Combined functional profiling of Transcription Rate (TR) and RNA Stability (RS) using GO Biological Process

140 significant modules

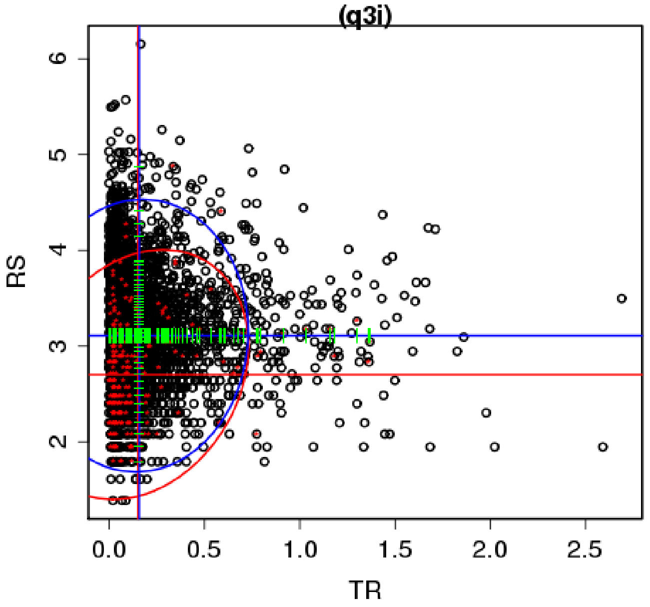
LOR indicates Log Odds Ratio of the coefficient or the interaction

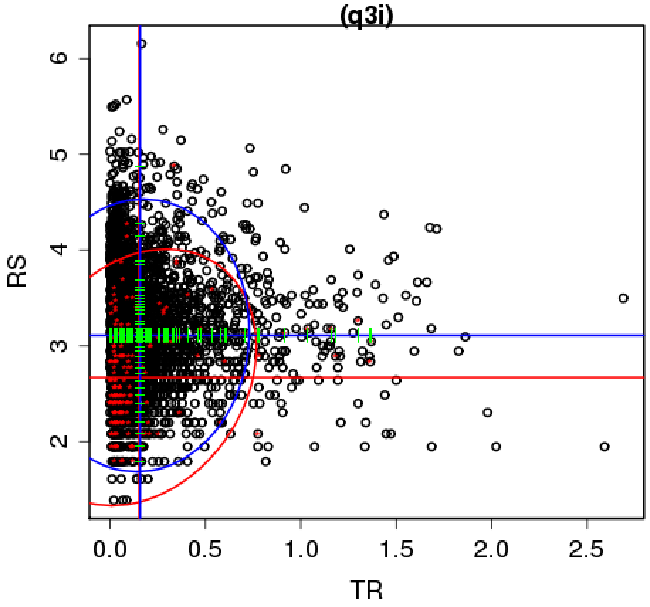
p indicates FDR adjusted p-value

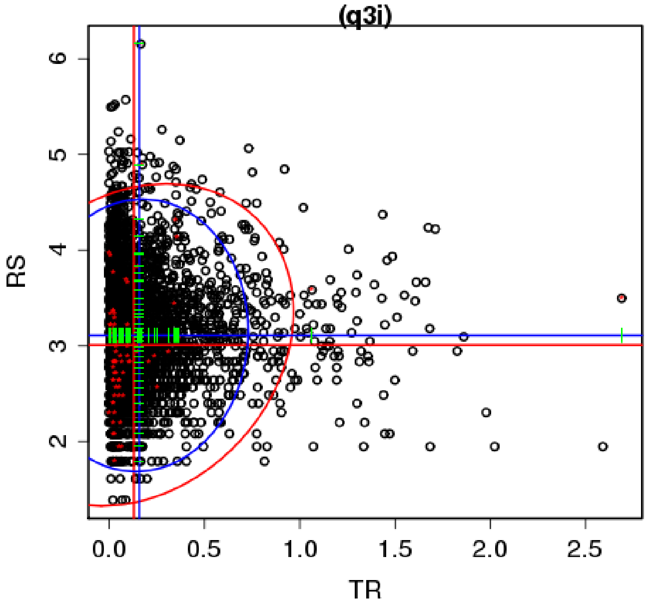
	LOR TR	LOR RS	LOR Inter	p TR	p RS	p Inter	pattern	name
GO:0022613	-4.69	-1.78	1.61	0.08	0.00	0.03	q3i	ribonucleoprotein complex biogenesis and assembly
GO:0042254	-5.05	-1.91	1.75	0.09	0.00	0.03	q3i	ribosome biogenesis
GO:0000746	-11.48	-0.73	3.17	0.06	0.02	0.03	q3i	conjugation
GO:0000747	-11.39	-0.74	3.16	0.06	0.02	0.03	q3i	conjugation with cellular fusion
GO:0019953	-11.87	-0.82	3.29	0.04	0.01	0.02	q3i	sexual reproduction
GO:0042221	-6.65	-0.12	2.05	0.02	0.60	0.01	q3i	response to chemical stimulus
GO:0051704	-11.98	-0.69	3.23	0.04	0.02	0.02	q3i	multi-organism process
GO:0000819	-30.49	-0.87	7.10	0.02	0.03	0.02	q3i	sister chromatid segregation
GO:0000070	-30.23	-0.78	7.01	0.03	0.07	0.03	q3i	mitotic sister chromatid segregation
GO:0006260	-20.35	-0.97	4.99	0.00	0.00	0.01	q3i	DNA replication
GO:0006261	-25.15	-1.31	6.28	0.00	0.00	0.01	q3i	DNA-dependent DNA replication
GO:0019725	-9.13	-0.38	2.71	0.02	0.15	0.01	q3i	cellular homeostasis
GO:0042592	-8.75	-0.30	2.59	0.02	0.27	0.01	q3i	homeostatic process
GO:0065004	12.12	-0.49	-4.60	0.00	0.21	0.02	q4i	protein-DNA complex assembly
GO:0006325	8.01	-0.47	-3.09	0.00	0.03	0.01	q4i	establishment and/or maintenance of chromatin architecture
GO:0006323	12.63	-0.48	-4.96	0.00	0.15	0.01	q4i	DNA packaging
GO:0006333	12.44	-0.40	-4.84	0.00	0.23	0.01	q4i	chromatin assembly or disassembly
GO:0031497	12.51	-0.44	-4.84	0.00	0.20	0.01	q4i	chromatin assembly
GO:0006082	0.58	0.56	-0.18	0.99	0.00	1.00	yh	organic acid metabolic process
GO:0006519	2.41	0.43	-0.88	0.66	0.02	0.58	yh	amino acid and derivative metabolic process
GO:0006520	2.44	0.45	-0.87	0.65	0.02	0.58	yh	amino acid metabolic process
GO:0006807	2.56	0.44	-1.01	0.61	0.01	0.46	yh	nitrogen compound metabolic process
GO:0009308	2.41	0.41	-0.89	0.65	0.03	0.57	yh	amine metabolic process
GO:0019752	0.58	0.56	-0.18	0.99	0.00	1.00	yh	carboxylic acid metabolic process
GO:0009056	-0.54	0.34	0.15	0.99	0.02	1.00	yh	catabolic process
GO:0044248	-0.21	0.38	0.09	0.99	0.01	1.00	yh	cellular catabolic process
GO:0005975	-0.32	0.87	0.01	0.99	0.00	1.00	yh	carbohydrate metabolic process
GO:0005996	-0.88	0.97	0.37	0.99	0.00	1.00	yh	monosaccharide metabolic process
GO:0006066	-0.97	0.76	0.31	0.99	0.00	1.00	yh	alcohol metabolic process
GO:0044262	-0.08	0.88	-0.07	1.00	0.00	1.00	yh	cellular carbohydrate metabolic process
GO:0019318	-1.03	0.93	0.43	0.99	0.00	1.00	yh	hexose metabolic process
GO:0032787	-1.77	0.75	0.58	0.99	0.00	1.00	yh	monocarboxylic acid metabolic process
GO:0006006	-1.37	0.95	0.61	0.99	0.00	1.00	yh	glucose metabolic process
GO:0006007	0.02	1.23	0.35	1.00	0.00	1.00	yh	glucose catabolic process
GO:0016052	-1.20	1.09	0.55	0.99	0.00	1.00	yh	carbohydrate catabolic process
GO:0019320	-0.44	1.16	0.44	0.99	0.00	1.00	yh	hexose catabolic process
GO:0044275	-1.20	1.09	0.55	0.99	0.00	1.00	yh	cellular carbohydrate catabolic process
GO:0046164	-0.86	1.15	0.56	0.99	0.00	1.00	yh	alcohol catabolic process
GO:0046365	-0.15	1.25	0.35	0.99	0.00	1.00	yh	monosaccharide catabolic process
GO:0006090	-0.15	1.15	0.45	0.99	0.01	1.00	yh	pyruvate metabolic process
GO:0006096	-0.93	1.13	0.65	0.99	0.01	1.00	yh	glycolysis
GO:0009063	5.11	1.04	-1.75	0.59	0.03	0.68	yh	amino acid catabolic process
GO:0009310	5.53	1.09	-1.99	0.56	0.02	0.61	yh	amine catabolic process
GO:0044270	5.53	1.09	-1.99	0.56	0.02	0.61	yh	nitrogen compound catabolic process
GO:0006084	5.12	1.35	-1.65	0.46	0.00	0.52	yh	acetyl-CoA metabolic process
GO:0006732	0.20	0.63	-0.10	0.99	0.01	1.00	yh	coenzyme metabolic process
GO:0051186	0.45	0.58	-0.10	0.99	0.01	1.00	yh	cofactor metabolic process
GO:0006091	1.50	0.40	-0.23	0.80	0.03	1.00	yh	generation of precursor metabolites and energy
GO:0006113	5.76	1.41	-1.76	0.46	0.01	0.61	yh	fermentation
GO:0015980	2.73	0.58	-0.66	0.48	0.02	0.70	yh	energy derivation by oxidation of organic compounds
GO:0019751	4.35	1.38	-1.11	0.66	0.02	0.92	yh	polyol metabolic process
GO:0006536	3.21	1.30	-0.86	0.99	0.03	1.00	yh	glutamate metabolic process
GO:0009084	3.78	0.98	-1.30	0.93	0.03	0.95	yh	glutamine family amino acid biosynthetic process
GO:0006537	3.28	1.37	-0.87	0.99	0.03	1.00	yh	glutamate biosynthetic process
GO:0006766	-1.01	0.63	0.23	0.99	0.05	1.00	yh	vitamin metabolic process
GO:0006767	-1.01	0.63	0.23	0.99	0.05	1.00	yh	water-soluble vitamin metabolic process
GO:0030435	4.76	0.56	-1.98	0.43	0.02	0.27	yh	sporulation
GO:0005984	-70.69	1.26	12.40	0.49	0.05	0.61	yh	disaccharide metabolic process
GO:0008645	-1.41	1.40	0.02	0.99	0.02	1.00	yh	hexose transport
GO:0015749	-1.41	1.40	0.02	0.99	0.02	1.00	yh	monosaccharide transport
GO:0006094	-0.30	1.11	0.57	0.99	0.03	1.00	yh	gluconeogenesis
GO:0019319	-0.14	0.98	0.50	0.99	0.05	1.00	yh	hexose biosynthetic process
GO:0046165	1.85	1.14	-0.05	0.99	0.01	1.00	yh	alcohol biosynthetic process
GO:0046364	-0.14	0.98	0.50	0.99	0.05	1.00	yh	monosaccharide biosynthetic process
GO:0006739	2.55	1.46	-0.49	0.99	0.00	1.00	yh	NADP metabolic process
GO:0006740	3.11	1.61	-0.58	0.95	0.00	1.00	yh	NADPH regeneration
GO:0006769	-0.60	0.89	0.32	0.99	0.03	1.00	yh	nicotinamide metabolic process
GO:0019362	-0.83	0.86	0.37	0.99	0.03	1.00	yh	pyridine nucleotide metabolic process
GO:0006098	2.55	1.46	-0.39	0.99	0.01	1.00	yh	pentose-phosphate shunt
GO:0006067	3.53	1.79	-1.08	0.99	0.00	1.00	yh	ethanol metabolic process
GO:0009072	7.43	1.06	-3.32	0.79	0.02	0.62	yh	aromatic amino acid family metabolic process

GO:0016042	18.81	1.09	-10.53	0.95	0.03	0.61	yh	lipid catabolic process
GO:0009081	5.35	1.11	-1.70	0.46	0.02	0.58	yh	branched chain family amino acid metabolic process
GO:0006081	-0.84	1.39	0.01	0.99	0.02	1.00	yh	aldehyde metabolic process
GO:0009109	4.88	1.30	-1.52	0.49	0.00	0.58	yh	coenzyme catabolic process
GO:0046356	4.97	1.35	-1.52	0.47	0.00	0.57	yh	acetyl-CoA catabolic process
GO:0051187	4.77	1.40	-1.46	0.49	0.00	0.59	yh	cofactor catabolic process
GO:0006100	5.29	1.19	-1.58	0.46	0.02	0.61	yh	
GO:0006099	4.97	1.35	-1.52	0.47	0.00	0.57	yh	tricarboxylic acid cycle
GO:0006071	4.12	1.26	-1.02	0.73	0.04	0.95	yh	glycerol metabolic process
GO:0044242	19.65	1.51	-9.69	0.56	0.00	0.43	yh	cellular lipid catabolic process
GO:0022607	3.20	-0.68	-1.01	0.17	0.00	0.29	yl	cellular component assembly
GO:0065003	2.62	-0.90	-0.67	0.42	0.00	0.64	yl	macromolecular complex assembly
GO:0006366	0.16	-0.63	-0.37	0.99	0.00	1.00	yl	transcription from RNA polymerase II promoter
GO:0006357	-0.32	-0.60	-0.35	0.99	0.02	1.00	yl	regulation of transcription from RNA polymerase II promoter
GO:0016568	2.18	-0.64	-1.61	0.99	0.01	0.84	yl	chromatin modification
GO:0009059	0.66	-0.49	0.26	0.99	0.00	0.95	yl	macromolecule biosynthetic process
GO:0000278	-6.84	-0.75	1.60	0.38	0.00	0.53	yl	mitotic cell cycle
GO:0051726	-7.52	-0.93	1.68	0.70	0.00	0.95	yl	regulation of cell cycle
GO:0006396	-5.40	-1.47	1.41	0.35	0.00	0.46	yl	RNA processing
GO:0008033	-0.88	-0.92	0.12	0.99	0.01	1.00	yl	tRNA processing
GO:0009451	-1.42	-1.49	-0.41	0.99	0.00	1.00	yl	RNA modification
GO:0006400	-5.93	-1.22	1.21	0.99	0.03	1.00	yl	tRNA modification
GO:0006401	-0.39	-1.02	0.04	0.99	0.02	1.00	yl	RNA catabolic process
GO:0006402	0.04	-1.00	-0.01	1.00	0.03	1.00	yl	mRNA catabolic process
GO:0016071	-2.19	-0.78	0.58	0.99	0.00	1.00	yl	mRNA metabolic process
GO:0006397	-3.22	-0.82	0.90	0.93	0.00	0.95	yl	mRNA processing
GO:0051325	-4.72	-0.88	1.03	0.97	0.02	1.00	yl	interphase
GO:0051329	-4.72	-0.88	1.03	0.97	0.02	1.00	yl	interphase of mitotic cell cycle
GO:0006486	-7.70	-0.93	1.80	0.79	0.02	0.95	yl	protein amino acid glycosylation
GO:0009100	-2.61	-0.87	0.54	0.99	0.02	1.00	yl	glycoprotein metabolic process
GO:0009101	-2.70	-0.90	0.59	0.99	0.02	1.00	yl	glycoprotein biosynthetic process
GO:0043413	-7.70	-0.93	1.80	0.79	0.02	0.95	yl	biopolymer glycosylation
GO:0000087	-9.82	-0.87	2.40	0.28	0.00	0.39	yl	M phase of mitotic cell cycle
GO:0007067	-9.74	-0.88	2.33	0.35	0.00	0.46	yl	mitosis
GO:0007088	-15.73	-1.30	3.79	0.58	0.02	0.74	yl	regulation of mitosis
GO:0016072	-5.48	-1.90	1.37	0.72	0.00	0.95	yl	rRNA metabolic process
GO:0006364	-5.46	-1.96	1.41	0.70	0.00	0.94	yl	rRNA processing
GO:0022618	-2.58	-1.46	1.13	0.70	0.00	0.39	yl	ribonucleoprotein complex assembly
GO:0006413	-2.22	-1.47	0.97	0.99	0.00	0.95	yl	translational initiation
GO:0007166	-5.86	-0.98	1.86	0.72	0.04	0.61	yl	cell surface receptor linked signal transduction
GO:0031137	-7.32	-1.61	2.54	0.58	0.02	0.39	yl	regulation of conjugation with cellular fusion
GO:0032005	-7.32	-1.61	2.54	0.58	0.02	0.39	yl	signal transduction during conjugation with cellular fusion
GO:0046999	-7.32	-1.61	2.54	0.58	0.02	0.39	yl	regulation of conjugation
GO:0000750	-7.32	-1.61	2.54	0.58	0.02	0.39	yl	pheromone-dependent signal transduction during conjugation with cellular fusion
GO:0006730	-5.70	-0.86	1.50	0.93	0.04	0.95	yl	one-carbon compound metabolic process
GO:0000054	-6.34	-1.35	1.94	0.95	0.05	0.95	yl	ribosome export from nucleus
GO:0033750	-6.34	-1.35	1.94	0.95	0.05	0.95	yl	ribosome localization
GO:0033753	-6.34	-1.35	1.94	0.95	0.05	0.95	yl	establishment of ribosome localization
GO:0006487	-8.84	-1.01	2.34	0.70	0.03	0.74	yl	protein amino acid N-linked glycosylation
GO:0032259	0.54	-1.21	-1.23	0.99	0.03	1.00	yl	methylation
GO:0043414	0.54	-1.21	-1.23	0.99	0.03	1.00	yl	biopolymer methylation
GO:0006338	1.03	-0.84	-1.39	0.99	0.01	1.00	yl	chromatin remodeling
GO:0040029	0.26	-0.88	-0.80	0.99	0.02	1.00	yl	regulation of gene expression, epigenetic
GO:0048519	-0.07	-0.52	-0.42	1.00	0.04	1.00	yl	negative regulation of biological process
GO:0048523	-0.18	-0.51	-0.39	0.99	0.04	1.00	yl	negative regulation of cellular process
GO:0006497	-14.22	-1.02	3.75	0.39	0.03	0.31	yl	protein amino acid lipidation
GO:0042157	-14.22	-1.02	3.75	0.39	0.03	0.31	yl	lipoprotein metabolic process
GO:0042158	-14.22	-1.02	3.75	0.39	0.03	0.31	yl	lipoprotein biosynthetic process
GO:0042255	-2.49	-1.80	1.31	0.82	0.00	0.39	yl	ribosome assembly
GO:0042257	-2.11	-1.73	1.25	0.93	0.00	0.39	yl	ribosomal subunit assembly
GO:0007062	-35.59	-1.24	7.67	0.46	0.04	0.58	yl	sister chromatid cohesion
GO:0042273	-4.79	-2.86	2.04	0.47	0.00	0.14	yl	ribosomal large subunit biogenesis
GO:0007064	-65.49	-1.42	14.17	0.19	0.03	0.18	yl	mitotic sister chromatid cohesion
GO:0050793	-15.23	-1.52	4.16	0.58	0.03	0.52	yl	regulation of developmental process
GO:0000154	16.04	-2.21	-8.62	0.95	0.02	0.95	yl	rRNA modification
GO:0030490	-12.30	-2.32	3.36	0.56	0.00	0.62	yl	maturation of SSU-rRNA
GO:0000027	-3.09	-2.38	1.60	0.79	0.00	0.38	yl	ribosomal large subunit assembly and maintenance
GO:0043681	0.46	-1.40	0.21	0.99	0.02	1.00	yl	protein import into mitochondrion
GO:0000114	-5.92	-2.25	1.88	0.99	0.02	1.00	yl	G1-specific transcription in mitotic cell cycle

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


GO:0022613
ribonucleoprotein complex biogenesis and assembly
(q3i)


GO:0042254
ribosome biogenesis
(q3i)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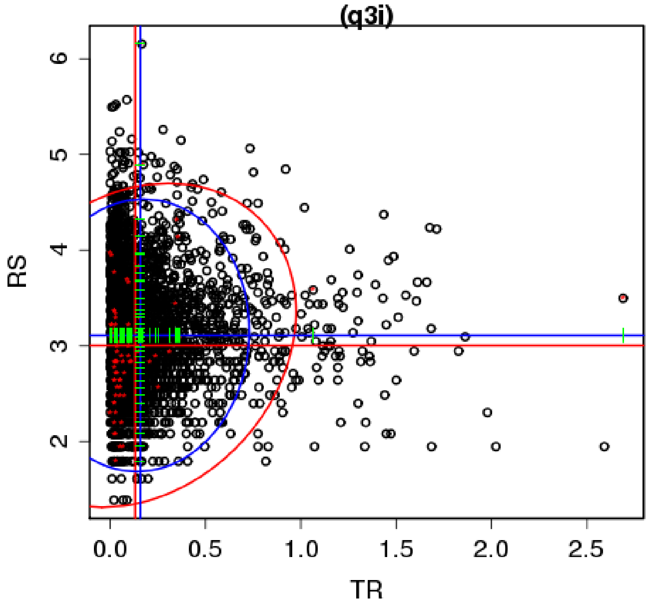
conjugation
(q3i)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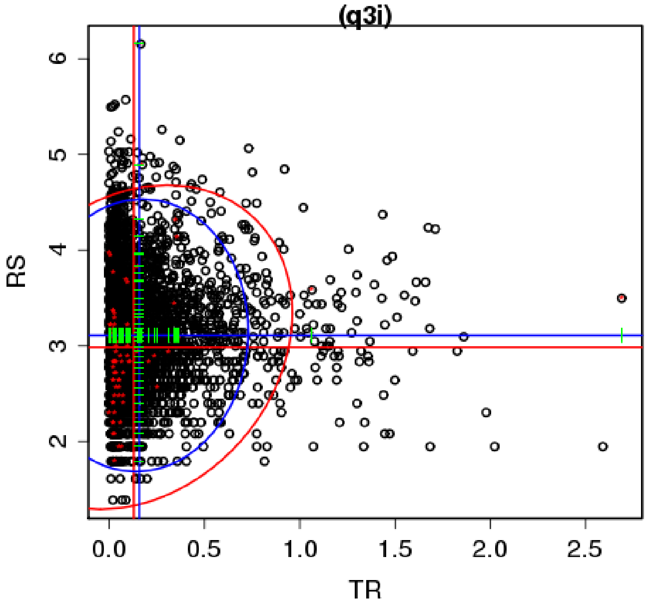
conjugation with cellular fusion
(q3i)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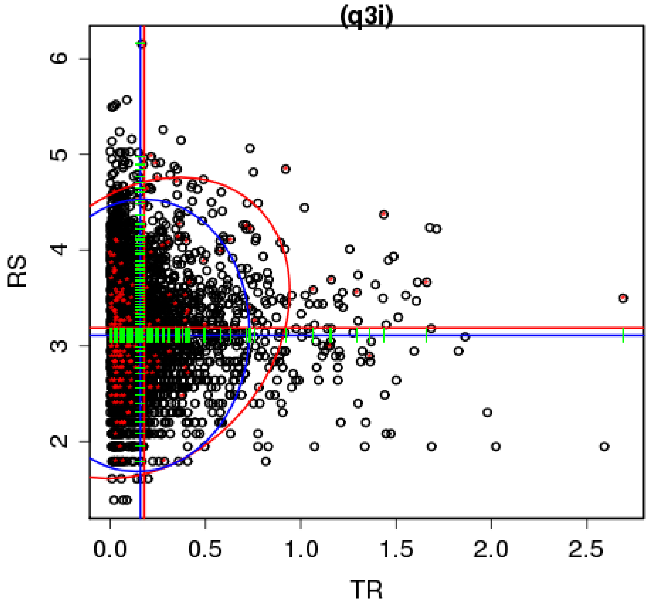
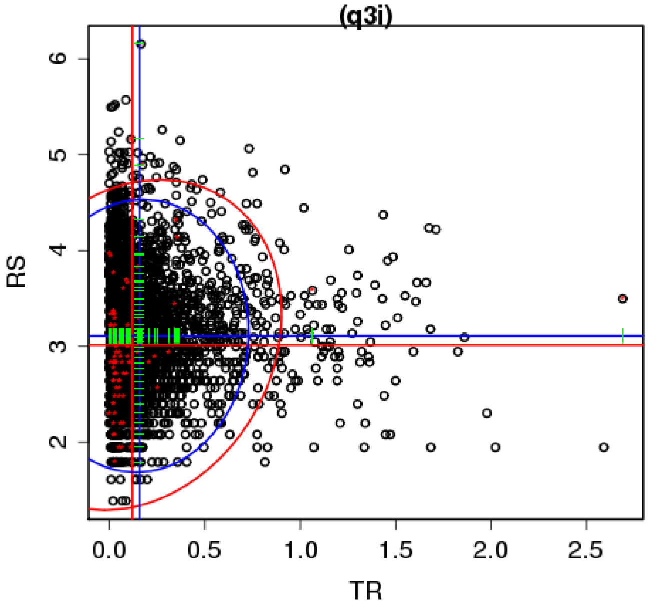
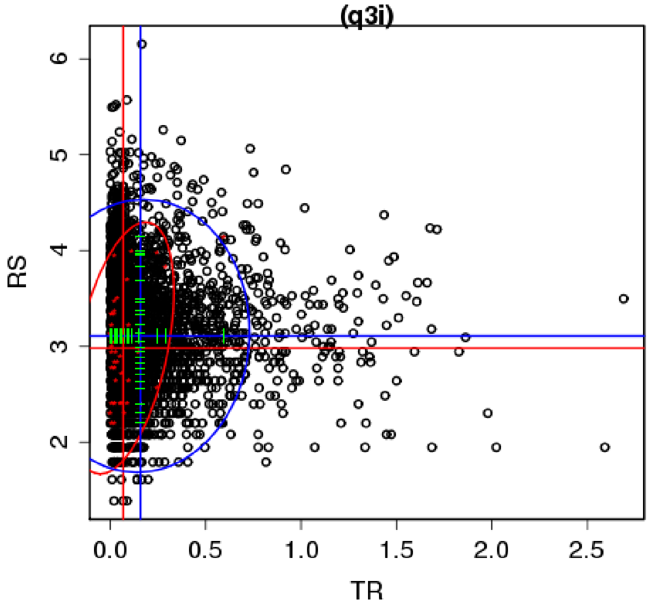
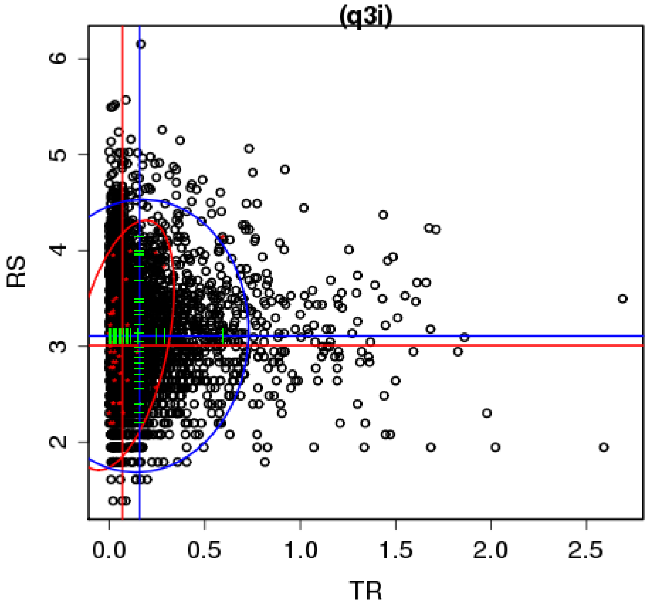
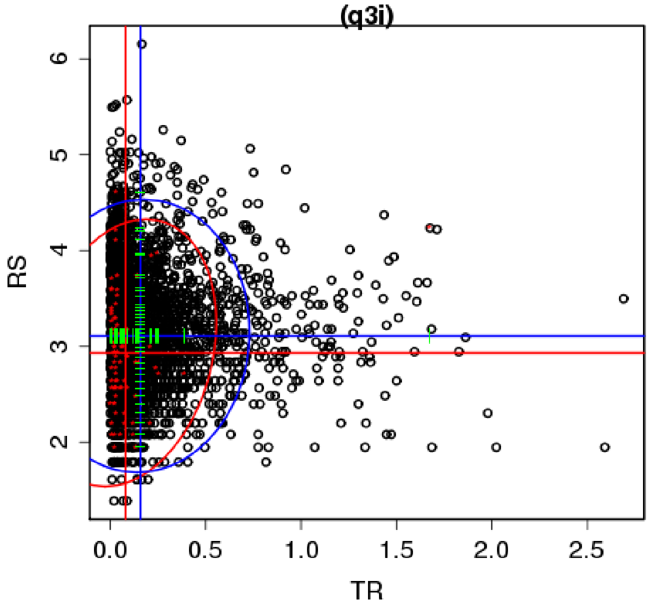
sexual reproduction
(q3i)

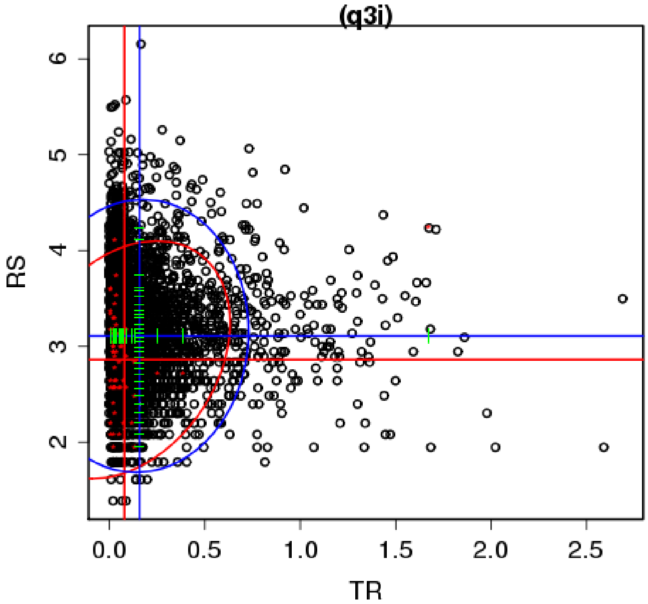

GO:0042221
response to chemical stimulus
(q3i)

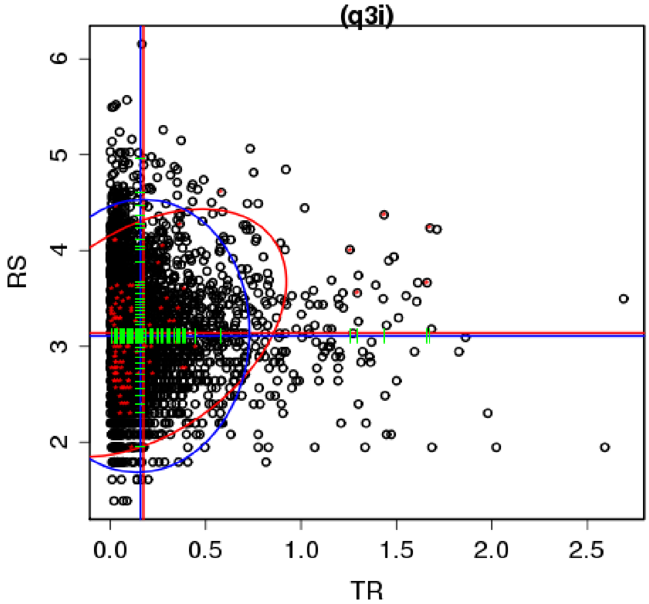

GO:0051704
multi-organism process
(q3i)


GO:0000819
sister chromatid segregation
(q3i)

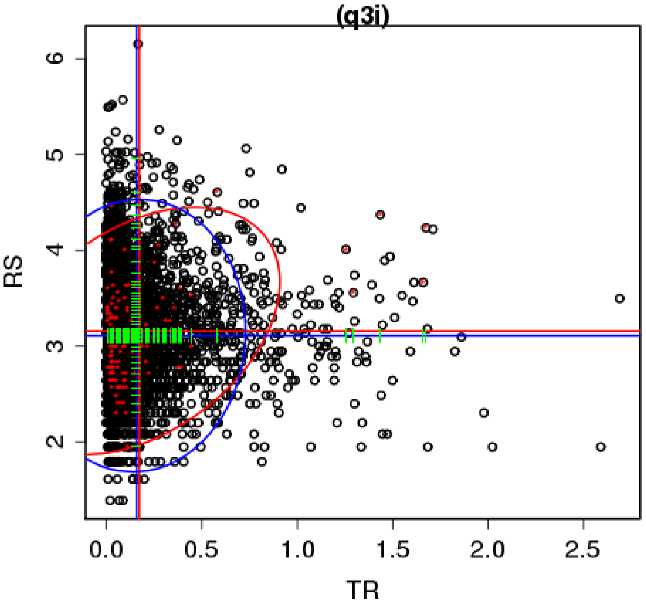

GO:0000070
mitotic sister chromatid segregation
(q3i)


GO:0006260
DNA replication
(q3i)

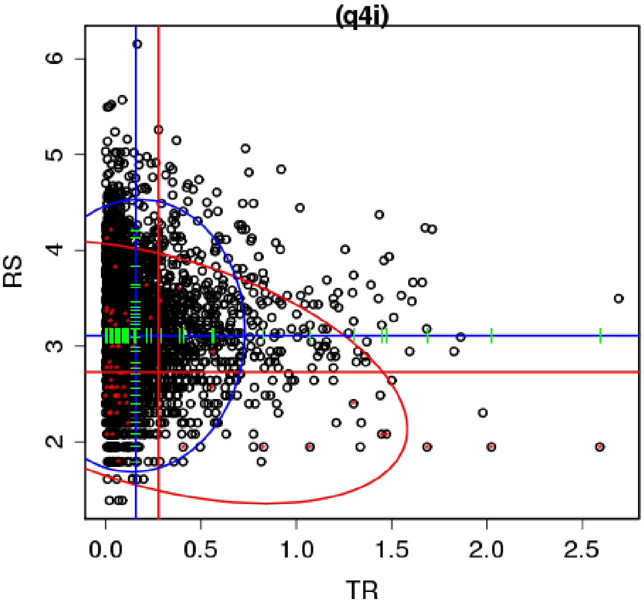

GO:0006261
DNA-dependent DNA replication
(q3i)


GO:0019725
cellular homeostasis
(q3i)

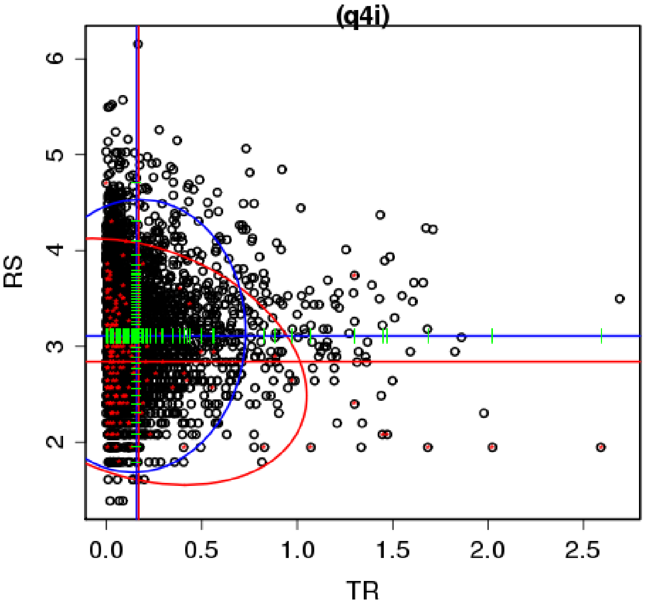
GO:0042592
homeostatic process
(q3i)



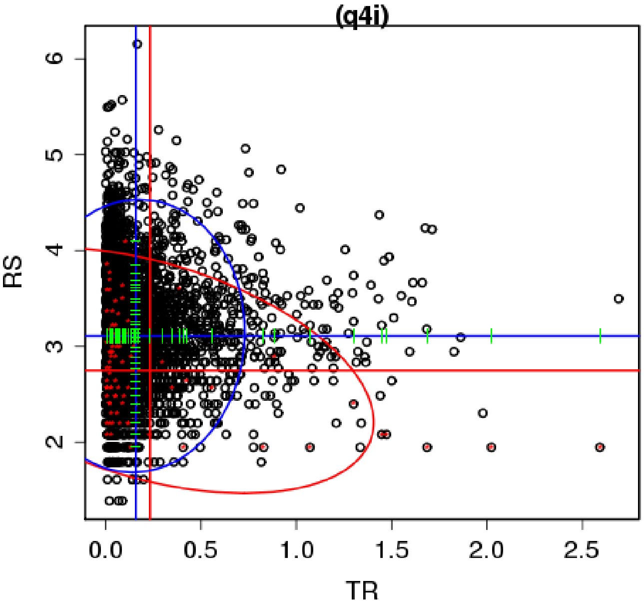
GO:0065004
protein-DNA complex assembly
(q4i)



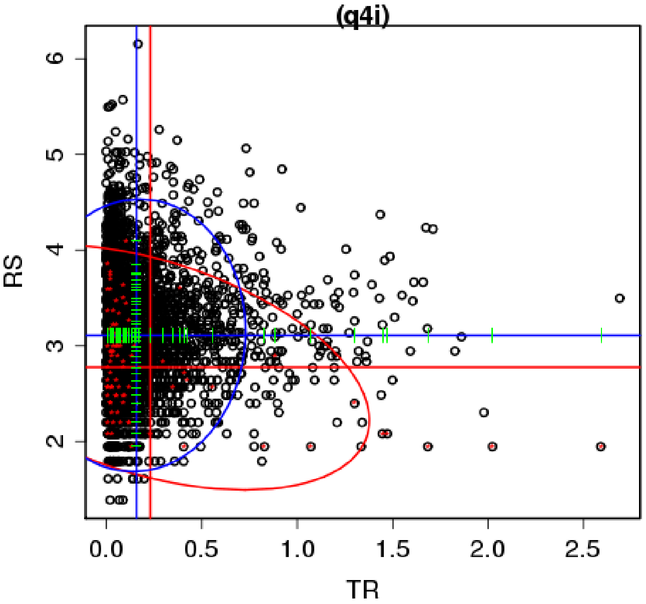
GO:0006325
establishment and/or maintenance of chromatin architec
(q4i)



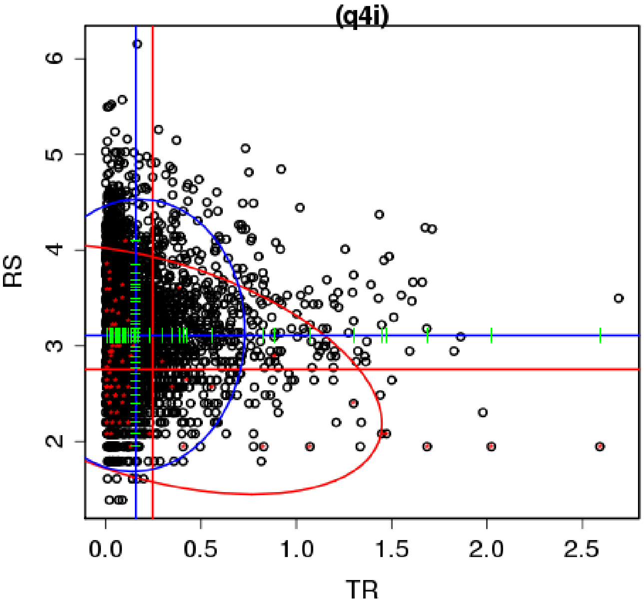
GO:0006323
DNA packaging
(q4i)



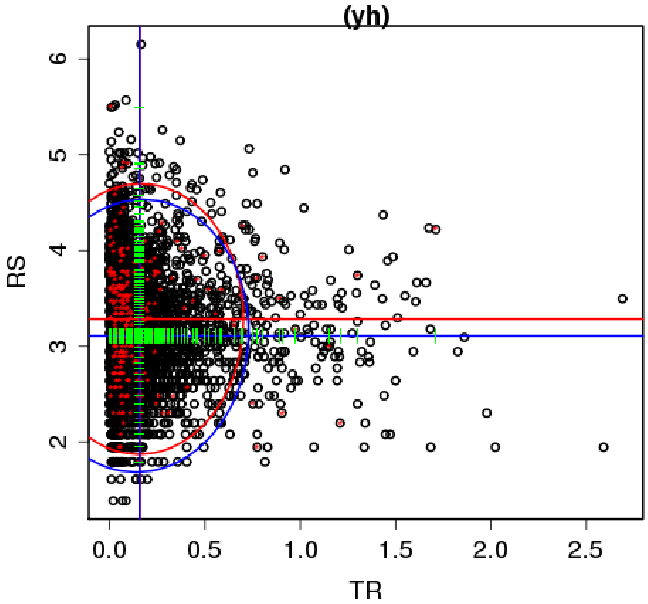
GO:0006333
chromatin assembly or disassembly
(q4i)



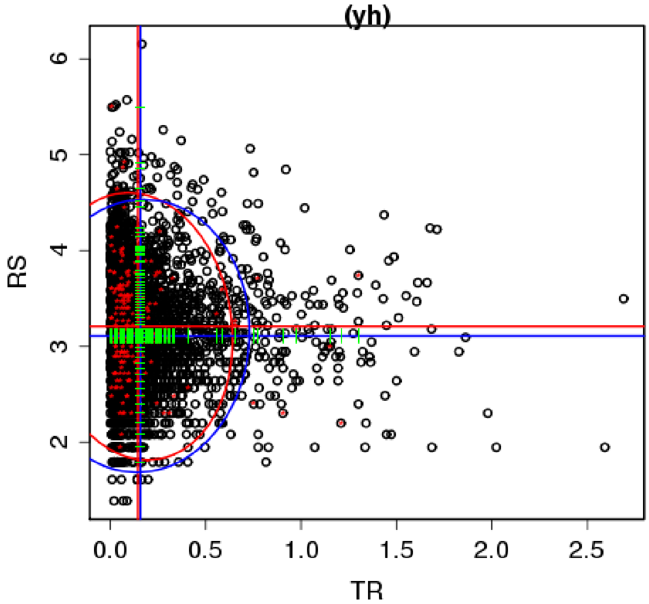
GO:0031497
chromatin assembly
(q4i)



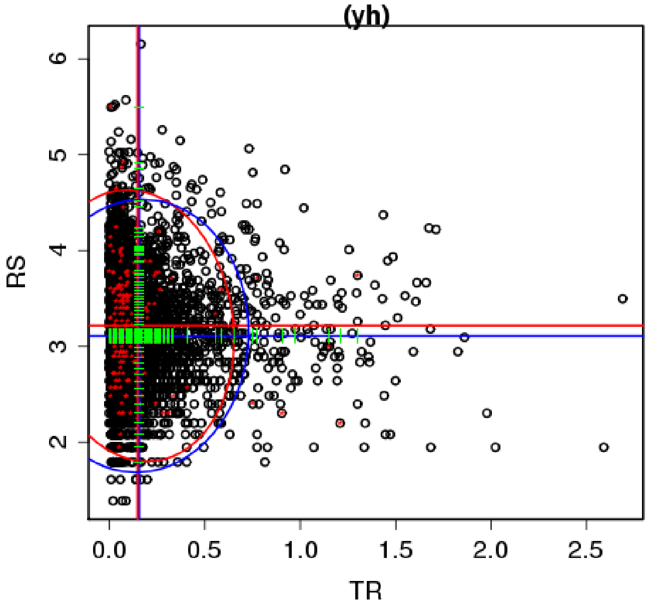
GO:0006082
organic acid metabolic process
(yh)



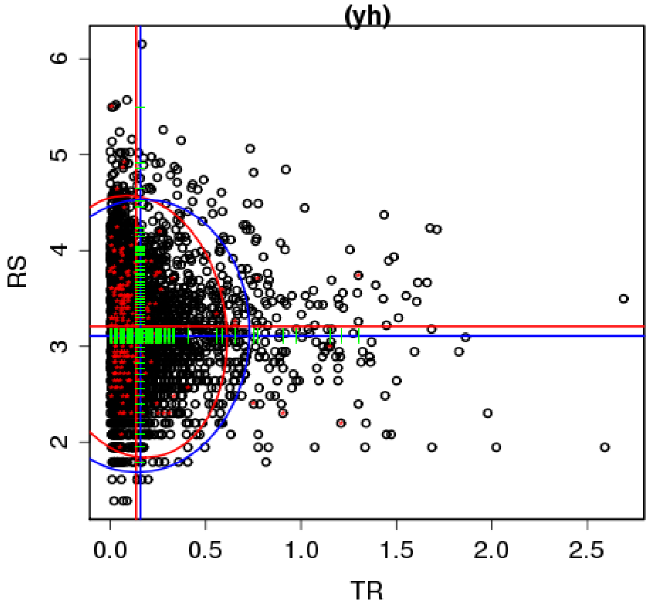
GO:0006519
amino acid and derivative metabolic process
(yh)



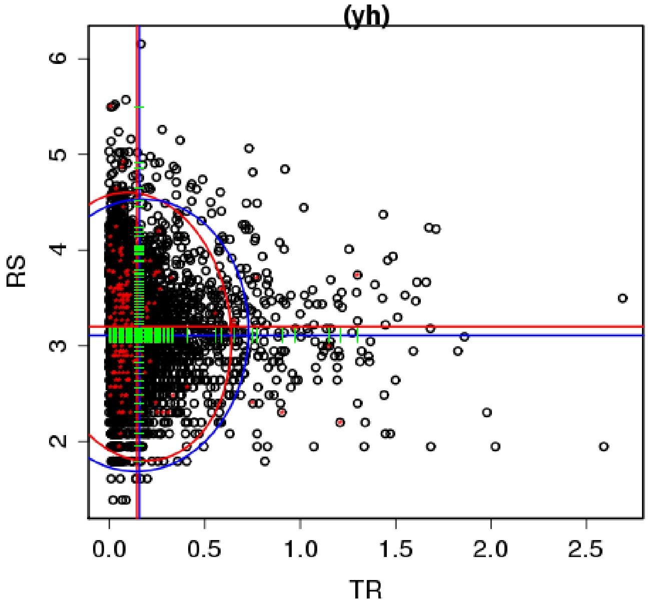
GO:0006520
amino acid metabolic process
(yh)



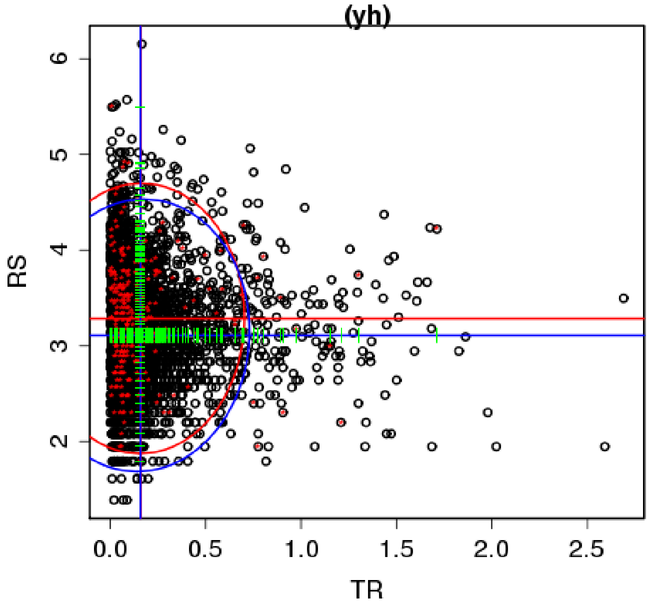
GO:0006807
nitrogen compound metabolic process
(yh)

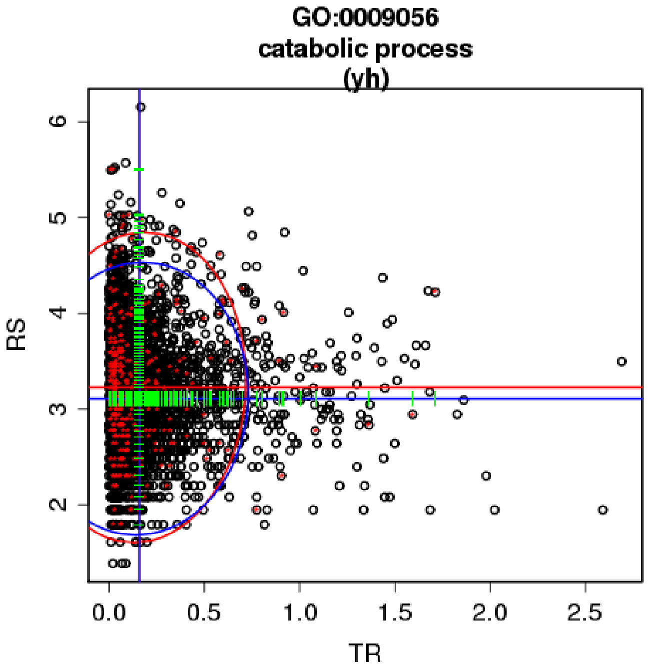


GO:0009308
amine metabolic process
(yh)

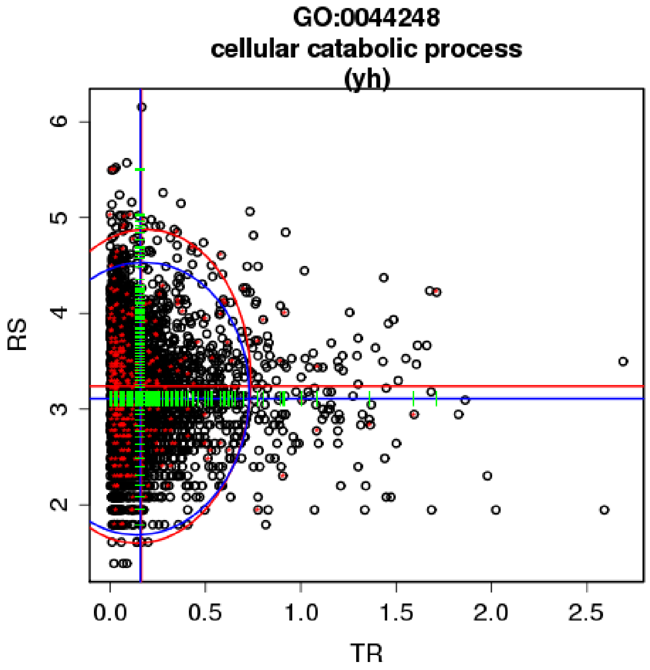


GO:0019752
carboxylic acid metabolic process
(yh)

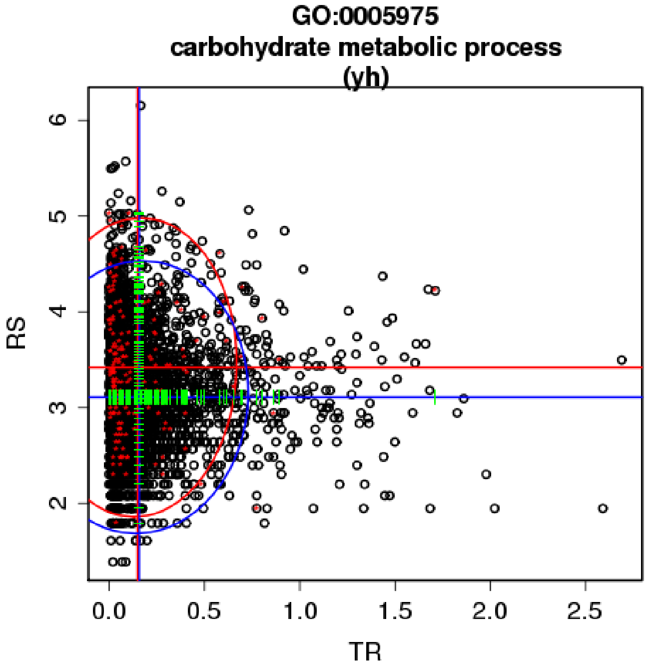




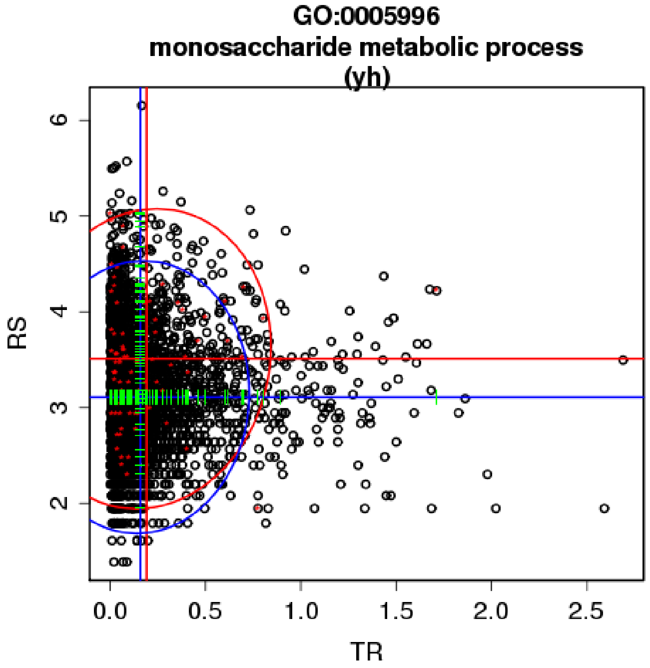
GO:0009056
catabolic process
(yh)



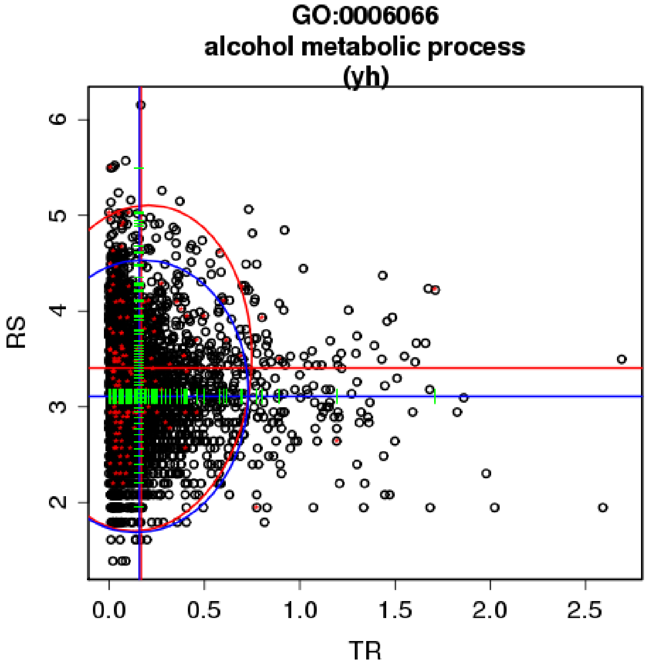
GO:0044248
cellular catabolic process
(yh)



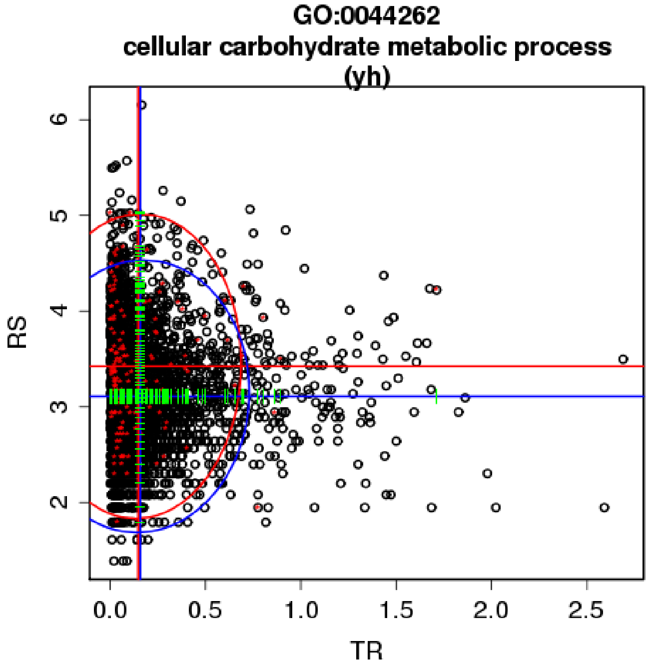
GO:0005975
carbohydrate metabolic process
(yh)



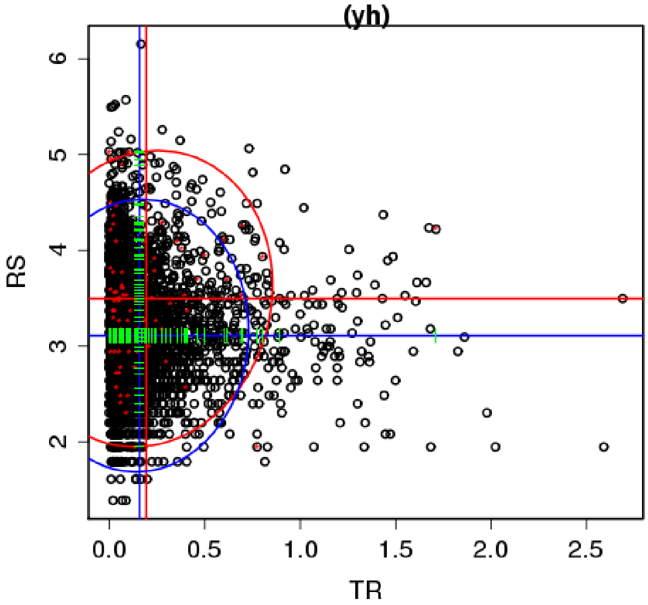
GO:0005996
monosaccharide metabolic process
(yh)



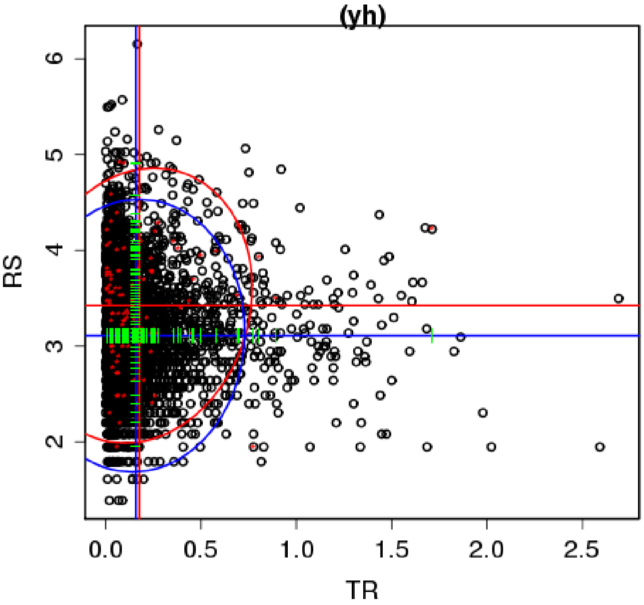
GO:0006066
alcohol metabolic process
(yh)



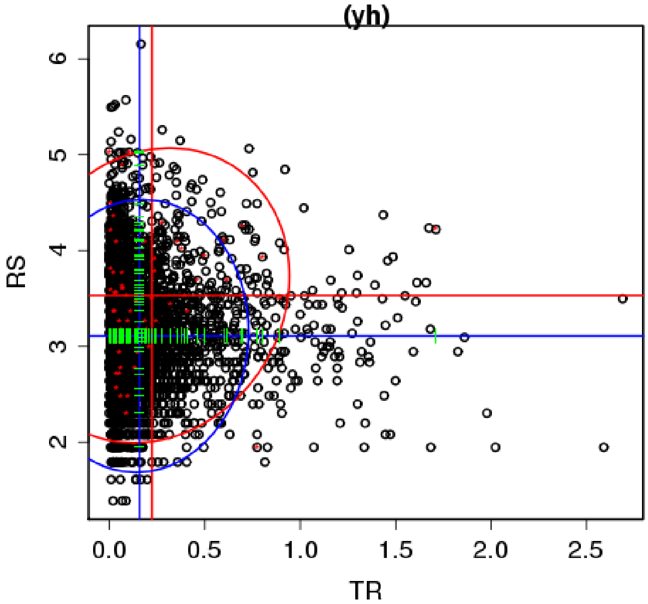
GO:0044262
cellular carbohydrate metabolic process
(yh)



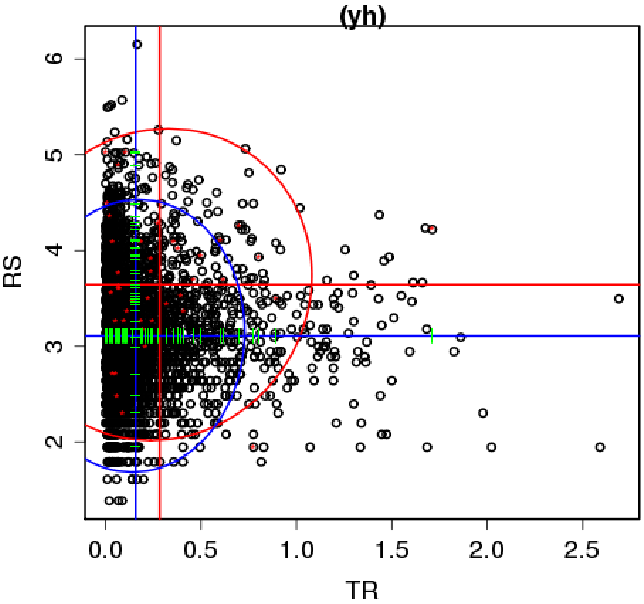
GO:0019318
hexose metabolic process
(yh)



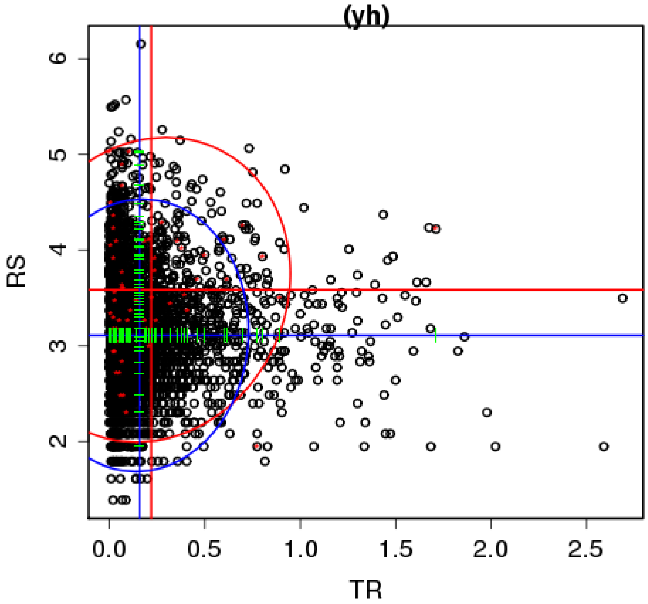
GO:0032787
monocarboxylic acid metabolic process
(yh)



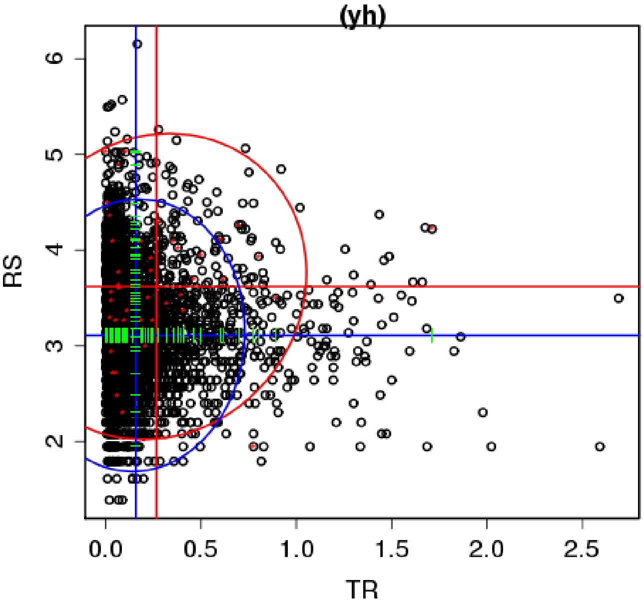
GO:0006006
glucose metabolic process
(yh)



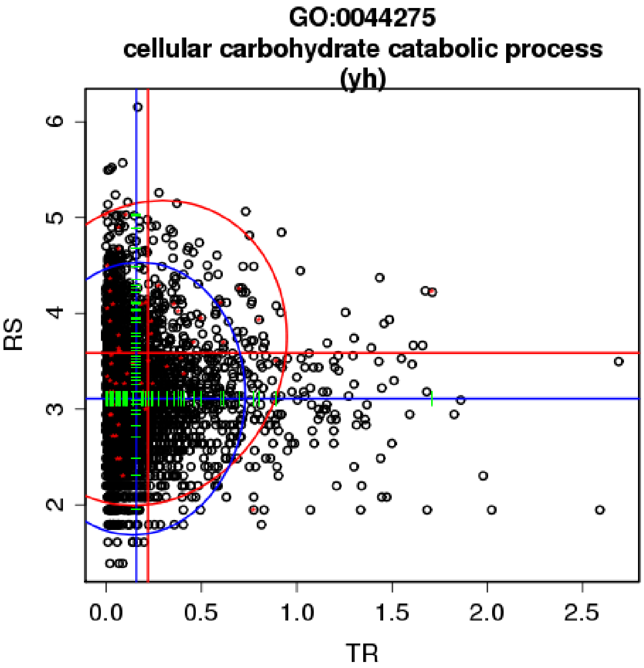
GO:0006007
glucose catabolic process
(yh)

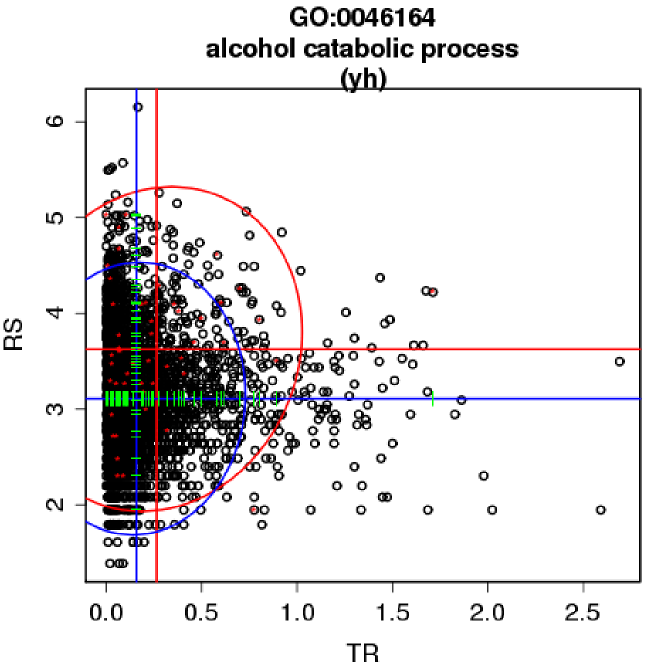


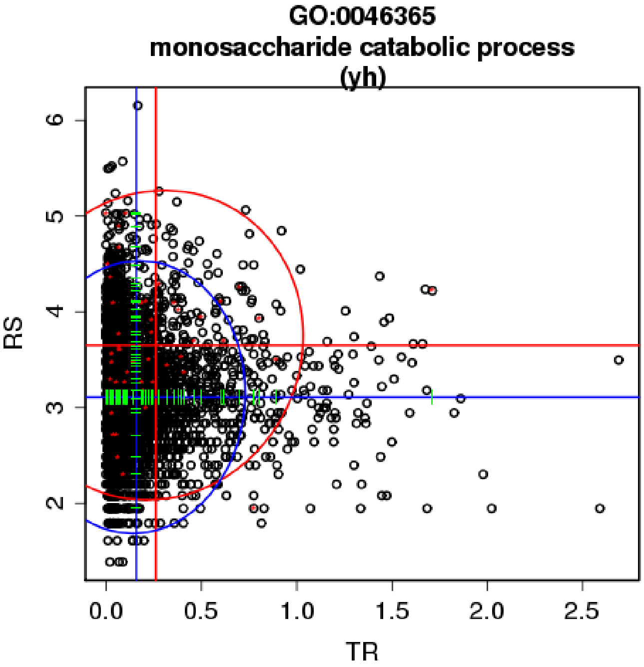
GO:0016052
carbohydrate catabolic process
(yh)

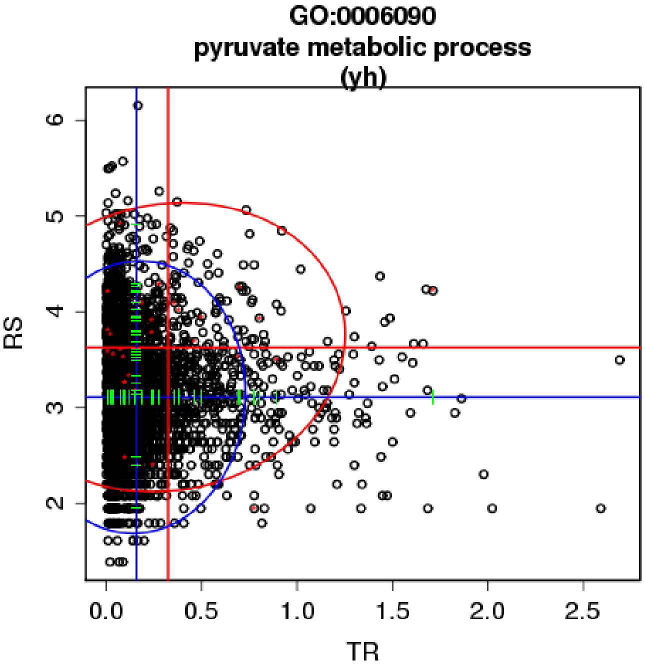


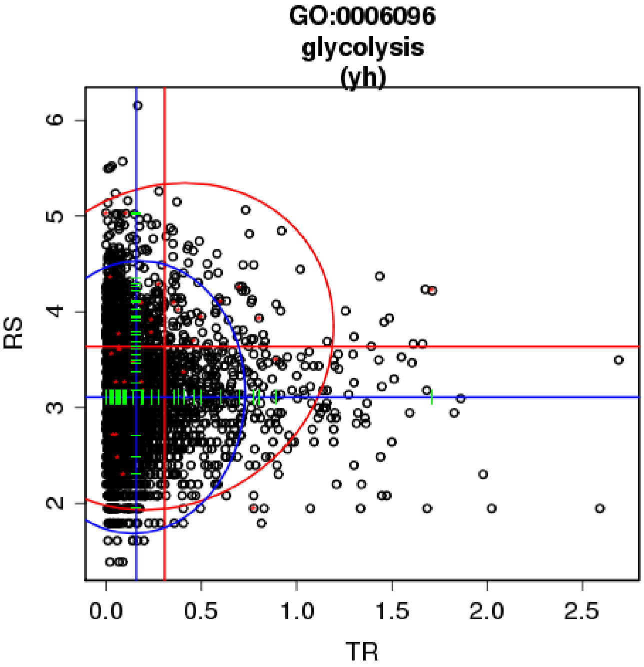
GO:0019320
hexose catabolic process
(yh)

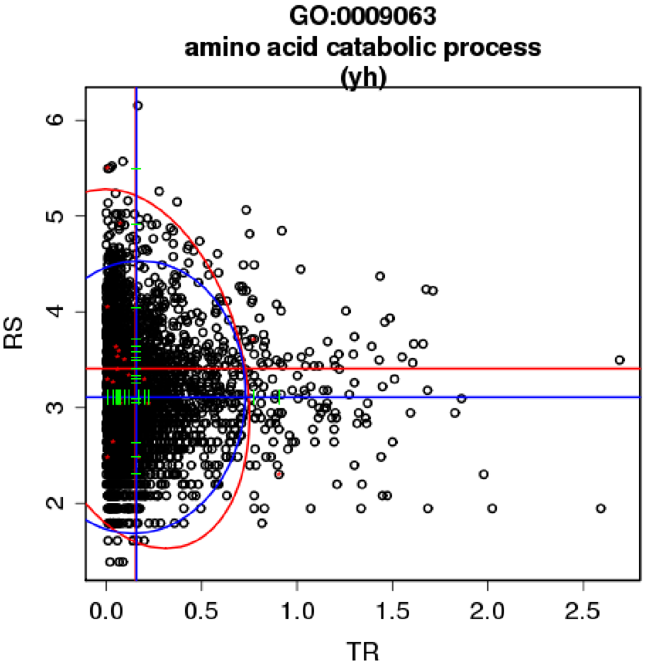

GO:0044275
cellular carbohydrate catabolic process
(yh)

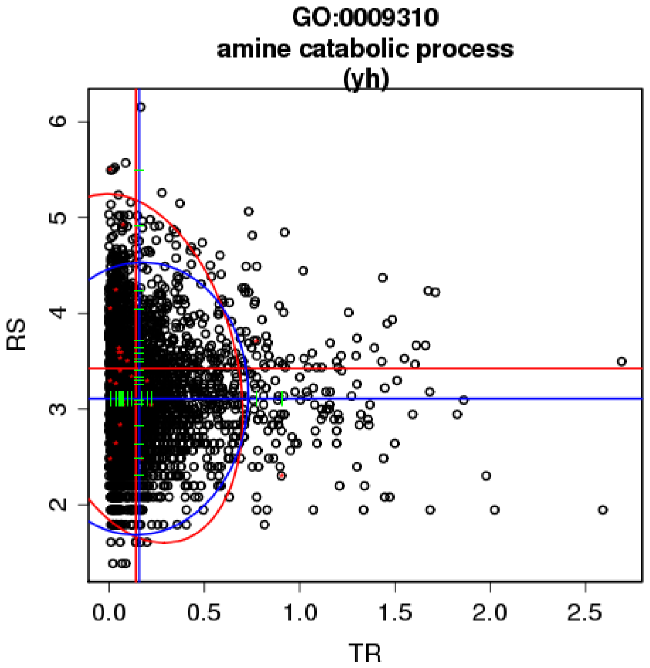

GO:0046164
alcohol catabolic process
(yh)

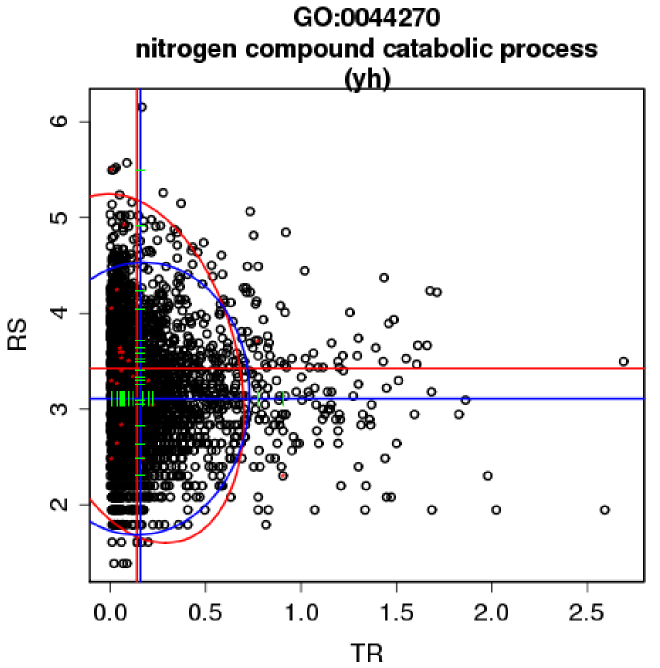

GO:0046365
monosaccharide catabolic process
(yh)

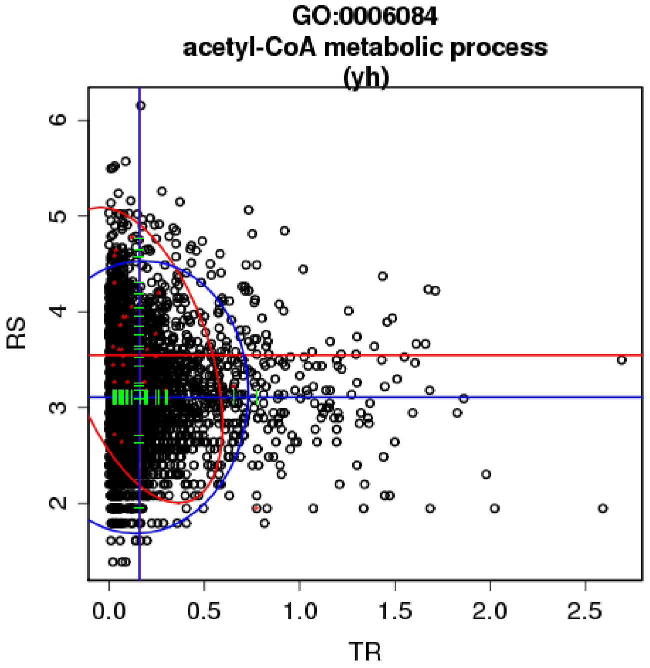

GO:0006090
pyruvate metabolic process
(yh)

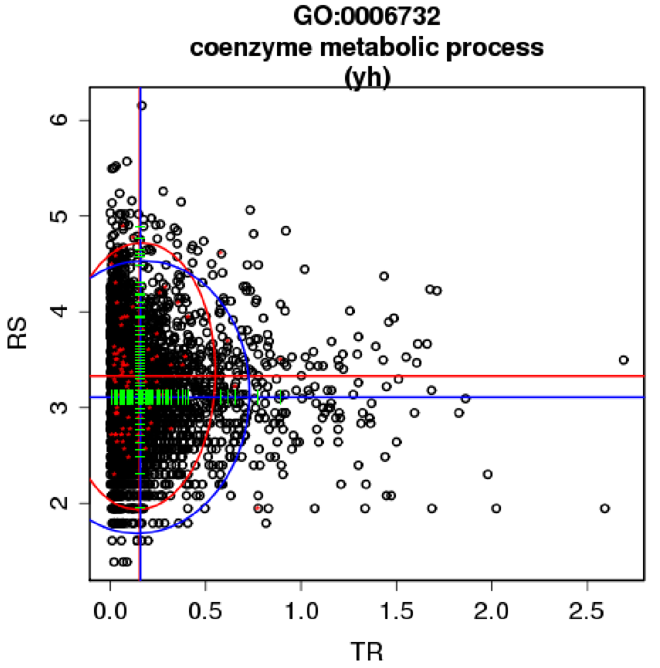

GO:0006096
glycolysis
(yh)

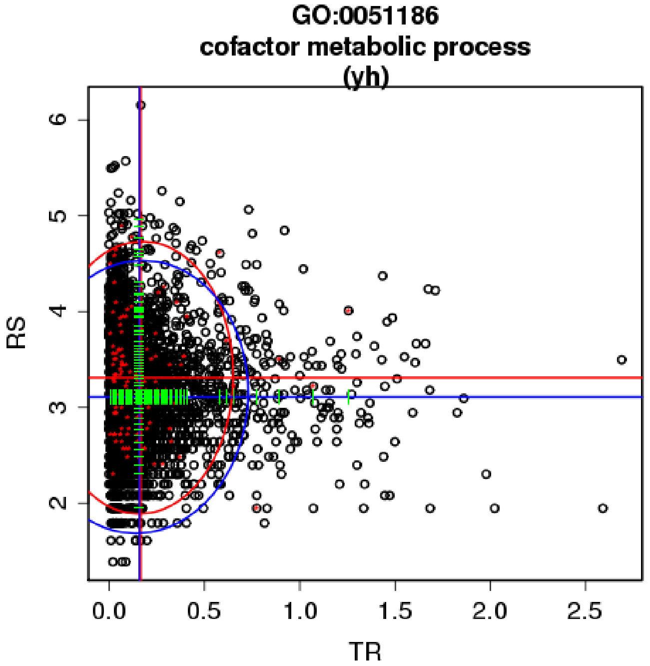

GO:0009063
amino acid catabolic process
(yh)

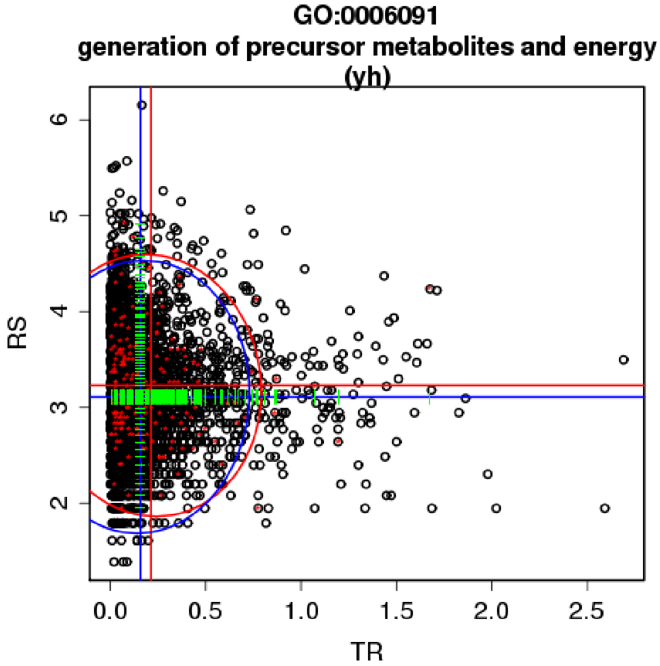

GO:0009310
amine catabolic process
(yh)


GO:0044270
nitrogen compound catabolic process
(yh)

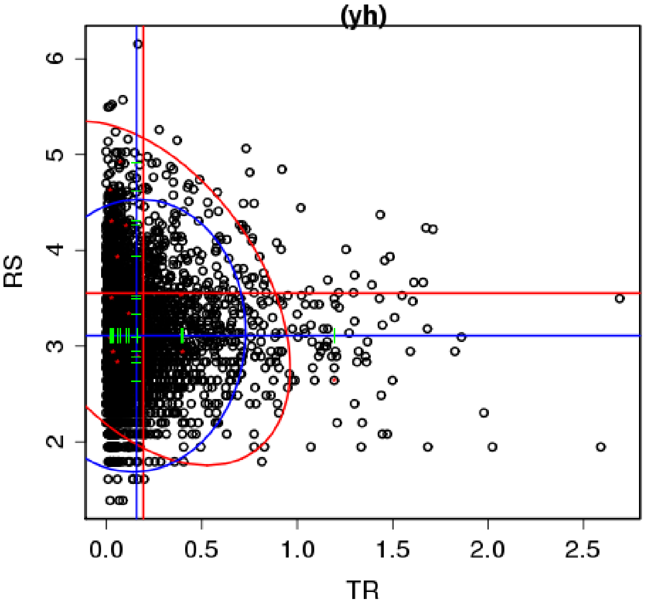

GO:0006084
acetyl-CoA metabolic process
(yh)


GO:0006732
coenzyme metabolic process
(yh)

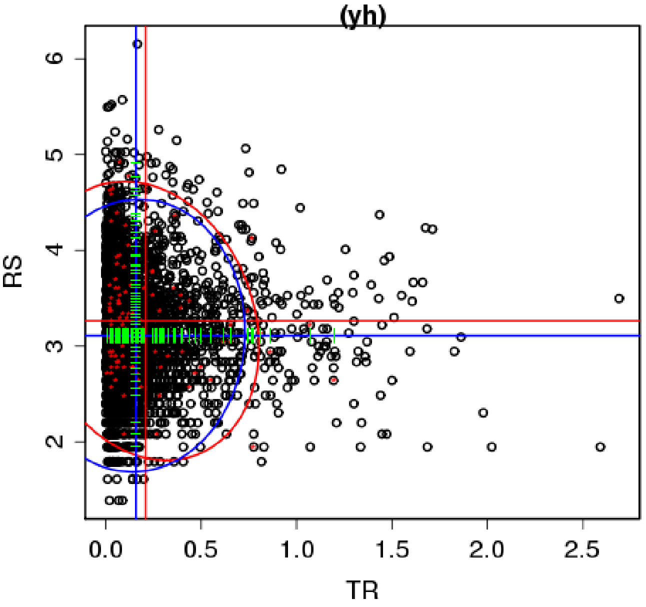

GO:0051186
cofactor metabolic process
(yh)


GO:0006091
generation of precursor metabolites and energy
(yh)

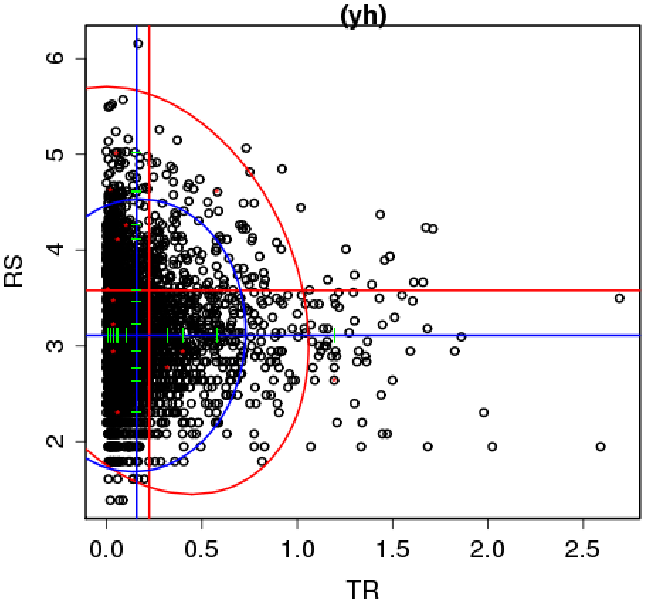
GO:0006113
fermentation
(yh)



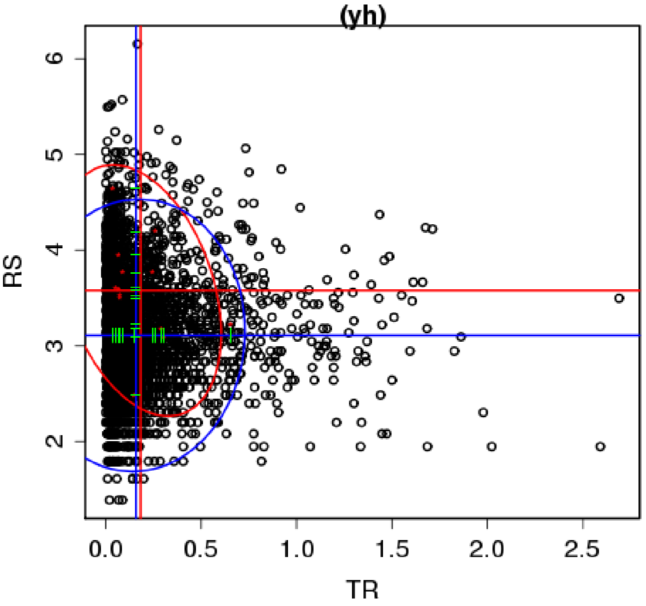
GO:0015980
energy derivation by oxidation of organic compounds
(yh)



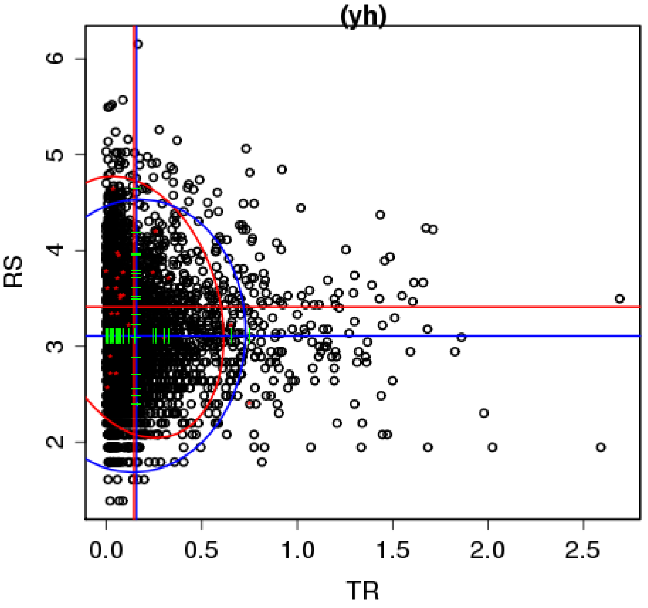
GO:0019751
polyol metabolic process
(yh)



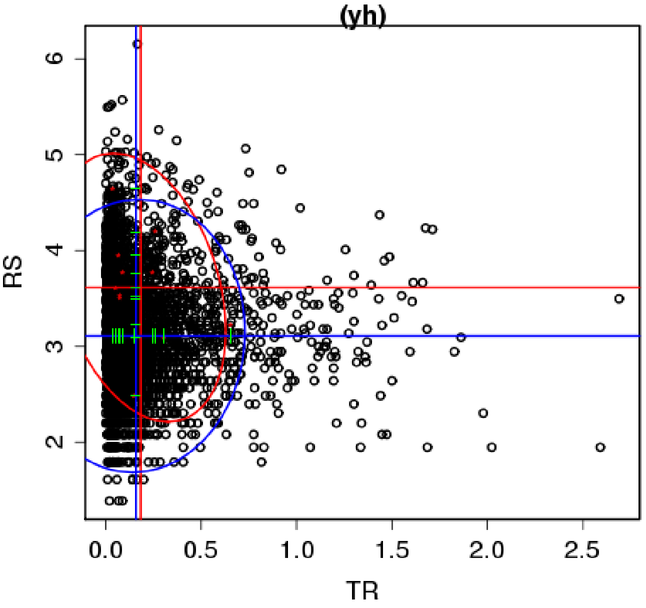
GO:0006536
glutamate metabolic process
(yh)

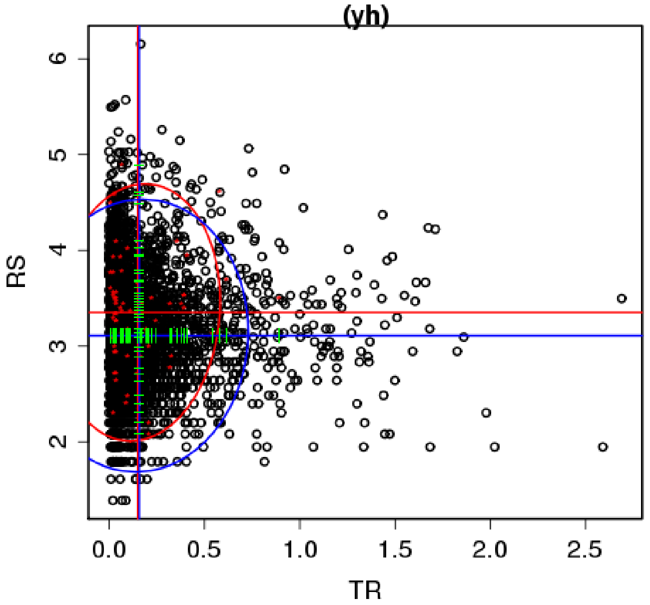


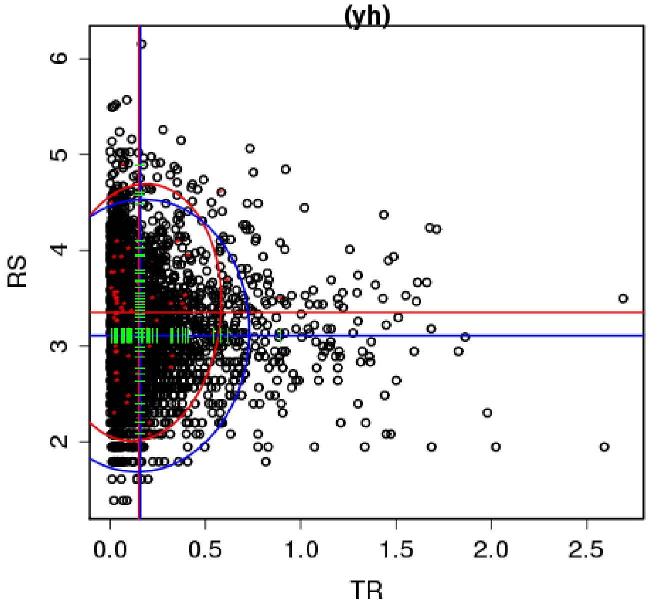
GO:0009084
glutamine family amino acid biosynthetic process
(yh)

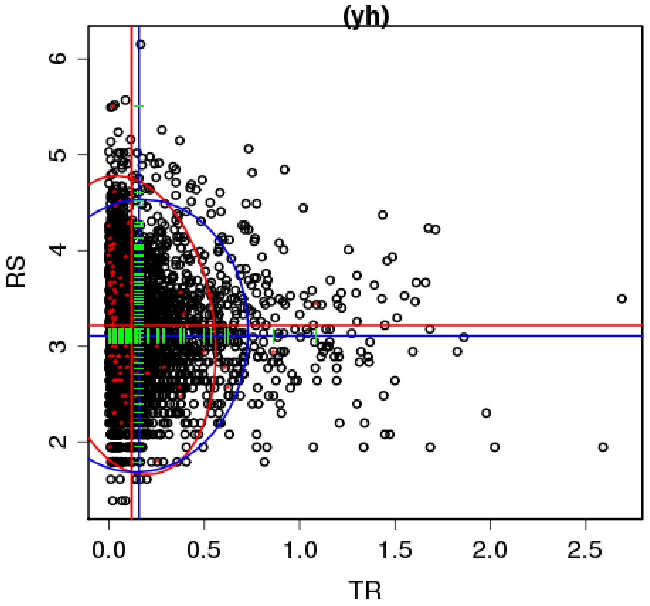


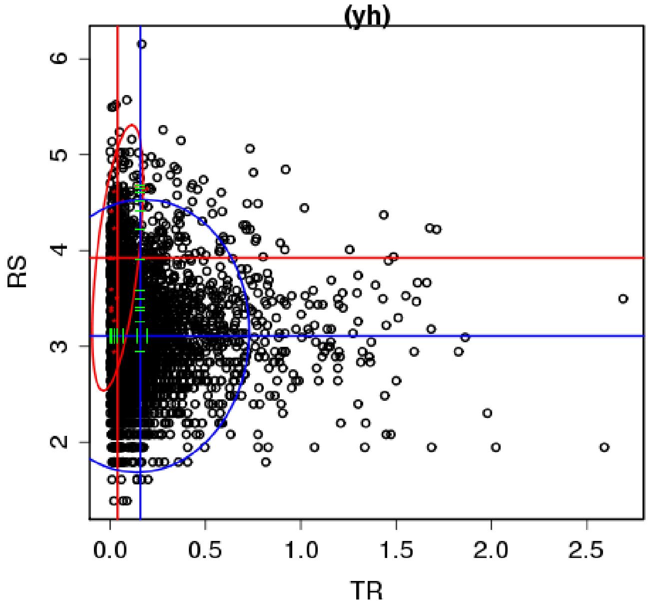
GO:0006537
glutamate biosynthetic process
(yh)

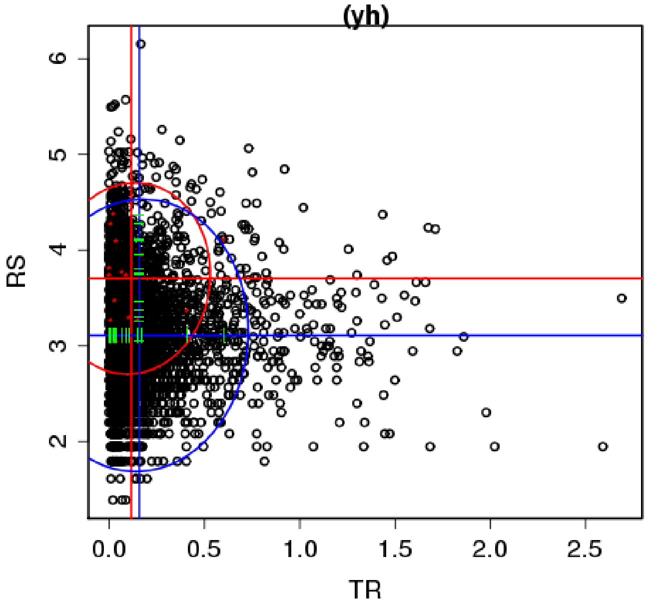


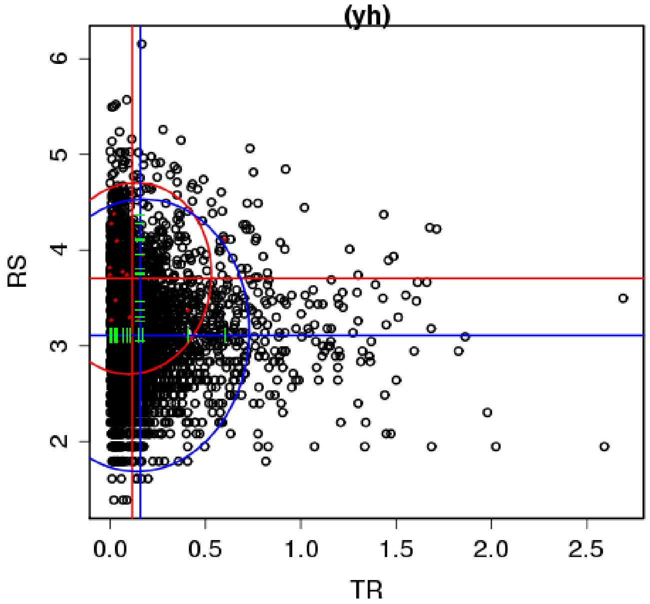

GO:0006766
vitamin metabolic process
(yh)

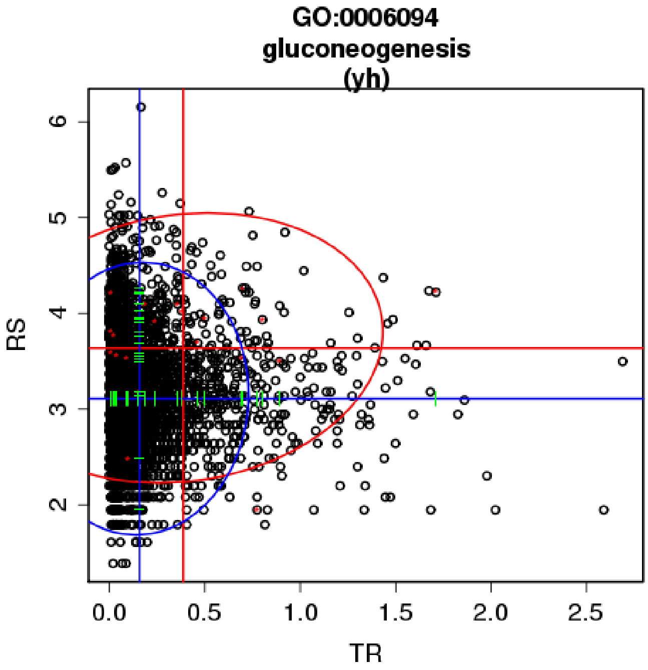

GO:0006767
water-soluble vitamin metabolic process
(yh)

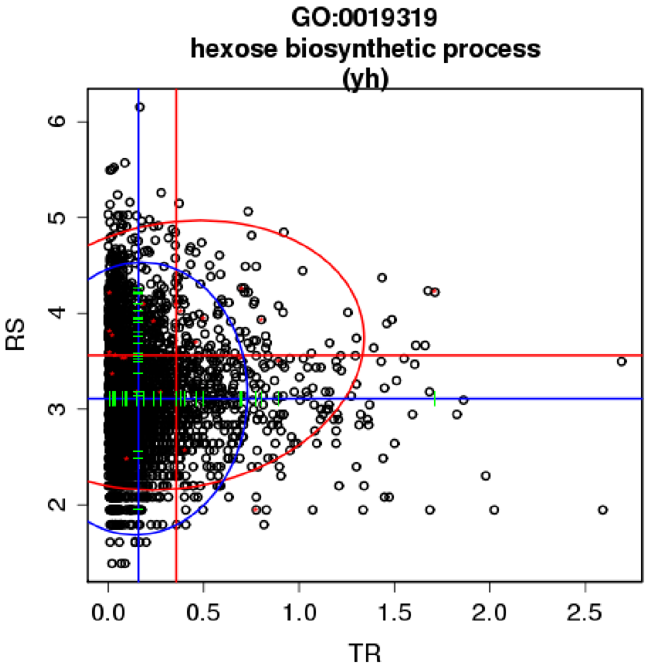

GO:0030435
sporulation
(yh)

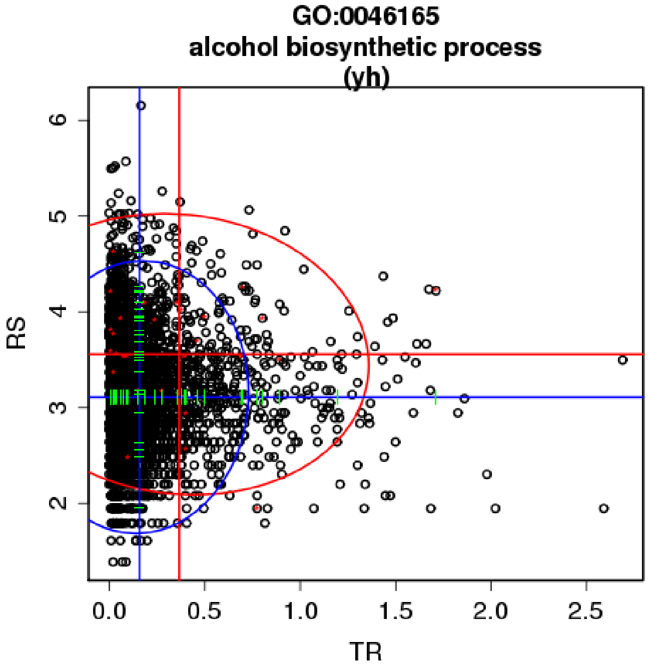

GO:0005984
disaccharide metabolic process
(yh)

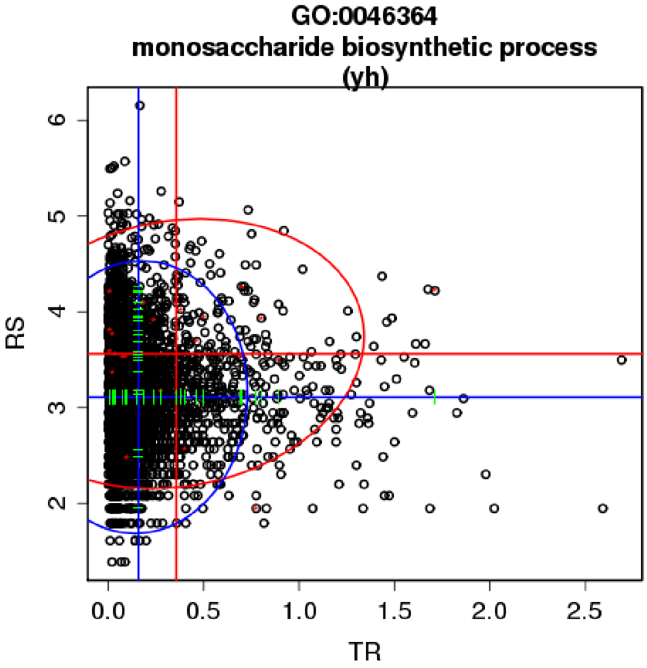

GO:0008645
hexose transport
(yh)

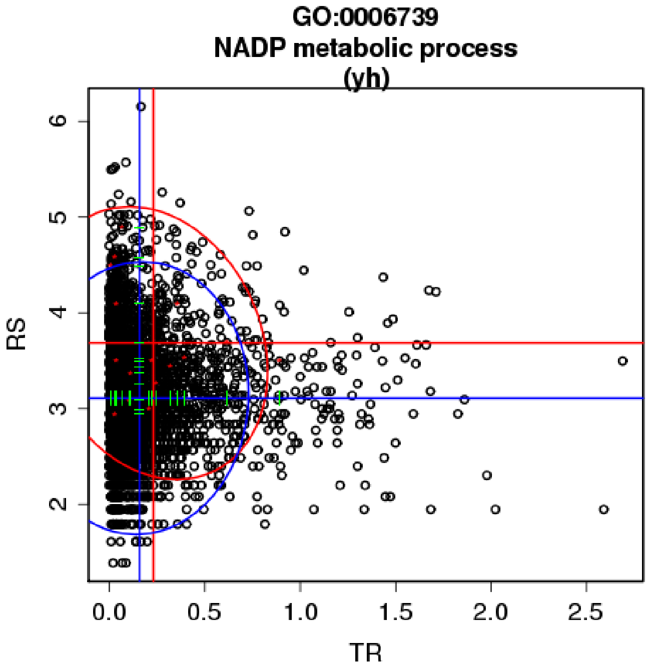

GO:0015749
monosaccharide transport
(yh)

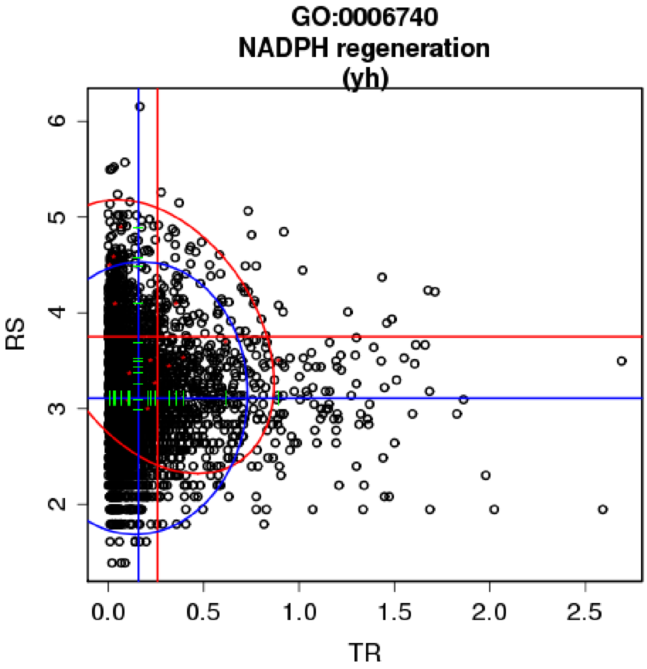

GO:0006094
gluconeogenesis
(yh)

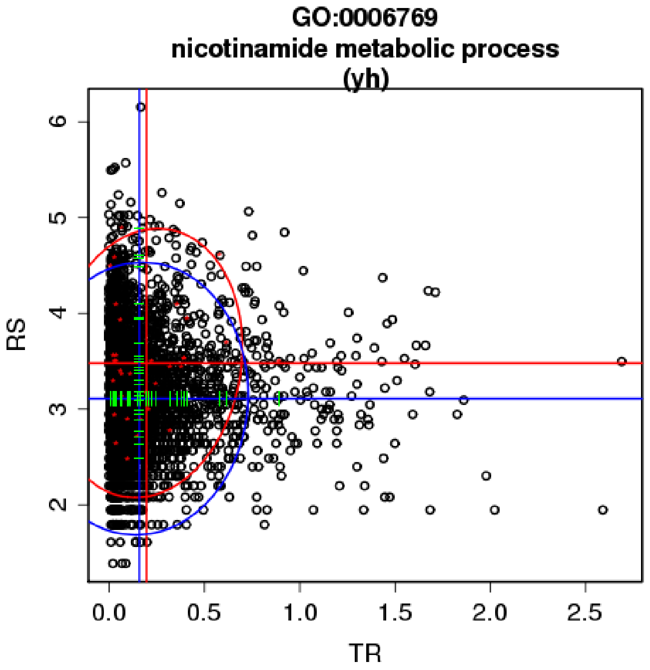

GO:0019319
hexose biosynthetic process
(yh)

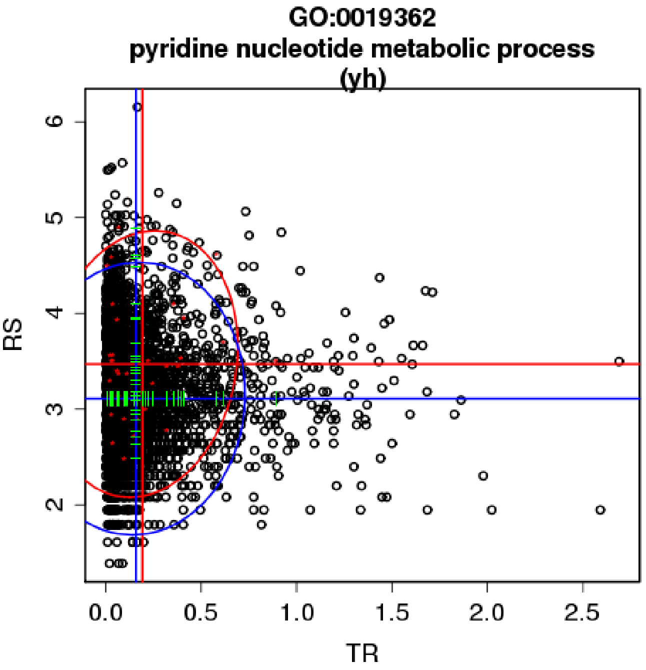

GO:0046165
alcohol biosynthetic process
(yh)

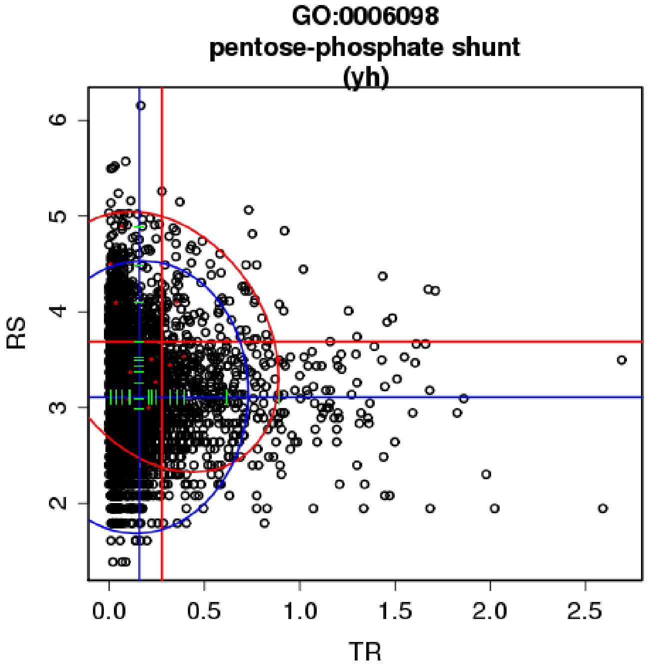

GO:0046364
monosaccharide biosynthetic process
(yh)

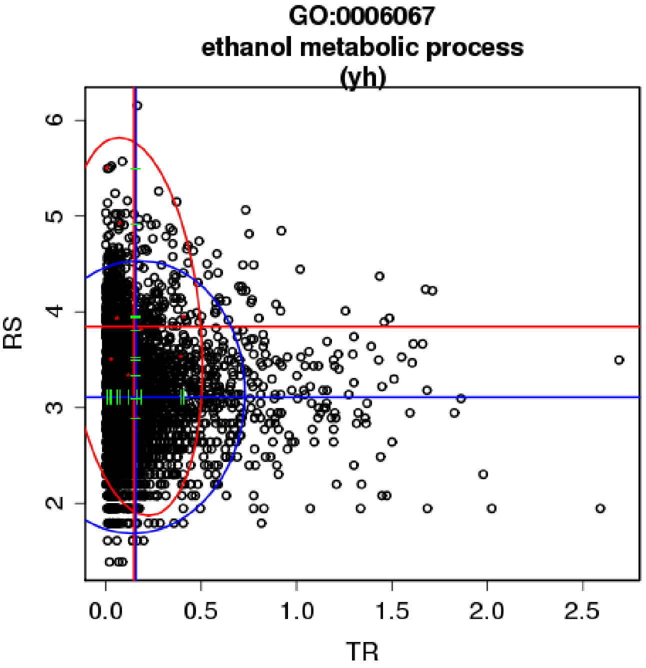

GO:0006739
NADP metabolic process
(yh)

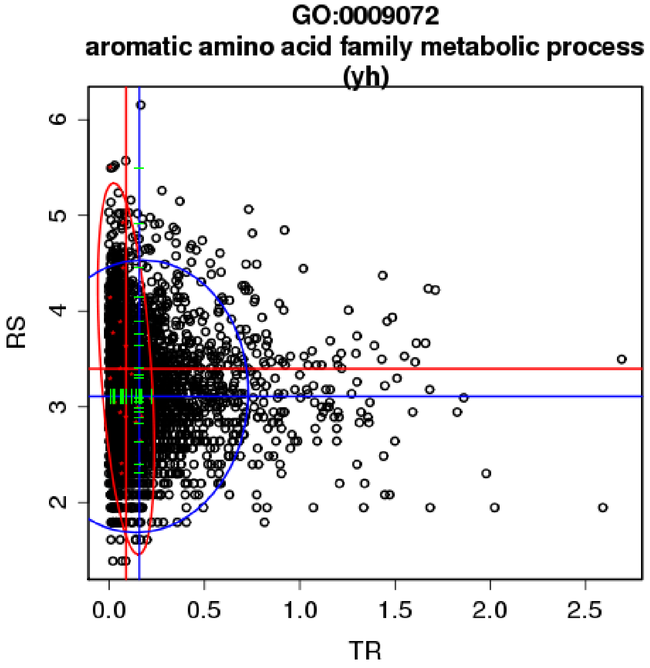

GO:0006740
NADPH regeneration
(yh)

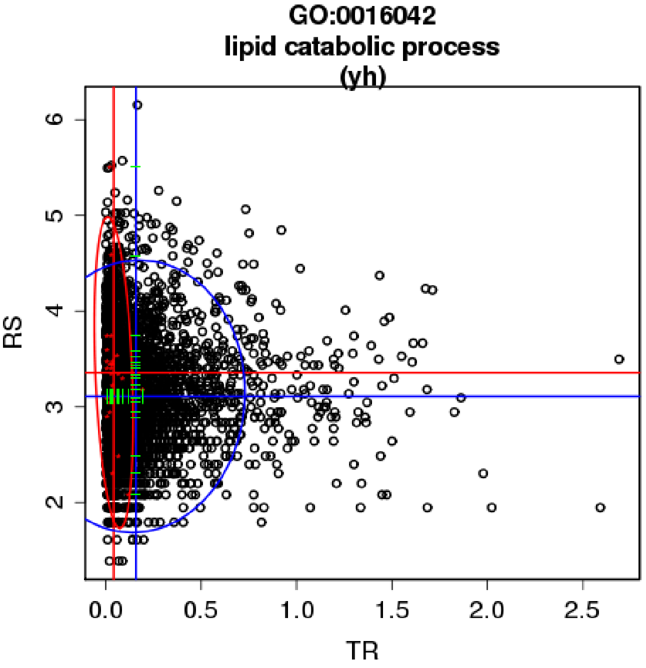

GO:0006769
nicotinamide metabolic process
(yh)

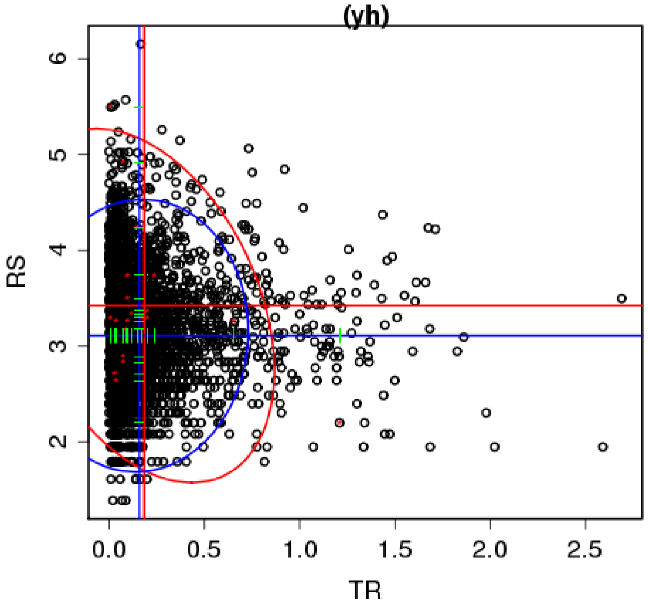

GO:0019362
pyridine nucleotide metabolic process
(yh)


GO:0006098
pentose-phosphate shunt
(yh)


GO:0006067
ethanol metabolic process
(yh)


GO:0009072
aromatic amino acid family metabolic process
(yh)


GO:0016042
lipid catabolic process
(yh)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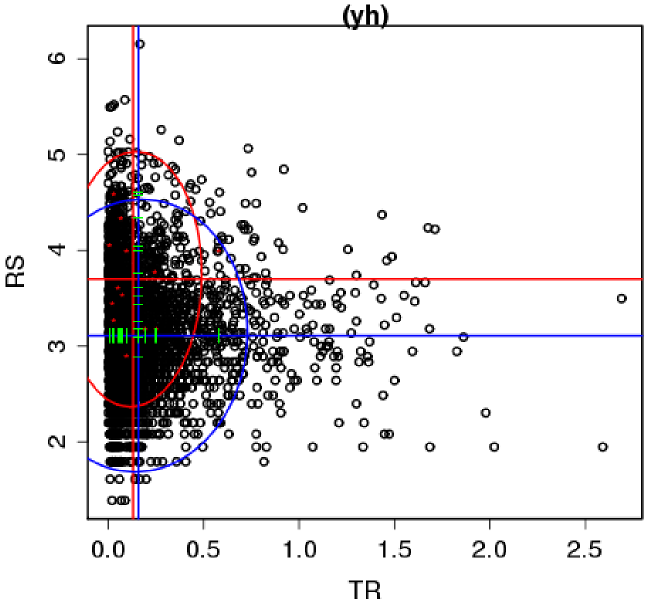
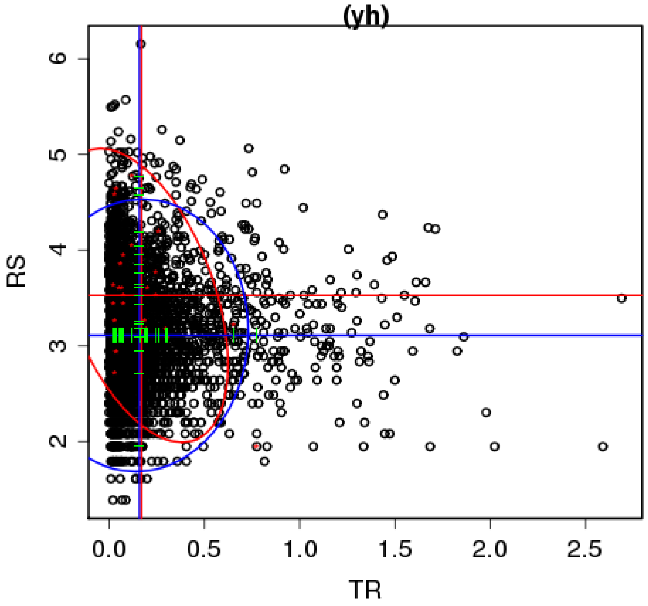
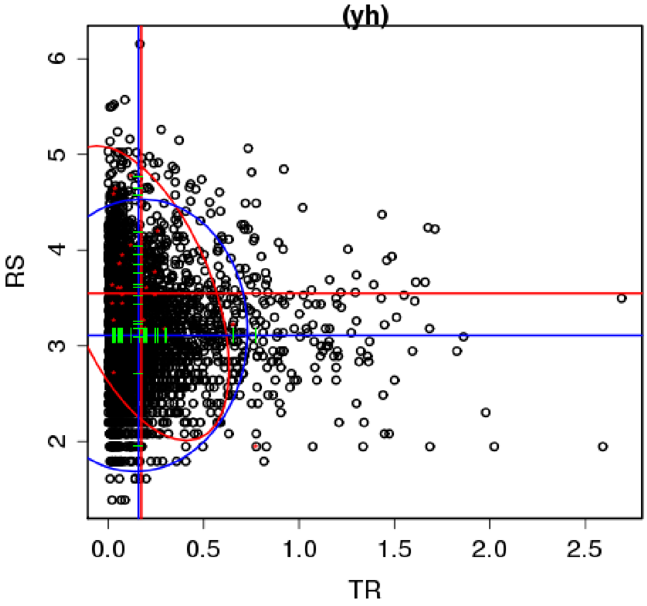
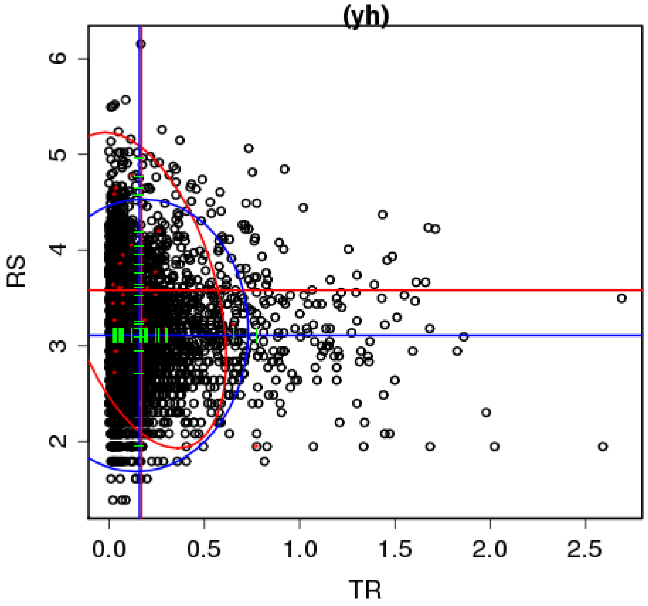
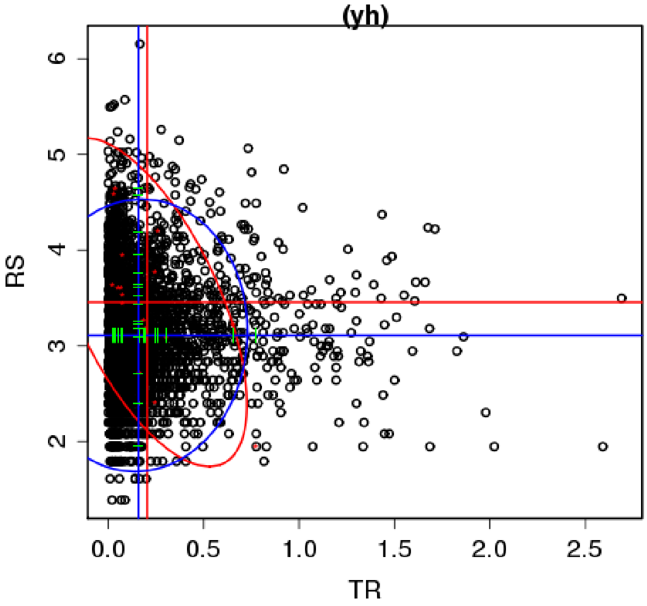
branched chain family amino acid metabolic process
(yh)


GO:0006081
aldehyde metabolic process
(yh)

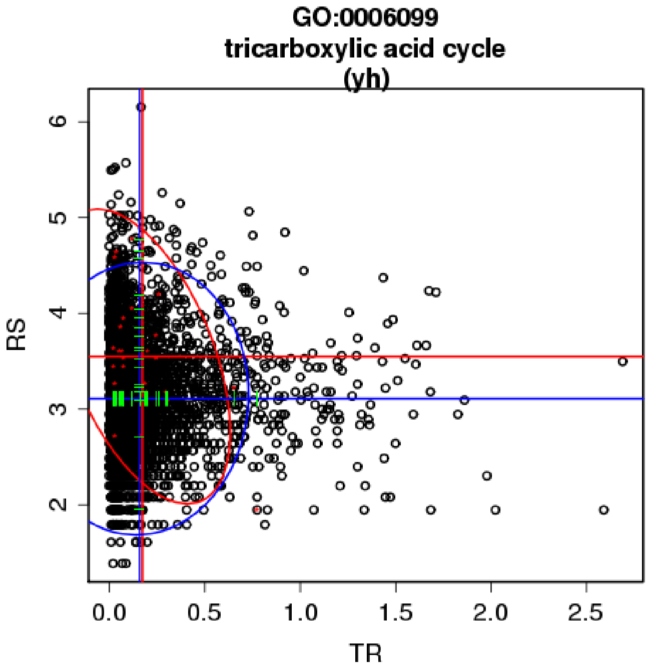

GO:0009109
coenzyme catabolic process
(yh)

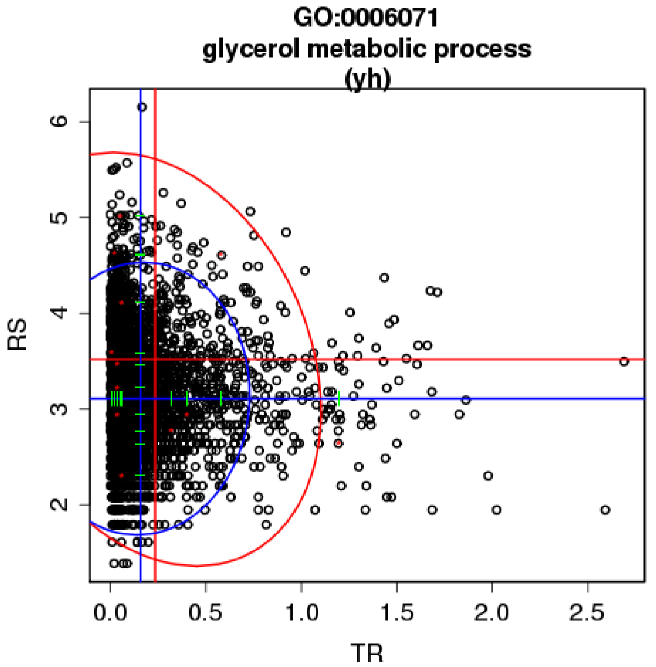

GO:0046356
acetyl-CoA catabolic process
(yh)

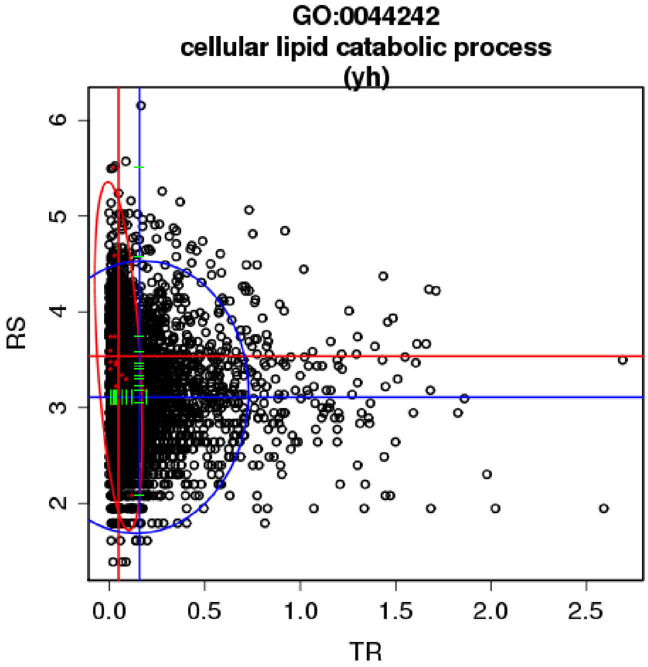

GO:0051187
cofactor catabolic process
(yh)

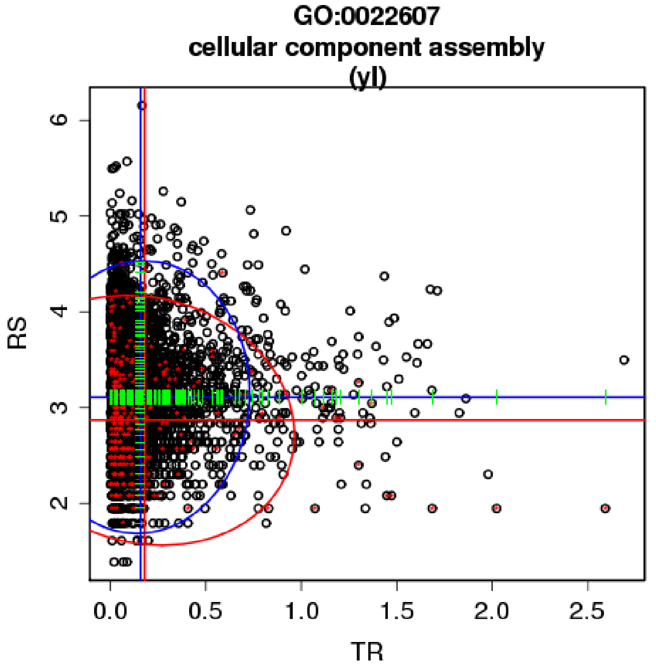

GO:0006100

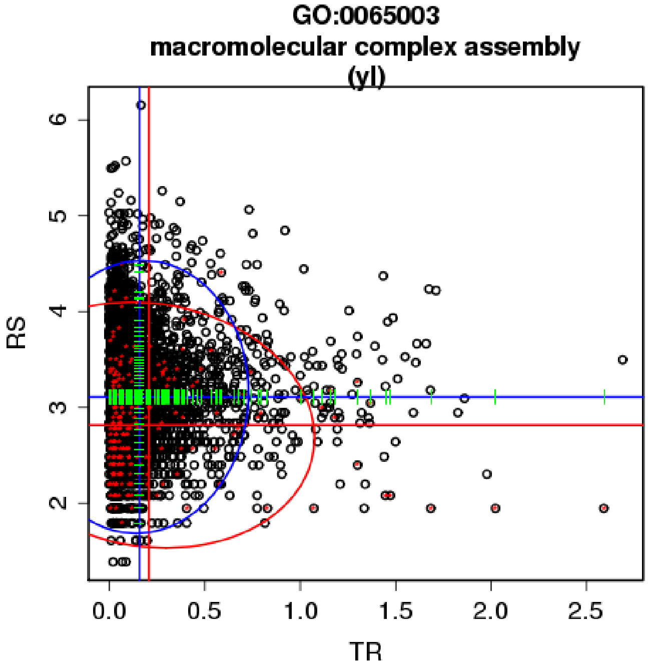
(yh)

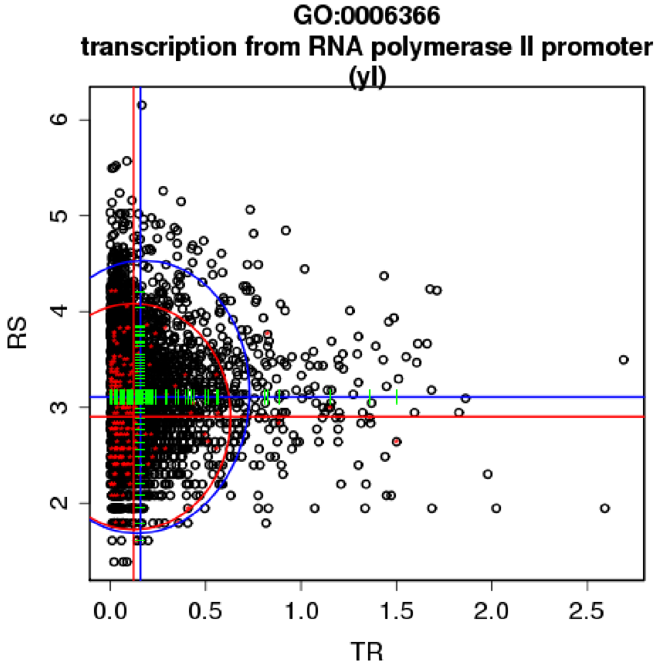

GO:0006099
tricarboxylic acid cycle
(yh)
RS
TR
6
5
4
3
2
0.0
0.5
1.0
1.5
2.0
2.5


GO:0006071
glycerol metabolic process
(yh)
RS
TR
6
5
4
3
2
0.0
0.5
1.0
1.5
2.0
2.5

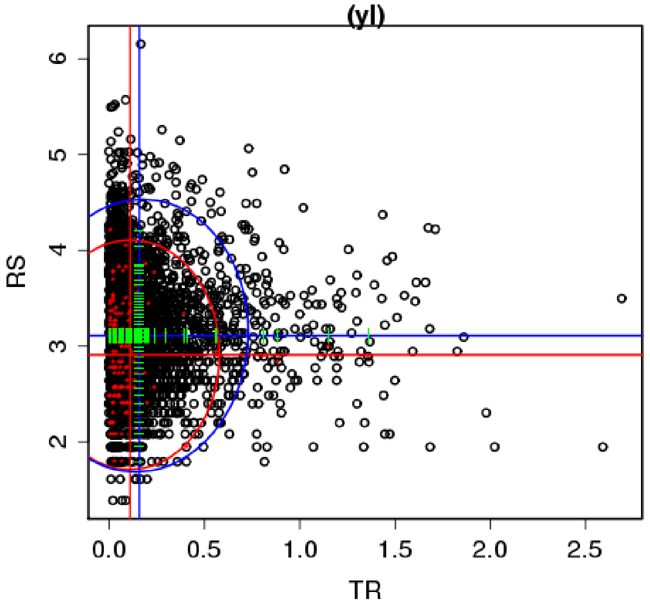

GO:0044242
cellular lipid catabolic process
(yh)
RS
TR
6
5
4
3
2
0.0
0.5
1.0
1.5
2.0
2.5


GO:0022607
cellular component assembly
(yl)
RS
TR
6
5
4
3
2
0.0
0.5
1.0
1.5
2.0
2.5

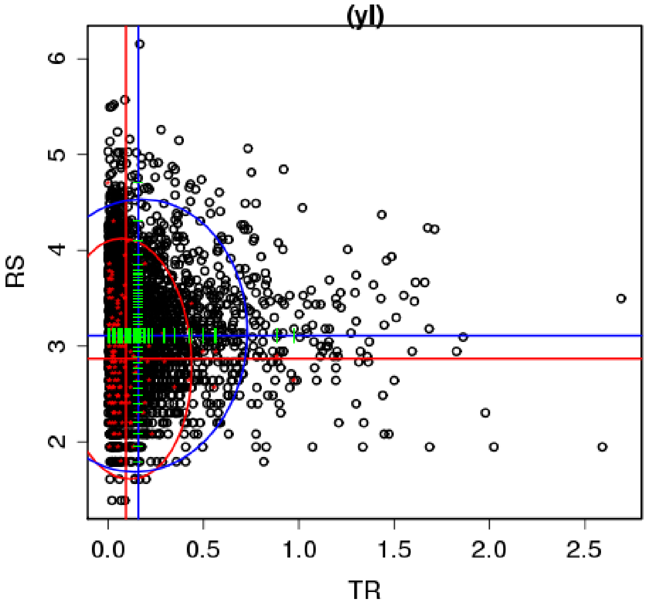

GO:0065003
macromolecular complex assembly
(yl)
RS
TR
6
5
4
3
2
0.0
0.5
1.0
1.5
2.0
2.5


GO:0006366
transcription from RNA polymerase II promoter
(yl)
RS
TR
6
5
4
3
2
0.0
0.5
1.0
1.5
2.0
2.5

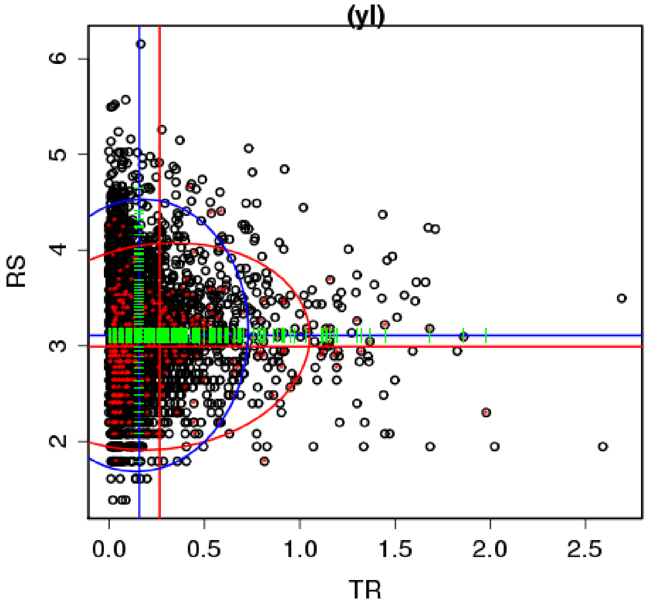
GO:0006357
egulation of transcription from RNA polymerase II prom
(yl)



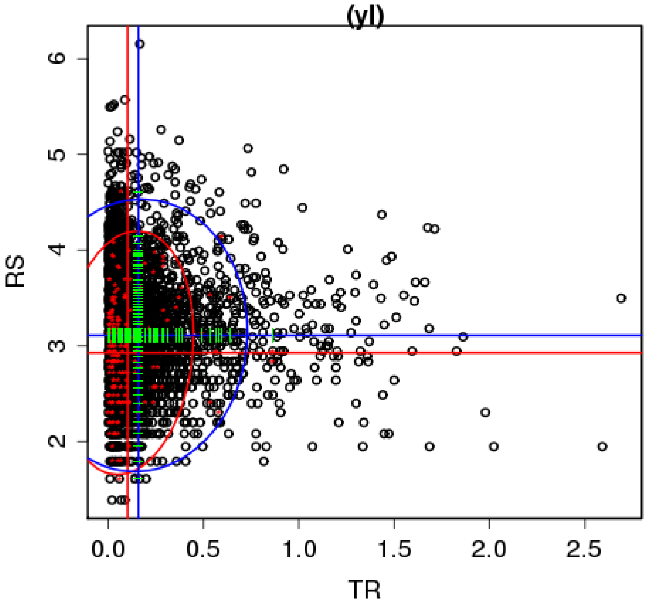
GO:0016568
chromatin modification
(yl)



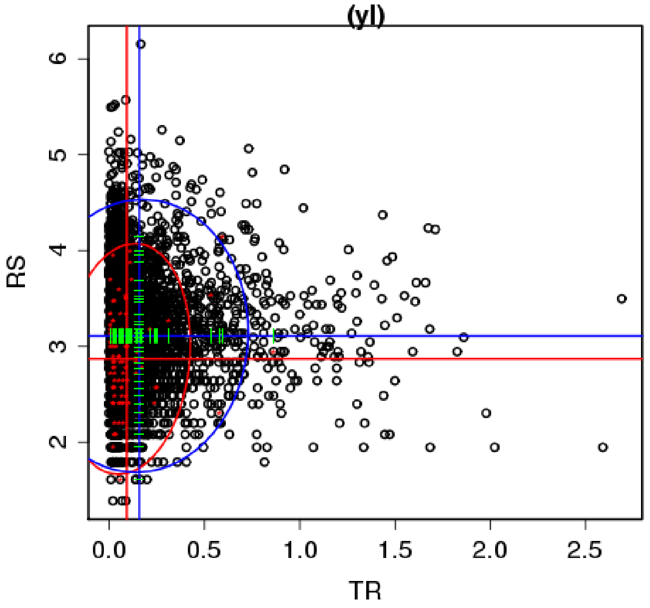
GO:0009059
macromolecule biosynthetic process
(yl)



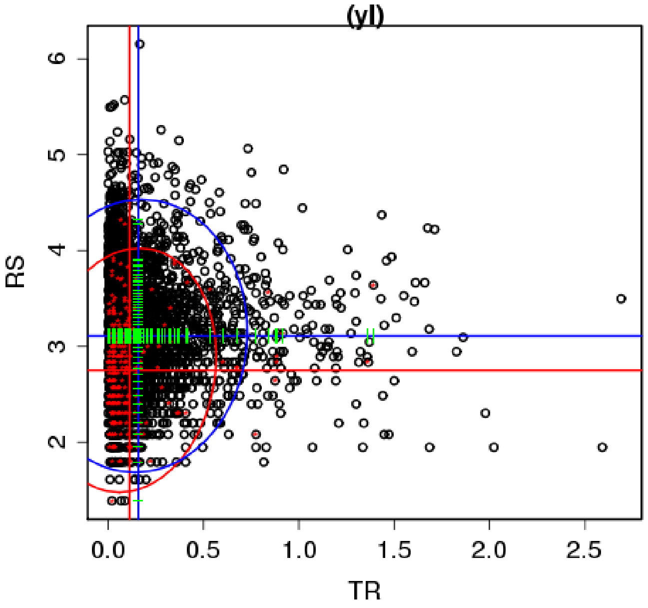
GO:0000278
mitotic cell cycle
(yl)

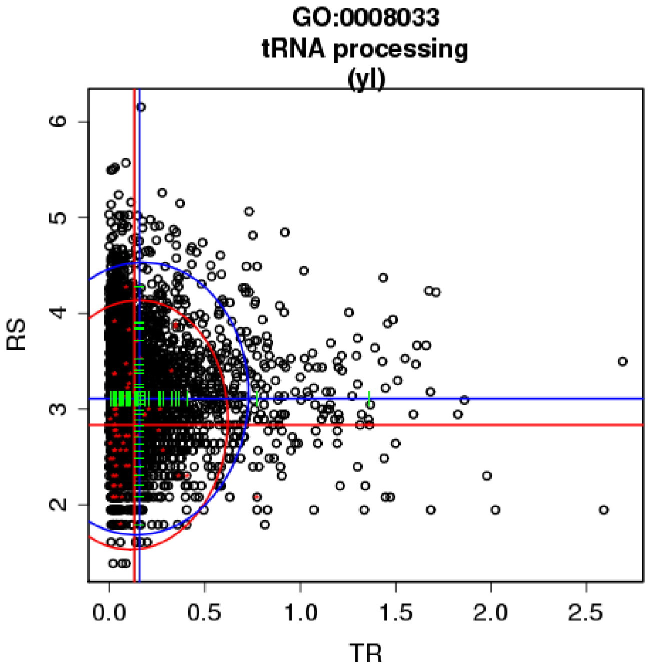


GO:0051726
regulation of cell cycle
(yl)

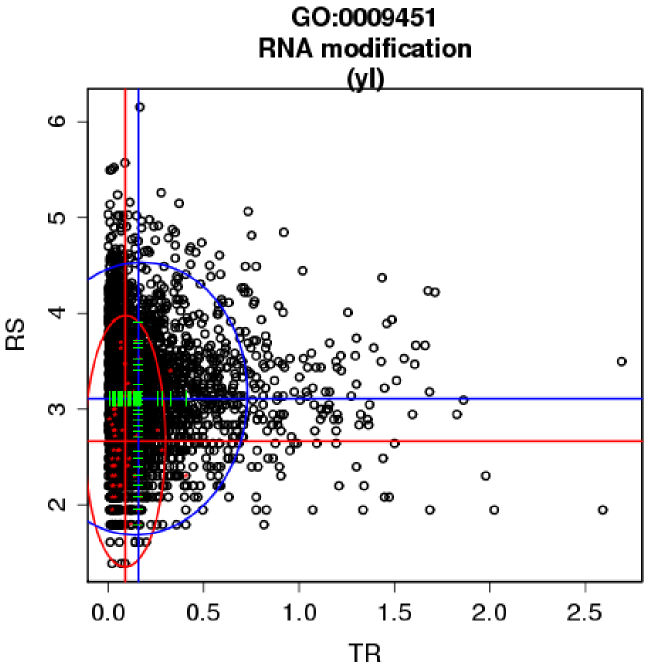


GO:0006396
RNA processing
(yl)

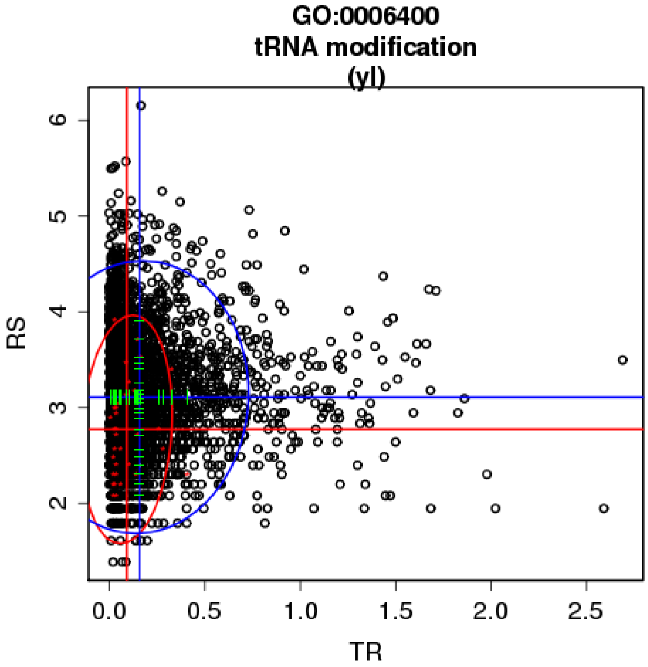




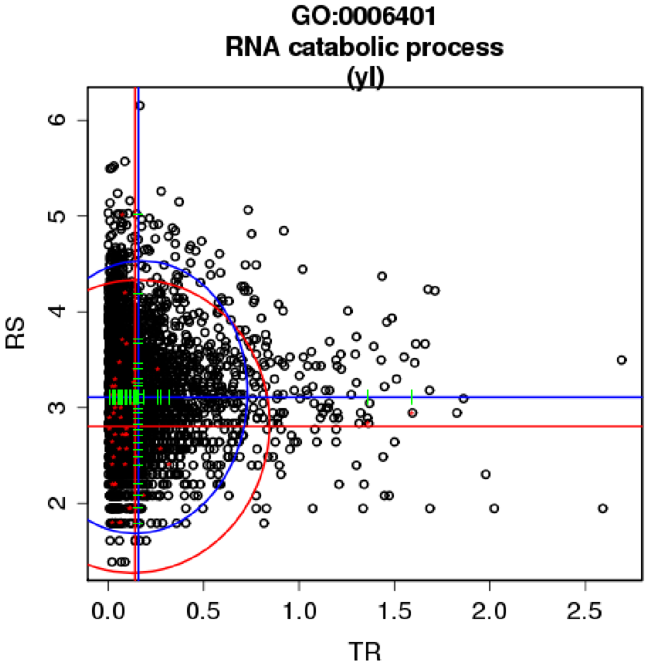
GO:0008033
tRNA processing
(yl)



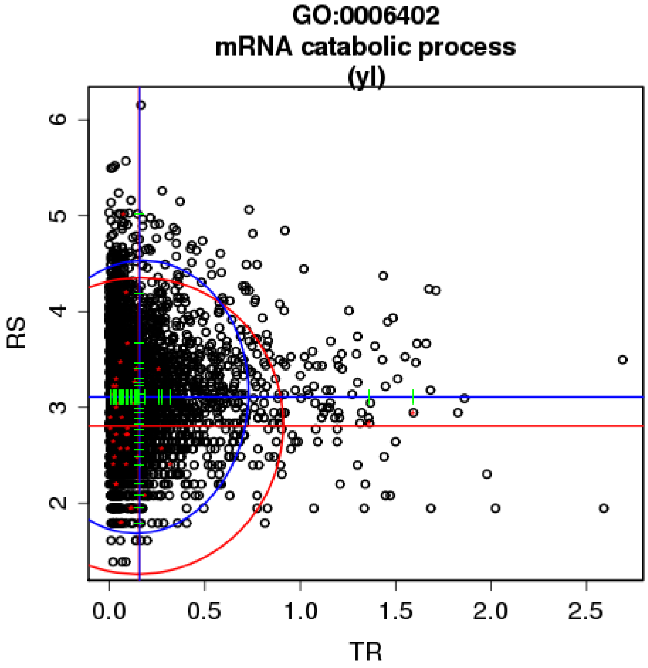
GO:0009451
RNA modification
(yl)



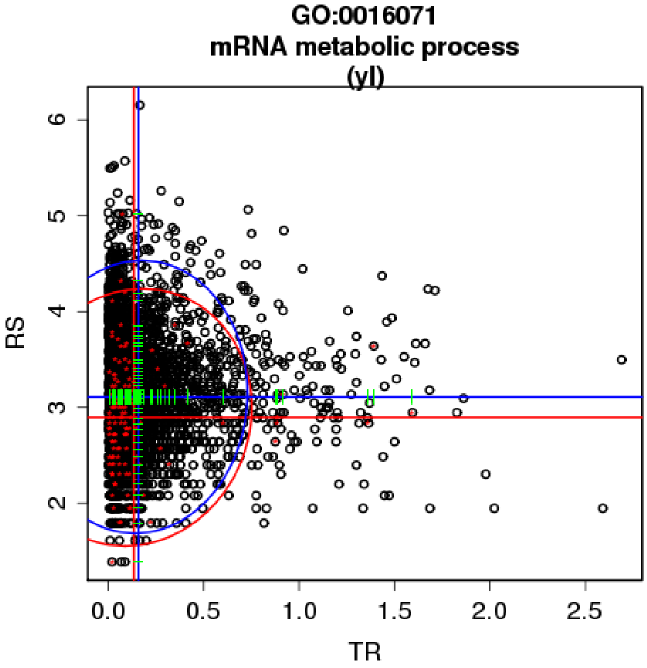
GO:0006400
tRNA modification
(yl)



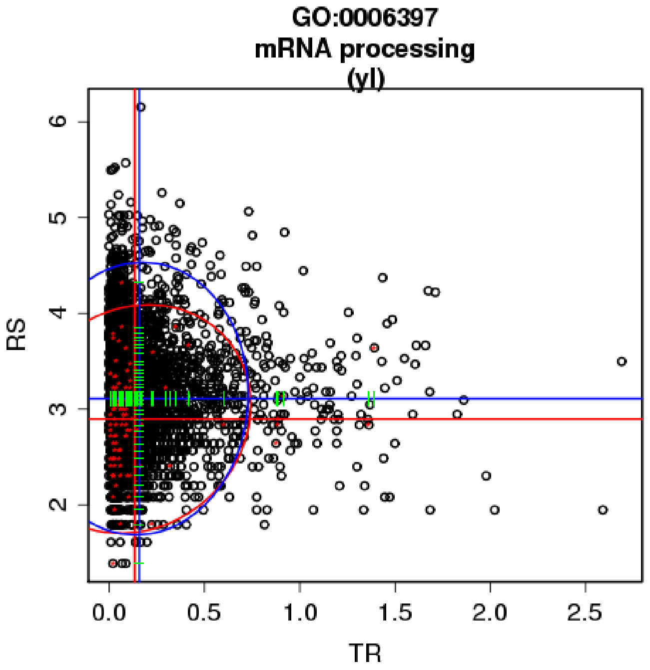
GO:0006401
RNA catabolic process
(yl)



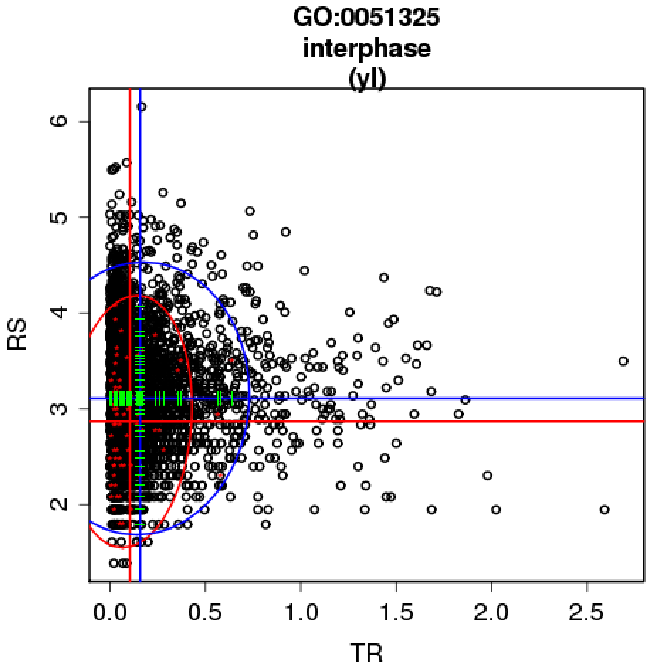
GO:0006402
mRNA catabolic process
(yl)



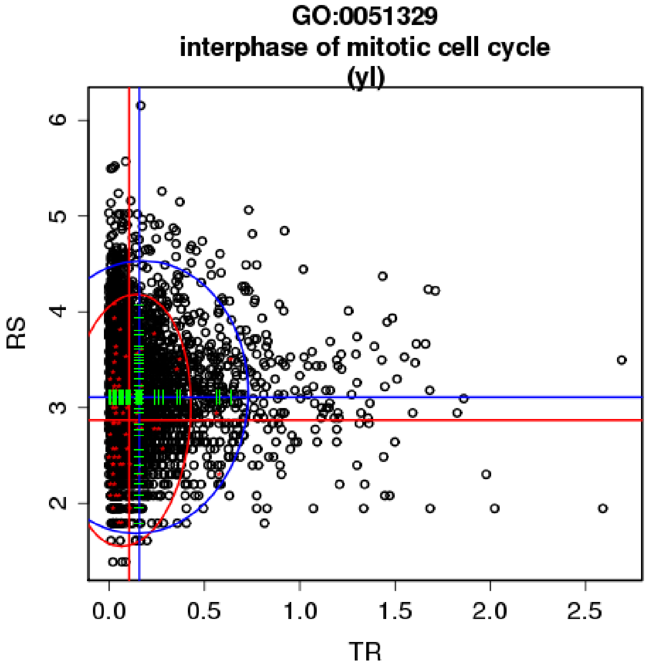
GO:0016071
mRNA metabolic process
(yl)



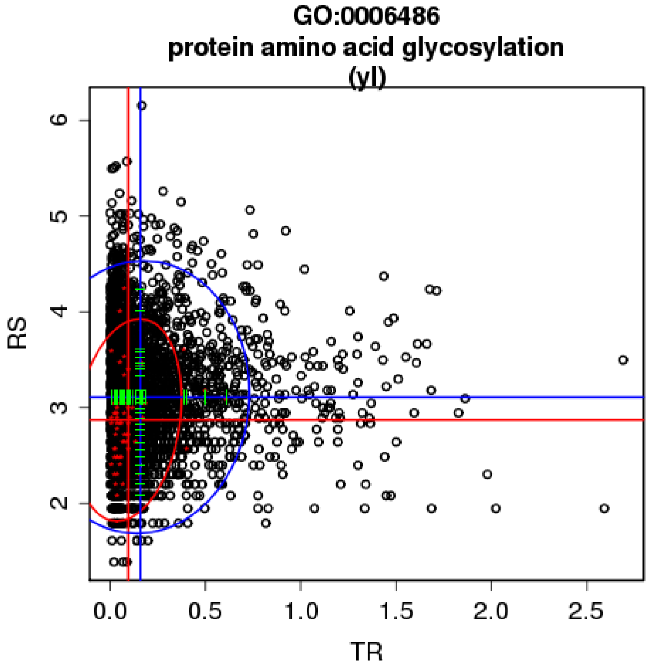
GO:0006397
mRNA processing
(yl)



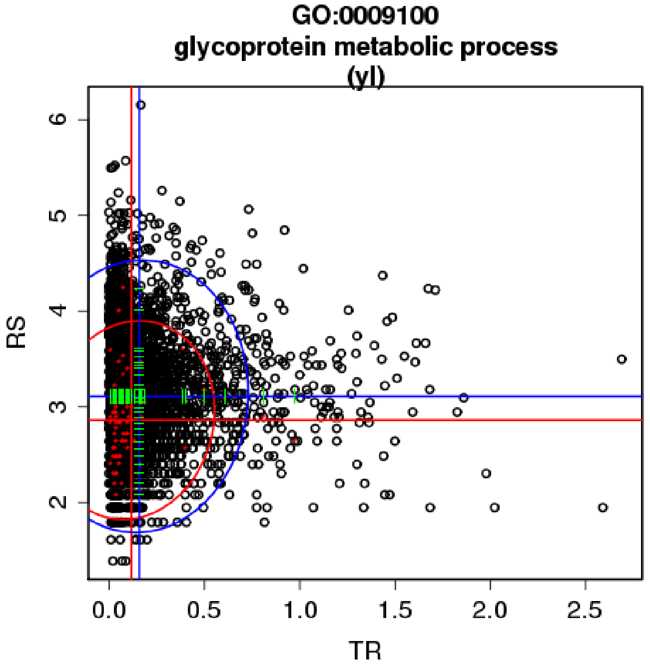
GO:0051325
interphase
(yl)



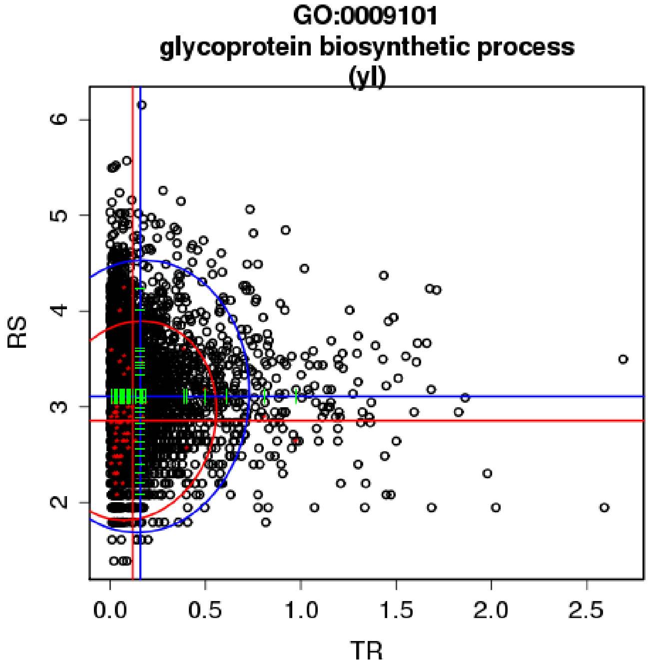
GO:0051329
interphase of mitotic cell cycle
(yl)



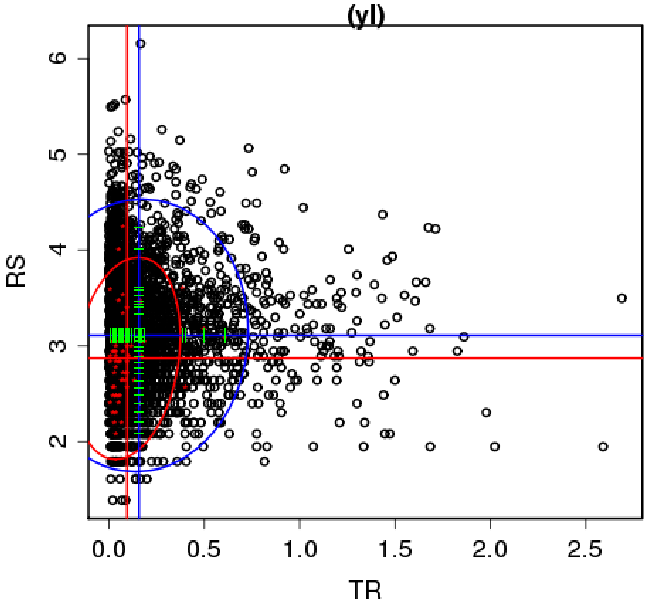
GO:0006486
protein amino acid glycosylation
(yl)



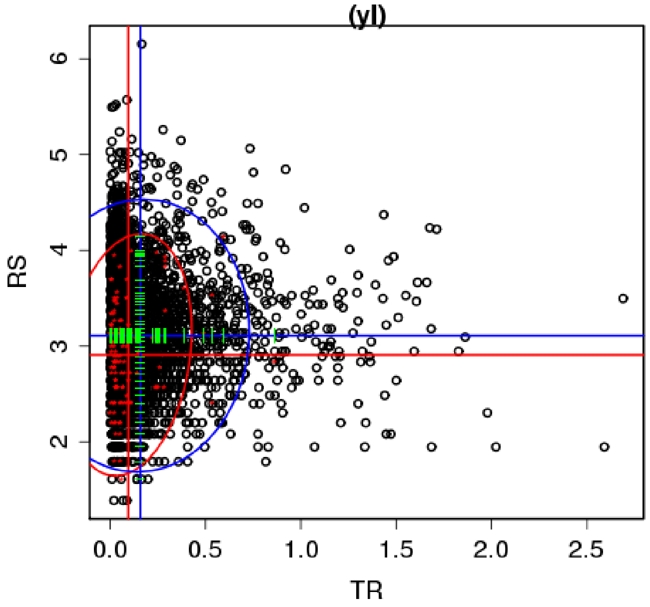
GO:0009100
glycoprotein metabolic process
(yl)



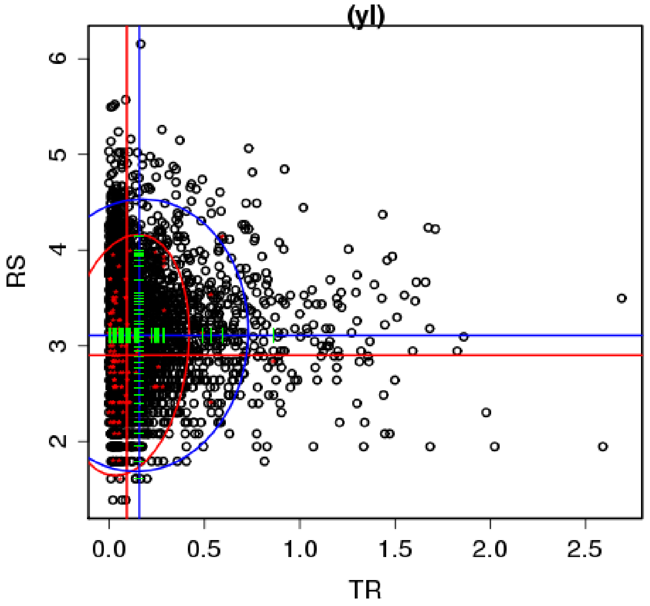
GO:0009101
glycoprotein biosynthetic process
(yl)



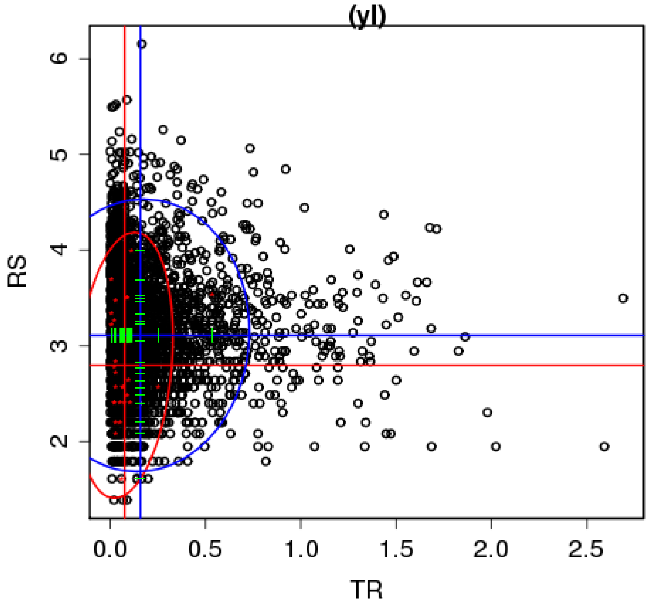
GO:0043413
biopolymer glycosylation
(yl)



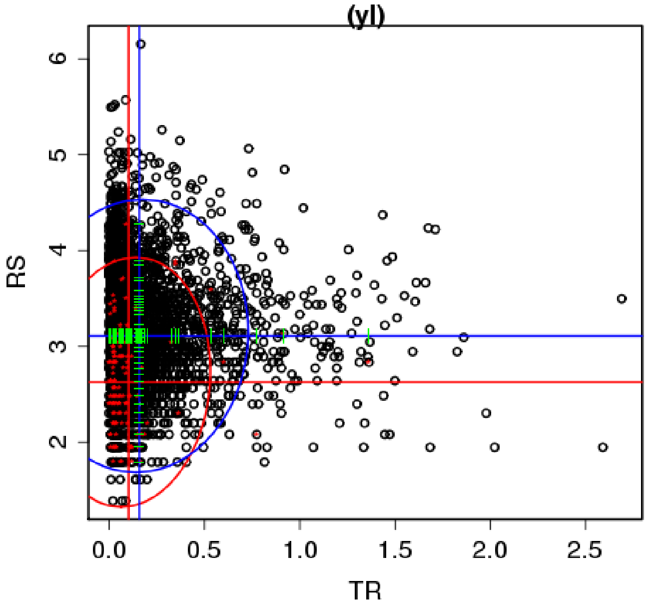
GO:0000087
M phase of mitotic cell cycle
(yl)



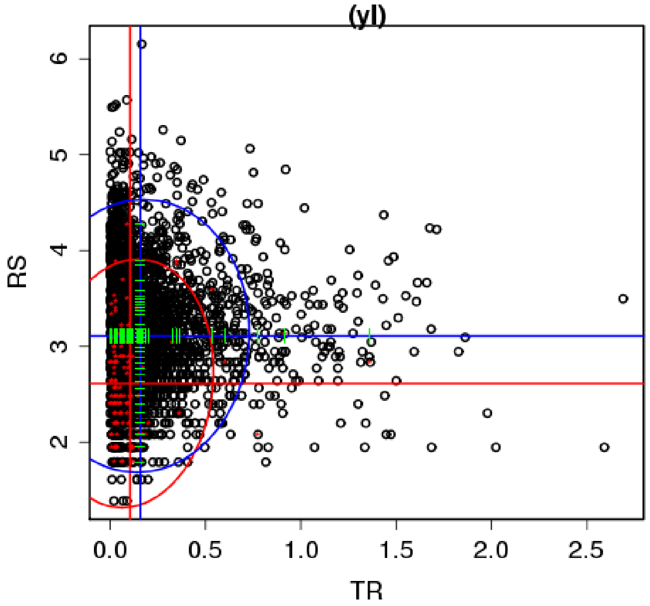
GO:0007067
mitosis
(yl)



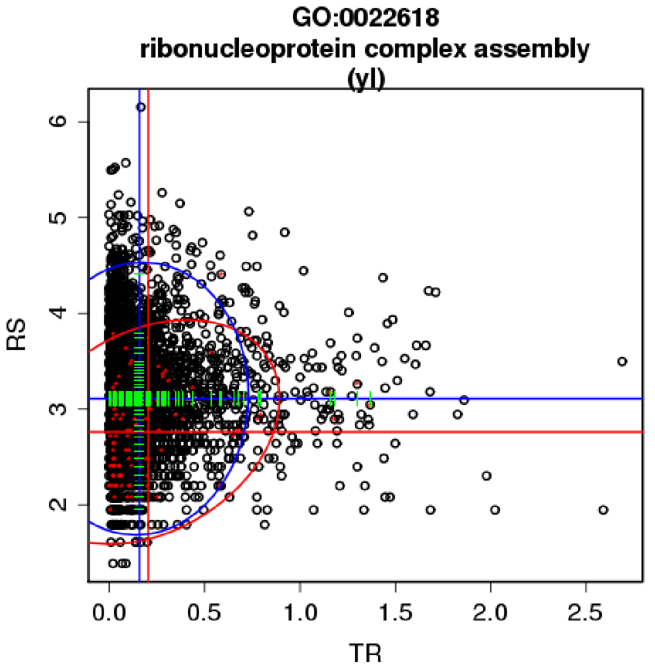
GO:0007088
regulation of mitosis
(yl)

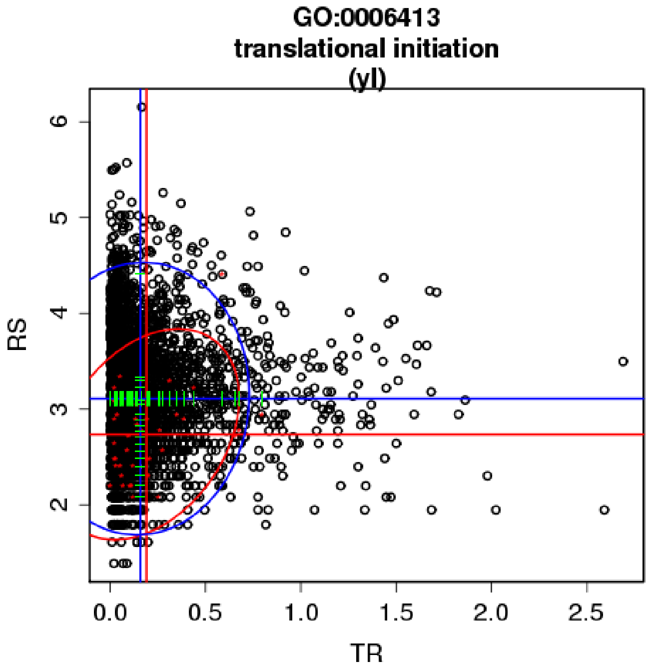


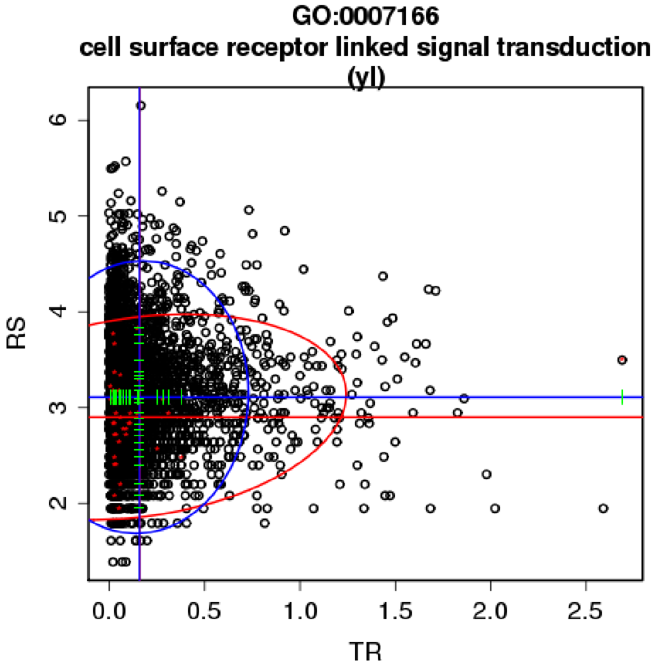
GO:0016072
rRNA metabolic process
(yl)

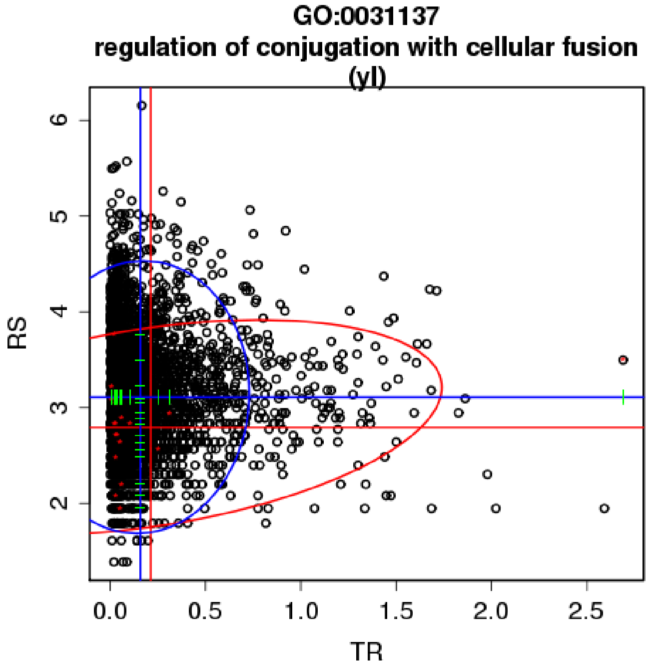


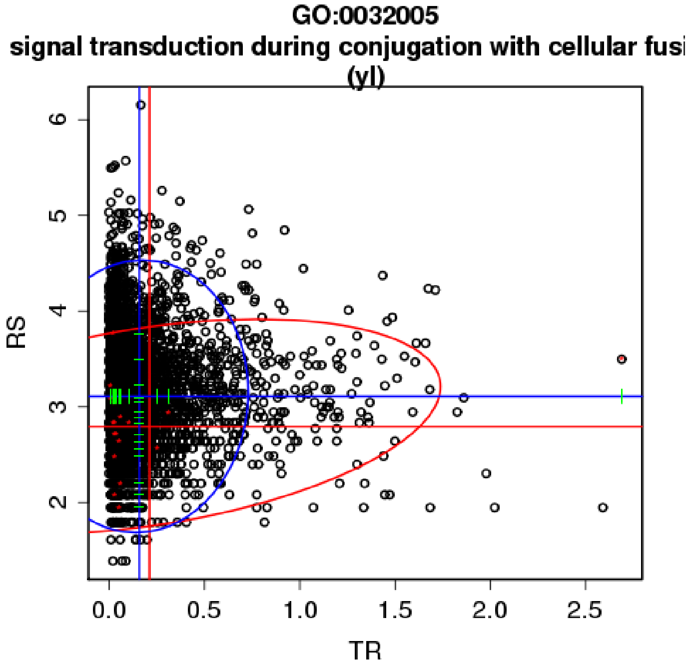
GO:0006364
rRNA processing
(yl)

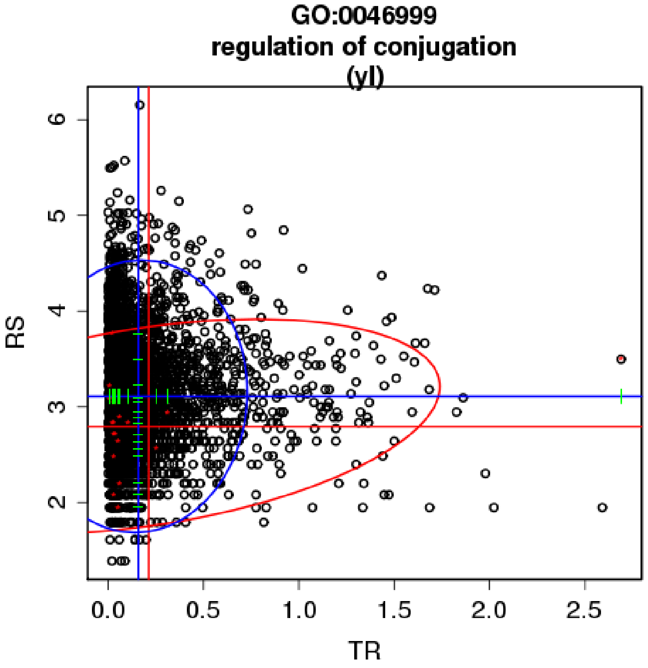

GO:0022618
ribonucleoprotein complex assembly
(yl)

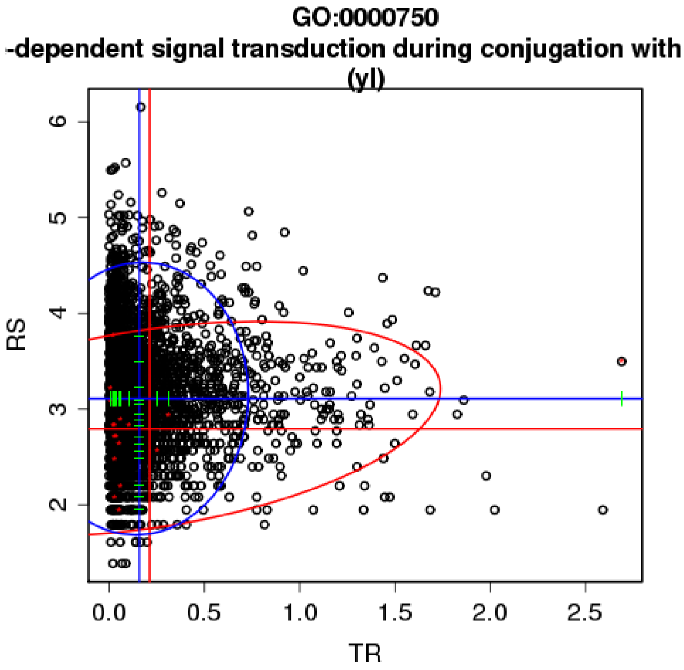

GO:0006413
translational initiation
(yl)

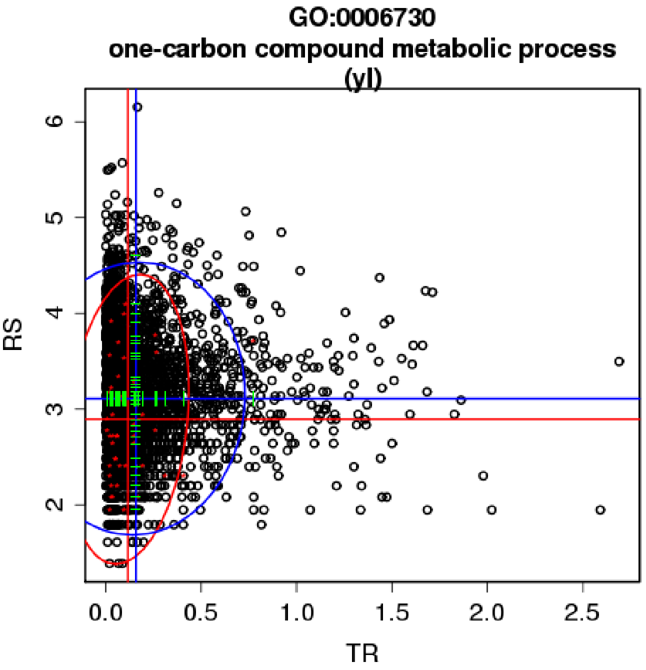

GO:0007166
cell surface receptor linked signal transduction
(yl)

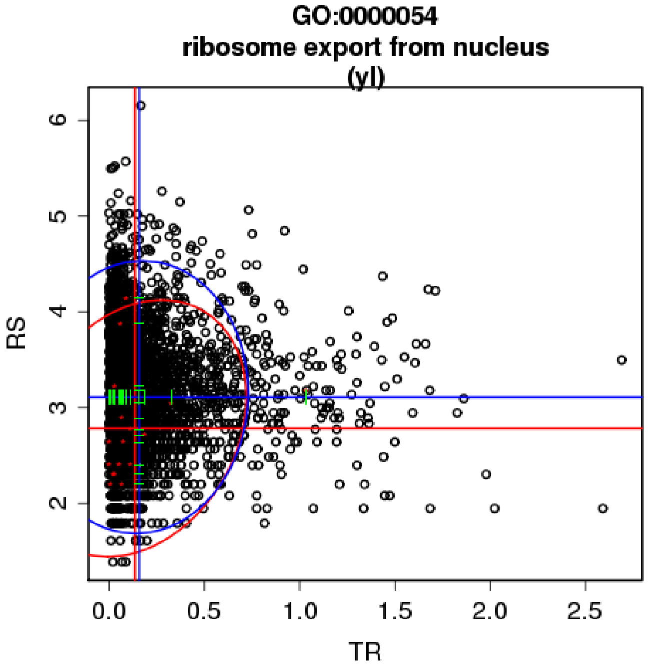

GO:0031137
regulation of conjugation with cellular fusion
(yl)

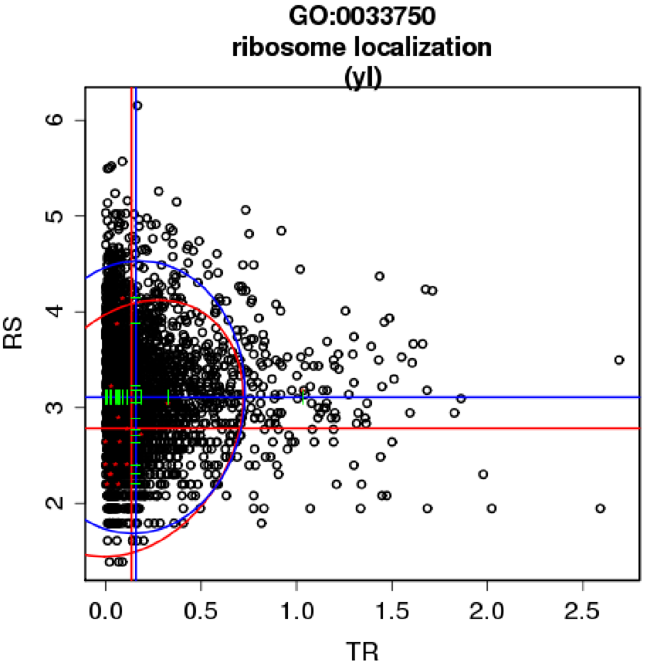

GO:0032005
signal transduction during conjugation with cellular fusi
(yl)

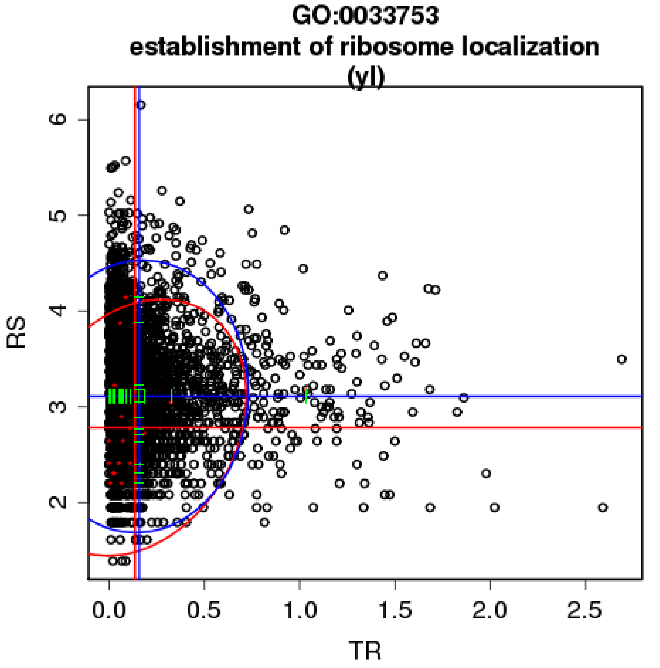

GO:0046999
regulation of conjugation
(yl)

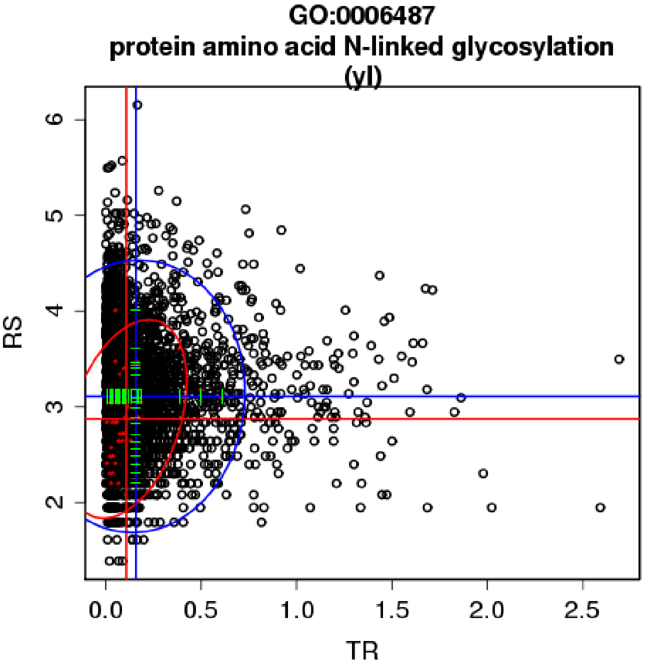

GO:0000750
-dependent signal transduction during conjugation with
(yl)


GO:0006730
one-carbon compound metabolic process
(yl)

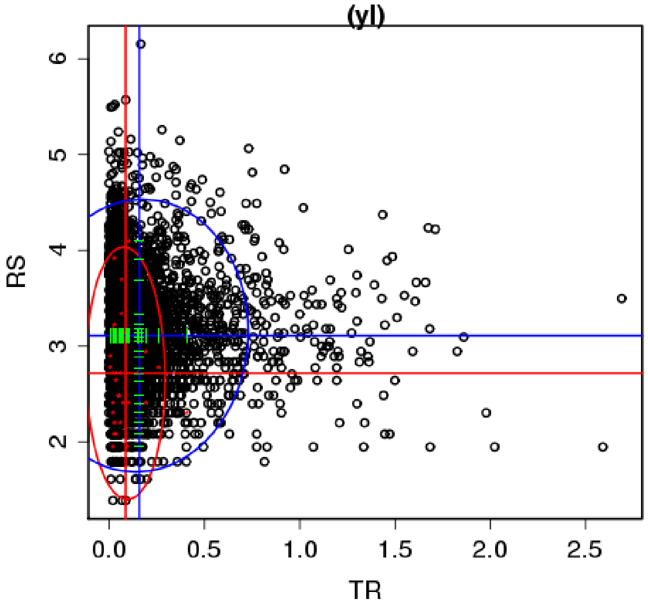

GO:0000054
ribosome export from nucleus
(yl)


GO:0033750
ribosome localization
(yl)

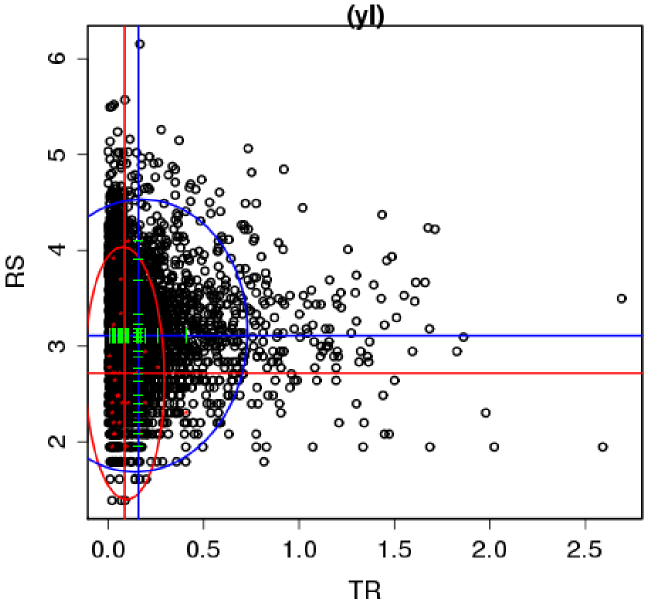

GO:0033753
establishment of ribosome localization
(yl)


GO:0006487
protein amino acid N-linked glycosylation
(yl)

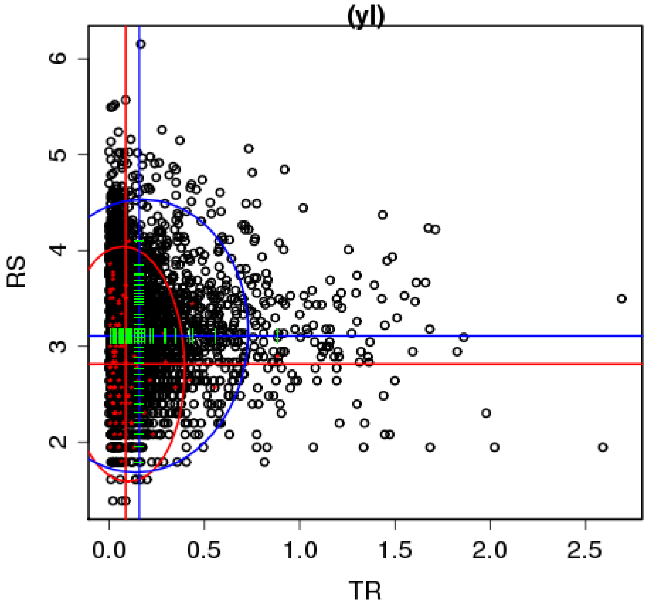
GO:0032259
methylation
(yl)



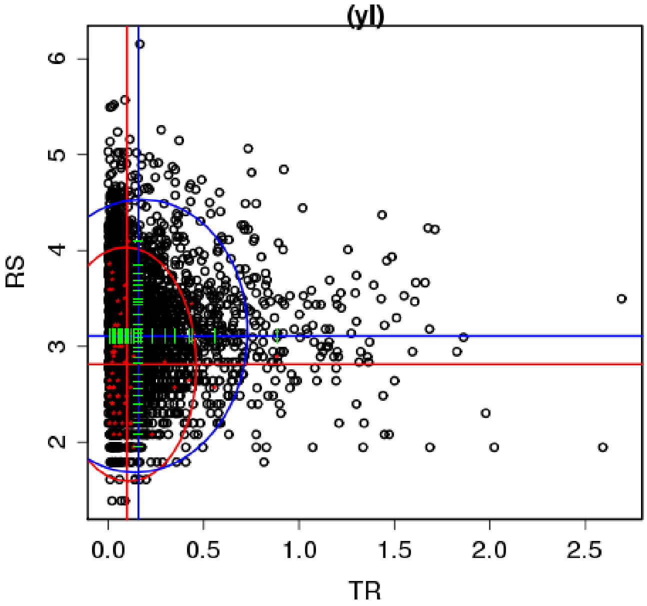
GO:0043414
biopolymer methylation
(yl)



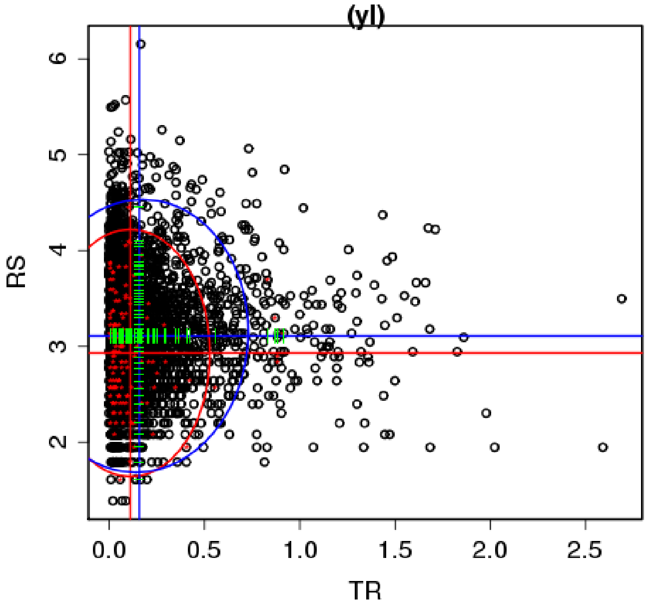
GO:0006338
chromatin remodeling
(yl)



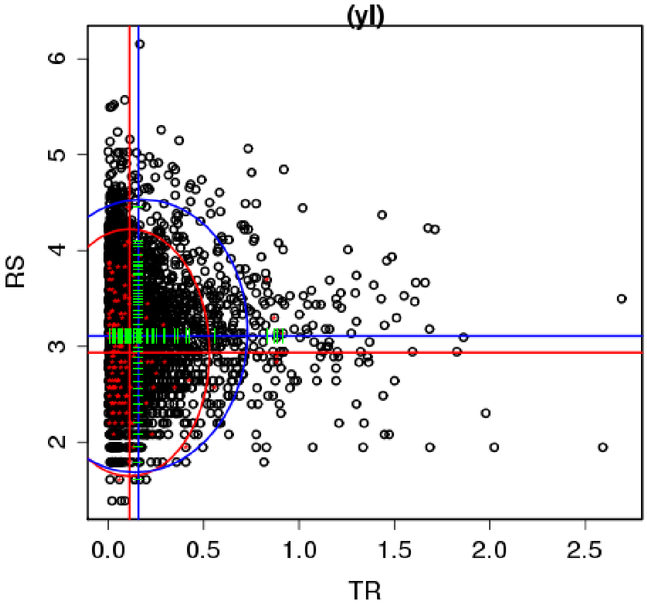
GO:0040029
regulation of gene expression, epigenetic
(yl)

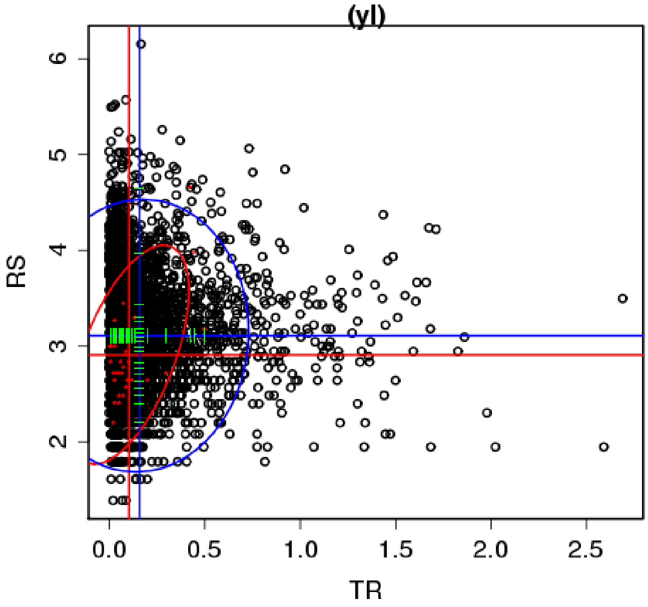


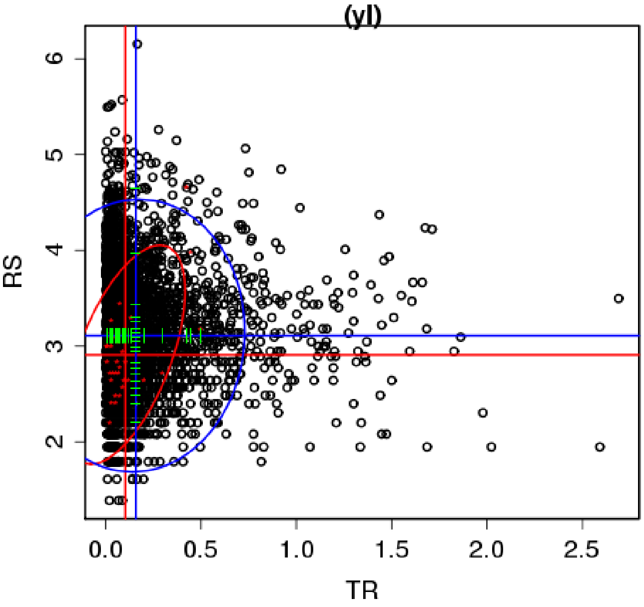
GO:0048519
negative regulation of biological process
(yl)

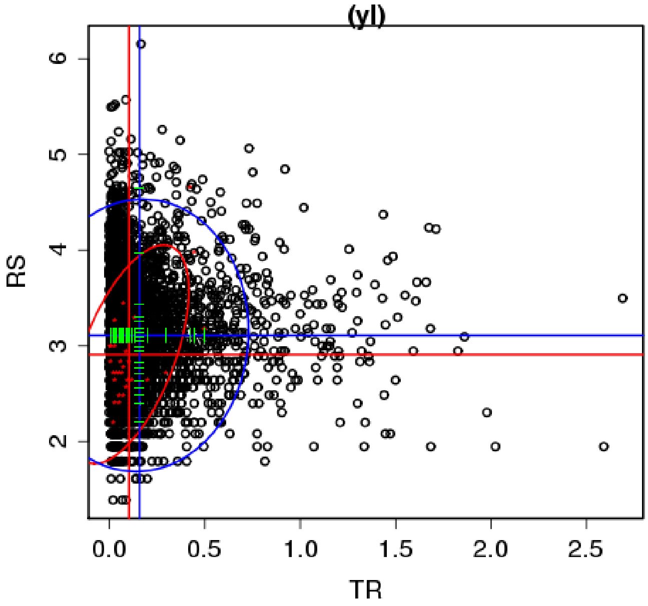


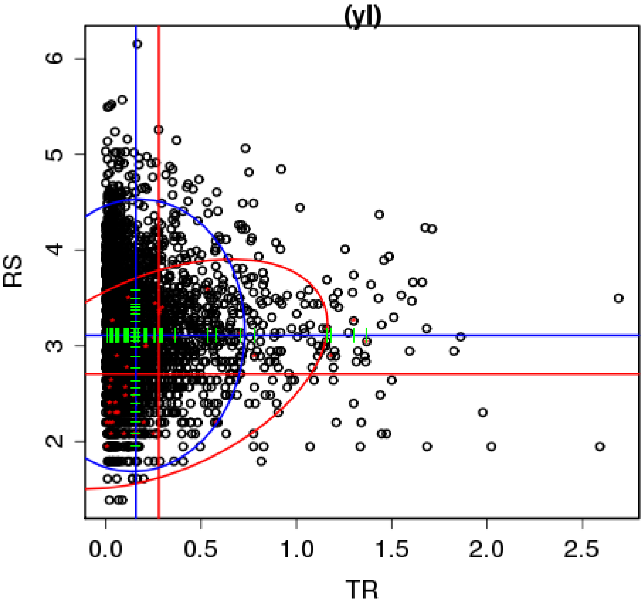
GO:0048523
negative regulation of cellular process
(yl)

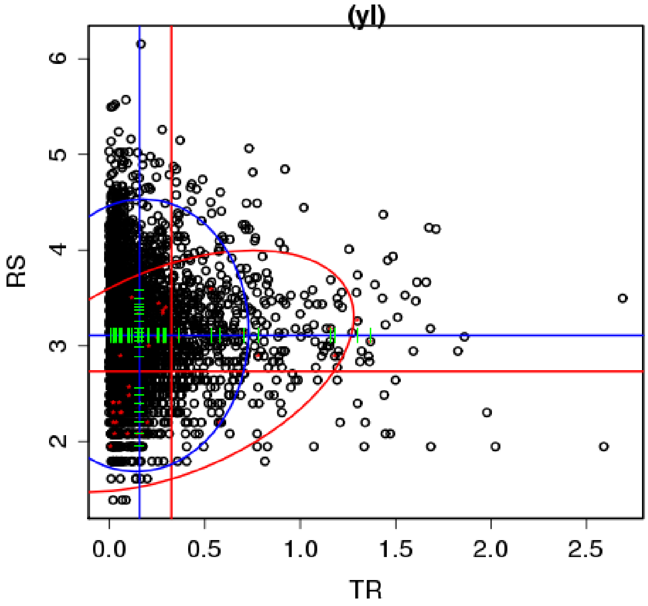


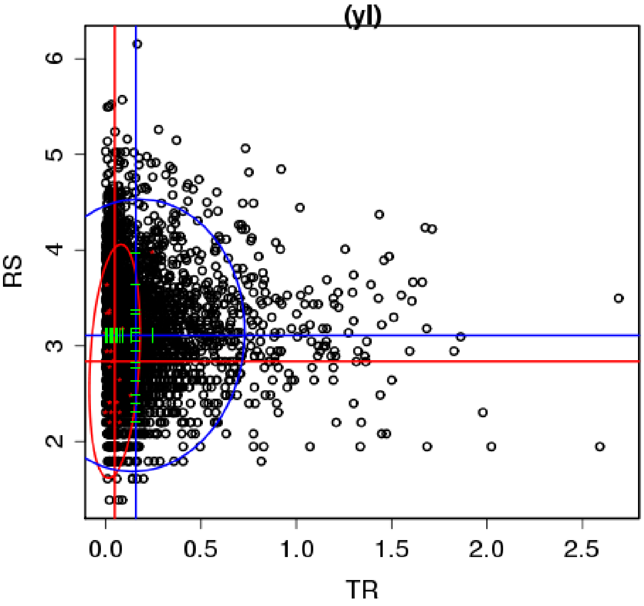

GO:0006497
protein amino acid lipidation
(yl)

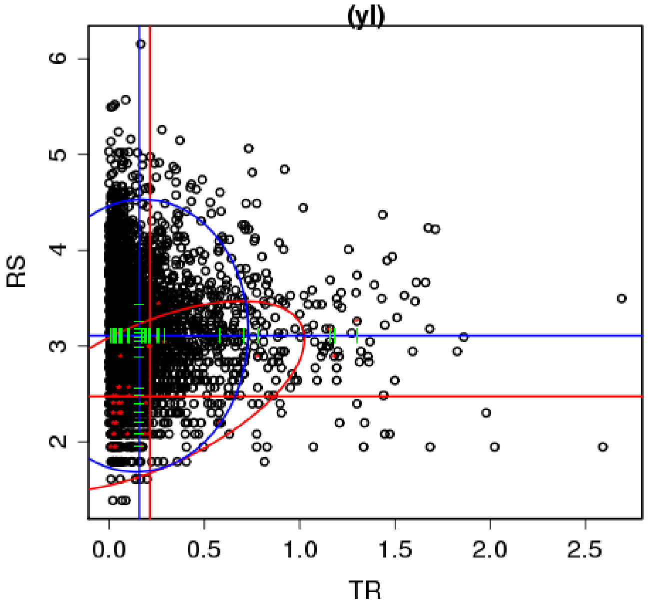

GO:0042157
lipoprotein metabolic process
(yl)

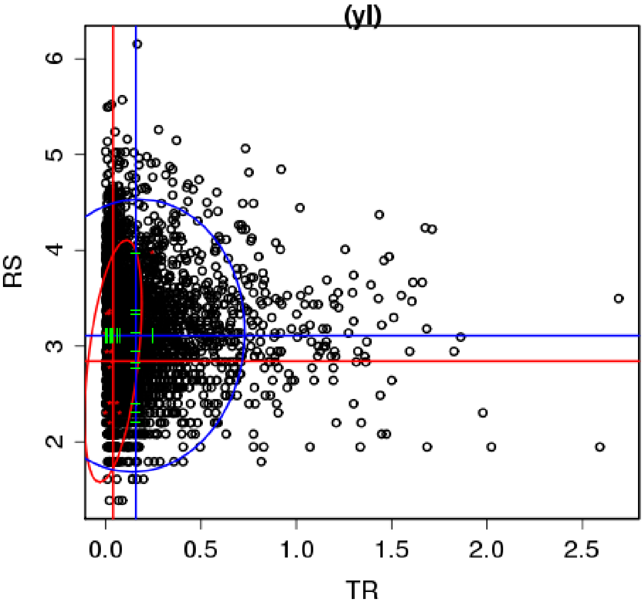

GO:0042158
lipoprotein biosynthetic process
(yl)

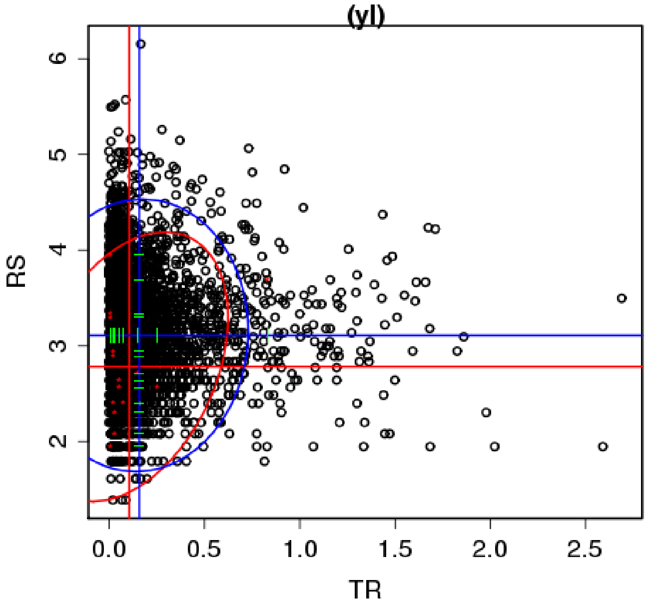

GO:0042255
ribosome assembly
(yl)

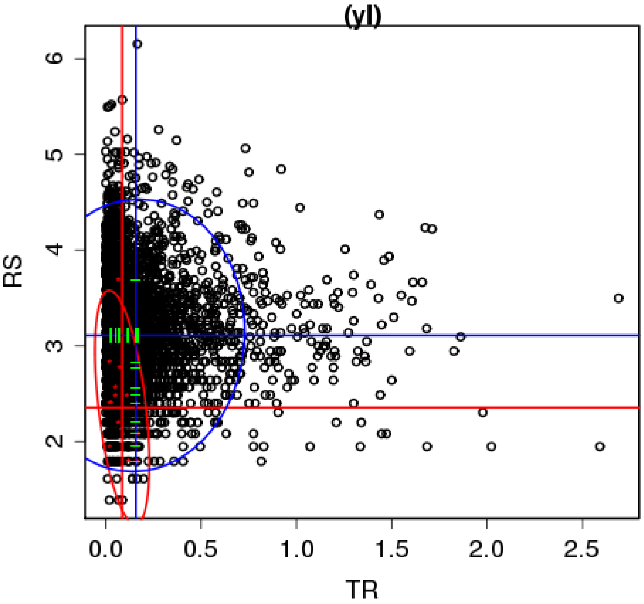

GO:0042257
ribosomal subunit assembly
(yl)

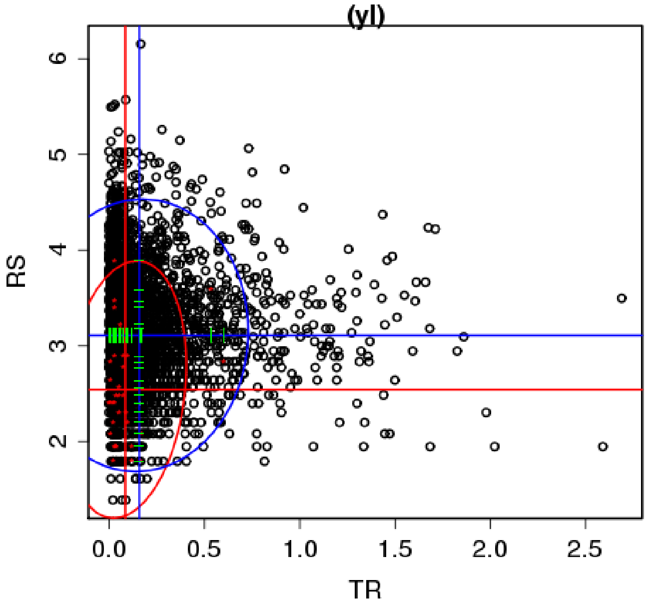

GO:0007062
sister chromatid cohesion
(yl)

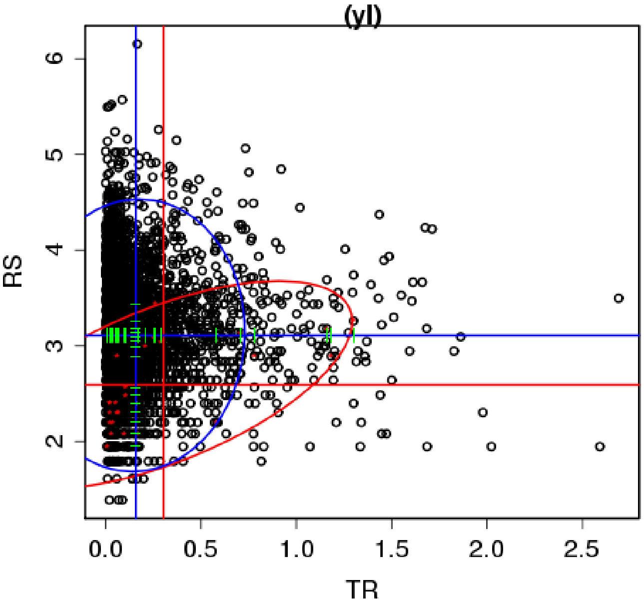

GO:0042273
ribosomal large subunit biogenesis
(yl)

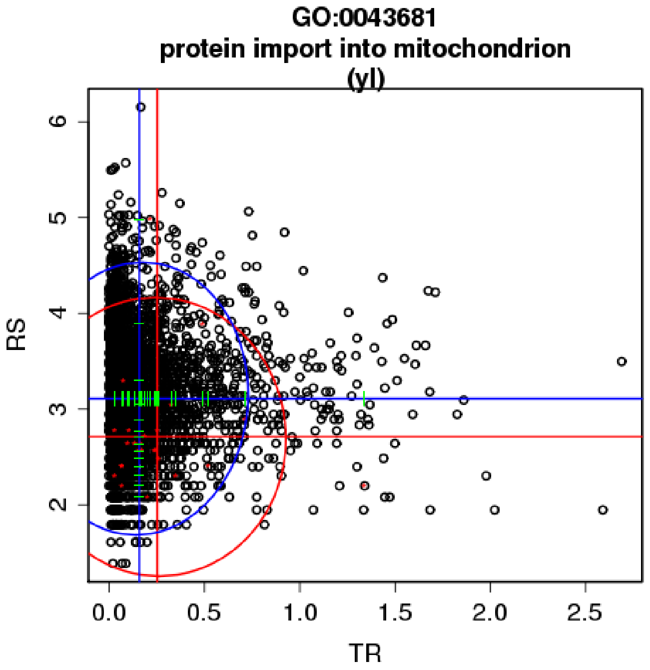

GO:0007064
mitotic sister chromatid cohesion
(yl)

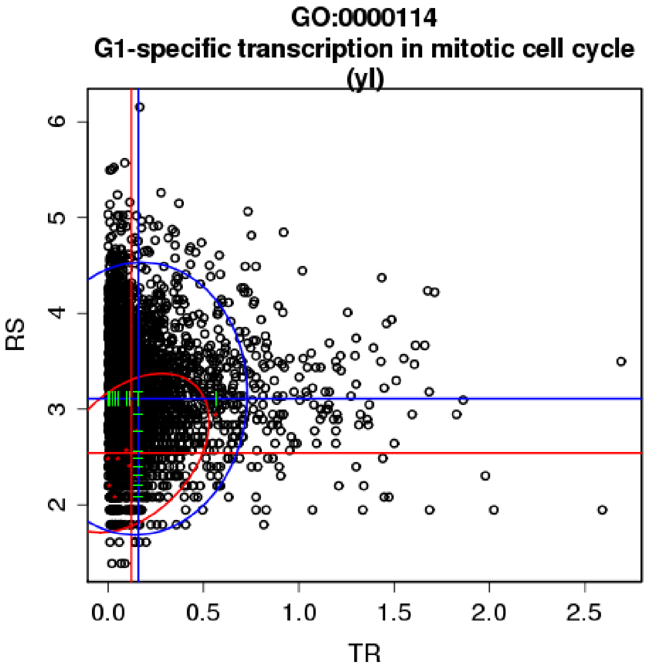

GO:0050793
regulation of developmental process
(yl)


GO:0000154
rRNA modification
(yl)


GO:0030490
maturation of SSU-rRNA
(yl)


GO:0000027
ribosomal large subunit assembly and maintenance
(yl)


GO:0043681
protein import into mitochondrion
(yl)
RS
TR
6
5
4
3
2
0.0
0.5
1.0
1.5
2.0
2.5


GO:0000114
G1-specific transcription in mitotic cell cycle
(yl)
RS
TR
6
5
4
3
2
0.0
0.5
1.0
1.5
2.0
2.5

Combined functional profiling of Transcription Rate (TR) and RNA Stability (RS) using KEGG pathways

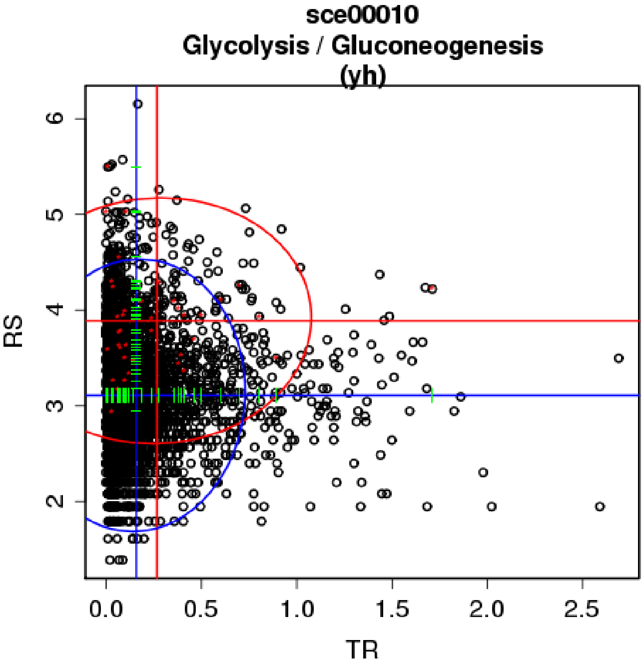
13 significant modules

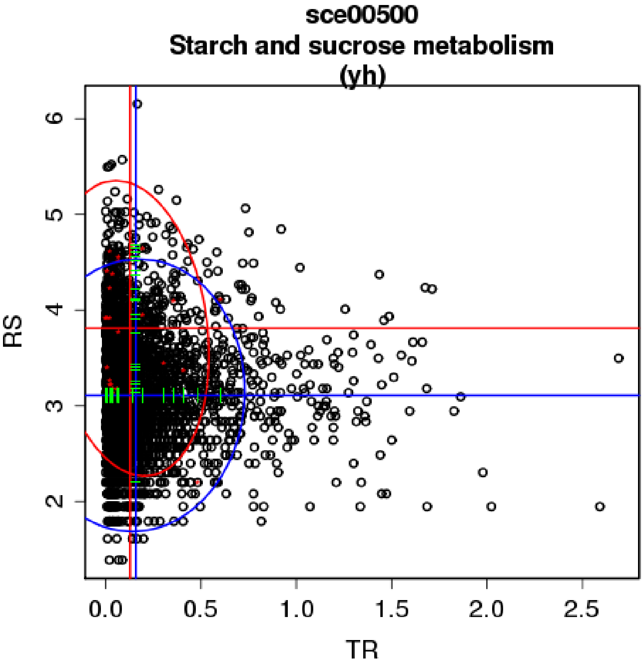
LOR indicates Log Odds Ratio of the coefficient or the interaction

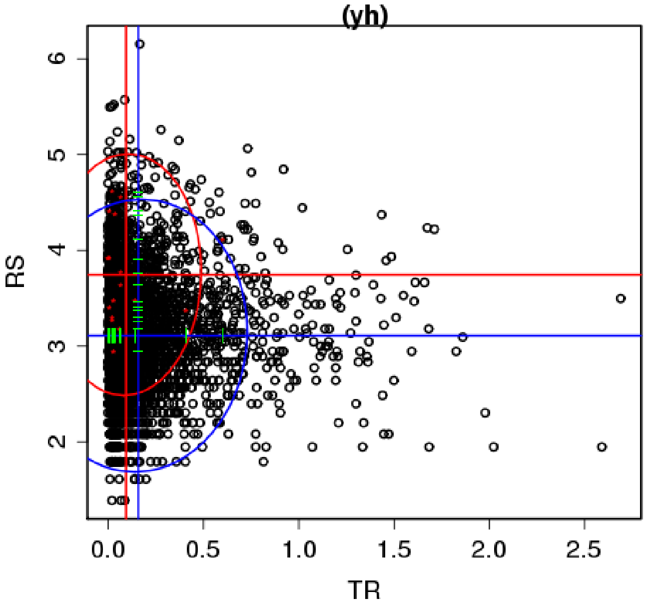
p indicates FDR adjusted p-value

	LOR TR	LOR RS	LOR Inter	p TR	p RS	p Inter	pattern	name
sce00010	-0.48	1.70	0.44	0.97	0.00	1.00	yh	Glycolysis / Gluconeogenesis
sce00500	3.80	1.77	-1.31	0.97	0.00	1.00	yh	Starch and sucrose metabolism
sce00052	-2.36	1.49	-0.06	0.97	0.00	1.00	yh	Galactose metabolism
sce00630	6.98	1.14	-2.59	0.75	0.03	1.00	yh	Glyoxylate and dicarboxylate metabolism
sce00030	0.27	0.96	0.08	0.97	0.04	1.00	yh	Pentose phosphate pathway
sce00020	4.71	1.28	-1.44	0.75	0.00	1.00	yh	Citrate cycle (TCA cycle)
sce04130	-0.35	-1.72	0.29	0.97	0.01	1.00	yl	SNARE interactions in vesicular transport
sce04111	-6.06	-0.78	1.09	0.93	0.01	1.00	yl	Cell cycle
sce00230	1.32	-0.97	-0.24	0.97	0.00	1.00	yl	Purine metabolism
sce04011	-5.61	-1.38	1.91	0.91	0.00	1.00	yl	MAPK signaling pathway
sce00240	1.45	-0.97	-0.24	0.97	0.01	1.00	yl	Pyrimidine metabolism
sce03050	0.68	-1.27	0.17	0.97	0.01	1.00	yl	Proteasome
sce03020	1.20	-2.20	-0.11	0.97	0.00	1.00	yl	RNA polymerase

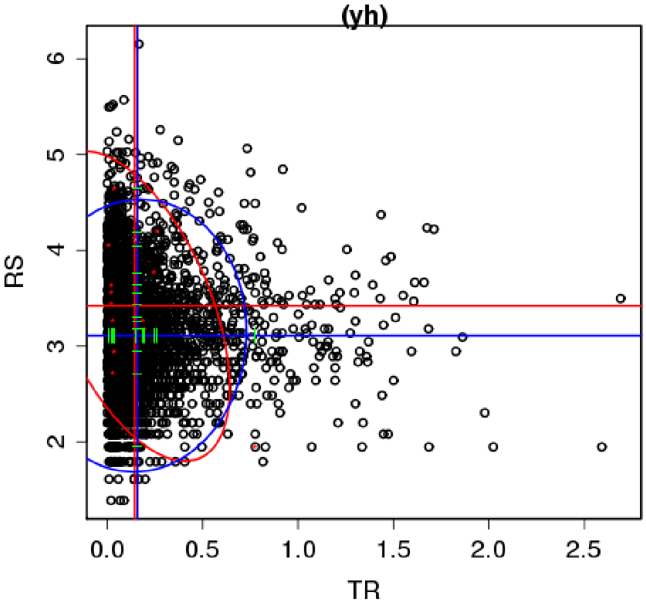
Table 1: LOR: log odds ratio; p: adjusted p-value FDR


sce00010
Glycolysis / Gluconeogenesis
(yh)

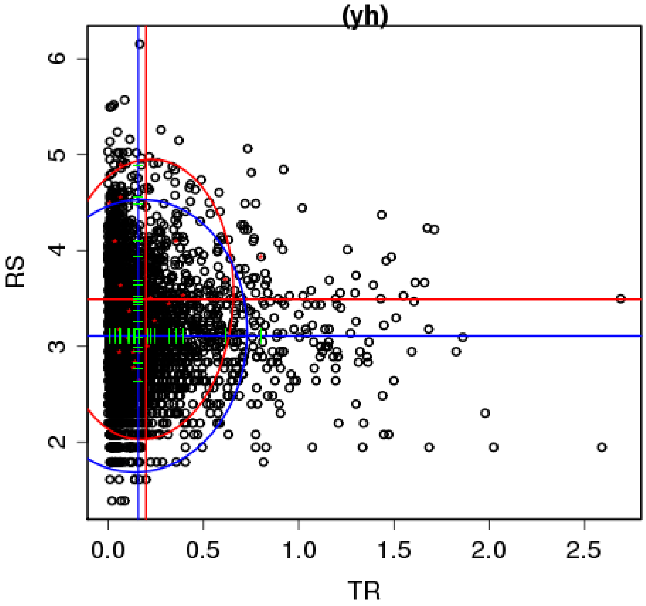

sce00500
Starch and sucrose metabolism
(yh)



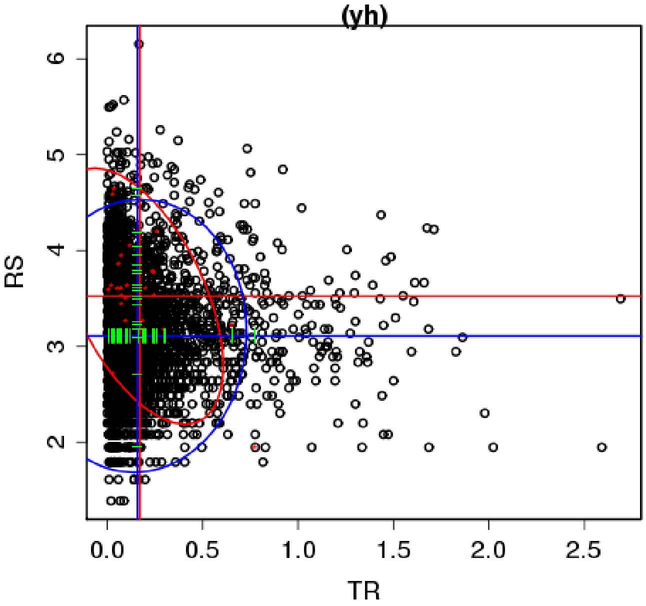
sce00052
Galactose metabolism
(yh)



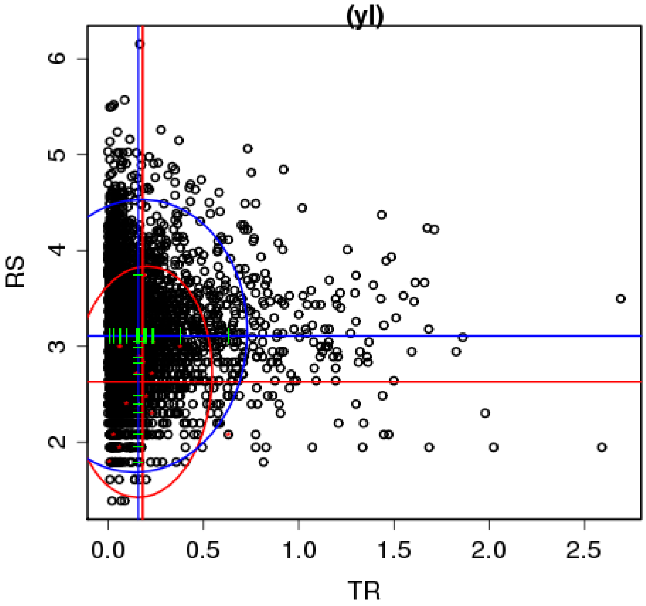
sce00630
Glyoxylate and dicarboxylate metabolism
(yh)



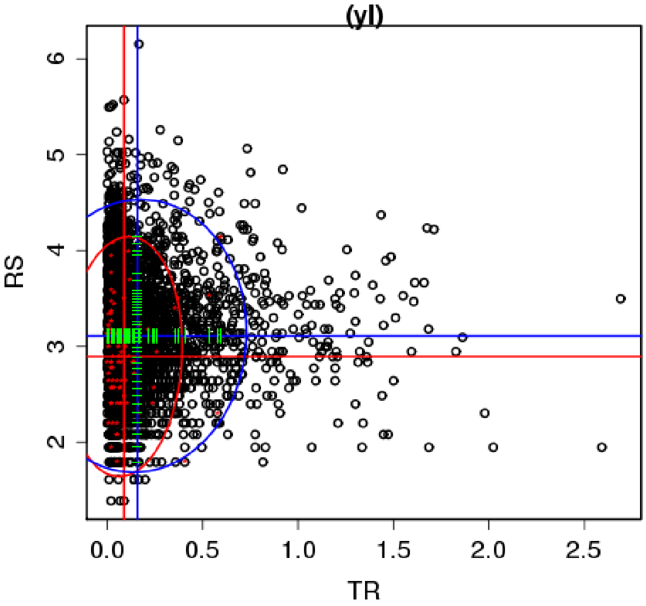
sce00030
Pentose phosphate pathway
(yh)



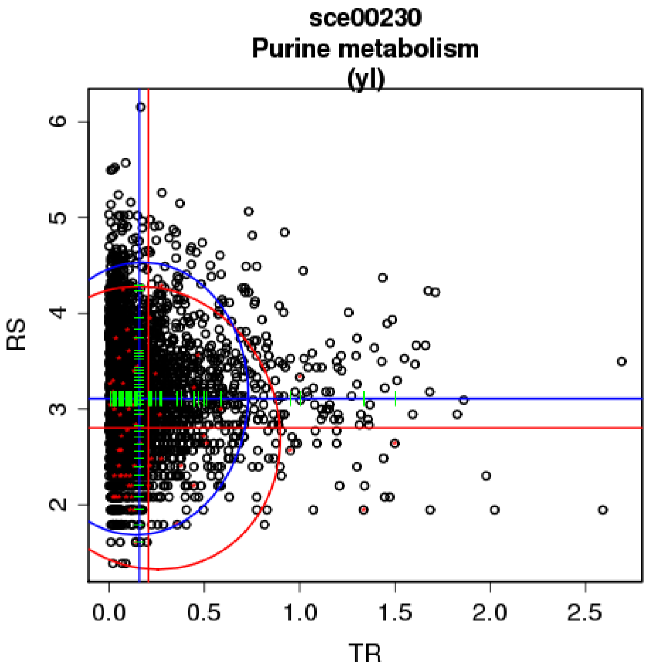
sce00020
Citrate cycle (TCA cycle)
(yh)

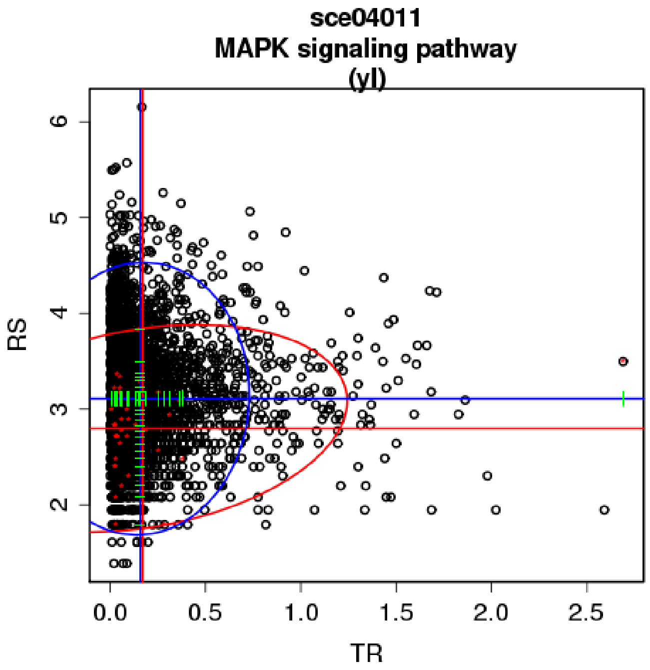


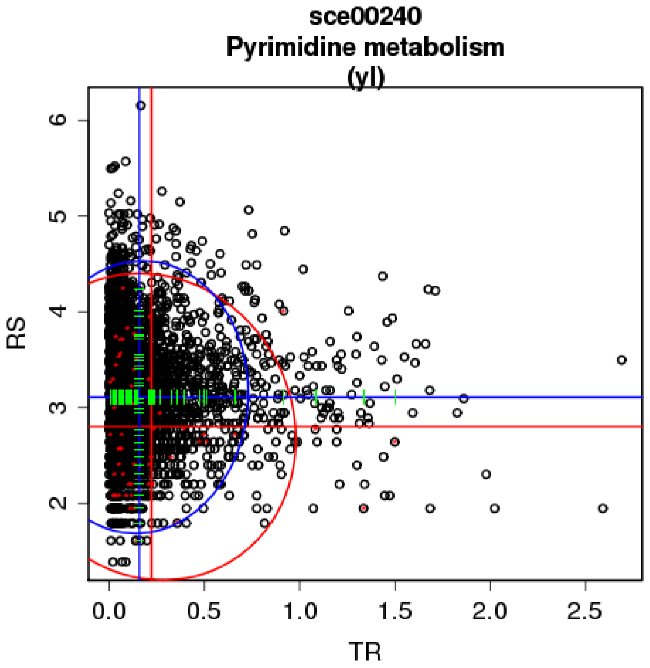
sce04130
SNARE interactions in vesicular transport
(yl)

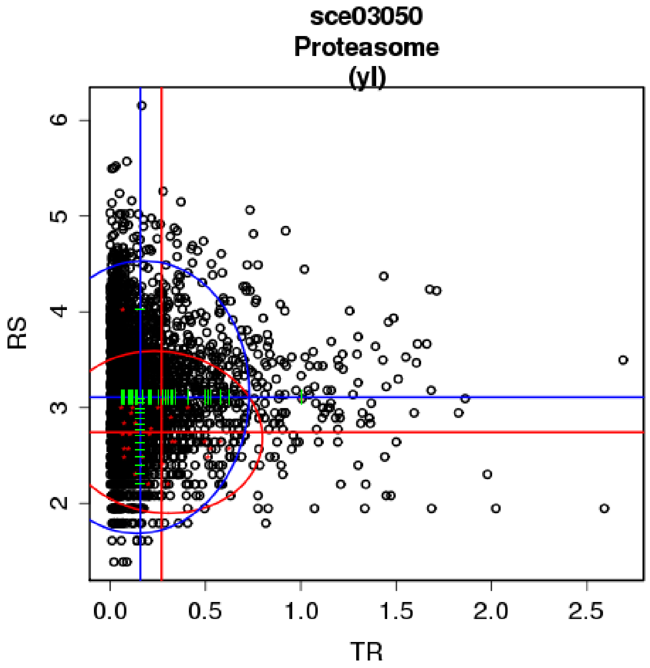


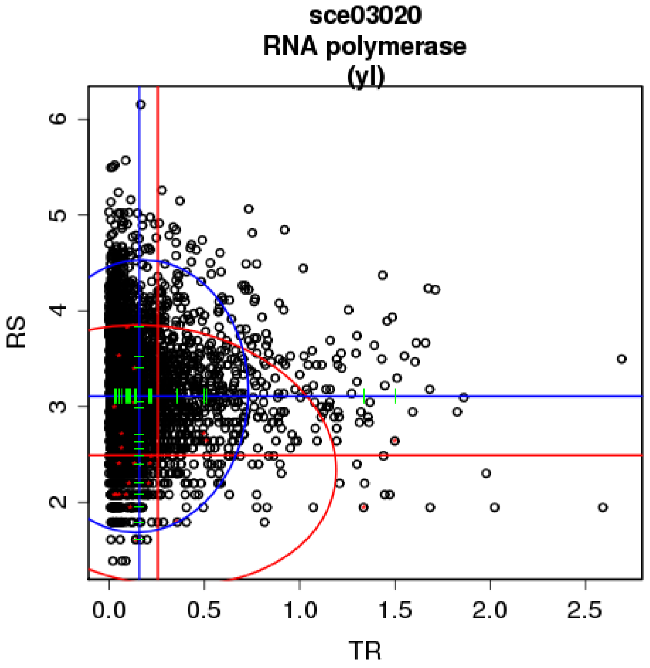
sce04111
Cell cycle
(yl)


sce00230
Purine metabolism
(yl)
RS
TR
6
5
4
3
2
0.0
0.5
1.0
1.5
2.0
2.5


sce04011
MAPK signaling pathway
(yl)
RS
TR
6
5
4
3
2
0.0
0.5
1.0
1.5
2.0
2.5


sce00240
Pyrimidine metabolism
(yl)
RS
TR
6
5
4
3
2
0.0
0.5
1.0
1.5
2.0
2.5


sce03050
Proteasome
(yl)
RS
TR
6
5
4
3
2
0.0
0.5
1.0
1.5
2.0
2.5


sce03020
RNA polymerase
(yl)
RS
TR
6
5
4
3
2
0.0
0.5
1.0
1.5
2.0
2.5