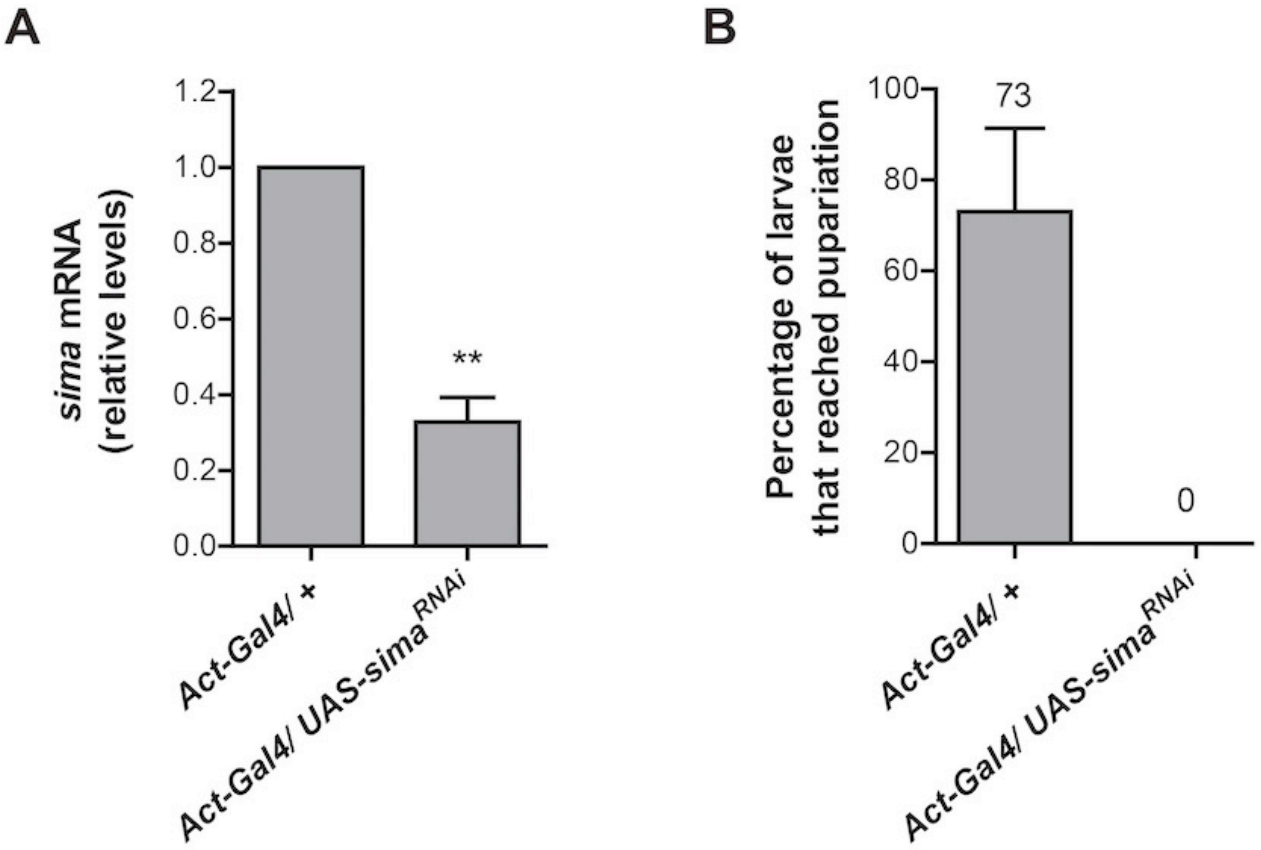
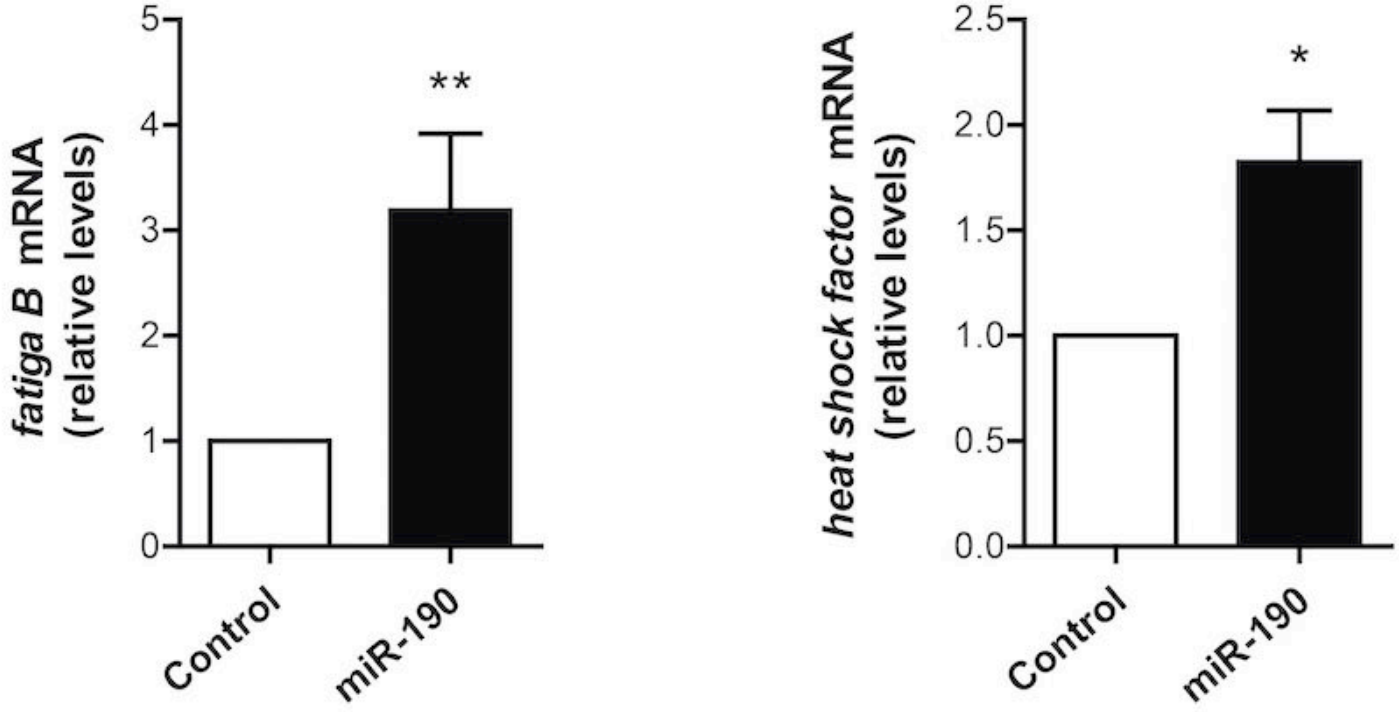
Supplemental Information

S1 Table. List of miRNAs evaluated in the screen.
A complete list of all UAS-miRNAs tested in the screen is presented.
doi:10.1371/journal.pgen.1006073.s001
(XLSX)

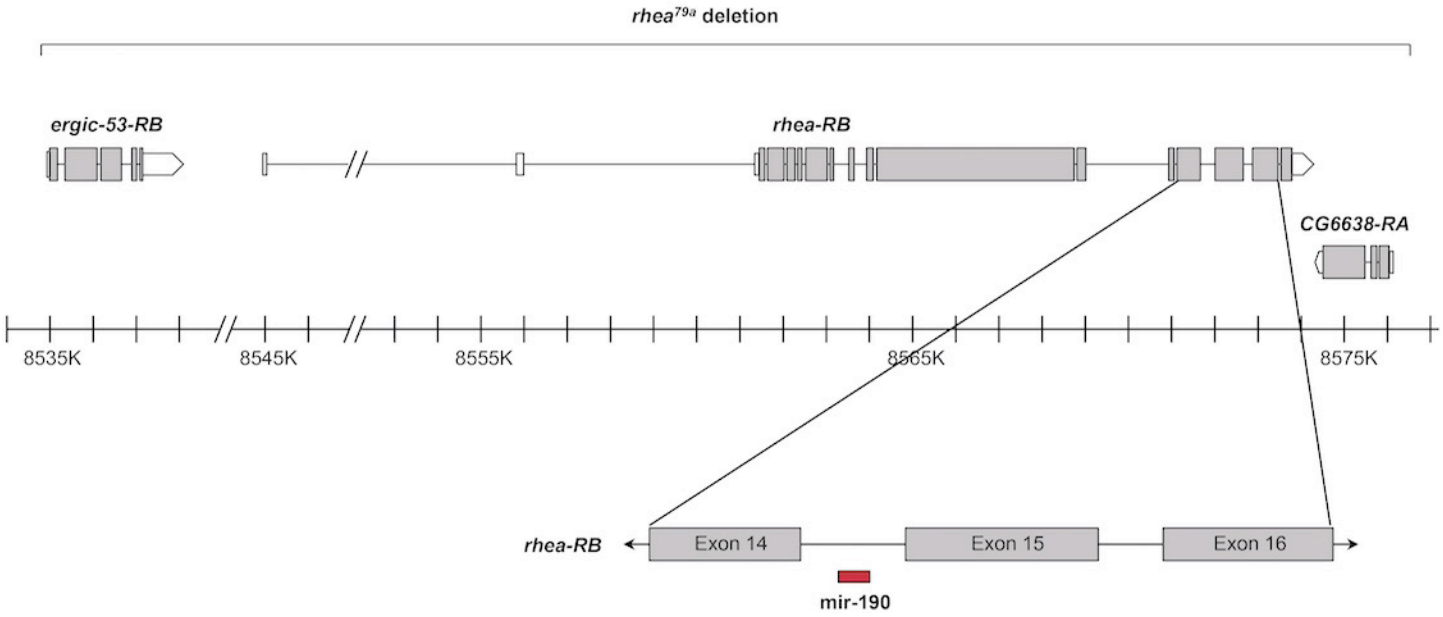
S1 Dataset. Data collection of all the figures.
doi:10.1371/journal.pgen.1006073.s007
(XLSX)



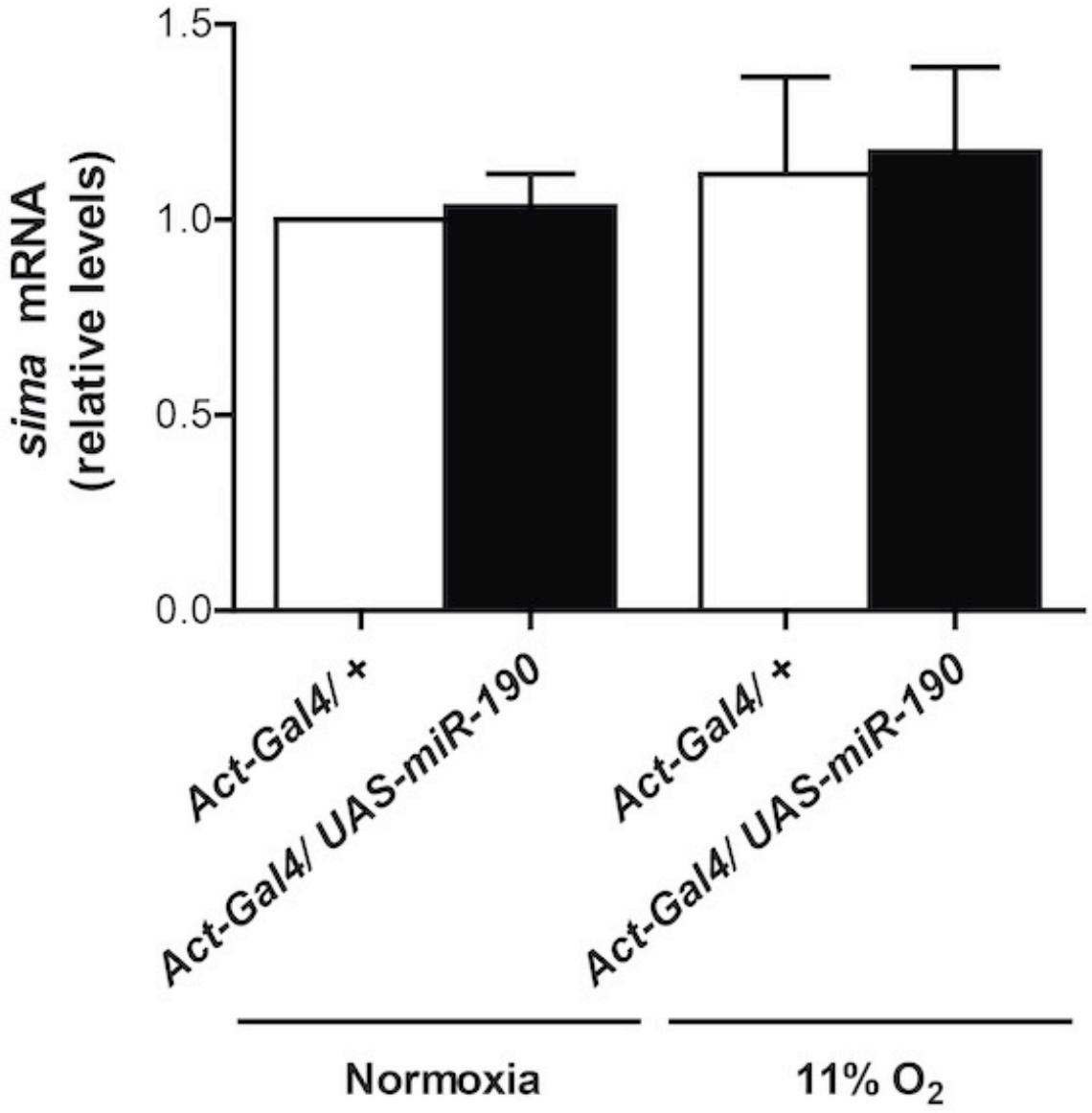
S1 Fig. Expression of sima RNAi is effective in reducing sima mRNA levels and provokes lethality in individuals exposed to hypoxia.
(A) Normoxic third instar larvae in which ubiquitous expression of sima RNAi was induced with an actin-Gal4 driver downregulated sima mRNA levels to 32% of their control siblings bearing the act-Gal4 driver only **$p<0.01$; unpaired two-tailed Student's t-test. Error bars represent SD; $n \geq 3$ per group. (B) sima silencing provoked lethality in larvae exposed to hypoxia. First instar larvae developed in normoxia that expressed sima RNAi were transferred to an incubator with 5% O2, and the number of larvae undergoing pupariation was recorded 7 days later in comparison with that of siblings exposed to the same treatment but carrying the act-Gal4 driver only. Error bars represent SD; $n \geq 20$ larvae per group.
doi:10.1371/journal.pgen.1006073.s002
(TIF)



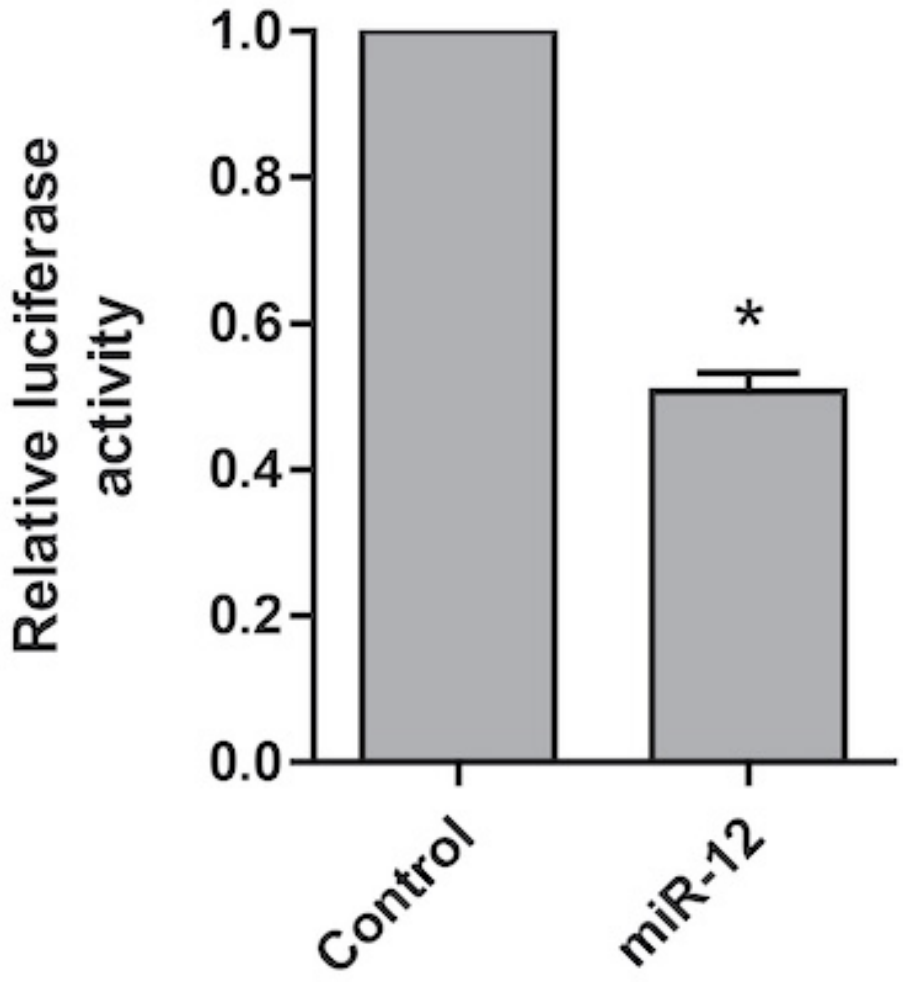
S2 Fig. miR-190 overexpression enhances induction of Sima endogenous target genes in cell culture in normoxia.
miR-190 was overexpressed in normoxic Drosophila S2R+ cells by transfection with 300 ng of a pAc-miR-190 plasmid or an empty vector as a control. Analysis by real time RT-PCR revealed that overexpression of the miRNA provoked upregulation of the endogenous Sima target genes fatiga B (fgaB) and heat shock factor (hsf). **$p<0.01$, *$p<0.05$; unpaired two-tailed Student's t-test (in FgaB quantitative RT-PCR, data were transformed using the reciprocal number to fulfill variance homogeneity criteria). Error bars represent SD; $n \geq 3$ per group.
doi:10.1371/journal.pgen.1006073.s003
(TIF)



S3 Fig. Schematic representation of the rhea locus including one of its introns where miR-190 is encoded.
Structure of the rhea-RB primary transcript is shown, along with those of transcripts of the two neighboring loci ergic-53-RB and CG6638-RA. Grey boxes represent coding exons, white boxes non-coding exons and lines introns. The region encompassing exon 14 to exon 16 of rhea-RB is amplified to show that miR-190 (red) is encoded within its intron 14. The rhea79a deletion (shown in the upper part of the scheme) covers the ergic-53, rhea and CG6638 loci.
doi:10.1371/journal.pgen.1006073.s004
(TIF)



S4 Fig. Overexpression of miR-190 does not affect sima mRNA levels.
Embryos ubiquitously overexpressing miR-190 under the control of an actin-Gal4 driver, were either kept in normoxia or exposed to mild hypoxia (11% O2) for 4 h. miR-190 overexpression did not affect sima transcript levels as compared to control embryos bearing the act-Gal4 driver only, as assessed by real time RT-PCR. Error bars represent SD; n ≥ 3 per group.
doi:10.1371/journal.pgen.1006073.s005
(TIF)



S5 Fig. miR-12-dependent downregulation of the CG10011 3'UTR reporter.
Drosophila S2R+ cells were co-transfected with the CG10011 3'UTR reporter along with a pAc-miR-12 overexpression plasmid, or an empty vector as a control. Another plasmid encoding Renilla luciferase was co-transfected for normalization. As expected, luciferase expression was strongly reduced in cells transfected with the miR-12 overexpression plasmid. *$p<0.05$; unpaired two-tailed Student's t-test. Error bars represent SD; $n \geq 3$ per group.
doi:10.1371/journal.pgen.1006073.s006
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