

Supplementary Files

Query	35	TTTATTTGAGTGAGTGGCCACGTGAACCTTATGATGACCCATGTAAGCAGTAACCTTTAG	94
Sbjct	128286	TTTATTTGAGTGAGTGGCCACGTGAACCTTATGATGACCCATGTAAGCAGTAACCTTTAG	128345
Query	95	AAAGCCTTCTTCCTAACCGTATCCGCTATTTTTATAACACACAGACTGTAAAAATAGAGT	154
Sbjct	128346	AAAGCCTTCTTCCTAACCATATCCGCTATTTTTATAACACACAGACTGTAAAAATAGGACT	128405
Query	155	AATAAGTCATAACAATATATTTTGTAACTGATTTTTATTTAACTGATTAATCATGTTTG	214
Sbjct	128406	AATAAGTCATAACAGTATCTTTTCGTTAACTGATTTTTATTTAAATTGATTAATCATGTTTG	128465
Query	215	TAACTTAGTTAGACAAGCtttttttttttttttaattaaaaatttaggtttaagtcaa	274
Sbjct	128466	TAACTTAGTTAGACAAGC--TTTTTTTAAAGTTTATGATTAATAAATTTAGGTTTAAAGTCAA	128523
Query	275	aaactgttcaaacataaaaaataaaataaattgaaaaagtttct-ttt----taaaaaa	328
Sbjct	128524	AAACTGTTCAAACAATAAAAAATAAAATAAATTAAGAGAGTTTCTATTTAAAAAATAAAAA	128583
Query	329	aagtctgcaaaatgaggtaaaaGGGGTTGGATAATTTCAATTCCAATAAAGCTTTTGCCTC	388
Sbjct	128584	AAGTCTGCAAAAATGAAGTAAATAGTTGATTATTTCAATTCCAATAGACTATTTCTTC	128643
Query	389	TTAAAGGGTAAATTTTGA-AACaaaaaaaTCAGTTTCTATTGAATTTATGGATTTGAG	447
Sbjct	128644	TTAAATGGTAAATTTTGAGAAC--AAAAAATCAGTTTCTATTGATTTATGGATTTAAG	128701
Query	448	TATGAGTAAAAATTAATATTTGTTTTATTCTGAAGGCCTGGAAACATTTCTTCCAAAGT	507
Sbjct	128702	TATGAGTAAAAATTAATATTTGTTTCAATCTGAAGGCCTGGAAACATTTCTTCC-AATT	128760
Query	508	TTAAATATAAATATTGTAATTTTAGTGTTTTAAAGAACAATTAGTCAGGGTTATTCCATC	567
Sbjct	128761	TTAAATATAAATATTGTAATTTTAGTGTTTTAAAGAACAATTAGTCCGGGTTATTCCATC	128820
Query	568	AAATACAGTAGATTTTGCAAAATCCGCTCTTGAAGTTAAGATGTTTGTATTGTGTTGTCTA	627
Sbjct	128821	AAATACAGTAGATTTTGCAAAATCCGCTCTTGAAGTTAAGATGTTTGTATTGTGTTGTCTA	128880
Query	628	AAATTGTCATTGTGCTTGTATTTTATGCTAAAAATTTTAAATGACAACATTTTATTA	687
Sbjct	128881	AAATTGTCATTGTGCTTGTATTTTATGCTAAAAATTTTAAATGACAACATTTTATTA	128940
Query	688	TACGTTTGGAAAACAGTAGACCCACAGAATCAAACAACTCAAACACAAAATGATCGTAA	747
Sbjct	128941	TACGTTTGGAAAACAGTAGACCCACAGAATCAAACAACTCAAACACAAAATGATCGTAA	129000
Query	748	TAAACAGATA-TT-ATTGTTCTTTTTTCAGTCAAACCTTATTT 787	
Sbjct	129001	AAAACAGATAGTTCATTGTTCTTTTTTCAGTCAAACCTTATTT 129042	
Query	838	TTAAATATTTAACATTGGCGGTTCAATTCGCTGTGGCAACCCCTGATTAATGGAGGGACT	897
Sbjct	129041	TTAAATATTTAACATTGGCGGTTCAATTCGCTGTGGCAACCCCTGATTAATGGAGGGACT	129100
Query	898	AAGCCAAAAAGAAAATGAATTAATTAATTTTAAACATTCATGAAATACGTATGTGAGCAT	957
Sbjct	129101	AAGCCAAAAAGAAAATGAATTAATTAATTTTAAACATTCATGAAATACGTATGTGAGCAT	129160
Query	958	ATGACAATAACAttttttttCATAGATAAAATCGAGAAGGTGGGACATGTCAAACCTCTCC	1017
Sbjct	129161	ATGACAATAACATTTTTTTTTCATAGATAAAATCGAGAAGGTGGGACATGTCAAACCTCTCC	129220
Query	1018	ATTTGAAAAGAGGACAAACACGTACATTTAGTAAACTATTC-CTGTTACGCTGGGT-AA	1075
Sbjct	129221	ATTTGAAAAGAGGACAAACACGTACATTTAGTAAACTATCCACTGTTACGCTTGGTTAA	129280

Query	1076	TTTC-AATTAACCTAC-TTAAACTGGAAAA-ATCCCAAATG-TGCTTC-AAAATCTGG	1130
Sbjct	129281	TTTCTAATTAGCCTACATTATAACTGGAAAACATCACAAACTTATGCTTCGAAAATCTGG	129340
Query	1131	AAAC-ACC-TATTGATAA-TATCCC-TCAAAA-TTGA-GAAGAAAAGGTAA-A-ATCC-T	1181
Sbjct	129341	AGACCACCATATTGATAAATATCCCATCAAAAATTGATGAAGATAATGTTAGACATCCCT	129400
Query	1182	CCTAA-CGCCTTTT-C-GTC-TAAAAG-GTCCAA-TGATT-CG-AAGGA	1222
Sbjct	129401	CCTAAGCGCCTTTTCTGTCATAAAAAGTGCCAAATGATTCGGAAGGA	129449

Supplementary Figure 1. BLASTn analysis of the forward sequencing result (zebrafish *abcb4* gene promoter). Wherewith, the query sequence is the sequence of zebrafish *abcb4* gene promoter obtained from First Base Laboratories Sdn. Bhd.

Supplementary Table 1. Summary of BLASTn analysis of the forward sequencing result (zebrafish *abcb4* gene promoter).

Gene name	Description of the highest score hit	Score (bits)	E-value	Identities	Gaps
<i>Abcb4</i>	Zebrafish DNA sequence from clone DKEY-24I24 in linkage group 16, complete sequence	1146 (620)	0.0	717/762 (94%)	14/762 (1%)

Query	686	TTAAATATCTAACATTGGCGGTTCAATGCGTTGTGGCAACCCCTGATTAATGGAGGGACT	745
Sbjct	129041	TTAAATATTTAACATTGGCGGTTCAATGCGCTGTGGCAACCCCTGATTAATGGAGGGACT	129100
Query	746	AAGCCAAAAGAAAATGAATTAATTAATTTTAAACATTCATGCAATACGTATGTGAGCAT	805
Sbjct	129101	AAGCCAAAAGAAAATGAATTAATTAATTTTAAACATTCATGAAATACGTATGTGAGCAT	129160
Query	806	ATGACTATAACATTTTGTATCGTAGATAAAATCGAGAAGGTGGCACATGTCAAGCTCTC	865
Sbjct	129161	ATGACAATAACATTTT-TTTTCATAGATAAAATCGAGAAGGTGGGACATGTCAAACCTC	129219
Query	866	CATCAGAAAAGAGGACCAACACGTACATTTAGTAACTATTCGACTGTTACGCTTGGTT	925
Sbjct	129220	CATTTGAAAAGAGGACAAACACGTACATTTAGTAACTA-TCCACTGTTACGCTTGGTT	129278
Query	926	AATTTCTAATTAGCATACATTATAACCGGAAAACATCACAAACATGTGCTTCGAAAATCT	985
Sbjct	129279	AATTTCTAATTAGCCTACATTATAACTGGAAAACATCACAAACTTATGCTTCGAAAATCT	129338
Query	986	GGAGACCACCATATTGATAAATATCCCATCAAAAATTGATGAAGATAACGTTAGACATCC	1045
Sbjct	129339	GGAGACCACCATATTGATAAATATCCCATCAAAAATTGATGAAGATAATGTTAGACATCC	129398
Query	1046	CTCTAAGCGCCTTTCTCTGTCATAAAAAGTGCCAAATGATTCGGAAGGAGATCTATAA	1105
Sbjct	129399	CTCTAAGCGCCTTTTCTGTCATAAAAAGTGCCAAATGATTCGGAAGGAGATCTATAA	129458
Query	1106	AGCATCCAGGCTGTGACGTAATCCCTAGAAACATAAAGTCAAGGCAGTATAAACGTGCGC	1165
Sbjct	129459	AGCATGCAGGCTGTGATGTAATCCCTAGAAACATAAAGTCAAGGCAGTATAAACGTGCGC	129518
Query	1166	GCGTCCGCATGCGTCAGATAGTCTCCAGTCCCGCGCCTCGCTGAGCTCATTGTGGAGG	1225
Sbjct	129519	GCGACCGCATCTGTCAGATAGTCTCCAGTCCCGCGCCTCGCTGAGCTCATTGTGGAGG	129578
Query	1226	GACAGCAGGGTGGGAAGAAGCCGTCAGAGCGGTAGGTATCTTTTCATTCA	1275
Sbjct	129579	GACAGCAGGGTGGGAAGAAGCCGTCAGAGCGGTAGGTATCTTTTCATTCA	129628

Supplementary Figure 2. BLASTn analysis of the reverse sequencing result (zebrafish *abcb4* gene promoter). Wherewith, the query sequence is the reverse-complement sequence of zebrafish *abcb4* gene promoter obtained from First Base Laboratories Sdn. Bhd.

Supplementary Table 2. Summary of BLASTn analysis of the reverse sequencing result (zebrafish *abcb4* gene promoter).

Gene name	Description of the highest score hit	Score (bits)	E-value	Identities	Gaps
<i>Abcb4</i>	Zebrafish DNA sequence from clone DKEY-24I24 in linkage group 16, complete sequence	928 (502)	0.0	561/590 (95%)	2/590 (0%)

Query	622	T T A A A T A T T T A A C A T T G G C G G T T C A T T G C G C T G T G G C A A C C C C T G A T T A A T G G A G G G A C T	681
Sbjct	129041	T T A A A T A T T T A A C A T T G G C G G T T C A T T G C G C T G T G G C A A C C C C T G A T T A A T G G A G G G A C T	129100
Query	682	A A G C C A A A A G A A A A T G A A T T A A T T A A T T T T T A A C A T T C A T G A A A T A C G T A T G T G A G C A T	741
Sbjct	129101	A A G C C A A A A G A A A A T G A A T T A A T T A A T T T T T A A C A T T C A T G A A A T A C G T A T G T G A G C A T	129160
Query	742	A T G A C A A T A A C A t t t t t t t t t t C A T A G A T A A A A T C G A G A A G G T G G G A C A T G T C A A A C T C T C	801
Sbjct	129161	A T G A C A A T A A C A - T T T T T T T C A T A G A T A A A A T C G A G A A G G T G G G A C A T G T C A A A C T C T C	129219
Query	802	C A T T T G A A A G A G G A C A A A C A C G T A C A T T T A G T A A A C T A T T C A C T G T T C A C G C T T G G T T A	861
Sbjct	129220	C A T T T G A A A G A G G A C A A A C A C G T A C A T T T A G T A A A C T A T C C A C T G T T C A C G C T T G G T T A	129279
Query	862	A T T T C T A A T T A G C C T A C A T T A T A A C T G G A A A A C A T C A C A A A C A T G T G C T T C G A A A A T C T G	921
Sbjct	129280	A T T T C T A A T T A G C C T A C A T T A T A A C T G G A A A A C A T C A C A A A C T T A T G C T T C G A A A A T C T G	129339
Query	922	G A G A C C A C C A T A T T G A T A A A T A T C C C A T C A A A A A T T G A T G A A G A T A A T G T T A G A C A T C C C	981
Sbjct	129340	G A G A C C A C C A T A T T G A T A A A T A T C C C A T C A A A A A T T G A T G A A G A T A A T G T T A G A C A T C C C	129399
Query	982	T C C T A A G C G C C T T T T T C T G T C A T A A A A G T G T C C A A A T G A T T T C G G A A G G A G A T C T A T A A A	1041
Sbjct	129400	T C C T A A G C G C C T T T T T C T G T C A T A A A A G T G T C C A A A T G A T T T C G G A A G G A G A T C T A T A A A	129459
Query	1042	G C A T G C A G G C T G T G A C G T A A T C C C T A G A A A C A T A A G G G C A A G G C A G T A T A A A C G T G C G C G	1101
Sbjct	129460	G C A T G C A G G C T G T G A T G T A A T C C C T A G A A A C A T A A A G T C A A G G C T G T A T A A A C G T G C G C G	129519
Query	1102	C G A C C G C G A T C T G T C A G A T A G T C C T C C A G T C C C G C G C C T C G C T G A G C T C	1150
Sbjct	129520	C G A C C G C G A T C T G T C A G A T A G T C C T C C A G T C C C G C G C C T C G C T G A G C T C	129568

Supplementary Figure 3. BLASTn analysis of the reverse sequencing result (first BLAST hits). Wherewith, the query sequence is the reverse-complement sequence of mutated zebrafish *abcb4* gene promoter that obtained from First Base Laboratories Sdn. Bhd. The sequence that framed in red color box indicates the mutation site, at which the bases AGT had been substituted into bases GGG, thus creating mutation in the AP-1 TFBS.

Supplementary Table 3. Summary of BLASTn analysis of the reverse sequencing result (first BLAST hits).

Gene name	Description of the highest score hit	Score (bits)	E-value	Identities	Gaps
<i>Abcb4</i>	Zebrafish DNA sequence from clone DKEY-24I24 in linkage group 16, complete sequence	931 (504)	0.0	521/529 (98%)	1/529 (0%)

Query	1	TGGAAC-TAGTTAGACAAGtttttttttttttagaataaaaaatttaggtttaagtca	59
Sbjct	128464	TGTAACCTAGTTAGACAAGCTTTTTTAAAGTTTATG-ATTAATAATTTAGGTTTAAAGTCA	128522
Query	60	aaaactgttcaacaataaaaaataaaa-tgaagaagtttct-ttt----taaaaa	112
Sbjct	128523	AAAACGTGTTCAACAATAAAAAATAAATAAATTAAGAAAGTTTCTATTTAAAAAATAAAA	128582
Query	113	aaaGTCTGCAAAATGAGGTAAAA-GGGTTTGATTATTTCAATCCAATAGACTTTTGCTT	171
Sbjct	128583	AAAGTCTGCAAAATGAAGTAAAATTAGTTTGATTATTTCAATCCAATAGACTATTTCTT	128642
Query	172	CTTAAATGGTAAATTT-GAGACaaaaaaaaTCAGTTTCTATTGAATTATTGGATTGA	230
Sbjct	128643	CTTAAATGGTAAATTTGAG--AACAAAAAATCAGTTTCTATTGATTATTGGATTAA	128700
Query	231	GTATGAGTAAAAATTAATATTTGTTTTATTCTGAAGGCCTGGAAACATTTCTTCAAAG	290
Sbjct	128701	GTATGAGTAAAAATTAATATTTGTTTCATTCTGAAGGCCTGGAAACATTTCTTCC-AAT	128759
Query	291	TTTAAATATAAATATTGTAATTTTAGTGTTTTAAAGAACAATTAGTCAGGGTTATTCCAT	350
Sbjct	128760	TTTAAATATAAATATTGTAATTTTAGTGTTTTAAAGAACAATTAGTCAGGGTTATTCCAT	128819
Query	351	CAAATACAGTAGATTTTGCAAAATCCGCTCTTGAAGTTAAGATGTTGTATTGTGTGTCT	410
Sbjct	128820	CAAATACAGTAGATTTTGCAAAATCCGCTCTTGAAGTTAAGATGTTGTATTGTGTGTCT	128879
Query	411	AAAATTGTCATTGTGCTTGTATTTTATGCTAAAAATTTTAAATGACAACATTTTATT	470
Sbjct	128880	AAAATTGTCATTGTGCTTGTATTTTATGCTAAAAATTTTAAATGACAACATTTTATT	128939
Query	471	ATACGTTTGAAAAACAGTAGACCCACAGAATCAAACAACTCAAACACAAAATGATCGTA	530
Sbjct	128940	ATACGTTTGAAAAACAGTAGACCCACAGAATCAAACAACTCAAACACAAAATGATCGTA	128999
Query	531	ATAAACAGATA-TT-ATTGTTCTTTTTCAGTCAAACCTTATTT	571
Sbjct	129000	AAAAACAGATAGTTCATTGTTCTTTTTCAGTCAAACCTTATTT	129042

Supplementary Figure 4. BLASTn analysis of the reverse sequencing result (second BLAST hits). Wherein, the query sequence is the reverse-complement sequence of mutated zebrafish *abcb4* gene promoter that obtained from First Base Laboratories Sdn. Bhd.

Supplementary Table 4. Summary of BLASTn analysis of the reverse sequencing result (second BLAST hits).

Gene name	Description of the highest score hit	Score (bits)	E-value	Identities	Gaps
<i>Abcb4</i>	Zebrafish DNA sequence from clone DKEY-24I24 in linkage group 16, complete sequence	863 (467)	0.0	547/583 (94%)	16/583 (2%)