

# Annex 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

No significant pathway

### 3.2 Cluster 1

No significant pathway

### 3.3 Cluster 10

No significant pathway

### 3.4 Cluster 11

No significant pathway

### 3.5 Cluster 12

No significant pathway

### 3.6 Cluster 13

No significant pathway

### 3.7 Cluster 14

	pathway	padj	NES
1	REACTOME SIGNALING BY RHO GTPASES MIRO GTPASES AND RHOBTB3	0.0014	1.3558
	NA		
	NA.1		
	NA.2		
	NA.3		
	NA.4		
	NA.5		
	NA.6		
	NA.7		
	NA.8		

Table 56: Top 10 up-regulated pathways for cluster 14

### 3.8 Cluster 15

No significant pathway

### 3.9 Cluster 16

No significant pathway

### 3.10 Cluster 17

No significant pathway

### 3.11 Cluster 18

No significant pathway

### 3.12 Cluster 19

No significant pathway

### 3.13 Cluster 2

No significant pathway

### 3.14 Cluster 20

No significant pathway

### 3.15 Cluster 21

No significant pathway

### 3.16 Cluster 22

No significant pathway

### 3.17 Cluster 23

No significant pathway

### 3.18 Cluster 24

No significant pathway

### 3.19 Cluster 25

	pathway	padj	NES
1	REACTOME SIGNALING BY RHO GTPASES MIRO GTPASES AND RHOBTB3	0.0002	1.4481
	NA		
	NA.1		
	NA.2		
	NA.3		
	NA.4		
	NA.5		
	NA.6		
	NA.7		
	NA.8		

Table 57: Top 10 up-regulated pathways for cluster 25

### 3.20 Cluster 26

No significant pathway

### 3.21 Cluster 27

No significant pathway

### 3.22 Cluster 28

No significant pathway

### 3.23 Cluster 29

No significant pathway

### 3.24 Cluster 3

No significant pathway

### 3.25 Cluster 30

No significant pathway

### 3.26 Cluster 31

	pathway	padj	NES
1	REACTOME SIGNALING BY RHO GTPASES MIRO GTPASES AND RHOBTB3	0.0004	1.4992
2	REACTOME INNATE IMMUNE SYSTEM	0.0010	1.3715
NA			
NA.1			
NA.2			
NA.3			
NA.4			
NA.5			
NA.6			
NA.7			

Table 58: Top 10 up-regulated pathways for cluster 31

### 3.27 Cluster 4

No significant pathway

### 3.28 Cluster 5

No significant pathway

### 3.29 Cluster 6

	pathway	padj	NES
1	REACTOME SIGNALING BY RHO GTPASES MIRO GTPASES AND RHOBTB3	0.0013	1.4173
2	REACTOME METABOLISM OF RNA	0.0014	1.4036
NA			
NA.1			
NA.2			
NA.3			
NA.4			
NA.5			
NA.6			
NA.7			

Table 59: Top 10 up-regulated pathways for cluster 6

### 3.30 Cluster 7

No significant pathway

### 3.31 Cluster 8

No significant pathway

### 3.32 Cluster 9

No significant pathway

## 4 Q3.2 Top 10 up-regulated pathways with adjustment for confon- dant effect

### 4.1 Cluster 0

No significant pathway

**4.2 Cluster 1**

No significant pathway

**4.3 Cluster 2**

No significant pathway

**4.4 Cluster 3**

No significant pathway

**4.5 Cluster 4**

No significant pathway

**4.6 Cluster 5**

No significant pathway

**4.7 Cluster 6**

	pathway	padj	NES
1	REACTOME METABOLISM OF RNA	0.0002	1.5175
2	REACTOME SIGNALING BY RHO GTPASES MIRO GTPASES AND RHOBTB3	0.0003	1.5020
	NA		
	NA.1		
	NA.2		
	NA.3		
	NA.4		
	NA.5		
	NA.6		
	NA.7		

Table 60: Top 10 up-regulated pathways for cluster 6 with adjustement for confondant effect

**4.8 Cluster 7**

No significant pathway

**4.9 Cluster 8**

No significant pathway

**4.10 Cluster 9**

No significant pathway

#### 4.11 Cluster 10

	pathway	padj	NES
1	REACTOME SIGNALING BY NUCLEAR RECEPTORS	0.0009	1.6972
2	REACTOME SIGNALING BY RECEPTOR TYROSINE KINASES	0.0013	1.5088
3	REACTOME SIGNALING BY RHO GTPASES MIRO GTPASES AND RHOBTB3	0.0009	1.4603
4	REACTOME METABOLISM OF RNA	0.0009	1.4597
5	REACTOME INNATE IMMUNE SYSTEM	0.0009	1.3220
	NA		
	NA.1		
	NA.2		
	NA.3		
	NA.4		

Table 61: Top 10 up-regulated pathways for cluster 10 with adjustement for confondant effect

#### 4.12 Cluster 11

No significant pathway

#### 4.13 Cluster 12

No significant pathway

#### 4.14 Cluster 13

No significant pathway

#### 4.15 Cluster 14

No significant pathway

#### 4.16 Cluster 15

No significant pathway

#### 4.17 Cluster 16

No significant pathway

#### 4.18 Cluster 17

No significant pathway

#### 4.19 Cluster 18

No significant pathway

#### 4.20 Cluster 19

No significant pathway

#### 4.21 Cluster 20

No significant pathway

#### 4.22 Cluster 21

No significant pathway

#### **4.23 Cluster 22**

No significant pathway

#### **4.24 Cluster 23**

No significant pathway

#### **4.25 Cluster 24**

No significant pathway

#### **4.26 Cluster 25**

No significant pathway

#### **4.27 Cluster 26**

No significant pathway

#### **4.28 Cluster 27**

No significant pathway

#### **4.29 Cluster 28**

No significant pathway

#### **4.30 Cluster 29**

No significant pathway

#### **4.31 Cluster 30**

No significant pathway

#### **4.32 Cluster 31**

No significant pathway