

Additional file 3

Name	Forward	Reverse	Size (bp)	E (%)	R ²
<i>Askopos</i>	TCTGGTAGTTCCTGCGTGTGAG	GCTCTTCAACCTCATCACCCA	55	104	0.998
<i>Sidkey-30j22.9</i>	GCAAGGTGTCACTCAAGGCAC	GTACTTCAGACCTGTGGAGGGTT	95	102	0.999
<i>Betaine aldehyde dehydrogenase</i>	GTATCCACCAAACGGCACTTC	GCAGGTACTCAGGCGAGCC	50	104	0.999
<i>Checkpoint 1</i>	GGCAGGTACTCATTCCAATTACAG	GAAACGGCTACCACATCCAAG	83	100	0.998
<i>Prohibitin 2</i>	GGAAGGACTACGACGAGCGAG	GGGACACCTGTGCTCTCTGTG	69	99	0.999
<i>Synthaxin 4</i>	GATGATGAAAATGAGGACAAAGC	CCCATCCTCCTCTGACTTCTTG	252	100	0.998
<i>18K hypothetical goldfish protein</i>	AGTTACTTCTTCTCCCGCAAGC	GATCCAACATCGAGGTCGTAAAC	122	93	0.999
<i>HR6A</i>	TATGTTTGGACATCCTACAGAATCG	CGGACTGTTGGGATTTGGTTC	58	98	0.999
<i>Tudor 5 protein</i>	CTGTCACTCTGAGGGCTTTATCC	TCTGCTGGATGTGGCTCCTC	88	100	0.997
HHC00057	CAGGTCGTCTGTTTTGCCATTC	CATAAAGAAGGTGGAAGCCAGG	146	92	0.999
HHC00068	ACATCTCCTCCCACGATTCA	TTGAGGAGTGCAACCCAATC	114	98	0.998
HHC00130	GGAGGGATCTTTGGTTTCTTTG	CAACAAGGAGAACCGCACAG	67	99	0.998
HHC00222	TACTGTGTAGATGCCACGAAAGAG	CCGTTGATGTCGTGGAGTTTG	96	97	0.999
HHC00255	ATAATACATCCCAAAGCCCAGAG	CACAATAAGGGGATAATACACAGAGA	198	104	0.999
HHC00309	GGACGGGGAGATTAGAGTCATC	GAGCCCAAGTCCTGGTATGCC	93	105	0.998
HHC00334	CCATGAGGTAGCAGTAGAGGAAGG	GCTGGTATTGTCCTGGCGAAG	115	95	0.997
HHC01010	GAAGAGAGGAAGAACATAAAGACGG	CATCCCTGAGTAGAGCACACTTG	149	93	0.999
HHC01015	CCACTAGAAGTGTGTGCAAGATC	CGTTTCCAGGTTTTTTGAATCC	85	97	0.998
HHC01032	CCGCATTGATGACTTTGATGTG	CTGGACTCATAGTGGCTAATTCACC	143	99	0.996

HHC01194	ACTAAGACCCAGCCAGCAGAAG	GGTGGAGGGAGGAGTTTCTTTG	179	99	0.999
HHC01310	TATGAGGAAGCGGTGGTTTG	GAGCCTGCCCAACCTTATCAT	75	98	0.998
HHC00005	CCGAGCGGAGGGATTAGC	CAGCCATCAGGTTGTCCACG	229	99	0.998
HHC00036	TAAACGGCTCTGTTGTCCCAT	GTACACGCTGTCGCTTCCAG	284	92	0.999
HHC00106	AGGCATCTGGCACAATGAGAAC	CTCTCTACTTCTGGGCAGGGAT	462	89	0.999
HHC00189	GGGTGGCTTCATCTCACTTC	GTTTGAACCCGTGTCGGAG	313	95	0.998
HHC00233	AACAGCCTGTCGGGTTTGTAAC	GATGCTGGGATCAGTGCTGC	211	92	0.997
HHC01306	TCGGCTTTTTTCCACTTCCTC	GGTGGGGGAATGTGAGAGAAG	262	98	0.999
HHC01032	CTATGATGGCAAGGGTATCGG	TTAGGGCTTACTAGCGAACGGG	297	99	0.998
HHC01385	GAACTACCAGAGGAGAGGGCAATC	CTTACCCAAAGACCCCATCCTG	127	98	0.997
HHC01481	GGGACTCATCTCGTGGGTCT	AGCAGTATTACTTGACCTCGCC	125	98	0.999
