

| Cluster | ID | Description | Gene Ratio | BgR Ratio | pvalue | p.adjust | qvalue |
|---------|---------------|---|------------|-------------------|--------------|----------------|----------------|
| 1 | GO:0 03019 | negative regulation of blood coagulation | 5/87 | 52/1 8493 | 4.48E -06 | 0.002 93928 | 0.002 60450 |
| 1 | GO:1 90004 | negative regulation of hemostasis | 5/87 | 52/1 8493 | 4.48E -06 | 0.002 93928 | 0.002 60450 |
| 1 | GO:0 05081 | negative regulation of coagulation | 5/87 | 56/1 8493 | 6.49E -06 | 0.002 93928 | 0.002 60450 |
| 1 | GO:0 06104 | negative regulation of wound healing | 5/87 | 72/1 8493 | 2.24E -05 | 0.004 94421 | 0.004 38106 |
| 1 | GO:0 03019 | regulation of blood coagulation | 5/87 | 77/1 8493 | 3.11E -05 | 0.004 94421 | 0.004 38106 |
| 1 | GO:1 90004 | regulation of hemostasis | 5/87 | 77/1 8493 | 3.11E -05 | 0.004 94421 | 0.004 38106 |
| 1 | GO:0 00300 | regionalization | 9/87 | 341/ 1849 3 | 3.21E -05 | 0.004 94421 | 0.004 38106 |
| 1 | GO:0 06104 | regulation of wound healing | 6/87 | 134/ 1849 3 | 4.04E -05 | 0.004 94421 | 0.004 38106 |
| 1 | GO:0 00758 | digestion | 6/87 | 135/ 1849 3 | 4.21E -05 | 0.004 94421 | 0.004 38106 |
| 1 | GO:0 05081 | regulation of coagulation | 5/87 | 82/1 8493 | 4.21E -05 | 0.004 94421 | 0.004 38106 |
| 1 | GO:0 03411 | positive regulation of heterotypic cell-cell adhesion | 3/87 | 15/1 8493 | 4.39E -05 | 0.004 94421 | 0.004 38106 |
| 1 | GO:0 01003 | response to metal ion | 9/87 | 358/ 1849 3 | 4.69E -05 | 0.004 94421 | 0.004 38106 |
| 1 | GO:1 90303 | negative regulation of response to wounding | 5/87 | 84/1 8493 | 4.73E -05 | 0.004 94421 | 0.004 38106 |
| 1 | GO:0 00995 | anterior/posterior pattern specification | 7/87 | 211/ 1849 3 | 6.15E -05 | 0.005 96925 | 0.005 28936 |
| 1 | GO:0 02260 | digestive system process | 5/87 | 97/1 8493 | 9.41E -05 | 0.008 52684 | 0.007 55563 |

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|---|---|------|------|-------|-------|-------|--|
| | GO:1 | | 160/ | 0.000 | 0.008 | 0.007 | |
| 1 | 90303 regulation of response to wounding | 6/87 | 1849 | 10817 | 64966 | 66447 | |
| | 4 | | 3 | 8 | 3 | 1 | |
| | GO:0 | | | | 0.008 | 0.007 | |
| 1 | 03027 maintenance of gastrointestinal epithelium | 3/87 | 20/1 | 0.000 | 64966 | 66447 | |
| | 7 | | 8493 | 1082 | 3 | 1 | |
| | GO:0 | | | 0.000 | 0.014 | 0.012 | |
| 1 | 03163 plasminogen activation | 3/87 | 24/1 | 18950 | 30779 | 67814 | |
| | 9 | | 8493 | 7 | 4 | 3 | |
| | GO:0 | | 434/ | 0.000 | 0.014 | 0.012 | |
| 1 | 00738 pattern specification process | 9/87 | 1849 | 20215 | 45968 | 81273 | |
| | 9 | | 3 | 9 | 9 | 7 | |
| | GO:0 | | | 0.000 | 0.014 | 0.012 | |
| 1 | 03411 regulation of heterotypic cell-cell adhesion | 3/87 | 25/1 | 21461 | 58330 | 92227 | |
| | 4 | | 8493 | 8 | 9 | 7 | |
| | GO:0 | | 152/ | 3.26E | 7.04E | 5.65E | |
| 2 | 03016 platelet activation | 9/85 | 1849 | -08 | -05 | -05 | |
| | 8 | | 3 | | | | |
| | GO:0 | | 287/ | 7.78E | 0.000 | 0.000 | |
| 2 | 03433 cell junction organization | 10/8 | 1849 | -07 | 79027 | 63440 | |
| | 0 | | 5 | 3 | 1 | 7 | |
| | GO:0 | | 76/1 | 1.33E | 0.000 | 0.000 | |
| 2 | 03410 homotypic cell-cell adhesion | 6/85 | 8493 | -06 | 79027 | 63440 | |
| | 9 | | | | 1 | 7 | |
| | GO:0 | | 238/ | 1.47E | 0.000 | 0.000 | |
| 2 | 03432 cell junction assembly | 9/85 | 1849 | -06 | 79027 | 63440 | |
| | 9 | | 3 | | 1 | 7 | |
| | GO:0 | | 493/ | 2.54E | 0.001 | 0.000 | |
| 2 | 05087 regulation of body fluid levels | 12/8 | 1849 | -06 | 09430 | 87847 | |
| | 8 | | 5 | 3 | 2 | 5 | |
| | GO:0 | | 95/1 | 4.94E | 0.001 | 0.001 | |
| 2 | 00704 cell-substrate junction assembly | 6/85 | 8493 | -06 | 77666 | 42625 | |
| | 4 | | | | 6 | 8 | |
| | GO:0 | | 57/1 | 6.32E | 0.001 | 0.001 | |
| 2 | 07052 platelet aggregation | 5/85 | 8493 | -06 | 94751 | 56340 | |
| | 7 | | | | 2 | 8 | |
| | GO:0 | | 36/1 | 2.19E | 0.005 | 0.004 | |
| 2 | 04507 positive regulation of viral genome replication | 4/85 | 8493 | -05 | 10618 | 09910 | |
| | 0 | | | | 5 | 2 | |
| | GO:0 | | 334/ | 2.26E | 0.005 | 0.004 | |
| 2 | 00759 blood coagulation | 9/85 | 1849 | -05 | 10618 | 09910 | |
| | 6 | | 3 | | 5 | 2 | |
| | GO:0 | | 339/ | 2.54E | 0.005 | 0.004 | |
| 2 | 00759 hemostasis | 9/85 | 1849 | -05 | 10618 | 09910 | |
| | 9 | | 3 | | 5 | 2 | |
| | GO:0 | | 340/ | 2.60E | 0.005 | 0.004 | |
| 2 | 05081 coagulation | 9/85 | 1849 | -05 | 10618 | 09910 | |
| | 7 | | 3 | | 5 | 2 | |

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|------|-------|---|------|--------------|----------------|-------|-------|-------|
| GO:0 | | | | | | | 0.006 | 0.005 |
| 2 | 05077 | positive regulation of axonogenesis | 5/85 | 81/1 8493 | 3.55E -05 | 37647 | 11885 | |
| | 2 | | | | | 1 | 2 | |
| GO:0 | | | | | | | 0.006 | 0.005 |
| 2 | 05165 | spindle localization | 4/85 | 42/1 8493 | 4.07E -05 | 75653 | 42395 | |
| | 3 | | | | | 4 | 5 | |
| GO:0 | | | | | | | 0.007 | 0.005 |
| 2 | 04852 | positive regulation of viral process | 5/85 | 86/1 8493 | 4.74E -05 | 29672 | 85760 | |
| | 4 | | | | | 1 | 2 | |
| GO:0 | | | | | | | 0.008 | 0.006 |
| 2 | 01077 | positive regulation of cell morphogenesis involved in differentiation | 6/85 | 147/ 1849 | 5.94E -05 | 54537 | 85998 | |
| | 0 | | | | | 3 | 4 | 6 |
| GO:0 | | | | | | | 0.008 | 0.006 |
| 2 | 00176 | neuron migration | 6/85 | 149/ 1849 | 6.41E -05 | 63682 | 93339 | |
| | 4 | | | | | 3 | 4 | 9 |
| GO:0 | | | | | | | 0.010 | 0.008 |
| 2 | 06156 | axon development | 10/8 | 493/ 1849 | 8.65E -05 | 97253 | 80843 | |
| | 4 | | | | | 5 | 3 | 8 |
| GO:0 | | | | | | | 0.010 | 0.008 |
| 2 | 00722 | integrin-mediated signaling pathway | 5/85 | 99/1 8493 | 9.28E -05 | 97486 | 81031 | |
| | 9 | | | | | 5 | 3 | |
| GO:0 | | | | | | | 0.010 | 0.008 |
| 2 | 00751 | muscle organ development | 9/85 | 403/ 1849 | 9.68E -05 | 97486 | 81031 | |
| | 7 | | | | | 3 | 5 | 3 |
| GO:0 | | | | | | | 0.010 | 0.008 |
| 2 | 04390 | positive regulation of multi-organism process | 6/85 | 162/ 1849 | 0.000 10176 | 97486 | 81031 | |
| | 2 | | | | | 3 | 5 | 3 |
| GO:0 | | | | | | | 1.82E | 1.55E |
| 3 | 00661 | SRP-dependent cotranslational protein targeting to membrane | 50/9 | 105/ 1849 | 1.01E -91 | 1.82E | 1.55E | -88 |
| | 4 | | | | | 5 | 3 | -88 |
| GO:0 | | | | | | | 1.10E | 9.38E |
| 3 | 00661 | cotranslational protein targeting to membrane | 50/9 | 109/ 1849 | 1.22E -90 | 1.10E | 9.38E | -88 |
| | 3 | | | | | 5 | 3 | -88 |
| GO:0 | | | | | | | 1.29E | 1.10E |
| 3 | 00018 | nuclear-transcribed mRNA catabolic process, nonsense-mediated decay | 51/9 | 120/ 1849 | 2.15E -90 | 1.29E | 1.10E | -87 |
| | 4 | | | | | 5 | 3 | -87 |
| GO:0 | | | | | | | 5.66E | 4.81E |
| 3 | 04504 | protein targeting to ER | 50/9 | 117/ 1849 | 1.26E -88 | 5.66E | 4.81E | -86 |
| | 7 | | | | | 5 | 3 | -86 |
| GO:0 | | | | | | | 3.92E | 3.33E |
| 3 | 07259 | establishment of protein localization to endoplasmic reticulum | 50/9 | 121/ 1849 | 1.09E -87 | 3.92E | 3.33E | -85 |
| | 9 | | | | | 5 | 3 | -85 |
| GO:0 | | | | | | | 1.77E | 1.51E |
| 3 | 07097 | protein localization to endoplasmic reticulum | 51/9 | 146/ 1849 | 5.90E -85 | 1.77E | 1.51E | -82 |
| | 2 | | | | | 5 | 3 | -82 |
| GO:0 | | | | | | | 1.03E | 8.77E |
| 3 | 00641 | translational initiation | 54/9 | 194/ 1849 | 4.01E -84 | 1.03E | 8.77E | -82 |
| | 3 | | | | | 5 | 3 | -82 |

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|------|---|------|----------|-------|-------|-------|
| GO:0 | | | | | | |
| 3 | 00095 nuclear-transcribed mRNA catabolic process | 51/9 | 207/1849 | 6.96E | 1.57E | 1.33E |
| 6 | | 5 | 3 | -76 | -73 | -73 |
| GO:0 | | | | | | |
| 3 | 00661 protein targeting to membrane | 50/9 | 198/1849 | 7.35E | 1.47E | 1.25E |
| 2 | | 5 | 3 | -75 | -72 | -72 |
| GO:0 | | | | | | |
| 3 | 00640 mRNA catabolic process | 55/9 | 307/1849 | 4.66E | 8.40E | 7.14E |
| 2 | | 5 | 3 | -74 | -72 | -72 |
| GO:0 | | | | | | |
| 3 | 00640 RNA catabolic process | 55/9 | 340/1849 | 2.02E | 3.32E | 2.82E |
| 1 | | 5 | 3 | -71 | -69 | -69 |
| GO:0 | | | | | | |
| 3 | 09015 establishment of protein localization to membrane | 53/9 | 317/1849 | 2.59E | 3.88E | 3.30E |
| 0 | | 5 | 3 | -69 | -67 | -67 |
| GO:0 | | | | | | |
| 3 | 00660 protein targeting | 54/9 | 424/1849 | 5.41E | 7.50E | 6.38E |
| 5 | | 5 | 3 | -64 | -62 | -62 |
| GO:0 | | | | | | |
| 3 | 04225 ribosome biogenesis | 26/9 | 282/1849 | 1.07E | 1.37E | 1.17E |
| 4 | | 5 | 3 | -25 | -23 | -23 |
| GO:0 | | | | | | |
| 3 | 02261 ribonucleoprotein complex biogenesis | 30/9 | 485/1849 | 1.47E | 1.76E | 1.50E |
| 3 | | 5 | 3 | -24 | -22 | -22 |
| GO:0 | | | | | | |
| 3 | 00218 cytoplasmic translation | 18/9 | 93/1 | 6.07E | 6.84E | 5.81E |
| 1 | | 5 | 8493 | -24 | -22 | -22 |
| GO:0 | | | | | | |
| 3 | 00636 rRNA processing | 18/9 | 205/1849 | 1.58E | 1.68E | 1.42E |
| 4 | | 5 | 3 | -17 | -15 | -15 |
| GO:0 | | | | | | |
| 3 | 01607 rRNA metabolic process | 18/9 | 240/1849 | 2.63E | 2.64E | 2.24E |
| 2 | | 5 | 3 | -16 | -14 | -14 |
| GO:0 | | | | | | |
| 3 | 04227 ribosomal small subunit biogenesis | 12/9 | 63/1 | 3.55E | 3.36E | 2.86E |
| 4 | | 5 | 8493 | -16 | -14 | -14 |
| GO:0 | | | | | | |
| 3 | 04227 ribosomal large subunit biogenesis | 12/9 | 73/1 | 2.34E | 2.11E | 1.80E |
| 3 | | 5 | 8493 | -15 | -13 | -13 |
| GO:0 | | | | | | |
| 4 | 03508 axoneme assembly | 8/42 | 61/1 | 9.41E | 2.23E | 1.95E |
| 2 | | | 8493 | -13 | -10 | -10 |
| GO:0 | | | | | | |
| 4 | 00334 cilium movement | 8/42 | 63/1 | 1.23E | 2.23E | 1.95E |
| 1 | | | 8493 | -12 | -10 | -10 |
| GO:0 | | | | | | |
| 4 | 00701 microtubule-based movement | 11/4 | 269/1849 | 1.44E | 1.74E | 1.53E |
| 8 | | 2 | 3 | -11 | -09 | -09 |

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|---|--|------|------|-------|-------|-------|
| | GO:0 | | 255/ | 0.002 | 0.046 | 0.041 |
| 4 | 00728 germ cell development | 4/42 | 1849 | 61920 | 98483 | 12368 |
| | 1 | | 3 | 9 | 8 | 8 |
| | GO:0 | | 458/ | | | |
| 7 | 00854 epidermis development | 16/9 | 1849 | 1.02E | 1.54E | 1.41E |
| | 4 | 3 | 3 | -09 | -06 | -06 |
| | GO:0 | | 12/1 | 2.22E | 1.67E | 1.53E |
| 7 | 03158 hemidesmosome assembly | 5/93 | 8493 | -09 | -06 | -06 |
| | 1 | | | | | |
| | GO:0 | | 112/ | 9.34E | 4.69E | 4.30E |
| 7 | 07026 cornification | 8/93 | 1849 | -08 | -05 | -05 |
| | 8 | | 3 | | | |
| | GO:0 | | 412/ | 1.42E | 5.37E | 4.92E |
| 7 | 04358 skin development | 13/9 | 1849 | -07 | -05 | -05 |
| | 8 | 3 | 3 | | | |
| | GO:0 | | 20/1 | 2.73E | 0.000 | 0.000 |
| 7 | 03027 maintenance of gastrointestinal epithelium | 4/93 | 8493 | -06 | 82284 | 75407 |
| | 7 | | | | 1 | 2 |
| | GO:0 | | 27/1 | 9.63E | 0.002 | 0.002 |
| 7 | 01066 epithelial structure maintenance | 4/93 | 8493 | -06 | 41776 | 21570 |
| | 9 | | | | 8 | 3 |
| | GO:0 | | 61/1 | 1.37E | 0.002 | 0.002 |
| 7 | 01626 O-glycan processing | 5/93 | 8493 | -05 | 95895 | 71165 |
| | 6 | | | | 1 | 7 |
| | GO:0 | | 224/ | 1.72E | 0.003 | 0.002 |
| 7 | 03142 keratinization | 8/93 | 1849 | -05 | 24081 | 96996 |
| | 4 | 3 | 3 | | 4 | 3 |
| | GO:0 | | 113/ | 2.25E | 0.003 | 0.003 |
| 7 | 04230 molting cycle | 6/93 | 1849 | -05 | 39588 | 11207 |
| | 3 | 3 | 3 | | 4 | 4 |
| | GO:0 | | 113/ | 2.25E | 0.003 | 0.003 |
| 7 | 04263 hair cycle | 6/93 | 1849 | -05 | 39588 | 11207 |
| | 3 | 3 | 3 | | 4 | 4 |
| | GO:0 | | 135/ | 6.13E | 0.007 | 0.007 |
| 7 | 00758 digestion | 6/93 | 1849 | -05 | 92107 | 25907 |
| | 6 | 3 | 3 | | 6 | 2 |
| | GO:0 | | 348/ | 6.40E | 0.007 | 0.007 |
| 7 | 03019 extracellular matrix organization | 9/93 | 1849 | -05 | 92107 | 25907 |
| | 8 | 3 | 3 | | 6 | 2 |
| | GO:0 | | 351/ | 6.83E | 0.007 | 0.007 |
| 7 | 00991 epidermal cell differentiation | 9/93 | 1849 | -05 | 92107 | 25907 |
| | 3 | 3 | 3 | | 6 | 2 |
| | GO:0 | | 95/1 | 0.000 | 0.012 | 0.011 |
| 7 | 00704 cell-substrate junction assembly | 5/93 | 8493 | 11702 | 41018 | 37300 |
| | 4 | | | 3 | 6 | 6 |
| | GO:0 | | 97/1 | 0.000 | 0.012 | 0.011 |
| 7 | 02260 digestive system process | 5/93 | 8493 | 12913 | 41018 | 37300 |
| | 0 | | | 8 | 6 | 6 |

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|---|---|------|------|-------|-------|-------|
| | GO:0 | | 299/ | 0.000 | 0.012 | 0.011 |
| 7 | 03021 keratinocyte differentiation | 8/93 | 1849 | 13176 | 41018 | 37300 |
| | 6 | | 3 | | 6 | 6 |
| | GO:0 | | 102/ | 0.000 | 0.014 | 0.013 |
| 7 | 00649 protein O-linked glycosylation | 5/93 | 1849 | 16364 | 50616 | 29381 |
| | 3 | | 3 | | 4 | 3 |
| | GO:0 | | 402/ | 0.000 | 0.015 | 0.014 |
| 7 | 04306 extracellular structure organization | 9/93 | 1849 | 19046 | 72122 | 40732 |
| | 2 | | 3 | 3 | | 1 |
| | GO:0 | | 238/ | 0.000 | 0.015 | 0.014 |
| 7 | 03432 cell junction assembly | 7/93 | 1849 | 19821 | 72122 | 40732 |
| | 9 | | 3 | | | 1 |
| | GO:0 | | 26/1 | 0.000 | 0.021 | 0.020 |
| 7 | 06070 cell differentiation involved in embryonic placenta development | 3/93 | 8493 | 29436 | 87457 | 04641 |
| | 6 | | | 3 | 8 | 3 |
| | GO:0 | | 11/1 | 1.10E | 2.58E | 2.15E |
| 8 | 04312 surfactant homeostasis | 5/90 | 8493 | -09 | -06 | -06 |
| | 9 | | | | | |
| | GO:0 | | 13/1 | 3.04E | 3.56E | 2.98E |
| 8 | 04887 chemical homeostasis within a tissue | 5/90 | 8493 | -09 | -06 | -06 |
| | 5 | | | | | |
| | GO:0 | | 221/ | 1.20E | 9.14E | 7.64E |
| 8 | 00189 tissue homeostasis | 10/9 | 1849 | -07 | -05 | -05 |
| | 4 | 0 | 3 | | | |
| | GO:0 | | 133/ | 2.74E | 9.14E | 7.64E |
| 8 | 03026 entry into host cell | 8/90 | 1849 | -07 | -05 | -05 |
| | 0 | | 3 | | | |
| | GO:0 | | 133/ | 2.74E | 9.14E | 7.64E |
| 8 | 04440 entry into host | 8/90 | 1849 | -07 | -05 | -05 |
| | 9 | | 3 | | | |
| | GO:0 | | 133/ | 2.74E | 9.14E | 7.64E |
| 8 | 05180 entry into cell of other organism involved in symbiotic interaction | 8/90 | 1849 | -07 | -05 | -05 |
| | 6 | | 3 | | | |
| | GO:0 | | 133/ | 2.74E | 9.14E | 7.64E |
| 8 | 05182 entry into other organism involved in symbiotic interaction | 8/90 | 1849 | -07 | -05 | -05 |
| | 8 | | 3 | | | |
| | GO:0 | | 289/ | 1.41E | 0.000 | 0.000 |
| 8 | 01905 viral life cycle | 10/9 | 1849 | -06 | 41332 | 34542 |
| | 8 | 0 | 3 | | 6 | 2 |
| | GO:0 | | 471/ | 2.93E | 0.000 | 0.000 |
| 8 | 04887 multicellular organismal homeostasis | 12/9 | 1849 | -06 | 76239 | 63714 |
| | 1 | 0 | 3 | | 4 | 4 |
| | GO:0 | | 425/ | 6.76E | 0.001 | 0.001 |
| 8 | 06024 anatomical structure homeostasis | 11/9 | 1849 | -06 | 58203 | 32213 |
| | 9 | 0 | 3 | | 7 | 2 |
| | GO:0 | | 209/ | 8.16E | 0.001 | 0.001 |
| 8 | 05170 interaction with host | 8/90 | 1849 | -06 | 73435 | 44942 |
| | 1 | | 3 | | 4 | 5 |

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| 8 | GO:1 90390 positive regulation of viral life cycle 2 | 5/90 | 60/1 8493 | 1.08E -05 | 0.002 10360 | 0.001 75801 | | |
| | | | | | 3 | 2 | | |
| 8 | GO:0 05090 leukocyte migration 0 | 11/90 | 478/ 1849 | 2.03E -05 | 0.003 64707 | 0.003 04791 | | |
| | | | 3 | | 7 | 6 | | |
| 8 | GO:0 00166 response to hypoxia 6 | 9/90 | 314/ 1849 | 2.21E -05 | 0.003 69690 | 0.003 08955 | | |
| | | | 3 | | 5 | 9 | | |
| 8 | GO:0 04306 extracellular structure organization 2 | 10/90 | 402/ 1849 | 2.56E -05 | 0.003 98946 | 0.003 33405 | | |
| | | | 3 | | | | | |
| 8 | GO:0 04671 viral entry into host cell 8 | 6/90 | 121/ 1849 | 2.75E -05 | 0.003 98946 | 0.003 33405 | | |
| | | | 3 | | | | | |
| 8 | GO:0 03629 response to decreased oxygen levels 3 | 9/90 | 325/ 1849 | 2.90E -05 | 0.003 98946 | 0.003 33405 | | |
| | | | 3 | | | | | |
| 8 | GO:0 07048 response to oxygen levels 2 | 9/90 | 349/ 1849 | 5.05E -05 | 0.006 55682 | 0.005 47963 | | |
| | | | 3 | | 3 | 4 | | |
| 8 | GO:0 04505 transcytosis 6 | 3/90 | 16/1 8493 | 5.96E -05 | 0.007 28721 | 0.006 09003 | | |
| | | | | | 7 | 5 | | |
| 8 | GO:0 04852 positive regulation of viral process 4 | 5/90 | 86/1 8493 | 6.23E -05 | 0.007 28721 | 0.006 09003 | | |
| | | | | | 7 | 5 | | |
| 9 | GO:0 01699 antibiotic metabolic process 9 | 5/77 | 152/ 1849 | 0.000 | 0.268 43106 | 0.252 63267 | 0.252 42305 | |
| | | | 3 | | 3 | 4 | 4 | |
| 9 | GO:0 01585 organic hydroxy compound transport 0 | 6/77 | 255/ 1849 | 0.000 | 0.268 67815 | 0.252 63267 | 0.252 42305 | |
| | | | 3 | | 7 | 4 | 4 | |
| 9 | GO:0 04312 surfactant homeostasis 9 | 2/77 | 11/1 8493 | 0.000 | 0.268 91855 | 0.252 63267 | 0.252 42305 | |
| | | | | | 5 | 4 | 4 | |
| 9 | GO:0 04510 intermediate filament cytoskeleton organization 4 | 3/77 | 49/1 8493 | 0.001 | 0.268 63267 | 0.252 42305 | 0.252 42305 | |
| | | | | | 11419 | 4 | 4 | |
| 9 | GO:0 04510 intermediate filament-based process 3 | 3/77 | 50/1 8493 | 0.001 | 0.268 18177 | 0.252 63267 | 0.252 42305 | |
| | | | | | 7 | 4 | 4 | |
| 9 | GO:0 04887 chemical homeostasis within a tissue 5 | 2/77 | 13/1 8493 | 0.001 | 0.268 29566 | 0.252 63267 | 0.252 42305 | |
| | | | | | 2 | 4 | 4 | |
| 9 | GO:0 00680 xenobiotic metabolic process 5 | 4/77 | 117/ 1849 | 0.001 | 0.268 44305 | 0.252 63267 | 0.252 42305 | |
| | | | 3 | | 7 | 4 | 4 | |

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|----|---|------|--------------|----------------|-------|-------|-------|-------|
| | GO:0 | | | | | | 0.268 | 0.252 |
| 9 | 00175 neural crest cell migration | 3/77 | 55/1 8493 | 0.001 55842 | 63267 | 42305 | | |
| | 5 | | | | 4 | 4 | | |
| | GO:0 | | | | | | 0.001 | 0.301 |
| 9 | 04244 progesterone metabolic process | 2/77 | 16/1 8493 | 97725 | 81585 | 60392 | | |
| | 8 | | | 8 | 6 | 3 | | |
| | GO:1 | | | | | | 0.002 | 0.301 |
| 9 | 90264 tertiary alcohol metabolic process | 2/77 | 17/1 8493 | 23485 | 81585 | 60392 | | |
| | 4 | | | 9 | 6 | 3 | | |
| | GO:0 | | | | | | 0.002 | 0.301 |
| 9 | 00758 digestion | 4/77 | 135/ 1849 | 43474 | 81585 | 60392 | | |
| | 6 | | 3 | 4 | 6 | 3 | | |
| | GO:0 | | | | | | 0.002 | 0.301 |
| 9 | 01890 ether metabolic process | 2/77 | 19/1 8493 | 7949 | 81585 | 60392 | | |
| | 4 | | | | 6 | 3 | | |
| | GO:0 | | | | | | 0.003 | 0.301 |
| 9 | 01613 glycoside metabolic process | 2/77 | 20/1 8493 | 09709 | 81585 | 60392 | | |
| | 7 | | | 1 | 6 | 3 | | |
| | GO:0 | | | | | | 0.003 | 0.301 |
| 9 | 00689 receptor-mediated endocytosis | 6/77 | 346/ 1849 | 19301 | 81585 | 60392 | | |
| | 8 | | 3 | 9 | 6 | 3 | | |
| | GO:0 | | | | | | 0.003 | 0.301 |
| 9 | 03019 extracellular matrix organization | 6/77 | 348/ 1849 | 28470 | 81585 | 60392 | | |
| | 8 | | 3 | 8 | 6 | 3 | | |
| | GO:0 | | | | | | 0.003 | 0.301 |
| 9 | 00608 cellular aldehyde metabolic process | 3/77 | 73/1 8493 | 50185 | 81585 | 60392 | | |
| | 1 | | | 2 | 6 | 3 | | |
| | GO:0 | | | | | | 0.003 | 0.318 |
| 9 | 03430 primary alcohol metabolic process | 3/77 | 76/1 8493 | 92301 | 22544 | 02333 | | |
| | 8 | | | 1 | 6 | 8 | | |
| | GO:0 | | | | | | 0.004 | 0.318 |
| 9 | 01403 neural crest cell development | 3/77 | 78/1 8493 | 22019 | 79438 | 55794 | | |
| | 2 | | | 3 | 6 | 7 | | |
| | GO:0 | | | | | | 0.004 | 0.318 |
| 9 | 01572 bile acid and bile salt transport | 2/77 | 25/1 8493 | 82477 | 79438 | 55794 | | |
| | 1 | | | 8 | 6 | 7 | | |
| | GO:0 | | | | | | 0.004 | 0.318 |
| 9 | 01403 mesenchymal cell development | 3/77 | 82/1 8493 | 85473 | 79438 | 55794 | | |
| | 1 | | | 7 | 6 | 7 | | |
| | GO:0 | | | | | | 5.49E | 1.05E |
| 10 | 00640 mRNA catabolic process | 14/9 | 307/ 1849 | 5.49E | 1.05E | 7.93E | | |
| | 2 | 5 | 3 | -10 | -06 | -07 | | |
| | GO:0 | | | | | | 2.06E | 1.97E |
| 10 | 00640 RNA catabolic process | 14/9 | 340/ 1849 | 2.06E | 1.97E | 1.49E | | |
| | 1 | 5 | 3 | -09 | -06 | -06 | | |
| | GO:0 | | | | | | 4.25E | 2.71E |
| 10 | 06024 anatomical structure homeostasis | 15/9 | 425/ 1849 | 4.25E | 2.71E | 2.04E | | |
| | 9 | 5 | 3 | -09 | -06 | -06 | | |

| | | | | | | |
|----------|--|------|------|-------|-------|-------|
| GO:0 | | 13/9 | 317/ | 8.54E | 3.55E | 2.68E |
| 10 09015 | establishment of protein localization to membrane | 5 | 1849 | -09 | -06 | -06 |
| GO:0 | | | 120/ | 1.11E | 3.55E | 2.68E |
| 10 00018 | nuclear-transcribed mRNA catabolic process, nonsense-mediated decay | 9/95 | 1849 | -08 | -06 | -06 |
| GO:0 | | | 265/ | 1.11E | 3.55E | 2.68E |
| 10 03164 | regulation of protein stability | 12/9 | 1849 | -08 | -06 | -06 |
| GO:0 | | | 218/ | 1.56E | 3.85E | 2.90E |
| 10 00645 | protein folding | 11/9 | 1849 | -08 | -06 | -06 |
| GO:0 | | | 169/ | 1.61E | 3.85E | 2.90E |
| 10 05082 | protein stabilization | 10/9 | 1849 | -08 | -06 | -06 |
| GO:0 | | | 36/1 | 2.69E | 5.72E | 4.32E |
| 10 04584 | negative regulation of mitotic metaphase/anaphase transition | 6/95 | 8493 | -08 | -06 | -06 |
| GO:1 | | | 37/1 | 3.20E | 6.12E | 4.62E |
| 10 90210 | negative regulation of metaphase/anaphase transition of cell cycle | 6/95 | 8493 | -08 | -06 | -06 |
| GO:0 | | | 185/ | 3.81E | 6.62E | 5.00E |
| 10 00081 | sister chromatid segregation | 10/9 | 1849 | -08 | -06 | -06 |
| GO:2 | | | 39/1 | 4.46E | 7.10E | 5.36E |
| 10 00081 | negative regulation of mitotic sister chromatid separation | 6/95 | 8493 | -08 | -06 | -06 |
| GO:1 | | | 40/1 | 5.22E | 7.41E | 5.59E |
| 10 90581 | negative regulation of chromosome separation | 6/95 | 8493 | -08 | -06 | -06 |
| GO:2 | | | 144/ | 5.45E | 7.41E | 5.59E |
| 10 00125 | negative regulation of chromosome organization | 9/95 | 1849 | -08 | -06 | -06 |
| GO:0 | | | 194/ | 5.97E | 7.41E | 5.59E |
| 10 00641 | translational initiation | 10/9 | 1849 | -08 | -06 | -06 |
| GO:1 | | | 375/ | 6.20E | 7.41E | 5.59E |
| 10 90199 | regulation of mitotic cell cycle phase transition | 13/9 | 1849 | -08 | -06 | -06 |
| GO:0 | | | 105/ | 6.66E | 7.49E | 5.66E |
| 10 00661 | SRP-dependent cotranslational protein targeting to membrane | 8/95 | 1849 | -08 | -06 | -06 |
| GO:0 | | | 42/1 | 7.08E | 7.52E | 5.67E |
| 10 03304 | negative regulation of mitotic sister chromatid segregation | 6/95 | 8493 | -08 | -06 | -06 |
| GO:0 | | | 109/ | 8.93E | 8.98E | 6.78E |
| 10 00661 | cotranslational protein targeting to membrane | 8/95 | 1849 | -08 | -06 | -06 |
| | | | 3 | | | |

| | | | | | | | |
|------|-------|---|-------|----------|----------|----------|----------|
| GO:0 | | | | | | | |
| 11 | 00695 | humoral immune response | 12/90 | 349/1849 | 1.24E-07 | 1.44E-05 | 1.08E-05 |
| GO:0 | | | | | | | |
| 11 | 00246 | immune receptors built from immunoglobulin superfamily domains | 12/90 | 354/1849 | 1.44E-07 | 1.45E-05 | 1.09E-05 |
| GO:0 | | | | | | | |
| 11 | 00191 | positive regulation of T cell mediated cytotoxicity | 5/90 | 26/1849 | 1.48E-07 | 1.45E-05 | 1.09E-05 |
| GO:0 | | | | | | | |
| 11 | 00247 | antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent | 5/90 | 26/1849 | 1.48E-07 | 1.45E-05 | 1.09E-05 |
| GO:0 | | | | | | | |
| 11 | 00269 | regulation of immune effector process | 13/90 | 439/1849 | 1.99E-07 | 1.85E-05 | 1.39E-05 |

Supplementary table5 The top 20 enrichment terms of the exemplar genes in other 9 cluster by NMF.