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French genomic evaluations have been based on a Marker-Assisted BLUP (MABLUP) approach where QTL were detected using a variable selection method. The evaluation software was modified to remove the existing constraint on number of QTL included. A set of new MABLUP models were tested using a set of 2574 Montbéliard bulls genotyped on the Illumina Bovine SNP50 BeadChip®. From 1000 to 6000 QTL detected with a BayesCpi approach were included. A model based on SNP only was compared with models based on haplotypes of 3, 4, or 5 SNP. The best SNP corresponding to a QTL position was completed with 2, 3 or 4 flanking SNP to build a haplotype. An alternative to this strategy was developed to select the haplotype with the largest number of "predictable" alleles from a window of 10 SNP around the QTL-SNP, where observed haplotype allele frequencies were used as indicators of "good predictability" in genomic evaluation. In the MABLUP model, a polygenic residual component explaining 10 to 50% of the genetic variance was also included in the model and was estimated either through the pedigree or from the SNP of the Illumina Bovine LD chip. The impact of all these scenarios on the correlation between observed daughter yield deviations and genomic estimated breeding values and on the regression slope in a regular validation test was measured and compared to other genomic selection approaches. The best combinations of these scenarios led to an average gain in correlation between 1.5 and 3% with a significant improvement of the regression slope. A reasonable final model for most traits includes 3K QTL haplotypes of 4 SNP and a residual polygenic component based on the LD SNP explaining 20 to 30% of the genetic variance. These results were used to improve the new French national genomic evaluation.