



### Looking for the “missing” Nelore genotypes

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SNP genotyping with High Density (HD) chips offers a relative low cost when compared to genotyping by re-sequencing using Next Generation Sequencing technologies, which is a significant advantage when a large number of individuals are under study. Currently, there are commercial HD chips for several economically important species, for very reasonable prices per sample. The Illumina BovineHD BeadChip includes more than 777,000 SNPs designed from sequence data derived from two cattle subspecies, *Bos taurus taurus* and *Bos taurus indicus*, and several composite breeds, selected for beef and/or dairy production. However, although those breeds share most part of their genomic sequence, some SNP probes designed based on one breed may not be fully compatible to others. Indeed, this chip has 29,968 loci that have been known to yield breed-specific lower call rates when compared to most loci on the panel, and which are usually removed from datasets as low quality data during Quality Control procedures. We examined BovineHD “missing” genotypes from a total of 1,709 Nelore DNA samples and used sequence data from eight animals to identify putative polymorphisms flanking the assayed SNPs. We only used information from markers “missing” in all samples, and located in exons, and manually curated those related to non-synonymous mutations (NSM). Preliminary analyses have revealed that most of the genes harboring those NSM are associated with disease resistance, immune system response and reproductive traits.

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