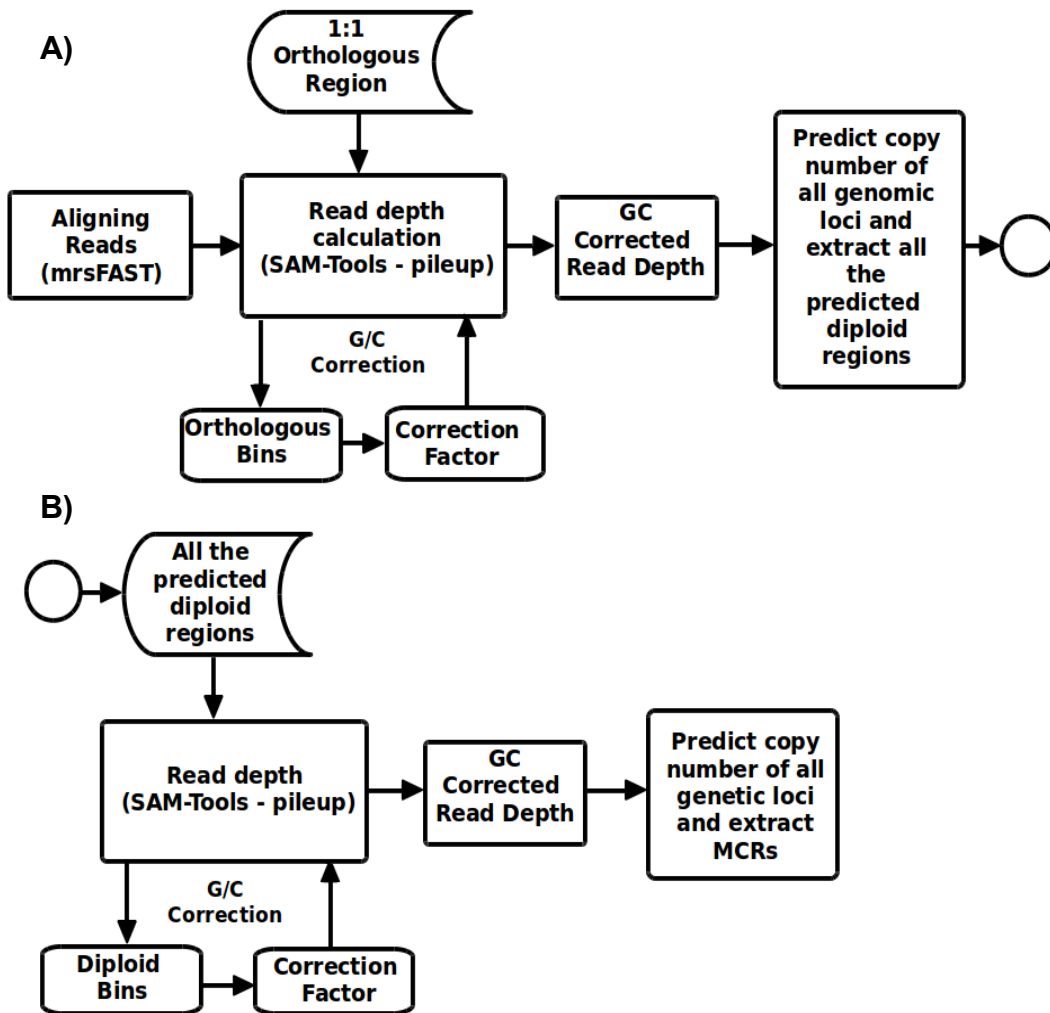


Supplementary Information

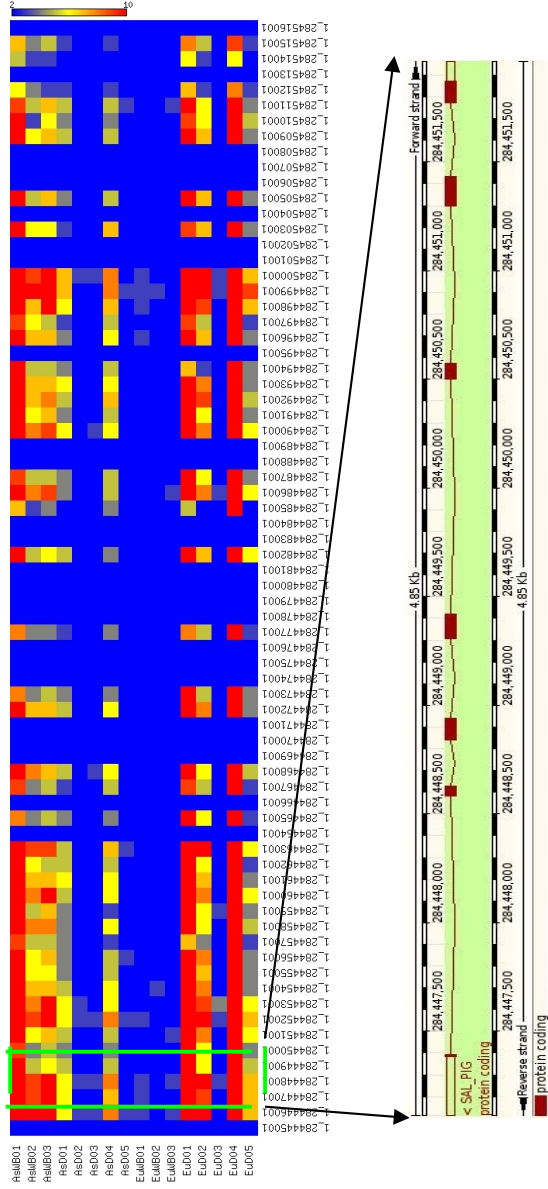
Supplementary Figure 1: Flow chart of the MCR detection process.

A) First step: Detection of diploid region using 1:1 orthologous region.

B) Refining step: Detection of MCRs using the predicted diploid region from the first step.



Supplementary Fig 2: The region in chromosome 1 with SAL1 gene.
 The region containing SAL1 gene (SSC1: 284447110-284451960) shows high copy number in some of the Asian individuals and European Domestic.



Supplementary Tables

Supplementary Table 1**A**: List of individuals with MCRs

Supplementary Table 1**B**: List of individuals used to form groups

Supplementary Table 2**A**: List of the CNVRs in the porcine genome.

Supplementary Table 2**B**: CNVRs distribution in the porcine genome.

Supplementary Table 2**C**: G/C percentage of the chromosome and region affected by CNVRs.

Supplementary Table 3**A**: Total genes overlapped by CNVRs with their exonic depth.

Supplementary Table 3**B**: Final list of genes overlapped by CNVRs.

Supplementary Table 3**C**: Orthologous genes overlapped by CNVRs.

Supplementary Table 3**D**: List of olfactory receptor genes overlapped by CNVRs.

Supplementary Table 4**A**: Gene ontology using BinGO package.

Supplementary Table 4**B**: General statistics of genes

Supplementary Table 4**C**: The list of qPCR primers

A,B,C,D,E represents sheets in each excel file.