ICD.xlsx – ICD±Transformation, Random Simulations (for SK1, YJM and Microscopy)

/RecombineSim

* ChrSizesS288cH4L2\_L2HG.txt – required by *RecombineSim*, designates internal chromosome sizes (in bp)
* /Event\_Tables – contains all relevant event tables
* ExpectedDistribution.m – determines the expected distribution of SNPs/INDELs by calculating the SNP/INDEL densities surrounding DSB hotspots. Pan et al. Spo11 data is used (/WeightedMaps/DSB\_WeightMap) to select 1000 sites per chromosome. Selection is weighted by hotspot frequency. For each of the 16,000 DSBs, the SNP/INDEL density is recorded ±Xbp. A smoothed CDF is then estimated using the *ksdensity* function.
* Hazard.m – required by RecombineSim, calculates Hazard functions for a given γ(α,β)
* InsertRows.m – required by RecombineSim, formats output .txt files
* moving\_average.m – required by RecombineSim, performs moving average smoothing for preweight maps
* normalize\_var.m – required by RecombineSim, normalizes variables between a specified range
* PolymorphismAnalysis.m – determines the observed distribution of SNPs/INDELs by calculating the SNP/INDEL densities surrounding CO midpoints. For each CO, the SNP/INDEL density is recorded ±Xbp. A smoothed CDF is then estimated using the *ksdensity* function.
* README – details on running *RecombineSim*
* RecombineSimMaturation.m – a combined script to run CO simulations
* replaceinfile.m – required by *RecombineSim*, formats output .txt files
* /VariantAnalysis
  + VariantTable\_SK1.txt / VariantTableYJM.txt – required by *RecombineSim* to determine left/right chromosomal boundaries
  + SK1\_VarAnalysis\_Input / YJM\_VarAnalysis\_Input – required by *PolymorphismAnalysis*, lists CO positions in a simplified format
* /WeightedMaps
  + CO\_WeightMap / DSB\_WeightMap / SK1\_SNP\_WeightMap / YJM\_SNP\_WeightMap – required by *RecombineSim* when pre-weighting CO formation.