



S1 Fig. Sliding-window test results using exon-sequencing of RA cases and controls. An accumulation of true rare missense variants ($MAF < 0.5\%$) predicted to be damaging was observed in the Protein kinase 1 domain of *TYK2*. Association results from 500 bp sliding window tests in SKAT-O restricted to nonsense variants (pink) and missense variants predicted to be damaging (red) are shown. Variants with $MAF > 1\%$ (indicated by a star) were excluded in the test. In *TYK2*, we further excluded the A928V and A53T variants with $0.5\% < MAF < 1\%$ (indicated by a star) that were independently investigated using Exomechip data. The light blue background highlights the coding sequence region with $P < 0.05$.