

## APPENDIX S2

# MeSH over-representation analysis (Swine)

This is a reproducible report written by an R Markdown.

### 1. Create a vector of background (universe) genes

We first create a vector of all genes.

```
library(biomaRt)
## access to biomaRt
mart <- useMart(biomart = "ensembl", dataset = "sscrofa_gene_ensembl")
univ.geneID <- getBM(attributes=c("ensembl_gene_id", "entrezgene", "hgnc_symbol"), mart = mart) # 27243
## remove genes with no corresponding Entrez Gene ID
univ.geneID2 <- univ.geneID[!is.na(univ.geneID[,2]),] # 18251
## remove duplicated Entrez Gene ID
univ.geneID3 <- univ.geneID2[!duplicated(univ.geneID2[,2]),] # 17130
```

### 2. Create a vector of significant genes

Secondly, we create a vector of significant genes by reading the file *sscGenes.txt*.

```
## read data
genes.ssc <- read.table("sscGenes2.txt", colClasses = c("character", rep("NULL", 5)), fill=TRUE,
                        header=FALSE, stringsAsFactors=FALSE)
colnames(genes.ssc) <- "ensembl_gene_id"
## merge two files
my.geneID <- merge(genes.ssc, univ.geneID3, by = "ensembl_gene_id") # 155
## remove duplicated Entrez Gene ID
my.geneID2 <- my.geneID[!duplicated(my.geneID$entrezgene),] # 152
```

### 3. GO enrichment analysis

We perform a GO analysis via the *GOstats* package.

```
library("org.Ss.eg.db")
library("GOstats")
paraGO <- new("GOHyperGParams", geneIds=my.geneID2[,2], universeGeneIds=univ.geneID3[,2],
              annotation="org.Ss.eg.db", ontology="BP", pvalueCutoff=0.05,
              conditional=TRUE, testDirection="over")
```

GO enrichment analysis for BP

```
BP <- hyperGTest(paraGO)
summary(BP)[,c(1,2,7)]
```

```
##           GOBPID           Pvalue
## 1   GO:0002125 2.414211e-06
## 2   GO:0070493 2.073360e-05
```

## 3 GO:0042631 7.252975e-05  
## 4 GO:2000484 7.252975e-05  
## 5 GO:0001992 2.163746e-04  
## 6 GO:0007621 2.163746e-04  
## 7 GO:0031394 2.163746e-04  
## 8 GO:0051970 2.163746e-04  
## 9 GO:2000778 2.163746e-04  
## 10 GO:0032849 4.303350e-04  
## 11 GO:0042711 4.303350e-04  
## 12 GO:2001279 4.303350e-04  
## 13 GO:0006112 4.865599e-04  
## 14 GO:0007204 5.818235e-04  
## 15 GO:0045819 7.132263e-04  
## 16 GO:0060180 7.132263e-04  
## 17 GO:0003015 7.462577e-04  
## 18 GO:0060986 8.312094e-04  
## 19 GO:0006506 9.499953e-04  
## 20 GO:0051459 1.040437e-03  
## 21 GO:0014049 1.063879e-03  
## 22 GO:0035810 1.063879e-03  
## 23 GO:0042713 1.063879e-03  
## 24 GO:0009251 1.218596e-03  
## 25 GO:0044247 1.218596e-03  
## 26 GO:0003084 1.481137e-03  
## 27 GO:0035025 1.481137e-03  
## 28 GO:0048523 1.522633e-03  
## 29 GO:0005976 1.597594e-03  
## 30 GO:0006664 1.920400e-03  
## 31 GO:0035815 1.963859e-03  
## 32 GO:0007625 2.510921e-03  
## 33 GO:0009415 2.510921e-03  
## 34 GO:0043084 2.510921e-03  
## 35 GO:2001244 2.510921e-03  
## 36 GO:0008272 3.121207e-03  
## 37 GO:0015939 3.121207e-03  
## 38 GO:0045723 3.121207e-03  
## 39 GO:0045907 3.121207e-03  
## 40 GO:0046457 3.121207e-03  
## 41 GO:0006874 3.137600e-03  
## 42 GO:0043270 3.319385e-03  
## 43 GO:0042158 3.534758e-03  
## 44 GO:0051209 3.534758e-03  
## 45 GO:0051282 3.534758e-03  
## 46 GO:0034329 3.622341e-03  
## 47 GO:0072507 4.522534e-03  
## 48 GO:0010460 4.527078e-03  
## 49 GO:0008645 4.633205e-03  
## 50 GO:0007015 4.767898e-03  
## 51 GO:0016053 4.770176e-03  
## 52 GO:0008643 6.006432e-03  
## 53 GO:0006693 6.172849e-03  
## 54 GO:0032892 6.172849e-03  
## 55 GO:0035338 6.172849e-03  
## 56 GO:0044062 6.172849e-03

## 57 GO:0051955 6.172849e-03  
## 58 GO:0044724 6.518355e-03  
## 59 GO:0044705 7.083061e-03  
## 60 GO:0006073 7.502866e-03  
## 61 GO:0042462 8.050112e-03  
## 62 GO:0051412 8.050112e-03  
## 63 GO:0031323 8.258403e-03  
## 64 GO:0000023 8.564280e-03  
## 65 GO:0002534 8.564280e-03  
## 66 GO:0002741 8.564280e-03  
## 67 GO:0005985 8.564280e-03  
## 68 GO:0006408 8.564280e-03  
## 69 GO:0009733 8.564280e-03  
## 70 GO:0009845 8.564280e-03  
## 71 GO:0010804 8.564280e-03  
## 72 GO:0035865 8.564280e-03  
## 73 GO:0035926 8.564280e-03  
## 74 GO:0042450 8.564280e-03  
## 75 GO:0043181 8.564280e-03  
## 76 GO:0043311 8.564280e-03  
## 77 GO:0046833 8.564280e-03  
## 78 GO:0050652 8.564280e-03  
## 79 GO:0051460 8.564280e-03  
## 80 GO:0060588 8.564280e-03  
## 81 GO:0070948 8.564280e-03  
## 82 GO:0070950 8.564280e-03  
## 83 GO:0070961 8.564280e-03  
## 84 GO:0070963 8.564280e-03  
## 85 GO:0071314 8.564280e-03  
## 86 GO:0071638 8.564280e-03  
## 87 GO:0072643 8.564280e-03  
## 88 GO:0090198 8.564280e-03  
## 89 GO:0097029 8.564280e-03  
## 90 GO:1900011 8.564280e-03  
## 91 GO:2000405 8.564280e-03  
## 92 GO:0031644 9.072985e-03  
## 93 GO:0051954 9.072985e-03  
## 94 GO:0010907 1.015067e-02  
## 95 GO:0035337 1.015067e-02  
## 96 GO:0046326 1.015067e-02  
## 97 GO:0044706 1.092574e-02  
## 98 GO:0060401 1.099555e-02  
## 99 GO:0035176 1.128218e-02  
## 100 GO:0045851 1.128218e-02  
## 101 GO:0055078 1.128218e-02  
## 102 GO:0010827 1.155903e-02  
## 103 GO:0006091 1.182295e-02  
## 104 GO:0061564 1.182295e-02  
## 105 GO:0044260 1.216307e-02  
## 106 GO:0051057 1.246654e-02  
## 107 GO:0051238 1.246654e-02  
## 108 GO:0002791 1.287311e-02  
## 109 GO:0072330 1.287311e-02  
## 110 GO:0030154 1.325425e-02

## 111 GO:0034332 1.334813e-02  
## 112 GO:0051453 1.370278e-02  
## 113 GO:0055082 1.452474e-02  
## 114 GO:0006084 1.498993e-02  
## 115 GO:0007618 1.498993e-02  
## 116 GO:0014068 1.498993e-02  
## 117 GO:1901879 1.498993e-02  
## 118 GO:0046474 1.666274e-02  
## 119 GO:0048812 1.682329e-02  
## 120 GO:0001771 1.705603e-02  
## 121 GO:0002248 1.705603e-02  
## 122 GO:0006478 1.705603e-02  
## 123 GO:0007402 1.705603e-02  
## 124 GO:0009438 1.705603e-02  
## 125 GO:0010015 1.705603e-02  
## 126 GO:0010054 1.705603e-02  
## 127 GO:0022622 1.705603e-02  
## 128 GO:0034137 1.705603e-02  
## 129 GO:0034140 1.705603e-02  
## 130 GO:0034141 1.705603e-02  
## 131 GO:0034351 1.705603e-02  
## 132 GO:0035089 1.705603e-02  
## 133 GO:0042256 1.705603e-02  
## 134 GO:0043148 1.705603e-02  
## 135 GO:0048149 1.705603e-02  
## 136 GO:0048765 1.705603e-02  
## 137 GO:0048767 1.705603e-02  
## 138 GO:0050653 1.705603e-02  
## 139 GO:0060252 1.705603e-02  
## 140 GO:0060385 1.705603e-02  
## 141 GO:0061339 1.705603e-02  
## 142 GO:0072608 1.705603e-02  
## 143 GO:0097211 1.705603e-02  
## 144 GO:2000098 1.705603e-02  
## 145 GO:0048667 1.736729e-02  
## 146 GO:0070873 1.771326e-02  
## 147 GO:0046467 1.810621e-02  
## 148 GO:0048699 1.812233e-02  
## 149 GO:0050880 1.885329e-02  
## 150 GO:0043471 1.914757e-02  
## 151 GO:0051592 1.961729e-02  
## 152 GO:0032642 2.062912e-02  
## 153 GO:0045913 2.062912e-02  
## 154 GO:1901570 2.062912e-02  
## 155 GO:0030072 2.166283e-02  
## 156 GO:0003044 2.215699e-02  
## 157 GO:0030004 2.215699e-02  
## 158 GO:0060048 2.215699e-02  
## 159 GO:0006766 2.284293e-02  
## 160 GO:0009311 2.373031e-02  
## 161 GO:0005975 2.399894e-02  
## 162 GO:0010256 2.401274e-02  
## 163 GO:0044262 2.524357e-02  
## 164 GO:0046883 2.524357e-02

## 165 GO:0070830 2.534820e-02  
## 166 GO:0071616 2.534820e-02  
## 167 GO:0002086 2.547586e-02  
## 168 GO:0002888 2.547586e-02  
## 169 GO:0006434 2.547586e-02  
## 170 GO:0006975 2.547586e-02  
## 171 GO:0030836 2.547586e-02  
## 172 GO:0032930 2.547586e-02  
## 173 GO:0045197 2.547586e-02  
## 174 GO:0048865 2.547586e-02  
## 175 GO:0050774 2.547586e-02  
## 176 GO:0060022 2.547586e-02  
## 177 GO:0060100 2.547586e-02  
## 178 GO:0070286 2.547586e-02  
## 179 GO:0090594 2.547586e-02  
## 180 GO:1902566 2.547586e-02  
## 181 GO:0044272 2.634016e-02  
## 182 GO:0046488 2.634016e-02  
## 183 GO:0045055 2.700981e-02  
## 184 GO:0019318 2.781812e-02  
## 185 GO:0032677 2.871429e-02  
## 186 GO:0046530 2.871429e-02  
## 187 GO:0015833 3.124993e-02  
## 188 GO:0045017 3.235683e-02  
## 189 GO:0048666 3.301916e-02  
## 190 GO:0032535 3.311166e-02  
## 191 GO:0051705 3.316839e-02  
## 192 GO:0051129 3.342271e-02  
## 193 GO:0010642 3.382437e-02  
## 194 GO:0014012 3.382437e-02  
## 195 GO:0021554 3.382437e-02  
## 196 GO:0030432 3.382437e-02  
## 197 GO:0034145 3.382437e-02  
## 198 GO:0048539 3.382437e-02  
## 199 GO:0051895 3.382437e-02  
## 200 GO:0060287 3.382437e-02  
## 201 GO:2000144 3.382437e-02  
## 202 GO:2000310 3.382437e-02  
## 203 GO:2000353 3.382437e-02  
## 204 GO:0002367 3.407657e-02  
## 205 GO:0021675 3.407657e-02  
## 206 GO:0050707 3.407657e-02  
## 207 GO:0048589 3.492128e-02  
## 208 GO:0032880 3.521664e-02  
## 209 GO:0044255 3.566352e-02  
## 210 GO:0044057 3.724675e-02  
## 211 GO:0019432 3.785067e-02  
## 212 GO:0030029 3.900379e-02  
## 213 GO:0003014 3.979510e-02  
## 214 GO:0007202 3.979510e-02  
## 215 GO:0010923 3.979510e-02  
## 216 GO:0030193 3.979510e-02  
## 217 GO:0046460 3.979510e-02  
## 218 GO:1900274 3.979510e-02

## 219 GO:2001233 3.979510e-02  
 ## 220 GO:0032990 4.049854e-02  
 ## 221 GO:0080090 4.117167e-02  
 ## 222 GO:0045823 4.121869e-02  
 ## 223 GO:0031344 4.129751e-02  
 ## 224 GO:0071356 4.177676e-02  
 ## 225 GO:0072659 4.177676e-02  
 ## 226 GO:0002278 4.210215e-02  
 ## 227 GO:0002447 4.210215e-02  
 ## 228 GO:0006527 4.210215e-02  
 ## 229 GO:0006684 4.210215e-02  
 ## 230 GO:0031579 4.210215e-02  
 ## 231 GO:0050655 4.210215e-02  
 ## 232 GO:0051709 4.210215e-02  
 ## 233 GO:0051873 4.210215e-02  
 ## 234 GO:0061099 4.210215e-02  
 ## 235 GO:0061245 4.210215e-02  
 ## 236 GO:0090224 4.210215e-02  
 ## 237 GO:0008217 4.302025e-02  
 ## 238 GO:0031960 4.302025e-02  
 ## 239 GO:0040011 4.367228e-02  
 ## 240 GO:0051146 4.420330e-02  
 ## 241 GO:0055114 4.439665e-02  
 ## 242 GO:2000021 4.535415e-02  
 ## 243 GO:0002683 4.540255e-02  
 ## 244 GO:0009914 4.648659e-02  
 ## 245 GO:0008152 4.660552e-02  
 ## 246 GO:0032956 4.661793e-02  
 ## 247 GO:0043436 4.723082e-02  
 ## 248 GO:0030003 4.742850e-02

##

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Term  
 maternal aggressive behavior  
 thrombin receptor signaling pathway  
 cellular response to water deprivation  
 positive regulation of interleukin-8 secretion  
 regulation of systemic arterial blood pressure by vasopressin  
 negative regulation of female receptivity  
 positive regulation of prostaglandin biosynthetic process  
 negative regulation of transmission of nerve impulse  
 positive regulation of interleukin-6 secretion  
 positive regulation of cellular pH reduction  
 maternal behavior  
 regulation of unsaturated fatty acid biosynthetic process  
 energy reserve metabolic process  
 positive regulation of cytosolic calcium ion concentration  
 positive regulation of glycogen catabolic process  
 female mating behavior  
 heart process  
 endocrine hormone secretion  
 GPI anchor biosynthetic process  
 regulation of corticotropin secretion  
 positive regulation of glutamate secretion  
 positive regulation of urine volume  
 sperm ejaculation

## 24 glucan catabolic process  
 ## 25 cellular polysaccharide catabolic process  
 ## 26 positive regulation of systemic arterial blood pressure  
 ## 27 positive regulation of Rho protein signal transduction  
 ## 28 negative regulation of cellular process  
 ## 29 polysaccharide metabolic process  
 ## 30 glycolipid metabolic process  
 ## 31 positive regulation of renal sodium excretion  
 ## 32 grooming behavior  
 ## 33 response to water  
 ## 34 penile erection  
 ## 35 positive regulation of intrinsic apoptotic signaling pathway  
 ## 36 sulfate transport  
 ## 37 pantothenate metabolic process  
 ## 38 positive regulation of fatty acid biosynthetic process  
 ## 39 positive regulation of vasoconstriction  
 ## 40 prostanoid biosynthetic process  
 ## 41 cellular calcium ion homeostasis  
 ## 42 positive regulation of ion transport  
 ## 43 lipoprotein biosynthetic process  
 ## 44 release of sequestered calcium ion into cytosol  
 ## 45 regulation of sequestering of calcium ion  
 ## 46 cell junction assembly  
 ## 47 divalent inorganic cation homeostasis  
 ## 48 positive regulation of heart rate  
 ## 49 hexose transport  
 ## 50 actin filament organization  
 ## 51 organic acid biosynthetic process  
 ## 52 carbohydrate transport  
 ## 53 prostaglandin metabolic process  
 ## 54 positive regulation of organic acid transport  
 ## 55 long-chain fatty-acyl-CoA biosynthetic process  
 ## 56 regulation of excretion  
 ## 57 regulation of amino acid transport  
 ## 58 single-organism carbohydrate catabolic process  
 ## 59 multi-organism reproductive behavior  
 ## 60 cellular glucan metabolic process  
 ## 61 eye photoreceptor cell development  
 ## 62 response to corticosterone  
 ## 63 regulation of cellular metabolic process  
 ## 64 maltose metabolic process  
 ## 65 cytokine production involved in inflammatory response  
 ## 66 positive regulation of cytokine secretion involved in immune response  
 ## 67 sucrose metabolic process  
 ## 68 snRNA export from nucleus  
 ## 69 response to auxin  
 ## 70 seed germination  
 ## 71 negative regulation of tumor necrosis factor-mediated signaling pathway  
 ## 72 cellular response to potassium ion  
 ## 73 chemokine (C-C motif) ligand 2 secretion  
 ## 74 arginine biosynthetic process via ornithine  
 ## 75 vacuolar sequestering  
 ## 76 positive regulation of eosinophil degranulation  
 ## 77 positive regulation of RNA export from nucleus

## 78 dermatan sulfate proteoglycan biosynthetic process, polysaccharide chain biosynthetic process  
 ## 79 negative regulation of corticotropin secretion  
 ## 80 negative regulation of lipoprotein lipid oxidation  
 ## 81 regulation of neutrophil mediated cytotoxicity  
 ## 82 regulation of neutrophil mediated killing of bacterium  
 ## 83 positive regulation of neutrophil mediated killing of symbiont cell  
 ## 84 positive regulation of neutrophil mediated killing of gram-negative bacterium  
 ## 85 cellular response to cocaine  
 ## 86 negative regulation of monocyte chemotactic protein-1 production  
 ## 87 interferon-gamma secretion  
 ## 88 negative regulation of chemokine secretion  
 ## 89 mature dendritic cell differentiation  
 ## 90 negative regulation of corticotropin-releasing hormone receptor activity  
 ## 91 negative regulation of T cell migration  
 ## 92 regulation of neurological system process  
 ## 93 positive regulation of amine transport  
 ## 94 positive regulation of glucose metabolic process  
 ## 95 fatty-acyl-CoA metabolic process  
 ## 96 positive regulation of glucose import  
 ## 97 multi-multicellular organism process  
 ## 98 cytosolic calcium ion transport  
 ## 99 social behavior  
 ## 100 pH reduction  
 ## 101 sodium ion homeostasis  
 ## 102 regulation of glucose transport  
 ## 103 generation of precursor metabolites and energy  
 ## 104 axon development  
 ## 105 cellular macromolecule metabolic process  
 ## 106 positive regulation of small GTPase mediated signal transduction  
 ## 107 sequestering of metal ion  
 ## 108 regulation of peptide secretion  
 ## 109 monocarboxylic acid biosynthetic process  
 ## 110 cell differentiation  
 ## 111 adherens junction organization  
 ## 112 regulation of intracellular pH  
 ## 113 cellular chemical homeostasis  
 ## 114 acetyl-CoA metabolic process  
 ## 115 mating  
 ## 116 positive regulation of phosphatidylinositol 3-kinase signaling  
 ## 117 regulation of protein depolymerization  
 ## 118 glycerophospholipid biosynthetic process  
 ## 119 neuron projection morphogenesis  
 ## 120 immunological synapse formation  
 ## 121 connective tissue replacement involved in inflammatory response wound healing  
 ## 122 peptidyl-tyrosine sulfation  
 ## 123 ganglion mother cell fate determination  
 ## 124 methylglyoxal metabolic process  
 ## 125 root morphogenesis  
 ## 126 trichoblast differentiation  
 ## 127 root system development  
 ## 128 positive regulation of toll-like receptor 2 signaling pathway  
 ## 129 negative regulation of toll-like receptor 3 signaling pathway  
 ## 130 positive regulation of toll-like receptor 3 signaling pathway  
 ## 131 negative regulation of glial cell apoptotic process



## 132 establishment of apical/basal cell polarity  
 ## 133 mature ribosome assembly  
 ## 134 mitotic spindle stabilization  
 ## 135 behavioral response to ethanol  
 ## 136 root hair cell differentiation  
 ## 137 root hair elongation  
 ## 138 chondroitin sulfate proteoglycan biosynthetic process, polysaccharide chain biosynthetic process  
 ## 139 positive regulation of glial cell proliferation  
 ## 140 axonogenesis involved in innervation  
 ## 141 establishment or maintenance of monopolar cell polarity  
 ## 142 interleukin-10 secretion  
 ## 143 cellular response to gonadotropin-releasing hormone  
 ## 144 negative regulation of smooth muscle cell-matrix adhesion  
 ## 145 cell morphogenesis involved in neuron differentiation  
 ## 146 regulation of glycogen metabolic process  
 ## 147 membrane lipid biosynthetic process  
 ## 148 generation of neurons  
 ## 149 regulation of blood vessel size  
 ## 150 regulation of cellular carbohydrate catabolic process  
 ## 151 response to calcium ion  
 ## 152 regulation of chemokine production  
 ## 153 positive regulation of carbohydrate metabolic process  
 ## 154 fatty acid derivative biosynthetic process  
 ## 155 peptide hormone secretion  
 ## 156 regulation of systemic arterial blood pressure mediated by a chemical signal  
 ## 157 cellular monovalent inorganic cation homeostasis  
 ## 158 cardiac muscle contraction  
 ## 159 vitamin metabolic process  
 ## 160 oligosaccharide metabolic process  
 ## 161 carbohydrate metabolic process  
 ## 162 endomembrane system organization  
 ## 163 cellular carbohydrate metabolic process  
 ## 164 regulation of hormone secretion  
 ## 165 tight junction assembly  
 ## 166 acyl-CoA biosynthetic process  
 ## 167 diaphragm contraction  
 ## 168 positive regulation of myeloid leukocyte mediated immunity  
 ## 169 seryl-tRNA aminoacylation  
 ## 170 DNA damage induced protein phosphorylation  
 ## 171 positive regulation of actin filament depolymerization  
 ## 172 positive regulation of superoxide anion generation  
 ## 173 establishment or maintenance of epithelial cell apical/basal polarity  
 ## 174 stem cell fate commitment  
 ## 175 negative regulation of dendrite morphogenesis  
 ## 176 hard palate development  
 ## 177 positive regulation of phagocytosis, engulfment  
 ## 178 axonemal dynein complex assembly  
 ## 179 inflammatory response to wounding  
 ## 180 regulation of eosinophil activation  
 ## 181 sulfur compound biosynthetic process  
 ## 182 phosphatidylinositol metabolic process  
 ## 183 regulated secretory pathway  
 ## 184 hexose metabolic process  
 ## 185 regulation of interleukin-8 production

## 186 photoreceptor cell differentiation  
 ## 187 peptide transport  
 ## 188 glycerolipid biosynthetic process  
 ## 189 neuron development  
 ## 190 regulation of cellular component size  
 ## 191 multi-organism behavior  
 ## 192 negative regulation of cellular component organization  
 ## 193 negative regulation of platelet-derived growth factor receptor signaling pathway  
 ## 194 peripheral nervous system axon regeneration  
 ## 195 optic nerve development  
 ## 196 peristalsis  
 ## 197 positive regulation of toll-like receptor 4 signaling pathway  
 ## 198 bone marrow development  
 ## 199 negative regulation of focal adhesion assembly  
 ## 200 epithelial cilium movement involved in determination of left/right asymmetry  
 ## 201 positive regulation of DNA-templated transcription, initiation  
 ## 202 regulation of N-methyl-D-aspartate selective glutamate receptor activity  
 ## 203 positive regulation of endothelial cell apoptotic process  
 ## 204 cytokine production involved in immune response  
 ## 205 nerve development  
 ## 206 regulation of cytokine secretion  
 ## 207 developmental growth  
 ## 208 regulation of protein localization  
 ## 209 cellular lipid metabolic process  
 ## 210 regulation of system process  
 ## 211 triglyceride biosynthetic process  
 ## 212 actin filament-based process  
 ## 213 renal system process  
 ## 214 activation of phospholipase C activity  
 ## 215 negative regulation of phosphatase activity  
 ## 216 regulation of blood coagulation  
 ## 217 neutral lipid biosynthetic process  
 ## 218 regulation of phospholipase C activity  
 ## 219 regulation of apoptotic signaling pathway  
 ## 220 cell part morphogenesis  
 ## 221 regulation of primary metabolic process  
 ## 222 positive regulation of heart contraction  
 ## 223 regulation of cell projection organization  
 ## 224 cellular response to tumor necrosis factor  
 ## 225 protein localization to plasma membrane  
 ## 226 eosinophil activation involved in immune response  
 ## 227 eosinophil mediated immunity  
 ## 228 arginine catabolic process  
 ## 229 sphingomyelin metabolic process  
 ## 230 membrane raft organization  
 ## 231 dermatan sulfate proteoglycan metabolic process  
 ## 232 regulation of killing of cells of other organism  
 ## 233 killing by host of symbiont cells  
 ## 234 negative regulation of protein tyrosine kinase activity  
 ## 235 establishment or maintenance of bipolar cell polarity  
 ## 236 regulation of spindle organization  
 ## 237 regulation of blood pressure  
 ## 238 response to corticosteroid  
 ## 239 locomotion

```

## 240 striated muscle cell differentiation
## 241 oxidation-reduction process
## 242 regulation of ion homeostasis
## 243 negative regulation of immune system process
## 244 hormone transport
## 245 metabolic process
## 246 regulation of actin cytoskeleton organization
## 247 oxoacid metabolic process
## 248 cellular cation homeostasis

```

GO enrichment analysis for MF

```

ontology(paraGO) <- "MF"
MF <- hyperGTest(paraGO)
summary(MF)[,c(1,2,7)]

```

```

##      GOMFID      Pvalue
## 1  GO:0000026 6.848844e-07
## 2  GO:0015057 2.721796e-06
## 3  GO:0003727 2.567893e-05
## 4  GO:0004313 7.849775e-05
## 5  GO:0004315 7.849775e-05
## 6  GO:0004316 7.849775e-05
## 7  GO:0004317 7.849775e-05
## 8  GO:0004319 7.849775e-05
## 9  GO:0004320 7.849775e-05
## 10 GO:0016295 7.849775e-05
## 11 GO:0016296 7.849775e-05
## 12 GO:0004314 2.341235e-04
## 13 GO:0016420 2.341235e-04
## 14 GO:0031681 2.341235e-04
## 15 GO:0031894 2.341235e-04
## 16 GO:0001653 2.890821e-04
## 17 GO:0031177 4.655251e-04
## 18 GO:0035064 5.982992e-04
## 19 GO:0000036 7.713683e-04
## 20 GO:0051192 7.713683e-04
## 21 GO:0016417 1.150336e-03
## 22 GO:0005000 2.122460e-03
## 23 GO:0008271 2.122460e-03
## 24 GO:0070402 2.713068e-03
## 25 GO:0017046 2.991566e-03
## 26 GO:0016888 4.097126e-03
## 27 GO:0016887 5.408714e-03
## 28 GO:0001965 5.743499e-03
## 29 GO:0004056 8.905043e-03
## 30 GO:0004462 8.905043e-03
## 31 GO:0004573 8.905043e-03
## 32 GO:0004967 8.905043e-03
## 33 GO:0005200 1.162867e-02
## 34 GO:1901682 1.216228e-02
## 35 GO:0016829 1.518246e-02
## 36 GO:0000340 1.773159e-02

```

## 37 GO:0004342 1.773159e-02  
 ## 38 GO:0004487 1.773159e-02  
 ## 39 GO:0004558 1.773159e-02  
 ## 40 GO:0030292 1.773159e-02  
 ## 41 GO:0051424 1.773159e-02  
 ## 42 GO:0097016 1.773159e-02  
 ## 43 GO:0097159 1.855111e-02  
 ## 44 GO:0000166 2.052172e-02  
 ## 45 GO:0033218 2.307389e-02  
 ## 46 GO:0016758 2.528449e-02  
 ## 47 GO:0004930 2.530484e-02  
 ## 48 GO:1901363 2.564289e-02  
 ## 49 GO:0019900 2.573614e-02  
 ## 50 GO:0004477 2.648032e-02  
 ## 51 GO:0004828 2.648032e-02  
 ## 52 GO:0050998 2.648032e-02  
 ## 53 GO:0005080 2.904388e-02  
 ## 54 GO:0016836 2.904388e-02  
 ## 55 GO:0016787 2.924347e-02  
 ## 56 GO:0004767 3.515192e-02  
 ## 57 GO:0050700 3.515192e-02  
 ## 58 GO:0005524 3.547224e-02  
 ## 59 GO:0030554 4.065333e-02  
 ## 60 GO:0016798 4.242920e-02  
 ## 61 GO:0015926 4.331240e-02  
 ## 62 GO:0004396 4.374706e-02  
 ## 63 GO:0004488 4.374706e-02

##	Term
## 1	alpha-1,2-mannosyltransferase activity
## 2	thrombin receptor activity
## 3	single-stranded RNA binding
## 4	[acyl-carrier-protein] S-acetyltransferase activity
## 5	3-oxoacyl-[acyl-carrier-protein] synthase activity
## 6	3-oxoacyl-[acyl-carrier-protein] reductase (NADPH) activity
## 7	3-hydroxypalmitoyl-[acyl-carrier-protein] dehydratase activity
## 8	enoyl-[acyl-carrier-protein] reductase (NADPH, B-specific) activity
## 9	oleoyl-[acyl-carrier-protein] hydrolase activity
## 10	myristoyl-[acyl-carrier-protein] hydrolase activity
## 11	palmitoyl-[acyl-carrier-protein] hydrolase activity
## 12	[acyl-carrier-protein] S-malonyltransferase activity
## 13	malonyltransferase activity
## 14	G-protein beta-subunit binding
## 15	V1A vasopressin receptor binding
## 16	peptide receptor activity
## 17	phosphopantetheine binding
## 18	methylated histone binding
## 19	ACP phosphopantetheine attachment site binding involved in fatty acid biosynthetic process
## 20	prosthetic group binding
## 21	S-acyltransferase activity
## 22	vasopressin receptor activity
## 23	secondary active sulfate transmembrane transporter activity
## 24	NADPH binding
## 25	peptide hormone binding
## 26	endodeoxyribonuclease activity, producing 5'-phosphomonoesters

```

## 27 ATPase activity
## 28 G-protein alpha-subunit binding
## 29 argininosuccinate lyase activity
## 30 lactoylglutathione lyase activity
## 31 mannosyl-oligosaccharide glucosidase activity
## 32 glucagon receptor activity
## 33 structural constituent of cytoskeleton
## 34 sulfur compound transmembrane transporter activity
## 35 lyase activity
## 36 RNA 7-methylguanosine cap binding
## 37 glucosamine-6-phosphate deaminase activity
## 38 methylenetetrahydrofolate dehydrogenase (NAD+) activity
## 39 alpha-1,4-glucosidase activity
## 40 protein tyrosine kinase inhibitor activity
## 41 corticotropin-releasing hormone binding
## 42 L27 domain binding
## 43 organic cyclic compound binding
## 44 nucleotide binding
## 45 amide binding
## 46 transferase activity, transferring hexosyl groups
## 47 G-protein coupled receptor activity
## 48 heterocyclic compound binding
## 49 kinase binding
## 50 methenyltetrahydrofolate cyclohydrolase activity
## 51 serine-tRNA ligase activity
## 52 nitric-oxide synthase binding
## 53 protein kinase C binding
## 54 hydro-lyase activity
## 55 hydrolase activity
## 56 sphingomyelin phosphodiesterase activity
## 57 CARD domain binding
## 58 ATP binding
## 59 adenylyl nucleotide binding
## 60 hydrolase activity, acting on glycosyl bonds
## 61 glucosidase activity
## 62 hexokinase activity
## 63 methylenetetrahydrofolate dehydrogenase (NADP+) activity

```

GO enrichment analysis for CC

```

ontology(paraGO) <- "CC"
CC <- hyperGTest(paraGO)
summary(CC)[,c(1,2,7)]

```

```

##      GOCCID      Pvalue
## 1  GO:0035102 1.662649e-05
## 2  GO:0005783 2.771039e-04
## 3  GO:0005737 6.205058e-04
## 4  GO:0005794 6.358349e-04
## 5  GO:0005622 9.076359e-04
## 6  GO:0042587 1.280729e-03
## 7  GO:0043227 1.724776e-03
## 8  GO:0005623 2.283221e-03

```

## 9 GO:0016235 3.285612e-03  
 ## 10 GO:0043229 5.918317e-03  
 ## 11 GO:0005923 6.125909e-03  
 ## 12 GO:0000323 6.612909e-03  
 ## 13 GO:0000133 7.959619e-03  
 ## 14 GO:0005618 7.959619e-03  
 ## 15 GO:0005767 7.959619e-03  
 ## 16 GO:0009941 1.585665e-02  
 ## 17 GO:0034098 1.585665e-02  
 ## 18 GO:0035748 1.585665e-02  
 ## 19 GO:0031300 1.611572e-02  
 ## 20 GO:0000792 1.797360e-02  
 ## 21 GO:0030173 2.069186e-02  
 ## 22 GO:0009506 2.369158e-02  
 ## 23 GO:0009570 2.369158e-02  
 ## 24 GO:0097025 2.369158e-02  
 ## 25 GO:0005902 2.817444e-02  
 ## 26 GO:0098588 2.830548e-02  
 ## 27 GO:0042175 3.074791e-02  
 ## 28 GO:0031045 3.146488e-02  
 ## 29 GO:0043219 3.146488e-02  
 ## 30 GO:0043220 3.146488e-02  
 ## 31 GO:0033268 3.917705e-02  
 ## 32 GO:0035145 3.917705e-02  
 ## 33 GO:0043196 3.917705e-02  
 ## 34 GO:0044435 3.917705e-02  
 ## 35 GO:0005765 4.579720e-02  
 ## 36 GO:0030054 4.679293e-02  
 ## 37 GO:0005829 4.796554e-02  
 ## 38 GO:0005887 4.887769e-02

##	Term
## 1	PRC1 complex
## 2	endoplasmic reticulum
## 3	cytoplasm
## 4	Golgi apparatus
## 5	intracellular
## 6	glycogen granule
## 7	membrane-bounded organelle
## 8	cell
## 9	aggresome
## 10	intracellular organelle
## 11	tight junction
## 12	lytic vacuole
## 13	polarisome
## 14	cell wall
## 15	secondary lysosome
## 16	chloroplast envelope
## 17	Cdc48p-Npl4p-Ufd1p AAA ATPase complex
## 18	myelin sheath abaxonal region
## 19	intrinsic component of organelle membrane
## 20	heterochromatin
## 21	integral component of Golgi membrane
## 22	plasmodesma
## 23	chloroplast stroma

```

## 24                               MPP7-DLG1-LIN7 complex
## 25                               microvillus
## 26                               bounding membrane of organelle
## 27 nuclear outer membrane-endoplasmic reticulum membrane network
## 28                               dense core granule
## 29                               lateral loop
## 30                               Schmidt-Lanterman incisure
## 31                               node of Ranvier
## 32                               exon-exon junction complex
## 33                               varicosity
## 34                               plastid part
## 35                               lysosomal membrane
## 36                               cell junction
## 37                               cytosol
## 38                               integral component of plasma membrane

```

#### 4. MeSH enrichment analysis

Then, we perform a MeSH ORA for the category **Chemicals and Drugs** by setting ‘category=“D”’.

```

library(meshr)
library(MeSH.db)
library("org.MeSH.Ssc.db")
meshParams <- new("MeSHHyperGParams", geneIds = my.geneID2[,2], universeGeneIds = univ.geneID3[,2],
                 annotation = "org.MeSH.Ssc.db", category = "D", database = "gene2pubmed",
                 pvalueCutoff = 0.05, pAdjust = "none")
meshR <- meshHyperGTest(meshParams)
summary(meshR)[!duplicated(summary(meshR)[,7]),c(1,2,7)]

```

##	MESHID	Pvalue	MESHTERM
## 1	D000213	0.008353484	Acyl Carrier Protein
## 210	D048630	0.008353484	Polyketide Synthases
## 214	D054890	0.008353484	Fatty Acid Synthase, Type I
## 17	D002245	0.016637643	Carbon Dioxide
## 169	D019298	0.016637643	Glucose-6-Phosphate
## 211	D051274	0.016637643	Glucose Transporter Type 3
## 101	D006593	0.024853048	Hexokinase
## 105	D006601	0.024853048	Hexoses
## 115	D008780	0.024853048	Methyltransferases
## 159	D018027	0.024853048	Receptors, Glucagon
## 201	D039601	0.024853048	Eukaryotic Initiation Factor-4A
## 233	D064429	0.024853048	Fatty Acid Synthases
## 55	D004763	0.033000266	Glucagon-Like Peptides
## 109	D006629	0.033000266	Hirudins
## 204	D044463	0.033000266	Receptor, PAR-1
## 3	D000577	0.041079859	Amides
## 48	D002457	0.041079859	Cell Extracts
## 60	D006003	0.041079859	Glycogen
## 119	D011770	0.041079859	Pyruvate Kinase
## 143	D012799	0.041079859	Sialyltransferases
## 153	D016211	0.041079859	Transforming Growth Factor alpha
## 162	D019158	0.041079859	N-Acetylneuraminic Acid
## 172	D019344	0.049092385	Lactic Acid

Switching to a different category is easily done by the ‘category<-’ function. Here, we use **Diseases** (category = “C”).

```
category(meshParams) <- "C"
meshR <- meshHyperGTest(meshParams)
summary(meshR)[!duplicated(summary(meshR)[,7]),c(1,2,7)]
```

MeSH ORA for **Anatomy** (category = “A”).

```
category(meshParams) <- "A"
meshR <- meshHyperGTest(meshParams)
summary(meshR)[!duplicated(summary(meshR)[,7]),c(1,2,7)]
```

```
##      MESHID      Pvalue      MESHTERM
## 1 D008841 0.03300027 Actin Cytoskeleton
```

MeSH ORA for **Phenomena and Processes** (category = “G”).

```
category(meshParams) <- "G"
meshR <- meshHyperGTest(meshParams)
summary(meshR)[!duplicated(summary(meshR)[,7]),c(1,2,7)]
```

```
##      MESHID      Pvalue      MESHTERM
## 39 D020134 0.02273332 Catalytic Domain
## 1  D004542 0.02485305      Ejaculation
## 24 D013076 0.02485305      Sperm Count
```

## 5. Session Information

```
sessionInfo()
```

```
## R version 3.1.2 (2014-10-31)
## Platform: x86_64-apple-darwin13.4.0 (64-bit)
##
## locale:
## [1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
##
## attached base packages:
## [1] grid      parallel  stats4    stats     graphics  grDevices  utils
## [8] datasets  methods   base
##
## other attached packages:
## [1] org.MeSH.Ssc.db_1.2.0      meshr_1.2.2
## [3] org.MeSH.Syn.db_1.2.0     org.MeSH.Bsu.168.db_1.2.0
## [5] org.MeSH.Atu.K84.db_1.2.0 org.MeSH.Aca.db_1.2.0
## [7] org.MeSH.Hsa.db_1.2.0     MeSH.PCR.db_1.2.0
## [9] MeSH.AOR.db_1.2.0        MeSH.db_1.2.0
## [11] MeSHDbi_1.2.0            org.Hs.eg.db_3.0.0
## [13] cummeRbund_2.8.2         Gviz_1.10.2
## [15] rtracklayer_1.26.2       GenomicRanges_1.18.3
```



```

## [17] fastcluster_1.1.13      reshape2_1.4
## [19] ggplot2_1.0.0           fdrtool_1.2.13
## [21] GOSTats_2.32.0          graph_1.44.0
## [23] Category_2.32.0         GO.db_3.0.0
## [25] Matrix_1.1-4            org.Ss.eg.db_3.0.0
## [27] RSQLite_1.0.0           DBI_0.3.1
## [29] AnnotationDbi_1.28.1    GenomeInfoDb_1.2.3
## [31] IRanges_2.0.0           S4Vectors_0.4.0
## [33] Biobase_2.26.0          BiocGenerics_0.12.1
## [35] biomaRt_2.22.0
##
## loaded via a namespace (and not attached):
## [1] acepack_1.3-3.3          annotate_1.44.0
## [3] AnnotationForge_1.8.1    base64enc_0.1-2
## [5] BatchJobs_1.5           BBmisc_1.8
## [7] BiocParallel_1.0.0       Biostrings_2.34.0
## [9] biovizBase_1.14.0       bitops_1.0-6
## [11] brew_1.0-6              BSgenome_1.34.0
## [13] checkmate_1.5.0         cluster_1.15.3
## [15] codetools_0.2-9         colorspace_1.2-4
## [17] dichromat_2.0-0         digest_0.6.4
## [19] evaluate_0.5.5          fail_1.2
## [21] foreach_1.4.2           foreign_0.8-61
## [23] formatR_1.0             Formula_1.1-2
## [25] genefilter_1.48.1       GenomicAlignments_1.2.1
## [27] GenomicFeatures_1.18.2  GSEABase_1.28.0
## [29] gtable_0.1.2            Hmisc_3.14-5
## [31] htmltools_0.2.6         iterators_1.0.7
## [33] knitr_1.8               lattice_0.20-29
## [35] latticeExtra_0.6-26     MASS_7.3-35
## [37] matrixStats_0.10.3      munsell_0.4.2
## [39] nnet_7.3-8              plyr_1.8.1
## [41] proto_0.3-10            R.methodsS3_1.6.1
## [43] RBGL_1.42.0             RColorBrewer_1.0-5
## [45] Rcpp_0.11.3             RCurl_1.95-4.3
## [47] rmarkdown_0.3.10       rpart_4.1-8
## [49] Rsamtools_1.18.2       scales_0.2.4
## [51] sendmailR_1.2-1         splines_3.1.2
## [53] stringr_0.6.2           survival_2.37-7
## [55] tools_3.1.2            VariantAnnotation_1.12.4
## [57] XML_3.98-1.1           xtable_1.7-4
## [59] XVector_0.6.0          yaml_2.1.13
## [61] zlibbioc_1.12.0

```