



Figure 3-figure supplement 4 Difference in runtime between windowWardD2 and linkedSNPHapCUT2 algorithms for phasing across a range of simulated data. Datasets have varied coverages, gamete numbers, and numbers of SNPs. Figure shows both CPU time and wall time. Points above the  $y = 0$  line represent datasets for which the windowWardD2 method performs faster. Evaluation of linkedSNPHapCUT2 does not include the time necessary to convert the files for use with HapCUT2. Panel (A) shows total user and system time. Panel (B) shows real time. Each point shows the difference in total time (in seconds) required for each phasing method (linkedSNPHapCUT2 minus windowWardD2). Number of gametes in each simulation is shown on the x axis. Only simulations for which both phasing methods were successful are shown (of the 432 datasets, 365 were successfully phased using windowWardD2 and 266 were successfully phased using linkedSNPHapCUT2); the file conversion together with calling HapCUT2 were allowed to time out after 3 days.