



Figure S3: Effect of different expected error filtering thresholds on haplotype recovery (no denoising applied). All filtered reads are mapped against the expected haplotypes (black circles). Not all reads are shared between both replicates (indicated by A or B instead of a circle). The 15 expected haplotypes are shown in black, while unexpected ones are highlighted in gray or blue. Error bars show the standard deviation of relative read abundance between both replicates, for the respective haplotype.