

Supplementary Material

The Supplementary Material for this article can be found online at the additional information tab for this paper:

1. Supplementary Figure

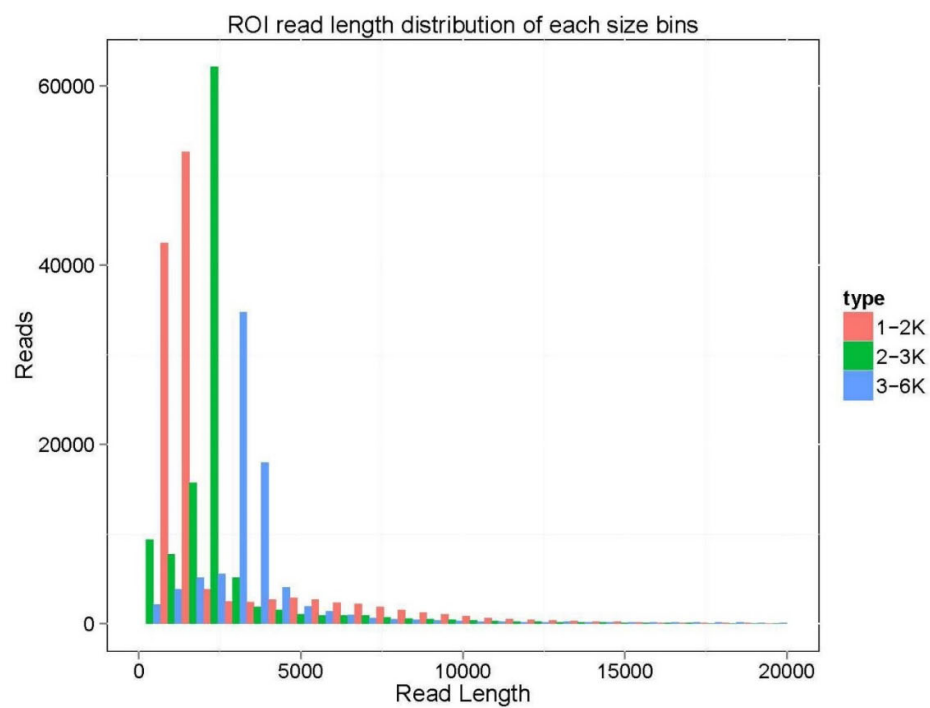


Figure S1. Summary of PacBio RS II single-molecule real-time (SMRT) sequencing.

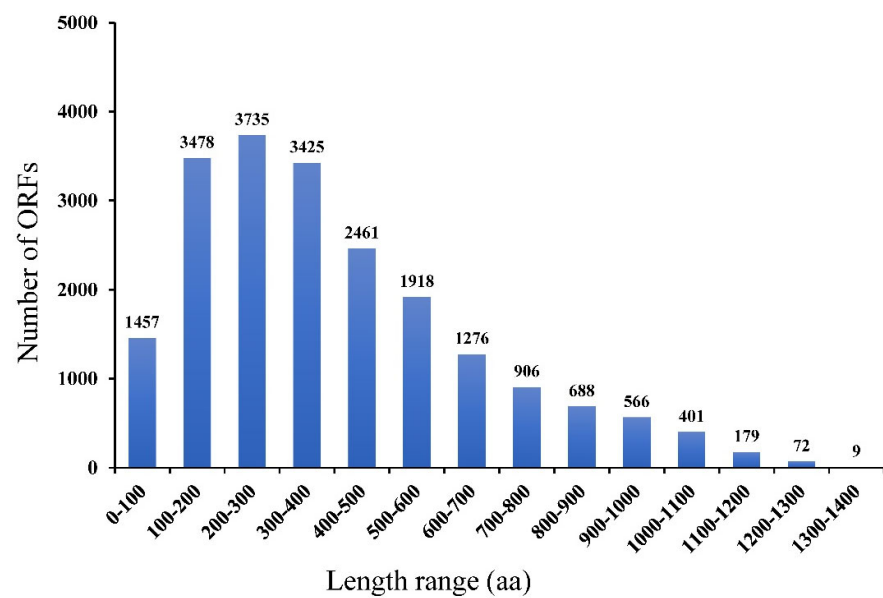


Figure S2. Length distribution of ORFs with new transcripts.

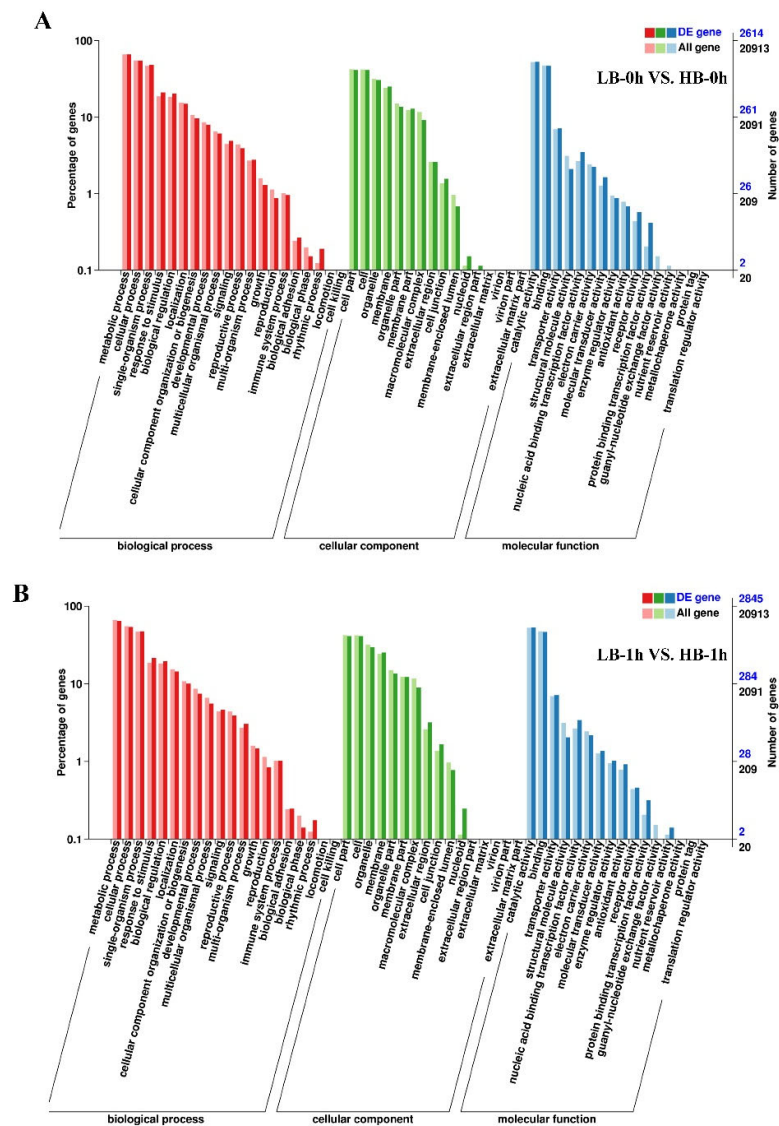


Figure S3. Gene ontology (GO) categorization of pear flesh DEGs. (A) GO analysis of DEGs between low browning (LB) and high browning (HB) at 0h in three main categories. (B) GO analysis of DEGs between low browning (LB) and high browning (HB) at 1h in three main categories.

2.Supplementary Table

Table S1. Primers designed for qRT-PCR validation

| Category | Transcript ID | Forward primer (5'-3') | Reverse primer (5'-3') |
|----------------|---------------|------------------------|------------------------|
| reference gene | YLS8 | TGAGGTGCTGGCTTCTGT | TGACCGTTGATGGATCGTA |
| | Pbr012851.1 | GAGGTTCCGGTTGCATTGT | GGTGACTTCGGAATGGCTTC |
| | Pbr024635.1 | ACAGGTGGACGGAGAGAATC | TGAGTCCGCAGAGAAACACT |
| | Pbr030350.1 | AAGCCTCAACCTCCCAAACA | TCTCCTGTGTGTACCCAACC |
| | Pbr036272.1 | GAAGCACGGGGACATAAACG | GTGAGACTTGTACGTTCCGC |
| | Pbr039972.1 | GAACCGATGCCATCCAAGTC | ACATAACCCACGTCACCAGT |
| | Pbr027985.1 | CGGTGCTGTTCAAGGTCCTA | CTTCGTTCTGAATCGCTCACC |
| | Pbr017290.1 | CAGAATCATGTTGACCGGC | GTTGTAGTCGAAGCTCTGCG |
| | Pbr006709.1 | TTGTCGGGGCTGATTCTCTT | AAGCCTTCCCCTCAAATGGA |
| | Pbr022422.1 | GCAGGTTCTGTGGATGTCCA | GAACGAGTTGCCATGATGGC |
| | Pbr022425.1 | CTGCTCCACAGATGAAGACC | TCAAGATGTTGAGCTGATCC |
| mRNA | PB.10426 | AGACTTTCTCTTTGGCGTGT | GCGACGTTTTAGTACTCTGGAG |
| | Pbr35186.1 | ATGAATCATGCCCGAATGCC | AGCAATCGTGGAAGTGAAGC |
| | Pbr000321.4 | ACCACAACCTACCCTCTTCCG | TCTTGCTAGGCCCTGGTCTA |
| | Pbr000322.1 | CCCACCTGACCTAACCAAGT | TCCGGAGTGAAGGCTTTGAT |
| | Pbr029378.1 | GCTTCGGAAACTTCGGTCAG | TGCTCGCAAAGATCATTCGG |
| | Pbr017091.1 | GGTGGACAGTATAAGGGCGA | TCCGGCTTCTTCCCTTGAAT |
| | Pbr026287.1 | ACCCACTTGAGCCTTACCTC | TCCTCCCAAGCATGACCATT |
| | Pbr022402.1 | TCTGCAACCAACTGTCAACG | GCACACTCTCAGCACAAAGA |
| | Pbr019531.1 | CTCGCTCTTCTGGATTGCAC | ATGCACTCGACATGTTTCCG |
| | Pbr020145.1 | CCAAGCCTCATCACTGGACT | TGAGAAAGGCAGAGGTCGTC |
| | Pbr033501.1 | AGGCTGTTGGGAAGGAGTTT | CCACCCACCCTTTCTTCGTA |
| | Pbr011477.1 | TACGCCCAAGACCAATTCCT | CAACGCTGACCAACTTGTGT |
| | Pbr013248.1 | CCCTAGAGTCACCGTCACTG | GCCCTTCCACCGCAAAATTA |
| | Pbr008363.1 | ACAACAACGTCACTCCATGC | AGAGGCATTGAGGGTCTGAC |
| | PB.14775 | TCCACAGCCTCAGGAAGAAC | TGCCAGCAGTACCGAAACTA |
| | Pbr001923.1 | GTGTGAACGAAGCAGGCATT | GCTGGATTCAACATGGGTCC |
| | PB.156.1 | GTTCTCCTCTTCCTGGGCTT | GCGCCTTGTTTGTCTGTTA |
| | PB.6461.1 | TTTTGATGGATTCTGTGGCGG | GAGCACCCAAACCCAAATGT |
| | PB.7534.1 | TCCGAGTCACACCCTTTCAA | TGCAGCCACGAAATTAGTCA |
| lcrRNA | PB.13941.1 | TCTACCACTGCTTGTCGGAA | CGTCGGCCTTAAATCCTGG |
| | PB.8714.2 | GGGAGTTGGAGAATTGAACCG | TGTTTCATCGGGGTACTCTCG |
| | PB.15038.3 | TGGATGTGGGTTGTGAAGGT | AGGAGGGCAAGAAGAAGCTT |

Table S2. The PacBio SMRT sequencing information of sand pear fruit

| Category | 1-2kb | 2-3kb | 3-6kb | All |
|--|---------|---------|--------|---------|
| Number of SMRT cells | 2 | 2 | 2 | 6 |
| Number of reads of Insert | 155,736 | 111,958 | 83,566 | 351,260 |
| Mean Read Length of Insert | 2,235 | 2,545 | 3,784 | 2,702 |
| Number of five prime reads | 87,476 | 73,389 | 49,472 | 210,337 |
| Number of three prime reads | 96,759 | 78,137 | 52,693 | 227,589 |
| Number of poly-A reads | 93,638 | 77,232 | 52,288 | 223,158 |
| Number of filtered short reads | 20,218 | 6,291 | 1,092 | 27,601 |
| Number of non-full-length reads | 62,831 | 42,706 | 41,892 | 147,429 |
| Number of full-length reads | 72,687 | 62,961 | 40,582 | 176,230 |
| Number of full-length non-chimeric reads | 72,370 | 62,718 | 40,545 | 175,633 |
| Average full-length non-chimeric read length | 1,416 | 2,170 | 3,160 | 2,087 |

Table S3 ICE cluster result statistics

| Category | 0-1kb | 1-2kb | 2-3kb | 3-6kb | over 6kb | All |
|---|--------|--------|--------|--------|----------|--------|
| Number of consensus isoforms | 2,277 | 30,396 | 23,745 | 12,118 | 586 | 69,122 |
| Average consensus isoforms read length | 882 | 1,509 | 2,440 | 3,455 | 9,052 | 2,213 |
| Number of polished high-quality isoforms | 2,084 | 26,080 | 15,627 | 4,003 | 3 | 47,797 |
| Number of polished low-quality isoforms | 193 | 4,316 | 8,118 | 8,115 | 583 | 21,325 |
| Percent of polished high-quality isoforms (%) | 91.52% | 85.80% | 65.81% | 33.03% | 0.51% | 69.15% |

Table S4 Samples sequencing data evaluation

| Samples | BMK-ID | ReadSum | BaseSum | GC(%) | Q30(%) |
|---------|--------|------------|---------------|-------|--------|
| LB-0h-1 | T46 | 25,507,834 | 7,630,726,334 | 47.93 | 90.6 |
| LB-0h-2 | T47 | 24,472,937 | 7,315,878,272 | 48.03 | 90.56 |
| LB-0h-3 | T48 | 32,836,015 | 9,827,758,228 | 47.6 | 91 |
| LB-1h-1 | T49 | 23,778,107 | 7,116,394,766 | 47.7 | 90.91 |
| LB-1h-2 | T50 | 25,380,678 | 7,597,335,016 | 47.5 | 90.71 |
| LB-1h-3 | T51 | 25,032,532 | 7,491,386,194 | 47.69 | 90.55 |
| HB-0h-1 | T67 | 24,972,213 | 7,469,504,092 | 47.94 | 91.16 |
| HB-0h-2 | T68 | 29,059,610 | 8,687,022,644 | 47.81 | 90.9 |
| HB-0h-3 | T69 | 24,952,821 | 7,464,325,128 | 47.84 | 90.91 |
| HB-1h-1 | T70 | 25,302,776 | 7,566,162,862 | 48.26 | 91.26 |
| HB-1h-2 | T71 | 27,750,072 | 8,301,809,460 | 47.91 | 91.28 |
| HB-1h-3 | T72 | 24,857,794 | 7,437,296,976 | 47.67 | 91.24 |

Table S5. Annotation of new transcript datasets to eight public databases

| Annotated Database | Annotated Number | 300<=length<1000 | length>=1000 |
|----------------------|------------------|------------------|--------------|
| COG_Annotation | 8,255 | 184 | 8,071 |
| GO_Annotation | 12,584 | 313 | 12,271 |
| KEGG_Annotation | 9,115 | 252 | 8,863 |
| KOG_Annotation | 12,346 | 264 | 12,082 |
| Pfam_Annotation | 17,425 | 351 | 17,074 |
| Swissprot_Annotation | 14,586 | 320 | 14,266 |
| eggNOG_Annotation | 20,562 | 468 | 20,094 |
| nr_Annotation | 17,531 | 409 | 17,122 |
| All_Annotated | 21,074 | 490 | 20,584 |

COG, clusters of orthologous groups; GO, gene ontology; KEGG, kyoto encyclopedia of genes and genomes; KOG,euKaryotic Ortholog Groups; Pfam,Protein family;Swiss-Prot, a well-annotated and manually checked protein database; eggNOG, evolutionary genealogy of genes: non-supervised orthologous groups; nr, a NCBI non-redundant protein database.

Table S6. Summary of annotated differentially expressed genes between LB and HB sand pear flesh at 0h and 1h

| DEG Set | Total | COG | eggNOG | NR | Pfam | Swiss-Prot | GO | KEGG |
|----------------|-------|------|--------|------|------|------------|------|------|
| LB VS HB at 0h | 4738 | 1906 | 4542 | 4651 | 3946 | 3492 | 2614 | 1697 |
| LB VS HB at 1h | 5192 | 2078 | 4980 | 5106 | 4340 | 3843 | 2845 | 1777 |

Table S7. KEGG pathway enrichment of LB vs. HB at 0h and 1h in RNA-Seq

| LB-0h vs. HB-0h | | | | | |
|---|---------|---------------------------------|-----------------------------------|-------------|-------------------|
| #Kegg_pathway | ko_id | Cluter_frequency | Genome_frequency | P-value | Corrected_P-value |
| Phenylalanine, tyrosine and tryptophan biosynthesis | ko00400 | 24 out of 969 2.47678018575851% | 79 out of 8004 0.987006496751624% | 1.16E-05 | 0.00137 |
| Protein processing in endoplasmic reticulum | ko04141 | 71 out of 969 7.32714138286894% | 412 out of 8004 5.14742628685657% | 0.001101928 | 0.13003 |
| Galactose metabolism | ko00052 | 22 out of 969 2.2703818369453% | 92 out of 8004 1.14942528735632% | 0.001160464 | 0.13693 |
| Plant hormone signal transduction | ko04075 | 73 out of 969 7.53353973168215% | 443 out of 8004 5.53473263368316% | 0.003202532 | 0.3779 |
| Flavonoid biosynthesis | ko00941 | 18 out of 969 1.85758513931889% | 78 out of 8004 0.974512743628186% | 0.004732565 | 0.55844 |
| Taurine and hypotaurine metabolism | ko00430 | 8 out of 969 0.825593395252838% | 24 out of 8004 0.299850074962519% | 0.005547423 | 0.6546 |
| Ubiquinone and other terpenoid-quinone biosynthesis | ko00130 | 14 out of 969 1.44478844169247% | 56 out of 8004 0.699650174912544% | 0.00574476 | 0.67788 |
| Circadian rhythm - plant | ko04712 | 17 out of 969 1.75438596491228% | 77 out of 8004 0.962018990504748% | 0.009433727 | 1 |
| Biosynthesis of amino acids | ko01230 | 64 out of 969 6.6047471620227% | 401 out of 8004 5.00999500249875% | 0.011347821 | 1 |
| Histidine metabolism | ko00340 | 10 out of 969 1.03199174406605% | 38 out of 8004 0.474762618690655% | 0.012719188 | 1 |
| Alanine, aspartate and glutamate metabolism | ko00250 | 18 out of 969 1.85758513931889% | 86 out of 8004 1.07446276861569% | 0.013399834 | 1 |
| Sulfur metabolism | ko00920 | 13 out of 969 1.34158926728586% | 56 out of 8004 0.699650174912544% | 0.014426297 | 1 |
| Brassinosteroid biosynthesis | ko00905 | 7 out of 969 0.722394220846233% | 23 out of 8004 0.28735632183908% | 0.0158985 | 1 |
| Biotin metabolism | ko00780 | 9 out of 969 0.928792569659443% | 35 out of 8004 0.43728135932034% | 0.020551053 | 1 |
| Butanoate metabolism | ko00650 | 8 out of 969 0.825593395252838% | 31 out of 8004 0.387306346826587% | 0.027711116 | 1 |
| Stilbenoid, diarylheptanoid and gingerol biosynthesis | ko00945 | 9 out of 969 0.928792569659443% | 38 out of 8004 0.474762618690655% | 0.034150411 | 1 |
| Porphyrin and chlorophyll metabolism | ko00860 | 14 out of 969 1.44478844169247% | 71 out of 8004 0.887056471764118% | 0.043120371 | 1 |
| Glycosaminoglycan degradation | ko00531 | 5 out of 969 0.515995872033024% | 20 out of 8004 0.249875062468766% | 0.085000441 | 1 |
| Plant-pathogen interaction | ko04626 | 45 out of 969 4.64396284829721% | 304 out of 8004 3.79810094952524% | 0.086413695 | 1 |
| Fatty acid biosynthesis | ko00061 | 16 out of 969 1.65118679050568% | 93 out of 8004 1.16191904047976% | 0.091707858 | 1 |
| Degradation of aromatic compounds | ko01220 | 4 out of 969 0.412796697626419% | 15 out of 8004 0.187406296851574% | 0.09815157 | 1 |

| | | | | | |
|--|---------|---------------------------------|-----------------------------------|-------------|---|
| Glycine, serine and threonine metabolism | ko00260 | 20 out of 969 2.0639834881321% | 123 out of 8004 1.53673163418291% | 0.102680466 | 1 |
| Flavone and flavonol biosynthesis | ko00944 | 1 out of 969 0.103199174406605% | 1 out of 8004 0.0124937531234383% | 0.121064468 | 1 |
| Steroid biosynthesis | ko00100 | 10 out of 969 1.03199174406605% | 58 out of 8004 0.72463768115942% | 0.157510022 | 1 |
| Glycerolipid metabolism | ko00561 | 17 out of 969 1.75438596491228% | 109 out of 8004 1.36181909045477% | 0.163487036 | 1 |
| Ascorbate and aldarate metabolism | ko00053 | 11 out of 969 1.13519091847265% | 67 out of 8004 0.837081459270365% | 0.181586946 | 1 |
| Tropane, piperidine and pyridine alkaloid biosynthesis | ko00960 | 8 out of 969 0.825593395252838% | 46 out of 8004 0.574712643678161% | 0.186437366 | 1 |
| Glyoxylate and dicarboxylate metabolism | ko00630 | 17 out of 969 1.75438596491228% | 113 out of 8004 1.41179410294853% | 0.202881024 | 1 |
| Inositol phosphate metabolism | ko00562 | 16 out of 969 1.65118679050568% | 106 out of 8004 1.32433783108446% | 0.207996706 | 1 |
| Terpenoid backbone biosynthesis | ko00900 | 12 out of 969 1.23839009287926% | 77 out of 8004 0.962018990504748% | 0.21671763 | 1 |
| N-Glycan biosynthesis | ko00510 | 11 out of 969 1.13519091847265% | 70 out of 8004 0.87456271864068% | 0.221737206 | 1 |
| Thiamine metabolism | ko00730 | 5 out of 969 0.515995872033024% | 27 out of 8004 0.337331334332834% | 0.222355712 | 1 |
| Peroxisome | ko04146 | 21 out of 969 2.1671826625387% | 147 out of 8004 1.83658170914543% | 0.240003271 | 1 |
| RNA transport | ko03013 | 40 out of 969 4.12796697626419% | 296 out of 8004 3.69815092453773% | 0.249119349 | 1 |
| One carbon pool by folate | ko00670 | 7 out of 969 0.722394220846233% | 44 out of 8004 0.549725137431284% | 0.279491581 | 1 |
| Synthesis and degradation of ketone bodies | ko00072 | 2 out of 969 0.206398348813209% | 9 out of 8004 0.112443778110945% | 0.298868642 | 1 |
| beta-Alanine metabolism | ko00410 | 10 out of 969 1.03199174406605% | 68 out of 8004 0.849575212393803% | 0.305389627 | 1 |
| Vancomycin resistance | ko01502 | 1 out of 969 0.103199174406605% | 3 out of 8004 0.0374812593703148% | 0.321033043 | 1 |
| Ether lipid metabolism | ko00565 | 8 out of 969 0.825593395252838% | 54 out of 8004 0.674662668665667% | 0.327685671 | 1 |
| Glycerophospholipid metabolism | ko00564 | 20 out of 969 2.0639834881321% | 151 out of 8004 1.88655672163918% | 0.368948395 | 1 |
| Nitrogen metabolism | ko00910 | 8 out of 969 0.825593395252838% | 57 out of 8004 0.712143928035982% | 0.385168603 | 1 |
| Vitamin B6 metabolism | ko00750 | 4 out of 969 0.412796697626419% | 26 out of 8004 0.324837581209395% | 0.387726228 | 1 |
| C5-Branched dibasic acid metabolism | ko00660 | 2 out of 969 0.206398348813209% | 11 out of 8004 0.137431284357821% | 0.391795011 | 1 |
| Propanoate metabolism | ko00640 | 7 out of 969 0.722394220846233% | 50 out of 8004 0.624687656171914% | 0.402557314 | 1 |
| Cysteine and methionine metabolism | ko00270 | 17 out of 969 1.75438596491228% | 130 out of 8004 1.62418790604698% | 0.405899293 | 1 |
| Pyruvate metabolism | ko00620 | 20 out of 969 2.0639834881321% | 155 out of 8004 1.93653173413293% | 0.416093694 | 1 |
| Other glycan degradation | ko00511 | 5 out of 969 0.515995872033024% | 35 out of 8004 0.43728135932034% | 0.420274327 | 1 |

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|---|---------|---------------------------------|-----------------------------------|-------------|---|
| Lysine degradation | ko00310 | 7 out of 969 0.722394220846233% | 52 out of 8004 0.649675162418791% | 0.44404852 | 1 |
| Arachidonic acid metabolism | ko00590 | 4 out of 969 0.412796697626419% | 28 out of 8004 0.349825087456272% | 0.444927332 | 1 |
| Photosynthesis - antenna proteins | ko00196 | 4 out of 969 0.412796697626419% | 28 out of 8004 0.349825087456272% | 0.444927332 | 1 |
| Sphingolipid metabolism | ko00600 | 6 out of 969 0.619195046439629% | 46 out of 8004 0.574712643678161% | 0.489324737 | 1 |
| Cyanoamino acid metabolism | ko00460 | 17 out of 969 1.75438596491228% | 137 out of 8004 1.71164417791104% | 0.496077698 | 1 |
| alpha-Linolenic acid metabolism | ko00592 | 13 out of 969 1.34158926728586% | 105 out of 8004 1.31184407796102% | 0.510511975 | 1 |
| Tryptophan metabolism | ko00380 | 6 out of 969 0.619195046439629% | 47 out of 8004 0.587206396801599% | 0.511132536 | 1 |
| Selenocompound metabolism | ko00450 | 3 out of 969 0.309597523219814% | 23 out of 8004 0.28735632183908% | 0.539238042 | 1 |
| Pantothenate and CoA biosynthesis | ko00770 | 7 out of 969 0.722394220846233% | 57 out of 8004 0.712143928035982% | 0.544673716 | 1 |
| Valine, leucine and isoleucine degradation | ko00280 | 9 out of 969 0.928792569659443% | 74 out of 8004 0.924537731134433% | 0.54770813 | 1 |
| Carbon fixation in photosynthetic organisms | ko00710 | 15 out of 969 1.54798761609907% | 125 out of 8004 1.56171914042979% | 0.556281822 | 1 |
| Riboflavin metabolism | ko00740 | 2 out of 969 0.206398348813209% | 15 out of 8004 0.187406296851574% | 0.557677763 | 1 |
| RNA degradation | ko03018 | 24 out of 969 2.47678018575851% | 201 out of 8004 2.51124437781109% | 0.562333848 | 1 |
| SNARE interactions in vesicular transport | ko04130 | 9 out of 969 0.928792569659443% | 75 out of 8004 0.937031484257871% | 0.564631865 | 1 |
| Phenylalanine metabolism | ko00360 | 20 out of 969 2.0639834881321% | 170 out of 8004 2.12393803098451% | 0.590775878 | 1 |
| Tyrosine metabolism | ko00350 | 7 out of 969 0.722394220846233% | 60 out of 8004 0.749625187406297% | 0.60123832 | 1 |
| Citrate cycle (TCA cycle) | ko00020 | 11 out of 969 1.13519091847265% | 95 out of 8004 1.18690654672664% | 0.610458529 | 1 |
| ABC transporters | ko02010 | 5 out of 969 0.515995872033024% | 45 out of 8004 0.562218890554723% | 0.649783989 | 1 |
| Purine metabolism | ko00230 | 38 out of 969 3.92156862745098% | 329 out of 8004 4.11044477761119% | 0.649933222 | 1 |
| Zeatin biosynthesis | ko00908 | 3 out of 969 0.309597523219814% | 28 out of 8004 0.349825087456272% | 0.676115678 | 1 |
| Lipoic acid metabolism | ko00785 | 1 out of 969 0.103199174406605% | 9 out of 8004 0.112443778110945% | 0.687144396 | 1 |
| Fatty acid elongation | ko00062 | 5 out of 969 0.515995872033024% | 47 out of 8004 0.587206396801599% | 0.688187864 | 1 |
| Glycosphingolipid biosynthesis - globo series | ko00603 | 2 out of 969 0.206398348813209% | 19 out of 8004 0.237381309345327% | 0.688782489 | 1 |
| Fatty acid metabolism | ko01212 | 18 out of 969 1.85758513931889% | 164 out of 8004 2.04897551224388% | 0.708555557 | 1 |
| Biosynthesis of unsaturated fatty acids | ko01040 | 8 out of 969 0.825593395252838% | 77 out of 8004 0.962018990504748% | 0.729965756 | 1 |
| Diterpenoid biosynthesis | ko00904 | 4 out of 969 0.412796697626419% | 40 out of 8004 0.499750124937531% | 0.730556741 | 1 |

| | | | | | |
|---|---------|---------------------------------|-----------------------------------|-------------|---|
| Folate biosynthesis | ko00790 | 2 out of 969 0.206398348813209% | 21 out of 8004 0.262368815592204% | 0.741371124 | 1 |
| Carbon metabolism | ko01200 | 46 out of 969 4.74716202270382% | 411 out of 8004 5.13493253373313% | 0.742462499 | 1 |
| Valine, leucine and isoleucine biosynthesis | ko00290 | 4 out of 969 0.412796697626419% | 41 out of 8004 0.512243878060969% | 0.748500921 | 1 |
| Glycosylphosphatidylinositol(GPI)-anchor biosynthesis | ko00563 | 4 out of 969 0.412796697626419% | 41 out of 8004 0.512243878060969% | 0.748500921 | 1 |
| Endocytosis | ko04144 | 24 out of 969 2.47678018575851% | 222 out of 8004 2.7736131934033% | 0.755466516 | 1 |
| Regulation of autophagy | ko04140 | 5 out of 969 0.515995872033024% | 51 out of 8004 0.637181409295352% | 0.756084531 | 1 |
| Arginine and proline metabolism | ko00330 | 13 out of 969 1.34158926728586% | 125 out of 8004 1.56171914042979% | 0.761598448 | 1 |
| Protein export | ko03060 | 8 out of 969 0.825593395252838% | 80 out of 8004 0.999500249875062% | 0.768455239 | 1 |
| Starch and sucrose metabolism | ko00500 | 41 out of 969 4.23116615067079% | 374 out of 8004 4.67266366816592% | 0.778861502 | 1 |
| Isoquinoline alkaloid biosynthesis | ko00950 | 3 out of 969 0.309597523219814% | 33 out of 8004 0.412293853073463% | 0.780461359 | 1 |
| Nicotinate and nicotinamide metabolism | ko00760 | 2 out of 969 0.206398348813209% | 23 out of 8004 0.28735632183908% | 0.786164092 | 1 |
| 2-Oxocarboxylic acid metabolism | ko01210 | 9 out of 969 0.928792569659443% | 91 out of 8004 1.13693153423288% | 0.788159244 | 1 |
| Fructose and mannose metabolism | ko00051 | 10 out of 969 1.03199174406605% | 103 out of 8004 1.28685657171414% | 0.815086554 | 1 |
| Glycolysis / Gluconeogenesis | ko00010 | 18 out of 969 1.85758513931889% | 178 out of 8004 2.22388805597201% | 0.826014599 | 1 |
| Phenylpropanoid biosynthesis | ko00940 | 33 out of 969 3.40557275541796% | 318 out of 8004 3.97301349325337% | 0.854360309 | 1 |
| Pyrimidine metabolism | ko00240 | 23 out of 969 2.37358101135191% | 230 out of 8004 2.8735632183908% | 0.864907356 | 1 |
| Phosphatidylinositol signaling system | ko04070 | 8 out of 969 0.825593395252838% | 90 out of 8004 1.12443778110945% | 0.867867638 | 1 |
| Pentose and glucuronate interconversions | ko00040 | 15 out of 969 1.54798761609907% | 158 out of 8004 1.97401299350325% | 0.875269361 | 1 |
| Ribosome biogenesis in eukaryotes | ko03008 | 14 out of 969 1.44478844169247% | 151 out of 8004 1.88655672163918% | 0.88904331 | 1 |
| Proteasome | ko03050 | 9 out of 969 0.928792569659443% | 103 out of 8004 1.28685657171414% | 0.890554449 | 1 |
| Fatty acid degradation | ko00071 | 6 out of 969 0.619195046439629% | 73 out of 8004 0.912043978010994% | 0.89083771 | 1 |
| Carotenoid biosynthesis | ko00906 | 5 out of 969 0.515995872033024% | 63 out of 8004 0.787106446776612% | 0.893412431 | 1 |
| Glutathione metabolism | ko00480 | 13 out of 969 1.34158926728586% | 144 out of 8004 1.79910044977511% | 0.902514708 | 1 |
| Amino sugar and nucleotide sugar metabolism | ko00520 | 19 out of 969 1.96078431372549% | 203 out of 8004 2.53623188405797% | 0.911150256 | 1 |
| Linoleic acid metabolism | ko00591 | 2 out of 969 0.206398348813209% | 32 out of 8004 0.399800099950025% | 0.913407179 | 1 |
| Cutin, suberine and wax biosynthesis | ko00073 | 3 out of 969 0.309597523219814% | 44 out of 8004 0.549725137431284% | 0.915043145 | 1 |

| | | | | | |
|---|---------|---------------------------------|-----------------------------------|-------------|---|
| Base excision repair | ko03410 | 5 out of 969 0.515995872033024% | 70 out of 8004 0.87456271864068% | 0.93757962 | 1 |
| Sulfur relay system | ko04122 | 1 out of 969 0.103199174406605% | 23 out of 8004 0.28735632183908% | 0.948818047 | 1 |
| Ribosome | ko03010 | 55 out of 969 5.67595459236326% | 556 out of 8004 6.94652673663168% | 0.960723211 | 1 |
| Monoterpenoid biosynthesis | ko00902 | 1 out of 969 0.103199174406605% | 26 out of 8004 0.324837581209395% | 0.965290522 | 1 |
| Pentose phosphate pathway | ko00030 | 5 out of 969 0.515995872033024% | 79 out of 8004 0.987006496751624% | 0.970018166 | 1 |
| Spliceosome | ko03040 | 31 out of 969 3.19917440660475% | 343 out of 8004 4.28535732133933% | 0.972680428 | 1 |
| Basal transcription factors | ko03022 | 4 out of 969 0.412796697626419% | 70 out of 8004 0.87456271864068% | 0.976613748 | 1 |
| Sesquiterpenoid and triterpenoid biosynthesis | ko00909 | 2 out of 969 0.206398348813209% | 46 out of 8004 0.574712643678161% | 0.980851902 | 1 |
| mRNA surveillance pathway | ko03015 | 16 out of 969 1.65118679050568% | 211 out of 8004 2.63618190904548% | 0.988222741 | 1 |
| Ubiquitin mediated proteolysis | ko04120 | 16 out of 969 1.65118679050568% | 221 out of 8004 2.76111944027986% | 0.993750018 | 1 |
| RNA polymerase | ko03020 | 6 out of 969 0.619195046439629% | 110 out of 8004 1.37431284357821% | 0.994201848 | 1 |
| Oxidative phosphorylation | ko00190 | 23 out of 969 2.37358101135191% | 295 out of 8004 3.68565717141429% | 0.994264857 | 1 |
| Aminoacyl-tRNA biosynthesis | ko00970 | 5 out of 969 0.515995872033024% | 111 out of 8004 1.38680659670165% | 0.998365644 | 1 |
| Phagosome | ko04145 | 6 out of 969 0.619195046439629% | 148 out of 8004 1.84907546226887% | 0.999835082 | 1 |
| DNA replication | ko03030 | 3 out of 969 0.309597523219814% | 114 out of 8004 1.42428785607196% | 0.999947772 | 1 |
| Photosynthesis | ko00195 | 12 out of 969 1.23839009287926% | 243 out of 8004 3.0359820089955% | 0.999965781 | 1 |
| Nucleotide excision repair | ko03420 | 3 out of 969 0.309597523219814% | 118 out of 8004 1.47426286856572% | 0.999966969 | 1 |
| Homologous recombination | ko03440 | 1 out of 969 0.103199174406605% | 83 out of 8004 1.03698150924538% | 0.999978971 | 1 |
| Mismatch repair | ko03430 | 1 out of 969 0.103199174406605% | 88 out of 8004 1.09945027486257% | 0.999989051 | 1 |

LB-1h vs. HB-1h

| #Kegg_pathway | ko_id | Cluter_frequency | Genome_frequency | P-value | Corrected_P-value |
|---|---------|-----------------------------------|-----------------------------------|-------------|-------------------|
| Galactose metabolism | ko00052 | 27 out of 1027 2.62901655306719% | 92 out of 8004 1.14942528735632% | 2.04E-05 | 0.0024 |
| Phenylalanine, tyrosine and tryptophan biosynthesis | ko00400 | 22 out of 1027 2.14216163583252% | 79 out of 8004 0.987006496751624% | 0.000270298 | 0.0319 |
| Ubiquinone and other terpenoid-quinone biosynthesis | ko00130 | 17 out of 1027 1.65530671859786% | 56 out of 8004 0.699650174912544% | 0.000440318 | 0.05196 |
| Plant-pathogen interaction | ko04626 | 56 out of 1027 5.45277507302824% | 304 out of 8004 3.79810094952524% | 0.002879213 | 0.33975 |
| Protein processing in endoplasmic reticulum | ko04141 | 72 out of 1027 7.01071080817916% | 412 out of 8004 5.14742628685657% | 0.00327907 | 0.38693 |
| Alanine, aspartate and glutamate metabolism | ko00250 | 20 out of 1027 1.94741966893866% | 86 out of 8004 1.07446276861569% | 0.005325293 | 0.62838 |
| Histidine metabolism | ko00340 | 11 out of 1027 1.07108081791626% | 38 out of 8004 0.474762618690655% | 0.006569975 | 0.77526 |
| Glycosaminoglycan degradation | ko00531 | 7 out of 1027 0.68159688412853% | 20 out of 8004 0.249875062468766% | 0.009552215 | 1 |
| Sulfur metabolism | ko00920 | 14 out of 1027 1.36319376825706% | 56 out of 8004 0.699650174912544% | 0.009553884 | 1 |
| Biotin metabolism | ko00780 | 10 out of 1027 0.973709834469328% | 35 out of 8004 0.43728135932034% | 0.010349933 | 1 |
| Biosynthesis of amino acids | ko01230 | 67 out of 1027 6.5238558909445% | 401 out of 8004 5.00999500249875% | 0.012518492 | 1 |
| Porphyrin and chlorophyll metabolism | ko00860 | 16 out of 1027 1.55793573515093% | 71 out of 8004 0.887056471764118% | 0.016109332 | 1 |
| Steroid biosynthesis | ko00100 | 13 out of 1027 1.26582278481013% | 58 out of 8004 0.72463768115942% | 0.029597701 | 1 |
| Circadian rhythm - plant | ko04712 | 16 out of 1027 1.55793573515093% | 77 out of 8004 0.962018990504748% | 0.033072866 | 1 |
| Degradation of aromatic compounds | ko01220 | 5 out of 1027 0.486854917234664% | 15 out of 8004 0.187406296851574% | 0.034233485 | 1 |
| Flavonoid biosynthesis | ko00941 | 16 out of 1027 1.55793573515093% | 78 out of 8004 0.974512743628186% | 0.036844833 | 1 |
| Stilbenoid, diarylheptanoid and gingerol biosynthesis | ko00945 | 9 out of 1027 0.876338851022395% | 38 out of 8004 0.474762618690655% | 0.04716511 | 1 |
| Photosynthesis - antenna proteins | ko00196 | 7 out of 1027 0.68159688412853% | 28 out of 8004 0.349825087456272% | 0.058773187 | 1 |
| Sphingolipid metabolism | ko00600 | 10 out of 1027 0.973709834469328% | 46 out of 8004 0.574712643678161% | 0.062990798 | 1 |
| Taurine and hypotaurine metabolism | ko00430 | 6 out of 1027 0.584225900681597% | 24 out of 8004 0.299850074962519% | 0.077604124 | 1 |
| Ascorbate and aldarate metabolism | ko00053 | 13 out of 1027 1.26582278481013% | 67 out of 8004 0.837081459270365% | 0.081340102 | 1 |
| Glyoxylate and dicarboxylate metabolism | ko00630 | 20 out of 1027 1.94741966893866% | 113 out of 8004 1.41179410294853% | 0.082420896 | 1 |
| Butanoate metabolism | ko00650 | 7 out of 1027 0.68159688412853% | 31 out of 8004 0.387306346826587% | 0.093358594 | 1 |
| Cysteine and methionine metabolism | ko00270 | 22 out of 1027 2.14216163583252% | 130 out of 8004 1.62418790604698% | 0.104103969 | 1 |

| | | | | | |
|---|---------|-----------------------------------|-----------------------------------|-------------|---|
| Riboflavin metabolism | ko00740 | 4 out of 1027 0.389483933787731% | 15 out of 8004 0.187406296851574% | 0.11587282 | 1 |
| Thiamine metabolism | ko00730 | 6 out of 1027 0.584225900681597% | 27 out of 8004 0.337331334332834% | 0.12313498 | 1 |
| Inositol phosphate metabolism | ko00562 | 18 out of 1027 1.75267770204479% | 106 out of 8004 1.32433783108446% | 0.12870001 | 1 |
| Arachidonic acid metabolism | ko00590 | 6 out of 1027 0.584225900681597% | 28 out of 8004 0.349825087456272% | 0.140688197 | 1 |
| Glycerolipid metabolism | ko00561 | 18 out of 1027 1.75267770204479% | 109 out of 8004 1.36181909045477% | 0.155214933 | 1 |
| Glycine, serine and threonine metabolism | ko00260 | 20 out of 1027 1.94741966893866% | 123 out of 8004 1.53673163418291% | 0.155980595 | 1 |
| Brassinosteroid biosynthesis | ko00905 | 5 out of 1027 0.486854917234664% | 23 out of 8004 0.28735632183908% | 0.163755457 | 1 |
| Peroxisome | ko04146 | 23 out of 1027 2.23953261927945% | 147 out of 8004 1.83658170914543% | 0.180942223 | 1 |
| Fatty acid biosynthesis | ko00061 | 15 out of 1027 1.46056475170399% | 93 out of 8004 1.16191904047976% | 0.20759005 | 1 |
| Glycosphingolipid biosynthesis - ganglio series | ko00604 | 2 out of 1027 0.194741966893866% | 7 out of 8004 0.087456271864068% | 0.223517184 | 1 |
| Plant hormone signal transduction | ko04075 | 62 out of 1027 6.03700097370983% | 443 out of 8004 5.53473263368316% | 0.245251315 | 1 |
| Amino sugar and nucleotide sugar metabolism | ko00520 | 29 out of 1027 2.82375851996105% | 203 out of 8004 2.53623188405797% | 0.294776533 | 1 |
| Synthesis and degradation of ketone bodies | ko00072 | 2 out of 1027 0.194741966893866% | 9 out of 8004 0.112443778110945% | 0.324487842 | 1 |
| One carbon pool by folate | ko00670 | 7 out of 1027 0.68159688412853% | 44 out of 8004 0.549725137431284% | 0.33249583 | 1 |
| Vancomycin resistance | ko01502 | 1 out of 1027 0.0973709834469328% | 3 out of 8004 0.0374812593703148% | 0.337690533 | 1 |
| Phenylalanine metabolism | ko00360 | 24 out of 1027 2.33690360272639% | 170 out of 8004 2.12393803098451% | 0.339366427 | 1 |
| Fructose and mannose metabolism | ko00051 | 15 out of 1027 1.46056475170399% | 103 out of 8004 1.28685657171414% | 0.340497574 | 1 |
| Selenocompound metabolism | ko00450 | 4 out of 1027 0.389483933787731% | 23 out of 8004 0.28735632183908% | 0.340627862 | 1 |
| Valine, leucine and isoleucine degradation | ko00280 | 11 out of 1027 1.07108081791626% | 74 out of 8004 0.924537731134433% | 0.349031221 | 1 |
| SNARE interactions in vesicular transport | ko04130 | 11 out of 1027 1.07108081791626% | 75 out of 8004 0.937031484257871% | 0.3661016 | 1 |
| Phosphatidylinositol signaling system | ko04070 | 13 out of 1027 1.26582278481013% | 90 out of 8004 1.12443778110945% | 0.368260772 | 1 |
| Tryptophan metabolism | ko00380 | 7 out of 1027 0.68159688412853% | 47 out of 8004 0.587206396801599% | 0.398662061 | 1 |
| Endocytosis | ko04144 | 30 out of 1027 2.92112950340798% | 222 out of 8004 2.7736131934033% | 0.409316823 | 1 |
| C5-Branched dibasic acid metabolism | ko00660 | 2 out of 1027 0.194741966893866% | 11 out of 8004 0.137431284357821% | 0.421786179 | 1 |
| Phenylpropanoid biosynthesis | ko00940 | 42 out of 1027 4.08958130477118% | 318 out of 8004 3.97301349325337% | 0.444917186 | 1 |
| Glycosphingolipid biosynthesis - globo series | ko00603 | 3 out of 1027 0.292112950340798% | 19 out of 8004 0.237381309345327% | 0.447974619 | 1 |

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|--|---------|-----------------------------------|-----------------------------------|-------------|---|
| Nitrogen metabolism | ko00910 | 8 out of 1027 0.778967867575463% | 57 out of 8004 0.712143928035982% | 0.451103583 | 1 |
| Other glycan degradation | ko00511 | 5 out of 1027 0.486854917234664% | 35 out of 8004 0.43728135932034% | 0.472670518 | 1 |
| Tyrosine metabolism | ko00350 | 8 out of 1027 0.778967867575463% | 60 out of 8004 0.749625187406297% | 0.511509866 | 1 |
| beta-Alanine metabolism | ko00410 | 9 out of 1027 0.876338851022395% | 68 out of 8004 0.849575212393803% | 0.514749301 | 1 |
| Glycolysis / Gluconeogenesis | ko00010 | 23 out of 1027 2.23953261927945% | 178 out of 8004 2.22388805597201% | 0.519931798 | 1 |
| Biosynthesis of unsaturated fatty acids | ko01040 | 10 out of 1027 0.973709834469328% | 77 out of 8004 0.962018990504748% | 0.535158114 | 1 |
| Terpenoid backbone biosynthesis | ko00900 | 10 out of 1027 0.973709834469328% | 77 out of 8004 0.962018990504748% | 0.535158114 | 1 |
| Carbon fixation in photosynthetic organisms | ko00710 | 16 out of 1027 1.55793573515093% | 125 out of 8004 1.56171914042979% | 0.545005908 | 1 |
| Tropane, piperidine and pyridine alkaloid biosynthesis | ko00960 | 6 out of 1027 0.584225900681597% | 46 out of 8004 0.574712643678161% | 0.549070618 | 1 |
| Sesquiterpenoid and triterpenoid biosynthesis | ko00909 | 6 out of 1027 0.584225900681597% | 46 out of 8004 0.574712643678161% | 0.549070618 | 1 |
| Carotenoid biosynthesis | ko00906 | 8 out of 1027 0.778967867575463% | 63 out of 8004 0.787106446776612% | 0.569578711 | 1 |
| Fatty acid elongation | ko00062 | 6 out of 1027 0.584225900681597% | 47 out of 8004 0.587206396801599% | 0.571081626 | 1 |
| Nicotinate and nicotinamide metabolism | ko00760 | 3 out of 1027 0.292112950340798% | 23 out of 8004 0.28735632183908% | 0.580994698 | 1 |
| Diterpenoid biosynthesis | ko00904 | 5 out of 1027 0.486854917234664% | 40 out of 8004 0.499750124937531% | 0.596259601 | 1 |
| alpha-Linolenic acid metabolism | ko00592 | 13 out of 1027 1.26582278481013% | 105 out of 8004 1.31184407796102% | 0.599577573 | 1 |
| Fatty acid degradation | ko00071 | 9 out of 1027 0.876338851022395% | 73 out of 8004 0.912043978010994% | 0.604283443 | 1 |
| Glycosylphosphatidylinositol(GPI)-anchor biosynthesis | ko00563 | 5 out of 1027 0.486854917234664% | 41 out of 8004 0.512243878060969% | 0.618973193 | 1 |
| Carbon metabolism | ko01200 | 51 out of 1027 4.96592015579357% | 411 out of 8004 5.13493253373313% | 0.626830006 | 1 |
| RNA transport | ko03013 | 36 out of 1027 3.50535540408958% | 296 out of 8004 3.69815092453773% | 0.663679772 | 1 |
| Vitamin B6 metabolism | ko00750 | 3 out of 1027 0.292112950340798% | 26 out of 8004 0.324837581209395% | 0.666358362 | 1 |
| Monoterpenoid biosynthesis | ko00902 | 3 out of 1027 0.292112950340798% | 26 out of 8004 0.324837581209395% | 0.666358362 | 1 |
| Glycerophospholipid metabolism | ko00564 | 18 out of 1027 1.75267770204479% | 151 out of 8004 1.88655672163918% | 0.668901433 | 1 |
| Lysine degradation | ko00310 | 6 out of 1027 0.584225900681597% | 52 out of 8004 0.649675162418791% | 0.672344057 | 1 |
| N-Glycan biosynthesis | ko00510 | 8 out of 1027 0.778967867575463% | 70 out of 8004 0.87456271864068% | 0.691093704 | 1 |

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|---|---------|-----------------------------------|-----------------------------------|-------------|---|
| Cyanoamino acid metabolism | ko00460 | 16 out of 1027 1.55793573515093% | 137 out of 8004 1.71164417791104% | 0.696003568 | 1 |
| ABC transporters | ko02010 | 5 out of 1027 0.486854917234664% | 45 out of 8004 0.562218890554723% | 0.701833907 | 1 |
| Ether lipid metabolism | ko00565 | 6 out of 1027 0.584225900681597% | 54 out of 8004 0.674662668665667% | 0.708261107 | 1 |
| Lipoic acid metabolism | ko00785 | 1 out of 1027 0.0973709834469328% | 9 out of 8004 0.112443778110945% | 0.709619774 | 1 |
| Protein export | ko03060 | 9 out of 1027 0.876338851022395% | 80 out of 8004 0.999500249875062% | 0.71406847 | 1 |
| Fatty acid metabolism | ko01212 | 19 out of 1027 1.85004868549172% | 164 out of 8004 2.04897551224388% | 0.71955588 | 1 |
| Purine metabolism | ko00230 | 39 out of 1027 3.79746835443038% | 329 out of 8004 4.11044477761119% | 0.730207714 | 1 |
| Arginine and proline metabolism | ko00330 | 14 out of 1027 1.36319376825706% | 125 out of 8004 1.56171914042979% | 0.747522802 | 1 |
| Pantothenate and CoA biosynthesis | ko00770 | 6 out of 1027 0.584225900681597% | 57 out of 8004 0.712143928035982% | 0.756922193 | 1 |
| Starch and sucrose metabolism | ko00500 | 44 out of 1027 4.28432327166504% | 374 out of 8004 4.67266366816592% | 0.758620084 | 1 |
| Folate biosynthesis | ko00790 | 2 out of 1027 0.194741966893866% | 21 out of 8004 0.262368815592204% | 0.771596584 | 1 |
| Valine, leucine and isoleucine biosynthesis | ko00290 | 4 out of 1027 0.389483933787731% | 41 out of 8004 0.512243878060969% | 0.789744289 | 1 |
| Citrate cycle (TCA cycle) | ko00020 | 10 out of 1027 0.973709834469328% | 95 out of 8004 1.18690654672664% | 0.793498068 | 1 |
| Linoleic acid metabolism | ko00591 | 3 out of 1027 0.292112950340798% | 32 out of 8004 0.399800099950025% | 0.797361837 | 1 |
| Sulfur relay system | ko04122 | 2 out of 1027 0.194741966893866% | 23 out of 8004 0.28735632183908% | 0.814058401 | 1 |
| Pentose and glucuronate interconversions | ko00040 | 17 out of 1027 1.65530671859786% | 158 out of 8004 1.97401299350325% | 0.816474564 | 1 |
| Cutin, suberine and wax biosynthesis | ko00073 | 4 out of 1027 0.389483933787731% | 44 out of 8004 0.549725137431284% | 0.833890279 | 1 |
| Glutathione metabolism | ko00480 | 15 out of 1027 1.46056475170399% | 144 out of 8004 1.79910044977511% | 0.841645452 | 1 |
| 2-Oxocarboxylic acid metabolism | ko01210 | 9 out of 1027 0.876338851022395% | 91 out of 8004 1.13693153423288% | 0.842185466 | 1 |
| Pyruvate metabolism | ko00620 | 16 out of 1027 1.55793573515093% | 155 out of 8004 1.93653173413293% | 0.857654584 | 1 |
| Oxidative phosphorylation | ko00190 | 32 out of 1027 3.11587147030185% | 295 out of 8004 3.68565717141429% | 0.871471566 | 1 |
| RNA degradation | ko03018 | 21 out of 1027 2.04479065238559% | 201 out of 8004 2.51124437781109% | 0.872613453 | 1 |
| Propanoate metabolism | ko00640 | 4 out of 1027 0.389483933787731% | 50 out of 8004 0.624687656171914% | 0.899167023 | 1 |
| Ubiquitin mediated proteolysis | ko04120 | 21 out of 1027 2.04479065238559% | 221 out of 8004 2.76111944027986% | 0.950220039 | 1 |
| Pentose phosphate pathway | ko00030 | 6 out of 1027 0.584225900681597% | 79 out of 8004 0.987006496751624% | 0.950382814 | 1 |
| RNA polymerase | ko03020 | 9 out of 1027 0.876338851022395% | 110 out of 8004 1.37431284357821% | 0.953810741 | 1 |

| | | | | | |
|------------------------------------|---------|-----------------------------------|-----------------------------------|-------------|---|
| Base excision repair | ko03410 | 5 out of 1027 0.486854917234664% | 70 out of 8004 0.87456271864068% | 0.955937968 | 1 |
| Spliceosome | ko03040 | 34 out of 1027 3.31061343719572% | 343 out of 8004 4.28535732133933% | 0.962273905 | 1 |
| Proteasome | ko03050 | 8 out of 1027 0.778967867575463% | 103 out of 8004 1.28685657171414% | 0.962718488 | 1 |
| Regulation of autophagy | ko04140 | 3 out of 1027 0.292112950340798% | 51 out of 8004 0.637181409295352% | 0.967553188 | 1 |
| mRNA surveillance pathway | ko03015 | 19 out of 1027 1.85004868549172% | 211 out of 8004 2.63618190904548% | 0.968097755 | 1 |
| Pyrimidine metabolism | ko00240 | 21 out of 1027 2.04479065238559% | 230 out of 8004 2.8735632183908% | 0.96896054 | 1 |
| Zeatin biosynthesis | ko00908 | 1 out of 1027 0.0973709834469328% | 28 out of 8004 0.349825087456272% | 0.97876269 | 1 |
| Ribosome biogenesis in eukaryotes | ko03008 | 12 out of 1027 1.16845180136319% | 151 out of 8004 1.88655672163918% | 0.979169321 | 1 |
| Homologous recombination | ko03440 | 5 out of 1027 0.486854917234664% | 83 out of 8004 1.03698150924538% | 0.986411879 | 1 |
| Isoquinoline alkaloid biosynthesis | ko00950 | 1 out of 1027 0.0973709834469328% | 33 out of 8004 0.412293853073463% | 0.989341285 | 1 |
| Aminoacyl-tRNA biosynthesis | ko00970 | 6 out of 1027 0.584225900681597% | 111 out of 8004 1.38680659670165% | 0.997139502 | 1 |
| Nucleotide excision repair | ko03420 | 6 out of 1027 0.584225900681597% | 118 out of 8004 1.47426286856572% | 0.998554739 | 1 |
| Ribosome | ko03010 | 50 out of 1027 4.86854917234664% | 556 out of 8004 6.94652673663168% | 0.998608394 | 1 |
| Phagosome | ko04145 | 8 out of 1027 0.778967867575463% | 148 out of 8004 1.84907546226887% | 0.999199931 | 1 |
| Basal transcription factors | ko03022 | 2 out of 1027 0.194741966893866% | 70 out of 8004 0.87456271864068% | 0.999270427 | 1 |
| DNA replication | ko03030 | 5 out of 1027 0.486854917234664% | 114 out of 8004 1.42428785607196% | 0.999395544 | 1 |
| Mismatch repair | ko03430 | 3 out of 1027 0.292112950340798% | 88 out of 8004 1.09945027486257% | 0.999478854 | 1 |
| Photosynthesis | ko00195 | 11 out of 1027 1.07108081791626% | 243 out of 8004 3.0359820089955% | 0.999997301 | 1 |

3. Supplementary Methods

3.1 LC-MS analyses

The powder samples of sand pears (0.1 g) were extracted with 1 mL 80% methanol. The extraction was performed by incubation for 30 min under sonication with occasional shaking. Next, the slurry was centrifuged at 19,000g for 10 min, the supernatant was placed on 10mL glass centrifuge tube and concentrated to dry in vacuum at 37 °C. The residue was redissolved in 150 μ L 80% methanol water solution and centrifuged for 10min at 14000g, then the supernatant was used for analysis.

The LC-MS/MS portion of the platform was based on a UHPLC system (1290 series, Agilent Technologies) equipped with an ACQUITY UPLC BEH Amide column (1.7 μ m, 2.1 mm \times 100 mm, Waters) and a triple quadrupole mass spectrometer (5500 QTRAP, AB SCIEX) in the multiple reaction monitoring (MRM) mode. Metabolites were detected in electrospray negative-ionization and positive-ionization mode. The 2 μ L samples were injected sequentially. The ACQUITY UPLC BEH Amide column (1.7 μ m, 2.1 mm \times 100 mm, Waters) was heated to 45 °C under a flow rate of 300 μ L/min. A gradient was used to separate the compounds consisted of solvent A (20 mM ammonium acetate, 50% acetonitrile, pH 9.5) and solvent B (100% acetonitrile). The gradient started at 5% solvent A for 1 min and increasing linearly to 35% solvent A over 11 min, and then increased linearly to 60% solvent A over 2 min, and then decreasing to 5% of solvent A in 2 min, then keeping for extra 2 min. QC samples were injected during acquisition.

The MS conditions were set as follows: Source Temperature 550°C, Ion Source Gas1(GAS1): 40, Ion Source Gas2(GAS2): 50, Curtain Gas(CUR): 35, Ion Spray Voltage Floating (ISVF) : -4500V; The mass spectrometer was operated with a dwell time of 200 ms. To construct the metabolite MRM library, each metabolite standard (50 mg/mL) was first analyzed by LC-MS/MS to get the optimal MRM transition parameters. Then the retention time of each metabolite was determined by measuring the corresponding MRM (Q1/Q3) transition individually. A standard mixture sample (6 standard mixtures) that contains all of the 6 metabolites was measured together and used as the reference peaks for metabolite identification. Raw MRM data files were processed by peak finding, alignment, and filtering using MultiQuant software.