

Figure S1. Clustal alignment of 4 GH45 genes.

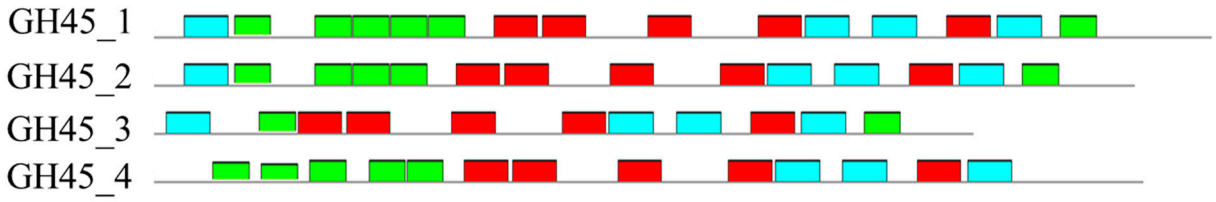


Figure S2. Gene structure variations among different GH45 copies.

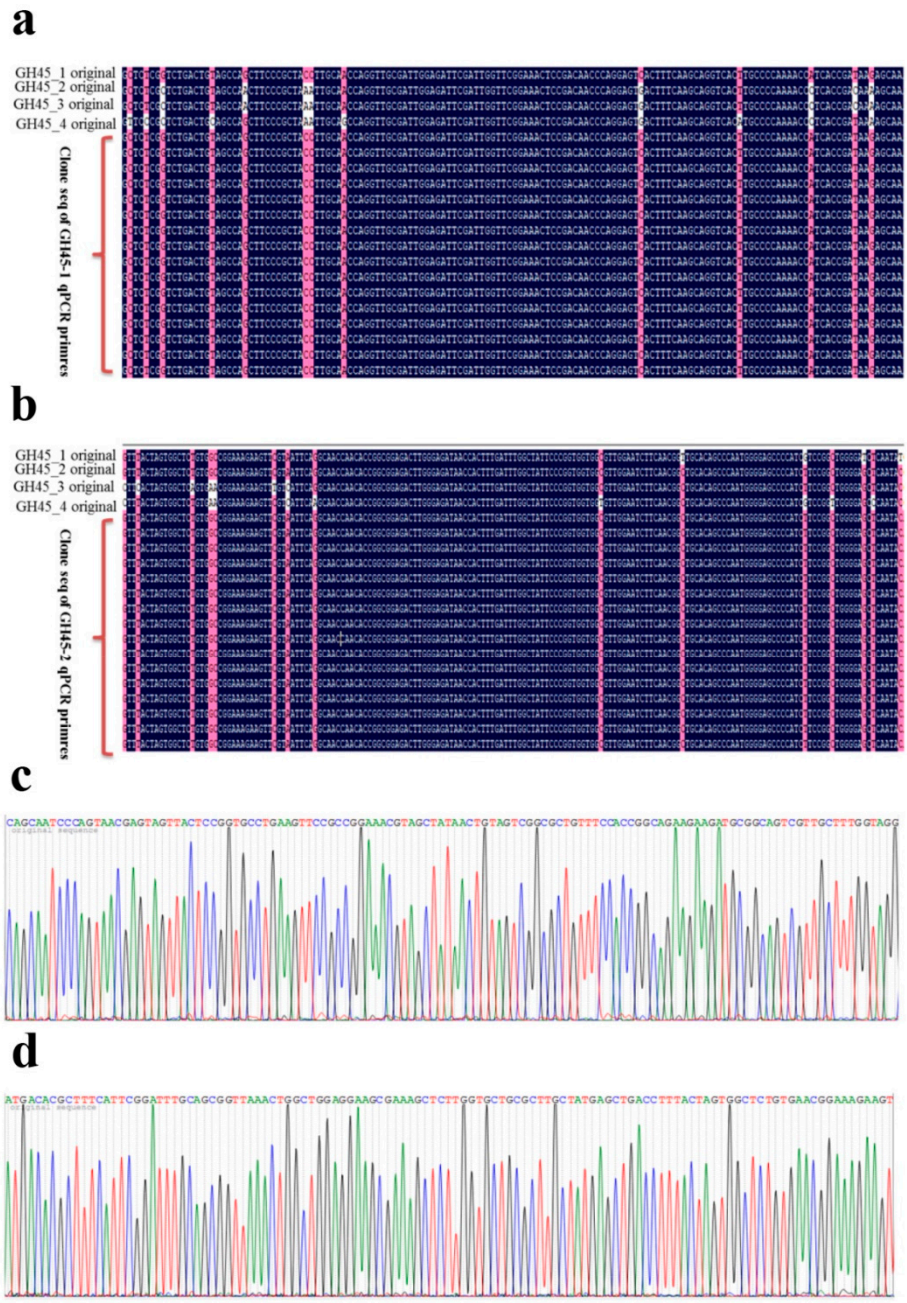


Figure S3. Clone sequencing results of GH45 qpcr primers;(a) Clone sequencing of GH45_1 qpcr amplification results (~20 clones), (b) Clone sequencing of GH45_2 qpcr amplification results (~20 clones), (c) Clone sequencing of GH45_3 qpcr amplification results—only one clone was sequenced since the primers were designed on highly divergent regions and(d) Clone sequencing of GH45_4 qpcr amplification results—only one clone was sequenced since the primers were designed on a highly specific region.

Table S1. Primer design for the GH45 RT-PCR assay.

ID	Sense Primer	Antisense Primer
45_1	TTGCTCTTATCGGTGATGG	GCGTTGTTGTTGGAGAAC
45_2	GGTGTTGGTTGCCTGAAT	CGTGGTGGAAGGTAAGAC
45_3	CTGCCGCATCTTCTTCTG	GCTGACTCCACCGTATTG
45_4	CCGCGACAACAACTACTG	GCATGTGACCTGCTTGAA

Table S2. Primer design for the long-range PCR assay.

ID	Primers
P1-Sense	CAGATATTCGGAGGACAAGTTCAT
P2-Sense	CTTACGTTCGCTTTCTAAATAGGG
P2-Antisense	CACATACCAAGTCGAATATCTGGA
P4-Antisense	TAGTTAGACAATGGAGGAGAACAG
P5-Antisense	TGATGTATATCTCGACCTGTAACTC

Table S3. Primer design for the GH45 qPCR assay.

ID	Sense Primer	Antisense Primer
q45_1	TTGCTCTTATCGGTGATGG	GCTCTCGGTCTGACTGTA
q45_2	GTTTACTAGTGGCTCTGTGGC	GTATTGAGCTCCCCAGCCGGAA
q45_3	CCTACCAAAGCAACGACTG	CAGCAATCCCAGTAACGAG
q45_4	CCGCGACAACAACTACTG	CAGCAATCCCAGTAACGAG