

Chr17_AsiSI_59204586

Blue lettering indicates the region analyzed (minimum 50nts, maximum 100 nts)

+OHT/PW

Clone#1

Clone	4	CGGGCCGCGCCGCTTCCTGGCTCCCCACCCTGCGCCGGCGGCCGCCCTGGCCACGTCACC	63
Sbjct	48	CGGGCCGCGCCGCTTCCTGGCTCCCCACCCTGCGCCGGCGGCCGCCCTGGCCACGTCACC	107
Query	64	GCCCGGCCAAGAGCG-----GTGTGAG-GCGGAGCTGTGAGGCGCA	103
Sbjct	108	GCCCGGCCAAGAGTGCCTGGGCGGCGGCGCGGGGTGCGATCGCGGAGCTGTGAGGCGCA	167
		AsiSI site	
Query	104	GGCAGGGCTCTGGGGCACCTAGAGACCGGGCCGGAGACGTGGCAGCCGCCCTGCCCGCC	163
Sbjct	168	GGCAGGGCTCTGGGGCACCTAGAGACCGGGCCGGAGACGTGGCAGCCGCCCTGCCCGCC	227
Query	164	AGAAAGTTTCCTAGAAAGTTTGCTGGGCGCGCGCG	197
Sbjct	228	AGAAAGTTTCCTAGAAAGTTTGCTGGGCGCGGGCG	261

Clone#5

Query	4	GGGCGCGCCGCTTCCTGGCTCCCCACCCTGCGCCGGCGGCCGCCCTGGCCACGTCACCGC	63
Sbjct	50	GGCCGCGCCGCTTCCTGGCTCCCCACCCTGCGCCGGCGGCCGCCCTGGCCACGTCACCGC	109
Query	64	CCGGCCAAGAGTGCCTGGGCGGCGGCGCGGGGTGCGATCGCGGAGCTGTGAGGCGCAGG	123
Sbjct	110	CCGGCCAAGAGTGCCTGGGCGGCGGCGCGGGGTGCGATCGCGGAGCTGTGAGGCGCAGG	169
		AsiSI site	
Query	124	CAGGGCTCT-GGGCACCTAGAGACCGGGCCGGAGACGTGGCAGCCGCCCTGCCCGCCAG	182
Sbjct	170	CAGGGCTCTGGGGCACCTAGAGACCGGGCCGGAGACGTGGCAGCCGCCCTGCCCGCCAG	229
Query	183	AAAGTTTCCTAGAAAGTTTGCTGGGCGCGCGCG	214
Sbjct	230	AAAGTTTCCTAGAAAGTTTGCTGGGCGCGGGCG	261

Clone#15

Query	25	GGA-CT-CGGGCCGCGCCGCTT-CTGGCTCCCCACCCTGCGCCGGCGGCCGCCCTGGCCA	81
Sbjct	41	GGATCTCCGGGCCGCGCCGCTTCCTGGCTCCCCACCCTGCGCCGGCGGCCGCCCTGGCCA	100
Query	82	CGTCACCGCCCGGCCAAGAGTGCCTGGGCGGCGGCGCGGGGTGCGATCGCGGAGCTGTG	141
Sbjct	101	CGTCACCGCCCGGCCAAGAGTGCCTGGGCGGCGGCGCGGGGTGCGATCGCGGAGCTGTG	160

Query	144	AGGCAGGGCTCTGGGGCACCTAAAAAACGGGGGCGGAAACTGGGAACCCCCCTCCCC	202
Sbjct	167	AGGCAGGGCTCTGGGGCACCTAGAGACCGGGG-CCGGAGACGTGGCAGCCGCCCTGCCCC	225
Query	203	CCAAAAAGTTTCCTAAAAATTTGCTGGGCGC	232
Sbjct	226	CCAGAAAGTTTCCTAGAAAGTTTGCTGGGCGC	256

Clone#28

Query	25	ATCTCCGGGCCGCGCCGCTTCCTGGCTCCCCACCCTGCGCCGGCGGCCGCCCTGGCCACG	83
Sbjct	43	ATCTCCGGGCCGCGCCGCTTCCTGGCTCCCCACCCTGCGCCGGCGGCCGCCCTGGCCACG	102
Query	84	TCACTCGCCCGGCCAAGAGTGCGTGGGCGGCGGCGCGGGGT GCGATCGC GGAGCTGTGA	143
Sbjct	103	TCAC-CGCCCGGCCAAGAGTGCGTGGGCGGCGGCGCGGGGT GCGATCGC GGAGCTGTGA	161
			AsiSI site
Query	144	GGCGCAGGCAGGGCTCTGGGGCACCTAGAGACCGGGGCCGAGACGTGGCAGCCGCCCTG	203
Sbjct	162	GGCGCAGGCAGGGCTCTGGGGCACCTAGAGACCGGGGCCGAGACGTGGCAGCCGCCCTG	221
Query	204	CCCGCCAGAAAGTTTCCTAGAAAGTTTGCTGGGCGCGCGCG	243
Sbjct	222	CCCGCCAGAAAGTTTCCTAGAAAGTTTGCTGGGCGCGGGCG	261

Clone#33

Query	26	CGGGCCGCGCCGCTTCCTGGCTCCCCACCCTGCGCCGGCGGCCGCCCTGGCCA-GGAACG	84
Sbjct	48	CGGGCCGCGCCGCTTCCTGGCTCCCCACCCTGCGCCGGCGGCCGCCCTGGCCACGTCACC	107
Query	85	GCCGAGCCAAGAGTGCGTGGGCGGCGGCGCGGGGT GCCATCTC GGAGCTGTGAGGCGCA	144
Sbjct	108	GCCCGGCCAAGAGTGCGTGGGCGGCGGCGCGGGGT GCGATCGC GGAGCTGTGAGGCGCA	167
Query	145	GGCAGGGCTCTGGGGCACCTAGAGACCGGGGCCGAGACGTGGCAGCCGCCCTGCCCGCC	204
Sbjct	168	GGCAGGGCTCTGGGGCACCTAGAGACCGGGGCCGAGACGTGGCAGCCGCCCTGCCCGCC	227
Query	205	AGAAAGTTTCCTAGAAAGTTTGCTGGGCGCGCGCG	238
Sbjct	228	AGAAAGTTTCCTAGAAAGTTTGCTGGGCGCGGGCG	261

+OHT/PW + ML216

Clone#5

Query	1	GATCTC-GGGCCGCGCCGCTTCCTGGCTCCCCACCCTGCGCCGGCGGCCGCCCTGGCCAC	59
Sbjct	42	GATCTCCGGGCGCGCCGCTTCCTGGCTCCCCACCCTGCGCCGGCGGCCGCCCTGGCCAC	101
Query	60	GTCACCGCCC GGCCAAGAGTCGGTGGGCGG--GCGCG-GGG TGCGATCGC GGAActGTGA	119
Sbjct	102	GTCACCGCCC GGCCAAGAGTGCGTGGGCGGCGGCGCGCGGT TGCGATCGC GGAGCTGTGA	161
		AsiSI site	
Query	120	GGCGCAGGCAGGGCTCTGGGGCACCTAGAGACCGGGGCCGAGACGTGGCAGCCGCCCTG	179
Sbjct	162	GGCGCAGGCAGGGCTCTGGGGCACCTAGAGACCGGGGCCGAGACGTGGCAGCCGCCCTG	221
Query	180	CCCGCCAGAAAGTTTCCTAGAAGTTTGCTGGGCGCGCGCG	219
Sbjct	222	CCCGCCAGAAAGTTTCCTAGAAGTTTGCTGGGCGCGGGCG	261

Clone#7

Query	26	GATCTC-GGGCCGCGCGCTTCCTGGCTCCCCACCCTGCGCCGGCGCCGCCCTGGCCAC	84
Sbjct	42	GATCTCCGGGCGCGCGCTTCCTGGCTCCCCACCCTGCGCCGGCGCCGCCCTGGCCAC	101
Query	85	GTCACCGCCC GGCCA-GAGT GCGTG GGGCGGCGGCGCGGGGT GCGATCGC GGAGCTGTGA	143
Sbjct	102	GTCACCGCCC GGCCAAGAGT GCGTG GGGCGGCGGCGCGGGGT GCGATCGC GGAGCTGTGA	161
		AsiSI site	
Query	144	GGCGCAGGCAGGGCTCTGGGGCACCTAGAGACCGGGGCCGAGACGTGGCAGCCGCCCTG	203
Sbjct	162	GGCGCAGGCAGGGCTCTGGGGCACCTAGAGACCGGGGCCGAGACGTGGCAGCCGCCCTG	221
Query	204	CCCGCCAGAAAGTTTCCTAGAAGTTTGCTGGGCGCGCGCG	244
Sbjct	222	CCCGCCAGAAAGTTTCCTAGAAGTTTGCTGGGCGCGGGCG	261

Clone#8

Query	29	CGGGCCGCGCCGCTTCCTGGCTCCCCACCCTGCGCCGGCGGCCGCCCTGGCCACGTCAAC	88
Sbjct	48	CGGGCCGCGCCGCTTCCTGGCTCCCCACCCTGCGCCGGCGGCCGCCCTGGCCACGTCAAC	107
Query	89	GCCC GGCCAAGAGTGC GTGGGCGGAGGCGCGCGGGT GCGATCGC GGAGCTGTGAGCGGCA	148
Sbjct	108	GCCC GGCCAAGAGTGC GTGGGCGGCGGCGCGCGGGT GCGATCGC GGAGCTGTGAGGCGCA	167
		AseI site	

[illegible]

Clone#12

Clone#13

Clone#17

			AsiSI site	
Query	129	GGCAGGGCTCTGGGGCACCTAGAGACCGGGGCCGGAGACGTGGCAGCCGCCCTGCCCGCC		188
Sbjct	168	GGCAGGGCTCTGGGGCACCTAGAGACCGGGGCCGGAGACGTGGCAGCCGCCCTGCCCGCC		227
Query	189	AGAAAGTTTCCTAGAAAGTTTGCTGGGCGCGCGCG	222	
Sbjct	228	AGAAAGTTTCCTAGAAAGTTTGCTGGGCGCGGGCG	261	

Clone#18

Query	26	ATCTCCGGGCGCGCCGCTTCCTGGCTCCCCACCCTGCGCCGGCGGGCGCCCTGGCCACG		84
Sbjct	43	ATCTCCGGGCGCGCCGCTTCCTGGCTCCCCACCCTGCGCCGGCGGGCGCCCTGGCCACG		102
Query	85	TCACCGCCCGGCCAAGAGTGCCTGGGCGGCGGCGCGGGT GCGATCGCGGAGCTGTGAG		144
Sbjct	103	TCACCGCCCGGCCAAGAGTGCCTGGGCGGCGGCGCGGGT GCGATCGCGGAGCTGTGAG		162
			AsiSI site	
Query	145	GCTGCAGGCAGGGCTCTGGGGCACCTAGAGACCGGGGCCGGAGACGTGGCAGCCGCCCTG		204
Sbjct	163	GC-GCAGGCAGGGCTCTGGGGCACCTAGAGACCGGGGCCGGAGACGTGGCAGCCGCCCTG		222
Query	205	CCGCCAGAAAGTTTCCTAGAAAGTTTGCTGGGCGCGCGCG	243	
Sbjct	223	CCGCCAGAAAGTTTCCTAGAAAGTTTGCTGGGCGCGGGCG	261	

Clone#21

Query	34	GCCGCGACGC-TCCTGGCT-CCC-CCCTGCGCCGGCGGGCGCCCTGGCC-CGTCACCGTC		89
Sbjct	51	GCCGCGCCGCTTCCTGGCTCCCCACCCTGCGCCGGCGGGCGCCCTGGCCACGTCACCGCC		110
Query	90	CGGTCAATAGTGCCTGGGCGGTGGCGCGCGGGT GCTATCGCGGAGCTGTGAGGCGCAGGC		149
Sbjct	111	CGGCCAAGAGTGCCTGGGCGGCGGCGCGCGGGT GCGATCGCGGAGCTGTGAGGCGCAGGC		170
			AsiSI site	
Query	150	AGGGCTCTGGGGCACCTAGAGACCGGGGCCGGAGACGTGGCAGCCGCCCTGCCCCCCTTA		209
Sbjct	171	AGGGCTCTGGGGCACCTAGAGACCGGGGCCGGAGACGTGGCAGCCGCCCTGCCCCCCTTA		230
Query	210	AAGTTTCCTAGAAAGTTTGCTGGGCGC	235	
Sbjct	231	AAGTTTCCTAGAAAGTTTGCTGGGCGC	256	

Clone#24

Query	23	GATCTCCGGGGGCGCGCCGCTTCCTGGCT-CCCACCCTGCGCCGGCGGGCGCCCTGGCC		81
Sbjct	42	GATCTCC--GGGCGCGCCGCTTCCTGGCTCCCCACCCTGCGCCGGCGGGCGCCCTGGCC		99
Query	82	ACGTACCTGCCC GGCCAAGAGTGCCTGGGCGGCGGCGCGGGT GCGATCGCGGAGCTG		141
Sbjct	100	ACGTACC-GCCCGGCCAAGAGTGCCTGGGCGGCGGCGCGGGT GCGATCGCGGAGCTG		158

				AsiSI site	
Query	142	TGAGGCGCAGGCAGGGCTCTGGGGCACCTAGAGACCGGGGCCGGAGACGTGGCAGCCGCC			201
Sbjct	159	TGAGGCGCAGGCAGGGCTCTGGGGCACCTAGAGACCGGGGCCGGAGACGTGGCAGCCGCC			218
Query	202	CTGCCCCCAGAAAGTTTCCTAGAAGTTTGCTGGGCGCGCGCG	244		
Sbjct	219	CTGCCCCCAGAAAGTTTCCTAGAAGTTTGCTGGGCGCGGGCG	261		

Clone#27

Query	31	CGGGCCGCGCCGCTTCCTGGCTCCCCACCCTGCGCCGGCGGCCGCCCTGGCCACGTCACC			90
Sbjct	48	CGGGCCGCGCCGCTTCCTGGCTCCCCACCCTGCGCCGGCGGCCGCCCTGGCCACGTCACC			107
Query	91	GCCCGGCCAAGAGTGCGTGGGCGGCGGCGCGGGGT GCGATCGC GGAGCTGTGAGGCGCA			150
Sbjct	108	GCCCGGCCAAGAGTGCGTGGGCGGCGGCGCGGGGT GCGATCGC GGAGCTGTGAGGCGCA			167
				AsiSI site	
Query	151	GGCAGGGCTCTGGGGCACCTAGAGACCGGGGCCGAAAAC-TGGCAGCCCCCTGGCCCCC			209
Sbjct	168	GGCAGGGCTCTGGGGCACCTAGAGACCGGGGCCGGAGACGTGGCAGCCGCCCTG-CCCGC			226
Query	210	CAAAAA-TTTCCTAAAAATTTGCTGGGC	236		
Sbjct	227	CAGAAAGTTTCCTAGAAGTTTGCTGGGC	254		

1

Clone#28

Query	27	GATCT-CGGGCGCGCCGCTTCCTGGCTCCCCACCCTGCGCCGGCGGCCGCCCTGGCCAC			85
Sbjct	42	GATCTCCGGGCGCGCCGCTTCCTGGCTCCCCACCCTGCGCCGGCGGCCGCCCTGGCCAC			101
Query	86	GTCACCGCCCGGCCAAGAGTGCTTGGGCGGCGGCGCGC--GT GCG-TCGCG GGAGCTGTGA			145
Sbjct	102	GTCACCGCCCGGCCAAGAGTGCGTGGGCGGCGGCGCGCGGGT GCGATCGC GGAGCTGTGA			161
				AsiSI site	
Query	146	GGCGCAGGCAGGGCTCTGGGGCACCTAGAGACCGGGGCCGGAAC-TGGGAGGCGCCCTG			204
Sbjct	162	GGCGCAGGCAGGGCTCTGGGGCACCTAGAGACCGGGGCCGGAGACGTGGCAGCCGCCCTG			221
Query	205	GCCGGCCGAAAGGTTTCTTGAAGTTTGGTGGGGGGGGCG	244		
Sbjct	222	CCCGCCAGAAAGTTTCCTAGAAGTTTGCTGGGCGCGGGCG	261		

Clone#31

Query	28	CGGGCCGCGCCGCTTCCTGGCT-CCCACCCTGCGCCGGCGGCCGCCCTGGCCACGTCACC			86
Sbjct	48	CGGGCCGCGCCGCTTCCTGGCTCCCCACCCTGCGCCGGCGGCCGCCCTGGCCACGTCACC			107
Query	87	GCCCGGCCAAGAGTGCGTGGGCGGCGGCGCGGGT GCGATCGC GGAGCTGTGAGGCGCA			146
Sbjct	108	GCCCGGCCAAGAGTGCGTGGGCGGCGGCGCGGGT GCGATCGC GGAGCTGTGAGGCGCA			167
				AsiSI site	

Query	147	GGCAGGGCTCTGGGGCACCTAGAGACC-GGGCCGGAGACGTGGCAGCCGCCCTGCCCGCC	205
Sbjct	168	GGCAGGGCTCTGGGGCACCTAGAGACCGGGCCGGAGACGTGGCAGCCGCCCTGCCCGCC	227
Query	206	AGAAAGTTTCCTAGAAAGTTTGCTGGGCGCGCGCG	239
Sbjct	228	AGAAAGTTTCCTAGAAAGTTTGCTGGGCGCGGGCG	261

Clone#32

Query	20	GGGATCTCCGGGCCGCGCCGCTTCCTGGCTCCCCACCCTGCGCCGGCGGCCGCCCTGGCC	77
Sbjct	40	GGGATCTCCGGGCCGCGCCGCTTCCTGGCTCCCCACCCTGCGCCGGCGGCCGCCCTGGCC	99
Query	78	ACGTCACCGCCCCGCCAAGAGTGCGTGGGCGGCGCGCGGGT GCGATCGC GGAGCTGT	137
Sbjct	100	ACGTCACCGCCCCGCCAAGAGTGCGTGGGCGGCGGCGCGCGGGT GCGATCGC GGAGCTGT	159
		AsiSI site	
Query	138	AGAGGCGCAGGCAGGGCTCTGGGGCACCTAGAGACCGGGGCCGGAGACGTGGCAGCCGCC	196
Sbjct	160	-GAGGCGCAGGCAGGGCTCTGGGGCACCTAGAGACCGGGGCCGGAGACGTGGCAGCCGCC	219
Query	197	TGCCCCGCCAGAAAGTTTCCTAGAAAGTTTGCTGGGCGCGCGCG	238
Sbjct	220	TGCCCCGCCAGAAAGTTTCCTAGAAAGTTTGCTGGGCGCGGGCG	261

Clone#33

Query	25	TCT-CGGGCGCGCCGCTTCCTGGCTCCCCACCCTGCGCCGGCGGCCGCCCTGGCCACGT	83
Sbjct	44	TCTCCGGGCGCGCCGCTTCCTGGCTCCCCACCCTGCGCCGGCGGCCGCCCTGGCCACGT	103
Query	84	CACCGCCCGGCCAAGAGTGCGTGGGCGGCGGCGCGCG-- TGCG-TCGCG -AGCTGTGAGG	143
Sbjct	104	CACCGCCCGGCCAAGAGTGCGTGGGCGGCGGCGCGCGGGT GCGATCGC GGAGCTGTGAGG	163
		AsiSI site	
Query	144	CGCAGGCAGGGCTCTGGGGCACCTAGAGACC-GGGCCGGAGACGTGGCAGCCGCCCTGCC	202
Sbjct	164	CGCAGGCAGGGCTCTGGGGCACCTAGAGACCGGGGCCGGAGACGTGGCAGCCGCCCTGCC	223
Query	203	CGCCAGAAAGTTTCCTAGAAAGTTTGCTGGGCGCGCGCG	240
Sbjct	224	CGCCAGAAAGTTTCCTAGAAAGTTTGCTGGGCGCGGGCG	261

Clone#34

Query	27	CGGGCCGCGCCGCTTCCTGGCTCCCCACCCTGCGCCGGCGGCCGCCCTGGCCACGTCACC	86
Sbjct	48	CGGGCCGCGCCGCTTCCTGGCTCCCCACCCTGCGCCGGCGGCCGCCCTGGCCACGTCACC	107
Query	87	GCCCGGCCAAGAGTGCTTGGGCGGCGGCGCGCGGGT GCGATCGC GGAGCTGTGAGGCGCA	146
Sbjct	108	GCCCGGCCAAGAGTGCGTGGGCGGCGGCGCGCGGGT GCGATCGC GGAGCTGTGAGGCGCA	167


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Query 147 GGCAGGGCTCTGGGGCACCTAGAGACCGGGGCCGAGAGACGTGGCAGCCGCCCTGCCCCG 206
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Sbjct 168 GGCAGGGCTCTGGGGCACCTAGAGACCGGGGCCG-GAGACGTGGCAGCCGCCCTGCCCCG 227
Query 207 AGAAAGTTTCCTAGAAAGTTTGCTGGGCGCGCGCG 240
          ||||||||||||||||||||||||||||| |||
Sbjct 228 AGAAAGTTTCCTAGAAAGTTTGCTGGGCGCGGGCG 261
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