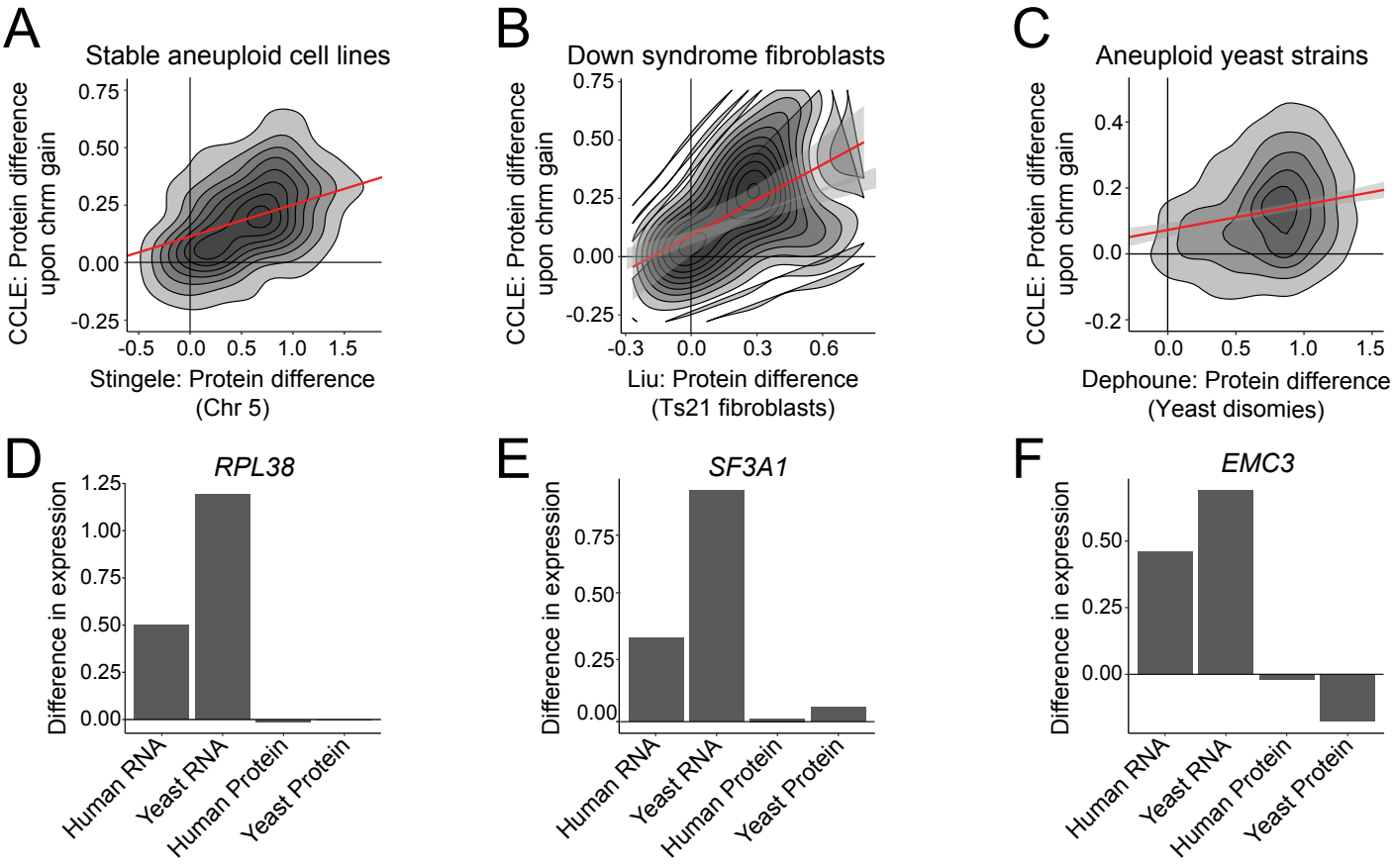
Supplemental Figure S6



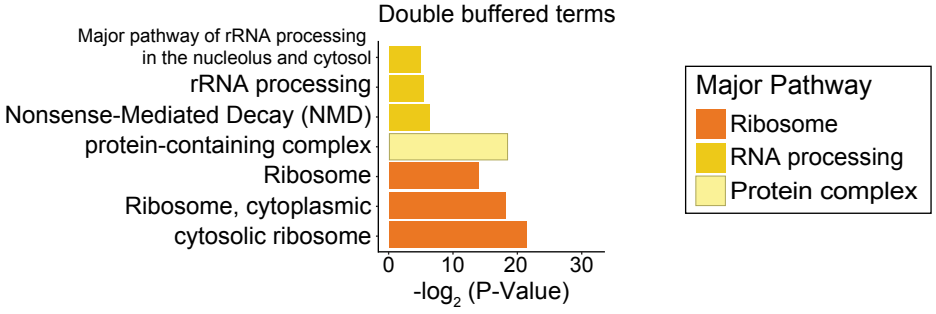
J

Protein correlation:	# genes	Corr	P-value	double buffered
A: Stable Chr 5 gain	372	0.431	$<5x10^{-10}$	73
B: Down syndrome fibrobl.	42	0.538	$<4x10^{-4}$	15
C: Yeast aneuploid strains	738	0.214	$<5x10^{-9}$	98

K

RNA correlation:	# genes	Corr	P-value
H: Stable Chr 5 gain	263	0.291	$<3x10^{-5}$
I: Down syndrome fibrobl.	93	0.294	$<5x10^{-3}$
J: Yeast aneuploid strains	725	0.073	0.049

L Gene types buffered in both CCLE and yeast disomies



Supplemental Figure S6. Patterns of protein buffering and scaling are evolutionarily conserved.

A-C) Two-dimensional density plots displaying the difference in protein expression upon chromosome gain, for genes encoded on that respective chromosome, in the CCLE dataset versus A) stable aneuploid cell lines with a gain for Chromosome 5, B) Down syndrome fibroblasts normalized to matched euploid controls, and C) haploid yeast with single chromosome disomies. Linear correlations (red) with 95% confidence interval (grey) are plotted against the data.

D-F) Bar graphs displaying the difference in protein or RNA expression in the CCLE dataset and aneuploid yeast, upon gain of the corresponding chromosome for three genes: D) *RPL38*, E) *SF3A1*, and F) *EMC3*.

G-I) Two-dimensional density plots displaying the difference in RNA expression upon chromosome gain, for genes encoded on that respective chromosome, in the CCLE dataset versus H) stable aneuploid cell lines with a gain for Chromosome 5, I) Down syndrome fibroblasts normalized relative to matched euploid controls, and J) haploid monosomic yeast with single chromosome disomies. Two dimensional density plots with linear correlations (red) with 95% confidence interval (grey) are plotted against the data.

J-K) Tables indicating the number of genes analyzed per condition, Pearson correlation coefficients, and corresponding p-values for protein expression differences examined in A-C and RNA expression differences examined H-I. The protein correlation table (K) also indicated how many genes are buffered in both the CCLE dataset and the indicated aneuploid dataset.

L) Bar graphs displaying the GO terms enriched among proteins buffered in both the CCLE and the aneuploid yeast dataset upon chromosome gain. The complete set of GO terms is included in Supplemental Table S8.