# Combined functional profiling of differential gene expression and prognosis using GO Biological Process

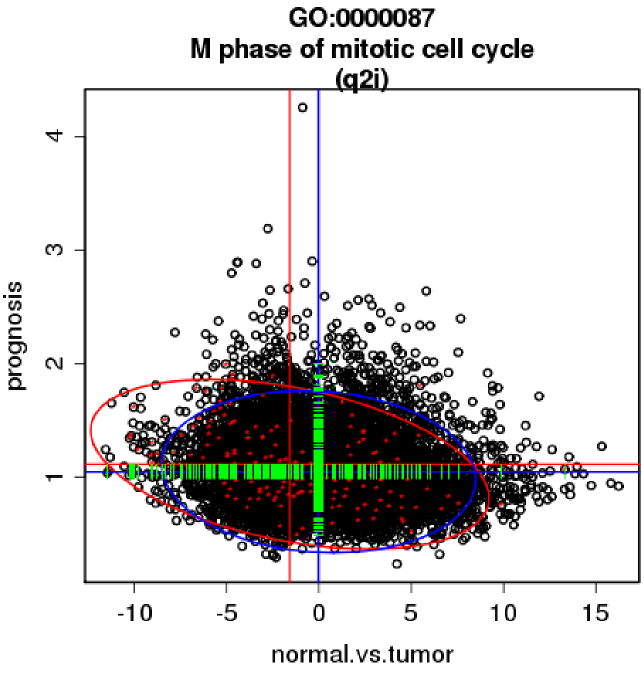
**29** significant modules

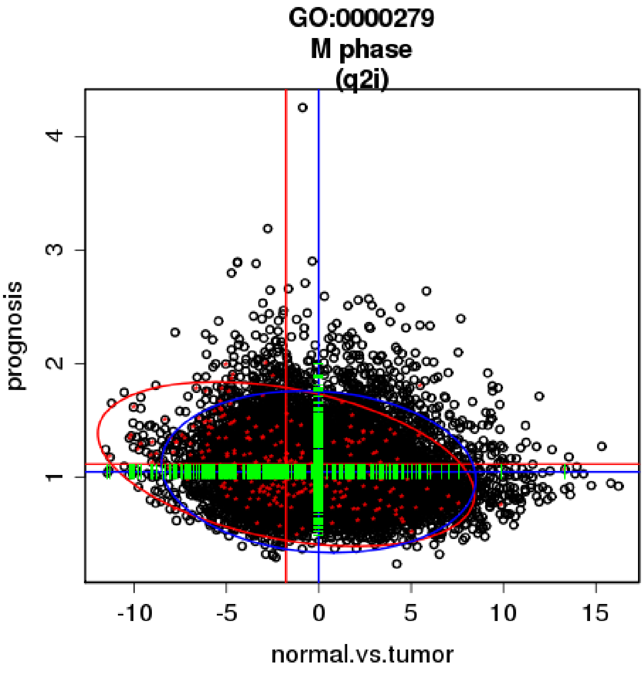
**LOR** indicates Log Odds Ratio of the coefficient or the interaction

**p** indicates FDR adjusted p-value

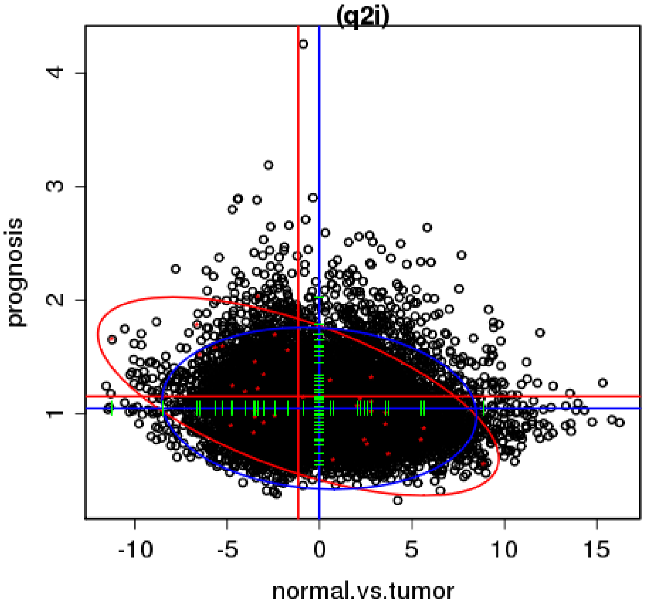
| | LOR normal vs tumor | LOR prognosis | LOR Inter | p normal vs tumor | p prognosis | p Inter | pattern | name |
|---|---|---|---|---|---|---|---|---|
| GO:0000087 | -0.45 | -0.08 | -0.42 | 0.01 | 0.81 | 0.00 | q2i | M phase of mitotic cell cycle |
| GO:0000279 | -0.53 | -0.07 | -0.38 | 0.04 | 0.85 | 0.00 | q2i | M phase |
| GO:0000910 | -0.27 | -0.09 | -0.57 | 0.01 | 0.95 | 0.00 | q2i | cytokinesis |
| GO:0007067 | -0.47 | -0.07 | -0.40 | 0.04 | 0.90 | 0.00 | q2i | mitosis |
| GO:0022618 | -0.22 | -0.33 | -0.42 | 0.03 | 0.21 | 0.00 | q2i | ribonucleoprotein complex assembly |
| GO:0051301 | -0.38 | -0.00 | -0.38 | 0.01 | 0.99 | 0.00 | q2i | cell division |
| GO:0051726 | -0.01 | 0.05 | -0.22 | 0.03 | 0.91 | 0.01 | q2i | regulation of cell cycle |
| GO:0045638 | 0.09 | -0.35 | -0.60 | 0.01 | 0.65 | 0.04 | q4i | negative regulation of myeloid cell differentiation |
| GO:0000226 | -0.08 | 0.16 | -0.31 | 0.11 | 0.47 | 0.02 | b24 | microtubule cytoskeleton organization and biogenesis |
| GO:0000278 | -0.34 | 0.04 | -0.28 | 0.11 | 0.94 | 0.00 | b24 | mitotic cell cycle |
| GO:0007346 | -0.30 | -0.08 | -0.39 | 0.07 | 0.90 | 0.00 | b24 | regulation of mitotic cell cycle |
| GO:0022403 | -0.42 | -0.00 | -0.31 | 0.09 | 0.99 | 0.00 | b24 | cell cycle phase |
| GO:0042254 | -0.40 | -0.45 | -0.42 | 0.19 | 0.10 | 0.01 | b24 | ribosome biogenesis |
| GO:0006412 | 0.06 | -0.28 | -0.20 | 0.02 | 0.01 | 0.07 | q4f | translation |
| GO:0006414 | 0.45 | -1.12 | -0.43 | 0.00 | 0.00 | 0.28 | q4f | translational elongation |
| GO:0042312 | 0.45 | 0.08 | -0.51 | 0.03 | 0.97 | 0.22 | xh | regulation of vasodilation |
| GO:0000209 | -0.25 | 0.55 | 0.13 | 0.94 | 0.01 | 1.00 | yh | protein polyubiquitination |
| GO:0006066 | 0.08 | 0.20 | -0.02 | 0.97 | 0.02 | 1.00 | yh | alcohol metabolic process |
| GO:0010033 | 0.05 | 0.29 | 0.00 | 0.99 | 0.02 | 1.00 | yh | response to organic substance |
| GO:0032944 | -0.17 | -0.70 | 0.06 | 0.97 | 0.02 | 1.00 | yl | regulation of mononuclear cell proliferation |
| GO:0042098 | -0.18 | -0.61 | 0.08 | 0.95 | 0.04 | 1.00 | yl | T cell proliferation |
| GO:0042110 | 0.03 | -0.38 | 0.14 | 0.75 | 0.03 | 0.86 | yl | T cell activation |
| GO:0042129 | -0.33 | -0.74 | -0.02 | 0.99 | 0.05 | 1.00 | yl | regulation of T cell proliferation |
| GO:0045321 | -0.04 | -0.28 | 0.06 | 0.92 | 0.03 | 1.00 | yl | leukocyte activation |
| GO:0046649 | -0.06 | -0.33 | 0.07 | 0.89 | 0.02 | 1.00 | yl | lymphocyte activation |
| GO:0046651 | -0.19 | -0.49 | -0.05 | 0.99 | 0.05 | 1.00 | yl | lymphocyte proliferation |
| GO:0050670 | -0.17 | -0.70 | 0.06 | 0.97 | 0.02 | 1.00 | yl | regulation of lymphocyte proliferation |
| GO:0051249 | -0.06 | -0.44 | 0.24 | 0.52 | 0.04 | 0.71 | yl | regulation of lymphocyte activation |
| GO:0022613 | -0.32 | -0.35 | -0.39 | 0.01 | 0.03 | 0.00 | no_rel | ribonucleoprotein complex biogenesis and assembly |

Table 1: LOR: log odds ratio; p: adjusted p-value FDR

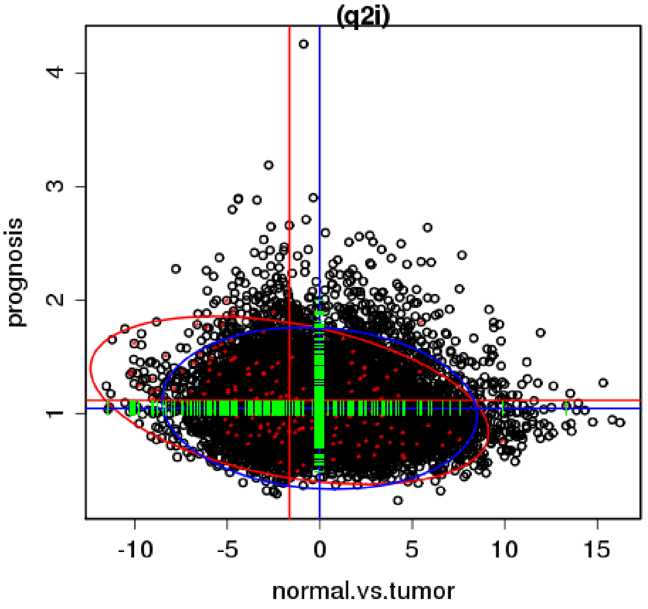




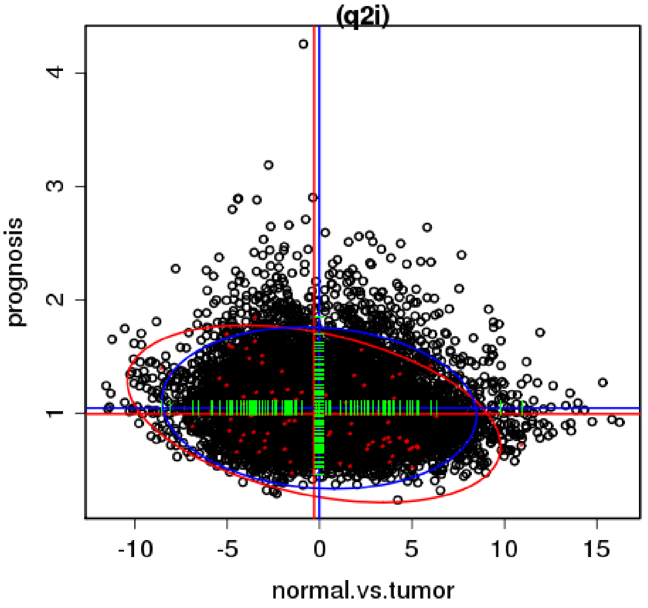
GO:0000910
cytokinesis
(q2i)



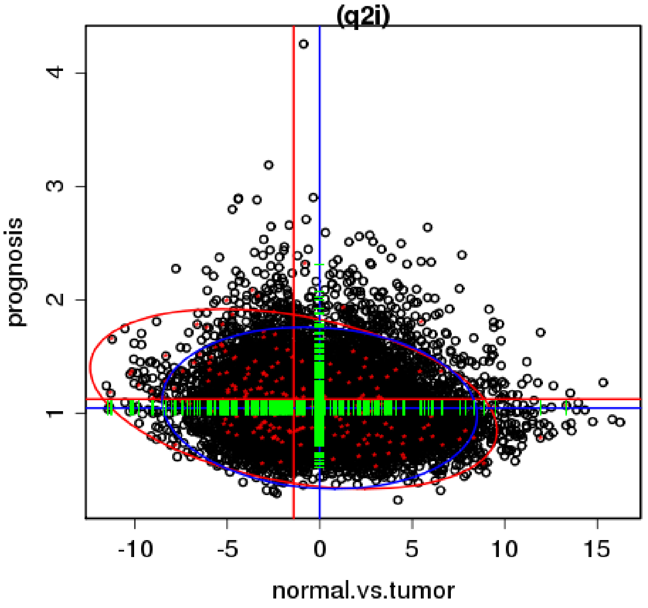
GO:0007067
mitosis
(q2i)



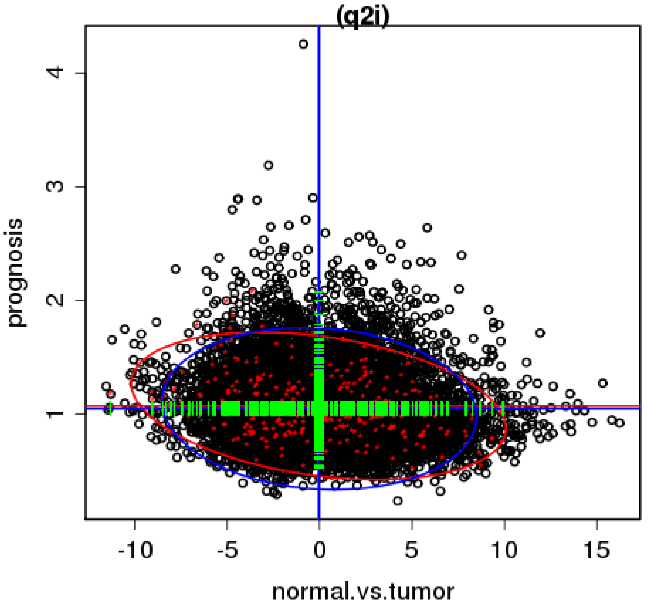
GO:0022618
ribonucleoprotein complex assembly
(q2i)



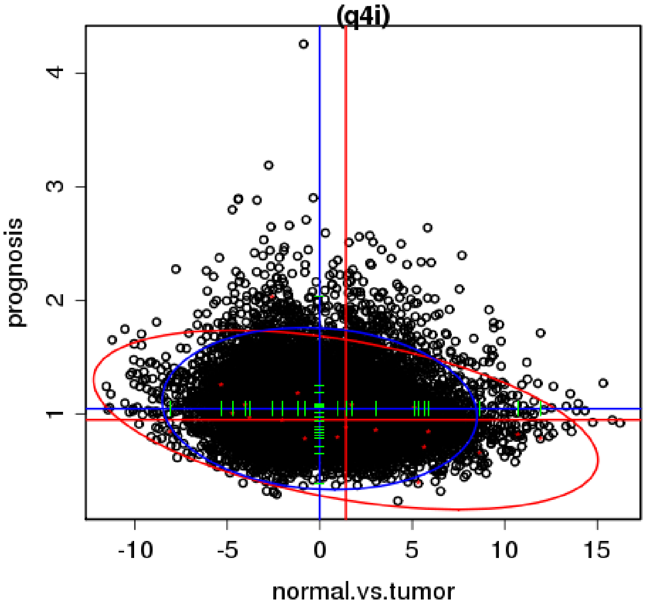
GO:0051301
cell division
(q2i)

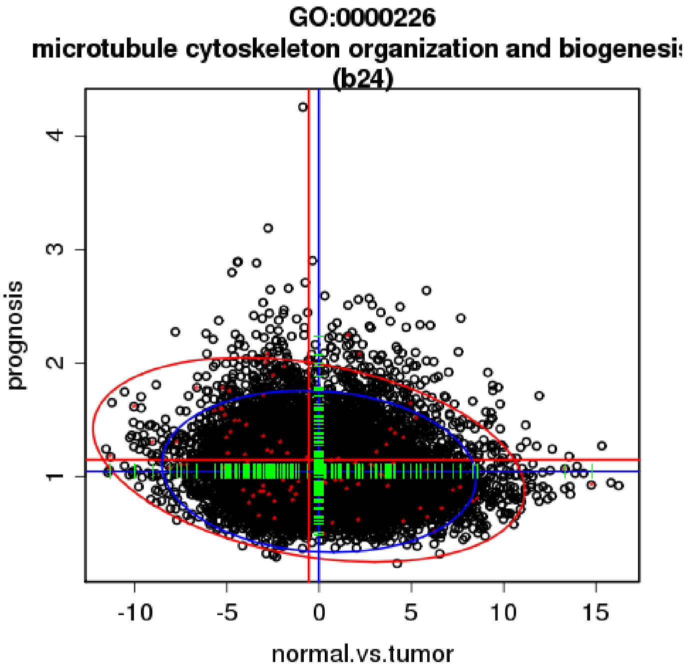


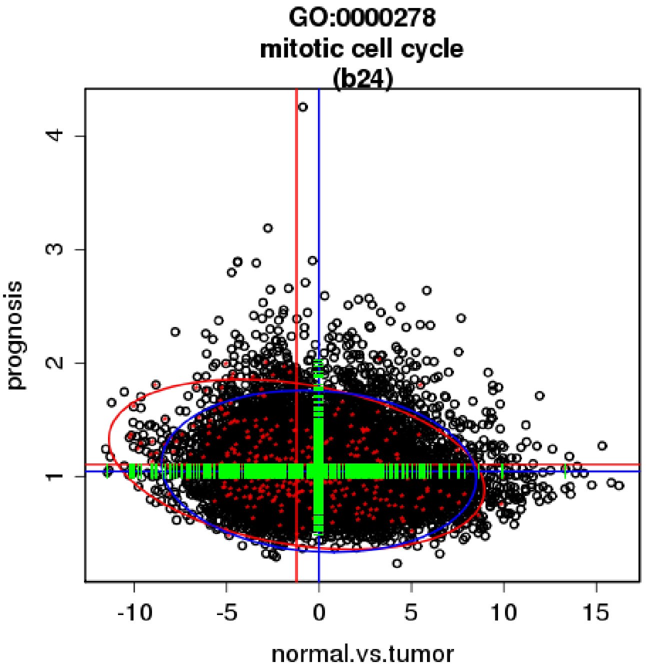
GO:0051726
regulation of cell cycle
(q2i)

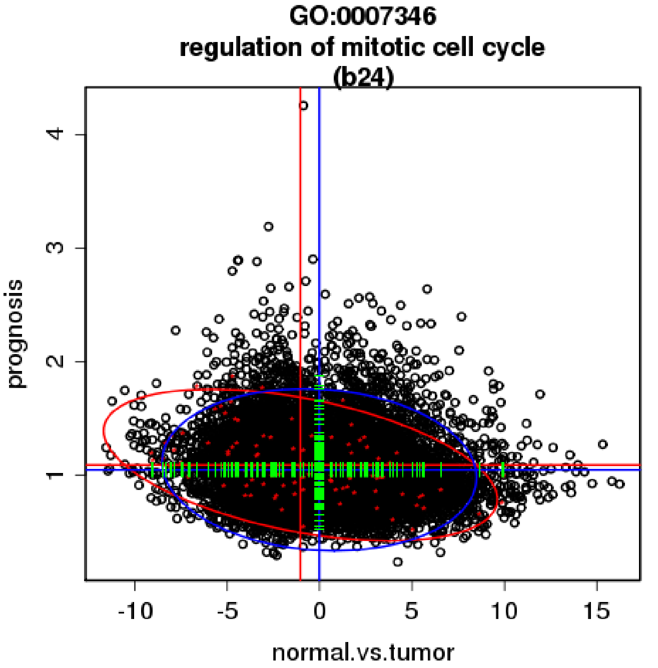


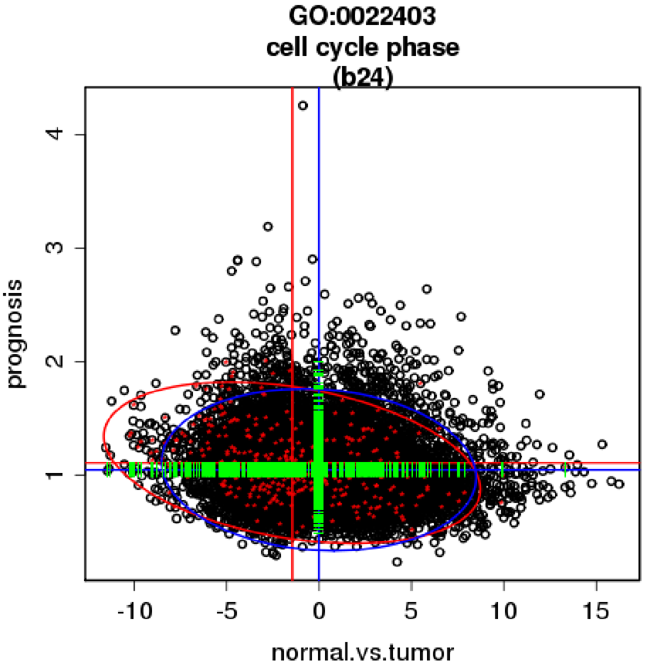
GO:0045638
negative regulation of myeloid cell differentiation
(q4i)

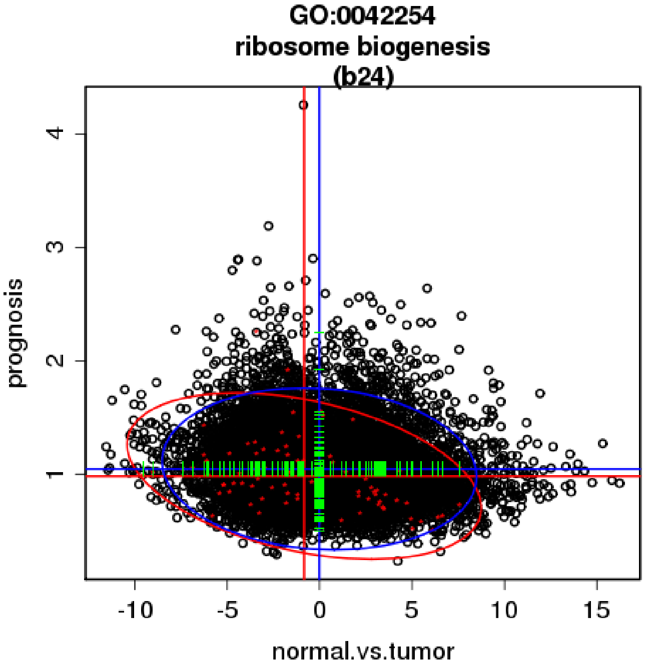


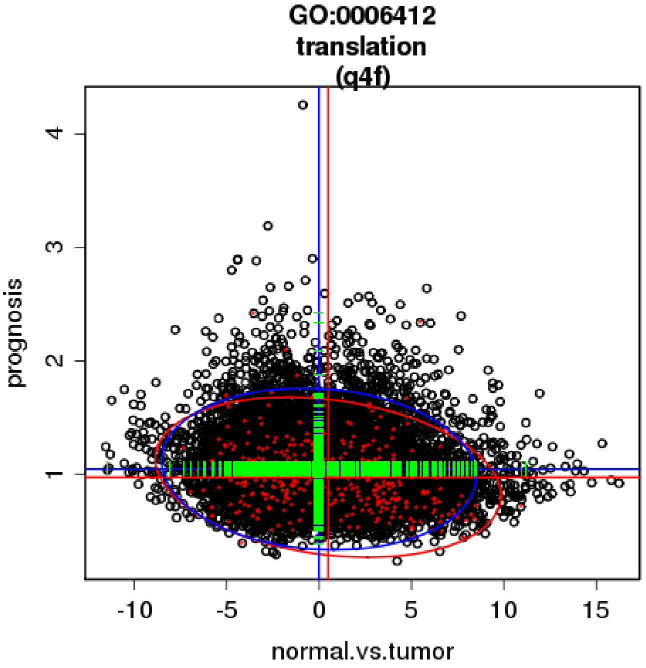

GO:0000226
microtubule cytoskeleton organization and biogenesis
(b24)
prognosis
1
2
3
4
-10
-5
0
5
10
15
normal.vs.tumor

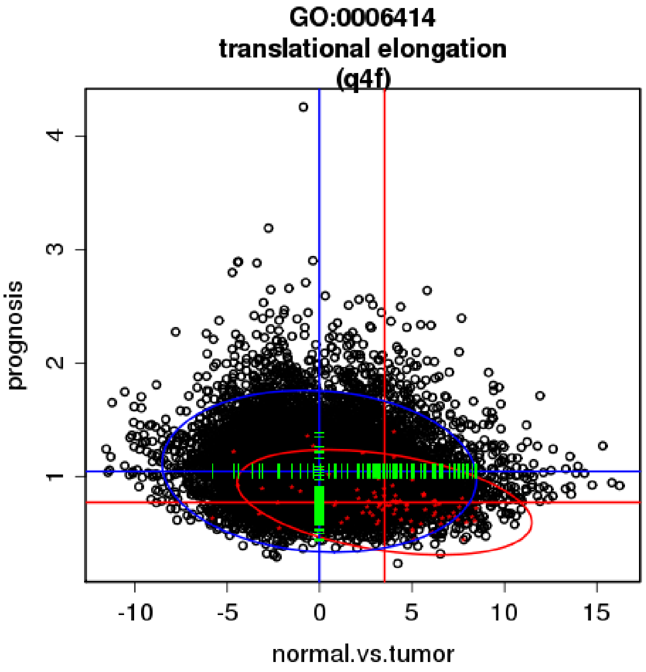

GO:0000278
mitotic cell cycle
(b24)
prognosis
1
2
3
4
-10
-5
0
5
10
15
normal.vs.tumor

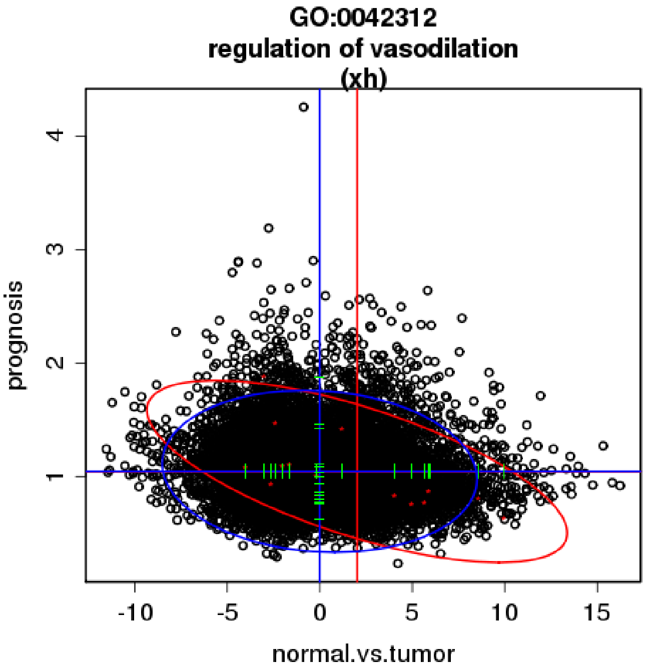

GO:0007346
regulation of mitotic cell cycle
(b24)
prognosis
1
2
3
4
-10
-5
0
5
10
15
normal.vs.tumor

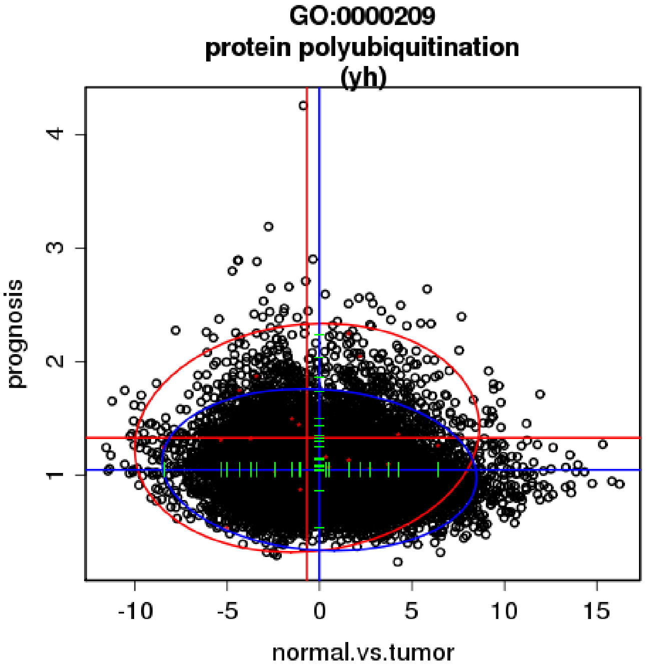

GO:0022403
cell cycle phase
(b24)
prognosis
1
2
3
4
-10
-5
0
5
10
15
normal.vs.tumor

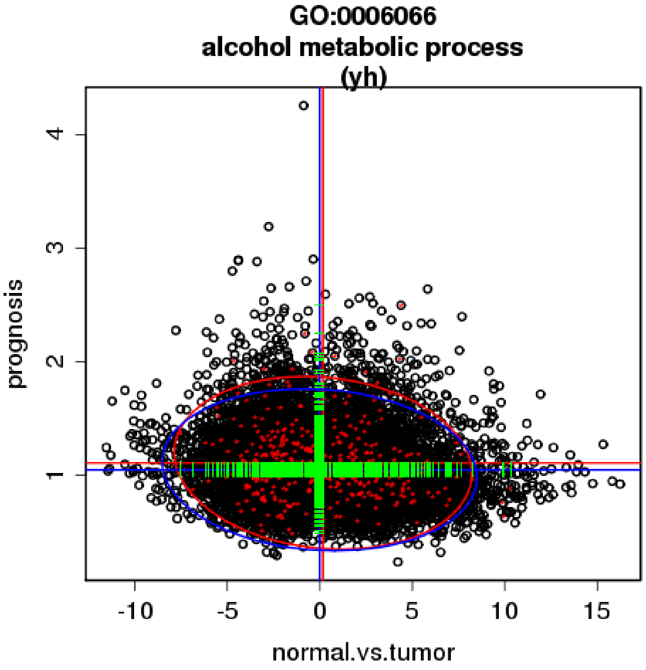

GO:0042254
ribosome biogenesis
(b24)
prognosis
1
2
3
4
-10
-5
0
5
10
15
normal.vs.tumor

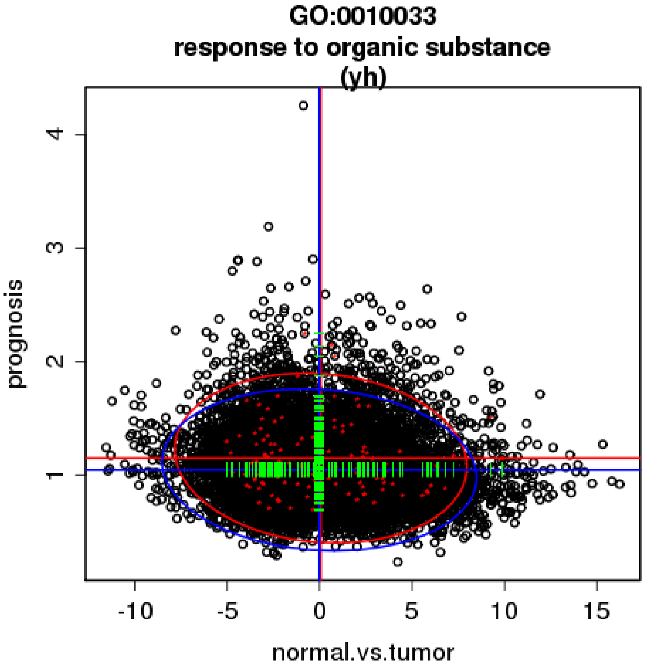

GO:0006412
translation
(q4f)
prognosis
1
2
3
4
-10
-5
0
5
10
15
normal.vs.tumor

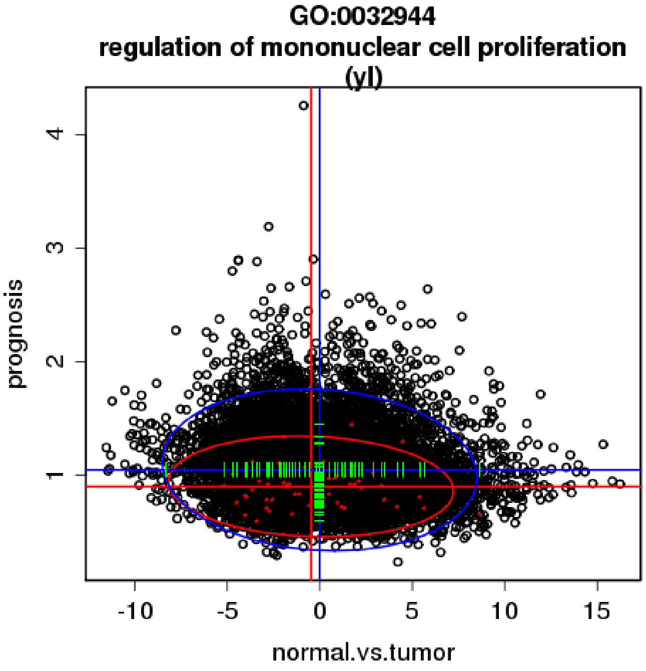

GO:0006414
translational elongation
(q4f)
prognosis
normal.vs.tumor
4
3
2
1
-10
-5
0
5
10
15

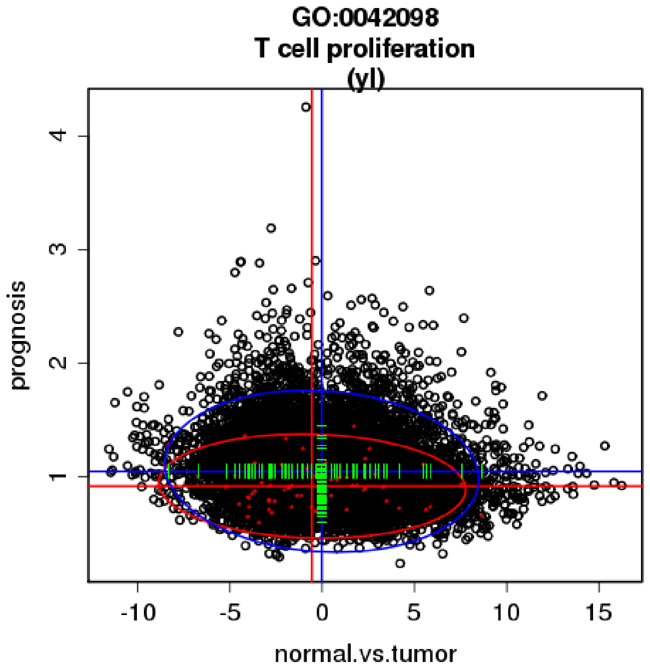

GO:0042312
regulation of vasodilation
(xh)
prognosis
normal.vs.tumor
4
3
2
1
-10
-5
0
5
10
15

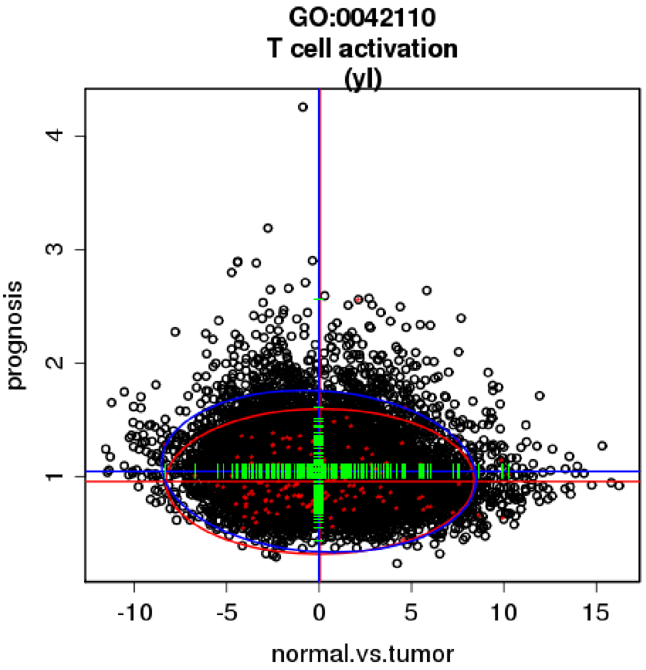

GO:0000209
protein polyubiquitination
(yh)
prognosis
normal.vs.tumor
4
3
2
1
-10
-5
0
5
10
15

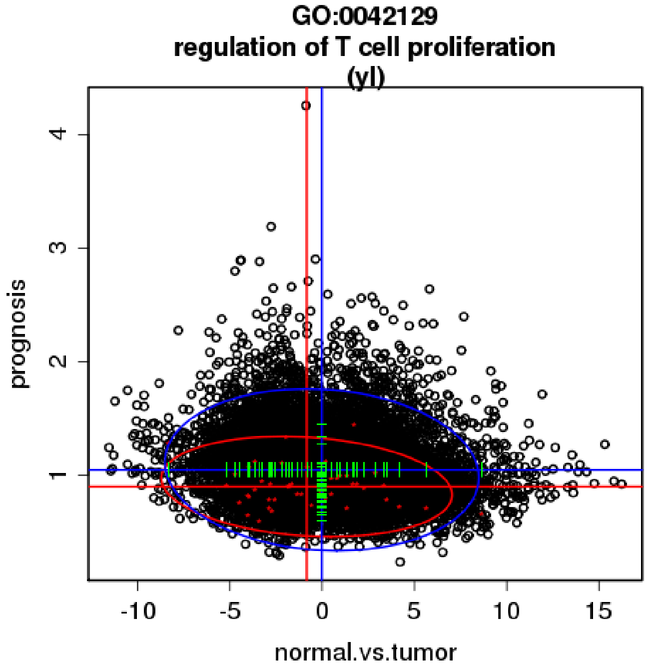

GO:0006066
alcohol metabolic process
(yh)
prognosis
normal.vs.tumor
4
3
2
1
-10
-5
0
5
10
15

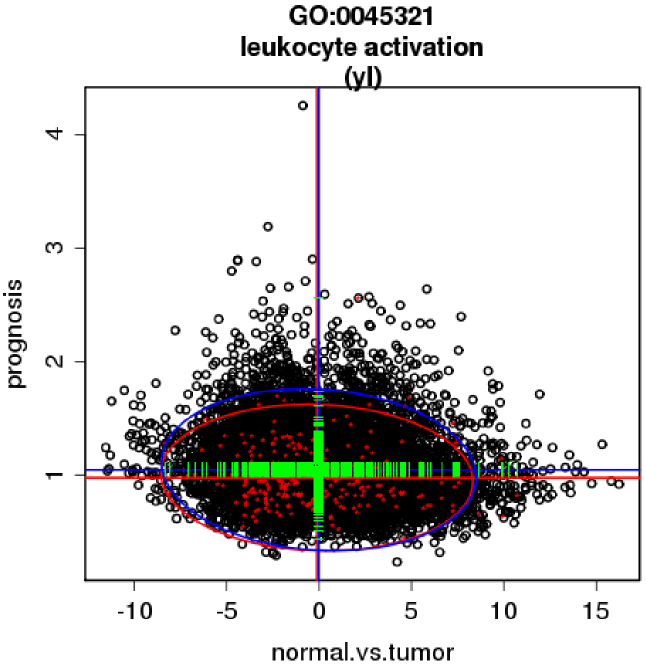

GO:0010033
response to organic substance
(yh)
prognosis
normal.vs.tumor
4
3
2
1
-10
-5
0
5
10
15

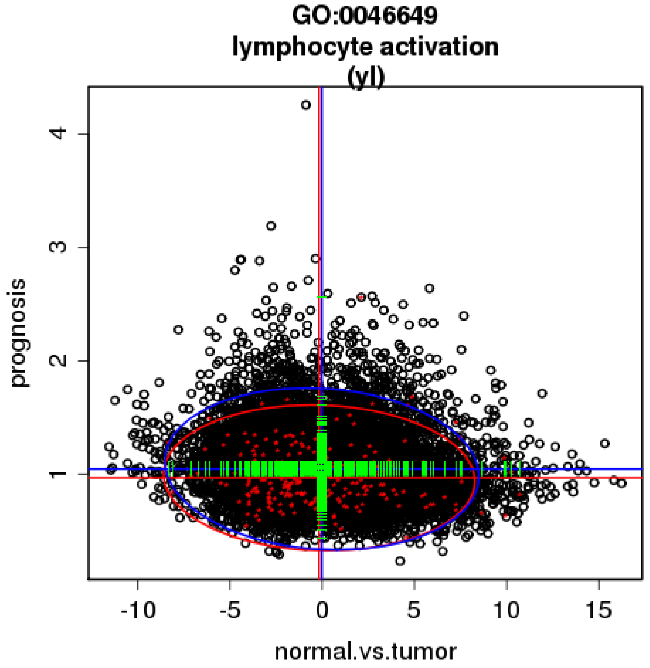

GO:0032944
regulation of mononuclear cell proliferation
(yl)
prognosis
normal.vs.tumor
4
3
2
1
-10
-5
0
5
10
15

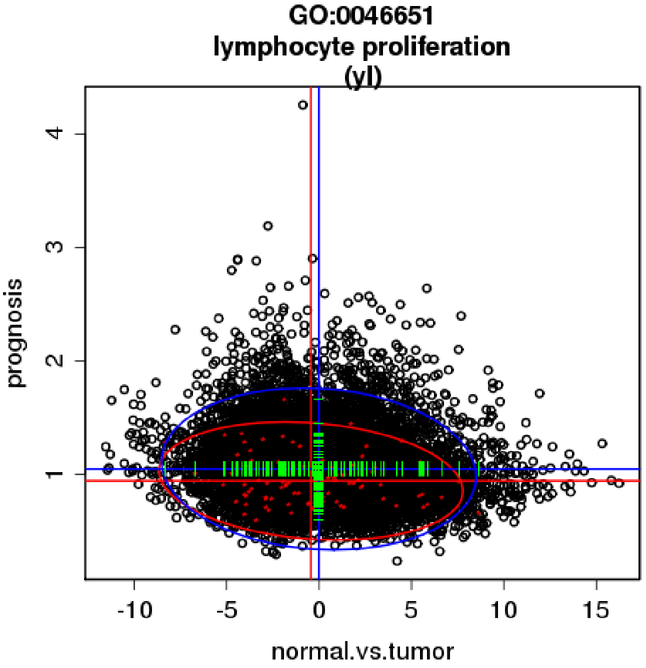

GO:0042098
T cell proliferation
(yl)

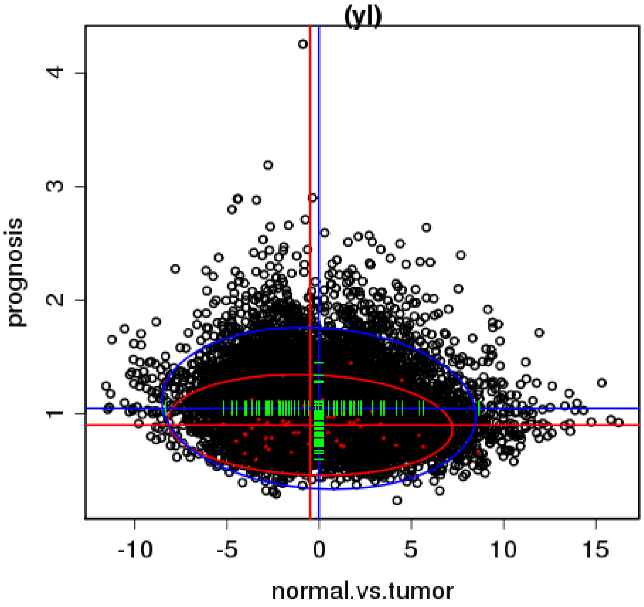

GO:0042110
T cell activation
(yl)

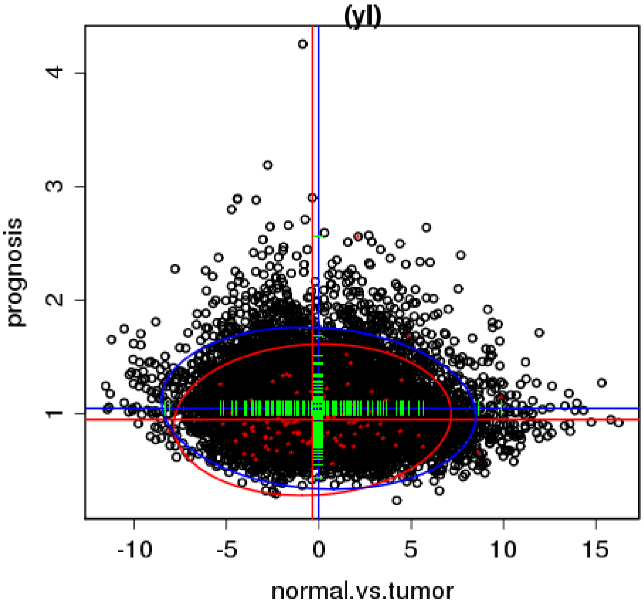

GO:0042129
regulation of T cell proliferation
(yl)

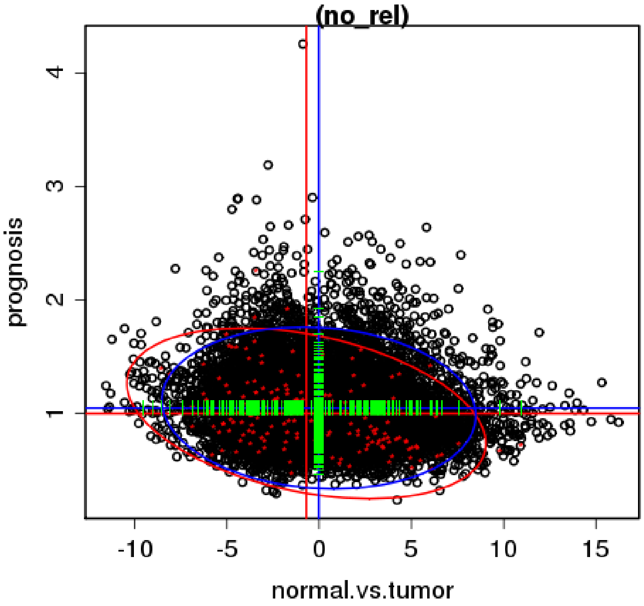

GO:0045321
leukocyte activation
(yl)


GO:0046649
lymphocyte activation
(yl)


GO:0046651
lymphocyte proliferation
(yl)


GO:0050670
regulation of lymphocyte proliferation
(yl)


GO:0051249
regulation of lymphocyte activation
(yl)


GO:0022613
ribonucleoprotein complex biogenesis and assembly
(no_rel)

# Combined functional profiling of differential gene expression and prognosis using KEGG pathways

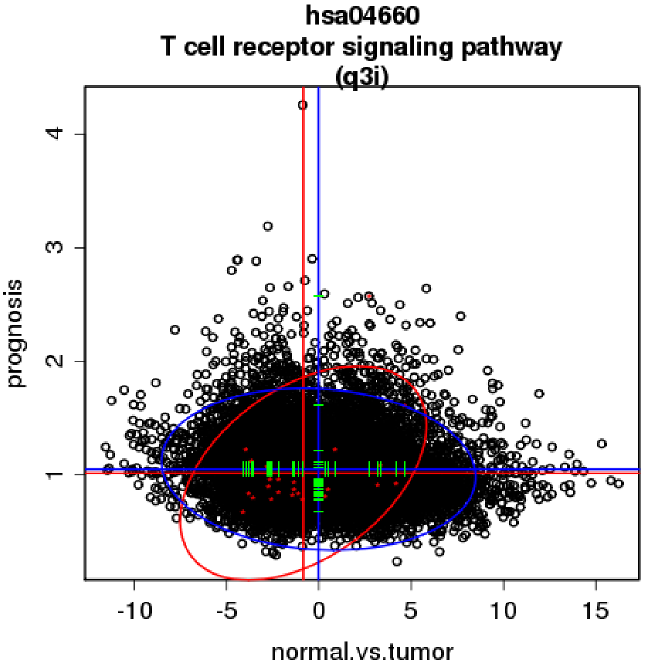
**6** significant modules

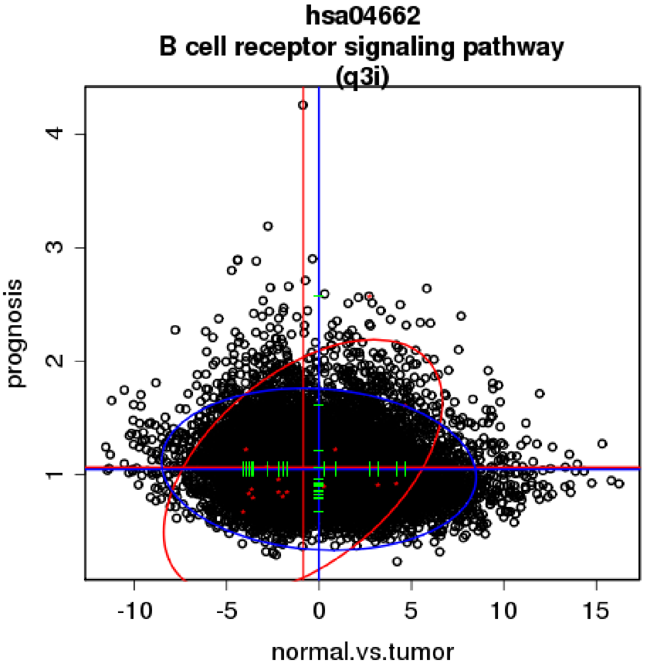
**LOR** indicates Log Odds Ratio of the coefficient or the interaction

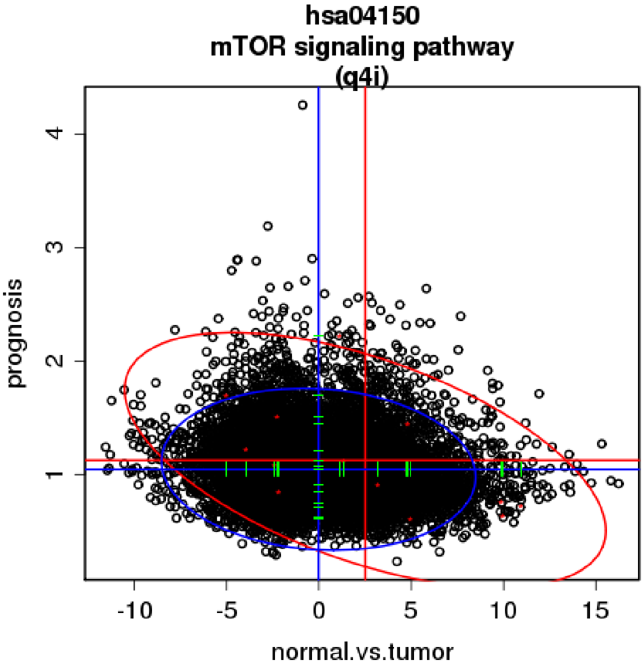
**p** indicates FDR adjusted p-value

| | LOR normal vs tumor | LOR prognosis | LOR Inter | p normal vs tumor | p prognosis | p Inter | pattern | name |
|---|---|---|---|---|---|---|---|---|
| hsa04660 | -0.26 | -0.18 | 0.53 | 0.03 | 0.81 | 0.04 | q3i | T cell receptor signaling pathway |
| hsa04662 | -0.36 | -0.05 | 0.58 | 0.03 | 0.90 | 0.04 | q3i | B cell receptor signaling pathway |
| hsa04150 | 0.67 | 0.30 | -0.48 | 0.00 | 0.57 | 0.05 | q4i | mTOR signaling pathway |
| hsa04140 | -0.77 | -0.85 | -0.78 | 0.10 | 0.31 | 0.01 | b24 | Regulation of autophagy |
| hsa04370 | -0.55 | 0.55 | 0.29 | 0.43 | 0.01 | 0.75 | yh | VEGF signaling pathway |
| hsa03010 | 0.11 | -1.65 | -0.49 | 0.43 | 0.04 | 0.75 | yl | Ribosome |

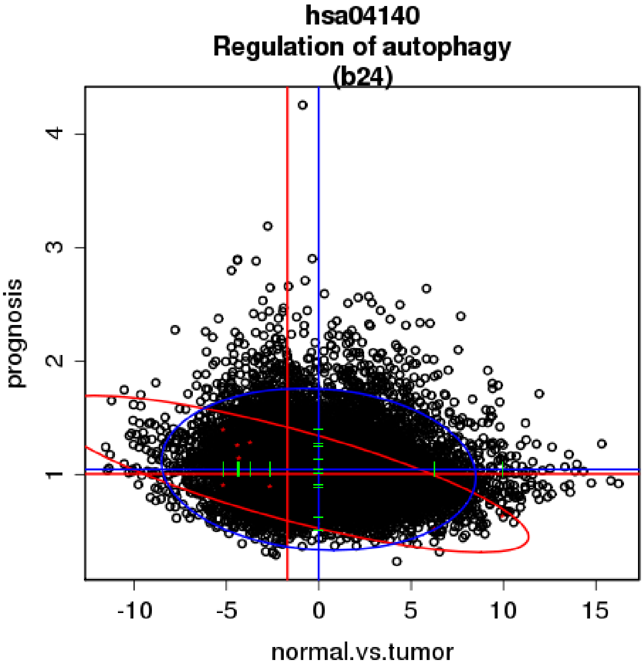
Table 1: LOR: log odds ratio; p: adjusted p-value FDR



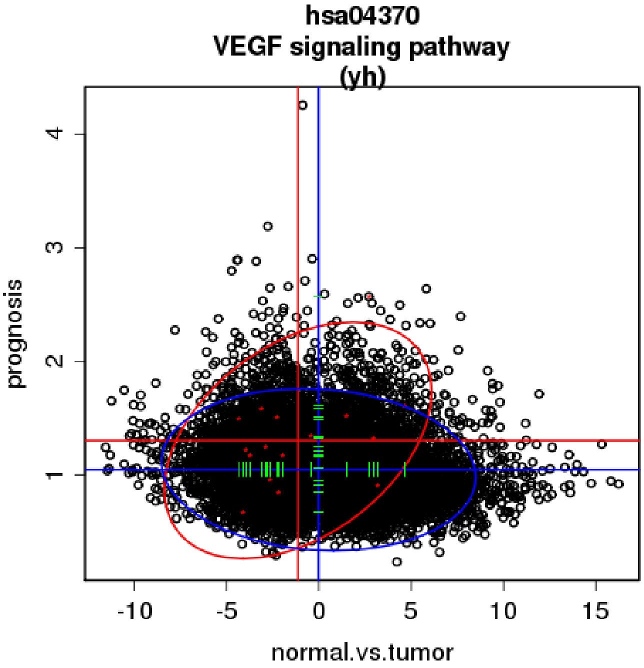




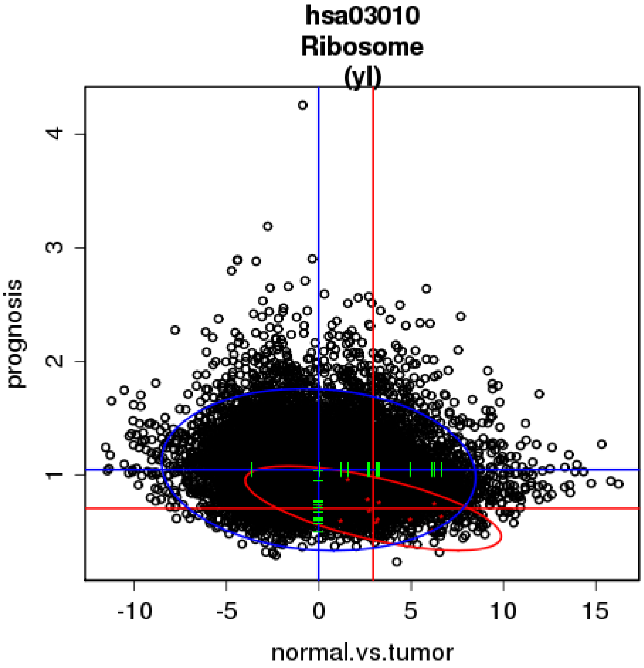
hsa04150
mTOR signaling pathway
(q4i)



hsa04140
Regulation of autophagy
(b24)



hsa04370
VEGF signaling pathway
(yh)



hsa03010
Ribosome
(yl)