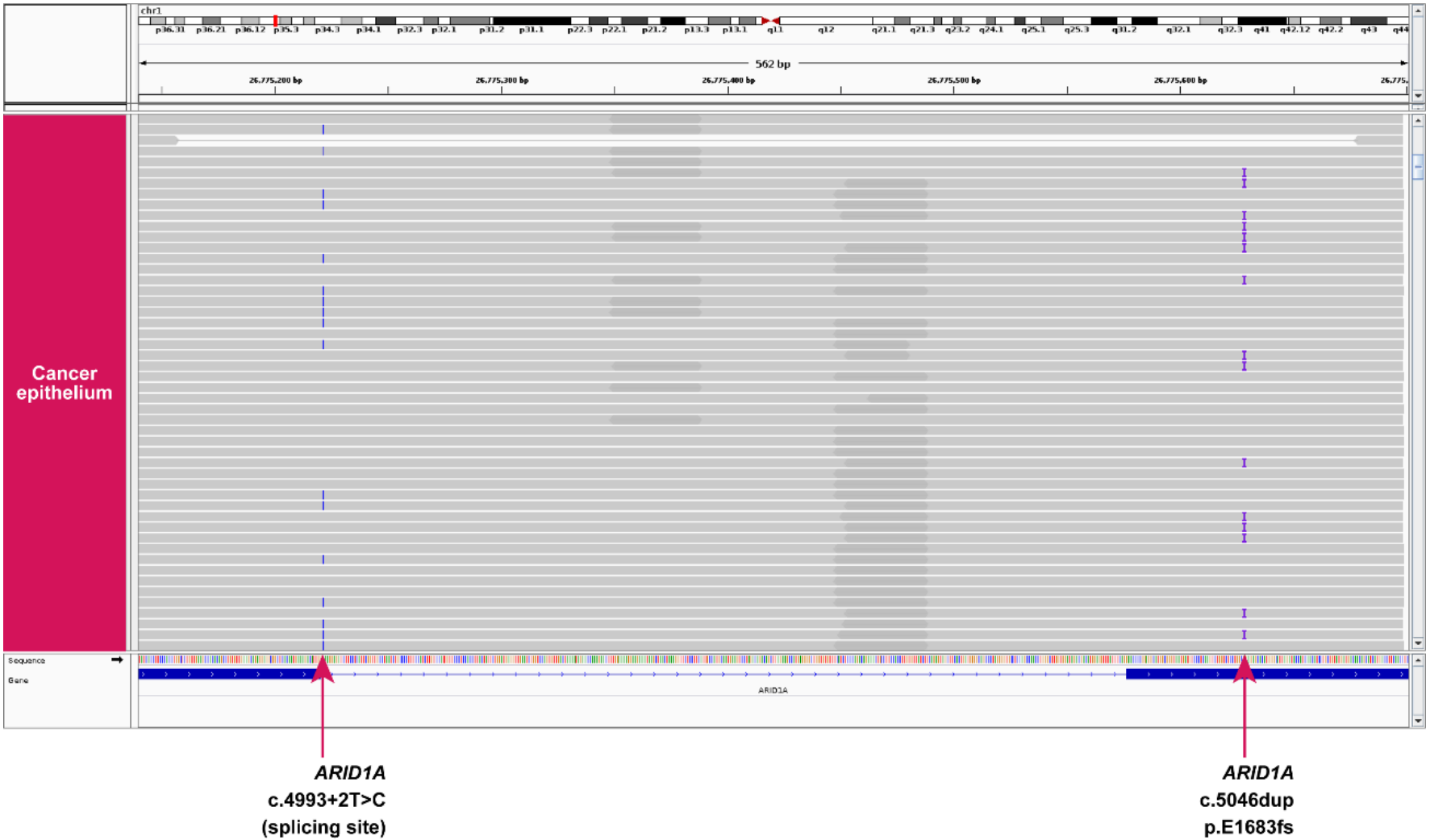

Figure S5. Haplotype phasing of two SNVs in *ARID1A*. Alignment of sequence reads around two *ARID1A* mutations in cancer epithelium samples based on amplicon sequencing in which PCR primers designed to amplify DNA fragments containing a splice donor site SNV (c.4993+2T>C) and a frameshift insertion (p.E1683fs). The alignment was visualized using IGV tools. These two mutations resided on distinct alleles and were therefore biallelic compound heterozygous mutations.