**Supplemental Item Legends**

File S1: Lists of strains, plasmids, and oligonucleotides used in this study.

File S2: White-to-opaque and opaque-to-white switching frequencies for the 172 strains tested in this study. Switching frequencies are normalized to the average of four wild type switching assays performed on the same day. When no switching events were detected for a strain, the switching frequency is indicated as less than one divided by the number of colonies counted. Statistical significance was calculated using Welch’s t-test with the Bonferroni Correction for multiple comparisons, an α = 0.05 gives final thresholds of 2.91 x 10-4 for white-to-opaque switching and 2.94 x 10-4 for opaque-to-white switching. In addition, this file contains the absolute switching rate and number of colonies counted for all deletion strains as well as the mean, standard deviation, and range of absolute switching rates for the wild type assays that were performed with each batch of strains. Cell type enrichment data are taken from a previous study (Tuch *et al.* 2010).

File S3: Supplemental Information, consisting of Supplemental Materials and Methods and Supplemental Results. Contains details on comparisons between white-to-opaque and opaque-to-white switching frequencies, GO terms, and genes whose transcripts are differentially regulated between cell types.

File S4: Testing for overrepresentation of genes affecting white-to-opaque or opaque-to-white switching in 42 GO-SLIM sets, She3 associated transcripts, two- or four-fold cell type enrichment, and genes with five-fold switching effects in the opposite direction. Statistical testing for overrepresentation used a Hypergeometric Distribution with the Bonferroni Correction, an α = 0.05 gives a final threshold of 1.04 x 10^-3. In addition, this file contains the lists of genes included in each of the categories tested.