCCACTGGCTCCTTCCAGACAGATCGGAAGAGCGGTTTCAG
chr19	49459601	49459640	BAX_8719	+	GTGACCTATGCACCAGACGTGCAGGGCAGTGAGCCCAGGGATGCTCCCCCTCAGATCTGTAGATCGGAAGAGCGGTTTCAG
chr19	49464105	49464144	BAX_8720	+	GTGACCTATGCACCAGACGTGATGGGCTGGACATTGGACTTCTCCGGGAGCGGCTGTTGAGATCGGAAGAGCGGTTTCAG
chr19	49464365	49464404	BAX_8721	+	GTGACCTATGCACCAGACGTATTATCATCTACCTGCTGACCTCCCAGTGACCCCTGACCTCAGATCGGAAGAGCGGTTTCAG
chr19	49464904	49464943	BAX_8722	+	GTGACCTATGCACCAGACGTTGCCTTGGACTGTGTTTTTCTCCATAAATTTATGGCATTAGATCGGAAGAGCGGTTTCAG
chr2	60679812	60679851	BCL11A_8723	+	GTGACCTATGCACCAGACGTGTTGGAGACAGGAGGGGAAAAAAGTACAGGTTGAGATCGGAAGAGCGGTTTCAG
chr2	60689570	60689609	BCL11A_8724	+	GTGACCTATGCACCAGACGTATACAAACCAACATCAATGTTTAACTAGGCGGGCAAGATCGGAAGAGCGGTTTCAG
chr2	60695979	60696018	BCL11A_8725	+	GTGACCTATGCACCAGACGTAAACCCAAATCAAGCACTACAGCTACAACAACAGTGCATCAGATCGGAAGAGCGGTTTCAG
chr2	60773446	60773485	BCL11A_8726	+	GTGACCTATGCACCAGACGTAGAAACAAAAGCACAATTTAGAGTGCCAGAGAGGACAGAGATCGGAAGAGCGGTTTCAG
chr2	60688263	60688302	BCL11A_8727	+	GTGACCTATGCACCAGACGTTCCGACTCGCCGGCCACCGAGTCTTCTCGCAAGTGTCCAGATCGGAAGAGCGGTTTCAG
chr2	60688699	60688738	BCL11A_8728	+	GTGACCTATGCACCAGACGTGTTCCGGGGAGCTCGGGGTTGGAGAGCCGTCGTCGGACTTAGATCGGAAGAGCGGTTTCAG
chr2	60689135	60689174	BCL11A_8729	+	GTGACCTATGCACCAGACGTATTCAACCGCAGCACCCTGTCAAAGGCACTCGGTTGAGATCGGAAGAGCGGTTTCAG
chr2	60687953	60687992	BCL11A_8730	+	GTGACCTATGCACCAGACGTGCGCAAACTCCCGTTCTCCGAGAGTGTCTCCGACGAGGAGATCGGAAGAGCGGTTTCAG
chr2	60688357	60688396	BCL11A_8731	+	GTGACCTATGCACCAGACGTGGTGGAAAGGCCCTCGCTGAAGTGTGCATGGAGCTGAGCACAGATCGGAAGAGCGGTTTCAG
chr2	60688761	60688800	BCL11A_8732	+	GTGACCTATGCACCAGACGTTGCATGTGGCTTCTCATGTGGCGTTCAGCTTGTGGCTAGATCGGAAGAGCGGTTTCAG
chr2	60689165	60689204	BCL11A_8733	+	GTGACCTATGCACCAGACGTGGGGTATGGGTGGCCAGGGCCATCTCTCCGCCCCAGGAGATCGGAAGAGCGGTTTCAG
chr22	23524437	23524476	BCR_8734	+	GTGACCTATGCACCAGACGTGACGCCACGTGCGTGGGCACACCTGCACGGGGGAGGAAAAAGATCGGAAGAGCGGTTTCAG
chr22	23596178	23596217	BCR_8735	+	GTGACCTATGCACCAGACGTATGGTGTACGTGTGGCAGAGGGCCAGGTGAGGCTCCCTGAGATCGGAAGAGCGGTTTCAG
chr22	23603252	23603291	BCR_8736	+	GTGACCTATGCACCAGACGTTTTAGGGAGCTGAGCAGGGCGGGATGGGCAGGGTGACAGAGATCGGAAGAGCGGTTTCAG
chr22	23610713	23610752	BCR_8737	+	GTGACCTATGCACCAGACGTGATGCCGTTTCAGACAGGTGCACCGCTGACTCCCACCTGTAAGATCGGAAGAGCGGTTTCAG
chr22	23613790	23613829	BCR_8738	+	GTGACCTATGCACCAGACGTCATGCTGAGGTCTCTGTGTGCCCTCGTCAGGGAGGCTGCTAGATCGGAAGAGCGGTTTCAG
chr22	23615972	23616011	BCR_8739	+	GTGACCTATGCACCAGACGTCAGGGGATGGCTTGGGTCCACCCATCCTGCTGAGCTGGGGAGATCGGAAGAGCGGTTTCAG
chr22	23626296	23626335	BCR_8740	+	GTGACCTATGCACCAGACGTATGTGCCCTTGCCAGCAGTGACCCACCCTGACTCTCAGATCGGAAGAGCGGTTTCAG
chr22	23627399	23627438	BCR_8741	+	GTGACCTATGCACCAGACGTGGGGAAAGCGGGGTTGGTGTGGTGCAGAGTGCAGGCAGATCGGAAGAGCGGTTTCAG
chr22	23629476	23629515	BCR_8742	+	GTGACCTATGCACCAGACGTGCTGTTCCGGCCCTCCTGCTCCTGGCCTGGGATGGGCAGATCGGAAGAGCGGTTTCAG
chr22	23630370	23630409	BCR_8743	+	GTGACCTATGCACCAGACGTTCTGTCCTGAGAGGGCTGGGCTTCAAACCATTAGGGCCAAGATCGGAAGAGCGGTTTCAG
chr22	23631819	23631858	BCR_8744	+	GTGACCTATGCACCAGACGTCCGTTTTCCGTGTACAGGGCACCTGCAGGGAGGGCAGGCAGAGATCGGAAGAGCGGTTTCAG
chr22	23632611	23632650	BCR_8745	+	GTGACCTATGCACCAGACGTGTTTTGGGGAGGAGGGTTGCAGCGGCCGAGCCAGGGTCTCCAGATCGGAAGAGCGGTTTCAG
chr22	23634836	23634875	BCR_8746	+	GTGACCTATGCACCAGACGTGATTTCCAGAGGGCCAGCCTGCCAGGTGGGGCAGCAGGATAGATCGGAAGAGCGGTTTCAG
chr22	23637353	23637392	BCR_8747	+	GTGACCTATGCACCAGACGTCATCCCTACCCCTCCCTGCCCGATGCATGGCGTCTTTTTAGATCGGAAGAGCGGTTTCAG
chr22	23651681	23651720	BCR_8748	+	GTGACCTATGCACCAGACGTGTTGGACTCTCTGGTGCCCACTTCCCCAGAAGGATAGGAGATCGGAAGAGCGGTTTCAG
chr22	23652631	23652670	BCR_8749	+	GTGACCTATGCACCAGACGTAGGGGCTTGGGCTCAGCAGTGCAGGCTGCTGCTCCCTCAAGATCGGAAGAGCGGTTTCAG
chr22	23654034	23654073	BCR_8750	+	GTGACCTATGCACCAGACGTGCTGCGCAGGACGGGATGGAGGTGTGGGCAATGGTGTCCAGATCGGAAGAGCGGTTTCAG
chr22	23655219	23655258	BCR_8751	+	GTGACCTATGCACCAGACGTGAGCCCTTGGCCTCATGGAGAGCTCTCCTCCAGTGCACAGATCGGAAGAGCGGTTTCAG
chr22	23656271	23656310	BCR_8752	+	GTGACCTATGCACCAGACGTTCTCCATGGCAGCCATGGGAGCTCCAGGTCGCCAGGCCGCAAGATCGGAAGAGCGGTTTCAG
chr22	23656912	23656951	BCR_8753	+	GTGACCTATGCACCAGACGTACAGGCTCCAGCCATGCAACCTGACCTGACAGAGGTGGAGATCGGAAGAGCGGTTTCAG
chr22	23657720	23657759	BCR_8754	+	GTGACCTATGCACCAGACGTCCATCTCCTGGAGGCGGACAGATGGCCTGGAACCTCTGGAGATCGGAAGAGCGGTTTCAG
chr22	23523584	23523623	BCR_8755	+	GTGACCTATGCACCAGACGTGACCCCCGCCAGCGTGCGCGCGCTCAGGTCCAACCTCGAAGATCGGAAGAGCGGTTTCAG
chr22	23524010	23524049	BCR_8756	+	GTGACCTATGCACCAGACGTTGGAAGGGGAGGGCAAGGGCCCGCTCCTGCGCAGCAGAGAGATCGGAAGAGCGGTTTCAG
chr17	76210519	76210558	BIRC5_8757	+	GTGACCTATGCACCAGACGTCCGGCTCCTGGGCTCCCCAGCCGCTTGGCTTGCCTGATCGGAAGAGCGGTTTCAG
chr17	76210881	76210920	BIRC5_8758	+	GTGACCTATGCACCAGACGTTCTGGCCAGCCTCGATGGGCTTGTTTTTGAAGTGTGATCGGAAGAGCGGTTTCAG

chr17	76212873	76212912	BIRC5_8759	+	GTGACCTATGCACCAGACGTGGAATAAGAACTGCTCAAACCCTGTTCATGTCTTTAGCAAGATCGGAAGAGCGGTTTCAG
chr17	76219646	76219685	BIRC5_8760	+	GTGACCTATGCACCAGACGTGCGGAGCTGCCTGGTCCAGAGTGGCTGCACCACTTCCAGGAGATCGGAAGAGCGGTTTCAG
chr17	76219749	76219788	BIRC5_8761	+	GTGACCTATGCACCAGACGTCAACATTTTCAAATTAGATGTTTCAACTGTGCTCTTGTTTAGATCGGAAGAGCGGTTTCAG
chr7	116165157	116165196	CAV1_8762	+	GTGACCTATGCACCAGACGTGTGGGGGGGCGCCGGCTCGGGCGTGCGGGGAGTGTCCGCTAGATCGGAAGAGCGGTTTCAG
chr7	116166754	116166793	CAV1_8763	+	GTGACCTATGCACCAGACGTGCGACCAACAGGGAAGGGCTGGGACAGCTCTCCTCTGGCAAGATCGGAAGAGCGGTTTCAG
chr7	116199352	116199391	CAV1_8764	+	GTGACCTATGCACCAGACGTAAGGATAGAAGTATACCTGATTTTTTCTTTTAAATTTAGATCGGAAGAGCGGTTTCAG
chr19	30303694	30303733	CCNE1_8765	+	GTGACCTATGCACCAGACGTGAAGAGACAGGTTGGGAGCATCCCCCCTCACCTGGGAGATCGGAAGAGCGGTTTCAG
chr19	30303955	30303994	CCNE1_8766	+	GTGACCTATGCACCAGACGTCCGGGGTGGGCTCTGTGGAGGTCTTCTCCCCCTGGGTAGATCGGAAGAGCGGTTTCAG
chr19	30308200	30308239	CCNE1_8767	+	GTGACCTATGCACCAGACGTACTCTGCCACATGGCTTCCAGGTCTTACTCCATGCTCCAGATCGGAAGAGCGGTTTCAG
chr19	30308459	30308498	CCNE1_8768	+	GTGACCTATGCACCAGACGTGTCTTCCTGTTCGCTTCATGAAAGCACTGAGCATTTCCAGAGATCGGAAGAGCGGTTTCAG
chr19	30311766	30311805	CCNE1_8769	+	GTGACCTATGCACCAGACGTTTCAAATATTTGTTCTATAATGTGTGTTATTTCTCGAGCTAGATCGGAAGAGCGGTTTCAG
chr19	30312735	30312774	CCNE1_8770	+	GTGACCTATGCACCAGACGTGTGAATTTTCCGGCCATTTTTAAATCGGTACGGCAGATCAGATCGGAAGAGCGGTTTCAG
chr19	30313048	30313087	CCNE1_8771	+	GTGACCTATGCACCAGACGTCCATCACGTCCGCTGGGGCCACTTCCCTGCAGCTGGAGTGAGATCGGAAGAGCGGTTTCAG
chr19	30313269	30313308	CCNE1_8772	+	GTGACCTATGCACCAGACGTTTTCCAGTGCATGCACAAAAGGTGTACTAAGCTTACATAGATCGGAAGAGCGGTTTCAG
chr19	30313521	30313560	CCNE1_8773	+	GTGACCTATGCACCAGACGTCTCCTTCTTTCAGTCTTCTTGCCAAATTTTAAACTGAGATCGGAAGAGCGGTTTCAG
chr19	30314695	30314734	CCNE1_8774	+	GTGACCTATGCACCAGACGTCTTCTCCACAAAGACAGTTGCGCGCCTGCTCCACGTTCTAGATCGGAAGAGCGGTTTCAG
chr7	14216535	14216574	DGKB_8775	+	GTGACCTATGCACCAGACGTATATTTTCATTGTTAAGTATTGCAAGGAAATCTTTATATTAAGATCGGAAGAGCGGTTTCAG
chr7	14217787	14217826	DGKB_8776	+	GTGACCTATGCACCAGACGTGATAGTGCCTTAAAGTTCAGATGTATACATATGTCCAAGATCGGAAGAGCGGTTTCAG
chr7	14378346	14378385	DGKB_8777	+	GTGACCTATGCACCAGACGTAAAAGAAAGAAACAGAAACGGAATATTTTATCTTTATTTTCAGATCGGAAGAGCGGTTTCAG
chr7	14385027	14385066	DGKB_8778	+	GTGACCTATGCACCAGACGTAAAGGAAGAAGCACCTTAGGCAATATCAATAACAGAGGGAGATCGGAAGAGCGGTTTCAG
chr7	14517861	14517900	DGKB_8779	+	GTGACCTATGCACCAGACGTAAAATAGAAAACAAAACAGGATGTTTATGATCCTATTAAGATCGGAAGAGCGGTTTCAG
chr7	14614008	14614047	DGKB_8780	+	GTGACCTATGCACCAGACGTAAAAAATACCTTGAGAAAAGAACTCTAACAAAATAAAAAAGATCGGAAGAGCGGTTTCAG
chr7	14620587	14620626	DGKB_8781	+	GTGACCTATGCACCAGACGTAAAAAATAACAATAAAGAAAATTTAAGTTTCAGATAAAGATCGGAAGAGCGGTTTCAG
chr7	14622773	14622812	DGKB_8782	+	GTGACCTATGCACCAGACGTAGCATGTTATGCGACATGTAATAGTTTAAAAATAAGATAGATCGGAAGAGCGGTTTCAG
chr7	14653049	14653088	DGKB_8783	+	GTGACCTATGCACCAGACGTAGTTATATACATGAAAAAATTATTAGGCCATTATATATGAGATCGGAAGAGCGGTTTCAG
chr7	14661130	14661169	DGKB_8784	+	GTGACCTATGCACCAGACGTGAAAATTTTGATAAAAATAAAAATTAGGAAAATAACATAAAGATCGGAAGAGCGGTTTCAG
chr7	14669907	14669946	DGKB_8785	+	GTGACCTATGCACCAGACGTGAAGTTTCATATGAAAGCTGAAAAAGAGTCAAACCTCAAACAGATCGGAAGAGCGGTTTCAG
chr7	14712663	14712702	DGKB_8786	+	GTGACCTATGCACCAGACGTAGAAAAGGGGATAGTATCAAATTTCTACATGACAACGCCTAAGATCGGAAGAGCGGTTTCAG
chr7	14722305	14722344	DGKB_8787	+	GTGACCTATGCACCAGACGTATGACAACATTTGATAAGAGGACACACTACATAATGCCAGATCGGAAGAGCGGTTTCAG
chr7	14722477	14722516	DGKB_8788	+	GTGACCTATGCACCAGACGTACAGGTACACAATACTCAGAGCTAATCCTGGTCTGGTTGATAGATCGGAAGAGCGGTTTCAG
chr7	14724998	14725037	DGKB_8789	+	GTGACCTATGCACCAGACGTGTAAGAGAACAGATTTCACTTAATGAAATAAACAGTGAAGATCGGAAGAGCGGTTTCAG
chr7	14733830	14733869	DGKB_8790	+	GTGACCTATGCACCAGACGTGGAGATAAGGGAAAATGGTGGTCAACCAATAAAATAAATAGATCGGAAGAGCGGTTTCAG
chr7	14737805	14737844	DGKB_8791	+	GTGACCTATGCACCAGACGTAAAGAGAGATAAAAAATAGATCAAGATCTTAGTGAGTTAGATCGGAAGAGCGGTTTCAG
chr7	14741366	14741405	DGKB_8792	+	GTGACCTATGCACCAGACGTAGAGGTGTTGAAAAAAGATTATAGGCCAAATAAGATCAATAGATCGGAAGAGCGGTTTCAG
chr7	14758321	14758360	DGKB_8793	+	GTGACCTATGCACCAGACGTAAATGCTTATATTTTTGTTAATTTTACAGTGATCTCAAGATCGGAAGAGCGGTTTCAG
chr7	14775830	14775869	DGKB_8794	+	GTGACCTATGCACCAGACGTAAAATGTAACATGTATTTAAGATCCAACCAAATGTTAAAGATCGGAAGAGCGGTTTCAG
chr7	14793584	14793623	DGKB_8795	+	GTGACCTATGCACCAGACGTAAAGAAAGAAAGAAATACATGTGTTAATGTAAGATACTTTAAGATCGGAAGAGCGGTTTCAG
chr7	14797367	14797406	DGKB_8796	+	GTGACCTATGCACCAGACGTACAGAAAACAAAAAATGTTTTATATGCACATACTGTGGTTAGATCGGAAGAGCGGTTTCAG
chr7	14880899	14880938	DGKB_8797	+	GTGACCTATGCACCAGACGTAGAAGCTCTGTACATAACCAGGTAAGAAATCTTTTATTCAAGATCGGAAGAGCGGTTTCAG
chr7	100401223	100401262	EPHB4_8798	+	GTGACCTATGCACCAGACGTAAAGGAGAGCTTGGTGACACCCTAGGTTCCCTGTGGCCGAGATCGGAAGAGCGGTTTCAG
chr7	100402954	100402993	EPHB4_8799	+	GTGACCTATGCACCAGACGTAAAGGATGGGGAGAAATGCTGATACCAGGCCAGTCCAGTCCGGGAGATCGGAAGAGCGGTTTCAG
chr7	100403327	100403366	EPHB4_8800	+	GTGACCTATGCACCAGACGTGGGAAGAAGCTCTGGGTGAGGCTGTCCAGGAAAAGCAAAGAGATCGGAAGAGCGGTTTCAG
chr7	100404202	100404241	EPHB4_8801	+	GTGACCTATGCACCAGACGTAGGAGAAAAGGTGAGCTGGGGGACTCACTGAGGACTCACAGATCGGAAGAGCGGTTTCAG
chr7	100405213	100405252	EPHB4_8802	+	GTGACCTATGCACCAGACGTGATAGGGTGGGGGCTTGGTGAGGACAGCCCACCACCCTTAGATCGGAAGAGCGGTTTCAG
chr7	100410627	100410666	EPHB4_8803	+	GTGACCTATGCACCAGACGTGGACCGCAGGCTCATCAGCTCTCCCCTCCAGTGTGGCCAGATCGGAAGAGCGGTTTCAG
chr7	100410841	100410880	EPHB4_8804	+	GTGACCTATGCACCAGACGTAGGCAGGGCCCGTTCAGCTGGGAATTAACCTCCACTGGACAGATCGGAAGAGCGGTTTCAG
chr7	100411349	100411388	EPHB4_8805	+	GTGACCTATGCACCAGACGTTGGGAAAGGAACAAAAGGTAAACTGAGTCACACATCTTTAAGATCGGAAGAGCGGTTTCAG
chr7	100411654	100411693	EPHB4_8806	+	GTGACCTATGCACCAGACGTAAAGGCTGCTGATCAGGAGAAACTGATGGTCTGTAGGAGAGATCGGAAGAGCGGTTTCAG
chr7	100414990	100415029	EPHB4_8807	+	GTGACCTATGCACCAGACGTGAGGTAGTGGGGTGGCGTCCACCAGGAAACCAAGTTCCCTAGATCGGAAGAGCGGTTTCAG
chr7	100416277	100416316	EPHB4_8808	+	GTGACCTATGCACCAGACGTACAGACACAGGGAACCCCTGTGCATGGTAGCTCTGTCCCAGATCGGAAGAGCGGTTTCAG
chr7	100417522	100417561	EPHB4_8809	+	GTGACCTATGCACCAGACGTCCAGGAGTCCAGGAGGCCAGCTGCTCGCGTGGTGAGATCGGAAGAGCGGTTTCAG
chr7	100417929	100417968	EPHB4_8810	+	GTGACCTATGCACCAGACGTAAAGCAATTCATCAAAAAGCATGCACAAAACATCCATCTGAGATCGGAAGAGCGGTTTCAG
chr7	100420300	100420339	EPHB4_8811	+	GTGACCTATGCACCAGACGTGGGGGAGGCACACCGCTGCTGTCCCCTCCCTGAGGACCAGATCGGAAGAGCGGTTTCAG
chr7	100421564	100421603	EPHB4_8812	+	GTGACCTATGCACCAGACGTAAAGAGTTCAGCAAGGGGCTGGGGAGCCGCCAGGGAGAGAGATCGGAAGAGCGGTTTCAG
chr7	100421906	100421945	EPHB4_8813	+	GTGACCTATGCACCAGACGTACAGAGACAGAGTCACTGGCTGGGGTGGGGAGGGAGGTAGATCGGAAGAGCGGTTTCAG
chr7	100424663	100424702	EPHB4_8814	+	GTGACCTATGCACCAGACGTCACTCGGCTAGGATCCGAATGAGTTTGGGGGGCCCTCGCAGATCGGAAGAGCGGTTTCAG
chr10	50667291	50667330	ERCC6_8815	+	GTGACCTATGCACCAGACGTAAAGCCTATACTGATATTTAATTTTCTAGTTTTATGCCAGATCGGAAGAGCGGTTTCAG
chr10	50668508	50668547	ERCC6_8816	+	GTGACCTATGCACCAGACGTAAAAGCATCACAGTAGATTAATGTTTCTTTTTGAGACTTAGATCGGAAGAGCGGTTTCAG



chr10	50669613	50669652	ERCC6_8817	+	GTGACCTATGCACCAGACGTAAGAAATAGCAAAGTGATATTTCTACTCTGTATGCAAGAAAAGATCGGAAGAGCGGTTTCAG
chr10	50678946	50678985	ERCC6_8818	+	GTGACCTATGCACCAGACGTAAGAAACACCCTAATACTATATTGTATCATCTTTGTCAAAGATCGGAAGAGCGGTTTCAG
chr10	50679177	50679216	ERCC6_8819	+	GTGACCTATGCACCAGACGTAAGAAAGATAAGCTGGTATAAAAACAATGTGTAGCTCTACCTAAGATCGGAAGAGCGGTTTCAG
chr10	50680527	50680566	ERCC6_8820	+	GTGACCTATGCACCAGACGTTGAGAGAGACCTCTCAACGAGAATCCTTCCAATGACAAGATCGGAAGAGCGGTTTCAG
chr10	50681085	50681124	ERCC6_8821	+	GTGACCTATGCACCAGACGTTGACACACAACACTGAGCACACACACTTAAGACCAGTTACAAGATCGGAAGAGCGGTTTCAG
chr10	50681644	50681683	ERCC6_8822	+	GTGACCTATGCACCAGACGTTGGGGGATAGGAGTTTGCAAAGCAATAACACATTCCAGAGATCGGAAGAGCGGTTTCAG
chr10	50682299	50682338	ERCC6_8823	+	GTGACCTATGCACCAGACGTTAAAGAGTACACTGTACACTGACCCATGACCCCATGTAAGATCGGAAGAGCGGTTTCAG
chr10	50684367	50684406	ERCC6_8824	+	GTGACCTATGCACCAGACGTTGAAAAACAAGGAACTATAATTTCAAAAAAAAATTAACAAGATCGGAAGAGCGGTTTCAG
chr10	50686527	50686566	ERCC6_8825	+	GTGACCTATGCACCAGACGTAGCAGAGAAGGGAACATTACTATATATGTTAAGGAACGCAGATCGGAAGAGCGGTTTCAG
chr10	50690920	50690959	ERCC6_8826	+	GTGACCTATGCACCAGACGTTAAAGGAAGCACCTTTTTATTAAATTTACCTTTTAGCAATCAGATCGGAAGAGCGGTTTCAG
chr10	50691573	50691612	ERCC6_8827	+	GTGACCTATGCACCAGACGTAATAAAATGGTAAAGTCAGTTTTAAATAAGAAGTGACACCAGATCGGAAGAGCGGTTTCAG
chr10	50701309	50701348	ERCC6_8828	+	GTGACCTATGCACCAGACGTACGTCCAAGAAGAAAACAACCATGAAAGAGCATATACAGTAGATCGGAAGAGCGGTTTCAG
chr10	50708753	50708792	ERCC6_8829	+	GTGACCTATGCACCAGACGTTAAACACCAACAAGAAAAGAGAAAATGGCAAATGGTGGATAAGATCGGAAGAGCGGTTTCAG
chr10	50714069	50714108	ERCC6_8830	+	GTGACCTATGCACCAGACGTAATAAAAAATCACATTTCCATTATTTTGATCACAAGACAGAAGATCGGAAGAGCGGTTTCAG
chr10	50732834	50732873	ERCC6_8831	+	GTGACCTATGCACCAGACGTAATAGCAATGCGTTTTCGACTAGCATGAAACTTTCCGAGGAGATCGGAAGAGCGGTTTCAG
chr10	50736582	50736621	ERCC6_8832	+	GTGACCTATGCACCAGACGTTAAATATAGAAGACAGAAAACAGCAATGAAGTGATTATTGAGATCGGAAGAGCGGTTTCAG
chr10	50738896	50738936	ERCC6_8833	+	GTGACCTATGCACCAGACGTAGATAAATTTGCTATTTTGCACCTGTATAACATTTTTATAAGATCGGAAGAGCGGTTTCAG
chr10	50741021	50741060	ERCC6_8834	+	GTGACCTATGCACCAGACGTTACTTAAAGAAAATAATAAGCCTTTTCGTTATAAGATCGGAAGAGCGGTTTCAG
chr10	50678592	50678631	ERCC6_8835	+	GTGACCTATGCACCAGACGTAGTTTTGCCTGTTCTGAAGAATTTGAACATTTCCCATTTAGATCGGAAGAGCGGTTTCAG
chr10	50732461	50732500	ERCC6_8836	+	GTGACCTATGCACCAGACGTCCCTCTTCTGGAGTTTCTTGATGTGCTTTTTCAAACGCTCAGATCGGAAGAGCGGTTTCAG
chr6	152163933	152163972	ESR1_8837	+	GTGACCTATGCACCAGACGTTGTTGAAAACGACTTCTATTTTTGATCCTATGAGCAGATCCAGATCGGAAGAGCGGTTTCAG
chr6	152201917	152201956	ESR1_8838	+	GTGACCTATGCACCAGACGTTCTCTCCAGGGGCCCTTGGGGATGGCCCTGGCCACCGCCAGATCGGAAGAGCGGTTTCAG
chr6	152265654	152265693	ESR1_8839	+	GTGACCTATGCACCAGACGTTAAGCGCAGCTTTTAAAGAGTCAATAGCTTTTCAAGAATTTAGATCGGAAGAGCGGTTTCAG
chr6	152332940	152332979	ESR1_8840	+	GTGACCTATGCACCAGACGTTAGGCTGTAGCTTAAAGAGTAGCATGTTCTTTACGATCATAGAGATCGGAAGAGCGGTTTCAG
chr6	152382270	152382309	ESR1_8841	+	GTGACCTATGCACCAGACGTTAACACAAGATAACTCAATGCTGGATGAAATGTTTATTGTAGATCGGAAGAGCGGTTTCAG
chr6	152415714	152415753	ESR1_8842	+	GTGACCTATGCACCAGACGTTGTGGGCTTCTACAGGAGAGACATAAAGAAAACATGCCAGATCGGAAGAGCGGTTTCAG
chr6	152420112	152420151	ESR1_8843	+	GTGACCTATGCACCAGACGTTGCTCCACACGGTTTCAGATAATCCCTGCTGCATTTTACCAGATCGGAAGAGCGGTTTCAG
chr7	128471054	128471093	FLNC_8844	+	GTGACCTATGCACCAGACGTTGGGGCGAGGGCACGGGCTGCGGGGATAGGGTCTGCCAAGATCGGAAGAGCGGTTTCAG
chr7	128475639	128475678	FLNC_8845	+	GTGACCTATGCACCAGACGTTGAGCAGCAGCATGGAGCCCTTAGCTCCCAAAGACAGAAGATCGGAAGAGCGGTTTCAG
chr7	128477322	128477361	FLNC_8846	+	GTGACCTATGCACCAGACGTAGATGGGGCAGGGGGAAAGGGGGCAGGGGCAGAGGTTGGAGATCGGAAGAGCGGTTTCAG
chr7	128477613	128477652	FLNC_8847	+	GTGACCTATGCACCAGACGTGCCCTGGCGGCCCTCTGGGCAGCTGGGCACATGTAGGCAGATCGGAAGAGCGGTTTCAG
chr7	128477820	128477859	FLNC_8848	+	GTGACCTATGCACCAGACGTTGCCGCTGGGGACAGAGGGATTCACTTGGGATTGGAACAGAGATCGGAAGAGCGGTTTCAG
chr7	128478129	128478168	FLNC_8849	+	GTGACCTATGCACCAGACGTTAGGCCCCCTGCCTGCGCTGCTCTTACATCCTTGGTTAGATCGGAAGAGCGGTTTCAG
chr7	128478494	128478533	FLNC_8850	+	GTGACCTATGCACCAGACGTTCCCGGGGTCAGGTGCAAGTGAAGCCCTGACCATTGTGGGGAGATCGGAAGAGCGGTTTCAG
chr7	128478868	128478907	FLNC_8851	+	GTGACCTATGCACCAGACGTTTCACTGCTCCCAAGGTAGCCCTTACCAGAGCCAGAGGCAGATCGGAAGAGCGGTTTCAG
chr7	128480225	128480264	FLNC_8852	+	GTGACCTATGCACCAGACGTTGAGCCAGGGTCTGAGGGTGGGGCTGGGGATCATAAGGAGATCGGAAGAGCGGTTTCAG
chr7	128480739	128480778	FLNC_8853	+	GTGACCTATGCACCAGACGTTGCGCCCCCATGCTGTCTGTCTAGGCCATCACAGGAGAGATCGGAAGAGCGGTTTCAG
chr7	128481035	128481074	FLNC_8854	+	GTGACCTATGCACCAGACGTTGGGGGGCAGGAGGAGGGAGTCTGCGGGGGAGGGCAGCAGAGATCGGAAGAGCGGTTTCAG
chr7	128481428	128481467	FLNC_8855	+	GTGACCTATGCACCAGACGTAGCTCACACACCTGCCCCGGGGTGGGGCAAGCTGGTTAGATCGGAAGAGCGGTTTCAG
chr7	128481632	128481671	FLNC_8856	+	GTGACCTATGCACCAGACGTTCCAGCTCTGCTGCCCTTACTACCCATGGCAGGGACCCAGATCGGAAGAGCGGTTTCAG
chr7	128482439	128482478	FLNC_8857	+	GTGACCTATGCACCAGACGTTCCGGCTGCCCGTGCACCCACACAGGAGGTTCCCTGAGGGAAGATCGGAAGAGCGGTTTCAG
chr7	128482763	128482802	FLNC_8858	+	GTGACCTATGCACCAGACGTTCCGGAAGGGTGGGTCTGGGAGGGGGCGGGGTGAGTCAAGATCGGAAGAGCGGTTTCAG
chr7	128483019	128483058	FLNC_8859	+	GTGACCTATGCACCAGACGTTCTGGTACTCACAGCAGATGCACCTGCCAGCTCCAGAAGATCGGAAGAGCGGTTTCAG
chr7	128483384	128483423	FLNC_8860	+	GTGACCTATGCACCAGACGTTGGGCAGGGGCTGGGACTGCCCTCAGGTTGGGGTTAGTGGAGATCGGAAGAGCGGTTTCAG
chr7	128483642	128483681	FLNC_8861	+	GTGACCTATGCACCAGACGTTCCCTCCCATCTACCGCCCGCCGCCCCAGAGCCCTAGATCGGAAGAGCGGTTTCAG
chr7	128483978	128484017	FLNC_8862	+	GTGACCTATGCACCAGACGTTCAAGACACCTGGGAGTGGGCTATTCCGGTAGGGTGAAGATCGGAAGAGCGGTTTCAG
chr7	128484331	128484370	FLNC_8863	+	GTGACCTATGCACCAGACGTAGGAGCTGGTTGGGGCTGGGAGTTGGGGACTTGTGGAAAGATCGGAAGAGCGGTTTCAG
chr7	128485320	128485359	FLNC_8864	+	GTGACCTATGCACCAGACGTAGGAGGAGCCAAGAAAGTCAAGTGGCAGGTGCAGGAGCTAGATCGGAAGAGCGGTTTCAG
chr7	128486228	128486267	FLNC_8865	+	GTGACCTATGCACCAGACGTTGGGGCCAGGCTAGTGGGCAGGGCTGGGCAAGTGGGCAGGAGATCGGAAGAGCGGTTTCAG
chr7	128486528	128486567	FLNC_8866	+	GTGACCTATGCACCAGACGTTCTTTGCTAGCCTAAATCTGTGACCACCTTTCCAGCCAGATCGGAAGAGCGGTTTCAG
chr7	128486970	128487009	FLNC_8867	+	GTGACCTATGCACCAGACGTAGATGGTGGGGCTCAGGGAAGACAAGGAGGTTGCAGAGATCGGAAGAGCGGTTTCAG
chr7	128487929	128487968	FLNC_8868	+	GTGACCTATGCACCAGACGTTCCGGGCGAGGGAGGAGGAGGCTGGGGCAGGACGCCGGAAGATCGGAAGAGCGGTTTCAG
chr7	128488133	128488172	FLNC_8869	+	GTGACCTATGCACCAGACGTTGCCCTGGGCTCCTGTGCTGCGGCTGAGCTCTGGGGTGTCTAGATCGGAAGAGCGGTTTCAG
chr7	128488782	128488821	FLNC_8870	+	GTGACCTATGCACCAGACGTTGTCATCCACCCCGAGGTCATGCTCCAGGCACAGGGGAGATCGGAAGAGCGGTTTCAG
chr7	128489047	128489086	FLNC_8871	+	GTGACCTATGCACCAGACGTACCCGCTGCCCGTGCCTGCTACCACCCAGCCCTCAAAAAGATCGGAAGAGCGGTTTCAG
chr7	128489269	128489308	FLNC_8872	+	GTGACCTATGCACCAGACGTTTTCTCTCTCTTCTTGGTGGGCGAGGGTGGTTGGCGGAGATCGGAAGAGCGGTTTCAG
chr7	128489643	128489682	FLNC_8873	+	GTGACCTATGCACCAGACGTTAGCCACCAAGTACTAGTGGCTGGGAGGGGGCTGGAGATCGGAAGAGCGGTTTCAG
chr7	128491008	128491047	FLNC_8874	+	GTGACCTATGCACCAGACGTTGCTGGGCTGGGCTGGGGCTGGGTGAGAGGAGCAGGCCAGATCGGAAGAGCGGTTTCAG

chr7	128491425	128491464	FLNC_8875	+	GTGACCTATGCACCAGACGTTGCAGGTGCGAGGCTGGGGTGGAGACTCACCAGGGGCAGGAGATCGGAAGAGCGGTTTCAG
chr7	128491693	128491732	FLNC_8876	+	GTGACCTATGCACCAGACGTTGTATGGGCATGTACAGCCCATGAGGCACACACCCGCATAGATCGGAAGAGCGGTTTCAG
chr7	128492817	128492856	FLNC_8877	+	GTGACCTATGCACCAGACGTGGCCTCACGGGGACCTCAGGGGTGGGGGCCACAGGATGCAGATCGGAAGAGCGGTTTCAG
chr7	128493096	128493135	FLNC_8878	+	GTGACCTATGCACCAGACGTCCCCAGAGAGCCCCATTCCAGCGGGTGCCTCCCACAGGCAGATCGGAAGAGCGGTTTCAG
chr7	128493686	128493725	FLNC_8879	+	GTGACCTATGCACCAGACGTGGGCAGAGGTCGTTGGCGAGAGACAGGGAGGCCAGGAGGCAGATCGGAAGAGCGGTTTCAG
chr7	128493902	128493941	FLNC_8880	+	GTGACCTATGCACCAGACGTGGAGGACCCCTGGTGGGGCGGGTGTGGGAGAGGGTGGCAGATCGGAAGAGCGGTTTCAG
chr7	128494320	128494320	FLNC_8881	+	GTGACCTATGCACCAGACGTGCACACTGGGCCGGCCGGTCTCACGGCGGGATGGGAGGGAGATCGGAAGAGCGGTTTCAG
chr7	128494747	128494786	FLNC_8882	+	GTGACCTATGCACCAGACGTGGTGGCCAGGAGTGGGGATGAAGTCAGGGCAGCCAGTGTGAGATCGGAAGAGCGGTTTCAG
chr7	128494977	128495016	FLNC_8883	+	GTGACCTATGCACCAGACGTACACTGGCAGTGGGGCTGGGCCGCCTGACCTTCCAGACTAGATCGGAAGAGCGGTTTCAG
chr7	128495379	128495418	FLNC_8884	+	GTGACCTATGCACCAGACGTAGGGTGGGGGTGGAGGGTTTCTGCTATCTGAGAGATGGGCAGATCGGAAGAGCGGTTTCAG
chr7	128496715	128496754	FLNC_8885	+	GTGACCTATGCACCAGACGTCTGCCCTGCCAAGTCCCTTCCGGGCTGGGGCCTTCTGGAGATCGGAAGAGCGGTTTCAG
chr7	128496986	128497025	FLNC_8886	+	GTGACCTATGCACCAGACGTGGAGCTGGGGAACAGGTGACTTCTGGGGTGTCTGGCCAAGATCGGAAGAGCGGTTTCAG
chr7	128497401	128497440	FLNC_8887	+	GTGACCTATGCACCAGACGTGTTTGGGGAGGTCCACCCAGCTGCAGCCAGCCAGCCAGATCGGAAGAGCGGTTTCAG
chr7	128498282	128498321	FLNC_8888	+	GTGACCTATGCACCAGACGTGGGGGAGGGCGTCTCCGGGGTGTGAGCAAGAAGCCGTCAAGATCGGAAGAGCGGTTTCAG
chr7	128485021	128485060	FLNC_8889	+	GTGACCTATGCACCAGACGTGGCAAGGTCGGTGTAGGCAGCCACCTTCACTGTGGACTGCTAGATCGGAAGAGCGGTTTCAG
chr2	216226360	216226399	FN1_8890	+	GTGACCTATGCACCAGACGTGGAAGAAGGAAAAAAATTAGTGGCAAATAGTAAAGTAGATCGGAAGAGCGGTTTCAG
chr2	216226813	216226852	FN1_8891	+	GTGACCTATGCACCAGACGTAGAGCAGGAAAGTCAAATGGGTTTATGATAAAGTGGAGATCGGAAGAGCGGTTTCAG
chr2	216229719	216229758	FN1_8892	+	GTGACCTATGCACCAGACGTACACAAGACAGTGCACCGCAATGAGAAACAATAGTGCAGATCGGAAGAGCGGTTTCAG
chr2	216230364	216230403	FN1_8893	+	GTGACCTATGCACCAGACGTGGGGAAAGTCAGGACAAAAAGTTATTTGTATATTCTGACAGATCGGAAGAGCGGTTTCAG
chr2	216232761	216232800	FN1_8894	+	GTGACCTATGCACCAGACGTAAAGGAAGAAAAAGCAAAAAGACATCTTATTAATCGATTAGATCGGAAGAGCGGTTTCAG
chr2	216235166	216235205	FN1_8895	+	GTGACCTATGCACCAGACGTCCGTACATCCAAAGCAGAGAGAAAGCATTATAGTGTAGGAAAGATCGGAAGAGCGGTTTCAG
chr2	216236749	216236788	FN1_8896	+	GTGACCTATGCACCAGACGTATTTGGATTGAGTCCCGGACCGTGTGGGTACAGGTGATAGAGATCGGAAGAGCGGTTTCAG
chr2	216237109	216237148	FN1_8897	+	GTGACCTATGCACCAGACGTGAGGTTAGAGTCAAAAGCAAAAGCGCATTAAAGTCCAGGAGATCGGAAGAGCGGTTTCAG
chr2	216237034	216237073	FN1_8898	+	GTGACCTATGCACCAGACGTAACATCCAAAGTCTCTGGTCCATGAAAGTTGGGGTGTGGAAGATCGGAAGAGCGGTTTCAG
chr2	216238145	216238184	FN1_8899	+	GTGACCTATGCACCAGACGTAATAGAACCATCACATTATGTCATGGGCTCAGCTAGTCAAGATCGGAAGAGCGGTTTCAG
chr2	216240127	216240166	FN1_8900	+	GTGACCTATGCACCAGACGTACAAAATTAAGTCTCTAAGAAGGCAATAACCAAGAAAATAGATCGGAAGAGCGGTTTCAG
chr2	216240452	216240491	FN1_8901	+	GTGACCTATGCACCAGACGTAGAAGAGATGATTTTTAACAGTCTTGTCTTTTACTAGGAAGATCGGAAGAGCGGTTTCAG
chr2	216241408	216241447	FN1_8902	+	GTGACCTATGCACCAGACGTGCATAGCTAGAGATTAGTGCCTGCTTGGCTCATCCATGTAAGATCGGAAGAGCGGTTTCAG
chr2	216242996	216243035	FN1_8903	+	GTGACCTATGCACCAGACGTAAGGGCATGGTAGCTTTAGCAACGTCCTCAACTGAAACCAGATCGGAAGAGCGGTTTCAG
chr2	216244051	216244090	FN1_8904	+	GTGACCTATGCACCAGACGTTGTCATTTGGTTAGGTTTACTTATAGGAAATGGGGGAAAAAGATCGGAAGAGCGGTTTCAG
chr2	216245814	216245853	FN1_8905	+	GTGACCTATGCACCAGACGTAATTAATGGTAAGAGTTATGTGAAAAGCAAGTTGTGAAAAGATCGGAAGAGCGGTTTCAG
chr2	216247059	216247098	FN1_8906	+	GTGACCTATGCACCAGACGTAGTGAAGCAAAATGCAACATCCACGTCATCCACTATAAAGATCGGAAGAGCGGTTTCAG
chr2	216248217	216248256	FN1_8907	+	GTGACCTATGCACCAGACGTAAGCAGGGAGAAAACAGTGAAGCCCACTCCTTGGAGACAAGATCGGAAGAGCGGTTTCAG
chr2	216248918	216248957	FN1_8908	+	GTGACCTATGCACCAGACGTAAGGTTAGTTAGTTCAGAGTGTGAGGGGTTTAGAGCTACTTGGAGATCGGAAGAGCGGTTTCAG
chr2	216249710	216249749	FN1_8909	+	GTGACCTATGCACCAGACGTAAGGAAAATTTTTACATCCGTAATTTTTCAAACAATATTCAGATCGGAAGAGCGGTTTCAG
chr2	216251692	216251731	FN1_8910	+	GTGACCTATGCACCAGACGTACCCGGGGGAGGAAGAGAAAAAAGAAAAAGACACCAAGATCGGAAGAGCGGTTTCAG
chr2	216253035	216253074	FN1_8911	+	GTGACCTATGCACCAGACGTAATGGGGCTTATTTAAAACCTCTGCTCAAAGCATGAGAAGATCGGAAGAGCGGTTTCAG
chr2	216256548	216256587	FN1_8912	+	GTGACCTATGCACCAGACGTACAAGAAGGAAAGACTCAGTTAATGTAATTTTTAAAATTAAGATCGGAAGAGCGGTTTCAG
chr2	216257937	216257976	FN1_8913	+	GTGACCTATGCACCAGACGTACAAGCAAAAGGGAGGGGAGGCCAAAAGGAAAATAGAGGGAGATCGGAAGAGCGGTTTCAG
chr2	216259453	216259492	FN1_8914	+	GTGACCTATGCACCAGACGTAAGAAAAGGGAAGTTATTGCACAGAGGATCTGTGAGCCAGAGATCGGAAGAGCGGTTTCAG
chr2	216261957	216261996	FN1_8915	+	GTGACCTATGCACCAGACGTAGAACAATTTTAAAAGTCAAAGCTGACACAAAAGCTTGGACAGATCGGAAGAGCGGTTTCAG
chr2	216262582	216262621	FN1_8916	+	GTGACCTATGCACCAGACGTGAATGCAAAGTAAACACCAAGGACAAATATTTCCAGAGGAAGATCGGAAGAGCGGTTTCAG
chr2	216264085	216264124	FN1_8917	+	GTGACCTATGCACCAGACGTGAATCAATGCACATATTTAAAACCTCAAACCTCACAGATGATAGATCGGAAGAGCGGTTTCAG
chr2	216269389	216269428	FN1_8918	+	GTGACCTATGCACCAGACGTAGATGAAACATGCCAAGAAATTTAGATCAGTAATGATCAGATCGGAAGAGCGGTTTCAG
chr2	216271244	216271283	FN1_8919	+	GTGACCTATGCACCAGACGTAGAGTCAACTGGTCACTTACATCTCTGCTGAAGATTACTAGATCGGAAGAGCGGTTTCAG
chr2	216272055	216272094	FN1_8920	+	GTGACCTATGCACCAGACGTATGAGCAAAAGTAAAGTGCAGCTGTTTTCTTTGAGACAGAGATCGGAAGAGCGGTTTCAG
chr2	216272931	216272970	FN1_8921	+	GTGACCTATGCACCAGACGTAAGAAAAGTGGGGCAAAACAGTCAGGAAGTGTACTACAGGCAGATCGGAAGAGCGGTTTCAG
chr2	216273160	216273199	FN1_8922	+	GTGACCTATGCACCAGACGTAAGAAAAGGTAACATAATCAGAGCAAACCTAGTCCCTCAAAGATCGGAAGAGCGGTTTCAG
chr2	216274473	216274512	FN1_8923	+	GTGACCTATGCACCAGACGTACAGAAAAGGGAAAAGTCCAGCTTCACTATCAGAAAATAGATCGGAAGAGCGGTTTCAG
chr2	216279692	216279731	FN1_8924	+	GTGACCTATGCACCAGACGTAAGTGTAGCATTTAATTATCTTGAATATTCACCTCACTCAAGATCGGAAGAGCGGTTTCAG
chr2	216284119	216284158	FN1_8925	+	GTGACCTATGCACCAGACGTTGGAAGGAAAAGATAAACAGCCTTGAAGACTTATAACTACAGATCGGAAGAGCGGTTTCAG
chr2	216285535	216285574	FN1_8926	+	GTGACCTATGCACCAGACGTAAGCAGGTGAGTGAGAACTTTTTAAAGTTCCATTGAAGATCGGAAGAGCGGTTTCAG
chr2	216286977	216287016	FN1_8927	+	GTGACCTATGCACCAGACGTATGGATAAGAAATGCACTTGATAAATGATCACCAGGTCTAAGATCGGAAGAGCGGTTTCAG
chr2	216288260	216288299	FN1_8928	+	GTGACCTATGCACCAGACGTCAATACACAACAAGAAGGAAAAGATTACCGCTGAGCTTTAGATCGGAAGAGCGGTTTCAG
chr2	216289059	216289098	FN1_8929	+	GTGACCTATGCACCAGACGTAATCAAAAGAGTGTGAGTAAACAGAGATGCTTTATCTCCAGATCGGAAGAGCGGTTTCAG
chr2	216290019	216290058	FN1_8930	+	GTGACCTATGCACCAGACGTGAAAAGGGAATGTCACAAAACCTGGGTGAGAGAAGACAATAGATCGGAAGAGCGGTTTCAG
chr2	216293072	216293111	FN1_8931	+	GTGACCTATGCACCAGACGTAAGGAAAAGCATAACATCAGTCCAGAGTCCGAAATGAGATCGGAAGAGCGGTTTCAG
chr2	216295586	216295625	FN1_8932	+	GTGACCTATGCACCAGACGTAATTTGGAAGAAAACAGGAAAAAAGTTATTTGAAATTGAGATCGGAAGAGCGGTTTCAG

chr2	216296698	216296737	FN1_8933	+	GTGACCTATGCACCAGACGTTACAACGAAATGTTAGGAGAGGGCAGAACAGATTTTTTTAGATCGGAAGAGCGGTTTCCAG
chr2	216298195	216298234	FN1_8934	+	GTGACCTATGCACCAGACGTAAGGAAAGTCCATGTGAGCCTCACTTAGGTACAAGCTTTTATAGATCGGAAGAGCGGTTCCAG
chr2	216299558	216299597	FN1_8935	+	GTGACCTATGCACCAGACGTTTGAAGGAAACGTTACATTTGCATTTCTCCTTTTCCCAAAGATCGGAAGAGCGGTTCCAG
chr2	216300536	216300575	FN1_8936	+	GTGACCTATGCACCAGACGTTGGGGGAGAGACGCCCGACCGGGAGGCAAGTTGCCACCAAGATCGGAAGAGCGGTTCCAG
chr3	119545713	119545752	GSK3B_8937	+	GTGACCTATGCACCAGACGTTAAAAGTCCCAAGAGAGAGCATGAGCAATGCTATAACAACAAGATCGGAAGAGCGGTTCCAG
chr3	119562211	119562250	GSK3B_8938	+	GTGACCTATGCACCAGACGTTTAAAGACAATAAGGTAGAGTCCACTTTAACTTTGTATGAGATCGGAAGAGCGGTTCCAG
chr3	119582463	119582502	GSK3B_8939	+	GTGACCTATGCACCAGACGTTAAAAAAGGGAAGAACAATTAATGTTTATTTTAAAGAACAGATCGGAAGAGCGGTTCCAG
chr3	119585486	119585525	GSK3B_8940	+	GTGACCTATGCACCAGACGTTAATGCAGTGAATAATCCAACAGGGGAAAGTCAATCCAAGATCGGAAGAGCGGTTCCAG
chr3	119595366	119595405	GSK3B_8941	+	GTGACCTATGCACCAGACGTAGCAAGTTATTGCCATCTTTTCTATATATTTACAAATTTAGATCGGAAGAGCGGTTCCAG
chr3	119624710	119624749	GSK3B_8942	+	GTGACCTATGCACCAGACGTAAGAAAAAGAACGCTTATAAATACTTCATAGCTTGAGCTGAGATCGGAAGAGCGGTTCCAG
chr3	119631668	119631707	GSK3B_8943	+	GTGACCTATGCACCAGACGTTAAAATAAAAAATAAAAAAGCAGAATTTCTTTAAATCTAAACAGATCGGAAGAGCGGTTCCAG
chr3	119635032	119635071	GSK3B_8944	+	GTGACCTATGCACCAGACGTTAGTAGAAATTAATAAATCTTCCTATTTCTAAACAAATCAGATCGGAAGAGCGGTTCCAG
chr3	119642341	119642380	GSK3B_8945	+	GTGACCTATGCACCAGACGTTTATTTAAAAACAAAAAACAAACAGATTAGAAACTGGAGATCGGAAGAGCGGTTCCAG
chr3	119666209	119666248	GSK3B_8946	+	GTGACCTATGCACCAGACGTTAACACATAAAAAATATATTTTTAAAGGATAACAGCTATTCAAGATCGGAAGAGCGGTTCCAG
chr3	119721097	119721136	GSK3B_8947	+	GTGACCTATGCACCAGACGTTAAAGGAAATTTTTTTTTCACGAGAACTGTAAGGAATTTAAAGATCGGAAGAGCGGTTCCAG
chr3	119812292	119812331	GSK3B_8948	+	GTGACCTATGCACCAGACGTTTTCGCGAATCACCTTTTCTTCTCCTTCTCTCTTCTCTCTAGATCGGAAGAGCGGTTCCAG
chr6	114262263	114262302	HDAC2_8949	+	GTGACCTATGCACCAGACGTAGGCAATGTGAAATATAAAAATGGCACACTTTGGTGTAAAGATCGGAAGAGCGGTTCCAG
chr6	114264681	114264720	HDAC2_8950	+	GTGACCTATGCACCAGACGTTTATTTAAATAAATTTTGACAAAAACAGACTCACAGTTTTATAGATCGGAAGAGCGGTTCCAG
chr6	114265585	114265624	HDAC2_8951	+	GTGACCTATGCACCAGACGTCATGCAAAGTTTTATTGACAAAAATTAATTTTCTTTGCAAGTATGATCGGAAGAGCGGTTCCAG
chr6	114266645	114266684	HDAC2_8952	+	GTGACCTATGCACCAGACGTTCAATAAAATAAAGTTACATATTACAAGCTCAGTTTTTCAAGATCGGAAGAGCGGTTCCAG
chr6	114267323	114267362	HDAC2_8953	+	GTGACCTATGCACCAGACGTTAAGATTTGGGTAACAACAAAATCTGCATACTGCAACAGTTAGATCGGAAGAGCGGTTCCAG
chr6	114270262	114270301	HDAC2_8954	+	GTGACCTATGCACCAGACGTGATAACAATGTTAGCATCTCCAATAACATTCTGAAATTCAGATCGGAAGAGCGGTTCCAG
chr6	114270435	114270474	HDAC2_8955	+	GTGACCTATGCACCAGACGTTAATTAATGATCTTAGAGAAATTTCTATAATAAAAAGTAGATCGGAAGAGCGGTTCCAG
chr6	114274593	114274632	HDAC2_8956	+	GTGACCTATGCACCAGACGTTTATTAATAAGTTTTGGTTTTCTTTAAAGGTTCTAAGATGATCGGAAGAGCGGTTCCAG
chr6	114277326	114277365	HDAC2_8957	+	GTGACCTATGCACCAGACGTGAAACAAGATAGACCTTTTAAACATTTATCATAAAAAGTAGATCGGAAGAGCGGTTCCAG
chr6	114277868	114277907	HDAC2_8958	+	GTGACCTATGCACCAGACGTTGGATTTCTTAATTTCAACACATTCTGCAAATTAATGAAAGATCGGAAGAGCGGTTCCAG
chr6	114279941	114279980	HDAC2_8959	+	GTGACCTATGCACCAGACGTTAAATAATGTCAGAAGTGTGGAATTAACAACCGGTTATATCAGATCGGAAGAGCGGTTCCAG
chr6	114281193	114281232	HDAC2_8960	+	GTGACCTATGCACCAGACGTTAAAGACACAAAATAACAGACAAGAGACCCTCCATAGATCGGAAGAGCGGTTCCAG
chr6	114292365	114292404	HDAC2_8961	+	GTGACCTATGCACCAGACGTTCCACGGGGGAGAAAGGGGACAGGCTGGAGAGGAGCCAGATCGGAAGAGCGGTTCCAG
chr7	27203471	27203510	HOXA9_8962	+	GTGACCTATGCACCAGACGTGAGAACAATCTGGTATTAGGACAGAGAAGACGCCACATCCCGCAGATCGGAAGAGCGGTTCCAG
chr7	27205087	27205126	HOXA9_8963	+	GTGACCTATGCACCAGACGTAGCGCCTGGCCCGCCCGGCCAGCCACGGAAATTTATGAAAGATCGGAAGAGCGGTTCCAG
chr7	27204797	27204836	HOXA9_8964	+	GTGACCTATGCACCAGACGTGGTGACGTAGGGGTGGTGGTATGGTGGTGGTACACCGCAGATCGGAAGAGCGGTTCCAG
chr11	64572299	64572338	MEN1_8965	+	GTGACCTATGCACCAGACGTGGGGAGAGCAAGGTGAGAGCAAGGTTGCCGGCCAGTGGCTAGATCGGAAGAGCGGTTCCAG
chr11	64572681	64572720	MEN1_8966	+	GTGACCTATGCACCAGACGTGGGAAGGGGACAGCATGCTCTTACTCACCCCTTAAGATCGGAAGAGCGGTTCCAG
chr11	64573253	64573292	MEN1_8967	+	GTGACCTATGCACCAGACGTAGTGGGGTCTGCTGAGGGTCTGAAAGGGGCTCACCATCGGATCGGAAGAGCGGTTCCAG
chr11	64573851	64573890	MEN1_8968	+	GTGACCTATGCACCAGACGTGTGAGGCAGAGGATCCTCAGGGAGGCAGCCCCAGCTGCCAGATCGGAAGAGCGGTTCCAG
chr11	64574581	64574620	MEN1_8969	+	GTGACCTATGCACCAGACGTATCATAATTCAGGCTGCCACCCAGCCCCGGCCTCACCAAGATCGGAAGAGCGGTTCCAG
chr11	64574702	64574741	MEN1_8970	+	GTGACCTATGCACCAGACGTAAGGAGAGAGTTATGAGCCACGGAACAGGGAGGAGAACCGAGATCGGAAGAGCGGTTCCAG
chr11	64575163	64575202	MEN1_8971	+	GTGACCTATGCACCAGACGTGATGAGATCATTATGTCTCATGATGGCCACCCTGTGCCTAGATCGGAAGAGCGGTTCCAG
chr11	64575582	64575621	MEN1_8972	+	GTGACCTATGCACCAGACGTGGGAGGTAATGAAAGAGGGTCTGTGCTTTAATACATGGGAGATCGGAAGAGCGGTTCCAG
chr11	64577592	64577631	MEN1_8973	+	GTGACCTATGCACCAGACGTGGTGGCGCCGGCTGCAAGGCTCAAGCCGGGGAGGGAGATCGGAAGAGCGGTTCCAG
chr22	36678842	36678881	MYH9_8974	+	GTGACCTATGCACCAGACGTAGGTAGAAGCAGAGGGTACAGCGGGCCCGGCCAGGCCAGGGAGATCGGAAGAGCGGTTCCAG
chr22	36680322	36680361	MYH9_8975	+	GTGACCTATGCACCAGACGTGGACGTGTGGCCCGTGGCCCGGTTAGGGGCTCTGGGCGTAGATCGGAAGAGCGGTTCCAG
chr22	36680568	36680607	MYH9_8976	+	GTGACCTATGCACCAGACGTGACAAGGTGGCTCAGAGGGAAACACCTCTTCAGAGGGTCAGATCGGAAGAGCGGTTCCAG
chr22	36681386	36681425	MYH9_8977	+	GTGACCTATGCACCAGACGTAGGGCCAGTACCTTTGGGAGGGCTGGGGCCCTGGCTGGAAGATCGGAAGAGCGGTTCCAG
chr22	36681838	36681877	MYH9_8978	+	GTGACCTATGCACCAGACGTGGCGGGAGAAGTGAAGGGCTACCTCGGGACACACTGGAGATCGGAAGAGCGGTTCCAG
chr22	36682010	36682049	MYH9_8979	+	GTGACCTATGCACCAGACGTGACCCAGAGTGTGACCTAAAGGCAGCCACAGCCCCACAAGAGATCGGAAGAGCGGTTCCAG
chr22	36682903	36682942	MYH9_8980	+	GTGACCTATGCACCAGACGTGACAGAGGCTTGGCACCCACCCAGCTCCTTGGCCCTCAAGATCGGAAGAGCGGTTCCAG
chr22	36684470	36684509	MYH9_8981	+	GTGACCTATGCACCAGACGTGAACATCAACAATTTGGGAAGCTGGACCCACTGGGAGACCAGATCGGAAGAGCGGTTCCAG
chr22	36684996	36685035	MYH9_8982	+	GTGACCTATGCACCAGACGTGAGAGCCCAAGTCAAGGAGCAAAGGGACTGGCAGGTACCTGAGATCGGAAGAGCGGTTCCAG
chr22	36685354	36685393	MYH9_8983	+	GTGACCTATGCACCAGACGTGGTGGCCACCATGAGGCTCAGGCTACGGCCCCACAGGATCGGAAGAGCGGTTCCAG
chr22	36688320	36688359	MYH9_8984	+	GTGACCTATGCACCAGACGTGCAAGGTAAGACATGCCAGATGGCACCCTGCTCAGGAGATCGGAAGAGCGGTTCCAG
chr22	36689538	36689577	MYH9_8985	+	GTGACCTATGCACCAGACGTGTTGAGAGGGGTGCGGGTCTTAGGAGGGTGGTGTCCAAAAGATCGGAAGAGCGGTTCCAG
chr22	36689920	36689959	MYH9_8986	+	GTGACCTATGCACCAGACGTGGGGGAGACACAAAGGACCATGGACCCACCCCACTGCTCAGATCGGAAGAGCGGTTCCAG
chr22	36690355	36690394	MYH9_8987	+	GTGACCTATGCACCAGACGTAGAAAGCAAAGACGTGAGTGGGGCCCTCTGACACAAGGCAGATCGGAAGAGCGGTTCCAG
chr22	36691133	36691172	MYH9_8988	+	GTGACCTATGCACCAGACGTTAAATCCCCTCAGAGTGGAGGCCGGGATGCTGGAGCGAGGATCGGAAGAGCGGTTCCAG
chr22	36691774	36691813	MYH9_8989	+	GTGACCTATGCACCAGACGTGACCACCAACATCAGTATAAGGAGATTTACCTCCAAGGATCGGAAGAGCGGTTCCAG
chr22	36693071	36693110	MYH9_8990	+	GTGACCTATGCACCAGACGTGGGGAGGCCACATAGCCCTCAGTGCATGGTTCTGTCTAGATCGGAAGAGCGGTTCCAG

chr22	36695099	36695138	MYH9_8991	+	GTGACCTATGCACCAGACGTGGGAGTAGGCTGGCATTAGTGTGGTTGAGCACAGAACAAGATCGGAAGAGCGGTTTCAG
chr22	36696321	36696360	MYH9_8992	+	GTGACCTATGCACCAGACGTCCAGAGACACGGTAAGGACAGCAGGCCAGAGGCATGGCCAGATCGGAAGAGCGGTTTCAG
chr22	36697114	36697153	MYH9_8993	+	GTGACCTATGCACCAGACGTCAAGTGGAAAAACAAGCTCCTCGCAACACCCTCAAGCCAAGATCGGAAGAGCGGTTTCAG
chr22	36697722	36697761	MYH9_8994	+	GTGACCTATGCACCAGACGTAGATAGAGGTAGAGACATGCTCGGCTGGAAGATGCCCGCCAGATCGGAAGAGCGGTTTCAG
chr22	36698733	36698772	MYH9_8995	+	GTGACCTATGCACCAGACGTAGGAACATGGTCACGCGGGAGCAGTGGACAGCAGACCCGAAGATCGGAAGAGCGGTTTCAG
chr22	36700212	36700251	MYH9_8996	+	GTGACCTATGCACCAGACGTGGAGCAGGCCGCTTTACCTGCCACAGCTGCCACAGCTCAGATCGGAAGAGCGGTTTCAG
chr22	36701159	36701198	MYH9_8997	+	GTGACCTATGCACCAGACGTAAAAGTAGAGCTGGTGCATTTACCCATTGCCTCGATTCCAAGATCGGAAGAGCGGTTTCAG
chr22	36702108	36702147	MYH9_8998	+	GTGACCTATGCACCAGACGTAAACACATGCATGCGGCTCCTACTTCCGTGCCCTAGAACAGTAGATCGGAAGAGCGGTTTCAG
chr22	36702664	36702703	MYH9_8999	+	GTGACCTATGCACCAGACGTACAGAGAACACGTGAGTGCCACACAGTTGCAGCTGGGTAGATCGGAAGAGCGGTTTCAG
chr22	36705452	36705491	MYH9_9000	+	GTGACCTATGCACCAGACGTGACAGAGGCAGGAGTCAACAGCTGCGCTGGGGACATGTGTAGATCGGAAGAGCGGTTTCAG
chr22	36708278	36708317	MYH9_9001	+	GTGACCTATGCACCAGACGTGCGCAGCATCAGCACAGGTGAGTGACCCCTGGGAGGGGCACAGATCGGAAGAGCGGTTTCAG
chr22	36710374	36710413	MYH9_9002	+	GTGACCTATGCACCAGACGTAGAAAACAATGTCAGAGAGACGCCAACCCCTGCACATAAGAAAGATCGGAAGAGCGGTTTCAG
chr22	36714381	36714420	MYH9_9003	+	GTGACCTATGCACCAGACGTTCAGAGATAAGAGAGGGGACAAAAAGTCCCTAATTAGACCCAGATCGGAAGAGCGGTTTCAG
chr22	36715691	36715730	MYH9_9004	+	GTGACCTATGCACCAGACGTAATCAGAGGCAGCTCAGAAGCAGACATGGGTGATGGTGATAGATCGGAAGAGCGGTTTCAG
chr22	36716419	36716458	MYH9_9005	+	GTGACCTATGCACCAGACGTTGGAGGGCAAGGGCGCCTCAGCGAGGTGCTGAAAGTGAGAGATCGGAAGAGCGGTTTCAG
chr22	36716952	36716991	MYH9_9006	+	GTGACCTATGCACCAGACGTATTAAGGAGCAACAAGCTGGGGAGAAGGCAAGCCCTCCAGATCGGAAGAGCGGTTTCAG
chr22	36717877	36717916	MYH9_9007	+	GTGACCTATGCACCAGACGTAAAGGATAGCAAGAGATCAGAGGTGCCCTGACATGGGGAGAGATCGGAAGAGCGGTTTCAG
chr22	36718577	36718616	MYH9_9008	+	GTGACCTATGCACCAGACGTCCCAGGCGAGTGAAGGCGGGACAGCAGCTGGGCTGCAGATCGGAAGAGCGGTTTCAG
chr22	36722717	36722756	MYH9_9009	+	GTGACCTATGCACCAGACGTAGGCAAGGAAGTCCCGGGCTTAGGCATGCCAAGTCCCTTGAGATCGGAAGAGCGGTTTCAG
chr22	36723544	36723583	MYH9_9010	+	GTGACCTATGCACCAGACGTGAAGACATCAGATTAACCTCCCGCCAGATGCAAAAAGCCTCCAGATCGGAAGAGCGGTTTCAG
chr22	36737582	36737621	MYH9_9011	+	GTGACCTATGCACCAGACGTGAGCGGCAGATAGGAACAGGTTAGGAAGTTTGATTCTCAGAGATCGGAAGAGCGGTTTCAG
chr22	36745292	36745331	MYH9_9012	+	GTGACCTATGCACCAGACGTAGCCAGGACCTAAGCGGGGAGGAGAAGGACAACACATTACAGATCGGAAGAGCGGTTTCAG
chr8	71025889	71025928	NCOA2_9013	+	GTGACCTATGCACCAGACGTACAGATAAAAAGTTGTGAAACATCTTTGAGGTTTTGAAAAAGATCGGAAGAGCGGTTTCAG
chr8	71033637	71033676	NCOA2_9014	+	GTGACCTATGCACCAGACGTGAAGACAGGACAGTGGCTACGCAGCAGGACAAGTGTCCAAGAGATCGGAAGAGCGGTTTCAG
chr8	71036328	71036367	NCOA2_9015	+	GTGACCTATGCACCAGACGTATGGAAAGATTGAATGAATGTTACAGCTTGCTGGTATCCAAGATCGGAAGAGCGGTTTCAG
chr8	71037111	71037150	NCOA2_9016	+	GTGACCTATGCACCAGACGTAAAACAGAAACAGAAATCCAAAAGAGACTGTTAGTTATATAGATCGGAAGAGCGGTTTCAG
chr8	71039293	71039332	NCOA2_9017	+	GTGACCTATGCACCAGACGTGGGCAACACATGGAGGAAAATGTCGGGGACAGACATAGATAGATCGGAAGAGCGGTTTCAG
chr8	71040756	71040795	NCOA2_9018	+	GTGACCTATGCACCAGACGTACAAACAGGATGAATACATTTTAAGAACAAGATACATTTTATAGATCGGAAGAGCGGTTTCAG
chr8	71041226	71041265	NCOA2_9019	+	GTGACCTATGCACCAGACGTAGTCCCAATAACAACAAATAATTAACCATAAAAACAGAGATCGGAAGAGCGGTTTCAG
chr8	71044248	71044287	NCOA2_9020	+	GTGACCTATGCACCAGACGTAGAAAATGTCACCTTTGGGCAATGAAAAGCTAGTTGATTAGATCGGAAGAGCGGTTTCAG
chr8	71050578	71050617	NCOA2_9021	+	GTGACCTATGCACCAGACGTAGAAGAAAAAATCTTACATCTTAAATCAAGGAAGCATTAGATCGGAAGAGCGGTTTCAG
chr8	71053645	71053684	NCOA2_9022	+	GTGACCTATGCACCAGACGTGCCAAAGAAAACAGAGATGCAAGTGAACATATTAGATCGGAAGAGCGGTTTCAG
chr8	71057094	71057133	NCOA2_9023	+	GTGACCTATGCACCAGACGTAAACAAATGAAAATGGAAGTTAATATAGGATAATGGAAGAAAGATCGGAAGAGCGGTTTCAG
chr8	71060729	71060768	NCOA2_9024	+	GTGACCTATGCACCAGACGTCAAACAGAAAGTTTATCCAGTCTACTCTAAGAGTAGACAAGATCGGAAGAGCGGTTTCAG
chr8	71069486	71069525	NCOA2_9025	+	GTGACCTATGCACCAGACGTAGAAGAAAAAATTAAGATAAAAAGAAAAAATCTTAGAGATCGGAAGAGCGGTTTCAG
chr8	71071898	71071937	NCOA2_9026	+	GTGACCTATGCACCAGACGTGCAAGGAAACAGAGGCAGCTTTAGAAAAAATGAGGAGATCGGAAGAGCGGTTTCAG
chr8	71075100	71075139	NCOA2_9027	+	GTGACCTATGCACCAGACGTACAGCAGGCATTATACCTACATGTTGATCTATTCTTTATAGATCGGAAGAGCGGTTTCAG
chr8	71075812	71075851	NCOA2_9028	+	GTGACCTATGCACCAGACGTACATGTTTACATTTATCATATTTGGGCTTTCTAGTGATTAGATCGGAAGAGCGGTTTCAG
chr8	71079000	71079039	NCOA2_9029	+	GTGACCTATGCACCAGACGTCAAAGTAAATCCAGTTTTACAAAGAAACAAACATCAGATTAGATCGGAAGAGCGGTTTCAG
chr8	71082625	71082664	NCOA2_9030	+	GTGACCTATGCACCAGACGTAAAGTACAATTTGTTAGAAAGATGCAACATAACATCAGATCGGAAGAGCGGTTTCAG
chr8	71087105	71087144	NCOA2_9031	+	GTGACCTATGCACCAGACGTCAATAAGTGTGAATTAATGGCAGTGCATTTTCAAGGACAGATCGGAAGAGCGGTTTCAG
chr8	71126321	71126360	NCOA2_9032	+	GTGACCTATGCACCAGACGTGAAACACATTTTTATGATGATTTTGAAGAAAGAGCTATTGTAGATCGGAAGAGCGGTTTCAG
chr8	71128991	71129030	NCOA2_9033	+	GTGACCTATGCACCAGACGTTATCAGCAACTAAAACAGAAAACAGAGAAGAGGAAAGAAAGATCGGAAGAGCGGTTTCAG
chr8	71068639	71068678	NCOA2_9034	+	GTGACCTATGCACCAGACGTGGCTCCATCTGATCAGATTTGGTGGTGCAGCAGCTGCAGGAAGATCGGAAGAGCGGTTTCAG
chr8	71069062	71069101	NCOA2_9035	+	GTGACCTATGCACCAGACGTAAAGTCTCTGCAGGGGAAAACGACTGGGTGGGATTCGAGAGATCGGAAGAGCGGTTTCAG
chr20	5096019	5096058	PCNA_9036	+	GTGACCTATGCACCAGACGTGGAAGTGTAACTGAGGAGTGTATACATATGAAGATCGGAAGAGCGGTTTCAG
chr20	5098321	5098360	PCNA_9037	+	GTGACCTATGCACCAGACGTCAAAAATTTTCCAAAAGTTAATTGTTAGAAATTTAATGATAGATCGGAAGAGCGGTTTCAG
chr20	5099334	5099373	PCNA_9038	+	GTGACCTATGCACCAGACGTAAAGCAGATGCTTTTGAGAAATACTGACACAGAGTTTTGAAGATCGGAAGAGCGGTTTCAG
chr20	5099523	5099562	PCNA_9039	+	GTGACCTATGCACCAGACGTGGAGACACATGCTTTAAAATCAACGCCGTCTGCTGAAGGGAGATCGGAAGAGCGGTTTCAG
chr20	5100455	5100494	PCNA_9040	+	GTGACCTATGCACCAGACGTTGGCAACAACGCCGCTACAGGCAGCGGGAAAGGAGGAAAGAGATCGGAAGAGCGGTTTCAG
chr15	74287293	74287332	PML_9041	+	GTGACCTATGCACCAGACGTGTTAGGGATGATGGGTTAAGCTTTGTTGGTTTGTGTGATCGGAAGAGCGGTTTCAG
chr15	74290828	74290867	PML_9042	+	GTGACCTATGCACCAGACGTCCGCACAGGTGGGGTGGTGCATCCAAGTACCAGTGAAGATCGGAAGAGCGGTTTCAG
chr15	74315760	74315799	PML_9043	+	GTGACCTATGCACCAGACGTACGCCACCTTCTGGGCGGCTGTGCCTCTGCTGCACCCTAGATCGGAAGAGCGGTTTCAG
chr15	74317279	74317318	PML_9044	+	GTGACCTATGCACCAGACGTTTTGAGGTCTGAAGGGTGGTGGTGGGGCCAGCAGGTCAAGATCGGAAGAGCGGTTTCAG
chr15	74325067	74325106	PML_9045	+	GTGACCTATGCACCAGACGTCCCCAGCCCCAGCCTTCCCTCTGAAGGCCTGAGTTCCACAGATCGGAAGAGCGGTTTCAG
chr15	74325766	74325805	PML_9046	+	GTGACCTATGCACCAGACGTGGGTAGGGCAGTGGCCTGGGTGCTGCCGCCAGGGTCTGGAGATCGGAAGAGCGGTTTCAG
chr15	74325774	74325813	PML_9047	+	GTGACCTATGCACCAGACGTGAGTGGCTGGTGCCTGCCGCCAGGGTCTGGGCGTTCGAGATCGGAAGAGCGGTTTCAG
chr15	74326847	74326886	PML_9048	+	GTGACCTATGCACCAGACGTGGAAGACTGAGTCCGAAAACCTCGGTGAGTGGCCAGAAAGATCGGAAGAGCGGTTTCAG

chr15	74326882	74326921	PML_9049	+	GTGACCTATGCACCAGACGTGAGGTTCCAGCCAGGACTCCTGCCTCCCCCATTTTCAGAGATCGGAAGAGCGGTTTCAG
chr15	74327008	74327047	PML_9050	+	GTGACCTATGCACCAGACGTGTGCTGAGGACAGTCTCCAATGACAGCTGCATGCCTGGAAGATCGGAAGAGCGGTTTCAG
chr15	74328303	74328342	PML_9051	+	GTGACCTATGCACCAGACGTCTTCTCTTGTAACTTGCAGCCAAACCCCTGCCCGGCCAGATCGGAAGAGCGGTTTCAG
chr15	74335491	74335530	PML_9052	+	GTGACCTATGCACCAGACGTCTGGGGCTACCCACCCCTTCTAATTTAGTCTCTGAGTAGATCGGAAGAGCGGTTTCAG
chr15	74335532	74335571	PML_9053	+	GTGACCTATGCACCAGACGTCCAAAAAAGAGTGCAGGCAGAGCCATCTGCCAGGCCAGGAGATCGGAAGAGCGGTTTCAG
chr15	74337360	74337399	PML_9054	+	GTGACCTATGCACCAGACGTTGACCAGCTTGGAGTCTCTGGTGGCCAGAGAGGGATGGGGAGATCGGAAGAGCGGTTTCAG
chr15	74315469	74315508	PML_9055	+	GTGACCTATGCACCAGACGTGAGCAGCGGGTACCAGCTGAGGACTACGAGGAGATGGCCAGTAGATCGGAAGAGCGGTTTCAG
chr15	74327913	74327952	PML_9056	+	GTGACCTATGCACCAGACGTATCCTGCCAATGCCAGGAACATCCTGCCAGCTGCAAAGAGATCGGAAGAGCGGTTTCAG
chr15	74336966	74337005	PML_9057	+	GTGACCTATGCACCAGACGTCTCCTCGAGGTCTCCCGGGCCCCAGCTGGCCAGCATGAGATCGGAAGAGCGGTTTCAG
chr3	12393184	12393223	PPARG_9058	+	GTGACCTATGCACCAGACGTTCAGATACCGGTATTGGGGAGCTGGGGGCAATTTATGTAAGATCGGAAGAGCGGTTTCAG
chr3	12421441	12421480	PPARG_9059	+	GTGACCTATGCACCAGACGTATTTTCACTTTTCAGACTACTAGGACTAGAATTTGGACTCAGATCGGAAGAGCGGTTTCAG
chr3	12423001	12423040	PPARG_9060	+	GTGACCTATGCACCAGACGTAAAAAGTCTTCAAAGAAATTTGAAACTTTTATTTTCAAGATCGGAAGAGCGGTTTCAG
chr3	12434262	12434301	PPARG_9061	+	GTGACCTATGCACCAGACGTAGTGCATACCATATCCTTTATTATTCTATTATAGCTGCCAGATCGGAAGAGCGGTTTCAG
chr3	12447591	12447630	PPARG_9062	+	GTGACCTATGCACCAGACGTCTTCTGCTCTTCTATTGGGGAGGCGGGAAGTTGTTTTGGAGATCGGAAGAGCGGTTTCAG
chr3	12458664	12458703	PPARG_9063	+	GTGACCTATGCACCAGACGTCTTTTGTATCTCTATGAAAGAGGGTGGGATGATGGTGGGAGATCGGAAGAGCGGTTTCAG
chr3	12475655	12475694	PPARG_9064	+	GTGACCTATGCACCAGACGTGAGCCACTGCCAACATTTCCCTTCTTCCAGTTGCACATATAGATCGGAAGAGCGGTTTCAG
chr4	23797559	23797598	PPARGC1A_9065	+	GTGACCTATGCACCAGACGTACCAAAGCCAGTTAGATACACACTTTGGCTGATGGCCATTAGATCGGAAGAGCGGTTTCAG
chr4	23803515	23803554	PPARGC1A_9066	+	GTGACCTATGCACCAGACGTGAAAGAAAGTTCAAAGCTGGTTAAGAAGTATTAGTATATAGATCGGAAGAGCGGTTTCAG
chr4	23803979	23804018	PPARGC1A_9067	+	GTGACCTATGCACCAGACGTAAAGAAAGGAGAGATTCTGGAGTGGGAAAAAGCTAGCCAGATCGGAAGAGCGGTTTCAG
chr4	23814501	23814540	PPARGC1A_9068	+	GTGACCTATGCACCAGACGTAACTTTTACTAAGTCAACCACCTCAATTTTTCATGAGCAGATCGGAAGAGCGGTTTCAG
chr4	23814759	23814798	PPARGC1A_9069	+	GTGACCTATGCACCAGACGTGGAGAAAAGCAAAAAGGGCATTGCAACTGCCACTTAACCAGATCGGAAGAGCGGTTTCAG
chr4	23825987	23826026	PPARGC1A_9070	+	GTGACCTATGCACCAGACGTGGGCACATTTATAAAAAAACTGAAATGGAGTTGCTGTAAGATCGGAAGAGCGGTTTCAG
chr4	23826142	23826181	PPARGC1A_9071	+	GTGACCTATGCACCAGACGTAAAAAGAACTAATATTGATATTTAGTGTCTTTTAGAAGATCGGAAGAGCGGTTTCAG
chr4	23830238	23830277	PPARGC1A_9072	+	GTGACCTATGCACCAGACGTAGGCAATAAAGAAAGCTAAATTTAGTCAACTGAACTTATCAGATCGGAAGAGCGGTTTCAG
chr4	23831219	23831258	PPARGC1A_9073	+	GTGACCTATGCACCAGACGTATCAGGGAAAGGGAAAGCAAGTAAAGTTATGCATCTTTAGATCGGAAGAGCGGTTTCAG
chr4	23833385	23833424	PPARGC1A_9074	+	GTGACCTATGCACCAGACGTAGAAAAAAACAGAAAGATGTGAGTTGACCTGGGAGGACAGGATCGGAAGAGCGGTTTCAG
chr4	23886565	23886604	PPARGC1A_9075	+	GTGACCTATGCACCAGACGTGAGAAAAAAAATTTAAAAAGCTTCCATTAACCACAGGAGATCGGAAGAGCGGTTTCAG
chr4	23891591	23891630	PPARGC1A_9076	+	GTGACCTATGCACCAGACGTAACTGACGCCAGTCAAGCTTTTTCACTCCAATCCACAGTGAGATCGGAAGAGCGGTTTCAG
chr4	23815781	23815820	PPARGC1A_9077	+	GTGACCTATGCACCAGACGTTTGCTTGCCCTCAAAGTCTCTCAGGTAGCACTGTCTGAGATCGGAAGAGCGGTTTCAG
chr17	38487659	38487698	RARA_9078	+	GTGACCTATGCACCAGACGTGTGTGGGGCTGGGGTGGGAAGGGACTGTGGAGGGTGCAAGATCGGAAGAGCGGTTTCAG
chr17	38499130	38499169	RARA_9079	+	GTGACCTATGCACCAGACGTGCCTCTCAGTCTGCTGTTGTAGGGGGTGGGAGTGGGCGGTAGATCGGAAGAGCGGTTTCAG
chr17	38504727	38504766	RARA_9080	+	GTGACCTATGCACCAGACGTGGGGTCAATGGGAAGGACAGCTTGATGAGGTCAATGGGATAGATCGGAAGAGCGGTTTCAG
chr17	38506188	38506227	RARA_9081	+	GTGACCTATGCACCAGACGTAGGGCAGGGGCCAGTCCCGCCTCAGTTGGGGTCTCAGAAGATCGGAAGAGCGGTTTCAG
chr17	38508333	38508372	RARA_9082	+	GTGACCTATGCACCAGACGTCCCCCGCTGCAGGGTGGGATTTGCCAGGGCCACAGGAGATCGGAAGAGCGGTTTCAG
chr17	38508770	38508809	RARA_9083	+	GTGACCTATGCACCAGACGTGCCCTGGCCCTGGCCAGCCAGCCTGCCCTGTGTCTGGGTAGAGATCGGAAGAGCGGTTTCAG
chr17	38510769	38510808	RARA_9084	+	GTGACCTATGCACCAGACGTGGCCTGGGCTGGGGCTGGGCTGGGACGGGGTGCAGCCAGATCGGAAGAGCGGTTTCAG
chr17	38511684	38511723	RARA_9085	+	GTGACCTATGCACCAGACGTGAGGGGTACCGGCCCCGACACCTGGCCAGGAGATCGGAAGAGCGGTTTCAG
chr17	38512489	38512528	RARA_9086	+	GTGACCTATGCACCAGACGTACATGGACACAGCCCTCGCCCTCCGCCCGGCTTTTCTCAGATCGGAAGAGCGGTTTCAG
chr5	36152383	36152422	SKP2_9087	+	GTGACCTATGCACCAGACGTGCAAAAAGGGGAAGAGCATGAAATGGACCCCTTAAATAAAGATCGGAAGAGCGGTTTCAG
chr5	36153155	36153194	SKP2_9088	+	GTGACCTATGCACCAGACGTGAGGGTAAAAATGTGAGTTATGCAAGGGTGGATTTAGCTAGATCGGAAGAGCGGTTTCAG
chr5	36163869	36163908	SKP2_9089	+	GTGACCTATGCACCAGACGTTCACCCCTTTGGCAAACGTAGGGGAGGAAGAGGAGGAAGATCGGAAGAGCGGTTTCAG
chr5	36166775	36166814	SKP2_9090	+	GTGACCTATGCACCAGACGTAAATCCCTGGAAGAAAGACTATTTCTAAATTTTCGAGGTAGAAGATCGGAAGAGCGGTTTCAG
chr5	36168560	36168599	SKP2_9091	+	GTGACCTATGCACCAGACGTGGCAGAGTGCACAAGGCAGTTGATTTTATGTGATGAAAGATCGGAAGAGCGGTTTCAG
chr5	36170555	36170594	SKP2_9092	+	GTGACCTATGCACCAGACGTGTGAGACTTGATTATAGACTCTTATGTCAAACGTAATAATAGATCGGAAGAGCGGTTTCAG
chr5	36171846	36171885	SKP2_9093	+	GTGACCTATGCACCAGACGTCAAAGCTGGACACTGAGGCCTTCAACAATAATAGATGAGATCGGAAGAGCGGTTTCAG
chr5	36177129	36177168	SKP2_9094	+	GTGACCTATGCACCAGACGTAAATGTTTATTGTTTATAGTCAAAAGTGAAGAACTTTGATTTAGATCGGAAGAGCGGTTTCAG
chr5	36177405	36177444	SKP2_9095	+	GTGACCTATGCACCAGACGTGTTTGTGTTTAAATGCTTAATAGAAGGCAGGAAACAACAGAGATCGGAAGAGCGGTTTCAG
chr5	36182144	36182183	SKP2_9096	+	GTGACCTATGCACCAGACGTGCAGGATGGTGTCTCTTTAGAACAGGGAAATAGGCAAGATCGGAAGAGCGGTTTCAG
chr5	36184124	36184163	SKP2_9097	+	GTGACCTATGCACCAGACGTATAAAAATGAGTGTCTAAACTAAGTTGATTTCTTTTTTAGATCGGAAGAGCGGTTTCAG
chr16	11349346	11349385	SOCS1_9098	+	GTGACCTATGCACCAGACGTGGGCCAGCCGGAGGGTGGGCCATAGCGTCCGGGGGTGCGAGATCGGAAGAGCGGTTTCAG
chr16	11349028	11349067	SOCS1_9099	+	GTGACCTATGCACCAGACGTACCAGGAAGTGCACCGGCTGGCCGCGCAGCCGCTCGTAGATCGGAAGAGCGGTTTCAG
chr2	39213467	39213506	SOS1_9100	+	GTGACCTATGCACCAGACGTAAAAAGAAATAAAATACACATTTATAAATTTATGAAGTGAAGATCGGAAGAGCGGTTTCAG
chr2	39214743	39214782	SOS1_9101	+	GTGACCTATGCACCAGACGTAAATTTTTAAGAAAAAGTCCACAGGAATTTTATTTTCATAGATCGGAAGAGCGGTTTCAG
chr2	39216466	39216505	SOS1_9102	+	GTGACCTATGCACCAGACGTAAACAAGAAAAAGTAGATTTTTTTCTTTTCTATTGATATATTAGATCGGAAGAGCGGTTTCAG
chr2	39222539	39222578	SOS1_9103	+	GTGACCTATGCACCAGACGTATCAAAAAGAAACACAATACTTTAAACACTGTAGTAGAAAGAGATCGGAAGAGCGGTTTCAG
chr2	39224577	39224616	SOS1_9104	+	GTGACCTATGCACCAGACGTAAATGGAATGATTTCAAGGATAAAGAAAGAAATGCAAGTAGATCGGAAGAGCGGTTTCAG
chr2	39233681	39233720	SOS1_9105	+	GTGACCTATGCACCAGACGTAAAAAATAGGCCTAAGTTTACAAAAGAAATCAAAGCTTTAGATCGGAAGAGCGGTTTCAG
chr2	39234345	39234384	SOS1_9106	+	GTGACCTATGCACCAGACGTAAAAAAGTGAACATAAAGTTTTAGAGTTTTTCCAATAAAAGATCGGAAGAGCGGTTTCAG

chr2	39237855	39237894	SOS1_9107	+	GTGACCTATGCACCAGACGTCAATACATAATTCTACATGACACTTTTTCTCTAATATAGAGATCGGAAGAGCGGTTTCAG
chr2	39240715	39240754	SOS1_9108	+	GTGACCTATGCACCAGACGTAAACACAGAATTGAATTACATGGGAATCAAACATAAATGTTAGATCGGAAGAGCGGTTTCAG
chr2	39241141	39241180	SOS1_9109	+	GTGACCTATGCACCAGACGTATAGAACAAATTAATGAAAAAGACTAATTATATCGAGTTATAGATCGGAAGAGCGGTTTCAG
chr2	39241998	39242037	SOS1_9110	+	GTGACCTATGCACCAGACGTAAAGGAAAAATATCTTATTAACCTCTATGATTCAAAATGAAGATCGGAAGAGCGGTTTCAG
chr2	39250377	39250416	SOS1_9111	+	GTGACCTATGCACCAGACGTGAAAAAGACATATTAGTACATAGATGACAGAAAACCTAGAGATCGGAAGAGCGGTTTCAG
chr2	39251289	39251328	SOS1_9112	+	GTGACCTATGCACCAGACGTAAATGACAAATCTGAACCCAGTAGTACATTTTTGGATAAAAAGATCGGAAGAGCGGTTTCAG
chr2	39262462	39262501	SOS1_9113	+	GTGACCTATGCACCAGACGTAAAGTGATTTAATTTTTTTTTTAAAGTTTACTTTTTTCAGACATAGATCGGAAGAGCGGTTTCAG
chr2	39262652	39262691	SOS1_9114	+	GTGACCTATGCACCAGACGTAAAGAAGGTAAACATAAAATTTACCATTACAAACACAAAGATCGGAAGAGCGGTTTCAG
chr2	39278439	39278478	SOS1_9115	+	GTGACCTATGCACCAGACGTGAAAACACATTAATTCAGTGAGGCTGTATTATTATAATATAGATCGGAAGAGCGGTTTCAG
chr2	39281975	39282014	SOS1_9116	+	GTGACCTATGCACCAGACGTAGAGATATAAAAAAGTATAATAAAATATGAAGCTTTCGTAAGATCGGAAGAGCGGTTTCAG
chr2	39284018	39284057	SOS1_9117	+	GTGACCTATGCACCAGACGTAAAGAAAAAGCATGTTTAAACATCATATACTGTACATTTAAGATCGGAAGAGCGGTTTCAG
chr2	39285956	39285995	SOS1_9118	+	GTGACCTATGCACCAGACGTAGGAAAAACAACTAAGCAAAAAATATTAATAATAGTGCAGATCGGAAGAGCGGTTTCAG
chr2	39294905	39294944	SOS1_9119	+	GTGACCTATGCACCAGACGTAAAGCAAAGTAAATAAAATGTGGTTCCATATCATTAAACAGATCGGAAGAGCGGTTTCAG
chr2	39347574	39347613	SOS1_9120	+	GTGACCTATGCACCAGACGTGGGCGCCTCTGGGCGGGGAGAGGGGCGCGCGCCGGGCAGATCGGAAGAGCGGTTTCAG
chr2	39250049	39250088	SOS1_9121	+	GTGACCTATGCACCAGACGTGTGTCTATCTTTATCATAAATTTGTACCTTTCGCATAAAAAAGATCGGAAGAGCGGTTTCAG
chr20	36012817	36012856	SRC_9122	+	GTGACCTATGCACCAGACGTGGGCGCGCGGGGTCCTCGCCACCTGGGGCCACGGCGGAGATCGGAAGAGCGGTTTCAG
chr20	36014588	36014627	SRC_9123	+	GTGACCTATGCACCAGACGTCTTCCCTATTGCCCTCAGGGCTGGGTGGTGGGACTTCAAGATCGGAAGAGCGGTTTCAG
chr20	36022407	36022446	SRC_9124	+	GTGACCTATGCACCAGACGTCTCTGGCTGCTTACCCTGCTTCCCTGGACACTGCCGGAGATCGGAAGAGCGGTTTCAG
chr20	36024725	36024764	SRC_9125	+	GTGACCTATGCACCAGACGTCTCCGAGGGCGGAGGGCGGGCGGCAAGCCTCAGCTGCAAGATCGGAAGAGCGGTTTCAG
chr20	36026268	36026307	SRC_9126	+	GTGACCTATGCACCAGACGTGCCCTGCCCTCGGGAGAGGCATCCACCCCCACCCCGTGAGATCGGAAGAGCGGTTTCAG
chr20	36028708	36028747	SRC_9127	+	GTGACCTATGCACCAGACGTGGCGGCGGGGCGAGGGGCGAGGGGCACCTCCGGACAGGGCAAGATCGGAAGAGCGGTTTCAG
chr20	36030092	36030131	SRC_9128	+	GTGACCTATGCACCAGACGTCCCTCCCGCCTCCCCACACCCCTTGGTCTCAAGCACCCAGAGATCGGAAGAGCGGTTTCAG
chr20	36031793	36031832	SRC_9129	+	GTGACCTATGCACCAGACGTGCCAGCCGCTTCTCGGCTGGATCCTGGGCTGGTGGAGATCGGAAGAGCGGTTTCAG
chr9	27158151	27158190	TEK_9130	+	GTGACCTATGCACCAGACGTCTTAAGTTTTGGCGAGGTAGGCCACTGAGGAACACAAAGATCGGAAGAGCGGTTTCAG
chr9	27168614	27168653	TEK_9131	+	GTGACCTATGCACCAGACGTGTTTCATTGCTTTCCCCAGTATGATGTGAGATATCAGATAAGATCGGAAGAGCGGTTTCAG
chr9	27172756	27172795	TEK_9132	+	GTGACCTATGCACCAGACGTAGACTTGATAAGTAAGCTGTGGATTTAAAAAGCCATCGTTAGATCGGAAGAGCGGTTTCAG
chr9	27173371	27173410	TEK_9133	+	GTGACCTATGCACCAGACGTATCACACCTTGACAGAGGATGTTCTAGCAGGTATATAAAGATCGGAAGAGCGGTTTCAG
chr9	27180377	27180416	TEK_9134	+	GTGACCTATGCACCAGACGTGTAACACTGTAGTCAGGGCCATGTTTCAGCATGTCTGAATGATCGGAAGAGCGGTTTCAG
chr9	27183619	27183658	TEK_9135	+	GTGACCTATGCACCAGACGTTTCTTAATTTGCCCTTCTAAAGCATGAGATGCTTCAGTGCAGATCGGAAGAGCGGTTTCAG
chr9	27185638	27185677	TEK_9136	+	GTGACCTATGCACCAGACGTTCCTCCAGAAAAAGGGATGTCCTTGATGCATTATGTTTAGATCGGAAGAGCGGTTTCAG
chr9	27190699	27190738	TEK_9137	+	GTGACCTATGCACCAGACGTGACAGGATAGATGCCAGCTGGGATGTGGCACCCAGGAGAAAGATCGGAAGAGCGGTTTCAG
chr9	27192632	27192671	TEK_9138	+	GTGACCTATGCACCAGACGTGCCAACAGGCATTTATTCATGAGCTGGGTGGGAGGGGAGAGATCGGAAGAGCGGTTTCAG
chr9	27197608	27197647	TEK_9139	+	GTGACCTATGCACCAGACGTGATGCTGCTCCAGCCTCATCTGAGCAATAAGGGGCTACCAGATCGGAAGAGCGGTTTCAG
chr9	27203128	27203167	TEK_9140	+	GTGACCTATGCACCAGACGTGGACAAGTATTTACATAGGATACCCTGCAGCCCTATAGAGATCGGAAGAGCGGTTTCAG
chr9	27205074	27205113	TEK_9141	+	GTGACCTATGCACCAGACGTATCTTCCCTACTAGCTAATAAGGGGCAAGTCCAAGTACAGGCAGATCGGAAGAGCGGTTTCAG
chr9	27206801	27206840	TEK_9142	+	GTGACCTATGCACCAGACGTGACCAGATAGATGCCAGCTGGGATGTGGCACCCAGGAGAAAGATCGGAAGAGCGGTTTCAG
chr9	27209240	27209279	TEK_9143	+	GTGACCTATGCACCAGACGTCTTTTCTGCTTTTCTGCCAGAGTTTTTATAAACAGACAGATCGGAAGAGCGGTTTCAG
chr9	27212906	27212945	TEK_9144	+	GTGACCTATGCACCAGACGTAGGACTTCGCTTTGGATATCTTTCTGTTGGAGTTCCTCTAGATCGGAAGAGCGGTTTCAG
chr9	27213606	27213645	TEK_9145	+	GTGACCTATGCACCAGACGTGACACAGACATGATCGCATCCTTTCCGAGGTAATCCCTAGATCGGAAGAGCGGTTTCAG
chr9	27217767	27217806	TEK_9146	+	GTGACCTATGCACCAGACGTCTTCTATTGCCAAGGATTTTTTTCCCTCCGAAACATAGATCGGAAGAGCGGTTTCAG
chr9	27218826	27218865	TEK_9147	+	GTGACCTATGCACCAGACGTATGTTTATCTACCAGTGAGACTTAGGCAAAAGTGAGTGCAGATCGGAAGAGCGGTTTCAG
chr9	27220154	27220193	TEK_9148	+	GTGACCTATGCACCAGACGTCTCATCTGGGGCTATTTTGTCTTACCTTCCCTCTGTAGATCGGAAGAGCGGTTTCAG
chr9	27228314	27228353	TEK_9149	+	GTGACCTATGCACCAGACGTAAAGTCAGGCAGGAGATCTTAATTGGAATACCTGATGTGCAGATCGGAAGAGCGGTTTCAG
chr9	27229241	27229280	TEK_9150	+	GTGACCTATGCACCAGACGTCTGTATACCCTCTGTTTCCCTTCACTGGCATGGGAGACCAGATCGGAAGAGCGGTTTCAG
chr17	38545910	38545949	TOP2A_9151	+	GTGACCTATGCACCAGACGTAAAGCCCAGGTAACCTGCACATTTGTAATCTGACAACATAAGATCGGAAGAGCGGTTTCAG
chr17	38547903	38547942	TOP2A_9152	+	GTGACCTATGCACCAGACGTAAATGGAAGGAAAATAGTACATTTAAGCAACACATGAAAGATCGGAAGAGCGGTTTCAG
chr17	38548374	38548413	TOP2A_9153	+	GTGACCTATGCACCAGACGTAAAAAAAATCCTGACAACCAATTTCTAAATGTGTCAAGCAAGATCGGAAGAGCGGTTTCAG
chr17	38548604	38548643	TOP2A_9154	+	GTGACCTATGCACCAGACGTAAACATATACAAAAAATCAAAGAGGGTAGTAGGAGAAACAGATCGGAAGAGCGGTTTCAG
chr17	38549000	38549039	TOP2A_9155	+	GTGACCTATGCACCAGACGTGATAGAAATTAATCACTTTATATATAGACCCACTTTTCAGATCGGAAGAGCGGTTTCAG
chr17	38551802	38551841	TOP2A_9156	+	GTGACCTATGCACCAGACGTGCAAAGTTAGGGTTGGATATAGAATAAATCTGAACTATGAGATCGGAAGAGCGGTTTCAG
chr17	38552728	38552767	TOP2A_9157	+	GTGACCTATGCACCAGACGTGATATAAGAAGCAAGTTAAATGTTAACAAAAACATACAGATCGGAAGAGCGGTTTCAG
chr17	38554904	38554943	TOP2A_9158	+	GTGACCTATGCACCAGACGTAAATACAAAATGATTAATATATGTATACAAGCAGCATGATCGGAAGAGCGGTTTCAG
chr17	38555200	38555239	TOP2A_9159	+	GTGACCTATGCACCAGACGTAAATAAAATCTAGCTTTATTAGAAAATGTGAAACATAAACAGATCGGAAGAGCGGTTTCAG
chr17	38555394	38555433	TOP2A_9160	+	GTGACCTATGCACCAGACGTAAAAGTAAACAGAGATAATGATTTTGTAGTAATATTTAGGAGATCGGAAGAGCGGTTTCAG
chr17	38556330	38556369	TOP2A_9161	+	GTGACCTATGCACCAGACGTAAAAACAAGATTAGAGCCAAGAATAGACAAATTTGGCTAAACAGATCGGAAGAGCGGTTTCAG
chr17	38556672	38556711	TOP2A_9162	+	GTGACCTATGCACCAGACGTAAATAATCTGAAGTTTCTAAATATAAGGCTTCTGAATAGAGATCGGAAGAGCGGTTTCAG
chr17	38556926	38556965	TOP2A_9163	+	GTGACCTATGCACCAGACGTAAATAAAAAAGCATGTTTTCTAAATGTGATACTAGACAGATCGGAAGAGCGGTTTCAG
chr17	38557344	38557383	TOP2A_9164	+	GTGACCTATGCACCAGACGTGAAAACAAGATGTTATTTTACAAAATACTGAATTTACAGATCGGAAGAGCGGTTTCAG

chr17	38559317	38559356	TOP2A_9165	+	GTGACCTATGCACCAGACGTA AAAAGATT CATAAGCTGAGGCTTTTACTAATACAATAAGATCGGAAGAGCGGTTTCAG
chr17	38560536	38560575	TOP2A_9166	+	GTGACCTATGCACCAGACGTA AATAAGAGCAAACGTAAGTATCCTCAATTTAACCAATTTAGATCGGAAGAGCGGTTTCAG
chr17	38560754	38560793	TOP2A_9167	+	GTGACCTATGCACCAGACGTA AATAGTATTACATGAGTCTACCGGTCTAAACAATGCTCAAGATCGGAAGAGCGGTTTCAG
chr17	38561146	38561185	TOP2A_9168	+	GTGACCTATGCACCAGACGTA AGGATGAAAAGATGCTACTGGTACTAATAGGCTAATAGGAGATCGGAAGAGCGGTTTCAG
chr17	38562756	38562795	TOP2A_9169	+	GTGACCTATGCACCAGACGTA AAAATACCAAGTTCCTTCATATAGTCTTTGTACAGGGTGTAGATCGGAAGAGCGGTTTCAG
chr17	38562952	38562991	TOP2A_9170	+	GTGACCTATGCACCAGACGTA AACAATGACTGTGGCTTTGTGACTGTGGGGTCCCCTGTAGATCGGAAGAGCGGTTTCAG
chr17	38563937	38563976	TOP2A_9171	+	GTGACCTATGCACCAGACGTA TATACCAAAAAAGCATCGCTTTATAAATTTGAAAAAGAAAGATCGGAAGAGCGGTTTCAG
chr17	38564893	38564932	TOP2A_9172	+	GTGACCTATGCACCAGACGTA AAGATT CATATTAGGGATCATATTAGGGAAGAAGGGATCAGATCGGAAGAGCGGTTTCAG
chr17	38567509	38567548	TOP2A_9173	+	GTGACCTATGCACCAGACGTA GTT GATATTAAGCCACTAAAAATGACTCATGCTTTATTAGATCGGAAGAGCGGTTTCAG
chr17	38567718	38567757	TOP2A_9174	+	GTGACCTATGCACCAGACGTA AAAATACCAAACCTGTAAAACTCAGTATCCTCAAATTTATAAGATCGGAAGAGCGGTTTCAG
chr17	38568081	38568120	TOP2A_9175	+	GTGACCTATGCACCAGACGTA TAAAGGTAACAGTATTAAGAAGTTATTA AAAAATAGGAGATCGGAAGAGCGGTTTCAG
chr17	38569234	38569273	TOP2A_9176	+	GTGACCTATGCACCAGACGTA AAGAATAGGAAACATGAAAAATCAAGTCATCTCACAAAAGATCGGAAGAGCGGTTTCAG
chr17	38569555	38569594	TOP2A_9177	+	GTGACCTATGCACCAGACGTA AATATGAAACACTATTTTTATTGTTACTATCTCATTGACAAAGATCGGAAGAGCGGTTTCAG
chr17	38569888	38569927	TOP2A_9178	+	GTGACCTATGCACCAGACGTA AGATTGAAAATTTGATTTTACAACACATTAACCGAATGCGATCGGAAGAGCGGTTTCAG
chr17	38572331	38572370	TOP2A_9179	+	GTGACCTATGCACCAGACGTA TAAAATATACATTTGTAAGAAATTAGTGTTTTAAGAAACAGATCGGAAGAGCGGTTTCAG
chr17	38572775	38572814	TOP2A_9180	+	GTGACCTATGCACCAGACGTA GGCAAAGAAATACTGTTATTTTTATTCTATATTCATTGTTAGATCGGAAGAGCGGTTTCAG
chr17	38573158	38573197	TOP2A_9181	+	GTGACCTATGCACCAGACGTA AAAAAAGAGAGAAGAAAGGGAATTTTTAATCATAAGTTAGATCGGAAGAGCGGTTTCAG
chr17	38574054	38574093	TOP2A_9182	+	GTGACCTATGCACCAGACGTA GTGAAAGGGGCTCAAGAACCCTGAAAGCGACTAAACAGGCAAGATCGGAAGAGCGGTTTCAG
chr1	154130208	154130247	TPM3_9183	+	GTGACCTATGCACCAGACGTA AAGGAGAGAAGTTACAAGAAC TAGAAGTAAATTTCAAGAGATCGGAAGAGCGGTTTCAG
chr1	154140427	154140466	TPM3_9184	+	GTGACCTATGCACCAGACGTA AGTAAGGATACTTAGGTGAGAAGGACTAGCATCAATCTAGATCGGAAGAGCGGTTTCAG
chr1	154141870	154141909	TPM3_9185	+	GTGACCTATGCACCAGACGTA CAGGAACACAGGGAGGAATGAGGGGACAGAGTGAAGAGAGATCGGAAGAGCGGTTTCAG
chr1	154142956	154142995	TPM3_9186	+	GTGACCTATGCACCAGACGTT ATGAAATTAGTCAGAACCAGAGATGAAGACAAAAGAAAGATCGGAAGAGCGGTTTCAG
chr1	154143198	154143237	TPM3_9187	+	GTGACCTATGCACCAGACGTA GATAGATAAAAATTTAGATGAGAAATTAGTCACACAGGAGATCGGAAGAGCGGTTTCAG
chr1	154143975	154144014	TPM3_9188	+	GTGACCTATGCACCAGACGTT TTAAGTACACAGGAGGAAAAGGAAAGGAAAGATCGGAAGAGCGGTTTCAG
chr1	154144591	154144630	TPM3_9189	+	GTGACCTATGCACCAGACGTT AGTACGCGGGATGGCACAAGCCAGGTTGTGGGGAGGGAGAGATCGGAAGAGCGGTTTCAG
chr1	154145465	154145504	TPM3_9190	+	GTGACCTATGCACCAGACGTA GATCCCAGTATAGCTTAGTGAAGCAAAGGAGCCATTTACAGATCGGAAGAGCGGTTTCAG
chr1	154145688	154145727	TPM3_9191	+	GTGACCTATGCACCAGACGTA GACAAAAGCAATACTGACACCCTGAGGAGTGTGTCTGATAGATCGGAAGAGCGGTTTCAG
chr1	154148735	154148774	TPM3_9192	+	GTGACCTATGCACCAGACGTA GAAAGAATGGACAAGGGAAAGCAGAGGCATGGAGAAAAGAGATCGGAAGAGCGGTTTCAG
chr1	154155606	154155645	TPM3_9193	+	GTGACCTATGCACCAGACGTA CAGTACTGCTCCGCTCCGGTCCAGTGCCTCCTCCGCTCGAGATCGGAAGAGCGGTTTCAG
chr1	154163798	154163837	TPM3_9194	+	GTGACCTATGCACCAGACGTC CAGAGAGTCAACACAAAAACACACAAAACAAACAAATCGAGATCGGAAGAGCGGTTTCAG
chr1	154164505	154164544	TPM3_9195	+	GTGACCTATGCACCAGACGTT GTTGGTAGGCTCACCTGTGAACACTGGAGAACTGGAGACAGATCGGAAGAGCGGTTTCAG
chr9	107546747	107546786	ABCA1_9196	+	GTGACCTATGCACCAGACGTA TTAAGATGGACCTTTATAAATACC ACTCAACTTGCTCATAGATCGGAAGAGCGGTTTCAG
chr9	107547931	107547970	ABCA1_9197	+	GTGACCTATGCACCAGACGTA AAAAAATACCCAAATGGAGGATCTCCAGAAA ACTATTTAAGATCGGAAGAGCGGTTTCAG
chr9	107548682	107548721	ABCA1_9198	+	GTGACCTATGCACCAGACGTA CAGAAAGAGGTTTTAGTTTTAGAGAGATTCTCTGTAACCAGATCGGAAGAGCGGTTTCAG
chr9	107549268	107549307	ABCA1_9199	+	GTGACCTATGCACCAGACGTA AATAAATAAGTCTTATTTTGTGGGGGAAAAAAAATCAAAGATCGGAAGAGCGGTTTCAG
chr9	107550346	107550385	ABCA1_9200	+	GTGACCTATGCACCAGACGTA AAAAGCACCTTGACTTTGGTCTGGCTTGGGAATTTTATCAGATCGGAAGAGCGGTTTCAG
chr9	107550859	107550898	ABCA1_9201	+	GTGACCTATGCACCAGACGTA CAGAAA ACTACTTAGATTTAAGCAGGTAGAGATACTCTAGATCGGAAGAGCGGTTTCAG
chr9	107553320	107553359	ABCA1_9202	+	GTGACCTATGCACCAGACGTA AGATTAAAGTTGTATAAGCAA ACTCTAAAACATGAATATAGATCGGAAGAGCGGTTTCAG
chr9	107554290	107554329	ABCA1_9203	+	GTGACCTATGCACCAGACGTA CAAAATGTAACATTCATAAGCCTCAGT GACTCACAGCTCAGATCGGAAGAGCGGTTTCAG
chr9	107555198	107555237	ABCA1_9204	+	GTGACCTATGCACCAGACGTA AAAACAAGAAAAATGAACTTTCAA ACTATTTTTCAGGACAGATCGGAAGAGCGGTTTCAG
chr9	107555592	107555631	ABCA1_9205	+	GTGACCTATGCACCAGACGTA ATGCAGAGATCCGGTCAAGATGGAGGGATCAA AAAACAAAGATCGGAAGAGCGGTTTCAG
chr9	107556802	107556841	ABCA1_9206	+	GTGACCTATGCACCAGACGTA AAAAAAAAATGGGAGGGAAGGGAGGGT GAGGGAGAGAAGATCGGAAGAGCGGTTTCAG
chr9	107558489	107558528	ABCA1_9207	+	GTGACCTATGCACCAGACGTA CAAAAAGATAAGTGTCTACTGAGAGTCCCTGCCTCCTTAGATCGGAAGAGCGGTTTCAG
chr9	107558716	107558755	ABCA1_9208	+	GTGACCTATGCACCAGACGTA AACAAAGACATCCAGTTACCCCTAA ATCAAATATACAAAGATCGGAAGAGCGGTTTCAG
chr9	107560890	107560929	ABCA1_9209	+	GTGACCTATGCACCAGACGTA AAGCGTGTGAAAATCTGAGGGGCTTTTGATGCGATTTAGGAGATCGGAAGAGCGGTTTCAG
chr9	107562280	107562319	ABCA1_9210	+	GTGACCTATGCACCAGACGTA CACTACAGTACAGTACAGTCCAGTCCCAACCCGGCTCCTAGATCGGAAGAGCGGTTTCAG
chr9	107562876	107562915	ABCA1_9211	+	GTGACCTATGCACCAGACGTA CAGAAACCTGCCTCAGTTGTGACTGTT CACATAGATAAGGAGATCGGAAGAGCGGTTTCAG
chr9	107564451	107564490	ABCA1_9212	+	GTGACCTATGCACCAGACGTA GCCTGACATTA AACCCAGACAGTGGGGTGCACAGTATCAGATCGGAAGAGCGGTTTCAG
chr9	107565608	107565647	ABCA1_9213	+	GTGACCTATGCACCAGACGTA AAGAAAACAAAAATCAGTTCAAAGAAAGCACTGAGCCTAAGATCGGAAGAGCGGTTTCAG
chr9	107567012	107567051	ABCA1_9214	+	GTGACCTATGCACCAGACGTA TAAAAACCAAGCATACGGGCTTTTATAGACAAGAATGAAGATCGGAAGAGCGGTTTCAG
chr9	107568722	107568761	ABCA1_9215	+	GTGACCTATGCACCAGACGTA AGACAGCAAGAGTAGGATTACAGAGATGGCTTGGCCTTAGATCGGAAGAGCGGTTTCAG
chr9	107571856	107571895	ABCA1_9216	+	GTGACCTATGCACCAGACGTA GAGAGGACGCCAGCTTAGTAATTCAT TAAAACAGCAAAAGATCGGAAGAGCGGTTTCAG
chr9	107573216	107573255	ABCA1_9217	+	GTGACCTATGCACCAGACGTA GCAGTGGAGGGGGCAGGGGGACAGCAGGAAACGGCAAGT GAGATCGGAAGAGCGGTTTCAG
chr9	107575014	107575053	ABCA1_9218	+	GTGACCTATGCACCAGACGTA CAACACTGAAGGTCACCTATTATCTTAGGTGTTTTCGGCAGATCGGAAGAGCGGTTTCAG
chr9	107576523	107576562	ABCA1_9219	+	GTGACCTATGCACCAGACGTA AGGAAAGAAATCCATACTTTATTTATTTACAACAAAACAGATCGGAAGAGCGGTTTCAG
chr9	107576767	107576806	ABCA1_9220	+	GTGACCTATGCACCAGACGTA GAGAGATGAGAACAATATAAGCACAACATTACGAGAGTAGATCGGAAGAGCGGTTTCAG
chr9	107578637	107578676	ABCA1_9221	+	GTGACCTATGCACCAGACGTA GAATGCAAGATGGCTCACTCAACTCAGAGGGGCTTCAGATCGGAAGAGCGGTTTCAG
chr9	107579696	107579735	ABCA1_9222	+	GTGACCTATGCACCAGACGTA AAGAGGAGGTGAGAACGGGTACGGGACGGAGCAAGGCAGAAAGATCGGAAGAGCGGTTTCAG

chr9	107581175	107581214	ABCA1_9223	+	GTGACCTATGCACCAGACGTCAAACACAAGGATGTGGGACAGGTGAGGCCCTCTCAGTTCTAGATCGGAAGAGCGGTTTCAG
chr9	107582015	107582054	ABCA1_9224	+	GTGACCTATGCACCAGACGTACAGAGCAAAGCAAACTCCAGACCAGCCCCAGACAGTGAAGATCGGAAGAGCGGTTTCAG
chr9	107582361	107582400	ABCA1_9225	+	GTGACCTATGCACCAGACGTGGAGGCAGGTCTGCTGGGCCCTACTGGATACCCAGAAAGATCGGAAGAGCGGTTTCAG
chr9	107583798	107583837	ABCA1_9226	+	GTGACCTATGCACCAGACGTAAATTTAGAAGTACAGAAGTCAAGGTTGACCTACCCCTAAAGATCGGAAGAGCGGTTTCAG
chr9	107584959	107584998	ABCA1_9227	+	GTGACCTATGCACCAGACGTAGAGAAGACAGAAATGAACCCACAGAAAGCACTGAGGAGTAGATCGGAAGAGCGGTTTCAG
chr9	107586870	107586909	ABCA1_9228	+	GTGACCTATGCACCAGACGTAGCAGCAGGTATGACCCAAGCTCAGCATATCCCAGTATTCAGATCGGAAGAGCGGTTTCAG
chr9	107588179	107588218	ABCA1_9229	+	GTGACCTATGCACCAGACGTGAGGAAAGTACAGTACCTTCCATTTCTGGTTCAGTCTCATTTAGATCGGAAGAGCGGTTTCAG
chr9	107589461	107589500	ABCA1_9230	+	GTGACCTATGCACCAGACGTAGAGACACATCAAATGTGCTGCCTCAACAATCCCAAGCACAGATCGGAAGAGCGGTTTCAG
chr9	107591430	107591469	ABCA1_9231	+	GTGACCTATGCACCAGACGTCAAGGAAGGACAAGGGGAGAAAGAAAGACACACGTGAGCCAGATCGGAAGAGCGGTTTCAG
chr9	107594119	107594158	ABCA1_9232	+	GTGACCTATGCACCAGACGTAAACAGCCTTCATGAGAAGCTTGGCAGCCAGACAACAAGCAGATCGGAAGAGCGGTTTCAG
chr9	107595063	107595102	ABCA1_9233	+	GTGACCTATGCACCAGACGTAGTGAGAAAAGTACAAGTAGTAAACACCAACTAAATCTTGAAGATCGGAAGAGCGGTTTCAG
chr9	107599388	107599427	ABCA1_9234	+	GTGACCTATGCACCAGACGTGTGGGGAGCCAGGACCCGACGAAAAAGGAGGAGAAGCACAAGATCGGAAGAGCGGTTTCAG
chr9	107599859	107599898	ABCA1_9235	+	GTGACCTATGCACCAGACGTGAGGAGAGACAATACTCATATGTCATGTCATATACTGATAGATCGGAAGAGCGGTTTCAG
chr9	107607861	107607900	ABCA1_9236	+	GTGACCTATGCACCAGACGTAAAGAAAACCTTTGTTTCTGAATTCAAATGTAAACCTGAAAAGATCGGAAGAGCGGTTTCAG
chr9	107620990	107621029	ABCA1_9237	+	GTGACCTATGCACCAGACGTTCATGCAAAGAGAGACAAGCACAAGAGGATTATGAAGATAGATCGGAAGAGCGGTTTCAG
chr9	107624092	107624131	ABCA1_9238	+	GTGACCTATGCACCAGACGTATAGTGTATTTATTTTATTTAGTAAAGTAACTCAAAAAAAGATCGGAAGAGCGGTTTCAG
chr9	107645449	107645488	ABCA1_9239	+	GTGACCTATGCACCAGACGTTGCAAGAAAAGGCCGAAAGCTTTAGCTAGGCCAAGCTGCTAGATCGGAAGAGCGGTTTCAG
chr9	107646860	107646899	ABCA1_9240	+	GTGACCTATGCACCAGACGTGAGGAGTAGAAAACACAGGAGGAGAAACATAATTCCCTGAGATCGGAAGAGCGGTTTCAG
chr9	107651487	107651526	ABCA1_9241	+	GTGACCTATGCACCAGACGTAAAGATAGAACTGTAAATTTAAAAATAATATGGATAAGATCGGAAGAGCGGTTTCAG
chr9	107665971	107666010	ABCA1_9242	+	GTGACCTATGCACCAGACGTCCAGCACCCCCAGCGTGTGGCTCGGGAGCCCTGGAAGGCAAGATCGGAAGAGCGGTTTCAG
chr19	1453152	1453191	APC2_9243	+	GTGACCTATGCACCAGACGTACATGGAGGAGGTGGGCTAGGGTCCCGGGTGGTGCCCCAGATCGGAAGAGCGGTTTCAG
chr19	1453347	1453386	APC2_9244	+	GTGACCTATGCACCAGACGTGGGCCACCCGACAGAGGGAGTGGGGGAGGCTGGGGGAAAAGATCGGAAGAGCGGTTTCAG
chr19	1453621	1453660	APC2_9245	+	GTGACCTATGCACCAGACGTGTGGGAACCCAGCCCTCGGCGAGCTGGGATGACTCGGTTCAGATCGGAAGAGCGGTTTCAG
chr19	1455267	1455306	APC2_9246	+	GTGACCTATGCACCAGACGTGCGGGAGCCAGGGGACCGCCGCGCCGACTCGAAGGTGAGATCGGAAGAGCGGTTTCAG
chr19	1455510	1455549	APC2_9247	+	GTGACCTATGCACCAGACGTGGGCGGGGTGGCGCGCGGTAGGCGGGGCCCTGCGCCAGTAGATCGGAAGAGCGGTTTCAG
chr19	1456163	1456202	APC2_9248	+	GTGACCTATGCACCAGACGTGGGCAGAGCCAGGGACCAGGGTGGTGTGCGGCCAGGCAGAGATCGGAAGAGCGGTTTCAG
chr19	1456414	1456453	APC2_9249	+	GTGACCTATGCACCAGACGTGGGTGAAACGGGGCTGGCGCAGCTGTCTGGGCTGGAAGGAGATCGGAAGAGCGGTTTCAG
chr19	1457253	1457292	APC2_9250	+	GTGACCTATGCACCAGACGTGGCCTGTGGGGCCCTCCGCGCAATTAACGTGCAGCTAGAGATCGGAAGAGCGGTTTCAG
chr19	1458070	1458109	APC2_9251	+	GTGACCTATGCACCAGACGTGAGTCCCTTGGGAAGCCCTCCAGCCCCGAACAGGTAGATCGGAAGAGCGGTTTCAG
chr19	1460330	1460369	APC2_9252	+	GTGACCTATGCACCAGACGTGCAGTGGGTGGGCTGGCCTTCTCCATCCAGTCTTCCAGAGATCGGAAGAGCGGTTTCAG
chr19	1460867	1460906	APC2_9253	+	GTGACCTATGCACCAGACGTGGGTGCTGGGAAAGCCTTCCAGGGTGTCCCTGATAGGCAGAGATCGGAAGAGCGGTTTCAG
chr19	1461163	1461202	APC2_9254	+	GTGACCTATGCACCAGACGTGGTGGCGGCGAGGATGCTTCTCAGTCACTGGAAGGAGAAGATCGGAAGAGCGGTTTCAG
chr19	1462187	1462226	APC2_9255	+	GTGACCTATGCACCAGACGTACCCCCCTACCCGACACACAGGACGCTGCGCTCGGGGCGGGAGATCGGAAGAGCGGTTTCAG
chr19	1470223	1470262	APC2_9256	+	GTGACCTATGCACCAGACGTGGGCTTCTGGAACGTTCTCTCCCGCCCTGCGGGCGGGTAGATCGGAAGAGCGGTTTCAG
chr19	1465624	1465663	APC2_9257	+	GTGACCTATGCACCAGACGTCCGGCTGCTTTGACGACAGCAGTACCGGCTGACCCCTGATCCCTGCGAGATCGGAAGAGCGGTTTCAG
chr19	1466084	1466123	APC2_9258	+	GTGACCTATGCACCAGACGTGAGCGGAGTGGCAGCGACGGTACTGCCACGCGAACAATAGATCGGAAGAGCGGTTTCAG
chr19	1466544	1466583	APC2_9259	+	GTGACCTATGCACCAGACGTCCAGGCCCCAGCGAGGGTGGTGCCTGGATGACAGTACTAGATCGGAAGAGCGGTTTCAG
chr19	1467004	1467043	APC2_9260	+	GTGACCTATGCACCAGACGTGCTACGTGAAGCGTTCCTGGACATCGCCGACTGCCGGGAAGATCGGAAGAGCGGTTTCAG
chr19	1467464	1467503	APC2_9261	+	GTGACCTATGCACCAGACGTCTGCACGTGACTCCGCGGAGGGCACGCGGTTCAACTTCTAGATCGGAAGAGCGGTTTCAG
chr19	1467924	1467963	APC2_9262	+	GTGACCTATGCACCAGACGTCCGACGGCCGGAAGGAGCCCTCCGCCGTTCAAGGCTGAGATCGGAAGAGCGGTTTCAG
chr19	1468384	1468423	APC2_9263	+	GTGACCTATGCACCAGACGTAATTGTACGTGCTGACAGGACAGGACGCTGCCACGCGAGATCGGAAGAGCGGTTTCAG
chr19	1468844	1468883	APC2_9264	+	GTGACCTATGCACCAGACGTGACCTCGGAGCTGGCGACGCTGAGCCAGCCCCCAGAAGCAGATCGGAAGAGCGGTTTCAG
chr19	1469304	1469343	APC2_9265	+	GTGACCTATGCACCAGACGTCCGGGCTTGGCGGCCCGGCTCCGAGCTGTCTCGGCCGAGATCGGAAGAGCGGTTTCAG
chr19	1469764	1469803	APC2_9266	+	GTGACCTATGCACCAGACGTCCCACATCTGCGCAGCAGCTTCCCGCCACGCGCCTGCCAGATCGGAAGAGCGGTTTCAG
chr20	54945407	54945446	AURKA_9267	+	GTGACCTATGCACCAGACGTACAATGATAAAATACAAAACACAGGTTAGAGAGATCAGATCGGAAGAGCGGTTTCAG
chr20	54945726	54945765	AURKA_9268	+	GTGACCTATGCACCAGACGTAGGGAGGCTCAGTTGATGCTCTCGTTTTATGATCACAGATCGGAAGAGCGGTTTCAG
chr20	54948623	54948662	AURKA_9269	+	GTGACCTATGCACCAGACGTAATATTGAAAGCCTATGTTTTAGATTTATATAACACAAGAGATCGGAAGAGCGGTTTCAG
chr20	54956638	54956677	AURKA_9270	+	GTGACCTATGCACCAGACGTGGATAAACATTCTAACACTTGGTTTGGAGCTCACAGAAGAAGATCGGAAGAGCGGTTTCAG
chr20	54958243	54958282	AURKA_9271	+	GTGACCTATGCACCAGACGTTTTGAACACTTTAGAATGTGAAGAAAAACAAGCTTTTCTAAGATCGGAAGAGCGGTTTCAG
chr20	54959391	54959430	AURKA_9272	+	GTGACCTATGCACCAGACGTTAAGTAAAAACCTGTTTTAGATAAATATATAGGATAAAGATCGGAAGAGCGGTTTCAG
chr20	54961600	54961639	AURKA_9273	+	GTGACCTATGCACCAGACGTAGAGAAAATAAATCTTGGCATTATGAAAGCAAAGATAGATCGGAAGAGCGGTTTCAG
chr20	54963264	54963303	AURKA_9274	+	GTGACCTATGCACCAGACGTAAGAAAAAGAAAGAACTTTAATTTGAACAAAAGCAACTGCAGATCGGAAGAGCGGTTTCAG
chr6	41903856	41903895	CCND3_9275	+	GTGACCTATGCACCAGACGTGGGAGAAGAGTGAAGGAGCAAACACTCCCCCATAGCATCTAGATCGGAAGAGCGGTTTCAG
chr6	41904430	41904469	CCND3_9276	+	GTGACCTATGCACCAGACGTTAATCTTGGAGAGGAGAAAGGGAACCATGAGAGAAGGAAAGATCGGAAGAGCGGTTTCAG
chr6	41904444	41904483	CCND3_9277	+	GTGACCTATGCACCAGACGTAGGAAAGGGAAACCATGAGAGAAGGAAACCTGAAGGATAACAGATCGGAAGAGCGGTTTCAG
chr6	41905143	41905182	CCND3_9278	+	GTGACCTATGCACCAGACGTGGGGAAAGGGTGGGCTCAGTGGCTGGAGAAGTGAAGAGGAAGATCGGAAGAGCGGTTTCAG
chr6	41908289	41908328	CCND3_9279	+	GTGACCTATGCACCAGACGTAAGACTTCTCAGCAGCTGCTCCTCACATACCTGGGAGATCGGAAGAGCGGTTTCAG
chr6	41908334	41908373	CCND3_9280	+	GTGACCTATGCACCAGACGTGCGCACAGTCTGCTGGGCTGAGGCTGGGGAACACAGAGATCGGAAGAGCGGTTTCAG



chr6	41909398	41909437	CCND3_9281	+	GTGACCTATGCACCAGACGTCGAACAGGCAGGGCGGGAGTGCGGGCTCGCGAGTCCCAAGAGATCGGAAGAGCGGTTTCAG
chrX	135730574	135730613	CD40LG_9282	+	GTGACCTATGCACCAGACGTCACCAAGCCTTTATTAACATAAATTTGGGGTCTTACTAATAGATCGGAAGAGCGGTTTCAG
chrX	135732567	135732606	CD40LG_9283	+	GTGACCTATGCACCAGACGTTAATTACTGGTAAAAGTGTCAATTGAAATATTTACTACATAGATCGGAAGAGCGGTTTCAG
chrX	135736600	135736639	CD40LG_9284	+	GTGACCTATGCACCAGACGTTATTTGCTAATTTCTATGAATGCCTAAAACTAAAAGGAAAGATCGGAAGAGCGGTTTCAG
chrX	135738588	135738627	CD40LG_9285	+	GTGACCTATGCACCAGACGTCAGCATCTGAGCGGTAGCCACCCAAGGGGAAAAGGCTGGGAAGATCGGAAGAGCGGTTTCAG
chrX	135741585	135741624	CD40LG_9286	+	GTGACCTATGCACCAGACGTTCTTGAGCCTGTGGTGGAGCTGACGCTGGGAGTCTTTCATAAGATCGGAAGAGCGGTTTCAG
chr13	28537517	28537556	CDX2_9287	+	GTGACCTATGCACCAGACGTTAAAGGTGGAGAAAAGCATTGTGGTGAAGATGTGAGGGAAAGATCGGAAGAGCGGTTTCAG
chr13	28539163	28539202	CDX2_9288	+	GTGACCTATGCACCAGACGTAGGAGAAAGTGAAGGGCTGAGAACTGCAAGGCAGCCCATCAGAGATCGGAAGAGCGGTTTCAG
chr13	28543154	28543193	CDX2_9289	+	GTGACCTATGCACCAGACGTGCCGGGAGCAGACCTCACCATGCTGCCTGGGGACCGACGAGATCGGAAGAGCGGTTTCAG
chr15	51503264	51503303	CYP19A1_9290	+	GTGACCTATGCACCAGACGTGATCAGACAGTTAGCCAGAAATATAAAGGCTAGAGTCACTAGATCGGAAGAGCGGTTTCAG
chr15	51504769	51504808	CYP19A1_9291	+	GTGACCTATGCACCAGACGTAGATAAAAGGAACAAAGAAAGGTAAATGTTAGTTCATCTGAGATCGGAAGAGCGGTTTCAG
chr15	51507440	51507479	CYP19A1_9292	+	GTGACCTATGCACCAGACGTGGAAGATGGGAAAAATTTGGAAAACTGAACTCAAAGTTTCAAGATCGGAAGAGCGGTTTCAG
chr15	51508025	51508064	CYP19A1_9293	+	GTGACCTATGCACCAGACGTAGTCAAAAATTTGCTATTTTTACTAGTATTAGACATCTAAGATCGGAAGAGCGGTTTCAG
chr15	51510863	51510902	CYP19A1_9294	+	GTGACCTATGCACCAGACGTAAAAAACACACATACACAAGAAAGAGCAGTTGAGCAAATAGATCGGAAGAGCGGTTTCAG
chr15	51514733	51514772	CYP19A1_9295	+	GTGACCTATGCACCAGACGTACATCAGAGAATCAGCCATCAGAACTCCAGGGCACACAAGATCGGAAGAGCGGTTTCAG
chr15	51520141	51520180	CYP19A1_9296	+	GTGACCTATGCACCAGACGTAGGAAACTTTGGTGTCAATTTTTAAGGGTCAAGGAACTCAGATCGGAAGAGCGGTTTCAG
chr15	51529217	51529256	CYP19A1_9297	+	GTGACCTATGCACCAGACGTTGTACAGACATAAGCAACATCTTAGTACACCAAAAATGAGATCGGAAGAGCGGTTTCAG
chr15	51535120	51535159	CYP19A1_9298	+	GTGACCTATGCACCAGACGTTGACCTGACAGAGGGGCCAATTTAGACTCCTGTGGAAATCAAGATCGGAAGAGCGGTTTCAG
chr20	31367962	31368001	DNMT3B_9299	+	GTGACCTATGCACCAGACGTGGCTATGGGGGCGAGCTGGGTGGGTACTTGGGCAAGAGAGATCGGAAGAGCGGTTTCAG
chr20	31368282	31368321	DNMT3B_9300	+	GTGACCTATGCACCAGACGTAGTGGGGACTGGGGTGGTGTACAGGCGTGACATAGTGAAGCAGATCGGAAGAGCGGTTTCAG
chr20	31369231	31369270	DNMT3B_9301	+	GTGACCTATGCACCAGACGTTGCTCTCCCTTTTTAGGGCTCAGGGACTTTGCTTTGGCAGATCGGAAGAGCGGTTTCAG
chr20	31372676	31372715	DNMT3B_9302	+	GTGACCTATGCACCAGACGTACACCTCGAGCCAAAGCACTTGTGGCCAACACTCTACATAAGATCGGAAGAGCGGTTTCAG
chr20	31374444	31374483	DNMT3B_9303	+	GTGACCTATGCACCAGACGTGAGTCCCAAGCCTCAGGCGAGTCTCTAACTGGGAGAGATCGGAAGAGCGGTTTCAG
chr20	31375268	31375307	DNMT3B_9304	+	GTGACCTATGCACCAGACGTGAGGGGCTCCTCGCCAGGGTGACTGAGGACCTGAACACGAGATCGGAAGAGCGGTTTCAG
chr20	31376829	31376868	DNMT3B_9305	+	GTGACCTATGCACCAGACGTGGAAGGGCAAGGGGTTCTGCAGGCTGAGGCTGTCCCTGCAGATCGGAAGAGCGGTTTCAG
chr20	31379525	31379564	DNMT3B_9306	+	GTGACCTATGCACCAGACGTGAGGGAAATGAGGGCTAAGCCCTGAGAGCAGGGATGAAGAGATCGGAAGAGCGGTTTCAG
chr20	31380587	31380626	DNMT3B_9307	+	GTGACCTATGCACCAGACGTGCCCATGGCAGCACCCGCTGCCTCTGCTGGTGGGACCAAGATCGGAAGAGCGGTTTCAG
chr20	31381412	31381451	DNMT3B_9308	+	GTGACCTATGCACCAGACGTCCTGTCCTTTGACTGTGCCCTGTTTCTATGCACCTTCTTAGATCGGAAGAGCGGTTTCAG
chr20	31383351	31383390	DNMT3B_9309	+	GTGACCTATGCACCAGACGTGGTACTGGGATCTGGACAGATGGGAGGAGCAGCTGCAGATCGGAAGAGCGGTTTCAG
chr20	31383511	31383550	DNMT3B_9310	+	GTGACCTATGCACCAGACGTCCTCCCTCCCATGTCATCCCTCCACACCTGGCTAGGGCTCAGATCGGAAGAGCGGTTTCAG
chr20	31384686	31384725	DNMT3B_9311	+	GTGACCTATGCACCAGACGTCTACTACTGCCCTGGACCTTCCCTCCCTTGCCTCCTCTAAAGATCGGAAGAGCGGTTTCAG
chr20	31385116	31385155	DNMT3B_9312	+	GTGACCTATGCACCAGACGTGGCCCTGTGGGGTGGATGTGGGTGGGCCCCCAAGGCTCCTAGATCGGAAGAGCGGTTTCAG
chr20	31386460	31386499	DNMT3B_9313	+	GTGACCTATGCACCAGACGTGGCTCCCGCCTCTACCACCACAGATCCCAAGGGGCACAGGGAGATCGGAAGAGCGGTTTCAG
chr20	31387145	31387184	DNMT3B_9314	+	GTGACCTATGCACCAGACGTGGAACTGGAGACACTGTCTCGTGCACAACAGGGTAAGATCGGAAGAGCGGTTTCAG
chr20	31388115	31388154	DNMT3B_9315	+	GTGACCTATGCACCAGACGTTTCTACTCTCGCGGCTCATCTCTTCTCTTTTTCCACAGATCGGAAGAGCGGTTTCAG
chr20	31388742	31388781	DNMT3B_9316	+	GTGACCTATGCACCAGACGTTTCTCTCTGGCAGTCCCTGGAGAGCCTATGTCACCTGACCAGATCGGAAGAGCGGTTTCAG
chr20	31389243	31389282	DNMT3B_9317	+	GTGACCTATGCACCAGACGTCTGGGGACCTGATTGTCACAGACAGCCAGGGCAGGAAAGAGATCGGAAGAGCGGTTTCAG
chr20	31390287	31390326	DNMT3B_9318	+	GTGACCTATGCACCAGACGTGCTCTTAGTGGGTGAGTAAACAGCCAAAGTTAAATATGTGAAGATCGGAAGAGCGGTTTCAG
chr20	31393224	31393263	DNMT3B_9319	+	GTGACCTATGCACCAGACGTCTGTGGCCCTCGGAAAAATGCACCTTGGTGACCTCCAAGTAGATCGGAAGAGCGGTTTCAG
chr20	31394144	31394183	DNMT3B_9320	+	GTGACCTATGCACCAGACGTTGCACTTGGAGAGGAAACTGTGTAGATCAAAACACAAAAGATCGGAAGAGCGGTTTCAG
chr20	31395720	31395759	DNMT3B_9321	+	GTGACCTATGCACCAGACGTTGCCAAAGCCACTGGGCTGTGTGCAGAGCCAGGACCAAGATCGGAAGAGCGGTTTCAG
chr19	45912994	45913033	ERCC1_9322	+	GTGACCTATGCACCAGACGTGGGAGAAAAAATGAGGAACCAGTCAATAAGGAGCTGTTAGATCGGAAGAGCGGTTTCAG
chr19	45917014	45917053	ERCC1_9323	+	GTGACCTATGCACCAGACGTAAAGCGAGGGGTCAGGGCAGTTGAGCACAAAAGCCTCCCAGATCGGAAGAGCGGTTTCAG
chr19	45917303	45917342	ERCC1_9324	+	GTGACCTATGCACCAGACGTTGGAGGCGAGGAGTGTGTCCGGAAGAAAGAAAGGCCAGCAAGAAGATCGGAAGAGCGGTTTCAG
chr19	45918229	45918268	ERCC1_9325	+	GTGACCTATGCACCAGACGTAGGATACAGGGCAGCCGGGAGGTGAGGTATCAGATTATAGAGATCGGAAGAGCGGTTTCAG
chr19	45922466	45922505	ERCC1_9326	+	GTGACCTATGCACCAGACGTACAGGACCGGGGTCAGGAGGTTGAGGAGTCTCAGTCTCTTAAGACAGATCGGAAGAGCGGTTTCAG
chr19	45923696	45923735	ERCC1_9327	+	GTGACCTATGCACCAGACGTACGAAGGGCAGAAGCCATCAATAGGGATGACCCTTGATAAAGATCGGAAGAGCGGTTTCAG
chr19	45924662	45924701	ERCC1_9328	+	GTGACCTATGCACCAGACGTAAAGGGAGTTTGCAGGGGACTGGTTGGGTGAGCAGAGGAAGATCGGAAGAGCGGTTTCAG
chr19	45926643	45926682	ERCC1_9329	+	GTGACCTATGCACCAGACGTAAAGGGAAGGTGCCAGGAGCGAGTGAGCCACTGGCGTCTAAGATCGGAAGAGCGGTTTCAG
chr16	14014240	14014279	ERCC4_9330	+	GTGACCTATGCACCAGACGTGCTGGCGCGGGAGTGAGGGGACTCCGAGAGTGTGAGGGCAGATCGGAAGAGCGGTTTCAG
chr16	14016079	14016118	ERCC4_9331	+	GTGACCTATGCACCAGACGTGAAATCTTATATAGTATGTAATTTGTACTTTTTTTAGATCGGAAGAGCGGTTTCAG
chr16	14020624	14020663	ERCC4_9332	+	GTGACCTATGCACCAGACGTTTATGTGCAAAAATATGATGACATATTGTGCATCTTTGTAGATCGGAAGAGCGGTTTCAG
chr16	14022103	14022142	ERCC4_9333	+	GTGACCTATGCACCAGACGTTCCTTTTAAGCACAGTTTATGTTGTAATTTAAAGAAAGATCGGAAGAGCGGTTTCAG
chr16	14024758	14024797	ERCC4_9334	+	GTGACCTATGCACCAGACGTAAAACTAATAATATCTAAGAGCTGATTTGAATAAGTAGATCGGAAGAGCGGTTTCAG
chr16	14026153	14026192	ERCC4_9335	+	GTGACCTATGCACCAGACGTGGGTTAAGTCTTTAAATGTGTTTTTATTTCCGATTTGGAGATCGGAAGAGCGGTTTCAG
chr16	14028170	14028209	ERCC4_9336	+	GTGACCTATGCACCAGACGTAGGAGATGAAAACATTTGCTTCCAAAATCTATCAAAATGAGAGATCGGAAGAGCGGTTTCAG
chr16	14029611	14029650	ERCC4_9337	+	GTGACCTATGCACCAGACGTAAAGATACAGACTTTCAGTTGCACAGTTCTTTAGGATTTAAGATCGGAAGAGCGGTTTCAG
chr16	14031726	14031765	ERCC4_9338	+	GTGACCTATGCACCAGACGTGAAAATCAGTATGAAAGCCCAACTACTATTGAAACCTTAGATCGGAAGAGCGGTTTCAG

chr16	14038703	14038742	ERCC4_9339	+	GTGACCTATGCACCAGACGTCACTTTGTGTCAGGCACCTCCATTGCTGCAAAAGGGGGCTGTAGATCGGAAGAGCGGTTTCAG
chr16	14042215	14042254	ERCC4_9340	+	GTGACCTATGCACCAGACGTCTGTTTTCTTATCCCATGCCTGTACTTTTTAGCCGCTCCTAGATCGGAAGAGCGGTTTCAG
chr16	14029312	14029351	ERCC4_9341	+	GTGACCTATGCACCAGACGTGAGATGTGCGAGGAAGGATATCGTCGAGAAATAAGCAGTAGAGATCGGAAGAGCGGTTTCAG
chr16	14041848	14041887	ERCC4_9342	+	GTGACCTATGCACCAGACGTGGATTCTCTGGTGCCCTCTCCTCATGCAACGGCGGAGTAGATCGGAAGAGCGGTTTCAG
chr17	41606122	41606161	ETV4_9343	+	GTGACCTATGCACCAGACGTAGAGAAGGTCTGGTCAGCCTGGCTACGCCGCCAGCCTTTGAGATCGGAAGAGCGGTTTCAG
chr17	41606615	41606654	ETV4_9344	+	GTGACCTATGCACCAGACGTAAACAGTTTTGGGTAGAGTGCTACCTTGGCAGAGGAAAGATCGGAAGAGCGGTTTCAG
chr17	41607055	41607094	ETV4_9345	+	GTGACCTATGCACCAGACGTGAAAATAGGAGGTGGGGTGTGGTCTTTTTGGTCCCCAGATCGGAAGAGCGGTTTCAG
chr17	41607331	41607370	ETV4_9346	+	GTGACCTATGCACCAGACGTAAATTGGGGTTGCTCAGATCTGGGGTTTACCAGATGAGAAGATCGGAAGAGCGGTTTCAG
chr17	41607560	41607599	ETV4_9347	+	GTGACCTATGCACCAGACGTAGAAGGGGTGATGTGAGAAGTGGCTTGGGGTGGAGCTCGAAGATCGGAAGAGCGGTTTCAG
chr17	41610318	41610357	ETV4_9348	+	GTGACCTATGCACCAGACGTGGATGGAGAAGGAGAGAAGAACTTTAAATTAATCCAGATCGGAAGAGCGGTTTCAG
chr17	41610727	41610766	ETV4_9349	+	GTGACCTATGCACCAGACGTGAAGGAGACAGGGGTGAGGGGCGAGAGAAGCTGGAAGAACAGATCGGAAGAGCGGTTTCAG
chr17	41611364	41611403	ETV4_9350	+	GTGACCTATGCACCAGACGTGGAGGGGACAGAGCAGGCCAGGCCTGCACACAAGAGGAGATCGGAAGAGCGGTTTCAG
chr17	41613858	41613897	ETV4_9351	+	GTGACCTATGCACCAGACGTAAAGTCAGAGGTGAGTTTGGGGCGAGCCCTGGTTGTCTCCAGATCGGAAGAGCGGTTTCAG
chr17	41622401	41622440	ETV4_9352	+	GTGACCTATGCACCAGACGTAAATAGTGAATTGGAGGTGAGGTGGAGGGGACGGTAAGAGAGATCGGAAGAGCGGTTTCAG
chr17	41622746	41622785	ETV4_9353	+	GTGACCTATGCACCAGACGTGGGGAGAATGCCCGGAGTCACCTGAGGCGCTTAGTCTAGATCGGAAGAGCGGTTTCAG
chr17	41622996	41623035	ETV4_9354	+	GTGACCTATGCACCAGACGTCTCCGCCGACGGCCGGGGCCCCAAGCGGGGGCCGAGAAGATCGGAAGAGCGGTTTCAG
chr15	91428499	91428538	FES_9355	+	GTGACCTATGCACCAGACGTATGGACTCTGGTGGTGTGGTGTATCGCTTCTCCTAGATCGGAAGAGCGGTTTCAG
chr15	91428826	91428865	FES_9356	+	GTGACCTATGCACCAGACGTAGACTGGGGCTGGGTCATTCTGTCTAAATTTTGAGCCAGATCGGAAGAGCGGTTTCAG
chr15	91430298	91430337	FES_9357	+	GTGACCTATGCACCAGACGTCCCTTGTCTGGCAGGGAGGGAATCCGAAGCCAGTGCTGACAGATCGGAAGAGCGGTTTCAG
chr15	91430611	91430650	FES_9358	+	GTGACCTATGCACCAGACGTAGCCCGTCCCCTGGCCCCACCCTTGGAGCCCTAAGCAGATCGGAAGAGCGGTTTCAG
chr15	91432684	91432723	FES_9359	+	GTGACCTATGCACCAGACGTCTCCTGTCTGCTGGGCCAGGGCTGCTGGCCTGTCCACAGATCGGAAGAGCGGTTTCAG
chr15	91432877	91432916	FES_9360	+	GTGACCTATGCACCAGACGTGCTTTGACCTGGGTGCGCGGGGGCTCCCAGCAGACCACAGATCGGAAGAGCGGTTTCAG
chr15	91433203	91433242	FES_9361	+	GTGACCTATGCACCAGACGTCCCTGCCTGCAGCAGCCTCTGGCCCTCCCTCCCTACAGATCGGAAGAGCGGTTTCAG
chr15	91433519	91433558	FES_9362	+	GTGACCTATGCACCAGACGTCCATCCCGCGCCGTGCTCCCGCCAGCCCTGGCCACCTGGAGATCGGAAGAGCGGTTTCAG
chr15	91433725	91433764	FES_9363	+	GTGACCTATGCACCAGACGTCCCAGCCTGGGCCCCCTACTGTTGTGTTTGCAGTTTAATAGATCGGAAGAGCGGTTTCAG
chr15	91434432	91434471	FES_9364	+	GTGACCTATGCACCAGACGTCTGGGACCCGAGCCTTCCAGGCCCTACTTCCCCTCCCTAGATCGGAAGAGCGGTTTCAG
chr15	91434917	91434956	FES_9365	+	GTGACCTATGCACCAGACGTACCAGCCTGGCCCATGCCACTGTGGCAGGGCTTGGGAAGATCGGAAGAGCGGTTTCAG
chr15	91435352	91435391	FES_9366	+	GTGACCTATGCACCAGACGTCTCTGCTGGCCTCTGTGCTGGCAGCTTCTCCTGAGTCAGATCGGAAGAGCGGTTTCAG
chr15	91436066	91436105	FES_9367	+	GTGACCTATGCACCAGACGTAATGATCACCCAGGGTCCCAGCAGAGGTACAGATCGGAAGAGCGGTTTCAG
chr15	91436435	91436474	FES_9368	+	GTGACCTATGCACCAGACGTGGCGCTGAGCTCCAGGTAGGGCCGCGCAGCCTGGTCAGGTGAGATCGGAAGAGCGGTTTCAG
chr15	91436655	91436694	FES_9369	+	GTGACCTATGCACCAGACGTGGTGCCACGGGCCCTGCCAACACCCCGACCAGAGTCAAAGATCGGAAGAGCGGTTTCAG
chr15	91437052	91437091	FES_9370	+	GTGACCTATGCACCAGACGTCTGCTACCCCTGGACTCCATGGCCAGAGGGCCAGGCCTGGAGATCGGAAGAGCGGTTTCAG
chr15	91437299	91437338	FES_9371	+	GTGACCTATGCACCAGACGTGTGATGACAGCAGCCTCAGGCTGCACCCTTCCAGATGAGATCGGAAGAGCGGTTTCAG
chr15	91438799	91438838	FES_9372	+	GTGACCTATGCACCAGACGTCCCTTCTCAAGCTGGTGGCCTGCAGGCCTAGGTGCAGCAGATCGGAAGAGCGGTTTCAG
chr4	144258424	144258463	GAB1_9373	+	GTGACCTATGCACCAGACGTCTCGGGCCACCACTCCGCGGCCCTCGGCCCTCCAGCCCTAGATCGGAAGAGCGGTTTCAG
chr4	144336935	144336974	GAB1_9374	+	GTGACCTATGCACCAGACGTGATATTACTATTCAACTGAATTCTTCTTTTCTGCTACATAGATCGGAAGAGCGGTTTCAG
chr4	144354880	144354919	GAB1_9375	+	GTGACCTATGCACCAGACGTATGCCATGTGAGAGAGAGACAGAGCGTGTGTATGTGTAGATCGGAAGAGCGGTTTCAG
chr4	144359764	144359803	GAB1_9376	+	GTGACCTATGCACCAGACGTGTGGACTTCTTCTATTAGAGTTAATGATAGAAAATCGAGATCGGAAGAGCGGTTTCAG
chr4	144361051	144361090	GAB1_9377	+	GTGACCTATGCACCAGACGTGGACTTTGGCATCATCAAGTGTATTTTCTAATGCTAAATCAGATCGGAAGAGCGGTTTCAG
chr4	144361546	144361585	GAB1_9378	+	GTGACCTATGCACCAGACGTATGCGCAAAGTAAAGGCTTGGGAGTGCCAAGTTAGATCAGATCGGAAGAGCGGTTTCAG
chr4	144378933	144378972	GAB1_9379	+	GTGACCTATGCACCAGACGTAGCACCCAGCTGTATGGGGCTATGGGAATTTATTTGAGATCGGAAGAGCGGTTTCAG
chr4	144380642	144380681	GAB1_9380	+	GTGACCTATGCACCAGACGTGTCTAAATATGTAGTTGTGTGAATAATGTGACTATCTAGATCGGAAGAGCGGTTTCAG
chr4	144381651	144381690	GAB1_9381	+	GTGACCTATGCACCAGACGTTTTAACTTTTCCCTTCTGAGCAGCCCTTTTCACTTATAGATCGGAAGAGCGGTTTCAG
chr4	144387389	144387428	GAB1_9382	+	GTGACCTATGCACCAGACGTGTGACATGTCTCTTTTGTATACAGTTAGTTTACACTTATAGATCGGAAGAGCGGTTTCAG
chr4	144390353	144390392	GAB1_9383	+	GTGACCTATGCACCAGACGTGTGCCATTTCTGAACAAAAGAAAAGTGAATTGTAAGATAAGATCGGAAGAGCGGTTTCAG
chr4	144359463	144359502	GAB1_9384	+	GTGACCTATGCACCAGACGTATGATTTAGTATTAGTTACTTCCCAACACCTGTTAAAGATCGGAAGAGCGGTTTCAG
chr7	81332084	81332123	HGF_9385	+	GTGACCTATGCACCAGACGTGACATACAAAACAAAGTATTATTAGGAATTAATAAAGAGATCGGAAGAGCGGTTTCAG
chr7	81334862	81334901	HGF_9386	+	GTGACCTATGCACCAGACGTGCAAAAACATACAATAAGGTGAGAAAAGTAAGAAAACAAAGATCGGAAGAGCGGTTTCAG
chr7	81335080	81335119	HGF_9387	+	GTGACCTATGCACCAGACGTAAATACAATGGTAAGTACTCTCAACTGGATTCAACACAAAGATCGGAAGAGCGGTTTCAG
chr7	81335754	81335793	HGF_9388	+	GTGACCTATGCACCAGACGTGGAATAAATTTAAATGTAAACATAATAATTTCAAATTCAGATCGGAAGAGCGGTTTCAG
chr7	81336691	81336730	HGF_9389	+	GTGACCTATGCACCAGACGTGAGAAAAGAGAACAAGTAAACATCTGTGCAGAAAAGATGAAGATCGGAAGAGCGGTTTCAG
chr7	81339570	81339609	HGF_9390	+	GTGACCTATGCACCAGACGTACCAAAACATAACATTTTTTAAATAAGAAATTTGAAATAATAGATCGGAAGAGCGGTTTCAG
chr7	81340846	81340885	HGF_9391	+	GTGACCTATGCACCAGACGTAAATGTATAGATAAATACACAATTCATATATGATATATAGATCGGAAGAGCGGTTTCAG
chr7	81346692	81346731	HGF_9392	+	GTGACCTATGCACCAGACGTAAACAGGCCCTGACATCACAAAGATGCTCATTCATCCAAGAGATCGGAAGAGCGGTTTCAG
chr7	81350174	81350213	HGF_9393	+	GTGACCTATGCACCAGACGTAAATATACAGAATAAGTCCAATGAATATCAAGGCAGATAAAGATCGGAAGAGCGGTTTCAG
chr7	81355344	81355383	HGF_9394	+	GTGACCTATGCACCAGACGTAAAGCATGTTAATGTAATTTGCCGGAGTCTTACGTTGGTAGATCGGAAGAGCGGTTTCAG
chr7	81359106	81359145	HGF_9395	+	GTGACCTATGCACCAGACGTAAAACAACAAAACAAAACATATATAAAATCTTTGAAAGATCGGAAGAGCGGTTTCAG
chr7	81372276	81372315	HGF_9396	+	GTGACCTATGCACCAGACGTAAAGTAGGTAAAAGGATACAGGATTGAAAGGTAAGAACTAAGATCGGAAGAGCGGTTTCAG

chr7	81372798	81372837	HGF_9397	+	GTGACCTATGCACCAGACGTCACCAAGAAAAGTGTACAGTAAATCTGCCTGGAAACACCAAGATCGGAAGAGCGGTTTCAG
chr7	81374447	81374486	HGF_9398	+	GTGACCTATGCACCAGACGTTAAAGTATGGCATGTTAATTGTTTCTGCAGCAAAATCAAAGATCGGAAGAGCGGTTTCAG
chr7	81381589	81381628	HGF_9399	+	GTGACCTATGCACCAGACGTAATGATAATCATTACAGTATAAGAGCATGCAACTTTTTTTAGATCGGAAGAGCGGTTTCAG
chr7	81381574	81381613	HGF_9400	+	GTGACCTATGCACCAGACGTAAGAGCTAGTTTTAAATGATAATCATTACAGTATAAGAGATCGGAAGAGCGGTTTCAG
chr7	81386630	81386669	HGF_9401	+	GTGACCTATGCACCAGACGTAAGTAGATAAAATATTGCAACTATGCAAAACATATGCAGAGATCGGAAGAGCGGTTTCAG
chr7	81388131	81388170	HGF_9402	+	GTGACCTATGCACCAGACGTTATCAGAATGAAAAGAAGAAACTACTATTATACAGTAAGATCGGAAGAGCGGTTTCAG
chr7	81392199	81392238	HGF_9403	+	GTGACCTATGCACCAGACGTCAAAATGTTTTAAAAAATAAACATTGGAGAAATGTTTTTAGATCGGAAGAGCGGTTTCAG
chr7	81399298	81399337	HGF_9404	+	GTGACCTATGCACCAGACGTGACGGGCTGGCGGATCCCTCTGGAGGAGATGCCTGGGTGAAGATCGGAAGAGCGGTTTCAG
chr12	68549278	68549317	IFNG_9405	+	GTGACCTATGCACCAGACGTAGAAAAGAGCAAAATTAATTTCCAGGCATATAAGCCATCAGAGATCGGAAGAGCGGTTTCAG
chr12	68551886	68551925	IFNG_9406	+	GTGACCTATGCACCAGACGTAAGAGCACAACAAGAGGATGATGTGAATTTATCCATCAGAAGATCGGAAGAGCGGTTTCAG
chr12	68552050	68552089	IFNG_9407	+	GTGACCTATGCACCAGACGTAAGAAAGAAAAAATTGGTTTTACAATTAGCCATAAATTGCCAGATCGGAAGAGCGGTTTCAG
chr12	68553406	68553445	IFNG_9408	+	GTGACCTATGCACCAGACGTAGAATTAAGCCAAAGAGTTGAAATCAGTAGTTCTTGATAGATCGGAAGAGCGGTTTCAG
chr6	160390438	160390477	IGF2R_9409	+	GTGACCTATGCACCAGACGTCGCCCGGACGCAAGGCTCCGCTCGCGGTCGCCGGGTGACAGATCGGAAGAGCGGTTTCAG
chr6	160412366	160412405	IGF2R_9410	+	GTGACCTATGCACCAGACGTTACCTGAAATTAAGATTGGATTGGCAATATGATCCCAATTAGATCGGAAGAGCGGTTTCAG
chr6	160430177	160430216	IGF2R_9411	+	GTGACCTATGCACCAGACGTACAGGCCTTGATGTATTTCTTAAAAAAGGTCTGAGATCGGAAGAGCGGTTTCAG
chr6	160431828	160431867	IGF2R_9412	+	GTGACCTATGCACCAGACGTAACCTCAAATTCATGCTTATGAAGTAACTCTGGGGAACAGATCGGAAGAGCGGTTTCAG
chr6	160445747	160445786	IGF2R_9413	+	GTGACCTATGCACCAGACGTTTGTTGGGGCTGAGGGGGTGGTGGTGGAGGATTTCTTCTATAGATCGGAAGAGCGGTTTCAG
chr6	160448357	160448396	IGF2R_9414	+	GTGACCTATGCACCAGACGTGCTCGGAGTCTGCTGTGCTGCTTAAATGCTCCAGCAAGACATCGGAAGAGCGGTTTCAG
chr6	160450698	160450737	IGF2R_9415	+	GTGACCTATGCACCAGACGTCGTCTCCTGATCACTAATGTGGCGCACAGTAGCCTGGTTAGATCGGAAGAGCGGTTTCAG
chr6	160453756	160453795	IGF2R_9416	+	GTGACCTATGCACCAGACGTGCTTTCTGCCTCCTGGCGTCTTAGGAAGAAGGGGATCGAGATCGGAAGAGCGGTTTCAG
chr6	160455565	160455604	IGF2R_9417	+	GTGACCTATGCACCAGACGTGCTGGAGTTCAGCCCTCCTCTTGCATTTCATGGCATGTAGATCGGAAGAGCGGTTTCAG
chr6	160461767	160461806	IGF2R_9418	+	GTGACCTATGCACCAGACGTCCTTGCATGCGGGTCTTAGTCCACATGCTCATGGAACATAGATCGGAAGAGCGGTTTCAG
chr6	160464331	160464370	IGF2R_9419	+	GTGACCTATGCACCAGACGTCCTGGATGGAAGATCTAGTGTGATGCTTTCTAGGGATCCAGATCGGAAGAGCGGTTTCAG
chr6	160465700	160465739	IGF2R_9420	+	GTGACCTATGCACCAGACGTTAAAAAGCTGAAATTTCTGCTTCTGCCAGGTCCAGATCGGAAGAGCGGTTTCAG
chr6	160466925	160466964	IGF2R_9421	+	GTGACCTATGCACCAGACGTAAGCAGGACCTCTGCTTAAATGTGACTTGAACCACTTAAAGATCGGAAGAGCGGTTTCAG
chr6	160467688	160467727	IGF2R_9422	+	GTGACCTATGCACCAGACGTTCTCAGTTCTGTTTCATTCTTAGGCATTATATGCTAAGAAAGATCGGAAGAGCGGTTTCAG
chr6	160468379	160468418	IGF2R_9423	+	GTGACCTATGCACCAGACGTTTGTCCCTCATCGCGCTCCCTGAGGATACTCATGCCCTGTGAGATCGGAAGAGCGGTTTCAG
chr6	160468950	160468989	IGF2R_9424	+	GTGACCTATGCACCAGACGTGTCAGTGCTCTGTTTTGGCCTGGTACAGATGCTGAGGTAGATCGGAAGAGCGGTTTCAG
chr6	160469586	160469625	IGF2R_9425	+	GTGACCTATGCACCAGACGTTTCTGCTGTTCTCCTTTGCCCTCAATCCATGACTGAGATCGGAAGAGCGGTTTCAG
chr6	160471695	160471734	IGF2R_9426	+	GTGACCTATGCACCAGACGTCCTGCTGGCTGGTGGCCTTCACTGCTGCATTTTTGACTGTAGATCGGAAGAGCGGTTTCAG
chr6	160477568	160477607	IGF2R_9427	+	GTGACCTATGCACCAGACGTTTTACCTGGCCCTCGTCTGAGTGCCTGCTGGACATCCAGATCGGAAGAGCGGTTTCAG
chr6	160479167	160479206	IGF2R_9428	+	GTGACCTATGCACCAGACGTTATGATGCATTTCCAGTTTGCTTTGAAACAGGGGGAGAGTAGATCGGAAGAGCGGTTTCAG
chr6	160480141	160480180	IGF2R_9429	+	GTGACCTATGCACCAGACGTAGCCATGTTGTTTTGTAGCTAAAAAGGGCCCTGGTGGCTCAGATCGGAAGAGCGGTTTCAG
chr6	160482689	160482728	IGF2R_9430	+	GTGACCTATGCACCAGACGTTGCTGCTCTTGTGCGCTGTTTCATTTTATAGAGCAAGATCGGAAGAGCGGTTTCAG
chr6	160482971	160483010	IGF2R_9431	+	GTGACCTATGCACCAGACGTAGACCAAGCAGTAAAGATGATGTTGCTGGGTTGACTCCATCCATGATCGGAAGAGCGGTTTCAG
chr6	160483662	160483701	IGF2R_9432	+	GTGACCTATGCACCAGACGTGCTGTCCTACAAGTCAATTTAAATGTATAGAGTAGCAGAGATCGGAAGAGCGGTTTCAG
chr6	160485574	160485613	IGF2R_9433	+	GTGACCTATGCACCAGACGTACCGACGGCCCTCAGCGGGTCTTCTCCCAACCCTCAGGCAGATCGGAAGAGCGGTTTCAG
chr6	160485944	160485983	IGF2R_9434	+	GTGACCTATGCACCAGACGTGGATGTGTTGCTCTTTGGACAGACTAATTGGTATGATAGATCGGAAGAGCGGTTTCAG
chr6	160489428	160489467	IGF2R_9435	+	GTGACCTATGCACCAGACGTGCTCCTCGTGGGGTGGTGTGTCAGTGAAGTGTATCACAGAGATCGGAAGAGCGGTTTCAG
chr6	160491101	160491140	IGF2R_9436	+	GTGACCTATGCACCAGACGTGTTCTGACCTTCTGCTGTTGCAGCTTTGGGAATGAGCAGATCGGAAGAGCGGTTTCAG
chr6	160493079	160493118	IGF2R_9437	+	GTGACCTATGCACCAGACGTGTCAGTCCTTACCCTCAGCCAGGTGAGAGACGGTGCAGATCGGAAGAGCGGTTTCAG
chr6	160493927	160493966	IGF2R_9438	+	GTGACCTATGCACCAGACGTTGGTCTCTCGTGTGTTGCTGACTCTCCCGTCTCTGGGGAGATCGGAAGAGCGGTTTCAG
chr6	160494512	160494551	IGF2R_9439	+	GTGACCTATGCACCAGACGTAGATGGGACGGGAGAGTGCATGTCAGTGCCTGGCTGCAGATCGGAAGAGCGGTTTCAG
chr6	160495018	160495057	IGF2R_9440	+	GTGACCTATGCACCAGACGTCAAATCCAAAGGGTGAGATAATTTTTGCAAGACTTTTAGTAGATCGGAAGAGCGGTTTCAG
chr6	160497039	160497078	IGF2R_9441	+	GTGACCTATGCACCAGACGTGCTGTGACGATCTAGATGCTCAACTCGGGTGTAGTGAGCAGATCGGAAGAGCGGTTTCAG
chr6	160499405	160499444	IGF2R_9442	+	GTGACCTATGCACCAGACGTCAACCTGGCGTGTGTTGGTGCAGGTGACCAGGTGACCAGATCGGAAGAGCGGTTTCAG
chr6	160500830	160500869	IGF2R_9443	+	GTGACCTATGCACCAGACGTGCAATGAGGTAAATAAATCAAGCTCATAGTAAACTAGAAGATCGGAAGAGCGGTTTCAG
chr6	160501318	160501357	IGF2R_9444	+	GTGACCTATGCACCAGACGTGGCTCCGCTCCCCACATGGCTGGGGCCTTGATACTGTAGATCGGAAGAGCGGTTTCAG
chr6	160505227	160505266	IGF2R_9445	+	GTGACCTATGCACCAGACGTTCCAGTCCACCCGGCGCCACACCCTCAGCATGTGAACAGATCGGAAGAGCGGTTTCAG
chr6	160506174	160506213	IGF2R_9446	+	GTGACCTATGCACCAGACGTTGGGCTCTGCTTGGTTCAAGGAGCAGCATCTGAACCGAGATCGGAAGAGCGGTTTCAG
chr6	160509190	160509229	IGF2R_9447	+	GTGACCTATGCACCAGACGTTGGGGCTCAGAGCGGGATGTGCACTGAGCATACTGGAGATCGGAAGAGCGGTTTCAG
chr6	160510296	160510335	IGF2R_9448	+	GTGACCTATGCACCAGACGTCGTTTCCCTCTGAGCTGAAATGTGTTCAAATAAACAAGATCGGAAGAGCGGTTTCAG
chr6	160511146	160511185	IGF2R_9449	+	GTGACCTATGCACCAGACGTGCTTCCACAAAGTTCCACATTTAACTTCTCCAAGGAAGAGATCGGAAGAGCGGTTTCAG
chr6	160517668	160517707	IGF2R_9450	+	GTGACCTATGCACCAGACGTCATCCGGAAGCTTAGCACTTGACCCACATCTTCCCTTAAAGATCGGAAGAGCGGTTTCAG
chr6	160523714	160523753	IGF2R_9451	+	GTGACCTATGCACCAGACGTGGCAGGGCAGGTTGGGGCGGGTGGATTGCATGCCTCCCATAAAGATCGGAAGAGCGGTTTCAG
chr6	160524858	160524897	IGF2R_9452	+	GTGACCTATGCACCAGACGTGGCGAGTCTTTGAAGGCCCTGCCCTCCCGGCCCTGTAGATCGGAAGAGCGGTTTCAG
chr6	160526127	160526166	IGF2R_9453	+	GTGACCTATGCACCAGACGTCTGCGAGGACGACCGGAGCCGAGCAGCCACCTAGATCGGAAGAGCGGTTTCAG
chr19	7117432	7117471	INSR_9454	+	GTGACCTATGCACCAGACGTCAGTCAACGCTGGTGAGTCTGGGGCCCTGCCACGCAGATCGGAAGAGCGGTTTCAG

chr19	7120771	7120810	INSR_9455	+	GTGACCTATGCACCAGACGTAAAAGGTTACACGCTCTTAACCTTACGCTTGGTCCTAGAGATCGGAAGAGCGGTTTCAG
chr19	7122795	7122834	INSR_9456	+	GTGACCTATGCACCAGACGTAAACACGGGGTGGTGTTCAGCAGCACTGGGATCCGAGGAAGATCGGAAGAGCGGTTTCAG
chr19	7123011	7123050	INSR_9457	+	GTGACCTATGCACCAGACGTAGCAACCAGGGTCTTGGAGGAGGGTCCGTGATTCGACTCAGATCGGAAGAGCGGTTTCAG
chr19	7125549	7125588	INSR_9458	+	GTGACCTATGCACCAGACGTCTTATCTACACAGCATCCTTGGAGGATCCCTTGGGGGTCTAGATCGGAAGAGCGGTTTCAG
chr19	7126673	7126712	INSR_9459	+	GTGACCTATGCACCAGACGTAAAACGAGGCACGTAGCTTGGATTCTCATGGACTCTGAGATCGGAAGAGCGGTTTCAG
chr19	7128976	7129015	INSR_9460	+	GTGACCTATGCACCAGACGTATAAGAAAATATATGTTTCATATCAATGTGTTTCCAACAAGATCGGAAGAGCGGTTTCAG
chr19	7132339	7132378	INSR_9461	+	GTGACCTATGCACCAGACGTAGAGAGGAGGAAGAGGGTGGCTGAGCTTGGACATCTGAGATCGGAAGAGCGGTTTCAG
chr19	7143112	7143151	INSR_9462	+	GTGACCTATGCACCAGACGTAGTAGGACATGATGATGACACCATCACCATCATTTTTTTAGATCGGAAGAGCGGTTTCAG
chr19	7150554	7150593	INSR_9463	+	GTGACCTATGCACCAGACGTAAAACCAACGCCTTTGAGGACAGAGGGAACCTCATTAGACAGATCGGAAGAGCGGTTTCAG
chr19	7163221	7163260	INSR_9464	+	GTGACCTATGCACCAGACGTGAAAAGGAAATGGGTCCATCATGAGAAACAGTGTGCAAAGAGATCGGAAGAGCGGTTTCAG
chr19	7166426	7166465	INSR_9465	+	GTGACCTATGCACCAGACGTAAAACAGCAGAAGGCGAGTTACCCTTACAAGACCGTCACACAGATCGGAAGAGCGGTTTCAG
chr19	7168116	7168155	INSR_9466	+	GTGACCTATGCACCAGACGTAAAACAAAAGGCAAAAATGAGCTATTTTCAGTGATTTTCAGATCGGAAGAGCGGTTTCAG
chr19	7170773	7170812	INSR_9467	+	GTGACCTATGCACCAGACGTAAACACACACATCTAGTCACTTCAACGGCTGGTCTTTCACAAAGATCGGAAGAGCGGTTTCAG
chr19	7172456	7172495	INSR_9468	+	GTGACCTATGCACCAGACGTGAGAGAATATCCAGTGGGTTTCTATAGACATATTTCAATCAGATCGGAAGAGCGGTTTCAG
chr19	7174753	7174792	INSR_9469	+	GTGACCTATGCACCAGACGTAGCAGAGAGAGAGAGAAAAGAGAAAGGGGAGGGGGGTGTCAAGATCGGAAGAGCGGTTTCAG
chr19	7267918	7267957	INSR_9470	+	GTGACCTATGCACCAGACGTAAATGAACAGAAAAGCAAGACAGGTGAGCAGACGCACGGTGAGATCGGAAGAGCGGTTTCAG
chr19	7293913	7293952	INSR_9471	+	GTGACCTATGCACCAGACGTGCGCGGGGTCTCCTCGGATCAGAGCGCGCGCGCTGCCAGATCGGAAGAGCGGTTTCAG
chr19	7267642	7267681	INSR_9472	+	GTGACCTATGCACCAGACGTGAGCAGCAGCTAGTAAAGACAGCTGTGATCCCCGGAGATCGGAAGAGCGGTTTCAG
chr10	3821793	3821832	KLF6_9473	+	GTGACCTATGCACCAGACGTAAATGCAAGCACAGAAGAGTTAGTTCCATCCCTTGCAGATCGGAAGAGCGGTTTCAG
chr10	3822432	3822471	KLF6_9474	+	GTGACCTATGCACCAGACGTAGCACAGGACAAGCAGCCATGACTTCACTGACCCGCAGAAGATCGGAAGAGCGGTTTCAG
chr10	3824417	3824456	KLF6_9475	+	GTGACCTATGCACCAGACGTGAACACAGAGAAGGCACGTGATTGCCATGACGACCAAAAAGATCGGAAGAGCGGTTTCAG
chr10	3827217	3827256	KLF6_9476	+	GTGACCTATGCACCAGACGTGTTGGACGGAGCCCGCGTCCGCGAGGGGCGCGGAGGCGCGCAGATCGGAAGAGCGGTTTCAG
chr10	3824130	3824169	KLF6_9477	+	GTGACCTATGCACCAGACGTAGGTAACCTGGCCGTGGGAGAAATTCCTCGGAGCTGCAGATCGGAAGAGCGGTTTCAG
chr1	43803609	43803648	MPL_9478	+	GTGACCTATGCACCAGACGTGAGAGCTGGAGTGGAGTACCTATGCCAGGAAGAGGCCAGATCGGAAGAGCGGTTTCAG
chr1	43803913	43803952	MPL_9479	+	GTGACCTATGCACCAGACGTGACTGTGCCCACTCCCATGTATCTGTCCCTGCACTTAGAGATCGGAAGAGCGGTTTCAG
chr1	43804402	43804441	MPL_9480	+	GTGACCTATGCACCAGACGTTCCTCCTGTACCCTGCCCTCCACTTGCTGCCCCAGTAGATCGGAAGAGCGGTTTCAG
chr1	43805251	43805290	MPL_9481	+	GTGACCTATGCACCAGACGTCTTCTTCTGCCCACTCTTATCTCCATCTTCAATCTTGGATCGGAAGAGCGGTTTCAG
chr1	43805808	43805847	MPL_9482	+	GTGACCTATGCACCAGACGTAAAGAAATGAGGAGATGGGGAGGAGATAAAAGAATATCTCAGATCGGAAGAGCGGTTTCAG
chr1	43806195	43806234	MPL_9483	+	GTGACCTATGCACCAGACGTAACTGCTAGTTAGGTTGGTGTGATGGGAGTGAGCCACAAGATCGGAAGAGCGGTTTCAG
chr1	43812311	43812350	MPL_9484	+	GTGACCTATGCACCAGACGTCTTCTCATTCTCCACATAGTTCCACCCCACTGAAAGATCGGAAGAGCGGTTTCAG
chr1	43812616	43812655	MPL_9485	+	GTGACCTATGCACCAGACGTGCAACAAATGCCACAGACCTCACTACGCAGGGATCCCTAGATCGGAAGAGCGGTTTCAG
chr1	43815041	43815080	MPL_9486	+	GTGACCTATGCACCAGACGTGCCAGGCAGGAGACTGCGGGTGGACCAGGTGGAGCCGAAAGATCGGAAGAGCGGTTTCAG
chr1	43817985	43818024	MPL_9487	+	GTGACCTATGCACCAGACGTTCCTCCCTGTGCCACCACCAAGCTGCCTGGTACTGAGATCGGAAGAGCGGTTTCAG
chr1	43818454	43818493	MPL_9488	+	GTGACCTATGCACCAGACGTCTCACTCCAGTCCCTGGACAGCTAACTCTCGAGACAGATCGGAAGAGCGGTTTCAG
chr1	45795120	45795159	MUTYH_9489	+	GTGACCTATGCACCAGACGTGGAAGAGGAGGGCCCTTTAGTTGGGGAGGGGAGCAGATCGGAAGAGCGGTTTCAG
chr1	45796240	45796279	MUTYH_9490	+	GTGACCTATGCACCAGACGTAGACAGGGAGGTGAGGGCTGGCCTTTTTGCAAAAGAGATAGATCGGAAGAGCGGTTTCAG
chr1	45797017	45797056	MUTYH_9491	+	GTGACCTATGCACCAGACGTGGTCAAGGGTTCAAATAGGCCTGTGGATATAGCCTCAAAGATCGGAAGAGCGGTTTCAG
chr1	45797239	45797278	MUTYH_9492	+	GTGACCTATGCACCAGACGTGGGCAGCCAGGAGGGGTACGGCCCTAGCTGCCGATTCAGATCGGAAGAGCGGTTTCAG
chr1	45797532	45797571	MUTYH_9493	+	GTGACCTATGCACCAGACGTAGATCCCGAACCCCTACTCAAGCCAAGAGGGCTTTAGGGGAGATCGGAAGAGCGGTTTCAG
chr1	45797769	45797808	MUTYH_9494	+	GTGACCTATGCACCAGACGTGAGGGTGTGATGTATAGGGCAGACTCCTTAGGACTAGATCGGAAGAGCGGTTTCAG
chr1	45797993	45798032	MUTYH_9495	+	GTGACCTATGCACCAGACGTGGAACACTGCTGTGAAGCAGACTCCCTTTGCAGACACCCAGATCGGAAGAGCGGTTTCAG
chr1	45798171	45798210	MUTYH_9496	+	GTGACCTATGCACCAGACGTGGGGCCAAAGAGTTAGCCTGGGCTGGGAGGAAGGAGGCTGAGATCGGAAGAGCGGTTTCAG
chr1	45798370	45798409	MUTYH_9497	+	GTGACCTATGCACCAGACGTGCAAGACTCAAGATTATAAGACCCAAAGACTCCTGGGTAGATCGGAAGAGCGGTTTCAG
chr1	45798517	45798556	MUTYH_9498	+	GTGACCTATGCACCAGACGTGATCAGAGGTCAAAGAGATCACCCGTCAGTCCCTTATTGAGATCGGAAGAGCGGTTTCAG
chr1	45798642	45798681	MUTYH_9499	+	GTGACCTATGCACCAGACGTAGGCAGGCAGAAAGAGACAAGGTCAAGGGTGAAGGTGGTAAAGATCGGAAGAGCGGTTTCAG
chr1	45798853	45798892	MUTYH_9500	+	GTGACCTATGCACCAGACGTGGGTTGGCATGGAGCAGCTGAGATGCCCTACCTGGAGATCGGAAGAGCGGTTTCAG
chr1	45799007	45799046	MUTYH_9501	+	GTGACCTATGCACCAGACGTAAACCCAGATGAGGAGTTAGGGTGGAGGGGGCTGGGTGCCAGATCGGAAGAGCGGTTTCAG
chr1	45799244	45799283	MUTYH_9502	+	GTGACCTATGCACCAGACGTCCCAGGACTCAGCAATCATCCCTGCACAGGCTGTGCATAGATCGGAAGAGCGGTTTCAG
chr1	45799247	45799286	MUTYH_9503	+	GTGACCTATGCACCAGACGTAGGACACTCAGCAATCATCCCTGCACAGGCTGTGCATCAGAGATCGGAAGAGCGGTTTCAG
chr1	45799277	45799316	MUTYH_9504	+	GTGACCTATGCACCAGACGTTGTGCATCAGGGTCTTGGGACACAGCAGCCTGTGGCAGTAAGATCGGAAGAGCGGTTTCAG
chr1	45799286	45799325	MUTYH_9505	+	GTGACCTATGCACCAGACGTGGTCTTGGGACACAGCAGCCTGTGGCAGTATGCTCCACAGATCGGAAGAGCGGTTTCAG
chr1	45800188	45800227	MUTYH_9506	+	GTGACCTATGCACCAGACGTGAAACAGCCAGCCAGACAGTCAGTCAATGAGGACAGATCGGAAGAGCGGTTTCAG
chr1	45800194	45800233	MUTYH_9507	+	GTGACCTATGCACCAGACGTAAAGACCCAGCCAAAGCAGTCAGTCACAATGAGGCCAAATAGATCGGAAGAGCGGTTTCAG
chr1	45805937	45805976	MUTYH_9508	+	GTGACCTATGCACCAGACGTAGTGACGATGGCGAGTTTCAGCTCCCGCAGCTCCGACGAGATCGGAAGAGCGGTTTCAG
chr1	40363653	40363692	MYCL1_9509	+	GTGACCTATGCACCAGACGTAAAGAGATCAAGAGAAGAAACACATCCATGAGAAACAAGATCGGAAGAGCGGTTTCAG
chr1	40367117	40367156	MYCL1_9510	+	GTGACCTATGCACCAGACGTTCGGGAGGGGAAGGGGGACGTGCTGACCCGGTGCCGCCAGATCGGAAGAGCGGTTTCAG
chr1	40363353	40363392	MYCL1_9511	+	GTGACCTATGCACCAGACGTCCCTTACAGGTGGGGACCTCAGTCACTCTTCATCCTCCAGATCGGAAGAGCGGTTTCAG
chr1	40366806	40366845	MYCL1_9512	+	GTGACCTATGCACCAGACGTCCGAGAAGCCCTCCACATGCACTACCGGCTGATGGAAGATCGGAAGAGCGGTTTCAG

chr5	142658987	142659026	NR3C1_9513	+	GTGACCTATGCACCAGACGTGATAATCTACGTTTTAGAAGCTCTTTTTGAAACTTAACAGATCGGAAGAGCGGTTTCAG
chr5	142661617	142661656	NR3C1_9514	+	GTGACCTATGCACCAGACGTAGATATGGTAATGATCAGGCTTCCAATTGGTCAGTGGGAAGATCGGAAGAGCGGTTTCAG
chr5	142675166	142675205	NR3C1_9515	+	GTGACCTATGCACCAGACGTAAATAGCAGGGTATTAGTTAGAATACTGCTACTTCCCCAGATCGGAAGAGCGGTTTCAG
chr5	142678388	142678427	NR3C1_9516	+	GTGACCTATGCACCAGACGTAGAAATAAAGGTATGAGGCAACTCTTCAGAAGATCATCAGATCGGAAGAGCGGTTTCAG
chr5	142680339	142680378	NR3C1_9517	+	GTGACCTATGCACCAGACGTTAAACAATAACATAGAAATGAATGTAATGGGAAGGTCTAGATCGGAAGAGCGGTTTCAG
chr5	142689789	142689828	NR3C1_9518	+	GTGACCTATGCACCAGACGTAAAAGGCAGTATAAAGTTTCACAGGCTTCAAACATATAGATCGGAAGAGCGGTTTCAG
chr5	142693744	142693783	NR3C1_9519	+	GTGACCTATGCACCAGACGTGGAAGAACAGTGTATGATTTAACTGTCAAAGGAATATCAAGATCGGAAGAGCGGTTTCAG
chr5	142780415	142780454	NR3C1_9520	+	GTGACCTATGCACCAGACGTCAACTACAAAAACAAAAACAAAAACGCGGGGAAAACATCAAGATCGGAAGAGCGGTTTCAG
chr5	142779625	142779664	NR3C1_9521	+	GTGACCTATGCACCAGACGTATTATCCTTAATTTTTGGGTTTAGTGCCGGTAAAATGAGAAGATCGGAAGAGCGGTTTCAG
chr5	142780019	142780058	NR3C1_9522	+	GTGACCTATGCACCAGACGTAGGTTTGCAATGCTTTCTTCCAAAAGCTTTAAGTCTGTTTAGATCGGAAGAGCGGTTTCAG
chr18	39535335	39535374	PIK3C3_9523	+	GTGACCTATGCACCAGACGTACTCGGGACAGGGAGTGGGATTGCTGGGGCGTAGGGACGTAGATCGGAAGAGCGGTTTCAG
chr18	39537734	39537773	PIK3C3_9524	+	GTGACCTATGCACCAGACGTTTTGGTCATGGTATGTTACAGACTGTTCTTACCTTTCTAGATCGGAAGAGCGGTTTCAG
chr18	39542608	39542647	PIK3C3_9525	+	GTGACCTATGCACCAGACGTTGTGGTCTCATCTGTAGGAGGTAGCAGCTTTCTGACCCAGATCGGAAGAGCGGTTTCAG
chr18	39550431	39550470	PIK3C3_9526	+	GTGACCTATGCACCAGACGTTTCAATTTGGAACAGGTGCAAAGCTCTGACTGATGTCTATTGAGATCGGAAGAGCGGTTTCAG
chr18	39570529	39570568	PIK3C3_9527	+	GTGACCTATGCACCAGACGTTGGAAGTGTGTTGGTCTCTAAAGTAGAGGGGAGAGGAAAAGATCGGAAGAGCGGTTTCAG
chr18	39573316	39573355	PIK3C3_9528	+	GTGACCTATGCACCAGACGTTGCAATTTTTTATGAAAGTACTTTTTCTCAGAGTAAATAGATCGGAAGAGCGGTTTCAG
chr18	39575969	39576008	PIK3C3_9529	+	GTGACCTATGCACCAGACGTTTGAATATTAATTTAAAATAGTTAAATGGGTGTTCTGAGATCGGAAGAGCGGTTTCAG
chr18	39576705	39576744	PIK3C3_9530	+	GTGACCTATGCACCAGACGTTGAATTTTCATATTAATAATTTTACCTAACCAACTTTGTTAGATCGGAAGAGCGGTTTCAG
chr18	39584516	39584555	PIK3C3_9531	+	GTGACCTATGCACCAGACGTATTTATTCTGCTTCAATGGGTCAATTTTAAACTAGAGCAGATCGGAAGAGCGGTTTCAG
chr18	39593571	39593610	PIK3C3_9532	+	GTGACCTATGCACCAGACGTCCAGGGAGGACATATTTCTAGTTTGTAAATTTTTCCCTTAGATCGGAAGAGCGGTTTCAG
chr18	39595541	39595580	PIK3C3_9533	+	GTGACCTATGCACCAGACGTAGCTTTTTCCAGCTTCCATAGGAGAGATCCTACTGCATGAAGATCGGAAGAGCGGTTTCAG
chr18	39600680	39600719	PIK3C3_9534	+	GTGACCTATGCACCAGACGTATAATTTCTGTTTATTCTTATTACCTTAAGAATTATAGATCGGAAGAGCGGTTTCAG
chr18	39609416	39609455	PIK3C3_9535	+	GTGACCTATGCACCAGACGTGGTGTATGCTTTTTGTTCTAATAGACCTTGGCATCAGAAAGATCGGAAGAGCGGTTTCAG
chr18	39613932	39613971	PIK3C3_9536	+	GTGACCTATGCACCAGACGTTGGATTTAATGTATTTAATGTGAACATTTCTAAGACATCGGAAGAGCGGTTTCAG
chr18	39617795	39617834	PIK3C3_9537	+	GTGACCTATGCACCAGACGTTCTTATGTTGGTGGGAACATTTTTTTCGTTTGGAAACAGATCGGAAGAGCGGTTTCAG
chr18	39618825	39618864	PIK3C3_9538	+	GTGACCTATGCACCAGACGTTTACATCATTATTTACTTTAGTGTACATTGTGTGAAGATCGGAAGAGCGGTTTCAG
chr18	39620716	39620755	PIK3C3_9539	+	GTGACCTATGCACCAGACGTTAATAAAGATTATGCAATTCATGAATATATTTCTGTCAAAAGATCGGAAGAGCGGTTTCAG
chr18	39623792	39623831	PIK3C3_9540	+	GTGACCTATGCACCAGACGTCAGGCTATTACTTTCCATTGATCAGATAAAGAAGAGCAGGAGATCGGAAGAGCGGTTTCAG
chr18	39629580	39629619	PIK3C3_9541	+	GTGACCTATGCACCAGACGTGACTACCCAGTAGACATACTTTATATGCCCATGGTTTAGATCGGAAGAGCGGTTTCAG
chr18	39638026	39638065	PIK3C3_9542	+	GTGACCTATGCACCAGACGTTTGCTTGGCCAGACAGAAATTTGGGTAAATTTATTTTTAGATCGGAAGAGCGGTTTCAG
chr18	39644805	39644844	PIK3C3_9543	+	GTGACCTATGCACCAGACGTAGTAACATAAATGAAGAGCTCTTCTGTATAATTTTTCCATAGATCGGAAGAGCGGTTTCAG
chr18	39647488	39647527	PIK3C3_9544	+	GTGACCTATGCACCAGACGTTGAGTGCAGTGCATTTTTCTCACCTTCTCCGTGTACTGCCAGATCGGAAGAGCGGTTTCAG
chr18	39661112	39661151	PIK3C3_9545	+	GTGACCTATGCACCAGACGTGACCCATCAAGATGCTTGGCTCAATAAGAAAACACGTTAAGATCGGAAGAGCGGTTTCAG
chr1	9775838	9775877	PIK3CD_9546	+	GTGACCTATGCACCAGACGTGAGTGGGCCGCTGCGCCGGCTGCCCTGCCCTGCCCCACAGATCGGAAGAGCGGTTTCAG
chr1	9776147	9776186	PIK3CD_9547	+	GTGACCTATGCACCAGACGTGCGTGGCCCTGCCGCTGAGGCTGCTCTGTCCATGGGGAGAGATCGGAAGAGCGGTTTCAG
chr1	9776688	9776727	PIK3CD_9548	+	GTGACCTATGCACCAGACGTTGAGGCCCTCTGCACTCTGGGCTCCCAACGCCCTGGATAGAGATCGGAAGAGCGGTTTCAG
chr1	9777177	9777216	PIK3CD_9549	+	GTGACCTATGCACCAGACGTGCCCTCCGCCTCCCCTCTGAGCCACCCTTCTTTCCACCTAGATCGGAAGAGCGGTTTCAG
chr1	9777695	9777734	PIK3CD_9550	+	GTGACCTATGCACCAGACGTTGGGATAGTGGGAGAGACACTGTTTTTTGCACAAAACAAGATCGGAAGAGCGGTTTCAG
chr1	9778984	9779023	PIK3CD_9551	+	GTGACCTATGCACCAGACGTGGGCCCGGCTGGGAGGGGTGCAGACCSCCGGAGACCAGTACAGATCGGAAGAGCGGTTTCAG
chr1	9780086	9780125	PIK3CD_9552	+	GTGACCTATGCACCAGACGTGCCACGGAGGGAGAGCGGTTGGGAGTGTGAGGGTCCAGAGATCGGAAGAGCGGTTTCAG
chr1	9780311	9780350	PIK3CD_9553	+	GTGACCTATGCACCAGACGTCCCCCGCCGCTGAGGCTGAGGGGCTGGCCGGAGCTCTCAGATCGGAAGAGCGGTTTCAG
chr1	9780730	9780769	PIK3CD_9554	+	GTGACCTATGCACCAGACGTTGGGGGTGTGGGGTGGGGGGCATGGAGCCGGCGTGAACAGATCGGAAGAGCGGTTTCAG
chr1	9780978	9781017	PIK3CD_9555	+	GTGACCTATGCACCAGACGTAGGGCCACCTGGGGCGGAGCTGGGGGCGAGACCAGCCTAGATCGGAAGAGCGGTTTCAG
chr1	9781317	9781356	PIK3CD_9556	+	GTGACCTATGCACCAGACGTGCTGGGCGCTCCCACCTTCTCCAGAGGGCAGCTGTGTCTTAGATCGGAAGAGCGGTTTCAG
chr1	9781656	9781695	PIK3CD_9557	+	GTGACCTATGCACCAGACGTTTCCCCAGCCGTTCTGTGGGAATCCCAGCCCTGAGTCTAGTCTCGGAAGAGCGGTTTCAG
chr1	9781929	9781968	PIK3CD_9558	+	GTGACCTATGCACCAGACGTAGGCCCTGGGGCGGGCAGGGGCGGCCCTGAGCCTGAGATCGGAAGAGCGGTTTCAG
chr1	9782222	9782261	PIK3CD_9559	+	GTGACCTATGCACCAGACGTGCCCGCCACAAGGGTCTCCACCCCTGGGAGGCGGTAGATCGGAAGAGCGGTTTCAG
chr1	9782425	9782464	PIK3CD_9560	+	GTGACCTATGCACCAGACGTGGCCTCCCCACACCCCGCCTGTACTGCCCTGGGGGCTCTAGATCGGAAGAGCGGTTTCAG
chr1	9782675	9782714	PIK3CD_9561	+	GTGACCTATGCACCAGACGTCCACCCACATCGTCCCTTGGTGTCTGTGCCAGCCTGGGAGATCGGAAGAGCGGTTTCAG
chr1	9783361	9783400	PIK3CD_9562	+	GTGACCTATGCACCAGACGTGGCCAGGGATAGGTTCCCTCTCTTCCAAGAGGTGTGGAGATCGGAAGAGCGGTTTCAG
chr1	9784161	9784200	PIK3CD_9563	+	GTGACCTATGCACCAGACGTTGGTGTGGCGGCTGCTGTGGGACTTTGGCTTCTGCCCCAGATCGGAAGAGCGGTTTCAG
chr1	9784490	9784529	PIK3CD_9564	+	GTGACCTATGCACCAGACGTTGCCGCCACAGATGCCCCCTCGGTTGGGGCCCAAGGAGATCGGAAGAGCGGTTTCAG
chr1	9785005	9785044	PIK3CD_9565	+	GTGACCTATGCACCAGACGTGGCAGGAGACTGCTGTGCCAGTGGACTTCCAAGCCCTGCAGATCGGAAGAGCGGTTTCAG
chr1	9787115	9787154	PIK3CD_9566	+	GTGACCTATGCACCAGACGTGAGCCCTGGGCCCAAGAGGAGGCGGCTGCGGGTCTGGGGAGATCGGAAGAGCGGTTTCAG
chr19	18267022	18267061	PIK3R2_9567	+	GTGACCTATGCACCAGACGTAGCAGGGGCCCTGGAAGGGGGTGGTCCCTCAGACCCTAGATCGGAAGAGCGGTTTCAG
chr19	18271790	18271829	PIK3R2_9568	+	GTGACCTATGCACCAGACGTGCCTCAATGGGTTGGGAGGAGGCTGGGGGCCCAAGTACAAGATCGGAAGAGCGGTTTCAG
chr19	18272006	18272045	PIK3R2_9569	+	GTGACCTATGCACCAGACGTTGGTGGCTGGGCTGCTGTGGGACTTTGGCTTCTGCCCCAGATCGGAAGAGCGGTTTCAG
chr19	18272872	18272911	PIK3R2_9570	+	GTGACCTATGCACCAGACGTTGTATTGCTGTCTTTCTCCCGTTGGGGCCGTAATACAGATCGGAAGAGCGGTTTCAG

chr19	18273131	18273170	PIK3R2_9571	+	GTGACCTATGCACCAGACGTGGCAGGGGGCCAGGGACCAAGGAGGTGTACAGGGTGAGCAGATCGGAAGAGCGGTTTCAG
chr19	18273327	18273366	PIK3R2_9572	+	GTGACCTATGCACCAGACGTGCCCTGCAAGGATAACCGGGGGTACAGGTCACAGAGACAGATCGGAAGAGCGGTTTCAG
chr19	18273968	18274007	PIK3R2_9573	+	GTGACCTATGCACCAGACGTGCCTGGGAGCCAGGGAGGGTAGCACCTGGCTGGCCCCAGGAGATCGGAAGAGCGGTTTCAG
chr19	18274209	18274248	PIK3R2_9574	+	GTGACCTATGCACCAGACGTCCCCGTACATGAGGGAAACCGAGACATAGAGGGGCAGTGGAGATCGGAAGAGCGGTTTCAG
chr19	18278127	18278166	PIK3R2_9575	+	GTGACCTATGCACCAGACGTGCTCCATACTTCCCTGCCGCTCCCTGGCGACTGCTGCGGCACATCGGAAGAGCGGTTTCAG
chr19	18279717	18279756	PIK3R2_9576	+	GTGACCTATGCACCAGACGTGCGCAGCGGTGGGGATTCCCCTGCCCTCCCTCCAGAGCTCTCAAGATCGGAAGAGCGGTTTCAG
chr19	18280115	18280154	PIK3R2_9577	+	GTGACCTATGCACCAGACGTCCCGGCCCAAGCAGAGCCGCCCTTGGCCCGTCTGCGCCGAGATCGGAAGAGCGGTTTCAG
chr7	113520191	113520230	PPP1R3A_9578	+	GTGACCTATGCACCAGACGTAAAAACAACAAAGAAATAATGACCATAAGATCTTTTAAAAAGATCGGAAGAGCGGTTTCAG
chr7	113522229	113522268	PPP1R3A_9579	+	GTGACCTATGCACCAGACGTAATATAATTGTCCATGTGAAGATTGTTTTAATTGTAGACAGATCGGAAGAGCGGTTTCAG
chr7	113522386	113522425	PPP1R3A_9580	+	GTGACCTATGCACCAGACGTAAAAAGAAAATGTATATGTTTTTCTGGGACTGCATCTTCAGATCGGAAGAGCGGTTTCAG
chr7	113559062	113559101	PPP1R3A_9581	+	GTGACCTATGCACCAGACGTGATATCAATAAGAGAGAAGCTGACGACTAGTAGAGGCTGAGATCGGAAGAGCGGTTTCAG
chr7	113558671	113558710	PPP1R3A_9582	+	GTGACCTATGCACCAGACGTTTTTCTGTTTGGATTTGTTCATAAGATCTTCTTTTGAAGATCGGAAGAGCGGTTTCAG
chr7	113518268	113518307	PPP1R3A_9583	+	GTGACCTATGCACCAGACGTATTTCTTCTGTTTGAATTCAAAATATTTTCTGATTTCTGATAGATCGGAAGAGCGGTTTCAG
chr7	113518748	113518787	PPP1R3A_9584	+	GTGACCTATGCACCAGACGTTTCATTGTATAGATTACACTACTGTATCTCGTTGACAAAAAGATCGGAAGAGCGGTTTCAG
chr7	113519228	113519267	PPP1R3A_9585	+	GTGACCTATGCACCAGACGTCCACCTGATTTTTCTTCAACTTGGAAAAGATAATCATTCCAGATCGGAAGAGCGGTTTCAG
chr7	113519708	113519747	PPP1R3A_9586	+	GTGACCTATGCACCAGACGTTTTACTTCAATATTTTAGTCTCCCTCATGTTTTTATAGATCGGAAGAGCGGTTTCAG
chr11	111597792	111597831	PPP2R1B_9587	+	GTGACCTATGCACCAGACGTAAACAGCATGTTGCTGCCAGCAGGAAGAGGGGCCACTTTTCAGATCGGAAGAGCGGTTTCAG
chr11	111608304	111608343	PPP2R1B_9588	+	GTGACCTATGCACCAGACGTAGACAGTGGCGCTGTAACTGTCCTGACCAGGGCACATCCAGATCGGAAGAGCGGTTTCAG
chr11	111612347	111612386	PPP2R1B_9589	+	GTGACCTATGCACCAGACGTCCAAAACAAATCAGGTTAGTGGTACAGAAAAGTTACGAAACAGATCGGAAGAGCGGTTTCAG
chr11	111612879	111612918	PPP2R1B_9590	+	GTGACCTATGCACCAGACGTAAAGTATTATCTGTGAAAGACAGTCTAATGGGCCATAGAAAGATCGGAAGAGCGGTTTCAG
chr11	111613400	111613439	PPP2R1B_9591	+	GTGACCTATGCACCAGACGTAAAGTAAGATGGCACATTTAAATACTTTAAAAAATTCCAAAGATCGGAAGAGCGGTTTCAG
chr11	111614265	111614304	PPP2R1B_9592	+	GTGACCTATGCACCAGACGTGGTCAAAAACATGTTCTCATATCGCTTATTGTTTTTAAAGATCGGAAGAGCGGTTTCAG
chr11	111618749	111618788	PPP2R1B_9593	+	GTGACCTATGCACCAGACGTAGAAGATCCATTAAACATATTGCCAAAATTCAGAAATAAGATCGGAAGAGCGGTTTCAG
chr11	111623067	111623106	PPP2R1B_9594	+	GTGACCTATGCACCAGACGTAAAGACCCCAAAAAGCACACATTTAAAAATCAAGTACTCTGAGATCGGAAGAGCGGTTTCAG
chr11	111624312	111624351	PPP2R1B_9595	+	GTGACCTATGCACCAGACGTATCGAAATTAAGAGCCTTTATTACAAGACAACAGAACTTAGATCGGAAGAGCGGTTTCAG
chr11	111625304	111625343	PPP2R1B_9596	+	GTGACCTATGCACCAGACGTAAAGAAAAAAGAATGCTTTCACAGGGCCATTACAAAGAGATCGGAAGAGCGGTTTCAG
chr11	111625829	111625868	PPP2R1B_9597	+	GTGACCTATGCACCAGACGTATTTGAAACGGGTTTTAATGTATACTAACAAAAGAATTAACAGATCGGAAGAGCGGTTTCAG
chr11	111626185	111626224	PPP2R1B_9598	+	GTGACCTATGCACCAGACGTAAATTTCTGTAATTCAGACATTTACTGAGACCCATGGGGAGATCGGAAGAGCGGTTTCAG
chr11	111630686	111630725	PPP2R1B_9599	+	GTGACCTATGCACCAGACGTAAACAATGAAGGTATTTCCCATCAATAACACTGAATAAAAGATCGGAAGAGCGGTTTCAG
chr11	111631786	111631825	PPP2R1B_9600	+	GTGACCTATGCACCAGACGTAAAAAGGAAAACAGAGAAGAATAATTTGAAATCAGGTAGATCGGAAGAGCGGTTTCAG
chr11	111635640	111635679	PPP2R1B_9601	+	GTGACCTATGCACCAGACGTCAACAACAGGACTCATCAACATGGATAGCTCTCCACAGCAGATCGGAAGAGCGGTTTCAG
chr11	111636119	111636158	PPP2R1B_9602	+	GTGACCTATGCACCAGACGTGAAAAGTAGAAAAGAAACAATGAAAAGAAACGGCTGAATTAGATCGGAAGAGCGGTTTCAG
chr12	70915302	70915341	PTPRB_9603	+	GTGACCTATGCACCAGACGTGAACACTGTAATTAGAGACTGCCGCAGGGTGTGTGTCATAATAGATCGGAAGAGCGGTTTCAG
chr12	70918382	70918421	PTPRB_9604	+	GTGACCTATGCACCAGACGTGCAAGAACTGTCAGAGGGCCGCTTCTCATGATAAGATCGGAAGAGCGGTTTCAG
chr12	70925961	70926000	PTPRB_9605	+	GTGACCTATGCACCAGACGTGGCAAAAGGAAAGATTGAGCCTTTTTATAAATTTGCCTTAGATCGGAAGAGCGGTTTCAG
chr12	70928442	70928481	PTPRB_9606	+	GTGACCTATGCACCAGACGTAGAGAGCAGGATAAAAAGGAACTGTCCAATGCAAACCTTAGATCGGAAGAGCGGTTTCAG
chr12	70928746	70928785	PTPRB_9607	+	GTGACCTATGCACCAGACGTACAGACAGAAAAACATGAGTCCGAAAAGTACTCTTGTAGATCGGAAGAGCGGTTTCAG
chr12	70929950	70929989	PTPRB_9608	+	GTGACCTATGCACCAGACGTTTTACAATATGGAGAGTCAAGAAACATGGCCCTTTCAGAAAGATCGGAAGAGCGGTTTCAG
chr12	70932805	70932844	PTPRB_9609	+	GTGACCTATGCACCAGACGTAAATATGAGTTTGTAAGTGGAGAATGAAATAGAATAAAAGATCGGAAGAGCGGTTTCAG
chr12	70933497	70933536	PTPRB_9610	+	GTGACCTATGCACCAGACGTAAATGAAAACAAACAGAAAAGAGTTACTGCAGAAAAGGAAAAGATCGGAAGAGCGGTTTCAG
chr12	70933635	70933674	PTPRB_9611	+	GTGACCTATGCACCAGACGTAAAGCAAAAAGAGCAAGACTTTGTTGACAAATTTACATAAAGATCGGAAGAGCGGTTTCAG
chr12	70933813	70933852	PTPRB_9612	+	GTGACCTATGCACCAGACGTAGGGAGATAACTTTTTATTCTGATTATGATACTTGGCTTGAAGATCGGAAGAGCGGTTTCAG
chr12	70934748	70934787	PTPRB_9613	+	GTGACCTATGCACCAGACGTCCAGATAGAAAACAAACAGCAGGTGGGAAAATTAGTGTAGATCGGAAGAGCGGTTTCAG
chr12	70938454	70938493	PTPRB_9614	+	GTGACCTATGCACCAGACGTAAACCGATTTATTTAAATATAAATAGTTGTTGAAACACAGTAGATCGGAAGAGCGGTTTCAG
chr12	70946811	70946850	PTPRB_9615	+	GTGACCTATGCACCAGACGTAAACCCACAGTTAAGGACTGCCTTTCTGTGACTTAGGTGAGATCGGAAGAGCGGTTTCAG
chr12	70949100	70949139	PTPRB_9616	+	GTGACCTATGCACCAGACGTAGGTGGGGAAGCAACAGAAAGACTGTCACACTCTGCTTTTCAGATCGGAAGAGCGGTTTCAG
chr12	70949939	70949978	PTPRB_9617	+	GTGACCTATGCACCAGACGTGAGAGGAGGCAACACTTTTTCAGAACTCAGGGAGAATTTTTAGATCGGAAGAGCGGTTTCAG
chr12	70953415	70953454	PTPRB_9618	+	GTGACCTATGCACCAGACGTGAGAAAAGTAAAAATCATAATACAGCTATGCCATAACAGATCGGAAGAGCGGTTTCAG
chr12	70954725	70954764	PTPRB_9619	+	GTGACCTATGCACCAGACGTAGAAAAATGTTACTGAGAACAACAAACAGCAAGCATAGATCGGAAGAGCGGTTTCAG
chr12	70956898	70956937	PTPRB_9620	+	GTGACCTATGCACCAGACGTGAGGAGCAAGAGAATGAGGGAGGGAATGCAGTGAGGAGAGATCGGAAGAGCGGTTTCAG
chr12	70960495	70960534	PTPRB_9621	+	GTGACCTATGCACCAGACGTACAAGTGGAGCAACAAAATACAGATTTTACTACTTAGGTTAGATCGGAAGAGCGGTTTCAG
chr12	70963729	70963768	PTPRB_9622	+	GTGACCTATGCACCAGACGTAAATAAATTTAAAGTCAATCAGATAAGACTTGTAGAAATGAACTGTGAGATCGGAAGAGCGGTTTCAG
chr12	70965080	70965119	PTPRB_9623	+	GTGACCTATGCACCAGACGTAAATGAGAAGACATTTCAAGAAAGGAACTGATCAGAGTTTAGATCGGAAGAGCGGTTTCAG
chr12	70965878	70965917	PTPRB_9624	+	GTGACCTATGCACCAGACGTAAACAGAGTAACATAAATTTATGAATTCTGAGTGAGTAAGATCGGAAGAGCGGTTTCAG
chr12	70970436	70970475	PTPRB_9625	+	GTGACCTATGCACCAGACGTGAAAAGTGGGGGCGGGGGGGGGGGAAAGGGGGATTCAAAGATCGGAAGAGCGGTTTCAG
chr12	70975093	70975132	PTPRB_9626	+	GTGACCTATGCACCAGACGTAGACAGAAAGAAAACAAATGACACTTAGTACCTTAAAGAGATCGGAAGAGCGGTTTCAG
chr12	70981058	70981097	PTPRB_9627	+	GTGACCTATGCACCAGACGTAGCAATGGATGGGTCTATTGATGGACTGAGGCATATTCAGATCGGAAGAGCGGTTTCAG
chr12	70984024	70984063	PTPRB_9628	+	GTGACCTATGCACCAGACGTAAATGATGTCAAAAAGGAGATATTACAGACCAAAAAGTAAGATCGGAAGAGCGGTTTCAG

chr12	70986336	70986375	PTPRB_9629	+	GTGACCTATGCACCAGACGTAAGAACAGAAAGGAGACTTTTACTCAGGATCTCTCACAGAGATCGGAAGAGCGGTTCCAG
chr12	70988515	70988554	PTPRB_9630	+	GTGACCTATGCACCAGACGTAAAATGCATGTCCAAATGTCATTAATAATTCCCTTATAGGAGATCGGAAGAGCGGTTCCAG
chr12	71003130	71003169	PTPRB_9631	+	GTGACCTATGCACCAGACGTATCAGACACAACAGTTAAAGTCCACAGTCTGGACTGCCTAAGATCGGAAGAGCGGTTCCAG
chr12	71003605	71003644	PTPRB_9632	+	GTGACCTATGCACCAGACGTAGTTAAGATCCAGAGGAGACCCAGGGGGCTGGACGTGGGAAGATCGGAAGAGCGGTTCCAG
chr12	71016437	71016476	PTPRB_9633	+	GTGACCTATGCACCAGACGTGAAAAGATAGTTGCAAAGATTATTCTCATGTTTTATGAATAGATCGGAAGAGCGGTTCCAG
chr12	71029857	71029896	PTPRB_9634	+	GTGACCTATGCACCAGACGTAAAAGCTCATAAAGCACTATGTAGCAAATATGAGGCCAAGATCGGAAGAGCGGTTCCAG
chr12	71031186	71031225	PTPRB_9635	+	GTGACCTATGCACCAGACGTGCAACTGTTCCATGTTGGGAAAAAATAAATCTCAGATCGGAAGAGCGGTTCCAG
chr6	117622311	117622350	ROS1_9636	+	GTGACCTATGCACCAGACGTGGGGAAAGATGGGAAAGTAAATAGCAATTGGATATAAATTAAGATCGGAAGAGCGGTTCCAG
chr6	117630102	117630141	ROS1_9637	+	GTGACCTATGCACCAGACGTAGAGGGTTTGTCTTAATTATACCTATTACAAACACCAGGAGATCGGAAGAGCGGTTCCAG
chr6	117638446	117638485	ROS1_9638	+	GTGACCTATGCACCAGACGTGAAAAGACACAGGCTGGATGATATGACAGAAGCAGGAGTCCAGATCGGAAGAGCGGTTCCAG
chr6	117639426	117639465	ROS1_9639	+	GTGACCTATGCACCAGACGTAAAAACAAGTCAGGAATCAGTATAGCAGACATTTCTGTGAGATCGGAAGAGCGGTTCCAG
chr6	117641204	117641243	ROS1_9640	+	GTGACCTATGCACCAGACGTGCAACATTTTGTCTCCCCCCTCCACATATATAGGTTGAGATCGGAAGAGCGGTTCCAG
chr6	117642568	117642607	ROS1_9641	+	GTGACCTATGCACCAGACGTAAAAATGACAATAATTCACAAAATAAAATATTGCTTCTTTTATAGATCGGAAGAGCGGTTCCAG
chr6	117645589	117645628	ROS1_9642	+	GTGACCTATGCACCAGACGTAAATCAGAAAAAGAAATTAATTCATAGATAAAAGCTAAGTAGATCGGAAGAGCGGTTCCAG
chr6	117647588	117647627	ROS1_9643	+	GTGACCTATGCACCAGACGTAAATAATACAGAAAATATACATGACATATACCTGTATAGATCGGAAGAGCGGTTCCAG
chr6	117650620	117650659	ROS1_9644	+	GTGACCTATGCACCAGACGTAAAAAGAAAATATTGGTTGATATGTTTGAAGTAAATCTAGATCGGAAGAGCGGTTCCAG
chr6	117658514	117658553	ROS1_9645	+	GTGACCTATGCACCAGACGTAAAGTCTCGATTAAATTTTTTTTCTCTAAGAAAATATTAGATCGGAAGAGCGGTTCCAG
chr6	117662485	117662524	ROS1_9646	+	GTGACCTATGCACCAGACGTAAAAAGCAACTTGTCTTAAAGTTGAGGCCTTGCACTTGAGATCGGAAGAGCGGTTCCAG
chr6	117662806	117662845	ROS1_9647	+	GTGACCTATGCACCAGACGTTAGCAAGGAATGATAAAGGATGCTGCAATAGCACTGAAAAGAGATCGGAAGAGCGGTTCCAG
chr6	117663718	117663757	ROS1_9648	+	GTGACCTATGCACCAGACGTTTTTTAAAAATCAACATCTTATTTTTAACATTTTATACAAGATCGGAAGAGCGGTTCCAG
chr6	117665436	117665475	ROS1_9649	+	GTGACCTATGCACCAGACGTAAAGAAACAAAAGATTAAATATCTATACTATATATAGAGATCGGAAGAGCGGTTCCAG
chr6	117674343	117674382	ROS1_9650	+	GTGACCTATGCACCAGACGTGATAAGGAATATAAAGAACAATAAATTAATCTTACATTTTATAGATCGGAAGAGCGGTTCCAG
chr6	117678089	117678128	ROS1_9651	+	GTGACCTATGCACCAGACGTAAAAAAGTCCCCCAACTTAATGAGTAAAATACATCATTAGATCGGAAGAGCGGTTCCAG
chr6	117679183	117679222	ROS1_9652	+	GTGACCTATGCACCAGACGTGGTAGACACAGCCAAAGAGAGATGGTTATTTTTTAAAGATCGGAAGAGCGGTTCCAG
chr6	117681185	117681224	ROS1_9653	+	GTGACCTATGCACCAGACGTAAAAACATGTAGATAATATGCATGAGAAAAGTACTTTAGATCGGAAGAGCGGTTCCAG
chr6	117681579	117681618	ROS1_9654	+	GTGACCTATGCACCAGACGTGAAAACAAAATTCATTGATGAGTTCTCCGTGGCAACAGATCGGAAGAGCGGTTCCAG
chr6	117684039	117684078	ROS1_9655	+	GTGACCTATGCACCAGACGTGAGGGACAGGTTAGAGCAGAAAAGAATATAAAGAATATAAAGAGATCGGAAGAGCGGTTCCAG
chr6	117686378	117686417	ROS1_9656	+	GTGACCTATGCACCAGACGTACAGAAAAAATTTTCTCAGGGAGAGAATTATAAATAGATCGGAAGAGCGGTTCCAG
chr6	117686915	117686954	ROS1_9657	+	GTGACCTATGCACCAGACGTAAAACAAAAGAAAATGAGGAAAGATAAGGATTTAGATCGGAAGAGCGGTTCCAG
chr6	117687464	117687503	ROS1_9658	+	GTGACCTATGCACCAGACGTATAACACCAATTAGTGTGTTCTGGAGTGGTGGAGGATCGGAAGAGCGGTTCCAG
chr6	117700333	117700372	ROS1_9659	+	GTGACCTATGCACCAGACGTAGTAAGGTAAGAAAATAAACCAATACATGTTTGAAGCATAGATCGGAAGAGCGGTTCCAG
chr6	117704682	117704721	ROS1_9660	+	GTGACCTATGCACCAGACGTAAATTGATGGCCAGTTAATGGCTTCAAGTGACATTATTAGATCGGAAGAGCGGTTCCAG
chr6	117707035	117707074	ROS1_9661	+	GTGACCTATGCACCAGACGTAGTGAATGATTAGCAGTTATTTTTTCATACATACCAACAAGATCGGAAGAGCGGTTCCAG
chr6	117708173	117708212	ROS1_9662	+	GTGACCTATGCACCAGACGTAAAAAGAAATAAAAGAAACATCAGGAAAAGCAACTTTAGATCGGAAGAGCGGTTCCAG
chr6	117709208	117709247	ROS1_9663	+	GTGACCTATGCACCAGACGTAAAACCAAGGATTTCCATAAATTCACCTACAGCCTCATCTAGATCGGAAGAGCGGTTCCAG
chr6	117711020	117711059	ROS1_9664	+	GTGACCTATGCACCAGACGTAAACAAAAGAAACCTCATGAGATTGAGTCCAAAGGTTGATGAGATCGGAAGAGCGGTTCCAG
chr6	117714495	117714534	ROS1_9665	+	GTGACCTATGCACCAGACGTAAAAATATACCGGTAGGATTAGCATCTGTCTATACAGCAAGATCGGAAGAGCGGTTCCAG
chr6	117715520	117715559	ROS1_9666	+	GTGACCTATGCACCAGACGTGCAAGTGCACACACATTATATATAACAACCAGGACAAGATCGGAAGAGCGGTTCCAG
chr6	117715912	117715951	ROS1_9667	+	GTGACCTATGCACCAGACGTCAACACAATTTGCAGACAGGTAGACCAACCACAGGTACACAGATCGGAAGAGCGGTTCCAG
chr6	117717438	117717477	ROS1_9668	+	GTGACCTATGCACCAGACGTAAACAATTTGGAGAGACGTGTTTCATGTCATGGTGTGAAAGATCGGAAGAGCGGTTCCAG
chr6	117718290	117718329	ROS1_9669	+	GTGACCTATGCACCAGACGTAAATGGTATGATGATGACAGAAAAATGTGCAAGCATGATAGATCGGAAGAGCGGTTCCAG
chr6	117724451	117724490	ROS1_9670	+	GTGACCTATGCACCAGACGTGAGTGATCAATCATCAGCATTATAGAATCAGCACCCCAAGATCGGAAGAGCGGTTCCAG
chr6	117725602	117725641	ROS1_9671	+	GTGACCTATGCACCAGACGTAAACAAGATTACTACCACGCACTCCTGTCCATCAGGCAGATCGGAAGAGCGGTTCCAG
chr6	117730816	117730855	ROS1_9672	+	GTGACCTATGCACCAGACGTGAGGGAGCATTGACAGTCAAGGGCACTTGATACTGGTTTTAGATCGGAAGAGCGGTTCCAG
chr6	117737491	117737530	ROS1_9673	+	GTGACCTATGCACCAGACGTCAATAACAGACAATGGTGAATGATTGAAAGAAATGTGACTTTAGATCGGAAGAGCGGTTCCAG
chr6	117739680	117739719	ROS1_9674	+	GTGACCTATGCACCAGACGTGAAGGAGGTAGTAACACAGCCATCAGTACTGGTTCGAAGATCGGAAGAGCGGTTCCAG
chr6	117746830	117746869	ROS1_9675	+	GTGACCTATGCACCAGACGTATGGCAGTTTTTAGATGGCCGGTCTAATTTTTCTCATTTAGATCGGAAGAGCGGTTCCAG
chr6	166826386	166826425	RPS6KA2_9676	+	GTGACCTATGCACCAGACGTGAAGACAAGGGTGAGAGCCGCGGCGCTCACTCCAGGGGTAGATCGGAAGAGCGGTTCCAG
chr6	166827430	166827469	RPS6KA2_9677	+	GTGACCTATGCACCAGACGTAGGTCATGAGAGTGGGGGGATGGTTGGATCAATTTGTGCTAGATCGGAAGAGCGGTTCCAG
chr6	166831841	166831880	RPS6KA2_9678	+	GTGACCTATGCACCAGACGTAGACAAATTTGTGGTAAAGACCTGTTATTTTACAACCTAAAGATCGGAAGAGCGGTTCCAG
chr6	166833457	166833496	RPS6KA2_9679	+	GTGACCTATGCACCAGACGTACGACAGGACACCCGCTTCACTAAGGACATTCAGATCGGAAGAGCGGTTCCAG
chr6	166836916	166836955	RPS6KA2_9680	+	GTGACCTATGCACCAGACGTGAAGGCAGATGCCTACTTGGGGGTGAGGACTGAGCAGGATCGGAAGAGCGGTTCCAG
chr6	166844110	166844149	RPS6KA2_9681	+	GTGACCTATGCACCAGACGTGAGAAGGGGCGCACACGTCAACCAGGCTGGTTGCTGTGAAAGATCGGAAGAGCGGTTCCAG
chr6	166845989	166846028	RPS6KA2_9682	+	GTGACCTATGCACCAGACGTCAACAGCACATGGCAGTGAGGGGTCTACTTTAGGCTTTCGGAGATCGGAAGAGCGGTTCCAG
chr6	166862348	166862387	RPS6KA2_9683	+	GTGACCTATGCACCAGACGTACCAGAGAGAAGAAGATTGTCGGAACCTCACACGAGGGGAGATCGGAAGAGCGGTTCCAG
chr6	166864732	166864771	RPS6KA2_9684	+	GTGACCTATGCACCAGACGTGAGGGGAGGTTAGATGCCACGAAAGCTGGGTGACCTAGATCGGAAGAGCGGTTCCAG
chr6	166873050	166873089	RPS6KA2_9685	+	GTGACCTATGCACCAGACGTGAAGGAAAGCAAGACAGGCCTGAGGATGCACAGACATTGAGATCGGAAGAGCGGTTCCAG
chr6	166883404	166883443	RPS6KA2_9686	+	GTGACCTATGCACCAGACGTACAGAAATGATCATCAGAACAATAAAGATGGGGTCTAGATCGGAAGAGCGGTTCCAG

chr6	166902420	166902459	RPS6KA2_9687	+	GTGACCTATGCACCAGACGTAGATCCTATTTTAGGATCTATTTTAGGAGAACAAGGACAAAGATCGGAAGAGCGGTTTCAG
chr6	166904240	166904279	RPS6KA2_9688	+	GTGACCTATGCACCAGACGTACACAGAGCACAGTGAGTTTCATTCATCCAGATGGACCCGGAGATCGGAAGAGCGGTTTCAG
chr6	166912149	166912188	RPS6KA2_9689	+	GTGACCTATGCACCAGACGTACACAGCACACACTGCCTCAGTCTCTGGGTGTGTTCCGGAGATCGGAAGAGCGGTTTCAG
chr6	166914423	166914462	RPS6KA2_9690	+	GTGACCTATGCACCAGACGTGGGAGAGAAAACAGATGCTTTAGAAAAGAGACCCAGCTGCAGATCGGAAGAGCGGTTTCAG
chr6	166921781	166921820	RPS6KA2_9691	+	GTGACCTATGCACCAGACGTGACAGACCCGCAATTTTGACAGCTTGTCGAATGTCTGTGGAGATCGGAAGAGCGGTTTCAG
chr6	166923856	166923895	RPS6KA2_9692	+	GTGACCTATGCACCAGACGTAAAAGATAAAGGCTTTTCATGAGGCGAGAAATAAGAGTTCTAGATCGGAAGAGCGGTTTCAG
chr6	166944812	166944851	RPS6KA2_9693	+	GTGACCTATGCACCAGACGTGAAACCGGAAACATCAGAAACCCGTAAGACTTCAAACCTCCAGATCGGAAGAGCGGTTTCAG
chr6	166952283	166952322	RPS6KA2_9694	+	GTGACCTATGCACCAGACGTGCGGCACGGGTGAGAAAACACCCGCGAGGAGTCCCTCAGAAGATCGGAAGAGCGGTTTCAG
chr6	167040518	167040557	RPS6KA2_9695	+	GTGACCTATGCACCAGACGTCCAGCCCGGAGCAGCCGACGGGCCGGGGACGCGCATCCAGATCGGAAGAGCGGTTTCAG
chr6	167271758	167271797	RPS6KA2_9696	+	GTGACCTATGCACCAGACGTAGATAGATGTTAAAGATGGTTAGCATTGCCATGTGTTTGTAGATCGGAAGAGCGGTTTCAG
chr6	167275669	167275708	RPS6KA2_9697	+	GTGACCTATGCACCAGACGTTCCTTTCTGCTGGTCGAGTATTGATAGTAGGAAAGGAAAAGATCGGAAGAGCGGTTTCAG
chr1	17345464	17345503	SDHB_9698	+	GTGACCTATGCACCAGACGTGAGAAAAGAAATCAATAACAAATGATAACTGAAACTGAAAGAGATCGGAAGAGCGGTTTCAG
chr1	17349236	17349275	SDHB_9699	+	GTGACCTATGCACCAGACGTGAGGATGATTAGCTGAGCTGCCAATCAACAGGCCAGAGCCGAGATCGGAAGAGCGGTTTCAG
chr1	17350580	17350619	SDHB_9700	+	GTGACCTATGCACCAGACGTAGAAAAGAGAGGCAGGAGCTTGTGACGGGAGAGACTCTGCAGATCGGAAGAGCGGTTTCAG
chr1	17355242	17355281	SDHB_9701	+	GTGACCTATGCACCAGACGTCCACACATTAACACATCCTCACCCATATCCGGAATCAGTCAGATCGGAAGAGCGGTTTCAG
chr1	17359651	17359690	SDHB_9702	+	GTGACCTATGCACCAGACGTAAAATATCCAGTGGTATTTATGTAACGTTCAACCTCCCTAAGATCGGAAGAGCGGTTTCAG
chr1	17371394	17371433	SDHB_9703	+	GTGACCTATGCACCAGACGTAAAAGTTACAAAAAGGAAAAAATTAGAAATACAAGAGATCGGAAGAGCGGTTTCAG
chr1	17380525	17380564	SDHB_9704	+	GTGACCTATGCACCAGACGTGACGTGACCGTCCAGCCACCCCTTAACCCGAGGTCGCTCTCCGAGATCGGAAGAGCGGTTTCAG
chr12	53775608	53775647	SP1_9705	+	GTGACCTATGCACCAGACGTATCATAGAGTGGGAAAGGTTGAGAAAGATGTAATATTCAGATCGGAAGAGCGGTTTCAG
chr12	53777417	53777456	SP1_9706	+	GTGACCTATGCACCAGACGTCAATCTTGTCATTATTGGGAACCACTTAGCATCGTAAGATCGGAAGAGCGGTTTCAG
chr12	53800548	53800587	SP1_9707	+	GTGACCTATGCACCAGACGTCCAGCCAGTTTCTTACAATATAAAGAAAATTAATAGATAGATCGGAAGAGCGGTTTCAG
chr12	53803356	53803395	SP1_9708	+	GTGACCTATGCACCAGACGTGCCTATGGGAGAGAAAATAGTAATAGACTAGAATGAAAAGATCGGAAGAGCGGTTTCAG
chr12	53805035	53805074	SP1_9709	+	GTGACCTATGCACCAGACGTCCGGGCCAGAGACATATGGCCATACCCCTAACCCGGAGATCGGAAGAGCGGTTTCAG
chr12	53776282	53776321	SP1_9710	+	GTGACCTATGCACCAGACGTGGCAACAGCTGCAGTTTGTCTGCTGGCCACTGGGGCCCAAGTCCAGATCGGAAGAGCGGTTTCAG
chr12	53776660	53776699	SP1_9711	+	GTGACCTATGCACCAGACGTGGTATCATACAAGCCAGTCCAGCTCCTTTTTACCAAGATCGGAAGAGCGGTTTCAG
chr12	53777038	53777077	SP1_9712	+	GTGACCTATGCACCAGACGTAGAACCTCCAGCTTCAGGCTGTTCCAACTCTGGTCCCATAGATCGGAAGAGCGGTTTCAG
chr15	39874136	39874175	THBS1_9713	+	GTGACCTATGCACCAGACGTGTGGCACCTTTAGGGGAAGGAGGGACAGGAAGAGGTCGATAGATCGGAAGAGCGGTTTCAG
chr15	39874964	39875003	THBS1_9714	+	GTGACCTATGCACCAGACGTTCCTCTGAGCCCTGCTCCGTGGGATCATCTGCTAGACAGGAGATCGGAAGAGCGGTTTCAG
chr15	39875904	39875943	THBS1_9715	+	GTGACCTATGCACCAGACGTCTCTATTTTAGGCCACATAGGGAATCGGGGGAATCCAGATCGGAAGAGCGGTTTCAG
chr15	39876399	39876438	THBS1_9716	+	GTGACCTATGCACCAGACGTCTGACACCCAGCCGTTAGACTGAACCCCTGGAAGGTTTATAGATCGGAAGAGCGGTTTCAG
chr15	39876634	39876673	THBS1_9717	+	GTGACCTATGCACCAGACGTTCACCAGCCAGAATAAGAATCGACGGCTTTTGTGTTGAACAGATCGGAAGAGCGGTTTCAG
chr15	39877775	39877814	THBS1_9718	+	GTGACCTATGCACCAGACGTCAAATGGCAGTAGCTATTTCTCAGTACTAGGTCAGTCTAAGATCGGAAGAGCGGTTTCAG
chr15	39879732	39879771	THBS1_9719	+	GTGACCTATGCACCAGACGTGAGCCCTCAGGGACGTGGAGAATGACCTGTCTTGTGATCGGAAGAGCGGTTTCAG
chr15	39880430	39880469	THBS1_9720	+	GTGACCTATGCACCAGACGTGGTCGCTGCAAGGGTGAGCATGGGCAGCAGCTCTGCCAAGATCGGAAGAGCGGTTTCAG
chr15	39880911	39880950	THBS1_9721	+	GTGACCTATGCACCAGACGTGACGCCAGGATGAAACCCAGCCAGGAGCTTTGCTCTTTTACAGATCGGAAGAGCGGTTTCAG
chr15	39881298	39881337	THBS1_9722	+	GTGACCTATGCACCAGACGTGATGGGGCTCCGAGTTTCTGGATCTAGGAAAGCAGCTAACAGATCGGAAGAGCGGTTTCAG
chr15	39881566	39881605	THBS1_9723	+	GTGACCTATGCACCAGACGTCTAGACGAGTAACCCAGAGGACAGGAGGAGCTGTCTTGACAGATCGGAAGAGCGGTTTCAG
chr15	39882235	39882274	THBS1_9724	+	GTGACCTATGCACCAGACGTGTCCCTTTGTGTCCTCCAGAAAAGAGGGCCCATCACCTTATAGATCGGAAGAGCGGTTTCAG
chr15	39882835	39882874	THBS1_9725	+	GTGACCTATGCACCAGACGTTCCTATCCCTTTTTCATCTTTTTCAGTTACGACACAGCCAGATCGGAAGAGCGGTTTCAG
chr15	39883562	39883601	THBS1_9726	+	GTGACCTATGCACCAGACGTGCCGTGATCAGAGGCCCGCGGGAGACAGGAGATGCACAGAGATCGGAAGAGCGGTTTCAG
chr15	39883835	39883874	THBS1_9727	+	GTGACCTATGCACCAGACGTGGACTCCTTTTCAGAGTCTTTTCAGTAACTGTTGGAAATATCAGATCGGAAGAGCGGTTTCAG
chr15	39885014	39885053	THBS1_9728	+	GTGACCTATGCACCAGACGTGGAGCCACTTTCTAAGACAGGGACTGCTGGCACAGCTGTGAGATCGGAAGAGCGGTTTCAG
chr15	39885439	39885478	THBS1_9729	+	GTGACCTATGCACCAGACGTAGTTCTTAGATCCTAAGAGACTGATGCATACATGGGAAAAGATCGGAAGAGCGGTTTCAG
chr15	39885880	39885919	THBS1_9730	+	GTGACCTATGCACCAGACGTAAAGCCTGGAACAGAGAGAGGACTTATGGGTGCCTGACTAAGATCGGAAGAGCGGTTTCAG
chr15	39886408	39886447	THBS1_9731	+	GTGACCTATGCACCAGACGTACTGACCTTTTACTTACAGTCACTAGGGGACAAAAGATCGGAAGAGCGGTTTCAG
chr15	39886652	39886691	THBS1_9732	+	GTGACCTATGCACCAGACGTATCAGCTGAATGTACCTGAGACTGATGATCTCTATTTTACAGATCGGAAGAGCGGTTTCAG
chr15	39887581	39887620	THBS1_9733	+	GTGACCTATGCACCAGACGTGTTGATTGAAAGACTGATCATAAACCAATGCTGGTATTGCAGATCGGAAGAGCGGTTTCAG
chr15	39874684	39874723	THBS1_9734	+	GTGACCTATGCACCAGACGTGTGCCAATGGCAAGGCGGGCACCCCTGGACCTCAGCTGAAGATCGGAAGAGCGGTTTCAG
chr1	3599005	3599044	TP73_9735	+	GTGACCTATGCACCAGACGTGGCTGGCCAGAGCTGGGGGCCCCCTGGGAGGACTCTAGATCGGAAGAGCGGTTTCAG
chr1	3599755	3599794	TP73_9736	+	GTGACCTATGCACCAGACGTGGGCTGCCCTCTGCAAGAGGACTGGAGTGGGGACAACAAAAGATCGGAAGAGCGGTTTCAG
chr1	3607519	3607558	TP73_9737	+	GTGACCTATGCACCAGACGTCCGCCATCATAGGATCTTCGCGGACTTTGCGGGGAAAGATCGGAAGAGCGGTTTCAG
chr1	3638782	3638821	TP73_9738	+	GTGACCTATGCACCAGACGTCCAGCTCCTCTGCCACGGTGGCAGTTTCCGAGCATCCAGATCGGAAGAGCGGTTTCAG
chr1	3640044	3640083	TP73_9739	+	GTGACCTATGCACCAGACGTAGCCAGGCTGTGCCAGGGCCCTGCAGTCAGCTGTACGGGAGATCGGAAGAGCGGTTTCAG
chr1	3643799	3643838	TP73_9740	+	GTGACCTATGCACCAGACGTGGCACAGGGGTGGAGGTGGGACAGGGCTGGGACAGGCAGAGATCGGAAGAGCGGTTTCAG
chr1	3644345	3644384	TP73_9741	+	GTGACCTATGCACCAGACGTGGCCAGGGAACTGGACCGTGTGGGAGGAGAAGGGGACAAGATCGGAAGAGCGGTTTCAG
chr1	3644792	3644831	TP73_9742	+	GTGACCTATGCACCAGACGTGCTCCTGCCACGGCAGCCGGAGACCTGCCCTCACCTGTGCAGATCGGAAGAGCGGTTTCAG
chr1	3646023	3646062	TP73_9743	+	GTGACCTATGCACCAGACGTCTAGCCACAGTCTAGTGTGGGAAAGGACATGCTTAAGATCGGAAGAGCGGTTTCAG
chr1	3646723	3646762	TP73_9744	+	GTGACCTATGCACCAGACGTGGGACGTGCCGGCCAGGGCAGGGGAGGCCACTAGATCGGAAGAGCGGTTTCAG



chr1	3647640	3647679	TP73_9745	+	GTGACCTATGCACCAGACGTTGCCGAGGGCCTGAGCATGTGCTGTACCCTGTCTGTTCAAGATCGGAAGAGCGGTTTCAG
chr1	3648130	3648169	TP73_9746	+	GTGACCTATGCACCAGACGTTGGGTGGACCCCGCTCTGCAGAGGCAGTAGCTGGAGGGGCCAGATCGGAAGAGCGGTTTCAG
chr1	3648131	3648170	TP73_9747	+	GTGACCTATGCACCAGACGTTGGGTGGACCCCGCTCTGCAGAGGCAGTAGCTGGAGGGGGCCAGATCGGAAGAGCGGTTTCAG
chr1	3649337	3649376	TP73_9748	+	GTGACCTATGCACCAGACGTTGCAGTACCGCATGACCATCTGGCGGGCCTGCAGGACCTGAGATCGGAAGAGCGGTTTCAG
chr1	3649654	3649693	TP73_9749	+	GTGACCTATGCACCAGACGTTGGCTGCAGCTCGGCCACCGCCAGAGACCACAGATCGGCAGATCGGAAGAGCGGTTTCAG
chr12	121746505	121746544	ANAPC5_9750	+	GTGACCTATGCACCAGACGTTGGGAAAAATAACACACACATTTAACTCAACCCTTCCAGTAAGATCGGAAGAGCGGTTTCAG
chr12	121747677	121747716	ANAPC5_9751	+	GTGACCTATGCACCAGACGTTAGCATGTGCCACTGTACATACCACAAACCCTGCCCCTTCAGATCGGAAGAGCGGTTTCAG
chr12	121756238	121756277	ANAPC5_9752	+	GTGACCTATGCACCAGACGTAGAGGAAAAACAGGATGAGAAGATCCACCACCACATCTCAGATCGGAAGAGCGGTTTCAG
chr12	121756422	121756461	ANAPC5_9753	+	GTGACCTATGCACCAGACGTATCAAAATGAACACAAGTGTTTAACTAGTCACTTTGAGGAGATCGGAAGAGCGGTTTCAG
chr12	121757632	121757671	ANAPC5_9754	+	GTGACCTATGCACCAGACGTAAAAAAACACAATTAAGTACAAAATGGCGAATGTTTCATCTAGATCGGAAGAGCGGTTTCAG
chr12	121758273	121758312	ANAPC5_9755	+	GTGACCTATGCACCAGACGTAAACACACAATTTGATCAGCATAACCTGTGTTGAATCCACAAGATCGGAAGAGCGGTTTCAG
chr12	121765045	121765084	ANAPC5_9756	+	GTGACCTATGCACCAGACGTAGAGGGAACGATTTTCCCTTTCAGCAGCAGACCTGGCTGCAGATCGGAAGAGCGGTTTCAG
chr12	121766272	121766311	ANAPC5_9757	+	GTGACCTATGCACCAGACGTAGGGACTGTATCCAGGGAGGCCGAGGTACTAAGGGACAAGATCGGAAGAGCGGTTTCAG
chr12	121766311	121766350	ANAPC5_9758	+	GTGACCTATGCACCAGACGTAGATATACCCACGACCCAAGATAGAGATTACATGACAGAAAGATCGGAAGAGCGGTTTCAG
chr12	121768486	121768525	ANAPC5_9759	+	GTGACCTATGCACCAGACGTAAATCATCAAAATATATATAACAGTGGCAATGGCTGATGAGATCGGAAGAGCGGTTTCAG
chr12	121769242	121769281	ANAPC5_9760	+	GTGACCTATGCACCAGACGTACTAAACATTAATATCCCATAAATAACACAACATGCATAGATCGGAAGAGCGGTTTCAG
chr12	121773537	121773576	ANAPC5_9761	+	GTGACCTATGCACCAGACGTTAAATCAATGTATTTAAACGCTGTAATATCTCTGGTAGATCGGAAGAGCGGTTTCAG
chr12	121775206	121775245	ANAPC5_9762	+	GTGACCTATGCACCAGACGTAAAAATGGTACTCAGTAGAAAGGTCATAAACAATGATCGGAAGAGCGGTTTCAG
chr12	121779883	121779922	ANAPC5_9763	+	GTGACCTATGCACCAGACGTTAAAAAAACAAAAATAGTAAAGAAATACAAAAAGTAAAAAGATCGGAAGAGCGGTTTCAG
chr12	121783845	121783884	ANAPC5_9764	+	GTGACCTATGCACCAGACGTAGACGAGAGACAAGGGGAAAGCATTAACTGACATCCAGGCAGATCGGAAGAGCGGTTTCAG
chr12	121784809	121784848	ANAPC5_9765	+	GTGACCTATGCACCAGACGTCGTGAATGAGAAAATCGAGGTGCATATTTTGAAGAGCCCTTAGATCGGAAGAGCGGTTTCAG
chr12	121784819	121784858	ANAPC5_9766	+	GTGACCTATGCACCAGACGTAAATCGAGGTGCATATTTTGAAGAGCCCTTTGAATAATTAGATCGGAAGAGCGGTTTCAG
chr12	121785695	121785734	ANAPC5_9767	+	GTGACCTATGCACCAGACGTGAGAGATAGGGAGGTATGGATTTAAAGAGCTGGAGATGAGATCGGAAGAGCGGTTTCAG
chr12	121790154	121790193	ANAPC5_9768	+	GTGACCTATGCACCAGACGTGAACTAAGTCTCGGGCCGCGGCTGCGGCCAGTTGTCAGATCGGAAGAGCGGTTTCAG
chr3	142168455	142168494	ATR_9769	+	GTGACCTATGCACCAGACGTGAAACATAAAAACAAAAACAGATGTTAATAATTTGGAATTAGATCGGAAGAGCGGTTTCAG
chr3	142172086	142172125	ATR_9770	+	GTGACCTATGCACCAGACGTAACAATATTATGGTATGATGTTATCTTTGCAAGAAGAAAAGATCGGAAGAGCGGTTTCAG
chr3	142176608	142176647	ATR_9771	+	GTGACCTATGCACCAGACGTATACATTTTTATTACAAACTAACAAATGTTAGAATTTAAAAAAGATCGGAAGAGCGGTTTCAG
chr3	142178236	142178275	ATR_9772	+	GTGACCTATGCACCAGACGTGAGTGATATCCATTAATCACATCAGCCAATGAAAAAGGAGATCGGAAGAGCGGTTTCAG
chr3	142180943	142180982	ATR_9773	+	GTGACCTATGCACCAGACGTATACACATAAAATTTAAAAACAAGTAACTCAAAATTCAGATCGGAAGAGCGGTTTCAG
chr3	142184093	142184132	ATR_9774	+	GTGACCTATGCACCAGACGTATGAGTTTATATATTGAAATTTAGGGCCAAAATTTCTGTGATAAGATCGGAAGAGCGGTTTCAG
chr3	142185386	142185425	ATR_9775	+	GTGACCTATGCACCAGACGTTAAATAGTGCATTTAATTTGTTTTACCTTAAATCCACTAGATCGGAAGAGCGGTTTCAG
chr3	142186921	142186960	ATR_9776	+	GTGACCTATGCACCAGACGTAAAGAGTTAAATGTCATAAAAAGAGTTTTATACAGGATTTAGATCGGAAGAGCGGTTTCAG
chr3	142188422	142188461	ATR_9777	+	GTGACCTATGCACCAGACGTAAATAAGTTTAAAAACAATAAAGGAAAGAGAAAAATCAGAGATCGGAAGAGCGGTTTCAG
chr3	142189036	142189075	ATR_9778	+	GTGACCTATGCACCAGACGTATAGACAAGAACACTATTAGCATAGCTGTCATTTTTATAAGATCGGAAGAGCGGTTTCAG
chr3	142204135	142204174	ATR_9779	+	GTGACCTATGCACCAGACGTGAAACATAGGATACCTCACTCAAGAAAATCCACGCTATGCTAGATCGGAAGAGCGGTTTCAG
chr3	142212164	142212203	ATR_9780	+	GTGACCTATGCACCAGACGTAAAGGCAACAATAAGCCTTTTAAATTTAAAAACATACTTCTAGATCGGAAGAGCGGTTTCAG
chr3	142215373	142215412	ATR_9781	+	GTGACCTATGCACCAGACGTTAAACAACACATTGGTGAGAGAGACCATTGGTAAAGGTACAAGATCGGAAGAGCGGTTTCAG
chr3	142216045	142216084	ATR_9782	+	GTGACCTATGCACCAGACGTATAGAGCCTATGTTAAAATGTTATCATATTCAGCCTTATAGATCGGAAGAGCGGTTTCAG
chr3	142217627	142217666	ATR_9783	+	GTGACCTATGCACCAGACGTAATGAAGAGTCAAGAAATGTCACGGTAGCTGGGTCCAAGAAGATCGGAAGAGCGGTTTCAG
chr3	142218571	142218610	ATR_9784	+	GTGACCTATGCACCAGACGTTAAACCCATATCAACTAACTTTAATTTTAAAGGTGACAAGATCGGAAGAGCGGTTTCAG
chr3	142224156	142224195	ATR_9785	+	GTGACCTATGCACCAGACGTTGATTAATAAAAAACAATCAAAAACAAGAAAAAACAACAATGAGATCGGAAGAGCGGTTTCAG
chr3	142226962	142227001	ATR_9786	+	GTGACCTATGCACCAGACGTTAAAAAGTTGAGTAAATTAAGACTTATAAGATAAAATTTAAGATCGGAAGAGCGGTTTCAG
chr3	142232491	142232530	ATR_9787	+	GTGACCTATGCACCAGACGTTAAATGTGTAGACAGTAACACACTTTCACATATTGATTAAGATCGGAAGAGCGGTTTCAG
chr3	142234368	142234407	ATR_9788	+	GTGACCTATGCACCAGACGTGAAAAATTTGTTTTATTAAAAAGATAAAATCCACCTGTTTTAGATCGGAAGAGCGGTTTCAG
chr3	142238637	142238676	ATR_9789	+	GTGACCTATGCACCAGACGTATATTTTACATTTGTAAGTCCACAGTGAAGCAGATAACGCAGATCGGAAGAGCGGTTTCAG
chr3	142241694	142241733	ATR_9790	+	GTGACCTATGCACCAGACGTTAAAAAAAGTAAAAAATAAAATTCACAGATGCTATAAATTTAGATCGGAAGAGCGGTTTCAG
chr3	142243052	142243091	ATR_9791	+	GTGACCTATGCACCAGACGTAGTAGAAAGAAAATTTATACGTAATTTCTACAAAAGTAAAGATCGGAAGAGCGGTTTCAG
chr3	142254058	142254097	ATR_9792	+	GTGACCTATGCACCAGACGTAGCACAGAGACAGAACTTATAATCAACTATTTTTAAACAAGATCGGAAGAGCGGTTTCAG
chr3	142255054	142255093	ATR_9793	+	GTGACCTATGCACCAGACGTGTTGGAATAAAAAGAATTTATTGCCAAAGAATGAATCTAGATCGGAAGAGCGGTTTCAG
chr3	142259887	142259926	ATR_9794	+	GTGACCTATGCACCAGACGTAAAGTAGTCTTCAGAGTAAAGCTTATAAACATGCTGCCAGAGATCGGAAGAGCGGTTTCAG
chr3	142261610	142261649	ATR_9795	+	GTGACCTATGCACCAGACGTTAAACAGATAAATGTAAGCTTTACAGAGATTGAATTTCTAGATCGGAAGAGCGGTTTCAG
chr3	142266763	142266802	ATR_9796	+	GTGACCTATGCACCAGACGTTGACATGTTAAAAAAAATTTTTCTTCTCATCTAATATCCAGATCGGAAGAGCGGTTTCAG
chr3	142268526	142268565	ATR_9797	+	GTGACCTATGCACCAGACGTATGCAACAATTACAAAAAGTACATTTGTCTGGGTGAAAAAGATCGGAAGAGCGGTTTCAG
chr3	142272593	142272632	ATR_9798	+	GTGACCTATGCACCAGACGTTAAAATTAACCTGTTAAAGAAAATTTTAGAGCTAGTTGACAGATCGGAAGAGCGGTTTCAG
chr3	142272868	142272907	ATR_9799	+	GTGACCTATGCACCAGACGTAGAGTATACAATACCTAATTTAACAATATAAAATGTCAAAGGATCGGAAGAGCGGTTTCAG
chr3	142274992	142275031	ATR_9800	+	GTGACCTATGCACCAGACGTTAAAAAAGTACTAAACTTTTCTGCCTAATTTTGTGGTAGATCGGAAGAGCGGTTTCAG
chr3	142277629	142277668	ATR_9801	+	GTGACCTATGCACCAGACGTTACAAAAAAGTCAATAATTTTCTTAACTCATATAGATCGGAAGAGCGGTTTCAG
chr3	142278294	142278333	ATR_9802	+	GTGACCTATGCACCAGACGTTACATTTTTGTTAAAAAAATTGAATTAAGATTGAATTTGATAGATCGGAAGAGCGGTTTCAG

chr3 142279307 142279346 ATR\_9803 + GTGACCTATGCACCAGACGTGAATATAGTAGAGATATTCATATGCAATATAAATTTGGAGATCGGAAGAGCGGTTTCAG  
chr3 142280274 142280313 ATR\_9804 + GTGACCTATGCACCAGACGTAAAAATAATTTCCAGAAATATTTCTTAGAAAAATATATTTAGATCGGAAGAGCGGTTTCAG  
chr3 142281962 142282001 ATR\_9805 + GTGACCTATGCACCAGACGTAAACAAAAAGATATTAATAAACAAGTATATCCGAAGTGCAGATCGGAAGAGCGGTTTCAG  
chr3 142285114 142285153 ATR\_9806 + GTGACCTATGCACCAGACGTAAAGATTCATTTAAAGAGTGCATGACAAATTAACAATGGTAGATCGGAAGAGCGGTTTCAG  
chr3 142287007 142287046 ATR\_9807 + GTGACCTATGCACCAGACGTAAATAAAGCTTTTAAATCCTTAAAGTCACTCAGTTTCATTAGATCGGAAGAGCGGTTTCAG  
chr3 142297557 142297596 ATR\_9808 + GTGACCTATGCACCAGACGTGAGGCACTAGTCAACCACGCCAACCGGGTTCCCGGGCGTAGATCGGAAGAGCGGTTTCAG  
chr3 142281523 142281562 ATR\_9809 + GTGACCTATGCACCAGACGTACCACACTTAGCAGAACACAACTATCTGCCAAAGTAAAGATCGGAAGAGCGGTTTCAG  
chr19 45252314 45252353 BCL3\_9810 + GTGACCTATGCACCAGACGTCCCGAGGGTCCCGGGCGGGTGGGATCCACACAGAGCATAGAGATCGGAAGAGCGGTTTCAG  
chr19 45254648 45254687 BCL3\_9811 + GTGACCTATGCACCAGACGTGCCCTATTAAGGGGAGGGGTGGTTGGGAAGACCAGCCGAGATCGGAAGAGCGGTTTCAG  
chr19 45260489 45260528 BCL3\_9812 + GTGACCTATGCACCAGACGTACCOCGGGGCACCGCTGGGCTGCCAGCGACCTGGAGTGCAGATCGGAAGAGCGGTTTCAG  
chr19 45260683 45260722 BCL3\_9813 + GTGACCTATGCACCAGACGTACTAGGAGCTGGGAGGGAGCGGGCCCTTAGCAGGGGCGGGAGATCGGAAGAGCGGTTTCAG  
chr19 45260991 45261030 BCL3\_9814 + GTGACCTATGCACCAGACGTCCCCCTGAGCCTCGCGCCACCCCTATCCTTGACCCCAAAGATCGGAAGAGCGGTTTCAG  
chr19 45261681 45261720 BCL3\_9815 + GTGACCTATGCACCAGACGTGCAGCTGGGACATGCCCTTGACACAGTGTGCCGCGGGAGATCGGAAGAGCGGTTTCAG  
chr19 45262883 45262922 BCL3\_9816 + GTGACCTATGCACCAGACGTGGGGCAGATCTTGGACTCATGAGGAGGGGCCCCCTGCCAGATCGGAAGAGCGGTTTCAG  
chr2 32582565 32582604 BIRC6\_9817 + GTGACCTATGCACCAGACGTGCAGCGCCGGGCGGGCGGAAGCCGGGAAAGAGCCGTGCAGATCGGAAGAGCGGTTTCAG  
chr2 32602848 32602887 BIRC6\_9818 + GTGACCTATGCACCAGACGTATAAGTATCAATGTGGTCCCTACTTAATGTAATCTTAGAAGATCGGAAGAGCGGTTTCAG  
chr2 32605369 32605408 BIRC6\_9819 + GTGACCTATGCACCAGACGTAAATAGATGGCTTTTGGGTTATATTACAATGGACACCAGATCGGAAGAGCGGTTTCAG  
chr2 32614022 32614061 BIRC6\_9820 + GTGACCTATGCACCAGACGTGACTTAACAAGAGTGACAGTGCAGATGAGATGATTAGTTTAGATCGGAAGAGCGGTTTCAG  
chr2 32617229 32617268 BIRC6\_9821 + GTGACCTATGCACCAGACGTAAATAAAAAAATACTTTTCTCAGTAGGCCCTTTGTAGCCAGATCGGAAGAGCGGTTTCAG  
chr2 32620672 32620711 BIRC6\_9822 + GTGACCTATGCACCAGACGTATGTTTCTGGGCATAATAGGCTAAGTCAAGTCAGTCGTGTAATAAGATCGGAAGAGCGGTTTCAG  
chr2 32626464 32626503 BIRC6\_9823 + GTGACCTATGCACCAGACGTATTTGAAGTAAACAATAGTAATTGAAAAAAGATCAGTTAGATCGGAAGAGCGGTTTCAG  
chr2 32626702 32626741 BIRC6\_9824 + GTGACCTATGCACCAGACGTGTTTGTAGTAGTATTAATAGATGTTACATGTTTTCCTAAGATCGGAAGAGCGGTTTCAG  
chr2 32631636 32631675 BIRC6\_9825 + GTGACCTATGCACCAGACGTAGTAGATATGATAATGATTTAAAAATCTTACACAGTTGAGATCGGAAGAGCGGTTTCAG  
chr2 32641242 32641281 BIRC6\_9826 + GTGACCTATGCACCAGACGTGATTATGTTACTAATACTTATAAATCCATGTATATGGAGATCGGAAGAGCGGTTTCAG  
chr2 32656169 32656208 BIRC6\_9827 + GTGACCTATGCACCAGACGTCCCAAGATAATTAATTTAAGTCCATCTTGTGTATTTGAGATCGGAAGAGCGGTTTCAG  
chr2 32658883 32658922 BIRC6\_9828 + GTGACCTATGCACCAGACGTATCAAAATTTATCTTTGAAGATTTTATTTGTGGTTGATTAGATCGGAAGAGCGGTTTCAG  
chr2 32660664 32660703 BIRC6\_9829 + GTGACCTATGCACCAGACGTATAGAGCTGTTGCCATGACAGTAAAGGAGTAGTGATAGATCGGAAGAGCGGTTTCAG  
chr2 32661263 32661302 BIRC6\_9830 + GTGACCTATGCACCAGACGTACATTTTACAAAAGCAAAATTAATAATACCACAGTTGTAAGATCGGAAGAGCGGTTTCAG  
chr2 32664765 32664804 BIRC6\_9831 + GTGACCTATGCACCAGACGTGCATTTTGAACAATAACAATACAGTTTAAACATTTGGAGATCGGAAGAGCGGTTTCAG  
chr2 32666541 32666580 BIRC6\_9832 + GTGACCTATGCACCAGACGTGCATTTGTTGTTATCTTACAGTAATGAAAGTGACAGATCGGAAGAGCGGTTTCAG  
chr2 32667305 32667344 BIRC6\_9833 + GTGACCTATGCACCAGACGTAAAAATTTGCTTACCCTGTTGATTGCCTTTTATAGTAAAGATCGGAAGAGCGGTTTCAG  
chr2 32667534 32667573 BIRC6\_9834 + GTGACCTATGCACCAGACGTAAAAAGTGAAGCATACTTTCTAGGTACACCTGCAATTAGATCGGAAGAGCGGTTTCAG  
chr2 32668667 32668706 BIRC6\_9835 + GTGACCTATGCACCAGACGTAAATTTAATCACAATAGTTATAGTCATATGGAACATCTAGATCGGAAGAGCGGTTTCAG  
chr2 32670747 32670786 BIRC6\_9836 + GTGACCTATGCACCAGACGTATCTAATGACTAATAATAGCGCTCTGAGTATGATCAAGATCGGAAGAGCGGTTTCAG  
chr2 32674007 32674046 BIRC6\_9837 + GTGACCTATGCACCAGACGTCTTTTAAAGGAAATCTGAAATGTTGTATCTTGATCTTGATCGGAAGAGCGGTTTCAG  
chr2 32679021 32679060 BIRC6\_9838 + GTGACCTATGCACCAGACGTGGTATATACCTTCTTTTATTATATACTTTATGCAGTAATAGATCGGAAGAGCGGTTTCAG  
chr2 32688460 32688499 BIRC6\_9839 + GTGACCTATGCACCAGACGTATTTGGCTCTTTGTTTCATGCTGCTCTAAACTTCAAAGCAGATCGGAAGAGCGGTTTCAG  
chr2 32689902 32689941 BIRC6\_9840 + GTGACCTATGCACCAGACGTAAAAATAGGTGTTGGCTTAGACATTTAAAAATATCTTGAGATCGGAAGAGCGGTTTCAG  
chr2 32692818 32692857 BIRC6\_9841 + GTGACCTATGCACCAGACGTAAAGAAAGTAAATGATACGCTTTCTATGTTTCTGACAAAAGATCGGAAGAGCGGTTTCAG  
chr2 32693190 32693229 BIRC6\_9842 + GTGACCTATGCACCAGACGTAGTGCAAATTTAATGTTATTGAAACTTTGTATTTATATAGATCGGAAGAGCGGTTTCAG  
chr2 32693862 32693901 BIRC6\_9843 + GTGACCTATGCACCAGACGTGGCTTACATTTTAAAGGCTGGAAATATACTTAGATGTTAAGATCGGAAGAGCGGTTTCAG  
chr2 32694693 32694732 BIRC6\_9844 + GTGACCTATGCACCAGACGTAAATGTTGGAGGTTTGTATTAAATGATGTGACTTTTCAGATCGGAAGAGCGGTTTCAG  
chr2 32695380 32695419 BIRC6\_9845 + GTGACCTATGCACCAGACGTAAAGCAGTGTCTTTAGTAAAAACAATATCCTGCAATAAGATCGGAAGAGCGGTTTCAG  
chr2 32696203 32696242 BIRC6\_9846 + GTGACCTATGCACCAGACGTGGAGAGGTTTCTGACAGGTATCAGAAGTTTAAATAATATAGATCGGAAGAGCGGTTTCAG  
chr2 32701423 32701462 BIRC6\_9847 + GTGACCTATGCACCAGACGTACTTTTCAATATAGTATCTCAGAAAAGTCAAGGATTAAGATCGGAAGAGCGGTTTCAG  
chr2 32703897 32703936 BIRC6\_9848 + GTGACCTATGCACCAGACGTATTTTTCTCATAGATGTGCAAAATACCTTGTCATTTAGATCGGAAGAGCGGTTTCAG  
chr2 32704696 32704735 BIRC6\_9849 + GTGACCTATGCACCAGACGTACATTATGTTTCTTCTTTATTCTATTAAATGGAACATGTAGATCGGAAGAGCGGTTTCAG  
chr2 32707661 32707700 BIRC6\_9850 + GTGACCTATGCACCAGACGTGTTTATATTTAAGACATATGCTATTCTTAAACAAGTCTAGATCGGAAGAGCGGTTTCAG  
chr2 32710837 32710876 BIRC6\_9851 + GTGACCTATGCACCAGACGTGACCATTTTTAGAGTATTCAGATGAATGATTCAGCTCTTAGATCGGAAGAGCGGTTTCAG  
chr2 32712879 32712918 BIRC6\_9852 + GTGACCTATGCACCAGACGTAGGAGAAATGGTGTATTTTACATATTATTGTTAGCTGGAGATCGGAAGAGCGGTTTCAG  
chr2 32713792 32713831 BIRC6\_9853 + GTGACCTATGCACCAGACGTTTAGGAGAAAAACATATGATCTAATAAGCAAGCTTAAAGATCGGAAGAGCGGTTTCAG  
chr2 32715229 32715268 BIRC6\_9854 + GTGACCTATGCACCAGACGTAAATTTATTCAATTAATCTGACATATACTTAGATGTTAAGATCGGAAGAGCGGTTTCAG  
chr2 32716636 32716675 BIRC6\_9855 + GTGACCTATGCACCAGACGTGTTTAGCCTGGCATATGCCAGACTATTCAATAAACAGTAAGATCGGAAGAGCGGTTTCAG  
chr2 32718745 32718784 BIRC6\_9856 + GTGACCTATGCACCAGACGTGTACTAATTTGTTCTGATATAGAAGTAACATGTAATTAGATCGGAAGAGCGGTTTCAG  
chr2 32725187 32725226 BIRC6\_9857 + GTGACCTATGCACCAGACGTAGAAATTAATCTTACCATTGCTCTGATACTATAACTGGAGATCGGAAGAGCGGTTTCAG  
chr2 32726966 32727005 BIRC6\_9858 + GTGACCTATGCACCAGACGTGCCAACACAGTTCAGTGATTCAAATAAATTTATTGCGAAGATCGGAAGAGCGGTTTCAG  
chr2 32727969 32728008 BIRC6\_9859 + GTGACCTATGCACCAGACGTATTTCAACTATCAATTTAAGTAAATGTAGATGATGATGATCGGAAGAGCGGTTTCAG  
chr2 32728314 32728353 BIRC6\_9860 + GTGACCTATGCACCAGACGTGTTTACTAAATCTTACTTATGTGAATTTACTAGTTTATTAGATCGGAAGAGCGGTTTCAG

chr2	32730283	32730322	BIRC6_9861	+	GTGACCTATGCACCAGACGTTTTTATAAAGAAGCATCATGAGAACAAGCTTTAATTTAGAAGATCGGAAGAGCGGTTTCAG
chr2	32735072	32735111	BIRC6_9862	+	GTGACCTATGCACCAGACGCTACTTTGATATTTAAATGTTTACATATCTGTAAAGTAACAGAGATCGGAAGAGCGGTTTCAG
chr2	32735712	32735751	BIRC6_9863	+	GTGACCTATGCACCAGACGTATTTTTTCATTTAATTAAGCACACACATGCACATAATCATGAGATCGGAAGAGCGGTTTCAG
chr2	32738232	32738271	BIRC6_9864	+	GTGACCTATGCACCAGACGTTTTGTGAAATCTTTTTATCCCCAGTACTAGATCAGTTAAGATCGGAAGAGCGGTTTCAG
chr2	32740848	32740887	BIRC6_9865	+	GTGACCTATGCACCAGACGTAAAATAACTTACATTTTTAGTTGTTTTATTACATAAGAAAGAGATCGGAAGAGCGGTTTCAG
chr2	32743475	32743514	BIRC6_9866	+	GTGACCTATGCACCAGACGTAAACATTAATCATTGGCTGTGTATACATGTATTTTACAATAGATCGGAAGAGCGGTTTCAG
chr2	32744024	32744063	BIRC6_9867	+	GTGACCTATGCACCAGACGTTTTAAGTATTTAGTTTGTAACTTTATGTTTTGATGTATAGATCGGAAGAGCGGTTTCAG
chr2	32750097	32750136	BIRC6_9868	+	GTGACCTATGCACCAGACGTTATTTTTTATAATCTTGATTTTTGGTGTCTATAAAAAAGATCGGAAGAGCGGTTTCAG
chr2	32750706	32750745	BIRC6_9869	+	GTGACCTATGCACCAGACGTTCAATGAATAAACGTCAAAGAAATTTAGTAGCCTTAAAAAGATCGGAAGAGCGGTTTCAG
chr2	32754902	32754941	BIRC6_9870	+	GTGACCTATGCACCAGACGTAAATACTACTTTAAAAAATTACAGACTGTCATACAAAAGAGGCAGATCGGAAGAGCGGTTTCAG
chr2	32756629	32756668	BIRC6_9871	+	GTGACCTATGCACCAGACGTATTTCCCTAATCGAGTATATCATTCCATAGCTAAGCCCTTCAGATCGGAAGAGCGGTTTCAG
chr2	32768619	32768658	BIRC6_9872	+	GTGACCTATGCACCAGACGTAGTATTAATTTTATCAACACATATGTGAATAGTTGTGTAAAGATCGGAAGAGCGGTTTCAG
chr2	32770938	32770977	BIRC6_9873	+	GTGACCTATGCACCAGACGTTTTTAATTTAGTTTCAAGTTTAAACATTTAGTTTAAACAAATAGATTTAATTAAGATCGGAAGAGCGGTTTCAG
chr2	32774559	32774598	BIRC6_9874	+	GTGACCTATGCACCAGACGTCTGTAAATGTGTCTGTGGATGAATAATTTGTTTGCTTAAGATCGGAAGAGCGGTTTCAG
chr2	32800444	32800483	BIRC6_9875	+	GTGACCTATGCACCAGACGTCAATGTTCAATTTCTCTTGAGTTGCTCTAACAATGTTTTAGATCGGAAGAGCGGTTTCAG
chr2	32819138	32819177	BIRC6_9876	+	GTGACCTATGCACCAGACGTTTTCTCTATATGCCACTTTTCATTTGATGTAAGAGATGTTTAGATCGGAAGAGCGGTTTCAG
chr2	32820222	32820261	BIRC6_9877	+	GTGACCTATGCACCAGACGTATTTTTGATTTGCTTAAGATCTCACITTCCTATTTTTTTAGATCGGAAGAGCGGTTTCAG
chr2	32823046	32823085	BIRC6_9878	+	GTGACCTATGCACCAGACGTATGATAAAGCACTCCCTTATCTCCCTTGCTCATCTAGATCGGAAGAGCGGTTTCAG
chr2	32824978	32825017	BIRC6_9879	+	GTGACCTATGCACCAGACGTTGCAATTTTTGTTTCAAATGCCAATGATTGTATACAAAGAGATCGGAAGAGCGGTTTCAG
chr2	32828161	32828200	BIRC6_9880	+	GTGACCTATGCACCAGACGTTTTCTGTGACATTTTCACTTAAGAAATAAAGAACTGTGAAGATCGGAAGAGCGGTTTCAG
chr2	32832721	32832760	BIRC6_9881	+	GTGACCTATGCACCAGACGTAAAATTAGTGAAACTTTTGTAAAGACATTTTACAATAAGATCGGAAGAGCGGTTTCAG
chr2	32836660	32836699	BIRC6_9882	+	GTGACCTATGCACCAGACGTCTCTTAACAGGAGCCTTGTTGCTTTAAGAGTTGTGTAATAGATCGGAAGAGCGGTTTCAG
chr2	32842982	32843021	BIRC6_9883	+	GTGACCTATGCACCAGACGTTGGGACTCATAGACAAAAGGCTCGAAGCACAAGCCAAAGATCGGAAGAGCGGTTTCAG
chr2	32724905	32724944	BIRC6_9884	+	GTGACCTATGCACCAGACGTTTTAATTTGTTAAAACATTTGTTAACTTTTAGTGCAGCTGCCATGATCGGAAGAGCGGTTTCAG
chr2	32740457	32740496	BIRC6_9885	+	GTGACCTATGCACCAGACGTATAGATTTTCCAGGACAAAACAGGCGCCATCATGTCCAGATCGGAAGAGCGGTTTCAG
chr2	32640312	32640351	BIRC6_9886	+	GTGACCTATGCACCAGACGTATTATGAGTAAAGTTTGCATGATGATGGTTTTACTGTTAGATCGGAAGAGCGGTTTCAG
chr2	32640777	32640816	BIRC6_9887	+	GTGACCTATGCACCAGACGTTGTACAGACTCCTTTAATAATTAGCCTGAGCAGAGGAATAGATCGGAAGAGCGGTTTCAG
chr17	59761512	59761551	BRIP1_9888	+	GTGACCTATGCACCAGACGTAGAATTTAAGAGATTTAACTTTCTGCTCCTAGCTAACATAGATCGGAAGAGCGGTTTCAG
chr17	59763537	59763576	BRIP1_9889	+	GTGACCTATGCACCAGACGTAGGTAAACCCAGGGAATTTGGTTACTTATTTAAAAGATCGGAAGAGCGGTTTCAG
chr17	59770884	59770923	BRIP1_9890	+	GTGACCTATGCACCAGACGTATCGGAAAAGTCAAATAAATTAATAACTCGGAATAAATCAGATCGGAAGAGCGGTTTCAG
chr17	59820506	59820545	BRIP1_9891	+	GTGACCTATGCACCAGACGTAGAAAAAGCATATCCAAAATTTCTAGAAATTTGCTTATTTCAGATCGGAAGAGCGGTTTCAG
chr17	59821963	59822002	BRIP1_9892	+	GTGACCTATGCACCAGACGTGAAAAGAAAAAATGATTTTTTGTGTGTCTAGCTAAACAAAAGATCGGAAGAGCGGTTTCAG
chr17	59853934	59853973	BRIP1_9893	+	GTGACCTATGCACCAGACGTAAATGTCATTATTAGAGTTATGCCTGAAAAGGCATGGAAGATCGGAAGAGCGGTTTCAG
chr17	59858377	59858416	BRIP1_9894	+	GTGACCTATGCACCAGACGTAGAAATGCTAATTAAGTGGCAAACATTTAAAACCTATGAGATCGGAAGAGCGGTTTCAG
chr17	59861796	59861835	BRIP1_9895	+	GTGACCTATGCACCAGACGTTTACCATTAAGTATAGAGGGGTTGGGAGGAAATTTGAAAAGATCGGAAGAGCGGTTTCAG
chr17	59871101	59871140	BRIP1_9896	+	GTGACCTATGCACCAGACGTATAAAAAAATTTGTGTCAACCAAGTATCATCCTTACACACACAGATCGGAAGAGCGGTTTCAG
chr17	59876671	59876710	BRIP1_9897	+	GTGACCTATGCACCAGACGTAAAGAATTTTCTTGTAACATTTGGCAAATAGATTTAAAGATCGGAAGAGCGGTTTCAG
chr17	59878846	59878885	BRIP1_9898	+	GTGACCTATGCACCAGACGTATATGCATAACTGAAATGTGAACCAATATTAGCATAGAAGAGATCGGAAGAGCGGTTTCAG
chr17	59886129	59886168	BRIP1_9899	+	GTGACCTATGCACCAGACGTGGAAGAAACGATAACTAATATCTAACTACCATAAAAAAGATCGGAAGAGCGGTTTCAG
chr17	59924592	59924631	BRIP1_9900	+	GTGACCTATGCACCAGACGTAGAACCAAAATGAAGTTAAGTGAAGTGAAGTTAACTAGATCGGAAGAGCGGTTTCAG
chr17	59926628	59926667	BRIP1_9901	+	GTGACCTATGCACCAGACGTTAATTTAAAAAAAACAGCATAAATAAATCTACAGGTAGGCAAGATCGGAAGAGCGGTTTCAG
chr17	59934603	59934642	BRIP1_9902	+	GTGACCTATGCACCAGACGTAGAACAATCTATTTATAATATATCTAATTAATAAACATCAGATCGGAAGAGCGGTTTCAG
chr17	59937279	59937318	BRIP1_9903	+	GTGACCTATGCACCAGACGTAGAACAATGAAAATAATAAACATATTAACTTTATAAAGAGATCGGAAGAGCGGTTTCAG
chr17	59938911	59938950	BRIP1_9904	+	GTGACCTATGCACCAGACGTTGTTTATTTCAAGTTCTTAACACTACAACGAAATGAAAATGAGATCGGAAGAGCGGTTTCAG
chr17	59761089	59761128	BRIP1_9905	+	GTGACCTATGCACCAGACGTAGACAATTCAGTCTGGATCCAGGCTTCTTCAGAACAGAGATCGGAAGAGCGGTTTCAG
chr16	88943694	88943733	CBFA2T3_9906	+	GTGACCTATGCACCAGACGTGCAGAGGGCTGACAGGCTCAGGCTGGGCTCGGCCACCCGATCAGATCGGAAGAGCGGTTTCAG
chr16	88945879	88945918	CBFA2T3_9907	+	GTGACCTATGCACCAGACGTGCATGGCGAGGGCTGGCGGTCACATGGGCCATCCAGATGGAGATCGGAAGAGCGGTTTCAG
chr16	88947207	88947246	CBFA2T3_9908	+	GTGACCTATGCACCAGACGTGGCCGGCGTCAACACAGGATGGGCCACGGCTGCCCTCCAGATCGGAAGAGCGGTTTCAG
chr16	88947908	88947947	CBFA2T3_9909	+	GTGACCTATGCACCAGACGTGCGGCACAGCCTTCAAGACCTCAGAGGGACCGGGACGCACAGATCGGAAGAGCGGTTTCAG
chr16	88949180	88949219	CBFA2T3_9910	+	GTGACCTATGCACCAGACGTGGGAGGTGCACGCTTAGTCCCACCCACAGCCAGTCTCTGAGATCGGAAGAGCGGTTTCAG
chr16	88951688	88951727	CBFA2T3_9911	+	GTGACCTATGCACCAGACGTGAGCAGGTGGGGCGAGGGCAGTGGACATGGATGAAACCGAGATCGGAAGAGCGGTTTCAG
chr16	88952561	88952600	CBFA2T3_9912	+	GTGACCTATGCACCAGACGTGGAAGGAGGGCTGGTGGTACGATGCAGGGGTGCACAGCCAGATCGGAAGAGCGGTTTCAG
chr16	88958390	88958429	CBFA2T3_9913	+	GTGACCTATGCACCAGACGTGAAAACCCACCTCACATCAGCACCCTCGGCATGTGAGCCAGATCGGAAGAGCGGTTTCAG
chr16	88958904	88958943	CBFA2T3_9914	+	GTGACCTATGCACCAGACGTGAAGCGGACATGAGGACACAAAGGTGATGGTGACAACAAGATCGGAAGAGCGGTTTCAG
chr16	88964571	88964610	CBFA2T3_9915	+	GTGACCTATGCACCAGACGTAAATAAGAAAGAACACGCTGTGAGGAGGGCGTGGGCAGGAGAGATCGGAAGAGCGGTTTCAG
chr16	88968043	88968082	CBFA2T3_9916	+	GTGACCTATGCACCAGACGTTTGGCTTTCCTGTCCACTGGGGCTGCGACCAACGGAGAAAAGATCGGAAGAGCGGTTTCAG
chr16	88968075	88968114	CBFA2T3_9917	+	GTGACCTATGCACCAGACGTGGAAGAAAGACCTGCGTGAAGAGGCTAAGTGCAAAAGAGATCGGAAGAGCGGTTTCAG
chr16	89043226	89043265	CBFA2T3_9918	+	GTGACCTATGCACCAGACGTACCCCTCAGGGGCCAACCTGGAGCCAGGACAGGCTCTACAGATCGGAAGAGCGGTTTCAG

chr1	193091472	193091511	CDC73_9919	+	GTGACCTATGCACCAGACGTCATGGCTGTGGCCAGGGGTGGCAGGGCAGAGTTGGGCGCAGATCGGAAGAGCGGTTCCAG
chr1	193104594	193104633	CDC73_9920	+	GTGACCTATGCACCAGACGTTTGCATATTTATATTGAACCTTTCAGAAAGCCATTCCAAAAAGATCGGAAGAGCGGTTCCAG
chr1	193104730	193104769	CDC73_9921	+	GTGACCTATGCACCAGACGTTGTATTTAAACAATTTTATTTATATTGTTATTGAAATTGAGATCGGAAGAGCGGTTCCAG
chr1	193107314	193107353	CDC73_9922	+	GTGACCTATGCACCAGACGTTTTTTAAGTAGAAAAGTAGGTAGTTAGATATATGTAAGAGAGATCGGAAGAGCGGTTCCAG
chr1	193111207	193111246	CDC73_9923	+	GTGACCTATGCACCAGACGTTATTTACTCATTGAGGTGAGAGAGAGAGAGAGAAGATCGGAAGAGCGGTTCCAG
chr1	193117106	193117145	CDC73_9924	+	GTGACCTATGCACCAGACGTTTACTGCTTTACAGTAGATTAATGAAGTTGCCACTTATAGATCGGAAGAGCGGTTCCAG
chr1	193119523	193119562	CDC73_9925	+	GTGACCTATGCACCAGACGTTAACTCTTATCTTCCCGTAGTTGGTTGGTTGTTGACTTGGATCGGAAGAGCGGTTCCAG
chr1	193121585	193121624	CDC73_9926	+	GTGACCTATGCACCAGACGTTTGGCTGTAGATGTTCTTTTGTCCAGGGATTTTATGTGAAGATCGGAAGAGCGGTTCCAG
chr1	193172993	193173032	CDC73_9927	+	GTGACCTATGCACCAGACGTAGAACTTTGCTTTTTGTTTTCTTCAAAGATCGTAACAGAGATCGGAAGAGCGGTTCCAG
chr1	193181241	193181280	CDC73_9928	+	GTGACCTATGCACCAGACGTGCATATGATTTAAACTTAACCTTAAAAAGTAAATGATTGAGATCGGAAGAGCGGTTCCAG
chr1	193181618	193181657	CDC73_9929	+	GTGACCTATGCACCAGACGTTATTAACACTACCTGTACGTAGGATATTGAGATACCATGAGATCGGAAGAGCGGTTCCAG
chr1	193202295	193202334	CDC73_9930	+	GTGACCTATGCACCAGACGTCCTATATATATCTTTCCAGAGTGTGAACCCAAGAGATCGGAAGAGCGGTTCCAG
chr1	193205497	193205536	CDC73_9931	+	GTGACCTATGCACCAGACGTCCTTTGTATTTACTGTATCCAGATAGAAAATGTTCTCATTAGATCGGAAGAGCGGTTCCAG
chr1	193219012	193219051	CDC73_9932	+	GTGACCTATGCACCAGACGTTTCTAAATATGCTTGTGTGTTTTATTGTAATTTTCTAGATCGGAAGAGCGGTTCCAG
chr1	193219853	193219892	CDC73_9933	+	GTGACCTATGCACCAGACGTTCCCTCCATTTCTGGAAATTGAGACTCAAGCTTTATGAATTAGATCGGAAGAGCGGTTCCAG
chr5	68530879	68530918	CDK7_9934	+	GTGACCTATGCACCAGACGTCGTGAAGGACGGGGAGGGGCCCAAGCGGACAGCCCGCGCAGATCGGAAGAGCGGTTCCAG
chr5	68531291	68531330	CDK7_9935	+	GTGACCTATGCACCAGACGTTTTTATGTTGTTTTAAAGTCTCCTTGAAGATGCTGTATAGATCGGAAGAGCGGTTCCAG
chr5	68550507	68550546	CDK7_9936	+	GTGACCTATGCACCAGACGTTCAAACCTGTTACTGGGATTTGGGACTCTGCCTTTTCTTAAGATCGGAAGAGCGGTTCCAG
chr5	68551366	68551405	CDK7_9937	+	GTGACCTATGCACCAGACGTTGATTCCTGGAGAAATCCTTTGTCCAGTTTATCAAACAAGATCGGAAGAGCGGTTCCAG
chr5	68553991	68554030	CDK7_9938	+	GTGACCTATGCACCAGACGTTAATATTGCTTCTTTATACTAGTCAAGTTTTATATAGCCAAGATCGGAAGAGCGGTTCCAG
chr5	68555774	68555813	CDK7_9939	+	GTGACCTATGCACCAGACGTCCTAAAGCTACATGTGCAGGAGTTGATCAGAAATGAGCAAGATCGGAAGAGCGGTTCCAG
chr5	68558142	68558181	CDK7_9940	+	GTGACCTATGCACCAGACGTATTAATGTACGCACCTTAATATTGTTGTTGCAGTTATTTGAGATCGGAAGAGCGGTTCCAG
chr5	68565131	68565170	CDK7_9941	+	GTGACCTATGCACCAGACGTATGCATTTTCTTAAATGTAATTAGGACTCTGTAAGTTAGATCGGAAGAGCGGTTCCAG
chr5	68568879	68568918	CDK7_9942	+	GTGACCTATGCACCAGACGTTGATCTTTTATACTGAAATATAAAAATAATCTTAACAGATCGGAAGAGCGGTTCCAG
chr5	68572528	68572567	CDK7_9943	+	GTGACCTATGCACCAGACGTCACCTTTTAAAGAAATTAATGAATTGAAAACTCCAAAAGATCGGAAGAGCGGTTCCAG
chr5	68572973	68573012	CDK7_9944	+	GTGACCTATGCACCAGACGTGGACAACATTTACTACTGAGGGAAAATAGCCAAAAGCAAGATCGGAAGAGCGGTTCCAG
chr17	57697545	57697584	CLTC_9945	+	GTGACCTATGCACCAGACGTGCCCGGCTGGTGAGGGCTGTGGAGAAGGTGGTAGAAGGAGATCGGAAGAGCGGTTCCAG
chr17	57725038	57725077	CLTC_9946	+	GTGACCTATGCACCAGACGTTAATTTTATGAAGAAGAGGTTTGAACAACCGGTTGTAGATCGGAAGAGCGGTTCCAG
chr17	57725773	57725812	CLTC_9947	+	GTGACCTATGCACCAGACGTCCTTTGGTAATTTTAAATGAGAATCTGTATTGGCTTTAGATCGGAAGAGCGGTTCCAG
chr17	57728688	57728727	CLTC_9948	+	GTGACCTATGCACCAGACGTCAAATAAATGACTTTTTTAAAAATCTCTCCTCTTAAAGAAGATCGGAAGAGCGGTTCCAG
chr17	57733399	57733438	CLTC_9949	+	GTGACCTATGCACCAGACGTCCTGAAACTTAAGCAATAAAAATAAGATAACCTGATGAGTTAGATCGGAAGAGCGGTTCCAG
chr17	57737960	57737999	CLTC_9950	+	GTGACCTATGCACCAGACGTATGAAAATGAAGTTGTGCATGACATTAATCCATTGTTAATAAGATCGGAAGAGCGGTTCCAG
chr17	57739015	57739054	CLTC_9951	+	GTGACCTATGCACCAGACGTTTATGTTGACATAATCTTGTCTTTGGTTGCATTAATATGAAGATCGGAAGAGCGGTTCCAG
chr17	57741366	57741405	CLTC_9952	+	GTGACCTATGCACCAGACGTTGAAACACATCTCAGCATGAATTCATTGAAGCATGACAAGATCGGAAGAGCGGTTCCAG
chr17	57742281	57742320	CLTC_9953	+	GTGACCTATGCACCAGACGTAAAAATATTTGTAGAAGCTGATGAAATGGAGAGTGAGATCGGAAGAGCGGTTCCAG
chr17	57743612	57743651	CLTC_9954	+	GTGACCTATGCACCAGACGTTAATGCTTTTTAGGCATGTTTCCAACTTGTTTAGTAATAGATCGGAAGAGCGGTTCCAG
chr17	57744016	57744055	CLTC_9955	+	GTGACCTATGCACCAGACGTTTCTTACCTAATAGATGGTGTAGTTGTGATTAATAGGTAAGATCGGAAGAGCGGTTCCAG
chr17	57744349	57744388	CLTC_9956	+	GTGACCTATGCACCAGACGTGTTTTGAGTTTTTAAAAAAGTACTTAAGGTAGCCAAGAAGATCGGAAGAGCGGTTCCAG
chr17	57746312	57746351	CLTC_9957	+	GTGACCTATGCACCAGACGTTTGGAGTAATGTGTTTTCTGGTTGGATTCCAGGTTAGCAGTAGATCGGAAGAGCGGTTCCAG
chr17	57751144	57751183	CLTC_9958	+	GTGACCTATGCACCAGACGTTGTAGTAAATGTAAGGTAATCTTACTATAGATTTTATAGATCGGAAGAGCGGTTCCAG
chr17	57752215	57752254	CLTC_9959	+	GTGACCTATGCACCAGACGTTTAAACAGGATAAGTACTTTCTTAACATGGCAATAGATCGGAAGAGCGGTTCCAG
chr17	57754560	57754599	CLTC_9960	+	GTGACCTATGCACCAGACGTCAGCTGAATATGTAGAGAAGCTGCATTTTTAAAAACCTGAGATCGGAAGAGCGGTTCCAG
chr17	57756891	57756930	CLTC_9961	+	GTGACCTATGCACCAGACGTCAAATGTGTTATGGCTGTCAGTAAAAATATACATTTTATAGATCGGAAGAGCGGTTCCAG
chr17	57758429	57758468	CLTC_9962	+	GTGACCTATGCACCAGACGTAGAGGGATCCATTTGGCTATTATAGTCAGTCTTTAATAAAAAGATCGGAAGAGCGGTTCCAG
chr17	57758850	57758889	CLTC_9963	+	GTGACCTATGCACCAGACGTAGATTACCTAAGTTGAATTAACACTAAACTGTGCTATGAGGAGATCGGAAGAGCGGTTCCAG
chr17	57759211	57759250	CLTC_9964	+	GTGACCTATGCACCAGACGTTTACCTTATGTTTGAACCTCATAAAATGATTAAGATCGGAAGAGCGGTTCCAG
chr17	57759800	57759839	CLTC_9965	+	GTGACCTATGCACCAGACGTTTTTTCAGATTTAAGAAAACTAGTTGGGCTACTTGATTAGATCGGAAGAGCGGTTCCAG
chr17	57760165	57760204	CLTC_9966	+	GTGACCTATGCACCAGACGTTCCAAAGTTTGGTGAAGAATTAAGAAACGCTATTTAAACAGATCGGAAGAGCGGTTCCAG
chr17	57760386	57760425	CLTC_9967	+	GTGACCTATGCACCAGACGTGACTTTTTATATGACCTGAGATCTTTTACCATAGATATTCTAGATCGGAAGAGCGGTTCCAG
chr17	57760634	57760673	CLTC_9968	+	GTGACCTATGCACCAGACGTATTGTAACACAGTGAAGCAACTGTGTAGTTAAAACATGATGATCGGAAGAGCGGTTCCAG
chr17	57760908	57760947	CLTC_9969	+	GTGACCTATGCACCAGACGTTCTCAGAAGATAAAGGATTAGAAGGAGAAGCTCATTAAAGATCGGAAGAGCGGTTCCAG
chr17	57761128	57761167	CLTC_9970	+	GTGACCTATGCACCAGACGTAATTTTAAACCAAAGCTTACATGCAAGGAATTAGGACATAAGATCGGAAGAGCGGTTCCAG
chr17	57761357	57761396	CLTC_9971	+	GTGACCTATGCACCAGACGTTTTGATCTTGCACATAATCTCAAGACTCATAAAGTTATGTAGATCGGAAGAGCGGTTCCAG
chr17	57762598	57762637	CLTC_9972	+	GTGACCTATGCACCAGACGTTTGGGGGCGAGGGCTGTTTTAAACCAGGCCTAAAATGGTATAGATCGGAAGAGCGGTTCCAG
chr17	57763180	57763219	CLTC_9973	+	GTGACCTATGCACCAGACGTTTCTAAGTGTATTCAGAAGTATTTCTTGCATGTAATAAGATCGGAAGAGCGGTTCCAG
chr17	57768083	57768122	CLTC_9974	+	GTGACCTATGCACCAGACGTTCTGTAACCTCAAAAAATTCATTAGCAAAATTTAATAAGATCGGAAGAGCGGTTCCAG
chr17	57771224	57771263	CLTC_9975	+	GTGACCTATGCACCAGACGTTGATCCTGTAGTCACATTTTCTGACTGAAACATCGTCTAGATCGGAAGAGCGGTTCCAG
chr8	113237170	113237209	CSMD3_9976	+	GTGACCTATGCACCAGACGTTGATGATTAGCTATGTGTTAACTTTCTCCAGAAACAAGATCGGAAGAGCGGTTCCAG

chr8	113243872	113243911	CSMD3_9977	+	GTGACCTATGCACCAGACGTTTAAACAGCCTAAATATACTTGAATACTGGCCATAGCTATAAGATCGGAAGAGCGGTTTCAG
chr8	113246717	113246756	CSMD3_9978	+	GTGACCTATGCACCAGACGCTAAGGACATTTTAGTCTACTTAACTTTGTAAATAGTTATAAGATCGGAAGAGCGGTTTCAG
chr8	113249588	113249627	CSMD3_9979	+	GTGACCTATGCACCAGACGTATTAATATACCACACATTAATTTTACAATGCCATATAAAAGATCGGAAGAGCGGTTTCAG
chr8	113256813	113256852	CSMD3_9980	+	GTGACCTATGCACCAGACGTAAAAGAGAACAATGTAATTTTCTATAGATATGTTAAGAAGATCGGAAGAGCGGTTTCAG
chr8	113259371	113259410	CSMD3_9981	+	GTGACCTATGCACCAGACGTTTAAAGAGAGGAAAAAATATTCCCCTACAACTTCAAATAAGATCGGAAGAGCGGTTTCAG
chr8	113266566	113266605	CSMD3_9982	+	GTGACCTATGCACCAGACGTGATTAAGATATTAGTCTTTAAATTTACAATAGATAAGATCGGAAGAGCGGTTTCAG
chr8	113267667	113267706	CSMD3_9983	+	GTGACCTATGCACCAGACGTAAAAGAGCCTTATATCAAGATTAGTATACAGCAGAAAGATCGGAAGAGCGGTTTCAG
chr8	113276052	113276091	CSMD3_9984	+	GTGACCTATGCACCAGACGTATTAAGAGTATTAGACACAGCTGTTGAAATATCCTGAGCAGATCGGAAGAGCGGTTTCAG
chr8	113277830	113277869	CSMD3_9985	+	GTGACCTATGCACCAGACGTTGGATTAGAAGAGCAGATGTTTAAAGATGAGGCATGTTTAAAGATCGGAAGAGCGGTTTCAG
chr8	113293590	113293629	CSMD3_9986	+	GTGACCTATGCACCAGACGTAAGTGTTTAAGAGTATATATAAAAAATGCAATCAGAAATAGATCGGAAGAGCGGTTTCAG
chr8	113299486	113299525	CSMD3_9987	+	GTGACCTATGCACCAGACGTGTACAGTTCAAGTTAACCAATTTCCATAAACATTTATTAAGATCGGAAGAGCGGTTTCAG
chr8	113303935	113303974	CSMD3_9988	+	GTGACCTATGCACCAGACGTGACAATTTTGAACATATGTTTGAATAATATACATATAAGATCGGAAGAGCGGTTTCAG
chr8	113304950	113304989	CSMD3_9989	+	GTGACCTATGCACCAGACGTGTGGCAGGAGGACAGGGAAGGAAACACAGAAAAAATATAGATCGGAAGAGCGGTTTCAG
chr8	113308246	113308285	CSMD3_9990	+	GTGACCTATGCACCAGACGTTTATAAAGTAATATTTTAACTGTTGATTTGTTTTATTTAGATCGGAAGAGCGGTTTCAG
chr8	113314206	113314245	CSMD3_9991	+	GTGACCTATGCACCAGACGTATAAATAAAAAATCCTTAAAGATATAGTCAAGCTGCAAGATCGGAAGAGCGGTTTCAG
chr8	113317155	113317194	CSMD3_9992	+	GTGACCTATGCACCAGACGTACCAAAGGGTGAATTTGCTAACAAATCACTATATCTCAACAGATCGGAAGAGCGGTTTCAG
chr8	113318432	113318471	CSMD3_9993	+	GTGACCTATGCACCAGACGTATACACAAGCAAATCGTATAAACAGAAAAATGTTTAAAGATCGGAAGAGCGGTTTCAG
chr8	113323406	113323445	CSMD3_9994	+	GTGACCTATGCACCAGACGTGAAAAAATAAGCTGTTTAAATTAATGAATCAGAAATTTAAGATCGGAAGAGCGGTTTCAG
chr8	113326292	113326331	CSMD3_9995	+	GTGACCTATGCACCAGACGTAAAATAAAAAATTTAGATAAAGCTAATTTATTTCTCATTAGATCGGAAGAGCGGTTTCAG
chr8	113326857	113326896	CSMD3_9996	+	GTGACCTATGCACCAGACGTAAAATGTCATTAATAATGCCAGTCTTTTAGAGCCTCAGTAGATCGGAAGAGCGGTTTCAG
chr8	113331190	113331229	CSMD3_9997	+	GTGACCTATGCACCAGACGTAAAAGAGGGGAGGTTTCATATAAGCAACAGGTGATGATAAAGATCGGAAGAGCGGTTTCAG
chr8	113332221	113332260	CSMD3_9998	+	GTGACCTATGCACCAGACGTAAACAAAGTGTTTATTTCTTTTCTGTGCGACTACATGTATAGATCGGAAGAGCGGTTTCAG
chr8	113347714	113347753	CSMD3_9999	+	GTGACCTATGCACCAGACGTAGGATTTGGAAAGGAGGAGAGATCAAGATTTGATTTGGAAGATCGGAAGAGCGGTTTCAG
chr8	113349069	113349108	CSMD3_10000	+	GTGACCTATGCACCAGACGTATGTCACAAACAAATATGTTTAAATTTAAATAAACTAGATCGGAAGAGCGGTTTCAG
chr8	113349971	113350010	CSMD3_10001	+	GTGACCTATGCACCAGACGTGAAAAAGAAAGACATTTTTTCTTTCCAAATTTTCAGAGGCCAGATCGGAAGAGCGGTTTCAG
chr8	113353926	113353965	CSMD3_10002	+	GTGACCTATGCACCAGACGTAAACAAACAGAATGCTACTTTTATTTGCTTTACCGAATTAAGATCGGAAGAGCGGTTTCAG
chr8	113358453	113358492	CSMD3_10003	+	GTGACCTATGCACCAGACGTACAGAAATCCAAAGTAAACAGAGTAGAGGAATAATTTACAGATCGGAAGAGCGGTTTCAG
chr8	113363484	113363523	CSMD3_10004	+	GTGACCTATGCACCAGACGTAAAATGATGTGGTTTCAGTACACATACATAAAAAAGTTTAAAGATCGGAAGAGCGGTTTCAG
chr8	113364774	113364813	CSMD3_10005	+	GTGACCTATGCACCAGACGTTTAAATGATACAATTTAAGTAACTTTCAAGTGATAAATCGATCGGAAGAGCGGTTTCAG
chr8	113392696	113392735	CSMD3_10006	+	GTGACCTATGCACCAGACGTATAGTAAAGGCAAGCAATGACCACATAAAGTACTATAGATCGGAAGAGCGGTTTCAG
chr8	113395903	113395942	CSMD3_10007	+	GTGACCTATGCACCAGACGTATAATTACAGGTAAGAATACACATTTCTAACCAGATACACAGATCGGAAGAGCGGTTTCAG
chr8	113403028	113403067	CSMD3_10008	+	GTGACCTATGCACCAGACGTAGCAGTCCAAAGAGAGGGAGTTAATTTCTAATGCAAAAGGATAGATCGGAAGAGCGGTTTCAG
chr8	113420653	113420692	CSMD3_10009	+	GTGACCTATGCACCAGACGTAAACAAACACTAAGATATCATAATAATTTTTCATTTCAGTAAGATCGGAAGAGCGGTTTCAG
chr8	113421272	113421311	CSMD3_10010	+	GTGACCTATGCACCAGACGTGGAACCCGAGAGCAAAACAAATCACCACCATCCAAAAAGATCGGAAGAGCGGTTTCAG
chr8	113484947	113484986	CSMD3_10011	+	GTGACCTATGCACCAGACGTATGGCAAAAATATCATTTTTAGAAAAAGTTTAAAAAATAGATCGGAAGAGCGGTTTCAG
chr8	113519069	113519108	CSMD3_10012	+	GTGACCTATGCACCAGACGTAAACAAACAAATAAAATCTCTTTAAACATTAATACAATTTAAGATCGGAAGAGCGGTTTCAG
chr8	113529465	113529504	CSMD3_10013	+	GTGACCTATGCACCAGACGTACAGAGACAAAATTTAGTTTTGATACTACCAAAATCAAGATCGGAAGAGCGGTTTCAG
chr8	113563113	113563152	CSMD3_10014	+	GTGACCTATGCACCAGACGTACCATATTTCTCTGATTTTTTAAACAAGGATTTCAACTTTAGATCGGAAGAGCGGTTTCAG
chr8	113564960	113564999	CSMD3_10015	+	GTGACCTATGCACCAGACGTATAATAGAAATTTAAGCCACAATTTAATGCCAATTTTCAGATCGGAAGAGCGGTTTCAG
chr8	113569194	113569233	CSMD3_10016	+	GTGACCTATGCACCAGACGTAATATAAATGATTAAGGCCAAAATTTAGGAGGAGGATTTAGATCGGAAGAGCGGTTTCAG
chr8	113599475	113599514	CSMD3_10017	+	GTGACCTATGCACCAGACGTAAACAGAAATTTAGAAAGTACAGTTAATAGATAGCAGTATCAAGATCGGAAGAGCGGTTTCAG
chr8	113649245	113649284	CSMD3_10018	+	GTGACCTATGCACCAGACGTGAGAGAAAAATTTCCCGCGGGGAGGAAAGGACAAAGAAAGATCGGAAGAGCGGTTTCAG
chr8	113651151	113651190	CSMD3_10019	+	GTGACCTATGCACCAGACGTAAATAGAAACACTGAATTTACAGGTAGATCAGTAAACACAGATCGGAAGAGCGGTTTCAG
chr8	113657465	113657504	CSMD3_10020	+	GTGACCTATGCACCAGACGTAAAGAAACAGATCCATGTGATCAGCAGTGAGAGAGACAGAGATCGGAAGAGCGGTTTCAG
chr8	113662589	113662628	CSMD3_10021	+	GTGACCTATGCACCAGACGTAAAGGGAAGAAATAAAGATAGTAAAGTGGTGGGATTTGGAGAGATCGGAAGAGCGGTTTCAG
chr8	113668581	113668620	CSMD3_10022	+	GTGACCTATGCACCAGACGTAAAGACACATGTGAAAATATTTAGAATTAACACTATATAAGATCGGAAGAGCGGTTTCAG
chr8	113678655	113678694	CSMD3_10023	+	GTGACCTATGCACCAGACGTAAATCAGACAAGTAAGAATAAAACATTTCAAGATAAATCGCAGATCGGAAGAGCGGTTTCAG
chr8	113694876	113694915	CSMD3_10024	+	GTGACCTATGCACCAGACGTATGCAAAAGAAAAATACACAAACAAACAAATTTAGCCAGAGATCGGAAGAGCGGTTTCAG
chr8	113697972	113698011	CSMD3_10025	+	GTGACCTATGCACCAGACGTAGGAAGATTTAGAAATCAATAAATATTTCAAAAAATAATATAGATCGGAAGAGCGGTTTCAG
chr8	113702290	113702329	CSMD3_10026	+	GTGACCTATGCACCAGACGTAGAAGATAAAAGTCACCTTCCAAAGGGTTGACGGCATATGAAGATCGGAAGAGCGGTTTCAG
chr8	113812514	113812553	CSMD3_10027	+	GTGACCTATGCACCAGACGTATGGCAAAAAGAGGAGAGATGGGTTATTAACACTCCTCAGATCGGAAGAGCGGTTTCAG
chr8	113842029	113842068	CSMD3_10028	+	GTGACCTATGCACCAGACGTACAGAAACATGCAACTATGCACTGCGTTGTGCAATAAAGATCGGAAGAGCGGTTTCAG
chr8	113871506	113871545	CSMD3_10029	+	GTGACCTATGCACCAGACGTAAATGCAATTTTAAAAAGATGAACATATGTCACATGTAATAAAGATCGGAAGAGCGGTTTCAG
chr8	113933991	113934030	CSMD3_10030	+	GTGACCTATGCACCAGACGTATAAAAGAGAAAAAATATGATAAGAAAGATGCAACATAATAGATCGGAAGAGCGGTTTCAG
chr8	113960117	113960156	CSMD3_10031	+	GTGACCTATGCACCAGACGTAGGGAAAAAAGAAAAAGAAACAAATATATGTGATTAGAAGATCGGAAGAGCGGTTTCAG
chr8	113967001	113967040	CSMD3_10032	+	GTGACCTATGCACCAGACGTAAACAAACAAACAAATGATCAGGAATAACAATTTTAAAAAGATCGGAAGAGCGGTTTCAG
chr8	113988388	113988427	CSMD3_10033	+	GTGACCTATGCACCAGACGTAGTACGACTAGATGCTAACTTTTCTTTAAATTTGTAGATCGGAAGAGCGGTTTCAG
chr8	114031419	114031458	CSMD3_10034	+	GTGACCTATGCACCAGACGTAAAGACAACAACAAAAATTTAAAAAGCTTTTTCAGCAGTAGATCGGAAGAGCGGTTTCAG

chr8	114111203	114111242	CSMD3_10035	+	GTGACCTATGCACCAGACGTTGACAAAATATTTCAGTTGTAAGTTATTGAGATAAATGCAAAGATCGGAAGAGCGGTTTCAG
chr8	114186156	114186195	CSMD3_10036	+	GTGACCTATGCACCAGACGTGAGGAAAAGGAGAGTTTACAGTTATTTCAATAAGCAGTTAGATCGGAAGAGCGGTTTCAG
chr8	114290944	114290983	CSMD3_10037	+	GTGACCTATGCACCAGACGTATGGAATTAATTGTTAGAGACATAATCATTTTATCTAAGAAGATCGGAAGAGCGGTTTCAG
chr8	114327033	114327072	CSMD3_10038	+	GTGACCTATGCACCAGACGTAGACAATAAACAGACATTAAATATTATAAATCAAGAACAAGATCGGAAGAGCGGTTTCAG
chr8	114389035	114389074	CSMD3_10039	+	GTGACCTATGCACCAGACGTTGTGCTGAAGAGGTTGTTTATGAGTCGCAACAACCGGCCAAGATCGGAAGAGCGGTTTCAG
chr8	114449094	114449133	CSMD3_10040	+	GTGACCTATGCACCAGACGTAGCTCCTAATTCCTGCTCCTCAGCCCGGCAGTGGAGTTAGATCGGAAGAGCGGTTTCAG
chr19	1969969	1970008	CSNK1G2_10041	+	GTGACCTATGCACCAGACGTGCTCGTGGTGGTAGGTTGGGTCGGGAGGCTGCTGCAGGGCCAGATCGGAAGAGCGGTTTCAG
chr19	1978355	1978394	CSNK1G2_10042	+	GTGACCTATGCACCAGACGTCCCTCCACCCCACCCCGCTGACGTGCCCCAGGGATTTAGATCGGAAGAGCGGTTTCAG
chr19	1979258	1979297	CSNK1G2_10043	+	GTGACCTATGCACCAGACGTAGGCCGGGCAGGCCGGGCGGGAGCAGGGCGGGAGCAAGGAGATCGGAAGAGCGGTTTCAG
chr19	1979653	1979692	CSNK1G2_10044	+	GTGACCTATGCACCAGACGTGGGTGCCGGTATGTGGGAGCGGGGACCGGAAACTGCCAGATCGGAAGAGCGGTTTCAG
chr19	1979845	1979884	CSNK1G2_10045	+	GTGACCTATGCACCAGACGTGGCGGGACCCGCCAGGGAGGGGCATGGCGGCCAGAGATCGGAAGAGCGGTTTCAG
chr19	1980027	1980066	CSNK1G2_10046	+	GTGACCTATGCACCAGACGTGGGCGGTGCCTTCGGGGAGTGGGGGTGCCTGGTCCCAGATCGGAAGAGCGGTTTCAG
chr19	1980213	1980252	CSNK1G2_10047	+	GTGACCTATGCACCAGACGTGTGCAGCCCCCTGAATCTTCCGTCCGTGCAGCCCCCTGGGCGAGATCGGAAGAGCGGTTTCAG
chr5	138117729	138117768	CTNNA1_10048	+	GTGACCTATGCACCAGACGTGAAAACACAATAACATTGTAACATGGTTCATAGCACAGGAGATCGGAAGAGCGGTTTCAG
chr5	138119072	138119111	CTNNA1_10049	+	GTGACCTATGCACCAGACGTACTGCTTTTTAGGTAAGAGAGGCAGGCCCTTTCTAGAAAAGATCGGAAGAGCGGTTTCAG
chr5	138145904	138145943	CTNNA1_10050	+	GTGACCTATGCACCAGACGTAGGCCTATGTCTGTAATTTGTTCTATCACAGGAAGATTGCAGATCGGAAGAGCGGTTTCAG
chr5	138148002	138148041	CTNNA1_10051	+	GTGACCTATGCACCAGACGTGATTTGGGGATATATTAAGTTGTTCAATTTTACTATCTAGAGATCGGAAGAGCGGTTTCAG
chr5	138160499	138160538	CTNNA1_10052	+	GTGACCTATGCACCAGACGTCTTGGGTGGAATTTCCAGCTCTTGACCATCCCCAAAAGATCGGAAGAGCGGTTTCAG
chr5	138163418	138163457	CTNNA1_10053	+	GTGACCTATGCACCAGACGTACGCTTTTCTTTGAAAGTAAGATTTTATGGATGAGGAGTTAGATCGGAAGAGCGGTTTCAG
chr5	138221992	138222031	CTNNA1_10054	+	GTGACCTATGCACCAGACGTTGAAAGTGCTGATTGTTTTCTAAGTTCTCAATTTTGTAGAGATCGGAAGAGCGGTTTCAG
chr5	138223342	138223381	CTNNA1_10055	+	GTGACCTATGCACCAGACGTAGCAGTTTCATTGACTTGTAGGCACTTGGTGAAGTGTGAGATCGGAAGAGCGGTTTCAG
chr5	138240141	138240180	CTNNA1_10056	+	GTGACCTATGCACCAGACGTACTGACACTGGTGACAGCATAACCAAATTAATTTTATTAGATCGGAAGAGCGGTTTCAG
chr5	138253598	138253637	CTNNA1_10057	+	GTGACCTATGCACCAGACGTGGTTCCTCCAGGAAGTATGTGAAGATGTCATAATTACTTAGATCGGAAGAGCGGTTTCAG
chr5	138260410	138260449	CTNNA1_10058	+	GTGACCTATGCACCAGACGTCTCCCTTTCCAGTTCTGCACACACCCGACCTAGTGAAGATCGGAAGAGCGGTTTCAG
chr5	138261107	138261146	CTNNA1_10059	+	GTGACCTATGCACCAGACGTGCATTTCAGACGCTTAAACAGCTTCTTTCTATCATTTCAGATCGGAAGAGCGGTTTCAG
chr5	138265056	138265095	CTNNA1_10060	+	GTGACCTATGCACCAGACGTGCTCCGTGGGCGAGTTCAGCTTGTGCTGCCACTTTCCCTAGATCGGAAGAGCGGTTTCAG
chr5	138266354	138266393	CTNNA1_10061	+	GTGACCTATGCACCAGACGTCCCCGGCCCCACCCAGGCTGCACAGGGGCTACTTTCTCCAGATCGGAAGAGCGGTTTCAG
chr5	138266635	138266674	CTNNA1_10062	+	GTGACCTATGCACCAGACGTGACTTGCCAGGTGGGTCTCCAAGCTCCTCCTGGGGCTCAGAGATCGGAAGAGCGGTTTCAG
chr5	138268412	138268451	CTNNA1_10063	+	GTGACCTATGCACCAGACGTGTGAACAAAAGAGGGCCAGTGGGAACGTGCTGACCCTTAGATCGGAAGAGCGGTTTCAG
chr5	138269789	138269828	CTNNA1_10064	+	GTGACCTATGCACCAGACGTGCCGGCCGCCCCACCCCTCGGGGCTCCTGAATACAGTCAGATCGGAAGAGCGGTTTCAG
chr2	38298464	38298503	CYP1B1_10065	+	GTGACCTATGCACCAGACGTTTTAATGTGGAGAGAGAAAAGCAAGTGAAGCAAAATTTTAAAGATCGGAAGAGCGGTTTCAG
chr2	38302542	38302581	CYP1B1_10066	+	GTGACCTATGCACCAGACGTGAGAGGAGAAGGCGTGACACTCAGGGGTGCAGAGACAGGAAGATCGGAAGAGCGGTTTCAG
chr2	38298169	38298208	CYP1B1_10067	+	GTGACCTATGCACCAGACGTGCTGGATCAAAAGTTCTCCGGGTTAGGCCACTTCACTGGGTAGATCGGAAGAGCGGTTTCAG
chr2	38301846	38301885	CYP1B1_10068	+	GTGACCTATGCACCAGACGTTCGTTGCTGGCTGAGCACTCAGGCACTCGGGGTCTGCTGATCGGAAGAGCGGTTTCAG
chr2	38302193	38302232	CYP1B1_10069	+	GTGACCTATGCACCAGACGTGGCCGAGCCCTGTGCAGCCAGGGCTGTGGATGCGCAGATCGGAAGAGCGGTTTCAG
chr11	47236825	47236864	DDB2_10070	+	GTGACCTATGCACCAGACGTTGCCTGCTGCTTGAATATTTCCGCCTTTTAGGGTGTGCGAGATCGGAAGAGCGGTTTCAG
chr11	47238034	47238073	DDB2_10071	+	GTGACCTATGCACCAGACGTTTTGCCTCAAGTCTCAAGGGTTACACGTGCATTTTTAAGATCGGAAGAGCGGTTTCAG
chr11	47254521	47254560	DDB2_10072	+	GTGACCTATGCACCAGACGTTAACTAGCAGGGGAAAGGGCTTCTAAGCTTAGGTGTAGTTAGATCGGAAGAGCGGTTTCAG
chr11	47256234	47256273	DDB2_10073	+	GTGACCTATGCACCAGACGTGAGGTCCTGCCTTTCCCTCCCTCACCCCACTCGGTTTCAGATCGGAAGAGCGGTTTCAG
chr11	47256496	47256535	DDB2_10074	+	GTGACCTATGCACCAGACGTCCAGACTCATCTCTCAGCAGCCCTGCTGCTGACCAAGATCGGAAGAGCGGTTTCAG
chr11	47256974	47257013	DDB2_10075	+	GTGACCTATGCACCAGACGTGGGAAGGAGCTCGCAAGAGGCTGTGATCATGAGGCAGATCGGAAGAGCGGTTTCAG
chr11	47259563	47259602	DDB2_10076	+	GTGACCTATGCACCAGACGTGGTCTCAATAATGATGGGAGGAAGCAGGGATTCAACCTAGATCGGAAGAGCGGTTTCAG
chr11	47259745	47259784	DDB2_10077	+	GTGACCTATGCACCAGACGTGGAGAATGTCTGACTTGCCAAAGTCCGATCCTACTTCCAGATCGGAAGAGCGGTTTCAG
chr11	47260411	47260450	DDB2_10078	+	GTGACCTATGCACCAGACGTAGAAGGTGTGGGCCAGACAAGGCCCTTGAGCCACACATGAGATCGGAAGAGCGGTTTCAG
chr7	137076093	137076132	DGKI_10079	+	GTGACCTATGCACCAGACGTATGAGAAAAAAAGAGAGAGATAGACACAAAGATCGGAAGAGCGGTTTCAG
chr7	137080454	137080493	DGKI_10080	+	GTGACCTATGCACCAGACGTGATGAAATGGGAAACCACCATAGAGGGTTGGAGCAGCAGATCGGAAGAGCGGTTTCAG
chr7	137082170	137082209	DGKI_10081	+	GTGACCTATGCACCAGACGTAGAAAGCAAGATGACCGTCAAAAATAAGCTCAAAAATAAAGATCGGAAGAGCGGTTTCAG
chr7	137092752	137092791	DGKI_10082	+	GTGACCTATGCACCAGACGTAGACATAAAAAAGAAGCTCAGGCAGAAATTCGGAACAAGGAGATCGGAAGAGCGGTTTCAG
chr7	137096964	137097003	DGKI_10083	+	GTGACCTATGCACCAGACGTCAAAAGAGAGATGCCATTAGTAGAAGACCCCTTATTAAAGATCGGAAGAGCGGTTTCAG
chr7	137128859	137128898	DGKI_10084	+	GTGACCTATGCACCAGACGTATAATAAGCATGATCAATTTTTATATGATAATTATAATGAGATCGGAAGAGCGGTTTCAG
chr7	137148368	137148407	DGKI_10085	+	GTGACCTATGCACCAGACGTGAAGGGCACCGATGATTAACATTCAAAGTCAGCCAGTAGATCGGAAGAGCGGTTTCAG
chr7	137150792	137150831	DGKI_10086	+	GTGACCTATGCACCAGACGTACAGAAGCTGATGCATGGAAGAAATAACAAAACAAGTATTAGATCGGAAGAGCGGTTTCAG
chr7	137151669	137151708	DGKI_10087	+	GTGACCTATGCACCAGACGTAAAGCGATCAGCAGAAGTTGCTAGGGGAAAAAAATGCAGAGATCGGAAGAGCGGTTTCAG
chr7	137154376	137154415	DGKI_10088	+	GTGACCTATGCACCAGACGTACACACACACTCTAGTGGCTGCATTTCAATAACCTGATGGAGATCGGAAGAGCGGTTTCAG
chr7	137170175	137170214	DGKI_10089	+	GTGACCTATGCACCAGACGTAATGAAAAAAAATCCATACCTTAAATATAGTTTGAACAAGATCGGAAGAGCGGTTTCAG
chr7	137172446	137172485	DGKI_10090	+	GTGACCTATGCACCAGACGTAGGAAGAAGAAAATCTAAAATAACATTTGATTTTTCTAGATCGGAAGAGCGGTTTCAG
chr7	137206723	137206762	DGKI_10091	+	GTGACCTATGCACCAGACGTAGAACCAGTGTGCAGATAAAATGAGAGAGCGGAATTGAGATCGGAAGAGCGGTTTCAG
chr7	137237325	137237364	DGKI_10092	+	GTGACCTATGCACCAGACGTAAAGAGTCAAGGGGACAAAGGAGTTAGTTATTATTTAAGAAGATCGGAAGAGCGGTTTCAG

chr7	137256043	137256082	DGKI_10093	+	GTGACCTATGCACCAGACGTAGATTAAGACAGAAGTAAATATGTCCATCCTTCTCATGAGATCGGAAGAGCGGTTTCAG
chr7	137257595	137257634	DGKI_10094	+	GTGACCTATGCACCAGACGTGAAAAACAGAAAAGGGGTTTTGAAGTAGTCACAAGTCTAAAAGATCGGAAGAGCGGTTTCAG
chr7	137262041	137262080	DGKI_10095	+	GTGACCTATGCACCAGACGTGGGAAATAAAGAAGAAATTCGTAATTACATGGTGATAAGATCGGAAGAGCGGTTTCAG
chr7	137263082	137263121	DGKI_10096	+	GTGACCTATGCACCAGACGTGAAAAAGTAGTTTTGTATGGAGACCTCACTAAAGGTAGCAGATCGGAAGAGCGGTTTCAG
chr7	137266685	137266724	DGKI_10097	+	GTGACCTATGCACCAGACGTAAACAAAGACAGAGGCAAAATTTTGTGTGCCAGGCAGAAAAGATCGGAAGAGCGGTTTCAG
chr7	137270103	137270142	DGKI_10098	+	GTGACCTATGCACCAGACGTAGAGAACATCCATTGCTGTCAGAGTGGAGAACAGTGAAGATCGGAAGAGCGGTTTCAG
chr7	137271967	137272006	DGKI_10099	+	GTGACCTATGCACCAGACGTTCGGGGGCCAGAAGAGATAAAGAATAAATAAGTTAAGATCGGAAGAGCGGTTTCAG
chr7	137282664	137282703	DGKI_10100	+	GTGACCTATGCACCAGACGTAAAGAAGAAAAAGTAAACAAAAGAACATTTCACTGGCTAAGATCGGAAGAGCGGTTTCAG
chr7	137284662	137284701	DGKI_10101	+	GTGACCTATGCACCAGACGTAAATACACAAAAAGGCAATAATAGGAAGAAATTTCCCAAAGATCGGAAGAGCGGTTTCAG
chr7	137293821	137293860	DGKI_10102	+	GTGACCTATGCACCAGACGTCAATCAGCACTGTTAGGATACACATCCATGGCTTGAAAGGAGATCGGAAGAGCGGTTTCAG
chr7	137294366	137294405	DGKI_10103	+	GTGACCTATGCACCAGACGTAGAGAGAAATGCCTGAGCTCAGAGGCCAGCCAGCCCAGGAGATCGGAAGAGCGGTTTCAG
chr7	137304697	137304736	DGKI_10104	+	GTGACCTATGCACCAGACGTAATAAGCCAGTAAACAATTTCTGGTCAAAGAGTAATGCTGAGATCGGAAGAGCGGTTTCAG
chr7	137308311	137308350	DGKI_10105	+	GTGACCTATGCACCAGACGTAGAACAAGAGACAGATAATTTAAACCACCTCAGTTACAGAGATCGGAAGAGCGGTTTCAG
chr7	137339545	137339584	DGKI_10106	+	GTGACCTATGCACCAGACGTAAAAAGAAAGTATATTATATTAGAGATAAGCATCAGACTAAGATCGGAAGAGCGGTTTCAG
chr7	137341297	137341336	DGKI_10107	+	GTGACCTATGCACCAGACGTCAATTCAAAAGACAAAAAGAAATGTTAACAGTCTGTTCTAGATCGGAAGAGCGGTTTCAG
chr7	137363409	137363448	DGKI_10108	+	GTGACCTATGCACCAGACGTAAAGACCCACTGACATCAATTTTTTTTTTCCAGGGATAAGAGATCGGAAGAGCGGTTTCAG
chr6	10984150	10984189	ELOVL2_10109	+	GTGACCTATGCACCAGACGTTGTATATTTGAAGAGAAAAATAAAAAGGTTATTTAATAAAGATCGGAAGAGCGGTTTCAG
chr6	10990081	10990120	ELOVL2_10110	+	GTGACCTATGCACCAGACGTACAGAGGCCATCTGTGAGCGGGCAGGCTGTGCCACAAGATCGGAAGAGCGGTTTCAG
chr6	10990686	10990725	ELOVL2_10111	+	GTGACCTATGCACCAGACGTACAGTATAAAAATCACTATTCTTCCAGGAAGGACTGTTCAAGATCGGAAGAGCGGTTTCAG
chr6	10995422	10995461	ELOVL2_10112	+	GTGACCTATGCACCAGACGTTTTGTAAGGGGAGAAAAGGGTGAGAAATGGCAGTGTTCCTAGATCGGAAGAGCGGTTTCAG
chr6	11000408	11000447	ELOVL2_10113	+	GTGACCTATGCACCAGACGTACCAGAAAAGAAAAGAAAACAACATCAGCACAGAATTTAGATCGGAAGAGCGGTTTCAG
chr6	11005803	11005842	ELOVL2_10114	+	GTGACCTATGCACCAGACGTACACATACAGTGAAGATCCTGAGGAATGATGCTCCTGTTTAGATCGGAAGAGCGGTTTCAG
chr6	11011053	11011092	ELOVL2_10115	+	GTGACCTATGCACCAGACGTAAGAAAAAATGATTTAAGTGTTTTTTTCTCTTTTTTTGAGATCGGAAGAGCGGTTTCAG
chr6	1104474	11044513	ELOVL2_10116	+	GTGACCTATGCACCAGACGTGGCTGTGGCGCGGACCTCCCGGGCGGCGATGCGCTGTAGATCGGAAGAGCGGTTTCAG
chr12	132446510	132446549	EP400_10117	+	GTGACCTATGCACCAGACGTGGAGTTAATTTGTTTAGTACAAATCTTCTAGATGATCAGAAGATCGGAAGAGCGGTTTCAG
chr12	132464349	132464388	EP400_10118	+	GTGACCTATGCACCAGACGTACGGCTAGCGTGGCCCTCGGAATGCCCCCTCTCTTTGGGAGATCGGAAGAGCGGTTTCAG
chr12	132466152	132466191	EP400_10119	+	GTGACCTATGCACCAGACGTGCAGCAGAGCCAGCTCCCGCTCAGGAGCAGGCAGCACACAGATCGGAAGAGCGGTTTCAG
chr12	132467034	132467073	EP400_10120	+	GTGACCTATGCACCAGACGTAGATAGAGGAAAAAAGAAAATGGTTGCAGGATTTGCTGAGATCGGAAGAGCGGTTTCAG
chr12	132471363	132471402	EP400_10121	+	GTGACCTATGCACCAGACGTTTAAGAAAGTTGAAATGTACTCCAGTTGGTGAAGCACAAGATCGGAAGAGCGGTTTCAG
chr12	132472446	132472485	EP400_10122	+	GTGACCTATGCACCAGACGTTCGGTGAGCTGCTGTGCTGTGTGCGTGTGCGTGGGGGCTAGATCGGAAGAGCGGTTTCAG
chr12	132474660	132474699	EP400_10123	+	GTGACCTATGCACCAGACGTCCGTTGTCATGGGGTCTGAAGAATCAGTCTGTCGGAGCTGAGATCGGAAGAGCGGTTTCAG
chr12	132475270	132475309	EP400_10124	+	GTGACCTATGCACCAGACGTTTTAAAAAAGGCTCACACGCTTGGTGATTTTGTTCGAGATCGGAAGAGCGGTTTCAG
chr12	132476012	132476051	EP400_10125	+	GTGACCTATGCACCAGACGTGGTTGTTACTGTCTGTGTGAGAGAGGAGTAGAAGCAGCTAGATCGGAAGAGCGGTTTCAG
chr12	132476786	132476825	EP400_10126	+	GTGACCTATGCACCAGACGTCTCAGCAGCTATTTGTCTCAGGCTGCTGATGAGAGATCGGAAGAGCGGTTTCAG
chr12	132479512	132479551	EP400_10127	+	GTGACCTATGCACCAGACGTGCTACCTTATAAACACTCAGTAAAGTAAAAAGAAACATTTAGATCGGAAGAGCGGTTTCAG
chr12	132489740	132489779	EP400_10128	+	GTGACCTATGCACCAGACGTAGCCTTTGGAAGAATTCAGGGTAAAAAGCAGAAGCCGGAGAGATCGGAAGAGCGGTTTCAG
chr12	132490858	132490897	EP400_10129	+	GTGACCTATGCACCAGACGTAAAGCTTTCAAGTGTGGGATGGCCCTTTGAGAGACAGAGCAAGATCGGAAGAGCGGTTTCAG
chr12	132491433	132491472	EP400_10130	+	GTGACCTATGCACCAGACGTGCTAGTTTTTTAAACAATACCTATTTGCTAGGACTTACCTAGATCGGAAGAGCGGTTTCAG
chr12	132496190	132496229	EP400_10131	+	GTGACCTATGCACCAGACGTTTTAAACATAAAAATAAGCTAAACAGAAAGCCATGTTAATAGATCGGAAGAGCGGTTTCAG
chr12	132497734	132497773	EP400_10132	+	GTGACCTATGCACCAGACGTTACGCGCTTGTCAATGAGTGTCTTTGTCTGTTGATGTAGAAGATCGGAAGAGCGGTTTCAG
chr12	132498220	132498259	EP400_10133	+	GTGACCTATGCACCAGACGTTTTCTGCCATTTCAAGTAAATTAACATGCGTATGCTGATCGGAAGAGCGGTTTCAG
chr12	132498469	132498508	EP400_10134	+	GTGACCTATGCACCAGACGTGCTCTGGGCATGTGCCCCCTTTGCTGTCCCTGCCTGTGAGAGATCGGAAGAGCGGTTTCAG
chr12	132502277	132502316	EP400_10135	+	GTGACCTATGCACCAGACGTGATCCAGAAAGCGGAATTAAGTGTGGATATCTTTCTAGGAGATCGGAAGAGCGGTTTCAG
chr12	132502932	132502971	EP400_10136	+	GTGACCTATGCACCAGACGTCCCAGAGGACGCGGGAGGGTGGCTCCCAGGGCCCCACAGATCGGAAGAGCGGTTTCAG
chr12	132504774	132504813	EP400_10137	+	GTGACCTATGCACCAGACGTGATGTTGCTGTCTCCGCTTATGGAGTGTGTTTGTGGGAGATCGGAAGAGCGGTTTCAG
chr12	132505877	132505916	EP400_10138	+	GTGACCTATGCACCAGACGTTCACTTCCAGTCTTCCAGTCTTCCATCTCTACCCAGAGGAAGATCGGAAGAGCGGTTTCAG
chr12	132508497	132508536	EP400_10139	+	GTGACCTATGCACCAGACGTGGATGAGAGAGCACTGATGCCAAAAATGACAAAAGCGCCTAGATCGGAAGAGCGGTTTCAG
chr12	132510360	132510399	EP400_10140	+	GTGACCTATGCACCAGACGTCTGAGCAGGAGGGAGACTTGGCTTGGATGCTCTTTTCTAGATCGGAAGAGCGGTTTCAG
chr12	132512087	132512126	EP400_10141	+	GTGACCTATGCACCAGACGTGAGCTTGAAGCCCGGTGCACGTGGACAGGTAGCTTTCCAAGATCGGAAGAGCGGTTTCAG
chr12	132512844	132512883	EP400_10142	+	GTGACCTATGCACCAGACGTCCCTCGTGACCTTTTCGGTGTCTCTGGCTGCATTGCACCCAGATCGGAAGAGCGGTTTCAG
chr12	132514459	132514498	EP400_10143	+	GTGACCTATGCACCAGACGTGTTGGGGCGTGGCCGTCGGGAGCTCACCCGCGCTGGAGATCGGAAGAGCGGTTTCAG
chr12	132514714	132514753	EP400_10144	+	GTGACCTATGCACCAGACGTCATTTTACATGTTCTCTGATGGGTGAGTCACTGCTGTTAGATCGGAAGAGCGGTTTCAG
chr12	132516705	132516744	EP400_10145	+	GTGACCTATGCACCAGACGTGCGGGGGATAGGATCAGGAGATGCAAAGACATCCACATATAGATCGGAAGAGCGGTTTCAG
chr12	132522349	132522388	EP400_10146	+	GTGACCTATGCACCAGACGTTTCAATGAGAGGCCTGAGGTGAGACCCGCCATGCGGCGGAGATCGGAAGAGCGGTTTCAG
chr12	132522652	132522691	EP400_10147	+	GTGACCTATGCACCAGACGTATTGAATCTGGCTGAAGAGTTGCACGGTGGGAGCCGCGGAGATCGGAAGAGCGGTTTCAG
chr12	132528018	132528057	EP400_10148	+	GTGACCTATGCACCAGACGTGTTTTCTTTACAACATACATATTTAAAAATTTGACGCTTAGATCGGAAGAGCGGTTTCAG
chr12	132528284	132528323	EP400_10149	+	GTGACCTATGCACCAGACGTCAAGTTTTGGTCTAGTAAAAAATTTGCAATATTTTTCAGAAGATCGGAAGAGCGGTTTCAG
chr12	132528867	132528906	EP400_10150	+	GTGACCTATGCACCAGACGTGCCGTTCCCTCTGCCCTTGTCCCTTCTGAGGGGCACAGATCGGAAGAGCGGTTTCAG

chr12	132529271	132529310	EP400_10151	+	GTGACCTATGCACCAGACGTCCCTCTCCCTTTGTGTCTGTGTGGGCAGCTTCTGTGAGTAGATCGGAAGAGCGGTTTCAG
chr12	132529509	132529548	EP400_10152	+	GTGACCTATGCACCAGACGTCGAGGGCGTACATGACCTGGGGGGGCCCTTGCCTGCAGAAAGATCGGAAGAGCGGTTTCAG
chr12	132530116	132530155	EP400_10153	+	GTGACCTATGCACCAGACGTGTGGTCTTTGTGCCAGCGGTGATGTGCGGTCAATTTTTCTAAGATCGGAAGAGCGGTTTCAG
chr12	132530456	132530495	EP400_10154	+	GTGACCTATGCACCAGACGTTCTCGTTTGTCCCTCGAGGAGAGCACAGGCAGGTGTGGTGAGATCGGAAGAGCGGTTTCAG
chr12	132535015	132535054	EP400_10155	+	GTGACCTATGCACCAGACGTTGAGTGCTCAATTTATGTTCAATGACTGAGTAGATTGCAGATCGGAAGAGCGGTTTCAG
chr12	132535211	132535250	EP400_10156	+	GTGACCTATGCACCAGACGTATTCGTGACACATTTGTACTGTTTGAAGGATTTCAATTCAGATCGGAAGAGCGGTTTCAG
chr12	132537780	132537819	EP400_10157	+	GTGACCTATGCACCAGACGTTGGGCCCTTCTGTTGAGTGGGAAAATGTGGTGACTGTGAAGATCGGAAGAGCGGTTTCAG
chr12	132538153	132538192	EP400_10158	+	GTGACCTATGCACCAGACGTCGCCTCTCCCGGGCTTCCCTCTACGGGAAGTCACCCACAAGATCGGAAGAGCGGTTTCAG
chr12	132539575	132539614	EP400_10159	+	GTGACCTATGCACCAGACGTTACAGAGATGCTGAAATGTGGACCCCATTTCTCTGGCGCAGATCGGAAGAGCGGTTTCAG
chr12	132539764	132539803	EP400_10160	+	GTGACCTATGCACCAGACGTCCTCACCTGGGTTGTGCACCTTGACTGCATTCTGCCGAAAAGATCGGAAGAGCGGTTTCAG
chr12	132546879	132546918	EP400_10161	+	GTGACCTATGCACCAGACGTGTGGGAGCTTCTCTGCCACACGCTGTGCTGTGGCGGTGAGATCGGAAGAGCGGTTTCAG
chr12	132547257	132547296	EP400_10162	+	GTGACCTATGCACCAGACGTCACAGAGCTTCAACGTCGCTGTCGCTTGTGGTTCAGTTCAGAGATCGGAAGAGCGGTTTCAG
chr12	132549442	132549481	EP400_10163	+	GTGACCTATGCACCAGACGTTTTCTGTTTTGTTTTCCAAAAGCAGCATTTTTTATGTTTTAGATCGGAAGAGCGGTTTCAG
chr12	132551525	132551564	EP400_10164	+	GTGACCTATGCACCAGACGTCAGCACACCCCTCCCGTCTGGGCTTGTAGCCTGGTTTACAAGATCGGAAGAGCGGTTTCAG
chr12	132552042	132552081	EP400_10165	+	GTGACCTATGCACCAGACGTTAGGGGATTCTCACTTCTGGTCTATGCCAAGCCAAAGCTAGATCGGAAGAGCGGTTTCAG
chr12	132554197	132554236	EP400_10166	+	GTGACCTATGCACCAGACGTTAACAGGGTGAGGGCCCCAGGTGCAGGAGTGGTGCCTGCCGCGAGATCGGAAGAGCGGTTTCAG
chr12	132561149	132561188	EP400_10167	+	GTGACCTATGCACCAGACGTTAGCAAAGTGGAAACCTCACATTTCCAGGTCAGAAATAGATCGGAAGAGCGGTTTCAG
chr12	132562229	132562268	EP400_10168	+	GTGACCTATGCACCAGACGTAGGCTTGCCTCATCTAAAGCATAAAGCTACCTTCCCTACAAGATCGGAAGAGCGGTTTCAG
chr12	132445620	132445659	EP400_10169	+	GTGACCTATGCACCAGACGTAGGTGCCCTGGCCCTGGGCTGGCCTCTGCAGCAGCAGATCGGAAGAGCGGTTTCAG
chr12	132446065	132446104	EP400_10170	+	GTGACCTATGCACCAGACGTCTGCTCCCCGGGGCTGGGGGGCGCAGCGGGTTTGGGATGAAGATCGGAAGAGCGGTTTCAG
chr1	22895857	22895896	EPHA8_10171	+	GTGACCTATGCACCAGACGTGGCACTGGGGACAACGTCATCCCTCTGTGAGCAGAGAGAGATCGGAAGAGCGGTTTCAG
chr1	22903384	22903423	EPHA8_10172	+	GTGACCTATGCACCAGACGTCATGGCTGGCCATGGGTGTCAGCCGCGCAGCGGTGCTTGGTTCAGATCGGAAGAGCGGTTTCAG
chr1	22913139	22913178	EPHA8_10173	+	GTGACCTATGCACCAGACGTCCTCGAGTCCAGTACCCCTGAGCCCAAGACTGGCCCGGAGATCGGAAGAGCGGTTTCAG
chr1	22915710	22915749	EPHA8_10174	+	GTGACCTATGCACCAGACGTAAACTCCGTCCTCCGACGCTGCTGCTCCCGCAGCTTCCCTAGATCGGAAGAGCGGTTTCAG
chr1	22915883	22915922	EPHA8_10175	+	GTGACCTATGCACCAGACGTCACATCTATAAGTAAGAGAAAATCCCAAAGCTCAGAGGCAGATCGGAAGAGCGGTTTCAG
chr1	22919954	22919993	EPHA8_10176	+	GTGACCTATGCACCAGACGTCAGGACGGAGTGGGAGGGGCTGGGCCAGCAGGGCAGGGCCAGATCGGAAGAGCGGTTTCAG
chr1	22920190	22920229	EPHA8_10177	+	GTGACCTATGCACCAGACGTGGAGGGGGCGTGGGCGCGGAGCAGCCAGGTGCCAGGACAGATCGGAAGAGCGGTTTCAG
chr1	22921827	22921866	EPHA8_10178	+	GTGACCTATGCACCAGACGTTGGCCAGCCACCCAGCCCTCTCAAGCACCCGTACAGATCGGAAGAGCGGTTTCAG
chr1	22922677	22922716	EPHA8_10179	+	GTGACCTATGCACCAGACGTGGGCCGGTGGTCTGGGGCAGAGGGCAAGGCCACAGGGGGAAGATCGGAAGAGCGGTTTCAG
chr1	22923980	22924019	EPHA8_10180	+	GTGACCTATGCACCAGACGTGGGGTTGTGAGGGCGGGGCGCAGCATGGGGCAAGGTGGGGGAGATCGGAAGAGCGGTTTCAG
chr1	22924365	22924404	EPHA8_10181	+	GTGACCTATGCACCAGACGTGGCAAAGACAGCCTCCCTGCAGTGCCCTCTGCTGGAGATCGGAAGAGCGGTTTCAG
chr1	22924716	22924755	EPHA8_10182	+	GTGACCTATGCACCAGACGTCACCCTGCCTCTTGCATGGCTGGGGAGGGAGTCCAGAGATCGGAAGAGCGGTTTCAG
chr1	22925551	22925590	EPHA8_10183	+	GTGACCTATGCACCAGACGTCACACTCCTTCCGGCTAGACTGGGAGTGGGGAGATGGCGAGATCGGAAGAGCGGTTTCAG
chr1	22927314	22927353	EPHA8_10184	+	GTGACCTATGCACCAGACGTAGCCCTGGCAGGTCGCGGGCGGTGGAGCCTCAGGGTGCAGATCGGAAGAGCGGTTTCAG
chr1	22927592	22927631	EPHA8_10185	+	GTGACCTATGCACCAGACGTCACCCCTGCTCTTGGAGCCAGCTGCCTCCAGTATTAGATCGGAAGAGCGGTTTCAG
chr1	22927977	22928016	EPHA8_10186	+	GTGACCTATGCACCAGACGTGGTGGGGCTGGGGCCCATGCGTGTGGGGGAGGGGGGGGAGATCGGAAGAGCGGTTTCAG
chr1	22928245	22928284	EPHA8_10187	+	GTGACCTATGCACCAGACGTCAGGGGCCAGGCAGCCACCAAGCCACCCAGGTCATGCAGATCGGAAGAGCGGTTTCAG
chr1	22903052	22903091	EPHA8_10188	+	GTGACCTATGCACCAGACGTACGAGGTCGCAGTGTGGTCCCTCAGCAAGCGCGGCTAGATCGGAAGAGCGGTTTCAG
chr1	22915628	22915667	EPHA8_10189	+	GTGACCTATGCACCAGACGTTCAATGGCGTGTCCGACCTGAGCCCCGAGCCCCGCGGGCAGATCGGAAGAGCGGTTTCAG
chr1	23107989	23108028	EPHB2_10190	+	GTGACCTATGCACCAGACGTGGTCCCAAACTTGCATTTGTCCTCCAGATCCCTCAAGCAGATCGGAAGAGCGGTTTCAG
chr1	23111580	23111619	EPHB2_10191	+	GTGACCTATGCACCAGACGTGGTGGGGCACGTGCCCTGCAAAATGCATAGAAGTGGTTCAGATCGGAAGAGCGGTTTCAG
chr1	23189696	23189735	EPHB2_10192	+	GTGACCTATGCACCAGACGTGGGGCCCTCAAGGGCGATGGCTGGCCGAGTCCCAGGTCTAAGATCGGAAGAGCGGTTTCAG
chr1	23191716	23191755	EPHB2_10193	+	GTGACCTATGCACCAGACGTCGACGTGGGCCAGGGGAGTGGCCCATCGCGCTGTGCCAGAGATCGGAAGAGCGGTTTCAG
chr1	23208987	23209026	EPHB2_10194	+	GTGACCTATGCACCAGACGTCGCTGGGTGCTGTCCCATCACCCACCTCCCTGAGGGCCCCAGATCGGAAGAGCGGTTTCAG
chr1	23219550	23219589	EPHB2_10195	+	GTGACCTATGCACCAGACGTTCCAGGGGCAAGAGGAGGGGCACAGACTCCACAACAAGAAAGATCGGAAGAGCGGTTTCAG
chr1	23222084	23222123	EPHB2_10196	+	GTGACCTATGCACCAGACGTTCTCCAGGTTGGCCAGGCTGGCTGTCCAGATGGCTTCAGATCGGAAGAGCGGTTTCAG
chr1	23222982	23223021	EPHB2_10197	+	GTGACCTATGCACCAGACGTACCCAAGCGGGCTGGAACCCCTGGGCCCTTCACTGTGGTGTAGATCGGAAGAGCGGTTTCAG
chr1	23232613	23232652	EPHB2_10198	+	GTGACCTATGCACCAGACGTGGTACTCTCACATGTACTATGACCTTAGCCATGGCTGGTGTAGATCGGAAGAGCGGTTTCAG
chr1	23233461	23233500	EPHB2_10199	+	GTGACCTATGCACCAGACGTCGAAGAGGGCCAGGGGCCATGAATGGGGCAGGAAAAGGAAGATCGGAAGAGCGGTTTCAG
chr1	23234672	23234711	EPHB2_10200	+	GTGACCTATGCACCAGACGTGGCAGGGAACACCGGAGTTCACAGAGCCAGAGAAGAGGGCAAGATCGGAAGAGCGGTTTCAG
chr1	23235675	23235714	EPHB2_10201	+	GTGACCTATGCACCAGACGTAAGGGGATAGGCAAGCCCTCTGGCCACCCAGATGGGAGAGATCGGAAGAGCGGTTTCAG
chr1	23237079	23237118	EPHB2_10202	+	GTGACCTATGCACCAGACGTACCCTGGCCCTGCCAGCCAGGCCCTGCCCTTCCCGAGATCGGAAGAGCGGTTTCAG
chr1	23239103	23239142	EPHB2_10203	+	GTGACCTATGCACCAGACGTAGCCACTTCTGCTTGTACCTTAGCACCCCTCTCCACCGAGATCGGAAGAGCGGTTTCAG
chr1	23240074	23240113	EPHB2_10204	+	GTGACCTATGCACCAGACGTCCTCGGCTCACCTTCTCCAAGCCCCGCCCTCTGCCAGATCGGAAGAGCGGTTTCAG
chr1	23111237	23111276	EPHB2_10205	+	GTGACCTATGCACCAGACGTACACCGAGGTGCGGAGCTTCGACCTGTGTCCGCGAGCGGAGATCGGAAGAGCGGTTTCAG
chr21	39755856	39755895	ERG_10206	+	GTGACCTATGCACCAGACGTCAGGAGAGGAAGAAAACCTCAGTGAGCACAGGTTCCAGGAGATCGGAAGAGCGGTTTCAG
chr21	39762975	39763014	ERG_10207	+	GTGACCTATGCACCAGACGTAAGAAAAGTAAAGCTTCAATATGTAACATAGTAGATCGGAAGAGCGGTTTCAG
chr21	39763648	39763687	ERG_10208	+	GTGACCTATGCACCAGACGTAGAATACAAAGCAATTAGCTATAACAGATTTGGTTCACAGATCGGAAGAGCGGTTTCAG



chr21	39764377	39764416	ERG_10209	+	GTGACCTATGCACCAGACGTAAATAAATTGACTAAAAGATCAATCATGTAATTTTTATAAAGATCGGAAGAGCGGTTTCAG
chr21	39772578	39772617	ERG_10210	+	GTGACCTATGCACCAGACGTAAAGGAAAGACAAACATGTGAAGGCTTTTTGTTGGTTGTAGATCGGAAGAGCGGTTTCAG
chr21	39774570	39774609	ERG_10211	+	GTGACCTATGCACCAGACGTAAACAAAAAGCGACATCAAATGAAAAAAGAGAGAGATCGGAAGAGCGGTTTCAG
chr21	39775642	39775681	ERG_10212	+	GTGACCTATGCACCAGACGTTGGGAACACATTCACTCAATTCCTGAAGCCAGGGATCTTCAGATCGGAAGAGCGGTTTCAG
chr21	39795454	39795493	ERG_10213	+	GTGACCTATGCACCAGACGTTTGGCCACACTGCATTCATCAGGAGAGTTCTCGAGGAGAGATCGGAAGAGCGGTTTCAG
chr21	39795494	39795533	ERG_10214	+	GTGACCTATGCACCAGACGTAGAATAATTCTCCATTATAACAGCAATCAAAGAGCATGTAGATCGGAAGAGCGGTTTCAG
chr21	39817555	39817594	ERG_10215	+	GTGACCTATGCACCAGACGTAAAGAAACACATAATTCAAGACACTCCAACAGACAGTCATAGATCGGAAGAGCGGTTTCAG
chr21	39870315	39870354	ERG_10216	+	GTGACCTATGCACCAGACGTAGTTTATTGATCGTTAATAAATGTTAATAATAATTATTGCAGATCGGAAGAGCGGTTTCAG
chr21	39947635	39947674	ERG_10217	+	GTGACCTATGCACCAGACGTAAAGCCAGCCATCTACCAGCTGTTCCAGAACCTGACGGCTAAGATCGGAAGAGCGGTTTCAG
chr21	39755595	39755634	ERG_10218	+	GTGACCTATGCACCAGACGTGAACTTGTAGGCGTAGCGCTTCCCATGGACCTTGGTCATGAGATCGGAAGAGCGGTTTCAG
chr11	44129809	44129848	EXT2_10219	+	GTGACCTATGCACCAGACGTCTCATACAGCCCAGCCCCAGGAGATACTTGAGTGGCCCTAGATCGGAAGAGCGGTTTCAG
chr11	44130844	44130883	EXT2_10220	+	GTGACCTATGCACCAGACGTTATTTGGGGCTGCCTTATGATGGGTTCAAGATCATTTTGAGATCGGAAGAGCGGTTTCAG
chr11	44135862	44135901	EXT2_10221	+	GTGACCTATGCACCAGACGTTTCATCCAGCCAGCGGTGTCCTTTACTGAATCTGTAGATAGATCGGAAGAGCGGTTTCAG
chr11	44146545	44146584	EXT2_10222	+	GTGACCTATGCACCAGACGTTTCATTACCTCTCGCAAAGGCTCAGGAGAGTTTGCTTACAAGATCGGAAGAGCGGTTTCAG
chr11	44148516	44148555	EXT2_10223	+	GTGACCTATGCACCAGACGTCTCTTAGTAACTCTACATTAGTGGTTCTGCGTATATAAGATCGGAAGAGCGGTTTCAG
chr11	44151699	44151738	EXT2_10224	+	GTGACCTATGCACCAGACGTAAAGTCTTGGGGAGGTGACATGGGTGGTACCAGAAATGGTGGAGATCGGAAGAGCGGTTTCAG
chr11	44193303	44193342	EXT2_10225	+	GTGACCTATGCACCAGACGTTCCAGTGCATGCCACATGAGGCAATGGTCCAGCTGCAGGGAGATCGGAAGAGCGGTTTCAG
chr11	44219579	44219618	EXT2_10226	+	GTGACCTATGCACCAGACGTTTAGTGCCCTCTCAGCTGAGCAATTTGGATGGCCAAAAGATCGGAAGAGCGGTTTCAG
chr11	44228520	44228559	EXT2_10227	+	GTGACCTATGCACCAGACGTTTACACAGTGTGTTTATATGTTAATAATTACTTCTATGAGATCGGAAGAGCGGTTTCAG
chr11	44254057	44254096	EXT2_10228	+	GTGACCTATGCACCAGACGTGCAGTCTGGCAAGGTGACAAAAGTGAAGAAATGATACACAGATCGGAAGAGCGGTTTCAG
chr11	44257936	44257975	EXT2_10229	+	GTGACCTATGCACCAGACGTCTCCAACAAAAGTGCGCCTTAGCCTCTGATCTCTATTTCAGATCGGAAGAGCGGTTTCAG
chr11	44265848	44265887	EXT2_10230	+	GTGACCTATGCACCAGACGTTGGTGGAGGTCTGAATGTGAGGCTGGGACAGAGGGAGAGAAGATCGGAAGAGCGGTTTCAG
chr11	44129541	44129580	EXT2_10231	+	GTGACCTATGCACCAGACGTCTATCGCTGTGGCTTCAACCCAAAAGAACAAAATCAAGGTGAGATCGGAAGAGCGGTTTCAG
chr9	97864143	97864182	FANCC_10232	+	GTGACCTATGCACCAGACGTGACAGAAGAAGGCAAAATAAAACACTTTCCAGACAGATAGATCGGAAGAGCGGTTTCAG
chr9	97869562	97869601	FANCC_10233	+	GTGACCTATGCACCAGACGTGATTTTACAGGGGAGAGGTTAGGAAGAGGCAGGACAGACAGATCGGAAGAGCGGTTTCAG
chr9	97873930	97873969	FANCC_10234	+	GTGACCTATGCACCAGACGTGGCAGAACACATGGCAGTTGACAACCTAAATTTCTTCCAGATCGGAAGAGCGGTTTCAG
chr9	97877003	97877042	FANCC_10235	+	GTGACCTATGCACCAGACGTAGAGAGATACGTGACAGGGCAACTGAGGAAATGTCAAGCCAGATCGGAAGAGCGGTTTCAG
chr9	97879683	97879722	FANCC_10236	+	GTGACCTATGCACCAGACGTAGAAAATCCAAGAGCATGAACATTAAGATTGAAACGGAGATCGGAAGAGCGGTTTCAG
chr9	97887478	97887517	FANCC_10237	+	GTGACCTATGCACCAGACGTGAAAAGTCAGATCAAGACAGTAACTAAACAAGTAATCCGGCAAGATCGGAAGAGCGGTTTCAG
chr9	97888874	97888913	FANCC_10238	+	GTGACCTATGCACCAGACGTAGAAGACCATGAGAATGTGAAATATCAAGCACTTTTCTAGATCGGAAGAGCGGTTTCAG
chr9	97897795	97897834	FANCC_10239	+	GTGACCTATGCACCAGACGTGAAATAAAAATAAATTTAAACAGAAATGGCTCACTGAAAAGATCGGAAGAGCGGTTTCAG
chr9	97912380	97912419	FANCC_10240	+	GTGACCTATGCACCAGACGTAAATAAGAAATAACTCAAAATTAAGAGCCATGCATAATAGATCGGAAGAGCGGTTTCAG
chr9	97933436	97933475	FANCC_10241	+	GTGACCTATGCACCAGACGTAAATCAGTTGCAGGTTAACTCACGCTGCAAACAGGATTACAGATCGGAAGAGCGGTTTCAG
chr9	97934440	97934479	FANCC_10242	+	GTGACCTATGCACCAGACGTAAACAGAAAAATTAACCTCTTTAAAAGTAAATGCAAGTAGATCGGAAGAGCGGTTTCAG
chr9	98003036	98003075	FANCC_10243	+	GTGACCTATGCACCAGACGTGAAAACCTAATAAGTTTTATCAAGCAGAAAAAATCATTAAAGATCGGAAGAGCGGTTTCAG
chr9	98009809	98009848	FANCC_10244	+	GTGACCTATGCACCAGACGTAAATAAATAAATTTGGTCAGTAAAGGCATTATGCAACTTAGAAGATCGGAAGAGCGGTTTCAG
chr9	98011584	98011623	FANCC_10245	+	GTGACCTATGCACCAGACGTGCGAAAAGGTGATGTCCCTTACAGCAGCCTGTCCAGCACAGATCGGAAGAGCGGTTTCAG
chr9	35074224	35074263	FANCG_10246	+	GTGACCTATGCACCAGACGTAGAAGGATGATGCCTAAGGGTGAAGATTGGCAGAAAGCTAGATCGGAAGAGCGGTTTCAG
chr9	35074502	35074541	FANCG_10247	+	GTGACCTATGCACCAGACGTAGCCAGAGTACAGAGTCTTAGAACTTGACATAGTCTTAGAGATCGGAAGAGCGGTTTCAG
chr9	35075090	35075129	FANCG_10248	+	GTGACCTATGCACCAGACGTCTCCAAAGTCAAGAAGTGTCTCCAGCCTCACAGTCACAGATCGGAAGAGCGGTTTCAG
chr9	35075333	35075372	FANCG_10249	+	GTGACCTATGCACCAGACGTACACAGAACAGGGGTGAAGAGGAATCAAACTTTCAGAACTCAGATCGGAAGAGCGGTTTCAG
chr9	35075762	35075801	FANCG_10250	+	GTGACCTATGCACCAGACGTAGAAGAAGCAGTGTCTTGAAGGCATGAGCCACCATCCAGATCGGAAGAGCGGTTTCAG
chr9	35076036	35076075	FANCG_10251	+	GTGACCTATGCACCAGACGTAAAGCCATAAGCTCACCTAGGCCCTAGCAGGGAACCTAGATCGGAAGAGCGGTTTCAG
chr9	35076591	35076630	FANCG_10252	+	GTGACCTATGCACCAGACGTAAAGAAAAAATTTGATCTATAATCTTTGGGAGCCATACTTAGATCGGAAGAGCGGTTTCAG
chr9	35076878	35076917	FANCG_10253	+	GTGACCTATGCACCAGACGTAGGAGGACCGGGCTCAGTACCCTTACAAGCAAAAAGAGATCGGAAGAGCGGTTTCAG
chr9	35077109	35077148	FANCG_10254	+	GTGACCTATGCACCAGACGTTCAGGGTGTGAGCTTGGAGGCTATAGAGCAGGGTCAAGATCGGAAGAGCGGTTTCAG
chr9	35077407	35077446	FANCG_10255	+	GTGACCTATGCACCAGACGTAAAGGACAACCAAGAGCTCAAGGCTCAAACTCCTCGTCTAGATCGGAAGAGCGGTTTCAG
chr9	35078351	35078390	FANCG_10256	+	GTGACCTATGCACCAGACGTTACACACACATAGACACACACAGCTGAAGTAGCACCAGATCGGAAGAGCGGTTTCAG
chr9	35078744	35078783	FANCG_10257	+	GTGACCTATGCACCAGACGTAAATGTTGGTCTTACAGACTGCTCCCCATGGAAGATCCTCAGATCGGAAGAGCGGTTTCAG
chr9	35079249	35079288	FANCG_10258	+	GTGACCTATGCACCAGACGTAGGGAGGGGTTGCTCACTGAGGATCAATCTTTTTTCTCCAGATCGGAAGAGCGGTTTCAG
chr9	35079532	35079571	FANCG_10259	+	GTGACCTATGCACCAGACGTGCTGGCCCCGAGACCCAGAACCGGCTTAGGAAGGGTGAAGATCGGAAGAGCGGTTTCAG
chr1	11168354	11168393	MTOR_10260	+	GTGACCTATGCACCAGACGTAGAAACATAAATCTTACTCTTCTGGCAATCGATGCAGATCGGAAGAGCGGTTTCAG
chr1	11169438	11169477	MTOR_10261	+	GTGACCTATGCACCAGACGTCAAAGTAGAAATAACTGTAAGAATGGGAGCAATACAACAAGATCGGAAGAGCGGTTTCAG
chr1	11169797	11169836	MTOR_10262	+	GTGACCTATGCACCAGACGTAGAATAATCAATTAACAGAAAATCAAACACCAAAAAGCCACAGATCGGAAGAGCGGTTTCAG
chr1	11172985	11173024	MTOR_10263	+	GTGACCTATGCACCAGACGTAAATAAAGAGTATTGAAACATGCTTCAAATTTTGACTTGAAGATCGGAAGAGCGGTTTCAG
chr1	11174521	11174560	MTOR_10264	+	GTGACCTATGCACCAGACGTGACAGAGCCACTCACCACAGGAGTTACTAACTCTCCACCAGATCGGAAGAGCGGTTTCAG
chr1	11174955	11174994	MTOR_10265	+	GTGACCTATGCACCAGACGTATAAATGGGAAAAGCCAAATCAATGTTTATTCTTTACCAGATCGGAAGAGCGGTTTCAG
chr1	11175536	11175575	MTOR_10266	+	GTGACCTATGCACCAGACGTAGAAGACGATGAGGAGGGATCAACAGAGATAACGGATAGATCGGAAGAGCGGTTTCAG

chr1	11177154	11177193	MTOR_10267	+	GTGACCTATGCACCAGACGTGGAGTGCATGTGAACTACGGTTCTGGAACTTTAATTTCAAGATCGGAAGAGCGGTTTCAG
chr1	11181436	11181475	MTOR_10268	+	GTGACCTATGCACCAGACGTACACAACCTGTTACAGTAAGAGAGCAGCCTAAGACATGTAGTAGATCGGAAGAGCGGTTTCAG
chr1	11182194	11182233	MTOR_10269	+	GTGACCTATGCACCAGACGTACAGAAAAGCAGGGTTAGTGTACCGTAAAGAGAGTATACCCAGATCGGAAGAGCGGTTTCAG
chr1	11184701	11184740	MTOR_10270	+	GTGACCTATGCACCAGACGTCAAGTGGGAGCGGTGAGTGTACATCAGAGTCCCTCAGCTCTAGATCGGAAGAGCGGTTTCAG
chr1	11186864	11186903	MTOR_10271	+	GTGACCTATGCACCAGACGTTTACCAAAGGATTTAGTGTCTGCCTCCAGGGAAGAAATTTAGATCGGAAGAGCGGTTTCAG
chr1	11187212	11187251	MTOR_10272	+	GTGACCTATGCACCAGACGTAAAGCAGGACGTTTCAAGTTATCAAAGTCTCAACCAACAGATCGGAAGAGCGGTTTCAG
chr1	11187874	11187913	MTOR_10273	+	GTGACCTATGCACCAGACGTGAAAAGAGGAGGAAGACATCAAGAAATCAGCTAACCTCAGAGATCGGAAGAGCGGTTTCAG
chr1	11188194	11188233	MTOR_10274	+	GTGACCTATGCACCAGACGTAAACAGAAGAAACATCTATAAAGGAAATGTGGGTTGGGAAAAGATCGGAAGAGCGGTTTCAG
chr1	11188620	11188659	MTOR_10275	+	GTGACCTATGCACCAGACGTAAAAGACACAGTATGTAGCATATGAGACTTGAACAACCTAAGATCGGAAGAGCGGTTTCAG
chr1	11189019	11189058	MTOR_10276	+	GTGACCTATGCACCAGACGTAAATGAGAAAAGTACAGAAAATTTAGTTCCAGATTTTTGCAGATCGGAAGAGCGGTTTCAG
chr1	11190845	11190884	MTOR_10277	+	GTGACCTATGCACCAGACGTAGAAAAGGCAAGGACAGACACTGGAGCTGTGACCAACAGCAAGATCGGAAGAGCGGTTTCAG
chr1	11193265	11193304	MTOR_10278	+	GTGACCTATGCACCAGACGTAGAAAACAGCCCCATGACATTCCTCCTCAAACAGCCAGATCGGAAGAGCGGTTTCAG
chr1	11194534	11194573	MTOR_10279	+	GTGACCTATGCACCAGACGTACAAGGCACAGAGGCCACTTGGCTTGTGGCCAGCTTCAGATCGGAAGAGCGGTTTCAG
chr1	11199503	11199542	MTOR_10280	+	GTGACCTATGCACCAGACGTAGAGAAAAGTGGGTTATAGACAGAACTGGACAGCCAGGGAAGATCGGAAGAGCGGTTTCAG
chr1	11204823	11204862	MTOR_10281	+	GTGACCTATGCACCAGACGTCAAATCGCATTCCAACCTAATTACTGCACGAAACCTCAAAGATCGGAAGAGCGGTTTCAG
chr1	11205113	11205152	MTOR_10282	+	GTGACCTATGCACCAGACGTAAACAACCTTTGGGACTGAGCTGTGGACTTGGGAGCTTAGGAGATCGGAAGAGCGGTTTCAG
chr1	11206859	11206898	MTOR_10283	+	GTGACCTATGCACCAGACGTACACATAGACAGAAAAGCTCAAGGGGGTGGCTGGTTGGGAGATCGGAAGAGCGGTTTCAG
chr1	11210294	11210333	MTOR_10284	+	GTGACCTATGCACCAGACGTGAATTATATAGTACAGTAATCCAATCTCCTTAACTAAGATCGGAAGAGCGGTTTCAG
chr1	11217359	11217398	MTOR_10285	+	GTGACCTATGCACCAGACGTGAAAAGAAAAGACTGCTGTGAGGTACACAGAAGGATCGATCGGAAGAGCGGTTTCAG
chr1	11227585	11227624	MTOR_10286	+	GTGACCTATGCACCAGACGTAAAGGGAAAAGGTAGTTACTCAACAGGCTGAGGGTAGAGATCGGAAGAGCGGTTTCAG
chr1	11259471	11259510	MTOR_10287	+	GTGACCTATGCACCAGACGTGCAAACCTCACAGCACAGGAAAATGGCAGATGGGGCACAAGATCGGAAGAGCGGTTTCAG
chr1	11259771	11259810	MTOR_10288	+	GTGACCTATGCACCAGACGTAGAAGGTGGAAGGAGACCTCCCGTGCCTCTGCCTGAGATCGGAAGAGCGGTTTCAG
chr1	11264771	11264810	MTOR_10289	+	GTGACCTATGCACCAGACGTACAGGTGACAATGGAAAACATCAGTTTCAAGGGCCAATTAGATCGGAAGAGCGGTTTCAG
chr1	11269526	11269565	MTOR_10290	+	GTGACCTATGCACCAGACGTAGATTATAGAAAACCTATAACTCTACTAGATGCTTCTAGATCGGAAGAGCGGTTTCAG
chr1	11270974	11271013	MTOR_10291	+	GTGACCTATGCACCAGACGTAGGGGGAAGAGATGAGAAAATCATTCTGGAGAGTGGAGAGATCGGAAGAGCGGTTTCAG
chr1	11272542	11272581	MTOR_10292	+	GTGACCTATGCACCAGACGTCACTAACATACAGTAACTGCTAACATCAATCTCCAAGGAAGATCGGAAGAGCGGTTTCAG
chr1	11272976	11273015	MTOR_10293	+	GTGACCTATGCACCAGACGTGAGCAAAAGCATGGTGATGAATAGTCAGTCCCAAGTATCAGATCGGAAGAGCGGTTTCAG
chr1	11273634	11273673	MTOR_10294	+	GTGACCTATGCACCAGACGTAGAAAAGTCAAGGGAGCTGAGTCAAGTCCCTTTCTGATGAAGATCGGAAGAGCGGTTTCAG
chr1	11276302	11276341	MTOR_10295	+	GTGACCTATGCACCAGACGTCAAGAGTCAACCGTGGTATCATGAAGGACATTGAACAGATCGGAAGAGCGGTTTCAG
chr1	11288986	11289025	MTOR_10296	+	GTGACCTATGCACCAGACGTACAACAGAGAGTGTTAGAGCTACACATGGCATGACGTGACAGATCGGAAGAGCGGTTTCAG
chr1	11291122	11291161	MTOR_10297	+	GTGACCTATGCACCAGACGTAAAGGGAGGGAAGAAAACATTCATCACAAATGATTAGATCGGAAGAGCGGTTTCAG
chr1	11291502	11291541	MTOR_10298	+	GTGACCTATGCACCAGACGTACAAGAACACGATTCAATGAGCCAGTACGAGAGAAAAGAAAGATCGGAAGAGCGGTTTCAG
chr1	11292596	11292635	MTOR_10299	+	GTGACCTATGCACCAGACGTAAAAAGAGGGTGGCAGAAAGGGTTAGAAATCTGGCATTAAAGATCGGAAGAGCGGTTTCAG
chr1	11293555	11293594	MTOR_10300	+	GTGACCTATGCACCAGACGTAAAGTTATGAAAATGAATGCAGATTAGACTCTACTAGAAAAGATCGGAAGAGCGGTTTCAG
chr1	11294333	11294372	MTOR_10301	+	GTGACCTATGCACCAGACGTGAAAAGGCTCAATATTTCTCTATGGCAGAAAGACATTCTAGAAGATCGGAAGAGCGGTTTCAG
chr1	11298116	11298155	MTOR_10302	+	GTGACCTATGCACCAGACGTAAAGGACCTTTGAACATTTCTCATGATCCCATCACTCCAGATCGGAAGAGCGGTTTCAG
chr1	11298685	11298724	MTOR_10303	+	GTGACCTATGCACCAGACGTAGGCAGAGAGAAAACAGAATAAACACTGCTGCTGTAGACAAGATCGGAAGAGCGGTTTCAG
chr1	11300615	11300654	MTOR_10304	+	GTGACCTATGCACCAGACGTGAAAACAAGTACATAAGGGCTGGGCACATGACACTCAGTAGATCGGAAGAGCGGTTTCAG
chr1	11301749	11301788	MTOR_10305	+	GTGACCTATGCACCAGACGTATGGAGAGTGGCTAGTTGAGACATAATGACATTTCTTAATAGATCGGAAGAGCGGTTTCAG
chr1	11303368	11303407	MTOR_10306	+	GTGACCTATGCACCAGACGTAAAAGACAAGATAGATGCTCCAGGTCAGGGTTAGGGTCTAGATCGGAAGAGCGGTTTCAG
chr1	11307801	11307840	MTOR_10307	+	GTGACCTATGCACCAGACGTAAAGGATAAAGGGTTGGCAGGGAAGGATGAGGTGGAGCAGATCGGAAGAGCGGTTTCAG
chr1	11308162	11308201	MTOR_10308	+	GTGACCTATGCACCAGACGTGAGGAGGAAAAAATCATCTTTACTTATGACTGGCATTCAAGATCGGAAGAGCGGTTTCAG
chr1	11314041	11314080	MTOR_10309	+	GTGACCTATGCACCAGACGTAGACAGGGTGCTTCAATAGACAGAGTACAACCCAGAAGATCGGAAGAGCGGTTTCAG
chr1	11316260	11316299	MTOR_10310	+	GTGACCTATGCACCAGACGTAAAGCAAACCCGAGAACTCTCATTGGTACCAGAGTTTTTGTTCAGATCGGAAGAGCGGTTTCAG
chr1	11317233	11317272	MTOR_10311	+	GTGACCTATGCACCAGACGTGAGGAAAGGCAAAAGGTGATGATGGGGCGTATGCTGGCCAGAGATCGGAAGAGCGGTTTCAG
chr1	11318661	11318700	MTOR_10312	+	GTGACCTATGCACCAGACGTAGATAATAAGACAACAACTTCTAATAATTCTAATCTGAGATCGGAAGAGCGGTTTCAG
chr1	11319477	11319516	MTOR_10313	+	GTGACCTATGCACCAGACGTGGTTCTTTAGAGAGAAGTTTCTTTAATATTCTGGATAAGAGATCGGAAGAGCGGTTTCAG
chrX	48649747	48649786	GATA1_10314	+	GTGACCTATGCACCAGACGTTGAGTGGCTGTCTTGGCATTGGCTGAGTGTCTTTGGGGTTAGATCGGAAGAGCGGTTTCAG
chrX	48650639	48650678	GATA1_10315	+	GTGACCTATGCACCAGACGTCAAAAAAGGACAGGGAAGTTGAGGTGGGAGGGGTGGCCAAAGATCGGAAGAGCGGTTTCAG
chrX	48650886	48650925	GATA1_10316	+	GTGACCTATGCACCAGACGTAGACCTGCTTCACTTATACACAGGAACCCCTGTCCTCACAGATCGGAAGAGCGGTTTCAG
chrX	48652582	48652621	GATA1_10317	+	GTGACCTATGCACCAGACGTATGGCTCCAGAGGAGGGTGGTGTCTTCTCCTTGTAGATCGGAAGAGCGGTTTCAG
chr3	155588697	155588736	GMPS_10318	+	GTGACCTATGCACCAGACGTGGTCCCTGACAGACCCTCCCGCGGAGGCGTAGGCTCCAGATCGGAAGAGCGGTTTCAG
chr3	155611499	155611538	GMPS_10319	+	GTGACCTATGCACCAGACGTCACTAATCTTTTTCATGAGGAGATTGAACCTAGATTGTGGAAGATCGGAAGAGCGGTTTCAG
chr3	155615841	155615880	GMPS_10320	+	GTGACCTATGCACCAGACGTAAATTTGTTTTGAAAGCTTACTTATATTTTATCTGTTTGGATCGGAAGAGCGGTTTCAG
chr3	155621760	155621799	GMPS_10321	+	GTGACCTATGCACCAGACGTTTTAGATGAATAAGACAATAGTAATTAATAATTTAAAGAGATCGGAAGAGCGGTTTCAG
chr3	155624063	155624102	GMPS_10322	+	GTGACCTATGCACCAGACGTTAAAAATTTGCAGAGTTCATTTAAAAAATTTATCTGAAAGATCGGAAGAGCGGTTTCAG
chr3	155628685	155628724	GMPS_10323	+	GTGACCTATGCACCAGACGTATTATCTGGAACTTACAATAATTTATCAATAATTTGAGATCGGAAGAGCGGTTTCAG
chr3	155629079	155629118	GMPS_10324	+	GTGACCTATGCACCAGACGTACTCCAGAAAAGTTAATCTACATGTTAGGACTGTTTAAATAGATCGGAAGAGCGGTTTCAG

chr3	155632370	155632409	GMPS_10325	+	GTGACCTATGCACCAGACGTTTTTAATATCCTCAACATGTACTATTTTTGATGTGAATCTAGATCGGAAGAGCGGTTTCAG
chr3	155633992	155634031	GMPS_10326	+	GTGACCTATGCACCAGACGTTGAAAACCTTTTTTCATAAAGTAGATACATGGAAGTCTTCAGATCGGAAGAGCGGTTTCAG
chr3	155637138	155637177	GMPS_10327	+	GTGACCTATGCACCAGACGTGAACGAATTTTTGTTTGATTTCATCTTTAGACCTTCATGTTAGATCGGAAGAGCGGTTTCAG
chr3	155640102	155640141	GMPS_10328	+	GTGACCTATGCACCAGACGTATACAGCTAATCATTACAAGAAATTGAACGGATTCTTATTAGATCGGAAGAGCGGTTTCAG
chr3	155649680	155649719	GMPS_10329	+	GTGACCTATGCACCAGACGTCAGGAGACTAGGGTGGGGGCTTGTAATGGAAGGATGTATAGATCGGAAGAGCGGTTTCAG
chr3	155652846	155652885	GMPS_10330	+	GTGACCTATGCACCAGACGTCATGTTTTGATTACTACCCCTCTGAAACTAGTTTTGGAAAGATCGGAAGAGCGGTTTCAG
chr3	155654310	155654349	GMPS_10331	+	GTGACCTATGCACCAGACGTATTTTTTTCTAATGCAGCGTTCGAACTCTTACATTTAGATCGGAAGAGCGGTTTCAG
chr3	155655492	155655531	GMPS_10332	+	GTGACCTATGCACCAGACGTGTTCTATTAAGTACCGTGTGCAGTTTAAATTGATTAGAAAGATCGGAAGAGCGGTTTCAG
chrX	132670332	132670371	GPC3_10333	+	GTGACCTATGCACCAGACGTAAAGAGAAGGATTTGAAATGCAAGTCTACCCATAGCCTCAAGATCGGAAGAGCGGTTTCAG
chrX	132730638	132730677	GPC3_10334	+	GTGACCTATGCACCAGACGTACAACCAGGAATGCATCAGCTCTTCATATTTCTCAGGTGGAGATCGGAAGAGCGGTTTCAG
chrX	132795889	132795928	GPC3_10335	+	GTGACCTATGCACCAGACGTGAAGGTAAGAAAGGGTTTGTCAAAGAAAGTCCCAAACAAAGATCGGAAGAGCGGTTTCAG
chrX	132826533	132826572	GPC3_10336	+	GTGACCTATGCACCAGACGTAAACAAAACATCTGTGCATAAGAGGCAAGTAACTCAGTATAGATCGGAAGAGCGGTTTCAG
chrX	132834067	132834106	GPC3_10337	+	GTGACCTATGCACCAGACGTAAATGCAATATAATTATAGGCTACTTGTGCAGATATGATAAGATCGGAAGAGCGGTTTCAG
chrX	132888214	132888253	GPC3_10338	+	GTGACCTATGCACCAGACGTAAAAAAAAGAGACACAAAAATGTGTACAAATTAAGCAAGATCGGAAGAGCGGTTTCAG
chrX	133087249	133087288	GPC3_10339	+	GTGACCTATGCACCAGACGTCAAGGTTTTTCATGTTTCAGTAAGCAGGATCTCTCTCACAGATCGGAAGAGCGGTTTCAG
chrX	133119487	133119526	GPC3_10340	+	GTGACCTATGCACCAGACGTAGGGAGCTAGGAGAGCGCGGGAGAGTGGCAGCCGGAGCGAAGATCGGAAGAGCGGTTTCAG
chrX	132887866	132887905	GPC3_10341	+	GTGACCTATGCACCAGACGTGACTTGCAGTGTGAAACCTGGGTCTATAAAGCTTGGATCGGAAGAGCGGTTTCAG
chr2	239974843	239974882	HDAC4_10342	+	GTGACCTATGCACCAGACGTGCAAGAGAAGGAGATGGGGCGTGGGGCAGGTGCACCACAGATCGGAAGAGCGGTTTCAG
chr2	239975308	239975347	HDAC4_10343	+	GTGACCTATGCACCAGACGTGGGGTGAGGAAAGTCGCTCAGTGACTACAACCTAGCAGGAAGATCGGAAGAGCGGTTTCAG
chr2	239976540	239976579	HDAC4_10344	+	GTGACCTATGCACCAGACGTATGCATAAGAATATAAAGACTGCCAATATAATCCACACGTAGATCGGAAGAGCGGTTTCAG
chr2	239988562	239988601	HDAC4_10345	+	GTGACCTATGCACCAGACGTAAACGGGAGACTGCAGTGTGAACGGGGAGGACCAGCCAGATCGGAAGAGCGGTTTCAG
chr2	239990314	239990353	HDAC4_10346	+	GTGACCTATGCACCAGACGTCAAGGAGAAGGCGTTACTGGGTGAGCTGAAAGAGGGACGGGAGATCGGAAGAGCGGTTTCAG
chr2	240002899	240002938	HDAC4_10347	+	GTGACCTATGCACCAGACGTAAAGGAGAAACACACGCTCATGGACCCGAGCGGACCTGAGATCGGAAGAGCGGTTTCAG
chr2	240003928	240003967	HDAC4_10348	+	GTGACCTATGCACCAGACGTAGGGCAACTACTTACGGCTGAGGACGGTATTGAGGGTAGATCGGAAGAGCGGTTTCAG
chr2	240005949	240005988	HDAC4_10349	+	GTGACCTATGCACCAGACGTGAACGTGACGCTGGAGACGAAGCGCAGGTGGGGCGTGGCCAAGATCGGAAGAGCGGTTTCAG
chr2	240009321	240009360	HDAC4_10350	+	GTGACCTATGCACCAGACGTCAACAGACAGCCAGGAGAGACAAACAAAGACACACTTTGAGATCGGAAGAGCGGTTTCAG
chr2	240011823	240011862	HDAC4_10351	+	GTGACCTATGCACCAGACGTAAACACCCACAGTGAAGTCAACCTCCAGGCCACCGTCATAGATCGGAAGAGCGGTTTCAG
chr2	240016763	240016802	HDAC4_10352	+	GTGACCTATGCACCAGACGTGAGGGGAGACGGTCAGAGAGGCCAACGGGCACCGGCCAACGAGATCGGAAGAGCGGTTTCAG
chr2	240024603	240024642	HDAC4_10353	+	GTGACCTATGCACCAGACGTAGGGGAGAGACACTCACAGTTCGCAAGACTGCTGCTAGATCGGAAGAGCGGTTTCAG
chr2	240029890	240029929	HDAC4_10354	+	GTGACCTATGCACCAGACGTGCAGAGGGGCCAAGATTACGCGCACATCCAGGGGCCAGCCAGATCGGAAGAGCGGTTTCAG
chr2	240033419	240033458	HDAC4_10355	+	GTGACCTATGCACCAGACGTGAAACGGCCGTGTTGGCGGTTGCGGATGTCTCCCGCCCTAGATCGGAAGAGCGGTTTCAG
chr2	240037017	240037056	HDAC4_10356	+	GTGACCTATGCACCAGACGTGAGGTAAACACATGAAGCACAGAGAGCTGGGTCTCTGAGCAGATCGGAAGAGCGGTTTCAG
chr2	240048386	240048425	HDAC4_10357	+	GTGACCTATGCACCAGACGTCCAGTCTGAAGTAATTTGGAGGAAGAAACAGCAGAGGGGAAGATCGGAAGAGCGGTTTCAG
chr2	240056150	240056189	HDAC4_10358	+	GTGACCTATGCACCAGACGTCAAGCAGGATGCTCGGGTGGAAGGACCCATCACCCACCCAGATCGGAAGAGCGGTTTCAG
chr2	240056350	240056389	HDAC4_10359	+	GTGACCTATGCACCAGACGTAAACAGACAGTACCATCACAGTCTGTCACGGCCAAACATCAGATCGGAAGAGCGGTTTCAG
chr2	240061503	240061542	HDAC4_10360	+	GTGACCTATGCACCAGACGTAGAATAACCTGGTGAGTGTACTCCATGCGGAGGGAGGGAGATCGGAAGAGCGGTTTCAG
chr2	240066421	240066460	HDAC4_10361	+	GTGACCTATGCACCAGACGTAGGAGATGTCATTACAGCCAGGCAGACACCCTGGCTCAAAGATCGGAAGAGCGGTTTCAG
chr2	240078480	240078519	HDAC4_10362	+	GTGACCTATGCACCAGACGTGGCAAAGACAGATGTTTTAGTTTACCAGCGCACTGCCCCAGATCGGAAGAGCGGTTTCAG
chr2	240085630	240085669	HDAC4_10363	+	GTGACCTATGCACCAGACGTAGAAGCATAGCAGGGGGTGAAGTGTGGCTCTGCCCTACAAGATCGGAAGAGCGGTTTCAG
chr2	240098270	240098309	HDAC4_10364	+	GTGACCTATGCACCAGACGTAAAGGAGGAGACAGCGTCCAGGCCAGGCTCCACACACAGATCGGAAGAGCGGTTTCAG
chr2	240111784	240111823	HDAC4_10365	+	GTGACCTATGCACCAGACGTAAACAGCAGAGAGCCGGTCACTGCCGCCCTTTGCTTCCAGATCGGAAGAGCGGTTTCAG
chr2	240158371	240158410	HDAC4_10366	+	GTGACCTATGCACCAGACGTGAGAAGGCACTGGCTTCAGAACTGCGCGCATTTACGCCAAGATCGGAAGAGCGGTTTCAG
chr2	240274405	240274444	HDAC4_10367	+	GTGACCTATGCACCAGACGTGTCCACTCCTTTAAGTGATTGAAATGGCTCAAAATTTCCAGATCGGAAGAGCGGTTTCAG
chr6	34208670	34208709	HMGA1_10368	+	GTGACCTATGCACCAGACGTGGACAGCGCTGGTAGGGAGTCAAGTGGGTGTCCAAACCTTAGATCGGAAGAGCGGTTTCAG
chr6	34208703	34208742	HMGA1_10369	+	GTGACCTATGCACCAGACGTAAACCTTTGCTTCACTTGCTTACCTTTGGGGCTAGGGAAGATCGGAAGAGCGGTTTCAG
chr6	34210583	34210622	HMGA1_10370	+	GTGACCTATGCACCAGACGTAGATGGACTACCCTGGGTGGATGACTAGCAGAGATCCAGATCGGAAGAGCGGTTTCAG
chr6	34211306	34211345	HMGA1_10371	+	GTGACCTATGCACCAGACGTAAAGCAGACTGCTGCTTGCCTCTGGGCTCTTTTGGATGTAAGATCGGAAGAGCGGTTTCAG
chr6	34212672	34212711	HMGA1_10372	+	GTGACCTATGCACCAGACGTCCGCTGCTCCTCACTGGAGGAGCAGCTTCTTCTGGGACAGATCGGAAGAGCGGTTTCAG
chr2	176973881	176973920	HOXD11_10373	+	GTGACCTATGCACCAGACGTAAAGCGCCCTCACCCAGCCCACTCACCCACCTCCTTCCAGATCGGAAGAGCGGTTTCAG
chr2	209101904	209101943	IDH1_10374	+	GTGACCTATGCACCAGACGTGGAIAAAAAAAAAAGAAATTTAGTTGGTCTCTGATATGGTAAGATCGGAAGAGCGGTTTCAG
chr2	209103968	209104007	IDH1_10375	+	GTGACCTATGCACCAGACGTGGAIAAAAAAAAAACCAACTCCAATCATCTAGTTATAGAGATCGGAAGAGCGGTTTCAG
chr2	209104738	209104777	IDH1_10376	+	GTGACCTATGCACCAGACGTGGAGCATGAAGCGTTGGTGGTCCAACTGCATGAAGAGCACTAGATCGGAAGAGCGGTTTCAG
chr2	209106880	209106919	IDH1_10377	+	GTGACCTATGCACCAGACGTAAAGGTAAGAGAATAATAATAAGAAATTTGATTTTGTAGATCGGAAGAGCGGTTTCAG
chr2	209108339	209108378	IDH1_10378	+	GTGACCTATGCACCAGACGTGAAGCCAGTGAAGGAAAAAGGGAGAAAGAAATAAATGTAAGATCGGAAGAGCGGTTTCAG
chr2	209110159	209110198	IDH1_10379	+	GTGACCTATGCACCAGACGTGGGAAAAAGGTATAAAGAAAAAAAATACCTTAGCAGGAAGATCGGAAGAGCGGTTTCAG
chr2	209113395	209113434	IDH1_10380	+	GTGACCTATGCACCAGACGTAAAAATTAGAAGCAAAGTTTTTCAGACAAATGGATAGTTAAGATCGGAAGAGCGGTTTCAG
chr2	209116286	209116325	IDH1_10381	+	GTGACCTATGCACCAGACGTAAAAACCTAAAGAAAAAGAAAAATACATGCCTTGTCTATTAGATCGGAAGAGCGGTTTCAG
chr15	99192915	99192954	IGF1R_10382	+	GTGACCTATGCACCAGACGTGCCCGCCGCCCGGGCAACTGCGGAACTTTCTCCAGAGATCGGAAGAGCGGTTTCAG

chr15	99434877	99434916	IGF1R_10383	+	GTGACCTATGCACCAGACGTGCCACACGTTGGTCACTACCCGCCCCACCTCACCCGCCAAGATCGGAAGAGCGGTTTCAG
chr15	99440145	99440184	IGF1R_10384	+	GTGACCTATGCACCAGACGTCATCCCCCTGGAAAACCGGCTAGATCTCATGGTTTTCTTTAGATCGGAAGAGCGGTTTCAG
chr15	99442861	99442900	IGF1R_10385	+	GTGACCTATGCACCAGACGTCAAATTTTCATGAGCTGACGTTCTATTACAAAATAAGCAGCAGATCGGAAGAGCGGTTTCAG
chr15	99452139	99452178	IGF1R_10386	+	GTGACCTATGCACCAGACGTGCATCCAAAACACCGTGGGCCCAACCATCATGATAACAGCAGATCGGAAGAGCGGTTTCAG
chr15	99454681	99454720	IGF1R_10387	+	GTGACCTATGCACCAGACGTGCTTTGGGTGATGCCATTCTGTTGACAGGGCTACGAATTGGAGATCGGAAGAGCGGTTTCAG
chr15	99456522	99456561	IGF1R_10388	+	GTGACCTATGCACCAGACGCTAGACAAGCCGCCACCATCCACTTCTTCGCAAGCTCAAGATCGGAAGAGCGGTTTCAG
chr15	99459371	99459410	IGF1R_10389	+	GTGACCTATGCACCAGACGTAGCAGCGGCCCTGGACGGAGGTGTGACCGTTCATTCTCTGATAGATCGGAAGAGCGGTTTCAG
chr15	99460116	99460155	IGF1R_10390	+	GTGACCTATGCACCAGACGTCATGTGAAATTTTCAGTTGGCAAACCCTGCTCAGGCGGAGATCGGAAGAGCGGTTTCAG
chr15	99465671	99465710	IGF1R_10391	+	GTGACCTATGCACCAGACGTATCCAGCTGGCCCCATTGCCACCTTCTCACAACCTAGTGAGATCGGAAGAGCGGTTTCAG
chr15	99467252	99467291	IGF1R_10392	+	GTGACCTATGCACCAGACGTGGCAGTGGCCCCGTGCCTGCATGTACTTCCATCCATTGACAAGATCGGAAGAGCGGTTTCAG
chr15	99467924	99467963	IGF1R_10393	+	GTGACCTATGCACCAGACGTTGGAGGGGAGAAGAACCGTGGTAAAACCTGAAAGCAGGGTGAGATCGGAAGAGCGGTTTCAG
chr15	99472900	99472939	IGF1R_10394	+	GTGACCTATGCACCAGACGTGCAAAGTTTATGACACTTTCTGTGGCTGAGTGGTTTGTGATGAGATCGGAAGAGCGGTTTCAG
chr15	99473545	99473584	IGF1R_10395	+	GTGACCTATGCACCAGACGTGGGCCACCAGCACTGCCAGCGTGCAGGGCAGGTAGATCGGATCGGAAGAGCGGTTTCAG
chr15	99478293	99478332	IGF1R_10396	+	GTGACCTATGCACCAGACGTGTTCTGAAAAGCCAAAATGCAGCACAGGGAGAGGGTATCAGATCGGAAGAGCGGTTTCAG
chr15	99478666	99478705	IGF1R_10397	+	GTGACCTATGCACCAGACGTATTTCCACCGGTATTGCATGTTGCCTGGCCTGCTCTCTTTAGATCGGAAGAGCGGTTTCAG
chr15	99482600	99482639	IGF1R_10398	+	GTGACCTATGCACCAGACGTAGCTTTCCAGGTCTGGGCAAGAACATAAATCAGGTGTTTTAGATCGGAAGAGCGGTTTCAG
chr15	99486292	99486331	IGF1R_10399	+	GTGACCTATGCACCAGACGCTTTACTGTCATTGGCAGCCTGGAGCCCCAGCCTCGCACAGATCGGAAGAGCGGTTTCAG
chr15	99491948	99491987	IGF1R_10400	+	GTGACCTATGCACCAGACGTCTTGGGCCCTCCGTGCTCTTCTGAGTTCTTCTCAAATAAGATCGGAAGAGCGGTTTCAG
chr15	99500682	99500721	IGF1R_10401	+	GTGACCTATGCACCAGACGCTGAATCTGTGCAAACAGTAACGTGTGCGCACGCGCAGCGAGATCGGAAGAGCGGTTTCAG
chr15	99251074	99251113	IGF1R_10402	+	GTGACCTATGCACCAGACGTGGATATTGGGCTTTACAACCTGAGGAACATTACTCGGGGGAGATCGGAAGAGCGGTTTCAG
chr7	45954555	45954594	IGFBP3_10403	+	GTGACCTATGCACCAGACGTGAAAACAGAGACAGAGAAGTGAATGCTCCTGGGTCTGGTGAGATCGGAAGAGCGGTTTCAG
chr7	45956277	45956316	IGFBP3_10404	+	GTGACCTATGCACCAGACGTGGAAGGACCAGAGCAACAGATCACAGTTTTTACTCTAGAAGATCGGAAGAGCGGTTTCAG
chr7	45957049	45957088	IGFBP3_10405	+	GTGACCTATGCACCAGACGTCCAAGAGAGACAACACATGAGAGTCAATATCTATCAAGATCGGAAGAGCGGTTTCAG
chr7	45960750	45960789	IGFBP3_10406	+	GTGACCTATGCACCAGACGTTACCAGGACCGTCTGCTTGGCAGTGGCCGCGCAGGATGAGATCGGAAGAGCGGTTTCAG
chr3	123946922	123946961	KALRN_10407	+	GTGACCTATGCACCAGACGTGGGACTTTCTTTGTAAGGACCTAGAGAAGTTGTGTGAGATCGGAAGAGCGGTTTCAG
chr3	123953801	123953840	KALRN_10408	+	GTGACCTATGCACCAGACGTGGGGAATGGCCTGCAGGGGAGCGGGAGGGAGCTGGGCTGAGATCGGAAGAGCGGTTTCAG
chr3	123983548	123983587	KALRN_10409	+	GTGACCTATGCACCAGACGTTTTCTCTCTTAGCATCTTCTTTCCCTTCCCCTTCTGCCAGATCGGAAGAGCGGTTTCAG
chr3	123988113	123988152	KALRN_10410	+	GTGACCTATGCACCAGACGTAACAGGCCAAACCTGAGCCGGGATGGGGGTGAGGGAGCAGAGATCGGAAGAGCGGTTTCAG
chr3	124017771	124017810	KALRN_10411	+	GTGACCTATGCACCAGACGTGGGCTGTTCTCAGCAGCTGCCCTGGGAGTGGGAGATCGGAAGAGCGGTTTCAG
chr3	124045029	124045068	KALRN_10412	+	GTGACCTATGCACCAGACGTGAAAACCTGCAGCAGCTGCTGTTGGTAGAAGGGTTGGCAAGATCGGAAGAGCGGTTTCAG
chr3	124048850	124048889	KALRN_10413	+	GTGACCTATGCACCAGACGTAGCAGGGCAACCATGGTCTTGGGCATGTCTGCATGTGGGAGATCGGAAGAGCGGTTTCAG
chr3	124053353	124053392	KALRN_10414	+	GTGACCTATGCACCAGACGTCAGACCCCGTGTCCATTATCCATTCTAGGAGGCAGACCAGATCGGAAGAGCGGTTTCAG
chr3	124103894	124103933	KALRN_10415	+	GTGACCTATGCACCAGACGTCAGTGAGAGAGGGGACTTCTGTCCTGCCAGGGTCAGGTCAGATCGGAAGAGCGGTTTCAG
chr3	124117729	124117768	KALRN_10416	+	GTGACCTATGCACCAGACGTCGACAGGAGGGAGGTGGAGAGGGGCCAAGAAGTCTCTTAGATCGGAAGAGCGGTTTCAG
chr3	124132523	124132562	KALRN_10417	+	GTGACCTATGCACCAGACGTTCCGCTCATTCTCTGGCAGTGGGAGGATGATGAAAACAAGCAAGATCGGAAGAGCGGTTTCAG
chr3	124141836	124141875	KALRN_10418	+	GTGACCTATGCACCAGACGTCCTTTCTTCTCAGCCTGGGTTTCTCAGCCAGCTGAGCCAGATCGGAAGAGCGGTTTCAG
chr3	124149633	124149672	KALRN_10419	+	GTGACCTATGCACCAGACGTAATCTGGCTGCACTGCCTCCCTTCCCTTTCTGCTCTGTAGATCGGAAGAGCGGTTTCAG
chr3	124153383	124153422	KALRN_10420	+	GTGACCTATGCACCAGACGTAGACTGTGGGGCTTGTGGGGCTGAGATTGCCAGGGGGCCAAGATCGGAAGAGCGGTTTCAG
chr3	124157895	124157934	KALRN_10421	+	GTGACCTATGCACCAGACGTATTGTCATCGAAGGGCTCAGACTCCTGGCCTTGGCCGCTAGATCGGAAGAGCGGTTTCAG
chr3	124160917	124160956	KALRN_10422	+	GTGACCTATGCACCAGACGTCACCTGCCAGCCACCACTTCAAGCAGACACCCCTCCAGATCGGAAGAGCGGTTTCAG
chr3	124165134	124165173	KALRN_10423	+	GTGACCTATGCACCAGACGTCCTTTCCCTGGCAGCTATCTCAGTTCTGGGGAGCATAAGAAAGATCGGAAGAGCGGTTTCAG
chr3	124165743	124165782	KALRN_10424	+	GTGACCTATGCACCAGACGTTCCAGAGCCTCCCCAGATCCACCAGAAGCTCCATTAGATCGGAAGAGCGGTTTCAG
chr3	124174217	124174256	KALRN_10425	+	GTGACCTATGCACCAGACGTTGATGTCCTCTGGGACATCCCTTCTCATCTCCCTGAAGATCGGAAGAGCGGTTTCAG
chr3	124175586	124175625	KALRN_10426	+	GTGACCTATGCACCAGACGTCCTCCGCCAGCTAGCTGGCTCCCGTGACTATGCTGGGAGATCGGAAGAGCGGTTTCAG
chr3	124180814	124180853	KALRN_10427	+	GTGACCTATGCACCAGACGTCAGTAATCCGTTACAGCTATATGGAAAATGACATCCTAGATCGGAAGAGCGGTTTCAG
chr3	124181491	124181530	KALRN_10428	+	GTGACCTATGCACCAGACGTGGAGGGTCTCAGAGGTGCAGCACTTAGGCCGTAAAACAGCAGATCGGAAGAGCGGTTTCAG
chr3	124193590	124193629	KALRN_10429	+	GTGACCTATGCACCAGACGTTGAAATCCTTCTCCACTGCCATAACAGCTGGCAGCACTCAGATCGGAAGAGCGGTTTCAG
chr3	124196192	124196231	KALRN_10430	+	GTGACCTATGCACCAGACGTTTTTCCATTCTTGGCAGCTGATGAGCAGGTGAAATGCTAGATCGGAAGAGCGGTTTCAG
chr3	124201758	124201797	KALRN_10431	+	GTGACCTATGCACCAGACGTTCCCTCTCATCTCCCTCCACTGCCTACTGCCTGGGGCAAGATCGGAAGAGCGGTTTCAG
chr3	124207173	124207212	KALRN_10432	+	GTGACCTATGCACCAGACGTTCCAGCACTGGGGAAGCCTCCTCTCTTCTTGGACAGGGAGATCGGAAGAGCGGTTTCAG
chr3	124209742	124209781	KALRN_10433	+	GTGACCTATGCACCAGACGTCAGTGGGTGAGCAAGCAACTCCCTGCTTTCATAGAACCAGATCGGAAGAGCGGTTTCAG
chr3	124210282	124210321	KALRN_10434	+	GTGACCTATGCACCAGACGTCCTCTGCTAGGCCACAAACTAGGGTTGGGATAATAGAAAGATCGGAAGAGCGGTTTCAG
chr3	124211740	124211779	KALRN_10435	+	GTGACCTATGCACCAGACGTCCTCTCCCTCCAGCACTGCCTGCCTCACAGGCTTCCGGGTAGATCGGAAGAGCGGTTTCAG
chr3	124215271	124215310	KALRN_10436	+	GTGACCTATGCACCAGACGTGTCCTAACCTTCCCTCCCTGAGACTTCTTGATGGCTCAAAGATCGGAAGAGCGGTTTCAG
chr3	124237320	124237359	KALRN_10437	+	GTGACCTATGCACCAGACGTGGGACTTGTCCCTGCAGCTACCAGGGTATGCCGTGGCACCAGATCGGAAGAGCGGTTTCAG
chr3	124303764	124303803	KALRN_10438	+	GTGACCTATGCACCAGACGTTGGCGGGCTGGTGGCTTCTGTTAGCCAGACTGTCGCAGATCGGAAGAGCGGTTTCAG
chr3	124351561	124351600	KALRN_10439	+	GTGACCTATGCACCAGACGTTGGGCTGGAGTTGCCATCAGAGGGCTTCTGACATGAGATCGGAAGAGCGGTTTCAG
chr3	124352811	124352850	KALRN_10440	+	GTGACCTATGCACCAGACGTTTTACTTCTCACTTAAAAGAGCAACGTGCCGTGCATGATCGGAAGAGCGGTTTCAG

chr3	124356161	124356200	KALRN_10441	+	GTGACCTATGCACCAGACGTGTCCTGGAGGCAGTTCGTGTGTGTCTCACCTTCACTGAGATCGGAAGAGCGGTTTCAG
chr3	124369796	124369835	KALRN_10442	+	GTGACCTATGCACCAGACGTTCCCCAGTTCCTCCCTGTGGTGCACATGTGAGTGGCGGTGGAGATCGGAAGAGCGGTTTCAG
chr3	124374525	124374564	KALRN_10443	+	GTGACCTATGCACCAGACGTGGTTCCAGGTGGGTCTGTGGTACCCCAACCAGGAGCACGTAGATCGGAAGAGCGGTTTCAG
chr3	124376409	124376448	KALRN_10444	+	GTGACCTATGCACCAGACGTATGCTGCCCGGAGGATCCAGTGTCTGGGAATCCAGGACTAGATCGGAAGAGCGGTTTCAG
chr3	124376661	124376700	KALRN_10445	+	GTGACCTATGCACCAGACGTCCTCATACCTCCTCCCAAACCTCCTTACTAGGCTCATTAAAGATCGGAAGAGCGGTTTCAG
chr3	124377375	124377414	KALRN_10446	+	GTGACCTATGCACCAGACGTCAGGCTTTTGCTGAECTGGGTGGGGAGGAAAACCTCAGGCCAAGATCGGAAGAGCGGTTTCAG
chr3	124378315	124378354	KALRN_10447	+	GTGACCTATGCACCAGACGTGGGAGCTGGGTGAGGGTGGAGAAGGATCCATCAGGCTCAGATCGGAAGAGCGGTTTCAG
chr3	124379831	124379870	KALRN_10448	+	GTGACCTATGCACCAGACGTTGCTTGTAAATGCTTGTCTTCTTAGGGACCATATTGGATAAGATCGGAAGAGCGGTTTCAG
chr3	124380786	124380825	KALRN_10449	+	GTGACCTATGCACCAGACGTAAGATGCGTCTAAGCCCCTCTCTCCAGGACAATAGGAGAGATCGGAAGAGCGGTTTCAG
chr3	124385492	124385531	KALRN_10450	+	GTGACCTATGCACCAGACGTCATGTTGATGAGAAAGAGGCAAGGAAGAGCCAGTCTTGAGATCGGAAGAGCGGTTTCAG
chr3	124386041	124386080	KALRN_10451	+	GTGACCTATGCACCAGACGTGGCTTGGTTCCTTGCAGGGCTGTGTGAGGGGACTCCACGAAGATCGGAAGAGCGGTTTCAG
chr3	124390756	124390795	KALRN_10452	+	GTGACCTATGCACCAGACGTAATCATTACTCCCACCTTGTACTACGATGGCATAGCCTAGATCGGAAGAGCGGTTTCAG
chr3	124393472	124393511	KALRN_10453	+	GTGACCTATGCACCAGACGTCGTTGGCTTCCCGGGAGAGGAGTATGAGGATTAATAAAGATCGGAAGAGCGGTTTCAG
chr3	124397171	124397210	KALRN_10454	+	GTGACCTATGCACCAGACGTTATTCCGGAGCTGCGTCCCCACCTGTCATCCACTCCCACCAGATCGGAAGAGCGGTTTCAG
chr3	124398375	124398414	KALRN_10455	+	GTGACCTATGCACCAGACGTCATTGTTGCTCTATTTCCTACAATGATTGCCTTTTTTGAAGATCGGAAGAGCGGTTTCAG
chr3	124412689	124412728	KALRN_10456	+	GTGACCTATGCACCAGACGTAAGCATTAGAATTGGAAACATCGGGGATGGTTAAATAAATAGATCGGAAGAGCGGTTTCAG
chr3	124413361	124413400	KALRN_10457	+	GTGACCTATGCACCAGACGTTGCCCTAACATCAGCAACAGCAGCCCTTGTGACACAGAGATCGGAAGAGCGGTTTCAG
chr3	124416582	124416621	KALRN_10458	+	GTGACCTATGCACCAGACGTCCTGCTCTTCTTTTTCTTTTTCTTTTTAAACATTTAGATCGGAAGAGCGGTTTCAG
chr3	124418891	124418930	KALRN_10459	+	GTGACCTATGCACCAGACGTGCCAGCCCTGGCCCCCAGGCAGTGGGATTGAGGCACCTAGATCGGAAGAGCGGTTTCAG
chr3	124420974	124421013	KALRN_10460	+	GTGACCTATGCACCAGACGTAGTTTTATATCTTTCATTTCATGAACACCTAGCAACATCAAGATCGGAAGAGCGGTTTCAG
chr3	124431993	124432032	KALRN_10461	+	GTGACCTATGCACCAGACGTACGCCATCTCTCTAAAGTCGCCTGCATCCATTAGGTTAGAGATCGGAAGAGCGGTTTCAG
chr3	124438328	124438367	KALRN_10462	+	GTGACCTATGCACCAGACGTGCCCTATGGTTTCACATAGACGTGCAGTGTGAACCAAGAGATCGGAAGAGCGGTTTCAG
chr3	123987856	123987895	KALRN_10463	+	GTGACCTATGCACCAGACGTGGCCCTGTGGAGGAGCTGGCCGGGAGGGGCAGCGGCTGAGATCGGAAGAGCGGTTTCAG
chr3	124438055	124438094	KALRN_10464	+	GTGACCTATGCACCAGACGTCCTTCCATCTTCTGTGGTGTGAGCAATGCTGCCAGAGAAGATCGGAAGAGCGGTTTCAG
chr3	20082283	20082322	KAT2B_10465	+	GTGACCTATGCACCAGACGTGCCGCTCTCGGACCGCGGATGGGTGCTAGGGGCCAGCCAGATCGGAAGAGCGGTTTCAG
chr3	20113962	20114001	KAT2B_10466	+	GTGACCTATGCACCAGACGTAATCTTCAAGGAAAGTATAACGAGTTCATTGTAGCGTGAAGATCGGAAGAGCGGTTTCAG
chr3	20136911	20136950	KAT2B_10467	+	GTGACCTATGCACCAGACGTAACATTTTAAACATTTTCTCTCATTATTCAAATGTACCAGATCGGAAGAGCGGTTTCAG
chr3	20142971	20143010	KAT2B_10468	+	GTGACCTATGCACCAGACGTGAACGTTCTTTTCTTTGGCCCCATAAAGCCTGTTACAGAAGATCGGAAGAGCGGTTTCAG
chr3	20153290	20153329	KAT2B_10469	+	GTGACCTATGCACCAGACGTTTGTGCTGGTCTTTGTTTATGCCAGAGCTTGGGTTGAGATCGGAAGAGCGGTTTCAG
chr3	20156491	20156530	KAT2B_10470	+	GTGACCTATGCACCAGACGTTTTTACATGATCAGAAACACCAAGCAGGCAACCTGAAGATCGGAAGAGCGGTTTCAG
chr3	20161226	20161265	KAT2B_10471	+	GTGACCTATGCACCAGACGTAAGAGGGGATAAGAGAGGGCTGTGACTTGTCTCCAGGAGCTAGATCGGAAGAGCGGTTTCAG
chr3	20164307	20164346	KAT2B_10472	+	GTGACCTATGCACCAGACGTTAAACCTGGGCAGCCAGCTGGTAGACCTCTTCTGCTCTCCAGATCGGAAGAGCGGTTTCAG
chr3	20167616	20167655	KAT2B_10473	+	GTGACCTATGCACCAGACGTCCTTCTGTTCTTCTTCTTCTTCTTAAATGAAAGAGATCGGAAGAGCGGTTTCAG
chr3	20169052	20169091	KAT2B_10474	+	GTGACCTATGCACCAGACGTACCAAGCTCTTAGAAGAAGCAGAATGTGGGCTTCTCAGATCGGAAGAGCGGTTTCAG
chr3	20178555	20178594	KAT2B_10475	+	GTGACCTATGCACCAGACGTCACCAACGCAACACTGTTTTGTACTCCTTTTTCTTAATAGATCGGAAGAGCGGTTTCAG
chr3	20181867	20181906	KAT2B_10476	+	GTGACCTATGCACCAGACGTGGTTGACTCCCTTACTTCTGTACAGGCCAGTCTTAGCTGAGATCGGAAGAGCGGTTTCAG
chr3	20187933	20187972	KAT2B_10477	+	GTGACCTATGCACCAGACGTACCTTCTTTTAAAGCGAAATTTTTAGTAATGCCGTGGTAGATCGGAAGAGCGGTTTCAG
chr3	20189502	20189541	KAT2B_10478	+	GTGACCTATGCACCAGACGTCGGGCAGAGGATGTTAATGGAAGTGATTTTTTTTTTCCAGATCGGAAGAGCGGTTTCAG
chr3	20189809	20189848	KAT2B_10479	+	GTGACCTATGCACCAGACGTTCTTTTACCTCATGCAAAATTTTTGAAATGATTTCCAGATCGGAAGAGCGGTTTCAG
chr3	20189990	20190029	KAT2B_10480	+	GTGACCTATGCACCAGACGTTAACATTTTCAATAGATGATTTAAACTCTGGATGGCGGAGATCGGAAGAGCGGTTTCAG
chr3	20194028	20194067	KAT2B_10481	+	GTGACCTATGCACCAGACGTCCTCTGCTTCTTAGAAAACCTCAACAGCAGTGTGCCTAAAGAGATCGGAAGAGCGGTTTCAG
chr18	6942249	6942288	LAMA1_10482	+	GTGACCTATGCACCAGACGTAAGAAGAGAAGACAATCTTGCTTAATTTTTGTTGAAATGCAGATCGGAAGAGCGGTTTCAG
chr18	6943412	6943451	LAMA1_10483	+	GTGACCTATGCACCAGACGTATATCTTGGTGAGTTTTTGTGATTTAAGGAACACAGTCCAGATCGGAAGAGCGGTTTCAG
chr18	6947306	6947345	LAMA1_10484	+	GTGACCTATGCACCAGACGTCGAAGGAGGACCAAGTCAGGGTGTAGCGCTGCCAGGCCAGAGATCGGAAGAGCGGTTTCAG
chr18	6948566	6948605	LAMA1_10485	+	GTGACCTATGCACCAGACGTTGACATGCAAGATGAGACGTTGGTATTCTAATGGGAAGGAGATCGGAAGAGCGGTTTCAG
chr18	6949269	6949308	LAMA1_10486	+	GTGACCTATGCACCAGACGTGTGAAAACATGCAATTTTTTGAGGAATCGAAAAAATAGATCGGAAGAGCGGTTTCAG
chr18	6950981	6951020	LAMA1_10487	+	GTGACCTATGCACCAGACGTCGAAGTGTCTAGCGTTGAGAAAAGAACTTTTACTTTTTCATAGATCGGAAGAGCGGTTTCAG
chr18	6955475	6955514	LAMA1_10488	+	GTGACCTATGCACCAGACGTCACACAGGGACTCAGCCGCCACCCGAGCCCAACCCAGATCGGAAGAGCGGTTTCAG
chr18	6956775	6956814	LAMA1_10489	+	GTGACCTATGCACCAGACGTACAAGAGAGTGTTTTTCAAAATTAGGATATCACAACACAGTATCGGAAGAGCGGTTTCAG
chr18	6958672	6958711	LAMA1_10490	+	GTGACCTATGCACCAGACGTAATGGAGAAAATAAATGAAAAGCTTAAACATAATGAAATAGATCGGAAGAGCGGTTTCAG
chr18	6959502	6959541	LAMA1_10491	+	GTGACCTATGCACCAGACGTTGCATAGAGAAATTTCCAGACAAAACATTAATATGAGATCGGAAGAGCGGTTTCAG
chr18	6961769	6961808	LAMA1_10492	+	GTGACCTATGCACCAGACGTTGGATGGAACAGCATGGTGAGTTCCTAGCTGCGGCCAAAGATCGGAAGAGCGGTTTCAG
chr18	6962069	6962108	LAMA1_10493	+	GTGACCTATGCACCAGACGTGGGCATGAGAACAATCACAAAATTTGGGTTTTTAAATTCAGATCGGAAGAGCGGTTTCAG
chr18	6964813	6964852	LAMA1_10494	+	GTGACCTATGCACCAGACGTAGCACAGGCAAGAGATAAGAAAAGGAAAATCCCTTTCCATAGATCGGAAGAGCGGTTTCAG
chr18	6965442	6965481	LAMA1_10495	+	GTGACCTATGCACCAGACGTGAGAACACAGTCCCCAGGTTATAGCTTTATCCAGGTTTAGATCGGAAGAGCGGTTTCAG
chr18	6966307	6966346	LAMA1_10496	+	GTGACCTATGCACCAGACGTTGAAGAGATGAAATGAAATCCTTCTCAGGAGGGTAGAAAAGATCGGAAGAGCGGTTTCAG
chr18	6971991	6972030	LAMA1_10497	+	GTGACCTATGCACCAGACGTTCAAGCAAAACAATAAATATAAGCTGACCAAGCAAGATCGGAAGAGCGGTTTCAG
chr18	6973217	6973256	LAMA1_10498	+	GTGACCTATGCACCAGACGTCAAAGAAATGCAAAAATAAATTTTTCAGAAATTTCCAGTACAGATCGGAAGAGCGGTTTCAG

chr18	6975046	6975085	LAMA1_10499	+	GTGACCTATGCACCAGACGTAGGAATGAACGGGGATCAGTTTACACACTGGACTGTTTGCAGATCGGAAGAGCGGTTTCAG
chr18	6976090	6976129	LAMA1_10500	+	GTGACCTATGCACCAGACGTAAAATGAAAGTGTCCCATCATTTAGTGACACACACCGGCAGATCGGAAGAGCGGTTTCAG
chr18	6977891	6977930	LAMA1_10501	+	GTGACCTATGCACCAGACGTCAAGAAGGCAAGGGGTGGCAAGAAAGTTGGGGAGAGGAAAGATCGGAAGAGCGGTTTCAG
chr18	6978388	6978427	LAMA1_10502	+	GTGACCTATGCACCAGACGTTGTATATAAAAGCATGCACCTTCTGGTGCTTACACACAGAGAGATCGGAAGAGCGGTTTCAG
chr18	6980647	6980686	LAMA1_10503	+	GTGACCTATGCACCAGACGTGGAGAAAAATGTTTCCTTTTTCAGGTTAGCCTACAAAAAAGTAGATCGGAAGAGCGGTTTCAG
chr18	6982600	6982639	LAMA1_10504	+	GTGACCTATGCACCAGACGTGAACCATTTAAGCGTGGTGAGAGCAGGGCAGGGTGGAGTCAGATCGGAAGAGCGGTTTCAG
chr18	6983244	6983283	LAMA1_10505	+	GTGACCTATGCACCAGACGTGACCATTTTAGATACGTTTGTAGTAACTAAATCAAACCTTAACTGAGATCGGAAGAGCGGTTTCAG
chr18	6985410	6985449	LAMA1_10506	+	GTGACCTATGCACCAGACGTAAATTAATATTGTAATATATGCACATCTACTTAATAACAAGATCGGAAGAGCGGTTTCAG
chr18	6985653	6985692	LAMA1_10507	+	GTGACCTATGCACCAGACGTAAACGGCATTTAAAGGGTCTTCATAAAAGCAACCCTGCTTAGATCGGAAGAGCGGTTTCAG
chr18	6986357	6986396	LAMA1_10508	+	GTGACCTATGCACCAGACGTTGAATGGTTCACATAGTAAAGTAAATGAACAACAAAGCTCCAGATCGGAAGAGCGGTTTCAG
chr18	6992730	6992769	LAMA1_10509	+	GTGACCTATGCACCAGACGTAATTCATCAATTATTTAATAAGCCTCTCAAAGTGGCTAGAGATCGGAAGAGCGGTTTCAG
chr18	6993762	6993801	LAMA1_10510	+	GTGACCTATGCACCAGACGTAATAAGTCTCAGGCTTAGTTGACTTTAAGTAATTAGTTTAGATCGGAAGAGCGGTTTCAG
chr18	6995456	6995495	LAMA1_10511	+	GTGACCTATGCACCAGACGTTGGAGGAAACAAATTACAGATGCTCGAAGTAAATGTTCTAGATCGGAAGAGCGGTTTCAG
chr18	6997894	6997933	LAMA1_10512	+	GTGACCTATGCACCAGACGTAATTTTTAAAAGGAGAGTTAAAGTTAATGCGATGTGGTCAGATCGGAAGAGCGGTTTCAG
chr18	6999648	6999687	LAMA1_10513	+	GTGACCTATGCACCAGACGTGAAGGGACATAGGTGCAGACAGGATGGTCAATACCAGCTTAGATCGGAAGAGCGGTTTCAG
chr18	7000007	7000046	LAMA1_10514	+	GTGACCTATGCACCAGACGTAGAAATTTCTTTTTGAATTTTCAGATATACAATTTCCATCTAGATCGGAAGAGCGGTTTCAG
chr18	7002395	7002434	LAMA1_10515	+	GTGACCTATGCACCAGACGTACATTTAAAGGAAGGGGGAAAAAATGGGAAATTTGTTAGAAAGATCGGAAGAGCGGTTTCAG
chr18	7008617	7008657	LAMA1_10516	+	GTGACCTATGCACCAGACGTTACATGTTAAGAGAGGAAACGCTAACATTTGAAAAACTTTAGATCGGAAGAGCGGTTTCAG
chr18	7009376	7009415	LAMA1_10517	+	GTGACCTATGCACCAGACGTAGAACAACATTCAATTAAGCTCAGACGGCCAAATTTCTGACAAGATCGGAAGAGCGGTTTCAG
chr18	7010395	7010434	LAMA1_10518	+	GTGACCTATGCACCAGACGTATAAAGTGTGGTTTACTTCTCTGACAAAGCTTTTCAATCAAAGATCGGAAGAGCGGTTTCAG
chr18	7011489	7011528	LAMA1_10519	+	GTGACCTATGCACCAGACGTAAAGGAGGGGAAAGTGCACCTCAAATGCGAAGCTTTCCACAGATCGGAAGAGCGGTTTCAG
chr18	7012148	7012187	LAMA1_10520	+	GTGACCTATGCACCAGACGTGCAATAAAGGACTCGTTTTTGCTTAAAAAGAGATGTGAAGATCGGAAGAGCGGTTTCAG
chr18	7014061	7014100	LAMA1_10521	+	GTGACCTATGCACCAGACGTGGAAAACCAACTCAATTAATAAGGCAGATTTGATGCTTCCAGATCGGAAGAGCGGTTTCAG
chr18	7015868	7015907	LAMA1_10522	+	GTGACCTATGCACCAGACGTGAAATGCTGGTTGACATGCTGGTGATGTCATTAAAGAGATCGGAAGAGCGGTTTCAG
chr18	7016681	7016720	LAMA1_10523	+	GTGACCTATGCACCAGACGTAAAGGGGAGAAAAGTGGAAAACCAACATACGTTTTAATAAAAGATCGGAAGAGCGGTTTCAG
chr18	7017394	7017433	LAMA1_10524	+	GTGACCTATGCACCAGACGTGCACACAAGACATATTAACCTCCTACTTCTGAGGATGGTTAGATCGGAAGAGCGGTTTCAG
chr18	7023385	7023424	LAMA1_10525	+	GTGACCTATGCACCAGACGTGATTGAAAGTGGGATCAGACAAATGCAGTTACTTAAGGCCAGATCGGAAGAGCGGTTTCAG
chr18	7024476	7024515	LAMA1_10526	+	GTGACCTATGCACCAGACGTATTAGAAATGAACAAATTTTCCAATGGATGAAGCCGAATAGATCGGAAGAGCGGTTTCAG
chr18	7026116	7026155	LAMA1_10527	+	GTGACCTATGCACCAGACGTGCACCAGAGAATCAGCTAGGTTGCTTAAAGGATTTTCAGATCGGAAGAGCGGTTTCAG
chr18	7032186	7032225	LAMA1_10528	+	GTGACCTATGCACCAGACGTAGGAAAGTCAATCCTCTTTTCCACTACGTTACAAACAGAAAAGATCGGAAGAGCGGTTTCAG
chr18	7033105	7033144	LAMA1_10529	+	GTGACCTATGCACCAGACGTACAGATTGTTATGTGACTCACACGCTCGCAAATACATCTCAGATCGGAAGAGCGGTTTCAG
chr18	7036098	7036137	LAMA1_10530	+	GTGACCTATGCACCAGACGTTAAGCGAGAATGAACACGAAAGGGGAAAGACAATCACAGCAAGATCGGAAGAGCGGTTTCAG
chr18	7037761	7037800	LAMA1_10531	+	GTGACCTATGCACCAGACGTAATTCAGAATTTTGAAGTATGAAATAGAATTTACCTTAGAGATCGGAAGAGCGGTTTCAG
chr18	7038960	7038999	LAMA1_10532	+	GTGACCTATGCACCAGACGTGGGTAAGATAGCTTTTTGAAACCAATGTGCTGTCCAGATCGGAAGAGCGGTTTCAG
chr18	7040246	7040285	LAMA1_10533	+	GTGACCTATGCACCAGACGTAAACATGAACATGACCCAAAGTGAAGGCAAAAGAGGTTAAGATCGGAAGAGCGGTTTCAG
chr18	7042260	7042299	LAMA1_10534	+	GTGACCTATGCACCAGACGTGAGGTTGCCCTGGATTCTCTTACTAGAAAATAACAGCAATGAGATCGGAAGAGCGGTTTCAG
chr18	7043415	7043454	LAMA1_10535	+	GTGACCTATGCACCAGACGTATTTTTAACATCTCAATTAATTTACATAGCATGCCTTATAAGATCGGAAGAGCGGTTTCAG
chr18	7044849	7044888	LAMA1_10536	+	GTGACCTATGCACCAGACGTAGGAAGCCAAACGTAATTAGAAAATGTATCTGCTTATGTAGATCGGAAGAGCGGTTTCAG
chr18	7046377	7046416	LAMA1_10537	+	GTGACCTATGCACCAGACGTAGAAAGTTATGAACAAAAATTAACCTAGATTTTCAAGATCGGAAGAGCGGTTTCAG
chr18	7080097	7080136	LAMA1_10538	+	GTGACCTATGCACCAGACGTAATAAAAAACATGAATTCCTCTGGCTGTTGCTTTAAAAGATCGGAAGAGCGGTTTCAG
chr18	7080467	7080506	LAMA1_10539	+	GTGACCTATGCACCAGACGTAAATTTACCAATCAGTGCACCCTTGAATCCAAAGAAAAGATCGGAAGAGCGGTTTCAG
chr18	7117730	7117769	LAMA1_10540	+	GTGACCTATGCACCAGACGTCCGCCACTCGGTGGGTTCTGGGGAGAAAGCCGCGCCCGCAGATCGGAAGAGCGGTTTCAG
chr13	113951821	113951860	LAMP1_10541	+	GTGACCTATGCACCAGACGTGAGGGCGGGCCCTGGGAGCGCGGGACCGGGCGAGCCGAAGATCGGAAGAGCGGTTTCAG
chr13	113960932	113960971	LAMP1_10542	+	GTGACCTATGCACCAGACGTCCAGGGCACTTCATGCTTCCCTTGTGTGTGGAAAAGATGAGATCGGAAGAGCGGTTTCAG
chr13	113964188	113964227	LAMP1_10543	+	GTGACCTATGCACCAGACGTAATGGGGCCGATATGAAGTGATGAAAATGGGTTGGAGAGATCGGAAGAGCGGTTTCAG
chr13	113965193	113965232	LAMP1_10544	+	GTGACCTATGCACCAGACGTGACCTTGGCCCTTGGGCTGTGGTGATGGTTGGGTAGCTGGGAGATCGGAAGAGCGGTTTCAG
chr13	113973982	113974021	LAMP1_10545	+	GTGACCTATGCACCAGACGTGGCCCTCACCTGGGAGAGGGGACCGCACCGTAGGGCTGGAAGATCGGAAGAGCGGTTTCAG
chr13	113974796	113974835	LAMP1_10546	+	GTGACCTATGCACCAGACGTGGCGGCACCTCTCTGGGGGCGCCACTGTGCTCCACCACAGATCGGAAGAGCGGTTTCAG
chr13	113976053	113976092	LAMP1_10547	+	GTGACCTATGCACCAGACGTCCGAGGGCAGCTGTCGCGGGGTGTGGAGGAGCTGCTTCAGATCGGAAGAGCGGTTTCAG
chr13	113976747	113976786	LAMP1_10548	+	GTGACCTATGCACCAGACGTGCAGGCACAGCTGCAGGGCCCTCTGTCTCCTTCTCTGAGATCGGAAGAGCGGTTTCAG
chr11	18418526	18418565	LDHA_10549	+	GTGACCTATGCACCAGACGTGTCACCACTGGAAGCCATACCTTGACCCCATCCTTAGATCGGAAGAGCGGTTTCAG
chr11	18422568	18422607	LDHA_10550	+	GTGACCTATGCACCAGACGTGACTGCATAAAAATTGACAAGCTATAGTAAAATCAGATCGGAAGAGCGGTTTCAG
chr11	18424571	18424610	LDHA_10551	+	GTGACCTATGCACCAGACGTGTTATTTCTTTTTGTTTTGAAAAGATTATATAAAAAGTAGATCGGAAGAGCGGTTTCAG
chr11	18425369	18425408	LDHA_10552	+	GTGACCTATGCACCAGACGTTTTCAATTTGGCAACACAGAATATTAACATTTACTATTTTAGATCGGAAGAGCGGTTTCAG
chr11	18427130	18427169	LDHA_10553	+	GTGACCTATGCACCAGACGTGATGTATACGCTGCATTTGAATGCTTTTTGCTGGCTTTTAGATCGGAAGAGCGGTTTCAG
chr11	18428839	18428878	LDHA_10554	+	GTGACCTATGCACCAGACGTTGTCAATCATTCTACTGTCTAGGCTACAACAGGATTTAAGATCGGAAGAGCGGTTTCAG
chr2	33174023	33174062	LTBP1_10555	+	GTGACCTATGCACCAGACGTATGTTACAGTGGCCCTGCAGAGTAGGCAAAGTGGGGAGAGATCGGAAGAGCGGTTTCAG
chr2	33246284	33246323	LTBP1_10556	+	GTGACCTATGCACCAGACGTGAACTTTTCATTTAGCTAACAGATCATCTTAATTTACTCTCTAGATCGGAAGAGCGGTTTCAG

chr2	33335829	33335868	LTBP1_10557	+	GTGACCTATGCACCAGACGTTCTTATCAACCATTTTCCCAAGTTATGGTATCAGAGATTGAGATCGGAAGAGCGGTTTCAG
chr2	33360038	33360077	LTBP1_10558	+	GTGACCTATGCACCAGACGTCACCGTCCCTAACCTGTCCTACTGAGTCGAGTTTTATGAAGATCGGAAGAGCGGTTTCAG
chr2	33412158	33412197	LTBP1_10559	+	GTGACCTATGCACCAGACGTTTCATTCCGCCCATTTGCCAGACCTCTGTTAACCTGCCAAAGATCGGAAGAGCGGTTTCAG
chr2	33413929	33413968	LTBP1_10560	+	GTGACCTATGCACCAGACGTTACCGAGCCTGCTTTAGCAGTGTCTTACAGATATGGTATAGATCGGAAGAGCGGTTTCAG
chr2	33442732	33442771	LTBP1_10561	+	GTGACCTATGCACCAGACGTTTTCTCCTCACTCTTTGCAGGTTAATGTAGCATATCTGTTTAGATCGGAAGAGCGGTTTCAG
chr2	33447229	33447268	LTBP1_10562	+	GTGACCTATGCACCAGACGCTGAATTCATTGATGTGGACTCAACAGTTGTTTTGGCTTTAGATCGGAAGAGCGGTTTCAG
chr2	33468862	33468901	LTBP1_10563	+	GTGACCTATGCACCAGACGTTACTTTTTATTCTGTCTTTGGATTAATTGTCCTTTGGGAGATCGGAAGAGCGGTTTCAG
chr2	33477922	33477961	LTBP1_10564	+	GTGACCTATGCACCAGACGTCGCCAGCTGTATGCGCACATAGATTTCCAGCCACATGAGTAAGATCGGAAGAGCGGTTTCAG
chr2	33482589	33482628	LTBP1_10565	+	GTGACCTATGCACCAGACGTTAATGGATCATGGACTCTAGACATCTATCTGTGTGCTTTAGATCGGAAGAGCGGTTTCAG
chr2	33484688	33484727	LTBP1_10566	+	GTGACCTATGCACCAGACGTCATTGCTTGAAGTCTTTTTTTTTCAACGCTCAAAGTGATAGATCGGAAGAGCGGTTTCAG
chr2	33487902	33487941	LTBP1_10567	+	GTGACCTATGCACCAGACGTATCTGTGCTGTTTTGTCAGAGTATTCTGAATAAAAAATGTAAGATCGGAAGAGCGGTTTCAG
chr2	33488470	33488509	LTBP1_10568	+	GTGACCTATGCACCAGACGTTATTTTTACATATATACATCGAGGAGACGTTGGGCTAGATCGGAAGAGCGGTTTCAG
chr2	33498859	33498898	LTBP1_10569	+	GTGACCTATGCACCAGACGTTAGTTGACTAAATTTAAATATCAACATTTGAACAAGATCGGAAGAGCGGTTTCAG
chr2	33500168	33500207	LTBP1_10570	+	GTGACCTATGCACCAGACGTCATTCTTCTGCTTACAATTTCTTAGATCTGAGTTTTTAGATCGGAAGAGCGGTTTCAG
chr2	33501001	33501040	LTBP1_10571	+	GTGACCTATGCACCAGACGTTGAGAGTGTTCAGCACACATGACGGTGATGTGCAGGGTTGAGATCGGAAGAGCGGTTTCAG
chr2	33505236	33505275	LTBP1_10572	+	GTGACCTATGCACCAGACGTTAGTGTACTTATCAAGATTTGTTTTCTTCTGCATGGCCCAAGATCGGAAGAGCGGTTTCAG
chr2	33518360	33518399	LTBP1_10573	+	GTGACCTATGCACCAGACGTTGATCAAGTTTTCCCATTTTTAACTTCATTTAAATAAGATCGGAAGAGCGGTTTCAG
chr2	33525651	33525690	LTBP1_10574	+	GTGACCTATGCACCAGACGTAGTAACATGAACTACTGAACTTTCAGCTTAAAGCACCTGGAGATCGGAAGAGCGGTTTCAG
chr2	33534634	33534673	LTBP1_10575	+	GTGACCTATGCACCAGACGTCCTTTTTTCCCGAGTCATTATTACGTAATTTCTCAATTAGATCGGAAGAGCGGTTTCAG
chr2	33540347	33540386	LTBP1_10576	+	GTGACCTATGCACCAGACGTCACATACGAATCATATTTGTTGTGTATAAAGAGAGAGGAAGATCGGAAGAGCGGTTTCAG
chr2	33568041	33568080	LTBP1_10577	+	GTGACCTATGCACCAGACGTAGATTTTTTCCCAACGTGTTTCACATGTCCCTAGGGAAAAAGATCGGAAGAGCGGTTTCAG
chr2	33572588	33572627	LTBP1_10578	+	GTGACCTATGCACCAGACGTGTGACACTGTGCAAGGGAATGACAGGCTCCTCTCAAAGACAGATCGGAAGAGCGGTTTCAG
chr2	33585857	33585896	LTBP1_10579	+	GTGACCTATGCACCAGACGTTAGTGGTAGAGTACACATTTGTTGGTTCACATGGTGTAGATCGGAAGAGCGGTTTCAG
chr2	33586593	33586632	LTBP1_10580	+	GTGACCTATGCACCAGACGTAGTGGAAACAAATTTTCAGCACATTTGTACATGTACATGATAGATCGGAAGAGCGGTTTCAG
chr2	33588596	33588635	LTBP1_10581	+	GTGACCTATGCACCAGACGTGGGGGATATAGTATGGTGTACTGTGAAATATACAGATGGAGATCGGAAGAGCGGTTTCAG
chr2	33589434	33589473	LTBP1_10582	+	GTGACCTATGCACCAGACGTAGGAGATGCAAACCTGTGTCCAAATACTATCATAAGATTAGATCGGAAGAGCGGTTTCAG
chr2	33590581	33590620	LTBP1_10583	+	GTGACCTATGCACCAGACGTATCCAATTCCTTCTGCAGGAGGCCTTTTGGGGACAAGTTCAAGATCGGAAGAGCGGTTTCAG
chr2	33614384	33614423	LTBP1_10584	+	GTGACCTATGCACCAGACGTTAACTTGTTCCTTTGATACTAAGTTGTGGTTGAAGATTAGATCGGAAGAGCGGTTTCAG
chr2	33622360	33622399	LTBP1_10585	+	GTGACCTATGCACCAGACGTCGTGTTTTATGGATACATTAATTTTTCTGACACCCGAGATCGGAAGAGCGGTTTCAG
chr2	33623623	33623662	LTBP1_10586	+	GTGACCTATGCACCAGACGTACATAAACCATAGCCCATTTCTGCACACTGTGTAAGGAAAGATCGGAAGAGCGGTTTCAG
chr16	30128122	30128161	MAPK3_10587	+	GTGACCTATGCACCAGACGTAGAGACAGCAAGGCTCAGGCCGTCATGGGGGATGCCTACAGATCGGAAGAGCGGTTTCAG
chr16	30128335	30128374	MAPK3_10588	+	GTGACCTATGCACCAGACGTGCAGGAGTCAGGGGTCACAGGGAAGACTGGAGGAGCTCCGAGATCGGAAGAGCGGTTTCAG
chr16	30128617	30128656	MAPK3_10589	+	GTGACCTATGCACCAGACGTGGAGGTGACTTGGTAAATGATCACCTCTTTCTTTCTGGGAAGATCGGAAGAGCGGTTTCAG
chr16	30129116	30129155	MAPK3_10590	+	GTGACCTATGCACCAGACGTGGAGGAAGTGTGAGCTCCTGGCCAGCCTCAACAGGGTTCAGATCGGAAGAGCGGTTTCAG
chr16	30129495	30129534	MAPK3_10591	+	GTGACCTATGCACCAGACGTACCTGCTAAGTGTGCTAGCCGCTCAAGGCCTCTGCAGCTAGATCGGAAGAGCGGTTTCAG
chr16	30129870	30129909	MAPK3_10592	+	GTGACCTATGCACCAGACGTTTTCCGAGACCCCCCAGGCAGGGGGCAGTGGGAGGCACTAGATCGGAAGAGCGGTTTCAG
chr16	30133338	30133377	MAPK3_10593	+	GTGACCTATGCACCAGACGTCCGAGAGAGGCTGCTGCTGTGGCCTTCAAAGGGGGAGTCAGATCGGAAGAGCGGTTTCAG
chr10	89265320	89265359	MINPP1_10594	+	GTGACCTATGCACCAGACGTGGGCGGCCGCTGTGCTGTCCCGTCTCCACCCGCCCTGAGATCGGAAGAGCGGTTTCAG
chr10	89268301	89268340	MINPP1_10595	+	GTGACCTATGCACCAGACGTTGTTGCTTTTTATTTGACTTAACAGTTAAATAATTTGAGATCGGAAGAGCGGTTTCAG
chr10	89280937	89280976	MINPP1_10596	+	GTGACCTATGCACCAGACGTTCAAAAAATGTGAAGTACATTTGAGTACTACTAAACTAGATCGGAAGAGCGGTTTCAG
chr10	89312246	89312285	MINPP1_10597	+	GTGACCTATGCACCAGACGTTAATTTAATCTTTAGGAATCTGCAATGAGTGATTACAGATCGGAAGAGCGGTTTCAG
chr10	89265001	89265040	MINPP1_10598	+	GTGACCTATGCACCAGACGTAGGCCCGCGGGTCCAGGGATGGCGGGGCTAGTAGTACCGGAGATCGGAAGAGCGGTTTCAG
chr11	118307670	118307709	MLL_10599	+	GTGACCTATGCACCAGACGTGAGGAACCCCCAGGTCGGGGTCTCGACCTCTGCGGAGCAGATCGGAAGAGCGGTTTCAG
chr11	118339570	118339609	MLL_10600	+	GTGACCTATGCACCAGACGTTTAAAGTGCATGGTGCCTTTTAAAGTTTTGTTTTGTTAGGAGAAGATCGGAAGAGCGGTTTCAG
chr11	118345041	118345080	MLL_10601	+	GTGACCTATGCACCAGACGTTCCACTTGGCTTAAACTAACAGTTTATTGAGCCCTTTAGATCGGAAGAGCGGTTTCAG
chr11	118347708	118347747	MLL_10602	+	GTGACCTATGCACCAGACGTTAAGGTCAACTCTTGAGTCCGGAACAGACTTTTGATTTGTTTAGATCGGAAGAGCGGTTTCAG
chr11	118348927	118348966	MLL_10603	+	GTGACCTATGCACCAGACGTGTTTCACTCTGAGATGTTGACCTCTCAACCATAAAGGTTGAGATCGGAAGAGCGGTTTCAG
chr11	118350964	118351003	MLL_10604	+	GTGACCTATGCACCAGACGTTAAAAAGGTCTTCCCCAAATGCTCCTTGCTTAAATGGTGTAGATCGGAAGAGCGGTTTCAG
chr11	118352818	118352857	MLL_10605	+	GTGACCTATGCACCAGACGTAGGGCAAGAAGGAATGCTGAACCACAAGTACTAACAATAAAGATCGGAAGAGCGGTTTCAG
chr11	118353221	118353260	MLL_10606	+	GTGACCTATGCACCAGACGTATTTGTTTCTCTGCCATTTCTCAGGGATGTATTCTATTTAGATCGGAAGAGCGGTTTCAG
chr11	118355040	118355079	MLL_10607	+	GTGACCTATGCACCAGACGTTCAAGTATCAAAAGTATTTGAGTGTCAAAGACTTTAAAGATCGGAAGAGCGGTTTCAG
chr11	118355701	118355740	MLL_10608	+	GTGACCTATGCACCAGACGTTCTGCTTCTTTGATCCCAAGGAAGTACATAAAATTTTTCAGATCGGAAGAGCGGTTTCAG
chr11	118360613	118360652	MLL_10609	+	GTGACCTATGCACCAGACGTCACATGATGCTCTTTTTATAGAGAACCACCATGTGACTATTAGATCGGAAGAGCGGTTTCAG
chr11	118360975	118361014	MLL_10610	+	GTGACCTATGCACCAGACGTAAGCCAGTTTTGCCAGCTTTCGGAGGTTGACTTGGTGTAGATCGGAAGAGCGGTTTCAG
chr11	118362035	118362074	MLL_10611	+	GTGACCTATGCACCAGACGTTTGGAGTCTTTTTATTTCAGTTTTCTCTTCTAGTACTAGATCGGAAGAGCGGTTTCAG
chr11	118362654	118362693	MLL_10612	+	GTGACCTATGCACCAGACGTTCTCATTTTTCTGAGAGCTTGTCTTAGGTAGTCTTTAAGATCGGAAGAGCGGTTTCAG
chr11	118363956	118363995	MLL_10613	+	GTGACCTATGCACCAGACGTTACTGAGCCATCAGAATTTCTAGCCAAATAAAGCTTGTAGATCGGAAGAGCGGTTTCAG
chr11	118365124	118365163	MLL_10614	+	GTGACCTATGCACCAGACGTTTACTAATTCATGTTTTTAAATGCTTACTTAAGTAATTAAGATCGGAAGAGCGGTTTCAG

chr11	118365493	118365532	MLL_10615	+	GTGACCTATGCACCAGACGTTTAGCATAACTTTTTTCTCCTCATCGGCTAGAAAATCTGAGATCGGAAGAGCGGTTTCAG
chr11	118366619	118366658	MLL_10616	+	GTGACCTATGCACCAGACGTAAAAGGAGAGTCGTCACCCATTTCCCTCTAGATGCAGATGAGATCGGAAGAGCGGTTTCAG
chr11	118367093	118367132	MLL_10617	+	GTGACCTATGCACCAGACGTTGCAACACAGGGCCCTAGTTAATACATACTCCAAAAGAACAGATCGGAAGAGCGGTTTCAG
chr11	118368799	118368838	MLL_10618	+	GTGACCTATGCACCAGACGTATGGGTAATTTTATGAAAGAGATTCCTCTCAGTTTCCAAGATCGGAAGAGCGGTTTCAG
chr11	118370146	118370185	MLL_10619	+	GTGACCTATGCACCAGACGTGCCTTGGTTATTGGGGAAGCCTGTATATATCATTGGGGAAAGATCGGAAGAGCGGTTTCAG
chr11	118370639	118370678	MLL_10620	+	GTGACCTATGCACCAGACGCTATAAAGAGGAAGAGCAGCCCAACCTGAACACACTAGATCGGAAGAGCGGTTTCAG
chr11	118372583	118372622	MLL_10621	+	GTGACCTATGCACCAGACGTTTATTGACCTACTTGACCTAAGAAGACTAGCCCAAAGACTAGCCGAAGAGCGGTTTCAG
chr11	118377372	118377411	MLL_10622	+	GTGACCTATGCACCAGACGTCAAACTAGCTAGGCTGGGCTGTGGGATTTTCATGTTGTAGATCGGAAGAGCGGTTTCAG
chr11	118378335	118378374	MLL_10623	+	GTGACCTATGCACCAGACGTGAATTCGCTTTTTAAGACTAAGCTCTCAGTTTTGTCCACCAGATCGGAAGAGCGGTTTCAG
chr11	118380844	118380883	MLL_10624	+	GTGACCTATGCACCAGACGTAAATCAGGTTGACCCATCAGCAGAAGCCCTGTTTCAGCTAGATCGGAAGAGCGGTTTCAG
chr11	118382751	118382790	MLL_10625	+	GTGACCTATGCACCAGACGTGAGGTTGTTATCCACTCTGTCTCAGAATATTATGGTAAAAGATCGGAAGAGCGGTTTCAG
chr11	118390518	118390557	MLL_10626	+	GTGACCTATGCACCAGACGTTTCTTTCTGCAGCAGTTTTGGTCTCGATTTTCTTATCAGATCGGAAGAGCGGTTTCAG
chr11	118390790	118390829	MLL_10627	+	GTGACCTATGCACCAGACGTAGTGGGGAGCATTAGAAACTGCTTTCCCTCTCCCTCCAGATCGGAAGAGCGGTTTCAG
chr11	118391611	118391650	MLL_10628	+	GTGACCTATGCACCAGACGTAATTTCTAGAAAAGATTACAGAAAACGAATGCAGTTTTTCAAGATCGGAAGAGCGGTTTCAG
chr11	118392143	118392182	MLL_10629	+	GTGACCTATGCACCAGACGTCACTTGCACTCACACAGTTCTTTTGTGTTGCTGTAGAAAAGATCGGAAGAGCGGTTTCAG
chr11	118392898	118392937	MLL_10630	+	GTGACCTATGCACCAGACGTCTCCCCAGTGTGGAGTGCAAGGAGCCGGGGCCATCCAAAGATCGGAAGAGCGGTTTCAG
chr11	118342829	118342868	MLL_10631	+	GTGACCTATGCACCAGACGCTCATTAACTTGAECTGAAAAGCCCGGAAAGTCCGGAAGATCGGAAGAGCGGTTTCAG
chr11	118343271	118343310	MLL_10632	+	GTGACCTATGCACCAGACGTTCCAGACTCTCTCAAATGTCTTCAAAGATCGACTCCCTCAGATCGGAAGAGCGGTTTCAG
chr11	118343713	118343752	MLL_10633	+	GTGACCTATGCACCAGACGTAGAACCCGACATTTAGGTGGACTCTTTAAAGCATTCTAGGAGATCGGAAGAGCGGTTTCAG
chr11	118344155	118344194	MLL_10634	+	GTGACCTATGCACCAGACGTAGGCTTAGTAGTTCTGAGCTCTCACCTCTCACCCCCCGTAGATCGGAAGAGCGGTTTCAG
chr11	118344597	118344636	MLL_10635	+	GTGACCTATGCACCAGACGTTGGGTAGGGTTTCCAAAGAGAAGGTTGTTGGTGAAGATGTAGATCGGAAGAGCGGTTTCAG
chr11	118373595	118373634	MLL_10636	+	GTGACCTATGCACCAGACGTGGAATTCCTAAACTGGCCCCACAGGTTTATAACACAACATAGATCGGAAGAGCGGTTTCAG
chr11	118374067	118374106	MLL_10637	+	GTGACCTATGCACCAGACGTTGATAAGATTGGTATAAAGCCCTTCTATGCCAGGATAGATCGGAAGAGCGGTTTCAG
chr11	118374539	118374578	MLL_10638	+	GTGACCTATGCACCAGACGTTGAAGAAGCATTGCAATCTCAGCAGCTCAACTGGGAAAGATCGGAAGAGCGGTTTCAG
chr11	118375011	118375050	MLL_10639	+	GTGACCTATGCACCAGACGTGCTCAGCTCAGCTCATTGGAGTCAAGCCGCAGAGTCCACAAGATCGGAAGAGCGGTTTCAG
chr11	118375483	118375522	MLL_10640	+	GTGACCTATGCACCAGACGTGGGAGAAGAGAGTAACCATCACAGAAAAATCTGTAGCCTCAGATCGGAAGAGCGGTTTCAG
chr11	118375955	118375994	MLL_10641	+	GTGACCTATGCACCAGACGTTGTGATGGAGACAATACTTACAGTATTGGGACCCATGGGAAGATCGGAAGAGCGGTTTCAG
chr11	118376427	118376466	MLL_10642	+	GTGACCTATGCACCAGACGTTTGGGGCTCACTTAACTTTCATCTCACCCGAATGTCCCAAGATCGGAAGAGCGGTTTCAG
chr11	118376899	118376938	MLL_10643	+	GTGACCTATGCACCAGACGTTGCTCCCTCCACTCAGACTCGGGCATAACAGCCGCTTCAGATCGGAAGAGCGGTTTCAG
chr7	151834020	151834059	MLL3_10644	+	GTGACCTATGCACCAGACGTTAAAGACACAGGGTAAGAAAAGCAGCAAGGAAGGCAATAAGATCGGAAGAGCGGTTTCAG
chr7	151836000	151836039	MLL3_10645	+	GTGACCTATGCACCAGACGTCCATGTCAGAAAAGTATTGTAAAAACAGCTAGAAGCAGCAGATCGGAAGAGCGGTTTCAG
chr7	151836355	151836394	MLL3_10646	+	GTGACCTATGCACCAGACGTAGTCAGTACAGTAAGTCATCAATGTGCGACTGAAACTCCCAGATCGGAAGAGCGGTTTCAG
chr7	151836887	151836926	MLL3_10647	+	GTGACCTATGCACCAGACGTGTGTGTACATACTCCAATTTATGTGACAAACAAGTCTTTTATAGATCGGAAGAGCGGTTTCAG
chr7	151841977	151842016	MLL3_10648	+	GTGACCTATGCACCAGACGTTGGCATATCAACAGGAAAAAATCAAGGAAAACTGAAGAAGATCGGAAGAGCGGTTTCAG
chr7	151842391	151842430	MLL3_10649	+	GTGACCTATGCACCAGACGTGCAAAAGCAGACACAAGACTCCCTTCTGATGGAGACTCAGATCGGAAGAGCGGTTTCAG
chr7	151843831	151843870	MLL3_10650	+	GTGACCTATGCACCAGACGTACAAAAACATAATTTTTATAGAAAATAGGATACAGTATAAAGATCGGAAGAGCGGTTTCAG
chr7	151846248	151846287	MLL3_10651	+	GTGACCTATGCACCAGACGTTAAAGAAAACCATGACAAAAGAAAAATAATCACAAAGCCCGGAGATCGGAAGAGCGGTTTCAG
chr7	151848103	151848142	MLL3_10652	+	GTGACCTATGCACCAGACGTAAAGAAAATGTGTGGGAATCTCAACAAGTCAAATTTAATAGATCGGAAGAGCGGTTTCAG
chr7	151848677	151848716	MLL3_10653	+	GTGACCTATGCACCAGACGTTCAACTTTTGTAGTAATAAAACACTGACTGATGACACAAGAGATCGGAAGAGCGGTTTCAG
chr7	151850050	151850089	MLL3_10654	+	GTGACCTATGCACCAGACGTGCAAAATGCTGATTAATTCACCAGAAGGCAACAGTGAAGATCGGAAGAGCGGTTTCAG
chr7	151851242	151851281	MLL3_10655	+	GTGACCTATGCACCAGACGTAGAGAAAAAAGAGGAAAATAGTGTAAATGGATTTTCAAAGATCGGAAGAGCGGTTTCAG
chr7	151851541	151851580	MLL3_10656	+	GTGACCTATGCACCAGACGTATAAACACACACATCAAAGTCTGCAAAATCCACCCTGGGGAGATCGGAAGAGCGGTTTCAG
chr7	151853153	151853192	MLL3_10657	+	GTGACCTATGCACCAGACGTAAAAACACAAAACCATAAATACATTGATCAATATTGATAAGATCGGAAGAGCGGTTTCAG
chr7	151853442	151853481	MLL3_10658	+	GTGACCTATGCACCAGACGTCCAAAAAATTTAAATTTATGCTACTGAGCGAATATGCAAGATCGGAAGAGCGGTTTCAG
chr7	151856168	151856207	MLL3_10659	+	GTGACCTATGCACCAGACGTTGAAAAGGGTAAAAAATAAGTGAACAATTTGATATTTGGAGATCGGAAGAGCGGTTTCAG
chr7	151860922	151860961	MLL3_10660	+	GTGACCTATGCACCAGACGTAAATGACTATTACTACTTATACAGCATAGGTAAGATCGGAAGAGCGGTTTCAG
chr7	151864474	151864513	MLL3_10661	+	GTGACCTATGCACCAGACGTATAAAATTCAGTTGTGTTAATTTTCAAAGAGTCCAACAAGATCGGAAGAGCGGTTTCAG
chr7	151866345	151866384	MLL3_10662	+	GTGACCTATGCACCAGACGTTAAAAATTTACAAATATGTTTATCCACATTTTCAGTTAAAGAGATCGGAAGAGCGGTTTCAG
chr7	151871338	151871377	MLL3_10663	+	GTGACCTATGCACCAGACGTAAATATAAAGTTACTTATTTTATAGTAATTAGTTCAACGTAAGATCGGAAGAGCGGTTTCAG
chr7	151877222	151877261	MLL3_10664	+	GTGACCTATGCACCAGACGTAGAAAACAAAAATCACTGGGATTTGTGGTAATTAATGGCTTAGATCGGAAGAGCGGTTTCAG
chr7	151879690	151879729	MLL3_10665	+	GTGACCTATGCACCAGACGTAGAAAAGAAAAAGCAATCATATTTAGTTAAGGAAGAAAAAGATCGGAAGAGCGGTTTCAG
chr7	151880252	151880291	MLL3_10666	+	GTGACCTATGCACCAGACGTAGAAAGAAAAAATTTCCAGATTTGTTAAATGTTTTAAGATCGGAAGAGCGGTTTCAG
chr7	151882727	151882766	MLL3_10667	+	GTGACCTATGCACCAGACGTAGAACAGAGTATAACACTTTCTCAGAGCCATGCTAATGATAGATCGGAAGAGCGGTTTCAG
chr7	151884572	151884611	MLL3_10668	+	GTGACCTATGCACCAGACGTATAAATATCTTTACTTTTATGAACATAAAAATACTTCTTAAAGATCGGAAGAGCGGTTTCAG
chr7	151884943	151884982	MLL3_10669	+	GTGACCTATGCACCAGACGTAAAAATAATTTCCGTTGGCATGATATTCACAAGTAACAAGGAGATCGGAAGAGCGGTTTCAG
chr7	151891224	151891263	MLL3_10670	+	GTGACCTATGCACCAGACGTAAACAATAATAGTAAACAAGATTAAGAGCTAGTAGGGTCCAGATCGGAAGAGCGGTTTCAG
chr7	151891357	151891396	MLL3_10671	+	GTGACCTATGCACCAGACGTTAAAAAATAAAGAAAAAGTAAACACTACTAATTCAGATCGGAAGAGCGGTTTCAG
chr7	151891664	151891703	MLL3_10672	+	GTGACCTATGCACCAGACGTAAAAAATAAATTTAAAGGTTACTTCAAGATCTCACACAGATCGGAAGAGCGGTTTCAG



chr7	151893107	151893146	MLL3_10673	+	GTGACCTATGCACCAGACGTTAAATATGTTTTTAAAAATTCAGTATTTCTCAGATATTAGATCGGAAGAGCGGTTTCAG
chr7	151896555	151896594	MLL3_10674	+	GTGACCTATGCACCAGACGTATAAGCACATACAAAATGGTTAGAAAATTTCTAAAAAGACAGATCGGAAGAGCGGTTTCAG
chr7	151900160	151900199	MLL3_10675	+	GTGACCTATGCACCAGACGTAGTCACATTTATAAATATGTGACATTTAAAAATTTCTAGACAGATCGGAAGAGCGGTTTCAG
chr7	151902321	151902360	MLL3_10676	+	GTGACCTATGCACCAGACGTAAGAAATTAGGTAAACTGATAAGTAATTTCTCCCTACATTAGATCGGAAGAGCGGTTTCAG
chr7	151904524	151904563	MLL3_10677	+	GTGACCTATGCACCAGACGTGTAATGTATACACAAAACCTGGAAGAACCTATCAAATATAAGATCGGAAGAGCGGTTTCAG
chr7	151917831	151917870	MLL3_10678	+	GTGACCTATGCACCAGACGTAATAAATCCCAAGGATCAAAAATTTAAACTTTTCAATTTAGATCGGAAGAGCGGTTTCAG
chr7	151919162	151919201	MLL3_10679	+	GTGACCTATGCACCAGACGTAAAAAATAAATCCAGGTAATTTCTTTTCAGAAAAGGTTAAAGTAGATCGGAAGAGCGGTTTCAG
chr7	151919778	151919817	MLL3_10680	+	GTGACCTATGCACCAGACGTCATATTTGTACATTTTTTTTTAAAAATGGAATACTGAGAGATCGGAAGAGCGGTTTCAG
chr7	151921275	151921314	MLL3_10681	+	GTGACCTATGCACCAGACGTAATCCCCCGAAAAGTCTCAATTTTATTTTCTAGTTACTAGATCGGAAGAGCGGTTTCAG
chr7	151921712	151921751	MLL3_10682	+	GTGACCTATGCACCAGACGTAAACAAACCAATCCATGTGATTTATGCATTAACCTAACATAAAGATCGGAAGAGCGGTTTCAG
chr7	151927123	151927162	MLL3_10683	+	GTGACCTATGCACCAGACGTGAAAACAGAACATATTTAAATGGAGACTAAGCTAAAAACAGATCGGAAGAGCGGTTTCAG
chr7	151927417	151927456	MLL3_10684	+	GTGACCTATGCACCAGACGTAAAAATACACAGAATACGAAGTTATATTTTTCACTTGTTTAGATCGGAAGAGCGGTTTCAG
chr7	151933029	151933068	MLL3_10685	+	GTGACCTATGCACCAGACGTGATTTGGGAAAAGTCAACATTTCTGTGACAGACCAAATAATAGATCGGAAGAGCGGTTTCAG
chr7	151935922	151935961	MLL3_10686	+	GTGACCTATGCACCAGACGTGCAGTTGAGAAAATAGATGTGTAATAACTCAGCAACATAAAAGATCGGAAGAGCGGTTTCAG
chr7	151945716	151945755	MLL3_10687	+	GTGACCTATGCACCAGACGTCAGAACATTTGTTATGGCAATGTACAACAAAATTTAAATAGATCGGAAGAGCGGTTTCAG
chr7	151947049	151947088	MLL3_10688	+	GTGACCTATGCACCAGACGTCACATTTATAAAAACTCTAAGGAGTCAAATTTCTGTAACAGATCGGAAGAGCGGTTTCAG
chr7	151948062	151948101	MLL3_10689	+	GTGACCTATGCACCAGACGTAATTTAATTTCTTTAGCTCAGAATGAGTTTTTTTCTTTGAGATCGGAAGAGCGGTTTCAG
chr7	151949186	151949225	MLL3_10690	+	GTGACCTATGCACCAGACGTAAGTATACTTAAATAAAAATTTCTAACATCGAGTTATATAGATCGGAAGAGCGGTTTCAG
chr7	151949811	151949850	MLL3_10691	+	GTGACCTATGCACCAGACGTGGAATAATAAATAAACAACAGTTTTGTTATGCATTTGTAAAGATCGGAAGAGCGGTTTCAG
chr7	151960226	151960265	MLL3_10692	+	GTGACCTATGCACCAGACGTAGATAGCATTATGATGCCTTATCTTTAAACTTATGTTTAGATCGGAAGAGCGGTTTCAG
chr7	151962305	151962344	MLL3_10693	+	GTGACCTATGCACCAGACGTCAGTGAAACAATGAAATGTTGTATAAGAAATTTAAATTTTAGATCGGAAGAGCGGTTTCAG
chr7	151970963	151971002	MLL3_10694	+	GTGACCTATGCACCAGACGTTAAAGGAGAGAAATCTCTTTATAAAACCTTGAAAAGGAATAGATCGGAAGAGCGGTTTCAG
chr7	152007171	152007210	MLL3_10695	+	GTGACCTATGCACCAGACGTAATAAATGAAAAGGAGCAAATGAGCAAACATAAAAAAATAGATCGGAAGAGCGGTTTCAG
chr7	152009042	152009081	MLL3_10696	+	GTGACCTATGCACCAGACGTAAATGAAAATAACTGTGAAAAGTGAACAAACAGCAAAAATTTAGATCGGAAGAGCGGTTTCAG
chr7	152012434	152012473	MLL3_10697	+	GTGACCTATGCACCAGACGTTGAAATGTAAGTCAGAGAAGGAGAAAAGTAGCTTTATTCAAGATCGGAAGAGCGGTTTCAG
chr7	152027835	152027874	MLL3_10698	+	GTGACCTATGCACCAGACGTGAAACAAGAGAAAACAAGAGTCAATTTTTGTTTATTATTAGATCGGAAGAGCGGTTTCAG
chr7	152055771	152055810	MLL3_10699	+	GTGACCTATGCACCAGACGTAAAAAATAAATAAGTACATAGAGTTAAATGTTAAATTTAGATCGGAAGAGCGGTTTCAG
chr7	152132882	152132921	MLL3_10700	+	GTGACCTATGCACCAGACGTAGGAAAAGCACATGGATCCCGGTCCTCCTCCTGGGGGCTAGATCGGAAGAGCGGTTTCAG
chr7	151945356	151945395	MLL3_10701	+	GTGACCTATGCACCAGACGTTTGTAGCCTTTCTATAACCAACTGTTCTCCTCAGGACATAAGATCGGAAGAGCGGTTTCAG
chr7	151845501	151845540	MLL3_10702	+	GTGACCTATGCACCAGACGTGGGCAAAGCATGTTTTGTCTTAAAAAACATGCATTTGTGAGATCGGAAGAGCGGTTTCAG
chr7	151845874	151845913	MLL3_10703	+	GTGACCTATGCACCAGACGTCATTTTCATCTCACAAGGTGGTTTTAAATGTCCCTTAGGAGATCGGAAGAGCGGTTTCAG
chr7	151859639	151859678	MLL3_10704	+	GTGACCTATGCACCAGACGTGGCCTGCTGCCATATTTGGGAGTGGATGGGCCACTGGTTTCAATCGGAAGAGCGGTTTCAG
chr7	151873741	151873780	MLL3_10705	+	GTGACCTATGCACCAGACGTTAATGTCTGAATTATCAGATTTCTCATTAGCAAGTAAACTAGATCGGAAGAGCGGTTTCAG
chr7	151878277	151878316	MLL3_10706	+	GTGACCTATGCACCAGACGTGCTGGTGGCTGAGAGTAAGGGCAGAAATTCAGGCTTTGAGATCGGAAGAGCGGTTTCAG
chr7	151860066	151860105	MLL3_10707	+	GTGACCTATGCACCAGACGTCACAGAAAATAAATTTAGGCTTCAACAAGGGATTGATGTTAGATCGGAAGAGCGGTTTCAG
chr7	151874196	151874235	MLL3_10708	+	GTGACCTATGCACCAGACGTATTGGAAGGTCTAGTTCCTCATTAAACATGCTTTTTCTTATAGATCGGAAGAGCGGTTTCAG
chr7	151878748	151878787	MLL3_10709	+	GTGACCTATGCACCAGACGTGCCTTGTATGCTGTGACACTGATCCATAAGGATCCTGAGAGATCGGAAGAGCGGTTTCAG
chr7	151860493	151860532	MLL3_10710	+	GTGACCTATGCACCAGACGTGGATTGTTGTCATCAAATTTCTACCCGAGGTGGTGGTCCACAGATCGGAAGAGCGGTTTCAG
chr7	151874651	151874690	MLL3_10711	+	GTGACCTATGCACCAGACGTTGGCACTTGTCCAAATCTGGGTGCACAGGTAGCTGATTAAGATCGGAAGAGCGGTTTCAG
chr7	151879219	151879258	MLL3_10712	+	GTGACCTATGCACCAGACGTGGAGTGGTCGAGGGTACCAACCATTTTGCATATGGATAGATCGGAAGAGCGGTTTCAG
chr3	49925006	49925045	MST1R_10713	+	GTGACCTATGCACCAGACGTAAAGGGATGTCAAGTTAAGGCAATTTCCACCAGGATTCAGATCGGAAGAGCGGTTTCAG
chr3	49927504	49927543	MST1R_10714	+	GTGACCTATGCACCAGACGTGGGGAGGTGAGGGGACTCAACTACCCCAAAATTTGGGGGAGATCGGAAGAGCGGTTTCAG
chr3	49928094	49928133	MST1R_10715	+	GTGACCTATGCACCAGACGTGGGAGAGGATCACACTTAGGACTGGCCCTTACCAGGCCCTAGATCGGAAGAGCGGTTTCAG
chr3	49928750	49928789	MST1R_10716	+	GTGACCTATGCACCAGACGTAGGTGGGTTGGTGGGCAAGGGCACAGCAGCTCCTTCTCCAAGATCGGAAGAGCGGTTTCAG
chr3	49929024	49929063	MST1R_10717	+	GTGACCTATGCACCAGACGTGCGCAAGTCAGGCAGGGCAGGGGCTCCCTTTATAAGGCAGATCGGAAGAGCGGTTTCAG
chr3	49929282	49929321	MST1R_10718	+	GTGACCTATGCACCAGACGTGTGCATAATGAGTCGATGAGGGGACTCCAGGCCAAGGAGATCGGAAGAGCGGTTTCAG
chr3	49932817	49932856	MST1R_10719	+	GTGACCTATGCACCAGACGTAGGGAAATGAGGAGCTTGATAGGGCAGGGGTGGCTTTAGCAGATCGGAAGAGCGGTTTCAG
chr3	49932992	49933031	MST1R_10720	+	GTGACCTATGCACCAGACGTAGAATCCTTGGTGGCTTGGCTTTCCAAGCTCCTAGGGGCCAGATCGGAAGAGCGGTTTCAG
chr3	49933324	49933363	MST1R_10721	+	GTGACCTATGCACCAGACGTGTGGCAACTCAGGCCAGCCTGTAGGCCCTCTGCCCGTGTAGATCGGAAGAGCGGTTTCAG
chr3	49933551	49933590	MST1R_10722	+	GTGACCTATGCACCAGACGTGGTCATGAGACCAGCCAGTGGCTGGCCCTACTTTTCAAGATCGGAAGAGCGGTTTCAG
chr3	49933848	49933887	MST1R_10723	+	GTGACCTATGCACCAGACGTCATATGAGATGATTAAGCCAGAACCCCACTGTGATTTAGATCGGAAGAGCGGTTTCAG
chr3	49934077	49934116	MST1R_10724	+	GTGACCTATGCACCAGACGTGGGTAGGTTAGGCTTTGGGTTGCTTCCAAGCTGGCTGATCGGAAGAGCGGTTTCAG
chr3	49934334	49934373	MST1R_10725	+	GTGACCTATGCACCAGACGTAAGAGATTGGGCTCAAGGTTACCCCTTTTGTGATGGCCAGATCGGAAGAGCGGTTTCAG
chr3	49934860	49934899	MST1R_10726	+	GTGACCTATGCACCAGACGTATAGAGGTGGCTTAGGCAGGTCCTCCACTCCAAGCCCTCAGATCGGAAGAGCGGTTTCAG
chr3	49935129	49935168	MST1R_10727	+	GTGACCTATGCACCAGACGTAGGGGAACCCCTGAGGTGAGCCAGGAATACACAGGCCAAGATCGGAAGAGCGGTTTCAG
chr3	49935655	49935694	MST1R_10728	+	GTGACCTATGCACCAGACGTGGAACAGCCCTGAGTCCATGTGGGGTTGGGCTCTCTCAAGATCGGAAGAGCGGTTTCAG
chr3	49936132	49936171	MST1R_10729	+	GTGACCTATGCACCAGACGTGAAGCAGGTGACTCAGGGTCCCTGGAGGGAGATCGGAAGAGCGGTTTCAG
chr3	49936439	49936478	MST1R_10730	+	GTGACCTATGCACCAGACGTTAGATGTGACAAAATGGGGTGGAGCAAGAGACCCAGGAGATCGGAAGAGCGGTTTCAG

chr3	49936707	49936746	MST1R_10731	+	GTGACCTATGCACCAGACGTTCCAGGGAAGGGGAGGAGTTCAGGGTTCAGCCTTGTCGCCCGAGATCGGAAGAGCGGTTTCAG
chr3	49941053	49941092	MST1R_10732	+	GTGACCTATGCACCAGACGTTGGGACCCTAGAGGATCCCTACCGGCCCTGGGCCTGGACCTAGATCGGAAGAGCGGTTTCAG
chr3	49940233	49940272	MST1R_10733	+	GTGACCTATGCACCAGACGTTGTACAGCTGGCCGGCTGTACAGTACAGGAGTATACGAAGAGATCGGAAGAGCGGTTTCAG
chr3	49940643	49940682	MST1R_10734	+	GTGACCTATGCACCAGACGTTGACCAGCGCAGGCAGCGCGGGATCCAGCACCGACCTTAGATCGGAAGAGCGGTTTCAG
chr1	155158696	155158735	MUC1_10735	+	GTGACCTATGCACCAGACGTTGGAAAAGAGATCCAGGGTGAGGAGCAAAGGTACCTCCTAAGATCGGAAGAGCGGTTTCAG
chr1	155159861	155159900	MUC1_10736	+	GTGACCTATGCACCAGACGTAGGAGGTTTGGCAGGCCATGGAGTGCCCTTACCAGGGGAGATCGGAAGAGCGGTTTCAG
chr1	155160063	155160102	MUC1_10737	+	GTGACCTATGCACCAGACGTAAAGCAGTGGTTCAGGGCAGCTCCAGAGGAGGGCCCTCAGATCGGAAGAGCGGTTTCAG
chr1	155160345	155160384	MUC1_10738	+	GTGACCTATGCACCAGACGTGAAAATGGGCACCTCAGCCACGGGTCCAGCTCCTGGCTCAAGATCGGAAGAGCGGTTTCAG
chr1	155160550	155160589	MUC1_10739	+	GTGACCTATGCACCAGACGTAGGGAAAGGACTCAGGCTTGATGCAAAGGGTGTGGACAGTAGATCGGAAGAGCGGTTTCAG
chr1	155160699	155160738	MUC1_10740	+	GTGACCTATGCACCAGACGTGGAATTAAGTGGAGGTTTTGAAATGTGAAAAGACAGGAAAAGATCGGAAGAGCGGTTTCAG
chr1	155160718	155160757	MUC1_10741	+	GTGACCTATGCACCAGACGTGAAATGTGAAAAGACAGGAAAAGAAAAGACCCCGATAGATCGGAAGAGCGGTTTCAG
chr1	155160772	155160811	MUC1_10742	+	GTGACCTATGCACCAGACGTGTCTGTGATTGGAGAGGTTGAGAGGAGTACCGTGCTATAGATCGGAAGAGCGGTTTCAG
chr1	155162085	155162124	MUC1_10743	+	GTGACCTATGCACCAGACGTTTTAGGGCTGTGGTAGCTGTAAAGAGTAAAGTCTATAGGATCGGAAGAGCGGTTTCAG
chr1	155162112	155162151	MUC1_10744	+	GTGACCTATGCACCAGACGTTTAAAGTCAAGGGTTGGTCTTTATGAAGAAAATAAGAGATCGGAAGAGCGGTTTCAG
chr1	155162645	155162684	MUC1_10745	+	GTGACCTATGCACCAGACGTAAATGGGTGGGAGGGGGCAGAACAGATTCAGGCAGGCGCAGATCGGAAGAGCGGTTTCAG
chr10	76603247	76603286	MYST4_10746	+	GTGACCTATGCACCAGACGTGAGTAATGTCTGTCATTCTCACTACTGTCCTTTTGTCTTAGATCGGAAGAGCGGTTTCAG
chr10	76719847	76719886	MYST4_10747	+	GTGACCTATGCACCAGACGTTTTTCCCTATGTGGTGTACAATGACTCCCATTTATCAGATCGGAAGAGCGGTTTCAG
chr10	76729544	76729583	MYST4_10748	+	GTGACCTATGCACCAGACGTCCCCGTAATCCCGCTCCAGTCACTTAATTCAGATAGATCGGAAGAGCGGTTTCAG
chr10	76729870	76729909	MYST4_10749	+	GTGACCTATGCACCAGACGTAAACTGTACTAAAGTATTTTTATTACATATTGGTTAGCAGATCGGAAGAGCGGTTTCAG
chr10	76732408	76732447	MYST4_10750	+	GTGACCTATGCACCAGACGTATCTTATCAAAAGAAATCATTTATGTTTTGCTTTAAATAAGATCGGAAGAGCGGTTTCAG
chr10	76736099	76736138	MYST4_10751	+	GTGACCTATGCACCAGACGTGGTCAAAGCTCCAACCAAACCTGCGTCCCGTCCCTTTCTCAGATCGGAAGAGCGGTTTCAG
chr10	76737206	76737245	MYST4_10752	+	GTGACCTATGCACCAGACGTGATCCACATTTAGTAGAAGTATAAGATGTGGCTTCTAAGATCGGAAGAGCGGTTTCAG
chr10	76739108	76739147	MYST4_10753	+	GTGACCTATGCACCAGACGTAAAGTCTGGCAGGTGATAACTTGAATGTACATATGTGAGAGATCGGAAGAGCGGTTTCAG
chr10	76741697	76741736	MYST4_10754	+	GTGACCTATGCACCAGACGTGTAATAAAAAAATTCAGCTTTTTGAAATCTAGTACTCCTAGATCGGAAGAGCGGTTTCAG
chr10	76745010	76745049	MYST4_10755	+	GTGACCTATGCACCAGACGTAGCCAGCATGACCTTCAATTTCTTTTTCAAATGTTTTGAGATCGGAAGAGCGGTTTCAG
chr10	76748881	76748920	MYST4_10756	+	GTGACCTATGCACCAGACGTTACTTTATTACTTTTCTGATCCAGGAAGCTGATGGCCGTAGATCGGAAGAGCGGTTTCAG
chr10	76780582	76780621	MYST4_10757	+	GTGACCTATGCACCAGACGTGGACCTGGGAGCTCCGTGGCTCAGGCATCCACACCCAGAGATCGGAAGAGCGGTTTCAG
chr10	76781054	76781093	MYST4_10758	+	GTGACCTATGCACCAGACGTTCTTTATCATCTAAGTTGTGTAACCTCAATCTTGTAGCAAGATCGGAAGAGCGGTTTCAG
chr10	76782000	76782039	MYST4_10759	+	GTGACCTATGCACCAGACGTGTTAGATTCTGTGAGTCGGCTTCAATCAAATCTTATAGATCGGAAGAGCGGTTTCAG
chr10	76785018	76785057	MYST4_10760	+	GTGACCTATGCACCAGACGTGAATGATAAAAACCTTACCCTTGAAGATGCTGTATCTGAAGATCGGAAGAGCGGTTTCAG
chr10	76790815	76790854	MYST4_10761	+	GTGACCTATGCACCAGACGTCAGTCCACAAAACCTACGGGGCATCACTATTGGATTGATCAGATCGGAAGAGCGGTTTCAG
chr10	76602936	76602975	MYST4_10762	+	GTGACCTATGCACCAGACGTGAATAAACTTTTAAAGGAGAGCAATTGAAGGACTTGAGGAGAGATCGGAAGAGCGGTTTCAG
chr10	76735633	76735672	MYST4_10763	+	GTGACCTATGCACCAGACGTCCACTTCTTCTCCCTCCTCCAGAGTTCTTCCAGCCAGTGTAGATCGGAAGAGCGGTTTCAG
chr10	76789109	76789148	MYST4_10764	+	GTGACCTATGCACCAGACGTAGAACAGGCCACGAGCAGGACCAAAAAGAACAGCAGGAAAGATCGGAAGAGCGGTTTCAG
chr10	76789535	76789574	MYST4_10765	+	GTGACCTATGCACCAGACGTGATGCCATCAGTTCAGATCATTCAAGCAAGTCTGATACAGATCGGAAGAGCGGTTTCAG
chr10	76789961	76790000	MYST4_10766	+	GTGACCTATGCACCAGACGTCTTATACGAGCGAATGGGTCAGAGTGATTTTTGGGGCTGGGAGATCGGAAGAGCGGTTTCAG
chr10	76790387	76790426	MYST4_10767	+	GTGACCTATGCACCAGACGTGCTGCCACCATCAGTCACAAATCTATGGCGCTCCCAGATCGGAAGAGCGGTTTCAG
chr12	78225495	78225534	NAV3_10768	+	GTGACCTATGCACCAGACGTGAAGTTACTGCAGACTTGTGTAGCTAAAATGCACATTTAGATCGGAAGAGCGGTTTCAG
chr12	78334227	78334266	NAV3_10769	+	GTGACCTATGCACCAGACGTCTTCTGAAAGAAAAGCATGAAAGTCTCTGCTCCCATCTCTAGATCGGAAGAGCGGTTTCAG
chr12	78334924	78334963	NAV3_10770	+	GTGACCTATGCACCAGACGTATTTATTCTCAATATATAATGCTATCTTCACTTCCAGAAGATCGGAAGAGCGGTTTCAG
chr12	78362493	78362532	NAV3_10771	+	GTGACCTATGCACCAGACGTGAAGTAGGGGAATGTGTTTCCAATGATTTGTGTAGATACAAGATCGGAAGAGCGGTTTCAG
chr12	78388662	78388701	NAV3_10772	+	GTGACCTATGCACCAGACGTATTCTCTAATTTATTGCTTATTAGTGATGCAAAATAAATAGATCGGAAGAGCGGTTTCAG
chr12	78392267	78392306	NAV3_10773	+	GTGACCTATGCACCAGACGTGTTACATCATTATGACACAAGTCCAACATGAGTCTTGTGAAGATCGGAAGAGCGGTTTCAG
chr12	78401236	78401275	NAV3_10774	+	GTGACCTATGCACCAGACGTCTCTGTTTTATCCACAGTTGTAATAATATTTACAGGCCCTACAGATCGGAAGAGCGGTTTCAG
chr12	78415653	78415692	NAV3_10775	+	GTGACCTATGCACCAGACGTTTCATCGATGCATAGGTCAAACCTAGGAATTTCCGTTACTTAGATCGGAAGAGCGGTTTCAG
chr12	78443892	78443931	NAV3_10776	+	GTGACCTATGCACCAGACGTATTTTGCATATTTGAGCCAAATAAGAAAATAAATACAGATCGGAAGAGCGGTTTCAG
chr12	78444938	78444977	NAV3_10777	+	GTGACCTATGCACCAGACGTCTGTTTCCGTCAGCATTGTGTGAAGAGGGGAGGTGGTCTAGATCGGAAGAGCGGTTTCAG
chr12	78452906	78452945	NAV3_10778	+	GTGACCTATGCACCAGACGTGATGATGATGAGTGAAGTAATTTATAGATCGGAAGAGCGGTTTCAG
chr12	78510695	78510734	NAV3_10779	+	GTGACCTATGCACCAGACGTCCACCTTTCTTTTTCCAGTGTCTTCCAGCTTTTTCCCCAGATCGGAAGAGCGGTTTCAG
chr12	78512088	78512127	NAV3_10780	+	GTGACCTATGCACCAGACGTGCTTTGGCAGCTGTTATGCAAAAGTGCTTTACTTTATTGTAGATCGGAAGAGCGGTTTCAG
chr12	78516219	78516258	NAV3_10781	+	GTGACCTATGCACCAGACGTCTGGAGCATTGATAACATCTTCCCCTCTTCCCTGCATAGATCGGAAGAGCGGTTTCAG
chr12	78520999	78521038	NAV3_10782	+	GTGACCTATGCACCAGACGTCCTCAGCAGTAATGCTACCTCTCTGTTGATGTAACCTAGATCGGAAGAGCGGTTTCAG
chr12	78522657	78522696	NAV3_10783	+	GTGACCTATGCACCAGACGTCTAAAATATTGATTTTTGTTTTGTTTCTTCCACCACCCTAGATCGGAAGAGCGGTTTCAG
chr12	78531156	78531195	NAV3_10784	+	GTGACCTATGCACCAGACGTAGGGGGATTAAAGATGAAGTCACTTTATTAAACCCTGAGAGATCGGAAGAGCGGTTTCAG
chr12	78534125	78534164	NAV3_10785	+	GTGACCTATGCACCAGACGTGCTGTAAAGAAAAGCTTTGCTTTTTGCCATTGCACACAGAAGATCGGAAGAGCGGTTTCAG
chr12	78540183	78540222	NAV3_10786	+	GTGACCTATGCACCAGACGTAATATGCAATTTTTAATTTTTCTATTTTTGATTGATTAGATCGGAAGAGCGGTTTCAG
chr12	78542710	78542749	NAV3_10787	+	GTGACCTATGCACCAGACGTTCAATTTTTAAAATATATTACAAACAAATTTTTATAGAGAAAAGATCGGAAGAGCGGTTTCAG
chr12	78553077	78553116	NAV3_10788	+	GTGACCTATGCACCAGACGTAATTTGCCACTGGAGTAAAAGAAAGACAGCAAATTTGATAGATCGGAAGAGCGGTTTCAG



chr5	176639207	176639246	NSD1_10847	+	GTGACCTATGCACCAGACGTCTAAATGTGATAAAAAAAAAAAAAAATTGGAGAAAAGTGCTGAAGATCGGAAGAGCGGTTTCAG
chr5	176662957	176662996	NSD1_10848	+	GTGACCTATGCACCAGACGTAAATTTTCAGCAAACCTTTCACCTGGTCCCTAGGAAACTGCAAAGATCGGAAGAGCGGTTTCAG
chr5	176665519	176665558	NSD1_10849	+	GTGACCTATGCACCAGACGTGTTGGGGTCTCAGTATTTGAGCAGATATGATTAGAGGAAGAGATCGGAAGAGCGGTTTCAG
chr5	176666877	176666916	NSD1_10850	+	GTGACCTATGCACCAGACGTTTTGTAAAGTTCTAAAAGAAATAAATCTCAGGAAATGAGAAAAGATCGGAAGAGCGGTTTCAG
chr5	176671282	176671321	NSD1_10851	+	GTGACCTATGCACCAGACGTGTTGAGATTTAAAAACGTAATGCAGTAGTAAGTTTGAAGTAGATCGGAAGAGCGGTTTCAG
chr5	176673808	176673847	NSD1_10852	+	GTGACCTATGCACCAGACGTGTTCTGTACTTTTCACCTTCTAAAGAGAACTACTTTTCAGATCGGAAGAGCGGTTTCAG
chr5	176675336	176675375	NSD1_10853	+	GTGACCTATGCACCAGACGTGTTTGCCCACTTGTTCATTCATGATGTTTCATCTTTAAAGATCGGAAGAGCGGTTTCAG
chr5	176678865	176678904	NSD1_10854	+	GTGACCTATGCACCAGACGTATCGAACGGTCTTCTCCAAAAGAAAGTTTGAATTTAAGAGATCGGAAGAGCGGTTTCAG
chr5	176684163	176684202	NSD1_10855	+	GTGACCTATGCACCAGACGTCTTATGTGGACAGTCTAATGTAAACCTCAGTTTAAATTAGATCGGAAGAGCGGTTTCAG
chr5	176687180	176687219	NSD1_10856	+	GTGACCTATGCACCAGACGTATTTCTTCTCTATTTGTAGTCTAAAAGGGGATTAATCAAGATCGGAAGAGCGGTTTCAG
chr5	176694730	176694769	NSD1_10857	+	GTGACCTATGCACCAGACGTAGAATAGCACTCATCTCTTTTACCATCCTCTGTTTCTTGAAGATCGGAAGAGCGGTTTCAG
chr5	176696819	176696858	NSD1_10858	+	GTGACCTATGCACCAGACGTCTTTTGTGTTCTCAGGCAACACAGACCTCTGTTACCTGAGATCGGAAGAGCGGTTTCAG
chr5	176700796	176700835	NSD1_10859	+	GTGACCTATGCACCAGACGTAAATCTTGGGGACCTCTCTAGAAAGAGAATGGAATAGCTAGATCGGAAGAGCGGTTTCAG
chr5	176707846	176707885	NSD1_10860	+	GTGACCTATGCACCAGACGTGCTAAATACCATACTTCTCCTCTTTGCAGTTGCTTGAGATCGGAAGAGCGGTTTCAG
chr5	176709593	176709632	NSD1_10861	+	GTGACCTATGCACCAGACGTGAAATGCTGTTTTCTACTGTTACAAGATTGTAATTTGTGAGATCGGAAGAGCGGTTTCAG
chr5	176710940	176710979	NSD1_10862	+	GTGACCTATGCACCAGACGTGTTTCAGGATCTGACAGTGCATCTGAATTTTCAGGGCTTTAGATCGGAAGAGCGGTTTCAG
chr5	176715937	176715976	NSD1_10863	+	GTGACCTATGCACCAGACGTCTAGACTTCTGCTTTGGGATTAGTGGTGCGGTCTCCCTAGATCGGAAGAGCGGTTTCAG
chr5	176719170	176719209	NSD1_10864	+	GTGACCTATGCACCAGACGTAAATCCATTTGACCGCTACTGCTTCTCCATCACTAGATCGGAAGAGCGGTTTCAG
chr5	176722471	176722510	NSD1_10865	+	GTGACCTATGCACCAGACGTGTCACATGACAAACAAGCTGCCCCAGGGTACCATTTGAGATCGGAAGAGCGGTTTCAG
chr5	176562578	176562617	NSD1_10866	+	GTGACCTATGCACCAGACGTGTGGACGATGCAGATGTAGATTTGAAATGGACCCAGAAAGATCGGAAGAGCGGTTTCAG
chr5	176721250	176721289	NSD1_10867	+	GTGACCTATGCACCAGACGTATAAGGTGAGAGACCTCGCTGGGTGAGGGACCAAATCCCAGATCGGAAGAGCGGTTTCAG
chr5	176721657	176721696	NSD1_10868	+	GTGACCTATGCACCAGACGTGACAGCCCTGTAGCTAAAGAAAAGCACTGAGGCCCTGTGGAGATCGGAAGAGCGGTTTCAG
chr5	176722064	176722103	NSD1_10869	+	GTGACCTATGCACCAGACGTGACCCAGGCCCTCTAGCCAAATCCCAGGCCCTGGTGAAGATCGGAAGAGCGGTTTCAG
chr5	176637074	176637113	NSD1_10870	+	GTGACCTATGCACCAGACGTACAGGGTCCACACTGCCCCAGAAAGTTTCTGTTTTCTAGATCGGAAGAGCGGTTTCAG
chr5	176637501	176637540	NSD1_10871	+	GTGACCTATGCACCAGACGTAAAGCCTCTCATTAGTAACTCACATACAGACCCTAATGGAGATCGGAAGAGCGGTTTCAG
chr5	176637928	176637967	NSD1_10872	+	GTGACCTATGCACCAGACGTATGAGAAAACAGGGATTCAAGTGACATAGAAACAGCAGTAGATCGGAAGAGCGGTTTCAG
chr5	176638355	176638394	NSD1_10873	+	GTGACCTATGCACCAGACGTGCAATATCTGCGGAGTTGCTGCTTCCCTACCTGGCTTAAGATCGGAAGAGCGGTTTCAG
chr5	176638782	176638821	NSD1_10874	+	GTGACCTATGCACCAGACGTCTTTTTGAAAACGGAAAGGCCAGAGCTGGACTCTGTAAGATCGGAAGAGCGGTTTCAG
chr11	117030750	117030789	PAFAH1B2_10875	+	GTGACCTATGCACCAGACGTAAAGGATGAGCGTGGTTCTTGGCTACTCATGTATATCCATAGATCGGAAGAGCGGTTTCAG
chr11	117031988	117032027	PAFAH1B2_10876	+	GTGACCTATGCACCAGACGTAGTTACTTGTCAATGTCATTAATCTTAAAGTCTGTTTTGGAAGATCGGAAGAGCGGTTTCAG
chr11	117034619	117034658	PAFAH1B2_10877	+	GTGACCTATGCACCAGACGTGTTGGTGGGTAGAGAGTTTGTATCTTTAGGTGAGCTGAGAGATCGGAAGAGCGGTTTCAG
chr11	117038426	117038465	PAFAH1B2_10878	+	GTGACCTATGCACCAGACGTTCAAGTGTAAATGACATCTCAGCTTCCCTCAGATCAGTTCTAAGATCGGAAGAGCGGTTTCAG
chr20	9520275	9520314	PAK7_10879	+	GTGACCTATGCACCAGACGTACACAGATACCAATCTGAGGCAACACAGACACCTAACCAGATCGGAAGAGCGGTTTCAG
chr20	9523378	9523417	PAK7_10880	+	GTGACCTATGCACCAGACGTACCCCTACTGGTTATCTCAGGCAAGGAGAAACATTCTGAAAGATCGGAAGAGCGGTTTCAG
chr20	9525152	9525191	PAK7_10881	+	GTGACCTATGCACCAGACGTAAAGGAATGAAACAACCTGCAATTTTAAAACAATGTCTGCAGATCGGAAGAGCGGTTTCAG
chr20	9538392	9538431	PAK7_10882	+	GTGACCTATGCACCAGACGTAAATAACATTTAAGGAACAAGACAGGTTTAAAGAACATCTTTAGATCGGAAGAGCGGTTTCAG
chr20	9543682	9543721	PAK7_10883	+	GTGACCTATGCACCAGACGTGGGAAATATACTTTGACTTGTGAAGATGAAGTTGCTTTTAGATCGGAAGAGCGGTTTCAG
chr20	9547042	9547081	PAK7_10884	+	GTGACCTATGCACCAGACGTAGACATGGATAGAGAATATTCACATGCTGGATCTGAATGCAGATCGGAAGAGCGGTTTCAG
chr20	9561588	9561627	PAK7_10885	+	GTGACCTATGCACCAGACGTTAGAGGGAATTTGTTTAAAGAAAATTTTCATGGATTTAAGATCGGAAGAGCGGTTTCAG
chr20	9624987	9625026	PAK7_10886	+	GTGACCTATGCACCAGACGTCTGGGAAATATAAATGGAAAAGGACGACCCATTTATATCAGATCGGAAGAGCGGTTTCAG
chr20	9561195	9561234	PAK7_10887	+	GTGACCTATGCACCAGACGTGAAAATCTGGCAAATCGGATTTCAAAGCTTACCTCAGATCGGAAGAGCGGTTTCAG
chr14	20811857	20811896	PARP2_10888	+	GTGACCTATGCACCAGACGTCAATATCGCGGGACGGCATCGCGGGGGCGGGCAGTCAGAAAGATCGGAAGAGCGGTTTCAG
chr14	20813257	20813296	PARP2_10889	+	GTGACCTATGCACCAGACGTAAAGTTCATGGGCCAGCAAAGGGTCTCTGGTAGGAGTGAAGATCGGAAGAGCGGTTTCAG
chr14	20813296	20813335	PARP2_10890	+	GTGACCTATGCACCAGACGTATCTGGGGATGATATCTTGTATTTTCAACTCCTATTTCTAGATCGGAAGAGCGGTTTCAG
chr14	20813634	20813673	PARP2_10891	+	GTGACCTATGCACCAGACGTCTGGAACCGATCTTCCAGTCCATGGATATCTCAGAGACATAGATCGGAAGAGCGGTTTCAG
chr14	20815083	20815122	PARP2_10892	+	GTGACCTATGCACCAGACGTAGAAGAGGTGACCAATATATTTAGACACTTCTTAGATCGGAAGAGCGGTTTCAG
chr14	20818792	20818831	PARP2_10893	+	GTGACCTATGCACCAGACGTTTATGAGATTTTATGAGTTGGCATTAGAAAGTCAGAAAGATCGGAAGAGCGGTTTCAG
chr14	20819292	20819331	PARP2_10894	+	GTGACCTATGCACCAGACGTAAAAGTGACTACAAAAAATATACCCTCCTCTTTCTTAGATAGATCGGAAGAGCGGTTTCAG
chr14	20822417	20822456	PARP2_10895	+	GTGACCTATGCACCAGACGTACATTTTCTCTGCATTCTCTCCTATAATTCCTAGCTCCAGATCGGAAGAGCGGTTTCAG
chr14	20823117	20823156	PARP2_10896	+	GTGACCTATGCACCAGACGTTGCTGTTACTCTCACTTTGTTCTTCTACCTATACATATCCAGATCGGAAGAGCGGTTTCAG
chr14	20823985	20824024	PARP2_10897	+	GTGACCTATGCACCAGACGTTATGATTTGAGACTTATATATCCCTTATACCAGTCTCCATAGATCGGAAGAGCGGTTTCAG
chr14	20824201	20824240	PARP2_10898	+	GTGACCTATGCACCAGACGTGATCATTTATTTTTCATATCTTGCACTTACCTTAACCACCTCAGATCGGAAGAGCGGTTTCAG
chr14	20824604	20824643	PARP2_10899	+	GTGACCTATGCACCAGACGTAGCTTTGCGTGTGGAAAGACACTCCTTGCCCGAAAAGTACAAGATCGGAAGAGCGGTTTCAG
chr14	20824859	20824898	PARP2_10900	+	GTGACCTATGCACCAGACGTTTGAAGTCTGGGAGGACACAGGGGAAAAGGGATACAGTAAAGATCGGAAGAGCGGTTTCAG
chr14	20825319	20825358	PARP2_10901	+	GTGACCTATGCACCAGACGTAGTATGTCTGTGATCTCTAGTTTATTAATCCAGTTTTTAGATCGGAAGAGCGGTTTCAG
chr14	20825690	20825729	PARP2_10902	+	GTGACCTATGCACCAGACGTAGAACCAGGAGGACTAGAAGACTCCTTTTGGCCAGATAAGAGATCGGAAGAGCGGTTTCAG
chr14	20825967	20826006	PARP2_10903	+	GTGACCTATGCACCAGACGTAAATAAACAGAGATCTGATCTTCAAGCAAAGAAATAAGAGATCGGAAGAGCGGTTTCAG
chr17	26881524	26881563	PIGS_10904	+	GTGACCTATGCACCAGACGTGAAGGGACAAAGGGTATACCAGTAAAGTCTTAGGCATTGGAGATCGGAAGAGCGGTTTCAG

chr17	26882090	26882129	PIGS_10905	+	GTGACCTATGCACCAGACGTATCGGAGTAAGATCAAGGTGGCTGAGACCACAAGGGCGGAAGATCGGAAGAGCGGTTTCAG
chr17	26883295	26883334	PIGS_10906	+	GTGACCTATGCACCAGACGTGAATGAGATTGCCACAACATCATAACCAGGCCCTTGCCAGAGATCGGAAGAGCGGTTTCAG
chr17	26887220	26887259	PIGS_10907	+	GTGACCTATGCACCAGACGTAGGAGTCAGGGAAAGTCAGAGGCTCTTTGTGGATCAAAGAAGAGATCGGAAGAGCGGTTTCAG
chr17	26888658	26888697	PIGS_10908	+	GTGACCTATGCACCAGACGTGAGCAAGAGACAGAATGCCATGGCTCAGAAAAGAAAGCCAGATCGGAAGAGCGGTTTCAG
chr17	26890551	26890590	PIGS_10909	+	GTGACCTATGCACCAGACGTGAACAGGTGGTACACCAAGAGCAAAACACCATTCATCTCAGATCGGAAGAGCGGTTTCAG
chr17	26890936	26890975	PIGS_10910	+	GTGACCTATGCACCAGACGTAAAGAAGTAGCAATGAAAGGGCAAGCATCATGCCCTAGATCGGAAGAGCGGTTTCAG
chr17	26897992	26898031	PIGS_10911	+	GTGACCTATGCACCAGACGTGAGCATCAGGGCCGTGAGTCTCCACCTTGCCGGGGGAGATCGGAAGAGCGGTTTCAG
chr17	26898217	26898256	PIGS_10912	+	GTGACCTATGCACCAGACGTGGGGAACCGACTGAGGGCCTGGA AACCGGGCTAGGGTACCGAGATCGGAAGAGCGGTTTCAG
chr17	26898525	26898564	PIGS_10913	+	GTGACCTATGCACCAGACGTGGCTGCTCCGGCCACCGTGGGGGCAGAGCTTCGTGAGCCTAGATCGGAAGAGCGGTTTCAG
chr12	133201407	133201446	POLE_10914	+	GTGACCTATGCACCAGACGTAAACAGGCACAGTGAGACCCAGTCCACTCAGAGAGAGGAGATCGGAAGAGCGGTTTCAG
chr12	133201591	133201630	POLE_10915	+	GTGACCTATGCACCAGACGTGCAGCCCGCTGGGCGCCAGCCCTCCCGCGCTGGCCAGACAGATCGGAAGAGCGGTTTCAG
chr12	133202367	133202406	POLE_10916	+	GTGACCTATGCACCAGACGTCAAGAGTGCAGAGTGCAGGCTCACCAGCCAGCCTCCAGACCACAAGATCGGAAGAGCGGTTTCAG
chr12	133202914	133202953	POLE_10917	+	GTGACCTATGCACCAGACGTACAGCCACATCGGGAAGGAGCTCCCGGGGCCCTCCCTGCAGATCGGAAGAGCGGTTTCAG
chr12	133209105	133209144	POLE_10918	+	GTGACCTATGCACCAGACGTAAAGGATGCTGAGGGAGGGGTCTGGGACCTGTCTGGCACTGAGATCGGAAGAGCGGTTTCAG
chr12	133209392	133209431	POLE_10919	+	GTGACCTATGCACCAGACGTGCACACACACCACAGGCCCTGAGTCGGGCTGCTGCAAAACAAGATCGGAAGAGCGGTTTCAG
chr12	133210975	133211014	POLE_10920	+	GTGACCTATGCACCAGACGTGACACAACCGCGGCTGTGTTTGACCATCGCGGCCCTGTAAGATCGGAAGAGCGGTTTCAG
chr12	133212621	133212660	POLE_10921	+	GTGACCTATGCACCAGACGTAGCATTTGAAGACGCTGCTTCAGTGAATCGACCTTGTCTAGATCGGAAGAGCGGTTTCAG
chr12	133214736	133214775	POLE_10922	+	GTGACCTATGCACCAGACGTGAGTAGTGAGATGCCGTGGAGCCACAGTATCGGAGAGAGATCGGAAGAGCGGTTTCAG
chr12	133215895	133215934	POLE_10923	+	GTGACCTATGCACCAGACGTAGGTGCACGACACCCTCGTACCCTCAGCCTCCACCGTGCAGATCGGAAGAGCGGTTTCAG
chr12	133218448	133218487	POLE_10924	+	GTGACCTATGCACCAGACGTAGACGCCATGCTCAGCCAGCATCTGCCAGCTCCAGCACCAGATCGGAAGAGCGGTTTCAG
chr12	133218994	133219033	POLE_10925	+	GTGACCTATGCACCAGACGTGCACAGGTCAGCACCAGGGGCACATCGCCGGGTCCAGAGAGAGATCGGAAGAGCGGTTTCAG
chr12	133219326	133219365	POLE_10926	+	GTGACCTATGCACCAGACGTGCAAAATGGAAGAAAGACCTGGGTGGACCCAGCCTCAAAGATCGGAAGAGCGGTTTCAG
chr12	133219593	133219632	POLE_10927	+	GTGACCTATGCACCAGACGTGCAGGCCACGTCAACCTCCCTCCGTCGGCAGGAGGAGTGGAGATCGGAAGAGCGGTTTCAG
chr12	133219927	133219966	POLE_10928	+	GTGACCTATGCACCAGACGTAAACAAGCCAGCTACCCCAAGATGTGGGAGGCAGGCACAAGATCGGAAGAGCGGTTTCAG
chr12	133220157	133220196	POLE_10929	+	GTGACCTATGCACCAGACGTGGGCAGACAGGCCGGCAAGGGCTGGATGTTGGGGGCTCTAGATCGGAAGAGCGGTTTCAG
chr12	133220574	133220613	POLE_10930	+	GTGACCTATGCACCAGACGTTACGACGATGATCTCGTCACTGGGCGTAAGTGGTAAATGCAGATCGGAAGAGCGGTTTCAG
chr12	133225669	133225708	POLE_10931	+	GTGACCTATGCACCAGACGTACACGGACATACAGCACATCACAGGACACACTGGAACCCAAAGATCGGAAGAGCGGTTTCAG
chr12	133226112	133226151	POLE_10932	+	GTGACCTATGCACCAGACGTTGGTGAGCACAGCCAGTGTGCAAGTGGTGAGATGGGAATGAGATCGGAAGAGCGGTTTCAG
chr12	133233855	133233894	POLE_10933	+	GTGACCTATGCACCAGACGTCCAACCCATCAGAGAGACCCCTGTGCTAATGCACAGAGATCGGAAGAGCGGTTTCAG
chr12	133234026	133234065	POLE_10934	+	GTGACCTATGCACCAGACGTAGGAACCGGCCACAGAAACACAGGTTGGCAGCAGCACAAGAGATCGGAAGAGCGGTTTCAG
chr12	133234567	133234606	POLE_10935	+	GTGACCTATGCACCAGACGTAAAGACAGGCACACAGCTCAGTAACAGTGA AAATCACCCAAAGATCGGAAGAGCGGTTTCAG
chr12	133236106	133236145	POLE_10936	+	GTGACCTATGCACCAGACGTACAATGGGTAA AACACTGCAGAAATCAAGGGGCAGAGTCTAGATCGGAAGAGCGGTTTCAG
chr12	133237761	133237800	POLE_10937	+	GTGACCTATGCACCAGACGTAAAAAAGGCAAGCACAGCAGTGGCAAGGAGCGCTGGGGAAGATCGGAAGAGCGGTTTCAG
chr12	133240745	133240784	POLE_10938	+	GTGACCTATGCACCAGACGTAGAGAGGAGCAAGGTCGTGAGTTCCTCCCTTTCCATTTCCACGATCGGAAGAGCGGTTTCAG
chr12	133241059	133241098	POLE_10939	+	GTGACCTATGCACCAGACGTACCAGAACTGGTGGGCTGGCTGGCTGCCATGCTCCTCCAGGAGATCGGAAGAGCGGTTTCAG
chr12	133242047	133242086	POLE_10940	+	GTGACCTATGCACCAGACGTGTAACATGGAGCACCTCACAGATCTTCCATTTTACATAGATCGGAAGAGCGGTTTCAG
chr12	133244245	133244284	POLE_10941	+	GTGACCTATGCACCAGACGTGGAGATGGGCAGAGCAGGTGGGTGAGATCTCCAGAGCAAGATCGGAAGAGCGGTTTCAG
chr12	133245099	133245138	POLE_10942	+	GTGACCTATGCACCAGACGTGGCAATGGGGGCAAGTTCAAAGGAGGCCACAGACACACCAGATCGGAAGAGCGGTTTCAG
chr12	133245334	133245373	POLE_10943	+	GTGACCTATGCACCAGACGTTGAGAAAGCACTTAGGGCTGGGCAGAGAGAGCTCCGACTCAGATCGGAAGAGCGGTTTCAG
chr12	133245536	133245575	POLE_10944	+	GTGACCTATGCACCAGACGTAGCGAACTCAGTAGAGGCTGGTACCAAAGCTTGCCTCTAGATCGGAAGAGCGGTTTCAG
chr12	133248919	133248958	POLE_10945	+	GTGACCTATGCACCAGACGTGATGAGACGAGGGGTGACAGGGGCAACACACCCACATAAGATCGGAAGAGCGGTTTCAG
chr12	133249436	133249475	POLE_10946	+	GTGACCTATGCACCAGACGTAAACAAAGGCTTCCAGCCAAAAGCAACACCAAAGGCCCTGAAGATCGGAAGAGCGGTTTCAG
chr12	133249874	133249913	POLE_10947	+	GTGACCTATGCACCAGACGTAAAGCCAGAGAGCAGGGCCATCAA AAATCAAGAGCCAGGAGATCGGAAGAGCGGTTTCAG
chr12	133250304	133250343	POLE_10948	+	GTGACCTATGCACCAGACGTAATGAGAAACAGAAAGCCAGGATGATTCTAACATGCAGCCCGAGATCGGAAGAGCGGTTTCAG
chr12	133252114	133252153	POLE_10949	+	GTGACCTATGCACCAGACGTAAAGAGGAGAGAGCAAGCAAGTGGCAGGTCAGGCTCTAATGAGATCGGAAGAGCGGTTTCAG
chr12	133252417	133252456	POLE_10950	+	GTGACCTATGCACCAGACGTGTCACAGACGTGTCAGAGGCTGTCCCTTCTTCTCAAGCAGATCGGAAGAGCGGTTTCAG
chr12	133252801	133252840	POLE_10951	+	GTGACCTATGCACCAGACGTTTCATTAGCAATCAGCACAAAGTCAGAGGCTGCAAAGCCAAAGATCGGAAGAGCGGTTTCAG
chr12	133253250	133253289	POLE_10952	+	GTGACCTATGCACCAGACGTAAATAAGCATAAAGCCAAGCTCTAACTCCCATTAGGCAGATCGGAAGAGCGGTTTCAG
chr12	133254040	133254079	POLE_10953	+	GTGACCTATGCACCAGACGTACAGTGTGCTAACTAGAGTTCATATCCAGGAAAGTCTAAGATCGGAAGAGCGGTTTCAG
chr12	133254316	133254355	POLE_10954	+	GTGACCTATGCACCAGACGTACAAGAGAGCAACTAACTCAGCTGCCAGGGTCTGGAGGAGAGATCGGAAGAGCGGTTTCAG
chr12	133256248	133256287	POLE_10955	+	GTGACCTATGCACCAGACGTAAGAGATCACGCTCATTTGTTCAAGAGAAATAGGACTTTAAGATCGGAAGAGCGGTTTCAG
chr12	133256643	133256682	POLE_10956	+	GTGACCTATGCACCAGACGTGACAATGAAAGGGCTTTCATTGGTAAATACATTTCTAGATCGGAAGAGCGGTTTCAG
chr12	133256819	133256858	POLE_10957	+	GTGACCTATGCACCAGACGTTCAACCAACCCATCCAGGGGTGATGAGAAAGAAGAAAGCGAAGATCGGAAGAGCGGTTTCAG
chr12	133257284	133257323	POLE_10958	+	GTGACCTATGCACCAGACGTATCAGTCAACACAGACACAAGACCATCTCTACACAGTAAAGATCGGAAGAGCGGTTTCAG
chr12	133257876	133257915	POLE_10959	+	GTGACCTATGCACCAGACGTGAAGGGAAACCCGCTGCTTAATTTGTAATGCCACTGCTGCAGATCGGAAGAGCGGTTTCAG
chr12	133263912	133263951	POLE_10960	+	GTGACCTATGCACCAGACGTGCTACCACCTCTGCTTCAGGGGAGAAATTTGGCCGCTCCAGATCGGAAGAGCGGTTTCAG
chr19	45883497	45883536	PPP1R13L_10961	+	GTGACCTATGCACCAGACGTACAGGATCTTCAGACATCGAGAGCTCCCACTCCATCAGATCGGAAGAGCGGTTTCAG
chr19	45885995	45886034	PPP1R13L_10962	+	GTGACCTATGCACCAGACGTCCACGGAGGGGAAGGTGAGAGCCTGGCCAGGGGTCCAGAGATCGGAAGAGCGGTTTCAG

chr19	45888997	45889036	PPP1R13L_10963	+	GTGACCTATGCACCAGACGTGGTGGGGGTTGCGGGGAACGATCGCTGAGAGGCTCGCCAGATCGGAAGAGCGGTTTCAG
chr19	45889226	45889265	PPP1R13L_10964	+	GTGACCTATGCACCAGACGTCGGGGGAGGGGGAAGACTCAGTCCCGCGGCTGGCATCTGCAGATCGGAAGAGCGGTTTCAG
chr19	45895609	45895648	PPP1R13L_10965	+	GTGACCTATGCACCAGACGTCAAGAGCCCATCAGAGGACAGGTCGCCAGGAGACCCAAAGATCGGAAGAGCGGTTTCAG
chr19	45899528	45899567	PPP1R13L_10966	+	GTGACCTATGCACCAGACGTGGAATCATTAGGGTCTGTGGGGCTGCCTCTCCTCCGGGTCAGATCGGAAGAGCGGTTTCAG
chr19	45899705	45899744	PPP1R13L_10967	+	GTGACCTATGCACCAGACGTGTTTCCAGGGAGGATGAGACGGGAGGGGTGGCGAGCCCCGAGATCGGAAGAGCGGTTTCAG
chr19	45900327	45900366	PPP1R13L_10968	+	GTGACCTATGCACCAGACGTGCCAGGGCTGTAGGGATGGATCAAAGGAGACATTAGTGGAGATCGGAAGAGCGGTTTCAG
chr19	45901416	45901455	PPP1R13L_10969	+	GTGACCTATGCACCAGACGTGGAGTGGAGTGGAGTGAAGGACCTGGCCCTCTGGCAGGGCCGGAGATCGGAAGAGCGGTTTCAG
chr19	45901587	45901626	PPP1R13L_10970	+	GTGACCTATGCACCAGACGTGGAGCGGGCGCCTGCATGGTGGGGAGGGAGGGAGCTGGCTAGATCGGAAGAGCGGTTTCAG
chr19	45900070	45900109	PPP1R13L_10971	+	GTGACCTATGCACCAGACGTGCCATCGAAGGCGCGGGGCCGGGGCGAGGTGCGCGGTCAGATCGGAAGAGCGGTTTCAG
chr8	30643834	30643873	PPP2CB_10972	+	GTGACCTATGCACCAGACGTCAAAAAAGGAAGCAATAAAGGATCTGACTTTTGCAAAGAAAGATCGGAAGAGCGGTTTCAG
chr8	30648842	30648881	PPP2CB_10973	+	GTGACCTATGCACCAGACGTAAAAAAATTTCATTTTTCATTATAATATTATGATTTTGAAGATCGGAAGAGCGGTTTCAG
chr8	30651605	30651644	PPP2CB_10974	+	GTGACCTATGCACCAGACGTAAAAAAGTACATGTACAATATTATCAGTCATACCTTTAGATCGGAAGAGCGGTTTCAG
chr8	30651808	30651847	PPP2CB_10975	+	GTGACCTATGCACCAGACGTTTAAACAAAAGAGAATGTATTTGTGTTTTACTAATCCAAAACAGATCGGAAGAGCGGTTTCAG
chr8	30655281	30655320	PPP2CB_10976	+	GTGACCTATGCACCAGACGTAGGAGTAAACCCATAGTAAAAATCACATTTTTACTAGTGTAGATCGGAAGAGCGGTTTCAG
chr8	30657282	30657321	PPP2CB_10977	+	GTGACCTATGCACCAGACGTAGTAAAATCAACAATTACAAGTAAAAACTATCATTTCTTAGATCGGAAGAGCGGTTTCAG
chr5	145969800	145969839	PPP2R2B_10978	+	GTGACCTATGCACCAGACGTGAGAGCAAAAGCAATGACATATCTTCACTGTCTTTTCTTTAGATCGGAAGAGCGGTTTCAG
chr5	145972636	145972675	PPP2R2B_10979	+	GTGACCTATGCACCAGACGTAAACATCGAGAAGGTCAGTTATTTTAAACAGTAATAGATCGGAAGAGCGGTTTCAG
chr5	145980034	145980073	PPP2R2B_10980	+	GTGACCTATGCACCAGACGTAAAGCAAAAGGCAAAATTTAATCTTCAACTCCATCACTGAAGATCGGAAGAGCGGTTTCAG
chr5	146017989	146018028	PPP2R2B_10981	+	GTGACCTATGCACCAGACGTGAGTCAAGGAAGGAACAGGAGAAGGAGGAGGAGCACTTGTAGATCGGAAGAGCGGTTTCAG
chr5	146030298	146030337	PPP2R2B_10982	+	GTGACCTATGCACCAGACGTAGAGAAACAATCATTTCAGAACCAAGATCTTCCATAGGAGATCGGAAGAGCGGTTTCAG
chr5	146070814	146070853	PPP2R2B_10983	+	GTGACCTATGCACCAGACGTCAACCAGATTAAAGTCAGAATTATAGTGAAGCAAGCTCAAGATCGGAAGAGCGGTTTCAG
chr5	146077718	146077757	PPP2R2B_10984	+	GTGACCTATGCACCAGACGTGGAATAACACAACAGATTAATCACAAGTACCAACTAGATCGGAAGAGCGGTTTCAG
chr5	146080716	146080755	PPP2R2B_10985	+	GTGACCTATGCACCAGACGTGAAGCAAAAGGCAATTAAGTAACTGCACACTTACTTTGAAGATCGGAAGAGCGGTTTCAG
chr5	146236109	146236148	PPP2R2B_10986	+	GTGACCTATGCACCAGACGTGGGCCAATTCTGCTGTGGTTCCTCCCTTAGATCGGAAGAGCGGTTTCAG
chr5	146257645	146257684	PPP2R2B_10987	+	GTGACCTATGCACCAGACGTCTTACTTGTGCGTGGGAACAGAGCCGGCAGACAAGTATCCAGATCGGAAGAGCGGTTTCAG
chr1	45288352	45288391	PTCH2_10988	+	GTGACCTATGCACCAGACGTACACCAGCCCCAGTAAAGCCACGGGCCCTGGGGCTCCCAGATCGGAAGAGCGGTTTCAG
chr1	45288851	45288890	PTCH2_10989	+	GTGACCTATGCACCAGACGTGGTGTGGGGGAGTCAGCCCAGGCCTGTCTGTGAGCCTGCAGATCGGAAGAGCGGTTTCAG
chr1	45289068	45289107	PTCH2_10990	+	GTGACCTATGCACCAGACGTAGAGTGGTCTGGAGCTCTCCTCTGCCAGTCATGGCCAGAGATCGGAAGAGCGGTTTCAG
chr1	45292070	45292109	PTCH2_10991	+	GTGACCTATGCACCAGACGTGAGGCTCACAGGGCTCCTGCCAGGAGGATGACAGCCAGATCGGAAGAGCGGTTTCAG
chr1	45292765	45292804	PTCH2_10992	+	GTGACCTATGCACCAGACGTAGAGAGGGCTGAAGGCCCTGGGCCAGGAGGCTGCAGCCAGATCGGAAGAGCGGTTTCAG
chr1	45292992	45293031	PTCH2_10993	+	GTGACCTATGCACCAGACGTCCAGGATAGGGTTCTATTAGCTGGTGGCCCCAGGGCTTTAGATCGGAAGAGCGGTTTCAG
chr1	45293397	45293436	PTCH2_10994	+	GTGACCTATGCACCAGACGTAGCAACTAAGCTGGAGACCCAGGGCTGCCCCAGCCAGATCGGAAGAGCGGTTTCAG
chr1	45293874	45293913	PTCH2_10995	+	GTGACCTATGCACCAGACGTTAGAGAGTGGATGACAGGCTGTGCTTGAATGCTGGTGTAGATCGGAAGAGCGGTTTCAG
chr1	45294097	45294136	PTCH2_10996	+	GTGACCTATGCACCAGACGTGACAGGAGGGGAATGAAGCTGGTCTGAGATCGGAAGAGCGGTTTCAG
chr1	45294314	45294353	PTCH2_10997	+	GTGACCTATGCACCAGACGTAGAGTGGGGCTGCCCTCAGGTCACAAAGGGAGGGCCGTAGATCGGAAGAGCGGTTTCAG
chr1	45294757	45294796	PTCH2_10998	+	GTGACCTATGCACCAGACGTAGAGGAGCGGGCAGCTGAGGACCCGTGAAGCCTGGTACTAGATCGGAAGAGCGGTTTCAG
chr1	45294995	45295034	PTCH2_10999	+	GTGACCTATGCACCAGACGTAAAGGGCAGTCTCAGGGCTCCCAGGGTGGGCACTGGTTGATCGGAAGAGCGGTTTCAG
chr1	45295216	45295255	PTCH2_11000	+	GTGACCTATGCACCAGACGTAGGGTGGATAGGAGGGGGCAGGAGGAGGGAATGCCCTCAGAGATCGGAAGAGCGGTTTCAG
chr1	45295444	45295483	PTCH2_11001	+	GTGACCTATGCACCAGACGTTGTGGGAGAACCAGGGGTGAGAGCTGGCCCAACACTGGAGATCGGAAGAGCGGTTTCAG
chr1	45295713	45295752	PTCH2_11002	+	GTGACCTATGCACCAGACGTACAGGAGGGTTAATGCTCAAGGCCCTGGCCGTGGATAACAGATCGGAAGAGCGGTTTCAG
chr1	45296726	45296765	PTCH2_11003	+	GTGACCTATGCACCAGACGTAGCCTATAGTTGGTGGGTCAGGAGCAAAAACCCAGCTAGATCGGAAGAGCGGTTTCAG
chr1	45297480	45297519	PTCH2_11004	+	GTGACCTATGCACCAGACGTTACCCCGGGCCACGTGAGTCTGCCCAACAACCTTTGTAGATCGGAAGAGCGGTTTCAG
chr1	45297727	45297766	PTCH2_11005	+	GTGACCTATGCACCAGACGTGAGGGGCATAGGAGATCAGCAGAAGAAGGGATTCCCACTAGATCGGAAGAGCGGTTTCAG
chr1	45298024	45298063	PTCH2_11006	+	GTGACCTATGCACCAGACGTAAACAGAGAAAGCTGGGGGGAAAGGGCCTAGGCGGGTCAAGATCGGAAGAGCGGTTTCAG
chr1	45307762	45307761	PTCH2_11007	+	GTGACCTATGCACCAGACGTAAAGAAAGGTCAGCCAGGCATCTGCCAACAATGCATGAAGATCGGAAGAGCGGTTTCAG
chr1	45308615	45308654	PTCH2_11008	+	GTGACCTATGCACCAGACGTATGGGGCCGCGGGCCGCCCAACCCGCTTATCTGGCCGAGATCGGAAGAGCGGTTTCAG
chr8	141675107	141675146	PTK2_11009	+	GTGACCTATGCACCAGACGTAGAATCACAAACAAATTTAGAACACACACAAGGATTTTTAGATCGGAAGAGCGGTTTCAG
chr8	141678534	141678573	PTK2_11010	+	GTGACCTATGCACCAGACGTAGAAGCCAGTCATTTTTCTGCTCTCCAGCAGATGGCTGAAGATCGGAAGAGCGGTTTCAG
chr8	141684514	141684553	PTK2_11011	+	GTGACCTATGCACCAGACGTAGAATGATTCCCAATTAAGTCATGTGCGTTAAGAAAGATTAAGATCGGAAGAGCGGTTTCAG
chr8	141685609	141685648	PTK2_11012	+	GTGACCTATGCACCAGACGTAGAAAAGTTCAGTCAATGCACCTGGTATATACACTTGGGCAAGATCGGAAGAGCGGTTTCAG
chr8	141696804	141696843	PTK2_11013	+	GTGACCTATGCACCAGACGTAAAAACAAAATCAAAATTTTCATTTTATTGAAAAATAGATCGGAAGAGCGGTTTCAG
chr8	141711132	141711171	PTK2_11014	+	GTGACCTATGCACCAGACGTGTTGAAAACAGCATATTAGCTCTCAATAGTCTATTTCATAGATCGGAAGAGCGGTTTCAG
chr8	141712817	141712856	PTK2_11015	+	GTGACCTATGCACCAGACGTGTAAGGAGGCAAGGTAATGTTCAACTATAACATCTGCACAAGATCGGAAGAGCGGTTTCAG
chr8	141716315	141716354	PTK2_11016	+	GTGACCTATGCACCAGACGTAAAGAGACATCATATGAATGAACCTTTTGATTTTGACAAAAGATCGGAAGAGCGGTTTCAG
chr8	141727819	141727858	PTK2_11017	+	GTGACCTATGCACCAGACGTAAACACATTTGCTTAGGGGAGCTGACAACCAGAGTTAGCAAGATCGGAAGAGCGGTTTCAG
chr8	141745565	141745604	PTK2_11018	+	GTGACCTATGCACCAGACGTGGAATGAAAACACAACAGTGCATGATGAAGAATTAAGATCGGAAGAGCGGTTTCAG
chr8	141749217	141749256	PTK2_11019	+	GTGACCTATGCACCAGACGTAATTTTAGAAAATAAATTTCCCTGTTGTTTATGCTTAAAGAAAGATCGGAAGAGCGGTTTCAG
chr8	141753440	141753479	PTK2_11020	+	GTGACCTATGCACCAGACGTAGAATTTAGACAAATAAGACTTAAATAAAGAAAACAAAACAGATCGGAAGAGCGGTTTCAG

chr8	141754877	141754916	PTK2_11021	+	GTGACCTATGCACCAGACGTAATGACCAAAAAGAAAAAAGAAATAGTGCCAAGATCGGAAGAGCGGTTTCAG
chr8	141762426	141762465	PTK2_11022	+	GTGACCTATGCACCAGACGTGAAATTATAGAATCACACACATGCACAAAAGGTTTTGCTAAGATCGGAAGAGCGGTTTCAG
chr8	141771372	141771411	PTK2_11023	+	GTGACCTATGCACCAGACGTAAATTCACACATCAATACTTAAGTAAAATATTCCAAATGTAGATCGGAAGAGCGGTTTCAG
chr8	141774400	141774439	PTK2_11024	+	GTGACCTATGCACCAGACGTAGAAAACAGATATGTTGAAAGAGGTTAAACATCTGACCTCCAGATCGGAAGAGCGGTTTCAG
chr8	141799636	141799675	PTK2_11025	+	GTGACCTATGCACCAGACGTCAAGAGCAAAAGCTGTAAGCCCTGCAATTTCCCCAGGACCCAGATCGGAAGAGCGGTTTCAG
chr8	141803494	141803533	PTK2_11026	+	GTGACCTATGCACCAGACGTAAAGAAAAGAGATGCATAAGGCTCTTTTCACTCCTTTTGAAGATCGGAAGAGCGGTTTCAG
chr8	141810686	141810725	PTK2_11027	+	GTGACCTATGCACCAGACGTAAAAGATAAAGAACAGACTTCATTGTTCTTCCCAGTAAGAGATCGGAAGAGCGGTTTCAG
chr8	141813760	141813799	PTK2_11028	+	GTGACCTATGCACCAGACGTGAAAGGTAAAATCTTTGACTACTCGGATAAAAACTCATTTAGATCGGAAGAGCGGTTTCAG
chr8	141828464	141828503	PTK2_11029	+	GTGACCTATGCACCAGACGTTGAAACAAGTGAGAACAGAGGTGGCAGAAGGAAAAAGAAAGATCGGAAGAGCGGTTTCAG
chr8	141829130	141829169	PTK2_11030	+	GTGACCTATGCACCAGACGTAAATTACCAAAACATCTTGTAAAATACAGCAATGAGTAAAAGATCGGAAGAGCGGTTTCAG
chr8	141840636	141840675	PTK2_11031	+	GTGACCTATGCACCAGACGTAAAAGAAAGCGTATTAACAAATAACACCACCAATCAATTAAGATCGGAAGAGCGGTTTCAG
chr8	141856432	141856471	PTK2_11032	+	GTGACCTATGCACCAGACGTGGAAGACATACATTTATATGTATATAAGGAATGTTTGTAGATCGGAAGAGCGGTTTCAG
chr8	141856788	141856827	PTK2_11033	+	GTGACCTATGCACCAGACGTAGGAATGGGAAAAACAGCAACTGTTTTAAAAGAAAAATATTAGATCGGAAGAGCGGTTTCAG
chr8	141874509	141874548	PTK2_11034	+	GTGACCTATGCACCAGACGTTTCAAAAACAGAACAAATTAGAAATCAGTCATTTTCTCAAAGATCGGAAGAGCGGTTTCAG
chr8	141900847	141900886	PTK2_11035	+	GTGACCTATGCACCAGACGTGATGCTAGGTATCTGTCAATTTCTGTAAAAGAACAATAAGATCGGAAGAGCGGTTTCAG
chr9	8317953	8317992	PTPRD_11036	+	GTGACCTATGCACCAGACGTCAATGAATGGGGAGAAAGCAAAAAGAGGGACCATGAGCATAAAGATCGGAAGAGCGGTTTCAG
chr9	8319977	8320016	PTPRD_11037	+	GTGACCTATGCACCAGACGTAAACAAGCGGATGTTACTGGGTGAGATGTTACAGCTCTTGAGATCGGAAGAGCGGTTTCAG
chr9	8331747	8331786	PTPRD_11038	+	GTGACCTATGCACCAGACGTAGAAGTGGGAAACACCTCCGCCCGCAAAAGAGAGCGGAGGAAAGATCGGAAGAGCGGTTTCAG
chr9	8339058	8339097	PTPRD_11039	+	GTGACCTATGCACCAGACGTAAAGATTAATGTTAAACTATGCAAAAGTATAAAGAACATTAGATCGGAAGAGCGGTTTCAG
chr9	8340480	8340519	PTPRD_11040	+	GTGACCTATGCACCAGACGTGAGAATGAAAAGAAATGTGTTAAAGTATTTAGAGAACATGCAGATCGGAAGAGCGGTTTCAG
chr9	8341279	8341318	PTPRD_11041	+	GTGACCTATGCACCAGACGTGGAIAAAAAAAAAAAGAAAAACCAACAAGATCATTTTCAGATCGGAAGAGCGGTTTCAG
chr9	8341989	8342028	PTPRD_11042	+	GTGACCTATGCACCAGACGTAAATAGAGAAGAAAAGCCCAATAAACCTATCAGAAAAATCAAGATCGGAAGAGCGGTTTCAG
chr9	8376101	8376140	PTPRD_11043	+	GTGACCTATGCACCAGACGTGGAATATCAGTCGAAATCTGTTTTCCAGCCTCAGGTGGAGATCGGAAGAGCGGTTTCAG
chr9	8376737	8376776	PTPRD_11044	+	GTGACCTATGCACCAGACGTCAAGTGCACACTCAGGGCAACTGCTCATCAATTTCTCTAAGATCGGAAGAGCGGTTTCAG
chr9	8389418	8389457	PTPRD_11045	+	GTGACCTATGCACCAGACGTAGGAGTGTTATTCAACCAGGTGAGCACATCACAAAGAGGAAAGATCGGAAGAGCGGTTTCAG
chr9	8404671	8404710	PTPRD_11046	+	GTGACCTATGCACCAGACGTAAAACAACATATACACAAAATCAATACTGAAAACCACAGATCGGAAGAGCGGTTTCAG
chr9	8436700	8436739	PTPRD_11047	+	GTGACCTATGCACCAGACGTAAAGCAAAGAAACACATTTGAAAACAAATGAAAATGATAGATCGGAAGAGCGGTTTCAG
chr9	8449848	8449887	PTPRD_11048	+	GTGACCTATGCACCAGACGTAAAATAGAAATTTAAGAAGAAAAGAAAATCAATTGAAACAGATCGGAAGAGCGGTTTCAG
chr9	8460582	8460621	PTPRD_11049	+	GTGACCTATGCACCAGACGTGCAGAGTCTATTTCAAGTATAAAATAATGACTTTCTAGATAGATCGGAAGAGCGGTTTCAG
chr9	8465686	8465725	PTPRD_11050	+	GTGACCTATGCACCAGACGTAAAAGTGGGAAACAGAAAAGCAACTGTAATAATAAACCAGAGATCGGAAGAGCGGTTTCAG
chr9	8471096	8471135	PTPRD_11051	+	GTGACCTATGCACCAGACGTATGAATAGATAAAAGTTAGGTTAGTTGAAAGGAGGAAAACAGATCGGAAGAGCGGTTTCAG
chr9	8484389	8484428	PTPRD_11052	+	GTGACCTATGCACCAGACGTAAAACCAATAAAAAAAAAAATCTGGTTATCAGAGAGGCAAAAGATCGGAAGAGCGGTTTCAG
chr9	8485335	8485374	PTPRD_11053	+	GTGACCTATGCACCAGACGTAGGAAAAACAGTGTATTTAAACTATTCTTAAAAACAGATGAAGATCGGAAGAGCGGTTTCAG
chr9	8486360	8486399	PTPRD_11054	+	GTGACCTATGCACCAGACGTGGGATGGAGTGTAAGCAACCACTGAACTGTTTACAAGATCGGAAGAGCGGTTTCAG
chr9	8492990	8493029	PTPRD_11055	+	GTGACCTATGCACCAGACGTAAAATAGAAATGCTGATTCAAAACATGCTACTAATGCTAGATCGGAAGAGCGGTTTCAG
chr9	8497279	8497318	PTPRD_11056	+	GTGACCTATGCACCAGACGTATAAGAAGGTTGGGAGGAAAACAAAATAAAAAAGAAAGATCGGAAGAGCGGTTTCAG
chr9	8499851	8499890	PTPRD_11057	+	GTGACCTATGCACCAGACGTATCATTGGATAAAAGAAATATAGGCACCTGTCCACCCTAGATCGGAAGAGCGGTTTCAG
chr9	8501070	8501109	PTPRD_11058	+	GTGACCTATGCACCAGACGTGATGAGTTAAAGGAGGATTTAAGTGAAGGACAGGAGTGAAGATCGGAAGAGCGGTTTCAG
chr9	8504416	8504455	PTPRD_11059	+	GTGACCTATGCACCAGACGTAAAGAGAATGTGGTCATCTTCAATTAAGGTTTCAATGAAATAGATCGGAAGAGCGGTTTCAG
chr9	8507445	8507484	PTPRD_11060	+	GTGACCTATGCACCAGACGTGGAGGCAATGATGAACTCACAAATCACCAGGATGATCAAGATCGGAAGAGCGGTTTCAG
chr9	8518440	8518479	PTPRD_11061	+	GTGACCTATGCACCAGACGTGGAAGATAAAAGACAAATGAACTACCCATCATCCCTATAATAAGATCGGAAGAGCGGTTTCAG
chr9	8521557	8521596	PTPRD_11062	+	GTGACCTATGCACCAGACGTACACAAGGGAAATGATAACATATACAAGGCAAGAAAAAGTAGATCGGAAGAGCGGTTTCAG
chr9	8523535	8523574	PTPRD_11063	+	GTGACCTATGCACCAGACGTGAGGGGTTTGTGATCGAGAACAATGAAATGAGGAAAGGAAAGATCGGAAGAGCGGTTTCAG
chr9	8525046	8525085	PTPRD_11064	+	GTGACCTATGCACCAGACGTATAAAATATATTGCCAAAGAGATGATCAGAGAAGGCTTTTCAGATCGGAAGAGCGGTTTCAG
chr9	8526655	8526694	PTPRD_11065	+	GTGACCTATGCACCAGACGTAAATGAATGCAAAATAAGATTAGAAAAGAAAGCATTAGTAGATCGGAAGAGCGGTTTCAG
chr9	8527364	8527403	PTPRD_11066	+	GTGACCTATGCACCAGACGTAAAATCAGAGAGAAAGACAGCAATAAAAAATATTATAGATCGGAAGAGCGGTTTCAG
chr9	8528790	8528829	PTPRD_11067	+	GTGACCTATGCACCAGACGTAAAGGTGATAGAAAACATTAGTTAATAAGTCAGATGCTCCAGATCGGAAGAGCGGTTTCAG
chr9	8633469	8633508	PTPRD_11068	+	GTGACCTATGCACCAGACGTAAACAATAGCTGTCACAGGTGTTGTTACAATTGTCTACCTAGATCGGAAGAGCGGTTTCAG
chr9	8636855	8636894	PTPRD_11069	+	GTGACCTATGCACCAGACGTAAAATAACATCACAGTTAAATTGAAAACGAAATACAGACAGATCGGAAGAGCGGTTTCAG
chr9	8733854	8733893	PTPRD_11070	+	GTGACCTATGCACCAGACGTGGCAGCAGCGTGCAGCAGCAGCTTGAATCACTGCCTCCGAGATCGGAAGAGCGGTTTCAG
chr9	8486066	8486105	PTPRD_11071	+	GTGACCTATGCACCAGACGTACTTCTGGAATGAAATCTCTTCCATCTCCTCCAGATCGGAAGAGCGGTTTCAG
chr9	8518149	8518188	PTPRD_11072	+	GTGACCTATGCACCAGACGTCTCTGAGGTTGTTGTCACAGGTTGCTGGAGGCCCCAGATCGGAAGAGCGGTTTCAG
chr14	68290355	68290394	RAD51L1_11073	+	GTGACCTATGCACCAGACGTTTTAACATTTTTATTGATAAGTTTTATGCACAAGTTAACTAGATCGGAAGAGCGGTTTCAG
chr14	68292305	68292344	RAD51L1_11074	+	GTGACCTATGCACCAGACGTATTTTATTATGATTTGATTATGAATGATTCTCATCTCATAGATCGGAAGAGCGGTTTCAG
chr14	68301924	68301963	RAD51L1_11075	+	GTGACCTATGCACCAGACGTAAATTTTTCGTACCTTCTTCCATTGACCTATAACCTTCAGAAGATCGGAAGAGCGGTTTCAG
chr14	68331867	68331906	RAD51L1_11076	+	GTGACCTATGCACCAGACGTTATTTTTCTATTATAATGTTTTACTTTTTGTAACCTATATAAGATCGGAAGAGCGGTTTCAG
chr14	68352716	68352755	RAD51L1_11077	+	GTGACCTATGCACCAGACGTTTAGATTTTTAGTTTTAGTAAGTGGCTGAAAGGTTTATGTAGATCGGAAGAGCGGTTTCAG
chr14	68758708	68758747	RAD51L1_11078	+	GTGACCTATGCACCAGACGTGTGCTGGAGAGGCTGAAACTTGACACTGACATAGAGCCAGATCGGAAGAGCGGTTTCAG

chr14	68878255	68878294	RAD51L1_11079	+	GTGACCTATGCACCAGACGTTGACAGTATTCTCTGACTATGAAGGTCGGGGAATGAGATAAGATCGGAAGAGCGGTTTCAG
chr14	68934978	68935017	RAD51L1_11080	+	GTGACCTATGCACCAGACGTTGGATTAAAGCCATTTCTTTAAAGCTTATGCTCAGTGCTGCCAGATCGGAAGAGCGGTTTCAG
chr7	151164308	151164347	RHEB_11081	+	GTGACCTATGCACCAGACGTAAGAACCACCAATCACAGTGTTAGTGTGAAGCCGAACCCAGATCGGAAGAGCGGTTTCAG
chr7	151167749	151167788	RHEB_11082	+	GTGACCTATGCACCAGACGTAATAAAAATTTAGTTAAAGTACTTTTGCTCTTCATTATATAAGATCGGAAGAGCGGTTTCAG
chr7	151168538	151168577	RHEB_11083	+	GTGACCTATGCACCAGACGTGAAAAAAGACAAACCAGTAAGTCCAGCATTTGTATTGCTAGATCGGAAGAGCGGTTTCAG
chr7	151168702	151168741	RHEB_11084	+	GTGACCTATGCACCAGACGTAAGAATAAATAGACATCCATTTTAAATGTTGAAGTTTGTAGATCGGAAGAGCGGTTTCAG
chr7	151174512	151174551	RHEB_11085	+	GTGACCTATGCACCAGACGTAAAAAATTTATCTTTGAGTAGTCTTCATATAGCATCACAAAAGATCGGAAGAGCGGTTTCAG
chr7	151181901	151181940	RHEB_11086	+	GTGACCTATGCACCAGACGTAAAGAAATTAACATTAGTTTAAAAAATTAACTCGAAAAAGATCGGAAGAGCGGTTTCAG
chr7	151188111	151188150	RHEB_11087	+	GTGACCTATGCACCAGACGTGAACAAGAGCTTAGTGTTGGCATATGAAGGTAAAAAGATCGGAAGAGCGGTTTCAG
chr3	49397826	49397865	RHOA_11088	+	GTGACCTATGCACCAGACGTAAAAAATAGTCCTTTTAGCTAATAGTGTGGCATACATAAGATCGGAAGAGCGGTTTCAG
chr3	49400070	49400109	RHOA_11089	+	GTGACCTATGCACCAGACGTAATGTAGAGAATTTGGGGATACATACAATTTCTATCTTGAAGATCGGAAGAGCGGTTTCAG
chr3	49405992	49406031	RHOA_11090	+	GTGACCTATGCACCAGACGTAAAAACAACCACAAGAGTCAAGGTTAATCCCCACCCCAAGATCGGAAGAGCGGTTTCAG
chr3	49413033	49413072	RHOA_11091	+	GTGACCTATGCACCAGACGTCAAAACACAGATTAACCTGCAATGCACAAGAAAGTCATAGATCGGAAGAGCGGTTTCAG
chr1	26863471	26863510	RPS6KA1_11092	+	GTGACCTATGCACCAGACGTTGGCCAGCACCCCTGAGCGAGGGGCTGTGGGGGATCCTGTTAGATCGGAAGAGCGGTTTCAG
chr1	26872537	26872576	RPS6KA1_11093	+	GTGACCTATGCACCAGACGTCGAATGTCTGGTCTGACCTGGCTGTGTCCCTTGACAGCAAGATCGGAAGAGCGGTTTCAG
chr1	26873485	26873524	RPS6KA1_11094	+	GTGACCTATGCACCAGACGTAGCCCATAGCTGTGAAGGCCAACACTCGTTCATGTTAGAGGTAGATCGGAAGAGCGGTTTCAG
chr1	26873772	26873811	RPS6KA1_11095	+	GTGACCTATGCACCAGACGTACACTCCCTGTGCGAGAACCCAGGCTGGCTGAGGGAGGCAGATCGGAAGAGCGGTTTCAG
chr1	26877979	26878018	RPS6KA1_11096	+	GTGACCTATGCACCAGACGTTGGCCCTGCCTAGCTTCTACCACCCACCCATCCTTCGCCCTAGATCGGAAGAGCGGTTTCAG
chr1	26878225	26878264	RPS6KA1_11097	+	GTGACCTATGCACCAGACGTATCTACTGCCAGAGGGCCCCGGGATGGAGCTGAGGGACGAAGATCGGAAGAGCGGTTTCAG
chr1	26879999	26880038	RPS6KA1_11098	+	GTGACCTATGCACCAGACGTCCCTCCAGCCCCACCCAGCCTCCCAGGGGAGGCCCTTTCAGATCGGAAGAGCGGTTTCAG
chr1	26880753	26880792	RPS6KA1_11099	+	GTGACCTATGCACCAGACGTGGCCCTGCCCCCTCGGGACCCAGGGGAGGACAGGACAAGAGATCGGAAGAGCGGTTTCAG
chr1	26881723	26881762	RPS6KA1_11100	+	GTGACCTATGCACCAGACGTGCCCTGCCCTGATAACAATGGACTCCTCCAAGCCCCAGCCAGATCGGAAGAGCGGTTTCAG
chr1	26882127	26882166	RPS6KA1_11101	+	GTGACCTATGCACCAGACGTCCAGCTCAGGGGAGGGGATGTGGCATGGGGAGCCGGTAAATCGGAAGAGCGGTTTCAG
chr1	26883220	26883259	RPS6KA1_11102	+	GTGACCTATGCACCAGACGTCCAGCCACCCACAGGGCTCGGGCAGGGCTCAGCCCTGGATCGGAAGAGCGGTTTCAG
chr1	26883602	26883641	RPS6KA1_11103	+	GTGACCTATGCACCAGACGTTATCTGTTTTGTCTGTCTTGGGCTGGTACAGGAGGGAAGCAGATCGGAAGAGCGGTTTCAG
chr1	26885439	26885478	RPS6KA1_11104	+	GTGACCTATGCACCAGACGTGAGGGGCTGCTGCTCCATTATCCTTTTCAAAGAATGGCAGATCGGAAGAGCGGTTTCAG
chr1	26887353	26887392	RPS6KA1_11105	+	GTGACCTATGCACCAGACGTTGACCACGTCTCGGCCAAGGCTGCTGGGTTGGGGGCAGGTAGATCGGAAGAGCGGTTTCAG
chr1	26887636	26887675	RPS6KA1_11106	+	GTGACCTATGCACCAGACGTGCTTAAAGACTGGGGTGGGGACAGGAACCTCAACTCTCAAGATCGGAAGAGCGGTTTCAG
chr1	26888165	26888204	RPS6KA1_11107	+	GTGACCTATGCACCAGACGTATTCGGGGAGGCAGTAGGGGATGCCAAGGGTCAATCATAGATCGGAAGAGCGGTTTCAG
chr1	26898112	26898151	RPS6KA1_11108	+	GTGACCTATGCACCAGACGTACGCTCCTCAGCTGTAAGAGTGAAGGGGAATGGAGCCAGATCGGAAGAGCGGTTTCAG
chr1	26898427	26898466	RPS6KA1_11109	+	GTGACCTATGCACCAGACGTCTGGCCCTGGACCCTCCCCACTCCTGCAGCCCTAGCACTTAGATCGGAAGAGCGGTTTCAG
chr1	26898795	26898834	RPS6KA1_11110	+	GTGACCTATGCACCAGACGTACGGGCTGCGTGGGCTTATTTGGAGGAGGGAGGCAGGGTCAGATCGGAAGAGCGGTTTCAG
chr1	26899863	26899902	RPS6KA1_11111	+	GTGACCTATGCACCAGACGTCTTTGGGCTGCTGGGCTCTGGGGGTCAGCCCAAGGTGGAGATCGGAAGAGCGGTTTCAG
chr1	26900742	26900742	RPS6KA1_11112	+	GTGACCTATGCACCAGACGTCATTCGGGCCACAGGGCTGTGCTAGCTTTGACACAGTCAGCAGATCGGAAGAGCGGTTTCAG
chr17	57987983	57988022	RPS6KB1_11113	+	GTGACCTATGCACCAGACGTATAAGAGATTTTCATTGTGTGTCTTCTTACAAGTAGGAGATCGGAAGAGCGGTTTCAG
chr17	57990176	57990215	RPS6KB1_11114	+	GTGACCTATGCACCAGACGTTTTTTGAAATGAGAGCTGTTGTCTGTCTTGAATAGATTGAAGATCGGAAGAGCGGTTTCAG
chr17	58003954	58003993	RPS6KB1_11115	+	GTGACCTATGCACCAGACGTAGAGTTTGGTGTAATTTTGCATTTGCTCCAGAACTGGAGATCGGAAGAGCGGTTTCAG
chr17	58007546	58007585	RPS6KB1_11116	+	GTGACCTATGCACCAGACGTTTTTTGTTGTTGCATAGATTCAGGTAATTAACAAGCAAAAGCAGATCGGAAGAGCGGTTTCAG
chr17	58009094	58009133	RPS6KB1_11117	+	GTGACCTATGCACCAGACGTACCGTAAACAATTTCTATAGTAAATAATCATCTTAAAAATCCAGATCGGAAGAGCGGTTTCAG
chr17	58011632	58011671	RPS6KB1_11118	+	GTGACCTATGCACCAGACGTTTAAACATAATGGTTTGGGGTAATAGCTAATTTACAGATCGGAAGAGCGGTTTCAG
chr17	58011896	58011935	RPS6KB1_11119	+	GTGACCTATGCACCAGACGTAGTTAAAAAGCTGCATTAATTGGTCTGTGCTGAGTCACAGATCGGAAGAGCGGTTTCAG
chr17	58012672	58012711	RPS6KB1_11120	+	GTGACCTATGCACCAGACGTTAAATGGTCACTGACACTACAAGATTCAATGACTAGGATTAGATCGGAAGAGCGGTTTCAG
chr17	58013649	58013688	RPS6KB1_11121	+	GTGACCTATGCACCAGACGTGCATCTTTGGTGTGTTGTTGGGGAAAGATAATGCTAGTTTTAAGATCGGAAGAGCGGTTTCAG
chr17	58018315	58018354	RPS6KB1_11122	+	GTGACCTATGCACCAGACGTGAATTTCCATGTAGTCAATGGGAAATTTTGTAGTGTGAGGATGAGATCGGAAGAGCGGTTTCAG
chr17	58022890	58022929	RPS6KB1_11123	+	GTGACCTATGCACCAGACGTCCTTTTCACTTTTTTTGTTTTTAAACAACCTACAAGATCGGAAGAGCGGTTTCAG
chr17	58024160	58024199	RPS6KB1_11124	+	GTGACCTATGCACCAGACGTCCTTTTAAGTAAATTAAGGCCAAAAAAGGTGAGAGGGAGATAGATCGGAAGAGCGGTTTCAG
chr8	92972756	92972795	RUNX1T1_11125	+	GTGACCTATGCACCAGACGTAGGCGAGAAGAAAGCAAGATCCCAAGTTAATCACTGTTAAAGATCGGAAGAGCGGTTTCAG
chr8	92983087	92983126	RUNX1T1_11126	+	GTGACCTATGCACCAGACGTGTCAGGCCAAACCAGACAAGAAAACCTCTCAGTTAGCCAGATCGGAAGAGCGGTTTCAG
chr8	92988212	92988251	RUNX1T1_11127	+	GTGACCTATGCACCAGACGTGATGGGAAGGGGTTGGAGAGAGGAGAGTACTGTAAGCAGATCGGAAGAGCGGTTTCAG
chr8	92998564	92998603	RUNX1T1_11128	+	GTGACCTATGCACCAGACGTAAGGGGAGAATAGGGAAAGACATATAATCATCACAATTAAGATCGGAAGAGCGGTTTCAG
chr8	92999211	92999250	RUNX1T1_11129	+	GTGACCTATGCACCAGACGTAGAGAAGGCTGAATAAACCCTAAAGCATTCAGTACACAACCAGATCGGAAGAGCGGTTTCAG
chr8	93004128	93004167	RUNX1T1_11130	+	GTGACCTATGCACCAGACGTAAAAACAAGAGTTTGTCTTCATCTATCCATGATTCAGAAACCAGATCGGAAGAGCGGTTTCAG
chr8	93017536	93017575	RUNX1T1_11131	+	GTGACCTATGCACCAGACGTATGACAGGAATGAGAGGACGGACTGAAAGTTTTCTTCTGTAGATCGGAAGAGCGGTTTCAG
chr8	93023330	93023369	RUNX1T1_11132	+	GTGACCTATGCACCAGACGTAAATATGTAGTATAAATACATTAGCTGTTGGTAAATAGTAGATCGGAAGAGCGGTTTCAG
chr8	93027059	93027098	RUNX1T1_11133	+	GTGACCTATGCACCAGACGTACAAAAATCAGAAGGAAGTCATAAACTTACAGAGAACATGAGATCGGAAGAGCGGTTTCAG
chr8	93029579	93029618	RUNX1T1_11134	+	GTGACCTATGCACCAGACGTTTTCTCAGTACGATCTGGAGGATGCCACCAAGAACATTAAGATCGGAAGAGCGGTTTCAG
chr8	93029602	93029641	RUNX1T1_11135	+	GTGACCTATGCACCAGACGTCCACCAGACATAAATTTTACTCCTTAAAGCACCTCAGTAGATCGGAAGAGCGGTTTCAG
chr8	93074791	93074830	RUNX1T1_11136	+	GTGACCTATGCACCAGACGTAGCCGTACCACACATAGAAATGGCTGTCTCCTAAAAGCAAGCAGATCGGAAGAGCGGTTTCAG



chr8	93088291	93088330	RUNX1T1_11137	+	GTGACCTATGCACCAGACGTTTCGCTCTGCTAATTTTCCTCTCTCTTTTCTGACTGGGACAAGATCGGAAGAGCGGTTTCAG
chr1	161284226	161284265	SDHC_11138	+	GTGACCTATGCACCAGACGTTGGGACTGGGAGTTGGTGCCTCGCGCCCTCCGGAGATCTGAGATCGGAAGAGCGGTTTCAG
chr1	161298298	161298337	SDHC_11139	+	GTGACCTATGCACCAGACGTATTCTGGAGCCAGAGAATCTAGAGGTAGTGGGTGAAAGTTAGATCGGAAGAGCGGTTTCAG
chr1	161310456	161310495	SDHC_11140	+	GTGACCTATGCACCAGACGTGTGTTTTACACACACATATGTGCTTCTTTGAAAACTTGAGATCGGAAGAGCGGTTTCAG
chr1	161326641	161326680	SDHC_11141	+	GTGACCTATGCACCAGACGTTCCGGATTGTCACATTTTCTCTGTGAAGGGAGTGGGGAGAAGATCGGAAGAGCGGTTTCAG
chr1	161332234	161332273	SDHC_11142	+	GTGACCTATGCACCAGACGTTCCAGCATCTCTCCACATATTTACATTCAACAGATCGGAAGAGCGGTTTCAG
chr1	161332341	161332380	SDHC_11143	+	GTGACCTATGCACCAGACGTATTCTTCAGATCTCCTTGGAGCAGTAGACTACCTGGTAGACAGATCGGAAGAGCGGTTTCAG
chr11	111957694	111957733	SDHD_11144	+	GTGACCTATGCACCAGACGTTTCCACCCCTGAGGTGCTTAGCGTAGCCTCCAGCCAGGGAAGATCGGAAGAGCGGTTTCAG
chr11	111958708	111958747	SDHD_11145	+	GTGACCTATGCACCAGACGTTCCATCGCTGCTGCTTTCTGGGCTCTAGCCATCTTTACCTAGATCGGAAGAGCGGTTTCAG
chr11	111959746	111959785	SDHD_11146	+	GTGACCTATGCACCAGACGTCAATTCCAAATATAGTTGCTGCTCAGTTTGTTTGCTGTGAGATCGGAAGAGCGGTTTCAG
chr11	111965705	111965744	SDHD_11147	+	GTGACCTATGCACCAGACGTTTCATACTTTGAAGAATTGATGTATGCCTCTTTGCCTCTGAGATCGGAAGAGCGGTTTCAG
chr10	88718586	88718625	SNCG_11148	+	GTGACCTATGCACCAGACGTATGGCAGGTTGGGACAGTGTGGTGCCCAAGGGTGAGTGAAGATCGGAAGAGCGGTTTCAG
chr10	88719442	88719481	SNCG_11149	+	GTGACCTATGCACCAGACGTCCAGGGCCAGGGGACACATGGGGATAGGACCCCTGGGGAGATCGGAAGAGCGGTTTCAG
chr10	88719896	88719935	SNCG_11150	+	GTGACCTATGCACCAGACGTGCCCTCAGACCTGCCAGTCTCTCCTGGGCCAGAAAAGGAGATCGGAAGAGCGGTTTCAG
chr10	88722443	88722482	SNCG_11151	+	GTGACCTATGCACCAGACGTGGCTCCTGGGGTGACCATGGGGGTTCTTGTTAGGGACAGATCGGAAGAGCGGTTTCAG
chr10	88722753	88722792	SNCG_11152	+	GTGACCTATGCACCAGACGTGCCACGTGGATGACCTGAAGAGCGCTCCTCTGCCCTTGAAGATCGGAAGAGCGGTTTCAG
chr12	93966823	93966862	SOCS2_11153	+	GTGACCTATGCACCAGACGTGATCGGCGCCGACGCTGCGGGAGGAGCGCCTCCCAAGAGATCGGAAGAGCGGTTTCAG
chr12	93968966	93969005	SOCS2_11154	+	GTGACCTATGCACCAGACGTTTTTTAAACATGTCTACATGAGTATCCGAATCGACAGATCGGAAGAGCGGTTTCAG
chr1	16174656	16174695	SPEN_11155	+	GTGACCTATGCACCAGACGTGAGGCCCGCGCCGCTCGCTCCTCGGGCGCCGCTTCCAGATCGGAAGAGCGGTTTCAG
chr1	16199642	16199681	SPEN_11156	+	GTGACCTATGCACCAGACGTAGGTTTCTGTAGGCAGGATTTTGTATTTGATATGGTGAAGATCGGAAGAGCGGTTTCAG
chr1	16203184	16203223	SPEN_11157	+	GTGACCTATGCACCAGACGTAGCCTTTTGTATAACAGATGAGCTAGCTTAAACAAATAGATCGGAAGAGCGGTTTCAG
chr1	16235987	16236026	SPEN_11158	+	GTGACCTATGCACCAGACGTGTGTAATGTCTTTCCCTCTGTGCTACTGAGGAATGAAGATCGGAAGAGCGGTTTCAG
chr1	16237807	16237846	SPEN_11159	+	GTGACCTATGCACCAGACGTAGCAAGCTGAGTTTGATTTACTCATCACACTGTTGAGATCGGAAGAGCGGTTTCAG
chr1	16242785	16242824	SPEN_11160	+	GTGACCTATGCACCAGACGTGTTTACTATGTAACAAATTTAGTCTTTGTCTATAACACATAGATCGGAAGAGCGGTTTCAG
chr1	16245557	16245596	SPEN_11161	+	GTGACCTATGCACCAGACGTTTGCATAAATTTATGTGCTGTTATGATTTGCTTTGTTTTAGATCGGAAGAGCGGTTTCAG
chr1	16246023	16246062	SPEN_11162	+	GTGACCTATGCACCAGACGTGTTTTGGTATGTGTTTCAGACTCTGACTCACTCGTCTTAGATCGGAAGAGCGGTTTCAG
chr1	16247489	16247528	SPEN_11163	+	GTGACCTATGCACCAGACGTTGACTTTAAACAGAAGCAAAAACAAAGTCTATTCAAAATCTAGATCGGAAGAGCGGTTTCAG
chr1	16248855	16248894	SPEN_11164	+	GTGACCTATGCACCAGACGTAAACTTACCAGTGAGCTTGATGTTTTAATAGTTTTAATAAGATCGGAAGAGCGGTTTCAG
chr1	16262772	16262811	SPEN_11165	+	GTGACCTATGCACCAGACGTGAGTATCTCCCATGCTGTTGGCATGTCTTGGGATGCGTGGAGATCGGAAGAGCGGTTTCAG
chr1	16264151	16264190	SPEN_11166	+	GTGACCTATGCACCAGACGTGCAGGGCTGCCCTTCTGGCCCCAAGTTTTATGCCATGAGATCGGAAGAGCGGTTTCAG
chr1	16264512	16264551	SPEN_11167	+	GTGACCTATGCACCAGACGTGAGGCCCGAGGTTGAGCAACTGCCCCACCTACAGGGAGGAAGAGATCGGAAGAGCGGTTTCAG
chr1	16265382	16265421	SPEN_11168	+	GTGACCTATGCACCAGACGTCTGTGTCCTTCCCTCACATGTACCCACAGGTGGGGCTGAGATCGGAAGAGCGGTTTCAG
chr1	16265933	16265972	SPEN_11169	+	GTGACCTATGCACCAGACGTGTTATACCTCAGTGAATCTTCCAGGGCTCTGCAGTAAAGATCGGAAGAGCGGTTTCAG
chr1	16255077	16255116	SPEN_11170	+	GTGACCTATGCACCAGACGTGTTGGAGCGCTATCAAAAATGAAAAGACAGATAAAGAAGATCGGAAGAGCGGTTTCAG
chr1	16255558	16255597	SPEN_11171	+	GTGACCTATGCACCAGACGTGGAAGGGGCTTCAAGCAATGTTGAAGTGGTGGAGAAAGATCGGAAGAGCGGTTTCAG
chr1	16256039	16256078	SPEN_11172	+	GTGACCTATGCACCAGACGTCAATCAAAAAGGCCATTTCCCTCAAACCACAGCTCAAACAGATCGGAAGAGCGGTTTCAG
chr1	16256520	16256559	SPEN_11173	+	GTGACCTATGCACCAGACGTCCAGTGTCCGACATGTTTCCCTCCATGAAGATGAGGATCCAGATCGGAAGAGCGGTTTCAG
chr1	16257001	16257040	SPEN_11174	+	GTGACCTATGCACCAGACGTCTAGTTCTTTAGAAAAGAAACAAATTTTACTCTTTTGAAGATCGGAAGAGCGGTTTCAG
chr1	16257482	16257521	SPEN_11175	+	GTGACCTATGCACCAGACGTTTCCATAGCAGATTTATGGAGCTCACACGGATGCAACAGAAGATCGGAAGAGCGGTTTCAG
chr1	16257963	16258002	SPEN_11176	+	GTGACCTATGCACCAGACGTCCCAGGCAGAGACAGTAGTCCAGAGCCTGACAGTACAGATCGGAAGAGCGGTTTCAG
chr1	16258444	16258483	SPEN_11177	+	GTGACCTATGCACCAGACGTGTAAGGAGCGTCTATGCAACCATGGAGTGCACCATGAAAACAGATCGGAAGAGCGGTTTCAG
chr1	16258925	16258964	SPEN_11178	+	GTGACCTATGCACCAGACGTGAGAAAAAACCGGCCCTGAAAAAACTCCAAATCAAAGAAGATCGGAAGAGCGGTTTCAG
chr1	16259406	16259445	SPEN_11179	+	GTGACCTATGCACCAGACGTATGACATTTCTGGGGAGCCAGAAAACCTCCAGCACCTCCAGATCGGAAGAGCGGTTTCAG
chr1	16259887	16259926	SPEN_11180	+	GTGACCTATGCACCAGACGTAAAGCAGAGTGAGAAAACCCCACTTCCACTCTCCTCAGTCAAGATCGGAAGAGCGGTTTCAG
chr1	16260368	16260407	SPEN_11181	+	GTGACCTATGCACCAGACGTTCTGCCCAAGTGTCACTTCCACAAGTGTCAACACGCAAGATCGGAAGAGCGGTTTCAG
chr1	16260849	16260888	SPEN_11182	+	GTGACCTATGCACCAGACGTATGTTCTCACACTGACTGACCGCACGGTGGGCACAGTATCGGAAGAGCGGTTTCAG
chr1	16261330	16261369	SPEN_11183	+	GTGACCTATGCACCAGACGTGCCCTCCATCCAAAGGCCCTCAAGCTCCTGCAGGCTATGCGAGATCGGAAGAGCGGTTTCAG
chr1	16261811	16261850	SPEN_11184	+	GTGACCTATGCACCAGACGTCTCGACCAAGTGGACCCGGGCCATCCTCATTCCCAAGGGAGATCGGAAGAGCGGTTTCAG
chr1	16262292	16262331	SPEN_11185	+	GTGACCTATGCACCAGACGTTGCACCCCTATACTGTGCCACGGATGTGAGGATCATGTTAGATCGGAAGAGCGGTTTCAG
chrX	48888123	48888162	TFE3_11186	+	GTGACCTATGCACCAGACGTTAGGGGTTGGGTGCAGGATAAGTAGGGTTTCCAGTCCCTCAGATCGGAAGAGCGGTTTCAG
chrX	48889070	48889109	TFE3_11187	+	GTGACCTATGCACCAGACGTCAAGTGGGAGGCAAGCAGAAATGCCACATGAGGAGTTTTCAGATCGGAAGAGCGGTTTCAG
chrX	48891066	48891105	TFE3_11188	+	GTGACCTATGCACCAGACGTGGGAGGAGGAGAAAGAGGATGGGAAAGAGTTGTCAATAGATCGGAAGAGCGGTTTCAG
chrX	48891308	48891347	TFE3_11189	+	GTGACCTATGCACCAGACGTGTTGAGTGTAGCAGGCCCTCTGAGCACAGGAAGGCAAGAAAAGATCGGAAGAGCGGTTTCAG
chrX	48891777	48891816	TFE3_11190	+	GTGACCTATGCACCAGACGTAGAGGGCAGAGAACCACCAGTTGGGAACAAACCAGGCTTAGATCGGAAGAGCGGTTTCAG
chrX	48895650	48895689	TFE3_11191	+	GTGACCTATGCACCAGACGTAAGTAAATATTATACAGGTTTAGAAGAAATTTGGGAGGGGAAAGATCGGAAGAGCGGTTTCAG
chrX	48895978	48896017	TFE3_11192	+	GTGACCTATGCACCAGACGTAGGTAGACAAGGAAAGAGAGGGGCAAGGCAGAACAGACAGATCGGAAGAGCGGTTTCAG
chrX	48896946	48896985	TFE3_11193	+	GTGACCTATGCACCAGACGTGGAATTTGGGCCATATTTAGTAAAGTCTCAAGATCGGAAGAGCGGTTTCAG
chrX	48898106	48898145	TFE3_11194	+	GTGACCTATGCACCAGACGTGGTAGAGTGGTGTGATTGATGAAGGACCTTATTCAGATCGGAAGAGCGGTTTCAG

chrX	48900763	48900802	TFE3_11195	+	GTGACCTATGCACCAGACGTCCCCGGGCGAGCCCTGCCAGGCCGGTCCGGCCCTCGGCCCGGAGATCGGAAGAGCGGTTCCAG
chr9	101891393	101891432	TGFBR1_11196	+	GTGACCTATGCACCAGACGTTAAAATTTTTTCCCTAGATACACAAGAAAACTCTTCATAGATCGGAAGAGCGGTTCCAG
chr9	101895032	101895071	TGFBR1_11197	+	GTGACCTATGCACCAGACGTTGTCTCTCTTTTTCTAAGACATCTTTTTAAAATTAAGCAGATCGGAAGAGCGGTTCCAG
chr9	101900382	101900421	TGFBR1_11198	+	GTGACCTATGCACCAGACGTTTTGCTTTTCCTTATGTTATATATAACAAGATCTCTTAAAGATCGGAAGAGCGGTTCCAG
chr9	101904996	101905035	TGFBR1_11199	+	GTGACCTATGCACCAGACGTAAGCAGTCTATTATTTAAGCTTTAAATTTTCATGAATAAAGATCGGAAGAGCGGTTCCAG
chr9	101907181	101907220	TGFBR1_11200	+	GTGACCTATGCACCAGACGTGAACAACATATATTAATCTTCTGAATCACCTTTTTTCAGATCGGAAGAGCGGTTCCAG
chr9	101908902	101908941	TGFBR1_11201	+	GTGACCTATGCACCAGACGTCCTCTCCCTCAGTAGTTGTATGATGAGCAGAAGTTGTTTCAGATCGGAAGAGCGGTTCCAG
chr9	101910077	101910116	TGFBR1_11202	+	GTGACCTATGCACCAGACGTCTTTTGATATTAGCAATTTTTCTAACTGCTTCTGCTTAAAGATCGGAAGAGCGGTTCCAG
chr9	101911598	101911637	TGFBR1_11203	+	GTGACCTATGCACCAGACGTTTGCCTGAACTCTCTTTTTTCTCAGATCTGCTCCTGGGAGATCGGAAGAGCGGTTCCAG
chr10	102896681	102896720	TLX1_11204	+	GTGACCTATGCACCAGACGTTCTGCCCTGTGGGACCCAGGCCACTCAGGGGTCACTGAAGATCGGAAGAGCGGTTCCAG
chr10	102891593	102891632	TLX1_11205	+	GTGACCTATGCACCAGACGTGGCTCCTACAACGTGAACATGGCCTTGGCAGGCCGCCCGGAGATCGGAAGAGCGGTTCCAG
chr3	195591069	195591108	TNK2_11206	+	GTGACCTATGCACCAGACGTGGAAACCACCAGCACAGTTAAACAGTTTACAGAAGGTTCAAGATCGGAAGAGCGGTTCCAG
chr3	195593898	195593937	TNK2_11207	+	GTGACCTATGCACCAGACGTGGGTGGCGGCCATGACACGCGGGCCAGGGCCACTAGATCGGAAGAGCGGTTCCAG
chr3	195594140	195594179	TNK2_11208	+	GTGACCTATGCACCAGACGTGCACACCCACCCTGTGACGACCACTAGGGCCCACTGCTCAGATCGGAAGAGCGGTTCCAG
chr3	195595591	195595630	TNK2_11209	+	GTGACCTATGCACCAGACGTAAGGGAGAGCCCAACAGGAAGGCAGTCAAGCAGGGTCTGGAGATCGGAAGAGCGGTTCCAG
chr3	195596423	195596462	TNK2_11210	+	GTGACCTATGCACCAGACGTGGCCATGCGGCACAGGGGGAGAGACAGCGGAGACAGAGATCGGAAGAGCGGTTCCAG
chr3	195597087	195597126	TNK2_11211	+	GTGACCTATGCACCAGACGTGAGAGCTGGGTCAAGAGAGCAGGGGAAGCGTGTGGAGGGGAGATCGGAAGAGCGGTTCCAG
chr3	195599352	195599391	TNK2_11212	+	GTGACCTATGCACCAGACGTGAGATGGCAGGTCAGTGGACGCCAGGGTGGCGGGGAGATCGGAAGAGCGGTTCCAG
chr3	195605229	195605268	TNK2_11213	+	GTGACCTATGCACCAGACGTAGGAAGTCTGTGCCAACTCTGGGACTGACGCCTGGGTAGAGATCGGAAGAGCGGTTCCAG
chr3	195605474	195605513	TNK2_11214	+	GTGACCTATGCACCAGACGTGGAGGTGCAGAGTTTACGACAAACAGAGCGCCAGCCCTAGATCGGAAGAGCGGTTCCAG
chr3	195606057	195606096	TNK2_11215	+	GTGACCTATGCACCAGACGTGAGGGTCAAAGAGAAAGCCCTCTCAACACCTACCTGCGAGATCGGAAGAGCGGTTCCAG
chr3	195609210	195609249	TNK2_11216	+	GTGACCTATGCACCAGACGTGGAGGAGGCAGGAGGAATGAGCTGGAGGACCCCTGCCCTTAGATCGGAAGAGCGGTTCCAG
chr3	195610191	195610230	TNK2_11217	+	GTGACCTATGCACCAGACGTGGGATTTGCAAGGACTCAGGACTTGCAGGTCAGACAGATCGGAAGAGCGGTTCCAG
chr3	195611915	195611954	TNK2_11218	+	GTGACCTATGCACCAGACGTGGCAGCGGGCCAGATGGAATCCAACACCCAGGGTCAAGATCGGAAGAGCGGTTCCAG
chr3	195613929	195613968	TNK2_11219	+	GTGACCTATGCACCAGACGTAGCGGGAAACCGCTGCTGTGAAGGCCGCGTAGCCCGAGAGATCGGAAGAGCGGTTCCAG
chr3	195615470	195615509	TNK2_11220	+	GTGACCTATGCACCAGACGTCCCAGCCTCTGTGGGGGAGGAGTGGCTCAGGGACAAGGGAGATCGGAAGAGCGGTTCCAG
chr3	195615488	195615527	TNK2_11221	+	GTGACCTATGCACCAGACGTAGGAGTGGCTCAGGGACAAGGGTTGTGGGGGGACAACAGGAGATCGGAAGAGCGGTTCCAG
chr3	195622298	195622337	TNK2_11222	+	GTGACCTATGCACCAGACGTTGCAGGGCCGCTACTGCGCTCAGCCCCATAGCCTCATCAGATCGGAAGAGCGGTTCCAG
chr3	195594691	195594730	TNK2_11223	+	GTGACCTATGCACCAGACGTAGGTGAGCTTGCAGCAGGGGAGGCGGAGATCGGAAGAGCGGTTCCAG
chr3	195595140	195595179	TNK2_11224	+	GTGACCTATGCACCAGACGTGCGCAGGGACCCCGCGCCACGACGGTGTGTTGATGGAAGATCGGAAGAGCGGTTCCAG
chr19	54072650	54072689	ZNF331_11225	+	GTGACCTATGCACCAGACGTATTTCTCTTCTTCTTCTGAGCTATGATATTTGCGTCTGTAGATCGGAAGAGCGGTTCCAG
chr19	54074995	54075034	ZNF331_11226	+	GTGACCTATGCACCAGACGTGCCTCAGATAACTTAGACTGCCTCCTGGAATATCCGCTCAGATCGGAAGAGCGGTTCCAG
chr19	54080379	54080418	ZNF331_11227	+	GTGACCTATGCACCAGACGTTGTAAGACTGTGGGAAGGCTTTTTCGATGGGGCTCAAGCCAGATCGGAAGAGCGGTTCCAG
chr19	54080797	54080836	ZNF331_11228	+	GTGACCTATGCACCAGACGTAATGTAAGGAGTGTGGGAAGGCTTTTCGCTGGGGTTCAGAGATCGGAAGAGCGGTTCCAG
chr11	10327356	10327395	ADM_11229	+	GTGACCTATGCACCAGACGTGCAGCGCTTCCCCTTTGCTGGTACTGGCAGGCAAGGGGAGATCGGAAGAGCGGTTCCAG
chr11	10327656	10327695	ADM_11230	+	GTGACCTATGCACCAGACGTCTGTGCTGTCCAGGGACGGGAGGGAAGGAGTGTGCGGAGATCGGAAGAGCGGTTCCAG
chr11	10328199	10328238	ADM_11231	+	GTGACCTATGCACCAGACGTCCCATGGTACAAGGAATAGTCGCGCAAGCATCCCCTGGTATCGGAAGAGCGGTTCCAG
chr14	20923873	20923912	APEX1_11232	+	GTGACCTATGCACCAGACGTGAAATCAGCCCTTCTTCTTAGAAGCTGCGGCGGGGTGTATAGATCGGAAGAGCGGTTCCAG
chr14	20924271	20924310	APEX1_11233	+	GTGACCTATGCACCAGACGTTTTGAGGGAAAGAGACATTTTTTAGTATTGAATGGTCTTAAGATCGGAAGAGCGGTTCCAG
chr14	20925030	20925069	APEX1_11234	+	GTGACCTATGCACCAGACGTATTGATCCTAATGCCTGAACTTCAAACCAATTGCTAAGATCGGAAGAGCGGTTCCAG
chr14	20925678	20925717	APEX1_11235	+	GTGACCTATGCACCAGACGTAATCACTTTGAGCCTGGGAAATAAGCCCCCTCAACTACAGATCGGAAGAGCGGTTCCAG
chr14	20925419	20925458	APEX1_11236	+	GTGACCTATGCACCAGACGTGCCAAAGGCTTCGGGGAAATTACTGCAGGCTGTGCCACTGGAGATCGGAAGAGCGGTTCCAG
chr19	41725393	41725432	AXL_11237	+	GTGACCTATGCACCAGACGTGGGGCTCCTTGGGGCAGGGATCCCTCGGAGGGGCTGGGAGATCGGAAGAGCGGTTCCAG
chr19	41726774	41726813	AXL_11238	+	GTGACCTATGCACCAGACGTACATCCCCGAATCCCACCTCCCTGTCACACAGAGGGAGATCGGAAGAGCGGTTCCAG
chr19	41727162	41727201	AXL_11239	+	GTGACCTATGCACCAGACGTGGGTGAGGGTCTGAGGGTCCAGGGACATGTGGCGCTCAGATCGGAAGAGCGGTTCCAG
chr19	41727972	41728011	AXL_11240	+	GTGACCTATGCACCAGACGTGGATGTGGGTGAGTCCGGAAGGGGCGGGCAGGGTCAAGATCGGAAGAGCGGTTCCAG
chr19	41736963	41737002	AXL_11241	+	GTGACCTATGCACCAGACGTTGGGAGGTGGGGAGCTGGCGTCAGAGGGTGGGGTTGGGAGATCGGAAGAGCGGTTCCAG
chr19	41737214	41737253	AXL_11242	+	GTGACCTATGCACCAGACGTCAAACCTTGGTTCACTTTCAGTCTCAGGCCTCCTCCACCCAAGATCGGAAGAGCGGTTCCAG
chr19	41744070	41744109	AXL_11243	+	GTGACCTATGCACCAGACGTTTGGGAGGGACACGTCAACCTGCCCCACCGACCTTGCAGATCGGAAGAGCGGTTCCAG
chr19	41744525	41744564	AXL_11244	+	GTGACCTATGCACCAGACGTCTGGTGGGATTGGAGTGGAGTGGCTTGGGGAGGAGGAGATCGGAAGAGCGGTTCCAG
chr19	41745230	41745269	AXL_11245	+	GTGACCTATGCACCAGACGTAGCCATGCCCACTGCTTCAACCTGCTCCTCCATGACAAGATCGGAAGAGCGGTTCCAG
chr19	41745636	41745675	AXL_11246	+	GTGACCTATGCACCAGACGTCCACACCCCATCTCTCTTCCCTACCCTCAACACTAGTAGATCGGAAGAGCGGTTCCAG
chr19	41748931	41748970	AXL_11247	+	GTGACCTATGCACCAGACGTACCACATGGGGAGGCTGTGTGGCCTGGGATGGAGAGGCTGAGATCGGAAGAGCGGTTCCAG
chr19	41749623	41749662	AXL_11248	+	GTGACCTATGCACCAGACGTCCTATGCCCACTGCCCTGGCTGGATCTAAAGGCTGTAGAGATCGGAAGAGCGGTTCCAG
chr19	41754525	41754564	AXL_11249	+	GTGACCTATGCACCAGACGTGGCAGCATTACACACATCTTCTGAACTTCTGAGATCTGAGATCGGAAGAGCGGTTCCAG
chr19	41754736	41754775	AXL_11250	+	GTGACCTATGCACCAGACGTTGCACATGTGTAGGACCCCTCCTCCTATGCCCTAGATCGGAAGAGCGGTTCCAG
chr19	41758359	41758398	AXL_11251	+	GTGACCTATGCACCAGACGTTGCAGATTCAAGGGCTTACAAGCCCTAGGAGATCGGAAGAGCGGTTCCAG
chr19	41759624	41759663	AXL_11252	+	GTGACCTATGCACCAGACGTTTTCAGGGACCCCCCTTCCCTGCTGACTCCTCAGATCGGAAGAGCGGTTCCAG

chr19	41762527	41762566	AXL_11253	+	GTGACCTATGCACCAGACGTTCCCGCCAAGAGTGGGGAACCATGGGAGGGCATGGCTGAAGATCGGAAGAGCGGTTCCAG
chr19	41763545	41763584	AXL_11254	+	GTGACCTATGCACCAGACGTTTAGGTCTCCCCAACCCAGAATTCATTTCAAACCCCTGAAGATCGGAAGAGCGGTTCCAG
chr19	41765820	41765859	AXL_11255	+	GTGACCTATGCACCAGACGTCACCTGGTACTCCCTCTCAGGATCCAAGCTAAGCACTGCCAGATCGGAAGAGCGGTTCCAG
chr11	102196307	102196346	BIRC3_11256	+	GTGACCTATGCACCAGACGTTGAAATTCCTTTGCAAAATTCCTGTGATATCATGAGATTAGATCGGAAGAGCGGTTCCAG
chr11	102198872	102198911	BIRC3_11257	+	GTGACCTATGCACCAGACGTTTCTTTTTTAAATATTGGTTGCCATCAGAGAAATTCCTTAGATCGGAAGAGCGGTTCCAG
chr11	102199687	102199726	BIRC3_11258	+	GTGACCTATGCACCAGACGTTGGATAAATGAATGCATTAAATAGAGTCATTTGGTACAGATCGGAAGAGCGGTTCCAG
chr11	102201983	102202022	BIRC3_11259	+	GTGACCTATGCACCAGACGTTTAAATACAGTCTTTTTAATAAGATTGATATCAGTAGATCGGAAGAGCGGTTCCAG
chr11	102207543	102207582	BIRC3_11260	+	GTGACCTATGCACCAGACGTTAATATTTTTAAATCAATAGAGAACCATTGTCTTTTTTTCTAGATCGGAAGAGCGGTTCCAG
chr11	102207844	102207883	BIRC3_11261	+	GTGACCTATGCACCAGACGTTAAACATCGTCTAAACTTTAGAATTAATTTATTAATGTATAGATCGGAAGAGCGGTTCCAG
chr11	102195677	102195716	BIRC3_11262	+	GTGACCTATGCACCAGACGTTAAACTCCAGAGCAAAATCAAGATTTTTCTGCCTTGATGAGAGATCGGAAGAGCGGTTCCAG
chr14	54417617	54417656	BMP4_11263	+	GTGACCTATGCACCAGACGTTTGAAGGAAGGGGAAAAAGAAAAGCATATGAACTTTTAGATCGGAAGAGCGGTTCCAG
chr14	54418951	54418990	BMP4_11264	+	GTGACCTATGCACCAGACGTTGGAGGGGGAGGGAGTGGAAAGTTAAAGAATAAATAACAGATCGGAAGAGCGGTTCCAG
chr14	54417188	54417227	BMP4_11265	+	GTGACCTATGCACCAGACGTTCCACTCCCTTGAGTGAACGATCGCTAATCCTGACATCGGAAAGAGCGGTTCCAG
chr10	88635853	88635892	BMPR1A_11266	+	GTGACCTATGCACCAGACGTTTCATTTTAGTAATGTATGTGTATATAAAAAAGCACTAAGATCGGAAGAGCGGTTCCAG
chr10	88649992	88650031	BMPR1A_11267	+	GTGACCTATGCACCAGACGTTATGCAGCCCTCTTAAAGAGTTAGGAGAAATAGAGTTGCATAGATCGGAAGAGCGGTTCCAG
chr10	88651997	88652036	BMPR1A_11268	+	GTGACCTATGCACCAGACGTTATTTGGGACCCATGAGACAAAAGAGGGAGGGCCATATGAAGATCGGAAGAGCGGTTCCAG
chr10	88659658	88659697	BMPR1A_11269	+	GTGACCTATGCACCAGACGTCGAGAAAAGTCGGAGCATGCTTTCTCAAAATATCTTCTCTGGAGATCGGAAGAGCGGTTCCAG
chr10	88659894	88659933	BMPR1A_11270	+	GTGACCTATGCACCAGACGTTATTTTTGAAGCAAATATTTTGCAAAATATTAGATGATCGGAAGAGCGGTTCCAG
chr10	88672152	88672191	BMPR1A_11271	+	GTGACCTATGCACCAGACGTCGTTTCTATAGACATGAATGGTGTGTTGATTTAGAATGTGAGATCGGAAGAGCGGTTCCAG
chr10	88677094	88677133	BMPR1A_11272	+	GTGACCTATGCACCAGACGTTACTGATTCAGTCAATTTTCTTTTTGACAAGGCTAGTGAGGAGATCGGAAGAGCGGTTCCAG
chr10	88679237	88679276	BMPR1A_11273	+	GTGACCTATGCACCAGACGTTTGGCCCCACTGTTTTGAAATATTTTAAATTTCCAAAAGAGATCGGAAGAGCGGTTCCAG
chr10	88681463	88681502	BMPR1A_11274	+	GTGACCTATGCACCAGACGTTGAGTAGTCTGATTATGTTGATTTACTCATTTTTAAAGATCGGAAGAGCGGTTCCAG
chr10	88683274	88683313	BMPR1A_11275	+	GTGACCTATGCACCAGACGTTCTCAGTCCCCTGAAGAAGTATTGTAATGCTGAAATGCCACCAATAGATCGGAAGAGCGGTTCCAG
chr10	88683487	88683526	BMPR1A_11276	+	GTGACCTATGCACCAGACGTTCAAAGGTACAGAAATGAGAAATGAGACAAAGGCTGTTTTTACCAGATCGGAAGAGCGGTTCCAG
chr3	48200586	48200625	CDC25A_11277	+	GTGACCTATGCACCAGACGTTAGGAGAGAATAAGGTTAGGGTACACCTGCCTCACACCCACAGATCGGAAGAGCGGTTCCAG
chr3	48200956	48200995	CDC25A_11278	+	GTGACCTATGCACCAGACGTTGAAGGAAGGCCAAAGCAGGGTTAGCTTTCCAGCACAGCAAGATCGGAAGAGCGGTTCCAG
chr3	48205938	48205977	CDC25A_11279	+	GTGACCTATGCACCAGACGTTAACAGAGACCCCTTGAACCTGCACGTTTCACACATGAAGTAGATCGGAAGAGCGGTTCCAG
chr3	48207235	48207274	CDC25A_11280	+	GTGACCTATGCACCAGACGTTAAATTAGGAGAAATCAACTTTGACCCTCAGGGAAAACCTAAGATCGGAAGAGCGGTTCCAG
chr3	48207394	48207433	CDC25A_11281	+	GTGACCTATGCACCAGACGTTAAAAGATACTAGAGAATCTGAAAGCCTATATATAGATCGGAAGAGCGGTTCCAG
chr3	48209445	48209484	CDC25A_11282	+	GTGACCTATGCACCAGACGTTCAAAGGTACAGAAATGAGAAATGAGACAAAGGCTGTTTTGAACTTTAGATCGGAAGAGCGGTTCCAG
chr3	48215958	48215997	CDC25A_11283	+	GTGACCTATGCACCAGACGTTAAAAACAGACAGACCCATCTTTCATTAACCTGTTTCACAGATCGGAAGAGCGGTTCCAG
chr3	48218943	48218982	CDC25A_11284	+	GTGACCTATGCACCAGACGTTAGTGAAGAAAACCTGATTTTTAAAAAGAGCCTGTAGAGACTAACATAGATCGGAAGAGCGGTTCCAG
chr3	48219489	48219528	CDC25A_11285	+	GTGACCTATGCACCAGACGTTAAATTCATGGATTATAATGAGAGCTCTGATCCACTTTCAAGATCGGAAGAGCGGTTCCAG
chr3	48222341	48222380	CDC25A_11286	+	GTGACCTATGCACCAGACGTTAGTTGAGACACTACTGTCCATGAAAACCAACTCAGGCCAGATCGGAAGAGCGGTTCCAG
chr3	48224531	48224570	CDC25A_11287	+	GTGACCTATGCACCAGACGTTAAAAGGAAAATAATTAAGGACACAAAATAAAATTTAGATCGGAAGAGCGGTTCCAG
chr3	48225337	48225376	CDC25A_11288	+	GTGACCTATGCACCAGACGTTATCAGAAGGTAATAATGAGAATAAAAACAAGTAAAGAGGTAGATCGGAAGAGCGGTTCCAG
chr3	48226196	48226235	CDC25A_11289	+	GTGACCTATGCACCAGACGTTAAAAAACCTCTCAAGAAATAATCAAAAAACACCATTTAGATCGGAAGAGCGGTTCCAG
chr3	48228280	48228319	CDC25A_11290	+	GTGACCTATGCACCAGACGTCAGAATAAACCCATGAATGATTTATAGGATATAATTAAGATCGGAAGAGCGGTTCCAG
chr2	175665026	175665065	CHN1_11291	+	GTGACCTATGCACCAGACGTTCAAGTACAGGAATAAATGACTTTGTGTAAGCCATATGTTTCAGATCGGAAGAGCGGTTCCAG
chr2	175666551	175666590	CHN1_11292	+	GTGACCTATGCACCAGACGTTAAGTGAATACCAAGAAGAAAAGAAAATAACACAAAACCTGAAGATCGGAAGAGCGGTTCCAG
chr2	175673781	175673820	CHN1_11293	+	GTGACCTATGCACCAGACGTTTGAAGAAAATAAAAAGTAAATATCTGATTTACAGGACAGATCGGAAGAGCGGTTCCAG
chr2	175676327	175676366	CHN1_11294	+	GTGACCTATGCACCAGACGTTAACTAGTTAGTTTTCTTTGAATTATGCCTTTTCTTCAGATAGATCGGAAGAGCGGTTCCAG
chr2	175677221	175677260	CHN1_11295	+	GTGACCTATGCACCAGACGTTAATAAGAAAGGAAACATTCATATATTTTTCAGAGTTTATAGATCGGAAGAGCGGTTCCAG
chr2	175689257	175689296	CHN1_11296	+	GTGACCTATGCACCAGACGTTAAAAGAGGGGCAAAGTCAAGGAAAGGGGAAACACACGGATGAGATCGGAAGAGCGGTTCCAG
chr2	175711696	175711735	CHN1_11297	+	GTGACCTATGCACCAGACGTTGCAAAGAGTTTTAGAGGTTCCAGAGTTGTACAGACCTAGATCGGAAGAGCGGTTCCAG
chr2	175742867	175742906	CHN1_11298	+	GTGACCTATGCACCAGACGTTAAAGTGGAAAGATGTTTTAAAGAAAGTAAGCAACTGAAAGATCGGAAGAGCGGTTCCAG
chr2	175779910	175779949	CHN1_11299	+	GTGACCTATGCACCAGACGTTAAGTCTATTTCAGAAACTGTGCTTTCTACATTTTTCAATAAAGATCGGAAGAGCGGTTCCAG
chr2	175783304	175783343	CHN1_11300	+	GTGACCTATGCACCAGACGTTAGCAAAAAAACAGGCATATTTGAAAAATGCAAAATGTGCAAGATCGGAAGAGCGGTTCCAG
chr2	175809682	175809721	CHN1_11301	+	GTGACCTATGCACCAGACGTTGAGAAACAAAAGTGTCAATGTCCCTTACATAGAACTTAAGATCGGAAGAGCGGTTCCAG
chr2	175816941	175816980	CHN1_11302	+	GTGACCTATGCACCAGACGTTAAACATCAAATTAACATTACTGAATATTTAAATTTAAATAGATCGGAAGAGCGGTTCCAG
chr2	175869651	175869690	CHN1_11303	+	GTGACCTATGCACCAGACGTTCCGCGCCCGCCGAGTCCAGCGCTCCTCCCAGGCGGAGATCGGAAGAGCGGTTCCAG
chr12	57910974	57911013	DDIT3_11304	+	GTGACCTATGCACCAGACGTTAGGAAAGGGAACATAGATATAGTGAAGAAAGGAAAGATCGGAAGAGCGGTTCCAG
chr12	57911200	57911239	DDIT3_11305	+	GTGACCTATGCACCAGACGTTGGATCAGTCTGAAAAGCACATCTGCAGGATAATGGGGAGAGATCGGAAGAGCGGTTCCAG
chr3	185867988	185868027	DGKG_11306	+	GTGACCTATGCACCAGACGTTAGAGGCAGAAATGAATAGTGGCATGCAAACTCAGTAGCAGATCGGAAGAGCGGTTCCAG
chr3	185879463	185879502	DGKG_11307	+	GTGACCTATGCACCAGACGTTGAACACCAAGAGAACAACAGTGAGCTTTTTCAAGTGGGAGAGATCGGAAGAGCGGTTCCAG
chr3	185882818	185882857	DGKG_11308	+	GTGACCTATGCACCAGACGTTAGACAGCAAAAGTAGTGATACACATCTCTGTCTTCAAGATCGGAAGAGCGGTTCCAG
chr3	185906179	185906218	DGKG_11309	+	GTGACCTATGCACCAGACGTTAGAGAAAAGGCACTGTTAGTGTCTTACTAGTGTGTCAACAAGATCGGAAGAGCGGTTCCAG
chr3	185929685	185929724	DGKG_11310	+	GTGACCTATGCACCAGACGTTAAGCAGAGAGATGCTCAATATTCACATTTGAAATGCTCAGATCGGAAGAGCGGTTCCAG

chr3	185960368	185960407	DGKG_11311	+	GTGACCTATGCACCAGACGTAAAGAGACAAAGCAGATCCTTGGTGAGTGGTCATGACAGTGAAGATCGGAAGAGCGGTTTCAG
chr3	185969719	185969758	DGKG_11312	+	GTGACCTATGCACCAGACGTCAGCACTGCATTTGCCACCACAGCAGAAAGGCTGTATTCATAGATCGGAAGAGCGGTTTCAG
chr3	185970982	185971021	DGKG_11313	+	GTGACCTATGCACCAGACGTCACAGAGGAACAGAGAACCATATGCCATGGGACTGTAGAAAGATCGGAAGAGCGGTTTCAG
chr3	185975739	185975778	DGKG_11314	+	GTGACCTATGCACCAGACGTGAAGAAAGGCCAAAATGGGCTTGTTACTAGTTCGACAGTGAAGATCGGAAGAGCGGTTTCAG
chr3	185979578	185979617	DGKG_11315	+	GTGACCTATGCACCAGACGTTAAAAGAAAAGAAATAGTCTGCTTCATCCAATAGGGGGAGATCGGAAGAGCGGTTTCAG
chr3	185983106	185983145	DGKG_11316	+	GTGACCTATGCACCAGACGTAAAGGAAAAGCAAGCATCTTTTGGAAAAAGAGCCTAACAGATCGGAAGAGCGGTTTCAG
chr3	185985677	185985616	DGKG_11317	+	GTGACCTATGCACCAGACGTAAATGAAAAAGAGAGTGAAGTGAAAGTAGCAAAGAAAACATAGATCGGAAGAGCGGTTTCAG
chr3	185986717	185986756	DGKG_11318	+	GTGACCTATGCACCAGACGTGAAGCGAACGATGCCAGGAAAATGGCAGAACCATGTCCCAGATCGGAAGAGCGGTTTCAG
chr3	185990143	185990182	DGKG_11319	+	GTGACCTATGCACCAGACGTAAAAAGTCAAGGCAGGTGCTTGTGAATAGCCAGCTAGGAAAAGATCGGAAGAGCGGTTTCAG
chr3	185993464	185993503	DGKG_11320	+	GTGACCTATGCACCAGACGTAATAGGAGGTGAGACCCCAAGCTGGCTGCCCTGAGATGGAAGATCGGAAGAGCGGTTTCAG
chr3	185997773	185997812	DGKG_11321	+	GTGACCTATGCACCAGACGTCAAAGAGCAATCATTGTCCATTTTCATCATCGACATGTCTAGATCGGAAGAGCGGTTTCAG
chr3	185998544	185998583	DGKG_11322	+	GTGACCTATGCACCAGACGTGCAAAGGGAGAAAATCAAAGTGACACAACAGAGATGTAGATCGGAAGAGCGGTTTCAG
chr3	186002509	186002548	DGKG_11323	+	GTGACCTATGCACCAGACGTCAACAGAGGTAAGCCTTGAAGTGCCCTTAAGAAGCGCGGAGATCGGAAGAGCGGTTTCAG
chr3	186006680	186006719	DGKG_11324	+	GTGACCTATGCACCAGACGTCAAAGGAAAACATCCAAGGACATTTTCTGTTTAGTAAATAGATCGGAAGAGCGGTTTCAG
chr3	186015283	186015322	DGKG_11325	+	GTGACCTATGCACCAGACGTAAAAGAAGATTTAAAGACCAACCCAGGCCCTCTAGCTTCTAGATCGGAAGAGCGGTTTCAG
chr3	186024777	186024816	DGKG_11326	+	GTGACCTATGCACCAGACGTACAAATTCACATGTGAAACACTGGCAAATAGCTAATGGAAGAGATCGGAAGAGCGGTTTCAG
chr3	186038259	186038298	DGKG_11327	+	GTGACCTATGCACCAGACGTTATGTGAGTGGCTAAAGGGCAGTGATGGAGTTTGTTCACAGATCGGAAGAGCGGTTTCAG
chr8	120569942	120569981	ENPP2_11328	+	GTGACCTATGCACCAGACGTAAACAGAAAAATCAGAATCGAATTTTCCAGAGGAGTTTAGATCGGAAGAGCGGTTTCAG
chr8	120575264	120575303	ENPP2_11329	+	GTGACCTATGCACCAGACGTGAAGTAAAACGAAGTACAGTTGATGAGTTGATGTTGAAGAGATCGGAAGAGCGGTTTCAG
chr8	120577206	120577245	ENPP2_11330	+	GTGACCTATGCACCAGACGTACAAAAATCCAAAAATCAATTTATTCATGAAGAAAACCTCTAGATCGGAAGAGCGGTTTCAG
chr8	120580503	120580542	ENPP2_11331	+	GTGACCTATGCACCAGACGTGGAAAACAAATAGTATACGTTGCTTACCAAATCTATATCAGATCGGAAGAGCGGTTTCAG
chr8	120581621	120581660	ENPP2_11332	+	GTGACCTATGCACCAGACGTGTGACAGGGCACTCAGCAATGCCGTGGCTCTGTTACGAACGAGATCGGAAGAGCGGTTTCAG
chr8	120583092	120583131	ENPP2_11333	+	GTGACCTATGCACCAGACGTAAAAAAATAACTGTGTTAGTGCATATAAATTTTACATAGATCGGAAGAGCGGTTTCAG
chr8	120592418	120592457	ENPP2_11334	+	GTGACCTATGCACCAGACGTGAAAACCAAGTAAAGGAAAAGAAAGCAAAATCAGAAATGTAGATCGGAAGAGCGGTTTCAG
chr8	120594853	120594892	ENPP2_11335	+	GTGACCTATGCACCAGACGTAAAAGAAAAGGAGGCGAGGTGCTTCTTATATTTTTTTTATGATGAGATCGGAAGAGCGGTTTCAG
chr8	120596055	120596094	ENPP2_11336	+	GTGACCTATGCACCAGACGTAAAAGAAAAACAAAACAGTAAAGCATTGTTAGGTAGGAAAAGATCGGAAGAGCGGTTTCAG
chr8	120596300	120596339	ENPP2_11337	+	GTGACCTATGCACCAGACGTACAAATTCATGATTAGTTAGAATTTCTCATGAAATTACTTAGATCGGAAGAGCGGTTTCAG
chr8	120598564	120598603	ENPP2_11338	+	GTGACCTATGCACCAGACGTAATGAAATCAGACTTCAAGTGAATGTCTTTTGGAAAAAGATCGGAAGAGCGGTTTCAG
chr8	120599326	120599365	ENPP2_11339	+	GTGACCTATGCACCAGACGTAGAGGAGAAAGATTTCAAAGAAATAACAACCATACCAAAGATCGGAAGAGCGGTTTCAG
chr8	120602881	120602920	ENPP2_11340	+	GTGACCTATGCACCAGACGTGGAGAAAAGAAATTTTTCAAGCAAGACTAAAACGAAAATAGATCGGAAGAGCGGTTTCAG
chr8	120606111	120606150	ENPP2_11341	+	GTGACCTATGCACCAGACGTGAAGCAAGTTAGTCCCCACAGGGTTTTCTTTCTTTCCCTTAGATCGGAAGAGCGGTTTCAG
chr8	120608253	120608292	ENPP2_11342	+	GTGACCTATGCACCAGACGTGGATAGAGATGTCTGGACTCAGAAGTCGTCTGTCCCTCTGAGATCGGAAGAGCGGTTTCAG
chr8	120613001	120613040	ENPP2_11343	+	GTGACCTATGCACCAGACGTATTGGAAGGTTCAAGATCTCTCTAAACACATGTAACAAGATCGGAAGAGCGGTTTCAG
chr8	120613713	120613752	ENPP2_11344	+	GTGACCTATGCACCAGACGTAAAGCAAAGCAAGCATGTTGTAGTTCATTTCCGCAAAAAGATCGGAAGAGCGGTTTCAG
chr8	120620228	120620267	ENPP2_11345	+	GTGACCTATGCACCAGACGTAAAATATAAGCCGCTTAAAATGTGGTCTGTGTTTTTTGTCAAAGATCGGAAGAGCGGTTTCAG
chr8	120628635	120628674	ENPP2_11346	+	GTGACCTATGCACCAGACGTAAAGCAAATTTATTGTTAAAATAACAATACATAATCCACAAGATCGGAAGAGCGGTTTCAG
chr8	120629494	120629533	ENPP2_11347	+	GTGACCTATGCACCAGACGTAATGCAATATTAGAACAAGAGAACCAACAGGAATTGCTAGATCGGAAGAGCGGTTTCAG
chr8	120629814	120629853	ENPP2_11348	+	GTGACCTATGCACCAGACGTAAACATTAAGCTTTTAGAAAACATTATACCAGAGTTGCCAGATCGGAAGAGCGGTTTCAG
chr8	120631555	120631594	ENPP2_11349	+	GTGACCTATGCACCAGACGTAATGGGTAATGTATTGTTGAATTAATACAAATGCCAAGATCGGAAGAGCGGTTTCAG
chr8	120633770	120633809	ENPP2_11350	+	GTGACCTATGCACCAGACGTCCTCAATAAAACATTTCACTGCTGCACACTAACCAATGAAGATCGGAAGAGCGGTTTCAG
chr8	120638971	120639010	ENPP2_11351	+	GTGACCTATGCACCAGACGTCAAAGAGCAAACAAAACAGTGAAGAGTGGTCAATGTACAGATCGGAAGAGCGGTTTCAG
chr8	120650778	120650817	ENPP2_11352	+	GTGACCTATGCACCAGACGTAAAGAGACCAAGTTGTCAAATACAGCTGGAGAAGACTAAAAGATCGGAAGAGCGGTTTCAG
chr8	120651031	120651070	ENPP2_11353	+	GTGACCTATGCACCAGACGTCTGGAAAGCCTTTTGCAGCGTGTCTCTTTGCCTTACGAGATCGGAAGAGCGGTTTCAG
chr1	16456925	16456964	EPHA2_11354	+	GTGACCTATGCACCAGACGTACGAAGGTCAAGGGCGCTGTTGCAGAAAGCCACTGAAACCAGATCGGAAGAGCGGTTTCAG
chr1	16458376	16458415	EPHA2_11355	+	GTGACCTATGCACCAGACGTCCCAGGCCAGTACCACACTGTGCCCTCTGGCTGGCCCCAGAGATCGGAAGAGCGGTTTCAG
chr1	16458779	16458818	EPHA2_11356	+	GTGACCTATGCACCAGACGTACAGGCCTACGCTCAGTGCAGGCCACCCCTGAACCCGCGAGGATCGGAAGAGCGGTTTCAG
chr1	16459874	16459913	EPHA2_11357	+	GTGACCTATGCACCAGACGTACAGGGTCAAGGGAGTGCCTGGTCAAGCCCGCATGAGGAGATCGGAAGAGCGGTTTCAG
chr1	16460112	16460151	EPHA2_11358	+	GTGACCTATGCACCAGACGTAAGGGTGGGGTACAGGCAGCTCAGGAGGGGCCCATGGAGATCGGAAGAGCGGTTTCAG
chr1	16460421	16460460	EPHA2_11359	+	GTGACCTATGCACCAGACGTCCCACGGGGAACCAATGCAGGGAGGTCAAGAGTCTGCAGATCGGAAGAGCGGTTTCAG
chr1	16461073	16461112	EPHA2_11360	+	GTGACCTATGCACCAGACGTAATCAGCTGATGACAAGGGAGTTCCCCACAATACAGAGATCGGAAGAGCGGTTTCAG
chr1	16461695	16461734	EPHA2_11361	+	GTGACCTATGCACCAGACGTGTGGCCGCGGAGGAGCAGGCGAGTGAAGGCGGCAGGGCAGGAGATCGGAAGAGCGGTTTCAG
chr1	16462276	16462315	EPHA2_11362	+	GTGACCTATGCACCAGACGTGAGGAGGGTGGGGTAAAGTGGGTAAGAGTGCCTACAGCAAGATCGGAAGAGCGGTTTCAG
chr1	16464691	16464730	EPHA2_11363	+	GTGACCTATGCACCAGACGTAGGAGGAGTCAAGTGTGCTGGTGGACCCAGGGCAGACGTCAGATCGGAAGAGCGGTTTCAG
chr1	16464936	16464975	EPHA2_11364	+	GTGACCTATGCACCAGACGTGAGGACAGACAGACACAAGGACATCAGTTCAATCTGCTTAGATCGGAAGAGCGGTTTCAG
chr1	16475553	16475592	EPHA2_11365	+	GTGACCTATGCACCAGACGTAAAGATACAGGTTAGTGTGGGCAAGTGCCTGGGGAACTGAAGATCGGAAGAGCGGTTTCAG
chr1	16477469	16477508	EPHA2_11366	+	GTGACCTATGCACCAGACGTGAAGGGAGGGGGTGAAGCTGGGGTGTCTTCAAGAGTCAAGATCGGAAGAGCGGTTTCAG
chr1	16482438	16482477	EPHA2_11367	+	GTGACCTATGCACCAGACGTTCCGCTCCGCTCCGCCAGCCGCTCCCGGAGATCGGAAGAGCGGTTTCAG
chr1	16475218	16475257	EPHA2_11368	+	GTGACCTATGCACCAGACGTGGCGTGCCTCGAAGTGCCTGCTGAGCGGTGATCTCATCGGGAGATCGGAAGAGCGGTTTCAG

chr21	40182041	40182080	ETS2_11369	+	GTGACCTATGCACCAGACGTAAGTCTTAATTTTTTTTTTAAATGGAAACTCGATCTCTAGATCGGAAGAGCGGTTTCAG
chr21	40185049	40185088	ETS2_11370	+	GTGACCTATGCACCAGACGCTCCTCAGACTTGACAATTTGTGCATGATTTTTCTAAGTAGTAGATCGGAAGAGCGGTTTCAG
chr21	40186327	40186366	ETS2_11371	+	GTGACCTATGCACCAGACGCTTTCTGAGCCTGCAGTGGTGAGAAGAACCACTTCAGAGATCGGAAGAGCGGTTTCAG
chr21	40186916	40186955	ETS2_11372	+	GTGACCTATGCACCAGACGTAACGTCTTACTTCTCCTTTGCCAGGATGAGCTGTGGCCGGAGATCGGAAGAGCGGTTTCAG
chr21	40189026	40189065	ETS2_11373	+	GTGACCTATGCACCAGACGTTTGATCTGCCCTTAAGAACTTTGTCTTCCAGTCTTCCCAGAGATCGGAAGAGCGGTTTCAG
chr21	40190581	40190620	ETS2_11374	+	GTGACCTATGCACCAGACGTAAGCATCTTTCAACAAGGCTGTTGCTTTGATTCTGAGAACAGATCGGAAGAGCGGTTTCAG
chr21	40191701	40191740	ETS2_11375	+	GTGACCTATGCACCAGACGTAACCTCCGAGACTGCGCCCTGGCCCGACTCTCTGGGTCTGTCCAGATCGGAAGAGCGGTTTCAG
chr21	40193639	40193678	ETS2_11376	+	GTGACCTATGCACCAGACGTAGCCCTGGGAAATCTCTGGGCTTGAACCTGATTTCCCTGAGATCGGAAGAGCGGTTTCAG
chr21	40194824	40194863	ETS2_11377	+	GTGACCTATGCACCAGACGTACCACCCTGAGCCGGCCCCAGGCTCGTGGACTGAGTGGGAAGATCGGAAGAGCGGTTTCAG
chr3	59738058	59738097	FHIT_11378	+	GTGACCTATGCACCAGACGTAAAAAAGGAAGAGGCTCTTTTCATGGGCCCTTGGGATCTCAGATCGGAAGAGCGGTTTCAG
chr3	59908151	59908190	FHIT_11379	+	GTGACCTATGCACCAGACGTACAAGAAAGAAAAAAATGTGATTATCTCCCCATGATTTAGATCGGAAGAGCGGTTTCAG
chr3	59997137	59997176	FHIT_11380	+	GTGACCTATGCACCAGACGTGAAAAACAACAGAGGTGAGAATAGATAGATGGTATCTCAGATCGGAAGAGCGGTTTCAG
chr3	59999889	59999928	FHIT_11381	+	GTGACCTATGCACCAGACGTGCTGTTAAGGCCCATGCTGTGCTGGCTTTGGGTAGTGTTCTAGATCGGAAGAGCGGTTTCAG
chr3	60522706	60522745	FHIT_11382	+	GTGACCTATGCACCAGACGTTTGAAGTCTAAAAAGAAAGACAATGGATAGTTATAAAATTAGATCGGAAGAGCGGTTTCAG
chr15	91419158	91419197	FURIN_11383	+	GTGACCTATGCACCAGACGTCCCCACAGGACACTGCCAGGGGGTGGGACCAGAGAAGACAAGATCGGAAGAGCGGTTTCAG
chr15	91419594	91419633	FURIN_11384	+	GTGACCTATGCACCAGACGTCCCCAGCCCCCTCTGCTGCCACCCTCCCCCTCCTGCTCAGATCGGAAGAGCGGTTTCAG
chr15	91419798	91419837	FURIN_11385	+	GTGACCTATGCACCAGACGTTTTCTTCCGCTGCTGGGACCTCTCCCCAGATGCACCATCAAGATCGGAAGAGCGGTTTCAG
chr15	91420265	91420304	FURIN_11386	+	GTGACCTATGCACCAGACGTGCTGGGGAGGGGCGGTGACTCCCTGCTGAGTGTGTCTAGAAAGATCGGAAGAGCGGTTTCAG
chr15	91420452	91420491	FURIN_11387	+	GTGACCTATGCACCAGACGTGCAGGCCCCGGTCTCTGCCCTCCCTTCTCTTTCTCCACTAGATCGGAAGAGCGGTTTCAG
chr15	91420856	91420895	FURIN_11388	+	GTGACCTATGCACCAGACGTGCCCTGGGCCACCCTGTCTTCAGGAGGGCCCTTCCAGTGGAAAGATCGGAAGAGCGGTTTCAG
chr15	91421545	91421584	FURIN_11389	+	GTGACCTATGCACCAGACGTGATCTGTCCAGCCCTGCGGGCAGGTTGGGTGCTGTCTTCCAGATCGGAAGAGCGGTTTCAG
chr15	91422217	91422256	FURIN_11390	+	GTGACCTATGCACCAGACGTCTGGGGTGGGGGCTGGGGAGATGGGGCTGTGGCTGGCAGATCGGAAGAGCGGTTTCAG
chr15	91422785	91422824	FURIN_11391	+	GTGACCTATGCACCAGACGTGGGGCCAGCGGCAACCTGTCCCTACCAGACTCTCTGATGATCGGAAGAGCGGTTTCAG
chr15	91423015	91423054	FURIN_11392	+	GTGACCTATGCACCAGACGTGCTGGCCCGGACCTGATCGGTGAGTTAGGTAGAAGCAAGATCGGAAGAGCGGTTTCAG
chr15	91423225	91423264	FURIN_11393	+	GTGACCTATGCACCAGACGTGACCCAGGCTGGGAGGGGCCAGTGGGACCTGAGAGTGCAGATCGGAAGAGCGGTTTCAG
chr15	91423514	91423553	FURIN_11394	+	GTGACCTATGCACCAGACGTGCTCCCTGCCCGCCCTGCCACGCGCCCGCTCTCACAGATCGGAAGAGCGGTTTCAG
chr15	91424056	91424095	FURIN_11395	+	GTGACCTATGCACCAGACGTCACTTGAAGGGTAGGGGTACGAGGTGGAGGGCTGGCAGGAAGATCGGAAGAGCGGTTTCAG
chr15	91424281	91424320	FURIN_11396	+	GTGACCTATGCACCAGACGTGGTGCTGTTGGGCTTTGGGGCCCTGAGTCTGGGGTAAAGGATCGGAAGAGCGGTTTCAG
chr15	91425119	91425158	FURIN_11397	+	GTGACCTATGCACCAGACGTGCCACCCCTCAAGCCTACCCTCTTGGGCACCTTTAGATCGGAAGAGCGGTTTCAG
chr15	91424822	91424861	FURIN_11398	+	GTGACCTATGCACCAGACGTGCGGGCAACCGCTGCGGGCAGGGCTGCTGCCCTCACACTAGATCGGAAGAGCGGTTTCAG
chr22	24376628	24376667	GSTT1_11399	+	GTGACCTATGCACCAGACGTAAGGGTACAGACTGGGGATGGATGGTTGTGAGGGCAGGGAAAGATCGGAAGAGCGGTTTCAG
chr22	24379522	24379561	GSTT1_11400	+	GTGACCTATGCACCAGACGTGGGGTTCATGATGGGTAAAGGAAGGGCACTGTGCTGGGTAAAGATCGGAAGAGCGGTTTCAG
chr22	24381798	24381837	GSTT1_11401	+	GTGACCTATGCACCAGACGTTCCAGCATGGTGGGTGGTGGGAGGAGAAGCTGAGCCCGCAGATCGGAAGAGCGGTTTCAG
chr22	24384242	24384281	GSTT1_11402	+	GTGACCTATGCACCAGACGTGCCAGCCTGACCGGAAACCAGGGGATCAGCAAACTCCAGATCGGAAGAGCGGTTTCAG
chr5	141001115	141001154	HDAC3_11403	+	GTGACCTATGCACCAGACGTAGGGAGAGAGTGCAGTCACTCTAAGTTCTAATCTTAGATCGGAAGAGCGGTTTCAG
chr5	141004943	141004982	HDAC3_11404	+	GTGACCTATGCACCAGACGTATGAGGAATACAGAGTGAGCAGTTTCCAGAGATTTCCAGAGATCGGAAGAGCGGTTTCAG
chr5	141005342	141005381	HDAC3_11405	+	GTGACCTATGCACCAGACGTAGAGGAGAAAGTATGGCTCAGACTGAGAAAGGCAGCTAACAGATCGGAAGAGCGGTTTCAG
chr5	141005649	141005688	HDAC3_11406	+	GTGACCTATGCACCAGACGTCCAGCAGAGGGGAGCAGGCTGACCAGTGGGCTGAAGGACAGATCGGAAGAGCGGTTTCAG
chr5	141005861	141005900	HDAC3_11407	+	GTGACCTATGCACCAGACGTGAACCAGAGGAAGATGTGGAGGAGTTATCAAAAGACAAGAGATCGGAAGAGCGGTTTCAG
chr5	141007535	141007574	HDAC3_11408	+	GTGACCTATGCACCAGACGTCAAACCCAGGAAAAGTGCAGTATCAGAAGATCGGAAGAGCGGTTTCAG
chr5	141007765	141007804	HDAC3_11409	+	GTGACCTATGCACCAGACGTGCAAAAGATGGGCACTGCCACCCCAAGGGGATGGGGAGAAGATCGGAAGAGCGGTTTCAG
chr5	141008217	141008256	HDAC3_11410	+	GTGACCTATGCACCAGACGTGTTGGTGGTGGTAGCCACACATGGGAAGCACCACAACCCAGATCGGAAGAGCGGTTTCAG
chr5	141008884	141008923	HDAC3_11411	+	GTGACCTATGCACCAGACGTGCCAAAGCCAGGGTCTGAGCTAGAAGTGAACCCCCAACCCAGATCGGAAGAGCGGTTTCAG
chr5	141009317	141009356	HDAC3_11412	+	GTGACCTATGCACCAGACGTACAGTGGTCTATAAAGAGAAGAGCAATTTCCCCTCCCAGCAGATCGGAAGAGCGGTTTCAG
chr5	141009494	141009533	HDAC3_11413	+	GTGACCTATGCACCAGACGTAACACCTAAGTACAGTCTTCTCCAGCCCTCAAGCTAGATCGGAAGAGCGGTTTCAG
chr5	141009703	141009742	HDAC3_11414	+	GTGACCTATGCACCAGACGTGAGGAACAAGTTGGAACCTCTGCCCTCTGTCTGGGCCCTAGATCGGAAGAGCGGTTTCAG
chr5	141014531	141014570	HDAC3_11415	+	GTGACCTATGCACCAGACGTAGACACAAGATGAACCCAGGCAGGGTCCAGCCCCCAGATCGGAAGAGCGGTTTCAG
chr5	141016208	141016247	HDAC3_11416	+	GTGACCTATGCACCAGACGTGGAGAAGAGAGTTCGTGAGTCTCACCCCTGGAGTTGCAAAGATCGGAAGAGCGGTTTCAG
chr19	10381913	10381952	ICAM1_11417	+	GTGACCTATGCACCAGACGTGTGGGGATTGCCGTCGGGCCAGTTCTCCGAAGCCCCGGGAAGATCGGAAGAGCGGTTTCAG
chr19	10385715	10385754	ICAM1_11418	+	GTGACCTATGCACCAGACGTGAGCCCGGAGGGCTGGACTAGGCCAGCCCGGTTGGGAGAGAAGATCGGAAGAGCGGTTTCAG
chr19	10394473	10394512	ICAM1_11419	+	GTGACCTATGCACCAGACGTAAGAAGCCAGCAGGGAGAAGTTGGAGGCTGGGGTATCCTGCAGATCGGAAGAGCGGTTTCAG
chr19	10395007	10395046	ICAM1_11420	+	GTGACCTATGCACCAGACGTGCCAGGGGCGAGTGGGGTCTTCTGGGGTGTGACATCGGAAGAGCGGTTTCAG
chr19	10395344	10395383	ICAM1_11421	+	GTGACCTATGCACCAGACGTCTGCTGGTCAATGGCCCTATCCCCCAAGGCCCAATCTCCAGATCGGAAGAGCGGTTTCAG
chr19	10395715	10395754	ICAM1_11422	+	GTGACCTATGCACCAGACGTGCGCGGGCAGAGCTGGGTGGGGCAGGGCCATGGACCTAAGATCGGAAGAGCGGTTTCAG
chr19	10395974	10396013	ICAM1_11423	+	GTGACCTATGCACCAGACGTGGACAGGCCCTCTTCTGCGCCTCCCATATTGGTGGCAGAGATCGGAAGAGCGGTTTCAG
chr4	123373028	123373067	IL2_11424	+	GTGACCTATGCACCAGACGTAATGTTAATTTTTTAAAGTACAGAGTAGTTTACCTTAGATCGGAAGAGCGGTTTCAG
chr4	123375019	123375058	IL2_11425	+	GTGACCTATGCACCAGACGTAATATCATGACTAGTTTACATAGAGTCAAGATCGGAAGAGCGGTTTCAG
chr4	123377369	123377408	IL2_11426	+	GTGACCTATGCACCAGACGTAATGTCATTTGTTAATAAGATGATCTCCAGCTAGATTAAGATCGGAAGAGCGGTTTCAG

chr4	123377606	123377645	IL2_11427	+	GTGACCTATGCACCAGACGTGTTGAGGTTACTGTGAGTAGTGATTAAGAGAGTGATAGGAGATCGGAAGAGCGGTTTCAG
chr10	6054870	6054909	IL2RA_11428	+	GTGACCTATGCACCAGACGTGAACAAAGTACGGTCATATGTGAACACGGCACCAAAAAGATCGGAAGAGCGGTTTCAG
chr10	6060093	6060132	IL2RA_11429	+	GTGACCTATGCACCAGACGTAGAGAGGGAGTTCCAGCAAAGGGCCCTGGGCTTGGCATGGGAGATCGGAAGAGCGGTTTCAG
chr10	6061473	6061512	IL2RA_11430	+	GTGACCTATGCACCAGACGTGAGATAAAGAGAGACTCCTGCTACCGTGACTTTAGGACAGATCGGAAGAGCGGTTTCAG
chr10	6061915	6061954	IL2RA_11431	+	GTGACCTATGCACCAGACGTGAGTAAGTATGCTGGTGGAGCTAAACACAGGAGTCAGGGAGATCGGAAGAGCGGTTTCAG
chr10	6063667	6063706	IL2RA_11432	+	GTGACCTATGCACCAGACGTGAAGGAATGCTCTGAAGGCAAGTTGGGGACAGCACCCGCAAGATCGGAAGAGCGGTTTCAG
chr10	6066367	6066387	IL2RA_11433	+	GTGACCTATGCACCAGACGTGAGATGGAAATGTCAGAGATAAATTCACAAATGCTTCATAGAGATCGGAAGAGCGGTTTCAG
chr10	6067999	6068038	IL2RA_11434	+	GTGACCTATGCACCAGACGTAAAGAAGCCTATTAGGAACTCAAGAGGCCCCAGGCAAGTAAGATCGGAAGAGCGGTTTCAG
chr10	6104125	6104164	IL2RA_11435	+	GTGACCTATGCACCAGACGTCTGGGACCAGCCGGGCGAGTAAGCGGAGGTCTTTCTCTAGATCGGAAGAGCGGTTTCAG
chr17	45331317	45331356	ITGB3_11436	+	GTGACCTATGCACCAGACGTCTCCGGCTCGGCAGCGTGCAGCTGCCCCAGGATCTGCGCAGATCGGAAGAGCGGTTTCAG
chr17	45351881	45351920	ITGB3_11437	+	GTGACCTATGCACCAGACGTGATACCAGACCTTGTCTTCTCCAGACTAAGCTGCTTTTAGATCGGAAGAGCGGTTTCAG
chr17	45360926	45360965	ITGB3_11438	+	GTGACCTATGCACCAGACGTGACTCTTTCGGGGAGAGACACTGAAGCAGGTGGGCATAGAAGATCGGAAGAGCGGTTTCAG
chr17	45362072	45362111	ITGB3_11439	+	GTGACCTATGCACCAGACGTCTCCAGACGCCAGGACAGCTCCTTTGCCCCAGGAAGGTAGATCGGAAGAGCGGTTTCAG
chr17	45363799	45363838	ITGB3_11440	+	GTGACCTATGCACCAGACGTAGGACTTGGAGTGCCAGGTGTGGCTGGCATAGATCAAAATAGATCGGAAGAGCGGTTTCAG
chr17	45367153	45367192	ITGB3_11441	+	GTGACCTATGCACCAGACGTCTCGGGCTTCTGGAGTGGGCCCTGTGATGGTGGGTGCCAGATCGGAAGAGCGGTTTCAG
chr17	45367651	45367690	ITGB3_11442	+	GTGACCTATGCACCAGACGTGTGCTGGGAAATGTCGCCGCGGAGAGTCCACCTCATTGGAGATCGGAAGAGCGGTTTCAG
chr17	45368465	45368504	ITGB3_11443	+	GTGACCTATGCACCAGACGTCTGGGCAGGGCCCTTTGCTCTGGAGACTCTGTGGGCACCAAGATCGGAAGAGCGGTTTCAG
chr17	45369945	45369984	ITGB3_11444	+	GTGACCTATGCACCAGACGTCTGGCCAGCCCTCTGCTGGAACCCACACCCTCATATAGATCGGAAGAGCGGTTTCAG
chr17	45376907	45376946	ITGB3_11445	+	GTGACCTATGCACCAGACGTAGTCTGGAGAGAGCCGGGAGGCTGGGAGGTAGGAGAGATAGATCGGAAGAGCGGTTTCAG
chr17	45377955	45377994	ITGB3_11446	+	GTGACCTATGCACCAGACGTCACATCTTAGAGTTGCACACACCCAGGTTCTAAATGTTTCAGATCGGAAGAGCGGTTTCAG
chr17	45380217	45380256	ITGB3_11447	+	GTGACCTATGCACCAGACGTCTGACGGCTCCCGGCCCTGCCCCAGGAGGGAGAGGAGAAGATCGGAAGAGCGGTTTCAG
chr17	45385014	45385053	ITGB3_11448	+	GTGACCTATGCACCAGACGTGGGCTGGGCGTTTTCTAAAGTCTTTGCTGAGACTCTTAAGATCGGAAGAGCGGTTTCAG
chr17	45387581	45387620	ITGB3_11449	+	GTGACCTATGCACCAGACGTTCCCTCAGATCATTATCAGCCTGTGCCAGATTGCAGGATCGGAAGAGCGGTTTCAG
chr19	17937730	17937769	JAK3_11450	+	GTGACCTATGCACCAGACGTGGGGACAGATAAATGGGCTGCTCTGACAGTCCAAGGAAAGATCGGAAGAGCGGTTTCAG
chr19	17941038	17941077	JAK3_11451	+	GTGACCTATGCACCAGACGTGGAGGAGCGCATGTGGTGGGGGAGGAGCCTCCGTGGTGGAGATCGGAAGAGCGGTTTCAG
chr19	17941440	17941479	JAK3_11452	+	GTGACCTATGCACCAGACGTGACAAGGCTTGAGATGCGAGGGGTAGAAAAGGACAGGAAAGATCGGAAGAGCGGTTTCAG
chr19	17942220	17942259	JAK3_11453	+	GTGACCTATGCACCAGACGTGCGGTGTGAGCGTGACAGAGGATCCCAGGATAATCCGGCAGATCGGAAGAGCGGTTTCAG
chr19	17942618	17942657	JAK3_11454	+	GTGACCTATGCACCAGACGTCCAGATCTGTCCACAGGGGCCACCCCTGCTCGTCCCCAGATCGGAAGAGCGGTTTCAG
chr19	17943528	17943567	JAK3_11455	+	GTGACCTATGCACCAGACGTGCGGGATGATGTCACAGCCAGCTGATGCTGCCCTAGATCGGAAGAGCGGTTTCAG
chr19	17943749	17943788	JAK3_11456	+	GTGACCTATGCACCAGACGTGGCATGGGCATGGTAAGCAGCGCCTCTCATCCTGGGCCAGATCGGAAGAGCGGTTTCAG
chr19	17945541	17945580	JAK3_11457	+	GTGACCTATGCACCAGACGTGAGGAGCAGTCGGTAATCCCCAACCAATAGACCCACCCAGATCGGAAGAGCGGTTTCAG
chr19	17945823	17945862	JAK3_11458	+	GTGACCTATGCACCAGACGTGAAAAGTGGGATCAGGGATCCACTTCTTGCCCTGCTCAGCAGATCGGAAGAGCGGTTTCAG
chr19	17946035	17946074	JAK3_11459	+	GTGACCTATGCACCAGACGTGACACACAGGAAAATGCCCGGGAGGTTTGTGAATGAAGAGATCGGAAGAGCGGTTTCAG
chr19	17946871	17946910	JAK3_11460	+	GTGACCTATGCACCAGACGTGCAGGGAGAGCGGGTTGGGAGACTGAAGTGCAC TTGTGAGATCGGAAGAGCGGTTTCAG
chr19	17948033	17948072	JAK3_11461	+	GTGACCTATGCACCAGACGTGGGGAGGAGAGAAGATGCGTGGGTTTTCTTCCACTCCAAGATCGGAAGAGCGGTTTCAG
chr19	17948883	17948922	JAK3_11462	+	GTGACCTATGCACCAGACGTAGGGGACAGCAGAAGAGGCCAGTGAGGGGTTCTCTGCAGGAGATCGGAAGAGCGGTTTCAG
chr19	17949210	17949249	JAK3_11463	+	GTGACCTATGCACCAGACGTAGGATGAGGGAGAAAAACCAGAAATCAGAGGTGAAAAGTGCAGATCGGAAGAGCGGTTTCAG
chr19	17950483	17950522	JAK3_11464	+	GTGACCTATGCACCAGACGTGAGTGGCCCTGAGTGGGACTGAGCGACAGACACTCTCCTAGATCGGAAGAGCGGTTTCAG
chr19	17951161	17951200	JAK3_11465	+	GTGACCTATGCACCAGACGTAGGTGAGAGGGAATGGGGAGGAGTCAGAGATAGAAGAAGATCGGAAGAGCGGTTTCAG
chr19	17952366	17952405	JAK3_11466	+	GTGACCTATGCACCAGACGTCAAGCGTCAGACCCAGTGAACCCAGGGGTGCCGGTCCCAGATCGGAAGAGCGGTTTCAG
chr19	17952582	17952621	JAK3_11467	+	GTGACCTATGCACCAGACGTGGGGAGTACCAGAGTGGGGCCCCAGCTGGACCCCGCCAAGATCGGAAGAGCGGTTTCAG
chr19	17953430	17953469	JAK3_11468	+	GTGACCTATGCACCAGACGTTGGAGGGGAGGGAGCCGCTCAGCGTCGGGAGGGGTCCAGATCGGAAGAGCGGTTTCAG
chr19	17953992	17954031	JAK3_11469	+	GTGACCTATGCACCAGACGTGCCACAGGGAGCATAGCTGAGGCCACCCAACCTTCAAGCCAGATCGGAAGAGCGGTTTCAG
chr19	17954311	17954350	JAK3_11470	+	GTGACCTATGCACCAGACGTAGGAGAGAACCCTGGGATGAAAGTGAACCCAGCCTCAGTAGATCGGAAGAGCGGTTTCAG
chr19	17954720	17954759	JAK3_11471	+	GTGACCTATGCACCAGACGTTGGTCCCACAGCTCCCTCCTGAGTCAACCCATCTGTGCCAGATCGGAAGAGCGGTTTCAG
chr19	17955237	17955276	JAK3_11472	+	GTGACCTATGCACCAGACGTTGCCTGGGGACAGAGAGAAAGGCCCTCAGTCTGTCAGATCGGAAGAGCGGTTTCAG
chr5	56111893	56111932	MAP3K1_11473	+	GTGACCTATGCACCAGACGTGGGCCGGGGTCGCGGGGGGACTTGGAGAGCGGGCAGAGGAGATCGGAAGAGCGGTTTCAG
chr5	56152588	56152627	MAP3K1_11474	+	GTGACCTATGCACCAGACGTATGGTTACCAGTTATAAGGAAGAAAGCATAGGAGGAAATAGATCGGAAGAGCGGTTTCAG
chr5	56155753	56155792	MAP3K1_11475	+	GTGACCTATGCACCAGACGTGTTACAACAAATATGTTAGTTTTTATAATTTTTAGCTTCAAGATCGGAAGAGCGGTTTCAG
chr5	56160772	56160811	MAP3K1_11476	+	GTGACCTATGCACCAGACGTTCCACATTTTATACTTTATTAGTAGTAGTATATGGTACTAAGATCGGAAGAGCGGTTTCAG
chr5	56161294	56161333	MAP3K1_11477	+	GTGACCTATGCACCAGACGTATAAATGCTTAGAGTAAAATTTAGCATATTCTTAGGATAGATCGGAAGAGCGGTTTCAG
chr5	56161815	56161854	MAP3K1_11478	+	GTGACCTATGCACCAGACGTTTAAGGCTTTCAAACATTAATCCAGTGTACTTTTTAATTAGATCGGAAGAGCGGTTTCAG
chr5	56167869	56167908	MAP3K1_11479	+	GTGACCTATGCACCAGACGTCCTTTTCTCCCTATGCTTACTCAACACAGTTGCTCTCTGAAGATCGGAAGAGCGGTTTCAG
chr5	56168560	56168599	MAP3K1_11480	+	GTGACCTATGCACCAGACGTTGAAATGATACGGATATGTTAATTTTTAAAAATTTCTCAAGATCGGAAGAGCGGTTTCAG
chr5	56168843	56168882	MAP3K1_11481	+	GTGACCTATGCACCAGACGCTTTTGTTTTCTATTCTCAAAGAAATTTATAGATCAATAGATCGGAAGAGCGGTTTCAG
chr5	56171148	56171187	MAP3K1_11482	+	GTGACCTATGCACCAGACGTTTATTCCATAATCATATTTGGGTTTTGGGGTTTTTGGAGATCGGAAGAGCGGTTTCAG
chr5	56174939	56174978	MAP3K1_11483	+	GTGACCTATGCACCAGACGTTTATGATGAACTTCAAACCTCTTGTCTTAAAAGTGCAGATCGGAAGAGCGGTTTCAG
chr5	56176640	56176679	MAP3K1_11484	+	GTGACCTATGCACCAGACGTTTCACTTAAAGGAATATAGCATATTTTATCATGTTCTGCAGATCGGAAGAGCGGTTTCAG

chr5	56177110	56177149	MAP3K1_11485	+	GTGACCTATGCACCAGACGTTTCTGAAATGTATTACTTGTATCTTCTACCTCCCTACAGATCGGAAGAGCGGTTTCAG
chr5	56179517	56179556	MAP3K1_11486	+	GTGACCTATGCACCAGACGTTAGTGTGAGCATATAAATGAAATGACTCAAATCACAAAATGAAAGATCGGAAGAGCGGTTTCAG
chr5	56180664	56180703	MAP3K1_11487	+	GTGACCTATGCACCAGACGTTGTTTAAATTAACAAATAGTAGTACGTTGATTTAACATTTTCAGATCGGAAGAGCGGTTTCAG
chr5	56183358	56183397	MAP3K1_11488	+	GTGACCTATGCACCAGACGTTCTTTGAGTGTGATGACAGAAAATATTTTGAATCTGTGAGATCGGAAGAGCGGTTTCAG
chr5	56184195	56184234	MAP3K1_11489	+	GTGACCTATGCACCAGACGTTGATAAAAATTAACCTTCTTTGTGCTAAAAGGAGTACAGCAGAAGATCGGAAGAGCGGTTTCAG
chr5	56189518	56189557	MAP3K1_11490	+	GTGACCTATGCACCAGACGTTAGATCAACTACAGTAGAAACAGGATGCTCAACAAGAGAAAAGATCGGAAGAGCGGTTTCAG
chr5	56178271	56178310	MAP3K1_11491	+	GTGACCTATGCACCAGACGTTGACTTGATCTGAACAGTAGTTCCAAATGTGATGACAGCTAGATCGGAAGAGCGGTTTCAG
chr5	179663537	179663576	MAPK9_11492	+	GTGACCTATGCACCAGACGTTAAAACCAAATAATAAAAATCTGAGGCACGACATTGCTGCAGATCGGAAGAGCGGTTTCAG
chr5	179663542	179663581	MAPK9_11493	+	GTGACCTATGCACCAGACGTTCAAATAATAAAAATCTGAGGCACGACATTGCTGCAAATCAGATCGGAAGAGCGGTTTCAG
chr5	179665414	179665453	MAPK9_11494	+	GTGACCTATGCACCAGACGTTAATACAAGTTAAAATGCTTAATCAGTTTTCTAAACAGTTTCAGATCGGAAGAGCGGTTTCAG
chr5	179666998	179667037	MAPK9_11495	+	GTGACCTATGCACCAGACGTTAATCATATGTAAGTCAACAGTAATGCCTCAAAAAAAAAATAGATCGGAAGAGCGGTTTCAG
chr5	179668166	179668205	MAPK9_11496	+	GTGACCTATGCACCAGACGTTAAACAAATATAAATTAATGCTGTTAATATAAACCAACAGAGATCGGAAGAGCGGTTTCAG
chr5	179669766	179669805	MAPK9_11497	+	GTGACCTATGCACCAGACGTTCTTGGAGAAAATCAACTGAAGTACCTGTATTACAGTAGATCGGAAGAGCGGTTTCAG
chr5	179674521	179674560	MAPK9_11498	+	GTGACCTATGCACCAGACGTTAATGAAATGATAAAAATTATGAAGTGCCATGAACAAAACAAAGATCGGAAGAGCGGTTTCAG
chr5	179674937	179674976	MAPK9_11499	+	GTGACCTATGCACCAGACGTTCCAGGGGATAAAAACAGCTAGAGTCCCCATCTTTTTAGATCGGAAGAGCGGTTTCAG
chr5	179676149	179676188	MAPK9_11500	+	GTGACCTATGCACCAGACGTTAATGGCTTAAATTAGTAAAATGAATGAAGCATGCTAAATAAGATCGGAAGAGCGGTTTCAG
chr5	179688833	179688872	MAPK9_11501	+	GTGACCTATGCACCAGACGTTAAAGTGCACTTATTTATTTGAAAATTCAAAAGTTCCCTTAGATCGGAAGAGCGGTTTCAG
chr5	179691850	179691889	MAPK9_11502	+	GTGACCTATGCACCAGACGTTAAAATTAATATACTCAATATGTCAATTTACTTTGATTACAGATCGGAAGAGCGGTTTCAG
chr5	179696420	179696459	MAPK9_11503	+	GTGACCTATGCACCAGACGTTGAAATATAATGCACAATCCATTAGAACGGTTTTGGAAAATAGATCGGAAGAGCGGTTTCAG
chr5	179707572	179707611	MAPK9_11504	+	GTGACCTATGCACCAGACGTTCTGCAATATCCCGAAGGGTGGGCAAGTTTCAGATCCCTTAGATCGGAAGAGCGGTTTCAG
chr2	16082987	16083026	MYCN_11505	+	GTGACCTATGCACCAGACGTTAACTCGGGTCCGGCTGCCTCCTGGGGCACTGGACCCCGAGATCGGAAGAGCGGTTTCAG
chr2	16086230	16086269	MYCN_11506	+	GTGACCTATGCACCAGACGTTAACTGGACAGTCACTGCCACTTTGCACATTTTGATTTTTAGATCGGAAGAGCGGTTTCAG
chr2	16082592	16082631	MYCN_11507	+	GTGACCTATGCACCAGACGTTACCGGCCGCGGCCCAACCCCGCGTTCCACCCCGCCAGTAGATCGGAAGAGCGGTTTCAG
chr2	16085927	16085966	MYCN_11508	+	GTGACCTATGCACCAGACGTTAGAGCTTGAGCCCCGAAACTCTGACTCGGAGGACAGTGAAGATCGGAAGAGCGGTTTCAG
chr9	134001147	134001186	NUP214_11509	+	GTGACCTATGCACCAGACGTTAACCAGGCGCTCCCTCCCTCTTTAGTCTGGCGTTGCCTAGATCGGAAGAGCGGTTTCAG
chr9	134003117	134003156	NUP214_11510	+	GTGACCTATGCACCAGACGTTGGTTTATGTTGCAAAGTAGAGAGAGGATGATGGTGGCATAGATCGGAAGAGCGGTTTCAG
chr9	134003881	134003920	NUP214_11511	+	GTGACCTATGCACCAGACGTTTATACTGTGATGTCAACATGAGAACCTAAGCAGATTTAGATCGGAAGAGCGGTTTCAG
chr9	134004875	134004914	NUP214_11512	+	GTGACCTATGCACCAGACGTTAAGGCTTTACACATGTAGCATACAATCATGGTCTACTAGATCGGAAGAGCGGTTTCAG
chr9	134006234	134006273	NUP214_11513	+	GTGACCTATGCACCAGACGTTCTTGAATCTTGAATTTTCTTAAGTTGCCACTTTTTAGATCGGAAGAGCGGTTTCAG
chr9	134008057	134008096	NUP214_11514	+	GTGACCTATGCACCAGACGTTCTTTCTTTGGGCTGACCTCTAATGACATGTTATAGATCGGAAGAGCGGTTTCAG
chr9	134008607	134008646	NUP214_11515	+	GTGACCTATGCACCAGACGTTGGAAGAAATTTCAATGTTTGAGAATTAGAGAAGTCTTCTAAGATCGGAAGAGCGGTTTCAG
chr9	134010402	134010441	NUP214_11516	+	GTGACCTATGCACCAGACGTTAGTCTGGACAGGGCATTCTGCTCTCACTGGAAGATCACAGATCGGAAGAGCGGTTTCAG
chr9	134014805	134014844	NUP214_11517	+	GTGACCTATGCACCAGACGTTCTGGTAGTTAGTGCAGAANAATAGTCTTCTTTCTAGTTAGGAGATCGGAAGAGCGGTTTCAG
chr9	134016108	134016147	NUP214_11518	+	GTGACCTATGCACCAGACGTTGCCTGCTTTATCAGTAAGGAATACCATGGGCTTGCACAGATCGGAAGAGCGGTTTCAG
chr9	134020152	134020191	NUP214_11519	+	GTGACCTATGCACCAGACGTTCTAAAGTTTGAATCTTCTGAGTTGGGTAGAATAATTTAGATCGGAAGAGCGGTTTCAG
chr9	134021702	134021741	NUP214_11520	+	GTGACCTATGCACCAGACGTTAAGCAGACAACCTTAGACCTCAGCCCTGCCTTCTCAGATTAGATCGGAAGAGCGGTTTCAG
chr9	134022982	134023021	NUP214_11521	+	GTGACCTATGCACCAGACGTTTACGCTTGAATGTTTGTTTATTAAATTTACTGCCCCAGATCGGAAGAGCGGTTTCAG
chr9	134025808	134025847	NUP214_11522	+	GTGACCTATGCACCAGACGTTTCTGAGGGTGTTTTCTGAAAGTAGCTGACAGACTTGGAGATCGGAAGAGCGGTTTCAG
chr9	134026163	134026202	NUP214_11523	+	GTGACCTATGCACCAGACGTTGGATACTTTTCTGAGTTGAATTGCATTTAAACAATTTAGATCGGAAGAGCGGTTTCAG
chr9	134027292	134027331	NUP214_11524	+	GTGACCTATGCACCAGACGTTATGTAATCTGTTAAAAGATTTAAAACAAGCTCATGTAGATCGGAAGAGCGGTTTCAG
chr9	134038571	134038610	NUP214_11525	+	GTGACCTATGCACCAGACGTTGACTTGCACATAAATAATGGTGAATGAATGCATGAACAGATCGGAAGAGCGGTTTCAG
chr9	134039353	134039392	NUP214_11526	+	GTGACCTATGCACCAGACGTTCTTCCAGTCTTTAACTCCCTTTATTCTCTTCCAAGTAAGATCGGAAGAGCGGTTTCAG
chr9	134039542	134039581	NUP214_11527	+	GTGACCTATGCACCAGACGTTCCAGTAACCTGGGCCTGTACATAGTGTAGAGGGTGTGGTGGAGATCGGAAGAGCGGTTTCAG
chr9	134049716	134049755	NUP214_11528	+	GTGACCTATGCACCAGACGTTAGTGGGAAAGGAAACTGTTTTCCCTATGATGTTTCTAACAGATCGGAAGAGCGGTTTCAG
chr9	134051019	134051058	NUP214_11529	+	GTGACCTATGCACCAGACGTTAGCCCATACTGTACAGAGGCTGATTATGAGCTGTCTGAGATCGGAAGAGCGGTTTCAG
chr9	134053808	134053847	NUP214_11530	+	GTGACCTATGCACCAGACGTTACTGCCCAGTGTGTTTCCAGCCCTGGCTGCTTCTGTAGTACGATCGGAAGAGCGGTTTCAG
chr9	134064529	134064568	NUP214_11531	+	GTGACCTATGCACCAGACGTTATTTTGTGTTTCTTGAAGTGAAGAAGCACTCCACAATAGATCGGAAGAGCGGTTTCAG
chr9	134067690	134067729	NUP214_11532	+	GTGACCTATGCACCAGACGTTAAAGTTTTATGGCAAATTAAGTCAATAGCTTCCAGATCGGAAGAGCGGTTTCAG
chr9	134070692	134070731	NUP214_11533	+	GTGACCTATGCACCAGACGTTGTGTTGAGTAGCACTACTCATGTGTTTTCTTAAATAAGAGATCGGAAGAGCGGTTTCAG
chr9	134074413	134074452	NUP214_11534	+	GTGACCTATGCACCAGACGTTGGAAGCTTTTACTTGTTCCTCTGCTATTTGAAAAGATCGGAAGAGCGGTTTCAG
chr9	134077115	134077154	NUP214_11535	+	GTGACCTATGCACCAGACGTTATGCTTTCACTTCACTGATCAACATGTCTCAAACCCATTCAAGATCGGAAGAGCGGTTTCAG
chr9	134090766	134090805	NUP214_11536	+	GTGACCTATGCACCAGACGTTTCCAGTCTTTCCAGTCCCTTGGTCCCTAATGCCATTGTACAGATCGGAAGAGCGGTTTCAG
chr9	134098328	134098367	NUP214_11537	+	GTGACCTATGCACCAGACGTTGCTATTTGTTATGTTATCTTTATATATGATTTGTTTAAAGATCGGAAGAGCGGTTTCAG
chr9	134103729	134103768	NUP214_11538	+	GTGACCTATGCACCAGACGTTGGGAGGGCCCTTGGGAACCCACAGCCAGCCAAAAGCAGATCGGAAGAGCGGTTTCAG
chr9	134106167	134106206	NUP214_11539	+	GTGACCTATGCACCAGACGTTACAGTTCTCCCTCACAAAGCAAAATGGTCCCTTCTGCCAGATCGGAAGAGCGGTTTCAG
chr9	134107706	134107745	NUP214_11540	+	GTGACCTATGCACCAGACGTTCCCTTTTGAAGTCTCACTTAAATAAAGCATAAATAAGAGATCGGAAGAGCGGTTTCAG
chr9	134108885	134108924	NUP214_11541	+	GTGACCTATGCACCAGACGTTGACGGCTTTCTGATCCCTGGGACCAACCCATCTCAGATCGGAAGAGCGGTTTCAG
chr9	134073063	134073102	NUP214_11542	+	GTGACCTATGCACCAGACGTTCCACTAGCAGTACACCACCAGCCACCCAGCACTTCTCAAGATCGGAAGAGCGGTTTCAG

chr9	134073513	134073552	NUP214_11543	+	GTGACCTATGCACCAGACGTCCAGCCTGCAGTCAGCAACTCTGGCACTGCAGCATCTAGTAGATCGGAAGAGCGGTTTCAG
chr9	134073963	134074002	NUP214_11544	+	GTGACCTATGCACCAGACGTGACGACAGCAGCTGCCACACCACAGGTCAGCAGCTCAGGGAGATCGGAAGAGCGGTTTCAG
chr11	100910013	100910052	PGR_11545	+	GTGACCTATGCACCAGACGTAAACAAATGAGTAGAAAAACATGTAATAAAAAATAAAATTCAGATCGGAAGAGCGGTTTCAG
chr11	100912844	100912883	PGR_11546	+	GTGACCTATGCACCAGACGTGACAATTAAGTGGCAGTTGTGTATAAAAAGATGACATTAGATCGGAAGAGCGGTTTCAG
chr11	100920801	100920840	PGR_11547	+	GTGACCTATGCACCAGACGTACACAATACACAAAAGAAAAAGCAACAGGAAAAAAAATAGAGATCGGAAGAGCGGTTTCAG
chr11	100922310	100922349	PGR_11548	+	GTGACCTATGCACCAGACGTAATTTAAAAATACAGTGACCATAAAAATGACTGAATTATCAGATCGGAAGAGCGGTTTCAG
chr11	100933494	100933533	PGR_11549	+	GTGACCTATGCACCAGACGTGAAAAAAAAGAAATTCATGTAATATATAAACTCCATAAGATCGGAAGAGCGGTTTCAG
chr11	100962618	100962657	PGR_11550	+	GTGACCTATGCACCAGACGTAAAAATGAGTCAAAATTTTACAAATATCTAAGATTCACTGAGATCGGAAGAGCGGTTTCAG
chr11	100996900	100996939	PGR_11551	+	GTGACCTATGCACCAGACGTAAAACAAAGTACTCCATTTATTTTTAAGTGCACCACATCAGATCGGAAGAGCGGTTTCAG
chr11	100999812	100999851	PGR_11552	+	GTGACCTATGCACCAGACGTCTCCCTTTTTCTCTCCCCCGTCTCCAGGAGGAGGAAAAAGATCGGAAGAGCGGTTTCAG
chr11	100998584	100998623	PGR_11553	+	GTGACCTATGCACCAGACGTCAACAAGGTAGGAACGCGGGGAGCGCGGGAGGCGCTCCGCGAGATCGGAAGAGCGGTTTCAG
chr11	100998993	100999032	PGR_11554	+	GTGACCTATGCACCAGACGTGGGGGACCGGGGAGCGCTCTGCTGCCGCCCCCGCGGAGATCGGAAGAGCGGTTTCAG
chr11	100999402	100999441	PGR_11555	+	GTGACCTATGCACCAGACGTGAGCGGGGAGGGCTGGGTTGGCTCTGCCCGGACCTGAGGGAGATCGGAAGAGCGGTTTCAG
chr22	46594499	46594538	PPARA_11556	+	GTGACCTATGCACCAGACGTGTTTTCTAGAAAAGTTTTATTTAGAAATGTTTTCTTCTCCAGATCGGAAGAGCGGTTTCAG
chr22	46611241	46611280	PPARA_11557	+	GTGACCTATGCACCAGACGTGCTGGAACAGGGCCTGGTGGCCGCCACCATCACTACTTAAGATCGGAAGAGCGGTTTCAG
chr22	46614309	46614348	PPARA_11558	+	GTGACCTATGCACCAGACGTGGCCCTGCACATTTCCAGTTCGTTCTCAGTTCCTCAGATCGGAAGAGCGGTTTCAG
chr22	46615922	46615961	PPARA_11559	+	GTGACCTATGCACCAGACGTGGCGCTGTTCTGGGTTCTTGGCAACATGGAACCAAGTGTAGATCGGAAGAGCGGTTTCAG
chr22	46628147	46628186	PPARA_11560	+	GTGACCTATGCACCAGACGTGATTAATCTGCTGGTATGCTACTGACAGGCTCCTGATCGGAAGAGCGGTTTCAG
chr22	46631288	46631327	PPARA_11561	+	GTGACCTATGCACCAGACGTATCAGCCACACTTTTTCCAGGAGTTCTGAAGCTGACAGCAAGATCGGAAGAGCGGTTTCAG
chr19	54385929	54385968	PRKCG_11562	+	GTGACCTATGCACCAGACGTGGGGCTGGGGGACTGGGGGACGAGGGGACTAGGGGTGCAGAGATCGGAAGAGCGGTTTCAG
chr19	54386459	54386498	PRKCG_11563	+	GTGACCTATGCACCAGACGTGGGACCGGGCTCCTGGGACCCTCAGGAGGTTGAGGGCTGAGATCGGAAGAGCGGTTTCAG
chr19	54387508	54387547	PRKCG_11564	+	GTGACCTATGCACCAGACGTGGACACCTGGTTCTCTCCTCGGGCGCTGCCCCCGCCCTCAGATCGGAAGAGCGGTTTCAG
chr19	54393014	54393053	PRKCG_11565	+	GTGACCTATGCACCAGACGTGGCGCTGCCAGGGCCCTCCAAAGCGCCGGTCTGGGTAGATCGGAAGAGCGGTTTCAG
chr19	54393282	54393321	PRKCG_11566	+	GTGACCTATGCACCAGACGTGCCCTCGCCTGGCCCGCCCTCCCAAGTGTGAGGAGATCGGAAGAGCGGTTTCAG
chr19	54395095	54395134	PRKCG_11567	+	GTGACCTATGCACCAGACGTGGTGCAGGGAAGGCAATGACAGCTGACAGAGAATGATCTGAGATCGGAAGAGCGGTTTCAG
chr19	54395908	54395947	PRKCG_11568	+	GTGACCTATGCACCAGACGTGGGCTGGGGCTGGGGATGGAGCGCAATATTACCATCTCCAGATCGGAAGAGCGGTTTCAG
chr19	54396340	54396379	PRKCG_11569	+	GTGACCTATGCACCAGACGTCTGGCTTCTCAAGGGAGCCAGCCAGCCTCCACGGTAGATCGGAAGAGCGGTTTCAG
chr19	54396656	54396695	PRKCG_11570	+	GTGACCTATGCACCAGACGTCCAGGGCGTTGAATGGAGGGGATTTTTGCCTACTTCTCTGAGATCGGAAGAGCGGTTTCAG
chr19	54401376	54401415	PRKCG_11571	+	GTGACCTATGCACCAGACGTGGGGTTCTGGGGTAAAGGAGGAGTGTGTGGGAAGTCCAGATCGGAAGAGCGGTTTCAG
chr19	54401893	54401932	PRKCG_11572	+	GTGACCTATGCACCAGACGTAGGGGCGGAGGGCTGTCTCCGGCGCTGCCCTTATCCAGTAGATCGGAAGAGCGGTTTCAG
chr19	54403589	54403628	PRKCG_11573	+	GTGACCTATGCACCAGACGTGCCAACAGAGAATGGTCGGGGTGGTGGGAAGGGGCGAGATAGATCGGAAGAGCGGTTTCAG
chr19	54403746	54403785	PRKCG_11574	+	GTGACCTATGCACCAGACGTCCAGGAATTTCCGTGGAGGAAATCACGCCCTGGAAGGGAAGATCGGAAGAGCGGTTTCAG
chr19	54404014	54404053	PRKCG_11575	+	GTGACCTATGCACCAGACGTCCCTGCTGCTGTTGACAGCTTGTAGATCCCTTAGAGGGTAGATCGGAAGAGCGGTTTCAG
chr19	54406418	54406457	PRKCG_11576	+	GTGACCTATGCACCAGACGTGGGGAGAAGCTGGTCTGGCTAAAAGAGACAGAGAGGGGAGATCGGAAGAGCGGTTTCAG
chr19	54408007	54408046	PRKCG_11577	+	GTGACCTATGCACCAGACGTCTGACTGCCAGCTTCTCCAGCTCAACAACACACACCCACATCGGAAGAGCGGTTTCAG
chr19	54409722	54409761	PRKCG_11578	+	GTGACCTATGCACCAGACGTCTCCAGGCAACAAAACCTGGTCCCTGAAGGGTGGGGTTAGATCGGAAGAGCGGTTTCAG
chr19	54410160	54410199	PRKCG_11579	+	GTGACCTATGCACCAGACGTGCCACTAGGTGTCCCAACGTCCCTCCGCGTGCAGGAGATCGGAAGAGCGGTTTCAG
chr1	198666049	198666088	PTPRC_11580	+	GTGACCTATGCACCAGACGTAAAAAGTTGTTAACTTAAATATCAGGGAATGTCAATTTAGAAAAGATCGGAAGAGCGGTTTCAG
chr1	198668844	198668883	PTPRC_11581	+	GTGACCTATGCACCAGACGTCTTTAGACTTGTGCAATATGAAAAGTACATGACGACTAAGATCGGAAGAGCGGTTTCAG
chr1	198671670	198671709	PTPRC_11582	+	GTGACCTATGCACCAGACGTGCTGCTTAGTAGTGTCTTACATATAGATAATGAAATGGAGATCGGAAGAGCGGTTTCAG
chr1	198672512	198672551	PTPRC_11583	+	GTGACCTATGCACCAGACGTCTCAGTCAGGCAGCCACCATCCCCATGTGCCTGGTGAAGATCGGAAGAGCGGTTTCAG
chr1	198673638	198673677	PTPRC_11584	+	GTGACCTATGCACCAGACGTTTACTTAGAATCAGCATACTCTACTTTGGAATAGCACTTTAGATCGGAAGAGCGGTTTCAG
chr1	198677401	198677440	PTPRC_11585	+	GTGACCTATGCACCAGACGTAAACATTGACCAGAGAATTTTTTTTTGTGGCACAATGTTGTAGATCGGAAGAGCGGTTTCAG
chr1	198678964	198679003	PTPRC_11586	+	GTGACCTATGCACCAGACGTACTTGCATTTATATGTAATAATTGCTTCTCTTCTCATGTTAGATCGGAAGAGCGGTTTCAG
chr1	198682212	198682251	PTPRC_11587	+	GTGACCTATGCACCAGACGTGTAAGATTTAAATTTTCAAGAAAAGAGAAATCAAGAATTTGAGATCGGAAGAGCGGTTTCAG
chr1	198685980	198686019	PTPRC_11588	+	GTGACCTATGCACCAGACGTGTTTTAATGCTTCTTCCATAAGTGTAAAAGCAAGGTAGATCGGAAGAGCGGTTTCAG
chr1	198687442	198687481	PTPRC_11589	+	GTGACCTATGCACCAGACGTGCTCTCTACATTAAGTACAACTACATTATAATGATAGATCGGAAGAGCGGTTTCAG
chr1	198698311	198698350	PTPRC_11590	+	GTGACCTATGCACCAGACGTATATTTTTGCTGATGACTATTCTTCCCTGCATTTGAATAGATCGGAAGAGCGGTTTCAG
chr1	198700866	198700905	PTPRC_11591	+	GTGACCTATGCACCAGACGTCTTTTGTATATGATGATAAATTCAGACATCAAGACAGTTTCAAGATCGGAAGAGCGGTTTCAG
chr1	198701530	198701569	PTPRC_11592	+	GTGACCTATGCACCAGACGTATTGAGTGCTGAATTCATATATTAGGCTACTTGATTATAGATCGGAAGAGCGGTTTCAG
chr1	198701696	198701735	PTPRC_11593	+	GTGACCTATGCACCAGACGTATTTGATTCTTCTTACACTACATTTTATTTCAGTCCAGATCGGAAGAGCGGTTTCAG
chr1	198703372	198703411	PTPRC_11594	+	GTGACCTATGCACCAGACGTGATAATTGATAATTTCTTTTGAATAAATTTATAGCACTAGATCGGAAGAGCGGTTTCAG
chr1	198703565	198703604	PTPRC_11595	+	GTGACCTATGCACCAGACGTAGAAGATTCATAGTGTGGTCTTGGGGTTAGGAAAACAAGAGATCGGAAGAGCGGTTTCAG
chr1	198711166	198711205	PTPRC_11596	+	GTGACCTATGCACCAGACGTGCAACAAAAAACAACAACAACAAAAAAGTCCAACAGAGATCGGAAGAGCGGTTTCAG
chr1	198711507	198711546	PTPRC_11597	+	GTGACCTATGCACCAGACGTACTTTAGTATTCTCATTGTTTTGGACTTAAAGATCGGAAGAGCGGTTTCAG
chr1	198717339	198717378	PTPRC_11598	+	GTGACCTATGCACCAGACGTATTTTTTTATTTTTTGATCAGATAAAGTTAAGCTTTTAGATCGGAAGAGCGGTTTCAG
chr1	198718689	198718728	PTPRC_11599	+	GTGACCTATGCACCAGACGTAAATTCGCAAAATCCCAAGCTTAAACATTTAAATAATAAGATCGGAAGAGCGGTTTCAG
chr1	198719766	198719805	PTPRC_11600	+	GTGACCTATGCACCAGACGTGTAAGATTTTCTTTAAGCTTCTGCTCAAAAACGTCAAGATCGGAAGAGCGGTTTCAG



chr1	198721511	198721550	PTPRC_11601	+	GTGACCTATGCACCAGACGTAATTTGGGGAGTATATTTCTTTGATATAATGGATCTGGTAAGATCGGAAGAGCGGTTTCAG
chr1	198721912	198721951	PTPRC_11602	+	GTGACCTATGCACCAGACGTTTTGGTGAATGTGCTCTCAAATCATATGCTTGACTTCAGATCGGAAGAGCGGTTTCAG
chr1	198723544	198723583	PTPRC_11603	+	GTGACCTATGCACCAGACGTTTACCATTGCTTTTAAACATGCTCGGAATTTTTTTTTTCTAGATCGGAAGAGCGGTTTCAG
chr1	198725321	198725360	PTPRC_11604	+	GTGACCTATGCACCAGACGTAATGAGGAACTCAAACCTCCTGTTAGCTGTTATTTCTAGATCGGAAGAGCGGTTTCAG
chr1	44010848	44010887	PTPRF_11605	+	GTGACCTATGCACCAGACGTCCTCCCAAGGTACAGATCTCCACAGGTTGAAAGGTGGCATAGATCGGAAGAGCGGTTTCAG
chr1	44019319	44019358	PTPRF_11606	+	GTGACCTATGCACCAGACGTGGTGGGAAGGGGTGCGCAGGGCTCAGGGTCTGCCACACTAGATCGGAAGAGCGGTTTCAG
chr1	44019623	44019662	PTPRF_11607	+	GTGACCTATGCACCAGACGTGGGAGACGTGGGACGTTGGCTGGGCTGCCGGGCTGAGCGTGGGAGATCGGAAGAGCGGTTTCAG
chr1	44035460	44035499	PTPRF_11608	+	GTGACCTATGCACCAGACGTGGCAGGGGTCAAGGGGCCATGCAGACCTCAGAACAAGCGTAGATCGGAAGAGCGGTTTCAG
chr1	44044602	44044641	PTPRF_11609	+	GTGACCTATGCACCAGACGTAGGCAGTGCCTGGCCCTGTCACCACAGAGCTGTGCTGCAAGATCGGAAGAGCGGTTTCAG
chr1	44054682	44054721	PTPRF_11610	+	GTGACCTATGCACCAGACGTGAGGTGCTGTAAACAGTGCCCTCCCTGTCATCTGGGAGGTAGATCGGAAGAGCGGTTTCAG
chr1	44057235	44057274	PTPRF_11611	+	GTGACCTATGCACCAGACGTGCATGCCGGCTGGGCAGCCAACAGCAGAGAAGGGGAGGCTAGATCGGAAGAGCGGTTTCAG
chr1	44057630	44057669	PTPRF_11612	+	GTGACCTATGCACCAGACGTGGCAGAGAAGCATGAGGGGCTCCTGGTCCCTGAGGGTAGATCGGAAGAGCGGTTTCAG
chr1	44063735	44063774	PTPRF_11613	+	GTGACCTATGCACCAGACGTCCACCCTGGGGCAGGGGAGGGGCGCTTCTGCCTCAGACACCAAGCATCGGAAGAGCGGTTTCAG
chr1	44064595	44064634	PTPRF_11614	+	GTGACCTATGCACCAGACGTGGGTGGTGGGGTGGCAGGGTGAAGCAGACAGCAGCATGAGATCGGAAGAGCGGTTTCAG
chr1	44067779	44067818	PTPRF_11615	+	GTGACCTATGCACCAGACGTGGTGTGCGAACCGGGACAAAGACATGGGTCAAGCTGGGCTCAGATCGGAAGAGCGGTTTCAG
chr1	44069215	44069254	PTPRF_11616	+	GTGACCTATGCACCAGACGTGGTCAAGACGACCTGAGGGTGGGGCAGCAGGAGGGCAGCAGATCGGAAGAGCGGTTTCAG
chr1	44069871	44069910	PTPRF_11617	+	GTGACCTATGCACCAGACGTGGACATGGCATCCCTCCCGAGTGTGGCTGCATCTGGGGAGATCGGAAGAGCGGTTTCAG
chr1	44070682	44070721	PTPRF_11618	+	GTGACCTATGCACCAGACGTGCCACCGCAGCTGAGCTGGCAGACACAGCCCTGCTGAGATCGGAAGAGCGGTTTCAG
chr1	44071125	44071164	PTPRF_11619	+	GTGACCTATGCACCAGACGTGAGGTATCGGGGAGGGCGGGCAGGGCTGGAGGTAACCAGATCGGAAGAGCGGTTTCAG
chr1	44071304	44071343	PTPRF_11620	+	GTGACCTATGCACCAGACGTAGGGGATGGGGACACTGACAGCCCCATTGCAGTGGTCAGCAGATCGGAAGAGCGGTTTCAG
chr1	44072140	44072179	PTPRF_11621	+	GTGACCTATGCACCAGACGTGCCGGCTGGCTGTGACAGCCCTGATTCCCTGGGCCTGGCAGATCGGAAGAGCGGTTTCAG
chr1	44072650	44072689	PTPRF_11622	+	GTGACCTATGCACCAGACGTCCCTCAGAGCTCCGGGAACCGGCCACTGCCCTCGCCTTTAGATCGGAAGAGCGGTTTCAG
chr1	44075180	44075219	PTPRF_11623	+	GTGACCTATGCACCAGACGTCTATGGCTGTGTCGCCAGCCAGCCAGCTAGCAGGCCTAGATCGGAAGAGCGGTTTCAG
chr1	44079397	44079436	PTPRF_11624	+	GTGACCTATGCACCAGACGTCCCGCCCCCTACCTATGCTGCCAGCCCTACCCAAACAGCCTCGGAAGAGCGGTTTCAG
chr1	44083250	44083289	PTPRF_11625	+	GTGACCTATGCACCAGACGTGGGGTGGCCCTCCCATCCCTTGTCTCCCCCTTGTAGCAGATCGGAAGAGCGGTTTCAG
chr1	44083593	44083632	PTPRF_11626	+	GTGACCTATGCACCAGACGTAGGGCCCTGCCAGGAGGGGGTGGGAAATGCCAGCCACAAGATCGGAAGAGCGGTTTCAG
chr1	44084431	44084470	PTPRF_11627	+	GTGACCTATGCACCAGACGTCCCCAGTGCATATCTTACCAGACACTGTAAGGACAGAGATCGGAAGAGCGGTTTCAG
chr1	44084884	44084923	PTPRF_11628	+	GTGACCTATGCACCAGACGTACAGTGCCACCCAGGGGTGGGTGGGGTGGGAGGTGGGGAGATCGGAAGAGCGGTTTCAG
chr1	44085255	44085294	PTPRF_11629	+	GTGACCTATGCACCAGACGTGTGGGCTGCTTGGCTCCAGGGCTAGACTGGTTCATGCAGATCGGAAGAGCGGTTTCAG
chr1	44085540	44085579	PTPRF_11630	+	GTGACCTATGCACCAGACGTATGTCACTGCCACCATTGCCCTACAGGGCCCTAGGCCTGAGATCGGAAGAGCGGTTTCAG
chr1	44085903	44085942	PTPRF_11631	+	GTGACCTATGCACCAGACGTCTTTCCCCAGGGCCCTGTACACCTGGGAGAACACCAAGATCGGAAGAGCGGTTTCAG
chr1	44086261	44086300	PTPRF_11632	+	GTGACCTATGCACCAGACGTGCATTGAGTGTGTCCATAACGCTGCCCTGTCCACAGCTGGAGATCGGAAGAGCGGTTTCAG
chr1	44086674	44086713	PTPRF_11633	+	GTGACCTATGCACCAGACGTCCCCCTGGAGGGCTGGGTGGGTGGGCCTGAAGGCCTGGCAGATCGGAAGAGCGGTTTCAG
chr1	44086914	44086953	PTPRF_11634	+	GTGACCTATGCACCAGACGTCCAGGCTGACGGGCCAGGGCCCTGGCAGCAGCGCTGGAGATCGGAAGAGCGGTTTCAG
chr1	44087685	44087724	PTPRF_11635	+	GTGACCTATGCACCAGACGTCTCTCCCTCCGCCACCCTGGCCCTGGGGCTCCGAGGGGAAGATCGGAAGAGCGGTTTCAG
chr1	44056944	44056983	PTPRF_11636	+	GTGACCTATGCACCAGACGTGCGCCGCTGCAGGCACGCATGTGAGCGCCAGCACCATGAGATCGGAAGAGCGGTTTCAG
chr1	44069581	44069620	PTPRF_11637	+	GTGACCTATGCACCAGACGTCAAACCTGCATGTGACAGGACTGACCACGTCTACCACAGAGATCGGAAGAGCGGTTTCAG
chr3	12626167	12626206	RAF1_11638	+	GTGACCTATGCACCAGACGTGCCAAGAATGCTCTCATTAGCTGTGTCTCAAAGACACAGAGATCGGAAGAGCGGTTTCAG
chr3	12626491	12626530	RAF1_11639	+	GTGACCTATGCACCAGACGTGAAAACAGCTGAGCTAATGGGGGGTGAATGAACAACAGATAGATCGGAAGAGCGGTTTCAG
chr3	12626763	12626802	RAF1_11640	+	GTGACCTATGCACCAGACGTCCCATATGACAAAAGTGCATTTATCACCATATGACAGGCAGATCGGAAGAGCGGTTTCAG
chr3	12627309	12627348	RAF1_11641	+	GTGACCTATGCACCAGACGTGTTAAGGACTCTGGTTTCAAGAAAGTCCAGTTAATTTAGATCGGAAGAGCGGTTTCAG
chr3	12629147	12629186	RAF1_11642	+	GTGACCTATGCACCAGACGTAAAAGAAATTTAAAAATAAGTTTGGGGGCATGAGTAGAGATCGGAAGAGCGGTTTCAG
chr3	12633302	12633341	RAF1_11643	+	GTGACCTATGCACCAGACGTAGTTGGCAGTCAAGTGAATGATCTCAGTCTTAGATCGGAAGAGCGGTTTCAG
chr3	12641318	12641357	RAF1_11644	+	GTGACCTATGCACCAGACGTTAGAGATCATTATATACTCCATGCAATGGTAATAATCTTAGATCGGAAGAGCGGTTTCAG
chr3	12641789	12641828	RAF1_11645	+	GTGACCTATGCACCAGACGTAAAGACAAAGCAAGCCACACAAAGGATAAGCCAAACAGAAAGATCGGAAGAGCGGTTTCAG
chr3	12641925	12641964	RAF1_11646	+	GTGACCTATGCACCAGACGTAAAAGCTGGTCAACTCTACACAAAAGATTCTAGATCGGAAGAGCGGTTTCAG
chr3	12645799	12645838	RAF1_11647	+	GTGACCTATGCACCAGACGTAAAAGAAAATTCATGATTGGCACTTAGGCTTTCATACTGGAGATCGGAAGAGCGGTTTCAG
chr3	12647809	12647848	RAF1_11648	+	GTGACCTATGCACCAGACGTGCAGGGAAAGACTGGTTTTAGGCTTGCAGTAATCTTACAAGATCGGAAGAGCGGTTTCAG
chr3	12650433	12650472	RAF1_11649	+	GTGACCTATGCACCAGACGTAAACACAGGTGTAATATGCTGAATAAATAAAGATGACAAGATCGGAAGAGCGGTTTCAG
chr3	12650845	12650884	RAF1_11650	+	GTGACCTATGCACCAGACGTTTTAAAAAAAACATGAAATGTTTAAACAAGATCAAAGTTAGATCGGAAGAGCGGTTTCAG
chr3	12653572	12653611	RAF1_11651	+	GTGACCTATGCACCAGACGTAGGACCACCTTTAGGACCAACACAGGCTGCAGCACCCCTTAGATCGGAAGAGCGGTTTCAG
chr3	12660231	12660270	RAF1_11652	+	GTGACCTATGCACCAGACGTAAACAATCTTAAACCTGTAAGAAACACAAATAATTGTAGATCGGAAGAGCGGTTTCAG
chr7	128829334	128829373	SMO_11653	+	GTGACCTATGCACCAGACGTCCGAGCCGGTCTGGGGGGCGGGAGGTGCCGCGGTAAGATAGATCGGAAGAGCGGTTTCAG
chr7	128843441	128843480	SMO_11654	+	GTGACCTATGCACCAGACGTTGTGAGACAAGGTCCAGGCTCTCTGGTTGGGCAGGACCGAGATCGGAAGAGCGGTTTCAG
chr7	128845264	128845303	SMO_11655	+	GTGACCTATGCACCAGACGTGGAGGGCAGGCCCGGGGGCCCTCAGCTGGAACGTGGGAAGATCGGAAGAGCGGTTTCAG
chr7	128845634	128845673	SMO_11656	+	GTGACCTATGCACCAGACGTTGGGAGCCAGAGGTGAAGGTACAGGGAGGAAGCTGAAGAGATCGGAAGAGCGGTTTCAG
chr7	128846221	128846260	SMO_11657	+	GTGACCTATGCACCAGACGTGGTAGGAACGGGAGCCTGGATGGGGTGAATTTGAGGGAAGATCGGAAGAGCGGTTTCAG
chr7	128846439	128846478	SMO_11658	+	GTGACCTATGCACCAGACGTACCAGGCCAGGACCTGGGGCAACAAAATACTGGGCAAGATCGGAAGAGCGGTTTCAG

chr7	128848703	128848742	SMO_11659	+	GTGACCTATGCACCAGACGTCGGGGGACTTCGGTCTGAGGTCTGGCCAGCCCAACTAGATCGGAAGAGCGGTTTCAG
chr7	128849249	128849288	SMO_11660	+	GTGACCTATGCACCAGACGTTGGCATGGAGGCGGCAGTGCTGGGAGCTGGAGCCAAAGCCAAAGATCGGAAGAGCGGTTTCAG
chr7	128850400	128850439	SMO_11661	+	GTGACCTATGCACCAGACGTCAGCCAGCCCCCTCTGCCCTGCCCGCCTCACCCCTCAGCCTAGATCGGAAGAGCGGTTTCAG
chr7	128850965	128851004	SMO_11662	+	GTGACCTATGCACCAGACGTCCTCTCTACCCGAGCCGCTGGCCCCGCGCTGCCCATAGATCGGAAGAGCGGTTTCAG
chr7	128851622	128851661	SMO_11663	+	GTGACCTATGCACCAGACGTTCAAGCTTCTGGAGGAAGTGGGGGGAGCACAGAGGCTGGAGATCGGAAGAGCGGTTTCAG
chr7	128852303	128852342	SMO_11664	+	GTGACCTATGCACCAGACGTCAGGACCTGGGACAGGAAAGAGAGAACCAATACCTTCAAAGATCGGAAGAGCGGTTTCAG
chr10	104264102	104264141	SUFU_11665	+	GTGACCTATGCACCAGACGTTGGCCGGGAGACGCGGAGCGGCGGCTGGAAAGGTTAAGATCGGAAGAGCGGTTTCAG
chr10	104269071	104269110	SUFU_11666	+	GTGACCTATGCACCAGACGTTGCCACCTGTTCTTTTATCCAGAGCCTTATTCTGAGGTCTTAGATCGGAAGAGCGGTTTCAG
chr10	104309874	104309913	SUFU_11667	+	GTGACCTATGCACCAGACGTAGGGCTGGCTGCTGTGCTGGTCTTTTCCATGAGCCTGGAGATCGGAAGAGCGGTTTCAG
chr10	104352492	104352531	SUFU_11668	+	GTGACCTATGCACCAGACGTTGGTGGACGCTGGCTCAAGCCTTCTGTGGGAAAGGCTCTAGATCGGAAGAGCGGTTTCAG
chr10	104353489	104353528	SUFU_11669	+	GTGACCTATGCACCAGACGTATGCAAGGTGGGAGCGCGGCTCCCTGGGCTGGGGTGGGAGATCGGAAGAGCGGTTTCAG
chr10	104353833	104353872	SUFU_11670	+	GTGACCTATGCACCAGACGTAGTGAGGAAAACCTTTCTAGCACCCCTGTCCCTAGGCTCTAGATCGGAAGAGCGGTTTCAG
chr10	104357061	104357100	SUFU_11671	+	GTGACCTATGCACCAGACGTTCACTCAGACTTCCACCCAGCCTTCTCTCTTCTTCCACAGATCGGAAGAGCGGTTTCAG
chr10	104359312	104359351	SUFU_11672	+	GTGACCTATGCACCAGACGTCAGTGTCCCTGGGCTGGAACAAGAGGACGACTTTTTTCTGAGATCGGAAGAGCGGTTTCAG
chr10	104375170	104375209	SUFU_11673	+	GTGACCTATGCACCAGACGTCAGCCCTGCCACACAGTTTACCCACAGCACCCAGCTCAGAGATCGGAAGAGCGGTTTCAG
chr10	104377196	104377235	SUFU_11674	+	GTGACCTATGCACCAGACGTCCTTTTTCTTCTCCCTCTTCTTCTTTCATAGACTTCTTGCAGATCGGAAGAGCGGTTTCAG
chr10	104389923	104389962	SUFU_11675	+	GTGACCTATGCACCAGACGTTGCCCTGCAGTGGCCAGCGGGAGCCAGCTGCTCCCCAGTAGATCGGAAGAGCGGTTTCAG
chr1	47685857	47685896	TAL1_11676	+	GTGACCTATGCACCAGACGTTGGAGGACAAGAGTTAGAGAAATGGGCTTGAGATCTTCCAGATCGGAAGAGCGGTTTCAG
chr1	47689781	47689820	TAL1_11677	+	GTGACCTATGCACCAGACGTTGAACGGGCAGATCACAAAGATCCCATTGTTGAGGGAGGGAAAGATCGGAAGAGCGGTTTCAG
chr1	47691571	47691610	TAL1_11678	+	GTGACCTATGCACCAGACGTTGACAGACAGACAAGCGGATGCCCGCTCTGACGACCCGCCAGATCGGAAGAGCGGTTTCAG
chr14	76425699	76425738	TGFB3_11679	+	GTGACCTATGCACCAGACGTACATGTCAAGTGAAGGTTGGAAGGCCAAGTCTCAGGCTGAGATCGGAAGAGCGGTTTCAG
chr14	76427430	76427469	TGFB3_11680	+	GTGACCTATGCACCAGACGTTAAACATTTATAGAAAATCAACTTAAACCACCAATAAAGAGATCGGAAGAGCGGTTTCAG
chr14	76429841	76429880	TGFB3_11681	+	GTGACCTATGCACCAGACGTTGAAGGAAATGACAATCTCTGTCTGAAGAGACAGCCAGATCGGAAGAGCGGTTTCAG
chr14	76432049	76432088	TGFB3_11682	+	GTGACCTATGCACCAGACGTGACAGAAATGATGAGAAAGCACTCTGTGTGATGGGAAAGATCGGAAGAGCGGTTTCAG
chr14	76437609	76437648	TGFB3_11683	+	GTGACCTATGCACCAGACGTGAGAAAGGAGTGAAGTACCCGAGACCAGGACAGAGTGGCCAGATCGGAAGAGCGGTTTCAG
chr14	76438072	76438111	TGFB3_11684	+	GTGACCTATGCACCAGACGTAAGCAGAGCAGAGGGCACAGCATGAGCGAGACATGCAGGAAGATCGGAAGAGCGGTTTCAG
chr14	76447247	76447286	TGFB3_11685	+	GTGACCTATGCACCAGACGTTGGAAGAGAGGCCAGGGGGACGGCAAGGCCTGGAGAGGAAGAGATCGGAAGAGCGGTTTCAG
chr17	76171042	76171081	TK1_11686	+	GTGACCTATGCACCAGACGTTGGACAGGAGTGGGTGAAGGGCCAGGACAGGAAGGAGGCAAGATCGGAAGAGCGGTTTCAG
chr17	76171261	76171300	TK1_11687	+	GTGACCTATGCACCAGACGTATGAAAGACAGAGGGCGCTCAGCCACTTACCAGGTGGGAGATCGGAAGAGCGGTTTCAG
chr17	76171710	76171749	TK1_11688	+	GTGACCTATGCACCAGACGTCACGTTGGAGAAAGAGTGTGAGAGCTTCCACCCAGCACAAAGATCGGAAGAGCGGTTTCAG
chr17	76178774	76178813	TK1_11689	+	GTGACCTATGCACCAGACGTTAAAGCCAGAGCGTGAAGCAGGGCCAGGGAGGCCAGAAGCCAAGATCGGAAGAGCGGTTTCAG
chr17	76181257	76181296	TK1_11690	+	GTGACCTATGCACCAGACGTAGAGAGGGTCAAGTGAAGTCCACGGCGGAGGAGTGGGAGAGATCGGAAGAGCGGTTTCAG
chr17	76182910	76182949	TK1_11691	+	GTGACCTATGCACCAGACGTAGGTGAGGTCAATTTGAGGGCCCGCCTGCGCGGATCCCTGAGATCGGAAGAGCGGTTTCAG
chr17	76183086	76183125	TK1_11692	+	GTGACCTATGCACCAGACGTTGGAAGTTCCACGAACCCGAGTACTCTCCAGGGCCGTCGCCAGATCGGAAGAGCGGTTTCAG
chr12	48238799	48238838	VDR_11693	+	GTGACCTATGCACCAGACGTTGGGATAGAGAAGAAGAGACTCAGCTCAGCTGGGCCAGATCGGAAGAGCGGTTTCAG
chr12	48240245	48240284	VDR_11694	+	GTGACCTATGCACCAGACGTTCAATGGCCAGTACTGCGGGCAGAGCTGAGGAGCCGCCAAGATCGGAAGAGCGGTTTCAG
chr12	48240602	48240641	VDR_11695	+	GTGACCTATGCACCAGACGTTGGGAGGGAAGGAGTCAAGTTACCAGTAAACGCCTTCAAGAGATCGGAAGAGCGGTTTCAG
chr12	48249595	48249634	VDR_11696	+	GTGACCTATGCACCAGACGTTGAGGGAAGAGAAGGAGCTATTTAAGGATACTTGGACCAGAGATCGGAAGAGCGGTTTCAG
chr12	48251043	48251082	VDR_11697	+	GTGACCTATGCACCAGACGTTAAGATGGGTTCTCAGACCCACATTTTGGGGTTGCCTTCTAGATCGGAAGAGCGGTTTCAG
chr12	48251482	48251521	VDR_11698	+	GTGACCTATGCACCAGACGTTGGAAGGGAGCTCAGGAGGGCTGCCAGCAGCTCCACAGGATCGGAAGAGCGGTTTCAG
chr12	48258971	48259010	VDR_11699	+	GTGACCTATGCACCAGACGTAGCACACACTGCCCTGCCCTGACTGAACCTCCGGCTCTAGATCGGAAGAGCGGTTTCAG
chr12	48272907	48272946	VDR_11700	+	GTGACCTATGCACCAGACGTACAGCAAGCAGGCCACGGTCAAGCCAGAGTCAAGTCCAGAGATCGGAAGAGCGGTTTCAG
chr4	89013544	89013583	ABCG2_11701	+	GTGACCTATGCACCAGACGTACAGAAAAAGAATATAAATTCATTCTAGCATCCGTCAAAGATCGGAAGAGCGGTTTCAG
chr4	89015822	89015861	ABCG2_11702	+	GTGACCTATGCACCAGACGTAGTGGGAGCAGGGCAAGGTAACAGTTTTAAATTTCAAGAAGATCGGAAGAGCGGTTTCAG
chr4	89016772	89016811	ABCG2_11703	+	GTGACCTATGCACCAGACGTTCAAATACTAAAAGTCAAGGCTGCTTGGTAAATTTATGCAAGATCGGAAGAGCGGTTTCAG
chr4	89018770	89018809	ABCG2_11704	+	GTGACCTATGCACCAGACGTTAAGAGAAGAGTAGTTAACCCAACTGCCTAGGTCACCGTAAGATCGGAAGAGCGGTTTCAG
chr4	89020611	89020650	ABCG2_11705	+	GTGACCTATGCACCAGACGTTAAATACGTATCATACTCCAAGATTAGTTTAAAGAACCAAGATCGGAAGAGCGGTTTCAG
chr4	89022482	89022521	ABCG2_11706	+	GTGACCTATGCACCAGACGTTAAGGGAAACCAATCACCAGCAGTCAACTCAGCATTCTTAGAGATCGGAAGAGCGGTTTCAG
chr4	89028429	89028468	ABCG2_11707	+	GTGACCTATGCACCAGACGTAGAAAAATGCAAAAAAGGGGAAGAGTTTCAATTAGAGATAGATCGGAAGAGCGGTTTCAG
chr4	89034716	89034755	ABCG2_11708	+	GTGACCTATGCACCAGACGTAGTGATAAAAAAGGAAACACAACAAGATAACAACAATTAGATCGGAAGAGCGGTTTCAG
chr4	89036221	89036260	ABCG2_11709	+	GTGACCTATGCACCAGACGTAGGCAGCTCAAAAACAACAACTTATGATCTTGGAAACAAGATCGGAAGAGCGGTTTCAG
chr4	89039423	89039462	ABCG2_11710	+	GTGACCTATGCACCAGACGTAGGAGACTCAAGTCACTTAAATCTGAAACTTGAAGATCGGAAGAGCGGTTTCAG
chr4	89052376	89052415	ABCG2_11711	+	GTGACCTATGCACCAGACGTATAGCATTATTAATGAGACATAATGATAATGAGTCTTTCTAGATCGGAAGAGCGGTTTCAG
chr4	89053080	89053119	ABCG2_11712	+	GTGACCTATGCACCAGACGTACATATATGTTGTGGGTCTAATAACCTATAAGAGAATAAGATCGGAAGAGCGGTTTCAG
chr4	89053798	89053837	ABCG2_11713	+	GTGACCTATGCACCAGACGTTAAAACAGACTGATTTACTATTCATTTAAGTCAAGTTCAGATCGGAAGAGCGGTTTCAG
chr4	89061158	89061197	ABCG2_11714	+	GTGACCTATGCACCAGACGTTTATCTTCTGACAGCAAAAAGCAATAGTAAGTTGATAAGATCGGAAGAGCGGTTTCAG
chr5	131290075	131290114	ACSL6_11715	+	GTGACCTATGCACCAGACGTTAAGTACGAAAAATCTTAAACAGATAAGAACACAGATTAGATCGGAAGAGCGGTTTCAG
chr5	131295311	131295350	ACSL6_11716	+	GTGACCTATGCACCAGACGTTCCATATGAGAAAAATTAACAAGACAAGAACACATTTCAAAGAGATCGGAAGAGCGGTTTCAG

chr5	131296325	131296364	ACSL6_11717	+	GTGACCTATGCACCAGACGTACCAAAGGAGAACACAGTATGACAAATGCATTTAAAGTAGATCGGAAGAGCGGTTTCAG
chr5	131298382	131298421	ACSL6_11718	+	GTGACCTATGCACCAGACGTGGACAAACAGCTTTATAAGAACATGGCACTCTCAAGCCTGAGATCGGAAGAGCGGTTTCAG
chr5	131302236	131302275	ACSL6_11719	+	GTGACCTATGCACCAGACGTAAAACCATGGCTTCTCTCAGCCACATCATGAGGAATCAGGAGATCGGAAGAGCGGTTTCAG
chr5	131305904	131305943	ACSL6_11720	+	GTGACCTATGCACCAGACGTAAACACAGAAGCCACACTATGGGCACACACCTCCAAGAGCAGATCGGAAGAGCGGTTTCAG
chr5	131307349	131307388	ACSL6_11721	+	GTGACCTATGCACCAGACGTAAAGAAGAGCTGCCAAATTTTGTGATGCTGAGATGGTGTAGATCGGAAGAGCGGTTTCAG
chr5	131308562	131308601	ACSL6_11722	+	GTGACCTATGCACCAGACGTAAAGTTGGAAGCAGCTGTCAGAGCCTGAATGTCTCATTTTCAGATCGGAAGAGCGGTTTCAG
chr5	131309104	131309143	ACSL6_11723	+	GTGACCTATGCACCAGACGTAGGACAGGAAGGGAGGAGTCCCTTAGGGTGGTCACTACTGAGATCGGAAGAGCGGTTTCAG
chr5	131310539	131310578	ACSL6_11724	+	GTGACCTATGCACCAGACGTAAAGAAGGAGCCAGGCAAGGCCCGGTGAGTCAAGTGGGTAGATCGGAAGAGCGGTTTCAG
chr5	131310674	131310713	ACSL6_11725	+	GTGACCTATGCACCAGACGTGGGCATGGGAGACAGAAAGGAAAGAAACACTGACAGGAAAGATCGGAAGAGCGGTTTCAG
chr5	131312425	131312464	ACSL6_11726	+	GTGACCTATGCACCAGACGTAAAGCAAGAAGTCAAATTAGTTGGAAACTCAAGGGCCACTAGATCGGAAGAGCGGTTTCAG
chr5	131321162	131321201	ACSL6_11727	+	GTGACCTATGCACCAGACGTGAGAAGAGGAGTGTGTTAGGGAGACCCAGTGTGGCCAGCCAGATCGGAAGAGCGGTTTCAG
chr5	131323930	131323969	ACSL6_11728	+	GTGACCTATGCACCAGACGTCCATCAAGGAGAGTCAGGCCATGTGGGCCAGGTGATGAGAGATCGGAAGAGCGGTTTCAG
chr5	131324608	131324647	ACSL6_11729	+	GTGACCTATGCACCAGACGTACATGAGGCGGGGGTGGGGAAGAAGGGGAGATTAGAGGGCAGATCGGAAGAGCGGTTTCAG
chr5	131325212	131325251	ACSL6_11730	+	GTGACCTATGCACCAGACGTATGTGGGGAAGTGTGGGAAAACAAGGACTCTTCAACAGGAGATCGGAAGAGCGGTTTCAG
chr5	131325868	131325907	ACSL6_11731	+	GTGACCTATGCACCAGACGTATAAGAAAGCCTTGTGTGTCAGAGAGGGGTGAGAGTGGGTGTAGATCGGAAGAGCGGTTTCAG
chr5	131326671	131326710	ACSL6_11732	+	GTGACCTATGCACCAGACGTAGCACCCGCCAGAGAAAGTTGGCTGAGGCAGGTAGGGGTGCAGATCGGAAGAGCGGTTTCAG
chr5	131329955	131329994	ACSL6_11733	+	GTGACCTATGCACCAGACGTCAAGAGTCAGATAAGGCAAGAGACCTGACGGGCAGGTTAGAGATCGGAAGAGCGGTTTCAG
chr20	43248499	43248538	ADA_11734	+	GTGACCTATGCACCAGACGTGTTTCAGAGAAGCAAAAAGATCAGGCAACTTGTAGTACCCAAGATCGGAAGAGCGGTTTCAG
chr20	43251304	43251343	ADA_11735	+	GTGACCTATGCACCAGACGTAGGTGTGTGGCTGGCAGGGATGGCCCCAGGCCATGCTGATAGATCGGAAGAGCGGTTTCAG
chr20	43251582	43251621	ADA_11736	+	GTGACCTATGCACCAGACGTGCAGAAATAGAGCCAAGTATGGGAGGAGGCAGTGAGGAGGGAGATCGGAAGAGCGGTTTCAG
chr20	43251730	43251769	ADA_11737	+	GTGACCTATGCACCAGACGTGAGAGCCAGGTGATGGGTGCCCTAGCGGGAGGGCCCCGCCAGATCGGAAGAGCGGTTTCAG
chr20	43252981	43253020	ADA_11738	+	GTGACCTATGCACCAGACGTGATGCCACCCAGGCTCTGTACCAGCACCATGGAGAGACAGATCGGAAGAGCGGTTTCAG
chr20	43254336	43254375	ADA_11739	+	GTGACCTATGCACCAGACGTAGAGGAGTAGGGATGGGCCTGAGGCAAAAAGGAGCCATAAGATCGGAAGAGCGGTTTCAG
chr20	43255251	43255290	ADA_11740	+	GTGACCTATGCACCAGACGTAAAGAAAGGGTTGGGAACAACCTTCCCAAGTCCCTTGGGAGATCGGAAGAGCGGTTTCAG
chr20	43257821	43257860	ADA_11741	+	GTGACCTATGCACCAGACGTAAACAGTGAAGTGGTGGACCAACCCGGGCAGGATCCAGGCAAGATCGGAAGAGCGGTTTCAG
chr20	43280259	43280298	ADA_11742	+	GTGACCTATGCACCAGACGTTGCGCCCCGGCGCTGCTCCCTCCGCCGCCGCTCGGTGGGTAGATCGGAAGAGCGGTTTCAG