

Supplementary Figure S3

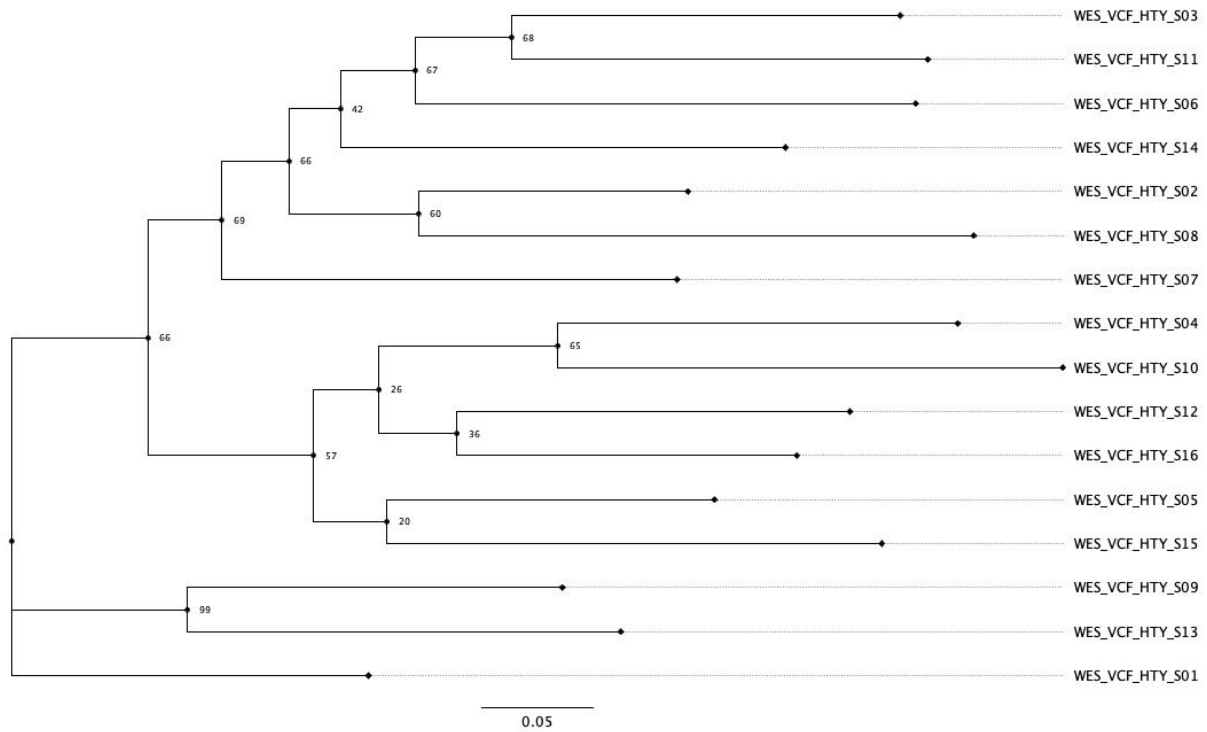


Figure S3. A phylogenetic tree constructed from SNPs detected in the 340 immune genes known to play roles in human gut microbiota. This unrooted tree was constructed using GTR+F+R2 as a model of nucleotide substitution. Numbers at the nodes are ultrafast bootstrap support (%). The Log-likelihood of this tree is -74062.3036 (s.e. 566.6104). Unconstrained log-likelihood (without tree) is -113874.0286. Akaike information criterion (AIC) score is 148202.6072, and a corrected Akaike information criterion (AICc) score is 148202.8000. Bayesian information criterion (BIC) score is 148502.6635. The total tree length (sum of branch lengths) is 3.5892, and the sum of internal branch lengths is equal to 0.6113 (17.0317% of tree length).