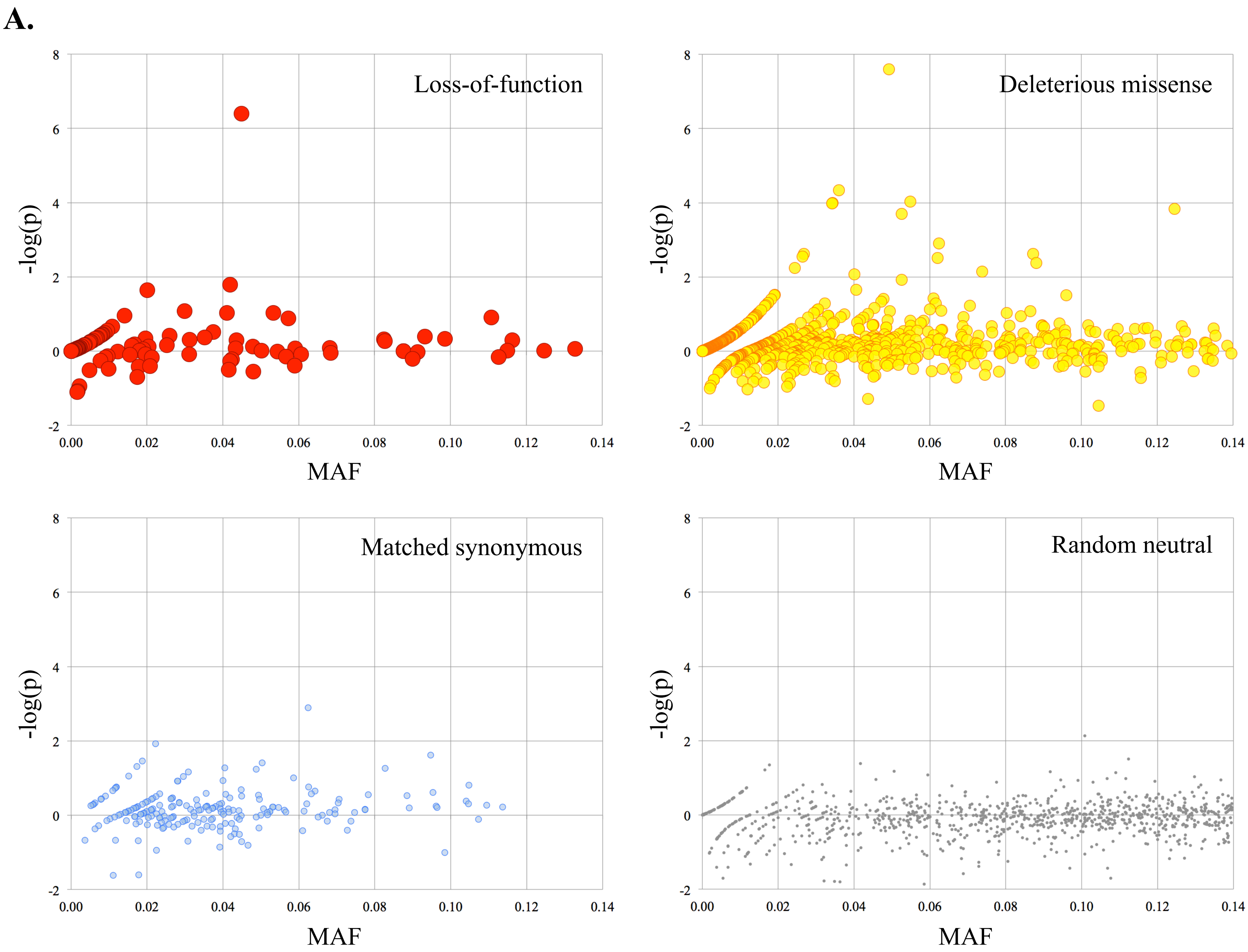
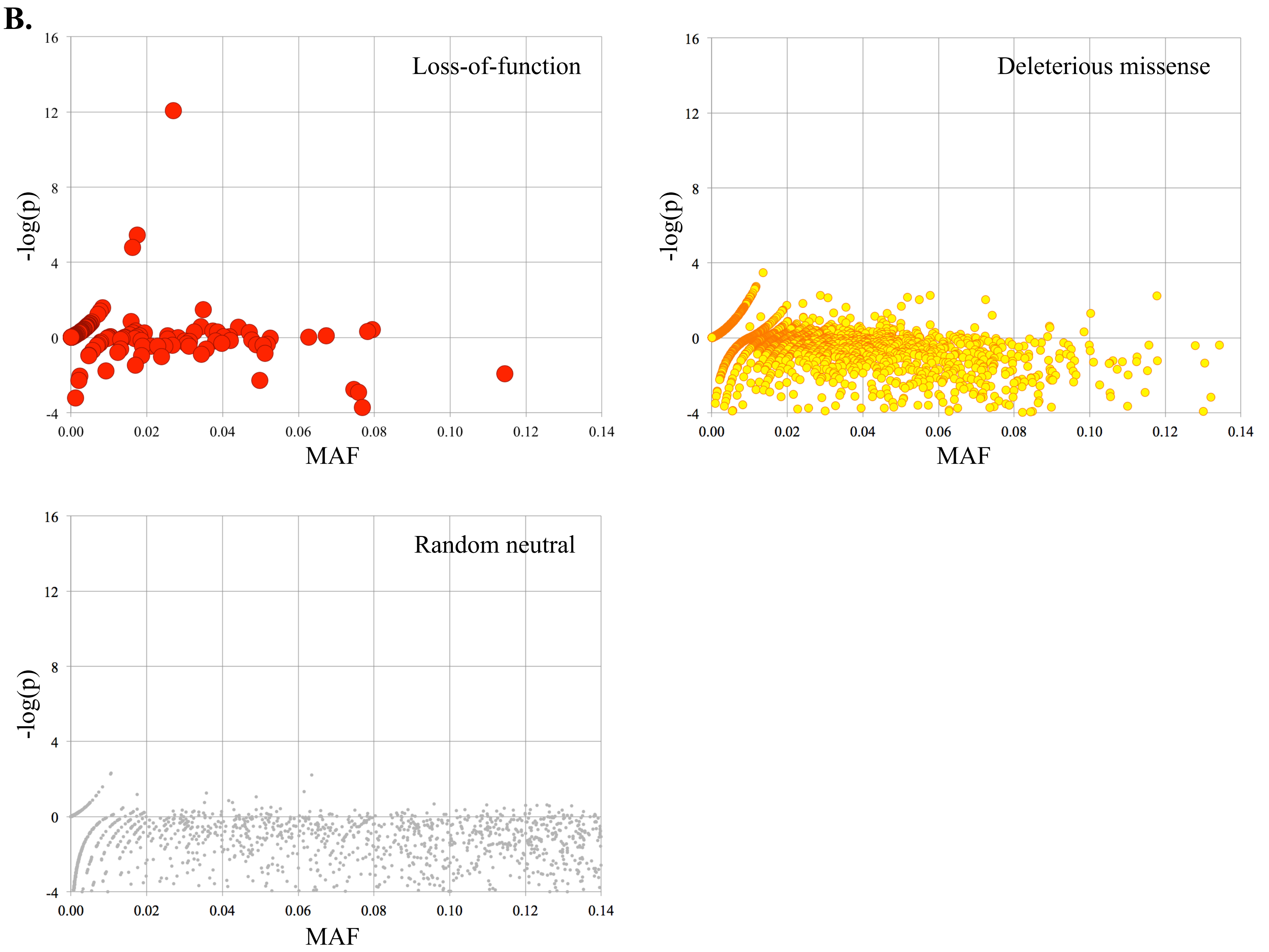

A.
Loss-of-function
Deleterious missense
Matched synonymous
Random neutral
-log(p)
MAF
8
6
4
2
0
-2
0.00
0.02
0.04
0.06
0.08
0.10
0.12
0.14


B.
Loss-of-function
Deleterious missense
Random neutral
-log(p)
16
12
8
4
0
-4
MAF
0.00
0.02
0.04
0.06
0.08
0.10
0.12
0.14

Supplemental Figure S1 : Statistical significance (-log p: Y-axis) of the depletion (positive values) or excess (negative values) in homozygotes shown separately for loss-of-function (red; defined as frame-shift, splice-site and stop-gain variants), missense (yellow), matched synonymous (blue), random neutral (small grey) variants ordered by minor allele frequency (MAF: X-axis), based on the genotyping of 6,385 healthy BBC (**A**) and 35,219 healthy NZDC (**B**) animals. For NZDC (**B**), MAF were computed across breeds (NZ Holstein-Friesian, NZ Jersey and NZ cross-bred), explaining the differences with the within breed MAF reported in Table 2, and the high proportion of variants with negative -log(p) values.