Chromatin protein complexes involved in gene repression in lamina-associated domains

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APPENDIX

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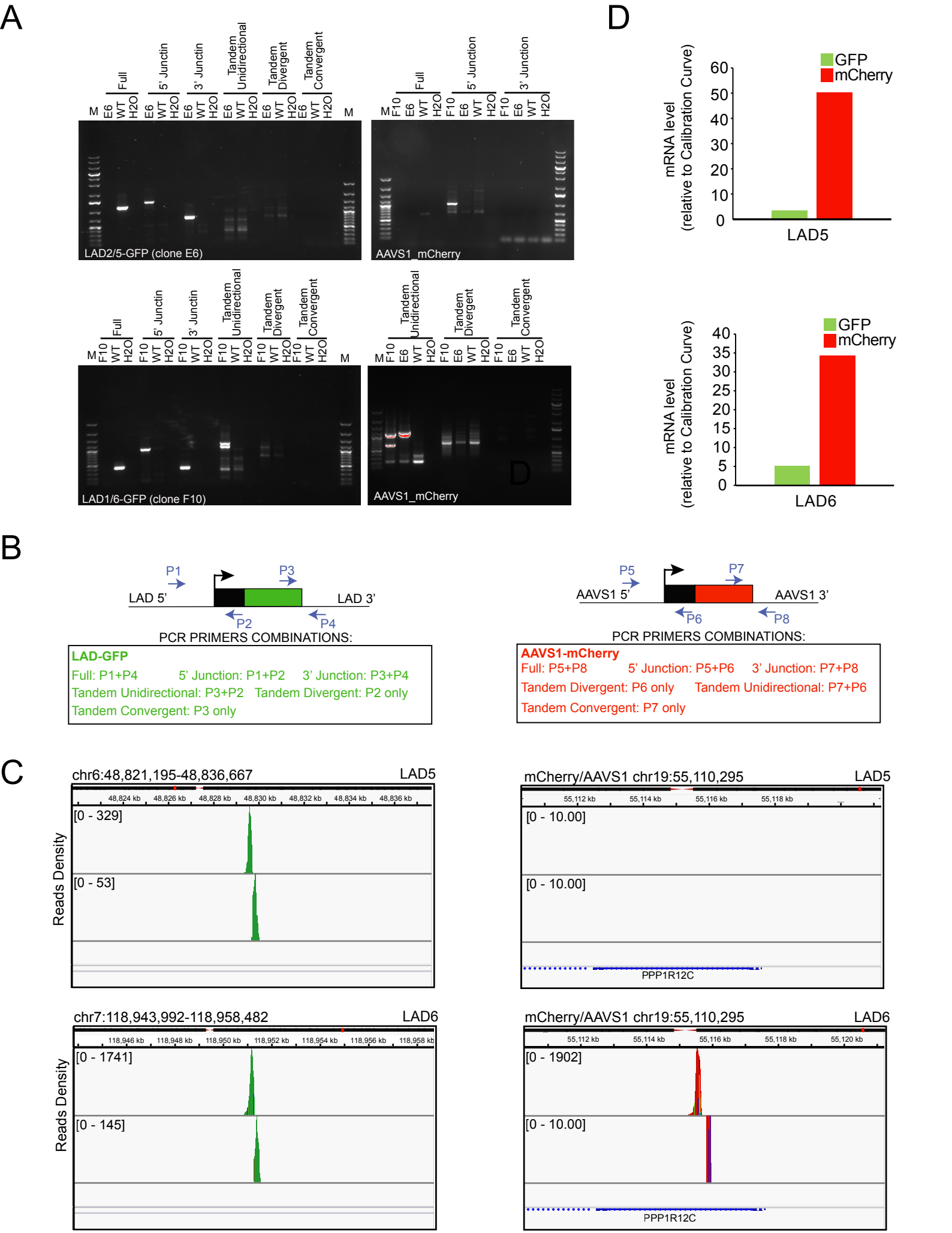
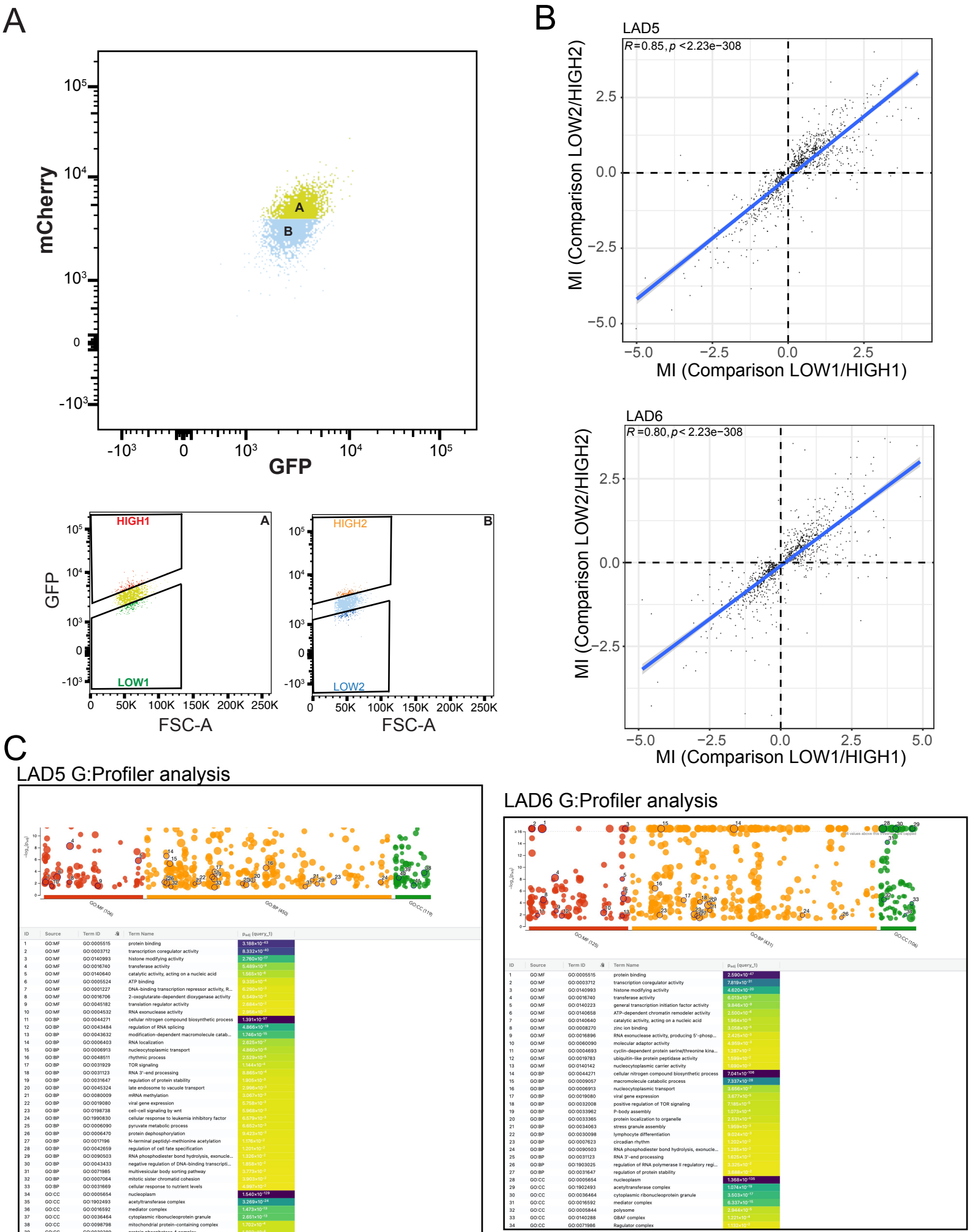
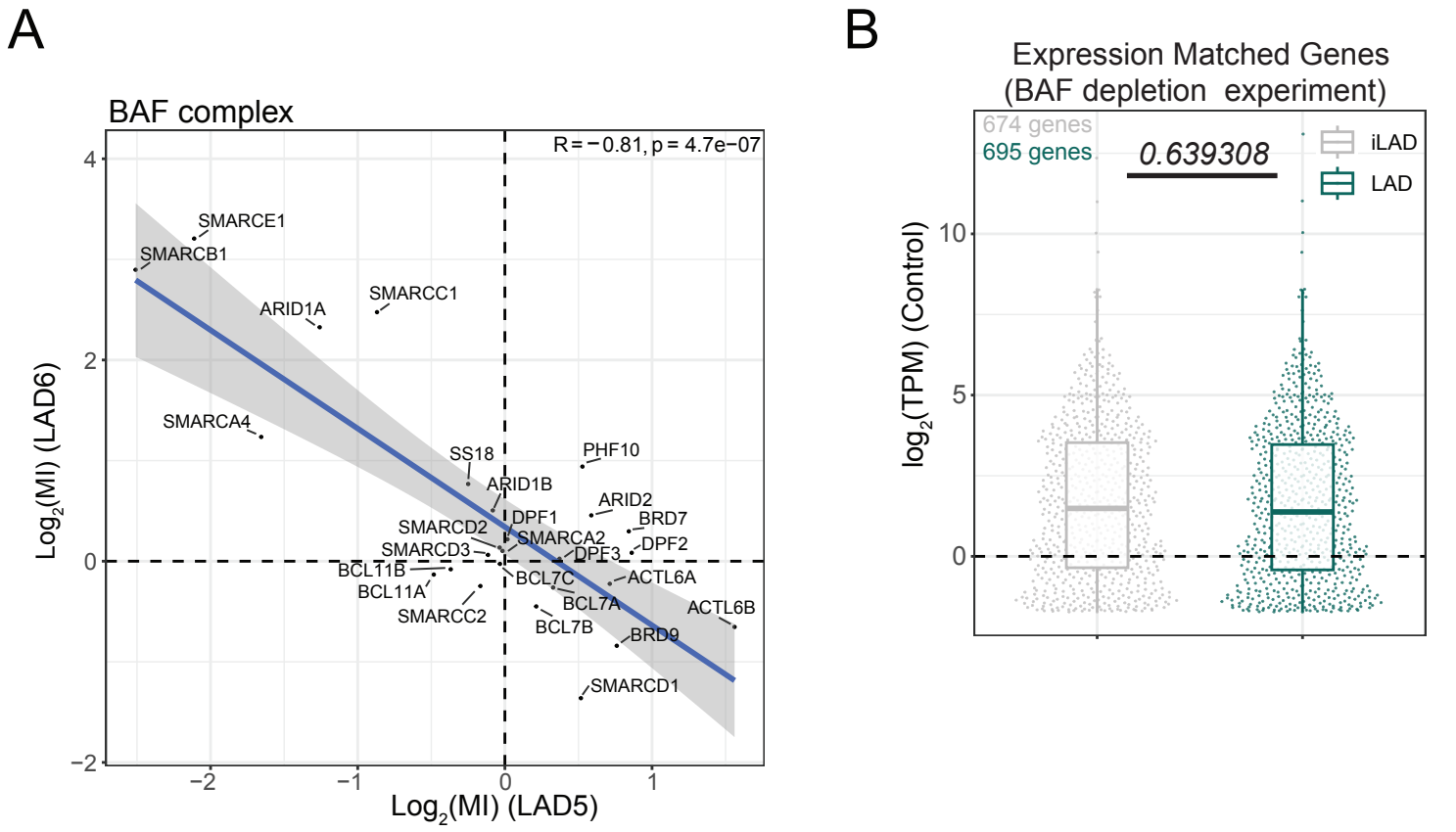


Appendix Figure S1 A) Genotyping PCR for GFP and mCherry reporters in the selected genomic locations. Genomic DNA from wild-type HAP1 cells was used as negative control. B) Schematic of all primer combinations used in the genotyping PCR. C) Tag-Map reads around integration sites for LAD-GFP reporters and AAVS1-mCherry. D) mRNA level for GFP and mCherry for the two LAD-reporter cell lines. mRNA levels were calculated by interpolating qPCR CT values on a calibration curve generated with GFP and mCherry plasmids to intrinsically normalize for primer efficiency.



Appendix Figure S2. A) Sorting strategy for the screen. Gene-trapped cells were divided in two bins according to mCherry fluorescent intensity (subgroup A and B, top panel). Each subgroup was further sorted according to GFP intensity (HIGH vs LOW, bottom panels). FSC-A is forward scattering area used for gating. B) Correlation plot between mutation indexes for significant hits (fcpv < 0.05) for LOW1/HIGH1 comparison vs LOW2/HIGH2 comparison (see also figure 1C) for GFP reporters. The blue line represents a linear model, Pearson correlation and P values are shown in the plot. B) G:Profiler analysis (Kolberg et al., 2023) for regulators of GFP reporters for LAD5 and LAD6 cell lines.



Appendix Figure S3 A) Correlation of LAD5 and LAD6 MIs from the screen for all subunits composing the BAF complex (cBAF and pBAF). The blue line represents a fitted linear model; Pearson correlation and P values are shown in the plots B) Gene expression levels for expression-matched LAD and iLAD genes in the BAF depletion experiments. Data are from Schick et al. 2019, and are the results from three biological replicates.

A

Jaeger et al Nat gen 2020

degron	MED1	MED6	MED10	MED12	MED14	MED26	MED28	MED31
up	0	78	12	0	67	0	0	0
down	3232	0	70	1	3046	0	6	0

Appendix Table S1. A) Number of differentially expressed genes following acute depletion of 8 different Mediator subunits (Jaeger et al., 2020)