APPENDIX

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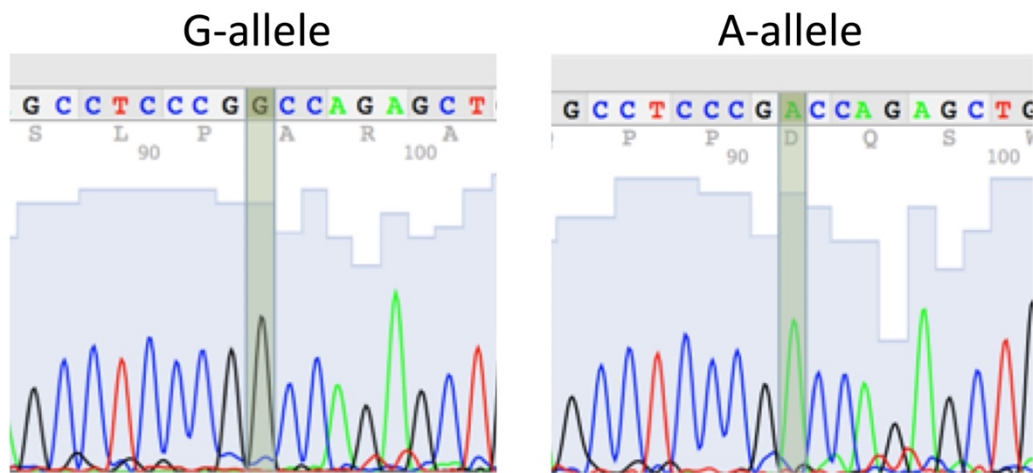
Appendix Fig S1. Generation of SNP-miR vectors.

Sanger sequence profiles of the miR-143/145 expression vectors utilized in the experiments shown in Fig 5.
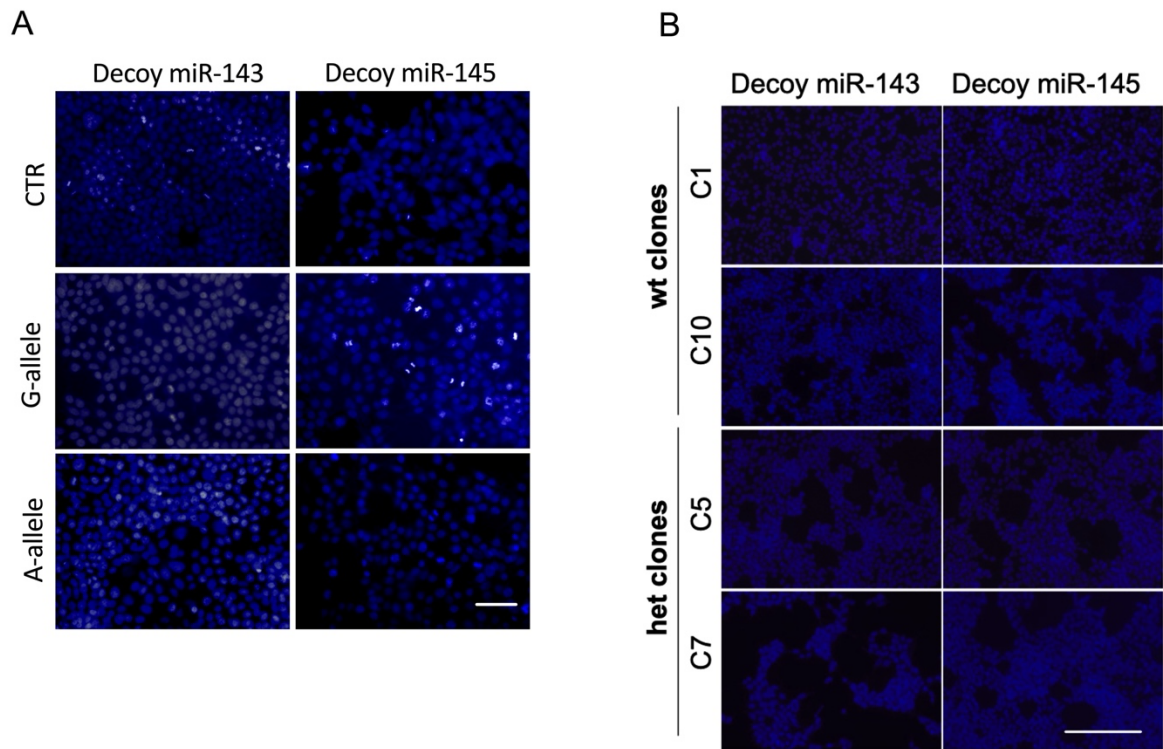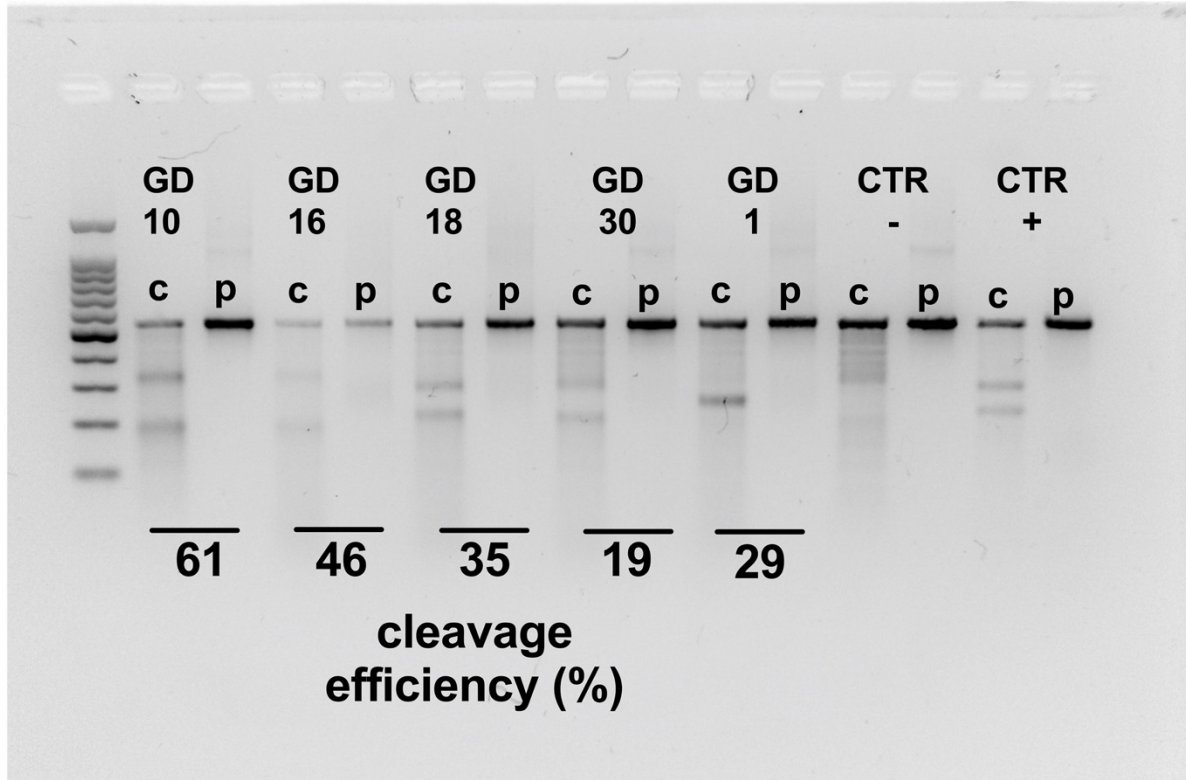
**Appendix Fig S2. DAPI staining related to the images shown in Figures 4B (A) and 5C (B)**. Scale bars: 50μm.

A

gaaacaaagaaaagaagagaaaaaaggtcaaggtttggtcctggggtgctc<u>aaatggcagg</u>
<u>*CCA*cagacaggaaacacagttgtgaggaattacaacagcctcccg**G**ccagagctggag</u>
<u>aggtggagcccaggtcccctctaacaccccttctcctggccaggttggagtcccgccacagg</u>
<u>ccaccagagcggagca</u>**GCGCAGCGCCCTGTCT**

B

Appendix Fig S3. Generation of CRISPR/CAS9 clones.

(A) Wild-type sequence of the genomic locus including *rs41291957*. The genetic variation was introduced using an oligonucleotide for HR carrying the A-allele. The oligonucleotide sequence is underlined and includes an A instead of a G; the PAM sequence of the selected sgRNA is identified in italics but is on the opposite strand (*NGG*); the sequence of the mature miR-143 sequence is shown in bold. (B) Guide efficiency test.
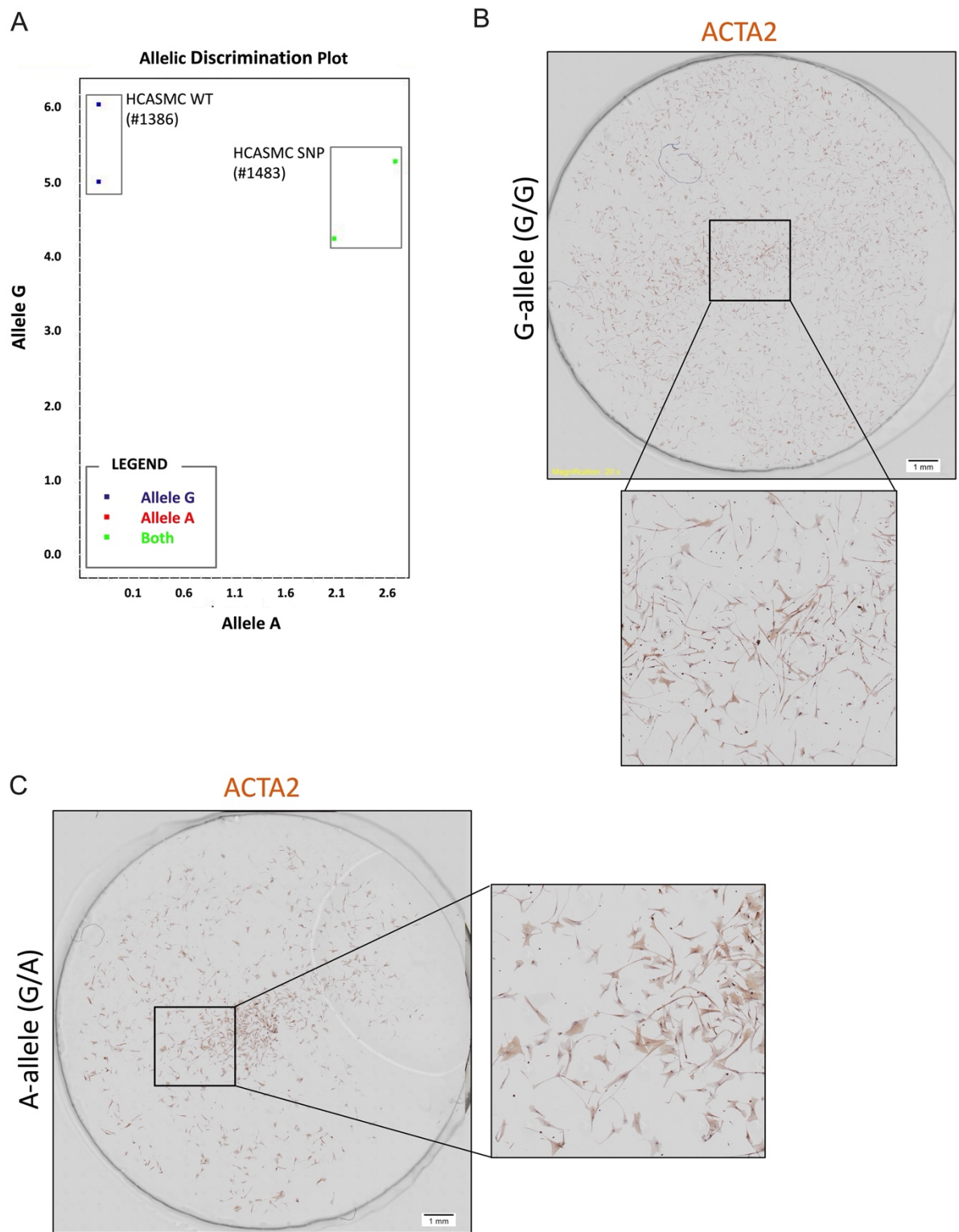
Appendix Fig S4. Allele discrimination analysis and ACTA2 staining of G- and A-allele HCASMCs.

(A) HCASMCs were genotyped also by qPCR using taqman probes. (B-C) ACTA2 staining of WT (B) and SNP (C) HCASMCs.