Figure S1. Additional controls. Heterozygosity for Cul-4 (B: Cul-4^{G1-3/+} pnr-GAL4, UAS-RNAi-mi/+ or for l(2)dtl (C: l(2)dtl^{f022613}+/; pnr-GAL4, UAS-RNAi-mi/+ alleles or expression of a RNAi directed against l(2)dtl (F: pnr-GAL4, UAS-RNAi-Rac2/l(2)dtl^{f022613}) suppress {minus} mutant bristle size reduction phenotype (A: pnr-GAL4, UAS-RNAi-mi/+), confirming the specificity to UAS-RNAi-mi. Expression of RNAi-Rac2 with the pnr-GAL4 driver results in a quasi-absence of microchaete and an absence of dorso-anterior macrochaete in the notum central part (E: pnr-GAL4, UAS-RNAi-Rac2/UAS-GFP). These phenotypes are not suppressed by heterozygosity for Cul-4 (F: pnr-GAL4, UAS-RNAi-Rac2/Cul-4^{G1-3}) or for l(2)dtl (C: pnr-GAL4, UAS-RNAi-Rac2/l(2)dtl^{f022613}) alleles or by expression of a RNAi directed against l(2)dtl (F: pnr-GAL4, UAS-RNAi-Rac2/l(2)dtl^{f022613}-1), ruling out that Cul-4 or l(2)dtl dosage reduction simply affects the RNAi pathway and abrogates GAL4-UAS-RNAi-mi function.
Tables S1-S4 are available for download at http://www.genetics.org/content/suppl/2011/11/18/genetics.111.136689.DC1 as excel files.

Table S1  Detailed results of the UAS-miRNA screen.
Nomenclature: P/R miRNA name@ landing site with P= pUASP.attB-SLIC and R=pUASP.attB-SLIC. Used landing sites are Fb= M(3xP3-RFP.attP)ZH-86Fb, P2= P(CaryP)attP2, P16= P(CaryP)attP16, VK= P8ac[yellow+]·attP-3B]VK00037.
UAS-(0/dsred2/GFP) - miRNA name - chromosome of insertion (X/II/III/? (not mapped)) – transgenic line.

Table S2  Collections of deficiencies used for the screen.

Table S3  A-D  Numbers of candidate genes predicted to be targeted by suppressor miRNAs and uncovered by suppressor deficiencies.

Table S4  Shortlisted candidates derived from intersecting both screens.
Genes highlighted in grey are uncovered by Df(2R)Exel7094.

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