“Deep sequencing of small RNAs from human skin reveals major alterations in the psoriasis miRNAome”

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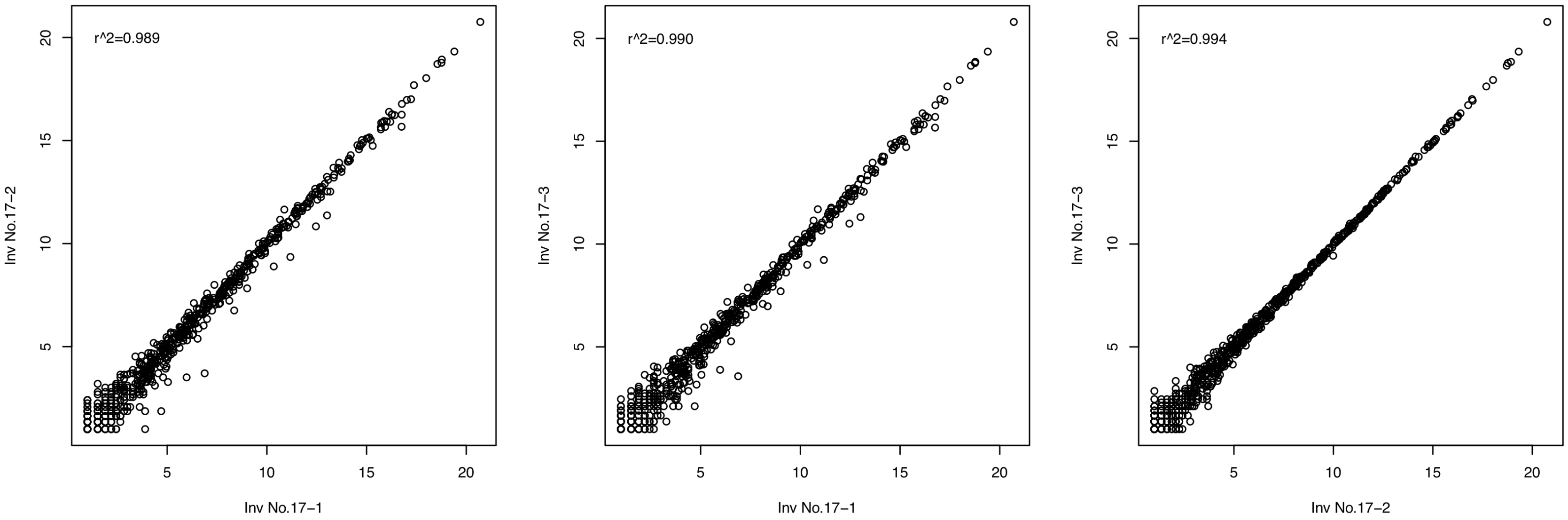
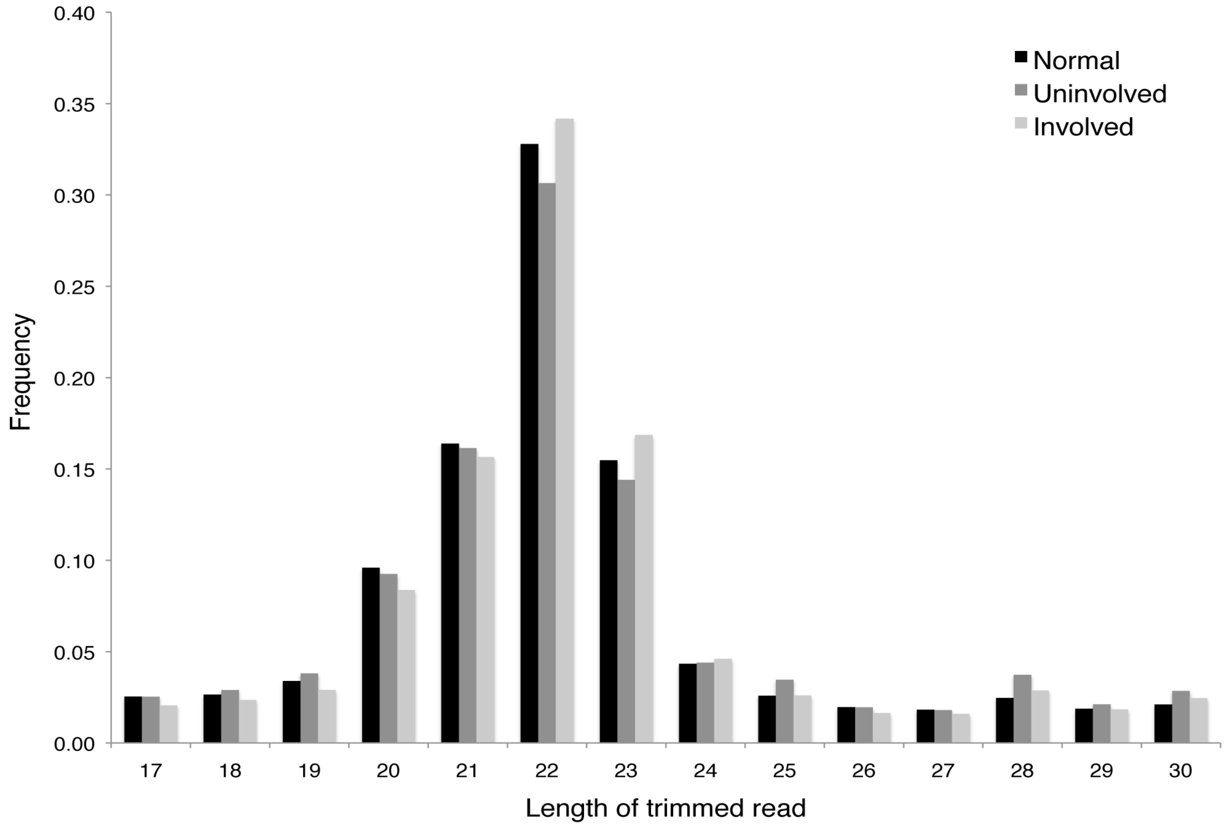
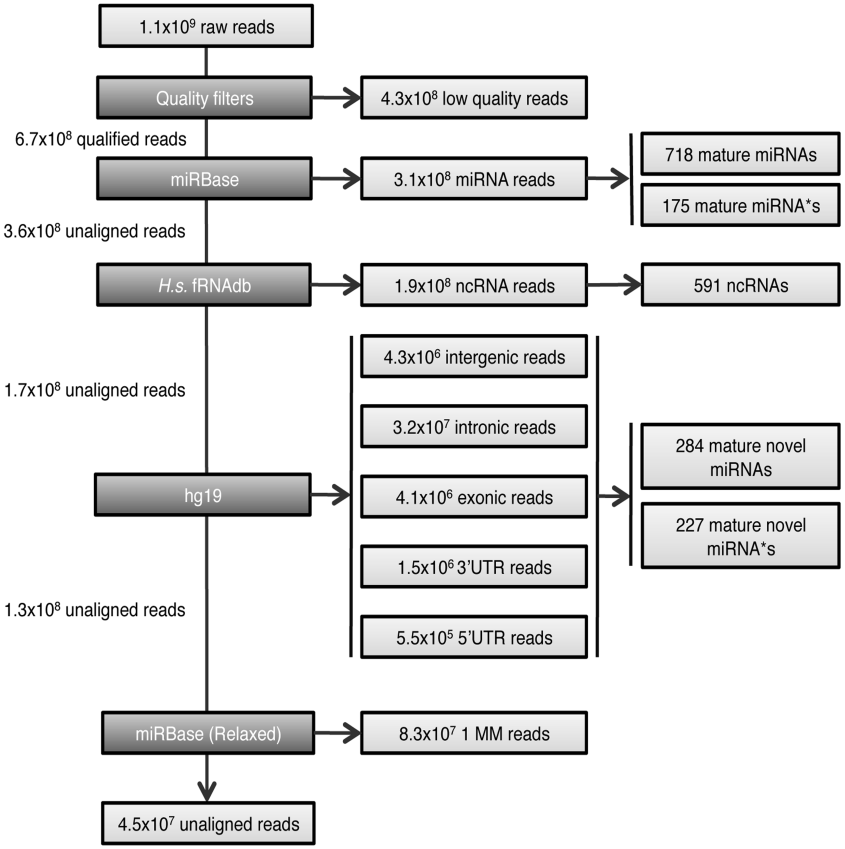
Supplementary figures and tables



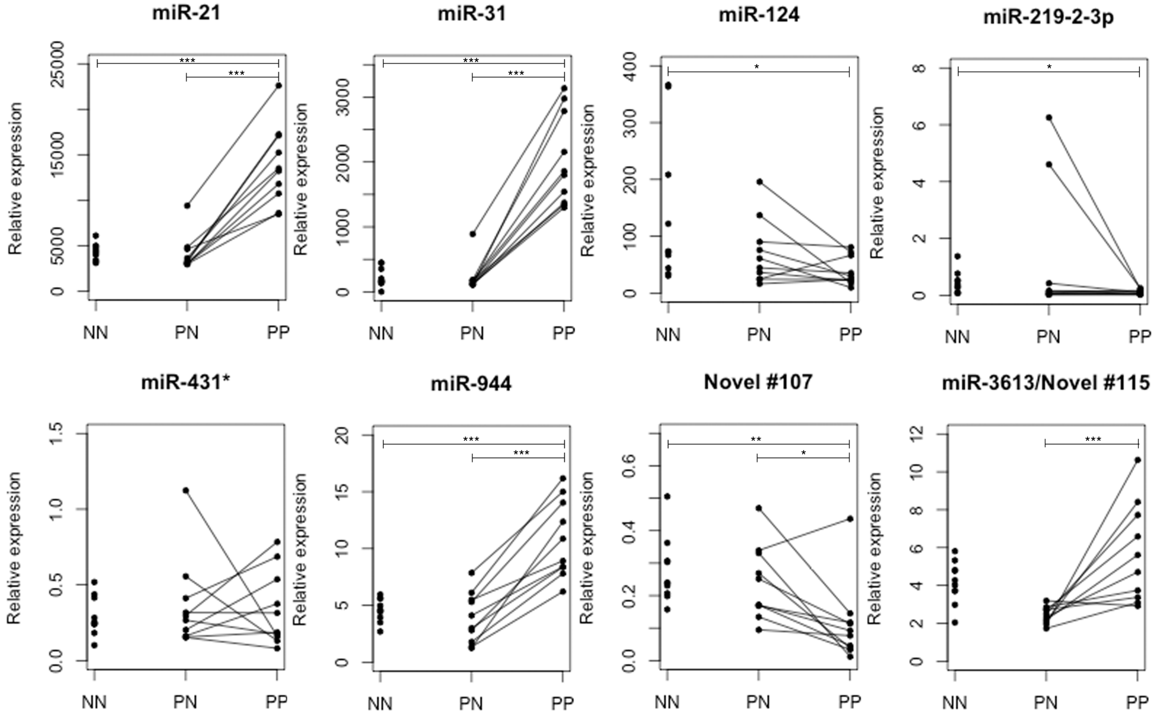
Supplementary Figure 1. Pairwise comparisons of normalized digital read counts in three technical replicates. RNA derived from a psoriatic skin biopsy "Inv #17" was prepared and sequenced independently three times. Each pairwise comparison is plotted separately. Numerical axes represent normalized digital read counts for indicated sample.



Supplementary figure 2. Length distribution of trimmed small RNA reads in normal, uninvolved psoriatic, and involved psoriatic skin.



Supplementary figure 3. Flowchart describing alignment of small RNA reads to human sequence databases. All reads aligned with zero mismatches, unless relaxed parameters are indicated (ie. 1MM=one mismatch). MiRNA* refers to mature miRNAs generated from the minor strand of the double stranded miRNA precursor. ncRNA refers to non-coding RNAs, such as tRNAs, piwi-interacting RNAs, snoRNAs, etc. in the *H. sapien* functional RNA database (see Materials and Methods).



Supplementary figure 4. Validation of differentially expressed known and novel miRNAs. qRT-PCR levels of differentially expressed miRNAs in ten NN, ten PN, and ten PP patients. Lines indicate matched uninvolved and involved samples from the same patient (***p<0.001, **p<0.01,*p<0.05). Relative expression was calculated with respect to the endogenous snoRNA Z30 (see Materials and Methods). Normal skin, NN; Uninvolved psoriatic skin, PN; Involved psoriatic skin, PP.