Comparison of miRNA/RTs

Key: ebc01 = Sabine’s prep 1 of the Ambion reference panel, ebc19 = Sabine’s prep 2 of the Ambion reference panel, eold = GSAF old prep and old sequencing run of the Ambion reference panel.

Linear scatter plots:

So it would appear that Sabine’s two preps agree with each other quite well while they do not agree well with the older prep. Since this pool should have all miRNA equally represented, but doesn’t by either method, it’s not clear what the “right answer” should be.

Log scatter plots:

5/27/11:
Analysis of log abundance (y axis) vs mir length (from 18 to 24, x axis) between Sabine’s two replicates:

![Box plot showing analysis results](image1)

and between sabine’s BC01 and the old BC20 SREk kit:

![Box plot showing analysis results](image2)

Shows some bias, but not a ton.

Significant bias for T between bc01 and bc19:

(NB: if you screen for 5’ dinucleotides without removing P2, you get a skewed result --these have a lot of P2).

Next step: any mutations at 3' end?

Any NT’s added at 5’ end?