

How do I merge data from the two different BeadChip versions?

After clustering the data from each version independently in GenomeStudio® data analysis software, the genotype calls can be exported and merged. This can be accomplished with open-source analysis applications such as PLINK (<http://pngu.mgh.harvard.edu/~purcell/plink/>), enabling data sets to be analyzed as one.

Will it be possible to cluster and merge v1 and v2 data sets within GenomeStudio software?

No. Projects that span the two BeadChip versions will have to be clustered outside of the GenomeStudio software.

Will Illumina manufacture new versions of the PorcineSNP60 BeadChip at some point in the future?

Illumina is building the bead pool for the v2 BeadChip to meet current and forecasted market demands. Should market demand warrant it, the manufacture of additional versions may be necessary.

What if my loci of interest are not represented on the v2 BeadChip?

The base content of the PorcineSNP60 v2 BeadChip was created using the v1 specifications. We've tried to provide as close to 100% content overlap between the versions as possible. In the unlikely event that there are loci of interest that are not represented on the v2 BeadChip, customers can cost-effectively add them onto the BeadChip with Add-On Content.

How much Add-On Content will be allowed on the v2 BeadChip?

The PorcineSNP60 v2 BeadChip can accommodate 90,000 beadtypes on the substrate, i.e. room for 25,000 beadtypes of Add-On Content, on top of 65,000 beadtypes of base content.

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