**Table S4.** Gene ontology analysis of significantly differentially methylated (DM) promoters in females related to males, given as a 30 toplist within different categories.

| | | | | **Occurence in** | | **Significance** | |
|---|---|---|---|---|---|---|---|
| **Category** | **GO ID** | **GO term** | **GO Level** | **Reference** | **Test list** | **Pval.** | **Pval. FDR-BH** |
| ***All DM promoters across breeds (30 homologs found of 55 loci included)*** | | | | | | | |
| | GO:0018345 | protein palmitoylation | 7 | 10 | 2 | 0.000 | 0.204 |
| | GO:0009615 | response to virus | 3, 4 | 200 | 4 | 0.001 | 0.381 |
| | GO:0007281 | germ cell development | 3, 4, 5 | 133 | 3 | 0.002 | 0.128 |
| | GO:0009994 | **oocyte differentiation** | 3, 4, 6, 7 | 36 | 2 | 0.002 | 0.124 |
| | GO:0048599 | **oocyte development** | 4, 5, 6, 7, 8 | 36 | 2 | 0.002 | 0.118 |
| | GO:0009607 | response to biotic stimulus | 2 | 485 | 5 | 0.003 | 0.119 |
| | GO:0008637 | apoptotic mitochondrial changes | 5, 6 | 40 | 2 | 0.003 | 0.134 |
| | GO:0016044 | cellular membrane organization | 2, 4 | 320 | 4 | 0.004 | 0.156 |
| | GO:0061024 | membrane organization | 3 | 322 | 4 | 0.004 | 0.153 |
| | GO:0006497 | protein lipidation | 6 | 46 | 2 | 0.004 | 0.156 |
| | GO:0001658 | **branching involved in ureteric bud morphogenesis** | 4, 5, 6, 7, 8 | 49 | 2 | 0.005 | 0.118 |
| | GO:0002376 | immune system process | 1 | 1383 | 8 | 0.005 | 0.116 |
| | GO:0042158 | lipoprotein biosynthetic process | 5 | 50 | 2 | 0.005 | 0.117 |
| | GO:0060675 | **ureteric bud morphogenesis** | 5, 6, 7 | 56 | 2 | 0.006 | 0.142 |
| | GO:0048477 | **oogenesis** | 5, 6 | 57 | 2 | 0.006 | 0.144 |
| | GO:0006921 | cellular component disassembly involved in apoptotic process | 5 | 68 | 2 | 0.008 | 0.142 |
| | GO:0007276 | **gamete generation** | 3, 4 | 415 | 4 | 0.009 | 0.146 |
| | GO:0033077 | T cell differentiation in thymus | 6, 7, 8, 9, 10 | 71 | 2 | 0.009 | 0.149 |
| | GO:0032501 | multicellular organismal process | 1 | 4702 | 16 | 0.009 | 0.152 |
| | GO:0072006 | nephron development | 3, 5, 6, 7 | 73 | 2 | 0.010 | 0.153 |
| | GO:0022037 | metencephalon development | 3, 4, 6, 7, 8 | 74 | 2 | 0.010 | 0.155 |
| | GO:0071845 | cellular component disassembly at cellular level | 4 | 227 | 3 | 0.010 | 0.159 |
| | GO:0042157 | lipoprotein metabolic process | 4 | 77 | 2 | 0.011 | 0.140 |
| | GO:0022411 | cellular component disassembly | 3 | 230 | 3 | 0.011 | 0.139 |
| | GO:0001656 | metanephros development | 5, 6, 7 | 80 | 2 | 0.011 | 0.147 |
| | GO:0051707 | response to other organism | 2, 3 | 460 | 4 | 0.012 | 0.156 |
| | GO:0019953 | **sexual reproduction** | 2 | 469 | 4 | 0.013 | 0.143 |
| | GO:0016050 | vesicle organization | 5 | 86 | 2 | 0.013 | 0.142 |
| | GO:0007292 | **female gamete generation** | 4, 5 | 87 | 2 | 0.013 | 0.143 |
| | GO:0008543 | fibroblast growth factor receptor signaling pathway | 5, 6, 7, 8 | 89 | 2 | 0.014 | 0.148 |
| ***Hypo DM promoters across breeds (8 homologs found of 24 loci included)*** | | | | | | | |
| | GO:0018345 | protein palmitoylation | 7 | 10 | 2 | 0.000 | **0.018** |
| | GO:0006497 | protein lipidation | 6 | 46 | 2 | 0.001 | 0.205 |
| | GO:0042158 | lipoprotein biosynthetic process | 5 | 50 | 2 | 0.001 | 0.162 |
| | GO:0042157 | lipoprotein metabolic process | 4 | 77 | 2 | 0.002 | **0.047** |
| | GO:0008543 | fibroblast growth factor receptor signaling pathway | 5, 6, 7, 8 | 89 | 2 | 0.003 | 0.060 |
| | GO:0071774 | response to fibroblast growth factor stimulus | 3, 5 | 105 | 2 | 0.003 | 0.058 |
| | GO:0044344 | cellular response to fibroblast growth factor stimulus | 4, 6 | 105 | 2 | 0.003 | 0.056 |
| | GO:0043543 | protein acylation | 6 | 123 | 2 | 0.005 | 0.063 |
| | GO:0007281 | germ cell development | 3, 4, 5 | 133 | 2 | 0.005 | 0.061 |
| | GO:0008219 | cell death | 2 | 1548 | 5 | 0.006 | 0.065 |
| | GO:0016265 | death | 1 | 1551 | 5 | 0.006 | 0.064 |
| | GO:0009607 | response to biotic stimulus | 2 | 485 | 3 | 0.007 | 0.067 |
| | GO:0009615 | response to virus | 3, 4 | 200 | 2 | 0.012 | 0.082 |
| | GO:0071363 | cellular response to growth factor stimulus | 5 | 212 | 2 | 0.013 | 0.087 |
| | GO:0070848 | response to growth factor stimulus | 4 | 226 | 2 | 0.015 | 0.090 |
| | GO:0022607 | cellular component assembly | 3 | 1275 | 4 | 0.016 | 0.094 |
| | GO:0044085 | cellular component biogenesis | 2 | 1394 | 4 | 0.022 | 0.110 |
| | GO:0016044 | cellular membrane organization | 2, 4 | 320 | 2 | 0.028 | 0.124 |
| | GO:0061024 | membrane organization | 3 | 322 | 2 | 0.028 | 0.121 |
| | GO:0071310 | cellular response to organic substance | 4 | 848 | 3 | 0.028 | 0.122 |
| | GO:0051704 | multi-organism process | 1 | 870 | 3 | 0.030 | 0.128 |
| | GO:0071844 | cellular component assembly at cellular level | 4 | 940 | 3 | 0.036 | 0.140 |
| | GO:0055114 | oxidation-reduction process | 2 | 946 | 3 | 0.037 | 0.140 |
| | GO:0003006 | **developmental process involved in reproduction** | 2, 3 | 402 | 2 | 0.041 | 0.147 |
| | GO:0007276 | **gamete generation** | 3, 4 | 415 | 2 | 0.044 | 0.152 |
| | GO:0045087 | innate immune response | 3, 4 | 441 | 2 | 0.048 | 0.157 |
| | GO:0051707 | response to other organism | 2, 3 | 460 | 2 | 0.052 | 0.165 |
| | GO:0019953 | **sexual reproduction** | 2 | 469 | 2 | 0.053 | 0.168 |
| | GO:0006184 | GTP catabolic process | 9, 10, 11, 12 | 470 | 2 | 0.054 | 0.168 |
| | GO:0046039 | GTP metabolic process | 8, 9, 10, 11 | 482 | 2 | 0.056 | 0.169 |
| ***Hyper DM promoters across breeds (18 homologs found of 31 loci included)*** | | | | | | | |
| | GO:0032501 | multicellular organismal process | 1 | 4702 | 13 | 0.000 | 0.277 |
| | GO:0022037 | metencephalon development | 3, 4, 6, 7, 8 | 74 | 2 | 0.004 | 0.214 |
| | GO:0016050 | vesicle organization | 5 | 86 | 2 | 0.005 | 0.248 |
| | GO:0001701 | in utero embryonic development | 6 | 308 | 3 | 0.005 | 0.185 |
| | GO:0030902 | hindbrain development | 3, 5, 6, 7 | 112 | 2 | 0.008 | 0.186 |
| | GO:0051607 | defense response to virus | 3, 4, 5 | 120 | 2 | 0.009 | 0.159 |
| | GO:0007275 | multicellular organismal development | 2 | 3449 | 9 | 0.009 | 0.156 |
| | GO:0042113 | B cell activation | 4, 5 | 146 | 2 | 0.013 | 0.177 |
| | GO:0032502 | developmental process | 1 | 3808 | 9 | 0.016 | 0.213 |
| | GO:0002376 | immune system process | 1 | 1383 | 5 | 0.017 | 0.203 |
| | GO:0043009 | chordate embryonic development | 5 | 499 | 3 | 0.019 | 0.219 |
| | GO:0009792 | embryo development ending in birth or egg hatching | 4 | 511 | 3 | 0.020 | 0.222 |
| | GO:0055085 | transmembrane transport | 2, 3, 4 | 944 | 4 | 0.020 | 0.223 |
| | GO:0006811 | ion transport | 3, 4 | 945 | 4 | 0.020 | 0.220 |
| | GO:0034645 | cellular macromolecule biosynthetic process | 4 | 3279 | 8 | 0.021 | 0.219 |
| | GO:0009615 | response to virus | 3, 4 | 200 | 2 | 0.023 | 0.229 |
| | GO:0009059 | macromolecule biosynthetic process | 3 | 3354 | 8 | 0.023 | 0.225 |
| | GO:0001666 | response to hypoxia | 3, 4 | 206 | 2 | 0.024 | 0.227 |
| | GO:0050900 | leukocyte migration | 2, 4, 5 | 209 | 2 | 0.025 | 0.220 |
| | GO:0034641 | cellular nitrogen compound metabolic process | 3 | 4837 | 10 | 0.026 | 0.213 |
| | GO:0044249 | cellular biosynthetic process | 3 | 4123 | 9 | 0.026 | 0.214 |
| | GO:0010467 | gene expression | 3 | 3426 | 8 | 0.026 | 0.212 |
| | GO:0070482 | response to oxygen levels | 3 | 222 | 2 | 0.027 | 0.215 |

|  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|
| GO:0040011 | locomotion | 1 | 1048 | 4 | 0.028 | 0.215 |
| GO:0071845 | cellular component disassembly at cellular level | 4 | 227 | 2 | 0.028 | 0.217 |
| GO:0006807 | nitrogen compound metabolic process | 2 | 4924 | 10 | 0.029 | 0.217 |
| GO:0022411 | cellular component disassembly | 3 | 230 | 2 | 0.029 | 0.208 |
| GO:0009058 | biosynthetic process | 2 | 4217 | 9 | 0.030 | 0.210 |
| GO:0090304 | nucleic acid metabolic process | 4, 5 | 3542 | 8 | 0.031 | 0.210 |
| GO:0006139 | nucleobase-containing compound metabolic process | 3, 4 | 4432 | 9 | 0.039 | 0.218 |
| ***All DM promoters in RJF( 12 homologs found of 22 loci included)*** |  |  |  |  |  |  |
| GO:0001701 | in utero embryonic development | 6 | 308 | 3 | 0.002 | 0.118 |
| GO:0032501 | multicellular organismal process | 1 | 4702 | 9 | 0.004 | 0.135 |
| GO:0043009 | chordate embryonic development | 5 | 499 | 3 | 0.007 | 0.121 |
| GO:0009792 | embryo development ending in birth or egg hatching | 4 | 511 | 3 | 0.008 | 0.118 |
| GO:0009790 | embryo development | 3 | 854 | 3 | 0.029 | 0.249 |
| GO:0055085 | transmembrane transport | 2, 3, 4 | 944 | 3 | 0.037 | 0.277 |
| GO:0006811 | ion transport | 3, 4 | 945 | 3 | 0.037 | 0.266 |
| GO:0032774 | RNA biosynthetic process | 4, 5, 6, 7 | 2529 | 5 | 0.039 | 0.271 |
| GO:0007275 | multicellular organismal development | 2 | 3449 | 6 | 0.039 | 0.263 |
| GO:0006366 | transcription from RNA polymerase II promoter | 5, 6, 7, 8, 9 | 1100 | 3 | 0.052 | 0.314 |
| GO:0032502 | developmental process | 1 | 3808 | 6 | 0.058 | 0.326 |
| GO:0016070 | RNA metabolic process | 4, 5, 6 | 3071 | 5 | 0.073 | 0.339 |
| GO:0065008 | regulation of biological quality | 2 | 2200 | 4 | 0.079 | 0.339 |
| GO:0034645 | cellular macromolecule biosynthetic process | 4 | 3279 | 5 | 0.088 | 0.334 |
| GO:0006355 | regulation of transcription, DNA-dependent | 5, 6, 7, 8, 9 | 2341 | 4 | 0.091 | 0.331 |
| GO:2001141 | regulation of RNA biosynthetic process | 5, 6, 7, 8 | 2358 | 4 | 0.093 | 0.330 |
| GO:0009059 | macromolecule biosynthetic process | 3 | 3354 | 5 | 0.094 | 0.328 |
| GO:0051252 | regulation of RNA metabolic process | 4, 5, 6, 7 | 2404 | 4 | 0.097 | 0.326 |
| GO:0010467 | gene expression | 3 | 3426 | 5 | 0.100 | 0.329 |
| GO:0048878 | chemical homeostasis | 4 | 700 | 2 | 0.100 | 0.318 |
| GO:0006351 | transcription, DNA-dependent | 4, 5, 6, 7, 8 | 2458 | 4 | 0.102 | 0.299 |
| GO:0006812 | cation transport | 4, 5 | 726 | 2 | 0.106 | 0.299 |
| GO:0090304 | nucleic acid metabolic process | 4, 5 | 3542 | 5 | 0.109 | 0.299 |
| GO:2000112 | regulation of cellular macromolecule biosynthetic process | 5, 6 | 2556 | 4 | 0.112 | 0.298 |
| GO:0010556 | regulation of macromolecule biosynthetic process | 4, 5 | 2615 | 4 | 0.118 | 0.295 |
| GO:0050896 | response to stimulus | 1 | 5834 | 3 | 0.121 | 0.299 |
| GO:0010468 | regulation of gene expression | 4, 5 | 2700 | 4 | 0.126 | 0.299 |
| GO:0034641 | cellular nitrogen compound metabolic process | 3 | 4837 | 6 | 0.127 | 0.298 |
| GO:0051716 | cellular response to stimulus | 2 | 4600 | 2 | 0.129 | 0.296 |
| GO:0006807 | nitrogen compound metabolic process | 2 | 4924 | 6 | 0.133 | 0.297 |
| ***Hypo DM promoters in RJF (3 homologs found of 9 loci included)**** |  |  |  |  |  |  |
| GO:0048878 | chemical homeostasis | 4 | 700 | 2 | 0.007 | 0.087 |
| GO:0042592 | homeostatic process | 3 | 1010 | 2 | 0.015 | 0.110 |
| GO:0065008 | regulation of biological quality | 2 | 2200 | 2 | 0.063 | 0.190 |
| GO:0065007 | biological regulation | 1 | 7420 | 2 | 0.399 | 0.521 |
| GO:0009987 | cellular process | 1 | 10797 | 2 | 0.403 | 0.514 |
| GO:0008152 | metabolic process | 1 | 8358 | 2 | 0.433 | 0.472 |
| ***Hyper DM promoter in RJF (9 homologs found of 13 loci included)*** |  |  |  |  |  |  |
| GO:0001701 | in utero embryonic development | 6 | 308 | 3 | 0.001 | 0.058 |
| GO:0032501 | multicellular organismal process | 1 | 4702 | 8 | 0.001 | **0.050** |
| GO:0043009 | chordate embryonic development | 5 | 499 | 3 | 0.003 | 0.076 |
| GO:0009792 | embryo development ending in birth or egg hatching | 4 | 511 | 3 | 0.003 | 0.061 |
| GO:0007275 | multicellular organismal development | 2 | 3449 | 6 | 0.008 | 0.094 |
| GO:0032774 | RNA biosynthetic process | 4, 5, 6, 7 | 2529 | 5 | 0.011 | 0.110 |
| GO:0009790 | embryo development | 3 | 854 | 3 | 0.013 | 0.115 |
| GO:0032502 | developmental process | 1 | 3808 | 6 | 0.014 | 0.105 |
| GO:0016070 | RNA metabolic process | 4, 5, 6 | 3071 | 5 | 0.025 | 0.163 |
| GO:0006366 | transcription from RNA polymerase II promoter | 5, 6, 7, 8, 9 | 1100 | 3 | 0.025 | 0.162 |
| GO:0034645 | cellular macromolecule biosynthetic process | 4 | 3279 | 5 | 0.032 | 0.184 |
| GO:0009059 | macromolecule biosynthetic process | 3 | 3354 | 5 | 0.034 | 0.193 |
| GO:0010467 | gene expression | 3 | 3426 | 5 | 0.037 | 0.201 |
| GO:0006355 | regulation of transcription, DNA-dependent | 5, 6, 7, 8, 9 | 2341 | 4 | 0.041 | 0.211 |
| GO:2001141 | regulation of RNA biosynthetic process | 5, 6, 7, 8 | 2358 | 4 | 0.041 | 0.208 |
| GO:0034641 | cellular nitrogen compound metabolic process | 3 | 4837 | 6 | 0.042 | 0.203 |
| GO:0090304 | nucleic acid metabolic process | 4, 5 | 3542 | 5 | 0.042 | 0.198 |
| GO:0051252 | regulation of RNA metabolic process | 4, 5, 6, 7 | 2404 | 4 | 0.044 | 0.194 |
| GO:0006807 | nitrogen compound metabolic process | 2 | 4924 | 6 | 0.045 | 0.193 |
| GO:0006351 | transcription, DNA-dependent | 4, 5, 6, 7, 8 | 2458 | 4 | 0.047 | 0.195 |
| GO:2000112 | regulation of cellular macromolecule biosynthetic process | 5, 6 | 2556 | 4 | 0.052 | 0.207 |
| GO:0010556 | regulation of macromolecule biosynthetic process | 4, 5 | 2615 | 4 | 0.056 | 0.215 |
| GO:0010468 | regulation of gene expression | 4, 5 | 2700 | 4 | 0.061 | 0.213 |
| GO:0031326 | regulation of cellular biosynthetic process | 4, 5 | 2785 | 4 | 0.067 | 0.216 |
| GO:0009889 | regulation of biosynthetic process | 3, 4 | 2809 | 4 | 0.068 | 0.217 |
| GO:0019219 | regulation of nucleobase-containing compound metabolic process | 4, 5 | 2832 | 4 | 0.070 | 0.212 |
| GO:0044249 | cellular biosynthetic process | 3 | 4123 | 5 | 0.071 | 0.212 |
| GO:0051171 | regulation of nitrogen compound metabolic process | 3, 4 | 2908 | 4 | 0.075 | 0.219 |
| GO:0009058 | biosynthetic process | 2 | 4217 | 5 | 0.077 | 0.220 |
| GO:0006139 | nucleobase-containing compound metabolic process | 3, 4 | 4432 | 5 | 0.090 | 0.212 |
| ***All DM promoters in WL ( 12 homologs found of 22 loci included)*** |  |  |  |  |  |  |
| GO:0018345 | protein palmitoylation | 7 | 10 | 2 | 0.000 | 0.121 |
| GO:0009615 | response to virus | 3, 4 | 200 | 4 | 0.000 | 0.146 |
| GO:0007281 | germ cell development | 3, 4, 5 | 133 | 3 | 0.001 | 0.435 |
| GO:0048599 | **oocyte development** | 4, 5, 6, 7, 8 | 36 | 2 | 0.002 | 0.406 |
| GO:0009994 | **oocyte differentiation** | 3, 4, 6, 7 | 36 | 2 | 0.002 | 0.325 |
| GO:0016044 | cellular membrane organization | 2, 4 | 320 | 4 | 0.002 | 0.273 |
| GO:0061024 | membrane organization | 3 | 322 | 4 | 0.002 | 0.239 |
| GO:0008637 | apoptotic mitochondrial changes | 5, 6 | 40 | 2 | 0.002 | 0.080 |
| GO:0006497 | protein lipidation | 6 | 46 | 2 | 0.003 | 0.101 |
| GO:0001658 | branching involved in ureteric bud morphogenesis | 4, 5, 6, 7, 8 | 49 | 2 | 0.003 | 0.110 |
| GO:0042158 | lipoprotein biosynthetic process | 5 | 50 | 2 | 0.003 | 0.110 |
| GO:0060675 | **ureteric bud morphogenesis** | 5, 6, 7 | 56 | 2 | 0.004 | 0.094 |
| GO:0048477 | **oogenesis** | 5, 6 | 57 | 2 | 0.004 | 0.095 |

|  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|
| GO:0007276 | **gamete generation** | 3, 4 | 415 | 4 | 0.004 | 0.095 |
| GO:0002376 | immune system process | 1 | 1383 | 7 | 0.004 | 0.104 |
| GO:0006921 | cellular component disassembly involved in apoptotic process | 5 | 68 | 2 | 0.005 | 0.106 |
| GO:0051707 | response to other organism | 2, 3 | 460 | 4 | 0.006 | 0.107 |
| GO:0033077 | T cell differentiation in thymus | 6, 7, 8, 9, 10 | 71 | 2 | 0.006 | 0.110 |
| GO:0019953 | **sexual reproduction** | 2 | 469 | 4 | 0.006 | 0.110 |
| GO:0072006 | nephron development | 3, 5, 6, 7 | 73 | 2 | 0.006 | 0.112 |
| GO:0022037 | metencephalon development | 3, 4, 6, 7, 8 | 74 | 2 | 0.006 | 0.113 |
| GO:0009607 | response to biotic stimulus | 2 | 485 | 4 | 0.007 | 0.101 |
| GO:0042157 | lipoprotein metabolic process | 4 | 77 | 2 | 0.007 | 0.103 |
| GO:0032502 | developmental process | 1 | 3808 | 12 | 0.007 | 0.106 |
| GO:0001656 | metanephros development | 5, 6, 7 | 80 | 2 | 0.007 | 0.107 |
| GO:0016050 | vesicle organization | 5 | 86 | 2 | 0.008 | 0.106 |
| GO:0007292 | **female gamete generation** | 4, 5 | 87 | 2 | 0.009 | 0.107 |
| GO:0008543 | fibroblast growth factor receptor signaling pathway | 5, 6, 7, 8 | 89 | 2 | 0.009 | 0.111 |
| GO:0001657 | **ureteric bud development** | 4 | 90 | 2 | 0.009 | 0.112 |
| GO:0008584 | **male gonad development** | 5, 6, 7 | 91 | 2 | 0.009 | 0.113 |
| ***Hypo DM promoters in WL (9 homologs found of 16 loci included)*** |  |  |  |  |  |  |
| GO:0018345 | protein palmitoylation | 7 | 10 | 2 | 0.000 | **0.010** |
| GO:0006497 | protein lipidation | 6 | 46 | 2 | 0.000 | 0.108 |
| GO:0042158 | lipoprotein biosynthetic process | 5 | 50 | 2 | 0.000 | 0.085 |
| GO:0042157 | lipoprotein metabolic process | 4 | 77 | 2 | 0.001 | **0.035** |
| GO:0008543 | fibroblast growth factor receptor signaling pathway | 5, 6, 7, 8 | 89 | 2 | 0.001 | **0.032** |
| GO:0044344 | cellular response to fibroblast growth factor stimulus | 4, 6 | 105 | 2 | 0.002 | **0.042** |
| GO:0071774 | response to fibroblast growth factor stimulus | 3, 5 | 105 | 2 | 0.002 | **0.041** |
| GO:0043543 | protein acylation | 6 | 123 | 2 | 0.003 | **0.040** |
| GO:0007281 | germ cell development | 3, 4, 5 | 133 | 2 | 0.003 | **0.045** |
| GO:0009615 | response to virus | 3, 4 | 200 | 2 | 0.007 | 0.057 |
| GO:0071363 | cellular response to growth factor stimulus | 5 | 212 | 2 | 0.008 | 0.057 |
| GO:0070848 | response to growth factor stimulus | 4 | 226 | 2 | 0.008 | 0.058 |
| GO:0008219 | cell death | 2 | 1548 | 4 | 0.011 | 0.067 |
| GO:0016265 | death | 1 | 1551 | 4 | 0.011 | 0.067 |
| GO:0071310 | cellular response to organic substance | 4 | 848 | 3 | 0.013 | 0.072 |
| GO:0051704 | multi-organism process | 1 | 870 | 3 | 0.014 | 0.073 |
| GO:0016044 | cellular membrane organization | 2, 4 | 320 | 2 | 0.016 | 0.081 |
| GO:0061024 | membrane organization | 3 | 322 | 2 | 0.016 | 0.081 |
| GO:0003006 | developmental process involved in reproduction | 2, 3 | 402 | 2 | 0.025 | 0.100 |
| GO:0007276 | gamete generation | 3, 4 | 415 | 2 | 0.026 | 0.101 |
| GO:0070887 | cellular response to chemical stimulus | 3 | 1150 | 3 | 0.028 | 0.108 |
| GO:0045087 | innate immune response | 3, 4 | 441 | 2 | 0.029 | 0.108 |
| GO:0051707 | response to other organism | 2, 3 | 460 | 2 | 0.031 | 0.110 |
| GO:0019953 | sexual reproduction | 2 | 469 | 2 | 0.032 | 0.111 |
| GO:0006184 | GTP catabolic process | 9, 10, 11, 12 | 470 | 2 | 0.032 | 0.111 |
| GO:0046039 | GTP metabolic process | 8, 9, 10, 11 | 482 | 2 | 0.034 | 0.115 |
| GO:0009607 | response to biotic stimulus | 2 | 485 | 2 | 0.034 | 0.113 |
| GO:0071495 | cellular response to endogenous stimulus | 3 | 487 | 2 | 0.035 | 0.114 |
| GO:0007166 | cell surface receptor signaling pathway | 3, 4, 5 | 2224 | 4 | 0.035 | 0.112 |
| GO:0048610 | cellular process involved in reproduction | 2, 3 | 496 | 2 | 0.036 | 0.114 |
| ***Hyper DM promoters in WL (15 homologs found of 23 loci included)*** |  |  |  |  |  |  |
| GO:0022037 | metencephalon development | 3, 4, 6, 7, 8 | 74 | 2 | 0.002 | 0.178 |
| GO:0001701 | in utero embryonic development | 6 | 308 | 3 | 0.003 | 0.191 |
| GO:0016050 | vesicle organization | 5 | 86 | 2 | 0.003 | 0.183 |
| GO:0032501 | multicellular organismal process | 1 | 4702 | 10 | 0.004 | 0.202 |
| GO:0030902 | hindbrain development | 3, 5, 6, 7 | 112 | 2 | 0.005 | 0.165 |
| GO:0051607 | defense response to virus | 3, 4, 5 | 120 | 2 | 0.006 | 0.156 |
| GO:0007275 | multicellular organismal development | 2 | 3449 | 8 | 0.008 | 0.153 |
| GO:0042113 | B cell activation | 4, 5 | 146 | 2 | 0.009 | 0.164 |
| GO:0043009 | chordate embryonic development | 5 | 499 | 3 | 0.011 | 0.164 |
| GO:0009792 | embryo development ending in birth or egg hatching | 4 | 511 | 3 | 0.012 | 0.168 |
| GO:0032502 | developmental process | 1 | 3808 | 8 | 0.014 | 0.174 |
| GO:0009615 | response to virus | 3, 4 | 200 | 2 | 0.016 | 0.192 |
| GO:0001666 | response to hypoxia | 3, 4 | 206 | 2 | 0.017 | 0.197 |
| GO:0070482 | response to oxygen levels | 3 | 222 | 2 | 0.019 | 0.206 |
| GO:0034645 | cellular macromolecule biosynthetic process | 4 | 3279 | 7 | 0.021 | 0.201 |
| GO:0044249 | cellular biosynthetic process | 3 | 4123 | 8 | 0.022 | 0.199 |
| GO:2000112 | regulation of cellular macromolecule biosynthetic process | 5, 6 | 2556 | 6 | 0.023 | 0.203 |
| GO:0009059 | macromolecule biosynthetic process | 3 | 3354 | 7 | 0.024 | 0.196 |
| GO:0009058 | biosynthetic process | 2 | 4217 | 8 | 0.025 | 0.194 |
| GO:0010556 | regulation of macromolecule biosynthetic process | 4, 5 | 2615 | 6 | 0.025 | 0.195 |
| GO:0010467 | gene expression | 3 | 3426 | 7 | 0.026 | 0.199 |
| GO:0010468 | regulation of gene expression | 4, 5 | 2700 | 6 | 0.029 | 0.189 |
| GO:0090304 | nucleic acid metabolic process | 4, 5 | 3542 | 7 | 0.031 | 0.192 |
| GO:0006139 | nucleobase-containing compound metabolic process | 3, 4 | 4432 | 8 | 0.032 | 0.196 |
| GO:0031326 | regulation of cellular biosynthetic process | 4, 5 | 2785 | 6 | 0.033 | 0.197 |
| GO:0009889 | regulation of biosynthetic process | 3, 4 | 2809 | 6 | 0.034 | 0.201 |
| GO:0002376 | immune system process | 1 | 1383 | 4 | 0.035 | 0.200 |
| GO:0016044 | cellular membrane organization | 2, 4 | 320 | 2 | 0.037 | 0.202 |
| GO:0061024 | membrane organization | 3 | 322 | 2 | 0.037 | 0.203 |
| GO:0009790 | embryo development | 3 | 854 | 3 | 0.042 | 0.208 |

Analysis was performed with human homologs using the Manteia web tool.

Note: Each promoter can represent more than one gene.

* Only 6 GO terms were found