Supplementary Table 1. Statistical results of basic information of seven public databases used for function annotation

|  |  |  |  |
| --- | --- | --- | --- |
| Database | Full name | Source | Vesrion and paramaters |
| Nr | NCBI non-redundant protein sequences | [https://www.ncbi.nlm.nih.gov/](https://www.ncbi.nlm.nih.gov/%22%20%5Co%20%22https%3A//www.ncbi.nlm.nih.gov/) | diamond v0.8.22e-value = 1e-5, --more-sensitive |
| Nt | NCBI nucleotide sequences | [https://www.ncbi.nlm.nih.gov/](https://www.ncbi.nlm.nih.gov/%22%20%5Co%20%22https%3A//www.ncbi.nlm.nih.gov/) | NCBI blast 2.2.28+e-value = 1e-5 |
| Pfam | Protein family | [http://pfam.sanger.ac.uk/](http://pfam.sanger.ac.uk/%22%20%5Co%20%22http%3A//pfam.sanger.ac.uk/) | HMMER 3.0 package，hmmscane-value = 0.01 |
| Swiss-Prot | Swiss-Prot | [http://www.ebi.ac.uk/uniprot/](http://www.ebi.ac.uk/uniprot/%22%20%5Co%20%22http%3A//www.ebi.ac.uk/uniprot/) | diamond v0.8.22e-value = 1e-5, --more-sensitive |
| KEGG | Kyoto Encyclopedia of Genes and Genomes | [http://www.genome.jp/kegg/](http://www.genome.jp/kegg/%C2%A0%22%20%5Co%20%22http%3A//www.genome.jp/kegg/%C2%A0)  | KAAS，KEGG Automatic Annotation Servere-value= 1e-10 |
| GO | Gene Ontology | [http://www.geneontology.org/](http://www.geneontology.org/%22%20%5Co%20%22http%3A//www.geneontology.org/) | Blast2GO v2.5e-value = 1e-6 |
| KOG/COG | COG: Clusters of Orthologous Groups of proteins | [http://www.ncbi.nlm.nih.gov/COG/](http://www.ncbi.nlm.nih.gov/COG/%22%20%5Co%20%22http%3A//www.ncbi.nlm.nih.gov/COG/) | diamond v0.8.22 |

Supplementary Table 2. Statistics of transcriptome assembly

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Species | Type | Total Nucleotides | Total Number | N50 | N90 | Mean Length | Median Length |
| Vf | Transcript | 129,562,931 | 185,805 | 1,151 | 268 | 697 | 355 |
| Unigene | 125,535,006 | 183,036 | 1,108 | 266 | 686 | 352 |
| Vvm | Transcript | 67,970,423 | 100,199 | 1,305 | 251 | 678 | 317 |
| Unigene | 66,927,794 | 98,933 | 1,309 | 250 | 676 | 315 |
| Vc | Transcript | 72,285,728 | 86,141 | 1,835 | 284 | 839 | 363 |
| Unigene | 71,299,275 | 85,094 | 1,847 | 283 | 838 | 360 |
| Vl | Transcript | 478,714,106 | 392,749 | 2,618 | 428 | 1,219 | 544 |
| Unigene | 243,388,639 | 271,031 | 860 | 241 | 898 | 538 |

Note: Vf: *Vulpes ferrilata*, Vvm: *Vulpes vulpes montana*, Vc: *Vulpes corsac*, Vl: *Vulpes lagopus*. N50/N90：The transcript obtained by splicing was arranged from long to short and then accumulated. When the cumulative length>=50%/90% of the total length, then the transcript length is considered N50/N90.

Supplementary Table 3. The result of CDS prediction

|  |  |  |
| --- | --- | --- |
| Species | Number of Blast to Protein database | Number of prediction by Estscan |
| Vf | 18,121 | 79,768 |
| Vvm | 17,247 | 43,337 |
| Vc | 16,639 | 36,282 |
| Vl | 33,491 | 22,701 |

Note：Vf: *Vulpes ferrilata*, Vvm: *Vulpes vulpes montana*, Vc: *Vulpes corsac*, Vl: *Vulpes lagopus*.

Supplementary Table 4. GO enrichment analysis of PSGs in *V. v. montana*

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| GO | property | List In GO | Background In GO | hyper\_p |
| GO:0000287 | magnesium ion binding | 1 | 7 | 0.113562242 |
| GO:0003676 | nucleic acid binding | 3 | 75 | 0.132436046 |
| GO:0003677 | DNA binding | 1 | 121 | 0.884728575 |
| GO:0003723 | RNA binding | 1 | 51 | 0.589496949 |
| GO:0003743 | translation initiation factor activity | 1 | 6 | 0.098136352 |
| GO:0003824 | catalytic activity | 2 | 55 | 0.240442517 |
| GO:0003924 | GTPase activity | 1 | 31 | 0.415982486 |
| GO:0004674 | protein serine/threonine kinase activity | 1 | 7 | 0.113562242 |
| GO:0005096 | GTPase activator activity | 1 | 8 | 0.128733548 |
| GO:0005102 | signaling receptor binding | 1 | 21 | 0.304553565 |
| GO:0005515 | protein binding | 3 | 353 | 0.958926388 |
| GO:0005525 | GTP binding | 1 | 44 | 0.535351782 |
| GO:0005576 | extracellular region | 2 | 62 | 0.285467477 |
| GO:0005577 | fibrinogen complex | 1 | 14 | 0.214637554 |
| GO:0005622 | intracellular anatomical structure | 2 | 35 | 0.118067143 |
| GO:0005634 | nucleus | 4 | 103 | 0.093514991 |
| GO:0005737 | cytoplasm | 1 | 70 | 0.70754794 |
| GO:0005783 | endoplasmic reticulum | 1 | 9 | 0.143654319 |
| GO:0005840 | ribosome | 1 | 26 | 0.362611975 |
| GO:0005882 | intermediate filament | 1 | 11 | 0.17276014 |
| GO:0008270 | zinc ion binding | 4 | 121 | 0.145727044 |
| GO:0008289 | lipid binding | 1 | 9 | 0.143654319 |
| GO:0008855 | exodeoxyribonuclease VII activity | 1 | 15 | 0.228136724 |
| GO:0009318 | exodeoxyribonuclease VII complex | 1 | 15 | 0.228136724 |
| GO:0015093 | ferrous iron transmembrane transporter activity | 1 | 13 | 0.20091087 |
| GO:0016020 | membrane | 2 | 153 | 0.751584482 |
| GO:0016021 | integral component of membrane | 5 | 182 | 0.190916208 |
| GO:0016209 | antioxidant activity | 1 | 8 | 0.128733548 |
| GO:0016491 | oxidoreductase activity | 2 | 55 | 0.240442517 |
| GO:0016757 | glycosyltransferase activity | 1 | 8 | 0.128733548 |
| GO:0019028 | viral capsid | 1 | 30 | 0.405665458 |
| GO:0030674 | protein-macromolecule adaptor activity | 1 | 14 | 0.214637554 |

Note: Property: The name of GO terms. List in GO: the PSGs enriched in this GO term. Background in GO: GO terms background of this species. Hyper\_P: *P*-value.

Supplementary Table 5. GO enrichment analysis of PSGs in *V. ferrilata*

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| GO | property | List In GO | Background In GO | hyper\_p |
| GO:0003924 | GTPase activity | 7 | 28 | 0.001853361 |
| GO:0005525 | GTP binding | 7 | 34 | 0.006013457 |
| GO:0016192 | vesicle-mediated transport | 3 | 12 | 0.04152219 |
| GO:0016491 | oxidoreductase activity | 6 | 40 | 0.047099438 |
| GO:0016020 | membrane | 7 | 55 | 0.070771409 |
| GO:0003735 | structural constituent of ribosome | 2 | 9 | 0.118087218 |
| GO:0005840 | ribosome | 2 | 9 | 0.118087218 |
| GO:0006412 | translation | 2 | 10 | 0.14136237 |
| GO:0016021 | integral component of membrane | 7 | 72 | 0.204249059 |
| GO:0007165 | signal transduction | 3 | 25 | 0.233284218 |
| GO:0003677 | DNA binding | 4 | 37 | 0.23371289 |
| GO:0003950 | NAD+ ADP-ribosyltransferase activity | 1 | 6 | 0.341478788 |
| GO:0006486 | protein glycosylation | 1 | 6 | 0.341478788 |
| GO:0006955 | immune response | 1 | 6 | 0.341478788 |
| GO:0008146 | sulfotransferase activity | 1 | 6 | 0.341478788 |
| GO:0008289 | lipid binding | 1 | 6 | 0.341478788 |
| GO:0016616 | oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor | 1 | 6 | 0.341478788 |
| GO:0046873 | metal ion transmembrane transporter activity | 1 | 6 | 0.341478788 |
| GO:0070403 | NAD+ binding | 1 | 6 | 0.341478788 |
| GO:0006281 | DNA repair | 1 | 7 | 0.385864409 |
| GO:0006357 | regulation of transcription by RNA polymerase II | 1 | 7 | 0.385864409 |
| GO:0008168 | methyltransferase activity | 1 | 7 | 0.385864409 |
| GO:0016757 | glycosyltransferase activity | 1 | 7 | 0.385864409 |
| GO:0030001 | metal ion transport | 1 | 7 | 0.385864409 |
| GO:0006355 | regulation of transcription, DNA-templated | 3 | 39 | 0.49344184 |
| GO:0004930 | G protein-coupled receptor activity | 1 | 12 | 0.567040183 |
| GO:0005576 | extracellular region | 1 | 12 | 0.567040183 |
| GO:0016787 | hydrolase activity | 1 | 12 | 0.567040183 |
| GO:0005085 | guanyl-nucleotide exchange factor activity | 1 | 13 | 0.596330207 |
| GO:0007186 | G protein-coupled receptor signaling pathway | 1 | 13 | 0.596330207 |
| GO:0005634 | nucleus | 2 | 33 | 0.662447888 |
| GO:0005975 | carbohydrate metabolic process | 1 | 16 | 0.672926184 |
| GO:0003676 | nucleic acid binding | 4 | 69 | 0.69449694 |
| GO:0046872 | metal ion binding | 1 | 18 | 0.71579732 |
| GO:0003700 | DNA-binding transcription factor activity | 1 | 20 | 0.753093518 |
| GO:0005509 | calcium ion binding | 1 | 20 | 0.753093518 |
| GO:0008270 | zinc ion binding | 2 | 40 | 0.763198475 |
| GO:0055085 | transmembrane transport | 1 | 23 | 0.800132507 |
| GO:0003723 | RNA binding | 2 | 44 | 0.808329352 |
| GO:0004672 | protein kinase activity | 1 | 28 | 0.859600648 |
| GO:0006468 | protein phosphorylation | 1 | 28 | 0.859600648 |
| GO:0005515 | protein binding | 13 | 271 | 0.939991965 |
| GO:0005524 | ATP binding | 2 | 80 | 0.976452049 |

Note: Property: The name of GO terms. List in GO: the PSGs enriched in this GO term. Background in GO: GO terms background of this species. Hyper\_P: *P*-value.

Supplementary Table 6. Significantly high expressed (p<0.05) genes in the high-altitude group compared with the low-altitude group

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Gene id | Vc | Vf | Vvm | Vl |
| *APBB1IP* | 3.42 | 7.786666667 | 6.496666667 | 0.751111111 |
| *EFHD2* | 31.49333333 | 32.39666667 | 69.91666667 | 26.8 |
| *Plek2* | 7.443333333 | 10.82333333 | 11.09666667 | 9.396666668 |
| *ASF1B* | 1.613333333 | 2.14 | 2.536666667 | 0.876666666 |
| *SEMA7A* | 34.5 | 56.46333333 | 40.23333333 | 14.90777778 |
| *EID3* | 1.56 | 3.13 | 23.59333333 | 1.628888889 |
| *NCL* | 85.14 | 115.09 | 86.61666667 | 49.41777778 |
| *LACTB* | 12.15 | 13.98 | 12.37333333 | 11.68111111 |
| *ACSS3* | 20.94 | 22.08666667 | 22.95333333 | 12.42111111 |
| *Slc25a14* | 4.256666667 | 30.02 | 4.553333333 | 2.616666667 |
| *TBC1D25* | 6.813333333 | 10.55 | 7.216666667 | 2.447777778 |
| *RNF146* | 18.71666667 | 24.80666667 | 19.54666667 | 4.89 |
| *SAMSN1* | 3.243333333 | 6.596666667 | 9.023333333 | 0.713333333 |
| *ANKRD22* | 0.88 | 1.916666667 | 6.593333333 | 0.716666667 |
| *ZNRF3* | 2.94 | 6.52 | 3.993333333 | 2.742222222 |
| *SNX14* | 15.47333333 | 25.59333333 | 15.53666667 | 5.371111111 |
| *FGL2* | 10.34666667 | 27.99333333 | 41.23333333 | 5.823333333 |
| *UTP3* | 15.08333333 | 20.23333333 | 22.47666667 | 9.274444445 |
| *AMBP* | 783.3366667 | 834.6766667 | 2274.936667 | 193.2866667 |
| *FST* | 1.093333333 | 7.586666667 | 13.8 | 0.735555556 |
| *Igfbp1* | 1.083333333 | 146.8266667 | 653.36 | 7.688888889 |
| *RLF* | 2.126666667 | 6.513333333 | 3.35 | 1.973333333 |
| *HSPA14* | 10.48666667 | 14.58666667 | 10.71333333 | 2.677777778 |
| *TMEM165* | 20.22 | 20.63 | 28.64666667 | 12.88222222 |
| *CLK2* | 9.73 | 11.04333333 | 15.16 | 3.446666667 |
| *TOP3B* | 6.583333333 | 8.05 | 6.893333333 | 5.702222222 |
| *KIAA1109* | 2.566666667 | 7.09 | 4.853333333 | 3.806666667 |
| *MBNL2* | 10.47666667 | 18.47 | 11.95 | 8.328888889 |
| *BNIP3L* | 14.20333333 | 25.33 | 22.06333333 | 14.16333334 |
| *SMARCE1* | 18.68 | 21.05 | 22.85333333 | 10.66666667 |
| *INSIG1* | 59.96666667 | 138.6433333 | 75.57333333 | 64.79777778 |
| *IRS2* | 4.343333333 | 11.12666667 | 9.21 | 8.987777779 |
| *CCDC173* | 1.333333333 | 3.28 | 2.09 | 0.975555556 |
| *C17orf80* | 4.57 | 5.546666667 | 12.95333333 | 2.074444444 |
| *DYNC2H1* | 2.28 | 2.936666667 | 3.47 | 1.541111111 |
| *ZDHHC14* | 10.54333333 | 24.76 | 11.10333333 | 2.1 |
| *SLC39A6* | 4.53 | 8.073333333 | 5.136666667 | 2.781111111 |
| *TSKU* | 6.613333333 | 9.916666667 | 62.06333333 | 4.407777777 |
| *SYNE3* | 1.98 | 2.823333333 | 3.473333333 | 1.157777778 |
| *APC* | 4.34 | 13.40666667 | 15.28666667 | 6.526666667 |
| *FAM109B* | 2.086666667 | 2.66 | 3.996666667 | 1.498888889 |
| *RHOC* | 177.5066667 | 248.52 | 275.9266667 | 95.42222223 |
| *WBP4* | 9.533333333 | 12.26666667 | 9.903333333 | 7.307777778 |
| *LRRK1* | 2.243333333 | 2.463333333 | 3.836666667 | 1.093333333 |
| *TPMT* | 7.566666667 | 12.5 | 9.49 | 7.775555556 |
| *ADGRD1* | 0.816666667 | 1.68 | 2.703333333 | 1.394444444 |
| *TOGARAM2* | 1.053333333 | 2.953333333 | 2.933333333 | 1.915555556 |
| *PSME4* | 5.793333333 | 10.81666667 | 7.233333333 | 4.473333333 |
| *ARHGEF5* | 1.883333333 | 2.636666667 | 2.926666667 | 1.35 |
| *SRBD1* | 2.636666667 | 2.773333333 | 3.3 | 2.022222222 |
| *THNSL1* | 3.78 | 4.72 | 4.14 | 2.793333333 |
| *PPM1F* | 7.743333333 | 12.38333333 | 14.73333333 | 8.054444444 |
| *KRR1* | 8.273333333 | 9.03 | 10.60666667 | 4.611111111 |
| *GPATCH1* | 3.26 | 3.64 | 3.363333333 | 1.912222222 |
| *RAB37* | 2.793333333 | 4.28 | 3.606666667 | 0.346666667 |
| *FBXO4* | 3.67 | 3.933333333 | 9.236666667 | 1.361111111 |
| *CSF3R* | 12.86 | 16.04666667 | 134.7866667 | 1.4 |
| *POLG2* | 2.833333333 | 2.993333333 | 5.07 | 1.807777778 |
| *R3HCC1L* | 4.2 | 4.706666667 | 5.366666667 | 2.246666667 |
| *SPSB1* | 2.02 | 3.463333333 | 6.006666667 | 1.353333333 |
| *RHNO1* | 2.48 | 4.403333333 | 2.593333333 | 1.335555556 |
| *IL1RAP* | 7.593333333 | 14.73 | 20.82 | 2.474444444 |
| *PCM1* | 3.206666667 | 17.67 | 9.273333333 | 5.093333333 |
| *FPGT* | 2.843333333 | 5.386666667 | 3.736666667 | 3.315555555 |
| *Dennd3* | 12.26333333 | 13.28333333 | 13.50666667 | 6.778888888 |
| *BOD1L1* | 2.613333333 | 7.146666667 | 3.886666667 | 2.917777778 |
| *CDC40* | 3.813333333 | 7.356666667 | 8.653333333 | 4.657777778 |
| *FGB* | 1068.573333 | 1649.213333 | 1962.973333 | 429.9777778 |
| *ARHGAP15* | 1.2 | 3.843333333 | 11.90666667 | 0.694444444 |
| *LIPH* | 1.006666667 | 2.153333333 | 3.106666667 | 1.766666667 |
| *PLIN2* | 76.97333333 | 165.9833333 | 81.26 | 40.59 |
| *Gramd4* | 10.01666667 | 10.07 | 12.55666667 | 6.821111111 |
| *ZBTB8A* | 1.443333333 | 2.43 | 1.746666667 | 0.713333333 |
| *ISG15* | 35.31 | 44.36 | 169.4433333 | 34.74666667 |
| *ATXN3* | 2.09 | 10.02333333 | 5.233333333 | 4.026666667 |

Note：Vf: *Vulpes ferrilata*, Vvm: *Vulpes vulpes montana*, Vc: *Vulpes corsac*, Vl: *Vulpes lagopus.*