



Supplementary Figure 6: Data aggregation identifies additional genetic interactions involving the *SHU* complex. Plot depicting the ε scores (y-axis) between 26 genes (x-axis) and the members of the *SHU* complex (*SHU1*, *SHU2*, *CSM2*, *PSY3*). Values represent the average of measurements from individual *SHU* members, and error bars represent the standard deviation from at least 3 unique gene pairs. Data points are color-coded according to interaction classification based on the analysis described in **Fig. 4** (red = aggravating, blue = alleviating, and dark grey = neutral). In most cases, interaction classification was the same for all *SHU* members. Three cases of classification inconsistency are represented by blended colors (1 of 4 interactions with *MUS81* was alleviating, 1 of 4 interactions with *HPR5* was alleviating, and 3 of 4 interactions with *SLX4* were aggravating). Despite not being classified as alleviating interactions, the epsilon measurements involving *MPH1*, *HR* genes (*RAD51*, *RAD52*, *RAD55*, *RAD57*), and others, were significantly greater than zero, however they were also significantly less than those between *SHU* members. This difference cannot be explained by differences in the fitness of associated single deletion mutants, since the fitness of *SHU* deletion strains was greater than or equal to the *HR* and *MPH1* deletion strains (**Fig. 2b**).