

Supplementary Information

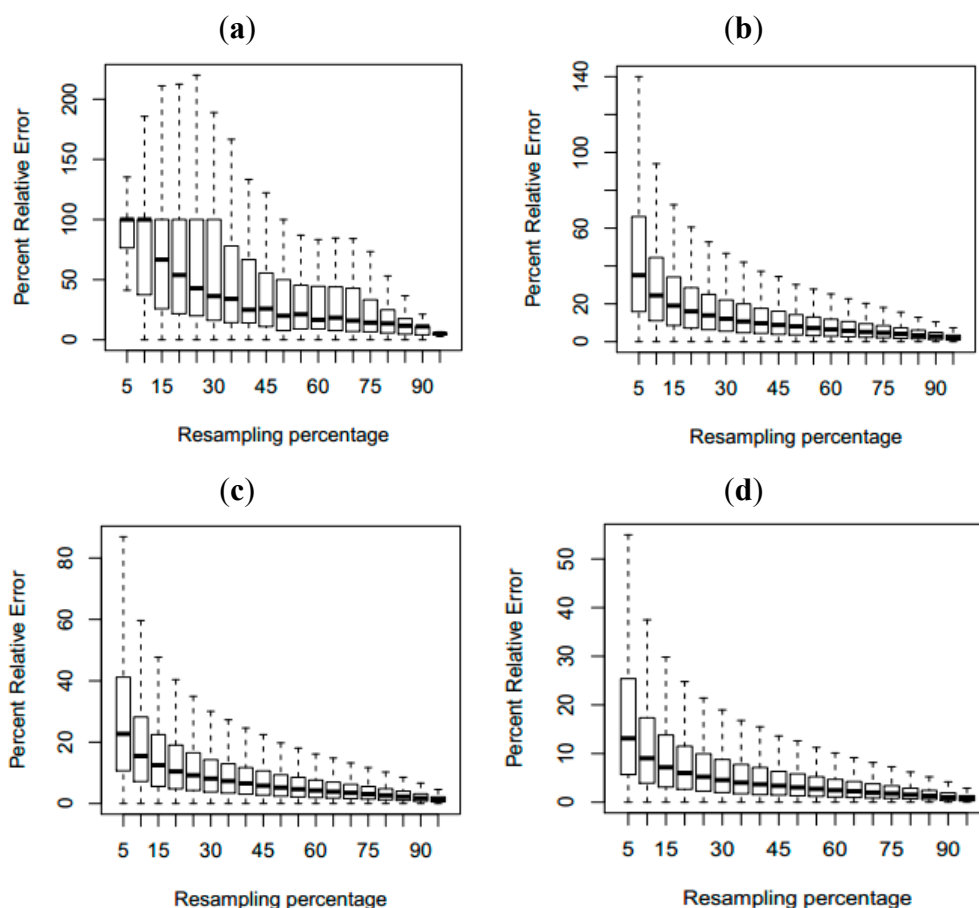


Figure S1. Saturation analysis of gene expression in red skin. **(a)** The saturated expression levels of transcripts with expression level ranked below 25 percentile with increasing RNA-seq data; **(b)** The saturated expression levels of transcripts with expression level ranked between 25 percentile and 50 percentile with increasing RNA-seq data; **(c)** The saturated expression levels of transcripts with expression level ranked between 50 percentile and 75 percentile with increasing RNA-seq data; **(d)** The saturated expression levels of transcripts with expression level ranked above 75 percentile with increasing RNA-seq data.

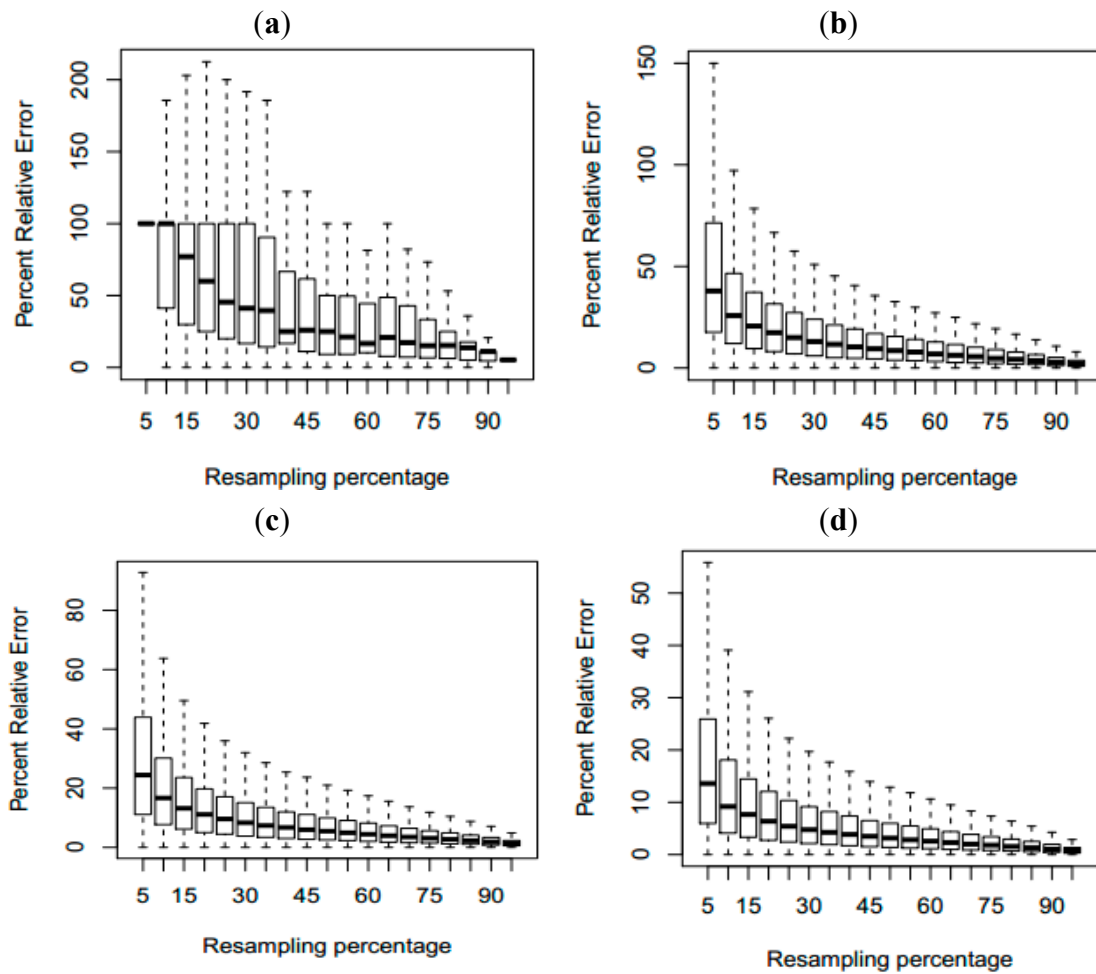


Figure S2. Saturation analysis of gene expression in white skin. **(a)** The saturated expression levels of transcripts with expression level ranked below 25 percentile with increasing RNA-seq data; **(b)** The saturated expression levels of transcripts with expression level ranked between 25 percentile and 50 percentile with increasing RNA-seq data; **(c)** The saturated expression levels of transcripts with expression level ranked between 50 percentile and 75 percentile with increasing RNA-seq data; **(d)** The saturated expression levels of transcripts with expression level ranked above 75 percentile with increasing RNA-seq data.

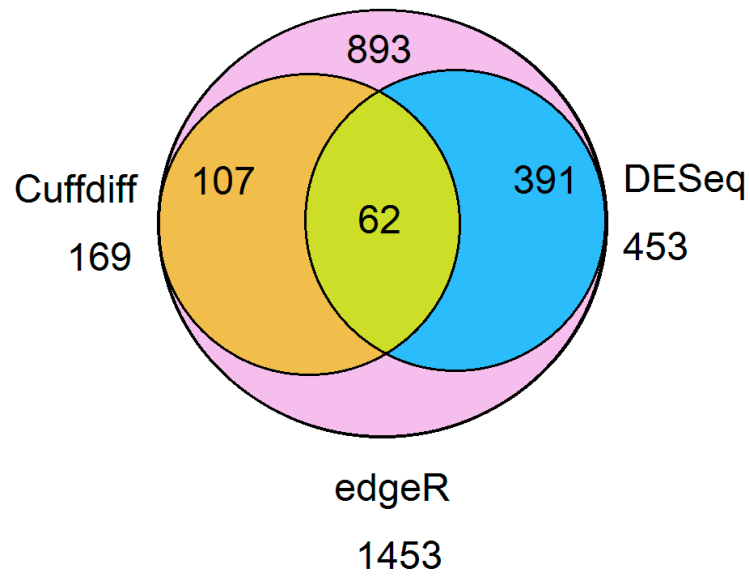


Figure S3. Crossover of DEGs results identified with different methods. The pink region represented unique DEGs identified with edgeR. The orange section showed the DEGs identified with Cuffdiff and edgeR and the blue section indicated DEGs identified with DESeq and edgeR. The central yellow section exhibited the consensus DEGs identified with all three methods.

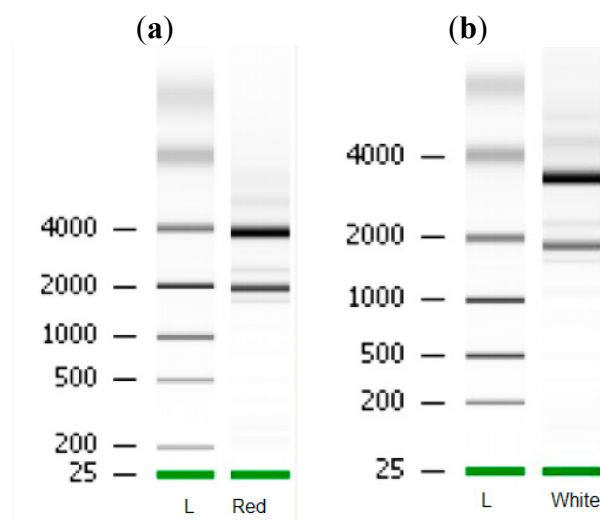


Figure S4. Gel electrophoresis with Bioanalyzer 2100. L: ladder. (a) Red: red skin; (b) White: white skin.

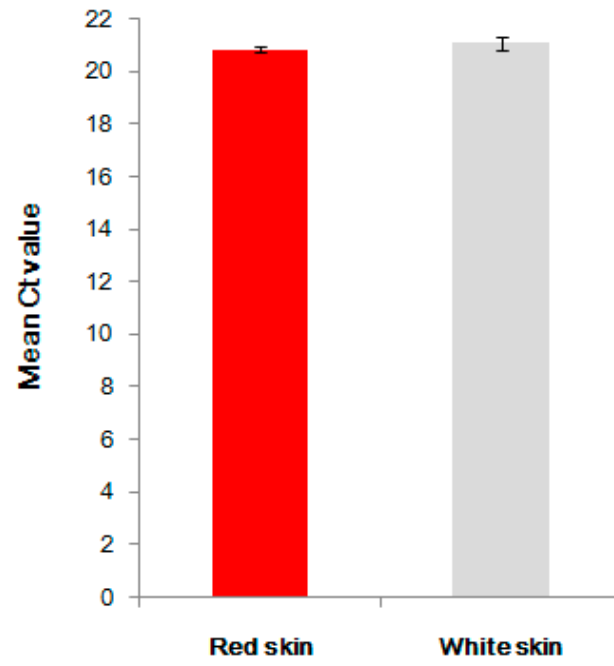


Figure S5. The normalized C_t values of β -actin in red skin and white skin.

Table S8. The specific primers for RT-qPCR including 52 DEGs and eight key enzymes in the melanin synthesis and the pteridine synthesis pathways.

| GenBank Accession | Gene Symbols | Forward Primer | Reverse Primer |
|-------------------------------|--------------------------|-----------------------|------------------------|
| M24113 | <i>beta-actin</i> | ACTACCTCATGAAGATCCTG | TTGCTGACCACATCTGCTG |
| FJ710827 | <i>18S rRNA</i> | GGGGAGTATGGTTGCAAAGC | CGCTCCACCAACTAAGAACG |
| The identified 52 DEGs | | | |
| Gene ID | Gene Symbols | Forward Primer | Reverse Primer |
| XLOC 041967 | <i>actn3b</i> | GAGATCCGTCGTCTGGAGAG | CCATTAGAGAGGCCGTTTCA |
| XLOC 044558 | <i>hspb11</i> | AGCACATTTCAGCCTCACCT | TCCAGGTTTTGCCTCATCTC |
| XLOC 010707 | <i>asb2a.1</i> | TGAGAAGGAGAACCCAGCAA | CGGCCACAAAGATAGGAGTG |
| XLOC 020562 | <i>gpib</i> | GGGATACACTGGGAAATCCA | CGATGCGATGATGAAGAGTG |
| XLOC 044449 | <i>usp28</i> | AGGAGTTGCTGGTGCTCCTA | TCATGGGGAGAGTTCCTCAC |
| XLOC 048918 | <i>gvs1</i> | GATGGCTGATTGAAGGCTCT | GAGGAGGTTTCGTCACACTGAG |
| XLOC 040360 | <i>prx</i> | CTCAGGGAAAAGGTCACTCG | TTCTGCACTTGCTTCACCAC |
| XLOC 048485 | <i>flnca</i> | GGGACAACAAAGATGGAACAG | TACAGCAAGGGACAAACCACT |
| XLOC 032972 | <i>ldb3b</i> | CACTCCAAGAATGGACTCACC | ATAGTAGCCTTCCCACCAGGA |
| XLOC 017077 | <i>jd2</i> | CGACTGAACACCACACCACA | ATCTCGGGGAGGTTTGTGTTG |
| XLOC 005340 | <i>txlnba</i> | GCAGGGAGCTTCAGAGACAT | TCCGCTCATACTGCTCTACG |
| XLOC 012134 | <i>txlnba</i> | GCTTCCAGAGCTTGTCCAAC | GGAATCTTTTGTGCCGTCTC |
| XLOC 027731 | <i>tnni2b.2</i> | GGCTGAGGAAAAGCAGGTAGT | TCGCCCTTGGTCACTTTAAC |
| XLOC 029054 | <i>neb</i> | GACAGAGGAGCACGATCAGG | TGACTTCTCATCGCCACAC |
| XLOC 037504 | <i>aldoab</i> | TACAGAACAACAGCGCAGCA | GAGTGAACAGCCGGATGAGT |
| XLOC 012413 | <i>jph1b</i> | CAAAGAGAGCAAACCCGAAC | GTGCCGTCAAGTGAGGAAAT |
| XLOC 034449 | <i>klhl31</i> | GGTCTCCTGTTTCGCTGTAGG | CAATAACTGTGCTGGCATGG |
| XLOC 043658 | <i>trdn</i> | AACAGGAAAGGCACAGAGAGC | GGTAGTCGTAGTGGTGGAGGA |
| XLOC 043281 | <i>myl3</i> | CTTAGGCAAACCCAAAGCTG | AGCGAGGACGTGTCTGAGTT |
| XLOC 049850 | <i>cox6a2</i> | ATACCCACACCTCCGCATT | TATTGGCATCTGAAGGGACAG |
| XLOC 020085 | <i>pygma</i> | TTACGAGAAAGACCCCAACG | CATTTCCCAGTCCAGCATCT |
| XLOC 047772 | <i>pygma</i> | GGTGTAGAGCCCACTCTGGA | GCAAGACAGGCATAGCTGGA |
| XLOC 039918 | <i>desma</i> | AGAATATCGGAGAGGCTGAGG | GATGCCCTTGAGAGAGTCGAT |
| XLOC 043184 | <i>myom1a</i> | GGCATCTTTGTTTCCAGGTG | CCGTTGGCTAAACGTCTGAT |
| XLOC 007687 | <i>CABZ01065679</i> | GGAATCTCACCCCTCCAAT | CTCTTCGCTGACAAACCACA |
| XLOC 043191 | <i>ckmt2a</i> | CAAGATCACCCCGAACAAC | GCCATTGTGTCTGTCTTGA |
| XLOC 038671 | <i>txlnbb</i> | TGGAGAGCTGTTCCAGTCTA | CTGCCTCTTCTCAACATCCT |
| XLOC 006362 | <i>mylk3</i> | GGAGGGTGGTGAATTGTTTG | CTTCTGGCGAGTCCAAAGTC |
| XLOC 049820 | <i>ptrfa</i> | TGGGCAAGAAGATGGGTAAG | AGGGCGGTACACGATAAGT |
| XLOC 034539 | <i>dusp27</i> | GTGCTTGTCGCTGCTTATCTC | GTCTCGTCATCGTCTTCGTCT |
| XLOC 013421 | <i>mlf1</i> | GGAAAACCGGAGAGAAGGAG | CTTTGTCATCCTGCGTGTGT |
| XLOC 012308 | <i>klf4a</i> | TTGTCGCTGAACATGATGAGG | GATGGTGCAGGTGCTAGGAT |
| XLOC 014119 | <i>junbb</i> | GTCCACCACCATCAGCTACC | CGTTCCTGGTTCTCCATGTC |
| XLOC 036958 | <i>si:dkeyp-69b9.3</i> | AATCAGACACAGGTGGACAGG | CCGATAGTAGGTGATGCTTG |
| XLOC 037669 | <i>ucp3</i> | CCACCAACTGCTGCTATCAA | GGTGCCAAATACTCCACGAT |
| XLOC 047593 | <i>si:ch211-270g19.5</i> | GTGTCCTGAGAGCCTGTGTGT | TAGTGGCAGTGAGAGGAATGG |
| XLOC 002126 | <i>slc16a3</i> | ACCACCTGGAGCAGTCGTATT | ACCTCCGTTGTCTTGGTTGTC |

Table S8. Cont.

| Gene ID | Gene Symbols | Forward Primer | Reverse Primer |
|-------------|-----------------------|-----------------------|-----------------------|
| XLOC 003593 | <i>tecra</i> | GGAGAGTCAGGTGAAGGCAG | GTGTGAAACCCAGCCAAGAT |
| XLOC 009384 | <i>ier2</i> | CACCATCTGCGTTGCTCTTA | GCCAGGATCAGCAGGAATAC |
| XLOC 012213 | | CTGCTGTCCTTGTGTTGTGC | CAGCCACAGACCCTGACTTT |
| XLOC 013877 | <i>pgam2</i> | GTGGGCAGGTTTAGCTCCAT | AAGGGTCTGAAAGAGGGTGAG |
| XLOC 015357 | <i>myh13(3 of 11)</i> | ACAAGCTGAGAGCCAAGAGC | CGTTGCATCCCTACTTCCAA |
| XLOC 015449 | <i>murc (1 of 2)</i> | GTCTTCTCGCGGGTCTTGTT | GGCTTGCTAACTTGGAGGTG |
| XLOC 018534 | <i>CABZ01080590</i> | GACAGGGCCATTCACTGTTT | TTGGGTGTCTGTGTTTCGTGT |
| XLOC 047486 | <i>obsn (1 of 2)</i> | GCACCCTCTGACTCTGGAAC | GTGGTGAAGAACACCCGTATG |
| XLOC 018681 | <i>pgam2</i> | CCAACACAAGGGGGTTTACA | CAGGGCAAGGTCAAAAAGTG |
| XLOC 023992 | <i>zgc:153911</i> | GGCTGATGGAGAACTCAGACA | GCGGTTTGTGTGTCAGTATG |
| XLOC 017474 | <i>btg2</i> | GCAGGCGCTATCAGACACTA | GATGCGGTAGGACACTTCGT |
| XLOC 022372 | <i>btg2</i> | CCTCTTGCCTTAACCACAGC | CCTGGGAAAACACGATCACT |
| XLOC 030124 | <i>tpm2</i> | CTGCCCTGACATTAACAGCA | ACCTCTCTCTGCAGCAGCTC |
| XLOC 017074 | <i>fos</i> | ACCAGTCATCCGACTCCTTG | GCTACATTTGGCAGGCATGT |
| XLOC 049242 | <i>ier2</i> | AACTTCCCCGGATACCCATA | CAAATCCCAGTCAGTCGTCA |

Eight key enzymes in the melanin synthesis and the pteridine synthesis pathways

| Gene ID | Gene Symbol | Forward Primer | Reverse Primer |
|-------------|--------------|------------------------|-----------------------|
| XLOC 002909 | <i>xdh</i> | CAGTTATGGTGTGGCCGTCT | CAGGTCCGCGAGTGTATAGGT |
| XLOC 004598 | <i>aim1</i> | AATAACAGCCGCGATACACC | GAAGGGTCTGCTGAAGTTGC |
| XLOC 036450 | <i>pam</i> | TCTATGCGGTGAATGGAGTG | TGCTGCGTCTCCTACAAAGA |
| XLOC 039905 | <i>fbxw4</i> | AGGACATTGAGCCATTGAGG | GATGGAGTTATCGCGTAGCC |
| XLOC 043728 | <i>gchfr</i> | GCCGAGTTGAGTTTGACAAGAG | GCTCCATGATTGCCTGAAAG |
| XLOC 044134 | <i>gch1</i> | ACTTTGACGGACGGGTGAAG | GGCAGGCTCATTTTCATTGTC |
| XLOC 051515 | <i>mc1r</i> | CGAACAGGTTTAGCACAGCA | ATGAAACGGGACTGGAGTTG |
| XLOC 050939 | <i>spra</i> | AGCTTCTCTCGGGGATGTGT | AGCTGATGTTGACGATGACG |

Table S9. The BS-PCR primers of *gpib* and *klf4a*.

| Gene ID | Gene Symbol | Forward Primer | Reverse Primer |
|-------------|--------------|------------------------------|------------------------------|
| XLOC 020562 | <i>gpib</i> | AGGTTAGTAAGGAATTTTGGTTTTT | CATTTTCTATATTTCAACCCAAAAT |
| XLOC 012308 | <i>klf4a</i> | GGATAGGTTTGTGGTTTTATTTTAATAG | TTTCCACACTAACACTATAAACTCTTTC |