



**S21 Fig. LocusZoom plots comparing the (A) discovery analysis, and (B) conditional analysis for the observed genetic association of nasal width near PAX1 at 20p11.22. Genetic association (left y-axis; log<sub>10</sub>-transformed p-values) is shown for genotyped SNPs**

depicted as stars and imputed SNPs depicted as circles. Shading of the points represent the linkage disequilibrium ( $r^2$ ) between each SNP and the rs2424399 (the top SNP from the discovery analysis), indicated by purple shading. The blue overlay shows the recombination rate (right y-axis). Positions of genes are shown below the plot. In the discovery analysis, a possible second peak in low-LD with the rs2424399 was observed around chromosomal position 22.0 Mb. After conditioning on rs2424399, variants at position 22.0 Mb showed some independent evidence of association, although not meeting genome-wide or suggestive thresholds for significance