Supplementary Information for

Doxorubicin induces an extensive transcriptional and metabolic rewiring in yeast cells

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Table S7: Primer sequences of the genes analyzed in RT-qPCR

Gene	**Primers**		**Gene**	**Primers**	
RFX1	Left	GGCTCCCATAAACCATCTCC	*HUG1*	Left	GTCAAGACCGGCTACTTATTCC
	Right	AGGTTGCCGTTGTGTTGC		Right	ACGTTCGACGGCAATGAT
CUP2	Left	GAAATTAAGGCCGACAGCAT	*NHP6A*	Left	GGACAAGTCGGCAAGAAGTT
	Right	CTTTGCTCAAGCGGATCG		Right	TCGTAAGGCTGCTTTTCCTC
PDR8	Left	TAGAGATACCACGGACAAGAACC	*HTB2*	Left	CCAAAGCTCCAGCTGAAAAG
	Right	TCTTTTGCATTACCTTGCAAATC		Right	TACCATCGACGGAGGTTGA
SRX1	Left	TCAAGGGACAGACGCTATATTATG	*BNA4*	Left	GGAAAGGCCATCCTACTCG
	Right	GGCGGTCGTATGCCTGTA		Right	TACCTTGGCCGTAAAATGGA
FRE7	Left	CCATTCTACAGACCTTGTGCAG	*ADH5*	Left	TGGTACTTTTCAAGAATACGCAAC
	Right	ATTATGCCTGCACGAACAGA		Right	CAAGATTGACGTTTGGTGGA
SGS1	Left	AGGGGGTGGTAAATCTCTTTG	*ENO1*	Left	TGTCCCATCTGGTGCTTCTA
	Right	TGTGTTTTACCCGATTTCACC		Right	TCCACTTGGATTTGTCACCA
REC104	Left	AGTGACACATTATATGACGATCCTTT	*SHM2*	Left	CTTTGGTTCCAGGTGGTGTC
	Right	CCTCTATTTCATCTCCTGCTTGA		Right	TCACCCATTCCTCTAGTGGTC
ATG39	Left	TGCATGAAAGCTCCTTTGC	*ARG4*	Left	GCGTTGAAAGACGAGATGCT
	Right	GTGTTCGATAGGACATCTGCAT		Right	CCAATTGCTTCAATACAGCAGA
YAP6	Left	CTCCCATCTCGCAATACCA			
	Right	GCGGTATCAGCACTGTTTTG			

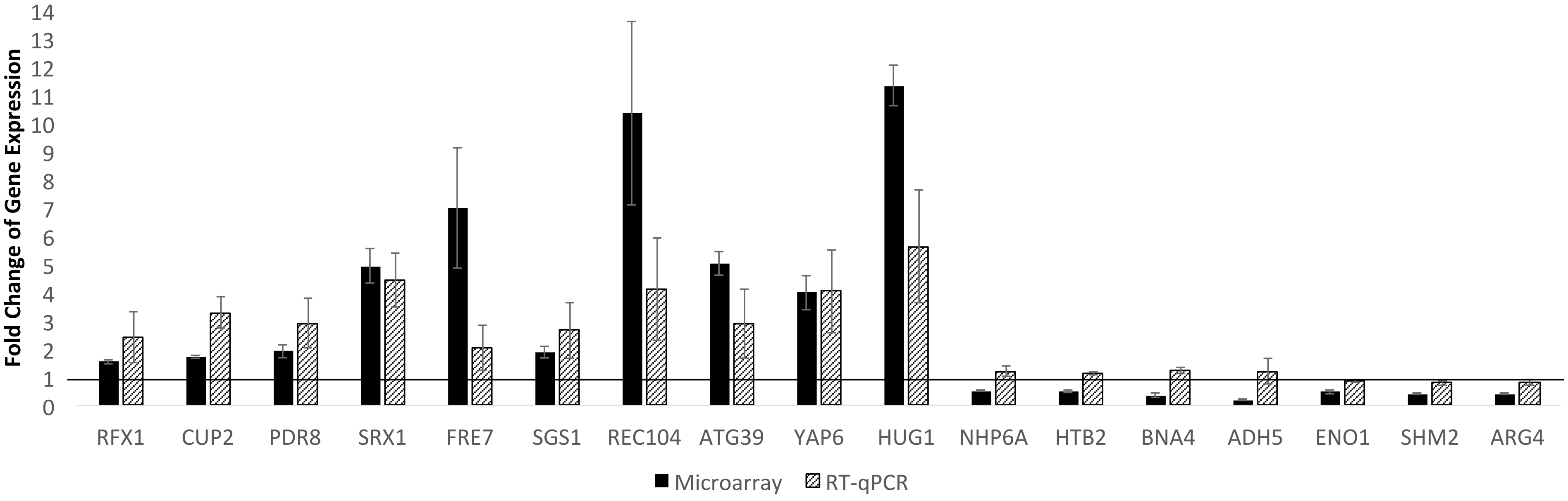

Figure S2: Comparison of fold change in the expression of selected differentially expressed genes in the presence of doxorubicin relative to control, obtained via microarray or RT-qPCR analysis. Error bars represent the standard errors.

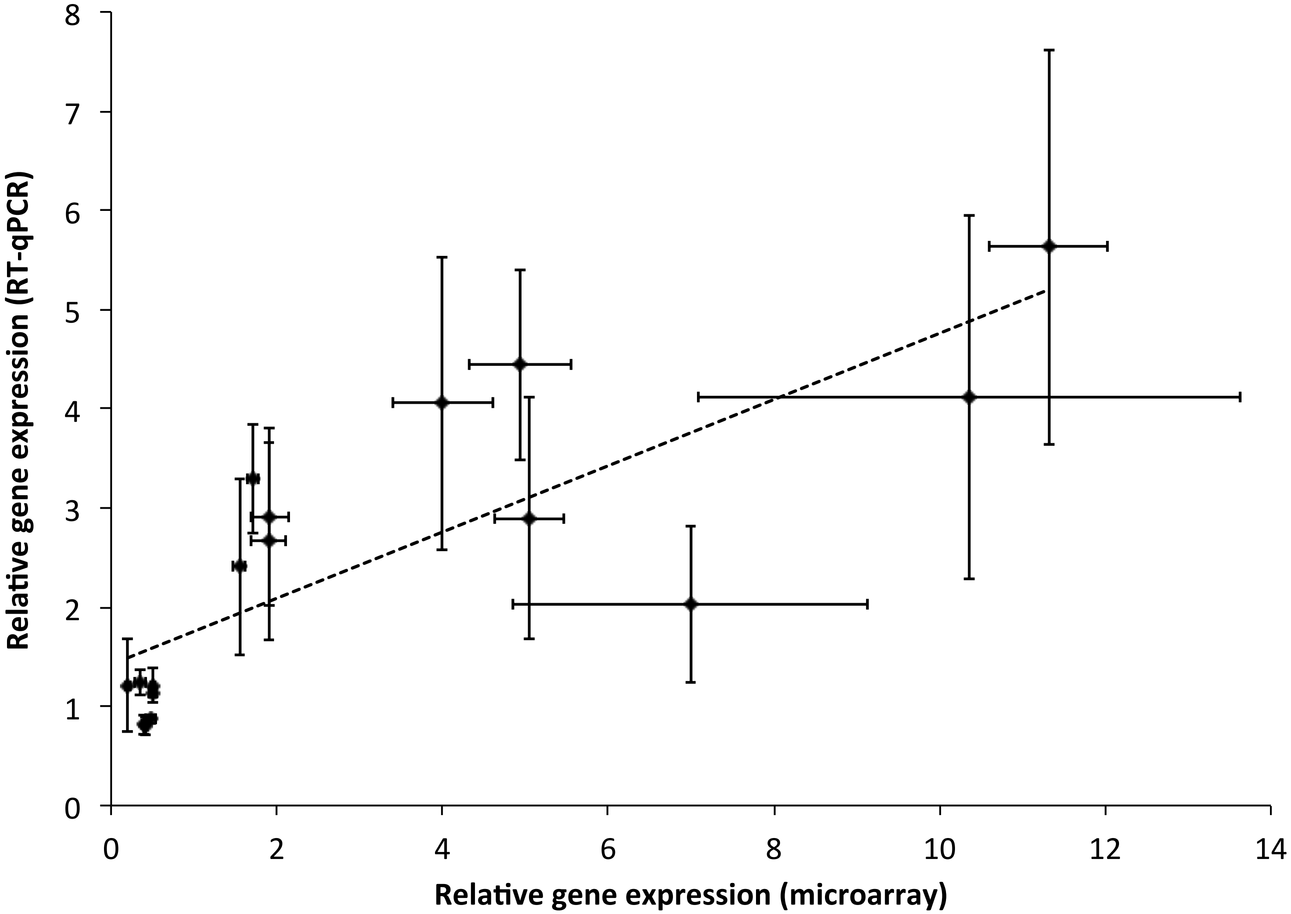

Figure S3: Correlation analysis of RT-qPCR and microarray data of selected differentially expressed genes. Line fit plot showed a significant correlation (r=0.8018, p-value=0.00011, n=17, df=15).