

Annex 1: Top 10 significant results by cluster

June 9, 2024

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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

	pathway	padj	NES
1	REACTOME SIGNALING BY RHO GTPASES MIRO GTPASES AND RHOBTB3	0.0006	1.4486
	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 10

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

No significant pathway

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	0.0001	1.4418
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

	pathway	padj	NES
1	REACTOME RHO GTPASE CYCLE	0.0008	1.4432
2	REACTOME SIGNALING BY RHO GTPASES MIRO GTPASES AND RHOBTB3	0.0007	1.3845
3	REACTOME TRANSPORT OF SMALL MOLECULES	0.0012	1.3414
NA			
NA.1			
NA.2			
NA.3			
NA.4			
NA.5			
NA.6			

Table 58: Top 10 up-regulated pathways for cluster 27

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	0.0003	1.4971
2	REACTOME INNATE IMMUNE SYSTEM	0.0011	1.3804
NA			
NA.1			
NA.2			
NA.3			
NA.4			
NA.5			
NA.6			
NA.7			

Table 59: 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

No significant pathway

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 adjustement 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	1.5225
2	REACTOME SIGNALING BY RHO GTPASES MIRO GTPASES AND RHOBTB3	0.0009	1.4999
	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 adjustment 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 ESR MEDIATED SIGNALING	0.0013	1.7869
2	REACTOME SIGNALING BY NUCLEAR RECEPTORS	0.0016	1.6954
3	REACTOME SIGNALING BY RECEPTOR TYROSINE KINASES	0.0013	1.5007
4	REACTOME SIGNALING BY RHO GTPASES MIRO GTPASES AND RHOBTB3	0.0004	1.4642
5	REACTOME METABOLISM OF RNA	0.0008	1.4642
6	REACTOME INNATE IMMUNE SYSTEM	0.0016	1.3388
	NA		
	NA.1		
	NA.2		
	NA.3		

Table 61: Top 10 up-regulated pathways for cluster 10 with adjustment 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