

## **SUPPLEMENTARY INFORMATION INDEX**

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Appendix of Statistical Analyses for Figure 1

Appendix of Statistical Analyses for Figure 2

Table S6. (in a separate file)

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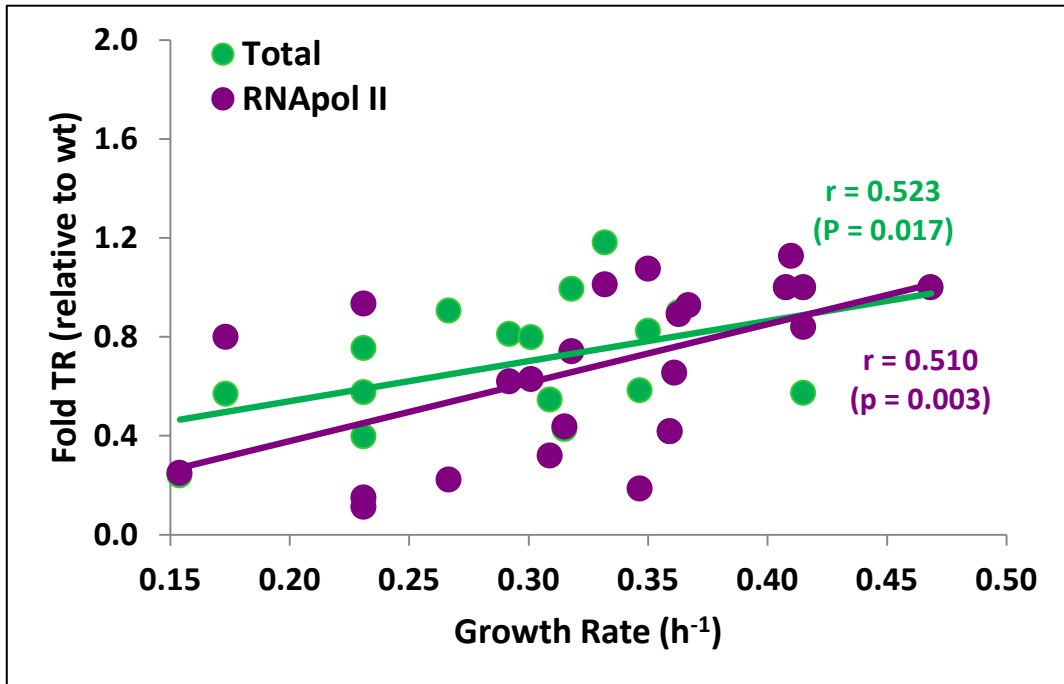
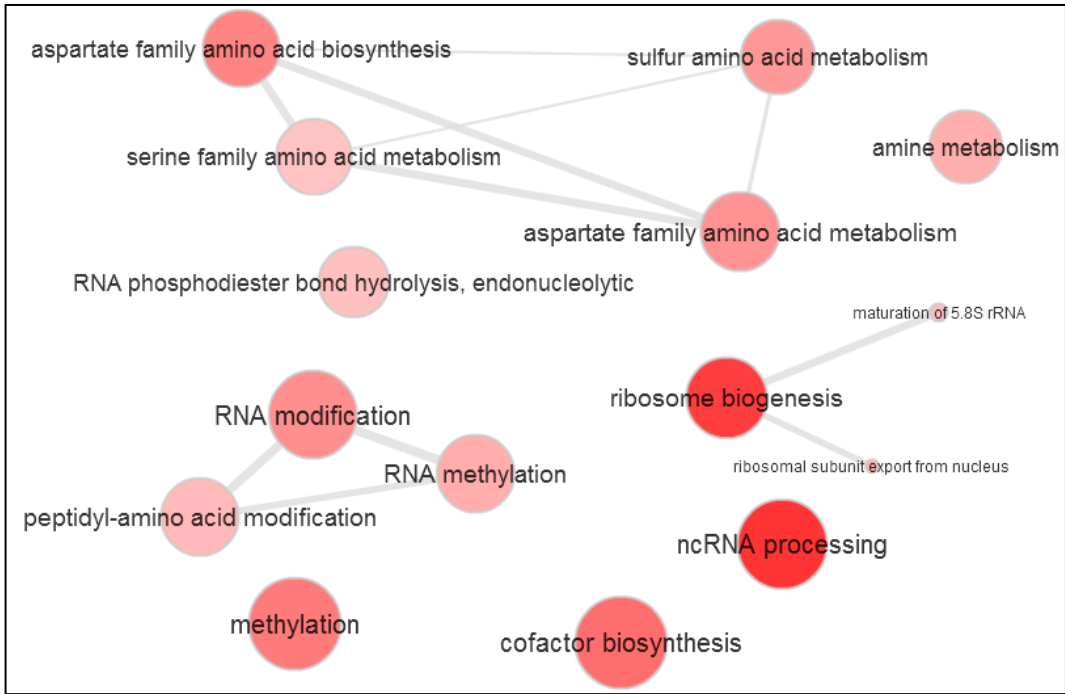


Figure S1.- Total and RNA pol II TR are similarly related to GR. See Figure 1 for comparison.

## Transcription Rate top

A



## Transcription Rate bottom

B

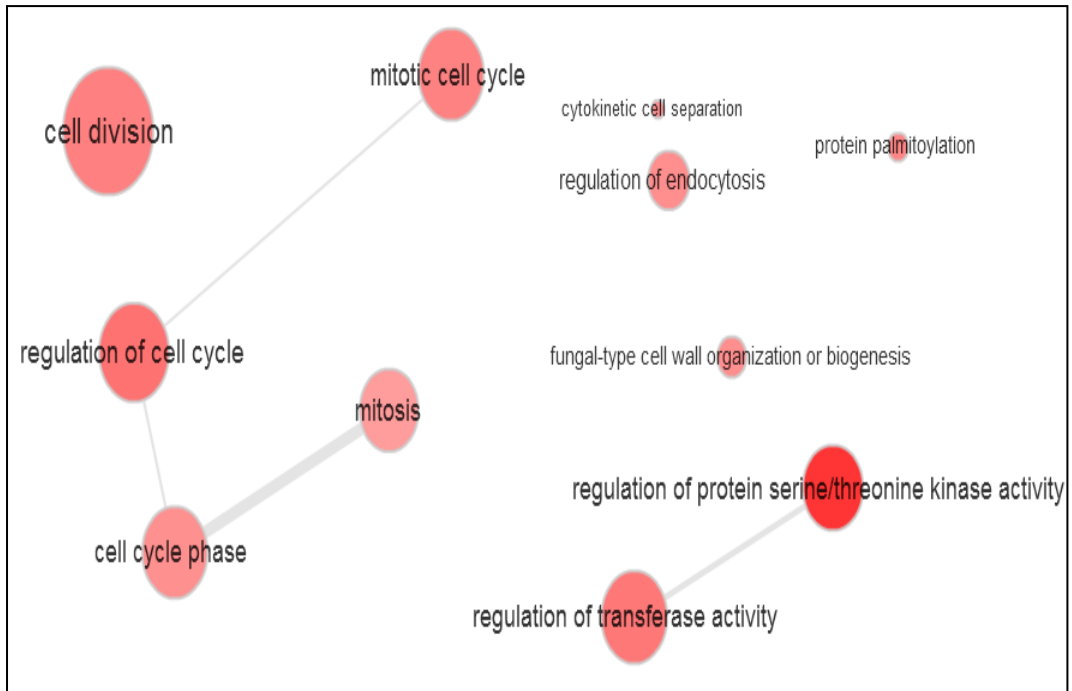
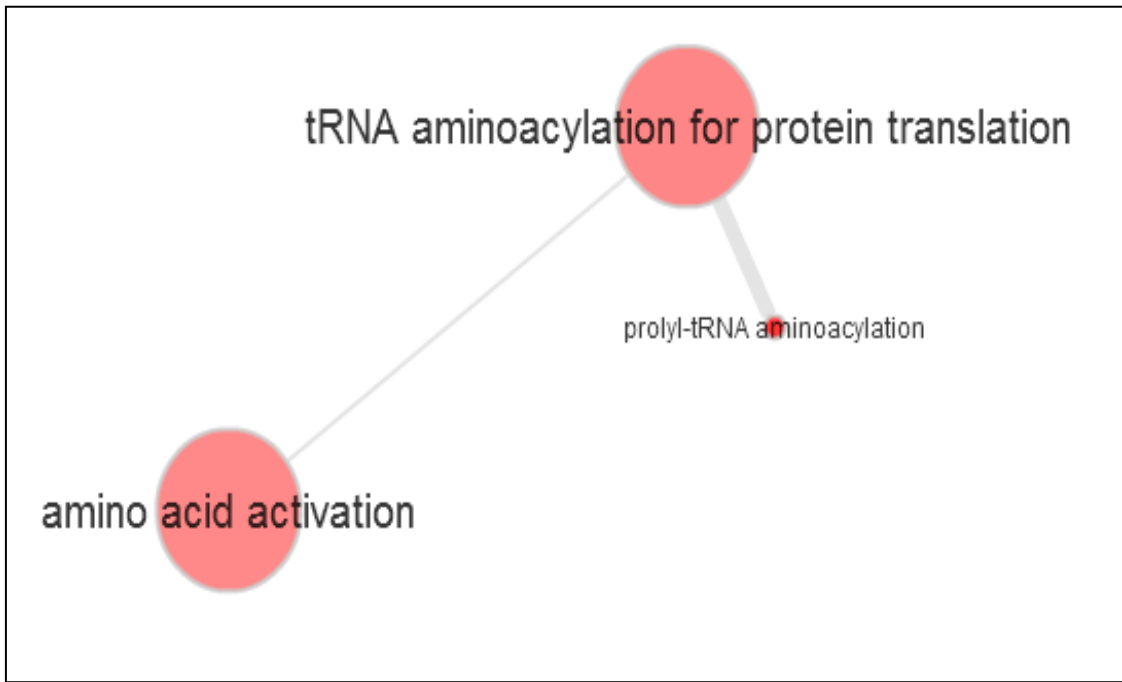


Figure S2

C

[mRNA] top



[mRNA] bottom

D

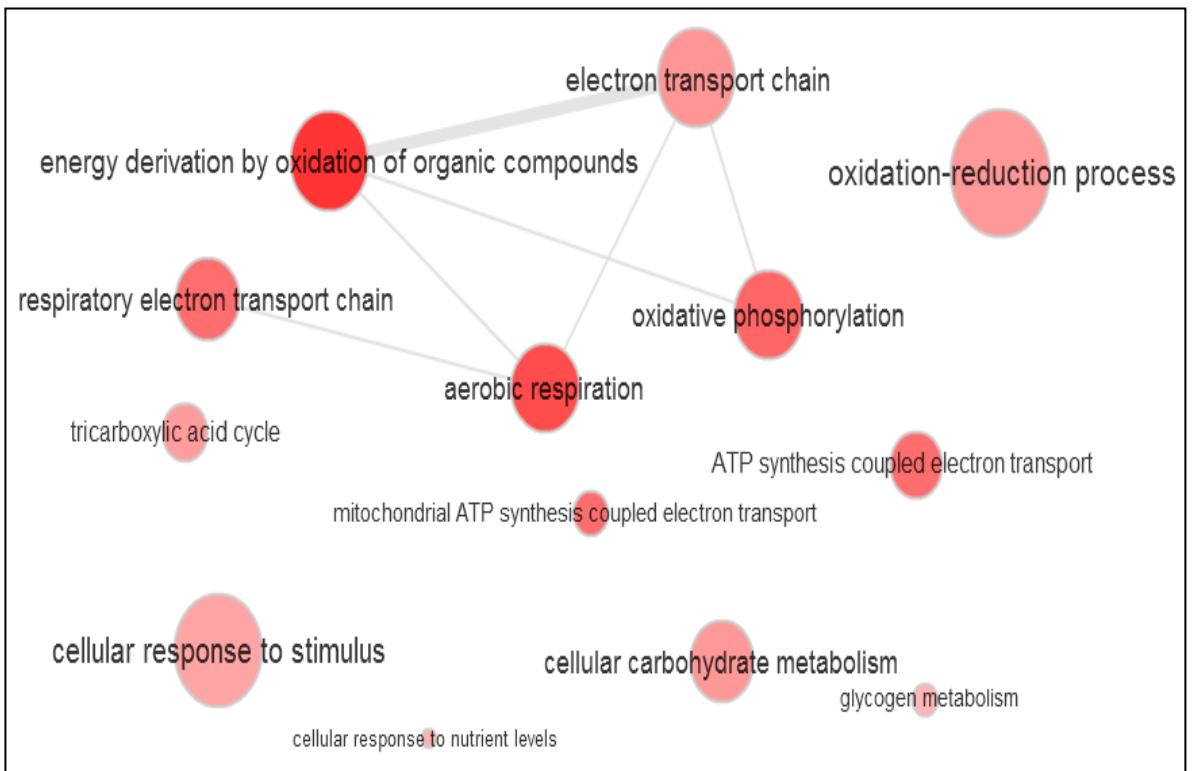
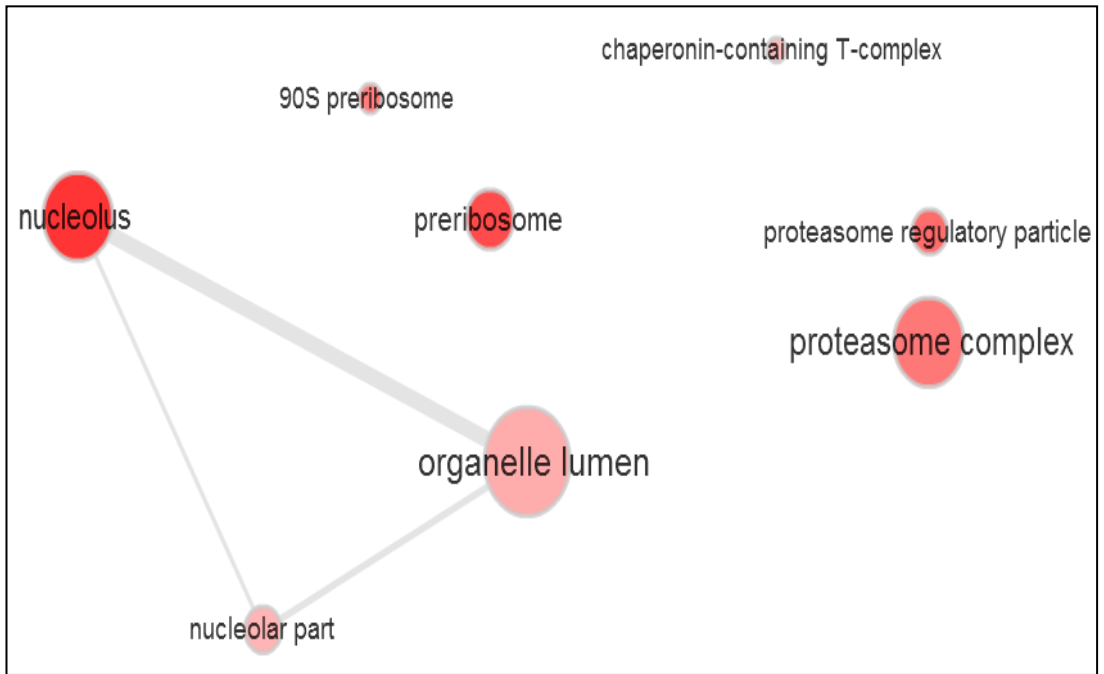


Figure S2

## Transcription Rate top (Cellular Component)

E



## [mRNA] bottom (Cellular Component)

F

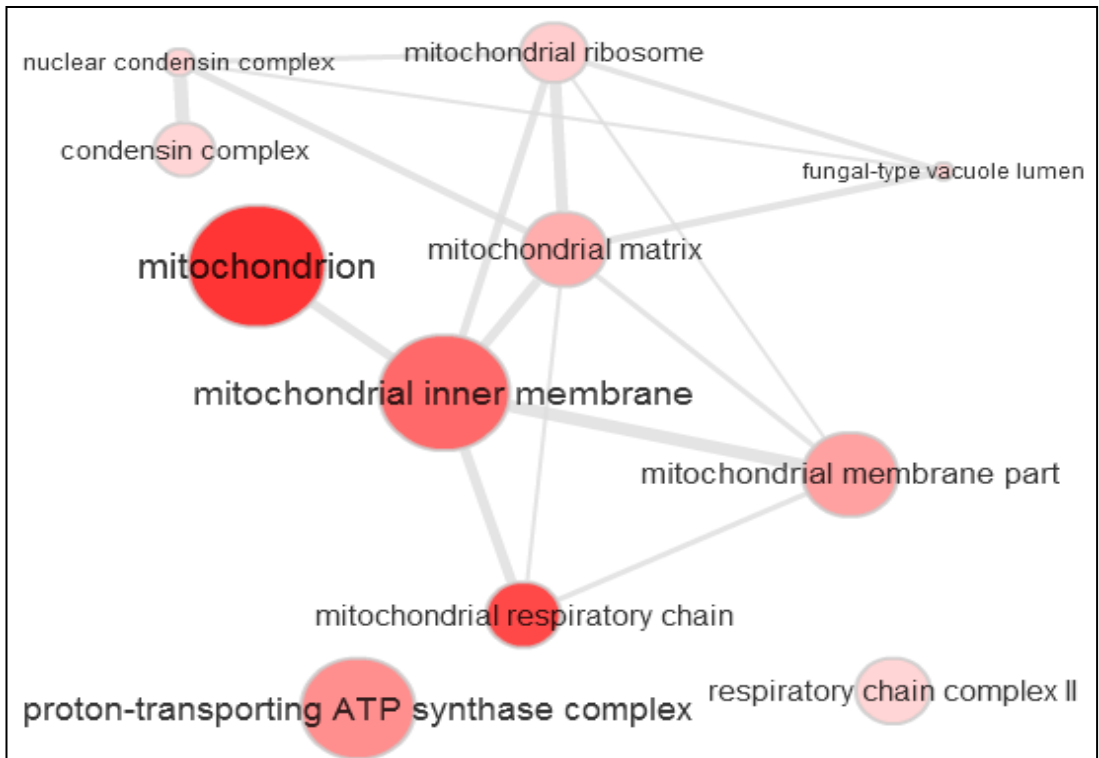
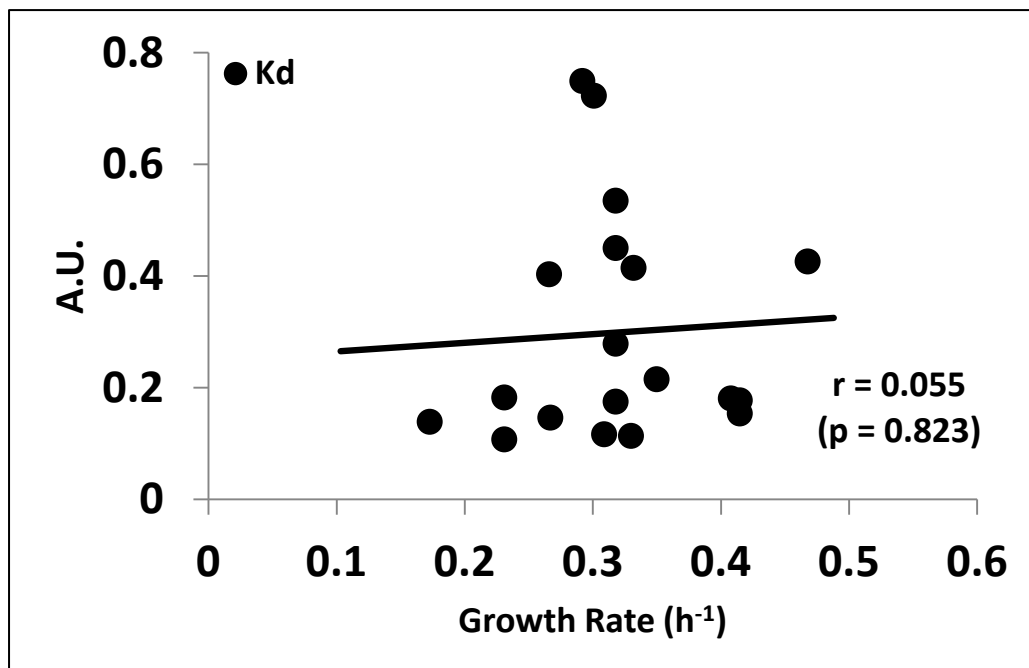
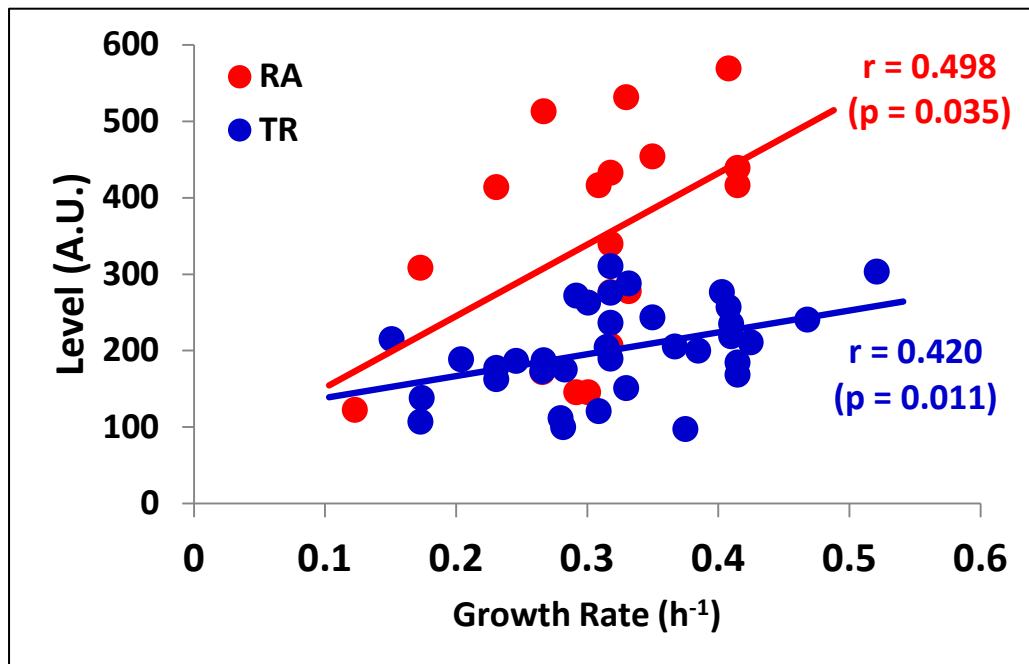


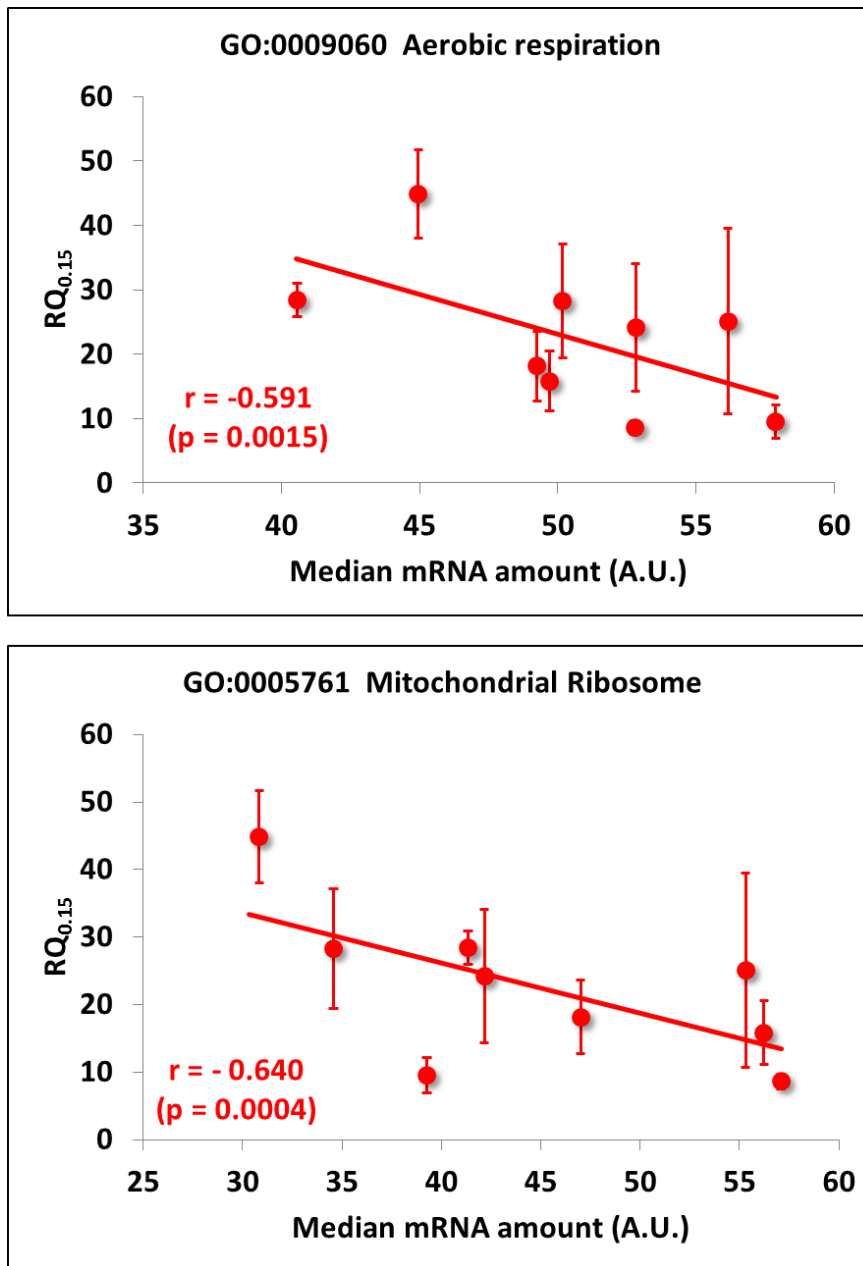
Figure S2.- GO enrichment searches for the highest positive and negative GR dependences in mRNA Transcription Rate and mRNA levels ([mRNA]). This figure is complementary to Fig. 2

ORF name	Gene name	Airoldi <i>et al.</i>	RA	TR
YEL040W	UTR2	up	up	up
YBL087C	RPL23A	up	up	up
YNL301C	RPL18B	up	up	up
YDL014W	NOP1	up	up	up
YGL076C	RPL7A	up	up	up
YOL120C	RPL18A	up	up	up
YDL081C	RPP1A	up	up	up
YDL130W	RPP1B	up	up	up
YEL026W	SNU13	up	up	up
YML056C	IMD4	up	up	up
YHR128W	FUR1	up	up	up
YMR242C	RPL20A	up	up	up
YOL039W	RPP2A	up	up	up
YGL031C	RPL24A	up	up	up
YLR406C	RPL31B	up	up	up
YGL156W	AMS1	down	down	down
YHR096C	HXT5	down	down	down
YJR008W	YJR008W	down	down	down
YGL121C	GPG1	down	down	down
YBL048W	YBL048W	down	down	down
<b>YOL052C-A</b>	<b>DDR2</b>	<b>down</b>	<b>down</b>	<b>up</b>
YJL161W	YJL161W	down	down	down
YOR338W	YOR338W	down	down	down
YBR169C	SSE2	down	down	down
YLL026W	HSP104	down	down	down
<b>Q0130</b>	<b>OLI1</b>	<b>down</b>	<b>down</b>	<b>up</b>
YDR258C	HSP78	down	down	down
YJL116C	NCA3	down	down	down
YDR171W	HSP42	down	down	down
YML128C	MSC1	down	down	down
<b>YDR379C-A</b>	<b>SDH6</b>	<b>down</b>	<b>down</b>	<b>up</b>
YLR178C	TFS1	down	down	down
YGR070W	ROM1	down	down	down
<b>YBR072W</b>	<b>HSP26</b>	<b>down</b>	<b>down</b>	<b>up</b>
YOR173W	DCS2	down	down	down
YGR032W	GSC2	down	down	down
YBL049W	MOH1	down	down	down
YHR138C	YHR138C	down	down	down
YLR312C	YLR312C	down	down	down
YPL186C	UIP4	down	down	down
YGR043C	YGR043C	down	down	down
YKR046C	PET10	down	down	down
YLR327C	YLR327C	down	down	down
YNL237W	YTP1	down	down	down
YCR021C	HSP30	down	down	down
<b>YIL136W</b>	<b>OM45</b>	<b>down</b>	<b>down</b>	<b>up</b>
<b>YGR142W</b>	<b>BTN2</b>	<b>down</b>	<b>down</b>	<b>up</b>
YIL160C	POT1	down	down	down
YDL085W	NDE2	down	down	down
YDL169C	UGX2	down	down	down
<b>YDR070C</b>	<b>FMP16</b>	<b>down</b>	<b>down</b>	<b>up</b>
YOL084W	PHM7	down	down	down
YGR088W	CTT1	down	down	down
YFL014W	HSP12	down	down	down
YGR248W	SOL4	down	down	down
YIR016W	YIR016W	down	down	down
YDL215C	GDH2	down	down	down

**Figure S3. Correspondence of the directionality in the correlation between Growth Rate and RA levels for Airoldi's Signature Genes in Airoldi's data and our data for RA and TR.**



**Figure S4.- Ribosomal proteins regulate their mRNA levels mainly at transcriptional level.** Data from all the RP mRNAs (113 genes) in dataset used in Fig. 1A. This figure is complementary to Fig. 3.



**Figure S5: The degree of respiration lowers at faster growth rates due to a decrease in respiratory gene transcripts.** Respiratory quotient (RQ) was quantified in YPD for nine yeast strains from the data set used in Fig. 1. The higher the RQ, the smaller the fraction of glucose metabolized by respiration. A lowering tendency for mRNA levels is seen for the genes coding for respiratory functions (GO:0009060 Aerobic Respiration, upper panel) and Mitochondrial Ribosome (GO:0005761 Mitochondrial Ribosome, lower panel) in the mutant strains with a lower RQ (higher respiration). Thus the negative correlation of mRNA levels with the GR for the mitochondria- and respiration-related genes seen (Figs. 3, 4) provokes lower respiratory rates when yeast cells grow faster. Pearson's correlation coefficients ( $r$ ) and associated  $p$ -values are shown.



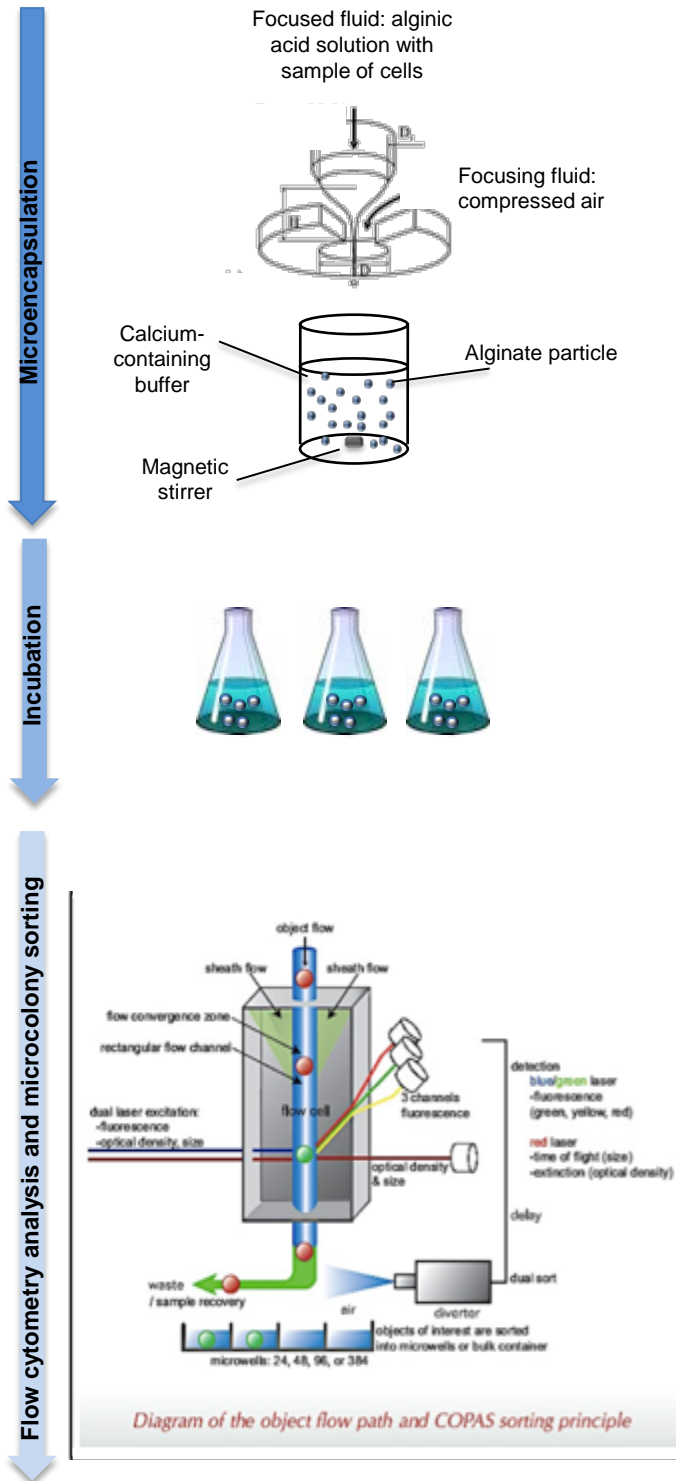


Figure S6. Cell microencapsulation, incubation, microcolony analysis and sorting.

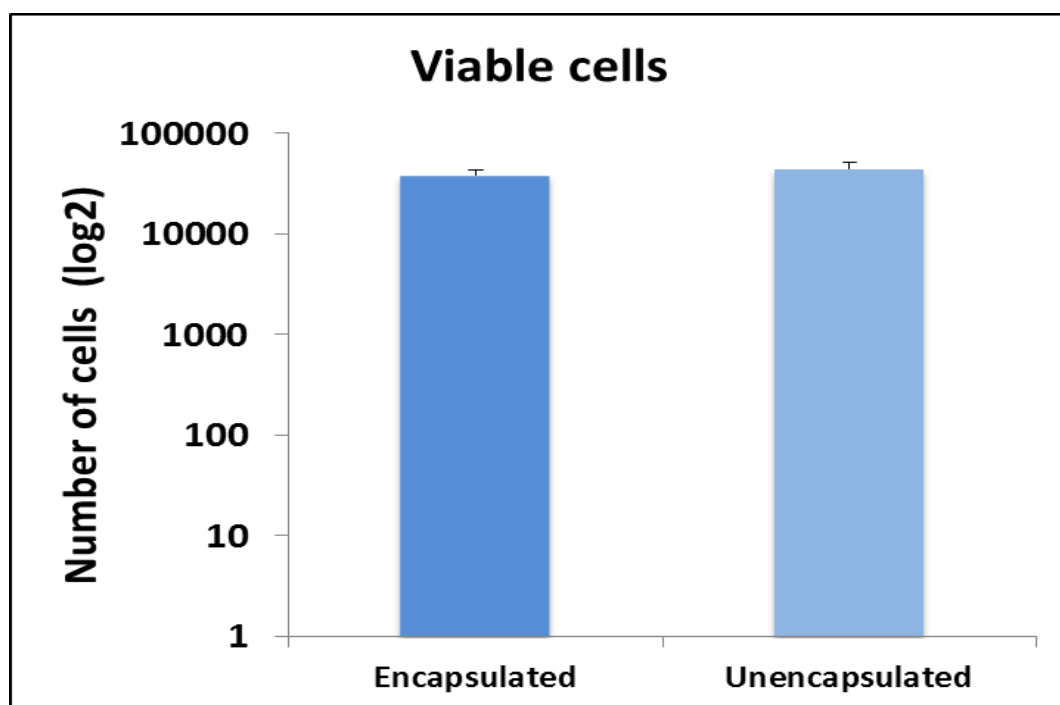
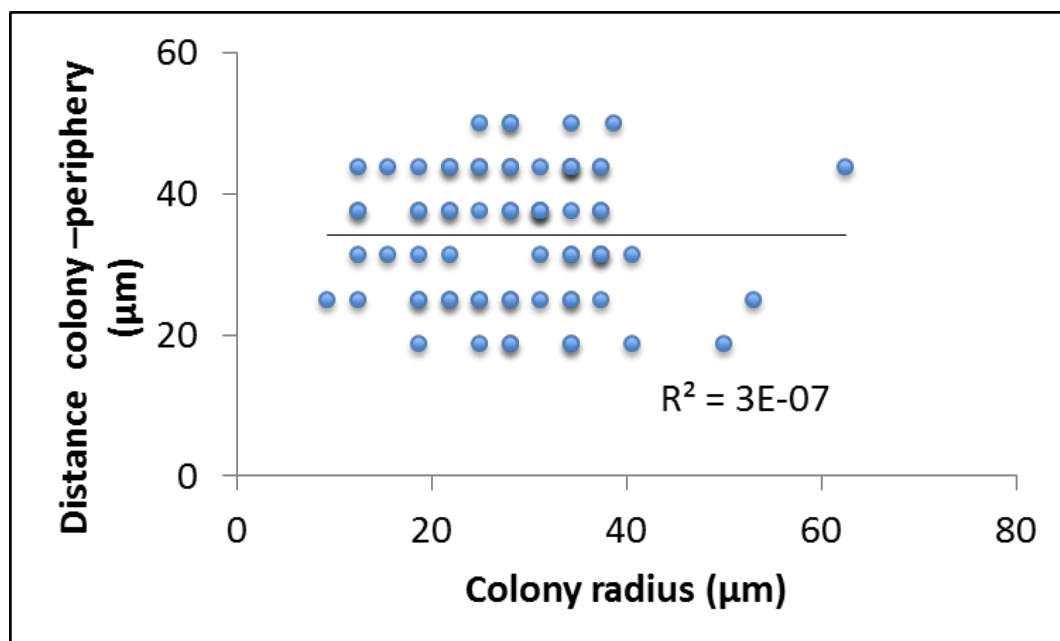
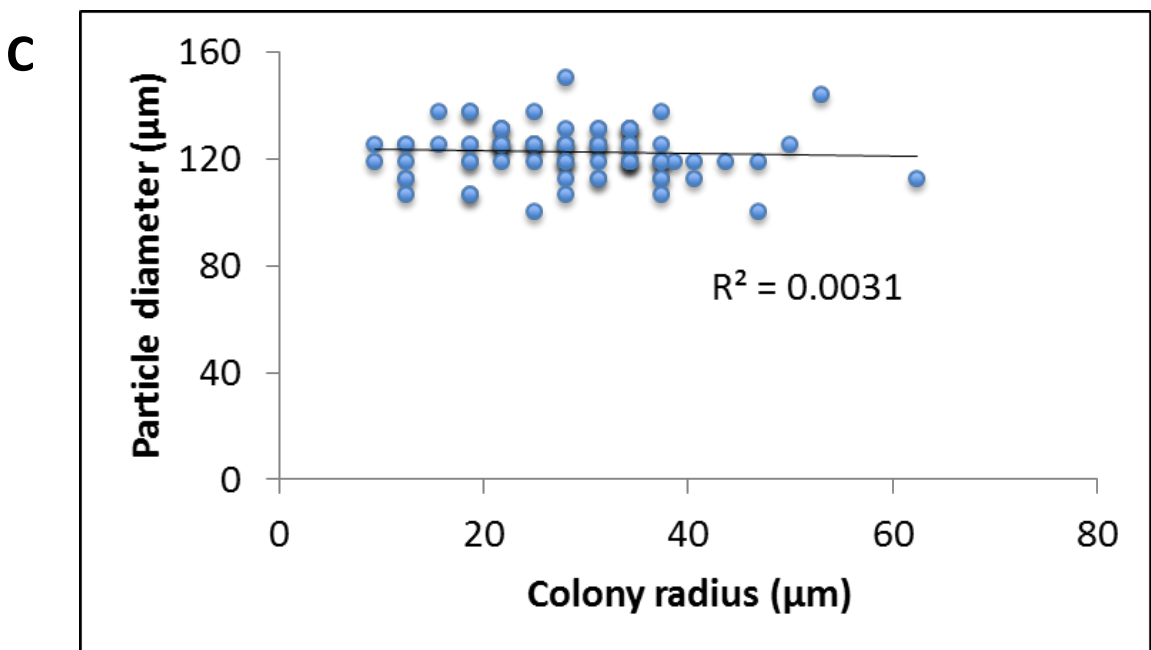
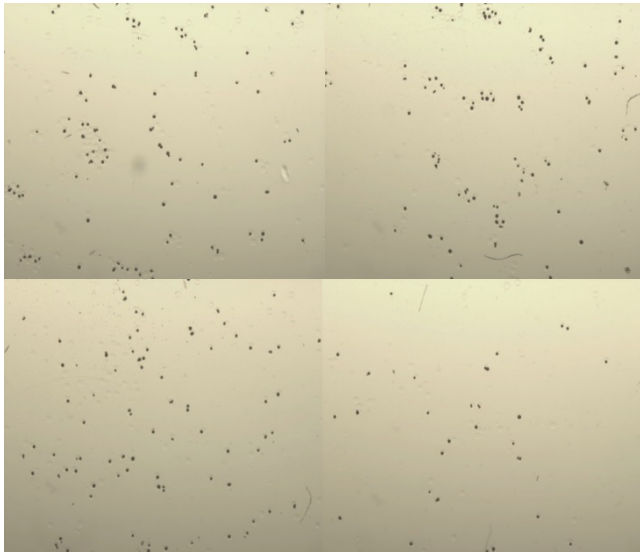
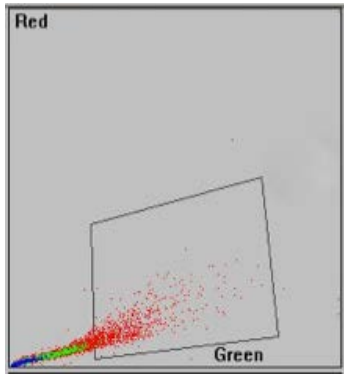
**A****B**

Figure S7



**Figure S7. Cells trapped in alginate particles remain fully viable and develop microcolonies without being influenced by the particle size or its location within the particle.** Panel A) Viability of the encapsulated cells of a standard experiment was compared with similar amount of cells, from the same culture, kept aside without being encapsulated. Cell viability was measured by its ability to form colonies on YPD agar plates. Average and standard deviation from three independent experiments is shown. Panel B) Size of 50 microcolonies grown during 14 hours in YPD medium and their distance to the external border of the alginate particle were measured and compared. No correlation was found. Panel C) Size of 50 microcolonies grown during 14 hours in YPD medium was compared to the size of their particles. No correlation was found. Tendency lines for linear regression and correlation coefficients are shown.

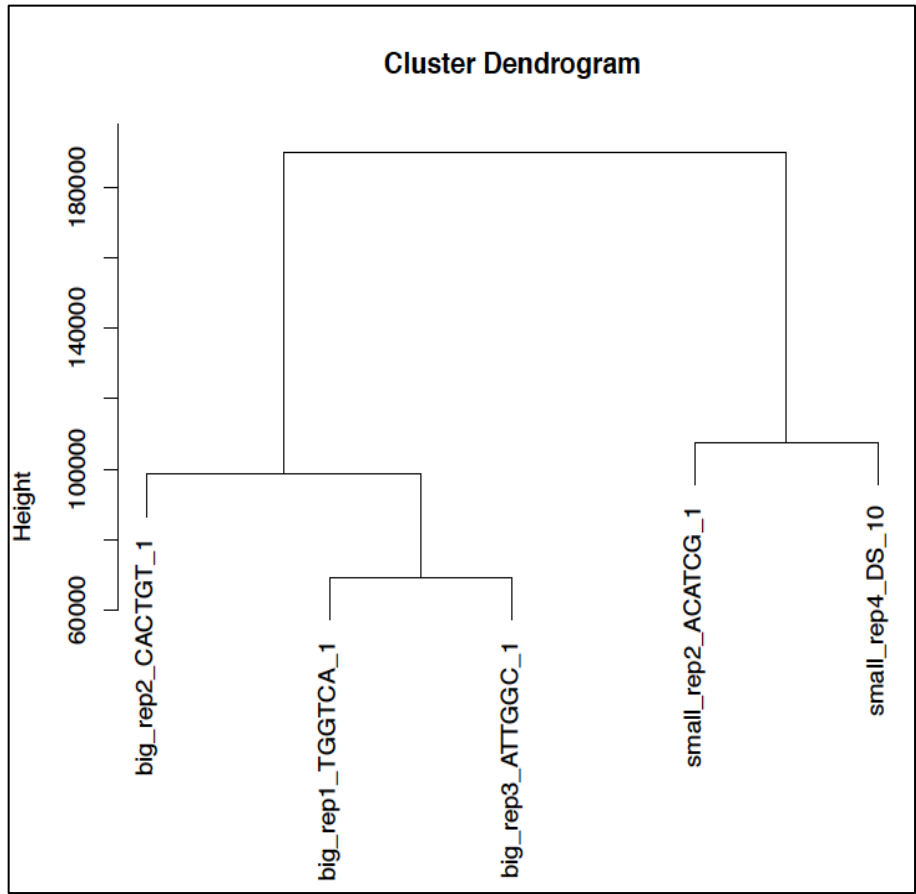
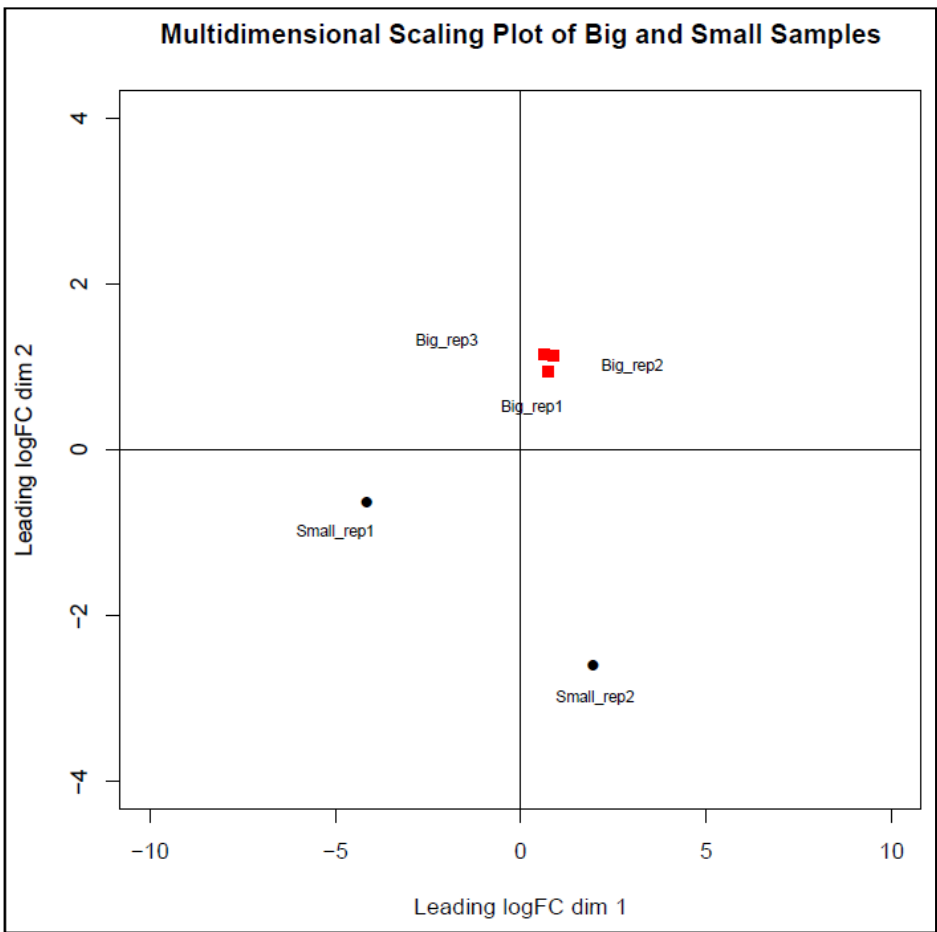
Big



Small



**Figure S8. Selection and sorting of big and small microcolonies.**

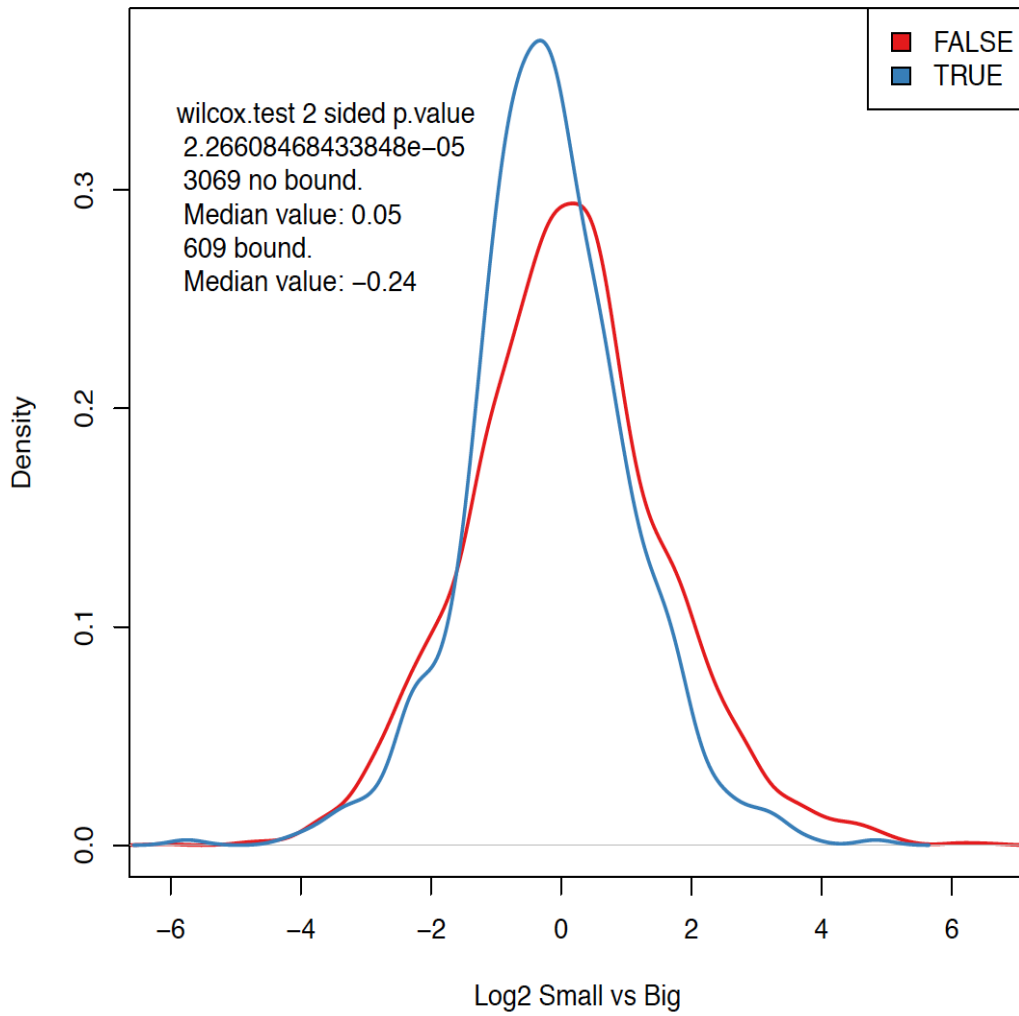


**Figure S9. Normalized quality check of microcolonies RNAseq results.**

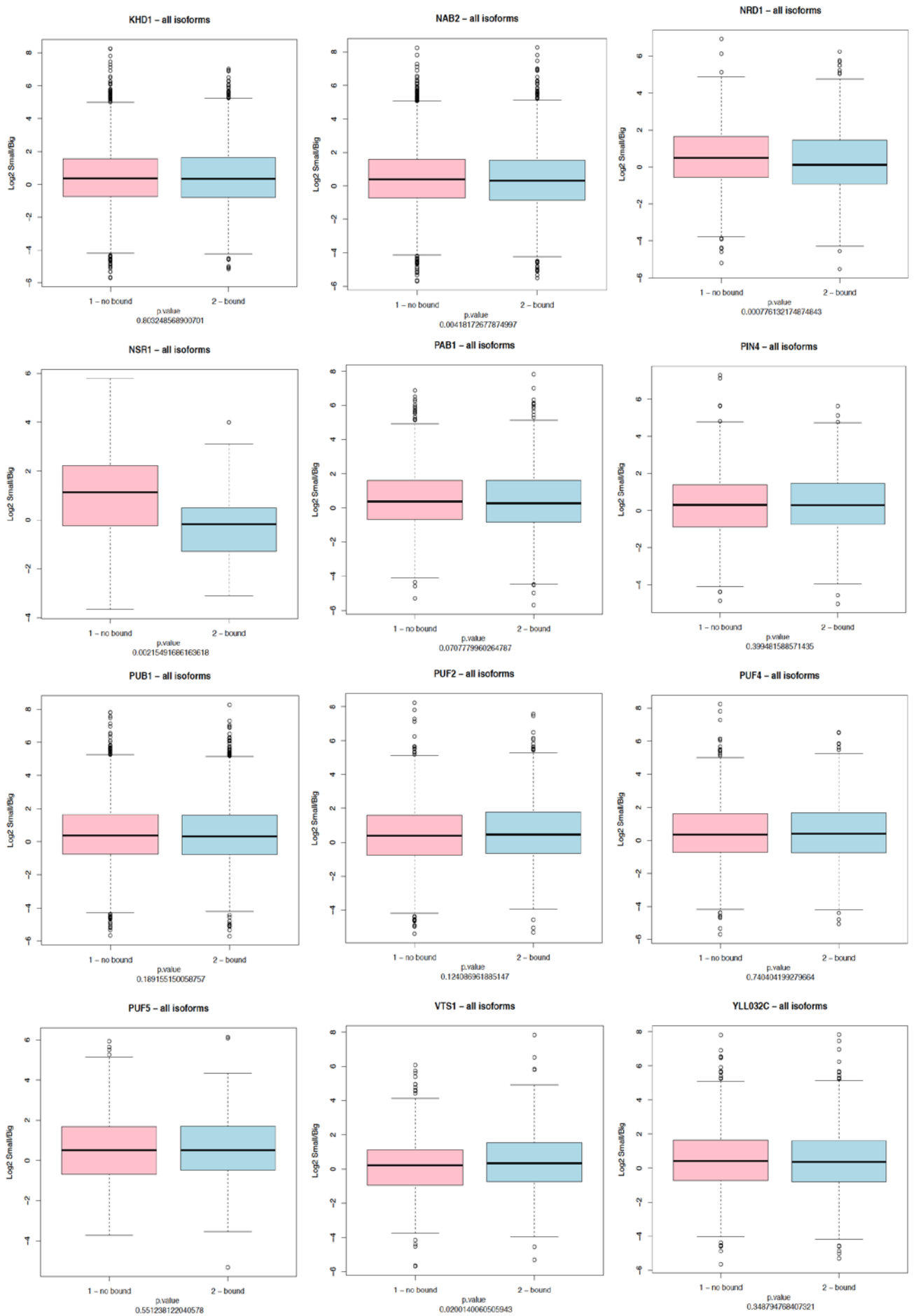
<b>Gene name</b>	<b>ORF name</b>	<b>log2 Fold</b>	<b>p-value</b>
MIG3	YER028C	-8.975	4.25E-05
POX1	YGL205W	-6.650	7.15E-05
YJR146W	YJR146W	-7.034	8.75E-05
HMS2	YJR147W	-7.034	8.75E-05
ELA1	YNL230C	-9.115	1.14E-04
YLR179C	YLR179C	-8.642	1.64E-04
CTF19	YPL018W	-9.039	1.79E-04
YCR087C-A	YCR087C-A	-8.478	2.02E-04
YNL092W	YNL092W	-6.589	4.92E-04
STP3	YLR375W	-5.626	6.38E-04
EMP65	YER140W	-6.148	7.22E-04
CMD1	YBR109C	-5.143	8.11E-04
NUP53	YMR153W	-6.090	1.03E-03
YLR312C	YLR312C	-7.882	1.03E-03
YPT53	YNL093W	-4.982	1.10E-03
CUE4	YML101C	-5.895	1.42E-03
HOT1	YMR172W	-7.410	1.43E-03
DON1	YDR273W	-4.214	1.91E-03

**Figure S10. mRNAs overrepresented in big microcolonies.**

### SRO9 binding site

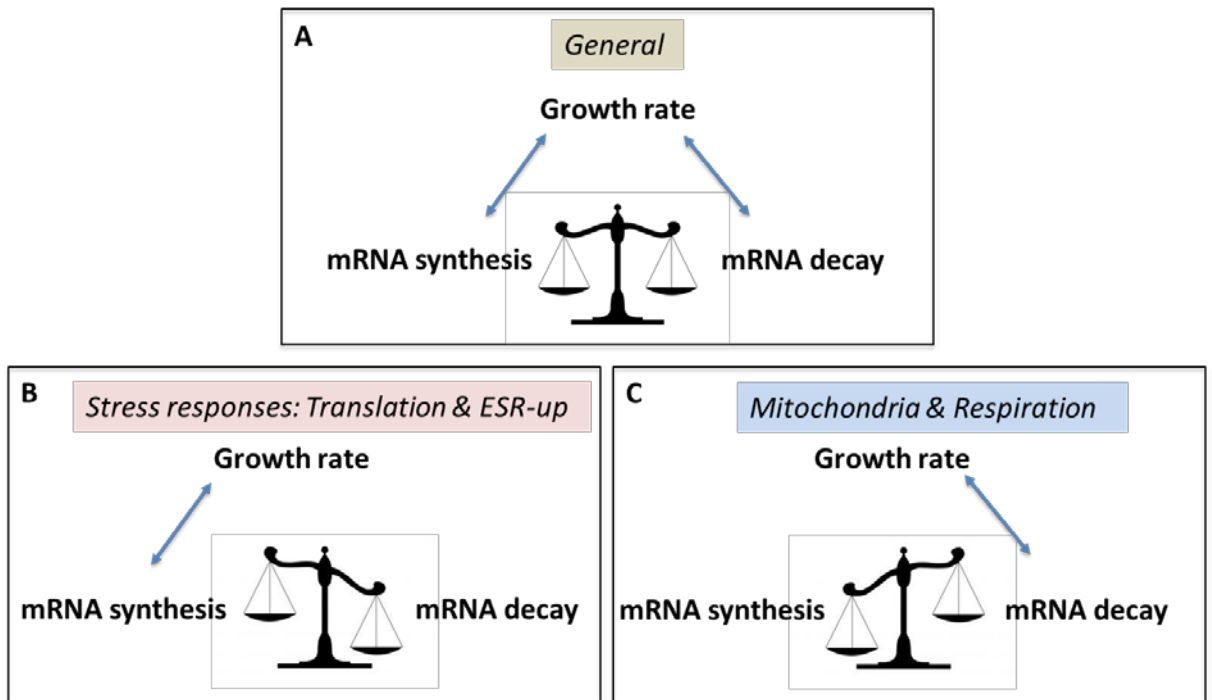


**Figure S11. mRNA bound by SRO9 are underrepresented in small microcolonies.**



**Figure S12. Relative distribution (small/big) of mRNA 3' isoforms containing binding sites for the indicated factors, compared to non-bound isoforms.**





**Figure S13. Model for the growth rate regulation of yeast gene expression.** A) The general control of mRNA synthesis and degradation machineries by the growth rate (GR) allows to maintain the general [mRNA] homeostasis and to adjust its turnover at a level compatible to an appropriate ratio between mRNA transmission from mother to daughter cells and the response capacity to environmental changes. The mechanistic cross-talk between transcription and mRNA decay ensures the maintenance of a constant mRNA concentration independently of the GR. B) For some gene functional categories, such as those affected in the environmental stress response (ESR) either down-regulated: translation-related genes and induced (ESR-up), the mRNA concentration is transcriptionally modified by the GR due to the uncoupling of the decay machinery. C) In the respiratory and mitochondrial-related genes, the GR controls the mRNA concentration by acting on mRNA degradation, while mRNA synthesis machinery remains uncoupled.

**Table S1A.** List of strains/samples from our laboratory used in this study indicating the culture conditions as well as the experimentally calculated Growth Rate.

Sample	Strain name	Genetic background	Culture medium	Temp. (°C)	Growth Rate (h <sup>-1</sup> )
1	BQS252	S288C	YPD	28	0.468
2	BQS252	S288C	YPGal	28	0.359
3	YMC458 wt	S288C	YPD	28	0.408
4	YMC461 xrn1-D208A	S288C	YPD	28	0.231
5	YMC511 xrn1Δ	S288C	YPD	28	0.267
6	BY4741 rai1Δ	S288C	YPD	28	0.204
7	BY4741 wt	S288C	YPD	28	0.415
8	BY4741 rpb4Δ	S288C	YPD	28	0.231
9	BY4741 sfp1Δ	S288C	YPD	28	0.173
10	BY4741 dst1Δ	S288C	YPD	28	0.415
11	BY4741 wt	S288C	YPGal	28	0.347
12	BY4741 rpb4Δ	S288C	YPGal	28	0.231
13	BY4741 sfp1Δ	S288C	YPGal	28	0.154
14	BY4741 dst1Δ	S288C	YPGal	28	0.315
15	GYLR-4B	S288C	YPD	23	0.246
16	GYLR-4B	S288C	YPD	30	0.425
17	GYLR-4B	S288C	YPD	37	0.375
18	RAP1	SCR101	YPD	28	0.283
19	rap1Δsil	SCR101	YPD	28	0.151
20	tpk1Δ	S288C	YPD	28	0.521
21	tpk2Δ	S288C	YPD	28	0.403
22	SJY6-spt16Δ	S288C	YPD	28	0.282
23	HPR1	W303	YPRaff	26	0.264
24	hpr1-degron	W303	YPRaff	26	0.286
25	hpr1Δ	W303	YPRaff	26	0.174
26	mex67-5	S288C	YPD	26	0.280
27	BY4741 wt	S288C	YPD	30	0.415
28	BY4741 wt	S288C	YPD	35	0.415
29	BY4741 DMY2	S288C	YPD	30	0.367
30	BY4741 DMY2	S288C	YPD	35	0.361
31	src1Δ	S288C	YPD	28	0.350
32	sus1Δ	W303	YPD	28	0.330
33	sac3NM	S288C	YPD	28	0.318
34	sac3Δ	S288C	YPD	28	0.309
35	hog1Δ	W303	YPD	28	0.332
36	wt (t0-Os)	W303	YPD	28	0.318
37	wt (t0-Ox)	W303	YPD	28	0.318
38	wt (t0-HS)	W303	YPD	25	0.266
39	wt	W303	YPD	28	0.318
40	pub1Δ	W303	YPD	28	0.292
41	ngr1Δ	W303	YPD	28	0.301
42	pub1Δ	W303	YPGal	28	0.123

**Table S1B.** List of mutant strains from Sun *et al.* (2013) used in this study indicating the experimentally calculated Growth Rate. Cell volumes are expressed as fold relative to the wild type strain.

<b>Deleted Gene</b>	<b>GR (h<sup>-1</sup>)</b>	<b>Volume</b>
RAI1	0.2207	0.951
POP2	0.2302	1.366
DHH1	0.2391	0.976
XRN1	0.2483	1.659
RRP47	0.2791	1.155
LSM6	0.2928	1.170
CCR4	0.2985	1.441
RRP6	0.3138	0.956
PAT1	0.3188	1.074
PUF6	0.3274	1.010
SKI8	0.3315	0.956
LSM1	0.3336	0.956
HBS1	0.3356	1.038
SKI2	0.3368	0.990
PUB1	0.3465	0.891
PUF4	0.3470	0.956
RTT103	0.3479	0.990
DOM34	0.3485	0.891
ESC1	0.3495	0.943
SKI3	0.3499	0.976
TPA1	0.3524	0.910
PUF3	0.3535	1.024
UPF3	0.3544	1.125
DCS1	0.3549	0.793
PUF1	0.3553	0.956
AIR2	0.3558	0.956
UPF2	0.3566	1.125
EDC3	0.3567	0.956
AIR1	0.3574	0.976
PUF2	0.3579	0.943
SKI7	0.3589	0.956
SCD6	0.3614	0.943
DCS2	0.3632	0.943
CTH1	0.3659	0.976
SWT1	0.3685	0.976
NOT3	0.3756	0.943
PAN3	0.3784	0.990
PAN2	0.3840	1.038

**Table S2.** Description of GO terms found in the SAM analyses (represented in Figure 2). All represented searches are for the GO Biological Process.

**A.** Terms overrepresented in the top of correlation between TR and GR

GO_ID	p-value	Term
GO:0042254	<1E-10	ribosome biogenesis
GO:0022613	<1E-10	ribonucleoprotein complex biogenesis
GO:0006364	<1E-10	rRNA processing
GO:0034470	<1E-10	ncRNA processing
GO:0006412	<1E-10	translation
GO:0042274	<1E-10	ribosomal small subunit biogenesis
GO:0042273	<1E-10	ribosomal large subunit biogenesis
GO:0030490	<1E-10	maturation of SSU-rRNA
GO:0000470	1.651E-05	maturation of LSU-rRNA
GO:0000967	1.661E-05	rRNA 5'-end processing
GO:0043144	7.242E-04	snoRNA processing
GO:0006407	9.465E-04	rRNA export from nucleus
GO:0045739	2.299E-03	positive regulation of DNA repair
GO:0072395	2.299E-03	signal transduction involved in cell cycle checkpoint
GO:0006414	6.053E-03	translational elongation
GO:2000001	6.679E-03	regulation of DNA damage checkpoint
GO:1903311	7.544E-03	regulation of mRNA metabolic process
GO:0044267	1.029E-02	cellular protein metabolic process
GO:0031123	1.059E-02	RNA 3'-end processing
GO:0009304	1.139E-02	tRNA transcription

**B.** Terms overrepresented in the bottom of correlation between TR and GR

GO_ID	p-value	Term
GO:0006749	3.705E-07	glutathione metabolic process
GO:0006629	9.034E-07	lipid metabolic process
GO:0044699	3.652E-06	single-organism metabolic process
GO:0055114	1.232E-04	oxidation-reduction process
GO:0044255	6.624E-04	cellular lipid metabolic process
GO:0010906	6.754E-04	regulation of glucose metabolic process
GO:0006111	2.362E-03	regulation of gluconeogenesis
GO:0070129	2.362E-03	regulation of mitochondrial translation
GO:0006575	2.492E-03	cellular modified amino acid metabolic process
GO:0010565	3.101E-03	regulation of cellular ketone metabolic process
GO:0045333	3.582E-03	cellular respiration
GO:0006793	5.034E-03	phosphorus metabolic process
GO:0006518	5.427E-03	peptide metabolic process
GO:0006508	5.879E-03	proteolysis
GO:0009060	1.884E-02	aerobic respiration
GO:0070585	2.234E-02	protein localization to mitochondrion
GO:0022904	3.492E-02	respiratory electron transport chain
GO:0042775	3.492E-02	mitochondrial ATP synthesis coupled electron transport
GO:0006635	3.541E-02	fatty acid beta-oxidation

Table S2 continued

## C. Terms overrepresented in the top of correlation between RA and GR

GO_ID	p-value	Term
GO:0034470	1.14E-08	ncRNA processing
GO:0032259	4.65E-08	methylation
GO:0034660	5.04E-08	ncRNA metabolic process
GO:0043414	1.315E-07	macromolecule methylation
GO:0042254	1.749E-07	ribosome biogenesis
GO:0008033	4.065E-07	tRNA processing
GO:0009066	1.3811E-06	aspartate family amino acid metabolic process
GO:1901566	1.6068E-06	organonitrogen compound biosynthetic process
GO:0009309	3.5365E-06	amine biosynthetic process
GO:0016053	3.6877E-06	organic acid biosynthetic process
GO:0019752	7.2196E-06	carboxylic acid metabolic process
GO:0006082	8.0162E-06	organic acid metabolic process
GO:0022613	8.5781E-06	ribonucleoprotein complex biogenesis
GO:0009304	1.0783E-05	tRNA transcription
GO:0042797	1.0783E-05	tRNA transcription from RNA polymerase III promoter
GO:0001510	1.0799E-05	RNA methylation
GO:0044281	4.0242E-05	small molecule metabolic process
GO:0000097	0.000257	sulfur amino acid biosynthetic process
GO:0006457	0.000345	protein folding
GO:0000096	0.000464	sulfur amino acid metabolic process
GO:0000103	0.000590	sulfate assimilation
GO:0006396	0.000951	RNA processing

## D. Terms overrepresented in the bottom of correlation between RA and GR

GO_ID	p-value	Term
GO:0005761	5.2E-09	mitochondrial ribosome
GO:0005759	2.932E-07	mitochondrial matrix
GO:0005618	4.885E-07	cell wall
GO:0030312	4.885E-07	external encapsulating structure
GO:0044429	7.75E-07	mitochondrial part
GO:0009277	1.1134E-06	fungal-type cell wall
GO:0005576	1.5036E-06	extracellular region
GO:0031225	2.2227E-06	anchored to membrane
GO:0044391	2.511E-06	ribosomal subunit
GO:0005739	3.0347E-06	mitochondrion
GO:0005773	4.0752E-06	vacuole
GO:0005762	5.5708E-06	mitochondrial large ribosomal subunit
GO:0031224	8.3334E-06	intrinsic to membrane
GO:0000323	0.00013	lytic vacuole
GO:0034657	0.00055	GID complex
GO:0044437	0.00062	vacuolar part
GO:0005763	0.00151	mitochondrial small ribosomal subunit

Table S2 continued

## E. Terms overrepresented in the top of correlation between kd and GR

GO_ID	p-value	Term
GO:0044429	9.716E-05	mitochondrial part
GO:0005761	0.000359	mitochondrial ribosome
GO:0005759	0.000466	mitochondrial matrix
GO:0071013	0.000659	catalytic step 2 spliceosome
GO:0031305	0.001059	integral to mitochondrial inner membrane
GO:0000151	0.001429	ubiquitin ligase complex
GO:0031304	0.001700	intrinsic to mitochondrial inner membrane
GO:0044391	0.001835	ribosomal subunit
GO:0031461	0.002083	cullin-RING ubiquitin ligase complex
GO:0031966	0.002292	mitochondrial membrane
GO:0033186	0.005752	CAF-1 complex
GO:0044437	0.008078	vacuolar part
GO:0005774	0.010512	vacuolar membrane
GO:0005743	0.013854	mitochondrial inner membrane
GO:0005778	0.014534	peroxisomal membrane
GO:0031903	0.014534	microbody membrane

## F. Terms overrepresented in the bottom of correlation between kd and GR

GO_ID	p-value	Term
GO:0042254	1.2672E-06	ribosome biogenesis
GO:0070085	1.7431E-06	glycosylation
GO:0006486	1.796E-06	protein glycosylation
GO:1901137	4.5284E-06	carbohydrate derivative biosynthetic process
GO:0034470	1.5003E-05	ncRNA processing
GO:0006364	3.2938E-05	rRNA processing
GO:0016072	4.6444E-05	rRNA metabolic process
GO:0022613	0.000169	ribonucleoprotein complex biogenesis
GO:0009066	0.000178	aspartate family amino acid metabolic process
GO:0034660	0.000209	ncRNA metabolic process
GO:0042274	0.000236	ribosomal small subunit biogenesis
GO:0051168	0.000249	nuclear export
GO:0016053	0.000267	organic acid biosynthetic process
GO:0046394	0.000267	carboxylic acid biosynthetic process
GO:0000054	0.000373	ribosomal subunit export from nucleus
GO:0033750	0.000373	ribosome localization
GO:0030488	0.000582	tRNA methylation
GO:0042273	0.000928	ribosomal large subunit biogenesis
GO:0042790	0.001098	transcription of nuclear large rRNA transcript from RNA polymerase I promoter
GO:0009067	0.001127	aspartate family amino acid biosynthetic process
GO:1901566	0.001227	organonitrogen compound biosynthetic process

**Table S3.** Description of GO terms found in the SAM analyses (represented in Figure S3). All searches correspond to Biological Process GO Term except the indicated ones.

**A.** Terms overrepresented in the top of correlation between TR and GR

GO_ID	p-value	Term
GO:0034470	<1E-10	ncRNA processing
GO:0042254	<1E-10	ribosome biogenesis
GO:0022613	<1E-10	ribonucleoprotein complex biogenesis
GO:0006364	<1E-10	rRNA processing
GO:0042273	<1E-10	ribosomal large subunit biogenesis
GO:0051188	<1E-10	cofactor biosynthetic process
GO:0009309	<1E-10	amine biosynthetic process
GO:0032259	<1E-10	methylation
GO:0009067	3.6E-09	aspartate family amino acid biosynthetic process
GO:0009086	1.47E-08	methionine biosynthetic process
GO:0009451	1.74E-08	RNA modification
GO:0008033	1.79E-08	tRNA processing
GO:0009066	3.75E-08	aspartate family amino acid metabolic process
GO:0000096	8.16E-08	sulfur amino acid metabolic process
GO:0019752	1.875E-07	carboxylic acid metabolic process
GO:0008652	1.931E-07	cellular amino acid biosynthetic process
GO:0006400	5.095E-07	tRNA modification
GO:0042274	1.5827E-06	ribosomal small subunit biogenesis
GO:0001510	2.4689E-06	RNA methylation
GO:0009308	2.6218E-06	amine metabolic process
GO:0044272	4.0904E-06	sulfur compound biosynthetic process
GO:0000054	5.3627E-06	ribosomal subunit export from nucleus
GO:0018193	1.5536E-05	peptidyl-amino acid modification
GO:0000460	2.6593E-05	maturation of 5.8S rRNA
GO:0090502	4.2895E-05	RNA phosphodiester bond hydrolysis, endonucleolytic
GO:0009069	7.5152E-05	serine family amino acid metabolic process

**B.** Terms overrepresented in the bottom of correlation between TR and GR

GO_ID	p-value	Term
GO:0071900	5.3594E-06	regulation of protein serine/threonine kinase activity
GO:0000079	1.5575E-05	regulation of cyclin-dependent protein kinase activity
GO:0051726	0.000215	regulation of cell cycle
GO:0051338	0.000307	regulation of transferase activity
GO:0051301	0.000499	cell division
GO:0000278	0.000566	mitotic cell cycle
GO:0018345	0.000756	protein palmitoylation
GO:0001932	0.000760	regulation of protein phosphorylation
GO:0071852	0.001140	fungal-type cell wall organization or biogenesis
GO:0030100	0.001144	regulation of endocytosis
GO:0022403	0.001310	cell cycle phase
GO:0000920	0.001352	cytokinetic cell separation

Table S3 continued

GO:0042325	0.001986	regulation of phosphorylation
GO:0022604	0.002313	regulation of cell morphogenesis
GO:0000087	0.002650	M phase of mitotic cell cycle
GO:0007067	0.002683	mitosis

**C.** Terms overrepresented in the top of correlation between RA and GR

GO_ID	p-value	Term
GO:0006433	0.00071717	prolyl-tRNA aminoacylation
GO:0006418	0.01358219	tRNA aminoacylation for protein translation
GO:0043038	0.01465051	amino acid activation
GO:0043039	0.01465051	tRNA aminoacylation

**D.** Terms overrepresented in the bottom of correlation between RA and GR

GO_ID	p-value	Term
GO:0015980	1.3E-08	energy derivation by oxidation of organic compounds
GO:0009060	1.173E-07	aerobic respiration
GO:0045333	5.207E-07	cellular respiration
GO:0006119	1.2708E-06	oxidative phosphorylation
GO:0022904	2.389E-06	respiratory electron transport chain
GO:0042773	2.389E-06	ATP synthesis coupled electron transport
GO:0042775	2.389E-06	mitochondrial ATP synthesis coupled electron transport
GO:0022900	8.0639E-05	electron transport chain
GO:0055114	0.000108	oxidation-reduction process
GO:0044262	0.000109	cellular carbohydrate metabolic process
GO:0006099	0.000141	tricarboxylic acid cycle
GO:0031669	0.001066	cellular response to nutrient levels
GO:0005977	0.001478	glycogen metabolic process

**E.** Terms overrepresented in the top of correlation between TR and GR (Cellular Component)

GO_ID	p-value	Term
GO:0005730	<1E-10	nucleolus
GO:0030684	<1E-10	preribosome
GO:0030687	<1E-10	preribosome, large subunit precursor
GO:0005838	3.80E-07	proteasome regulatory particle
GO:0000502	1.3304E-06	proteasome complex
GO:0030686	2.3964E-06	90S preribosome
GO:0005829	0.000197	cytosol
GO:0044452	0.000621	nucleolar part
GO:0005832	0.001030	chaperonin-containing T-complex



Table S3 continued

## F. Terms overrepresented in the bottom of correlation between RA and GR (Cellular Component)

<b>GO_ID</b>	<b>p-value</b>	<b>Term</b>
GO:0005739	1.5E-09	mitochondrion
GO:0005746	1.23E-08	mitochondrial respiratory chain
GO:0005743	2.902E-07	mitochondrial inner membrane
GO:0070469	1.9286E-06	respiratory chain
GO:0005753	1.3735E-05	mitochondrial proton-transporting ATP synthase complex
GO:0045259	1.3735E-05	proton-transporting ATP synthase complex
GO:0031966	3.8641E-05	mitochondrial membrane
GO:0005751	0.000227	mitochondrial respiratory chain complex IV
GO:0005759	0.000256	mitochondrial matrix
GO:0045275	0.001851	respiratory chain complex III
GO:0031461	0.006071	cullin-RING ubiquitin ligase complex
GO:0000313	0.006342	organellar ribosome
GO:0005761	0.006342	mitochondrial ribosome
GO:0000796	0.015103	condensin complex
GO:0000328	0.018366	fungal-type vacuole lumen

**Table S4.** Gene Ontology (GO) terms significantly overrepresented in the GSA analyses

## A. GO terms significantly overrepresented in the top of correlation between TR and GR

<b>GO_ID</b>	<b>p-value</b>							
1	GO:0000049	0.0007	35	GO:0050684	0.0145	70	GO:0022627	0.0267
2	GO:0000056	0.0019	36	GO:0000472	0.0146	71	GO:0042790	0.028
3	GO:0006405	0.0025	37	GO:0031126	0.0155	72	GO:0006913	0.0288
4	GO:0043628	0.0026	38	GO:0007004	0.0157	73	GO:0051169	0.0288
5	GO:0044452	0.003	39	GO:0000460	0.0159	74	GO:0000459	0.0291
6	GO:0050658	0.0038	40	GO:0000466	0.0159	75	GO:0090503	0.0291
7	GO:0051236	0.0038	41	GO:0034470	0.0159	76	GO:0006278	0.031
8	GO:0030515	0.0048	42	GO:0016074	0.0161	77	GO:0000027	0.0314
9	GO:0050657	0.0053	43	GO:0031125	0.0163	78	GO:0042255	0.0323
10	GO:0000463	0.0056	44	GO:0042273	0.0164	79	GO:2001251	0.0327
11	GO:0000470	0.0056	45	GO:0034660	0.0167	80	GO:0043634	0.0357
12	GO:0015931	0.0076	46	GO:0004004	0.0168	81	GO:0071029	0.0357
13	GO:0051168	0.0076	47	GO:0042274	0.0172	82	GO:0071046	0.0357
14	GO:0006403	0.0079	48	GO:0042254	0.0173	83	GO:0070925	0.0363
15	GO:0000080	0.0081	49	GO:0005730	0.018	84	GO:0051536	0.0365
16	GO:0051318	0.0081	50	GO:0000447	0.0182	85	GO:0051540	0.0365
17	GO:0090501	0.0101	51	GO:0006364	0.0184	86	GO:0043144	0.0375
18	GO:0032040	0.0103	52	GO:0010833	0.0186	87	GO:0051325	0.0378
19	GO:0090502	0.0111	53	GO:0030490	0.0186	88	GO:0051329	0.0378
20	GO:0000469	0.0115	54	GO:0000462	0.0187	89	GO:0022626	0.0401
21	GO:0005732	0.0115	55	GO:0016072	0.0193	90	GO:0045899	0.0401
22	GO:0000967	0.0121	56	GO:0071025	0.0196	91	GO:0001054	0.0402
23	GO:0034471	0.0121	57	GO:0071027	0.0196	92	GO:0005736	0.0402
24	GO:0031123	0.0124	58	GO:0003724	0.0209	93	GO:0007064	0.0418
25	GO:0030686	0.0126	59	GO:0045898	0.0212	94	GO:0044445	0.0422
26	GO:0008186	0.0127	60	GO:0022613	0.0215	95	GO:0002181	0.0424
27	GO:0000480	0.0129	61	GO:0009451	0.0224	96	GO:0000176	0.0438
28	GO:0000966	0.0129	62	GO:0030684	0.0233	97	GO:0008033	0.0442
29	GO:0000478	0.0131	63	GO:0000084	0.0239	98	GO:0001522	0.0446
30	GO:0000479	0.0131	64	GO:0051320	0.0239	99	GO:0070847	0.0448
31	GO:0000114	0.0142	65	GO:0032844	0.0242	100	GO:0030687	0.045
32	GO:0006407	0.0144	66	GO:0016078	0.0252	101	GO:0051537	0.0451
33	GO:0051029	0.0144	67	GO:0071038	0.0252	102	GO:0022625	0.0453
34	GO:0003723	0.0145	68	GO:0016073	0.0254			
			69	GO:0006399	0.0256			

Table S4 continued

## B. GO terms significantly overrepresented in in the bottom of correlation between TR and GR

	<b>GO_ID</b>	<b>p-value</b>						
1	GO:0006749	0.0005	46	GO:0031668	0.0178	92	GO:0032511	0.0342
2	GO:0006518	0.0012	47	GO:0071496	0.0178	93	GO:0045834	0.0346
3	GO:0005811	0.0022	48	GO:0031968	0.018	94	GO:0019898	0.0355
4	GO:0006111	0.0022	49	GO:0046914	0.0183	95	GO:0033613	0.0357
5	GO:0016788	0.0027	50	GO:0001010	0.0185	96	GO:0006631	0.0359
6	GO:0019932	0.0029	51	GO:0045182	0.0185	97	GO:0010906	0.0364
7	GO:0008610	0.003	52	GO:0042180	0.0186	98	GO:0051604	0.0368
8	GO:0042578	0.0032	53	GO:0009898	0.0187	99	GO:0015718	0.0369
9	GO:0006629	0.0033	54	GO:0030100	0.0189	100	GO:0010677	0.037
10	GO:0010676	0.0034	55	GO:0006900	0.0193	101	GO:0045912	0.037
11	GO:0045913	0.0034	56	GO:0008204	0.0193	102	GO:0042558	0.0375
12	GO:0006575	0.0035	57	GO:0016128	0.0193	103	GO:0032182	0.0385
13	GO:0042219	0.0035	58	GO:0019867	0.0195	104	GO:0042398	0.0388
14	GO:0006665	0.0051	59	GO:0031667	0.02	105	GO:0000132	0.0392
15	GO:0000959	0.0059	60	GO:0051186	0.0204	106	GO:0051294	0.0392
16	GO:0043603	0.0063	61	GO:0006734	0.0207	107	GO:0005886	0.0403
17	GO:0016765	0.0068	62	GO:0070131	0.0209	108	GO:0010033	0.0403
18	GO:1901615	0.0075	63	GO:0009605	0.0214	109	GO:0044262	0.0404
19	GO:0016791	0.0079	64	GO:0009991	0.0214	110	GO:0072330	0.0409
20	GO:0043255	0.0083	65	GO:0008287	0.0228	111	GO:0000754	0.0417
21	GO:0006109	0.0089	66	GO:0006633	0.0239	112	GO:0023058	0.0417
22	GO:0010675	0.0095	67	GO:0071310	0.0243	113	GO:0042559	0.0429
23	GO:0006066	0.0096	68	GO:0044107	0.0246	114	GO:0010876	0.043
24	GO:0006984	0.0098	69	GO:0015203	0.0255	115	GO:0019208	0.0434
25	GO:0030968	0.0098	70	GO:0045121	0.0258	116	GO:0006720	0.0439
26	GO:0034620	0.0098	71	GO:0016310	0.0261	117	GO:0008299	0.0439
27	GO:0034976	0.0098	72	GO:0006986	0.0267	118	GO:0030950	0.0439
28	GO:0051213	0.0098	73	GO:0035556	0.027	119	GO:0030952	0.0439
29	GO:0035967	0.0103	74	GO:0016616	0.0277	120	GO:0060627	0.0442
30	GO:0044255	0.0103	75	GO:0030117	0.0282	121	GO:0000023	0.0445
31	GO:0010565	0.0126	76	GO:0048475	0.0282	122	GO:0019674	0.0453
32	GO:0007154	0.0129	77	GO:0070129	0.0284	123	GO:0009108	0.0461
33	GO:0046653	0.0129	78	GO:0030036	0.0289	124	GO:0004659	0.0462
34	GO:0090114	0.013	79	GO:0012507	0.0291	125	GO:0016790	0.0463
35	GO:0006732	0.0135	80	GO:0019200	0.0292	126	GO:0000151	0.0465
36	GO:0007165	0.0135	81	GO:0046686	0.0293	127	GO:0006081	0.0466
37	GO:0023052	0.0135	82	GO:0016301	0.0299	128	GO:0010821	0.0469
38	GO:0044700	0.0135	83	GO:0000920	0.0309	129	GO:0045324	0.047
39	GO:0008237	0.0149	84	GO:0016614	0.0314	130	GO:0016491	0.0473
40	GO:0005741	0.0154	85	GO:0008599	0.0323	131	GO:0004091	0.0477
41	GO:0035966	0.0155	86	GO:0006696	0.0324	132	GO:0006508	0.0484
42	GO:0006637	0.0157	87	GO:0016129	0.0324	133	GO:0016772	0.0484
43	GO:0035383	0.0157	88	GO:0044108	0.0324	134	GO:0016705	0.049
44	GO:0031669	0.0161	89	GO:0010822	0.0327	135	GO:0007034	0.0491
45	GO:0016485	0.0167	90	GO:0009396	0.0331	136	GO:0006623	0.0495
			91	GO:0006760	0.0332			

Table S4 continued

## C. GO terms significantly overrepresented in the top of correlation between RA and GR

	<b>GO_ID</b>	<b>p-values</b>		<b>GO_ID</b>	<b>p-values</b>		<b>GO_ID</b>	<b>p-values</b>
1	GO:0008135	0.0006	34	GO:0051168	0.0122	68	GO:0008156	0.0339
2	GO:0004812	0.0007	35	GO:0016835	0.0129	69	GO:0031225	0.034
3	GO:0016875	0.0007	36	GO:0022625	0.0134	70	GO:0015931	0.0345
4	GO:0016876	0.0007	37	GO:0006399	0.0137	71	GO:0005779	0.0349
5	GO:0006418	0.0009	38	GO:0006488	0.0145	72	GO:0031231	0.0349
6	GO:0043038	0.0009	39	GO:0000027	0.0154	73	GO:0006475	0.0351
7	GO:0043039	0.0009	40	GO:0006473	0.0155	74	GO:0018393	0.0351
8	GO:0046695	0.0016	41	GO:0006267	0.0163	75	GO:0018394	0.0351
9	GO:0031365	0.0033	42	GO:0036388	0.0163	76	GO:0015215	0.0355
10	GO:0046112	0.0039	43	GO:0070925	0.0163	77	GO:0015934	0.0358
11	GO:0042255	0.0046	44	GO:1902299	0.0163	78	GO:0006417	0.036
12	GO:0019395	0.005	45	GO:0030488	0.0165	79	GO:0009123	0.0361
13	GO:0034440	0.005	46	GO:0006414	0.0175	80	GO:0006797	0.0374
14	GO:0000028	0.0062	47	GO:0022618	0.0177	81	GO:0016741	0.038
15	GO:0000124	0.0068	48	GO:0003723	0.0191	82	GO:0032947	0.038
16	GO:0000054	0.0076	49	GO:0006412	0.0198	83	GO:0030686	0.0384
17	GO:0003743	0.0076	50	GO:0009129	0.0203	84	GO:0044445	0.0385
18	GO:0033750	0.0076	51	GO:0009130	0.0203	85	GO:0034397	0.0397
19	GO:0033753	0.0076	52	GO:0071826	0.0204	86	GO:0000049	0.0424
20	GO:0071166	0.0076	53	GO:0006413	0.0222	87	GO:0018205	0.0426
21	GO:0071426	0.0076	54	GO:0001510	0.0232	88	GO:0006520	0.0429
22	GO:0071428	0.0076	55	GO:0006913	0.0251	89	GO:0009082	0.0429
23	GO:0009081	0.0081	56	GO:0051169	0.0251	90	GO:0005656	0.0436
24	GO:0051640	0.0085	57	GO:0031160	0.0258	91	GO:0036387	0.0436
25	GO:0042398	0.0088	58	GO:0000002	0.0269	92	GO:0000055	0.0445
26	GO:0043543	0.0091	59	GO:0009124	0.0275	93	GO:0033260	0.045
27	GO:0070461	0.0093	60	GO:0051656	0.0282	94	GO:0044786	0.045
28	GO:0006730	0.0099	61	GO:1901264	0.0288	95	GO:0000767	0.0465
29	GO:0005619	0.0102	62	GO:1901677	0.0296	96	GO:0005840	0.0472
30	GO:0006448	0.0105	63	GO:0022626	0.0297	97	GO:0016573	0.0472
31	GO:0006220	0.0117	64	GO:0006450	0.0308	98	GO:0043021	0.0473
32	GO:0006221	0.0117	65	GO:0050000	0.0308	99	GO:0009156	0.049
33	GO:0006575	0.0122	66	GO:0042273	0.0324	100	GO:0030658	0.049
			67	GO:0015605	0.033			

Table S4 continued

## D. GO terms significantly overrepresented in the bottom of correlation between RA and GR

	<b>GO_ID</b>	<b>p-values</b>		<b>GO_ID</b>	<b>p-values</b>		<b>GO_ID</b>	<b>p-values</b>
1	GO:0010648	0.002	31	GO:0006915	0.0185	61	GO:0004842	0.0317
2	GO:0016567	0.002	32	GO:0008219	0.0185	62	GO:0016881	0.033
3	GO:0048585	0.0029	33	GO:0012501	0.0185	63	GO:0048583	0.0331
4	GO:0070647	0.0033	34	GO:0016265	0.0185	64	GO:0003777	0.034
5	GO:0042787	0.0036	35	GO:0031109	0.0185	65	GO:0070887	0.0341
6	GO:0009968	0.0037	36	GO:0042221	0.019	66	GO:0042493	0.0346
7	GO:0023057	0.0037	37	GO:0019787	0.0191	67	GO:0051056	0.0352
8	GO:0031461	0.0038	38	GO:0009605	0.0195	68	GO:0006914	0.036
9	GO:0000279	0.0041	39	GO:0009991	0.0195	69	GO:0000940	0.0365
10	GO:0023051	0.005	40	GO:0042594	0.0216	70	GO:0000942	0.0365
11	GO:0009225	0.0056	41	GO:0031668	0.022	71	GO:0006111	0.037
12	GO:0030162	0.0058	42	GO:0071496	0.022	72	GO:0045185	0.037
13	GO:0009966	0.0073	43	GO:0046578	0.0223	73	GO:0008287	0.0371
14	GO:0030246	0.0082	44	GO:0031396	0.0226	74	GO:0051015	0.038
15	GO:0032446	0.0082	45	GO:0000429	0.0229	75	GO:0009267	0.0385
16	GO:0007265	0.0091	46	GO:0000001	0.0232	76	GO:0016236	0.0388
17	GO:0000151	0.0101	47	GO:0005680	0.0237	77	GO:0005381	0.039
18	GO:0006081	0.0107	48	GO:0032270	0.0244	78	GO:0022900	0.039
19	GO:0010646	0.0107	49	GO:0007266	0.026	79	GO:0016042	0.0418
20	GO:0031145	0.0111	50	GO:0044767	0.0264	80	GO:0043255	0.0422
21	GO:0008599	0.0122	51	GO:0051235	0.0268	81	GO:0016558	0.0429
22	GO:0051247	0.0135	52	GO:0048311	0.0277	82	GO:0006109	0.0432
23	GO:0042176	0.014	53	GO:0007165	0.0291	83	GO:0000749	0.044
24	GO:0000152	0.0146	54	GO:0023052	0.0291	84	GO:0009060	0.0468
25	GO:0031667	0.0146	55	GO:0044700	0.0291	85	GO:0004860	0.0474
26	GO:0017004	0.0148	56	GO:0032507	0.0305	86	GO:0031625	0.0482
27	GO:0031669	0.0161	57	GO:0032502	0.0311	87	GO:0044389	0.0482
28	GO:0045990	0.0164	58	GO:0031110	0.0312	88	GO:0051336	0.0491
29	GO:0000045	0.017	59	GO:0046173	0.0312	89	GO:0009896	0.0496
30	GO:0007154	0.0181	60	GO:0000753	0.0316	90	GO:0051651	0.0496

**Table S5.** Gene Ontology (GO) terms significantly overrepresented in the GSA analyses of the data from Sun et al. (2013).

A. GO terms significantly overrepresented in the top of correlation between TR and GR

	<b>GO_ID</b>	<b>p-value</b>						
1	GO:0070566	0.0037	43	GO:0030137	0.0187	86	GO:0032986	0.0343
2	GO:0019359	0.0041	44	GO:0051186	0.0188	87	GO:0033202	0.0351
3	GO:0006457	0.0043	45	GO:0000054	0.0197	88	GO:0016772	0.0357
4	GO:0009435	0.0048	46	GO:0033750	0.0197	89	GO:0009072	0.036
5	GO:0019363	0.0069	47	GO:0033753	0.0197	90	GO:0006368	0.0363
6	GO:0016853	0.0072	48	GO:0043604	0.0197	91	GO:0016586	0.0369
7	GO:0016835	0.0073	49	GO:0071166	0.0197	92	GO:0006520	0.0377
8	GO:0009108	0.0075	50	GO:0071426	0.0197	93	GO:0018208	0.0379
9	GO:0009308	0.0084	51	GO:0071428	0.0197	94	GO:0006733	0.0383
10	GO:0009309	0.0085	52	GO:0008757	0.0218	95	GO:0000002	0.0384
11	GO:0016779	0.0085	53	GO:0005829	0.0221	96	GO:0072525	0.0395
12	GO:0051087	0.009	54	GO:0008175	0.0221	97	GO:0008652	0.0399
13	GO:0051082	0.0102	55	GO:0044272	0.0227	98	GO:0016053	0.0404
14	GO:0051188	0.0105	56	GO:0046496	0.0234	99	GO:0046394	0.0404
15	GO:0009067	0.0112	57	GO:0030488	0.0236	100	GO:0043650	0.0409
16	GO:0006576	0.012	58	GO:0006790	0.024	101	GO:0055086	0.0412
17	GO:0060590	0.0128	59	GO:0008173	0.024	102	GO:0006890	0.0421
18	GO:0006284	0.0131	60	GO:0044106	0.0253	103	GO:0006612	0.0425
19	GO:0000096	0.0137	61	GO:0005838	0.026	104	GO:1901566	0.0426
20	GO:0000097	0.0137	62	GO:0022624	0.026	105	GO:0016866	0.0427
21	GO:0009086	0.0138	63	GO:0030687	0.0263	106	GO:0042273	0.0432
22	GO:0044445	0.0139	64	GO:0043414	0.0273	107	GO:0019752	0.0434
23	GO:0034243	0.014	65	GO:0043248	0.0275	108	GO:0006082	0.0439
24	GO:0009066	0.0143	66	GO:0016810	0.0277	109	GO:0009069	0.0442
25	GO:0043094	0.0144	67	GO:0006760	0.0278	110	GO:0003690	0.0445
26	GO:0032259	0.0147	68	GO:0042558	0.0278	111	GO:0043436	0.0448
27	GO:0006732	0.0151	69	GO:0000413	0.028	112	GO:0006354	0.0452
28	GO:0006555	0.0154	70	GO:0003755	0.028	113	GO:0008033	0.0455
29	GO:0019674	0.0155	71	GO:0016859	0.028	114	GO:0018193	0.0455
30	GO:0016814	0.0163	72	GO:0000502	0.0289	115	GO:0072524	0.0457
31	GO:0016741	0.0169	73	GO:0001510	0.0297	116	GO:0016836	0.0462
32	GO:0031072	0.017	74	GO:0006400	0.0298	117	GO:0018022	0.0463
33	GO:0050661	0.0171	75	GO:0019362	0.0298	118	GO:0009070	0.0464
34	GO:0009396	0.0174	76	GO:0009165	0.0303	119	GO:0006333	0.0467
35	GO:0042559	0.0174	77	GO:1901605	0.0316	120	GO:0000463	0.0474
36	GO:0006575	0.0175	78	GO:0003743	0.0322	121	GO:0008408	0.0483
37	GO:0005525	0.018	79	GO:0006720	0.0323	122	GO:0006446	0.0485
38	GO:0019001	0.018	80	GO:0008299	0.0323	123	GO:0006479	0.0499
39	GO:0032561	0.018	81	GO:0043648	0.0324	124	GO:0008213	0.0499
40	GO:0008168	0.0181	82	GO:0009451	0.0337			
41	GO:0032968	0.0181	83	GO:1901293	0.0337			
42	GO:0042398	0.0182	84	GO:0006337	0.0343			
			85	GO:0031498	0.0343			

Table S5. Continued

## B. GO terms significantly overrepresented in in the bottom of correlation between TR and GR

	<b>GO_ID</b>	<b>p-value</b>						
1	GO:0000982	0.0036	35	GO:0007154	0.0226	70	GO:0009605	0.0361
2	GO:0001077	0.005	36	GO:0065009	0.0227	71	GO:0009991	0.0361
3	GO:0001228	0.005	37	GO:0019932	0.0231	72	GO:0032506	0.0362
4	GO:0000429	0.0081	38	GO:0019899	0.0232	73	GO:0001071	0.0376
5	GO:0000436	0.0095	39	GO:0000977	0.0234	74	GO:0003700	0.0376
6	GO:0000920	0.0104	40	GO:0001012	0.0238	75	GO:0007091	0.038
7	GO:0051128	0.0109	41	GO:0009651	0.0244	76	GO:0009653	0.038
8	GO:0050793	0.0113	42	GO:0000079	0.0256	77	GO:0048856	0.038
9	GO:0022603	0.0116	43	GO:0006972	0.0256	78	GO:0000307	0.0384
10	GO:0007120	0.0138	44	GO:0030100	0.0259	79	GO:0051726	0.0397
11	GO:0000080	0.0141	45	GO:0000437	0.0262	80	GO:0031669	0.04
12	GO:0051318	0.0141	46	GO:0042594	0.0265	81	GO:0000003	0.0401
13	GO:0000987	0.0151	47	GO:0048869	0.027	82	GO:0032989	0.0402
14	GO:0001159	0.0155	48	GO:0001932	0.0271	83	GO:0048584	0.041
15	GO:0000981	0.0157	49	GO:0001101	0.0273	84	GO:0019207	0.0413
16	GO:0022604	0.0161	50	GO:0000083	0.0282	85	GO:0048610	0.0414
17	GO:0043086	0.0167	51	GO:0008028	0.0283	86	GO:0006468	0.042
18	GO:0001078	0.0183	52	GO:0007033	0.029	87	GO:0015748	0.0424
19	GO:0001227	0.0183	53	GO:0042325	0.0291	88	GO:0045991	0.0427
20	GO:0045944	0.0194	54	GO:0050790	0.0292	89	GO:0048585	0.0433
21	GO:0005576	0.0195	55	GO:0045990	0.0296	90	GO:0031668	0.0436
22	GO:0005618	0.02	56	GO:0031225	0.0297	91	GO:0071496	0.0436
23	GO:0030312	0.02	57	GO:0007096	0.0299	92	GO:0000430	0.0443
24	GO:0032101	0.02	58	GO:0000978	0.0307	93	GO:0046015	0.0443
25	GO:0032104	0.02	59	GO:0016747	0.0314	94	GO:0051321	0.0443
26	GO:0032107	0.02	60	GO:0044092	0.0314	95	GO:0000902	0.046
27	GO:0019900	0.0201	61	GO:0047484	0.0319	96	GO:0030865	0.0467
28	GO:0019901	0.0201	62	GO:0045013	0.0322	97	GO:0030866	0.0467
29	GO:0045859	0.0203	63	GO:0019887	0.0324	98	GO:1900428	0.0469
30	GO:0009277	0.0205	64	GO:0051301	0.0327	99	GO:0031399	0.047
31	GO:0043900	0.0205	65	GO:0016538	0.0328	100	GO:0042144	0.0471
32	GO:0071900	0.0206	66	GO:0031667	0.0339	101	GO:0004872	0.048
33	GO:0043549	0.0208	67	GO:0006357	0.0343	102	GO:0080134	0.0498
34	GO:0051338	0.0208	68	GO:0000976	0.0357			
			69	GO:0070491	0.0358			

Table S5. Continued

## C. GO terms significantly overrepresented in the top of correlation between RA and GR

	<b>GO_ID</b>	<b>p-values</b>						
1	GO:0006893	0.003	34	GO:1901605	0.019	68	GO:0019752	0.0317
2	GO:0016853	0.004	35	GO:0051082	0.0191	69	GO:0005666	0.0318
3	GO:0018193	0.0045	36	GO:0009165	0.0196	70	GO:0006082	0.0325
4	GO:0006575	0.0055	37	GO:0019363	0.0199	71	GO:0046496	0.0328
5	GO:0009435	0.0066	38	GO:0043604	0.0199	72	GO:0008168	0.0338
6	GO:0006457	0.0071	39	GO:1901293	0.0201	73	GO:0032259	0.0342
7	GO:0005829	0.0079	40	GO:0006790	0.0207	74	GO:0009304	0.0352
8	GO:0006576	0.0086	41	GO:0044272	0.0218	75	GO:0030011	0.0352
9	GO:0000413	0.0092	42	GO:0006890	0.022	76	GO:0042797	0.0352
10	GO:0003755	0.0092	43	GO:0050661	0.022	77	GO:0006760	0.0356
11	GO:0016859	0.0092	44	GO:0003690	0.024	78	GO:0042558	0.0356
12	GO:0018208	0.0095	45	GO:0051087	0.024	79	GO:0008175	0.0361
13	GO:0009066	0.01	46	GO:0005548	0.0243	80	GO:0006541	0.0373
14	GO:0009308	0.0104	47	GO:0016053	0.0243	81	GO:0005525	0.0375
15	GO:0019359	0.0104	48	GO:0046394	0.0243	82	GO:0019001	0.0375
16	GO:0009123	0.0124	49	GO:0031365	0.0248	83	GO:0032561	0.0375
17	GO:0009124	0.0124	50	GO:0009070	0.0253	84	GO:1901607	0.0388
18	GO:0009072	0.0128	51	GO:0042398	0.0254	85	GO:0070566	0.0391
19	GO:1901606	0.0135	52	GO:0006520	0.0259	86	GO:0008757	0.0403
20	GO:0009067	0.0136	53	GO:0044106	0.0259	87	GO:0043648	0.0406
21	GO:0009309	0.0139	54	GO:0009396	0.026	88	GO:0006284	0.0428
22	GO:0009156	0.014	55	GO:0042559	0.026	89	GO:0006334	0.0449
23	GO:0009161	0.014	56	GO:0016741	0.0262	90	GO:0055086	0.0464
24	GO:1901677	0.0144	57	GO:0006612	0.0265	91	GO:0008173	0.0469
25	GO:0006555	0.0151	58	GO:0009069	0.0271	92	GO:0006470	0.0473
26	GO:1901566	0.0156	59	GO:0019674	0.0272	93	GO:0006400	0.0476
27	GO:0000097	0.0158	60	GO:0016746	0.0278	94	GO:0009310	0.0476
28	GO:0009086	0.0158	61	GO:0060590	0.0285	95	GO:0019362	0.0485
29	GO:0000096	0.0163	62	GO:0016311	0.0299	96	GO:0031334	0.049
30	GO:0045833	0.0175	63	GO:0008652	0.0301	97	GO:0044283	0.0492
31	GO:0051055	0.0175	64	GO:0016866	0.0304	98	GO:0017025	0.0493
32	GO:0043094	0.0188	65	GO:0030488	0.0304			
33	GO:0044445	0.0189	66	GO:0009063	0.0313			
			67	GO:0043436	0.0316			



Table S5. Continued

## D. GO terms significantly overrepresented in the bottom of correlation between RA and GR

	<b>GO_ID</b>	<b>p-values</b>						
1	GO:0000920	0.0033	32	GO:0044767	0.0256	64	GO:0009272	0.0402
2	GO:0022414	0.0047	33	GO:0006111	0.0259	65	GO:0022603	0.0408
3	GO:0043900	0.0086	34	GO:0031225	0.0261	66	GO:0048646	0.0413
4	GO:0048869	0.0091	35	GO:0050790	0.0262	67	GO:0006476	0.0414
5	GO:0001403	0.011	36	GO:0000003	0.0264	68	GO:0022604	0.0414
6	GO:0004407	0.0123	37	GO:0009651	0.0268	69	GO:0044182	0.0417
7	GO:0033558	0.0123	38	GO:0022413	0.027	70	GO:0071310	0.0419
8	GO:0033692	0.0134	39	GO:0007033	0.0281	71	GO:0042325	0.043
9	GO:0032502	0.0139	40	GO:0043549	0.0282	72	GO:0001932	0.0431
10	GO:0019932	0.0142	41	GO:0051338	0.0282	73	GO:0000754	0.0433
11	GO:0000271	0.0144	42	GO:0045859	0.0291	74	GO:0023058	0.0433
12	GO:0032101	0.0148	43	GO:0003006	0.0296	75	GO:0042546	0.0444
13	GO:0032104	0.0148	44	GO:0000982	0.0298	76	GO:0071900	0.0447
14	GO:0032107	0.0148	45	GO:0005576	0.0298	77	GO:0000307	0.045
15	GO:0006896	0.0149	46	GO:0000083	0.0305	78	GO:0016811	0.0453
16	GO:0016575	0.0153	47	GO:0044092	0.0306	79	GO:0004553	0.0456
17	GO:0036267	0.0156	48	GO:0019900	0.0308	80	GO:0048584	0.0461
18	GO:0001077	0.0171	49	GO:0019901	0.0308	81	GO:0051651	0.0461
19	GO:0001228	0.0171	50	GO:0001078	0.0321	82	GO:0070726	0.0461
20	GO:0019899	0.0176	51	GO:0001227	0.0321	83	GO:0000422	0.0462
21	GO:0065009	0.0184	52	GO:0009277	0.0324	84	GO:0043934	0.0482
22	GO:0019213	0.0197	53	GO:0005618	0.0327	85	GO:2000242	0.0482
23	GO:0050793	0.0206	54	GO:0030312	0.0327	86	GO:0006073	0.0491
24	GO:0048610	0.0207	55	GO:0051235	0.0346	87	GO:0044042	0.0491
25	GO:0044264	0.0232	56	GO:0006094	0.0347	88	GO:0017016	0.0493
26	GO:0030154	0.0234	57	GO:0019319	0.0347	89	GO:0031267	0.0493
27	GO:0001101	0.0235	58	GO:0046364	0.0347	90	GO:0000079	0.0497
28	GO:0009653	0.0236	59	GO:0005976	0.0356			
29	GO:0048856	0.0236	60	GO:0010033	0.0364			
30	GO:0005546	0.0243	61	GO:0016051	0.0372			
31	GO:0043086	0.0243	62	GO:2000241	0.038			
			63	GO:0007154	0.0387			

Table S5. Continued

## E. GO terms significantly overrepresented in the top of correlation between Kd and GR

<b>GO_ID</b>	<b>p-values</b>							
1	GO:0071310	0.0019	32	GO:0006511	0.0232	64	GO:0016874	0.0385
2	GO:0016567	0.004	33	GO:0003006	0.0236	65	GO:0004842	0.039
3	GO:0000386	0.0052	34	GO:0005057	0.0238	66	GO:0006743	0.0397
4	GO:0006515	0.0067	35	GO:0044093	0.024	67	GO:0006744	0.0397
5	GO:0043130	0.0075	36	GO:0044257	0.0244	68	GO:0042181	0.0397
6	GO:0000749	0.0086	37	GO:0019941	0.0245	69	GO:0042375	0.0397
7	GO:0052689	0.0094	38	GO:0000746	0.0252	70	GO:0045426	0.0397
8	GO:0032266	0.0098	39	GO:0019740	0.0264	71	GO:1901661	0.0397
9	GO:0000152	0.0109	40	GO:0022414	0.0273	72	GO:1901663	0.0397
10	GO:0006896	0.0111	41	GO:0051345	0.0279	73	GO:0006623	0.0401
11	GO:0032446	0.0113	42	GO:0046349	0.0289	74	GO:0072665	0.0401
12	GO:0010033	0.0117	43	GO:0005099	0.029	75	GO:0072666	0.0401
13	GO:0019953	0.012	44	GO:0031625	0.0295	76	GO:0032851	0.0403
14	GO:0005680	0.0134	45	GO:0044389	0.0295	77	GO:0000183	0.0405
15	GO:0032182	0.0134	46	GO:0000109	0.0304	78	GO:0070887	0.0412
16	GO:0071444	0.0145	47	GO:0009118	0.0304	79	GO:0043161	0.0414
17	GO:0000151	0.0146	48	GO:0030811	0.0304	80	GO:0043596	0.0419
18	GO:0070647	0.0167	49	GO:0033121	0.0304	81	GO:0004091	0.0424
19	GO:0051603	0.0177	50	GO:0007186	0.0312	82	GO:0042180	0.0433
20	GO:0006023	0.0203	51	GO:0007034	0.0318	83	GO:0000165	0.0444
21	GO:0006031	0.0203	52	GO:0005096	0.0322	84	GO:0006270	0.0446
22	GO:1901073	0.0203	53	GO:0007166	0.0325	85	GO:0051336	0.0457
23	GO:0005546	0.0204	54	GO:0022413	0.0337	86	GO:0031304	0.0458
24	GO:0000747	0.0205	55	GO:0031305	0.034	87	GO:0006508	0.0469
25	GO:0032313	0.0205	56	GO:0000750	0.0346	88	GO:0071006	0.0473
26	GO:0032483	0.0205	57	GO:0032005	0.0346	89	GO:0071012	0.0473
27	GO:0031461	0.0206	58	GO:0035822	0.0351	90	GO:0033674	0.0478
28	GO:0006808	0.0208	59	GO:0005097	0.0352	91	GO:0051347	0.0478
29	GO:0032258	0.0209	60	GO:0006312	0.0358	92	GO:0043162	0.0486
30	GO:0043085	0.0209	61	GO:0031145	0.037	93	GO:0022604	0.0489
31	GO:0030163	0.0224	62	GO:0006140	0.0384	94	GO:0034629	0.0498
			63	GO:1900542	0.0384			

Table S5. Continued

## F. GO terms significantly overrepresented in the bottom of correlation between Kd and GR

	<b>GO_ID</b>	<b>p-values</b>						
1	GO:0006487	0.0007	34	GO:0016311	0.0163	68	GO:0002181	0.0327
2	GO:0048471	0.0015	35	GO:1901605	0.0175	69	GO:0006730	0.0337
3	GO:0035770	0.0034	36	GO:0005794	0.018	70	GO:0018208	0.0337
4	GO:0016050	0.0044	37	GO:1901607	0.0186	71	GO:0007029	0.0345
5	GO:0009066	0.0049	38	GO:0009070	0.0202	72	GO:0009165	0.0345
6	GO:0070085	0.0054	39	GO:0044445	0.0206	73	GO:0000413	0.0347
7	GO:0006486	0.0057	40	GO:0005789	0.021	74	GO:0003755	0.0347
8	GO:0043413	0.0057	41	GO:0042175	0.0212	75	GO:0016859	0.0347
9	GO:0006900	0.0059	42	GO:0005783	0.0218	76	GO:0006890	0.0354
10	GO:0016757	0.0065	43	GO:0009123	0.022	77	GO:0006665	0.0355
11	GO:0000139	0.0066	44	GO:0009124	0.022	78	GO:0016482	0.0367
12	GO:0009156	0.0066	45	GO:0044432	0.0223	79	GO:0072668	0.037
13	GO:0009161	0.0066	46	GO:0070972	0.0225	80	GO:0030658	0.0386
14	GO:0031984	0.0067	47	GO:0045047	0.0229	81	GO:0008080	0.039
15	GO:0031985	0.0067	48	GO:0072599	0.0229	82	GO:0031497	0.0391
16	GO:0000932	0.0069	49	GO:1901566	0.0229	83	GO:1901677	0.0393
17	GO:1901137	0.0073	50	GO:0044283	0.023	84	GO:0012506	0.04
18	GO:0044431	0.0078	51	GO:0008652	0.0238	85	GO:0030659	0.04
19	GO:0009100	0.0087	52	GO:0016410	0.0238	86	GO:0009260	0.0408
20	GO:0009101	0.0087	53	GO:0044711	0.0238	87	GO:0043094	0.0427
21	GO:0005795	0.0088	54	GO:0042790	0.0239	88	GO:0005751	0.0432
22	GO:0005829	0.0091	55	GO:0016853	0.0243	89	GO:0045277	0.0432
23	GO:0006888	0.0096	56	GO:0006457	0.0253	90	GO:1901293	0.0445
24	GO:0016758	0.0096	57	GO:0017025	0.0262	91	GO:0022626	0.0448
25	GO:0035303	0.0102	58	GO:0030148	0.0262	92	GO:0043604	0.0449
26	GO:0012507	0.0103	59	GO:0031365	0.0263	93	GO:0072522	0.046
27	GO:0007264	0.0111	60	GO:0010494	0.0269	94	GO:0005548	0.0471
28	GO:0006893	0.0118	61	GO:0006612	0.029	95	GO:1901135	0.0478
29	GO:0016053	0.0139	62	GO:0000289	0.0298	96	GO:0030135	0.0485
30	GO:0046394	0.0139	63	GO:0008565	0.0301	97	GO:0046467	0.0489
31	GO:0009067	0.0143	64	GO:0005525	0.0307	98	GO:0030173	0.0492
32	GO:0046390	0.0154	65	GO:0019001	0.0307	99	GO:0031228	0.0492
33	GO:0018193	0.016	66	GO:0032561	0.0307			
			67	GO:0030134	0.0314			

## Appendix for statistical analysis of Figure 1 data

We are evaluating the relationship between GR and TR, RA and  $k_d$  (see details in the paper).

### First data set (GRO experiments, Figure 1A)

Read the data.

```
x = read.csv("Datos_all_y_sin_RPs-RiBi_figura1A.csv", sep=";", dec=",")
```

We analyze the coefficient of correlation.

```
cor.test(x$GR, x$A11)
```

```
##  
## Pearson's product-moment correlation  
##  
## data: x$GR and x$A11  
## t = 3.1349, df = 28, p-value = 0.004013  
## alternative hypothesis: true correlation is not equal to 0  
## 95 percent confidence interval:  
## 0.1830516 0.7350057  
## sample estimates:  
## cor  
## 0.5097067
```

The estimated value is 0.5097067. If we test the null hypothesis of a null correlation coefficient the corresponding p-value is 0.004013 i.e. we can reject the null hypothesis with a strong evidence. It is true that the confidence interval at 95% for the coefficient of correlation is wide, [0.183051, 0.7350057] but the value 0 is not included. It is known with a high confidence level (0.995) that the corresponding confidence interval does not contain the value 0.

```
cor.test(x$GR, x$A11, conf.level=0.995)
```

```
##  
## Pearson's product-moment correlation  
##  
## data: x$GR and x$A11  
## t = 3.1349, df = 28, p-value = 0.004013  
## alternative hypothesis: true correlation is not equal to 0  
## 99.5 percent confidence interval:  
## 0.02211598 0.80141218  
## sample estimates:  
## cor  
## 0.5097067
```

## Using Sun et al (2013) data set (Figure 1B-E)

Read the data.

```
y = read.csv("Datos_globales_Cramer_para_figura_1_B_C_D.csv", sep=";", dec=",")
```

Now, the correlation coefficient between GR and TR, RA and  $k_d$ .

First, with TR.

```
cor.test(y$GR,y$TR)

##
## Pearson's product-moment correlation
##
## data: y$GR and y$TR
## t = 2.0663, df = 36, p-value = 0.04605
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  0.006618135 0.584458001
## sample estimates:
##          cor
## 0.3256126
```

We have an estimated value for the coefficient of correlation of 0.3256126. The p-value is 0.04. We can reject the null hypothesis at the usual significance level of 0.05.

Now, we investigate the relationship between GR and RA.

```
cor.test(y$GR,y$mRNA)

##
## Pearson's product-moment correlation
##
## data: y$GR and y$RA
## t = -0.1113, df = 36, p-value = 0.912
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.3362361 0.3029331
## sample estimates:
##          cor
## -0.01854632
```

The p-value is very close to 1. There is no linear relation between GR and RA.

Finally, GR with  $k_d$ .

```
cor.test(y$GR,y$kd)

##
## Pearson's product-moment correlation
```

```
##
## data: y$GR and y$kd
## t = 2.1249, df = 36, p-value = 0.04053
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  0.01584044 0.59049812
## sample estimates:
##      cor
## 0.3338333
```

The behavior of GR with regard TR is similar, as it is described in the paper.

## A different point of view not included in the paper

A major conclusion from our study is that the level of mRNA (RA) does not depend on the GR. The dependence of RA is with respect to TR and  $k_d$ . In order to verify it we fit a linear model where the response is RA and the predictors are the TR,  $k_d$  and GR.

We fit the model.

```
RA.fit = lm(RA ~ TR + kd + GR, data=y)
summary(RA.fit)

##
## Call:
## lm(formula = RA ~ TR + kd + GR, data = y)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.214897 -0.032192 -0.004148  0.044653  0.198761
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  1.24579    0.11948  10.427 3.96e-12 ***
## TR           1.34754    0.09243  14.579 3.44e-16 ***
## kd          -2.27123    0.16789 -13.528 3.04e-15 ***
## GR          -0.34141    0.37616  -0.908   0.37
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.08904 on 34 degrees of freedom
## Multiple R-squared:  0.8623, Adjusted R-squared:  0.8501
## F-statistic: 70.96 on 3 and 34 DF,  p-value: 1.023e-14
```

Let us see a usual summary of the fit.

```
summary(RA.fit)

##
## Call:
## lm(formula = RA ~ TR + kd + GR, data = y)
##
## Residuals:
```

```
##           Min           1Q       Median           3Q           Max
## -0.214897 -0.032192 -0.004148  0.044653  0.198761
##
## Coefficients:
##           Estimate Std. Error t value Pr(>|t|)
## (Intercept)  1.24579    0.11948  10.427 3.96e-12 ***
## TR           1.34754    0.09243  14.579 3.44e-16 ***
## kd          -2.27123    0.16789 -13.528 3.04e-15 ***
## GR          -0.34141    0.37616  -0.908  0.37
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.08904 on 34 degrees of freedom
## Multiple R-squared:  0.8623, Adjusted R-squared:  0.8501
## F-statistic: 70.96 on 3 and 34 DF,  p-value: 1.023e-14
```

It can be observed in the last column of the coefficients part of the output that we can not reject that the coefficient of the GR is null. The p-value is 0.37. However, if we consider the null hypothesis of a null value for the coefficient of TR and  $k_d$  the observed p-values are  $3.44e-16$  and  $3.04e-15$ , i.e. extremely significant. Moreover, the  $R^2$  is quite good: 0.8623.

If we apply a variable selection of the model then

```
library(MASS)
(RA.fit.sel = stepAIC(RA.fit))

## Start:  AIC=-180.04
## RA ~ TR + kd + GR
##
##           Df Sum of Sq      RSS      AIC
## - GR       1  0.00653 0.27611 -181.13
## <none>      0.26958 -180.04
## - kd       1  1.45111 1.72069 -111.61
## - TR       1  1.68517 1.95475 -106.76
##
## Step:  AIC=-181.13
## RA ~ TR + Kd
##
##           Df Sum of Sq      RSS      AIC
## <none>      0.27611 -181.13
## - kd       1  1.4780 1.75409 -112.87
## - TR       1  1.6802 1.95631 -108.73
##
## Call:
## lm(formula = RA ~ TR + kd, data = y)
##
## Coefficients:
## (Intercept)           TR           kd
##           1.143           1.345          -2.284
```

i.e. the variable GR is removed. A summary of the final model is

```
summary(RA.fit.sel)
```

```

##
## Call:
## lm(formula = RA ~ TR + kd, data = y)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.202867 -0.035389 -0.006959  0.047701  0.223526
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  1.14316    0.03849   29.70 < 2e-16 ***
## TR           1.34487    0.09215   14.59 < 2e-16 ***
## kd          -2.28405    0.16687  -13.69 1.29e-15 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.08882 on 35 degrees of freedom
## Multiple R-squared:  0.8589, Adjusted R-squared:  0.8509
## F-statistic: 106.6 on 2 and 35 DF,  p-value: 1.301e-15

```



# Appendix for statistical analysis of Figure 2 data

## *Statistical Analysis*

February 4, 2015

### *Contents*

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This document contains the description of the data processing and statistical analyses performed in the paper associated.

### 1 *Data sets*

MICROARRAYS from different experiments have been used. We have generated three different data sets.

- Gene expression: yeastgrowthRA.rda
- Transcription rate: yeastgrowthRA.rda
- Ratio between the transcription rate and gene expression yeastgrowthTRA.rda

We will illustrate using the yeastgrowthRA.rda. The code is included in order to reproduce the analysis performed. They can be loaded with

```
library(Biobase)
load("yeastgrowthRA.rda")
eset = yeastgrowthRA
```

The analysis for the other two data sets can be reproduced by replacing yeastgrowthRA by yeastgrowthTR and yeastgrowthTRA. The data set is an object of class ExpressionSet ([Gentleman et al. \[2014\]](#)).

```
class(eset)
## [1] "ExpressionSet"
## attr(,"package")
## [1] "Biobase"
```

A quantile normalization ([Bolstad \[2008\]](#)) have been applied to the gene expression matrix.

```
library(limma)
exprs0 = normalizeBetweenArrays(exprs(eset))
exprs(eset) = exprs0
```

The missing values have been removed using a **KNNimpute algorithm** proposed in [Troyanskaya et al. \[2001\]](#) and implemented in the R package [Hastie et al. \[2014\]](#).

```
library(impute)
exprs1 = impute.knn(exprs(eset))$data
exprs(eset) = exprs1
```

## 2 Differential expression

THE GROWTH RATE is the important phenotypic variable. This variable can be visualized using

```
pData(eset)[,"growthrate"]
```

The association between this variable and the expression profile of each gene has been tested using the SAM (Significance Analysis of Microarrays) method. It was proposed in [Tusher et al. \[2001\]](#). However, the best document to know the procedure is <http://www-stat.stanford.edu/~tibs/SAM/sam.pdf>. We identify genes with a positive or negative association with the growth rate (up and low genes). For a given false discovery rate we will have two groups of significant low and high genes.

The next code <sup>1</sup> will serve as an illustration.

<sup>1</sup> The whole code will be send under request.

```
data = list(x = exprs(eset), y = y0, geneid = featureNames(eset),
           genenames = featureNames(eset), logged2=TRUE)
samr.obj = samr(data, resp.type="Quantitative", nperms=10000)
genes.up.lo = ifelse(samr.obj$tt > 0, "up", "lo")
sam.pval = samr.pvalues.from.perms(samr.obj$tt, samr.obj$ttstar)
```

## 3 Fisher tests

FOR EACH GROUP of genes previously obtained (low and high) we have considered the possible association with each group defined using Gene Ontology. The different classification criteria used there

has been used i.e. biological process, molecular function and cellular component.

The association has been tested using a one-tail Fisher test. The function `hyperGTest` included in the R package [Gentleman and Falcon \[2014\]](#) has been used. The following code is a short illustration.

```
seleccionAnotada = is.element(geneIds(g1), mappedkeys(org.Sc.sgdENTREZID))
universoAnotado = is.element(featureNames(eset), mappedkeys(org.Sc.sgdENTREZID))
seleccion = geneIds(g1)[seleccionAnotada]
universo = featureNames(eset)[universoAnotado]
params <- new("GOHyperGParams", geneIds = seleccion, universeGeneIds = universo,
             annotation = annotation(eset), ontology = "BP",
             pvalueCutoff = 0.05, conditional = FALSE, testDirection = "over")
overRepresented1 <- hyperGTest(params)
```

#### 4 Gene set analysis

IT HAS been performed a **gene set enrichment analysis** using the procedure GSA proposed in [Efron and Tibshirani \[2007\]](#). In particular, we have used the R package [Efron and Tibshirani \[2010, GSA\]](#). The gene sets have been made using the Gene Ontology categories.

We show an example.

```
yg.gsa = GSA(exprs(eset), y0, genenames = featureNames(eset),
            genesets = geneIds(eset.gsc), resp.type = "Quantitative",
            minsize = 5, nperms = 10000)
```

#### 5 The whole code

SOME PARTS of code have been showed above. The whole analyses cannot reproduce with them. Any reader interested in the whole scripts can request to the authors and we will send it.

#### References

Ben Bolstad. *Methods in Microarray Normalization*, chapter 3, pages 41–60. Number 10 in Drug Discovery Series. CRC Press, 2008.

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