**Table S1:** GO terms enriched for the exclusive ‘TGdL’ genes

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | | |  |  | |  |
| GO ID | term\_type | Term | pvalue | | FDR |  |
| GO:0042908 | P | xenobiotic transport | 1.9e-10 | 1.1e-07 | |  |
| GO:0006508 | P | proteolysis | 3.8e-05 | 0.011 | |  |
| GO:0019725 | P | cellular homeostasis | 0.0016 | 0.32 | |  |
| GO:0042592 | P | homeostatic process | 0.0027 | 0.4 | |  |
| GO:0045454 | P | cell redox homeostasis | 0.0034 | 0.41 | |  |
| GO:0019538 | P | protein metabolic process | 0.0058 | 0.52 | |  |
| GO:0006468 | P | protein phosphorylation | 0.0061 | 0.52 | |  |
| GO:0044765 | P | single-organism transport | 0.0077 | 0.57 | |  |
| GO:0055114 | P | oxidation-reduction process | 0.013 | 0.71 | |  |
| GO:0035556 | P | intracellular signal transduction | 0.012 | 0.71 | |  |
| GO:1902578 | P | single-organism localization | 0.011 | 0.71 | |  |
| GO:0016310 | P | phosphorylation | 0.014 | 0.71 | |  |
| GO:0065008 | P | regulation of biological quality | 0.016 | 0.74 | |  |
| GO:0008104 | P | protein localization | 0.39 | 1 | |  |
| GO:0080090 | P | regulation of primary metabolic process | 1 | 1 | |  |
| GO:0019222 | P | regulation of metabolic process | 1 | 1 | |  |
| GO:0044281 | P | small molecule metabolic process | 0.51 | 1 | |  |
| GO:1901362 | P | organic cyclic compound biosynthetic process | 1 | 1 | |  |
| GO:1901360 | P | organic cyclic compound metabolic process | 1 | 1 | |  |
| GO:0051716 | P | cellular response to stimulus | 0.19 | 1 | |  |
| GO:0044711 | P | single-organism biosynthetic process | 0.99 | 1 | |  |
| GO:0070727 | P | cellular macromolecule localization | 0.21 | 1 | |  |
| GO:0043043 | P | peptide biosynthetic process | 0.99 | 1 | |  |
| GO:0016311 | P | dephosphorylation | 0.22 | 1 | |  |
| GO:0033036 | P | macromolecule localization | 0.62 | 1 | |  |
| GO:0060255 | P | regulation of macromolecule metabolic process | 1 | 1 | |  |
| GO:0045184 | P | establishment of protein localization | 0.35 | 1 | |  |
| GO:2001141 | P | regulation of RNA biosynthetic process | 1 | 1 | |  |
| GO:0043436 | P | oxoacid metabolic process | 0.73 | 1 | |  |
| GO:0046483 | P | heterocycle metabolic process | 1 | 1 | |  |
| GO:0044700 | P | single organism signaling | 0.031 | 1 | |  |
| GO:1901564 | P | organonitrogen compound metabolic process | 0.98 | 1 | |  |
| GO:0006082 | P | organic acid metabolic process | 0.71 | 1 | |  |
| GO:1901566 | P | organonitrogen compound biosynthetic process | 1 | 1 | |  |
| GO:0019637 | P | organophosphate metabolic process | 0.9 | 1 | |  |
| GO:0019438 | P | aromatic compound biosynthetic process | 1 | 1 | |  |
| GO:0007165 | P | signal transduction | 0.031 | 1 | |  |
| GO:0006950 | P | response to stress | 0.88 | 1 | |  |
| GO:0006807 | P | nitrogen compound metabolic process | 1 | 1 | |  |
| GO:0050789 | P | regulation of biological process | 0.82 | 1 | |  |
| GO:0097659 | P | nucleic acid-templated transcription | 1 | 1 | |  |
| GO:0044267 | P | cellular protein metabolic process | 0.44 | 1 | |  |
| GO:0090304 | P | nucleic acid metabolic process | 1 | 1 | |  |
| GO:0051186 | P | cofactor metabolic process | 0.58 | 1 | |  |
| GO:0044260 | P | cellular macromolecule metabolic process | 0.99 | 1 | |  |
| GO:0006886 | P | intracellular protein transport | 0.16 | 1 | |  |
| GO:0065007 | P | biological regulation | 0.82 | 1 | |  |
| GO:0018130 | P | heterocycle biosynthetic process | 1 | 1 | |  |
| GO:0006812 | P | cation transport | 0.76 | 1 | |  |
| GO:0006811 | P | ion transport | 0.93 | 1 | |  |
| GO:0006810 | P | transport | 0.62 | 1 | |  |
| GO:0009889 | P | regulation of biosynthetic process | 1 | 1 | |  |
| GO:0044710 | P | single-organism metabolic process | 0.41 | 1 | |  |
| GO:0050794 | P | regulation of cellular process | 0.75 | 1 | |  |
| GO:0043412 | P | macromolecule modification | 0.079 | 1 | |  |
| GO:0036211 | P | protein modification process | 0.065 | 1 | |  |
| GO:0008152 | P | metabolic process | 0.58 | 1 | |  |
| GO:0034654 | P | nucleobase-containing compound biosynthetic process | 1 | 1 | |  |
| GO:0051234 | P | establishment of localization | 0.63 | 1 | |  |
| GO:0016070 | P | RNA metabolic process | 1 | 1 | |  |
| GO:0044271 | P | cellular nitrogen compound biosynthetic process | 1 | 1 | |  |
| GO:0046907 | P | intracellular transport | 0.35 | 1 | |  |
| GO:0050896 | P | response to stimulus | 0.66 | 1 | |  |
| GO:0006355 | P | regulation of transcription, DNA-templated | 1 | 1 | |  |
| GO:0010556 | P | regulation of macromolecule biosynthetic process | 1 | 1 | |  |
| GO:0006351 | P | transcription, DNA-templated | 1 | 1 | |  |
| GO:0006518 | P | peptide metabolic process | 0.99 | 1 | |  |
| GO:0032774 | P | RNA biosynthetic process | 1 | 1 | |  |
| GO:0006732 | P | coenzyme metabolic process | 0.36 | 1 | |  |
| GO:0044249 | P | cellular biosynthetic process | 1 | 1 | |  |
| GO:0034641 | P | cellular nitrogen compound metabolic process | 1 | 1 | |  |
| GO:0023052 | P | signaling | 0.031 | 1 | |  |
| GO:0034645 | P | cellular macromolecule biosynthetic process | 1 | 1 | |  |
| GO:0044699 | P | single-organism process | 0.3 | 1 | |  |
| GO:0006139 | P | nucleobase-containing compound metabolic process | 1 | 1 | |  |
| GO:0009987 | P | cellular process | 0.99 | 1 | |  |
| GO:0006725 | P | cellular aromatic compound metabolic process | 1 | 1 | |  |
| GO:1903506 | P | regulation of nucleic acid-templated transcription | 1 | 1 | |  |
| GO:0055085 | P | transmembrane transport | 0.22 | 1 | |  |
| GO:0055086 | P | nucleobase-containing small molecule metabolic process | 0.51 | 1 | |  |
| GO:0043604 | P | amide biosynthetic process | 0.99 | 1 | |  |
| GO:0043603 | P | cellular amide metabolic process | 0.99 | 1 | |  |
| GO:1901135 | P | carbohydrate derivative metabolic process | 0.72 | 1 | |  |
| GO:0051252 | P | regulation of RNA metabolic process | 1 | 1 | |  |
| GO:0043170 | P | macromolecule metabolic process | 0.63 | 1 | |  |
| GO:0031326 | P | regulation of cellular biosynthetic process | 1 | 1 | |  |
| GO:0031323 | P | regulation of cellular metabolic process | 1 | 1 | |  |
| GO:0019752 | P | carboxylic acid metabolic process | 0.72 | 1 | |  |
| GO:0006520 | P | cellular amino acid metabolic process | 0.48 | 1 | |  |
| GO:2000112 | P | regulation of cellular macromolecule biosynthetic process | 1 | 1 | |  |
| GO:0071704 | P | organic substance metabolic process | 0.79 | 1 | |  |
| GO:0010467 | P | gene expression | 1 | 1 | |  |
| GO:0071702 | P | organic substance transport | 0.52 | 1 | |  |
| GO:0010468 | P | regulation of gene expression | 1 | 1 | |  |
| GO:1901576 | P | organic substance biosynthetic process | 1 | 1 | |  |
| GO:0019219 | P | regulation of nucleobase-containing compound metabolic process | 1 | 1 | |  |
| GO:0034613 | P | cellular protein localization | 0.21 | 1 | |  |
| GO:0006464 | P | cellular protein modification process | 0.065 | 1 | |  |
| GO:0009058 | P | biosynthetic process | 1 | 1 | |  |
| GO:0009059 | P | macromolecule biosynthetic process | 1 | 1 | |  |
| GO:0044763 | P | single-organism cellular process | 0.87 | 1 | |  |
| GO:0051171 | P | regulation of nitrogen compound metabolic process | 1 | 1 | |  |
| GO:0051649 | P | establishment of localization in cell | 0.37 | 1 | |  |
| GO:0007154 | P | cell communication | 0.082 | 1 | |  |
| GO:0051179 | P | localization | 0.66 | 1 | |  |
| GO:0051641 | P | cellular localization | 0.44 | 1 | |  |
| GO:0044238 | P | primary metabolic process | 0.86 | 1 | |  |
| GO:0005975 | P | carbohydrate metabolic process | 1 | 1 | |  |
| GO:0044237 | P | cellular metabolic process | 1 | 1 | |  |
| GO:0006796 | P | phosphate-containing compound metabolic process | 0.031 | 1 | |  |
| GO:0006793 | P | phosphorus metabolic process | 0.032 | 1 | |  |
| GO:0015031 | P | protein transport | 0.33 | 1 | |  |
| GO:0006412 | P | translation | 0.99 | 1 | |  |
| GO:0008234 | F | cysteine-type peptidase activity | 1.9e-13 | 1.2e-10 | |  |
| GO:0004523 | F | RNA-DNA hybrid ribonuclease activity | 1.2e-11 | 3.5e-09 | |  |
| GO:0016891 | F | endoribonuclease activity, producing 5'-phosphomonoesters | 6.9e-11 | 1.4e-08 | |  |
| GO:0016893 | F | endonuclease activity, active with either ribo- or deoxyribonucleic acids and producing 5'-phosphomonoesters | 1.5e-10 | 1.6e-08 | |  |
| GO:0008559 | F | xenobiotic-transporting ATPase activity | 1.9e-10 | 1.6e-08 | |  |
| GO:0090484 | F | drug transporter activity | 1.9e-10 | 1.6e-08 | |  |
| GO:0015238 | F | drug transmembrane transporter activity | 1.9e-10 | 1.6e-08 | |  |
| GO:0004540 | F | ribonuclease activity | 3.1e-10 | 2.3e-08 | |  |
| GO:0004521 | F | endoribonuclease activity | 3.9e-10 | 2.6e-08 | |  |
| GO:0004519 | F | endonuclease activity | 1.3e-08 | 8.00E-07 | |  |
| GO:0001871 | F | pattern binding | 4.7e-08 | 2.3e-06 | |  |
| GO:0030247 | F | polysaccharide binding | 4.7e-08 | 2.3e-06 | |  |
| GO:0004470 | F | malic enzyme activity | 1.5e-07 | 6.4e-06 | |  |
| GO:0004471 | F | malate dehydrogenase (decarboxylating) (NAD+) activity | 1.5e-07 | 6.4e-06 | |  |
| GO:0004518 | F | nuclease activity | 3.5e-07 | 1.4e-05 | |  |
| GO:0030246 | F | carbohydrate binding | 5.7e-07 | 2.1e-05 | |  |
| GO:0070011 | F | peptidase activity, acting on L-amino acid peptides | 3.4e-06 | 0.00012 | |  |
| GO:0016615 | F | malate dehydrogenase activity | 5.4e-06 | 0.00018 | |  |
| GO:0008233 | F | peptidase activity | 6.00E-06 | 0.00019 | |  |
| GO:0016616 | F | oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor | 1.6e-05 | 0.00047 | |  |
| GO:0016787 | F | hydrolase activity | 2.7e-05 | 0.00076 | |  |
| GO:0015276 | F | ligand-gated ion channel activity | 4.1e-05 | 0.0011 | |  |
| GO:0022834 | F | ligand-gated channel activity | 4.1e-05 | 0.0011 | |  |
| GO:0016614 | F | oxidoreductase activity, acting on CH-OH group of donors | 5.2e-05 | 0.0013 | |  |
| GO:0003924 | F | GTPase activity | 8.7e-05 | 0.0021 | |  |
| GO:0099600 | F | transmembrane receptor activity | 9.1e-05 | 0.0021 | |  |
| GO:0000166 | F | nucleotide binding | 0.00027 | 0.0055 | |  |
| GO:0035639 | F | purine ribonucleoside triphosphate binding | 0.00025 | 0.0055 | |  |
| GO:1901265 | F | nucleoside phosphate binding | 0.00027 | 0.0055 | |  |
| GO:0060089 | F | molecular transducer activity | 0.00037 | 0.0067 | |  |
| GO:0005525 | F | GTP binding | 0.00037 | 0.0067 | |  |
| GO:0032561 | F | guanyl ribonucleotide binding | 0.00037 | 0.0067 | |  |
| GO:0004872 | F | receptor activity | 0.00037 | 0.0067 | |  |
| GO:0036094 | F | small molecule binding | 0.00038 | 0.0067 | |  |
| GO:0019001 | F | guanyl nucleotide binding | 0.0005 | 0.0084 | |  |
| GO:0051287 | F | NAD binding | 0.00052 | 0.0085 | |  |
| GO:0017111 | F | nucleoside-triphosphatase activity | 0.00055 | 0.0088 | |  |
| GO:0032553 | F | ribonucleotide binding | 0.0006 | 0.0094 | |  |
| GO:0003824 | F | catalytic activity | 0.00074 | 0.011 | |  |
| GO:0097367 | F | carbohydrate derivative binding | 0.00081 | 0.012 | |  |
| GO:0032555 | F | purine ribonucleotide binding | 0.00093 | 0.012 | |  |
| GO:0032550 | F | purine ribonucleoside binding | 0.00093 | 0.012 | |  |
| GO:0016820 | F | hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances | 0.00089 | 0.012 | |  |
| GO:0042626 | F | ATPase activity, coupled to transmembrane movement of substances | 0.00089 | 0.012 | |  |
| GO:0043492 | F | ATPase activity, coupled to movement of substances | 0.00089 | 0.012 | |  |
| GO:0001883 | F | purine nucleoside binding | 0.00093 | 0.012 | |  |
| GO:0016462 | F | pyrophosphatase activity | 0.00097 | 0.012 | |  |
| GO:0032549 | F | ribonucleoside binding | 0.001 | 0.012 | |  |
| GO:0017076 | F | purine nucleotide binding | 0.001 | 0.012 | |  |
| GO:0001882 | F | nucleoside binding | 0.001 | 0.012 | |  |
| GO:0050662 | F | coenzyme binding | 0.0011 | 0.012 | |  |
| GO:0016818 | F | hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides | 0.0011 | 0.013 | |  |
| GO:0022836 | F | gated channel activity | 0.0012 | 0.013 | |  |
| GO:0016817 | F | hydrolase activity, acting on acid anhydrides | 0.0013 | 0.014 | |  |
| GO:0015405 | F | P-P-bond-hydrolysis-driven transmembrane transporter activity | 0.0017 | 0.018 | |  |
| GO:0015399 | F | primary active transmembrane transporter activity | 0.0017 | 0.018 | |  |
| GO:0048037 | F | cofactor binding | 0.0017 | 0.018 | |  |
| GO:0042910 | F | xenobiotic transporter activity | 0.0031 | 0.031 | |  |
| GO:0016887 | F | ATPase activity | 0.0033 | 0.033 | |  |
| GO:0005509 | F | calcium ion binding | 0.0033 | 0.033 | |  |
| GO:0022803 | F | passive transmembrane transporter activity | 0.0053 | 0.051 | |  |
| GO:0015267 | F | channel activity | 0.0053 | 0.051 | |  |
| GO:0042623 | F | ATPase activity, coupled | 0.0056 | 0.053 | |  |
| GO:0016788 | F | hydrolase activity, acting on ester bonds | 0.006 | 0.056 | |  |
| GO:0005524 | F | ATP binding | 0.0065 | 0.06 | |  |
| GO:0004672 | F | protein kinase activity | 0.0076 | 0.068 | |  |
| GO:0005216 | F | ion channel activity | 0.0078 | 0.068 | |  |
| GO:0022838 | F | substrate-specific channel activity | 0.0078 | 0.068 | |  |
| GO:0016491 | F | oxidoreductase activity | 0.0082 | 0.071 | |  |
| GO:0016684 | F | oxidoreductase activity, acting on peroxide as acceptor | 0.01 | 0.085 | |  |
| GO:1901363 | F | heterocyclic compound binding | 0.012 | 0.1 | |  |
| GO:0097159 | F | organic cyclic compound binding | 0.012 | 0.1 | |  |
| GO:0016773 | F | phosphotransferase activity, alcohol group as acceptor | 0.013 | 0.11 | |  |
| GO:0016209 | F | antioxidant activity | 0.018 | 0.14 | |  |
| GO:0030554 | F | adenyl nucleotide binding | 0.018 | 0.14 | |  |
| GO:0032559 | F | adenyl ribonucleotide binding | 0.018 | 0.14 | |  |
| GO:0016301 | F | kinase activity | 0.021 | 0.16 | |  |
| GO:0016903 | F | oxidoreductase activity, acting on the aldehyde or oxo group of donors | 0.032 | 0.24 | |  |
| GO:0005215 | F | transporter activity | 0.034 | 0.26 | |  |
| GO:0016772 | F | transferase activity, transferring phosphorus-containing groups | 0.047 | 0.35 | |  |
| GO:0022857 | F | transmembrane transporter activity | 0.063 | 0.46 | |  |
| GO:0004601 | F | peroxidase activity | 0.066 | 0.48 | |  |
| GO:0016853 | F | isomerase activity | 0.09 | 0.64 | |  |
| GO:0022892 | F | substrate-specific transporter activity | 0.098 | 0.69 | |  |
| GO:0022804 | F | active transmembrane transporter activity | 0.11 | 0.74 | |  |
| GO:0005488 | F | binding | 0.12 | 0.85 | |  |
| GO:0008236 | F | serine-type peptidase activity | 0.22 | 1 | |  |
| GO:0016740 | F | transferase activity | 0.51 | 1 | |  |
| GO:0016741 | F | transferase activity, transferring one-carbon groups | 0.49 | 1 | |  |
| GO:0017171 | F | serine hydrolase activity | 0.22 | 1 | |  |
| GO:0003723 | F | RNA binding | 0.92 | 1 | |  |
| GO:0003677 | F | DNA binding | 1 | 1 | |  |
| GO:0008168 | F | methyltransferase activity | 0.41 | 1 | |  |
| GO:0016757 | F | transferase activity, transferring glycosyl groups | 0.81 | 1 | |  |
| GO:0020037 | F | heme binding | 0.93 | 1 | |  |
| GO:0043169 | F | cation binding | 0.98 | 1 | |  |
| GO:0015075 | F | ion transmembrane transporter activity | 0.18 | 1 | |  |
| GO:0042578 | F | phosphoric ester hydrolase activity | 0.42 | 1 | |  |
| GO:0043168 | F | anion binding | 0.37 | 1 | |  |
| GO:0016705 | F | oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen | 0.84 | 1 | |  |
| GO:0043167 | F | ion binding | 0.96 | 1 | |  |
| GO:0005506 | F | iron ion binding | 0.83 | 1 | |  |
| GO:0009055 | F | electron carrier activity | 0.29 | 1 | |  |
| GO:0022891 | F | substrate-specific transmembrane transporter activity | 0.19 | 1 | |  |
| GO:0046906 | F | tetrapyrrole binding | 0.93 | 1 | |  |
| GO:0046872 | F | metal ion binding | 0.99 | 1 | |  |
| GO:0005515 | F | protein binding | 0.93 | 1 | |  |
| GO:0004175 | F | endopeptidase activity | 0.61 | 1 | |  |
| GO:0003676 | F | nucleic acid binding | 0.47 | 1 | |  |
| GO:0005198 | F | structural molecule activity | 0.84 | 1 | |  |
| GO:0003735 | F | structural constituent of ribosome | 0.9 | 1 | |  |
| GO:0046914 | F | transition metal ion binding | 1 | 1 | |  |
| GO:0030529 | C | intracellular ribonucleoprotein complex | 0.93 | 1 | |  |
| GO:0016021 | C | integral component of membrane | 0.6 | 1 | |  |
| GO:0016020 | C | membrane | 0.8 | 1 | |  |
| GO:0044422 | C | organelle part | 1 | 1 | |  |
| GO:0043234 | C | protein complex | 1 | 1 | |  |
| GO:0043231 | C | intracellular membrane-bounded organelle | 1 | 1 | |  |
| GO:1990904 | C | ribonucleoprotein complex | 0.94 | 1 | |  |
| GO:0043232 | C | intracellular non-membrane-bounded organelle | 1 | 1 | |  |
| GO:0043229 | C | intracellular organelle | 1 | 1 | |  |
| GO:0005622 | C | intracellular | 1 | 1 | |  |
| GO:0043227 | C | membrane-bounded organelle | 1 | 1 | |  |
| GO:0031224 | C | intrinsic component of membrane | 0.62 | 1 | |  |
| GO:0044425 | C | membrane part | 0.55 | 1 | |  |
| GO:0005840 | C | ribosome | 0.82 | 1 | |  |
| GO:0044444 | C | cytoplasmic part | 0.99 | 1 | |  |
| GO:0032991 | C | macromolecular complex | 1 | 1 | |  |
| GO:0044464 | C | cell part | 1 | 1 | |  |
| GO:0005623 | C | cell | 1 | 1 | |  |
| GO:0043228 | C | non-membrane-bounded organelle | 1 | 1 | |  |
| GO:0005737 | C | cytoplasm | 0.97 | 1 | |  |
| GO:0044424 | C | intracellular part | 1 | 1 | |  |
| GO:0044446 | C | intracellular organelle part | 1 | 1 | |  |
| GO:0098796 | C | membrane protein complex | 0.43 | 1 | |  |
| GO:0043226 | C | organelle | 1 | 1 | |  |