



Figure S5 Bottom track, line with a candidate *de novo* mutation that was eliminated from analysis due as a suspected error. This was decided based on the presence of highly divergent reads containing the majority of non-reference bases in this region, including the *de novo* mutant base. This is likely an issue of collapsed, divergent duplicates in the reference genome. Top track, sample line not carrying evidence of a *de novo* mutation but still showing evidence of a hidden duplication.