Supplemental Material

Supplementary figure legends

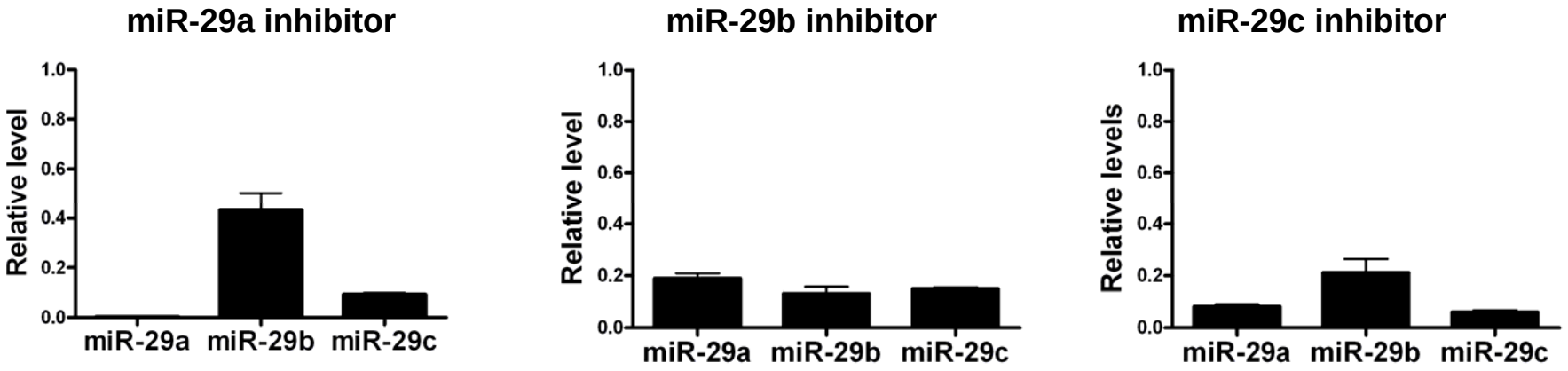
Figure I: HDF cells were treated with miR-29a-b or-c inhibitor (90nM) and RNAs were isolated 48 h post-treatment. qPCR values of miR-29abc were normalized to 5S and then compared to those in a control group, which were set as 1. Data are mean ± SEM.

Figure II: VSM or human dermal fibroblast (HDF) were treated with control mimic/inhibitor, miR-29a mimic (29a-M) or miR-29a inhibitor (29a-I) and the levels of several genes implaicted in elastic matrix biogenesis assessed by qPCR. Data are mean ± SEM, n= 3.

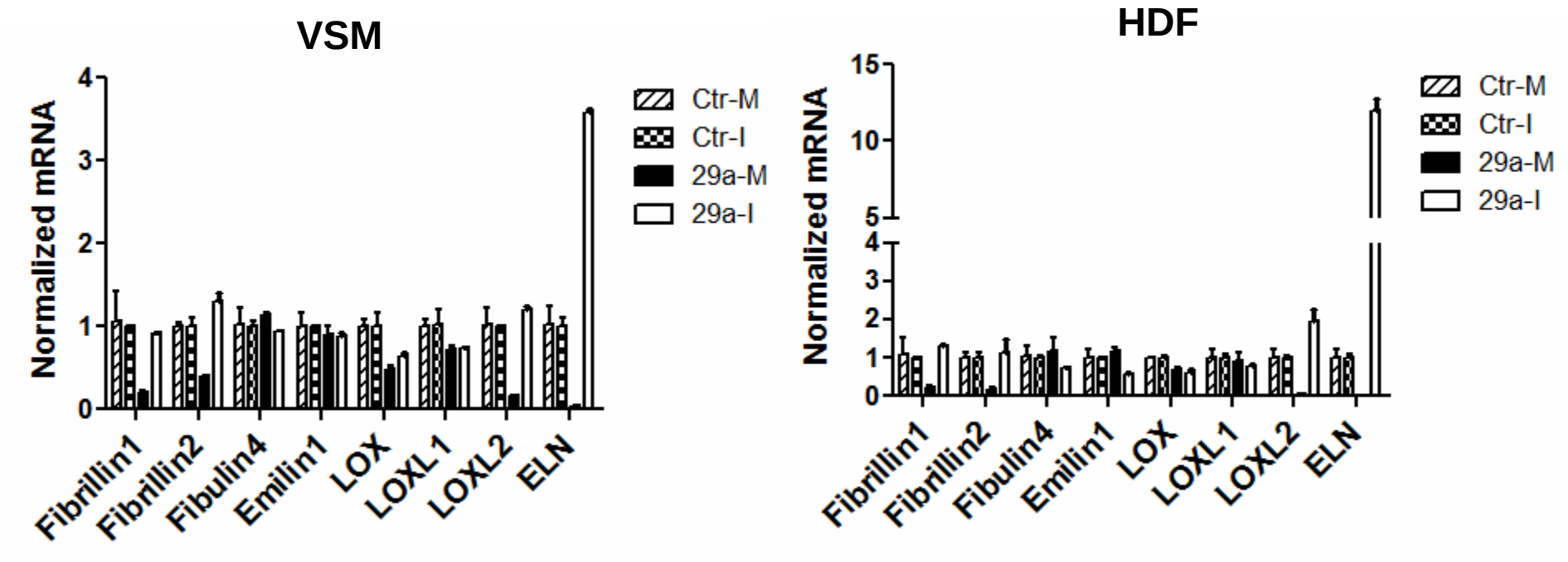
Figure III: In A, the levels of miR-29a were measured in VSM, SVAS (left panel),or WBS (donor 1, right panel). In B, the levels of miR-29a (left panel) , ELN (center panel) and COL1A1 (right panel) were measured in normal fibroblasts (NF) and an additional WBS donor.

Figure IV. Genotyping of two WBS donors.

Supplemental Figure I

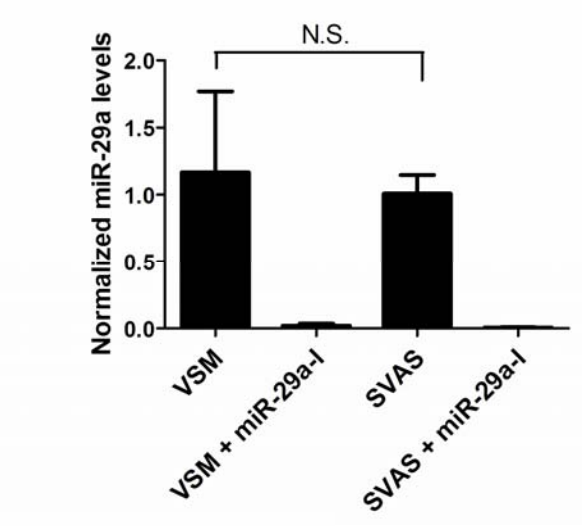


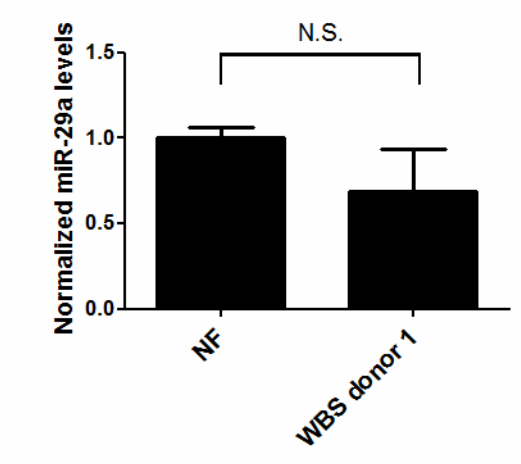
Supplemental Figure II



Supplemental Figure III

A





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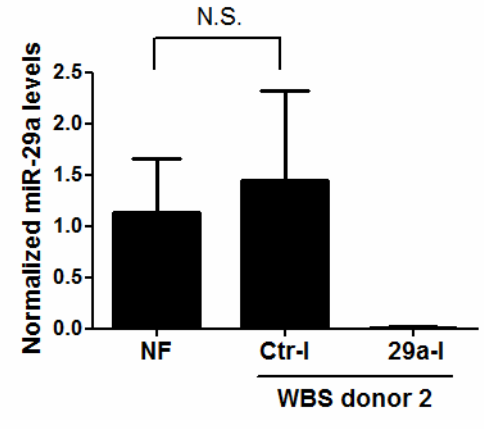

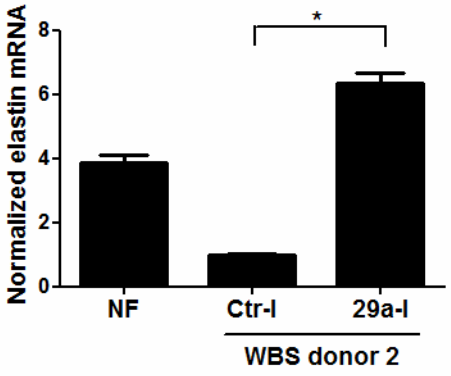

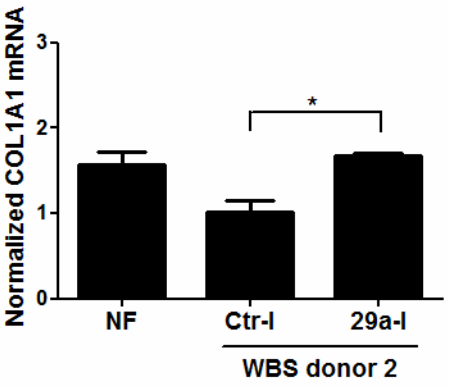

Supplemental figure IV

Method and outcome of genetic sequence of WBS specimens:

A Chromosome Microarray Comparative Genomic Hybridization (CM-CGH) test was performed on a slide with an array of 180,000 60-mer oligonucleotide probes (Agilent 180K) in Yale cytogenetics laboratory.

WBS donor 1
The analysis of signal patterns revealed an XY male with a 822 Kb microduplication at 5q12.3 (chr5:65,489,514-66,312,145, involving genes SFRS12 and MAST4) and 1.413 Mb microdeletion at 7q11.23 (chr7:72,364,314-73,777,467.NCBI36/hg18, including genes from TRIM50 to GTF2I). The 7q11.23 microdeletion is pathognomonic for Williams-Beuren syndrome (OMIM #194050).

WBS donor 2
The analysis of signal patterns revealed an XY male with a 1.413 Mb microdeletion at 7q11.23 (chr7:72,364,314-73,777,467.NCBI36/hg18, including genes from TRIM50 to GTF2I). The 7q11.23 microdeletion is pathognomonic for Williams-Beuren syndrome (OMIM #194050).