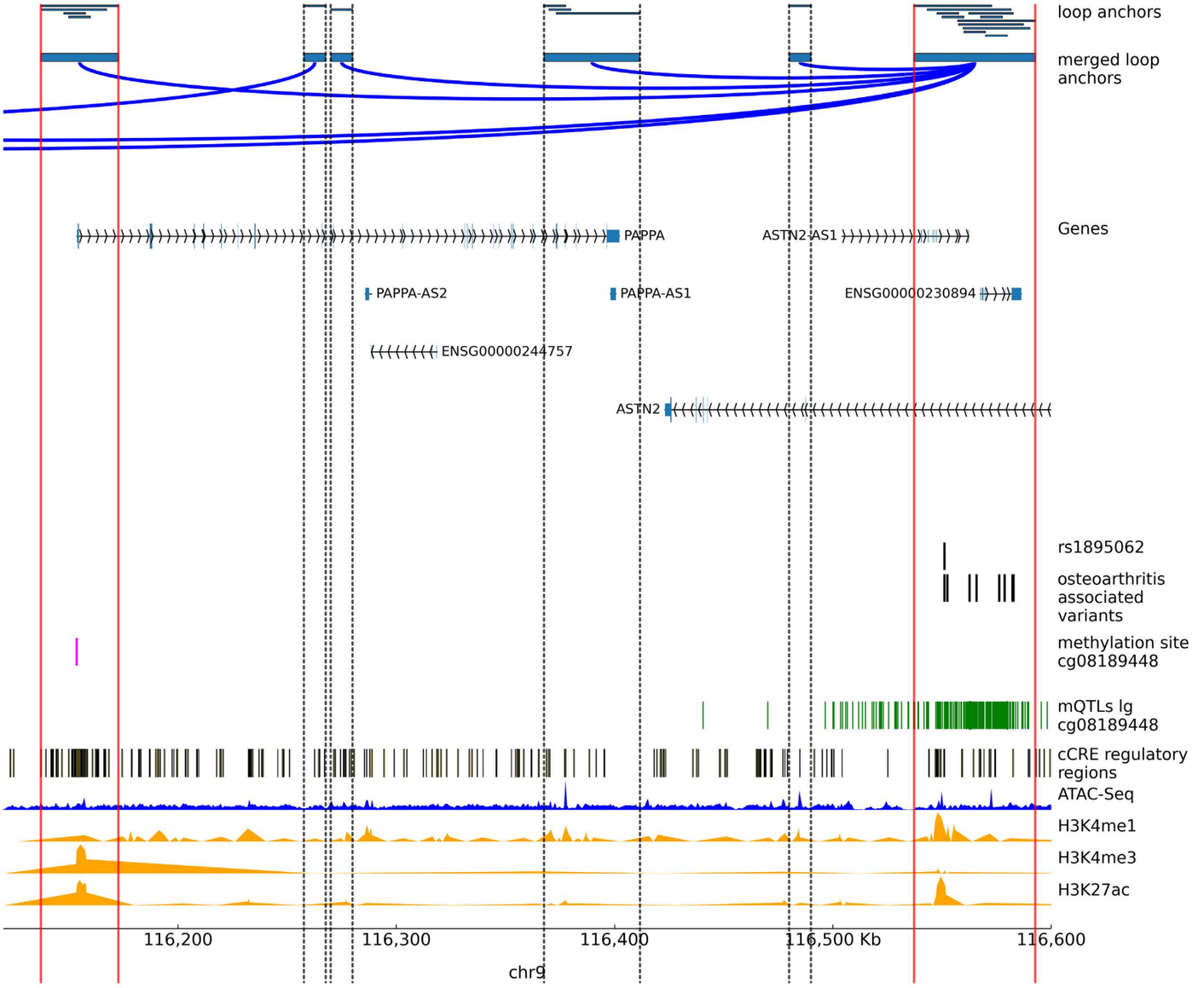

Supplemental Figure 11 **Identification of enhancer – promoter loops linked with osteoarthritis lead variant rs1321917 on chromosome 9**
Zoomed in plot of the identified enhancer – promoter loop associated to lead variant rs1321917. Horizontal red lines show the region of loop anchors with active promoter and enhancer regions throughout the plotting area. Horizontal dotted black lines show other identified loop anchor regions without any active enhancer/promoter region. *Loop anchors* show all identified loop anchors with the different loop calling algorithms used in this study as green bars at their respective location on the plotted chromosome region. The *merged loop anchors* show the region used for the final analysis after merging the several locally identified loop anchors. Putative identified loops are connected with a blue arc. *Genes* are the position of transcribed regions as identified in ENSEMBL genes version 110. *Osteoarthritis associated variants* are variants from the 95% credible set of a study by Boer, Hatzikotoulas, Southam et al.[3] with a posterior probability of > 3% identified to reside in loop anchors called in this study. In addition, the position of the credible set variant residing in an enhancer region, *rs1895062* , is shown in a separate track. Associated methylation QTL (mQTL) methylation sites and the respective positions of mQTLs in low grade (lg) degraded cartilage were identified by Kreitmaier et al.[41]. c*CRE regulatory regions* shows all cis regulatory elements (cCRE) as identified in version3 from the ENCODE registry[30]. ATAC Seq[11] (n = 8) and histone mark signal tracks for H3K4me1, H3K4me3 and H3K27ac[12] (n = 3) were averaged and merged into one track from the replicates of the public data repositories, Genomic co-ordinates (GRCh38) are given below the plot