Genome-wide analysis suggests a differential microRNA signature associated with normal and diabetic human corneal limbus

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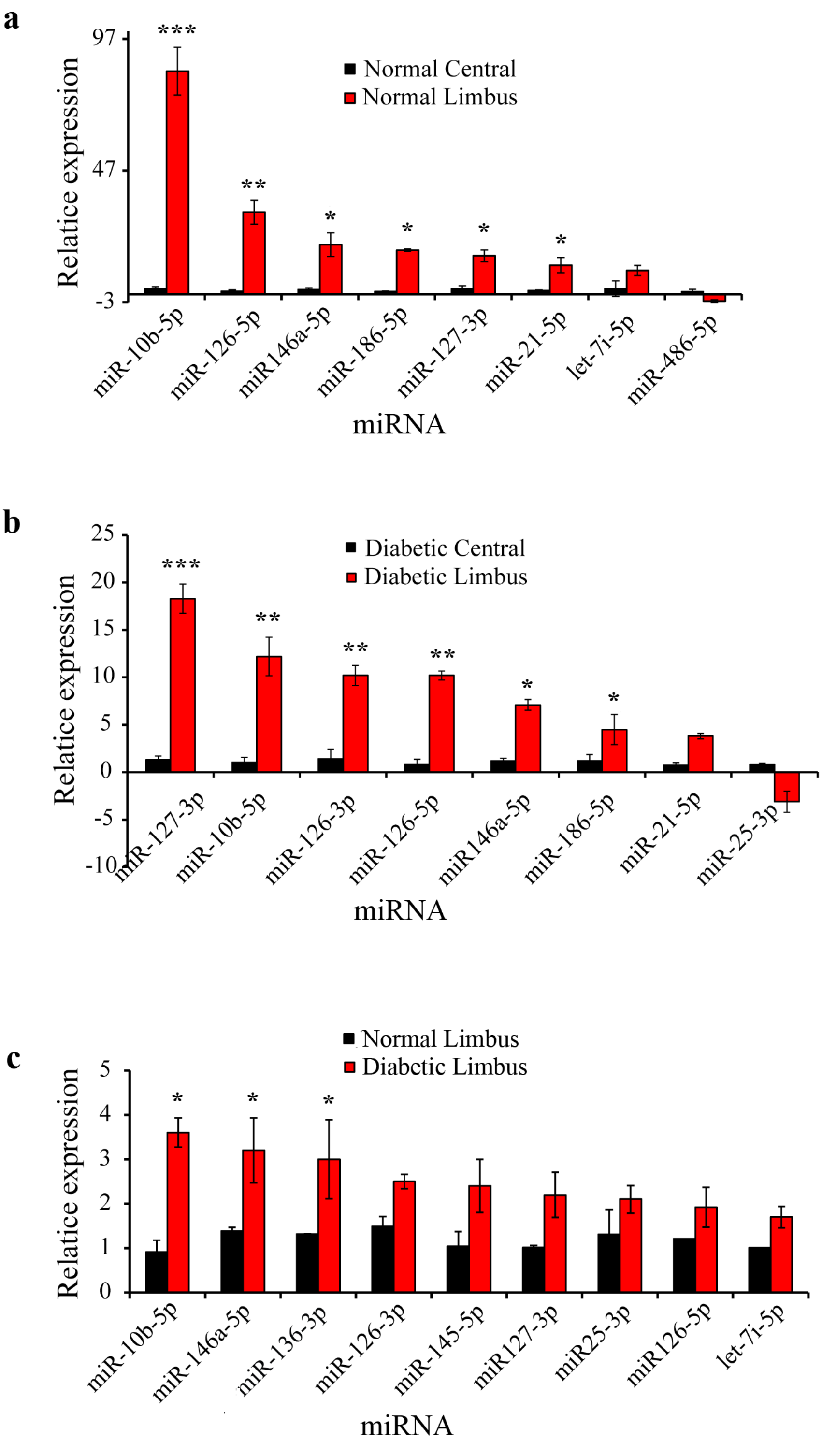
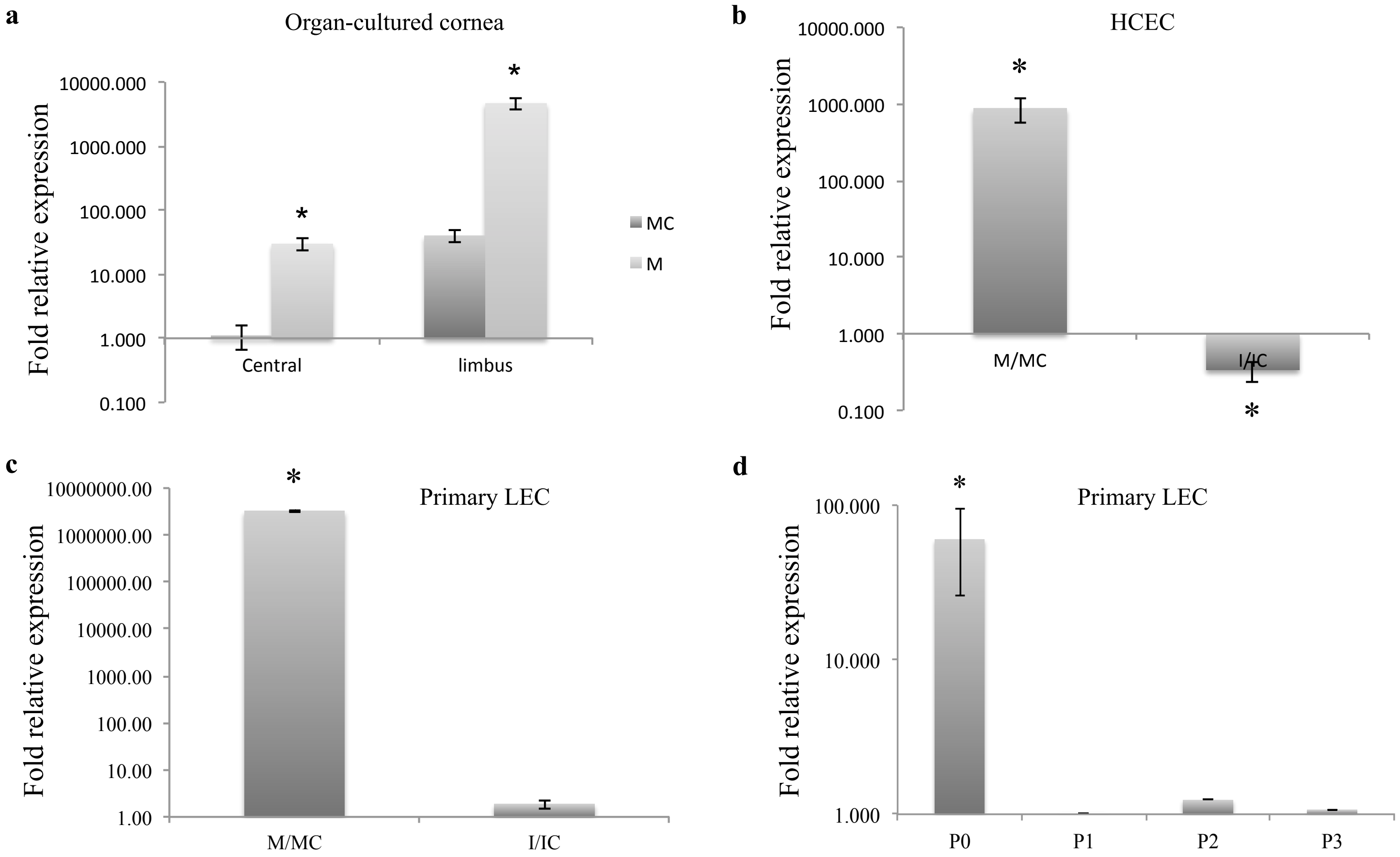


Supplementary Figure S1. QRT-PCR validation of differentially expressed miRNAs. Validation of differentially expressed miRNAs in ex vivo central cornea and limbus by QRT-PCR **(a)** Normal limbus vs. central cornea ; **(b)** Diabetic limbus vs. central cornea; **(c)** Diabetic vs. Normal limbus. Bars represent SEM of pooled values (n = 4). Each sample was run in triplicate. Signals were normalized to the U75 housekeeping miRNA run in parallel. A comparative threshold cycle (Ct) method (ΔΔCt) was used to calculate relative miRNA expression. *** $p<0.001$, ** $p<0.01$ and * $p<0.05$ by paired two-tailed t test.



Supplementary Figure S2. QRT-PCR. (**a**) miR-10b (M) significant overexpression in transfected central and limbal human organ-cultured cornea in comparison to corresponding mimic control (MC). **(b)** miR-10b significant increase or decrease in HCEC transfected with miR-10b mimic (M) or its inhibitor (I), respectively, in comparison to their corresponding controls, MC or IC. (**c**) miR-10b significant increase in primary LEC transfected with miR-10b mimic (M) in comparison to mimic control (MC), with no expression observed in MC, I or IC. **(d)** miR-10b significant expression in isolated primary LEC, not yet cultured at passage zero (P0), but no expression was observed in later passages, P1, P2 and P3 LEC.