**SUPPLEMENTARY FIGURE LEGEND**

**Supplementary Figure 1.** Variants detected in asthmatic and non-asthmatic horses with Genome Analysis Toolkit (GATK). The Venn diagram was generated with SeqMule to identify variants present in all asthmatics before (red) and after challenge (green), and in non-asthmatics before (turquoise) and after challenge (purple).

**Supplementary Figure 2.** Predicted effect of variants in all (left) and coding (right) regions for asthmatic horses before (upper) and after (lower) challenge. Analysis was done using Ensembl Variant Effect Predictor (VEP) tools.

**Supplementary Figure 3.** Predicted effect of variants from all (left) and coding (right) regions for asthmatic horses before (upper) and after (lower) challenge. Analysis was done using Ensembl Variant Effect Predictor (VEP) tools.

**Supplementary Figure 4.** Results of analysis of *PACRG* (A) and *RTTN* (B) mutations with PolyPhen2 software. Mutations were predicted as probably damaging in PACRG and RTTN proteins with confidence scores of 0.993 and 0.979, respectively.