

Supplemental_Table_S9. Primers to analyze mutations introduced in wild-type entry clones

BA_ID	DNA variant	Sequence (5'-3')	Genomic position (hg19)	cDNA position (hg19)	Primer ID
BA1	c.160+5G>C	GGGCTGTGTCTGCTCTGG	94578702	67-80	21050
BA1	c.161G>T	AACACTCAGTGCTCCATGCTC	94576914	302+80	61709
BA1	c.302+4A>C	TGAAGGAGGACATCAGAGGG	94577250	161-115	61708
BA1	c.303-3C>G	CTCTAGACTTAACGTGGATGAG	94573919	442+214	61710
BA4	c.768G>T	ACACAAGGTATTTCCAGGTTC	94564636	571-89	61712
BA7	c.859-9T>C	GCAGCTGGATTAAGGATTG	94546416	859-142	65005
BA7	c.1100-6T>A	CATTCCAGTGATGACTGTGGA	94544731	1239+147	61716
BA11	c.1937+13T>G	TCTAAAGACATGGAAGCCTTG	94528051	1937+82	61724
BA12	c.2382+5G>C	CCTGTACATTTTAGCCTCACG	94522010	2382+147	57174
BA12	c.2588G>C	TGGAAGGGGTAGTCTTTCTGG	94517426	2588-172	61727
BA15	c.2919-10T>C	TATCTCTGCCTGTGCCAG	94510058	3050+111	1573
BA15	c.2919-6C>A	TATCTCTGCCTGTGCCAG	94510058	3050+111	1573
BA15	c.3050+5G>A	ACTGAACCTGGTGTGGGG	94510382	2919-82	1572
BA16	c.3522+5del	TCTATGTTGCACCAAACCGC	94506512	3522+253	75373
BA17	c.3607G>A	CTTTGGAATGAAGGAAGAAG	94505436	3607+163	61733
BA17	c.3607+3A>T	CTTTGGAATGAAGGAAGAAG	94505436	3607+163	61733
BA17	c.3812A>G	GATAGTTGCTATGCTTGGGTG	94502592	3813+109	61735
BA17	c.3813G>C	GATAGTTGCTATGCTTGGGTG	94502592	3813+109	61735
BA18	c.3862+3A>G	GTCGTAATGGATTTTCTTCCC	94502461	3814-117	61736
BA19	c.4128G>A	GCTACCAGCCTGGTATTTATTG	94497732	3863-133	1584
BA19	c.4253+4C>T	ACCCTGCTTATTATGTTCCCC	94496836	4129-160	61737
BA19	c.4253+5G>T	ACCCTGCTTATTATGTTCCCC	94496836	4129-160	61737
BA19	c.4253+5G>A	ACCCTGCTTATTATGTTCCCC	94496836	4129-160	61737
BA20	c.4538A>G	AAACATCACCCAGCTGTTCC	94495136	4404	70580
BA20	c.4538A>C	AAACATCACCCAGCTGTTCC	94495136	4404	70580
BA21	c.4634G>A	TGCCCTGATCATACATAAATTG	94490428	4634+82	61743
BA22	c.4667G>C	CAAAATGAATGTTTGGGAAAG	94489055	4635-81	61744
BA23	c.4773G>C	CAGCAGTGGGAAAAGAGT	94487673	4668-166	61746
BA23	c.4773+3A>G	CAGCAGTGGGAAAAGAGT	94487673	4668-166	61746

BA23	c.4773+5G>A	CAGCAGTGGGAAAAGAGT	94487673	4668-166	61746
BA23	c.5196+3_5196+8del	GTGTAAGGCCTTCCCAAAG	94485410	5019-95	61749
BA23	c.5196+3_5196+6del	GTGTAAGGCCTTCCCAAAG	94485410	5019-95	61749
BA25	c.5312+3A>T	AGAGTGAGAGACCAGGCAG	94481679	5197-269	61750
BA25	c.5313-3C>G	CGATGAACAGATTAGCACAGA	94480173	5386	68616
BA25	c.5460+5G>A	TAGGGAGGAAGAAAGTGGCA	94479986	5460+113	61753
BA26	c.5461-10T>C	CATAGACATCTGTCACAGCCTG	94476848	5554	68147
BA26	c.5461-8T>G	CATAGACATCTGTCACAGCCTG	94476848	5554	68147
BA26	c.5584G>C	CTGCAAGGACTCTCTGTCTG	94477067	5461-126	61754
BA26	c.5584+5G>A	AGCAGGGTCAGGAGGAAGTAC	94476406	5664	68149
BA26	c.5584+6T>C	AGTCCTACTTCTCTGTTTCAGACG	94476962	5461-21	68148
BA27	c.5585-10T>C	AGCAGGGTCAGGAGGAAGTAC	94476406	5664	68149
BA27	c.5836-3C>A	CGAGATGTCTCAGTACTCACCAC	94474018	5836-165	74606
BA27	c.5714+5G>A	CTGATTGGGAAGAACCTGTTT	94476450	5620	68617
BA27	c.5898+5del	TTTCTCATGTGGCTAGTGAAG	94473658	5898+133	65517
BA29	c.6478A>G	ATCAGAGAAGGGAGGGCTGT	94466595	6349	42822
BA29	c.6479+4A>G	ATCAGAGAAGGGAGGGCTGT	94466595	6349	42822