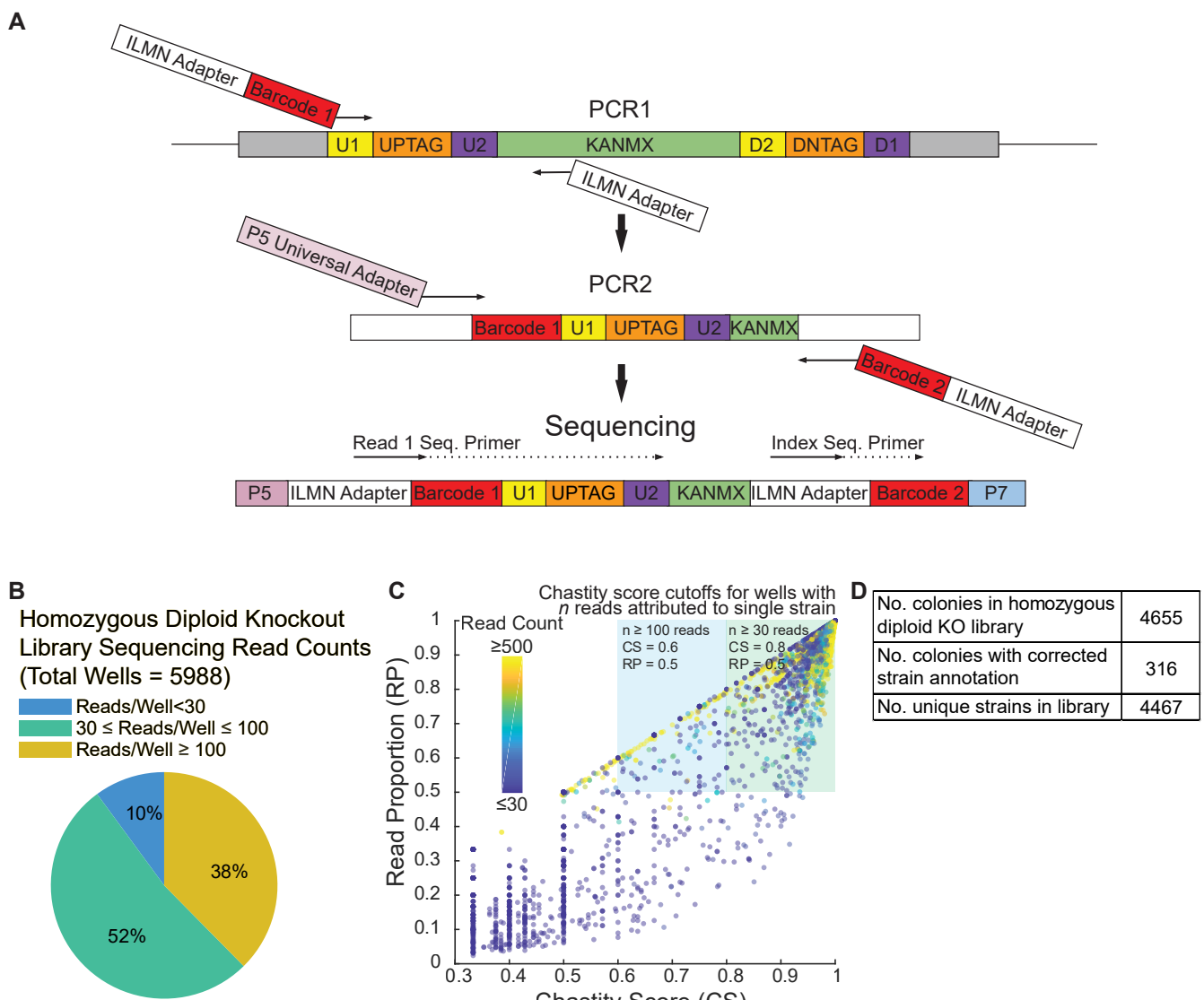

Figure S1: Diploid library strain identification via barcode sequencing. A) Schematic demonstrating PCR and sequencing strategy. Barcode 1 contained eight bp specifying well location and a 12 base pair unique molecular identifier. Barcode 2 was an Illumina index barcode that was used to identify the source plate. B) Pie chart demonstrating number of reads per well across ~6000 wells in the library. Most wells had at least 30X coverage. Wells with <30 reads were found to lack yeast growth (not shown). C) Scatter plot of read proportion (RP) versus chastity score (CS). Shaded blue area represents RP and CS cutoffs for wells with ≥ 100 reads. Shaded green area represents more stringent RP and CS cutoffs for wells with 30 ≤ reads < 100. D) The cutoffs described above resulted in correction of strain annotation for 316 wells, totaling to 4467 unique strains.