

Table S1. Gene ontology classifications of DEGs with functional annotation.

| GO term | P-value | Gene ID | Description | Fold change | P-value |
|------------------------------------|----------|------------------|--|-------------|-----------|
| GO:0006626 | | | | | |
| Protein targeting to mitochondrion | 4.88E-03 | GRMZM2G180971 | EF-hand-like domain;Mitochondrial carrier protein | 4.45 | 2.52E-04 |
| | | GRMZM2G058432 | Mitochondrial inner membrane translocase complex | 3.48 | 1.31E-25 |
| | | GRMZM2G174738 | Mitochondrial carrier protein | 2.07 | 2.36E-08 |
| | | GRMZM2G144101 | Mitochondrial inner membrane translocase complex | 2.06 | 6.30E-13 |
| | | GRMZM2G002440 | GrpE nucleotide exchange factor | 2.48 | 2.43E-04 |
| | | GRMZM2G314434 | Plant specific mitochondrial import receptor subunit TOM20 | 2.69 | 8.95E-11 |
| | | GRMZM2G024823 | Mitochondrial substrate/solute carrier | 3.01 | 7.53E-05 |
| | | GRMZM2G067877 | Mitochondrial substrate/solute carrier | 2.91 | 1.26E-11 |
| | | GRMZM2G436593 | Mitochondrial substrate/solute carrier | 2.75 | 6.45E-04 |
| | | GRMZM2G075003 | Mitochondrial inner membrane translocase complex | 2.05 | 4.44E-05 |
| | | GRMZM2G319878 | Mitochondrial inner membrane translocase complex | 3.83 | 3.44E-08 |
| | | GRMZM2G030312 | GrpE nucleotide exchange factor | 4.39 | 2.32E-19 |
| | | GRMZM2G100402 | Plant specific mitochondrial import receptor subunit TOM20 | 3.66 | 2.30E-11 |
| | | GRMZM2G127173 | Mitochondrial substrate/solute carrier | 4.18 | 2.47E-04 |
| GO:0006334 | | | | | |
| Nucleosome assembly | 6.75E-20 | GRMZM2G121186 | Nucleosome assembly protein (NAP) | 3.52 | 2.15E-17 |
| | | AC216889.3_FG008 | Histone H2A;Histone-fold | 6.89 | 1.36E-12 |
| | | GRMZM2G151826 | Histone H2A;Histone core;Histone-fold | 5.25 | 2.22E-19 |
| | | GRMZM2G177937 | Thioredoxin, conserved site | 4.24 | 3.76E-08 |
| | | GRMZM2G079089 | Histone H2B;Histone core;Histone-fold | 2.38 | 1.94E-17 |
| | | GRMZM2G401308 | Histone H1/H5 | 2.23 | 5.86E-24 |
| | | GRMZM2G448458 | Histone H2A;Histone core;Histone-fold | 13.87 | 7.26E-04 |
| | | GRMZM2G063896 | Histone H4 | 5.93 | 1.38E-74 |
| | | GRMZM2G479684 | Histone H4 | 5.49 | 5.54E-171 |
| | | GRMZM2G046841 | Histone H2B;Histone core;Histone-fold | 3.29 | 1.21E-08 |
| | | GRMZM2G056231 | Histone H2A;Histone core;Histone-fold | 6.10 | 6.39E-38 |
| | | GRMZM2G181153 | Histone H4 | 4.56 | 8.71E-27 |
| | | GRMZM2G349651 | Histone H4 | 7.82 | 2.27E-34 |
| | | GRMZM2G401147 | Histone H2B;Histone core;Histone-fold | 6.11 | 2.36E-83 |
| | | GRMZM2G008865 | Histone H2A;Histone core;Histone-fold | 4.60 | 2.09E-03 |
| | | AC191069.3_FG004 | I GR protein motif | 2.66 | 1.50E-07 |
| | | GRMZM2G163939 | Histone H2B;Histone core;Histone-fold | 4.31 | 7.57E-51 |
| | | GRMZM2G003306 | Histone H2A;Histone core;Histone-fold | 6.53 | 6.29E-109 |
| | | GRMZM2G047813 | Histone H2A;Histone core;Histone-fold | 6.44 | 2.11E-70 |
| | | GRMZM2G054651 | TB2/DP1/HVA22 related protein | 0.37 | 2.16E-04 |
| | | GRMZM2G069911 | Histone H1/H5 | 3.36 | 8.68E-14 |
| | | GRMZM2G305027 | Histone H2B;Histone core;Histone-fold | 2.64 | 2.40E-07 |
| | | GRMZM2G140051 | Nucleosome assembly protein (NAP) | 3.08 | 9.01E-19 |

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| GRMZM2G112912 | Histone H2B;Histone core;Histone-fold | 7.14 | 9.08E-37 |
| GRMZM2G034157 | Heat shock protein Hsp20 | 7.37 | 2.07E-102 |
| GRMZM2G122437 | Heavy metal transport/detoxification protein | 0.35 | 2.02E-25 |
| GRMZM2G145758 | Histone core;Histone-fold;Histone H3 | 4.98 | 1.29E-14 |
| GRMZM2G387076 | Histone core;Histone-fold;Histone H3 | 5.91 | 1.21E-59 |
| GRMZM2G450937 | Leucine-rich repeat;Ribosomal protein L19/L19e | 3.18 | 5.03E-14 |
| GRMZM2G073275 | Histone H4 | 6.13 | 6.86E-69 |
| GRMZM2G118355 | Histone core;Histone-fold;Histone H3 | 2.65 | 1.22E-46 |
| GRMZM2G106133 | Histone H1/H5 | 2.19 | 1.74E-07 |
| GRMZM2G171387 | Histone core;Histone-fold;Histone H3 | 2.14 | 2.17E-42 |
| GRMZM2G084521 | Cyclophilin-type peptidyl-prolyl cis-trans isomerase | 2.11 | 2.82E-07 |
| GRMZM2G305046 | Histone H2A;Histone core;Histone-fold | 4.30 | 1.93E-20 |
| GRMZM2G072855 | Histone H4 | 6.32 | 2.23E-23 |
| GRMZM2G472696 | Histone H2B;Histone core;Histone-fold | 2.36 | 3.02E-34 |
| GRMZM2G306258 | Histone H2B;Histone core;Histone-fold | 5.91 | 1.09E-39 |
| GRMZM2G071959 | Histone H2B;Histone core;Histone-fold | 4.07 | 5.66E-45 |
| GRMZM2G332838 | Histone H4 | 5.97 | 2.47E-108 |
| GRMZM2G016232 | Histone H4 | 3.15 | 1.20E-29 |
| GRMZM2G080274 | Histone H1/H5 | 5.32 | 3.77E-17 |
| GRMZM2G042047 | Histone H2A;Histone core;Histone-fold | 2.63 | 3.58E-05 |
| GRMZM2G151726 | Histone H2A;Histone core;Histone-fold | 2.60 | 9.70E-15 |
| GRMZM2G447984 | Histone core;Histone-fold;Histone H3 | 7.24 | 1.83E-17 |
| AC212565.3_FG001 | Histone H4 | 4.12 | 6.53E-68 |
| GRMZM5G864735 | Histone core;Histone-fold;Histone H3 | 5.53 | 2.32E-04 |
| GRMZM2G141432 | Histone H2B;Histone core;Histone-fold | 2.06 | 1.66E-09 |
| GRMZM2G130079 | Histone core;Histone-fold;Histone H3 | 6.34 | 5.97E-06 |
| GRMZM2G084195 | Histone H4 | 8.42 | 5.72E-117 |
| GRMZM2G057852 | Histone H2B;Histone core;Histone-fold | 3.74 | 9.07E-08 |
| AC196961.2_FG003 | Histone H4, conserved site | 20.71 | 9.31E-41 |
| GRMZM2G421279 | Histone H4 | 6.46 | 5.42E-105 |
| GRMZM2G146358 | Ribosomal protein L19/L19e conserved site | 2.51 | 1.92E-18 |
| GRMZM2G144995 | NOP5, N-terminal | 2.03 | 8.78E-07 |
| GRMZM2G176707 | Nucleosome assembly protein (NAP) | 4.98 | 3.72E-10 |
| GRMZM2G109448 | Histone H2A;Histone core;Histone-fold | 7.05 | 1.57E-37 |
| GRMZM2G121221 | Histone H1/H5 | 4.22 | 3.32E-15 |
| GRMZM2G164020 | Histone H1/H5 | 4.81 | 2.15E-49 |
| GRMZM2G003002 | Histone H1/H5 | 6.96 | 2.77E-09 |
| GRMZM2G119071 | Histone H2B;Histone core;Histone-fold | 7.26 | 1.36E-12 |
| GRMZM2G046055 | Histone H2A;Histone core;Histone-fold | 2.41 | 2.53E-21 |
| GRMZM2G107540 | Histone H2A;Histone core;Histone-fold | 2.31 | 3.44E-05 |
| GRMZM2G342515 | Histone H2B;Histone core;Histone-fold | 8.41 | 1.80E-69 |
| GRMZM2G304575 | Histone H2B;Histone core;Histone-fold | 4.93 | 1.09E-42 |
| GRMZM2G078314 | Histone core;Histone-fold;Histone H3 | 7.69 | 9.37E-65 |
| GRMZM2G157470 | Methyl-CpG DNA binding | 2.47 | 3.87E-03 |

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|--------------------|----------|------------------|--|---------|-----------|
| | | GRMZM2G004878 | Histone H1/H5 | 3.69 | 1.97E-10 |
| | | GRMZM2G050833 | Histone H2A;Histone core;Histone-fold | 2.52 | 9.77E-11 |
| | | GRMZM2G130746 | Histone H2A;Histone core;Histone-fold | 2.14 | 3.21E-10 |
| | | GRMZM2G149178 | Histone H4 | 4.57 | 7.26E-55 |
| | | GRMZM2G041381 | Histone H2A;Histone core;Histone-fold | 5.22 | 2.48E-04 |
| | | GRMZM5G883764 | Histone H2A;Histone core;Histone-fold | 4.62 | 2.27E-33 |
| | | AC233865.1_FG001 | Histone H4 | 3.72 | 6.47E-47 |
| GO:0044429 | 8.43E-13 | GRMZM2G157018 | ATPase,mitochondrial | 2.31 | 7.57E-39 |
| Mitochondrial part | | GRMZM2G144101 | Mitochondrial inner membrane translocase complex | 2.06 | 6.30E-13 |
| | | GRMZM2G135186 | Mitochondrial substrate/solute carrier | 2.93 | 1.43E-24 |
| | | GRMZM2G105207 | ETC complex I subunit conserved region | 2.22 | 2.95E-05 |
| | | AC194341.4_FG002 | ATPase,mitochondrial | 2.28 | 2.61E-21 |
| | | GRMZM2G010933 | Cytochrome c oxidase copper chaperone | 31.26 | 5.63E-17 |
| | | GRMZM2G321404 | Mitochondrial inner membrane translocase complex | 8.85 | 1.25E-06 |
| | | GRMZM2G042078 | ATPase,mitochondrial | 3.43 | 5.11E-15 |
| | | GRMZM2G152827 | Mitochondrial substrate/solute carrier | 3.65 | 5.57E-30 |
| | | GRMZM2G064753 | Cytochrome c oxidase, subunit Vb | 2.52 | 2.78E-09 |
| | | GRMZM2G120876 | Porin, eukaryotic type | 4.19 | 1.71E-16 |
| | | GRMZM2G171476 | Ubiquinol-cytochrome C reductase | 2.97 | 3.45E-24 |
| | | GRMZM2G146670 | Porin, eukaryotic type | 4.09 | 1.73E-18 |
| | | GRMZM2G150616 | Porin, eukaryotic type | 3.58 | 8.54E-27 |
| | | GRMZM2G038375 | Mitochondrial inner membrane translocase complex | 2.41 | 5.73E-09 |
| | | GRMZM2G125669 | Alternative oxidase | 1162.37 | 6.74E-47 |
| | | GRMZM2G058432 | Mitochondrial inner membrane translocase complex | 3.48 | 1.31E-25 |
| | | GRMZM2G048013 | Cytochrome c oxidase, subunit VIIa | 2.25 | 8.50E-12 |
| | | GRMZM2G412296 | Cytochrome c oxidase, subunit VIIa | 4.11 | 9.06E-15 |
| | | GRMZM2G071071 | EF-hand-like domain;Mitochondrial Rho-like | 5.91 | 3.29E-39 |
| | | GRMZM2G100402 | Plant specific mitochondrial import receptor subunit TOM20 | 3.66 | 2.30E-11 |
| | | GRMZM2G167463 | Mitochondrial inner membrane translocase complex | 4.47 | 1.18E-13 |
| | | GRMZM2G015401 | Mitochondrial substrate/solute carrier | 2.95 | 7.73E-04 |
| | | GRMZM2G319878 | Mitochondrial inner membrane translocase complex | 3.83 | 3.44E-08 |
| | | GRMZM2G103771 | Mitochondrial inner membrane translocase complex | 0.03 | 1.05E-14 |
| | | GRMZM2G134738 | Cytochrome c oxidase, subunit Vb | 3.33 | 4.58E-22 |
| | | GRMZM2G069229 | ATPase,mitochondrial | 8.85 | 1.13E-07 |
| | | GRMZM2G024823 | Mitochondrial substrate/solute carrier | 3.01 | 7.53E-05 |
| | | GRMZM2G067877 | Mitochondrial substrate/solute carrier | 2.91 | 1.26E-11 |
| | | GRMZM2G018417 | Porin, eukaryotic type | 5.27 | 4.12E-09 |
| | | GRMZM2G115049 | Porin, eukaryotic type | 10.49 | 7.79E-128 |
| | | GRMZM2G064600 | Mitochondrial inner membrane translocase complex | 6.16 | 2.92E-11 |
| GO:0003942 | 3.08E-08 | GRMZM2G134982 | Translation elongation factor EFTu/EF1A | 3.60 | 6.19E-04 |
| GTPase activity | | GRMZM2G113250 | Translation elongation factor EFTu/EF1A | 2.87 | 2.88E-29 |
| | | GRMZM2G043822 | Beta tubulin, autoregulation binding site | 3.70 | 8.04E-41 |

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|------------------|---|-------|-----------|
| GRMZM2G343543 | Translation elongation factor EFTu/EF1A | 2.85 | 2.90E-33 |
| AC197246.3_FG001 | Ras GTPase;Small GTP-binding protein | 3.00 | 4.27E-05 |
| GRMZM2G157334 | Ras GTPase;Ras small GTPase;Ran GTPase | 2.54 | 8.19E-25 |
| AC203173.3_FG004 | Translation elongation factor EFTu/EF1A, domain 2 | 2.22 | 6.72E-26 |
| GRMZM2G110509 | Translation elongation factor EFTu/EF1A, domain 2 | 2.80 | 3.16E-26 |
| GRMZM2G037204 | Ras GTPase;Small GTP-binding protein | 2.52 | 2.40E-07 |
| GRMZM2G128688 | Translation elongation factor EFTu/EF1A, domain 2 | 4.10 | 7.83E-07 |
| GRMZM2G071790 | Beta tubulin, autoregulation binding site | 4.86 | 2.75E-40 |
| GRMZM2G066191 | Beta tubulin, autoregulation binding site | 8.28 | 6.50E-04 |
| GRMZM2G056393 | Translation elongation factor EFTu/EF1A, domain 2 | 3.15 | 9.64E-05 |
| GRMZM2G122805 | Ras GTPase | 3.37 | 1.96E-05 |
| GRMZM2G129155 | Dynamin GTPase effector | 3.66 | 5.65E-06 |
| GRMZM2G151193 | Translation elongation factor EFTu/EF1A, domain 2 | 2.50 | 2.09E-18 |
| GRMZM2G149717 | Dynamin central domain;Dynamin | 2.70 | 2.06E-04 |
| GRMZM5G850607 | Protein synthesis factor, GTP-binding | 2.75 | 2.34E-16 |
| GRMZM2G117900 | Translation elongation factor EFTu/EF1A, domain 2 | 2.20 | 5.00E-07 |
| GRMZM2G316232 | Protein synthesis factor, GTP-binding | 5.31 | 2.04E-03 |
| GRMZM2G099167 | Beta tubulin, autoregulation binding site | 3.60 | 6.97E-11 |
| GRMZM2G098129 | Guanylate-binding protein, N-terminal | 5.17 | 3.55E-03 |
| GRMZM2G022269 | Translation elongation factor EFTu/EF1A, domain 2 | 4.08 | 6.89E-21 |
| GRMZM2G108766 | Beta tubulin, autoregulation binding site | 3.85 | 1.74E-03 |
| GRMZM2G107654 | Translation elongation factor EFTu/EF1A, domain 2 | 2.13 | 1.15E-11 |
| GRMZM2G157462 | Dynamin central domain;Dynamin | 2.07 | 3.28E-04 |
| GRMZM2G095851 | Translation elongation factor EFTu/EF1A, domain 2 | 2.31 | 1.96E-20 |
| AC234515.1_FG003 | Beta tubulin, autoregulation binding site | 4.02 | 3.64E-06 |
| GRMZM2G023418 | Translation elongation factor EFTu/EF1A, domain 2 | 2.78 | 1.01E-04 |
| GRMZM2G313678 | Translation elongation factor EFTu/EF1A, domain 2 | 4.40 | 7.99E-07 |
| GRMZM2G172932 | Beta tubulin, autoregulation binding site | 3.56 | 7.72E-14 |
| GRMZM2G028313 | Translation elongation factor EFTu/EF1A, domain 2 | 2.13 | 1.72E-07 |
| GRMZM2G149768 | Translation elongation factor EFTu/EF1A, domain 2 | 2.23 | 2.92E-51 |
| GRMZM2G152466 | Tubulin/FtsZ, GTPase domain | 4.84 | 5.65E-176 |
| GRMZM2G005516 | Tubulin/FtsZ, GTPase domain | 2.55 | 1.23E-03 |
| GRMZM2G164696 | Beta tubulin, autoregulation binding site | 3.96 | 9.52E-17 |
| GRMZM2G354604 | Ras GTPase;Ran GTPase;Small GTP-binding protein | 3.59 | 9.29E-196 |
| GRMZM2G153541 | Translation elongation factor EFTu/EF1A, domain 2 | 3.51 | 9.42E-175 |
| GRMZM2G083243 | Beta tubulin, autoregulation binding site | 7.81 | 9.60E-14 |
| GRMZM2G133802 | Beta tubulin, autoregulation binding site | 2.95 | 3.64E-07 |
| GRMZM2G011216 | Protein synthesis factor, GTP-binding | 6.38 | 9.75E-46 |
| GRMZM2G153292 | Tubulin/FtsZ, GTPase domain | 5.69 | 3.34E-210 |
| GRMZM2G154218 | Translation elongation factor EFTu/EF1A, domain 2 | 2.14 | 1.04E-77 |
| AC233866.1_FG006 | Translation elongation factor EFTu/EF1A, domain 2 | 3.18 | 5.47E-59 |
| GRMZM2G057535 | Translation elongation factor EFTu/EF1A, domain 2 | 19.51 | 5.09E-05 |
| GRMZM2G416142 | Ras GTPase;Small GTP-binding protein | 2.62 | 1.52E-04 |
| GRMZM2G314647 | Dynamin central domain;Dynamin | 2.90 | 5.76E-04 |

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| | | GRMZM2G156476 | Ras GTPase;Small GTP-binding protein | 2.72 | 1.60E-03 |
| | | AC209819.3_FG012 | Ras GTPase;Small GTPase, Rho type" | 2.14 | 2.67E-03 |
| | | GRMZM2G001327 | Translation elongation factor EFTu/EF1A, domain 2 | 2.17 | 1.85E-27 |
| | | GRMZM2G180335 | Dynamin central domain;Dynamin | 3.72 | 1.47E-07 |
| GO:000097 | | | | | |
| Sulfur amino acid biosynthetic process | 5.46E-04 | GRMZM2G149751 | Cobalamin-independent methionine synthase | 3.34 | 4.50E-09 |
| | | GRMZM2G165998 | RmlC-like jelly roll fold | 4.45 | 3.12E-25 |
| | | GRMZM2G013430 | Serine acetyltransferase, N-terminal | 6.33 | 7.05E-04 |
| | | GRMZM2G076885 | Semialdehyde dehydrogenase, dimerisation domain | 2.45 | 5.58E-06 |
| | | GRMZM2G165747 | Cobalamin-independent methionine synthase | 3.43 | 2.15E-07 |
| | | GRMZM2G165622 | Cysteine synthase/cystathionine beta-synthase P-phosphate-binding site | 6.76 | 8.71E-09 |
| | | GRMZM2G328893 | Cysteine synthase K/M | 7.36 | 3.46E-08 |
| | | GRMZM2G036708 | Cysteine synthase K/M | 3.09 | 2.21E-07 |
| | | GRMZM2G574782 | HAD-like domain;Methylthioribulose-1-phosphate dehydratase | 2.40 | 1.93E-05 |
| | | GRMZM2G112149 | Cobalamin-independent methionine synthase | 3.49 | 2.09E-09 |
| | | GRMZM2G005887 | Cysteine synthase K/M | 2.59 | 1.90E-32 |
| | | GRMZM2G048740 | Serine acetyltransferase, N-terminal | 2.38 | 1.86E-03 |
| GO:0006418 | | | | | |
| tRNA aminoacylation for protein translation | 4.28E-03 | GRMZM2G148709 | Arginyl-tRNA synthetase, class Ic | 2.27 | 5.01E-07 |
| | | GRMZM2G083836 | Nucleic acid-binding, OB-fold | 3.99 | 5.80E-17 |
| | | GRMZM2G701193 | Cysteinyl-tRNA synthetase/mycothiol ligase | 9.85 | 9.99E-04 |
| | | GRMZM2G101463 | Phenylalanyl-tRNA synthetase, class IIc, alpha subunit | 2.31 | 2.10E-08 |
| | | GRMZM2G013773 | Valyl/Leucyl/Isoleucyl-tRNA synthetase, class Ia, editing | 9.76 | 4.56E-11 |
| | | GRMZM2G029027 | Arginyl-tRNA synthetase, class Ic | 2.46 | 2.86E-04 |
| | | GRMZM2G107089 | Anticodon-binding | 2.75 | 2.19E-05 |
| | | GRMZM2G094123 | Anticodon-binding | 2.01 | 6.09E-09 |
| | | GRMZM2G002687 | Tryptophanyl-tRNA synthetase, class Ib | 2.25 | 7.02E-06 |
| | | GRMZM2G041797 | Anticodon-binding | 3.49 | 1.58E-03 |
| | | GRMZM5G821551 | Anticodon-binding | 3.43 | 6.32E-08 |
| | | GRMZM2G071871 | Nucleic acid-binding, OB-fold | 4.69 | 1.35E-12 |
| | | GRMZM2G012404 | RNA-binding S4 | 6.74 | 3.58E-03 |
| | | GRMZM2G172101 | Seryl-tRNA synthetase, class Iia | 2.82 | 1.36E-03 |
| | | GRMZM5G817976 | Prolyl-tRNA synthetase, class Iia, prokaryotic-type | 2.85 | 3.45E-11 |
| | | GRMZM2G057491 | Glutathione S-transferase, C-terminal-like | 11.76 | 3.49E-06 |
| | | GRMZM2G046932 | Glutathione S-transferase, C-terminal-like | 2.50 | 7.04E-09 |
| | | GRMZM2G386714 | Lysyl-tRNA synthetase, class II, C-terminal | 4.39 | 1.50E-04 |
| | | GRMZM2G000481 | Rossmann-like alpha/beta/alpha sandwich fold | 3.33 | 1.58E-03 |
| | | GRMZM2G082271 | Phosphoesterase, DHHA1 | 2.34 | 1.18E-05 |

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|-----------------------------|----------|------------------|--|--------|-----------|
| | | GRMZM5G874500 | Cysteinyl-tRNA synthetase/mycothiol ligase | 2.01 | 7.10E-06 |
| | | GRMZM2G090487 | FAD-dependent pyridine nucleotide-disulphide oxidoreductase | 346.60 | 5.11E-03 |
| | | GRMZM2G146589 | Lysyl-tRNA synthetase, class II, C-terminal | 3.56 | 2.70E-32 |
| | | GRMZM2G019121 | Nucleic acid-binding, OB-fold | 2.95 | 1.81E-10 |
| | | GRMZM2G117870 | Valyl/Leucyl/Isoleucyl-tRNA synthetase, class Ia, editing | 2.08 | 3.50E-04 |
| GO:0045735 | | | | | |
| Nutrient reservoir activity | 9.05E-08 | GRMZM2G078441 | RmlC-like jelly roll fold;Cupin 1 | 0.23 | 2.40E-12 |
| | | GRMZM2G410134 | Bifunctional inhibitor/plant lipid transfer protein/seed storage | 0.24 | 0.00E+00 |
| | | GRMZM2G008341 | Zein seed storage protein | 0.00 | 5.39E-18 |
| | | GRMZM2G045387 | Zein seed storage protein | 0.00 | 0.00E+00 |
| | | GRMZM2G160739 | Zein seed storage protein | 0.00 | 0.00E+00 |
| | | GRMZM2G044152 | Zein seed storage protein | 0.00 | 9.65E-282 |
| | | AF546187.1_FG007 | Zein seed storage protein | 0.01 | 0.00E+00 |
| | | AF546187.1_FG001 | Zein seed storage protein | 0.00 | 0.00E+00 |
| | | GRMZM2G088441 | Zein seed storage protein | 0.00 | 0.00E+00 |
| | | GRMZM2G404688 | Bifunctional inhibitor/plant lipid transfer protein/seed storage | 0.15 | 1.47E-14 |
| | | GRMZM2G044625 | Zein seed storage protein | 0.00 | 0.00E+00 |
| | | GRMZM2G088273 | Zein seed storage protein | 0.00 | 1.37E-12 |
| | | GRMZM2G053120 | Zein seed storage protein | 0.01 | 4.02E-15 |
| | | AF546188.1_FG005 | Zein seed storage protein | 0.01 | 0.00E+00 |
| | | AF546188.1_FG007 | Zein seed storage protein | 0.01 | 0.00E+00 |
| | | AF546188.1_FG001 | Zein seed storage protein | 0.01 | 0.00E+00 |
| | | AF546188.1_FG003 | Zein seed storage protein | 0.02 | 2.25E-48 |
| | | GRMZM2G138689 | Gliadin/LMW glutenin | 0.00 | 0.00E+00 |
| | | GRMZM2G054916 | RmlC-like jelly roll fold;Cupin 1 | 0.03 | 4.47E-09 |
| | | GRMZM2G162992 | K Homology, type 1;K Homology | 2.08 | 9.75E-05 |
| | | GRMZM2G353268 | Zein seed storage protein | 0.00 | 0.00E+00 |
| | | GRMZM2G059620 | Zein seed storage protein | 0.00 | 0.00E+00 |
| | | GRMZM2G026703 | RmlC-like jelly roll fold;Cupin 1 | 0.00 | 1.14E-08 |
| | | GRMZM2G008913 | Zein seed storage protein | 0.00 | 4.31E-30 |
| | | GRMZM2G060429 | Bifunctional inhibitor/plant lipid transfer protein/seed storage | 0.07 | 0.00E+00 |
| | | GRMZM2G026939 | Zein seed storage protein | 0.00 | 0.00E+00 |
| | | GRMZM2G067919 | RmlC-like jelly roll fold;Cupin 1 | 0.18 | 1.68E-24 |
| | | GRMZM2G388461 | Zein seed storage protein | 0.00 | 0.00E+00 |
| | | AC191050.3_FG003 | RmlC-like jelly roll fold;Cupin 1 | 0.14 | 2.65E-12 |
| | | GRMZM2G166141 | RmlC-like jelly roll fold | 0.07 | 9.48E-13 |
| | | GRMZM2G346897 | Zein seed storage protein | 0.00 | 0.00E+00 |
| | | GRMZM2G346895 | Zein seed storage protein | 0.00 | 9.84E-282 |
| | | GRMZM2G397687 | Zein seed storage protein | 0.00 | 0.00E+00 |
| | | GRMZM2G088365 | Zein seed storage protein | 0.00 | 1.25E-52 |
| | | GRMZM2G404459 | Zein seed storage protein | 0.01 | 3.59E-03 |
| GO:0033279 | 3.01E-03 | GRMZM2G327564 | Ribosomal protein L24, SH3-like | 2.31 | 8.30E-24 |

Ribosomal subunit

| | | | |
|------------------|--|------|----------|
| GRMZM2G064640 | RNA-binding S4 | 2.39 | 1.65E-13 |
| GRMZM2G078985 | Ribosomal protein S7 | 2.69 | 2.08E-22 |
| GRMZM5G832108 | RNA-binding S4 | 2.13 | 4.37E-13 |
| GRMZM2G090422 | Ribosomal protein L13 | 2.50 | 9.24E-53 |
| GRMZM2G163561 | Nucleic acid-binding, OB-fold | 2.12 | 2.74E-17 |
| GRMZM2G070649 | Translation protein SH3-like, subgroup | 3.03 | 3.22E-04 |
| AC233949.1_FG004 | ATPase, AAA-type, VAT, N-terminal | 6.09 | 2.26E-19 |
| GRMZM2G092719 | Ribosomal protein S2, conserved site | 3.30 | 3.44E-15 |
| GRMZM2G058923 | Ribosomal protein L18e/L15 | 2.14 | 1.85E-03 |
| GRMZM2G036765 | ATPase, AAA-type, VAT, N-terminal | 4.83 | 3.89E-18 |
| GRMZM2G091921 | Ribosomal protein L32p | 3.81 | 1.42E-14 |
| GRMZM2G122290 | Ribosomal protein L1 | 2.89 | 5.76E-04 |
| GRMZM2G168149 | Ribosomal protein S5, C-terminal | 2.05 | 1.87E-22 |
| GRMZM2G703490 | ATPase, AAA-type, VAT, N-terminal | 5.22 | 7.18E-04 |
| GRMZM2G140609 | Ribosomal protein S12/S23 | 2.76 | 1.06E-07 |
| GRMZM2G126821 | Ribosomal protein S2, conserved site | 2.15 | 1.48E-08 |
| GRMZM2G092663 | Ribosomal protein S5, C-terminal | 2.31 | 9.20E-11 |
| GRMZM2G110952 | Protein of unknown function DUF966 | 2.43 | 1.83E-19 |
| GRMZM2G170336 | Ribosomal protein S10, eukaryotic/archaeal | 2.68 | 3.33E-08 |
| GRMZM2G119169 | Ribosomal protein L22/L17 | 2.48 | 5.05E-10 |
| AC210013.4_FG019 | Ribosomal protein S5, C-terminal | 2.33 | 1.54E-30 |
| GRMZM2G163769 | Ribosomal protein L22/L17 | 2.48 | 1.84E-05 |

GO:0030662

Coated vesicle
membrane

1.64E-03

| | | | |
|------------------|---|-------|----------|
| GRMZM2G073792 | Clathrin, heavy chain, propeller repeat | 2.83 | 8.89E-05 |
| GRMZM2G143725 | Sec23/Sec24 beta-sandwich | 2.19 | 4.60E-03 |
| GRMZM2G085295 | Clathrin, heavy chain, propeller repeat | 18.31 | 1.26E-05 |
| GRMZM5G874869 | Zinc finger, Sec23/Sec24-type | 6.89 | 1.32E-04 |
| GRMZM2G057576 | Clathrin, heavy chain, propeller repeat | 2.93 | 2.25E-06 |
| GRMZM2G011101 | Coatomer, beta subunit | 2.76 | 3.32E-05 |
| GRMZM5G826171 | Sec23/Sec24 beta-sandwich | 2.86 | 9.43E-06 |
| AC155622.2_FG001 | Coatomer, alpha subunit, C-terminal | 2.24 | 2.09E-04 |
| GRMZM2G378906 | Coatomer, beta subunit | 3.40 | 1.64E-06 |
| GRMZM2G048377 | Clathrin, heavy chain, propeller repeat | 17.95 | 7.26E-04 |
| GRMZM2G075680 | Zinc finger, Sec23/Sec24-type | 4.42 | 8.99E-05 |
| GRMZM2G010054 | WD40/YVTN repeat-like-containing domain | 2.25 | 1.56E-03 |

GO:0006119

Oxidative
phosphorylation

8.53E-04

| | | | |
|------------------|--|------|----------|
| GRMZM2G157018 | ATPase, F0 complex, subunit D, mitochondrial | 2.31 | 7.57E-39 |
| GRMZM2G070360 | ATPase, V1/A1 complex, subunit E | 2.02 | 8.37E-07 |
| GRMZM2G181151 | ATPase, F1/V1/A1 complex, alpha/beta subunit, N-terminal | 2.18 | 8.94E-09 |
| GRMZM2G101020 | ATPase, V0 complex, proteolipid subunit C | 3.23 | 1.45E-12 |
| AC194341.4_FG002 | ATPase, F0 complex, subunit G, mitochondrial | 2.28 | 2.61E-21 |

| | | | |
|---------------|--|------|----------|
| GRMZM2G009638 | ATPase, F1 complex, gamma subunit conserved site | 2.39 | 4.64E-17 |
| GRMZM2G138220 | ATPase, F1 complex, delta/epsilon subunit | 2.06 | 1.34E-05 |
| GRMZM2G042078 | ATPase, F0 complex, subunit G, mitochondrial | 3.43 | 5.11E-15 |
| GRMZM2G079777 | ATPase, V1/A1 complex, subunit D | 2.42 | 3.95E-06 |
| GRMZM2G021331 | ATPase, F1/V1/A1 complex, alpha/beta subunit, N-terminal | 2.47 | 4.04E-20 |
| GRMZM2G113408 | ATPase, F1/V1/A1 complex, alpha/beta subunit, N-terminal | 3.37 | 8.35E-60 |
| GRMZM2G321725 | ATPase, F1 complex, gamma subunit conserved site | 2.60 | 8.59E-19 |
| GRMZM2G144372 | ATPase, V1 complex, subunit C | 2.67 | 2.40E-07 |
| GRMZM2G128995 | ATPase, V1 complex, subunit C | 2.02 | 6.60E-04 |
| GRMZM2G156068 | ATPase, F1 complex, OSCP/delta subunit | 2.81 | 1.01E-53 |
| GRMZM2G069458 | ATPase, F1 complex, gamma subunit domain | 4.01 | 3.01E-25 |
| GRMZM2G041275 | ATPase, F1/V1/A1 complex, alpha/beta subunit, N-terminal | 3.16 | 1.65E-14 |
| GRMZM2G171628 | ATPase, F1 complex, delta/epsilon subunit | 2.16 | 1.75E-17 |
| GRMZM2G177005 | ATPase, V0 complex, proteolipid subunit C | 2.74 | 5.38E-15 |
| GRMZM2G078839 | ATPase, V1/A1 complex, subunit E | 2.66 | 4.66E-04 |
| GRMZM2G069229 | ATPase, F0 complex, subunit G, mitochondrial | 8.85 | 1.13E-07 |
| GRMZM2G421857 | ATPase, F1/V1/A1 complex, alpha/beta subunit, N-terminal | 2.06 | 1.69E-14 |
| GRMZM2G021635 | ATPase, V1/A1 complex, subunit D | 2.34 | 1.55E-03 |
| GRMZM2G028432 | ATPase, V0 complex, proteolipid subunit C | 2.14 | 4.87E-07 |
| GRMZM2G058910 | ATPase, V0/A0 complex, 116kDa subunit | 2.12 | 1.54E-03 |
