



Fig S6. Inconsistency among different short-read datasets. **(A)** The TSM solution explaining a cluster of three base differences (and not explaining one nearby difference). **(B)** The Platinum data have one supporting read (left; red box) whereas the Chromium data have none; an independent dataset has multiple supporting reads (red box), but these are associated with flanking changes (blue box) creating more than two haplotypes. A plausible explanation is the mismapping of reads from another locus. Data were visualized with IGV (Thorvaldsdóttir et al. 2013).