**Table S2:** GO terms enriched for the ‘TGdL’ and ‘Tombul’ shared genes

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | | |  |  |  |
| **GO ID** | **term\_type** | **Term** | **pvalue** | **FDR** |  |
| GO:0044092 | P | negative regulation of molecular function | 1.2e-10 | 5.1e-08 |  |
| GO:0043086 | P | negative regulation of catalytic activity | 1.2e-10 | 5.1e-08 |  |
| GO:0050790 | P | regulation of catalytic activity | 6.2e-06 | 0.0015 |  |
| GO:0065009 | P | regulation of molecular function | 7.2e-06 | 0.0015 |  |
| GO:0071215 | P | cellular response to abscisic acid stimulus | 0.00064 | 0.067 |  |
| GO:0097306 | P | cellular response to alcohol | 0.00064 | 0.067 |  |
| GO:0071229 | P | cellular response to acid chemical | 0.00064 | 0.067 |  |
| GO:0009738 | P | abscisic acid-activated signaling pathway | 0.00064 | 0.067 |  |
| GO:0006952 | P | defense response | 0.0011 | 0.084 |  |
| GO:0097305 | P | response to alcohol | 0.0011 | 0.084 |  |
| GO:0009737 | P | response to abscisic acid | 0.0011 | 0.084 |  |
| GO:0071396 | P | cellular response to lipid | 0.0016 | 0.11 |  |
| GO:0050896 | P | response to stimulus | 0.0019 | 0.12 |  |
| GO:1901701 | P | cellular response to oxygen-containing compound | 0.0022 | 0.12 |  |
| GO:0001101 | P | response to acid chemical | 0.0022 | 0.12 |  |
| GO:0009755 | P | hormone-mediated signaling pathway | 0.0032 | 0.14 |  |
| GO:0071495 | P | cellular response to endogenous stimulus | 0.0032 | 0.14 |  |
| GO:0032870 | P | cellular response to hormone stimulus | 0.0032 | 0.14 |  |
| GO:0033993 | P | response to lipid | 0.0029 | 0.14 |  |
| GO:0006928 | P | movement of cell or subcellular component | 0.0039 | 0.15 |  |
| GO:0071310 | P | cellular response to organic substance | 0.0039 | 0.15 |  |
| GO:0007018 | P | microtubule-based movement | 0.0039 | 0.15 |  |
| GO:0070887 | P | cellular response to chemical stimulus | 0.0051 | 0.19 |  |
| GO:1901700 | P | response to oxygen-containing compound | 0.0065 | 0.23 |  |
| GO:0006950 | P | response to stress | 0.0088 | 0.3 |  |
| GO:0007165 | P | signal transduction | 0.01 | 0.31 |  |
| GO:0044700 | P | single organism signaling | 0.01 | 0.31 |  |
| GO:0023052 | P | signaling | 0.01 | 0.31 |  |
| GO:0007017 | P | microtubule-based process | 0.014 | 0.4 |  |
| GO:0071705 | P | nitrogen compound transport | 0.016 | 0.45 |  |
| GO:0009719 | P | response to endogenous stimulus | 0.025 | 0.67 |  |
| GO:0009725 | P | response to hormone | 0.025 | 0.67 |  |
| GO:0010033 | P | response to organic substance | 0.034 | 0.88 |  |
| GO:0008104 | P | protein localization | 0.39 | 1 |  |
| GO:0080090 | P | regulation of primary metabolic process | 0.85 | 1 |  |
| GO:0019222 | P | regulation of metabolic process | 0.83 | 1 |  |
| GO:1901362 | P | organic cyclic compound biosynthetic process | 0.94 | 1 |  |
| GO:0071840 | P | cellular component organization or biogenesis | 0.82 | 1 |  |
| GO:0051716 | P | cellular response to stimulus | 0.05 | 1 |  |
| GO:0044711 | P | single-organism biosynthetic process | 1 | 1 |  |
| GO:0070727 | P | cellular macromolecule localization | 0.32 | 1 |  |
| GO:0043043 | P | peptide biosynthetic process | 0.92 | 1 |  |
| GO:0010467 | P | gene expression | 1 | 1 |  |
| GO:0055085 | P | transmembrane transport | 0.36 | 1 |  |
| GO:0033036 | P | macromolecule localization | 0.63 | 1 |  |
| GO:0060255 | P | regulation of macromolecule metabolic process | 0.86 | 1 |  |
| GO:0045184 | P | establishment of protein localization | 0.33 | 1 |  |
| GO:0030163 | P | protein catabolic process | 0.42 | 1 |  |
| GO:2001141 | P | regulation of RNA biosynthetic process | 0.89 | 1 |  |
| GO:0043436 | P | oxoacid metabolic process | 0.98 | 1 |  |
| GO:0055114 | P | oxidation-reduction process | 0.044 | 1 |  |
| GO:0046483 | P | heterocycle metabolic process | 1 | 1 |  |
| GO:1901564 | P | organonitrogen compound metabolic process | 1 | 1 |  |
| GO:0043603 | P | cellular amide metabolic process | 0.94 | 1 |  |
| GO:1901566 | P | organonitrogen compound biosynthetic process | 0.99 | 1 |  |
| GO:0019538 | P | protein metabolic process | 0.77 | 1 |  |
| GO:0019637 | P | organophosphate metabolic process | 0.95 | 1 |  |
| GO:0019438 | P | aromatic compound biosynthetic process | 0.91 | 1 |  |
| GO:0044281 | P | small molecule metabolic process | 1 | 1 |  |
| GO:0022607 | P | cellular component assembly | 0.64 | 1 |  |
| GO:0034645 | P | cellular macromolecule biosynthetic process | 0.94 | 1 |  |
| GO:0006807 | P | nitrogen compound metabolic process | 1 | 1 |  |
| GO:0035556 | P | intracellular signal transduction | 0.25 | 1 |  |
| GO:0043170 | P | macromolecule metabolic process | 0.99 | 1 |  |
| GO:0050789 | P | regulation of biological process | 0.77 | 1 |  |
| GO:0097659 | P | nucleic acid-templated transcription | 0.87 | 1 |  |
| GO:0044267 | P | cellular protein metabolic process | 0.81 | 1 |  |
| GO:1901575 | P | organic substance catabolic process | 0.93 | 1 |  |
| GO:0044260 | P | cellular macromolecule metabolic process | 0.99 | 1 |  |
| GO:0006886 | P | intracellular protein transport | 0.25 | 1 |  |
| GO:0016043 | P | cellular component organization | 0.83 | 1 |  |
| GO:0065003 | P | macromolecular complex assembly | 0.4 | 1 |  |
| GO:0065007 | P | biological regulation | 0.34 | 1 |  |
| GO:1901360 | P | organic cyclic compound metabolic process | 1 | 1 |  |
| GO:0018130 | P | heterocycle biosynthetic process | 0.94 | 1 |  |
| GO:0006629 | P | lipid metabolic process | 0.99 | 1 |  |
| GO:0006812 | P | cation transport | 0.5 | 1 |  |
| GO:0006811 | P | ion transport | 0.6 | 1 |  |
| GO:0006810 | P | transport | 0.43 | 1 |  |
| GO:0009889 | P | regulation of biosynthetic process | 0.88 | 1 |  |
| GO:0044710 | P | single-organism metabolic process | 0.72 | 1 |  |
| GO:0050794 | P | regulation of cellular process | 0.69 | 1 |  |
| GO:0043412 | P | macromolecule modification | 0.82 | 1 |  |
| GO:0036211 | P | protein modification process | 0.7 | 1 |  |
| GO:0008152 | P | metabolic process | 0.91 | 1 |  |
| GO:0034654 | P | nucleobase-containing compound biosynthetic process | 0.91 | 1 |  |
| GO:0051234 | P | establishment of localization | 0.38 | 1 |  |
| GO:0016070 | P | RNA metabolic process | 1 | 1 |  |
| GO:0044271 | P | cellular nitrogen compound biosynthetic process | 0.98 | 1 |  |
| GO:0046907 | P | intracellular transport | 0.21 | 1 |  |
| GO:0006355 | P | regulation of transcription, DNA-templated | 0.89 | 1 |  |
| GO:0010556 | P | regulation of macromolecule biosynthetic process | 0.88 | 1 |  |
| GO:0006351 | P | transcription, DNA-templated | 0.87 | 1 |  |
| GO:0006518 | P | peptide metabolic process | 0.93 | 1 |  |
| GO:0032774 | P | RNA biosynthetic process | 0.87 | 1 |  |
| GO:0016310 | P | phosphorylation | 0.76 | 1 |  |
| GO:0044248 | P | cellular catabolic process | 0.62 | 1 |  |
| GO:0044249 | P | cellular biosynthetic process | 1 | 1 |  |
| GO:0034641 | P | cellular nitrogen compound metabolic process | 1 | 1 |  |
| GO:0007154 | P | cell communication | 0.045 | 1 |  |
| GO:0044699 | P | single-organism process | 0.49 | 1 |  |
| GO:0006139 | P | nucleobase-containing compound metabolic process | 1 | 1 |  |
| GO:0009057 | P | macromolecule catabolic process | 0.79 | 1 |  |
| GO:0006508 | P | proteolysis | 0.5 | 1 |  |
| GO:0006996 | P | organelle organization | 0.85 | 1 |  |
| GO:0032501 | P | multicellular organismal process | 0.64 | 1 |  |
| GO:0009987 | P | cellular process | 1 | 1 |  |
| GO:1903506 | P | regulation of nucleic acid-templated transcription | 0.89 | 1 |  |
| GO:0009058 | P | biosynthetic process | 1 | 1 |  |
| GO:0030001 | P | metal ion transport | 0.37 | 1 |  |
| GO:0006979 | P | response to oxidative stress | 0.044 | 1 |  |
| GO:0043604 | P | amide biosynthetic process | 0.92 | 1 |  |
| GO:0006082 | P | organic acid metabolic process | 0.99 | 1 |  |
| GO:1901135 | P | carbohydrate derivative metabolic process | 0.96 | 1 |  |
| GO:0051252 | P | regulation of RNA metabolic process | 0.9 | 1 |  |
| GO:0043933 | P | macromolecular complex subunit organization | 0.38 | 1 |  |
| GO:0031326 | P | regulation of cellular biosynthetic process | 0.88 | 1 |  |
| GO:0031323 | P | regulation of cellular metabolic process | 0.8 | 1 |  |
| GO:0019752 | P | carboxylic acid metabolic process | 0.98 | 1 |  |
| GO:0090304 | P | nucleic acid metabolic process | 1 | 1 |  |
| GO:0034622 | P | cellular macromolecular complex assembly | 0.35 | 1 |  |
| GO:0071822 | P | protein complex subunit organization | 0.34 | 1 |  |
| GO:2000112 | P | regulation of cellular macromolecule biosynthetic process | 0.88 | 1 |  |
| GO:0071704 | P | organic substance metabolic process | 0.99 | 1 |  |
| GO:0071702 | P | organic substance transport | 0.14 | 1 |  |
| GO:0010468 | P | regulation of gene expression | 0.89 | 1 |  |
| GO:0006468 | P | protein phosphorylation | 0.59 | 1 |  |
| GO:1901576 | P | organic substance biosynthetic process | 1 | 1 |  |
| GO:0019219 | P | regulation of nucleobase-containing compound metabolic process | 0.92 | 1 |  |
| GO:0006725 | P | cellular aromatic compound metabolic process | 1 | 1 |  |
| GO:0034613 | P | cellular protein localization | 0.32 | 1 |  |
| GO:0006464 | P | cellular protein modification process | 0.7 | 1 |  |
| GO:0015031 | P | protein transport | 0.32 | 1 |  |
| GO:0044765 | P | single-organism transport | 0.84 | 1 |  |
| GO:0009059 | P | macromolecule biosynthetic process | 0.95 | 1 |  |
| GO:0044763 | P | single-organism cellular process | 0.83 | 1 |  |
| GO:0051171 | P | regulation of nitrogen compound metabolic process | 0.89 | 1 |  |
| GO:0051649 | P | establishment of localization in cell | 0.14 | 1 |  |
| GO:0042221 | P | response to chemical | 0.049 | 1 |  |
| GO:0009056 | P | catabolic process | 0.84 | 1 |  |
| GO:0051179 | P | localization | 0.41 | 1 |  |
| GO:1902578 | P | single-organism localization | 0.87 | 1 |  |
| GO:0051641 | P | cellular localization | 0.19 | 1 |  |
| GO:0044238 | P | primary metabolic process | 0.99 | 1 |  |
| GO:0005975 | P | carbohydrate metabolic process | 0.31 | 1 |  |
| GO:0044237 | P | cellular metabolic process | 1 | 1 |  |
| GO:0006796 | P | phosphate-containing compound metabolic process | 0.81 | 1 |  |
| GO:0044085 | P | cellular component biogenesis | 0.63 | 1 |  |
| GO:0006793 | P | phosphorus metabolic process | 0.82 | 1 |  |
| GO:0006259 | P | DNA metabolic process | 0.67 | 1 |  |
| GO:0006412 | P | translation | 0.91 | 1 |  |
| GO:0004523 | F | RNA-DNA hybrid ribonuclease activity | 5.8e-23 | 3.3e-20 |  |
| GO:0016891 | F | endoribonuclease activity, producing 5'-phosphomonoesters | 1.5e-21 | 4.3e-19 |  |
| GO:0016893 | F | endonuclease activity, active with either ribo- or deoxyribonucleic acids and producing 5'-phosphomonoesters | 5.9e-21 | 1.1e-18 |  |
| GO:0004521 | F | endoribonuclease activity | 3.5e-20 | 4.9e-18 |  |
| GO:0004540 | F | ribonuclease activity | 1.9e-19 | 2.2e-17 |  |
| GO:0004519 | F | endonuclease activity | 2.1e-17 | 2.00E-15 |  |
| GO:0004518 | F | nuclease activity | 1.9e-16 | 1.6e-14 |  |
| GO:0046910 | F | pectinesterase inhibitor activity | 1.5e-10 | 1.00E-08 |  |
| GO:0004857 | F | enzyme inhibitor activity | 8.3e-09 | 5.3e-07 |  |
| GO:0030234 | F | enzyme regulator activity | 2.2e-06 | 0.00012 |  |
| GO:0005507 | F | copper ion binding | 3.00E-06 | 0.00016 |  |
| GO:0098772 | F | molecular function regulator | 6.3e-06 | 0.00027 |  |
| GO:0016788 | F | hydrolase activity, acting on ester bonds | 6.1e-06 | 0.00027 |  |
| GO:0020037 | F | heme binding | 1.9e-05 | 0.00073 |  |
| GO:0046906 | F | tetrapyrrole binding | 1.9e-05 | 0.00073 |  |
| GO:0044212 | F | transcription regulatory region DNA binding | 3.8e-05 | 0.0012 |  |
| GO:0001067 | F | regulatory region nucleic acid binding | 3.8e-05 | 0.0012 |  |
| GO:0000975 | F | regulatory region DNA binding | 3.8e-05 | 0.0012 |  |
| GO:0008061 | F | chitin binding | 0.00023 | 0.0069 |  |
| GO:0005506 | F | iron ion binding | 0.00079 | 0.022 |  |
| GO:0016705 | F | oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen | 0.00088 | 0.024 |  |
| GO:0046872 | F | metal ion binding | 0.0028 | 0.074 |  |
| GO:0003777 | F | microtubule motor activity | 0.0039 | 0.097 |  |
| GO:0043169 | F | cation binding | 0.0047 | 0.11 |  |
| GO:0046914 | F | transition metal ion binding | 0.0059 | 0.13 |  |
| GO:0043167 | F | ion binding | 0.0067 | 0.15 |  |
| GO:0010333 | F | terpene synthase activity | 0.0076 | 0.16 |  |
| GO:0016838 | F | carbon-oxygen lyase activity, acting on phosphates | 0.013 | 0.26 |  |
| GO:0016209 | F | antioxidant activity | 0.014 | 0.28 |  |
| GO:0003774 | F | motor activity | 0.016 | 0.3 |  |
| GO:0004601 | F | peroxidase activity | 0.017 | 0.31 |  |
| GO:0016684 | F | oxidoreductase activity, acting on peroxide as acceptor | 0.021 | 0.38 |  |
| GO:0004252 | F | serine-type endopeptidase activity | 0.022 | 0.38 |  |
| GO:0016491 | F | oxidoreductase activity | 0.046 | 0.76 |  |
| GO:0005509 | F | calcium ion binding | 0.048 | 0.77 |  |
| GO:0003690 | F | double-stranded DNA binding | 0.062 | 0.98 |  |
| GO:1901363 | F | heterocyclic compound binding | 0.53 | 1 |  |
| GO:0003735 | F | structural constituent of ribosome | 0.71 | 1.00E+00 |  |
| GO:0046983 | F | protein dimerization activity | 0.48 | 1 |  |
| GO:0016740 | F | transferase activity | 0.86 | 1.00E+00 |  |
| GO:0016741 | F | transferase activity, transferring one-carbon groups | 0.51 | 1 |  |
| GO:0016746 | F | transferase activity, transferring acyl groups | 0.38 | 1 |  |
| GO:0016747 | F | transferase activity, transferring acyl groups other than amino-acyl groups | 0.35 | 1 |  |
| GO:0008092 | F | cytoskeletal protein binding | 0.42 | 1 |  |
| GO:0004672 | F | protein kinase activity | 0.56 | 1 |  |
| GO:0016818 | F | hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides | 0.92 | 1 |  |
| GO:0016817 | F | hydrolase activity, acting on acid anhydrides | 0.92 | 1 |  |
| GO:0097367 | F | carbohydrate derivative binding | 0.91 | 1 |  |
| GO:0005524 | F | ATP binding | 0.98 | 1 |  |
| GO:0016757 | F | transferase activity, transferring glycosyl groups | 0.95 | 1 |  |
| GO:0004553 | F | hydrolase activity, hydrolyzing O-glycosyl compounds | 0.28 | 1 |  |
| GO:0005525 | F | GTP binding | 0.86 | 1 |  |
| GO:0015631 | F | tubulin binding | 0.18 | 1 |  |
| GO:0005488 | F | binding | 0.28 | 1 |  |
| GO:0003676 | F | nucleic acid binding | 0.46 | 1 |  |
| GO:0003677 | F | DNA binding | 0.96 | 1 |  |
| GO:0008168 | F | methyltransferase activity | 0.42 | 1 |  |
| GO:0032549 | F | ribonucleoside binding | 0.98 | 1 |  |
| GO:0017076 | F | purine nucleotide binding | 0.99 | 1 |  |
| GO:0008236 | F | serine-type peptidase activity | 0.11 | 1 |  |
| GO:0016787 | F | hydrolase activity | 0.13 | 1 |  |
| GO:0043565 | F | sequence-specific DNA binding | 0.48 | 1 |  |
| GO:0003824 | F | catalytic activity | 0.35 | 1 |  |
| GO:0016758 | F | transferase activity, transferring hexosyl groups | 0.89 | 1 |  |
| GO:0004842 | F | ubiquitin-protein transferase activity | 0.27 | 1 |  |
| GO:0022890 | F | inorganic cation transmembrane transporter activity | 0.73 | 1 |  |
| GO:0022892 | F | substrate-specific transporter activity | 0.82 | 1 |  |
| GO:0016462 | F | pyrophosphatase activity | 0.91 | 1 |  |
| GO:0016773 | F | phosphotransferase activity, alcohol group as acceptor | 0.63 | 1 |  |
| GO:0016772 | F | transferase activity, transferring phosphorus-containing groups | 0.8 | 1 |  |
| GO:0016301 | F | kinase activity | 0.69 | 1 |  |
| GO:0015075 | F | ion transmembrane transporter activity | 0.79 | 1 |  |
| GO:0032559 | F | adenyl ribonucleotide binding | 0.98 | 1 |  |
| GO:0032555 | F | purine ribonucleotide binding | 0.98 | 1 |  |
| GO:0032550 | F | purine ribonucleoside binding | 0.98 | 1 |  |
| GO:0032553 | F | ribonucleotide binding | 0.99 | 1 |  |
| GO:0008270 | F | zinc ion binding | 0.95 | 1 |  |
| GO:0035639 | F | purine ribonucleoside triphosphate binding | 0.99 | 1 |  |
| GO:0016798 | F | hydrolase activity, acting on glycosyl bonds | 0.34 | 1 |  |
| GO:0000166 | F | nucleotide binding | 0.99 | 1 |  |
| GO:0016829 | F | lyase activity | 0.35 | 1 |  |
| GO:0000287 | F | magnesium ion binding | 0.12 | 1 |  |
| GO:0032561 | F | guanyl ribonucleotide binding | 0.86 | 1 |  |
| GO:0015291 | F | secondary active transmembrane transporter activity | 0.29 | 1 |  |
| GO:0005198 | F | structural molecule activity | 0.85 | 1 |  |
| GO:0005215 | F | transporter activity | 0.51 | 1 |  |
| GO:0017171 | F | serine hydrolase activity | 0.11 | 1 |  |
| GO:0030554 | F | adenyl nucleotide binding | 0.98 | 1 |  |
| GO:0001071 | F | nucleic acid binding transcription factor activity | 0.38 | 1 |  |
| GO:0005515 | F | protein binding | 0.77 | 1 |  |
| GO:0016835 | F | carbon-oxygen lyase activity | 0.14 | 1 |  |
| GO:0008233 | F | peptidase activity | 0.81 | 1 |  |
| GO:0097159 | F | organic cyclic compound binding | 0.53 | 1 |  |
| GO:0004175 | F | endopeptidase activity | 0.24 | 1 |  |
| GO:0017111 | F | nucleoside-triphosphatase activity | 0.89 | 1 |  |
| GO:0001883 | F | purine nucleoside binding | 0.98 | 1 |  |
| GO:0001882 | F | nucleoside binding | 0.98 | 1 |  |
| GO:0019001 | F | guanyl nucleotide binding | 0.88 | 1 |  |
| GO:0022857 | F | transmembrane transporter activity | 0.47 | 1 |  |
| GO:0019787 | F | ubiquitin-like protein transferase activity | 0.28 | 1 |  |
| GO:0070011 | F | peptidase activity, acting on L-amino acid peptides | 0.78 | 1 |  |
| GO:1901265 | F | nucleoside phosphate binding | 0.99 | 1 |  |
| GO:0022804 | F | active transmembrane transporter activity | 0.73 | 1 |  |
| GO:0008324 | F | cation transmembrane transporter activity | 0.43 | 1 |  |
| GO:0036094 | F | small molecule binding | 0.99 | 1 |  |
| GO:0022891 | F | substrate-specific transmembrane transporter activity | 0.78 | 1 |  |
| GO:0003700 | F | transcription factor activity, sequence-specific DNA binding | 0.38 | 1 |  |
| GO:0048037 | F | cofactor binding | 0.94 | 1 |  |
| GO:0031224 | C | intrinsic component of membrane | 0.88 | 1 |  |
| GO:0016021 | C | integral component of membrane | 0.86 | 1 |  |
| GO:0016020 | C | membrane | 0.51 | 1 |  |
| GO:0032991 | C | macromolecular complex | 1 | 1 |  |
| GO:0043234 | C | protein complex | 1 | 1 |  |
| GO:0043231 | C | intracellular membrane-bounded organelle | 0.94 | 1 |  |
| GO:0044422 | C | organelle part | 1 | 1 |  |
| GO:0044464 | C | cell part | 1 | 1 |  |
| GO:0044424 | C | intracellular part | 0.99 | 1 |  |
| GO:0043229 | C | intracellular organelle | 0.98 | 1 |  |
| GO:0043227 | C | membrane-bounded organelle | 0.94 | 1 |  |
| GO:0012505 | C | endomembrane system | 0.67 | 1 |  |
| GO:0044444 | C | cytoplasmic part | 0.95 | 1 |  |
| GO:0005737 | C | cytoplasm | 0.95 | 1 |  |
| GO:0030529 | C | intracellular ribonucleoprotein complex | 0.79 | 1 |  |
| GO:0005840 | C | ribosome | 0.72 | 1 |  |
| GO:0005622 | C | intracellular | 0.99 | 1 |  |
| GO:1990904 | C | ribonucleoprotein complex | 0.82 | 1 |  |
| GO:0005623 | C | cell | 1 | 1 |  |
| GO:0043228 | C | non-membrane-bounded organelle | 0.95 | 1 |  |
| GO:0044425 | C | membrane part | 0.95 | 1 |  |
| GO:0043232 | C | intracellular non-membrane-bounded organelle | 0.95 | 1 |  |
| GO:0005634 | C | nucleus | 0.91 | 1 |  |
| GO:0044446 | C | intracellular organelle part | 1 | 1 |  |
| GO:0043226 | C | organelle | 0.98 | 1 |  |