The Supplementary Table S1-S2

Table S1.Overview of the sequencing reads alignment to the reference genome

Sample	Clean Reads	Mapped Reads	Uniq Mapped Reads	Multiple Map Reads	GC Content	(%)≥Q30
H1	48,911,196	46,744,271 (95.57%)	45,332,170 （92.68%）	1,412,101 (2.89%)	53.84%	95.46%
H2	52,626,036	49,974,510 (94.96%)	48,425,710 （92.02%）	1,548,800 (2.94%)	53.20%	95.52%
H3	48,352,530	46,370,897 (95.90%)	45,006,450 （93.08%）	1,364,447 (2.82%)	53.42%	95.39%
H4	46,259,594	44,115,880 (95.37%)	42,752,634 （92.42%）	1,363,246 (2.95%)	53.11%	95.25%
X1	46,758,086	32,513,488 (69.54%)	31,664,157 （67.72%）	849,331 (1.82%)	50.80%	95.01%
X2	40,761,760	30,283,325 (74.29%)	29,279,572 （71.83%）	1,003,753 (2.46%)	52.26%	94.82%
X3	50,006,008	36,339,224 (72.67%)	35,190,724 （70.37%）	1,148,500 (2.30%)	52.35%	95.17%
X4	53,124,936	38,975,952 (73.37%)	37,826,214 （71.20%）	1,149,738 (2.16%)	52.35%	95.22%

Table S2. Primer information

Gene	Accession No.	Primer sequences (5'-3')	Products length (bp)
CRYAB	NM_174290.2	F:ATGAAGAGCGCCAGGATGAAC R:AGTAATGGCGAGAGGGTCCA	92
GAMT	NM_001038544.2	F:ACCCTGCCAGACAGTCACTT R:GGAAGGCATGGTCCCGAATG	106
NT5DC2	XM_003587635.2	F:ACTTGATGAGAAGGGCTCGC R:GTCAAACAGGTTTCCCTGCC	85
CALM1	NM_001242572.1	F:GGCACCATTGACTTCCCAGA R:ACCCGTTGCCATCCTTATCG	115
MYH1	XM_010815980.3	F:TACCCTGGGGATGAGTATGAC R:ATCAAAGACCCTGCCTTGGAG	91
COX6C	NM_001244111.1	F:TTTGGACTCTTTCGGCCACC R:TTCTTCTCGACGACTCAACCG	131
COX7C	XM_005209728.4	F:GTGAGGTAAGGAGCGGTAG R:ATAGTGGCTCCGACGAAC	140
PGM1	NM_001076903.1	F:GGGGACGGCAGGTTCTACAT R:AACCAAGCGACCAATCCCG	81