

Supplementary Figures

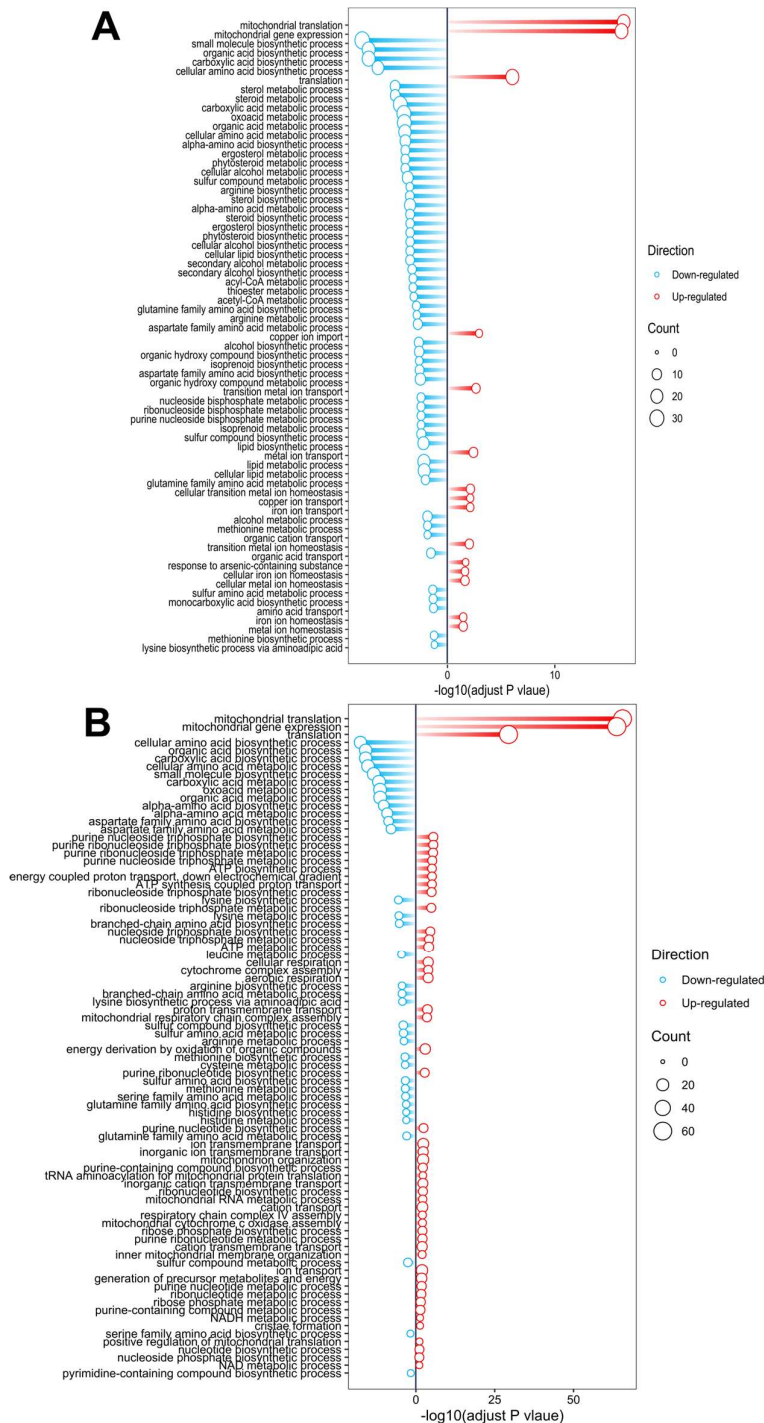


Figure S1: GO term enrichment analyses: The GO term (Molecular Function) analyses show significantly enriched terms for (A) positively responding versus non-responding and (B) positively responding versus negatively responding strains.

A		B	
MET32	91.9	SFP1	83.2
MSN2	36.6	CST6	39.2
MSN4	12.8	GCR1	34.9
AFT1	9.9	HSF1	26
HCM1	7.1	RAP1	23.2
GCN5	5.9	SPT20	22
MED2	5.6	FHL1	12.8
HAP4	5.4	FKH2	12.5
AFT2	4.9	HF11	4.9
MET4	3.9	SPT10	4.5
RIM101	3.8	REB1	3.3
ZAP1	2.7	URE2	2.1
XBP1	2.6	PIP2	2.1

Up-regulated Down-regulated

Figure S2. Transcription factor enrichment analyses for non-responding strains analyzed under CR condition. Significantly enriched TFs for (A) up- and (B) down-regulated DEGs obtained under CR conditions for non-responding strains. The color index and the number show the significance of the enrichment score ($-\log_{10}$, adjusted P -value).

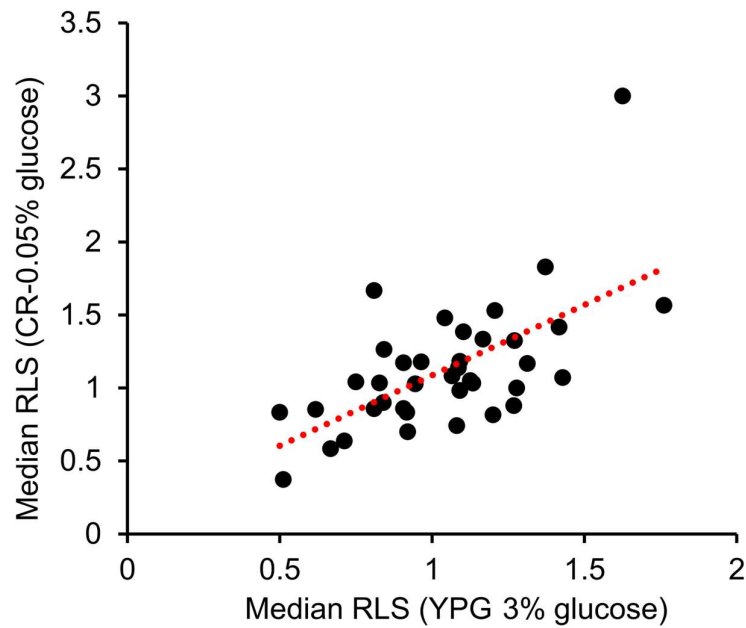


Figure S3. A positive correlation of median RLS phenotype between YPG and CR medium was observed. A significant correlation was observed between median RLS in YPG and median RLS in CR, wherein glycerol-induced CR-induced respiration approximately equally extends the RLS of those strains we tested ($R^2 = 0.62$, Padj value = 2.29×10^{-4}).