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Supplementary data

# The First Insight into Transcriptome Profile of Herbaceous Plant *Nervilia fordii* Based on RNA-seq

**Qionglin HUANG, Lingling LIANG, Rui HE*, Xinye MA, Ruoting ZHAN, Weiwen CHEN***

## Table S 1 281 KEGG pathways annotated from unigenes of *N. fordii*

| | Pathway | DEGs genes with pathway annotation (14215) | All genes with pathway annotation (28970) | Pvalue | Qvalue | Pathway ID |
|---|---|---|---|---|---|---|
| **1** | Ribosome | 1250 (8.79%) | 1894 (6.54%) | 2.375574e-53 | 6.651607e-51 | ko03010 |
| **2** | Metabolic pathways | 4030 (28.35%) | 7639 (26.37%) | 3.180003e-14 | 4.452004e-12 | ko01100 |
| **3** | Microbial metabolism in diverse environments | 965 (6.79%) | 1691 (5.84%) | 6.778953e-12 | 6.327023e-10 | ko01120 |
| **4** | Biosynthesis of secondary metabolites | 1879 (13.22%) | 3452 (11.92%) | 1.035225e-11 | 7.246575e-10 | ko01110 |
| **5** | MAPK signaling pathway | 281 (1.98%) | 446 (1.54%) | 1.685610e-09 | 9.439416e-08 | ko04010 |
| **6** | Phenylpropanoid biosynthesis | 298 (2.1%) | 479 (1.65%) | 3.742764e-09 | 1.746623e-07 | ko00940 |
| **7** | Antigen processing and presentation | 255 (1.79%) | 404 (1.39%) | 7.342417e-09 | 2.936967e-07 | ko04612 |
| **8** | Tryptophan metabolism | 159 (1.12%) | 237 (0.82%) | 1.402616e-08 | 4.909156e-07 | ko00380 |
| **9** | Fc gamma R-mediated phagocytosis | 746 (5.25%) | 1340 (4.63%) | 4.191972e-07 | 1.304169e-05 | ko04666 |
| **10** | Endocytosis | 818 (5.75%) | 1479 (5.11%) | 4.716202e-07 | 1.320537e-05 | ko04144 |

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| **11** | Stilbenoid, diarylheptanoid and gingerol biosynthesis | 137 (0.96%) | 210 (0.72%) | 1.546111e-06 | 3.935555e-05 | ko00945 |
| **12** | Fatty acid metabolism | 193 (1.36%) | 310 (1.07%) | 1.815826e-06 | 4.236927e-05 | ko00071 |
| **13** | Viral myocarditis | 92 (0.65%) | 133 (0.46%) | 2.014992e-06 | 4.339983e-05 | ko05416 |
| **14** | Limonene and pinene degradation | 161 (1.13%) | 255 (0.88%) | 3.887193e-06 | 7.774386e-05 | ko00903 |
| **15** | Phagosome | 290 (2.04%) | 492 (1.7%) | 5.882558e-06 | 1.097519e-04 | ko04145 |
| **16** | Leukocyte transendothelial migration | 80 (0.56%) | 115 (0.4%) | 6.526765e-06 | 1.097519e-04 | ko04670 |
| **17** | Chloroalkane and chloroalkene degradation | 97 (0.68%) | 144 (0.5%) | 6.663511e-06 | 1.097519e-04 | ko00625 |
| **18** | Citrate cycle (TCA cycle) | 226 (1.59%) | 375 (1.29%) | 7.611911e-06 | 1.184075e-04 | ko00020 |
| **19** | Flavonoid biosynthesis | 139 (0.98%) | 218 (0.75%) | 8.18012e-06 | 1.205491e-04 | ko00941 |
| **20** | Ether lipid metabolism | 610 (4.29%) | 1100 (3.8%) | 8.880561e-06 | 1.243279e-04 | ko00565 |
| **21** | Valine, leucine and isoleucine degradation | 215 (1.51%) | 358 (1.24%) | 1.725102e-05 | 2.300136e-04 | ko00280 |
| **22** | GnRH signaling pathway | 669 (4.71%) | 1223 (4.22%) | 3.181859e-05 | 4.049639e-04 | ko04912 |
| **23** | Arrhythmogenic right ventricular cardiomyopathy (ARVC) | 56 (0.39%) | 78 (0.27%) | 3.750093e-05 | 4.534852e-04 | ko05412 |
| **24** | Arginine and proline metabolism | 204 (1.44%) | 341 (1.18%) | 3.887016e-05 | 4.534852e-04 | ko00330 |
| **25** | Shigellosis | 144 (1.01%) | 232 (0.8%) | 4.327258e-05 | 4.846529e-04 | ko05131 |
| **26** | Bisphenol degradation | 111 (0.78%) | 175 (0.6%) | 8.737167e-05 | 9.409257e-04 | ko00363 |
| **27** | Tight junction | 153 (1.08%) | 251 (0.87%) | 9.522363e-05 | 9.640737e-04 | ko04530 |
| **28** | Photosynthesis - antenna proteins | 58 (0.41%) | 83 (0.29%) | 9.640737e-05 | 9.640737e-04 | ko00196 |
| **29** | Glycolysis / Gluconeogenesis | 301 (2.12%) | 527 (1.82%) | 0.0001123492 | 1.067736e-03 | ko00010 |
| **30** | Glycerophospholipid metabolism | 676 (4.76%) | 1247 (4.3%) | 0.0001144003 | 1.067736e-03 | ko00564 |

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| **31** | PPAR signaling pathway | 167 (1.17%) | 279 (0.96%) | 0.0001784382 | 1.611655e-03 | ko03320 |
| **32** | Biosynthesis of unsaturated fatty acids | 144 (1.01%) | 237 (0.82%) | 0.0001856014 | 1.611655e-03 | ko01040 |
| **33** | Photosynthesis | 103 (0.72%) | 163 (0.56%) | 0.000189945 | 1.611655e-03 | ko00195 |
| **34** | Nitrogen metabolism | 141 (0.99%) | 233 (0.8%) | 0.0002776942 | 2.286893e-03 | ko00910 |
| **35** | Hypertrophic cardiomyopathy (HCM) | 91 (0.64%) | 144 (0.5%) | 0.0004341815 | 3.473452e-03 | ko05410 |
| **36** | Glycine, serine and threonine metabolism | 119 (0.84%) | 195 (0.67%) | 0.0005028105 | 3.698425e-03 | ko00260 |
| **37** | Two-component system | 63 (0.44%) | 95 (0.33%) | 0.0005050226 | 3.698425e-03 | ko02020 |
| **38** | Pyruvate metabolism | 250 (1.76%) | 439 (1.52%) | 0.0005139261 | 3.698425e-03 | ko00620 |
| **39** | Protein processing in endoplasmic reticulum | 554 (3.9%) | 1023 (3.53%) | 0.0005151378 | 3.698425e-03 | ko04141 |
| **40** | NOD-like receptor signaling pathway | 92 (0.65%) | 147 (0.51%) | 0.0006496561 | 4.541610e-03 | ko04621 |
| **41** | Polycyclic aromatic hydrocarbon degradation | 119 (0.84%) | 196 (0.68%) | 0.0006650215 | 4.541610e-03 | ko00624 |
| **42** | Gap junction | 140 (0.98%) | 235 (0.81%) | 0.0007469134 | 4.979423e-03 | ko04540 |
| **43** | Phenylalanine metabolism | 163 (1.15%) | 278 (0.96%) | 0.0008153894 | 5.309512e-03 | ko00360 |
| **44** | Prostate cancer | 141 (0.99%) | 238 (0.82%) | 0.0009879358 | 6.286864e-03 | ko05215 |
| **45** | Pathogenic Escherichia coli infection | 188 (1.32%) | 326 (1.13%) | 0.001063542 | 6.617595e-03 | ko05130 |
| **46** | Huntington's disease | 480 (3.38%) | 888 (3.07%) | 0.001417042 | 8.625473e-03 | ko05016 |
| **47** | Regulation of actin cytoskeleton | 232 (1.63%) | 411 (1.42%) | 0.001505059 | 8.966309e-03 | ko04810 |
| **48** | Aminobenzoate degradation | 127 (0.89%) | 215 (0.74%) | 0.001981588 | 1.143254e-02 | ko00627 |
| **49** | Pentose and glucuronate interconversions | 142 (1%) | 243 (0.84%) | 0.002030948 | 1.143254e-02 | ko00040 |
| **50** | Propanoate metabolism | 151 (1.06%) | 260 (0.9%) | 0.002115779 | 1.143254e-02 | ko00640 |

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| **51** | Focal adhesion | 159 (1.12%) | 275 (0.95%) | 0.002122576 | 1.143254e-02 | ko04510 |
| **52** | Bacterial invasion of epithelial cells | 103 (0.72%) | 171 (0.59%) | 0.002123186 | 1.143254e-02 | ko05100 |
| **53** | Retinol metabolism | 36 (0.25%) | 52 (0.18%) | 0.002577126 | 1.361501e-02 | ko00830 |
| **54** | mTOR signaling pathway | 136 (0.96%) | 233 (0.8%) | 0.002638323 | 1.368019e-02 | ko04150 |
| **55** | Primary bile acid biosynthesis | 22 (0.15%) | 29 (0.1%) | 0.003005039 | 1.507366e-02 | ko00120 |
| **56** | Long-term depression | 76 (0.53%) | 123 (0.42%) | 0.003014732 | 1.507366e-02 | ko04730 |
| **57** | Dilated cardiomyopathy | 68 (0.48%) | 110 (0.38%) | 0.004766293 | 2.341337e-02 | ko05414 |
| **58** | Acute myeloid leukemia | 69 (0.49%) | 112 (0.39%) | 0.005050049 | 2.437955e-02 | ko05221 |
| **59** | Osteoclast differentiation | 77 (0.54%) | 127 (0.44%) | 0.005717588 | 2.652361e-02 | ko04380 |
| **60** | Pancreatic secretion | 51 (0.36%) | 80 (0.28%) | 0.005719562 | 2.652361e-02 | ko04972 |
| **61** | Amyotrophic lateral sclerosis (ALS) | 66 (0.46%) | 107 (0.37%) | 0.005778358 | 2.652361e-02 | ko05014 |
| **62** | Carbon fixation in photosynthetic organisms | 174 (1.22%) | 310 (1.07%) | 0.007249568 | 3.229922e-02 | ko00710 |
| **63** | Butanoate metabolism | 89 (0.63%) | 150 (0.52%) | 0.007267325 | 3.229922e-02 | ko00650 |
| **64** | Flavone and flavonol biosynthesis | 46 (0.32%) | 72 (0.25%) | 0.007961996 | 3.483373e-02 | ko00944 |
| **65** | Toxoplasmosis | 296 (2.08%) | 546 (1.88%) | 0.008544348 | 3.614370e-02 | ko05145 |
| **66** | Alzheimer's disease | 296 (2.08%) | 546 (1.88%) | 0.008544348 | 3.614370e-02 | ko05010 |
| **67** | Glyoxylate and dicarboxylate metabolism | 144 (1.01%) | 254 (0.88%) | 0.00864867 | 3.614370e-02 | ko00630 |
| **68** | Adherens junction | 137 (0.96%) | 241 (0.83%) | 0.009068868 | 3.734240e-02 | ko04520 |
| **69** | Caffeine metabolism | 11 (0.08%) | 13 (0.04%) | 0.00940522 | 3.816611e-02 | ko00232 |
| **70** | Naphthalene degradation | 36 (0.25%) | 55 (0.19%) | 0.01044862 | 4.160579e-02 | ko00626 |

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| **71** | RNA transport | 635 (4.47%) | 1213 (4.19%) | 0.01055004 | 4.160579e-02 | ko03013 |
| **72** | Vibrio cholerae infection | 125 (0.88%) | 220 (0.76%) | 0.01247198 | 4.850214e-02 | ko05110 |
| **73** | Fc epsilon RI signaling pathway | 68 (0.48%) | 114 (0.39%) | 0.01484394 | 5.668524e-02 | ko04664 |
| **74** | ErbB signaling pathway | 75 (0.53%) | 127 (0.44%) | 0.0149811 | 5.668524e-02 | ko04012 |
| **75** | Phototransduction - fly | 83 (0.58%) | 142 (0.49%) | 0.01536245 | 5.735315e-02 | ko04745 |
| **76** | Lysosome | 214 (1.51%) | 392 (1.35%) | 0.0156869 | 5.779384e-02 | ko04142 |
| **77** | Lysine degradation | 106 (0.75%) | 186 (0.64%) | 0.01804037 | 6.560135e-02 | ko00310 |
| **78** | Vitamin B6 metabolism | 26 (0.18%) | 39 (0.13%) | 0.02015635 | 7.235613e-02 | ko00750 |
| **79** | Parkinson's disease | 269 (1.89%) | 501 (1.73%) | 0.02048345 | 7.259957e-02 | ko05012 |
| **80** | Drug metabolism - cytochrome P450 | 78 (0.55%) | 134 (0.46%) | 0.02081316 | 7.284606e-02 | ko00982 |
| **81** | Rheumatoid arthritis | 72 (0.51%) | 123 (0.42%) | 0.02184008 | 7.527530e-02 | ko05323 |
| **82** | Benzoate degradation | 52 (0.37%) | 86 (0.3%) | 0.02204491 | 7.527530e-02 | ko00362 |
| **83** | Steroid biosynthesis | 55 (0.39%) | 92 (0.32%) | 0.02512855 | 8.477101e-02 | ko00100 |
| **84** | Carbon fixation pathways in prokaryotes | 96 (0.68%) | 169 (0.58%) | 0.02607216 | 8.690720e-02 | ko00720 |
| **85** | Metabolism of xenobiotics by cytochrome P450 | 71 (0.5%) | 122 (0.42%) | 0.0266479 | 8.764700e-02 | ko00980 |
| **86** | Selenocompound metabolism | 64 (0.45%) | 109 (0.38%) | 0.02711494 | 8.764700e-02 | ko00450 |
| **87** | Ascorbate and aldarate metabolism | 131 (0.92%) | 236 (0.81%) | 0.02726432 | 8.764700e-02 | ko00053 |
| **88** | Peroxisome | 242 (1.7%) | 451 (1.56%) | 0.02754620 | 8.764700e-02 | ko04146 |
| **89** | RNA polymerase | 225 (1.58%) | 418 (1.44%) | 0.02795619 | 8.795206e-02 | ko03020 |
| **90** | Pancreatic cancer | 77 (0.54%) | 134 (0.46%) | 0.03121191 | 9.611683e-02 | ko05212 |

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| **91** | Cardiac muscle contraction | 61 (0.43%) | 104 (0.36%) | 0.03123797 | 9.611683e-02 | ko04260 |
| **92** | Alanine, aspartate and glutamate metabolism | 144 (1.01%) | 262 (0.9%) | 0.03176695 | 9.668202e-02 | ko00250 |
| **93** | Methane metabolism | 179 (1.26%) | 330 (1.14%) | 0.03317943 | 9.989506e-02 | ko00680 |
| **94** | Epithelial cell signaling in Helicobacter pylori infection | 66 (0.46%) | 114 (0.39%) | 0.03619391 | 1.078116e-01 | ko05120 |
| **95** | Type I diabetes mellitus | 24 (0.17%) | 37 (0.13%) | 0.03878331 | 1.131501e-01 | ko04940 |
| **96** | Systemic lupus erythematosus | 98 (0.69%) | 175 (0.6%) | 0.03879433 | 1.131501e-01 | ko05322 |
| **97** | Adipocytokine signaling pathway | 71 (0.5%) | 124 (0.43%) | 0.04097735 | 1.182851e-01 | ko04920 |
| **98** | Natural killer cell mediated cytotoxicity | 73 (0.51%) | 128 (0.44%) | 0.04283625 | 1.223893e-01 | ko04650 |
| **99** | Melanoma | 51 (0.36%) | 87 (0.3%) | 0.04654463 | 1.316414e-01 | ko05218 |
| **100** | Oxidative phosphorylation | 325 (2.29%) | 621 (2.14%) | 0.05417756 | 1.516972e-01 | ko00190 |
| **101** | TGF-beta signaling pathway | 100 (0.7%) | 181 (0.62%) | 0.05542582 | 1.536557e-01 | ko04350 |
| **102** | beta-Alanine metabolism | 115 (0.81%) | 210 (0.72%) | 0.05619086 | 1.542494e-01 | ko00410 |
| **103** | Endometrial cancer | 61 (0.43%) | 107 (0.37%) | 0.06054546 | 1.645896e-01 | ko05213 |
| **104** | Taurine and hypotaurine metabolism | 16 (0.11%) | 24 (0.08%) | 0.06347497 | 1.708942e-01 | ko00430 |
| **105** | Fat digestion and absorption | 21 (0.15%) | 33 (0.11%) | 0.0662733 | 1.767288e-01 | ko04975 |
| **106** | VEGF signaling pathway | 79 (0.56%) | 142 (0.49%) | 0.06874481 | 1.815901e-01 | ko04370 |
| **107** | Purine metabolism | 375 (2.64%) | 724 (2.5%) | 0.07365915 | 1.927529e-01 | ko00230 |
| **108** | Valine, leucine and isoleucine biosynthesis | 86 (0.6%) | 156 (0.54%) | 0.07519146 | 1.949408e-01 | ko00290 |
| **109** | Pathways in cancer | 214 (1.51%) | 406 (1.4%) | 0.07663615 | 1.968635e-01 | ko05200 |
| **110** | Fatty acid elongation in mitochondria | 7 (0.05%) | 9 (0.03%) | 0.08097443 | 2.046158e-01 | ko00062 |

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| **111** | B cell receptor signaling pathway | 79 (0.56%) | 143 (0.49%) | 0.08111553 | 2.046158e-01 | ko04662 |
| **112** | Benzoxazinoid biosynthesis | 15 (0.11%) | 23 (0.08%) | 0.08949071 | 2.222558e-01 | ko00402 |
| **113** | Measles | 241 (1.7%) | 461 (1.59%) | 0.08969611 | 2.222558e-01 | ko05162 |
| **114** | Cysteine and methionine metabolism | 154 (1.08%) | 290 (1%) | 0.09298834 | 2.283924e-01 | ko00270 |
| **115** | Tropane, piperidine and pyridine alkaloid biosynthesis | 36 (0.25%) | 62 (0.21%) | 0.09818201 | 2.390519e-01 | ko00960 |
| **116** | Diterpenoid biosynthesis | 37 (0.26%) | 64 (0.22%) | 0.1009288 | 2.436212e-01 | ko00904 |
| **117** | Type II diabetes mellitus | 59 (0.42%) | 106 (0.37%) | 0.1032810 | 2.462140e-01 | ko04930 |
| **118** | C5-Branched dibasic acid metabolism | 12 (0.08%) | 18 (0.06%) | 0.1037616 | 2.462140e-01 | ko00660 |
| **119** | Chemokine signaling pathway | 94 (0.66%) | 174 (0.6%) | 0.1083420 | 2.549224e-01 | ko04062 |
| **120** | Histidine metabolism | 70 (0.49%) | 128 (0.44%) | 0.1177972 | 2.748601e-01 | ko00340 |
| **121** | T cell receptor signaling pathway | 62 (0.44%) | 113 (0.39%) | 0.1268598 | 2.935599e-01 | ko04660 |
| **122** | Glioma | 85 (0.6%) | 158 (0.55%) | 0.1329267 | 3.050777e-01 | ko05214 |
| **123** | Dorso-ventral axis formation | 42 (0.3%) | 75 (0.26%) | 0.1385507 | 3.104653e-01 | ko04320 |
| **124** | MAPK signaling pathway - fly | 42 (0.3%) | 75 (0.26%) | 0.1385507 | 3.104653e-01 | ko04013 |
| **125** | Tyrosine metabolism | 92 (0.65%) | 172 (0.59%) | 0.1386006 | 3.104653e-01 | ko00350 |
| **126** | Prion diseases | 103 (0.72%) | 194 (0.67%) | 0.1461496 | 3.247769e-01 | ko05020 |
| **127** | Small cell lung cancer | 17 (0.12%) | 28 (0.1%) | 0.1481799 | 3.266958e-01 | ko05222 |
| **128** | Non-small cell lung cancer | 50 (0.35%) | 91 (0.31%) | 0.1542872 | 3.375033e-01 | ko05223 |
| **129** | Aldosterone-regulated sodium reabsorption | 38 (0.27%) | 68 (0.23%) | 0.1577085 | 3.423130e-01 | ko04960 |
| **130** | Glycerolipid metabolism | 131 (0.92%) | 250 (0.86%) | 0.1598928 | 3.443504e-01 | ko00561 |

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| **131** | Mineral absorption | 19 (0.13%) | 32 (0.11%) | 0.1611068 | 3.443504e-01 | ko04978 |
| **132** | Bladder cancer | 44 (0.31%) | 80 (0.28%) | 0.1708576 | 3.624252e-01 | ko05219 |
| **133** | Cyanoamino acid metabolism | 92 (0.65%) | 174 (0.6%) | 0.1758934 | 3.703019e-01 | ko00460 |
| **134** | Brassinosteroid biosynthesis | 15 (0.11%) | 25 (0.09%) | 0.1858632 | 3.883709e-01 | ko00905 |
| **135** | Collecting duct acid secretion | 38 (0.27%) | 69 (0.24%) | 0.1899010 | 3.938687e-01 | ko04966 |
| **136** | Regulation of autophagy | 87 (0.61%) | 165 (0.57%) | 0.1935579 | 3.955928e-01 | ko04140 |
| **137** | Pentose phosphate pathway | 87 (0.61%) | 165 (0.57%) | 0.1935579 | 3.955928e-01 | ko00030 |
| **138** | Axon guidance | 78 (0.55%) | 148 (0.51%) | 0.2105899 | 4.271746e-01 | ko04360 |
| **139** | RIG-I-like receptor signaling pathway | 32 (0.23%) | 58 (0.2%) | 0.2120617 | 4.271746e-01 | ko04622 |
| **140** | Renal cell carcinoma | 87 (0.61%) | 166 (0.57%) | 0.2159668 | 4.319336e-01 | ko05211 |
| **141** | Vascular smooth muscle contraction | 130 (0.91%) | 252 (0.87%) | 0.2295655 | 4.558748e-01 | ko04270 |
| **142** | Progesterone-mediated oocyte maturation | 146 (1.03%) | 284 (0.98%) | 0.2316879 | 4.568494e-01 | ko04914 |
| **143** | Circadian rhythm - mammal | 25 (0.18%) | 45 (0.16%) | 0.2352140 | 4.585870e-01 | ko04710 |
| **144** | Colorectal cancer | 81 (0.57%) | 155 (0.54%) | 0.2369669 | 4.585870e-01 | ko05210 |
| **145** | Vitamin digestion and absorption | 2 (0.01%) | 2 (0.01%) | 0.2407582 | 4.585870e-01 | ko04977 |
| **146** | D-Arginine and D-ornithine metabolism | 2 (0.01%) | 2 (0.01%) | 0.2407582 | 4.585870e-01 | ko00472 |
| **147** | Penicillin and cephalosporin biosynthesis | 2 (0.01%) | 2 (0.01%) | 0.2407582 | 4.585870e-01 | ko00311 |
| **148** | Zeatin biosynthesis | 190 (1.34%) | 375 (1.29%) | 0.2838448 | 5.348385e-01 | ko00908 |
| **149** | Synthesis and degradation of ketone bodies | 25 (0.18%) | 46 (0.16%) | 0.2846105 | 5.348385e-01 | ko00072 |
| **150** | Protein export | 74 (0.52%) | 143 (0.49%) | 0.2880782 | 5.357131e-01 | ko03060 |

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| **151** | Drug metabolism - other enzymes | 27 (0.19%) | 50 (0.17%) | 0.2889024 | 5.357131e-01 | ko00983 |
| **152** | Toluene degradation | 3 (0.02%) | 4 (0.01%) | 0.2986385 | 5.465280e-01 | ko00623 |
| **153** | Fluorobenzoate degradation | 3 (0.02%) | 4 (0.01%) | 0.2986385 | 5.465280e-01 | ko00364 |
| **154** | Protein digestion and absorption | 48 (0.34%) | 92 (0.32%) | 0.3111558 | 5.657378e-01 | ko04974 |
| **155** | Plant hormone signal transduction | 572 (4.02%) | 1149 (3.97%) | 0.3212097 | 5.802498e-01 | ko04075 |
| **156** | Primary immunodeficiency | 4 (0.03%) | 6 (0.02%) | 0.3264245 | 5.858901e-01 | ko05340 |
| **157** | Toll-like receptor signaling pathway | 160 (1.13%) | 318 (1.1%) | 0.347936 | 6.183617e-01 | ko04620 |
| **158** | Fatty acid biosynthesis | 63 (0.44%) | 123 (0.42%) | 0.3489327 | 6.183617e-01 | ko00061 |
| **159** | Polyketide sugar unit biosynthesis | 6 (0.04%) | 10 (0.03%) | 0.3542171 | 6.237785e-01 | ko00523 |
| **160** | Sphingolipid metabolism | 81 (0.57%) | 160 (0.55%) | 0.37598 | 6.538268e-01 | ko00600 |
| **161** | Thyroid cancer | 66 (0.46%) | 130 (0.45%) | 0.3816003 | 6.538268e-01 | ko05216 |
| **162** | Salivary secretion | 65 (0.46%) | 128 (0.44%) | 0.3819699 | 6.538268e-01 | ko04970 |
| **163** | Hepatitis C | 57 (0.4%) | 112 (0.39%) | 0.3848717 | 6.538268e-01 | ko05160 |
| **164** | Indole alkaloid biosynthesis | 14 (0.1%) | 26 (0.09%) | 0.3853061 | 6.538268e-01 | ko00901 |
| **165** | African trypanosomiasis | 19 (0.13%) | 36 (0.12%) | 0.3900934 | 6.538268e-01 | ko05143 |
| **166** | Glycosphingolipid biosynthesis - ganglio series | 21 (0.15%) | 40 (0.14%) | 0.3910404 | 6.538268e-01 | ko00604 |
| **167** | Isoquinoline alkaloid biosynthesis | 32 (0.23%) | 62 (0.21%) | 0.391851 | 6.538268e-01 | ko00950 |
| **168** | RNA degradation | 656 (4.61%) | 1326 (4.58%) | 0.3922961 | 6.538268e-01 | ko03018 |
| **169** | Ribosome biogenesis in eukaryotes | 674 (4.74%) | 1364 (4.71%) | 0.4075464 | 6.752248e-01 | ko03008 |
| **170** | Various types of N-glycan biosynthesis | 57 (0.4%) | 113 (0.39%) | 0.4211365 | 6.936366e-01 | ko00513 |

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|---|---|---|---|---|---|---|
| **171** | Vasopressin-regulated water reabsorption | 43 (0.3%) | 85 (0.29%) | 0.4314736 | 7.065065e-01 | ko04962 |
| **172** | Starch and sucrose metabolism | 266 (1.87%) | 538 (1.86%) | 0.4474729 | 7.284443e-01 | ko00500 |
| **173** | Chronic myeloid leukemia | 45 (0.32%) | 90 (0.31%) | 0.4712476 | 7.627129e-01 | ko05220 |
| **174** | Calcium signaling pathway | 131 (0.92%) | 265 (0.91%) | 0.4767339 | 7.633146e-01 | ko04020 |
| **175** | Biosynthesis of vancomycin group antibiotics | 5 (0.04%) | 9 (0.03%) | 0.4770716 | 7.633146e-01 | ko01055 |
| **176** | Monoterpenoid biosynthesis | 2 (0.01%) | 3 (0.01%) | 0.4860212 | 7.718562e-01 | ko00902 |
| **177** | Glycosaminoglycan biosynthesis - keratan sulfate | 1 (0.01%) | 1 (0%) | 0.49068 | 7.718562e-01 | ko00533 |
| **178** | Sesquiterpenoid biosynthesis | 1 (0.01%) | 1 (0%) | 0.49068 | 7.718562e-01 | ko00909 |
| **179** | alpha-Linolenic acid metabolism | 82 (0.58%) | 167 (0.58%) | 0.5272459 | 8.247422e-01 | ko00592 |
| **180** | Bacterial secretion system | 12 (0.08%) | 24 (0.08%) | 0.5442673 | 8.466380e-01 | ko03070 |
| **181** | Inositol phosphate metabolism | 108 (0.76%) | 221 (0.76%) | 0.5503532 | 8.513751e-01 | ko00562 |
| **182** | Basal cell carcinoma | 10 (0.07%) | 20 (0.07%) | 0.555004 | 8.538523e-01 | ko05217 |
| **183** | Glucosinolate biosynthesis | 6 (0.04%) | 12 (0.04%) | 0.587362 | 8.938117e-01 | ko00966 |
| **184** | DDT degradation | 6 (0.04%) | 12 (0.04%) | 0.587362 | 8.938117e-01 | ko00351 |
| **185** | Insulin signaling pathway | 213 (1.5%) | 438 (1.51%) | 0.5919446 | 8.959162e-01 | ko04910 |
| **186** | Geraniol degradation | 14 (0.1%) | 29 (0.1%) | 0.6061696 | 9.106973e-01 | ko00281 |
| **187** | Caprolactam degradation | 13 (0.09%) | 27 (0.09%) | 0.6126573 | 9.106973e-01 | ko00930 |
| **188** | Cell cycle - Caulobacter | 24 (0.17%) | 50 (0.17%) | 0.6146635 | 9.106973e-01 | ko04112 |
| **189** | Leishmaniasis | 134 (0.94%) | 277 (0.96%) | 0.6147207 | 9.106973e-01 | ko05140 |
| **190** | Tetracycline biosynthesis | 11 (0.08%) | 23 (0.08%) | 0.6276017 | 9.248867e-01 | ko00253 |

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|---|---|---|---|---|---|---|
| **191** | Other glycan degradation | 44 (0.31%) | 92 (0.32%) | 0.6339197 | 9.293064e-01 | ko00511 |
| **192** | Anthocyanin biosynthesis | 3 (0.02%) | 6 (0.02%) | 0.6386312 | 9.313372e-01 | ko00942 |
| **193** | Glycosphingolipid biosynthesis - globo series | 17 (0.12%) | 36 (0.12%) | 0.6505404 | 9.437892e-01 | ko00603 |
| **194** | Taste transduction | 22 (0.15%) | 47 (0.16%) | 0.6753487 | 9.721446e-01 | ko04742 |
| **195** | Carotenoid biosynthesis | 65 (0.46%) | 137 (0.47%) | 0.6793417 | 9.721446e-01 | ko00906 |
| **196** | N-Glycan biosynthesis | 64 (0.45%) | 135 (0.47%) | 0.681714 | 9.721446e-01 | ko00510 |
| **197** | Glycosaminoglycan degradation | 40 (0.28%) | 85 (0.29%) | 0.6839732 | 9.721446e-01 | ko00531 |
| **198** | Phototransduction | 37 (0.26%) | 79 (0.27%) | 0.6947067 | 9.798302e-01 | ko04744 |
| **199** | Lysine biosynthesis | 27 (0.19%) | 58 (0.2%) | 0.6963793 | 9.798302e-01 | ko00300 |
| **200** | Chlorocyclohexane and chlorobenzene degradation | 9 (0.06%) | 20 (0.07%) | 0.7207407 | 1.000000e+00 | ko00361 |
| **201** | Nicotinate and nicotinamide metabolism | 30 (0.21%) | 65 (0.22%) | 0.7236399 | 1.000000e+00 | ko00760 |
| **202** | Neurotrophin signaling pathway | 208 (1.46%) | 436 (1.51%) | 0.7327179 | 1.000000e+00 | ko04722 |
| **203** | Pyrimidine metabolism | 307 (2.16%) | 641 (2.21%) | 0.7392595 | 1.000000e+00 | ko00240 |
| **204** | Neuroactive ligand-receptor interaction | 1 (0.01%) | 2 (0.01%) | 0.7406018 | 1.000000e+00 | ko04080 |
| **205** | Glutathione metabolism | 108 (0.76%) | 229 (0.79%) | 0.7406554 | 1.000000e+00 | ko00480 |
| **206** | Novobiocin biosynthesis | 11 (0.08%) | 25 (0.09%) | 0.7596792 | 1.000000e+00 | ko00401 |
| **207** | Circadian rhythm - plant | 118 (0.83%) | 251 (0.87%) | 0.7634782 | 1.000000e+00 | ko04712 |
| **208** | Arachidonic acid metabolism | 16 (0.11%) | 36 (0.12%) | 0.7644512 | 1.000000e+00 | ko00590 |
| **209** | Biosynthesis of ansamycins | 6 (0.04%) | 14 (0.05%) | 0.7670132 | 1.000000e+00 | ko01051 |
| **210** | Sulfur metabolism | 36 (0.25%) | 79 (0.27%) | 0.7687797 | 1.000000e+00 | ko00920 |

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|---|---|---|---|---|---|---|
| **211** | Linoleic acid metabolism | 28 (0.2%) | 62 (0.21%) | 0.7710556 | 1.000000e+00 | ko00591 |
| **212** | ECM-receptor interaction | 5 (0.04%) | 12 (0.04%) | 0.787679 | 1.000000e+00 | ko04512 |
| **213** | Non-homologous end-joining | 13 (0.09%) | 30 (0.1%) | 0.7910465 | 1.000000e+00 | ko03450 |
| **214** | Fructose and mannose metabolism | 88 (0.62%) | 190 (0.66%) | 0.7978357 | 1.000000e+00 | ko00051 |
| **215** | Atrazine degradation | 2 (0.01%) | 5 (0.02%) | 0.8006544 | 1.000000e+00 | ko00791 |
| **216** | Pantothenate and CoA biosynthesis | 49 (0.34%) | 108 (0.37%) | 0.8068115 | 1.000000e+00 | ko00770 |
| **217** | Phosphonate and phosphinate metabolism | 4 (0.03%) | 10 (0.03%) | 0.8124494 | 1.000000e+00 | ko00440 |
| **218** | Terpenoid backbone biosynthesis | 193 (1.36%) | 411 (1.42%) | 0.8188936 | 1.000000e+00 | ko00900 |
| **219** | Carbohydrate digestion and absorption | 10 (0.07%) | 24 (0.08%) | 0.823566 | 1.000000e+00 | ko04973 |
| **220** | Porphyrin and chlorophyll metabolism | 59 (0.42%) | 130 (0.45%) | 0.8237463 | 1.000000e+00 | ko00860 |
| **221** | p53 signaling pathway | 61 (0.43%) | 135 (0.47%) | 0.8391101 | 1.000000e+00 | ko04115 |
| **222** | Melanogenesis | 102 (0.72%) | 222 (0.77%) | 0.8417038 | 1.000000e+00 | ko04916 |
| **223** | Chagas disease (American trypanosomiasis) | 140 (0.98%) | 302 (1.04%) | 0.8425525 | 1.000000e+00 | ko05142 |
| **224** | Phosphatidylinositol signaling system | 114 (0.8%) | 249 (0.86%) | 0.865458 | 1.000000e+00 | ko04070 |
| **225** | Biosynthesis of siderophore group nonribosomal peptides | 1 (0.01%) | 3 (0.01%) | 0.8678921 | 1.000000e+00 | ko01053 |
| **226** | Betalain biosynthesis | 1 (0.01%) | 3 (0.01%) | 0.8678921 | 1.000000e+00 | ko00965 |
| **227** | Phenylalanine, tyrosine and tryptophan biosynthesis | 42 (0.3%) | 96 (0.33%) | 0.8742619 | 1.000000e+00 | ko00400 |
| **228** | Lipoic acid metabolism | 4 (0.03%) | 11 (0.04%) | 0.8742984 | 1.000000e+00 | ko00785 |
| **229** | Renin-angiotensin system | 24 (0.17%) | 57 (0.2%) | 0.882224 | 1.000000e+00 | ko04614 |
| **230** | MAPK signaling pathway - yeast | 33 (0.23%) | 77 (0.27%) | 0.8862204 | 1.000000e+00 | ko04011 |

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|---|---|---|---|---|---|---|
| **231** | Spliceosome | 660 (4.64%) | 1390 (4.8%) | 0.8924857 | 1.000000e+00 | ko03040 |
| **232** | Other types of O-glycan biosynthesis | 10 (0.07%) | 26 (0.09%) | 0.9000465 | 1.000000e+00 | ko00514 |
| **233** | Olfactory transduction | 44 (0.31%) | 102 (0.35%) | 0.9033067 | 1.000000e+00 | ko04740 |
| **234** | Wnt signaling pathway | 153 (1.08%) | 335 (1.16%) | 0.9042515 | 1.000000e+00 | ko04310 |
| **235** | Folate biosynthesis | 32 (0.23%) | 76 (0.26%) | 0.9086259 | 1.000000e+00 | ko00790 |
| **236** | Sulfur relay system | 9 (0.06%) | 24 (0.08%) | 0.9103493 | 1.000000e+00 | ko04122 |
| **237** | Jak-STAT signaling pathway | 22 (0.15%) | 54 (0.19%) | 0.9137064 | 1.000000e+00 | ko04630 |
| **238** | Lipopolysaccharide biosynthesis | 6 (0.04%) | 17 (0.06%) | 0.917168 | 1.000000e+00 | ko00540 |
| **239** | Gastric acid secretion | 44 (0.31%) | 103 (0.36%) | 0.9179898 | 1.000000e+00 | ko04971 |
| **240** | Styrene degradation | 7 (0.05%) | 20 (0.07%) | 0.9321161 | 1.000000e+00 | ko00643 |
| **241** | Amoebiasis | 34 (0.24%) | 82 (0.28%) | 0.9322464 | 1.000000e+00 | ko05146 |
| **242** | Oocyte meiosis | 184 (1.29%) | 406 (1.4%) | 0.9420455 | 1.000000e+00 | ko04114 |
| **243** | Basal transcription factors | 107 (0.75%) | 242 (0.84%) | 0.9432336 | 1.000000e+00 | ko03022 |
| **244** | Ubiquinone and other terpenoid-quinone biosynthesis | 41 (0.29%) | 99 (0.34%) | 0.9484443 | 1.000000e+00 | ko00130 |
| **245** | Aminoacyl-tRNA biosynthesis | 82 (0.58%) | 189 (0.65%) | 0.9497655 | 1.000000e+00 | ko00970 |
| **246** | One carbon pool by folate | 28 (0.2%) | 70 (0.24%) | 0.9498837 | 1.000000e+00 | ko00670 |
| **247** | Galactose metabolism | 87 (0.61%) | 200 (0.69%) | 0.9508864 | 1.000000e+00 | ko00052 |
| **248** | Long-term potentiation | 110 (0.77%) | 250 (0.86%) | 0.9530434 | 1.000000e+00 | ko04720 |
| **249** | Apoptosis | 125 (0.88%) | 283 (0.98%) | 0.9570923 | 1.000000e+00 | ko04210 |
| **250** | Proximal tubule bicarbonate reclamation | 20 (0.14%) | 53 (0.18%) | 0.9638715 | 1.000000e+00 | ko04964 |

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|---|---|---|---|---|---|---|
| **251** | Amino sugar and nucleotide sugar metabolism | 149 (1.05%) | 336 (1.16%) | 0.9639454 | 1.000000e+00 | ko00520 |
| **252** | Peptidoglycan biosynthesis | 1 (0.01%) | 5 (0.02%) | 0.9657383 | 1.000000e+00 | ko00550 |
| **253** | Bile secretion | 113 (0.79%) | 260 (0.9%) | 0.970034 | 1.000000e+00 | ko04976 |
| **254** | Cell cycle - yeast | 157 (1.1%) | 356 (1.23%) | 0.973914 | 1.000000e+00 | ko04111 |
| **255** | Cell cycle | 171 (1.2%) | 387 (1.34%) | 0.9765616 | 1.000000e+00 | ko04110 |
| **256** | Biotin metabolism | 6 (0.04%) | 21 (0.07%) | 0.9835518 | 1.000000e+00 | ko00780 |
| **257** | ABC transporters | 102 (0.72%) | 244 (0.84%) | 0.9905942 | 1.000000e+00 | ko02010 |
| **258** | Base excision repair | 55 (0.39%) | 140 (0.48%) | 0.9921348 | 1.000000e+00 | ko03410 |
| **259** | Notch signaling pathway | 29 (0.2%) | 80 (0.28%) | 0.9923301 | 1.000000e+00 | ko04330 |
| **260** | Proteasome | 47 (0.33%) | 122 (0.42%) | 0.9925777 | 1.000000e+00 | ko03050 |
| **261** | Thiamine metabolism | 6 (0.04%) | 23 (0.08%) | 0.9932007 | 1.000000e+00 | ko00730 |
| **262** | Circadian rhythm - fly | 16 (0.11%) | 49 (0.17%) | 0.993238 | 1.000000e+00 | ko04711 |
| **263** | Butirosin and neomycin biosynthesis | 1 (0.01%) | 8 (0.03%) | 0.995476 | 1.000000e+00 | ko00524 |
| **264** | Hedgehog signaling pathway | 33 (0.23%) | 93 (0.32%) | 0.9970113 | 1.000000e+00 | ko04340 |
| **265** | Cytosolic DNA-sensing pathway | 23 (0.16%) | 69 (0.24%) | 0.997159 | 1.000000e+00 | ko04623 |
| **266** | Ubiquitin mediated proteolysis | 210 (1.48%) | 492 (1.7%) | 0.9981841 | 1.000000e+00 | ko04120 |
| **267** | Meiosis - yeast | 90 (0.63%) | 227 (0.78%) | 0.998295 | 1.000000e+00 | ko04113 |
| **268** | Streptomycin biosynthesis | 12 (0.08%) | 43 (0.15%) | 0.9985815 | 1.000000e+00 | ko00521 |
| **269** | mRNA surveillance pathway | 261 (1.84%) | 607 (2.1%) | 0.9989285 | 1.000000e+00 | ko03015 |
| **270** | Riboflavin metabolism | 15 (0.11%) | 52 (0.18%) | 0.9990648 | 1.000000e+00 | ko00740 |

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| **271** | Glycosaminoglycan biosynthesis - heparan sulfate | 6 (0.04%) | 30 (0.1%) | 0.999765 | 1.000000e+00 | ko00534 |
| **272** | Glycosylphosphatidylinositol(GPI)-anchor biosynthesis | 14 (0.1%) | 53 (0.18%) | 0.999779 | 1.000000e+00 | ko00563 |
| **273** | Glycosaminoglycan biosynthesis - chondroitin sulfate | 4 (0.03%) | 24 (0.08%) | 0.999807 | 1.000000e+00 | ko00532 |
| **274** | D-Glutamine and D-glutamate metabolism | 4 (0.03%) | 27 (0.09%) | 0.9999638 | 1.000000e+00 | ko00471 |
| **275** | SNARE interactions in vesicular transport | 26 (0.18%) | 97 (0.33%) | 0.9999978 | 1.000000e+00 | ko04130 |
| **276** | Homologous recombination | 60 (0.42%) | 193 (0.67%) | 0.9999999 | 1.000000e+00 | ko03440 |
| **277** | Nucleotide excision repair | 77 (0.54%) | 242 (0.84%) | 1 | 1.000000e+00 | ko03420 |
| **278** | Plant-pathogen interaction | 523 (3.68%) | 1258 (4.34%) | 1 | 1.000000e+00 | ko04626 |
| **279** | Mismatch repair | 22 (0.15%) | 106 (0.37%) | 1 | 1.000000e+00 | ko03430 |
| **280** | DNA replication | 29 (0.2%) | 124 (0.43%) | 1 | 1.000000e+00 | ko03030 |
| **281** | Steroid hormone biosynthesis | 0 (0.00%) | 2 (0.15%) | | | ko00140 |

**Table S 2 Candidate gene involved in flavonoids biosynthesis pathway**

| Enzyme | E.C. No. | Gene ID | Length/bp | RPKM in Leaf | RPKM in Corm | Subject in Nr database | Similarity | E-value |
|---|---|---|---|---|---|---|---|---|
| PAL | [4.3.1.24] | Unigene283 | 1743 | 8.41 | 49.11 | *Dendrobium candidum* JQ765748 | 78% | 0 |
| C4H | [1.14.13.11] | Unigene37438 | 597 | 1.56 | 6.15 | *Bambusa oldhamii* GU188741 | 80% | 1.00E-102 |
| 4CL | [6.2.1.12] | Unigene304 | 1623 | 0.11 | 2.49 | *Ruta graveolens* EU196764 | 71% | 0 |
| ACC | [6.4.1.2] | Unigene8800 | 874 | 6.65 | 11.98 | *Elaeis guineensis* DQ531848 | 84% | 1.00E-131 |
| CHS | [EC2.3.1.74] | Unigene25541 | 1592 | 27.16 | 142.48 | *Oncidium Gower Ramsey* DQ118023 | 83% | 0 |
| CHI | [EC5.1.1.6] | Unigene124078 | 204 | 0.28 | 0.79 | *Olea europaea* GU646679 | 99% | 3.00E-29 |
| FSII | [1.14.11.22] | Unigene109602 | 874 | 0.52 | 2.78 | *Iris x hollandica* AB284260 | 69% | 2.00E-72 |
| F3H | [1.14.11.9] | Unigene133003 | 248 | 0.15 | 0.61 | *Ipomoea batatas* EF108572 | 79% | 9.00E-39 |
| FLS | [1.14.11.23] | Unigene5065 | 1013 | 28.78 | 13.14 | *Dendrobium hybrid cultivar* KC345018 | 82% | 0 |
| DFR | [1.1.1.219] | Unigene23147 | 1263 | 36.61 | 23.81 | *Vitis vinifera* XM_002275159 | 74% | 1.00E-142 |
| ANS | [1.14.11.19] | Unigene30820 | 1227 | 62.78 | 253.18 | *Zea mays* NM_001158666 | 70% | 8.00E-92 |
| UFGT | [2.4.1.115] | Unigene27719 | 328 | 35.30 | 8.98 | *Lycium barbarum* AB360626 | 67% | 3.00E-28 |

**Table S 3 Candidate gene involved in Terpenoids biosynthesis pathway**

| Enzyme | E.C. No. | Gene ID | Length/bp | RPKM in Leaf | RPKM in Corm | Subject in Nr database | Similarity | E-value |
|---|---|---|---|---|---|---|---|---|
| AACT | [2.3.1.9] | Unigene3079 | 1786 | 9.35 | 13.76 | *Vanda hybrid cultivar* JF911348 | 89% | 0 |
| HMGS | [2.3.3.10] | Unigene79770 | 904 | 16.00 | 0.40 | *Camellia sinensis* JQ390224 | 79% | 3.00E-68 |
| HMGR | [1.1.1.88] | Unigene25402 | 2169 | 47.87 | 59.98 | *Dendrobium officinale* JX909333 | 87% | 0 |
| MK | [2.7.1.36] | Unigene16258 | 1616 | 10.24 | 13.44 | *Vitis vinifera* XM_002284777 | 69% | 1.00E-140 |
| PMK | [2.7.4.2] | Unigene9021 | 985 | 3.51 | 3.29 | *Hevea brasiliensis* AF429385 | 71% | 1.00E-83 |
| MVD | [4.1.1.33] | Unigene46088 | 964 | 5.63 | 0.00 | *Pana ginseng* GU565096 | 88% | 9.00E-75 |
| DXS | [2.2.1.7] | Unigene16585 | 3828 | 23.33 | 11.91 | *Elaeis guineensis* AY583783 | 80% | 0 |
| DXR | [1.1.1.267] | Unigene109510 | 1226 | 3.87 | 6.96 | *Vanda hybrid cultivar* EU145744 | 85% | 1.00E-155 |
| MCT | [2.7.7.60] | Unigene925 | 1872 | 3.51 | 5.89 | *Hevea brasiliensis* AB294703 | 75% | 1.00E-91 |
| CMK | [2.7.1.148] | Unigene15573 | 1339 | 13.51 | 10.57 | *Vanda hybrid cultivar* GU942924 | 85% | 0 |
| MCS | [4.6.1.12] | Unigene50413 | 289 | 1.05 | 0.00 | *Vitis vinifera* XM_002278370 | 78% | 5.00E-30 |
| HDS | [1.17.7.1] | Unigene38228 | 2752 | 7.50 | 4.62 | *Hevea brasiliensis* AB294707 | 81% | 0 |
| HDR | [1.17.1.2] | Unigene10848 | 1776 | 65.32 | 45.29 | *Oncidium hybrid cultivar* EU908200 | 83% | 0 |
| IPI | [5.3.3.2] | Unigene76830 | 284 | 4.68 | 2.43 | *Ipomoea batatas* DQ150100 | 72% | 2.00E-6 |
| FPPS | [2.5.1.10] | Unigene29801 | 1502 | 39.20 | 34.60 | *Dendrobium officinale* JX679465 | 88% | 1.00E-163 |
| GPPS | [2.5.1.1] | Unigene84310 | 942 | 0.00 | 0.38 | *Quercus robur* AJ298245 | 73% | 4.00E-90 |
| GGPPS | [2.5.1.29] | Unigene9865 | 1399 | 11.67 | 21.09 | *Brachypodium distachyon* XM_003562778 | 70% | 1.00E-116 |
| SS | [4.2.3.6] | Unigene93983 | 596 | 0.00 | 4.89 | *Zingiber zerumbet* AB247333 | 70% | 4.00E-22 |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| SQQ | [2.5.1.21] | Unigene14254 | 1555 | 6.10 | 2.82 | *Oryza sativa* AB007501 | 77% | 1.00E-165 |

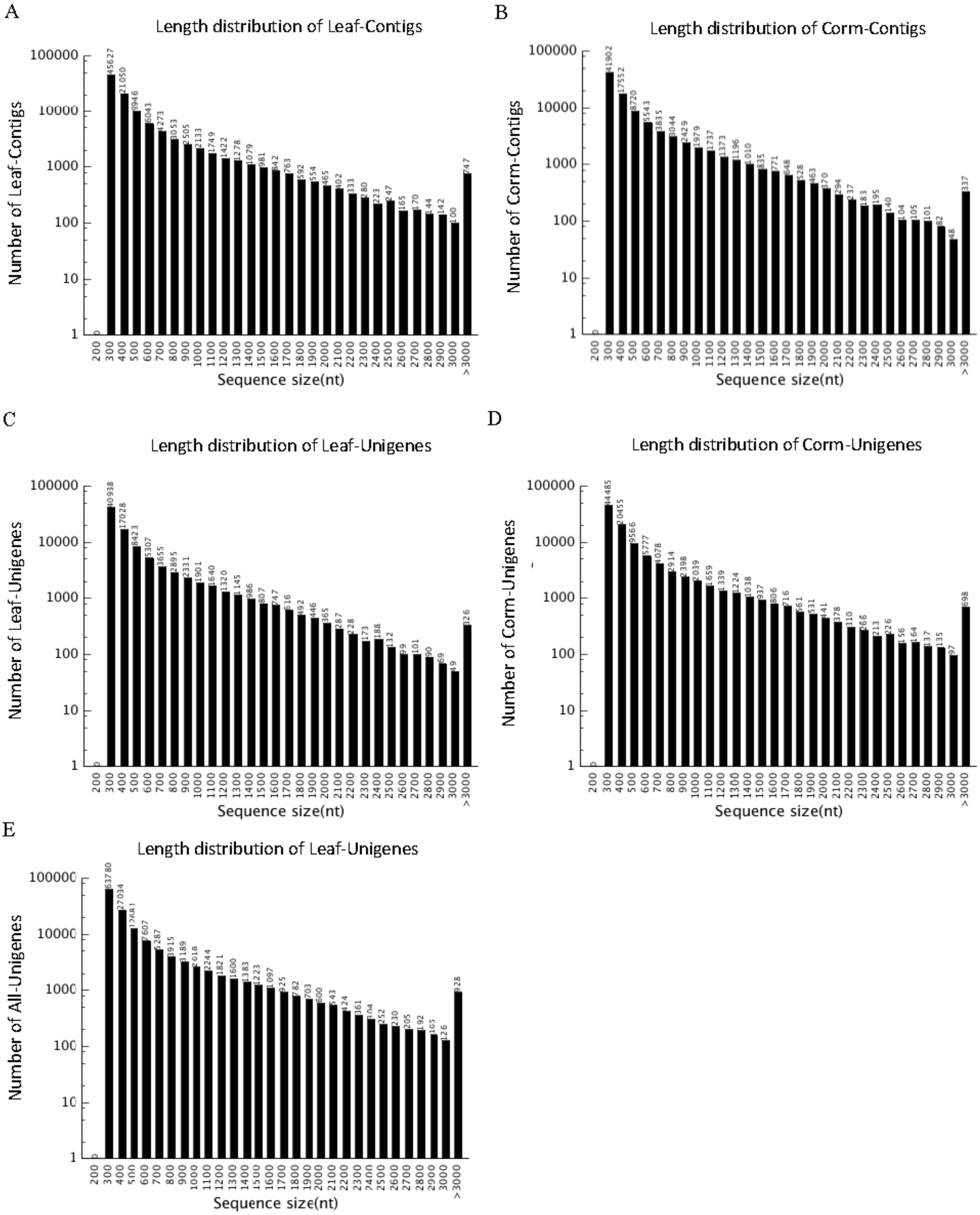

**Figure S1 Overview of the *N. fordii* tissues transcriptome assembly. A**. The length distribution of contigs assembled from clean reads of leaf tissue. **B**. The length distribution of contigs assembled from clean reads of corm tissue. **C**. The length distribution of unigenes obtained from trinity of leaf tissue. **D**. The length distribution of unigenes obtained from trinity of corm tissue. **E**. The length distribution of unigenes clustered from unigenes of two tissues.