Supplementary Table 2. Mutational hotspots of the 50 tumor-related genes assessed by Ion AmpliSeq Cancer Hotspot Panel v2.

Gene symbol	Accession number	Mutations deposited in Catalogue of Somatic Mutations in Cancer (COSMIC) database (https://cancer.sanger.ac.uk)						Amplicon ID	Reference sequence of library insert
		COSMIC ID	Codon number and mutation	Amino acid substitution	Strand	Chromosome position (hg19)			
SMARCB1	NM_003073.2	1002	c.118C>T	p.R40*	+	22:24139467-24139467		CHP2_SMARCB1_1	CCTCCGTATGTTCCGAGGTTCTCTGCTCATCAAGGAGTACCCTCACTGTGGAAGAGGAAGCTAGCACTGTGGAAGAGGAAGAAATTGCATCTGTCACACATGGTAAAAGAAGAAAT
BRI3	NM_001021	1042	c.210T-2A>G	p.?	+	13:49039665-49039665		CHP2_BRI3_1	CCTCCCATGGTTCCGAGGTTCTCTGCTCATCAAGGATACCCTCACTGTGGAAGAGGAAGCTAGCACTGTGGAAGAGGAAGAATATTAGACCTTAAATTCAAAATCATT
SMARCB1	NM_003073.2	1057	c.1144delG	p.A382fs*	+	22:24176357-24176357		CHP2_SMARCB1_4	CCTTGGGAAGGGCAGCGCCCAGGCTGGGAGGCTGGCCCCGACTCATTGCCTCTCCCCACTCCTCTTCCAGGCCGAGTGAGGGCGTCTTGCCAACACGGCCCCGGCCTGGTAAACCAGCCCATCAGCACACCGGCTCCC
SMARCB1	NM_003073.2	1060	c.1144delG	p.A382fs*	+	22:24176357-24176357		CHP2_SMARCB1_4	CCTTGGGAAGGGCAGCGCCCAGGCTGGGAGGCTGGCCCCGACTCATTGCCTCTCCCCACTCCTCTTCCAGGCCGAGTGAGGGCGTCTTGCCAACACGGCCCCGGCCTGGTAAACCAGCCCATCAGCACACCGGCTCCC
TP53	NM_000546	10645	c.527G>T	p.C176F	+	17:7578406-7578406		CHP2_TP53_1	CCAGGCCCCAGCTGCTCACCATCGCTATCTGAGCAGCGCTCATGGTGGGGGCAGCGCCTCACACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGCCATGGGCGTGGGCAGGCCAGCTGA
TP53	NM_000546	10646	c.725G>A	p.C242Y	+	17:7575756-7575756		CHP2_TP53_1	CCAGGTGTGATGTGTGAGGATGGGCCTCCGGTTCATGCCGCCCATGCAGGAACTGTTACACATGTAGTTGTAGTGGATGGTGGTCACTGCAGGCCAACCTAG
TP53	NM_000546	10647	c.404G>T	p.C135F	+	17:7578326-7578326		CHP2_TP53_1	CCAGACTGCCTCTCGCTTAGTGCTGTGCTGATGGTACAGGAGGAAGAGGAGGCAGGGCTCAGATGGCCTGGTCTGCCAGTGTGCAGGGCCGCATCAGGTCACGACACCGCACCAGGGCAGCTGCG
TP53	NM_000546	10648	c.524G>A	p.R175H	+	17:7578406-7578406		CHP2_TP53_1	CCAGACTGCCTCTCGCTTAGTGCTGTGCTGATGGTACAGGAGGAAGAGGAGGCAGGGCTCAGATGGCCTGGTCTGCCAGTGTGCAGGGCCGCATCAGGTCACGACACCGCACCAGGGCAGCTGCG
TP53	NM_000546	10650	c.526C>T	p.P177S	+	17:7578400-7578400		CHP2_TP53_1	CCAGACTGCCTCTCGCTTAGTGCTGTGCTGATGGTACAGGAGGAAGAGGAGGCAGGGCTCAGATGGCCTGGTCTGCCAGTGTGCAGGGCCGCATCAGGTCACGACACCGCACCAGGGCAGCTGCG
TP53	NM_000546	10651	c.539C>G	p.P177R	+	17:7578400-7578400		CHP2_TP53_4	CCAGCCCCAGCTGCTCACCATCGCTATCTGAGCAGCGCTCATGGTGGGGGCAGCGCCTCACAACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGCCATGGGCGTGGGCAGGCCAGCTGAGCA
TP53	NM_000546	10654	c.637C>T	p.R213*	+	17:7578212-7578212		CHP2_TP53_2	GGCGGGCACTGGGAGCACCACCACACTGTGCGAAGGTTTCTGTCCTCACGCGCGAATTTCCCGCCATGGCTGACTAGTGGATCCGAGCTCGGTACCAAGCTTGTACAAGAGAGCACAGAGCAGA
TP53	NM_000546	10656	c.742C>T	p.R248W	+	17:7577539-7577539		CHP2_TP53_1	CCAGTGTGATGATGATGTGAGGATGGGCCTCCGTTCATGCCGCCCATGCAGGAACTGTTACACATGTAGTTGTAGTGGATGGTGGTCACTGCAGGCCAACCTAGAGTGGGCAGAGCAGTCTCCTGA
TP53	NM_000546	10659	c.817C>T	p.R273C	+	17:7577121-7577121		CHP2_TP53_1	TACCTCGCTTAGTGCTCCCTGGGGGCAGCTGCTGGTGAGGACTCCCCTTTCTTGCGGAGATTCTCTTCTCTGTGCGCCGGTCTCTCCCAGGACAGGCACACACACGCACCTCAAAGCTGTTCCGTCCCAGTAGATT
TP53	NM_000546	10660	c.818G>A	p.R273H	+	17:7577120-7577120		CHP2_TP53_1	TACCTCGCTTAGTGCTCCCTGGGGGCAGCTGCTGGTGAGGACTCCCCTTTCTTGCGGAGATTCTCTTCTCTGTGCGCCGGTCTCTCCCAGGACAGGCACACACACGCACCTCAAAGCTGTTCCGTCCCAGTAGATT
TP53	NM_000546	10662	c.743G>A	p.R248Q	+	17:7577538-7577538		CHP2_TP53_1	CCAGTGTGATGATGATGTGAGGATGGGCCTCCGTTCATGCCGCCCATGCAGGAACTGTTACACATGTAGTTGTAGTGGATGGTGGTCACTGCAGGCCAACCTAG
TP53	NM_000546	10663	c.916C>T	p.R306*	+	17:7577022-7577022		CHP2_TP53_1	CCAGACCGCTTCTATGCTGCAGGACGGATCCGAGTCTAGAGGGCAGGGTCTTCTTCCTCCTCCGCCCCGCCCTGCAGGAGCGCACGTACGCGCTGTCGATGTGCATGAGGGTCACGTACTGACGATCT
TP53	NM_000546	10667	c.646G>A	p.V216M	+	17:7578265-7578265		CHP2_TP53_3	GGCGGGCCTATAGGGCACCACCACACTATGTCGAAAAGTGTTTCTGTCATCCAAATACTCCACACGCAAATTTCCTTCCACTCGGATAAGATGCTGAGGAGGGGCCAGCACTGAAGGACA
TP53	NM_000546	10668	c.745A>G	p.R249G	+	17:7577536-7577536		CHP2_TP53_2	CGAGTGTGATGATGTGAGGATGGGCCTCCGGTTCATGCCGCCCATGCAGGAACTGTTACACATGTAGTTGTAGTGGATGGTGGTCACTGCAGGCCAACCTAG
TP53	NM_000546	10670	c.466G>T	p.V157F	+	17:7578646-7578646		CHP2_TP53_3	GGCGGGCCTATAGGGCACCACCACACTATGTCGAAAAGTGTTTCTGTCATCCAAATACTCCACACGCAAATTTCCTTCCACTCGGATAAGATGCTGAGGAGGGGCCAGCACTGAAGGACA
TP53	NM_000546	10672	c.737C>T	p.H193Y	+	17:7578272-7578272		CHP2_TP53_2	GGCGGGCCTATAGGGCACCACCACACTATGTCGAAAAGTGTTTCTGTCATCCAAATACTCCACACGCAAATTTCCTTCCACTCGGATAAGATGCTGAGGAGGGGCCAGCACTGAAGGACA
TP53	NM_000546	10684	c.401T>C	p.C133R	+	17:7578671-7578671		CHP2_TP53_3	GGCAGTTGGGAGCACCACCACACTGTGCGAAGGTTTCTGTCCTCACGCGCGAATTTCCCGCCATGGCTGACTAGTGGATCCGAGCTCGGTACCAAGCTTGTACAAGAGAGCACAGAGCAGA
TP53	NM_000546	10687	c.527G>A	p.R176H	+	17:7578403-7578403		CHP2_TP53_1	CCAGACCCCAGCTGCTCACCATCGCTATCTGAGCAGCGCTCATGGTGGGGGCAGCGCCTCACAACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGCCATGGGCGTGGGCAGGCCAGCTGAGCA
TP53	NM_000546	10690	c.472C>A	p.R158S	+	17:7578457-7578457		CHP2_TP53_1	CCAGACCCCAGCTGCTCACCATCGCTATCTGAGCAGCGCTCATGGTGGGGGCAGCGCCTCACAACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGCCATGGGCGTGGGCAGGCCAGCTGAGCA
TP53	NM_000546	10701	c.824G>T	p.C275F	+	17:7577114-7577114		CHP2_TP53_1	TACCTCGCTTAGTGCTCCCTGGGGGCAGCTGCTGGTGAGGACTCCCCTTTCTTGCGGAGATTCTCTTCTCTGTGCGCCGGTCTCTCCCAGGACAGGCACACACACGCACCTCAAAGCTGTTCCGTCCCAGTAGATT
TP53	NM_000546	10704	c.844C>T	p.R282W	+	17:7577014-7577014		CHP2_TP53_1	TACCTCGCTTAGTGCTCCCTGGGGGCAGCTGCTGGTGAGGACTCCCCTTTCTTGCGGAGATTCTCTTCTCTGTGCGCCGGTCTCTCCCAGGACAGGCACACACACGCACCTCAAAGCTGTTCCGTCCCAGTAGATT
TP53	NM_000546	10705	c.586C>T	p.R196*	+	17:7578263-7578263		CHP2_TP53_2	GGCGGGCCTATAGGGCACCACCACACTATGTCGAAAAGTGTTTCTGTCATCCAAATACTCCACACGCAAATTTCCTTCCACTCGGATAAGATGCTGAGGAGGGGCCAGCACTGAAGGACA
TP53	NM_000546	10706	c.548C>G	p.S183*	+	17:7578382-7578382		CHP2_TP53_1	CCAGCCCCAGCTGCTCACCATCGCTATCTGAGCAGCGCTCATGGTGGGGGCAGCGCCTCACAACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGCCATGGGCGTGGGCAGGCCAGCTGAGCA
TP53	NM_000546	10709	c.722C>G	p.S241C	+	17:7577559-7577559		CHP2_TP53_1	CCAGTGTGATGATGATGTGAGGATGGGCCTCCGTTCATGCCGCCCATGCAGGAACTGTTACACATGTAGTTGTAGTGGATGGTGGTCACTGCAGGCCAACCTAG
TP53	NM_000546	10710	c.892G>T	p.E298*	+	17:7577046-7577046		CHP2_TP53_1	TACCTCGCTTAGTGCTCCCTGGGGGCAGCTGCTGGTGAGGACTCCCCTTTCTTGCGGAGATTCTCTTCTCTGTGCGCCGGTCTCTCCCAGGACAGGCACACACACGCACCTCAAAGCTGTTCCGTCCCAGTAGATT
TP53	NM_000546	10714	c.473G>T	p.R158L	+	17:7578457-7578457		CHP2_TP53_1	CCAGCCCCAGCTGCTCACCATCGCTATCTGAGCAGCGCTCATGGTGGGGGCAGCGCCTCACAACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGCCATGGGCGTGGGCAGGCCAGCTGAGCA
TP53	NM_000546	10715	c.695T>A	p.I232N	+	17:7577586-7577586		CHP2_TP53_1	CCAGTGTGATGATGATGTGAGGATGGGCCTCCGGTTCATGCCGCCCATGCAGGAACTGTTACACATGTAGTTGTAGTGGATGGTGGTCACTGCAGGCCAACCTAG
TP53	NM_000546	10716	c.329C>T	p.R110L	+	17:7579013-7579013		CHP2_TP53_2	GCCCAGACGAGGAACGCAGCCGGCGCTGGCCTGGTAGGTTTCTGGGAAGGGACACAGAGAGAGCAGGGCCGGGCCGGGCTGGGTGGAGGGGCACGGGCTGGTGCAGGGGCCACGGGGGCAGCAGCCTC
TP53	NM_000546	10718	c.524G>T	p.R175L	+	17:7578406-7578406		CHP2_TP53_1	CCAGACCCCAGCTGCTCACCATCGCTATCTGAGCAGCGCTCATGGTGGGGGCAGCGCCTCACAACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGCCATGGGCGTGGGCAGGCCAGCTGAGCA
TP53	NM_000546	10719	c.811G>A	p.E271K	+	17:7577127-7577127		CHP2_TP53_1	TACCTCGCTTAGTGCTCCCTGGGGGCAGCTGCTGGTGAGGACTCCCCTTTCTTGCGGAGATTCTCTTCTCTGTGCGCCGGTCTCTCCCAGGACAGGCACACACACGCACCTCAAAGCTGTTCCGTCCCAGTAGATT
TP53	NM_000546	10722	c.853G>A	p.E285K	+	17:7577086-7577086		CHP2_TP53_1	TACCTCGCTTAGTGCTCCCTGGGGGCAGCTGCTGGTGAGGACTCCCCTTTCTTGCGGAGATTCTCTTCTCTGTGCGCCGGTCTCTCCCAGGACAGGCACACACACGCACCTCAAAGCTGTTCCGTCCCAGTAGATT
TP53	NM_000546	10724	c.839G>C	p.R280T	+	17:7577099-7577099		CHP2_TP53_1	TACCTCGCTTAGTGCTCCCTGGGGGCAGCTGCTGGTGAGGACTCCCCTTTCTTGCGGAGATTCTCTTCTCTGTGCGCCGGTCTCTCCCAGGACAGGCACACACACGCACCTCAAAGCTGTTCCGTCCCAGTAGATT
TP53	NM_000546	10725	c.781A>G	p.T261A	+	17:7577158-7577158		CHP2_TP53_1	CCAGTGTGATGATGATGTGAGGATGGGCCTCCGGTTCATGCCGCCCATGCAGGAACTGTTACACATGTAGTTGTAGTGGATGGTGGTCACTGCAGGCCAACCTAG
TP53	NM_000546	10726	c.856G>A	p.E286K	+	17:7577082-7577082		CHP2_TP53_1	TACCTCGCTTAGTGCTCCCTGGGGGCAGCTGCTGGTGAGGACTCCCCTTTCTTGCGGAGATTCTCTTCTCTGTGCGCCGGTCTCTCCCAGGACAGGCACACACACGCACCTCAAAGCTGTTCCGTCCCAGTAGATT
TP53	NM_000546	10728	c.839G>A	p.R280K	+	17:7577099-7577099		CHP2_TP53_1	TACCTCGCTTAGTGCTCCCTGGGGGCAGCTGCTGGTGAGGACTCCCCTTTCTTGCGGAGATTCTCTTCTCTGTGCGCCGGTCTCTCCCAGGACAGGCACACACACGCACCTCAAAGCTGTTCCGTCCCAGTAGATT
TP53	NM_000546	10731	c.707A>G	p.Y236C	+	17:7577574-7577574		CHP2_TP53_6	CCAGTGTGATGATGTGAGGATGGGCCTCCGGTTCATGCCGCCCATGCAGGAACTGTTACACATGTAGTTGTAGTGGATGGTGGTCACTGCAGGCCAACCTAG
TP53	NM_000546	10733	c.574C>T	p.Q192*	+	17:7578275-7578275		CHP2_TP53_1	GGCGGGCCTATAGGGCACCACCACACTATGTCGAAAAGTGTTTCTGTCATCCAAATACTCCACACGCAAATTTCCTTCCACTCGGATAAGATGCTGAGGAGGGGCCAGCACTGAAGGACA
TP53	NM_000546	10735	c.638G>A	p.R213Q	+	17:7578151-7578151		CHP2_TP53_1	GGCGGGCCTATAGGGCACCACCACACTATGTCGAAAAGTGTTTCTGTCATCCAAATACTCCACACGCAAATTTCCTTCCACTCGGATAAGATGCTGAGGAGGGGCCAGCACTGAAGGACA
TP53	NM_000546	10738	c.542G>A	p.R181H	+	17:7578388-7578388		CHP2_TP53_1	CCAGACCCCAGCTGCTCACCATCGCTATCTGAGCAGCGCTCATGGTGGGGGCAGCGCCTCACAACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGCCATGGGCGTGGGCAGGCCAGCTGAGCA
TP53	NM_000546	10739	c.481G>A	p.A161T	+	17:7578449-7578449		CHP2_TP53_1	CCAGCCCCAGCTGCTCACCATCGCTATCTGAGCAGCGCTCATGGTGGGGGCAGCGCCTCACAACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGCCATGGGCGTGGGCAGGCCAGCTGAGCA
TP53	NM_000546	10742	c.578A>G	p.H193R	+	17:7578271-7578271		CHP2_TP53_1	GGCGGGCCTATAGGGCACCACCACACTATGTCGAAAAGTGTTTCTGTCATCCAAATACTCCACACGCAAATTTCCTTCCACTCGGATAAGATGCTGAGGAGGGGCCAGCACTGAAGGACA
TP53	NM_000546	10743	c.848G>C	p.S283P	+	17:7577109-7577109		CHP2_TP53_1	TACCTCGCTTAGTGCTCCCTGGGGGCAGCTGCTGGTGAGGACTCCCCTTTCTTGCGGAGATTCTCTTCTCTGTGCGCCGGTCTCTCCCAGGACAGGCACACACACGCACCTCAAAGCTGTTCCGTCCCAGTAGATT
TP53	NM_000546	10749	c.836G>T	p.C277F	+	17:7577108-7577108		CHP2_TP53_1	TACCTCGCTTAGTGCTCCCTGGGGGCAGCTGCTGGTGAGGACTCCCCTTTCTTGCGGAGATTCTCTTCTCTGTGCGCCGGTCTCTCCCAGGACAGGCACACACACGCACCTCAAAGCTGTTCCGTCCCAGTAGATT
TP53	NM_000546	10750	c.488A>T	p.K164*	+	17:7578446-7578446		CHP2_TP53_1	CCAGACCCCAGCTGCTCACCATCGCTATCTGAGCAGCGCTCATGGTGGGGGCAGCGCCTCACAACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGCCATGGGCGTGGGCAGGCCAGCTGAGCA
TP53	NM_000546	10756	c.827C>T	p.A276V	+	17:7577111-7577111		CHP2_TP53_1	TACCTCGCTTAGTGCTCCCTGGGGGCAGCTGCTGGTGAGGACTCCCCTTTCTTGCGGAGATTCTCTTCTCTGTGCGCCGGTCTCTCCCAGGACAGGCACACACACGCACCTCAAAGCTGTTCCGTCCCAGTAGATT
TP53	NM_000546	10757	c.738G>C	p.M246I	+	17:7577543-7577543		CHP2_TP53_1	CCAGTGTGATGATGATGTGAGGATGGGCCTCCGGTTCATGCCGCCCATGCAGGAACTGTTACACATGTAGTTGTAGTGGATGGTGGTCACTGCAGGCCAACCTAG
TP53	NM_000546	10758	c.659A>G	p.Y220C	+	17:7578139-7578139		CHP2_TP53_1	GGCGGGCCTATAGGGCACCACCACACTATGTCGAAAAGTGTTTCTGTCATCCAAATACTCCACACGCAAATTTCCTTCCACTCGGATAAGATGCTGAGGAGGGGCCAGCACTGAAGGACA
TP53	NM_000546	10760	c.467G>C	p.R156P	+	17:7578463-7578463		CHP2_TP53_1	CCAGCCCCAGCTGCTCACCATCGCTATCTGAGCAGCGCTCATGGTGGGGGCAGCGCCTCACAACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGCCATGGGCGTGGGCAGGCCAGCTGAGCA
TP53	NM_000546	10762	c.490G>C	p.E164Q	+	17:7578440-7578440		CHP2_TP53_1	CCAGACCCCAGCTGCTCACCATCGCTATCTGAGCAGCGCTCATGGTGGGGGCAGCGCCTCACAACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGCCATGGGCGTGGGCAGGCCAGCTGAGCA
TP53	NM_000546	10768	c.533C>T	p.H177Y	+	17:7578395-7578395		CHP2_TP53_1	CCAGACCCCAGCTGCTCACCATCGCTATCTGAGCAGCGCTCATGGTGGGGGCAGCGCCTCACAACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGCCATGGGCGTGGGCAGGCCAGCTGAGCA
TP53	NM_000546	10769	c.820G>T	p.V274F	+	17:7577116-7577116		CHP2_TP53_1	TACCTCGCTTAGTGCTCCCTGGGGGCAGCTGCTGGTGAGGACTCCCCTTTCTTGCGGAGATTCTCTTCTCTGTGCGCCGGTCTCTCCCAGGACAGGCACACACACGCACCTCAAAGCTGTTCCGTCCCAGTAGATT
TP53	NM_000546	10770	c.1045G>T	p.E349*	+	17:7573982-7573982		CHP2_TP53_4	CACCTGGAGTGAGCCCTGCTCCCCCCTGGCTCCTTCCCAGCCTGGGCATCCTTGAGTTCCAAGGCCTCATTCAGCTCCTGGACACATCTGAAGCGCTCACGCCCACGGATCT
TP53	NM_000546	10771	c.790C>T	p.P230L	+	17:7577532-7577532		CHP2_TP53_1	CCAGTGTGATGATGTGAGGATGGGCCTCCGGTTCATGCCGCCCATGCAGGAACTGTTACACATGTAGTTGTAGTGGATGGTGGTCACTGCAGGCCAACCTAG
TP53	NM_000546	10777	c.713A>G	p.N238S	+	17:7577566-7577566		CHP2_TP53_1	CCAGTGTGATGATGTGAGGATGGGCCTCCGGTTCATGCCGCCCATGCAGGAACTGTTACACATGTAGTTGTAGTGGATGGTGGTCACTGCAGGCCAACCTAG
TP53	NM_000546	10779	c.818G>T	p.R273L	+	17:7577120-7577120		CHP2_TP53_1	TACCTCGCTTAGTGCTCCCTGGGGGCAGCTGCTGGTGAGGACTCCCCTTTCTTGCGGAGATTCTCTTCTCTGTGCGCCGGTCTCTCCCAGGACAGGCACACACACGCACCTCAAAGCTGTTCCGTCCCAGTAGATT
TP53	NM_000546	10785	c.743G>C	p.R248S	+	17:7577534-7577534		CHP2_TP53_1	CCAGTGTGATGATGTGAGGATGGGCCTCCGGTTCATGCCGCCCATGCAGGAACTGTTACACATGTAGTTGTAGTGGATGGTGGTCACTGCAGGCCAACCTAG
TP53	NM_000546	10788	c.764T>G	p.I255S	+	17:7577517-7577517		CHP2_TP53_1	CCAGTGTGATGATGTGAGGATGGGCCTCCGGTTCATGCCGCCCATGCAGGAACTGTTACACATGTAGTTGTAGTGGATGGTGGTCACTGCAGGCCAACCTAG
TP53	NM_000546	10790	c.455C>T	p.P152L	+	17:7578475-7578475		CHP2_TP53_1	CCAGCCCCAGCTGCTCACCATCGCTATCTGAGCAGCGCTCATGGTGGGGGCAGCGCCTCACAACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGCCATGGGCGTGGGCAGGCCAGCTGAGCA
TP53	NM_000546	10794	c.796G>A	p.G266R	+	17:7577142-7577142		CHP2_TP53_7	TACCTCGCTTAGTGCTCCCTGGGGGCAGCTGCTGGTGAGGACTCCCCTTTCTTGCGGAGATTCTCTTCTCTGTGCGCCGGTCTCTCCCAGGACAGGCACACACACGCACCTCAAAGCTGTTCCGTCCCAGTAGATT
ERBB4	NM_005235	108015	c.2886G>A	p.G958R	+	2:212368940-212368940		CHP2_ERBB4_8	AATAGTGCAGATGGGCAGCCCACAGTGCTGCAACATGTCTCTTTTCTCTTCTCAAAAATCAGGAATTCTCGCGTTGGAATTTCATCATATAGGT
TP53	NM_000546	10801	c.404G>A	p.C135Y	+	17:7578326-7578326		CHP2_TP53_1	GCCAGTTGGGAGCACCACCACACTGTGCGAAGGTTTCTGTCCTCACGCGCGAATTTCCCGCCATGGCTGACTAGTGGATCCGAGCTCGGTACCAAGCTTGTACAAGAGAGCACAGAGCAGA
TP53	NM_000546	10804	c.610G>T	p.E204*	+	17:7578239-7578239		CHP2_TP53_4	GGCGGGCCATAGGGCACCACCACACTATGTCGAAAAGTGTTTCTGTCATCCAAATACTCCACACGCAAATTTCCTTCCACTCGGATAAGATGCTGAGGAGGGGCCAGCACTGAAGGACA
TP53	NM_000546	10808	c.488A>G	p.Y163C	+	17:7578447-7578447		CHP2_TP53_1	CCAGACCCCAGCTGCTCACCATCGCTATCTGAGCAGCGCTCATGGTGGGGGCAGCGCCTCACAACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGCCATGGGCGTGGGCAGGCCAGCTGAGCA
TP53	NM_000546	10810	c.725G>T	p.C242F	+	17:7575756-7575756		CHP2_TP53_1	CCAGTGTGATGATGTGAGGATGGGCCTCCGGTTCATGCCGCCCATGCAGGAACTGTTACACATGTAGTTGTAGTGGATGGTGGTCACTGCAGGCCAACCTAG
TP53	NM_000546	10812	c.722C>T	p.S241F	+	17:7577559-7577559		CHP2_TP53_1	CCAGTGTGATGATGTGAGGATGGGCCTCCGGTTCATGCCGCCCATGCAGGAACTGTTACACATGTAGTTGTAGTGGATGGTGGTCACTGCAGGCCAACCTAG
TP53	NM_000546	10813	c.394A>G	p.K132E	+	17:7578536-7578536		CHP2_TP53_1	GCCAGTTGGGAGCACCACCACACTGTGCGAAGGTTTCTGTCCTCACGCGCGAATTTCCCGCCATGGCTGACTAGTGGATCCGAGCTCGGTACCAAGCTTGTACAAGAGAGCACAGAGCAGA
TP53	NM_000546	10814	c.832C>G	p.P278A	+	17:7577088-7577088		CHP2_TP53_1	TACCTCGCTTAGTGCTCCCTGGGGGCAGCTGCTGGTGAGGACTCCCCTTTCTTGCGGAGATTCTCTTCTCTGTGCGCCGGTCTCTCCCAGGACAGGCACACACACGCACCTCAAAGCTGTTCCGTCCCAGTAGATT
TP53	NM_000546	10817	c.743G>T	p.R249S	+	17:7577534-7577534		CHP2_TP53_1	CCAGTGTGATGATGTGAGGATGGGCCTCCGGTTCATGCCGCCCATGCAGGAACTGTTACACATGTAGTTGTAGTGGATGGTGGTCACTGCAGGCCAACCTAG
TP53	NM_000546	10834	c.711G>A	p.M237I	+	17:7577570-7577570		CHP2_TP53_1	CCAGTGTGATGATGTGAGGATGGGCCTCCGGTTCATGCCGCCCATGCAGGAACTGTTACACATGTAGTTGTAGTGGATGGTGGTCACTGCAGGCCAACCTAG
TP53	NM_000546	10836	c.886G>T	p.E296*	+	17:7577052-7577052		CHP2_TP53_1	TACCTCGCTTAGTGCTCCCTGGGGGCAGCTGCTGGTGAGGACTCCCCTTTCTTGCGGAGATTCTCTTCTCTGTGCGCCGGTCTCTCCCAGGACAGGCACACACACGCACCTCAAAGCTGTTCCGTCCCAGTAGATT
FBXW7_ENST00000542231	ENST00000342231	108571	c.790C>T	p.R266C	+	4:153472389-153472389		CHP2_FBXW7_4	TTGAACACAGCGGCAGCTGCTGCACAATGACCCATCAAAACATGTAAACACTGGGCTGCTCAATATCCAAACCCTCAAAGGTGGGCTCTGCAG
FBXW7_ENST00000281708	ENST00000281708	108572	c.1513C>T	p.R505C	+	4:153472389-153472389		CHP2_FBXW7_4	TTGAACACAGCGGCAGCTGCTGCACAATGACCCATCAAAACATGTAAACACTGGGCTGCTCAATATCCAAACCCTCAAAGGTGGGCTCTGCAG
TP53	NM_000546	10859	c.814G>T	p.V272L	+	17:7577124-7577124		CHP2_TP53_7	TACCTCGCTTAGTGCTCCCTGGGGGCAGCTGCTGGTGAGGACTCCCCTTTCTTGCGGAGATTCTCTTCTCTGTGCGCCGGTCTCTCCCAGGACAGGCACACACACGCACCTCAAAGCTGTTCCGTCCCAGTAGATT
TP53	NM_000546	10862	c.374C>T	p.T125M	+	17:7578554-7578554		CHP2_TP53_1	GCCAGTTGGGAGCACCACCACACTGTGCGAAGGTTTCTGTCCTCACGCGCGAATTTCCCGCCATGGCTGACTAGTGGATCCGAGCTCGGTACCAAGCTTGTACAAGAGAGCACAGAGCAGA
TP53	NM_000546	10863	c.833C>T	p.P278L	+	17:7577105-7577105		CHP2_TP53_1	TACCTCGCTTAGTGCTCCCTGGGGGCAGCTGCTGGTGAGGACTCCCCTTTCTTGCGGAGATTCTCTTCTCTGTGCGCCGGTCTCTCCCAGGACAGGCACACACACGCACCTCAAAGCTGTTCCGTCCCAGTAGATT
TP53	NM_000546	10867	c.793G>A	p.G266E	+	17:7577141-7577141		CHP2_TP53_7	TACCTCGCTTAGTGCTCCCTGGGGGCAGCTGCTGGTGAGGACTCCCCTTTCTTGCGGAGATTCTCTTCTCTGTGCGCCGGTCTCTCCCAGGACAGGCACACACACGCACCTCAAAGCTGTTCCGTCCCAGTAGATT
TP53	NM_000546	10870	c.523C>G	p.R175G	+	17:7578407-7578407		CHP2_TP53_1	CCAGACCCCAGCTGCTCACCATCGCTATCTGAGCAGCGCTCATGGTGGGGGCAGCGCCTCACAACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGCCATGGGCGTGGGCAGGCCAGCTGAGCA
TP53	NM_000546	10883	c.731G>A	p.G244D	+	17:7577539-7577539		CHP2_TP53_1	CCAGTGTGATGATGTGAGGATGGGCCTCCGGTTCATGCCGCCCATGCAGGAACTGTTACACATGTAGTTGTAGTGGATGGTGGTCACTGCAGGCCAACCTAG
TP53	NM_000546	10886	c.310C>T	p.Q104*	+	17:7579577-7579577		CHP2_TP53_3	GCCCAGACGAGGAACGCAGCCGGCGCTGGCCTGGTAGGTTTCTGGGAAGGGACACAGAGAGAGCAGGGCCGGGCCGGGCTGGGTGGAGGGGCACGGGCTGGTGCAGGGGCCACGGGGGCAGCAGCCTC
TP53	NM_000546	10887	c.833C>G	p.P278R	+	17:7577105-7577105		CHP2_TP53_1	TACCTCGCTTAGTGCTCCCTGGGGGCAGCTGCTGGTGAGGACTCCCCTTTCTTGCGGAGATTCTCTTCTCTGTGCGCCGGTCTCTCCCAGGACAGGCACACACACGCACCTCAAAGCTGTTCCGTCCCAGTAGATT
TP53	NM_000546	10888	c.378C>A	p.S126*	+	17:7578552-7578552		CHP2_TP53_1	GCCAGTTGGGAGCACCACCACACTGTGCGAAGGTTTCTGTCCTCACGCGCGAATTTCCCGCCATGGCTGACTAGTGGATCCGAGCTCGGTACCAAGCTTGTACAAGAGAGCACAGAGCAGA
TP53	NM_000546	10889	c.536A>G	p.H179R	+	17:7578394-7578394		CHP2_TP53_1	CCAGACCCCAGCTGCTCACCATCGCTATCTGAGCAGCGCTCATGGTGGGGGCAGCGCCTCACAACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGCCATGGGCGTGGGCAGGCCAGCTGAGCA
TP53	NM_000546	10891	c.814G>A	p.V272M	+	17:7577124-7577124		CHP2_TP53_7	TACCTCGCTTAGTGCTCCCTGGGGGCAGCTGCTGGTGAGGACTCCCCTTTCTTGCGGAGATTCTCTTCTCTGTGCGCCGGTCTCTCCCAGGACAGGCACACACACGCACCTCAAAGCTGTTCCGTCCCAGTAGATT
TP53	NM_000546	10893	c.824G>A	p.C275Y	+	17:7577114-7577114		CHP2_TP53_7	TACCTCGCTTAGTGCTCCCTGGGGGCAGCTGCTGGTGAGGACTCCCCTTTCTTGCGGAGATTCTCTTCTCTGTGCGCCGGTCTCTCCCAGGACAGGCACACACACGCACCTCAAAGCTGTTCCGTCCCAGTAGATT
SMARCB1	NM_003073.2	1080	c.1119+6G>A	p.?	+	22:24176287-24176287		CHP2_SMARCB1_4	CCTTGGGAAGGGCAGCGCCCAGGCTGGGAGGCTGGCCCCGACTCATTGCCTCTCCCCACTCCTCTTCCAGGCCGAGTGAGGGCGTCTTGCCAACACGGCCCCGGCCTGGTAAACCAGCCCATCAGCACACCGGCTCCC
TP53	NM_000546	10911	c.847C>T	p.R283C	+	17:7577091-7577091		CHP2_TP53_1	TACCTCGCTTAGTGCTCCCTGGGGGCAGCTGCTGGTGAGGACTCCCCTTTCTTGCGGAGATTCTCTTCTCTGTGCGCCGGTCTCTCCCAGGACAGGCACACACACGCACCTCAAAGCTGTTCCGTCCCAGTAGATT
TP53	NM_000546	10912	c.463A>C	p.T155P	+	17:7578467-7578467		CHP2_TP53_1	CCAGCCCCAGCTGCTCACCATCGCTATCTGAGCAGCGCTCATGGTGGGGGCAGCGCCTCACAACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGCCATGGGCGTGGGCAGGCCAGCTGAGCA
TP53	NM_000546	10931	c.751A>C	p.I251L	+	17:7577538-7577538		CHP2

TP53 ENST00000245858	ENST00000245858	120006	c.463C>T	p.R155W	-	17:7577539-7577539	CHP2_TP53_6	CCAGGTGTGATGATGGTGAGGATGGGCCTCGGTTCATGCCGCCCATGCAGGAACTGTTACACATGATTGTGATGGATGTGGTTACAGTCAGAGCAACCTAG
TP53 ENST00000268305	ENST00000268305	120007	c.742C>T	p.R248W	-	17:7577539-7577539	CHP2_TP53_6	CCAGGTGTGATGATGGTGAGGATGGGCCTCGGTTCATGCCGCCCATGCAGGAACTGTTACACATGATTGTGATGGATGTGGTTACAGTCAGAGCAACCTAG
KIT	NM_000222	1200	c.1663_1710del51	p.V555_I571del	+	4:55593097-55593647	CHP2_KIT_4	CCACAGAAACCCATGTATGAAGTACAGTGGAAGGTTGTTGAGGAGATAAATGGAACAAACTATTGTTTACATAGACCCACACACACTTCTTTATGTACACAAAG
TP53	NM_000546	12013	c.733G>C	p.G244A	-	17:7577546-7577550	CHP2_TP53_6	CCAGGTGTGATGATGGTGAGGATGGGCCTCGGTTCATGCCGCCCATGCAGGAACTGTTACACATGATTGTGATGGATGTGGTTACAGTCAGAGCAACCTAG
KIT	NM_000222	1201	c.1660_1668delCTACAG	p.Y555_Q556del	+	4:55593097-55593660	CHP2_KIT_4	CCACAGAAACCCATGTATGAAGTACAGTGGAAGGTTGTTGAGGAGATAAATGGAACAAACTATTGTTTACATAGACCCACACACACTTCTTTATGTACACAAAG
KIT	NM_000222	1202	c.1663_1680del18	p.V555_V560del	+	4:55593097-55593654	CHP2_KIT_4	CCACAGAAACCCATGTATGAAGTACAGTGGAAGGTTGTTGAGGAGATAAATGGAACAAACTATTGTTTACATAGACCCACACACACTTCTTTATGTACACAAAG
KIT	NM_000222	1203	c.1663_1710del57	p.V555_F571del	+	4:55593097-55593653	CHP2_KIT_4	CCACAGAAACCCATGTATGAAGTACAGTGGAAGGTTGTTGAGGAGATAAATGGAACAAACTATTGTTTACATAGACCCACACACACTTCTTTATGTACACAAAG
KIT	NM_000222	1204	c.1666_1680del15	p.Q556_V560del	+	4:55593600-55593654	CHP2_KIT_4	CCACAGAAACCCATGTATGAAGTACAGTGGAAGGTTGTTGAGGAGATAAATGGAACAAACTATTGTTTACATAGACCCACACACACTTCTTTATGTACACAAAG
KIT	NM_000222	1205	c.1666_1728del63	p.Q556_L576del	-	4:55593600-55593662	CHP2_KIT_4	CCACAGAAACCCATGTATGAAGTACAGTGGAAGGTTGTTGAGGAGATAAATGGAACAAACTATTGTTTACATAGACCCACACACACTTCTTTATGTACACAAAG
TP53 ENST00000268305	ENST00000268305	120015	c.733C>A	p.G245S	-	17:7577546-7577550	CHP2_TP53_6	CCAGGTGTGATGATGGTGAGGATGGGCCTCGGTTCATGCCGCCCATGCAGGAACTGTTACACATGATTGTGATGGATGTGGTTACAGTCAGAGCAACCTAG
TP53 ENST00000445445	ENST00000445445	120016	c.733G>A	p.G245S	-	17:7577548-7577548	CHP2_TP53_6	CCAGGTGTGATGATGGTGAGGATGGGCCTCGGTTCATGCCGCCCATGCAGGAACTGTTACACATGATTGTGATGGATGTGGTTACAGTCAGAGCAACCTAG
TP53 ENST00000445445	ENST00000445445	120017	c.454C>A	p.L152S	-	17:7577548-7577548	CHP2_TP53_6	CCAGGTGTGATGATGGTGAGGATGGGCCTCGGTTCATGCCGCCCATGCAGGAACTGTTACACATGATTGTGATGGATGTGGTTACAGTCAGAGCAACCTAG
TP53 ENST00000268305	ENST00000268305	120042	c.517G>C	p.V173L	-	17:7578413-7578413	CHP2_TP53_4	CCAGCCCCCGCTGCTACCATCTGCTATCTGAGCACGCGCTCATGGTGGGGGCACGCGCCTCACAACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGCCATGGGCGCGGACGCGGGTGCCGGGCGGGGGCGTG
TP53 ENST00000445445	ENST00000445445	120043	c.517C>T	p.V173L	-	17:7578413-7578413	CHP2_TP53_4	CCAGCCCCCGCTGCTACCATCTGCTATCTGAGCACGCGCTCATGGTGGGGGCACGCGCCTCACAACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGCCATGGGCGCGGACGCGGGTGCCGGGCGGGGGCGTG
TP53 ENST00000445445	ENST00000445445	120044	c.216C>G	p.V66L	-	17:7578413-7578413	CHP2_TP53_4	CCAGCCCCCGCTGCTACCATCTGCTATCTGAGCACGCGCTCATGGTGGGGGCACGCGCCTCACAACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGCCATGGGCGCGGACGCGGGTGCCGGGCGGGGGCGTG
TP53 ENST00000445445	ENST00000445445	120045	c.215G>C	p.V66L	-	17:7578413-7578413	CHP2_TP53_4	CCAGCCCCCGCTGCTACCATCTGCTATCTGAGCACGCGCTCATGGTGGGGGCACGCGCCTCACAACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGCCATGGGCGCGGACGCGGGTGCCGGGCGGGGGCGTG
KIT	NM_000222	1210	c.1667_1674delGTGGA	p.W557_K558del	+	4:55593601-55593647	CHP2_KIT_4	CCACAGAAACCCATGTATGAAGTACAGTGGAAGGTTGTTGAGGAGATAAATGGAACAAACTATTGTTTACATAGACCCACACACACTTCTTTATGTACACAAAG
KIT	NM_000222	1211	c.1668_1674delTGGAA	p.W557_K558del	+	4:55593602-55593607	CHP2_KIT_4	CCACAGAAACCCATGTATGAAGTACAGTGGAAGGTTGTTGAGGAGATAAATGGAACAAACTATTGTTTACATAGACCCACACACACTTCTTTATGTACACAAAG
KIT	NM_000222	1213	c.1668_1695del12	p.Q556_V565del	+	4:55593602-55593654	CHP2_KIT_4	CCACAGAAACCCATGTATGAAGTACAGTGGAAGGTTGTTGAGGAGATAAATGGAACAAACTATTGTTTACATAGACCCACACACACTTCTTTATGTACACAAAG
KIT	NM_000222	1216	c.1669T>A	p.W557R	+	4:55593603-55593603	CHP2_KIT_4	CCACAGAAACCCATGTATGAAGTACAGTGGAAGGTTGTTGAGGAGATAAATGGAACAAACTATTGTTTACATAGACCCACACACACTTCTTTATGTACACAAAG
KIT	NM_000222	1217	c.1669_1674delTGGAAG	p.W557_K558del	+	4:55593603-55593647	CHP2_KIT_4	CCACAGAAACCCATGTATGAAGTACAGTGGAAGGTTGTTGAGGAGATAAATGGAACAAACTATTGTTTACATAGACCCACACACACTTCTTTATGTACACAAAG
KIT	NM_000222	1218	c.1669_1674del6	p.W557_V559del	+	4:55593603-55593611	CHP2_KIT_4	CCACAGAAACCCATGTATGAAGTACAGTGGAAGGTTGTTGAGGAGATAAATGGAACAAACTATTGTTTACATAGACCCACACACACTTCTTTATGTACACAAAG
KIT	NM_000222	1219	c.1669T>C	p.W557R	-	4:55593603-55593603	CHP2_KIT_4	CCACAGAAACCCATGTATGAAGTACAGTGGAAGGTTGTTGAGGAGATAAATGGAACAAACTATTGTTTACATAGACCCACACACACTTCTTTATGTACACAAAG
KIT	NM_000222	1220	c.1669_1674delTGG	p.W557del	+	4:55593603-55593608	CHP2_KIT_4	CCACAGAAACCCATGTATGAAGTACAGTGGAAGGTTGTTGAGGAGATAAATGGAACAAACTATTGTTTACATAGACCCACACACACTTCTTTATGTACACAAAG
KIT	NM_000222	1221	c.1669T>G	p.W557G	-	4:55593603-55593603	CHP2_KIT_4	CCACAGAAACCCATGTATGAAGTACAGTGGAAGGTTGTTGAGGAGATAAATGGAACAAACTATTGTTTACATAGACCCACACACACTTCTTTATGTACACAAAG
KIT	NM_000222	1223	c.1669_1680del12	p.W557_V560del	+	4:55593603-55593654	CHP2_KIT_4	CCACAGAAACCCATGTATGAAGTACAGTGGAAGGTTGTTGAGGAGATAAATGGAACAAACTATTGTTTACATAGACCCACACACACTTCTTTATGTACACAAAG
KIT	NM_000222	1226	c.1670_1675delGGAAGG	p.W557_V559>F	-	4:55593604-55593609	CHP2_KIT_4	CCACAGAAACCCATGTATGAAGTACAGTGGAAGGTTGTTGAGGAGATAAATGGAACAAACTATTGTTTACATAGACCCACACACACTTCTTTATGTACACAAAG
KIT	NM_000222	1227	c.1671_1676delG	p.W557C	-	4:55593605-55593605	CHP2_KIT_4	CCACAGAAACCCATGTATGAAGTACAGTGGAAGGTTGTTGAGGAGATAAATGGAACAAACTATTGTTTACATAGACCCACACACACTTCTTTATGTACACAAAG
TP53	NM_000546	12296	c.292C>T	p.P98S	-	17:7579305-7579395	CHP2_TP53_2	GCCCAGACGGAAACCGTGCCTGGCCTGGTAGTTTTCTGGGAAGGGACAGAAGATGACAGGGGCCAGGAGGGGGCTGGTGCAGGGGCCGCCGGTGTAGGGCTGCAGGGGCCACGGGGGCAGCAGCCTC
KIT	NM_000222	1229	c.1670_1717del48	p.W557_R571>S	-	4:55593604-55593651	CHP2_KIT_4	CCACAGAAACCCATGTATGAAGTACAGTGGAAGGTTGTTGAGGAGATAAATGGAACAAACTATTGTTTACATAGACCCACACACACTTCTTTATGTACACAAAG
KIT	NM_000222	1232	c.1671_1676delG	p.W557_V560>C	-	4:55593605-55593613	CHP2_KIT_4	CCACAGAAACCCATGTATGAAGTACAGTGGAAGGTTGTTGAGGAGATAAATGGAACAAACTATTGTTTACATAGACCCACACACACTTCTTTATGTACACAAAG
GNAS ENST00000371100	ENST00000371100	123397	c.2539C>T	p.R846C	-	20:57484420-57484420	CHP2_GNAS_1	TGGTTTCAGGACCTGCTTGCTGCCGTGTCCTGCTGACTTCTGGAACTCTTTGGAACCAGTTCCAGGTGGGACCAAGTCCACCTTCCAGTAAGCCAACTGTTCACCTTTTAAT
KIT	NM_000222	1233	c.1671_1676delGAGGGT	p.W557_V559>C	-	4:55593604-55593612	CHP2_KIT_4	CCACAGAAACCCATGTATGAAGTACAGTGGAAGGTTGTTGAGGAGATAAATGGAACAAACTATTGTTTACATAGACCCACACACACTTCTTTATGTACACAAAG
KIT	NM_000222	1234	c.1672_1680del9	pK558_V560del	-	4:55593606-55593614	CHP2_KIT_4	CCACAGAAACCCATGTATGAAGTACAGTGGAAGGTTGTTGAGGAGATAAATGGAACAAACTATTGTTTACATAGACCCACACACACTTCTTTATGTACACAAAG
KIT	NM_000222	1235	c.1672_1675GATGAAGGTT	pK558_V559>FD	-	4:55593606-55593617	CHP2_KIT_4	CCACAGAAACCCATGTATGAAGTACAGTGGAAGGTTGTTGAGGAGATAAATGGAACAAACTATTGTTTACATAGACCCACACACACTTCTTTATGTACACAAAG
HRAS ENST00000397594	ENST00000397594	123649	c.181C>A	p.Q61K	-	11:533875-533875	CHP2_HRAS_2	CACACACGCAGGACCTCCCCCGGTGGCGCATGTACTGGCCTGCTGCTGCTCTGCGGCCGGCGGTACTGCAGCATTCTCGCAGGCTGTCCAGGATGTCCACGGTCATCATGGCAGCCTTGG
EGFR	NM_005228	12366	c.2573T>A	p.L858M	-	7:5529553-5529553	CHP2_EGFR_8	TTTGGGCTGGCCAAACTGCTGGGTGCGGAAGAGAAGAATACCATGCAGAAGGAGGCAAGTAAGGAGGTGGCTTTAGTTCAGCCAGCATTTTCCTGACACCAGGGACCAGGCTGCCTTTC
EGFR	NM_005228	12367	c.2237_2256del18	p.E746_S752>A	-	7:5524268-5524268	CHP2_EGFR_5	TAGGGACTCTGGATCCCAGAAGGTGAGAAGTTAAATTCCCGTCGCTATCAAGGAATTAAGAGAAGCAACATCTCTGGCCAAGCCAACAAGGAAATCCTCGATGTGATGTTCTTTGCTTGTGTGCAG
EGFR	NM_005228	12369	c.2240_2256del15	p.L747_T751del	-	7:5524270-5524268	CHP2_EGFR_5	TAGGGACTCTGGATCCCAGAAGGTGAGAAGTTAAATTCCCGTCGCTATCAAGGAATTAAGAGAAGCAACATCTCTGGCCAAGCCAACAAGGAAATCCTCGATGTGATGTTCTTTGCTTGTGTGCAG
EGFR	NM_005228	12370	c.2240_2257del18	p.L747_P753>S	-	7:5524270-5524247	CHP2_EGFR_5	TAGGGACTCTGGATCCCAGAAGGTGAGAAGTTAAATTCCCGTCGCTATCAAGGAATTAAGAGAAGCAACATCTCTGGCCAAGCCAACAAGGAAATCCTCGATGTGATGTTCTTTGCTTGTGTGCAG
EGFR	NM_005228	12371	c.2126A>T	p.E709V	-	7:5524178-5524178	CHP2_EGFR_4	GTGGGAGAAGCTTCCCAACCAAGCTCTCTTGGGATCTTGAAGGAAACTGAATTAAAAAGATACAAAGTGCTGGGCTCCGGTGCGTTCGGCACGGT
EGFR	NM_005228	12372	c.2159C>T	p.S720F	-	7:5524145-5524171	CHP2_EGFR_4	CTCCTCCTCCTCCTCCTCCGCCGCCG

NOTCH1	NM_017617.2	13070		c.7389dupC		p.P2463fs*15	-	9:139398805-139398805	CHIP2_NOTCH1_3
NOTCH1	NM_017617.2	13081		c.7403C>A		p.S2468*	-	9:139398791-139398791	CHIP2_NOTCH1_3
KIT	NM_000222	1310		c.2404G>T		p.D801Y	-	4:55599220-55599220	CHIP2_KIT_8
APC	NM_000038	13113		c.3927_3931delAAAGA		p.E1309fs*4	+	5:112175218-112175222	CHIP2_APC_3
SMAD4	NM_005359.3	13115		c.415C>G		p.S14*	-	18:48576671-48576671	CHIP2_SMAD4_2
RB1	NM_000321	13117		c.2853C>T		p.Q951*	-	13:49033916-49033916	CHIP2_RB1_8
TP53	NM_000546	13119		c.322_324delGGT		p.G108del	-	17:7579360-7579363	CHIP2_TP53_2
KIT	NM_000222	1311		c.2446G>A		p.D816H	-	4:55599320-55599320	CHIP2_KIT_8
TP53	NM_000546	13120		c.626_627delGA		p.R209fs*6	-	17:7578222-7578223	CHIP2_TP53_5
APC	NM_000038	13121		c.4899C>T		p.Q1567*	+	5:112178661-112178690	CHIP2_APC_4
APC	NM_000038	13123		c.4729G>T		p.E1577*	+	5:112176028-112178020	CHIP2_APC_4
APC	NM_000038	13125		c.3348C>T		p.R1114*	+	5:112156031-112158031	CHIP2_APC_2
APC	NM_000038	13127		c.4348C>T		p.R1450*	+	5:112175639-112178639	CHIP2_APC_3
KIT	NM_000222	1312		c.2446_2447GA>TT		p.D816F	-	4:55599320-55599321	CHIP2_KIT_8
PTEN	NM_000314.4	13135		c.521T>C		p.L188R	-	10:89692539-89692539	CHIP2_PTEN_3
SMAD	NM_005631.3	13145		c.950C>T		p.R199W	+	7:128845101-128845101	CHIP2_SMD_1
SMAD	NM_005631.3	13146		c.1604G>T		p.W535L	+	7:128850341-128850341	CHIP2_SMD_4
TP53, *ENST00000620305*	ENST00000620305	13147*a*		c.747G>C		p.R249S	-	17:7575534-7575534	CHIP2_TP53_4
TP53, *ENST00000413465*	ENST00000413465	13147*b*		c.747G>C		p.R249S	-	17:7575534-7575534	CHIP2_TP53_4
SMAD	NM_005631.3	13147		c.970G>A		p.A324T	+	7:128846048-128846048	CHIP2_SMD_2
TP53, *ENST00000620305*	ENST00000620305	13148		c.466G>T		p.V156F	-	17:7578406-7578406	CHIP2_TP53_4
TP53, *ENST00000413465*	ENST00000413465	13148*1*		c.466G>T		p.V156F	-	17:7578406-7578406	CHIP2_TP53_4
TP53, *ENST00000045858*	ENST00000045858	13148*2*		c.190G>T		p.V64F	-	17:7578461-7578461	CHIP2_TP53_4
TP53, *ENST00000413115*	ENST00000413115	13148*3*		c.73G>T		p.V25F	-	17:7578461-7578461	CHIP2_TP53_4
SMAD	NM_005631.3	13148		c.1210G>A		p.V404M	+	7:128846074-128846074	CHIP2_SMD_3
KIT	NM_000222	1314		c.2447A>T		p.D816V	-	4:55599321-55599321	CHIP2_KIT_8
SMAD	NM_005631.3	13150		c.1918A>G		p.T640A	+	7:128851893-128851893	CHIP2_SMD_5
TP53, *ENST00000620305*	ENST00000620305	13151*a*		c.559+1G>A		p.?	-	17:7578370-7578370	CHIP2_TP53_4
TP53, *ENST00000413465*	ENST00000413465	13151*b*		c.559+1G>A		p.?	-	17:7578370-7578370	CHIP2_TP53_4
TP53, *ENST00000045858*	ENST00000045858	13151*c*		c.280+1G>A		p.?	-	17:7578370-7578370	CHIP2_TP53_4
TP53, *ENST00000413115*	ENST00000413115	13151*d*		c.163+1G>A		p.?	-	17:7578370-7578370	CHIP2_TP53_4
ABL1	X16416	13154		c.1159T>A		p.L387M	+	9:133768328-133768328	CHIP2_ABL1_4
KIT	NM_000222	1315		c.2451A>G		p.K818R	-	4:55599327-55599327	CHIP2_KIT_8
CTNNB1	NM_001904	13168		c.1049T>C		p.I35T	-	3:41266107-41266107	CHIP2_CTNNB1_1
KIT	NM_000222	1316		c.2489A>G		p.D830G	-	4:55599364-55599364	CHIP2_KIT_8
ERBB2	NM_004448	13170		c.2389G>C		p.D796H	-	17:37880261-37880261	CHIP2_ERBB2_1
CTNNB1	NM_001904	13175		c.1138G>A		p.E46K	-	3:41266141-41266141	CHIP2_CTNNB1_1
KIT	NM_000222	1317		c.2485A>T		p.D829V	-	4:55599353-55599353	CHIP2_KIT_8
EGFR	NM_005228	13180		c.2388C>T		p.L738F	+	7:55242018-55242018	CHIP2_EGFR_5
EGFR	NM_005228	13181		c.2384G>A		p.P735L	+	7:55242024-55242024	CHIP2_EGFR_5
EGFR	NM_005228	13182		c.2203G>A		p.G735S	+	7:55242403-55242403	CHIP2_EGFR_5
EGFR	NM_005228	13183		c.2225T>C		p.V742A	+	7:55242381-55242381	CHIP2_EGFR_5
EGFR	NM_005228	13184		c.2236G>A		p.E746K	+	7:55242466-55242466	CHIP2_EGFR_5
EGFR	NM_005228	13185		c.2252C>T		p.T751I	+	7:55242465-55242465	CHIP2_EGFR_5
EGFR	NM_005228	13186		c.2255C>A		p.S752Y	+	7:55242485-55242485	CHIP2_EGFR_5
EGFR	NM_005228	13188		c.2281G>A		p.D761N	+	7:55242511-55242511	CHIP2_EGFR_5
EGFR	NM_005228	13189		c.2351C>T		p.S784F	+	7:55246053-55246053	CHIP2_EGFR_6
EGFR	NM_005228	13190		c.2375T>C		p.L792P	+	7:55246077-55246077	CHIP2_EGFR_6
EGFR	NM_005228	13192		c.2429G>A		p.G810S	+	7:55249154-55249154	CHIP2_EGFR_7
EGFR	NM_005228	13197		c.2599G>A		p.A867T	+	7:55259532-55259532	CHIP2_EGFR_8
EGFR	NM_005228	13198		c.2603G>A		p.G868D	+	7:55259538-55259538	CHIP2_EGFR_8
KIT	NM_000222	1321		c.2461T>A		p.N821K	-	4:55599340-55599340	CHIP2_KIT_8
CTNNA2	NM_004077	13201		c.383C>G		p.V128*	-	9:2197097-2197097	CHIP2_CDKN2A_2
CTNNA2	NM_004077	13202		c.151-2A>T		p.?	-	9:2197288-2197288	CHIP2_CDKN2A_2
CTNNA2	NM_004077	13203		c.151-1G>A		p.?	-	9:2197288-2197288	CHIP2_CDKN2A_2
CTNNA2	NM_004077	13204		c.242C>T		p.P81L	-	9:2197116-2197116	CHIP2_CDKN2A_2
CTNNA2	NM_004077	13207		c.343G>T		p.V115L	-	9:2197015-2197015	CHIP2_CDKN2A_2
KIT	NM_000222	1322		c.2464T>G		p.S822K	-	4:55599346-55599346	CHIP2_KIT_8
KIT	NM_000222	1323		c.2474T>C		p.V825A	-	4:55599348-55599348	CHIP2_KIT_8
CTNNA2	NM_004077	13250		c.2515G>A		p.E839K	-	4:5560204-5560204	CHIP2_KIT_9
CTNNA2	NM_004077	13252		c.170C>T		p.A57V	-	9:2197184-2197184	CHIP2_CDKN2A_1
CTNNA2	NM_004077	13254		c.313delG		p.D105fs*41	-	9:2197165-2197165	CHIP2_CDKN2A_2
KIT	NM_000222	1326		c.1589_1594insGACCTAT		c.530dupATG	-	4:55593635-55593186	CHIP2_KIT_2
CTNNA2	NM_004077	13274		c.251A>G		p.D84G	-	9:2197187-2197187	CHIP2_CDKN2A_2
CTNNA2	NM_004077	13276		c.115T>C		p.Y51A	-	9:2197286-2197286	CHIP2_CDKN2A_2
KIT	NM_000222	1327		c.1654_1668delI15		p.M552_G556del	-	4:55593588-55593682	CHIP2_KIT_4
CTNNA2	NM_004077	13280		c.206G>T		p.G69V	-	9:2197151-2197151	CHIP2_CDKN2A_2
CTNNA2	NM_004077	13281		c.205G>T		p.E69*	-	9:2197153-2197153	CHIP2_CDKN2A_2
CTNNA2	NM_004077	13289		c.231_232delTC		p.L78fs*41	-	9:2197126-2197127	CHIP2_CDKN2A_2
KIT	NM_000222	1328		c.1655_1676delI6		p.M552_W559del	-	4:55593589-55593682	CHIP2_KIT_4
CTNNA2	NM_004077	13294		c.376G>T		p.V126F	-	9:2197062-2197062	CHIP2_CDKN2A_2
CTNNA2	NM_004077	13295		c.251A>T		p.D84V	-	9:2197187-2197187	CHIP2_CDKN2A_2
CTNNA2	NM_004077	13296		c.358G>A		p.E120K	-	9:2197100-2197100	CHIP2_CDKN2A_2
CTNNA2	NM_004077	13297		c.249_250insTT		p.D84fs*63	-	9:2197188-2197189	CHIP2_CDKN2A_2
CTNNA2	NM_004077	13298		c.394G>C		p.A132P	-	9:2197064-2197064	CHIP2_CDKN2A_2
CTNNA2	NM_004077	13299		c.250G>T		p.D84Y	-	9:2197188-2197188	CHIP2_CDKN2A_2
KIT	NM_000222	1329		c.1660_1676delI15		p.E554_K560del	-	4:55593585-55593680	CHIP2_KIT_4
CTNNA2	NM_004077	13300		c.335G>T		p.R112*	-	9:2197083-2197083	CHIP2_CDKN2A_2
KIT	NM_000222	1330		c.1667_1681delI15		p.W557_E561del	-	4:55593646-55593682	CHIP2_KIT_4
FBXW7	NM_033632.1	13315		c.1393_1394GC>TA		p.R465Y	-	4:153409844-153409885	CHIP2_FBXW7_3
KIT	NM_000222	13167		c.2447A>T		p.A816S	-	4:55599321-55599321	CHIP2_KIT_8
EGFR	NM_005228	13189		c.2236_2256delI21		p.E746_S752del	-	7:55242466-55242486	CHIP2_EGFR_5
EGFR	NM_005228	13197		c.2239_2257>T		p.L747_P753>S	-	7:55242468-55242487	CHIP2_EGFR_5
EGFR	NM_005228	13207		c.2252_2276delI24		p.T751_P758del	-	7:55242465-55242485	CHIP2_EGFR_5
KIT	NM_000222	1332		c.1669_1683delI15		p.W557_E561del	-	4:55593603-55593682	CHIP2_KIT_4
KIT	NM_000222	1333		c.1679_1684TT>AC		p.V560T	-	4:55593633-55593682	CHIP2_KIT_4
KIT	NM_000222	1334		c.1702_1722delI21		p.V568_I574del	-	4:55593636-55593686	CHIP2_KIT_4
IDH2	NM_002168.2	13367		c.514G>C		p.R172S	-	2:96631437-96631437	CHIP2_IDH2_1
PTEN	NM_000314.4	13713		c.710_780delA		p.K268fs*6	-	10:89717755-89717755	CHIP2_PTEN_6
KIT	NM_000222	13754		c.1711_1726delI18		p.I571_L576del	-	4:55593645-55593682	CHIP2_KIT_4
CTNNA2	NM_004077	13763		c.1687T>A		p.Y563N	-	4:55593665-55593690	CHIP2_KIT_4
KIT	NM_000222	13764		c.1663G>A		p.V555I	-	4:55593597-55593597	CHIP2_KIT_4
KIT	NM_000222	13767		c.2598G>A		p.W835*	-	4:55602737-55602737	CHIP2_KIT_9
EGFR	NM_005228	13400		c.2457G>A		p.V819V	-	7:55249159-55249159	CHIP2_EGFR_7
TP53	NM_000546	13421		c.814delC		p.Y272fs*73	-	17:7577126-7577134	CHIP2_TP53_7
EGFR	NM_005228	13427		c.2126A>C		p.E709A	-	7:55241675-55241675	CHIP2_EGFR_4
EGFR	NM_005228	13432		c.2315G>T		p.W771*	-	7:55242435-55242435	CHIP2_EGFR_5
EGFR	NM_005228	13433		c.2318A>G		p.H773R	-	7:55242438-55242438	CHIP2_EGFR_5
CTNNA2	NM_004077	13436		c.155T>A		p.M52K	-	9:2197285-2197285	CHIP2_CDKN2A_2
CTNNA2	NM_004077	13440		c.283C>T		p.A48V	-	9:2197155-2197155	CHIP2_CDKN2A_2
PTEN	NM_000314.4	13452		c.863delA		p.I288fs*5	-	10:89720712-89720712	CHIP2_PTEN_7
CTNNA2	NM_004077	13465		c.349T>A		p.H132Q	-	9:2197066-2197066	CHIP2_CDKN2A_2
CTNNA2	NM_004077	13474		c.229G>A		p.D74N	-	9:2197138-2197138	CHIP2_CDKN2A_2
CTNNA2	NM_004077	13486		c.116G>T		p.S41*	-	9:2197177-2197177	CHIP2_CDKN2A_2
CTNNA2	NM_004077	13488		c.259G>A		p.D84N	-	9:2197188-2197188	CHIP2_CDKN2A_2
CTNNA2	NM_004077	13489		c.323G>T		p.G108V	-	9:2197016-2197016	CHIP2_CDKN2A_2
CTNNA2	NM_004077	13491		c.232_233delCT		p.L78fs*41	-	9:2197125-2197126	CHIP2_CDKN2A_2
CTNNA2	NM_004077	13493		c.174_189delI6		p.V59fs*82	-	9:2197169-2197184	CHIP2_CDKN2A_2
CTNNA2	NM_004077	13494		c.168_173delI4		p.M56fs*61	-	9:2197175-2197180	CHIP2_CDKN2A_2
CTNNA2	NM_004077	13496		c.153G>A		p.V51I	-	9:2197287-2197287	CHIP2_CDKN2A_2
CTNNA2	NM_004077	13504		c.118T>C		p.L63P	-	9:2197176-2197176	CHIP2_CDKN2A_2
CTNNA2	NM_004077	13505		c.316G>A		p.V106M	-	9:2197082-2197082	CHIP2_CDKN2A_2
CTNNA2	NM_004077	13520		c.223C>G		p.D108H	-	9:2197016-2197016	CHIP2_CDKN2A_2
CTNNA2	NM_004077	13524		c.227_230dCG>TT		p.R80*	-	9:2197126-2197127	CHIP2_CDKN2A_2
CTNNA2	NM_004077	13531		c.151-1G>A		p.?	-	9:2197288-2197288	CHIP2_CDKN2A_2
CTNNA2	NM_004077	13534		c.373C>A		p.Q125N	-	9:2197065-2197065	CHIP2_CDKN2A_2
CTNNA2	NM_004077	13540		c.355G>C		p.E119Q	-	9:2197083-2197083	CHIP2_CDKN2A_2
CTNNA2	NM_004077	13546		c.221C>T		p.D74V	-	9:2197137-2197137	CHIP2_CDKN2A_2
CTNNA2	NM_004077	13548		c.364G>A		p.G122S	-	9:2197094-2197094	CHIP2_CDKN2A_2
KIT	NM_005228	13553		c.2572_2573CA>TC		p.L858R	-	7:55259515-55259516	CHIP2_EGFR_8
EGFR	NM_005228	13556		c.2253_2276delI24		p.S752_T758del	-	7:55242463-55242486	CHIP2_EGFR_5
CTNNA2	NM_004077	13567		c.218C>A		p.C72*	-	9:2197142-2197142	CHIP2_CDKN2A_2
CTNNA2	NM_004077	13568		c.225delC		p.A76fs*70	-	9:2197132-2197132	CHIP2_CDKN2A_2
PIK3CA	NM_006218.1	13570		c.331A>C		p.K111E	-	3:178910644-178910644	PIK3CA_2
PIK3CA	NM_006218.3	13594		c.3046G>A		p.E1012Q	-	3:178952611-178952611	PIK3CA_10
CTNNA2	NM_004077	13604		c.202G>A		p.A68T	-	9:2197156-2197156	CHIP2_CDKN2A_2
CTNNA2	NM_004077	13607		c.314delC		p.L104fs*42	-	9:2197084-2197084	CHIP2_CDKN2A_2
CTNNA2	NM_004077	13608		c.371G>A		p.R124H	-	9:2197067-2197067	CHIP2_CDKN2A_2
CTNNA2	NM_004077	13613		c.259G>C		p.D84H	-	9:2197188-2197188	CHIP2_CDKN2A_2
CTNNA2	NM_004077	13619		c.363delG		p.G122fs*24	-	9:2197095-2197095	CHIP2_CDKN2A_2
CTNNA2	NM_004077	13633		c.386A>G		p.Y129C	-	9:2197072-2197072	CHIP2_CDKN2A_2
CTNNA2	NM_004077	13642		c.228_229insT		p.T77fs*43	-	9:2197139-2197139	CHIP2_CDKN2A_2
CTNNA2	NM_004077	13645		c.366C>A		p.G122G	-	9:2197092-2197092	CHIP2_CDKN2A_2
CTNNA2	NM_004077	13675		c.380C>T		p.A102V	-	9:2197069-2197069	CHIP2_CDKN2A_2
SRC	NM_005417	1369		c.1591C>T		p.Q531*	+	20:36631762-36631762	CHIP2_SRC_1
TP53, *ENST00000620305*	ENST00000620305	13687		c.853G>A		p.E285K	-	17:7577085-7577085	CHIP2_TP53_7
CTNNA2	NM_004077	13713		c.340C>T		p.P114S	-	9:2197084-2197084	CHIP2_CDKN2A_2
KIT	NM_000222	13717		c.2806A>T		p.I936V	-	5:112175218-112175222	CHIP2_APC_3
APC	NM_000038	13727		c.3922A>T		p.K1308*	+	5:112175218-112175222	CHIP2_APC_3
APC	NM_000038	13728		c.3907C>T		p.Q1303*	+	5:112175198-112175198	CHIP2_APC_3
CTNNA2	NM_004077	13754		c.157_174delI18		p.M53_R58del	-	9:2197166-2197183	CHIP2_CDKN2A_2
CTNNA2	NM_004077	13766		c.227C>T		p.A76V	-	9:2197131-2197131	CHIP2_CDKN2A_2
CTNNA2	NM_004077	13779		c.168_161insA		p.M54fs*56	-	9:2197175-2197179	CHIP2_CDKN2A_2
CTNNA2	NM_004077	13782		c.187C>G		p.L63V	-	9:2197171-2197171	CHIP2_CDKN2A_2
CTNNA2	NM_004077	13803		c.230_233delCT		p.L78fs*41	-	9:2197127-2197128	CHIP2_CDKN2A_2
CTNNA2	NM_004077	13807		c.346G>T		p.D116Y	-	9:2197083-2197083	CHIP2_CDKN2A_2
CTNNA2	NM_004077	13815		c.209C>T		p.T70L	-	9:2197149-2197149	CHIP2_CDKN2A_2
CTNNA2	NM_004077	13827		c.373C>T		p.V126V	-	9:2197066-2197066	CHIP2_CDKN2A_2
CTNNA2	NM_004077	13830		c.341C>A		p.P114H	-	9:2197083-2197083	CHIP2_CDKN2A_2
APC	NM_000038	13864		c.4393_4394delAG		p.S1465fs*3	+	5:112178444-112178444	CHIP2_APC_3
APC	NM_000038	13872		c.3286C>T		p.Q1096*	+	5:112174577-112174577	CHIP2_APC_2
APC	NM_000038	13879		c.4619G>T		p.E1547*	+	5:112178930-112178930	CHIP2_APC_3
TP53, *ENST00000620305*	ENST00000620305	13894		c.832C>T		p.P278S	-	17:7577106-7577106	CHIP2_TP53_7
CTNNA2	NM_004077	13965		c.156G>C		p.M52I	-	9:2197182-2197182	CHIP2_CDKN2A_2
CTNNA2	NM_004077	13972		c.194T>C		p.L65P	-	9:2197164-2197164	CHIP2_CDKN2A_2
EZH2, *ENST00000320595*	ENST00000320595	13994		c.1884T>A		p.Y982N	-	7:148508728-148508728	CHIP2_EZH2_1
EGFR	NM_005228	13979		c.2573T>G		p.L858R	-	7:55259516-55259516	CHIP2_EGFR_8
PTEN	NM_000314.4	13981		c.752G>A		p.G251D	-	10:89717727-89717727	CHIP2_PTEN_6
PTPN11	NM_002834.3	13993		c.1521G>A		p.T52S	+	12:112881139-112881139	CHIP2_PTPN11_1
CTNNA2	NM_004077	14057		c.731C>T		p.G245*	-	9:2197269-2197269	CHIP2_CDKN2A_2
ERBB2	NM_004448	14060		c.2264T>C		p.L755S	-	17:37880220-37880220	CHIP2_ERBB2_1
ERBB2	NM_004448	14062		c.2329G>T		p.V777L	-	17:37880486-37880486	CHIP2_ERBB2_2
ERBB2	NM_004448	14064		c.2329G>A		p.V777M	-	17:37880486-37881000	CHIP2_ERBB2_2
ERBB2	NM_004448	14065		c.2524G>A		p.V842I	-	17:37881152-37881152	CHIP2_ERBB2_3
EGFR	NM_005228	14068		c.2389G>A		p.D797N	-	7:55249010-55249010	CHIP2_EGFR_6
EGFR	NM_005228	14070		c.2588G>C		p.G863D	-	7:55259530-55259530	CHIP2_EGFR_8
PTEN	NM_000314.4	14087		c.165_259delI5		p.L56_Q86del	-	10:89685276-89687264	CHIP2_PTEN_4
SMAD4	NM_005359.3	14096		c.1333C>T		p.R445*	+	18:48603032-48603032	CHIP2_SMAD4_8
SMAD4	NM_005359.3	14105		c.1394_1395delAC		p.A466fs*28	+	18:48603091-48603092	CHIP2_SMAD4_8
SMAD4	NM_005359.3	14110		c.989A>C		p.E330A	+	18:48591828-48591828	CHIP2_SMAD4_6
SMAD4	NM_005359.3	14111		c.1028C>G		p.S343*	+	18:48591865-48591865	CHIP2_SMAD4_6
SMAD4	NM_005359.3	14113		c.1496G>A		p.R497H	+	18:48604668-48604668	CHIP2_SMAD4_9
SMAD4	NM_005359.3	14115		c.1590C>T		p.G530=	+	18:48604774-48604774	CHIP2_SMAD4_9
SMAD4	NM_005359.3	14118		c.502G>T		p.G168*	+	18:48581198-48581198	CHIP2_SMAD4_3
SMAD4	NM_005359.3	14121		c.1035_1036delTT		p.F339_S345del	+	18:48591852-48591866	CHIP2_SMAD4_6
SMAD4	NM_005359.3	14122		c.1082G>A		p.R361H	+	18:48591919-48591919	CHIP2_SMAD4_6
SMAD4	NM_005359.3	14124		c.1340_1365delI25		p.Q448fs*20	+	18:48603940-48603940	CHIP2_SMAD4_8
SMAD4	NM_005359.3	14126		c.1519A>C		p.K507Q	+	18:48604607-48604607	CHIP2_SMAD4_9
SMAD4	NM_005359.3	14129		c.1543A>T		p.R515*	+	18:48604721-48604721	CHIP2_SMAD4_9
SMAD4	NM_005359.3	14134		c.1576G>T		p.E526*	+	18:48604754-48604754	CHIP2_SMAD4_9
SMAD4	NM_005359.3	14135		c.1051G>C		p.D351H	+	18:48591888-48591888	CHIP2_SMAD4_6
SMAD4	NM_005359.3	14140		c.1081C>T		p.R361C	+	18:48591918-48591918	CHIP2_SMAD4_6
SMAD4	NM_005359.3	14163		c.931C>T		p.Q311*	+	18:48586202-48586202	CHIP2_SMAD4_5
SMAD4	NM_005359.3	14167		c.955+5G>C		p.?	-	18:48586291-48586291	CHIP2_SMAD4_5
SMAD4	NM_005359.3	14174		c.1253G>T		p.G418V	-	18:48589409-48589409	CHIP2_SMAD4_7
SMAD4	NM_005359.3	14175		c.1256C>G		p.T419*	-	18:48589485-48589485	CHIP2_SMAD4_7
SMAD4	NM_005359.3	14177		c.1546_1555delCAGCACAT		p.S517fs*7	-	18:48604726-48604735	CHIP2_SMAD4_9
KRAS	NM_004985	14200		c.35_36GT>AC		p.G12D	-	12:25398281-25398284	CHIP2_KRAS_1
SMAD4	NM_005359.3	14215		c.313C>T		p.A105V	-	18:48575139-48575139	CHIP2_SMAD4_1
SMAD4	NM_005359.3	14216		c.363_364insA		p.C122fs*2	-	18:48575160-48575161	CHIP2_SMAD4_1
SMAD4	NM_005359.3	14217		c.776_777delAT		p.T258fs*4	-	18:48584601-48584604	CHIP2_SMAD4_4
SMAD4	NM_005359.3	14218		c.1018G>T		p.V339C	-	18:48591905-48591905	CHIP2_SMAD4_6
SMAD4	NM_005359.3	14221		c.1496G>A		p.C499Y	-	18:48604674-48604674	CHIP2_SMAD4_9
SMAD4	NM_005359.3	14229		c.1229_1238insCA		p.Q410fs*9	-	18:48591478-48591479	CHIP2_SMAD4_6
SMAD4	NM_005359.3	14232		c.1064A>G		p.D355G	-	18:48591901-48591901	CHIP2_SMAD4_6
SMAD4	NM_005359.3	14240		c.2234A>T		p.K745I	-	18:48603944-48603944	CHIP2_SMAD4_8
SMAD4	NM_005359.3	14249		c.1156G>C		p.G386R	-	18:48593485-48593485	CHIP2_SMAD4_7
CTNNA2	NM_004077	14253		c.197A>C		p.H66P	-	9:2197161-2197161	CHIP2_CDKN2A_2
CTNNA2	NM_004077	14254		c.151-4G>C		p.?	-	9:2197281-2197281	CHIP2_CDKN2A_2
CTNNB1	NM_001904	14256		c.73_96delD4		p.WQQQSYLDS27	-	3:41266076-41266089	CHIP2_CTNNB1_1
PTPN11	NM_002834.3	14269		c.182A>G		p.D61G	-	12:112881640-112881640	CHIP2_PTPN11_2
PTPN11	NM_002834.3	14271		c.1580G>T		p.G503V	+	12:112926888-112926888	CHIP2_PTPN11_2
TSC1	NM_000368.4	14278		c.4856delA		p.L1619fs*24	-	9:135812-135812	CHIP2_VHL_2
MPL	NM_005373.1	142839		c.1544G>C		p.W515S	-	1:43815089-43815089	CHIP2_MPL_1
VHL	NM_000551.2	14284		c.429C>G		p.D143E	-	3:10188286-10188286	CHIP2_VHL_1
VHL	NM_000551.2	14302		c.394delA		p.N131fs*28	-	3:10188248-10188248	CHIP2_VHL_1
VHL	NM_000551.2	14305		c.266T>A		p.L89H	-	3:10187797-10187797	CHIP2_VHL_1
VHL	NM_000551.2	14307		c.496G>A		p.V166I	-	3:10191485-10191485	CHIP2_VHL_1
VHL	NM_000551.2	14309		c.478G>A		p.E160K	-	3:10191485-10191485	CHIP2_VHL_1
VHL	NM_000551.2	14310		c.349T>C		p.W117R	-	3:10188286-10188286	CHIP2_VHL_1
VHL	NM_000551.2	14311		c.499C>T		p.R167W	-	3:10191586-10191586	CHIP2_VHL_1
VHL	NM_000551.2	14312		c.353T>C		p.L118P	-	3:10188210-10188210	CHIP2_VHL_1
VHL	NM_000551.2	14328		c.294C>G		p.Y98*	-	3:10188209-10188209	CHIP2_VHL_1
VHL	NM_000551.2	14328		c.351G>T		p.W117C	-	3:10188209-10188209	CHIP2_VHL_1
VHL	NM_000551.2	14346		c.266T>C		p.L89P	-	3:10187797-10187797	CHIP2_VHL_1
VHL	NM_000551.2	14348		c.301C>T		p.L101L	-	3:10188302-10188302	CHIP2_VHL_1
VHL	NM_000551.2	14349		c.294_294delCTATGG		p.Y97_W98delI	-	3:10188209-10188214	CHIP2_VHL_1
VHL	NM_000551.2	14355		c.488T>C		p.L163P	-	3:10191485-10191485	CHIP2_VHL_1
VHL	NM_000551.2	14356		c.394C>T		p.Q132*	-	3:10188251-10188251	CHIP2_VHL_1
VHL	NM_000551.2	14362		c.281T>G		p.L128R	-	3:10188238-10188238	CHIP2_VHL_1
VHL	NM_000551.2	14368		c.473T>A		p.L158Q	-	3:10191480-10191480	CHIP2_VHL_1
VHL	NM_000551.2	14373		c.490G>T		p.E164*	-	3:10191485-10191485	CHIP2_VHL_1
VHL	NM_000551.2	14374		c.514C>T		p.R171W	-	3:10191510-10191510	CHIP2_VHL_1
VHL	NM_000551.2	14376		c.464-1G>A		p.?	-	3:10191470-10191470	CHIP2_VHL_1
VHL	NM_000551.2	14382		c.245G>C		p.R82P	-	3:10187796-10187796	CHIP2_VHL_1
VHL	NM_000551.2	14383		c.413C>G		p.P138R	-	3:10188270-10188270	CHIP2_VHL_1
VHL	NM_000551.2	14386		c.309delT		p.G104fs*55	-	3:10188048-10188048	CHIP2_VHL_1
VHL	NM_000551.2	14387		c.477T>C		p.L159P	-	3:10191480-10191480	CHIP2_VHL_1
VHL	NM_000551.2	14390		c.269A>T		p.N90I	-	3:10188088-10188088	CHIP2_VHL_1
VHL	NM_000551.2	14391		c.404delA		p.T135fs*5	-	3:10188239-10188239	CHIP2_VHL_1
VHL	NM_000551.2	14392		c.377A>G		p.D126G	-	3:10188234-10188234	CHIP2_VHL_1
VHL	NM_000551.2	14393		c.314delG		p.G104fs*55	-	3:10188042-10188042	CHIP2_VHL_1
VHL	NM_000551.2	14397		c.498C>T		p.Q166*	-	3:10191487-10191487	CHIP2_VHL_1
VHL	NM_000551.2	14399		c.353G>A		p.W117*	-	3:10188208-10188208	CHIP2_VHL_1
VHL	NM_000551.2	14400

Y3L	NM_000551.2	144971	c.244C>G	p.R82G	+	3:10183775-10183775	CHP2_VHL_1	CGCAGCTGCGGCGGCGCCAGGCCTACCCACGCTGCGCGCTGGCGCTGCCCGCCGCCGCCGCCG
BRAF	NM_004333	144982	c.1797_1798insACA	p.T599_V600insT	-	7:140453137-140453138	CHP2_BRAF_2	TCAAACTGATGGGACCCACTCCATCGAGATTTCACTGTAGCTAGACCAAAATCACCTATTTTTACTGTGAGGTTCTATGAAGAAATATATCTGGGTGTAGTAAGTAAAGGAAAACAG
TP53	NM_000546	146240	c.806_808delGCT	p.S269_I270del	-	17:7577138-7577152	CHP2_TP53_7	TACCTGGCTAGTGCTCCCTGGAGGGCAGCTGCTGGTGGAGGCTCCCCTTCTTGGTGGGGATCTTCTGCTCTGATGGGTCAGCAGGCACAACACACGCACCTCAAAGCTGTTCCGTCCCCAGTAGATT
NPM1	NM_002520.4	158600	c.861_862insTGCA	p.W288fs*9	+	5:170837545-170837546	CHP2_NPM1_1	TAACCAATTTCTTTTTTTTTTTTTCCAGGCTATTCAAGATCTCTGAGCAGCTGTTGAAGAAATGTTTAAGAAAATTGTTTAAAAAATTTTCCGTCTTATTTCAT
FLT3	Z26652	158601	c.1782_1783insTTCAGATCACTTCTCAGTTGATTTC	p.F594_R595insSDNSTYYVDF	-	13:28608258-28608274	CHP2_FLT3_2	AATTTTCTCTTGAGAACTCCCATTTGAGATCATATTCATTTCTCTGAAATCACGTAGAAGTACTCATTATCTGAGGAGCCGGTCACCTGTACCTCTGTAGCTGGCTTTCATACCTAAA
FLT3	Z26652	158603	c.1797_1798insCCGGCTCCTCAGATAATGAGTACTTCTACGTT GATTTCAGGGAATATGAAATATCGCC	p.V599_D600insPAPQNMSTSTLSENNNIA	-	13:28608258-28608259	CHP2_FLT3_2	AATTTTCTCTTGAGAACTCCCATTTGAGATCATATTCATTTCTCTGAAATCACGTAGAAGTACTCATTATCTGAGGAGCCGGTCACCTGTACCTCTGTAGCTGGCTTTCATACCTAAA
NPM1	NM_002520.4	158604	c.859_860insTTCG	p.W288fs*9	+	5:170837543-170837544	CHP2_NPM1_1	TAACCAATTTCTTTTTTTTTTTTTCCAGGCTATTCAAGATCTCTGAGCAGCTGTTGAAGAAATGTTTAAGAAAATTTTCGTTTTAAAAAATTTTCCGTCTTATTTCAT
FLT3	Z26652	158605	c.1799_1800insATAGATAATGAATATGAATATGA	p.V599_D600insEYEYEEYY	-	13:28608256-28608257	CHP2_FLT3_2	AATTTTCTCTTGAGAACTCCCATTTGAGATCATATTCATTTCTCTGAAATCACGTAGAAGTACTCATTATCTGAGGAGCCGGTCACCTGTACCTCTGTAGCTGGCTTTCATACCTAAA
TP53 ENST00000414345	ENST00000414345	165072	c.781A>G	p.T261A*	+	17:7577500-7577500	CHP2_TP53_4	CCAGGTGTGATGTGTGAGGATGGGCCTCCGGTTCATGCCGCCCATGCAGGAACTGTTACACATGTAGTTGTATGGATGTGGTGGTACAGTCAGAGCCAACCTAG
TP53 ENST00000268305	ENST00000268305	165073	c.781A>G	p.T261A*	+	17:7577500-7577500	CHP2_TP53_4	CCAGGTGTGATGTGTGAGGATGGGCCTCCGGTTCATGCCGCCCATGCAGGAACTGTTACACATGTAGTTGTATGGATGTGGTGGTACAGTCAGAGCCAACCTAG
TP53 ENST00000455839	ENST00000455839	165074	c.422A>C	p.Y141C*	+	17:7577086-7577088	CHP2_TP53_5	CCAGTGTGTGATGTGTGAGGATGGGCCTCCGGTTCATGCCGCCCATGCAGGTCTGCACCTGTGTGCAGTGCAGGCCAGCCTGCAGGGGCAGCTACGCCACACCGCCGCCGCCGC

APC	NM_000038	19616	c.4463T>G	p.L1488*	+	5:112175754-112175754	CHP2_APC_6	GATGCTGATACTTTATCATTTGCCACGGAAAGTACTCCAGATGGATTTTCTTGTTCATCCAGCTGAGTCCTTGAGCCTCGATGAGCCATTTATACAGAAAGATGTGGAATTAAGAAT
APC	NM_000038	19617	c.4464delA	p.L1488fs*19	+	5:112175755-112175755	CHP2_APC_6	GATGCTGATACTTTATCATTTGCCACGGAAAGTACTCCAGATGGATTTTCTTGTTCATCCAGCCTGAGTGCTCTGAGCCTCGATGAGCCATTTATACAGAAAGATGTGGAATTAAGAAT
APC	NM_000038	19626	c.4469delG	p.G1490fs*13	+	5:112175771-112175771	CHP2_APC_6	GATGCTGATACTTTATCATTTGCCACGGAAAGTACTCCAGATGGATTTTCTTGTTCATCCAGCCTGAGTGCTCTGAGCCTCGATGAGCCATTTATACAGAAAGATGTGGAATTAAGAAT
APC	NM_000038	19629	c.4469delC	p.P1493s*10	+	5:112175780-112175780	CHP2_APC_6	GATGCTGATACTTTATCATTTGCCACGGAAAGTACTCCAGATGGATTTTCTTGTTCATCCAGCCTGAGTGCTCTGAGCCTCGATGAGCCATTTATACAGAAAGATGTGGAATTAAGAAT
APC	NM_000038	19652	c.4483T>A	p.S1155P	+	5:112175544-112175544	CHP2_APC_6	TATCTTCAGATACGCCAGGCACAAGCTGTTGATTTTTCTCAGGAGGCGAAATCTCCTCCAAGTGGTGCTGCAGACACCAAGCTCGACACTATGTTCAGGAGACCCCACTCATGTTT
APC	NM_000038	19664	c.3919delA	p.I1307fs*	+	5:112175210-112175210	CHP2_APC_3	GATGAAATAGGATGAATCAGACGACACAGGAAGCAGATTCTGCTAATACCTGCAAATAGCAGAAATAAAAGAAAAGATTGGAACTAGGTCAGCTGGAGATCCTGTGAGCGAAGTTCCAGCAGT
APC	NM_000038	19667	c.4465_4466insAC	p.L1489fs*19	+	5:112175756-112175757	CHP2_APC_6	GATGCTGATACTTTATCATTTGCCACGGAAAGTACTCCAGATGGATTTTCTTGTTCATCCAGCCTGAGTGCTCTGAGCCTCGATGAGCCATTTATACAGAAAGATGTGGAATTAAGAAT
APC	NM_000038	19674	c.4482_4484insA	p.S1495fs*9	+	5:112175774-112175775	CHP2_APC_6	GATGCTGATACTTTATCATTTGCCACGGAAAGTACTCCAGATGGATTTTCTTGTTCATCCAGCCTGAGTGCTCTGAGCCTCGATGAGCCATTTATACAGAAAGATGTGGAATTAAGAAT
FLT3	Z36652	19686	c.2598C>G	p.I836M	+	13:28592637-28592637	CHP2_FLT3_4	ATAAGTAGGAAATAAGCAGGCCTCACATTGCCCTCGGACAACATAGTTGGAACATCACTCATGGATATCTCGAGCCAATCCAAAGTCACA
APC	NM_000038	19688	c.4386_4387delGA	p.S1463fs*5	+	5:112175677-112175678	CHP2_APC_5	CCCCTGGACAAACACAATGTCCCACAGCAGCTGATGCAGCACTCCTCCTGCAGCTCTCCAAAGCTGCAAAAGGAGGAGGAGAGTGGACCTAAGCAAGCTGC
FLT3	Z36652	19692	c.2525A>G	p.Y842C	+	13:28592620-28592620	CHP2_FLT3_4	ATAAGTAGGAAATAAGCAGGCCTCACATTGCCCTGCACAACATAGTTGGAACATCACTATGATATCTCGAGCCAATCCAAAGTCACA
APC	NM_000038	19694	c.4386_4387delGA	p.E1463fs*	+	5:112175677-112175688	CHP2_APC_5	GCCCTGGACAAACACATGTCCCACAGCAGCTGATGCAGCACTCCTCCTGCAGCTCTCCAAAGCTGCAAAAGGAGGAGGAGAGTGGACCTAAGCAAGCTGC
APC	NM_000038	19695	c.4460_4461insA	p.T1556fs*	+	5:112175951-112175952	CHP2_APC_7	GAATCAAATAAAAACCAAGAGAAAGAGGGCAAAAAACATTATGATTCTGAAAAGGACCATTTATAGTGATTCAGATGATGTATTTGAAATATCTAGAAGAATGTATATTTCTG
APC	NM_000038	19696	c.4517delG	p.P1573fs*42	+	5:112175988-112175988	CHP2_APC_4	TATCTTCAGATACGCCAGGCACAAGCTGTTGATTTTTCTCAGGAGCGAAATCTCCTCCAAGGTGGTGCTGCAGACACCAAGCTCGACACTATGTTCAGGAGACCCCACTCATGTTT
APC	NM_000038	19701	c.4861_4862delTT	p.S1155fs*19	+	5:112175544-112175545	CHP2_APC_6	TATCTTCAGATACGCCAGGCACAAGCTGTTGATTTTCTCAGGAGGCGAAATCTCCTCCAAGTGGTGCTGCAGACACCAAGCTCGACACTATGTTCAGGAGACCCCACTCATGTTT
APC	NM_000038	19705	c.4381A>T	p.R1435*	+	5:112175594-112175594	CHP2_APC_5	GCCCTGGACAACACATGTCACCCACAGCAGAGTAAACACCTCCCACCCTCCAAACAGCTCCAAACCAAGGGAGAGTACCTAAAAATAAAGACCACTTGCTGAAAAGAGGAGGAGTGGACCTAAGCAAGCTGC
APC	NM_000038	19714	c.4470delA	p.E1491fs*13	+	5:112175907-112175907	CHP2_APC_6	GATGCTGATACTTTATCATTTGCCACGGAAAGTACTCCAGATGGATTTTCTTGTTCATCCAGCCTGAGTGCTCTGAGCCTCGATGAGCCATTTATACAGAAAGATGTGGAATTAAGAAT
APC	NM_000038	19718	c.4660_4661insG	p.E1554fs*5	+	5:112175961-112175962	CHP2_APC_7	GAATCAAATAAAAACCAAGAGAAAGAGGGCAAAAAACATTATGATTCTGAAAAGGACCATTTATAGTGATTCAGATGATGTATTTGAAATATCTAGAAGAATGTATATTTCTG
CDH1	NM_004360.2	19747	c.1387G>T	p.E31*	+	16:68846086-68846086	CHP2_CDH1_2	GATCTCCTCTGCAGAGTTTCCCTGCGTATCCCTGGTGGTTCAAGCTGCTGACCTTCAAGGTGAGGGGTTAAGCACAACAGCACGACTGTGATCACAGTCACTGACACCAACGATATCCTCGATC
CDH1	NM_004360.2	19748	c.1388G>C	p.D37H	+	16:68846137-68846137	CHP2_CDH1_2	GATCTCCTCTGCAGAGTTTCCCTGCGTATCCCTGGTGGTTCAAGCTGCTGACCTTCAAGGTGAGGGGTTAAGCACAACAGCACGACTGTGATCACAGTCACTGACACCAACGATATCCTCGATC
CDH1	NM_004360.2	19751	c.1394G>A	p.D40N	+	16:68847324-68847324	CHP2_CDH1_2	GATCTCCTCTGCAGAGTTTCCCTGCGTATCCCTGGTGGTTCAAGCTGCTGACCTTCAAGGTGAGGGGTTAAGCACAACAGCACGACTGTGATCACAGTCACTGACACCAACGATATCCTCGATC
CDH1	NM_004360.2	19753	c.1027dupC	p.L343fs*13	+	16:68846056-68846056	CHP2_CDH1_2	GATCTCCTCTGCAGAGTTTCCCTGCGTATCCCTGGTGGTTCAAGCTGCTGACCTTCAAGGTGAGGGGTTAAGCACAACAGCACGACTGTGATCACAGTCACTGACACCAACGATATCCTCGATC
CDH1	NM_004360.2	19754	c.1009-1G>A	p.?	+	16:68846037-68846037	CHP2_CDH1_2	GATCTCCTCTGCAGAGTTTCCCTGCGTATCCCTGGTGGTTCAAGCTGCTGACCTTCAAGGTGAGGGGTTAAGCACAACAGCACGACTGTGATCACAGTCACTGACACCAACGATATCCTCGATC
CDH1	NM_004360.2	19761	c.1396_1396delCCCA	p.I1396fs*17	+	16:68847224-68847227	CHP2_CDH1_2	TTCTTTTGCTCTGCAGTACAAGCTGGGCAAGGAGGTGGGAGGGGTGGTGGTGGTGGTGGTGCTGATCCTCAGTCCAGGCTCCTCAGTCCAGCCTCCAGCTCCAGCTCCAG

GNAS	NM_000516.3	27888	c.680A>T	p.Q227L	+	20:57484936-57484986	CHP2_GNAS_2	TCCTCCCCCACCAGCATGTTTGACGTGGGTGGCCAGCGCGTAGAACGCCGCAGATGATCGCTGTGGGCTTGGCTTCCACGGTGAGATGCTGTGGGGTTGGGCTTGTTCGAAAGACGCT
GNAS	NM_000516.3	27895	c.683G>A	p.R201H	+	20:57484421-57484421	CHP2_GNAS_1	TGTTTCAGGACCTGCTTCGCTGCCGTCCTCTGACTTCTGGAATCTTTGGAGCCAAGTTCCAGGTGGGACAAAGTCACTTCCAGTAAGCCAACTGTCACCTTTTTAAT
GNAS	NM_000516.3	27896	c.684A>C	p.Q228H	+	20:57484936-57484986	CHP2_GNAS_2	TCCTCCCCCACCAGCATGTTTGACGTGGGTGGCCAGCGCGTAGAACGCCGCAGATGATCGCTGTGGGCTTGGCTTCCACGGTGAGATGCTGTGGGGTTGGGCTTGTTCGAAAGACGCT
GNAS	NM_000516.3	27899	c.691C>A	p.R201S	+	20:57484420-57484420	CHP2_GNAS_1	TGTTTCAGGACCTGCTTCGCTGCCGTCCTCTGACTTCTGGAATCTTTGGAGCCAAGTTCCAGGTGGGACAAAGTCACTTCCAGTAAGCCAACTGTCACCTTTTTAAT
GNAS	NM_000516.3	27900	c.691C>T	p.Q227H	+	20:57484936-57484986	CHP2_GNAS_2	TCCTCCCCCACCAGCATGTTTGACGTGGGTGGCCAGCGCGTAGAACGCCGCAGATGATCGCTGTGGGCTTGGCTTCCACGGTGAGATGCTGTGGGGTTGGGCTTGTTCGAAAGACGCT
FLT3	Z16652	27906	c.1796A>T	p.Y599F	+	13:28608260-28608260	CHP2_FLT3_2	AATTTTCTCTTGGAAACTCCCATTTGAGATCATATTTCTCTGAAATCACGTAGAAGTACTCATTATCTGAGGAGCCGGTCACCTGATCACTCTGTAGCTGGCTTTCATACCTAAA
KIT	NM_000222	27909	c.1656_1678del18	p.Y553_K558>	+	4:55593590-55593607	CHP2_KIT_4	CCACAGAAACCCATGATTTTCTTGGTTCTCTTCCTGCATGGTGGTCAGTGATAATGGAAAGTCAATGTTTAACTGCAAGTCTTCTTATGATACAAAATGGGGATTTCCAGAAAC
KIT	NM_000222	27910	c.2431T>C	p.F811T	+	4:55590307-55590307	CHP2_KIT_5	GGTCGGATCACAAGATTTGTGATTTTGGTCTGACCAGACATCAGAATGATCTAATATATGTGGTTAAGGAAC
BRAF	NM_004333	27912	c.1405_1407GGA>AGT	p.G469S	+	7:140481401-140481403	CHP2_BRAF_1	GTAGACTGTTCCAAATGATCCAGATCCAATTCTTTGTCCACTGTAATCTGCCCATCAGGAATCTCCCAATCATCACTCCAGTCCCGTCTACCAAGTGTTTCTTGTAAAAACAGTAAAAAAG
APC	NM_000038	27993	c.4366A>G	p.R1456G	+	5:112175639-112175651	CHP2_APC_5	GCCCTGGCAACAACCAGATTTCTCCTCCTCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAACAGCTCAACAGCTGCTCAAAAATGAAAGACACCTACTGCTGAAAGAGGAGGATGGAACCTAAGCAAGCTGC
BRAF	NM_004333	28010	c.1759C>T	p.L594F	+	7:140453185-140453185	CHP2_BRAF_2	TCAAACTGAGTGGGACCATCCTCTCATCCGATGTTTCACTGTGATGGTCTAGCTACAAATATTACAGGTAGATTTGTGGAGGTAGTAGAGTAAAGGAAACAG
KIT	NM_000222	28026	c.1621A>C	p.M541L	+	4:55593464-55593464	CHP2_KIT_3	GCTGATTTGGTTTGGATTTGGTATGATGGATATTATTGTGGAATGGTTCTCTACAAATATTACAGGTAGATTTGTGGAGGTAGTAGAGTAAAGGAAACAG
FLT3	Z16652	28042	c.1352C>T	p.S451F	+	13:28610138-28610138	CHP2_FLT3_1	TCTTCCAGGTCCACAAGATGGTAATGGGTATCATCCTGAGAAAACAGGAGCGCTGACTTGCGTGATGCTTCTGCGAGCACTTGAGGTTTCCCTAT
FLT3	Z16652	28044	c.1715A>G	p.Y572C	+	13:28608441-28608441	CHP2_FLT3_2	AATTTTCTCTTGGAAACTCCCATTTGAGATCATATTTCATCTTTCTCTGAAATCACGTAGAAGTACTCATTATCTGAGGAGCCGGTCACCTGATCACTCTGTAGCTGGCTTTCATACCTAAA
FLT3	Z16652	28047	c.2503C>A	p.R834Q	+	13:28505604-28505604	CHP2_FLT3_4	ATAAGTAGGAAAATAAGCCAAGCAGCCTCCCTCATAGTCATCTGGAATCTCAGCTCATCTCTGCTGTTCTTCTGCTGCTG

TP53	NM_000546	43723		c.398T>C	p.M133T	-	17:7578532-7578532	CHP2_TP53_3	GCCAGTTGGGAAACATCTTGTTGAGGGCAGGGGGAGTACTGTAGGAAGAGGAAGACAGAGTTGAAAGTCAAGGGCACAAGTGA
TP53	NM_000546	43725		c.862A>T	p.N288Y	-	17:7578376-7578376	CHP2_TP53_3	TACCTCGCTTAGTGCTCCCTGGGGGCAGCTGCTGGTGAGGGCTCCCCTTTCTTGCGGAGATTTCTCTTCTCTGTGCGCCGGTCTCTCCCAGGACAGGCACAAACACGCACCTCAAAGCTGTTCCGTCCCAGTAGATT
TP53	NM_000546	43728		c.727A>T	p.M243L	-	17:7578554-7577554	CHP2_TP53_3	CCAGGTGTGATGATGGTGAGGTGGGGCCTCGGTCATGCCGCCCATGCAGGAACTGTTACACATGATGGTTGGTGAGTGGTTGATAGATGCCATGGCGCGGACGCGGGCTGCCGGGCGGGGGTGTG
TP53	NM_000546	43728		c.543C>T	p.R181R	-	17:7578387-7578387	CHP2_TP53_3	CCAGGCCCCAGCTGCTACCATCTGCTACTGAGCAGCGCTCATGGTGGGGGCAGCGCCTCACAACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGCCATGGCGCGGACGCGGGCTGCCGGGCGGGGGTGTG
TP53	NM_000546	43730		c.398T>G	p.M133R	-	17:7578532-7578532	CHP2_TP53_3	GCCAGTTGGGAAACATCTTGTTGAGGGCAGGGGGAGTACTGTAGGAAGAGGAAGACAGAGTTGAAAGTCAAGGGCACAAGTGA
TP53	NM_000546	43732		c.517delG	p.V173fs*	-	17:7578413-7578413	CHP2_TP53_4	CCAGGCCCCAGCTGCTACCATCTGCTACTGAGCAGCGCTCATGGTGGGGGCAGCGCCTCACAACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGCCATGGCGCGGACGCGGGCTGCCGGGCGGGGGTGTG
TP53	NM_000546	43734		c.526C>A	p.L176*	-	17:7578402-7578402	CHP2_TP53_4	CCAGGCCCCAGCTGCTACCATCTGCTACTGAGCAGCGCTCATGGTGGGGGCAGCGCCTCACAACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGCCATGGCGCGGACGCGGGCTGCCGGGCGGGGGTGTG
TP53	NM_000546	43737		c.836G>A	p.C279Y	-	17:7577708-7577708	CHP2_TP53_7	TACCTCGCTTAGTGCTCCCTGGGGGCAGCTGCTGGTGAGGGCTCCCCTTTCTTGCGGAGATTTCTCTTCTCTGTGCGCCGGTCTCTCCCAGGACAGGCACAAACACGCACCTCAAAGCTGTTCCGTCCCAGTAGATT
TP53	NM_000546	43739		c.467G>A	p.R156H	-	17:7578663-7578663	CHP2_TP53_4	CCAGGCCCCAGCTGCTACCATCTGCTACTGAGCAGCGCTCATGGTGGGGGCAGCGCCTCACAACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGCCATGGCGCGGACGCGGGCTGCCGGGCGGGGGTGTG
TP53	NM_000546	43743		c.914A>G	p.K305R	-	17:7578324-7578324	CHP2_TP53_4	TACCTCGCTTAGTGCTCCCTGGGGGCAGCTGCTGGTGAGGGCTCCCCTTTCTTGCGGAGATTTCTCTTCTCTGTGCGCCGGTCTCTCCCAGGACAGGCACAAACACGCACCTCAAAGCTGTTCCGTCCCAGTAGATT
TP53	NM_000546	43744		c.466C>A	p.R156S	-	17:7578664-7578664	CHP2_TP53_4	CCAGGCCCCAGCTGCTACCATCTGCTACTGAGCAGCGCTCATGGTGGGGGCAGCGCCTCACAACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGCCATGGCGCGGACGCGGGCTGCCGGGCGGGGGTGTG
TP53	NM_000546	43746		c.881A>G	p.E294G	-	17:7577557-7577557	CHP2_TP53_7	TACCTCGCTTAGTGCTCCCTGGGGGCAGCTGCTGGTGAGGGCTCCCCTTTCTTGCGGAGATTTCTCTTCTCTGTGCGCCGGTCTCTCCCAGGACAGGCACAAACACGCACCTCAAAGCTGTTCCGTCCCAGTAGATT
TP53	NM_000546	43747		c.872A>G	p.K291R	-	17:7577666-7577666	CHP2_TP53_7	TACCTCGCTTAGTGCTCCCTGGGGGCAGCTGCTGGTGAGGGCTCCCCTTTCTTGCGGAGATTTCTCTTCTCTGTGCGCCGGTCTCTCCCAGGACAGGCACAAACACGCACCTCAAAGCTGTTCCGTCCCAGTAGATT
TP53	NM_000546	43749		c.959G>A	p.G199R	-	17:7578254-7578254	CHP2_TP53_3	GGCGGGCCATGAGGGCACCACCACACTATGTCGAAAAGGTGTTTCTGTCATCCAAATACTCCACACGCAAATTTCCTTCCACTCGGATAAGATGCTGAGGAGGGGCCAGACCTAAGAGCA
TP53	NM_000546	43750		c.815G>T	p.S271*	-	17:7577727-7577727	CHP2_TP53_7	TACCTCGCTTAGTGCTCCCTGGGGGCAGCTGCTGGTGAGGGCTCCCCTTTCTTGCGGAGATTTCTCTTCTCTGTGCGCCGGTCTCTCCCAGGACAGGCACAAACACGCACCTCAAAGCTGTTCCGTCCCAGTAGATT
TP53	NM_000546	43753		c.560-1G>A	p.?	-	17:7578280-7578280	CHP2_TP53_3	GGCGGGCCATGAGGGCACCACCACACTATGTCGAAAAGGTGTTTCTGTCATCCAAATACTCCACACGCAAATTTCCTTCCACTCGGATAAGATGCTGAGGAGGGGCCAGACCTAAGAGCA
TP53	NM_000546	43755		c.833C>A	p.P278H	-	17:7577706-7577706	CHP2_TP53_7	TACCTCGCTTAGTGCTCCCTGGGGGCAGCTGCTGGTGAGGGCTCCCCTTTCTTGCGGAGATTTCTCTTCTCTGTGCGCCGGTCTCTCCCAGGACAGGCACAAACACGCACCTCAAAGCTGTTCCGTCCCAGTAGATT
TP53	NM_000546	43761		c.612G>A	p.E204E	-	17:7578237-7578237	CHP2_TP53_3	GGCGGGCCATGAGGGCACCACCACACTATGTCGAAAAGGTGTTTCTGTCATCCAAATACTCCACACGCAAATTTCCTTCCACTCGGATAAGATGCTGAGGAGGGGCCAGACCTAAGAGCA
TP53	NM_000546	43765		c.727A>C	p.M243L	-	17:7578554-7577554	CHP2_TP53_4	CCAGGTGTGATGATGGTGAGGTGGGGCCTCGGTCATGCCGCCCATGCAGGAACTGTTACACATGATGGTTGGTGAGTGGTTGATAGATGCCATGGCGCGGACGCGGGCTGCCGGGCGGGGGTGTG
TP53	NM_000546	43766		c.899C>T	p.P300L	-	17:7578309-7578309	CHP2_TP53_7	TACCTCGCTTAGTGCTCCCTGGGGGCAGCTGCTGGTGAGGGCTCCCCTTTCTTGCGGAGATTTCTCTTCTCTGTGCGCCGGTCTCTCCCAGGACAGGCACAAACACGCACCTCAAAGCTGTTCCGTCCCAGTAGATT
TP53	NM_000546	43767		c.404C>T	p.P135L	-	17:7578754-7578754	CHP2_TP53_3	GCCAGTTGGGAAACATCTTGTTGAGGGCAGGGGGAGTACTGTAGGAAGAGGAAGACAGAGTTGAAAGTCAAGGGCACAAGTGA
TP53	NM_000546	43768		c.700T>G	p.Y234D	-	17:7577581-7577581	CHP2_TP53_4	CCAGGTGTGATGATGGTGAGGTGGGGCCTCGGTCATGCCGCCCATGCAGGAACTGTTACACATGATGGTTGGTGAGTGGTTGATAGATGCCATGGCGCGGACGCGGGCTGCCGGGCGGGGGTGTG
TP53	NM_000546	43772		c.538G>A	p.E180K	-	17:7578392-7578392	CHP2_TP53_4	CCAGGCCCCAGCTGCTACCATCTGCTACTGAGCAGCGCTCATGGTGGGGGCAGCGCCTCACAACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGCCATGGCGCGGACGCGGGCTGCCGGGCGGGGGTGTG
TP53	NM_000546	43773		c.913A>T	p.K305*	-	17:7578325-7578325	CHP2_TP53_4	TACCTCGCTTAGTGCTCCCTGGGGGCAGCTGCTGGTGAGGGCTCCCCTTTCTTGCGGAGATTTCTCTTCTCTGTGCGCCGGTCTCTCCCAGGACAGGCACAAACACGCACCTCAAAGCTGTTCCGTCCCAGTAGATT
TP53	NM_000546	43776		c.861G>A	p.E287E	-	17:7577977-7577977	CHP2_TP53_7	TACCTCGCTTAGTGCTCCCTGGGGGCAGCTGCTGGTGAGGGCTCCCCTTTCTTGCGGAGATTTCTCTTCTCTGTGCGCCGGTCTCTCCCAGGACAGGCACAAACACGCACCTCAAAGCTGTTCCGTCCCAGTAGATT
TP53	NM_000546	43777		c.603C>T	p.I201I	-	17:7578246-7578246	CHP2_TP53_3	CCAGGTGTGATGATGGTGAGGTGGGGCCTCGGTCATGCCGCCCATGCAGGAACTGTTACACATGATGGTTGGTGAGTGGTTGATAGATGCCATGGCGCGGACGCGGGCTGCCGGGCGGGGGTGTG
TP53	NM_000546	43778		c.713G>T	p.C238F	-	17:7577568-7577568	CHP2_TP53_3	CCAGGTGTGATGATGGTGAGGTGGGGCCTCGGTCATGCCGCCCATGCAGGAACTGTTACACATGATGGTTGGTGAGTGGTTGATAGATGCCATGGCGCGGACGCGGGCTGCCGGGCGGGGGTGTG
TP53	NM_000546	43779		c.589G>A	p.V197M	-	17:7578138-7578138	CHP2_TP53_3	GGCGGGCCATGAGGGCACCACCACACTATGTCGAAAAGGTGTTTCTGTCATCCAAATACTCCACACGCAAATTTCCTTCCACTCGGATAAGATGCTGAGGAGGGGCCAGACCTAAGAGCA
TP53	NM_000546	43781		c.472delC	p.R158fs*12	-	17:7578479-7578479	CHP2_TP53_4	CCAGGCCCCAGCTGCTACCATCTGCTACTGAGCAGCGCTCATGGTGGGGGCAGCGCCTCACAACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGCCATGGCGCGGACGCGGGCTGCCGGGCGGGGGTGTG
TP53	NM_000546	43782		c.576G>A	p.Q192Q	-	17:7578273-7578273	CHP2_TP53_3	GGCGGGCCATGAGGGCACCACCACACTATGTCGAAAAGGTGTTTCTGTCATCCAAATACTCCACACGCAAATTTCCTTCCACTCGGATAAGATGCTGAGGAGGGGCCAGACCTAAGAGCA
TP53	NM_000546	43787		c.215C>A	p.V97M	-	17:7579470-7579470	CHP2_TP53_2	GCCCAGACGGAAACCCATGAGCTGCCCTGGTAGGTTTTCTGGGAAGGGACAGAAGATGACAGGGGCCAGGAGGGGCTGGTGCAGGGGCCGCCGGTGTAGGAGCTGCTGGTACAGGGCCAGCAGCCTC
TP53	NM_000546	43793		c.617T>A	p.L206*	-	17:7578232-7578232	CHP2_TP53_3	GGCGGGCCATGAGGGCACCACCACACTATGTCGAAAAGGTGTTTCTGTCATCCAAATACTCCACACGCAAATTTCCTTCCACTCGGATAAGATGCTGAGGAGGGGCCAGACCTAAGAGCA
TP53	NM_000546	43795		c.1025delC	p.P342Qfs*3	-	17:7578004-7578004	CHP2_TP53_4	CACCTGGAGATGAGGCTGCTCCCCCCATGCTGATGCAGATAGCATGCTGGGGCTGTGGTGGGGTGGGGGGGAGCGCGTGGGCTGGCAGGGCAGGGGGCAGGTGTGGGAGGGGTGTGGGGGATGCAT
TP53	NM_000546	43797		c.558G>C	p.D184H	-	17:7578380-7578380	CHP2_TP53_4	CCAGGCCCCAGCTGCTACCATCTGCTACTGAGCAGCGCTCATGGTGGGGGCAGCGCCTCACAACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGCCATGGCGCGGACGCGGGCTGCCGGGCGGGGGTGTG
TP53	NM_000546	43801		c.716A>C	p.Y239T	-	17:7577557-7577557	CHP2_TP53_7	CCAGGTGTGATGATGGTGAGGTGGGGCCTCGGTCATGCCGCCCATGCAGGAACTGTTACACATGATGGTTGGTGAGTGGTTGATAGATGCCATGGCGCGGACGCGGGCTGCCGGGCGGGGGTGTG
TP53	NM_000546	43806		c.689C>A	p.T230N	-	17:7577592-7577592	CHP2_TP53_4	CCAGGTGTGATGATGGTGAGGTGGGGCCTCGGTCATGCCGCCCATGCAGGAACTGTTACACATGATGGTTGGTGAGTGGTTGATAGATGCCATGGCGCGGACGCGGGCTGCCGGGCGGGGGTGTG
TP53	NM_000546	43807		c.637delC	p.R213fs*54	-	17:7578212-7578212	CHP2_TP53_3	GGCGGGCCATGAGGGCACCACCACACTATGTCGAAAAGGTGTTTCTGTCATCCAAATACTCCACACGCAAATTTCCTTCCACTCGGATAAGATGCTGAGGAGGGGCCAGACCTAAGAGCA
TP53	NM_000546	43809		c.808T>A	p.F270I	-	17:7577739-7577739	CHP2_TP53_7	TACCTCGCTTAGTGCTCCCTGGGGGCAGCTGCTGGTGAGGGCTCCCCTTTCTTGCGGAGATTTCTCTTCTCTGTGCGCCGGTCTCTCCCAGGACAGGCACAAACACGCACCTCAAAGCTGTTCCGTCCCAGTAGATT
TP53	NM_000546	43814		c.583C>G	p.R194P	-	17:7578262-7578262	CHP2_TP53_3	GGCGGGCCATGAGGGCACCACCACACTATGTCGAAAAGGTGTTTCTGTCATCCAAATACTCCACACGCAAATTTCCTTCCACTCGGATAAGATGCTGAGGAGGGGCCAGACCTAAGAGCA
TP53	NM_000546	43820		c.488C>G	p.T163*	-	17:7578441-7578441	CHP2_TP53_4	CCAGGCCCCAGCTGCTACCATCTGCTACTGAGCAGCGCTCATGGTGGGGGCAGCGCCTCACAACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGCCATGGCGCGGACGCGGGCTGCCGGGCGGGGGTGTG
TP53	NM_000546	43823		c.825T>C	p.C275W	-	17:7577113-7577113	CHP2_TP53_7	TACCTCGCTTAGTGCTCCCTGGGGGCAGCTGCTGGTGAGGGCTCCCCTTTCTTGCGGAGATTTCTCTTCTCTGTGCGCCGGTCTCTCCCAGGACAGGCACAAACACGCACCTCAAAGCTGTTCCGTCCCAGTAGATT
TP53	NM_000546	43826		c.760T>A	p.Y254N	-	17:7577647-7577647	CHP2_TP53_7	TACCTCGCTTAGTGCTCCCTGGGGGCAGCTGCTGGTGAGGGCTCCCCTTTCTTGCGGAGATTTCTCTTCTCTGTGCGCCGGTCTCTCCCAGGACAGGCACAAACACGCACCTCAAAGCTGTTCCGTCCCAGTAGATT
TP53	NM_000546	43827		c.581T>C	p.L194P	-	17:7578266-7578266	CHP2_TP53_3	GGCGGGCCATGAGGGCACCACCACACTATGTCGAAAAGGTGTTTCTGTCATCCAAATACTCCACACGCAAATTTCCTTCCACTCGGATAAGATGCTGAGGAGGGGCCAGACCTAAGAGCA
TP53	NM_000546	43828		c.544T>A	p.C182S	-	17:7578386-7578386	CHP2_TP53_4	CCAGGCCCCAGCTGCTACCATCTGCTACTGAGCAGCGCTCATGGTGGGGGCAGCGCCTCACAACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGCCATGGCGCGGACGCGGGCTGCCGGGCGGGGGTGTG
TP53	NM_000546	43829		c.752T>G	p.I251S	-	17:7577529-7577529	CHP2_TP53_7	CCAGTGTGATGATGGTGAGGTGGGGCCTCGGTCATGCCGCCCATGCAGGAACTGTTACACATGATGGTTGGTGAGTGGTTGATAGATGCCATGGCGCGGACGCGGGCTGCCGGGCGGGGGTGTG
TP53	NM_000546	43831		c.472_475delCCGCG	p.R158fs*11	-	17:7578455-7578455	CHP2_TP53_4	CCAGGCCCCAGCTGCTACCATCTGCTACTGAGCAGCGCTCATGGTGGGGGCAGCGCCTCACAACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGCCATGGCGCGGACGCGGGCTGCCGGGCGGGGGTGTG
TP53	NM_000546	43833		c.754A>C	p.H252P	-	17:7577547-7577547	CHP2_TP53_7	GGCGGGCCATGAGGGCACCACCACACTATGTCGAAAAGGTGTTTCTGTCATCCAAATACTCCACACGCAAATTTCCTTCCACTCGGATAAGATGCTGAGGAGGGGCCAGACCTAAGAGCA
TP53	NM_000546	43836		c.475G>C	p.A159P	-	17:7578455-7578455	CHP2_TP53_4	CCAGGCCCCAGCTGCTACCATCTGCTACTGAGCAGCGCTCATGGTGGGGGCAGCGCCTCACAACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGCCATGGCGCGGACGCGGGCTGCCGGGCGGGGGTGTG
TP53	NM_000546	43837		c.843C>G	p.D281E	-	17:7577990-7577990	CHP2_TP53_7	TACCTCGCTTAGTGCTCCCTGGGGGCAGCTGCTGGTGAGGGCTCCCCTTTCTTGCGGAGATTTCTCTTCTCTGTGCGCCGGTCTCTCCCAGGACAGGCACAAACACGCACCTCAAAGCTGTTCCGTCCCAGTAGATT
TP53	NM_000546	43841		c.560-1G>T	p.?	-	17:7578280-7578280	CHP2_TP53_3	GGCGGGCCATGAGGGCACCACCACACTATGTCGAAAAGGTGTTTCTGTCATCCAAATACTCCACACGCAAATTTCCTTCCACTCGGATAAGATGCTGAGGAGGGGCCAGACCTAAGAGCA
TP53	NM_000546	43843		c.817C>G	p.R273G	-	17:7577721-7577721	CHP2_TP53_7	TACCTCGCTTAGTGCTCCCTGGGGGCAGCTGCTGGTGAGGGCTCCCCTTTCTTGCGGAGATTTCTCTTCTCTGTGCGCCGGTCTCTCCCAGGACAGGCACAAACACGCACCTCAAAGCTGTTCCGTCCCAGTAGATT
TP53	NM_000546	43844		c.617T>G	p.V205D	-	17:7578236-7578236	CHP2_TP53_3	GGCGGGCCATGAGGGCACCACCACACTATGTCGAAAAGGTGTTTCTGTCATCCAAATACTCCACACGCAAATTTCCTTCCACTCGGATAAGATGCTGAGGAGGGGCCAGACCTAAGAGCA
TP53	NM_000546	43846		c.487T>C	p.Y163H	-	17:7578443-7578443	CHP2_TP53_4	CCAGGCCCCAGCTGCTACCATCTGCTACTGAGCAGCGCTCATGGTGGGGGCAGCGCCTCACAACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGCCATGGCGCGGACGCGGGCTGCCGGGCGGGGGTGTG
TP53	NM_000546	43848		c.472C>T	p.R158C	-	17:7578479-7578479	CHP2_TP53_4	CCAGGCCCCAGCTGCTACCATCTGCTACTGAGCAGCGCTCATGGTGGGGGCAGCGCCTCACAACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGCCATGGCGCGGACGCGGGCTGCCGGGCGGGGGTGTG
TP53	NM_000546	43850		c.659A>C	p.Y220S	-	17:7578190-7578190	CHP2_TP53_3	GGCGGGCCATGAGGGCACCACCACACTATGTCGAAAAGGTGTTTCTGTCATCCAAATACTCCACACGCAAATTTCCTTCCACTCGGATAAGATGCTGAGGAGGGGCCAGACCTAAGAGCA
TP53	NM_000546	43851		c.586T>C	p.M196T	-	17:7578142-7578142	CHP2_TP53_3	GGCGGGCCATGAGGGCACCACCACACTATGTCGAAAAGGTGTTTCTGTCATCCAAATACTCCACACGCAAATTTCCTTCCACTCGGATAAGATGCTGAGGAGGGGCCAGACCTAAGAGCA
TP53	NM_000546	43853		c.684C>G	p.D228E	-	17:7577597-7577597	CHP2_TP53_4	CCAGGTGTGATGATGGTGAGGTGGGGCCTCGGTCATGCCGCCCATGCAGGAACTGTTACACATGATGGTTGGTGAGTGGTTGATAGATGCCATGGCGCGGACGCGGGCTGCCGGGCGGGGGTGTG
TP53	NM_000546	43859		c.594delA	p.S200fs*47	-	17:7578251-7578251	CHP2_TP53_3	GGCGGGCCATGAGGGCACCACCACACTATGTCGAAAAGGTGTTTCTGTCATCCAAATACTCCACACGCAAATTTCCTTCCACTCGGATAAGATGCTGAGGAGGGGCCAGACCTAAGAGCA
TP53	NM_000546	43860		c.704A>T	p.N235I	-	17:7577577-7577577	CHP2_TP53_7	CCAGTGTGATGATGGTGAGGTGGGGCCTCGGTCATGCCGCCCATGCAGGAACTGTTACACATGATGGTTGGTGAGTGGTTGATAGATGCCATGGCGCGGACGCGGGCTGCCGGGCGGGGGTGTG
TP53	NM_000546	43861		c.502C>T	p.H168Y	-	17:7578429-7578429	CHP2_TP53_4	CCAGGCCCCAGCTGCTACCATCTGCTACTGAGCAGCGCTCATGGTGGGGGCAGCGCCTCACAACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGCCATGGCGCGGACGCGGGCTGCCGGGCGGGGGTGTG
TP53	NM_000546	43862		c.683A>C	p.D228A	-	17:7577598-7577598	CHP2_TP53_4	CCAGTGTGATGATGGTGAGGTGGGGCCTCGGTCATGCCGCCCATGCAGGAACTGTTACACATGATGGTTGGTGAGTGGTTGATAGATGCCATGGCGCGGACGCGGGCTGCCGGGCGGGGGTGTG
TP53	NM_000546	43864		c.739A>T	p.N247Y	-	17:7577542-7577542	CHP2_TP53_7	CCAGTGTGATGATGGTGAGGTGGGGCCTCGGTCATGCCGCCCATGCAGGAACTGTTACACATGATGGTTGGTGAGTGGTTGATAGATGCCATGGCGCGGACGCGGGCTGCCGGGCGGGGGTGTG
TP53	NM_000546	43865		c.761A>C	p.Y254S	-	17:7577646-7577646	CHP2_TP53_7	CCAGTGTGATGATGGTGAGGTGGGGCCTCGGTCATGCCGCCCATGCAGGAACTGTTACACATGATGGTTGGTGAGTGGTTGATAGATGCCATGGCGCGGACGCGGGCTGCCGGGCGGGGGTGTG
TP53	NM_000546	43868		c.698C>T	p.T230I	-	17:7577592-7577592	CHP2_TP53_4	CCAGTGTGATGATGGTGAGGTGGGGCCTCGGTCATGCCGCCCATGCAGGAACTGTTACACATGATGGTTGGTGAGTGGTTGATAGATGCCATGGCGCGGACGCGGGCTGCCGGGCGGGGGTGTG
TP53	NM_000546	43871		c.746G>T	p.R249M	-	17:7577555-7577555	CHP2_TP53_7	CCAGTGTGATGATGGTGAGGTGGGGCCTCGGTCATGCCGCCCATGCAGGAACTGTTACACATGATGGTTGGTGAGTGGTTGATAGATGCCATGGCGCGGACGCGGGCTGCCGGGCGGGGGTGTG
TP53	NM_000546	43872		c.560-1G>C	p.?	-	17:7578280-7578280	CHP2_TP53_3	GGCGGGCCATGAGGGCACCACCACACTATGTCGAAAAGGTGTTTCTGTCATCCAAATACTCCACACGCAAATTTCCTTCCACTCGGATAAGATGCTGAGGAGGGGCCAGACCTAAGAGCA
TP53	NM_000546	43878		c.812A>G	p.E271G	-	17:7577726-7577726	CHP2_TP53_7	TACCTCGCTTAGTGCTCCCTGGGGGCAGCTGCTGGTGAGGGCTCCCCTTTCTTGCGGAGATTTCTCTTCTCTGTGCGCCGGTCTCTCCCAGGACAGGCACAAACACGCACCTCAAAGCTGTTCCGTCCCAGTAGATT
TP53	NM_000546	43881		c.757A>T	p.T253S	-	17:7577524-7577524	CHP2_TP53_7	CCAGTGTGATGATGGTGAGGTGGGGCCTCGGTCATGCCGCCCATGCAGGAACTGTTACACATGATGGTTGGTGAGTGGTTGATAGATGCCATGGCGCGGACGCGGGCTGCCGGGCGGGGGTGTG
TP53	NM_000546	43882		c.1010G>A	p.R337H	-	17:7574817-7574817	CHP2_TP53_8	CACCTGGAGTGAGGCCTGCTCCCCCCTGCCTCCCTTCCAGCCTGGGCATCCTTGAGTTCCAAGGCTCATTCAGCTCCTGGACACATCTGAAGCGCTCACGCCCACGGATCT
TP53	NM_000546	43889		c.691A>T	p.I231S	-	17:7577590-7577590	CHP2_TP53_4	CCAGTGTGATGATGGTGAGGTGGGGCCTCGGTCATGCCGCCCATGCAGGAACTGTTACACATGATGGTTGGTGAGTGGTTGATAGATGCCATGGCGCGGACGCGGGCTGCCGGGCGGGGGTGTG
TP53	NM_000546	43891		c.488G>A	p.M163I	-	17:7578459-7578459	CHP2_TP53_4	CCAGGCCCCAGCTGCTACCATCTGCTACTGAGCAGCGCTCATGGTGGGGGCAGCGCCTCACAACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGCCATGGCGCGGACGCGGGCTGCCGGGCGGGGGTGTG
TP53	NM_000546	43896		c.818G>C	p.R273P	-	17:7577720-7577720	CHP2_TP53_7	TACCTCGCTTAGTGCTCCCTGGGGGCAGCTGCTGGTGAGGGCTCCCCTTTCTTGCGGAGATTTCTCTTCTCTGTGCGCCGGTCTCTCCCAGGACAGGCACAAACACGCACCTCAAAGCTGTTCCGTCCCAGTAGATT
TP53	NM_000546	43898		c.485T>G	p.I162S	-	17:7578445-7578445	CHP2_TP53_4	CCAGGCCCCAGCTGCTACCATCTGCTACTGAGCAGCGCTCATGGTGGGGGCAGCGCCTCACAACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGCCATGGCGCGGACGCGGGCTGCCGGGCGGGGGTGTG
TP53	NM_000546	43900		c.578T>G	p.V126D	-	17:7578154-7578154	CHP2_TP53_3	GGCGGGCCATGAGGGCACCACCACACTATGTCGAAAAGGTGTTTCTGTCATCCAAATACTCCACACGCAAATTTCCTTCCACTCGGATAAGATGCTGAGGAGGGGCCAGACCTAAGAGCA
TP53	NM_000546	43902		c.823T>C	p.C275R	-	17:7577715-7577715	CHP2_TP53_7	TACCTCGCTTAGTGCTCCCTGGGGGCAGCTGCTGGTGAGGGCTCCCCTTTCTTGCGGAGATTTCTCTTCTCTGTGCGCCGGTCTCTCCCAGGACAGGCACAAACACGCACCTCAAAGCTGTTCCGTCCCAGTAGATT
TP53	NM_000546	43903		c.470T>C	p.V157G	-	17:7578480-7578480	CHP2_TP53_4	CCAGGCCCCAGCTGCTACCATCTGCTACTGAGCAGCGCTCATGGTGGGGGCAGCGCCTCACAACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGCCATGGCGCGGACGCGGGCTGCCGGGCGGGGGTGTG
TP53	NM_000546	43905		c.594T>G	p.Y198X	-	17:7578279-7578279	CHP2_TP53_3	GGCGGGCCATGAGGGCACCACCACACTATGTCGAAAAGGTGTTTCTGTCATCCAAATACTCCACACGCAAATTTCCTTCCACTCGGATAAGATGCTGAGGAGGGGCCAGACCTAAGAGCA
TP53	NM_000546	43906		c.840C>A	p.D281E	-	17:7577995-7577995	CHP2_TP53_7	TACCTCGCTTAGTGCTCCCTGGGGGCAGCTGCTGGTGAGGGCTCCCCTTTCTTGCGGAGATTTCTCTTCTCTGTGCGCCGGTCTCTCCCAGGACAGGCACAAACACGCACCTCAAAGCTGTTCCGTCCCAGTAGATT
TP53	NM_000546	43909		c.817C>A	p.R273S	-	17:7577721-7577721	CHP2_TP53_7	TACCTCGCTTAGTGCTCCCTGGGGGCAGCTGCTGGTGAGGGCTCCCCTTTCTTGCGGAGATTTCTCTTCTCTGTGCGCCGGTCTCTCCCAGGACAGGCACAAACACGCACCTCAAAGCTGTTCCGTCCCAGTAGATT
TP53	NM_000546	43910		c.245C>T	p.P82L	-	17:7579442-7579442	CHP2_TP53_2	GCCCAGACGGAAACCCATGAGCTGCCCTGGTAGGTTTTCTGGGAAGGGACAGAAGATGACAGGGGCCAGGAGGGGCTGGTGCAGGGGCCGCCGGTGTAGGAGCTGCTGGTACAGGGCCAGCAGCCTC
TP53	NM_000546	43912		c.395A>C	p.K132T	-	17:7578535-7578535	CHP2_TP53_3	GGCGGGCCATGAGGGCACCACCACACTATGTCGAAAAGGTGTTTCTGTCATCCAAATACTCCACACGCAAATTTCCTTCCACTCGGATAAGATGCTGAGGAGGGGCCAGACCTAAGAGCA
TP53	NM_000546	43915		c.886C>T	p.H296Y	-	17:7577952-7577952	CHP2_TP53_7	TACCTCGCTTAGTGCTCCCTGGGGGCAGCTGCTGGTGAGGGCTCCCCTTTCTTGCGGAGATTTCTCTTCTCTGTGCGCCGGTCTCTCCCAGGACAGGCACAAACACGCACCTCAAAGCTGTTCCGTCCCAGTAGATT
TP53	NM_000546	43918		c.809T>A	p.F270Y	-	17:7577729-7577729	CHP2_TP53_7	TACCTCGCTTAGTGCTCCCTGGGGGCAGCTGCTGGTGAGGGCTCCCCTTTCTTGCGGAGATTTCTCTTCTCTGTGCGCCGGTCTCTCCCAGGACAGGCACAAACACGCACCTCAAAGCTGTTCCGTCCCAGTAGATT
TP53	NM_000546	43919		c.856G>T	p.E286*	-	17:7577982-7577982	CHP2_TP53_7	TACCTCGCTTAGTGCTCCCTGGGGGCAGCTGCTGGTGAGGGCTCCCCTTTCTTGCGGAGATTTCTCTTCTCTGTGCGCCGGTCTCTCCCAGGACAGGCACAAACACGCACCTCAAAGCTGTTCCGTCCCAGTAGATT
TP53	NM_000546	43920		c.680C>T	p.S227F	-	17:7577601-7577601	CHP2_TP53_4	CCAGGTGTGATGATGGTGAGGTGGGGCCTCGGTCATGCCGCCCATGCAGGAACTGTTACACATGATGGTTGGTGAGTGGTTGATAGATGCCATGGCGCGGACGCGGGCTGCCGGGCGGGGGTGTG
TP53	NM_000546	43923		c.880G>A	p.R293Q	-	17:7577738-7577738	CHP2_TP53_7	TACCTCGCTTAGTGCTCCCTGGGGGCAGCTGCTGGTGAGGGCTCCCCTTTCTTGCGGAGATTTCTCTTCTCTGTGCGCCGGTCTCTCCCAGGACAGGCACAAACACGCACCTCAAAGCTGTTCCGTCCCAGTAGATT
TP53	NM_000546	43927		c.559+9C>T	p.?	-	17:7578362-7578362	CHP2_TP53_3	GGCGGGCCATGAGGGCACCACCACACTATGTCGAAAAGGTGTTTCTGTCATCCAAATACTCCACACGCAAATTTCCTTCCACTCGGATAAGATGCTGAGGAGGGGCCAGACCTAAGAGCA
TP53	NM_000546	43928		c.615T>A	p.Y205*	-	17:7578234-7578234	CHP2_TP53_3	GGCGGGCCATGAGGGCACCACCACACTATGTCGAAAAGGTGTTTCTGTCATCCAAATACTCCACACGCAAATTTCCTTCCACTCGGATAAGATGCTGAGGAGGGGCCAGACCTAAGAGCA
TP53	NM_000546	43929		c.582C>G	p.L194L	-	17:7578267-7578267	CHP2_TP53_3	GGCGGGCCATGAGGGCACCACCACACTATGTCGAAAAGGTGTTTCTGTCATCCAAATACTCCACACGCAAATTTCCTTCCACTCGGATAAGATGCTGAGGAGGGGCCAGACCTAAGAGCA
TP53	NM_000546	43931		c.523C>A	p.R175S	-	17:7578407-7578407	CHP2_TP53_4	CCAGGCCCCAGCTGCTACCATCTGCTACTGAGCAGCGCTCATGGTGGGGGCAGCGCCTCACAACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGCCATGGCGCGGACGCGGGCTGCCGGGCGGGGGTGTG
TP53	NM_000546	43934		c.471C>A	p.S157V	-	17:7578479-7578479	CHP2_TP53_4	CCAGGCCCCAGCTGCTACCATCTGCTACTGAGCAGCGCTCATGGTGGGGGCAGCGCCTCACAACCTCCGTCATGT

TP53	NM_000546	44301	c.468C>G	p.R156R	-	17:7578462-7578462	CHP2_TP53_4	CCAGCCCCAGCTGCTCACCATCGCTATCTGGGACAGCCCTCATGGTGGGGGCAGCGCCTCACCACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGGCCAGGGGCGCGGGTGCCGGGCGGGGGTGTG	
TP53	NM_000546	44303	c.463A>G	p.T155A	-	17:7578467-7578467	CHP2_TP53_4	CCAGCCCCAGCTGCTCACCATCGCTATCTGAGCACGCGCTCATGGTGGGGGCAGCGCCTCACCACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGGCCAGGGGCGCGGGTGCCGGGCGGGGGTGTG	
TP53	NM_000546	44305	c.459T>A	p.M148K	-	17:7578471-7578471	CHP2_TP53_4	CCAGCCCCAGCTGCTCACCATCGCTATCTGAGCAGCGCTCATGGTGGGGGCAGCGCCTCACCACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGGCCAGGGGCGCGGGTGCCGGGCGGGGGTGTG	
TP53	NM_000546	44306	c.849G>C	p.R282P	-	17:7577093-7577093	CHP2_TP53_3	TACCTCGCCTTAGTGCTCCTGGGGGCAGCTCGTGGTGAGGGCTCCCCTTTTGTTGCGGAGATTTCTTCTTCTGCTGTGCAGTGCTGCTCACACATCCTGCGTGGGCAAGCTGACCGCATCAGAGATT	
TP53	NM_000546	44308	c.494A>G	p.Q165R	-	17:7578436-7578436	CHP2_TP53_4	CCAGCCCCAGCTGCTCACCATCGCTATCTGCGACGCGCTCATGGTGGGGGCAGCGCCTCACCACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGGCCAGGGGCGCGGGTGCCGGGCGGGGGTGTG	
TP53	NM_000546	44310	c.738G>A	p.M246I	-	17:7577543-7577543	CHP2_TP53_6	CCAGGTGTGATGTGTGAGGATGGGCCTCCGGTTCATGCCGCCCCATGCAGGAACTGTTACACATGATGGTTGTAGTGGATGTGGTGCTACGTCAGGTCACAGGCCAACCTAG	
TP53	NM_000546	44312	c.511G>A	p.E171K	-	17:7578419-7578419	CHP2_TP53_4	CCAGCCCCAGCTGCTCACCATCGCTATCTGGAGCAGCGCTCATGGTGGGGGCAGCGCCTCACACACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGGCCAGGGGCGCGGGTGCCGGGCGGGGGTGTG	
TP53	NM_000546	44313	c.686G>A	p.C229Y	-	17:7577996-7577996	CHP2_TP53_5	GCCAGGTGTGATGTGTGAGGATGGGCCTCCGGTTCATGCCGCCCCATGCAGGAACTGTTACACATGATGGTTGTAGTGGATGTGGTGCTACGTCAGGTCACAGGCCAACCTAG	
TP53	NM_000546	44317	c.635T>A	p.V211E	-	17:7578196-7578196	CHP2_TP53_5	GGCGGGCCTCATGGGCACCACCACACTATGTCGAAAAGTGTTTCTGTCATCCAAATACTCCACACGCAAATTTCCTTCCACTCGGATAAGATGCTGAGGAGGGGCCAGACCTAAGAGCAC	
TP53	NM_000546	44319	c.483C>A	p.C15*	-	17:7578525-7578525	CHP2_TP53_4	GCCAGTGGTGATGTGTGAGGATGGGCCTCCGGTTCATGCCGCCCCATGCAGGAACTGTTACACATGATGGTTGTAGTGGATGTGGTGCTACGTCAGGTCACAGGCCAACCTAG	
TP53	NM_000546	44320	c.484A>T	p.I162F	-	17:7578446-7578446	CHP2_TP53_4	CCAGCCCCAGCTGCTCACCATCGCTATCTGAGCAGCGCTCATGGTGGGGGCAGCGCCTCACACACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGGCCAGGGGCGCGGGTGCCGGGCGGGGGTGTG	
TP53	NM_000546	44321	c.712T>C	p.C238R	-	17:7577569-7577569	CHP2_TP53_6	CCAGGTGTGATGTGTGAGGATGGGCCTCCGGTTCATGCCGCCCCATGCAGGAACTGTTACACATGATGGTTGTAGTGGATGTGGTGCTACGTCAGGTCACAGGCCAACCTAG	
TP53	NM_000546	44322	c.728T>A	p.M243K	-	17:7577533-7577533	CHP2_TP53_6	CCAGGTGTGATGTGTGAGGATGGGCCTCCGGTTCATGCCGCCCCATGCAGGAACTGTTACACATGATGGTTGTAGTGGATGTGGTGCTACGTCAGGTCACAGGCCAACCTAG	
TP53	NM_000546	44326	c.786T>C	p.Y266H	-	17:7577375-7577375	CHP2_TP53_6	CCAGGTGTGATGTGTGAGGATGGGCCTCCGGTTCATGCCGCCCCATGCAGGAACTGTTACACATGATGGTTGTAGTGGATGTGGTGCTACGTCAGGTCACAGGCCAACCTAG	
TP53	NM_000546	44327	c.514T>C	p.V171A	-	17:7578412-7578412	CHP2_TP53_4	CCAGCCCCAGCTGCTCACCATCGCTATCTGGAGCAGCGCTCATGGTGGGGGCAGCGCCTCACACACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGGCCAGGGGCGCGGGTGCCGGGCGGGGGTGTG	
TP53	NM_000546	44328	c.478A>G	p.M160V	-	17:7578452-7578452	CHP2_TP53_4	CCAGCCCCAGCTGCTCACCATCGCTATCTGGAGCAGCGCTCATGGTGGGGGCAGCGCCTCACACACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGGCCAGGGGCGCGGGTGCCGGGCGGGGGTGTG	
TP53	NM_000546	44329	c.476T>A	p.V159D	-	17:7578454-7578454	CHP2_TP53_4	CCAGCCCCAGCTGCTCACCATCGCTATCTGGAGCAGCGCTCATGGTGGGGGCAGCGCCTCACACACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGGCCAGGGGCGCGGGTGCCGGGCGGGGGTGTG	
TP53	NM_000546	44334	c.649G>T	p.V217L	-	17:7578280-7578280	CHP2_TP53_5	GGCGGGCCTCATGGGCACCACCACACTATGTCGAAAAGTGTTTCTGTCATCCAAATACTCCACACGCAAATTTCCTTCCACTCGGATAAGATGCTGAGGAGGGGCCAGACCTAAGAGCAC	
TP53	NM_000546	44336	c.494delC	p.Q165Sfs*3	-	17:7578436-7578436	CHP2_TP53_4	CCAGCCCCAGCTGCTCACCATCGCTATCTGGGACAGCCCTCATGGTGGGGGCAGCGCCTCACCACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGGCCAGGGGCGCGGGTGCCGGGCGGGGGTGTG	
TP53	NM_000546	44338	c.845G>A	p.R282Q	-	17:7577093-7577093	CHP2_TP53_7	TACCTCGCCTTAGTGCTCCTGGGGGCAGCTCGTGGTGAGGGCTCCCCTTTTGTTGCGGAGATTTCTTCTTCTGCTGTGCAGTGCTGCTCACACATCCTGCGTGGGCAAGCTGACCGCATCAGAGATT	
TP53	NM_000546	44343	c.547T>G	p.S183P	-	17:7578377-7578377	CHP2_TP53_4	CCAGCCCCAGCTGCTCACCATCGCTATCTGGAGCAGCGCTCATGGTGGGGGCAGCGCCTCACACACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGGCCAGGGGCGCGGGTGCCGGGCGGGGGTGTG	
TP53	NM_000546	44345	c.915G>T	p.K305N	-	17:7577023-7577023	CHP2_TP53_7	TACCTCGCCTTAGTGCTCCTGGGGGCAGCTCGTGGTGAGGGCTCCCCTTTTGTTGCGGAGATTTCTTCTTCTGCTGTGCAGTGCTGCTCACACATCCTGCGTGGGCAAGCTGACCGCATCAGAGATT	
TP53	NM_000546	44346	c.875A>C	p.K292T	-	17:7577063-7577063	CHP2_TP53_7	TACCTCGCCTTAGTGCTCCTGGGGGCAGCTCGTGGTGAGGGCTCCCCTTTTGTTGCGGAGATTTCTTCTTCTGCTGTGCAGTGCTGCTCACACATCCTGCGTGGGCAAGCTGACCGCATCAGAGATT	
TP53	NM_000546	44349	c.566C>T	a.189V	-	17:7578203-7578203	CHP2_TP53_5	GGCGGGCCTCATGGGCACCACCACACTATGTCGAAAAGTGTTTCTGTCATCCAAATACTCCACACGCAAATTTCCTTCCACTCGGATAAGATGCTGAGGAGGGGCCAGACCTAAGAGCAC	
TP53	NM_000546	44350	c.699C>G	p.H233Q	-	17:7577582-7577582	CHP2_TP53_6	CCAGTGTGTGATGTGTGAGGATGGGCCTCCGGTTCATGCCGCCCCATGCAGGAACTGTTACACATGATGGTTGTAGTGGATGTGGTGCTACGTCAGGTCACAGGCCAACCTAG	
TP53	NM_000546	44351	c.572C>T	p.P191L	-	17:7578275-7578275	CHP2_TP53_5	GGCGGGCCTCATGGGCACCACCACACTATGTCGAAAAGTGTTTCTGTCATCCAAATACTCCACACGCAAATTTCCTTCCACTCGGATAAGATGCTGAGGAGGGGCCAGACCTAAGAGCAC	
TP53	NM_000546	44352	c.858A>C	p.T286P	-	17:7577088-7577088	CHP2_TP53_7	TACCTCGCCTTAGTGCTCCTGGGGGCAGCTCGTGGTGAGGGCTCCCCTTTTGTTGCGGAGATTTCTTCTTCTGCTGTGCAGTGCTGCTCACACATCCTGCGTGGGCAAGCTGACCGCATCAGAGATT	
TP53	NM_000546	44358	c.624G>T	p.R208Ser74	-	17:7578494-7578494	CHP2_TP53_4	GGCGGGCCTCATGGGCACCACCACACTATGTCGAAAAGTGTTTCTGTCATCCAAATACTCCACACGCAAATTTCCTTCCACTCGGATAAGATGCTGAGGAGGGGCCAGACCTAAGAGCAC	
TP53	NM_000546	44360	c.686_687delGT	p.C229fs*10	-	17:7577594-7577595	CHP2_TP53_6	CCAGGTGTGATGTGTGAGGATGGGCCTCCGGTTCATGCCGCCCCATGCAGGAACTGTTACACATGATGGTTGTAGTGGATGTGGTGCTACGTCAGGTCACAGGCCAACCTAG	
TP53	NM_000546	44365	c.607G>T	p.V203L	-	17:7578242-7578242	CHP2_TP53_5	GGCGGGCCTCATGGGCACCACCACACTATGTCGAAAAGTGTTTCTGTCATCCAAATACTCCACACGCAAATTTCCTTCCACTCGGATAAGATGCTGAGGAGGGGCCAGACCTAAGAGCAC	
TP53	NM_000546	44367	c.458C>T	p.P153L	-	17:7578472-7578472	CHP2_TP53_4	CCAGCCCCAGCTGCTCACCATCGCTATCTGGAGCAGCGCTCATGGTGGGGGCAGCGCCTCACACACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGGCCAGGGGCGCGGGTGCCGGGCGGGGGTGTG	
TP53	NM_000546	44371	c.653delA	p.T218fs*36	-	17:7578218-7578218	CHP2_TP53_5	GGCGGGCCTCATGGGCACCACCACACTATGTCGAAAAGTGTTTCTGTCATCCAAATACTCCACACGCAAATTTCCTTCCACTCGGATAAGATGCTGAGGAGGGGCCAGACCTAAGAGCAC	
TP53	NM_000546	44372	c.646delC	p.H216fs*33	-	17:7578280-7578280	CHP2_TP53_5	GGCGGGCCTCATGGGCACCACCACACTATGTCGAAAAGTGTTTCTGTCATCCAAATACTCCACACGCAAATTTCCTTCCACTCGGATAAGATGCTGAGGAGGGGCCAGACCTAAGAGCAC	
TP53	NM_000546	44375	c.659T>G	p.V217G	-	17:7578199-7578199	CHP2_TP53_5	GGCGGGCCTCATGGGCACCACCACACTATGTCGAAAAGTGTTTCTGTCATCCAAATACTCCACACGCAAATTTCCTTCCACTCGGATAAGATGCTGAGGAGGGGCCAGACCTAAGAGCAC	
TP53	NM_000546	44378	c.724C>A	p.Q242*	-	17:7577555-7577555	CHP2_TP53_6	CCAGGTGTGATGTGTGAGGATGGGCCTCCGGTTCATGCCGCCCCATGCAGGAACTGTTACACATGATGGTTGTAGTGGATGTGGTGCTACGTCAGGTCACAGGCCAACCTAG	
TP53	NM_000546	44380	c.376T>A	p.Y126N	-	17:7578554-7578554	CHP2_TP53_3	GCCAGTTGGGCAAACTGACCGCATCAGAGATTCTTGAGGGCAGGGGGATACTGTAGGAGAAGGAAGGAGACAGAGTTGAAAGTCAGGGCACAAGTGA	
TP53	NM_000546	44383	c.518T>G	p.V173G	-	17:7578412-7578412	CHP2_TP53_4	CCAGCCCCAGCTGCTCACCATCGCTATCTGGAGCAGCGCTCATGGTGGGGGCAGCGCCTCACACACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGGCCAGGGGCGCGGGTGCCGGGCGGGGGTGTG	
TP53	NM_000546	44384	c.518G>A	p.T173I	-	17:7578420-7578420	CHP2_TP53_4	CCAGCCCCAGCTGCTCACCATCGCTATCTGGAGCAGCGCTCATGGTGGGGGCAGCGCCTCACACACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGGCCAGGGGCGCGGGTGCCGGGCGGGGGTGTG	
TP53	NM_000546	44387	c.491A>C	p.K164T	-	17:7578439-7578439	CHP2_TP53_4	CCAGCCCCAGCTGCTCACCATCGCTATCTGGAGCAGCGCTCATGGTGGGGGCAGCGCCTCACACACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGGCCAGGGGCGCGGGTGCCGGGCGGGGGTGTG	
TP53	NM_000546	44388	c.853G>T	p.E285*	-	17:7577088-7577088	CHP2_TP53_7	TACCTCGCCTTAGTGCTCCTGGGGGCAGCTCGTGGTGAGGGCTCCCCTTTTGTTGCGGAGATTTCTTCTTCTGCTGTGCAGTGCTGCTCACACATCCTGCGTGGGCAAGCTGACCGCATCAGAGATT	
TP53	NM_000546	44390	c.838A>T	p.R280*	-	17:7577108-7577108	CHP2_TP53_7	TACCTCGCCTTAGTGCTCCTGGGGGCAGCTCGTGGTGAGGGCTCCCCTTTTGTTGCGGAGATTTCTTCTTCTGCTGTGCAGTGCTGCTCACACATCCTGCGTGGGCAAGCTGACCGCATCAGAGATT	
TP53	NM_000546	44391	c.480C>T	p.Y163Y	-	17:7578441-7578441	CHP2_TP53_4	CCAGCCCCAGCTGCTCACCATCGCTATCTGGAGCAGCGCTCATGGTGGGGGCAGCGCCTCACACACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGGCCAGGGGCGCGGGTGCCGGGCGGGGGTGTG	
TP53	NM_000546	44393	c.821T>C	p.V274A	-	17:7577117-7577117	CHP2_TP53_6	TACCTCGCCTTAGTGCTCCTGGGGGCAGCTCGTGGTGAGGGCTCCCCTTTTGTTGCGGAGATTTCTTCTTCTGCTGTGCAGTGCTGCTCACACATCCTGCGTGGGCAAGCTGACCGCATCAGAGATT	
TP53	NM_000546	44396	c.382delC	p.P128fs*42	-	17:7578548-7578548	CHP2_TP53_3	GCCAGTTGGGCAAACTTTGTTGAGGGCAGGGGGATACTGTAGGAGAAGGAAGGAGACAGAGTTGAAAGTCAGGGCACAAGTGA	
TP53	NM_000546	44397	c.382C>T	p.P128S	-	17:7578548-7578548	CHP2_TP53_3	GCCAGTTGGGCAAACTTTGTTGAGGGCAGGGGGATACTGTAGGAGAAGGAAGGAGACAGAGTTGAAAGTCAGGGCACAAGTGA	
TP53	NM_000546	44398	c.682G>A	p.D228N	-	17:7577990-7577990	CHP2_TP53_5	CCAGGTGTGATGTGTGAGGATGGGCCTCCGGTTCATGCCGCCCCATGCAGGAACTGTTACACATGATGGTTGTAGTGGATGTGGTGCTACGTCAGGTCACAGGCCAACCTAG	
TP53	NM_000546	44399	c.673C>T	p.G225V	-	17:7578004-7578004	CHP2_TP53_5	CCAGGTGTGATGTGTGAGGATGGGCCTCCGGTTCATGCCGCCCCATGCAGGAACTGTTACACATGATGGTTGTAGTGGATGTGGTGCTACGTCAGGTCACAGGCCAACCTAG	
TP53	NM_000546	44405	c.37delG	p.Y12Lfs_K132delYSPALNK	-	17:7578534-7578534	CHP2_TP53_3	GCCAGTTGGGCAAACTTTGTTGAGGGCAGGGGGATACTGTAGGAGAAGGAAGGAGACAGAGTTGAAAGTCAGGGCACAAGTGA	
TP53	NM_000546	44407	c.642T>G	p.H214Q	-	17:7578297-7578297	CHP2_TP53_5	GGCGGGCCTCATGGGCACCACCACACTATGTCGAAAAGTGTTTCTGTCATCCAAATACTCCACACGCAAATTTCCTTCCACTCGGATAAGATGCTGAGGAGGGGCCAGACCTAAGAGCAC	
TP53	NM_000546	44411	c.608T>A	p.V203E	-	17:7578241-7578241	CHP2_TP53_5	GGCGGGCCTCATGGGCACCACCACACTATGTCGAAAAGTGTTTCTGTCATCCAAATACTCCACACGCAAATTTCCTTCCACTCGGATAAGATGCTGAGGAGGGGCCAGACCTAAGAGCAC	
TP53	NM_000546	44412	c.832C>A	p.L278I	-	17:7577096-7577096	CHP2_TP53_7	TACCTCGCCTTAGTGCTCCTGGGGGCAGCTCGTGGTGAGGGCTCCCCTTTTGTTGCGGAGATTTCTTCTTCTGCTGTGCAGTGCTGCTCACACATCCTGCGTGGGCAAGCTGACCGCATCAGAGATT	
TP53	NM_000546	44413	c.484A>G	p.I162V	-	17:7578446-7578446	CHP2_TP53_4	CCAGCCCCAGCTGCTCACCATCGCTATCTGGAGCAGCGCTCATGGTGGGGGCAGCGCCTCACACACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGGCCAGGGGCGCGGGTGCCGGGCGGGGGTGTG	
TP53	NM_000546	44415	c.711G>C	p.M237I	-	17:7577370-7577370	CHP2_TP53_6	CCAGGTGTGATGTGTGAGGATGGGCCTCCGGTTCATGCCGCCCCATGCAGGAACTGTTACACATGATGGTTGTAGTGGATGTGGTGCTACGTCAGGTCACAGGCCAACCTAG	
TP53	NM_000546	44416	c.458C>A	p.P153P	-	17:7578471-7578471	CHP2_TP53_4	CCAGCCCCAGCTGCTCACCATCGCTATCTGGAGCAGCGCTCATGGTGGGGGCAGCGCCTCACACACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGGCCAGGGGCGCGGGTGCCGGGCGGGGGTGTG	
TP53	NM_000546	44417	c.918delA	p.T304fs*41	-	17:7577028-7577028	CHP2_TP53_7	TACCTCGCCTTAGTGCTCCTGGGGGCAGCTCGTGGTGAGGGCTCCCCTTTTGTTGCGGAGATTTCTTCTTCTGCTGTGCAGTGCTGCTCACACATCCTGCGTGGGCAAGCTGACCGCATCAGAGATT	
TP53	NM_000546	44424	c.598T>A	p.Y97N	-	17:7578359-7578359	CHP2_TP53_5	GGCGGGCCTCATGGGCACCACCACACTATGTCGAAAAGTGTTTCTGTCATCCAAATACTCCACACGCAAATTTCCTTCCACTCGGATAAGATGCTGAGGAGGGGCCAGACCTAAGAGCAC	
TP53	NM_000546	44426	c.568C>G	p.P190A	-	17:7578281-7578281	CHP2_TP53_5	GGCGGGCCTCATGGGCACCACCACACTATGTCGAAAAGTGTTTCTGTCATCCAAATACTCCACACGCAAATTTCCTTCCACTCGGATAAGATGCTGAGGAGGGGCCAGACCTAAGAGCAC	
TP53	NM_000546	44428	c.741C>T	p.S247S	-	17:7577744-7577744	CHP2_TP53_6	CCAGGTGTGATGTGTGAGGATGGGCCTCCGGTTCATGCCGCCCCATGCAGGAACTGTTACACATGATGGTTGTAGTGGATGTGGTGCTACGTCAGGTCACAGGCCAACCTAG	
TP53	NM_000546	44431	c.505A>G	p.M169V	-	17:7578425-7578425	CHP2_TP53_4	CCAGCCCCAGCTGCTCACCATCGCTATCTGGAGCAGCGCTCATGGTGGGGGCAGCGCCTCACACACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGGCCAGGGGCGCGGGTGCCGGGCGGGGGTGTG	
TP53	NM_000546	44433	c.872A>C	p.K291T	-	17:7577066-7577066	CHP2_TP53_7	TACCTCGCCTTAGTGCTCCTGGGGGCAGCTCGTGGTGAGGGCTCCCCTTTTGTTGCGGAGATTTCTTCTTCTGCTGTGCAGTGCTGCTCACACATCCTGCGTGGGCAAGCTGACCGCATCAGAGATT	
TP53	NM_000546	44438	c.568C>A	p.P190T	-	17:7578281-7578281	CHP2_TP53_5	GGCGGGCCTCATGGGCACCACCACACTATGTCGAAAAGTGTTTCTGTCATCCAAATACTCCACACGCAAATTTCCTTCCACTCGGATAAGATGCTGAGGAGGGGCCAGACCTAAGAGCAC	
TP53	NM_000546	44439	c.659C>T	p.P219L	-	17:7578199-7578199	CHP2_TP53_5	GGCGGGCCTCATGGGCACCACCACACTATGTCGAAAAGTGTTTCTGTCATCCAAATACTCCACACGCAAATTTCCTTCCACTCGGATAAGATGCTGAGGAGGGGCCAGACCTAAGAGCAC	
TP53	NM_000546	44441	c.813G>C	p.E271D	-	17:7577125-7577125	CHP2_TP53_6	TACCTCGCCTTAGTGCTCCTGGGGGCAGCTCGTGGTGAGGGCTCCCCTTTTGTTGCGGAGATTTCTTCTTCTGCTGTGCAGTGCTGCTCACACATCCTGCGTGGGCAAGCTGACCGCATCAGAGATT	
TP53	NM_000546	44443	c.820G>C	p.V274L	-	17:7577118-7577118	CHP2_TP53_6	TACCTCGCCTTAGTGCTCCTGGGGGCAGCTCGTGGTGAGGGCTCCCCTTTTGTTGCGGAGATTTCTTCTTCTGCTGTGCAGTGCTGCTCACACATCCTGCGTGGGCAAGCTGACCGCATCAGAGATT	
TP53	NM_000546	44446	c.873C>G	p.K291N	-	17:7577065-7577065	CHP2_TP53_7	TACCTCGCCTTAGTGCTCCTGGGGGCAGCTCGTGGTGAGGGCTCCCCTTTTGTTGCGGAGATTTCTTCTTCTGCTGTGCAGTGCTGCTCACACATCCTGCGTGGGCAAGCTGACCGCATCAGAGATT	
TP53	NM_000546	44447	c.287C>T	p.S96F	-	17:7579480-7579480	CHP2_TP53_1	GCCCAGACGTCAAAAGTCAGTCAGTCGCCTGGTAGGTTTTCTGGGAAAGGGACACAGAAGATCACAGGGGCCAGGAGGGGGCTGGTGCAGGGGCCACGCGGGGAGACGCTGCTGGTGCAGGGGCCACGCGGGGAGACGCAGCCTC	
TP53	NM_000546	44448	c.821T>A	p.V274D	-	17:7577117-7577117	CHP2_TP53_6	TACCTCGCCTTAGTGCTCCTGGGGGCAGCTCGTGGTGAGGGCTCCCCTTTTGTTGCGGAGATTTCTTCTTCTGCTGTGCAGTGCTGCTCACACATCCTGCGTGGGCAAGCTGACCGCATCAGAGATT	
TP53	NM_000546	44451	c.874A>G	p.K292E	-	17:7577064-7577064	CHP2_TP53_7	TACCTCGCCTTAGTGCTCCTGGGGGCAGCTCGTGGTGAGGGCTCCCCTTTTGTTGCGGAGATTTCTTCTTCTGCTGTGCAGTGCTGCTCACACATCCTGCGTGGGCAAGCTGACCGCATCAGAGATT	
TP53	NM_000546	44453	c.399C>G	p.Y133*	-	17:7579378-7579378	CHP2_TP53_2	GCCCAGACGTCAAAAGTCAGTCAGTCCTGGTAGGTTTTCTGGGAAAGGGACACAGAAGATCACAGGGGCCAGGAGGGGGCTGGTGCAGGGGCCACGCGGGGAGACGCTGCTGGTGCAGGGGCCACGCGGGGAGACGCAGCCTC	
TP53	NM_000546	44457	c.751_759delATCTCACC	p.I251_T253delILT	-	17:7577522-7577500	CHP2_TP53_6	CCAGGTGTGATGTGTGAGGATGGGCCTCCGGTTCATGCCGCCCCATGCAGGAACTGTTACACATGATGGTTGTAGTGGATGTGGTGCTACGTCAGGTCACAGGCCAACCTAG	
TP53	NM_000546	44458	c.688_698delTT	p.T230fs*6	-	17:7577583-7577583	CHP2_TP53_6	CCAGGTGTGATGTGTGAGGATGGGCCTCCGGTTCATGCCGCCCCATGCAGGAACTGTTACACATGATGGTTGTAGTGGATGTGGTGCTACGTCAGGTCACAGGCCAACCTAG	
TP53	NM_000546	44460	c.757_760GACCCA	p.T253fs*91	-	17:7577521-7577524	CHP2_TP53_6	CCAGGTGTGATGTGTGAGGATGGGCCTCCGGTTCATGCCGCCCCATGCAGGAACTGTTACACATGATGGTTGTAGTGGATGTGGTGCTACGTCAGGTCACAGGCCAACCTAG	
TP53	NM_000546	44463	c.846G>T	p.R283L	-	17:7577090-7577090	CHP2_TP53_7	TACCTCGCCTTAGTGCTCCTGGGGGCAGCTCGTGGTGAGGGCTCCCCTTTTGTTGCGGAGATTTCTTCTTCTGCTGTGCAGTGCTGCTCACACATCCTGCGTGGGCAAGCTGACCGCATCAGAGATT	
TP53	NM_000546	44464	c.749_750CC>AG	p.P250Q	-	17:7577531-7577532	CHP2_TP53_6	CCAGGTGTGATGTGTGAGGATGGGCCTCCGGTTCATGCCGCCCCATGCAGGAACTGTTACACATGATGGTTGTAGTGGATGTGGTGCTACGTCAGGTCACAGGCCAACCTAG	
TP53	NM_000546	44467	c.497C>G	p.S166*	-	17:7578433-7578433	CHP2_TP53_4	CCAGCCCCAGCTGCTCACCATCGCTATCTGGAGCAGCGCTCATGGTGGGGGCAGCGCCTCACACACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGGCCAGGGGCGCGGGTGCCGGGCGGGGGTGTG	
TP53	NM_000546	44469	c.812A>T	p.E271V	-	17:7577126-7577126	CHP2_TP53_6	TACCTCGCCTTAGTGCTCCTGGGGGCAGCTCGTGGTGAGGGCTCCCCTTTTGTTGCGGAGATTTCTTCTTCTGCTGTGCAGTGCTGCTCACACATCCTGCGTGGGCAAGCTGACCGCATCAGAGATT	
TP53	NM_000546	44470	c.845G>T	p.R282L	-	17:7577093-7577093	CHP2_TP53_7	TACCTCGCCTTAGTGCTCCTGGGGGCAGCTCGTGGTGAGGGCTCCCCTTTTGTTGCGGAGATTTCTTCTTCTGCTGTGCAGTGCTGCTCACACATCCTGCGTGGGCAAGCTGACCGCATCAGAGATT	
TP53	NM_000546	44474	c.392A>G	p.N131S	-	17:7578538-7578538	CHP2_TP53_3	GCCAGTTGGGCAAACTTTGTTGAGGGCAGGGGGATACTGTAGGAGAAGGAAGGAGACAGAGTTGAAAGTCAGGGCACAAGTGA	
TP53	NM_000546	44475	c.871A>T	p.K291*	-	17:7577067-7577067	CHP2_TP53_7	TACCTCGCCTTAGTGCTCCTGGGGGCAGCTCGTGGTGAGGGCTCCCCTTTTGTTGCGGAGATTTCTTCTTCTGCTGTGCAGTGCTGCTCACACATCCTGCGTGGGCAAGCTGACCGCATCAGAGATT	
TP53	NM_000546	44476	c.749C>A	p.P250H	-	17:7577532-7577532	CHP2_TP53_6	CCAGGTGTGATGTGTGAGGATGGGCCTCCGGTTCATGCCGCCCCATGCAGGAACTGTTACACATGATGGTTGTAGTGGATGTGGTGCTACGTCAGGTCACAGGCCAACCTAG	
TP53	NM_000546	44481	c.311G>T	p.G105C	-	17:7579474-7579474	CHP2_TP53_1	GCCCAGACGTCAAAAGTCAGTCAGTCCTGGTAGGTTTTCTGGGAAAGGGACACAGAAGATCACAGGGGCCAGGAGGGGGCTGGTGCAGGGGCCACGCGGGGAGACGCTGCTGGTGCAGGGGCCACGCGGGGAGACGCAGCCTC	
TP53	NM_000546	44482	c.273G>A	p.W91*	-	17:7579614-7579614	CHP2_TP53_1	GCCCAGACGTCAAAAGTCAGTCAGTCCTGGTAGGTTTTCTGGGAAAGGGACACAGAAGATCACAGGGGCCAGGAGGGGGCTGGTGCAGGGGCCACGCGGGGAGACGCTGCTGGTGCAGGGGCCACGCGGGGAGACGCAGCCTC	
TP53	NM_000546	44495	c.559-12T>A	p.?	-	17:7578369-7578369	CHP2_TP53_5	CCAGCCCCAGCTGCTCACCATCGCTATCTGGAGCAGCGCTCATGGTGGGGGCAGCGCCTCACACACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGGCCAGGGGCGCGGGTGCCGGGCGGGGGTGTG	
TP53	NM_000546	44502	c.599A>G	p.N200S	-	17:7578250-7578250	CHP2_TP53_5	GGCGGGCCTCATGGGCACCACCACACTATGTCGAAAAGTGTTTCTGTCATCCAAATACTCCACACGCAAATTTCCTTCCACTCGGATAAGATGCTGAGGAGGGGCCAGACCTAAGAGCAC	
TP53	NM_000546	44505	c.660T>C	p.Y220*	-	17:7578189-7578189	CHP2_TP53_5	GGCGGGCCTCATGGGCACCACCACACTATGTCGAAAAGTGTTTCTGTCATCCAAATACTCCACACGCAAATTTCCTTCCACTCGGATAAGATGCTGAGGAGGGGCCAGACCTAAGAGCAC	
TP53	NM_000546	44508	c.401T>C	p.F134S	-	17:7578529-7578529	CHP2_TP53_4	GCCAGTTGGGCAAACTTTGTTGAGGGCAGGGGGATACTGTAGGAGAAGGAAGGAGACAGAGTTGAAAGTCAGGGCACAAGTGA	
TP53	NM_000546	44510	c.717C>G	p.N239K	-	17:7577564-7577564	CHP2_TP53_6	CCAGGTGTGATGTGTGAGGATGGGCCTCCGGTTCATGCCGCCCCATGCAGGAACTGTTACACATGATGGTTGTAGTGGATGTGGTGCTACGTCAGGTCACAGGCCAACCTAG	
TP53	NM_000546	44511	c.733C>A	p.L245I	-	17:7577548-7577548	CHP2_TP53_6	CCAGGTGTGATGTGTGAGGATGGGCCTCCGGTTCATGCCGCCCCATGCAGGAACTGTTACACATGATGGTTGTAGTGGATGTGGTGCTACGTCAGGTCACAGGCCAACCTAG	
TP53	NM_000546	44512	c.740A>G	p.N247S	-	17:7577541-7577541	CHP2_TP53_6	CCAGGTGTGATGTGTGAGGATGGGCCTCCGGTTCATGCCGCCCCATGCAGGAACTGTTACACATGATGGTTGTAGTGGATGTGGTGCTACGTCAGGTCACAGGCCAACCTAG	
TP53	NM_000546	44513	c.732C>A	p.G244G	-	17:7577549-7577549	CHP2_TP53_6	CCAGGTGTGATGTGTGAGGATGGGCCTCCGGTTCATGCCGCCCCATGCAGGAACTGTTACACATGATGGTTGTAGTGGATGTGGTGCTACGTCAGGTCACAGGCCAACCTAG	
TP53	NM_000546	44514	c.724T>G	p.M242R	-	17:7577555-7577555	CHP2_TP53_6	CCAGGTGTGATGTGTGAGGATGGGCCTCCGGTTCATGCCGCCCCATGCAGGAACTGTTACACATGATGGTTGTAGTGGATGTGGTGCTACGTCAGGTCACAGGCCAACCTAG	
TP53	NM_000546	44517	c.519G>A	p.V173V	-	17:7578411-7578411	CHP2_TP53_4	CCAGCCCCAGCTGCTCACCATCGCTATCTGGAGCAGCGCTCATGGTGGGGGCAGCGCCTCACACACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGGCCAGGGGCGCGGGTGCCGGGCGGGGGTGTG	
TP53	NM_000546	44518	c.522C>A	p.R174I	-	17:7578408-7578408	CHP2_TP53_4	CCAGCCCCAGCTGCTCACCATCGCTATCTGGAGCAGCGCTCATGGTGGGGGCAGCGCCTCACACACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGGCCAGGGGCGCGGGTGCCGGGCGGGGGTGTG	
TP53	NM_000546	44521	c.490A>C	p.K164Q	-	17:7578440-7578440	CHP2_TP53_4	CCAGCCCCAGCTGCTCACCATCGCTATCTGGAGCAGCGCTCATGGTGGGGGCAGCGCCTCACAC

TP53	NM_000546	44948	c.526T>C	p.C176R	-	17:7578406-7578406	CHP2_TP53_4	CHP2_TP53_4	CCAGCCCCAGCTGCTACCATGCTGATGCAGCAGCCTGACAGATGGCCATGGCCGGGGCGGGCGGTGTG
TP53	NM_000546	44953	c.700_702delTAC	p.Y234del	-	17:7577539-7577581	CHP2_TP53_5	CHP2_TP53_5	CCAGTGTGATGATGGTGAGGATGGGCCTCGGTTCATGCCGCCCATGCAGGAACTGTTACACATGATAGTTGTAGTGGATGATGGTGGTACAGTCAGAGCCAACCTAG
TP53	NM_000546	44956	c.808T>G	p.F270V	-	17:7576850-7577138	CHP2_TP53_7	CHP2_TP53_7	TACCTGCCTCATGTCCTCCTGGGGGCAGCTGCTGGTGAGGGACCTCGTGGTGATGGGCCTCGGTTCATGCCGCCCATGCAGGAACTGTTACACATGATAGTTGTAGTGGATGATGGTGGTACAGTCAGAGCCAACCTAG
TP53	NM_000546	44960	c.788C>G	p.T263R	-	17:7577035-7577373	CHP2_TP53_7	CHP2_TP53_7	CCAGTGTGATGATGGTGAGGATGGGCCTCGGTTCATGCCGCCCATGCAGGAACTGTTACACATGATAGTTGTAGTGGATGATGGTGGTACAGTCAGAGCCAACCTAG
TP53	NM_000546	44964	c.719C>T	p.S240T	-	17:7577562-7577562	CHP2_TP53_7	CHP2_TP53_7	CCAGTGTGATGATGGTGAGGATGGGCCTCGGTTCATGCCGCCCATGCAGGAACTGTTACACATGATAGTTGTAGTGGATGATGGTGGTACAGTCAGAGCCAACCTAG
TP53	NM_000546	44965	c.709A>T	p.M237L	-	17:7577572-7577572	CHP2_TP53_6	CHP2_TP53_6	CCAGTGTGATGATGGTGAGGATGGGCCTCGGTTCATGCCGCCCATGCAGGAACTGTTACACATGATAGTTGTAGTGGATGATGGTGGTACAGTCAGAGCCAACCTAG
TP53	NM_000546	44968	c.383G>A	p.A129T	-	17:7578545-7578545	CHP2_TP53_2	CHP2_TP53_2	GCCAGTTGGCCAAACACTTTGTTGGGGCAGGGGAGTACTGTAGGAGAAGGAAGGAGACAGGTGAAAGGTCAGGGCACAGATGA
TP53	NM_000546	44971	c.534C>T	p.H178H	-	17:7578396-7578396	CHP2_TP53_4	CHP2_TP53_4	CCAGCCCCAGCTGCTACCATGCTGATCTGAGCAGCGCTCATGGTGGGGGCAGCGCTCACACACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGCCATGGCCGGGGCGGGCGGTGTG
TP53	NM_000546	44972	c.831T>A	p.C277*	-	17:7577107-7577107	CHP2_TP53_7	CHP2_TP53_7	TACCTGCCTCATGTCCTCCTGGGGGCAGCTGCTGGTGAGGGACCTCGTGGTGATGGGCCTCGGTTCATGCCGCCCATGCAGGAACTGTTACACATGATAGTTGTAGTGGATGATGGTGGTACAGTCAGAGCCAACCTAG
TP53	NM_000546	44973	c.514T>C	p.V172V	-	17:7578414-7578414	CHP2_TP53_4	CHP2_TP53_4	CCAGCCCCAGCTGCTACCATGCTGATCTGAGCAGCGCTCATGGTGGGGGCAGCGCTCACACACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGCCATGGCCGGGGCGGGCGGTGTG
TP53	NM_000546	44979	c.645T>G	p.S215R	-	17:7578206-7578206	CHP2_TP53_4	CHP2_TP53_4	GGCAGGCCATGCAGGAACTGTTACACATGATAGTTGTAGTGGATGATGGTGGTACAGTCAGAGCCAACCTAGGGGGCCTATGGGAGAGCCGCCTGAGGTTCATGCCGCCCATGCAGGAACTGTTACACATGATAGTTGTAGTGGATGATGGTGGTACAGTCAGAGCCAACCTAGGGGGCAGCAGCCTGACAGATGGCCATGGCCGGGGCGGGCGGTGTG
TP53	NM_000546	44986	c.382G>C	p.E128Q	-	17:7578407-7578407	CHP2_TP53_2	CHP2_TP53_2	GCCAGTTGGCCAAACACTTTGTTGGGGCAGGGGAGTACTGTAGGAGAAGGAAGGAGACAGGTGAAAGGTCAGGGCACAGATGA
TP53	NM_000546	44996	c.515T>C	p.V172A	-	17:7578415-7578415	CHP2_TP53_4	CHP2_TP53_4	CCAGCCCCAGCTGCTACCATGCTGATCTGAGCAGCGCTCATGGTGGGGGCAGCGCTCACACACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGCCATGGCCGGGGCGGGCGGTGTG
BRAF	NM_004333	449	c.1391G>A	p.G464E	-	7:140481417-140481417	CHP2_BRAF_1	CHP2_BRAF_1	GTAGACTGTTCCAAATGATCCAGATCCAATTCTTTGCTCCACTGTAATACTCTCCATCATCACTCAGTACTCCTCCAATCATCTCCAGTCCTGCTCATCCAAGTCTTTCTGATAAAAACAGTAAAAAAG
TP53	NM_000546	45005	c.758A>G	p.N253S	-	17:7577942-7577942	CHP2_TP53_7	CHP2_TP53_7	CCAGTGTGATGATGGTGAGGATGGGCCTCGGTTCATGCCGCCCATGCAGGAACTGTTACACATGATAGTTGTAGTGGATGATGGTGGTACAGTCAGAGCCAACCTAG
TP53	NM_000546	45015	c.380_381CC>TT	p.S127F	-	17:7578549-7578550	CHP2_TP53_3	CHP2_TP53_3	GCCAGTTGGCCAAACACTTTGTTGGGGCAGGGGAGTACTGTAGGAGAAGGAAGGAGACAGGTGAAAGGTCAGGGCACAGATGA
TP53	NM_000546	45016	c.722_723CT>TT	p.S241F	-	17:7577556-7577557	CHP2_TP53_7	CHP2_TP53_7	CCAGTGTGATGATGGTGAGGATGGGCCTCGGTTCATGCCGCCCATGCAGGAACTGTTACACATGATAGTTGTAGTGGATGATGGTGGTACAGTCAGAGCCAACCTAG
TP53	NM_000546	45019	c.471_472CC>TT	p.R158C	-	17:7578458-7578459	CHP2_TP53_5	CHP2_TP53_5	CCAGCCCCAGCTGCTACCATGCTGATCTGAGCAGCGCTCATGGTGGGGGCAGCGCTCACACACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGCCATGGCCGGGGCGGGCGGTGTG
TP53	NM_000546	45021	c.585_586delCT	p.R196*	-	17:7578262-7578264	CHP2_TP53_6	CHP2_TP53_6	CCAGCCCCAGCTGCTACCATGCTGATCTGAGCAGCGCTCATGGTGGGGGCAGCGCTCACACACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGCCATGGCCGGGGCGGGCGGTGTG
TP53	NM_000546	45025	c.488A>C	p.Y163S	-	17:7578442-7578442	CHP2_TP53_4	CHP2_TP53_4	CCAGCCCCAGCTGCTACCATGCTGATCTGAGCAGCGCTCATGGTGGGGGCAGCGCTCACACACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGCCATGGCCGGGGCGGGCGGTGTG
TP53	NM_000546	45028	c.560-2A>T	p.?	-	17:7578289-7578289	CHP2_TP53_5	CHP2_TP53_5	GCCAGTTGGCCAAACACTTTGTTGGGGCAGGGGAGTACTGTAGGAGAAGGAAGGAGACAGGTGAAAGGTCAGGGCACAGATGA
TP53	NM_000546	45028	c.684C>T	p.D228D	-	17:7577997-7577997	CHP2_TP53_6	CHP2_TP53_6	CAGGTGTGATGATGGTGAGGATGGGCCTCGGTTCATGCCGCCCATGCAGGAACTGTTACACATGATAGTTGTAGTGGATGATGGTGGTACAGTCAGAGCCAACCTAG
TP53	NM_000546	45029	c.585_591delGT	p.A189_V197delAPPGHLIEV	-	17:7578258-7578284	CHP2_TP53_5	CHP2_TP53_5	GGCGGCCCATAGGGCACCACCACCACTATGGAAAAGTGTTTCTGTCATCCAAATACTCCACACGCAAATTTCCTTCCATCTGGATAAGATGCTGAGGAGGGGCCAGACCTAGAAGGGA
TP53	NM_000546	45032	c.716T>G	p.M238R	-	17:7577571-7577571	CHP2_TP53_7	CHP2_TP53_7	CCAGTGTGATGATGGTGAGGATGGGCCTCGGTTCATGCCGCCCATGCAGGAACTGTTACACATGATAGTTGTAGTGGATGATGGTGGTACAGTCAGAGCCAACCTAG
TP53	NM_000546	45034	c.748_749GC>AA	p.P250N	-	17:7577532-7577533	CHP2_TP53_7	CHP2_TP53_7	CCAGTGTGATGATGGTGAGGATGGGCCTCGGTTCATGCCGCCCATGCAGGAACTGTTACACATGATAGTTGTAGTGGATGATGGTGGTACAGTCAGAGCCAACCTAG
TP53	NM_000546	45035	c.761T>G	p.I254S	-	17:7577520-7577520	CHP2_TP53_7	CHP2_TP53_7	CCAGTGTGATGATGGTGAGGATGGGCCTCGGTTCATGCCGCCCATGCAGGAACTGTTACACATGATAGTTGTAGTGGATGATGGTGGTACAGTCAGAGCCAACCTAG
TP53	NM_000546	45040	c.321C>A	p.Y107*	-	17:7579366-7579366	CHP2_TP53_2	CHP2_TP53_2	GCCCAGACGAGGAAGCGTCAGCTGCCTGGTAGGTTTTCTGGGAAGGGACACAGAAGATGACAGGGGCCAGAGGGGGCTGGTGCAGGGGGCCGCCGCTGTAGGAGCTGCTGGTGCAGGGGCCACGGGGCAGCAGCCTG
TP53	NM_000546	45044	c.576G>T	p.E192D	-	17:7578673-7578673	CHP2_TP53_5	CHP2_TP53_5	CCAGTGTGATGATGGTGAGGATGGGCCTCGGTTCATGCCGCCCATGCAGGAACTGTTACACATGATAGTTGTAGTGGATGATGGTGGTACAGTCAGAGCCAACCTAG
TP53	NM_000546	45045	c.695T>G	p.I232S	-	17:7577586-7577586	CHP2_TP53_6	CHP2_TP53_6	CAGGTGTGATGATGGTGAGGATGGGCCTCGGTTCATGCCGCCCATGCAGGAACTGTTACACATGATAGTTGTAGTGGATGATGGTGGTACAGTCAGAGCCAACCTAG
TP53	NM_000546	45046	c.542G>C	p.R181P	-	17:7578388-7578388	CHP2_TP53_6	CHP2_TP53_6	CCAGCCCCAGCTGCTACCATGCTGATCTGAGCAGCGCTCATGGTGGGGGCAGCGCTCACACACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGCCATGGCCGGGGCGGGCGGTGTG
TP53	NM_000546	45047	c.515T>G	p.V172G	-	17:7578414-7578414	CHP2_TP53_4	CHP2_TP53_4	CCAGCCCCAGCTGCTACCATGCTGATCTGAGCAGCGCTCATGGTGGGGGCAGCGCTCACACACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGCCATGGCCGGGGCGGGCGGTGTG
TP53	NM_000546	45050	c.871A>G	p.K291E	-	17:7577867-7577867	CHP2_TP53_7	CHP2_TP53_7	TACCTGCCTCATGTCCTCCTGGGGGCAGCTGCTGGTGAGGGACCTCGTGGTGATGGGCCTCGGTTCATGCCGCCCATGCAGGAACTGTTACACATGATAGTTGTAGTGGATGATGGTGGTACAGTCAGAGCCAACCTAG
TP53	NM_000546	45051	c.559A>G	p.I187V	-	17:7578275-7578275	CHP2_TP53_5	CHP2_TP53_5	GGCAGGCCATGCAGGAACTGTTACACATGATAGTTGTAGTGGATGATGGTGGTACAGTCAGAGCCAACCTAGGGGGCCTATGGGAGAGCCGCCTGAGGTTCATGCCGCCCATGCAGGAACTGTTACACATGATAGTTGTAGTGGATGATGGTGGTACAGTCAGAGCCAACCTAGGGGGCAGCAGCCTGACAGATGGCCATGGCCGGGGCGGGCGGTGTG
TP53	NM_000546	45055	c.715_720delAACAGT	p.N239_S240delNS	-	17:7577561-7577566	CHP2_TP53_7	CHP2_TP53_7	CCAGTGTGATGATGGTGAGGATGGGCCTCGGTTCATGCCGCCCATGCAGGAACTGTTACACATGATAGTTGTAGTGGATGATGGTGGTACAGTCAGAGCCAACCTAG
TP53	NM_000546	45057	c.475delG	p.A159fs*11	-	17:7578453-7578453	CHP2_TP53_5	CHP2_TP53_5	GGCAGGCCATGCAGGAACTGTTACACATGATAGTTGTAGTGGATGATGGTGGTACAGTCAGAGCCAACCTAGGGGGCCTATGGGAGAGCCGCCTGAGGTTCATGCCGCCCATGCAGGAACTGTTACACATGATAGTTGTAGTGGATGATGGTGGTACAGTCAGAGCCAACCTAGGGGGCAGCAGCCTGACAGATGGCCATGGCCGGGGCGGGCGGTGTG
TP53	NM_000546	45069	c.886delC	p.H296fs*40	-	17:7577052-7577052	CHP2_TP53_7	CHP2_TP53_7	TACCTGCCTCATGTCCTCCTGGGGGCAGCTGCTGGTGAGGGACCTCGTGGTGATGGGCCTCGGTTCATGCCGCCCATGCAGGAACTGTTACACATGATAGTTGTAGTGGATGATGGTGGTACAGTCAGAGCCAACCTAG
TP53	NM_000546	45074	c.829T>G	p.C277G	-	17:7577108-7577108	CHP2_TP53_7	CHP2_TP53_7	TACCTGCCTCATGTCCTCCTGGGGGCAGCTGCTGGTGAGGGACCTCGTGGTGATGGGCCTCGGTTCATGCCGCCCATGCAGGAACTGTTACACATGATAGTTGTAGTGGATGATGGTGGTACAGTCAGAGCCAACCTAG
TP53	NM_000546	45077	c.396C>T	p.L132L	-	17:7578640-7578640	CHP2_TP53_2	CHP2_TP53_2	GCCAGTTGGCCAAACACTTTGTTGGGGCAGGGGAGTACTGTAGGAGAAGGAAGGAGACAGGTGAAAGGTCAGGGCACAGATGA
TP53	NM_000546	45084	c.746G>A	p.R248H	-	17:7577537-7577537	CHP2_TP53_7	CHP2_TP53_7	CCAGTGTGATGATGGTGAGGATGGGCCTCGGTTCATGCCGCCCATGCAGGAACTGTTACACATGATAGTTGTAGTGGATGATGGTGGTACAGTCAGAGCCAACCTAG
TP53	NM_000546	45089	c.487A>C	p.Q163P	-	17:7578452-7578452	CHP2_TP53_5	CHP2_TP53_5	GGCAGTTGGCCAAACACTTTGTTGGGGCAGGGGAGTACTGTAGGAGAAGGAAGGAGACAGGTGAAAGGTCAGGGCACAGATGA
TP53	NM_000546	45091	c.755T>A	p.L252H	-	17:7577526-7577526	CHP2_TP53_7	CHP2_TP53_7	CCAGTGTGATGATGGTGAGGATGGGCCTCGGTTCATGCCGCCCATGCAGGAACTGTTACACATGATAGTTGTAGTGGATGATGGTGGTACAGTCAGAGCCAACCTAG
BRAF	NM_004333	450	c.1391G>T	p.G464V	-	7:140481417-140481417	CHP2_BRAF_1	CHP2_BRAF_1	GTAGACTGTTCCAAATGATCCAGATCCAATTCTTTGCTCCACTGTAATACTCTCCATCATCACTCAGTACTCCTCCAATCATCTCCAGTCCTGCTCATCCAAGTCTTTCTGATAAAAACAGTAAAAAAG
TP53	NM_000546	45101	c.913_914AG>TAA	p.K305*	-	17:7577023-7577023	CHP2_TP53_7	CHP2_TP53_7	TACCTGCCTCATGTCCTCCTGGGGGCAGCTGCTGGTGAGGGACCTCGTGGTGATGGGCCTCGGTTCATGCCGCCCATGCAGGAACTGTTACACATGATAGTTGTAGTGGATGATGGTGGTACAGTCAGAGCCAACCTAG
TP53	NM_000546	45103	c.493C>A	p.R164L	-	17:7578438-7578438	CHP2_TP53_5	CHP2_TP53_5	GGCAGGCCATGCAGGAACTGTTACACATGATAGTTGTAGTGGATGATGGTGGTACAGTCAGAGCCAACCTAGGGGGCCTATGGGAGAGCCGCCTGAGGTTCATGCCGCCCATGCAGGAACTGTTACACATGATAGTTGTAGTGGATGATGGTGGTACAGTCAGAGCCAACCTAGGGGGCAGCAGCCTGACAGATGGCCATGGCCGGGGCGGGCGGTGTG
TP53	NM_000546	45109	c.831T>C	p.C277C	-	17:7577107-7577107	CHP2_TP53_7	CHP2_TP53_7	TACCTGCCTCATGTCCTCCTGGGGGCAGCTGCTGGTGAGGGACCTCGTGGTGATGGGCCTCGGTTCATGCCGCCCATGCAGGAACTGTTACACATGATAGTTGTAGTGGATGATGGTGGTACAGTCAGAGCCAACCTAG
TP53	NM_000546	45110	c.650T>C	p.V217A	-	17:7578199-7578199	CHP2_TP53_5	CHP2_TP53_5	GGCAGGCCATGCAGGAACTGTTACACATGATAGTTGTAGTGGATGATGGTGGTACAGTCAGAGCCAACCTAGGGGGCCTATGGGAGAGCCGCCTGAGGTTCATGCCGCCCATGCAGGAACTGTTACACATGATAGTTGTAGTGGATGATGGTGGTACAGTCAGAGCCAACCTAGGGGGCAGCAGCCTGACAGATGGCCATGGCCGGGGCGGGCGGTGTG
TP53	NM_000546	45111	c.469_470delCTCCG	p.V157fs*22	-	17:7578475-7578461	CHP2_TP53_5	CHP2_TP53_5	CAGGTGTGATGATGGTGAGGATGGGCCTCGGTTCATGCCGCCCATGCAGGAACTGTTACACATGATAGTTGTAGTGGATGATGGTGGTACAGTCAGAGCCAACCTAG
TP53	NM_000546	45114	c.782C>A	p.T261N	-	17:7577519-7577519	CHP2_TP53_7	CHP2_TP53_7	CCAGTGTGATGATGGTGAGGATGGGCCTCGGTTCATGCCGCCCATGCAGGAACTGTTACACATGATAGTTGTAGTGGATGATGGTGGTACAGTCAGAGCCAACCTAG
TP53	NM_000546	45115	c.648C>G	p.H216Q	-	17:7578200-7578200	CHP2_TP53_5	CHP2_TP53_5	GGCAGGCCATGCAGGAACTGTTACACATGATAGTTGTAGTGGATGATGGTGGTACAGTCAGAGCCAACCTAGGGGGCCTATGGGAGAGCCGCCTGAGGTTCATGCCGCCCATGCAGGAACTGTTACACATGATAGTTGTAGTGGATGATGGTGGTACAGTCAGAGCCAACCTAGGGGGCAGCAGCCTGACAGATGGCCATGGCCGGGGCGGGCGGTGTG
TP53	NM_000546	45116	c.742delC	p.R248fs*7	-	17:7577539-7577539	CHP2_TP53_7	CHP2_TP53_7	CCAGTGTGATGATGGTGAGGATGGGCCTCGGTTCATGCCGCCCATGCAGGAACTGTTACACATGATAGTTGTAGTGGATGATGGTGGTACAGTCAGAGCCAACCTAG
TP53	NM_000546	45128	c.469G>C	p.V157L	-	17:7578476-7578476	CHP2_TP53_5	CHP2_TP53_5	CAGGTGTGATGATGGTGAGGATGGGCCTCGGTTCATGCCGCCCATGCAGGAACTGTTACACATGATAGTTGTAGTGGATGATGGTGGTACAGTCAGAGCCAACCTAG
TP53	NM_000546	45122	c.845T>A	p.I282N	-	17:7578204-7578204	CHP2_TP53_5	CHP2_TP53_5	GGCGGGCCATAGGGCACCACCACCACTATGTCGAAAAGTGTTTCTGTCATCCAAATACTCCACACGCAAATTTCCTTCCATCTGGATAAGATGCTGAGGAGGGGCCAGACCTAGAAGGGA
TP53	NM_000546	45128	c.91C>T	p.T394I	-	17:7579927-7579927	CHP2_TP53_2	CHP2_TP53_2	TACCTGCCTCATGTCCTCCTGGGGGCAGCTGCTGGTGAGGGACCTCGTGGTGATGGGCCTCGGTTCATGCCGCCCATGCAGGAACTGTTACACATGATAGTTGTAGTGGATGATGGTGGTACAGTCAGAGCCAACCTAG
TP53	NM_000546	45131	c.38A>T	p.P12L	-	17:7579547-7579547	CHP2_TP53_2	CHP2_TP53_2	GCCATGGTTGGAAAACACTTTGTTGGGGCAGGGGAGTACTGTAGGAGAAGGAAGGAGACAGGTGAAAGGTCAGGGCACAGATGA
TP53	NM_000546	45134	c.715_726delI12	p.N239_C242delNSSC	-	17:7577555-7577566	CHP2_TP53_7	CHP2_TP53_7	CCAGTGTGATGATGGTGAGGATGGGCCTCGGTTCATGCCGCCCATGCAGGAACTGTTACACATGATAGTTGTAGTGGATGATGGTGGTACAGTCAGAGCCAACCTAG
TP53	NM_000546	45138	c.853G>C	p.E285Q	-	17:7577885-7577885	CHP2_TP53_7	CHP2_TP53_7	TACCTGCCTCATGTCCTCCTGGGGGCAGCTGCTGGTGAGGGACCTCGTGGTGATGGGCCTCGGTTCATGCCGCCCATGCAGGAACTGTTACACATGATAGTTGTAGTGGATGATGGTGGTACAGTCAGAGCCAACCTAG
TP53	NM_000546	45140	c.572_574delCTC	p.P191del	-	17:7578275-7578273	CHP2_TP53_5	CHP2_TP53_5	GGCAGGCCATGCAGGAACTGTTACACATGATAGTTGTAGTGGATGATGGTGGTACAGTCAGAGCCAACCTAGGGGGCCTATGGGAGAGCCGCCTGAGGTTCATGCCGCCCATGCAGGAACTGTTACACATGATAGTTGTAGTGGATGATGGTGGTACAGTCAGAGCCAACCTAGGGGGCAGCAGCCTGACAGATGGCCATGGCCGGGGCGGGCGGTGTG
TP53	NM_000546	45154	c.466C>G	p.R156G	-	17:7578444-7578444	CHP2_TP53_5	CHP2_TP53_5	CCAGCCCCAGCTGCTACCATGCTGATCTGAGCAGCGCTCATGGTGGGGGCAGCGCTCACACACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGCCATGGCCGGGGCGGGCGGTGTG
TP53	NM_000546	45157	c.688delA	p.T230fs*17	-	17:7577991-7577991	CHP2_TP53_6	CHP2_TP53_6	CAGGTGTGATGATGGTGAGGATGGGCCTCGGTTCATGCCGCCCATGCAGGAACTGTTACACATGATAGTTGTAGTGGATGATGGTGGTACAGTCAGAGCCAACCTAG
TP53	NM_000546	45162	c.799delA	p.M267fs*10	-	17:7577372-7577372	CHP2_TP53_6	CHP2_TP53_6	CAGTGTGATGATGGTGAGGATGGGCCTCGGTTCATGCCGCCCATGCAGGAACTGTTACACATGATAGTTGTAGTGGATGATGGTGGTACAGTCAGAGCCAACCTAG
TP53	NM_000546	45168	c.722_724delCCT	p.S241del	-	17:7577555-7577559	CHP2_TP53_7	CHP2_TP53_7	CCAGTGTGATGATGGTGAGGATGGGCCTCGGTTCATGCCGCCCATGCAGGAACTGTTACACATGATAGTTGTAGTGGATGATGGTGGTACAGTCAGAGCCAACCTAG
TP53	NM_000546	45169	c.326T>C	p.F109S	-	17:7579561-7579561	CHP2_TP53_2	CHP2_TP53_2	GCCGAGCGGGAAGCCGCTGAGCTGCCTGGTAGGTTTTCTGGGAAGGGACACAGAAGATGACAGGGGCCAGAGGGGGCTGGTGCAGGGGGCCGCCGCTGTAGGAGCTGCTGGTGCAGGGGCCACGGGGCAGCAGCCTG
TP53	NM_000546	45172	c.761A>T	p.N253V	-	17:7577520-7577520	CHP2_TP53_7	CHP2_TP53_7	CCAGTGTGATGATGGTGAGGATGGGCCTCGGTTCATGCCGCCCATGCAGGAACTGTTACACATGATAGTTGTAGTGGATGATGGTGGTACAGTCAGAGCCAACCTAG
TP53	NM_000546	45178	c.832delC	p.P278fs*67	-	17:7577506-7577506	CHP2_TP53_7	CHP2_TP53_7	TACCTGCCTCATGTCCTCCTGGGGGCAGCTGCTGGTGAGGGACCTCGTGGTGATGGGCCTCGGTTCATGCCGCCCATGCAGGAACTGTTACACATGATAGTTGTAGTGGATGATGGTGGTACAGTCAGAGCCAACCTAG
TP53	NM_000546	45179	c.313G>C	p.G105R	-	17:7579374-7579374	CHP2_TP53_2	CHP2_TP53_2	GCCAGACGCAGGAAGCCGCTGAGCTGCCTGGTAGGTTTTCTGGGAAGGGACACAGAAGATGACAGGGGCCAGAGGGGGCTGGTGCAGGGGGCCGCCGCTGTAGGAGCTGCTGGTGCAGGGGCCACGGGGCAGCAGCCTG
TP53	NM_000546	45184	c.902delC	p.P301fs*44	-	17:7576936-7576936	CHP2_TP53_8	CHP2_TP53_8	TACCTGCCTCATGTCCTCCTGGGGGCAGCTGCTGGTGAGGGACCTCGTGGTGATGGGCCTCGGTTCATGCCGCCCATGCAGGAACTGTTACACATGATAGTTGTAGTGGATGATGGTGGTACAGTCAGAGCCAACCTAG
TP53	NM_000546	45187	c.498_499delGG	p.K166fs*22	-	17:7578431-7578440	CHP2_TP53_5	CHP2_TP53_5	GGCAGGCCATGCAGGAACTGTTACACATGATAGTTGTAGTGGATGATGGTGGTACAGTCAGAGCCAACCTAGGGGGCCTATGGGAGAGCCGCCTGAGGTTCATGCCGCCCATGCAGGAACTGTTACACATGATAGTTGTAGTGGATGATGGTGGTACAGTCAGAGCCAACCTAGGGGGCAGCAGCCTGACAGATGGCCATGGCCGGGGCGGGCGGTGTG
TP53	NM_000546	45188	c.847delC	p.R283fs*62	-	17:7577991-7577991	CHP2_TP53_7	CHP2_TP53_7	TACCTGCCTCATGTCCTCCTGGGGGCAGCTGCTGGTGAGGGACCTCGTGGTGATGGGCCTCGGTTCATGCCGCCCATGCAGGAACTGTTACACATGATAGTTGTAGTGGATGATGGTGGTACAGTCAGAGCCAACCTAG
TP53	NM_000546	45194	c.487delT	p.Y163fs*	-	17:7578443-7578443	CHP2_TP53_5	CHP2_TP53_5	CCAGCCCCAGCTGCTACCATGCTGATCTGAGCAGCGCTCATGGTGGGGGCAGCGCTCACACACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGCCATGGCCGGGGCGGGCGGTGTG
TP53	NM_000546	45198	c.535C>T	p.S185S	-	17:7578375-7578375	CHP2_TP53_5	CHP2_TP53_5	CCAGCCCCAGCTGCTACCATGCTGATCTGAGCAGCGCTCATGGTGGGGGCAGCGCTCACACACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGCCATGGCCGGGGCGGGCGGTGTG
BRAF	NM_004333	451	c.1397G>T	p.G466V	-	7:140481411-140481411	CHP2_BRAF_1	CHP2_BRAF_1	GTAGACTGTTCCAAATGATCCAGATCCAATTCTTTGCTCCACTGTAATACTCTCCATCATCACTCAGTACTCCTCCAATCATCTCCAGTCCTGCTCATCCAAGTCTTTCTGATAAAAACAGTAAAAAAG
TP53	NM_000546	45208	c.233C>T	p.A79V	-	17:7579664-7579664	CHP2_TP53_2	CHP2_TP53_2	GCCCAGACGAGGAAGCCGCTGAGCTGCCTGGTAGGTTTTCTGGGAAGGGACACAGAAGATGACAGGGGCCAGAGGGGGCTGGTGCAGGGGGCCGCCGCTGTAGGAGCTGCTGGTGCAGGGGCCACGGGGCAGCAGCCTG
TP53	NM_000546	45233	c.884C>T	p.P295L	-	17:7577954-7577954	CHP2_TP53_7	CHP2_TP53_7	TACCTGCCTCATGTCCTCCTGGGGGCAGCTGCTGGTGAGGGACCTCGTGGTGATGGGCCTCGGTTCATGCCGCCCATGCAGGAACTGTTACACATGATAGTTGTAGTGGATGATGGTGGTACAGTCAGAGCCAACCTAG
TP53	NM_000546	45240	c.568G>T	p.G190V	-	17:7578289-7578289	CHP2_TP53_5	CHP2_TP53_5	GGCAGGCCATGCAGGAACTGTTACACATGATAGTTGTAGTGGATGATGGTGGTACAGTCAGAGCCAACCTAGGGGGCCTATGGGAGAGCCGCCTGAGGTTCATGCCGCCCATGCAGGAACTGTTACACATGATAGTTGTAGTGGATGATGGTGGTACAGTCAGAGCCAACCTAGGGGGCAGCAGCCTGACAGATGGCCATGGCCGGGGCGGGCGGTGTG
TP53	NM_000546	45248	c.895A>T	p.S299C	-	17:7577133-7577133	CHP2_TP53_7	CHP2_TP53_7	TACCTGCCTCATGTCCTCCTGGGGGCAGCTGCTGGTGAGGGACCTCGTGGTGATGGGCCTCGGTTCATGCCGCCCATGCAGGAACTGTTACACATGATAGTTGTAGTGGATGATGGTGGTACAGTCAGAGCCAACCTAG
TP53	NM_000546	45253	c.611A>G	p.E204G	-	17:7578238-7578238	CHP2_TP53_5	CHP2_TP53_5	GGCGGGCCATAGGGCACCACCACCACTATGTCGAAAAGTGTTTCTGTCATCCAAATACTCCACACGCAAATTTCCTTCCATCTGGATAAGATGCTGAGGAGGGGCCAGACCTAGAAGGGA
TP53	NM_000546	45257	c.626G>C	p.R209T	-	17:7578222-7578222	CHP2_TP53_5	CHP2_TP53_5	GGCAGGCCATGCAGGAACTGTTACACATGATAGTTGTAGTGGATGATGGTGGTACAGTCAGAGCCAACCTAGGGGGCCTATGGGAGAGCCGCCTGAGGTTCATGCCGCCCATGCAGGAACTGTTACACATGATAGTTGTAGTGGATGATGGTGGTACAGTCAGAGCCAACCTAGGGGGCAGCAGCCTGACAGATGGCCATGGCCGGGGCGGGCGGTGTG
TP53	NM_000546	45261	c.720T>A	p.S240R	-	17:7577551-7577561	CHP2_TP53_7	CHP2_TP53_7	CCAGTGTGATGATGGTGAGGATGGGCCTCGGTTCATGCCGCCCATGCAGGAACTGTTACACATGATAGTTGTAGTGGATGATGGTGGTACAGTCAGAGCCAACCTAG
TP53	NM_000546	45268	c.827C>A	p.A276D	-	17:7577111-7577111	CHP2_TP53_7	CHP2_TP53_7	TACCTGCCTCATGTCCTCCTGGGGGCAGCTGCTGGTGAGGGACCTCGTGGTGATGGGCCTCGGTTCATGCCGCCCATGCAGGAACTGTTACACATGATAGTTGTAGTGGATGATGGTGGTACAGTCAGAGCCAACCTAG
TP53	NM_000546	45275	c.559G>T	p.G187C	-	17:7578371-7578371	CHP2_TP53_5	CHP2_TP53_5	CCAGCCCCAGCTGCTACCATGCTGATCTGAGCAGCGCTCATGGTGGGGGCAGCGCTCACACACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGCCATGGCCGGGGCGGGCGGTGTG
TP53	NM_000546	45277	c.1025G>C	p.R342P	-	17:7576148-7576148	CHP2_TP53_8	CHP2_TP53_8	GGCGGGCCATAGGGCACCACCACCACTATGTCGAAAAGTGTTTCTGTCATCCAAATACTCCACACGCAAATTTCCTTCCATCTGGATAAGATGCTGAGGAGGGGCCAGACCTAGAAGGGA
TP53	NM_000546	45277	c.856delG	p.E286fs*59	-	17:7577882-7577882	CHP2_TP53_7	CHP2_TP53_7	TACCTGCCTCATGTCCTCCTGGGGGCAGCTGCTGGTGAGGGACCTCGTGGTGATGGGCCTCGGTTCATGCCGCCCATGCAGGAACTGTTACACATGATAGTTGTAGTGGATGATGGTGGTACAGTCAGAGCCAACCTAG
TP53	NM_000546	45278	c.1025G>A	p.R342Q	-	17:7576982-7576982	CHP2_TP53_8	CHP2_TP53_8	CACCTGGGATGGACCTGCTCCCCCTGGCTCCTTCCCAGCCTGGGACATCCTTGAGTTCCAAGGCTCATTCAGCTCCTGGAACATCTCGAAGCGCTCACGCCACGGATCT
TP53	NM_000546	45284	c.813C>A	p.S271E	-	17:7577125-7577125	CHP2_TP53_7	CHP2_TP53_7	TACCTGCCTCATGTCCTCCTGGGGGCAGCTGCTGGTGAGGGACCTCGTGGTGATGGGCCTCGGTTCATGCCGCCCATGCAGGAACTGTTACACATGATAGTTGTAGTGGATGATGGTGGTACAGTCAGAGCCAACCTAG
TP53	NM_000546	45286	c.475G>T	p.A159S	-	17:7578455-7578455	CHP2_TP53_5	CHP2_TP53_5	CCAGCCCCAGCTGCTACCATGCTGATCTGAGCAGCGCTCATGGTGGGGGCAGCGCTCACACACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGCCATGGCCGGGGCGGGCGGTGTG
TP53	NM_000546	45288	c.213C>G	p.Y71X	-	17:7579470-7579470	CHP2_T

TP53	NM_000546	46336	c.712T>G	p.C238G	-	17:7577569-7577569	CHP2_TP53_6	CCAGGTGTGATGATGGTGAGGATGGGCCTCGGTTCATGCCGCCCATGCAGGAACTGTTACACGTGCATTGTAGTGGTGATGGTGGTGACAGTCACAGAGCCAACCTAG
TP53	NM_000546	46348	c.1046G>T	p.L348F	-	17:7573983-7573983	CHP2_TP53_8	CACCTGGAGTGAGCCCTGCTCCCCCCTGGCTCCTTCCCAGCCTGGGCATCCTTGAGTTCCAAGGCCTCATTCAGCTCTCGGAACATCTCGAAGCGCTCACGCCCACGGATCT
TP53	NM_000546	46393	c.520_536delT	p.F174fs*7	-	17:7578394-7578416	CHP2_TP53_4	CCAGCCCCACGCTGCTCACCACTCGCTATCTGGAGCAGCTCTGCATCATCTGGGGGCACGCGCTCACACACTCTGTCGTGTGACTGCTTGTAGATGGGCATGGGCGCCAGGCTGTGAAA
BRAF	NM_004333	463	c.1756G>A	p.E586K	-	7:140453179-140453179	CHP2_BRAF_2	TCAAACTGATGGGACCCACTCCATCGAGATTTCACTGTAGCTAGACCAAAATCACCTATTTTTACTGTGAGGTCTTCATGAAGAAATATATCTGAGGTGTAGTAAGTAAAGGAAACAG
BRAF	NM_004333	464	c.1780A>T	p.I594F/A	-	7:140453145-140453155	CHP2_BRAF_2	TCAAACTGATGGGACCCACTCCATCGAGATTTCACTGTAGCTAGACCAAAATCACCTATTTTTACTGTGAGGTCTTCATGAAGAAATATATCTGAGGTGTAGTAAGTAAAGGAAACAG
BRAF	NM_004333	465	c.1781C>G	p.D587E	-	7:140453144-140453174	CHP2_BRAF_2	TCAAACTGATGGGACCCACTCCATCGAGATTTCACTGTAGCTAGACCAAAATCACCTATTTTTACTGTGAGGTCTTCATGAAGAAATATATCTGAGGTGTAGTAAGTAAAGGAAACAG
BRAF	NM_004333	466	c.1781A>T	p.D594V	-	7:140453144-140453154	CHP2_BRAF_2	TCAAACTGATGGGACCCACTCCATCGAGATTTCACTGTAGCTAGACCAAAATCACCTATTTTTACTGTGAGGTCTTCATGAAGAAATATATCTGAGGTGTAGTAAGTAAAGGAAACAG
BRAF	NM_004333	467	c.1781A>G	p.D594G	-	7:140453144-140453154	CHP2_BRAF_2	TCAAACTGATGGGACCCACTCCATCGAGATTTCACTGTAGCTAGACCAAAATCACCTATTTTTACTGTGAGGTCTTCATGAAGAAATATATCTGAGGTGTAGTAAGTAAAGGAAACAG
BRAF	NM_004333	468	c.1785T>G	p.F595L	-	7:140453150-140453150	CHP2_BRAF_2	TCAAACTGATGGGACCCACTCCATCGAGATTTCACTGTAGCTAGACCAAAATCACCTATTTTTACTGTGAGGTCTTCATGAAGAAATATATCTGAGGTGTAGTAAGTAAAGGAAACAG
BRAF	NM_004333	469	c.1786G>C	p.G596R	-	7:140453149-140453149	CHP2_BRAF_2	TCAAACTGATGGGACCCACTCCATCGAGATTTCACTGTAGCTAGACCAAAATCACCTATTTTTACTGTGAGGTCTTCATGAAGAAATATATCTGAGGTGTAGTAAGTAAAGGAAACAG
BRAF	NM_004333	470	c.1789C>G	p.L597V	-	7:140453146-140453146	CHP2_BRAF_2	TCAAACTGATGGGACCCACTCCATCGAGATTTCACTGTAGCTAGACCAAAATCACCTATTTTTACTGTGAGGTCTTCATGAAGAAATATATCTGAGGTGTAGTAAGTAAAGGAAACAG
BRAF	NM_004333	471	c.1790T>G	p.L597R	-	7:140453145-140453145	CHP2_BRAF_2	TCAAACTGATGGGACCCACTCCATCGAGATTTCACTGTAGCTAGACCAAAATCACCTATTTTTACTGTGAGGTCTTCATGAAGAAATATATCTGAGGTGTAGTAAGTAAAGGAAACAG
BRAF	NM_004333	472	c.1796C>T	p.T599I	-	7:140453139-140453139	CHP2_BRAF_2	TCAAACTGATGGGACCCACTCCATCGAGATTTCACTGTAGCTAGACCAAAATCACCTATTTTTACTGTGAGGTCTTCATGAAGAAATATATCTGAGGTGTAGTAAGTAAAGGAAACAG
BRAF	NM_004333	473	c.1798_1799GT>AA	p.V600K	-	7:140453136-140453137	CHP2_BRAF_2	TCAAACTGATGGGACCCACTCCATCGAGATTTCACTGTAGCTAGACCAAAATCACCTATTTTTACTGTGAGGTCTTCATGAAGAAATATATCTGAGGTGTAGTAAGTAAAGGAAACAG
BRAF	NM_004333	474	c.1799_1799GT>AC	p.V600E	-	7:140453136-140453137	CHP2_BRAF_2	TCAAACTGATGGGACCCACTCCATCGAGATTTCACTGTAGCTAGACCAAAATCACCTATTTTTACTGTGAGGTCTTCATGAAGAAATATATCTGAGGTGTAGTAAGTAAAGGAAACAG
BRAF	NM_004333	475	c.1799_1800TG>AA	p.V600E	-	7:140453135-140453136	CHP2_BRAF_2	TCAAACTGATGGGACCCACTCCATCGAGATTTCACTGTAGCTAGACCAAAATCACCTATTTTTACTGTGAGGTCTTCATGAAGAAATATATCTGAGGTGTAGTAAGTAAAGGAAACAG
BRAF	NM_004333	476	c.1799T>A	p.V600E	-	7:140453136-140453136	CHP2_BRAF_2	TCAAACTGATGGGACCCACTCCATCGAGATTTCACTGTAGCTAGACCAAAATCACCTATTTTTACTGTGAGGTCTTCATGAAGAAATATATCTGAGGTGTAGTAAGTAAAGGAAACAG
BRAF	NM_004333	477	c.1799_1800TG>GT	p.V600D	-	7:140453135-140453136	CHP2_BRAF_2	TCAAACTGATGGGACCCACTCCATCGAGATTTCACTGTAGCTAGACCAAAATCACCTATTTTTACTGTGAGGTCTTCATGAAGAAATATATCTGAGGTGTAGTAAGTAAAGGAAACAG
BRAF	NM_004333	478	c.1801A>G	p.K601E	-	7:140453134-140453134	CHP2_BRAF_2	TCAAACTGATGGGACCCACTCCATCGAGATTTCACTGTAGCTAGACCAAAATCACCTATTTTTACTGTGAGGTCTTCATGAAGAAATATATCTGAGGTGTAGTAAGTAAAGGAAACAG
HRAS	NM_005343	479	c.33C>T	p.A11A	-	11:534290-534290	CHP2_HRAS_1	GGGGCTGTATTCGTCACAAAATGGTTCTGGATCAGCTGGATGGTGCAGGCACTCTTGCCCACACCGCCGGCGCCCACCACCAGC
HRAS	NM_005343	480	c.34G>A	p.G12S	-	11:534289-534289	CHP2_HRAS_1	GGGGCTGTATTCGTCACAAAATGGTTCTGGATCAGCTGGATGGTGCAGGCACTCTTGCCCACACCGCCGGCGCCCACCACCAGC
HRAS	NM_005343	481	c.34G>T	p.G12C	-	11:534289-534289	CHP2_HRAS_1	GGGGCTGTATTCGTCACAAAATGGTTCTGGATCAGCTGGATGGTGCAGGCACTCTTGCCCACACCGCCGGCGCCCACCACCAGC
HRAS	NM_005343	482	c.34G>C	p.G12R	-	11:534289-534289	CHP2_HRAS_1	GGGGCTGTATTCGTCACAAAATGGTTCTGGATCAGCTGGATGGTGCAGGCACTCTTGCCCACACCGCCGGCGCCCACCACCAGC
ERBB4	NM_005235	48361	c.2804A>T	p.K935I	-	2:212389842-212389842	CHP2_ERBB4_8	AATAGTGCAGATGGGAGGCTGAGGCAAAGCGTTCTCTTTTCTCAAAATCATGGGATTTCTGCGTTGGAATTCCATCATAGGGT
ERBB4	NM_005235	48362	c.2791G>T	p.D931Y	-	2:212389855-212389855	CHP2_ERBB4_8	AATAGTGCAGATGGGAGGCTGAGGCAAAGCGTTCTCTTTTCTCAAAATCATGGGATTTCTGCGTTGGAATTCCATCATAGGGT
ERBB4	NM_005235	48363	c.1853A>C	p.H618P	-	2:212539015-212539015	CHP2_ERBB4_7	GGGTGCAGTTGGAGTTGGAGCATGGGTGGCACTCCGGATCTGGATCAGCATACTGGAAAATGAAACTGTTGCCCCTGTAAGCCATCTGGGCATTTTTCCACAGCATTTGGGGCCATCTTTAAAATGAGAGGC
ERBB4	NM_005235	48364	c.1784A>T	p.D595V	-	2:212539135-212539135	CHP2_ERBB4_7	GGGTGCAGTTGGAGTTGGAGCATGGGTGGCACTCCGGATCTGGATCAGCATACTGGAAAATGAAACTGTTGCCCCTGTAAGCCATCTGGGCATTTTTCCACAGCATTTGGGGCCATCTTTAAAATGAGAGGC
ERBB4	NM_005235	48365	c.1042G>T	p.E348*	-	2:212621557-212621557	CHP2_ERBB4_6	TCAAATTTATTGATCTTTCTCTTTCTCTTTCT

CTNNB1	NM_001904	5689	c.134C>G	p.S45C	+	3:41266137-41266137	CHP2_CTNNB1_1	GTTGGACATGGCCATGGAACCAGACAGAAAAGCGGCTGTTAGTCACTGGCAGCAACAGTCTTACCTGGACTCTGGAATCCATTCTGGTGCCACTACCACAGCTCCTTCTCTGAGTGGT
CTNNB1	NM_001904	5690	c.95A>C	p.D32A	+	3:41266098-41266098	CHP2_CTNNB1_1	GTTGGACATGGCCATGGAACCAGACAGAAAAGCGGCTGTTAGTCACTGGCAGCAACAGTCTTACCTGGACTCTGGAATCCATTCTGGTGCCACTACCACAGCTCCTTCTCTGAGTGGT
CTNNB1	NM_001904	5691	c.95A>T	p.D32V	+	3:41266098-41266098	CHP2_CTNNB1_1	GTTGGACATGGCCATGGAACCAGACAGAAAAGCGGCTGTTAGTCACTGGCAGCAACAGTCTTACCTGGACTCTGGAATCCATTCTGGTGCCACTACCACAGCTCCTTCTCTGAGTGGT
CTNNB1	NM_001904	5692	c.134C>A	p.S45Y	+	3:41266137-41266137	CHP2_CTNNB1_1	GTTGGACATGGCCATGGAACCAGACAGAAAAGCGGCTGTTAGTCACTGGCAGCAACAGTCTTACCTGGACTCTGGAATCCATTCTGGTGCCACTACCACAGCTCCTTCTCTGAGTGGT
CTNNB1	NM_001904	5694	c.86C>T	p.S29F	+	3:41266089-41266089	CHP2_CTNNB1_1	GTTGGACATGGCCATGGAACCAGACAGAAAAGCGGCTGTTAGTCACTGGCAGCAACAGTCTTACCTGGACTCTGGAATCCATTCTGGTGCCACTACCACAGCTCCTTCTCTGAGTGGT
CTNNB1	NM_001904	5696	c.125C>T	p.T42I	+	3:41266128-41266128	CHP2_CTNNB1_1	GTTGGACATGGCCATGGAACCAGACAGAAAAGCGGCTGTTAGTCACTGGCAGCAACAGTCTTACCTGGACTCTGGAATCCATTCTGGTGCCACTACCACAGCTCCTTCTCTGAGTGGT
CTNNB1	NM_001904	5699	c.128C>T	p.A43V	+	3:41266131-41266131	CHP2_CTNNB1_1	GTTGGACATGGCCATGGAACCAGACAGAAAAGCGGCTGTTAGTCACTGGCAGCAACAGTCTTACCTGGACTCTGGAATCCATTCTGGTGCCACTACCACAGCTCCTTCTCTGAGTGGT
NRAS	NM_002524	569	c.37G>C	p.G13R	+	1:115258745-115258745	CHP2_NRAS_1	TCATCTACAAAGTGGTTCTGGATTAGCTGGATTGTCAGTGCGCTTTTCCCCAACACCACCTGCTCAACCACCACCAGTTGTACT
CTNNB1	NM_001904	5701	c.122C>G	p.T41S	+	3:41266125-41266125	CHP2_CTNNB1_1	GTTGGACATGGCCATGGAACCAGACAGAAAAGCGGCTGTTAGTCACTGGCAGCAACAGTCTTACCTGGACTCTGGAATCCATTCTGGTGCCACTACCACAGCTCCTTCTCTGAGTGGT
CTNNB1	NM_001904	5702	c.59C>T	p.A20V	+	3:41266062-41266062	CHP2_CTNNB1_1	GTTGGACATGGCCATGGAACCAGACAGAAAAGCGGCTGTTAGTCACTGGCAGCAACAGTCTTACCTGGACTCTGGAATCCATTCTGGTGCCACTACCACAGCTCCTTCTCTGAGTGGT
CTNNB1	NM_001904	5703	c.106C>T	p.H36Y	+	3:41266109-41266109	CHP2_CTNNB1_1	GTTGGACATGGCCATGGAACCAGACAGAAAAGCGGCTGTTAGTCACTGGCAGCAACAGTCTTACCTGGACTCTGGAATCCATTCTGGTGCCACTACCACAGCTCCTTCTCTGAGTGGT
CTNNB1	NM_001904	5704	c.113C>T	p.P44S	+	3:41266116-41266116	CHP2_CTNNB1_1	GTTGGACATGGCCATGGAACCAGACAGAAAAGCGGCTGTTAGTCACTGGCAGCAACAGTCTTACCTGGACTCTGGAATCCATTCTGGTGCCACTACCACAGCTCCTTCTCTGAGTGGT
CTNNB1	NM_001904	5706	c.65T>C	p.V22A	+	3:41266068-41266068	CHP2_CTNNB1_1	GTTGGACATGGCCATGGAACCAGACAGAAAAGCGGCTGTTAGTCACTGGCAGCAACAGTCTTACCTGGACTCTGGAATCCATTCTGGTGCCACTACCACAGCTCCTTCTCTGAGTGGT
CTNNB1	NM_001904	5708	c.113C>T	p.T38I	+	3:41266122-41266122	CHP2_CTNNB1_1	GTTGGACATGGCCATGGAACCAGACAGAAAAGCGGCTGTTAGTCACTGGCAGCAACAGTCTTACCTGGACTCTGGAATCCATTCTGGTGCCACTACCACAGCTCCTTCTCTGAGTGGT
NRAS	NM_002524	570	c.37G>T	p.G13C	+	1:115258745-115258745	CHP2_NRAS_1	TCATCTACAAAGTGGTTCTGGATTAGCTGGATTGTCAGTGCGCTTTTCCCCAACACCACCTGCTCAACCACCACCAGTTGTACT
CTNNB1	NM_001904	5713	c.113G>A	p.G38D	+	3:41266116-41266116	CHP2_CTNNB1_1	GTTGGACATGGCCATGGAACCAGACAGAAAAGCGGCTGTTAGTCACTGGCAGCAACAGTCTTACCTGGACTCTGGAATCCATTCTGGTGCCACTACCACAGCTCCTTCTCTGAGTGGT
CTNNB1	NM_001904	5714	c.67A>C	p.S23R	+	3:41266070-41266070	CHP2_CTNNB1_1	GTTGGACATGGCCATGGAACCAGACAGAAAAGCGGCTGTTAGTCACTGGCAGCAACAGTCTTACCTGGACTCTGGAATCCATTCTGGTGCCACTACCACAGCTCCTTCTCTGAGTGGT
CTNNB1	NM_001904	5716	c.121A>T	p.T41S	+	3:41266124-41266124	CHP2_CTNNB1_1	GTTGGACATGGCCATGGAACCAGACAGAAAAGCGGCTGTTAGTCACTGGCAGCAACAGTCTTACCTGGACTCTGGAATCCATTCTGGTGCCACTACCACAGCTCCTTCTCTGAGTGGT
CTNNB1	NM_001904	5717	c.121C>T	p.T41T	+	3:41266124-41266124	CHP2_CTNNB1_1	GTTGGACATGGCCATGGAACCAGACAGAAAAGCGGCTGTTAGTCACTGGCAGCAACAGTCTTACCTGGACTCTGGAATCCATTCTGGTGCCACTACCACAGCTCCTTCTCTGAGTGGT
NRAS	NM_002524	571	c.37G>A	p.G13S	+	1:115258745-115258745	CHP2_NRAS_1	TCATCTACAAAGTGGTTCTGGATTAGCTGGATTGTCAGTGCGCTTTTCCCCAACACCACCTGCTCAACCACCACCAGTTGTACT
CTNNB1	NM_001904	5721	c.91C>T	p.L31L	+	3:41266084-41266084	CHP2_CTNNB1_1	GTTGGACATGGCCATGGAACCAGACAGAAAAGCGGCTGTTAGTCACTGGCAGCAACAGTCTTACCTGGACTCTGGAATCCATTCTGGTGCCACTACCACAGCTCCTTCTCTGAGTGGT
NRAS	NM_002524	572	c.38_39GT>TC	p.G13V	+	1:115258743-115258744	CHP2_NRAS_1	TCATCTACAAAGTGGTTCTGGATTAGCTGGATTGTCAGTGCGCTTTTCCCCAACACCACCTGCTCAACCACCACCAGTTGTACT
CTNNB1	NM_001904	5730	c.122C>A	p.T41N	+	3:41266125-41266125	CHP2_CTNNB1_1	GTTGGACATGGCCATGGAACCAGACAGAAAAGCGGCTGTTAGTCACTGGCAGCAACAGTCTTACCTGGACTCTGGAATCCATTCTGGTGCCACTACCACAGCTCCTTCTCTGAGTGGT
CTNNB1	NM_001904	5732	c.122C>G	p.T42R	+	3:41266125-41266125	CHP2_CTNNB1_1	GTTGGACATGGCCATGGAACCAGACAGAAAAGCGGCTGTTAGTCACTGGCAGCAACAGTCTTACCTGGACTCTGGAATCCATTCTGGTGCCACTACCACAGCTCCTTCTCTGAGTGGT
CTNNB1	NM_001904	5738	c.61G>A	p.A21T	+	3:41266068-41266068	CHP2_CTNNB1_1	GTTGGACATGGCCATGGAACCAGACAGAAAAGCGGCTGTTAGTCACTGGCAGCAACAGTCTTACCTGGACTCTGGAATCCATTCTGGTGCCACTACCACAGCTCCTTCTCTGAGTGGT
NRAS	NM_002524	573	c.38G>A	p.G13D	+	1:115258743-115258744	CHP2_NRAS_1	TCATCTACAAAGTGGTTCTGGATTAGCTGGATTGTCAGTGCGCTTTTCCCCAACACCACCTGCTCAACCACCACCAGTTGTACT
CTNNB1	NM_001904	5744	c.127G>C	p.A43P	+	3:41266130-41266130	CHP2_CTNNB1_1	GTTGGACATGGCCATGGAACCAGACAGAAAAGCGGCTGTTAGTCACTGGCAGCAACAGTCTTACCTGGACTCTGGAATCCATTCTGGTGCCACTACCACAGCTCCTTCTCTGAGTGGT
CTNNB1	NM_001904	5747	c.37G>A	p.A13T	+	3:41266070-41266070	CHP2_CTNNB1_1	GTTGGACATGGCCATGGAACCAGACAGAAAAGCGGCTGTTAGTCACTGGCAGCAACAGTCTTACCTGGACTCTGGAATCCATTCTGGTGCCACTACCACAGCTCCTTCTCTGAGTGGT
CTNNB1	NM_001904	5749	c.74G>T	p.W25L	+	3:41266077-41266077	CHP2_CTNNB1_1	GTTGGACATGGCCATGGAACCAGACAGAAAAGCGGCTGTTAGTCACTGGCAGCAACAGTCTTACCTGGACTCTGGAATCCATTCTGGTGCCACTACCACAGCTCCTTCTCTGAGTGGT
NRAS	NM_002524	574	c.38G>T	p.G13V	+	1:115258744-115258744	CHP2_NRAS_1	TCATCTACAAAGTGGTTCTGGATTAGCTGGATTGTCAGTGCGCTTTTCCCCAACACCACCTGCTCAACCACCACCAGTTGTACT
CTNNB1	NM_001904	5753	c.109C>G	p.A39G	+	3:41266110-41266110	CHP2_CTNNB1_1	GTTGGACATGGCCATGGAACCAGACAGAAAAGCGGCTGTTAGTCACTGGCAGCAACAGTCTTACCTGGACTCTGGAATCCATTCTGGTGCCACTACCACAGCTCCTTCTCTGAGTGGT
CTNNB1	NM_001904	5758	c.127G>A	p.A43T	+	3:41266130-41266130	CHP2_CTNNB1_1	GTTGGACATGGCCATGGAACCAGACAGAAAAGCGGCTGTTAGTCACTGGCAGCAACAGTCTTACCTGGACTCTGGAATCCATTCTGGTGCCACTACCACAGCTCCTTCTCTGAGTGGT
NRAS	NM_002524	575	c.38G>C	p.G13A	+	1:115258744-115258744	CHP2_NRAS_1	TCATCTACAAAGTGGTTCTGGATTAGCTGGATTGTCAGTGCGCTTTTCCCCAACACCACCTGCTCAACCACCACCAGTTGTACT
CTNNB1	NM_001904	5761	c.131C>T	p.P44L	+	3:41266134-41266134	CHP2_CTNNB1_1	GTTGGACATGGCCATGGAACCAGACAGAAAAGCGGCTGTTAGTCACTGGCAGCAACAGTCTTACCTGGACTCTGGAATCCATTCTGGTGCCACTACCACAGCTCCTTCTCTGAGTGGT
CTNNB1	NM_001904	5762	c.115G>A	p.G39S	+	3:41266116-41266116	CHP2_CTNNB1_1	GTTGGACATGGCCATGGAACCAGACAGAAAAGCGGCTGTTAGTCACTGGCAGCAACAGTCTTACCTGGACTCTGGAATCCATTCTGGTGCCACTACCACAGCTCCTTCTCTGAGTGGT
NRAS	NM_002524	576	c.37T>C	p.G13G	+	1:115258743-115258743	CHP2_NRAS_1	TCATCTACAAAGTGGTTCTGGATTAGCTGGATTGTCAGTGCGCTTTTCCCCAACACCACCTGCTCAACCACCACCAGTTGTACT
PTEN	NM_000314	5775	c.1002_1003CC>TT	p.R335*	+	10:89728851-89728852	CHP2_PTEN_8	CAAGGAATATCTAGTACTTACTTTAACAAAAAATGATCTTGACAAAGCAAATAAAGACAAAGCAAACGCAACCGATACTTTTCTCCAAATTTTAAGGTCAGTTAAATTAAACATTTTGTGG
NRAS	NM_002524	577	c.35G>A	p.A18T	+	1:115258750-115258750	CHP2_NRAS_1	TCATCTACAAAGTGGTTCTGGATTAGCTGGATTGTCAGTGCGCTTTTCCCCAACACCACCTGCTCAACCACCACCAGTTGTACT
NRAS	NM_002524	579	c.181_182CA>AG	p.Q61R	+	1:115256529-115256530	CHP2_NRAS_2	TCCTCTATGGCACTGTACTCTTCTGTCCAGCTGTATCCACGAACAACGGTTTCACCATCTATAACCAGTTG
PTEN	NM_000314	5801	c.968delA	p.N323fs*23	+	10:89728617-89728617	CHP2_PTEN_7	CAAGGAATATCTAGTACTTACTTTAACAAAAAATGATCTTGACAAAGCAAATAAAGACAAAGCAAACGCAACCGATACTTTTCTCCAAATTTTAAGGTCAGTTAAATTAAACATTTTGTGG
NRAS	NM_002524	580	c.181C>A	p.Q61K	+	1:115256530-115256530	CHP2_NRAS_2	TCTCTCATGGCACTGTACTCTTCTGTCCAGCTGTATCCACGAACAACGGTTTCACCATCTATAACCAGTTG
PTEN	NM_000314	5811	c.188delA	p.N63fs*58	+	10:89685256-89685256	CHP2_PTEN_2	TTTGTTTTTAAGGTTTTGGATTCAAGCATAAAAACAACAAGATATACATCTGTAATGTTTTCTTTATTTTGCTGCCAAAAGGTTTCACCATCTATAACCAGTTG
PTEN	NM_000314	5812	c.391delA	p.T131fs*3	+	10:89692907-89692907	CHP2_PTEN_3	CTTATCAAACCTTTTGGAAGATCTTGACAATGGCTAAGTGAAGATGACAATCATGTTGCAGCAATTCACTGTAAAGCTGGAAAGGAGCAGACGCTGGTGATATGAT
PTEN	NM_000314	5814	c.995delC	p.D331fs*13	+	10:89728642-89728642	CHP2_PTEN_8	CAAGGAATATCTAGTACTTACTTTAACAAAAAATGATCTTGACAAAGCAAATAAAGACAAAGCAAACGCAACCGATACTTTTCTCCAAATTTTAAGGTCAGTTAAATTAAACATTTTGTGG
PTEN	NM_000314	5816	c.867delA	p.V290fs*	+	10:89728716-89728716	CHP2_PTEN_7	CCAGAGGAAACCTCAGAAAAAGTAGAAAATGGAAGTCTATGTGATCAGAAAA
PTEN	NM_000314	5817	c.389delG	p.R130fs*	+	10:89692905-89692905	CHP2_PTEN_3	CTTATCAAACCTTTTGGAAGATCTTGACAATGGCTAAGTGAAGATGACAATCATGTTGCAGCAATTCACTGTAAAGCTGGAAAGGAGCAGACGCTGGTGATATGAT
PTEN	NM_002524	581	c.181C>T	p.Q61E	+	1:115256530-115256530	CHP2_NRAS_2	TCTCTCATGGCACTGTACTCTTCTGTCCAGCTGTATCCACGAACAACGGTTTCACCATCTATAACCAGTTG
PTEN	NM_000314	5822	c.734delG	p.F246fs*	+	10:89717713-89717713	CHP2_PTEN_6	CCACACGACGGGAAGACAAGTTCATGTACTTTGGTTCCCTCAGCCGTTACCTGTGTGTGGTGATATCAAAGTAGAGTTCTTCCAAAACAGAACAAGATGCTAAAAAGGTTT
PTEN	NM_000314	5823	c.963delA	p.F321fs*23	+	10:89728612-89728612	CHP2_PTEN_8	CAAGGAATATCTAGTACTTACTTTAACAAAAAATGATCTTGACAAAGCAAATAAAGACAAAGCAAACGCAACCGATACTTTTCTCCAAATTTTAAGGTCAGTTAAATTAAACATTTTGTGG
PTEN	NM_000314	5824	c.374delT	p.C124fs*10	+	10:89692846-89692846	CHP2_PTEN_3	CTTATCAAACCTTTTGGAAGATCTTGACAATGGCTAAGTGAAGATGACAATCATGTTGCAGCAATTCACTGTAAAGCTGGAAAGGAGCAGACGCTGGTGATATGAT
PTEN	NM_000314	5825	c.517delC	p.R173fs*10	+	10:89716849-89716849	CHP2_PTEN_4	CAATTTATGTAAAATAACTATAATGAAAGTCTTTTTTTCTGCTCACCAGGGAGTAAATTTTTTTCTGCATCAGGAGGTATGTGTATTATTATAGCTACCTGTTAAAGA
PTEN	NM_002524	582	c.182A>C	p.Q61P	+	1:115256529-115256529	CHP2_NRAS_2	TCTCTCATGGCACTGTACTCTTCTGTCCAGCTGTATCCACGAACAACGGTTTCACCATCTATAACCAGTTG
NRAS	NM_002524	583	c.182A>T	p.Q61L	+	1:115256529-115256529	CHP2_NRAS_2	TCTCTCATGGCACTGTACTCTTCTGTCCAGCTGTATCCACGAACAACGGTTTCACCATCTATAACCAGTTG
PTEN	NM_000314	5840	c.321_324delTCTTGA	p.L108_D109del	+	10:89692837-89692842	CHP2_PTEN_3	CTTATCAAACCTTTTGGAAGATCTTGACAATGGCTAAGTGAAGATGACAATCATGTTGCAGCAATTCACTGTAAAGCTGGAAAGGAGCAGACGCTGGTGATATGAT
PTEN	NM_000314	5841	c.348delC	p.D116fs*18	+	10:89692844-89692844	CHP2_PTEN_3	CTTATCAAACCTTTTGGAAGATCTTGACAATGGCTAAGTGAAGATGACAATCATGTTGCAGCAATTCACTGTAAAGCTGGAAAGGAGCAGACGCTGGTGATATGAT
PTEN	NM_000314	5842	c.337delT	p.Y110fs*15	+	10:89692837-89692837	CHP2_PTEN_3	CTTATCAAACCTTTTGGAAGATCTTGACAATGGCTAAGTGAAGATGACAATCATGTTGCAGCAATTCACTGTAAAGCTGGAAAGGAGCAGACGCTGGTGATATGAT
PTEN	NM_002524	584	c.182A>G	p.Q61R	+	1:115256529-115256529	CHP2_NRAS_2	TCTCTCATGGCACTGTACTCTTCTGTCCAGCTGTATCCACGAACAACGGTTTCACCATCTATAACCAGTTG
NRAS	NM_002524	585	c.183A>T	p.Q61H	+	1:115256528-115256528	CHP2_NRAS_2	TCTCTCATGGCACTGTACTCTTCTGTCCAGCTGTATCCACGAACAACGGTTTCACCATCTATAACCAGTTG
PTEN	NM_000314	5869	c.189delG	p.F137fs*7	+	10:89692890-89692890	CHP2_PTEN_3	CAAGGAATATCTAGTACTTACTTTAACAAAAAATGATCTTGACAAAGCAAATAAAGACAAAGCAAACGCAACCGATACTTTTCTCCAAATTTTAAGGTCAGTTAAATTAAACATTTTGTGG
NRAS	NM_002524	586	c.183A>C	p.Q61H	+	1:115256528-115256528	CHP2_NRAS_2	TCTCTCATGGCACTGTACTCTTCTGTCCAGCTGTATCCACGAACAACGGTTTCACCATCTATAACCAGTTG
PTEN	NM_000314	5878	c.46_47insT	p.Y16fs*28	+	10:89642672-89642673	CHP2_PTEN_1	CAGCCACGGGCTCCCGGACATGACGCCATCATCAAGGAGATCGTTGAGCAGGAAACAAAGGGAGATATCAAGAGGTGGATTCGACTTAGACTT
NRAS	NM_002524	587	c.183A>G	p.Q61Q	+	1:115256528-115256528	CHP2_NRAS_2	TCTCTCATGGCACTGTACTCTTCTGTCCAGCTGTATCCACGAACAACGGTTTCACCATCTATAACCAGTTG
PTEN	NM_000314	5885	c.353_354insA	p.H118fs*	+	10:89692669-89692670	CHP2_PTEN_3	CTTATCAAACCTTTTGGAAGATCTTGACAATGGCTAAGTGAAGATGACAATCATGTTGCAGCAATTCACTGTAAAGCTGGAAAGGAGCAGACGCTGGTGATATGAT
PTEN	NM_000314	5887	c.711_712delAG	p.K237fs*19	+	10:89716646-89716647	CHP2_PTEN_4	CCACACGACGGGAAGACAAGTTCATGTACTTTGGTTCCCTCAGCCGTTACCTGTGTGTGGTGATATCAAAGTAGAGTTCTTCCAAAACAGAACAAGATGCTAAAAAGGTTT
PTEN	NM_000314	5888	c.723_724insTT	p.E242fs*15	+	10:89717638-89717639	CHP2_PTEN_5	CCACACGACGGGAAGACAAGTTCATGTACTTTGGTTCCCTCAGCCGTTACCTGTGTGTGGTGATATCAAAGTAGAGTTCTTCCAAAACAGAACAAGATGCTAAAAAGGTTT
NRAS	NM_002524	589	c.181A>T	p.Q61*	+	1:115256530-115256518	CHP2_NRAS_2	TCTCTCATGGCACTGTACTCTTCTGTCCAGCTGTATCCACGAACAACGGTTTCACCATCTATAACCAGTTG
PTEN	NM_000314	5907	c.493-12delT	p.?	+	10:89711863-89711863	CHP2_PTEN_4	CAATTTATGTAAAATAACTATAATGGAACATTTTTTTTCAATTTGGCTTCTCTTTTTTTCTGCTCACCAGGGAGTAAATTTTTTTCTGCATCAGGAGGTATGTGTATTATTATAGCTACCTGTTAAAGA
PTEN	NM_000314	5915	c.1-9C>G	p.?	+	10:89624218-89624218	CHP2_PTEN_1	CAGCCACGGGCTCCCGGACATGACGCCATCATCAAGGAGATCGTTGAGCAGGAAACAAAGGGAGATATCAAGAGGTGGATTCGACTTAGACTT
PTEN	NM_000314	5916	c.209+5G>A	p.?	+	10:89685319-89685319	CHP2_PTEN_2	TTTGTTTTAAGGTTTTGGATTCAAGCATAAAAACAACAAGATATACATCTGTAATGTTTTCTTTATTGTGCTGCCAAAAGGTTTCACCATCTATAACAACTATTAAGTGAA
PTEN	NM_000314	5957	c.1026-1G>T	p.?	+	10:89728876-89728876	CHP2_PTEN_9	CAAGGAATATCTAGTACTTACTTTAACAAAAAATGATCTTGACAAAGCAAATAAAGACAAAGCAAACGCAACCGATACTTTTCTCCAAATTTTAAGGTCAGTTAAATTAAACATTTTGTGG
PTEN	NM_000314	5958	c.165-1G>T	p.?	+	10:89685260-89685260	CHP2_PTEN_2	TTTGTTTTAAGGTTTTGGATTCAAGCATAAAAACAACAAGATATACATCTGTAATGTTTTCTTTATTGTGCTGCCAAAAGGTTTCACCATCTATAACAACTATTAAGTGAA
PTEN	NM_000314	5959	c.165-2A>C	p.?	+	10:89685268-89685268	CHP2_PTEN_2	TTTGTTTTAAGGTTTTGGATTCAAGCATAAAAACAACCATACAAGATATACATCTGTAATGTTTTCTTTATTGTGCTGCCAAAAGGTTTCACCATCTATAACAACTATTAAGTGAA
PTEN	NM_000314	5960	c.165-1G>A	p.?	+	10:89685260-89685260	CHP2_PTEN_2	TTTGTTTTAAGGTTTTGGATTCAAGCATAAAAACAACAAGATATACATCTGTAATGTTTTCTTTATTGTGCTGCCAAAAGGTTTCACCATCTATAACAACTATTAAGTGAA
PTEN	NM_000314	5961	c.493-1G>A	p.?	+	10:89711874-89711874	CHP2_PTEN_4	CAATTTATGTAAAATAACTATAATGGAACATTTTTTTCAATTTGGCTTCTCTTTTTTTCTGCTCACCAGGGAGTAAATTTTTTTCTGCATCAGGAGGTATGTGTATTATTATAGCTACCTGTTAAAGA
PTEN	NM_000314	5974	c.209+1G>C	p.?	+	10:89685315-89685315	CHP2_PTEN_2	TTTGTTTTAAGGTTTTGGATTCAAGCATAAAAACCATACAAGATATACATCTGTAAGTGTTTTCTTTATTGTGCTGCCAAAAGGTTTCACCATCTATAACAACTATTAAGTGAA
PTEN	NM_000314	5975	c.209+1delGT	p.?	+	10:89685315-89685316	CHP2_PTEN_2	TTTGTTTTAAGGTTTTGGATTCAAGCATAAAAACCATACAAGATATACATCTGTAAGTGTTTTCTTTATTGTGCTGCCAAAAGGTTTCACCATCTATAACAACTATTAAGTGAA
PTEN	NM_000314	5976	c.209+1G>T	p.?	+	10:89685315-89685315	CHP2_PTEN_2	TTTGTTTTAAGGTTTTGGATTCAAGCATAAAAACCATACAAGATATACATCTGTAAGTGTTTTCTTTATTGTGCTGCCAAAAGGTTTCACCATCTATAACAACTATTAAGTGAA
PTEN	NM_000314	5979	c.209+1delGTAA	p.?	+	10:89685315-89685318	CHP2_PTEN_2	TTTGTTTTAAGGTTTTGGATTCAAGCATAAAAACCATACAAGATATACATCTGTAAGTGTTTTCTTTATTGTGCTGCCAAAAGGTTTCACCATCTATAACAACTATTAAGTGAA
FGFR1	NM_000604	601	c.374C>T	p.S125L	+	8:38285938-38285938	CHP2_FGFR1_1	ACAGTGTCTCACGCATACTGGTTTGGTTGGTATCTGTTTCTTTCTCCTCGAAGGAGGGTATCATCATCATCATCATCTCCTCCGAGGAGGGAGGAGCATCTATGGGAAGAAGAAGGGGCAC
CTNNB1	NM_001904	6050	c.64_144delG	p.V22_G28del	+	3:41266067-41266152	CHP2_CTNNB1_1	GTTGGACATGGCCATGGAACCAGACAGAAAAGCGGCTGTTAGTCACTGGCAGCAACAGTCTTACCTGGACTCTGGAATCCATTCTGGTGCCACTACCACAGCTCCTTCTCTGAGTGGT
CTNNB1	NM_001904	6052	c.64_99delC96	p.V22_S33del	+	3:41266067-41266102	CHP2_CTNNB1_1	GTTGGACATGGCCATGGAACCAGACAGAAAAGCGGCTGTTAGTCACTGGCAGCAACAGTCTTACCTGGACTCTGGAATCCATTCTGGTGCCACTACCACAGCTCCTTCTCTGAGTGGT
CTNNB1	NM_001904	6057	c.67_99delD3	p.S23_S33del	+	3:41266070-41266102	CHP2_CTNNB1_1	GTTGGACATGGCCATGGAACCAGACAGAAAAGCGGCTGTTAGTCACTGGCAGCAACAGTCTTACCTGGACTCTGGAATCCATTCTGGTGCCACTACCACAGCTCCTTCTCTGAGTGGT
CTNNB1	NM_001904	6064	c.74_97delG4	p.W25_D32del	+	3:41266077-41266100	CHP2_CTNNB1_1	GTTGGACATGGCCATGGAACCAGACAGAAAAGCGGCTGTTAGTCACTGGCAGCAACAGTCTTACCTGGACTCTGGAATCCATTCTGGTGCCACTACCACAGCTCCTTCTCTGAGTGGT
CTNNB1	NM_001904	6076	c.88_99delG2	p.V30_S33del	+	3:41266091-41266100	CHP2_CTNNB1_1	GTTGGACATGGCCATGGAACCAGACAGAAAAGCGGCTGTTAGTCACTGGCAGCAACAGTCTTACCTGGACTCTGGAATCCATTCTGGTGCCACTACCACAGCTCCTTCTCTGAGTGGT
CTNNB1	NM_001904	6088	c.97_98TC>CT	p.S33L	+	3:41266100-41266101	CHP2_CTNNB1_1	GTTGGACATGGCCATGGAACCAGACAGAAAAGCGGCTGTTAGTCACTGGCAGCAACAGTCTTACCTGGACTCTGGAATCCATTCTGGTGCCACTACCACAGCTCCTTCTCTGAGTGGT
CTNNB1	NM_001904	6089	c.97_98TC>AA	p.S33N	+	3:41266100-41266101	CHP2_CTNNB1_1	GTTGGACATGGCCATGGAACCAGACAGAAAAGCGGCTGTTAGTCACTGGCAGCAACAGTCTTACCTGGACTCTGGAATCCATTCTGGTGCCACTACCACAGCTCCTTCTCTGAGTGGT
BRAF	NM_004333	6137	c.1799T>CA	p.V600Q	+	7:140453136-140453137	CHP2_BRAF_2	TCAACTAATCATAGGTCTATTTATTCTTGTGATTTTAGTCTTCTGTAGGTGATTTATCTTTGAGGTGTTCATAGTCAGGAAGTCTTTACAGTCCAGAGAATAGGCCTGATGGTCAGGGA
CTNNB1	NM_001904	6140	c.121G>T	p.T40T	+	3:41266123-41266123	CHP2_CTNNB1_1	GTTGGACATGGCCATGGAACCAGACAGAAAAGCGGCTGTTAGTCACTGGCAGCAACAGTCTTACCTGGACTCTGGAATCCATTCTGGTGCCACTACCACAGCTCCTTCTCTGAGTGGT
PIK3CA	NM_006218.1	6147	c.1636C>G	p.Q546E	+	3:178936094-178936094	CHP2_PIK3CA_7	ATTAAGGGAAAATGGCAAAAGACAGCTCAAAGCAATTTCTACAGTGAGATCTCTCTTCTGGAAATCACTGAGCAGGAGGAAGAAGT
PTEN	NM_000314	6206	c.314C>T	p.C105R	+	10:89692905-89692905	CHP2_PTEN_3	CTTATCAAACCTTTTGGAAGATCTTGACAATGGCTAAGTGAAGATGACAATCATGTTGCAGCAATTCACTGTAAAGCTGGAAAGGAGCAGACGCTGGTGATATGAT
EGFR	NM_005228	6209	c.2240_2251del12	p.I747_T750del	+	7:55242470-55242481	CHP2_EGFR_5	TAGGGACTCTGGATCCCAGAAGGTGAGAAGAGTTAAAATTCCCGTCGCTATCAAGGAATTAAGAGAAGCAACATCTCTCGCACAAGCCACAAGGAAATCCTCGATGTGGATTTCTGCTTTGCTGTGGTGGGG
EGFR	NM_005228	6213	c.2282T>A	p.L761Q	+	7:55259515-55259515	CHP2_EGFR_8	TTTGGGCTGGCCCAAACTGCTGACATGGATCATATGTGGATGCAGATGTTTGCTTGACCTCAGGACCACTTGGTCTCCTGCACCAGCAGCTACTCCCTTCAGCGTCAGCAGGGGGCAGCAGCT
EGFR	NM_005228	6218	c.2239_2245delB	p.I747_E749del	+	7:55242469-55242477	CHP2_EGFR_5	TAGGGACTCTGGATCCCAGAAGGTGAGAAGAGTTAAAATTCCCGTCGCTATCAAGGAATTAAGAGAAGCAACATCTCTCGCACAAGCCACAAGGAAATCCTCGATGTGGATTTCTGCTTTGCTGTGGTGGGG
EGFR	NM_005228	6220	c.2238_2255delA18	p.E746_S752-I	+	7:55242468-55242477	CHP2_EGFR_5	TAGGGACTCTGGATCCCAGAAGGTGAGAAGAGTTAAAATTCCCGTCGCTATCAAGGAATTAAGAGAAGCAACATCTCTCGCACAAGCCACAAGGAAATCCTCGATGTGGATTTCTGCTTTGCTGTGGTGGGG
EGFR	NM_005228	6223	c.2235_2249delG15	p.E746_A750del	+	7:55242465-55242479	CHP2_EGFR_5	TAGGGACTCTGGATCCCAGAAGGTGAGAAGAGTTAAAATTCCCGTCGCTATCAAGGAATTAAGAGAAGCAACATCTCTCGCACAAGCCACAAGGAAATCCTCGATGTGGATTTCTGCTTTGCTGTGGTGGGG
EGFR	NM_005228	6224	c.2573T>G	p.L858R	+	7:55259515-55259515	CHP2_EGFR_8	TTTGGGCTGGCCCAAACTGCTGACATGGATCATATGTGGATGCAGATGTTTGCTTGACCTCAGGACCACTTGGTCTCCTGCACCAGCAGCTACTCCCTTCAGCGTCAGCAGGGGGCAGCAGCT
EGFR	NM_005228	6225	c.2236_2250delG15	p.E746_A750del	+	7:55242466-55242480	CHP2_EGFR_5	TAGGGACTCTGGATCCCAGAAGGTGAGAAGAGTTAAAATTCCCGTCGCTATCAAGGAATTAAGAGAAGCAACATCTCTCGCACAAGCCACAAGGAAATCCTCGATGTGGATTTCTGCTTTGCTGTGGTGGGG
EGFR	NM_005228	6226	c.2226C>T	p.R776C	+	7:55249058-55249058	CHP2_EGFR_6	GTGCGCTCTCCCTCCCTCCCAGGAAGCCTGATGGGCCGGCGGTGGCGAAGCCCATCGTGGCCGCTGGTGGGCATCTGGCTCGCCATCGCCTGCTGGGCAGCTGGCTCCTGGGCTGCTCGCC
EGFR	NM_005228	6239	c.2156G>C	p.G719A	+	7:55241708-55241708	CHP2_EGFR_4	CTCAAAAGGATCATCTCCAACATCGCCAGCAAGGATGATTTTGGGCTGGCCCGCCTGTGCAGCTGACATGGGCGATGTTGTCTGCAGCCCCTCATCTTCCTCTCCTCCTCCTCCTCCTCCTCC
EGFR	NM_005228	6240	c.2369C>T	p.T790M	+	7:55249071-55249071	CHP2_EGFR_6	GTGCGCTCTCCCTCCCTCCCAGGAAGCCTGATGGGCCGGCGGTGGCGAAGCCCATCGCCGTGCCGCCGCTGGGCCATCTGGCTCGCCATCGCCTGCTGGGCAGCTGGCTCCTGGGCTGCTCGCC
EGFR	NM_005228	6241	c.2361G>T	p.S787I	+	7:55249058-55249058	CHP2_EGFR_6	GTGCGCTCTCCCTCCCTCCCAGGAAGCCTGATGGGCCGGCGGTGG

TP53 ENST00000415465	ENST00000415465	99020	c.743G>A	p.R248Q	-	17:7577538-7577538	CHP2_TP53_6	CCAGGTGTGATGTGGTGAGGATGGGCCTCCGGTTCATGCCGCCCATGCAGGAACTGTTACACATGTAGTTGTAGTGGATGTGGTACAGTCAGAGCCAACCTAG		
TP53 ENST00000245858	ENST00000245858	99021	c.464G>A	p.R155Q	-	17:7577538-7577538	CHP2_TP53_6	CCAGGTGTGATGTGGTGAGGATGGGCCTCCGGTTCATGCCGCCCATGCAGGAACTGTTACACATGTAGTTGTAGTGGATGTGGTACAGTCAGAGCCAACCTAG		
TP53 ENST00000415465	ENST00000415465	99022	c.524G>A	p.R175H	-	17:7578406-7578406	CHP2_TP53_4	CCAGCCCCATGCTGCTACCATCTGCTATCTGAGCAGCGCTCATGGTGGGGGCAGCGCCTCACACACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGGCGGGAGTTTCTTTGATGATGGCCTGGGTCAGATGGCCATCACTGGCGCGGGCGCGGGTGCCGGGCGGGGGCTGTG		
TP53 ENST00000415315	ENST00000415315	99023	c.128G>A	p.R43H	-	17:7578406-7578406	CHP2_TP53_4	CCAGCCCCATGCTGCTACCATCTGCTATCTGAGCAGCGCTCATGGTGGGGGCAGCGCCTCACACACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGGCGGGAGTTTCTTTGATGATGGCCTGGGTCAGATGGCCATCACTGGCGCGGGCGCGGGTGCCGGGCGGGGGCTGTG		
TP53 ENST00000245858	ENST00000245858	99024	c.245G>A	p.R82H	-	17:7578406-7578406	CHP2_TP53_4	CCAGCCCCATGCTGCTACCATCTGCTATCTGAGCAGCGCTCATGGTGGGGGCAGCGCCTCACACACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGGCGGGAGTTTCTTTGATGATGGCCTGGGTCAGATGGCCATCACTGGCGCGGGCGCGGGTGCCGGGCGGGGGCTGTG		
4AK	NM_00434	99137	c.3586C>A	p.L1196M	-	2:29443631-29443631	CHP2_ALK_1	GTCTCCCCCCCGCCATGAGCTCCAGCAGGATGAACCGGGGGCAGGGATTGCAGGCTCACCCCAATGCACGGGACACATGTTCTGGTGGTTGAATTTGCTGCAGAGCAGAGAGGGAGTGTAACCAAA		
CDKN2A ENST00000446177	ENST00000446177	99191	c.238C>T	p.R80*	-	9:21971128-21971128	CHP2_CDKN2A_1	GCCCTCCCGGGCAGCGTCTGTGCACGGGTGGGGTGCTGGGGCTGGGGTGCGGGGTCGGGGTCGGGCAGTTGGGCTCCGCCCGTGGAGCAGCAGCAGCTCCGCCACTGCTGCGCTGCCATCATCATGACCTGCCAGAGAGA		
SMARCB1	NM_003073.2	991	c.1441C>A	p.V45*	-	22:24139990-24139990	CHP2_SMARCB1_1	CCTTCCGTATGTTCCTGAGGTTCTCTGTACAGGAGATACCCCACACTCTGGAGGCGACTAGCCACTGGGAGAGAGGGAAAAAATAGTTGCATCGTCACATGGTAAAAAAC		
SMARCB1	NM_003073.2	992	c.472C>T	p.R158*	+	22:24142240-24142240	CHP2_SMARCB1_2	GTGCCATGCTCCACAACCATCACACAGGAACCGCATGGGGCCGAGACAAGAAGAAGCTTCCCCCTTTGGTGTGGATGCATGCTGCACTCACCCTCCGTGCTGATTCCGGC		
SMARCB1	NM_003073.2	993	c.601C>T	p.R201*	+	22:24145652-24145652	CHP2_SMARCB1_3	TCAGCTTCATGGTCTGGACCTGGACTGTGATGCTCCAGGCTGTGGATGCTCACTCAGCCGGGCTGGACATGTGGTGGTCCCTGCGGGCAGGACGCTGCGGAAGCTCCTCACCTG		
TP53 ENST00000415465	ENST00000415465	99598	c.404G>A	p.C135Y	-	17:7578326-7578326	CHP2_TP53_3	GCCAGTTGGCAAAACATCTTGGTTGAGGGCAGGGGAGTACTGTAGGAGAAGGAAGGAGACAGAGTTGAAAGTCAGGGCACAAGTGA		
TP53 ENST00000415115	ENST00000415115	99599	c.401-A	p.C7Y	-	17:7578326-7578326	CHP2_TP53_3	GCCAGTTGGCAAAACATCTTGGTTGAGGGCAGGGGAGTACTGTAGGAGAAGGAAGGAGACAGAGTTGAAAGTCAGGGCACAAGTGA		
TP53 ENST00000245858	ENST00000245858	99600	c.125G>A	p.C42Y	-	17:7578326-7578326	CHP2_TP53_3	GCCAGTTGGCAAAACATCTTGGTTGAGGGCAGGGGAGTACTGTAGGAGAAGGAAGGAGACAGAGTTGAAAGTCAGGGCACAAGTGA		
TP53 ENST00000269305	ENST00000269305	99601	c.404G>A	p.C135Y	-	17:7578326-7578326	CHP2_TP53_2	GCCAGTTGGCAAAACATCTTGGTTGAGGGCAGGGGAGTACTGTAGGAGAAGGAAGGAGACAGAGTTGAAAGTCAGGGCACAAGTGA		
TP53 ENST00000269305	ENST00000269305*	99602	c.743G>A	p.R248Q	-	17:7577538-7577538	CHP2_TP53_6	CCAGGTGTGATGTGGTGAGGATGGGCCTCCGGTTCATGCCGCCCATGCAGGAACTGTTACACATGTAGTTGTAGTGGATGTGGTACAGTCAGAGCCAACCTAG		
FBXW7_NM_018315_2	NM_018315.2	99603	c.1273C>G	p.R425G	-	4:153472389-153472389	CHP2_FBXW7_4	TTGAACACAGCGGACTGCTGCAACATGACCCATCAAAACATGTAAACACTGGCCTGCTCTAATATCCCAAACCCTAAGAGTGGCCATCTCGAG		
FBXW7	NM_033632.1	99604	c.1513C>T	p.R505G	-	4:153472389-153472389	CHP2_FBXW7_4	TTGAACACAGCGGACTGCTGCAACATGACCCATCAAAACATGTAAACACTGGCCTGCTCTAATATCCCAAACCCTAAGAGTGGCCATCTCGAG		
FBXW7_ENST00000534231	ENST00000534231	99605	c.796C>G	p.R266G	-	4:153472389-153472389	CHP2_FBXW7_4	TTGAACACAGCGGACTGCTGCAACATGACCCATCAAAACATGTAAACACTGGCCTGCTCTAATATCCCAAACCCTAAGAGTGGCCATCTCGAG		
FBXW7_ENST00000261708	ENST00000261708	99606	c.1513C>G	p.R505G	-	4:153472389-153472389	CHP2_FBXW7_4	TTGAACACAGCGGACTGCTGCAACATGACCCATCAAAACATGTAAACACTGGCCTGCTCTAATATCCCAAACCCTAAGAGTGGCCATCTCGAG		
TP53 ENST00000415465	ENST00000415465	99615	c.637C>T	p.R213*	-	17:7578212-7578212	CHP2_TP53_5	GGCGGGCCTATAGGGCACCACCACACTATGTCGAAAAGTGTTTCTGTCATCCAAATACTCCACACGCAAATTTCCTTCCCACTCGGATAAGATGCTGAGGAGGGGCCAGACCTAAGAGCA		
TP53 ENST00000415115	ENST00000415115	99616	c.241C>T	p.R81*	-	17:7578212-7578212	CHP2_TP53_5	GGCGGGCCTATAGGGCACCACCACACTATGTCGAAAAGTGTTTCTGTCATCCAAATACTCCACACGCAAATTTCCTTCCCACTCGGATAAGATGCTGAGGAGGGGCCAGACCTAAGAGCA		
TP53 ENST00000245858	ENST00000245858	99617	c.338C>T	p.R180*	-	17:7578212-7578212	CHP2_TP53_5	GGCGGGCCTATAGGGCACCACCACACTATGTCGAAAAGTGTTTCTGTCATCCAAATACTCCACACGCAAATTTCCTTCCCACTCGGATAAGATGCTGAGGAGGGGCCAGACCTAAGAGCA		
TP53 ENST00000269305	ENST00000269305	99618	c.637C>T	p.R213*	-	17:7578212-7578212	CHP2_TP53_5	GGCGGGCCTATAGGGCACCACCACACTATGTCGAAAAGTGTTTCTGTCATCCAAATACTCCACACGCAAATTTCCTTCCCACTCGGATAAGATGCTGAGGAGGGGCCAGACCTAAGAGCA		
TP53 ENST00000415465	ENST00000415465	99624	c.713G>T	c.238F	-	17:7577568-7577568	CHP2_TP53_5	CCAGGTGTGATGTGGTGAGGATGGGCCTCCGGTTCATGCCGCCCATGCAGGAACTGTTACACATGTAGTTGTAGTGGATGTGGTACAGTCAGAGCCAACCTAG		
TP53 ENST00000245858	ENST00000245858	99625	c.434G>T	c.145F	-	17:7577568-7577568	CHP2_TP53_6	CCAGGTGTGATGTGGTGAGGATGGGCCTCCGGTTCATGCCGCCCATGCAGGAACTGTTACACATGTAGTTGTAGTGGATGTGGTACAGTCAGAGCCAACCTAG		
TP53 ENST00000269305	ENST00000269305	99626	c.713G>T	c.238F	-	17:7577568-7577568	CHP2_TP53_5	CCAGGTGTGATGTGGTGAGGATGGGCCTCCGGTTCATGCCGCCCATGCAGGAACTGTTACACATGTAGTTGTAGTGGATGTGGTACAGTCAGAGCCAACCTAG		
TP53 ENST00000415465	ENST00000415465	99638	c.517G>T	p.V173L	-	17:7578413-7578413	CHP2_TP53_4	CCAGCCCCATGCTGCTACCATCTGCTATCTGAGCAGCGCTCATGGTGGGGGCAGCGCCTCACACACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGGCGGGAGTTTCTTTGATGATGGCCTGGGTCAGATGGCCATCACTGGCGCGGGCGCGGGTGCCGGGCGGGGGCTGTG		
TP53 ENST00000415115	ENST00000415115	99639	c.121G>T	p.V41L	-	17:7578413-7578413	CHP2_TP53_4	CCAGCCCCATGCTGCTACCATCTGCTATCTGAGCAGCGCTCATGGTGGGGGCAGCGCCTCACACACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGGCGGGAGTTTCTTTGATGATGGCCTGGGTCAGATGGCCATCACTGGCGCGGGCGCGGGTGCCGGGCGGGGGCTGTG		
TP53 ENST00000245858	ENST00000245858	99640	c.238G>T	p.V96L	-	17:7578413-7578413	CHP2_TP53_4	CCAGCCCCATGCTGCTACCATCTGCTATCTGAGCAGCGCTCATGGTGGGGGCAGCGCCTCACACACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGGCGGGAGTTTCTTTGATGATGGCCTGGGTCAGATGGCCATCACTGGCGCGGGCGCGGGTGCCGGGCGGGGGCTGTG		
TP53 ENST00000269305	ENST00000269305	99641	c.517G>T	p.V173L	-	17:7578413-7578413	CHP2_TP53_4	CCAGCCCCATGCTGCTACCATCTGCTATCTGAGCAGCGCTCATGGTGGGGGCAGCGCCTCACACACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGGCGGGAGTTTCTTTGATGATGGCCTGGGTCAGATGGCCATCACTGGCGCGGGCGCGGGTGCCGGGCGGGGGCTGTG		
TP53 ENST00000415465	ENST00000415465	99646	c.711G>A	p.M237I	-	17:7577570-7577570	CHP2_TP53_6	CCAGGTGTGATGTGGTGAGGATGGGCCTCCGGTTCATGCCGCCCATGCAGGAACTGTTACACATGTAGTTGTAGTGGATGTGGTACAGTCAGAGCCAACCTAG		
TP53 ENST00000245858	ENST00000245858	99647	c.436G>A	p.M144I	-	17:7577570-7577570	CHP2_TP53_6	CCAGGTGTGATGTGGTGAGGATGGGCCTCCGGTTCATGCCGCCCATGCAGGAACTGTTACACATGTAGTTGTAGTGGATGTGGTACAGTCAGAGCCAACCTAG		
TP53 ENST00000269305	ENST00000269305	99648	c.711G>A	p.M237I	-	17:7577570-7577570	CHP2_TP53_6	CCAGGTGTGATGTGGTGAGGATGGGCCTCCGGTTCATGCCGCCCATGCAGGAACTGTTACACATGTAGTTGTAGTGGATGTGGTACAGTCAGAGCCAACCTAG		
HRAS ENST00000397594	ENST00000397594	99664	c.182A>T	p.Q61L	-	11:533874-533874	CHP2_HRAS_2	CACACACAGGAAGGCCTCCCCCGGTGGCGATGTACTGGTCCCGCACTGGCGCTGTACTTCTCCTGGCCGGGCGATCCAGGATATGTCCAACAGGCACGTCTCCCCATCAATGACCACCTGC		
TP53 ENST00000415465	ENST00000415465	99665	c.596C>T	p.R199*	-	17:7578263-7578263	CHP2_TP53_5	GGCGGGCCTATAGGGCACCACCACACTATGTCGAAAAGTGTTTCTGTCATCCAAATACTCCACACGCAAATTTCCTTCCCACTCGGATAAGATGCTGAGGAGGGGCCAGACCTAAGAGCA		
TP53 ENST00000415115	ENST00000415115	99666	c.190C>T	p.R64*	-	17:7578263-7578263	CHP2_TP53_5	GGCGGGCCTATAGGGCACCACCACACTATGTCGAAAAGTGTTTCTGTCATCCAAATACTCCACACGCAAATTTCCTTCCCACTCGGATAAGATGCTGAGGAGGGGCCAGACCTAAGAGCA		
TP53 ENST00000245858	ENST00000245858	99667	c.307C>T	p.R103*	-	17:7578263-7578263	CHP2_TP53_5	GGCGGGCCTATAGGGCACCACCACACTATGTCGAAAAGTGTTTCTGTCATCCAAATACTCCACACGCAAATTTCCTTCCCACTCGGATAAGATGCTGAGGAGGGGCCAGACCTAAGAGCA		
TP53 ENST00000269305	ENST00000269305	99668	c.596C>T	p.R196*	-	17:7578263-7578263	CHP2_TP53_5	GGCGGGCCTATAGGGCACCACCACACTATGTCGAAAAGTGTTTCTGTCATCCAAATACTCCACACGCAAATTTCCTTCCCACTCGGATAAGATGCTGAGGAGGGGCCAGACCTAAGAGCA		
TP53 ENST00000415465	ENST00000415465	99718	c.659A>G	p.Y220C	-	17:7578190-7578190	CHP2_TP53_5	GGCGGGCCTATAGGGCACCACCACACTATGTCGAAAAGTGTTTCTGTCATCCAAATACTCCACACGCAAATTTCCTTCCCACTCGGATAAGATGCTGAGGAGGGGCCAGACCTAAGAGCA		
TP53 ENST00000245858	ENST00000245858	99719	c.380A>G	p.Y127C	-	17:7578190-7578190	CHP2_TP53_5	GGCGGGCCTATAGGGCACCACCACACTATGTCGAAAAGTGTTTCTGTCATCCAAATACTCCACACGCAAATTTCCTTCCCACTCGGATAAGATGCTGAGGAGGGGCCAGACCTAAGAGCA		
TP53 ENST00000269305	ENST00000269305*	99720	c.659A>G	p.Y220C	-	17:7578190-7578190	CHP2_TP53_5	GGCGGGCCTATAGGGCACCACCACACTATGTCGAAAAGTGTTTCTGTCATCCAAATACTCCACACGCAAATTTCCTTCCCACTCGGATAAGATGCTGAGGAGGGGCCAGACCTAAGAGCA		
TP53 ENST00000415465	ENST00000415465	99721	c.814C>T	p.R272*	-	17:7577046-7577046	CHP2_TP53_3	CACCTGCAGTCATGGCTCCCTGGGGGCAGCTCGTGGTGAGGACTCCCCTTTCTTGCGGAGATTTCTCTTCTCTGTGCGCCGGTCTCTCCCCAGGACGGATCT		
TP53 ENST00000269305	ENST00000269305*	99721	c.812C>G	p.P271A	-	17:7577046-7577046	CHP2_TP53_3	CACCTGCAGTCATGGCTCCCTGGGGGCAGCTCGTGGTGAGGACTCCCCTTTCTTGCGGAGATTTCTCTTCTCTGTGCGCCGGTCTCTCCCCAGGACGGATCT		
TP53 ENST00000269305	ENST00000269305*	99729	c.818G>A	p.R273H	-	17:7577038-7577038	CHP2_TP53_3	CACCTGCAGTCATGGCTCCCTGGGGGCAGCTCGTGGTGAGGACTCCCCTTTCTTGCGGAGATTTCTCTTCTCTGTGCGCCGGTCTCTCCCCAGGACGGATCT		
APC	NM_000038	99778	c.4484G>T	p.S1495I	+	5:112157775-112157775	CHP2_APC_6	GATGCTGATACTTTATTACATTTTGCCACGGAAAGTACTCCAGATGGATTTTCTTGTTCATCCAGCCTGAGTGCTCTGAGCCTCGATGAGCCATTTATACAGAAAGATGTGGAATTAAGAAT		
TP53 ENST00000269305	ENST00000269305	99914	c.524G>A	p.R175H	-	17:7578406-7578406	CHP2_TP53_4	CCAGCCCCATGCTGCTACCATCTGCTATCTGAGCAGCGCTCATGGTGGGGGCAGCGCCTCACACACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGGCGGGAGTTTCTTTGATGATGGCCTGGGTCAGATGGCCATCACTGGCGCGGGCGCGGGTGCCGGGCGGGGGCTGTG		
HRAS ENST00000397594	ENST00000397594	99915	c.35G>A	p.G12D	-	11:534267-534268	CHP2_HRAS_1	GGGATCGTATTTCTGTCTGCTCCACAAAATGGTTCTGGACTCAGTTGGATGGTAGCAGCTCCTCACCACCTGCCCTCCCTCTCCTCCTCCTCCTCCTCCTCCTCC		
TP53 ENST00000415465	ENST00000415465	99916	c.578A>T	p.H193L	-	17:7578271-7578271	CHP2_TP53_3	GGCGGGCCTATAGGGCACCACCACACTATGTCGAAAAGTGTTTCTGTCATCCAAATACTCCACACGCAAATTTCCTTCCCACTCGGATAAGATGCTGAGGAGGGGCCAGACCTAAGAGCA		
TP53 ENST00000415115	ENST00000415115	99917	c.182A>T	p.H61L	-	17:7578271-7578271	CHP2_TP53_3	GGCGGGCCTATAGGGCACCACCACACTATGTCGAAAAGTGTTTCTGTCATCCAAATACTCCACACGCAAATTTCCTTCCCACTCGGATAAGATGCTGAGGAGGGGCCAGACCTAAGAGCA		
TP53 ENST00000245858	ENST00000245858	99918	c.299A>T	p.H100L	-	17:7578271-7578271	CHP2_TP53_3	GGCGGGCCTATAGGGCACCACCACACTATGTCGAAAAGTGTTTCTGTCATCCAAATACTCCACACGCAAATTTCCTTCCCACTCGGATAAGATGCTGAGGAGGGGCCAGACCTAAGAGCA		
TP53 ENST00000269305	ENST00000269305*	99919	c.578A>T	p.H193L	-	17:7578271-7578271	CHP2_TP53_3	GGCGGGCCTATAGGGCACCACCACACTATGTCGAAAAGTGTTTCTGTCATCCAAATACTCCACACGCAAATTTCCTTCCCACTCGGATAAGATGCTGAGGAGGGGCCAGACCTAAGAGCA		
TP53 ENST00000269305	ENST00000269305*	99924	c.856G>A	p.E286K	-	17:7577682-7577682	CHP2_TP53_7	TACCTCGCTTAGTGCTCCCTGGGGGCAGCTCGTGGTGAGGACTCCCCTTTCTTGCGGAGATTTCTCTTCTCTGTGCGCCGGTCTCTCCCCAGGACGGATCT		
TP53 ENST00000269305	ENST00000269305*	99925	c.844C>T	p.R282W	-	17:7577694-7577694	CHP2_TP53_7	TACCTCGCTTAGTGCTCCCTGGGGGCAGCTCGTGGTGAGGACTCCCCTTTCTTGCGGAGATTTCTCTTCTCTGTGCGCCGGTCTCTCCCCAGGACGGATCT		
TP53 ENST00000415465	ENST00000415465	99928	c.329G>T	p.R110L	-	17:7579358-7579358	CHP2_TP53_2	GCCCAGACGGAAGATCCGTAGCTGCCTCGGTAGTGTTTCTTGGGAAGGGACACAGAAGATGACAGGGGCCAGGAGGGGGCTGGTGCAGGGGCCACGGGCAGGCAGCCTC		
TP53 ENST00000269305	ENST00000269305*	99929	c.329G>T	p.R110L	-	17:7579358-7579358	CHP2_TP53_2	GCCCAGACGGAAGATCCGTAGCTGCCTCGGTAGTGTTTCTTGGGAAGGGACACAGAAGATGACAGGGGCCAGGAGGGGGCTGGTGCAGGGGCCACGGGCAGGCAGCCTC		
TP53 ENST00000269305	ENST00000269305*	99932	c.824G>T	p.C275F	-	17:7577114-7577114	CHP2_TP53_1	TACCTGCGTTAGTGCTCCCTGGGGGCAGCTCGTGGTGAGGACTCCCCTTTCTTGCGGAGATTTCTCTTCTCTGTGCGCCGGTCTCTCCCCAGGACGGATCT		
TP53 ENST00000269305	ENST00000269305*	99933	c.817C>T	p.R272C	-	17:7577121-7577121	CHP2_TP53_1	TACCTGCGTTAGTGCTCCCTGGGGGCAGCTCGTGGTGAGGACTCCCCTTTCTTGCGGAGATTTCTCTTCTCTGTGCGCCGGTCTCTCCCCAGGACGGATCT		
CDKN2A ENST00000261570	ENST00000261570 v02	99935	c.404C>T	p.P135L	-	9:21971128-21971128	CHP2_CDKN2A_1	GGCCTCCCGGGCAGCGTCTGTGCACGGGTGGGGTGCTGGGGCTGGGGTGCGGGGTCGGGGTCGGGCAGTTGGGCTCCGCCCTGTGGAGCAGCAGCAGCTCCGCCACTGCTGCGCTGCCATCATCATGACCTGCCAGAGAGA		
TP53 ENST00000415465	ENST00000415465	99944	c.378C>G	p.Y126*	-	17:7578552-7578552	CHP2_TP53_3	GCCAGTTGGCAAAACATCTTGGTTGAGGGCAGGGGAGTACTGTAGGAGAAGGAAGGAGACAGAGTTGAAAGTCAGGGCACAAGTGA		
TP53 ENST00000245858	ENST00000245858	99945	c.99C>G	p.Y33*	-	17:7578552-7578552	CHP2_TP53_3	GCCAGTTGGCAAAACATCTTGGTTGAGGGCAGGGGAGTACTGTAGGAGAAGGAAGGAGACAGAGTTGAAAGTCAGGGCACAAGTGA		
TP53 ENST00000415465	ENST00000415465	99946	c.378C>G	p.Y126*	-	17:7578552-7578552	CHP2_TP53_3	GCCAGTTGGCAAAACATCTTGGTTGAGGGCAGGGGAGTACTGTAGGAGAAGGAAGGAGACAGAGTTGAAAGTCAGGGCACAAGTGA		
TP53 ENST00000269305	ENST00000269305*	99947	c.916C>T	p.R306*	-	17:7577922-7577922	CHP2_TP53_1	TACCTCGCTTAGTGCTCCCTGGGGGCAGCTCGTGGTGAGGACTCCCCTTTCTTGCGGAGATTTCTCTTCTCTGTGCGCCGGTCTCTCCCCAGGACGGATCT		
TP53 ENST00000269305	ENST00000269305*	99950	c.814G>A	p.V272M	-	17:7577124-7577124	CHP2_TP53_1	TACCTCGCTTAGTGCTCCCTGGGGGCAGCTCGTGGTGAGGACTCCCCTTTCTTGCGGAGATTTCTCTTCTCTGTGCGCCGGTCTCTCCCCAGGACGGATCT		
TP53 ENST00000269305	ENST00000269305*	99952	c.797G>T	c.G266V	-	17:7577141-7577141	CHP2_TP53_1	TACCTCGCTTAGTGCTCCCTGGGGGCAGCTCGTGGTGAGGACTCCCCTTTCTTGCGGAGATTTCTCTTCTCTGTGCGCCGGTCTCTCCCCAGGACGGATCT		
EBRB2	NM_004448	681	c.2318_2318insP	p.S773P_P774insGS	+	17:37808086-37808087	CHP2_ERBB2_2	CCTCTCAGCGTCACTCTTCTGCTCCTCGGGAGACATCGTGATGGGCTGGTGTGGGCTCCCCATATGTCTCCGGCTTCTGGGCATCTGCGGTGCAGCTGGT		
EBRB2	NM_004448	682	c.2322_2323insLT	p.M774_A775insAYVM	+	17:37808995-37808994	CHP2_ERBB2_2	CCTCTCAGCGTCACTCTTCTGCTCCTCGGGAAGCATCGTGATGGGCTGGTGTGGGCTCCCCATATGTCTCCGGCTTCTGGGCATCTGCGTGCAGCTGGT		
EGFR	NM_005228	6319	c.2346G>C	p.A750P	-	7:55242078-55242078	CHP2_EGFR_5	TAGGGAGCTCTGGATCCACGTGCCTCGCTCATCAGGATCATCGTGATGGGTCACGTGGCCAGCGTGGACGCCGCTGCTTGGGCATCTGCCTGGACCATGCCA		
EGFR	NM_005228	12376	c.2369_2368ins9	p.V789_D770insASV	+	7:55240009-55240010	CHP2_EGFR_6	GTGCCTCTCCTCCTCCTCCAGGAAGCCTACGTGATGGCCAGCGTGGACACACCCCACGTGCCCGCCTGCTGGGCATCTGCCTGACCTCATCCACCGTGCAGCTCATCACGCAGCTCATGCCCTTCGGC		
EGFR	NM_005228	12381	c.2319_2320insP	p.H773_V774insNPH	+	7:55240021-55240022	CHP2_EGFR_6	GTGCCTCTCCTCCTCCTCCAGGAAGCCTACGTGATGGCCAGCGTGGACACACCCCACGTGCCCGCCTGCTGGGCATCTGCCTGACCTCATCCACCGTGCAGCTCATCACGCAGCTCATGCCCTTCGGC		
EBRB2	NM_004448	12556	c.2340_2341ins9	p.P780_Y781insGSP	+	17:37881011-37881012	CHP2_ERBB2_2	CCTCTCAGCGTCACTCTTCTGCTCCTCGGGAAGCATCGTGATGGGCTGGTGTGGGCTCCCCATATGTCTCCGGCTTCTGGGCATCTGCCTGACCTCATCCACCGTGCAGCTCATCACGCAGCTGGT		
EBRB2	NM_004448	12558	c.2325_2326ins12	p.A775_G776insYVMA	+	17:37880996-37880997	CHP2_ERBB2_2	CCTCTCAGCGTCACTCTTCTGCTCCTCGGGAAGCATCGTGATGGGCTGGTGTGGGCTCCCCATATGTCTCCGGCTTCTGGGCATCTGCCTGACCTCATCCACCGTGCAGCTCATCACGCAGCTGGT		
EGFR	NM_005228	13428	c.2311_2312ins9	p.H770_N771insSVD	+	7:55240061-55240062	CHP2_EGFR_6	GTGCCTCTCCTCCTCCTCCAGGAAGCCTACGTGATGGCCAGCGTGGACACACCCCACGTGCCCGCCTGCTGGGCATCTGCCTGACCTCATCCACCGTGCAGCTCATCACGCAGCTCATGCCCTTCGGC		
FLT3	Z36452	19737	c.1693_1804ins81	p.I581_K602ins27	+	13:28688252-28688253	CHP2_FLT3_2	AATTTTCTCTTGGAAACTCCCATTTGAGATCATATTCATATTCTCTGAAATCACGTAGAAGTACTCATTATCTGAGGAGCCGGTCACCTGTACCATCTGTAGCTGGCTTTCATACCTAAA		
FLT3	Z36452	19798	c.1887_1888ins18	p.K602_W603insYSTDLK	+	13:28688246-28688249	CHP2_FLT3_2	AATTTTCTCTTGGAAACTCCCATTTGAGATCATATTCATATTCTCTGAAATCACGTAGAAGTACTCATTATCTGAGGAGCCGGTCACCTGTACCATCTGTAGCTGGCTTTCATACCTAAA		
EBRB2	NM_004448	20959	c.2324_2325ins12	p.A775_G776insYVMA	+	17:37880995-37880996	CHP2_ERBB2_2	CCTCTCAGCGTCACTCTTCTGCTCCTCGGGAAGCATCGTGATGGGCTGGTGTGGGCTCCCCATATGTCTCCGGCTTCTGGGCATCTGCCTGACCTCATCCACCGTGCAGCTCATCACGCAGCTGGT		
FLT3	Z36452	27979	c.1788_1789ins36	p.E596_Y597insI2	+	13:28688267-28688268	CHP2_FLT3_2	AATTTTCTCTTGGAAACTCCCATTTGAGATCATATTCATATTCTCTGAAATCACGTAGAAGTACTCATTATCTGAGGAGCCGGTCACCTGTACCATCTGTAGCTGGCTTTCATACCTAAA		
FLT3	Z36452	28771	c.1811_1812insA9	p.W605_E606insDREYEYDILKW	+	13:28688244-28688245	CHP2_FLT3_2	AATTTTCTCTTGGAAACTCCCATTTGAGATCATATTCATATTCTCTGAAATCACGTAGAAGTACTCATTATCTGAGGAGCCGGTCACCTGTACCATCTGTAGCTGGCTTTCATACCTAAA		
FLT3	Z36452	28921	c.1788_1789ins45	p.Y597_D600ins15	+	13:28688257-28688258	CHP2_FLT3_2	AATTTTCTCTTGGAAACTCCCATTTGAGATCATATTCATATTCTCTGAAATCACGTAGAAGTACTCATTATCTGAGGAGCCGGTCACCTGTACCATCTGTAGCTGGCTTTCATACCTAAA		
PIK3CA	NM_006218.1	12558	c.3446C>T	p.R115L	-	3:178916957-178916957	CHP2_PIK3CA_2	AACCGTGAAGAAAAAGATCTCTAATCAACTGAAAATTTGGTATGATACAATATCCTATTCTAAAATGCAAATAACCATAAAGCTTAACTGTTGTCCCTTTCTAAAATAT		
PIK3CA	NM_006218.1	12579	c.178C>A	p.Q60K	+	3:178916791-178916791	CHP2_PIK3CA_1	AAATACCCCCTCCCATCAACTTCTTCAAGATGAAATCTTCTTACATTTTGGTAAGTGTTACTCAAGAAGCAGAAAGGGAAAGGAAGAATTTTTTGATGAAACAGACGACTTT		
PIK3CA	NM_006218.1	12589	c.275T>G	p.F99L	-	3:178947852-178947852	CHP2_PIK3CA_9	AGTGTCCAGTGCTGGATACTGGTGCAGCACTTCTCATTTTGATGAGATGTGGAGGATGTGTCACATAGTACACATCATCTGGTGAA		
GNAQ	NM_002072.2	112932	c.625C>A	p.Q209K	-	9:80409408-80409489	CHP2_GNAQ_1	TACCTCATGTGCTGACTCCCGAGGAACTTGATCATATTCACTAAGCGCTACTAGAAACATGATAGAGGTGACATTTTAAACGACGTGTATCCATTTTCTTCTCTCTGACCTTGGACCCCTCAC		
PIK3CA	NM_006218.1	14852	c.332A>G	p.K111R	+	3:178916945-178916945	CHP2_PIK3CA_2	AACCGTGAAGAAAAAGATCTCTAATCGAGAAATTGGATGATACAATATCCTATTCTAAAATGCAAATAACCATAAAGCTTAACTGTTGTCCCTTTCTAAAATAT		
PIK3CA	NM_006218.1	16484	c.2186C>A	p.H88N	+	3:178918851-178918851	CHP2_PIK3CA_1	AAATACCCCCTCCCATCAACTTCTTCAAGATGAAATCTTCTTACATTTTGTATAAGTGTTACTCAAGAAGCAGAAAGGGAAAGGAAGAATTTTTTGATGAAACAGACGACTTT		
PIK3CA	NM_006218.1	16654	c.337_3424dUTCAAT	p.S113_N1144dLN	+	3:178916950-178916955	CHP2_PIK3CA_2	AACCGTGAAGAAAAAGATCTCTAATCGAGAAATTGGATGATACAATATCCTATTCTAAAATGCAAATAACCATAAAGCTTAACTGTTGTCCCTTTCTAAAATAT		
GNAS	NM_000516.3	192557	c.694C>T	p.R231W	-	20:57484615-57484615	CHP2_GNAS_2	TCCTCCCCACCAGCATGTTTGAGCTGGGCTGGCCAGCGCGATGAAACGCCGCAAGTGGATCCAGTGCTTCACGCTAGGATGCTGTGGGCTTGGCTGTTCGTAAAGAACGCT		
GNAS ENST00000371100	ENST00000371100	192558	c.2620G>T	p.R876N	+	20:57484615-57484615	CHP2_GNAS_2	TCCTCCCCACCAGCATGTTTGAGCTGGGCTGGCCAGCGCGATGAAACGCCGCAAGTGGATCCAGTGCTTCACGCTAGGATGCTGTGGGCTTGGCTGTTCGTAAAGAACGCT		
MET	NM_000245	201908	c.3350G>A	p.D1117G	+	7:116417074-116417079	CHP2_MET_5	CTTTCTTTTGCACAGGGCATTTTGGTTGTTATATCATGGGACTTTGTTGGACAAATGTGCTGTGAAATCTTGACAGTAGCAGTCAGATGGTAGTTTTTATTTA		
PIK3CA	NM_006218.1	21448	c.337_339delCTC	p.L113del	+	3:178916950-178916952	CHP2_PIK3CA_2	AACCGTGAAGAAAAAGATCTCTAATCGAGAAATTGGATGATACAATATCCTATTCTAAAATGCAAATAACCATAAAGCTTAACTGTTGTCCCTTTCTAAAATAT		
IDH1	NM_005896.2	227566	c.415A>T	p.I139F	-	15:96619938-96619938	CHP2_IDH1_1	GCCATGGGCTGTCCTGCCAATGTGATGGGCTTGGTCCAGCCAGGGACCTAGGGCTGGGATGTTTTTGCAGATGATGGGCTCCCGGAAGACAGTCCCCCCCAGGATGTTCCGGATAGTTCCATTGGGACTT		
PIK3CA	NM_006218.1	230820	c.1396C>T	p.P466S	+	3:178928116-178928118	CHP2_PIK3CA_6	CATGGATTAGAAGATTTGCTGAACCCTATTGGTGTTACTGGATCAAATCCAAATAAAAGTAAGGTTTTATTGTCATAAATT