

Annexe

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1 Q3.1 Top 10 up-regulated transcripts without adjustment for confondant effect

1.1 Cluster 0

| | gene | log2FoldChange | padj |
|----|--------------------|----------------|--------|
| 1 | ENSG00000210156.1 | 2.5397 | 0.0000 |
| 2 | ENSG00000281181.1 | 2.3406 | 0.0000 |
| 3 | ENSG00000124159.15 | 1.8320 | 0.0000 |
| 4 | ENSG00000223609.7 | 1.8241 | 0.0000 |
| 5 | ENSG00000210140.1 | 1.6348 | 0.0000 |
| 6 | ENSG00000202538.1 | 1.5935 | 0.0000 |
| 7 | ENSG00000118972.1 | 1.5324 | 0.0000 |
| 8 | ENSG00000086506.2 | 1.4671 | 0.0000 |
| 9 | ENSG00000158578.18 | 1.4460 | 0.0000 |
| 10 | ENSG00000206172.8 | 1.4459 | 0.0000 |

Table 1: Top 10 up-regulated transcripts for cluster 0

1.2 Cluster 1

| | gene | log2FoldChange | padj |
|----|--------------------|----------------|--------|
| 1 | ENSG00000210156.1 | 2.2671 | 0.0000 |
| 2 | ENSG00000281181.1 | 1.8488 | 0.0000 |
| 3 | ENSG00000281383.1 | 1.4370 | 0.0000 |
| 4 | ENSG00000202538.1 | 1.3242 | 0.0000 |
| 5 | ENSG00000164821.4 | 1.2449 | 0.0000 |
| 6 | ENSG00000259384.6 | 1.2218 | 0.0000 |
| 7 | ENSG00000137392.9 | 1.1493 | 0.0000 |
| 8 | ENSG00000172232.9 | 1.1267 | 0.0000 |
| 9 | ENSG00000110245.11 | 1.0570 | 0.0000 |
| 10 | ENSG00000279691.1 | 1.0513 | 0.0000 |

Table 2: Top 10 up-regulated transcripts for cluster 1

1.3 Cluster 2

| | gene | log2FoldChange | padj |
|---|--------------------|----------------|--------|
| 1 | ENSG00000210156.1 | 2.1983 | 0.0000 |
| 2 | ENSG00000281181.1 | 1.9498 | 0.0000 |
| 3 | ENSG00000210140.1 | 1.5320 | 0.0000 |
| 4 | ENSG00000281383.1 | 1.4409 | 0.0000 |
| 5 | ENSG00000262902.1 | 1.1566 | 0.0000 |
| 6 | ENSG00000202538.1 | 1.1543 | 0.0000 |
| 7 | ENSG00000179751.6 | 1.1436 | 0.0000 |
| 8 | ENSG00000137392.9 | 1.0442 | 0.0000 |
| 9 | ENSG00000168928.12 | 1.0308 | 0.0000 |

Table 3: Top 10 up-regulated transcripts for cluster 2

1.4 Cluster 3

| | gene | log2FoldChange | padj |
|----|--------------------|----------------|--------|
| 1 | ENSG00000210154.1 | 2.0926 | 0.0000 |
| 2 | ENSG00000202538.1 | 1.5827 | 0.0000 |
| 3 | ENSG00000200879.1 | 1.4256 | 0.0000 |
| 4 | ENSG00000259710.1 | 1.3485 | 0.0000 |
| 5 | ENSG00000277581.1 | 1.3335 | 0.0000 |
| 6 | ENSG00000267703.1 | 1.3278 | 0.0000 |
| 7 | ENSG00000260799.1 | 1.3239 | 0.0000 |
| 8 | ENSG00000169429.10 | 1.3133 | 0.0000 |
| 9 | ENSG00000237070.1 | 1.2797 | 0.0000 |
| 10 | ENSG00000118972.1 | 1.2757 | 0.0000 |

Table 4: Top 10 up-regulated transcripts for cluster 3

1.5 Cluster 4

| | gene | log2FoldChange | padj |
|----|--------------------|----------------|--------|
| 1 | ENSG00000158578.18 | 2.9068 | 0.0000 |
| 2 | ENSG00000213934.6 | 2.9066 | 0.0000 |
| 3 | ENSG00000260592.1 | 2.8063 | 0.0000 |
| 4 | ENSG00000169877.9 | 2.7608 | 0.0000 |
| 5 | ENSG00000188536.12 | 2.6596 | 0.0000 |
| 6 | ENSG00000196565.13 | 2.4875 | 0.0000 |
| 7 | ENSG00000215182.8 | 2.4850 | 0.0000 |
| 8 | ENSG00000206177.6 | 2.4165 | 0.0000 |
| 9 | ENSG00000261039.2 | 2.3931 | 0.0000 |
| 10 | ENSG00000095752.6 | 2.3751 | 0.0000 |

Table 5: Top 10 up-regulated transcripts for cluster 4

1.6 Cluster 5

| | gene | log2FoldChange | padj |
|----|--------------------|----------------|--------|
| 1 | ENSG00000210156.1 | 2.3618 | 0.0000 |
| 2 | ENSG00000210154.1 | 2.2689 | 0.0000 |
| 3 | ENSG00000281181.1 | 1.9596 | 0.0000 |
| 4 | ENSG00000108342.12 | 1.6685 | 0.0000 |
| 5 | ENSG00000281383.1 | 1.4671 | 0.0000 |
| 6 | ENSG00000118972.1 | 1.4470 | 0.0000 |
| 7 | ENSG00000202538.1 | 1.4464 | 0.0000 |
| 8 | ENSG00000210140.1 | 1.4281 | 0.0000 |
| 9 | ENSG00000164821.4 | 1.2934 | 0.0000 |
| 10 | ENSG00000172232.9 | 1.2923 | 0.0000 |

Table 6: Top 10 up-regulated transcripts for cluster 5

1.7 Cluster 6

| | gene | log2FoldChange | padj |
|---|--------------------|----------------|--------|
| 1 | ENSG00000248713.1 | 1.2854 | 0.0000 |
| 2 | ENSG00000073737.16 | 1.0690 | 0.0000 |
| 3 | ENSG00000223617.1 | 1.0666 | 0.0000 |
| 4 | ENSG00000231013.1 | 1.0187 | 0.0000 |

Table 7: Top 10 up-regulated transcripts for cluster 6

1.8 Cluster 7

| | gene | log2FoldChange | padj |
|----|--------------------|----------------|--------|
| 1 | ENSG00000281181.1 | 2.2393 | 0.0000 |
| 2 | ENSG00000202538.1 | 2.1307 | 0.0000 |
| 3 | ENSG00000174697.4 | 2.0061 | 0.0000 |
| 4 | ENSG00000281383.1 | 1.8399 | 0.0000 |
| 5 | ENSG00000181092.9 | 1.6299 | 0.0000 |
| 6 | ENSG00000254211.5 | 1.6232 | 0.0000 |
| 7 | ENSG00000124159.15 | 1.5154 | 0.0008 |
| 8 | ENSG00000130876.11 | 1.4476 | 0.0000 |
| 9 | ENSG00000187288.10 | 1.4213 | 0.0000 |
| 10 | ENSG00000166819.11 | 1.4000 | 0.0000 |

Table 8: Top 10 up-regulated transcripts for cluster 7

1.9 Cluster 8

| | gene | log2FoldChange | padj |
|----|--------------------|----------------|--------|
| 1 | ENSG00000110680.12 | 2.7624 | 0.0000 |
| 2 | ENSG00000229807.10 | 2.6810 | 0.0000 |
| 3 | ENSG00000270641.1 | 2.3376 | 0.0008 |
| 4 | ENSG00000134240.11 | 2.2957 | 0.0000 |
| 5 | ENSG00000180053.7 | 2.2034 | 0.0000 |
| 6 | ENSG00000283378.1 | 2.0152 | 0.0000 |
| 7 | ENSG00000279431.1 | 1.8317 | 0.0001 |
| 8 | ENSG00000178233.17 | 1.7337 | 0.0000 |
| 9 | ENSG00000257647.1 | 1.6973 | 0.0000 |
| 10 | ENSG00000073737.16 | 1.6461 | 0.0000 |

Table 9: Top 10 up-regulated transcripts for cluster 8

1.10 Cluster 9

| | gene | log2FoldChange | padj |
|----|--------------------|----------------|--------|
| 1 | ENSG00000210154.1 | 2.3534 | 0.0000 |
| 2 | ENSG00000281181.1 | 2.0067 | 0.0000 |
| 3 | ENSG00000140465.13 | 1.5961 | 0.0000 |
| 4 | ENSG00000179914.4 | 1.4568 | 0.0000 |
| 5 | ENSG00000202538.1 | 1.4368 | 0.0000 |
| 6 | ENSG00000210140.1 | 1.4310 | 0.0000 |
| 7 | ENSG00000102854.15 | 1.2138 | 0.0000 |
| 8 | ENSG00000086506.2 | 1.1990 | 0.0000 |
| 9 | ENSG00000169347.16 | 1.1893 | 0.0000 |
| 10 | ENSG00000108342.12 | 1.1760 | 0.0000 |

Table 10: Top 10 up-regulated transcripts for cluster 9

1.11 Cluster 10

No significant transcript

1.12 Cluster 11

| | gene | log2FoldChange | padj |
|----|--------------------|----------------|--------|
| 1 | ENSG00000210191.1 | 3.8454 | 0.0000 |
| 2 | ENSG00000223609.7 | 3.6328 | 0.0000 |
| 3 | ENSG00000086506.2 | 3.2895 | 0.0000 |
| 4 | ENSG00000179914.4 | 2.9044 | 0.0000 |
| 5 | ENSG00000281181.1 | 2.6384 | 0.0000 |
| 6 | ENSG00000158578.18 | 2.5955 | 0.0000 |
| 7 | ENSG00000260592.1 | 2.5845 | 0.0000 |
| 8 | ENSG00000213934.6 | 2.5189 | 0.0000 |
| 9 | ENSG00000176840.11 | 2.5185 | 0.0000 |
| 10 | ENSG00000283907.1 | 2.4638 | 0.0000 |

Table 11: Top 10 up-regulated transcripts for cluster 11

1.13 Cluster 12

| | gene | log2FoldChange | padj |
|----|--------------------|----------------|--------|
| 1 | ENSG00000281181.1 | 2.3840 | 0.0000 |
| 2 | ENSG00000202538.1 | 1.8674 | 0.0000 |
| 3 | ENSG00000151365.2 | 1.5169 | 0.0000 |
| 4 | ENSG00000146678.9 | 1.4277 | 0.0000 |
| 5 | ENSG00000174697.4 | 1.3273 | 0.0000 |
| 6 | ENSG00000006128.11 | 1.2608 | 0.0000 |
| 7 | ENSG00000128510.10 | 1.2010 | 0.0000 |
| 8 | ENSG00000283907.1 | 1.1917 | 0.0000 |
| 9 | ENSG00000215182.8 | 1.1266 | 0.0000 |
| 10 | ENSG00000211660.3 | 1.1219 | 0.0000 |

Table 12: Top 10 up-regulated transcripts for cluster 12

1.14 Cluster 13

| | gene | log2FoldChange | padj |
|----|--------------------|----------------|--------|
| 1 | ENSG00000140465.13 | 2.4286 | 0.0000 |
| 2 | ENSG00000281181.1 | 2.0570 | 0.0000 |
| 3 | ENSG00000118972.1 | 1.7030 | 0.0000 |
| 4 | ENSG00000281383.1 | 1.6919 | 0.0000 |
| 5 | ENSG00000283907.1 | 1.5013 | 0.0000 |
| 6 | ENSG00000283209.1 | 1.4903 | 0.0000 |
| 7 | ENSG00000004939.13 | 1.4224 | 0.0000 |
| 8 | ENSG00000272799.1 | 1.4140 | 0.0000 |
| 9 | ENSG00000279691.1 | 1.4105 | 0.0000 |
| 10 | ENSG00000262902.1 | 1.4102 | 0.0000 |

Table 13: Top 10 up-regulated transcripts for cluster 13

1.15 Cluster 14

| | gene | log2FoldChange | padj |
|---|--------------------|----------------|--------|
| 1 | ENSG00000281181.1 | 1.7916 | 0.0007 |
| 2 | ENSG00000137392.9 | 1.7267 | 0.0010 |
| 3 | ENSG00000202538.1 | 1.5840 | 0.0002 |
| 4 | ENSG00000170890.13 | 1.3837 | 0.0015 |
| 5 | ENSG00000170827.9 | 1.2792 | 0.0005 |
| 6 | ENSG00000010438.16 | 1.1808 | 0.0003 |
| 7 | ENSG00000162438.11 | 1.1525 | 0.0005 |
| 8 | ENSG00000073737.16 | 1.1220 | 0.0001 |
| 9 | ENSG00000250746.1 | 1.0015 | 0.0001 |

Table 14: Top 10 up-regulated transcripts for cluster 14

1.16 Cluster 15

| | gene | log2FoldChange | padj |
|----|--------------------|----------------|--------|
| 1 | ENSG00000210154.1 | 2.2148 | 0.0000 |
| 2 | ENSG00000140465.13 | 2.0216 | 0.0000 |
| 3 | ENSG00000281181.1 | 1.7257 | 0.0000 |
| 4 | ENSG00000086506.2 | 1.4677 | 0.0000 |
| 5 | ENSG00000179914.4 | 1.3641 | 0.0000 |
| 6 | ENSG00000202538.1 | 1.3487 | 0.0000 |
| 7 | ENSG00000169429.10 | 1.2953 | 0.0000 |
| 8 | ENSG00000266378.1 | 1.2936 | 0.0000 |
| 9 | ENSG00000210195.2 | 1.2886 | 0.0000 |
| 10 | ENSG00000169245.5 | 1.2805 | 0.0000 |

Table 15: Top 10 up-regulated transcripts for cluster 15

1.17 Cluster 16

| | gene | log2FoldChange | padj |
|----|--------------------|----------------|--------|
| 1 | ENSG00000210191.1 | 2.8695 | 0.0000 |
| 2 | ENSG00000210156.1 | 2.6294 | 0.0000 |
| 3 | ENSG00000086506.2 | 2.5888 | 0.0000 |
| 4 | ENSG00000158578.18 | 2.2732 | 0.0000 |
| 5 | ENSG00000206172.8 | 2.2046 | 0.0000 |
| 6 | ENSG00000004939.13 | 2.1860 | 0.0000 |
| 7 | ENSG00000260592.1 | 2.1850 | 0.0000 |
| 8 | ENSG00000169877.9 | 2.1849 | 0.0000 |
| 9 | ENSG00000213934.6 | 2.1419 | 0.0000 |
| 10 | ENSG00000188536.12 | 2.1169 | 0.0000 |

Table 16: Top 10 up-regulated transcripts for cluster 16

1.18 Cluster 17

| | gene | log2FoldChange | padj |
|----|--------------------|----------------|--------|
| 1 | ENSG00000281181.1 | 5.1242 | 0.0000 |
| 2 | ENSG00000281383.1 | 3.7459 | 0.0000 |
| 3 | ENSG00000202538.1 | 3.3581 | 0.0000 |
| 4 | ENSG00000124159.15 | 2.5998 | 0.0000 |
| 5 | ENSG00000086506.2 | 2.4133 | 0.0000 |
| 6 | ENSG00000105664.10 | 2.2957 | 0.0000 |
| 7 | ENSG00000223609.7 | 2.2255 | 0.0002 |
| 8 | ENSG00000171951.4 | 1.9575 | 0.0000 |
| 9 | ENSG00000095752.6 | 1.8639 | 0.0000 |
| 10 | ENSG00000149948.13 | 1.7847 | 0.0000 |

Table 17: Top 10 up-regulated transcripts for cluster 17

1.19 Cluster 18

| | gene | log2FoldChange | padj |
|---|--------------------|----------------|--------|
| 1 | ENSG00000128965.11 | 1.3977 | 0.0000 |
| 2 | ENSG00000103888.16 | 1.1822 | 0.0002 |
| 3 | ENSG00000248923.1 | 1.1284 | 0.0012 |

Table 18: Top 10 up-regulated transcripts for cluster 18

1.20 Cluster 19

| | gene | log2FoldChange | padj |
|----|--------------------|----------------|--------|
| 1 | ENSG00000172179.11 | 2.4814 | 0.0000 |
| 2 | ENSG00000259384.6 | 2.3679 | 0.0000 |
| 3 | ENSG00000176840.11 | 2.1539 | 0.0000 |
| 4 | ENSG00000229859.9 | 1.8912 | 0.0001 |
| 5 | ENSG00000104826.12 | 1.7859 | 0.0000 |
| 6 | ENSG00000140465.13 | 1.7765 | 0.0000 |
| 7 | ENSG00000232810.3 | 1.7700 | 0.0000 |
| 8 | ENSG00000262902.1 | 1.7638 | 0.0000 |
| 9 | ENSG00000172232.9 | 1.7377 | 0.0000 |
| 10 | ENSG00000170827.9 | 1.7109 | 0.0000 |

Table 19: Top 10 up-regulated transcripts for cluster 19

1.21 Cluster 20

| | gene | log2FoldChange | padj |
|----|--------------------|----------------|--------|
| 1 | ENSG00000202538.1 | 1.5443 | 0.0000 |
| 2 | ENSG00000279431.1 | 1.2265 | 0.0000 |
| 3 | ENSG00000283265.1 | 1.1354 | 0.0000 |
| 4 | ENSG00000180053.7 | 1.1228 | 0.0000 |
| 5 | ENSG00000108759.3 | 1.1075 | 0.0001 |
| 6 | ENSG00000214940.8 | 1.1061 | 0.0002 |
| 7 | ENSG00000257647.1 | 1.0312 | 0.0000 |
| 8 | ENSG00000229807.10 | 1.0274 | 0.0006 |
| 9 | ENSG00000122735.15 | 1.0225 | 0.0000 |
| 10 | ENSG00000235832.2 | 1.0216 | 0.0000 |

Table 20: Top 10 up-regulated transcripts for cluster 20

1.22 Cluster 21

| | gene | log2FoldChange | padj |
|----|--------------------|----------------|--------|
| 1 | ENSG00000210154.1 | 2.4511 | 0.0000 |
| 2 | ENSG00000210156.1 | 2.3969 | 0.0000 |
| 3 | ENSG00000281181.1 | 2.0040 | 0.0000 |
| 4 | ENSG00000140465.13 | 1.6920 | 0.0000 |
| 5 | ENSG00000118972.1 | 1.6193 | 0.0000 |
| 6 | ENSG00000086506.2 | 1.4118 | 0.0000 |
| 7 | ENSG00000169877.9 | 1.3559 | 0.0000 |
| 8 | ENSG00000169245.5 | 1.3555 | 0.0000 |
| 9 | ENSG00000004939.13 | 1.3089 | 0.0000 |
| 10 | ENSG00000206172.8 | 1.3087 | 0.0000 |

Table 21: Top 10 up-regulated transcripts for cluster 21

1.23 Cluster 22

| | gene | log2FoldChange | padj |
|----|--------------------|----------------|--------|
| 1 | ENSG00000210154.1 | 2.5675 | 0.0000 |
| 2 | ENSG00000086506.2 | 2.0612 | 0.0000 |
| 3 | ENSG00000202538.1 | 1.9462 | 0.0000 |
| 4 | ENSG00000239839.6 | 1.6974 | 0.0000 |
| 5 | ENSG00000223609.7 | 1.6815 | 0.0000 |
| 6 | ENSG00000004939.13 | 1.6800 | 0.0000 |
| 7 | ENSG00000213934.6 | 1.6040 | 0.0000 |
| 8 | ENSG00000200879.1 | 1.6010 | 0.0000 |
| 9 | ENSG00000149516.13 | 1.5871 | 0.0000 |
| 10 | ENSG00000164821.4 | 1.5807 | 0.0000 |

Table 22: Top 10 up-regulated transcripts for cluster 22

1.24 Cluster 23

| | gene | log2FoldChange | padj |
|---|-------------------|----------------|--------|
| 1 | ENSG00000229828.2 | 1.2181 | 0.0000 |
| 2 | ENSG00000279431.1 | 1.2089 | 0.0000 |
| 3 | ENSG00000223617.1 | 1.0312 | 0.0000 |
| 4 | ENSG00000257647.1 | 1.0287 | 0.0000 |
| 5 | ENSG00000163082.9 | 1.0038 | 0.0000 |

Table 23: Top 10 up-regulated transcripts for cluster 23

1.25 Cluster 24

| | gene | log2FoldChange | padj |
|----|--------------------|----------------|--------|
| 1 | ENSG00000210154.1 | 2.3879 | 0.0000 |
| 2 | ENSG00000210156.1 | 2.2983 | 0.0000 |
| 3 | ENSG00000281181.1 | 2.0785 | 0.0000 |
| 4 | ENSG00000281383.1 | 1.5831 | 0.0000 |
| 5 | ENSG00000210140.1 | 1.4668 | 0.0000 |
| 6 | ENSG00000202538.1 | 1.3899 | 0.0000 |
| 7 | ENSG00000108342.12 | 1.3539 | 0.0000 |
| 8 | ENSG00000181143.15 | 1.2888 | 0.0000 |
| 9 | ENSG00000179914.4 | 1.2834 | 0.0000 |
| 10 | ENSG00000137392.9 | 1.2742 | 0.0000 |

Table 24: Top 10 up-regulated transcripts for cluster 24

1.26 Cluster 25

| | gene | log2FoldChange | padj |
|---|--------------------|----------------|--------|
| 1 | ENSG00000279431.1 | 1.0949 | 0.0000 |
| 2 | ENSG00000073737.16 | 1.0196 | 0.0000 |

Table 25: Top 10 up-regulated transcripts for cluster 25

1.27 Cluster 26

| | gene | log2FoldChange | padj |
|----|--------------------|----------------|--------|
| 1 | ENSG00000210156.1 | 2.2537 | 0.0000 |
| 2 | ENSG00000281181.1 | 1.9725 | 0.0000 |
| 3 | ENSG00000118972.1 | 1.5372 | 0.0000 |
| 4 | ENSG00000210140.1 | 1.4536 | 0.0000 |
| 5 | ENSG00000163435.15 | 1.3491 | 0.0000 |
| 6 | ENSG00000140465.13 | 1.3345 | 0.0000 |
| 7 | ENSG00000137392.9 | 1.3111 | 0.0000 |
| 8 | ENSG00000202538.1 | 1.2916 | 0.0000 |
| 9 | ENSG00000210154.1 | 1.2621 | 0.0000 |
| 10 | ENSG00000168928.12 | 1.2578 | 0.0000 |

Table 26: Top 10 up-regulated transcripts for cluster 26

1.28 Cluster 27

| | gene | log2FoldChange | padj |
|---|-------------------|----------------|--------|
| 1 | ENSG00000281181.1 | 1.4906 | 0.0000 |
| 2 | ENSG00000202538.1 | 1.3269 | 0.0000 |
| 3 | ENSG00000279431.1 | 1.0137 | 0.0000 |

Table 27: Top 10 up-regulated transcripts for cluster 27

1.29 Cluster 28

| | gene | log2FoldChange | padj |
|----|--------------------|----------------|--------|
| 1 | ENSG00000210156.1 | 2.2717 | 0.0000 |
| 2 | ENSG00000281181.1 | 2.0990 | 0.0000 |
| 3 | ENSG00000223609.7 | 2.0563 | 0.0000 |
| 4 | ENSG00000169429.10 | 1.7391 | 0.0000 |
| 5 | ENSG00000281383.1 | 1.6064 | 0.0000 |
| 6 | ENSG00000158578.18 | 1.5576 | 0.0000 |
| 7 | ENSG00000202538.1 | 1.5280 | 0.0000 |
| 8 | ENSG00000169245.5 | 1.5146 | 0.0000 |
| 9 | ENSG00000118972.1 | 1.5026 | 0.0000 |
| 10 | ENSG00000086506.2 | 1.5020 | 0.0000 |

Table 28: Top 10 up-regulated transcripts for cluster 28

1.30 Cluster 29

| | gene | log2FoldChange | padj |
|----|--------------------|----------------|--------|
| 1 | ENSG00000223609.7 | 3.3655 | 0.0000 |
| 2 | ENSG00000202538.1 | 3.2211 | 0.0000 |
| 3 | ENSG00000124159.15 | 2.6905 | 0.0000 |
| 4 | ENSG00000105664.10 | 2.5587 | 0.0000 |
| 5 | ENSG00000158578.18 | 2.4258 | 0.0000 |
| 6 | ENSG00000086506.2 | 2.3888 | 0.0000 |
| 7 | ENSG00000261039.2 | 2.3035 | 0.0000 |
| 8 | ENSG00000171951.4 | 2.1793 | 0.0000 |
| 9 | ENSG00000095752.6 | 2.1411 | 0.0000 |
| 10 | ENSG00000106483.11 | 2.1102 | 0.0000 |

Table 29: Top 10 up-regulated transcripts for cluster 29

1.31 Cluster 30

| | gene | log2FoldChange | padj |
|---|-------------------|----------------|--------|
| 1 | ENSG00000210195.2 | 1.7112 | 0.0000 |

Table 30: Top 10 up-regulated transcripts for cluster 30

1.32 Cluster 31

No significant transcript

2 Q3.1 Top 10 up-regulated transcript with ajustement for confondant effect

2.1 Cluster 0

| | gene | log2FoldChange | padj |
|---|-------------------|----------------|--------|
| 1 | ENSG00000223609.7 | 1.1369 | 0.0002 |

Table 31: Top 10 up-regulated transcripts for cluster 0 with ajustement for confondant effect

2.2 Cluster 1

No significant transcript

2.3 Cluster 2

No significant transcript

2.4 Cluster 3

| | gene | log2FoldChange | padj |
|---|--------------------|----------------|--------|
| 1 | ENSG00000270640.1 | 1.8560 | 0.0000 |
| 2 | ENSG00000215182.8 | 1.3792 | 0.0000 |
| 3 | ENSG00000264204.2 | 1.1567 | 0.0000 |
| 4 | ENSG00000159261.10 | 1.1012 | 0.0015 |
| 5 | ENSG00000200879.1 | 1.0460 | 0.0002 |
| 6 | ENSG00000095752.6 | 1.0370 | 0.0000 |

Table 32: Top 10 up-regulated transcripts for cluster 3 with ajustement for confondant effect

2.5 Cluster 4

| | gene | log2FoldChange | padj |
|----|--------------------|----------------|--------|
| 1 | ENSG00000171951.4 | 2.6749 | 0.0000 |
| 2 | ENSG00000159261.10 | 2.5414 | 0.0001 |
| 3 | ENSG00000223609.7 | 2.5085 | 0.0000 |
| 4 | ENSG00000095752.6 | 2.2721 | 0.0000 |
| 5 | ENSG00000261039.2 | 2.0630 | 0.0001 |
| 6 | ENSG00000268941.2 | 2.0243 | 0.0003 |
| 7 | ENSG00000106541.11 | 1.9935 | 0.0002 |
| 8 | ENSG00000149948.13 | 1.8640 | 0.0002 |
| 9 | ENSG00000124159.15 | 1.7444 | 0.0007 |
| 10 | ENSG00000106483.11 | 1.4863 | 0.0000 |

Table 33: Top 10 up-regulated transcripts for cluster 4 with ajustement for confondant effect

2.6 Cluster 5

| | gene | log2FoldChange | padj |
|---|--------------------|----------------|--------|
| 1 | ENSG00000163435.15 | 1.0765 | 0.0000 |

Table 34: Top 10 up-regulated transcripts for cluster 5 with ajustement for confondant effect

2.7 Cluster 6

No significant transcript

2.8 Cluster 7

| | gene | log2FoldChange | padj |
|----|--------------------|----------------|--------|
| 1 | ENSG00000174697.4 | 2.0496 | 0.0000 |
| 2 | ENSG00000151365.2 | 1.7741 | 0.0000 |
| 3 | ENSG00000181092.9 | 1.6654 | 0.0000 |
| 4 | ENSG00000254211.5 | 1.6275 | 0.0000 |
| 5 | ENSG00000187288.10 | 1.5227 | 0.0000 |
| 6 | ENSG00000166819.11 | 1.4918 | 0.0000 |
| 7 | ENSG00000130876.11 | 1.3605 | 0.0000 |
| 8 | ENSG00000166828.2 | 1.3040 | 0.0001 |
| 9 | ENSG00000133317.14 | 1.2826 | 0.0000 |
| 10 | ENSG00000145824.12 | 1.1655 | 0.0000 |

Table 35: Top 10 up-regulated transcripts for cluster 7 with ajustement for confondant effect

2.9 Cluster 8

| | gene | log2FoldChange | padj |
|---|--------------------|----------------|--------|
| 1 | ENSG00000229807.10 | 2.2735 | 0.0009 |
| 2 | ENSG00000246375.2 | 1.7102 | 0.0000 |
| 3 | ENSG00000162763.3 | 1.5895 | 0.0006 |
| 4 | ENSG00000283378.1 | 1.5257 | 0.0010 |
| 5 | ENSG00000241054.1 | 1.3848 | 0.0006 |
| 6 | ENSG00000198734.10 | 1.2633 | 0.0001 |
| 7 | ENSG00000250061.5 | 1.1986 | 0.0007 |

Table 36: Top 10 up-regulated transcripts for cluster 8 with ajustement for confondant effect

2.10 Cluster 9

No significant transcript

2.11 Cluster 10

| | gene | log2FoldChange | padj |
|---|--------------------|----------------|--------|
| 1 | ENSG00000219073.7 | 1.1604 | 0.0001 |
| 2 | ENSG00000142789.19 | 1.0556 | 0.0003 |

Table 37: Top 10 up-regulated transcripts for cluster 10 with adjustment for confondant effect

2.12 Cluster 11

| | gene | log2FoldChange | padj |
|----|--------------------|----------------|--------|
| 1 | ENSG00000277247.1 | 2.8346 | 0.0000 |
| 2 | ENSG00000189410.11 | 2.1225 | 0.0001 |
| 3 | ENSG00000223609.7 | 1.9738 | 0.0014 |
| 4 | ENSG00000149948.13 | 1.8667 | 0.0001 |
| 5 | ENSG00000086506.2 | 1.8515 | 0.0014 |
| 6 | ENSG00000124875.9 | 1.7872 | 0.0001 |
| 7 | ENSG00000239839.6 | 1.7854 | 0.0014 |
| 8 | ENSG00000163435.15 | 1.6569 | 0.0009 |
| 9 | ENSG00000229604.2 | 1.6353 | 0.0000 |
| 10 | ENSG00000101670.11 | 1.6247 | 0.0006 |

Table 38: Top 10 up-regulated transcripts for cluster 11 with adjustment for confondant effect

2.13 Cluster 12

| | gene | log2FoldChange | padj |
|----|--------------------|----------------|--------|
| 1 | ENSG00000151365.2 | 1.4695 | 0.0000 |
| 2 | ENSG00000174697.4 | 1.4452 | 0.0000 |
| 3 | ENSG00000202538.1 | 1.2194 | 0.0000 |
| 4 | ENSG00000105880.4 | 1.1673 | 0.0000 |
| 5 | ENSG00000254211.5 | 1.1559 | 0.0000 |
| 6 | ENSG00000181092.9 | 1.1122 | 0.0000 |
| 7 | ENSG00000146678.9 | 1.0632 | 0.0005 |
| 8 | ENSG00000215182.8 | 1.0605 | 0.0001 |
| 9 | ENSG00000006128.11 | 1.0396 | 0.0000 |
| 10 | ENSG00000166819.11 | 1.0377 | 0.0000 |

Table 39: Top 10 up-regulated transcripts for cluster 12 with adjustment for confondant effect

2.14 Cluster 13

| | gene | log2FoldChange | padj |
|---|--------------------|----------------|--------|
| 1 | ENSG00000185988.11 | 1.3936 | 0.0000 |
| 2 | ENSG00000272799.1 | 1.1348 | 0.0000 |
| 3 | ENSG00000279281.1 | 1.0549 | 0.0005 |

Table 40: Top 10 up-regulated transcripts for cluster 13 with adjustment for confondant effect

2.15 Cluster 14

| | gene | log2FoldChange | padj |
|---|--------------------|----------------|--------|
| 1 | ENSG00000010438.16 | 1.1909 | 0.0003 |
| 2 | ENSG00000162438.11 | 1.0712 | 0.0013 |

Table 41: Top 10 up-regulated transcripts for cluster 14 with adjustment for confondant effect

2.16 Cluster 15

| | gene | log2FoldChange | padj |
|---|-------------------|----------------|--------|
| 1 | ENSG00000223609.7 | 1.2400 | 0.0000 |

Table 42: Top 10 up-regulated transcripts for cluster 15 with adjustment for confondant effect

2.17 Cluster 16

| | gene | log2FoldChange | padj |
|----|--------------------|----------------|--------|
| 1 | ENSG00000223609.7 | 1.5988 | 0.0000 |
| 2 | ENSG00000159261.10 | 1.5516 | 0.0000 |
| 3 | ENSG00000215182.8 | 1.4767 | 0.0000 |
| 4 | ENSG00000237070.1 | 1.2521 | 0.0000 |
| 5 | ENSG00000228495.1 | 1.2404 | 0.0000 |
| 6 | ENSG00000169245.5 | 1.2301 | 0.0000 |
| 7 | ENSG00000241112.1 | 1.2216 | 0.0000 |
| 8 | ENSG00000206177.6 | 1.2016 | 0.0000 |
| 9 | ENSG00000267703.1 | 1.1947 | 0.0000 |
| 10 | ENSG00000086506.2 | 1.1716 | 0.0003 |

Table 43: Top 10 up-regulated transcripts for cluster 16 with adjustment for confondant effect

2.18 Cluster 17

| | gene | log2FoldChange | padj |
|----|--------------------|----------------|--------|
| 1 | ENSG00000169429.10 | 1.7999 | 0.0000 |
| 2 | ENSG00000149948.13 | 1.7278 | 0.0000 |
| 3 | ENSG00000103888.16 | 1.6323 | 0.0000 |
| 4 | ENSG00000124159.15 | 1.5569 | 0.0007 |
| 5 | ENSG00000095752.6 | 1.5507 | 0.0003 |
| 6 | ENSG00000281383.1 | 1.5111 | 0.0009 |
| 7 | ENSG00000210196.2 | 1.4883 | 0.0003 |
| 8 | ENSG00000171951.4 | 1.4869 | 0.0000 |
| 9 | ENSG00000060718.20 | 1.4805 | 0.0005 |
| 10 | ENSG00000166923.10 | 1.4775 | 0.0000 |

Table 44: Top 10 up-regulated transcripts for cluster 17 with adjustment for confondant effect

2.19 Cluster 18

| | gene | log2FoldChange | padj |
|---|--------------------|----------------|--------|
| 1 | ENSG00000062038.13 | 1.3323 | 0.0002 |
| 2 | ENSG00000248923.1 | 1.3163 | 0.0000 |
| 3 | ENSG00000103888.16 | 1.2854 | 0.0001 |
| 4 | ENSG00000135069.13 | 1.1049 | 0.0014 |

Table 45: Top 10 up-regulated transcripts for cluster 18 with adjustment for confondant effect

2.20 Cluster 19

| | gene | log2FoldChange | padj |
|----|--------------------|----------------|--------|
| 1 | ENSG00000172179.11 | 2.2017 | 0.0001 |
| 2 | ENSG00000140465.13 | 1.5658 | 0.0003 |
| 3 | ENSG00000176840.11 | 1.5456 | 0.0014 |
| 4 | ENSG00000259384.6 | 1.4193 | 0.0012 |
| 5 | ENSG00000256713.7 | 1.3759 | 0.0003 |
| 6 | ENSG00000170827.9 | 1.3690 | 0.0005 |
| 7 | ENSG00000104826.12 | 1.2968 | 0.0004 |
| 8 | ENSG00000244921.2 | 1.2365 | 0.0000 |
| 9 | ENSG00000198744.5 | 1.2041 | 0.0002 |
| 10 | ENSG00000010438.16 | 1.1691 | 0.0012 |

Table 46: Top 10 up-regulated transcripts for cluster 19 with adjustment for confondant effect

2.21 Cluster 20

| | gene | log2FoldChange | padj |
|---|-------------------|----------------|--------|
| 1 | ENSG00000215182.8 | 1.4007 | 0.0000 |

Table 47: Top 10 up-regulated transcripts for cluster 20 with adjustment for confondant effect

2.22 Cluster 21

| | gene | log2FoldChange | padj |
|---|--------------------|----------------|--------|
| 1 | ENSG00000185988.11 | 1.0874 | 0.0001 |

Table 48: Top 10 up-regulated transcripts for cluster 21 with adjustment for confondant effect

2.23 Cluster 22

| | gene | log2FoldChange | padj |
|---|-------------------|----------------|--------|
| 1 | ENSG00000239839.6 | 1.4162 | 0.0000 |
| 2 | ENSG00000200879.1 | 1.0568 | 0.0009 |
| 3 | ENSG00000237070.1 | 1.0291 | 0.0000 |
| 4 | ENSG00000077274.8 | 1.0056 | 0.0002 |

Table 49: Top 10 up-regulated transcripts for cluster 22 with adjustment for confondant effect

2.24 Cluster 23

| | gene | log2FoldChange | padj |
|---|-------------------|----------------|--------|
| 1 | ENSG00000174697.4 | 1.0171 | 0.0000 |

Table 50: Top 10 up-regulated transcripts for cluster 23 with adjustment for confondant effect

2.25 Cluster 24

No significant transcript

2.26 Cluster 25

| | gene | log2FoldChange | padj |
|---|-------------------|----------------|--------|
| 1 | ENSG00000214940.8 | 1.1796 | 0.0000 |

Table 51: Top 10 up-regulated transcripts for cluster 25 with adjustment for confondant effect

2.27 Cluster 26

| | gene | log2FoldChange | padj |
|---|--------------------|----------------|--------|
| 1 | ENSG00000163435.15 | 1.0422 | 0.0000 |

Table 52: Top 10 up-regulated transcripts for cluster 26 with adjustement for confondant effect

2.28 Cluster 27

No significant transcript

2.29 Cluster 28

| | gene | log2FoldChange | padj |
|---|--------------------|----------------|--------|
| 1 | ENSG00000163435.15 | 1.1236 | 0.0000 |
| 2 | ENSG00000159261.10 | 1.0506 | 0.0000 |
| 3 | ENSG00000169429.10 | 1.0347 | 0.0000 |
| 4 | ENSG00000239839.6 | 1.0173 | 0.0000 |

Table 53: Top 10 up-regulated transcripts for cluster 28 with adjustement for confondant effect

2.30 Cluster 29

| | gene | log2FoldChange | padj |
|----|--------------------|----------------|--------|
| 1 | ENSG00000183813.6 | 3.8872 | 0.0000 |
| 2 | ENSG00000102468.10 | 2.9228 | 0.0000 |
| 3 | ENSG00000257894.2 | 2.2761 | 0.0001 |
| 4 | ENSG00000178773.14 | 2.2342 | 0.0000 |
| 5 | ENSG00000261039.2 | 1.9669 | 0.0000 |
| 6 | ENSG00000202538.1 | 1.9596 | 0.0002 |
| 7 | ENSG00000167105.7 | 1.9554 | 0.0000 |
| 8 | ENSG00000215182.8 | 1.9496 | 0.0002 |
| 9 | ENSG00000095752.6 | 1.9404 | 0.0000 |
| 10 | ENSG00000146678.9 | 1.9214 | 0.0008 |

Table 54: Top 10 up-regulated transcripts for cluster 29 with adjustement for confondant effect

2.31 Cluster 30

| | gene | log2FoldChange | padj |
|---|-------------------|----------------|--------|
| 1 | ENSG00000210195.2 | 1.1028 | 0.0000 |

Table 55: Top 10 up-regulated transcripts for cluster 30 with adjustement for confondant effect

2.32 Cluster 31

No significant transcript

3 Q3.2 Top 10 up-regulated pathways without adjustment for confondant effect

3.1 Cluster 0

| | pathway | padj | NES |
|----|--|--------|--------|
| 1 | REACTOME_ERCC6_CSB_AND_EHMT2_G9A_POSITIVELY_REGULATE_RRNA_EXPRESSION | 0.0028 | 1.7165 |
| 2 | REACTOME_AMINE_LIGAND_BINDING_RECEPTORS | 0.0020 | 1.6721 |
| 3 | REACTOME_NUCLEOTIDE_SALVAGE | 0.0051 | 1.6072 |
| 4 | REACTOME_SCAVENGING_OF_HEME_FROM_PLASMA | 0.0027 | 1.6020 |
| 5 | REACTOME_DETOXIFICATION_OF_REACTIVE_OXYGEN_SPECIES | 0.0039 | 1.5645 |
| 6 | REACTOME_ACTIVATION_OF_RAC1 | 0.0066 | 1.5489 |
| 7 | REACTOME_GRB2_EVENTS_IN_ERBB2_SIGNALING | 0.0086 | 1.4917 |
| 8 | REACTOME_ROLE_OF_LAT2_NTAL_LAB_ON_CALCIIUM_MOBILIZATION | 0.0068 | 1.4024 |
| 9 | REACTOME_ARACHIDONIC_ACID_METABOLISM | 0.0087 | 1.3710 |
| 10 | REACTOME_AUTOPHAGY | 0.0053 | 1.3372 |

Table 56: Top 10 up-regulated pathways for cluster 0

3.2 Cluster 1

| | pathway | padj | NES |
|----|---|--------|--------|
| 1 | REACTOME_GENERATION_OF_SECOND_MESSENGER_MOLECULES | 0.0051 | 1.6022 |
| 2 | REACTOME_ACTIVATION_OF_PPARGC1A_PGC_1ALPHA_BY_PHOSPHORYLATION | 0.0065 | 1.5865 |
| 3 | REACTOME_INTERACTION_BETWEEN_L1_AND_ANKYRINS | 0.0061 | 1.5646 |
| 4 | REACTOME_CARNITINE_METABOLISM | 0.0069 | 1.5270 |
| 5 | REACTOME_INSULIN_RECEPTOR_RECYCLING | 0.0098 | 1.5189 |
| 6 | REACTOME_BLOOD_GROUP_SYSTEMS_BIOSYNTHESIS | 0.0093 | 1.5058 |
| 7 | REACTOME_SIGNALING_BY_NTRK3_TRKC | 0.0101 | 1.4768 |
| 8 | REACTOME_NCAM_SIGNALING_FOR_NEURITE_OUT_GROWTH | 0.0045 | 1.4231 |
| 9 | REACTOME_DETOXIFICATION_OF_REACTIVE_OXYGEN_SPECIES | 0.0095 | 1.4120 |
| 10 | REACTOME_SIGNALING_BY_INSULIN_RECEPTOR | 0.0072 | 1.3514 |

Table 57: Top 10 up-regulated pathways for cluster 1

3.3 Cluster 10

| | pathway |
|----|---|
| 1 | REACTOME_ECM_PROTEOGLYCANS |
| 2 | REACTOME_ESR_MEDIATED_SIGNALING |
| 3 | REACTOME_RHO_GTPASE_CYCLE |
| 4 | REACTOME_DISEASES_OF_SIGNAL_TRANSDUCTION_BY_GROWTH_FACTOR_RECEPTORS_AND_SECOND_MESS |
| 5 | REACTOME_SIGNALING_BY_RHO_GTPASES_MIRO_GTPASES_AND_RHOBTB3 |
| 6 | REACTOME_SIGNALING_BY_RECEPTOR_TYROSINE_KINASES |
| 7 | REACTOME_METABOLISM_OF_RNA |
| 8 | REACTOME_CELL_CYCLE |
| 9 | REACTOME_CYTOKINE_SIGNALING_IN_IMMUNE_SYSTEM |
| 10 | REACTOME_INNATE_IMMUNE_SYSTEM |

Table 58: Top 10 up-regulated pathways for cluster 10

3.4 Cluster 11

| | pathway | padj | NES |
|----|--|--------|--------|
| 1 | REACTOME_CHONDROITIN_SULFATE_BIOSYNTHESIS | 0.0026 | 1.7024 |
| 2 | REACTOME_GRB2_EVENTS_IN_ERBB2_SIGNALING | 0.0029 | 1.6670 |
| 3 | REACTOME_SCAVENGING_OF_HEME_FROM_PLASMA | 0.0023 | 1.6533 |
| 4 | REACTOME_ERCC6_CSB_AND_EHMT2_G9A_POSITIVELY_REGULATE_RRNA_EXPRESSION | 0.0033 | 1.6504 |
| 5 | REACTOME_SHC1_EVENTS_IN_ERBB4_SIGNALING | 0.0036 | 1.6413 |
| 6 | REACTOME_GENERATION_OF_SECOND_MESSENGER_MOLECULES | 0.0034 | 1.6227 |
| 7 | REACTOME_ACTIVATION_OF_RAC1 | 0.0063 | 1.6013 |
| 8 | REACTOME_PHASE_4_RESTING_MEMBRANE_POTENTIAL | 0.0049 | 1.5312 |
| 9 | REACTOME_SHC1_EVENTS_IN_ERBB2_SIGNALING | 0.0045 | 1.5225 |
| 10 | REACTOME_KERATINIZATION | 0.0051 | 1.4067 |

Table 59: Top 10 up-regulated pathways for cluster 11

3.5 Cluster 12

| | pathway | padj | NES |
|----|--|--------|--------|
| 1 | REACTOME_INWARDLY_RECTIFYING_K_CHANNELS | 0.0129 | 1.6700 |
| 2 | REACTOME_TRANSCRIPTIONAL_REGULATION_OF_TESTIS_DIFFERENTIATION | 0.0129 | 1.6500 |
| 3 | REACTOME_THROMBIN_SIGNALLING_THROUGH_PROTEINASE_ACTIVATED_RECEPTORS_PARS | 0.0166 | 1.5800 |
| 4 | REACTOME_G_BETA_GAMMA_SIGNALLING_THROUGH_CDC42 | 0.0197 | 1.5500 |
| 5 | REACTOME_G_PROTEIN_ACTIVATION | 0.0197 | 1.5300 |
| 6 | REACTOME_PROSTACYCLIN_SIGNALLING_THROUGH_PROSTACYCLIN_RECEPTOR | 0.0197 | 1.5300 |
| 7 | REACTOME_CA2_PATHWAY | 0.0152 | 1.5300 |
| 8 | REACTOME_PRESYNAPTIC_FUNCTION_OF_KAINATE_RECEPTORS | 0.0197 | 1.5100 |
| 9 | REACTOME_PROTEIN_UBIQUITINATION | 0.0191 | 1.4700 |
| 10 | REACTOME_GABA_RECEPTOR_ACTIVATION | 0.0197 | 1.4600 |

Table 60: Top 10 up-regulated pathways for cluster 12

3.6 Cluster 13

| | pathway | padj | NES |
|----|--|--------|--------|
| 1 | REACTOME_ERCC6_CSB_AND_EHMT2_G9A_POSITIVELY_REGULATE_RRNA_EXPRESSION | 0.0042 | 1.6696 |
| 2 | REACTOME_DETOXIFICATION_OF_REACTIVE_OXYGEN_SPECIES | 0.0034 | 1.6272 |
| 3 | REACTOME_SYNAPTIC_ADHESION_LIKE_MOLECULES | 0.0060 | 1.5462 |
| 4 | REACTOME_GENERATION_OF_SECOND_MESSENGER_MOLECULES | 0.0051 | 1.5298 |
| 5 | REACTOME_INTERACTION_BETWEEN_L1_AND_ANKYRINS | 0.0051 | 1.5144 |
| 6 | REACTOME_SIGNALING_BY_NTRK3_TRKC | 0.0075 | 1.5009 |
| 7 | REACTOME_SCAVENGING_OF_HEME_FROM_PLASMA | 0.0053 | 1.4840 |
| 8 | REACTOME_NCAM_SIGNALING_FOR_NEURITE_OUT_GROWTH | 0.0043 | 1.4785 |
| 9 | REACTOME_ROLE_OF_LAT2_NTAL_LAB_ON_CALCIIUM_MOBILIZATION | 0.0055 | 1.4467 |
| 10 | REACTOME_CREATION_OF_C4_AND_C2_ACTIVATORS | 0.0069 | 1.4063 |

Table 61: Top 10 up-regulated pathways for cluster 13

3.7 Cluster 14

| | pathway |
|----|--|
| 1 | REACTOME_ABERRANT_REGULATION_OF_MITOTIC_G1_S_TRANSITION_IN_CANCER_DUE_TO_RB1_DEFECTS |
| 2 | REACTOME_CTLA4_INHIBITORY_SIGNALING |
| 3 | REACTOME_EPHA_MEDIATED_GROWTH_CONE_COLLAPSE |
| 4 | REACTOME_ECM_PROTEOGLYCANS |
| 5 | REACTOME_APOPTOSIS |
| 6 | REACTOME_SIGNALING_BY_RHO_GTPASES_MIRO_GTPASES_AND_RHOBTB3 |
| 7 | REACTOME_RHO_GTPASE_CYCLE |
| 8 | REACTOME_CYTOKINE_SIGNALING_IN_IMMUNE_SYSTEM |
| 9 | REACTOME_MEMBRANE_TRAFFICKING |
| 10 | REACTOME_CELL_CYCLE |

Table 62: Top 10 up-regulated pathways for cluster 14

3.8 Cluster 15

| | pathway | padj | NES |
|----|---|--------|--------|
| 1 | REACTOME_DETOXIFICATION_OF_REACTIVE_OXYGEN_SPECIES | 0.0015 | 1.7440 |
| 2 | REACTOME_SCAVENGING_OF_HEME_FROM_PLASMA | 0.0013 | 1.7018 |
| 3 | REACTOME_CREATION_OF_C4_AND_C2_ACTIVATORS | 0.0020 | 1.6272 |
| 4 | REACTOME_STING_MEDIATED_INDUCION_OF_HOST_IMMUNE_RESPONSES | 0.0020 | 1.6188 |
| 5 | REACTOME_GENERATION_OF_SECOND_MESSENGER_MOLECULES | 0.0039 | 1.6075 |
| 6 | REACTOME_FCGR_ACTIVATION | 0.0030 | 1.5710 |
| 7 | REACTOME_ROLE_OF_LAT2_NTAL_LAB_ON_CALCIUM_MOBILIZATION | 0.0028 | 1.5593 |
| 8 | REACTOME_SYNAPTIC_ADHESION_LIKE_MOLECULES | 0.0043 | 1.5579 |
| 9 | REACTOME_TRAFFICKING_OF_GLUR2_CONTAINING_AMPA_RECEPTORS | 0.0033 | 1.5535 |
| 10 | REACTOME_INITIAL_TRIGGERING_OF_COMPLEMENT | 0.0031 | 1.5179 |

Table 63: Top 10 up-regulated pathways for cluster 15

3.9 Cluster 16

| | pathway | |
|----|---|-----|
| 1 | REACTOME_DETOXIFICATION_OF_REACTIVE_OXYGEN_SPECIES | 0.0 |
| 2 | REACTOME_SCAVENGING_OF_HEME_FROM_PLASMA | 0.0 |
| 3 | REACTOME_ERCC6_CSB_AND_EHMT2_G9A_POSITIVELY_REGULATE_RRNA_EXPRESSION | 0.0 |
| 4 | REACTOME_GENERATION_OF_SECOND_MESSENGER_MOLECULES | 0.0 |
| 5 | REACTOME_ACTIVATION_OF_RAC1 | 0.0 |
| 6 | REACTOME_DEFECTS_OF_CONTACT_ACTIVATION_SYSTEM_CAS_AND_KALLIKREIN_KININ_SYSTEM_KKS | 0.0 |
| 7 | REACTOME_NUCLEOTIDE_SALVAGE | 0.0 |
| 8 | REACTOME_ROLE_OF_LAT2_NTAL_LAB_ON_CALCIUM_MOBILIZATION | 0.0 |
| 9 | REACTOME_CREATION_OF_C4_AND_C2_ACTIVATORS | 0.0 |
| 10 | REACTOME_NETRIN_1_SIGNALING | 0.0 |

Table 64: Top 10 up-regulated pathways for cluster 16

3.10 Cluster 17

| | pathway | padj | NES |
|----|--|--------|--------|
| 1 | REACTOME_ABORTIVE_ELONGATION_OF_HIV_1_TRANSCRIPT_IN_THE_ABSENCE_OF_TAT | 0.0254 | 1.6010 |
| 2 | REACTOME_CASPASE_ACTIVATION_VIA_EXTRINSIC_APOPTOTIC_SIGNALING_PATHWAY | 0.0254 | 1.5182 |
| 3 | REACTOME_BASIGIN_INTERACTIONS | 0.0254 | 1.4889 |
| 4 | REACTOME_B_WICH_COMPLEX_POSITIVELY_REGULATES_RRNA_EXPRESSION | 0.0254 | 1.4414 |
| 5 | REACTOME_BASE_EXCISION_REPAIR | 0.0254 | 1.4301 |
| 6 | REACTOME_CHOLESTEROL_BIOSYNTHESIS | 0.0254 | 1.4174 |
| 7 | REACTOME_CYCLIN_A_B1_B2_ASSOCIATED_EVENTS_DURING_G2_M_TRANSITION | 0.0254 | 1.4031 |
| 8 | REACTOME_CONSTITUTIVE_SIGNALING_BY_ABERRANT_PI3K_IN_CANCER | 0.0254 | 1.3634 |
| 9 | REACTOME_CLASS_I_MHC_MEDIATED_ANTIGEN_PROCESSING_PRESENTATION | 0.0254 | 1.3000 |
| 10 | REACTOME_ANTIGEN_PROCESSING_UBIQUITINATION_PROTEASOME_DEGRADATION | 0.0254 | 1.2755 |

Table 65: Top 10 up-regulated pathways for cluster 17

3.11 Cluster 18

| | pathway | padj | NES |
|----|---|--------|--------|
| 1 | REACTOME_CTLA4_INHIBITORY_SIGNALING | 0.0127 | 1.7256 |
| 2 | REACTOME_TRANSCRIPTIONAL_REGULATION_BY_RUNX1 | 0.0043 | 1.6641 |
| 3 | REACTOME_DDX58_IFIH1_MEDIATED_INDUCION_OF_INTERFERON_ALPHA_BETA | 0.0127 | 1.6278 |
| 4 | REACTOME_CHROMOSOME_MAINTENANCE | 0.0127 | 1.6178 |
| 5 | REACTOME_CARGO_RECOGNITION_FOR_CLATHRIN_MEDIATED_ENDOCYTOSIS | 0.0127 | 1.5234 |
| 6 | REACTOME_CYTOPROTECTION_BY_HMOX1 | 0.0127 | 1.4104 |
| 7 | REACTOME_CLATHRIN_MEDIATED_ENDOCYTOSIS | 0.0127 | 1.3496 |
| 8 | REACTOME_SIGNALING_BY_RECEPTOR_TYROSINE_KINASES | 0.0043 | 1.3221 |
| 9 | REACTOME_CYTOKINE_SIGNALING_IN_IMMUNE_SYSTEM | 0.0127 | 1.2120 |
| 10 | REACTOME_CELL_CYCLE | 0.0127 | 1.1090 |

Table 66: Top 10 up-regulated pathways for cluster 18

3.12 Cluster 19

| | pathway | padj | NES |
|----|---|--------|--------|
| 1 | REACTOME_GENERATION_OF_SECOND_MESSENGER_MOLECULES | 0.0038 | 1.6617 |
| 2 | REACTOME_SYNAPTIC_ADHESION_LIKE_MOLECULES | 0.0045 | 1.6378 |
| 3 | REACTOME_INTERACTION_BETWEEN_L1_AND_ANKYRINS | 0.0046 | 1.6245 |
| 4 | REACTOME_SCAVENGING_OF_HEME_FROM_PLASMA | 0.0034 | 1.6225 |
| 5 | REACTOME_CARNITINE_METABOLISM | 0.0069 | 1.6209 |
| 6 | REACTOME_NCAM_SIGNALING_FOR_NEURITE_OUT_GROWTH | 0.0032 | 1.6086 |
| 7 | REACTOME_ROLE_OF_LAT2_NTAL_LAB_ON_CALCIIUM_MOBILIZATION | 0.0033 | 1.6023 |
| 8 | REACTOME_CREATION_OF_C4_AND_C2_ACTIVATORS | 0.0056 | 1.4972 |
| 9 | REACTOME_FCGR_ACTIVATION | 0.0070 | 1.4675 |
| 10 | REACTOME_SIGNALING_BY_INSULIN_RECEPTOR | 0.0068 | 1.4380 |

Table 67: Top 10 up-regulated pathways for cluster 19

3.13 Cluster 2

| | pathway | padj | NES |
|----|--|--------|--------|
| 1 | REACTOME_ERCC6_CSB_AND_EHMT2_G9A_POSITIVELY_REGULATE_RRNA_EXPRESSION | 0.0011 | 1.8467 |
| 2 | REACTOME_PLATELET_AGGREGATION_PLUG_FORMATION | 0.0050 | 1.5533 |
| 3 | REACTOME_ACTIVATED_NTRK2_SIGNALS_THROUGH_FRS2_AND_FRS3 | 0.0072 | 1.5474 |
| 4 | REACTOME_SIGNALING_BY_NTRK2_TRKB | 0.0055 | 1.5408 |
| 5 | REACTOME_AMINE_LIGAND_BINDING_RECEPTORS | 0.0053 | 1.5363 |
| 6 | REACTOME_SCAVENGING_OF_HEME_FROM_PLASMA | 0.0042 | 1.5143 |
| 7 | REACTOME_DETOXIFICATION_OF_REACTIVE_OXYGEN_SPECIES | 0.0058 | 1.5112 |
| 8 | REACTOME_AUTOPHAGY | 0.0040 | 1.4072 |
| 9 | REACTOME_ROLE_OF_LAT2_NTAL_LAB_ON_CALCIUM_MOBILIZATION | 0.0058 | 1.4069 |
| 10 | REACTOME_ARACHIDONIC_ACID_METABOLISM | 0.0079 | 1.3859 |

Table 68: Top 10 up-regulated pathways for cluster 2

3.14 Cluster 20

| | pathway |
|----|--|
| 1 | REACTOME_ABERRANT_REGULATION_OF_MITOTIC_G1_S_TRANSITION_IN_CANCER_DUE_TO_RB1_DEFECTS |
| 2 | REACTOME_FORMATION_OF_SENESCENCE_ASSOCIATED_HETEROCHROMATIN_FOCI_SAHF |
| 3 | REACTOME_ESTROGEN_DEPENDENT_NUCLEAR_EVENTS_DOWNSTREAM_OF_ESR_MEMBRANE_SIGNALING |
| 4 | REACTOME_ECM_PROTEOGLYCANS |
| 5 | REACTOME_SIGNALING_BY_WNT |
| 6 | REACTOME_SIGNALING_BY_INTERLEUKINS |
| 7 | REACTOME_RHO_GTPASE_CYCLE |
| 8 | REACTOME_SIGNALING_BY_RHO_GTPASES_MIRO_GTPASES_AND_RHOBTB3 |
| 9 | REACTOME_CYTOKINE_SIGNALING_IN_IMMUNE_SYSTEM |
| 10 | REACTOME_METABOLISM_OF_RNA |

Table 69: Top 10 up-regulated pathways for cluster 20

3.15 Cluster 21

| | pathway | padj | NES |
|----|--|--------|--------|
| 1 | REACTOME_ERCC6_CSB_AND_EHMT2_G9A_POSITIVELY_REGULATE_RRNA_EXPRESSION | 0.0024 | 1.7275 |
| 2 | REACTOME_DETOXIFICATION_OF_REACTIVE_OXYGEN_SPECIES | 0.0025 | 1.6662 |
| 3 | REACTOME_SCAVENGING_OF_HEME_FROM_PLASMA | 0.0040 | 1.5617 |
| 4 | REACTOME_ACTIVATION_OF_RAC1 | 0.0068 | 1.5558 |
| 5 | REACTOME_ETHANOL_OXIDATION | 0.0073 | 1.5066 |
| 6 | REACTOME_NUCLEOTIDE_SALVAGE | 0.0068 | 1.5009 |
| 7 | REACTOME_GENERATION_OF_SECOND_MESSENGER_MOLECULES | 0.0070 | 1.4759 |
| 8 | REACTOME_AUTOPHAGY | 0.0021 | 1.4471 |
| 9 | REACTOME_ANTIMICROBIAL_PEPTIDES | 0.0074 | 1.4188 |
| 10 | REACTOME_SELENOAMINO_ACID_METABOLISM | 0.0064 | 1.3840 |

Table 70: Top 10 up-regulated pathways for cluster 21

3.16 Cluster 22

| | pathway | padj | NES |
|----|--|--------|--------|
| 1 | REACTOME_SCAVENGING_OF_HEME_FROM_PLASMA | 0.0015 | 1.6832 |
| 2 | REACTOME_STING_MEDIATED_INDUCION_OF_HOST_IMMUNE_RESPONSES | 0.0037 | 1.6185 |
| 3 | REACTOME_DETOXIFICATION_OF_REACTIVE_OXYGEN_SPECIES | 0.0030 | 1.6030 |
| 4 | REACTOME_TRAFFICKING_OF_GLUR2_CONTAINING_AMPA_RECEPTORS | 0.0032 | 1.5959 |
| 5 | REACTOME_ROLE_OF_LAT2_NTAL_LAB_ON_CALCIIUM_MOBILIZATION | 0.0023 | 1.5711 |
| 6 | REACTOME_CREATION_OF_C4_AND_C2_ACTIVATORS | 0.0026 | 1.5543 |
| 7 | REACTOME_GENERATION_OF_SECOND_MESSENGER_MOLECULES | 0.0043 | 1.5531 |
| 8 | REACTOME_ERCC6_CSB_AND_EHMT2_G9A_POSITIVELY_REGULATE_RRNA_EXPRESSION | 0.0047 | 1.5352 |
| 9 | REACTOME_FCGR_ACTIVATION | 0.0036 | 1.5198 |
| 10 | REACTOME_INITIAL_TRIGGERING_OF_COMPLEMENT | 0.0039 | 1.4956 |

Table 71: Top 10 up-regulated pathways for cluster 22

3.17 Cluster 23

| | pathway |
|----|---|
| 1 | REACTOME_FORMATION_OF_SENESCENCE_ASSOCIATED_HETEROCHROMATIN_FOCI_SAHF |
| 2 | REACTOME_ECM_PROTEOGLYCANS |
| 3 | REACTOME_RHO_GTPASE_CYCLE |
| 4 | REACTOME_SIGNALING_BY_RHO_GTPASES_MIRO_GTPASES_AND_RHOBTB3 |
| 5 | REACTOME_DISEASES_OF_SIGNAL_TRANSDUCTION_BY_GROWTH_FACTOR_RECEPTORS_AND_SECOND_MESS |
| 6 | REACTOME_SIGNALING_BY_RECEPTOR_TYROSINE_KINASES |
| 7 | REACTOME_METABOLISM_OF_RNA |
| 8 | REACTOME_CYTOKINE_SIGNALING_IN_IMMUNE_SYSTEM |
| 9 | REACTOME_TRANSPORT_OF_SMALL_MOLECULES |
| 10 | REACTOME_INNATE_IMMUNE_SYSTEM |

Table 72: Top 10 up-regulated pathways for cluster 23

3.18 Cluster 24

| | pathway | padj | NES |
|----|--|--------|--------|
| 1 | REACTOME_ERCC6_CSB_AND_EHMT2_G9A_POSITIVELY_REGULATE_RRNA_EXPRESSION | 0.0033 | 1.6462 |
| 2 | REACTOME_DETOXIFICATION_OF_REACTIVE_OXYGEN_SPECIES | 0.0026 | 1.6370 |
| 3 | REACTOME_NUCLEOTIDE_LIKE_PURINERGIC_RECEPTORS | 0.0036 | 1.6230 |
| 4 | REACTOME_GENERATION_OF_SECOND_MESSENGER_MOLECULES | 0.0048 | 1.5651 |
| 5 | REACTOME_P2Y_RECEPTORS | 0.0044 | 1.5589 |
| 6 | REACTOME_SCAVENGING_OF_HEME_FROM_PLASMA | 0.0034 | 1.5341 |
| 7 | REACTOME_ACTIVATION_OF_RAC1 | 0.0060 | 1.5010 |
| 8 | REACTOME_ENDOSOMAL_VACUOLAR_PATHWAY | 0.0048 | 1.4959 |
| 9 | REACTOME_SIGNALING_BY_NTRK2_TRKB | 0.0072 | 1.4718 |
| 10 | REACTOME_AMINE_LIGAND_BINDING_RECEPTORS | 0.0083 | 1.4587 |

Table 73: Top 10 up-regulated pathways for cluster 24

3.19 Cluster 25

| | pathway |
|----|---|
| 1 | REACTOME_FORMATION_OF_SENESCENCE_ASSOCIATED_HETEROCHROMATIN_FOCI_SAHF |
| 2 | REACTOME_HIV_LIFE_CYCLE |
| 3 | REACTOME_DISEASES_OF_SIGNAL_TRANSDUCTION_BY_GROWTH_FACTOR_RECEPTORS_AND_SECOND_MESS |
| 4 | REACTOME_RHO_GTPASE_CYCLE |
| 5 | REACTOME_SIGNALING_BY_RHO_GTPASES_MIRO_GTPASES_AND_RHOBTB3 |
| 6 | REACTOME_SIGNALING_BY_RECEPTOR_TYROSINE_KINASES |
| 7 | REACTOME_METABOLISM_OF_RNA |
| 8 | REACTOME_CELL_CYCLE |
| 9 | REACTOME_CYTOKINE_SIGNALING_IN_IMMUNE_SYSTEM |
| 10 | REACTOME_INFECTIOUS_DISEASE |

Table 74: Top 10 up-regulated pathways for cluster 25

3.20 Cluster 26

| | pathway | padj | NES |
|----|--|--------|--------|
| 1 | REACTOME_GENERATION_OF_SECOND_MESSENGER_MOLECULES | 0.0022 | 1.6643 |
| 2 | REACTOME_SYNAPTIC_ADHESION_LIKE_MOLECULES | 0.0024 | 1.6236 |
| 3 | REACTOME_ERCC6_CSB_AND_EHMT2_G9A_POSITIVELY_REGULATE_RRNA_EXPRESSION | 0.0032 | 1.6087 |
| 4 | REACTOME_DETOXIFICATION_OF_REACTIVE_OXYGEN_SPECIES | 0.0024 | 1.5791 |
| 5 | REACTOME_SCAVENGING_OF_HEME_FROM_PLASMA | 0.0022 | 1.5567 |
| 6 | REACTOME_ACTIVATED_NTRK2_SIGNALS_THROUGH_FRS2_AND_FRS3 | 0.0045 | 1.5338 |
| 7 | REACTOME_BLOOD_GROUP_SYSTEMS_BIOSYNTHESIS | 0.0067 | 1.5097 |
| 8 | REACTOME_ACTIVATION_OF_RAC1 | 0.0043 | 1.5082 |
| 9 | REACTOME_CHONDROITIN_SULFATE_BIOSYNTHESIS | 0.0046 | 1.4935 |
| 10 | REACTOME_ROLE_OF_LAT2_NTAL_LAB_ON_CALCIUM_MOBILIZATION | 0.0053 | 1.4543 |

Table 75: Top 10 up-regulated pathways for cluster 26

3.21 Cluster 27

| | pathway |
|----|---|
| 1 | REACTOME_RHOG_GTPASE_CYCLE |
| 2 | REACTOME_INTERLEUKIN_4_AND_INTERLEUKIN_13_SIGNALING |
| 3 | REACTOME_RAC1_GTPASE_CYCLE |
| 4 | REACTOME_RHO_GTPASE_CYCLE |
| 5 | REACTOME_INTRACELLULAR_SIGNALING_BY_SECOND_MESSENGERS |
| 6 | REACTOME_MAPK_FAMILY_SIGNALING_CASCADES |
| 7 | REACTOME_SIGNALING_BY_WNT |
| 8 | REACTOME_SIGNALING_BY_INTERLEUKINS |
| 9 | REACTOME_DISEASES_OF_SIGNAL_TRANSDUCTION_BY_GROWTH_FACTOR_RECEPTORS_AND_SECOND_MESS |
| 10 | REACTOME_SIGNALING_BY_RECEPTOR_TYROSINE_KINASES |

Table 76: Top 10 up-regulated pathways for cluster 27

3.22 Cluster 28

| | pathway | padj | NES |
|----|--|--------|--------|
| 1 | REACTOME_DETOXIFICATION_OF_REACTIVE_OXYGEN_SPECIES | 0.0012 | 1.7632 |
| 2 | REACTOME_ERCC6_CSB_AND_EHMT2_G9A_POSITIVELY_REGULATE_RRNA_EXPRESSION | 0.0024 | 1.7205 |
| 3 | REACTOME_GENERATION_OF_SECOND_MESSENGER_MOLECULES | 0.0046 | 1.5977 |
| 4 | REACTOME_NUCLEOTIDE_LIKE_PURINERGIC_RECEPTORS | 0.0052 | 1.5898 |
| 5 | REACTOME_SYNAPTIC_ADHESION_LIKE_MOLECULES | 0.0050 | 1.5700 |
| 6 | REACTOME_STING_MEDIATED_INDUCION_OF_HOST_IMMUNE_RESPONSES | 0.0072 | 1.5350 |
| 7 | REACTOME_SCAVENGING_OF_HEME_FROM_PLASMA | 0.0043 | 1.5178 |
| 8 | REACTOME_ROLE_OF_LAT2_NTAL_LAB_ON_CALCIIUM_MOBILIZATION | 0.0085 | 1.4063 |
| 9 | REACTOME_NCAM_SIGNALING_FOR_NEURITE_OUT_GROWTH | 0.0075 | 1.4057 |
| 10 | REACTOME_O_GLYCOSYLATION_OF_TSR_DOMAIN_CONTAINING_PROTEINS | 0.0084 | 1.4043 |

Table 77: Top 10 up-regulated pathways for cluster 28

3.23 Cluster 29

| | pathway | padj | NES |
|----|---|------|-----|
| 1 | REACTOME_REGULATION_OF_GENE_EXPRESSION_IN_LATE_STAGE_BRANCHING_MORPHOGENESIS_PANCRE | | |
| 2 | REACTOME_RUNX3_REGULATES_NOTCH_SIGNALING | | |
| 3 | REACTOME_PURINE_SALVAGE | | |
| 4 | REACTOME_NUCLEOTIDE_SALVAGE | | |
| 5 | REACTOME_CLASS_C_3_METABOTROPIC_GLUTAMATE_PHEROMONE_RECEPTORS | | |
| 6 | REACTOME_ZBP1_DAI_MEDIATED_INDUCION_OF_TYPE_1_IFNS | | |
| 7 | REACTOME_TAK1_ACTIVATES_NFKB_BY_PHOSPHORYLATION_AND_ACTIVATION_OF_IKKK_COMPLEX | | |
| 8 | REACTOME_ETHANOL_OXIDATION | | |
| 9 | REACTOME_SCAVENGING_OF_HEME_FROM_PLASMA | | |
| 10 | REACTOME_SIGNALING_BY_NOTCH3 | | |

Table 78: Top 10 up-regulated pathways for cluster 29

3.24 Cluster 3

| | pathway | padj | NES |
|----|---|--------|--------|
| 1 | REACTOME_DETOXIFICATION_OF_REACTIVE_OXYGEN_SPECIES | 0.0009 | 1.8081 |
| 2 | REACTOME_SCAVENGING_OF_HEME_FROM_PLASMA | 0.0010 | 1.6894 |
| 3 | REACTOME_GENERATION_OF_SECOND_MESSENGER_MOLECULES | 0.0020 | 1.6887 |
| 4 | REACTOME_CREATION_OF_C4_AND_C2_ACTIVATORS | 0.0016 | 1.6031 |
| 5 | REACTOME_ENDOSOMAL_VACUOLAR_PATHWAY | 0.0035 | 1.5908 |
| 6 | REACTOME_ROLE_OF_LAT2_NTAL_LAB_ON_CALCIIUM_MOBILIZATION | 0.0018 | 1.5747 |
| 7 | REACTOME_NUCLEOTIDE_SALVAGE | 0.0032 | 1.5734 |
| 8 | REACTOME_AMINE_LIGAND_BINDING_RECEPTORS | 0.0032 | 1.5712 |
| 9 | REACTOME_TRAFFICKING_OF_GLUR2_CONTAINING_AMPA_RECEPTORS | 0.0032 | 1.5699 |
| 10 | REACTOME_INITIAL_TRIGGERING_OF_COMPLEMENT | 0.0030 | 1.5054 |

Table 79: Top 10 up-regulated pathways for cluster 3

3.25 Cluster 30

| | pathway | padj | NES |
|----|--|--------|--------|
| 1 | REACTOME_PURINE_SALVAGE | 0.0072 | 1.4717 |
| 2 | REACTOME_RESPONSE_TO_METAL_IONS | 0.0087 | 1.4256 |
| 3 | REACTOME_ERYTHROPOIETIN_ACTIVATES_RAS | 0.0088 | 1.4083 |
| 4 | REACTOME_ERCC6_CSB_AND_EHMT2_G9A_POSITIVELY_REGULATE_RRNA_EXPRESSION | 0.0089 | 1.3923 |
| 5 | REACTOME_NUCLEOTIDE_SALVAGE | 0.0088 | 1.3793 |
| 6 | REACTOME_SUMOYLATION_OF_TRANSCRIPTION_FACTORS | 0.0088 | 1.3762 |
| 7 | REACTOME_P2Y_RECEPTORS | 0.0107 | 1.3340 |
| 8 | REACTOME_GENERATION_OF_SECOND_MESSENGER_MOLECULES | 0.0112 | 1.2782 |
| 9 | REACTOME_POSITIVE_EPIGENETIC_REGULATION_OF_RRNA_EXPRESSION | 0.0108 | 1.2545 |
| 10 | REACTOME_SELENOAMINO_ACID_METABOLISM | 0.0096 | 1.2033 |

Table 80: Top 10 up-regulated pathways for cluster 30

3.26 Cluster 31

| | pathway | |
|----|---|--|
| 1 | REACTOME_SIGNALING_BY_RHO_GTPASES_MIRO_GTPASES_AND_RHOBTB3 | |
| 2 | REACTOME_RHO_GTPASE_CYCLE | |
| 3 | REACTOME_METABOLISM_OF_AMINO_ACIDS_AND_DERIVATIVES | |
| 4 | REACTOME_SIGNALING_BY_INTERLEUKINS | |
| 5 | REACTOME_DISEASES_OF_SIGNAL_TRANSDUCTION_BY_GROWTH_FACTOR_RECEPTORS_AND_SECOND_MESS | |
| 6 | REACTOME_SIGNALING_BY_RECEPTOR_TYROSINE_KINASES | |
| 7 | REACTOME_METABOLISM_OF_RNA | |
| 8 | REACTOME_CELLULAR_RESPONSES_TO_STIMULI | |
| 9 | REACTOME_CYTOKINE_SIGNALING_IN_IMMUNE_SYSTEM | |
| 10 | REACTOME_INNATE_IMMUNE_SYSTEM | |

Table 81: Top 10 up-regulated pathways for cluster 31

3.27 Cluster 4

| | pathway | padj | NES |
|----|--|--------|--------|
| 1 | REACTOME_NUCLEOTIDE_SALVAGE | 0.0014 | 1.7325 |
| 2 | REACTOME_SCAVENGING_OF_HEME_FROM_PLASMA | 0.0006 | 1.7152 |
| 3 | REACTOME_PURINE_SALVAGE | 0.0030 | 1.6378 |
| 4 | REACTOME_DETOXIFICATION_OF_REACTIVE_OXYGEN_SPECIES | 0.0030 | 1.6186 |
| 5 | REACTOME_ACTIVATION_OF_RAC1 | 0.0045 | 1.5900 |
| 6 | REACTOME_TRAF6_MEDIATED_IRF7_ACTIVATION_IN_TLR7_8_OR_9_SIGNALING | 0.0039 | 1.5678 |
| 7 | REACTOME_GENERATION_OF_SECOND_MESSENGER_MOLECULES | 0.0040 | 1.5433 |
| 8 | REACTOME_CREATION_OF_C4_AND_C2_ACTIVATORS | 0.0033 | 1.4987 |
| 9 | REACTOME_ROLE_OF_LAT2_NTAL_LAB_ON_CALCIUM_MOBILIZATION | 0.0036 | 1.4816 |
| 10 | REACTOME_INITIAL_TRIGGERING_OF_COMPLEMENT | 0.0051 | 1.3980 |

Table 82: Top 10 up-regulated pathways for cluster 4

3.28 Cluster 5

| | pathway | padj | NES |
|----|--|--------|--------|
| 1 | REACTOME_CHONDROITIN_SULFATE_BIOSYNTHESIS | 0.0046 | 1.6412 |
| 2 | REACTOME_SYNAPTIC_ADHESION_LIKE_MOLECULES | 0.0047 | 1.6357 |
| 3 | REACTOME_GENERATION_OF_SECOND_MESSENGER_MOLECULES | 0.0027 | 1.6337 |
| 4 | REACTOME_DETOXIFICATION_OF_REACTIVE_OXYGEN_SPECIES | 0.0051 | 1.6079 |
| 5 | REACTOME_NUCLEOTIDE_LIKE_PURINERGIC_RECEPTORS | 0.0052 | 1.5949 |
| 6 | REACTOME_SCAVENGING_OF_HEME_FROM_PLASMA | 0.0030 | 1.5936 |
| 7 | REACTOME_ERCC6_CSB_AND_EHMT2_G9A_POSITIVELY_REGULATE_RRNA_EXPRESSION | 0.0061 | 1.5564 |
| 8 | REACTOME_P2Y_RECEPTORS | 0.0063 | 1.5502 |
| 9 | REACTOME_ROLE_OF_LAT2_NTAL_LAB_ON_CALCIIUM_MOBILIZATION | 0.0048 | 1.5364 |
| 10 | REACTOME_NCAM_SIGNALING_FOR_NEURITE_OUT_GROWTH | 0.0055 | 1.4801 |

Table 83: Top 10 up-regulated pathways for cluster 5

3.29 Cluster 6

| | pathway | |
|----|---|--|
| 1 | REACTOME_FORMATION_OF_SENESCENCE_ASSOCIATED_HETEROCHROMATIN_FOCI_SAHF | |
| 2 | REACTOME_DISEASES_OF_SIGNAL_TRANSDUCTION_BY_GROWTH_FACTOR_RECEPTORS_AND_SECOND_MESS | |
| 3 | REACTOME_RHO_GTPASE_CYCLE | |
| 4 | REACTOME_SIGNALING_BY_RHO_GTPASES_MIRO_GTPASES_AND_RHOBTB3 | |
| 5 | REACTOME_SIGNALING_BY_INTERLEUKINS | |
| 6 | REACTOME_SIGNALING_BY_RECEPTOR_TYROSINE_KINASES | |
| 7 | REACTOME_METABOLISM_OF_RNA | |
| 8 | REACTOME_CYTOKINE_SIGNALING_IN_IMMUNE_SYSTEM | |
| 9 | REACTOME_TRANSPORT_OF_SMALL_MOLECULES | |
| 10 | REACTOME_CELLULAR_RESPONSES_TO_STIMULI | |

Table 84: Top 10 up-regulated pathways for cluster 6

3.30 Cluster 7

| | pathway | padj | NES |
|----|---|--------|--------|
| 1 | REACTOME_CA2_PATHWAY | 0.0165 | 1.6989 |
| 2 | REACTOME_G_PROTEIN_BETA_GAMMA_SIGNALLING | 0.0165 | 1.6980 |
| 3 | REACTOME_GLUCAGON_TYPE_LIGAND_RECEPTORS | 0.0165 | 1.6925 |
| 4 | REACTOME_ACTIVATION_OF_KAINATE_RECEPTORS_UPON_GLUTAMATE_BINDING | 0.0165 | 1.6829 |
| 5 | REACTOME_G_PROTEIN_ACTIVATION | 0.0165 | 1.6700 |
| 6 | REACTOME_GRB2_EVENTS_IN_ERBB2_SIGNALING | 0.0165 | 1.6402 |
| 7 | REACTOME_G2_M_DNA_DAMAGE_CHECKPOINT | 0.0165 | 1.6338 |
| 8 | REACTOME_EXTRA_NUCLEAR_ESTROGEN_SIGNALING | 0.0165 | 1.6292 |
| 9 | REACTOME_G_ALPHA_Q_SIGNALLING_EVENTS | 0.0165 | 1.5390 |
| 10 | REACTOME_GPCR_LIGAND_BINDING | 0.0165 | 1.3763 |

Table 85: Top 10 up-regulated pathways for cluster 7

3.31 Cluster 8

| | pathway |
|----|--|
| 1 | REACTOME FORMATION OF SENESCENCE ASSOCIATED HETEROCHROMATIN FOCI SAHF |
| 2 | REACTOME BUTYROPHILIN BTN FAMILY INTERACTIONS |
| 3 | REACTOME INTERLEUKIN 2 SIGNALING |
| 4 | REACTOME CTLA4 INHIBITORY SIGNALING |
| 5 | REACTOME ABERRANT REGULATION OF MITOTIC G1 S TRANSITION IN CANCER DUE TO RB1 DEFECTS |
| 6 | REACTOME CD209 DC SIGN SIGNALING |
| 7 | REACTOME EPHA MEDIATED GROWTH CONE COLLAPSE |
| 8 | REACTOME ECM PROTEOGLYCANS |
| 9 | REACTOME DDX58 IFIH1 MEDIATED INDUCTION OF INTERFERON ALPHA BETA |
| 10 | REACTOME GENE SILENCING BY RNA |

Table 86: Top 10 up-regulated pathways for cluster 8

3.32 Cluster 9

| | pathway | padj | NES |
|----|--|--------|--------|
| 1 | REACTOME ENDOSOMAL VACUOLAR PATHWAY | 0.0017 | 1.7368 |
| 2 | REACTOME SYNAPTIC ADHESION LIKE MOLECULES | 0.0028 | 1.6908 |
| 3 | REACTOME SCAVENGING OF HEME FROM PLASMA | 0.0008 | 1.6890 |
| 4 | REACTOME ROLE OF LAT2 NTAL LAB ON CALCIUM MOBILIZATION | 0.0017 | 1.6064 |
| 5 | REACTOME ACTIVATED NTRK2 SIGNALS THROUGH FRS2 AND FRS3 | 0.0050 | 1.6000 |
| 6 | REACTOME CHONDROITIN SULFATE BIOSYNTHESIS | 0.0056 | 1.5535 |
| 7 | REACTOME CREATION OF C4 AND C2 ACTIVATORS | 0.0031 | 1.5161 |
| 8 | REACTOME FCGR ACTIVATION | 0.0042 | 1.4837 |
| 9 | REACTOME CD22 MEDIATED BCR REGULATION | 0.0064 | 1.4756 |
| 10 | REACTOME INITIAL TRIGGERING OF COMPLEMENT | 0.0042 | 1.4618 |

Table 87: Top 10 up-regulated pathways for cluster 9

4 Q3.2 Top 10 up-regulated pathways with adjustement for confondant effect

4.1 Cluster 0

| | pathway | padj | NES |
|----|---|--------|--------|
| 1 | REACTOME NUCLEOTIDE SALVAGE | 0.0014 | 1.8397 |
| 2 | REACTOME ACTIVATION OF RAC1 | 0.0058 | 1.7446 |
| 3 | REACTOME CYTOSOLIC SULFONATION OF SMALL MOLECULES | 0.0062 | 1.6324 |
| 4 | REACTOME PURINE SALVAGE | 0.0067 | 1.6313 |
| 5 | REACTOME PYRIMIDINE SALVAGE | 0.0077 | 1.5936 |
| 6 | REACTOME ERCC6 CSB AND EHM2 G9A POSITIVELY REGULATE RRNA EXPRESSION | 0.0081 | 1.5600 |
| 7 | REACTOME AMINE LIGAND BINDING RECEPTORS | 0.0090 | 1.5038 |
| 8 | REACTOME HYALURONAN METABOLISM | 0.0086 | 1.5005 |
| 9 | REACTOME O GLYCOSYLATION OF TSR DOMAIN CONTAINING PROTEINS | 0.0098 | 1.4624 |
| 10 | REACTOME METABOLISM OF NUCLEOTIDES | 0.0101 | 1.3500 |

Table 88: Top 10 up-regulated pathways for cluster 0 with adjustement for confondant effect

4.2 Cluster 1

| | pathway |
|----|---|
| 1 | REACTOME SYNAPTIC ADHESION LIKE MOLECULES |
| 2 | REACTOME INFLAMMASOMES |
| 3 | REACTOME ADHERENS JUNCTIONS INTERACTIONS |
| 4 | REACTOME ACTIVATION OF THE PRE REPLICATIVE COMPLEX |
| 5 | REACTOME TP53 REGULATES TRANSCRIPTION OF SEVERAL ADDITIONAL CELL DEATH GENES WHOSE SPECIFIC ROLES IN P53 DEPENDENT APOPTOSIS REMAIN UNKNOWN |
| 6 | REACTOME RECYCLING OF BILE ACIDS AND SALTS |
| 7 | REACTOME BBSOME MEDIATED CARGO TARGETING TO CILIUM |
| 8 | REACTOME PROLONGED ERK ACTIVATION EVENTS |
| 9 | REACTOME PURINERGIC SIGNALING IN LEISHMANIASIS INFECTION |
| 10 | REACTOME SWITCHING OF ORIGINS TO A POST REPLICATIVE STATE |

Table 89: Top 10 up-regulated pathways for cluster 1 with adjustement for confondant effect

4.3 Cluster 2

| | pathway | padj | NES |
|----|--|--------|--------|
| 1 | REACTOME.ERCC6.CSB.AND.EHMT2.G9A.POSITIVELY.REGULATE.RRNA.EXPRESSION | 0.0080 | 1.7707 |
| 2 | REACTOME.ACTIVATED.NTRK2.SIGNALS.THROUGH.FRS2.AND.FRS3 | 0.0109 | 1.6270 |
| 3 | REACTOME.REGULATION.OF.TP53.ACTIVITY.THROUGH.ACETYLATION | 0.0110 | 1.5969 |
| 4 | REACTOME.ACTIVATION.OF.RAC1 | 0.0127 | 1.5906 |
| 5 | REACTOME.NUCLEOTIDE.SALVAGE | 0.0127 | 1.5471 |
| 6 | REACTOME.CYTOSOLIC.SULFONATION.OF.SMALL.MOLECULES | 0.0112 | 1.5414 |
| 7 | REACTOME.FOXO.MEDIATED.TRANSCRIPTION.OF.CELL.CYCLE.GENES | 0.0146 | 1.5037 |
| 8 | REACTOME.SEALING.OF.THE.NUCLEAR.ENVELOPE.NE.BY.ESCRT.III | 0.0140 | 1.4774 |
| 9 | REACTOME.ARACHIDONIC.ACID.METABOLISM | 0.0140 | 1.3798 |
| 10 | REACTOME.AUTOPHAGY | 0.0112 | 1.3412 |

Table 90: Top 10 up-regulated pathways for cluster 2 with adjustment for confondant effect

4.4 Cluster 3

| | pathway | padj | NES |
|----|--|--------|--------|
| 1 | REACTOME.STING.MEDIATED.INDUCTION.OF.HOST.IMMUNE.RESPONSES | 0.0013 | 1.8318 |
| 2 | REACTOME.IRF3.MEDIATED.INDUCTION.OF.TYPE.I.IFN | 0.0014 | 1.7682 |
| 3 | REACTOME.DETOXIFICATION.OF.REACTIVE.OXYGEN.SPECIES | 0.0074 | 1.5476 |
| 4 | REACTOME.INITIAL.TRIGGERING.OF.COMPLEMENT | 0.0040 | 1.5420 |
| 5 | REACTOME.ENDOSOMAL.VACUOLAR.PATHWAY | 0.0085 | 1.5411 |
| 6 | REACTOME.RESPONSE.TO.METAL.IONS | 0.0094 | 1.5201 |
| 7 | REACTOME.ZINC.TRANSPORTERS | 0.0075 | 1.5138 |
| 8 | REACTOME.CREATION.OF.C4.AND.C2.ACTIVATORS | 0.0069 | 1.5051 |
| 9 | REACTOME.NUCLEOTIDE.SALVAGE | 0.0094 | 1.4967 |
| 10 | REACTOME.SCAVENGING.OF.HEME.FROM.PLASMA | 0.0080 | 1.4778 |

Table 91: Top 10 up-regulated pathways for cluster 3 with adjustment for confondant effect

4.5 Cluster 4

| | pathway | padj | NES |
|----|---|--------|--------|
| 1 | REACTOME.PURINE.SALVAGE | 0.0007 | 1.8566 |
| 2 | REACTOME.NUCLEOTIDE.SALVAGE | 0.0023 | 1.7881 |
| 3 | REACTOME.TRANSPORT.OF.CONNEXONS.TO.THE.PLASMA.MEMBRANE | 0.0062 | 1.6337 |
| 4 | REACTOME.SYNTHESIS.OF.PIP3.AT.THE.EARLY.ENDOSOME.MEMBRANE | 0.0072 | 1.5874 |
| 5 | REACTOME.PHYSIOLOGICAL.FACTORS | 0.0103 | 1.5247 |
| 6 | REACTOME.POST.CHAPERONIN.TUBULIN.FOLDING.PATHWAY | 0.0122 | 1.4944 |
| 7 | REACTOME.GAP.JUNCTION.ASSEMBLY | 0.0110 | 1.4900 |
| 8 | REACTOME.ACTIVATION.OF.AMPK.DOWNSTREAM.OF.NMDARS | 0.0117 | 1.4782 |
| 9 | REACTOME.SEALING.OF.THE.NUCLEAR.ENVELOPE.NE.BY.ESCRT.III | 0.0120 | 1.4659 |
| 10 | REACTOME.GENERATION.OF.SECOND.MESSENGER.MOLECULES | 0.0117 | 1.4539 |

Table 92: Top 10 up-regulated pathways for cluster 4 with adjustment for confondant effect

4.6 Cluster 5

| | pathway | padj | NES |
|----|---|--------|--------|
| 1 | REACTOME.ENDOSOMAL.VACUOLAR.PATHWAY | 0.0029 | 1.7068 |
| 2 | REACTOME.RAF.INDEPENDENT.MAPK1.3.ACTIVATION | 0.0042 | 1.7046 |
| 3 | REACTOME.SIGNALING.BY.NTRK3.TRKC | 0.0046 | 1.6581 |
| 4 | REACTOME.NCAM.SIGNALING.FOR.NEURITE.OUT.GROWTH | 0.0054 | 1.5881 |
| 5 | REACTOME.ROLE.OF.LAT2.NTAL.LAB.ON.CALCIUM.MOBILIZATION | 0.0069 | 1.5578 |
| 6 | REACTOME.SYNAPTIC.ADHESSION.LIKE.MOLECULES | 0.0107 | 1.5550 |
| 7 | REACTOME.CHONDROITIN.SULFATE.BIOSYNTHESIS | 0.0107 | 1.5467 |
| 8 | REACTOME.SIGNALING.BY.INSULIN.RECEPTOR | 0.0058 | 1.5450 |
| 9 | REACTOME.GASTRIN.CREB.SIGNALLING.PATHWAY.VIA.PKC.AND.MAPK | 0.0107 | 1.5148 |
| 10 | REACTOME.CREATION.OF.C4.AND.C2.ACTIVATORS | 0.0109 | 1.4599 |

Table 93: Top 10 up-regulated pathways for cluster 5 with adjustment for confondant effect

4.7 Cluster 6

| | pathway | padj | NES |
|----|--|--------|--------|
| 1 | REACTOME.TRANSCRIPTIONAL.REGULATION.BY.RUNX1 | 0.0001 | 1.7394 |
| 2 | REACTOME.SIGNALING.BY.WNT | 0.0001 | 1.6567 |
| 3 | REACTOME.SIGNALING.BY.NUCLEAR.RECEPTORS | 0.0002 | 1.5887 |
| 4 | REACTOME.METABOLISM.OF.RNA | 0.0000 | 1.5194 |
| 5 | REACTOME.SIGNALING.BY.RHO.GTPASES.MIRO.GTPASES.AND.RHOBTB3 | 0.0000 | 1.5005 |
| 6 | REACTOME.RHO.GTPASE.CYCLE | 0.0001 | 1.4847 |
| 7 | REACTOME.SIGNALING.BY.RECEPTOR.TYROSINE.KINASES | 0.0001 | 1.4823 |
| 8 | REACTOME.CYTOKINE.SIGNALING.IN.IMMUNE.SYSTEM | 0.0001 | 1.4335 |
| 9 | REACTOME.TRANSPORT.OF.SMALL.MOLECULES | 0.0001 | 1.4275 |
| 10 | REACTOME.INNATE.IMMUNE.SYSTEM | 0.0001 | 1.3371 |

Table 94: Top 10 up-regulated pathways for cluster 6 with adjustment for confondant effect

4.8 Cluster 7

| | pathway | padj | NES |
|----|--|--------|--------|
| 1 | REACTOME.COOPERATION_OF_PDCL_PHL1_AND_TRIC_CCT_IN_G_PROTEIN_BETA_FOLDING | 0.0175 | 1.6514 |
| 2 | REACTOME.ACTIVATION_OF_KAINATE_RECEPTORS_UPON_GLUTAMATE_BINDING | 0.0175 | 1.6432 |
| 3 | REACTOME.ADP_SIGNALING_THROUGH_P2Y_PURINOCEPTOR_1 | 0.0175 | 1.6265 |
| 4 | REACTOME.ADRENALINE_NORADRENALINE_INHIBITS_INSULIN_SECRETION | 0.0175 | 1.6238 |
| 5 | REACTOME.ACTIVATION_OF_ATR_IN_RESPONSE_TO_REPLICATION_STRESS | 0.0175 | 1.6201 |
| 6 | REACTOME.CA2_PATHWAY | 0.0175 | 1.6194 |
| 7 | REACTOME.EXTRA_NUCLEAR_ESTROGEN_SIGNALING | 0.0175 | 1.5929 |
| 8 | REACTOME.CONSTITUTIVE_SIGNALING_BY_EGFRV8 | 0.0175 | 1.5801 |
| 9 | REACTOME.DEUBIQUITINATION | 0.0175 | 1.4003 |
| 10 | REACTOME.CLASS_A_1_RHODOPSIN_LIKE_RECEPTORS | 0.0175 | 1.3639 |

Table 95: Top 10 up-regulated pathways for cluster 7 with adjustment for confondant effect

4.9 Cluster 8

| | pathway | padj | NES |
|----|---|--------|--------|
| 1 | REACTOME.NEGATIVE_REGULATION_OF_NMDA_RECEPTOR_MEDIATED_NEURONAL_TRANSMISSION | 0.0037 | 1.6607 |
| 2 | REACTOME_TP53_REGULATES_TRANSCRIPTION_OF_SEVERAL_ADDITIONAL_CELL_DEATH_GENES_WHOSE_SPECIFIC_ROLES_IN_P53_DEPENDENT_APOPTOSIS_REMAIN_U | 0.0064 | 1.6339 |
| 3 | REACTOME.FORMATION_OF_SENESCENCE_ASSOCIATED_HETEROCHROMATIN_FOCI_SAHF | 0.0050 | 1.6308 |
| 4 | REACTOME.INTRACELLULAR_SIGNALING_BY_SECOND_MESSENGERS | 0.0118 | 1.5904 |
| 5 | REACTOME.RHO_GTPASE_CYCLE | 0.0087 | 1.5822 |
| 6 | REACTOME.MAPK_FAMILY_SIGNALING_CASCADES | 0.0062 | 1.5636 |
| 7 | REACTOME.SIGNALING_BY_INTERLEUKINS | 0.0055 | 1.5632 |
| 8 | REACTOME.SIGNALING_BY_RECEPTOR_TYROSINE_KINASES | 0.0064 | 1.5590 |
| 9 | REACTOME.CYTOKINE_SIGNALING_IN_IMMUNE_SYSTEM | 0.0072 | 1.5142 |
| 10 | REACTOME.TRANSPORT_OF_SMALL_MOLECULES | 0.0119 | 1.4662 |

Table 96: Top 10 up-regulated pathways for cluster 8 with adjustment for confondant effect

4.10 Cluster 9

| | pathway | padj | NES |
|----|--|--------|--------|
| 1 | REACTOME.SCAVENGING_OF_HEME_FROM_PLASMA | 0.0037 | 1.6607 |
| 2 | REACTOME.GABA_SYNTHESIS_RELEASE_REUPTAKE_AND_DEGRADATION | 0.0064 | 1.6339 |
| 3 | REACTOME_O_GLYCOSYLATION_OF_TSR_DOMAIN_CONTAINING_PROTEINS | 0.0050 | 1.6308 |
| 4 | REACTOME.CHONDROITIN_SULFATE_BIOSYNTHESIS | 0.0118 | 1.5904 |
| 5 | REACTOME.ADHERENS_JUNCTIONS_INTERACTIONS | 0.0087 | 1.5822 |
| 6 | REACTOME.CREATION_OF_C4_AND_C2_ACTIVATORS | 0.0062 | 1.5636 |
| 7 | REACTOME.INITIAL_TRIGGERING_OF_COMPLEMENT | 0.0055 | 1.5632 |
| 8 | REACTOME_ROLE_OF_LAT2_NTAL_LAB_ON_CALCIIUM_MOBILIZATION | 0.0064 | 1.5590 |
| 9 | REACTOME.FCGR_ACTIVATION | 0.0072 | 1.5142 |
| 10 | REACTOME_CD22_MEDIATED_BCR_REGULATION | 0.0119 | 1.4662 |

Table 97: Top 10 up-regulated pathways for cluster 9 with adjustment for confondant effect

4.11 Cluster 10

| | pathway | padj | NES |
|----|---|--------|--------|
| 1 | REACTOME.ESR_MEDIATED_SIGNALING | 0.0001 | 1.7877 |
| 2 | REACTOME.SIGNALING_BY_NUCLEAR_RECEPTORS | 0.0001 | 1.6804 |
| 3 | REACTOME.SIGNALING_BY_RECEPTOR_TYROSINE_KINASES | 0.0001 | 1.4854 |
| 4 | REACTOME.DISEASES_OF_SIGNAL_TRANSDUCTION_BY_GROWTH_FACTOR_RECEPTORS_AND_SECOND_MESSENGERS | 0.0001 | 1.4829 |
| 5 | REACTOME.SIGNALING_BY_INTERLEUKINS | 0.0001 | 1.4740 |
| 6 | REACTOME.SIGNALING_BY_RHO_GTPASES_MIRO_GTPASES_AND_RHOBTB3 | 0.0000 | 1.4695 |
| 7 | REACTOME.METABOLISM_OF_RNA | 0.0000 | 1.4688 |
| 8 | REACTOME.MEMBRANE_TRAFFICKING | 0.0001 | 1.3905 |
| 9 | REACTOME.CYTOKINE_SIGNALING_IN_IMMUNE_SYSTEM | 0.0001 | 1.3871 |
| 10 | REACTOME.INNATE_IMMUNE_SYSTEM | 0.0001 | 1.3392 |

Table 98: Top 10 up-regulated pathways for cluster 10 with adjustment for confondant effect

4.12 Cluster 11

| | pathway | padj | NES |
|----|---|--------|--------|
| 1 | REACTOME.CYTOSOLIC_SULFONATION_OF_SMALL_MOLECULES | 0.0088 | 1.8447 |
| 2 | REACTOME.CHONDROITIN_SULFATE_BIOSYNTHESIS | 0.0138 | 1.6831 |
| 3 | REACTOME.INSULIN_RECEPTOR_RECYCLING | 0.0131 | 1.6819 |
| 4 | REACTOME.SIGNALING_BY_ACTIVIN | 0.0147 | 1.6507 |
| 5 | REACTOME.BASIGIN_INTERACTIONS | 0.0138 | 1.5869 |
| 6 | REACTOME.RESOLUTION_OF_D_LOOP_STRUCTURES | 0.0138 | 1.5776 |
| 7 | REACTOME.TRANSFERRIN_ENDOCYTOSIS_AND_RECYCLING | 0.0147 | 1.5703 |
| 8 | REACTOME.AMINE_LIGAND_BINDING_RECEPTORS | 0.0148 | 1.5591 |
| 9 | REACTOME.SIGNALING_BY_INSULIN_RECEPTOR | 0.0158 | 1.4907 |
| 10 | REACTOME.POTASSIUM_CHANNELS | 0.0147 | 1.4025 |

Table 99: Top 10 up-regulated pathways for cluster 11 with adjustment for confondant effect

4.13 Cluster 12

| | pathway | padj | NES |
|----|---|--------|--------|
| 1 | REACTOME.TRANSCRIPTIONAL_REGULATION_OF_TESTIS_DIFFERENTIATION | 0.0126 | 1.6713 |
| 2 | REACTOME.HDMS_DEMETHYLATE_HISTONES | 0.0126 | 1.6630 |
| 3 | REACTOME.INWARDLY_RECTIFYING_K_CHANNELS | 0.0126 | 1.6524 |
| 4 | REACTOME.NEGATIVE_REGULATORS_OF_DDX58_IFIH1_SIGNALING | 0.0126 | 1.6252 |
| 5 | REACTOME.THROMBIN_SIGNALING_THROUGH_PROTEINASE_ACTIVATED_RECEPTORS_PARS | 0.0132 | 1.5931 |
| 6 | REACTOME.G.BETA.GAMMA_SIGNALLING_THROUGH_CDC42 | 0.0166 | 1.5856 |
| 7 | REACTOME.BLOOD_GROUP_SYSTEMS_BIOSYNTHESIS | 0.0166 | 1.5781 |
| 8 | REACTOME.PRESYNAPTIC_FUNCTION_OF_KAINATE_RECEPTORS | 0.0211 | 1.5491 |
| 9 | REACTOME.KERATAN_SULFATE_KERATIN_METABOLISM | 0.0211 | 1.5059 |
| 10 | REACTOME.CA2_PATHWAY | 0.0207 | 1.4754 |

Table 100: Top 10 up-regulated pathways for cluster 12 with adjustment for confondant effect

4.14 Cluster 13

| | pathway | padj | NES |
|----|--|--------|--------|
| 1 | REACTOME.BIOTIN_TRANSPORT_AND_METABOLISM | 0.0091 | 1.6129 |
| 2 | REACTOME.SYNAPTIC_ADHESION_LIKE_MOLECULES | 0.0124 | 1.5218 |
| 3 | REACTOME.NCAM_SIGNALING_FOR_NEURITE_OUT_GROWTH | 0.0088 | 1.5119 |
| 4 | REACTOME.INSULIN_RECEPTOR_RECYCLING | 0.0099 | 1.4999 |
| 5 | REACTOME.SUMOYLATION_OF_IMMUNE_RESPONSE_PROTEINS | 0.0138 | 1.4929 |
| 6 | REACTOME.NCAM1_INTERACTIONS | 0.0092 | 1.4859 |
| 7 | REACTOME.ADHERENS_JUNCTIONS_INTERACTIONS | 0.0144 | 1.4766 |
| 8 | REACTOME.RHOV_GTPASE_CYCLE | 0.0165 | 1.4275 |
| 9 | REACTOME.SCAVENGING_OF_HEME_FROM_PLASMA | 0.0155 | 1.3808 |
| 10 | REACTOME.INITIAL_TRIGGERING_OF_COMPLEMENT | 0.0135 | 1.3637 |

Table 101: Top 10 up-regulated pathways for cluster 13 with adjustment for confondant effect

4.15 Cluster 14

| | pathway | padj | NES |
|----|--|--------|--------|
| 1 | REACTOME.DEADENYLATION_OF_MRNA | 0.0067 | 1.8682 |
| 2 | REACTOME.NUCLEAR_RECEPTOR_TRANSCRIPTION_PATHWAY | 0.0077 | 1.7228 |
| 3 | REACTOME.RHOC_GTPASE_CYCLE | 0.0083 | 1.6190 |
| 4 | REACTOME.CILIUM_ASSEMBLY | 0.0067 | 1.4961 |
| 5 | REACTOME.SIGNALING_BY_NUCLEAR_RECEPTORS | 0.0067 | 1.4713 |
| 6 | REACTOME.ORGANELLE_BIOGENESIS_AND_MAINTENANCE | 0.0077 | 1.4116 |
| 7 | REACTOME.RHO_GTPASE_CYCLE | 0.0048 | 1.3712 |
| 8 | REACTOME.METABOLISM_OF_AMINO_ACIDS_AND_DERIVATIVES | 0.0077 | 1.3671 |
| 9 | REACTOME.SIGNALING_BY_RHO_GTPASES_MIRO_GTPASES_AND_RHOBTB3 | 0.0048 | 1.3035 |
| 10 | REACTOME.DEVELOPMENTAL_BIOLOGY | 0.0083 | 1.1967 |

Table 102: Top 10 up-regulated pathways for cluster 14 with adjustment for confondant effect

4.16 Cluster 15

| | pathway | padj | NES |
|----|---|--------|--------|
| 1 | REACTOME.INTERACTION_BETWEEN_L1_AND_ANKYRINS | 0.0055 | 1.5843 |
| 2 | REACTOME.CREATION_OF_C4_AND_C2_ACTIVATORS | 0.0045 | 1.5842 |
| 3 | REACTOME.ENDOSOMAL_VACUOLAR_PATHWAY | 0.0056 | 1.5832 |
| 4 | REACTOME.IRF3_MEDIATED_INDUCION_OF_TYPE_I_IFN | 0.0064 | 1.5585 |
| 5 | REACTOME.RAF_INDEPENDENT_MAPK1_3_ACTIVATION | 0.0064 | 1.5351 |
| 6 | REACTOME.ADHERENS_JUNCTIONS_INTERACTIONS | 0.0069 | 1.5304 |
| 7 | REACTOME.SCAVENGING_OF_HEME_FROM_PLASMA | 0.0070 | 1.4938 |
| 8 | REACTOME.INITIAL_TRIGGERING_OF_COMPLEMENT | 0.0056 | 1.4902 |
| 9 | REACTOME.ROLE_OF_LAT2_NTAL_LAB_ON_CALCIIUM_MOBILIZATION | 0.0072 | 1.4591 |
| 10 | REACTOME.CD22_MEDIATED_BCR_REGULATION | 0.0074 | 1.4377 |

Table 103: Top 10 up-regulated pathways for cluster 15 with adjustment for confondant effect

4.17 Cluster 16

| | pathway | padj | NES |
|----|---|--------|--------|
| 1 | REACTOME.SCAVENGING_OF_HEME_FROM_PLASMA | 0.0016 | 1.6775 |
| 2 | REACTOME.ROLE_OF_LAT2_NTAL_LAB_ON_CALCIIUM_MOBILIZATION | 0.0048 | 1.5823 |
| 3 | REACTOME.DETOXIFICATION_OF_REACTIVE_OXYGEN_SPECIES | 0.0048 | 1.5642 |
| 4 | REACTOME.GENERATION_OF_SECOND_MESSENGER_MOLECULES | 0.0049 | 1.5624 |
| 5 | REACTOME.NUCLEOTIDE_SALVAGE | 0.0074 | 1.5280 |
| 6 | REACTOME.CREATION_OF_C4_AND_C2_ACTIVATORS | 0.0062 | 1.5196 |
| 7 | REACTOME.ENDOSOMAL_VACUOLAR_PATHWAY | 0.0066 | 1.5173 |
| 8 | REACTOME.DCC_MEDIATED_ATTRACTIVE_SIGNALING | 0.0075 | 1.5133 |
| 9 | REACTOME.AMINE_LIGAND_BINDING_RECEPTORS | 0.0094 | 1.4672 |
| 10 | REACTOME.INITIAL_TRIGGERING_OF_COMPLEMENT | 0.0052 | 1.4656 |

Table 104: Top 10 up-regulated pathways for cluster 16 with adjustment for confondant effect

4.18 Cluster 17

| | pathway | padj | NES |
|----|--|--------|--------|
| 1 | REACTOME.G1S.SPECIFIC.TRANSCRIPTION | 0.0111 | 1.8989 |
| 2 | REACTOME.INTERCONVERSION_OF_NUCLEOTIDE_D1AND_TRIPHOSPHATES | 0.0111 | 1.8786 |
| 3 | REACTOME.APOPTOTIC.CLEAVAGE.OF.CELL.ADHESION.PROTEINS | 0.0249 | 1.5718 |
| 4 | REACTOME.BASE.EXCISION.REPAIR | 0.0249 | 1.5286 |
| 5 | REACTOME.B.WICHL.COMPLEX.POSITIVELY.REGULATES.RRNA.EXPRESSION | 0.0249 | 1.5117 |
| 6 | REACTOME.ACTIVATION_OF_GENE.EXPRESSION_BY_SREBF_SREBP | 0.0249 | 1.4265 |
| 7 | REACTOME.BIOLOGICAL.OXIDATIONS | 0.0249 | 1.4180 |
| 8 | REACTOME.ABORTIVE.ELONGATION_OF_HIV_1_TRANSCRIPT_IN_THE_ABSENCE_OF_TAT | 0.0249 | 1.4167 |
| 9 | REACTOME.BASIGIN.INTERACTIONS | 0.0249 | 1.4132 |
| 10 | REACTOME.ANTIGEN.PROCESSING_UBIQUITINATION_PROTEASOME.DEGRADATION | 0.0249 | 1.2880 |

Table 105: Top 10 up-regulated pathways for cluster 17 with adjustment for confondant effect

4.19 Cluster 18

| | pathway | padj | NES |
|----|---|--------|--------|
| 1 | REACTOME.MET.RECEPTOR.RECYCLING | 0.0188 | 2.7131 |
| 2 | REACTOME.LOSS.OF.FUNCTION.OF.MECP2.IN.RETT.SYNDROME | 0.0173 | 2.5978 |
| 3 | REACTOME.CASPASE.ACTIVATION.VIA.DEATH.RECEPTORS.IN.THE.PRESENCE.OF.LIGAND | 0.0192 | 2.4909 |
| 4 | REACTOME.TRAF6.MEDIATED.INDUCTION.OF.TAK1.COMPLEX.WITHIN.TLR4.COMPLEX | 0.0192 | 2.4909 |
| 5 | REACTOME.MECP2.REGULATES.NEURONAL.RECEPTORS.AND.CHANNELS | 0.0152 | 2.4373 |
| 6 | REACTOME.ACTIVATION.OF.IRF3.IRF7.MEDIATED.BY.TBK1.IKK.EPSILON | 0.0194 | 2.4362 |
| 7 | REACTOME.INNATE.IMMUNE.SYSTEM | 0.0033 | 1.4240 |
| 8 | REACTOME.NEUTROPHIL.DEGRANULATION | 0.0152 | 1.3372 |
| 9 | REACTOME.CYTOPROTECTION.BY.HMOX1 | 0.0173 | 1.2471 |
| 10 | REACTOME.CELLULAR.RESPONSE.TO.CHEMICAL.STRESS | 0.0173 | 1.2470 |

Table 106: Top 10 up-regulated pathways for cluster 18 with adjustment for confondant effect

4.20 Cluster 19

| | pathway | padj | NES |
|----|---|--------|--------|
| 1 | REACTOME.INSULIN.RECEPTOR.RECYCLING | 0.0162 | 1.8236 |
| 2 | REACTOME.GABA.SYNTHESIS.RELEASE.REUPTAKE.AND.DEGRADATION | 0.0162 | 1.6381 |
| 3 | REACTOME.ENERGY.DEPENDENT.REGULATION.OF.MTOR.BY.LKB1.AMPK | 0.0162 | 1.6317 |
| 4 | REACTOME.ACYL.CHAIN.REMODELLING.OF.PI | 0.0162 | 1.6181 |
| 5 | REACTOME.FORMATION.OF.FIBRIN.CLOT.CLOTTING.CASCADE | 0.0162 | 1.6156 |
| 6 | REACTOME.DEFECTS.OF.CONTACT.ACTIVATION.SYSTEM.CAS.AND.KALLIKREIN.KININ.SYSTEM.KKS | 0.0162 | 1.6072 |
| 7 | REACTOME.BLOOD.GROUP.SYSTEMS.BIOSYNTHESIS | 0.0162 | 1.6059 |
| 8 | REACTOME.CREB1.PHOSPHORYLATION.THROUGH.NMDA.RECEPTOR.MEDIATED.ACTIVATION.OF.RAS.SIGNALING | 0.0162 | 1.6050 |
| 9 | REACTOME.AMINO.ACIDS.REGULATE.MTORC1 | 0.0162 | 1.5214 |
| 10 | REACTOME.ACTIVATION.OF.NMDA.RECEPTORS.AND.POSTSYNAPTIC.EVENTS | 0.0162 | 1.5165 |

Table 107: Top 10 up-regulated pathways for cluster 19 with adjustment for confondant effect

4.21 Cluster 20

| | pathway | padj | NES |
|----|---|--------|--------|
| 1 | REACTOME.ABERRANT.REGULATION.OF.MITOTIC.G1S.TRANSITION.IN.CANCER.DUE.TO.RB1.DEFECTS | 0.0029 | 1.9536 |
| 2 | REACTOME.RUNX2.REGULATES.BONE.DEVELOPMENT | 0.0029 | 1.9502 |
| 3 | REACTOME.RUNX2.REGULATES.OSTEOBLAST.DIFFERENTIATION | 0.0088 | 1.9044 |
| 4 | REACTOME.FORMATION.OF.SENESCENCE.ASSOCIATED.HETEROCHROMATIN.FOCI.SAHF | 0.0106 | 1.8948 |
| 5 | REACTOME.REGULATION.OF.RUNX1.EXPRESSION.AND.ACTIVITY | 0.0106 | 1.6825 |
| 6 | REACTOME.DDX58.JFH1.MEDIATED.INDUCTION.OF.INTERFERON.ALPHA.BETA | 0.0106 | 1.5555 |
| 7 | REACTOME.SIGNALING.BY.WNT | 0.0029 | 1.4974 |
| 8 | REACTOME.APOPTOSIS | 0.0106 | 1.4549 |
| 9 | REACTOME.PROGRAMMED.CELL.DEATH | 0.0106 | 1.3193 |
| 10 | REACTOME.EXTRACELLULAR.MATRIX.ORGANIZATION | 0.0106 | 1.3028 |

Table 108: Top 10 up-regulated pathways for cluster 20 with adjustment for confondant effect

4.22 Cluster 21

| | pathway | padj | NES |
|----|--|--------|--------|
| 1 | REACTOME.ACTIVATION.OF.RAC1 | 0.0031 | 1.6999 |
| 2 | REACTOME.ERCC6.CSB.AND.EHMT2.G9A.POSITIVELY.REGULATE.RRNA.EXPRESSION | 0.0048 | 1.6851 |
| 3 | REACTOME.SYNTHESIS.SECRETION.AND.DEACYLATION.OF.GHRELIN | 0.0069 | 1.5864 |
| 4 | REACTOME.SCAVENGING.OF.HEME.FROM.PLASMA | 0.0039 | 1.5581 |
| 5 | REACTOME.NUCLEOTIDE.SALVAGE | 0.0059 | 1.5486 |
| 6 | REACTOME.GENERATION.OF.SECOND.MESSENGER.MOLECULES | 0.0051 | 1.5481 |
| 7 | REACTOME.PURINE.SALVAGE | 0.0068 | 1.5461 |
| 8 | REACTOME.ANTIMICROBIAL.PEPTIDES | 0.0040 | 1.5102 |
| 9 | REACTOME.TRAF6.MEDIATED.IRF7.ACTIVATION.IN.TLR7.8.OR.9.SIGNALING | 0.0083 | 1.4830 |
| 10 | REACTOME.SELENOAMINO.ACID.METABOLISM | 0.0078 | 1.3581 |

Table 109: Top 10 up-regulated pathways for cluster 21 with adjustment for confondant effect

4.23 Cluster 22

| | pathway | padj | NES |
|----|---|--------|--------|
| 1 | REACTOME.SCAVENGING_OF_HEME_FROM_PLASMA | 0.0018 | 1.6467 |
| 2 | REACTOME.INTERACTION_BETWEEN_L1_LAND_ANKYRINS | 0.0037 | 1.5756 |
| 3 | REACTOME.SIGNALING_BY_NTRK3_TRKC | 0.0063 | 1.5196 |
| 4 | REACTOME.CREATION_OF_C4_AND_C2_ACTIVATORS | 0.0044 | 1.4994 |
| 5 | REACTOME.INITIAL_TRIGGERING_OF_COMPLEMENT | 0.0049 | 1.4725 |
| 6 | REACTOME.ROLE_OF_LAT2_NTAL_LAB_ON_CALCIIUM_MOBILIZATION | 0.0052 | 1.4561 |
| 7 | REACTOME.ADHERENS_JUNCTIONS_INTERACTIONS | 0.0083 | 1.4080 |
| 8 | REACTOME.FCGR_ACTIVATION | 0.0069 | 1.3912 |
| 9 | REACTOME.NCAM_SIGNALING_FOR_NEURITE_OUT_GROWTH | 0.0077 | 1.3813 |
| 10 | REACTOME.CD22_MEDIATED_BCR_REGULATION | 0.0083 | 1.3598 |

Table 110: Top 10 up-regulated pathways for cluster 22 with adjustment for confondant effect

4.24 Cluster 23

| | pathway | padj | NES |
|----|--|--------|--------|
| 1 | REACTOME.BRANCHED_CHAIN_AMINO_ACID_CATABOLISM | 0.0004 | 1.9736 |
| 2 | REACTOME.METABOLISM_OF_AMINO_ACIDS_AND_DERIVATIVES | 0.0002 | 1.5545 |
| 3 | REACTOME.RHO_GTPASE_CYCLE | 0.0002 | 1.4726 |
| 4 | REACTOME.SIGNALING_BY_RHO_GTPASES_MIRO_GTPASES_AND_RHOBTB3 | 0.0001 | 1.4627 |
| 5 | REACTOME.METABOLISM_OF_RNA | 0.0002 | 1.4363 |
| 6 | REACTOME.TRANSPORT_OF_SMALL_MOLECULES | 0.0004 | 1.3724 |
| 7 | REACTOME.CELLULAR_RESPONSES_TO_STIMULI | 0.0004 | 1.3603 |
| 8 | REACTOME.CYTOKINE_SIGNALING_IN_IMMUNE_SYSTEM | 0.0004 | 1.3561 |
| 9 | REACTOME.INFECTIONOUS_DISEASE | 0.0004 | 1.3239 |
| 10 | REACTOME.INNATE_IMMUNE_SYSTEM | 0.0004 | 1.3083 |

Table 111: Top 10 up-regulated pathways for cluster 23 with adjustment for confondant effect

4.25 Cluster 24

| | pathway | padj | NES |
|----|---|--------|--------|
| 1 | REACTOME.CHONDROITIN_SULFATE_BIOSYNTHESIS | 0.0070 | 1.5747 |
| 2 | REACTOME.NCAM_SIGNALING_FOR_NEURITE_OUT_GROWTH | 0.0044 | 1.5383 |
| 3 | REACTOME.GENERATION_OF_SECOND_MESSENGER_MOLECULES | 0.0080 | 1.5133 |
| 4 | REACTOME.O_GLYCOSYLATION_OF_TSR_DOMAIN_CONTAINING_PROTEINS | 0.0077 | 1.5098 |
| 5 | REACTOME.RAF_INDEPENDENT_MAPK1_3_ACTIVATION | 0.0128 | 1.4582 |
| 6 | REACTOME.FOXO_MEDIATED_TRANSCRIPTION_OF_OXIDATIVE_STRESS_METABOLIC_AND_NEURONAL_GENES | 0.0122 | 1.4388 |
| 7 | REACTOME.INTERACTION_BETWEEN_L1_LAND_ANKYRINS | 0.0129 | 1.4240 |
| 8 | REACTOME.SYNTHESIS_OF_IP3_AND_IP4_IN_THE_CYTOSOL | 0.0136 | 1.4178 |
| 9 | REACTOME.DETOXIFICATION_OF_REACTIVE_OXYGEN_SPECIES | 0.0126 | 1.4097 |
| 10 | REACTOME.SCAVENGING_OF_HEME_FROM_PLASMA | 0.0120 | 1.4080 |

Table 112: Top 10 up-regulated pathways for cluster 24 with adjustment for confondant effect

4.26 Cluster 25

| | pathway | padj | NES |
|----|---|--------|--------|
| 1 | REACTOME.MITOCHONDRIAL_TRNA_AMINOACYLATION | 0.0054 | 1.9537 |
| 2 | REACTOME.RAC1_GTPASE_CYCLE | 0.0028 | 1.5148 |
| 3 | REACTOME.RHO_GTPASE_CYCLE | 0.0002 | 1.4597 |
| 4 | REACTOME.HIV_LIFE_CYCLE | 0.0054 | 1.4540 |
| 5 | REACTOME.CDC42_GTPASE_CYCLE | 0.0054 | 1.4439 |
| 6 | REACTOME.DNA_REPAIR | 0.0013 | 1.4337 |
| 7 | REACTOME.METABOLISM_OF_AMINO_ACIDS_AND_DERIVATIVES | 0.0013 | 1.3864 |
| 8 | REACTOME.SIGNALING_BY_INTERLEUKINS | 0.0013 | 1.3729 |
| 9 | REACTOME.INTRACELLULAR_SIGNALING_BY_SECOND_MESSENGERS | 0.0036 | 1.3490 |
| 10 | REACTOME.DISEASES_OF_SIGNAL_TRANSDUCTION_BY_GROWTH_FACTOR_RECEPTORS_AND_SECOND_MESSENGERS | 0.0030 | 1.3056 |

Table 113: Top 10 up-regulated pathways for cluster 25 with adjustment for confondant effect

4.27 Cluster 26

| | pathway | padj | NES |
|----|--|--------|--------|
| 1 | REACTOME.SCAVENGING_OF_HEME_FROM_PLASMA | 0.0020 | 1.8609 |
| 2 | REACTOME.SYNTHESIS_SECRETION_AND_DEACYLATION_OF_GHRELIN | 0.0048 | 1.7279 |
| 3 | REACTOME.ROLE_OF_LAT2_NTAL_LAB_ON_CALCIIUM_MOBILIZATION | 0.0039 | 1.7272 |
| 4 | REACTOME.CREATION_OF_C4_AND_C2_ACTIVATORS | 0.0044 | 1.6939 |
| 5 | REACTOME.SYNAPTIC_ADHESION_LIKE_MOLECULES | 0.0087 | 1.6214 |
| 6 | REACTOME.GASTRIN_CREB_SIGNALING_PATHWAY_VIA_PKC_AND_MAPK | 0.0090 | 1.6184 |
| 7 | REACTOME.CHONDROITIN_SULFATE_BIOSYNTHESIS | 0.0087 | 1.5929 |
| 8 | REACTOME.INITIAL_TRIGGERING_OF_COMPLEMENT | 0.0075 | 1.5876 |
| 9 | REACTOME.FCGR_ACTIVATION | 0.0090 | 1.5840 |
| 10 | REACTOME.CHONDROITIN_SULFATE_DERMATAN_SULFATE_METABOLISM | 0.0087 | 1.5698 |

Table 114: Top 10 up-regulated pathways for cluster 26 with adjustment for confondant effect

4.28 Cluster 27

| | pathway | padj | NES |
|----|--|--------|--------|
| 1 | REACTOME.RNA.POLYMERASE.III.TRANSCRIPTION.TERMINATION | 0.0186 | 1.9536 |
| 2 | REACTOME.NEGATIVE.REGULATION.OF.NMDA.RECEPTOR.MEDIATED.NEURONAL.TRANSMISSION | 0.0223 | 1.8000 |
| 3 | REACTOME.PKA.ACTIVATION.IN.GLUCAGON.SIGNALING | 0.0223 | 1.7881 |
| 4 | REACTOME.GLUTATHIONE.CONJUGATION | 0.0223 | 1.7407 |
| 5 | REACTOME.CELL.DEATH.SIGNALING.VIA.NRAGE.NRIF.AND.NADE | 0.0186 | 1.6526 |
| 6 | REACTOME.INTERLEUKIN.4.AND.INTERLEUKIN.13.SIGNALING | 0.0186 | 1.6092 |
| 7 | REACTOME.NRAGE.SIGNALS.DEATH.THROUGH.JNK | 0.0223 | 1.5709 |
| 8 | REACTOME.P75.NTR.RECEPTOR.MEDIATED.SIGNALING | 0.0223 | 1.4434 |
| 9 | REACTOME.RAC1.GTPASE.CYCLE | 0.0186 | 1.4304 |
| 10 | REACTOME.DEATH.RECEPTOR.SIGNALING | 0.0223 | 1.3495 |

Table 115: Top 10 up-regulated pathways for cluster 27 with adjustment for confondant effect

4.29 Cluster 28

| | pathway | padj | NES |
|----|---|--------|--------|
| 1 | REACTOME.DETOXIFICATION.OF.REACTIVE.OXYGEN.SPECIES | 0.0029 | 1.7468 |
| 2 | REACTOME.INSULIN.RECEPTOR.RECYCLING | 0.0089 | 1.5257 |
| 3 | REACTOME.ERCC6.CSB.AND.EHMT2.G9A.POSITIVELY.REGULATE.RRNA.EXPRESSION | 0.0145 | 1.4887 |
| 4 | REACTOME.DEFECTS.OF.CONTACT.ACTIVATION.SYSTEM.CAS.AND.KALLIKREIN.KININ.SYSTEM.KKS | 0.0145 | 1.4560 |
| 5 | REACTOME.ETHANOL.OXIDATION | 0.0104 | 1.4557 |
| 6 | REACTOME.GENERATION.OF.SECOND.MESSENGER.MOLECULES | 0.0140 | 1.4518 |
| 7 | REACTOME.SYNAPTIC.ADHESSION.LIKE.MOLECULES | 0.0149 | 1.4308 |
| 8 | REACTOME.INTERACTION.BETWEEN.L1.AND.ANKYRINS | 0.0149 | 1.4163 |
| 9 | REACTOME.RHOV.GTPASE.CYCLE | 0.0149 | 1.3911 |
| 10 | REACTOME.NCAM.SIGNALING.FOR.NEURITE.OUT.GROWTH | 0.0139 | 1.3894 |

Table 116: Top 10 up-regulated pathways for cluster 28 with adjustment for confondant effect

4.30 Cluster 29

| | pathway | padj | NES |
|----|--|--------|--------|
| 1 | REACTOME.VXPX.CARGO.TARGETING.TO.CILIUM | 0.0060 | 1.6725 |
| 2 | REACTOME.PTK6.REGULATES.RHO.GTPASES.RAS.GTPASE.AND.MAP.KINASES | 0.0057 | 1.6708 |
| 3 | REACTOME.SYNTHESIS.OF.LEUKOTRIENES.IT.AND.EOXINS.EX | 0.0060 | 1.6677 |
| 4 | REACTOME.PURINE.SALVAGE | 0.0073 | 1.6352 |
| 5 | REACTOME.SYNTHESIS.OF.PE | 0.0113 | 1.5637 |
| 6 | REACTOME.EICOSANOIDS | 0.0115 | 1.5547 |
| 7 | REACTOME.NUCLEOTIDE.SALVAGE | 0.0117 | 1.5386 |
| 8 | REACTOME.PHASE.4.RESTING.MEMBRANE.POTENTIAL | 0.0154 | 1.4891 |
| 9 | REACTOME.EPHB.MEDIATED.FORWARD.SIGNALING | 0.0130 | 1.4562 |
| 10 | REACTOME.ARACHIDONIC.ACID.METABOLISM | 0.0123 | 1.4323 |

Table 117: Top 10 up-regulated pathways for cluster 29 with adjustment for confondant effect

4.31 Cluster 30

| | pathway | padj | NES |
|----|--|--------|--------|
| 1 | REACTOME.SUMOYLATION.OF.TRANSCRIPTION.FACTORS | 0.0217 | 1.6052 |
| 2 | REACTOME.ASSEMBLY.OF.THE.HIV.VIRION | 0.0217 | 1.6038 |
| 3 | REACTOME.INFLAMMASOMES | 0.0217 | 1.5898 |
| 4 | REACTOME.SELENOAMINO.ACID.METABOLISM | 0.0194 | 1.5627 |
| 5 | REACTOME.NOTCH2.INTRACELLULAR.DOMAIN.REGULATES.TRANSCRIPTION | 0.0217 | 1.5522 |
| 6 | REACTOME.THE.NLRP3.INFLAMMASOME | 0.0223 | 1.5496 |
| 7 | REACTOME.GENERATION.OF.SECOND.MESSENGER.MOLECULES | 0.0217 | 1.5421 |
| 8 | REACTOME.SIGNALING.BY.NOTCH2 | 0.0223 | 1.4670 |
| 9 | REACTOME.EUKARYOTIC.TRANSLATION.ELONGATION | 0.0217 | 1.4088 |
| 10 | REACTOME.INFLUENZA.INFECTION | 0.0247 | 1.2349 |

Table 118: Top 10 up-regulated pathways for cluster 30 with adjustment for confondant effect

4.32 Cluster 31

| | pathway | padj | NES |
|----|--|--------|--------|
| 1 | REACTOME.BRANCHED.CHAIN.AMINO.ACID.CATABOLISM | 0.0010 | 1.9696 |
| 2 | REACTOME.METABOLISM.OF.AMINO.ACIDS.AND.DERIVATIVES | 0.0001 | 1.5999 |
| 3 | REACTOME.SIGNALING.BY.INTERLEUKINS | 0.0007 | 1.4249 |
| 4 | REACTOME.MEMBRANE.TRAFFICKING | 0.0003 | 1.4035 |
| 5 | REACTOME.RHO.GTPASE.CYCLE | 0.0010 | 1.3836 |
| 6 | REACTOME.SIGNALING.BY.RHO.GTPASES.MIRO.GTPASES.AND.RHOBTB3 | 0.0008 | 1.3652 |
| 7 | REACTOME.METABOLISM.OF.RNA | 0.0007 | 1.3591 |
| 8 | REACTOME.VESICLE.MEDIATED.TRANSPORT | 0.0003 | 1.3468 |
| 9 | REACTOME.CELLULAR.RESPONSES.TO.STIMULI | 0.0008 | 1.3127 |
| 10 | REACTOME.INNATE.IMMUNE.SYSTEM | 0.0008 | 1.2648 |

Table 119: Top 10 up-regulated pathways for cluster 31 with adjustment for confondant effect