

Prokaryotic Unidirectional Overlapping Genes Formation - Simulations with GC 50%

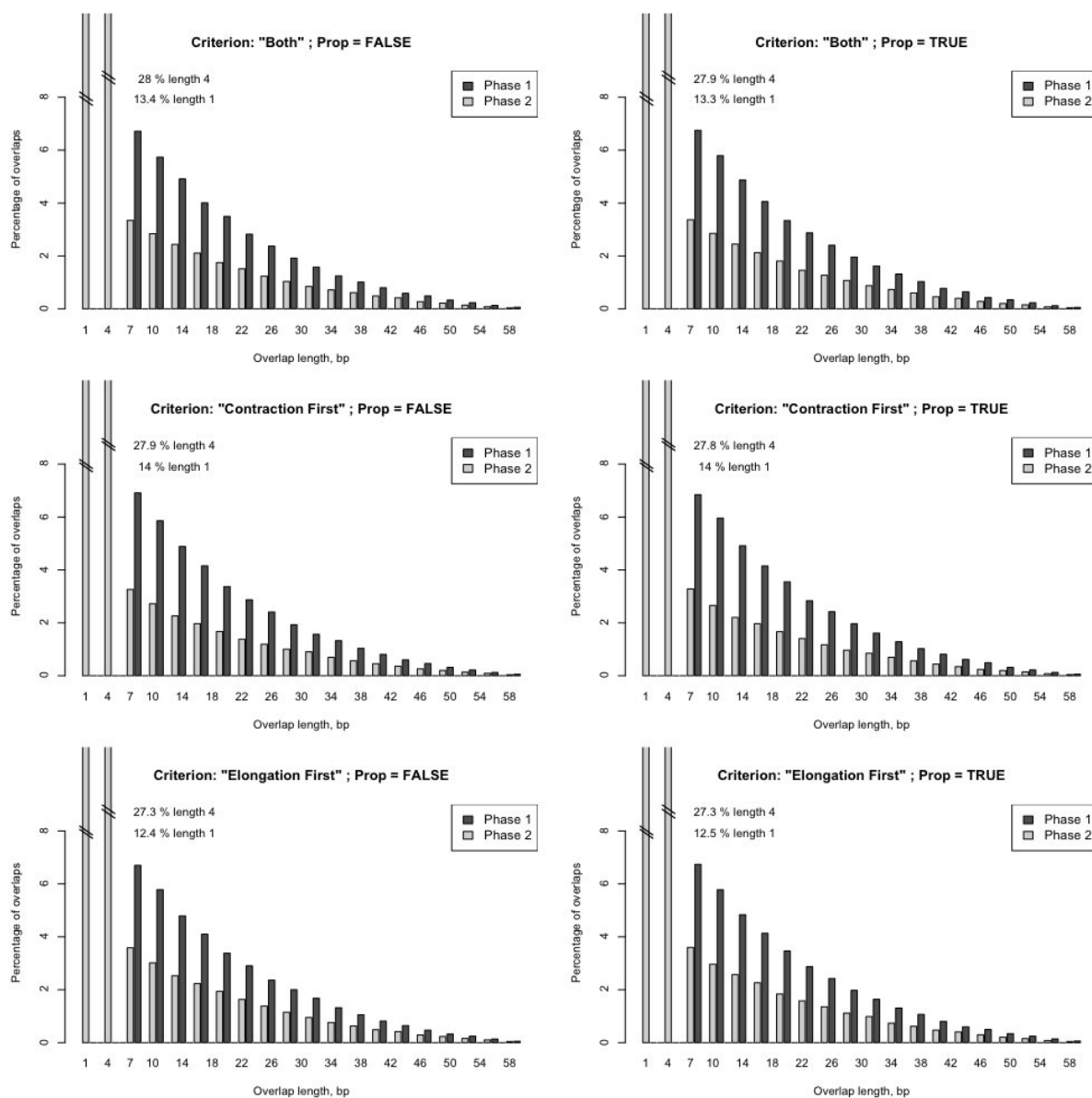


Figure S8 Hypothetical prokaryotic overlap lengths of unidirectional adjacent genes, calculated from simulated dataset (scenario 1). First set of simulations where gene size and intergenic distances were set to 63 bp and 60 bp + phase, respectively. Parameters: GC content = 50%; and all possible combinations between *criterion* ("Elongation First", "Both", "Contraction First") and *Proportions of start codons* (TRUE or FALSE). Frequency of overlaps in both phases was weighted according to the mutation rate between phase 1 and phase 2 simulations (see Material and Methods).