Supplementary Table S3. The table highlights the analysis ratio of the "Enrichment in Phenotype" section for the results of gene sets with a negative enrichment score.

NAME	NAME_GO	SIZE	ES	NES	NOM p-val	FDR q-val	FWER p-val
CYTOPLASMIC_TRANSLATION	GOBP_CYTOPLASMIC_TRANSLATION	34	-0.75312	-5.05323	0.00E+00	0.00E+00	0.00E+00
RIBOSOME	GOCC_RIBOSOME	39	-0.70015	-4.87546	0.00E+00	0.00E+00	0.00E+00
STRUCTURAL_CONSTITUENT_OF_RIBOSOME	GOMF_STRUCTURAL_CONSTITUENT_OF_RIBOSOME	36	-0.72597	-4.83902	0.00E+00	0.00E+00	0.00E+00
RIBOSOMAL_SUBUNIT	GOCC_RIBOSOMAL_SUBUNIT	33	-0.75283	-4.75978	0.00E+00	0.00E+00	0.00E+00
CYTOSOLIC_RIBOSOME	GOCC_CYTOSOLIC_RIBOSOME	33	-0.72472	-4.67105	0.00E+00	0.00E+00	0.00E+00

Legend: SIZE, number of genes in the gene set after filtering out those genes not in the expression dataset. **ES**, Enrichment score for the gene set; that is, the degree to which this gene set is overrepresented at the top or bottom of the ranked list of genes in the expression dataset. **NES**, Normalized enrichment score; that is, the enrichment score for the gene set after it has been normalized across analyzed gene sets. **NOM p-val**, Nominal p value; that is, the statistical significance of the enrichment score. The nominal p value is not adjusted for gene set size or multiple hypothesis testing; therefore, it is of limited use in comparing gene sets. **FDR q-val**, False discovery rate; that is, the estimated probability that the normalized enrichment score represents a false positive finding. **FWER p-val**, Familywise-error rate; that is, a more conservatively estimated probability that the normalized enrichment score represents a false positive finding. Because the goal of GSEA is to generate hypotheses, the GSEA team recommends focusing on the FDR statistic.