Supporting Information

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SI Materials and Methods

Mouse Strains and Genotyping. Genotyping was performed by PCR analysis using the following primers: Inv(*Nsi-Itga6*): mutant 56–134, WT 56–202; Inv(*Rel5-Itga6*): mutant 201–211, WT 201–202; Inv(*SB-Itga6*): mutant 25–202, WT 201–202; Inv(*Atf2-Itga6*): mutant 56–247, WT 201–202; Dup(*Nsi-Atf2*): 8–245; Dup(*Nsi-SB*): 8–27; Dup(*Rel5-Atf2*): 266–245; Dup(*Rel1-Rel5*): 163–87; Del(*SB-Atf2*): mutant 25–247, WT 233–235; Del(*8–13*): mutant 11–142, WT 141–142.

Primer sequences are listed below:

8: 5′-AAACGCATTTCTAAATCTTTGGT-3′,
11: 5′-CCAAGAACTTGCAGGGACATCTAGC-3′,
25: 5′-GTTTTCCCAGTCACGACGTTG-3′,
27: 5′-GTGCCGGAAACCAGGCAAAGC-3′,
56: 5′-CCGTCCAATGTGCGTGTTTTCC-3′,
87: 5′-GGCTGCTTTGGACAATGCTGG-3′,
134: 5′-GAGTTTCTCTTTGCTGTAATGAAGAGCTG-3′,
141: 5′-TGGAACAGAGAGCAAGGACG-3′,
142: 5′-AGTGTGGCCCTAAACGAAGG-3′,
163: 5′-GAGATTTTCATAACCCTGGATGCC-3′,
201: 5′-GACAGACTCTGTTAAATGCTGGCACAG-3′,
202: 5′-GCAAGCCACTTGGAAACAACTGTTAATGG-3′,
211: 5′-GGGAGTTACACCCCTCTTCACAC-3′,
233: 5′-GACAATCGTATGCATGGCATACTCGG-3′,
235: 5′-GATAGGAGTGACATTCAGACACGGC-3′,
245: 5′-GATAAGAGGTATGGGCTTAGGGTACG-3′,
247: 5′-GCCACTGGCCGAATATTACCTATTTTGTG-3′, and
266: 5′-AGCCCAACAGGGACTTTCCG-3′.

In the case of duplicated alleles, we discriminated between homozygous and heterozygous embryos by quantifying copy numbers of the mutant alleles by quantitative PCR using a primer pair mapping within the *LacZ* coding sequence in the reporter gene associated with the duplication (5′-ATCAGGATATGTGGCGGATGA-3′ and 5′- TGATTTGTGTAGTCGGTTTATGCA-3′).

Chromosome Conformation Capture Data Analysis. Quantitative differences in chromosome conformation capture interaction profiles were calculated using TAS software. Each interaction profile was normalized with input DNA and mismatch probe values. For each genotype and viewpoint, two replicate samples were processed. For the comparison of WT and Dup(*Nsi-SB*) intensities, datasets were normalized in parallel and scaled to equal median intensities. Differences in signal intensities between Dup(*Nsi-SB*) and WT profiles were considered significant for intervals displaying a P value lower than 0.001 over a minimal window of 100 bp (Wilcoxon signed-rank test). Arrowheads in Fig. 7 highlight a subset of these intervals.