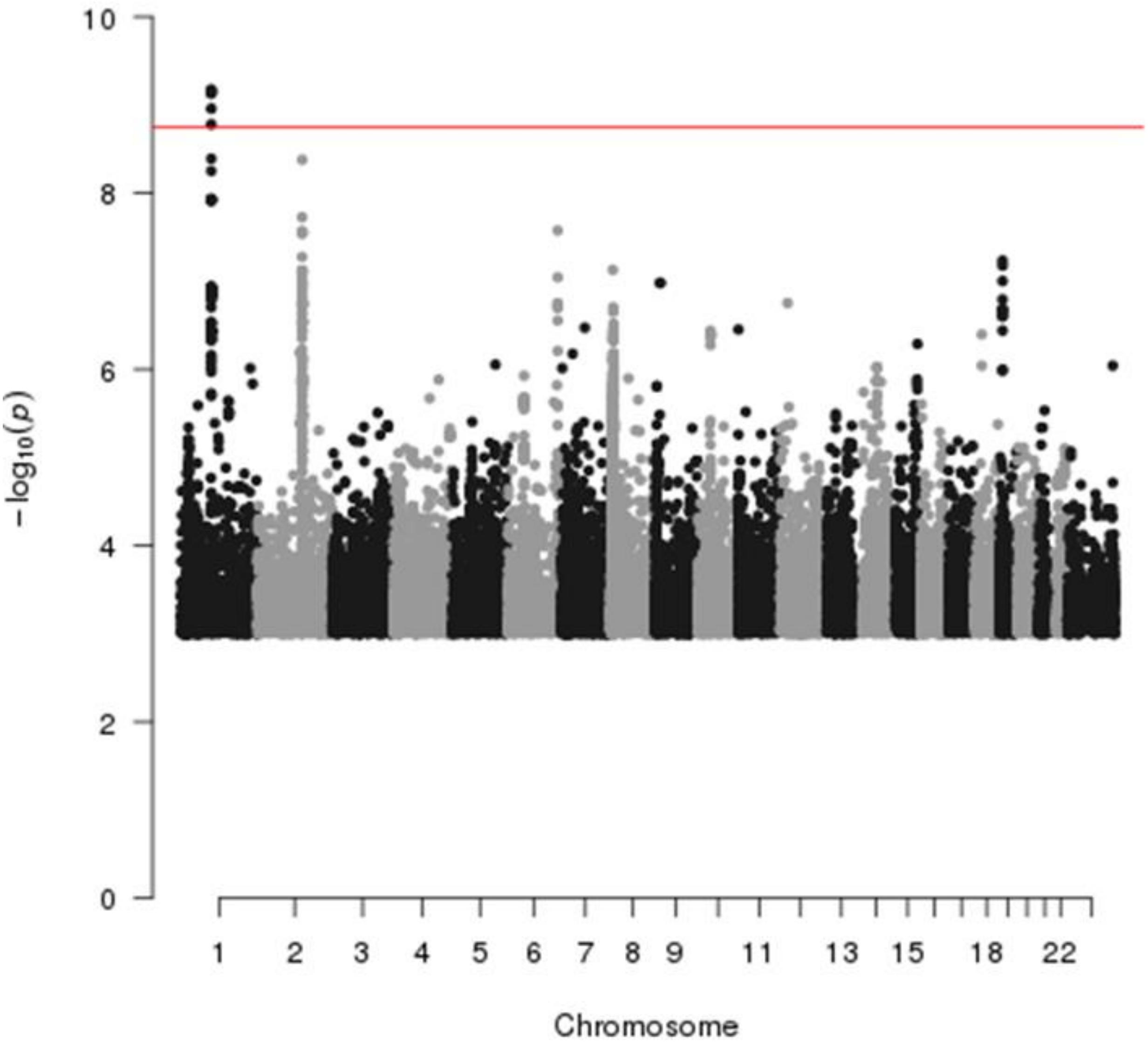
Supplementary Information

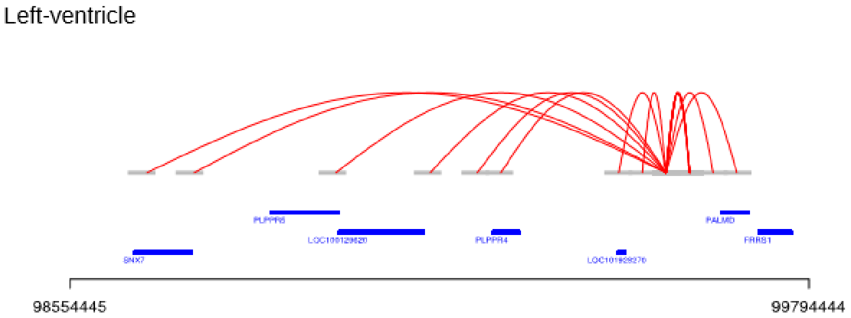
Genome-wide analysis yields new loci associating with aortic valve stenosis

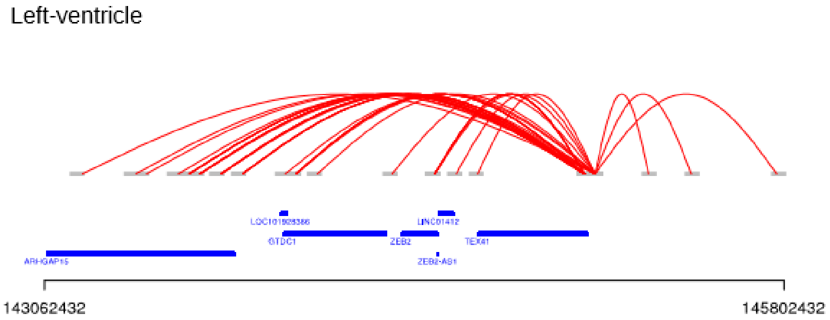
Helgadottir, *et.al.*

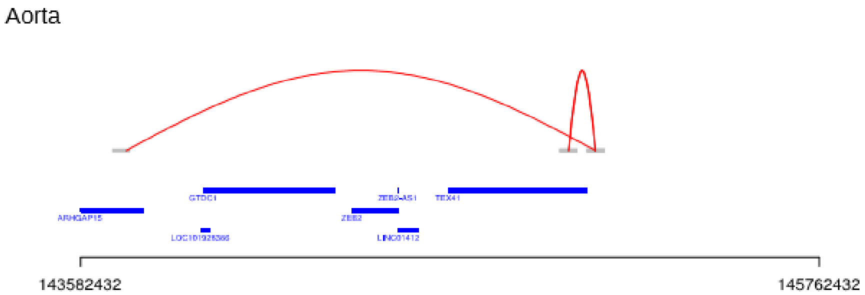


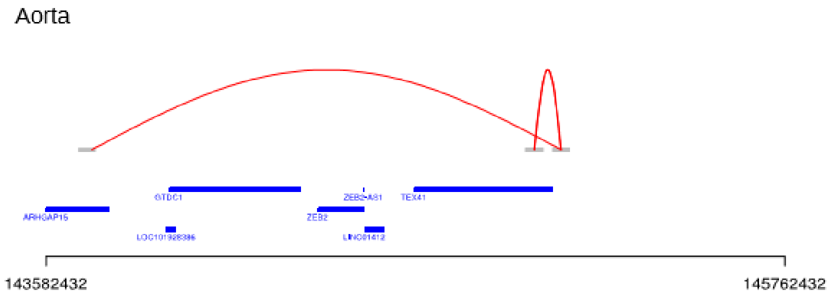
Supplementary Fig. 1

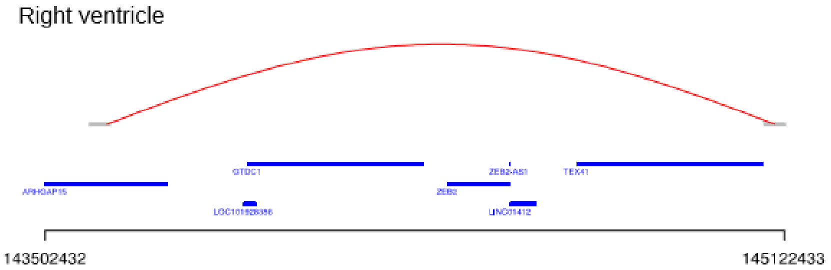
Manhattan plot for the discovery genome-wide association analysis. The red horizontal line indicates the genome-wide significance threshold for low-impact variants ($P < 4.6 \times 10^{-9}$).


Left-ventricle


Left-ventricle


Aorta


Aorta


Right ventricle

Supplementary Fig. 2

Shown are all chromatin interactions observed for the regulatory regions, to which AS risk variants at the *PALMD* locus (on the left-hand side) and at the *TEX41* locus (on the right-hand side) map to.

The chromatin interactions are shown for left- and right ventricular heart, and aorta tissue samples.

At the *PALMD* locus no chromatin interactions were observed in right ventricular tissue.