

Table S1. Primer sequences used for RT-qPCR in this study.

Marker	Forward Sequence (5'-3')	Reverse Sequence (5'-3')
<i>GLuRS</i>	GCTCTCCGCTCAAGTGAATACC	GATCAGTCCAGTCCTCCACCTT
<i>ALAD</i>	GGCATGGGCTTCTTGATGAGG	CCAGAGCAACATCCGTGTAGAC
<i>PBGD</i>	GAAGGATTGACATTGCCGTCCA	GTCTACGCAGAGAAGCACTTCC
<i>UROD</i>	GACGGCGTCATCCTGTTCTC	TGCGTAGAATCTTGAGCGACTC
<i>CPOX</i>	AAGCACCGTAATGAGCGTCG	TCAGTTGTTGCCATGCCTTGT
<i>POR</i>	TCATCCTCGGCTCCATCACC	CTCCTGCATCGTCAGCATGTT
<i>DVR</i>	CAGGTTCAATCAAGGTGCCGAT	CGTCATCTCGTCGCTGTACTC
<i>CAO</i>	GCATGGACTTCTGCTGGACAA	AGATGCCAGTGGTTGACAAGAC
<i>HCBR</i>	GCAGGAAGCAAGACATGGATGA	GCATTGGAGCAAGCCTGTCA
<i>CHLG</i>	GGGCACTGTTGTTAGCAGGG	GCCAATGTAGCTCGCACCAA
<i>NOL</i>	CACTGCTTCTCCTGGAATGGTC	GCAAGATCCTTGGTGGTGTCAA
<i>MgCH</i>	AAGATGGTTGCCGAAGTGGATG	ATGTCCTGGAGCTGCTTCTCA
<i>UBQ10</i> *	CTCATCTCCTCTCCTCGCATCA	CCACCAATCGGATCTAGCAACA

* Reference gene.

Table S2. Summary of genome mapping.

Sample	Total Clean Reads	Total Mapping Ratio [%]	Uniquely Mapping Ratio [%] *
<i>ch11</i>	29,328,341	97.93	90.26
Wild-type	25,306,787	96.84	89.16

* Unique mapping ratio: Percentage of reads that map to only one location in the reference genome. *ch11*, chlorophyll *b*-deficient mutant.

Table S3. Summary of gene mapping ratio.

Sample	Total Clean Reads	Total Mapping Ratio [%]	Uniquely Mapping Ratio [%] *
<i>ch11</i>	28,328,341	89.67	80.42
Wild-type	25,306,787	88.93	79.56

* Unique mapping ratio: The percentage of uniquely mapped reads. *ch11*, chlorophyll *b*-deficient mutant.