

**Table S1:** Comparison of the total runtime to phase whole-genome Hi-C data (format in hours:minutes) using HapCUT and HapCUT2. To assess the impact of the trans-error probability ( $\tau$ ) modeling on run time, HapCUT2 was run in three different ways: default (no trans-error modeling), Hi-C mode with a pre-computed  $\tau$  model and Hi-C mode that estimates  $\tau$  from the data.

<b>Method</b>	<b>Hi-C (30×)</b>	<b>Hi-C (40×)</b>	<b>Hi-C (90×)</b>
HapCUT	0:36	0:46	1:49
HapCUT2 (no trans-errors)	0:10	0:15	0:34
HapCUT2 (fixed $\tau$ model)	0:34	0:52	2:02
HapCUT2 (estimate $\tau$ from data)	3:05	4:38	9:11