

Description of Additional Supplementary Files

File Name: Supplementary Data 1

Description: **sPTB lead SNPs and LD SNPs for independent sPTB genomic regions.** Independent sPTB regions denoted by their lead SNP (SNP with lowest P-value) and SNPs in LD after clumping Zhang et. al. sPTB GWAS.

File Name: Supplementary Data 2

Description: **Heatmap z-score results in tabular format for Figure 2.** Each row represents an independent sPTB associated region denoted by the lead SNP (column 'rsid') and corresponding zscore for evolutionary measures (columns).

File Name: Supplementary Data 3

Description: **Heatmap p-value results in tabular format for Figure 2.** Each row represents an independent sPTB associated region denoted by the lead SNP (column 'rsid') and the corresponding empirical p-value obtained by comparing to the matched background distribution for difference evolutionary measures (columns).

File Name: Supplementary Data 4

Description: **1KG Individual IDs used for analysis.** Individual IDs and corresponding 1000 Genomes superpopulation assignment used for calculating evolutionary measures.

File Name: Supplementary Data 5

Description: **Cluster assignment and functional annotation for sPTB genomic regions.** The included regions are those with $-1.5 \leq \text{z-score} \leq 1.5$ from Figure 2. Each row represents the lead SNP and SNPs in LD for sPTB associated regions with an absolute value z-score ≥ 1.5 for any of the evolutionary measures evaluated. Columns include corresponding data for genomic position, nearest gene, statistics fro