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Extensive meta analysis of GWAS in humans has identified 697 significant SNP, however these SNP explain only 20% the total genetic variation. In order to compare the genetic architecture of stature in humans to stature in cattle, we performed a large meta-analysis using imputed sequence data. The 1000 Bull Genomes project provided a multi-breed reference population of 1,147 sequenced animals to impute SNP-chip genotypes up to whole genome sequence for 15 populations. The populations from Australia, Canada, Denmark, Finland, France, Germany, the Netherlands, and the USA represented the Angus, Fleckvieh, Holstein, Jersey, Montbeliarde, Normande, and Nordic Red Dairy Cattle breeds. Genome-wide association studies were performed on stature phenotypes for each of the populations. Individual GWAS studies revealed many QTL regions and several regions harboured good candidate genes, e.g. PLAG1, IGF2. Results from these GWAS studies were combined in a meta-analysis to increase the power for QTL detection and to refine QTL regions exploiting the different patterns of LD among the breeds. Results of this meta-analysis will be validated in an independent population to determine how much of the variation in stature can be explained by the significant SNP.