

Supplementary table 4: SLE Type 1/2 MEGENA module STRING statistics

| <i>mod.name</i> | <i>mod.annot</i> | <i>pcnt.PPI</i> | <i>mod.size</i> | <i>corr.type2</i> | <i>corr.SLEDAI</i> | <i>corr.PSD</i> | <i>num_nodes</i> | <i>num_edges</i> | <i>node_degree</i> | <i>p_value</i> |
|-----------------|---|-----------------|-----------------|-------------------|--------------------|-----------------|------------------|------------------|--------------------|----------------|
| 6.42.256.459 | Cell.Cycle. cell.cycle | 0.706 | 32 | -0.5448 | 0.3917 | -0.6619 | 30 | 194 | 12.93 | 0 |
| 10.157.367.514 | oxidative.phosphorylation,purine.nucleoside.triphosphate.metabolic.process | 0.65 | 23 | 0.513 | -0.5733 | 0.4006 | 20 | 78 | 7.8 | 0 |
| 6.42.256 | Cell.Cycle. mitotic.cell.cycle | 0.578 | 73 | -0.5919 | 0.4174 | -0.6903 | 60 | 498 | 16.6 | 0 |
| 10.157.367 | oxidative.phosphorylation,respiratory.chain | 0.577 | 32 | 0.5149 | -0.5866 | 0.3844 | 24 | 79 | 6.58 | 0 |
| 6.42 | Cell.Cycle. cell.cycle | 0.573 | 80 | -0.5739 | 0.3981 | -0.6778 | 65 | 521 | 16.03 | 0 |
| 6.36 | Monocyte. response.to.virus | 0.455 | 330 | -0.4474 | 0.447 | -0.3717 | 256 | 760 | 5.94 | 0 |
| 3.15.175.386 | Neutrophil. neutrophil.activation.involved.in.immune.response | 0.414 | 80 | -0.3746 | 0.2506 | -0.3084 | 67 | 128 | 3.82 | 0 |
| 6.36.230.438 | IFN. response.to.virus | 0.408 | 105 | -0.4013 | 0.3998 | -0.3051 | 81 | 251 | 6.2 | 0 |
| 6.36.230 | Monocyte. response.to.virus | 0.394 | 160 | -0.4321 | 0.4362 | -0.3456 | 126 | 465 | 7.38 | 0 |
| 10.157 | oxidative.phosphorylation,respiratory.chain | 0.385 | 57 | 0.4416 | -0.5346 | 0.3285 | 36 | 81 | 4.5 | 0 |
| 6.36.235 | transferase.activity,transferring.hexosyl.groups,protein.glycosylation | 0.385 | 54 | -0.523 | 0.508 | -0.4702 | 39 | 11 | 0.56 | 0.00025 |
| 6.36.230.439 | IFN. reg.of.viral.life.cycle | 0.316 | 27 | -0.4734 | 0.4735 | -0.3872 | 23 | 24 | 2.09 | 0 |
| 3.20 | Mono.Secreted. synapse.pruning | 0.31 | 38 | 0.5605 | -0.6045 | 0.5063 | 29 | 7 | 0.48 | 0.0024 |
| 5.22.218 | B.cells. cytokinesis | 0.3 | 41 | 0.3967 | -0.2124 | 0.4683 | 32 | 13 | 0.81 | 0.00000166 |
| 6.36.234 | extracellular.region,vesicle | 0.3 | 25 | -0.4665 | 0.5289 | -0.2784 | 20 | 4 | 0.4 | 0.0034 |
| 6.40 | cation.transmembrane.transporter.activity,carnitine.shuttle | 0.287 | 43 | 0.4326 | 0 | 0.2189 | 29 | 8 | 0.55 | 0.000079 |
| 6.40.252 | inflammatory.response,L-type.voltage-gated.calcium.channel.complex | 0.281 | 25 | 0.4767 | -0.2004 | 0.2681 | 19 | 5 | 0.53 | 0.00011 |
| 3.19.211 | small.molecule.biosynthetic.process,cellular.response.to.steroid.hormone.stimulus | 0.272 | 35 | -0.3821 | 0.2373 | 0 | 27 | 7 | 0.52 | 0.0043 |
| 7.49.271.472 | cellular.response.to.endogenous.stimulus,metal.ion.transmembrane.transporter.activity | 0.235 | 20 | 0.4631 | -0.4173 | 0.6095 | 17 | 2 | 0.24 | 0.0581 |
| 6.35.228 | protein-DNA.complex,chromatin | 0.233 | 77 | -0.3728 | 0.333 | -0.407 | 61 | 16 | 0.52 | 0.0042 |
| 6.37 | cerebral.cortex.radial.glia.guided.migration,telencephalon.glia.cell.migration | 0.231 | 92 | -0.5786 | 0.5231 | -0.4318 | 60 | 22 | 0.73 | 0.0000249 |
| 3.18 | T.cell. reg.of.neuron.death | 0.224 | 109 | -0.4121 | 0.3929 | -0.4392 | 76 | 20 | 0.53 | 0.0833 |
| 9.100.332 | cytosolic.large.ribosomal.subunit,structural.constituent.of.ribosome | 0.222 | 39 | 0.36 | 0 | 0.3609 | 18 | 2 | 0.22 | 0.3561 |
| 7.49.271.471 | posttranscriptional.reg.of.gene.expression,protein.targeting | 0.222 | 27 | 0.368 | -0.3951 | 0.644 | 24 | 5 | 0.42 | 0.1245 |
| 6.35.228.433 | nucleosome,DNA.packaging.complex | 0.202 | 42 | -0.3811 | 0.3303 | -0.3702 | 33 | 9 | 0.55 | 0.0172 |
| 3.20.216 | muscle.structure.development,muscle.organ.development | 0.2 | 24 | 0.6103 | -0.6323 | 0.5124 | 20 | 2 | 0.2 | 0.2141 |
| 6.37.240 | neurotransmitter.metabolic.process,reg.of.Wnt.signaling.pathway | 0.19 | 33 | -0.4776 | 0.373 | -0.3266 | 21 | 2 | 0.19 | 0.2795 |
| 6.37.239 | Rho.GTPase.binding,Rac.GTPase.binding | 0.174 | 32 | -0.6226 | 0.6181 | -0.4897 | 23 | 2 | 0.17 | 0.0996 |
| 10.158.371 | animal.organ.morphogenesis,reg.of.Wnt.signaling.pathway | 0.167 | 28 | -0.3681 | 0.4561 | -0.3992 | 24 | 2 | 0.17 | 0.1439 |
| 3.18.209 | cell.diff,polymeric.cytoskeletal.fiber | 0.15 | 53 | -0.5183 | 0.5029 | -0.5311 | 40 | 9 | 0.45 | 0.213 |
| 8.75 | phospholipid.transporter.activity,phospholipid.transport | 0.133 | 20 | -0.4442 | 0.4263 | -0.479 | 15 | 1 | 0.13 | 0.414 |
| 9.110 | spindle,C-5.sterol.desaturase.activity | 0.114 | 45 | 0.4903 | -0.3981 | 0.4448 | 35 | 2 | 0.11 | 0.4617 |
| 3.18.209.408 | reg.of.anatomical.structure.morphogenesis,forebrain.development | 0.108 | 49 | -0.5219 | 0.5038 | -0.5324 | 37 | 8 | 0.43 | 0.0749 |
| 8.76 | reg.of.apoptotic.signaling.pathway,pos.reg.of.apoptotic.signaling.pathway | 0.095 | 35 | -0.3597 | 0.3634 | -0.3104 | 21 | 1 | 0.1 | 0.6245 |
| 8.52 | meiotic.gene.conversion,gene.conversion | 0 | 27 | -0.3966 | 0.3193 | -0.3831 | 9 | 0 | 0 | 1 |
| 9.98 | reg.of.gene.expression,protein.localization.to.endoplasmic.reticulum | 0 | 20 | 0.4328 | -0.1893 | 0.3472 | 10 | 0 | 0 | 1 |
| 9.128 | reg.of.axon.extension,axon.extension | 0 | 22 | 0.4165 | -0.3147 | 0.3229 | 12 | 0 | 0 | 1 |
| 3.19.214 | pos.reg.of.antimicrobial.peptide.production,reg.of.antimicrobial.humoral.response | 0 | 21 | -0.41 | 0.3839 | -0.3093 | 14 | 0 | 0 | 1 |
| 9.110.349 | C-5.sterol.desaturase.activity,mannose.binding | 0 | 29 | 0.5126 | -0.4017 | 0.4991 | 24 | 0 | 0 | 1 |
| 9.110.349.510 | C-5.sterol.desaturase.activity,protein.localization.to.paranode.region.of.axon | 0 | 25 | 0.474 | -0.3596 | 0.4562 | 21 | 0 | 0 | 1 |