**Fig. S5** **Circos plots showing chromatin interactions between potential causal variants and distant genes.**

The outer layer shows all the SNPs with an association P < 0.05 in the MTAG analysis. SNPs in each genomic risk locus are colored according to their LD relationship with the index SNPs in the locus (red: r2 > 0.8, orange: 0.6 < r2 ≤ 0.8, green: 0.4 < r2 ≤ 0.6 , blue:0.2 < r2 ≤ 0.4). SNPs that are not in LD with any of the independent index SNPs ( r2 ≤ 0.2) are shown in gray. The rsID of the top associated potential causal SNPs is also displayed in the outermost layer. The inner layers show the chromosome ring. Genomic risk loci are highlighted in blue. Genes were mapped by chromatin interactions or eQTLs. If a candidate gene was mapped only by chromatin interactions or only by eQTLs, it was colored in orange or green, respectively. When the gene was mapped by both, it was colored in red. (a) painful gums (PG); (b) toothache (TA).

