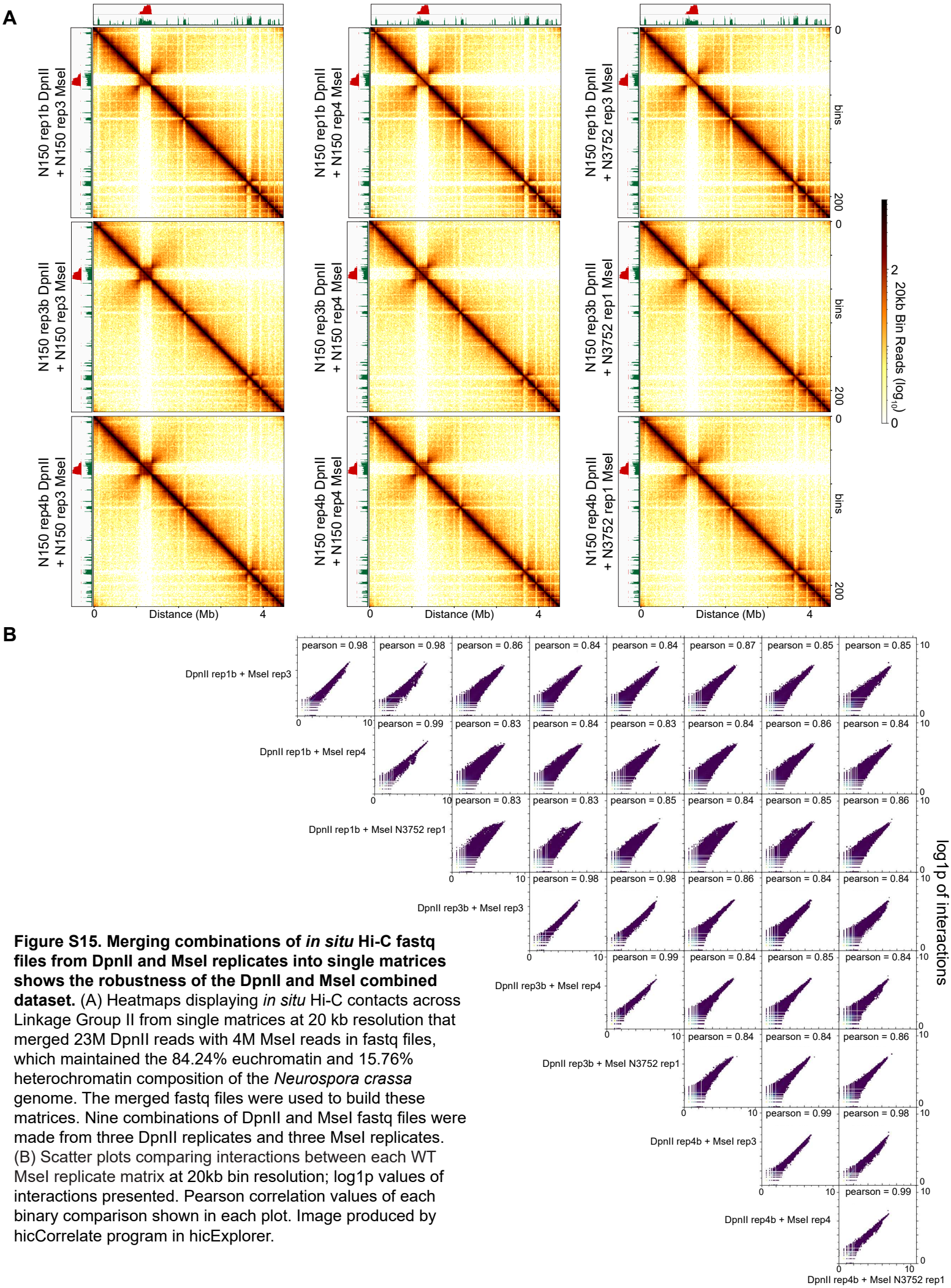

Figure S15. Merging combinations of *in situ* Hi-C fastq files from DpnII and MseI replicates into single matrices shows the robustness of the DpnII and MseI combined dataset. (A) Heatmaps displaying *in situ* Hi-C contacts across Linkage Group II from single matrices at 20 kb resolution that merged 23M DpnII reads with 4M MseI reads in fastq files, which maintained the 84.24% euchromatin and 15.76% heterochromatin composition of the *Neurospora crassa* genome. The merged fastq files were used to build these matrices. Nine combinations of DpnII and MseI fastq files were made from three DpnII replicates and three MseI replicates. (B) Scatter plots comparing interactions between each WT MseI replicate matrix at 20kb bin resolution; log1p values of interactions presented. Pearson correlation values of each binary comparison shown in each plot. Image produced by hicCorrelate program in hicExplorer.