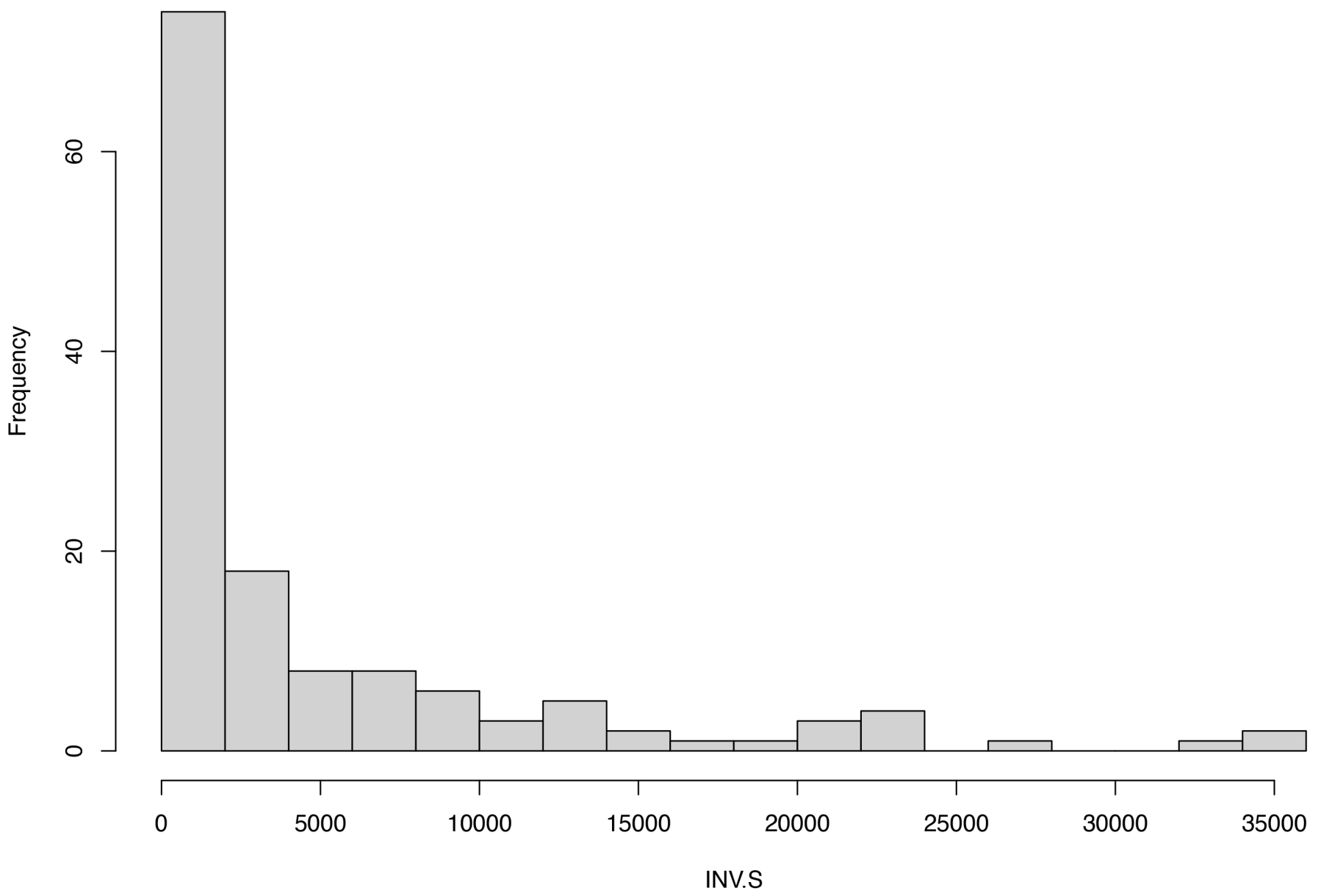
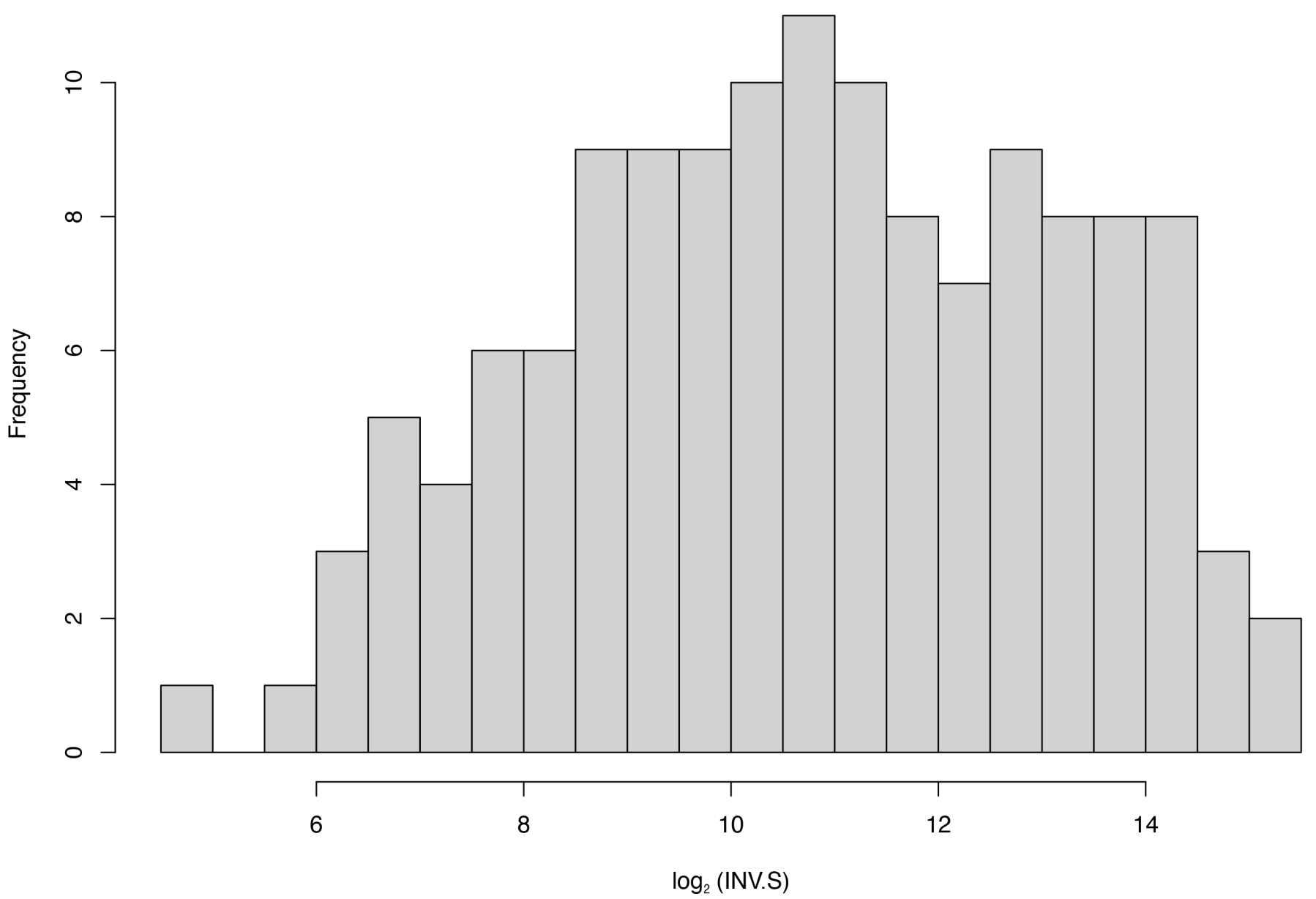


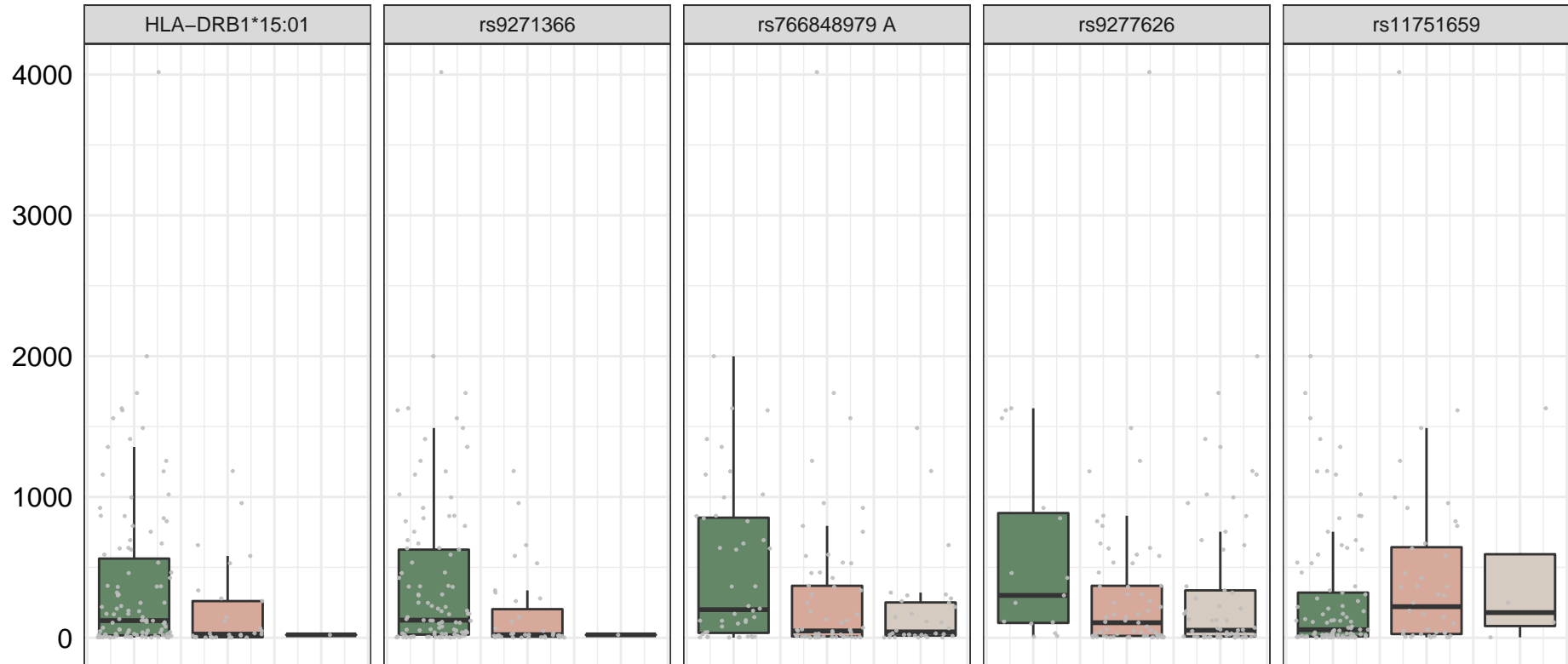
**INV.S distribution**



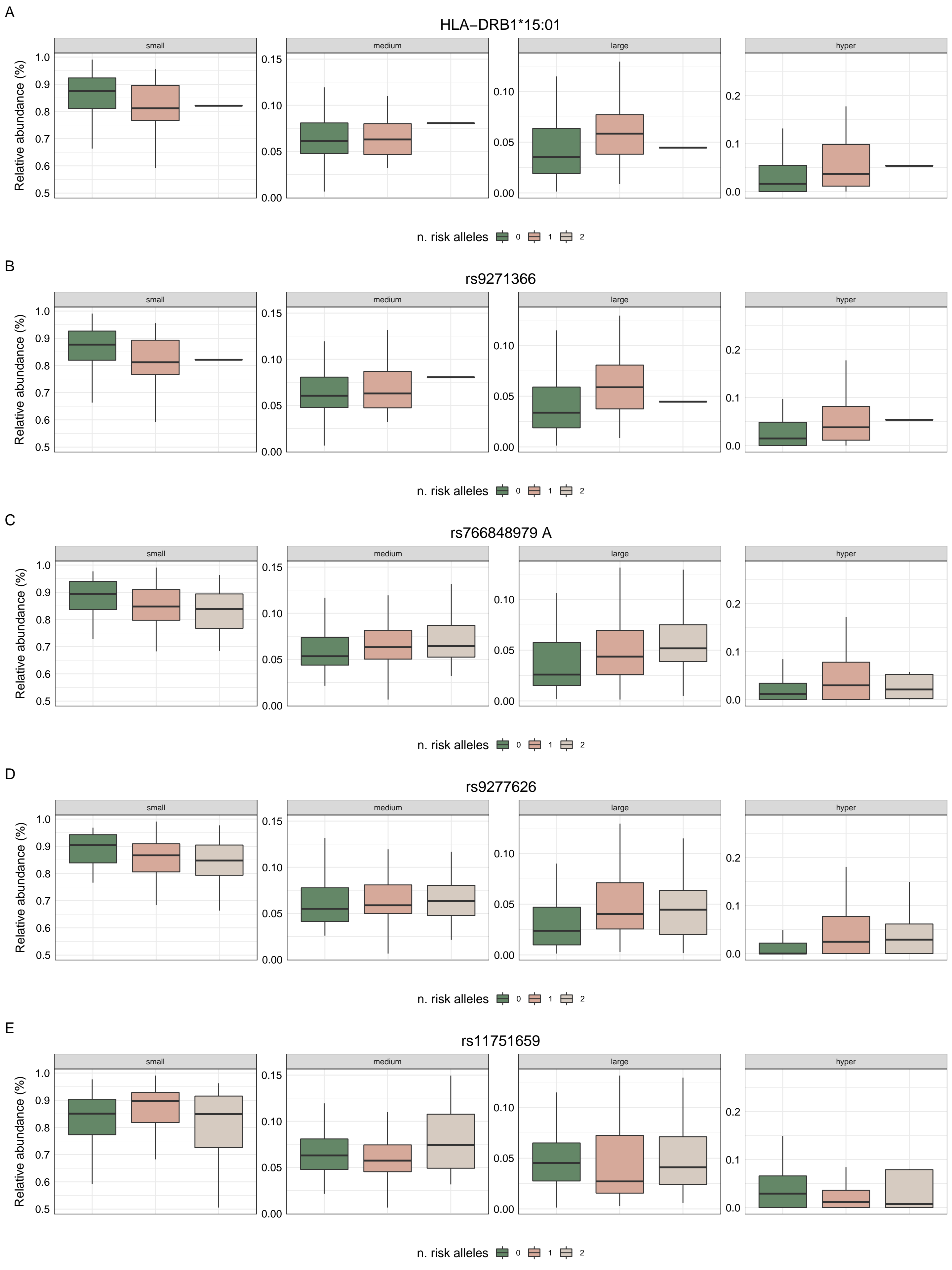
**normalized INV.S distribution**



Number of clonotypes



n. risk alleles 0 1 2



## Supplementary figures legend

**eFigure 1. Distribution of INV.S index.** The distribution of the INV.S index is shown before normalization (upper panel) and after normalization (lower panel).

**eFigure 2. Clonal proportion across MS-risk alleles.** The number of clonotypes occupying the 10% of the repertoire (clonal proportion) is plotted against the number of MS-risk allele in HLA-DRB1\*15:01, rs9271366, rs766848979 A, rs9277626 and rs11751659.

**eFigure 3. Clonal space homeostasis.** The percentage of the repertoire space occupied by clonotypes stratified according to their abundancy is plotted against the number of MS-risk allele in (A) HLA-DRB1\*15:01, (B) rs9271366, (C) rs766848979 A, (D) rs9277626, (E) rs11751659. P-values for each MS-risk allele and abundancy range according to regression analysis including age, sex and PC1 as covariates are significant for the following pairs: HLA-DRB1\*15:01 small ( $P=0.01$ ), large ( $P=0.045$ ) and hyperexpanded ( $P=0.01$ ); rs9271366 small ( $P=5.1 \times 10^{-3}$ ), large ( $P=0.018$ ) and hyperexpanded ( $P=9.23 \times 10^{-3}$ ); rs766848979 A small ( $P=6.2 \times 10^{-3}$ ) and large ( $P=3.6 \times 10^{-3}$ ); rs9277626 small ( $P=0.046$ ), and hyperexpanded ( $P=0.036$ ). Small:  $1 \times 10^{-5} < \text{frequency} < 1 \times 10^{-4}$ ; medium:  $1 \times 10^{-4} < \text{frequency} < 0.001$ ; large:  $0.001 < \text{frequency} < 0.01$ ; hyperexpanded: frequency  $> 0.01$ .