Supplementary Figure S1—Genomic assay (SearchLight DNA; Vidium Animal Health) analysis and annotation pipelines. A – Primary analysis is performed on a validated cloud-based bioinformatics pipeline for confident calling of single-nucleotide variants (SNVs), copy number variants (CNVs), and internal tandem duplications (ITDs). B – Candidate pathogenic variants are annotated according to predicted impact and filtered to remove common non-pathogenic single-nucleotide polymorphisms from the European Variant Archive (EVA) and Vidium Animal Health data, then annotated with human-to-canine-translated databases (COSMIC and cBioPortal) as well as biomarker associations from Vidium’s proprietary database (Vidium Insight; Vidium Animal Health).