**Table S3.** Gene ontology analysis of significantly differentially expressed (DE) genes 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 DE genes across breeds (242 homologs found of 315 probesets included)*** | | | | | | | |
| | GO:0007166 | cell surface receptor signaling pathway | 3, 4, 5 | 2224 | 18 | 0.000 | 0.234 |
| | GO:0023052 | signaling | 1 | 4227 | 47 | 0.000 | 0.215 |
| | GO:0009892 | negative regulation of metabolic process | 2, 3, 4 | 1162 | 6 | 0.000 | 0.153 |
| | GO:0006081 | cellular aldehyde metabolic process | 3 | 34 | 5 | 0.000 | 0.116 |
| | GO:0001574 | ganglioside biosynthetic process | 7, 8, 9, 10 | 8 | 3 | 0.000 | 0.104 |
| | GO:0007154 | cell communication | 2 | 4327 | 49 | 0.000 | 0.093 |
| | GO:0006672 | ceramide metabolic process | 7, 8 | 62 | 6 | 0.000 | 0.153 |
| | GO:0007186 | G-protein coupled receptor signaling pathway | 4, 5, 6 | 903 | 4 | 0.000 | 0.141 |
| | GO:0031324 | negative regulation of cellular metabolic process | 3, 4, 5 | 1085 | 6 | 0.001 | 0.132 |
| | GO:0007005 | mitochondrion organization | 5 | 177 | 10 | 0.001 | 0.124 |
| | GO:0065007 | biological regulation | 1 | 7420 | 100 | 0.001 | 0.123 |
| | GO:0000279 | M phase | 4, 5 | 477 | 18 | 0.001 | 0.114 |
| | GO:0046519 | sphingoid metabolic process | 6, 7 | 66 | 6 | 0.001 | 0.114 |
| | GO:0010605 | negative regulation of macromolecule metabolic process | 3, 4, 5 | 1057 | 6 | 0.001 | 0.118 |
| | GO:0010165 | response to X-ray | 5 | 26 | 4 | 0.001 | 0.115 |
| | GO:0045716 | positive regulation of low-density lipoprotein particle receptor biosynthetic process | 5, 6, 7, 8 | 3 | 2 | 0.001 | 0.114 |
| | GO:0022403 | cell cycle phase | 3, 4 | 756 | 24 | 0.001 | 0.120 |
| | GO:0071310 | cellular response to organic substance | 4 | 848 | 4 | 0.001 | 0.127 |
| | GO:0000278 | mitotic cell cycle | 3 | 688 | 22 | 0.001 | 0.154 |
| | GO:0007165 | signal transduction | 2, 3, 4 | 3830 | 45 | 0.001 | 0.146 |
| | GO:0001573 | ganglioside metabolic process | 7, 8, 9 | 14 | 3 | 0.001 | 0.146 |
| | GO:0006974 | response to DNA damage stimulus | 4 | 560 | 19 | 0.001 | 0.144 |
| | GO:0009890 | negative regulation of biosynthetic process | 3, 4, 5 | 906 | 5 | 0.002 | 0.150 |
| | GO:0051297 | centrosome organization | 5, 6, 8 | 53 | 5 | 0.002 | 0.146 |
| | GO:0072369 | regulation of lipid transport by positive regulation of transcription from RNA polymerase II promoter | 6, 7, 8, 9, 10, 11, 12 | 4 | 2 | 0.002 | 0.144 |
| | GO:0010988 | regulation of low-density lipoprotein particle clearance | 4, 5, 6 | 4 | 2 | 0.002 | 0.138 |
| | GO:0006396 | RNA processing | 4, 5, 6, 7 | 569 | 19 | 0.002 | 0.138 |
| | GO:0031327 | negative regulation of cellular biosynthetic process | 4, 5, 6 | 893 | 5 | 0.002 | 0.144 |
| | GO:0033554 | cellular response to stress | 3 | 991 | 28 | 0.002 | 0.142 |
| | GO:0006688 | glycosphingolipid biosynthetic process | 6, 7, 8 | 16 | 3 | 0.002 | 0.153 |
| ***Higher DE genes across breeds (52 genes found of 67 probesets included)*** | | | | | | | |
| | GO:0035261 | **external genitalia morphogenesis** | 4, 5, 6, 7 | 6 | 2 | 0.000 | 0.163 |
| | GO:0061010 | gall bladder development | 4, 5 | 6 | 2 | 0.000 | 0.082 |
| | GO:0040018 | positive regulation of multicellular organism growth | 3, 4, 5 | 34 | 3 | 0.000 | 0.063 |
| | GO:0034086 | maintenance of sister chromatid cohesion | 3, 4, 5, 7 | 8 | 2 | 0.000 | 0.076 |
| | GO:0034088 | maintenance of mitotic sister chromatid cohesion | 4, 5, 6, 7, 8, 9, 10 | 8 | 2 | 0.000 | 0.061 |
| | GO:0061038 | **uterus morphogenesis** | 3, 4, 5, 6 | 8 | 2 | 0.000 | 0.050 |
| | GO:0060324 | **face development** | 3, 4 | 42 | 3 | 0.000 | 0.051 |
| | GO:0071481 | cellular response to X-ray | 6 | 9 | 2 | 0.000 | **0.049** |
| | GO:0035117 | embryonic arm morphogenesis | 7, 8 | 9 | 2 | 0.000 | **0.043** |
| | GO:0035140 | arm morphogenesis | 6, 7 | 9 | 2 | 0.000 | **0.039** |
| | GO:0007064 | mitotic sister chromatid cohesion | 4, 5, 6, 7, 8, 9 | 10 | 2 | 0.000 | **0.044** |
| | GO:0031065 | positive regulation of histone deacetylation | 6, 7, 8, 9, 10, 11, 12 | 11 | 2 | 0.001 | **0.049** |
| | GO:0090312 | positive regulation of protein deacetylation | 6, 7, 8, 9 | 13 | 2 | 0.001 | 0.064 |
| | GO:0060322 | **head development** | 3 | 58 | 3 | 0.001 | 0.065 |
| | GO:0048703 | embryonic viscerocranium morphogenesis | 4, 5, 7, 8, 9 | 14 | 2 | 0.001 | 0.064 |
| | GO:0031063 | regulation of histone deacetylation | 6, 7, 8, 9, 11 | 15 | 2 | 0.001 | 0.069 |
| | GO:0090311 | regulation of protein deacetylation | 6, 7, 8 | 17 | 2 | 0.001 | 0.084 |
| | GO:0060065 | **uterus development** | 4, 5 | 18 | 2 | 0.002 | 0.089 |
| | GO:0042634 | regulation of hair cycle | 3, 4 | 18 | 2 | 0.002 | 0.084 |
| | GO:0035112 | **genitalia morphogenesis** | 3, 4, 5, 6 | 18 | 2 | 0.002 | 0.080 |
| | GO:0040014 | regulation of multicellular organism growth | 3, 4 | 81 | 3 | 0.002 | 0.111 |
| | GO:0032800 | receptor biosynthetic process | 4, 5 | 22 | 2 | 0.002 | 0.109 |
| | GO:0048557 | embryonic digestive tract morphogenesis | 4, 5, 6, 7 | 24 | 2 | 0.003 | 0.123 |
| | GO:0010165 | response to X-ray | 5 | 26 | 2 | 0.003 | 0.138 |
| | GO:0031058 | positive regulation of histone modification | 5, 6, 7, 8, 9, 10, 11 | 28 | 2 | 0.004 | 0.124 |
| | GO:0048562 | embryonic organ morphogenesis | 4, 5, 6 | 211 | 4 | 0.005 | 0.144 |
| | GO:0035115 | embryonic forelimb morphogenesis | 6, 7 | 31 | 2 | 0.005 | 0.142 |
| | GO:0007062 | sister chromatid cohesion | 3, 4, 6 | 31 | 2 | 0.005 | 0.138 |
| | GO:0060325 | face morphogenesis | 3, 4, 5, 6 | 32 | 2 | 0.005 | 0.142 |
| | GO:2001252 | positive regulation of chromosome organization | 4, 5, 6, 7 | 32 | 2 | 0.005 | 0.138 |
| ***Lower DE genes across breeds (191 genes found of 248 probesets included)*** | | | | | | | |
| | GO:0065007 | biological regulation | 1 | 7420 | 73 | 0.000 | 0.097 |
| | GO:0009892 | negative regulation of metabolic process | 2, 3, 4 | 1162 | 3 | 0.000 | 0.076 |
| | GO:0031324 | negative regulation of cellular metabolic process | 3, 4, 5 | 1085 | 3 | 0.000 | 0.124 |
| | GO:0010605 | negative regulation of macromolecule metabolic process | 3, 4, 5 | 1057 | 3 | 0.000 | 0.128 |
| | GO:0009890 | negative regulation of biosynthetic process | 3, 4, 5 | 906 | 2 | 0.000 | 0.106 |
| | GO:0007186 | G-protein coupled receptor signaling pathway | 4, 5, 6 | 903 | 2 | 0.000 | 0.094 |
| | GO:0031327 | negative regulation of cellular biosynthetic process | 4, 5, 6 | 893 | 2 | 0.000 | 0.093 |
| | GO:0007154 | cell communication | 2 | 4327 | 38 | 0.000 | 0.091 |
| | GO:0023052 | signaling | 1 | 4227 | 37 | 0.000 | 0.091 |
| | GO:0007005 | mitochondrion organization | 5 | 177 | 9 | 0.000 | 0.087 |
| | GO:0006281 | DNA repair | 5, 6, 7 | 392 | 14 | 0.001 | 0.080 |
| | GO:0009889 | regulation of biosynthetic process | 3, 4 | 2809 | 21 | 0.001 | 0.079 |
| | GO:0010556 | regulation of macromolecule biosynthetic process | 4, 5 | 2615 | 19 | 0.001 | 0.080 |
| | GO:0050794 | regulation of cellular process | 2, 3 | 6661 | 68 | 0.001 | 0.076 |
| | GO:0051297 | centrosome organization | 5, 6, 8 | 53 | 5 | 0.001 | 0.072 |
| | GO:0010468 | regulation of gene expression | 4, 5 | 2700 | 20 | 0.001 | 0.070 |
| | GO:0050789 | regulation of biological process | 1, 2 | 7035 | 73 | 0.001 | 0.067 |
| | GO:0031326 | regulation of cellular biosynthetic process | 4, 5 | 2785 | 21 | 0.001 | 0.066 |
| | GO:0007166 | cell surface receptor signaling pathway | 3, 4, 5 | 2224 | 15 | 0.001 | 0.066 |
| | GO:0010558 | negative regulation of macromolecule biosynthetic process | 4, 5, 6 | 821 | 2 | 0.001 | 0.075 |
| | GO:0031023 | microtubule organizing center organization | 4, 5, 7 | 58 | 5 | 0.001 | 0.076 |
| | GO:2000112 | regulation of cellular macromolecule biosynthetic process | 5, 6 | 2556 | 19 | 0.001 | 0.074 |
| | GO:0006081 | cellular aldehyde metabolic process | 3 | 34 | 4 | 0.001 | 0.074 |
| | GO:0006351 | transcription, DNA-dependent | 4, 5, 6, 7, 8 | 2458 | 18 | 0.001 | 0.072 |
| | GO:2001141 | regulation of RNA biosynthetic process | 5, 6, 7, 8 | 2358 | 17 | 0.001 | 0.074 |
| | GO:0032774 | RNA biosynthetic process | 4, 5, 6, 7 | 2529 | 19 | 0.001 | 0.077 |
| | GO:0006355 | regulation of transcription, DNA-dependent | 5, 6, 7, 8, 9 | 2341 | 17 | 0.001 | 0.078 |
| | GO:0006672 | ceramide metabolic process | 7, 8 | 62 | 5 | 0.001 | 0.079 |
| | GO:0006364 | rRNA processing | 6, 7, 8, 9 | 94 | 6 | 0.001 | 0.083 |
| | GO:2000113 | negative regulation of cellular macromolecule biosynthetic process | 5, 6, 7 | 781 | 2 | 0.001 | 0.083 |
| ***All DE genes in RJF (213 homologs found of 276 probesets included)*** | | | | | | | |
| | GO:0009892 | negative regulation of metabolic process | 2, 3, 4 | 1162 | 4 | 0.000 | 0.199 |
| | GO:0001574 | ganglioside biosynthetic process | 7, 8, 9, 10 | 8 | 3 | 0.000 | 0.171 |
| | GO:0031324 | negative regulation of cellular metabolic process | 3, 4, 5 | 1085 | 4 | 0.000 | 0.169 |
| | GO:0010605 | negative regulation of macromolecule metabolic process | 3, 4, 5 | 1057 | 4 | 0.000 | 0.176 |
| | GO:0006396 | RNA processing | 4, 5, 6, 7 | 569 | 19 | 0.000 | 0.178 |

| | | | | | | |
|---|---|---|---|---|---|---|
| GO:0010165 | response to X-ray | 5 | 26 | 4 | 0.000 | 0.171 |
| GO:0009890 | negative regulation of biosynthetic process | 3, 4, 5 | 906 | 3 | 0.001 | 0.160 |
| GO:0007186 | G-protein coupled receptor signaling pathway | 4, 5, 6 | 903 | 3 | 0.001 | 0.145 |
| GO:0007166 | cell surface receptor signaling pathway | 3, 4, 5 | 2224 | 17 | 0.001 | 0.138 |
| GO:0031327 | negative regulation of cellular biosynthetic process | 4, 5, 6 | 893 | 3 | 0.001 | 0.131 |
| GO:0045716 | positive regulation of low-density lipoprotein particle receptor biosynthetic process | 5, 6, 7, 8 | 3 | 2 | 0.001 | 0.123 |
| GO:0007005 | mitochondrion organization | 5 | 177 | 9 | 0.001 | 0.159 |
| GO:0051297 | centrosome organization | 5, 6, 8 | 53 | 5 | 0.001 | 0.149 |
| GO:0001573 | ganglioside metabolic process | 7, 8, 9 | 14 | 3 | 0.001 | 0.146 |
| GO:0010212 | response to ionizing radiation | 4 | 112 | 7 | 0.001 | 0.147 |
| GO:0010988 | regulation of low-density lipoprotein particle clearance | 4, 5, 6 | 4 | 2 | 0.001 | 0.166 |
| GO:0072369 | regulation of lipid transport by positive regulation of transcription from RNA polymerase II promoter | 6, 7, 8, 9, 10, 11, 12 | 4 | 2 | 0.001 | 0.156 |
| GO:0006081 | cellular aldehyde metabolic process | 3 | 34 | 4 | 0.001 | 0.158 |
| GO:0071479 | cellular response to ionizing radiation | 5 | 34 | 4 | 0.001 | 0.150 |
| GO:0031023 | microtubule organizing center organization | 4, 5, 7 | 58 | 5 | 0.001 | 0.144 |
| GO:0023052 | signaling | 1 | 4227 | 44 | 0.001 | 0.144 |
| GO:0006688 | glycosphingolipid biosynthetic process | 6, 7, 8 | 16 | 3 | 0.001 | 0.139 |
| GO:0010558 | negative regulation of macromolecule biosynthetic process | 4, 5, 6 | 821 | 3 | 0.001 | 0.134 |
| GO:0006672 | ceramide metabolic process | 7, 8 | 62 | 5 | 0.002 | 0.160 |
| GO:0007154 | cell communication | 2 | 4327 | 46 | 0.002 | 0.161 |
| GO:0072367 | regulation of lipid transport by regulation of transcription from RNA polymerase II promoter | 5, 6, 7, 8, 9, 10, 11 | 5 | 2 | 0.002 | 0.168 |
| GO:0006364 | rRNA processing | 6, 7, 8, 9 | 94 | 6 | 0.002 | 0.164 |
| GO:2000113 | negative regulation of cellular macromolecule biosynthetic process | 5, 6, 7 | 781 | 3 | 0.002 | 0.175 |
| GO:0006397 | mRNA processing | 5, 6, 7, 8 | 332 | 12 | 0.002 | 0.171 |
| GO:0046519 | sphingoid metabolic process | 6, 7 | 66 | 5 | 0.002 | 0.167 |
| ***Higher DE genes in RJF (38 genes found of 52 probesets included)*** | | | | | | |
| GO:0035261 | **external genitalia morphogenesis** | 4, 5, 6, 7 | 6 | 2 | 0.000 | 0.069 |
| GO:0061010 | gall bladder development | 4, 5 | 6 | 2 | 0.000 | **0.035** |
| GO:0060324 | face development | 3, 4 | 42 | 3 | 0.000 | **0.037** |
| GO:0034086 | maintenance of sister chromatid cohesion | 3, 4, 5, 7 | 8 | 2 | 0.000 | **0.032** |
| GO:0061038 | **uterus morphogenesis** | 3, 4, 5, 6 | 8 | 2 | 0.000 | **0.026** |
| GO:0034088 | maintenance of mitotic sister chromatid cohesion | 4, 5, 6, 7, 8, 9, 10 | 8 | 2 | 0.000 | **0.021** |
| GO:0071481 | cellular response to X-ray | 6 | 9 | 2 | 0.000 | **0.024** |
| GO:0035117 | embryonic arm morphogenesis | 7, 8 | 9 | 2 | 0.000 | **0.021** |
| GO:0035140 | arm morphogenesis | 6, 7 | 9 | 2 | 0.000 | **0.018** |
| GO:0007064 | mitotic sister chromatid cohesion | 4, 5, 6, 7, 8, 9 | 10 | 2 | 0.000 | **0.021** |
| GO:0031065 | positive regulation of histone deacetylation | 6, 7, 8, 9, 10, 11, 12 | 11 | 2 | 0.000 | **0.023** |
| GO:0060322 | head development | 3 | 58 | 3 | 0.000 | **0.024** |
| GO:0090312 | positive regulation of protein deacetylation | 6, 7, 8, 9 | 13 | 2 | 0.000 | **0.027** |
| GO:0048703 | embryonic viscerocranium morphogenesis | 4, 5, 7, 8, 9 | 14 | 2 | 0.000 | **0.029** |
| GO:0031063 | regulation of histone deacetylation | 6, 7, 8, 9, 11 | 15 | 2 | 0.001 | **0.032** |
| GO:0090311 | regulation of protein deacetylation | 6, 7, 8 | 17 | 2 | 0.001 | **0.038** |
| GO:0060065 | **uterus development** | 4, 5 | 18 | 2 | 0.001 | **0.040** |
| GO:0042634 | regulation of hair cycle | 3, 4 | 18 | 2 | 0.001 | **0.038** |
| GO:0035112 | **genitalia morphogenesis** | 3, 4, 5, 6 | 18 | 2 | 0.001 | **0.036** |
| GO:0032800 | receptor biosynthetic process | 4, 5 | 22 | 2 | 0.001 | 0.051 |
| GO:0048562 | embryonic organ morphogenesis | 4, 5, 6 | 211 | 4 | 0.001 | 0.055 |
| GO:0048557 | embryonic digestive tract morphogenesis | 4, 5, 6, 7 | 24 | 2 | 0.001 | 0.056 |
| GO:0010165 | response to X-ray | 5 | 26 | 2 | 0.002 | 0.062 |
| GO:0031058 | positive regulation of histone modification | 5, 6, 7, 8, 9, 10, 11 | 28 | 2 | 0.002 | 0.069 |
| GO:0007548 | **sex differentiation** | 3, 4 | 244 | 4 | 0.002 | 0.078 |
| GO:0042471 | ear morphogenesis | 5, 6, 7 | 114 | 3 | 0.002 | 0.075 |
| GO:0007062 | sister chromatid cohesion | 3, 4, 6 | 31 | 2 | 0.002 | 0.063 |
| GO:0035115 | embryonic forelimb morphogenesis | 6, 7 | 31 | 2 | 0.002 | 0.061 |
| GO:0060325 | face morphogenesis | 3, 4, 5, 6 | 32 | 2 | 0.003 | 0.063 |
| GO:2001252 | positive regulation of chromosome organization | 4, 5, 6, 7 | 32 | 2 | 0.003 | 0.062 |
| ***Lower DE genes in RJF (176 genes found of 224 probesets included)*** | | | | | | |
| GO:0009892 | negative regulation of metabolic process | 2, 3, 4 | 1162 | 2 | 0.000 | 0.078 |
| GO:0031324 | negative regulation of cellular metabolic process | 3, 4, 5 | 1085 | 2 | 0.000 | 0.094 |
| GO:0010605 | negative regulation of macromolecule metabolic process | 3, 4, 5 | 1057 | 2 | 0.000 | 0.065 |
| GO:0065007 | biological regulation | 1 | 7420 | 69 | 0.000 | 0.066 |
| GO:0051297 | centrosome organization | 5, 6, 8 | 53 | 5 | 0.000 | 0.105 |
| GO:0010556 | regulation of macromolecule biosynthetic process | 4, 5 | 2615 | 17 | 0.001 | 0.122 |
| GO:0031023 | microtubule organizing center organization | 4, 5, 7 | 58 | 5 | 0.001 | 0.105 |
| GO:0009889 | regulation of biosynthetic process | 3, 4 | 2809 | 19 | 0.001 | 0.097 |
| GO:0007186 | G-protein coupled receptor signaling pathway | 4, 5, 6 | 903 | 2 | 0.001 | 0.102 |
| GO:0031326 | regulation of cellular biosynthetic process | 4, 5 | 2785 | 19 | 0.001 | 0.100 |
| GO:0006364 | rRNA processing | 6, 7, 8, 9 | 94 | 6 | 0.001 | 0.110 |
| GO:2000112 | regulation of cellular macromolecule biosynthetic process | 5, 6 | 2556 | 17 | 0.001 | 0.109 |
| GO:0042254 | ribosome biogenesis | 5 | 131 | 7 | 0.001 | 0.104 |
| GO:0007154 | cell communication | 2 | 4327 | 36 | 0.001 | 0.100 |
| GO:0023052 | signaling | 1 | 4227 | 35 | 0.001 | 0.101 |
| GO:0006396 | RNA processing | 4, 5, 6, 7 | 569 | 16 | 0.001 | 0.097 |
| GO:0007005 | mitochondrion organization | 5 | 177 | 8 | 0.001 | 0.103 |
| GO:0016072 | rRNA metabolic process | 6, 7, 8 | 101 | 6 | 0.001 | 0.105 |
| GO:0050794 | regulation of cellular process | 2, 3 | 6661 | 64 | 0.001 | 0.114 |
| GO:0051172 | negative regulation of nitrogen compound metabolic process | 3, 4, 5 | 827 | 2 | 0.002 | 0.119 |
| GO:0045934 | negative regulation of nucleobase-containing compound metabolic process | 4, 5, 6 | 819 | 2 | 0.002 | 0.124 |
| GO:0022900 | electron transport chain | 3, 4 | 147 | 7 | 0.002 | 0.122 |
| GO:0050789 | regulation of biological process | 1, 2 | 7035 | 69 | 0.002 | 0.120 |
| GO:0006281 | DNA repair | 5, 6, 7 | 392 | 12 | 0.002 | 0.139 |
| GO:0007166 | cell surface receptor signaling pathway | 3, 4, 5 | 2224 | 15 | 0.002 | 0.143 |
| GO:0010468 | regulation of gene expression | 4, 5 | 2700 | 20 | 0.002 | 0.147 |
| GO:0032502 | developmental process | 1 | 3808 | 32 | 0.002 | 0.143 |
| GO:0018130 | heterocycle biosynthetic process | 4 | 355 | 11 | 0.003 | 0.167 |
| GO:0070841 | inclusion body assembly | 5 | 7 | 2 | 0.003 | 0.163 |
| GO:0022403 | cell cycle phase | 3, 4 | 756 | 18 | 0.003 | 0.160 |
| ***All DE genes in WL (165 homologs found of 204 probesets included)*** | | | | | | |
| GO:0007166 | cell surface receptor signaling pathway | 3, 4, 5 | 2224 | 7 | 0.000 | **0.008** |
| GO:0065007 | biological regulation | 1 | 7420 | 58 | 0.000 | **0.012** |
| GO:0050794 | regulation of cellular process | 2, 3 | 6661 | 53 | 0.000 | 0.068 |
| GO:0050789 | regulation of biological process | 1, 2 | 7035 | 58 | 0.000 | 0.085 |
| GO:0007154 | cell communication | 2 | 4327 | 30 | 0.000 | 0.091 |
| GO:0045716 | positive regulation of low-density lipoprotein particle receptor biosynthetic process | 5, 6, 7, 8 | 3 | 2 | 0.000 | 0.093 |
| GO:0023052 | signaling | 1 | 4227 | 30 | 0.000 | 0.105 |
| GO:0071479 | cellular response to ionizing radiation | 5 | 34 | 4 | 0.001 | 0.099 |
| GO:0006081 | cellular aldehyde metabolic process | 3 | 34 | 4 | 0.001 | 0.089 |
| GO:0000086 | G2/M transition of mitotic cell cycle | 3, 4, 5, 6, 7 | 135 | 7 | 0.001 | 0.109 |
| GO:0072369 | regulation of lipid transport by positive regulation of transcription from RNA polymerase II promoter | 6, 7, 8, 9, 10, 11, 12 | 4 | 2 | 0.001 | 0.107 |
| GO:0010988 | regulation of low-density lipoprotein particle clearance | 4, 5, 6 | 4 | 2 | 0.001 | 0.099 |
| GO:0006974 | response to DNA damage stimulus | 4 | 560 | 15 | 0.001 | 0.131 |
| GO:0072367 | regulation of lipid transport by regulation of transcription from RNA polymerase II promoter | 5, 6, 7, 8, 9, 10, 11 | 5 | 2 | 0.001 | 0.141 |
| GO:0022403 | cell cycle phase | 3, 4 | 756 | 18 | 0.001 | 0.137 |
| GO:0010212 | response to ionizing radiation | 4 | 112 | 6 | 0.001 | 0.142 |
| GO:0010984 | regulation of lipoprotein particle clearance | 3, 4, 5 | 6 | 2 | 0.002 | 0.175 |
| GO:0061010 | gall bladder development | 4, 5 | 6 | 2 | 0.002 | 0.166 |

| | | | | | | |
|---|---|---|---|---|---|---|
| GO:0035261 | **external genitalia morphogenesis** | 4, 5, 6, 7 | 6 | 2 | 0.002 | 0.157 |
| GO:0033554 | cellular response to stress | 3 | 991 | 21 | 0.002 | 0.167 |
| GO:0048583 | regulation of response to stimulus | 2, 3 | 1881 | 10 | 0.002 | 0.163 |
| GO:0046487 | glyoxylate metabolic process | 4, 7 | 7 | 2 | 0.002 | 0.189 |
| GO:0045714 | regulation of low-density lipoprotein particle receptor biosynthetic process | 5, 6, 7 | 7 | 2 | 0.002 | 0.181 |
| GO:0070841 | inclusion body assembly | 5 | 7 | 2 | 0.002 | 0.174 |
| GO:0007165 | signal transduction | 2, 3, 4 | 3830 | 29 | 0.003 | 0.171 |
| GO:0009889 | regulation of biosynthetic process | 3, 4 | 2809 | 19 | 0.003 | 0.176 |
| GO:0000278 | mitotic cell cycle | 3 | 688 | 16 | 0.003 | 0.172 |
| GO:0010468 | regulation of gene expression | 4, 5 | 2700 | 18 | 0.003 | 0.168 |
| GO:0010165 | response to X-ray | 5 | 26 | 3 | 0.003 | 0.163 |
| GO:0042254 | ribosome biogenesis | 5 | 131 | 6 | 0.003 | 0.165 |
| ***Higher DE genes in WL (32 genes found of 41 probesets included)*** | | | | | | |
| GO:0040018 | positive regulation of multicellular organism growth | 3, 4, 5 | 34 | 3 | 0.000 | **0.026** |
| GO:0061010 | gall bladder development | 4, 5 | 6 | 2 | 0.000 | **0.019** |
| GO:0035261 | **external genitalia morphogenesis** | 4, 5, 6, 7 | 6 | 2 | 0.000 | **0.013** |
| GO:0034086 | maintenance of sister chromatid cohesion | 3, 4, 5, 7 | 8 | 2 | 0.000 | **0.018** |
| GO:0061038 | **uterus morphogenesis** | 3, 4, 5, 6 | 8 | 2 | 0.000 | **0.014** |
| GO:0034088 | maintenance of mitotic sister chromatid cohesion | 4, 5, 6, 7, 8, 9, 10 | 8 | 2 | 0.000 | **0.012** |
| GO:0071481 | cellular response to X-ray | 6 | 9 | 2 | 0.000 | **0.013** |
| GO:0035117 | embryonic arm morphogenesis | 7, 8 | 9 | 2 | 0.000 | **0.011** |
| GO:0035140 | arm morphogenesis | 6, 7 | 9 | 2 | 0.000 | **0.010** |
| GO:0007064 | mitotic sister chromatid cohesion | 4, 5, 6, 7, 8, 9 | 10 | 2 | 0.000 | **0.011** |
| GO:0031065 | positive regulation of histone deacetylation | 6, 7, 8, 9, 10, 11, 12 | 11 | 2 | 0.000 | **0.013** |
| GO:0090312 | positive regulation of protein deacetylation | 6, 7, 8, 9 | 13 | 2 | 0.000 | **0.016** |
| GO:0048703 | embryonic viscerocranium morphogenesis | 4, 5, 7, 8, 9 | 14 | 2 | 0.000 | **0.017** |
| GO:0031063 | regulation of histone deacetylation | 6, 7, 8, 9, 11 | 15 | 2 | 0.000 | **0.019** |
| GO:0090311 | regulation of protein deacetylation | 6, 7, 8 | 17 | 2 | 0.000 | **0.023** |
| GO:0040014 | regulation of multicellular organism growth | 3, 4 | 81 | 3 | 0.000 | **0.021** |
| GO:0060065 | **uterus development** | 4, 5 | 18 | 2 | 0.001 | **0.022** |
| GO:0035112 | **genitalia morphogenesis** | 3, 4, 5, 6 | 18 | 2 | 0.001 | **0.021** |
| GO:0042634 | regulation of hair cycle | 3, 4 | 18 | 2 | 0.001 | **0.020** |
| GO:0048557 | embryonic digestive tract morphogenesis | 4, 5, 6, 7 | 24 | 2 | 0.001 | **0.034** |
| GO:0010165 | response to X-ray | 5 | 26 | 2 | 0.001 | **0.038** |
| GO:0048638 | regulation of developmental growth | 3, 4 | 110 | 3 | 0.001 | **0.037** |
| GO:0031058 | positive regulation of histone modification | 5, 6, 7, 8, 9, 10, 11 | 28 | 2 | 0.001 | **0.040** |
| GO:0007062 | sister chromatid cohesion | 3, 4, 6 | 31 | 2 | 0.002 | **0.047** |
| GO:0035115 | embryonic forelimb morphogenesis | 6, 7 | 31 | 2 | 0.002 | **0.045** |
| GO:2001252 | positive regulation of chromosome organization | 4, 5, 6, 7 | 32 | 2 | 0.002 | **0.046** |
| GO:0060325 | **face morphogenesis** | 3, 4, 5, 6 | 32 | 2 | 0.002 | **0.044** |
| GO:0000279 | M phase | 4, 5 | 477 | 5 | 0.002 | **0.044** |
| GO:0035264 | multicellular organism growth | 2 | 131 | 3 | 0.002 | **0.046** |
| GO:0071479 | cellular response to ionizing radiation | 5 | 34 | 2 | 0.002 | **0.045** |
| GO:0016575 | histone deacetylation | 7, 8, 10 | 35 | 2 | 0.002 | **0.045** |
| GO:0048701 | **embryonic cranial skeleton morphogenesis** | 6, 7, 8 | 37 | 2 | 0.002 | **0.048** |
| GO:0060323 | **head morphogenesis** | 3, 4, 5 | 38 | 2 | 0.002 | **0.049** |
| GO:0045927 | positive regulation of growth | 2, 3, 4 | 143 | 3 | 0.002 | **0.049** |
| ***Lower DE genes in RJF (134 genes found of 163 probesets included)*** | | | | | | |
| GO:0065007 | biological regulation | 1 | 7420 | 43 | 0.000 | **0.002** |
| GO:0050794 | regulation of cellular process | 2, 3 | 6661 | 39 | 0.000 | **0.009** |
| GO:0050789 | regulation of biological process | 1, 2 | 7035 | 43 | 0.000 | **0.010** |
| GO:0007166 | cell surface receptor signaling pathway | 3, 4, 5 | 2224 | 6 | 0.000 | **0.015** |
| GO:0006081 | cellular aldehyde metabolic process | 3 | 34 | 4 | 0.000 | 0.083 |
| GO:0010468 | regulation of gene expression | 4, 5 | 2700 | 11 | 0.000 | 0.073 |
| GO:0009889 | regulation of biosynthetic process | 3, 4 | 2809 | 12 | 0.000 | 0.076 |
| GO:0007154 | cell communication | 2 | 4327 | 24 | 0.000 | 0.078 |
| GO:0031326 | regulation of cellular biosynthetic process | 4, 5 | 2785 | 12 | 0.000 | 0.069 |
| GO:0048583 | regulation of response to stimulus | 2, 3 | 1881 | 6 | 0.001 | 0.081 |
| GO:0031323 | regulation of cellular metabolic process | 3, 4 | 3653 | 19 | 0.001 | 0.076 |
| GO:0023052 | signaling | 1 | 4227 | 24 | 0.001 | 0.089 |
| GO:0006281 | DNA repair | 5, 6, 7 | 392 | 11 | 0.001 | 0.102 |
| GO:0019222 | regulation of metabolic process | 2, 3 | 4057 | 23 | 0.001 | 0.099 |
| GO:0080090 | regulation of primary metabolic process | 3, 4 | 3560 | 19 | 0.001 | 0.094 |
| GO:0051171 | regulation of nitrogen compound metabolic process | 3, 4 | 2908 | 14 | 0.001 | 0.094 |
| GO:2001141 | regulation of RNA biosynthetic process | 5, 6, 7, 8 | 2358 | 10 | 0.001 | 0.096 |
| GO:0010556 | regulation of macromolecule biosynthetic process | 4, 5 | 2615 | 12 | 0.001 | 0.099 |
| GO:0006355 | regulation of transcription, DNA-dependent | 5, 6, 7, 8, 9 | 2341 | 10 | 0.001 | 0.095 |
| GO:0042254 | ribosome biogenesis | 5 | 131 | 6 | 0.001 | 0.098 |
| GO:0032501 | multicellular organismal process | 1 | 4702 | 29 | 0.001 | 0.095 |
| GO:0006351 | transcription, DNA-dependent | 4, 5, 6, 7, 8 | 2458 | 11 | 0.001 | 0.092 |
| GO:0000086 | G2/M transition of mitotic cell cycle | 3, 4, 5, 6, 7 | 135 | 6 | 0.001 | 0.099 |
| GO:0019219 | regulation of nucleobase-containing compound metabolic process | 4, 5 | 2832 | 14 | 0.001 | 0.097 |
| GO:2000112 | regulation of cellular macromolecule biosynthetic process | 5, 6 | 2556 | 12 | 0.002 | 0.097 |
| GO:0006364 | rRNA processing | 6, 7, 8, 9 | 94 | 5 | 0.002 | 0.097 |
| GO:0032502 | developmental process | 1 | 3808 | 22 | 0.002 | 0.095 |
| GO:0006396 | RNA processing | 4, 5, 6, 7 | 569 | 13 | 0.002 | 0.096 |
| GO:0051252 | regulation of RNA metabolic process | 4, 5, 6, 7 | 2404 | 11 | 0.002 | 0.093 |
| GO:0070841 | inclusion body assembly | 5 | 7 | 2 | 0.002 | 0.090 |

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