**Figure S1.** Frequency of recombinant regions as detected by PhiPack using single (intra-genic) vs. multiple (inter-genic) genes in ‘global’ subset and ‘local’ (Amerindian) subset of strains (as denoted in Fig. 1).

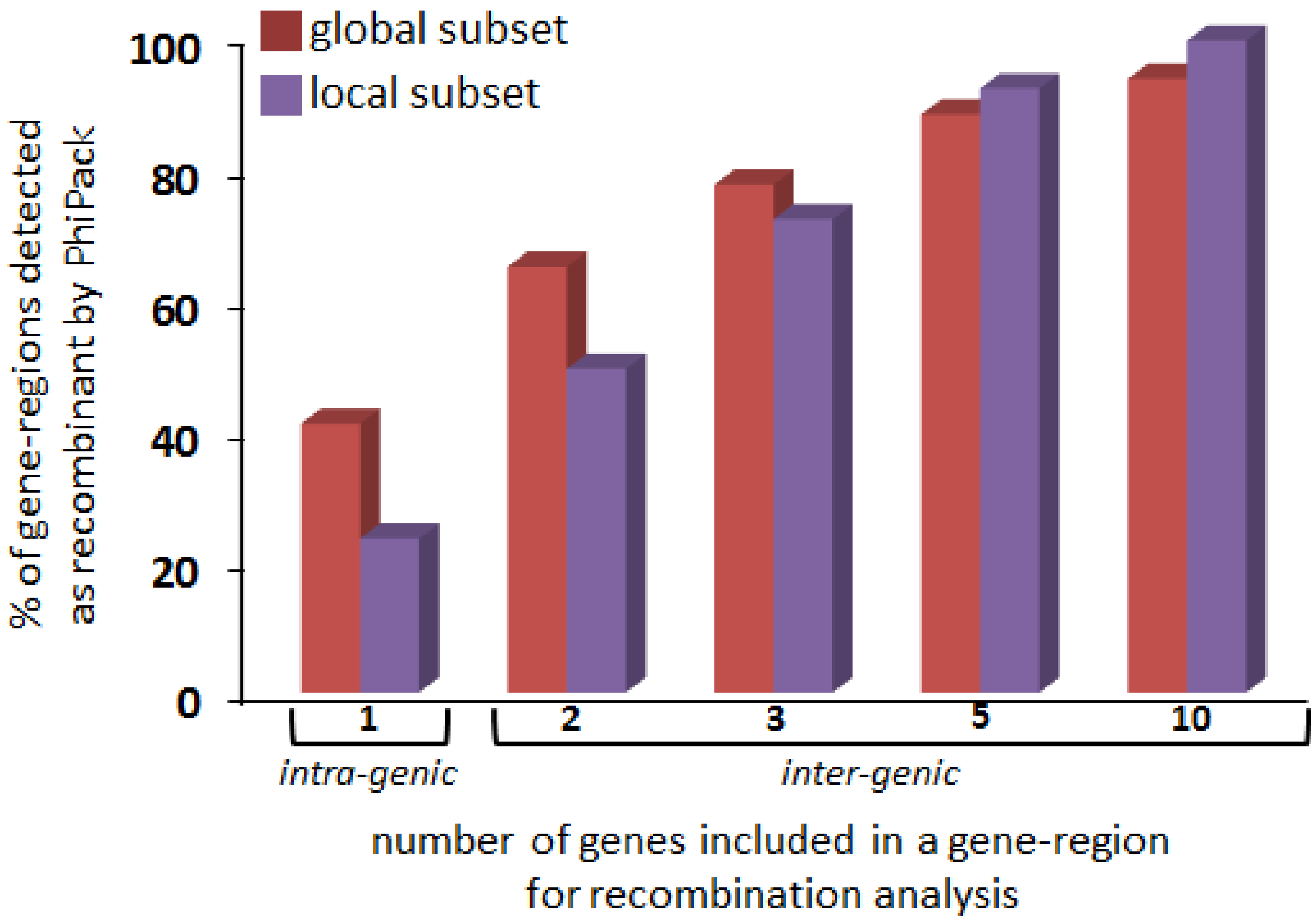
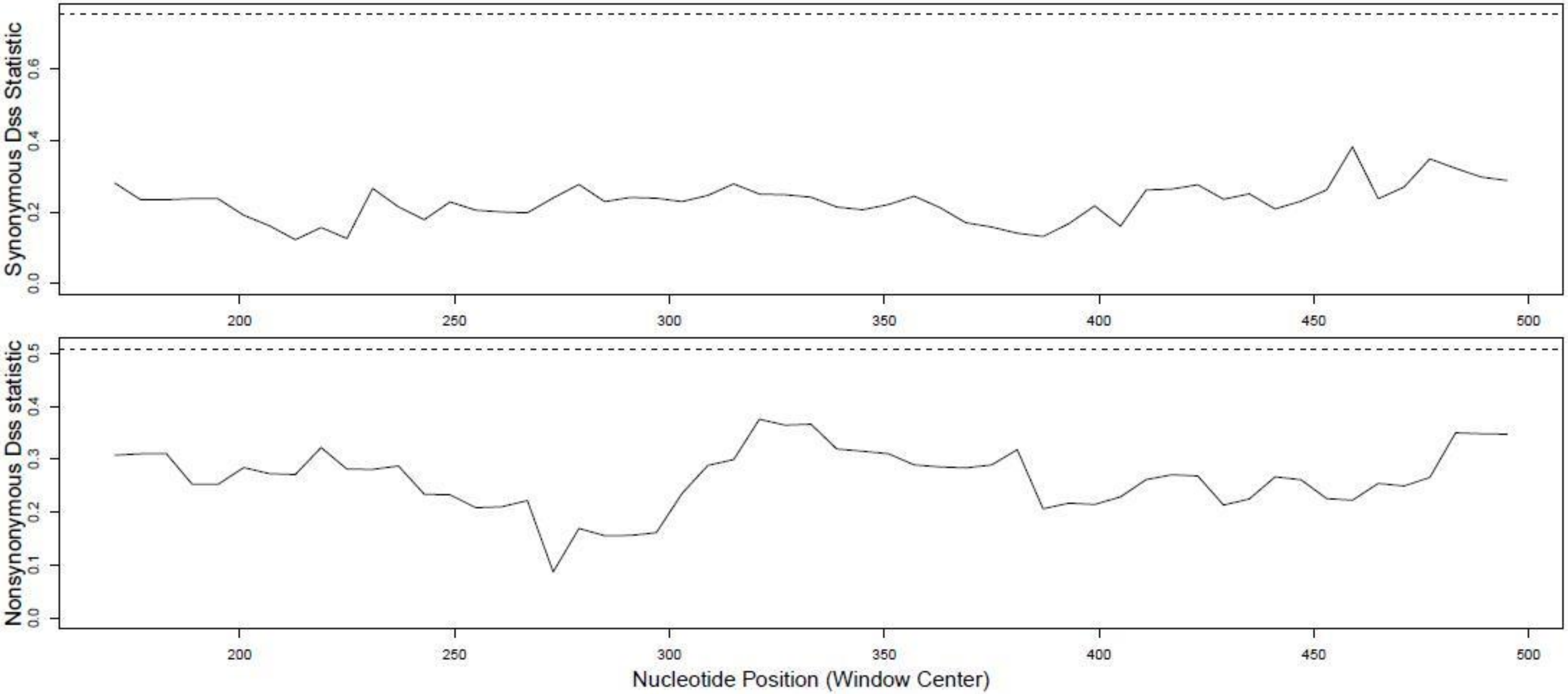


**Figure S2.** The synDss statistic landscapes for 50 randomly selected core genes of *H. pylori*: (A) 25 recombinant and (B) 25 non-recombinant, as designated by three recombination detection statistics in PhiPack software.

## (A) 25 randomly selected core genes designated as **recombinants** by PhiPack

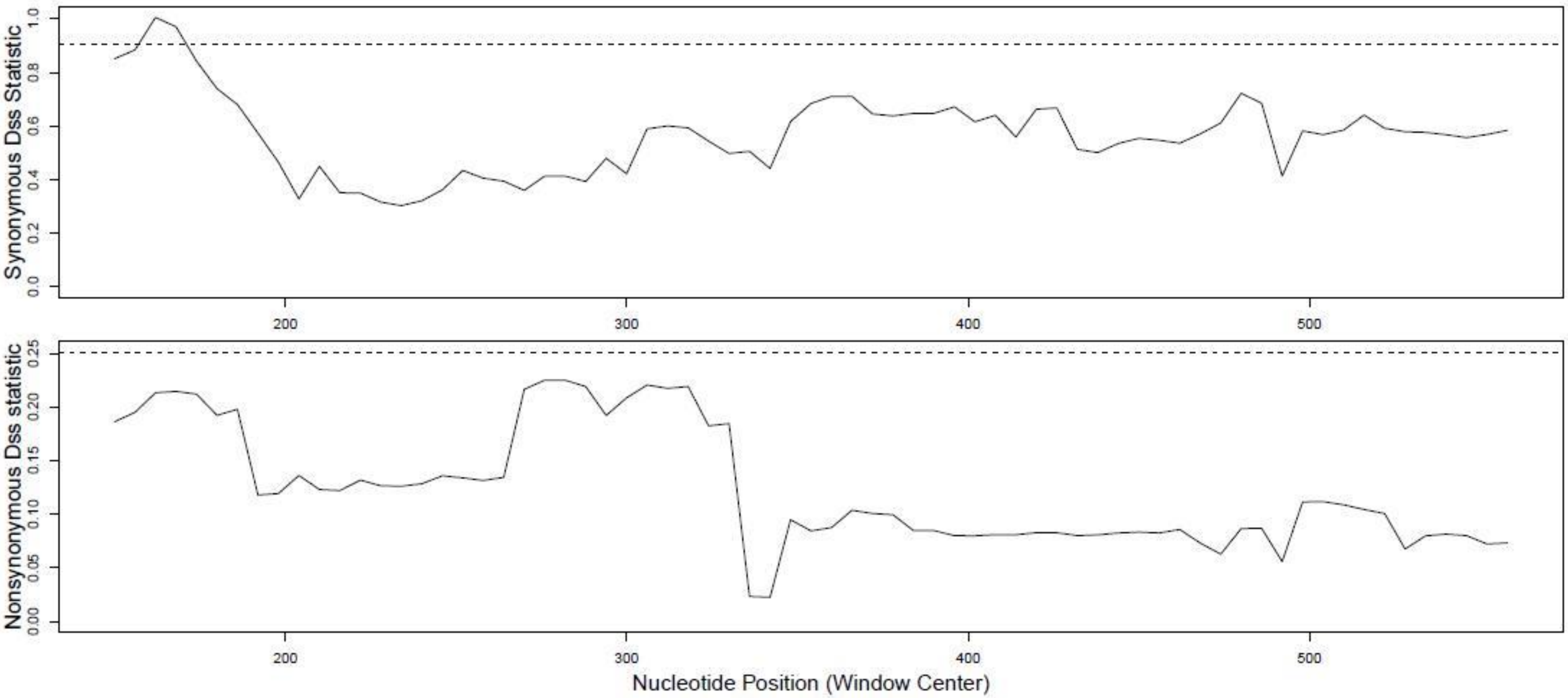
### HP_0029



Dss statistic landscapes for synonymous and nonsynonymous changes. Dotted horizontal lines represent the 95% significance level for each test, from a parametric bootstrap with 500 replicates.

(A) 25 randomly selected core genes designated as **recombinants** by PhiPack (CONTD.)

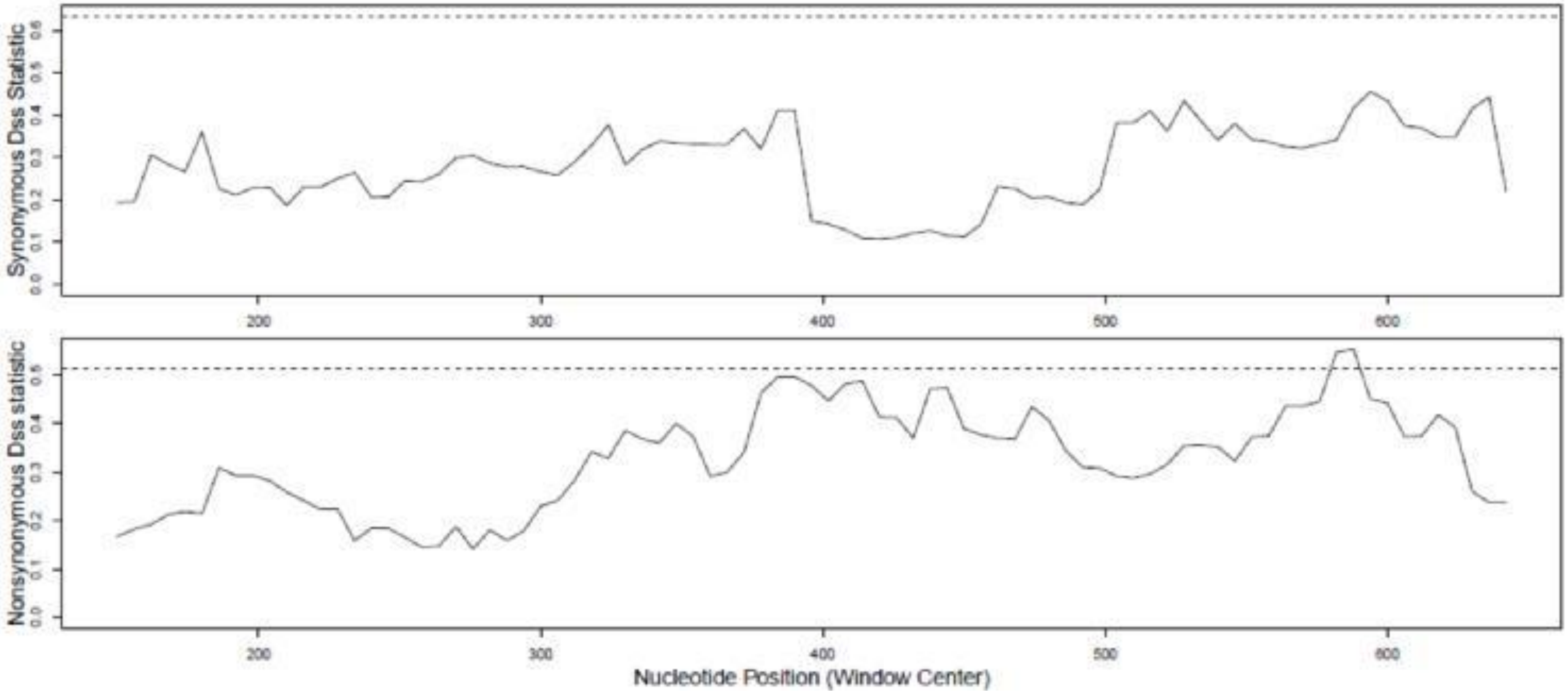
HP_0042



Dss statistic landscapes for synonymous and nonsynonymous changes. Dotted horizontal lines represent the 95% significance level for each test, from a parametric bootstrap with 500 replicates.

(A) 25 randomly selected core genes designated as **recombinants** by PhiPack (CONTD.)

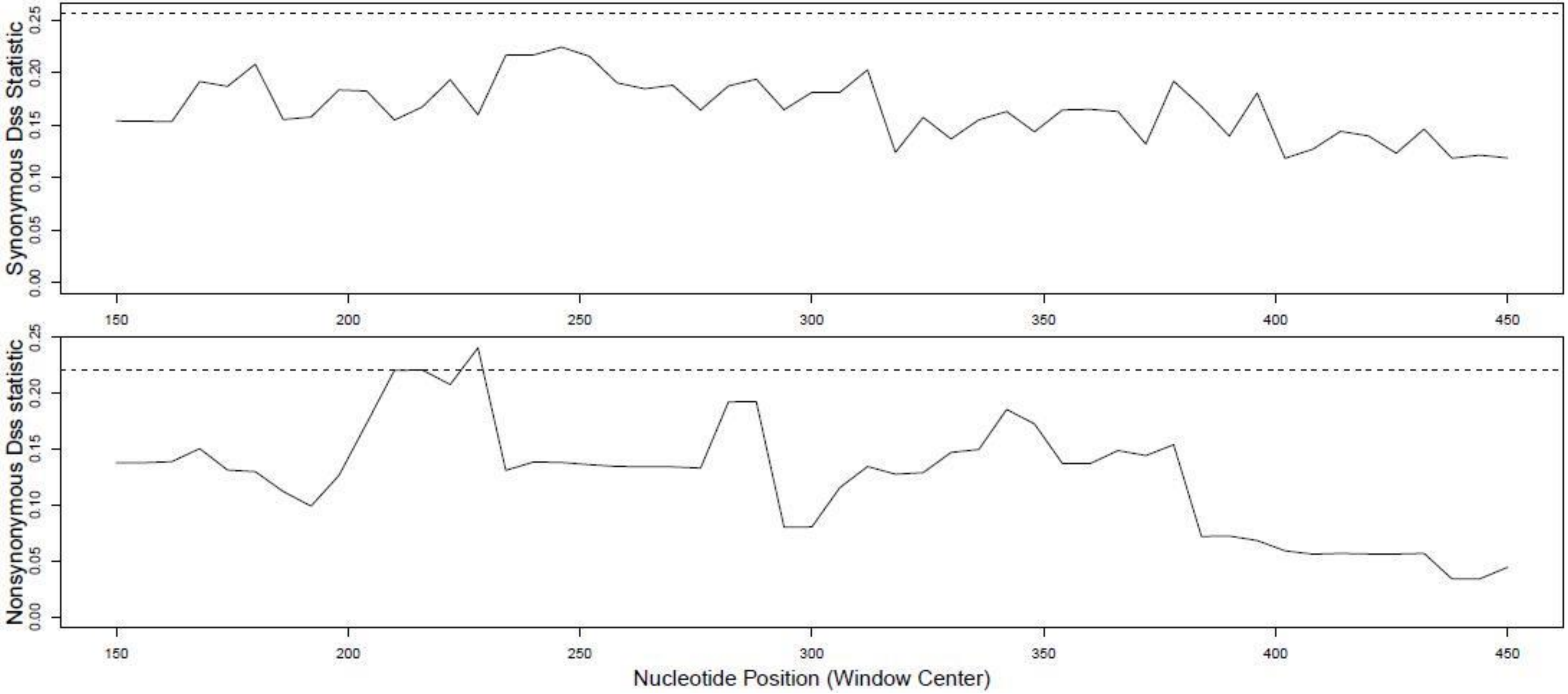
HP_0102



Dss statistic landscapes for synonymous and nonsynonymous changes. Dotted horizontal lines represent the 95% significance level for each test, from a parametric bootstrap with 500 replicates.

(A) 25 randomly selected core genes designated as **recombinants** by PhiPack (CONTD.)

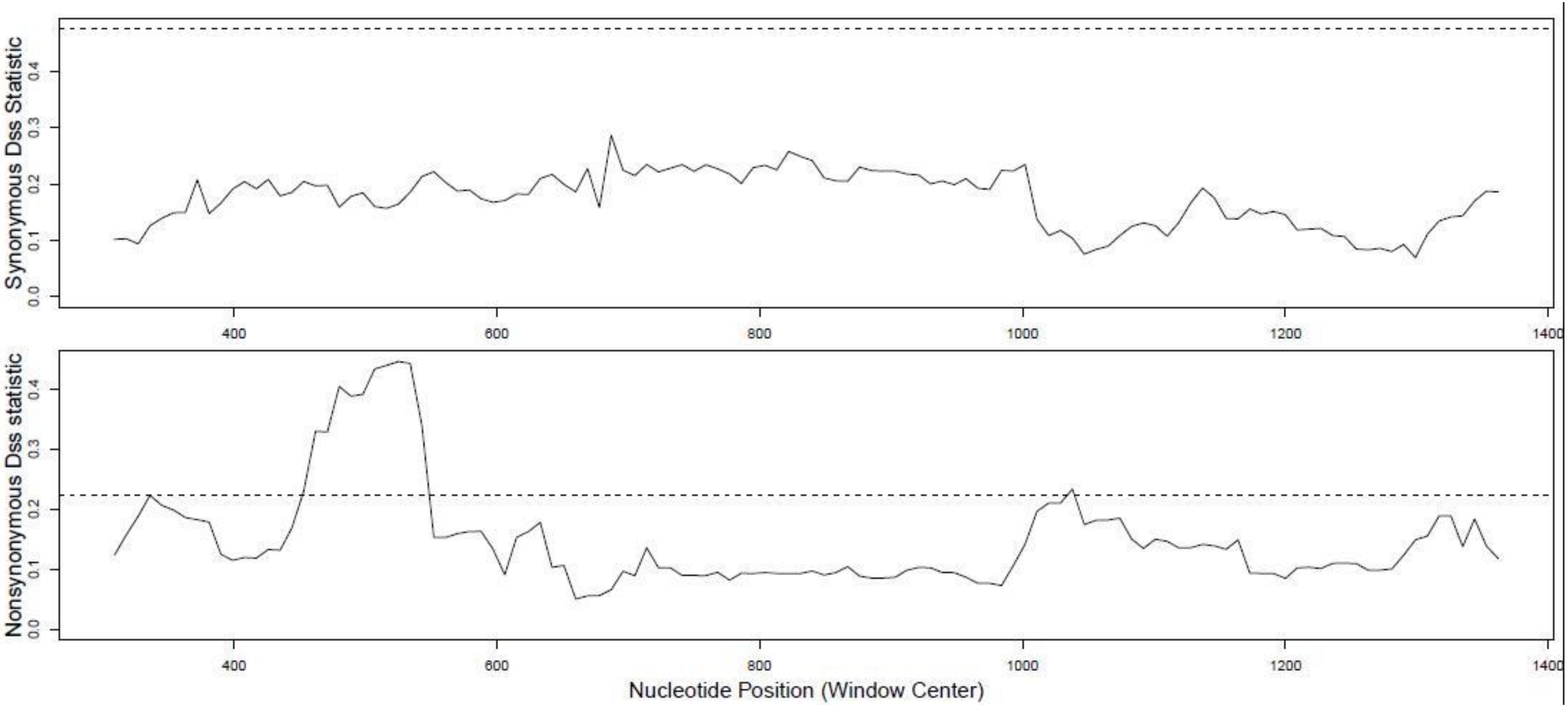
HP_0150



Dss statistic landscapes for synonymous and nonsynonymous changes. Dotted horizontal lines represent the 95% significance level for each test, from a parametric bootstrap with 500 replicates.

(A) 25 randomly selected core genes designated as **recombinants** by PhiPack (CONTD.)

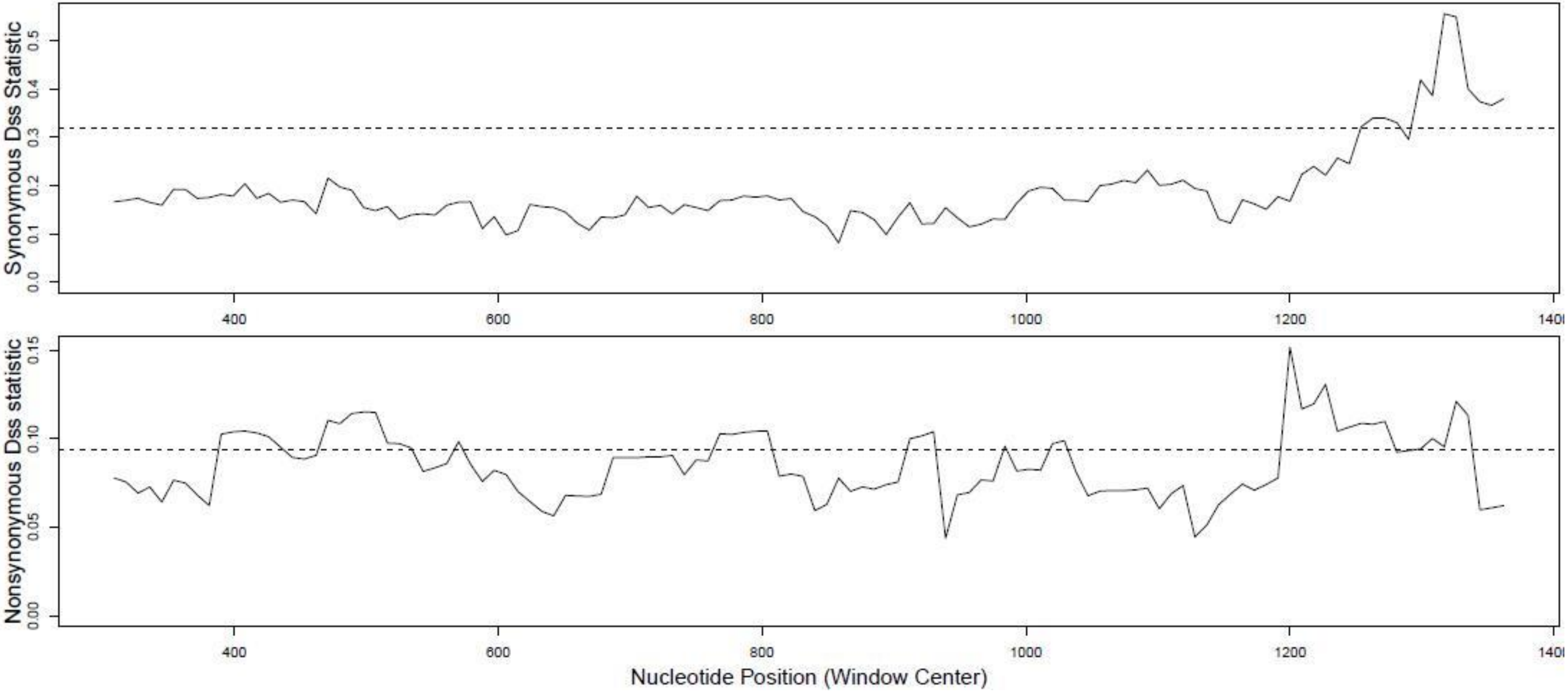
HP_0214



Dss statistic landscapes for synonymous and nonsynonymous changes. Dotted horizontal lines represent the 95% significance level for each test, from a parametric bootstrap with 500 replicates.

(A) 25 randomly selected core genes designated as **recombinants** by PhiPack (CONTD.)

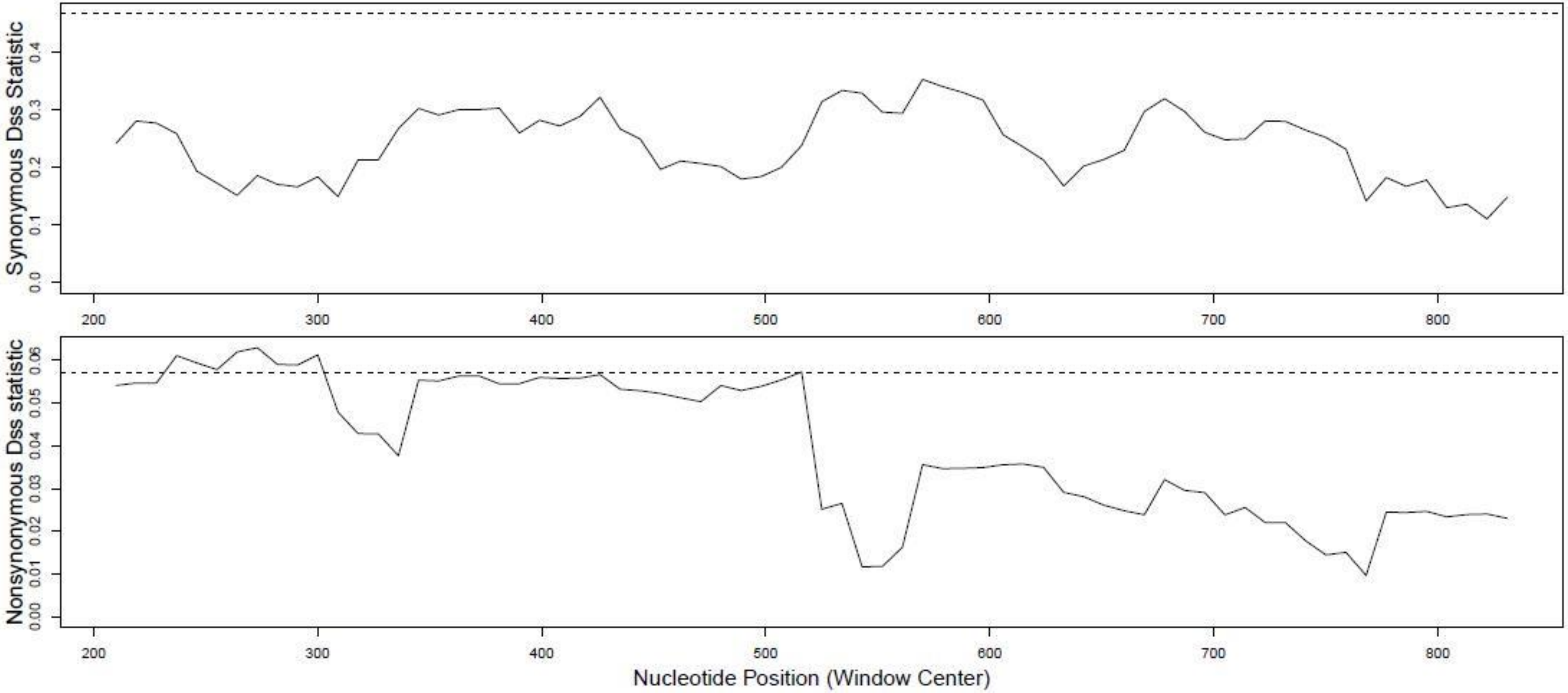
HP_0298



Dss statistic landscapes for synonymous and nonsynonymous changes. Dotted horizontal lines represent the 95% significance level for each test, from a parametric bootstrap with 500 replicates.

(A) 25 randomly selected core genes designated as **recombinants** by PhiPack (CONTD.)

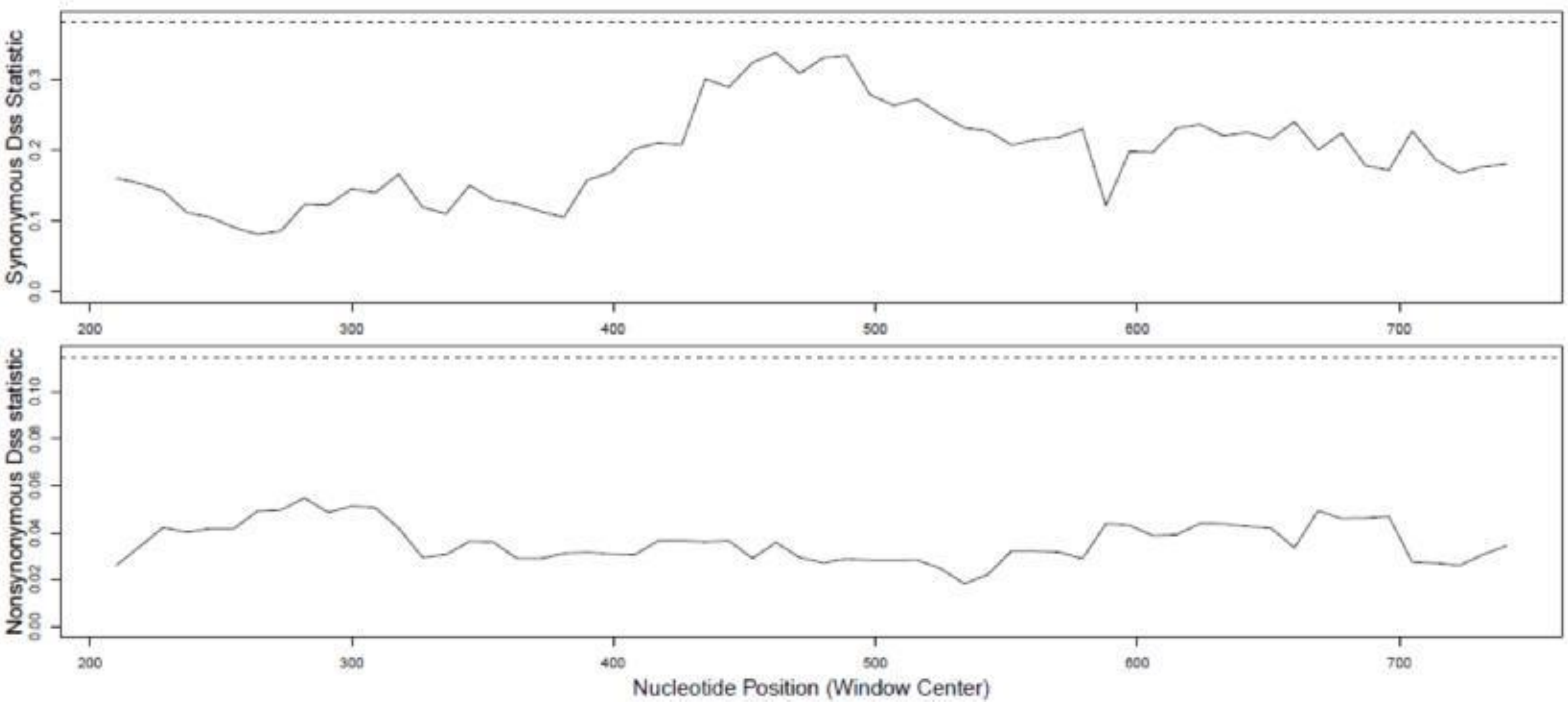
HP_0352



Dss statistic landscapes for synonymous and nonsynonymous changes. Dotted horizontal lines represent the 95% significance level for each test, from a parametric bootstrap with 500 replicates.

(A) 25 randomly selected core genes designated as **recombinants** by PhiPack (CONTD.)

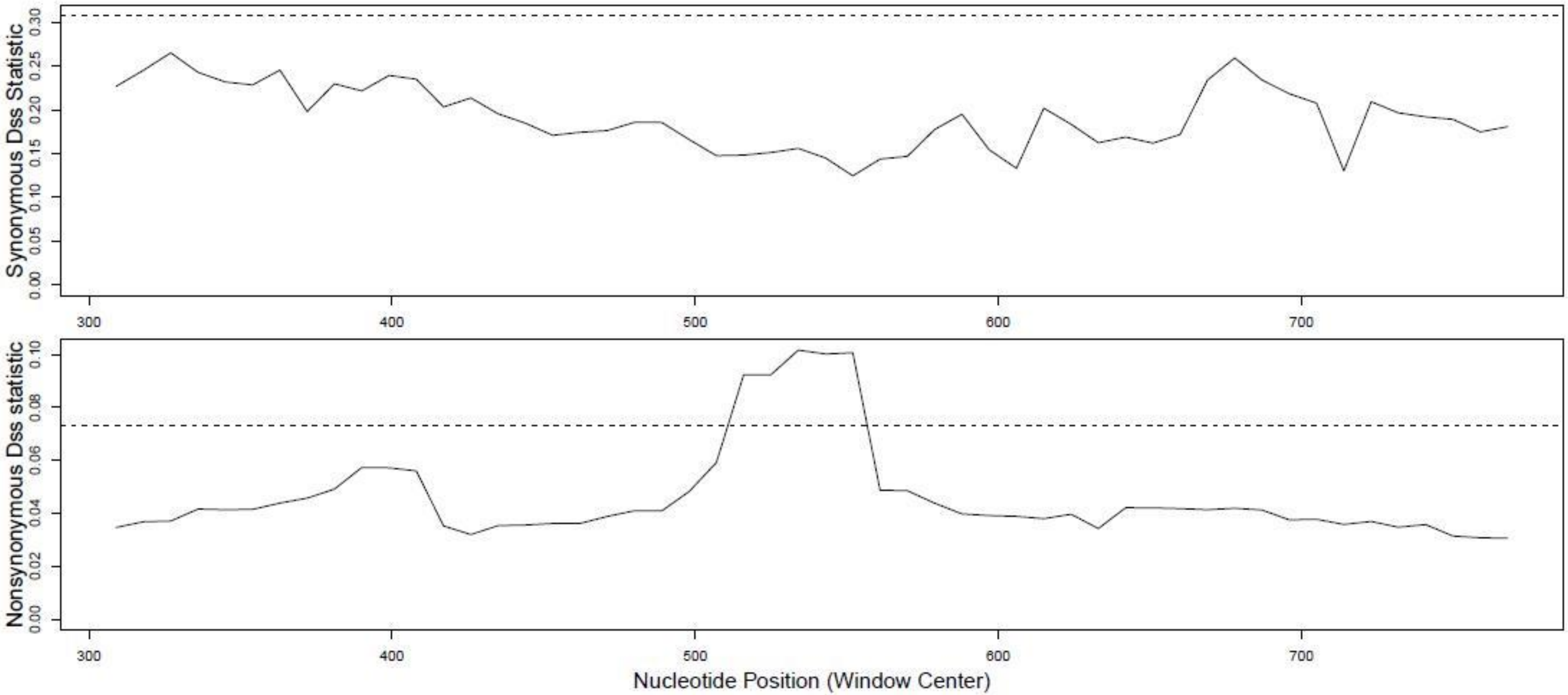
HP_0393



Dss statistic landscapes for synonymous and nonsynonymous changes. Dotted horizontal lines represent the 95% significance level for each test, from a parametric bootstrap with 500 replicates.

(A) 25 randomly selected core genes designated as **recombinants** by PhiPack (CONTD.)

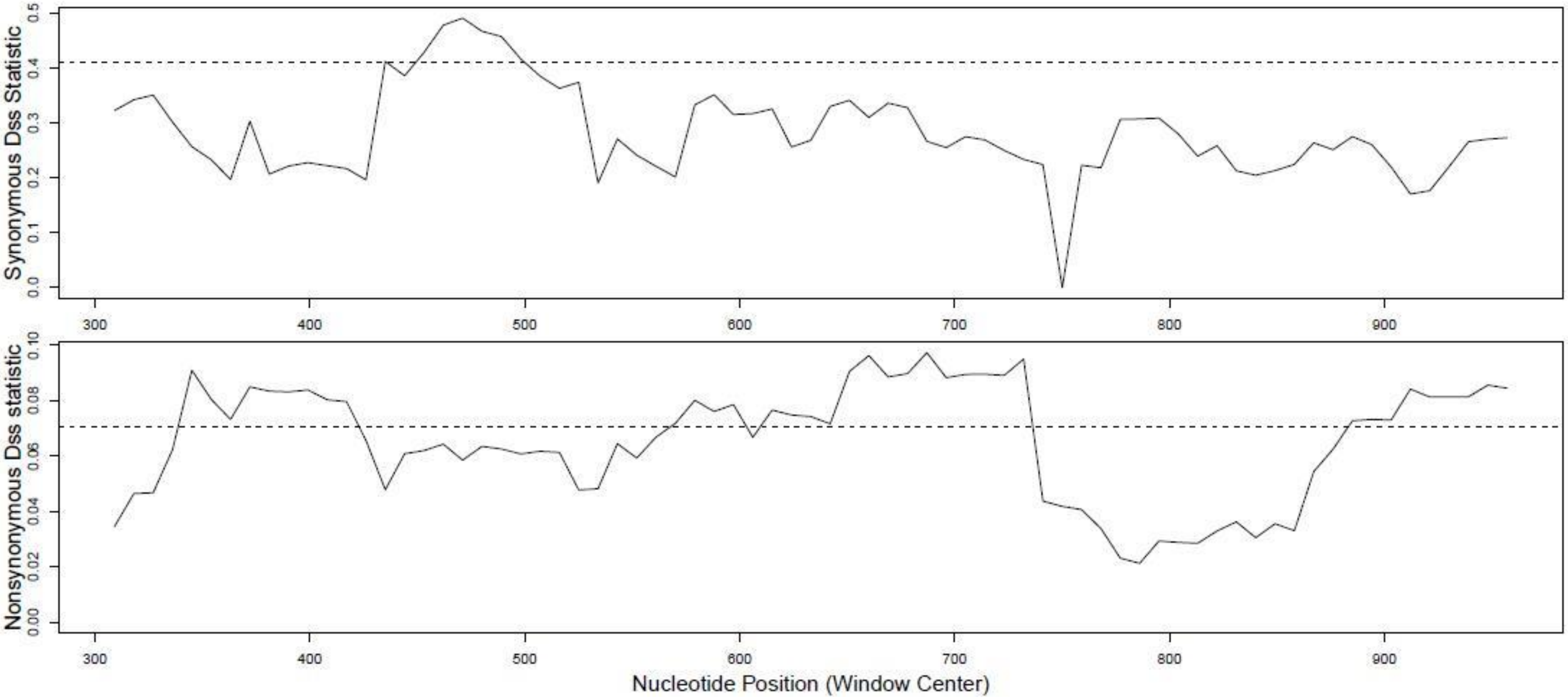
HP_0493



Dss statistic landscapes for synonymous and nonsynonymous changes. Dotted horizontal lines represent the 95% significance level for each test, from a parametric bootstrap with 500 replicates.

(A) 25 randomly selected core genes designated as **recombinants** by PhiPack (CONTD.)

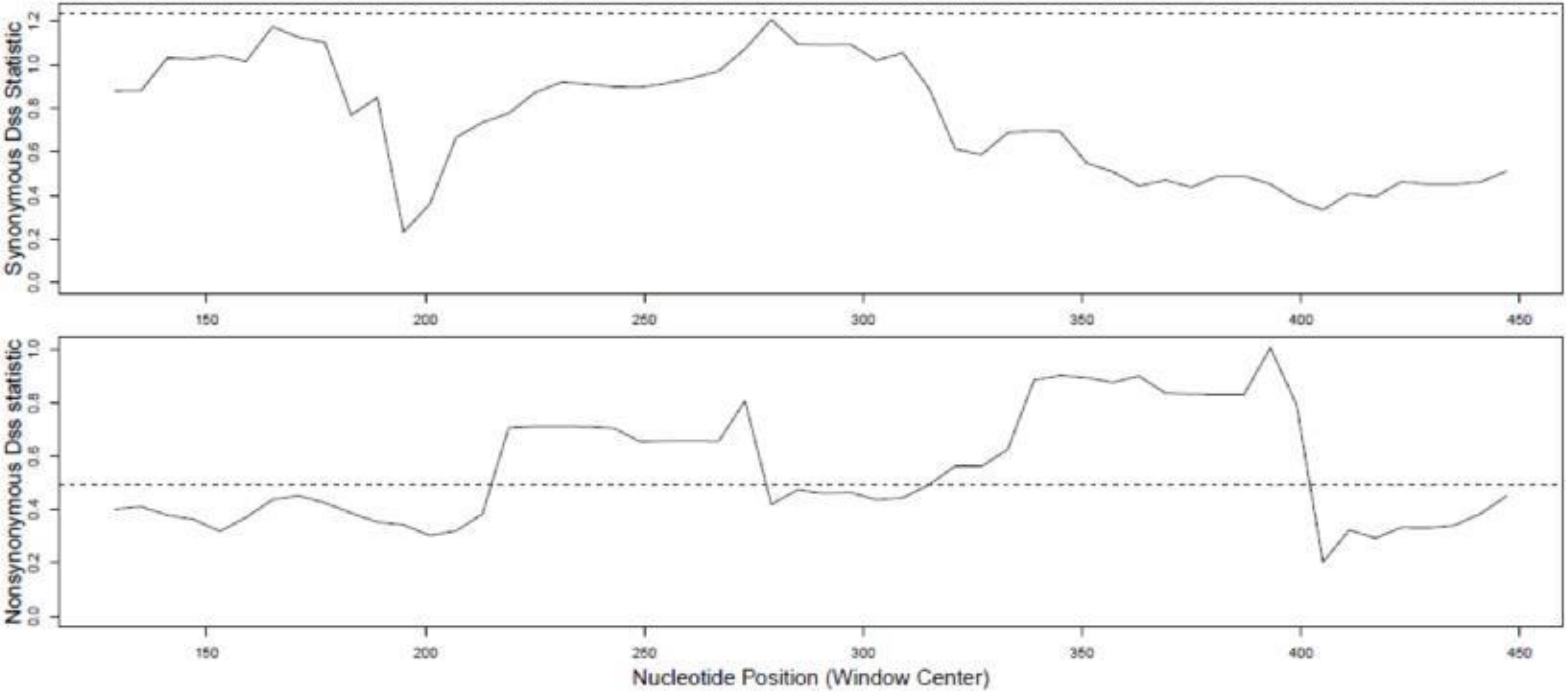
HP_0563



Dss statistic landscapes for synonymous and nonsynonymous changes. Dotted horizontal lines represent the 95% significance level for each test, from a parametric bootstrap with 500 replicates.

(A) 25 randomly selected core genes designated as **recombinants** by PhiPack (CONTD.)

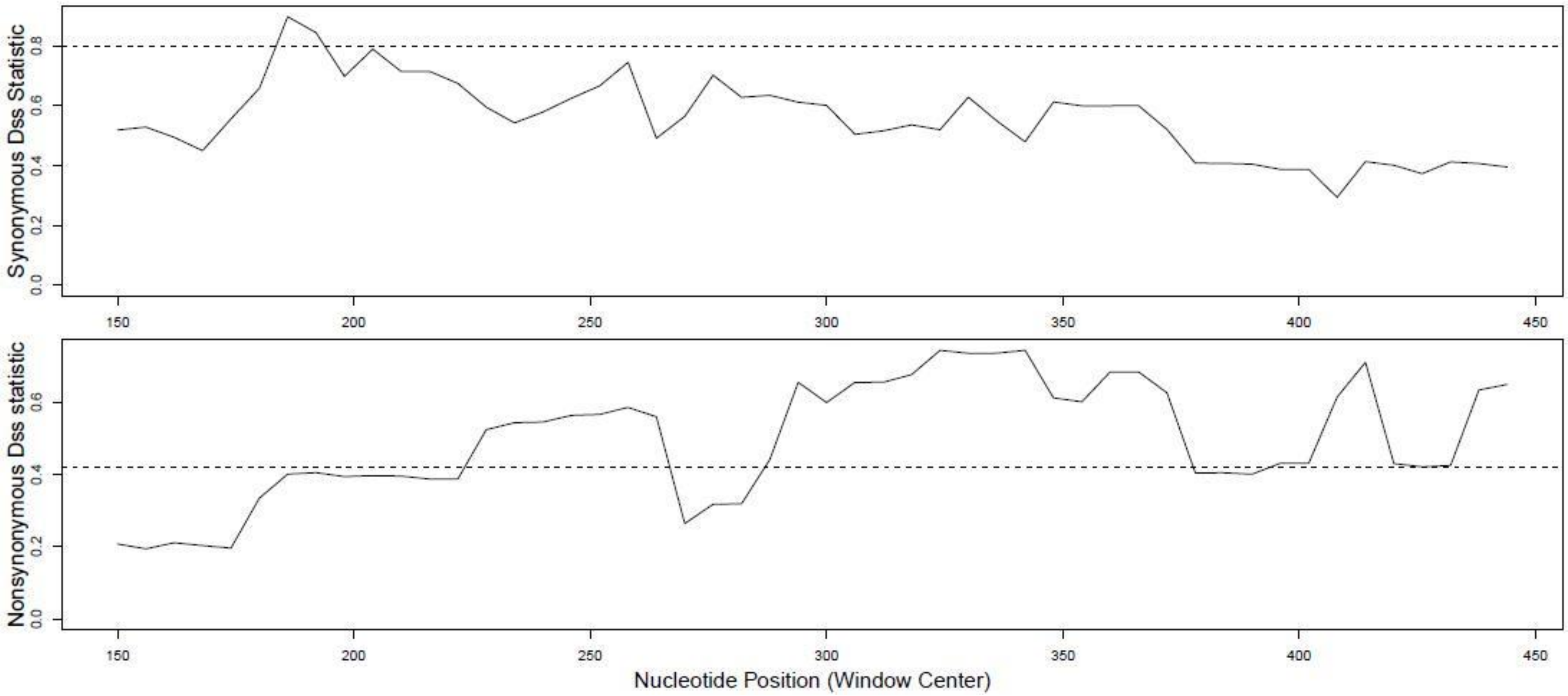
HP_0603



Dss statistic landscapes for synonymous and nonsynonymous changes. Dotted horizontal lines represent the 95% significance level for each test, from a parametric bootstrap with 500 replicates.

(A) 25 randomly selected core genes designated as **recombinants** by PhiPack (CONTD.)

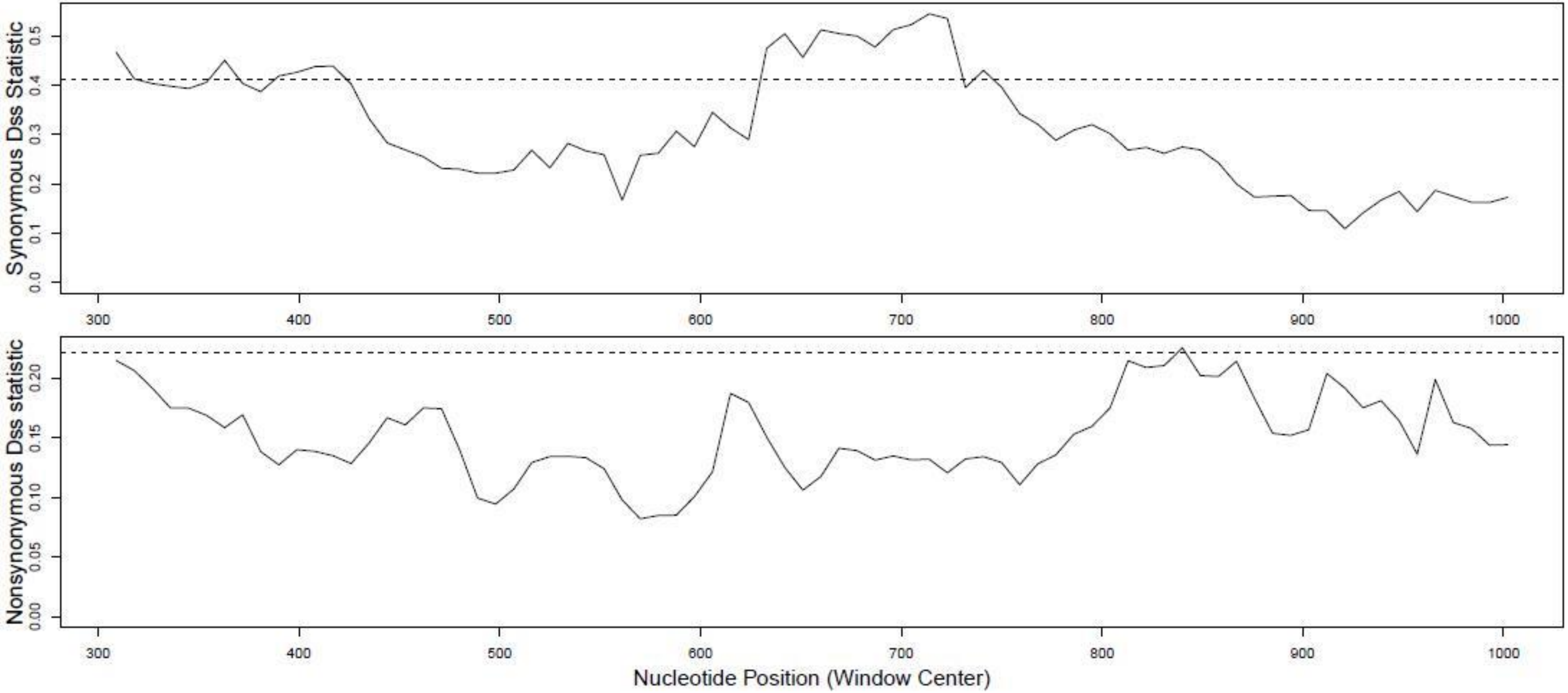
HP_0630



Dss statistic landscapes for synonymous and nonsynonymous changes. Dotted horizontal lines represent the 95% significance level for each test, from a parametric bootstrap with 500 replicates.

(A) 25 randomly selected core genes designated as **recombinants** by PhiPack (CONTD.)

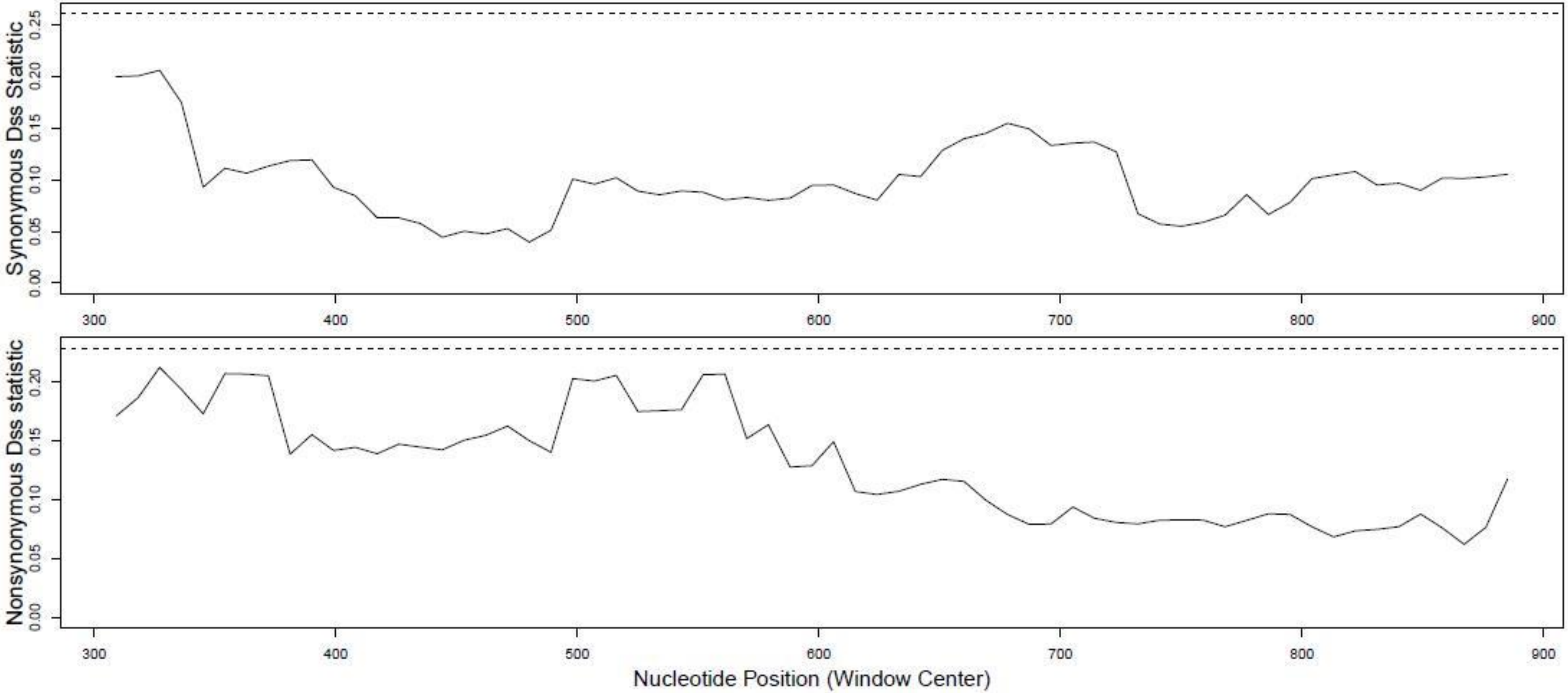
HP_0683



Dss statistic landscapes for synonymous and nonsynonymous changes. Dotted horizontal lines represent the 95% significance level for each test, from a parametric bootstrap with 500 replicates.

(A) 25 randomly selected core genes designated as **recombinants** by PhiPack (CONTD.)

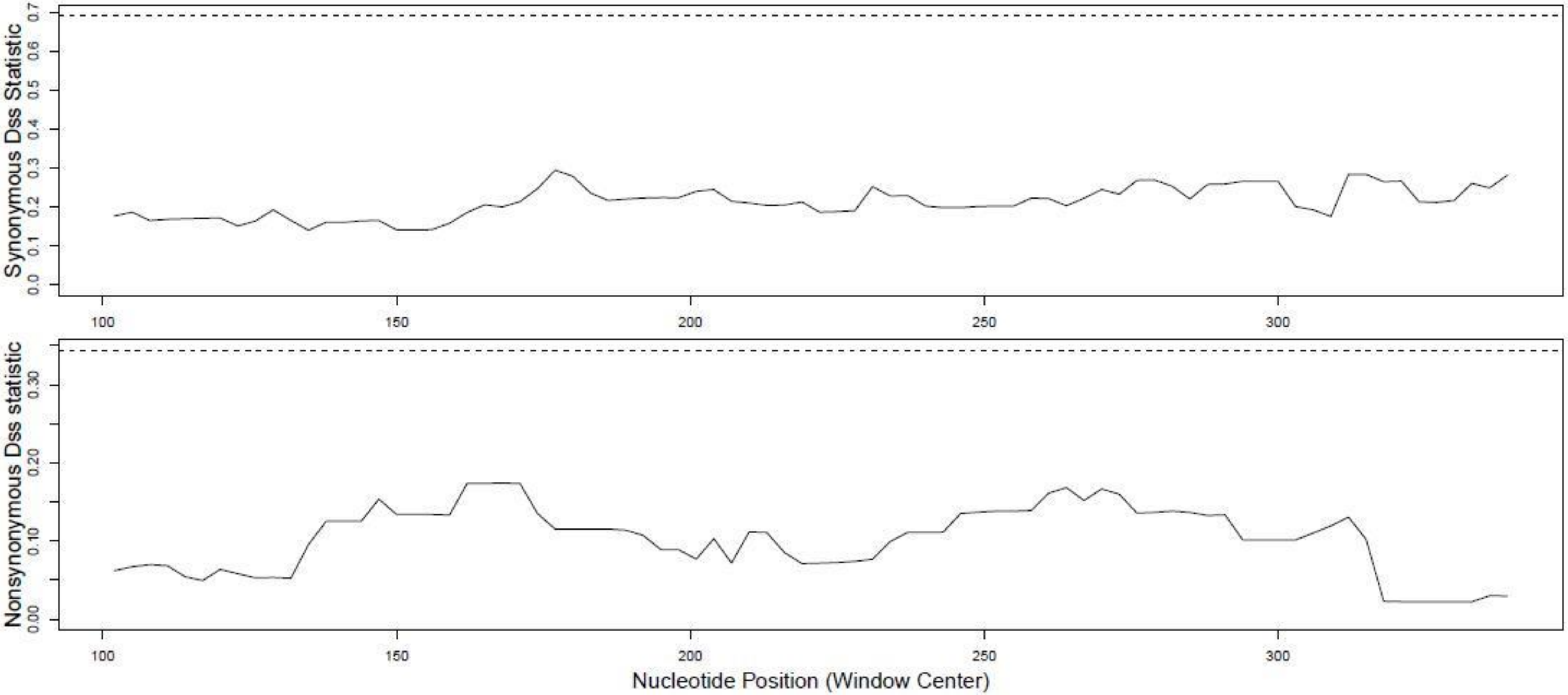
HP_0747



Dss statistic landscapes for synonymous and nonsynonymous changes. Dotted horizontal lines represent the 95% significance level for each test, from a parametric bootstrap with 500 replicates.

(A) 25 randomly selected core genes designated as **recombinants** by PhiPack (CONTD.)

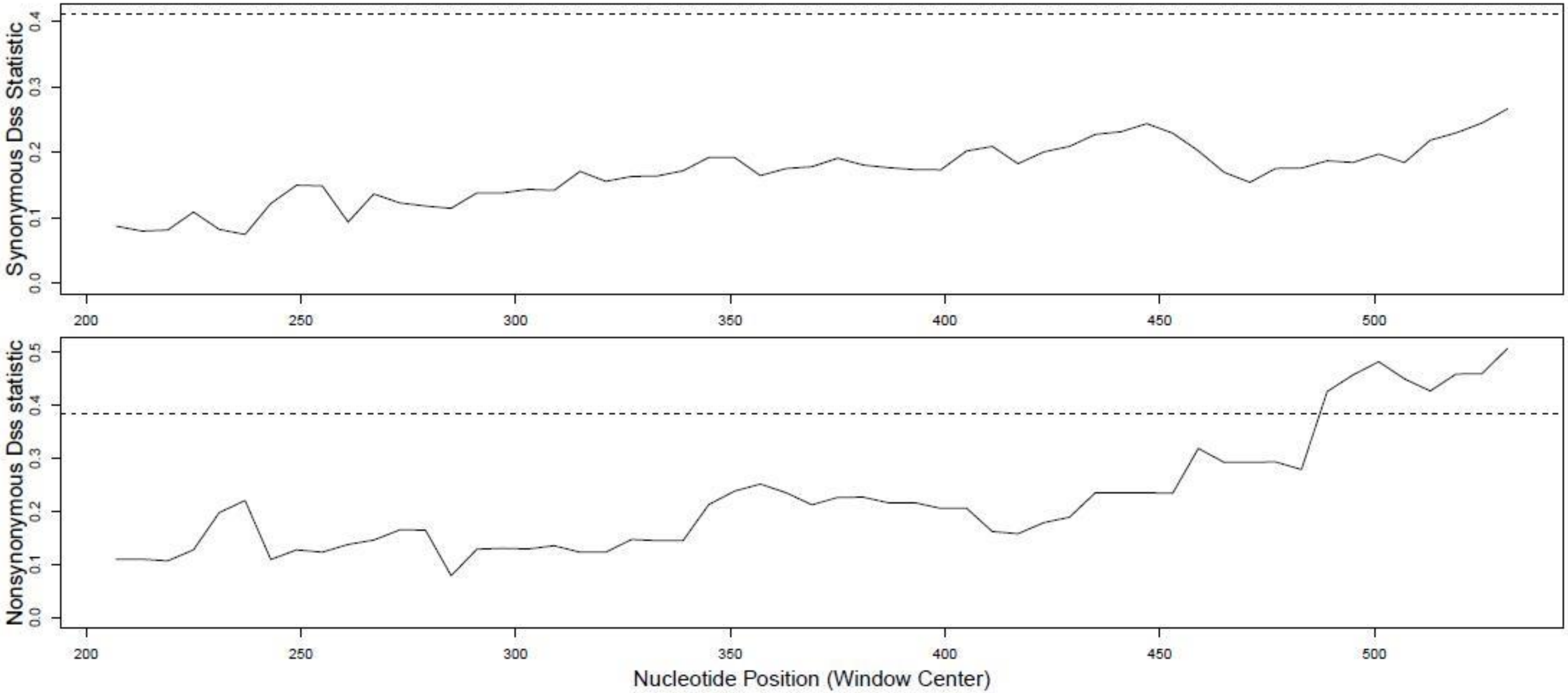
HP_0865



Dss statistic landscapes for synonymous and nonsynonymous changes. Dotted horizontal lines represent the 95% significance level for each test, from a parametric bootstrap with 500 replicates.

(A) 25 randomly selected core genes designated as **recombinants** by PhiPack (CONTD.)

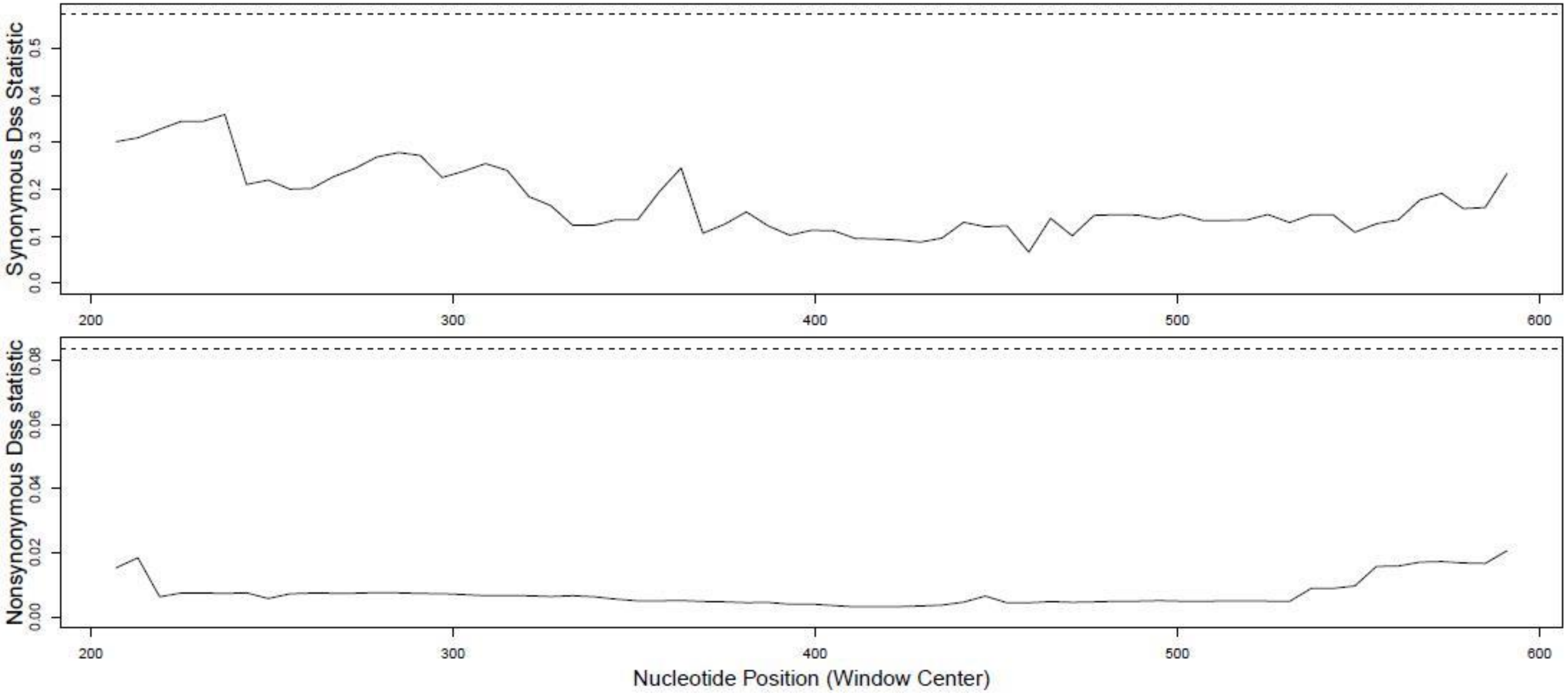
HP_0959



Dss statistic landscapes for synonymous and nonsynonymous changes. Dotted horizontal lines represent the 95% significance level for each test, from a parametric bootstrap with 500 replicates.

(A) 25 randomly selected core genes designated as **recombinants** by PhiPack (CONTD.)

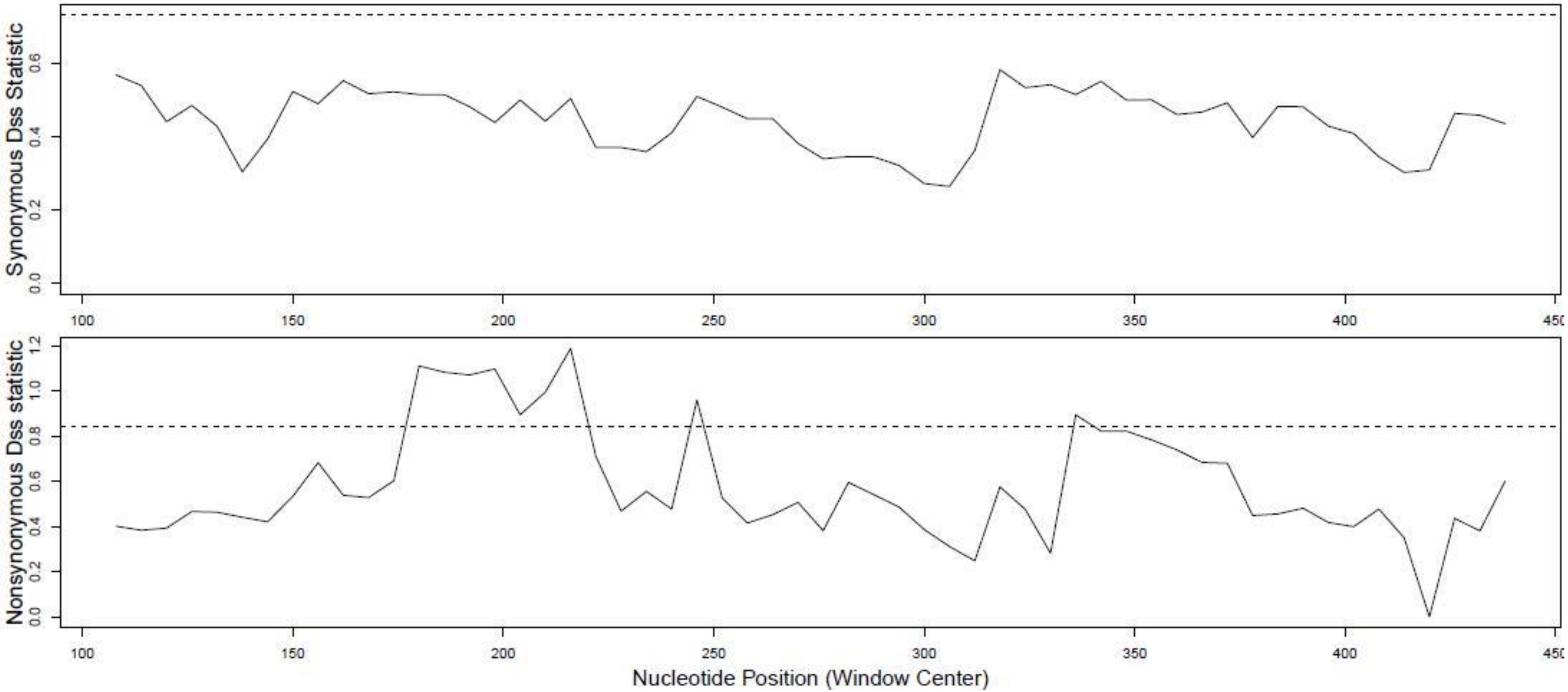
HP_1014



Dss statistic landscapes for synonymous and nonsynonymous changes. Dotted horizontal lines represent the 95% significance level for each test, from a parametric bootstrap with 500 replicates.

(A) 25 randomly selected core genes designated as **recombinants** by PhiPack (CONTD.)

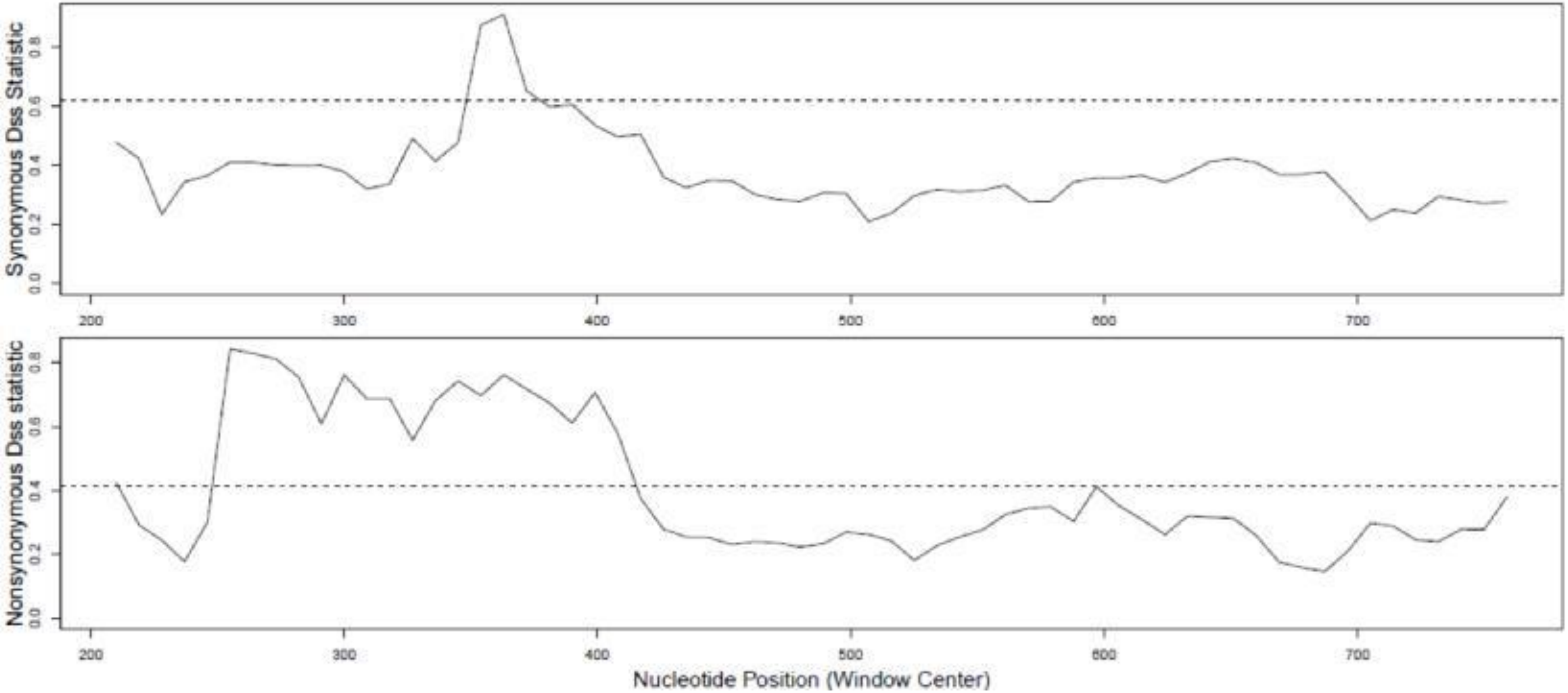
HP_1029



Dss statistic landscapes for synonymous and nonsynonymous changes. Dotted horizontal lines represent the 95% significance level for each test, from a parametric bootstrap with 500 replicates.

(A) 25 randomly selected core genes designated as **recombinants** by PhiPack (CONTD.)

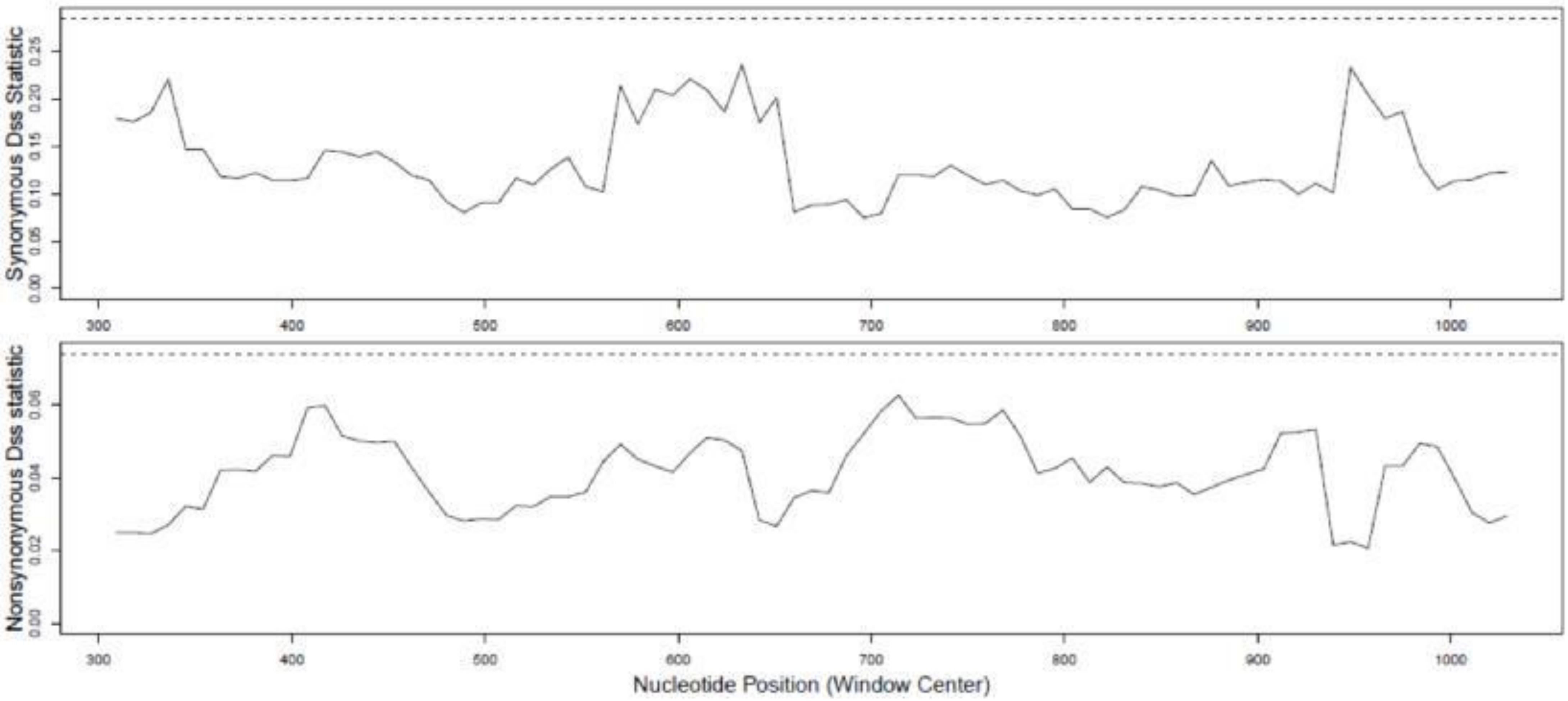
HP_1055



Dss statistic landscapes for synonymous and nonsynonymous changes. Dotted horizontal lines represent the 95% significance level for each test, from a parametric bootstrap with 500 replicates.

(A) 25 randomly selected core genes designated as **recombinants** by PhiPack (CONTD.)

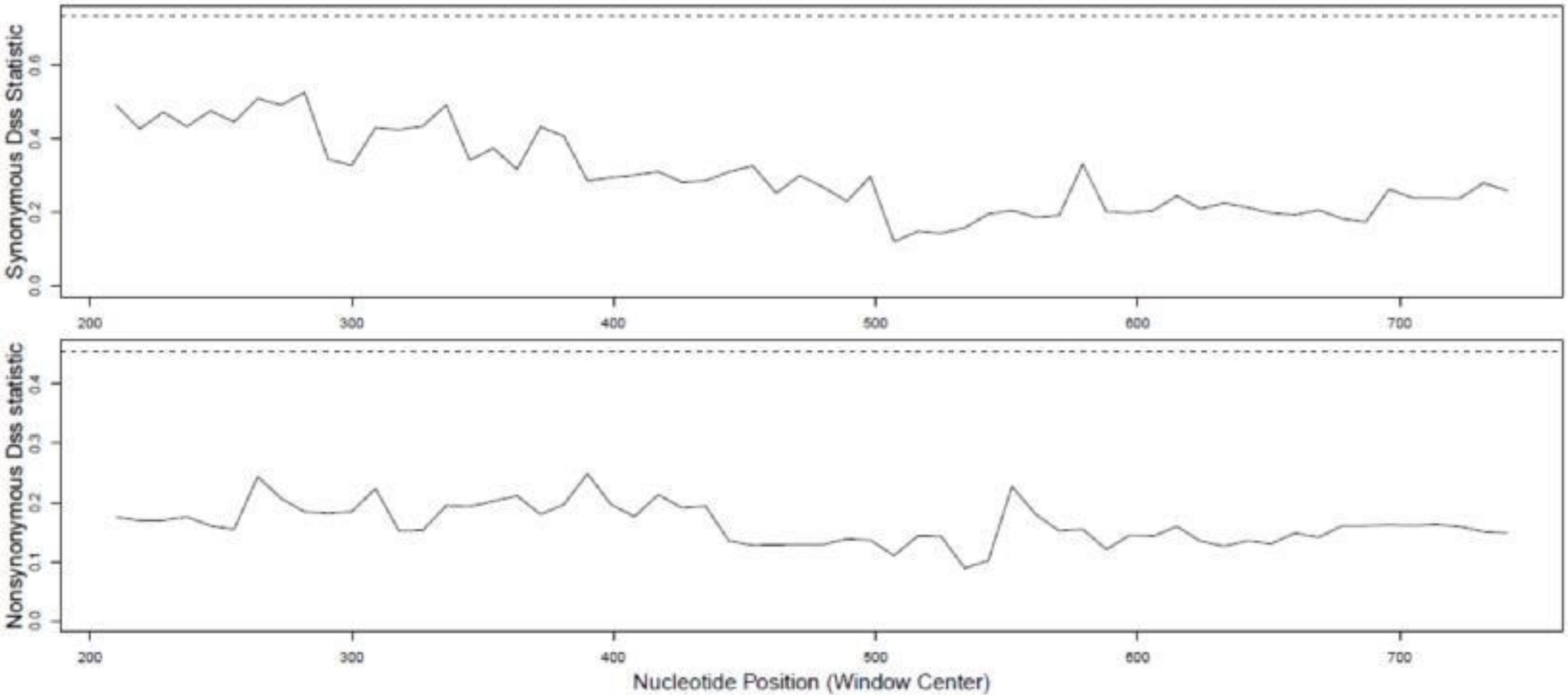
HP_1112



Dss statistic landscapes for synonymous and nonsynonymous changes. Dotted horizontal lines represent the 95% significance level for each test, from a parametric bootstrap with 500 replicates.

(A) 25 randomly selected core genes designated as **recombinants** by PhiPack (CONTD.)

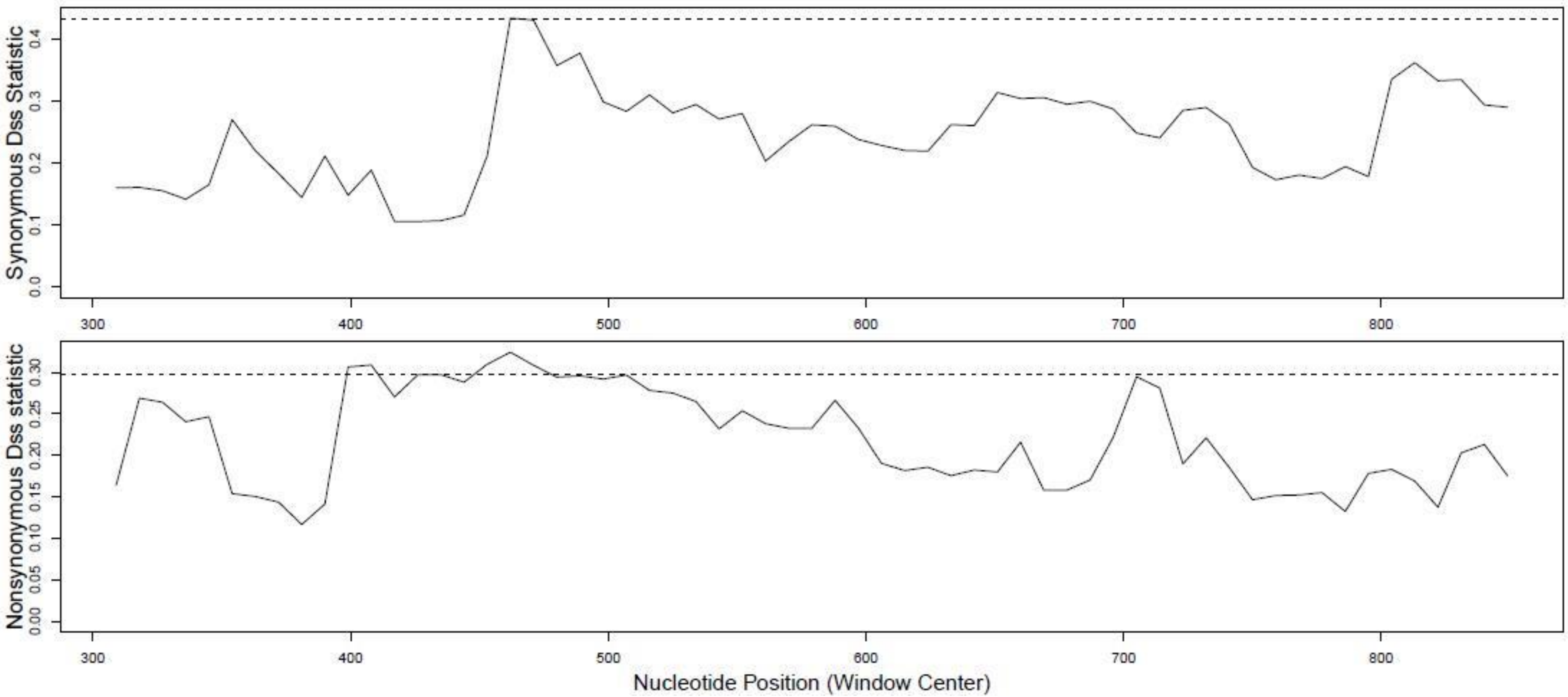
HP_1121



Dss statistic landscapes for synonymous and nonsynonymous changes. Dotted horizontal lines represent the 95% significance level for each test, from a parametric bootstrap with 500 replicates.

(A) 25 randomly selected core genes designated as **recombinants** by PhiPack (CONTD.)

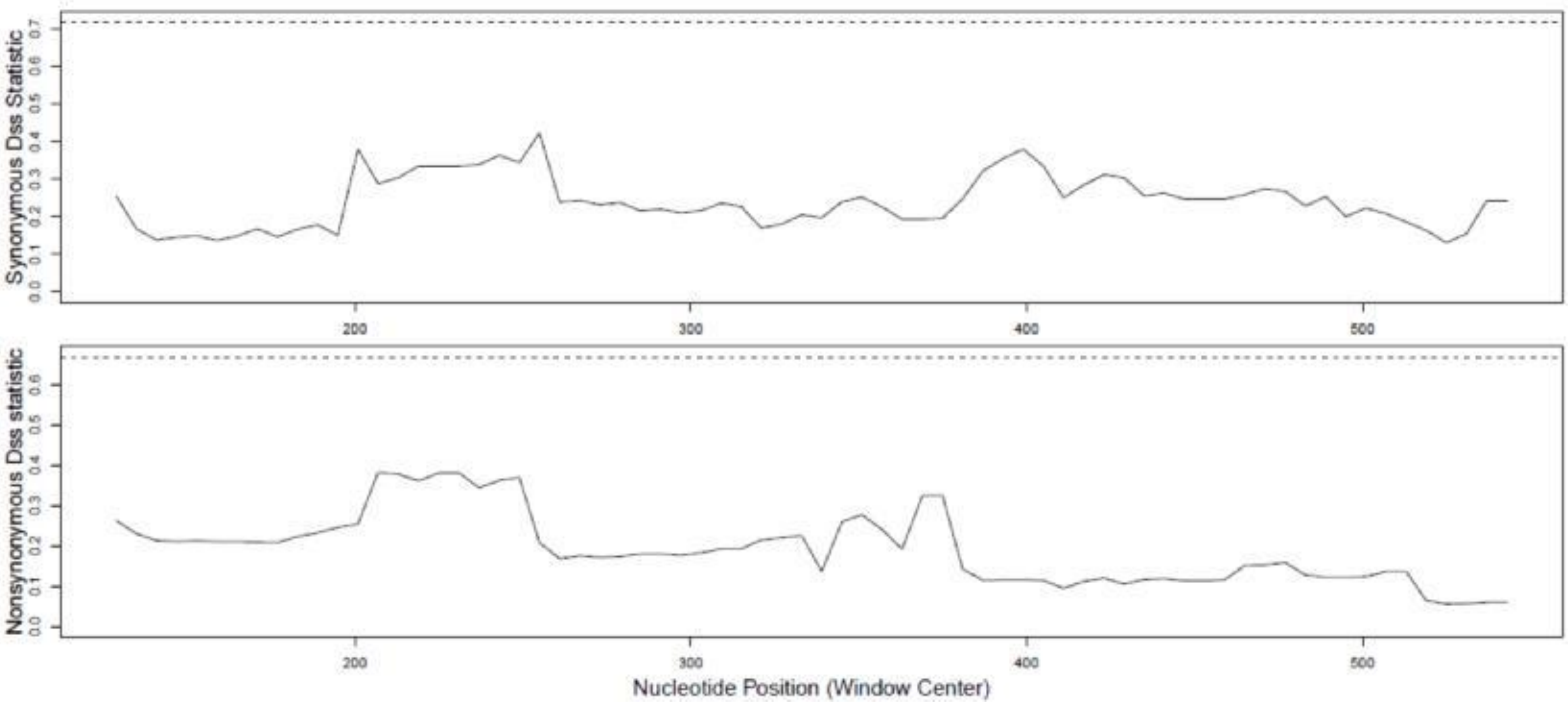
HP_1232



Dss statistic landscapes for synonymous and nonsynonymous changes. Dotted horizontal lines represent the 95% significance level for each test, from a parametric bootstrap with 500 replicates.

(A) 25 randomly selected core genes designated as **recombinants** by PhiPack (CONTD.)

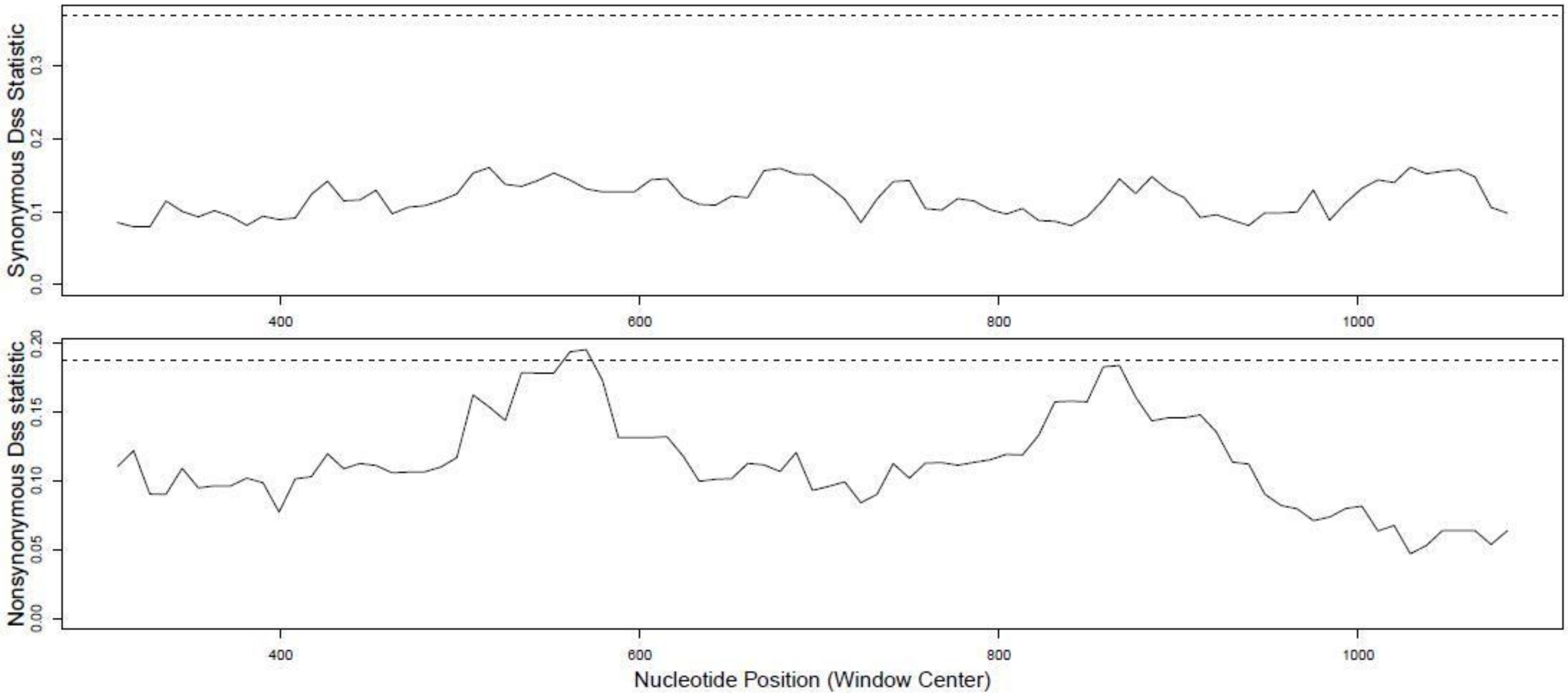
HP_1268



Dss statistic landscapes for synonymous and nonsynonymous changes. Dotted horizontal lines represent the 95% significance level for each test, from a parametric bootstrap with 500 replicates.

(A) 25 randomly selected core genes designated as **recombinants** by PhiPack (CONTD.)

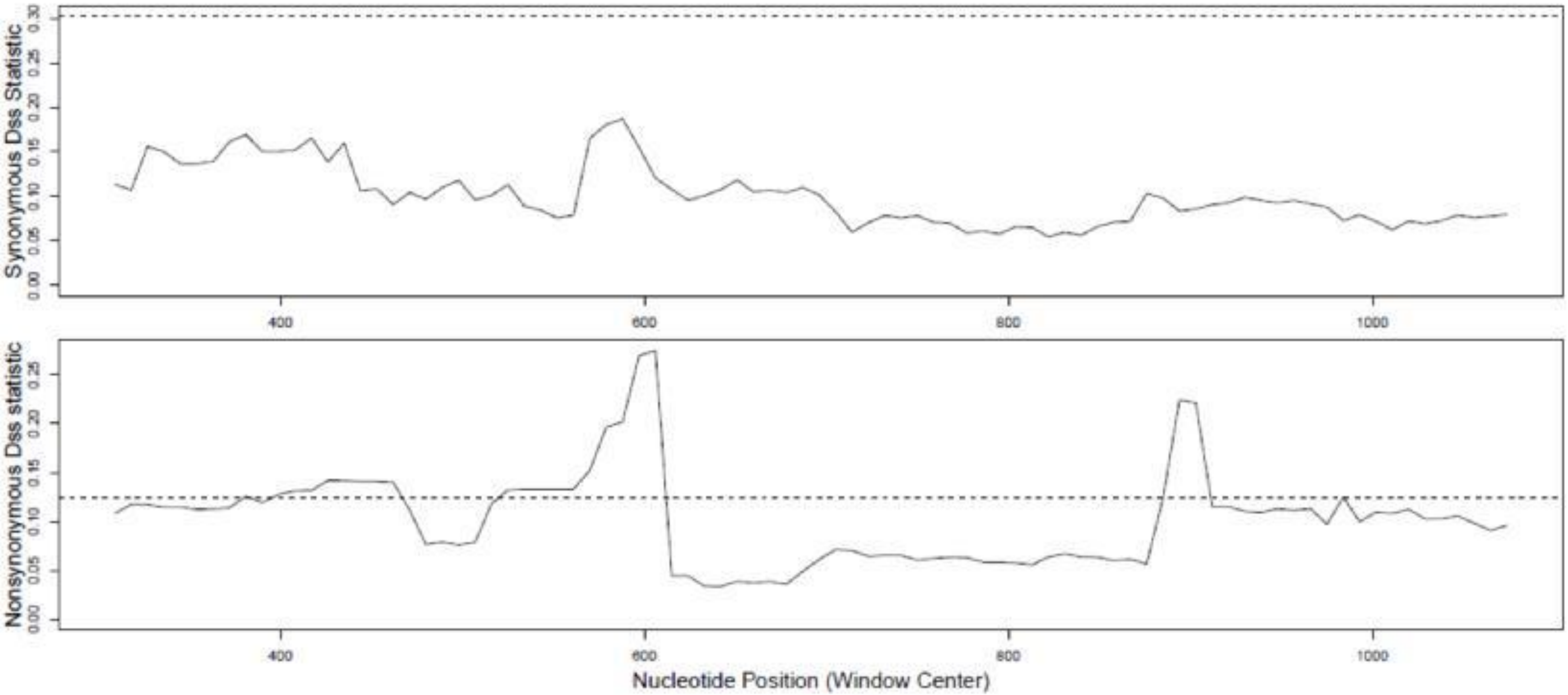
HP_1508



Dss statistic landscapes for synonymous and nonsynonymous changes. Dotted horizontal lines represent the 95% significance level for each test, from a parametric bootstrap with 500 replicates.

## (A) 25 randomly selected core genes designated as **recombinants** by PhiPack (CONTD.)

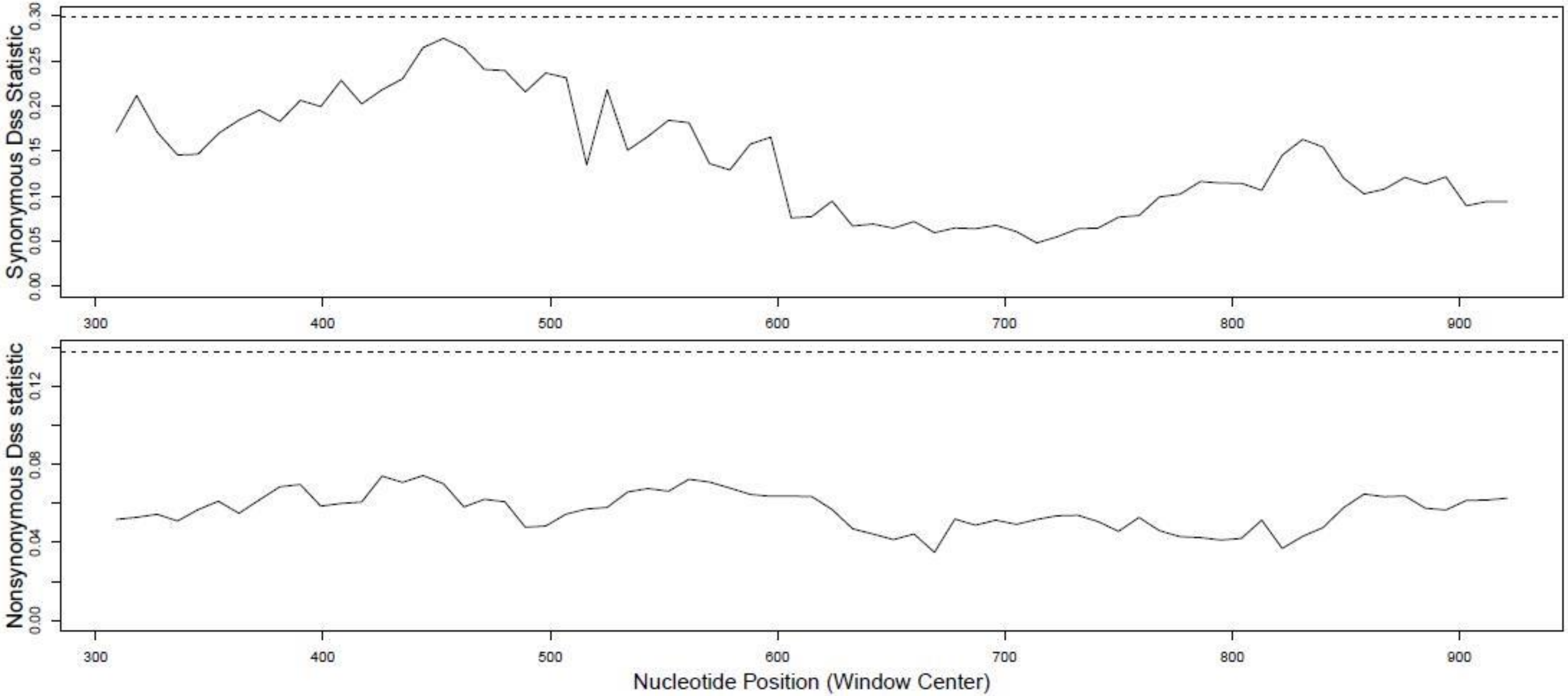
### HP_1529



Dss statistic landscapes for synonymous and nonsynonymous changes. Dotted horizontal lines represent the 95% significance level for each test, from a parametric bootstrap with 500 replicates.

(B) 25 randomly selected core genes designated as **non-recombinants** by PhiPack

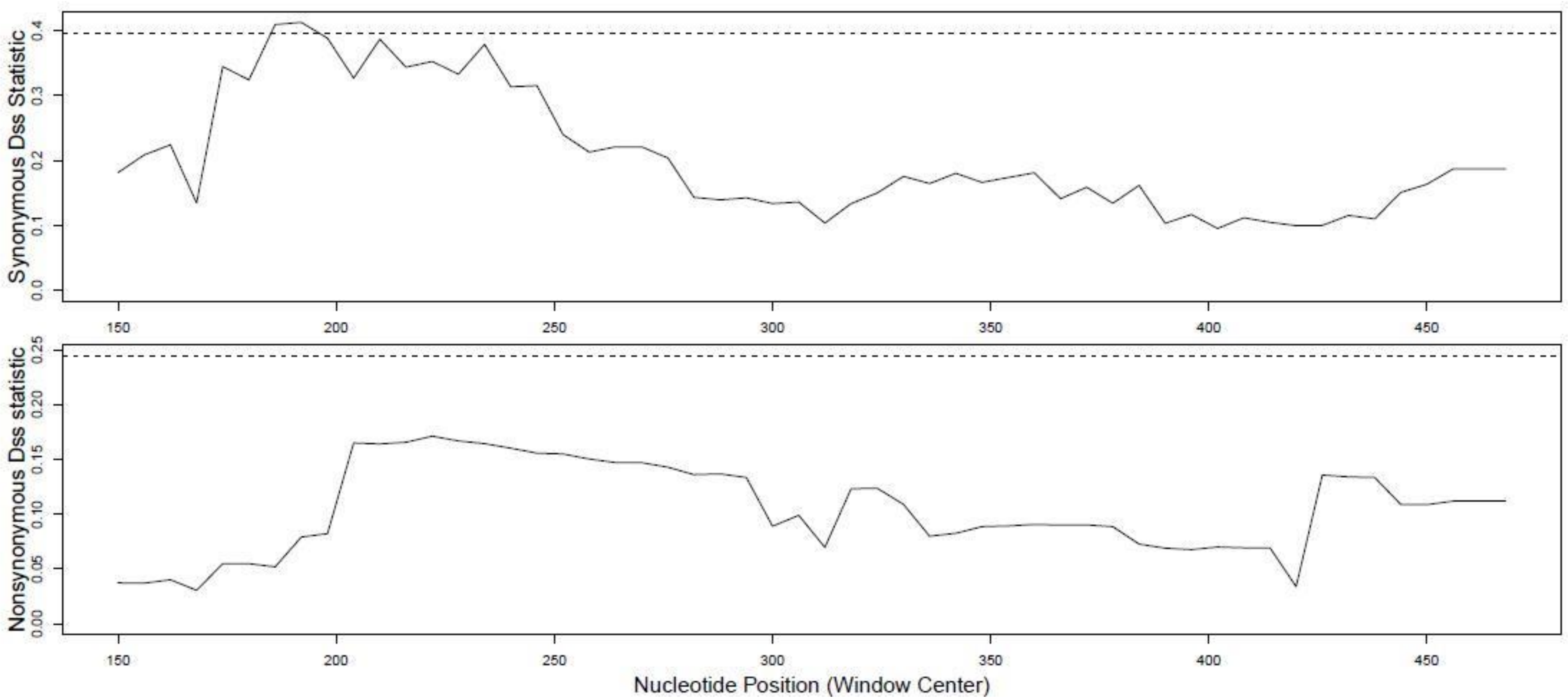
HP_0020



Dss statistic landscapes for synonymous and nonsynonymous changes. Dotted horizontal lines represent the 95% significance level for each test, from a parametric bootstrap with 500 replicates.

(B) 25 randomly selected core genes designated as **non-recombinants** by PhiPack (CONTD.)

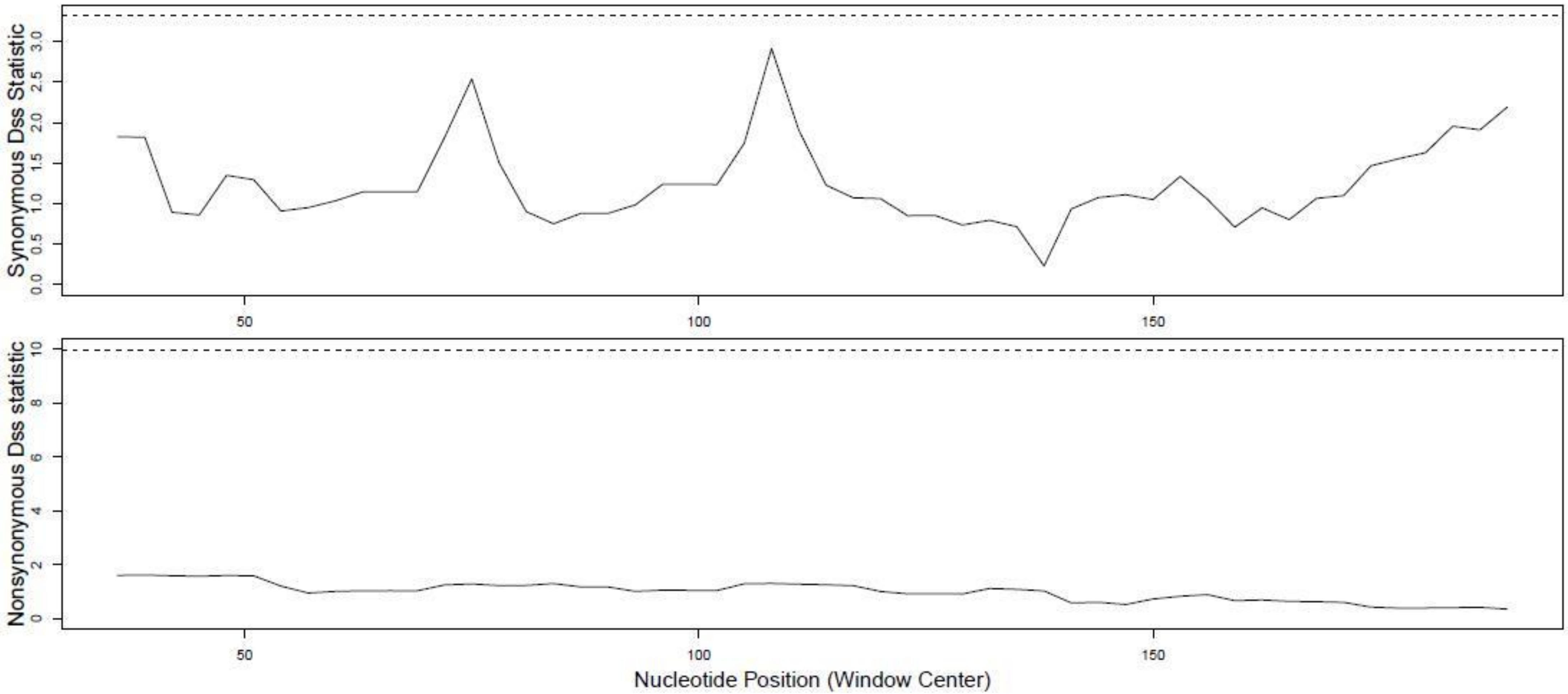
HP_0124



Dss statistic landscapes for synonymous and nonsynonymous changes. Dotted horizontal lines represent the 95% significance level for each test, from a parametric bootstrap with 500 replicates.

(B) 25 randomly selected core genes designated as **non-recombinants** by PhiPack (CONTD.)

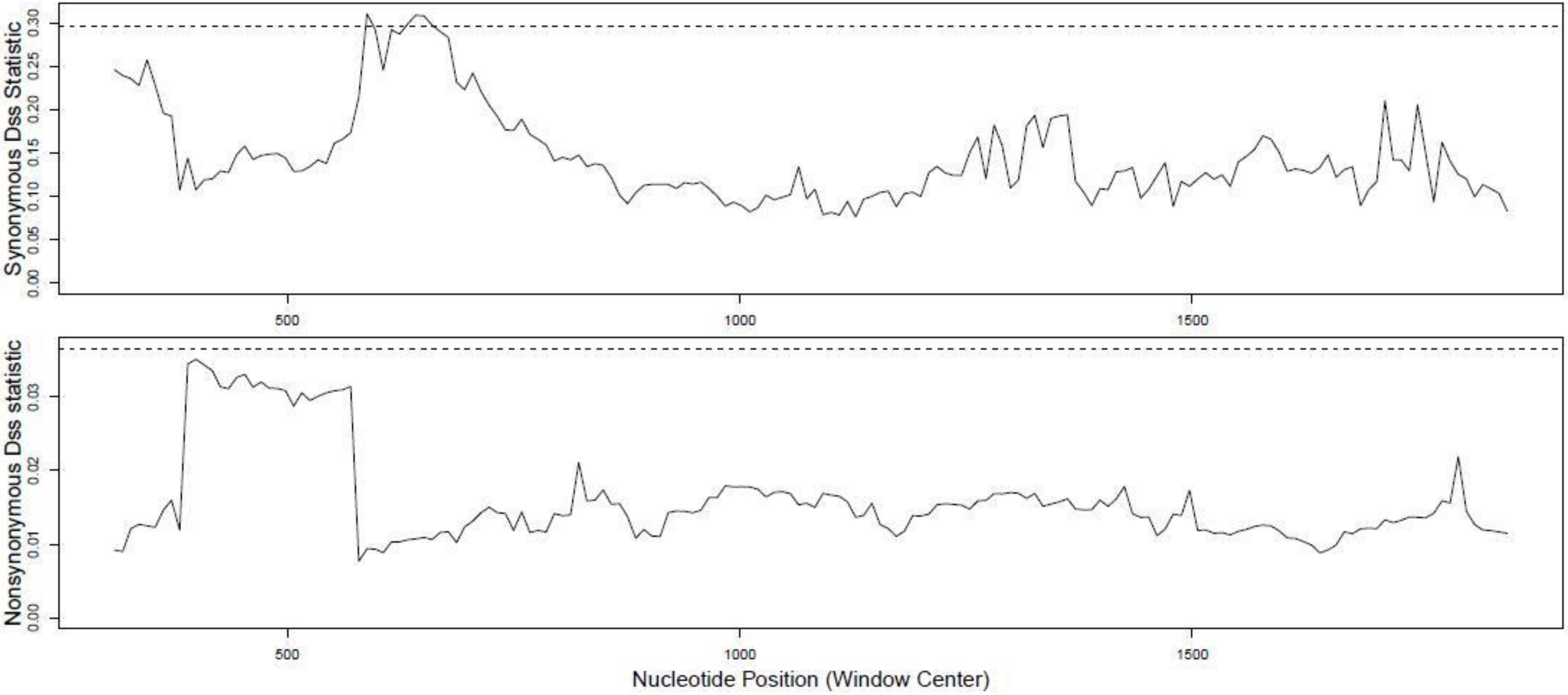
HP_0146



Dss statistic landscapes for synonymous and nonsynonymous changes. Dotted horizontal lines represent the 95% significance level for each test, from a parametric bootstrap with 500 replicates.

(B) 25 randomly selected core genes designated as **non-recombinants** by PhiPack (CONTD.)

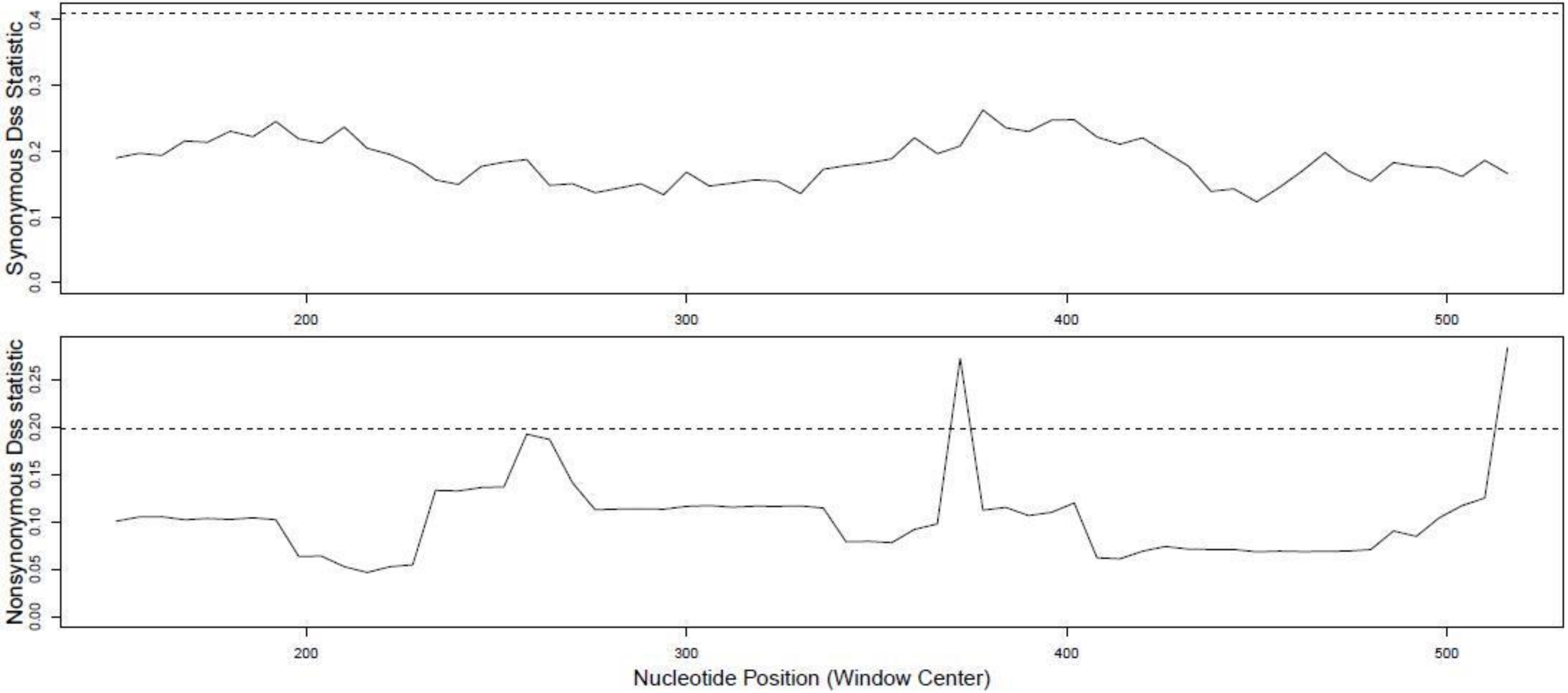
HP_0192



Dss statistic landscapes for synonymous and nonsynonymous changes. Dotted horizontal lines represent the 95% significance level for each test, from a parametric bootstrap with 500 replicates.

(B) 25 randomly selected core genes designated as **non-recombinants** by PhiPack (CONTD.)

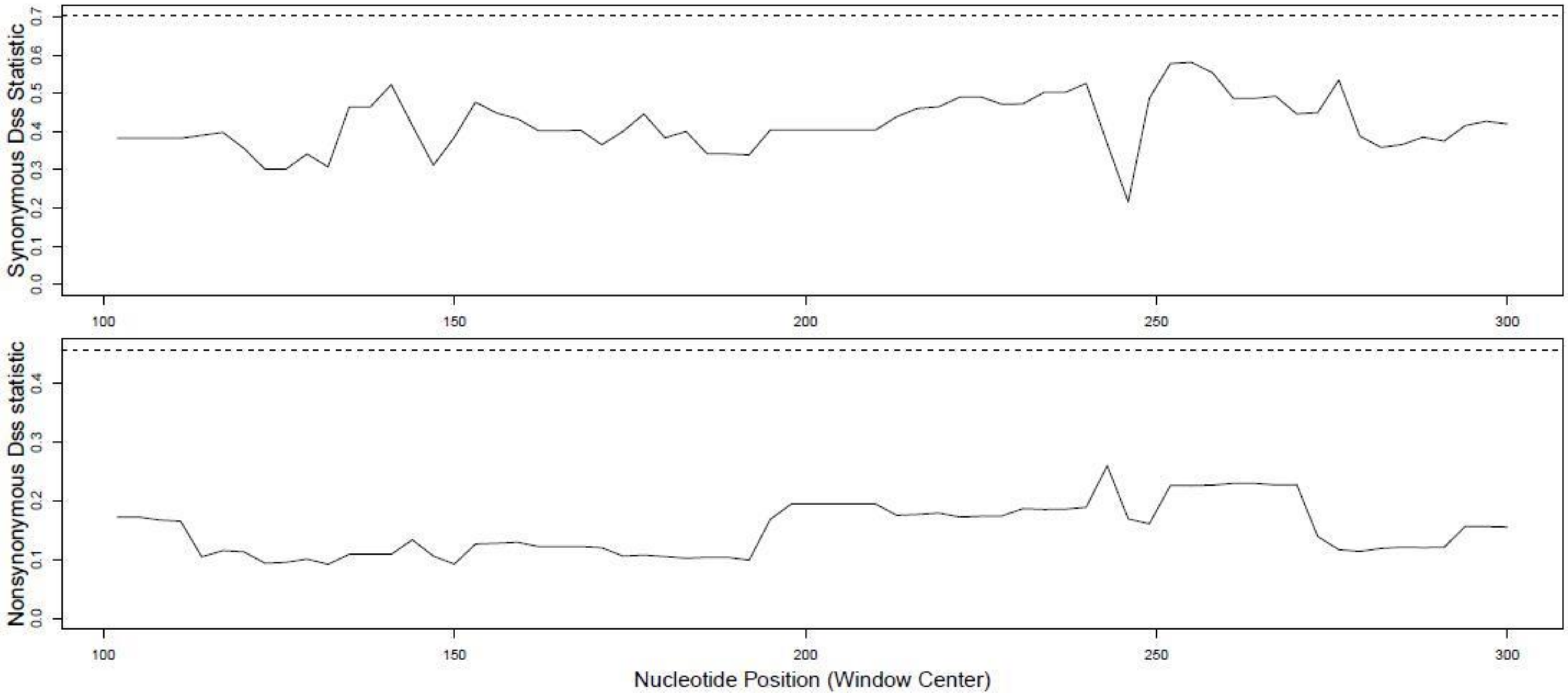
HP_0232



Dss statistic landscapes for synonymous and nonsynonymous changes. Dotted horizontal lines represent the 95% significance level for each test, from a parametric bootstrap with 500 replicates.

(B) 25 randomly selected core genes designated as **non-recombinants** by PhiPack (CONTD.)

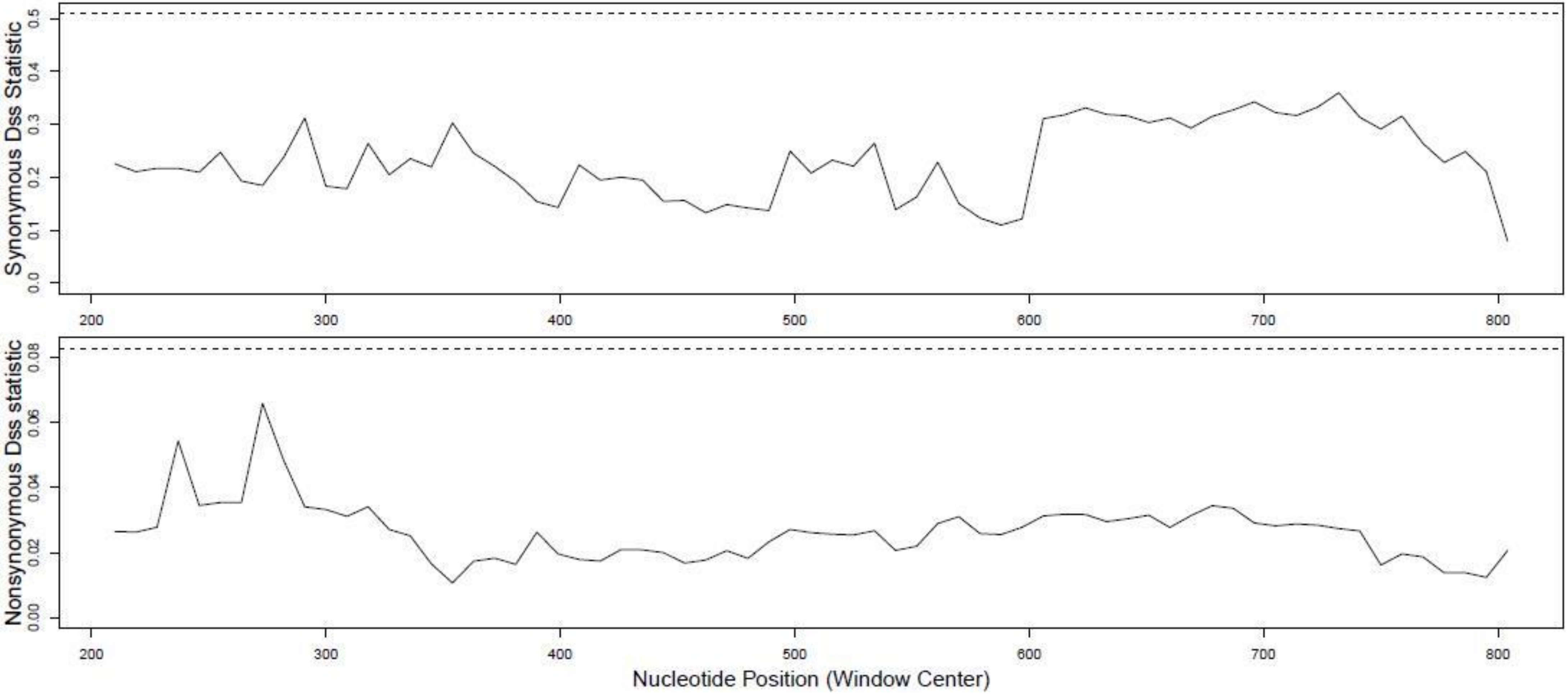
HP_0274



Dss statistic landscapes for synonymous and nonsynonymous changes. Dotted horizontal lines represent the 95% significance level for each test, from a parametric bootstrap with 500 replicates.

(B) 25 randomly selected core genes designated as **non-recombinants** by PhiPack (CONTD.)

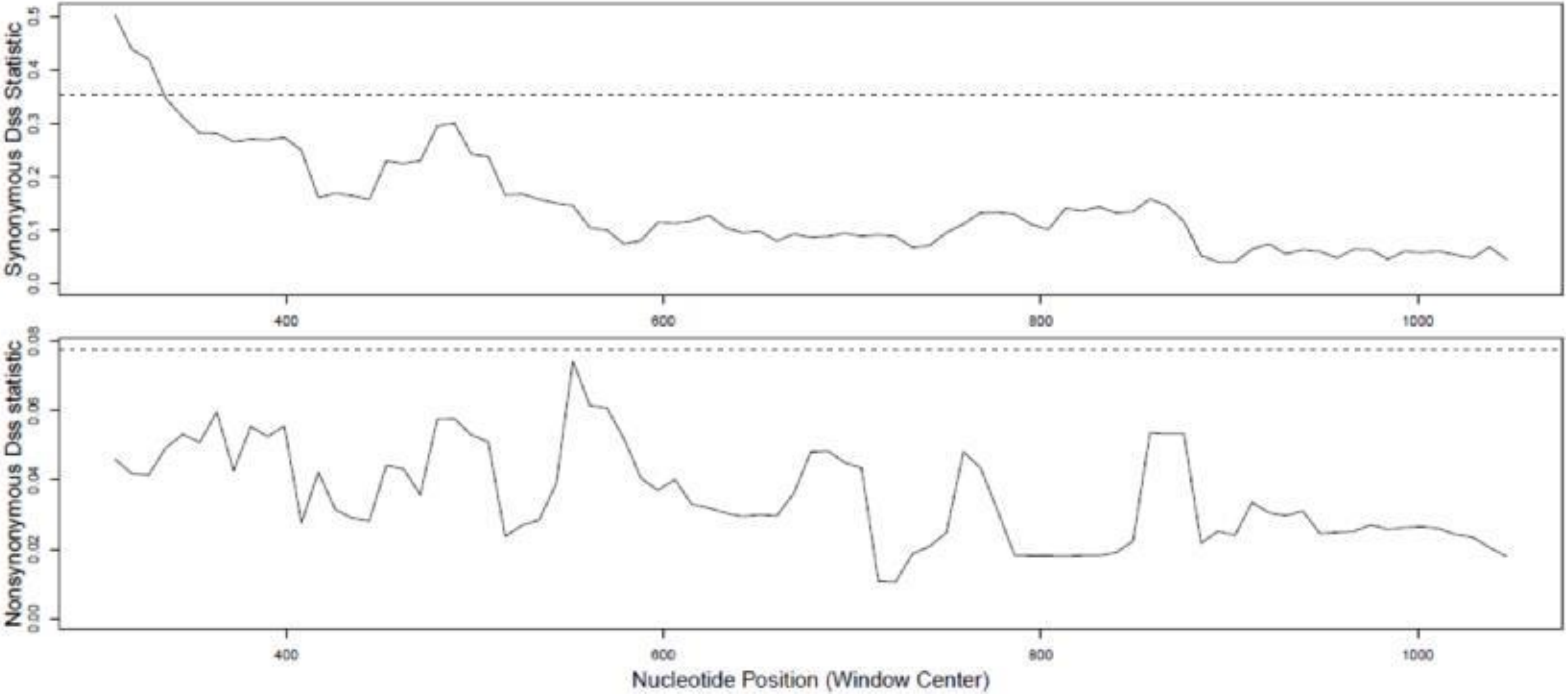
HP_0299



Dss statistic landscapes for synonymous and nonsynonymous changes. Dotted horizontal lines represent the 95% significance level for each test, from a parametric bootstrap with 500 replicates.

(B) 25 randomly selected core genes designated as **non-recombinants** by PhiPack (CONTD.)

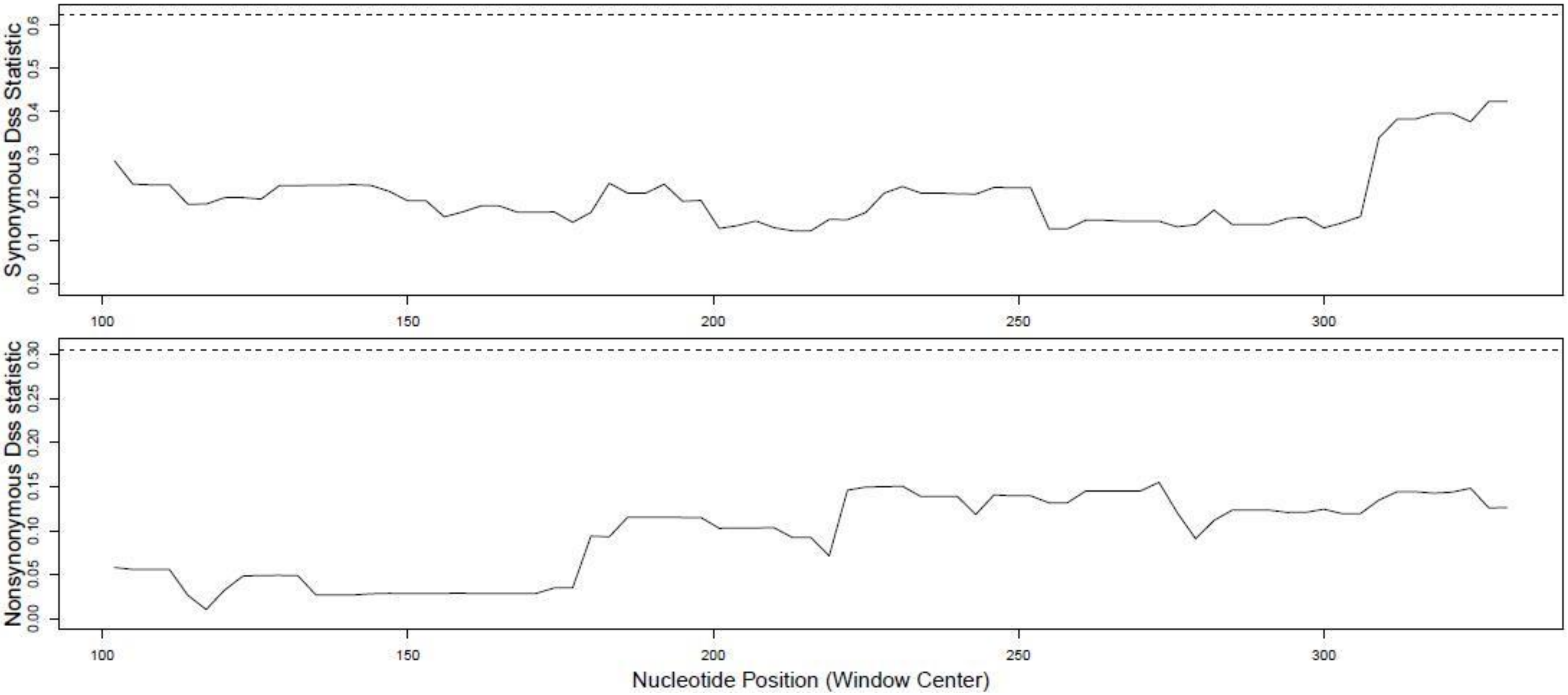
HP_0380



Dss statistic landscapes for synonymous and nonsynonymous changes. Dotted horizontal lines represent the 95% significance level for each test, from a parametric bootstrap with 500 replicates.

(B) 25 randomly selected core genes designated as **non-recombinants** by PhiPack (CONTD.)

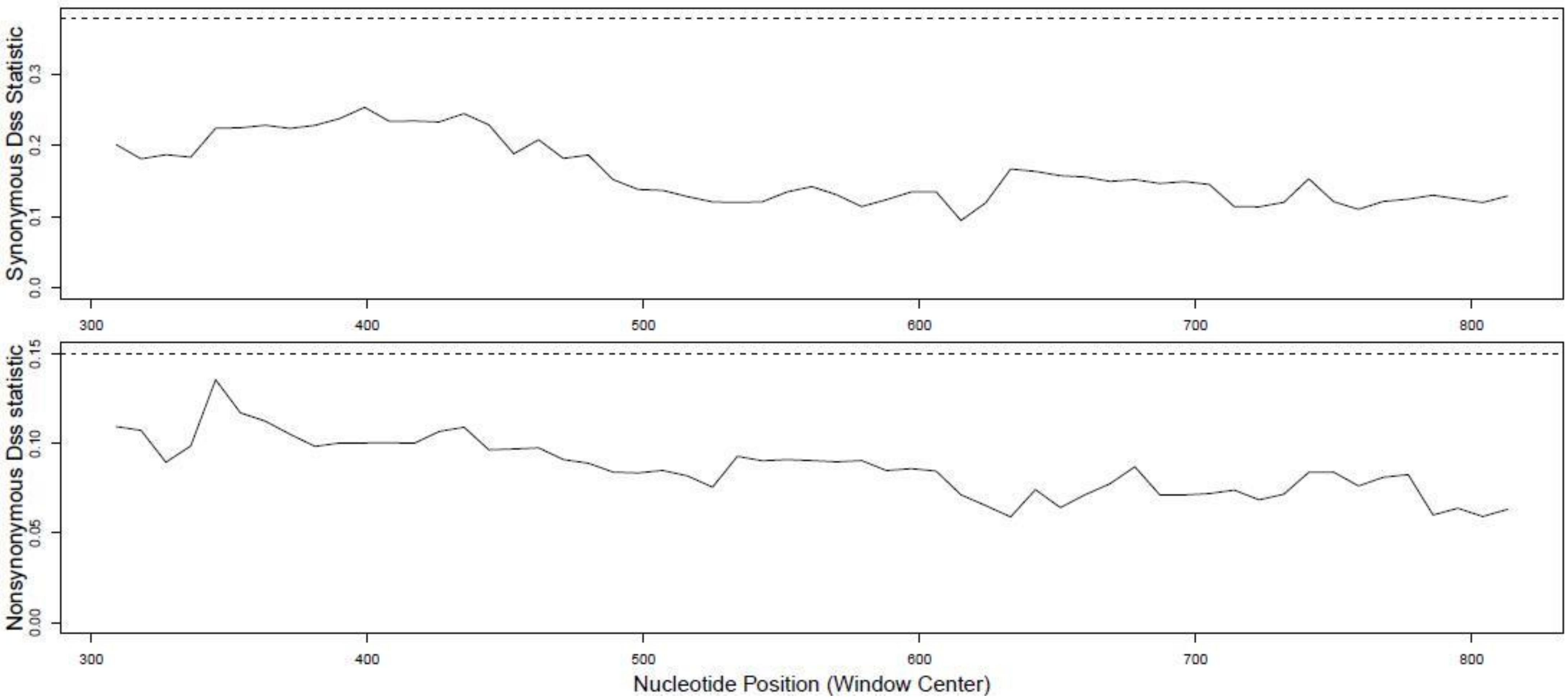
HP_0420



Dss statistic landscapes for synonymous and nonsynonymous changes. Dotted horizontal lines represent the 95% significance level for each test, from a parametric bootstrap with 500 replicates.

(B) 25 randomly selected core genes designated as **non-recombinants** by PhiPack (CONTD.)

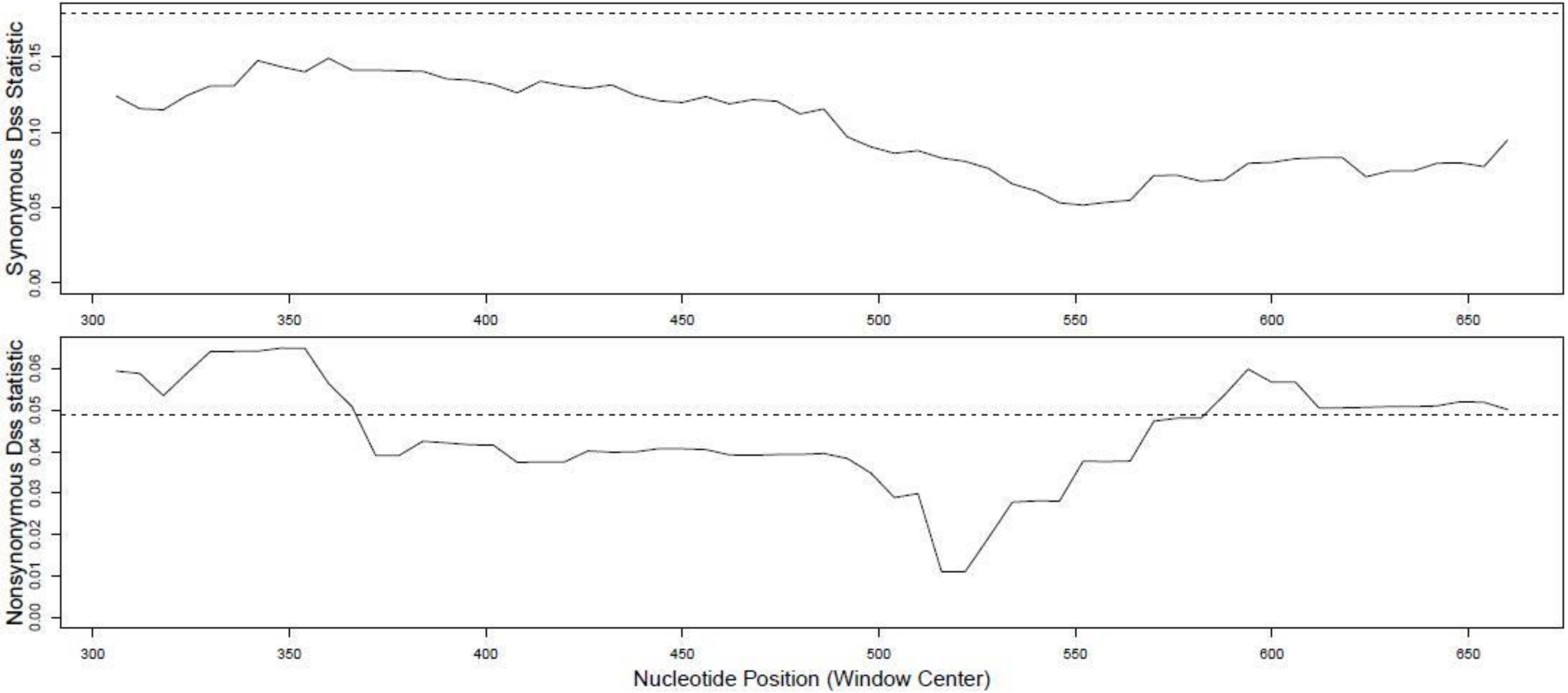
HP_0736



Dss statistic landscapes for synonymous and nonsynonymous changes. Dotted horizontal lines represent the 95% significance level for each test, from a parametric bootstrap with 500 replicates.

(B) 25 randomly selected core genes designated as **non-recombinants** by PhiPack (CONTD.)

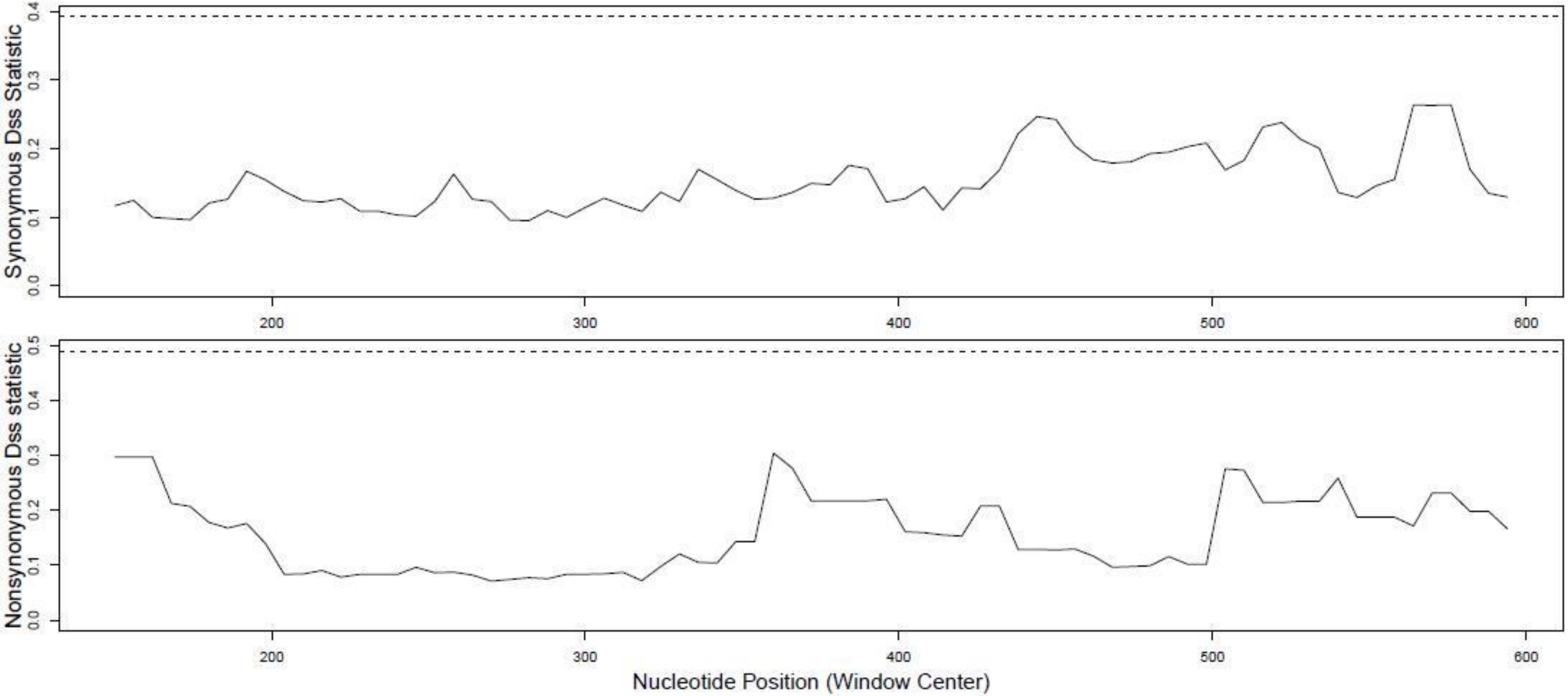
HP_0742



Dss statistic landscapes for synonymous and nonsynonymous changes. Dotted horizontal lines represent the 95% significance level for each test, from a parametric bootstrap with 500 replicates.

(B) 25 randomly selected core genes designated as **non-recombinants** by PhiPack (CONTD.)

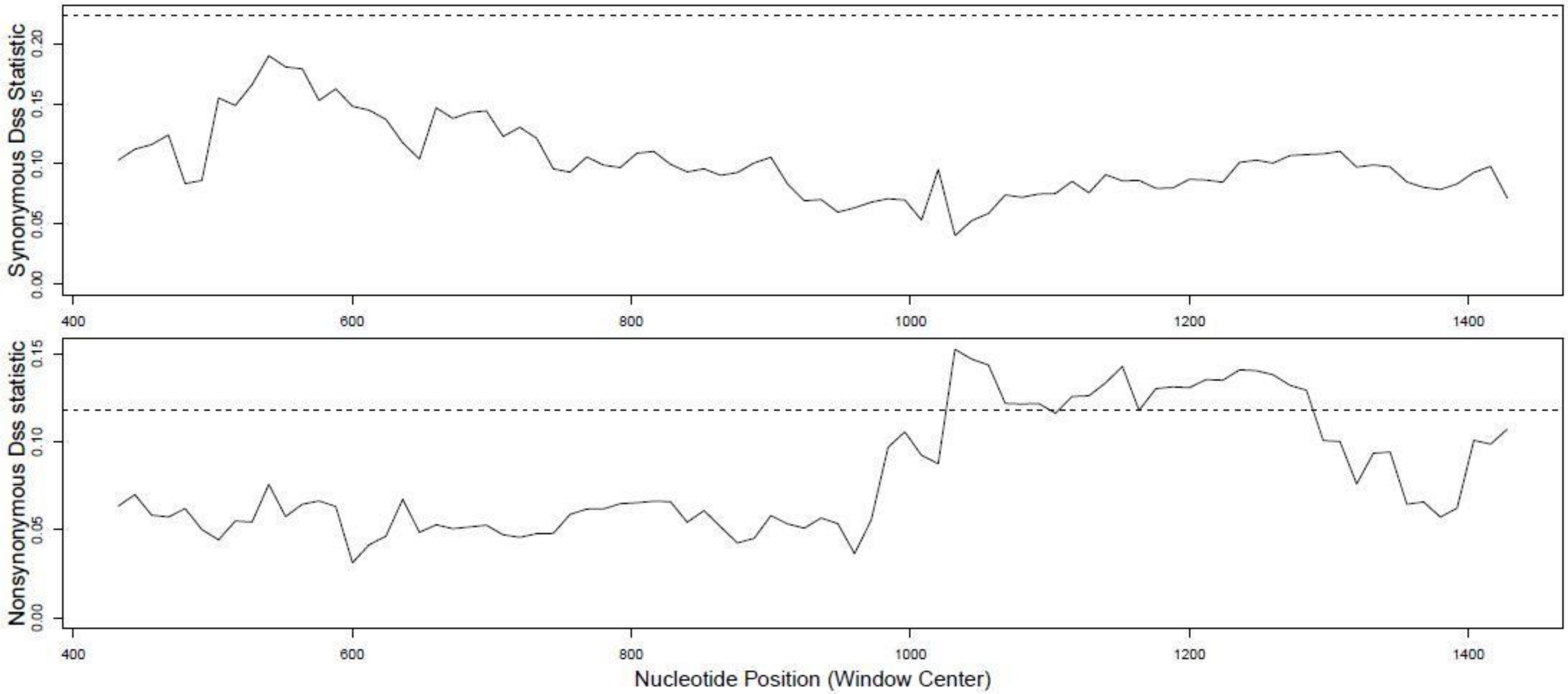
HP_0771



Dss statistic landscapes for synonymous and nonsynonymous changes. Dotted horizontal lines represent the 95% significance level for each test, from a parametric bootstrap with 500 replicates.

(B) 25 randomly selected core genes designated as **non-recombinants** by PhiPack (CONTD.)

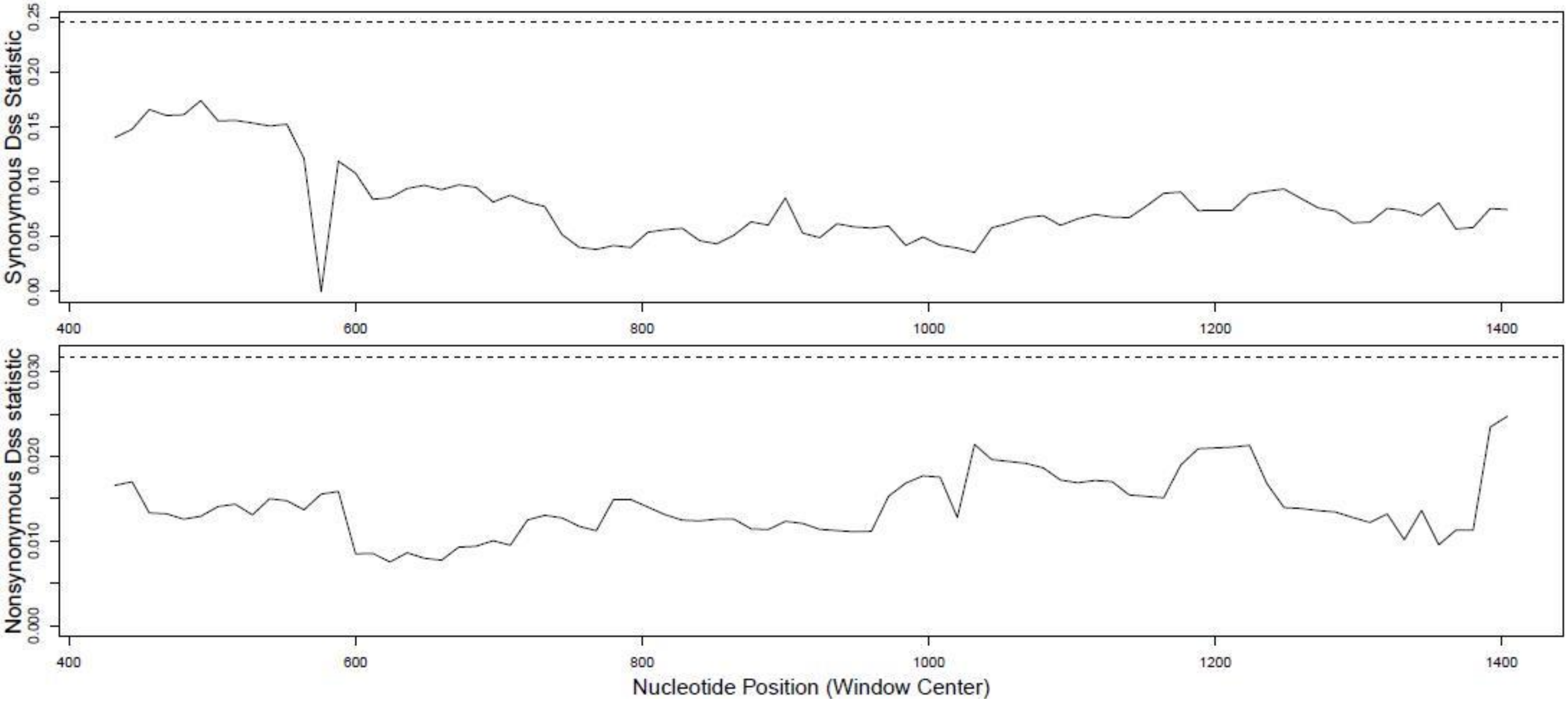
HP_0884



Dss statistic landscapes for synonymous and nonsynonymous changes. Dotted horizontal lines represent the 95% significance level for each test, from a parametric bootstrap with 500 replicates.

(B) 25 randomly selected core genes designated as **non-recombinants** by PhiPack (CONTD.)

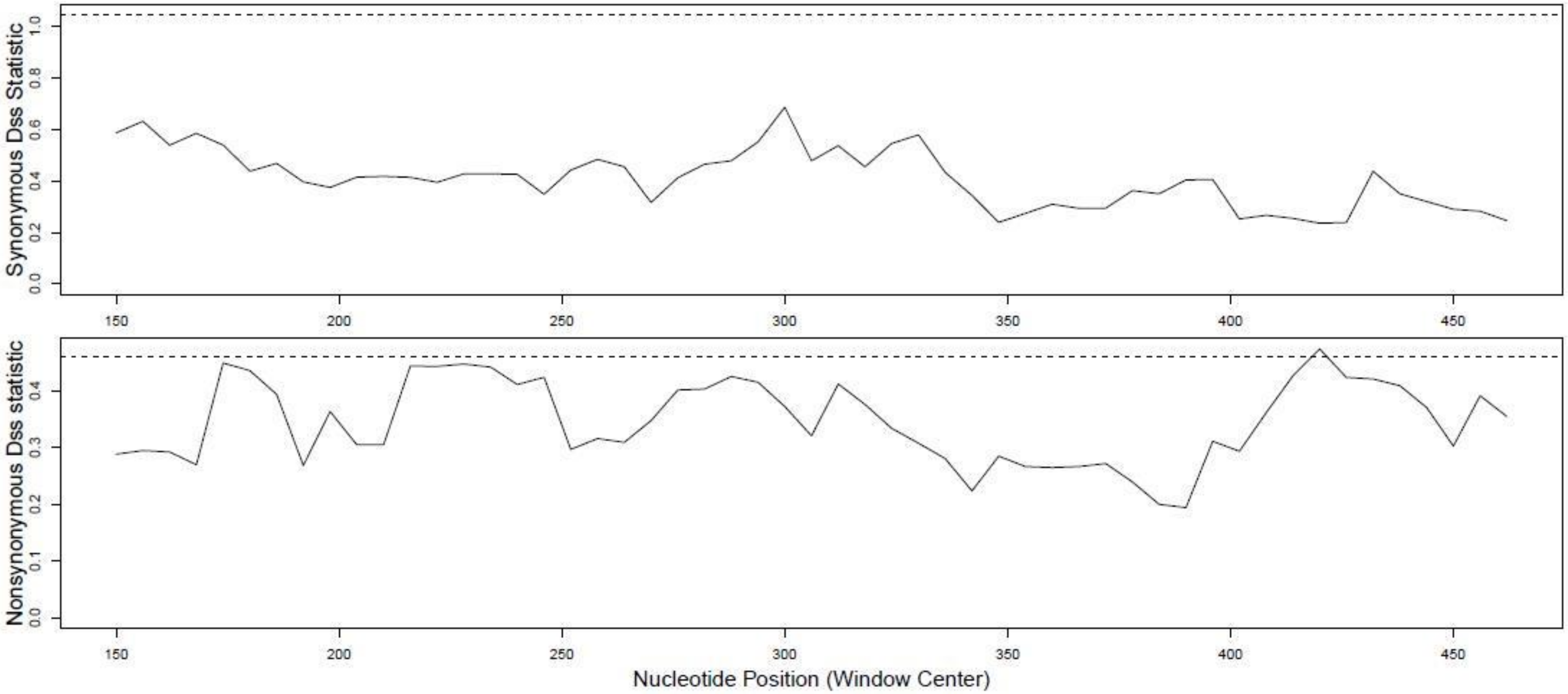
HP_0908



Dss statistic landscapes for synonymous and nonsynonymous changes. Dotted horizontal lines represent the 95% significance level for each test, from a parametric bootstrap with 500 replicates.

(B) 25 randomly selected core genes designated as **non-recombinants** by PhiPack (CONTD.)

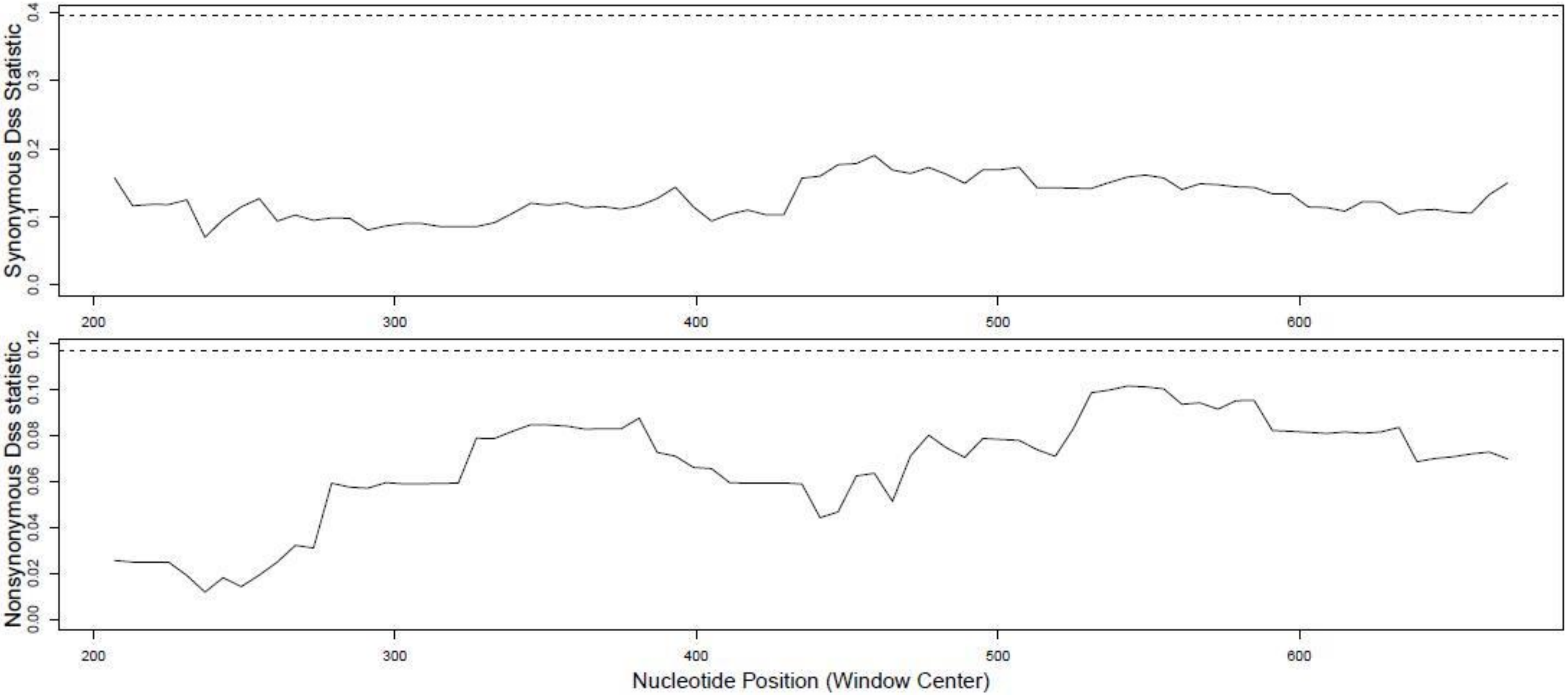
HP_0933



Dss statistic landscapes for synonymous and nonsynonymous changes. Dotted horizontal lines represent the 95% significance level for each test, from a parametric bootstrap with 500 replicates.

(B) 25 randomly selected core genes designated as **non-recombinants** by PhiPack (CONTD.)

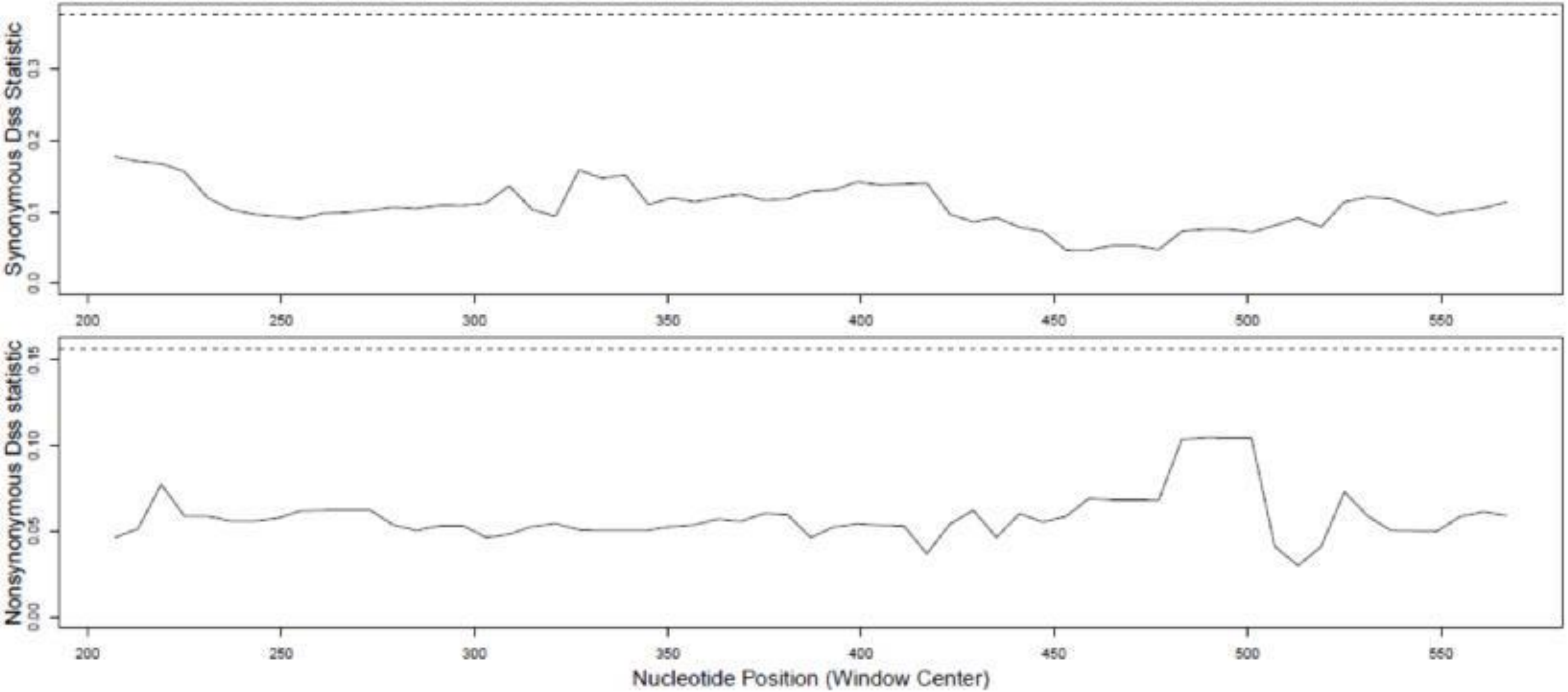
HP_0950



Dss statistic landscapes for synonymous and nonsynonymous changes. Dotted horizontal lines represent the 95% significance level for each test, from a parametric bootstrap with 500 replicates.

# (B) 25 randomly selected core genes designated as **non-recombinants** by PhiPack (CONTD.)

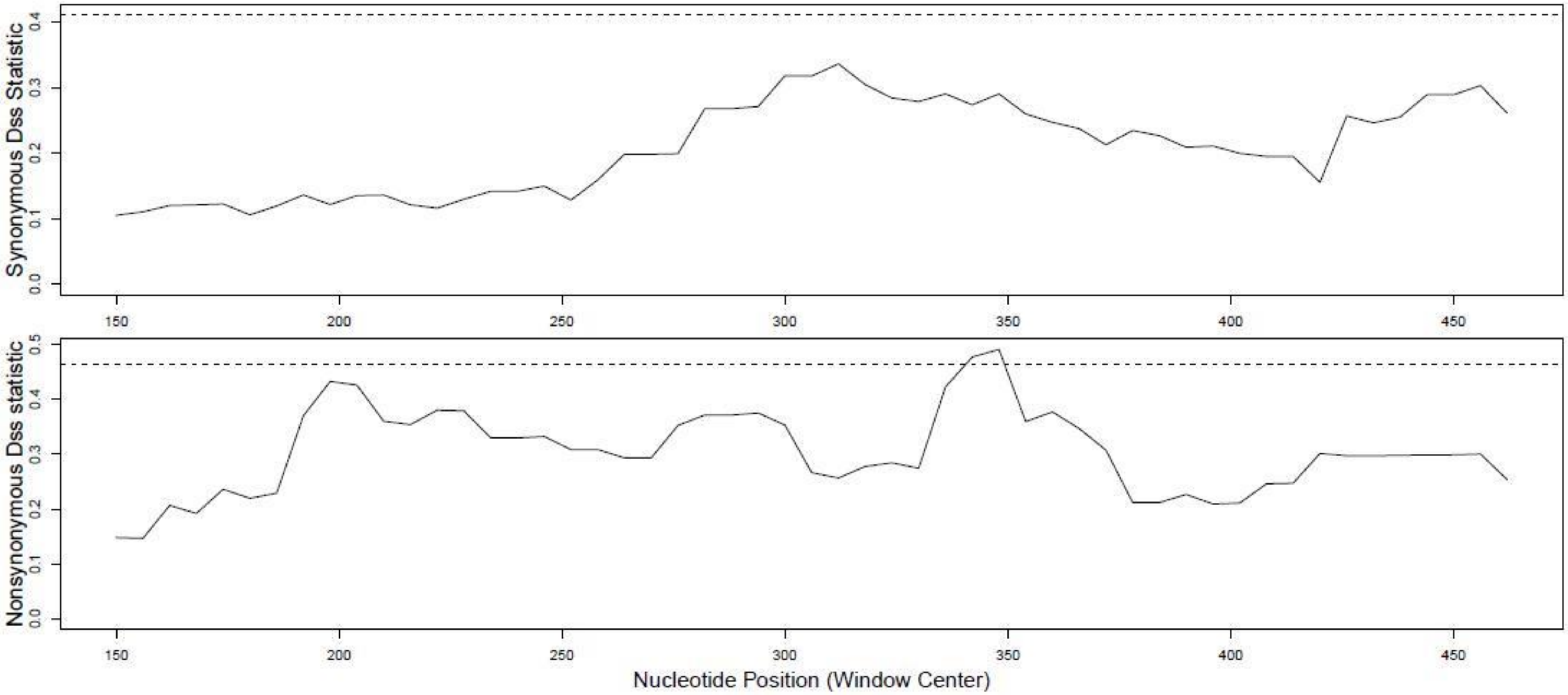
## HP_0958



Dss statistic landscapes for synonymous and nonsynonymous changes. Dotted horizontal lines represent the 95% significance level for each test, from a parametric bootstrap with 500 replicates.

(B) 25 randomly selected core genes designated as **non-recombinants** by PhiPack (CONTD.)

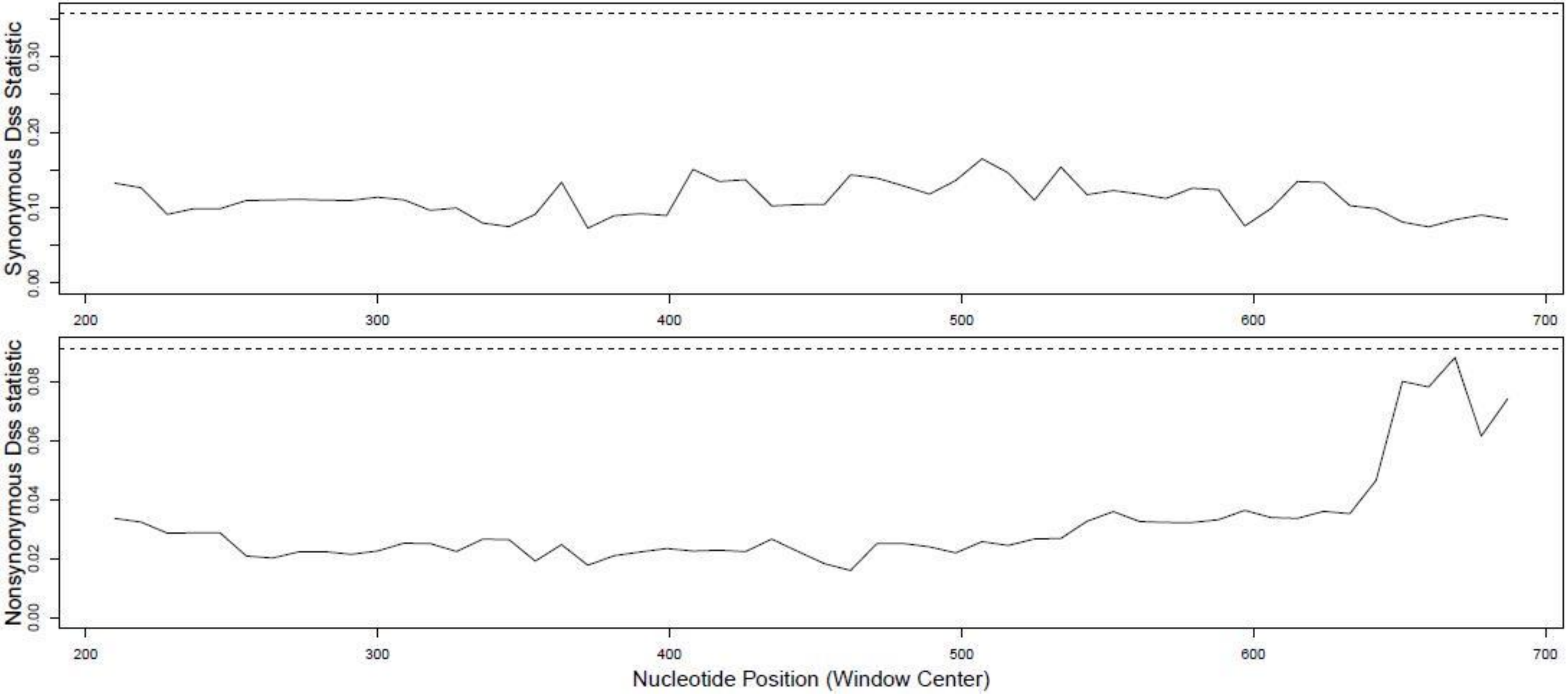
HP_1016



Dss statistic landscapes for synonymous and nonsynonymous changes. Dotted horizontal lines represent the 95% significance level for each test, from a parametric bootstrap with 500 replicates.

## (B) 25 randomly selected core genes designated as **non-recombinants** by PhiPack (CONTD.)

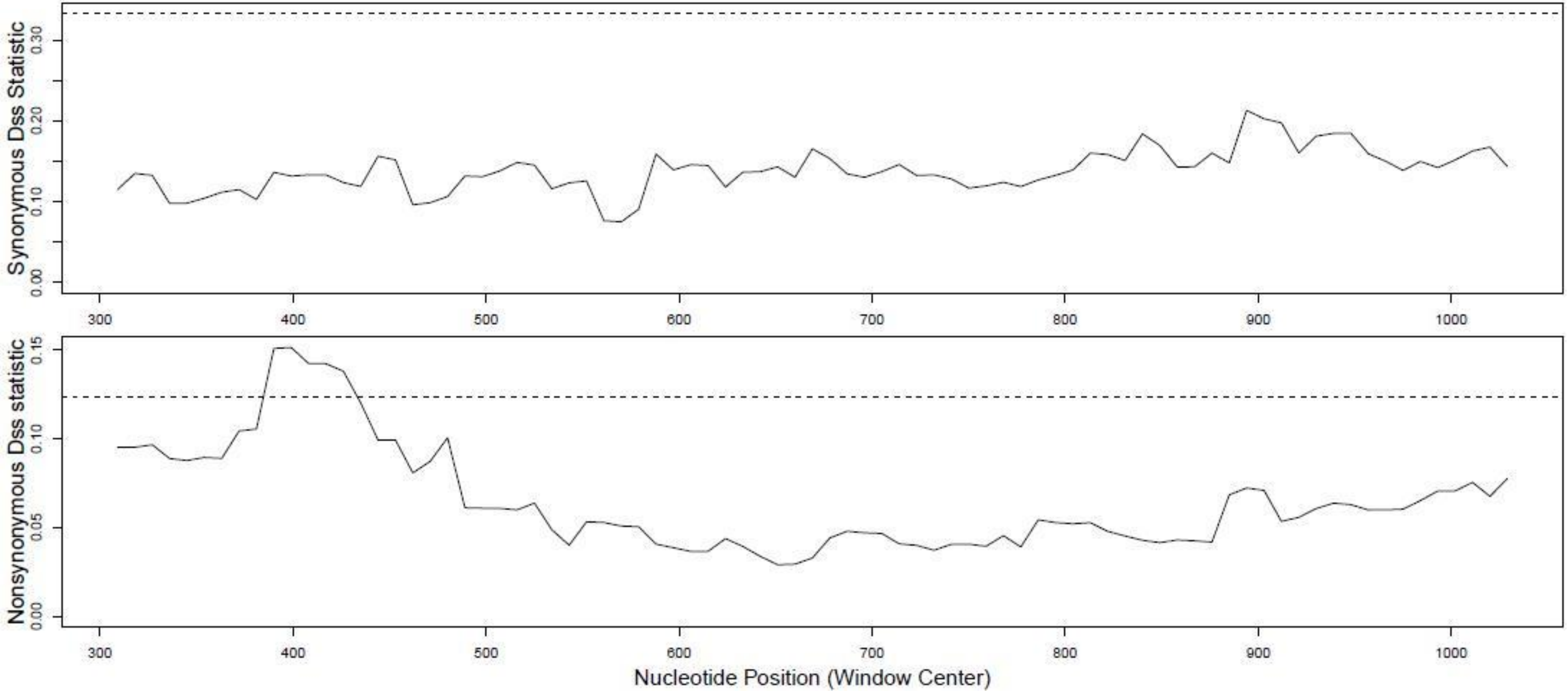
HP_1050



Dss statistic landscapes for synonymous and nonsynonymous changes. Dotted horizontal lines represent the 95% significance level for each test, from a parametric bootstrap with 500 replicates.

(B) 25 randomly selected core genes designated as **non-recombinants** by PhiPack (CONTD.)

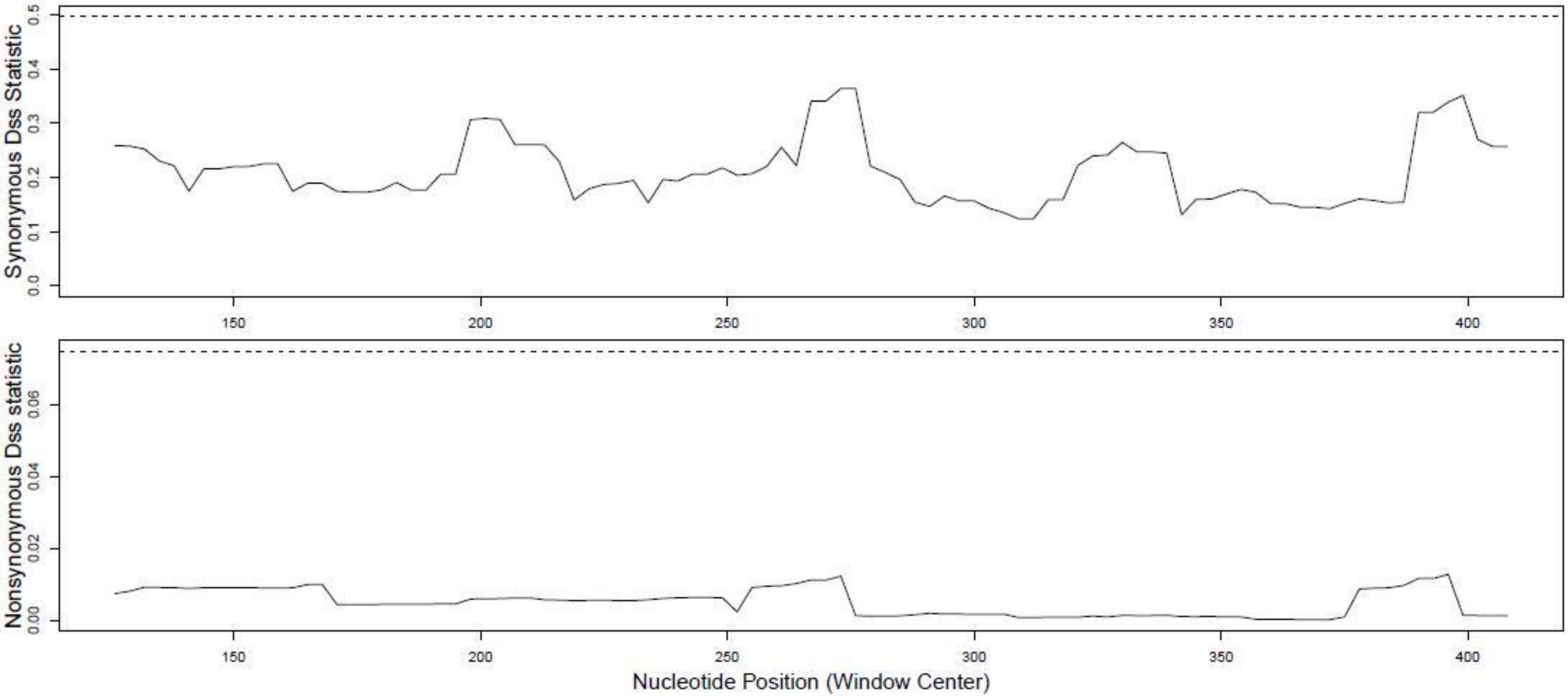
HP_1190



Dss statistic landscapes for synonymous and nonsynonymous changes. Dotted horizontal lines represent the 95% significance level for each test, from a parametric bootstrap with 500 replicates.

(B) 25 randomly selected core genes designated as **non-recombinants** by PhiPack (CONTD.)

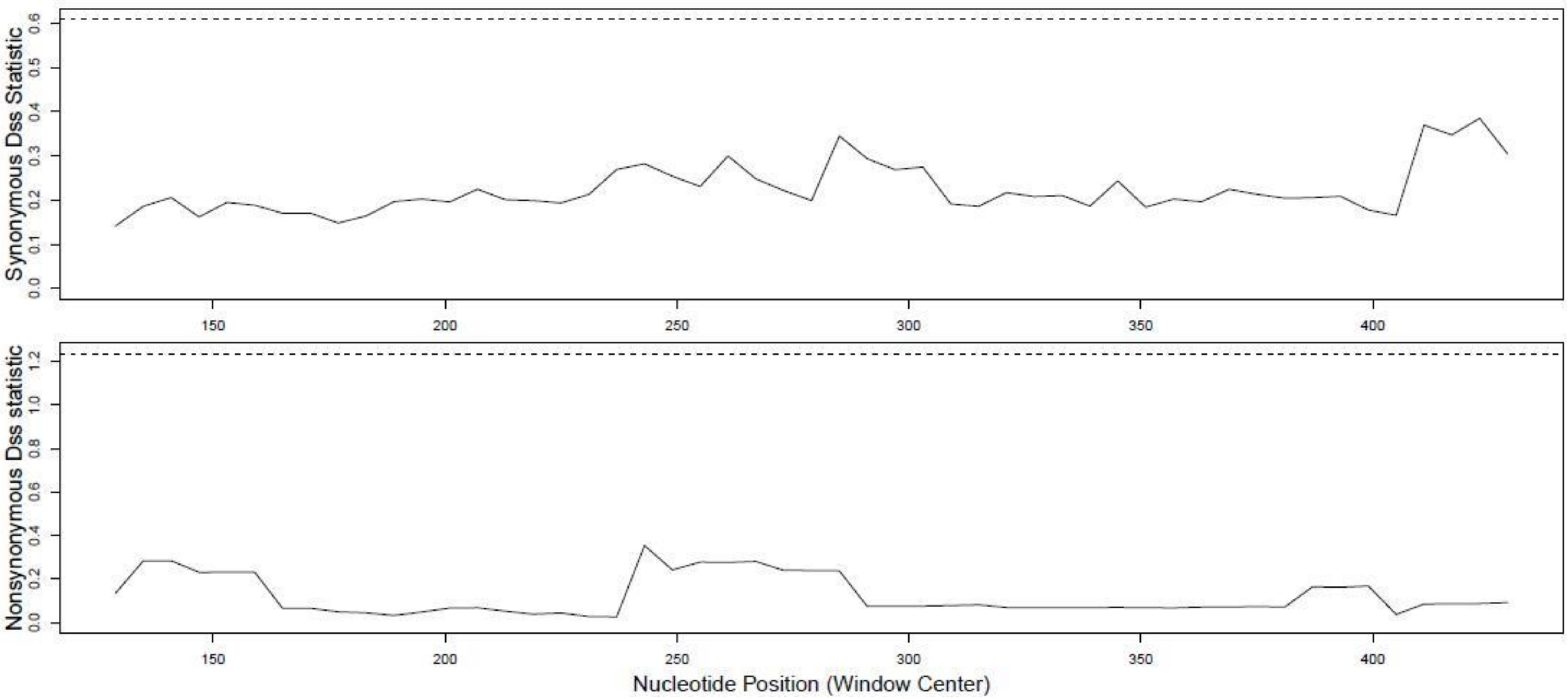
HP_1203



Dss statistic landscapes for synonymous and nonsynonymous changes. Dotted horizontal lines represent the 95% significance level for each test, from a parametric bootstrap with 500 replicates.

(B) 25 randomly selected core genes designated as **non-recombinants** by PhiPack (CONTD.)

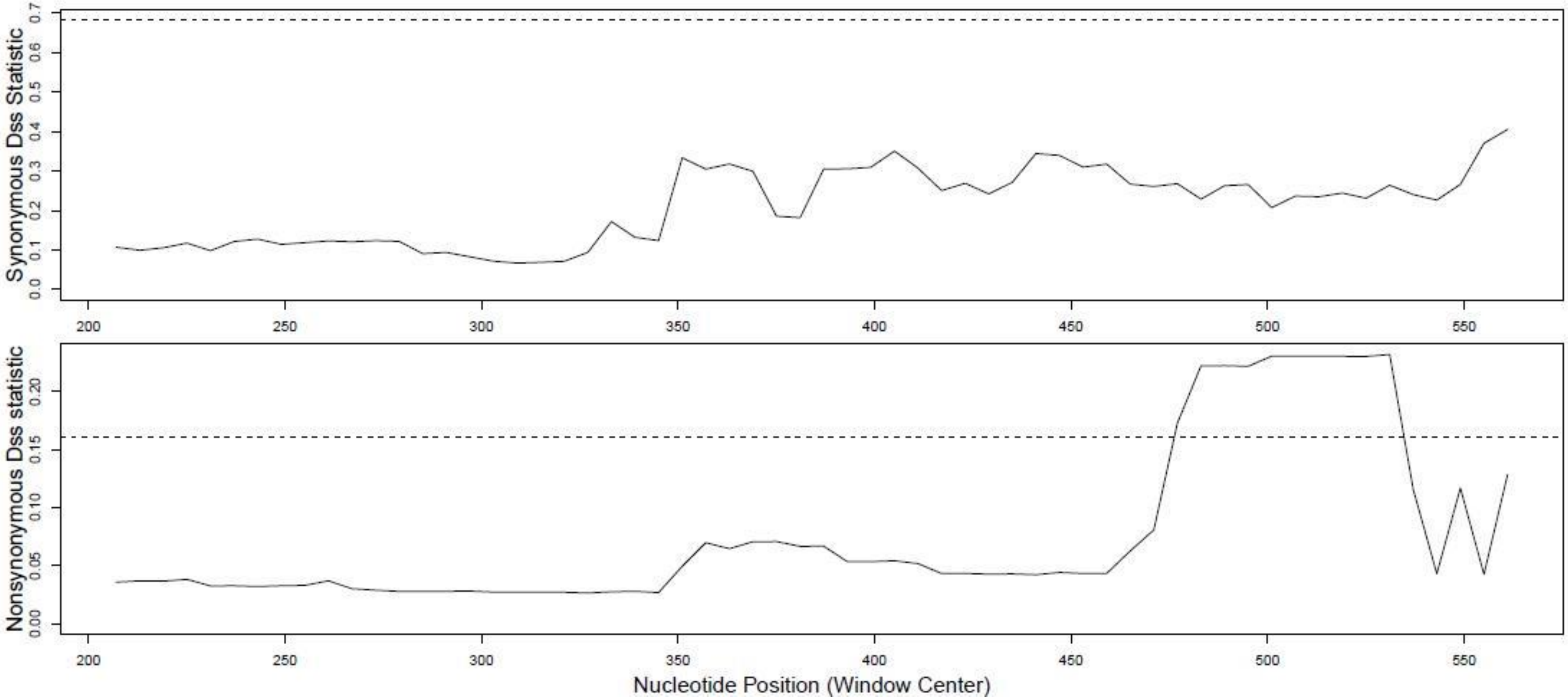
HP_1269



Dss statistic landscapes for synonymous and nonsynonymous changes. Dotted horizontal lines represent the 95% significance level for each test, from a parametric bootstrap with 500 replicates.

(B) 25 randomly selected core genes designated as **non-recombinants** by PhiPack (CONTD.)

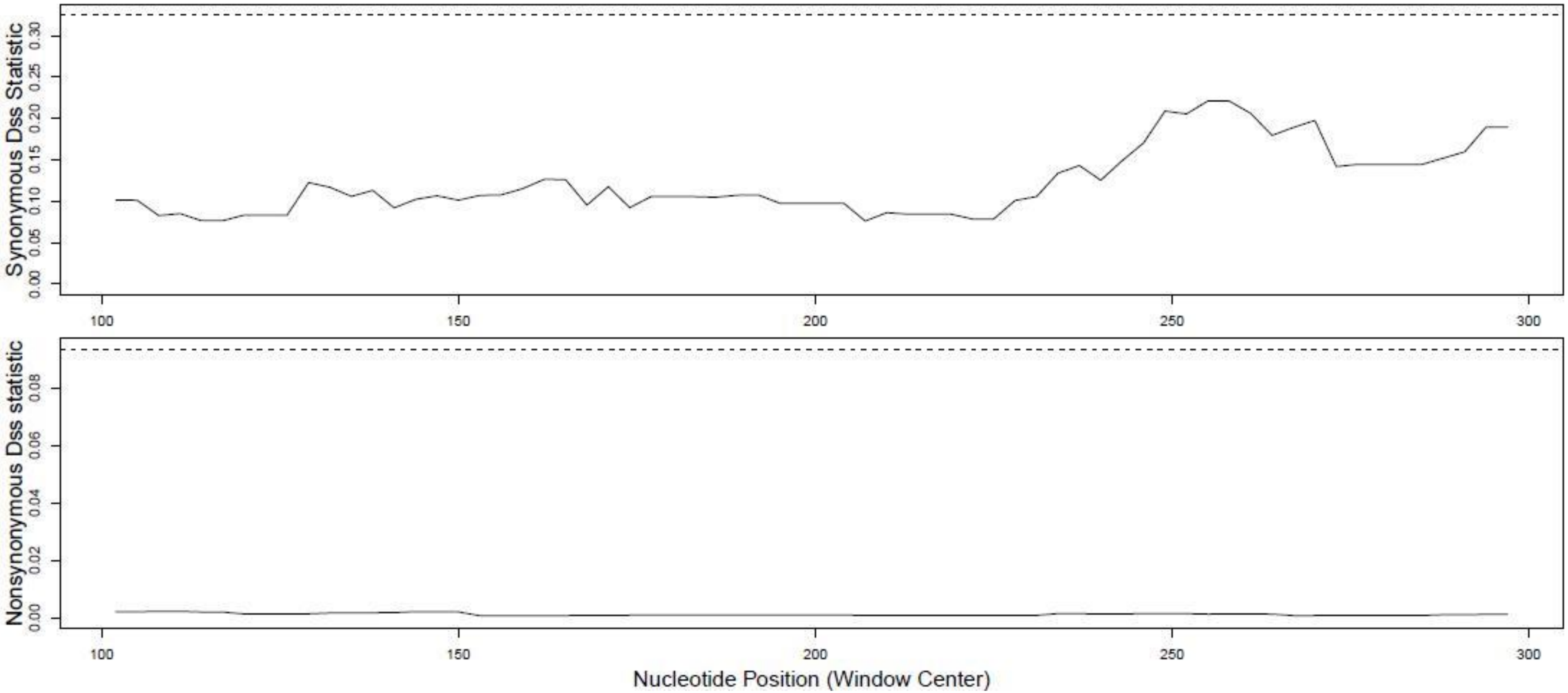
HP_1299



Dss statistic landscapes for synonymous and nonsynonymous changes. Dotted horizontal lines represent the 95% significance level for each test, from a parametric bootstrap with 500 replicates.

(B) 25 randomly selected core genes designated as **non-recombinants** by PhiPack (CONTD.)

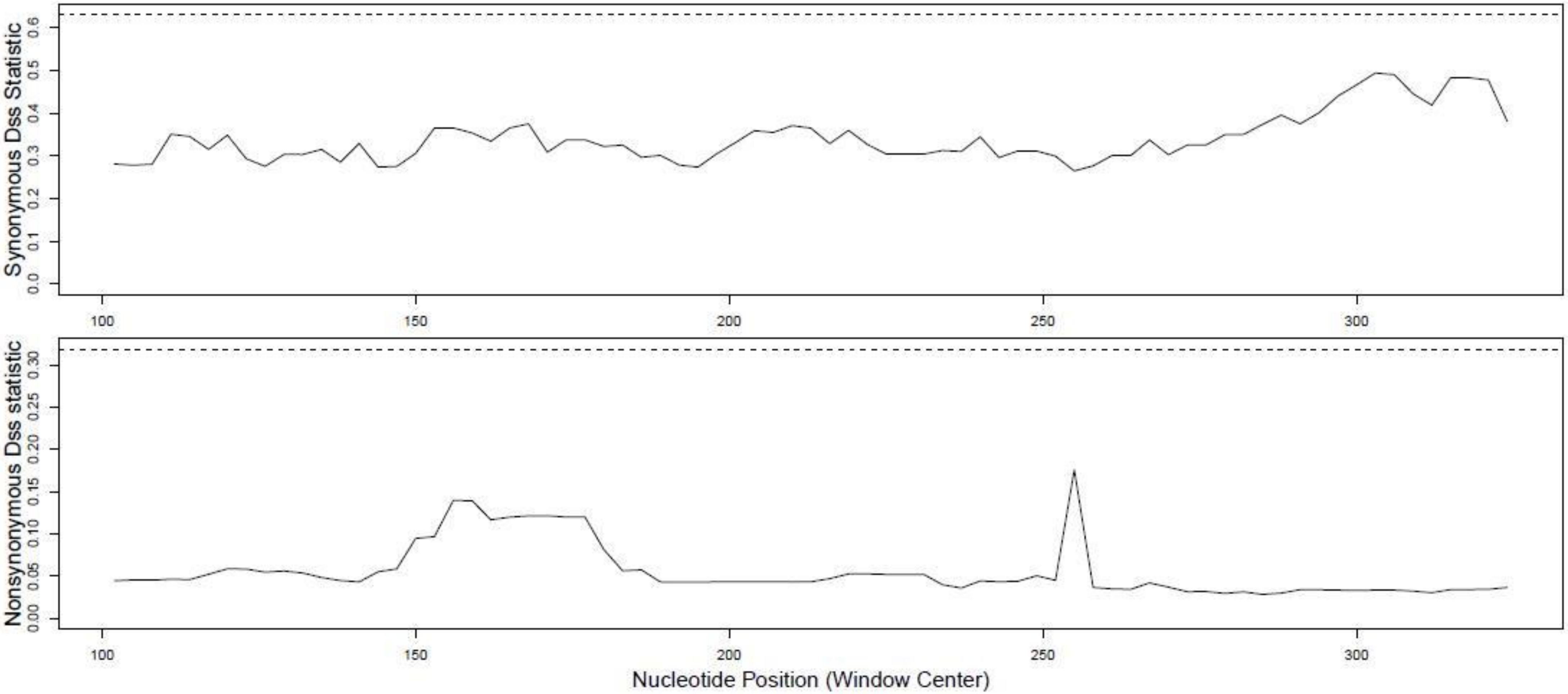
HP_1305



Dss statistic landscapes for synonymous and nonsynonymous changes. Dotted horizontal lines represent the 95% significance level for each test, from a parametric bootstrap with 500 replicates.

(B) 25 randomly selected core genes designated as **non-recombinants** by PhiPack (CONTD.)

HP_1559



Dss statistic landscapes for synonymous and nonsynonymous changes. Dotted horizontal lines represent the 95% significance level for each test, from a parametric bootstrap with 500 replicates.

**Figure S3.** Average frequency distribution of mutations in encoded proteins of randomly selected subsets of *H. pylori* non-recombinant core genes with convergent mutations.

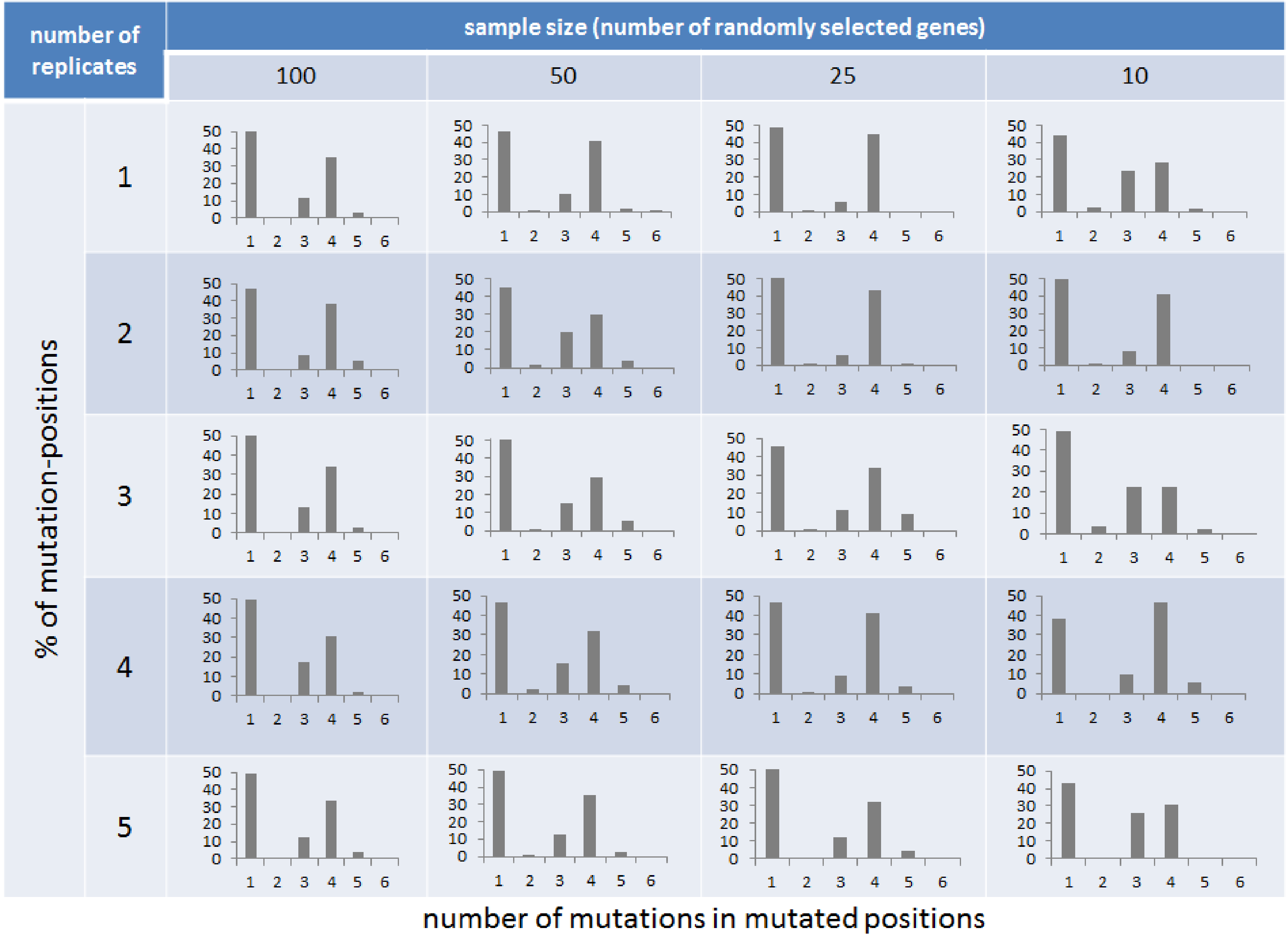
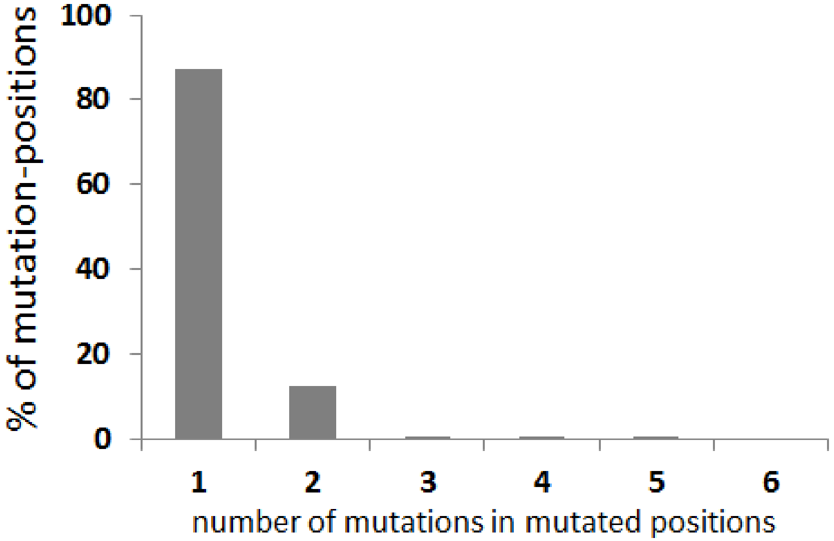
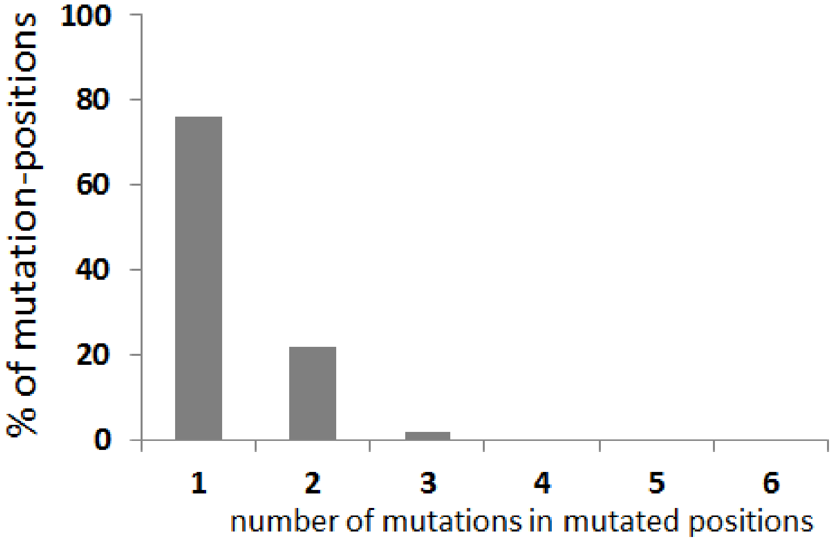


**Figure S4.** Average frequency distribution of mutations of encoded proteins in simulated datasets of 25 *H. pylori* genes (one of the randomly selected replicates from Figure S3) using two different mutation-rate constraints.



(a) Mutation rate same as of *H. pylori*



(b) Mutation rate twice of *H. pylori*