chr1	11167491	11167530	MTOR_1	-	AGATGTGCCCATCACGTTTTTTCTGAGGCTTTTGTACTTTAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11168187	11168226	MTOR_2	-	CTCTCAAAGTGACTTTGTTAAAATAAGCAATCAGGTCCCAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11169296	11169335	MTOR_3	-	CATGTGTTTACTTAAAAGGGACATAAAATCTGAGCACACTAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11169655	11169694	MTOR_4	-	CCTCTGAGGAACCGCACCAGTGACTAGCTCATTAAGAAAAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11172858	11172897	MTOR_5	-	CCACGGGAGGTCGCAAAGGCTCTCCCCCTTGTGCAGAGTGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11174324	11174363	MTOR_6	-	TCAAGTGCCTGGGAGCTGAGCTCAGTGGCTCACACCTGTAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11174819	11174858	MTOR_7	-	ATCGGGAACGAGCTGCTTCCAAATGGGATCAGGACAGTTAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11175402	11175441	MTOR_8	-	GTTCTAGAACCCCAACCTCATCTTCCCGGGTGATCACTTTAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11177010	11177049	MTOR_9	-	TAATTTGGTTTTTTTAGTCTTCTTTCTCCATTGTAGTTTTAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11181252	11181291	MTOR_10	-	GGGCCCTGCAGACCTGCGCTCTCCTGGAACCCCCACTCGCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11181985	11182024	MTOR_11	-	CGGCCACGAGAGCTAGTGCCCCTTCCGTGGCAGGGAATCTAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11184504	11184543	MTOR_12	-	ACCCTGAAATGGCAACAATTTGAGAAGTCTTCTGGTTTTTAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11186628	11186667	MTOR_13	-	TTGTGCACTTCTGTCACCCACTTCTCCCTCCTACACTGGCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11187016	11187055	MTOR_14	-	CAGGCTCCTGGCAGGGTTAACTGTCATTATAGTCCTTTCTAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11187630	11187669	MTOR_15	-	AAAAACACGAAAGGACATAACCCTGTAGAAATATTCTGCCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11188010	11188049	MTOR_16	-	GCCACTGTGGGGCTTCATAGACCCTGGTCCCTTAGCTGGTAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11188460	11188499	MTOR_17	-	ACTCTGGGCAGTTTCTCATCTAACCACTGGTTTGGTGGTCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11188861	11188900	MTOR_18	-	TTGGTTACAGGTGAAGGTGGCTCCAAGTCTCTCTTCTGTGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11189744	11189783	MTOR_19	-	AGGGAAGGATGCAACTCTGGTAGGCCATGTTAATGGCAAGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11190535	11190574	MTOR_20	-	CTTCTTCCTTATTAACAACCAACCAAGGTGCCAGGCTCTCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11193086	11193125	MTOR_21	-	GCAGGCCACCTGTGAGACCCAGCACCCTGGCTGGCTCGTGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11194357	11194396	MTOR_22	-	CACTGACCTGGGGCAAGTCATATTCCAGCCCTGTCATCCCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11199310	11199349	MTOR_23	-	CAATGCATCCAGAACAGACCACCTTCTCCAGAATGCTCGCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11199539	11199578	MTOR_24	-	ACCACCCACCCACATGGGCAGGTAGGGCCCCATGGTGTCCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11204654	11204693	MTOR_25	-	TAGAAAGCCCCAGTTCACCCACCTACCCCTACCCCTTCCAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11204974	11205013	MTOR_26	-	ACTATTCTGCACATTGTCATTTTTGAGGCTTATTTCCATAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11206682	11206721	MTOR_27	-	ACATGCACCCAGATCTCTCAGTGAGGAAAAGATTGTAGTGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11210132	11210171	MTOR_28	-	CCTCACAGGCACCCTGTGAAGGATGGGGTGAGTGAGGCTAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11217158	11217197	MTOR_29	-	TAGAATGATGGCATGTGTGGCTGCAAGAGACTTCGTCTCTAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11227448	11227487	MTOR_30	-	CATTCTTTTTGGAAAAGCAGGAGGTAGAGACTTGGCTAGGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11259264	11259303	MTOR_31	-	AACCCTTTTTAATTGCTGCCTTCATGCAAAATGACCTCTCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11259547	11259586	MTOR_32	-	TCCCCATTGTCCAGATGGAGGCTGACAGGGAACCAGCTGGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11264567	11264606	MTOR_33	-	TCAGGGCGGGTGGAGAAGATCAGCACATAGAAAACGATATAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11269318	11269357	MTOR_34	-	TGTTTCAGGTGACTGGGAAAGGAGAGCTCTGCTCTTCTCAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11270820	11270859	MTOR_35	-	CTTCTTTTCTGTTCTGAAGTCCCTGTTGTCTTTACTACTTAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11272318	11272357	MTOR_36	-	AGTCTGGACAGACAGGTGCTCTTCTGCCTTATTTGGAAAGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11272802	11272841	MTOR_37	-	CCTCTTTGGGACTAGCAATCTTTAAGCTTTAATGTTTTGTAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11273405	11273444	MTOR_38	-	TACGTCATCCTCCAGAGAGATTTTCTGATTTCCTCTGAGTAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11276154	11276193	MTOR_39	-	GTTAATGCTTTGGCCTCTTCCATGTTTGGGTCAAGGAAGGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11288674	11288713	MTOR_40	-	CAAACCCCAATCCTTCTCTTTCTCCTCTGCACCACACATGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11290931	11290970	MTOR_41	-	GGTAGCCATGAAAGACTTGCCAAGTTCTCACTCACAGAGCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11291306	11291345	MTOR_42	-	TGGCAAACTTGGTCTTTAAAGACTTTGCTGGGACGATGGCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11292442	11292481	MTOR_43	-	CTGCTTCCTGATTGAGCAAGACAGACCCCATGAGTCCAGGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11293404	11293443	MTOR_44	-	AGCTACTTTTTCCATAGCGGAGATAGGGTGGAAAAGAAACAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11294149	11294188	MTOR_45	-	CCGAGAGGCTGGTGCTTTCTCTGTGCGTTGTCATCAGCTCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11297849	11297888	MTOR_46	-	TGATGGCCAGACCCACAGGCAGGGAAGACAGGACTCTCGCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11298408	11298447	MTOR_47	-	CCAGACAGAAGGAATCTAGGGGAGTTAAGGAGCTTAGGACAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11300309	11300348	MTOR_48	-	ACAACGGCTCTTGCCAAGATAGTGAGAGATGCTGGAAACTAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11301559	11301598	MTOR_49	-	GAAACCTGAGCTTGCCCTGTATCAGCGTGAGGCTTGGCCCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11303120	11303159	MTOR_50	-	CTGTTATGATTTCACCTTCCACTCCATTTGGTTGGAGAGGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11307631	11307670	MTOR_51	-	CCATGGAAGACATCATTACCCATCTCAGGGTAAACAGGGAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11307825	11307864	MTOR_52	-	AGAGGCCCTTTCCCTCTTTTCCTAAGCTCCACACCTCACTAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11313845	11313884	MTOR_53	-	ACGGCAGAGGGGAGTCCAGGCTCCCCGTGTACCATTCTGTAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11315998	11316037	MTOR_54	-	GGCTCCATTCCCACCACTAGCAAAGCACATCTGCGTAGAGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11316939	11316978	MTOR_55	-	ACAGGGAGGAGCACAGCCAGGCTTGGGGAACGATGGTGTCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11318491	11318530	MTOR_56	-	AGTCTCTGGTCACAAAAACAACACACTCACCTTTGTGCCCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11319254	11319293	MTOR_57	-	GATCTGGGGCCAGTCATTGTGGGATGTGTGGGCTAAATGTAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr3	30648325	30648364	TGFBR2_58	-	GCTGCTCGTCATAGACCGAGCCCCCAGCGCAGCGGACGGCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG

chr3	30664640	30664679	TGFBR2_59	-	GGATAATTATATCCATCTCAGAGAGCTGTTTTTAAAATTAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr3	30686188	30686227	TGFBR2_60	-	AGAAAGATATATTAAATGATTATCCAACTGCCAGGCAGCCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr3	30691711	30691750	TGFBR2_61	-	GAGATTCATTGGAAGCGAGGGGAGAGGGAGAGAGAGAAAGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr3	30713079	30713118	TGFBR2_62	-	AACAAAACAAGGAGAGAAGGAGTTGGATGTGGTAGGTAAGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr3	30715546	30715585	TGFBR2_63	-	AACAGACAGTGAGGCCCATCATTTAATTCCAGCTGCCTTTAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr3	30729825	30729864	TGFBR2_64	-	AGCCAGCAAACACAGGGTCACTGAGAATGGCATGTGCAGCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr3	30732861	30732900	TGFBR2_65	-	AAAGAGATCCAAAGGGCACCATGAGTTGGTGGGCTCCGCGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr5	112090537	112090576	APC_66	-	CCTTGGACCTATAAGGTTAAAAAGGATTTTGAAATTCACTAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr5	112101972	112102011	APC_67	-	GAACACAATATATTAACATGAAATTCTAAATAACTTCAAGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr5	112102835	112102874	APC_68	-	TAGAAACAAGTTTTTATACAACAATTGCTTTAAGCAGTCTAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr5	112111275	112111314	APC_69	-	TTTTTTAAAAAAAGGTACGTTTAAACAATGCTAATAAAGAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr5	112116436	112116475	APC_70	-	AAATAATAAAAAAGTATCAATATCTTGTATTTACGTTAATAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr5	112128092	112128131	APC_71	-	ACAAGAAACCTAATTAGTTATGTTTTTATTAATAATATTAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr5	112136925	112136964	APC_72	-	GGAGTTAACATCAGTACATGCAAAAATGGTGTAGGCTTTCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr5	112151141	112151180	APC_73	-	AGCACATTATAGATGGTATAATTTAGACTATAGGTAAATAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr5	112154612	112154651	APC_74	-	AATGAGTTTAGAAACAAAATTACGACTTTAATATCCAAAAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr5	112157542	112157581	APC_75	-	AAATCAACATAAACCATAATGCTTTGTTATTTGAAGAGCAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr5	112162754	112162793	APC_76	-	AAGGGCAAGAGGAAAAAGACAATCATCTAAAATAAAACAAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr5	112163575	112163614	APC_77	-	AATACAGAATAGAGGATCATTAAAAAGACAACTTGAAGCCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr5	112164502	112164541	APC_78	-	ATCAATTTTAGATTAATTTATACATAAAATCATACTAGTTAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr5	112170597	112170636	APC_79	-	ACAGAATATGGGTCATCTAATTAGAGTTGGAATTTGTCTCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr5	112173199	112173238	APC_80	-	ATCAAGAGATCACAAAATTAAGGTCACAATGTGTATGCAGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr7	55086920	55086959	EGFR_81	-	CGAAGAGCTCGCTCCGGCTCTCCCGATCAATACTGGACGGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr7	55209928	55209967	EGFR_82	-	AAGACAGATATCACATGAAATACTGAGAAATGCAGAAAAAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr7	55210947	55210986	EGFR_83	-	AAAACATAAATGCGTGATTTCTCTTTTGAGGAACTCAAGAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr7	55214248	55214287	EGFR_84	-	ATGGAACTGCGGTGAGCACTCTTTCCAGCTCCTTTAAATTAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr7	55218936	55218975	EGFR_85	-	AAAGTAATAGATGCATATCTCAGTGAAATGATGAGAAACTAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr7	55220188	55220227	EGFR_86	-	GCAAAGGTTCCCTGTGAGCTGAAGAGTGAGGGTAGGATCAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr7	55221653	55221692	EGFR_87	-	GAGAGGACACGCTGGGCAAGTGAGGTAAGTACACTCAGCGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr7	55223472	55223511	EGFR_88	-	GAGCATGAAAGGAAGGTGATGACGGTGGCACCAGGTGCTCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr7	55224175	55224214	EGFR_89	-	AAGAGAGACGTGTATTCCGTTCACATTTGTTGGATTAAGAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr7	55224401	55224440	EGFR_90	-	CAACAGGGTGATTATTGATCACCAATCTCTACCAGTTAAAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr7	55224401	55224440	EGFR_91	-	CAACAGGGTGATTATTGATCACCAATCTCTACCAGTTAAAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr7	55225305	55225344	EGFR_92	-	GATGAAAGACTTCAGACACACACCACGTAGGAGTTTCTTTAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr7	55227781	55227820	EGFR_93	-	GAGAAGAAAAATCATGTGGTGAAAAATTATAAAAACAATGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr7	55229141	55229180	EGFR_94	-	AGAGTGGGTCACAGCAGTCAGTGACAGAGCAGGGACCCGAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr7	55231375	55231414	EGFR_95	-	GAAGAGGAAACCCGTCAGCCCACCCCTGAGACATTATTGCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr7	55232922	55232961	EGFR_96	-	GTGGAGAAAAATGTTCATGCATGTCTCTTTCTTTTCTCTTAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr7	55236165	55236204	EGFR_97	-	ATAGAAAGACATTAGAAAAATGACCACTAACATTTTTAATAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr7	55237949	55237988	EGFR_98	-	ATGGACAAGTACATTTCAATATGTGAGAGGCCTGGGGAGCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr7	55238817	55238856	EGFR_99	-	TGAAAGAGAAATATACATTTTTCTCATTCTACTTCTTTGGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr7	55240625	55240664	EGFR_100	-	GTGGAGGAACAAGGAAGGGTGAGGTTGCTGACAGATTCCAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr7	55241563	55241602	EGFR_101	-	CAAGAACACAGAGACAAGGGTCACCTCAGCCCTCACCATGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr7	55242364	55242403	EGFR_102	-	GAGAGAAGGAAGACGTTAACTGGCAATTGTGAGATGGTGCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr7	55248935	55248974	EGFR_103	-	GGAGAGGCACGTCAGTGTGGCTTCGCATGGTGGCCAGAAGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr7	55259361	55259400	EGFR_104	-	GAAGACCCTGCTGTGAGGGACAGATCATCATGGGAAGAAGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr7	55260408	55260447	EGFR_105	-	TGAGAGATGAGGCAGTGAGACAACTATTAGTTTCCCTCTGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr7	55266359	55266398	EGFR_106	-	GAAGCAAGAAAAGAAGGCAGTGGGATCATGAATGAACAATAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr7	55267958	55267997	EGFR_107	-	AATGAGAAAAAACAGTGCAATTAGAACACTGGAAGAAATGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr7	55268830	55268869	EGFR_108	-	GATTTTGAGGCTATTAGAATGGCCCGTAGAGATGCTATTCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr7	55269377	55269416	EGFR_109	-	AACAGAGAAGTTGCCCATGGAATGCTTGTACCACATCTCAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr7	55270159	55270198	EGFR_110	-	AAATGAGGGAAGGTTACTCCGGTCAGGGCTGCCCCAACTTAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr7	55272898	55272937	EGFR_111	-	AAAGAAATCAGAGGTGAAGTAATCAGCAAAGCACCATCCCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr12	25362678	25362717	KRAS_112	-	TACTTTTTTCTTAAGGCATACTAGTACAAGTGGTAATTTTAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr12	25368324	25368363	KRAS_113	-	TTAAGTTCAGCACATTAATTTTGGCAGAAAGCAGATGTCTAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr12	25378497	25378536	KRAS_114	-	CTGAAATAAATACAGATCTGTTTTCTGCAAAATCATAACTAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr12	25380117	25380156	KRAS_115	-	ATTGAATATAATAAGCTGACATTAAGGAGTAATTATAGTTAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr12	25398157	25398196	KRAS_116	-	TTTTAATATGCATATTACTGGTGCAGGACCATTCTTTGATAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG

chr14	103852316	103852355	MARK3_117	-	TTTAATTCTGCACAATGCGAGGGTCAAAACAAAACAGCACAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr14	103871362	103871401	MARK3_118	-	GCATACACAAAGATAAGGAAATGAGAGAACACAGAGTACTAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr14	103894673	103894712	MARK3_119	-	TAATAAATATTTATGGATTTTAAGAATTTAGTAATTATGGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr14	103915205	103915244	MARK3_120	-	AAACAAACAAAACACATAATCCCCCCAACACAAGTTATTAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr14	103918204	103918243	MARK3_121	-	GGAGAGGACACGGAAGAAAAAGAGACAAATGTCTGTATGCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr14	103923428	103923467	MARK3_122	-	GAGAAATAAAAGTAAGTAGAAATCCTACTTCTGAGTATTAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr14	103928691	103928730	MARK3_123	-	GAGACGCAGAGTCAGTCATCACTGGTGCAGATTCGTAATTAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr14	103931843	103931882	MARK3_124	-	AACATCAAGACAAAAATGAAATTTAGCCAAAATAGAATTAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr14	103932258	103932297	MARK3_125	-	GTACAGAGGAAAGAAAACGAGTAAGTCAACCTTTAGGTTTAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr14	103932629	103932668	MARK3_126	-	TAAACTGTTCATTAGCAGAGTAAAATGAAATATTCTGATAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr14	103933365	103933404	MARK3_127	-	GGCATAATACAGTTTATGTGTTTTGTTTGGGTAAGAAATCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr14	103934319	103934358	MARK3_128	-	ATGAGAAAAACAGAGCAAACCACAACACGAACCCAAATGGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr14	103941279	103941318	MARK3_129	-	GAGTTCATTTTTTAAATGACTGAATATAGTTTCAAGTTTTAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr14	103946673	103946712	MARK3_130	-	GGGCATTTTTGTCTTAAATTTATTTGGTAAATACAGTACAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr14	103958063	103958102	MARK3_131	-	AGAAAGTAAGAAGCTCTCAGAACATGATATACAAAAATTTAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr14	103964788	103964827	MARK3_132	-	TTAAGTAAAAAAAAAAAAAAATTAACAAAAATAACTCGCAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr14	103966442	103966481	MARK3_133	-	AGAATGTAGAAGCAGAGAGAAGAGGGAAAGAGAAAAGAAAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr14	103969168	103969207	MARK3_134	-	TAGAGGCAGGTTTATTTTTAATCGTACAGGAAAATCAACCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr14	105236627	105236666	AKT1_135	-	GACTGCGCTGGACGATAGCTTGGAGGGATGGAGAGGCGGCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr14	105237031	105237070	AKT1_136	-	ACTGCCTGCCCCCGCCCACTCCCTTTTCTCTCCACACTCAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr14	105238651	105238690	AKT1_137	-	TCCCCGCATATTCACGCGCACGCATGCTCCCCACATATCCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr14	105239164	105239203	AKT1_138	-	CCCATCCCAGCTACAGGCTACACCTCCATCCCCTCATCCCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr14	105239537	105239576	AKT1_139	-	CACCTGCGTGCATACGCGTTGCTGCGTCCCCACGTCCTGAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr14	105239741	105239780	AKT1_140	-	GGGCAGGCAGGGGGGCAGGGCCCTGGGGGCCTGGCGGCACAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr14	105240198	105240237	AKT1_141	-	GGGCTGCGGGGGATGGACTTCGCGGCCTGTGGGCCGCCCAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr14	105241224	105241263	AKT1_142	-	GCCCAGATGGGGCTGAAGGGCTGGGGCCAGGTAGCGACTCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr14	105241362	105241401	AKT1_143	-	GGCGGTGGGGCAGGGTGGAGATGAGGGTGCGGGGTGGCAGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr14	105241938	105241977	AKT1_144	-	TCCCCACTTCTGCCTGTGCCTGGGGCTGCCTTGGACTGTGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr14	105242945	105242984	AKT1_145	-	TGTGGCGGCCAGGCCAGGCACTTGGGCAGCCCCAGCGCTTAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr14	105246374	105246413	AKT1_146	-	CCTTGGCCTCTCGGGATTCAGATTTGGGGGGTTGGCTGGAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr14	105258884	105258923	AKT1_147	-	GCTGCCAGGGCTGGGCCTGGGGAGGGAGAGATGGGGGTAGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr17	7572876	7572915	TP53_148	-	TTCTTGTTCCCCACTGACAGCCTCCCACCCCCATCTCTCCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr17	7573876	7573915	TP53_149	-	TCAGCCCCTTCCTGGCCCTACTCCCCTGCCTTCCTAGGTTAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr17	7576486	7576525	TP53_150	-	TTGTAAGTTGAAAATGGATTTAATACACCTAATCTAAGGAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr17	7576574	7576613	TP53_151	-	AAAATGGTTCTATGACTTTGCCTGATACAGATGCTACTTGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr17	7576802	7576841	TP53_152	-	TTGGGACCTCTTATCAAGTGGAAAGTTTCCAGTCTAACACAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr17	7576968	7577007	TP53_153	-	AGGACAAGAAGCGGTGGAGGAGACCAAGGGTGCAGTTATGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr17	7577448	7577487	TP53_154	-	ACTTGCCACCCTGCACACTGGCCTGCTGTGCCCCAGCCTCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr17	7578126	7578165	TP53_155	-	CAACTGGGGTCTCTGGGAGGAGGGGTTAAGGGTGGTTGTCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr17	7578320	7578359	TP53_156	-	GGGGCTGGAGAGACGACAGGGCTGGTTGCCCAGGGTCCCCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr17	7579261	7579300	TP53_157	-	CTGAGGGGCTGGCTTCCATGAGACTTCAATGCCTGGCCGTAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr17	7579649	7579688	TP53_158	-	GGGTTGGGCTGGGGACCTGGAGGGCTGGGGACCTGGAGGGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr17	7579788	7579827	TP53_159	-	CCATTGGAAGGGCAGGCCCACCACCCCCACCCCAACCCCAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr18	48573366	48573405	SMAD4_160	-	TTTTCCTTTTAAATCAAATATGTCTCCAATTTCTGAAGCAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr18	48575005	48575044	SMAD4_161	-	AAACGACCATTTATTCATGTGTCACATTATGCAAGACACTAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr18	48575614	48575653	SMAD4_162	-	TAAAGGGGAAAACAAATGAAACATTAATCATTACAATGAAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr18	48581100	48581139	SMAD4_163	-	AATTAAACATATTTTAAATTTTTATAAGCTTCTATTCCCAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr18	48584444	48584483	SMAD4_164	-	AAGAAGACATTAACATGGTACATTCATAGATGTCATCTTAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr18	48584659	48584698	SMAD4_165	-	AGGCCCACATGGGTTAATTTGCTTTTATAAAGGCTGCCTAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr18	48586185	48586224	SMAD4_166	-	GACAACAAAAATTCCATTTTTATTTACTAAAAGTTGTCTAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr18	48591742	48591781	SMAD4_167	-	TAAATGGGAAAGAACATCCTCCCATGAGAAAGATATAAGGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr18	48593338	48593377	SMAD4_168	-	AAAAAGAAATTACATTTTATCTTGATAAGTATTTTAAATTAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr18	48602957	48602996	SMAD4_169	-	AAAACATTTCATACTATGAGTTCATAAAGAAAAATTCCATAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr18	48604575	48604614	SMAD4_170	-	AGATTTGGAAGACATCAGAGGGACAGGGTGATCTCTTCCCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr19	40739728	40739767	AKT2_171	-	CACGCAGAGGACGCACGCTCGCTGCCATCACCGCTGGGTGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr19	40740901	40740940	AKT2_172	-	GGGGCCCCCGCGCTGGTGTGCCTGCCCCAGGGGTGGAGGGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr19	40741119	40741158	AKT2_173	-	CTGCTTGCCCCAGCAGGACCCTCAGGGACCTGGCCCACTCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr19	40741746	40741785	AKT2_174	-	GCGTCGGCCCCACCCAGCCCAGCGCCAGCTGCTGCCACTGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG

chr19	40742113	40742152	AKT2_175	-	TTGGTGGGGGTAGGAACGTGTGAGGCCAAGGGTAGGGGGAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr19	40743825	40743864	AKT2_176	-	GGGTGTGCGCCAGGCTGACCTGTGGCATGCACACCACATGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr19	40744761	40744800	AKT2_177	-	GCTGCCTTGACTTTGCCCTCTGGGGCCTCCTTCTTTAGGGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr19	40745901	40745940	AKT2_178	-	CTCCCCTTCCCAGACAGTGTGAGGCCAGCCTTTGGACAGAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr19	40747794	40747833	AKT2_179	-	CGGGAATTGCGCTCGCGAGCCTCTGTGGGGGCTGCGGTCTAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr19	40748390	40748429	AKT2_180	-	GGAGCAGGGGTGGGGCTGCCAGCCTGCGGTGCCCCCACCCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr19	40761014	40761053	AKT2_181	-	GCCTCTGTGTGGCTGCCCTTGAGAGGGAGCAAGCCTGGTGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr19	40762782	40762821	AKT2_182	-	GGATGAGTGGGTCAGTGTTCTGGTGCTCACAGGATGGCTGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr19	40771078	40771117	AKT2_183	-	GCTTTTGCCCGCCAGATTCTTTCTCCCACGCTGGCTCCTCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11167567	11167606	MTOR_184	+	AGAAAGAAAAGGAATATTTTAATAATTTGAGCTTCTTCAAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11168353	11168392	MTOR_185	+	AGGAACAAAAACATTTCACTCTCTTCCTGGCAATCGATGCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11169437	11169476	MTOR_186	+	CAAAAGTAGAAATAACTGTAAGAATGGGAGCAATACAACAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11169796	11169835	MTOR_187	+	AGAAATCAATTAACAGAAAATTCAAACACCAAAAAGCCACAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11172984	11173023	MTOR_188	+	AAATAAAGAGTATTGAAACATGCTTCAAATTTTGACTTGAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11174520	11174559	MTOR_189	+	GACAGAGCCACTCACCACAGGAGTTACTAACTCTCCACCCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11174954	11174993	MTOR_190	+	ATAAATGGGAAAAGCCAAATCAATGTTTATTTTCTTTACCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11175535	11175574	MTOR_191	+	CAGAAGACAGATCAGGGAGGGATCAACAGAGATAACGGATAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11177153	11177192	MTOR_192	+	GGAGTGCATGTGAACTACGGTTCTGGAAACTTTAATTTCAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11181435	11181474	MTOR_193	+	ACACAACTGTTCAGTAAGAGAGCAGCCTAAGACATGTAGTAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11182193	11182232	MTOR_194	+	CAGAAAAGCAGGGTTAGTGTACCGTAAAGAGAGTATACCCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11184700	11184739	MTOR_195	+	CAGTGGGAGCGGTGAGTGTACATCAGAGGTCCTCAGCTCTAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11186863	11186902	MTOR_196	+	TTACCAAAGGATTTAGTGTTCTGCCTCCAGGGAAGAATTTAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11187211	11187250	MTOR_197	+	AAGCAGGCACGTTTTCAAGTTATCAAAGTCTCAACCAACCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11187873	11187912	MTOR_198	+	GAGAAGAAGGAGAGAAGCATCAAGAATCAGCTAACCTCAGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11188193	11188232	MTOR_199	+	AACAGAAGAAACATCTATAAAGGAAATGTGGGTTGGGGAAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11188619	11188658	MTOR_200	+	AAAAGACACAGTATGTAGCATATGAGACTTGAAACAACTAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11189018	11189057	MTOR_201	+	AATGAGAAAGTCACAGAAAATTTAGTTTCCCAGTTTTTGCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11189905	11189944	MTOR_202	+	ACACACGTGTTAGCGACACTCTTGCCTCTGCTTTCTCATCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11190844	11190883	MTOR_203	+	AGAAAGGCAAGGACAGACACTGGAGCTGTGACCAACAGCAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11193264	11193303	MTOR_204	+	AGAAACAAGCCCCCATGACATTCCCTCCTCAAAACAGCCCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11194533	11194572	MTOR_205	+	ACAAAGGCACAGAGAGCCACTTGGCTTGTGGCCCAGCTTCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11199502	11199541	MTOR_206	+	AGAGAAACTGGGTTATAGACAGAACTGGACAGCCCAGGGAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11199725	11199764	MTOR_207	+	CAGAAGTGAAGATTAGATATGTCTTCTGATACATTGTTTTAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11204822	11204861	MTOR_208	+	CAAATCGCATTCCAAACTAATTACTGCACGAACAATCCAAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11205112	11205151	MTOR_209	+	AACAACCCTTGGGACTGAGCTCTGGACTTGGGAGCTTAGGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11206858	11206897	MTOR_210	+	ACACATAGACAGAAAGCATCAAGGGGGTTGGCTGGTTGGGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11210293	11210332	MTOR_211	+	TGAATTATATAGTCAGATTAATCCAAATCTCCTTAAACTAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11217358	11217397	MTOR_212	+	GGAAAGAAAGACTGCTGTGAGGTACACAGAAGAAGGGATCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11227584	11227623	MTOR_213	+	AAAGGGAAAAGGTAGTTACACTCAACAGGTCTGAGGGTAGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11259470	11259509	MTOR_214	+	GCAAAACCTCACAGCACAGGAAAATGGCAGATGGGGCACAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11259770	11259809	MTOR_215	+	AGAAGGTGGAAAATGGAGAGACCTCCCGTGCCTCTGCCTGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11264770	11264809	MTOR_216	+	ACAGGTGACAATGGAAAACAATCAGTTTCAAGGGCCAATTAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11269525	11269564	MTOR_217	+	AGATTTATAGGAAACACCTATAACTCTACTAGATGCTTCTAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11270973	11271012	MTOR_218	+	AGGGGGAAGAGATGAGAAACTATCATTTTGGAGAGTGGAGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11272541	11272580	MTOR_219	+	CACTAACATACAGTAACTGCTAACATACAATCTCCAAGGAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11272975	11273014	MTOR_220	+	GAGCAAAAGCATGGTGATGAATAGTCAGGTCCCAAGTATCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11273633	11273672	MTOR_221	+	AGAAAAGTCAGAGGAGCTGAGTCAGGTCCCTTTCTGATGAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11276301	11276340	MTOR_222	+	CAAGAGGTCAACCAGCTGGTATCATGAAGGACATTGAACCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11288985	11289024	MTOR_223	+	ACAACAGAGAGTGTTAGAGCTACACATGGCATGACGTGACAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11291121	11291160	MTOR_224	+	AAGGGGAGGGAAAAAAGAAAACATTCATCACAACATGATTAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11291501	11291540	MTOR_225	+	ACAAGAACACGATTCAATGAGCCAGTACGAGAGAAAAGAAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11292595	11292634	MTOR_226	+	AAAAAGAGGGTGGCAGAAAGGGTTAGAAATTCTGGCATTAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11293554	11293593	MTOR_227	+	AAGTTATGAGAAAATGAATGCAGATTAGACTCTACTAGAAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11294332	11294371	MTOR_228	+	GAAAGGCTCATATGTTCTCTATGGCAGAAGACATTCTAGAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11298115	11298154	MTOR_229	+	AATGGAGCCTTTGAACATTTCCTCATGATCCCATCACTCCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11298684	11298723	MTOR_230	+	AGGCAGAGAGAAAACAGAATAAACACTGCTGCTGTAGACAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11300614	11300653	MTOR_231	+	GGAAACAAGTCACATAAGGGCTGGGCACATGACACTCAGTAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11301748	11301787	MTOR_232	+	ATGGAGAGTGGCTAGTTGAGACATAATGACATTCTTTAATAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG

chr1	11303367	11303406	MTOR_233	+	AAAAGACAAAGTAGATAGCTCCAGGTCAGGGTTAGGGTCTAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11307800	11307839	MTOR_234	+	AAGGATAAAGGGTTGGCAGGGGAAAAGTGAGGTGTGGAGCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11308161	11308200	MTOR_235	+	GAGGAGGAAAAAAATCATCTTTACTTATGACTGGCATTCAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11314040	11314079	MTOR_236	+	AGACAGGGTGCCTTCATTAGAGACAGAGTACAAACCCAGAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11316259	11316298	MTOR_237	+	AAGCAAACCGAGAACTCTCATTGGTACCAGAGTTTTGTTCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11317232	11317271	MTOR_238	+	GAGGAAGGCAAAAGGTGATGATGGGGCGTATGCTGGCCAGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11318660	11318699	MTOR_239	+	AGATATAATCAGAACAATTTCTAATAATTCTCTAACTGTGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr1	11319476	11319515	MTOR_240	+	GGTTCTTTAGAGAGAAGTTTCCTTTAATATTCTGGATAAGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr3	30648479	30648518	TGFBR2_241	+	CCCAGCCCGGGCTCGGCGGGGCGCCGGGGGTCTTCCTGGGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr3	30664775	30664814	TGFBR2_242	+	ATTAATTAATCTTTTCATCATTTTTCTATTTTTAGTCATGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr3	30686417	30686456	TGFBR2_243	+	CTTTTAAGAAGTTATTCTTTCTTTTCCCCTTTTTACATAAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr3	30691962	30692001	TGFBR2_244	+	TTCTCTTAAGGGTGTGGGACCTGAGATCTGTGCCAATTTTAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr3	30713939	30713978	TGFBR2_245	+	GCTAGTGCTAGATCCCCTTTACCTTGAGCCTGGCCTCACCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr3	30715748	30715787	TGFBR2_246	+	ACCAGCATCATTGTGTAGTGGTAAACTTGTCTTCAAAATAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr3	30730013	30730052	TGFBR2_247	+	AGTGTTTACAAAGGTCAGTAAGATTCAACCAAGTTGCCTCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr3	30733101	30733140	TGFBR2_248	+	GCAGGCTGGGCCATGTCCAAAGAGGCTGCCCCTCTCACCAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr5	112090732	112090771	APC_249	+	TGTGACTTTTAATTGTAGTTTATCCATTTTTATTCAGTATAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr5	112102117	112102156	APC_250	+	AAAAGGTGTTTTAAAATAATTTTTTAAGCTCAAATTGTCAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr5	112103097	112103136	APC_251	+	TTCATATAGTAAACATTGCCTTGTGTACTCCAGTTTATTGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr5	112111444	112111483	APC_252	+	TGGCAGTACAACTTATTTGAAACTTTAATAACTTGATATTAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr5	112116610	112116649	APC_253	+	TGTTTCTAAGTGATAAAACAGCGAAGAGCTATTAGGAATAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr5	112128236	112128275	APC_254	+	TGCCTTTCTTGTTTGTGGGTATAAAAATAGGTAGTTATTCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr5	112137090	112137129	APC_255	+	TATTTTATCATATTTTTTAAAATTATTTAAATATCAGAAAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr5	112151300	112151339	APC_256	+	ATTACAAACCCTGGTCACTAATGCCATGACTACTTTGCTAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr5	112155051	112155090	APC_257	+	TATAGTGTACATCGTAGTGCATGTTTCAAAGCAAATGTGAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr5	112157698	112157737	APC_258	+	AATGTTTTTTAATGACATAGACAATTACTGGTGGATTTTTAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr5	112162954	112162993	APC_259	+	ATAACATGTATTTCTTAAGATAGCTCAGGTATGAGTTAATAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr5	112163713	112163752	APC_260	+	GAATTTCACCTGTTTTTCTTTTTTCTCTTTTTCTTTGAGGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr5	112164679	112164718	APC_261	+	AAACATTTAGTACTATAATATGAATTTCATGTTTGGCTTTAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr5	112170872	112170911	APC_262	+	AGTTTTATATTACTTTTAAAGTACAGAATTCATACTCTCAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr5	112179833	112179872	APC_263	+	GAATGAAACTAAGAAAATTCTATGTTAATTACAACTGCTAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr7	55087068	55087107	EGFR_264	+	GTCTCGCCGGCTCCCGCGCCGCCCCCGGATCGCGCCCCGGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr7	55210140	55210179	EGFR_265	+	TTGATTTTCCTACACAAATAAAATTGGAGAAAATCTAAGTAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr7	55211191	55211230	EGFR_266	+	GGGATGCCAAGGCTGGGGGTTCATAAATGCAGACAGCAGTAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr7	55214443	55214482	EGFR_267	+	CATACACACTATCTCTGCCTCCAGCTCCTATGGGGGACAGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr7	55219065	55219104	EGFR_268	+	GAACAGCCTCAGACCCATGTGTGACCGCCCCTCTCTTCCTAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr7	55220367	55220406	EGFR_269	+	CCTCCAGCAGCCTCCCTGGAGCAGGCTGGGGCTGCACCCGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr7	55221855	55221894	EGFR_270	+	CTCTGTGGGCCCTCTAACTGGTCAGGCATCCTTGTCCCGCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr7	55223649	55223688	EGFR_271	+	CGCCGGTGTGCGGACGAGGCTTGTTCTCGGCTGCTGAGGCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr7	55224362	55224401	EGFR_272	+	GGTTCAGTTGCTTGTATAAAGAAAAACAAAATCTGCCTTTAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr7	55224535	55224574	EGFR_273	+	AATTATCACATGAATATAAATGGGAAATCAGTGTTTTAGAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr7	55224546	55224585	EGFR_274	+	GAATATAAATGGGAAATCAGTGTTTTAGAGAGAGAACTTTAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr7	55225456	55225495	EGFR_275	+	CACAGCCAAAGCCTGGTAGATTACATTTGCCTTTTTAGTTAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr7	55228041	55228080	EGFR_276	+	GCTTTCTGTTTAGTTTATGGAGTTGGTTCTAATGGGTCCTAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr7	55229334	55229373	EGFR_277	+	ATTTCTTTAATCCCCTTGCGTTGATCAAAAATAAGGCTCCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr7	55231526	55231565	EGFR_278	+	CTTGCTGCTATCCACGTCCATTTCATGGGAAGGGCCTTCAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr7	55233140	55233179	EGFR_279	+	AGTGAAGGAGAACAGAACATTTCCTCTCTTGCAAATTCAGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr7	55236232	55236271	EGFR_280	+	CTGTCTGACTTTAGTCTCCCACTAAAACTGCATTTCCTTTAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr7	55238247	55238286	EGFR_281	+	TTCACGTGTCTGTTCCCCCCGCTTTTCCTTTCTGCCACCCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr7	55238916	55238955	EGFR_282	+	ACAGCTCTGTGTCACATGGACCTCGTCAAGAATGACCACAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr7	55240827	55240866	EGFR_283	+	GTCCTGGGTGGGCTCAGGAGCCCTCGCACCCCGACAGGAAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr7	55241746	55241785	EGFR_284	+	TGGCACAGGCCTCTGGGCTGGGCCGCAGGGCCTCTCATGGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr7	55242523	55242562	EGFR_285	+	GCTTTGCTGTGTGGGGGTCCATGGCTCTGAACCTCAGGCCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr7	55249181	55249220	EGFR_286	+	AAGGGAGATACGGGGAGGGGAGATAAGGAGCCAGGATCCTAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr7	55259577	55259616	EGFR_287	+	GGCTTTAGGTCAGCCAGCATTTTCCTGACACCAGGGACCAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr7	55260544	55260583	EGFR_288	+	ATCCTGATGCTAATGAGTTTGTACTGAGGCCAAGCTGGCTAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr7	55266566	55266605	EGFR_289	+	GGTGGGTCTGTCCACACTGCCTAGCTGAGCCTTGGTGGCTAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr7	55268116	55268155	EGFR_290	+	CAGTCTGTGCTTCCATTGGGAAGAGTCCCTCTAATGAGCAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG

chr7	55269058	55269097	EGFR_291	+	TCTGTCTCTCTCTCTCTCTCAAGCTGTGTCTACTCATTTGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr7	55269485	55269524	EGFR_292	+	ACACCTTATAAGCCAGAATTTACAGCTCTCCACTATGGCTAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr7	55270328	55270367	EGFR_293	+	TGTCTGGAAACAGTCCTGCTCCTCAACCTCCTCGACCCACAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr7	55273320	55273359	EGFR_294	+	TAGTATGAGCCCTAAAAATCCAGACTCTTTCGATACCCAGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr12	25362855	25362894	KRAS_295	+	TAAAAAGTATTAAAATGTGAATATATACGATGGCTTCATGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr12	25368504	25368543	KRAS_296	+	AAACACAACTTCTTTAAAGTCTGTTGCATTGGTAAGAGTAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr12	25378717	25378756	KRAS_297	+	AAAAAAAGTTATAGCACAGTCATTAGTAACACAAATATCTAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr12	25380356	25380395	KRAS_298	+	AGAAACACAGTCTGGATTATTACAGTGCACCTTTTACTTCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr12	25398328	25398367	KRAS_299	+	CCTTATAATAAAAATAATGAAAATGTGACTATATTAGAACAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr14	103852427	103852466	MARK3_300	+	TGGGCGTTGTAGTTGGCGGACCTTCGGGGTGGCATTCGTGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr14	103871614	103871653	MARK3_301	+	GTTATGCTTATTTCTGTTATGACAGTTGCTCTGTTTATTTAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr14	103894787	103894826	MARK3_302	+	TTCAATGTCTAGTACTTTTTAAAAAATTATCGGTGCTAATAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr14	103915314	103915353	MARK3_303	+	CTTTTTTAAATATTTTGGGGTCTAAATACGTACTTGAAATAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr14	103918330	103918369	MARK3_304	+	TTTTATATATATTGGGTTTTTTTTCTTTCTCCCTTTTAAAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr14	103923559	103923598	MARK3_305	+	ATGTGTCTTTACTATGTCAATTTGATAATTTATCTCACTTAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr14	103928808	103928847	MARK3_306	+	GTGCCTCACTCAGTGTATGCTCTGTCTGTTTGTGTGCAGTAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr14	103932140	103932179	MARK3_307	+	CTGCACCCATGTACTTCACTAAACTAAAAGAAGTTTCCTAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr14	103932438	103932477	MARK3_308	+	AGGTGGAAACAAGCAGTAACTTTGGAGAGTCTTTAGAGTGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr14	103932789	103932828	MARK3_309	+	CATGCCTGCATGTTCATGTGTTTTTGTCTAAGTAACATATAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr14	103933538	103933577	MARK3_310	+	TCAGAAAGAGCTGAAATACCCTGTATGTAATTATTAGTTTAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr14	103934533	103934572	MARK3_311	+	GAGTATCCCAGTGCCTTCTCTTAGAGTCCAGGCAAGAGGTAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr14	103941557	103941596	MARK3_312	+	TTGAACTATAGAGTGGTCTTAGGGTGGTAGGGTTGGAACCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr14	103946837	103946876	MARK3_313	+	CTACCTGTTTGTAAGAAAAGTTGTTTTTCCCAAGAGAAATAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr14	103958381	103958420	MARK3_314	+	GGTGCTGGTTGTTTTGGAGTGAACACATAGAGCAAAAGGAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr14	103964875	103964914	MARK3_315	+	TATATACACATTTATTTTTCAATCCTCACTCCCAAATGGCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr14	103966547	103966586	MARK3_316	+	TGATTTTTACTTAAAATTTTTTTCAGGTGTTTACTTCATTAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr14	103969574	103969613	MARK3_317	+	ATGATGTAAATTAAGTAGCAATTAAAGTGTTTTCCTGAACAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr14	105236767	105236806	AKT1_318	+	AGACAGCTCAGACCCCGGTGCCCCACCTCCCTGCCACCTCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr14	105237194	105237233	AKT1_319	+	GGGCAGACGGGACAGTCATGAGCTTCGCTCCCCACTCCCAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr14	105238799	105238838	AKT1_320	+	GAAACAAGGCCACAGTGTCGGTACCGCCACCTGCCCAGGCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr14	105239439	105239478	AKT1_321	+	GGCAGATGGGCAGGACTCGGCATCAAGGGGTGTCCGGGACAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr14	105239726	105239765	AKT1_322	+	GGTGGCCTCAGGTCAGTGCCGCCAGGCCCCCAGGGCCCTGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr14	105239927	105239966	AKT1_323	+	CGCAACCTGAGGCACAGCCGTGGCTCGGGCCTCTGCCCCCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr14	105240327	105240366	AKT1_324	+	GGGGAGCTGGAACTGCGGCCCCACAGGCAGGACGGCAGCCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr14	105241350	105241389	AKT1_325	+	GGGCTGGGTGAGCTGCCACCCCGCACCCTCATCTCCACCCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr14	105241554	105241593	AKT1_326	+	GCACCAGGGTCAGCAAGCGGCGCTGCCAACAGTGCCCAGCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr14	105242146	105242185	AKT1_327	+	TCAGGTGAGGCTGCAGGCCTGTACCAGATCAGGAGCTCCAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr14	105243117	105243156	AKT1_328	+	GCAGAGCCTCTGTCTGCGTGCATCCCCCTGCCCCTCCCAGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr14	105246563	105246602	AKT1_329	+	GCGGGTGGTGAGAGCCACGCACACTCTACCCGTCAGACCCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr14	105258990	105259029	AKT1_330	+	GCTCCCGCGACGCTCACGCGCTCCTCTCAGGCTGGCGCTCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr17	7573018	7573057	TP53_331	+	CAGAAGCAGGGAGGAGAGATGACATCACATGAGTGAGAGGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr17	7574043	7574082	TP53_332	+	AGAGGAGGGGGAGAAGTAAGTATATACACAGTACCTGAGTAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr17	7576594	7576633	TP53_333	+	CAAAGTCATAGAACCATTTTCATGCTCTCTTTAACAATTTAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr17	7576667	7576706	TP53_334	+	TATATTATGGTATAAGTTGGTGTTCTGAAGTTAGTTAGCTAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr17	7576936	7576975	TP53_335	+	GGCAAGGAAAGGTGATAAAAGTGAATCTGAGGCATAACTGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr17	7577165	7577204	TP53_336	+	TAGGAAAAGAGAAGCAAGAGGCAGTAAGGAAATCAGGTCCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr17	7577618	7577657	TP53_337	+	ACACAGGCCCAAGATGAGGCCAGTGCGCCTTGGGGAGACCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr17	7578299	7578338	TP53_338	+	TCAGTGAGGAATCAGAGGCCTGGGGACCCTGGGCAACCAGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr17	7578564	7578603	TP53_339	+	AGGAAGGAGACAGAGTTGAAAGTCAGGGCACAAGTGAACAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr17	7579600	7579639	TP53_340	+	GTGAAAAGAGCAGTCAGAGGACCAGGTCCTCAGCCCCCCAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr17	7579731	7579770	TP53_341	+	AGAGCAGAAAGTCAGTCCCATGGAATTTTCGCTTCCCACAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr17	7579922	7579961	TP53_342	+	CGGAAGGCAGTCTGGCTGCTGCAAGAGGAAAAGTGGGGATAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr18	48573675	48573714	SMAD4_343	+	TAAGAGTTTTTCTATACCCTCTATGGTGGCAGATTTAAAAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr18	48575240	48575279	SMAD4_344	+	TTTGCTTTCATCCTAAGAAACATAAAGGGAAAAGGATCTCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr18	48575704	48575743	SMAD4_345	+	TGTTTCTTACTACTTTCTCTTTGTTTTGTCCTATCCTCTCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr18	48581373	48581412	SMAD4_346	+	GAATCAGATGTAGTCAGCAAGTTGAGTTTTCCTAATCATTAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr18	48584624	48584663	SMAD4_347	+	ACTTTAAAAAATCTTTTAAATAGTTGAGAAAAAAGTAGGCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr18	48584836	48584875	SMAD4_348	+	GTTTTTGTTGTAAGGGCTATTTTTTTTTTTTTTTTGGTAGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG

chr18	48586296	48586335	SMAD4_349	+	TTCAAAATTGATTTCCTGTATTTAGATTGATTTAGTGGTGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr18	48591986	48592025	SMAD4_350	+	TATAGTCAGATAGTTACTTTAAAAAATTGAGCATAGTACAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr18	48593567	48593606	SMAD4_351	+	ATTTTATTTGAATATTTTAGACTTAAAGCTCTATTTGTTGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr18	48603156	48603195	SMAD4_352	+	TTTTCATTCTTTTTTAAAGGTATAATAGTTGATATTTTTAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr18	48604847	48604886	SMAD4_353	+	CGTTGGGGCCCTTAACCTTATCAGGATGGTGGACTACAAAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr19	40739868	40739907	AKT2_354	+	CAGAGGTGGATGGGGAGGACCAGTCAGGAGAGGGCCTGGGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr19	40741064	40741103	AKT2_355	+	GAGGAGCTCAGGCTCAGGGACCCTGAGGCCAGGAGGCCTCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr19	40741267	40741306	AKT2_356	+	ACGGCCGTCAGCACCTGCCTCCCGGAGCAGCTGGGTTCGGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr19	40742021	40742060	AKT2_357	+	AGGAGAAATGAGGGCTGGGCCCGTGGCCCTGAGGCTGGCAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr19	40742302	40742341	AKT2_358	+	AGTCAACGGATCTCAGGTGCATGCTCCCAAGGCTTCCTGCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr19	40744008	40744047	AKT2_359	+	AAGGGGTGGGGAGAGGAGGTCAGGCCCCAGCCCACCCACCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr19	40744890	40744929	AKT2_360	+	AAGGCAGCAGGGTGGGAGGTGGGAGGGAGGAGGGCTCTGCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr19	40746027	40746066	AKT2_361	+	ACTGCGGGTGAGGGGCTGGTGGGCAACACCACACCTGCCCAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr19	40747986	40748025	AKT2_362	+	CAGGGAGAGTGGGGGCAGTCAGCGCCTGGCTCATGGCCCGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr19	40748604	40748643	AKT2_363	+	ACACACGTGAGTCCCAGCAGCCAGGAGTCCTGGGCCTCAGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr19	40761186	40761225	AKT2_364	+	AGGGAACAGACAGCAGGGGGCTGAGGGGATAGCCCTGCTAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr19	40762971	40763010	AKT2_365	+	GCAGGAAGGGAGGGAGAGAGGTTAGGACAAGGTTGAGTGAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG
chr19	40771184	40771223	AKT2_366	+	TGGTACGCTGTCACCTAGCTCGGGACAGCTCAGGGCAGCAAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGATCTCGTATGCCGTCTTCTGCTTG