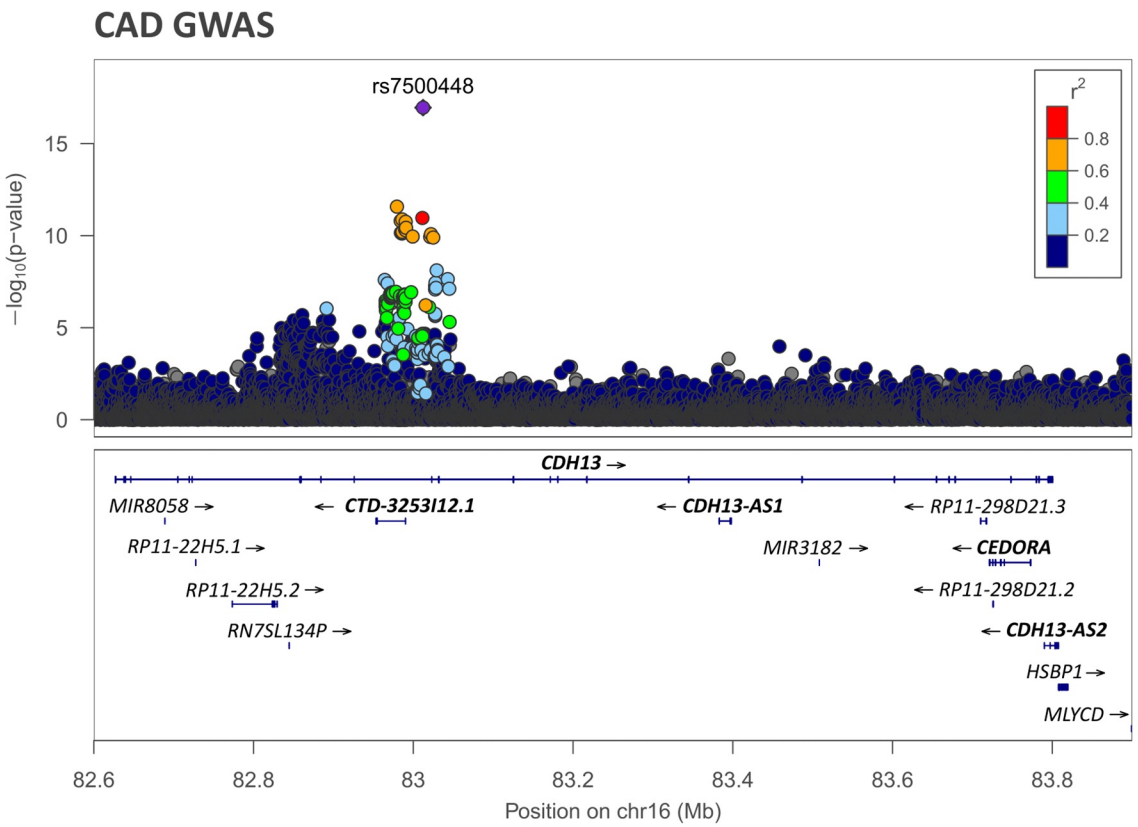
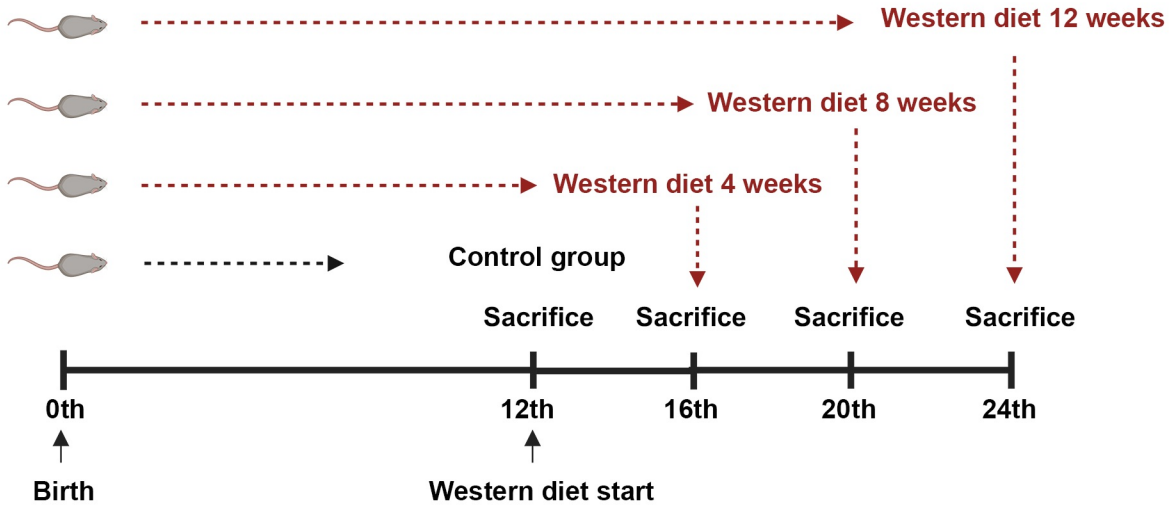
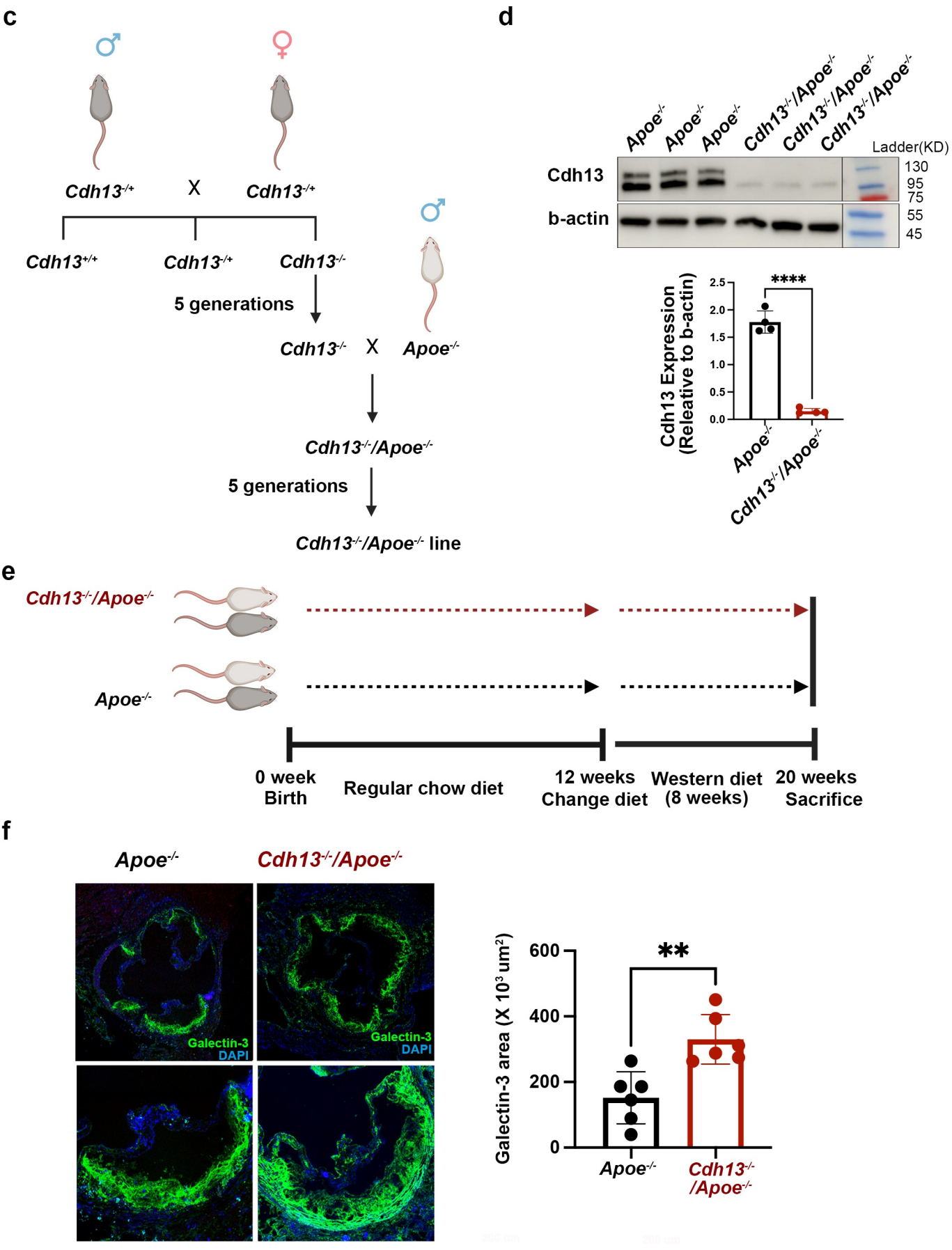
**a**



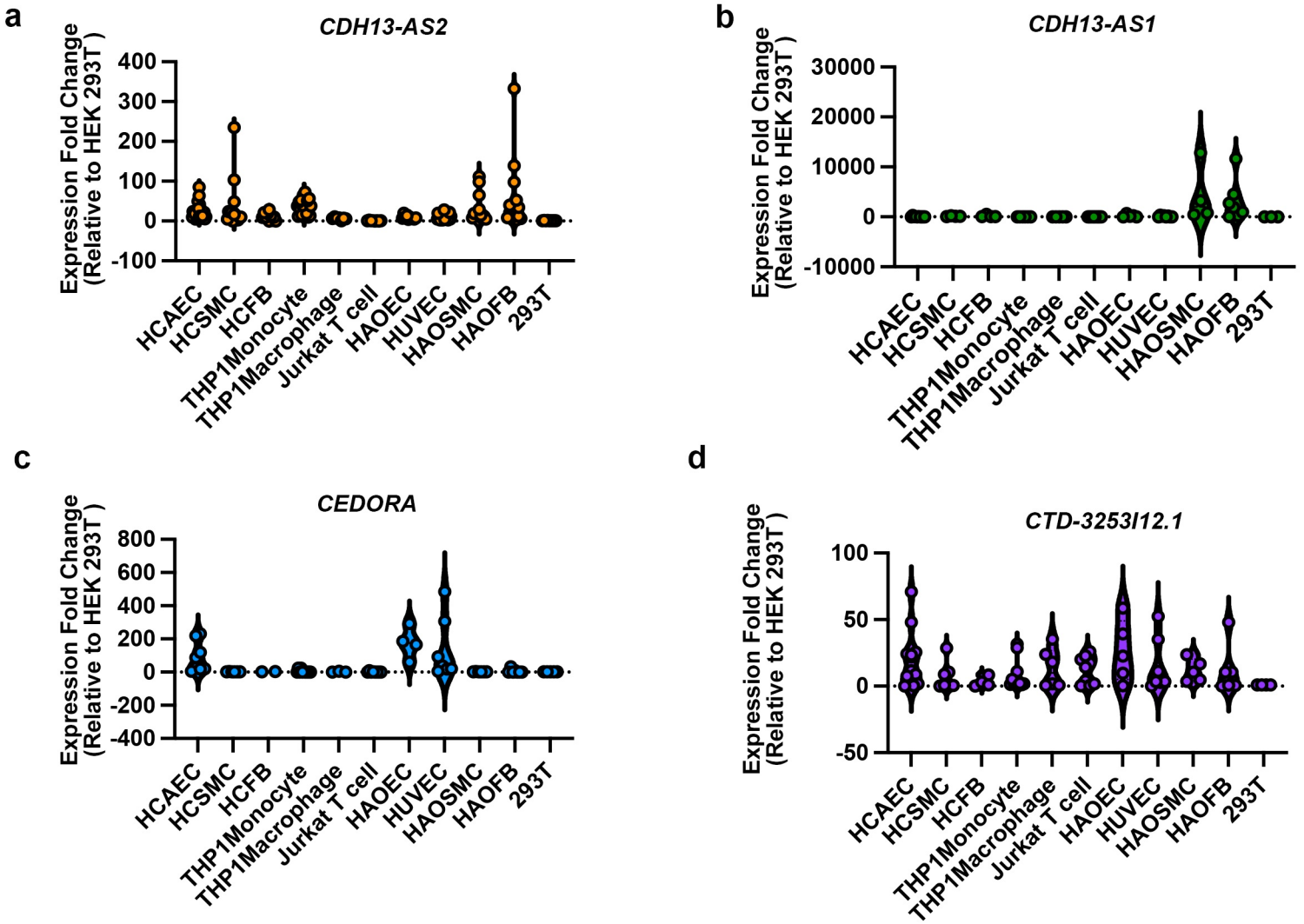

**b**



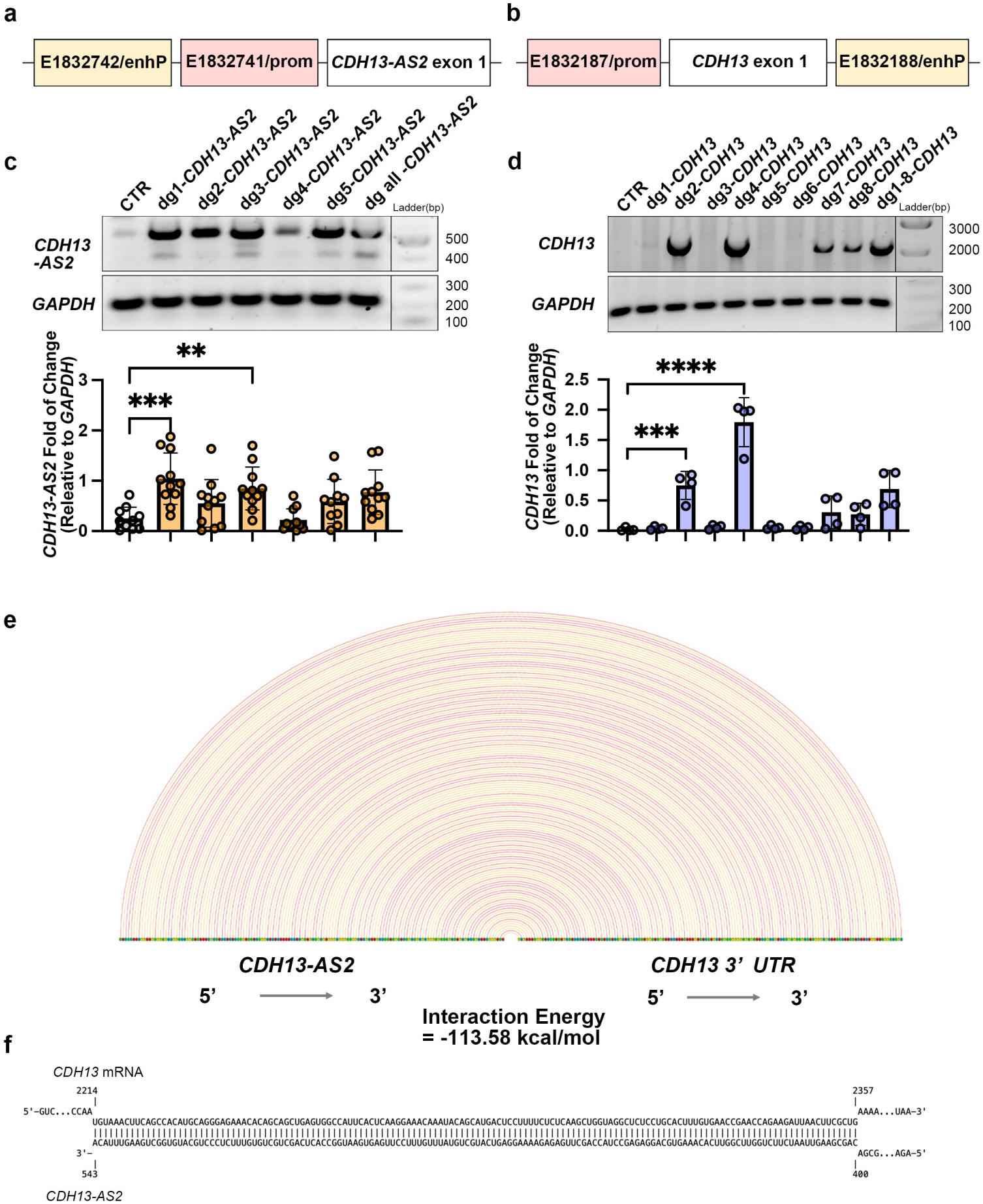

**Extended Data Fig.1: The *CDH13* CAD GWAS locus (a) and experimental scheme of exploring Cdh13 level during atherosclerosis development in mice. a,** The locus zoom plot was made based on the latest summary genetic statistic of CAD GWAS from the CARDIoGRAMplusC4D Consortium(Fig.1a and 1b). **b,** Atherosclerosis development was induced in Apoe$^{-/-}$ mice by weeks of Western diet feeding as indicated. Artery Cdh13 protein level was evaluated according to the time points(Fig.1c).



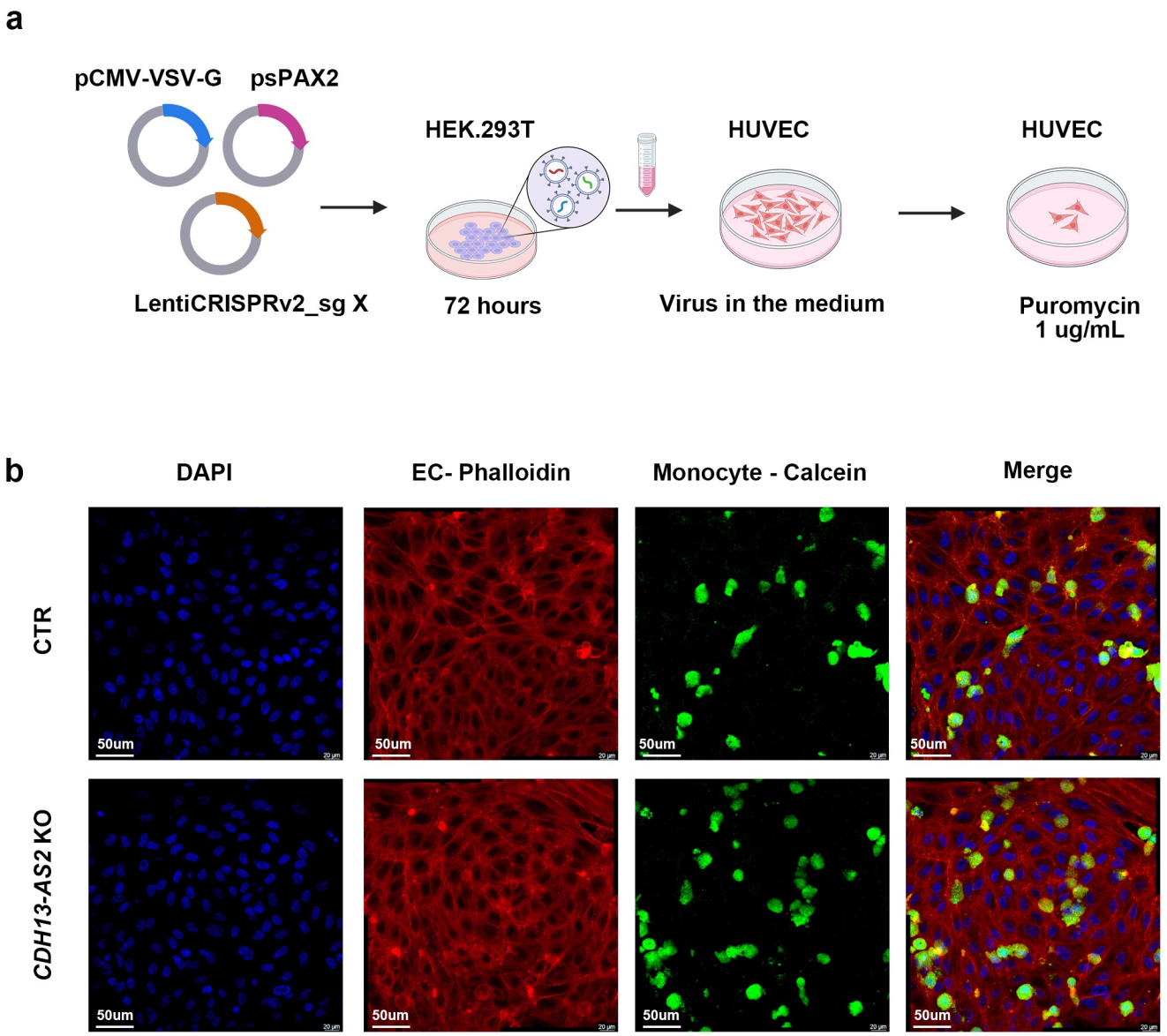

**Extended Data Fig.1: The *CDH13* CAD GWAS locus and experimental scheme of exploring Cdh13 level during atherosclerosis development in mice. c,** Generation of *Cdh13*$^{-/-}$/*Apoe*$^{-/-}$ transgenic mouse model(Fig.1e). **d,** Confirmation of Cdh13 knockout by Western blotting of protein level in mouse aortic tissue(unpaired t-test, ****, P ≤ 0.0001). **e,** The timeline to induce atherosclerosis phenotypes in transgenic mouse models(Fig.1e). **f,** In comparison to the *Apoe*$^{-/-}$ mice, *Cdh13*$^{-/-}$/*Apoe*$^{-/-}$ mice displayed increased leukocyte infiltration at the aortic roots marked by Galectin-3 staining. Unpaired t-test was used as the statistic method: **, P ≤ 0.01;



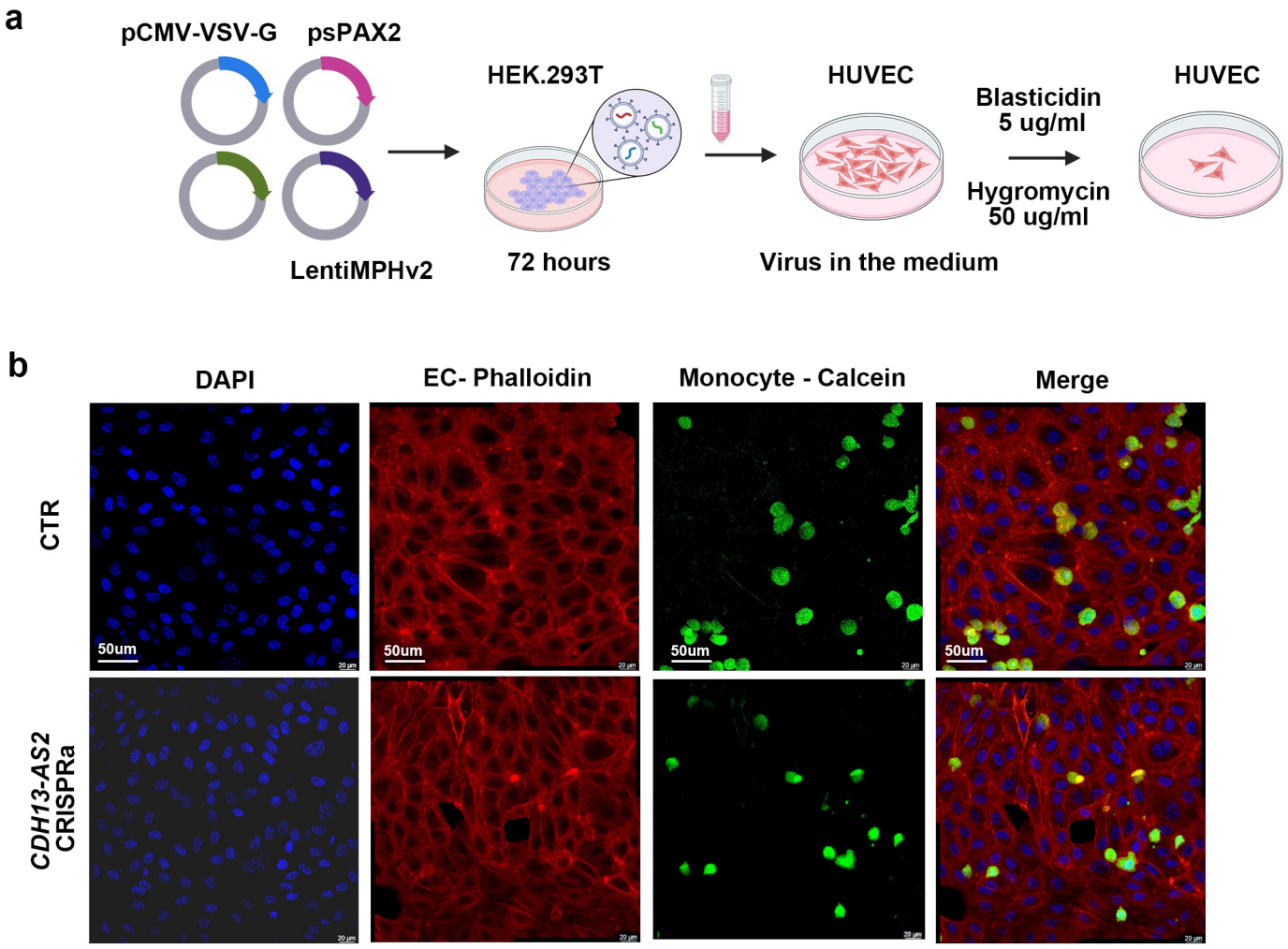

**Extended Data Fig.2: The expression of lncRNAs in vascular cell types**. **a** through **d,** LncRNAs expression in vascular cells. HUVECs, HAOEC, and HCAEC, human umbilical vein, aorta, and coronary artery endothelial cells; HAOSMC and HCSMC, human aorta and coronary artery smooth muscle cells; HCFB and HAOFB, human coronary artery and aorta fibroblasts; THP1, monocyte isolated from peripheral blood from an acute monocytic leukemia patient; macrophage, differentiated from THP1 via 100ng/ml phorbol 12-myristate 13-acetate (PMA) treatment for 72 hours; T cell, the immortalized line of human T lymphocyte cell, Jurkat. The four gene expressions were assessed by qPCR and the results were first normalized to GAPDH and then compared with HEK.293 T cells.



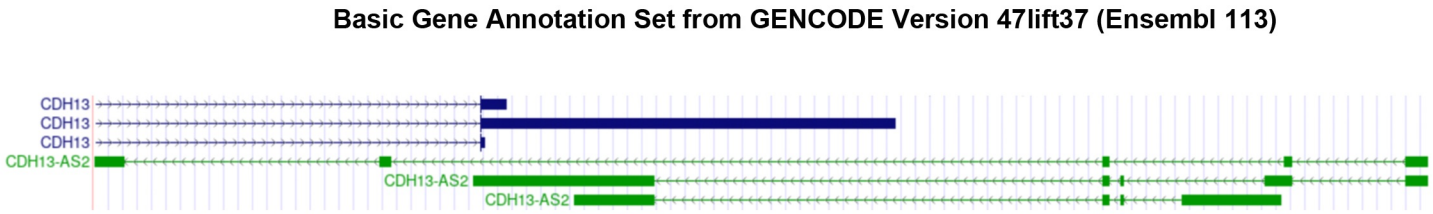

**Extended Data Fig.3: The binding of *CDH13* and *CDH13-AS2* by prediction and CRISPR-based transcriptional activation (CRISPRa) . a,b,** ENCODE IDs and positions of targeted promoter (prom) and enhancer (enhP) of *CDH13-AS2* **(a)** and *CDH13* **(b)**. **c,** For *CDH13-AS2*, five dgRNAs were tested individually or combined (dg1-5) (Ordinary one-way ANOVA multiple comparisons). **, P ≤ 0.01; ***, P ≤ 0.001. **d,** For *CDH13*, eight dgRNAs were tested individually or combined (dg1-8) (Ordinary one-way ANOVA multiple comparisons). ***, P ≤ 0.001; ****, P ≤ 0.0001. **e,f,** LncRRIsearch webtool predicts the pair-wise interaction of CDH13-AS2 with CDH13 3‘UTR with a local base-pairing interaction energy of -113.58 kcal/mol.




**Extended Data Fig.4: Workflow of generation of CRISPR knockout HUVEC lines and full images of the adhesion assay of Fig.4g. a,** HUVEC CRISPR knockout cell line generated by lentivirus treatment. **b,** Representative images of adhesion assay between control (CTR) and CDH13-AS2 KO HUVEC cells. HUVEC cells were labeled by phalloidin (red), TPH1 monocytes by calcein (green), and DNA by DAPI (blue).




**Extended Data Fig.5: Workflow of generation of CRISPR-based transcriptional activation (CRISPRa) cell line and full images of the adhesion assay of Fig.5g. a,** Workflow of CRISPRa in HUVEC cells. **b,** Representative images of adhesion assay between control (CTR) and CDH13-AS2 CRISPRa HUVEC cells. HUVEC cells were labeled by phalloidin (red), TPH1 monocytes by calcein (green), and DNA by DAPI (blue).




**Extended Data Fig.6: The genomic position of *CDH13-AS2* and *CDH13* 3'UTR.** The genome region of chr16:83,823,408-83,841,500 (GRCh37/hg19) was shown to visualize the full length of *CDH13-AS2*, *CDH13 3'UTR*, and the overlap of the two. Data was extracted from the UCSC Genome Browser on Human (GRCh37/hg19).