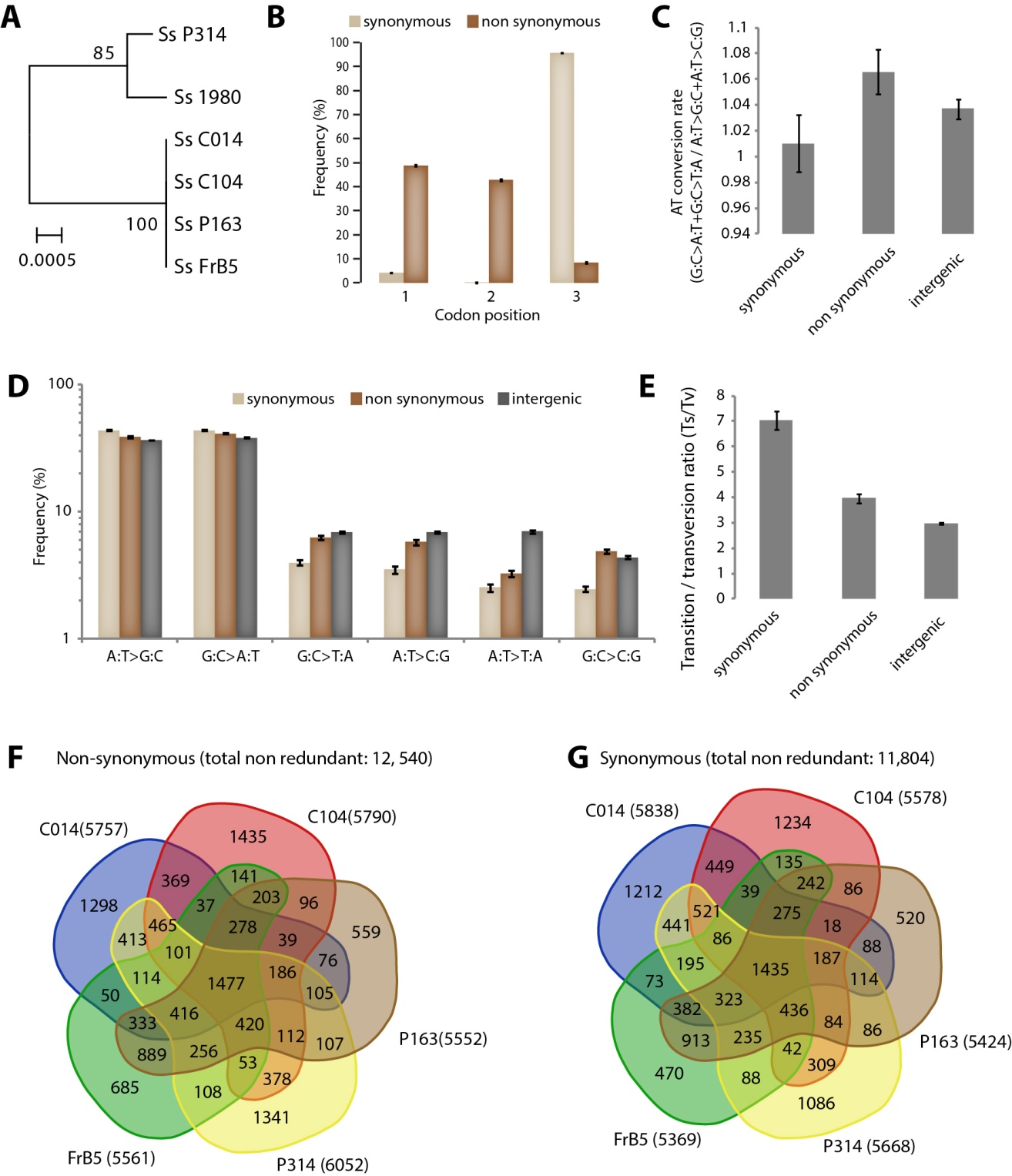
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**Figure 4 – figure supplement 2. Analysis of Single Nucleotide Polymorphisms (SNPs) in a natural population of the generalist plant pathogen *Sclerotinia sclerotiorum*. (A)** IGS-based phylogeny of the *S. sclerotiorum* isolates re-sequenced in this work. **(B)** Frequency of SNPs according to codon position and SNP type. **(C)** SNPs in coding regions do not show significant bias towards enrichment in A or T nucleotides as shown by the rate of AT conversion. **(D)** Frequency of each substitution type among synonymous, non-synonymous and intergenic SNPs shows higher transition rate among synonymous substitutions. **(E)** Transition / transversion ratio per SNP type shows ~3 fold increase in synonymous substitutions. **(B-E)** Error bars show the standard deviation of means for each isolate. Distribution of non-synonymous **(F)** and synonymous **(G)** SNPs among the five re-sequenced isolates.