

Description of Additional Supplementary Files

File Name: Supplementary Data 1

Description: Meta-data of the heart samples used in the study.

File Name: Supplementary Data 2

Description: TF enrichment in different cell types.

File Name: Supplementary Data 3

Description: Results of SNP fine-mapping analysis, and gene mapping.

File Name: Supplementary Data 4

Description: Comparing high PIP variants with variants with allele-specific activity using STARR-seq from van Ouwerkerk *et al.* 2020.

File Name: Supplementary Data 5

Description: Sum of PIPs for SNPs assigned to functional categories.

File Name: Supplementary Data 6

Description: SNPs chosen for experimental study.

File Name: Supplementary Data 7

Description: Colocalization result of fine-mapped SNPs with eQTLs.

File Name: Supplementary Data 8

Description: Gene mapping results, summarized at the gene level.

File Name: Supplementary Data 9

Description: Gene mapping results, summarized at the level of LD blocks.

File Name: Supplementary Data 10

Description: Information of genes at $PIP \geq 0.8$ with literature evidence.

File Name: Supplementary Data 11

Description: Loci where the mapped high PIP (≥ 0.8) genes are not the nearest genes.

File Name: Supplementary Data 12

Description: OMIM gene information.

File Name: Supplementary Data 13

Description: GO enrichment of genes with gene $PIP \geq 0.8$.

File Name: Supplementary Data 14

Description: GO enrichment of genes with gene $PIP \geq 0.5$ (from STRING).

File Name: Supplementary Data 15

Description: High PIP eQTLs and their categories.