

Supplemental_Table_S6. Gateway-tagged *ABCA4* primers to amplify genomic segments from bacterial artificial chromosome clone DNA

Wild-type fragment	Primer sequence with TAGS (5'-3')	Primer sequence without TAGS (5'-3')	Genomic position (hg 19)	cDNA position (hg 19)	Insert size (bp)
BA1_forward	GGGGACAAGTTTGTACAAAAAAGCAGGCTTCgaggtctggattttgttctg	GAGGCTGGATTTTGGTTCTG	94579137	67-515	7532
BA1_reverse	GGGGACCACTTTGTACAAGAAAGCTGGGTGtttcctcaaagaccgtgtcc	TTTCCTCAAAGACCGTGTCC	94571606	442+2527	
BA2_forward	GGGGACAAGTTTGTACAAAAAAGCAGGCTTCgtggtgaatgtggaagcctc	GTGGTGAATGTGGAAGCCTC	94577704	161-569	9809
BA2_reverse	GGGGACCACTTTGTACAAGAAAGCTGGGTGcaggttctgtagcctcggg	CAGGTTCTGTAGCCTCGGG	94567896	570+675	
BA3_forward	GGGGACAAGTTTGTACAAAAAAGCAGGCTTCgatcgctcaccatccttctc	GATCGCTCACCATCCTTGTC	94574767	303-495	10737
BA3_reverse	GGGGACCACTTTGTACAAGAAAGCTGGGTGaggtcaggagtgcaaacccag	AGGTCAGGGAGTCAAACCAG	94564031	768+319	
BA4_forward	GGGGACAAGTTTGTACAAAAAAGCAGGCTTCagctacttctcaacccacc	AGCTACTTCTCAACCCACC	94565172	571-625	9927
BA4_reverse	GGGGACCACTTTGTACAAGAAAGCTGGGTGgacctcaagtgtgcgtctg	GACCTCAAGTGATGCGTCTG	94555246	769-6249	
BA5_forward	GGGGACAAGTTTGTACAAAAAAGCAGGCTTCacggcatctaccactttg	ACGGCATCTACCCACTTTG	94560934	768+3416	8719
BA5_reverse	GGGGACCACTTTGTACAAGAAAGCTGGGTGtttggcacatatccttcag	TTTGGCACATATCCTTCCAG	94552216	769-3219	
BA6_forward	GGGGACAAGTTTGTACAAAAAAGCAGGCTTCgagaccgtttgacatgtccc	GAGACCGTTTGACATGTCCC	94558131	768+6219	9946
BA6_reverse	GGGGACCACTTTGTACAAGAAAGCTGGGTGcagctcgcaataatggaggg	CAGCTGCGAATAATGGAGGG	94548186	858+722	
BA7_forward	GGGGACAAGTTTGTACAAAAAAGCAGGCTTCaactctgtggcaattggag	AACACTGCTGGCAATTGGAG	94549585	769-588	6895
BA7_reverse	GGGGACCACTTTGTACAAGAAAGCTGGGTGagctactgtgtggagggtg	AGCTACTGTGTGGAGGGTG	94542691	1554+555	
BA8_forward	GGGGACAAGTTTGTACAAAAAAGCAGGCTTCggccttcattccaagcagtc	GGCCTTCATTCCAAGCAGTC	94544009	1356+137	9017
BA8_reverse	GGGGACCACTTTGTACAAGAAAGCTGGGTGggtccttcgagggttaaggag	GGTCTTCGAGGGTAAGGGAG	94534993	1555-6120	
BA9_forward	GGGGACAAGTTTGTACAAAAAAGCAGGCTTCtccaatcaccttttctcc	TTCCAATCACCTTTTCTCC	94538276	1554+4970	6157
BA9_reverse	GGGGACCACTTTGTACAAGAAAGCTGGGTGcctagaggcctgtgtgtctg	CCTAGAGGGCTTGTGGTCTG	94532120	1555-3247	
BA10_forward	GGGGACAAGTTTGTACAAAAAAGCAGGCTTCgctgggcactgttacatgtc	GCTGGGCACTGTTACATGTC	94537212	1554+6034	9508
BA10_reverse	GGGGACCACTTTGTACAAGAAAGCTGGGTGgctgcattattccagggtc	GCTGCATTATTCCAGGGCTC	94527705	1937+428	
BA11_forward	GGGGACAAGTTTGTACAAAAAAGCAGGCTTCtcttcctcctgtccttccc	TCTTCTCCTTGCTCTTCCC	94529368	1555-495	7812
BA11_reverse	GGGGACCACTTTGTACAAGAAAGCTGGGTGcagtgtcctttgtctgggtc	CAGTGCTCTTTGTCTGGGTC	94521557	2382+600	
BA12_forward	GGGGACAAGTTTGTACAAAAAAGCAGGCTTCgagaagggttgagactggac	GAGAAAGGGATTGAGACTGGAC	94528604	1760+64	11722
BA12_reverse	GGGGACCACTTTGTACAAGAAAGCTGGGTGgttctttgaaccctgaagtgg	GTTCTTTGAACCTGAAGTGG	94516883	2653+306	
BA13_forward	GGGGACAAGTTTGTACAAAAAAGCAGGCTTCcacgtgaggctaaaatgtacagg	CACGTGAGGCTAAAATGTACAGG	94522032	2382+125	8820
BA13_reverse	GGGGACCACTTTGTACAAGAAAGCTGGGTGttctcttagtcaccttgcttga	TTCTCTTAGTCACCTTGGCTTGA	94513213	2744-564	
BA14_forward	GGGGACAAGTTTGTACAAAAAAGCAGGCTTCgctctgtttcctttctcac	TGCCTCTGTTTCTTCTCAC	94517715	2588-461	8127
BA14_reverse	GGGGACCACTTTGTACAAGAAAGCTGGGTGgttcccttcttctccctc	GTTCCCTTCTTCTCCCCTC	94509589	3051-558	

BA15_forward	GGGGACAAGTTTGTACAAAAAAGCAGGCTTCcctcccagagtttagactgc	CCCTCCCAGAGTTAGACTGC	94513659	2743+765	5783
BA15_reverse	GGGGACCACTTTGTACAAGAAAGCTGGGTGacagaggagccacttccatc	ACAGAGGAGCCACTTCCATC	94507877	3328+440	
BA16_forward	GGGGACAAGTTTGTACAAAAAAGCAGGCTTCgcatgaactatgtaagccatcc	GCATGAACTATGTAAGCCATCC	94509227	3051-196	3951
BA16_reverse	GGGGACCACTTTGTACAAGAAAGCTGGGTGgctctcccagacactaagg	GCTCTCCCAGACACTAAGG	94505277	3607+322	
BA17_forward	GGGGACAAGTTTGTACAAAAAAGCAGGCTTCgacagaatctcgctgtctcg	GACAGAATCTCGTCTGTCTG	94507652	3328+665	6397
BA17_reverse	GGGGACCACTTTGTACAAGAAAGCTGGGTGagctttgctgtaccaggag	AGCTTTGCCTGTACCAGGAG	94501256	3862+1040	
BA18_forward	GGGGACAAGTTTGTACAAAAAAGCAGGCTTCtctcactcagcttggtcacc	TCTCACTCAGCTTGGTCACC	94503549	3608-662	6702
BA18_reverse	GGGGACCACTTTGTACAAGAAAGCTGGGTGgaatgttctggtggccactg	GAATGTTCTGGTGGCCACTG	94496867	4129-191	
BA19_forward	GGGGACAAGTTTGTACAAAAAAGCAGGCTTCcaccaagcatagcaactatc	CACCCAAGCATAGCAACTATC	94502592	3813+109	7036
BA19_reverse	GGGGACCACTTTGTACAAGAAAGCTGGGTGattctctggtgatgtcaatg	ATTCCTGGTGGATGTCAATG	94495557	4353-370	
BA20_forward	GGGGACAAGTTTGTACAAAAAAGCAGGCTTCgttttctgctttccaaacc	TGTTTCTGCTTTCCAAACCC	94497203	4128+131	7352
BA20_reverse	GGGGACCACTTTGTACAAGAAAGCTGGGTGcttgttctgatacgggctgc	CTTGTTCTGATACGGGCTGC	94489852	4634+658	
BA21_forward	GGGGACAAGTTTGTACAAAAAAGCAGGCTTCccactcaatcctgtctctg	CCCACTCAATCCTGCTCTG	94495895	4352+89	7312
BA21_reverse	GGGGACCACTTTGTACAAGAAAGCTGGGTGcttaaaaggaatgggccaag	CTTAAAGGAATGGGCCAAG	94488584	4667+358	
BA22_forward	GGGGACAAGTTTGTACAAAAAAGCAGGCTTCgtagcgtggcagtattggag	GTAGCGTGGCAGTATTGGAG	94490882	4540-278	4327
BA22_reverse	GGGGACCACTTTGTACAAGAAAGCTGGGTGaaagggaatggaaccaaag	AAAGGGAATGGAACCAAATG	94486556	5018+240	
BA23_forward	GGGGACAAGTTTGTACAAAAAAGCAGGCTTCagcaaccatcccaaactgag	AGCAACCATCCCAAAGTGA	94489590	4635-616	8402
BA23_reverse	GGGGACCACTTTGTACAAGAAAGCTGGGTGgtgctaccaccacaggacag	GTGCTACCACCACAGGACAG	94481189	5312+106	
BA24_forward	GGGGACAAGTTTGTACAAAAAAGCAGGCTTCcgcgaataaccatttaacc	CCGCAAATACCCATTTAACC	94485512	5019-197	8857
BA24_reverse	GGGGACCACTTTGTACAAGAAAGCTGGGTGacagaggcaccctaattcctc	ACAGAGGCACCCTAATCCTC	94476656	5584+162	
BA25_forward	GGGGACAAGTTTGTACAAAAAAGCAGGCTTCaggtgtctgctgagcttcttc	AGGTGTCTGCTGAGCTTCTTC	94482805	5197-1395	7441
BA25_reverse	GGGGACCACTTTGTACAAGAAAGCTGGGTGgtctctctccacacaaaag	TGCTCTCTCCACACAAAAG	94475365	5715-938	
BA26_forward	GGGGACAAGTTTGTACAAAAAAGCAGGCTTCcatgtgaactggccaagag	CCATGTGAACTGGCCAAGAG	94480932	5312+363	7037
BA26_reverse	GGGGACCACTTTGTACAAGAAAGCTGGGTGgagagcaaggagggaagag	GAGAGCAAGGAGGGGAAGAG	94473896	5836-43	
BA27_forward	GGGGACAAGTTTGTACAAAAAAGCAGGCTTCacaatggtagtgtccctgtg	ACAATGGTAGTTGCCCTGTG	94477525	5461-584	6892
BA27_reverse	GGGGACCACTTTGTACAAGAAAGCTGGGTGaggttaactccagcattttgc	AGGTAACCTCCAGCATTTTGC	94470634	6147+363	
BA28_forward	GGGGACAAGTTTGTACAAAAAAGCAGGCTTCtccactagccatgagaaaag	TCCACTAGCCACATGAGAAAAG	94473656	5898+135	7874
BA28_reverse	GGGGACCACTTTGTACAAGAAAGCTGGGTGgtgaatgagcacggcaaatg	GTGAATGAGCACGGCAATATG	94465783	6479+609	
BA29_forward	GGGGACAAGTTTGTACAAAAAAGCAGGCTTCgtctgtgtcccatatagaggag	GTCTGGTCCCCATACAGGAG	94467113	6282+301	4199
BA29_reverse	GGGGACCACTTTGTACAAGAAAGCTGGGTGgcaatcttcttctcaacc	GCAATCTTCTTCTCAACC	94462915	6729+502	
MG30_forward	GGGGACAAGTTTGTACAAAAAAGCAGGCTTCgctcactgtagccttgacctc	GCTCACTGTAGCCTTGACCTC	94463984	6480-318	1113
MG30_reverse	GGGGACCACTTTGTACAAGAAAGCTGGGTGggatgaacacagctcattgc	GGTATGAACACAGCTCATTGC	94462872	6729+545	
MG31_forward	GGGGACAAGTTTGTACAAAAAAGCAGGCTTCcgtgtgttatcatgtgccag	CCGTGTTGATCATGTGCCAG	94462397	6730-646	1267

MG31_reverse	<u>GGGGACCACTTTGTACAAGAAAGCTGGGT</u> Gtgggtgctccttacatggg	TGGTGTGCTCCTTACATGGG	94461031	6816+634	1507
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