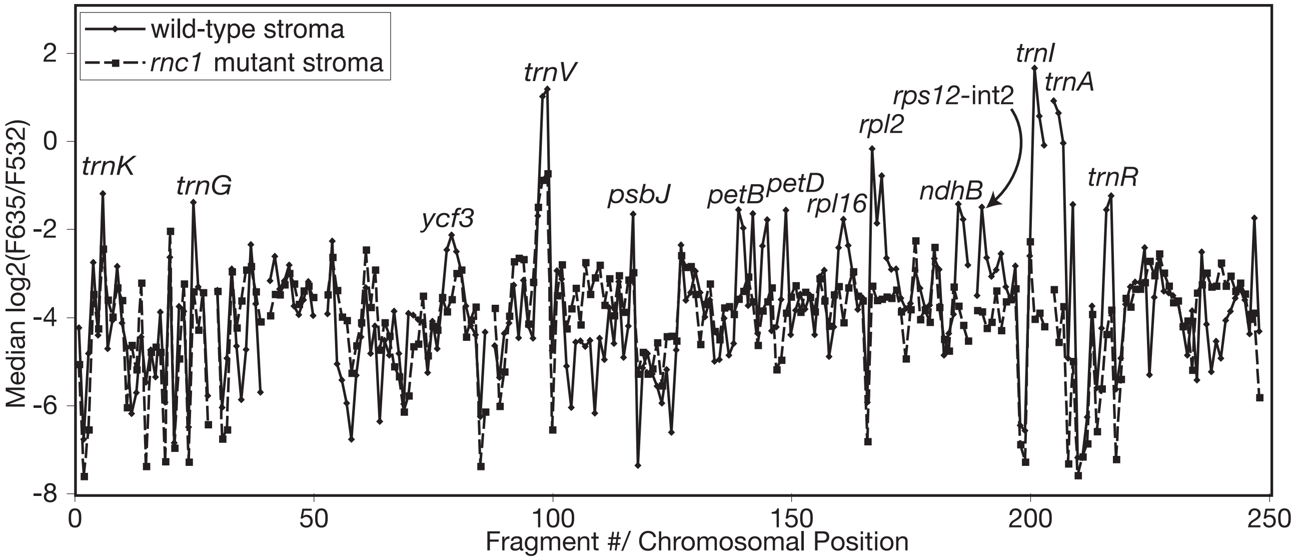
Supplemental Figure 1



Supplemental Figure 1. RIP-chip data showing enrichment of RNA sequences in RNC1 immunoprecipitations involving wild-type or rnc1-1/rnc1-2 mutant extract. Median log(2)-transformed enrichment ratios (F635/F532) of replicate spots across replicate experiments are plotted as a function of array fragment number, which were assigned based on their chromosomal position. The locus name is indicated for peaks that include fragments whose enrichment from wild-type stroma ranked in the top 15th percentile, and if the sequences showed significant differential enrichment from wild-type versus mutant stroma or from RNC1 versus PPR4 immunoprecipitations (P-value <3E-4). A large peak corresponding to trnV-UAC was observed with both the wild-type and mutant extract, but the statistical analysis in Supplemental Table 2 supports the notion that these sequences were preferentially enriched from the wild-type extract. RNC1 is not completely absent from the mutant extract, so it is expected that peaks corresponding to bona fide RNC1 ligands could be reduced but not eliminated when mutant extract is used for the immunoprecipitation.