

Table S14. Enriched GO terms in quinoa-specific orthologous groups

| GO ID | p Value | q Value | Term | Classification |
|------------|----------|----------|---------------------------------------------------------------------------------------|----------------|
| GO:0010329 | 5.30E-10 | 2.80E-07 | auxin efflux transmembrane transporter activity | MF |
| GO:0005515 | 8.86E-07 | 1.41E-04 | protein binding | MF |
| GO:0003677 | 1.54E-06 | 2.22E-04 | DNA binding | MF |
| GO:0003723 | 8.04E-06 | 9.12E-04 | RNA binding | MF |
| GO:0017016 | 2.26E-05 | 1.91E-03 | Ras GTPase binding | MF |
| GO:0016709 | 5.55E-05 | 3.54E-03 | oxidoreductase activity, acting on paired donors, with incorporation or reduction of | MF |
| GO:0046872 | 6.24E-05 | 3.54E-03 | metal ion binding | MF |
| GO:0004252 | 6.35E-05 | 3.54E-03 | serine-type endopeptidase activity | MF |
| GO:0042626 | 6.97E-05 | 3.69E-03 | ATPase activity, coupled to transmembrane movement of substances | MF |
| GO:0016740 | 1.28E-04 | 6.54E-03 | transferase activity | MF |
| GO:0047134 | 1.77E-04 | 7.40E-03 | protein-disulfide reductase activity | MF |
| GO:0001727 | 2.63E-04 | 9.72E-03 | lipid kinase activity | MF |
| GO:0009840 | 5.59E-11 | 4.43E-08 | chloroplastic endopeptidase Clp complex | CC |
| GO:0005739 | 4.28E-09 | 1.36E-06 | mitochondrion | CC |
| GO:0009507 | 9.61E-08 | 2.18E-05 | chloroplast | CC |
| GO:0009532 | 1.38E-07 | 2.73E-05 | plastid stroma | CC |
| GO:0005634 | 4.74E-07 | 8.36E-05 | nucleus | CC |
| GO:0005829 | 2.12E-06 | 2.81E-04 | cytosol | CC |
| GO:0005737 | 6.04E-06 | 7.38E-04 | cytoplasm | CC |
| GO:0005622 | 1.82E-05 | 1.81E-03 | intracellular | CC |
| GO:0032045 | 1.77E-04 | 7.40E-03 | guanyl-nucleotide exchange factor complex | CC |
| GO:0044599 | 2.63E-04 | 9.72E-03 | AP-5 adaptor complex | CC |
| GO:0002238 | 2.64E-09 | 1.05E-06 | response to molecule of fungal origin | BP |
| GO:0006351 | 1.01E-05 | 1.07E-03 | transcription, DNA-templated | BP |
| GO:0044550 | 2.31E-05 | 1.91E-03 | secondary metabolite biosynthetic process | BP |
| GO:0006355 | 2.40E-05 | 1.91E-03 | regulation of transcription, DNA-templated | BP |
| GO:0090602 | 2.41E-05 | 1.91E-03 | sieve element enucleation | BP |
| GO:0006624 | 2.52E-05 | 1.91E-03 | vacuolar protein processing | BP |
| GO:0090603 | 3.24E-05 | 2.34E-03 | sieve element differentiation | BP |
| GO:0035957 | 6.47E-05 | 3.54E-03 | positive regulation of starch catabolic process by positive regulation of transcripti | BP |
| GO:1900524 | 6.47E-05 | 3.54E-03 | positive regulation of flocculation via cell wall protein-carbohydrate interaction by | BP |
| GO:1900461 | 6.47E-05 | 3.54E-03 | positive regulation of pseudohyphal growth by positive regulation of transcription | BP |
| GO:0036095 | 6.47E-05 | 3.54E-03 | positive regulation of invasive growth in response to glucose limitation by positive | BP |
| GO:0048235 | 1.35E-04 | 6.68E-03 | pollen sperm cell differentiation | BP |
| GO:0006810 | 1.61E-04 | 7.40E-03 | transport | BP |
| GO:0051966 | 1.77E-04 | 7.40E-03 | regulation of synaptic transmission, glutamatergic | BP |
| GO:0060079 | 1.77E-04 | 7.40E-03 | excitatory postsynaptic potential | BP |
| GO:1900452 | 1.77E-04 | 7.40E-03 | regulation of long term synaptic depression | BP |
| GO:0010540 | 1.96E-04 | 7.97E-03 | basipetal auxin transport | BP |
| GO:0010981 | 2.45E-04 | 9.72E-03 | regulation of cell wall macromolecule metabolic process | BP |
| GO:0045892 | 2.63E-04 | 9.72E-03 | negative regulation of transcription, DNA-templated | BP |