

# Annexe 1: Top 10 significant results by cluster

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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 adjustement 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 adjustement 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 adjustement 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 adjustment 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 adjustment 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 adjustment 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 adjustment 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 CALCIUM 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	padj	NES
1	REACTOME ECM PROTEOGLYCANS	0.0003	1.8699
2	REACTOME ESR MEDIATED SIGNALING	0.0003	1.6754
3	REACTOME RHO GTPASE CYCLE	0.0003	1.4632
4	REACTOME DISEASES OF SIGNAL TRANSDUCTION BY GROWTH FACTOR RECEPTORS AND SECOND MESSENGERS	0.0003	1.4534
5	REACTOME SIGNALING BY RHO GTPASES MIRO GTPASES AND RHOBTB3	0.0000	1.4521
6	REACTOME SIGNALING BY RECEPTOR TYROSINE KINASES	0.0001	1.4417
7	REACTOME METABOLISM OF RNA	0.0001	1.4093
8	REACTOME CELL CYCLE	0.0003	1.3543
9	REACTOME CYTOKINE SIGNALING IN IMMUNE SYSTEM	0.0003	1.3402
10	REACTOME INNATE IMMUNE SYSTEM	0.0003	1.2778

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	1.6755
2	REACTOME TRANSCRIPTIONAL REGULATION OF TESTIS DIFFERENTIATION	0.0129	1.6597
3	REACTOME THROMBIN SIGNALLING THROUGH PROTEINASE ACTIVATED RECEPTORS PARS	0.0166	1.5895
4	REACTOME G BETA GAMMA SIGNALLING THROUGH CDC42	0.0197	1.5515
5	REACTOME G PROTEIN ACTIVATION	0.0197	1.5349
6	REACTOME PROSTACYCLIN SIGNALLING THROUGH PROSTACYCLIN RECEPTOR	0.0197	1.5334
7	REACTOME CA2 PATHWAY	0.0152	1.5332
8	REACTOME PRESYNAPTIC FUNCTION OF KAINATE RECEPTORS	0.0197	1.5142
9	REACTOME PROTEIN UBIQUITINATION	0.0191	1.4741
10	REACTOME GABA RECEPTOR ACTIVATION	0.0197	1.4606

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 CALCIUM 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	padj	NES
1	REACTOME ABERRANT REGULATION OF MITOTIC G1 S TRANSITION IN CANCER DUE TO RB1 DEFECTS	0.0021	2.0133
2	REACTOME CTLA4 INHIBITORY SIGNALING	0.0021	1.9958
3	REACTOME EPHA MEDIATED GROWTH CONE COLLAPSE	0.0021	1.8312
4	REACTOME ECM PROTEOGLYCANS	0.0021	1.6973
5	REACTOME APOPTOSIS	0.0021	1.4012
6	REACTOME SIGNALING BY RHO GTPASES MIRO GTPASES AND RHOBTB3	0.0001	1.3878
7	REACTOME RHO GTPASE CYCLE	0.0003	1.3816
8	REACTOME CYTOKINE SIGNALING IN IMMUNE SYSTEM	0.0021	1.2203
9	REACTOME MEMBRANE TRAFFICKING	0.0021	1.2163
10	REACTOME CELL CYCLE	0.0021	1.1944

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 INDUCTION 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	padj	NES
1	REACTOME DETOXIFICATION OF REACTIVE OXYGEN SPECIES	0.0017	1.7510
2	REACTOME SCAVENGING OF HEME FROM PLASMA	0.0012	1.6410
3	REACTOME ERCC6 CSB AND EHMT2 G9A POSITIVELY REGULATE RRNA EXPRESSION	0.0050	1.6382
4	REACTOME GENERATION OF SECOND MESSENGER MOLECULES	0.0056	1.5804
5	REACTOME ACTIVATION OF RAC1	0.0070	1.5606
6	REACTOME DEFECTS OF CONTACT ACTIVATION SYSTEM CAS AND KALLIKREIN KININ SYSTEM KKS	0.0065	1.5441
7	REACTOME NUCLEOTIDE SALVAGE	0.0065	1.5197
8	REACTOME ROLE OF LAT2 NTAL LAB ON CALCIUM MOBILIZATION	0.0065	1.4944
9	REACTOME CREATION OF C4 AND C2 ACTIVATORS	0.0070	1.4715
10	REACTOME NETRIN 1 SIGNALING	0.0065	1.4354

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 SIGNALLING 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 INDUCTION 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 CALCIUM 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	padj	NES
1	REACTOME ABERRANT REGULATION OF MITOTIC G1 S TRANSITION IN CANCER DUE TO RB1 DEFECTS	0.0012	2.0793
2	REACTOME FORMATION OF SENESCENCE ASSOCIATED HETEROCHROMATIN FOCI SAHF	0.0006	2.0603
3	REACTOME ESTROGEN DEPENDENT NUCLEAR EVENTS DOWNSTREAM OF ESR MEMBRANE SIGNALING	0.0016	1.9204
4	REACTOME ECM PROTEOGLYCANS	0.0012	1.8194
5	REACTOME SIGNALING BY WNT	0.0012	1.4817
6	REACTOME SIGNALING BY INTERLEUKINS	0.0012	1.3437
7	REACTOME RHO GTPASE CYCLE	0.0012	1.3367
8	REACTOME SIGNALING BY RHO GTPASES MIRO GTPASES AND RHOBTB3	0.0006	1.3004
9	REACTOME CYTOKINE SIGNALING IN IMMUNE SYSTEM	0.0014	1.2446
10	REACTOME METABOLISM OF RNA	0.0012	1.2423

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 INDUCTION 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 CALCIUM 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	padj	NES
1	REACTOME FORMATION OF SENESCENCE ASSOCIATED HETEROCHROMATIN FOCI SAHF	0.0006	1.9712
2	REACTOME ECM PROTEOGLYCANS	0.0005	1.8322
3	REACTOME RHO GTPASE CYCLE	0.0003	1.4029
4	REACTOME SIGNALING BY RHO GTPASES MIRO GTPASES AND RHOBTB3	0.0001	1.3976
5	REACTOME DISEASES OF SIGNAL TRANSDUCTION BY GROWTH FACTOR RECEPTORS AND SECOND MESSENGERS	0.0005	1.3701
6	REACTOME SIGNALING BY RECEPTOR TYROSINE KINASES	0.0006	1.3460
7	REACTOME METABOLISM OF RNA	0.0003	1.3312
8	REACTOME CYTOKINE SIGNALING IN IMMUNE SYSTEM	0.0007	1.2941
9	REACTOME TRANSPORT OF SMALL MOLECULES	0.0006	1.2722
10	REACTOME INNATE IMMUNE SYSTEM	0.0006	1.2230

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	padj	NES
1	REACTOME FORMATION OF SENESCENCE ASSOCIATED HETEROCHROMATIN FOCI SAHF	0.0003	2.0347
2	REACTOME HIV LIFE CYCLE	0.0004	1.6196
3	REACTOME DISEASES OF SIGNAL TRANSDUCTION BY GROWTH FACTOR RECEPTORS AND SECOND MESSENGERS	0.0001	1.4560
4	REACTOME RHO GTPASE CYCLE	0.0001	1.4367
5	REACTOME SIGNALING BY RHO GTPASES MIRO GTPASES AND RHOBTB3	0.0000	1.4352
6	REACTOME SIGNALING BY RECEPTOR TYROSINE KINASES	0.0004	1.3587
7	REACTOME METABOLISM OF RNA	0.0001	1.3572
8	REACTOME CELL CYCLE	0.0001	1.3368
9	REACTOME CYTOKINE SIGNALING IN IMMUNE SYSTEM	0.0003	1.3185
10	REACTOME INFECTIOUS DISEASE	0.0004	1.2394

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	padj	NES
1	REACTOME RHOG GTPASE CYCLE	0.0023	1.7602
2	REACTOME INTERLEUKIN 4 AND INTERLEUKIN 13 SIGNALING	0.0023	1.6243
3	REACTOME RAC1 GTPASE CYCLE	0.0012	1.4778
4	REACTOME RHO GTPASE CYCLE	0.0002	1.4683
5	REACTOME INTRACELLULAR SIGNALING BY SECOND MESSENGERS	0.0012	1.4458
6	REACTOME MAPK FAMILY SIGNALING CASCADES	0.0012	1.4323
7	REACTOME SIGNALING BY WNT	0.0023	1.4249
8	REACTOME SIGNALING BY INTERLEUKINS	0.0012	1.3627
9	REACTOME DISEASES OF SIGNAL TRANSDUCTION BY GROWTH FACTOR RECEPTORS AND SECOND MESSENGERS	0.0019	1.3406
10	REACTOME SIGNALING BY RECEPTOR TYROSINE KINASES	0.0012	1.3321

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 INDUCTION 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 CALCIUM 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 PANCREATIC BUD PRECURSOR CELLS	0.0033	1.6437
2	REACTOME RUNX3 REGULATES NOTCH SIGNALING	0.0048	1.5981
3	REACTOME PURINE SALVAGE	0.0044	1.5936
4	REACTOME NUCLEOTIDE SALVAGE	0.0055	1.5717
5	REACTOME CLASS C 3 METABOTROPIC GLUTAMATE PHEROMONE RECEPTORS	0.0073	1.5289
6	REACTOME ZBP1 DAI MEDIATED INDUCTION OF TYPE I IFNS	0.0080	1.5110
7	REACTOME TAK1 ACTIVATES NFKB BY PHOSPHORYLATION AND ACTIVATION OF IKKS COMPLEX	0.0063	1.4865
8	REACTOME ETHANOL OXIDATION	0.0080	1.4822
9	REACTOME SCAVENGING OF HEME FROM PLASMA	0.0073	1.4419
10	REACTOME SIGNALING BY NOTCH3	0.0073	1.4345

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 CALCIUM 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	padj	NES
1	REACTOME SIGNALING BY RHO GTPASES MIRO GTPASES AND RHOBTB3	0.0000	1.4988
2	REACTOME RHO GTPASE CYCLE	0.0001	1.4969
3	REACTOME METABOLISM OF AMINO ACIDS AND DERIVATIVES	0.0002	1.4960
4	REACTOME SIGNALING BY INTERLEUKINS	0.0002	1.4615
5	REACTOME DISEASES OF SIGNAL TRANSDUCTION BY GROWTH FACTOR RECEPTORS AND SECOND MESSENGERS	0.0002	1.4296
6	REACTOME SIGNALING BY RECEPTOR TYROSINE KINASES	0.0002	1.4261
7	REACTOME METABOLISM OF RNA	0.0001	1.4229
8	REACTOME CELLULAR RESPONSES TO STIMULI	0.0001	1.3996
9	REACTOME CYTOKINE SIGNALING IN IMMUNE SYSTEM	0.0002	1.3986
10	REACTOME INNATE IMMUNE SYSTEM	0.0000	1.3767

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 CALCIUM 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	padj	NES
1	REACTOME FORMATION OF SENESCENCE ASSOCIATED HETEROCHROMATIN FOCI SAHF	0.0001	2.0602
2	REACTOME DISEASES OF SIGNAL TRANSDUCTION BY GROWTH FACTOR RECEPTORS AND SECOND MESSENGERS	0.0002	1.4485
3	REACTOME RHO GTPASE CYCLE	0.0002	1.4264
4	REACTOME SIGNALING BY RHO GTPASES MIRO GTPASES AND RHOBTB3	0.0001	1.4182
5	REACTOME SIGNALING BY INTERLEUKINS	0.0003	1.4094
6	REACTOME SIGNALING BY RECEPTOR TYROSINE KINASES	0.0002	1.4088
7	REACTOME METABOLISM OF RNA	0.0001	1.4058
8	REACTOME CYTOKINE SIGNALING IN IMMUNE SYSTEM	0.0002	1.3673
9	REACTOME TRANSPORT OF SMALL MOLECULES	0.0002	1.3494
10	REACTOME CELLULAR RESPONSES TO STIMULI	0.0003	1.3099

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	padj	NES
1	REACTOME FORMATION OF SENESCENCE ASSOCIATED HETEROCHROMATIN FOCI SAHF	0.0111	2.1276
2	REACTOME BUTYROPHILIN BTN FAMILY INTERACTIONS	0.0224	1.9228
3	REACTOME INTERLEUKIN 2 SIGNALING	0.0224	1.8989
4	REACTOME CTLA4 INHIBITORY SIGNALING	0.0224	1.8529
5	REACTOME ABERRANT REGULATION OF MITOTIC G1 S TRANSITION IN CANCER DUE TO RB1 DEFECTS	0.0224	1.7735
6	REACTOME CD209 DC SIGN SIGNALING	0.0224	1.6381
7	REACTOME EPHA MEDIATED GROWTH CONE COLLAPSE	0.0224	1.5482
8	REACTOME ECM PROTEOGLYCANS	0.0224	1.3735
9	REACTOME DDX58 IFIH1 MEDIATED INDUCTION OF INTERFERON ALPHA BETA	0.0224	1.3536
10	REACTOME GENE SILENCING BY RNA	0.0224	1.3474

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 adjustment 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 EHMT2 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 adjustment for confondant effect

## 4.2 Cluster 1

	pathway	padj	NES
1	REACTOME SYNAPTIC ADHESION LIKE MOLECULES	0.0191	1.7800
2	REACTOME INFLAMMASOMES	0.0191	1.6472
3	REACTOME ADHERENS JUNCTIONS INTERACTIONS	0.0191	1.6328
4	REACTOME ACTIVATION OF THE PRE REPLICATIVE COMPLEX	0.0191	1.5673
5	REACTOME TP53 REGULATES TRANSCRIPTION OF SEVERAL ADDITIONAL CELL DEATH GENES WHOSE SPECIFIC ROLES IN P53 DEPENDENT APOPTOSIS REMAIN UNCERTAIN	0.0191	1.5603
6	REACTOME RECYCLING OF BILE ACIDS AND SALTS	0.0191	1.5589
7	REACTOME BBSOME MEDIATED CARGO TARGETING TO CILIUM	0.0194	1.5548
8	REACTOME PROLONGED ERK ACTIVATION EVENTS	0.0194	1.5480
9	REACTOME PURINERGIC SIGNALING IN LEISHMANIASIS INFECTION	0.0191	1.5433
10	REACTOME SWITCHING OF ORIGINS TO A POST REPLICATIVE STATE	0.0191	1.5049

Table 89: Top 10 up-regulated pathways for cluster 1 with adjustment 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 PIPS 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 ADHESION 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 RHOTB3	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 PHLP1 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 SIGNALLING 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 EGFRVIII	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	0.0017	2.0733
2	REACTOME TP53 REGULATES TRANSCRIPTION OF SEVERAL ADDITIONAL CELL DEATH GENES WHOSE SPECIFIC ROLES IN P53 DEPENDENT APOPTOSIS REMAIN UNCERTAIN	0.0027	1.9570
3	REACTOME FORMATION OF SENESCENCE ASSOCIATED HETEROCHROMATIN FOCI SAHF	0.0037	1.9018
4	REACTOME INTRACELLULAR SIGNALING BY SECOND MESSENGERS	0.0017	1.3656
5	REACTOME RHO GTPASE CYCLE	0.0017	1.3532
6	REACTOME MAPK FAMILY SIGNALING CASCADES	0.0018	1.3526
7	REACTOME SIGNALING BY INTERLEUKINS	0.0017	1.2894
8	REACTOME SIGNALING BY RECEPTOR TYROSINE KINASES	0.0017	1.2883
9	REACTOME CYTOKINE SIGNALING IN IMMUNE SYSTEM	0.0017	1.2836
10	REACTOME TRANSPORT OF SMALL MOLECULES	0.0017	1.2111

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 CALCIUM 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 ajustement 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 ajustement 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 SIGNALLING 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 ajustement 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 INDUCTION 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 CALCIUM 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 CALCIUM 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 G1 S SPECIFIC TRANSCRIPTION	0.0111	1.8989
2	REACTOME INTERCONVERSION OF NUCLEOTIDE DI AND 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 WICH 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 G1 S 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 IFIH1 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 AND 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 CALCIUM 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 RHOTB3	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 INFECTIOUS 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 AND 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 CALCIUM 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 SIGNALLING 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 SIGNALLING	0.0223	1.7881
4	REACTOME GLUTATHIONE CONJUGATION	0.0223	1.7407
5	REACTOME CELL DEATH SIGNALLING 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 SIGNALLING	0.0223	1.4434
9	REACTOME RAC1 GTPASE CYCLE	0.0186	1.4304
10	REACTOME DEATH RECEPTOR SIGNALLING	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 ADHESION 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 LT 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