# miRNA sequencing – early QC

sample	total reads	% map to genome	map to hsa mature miRNA seqs	% of total	annot to mature miRNA	% of total
HG00117	4,371,136	89%	142,584	3.3%	319,891	7%
HG00355	2,914,025	95%	121,710	4.2%	452,839	16%
NA06986	4,523,897	97%	209,420	4.6%	489,728	11%
NA19095	3,046,837	94%	81,426	2.7%	235,466	8%
NA20527	2,507,754	97%	79,203	3.2%	319,891	13%

These are from UNIGE samples, but similar results also from Kiel and Barcelona. We can quantify 100-300 miRNAs.

UNIGE small RNA seq

Will be rerun
-> read counts
2x
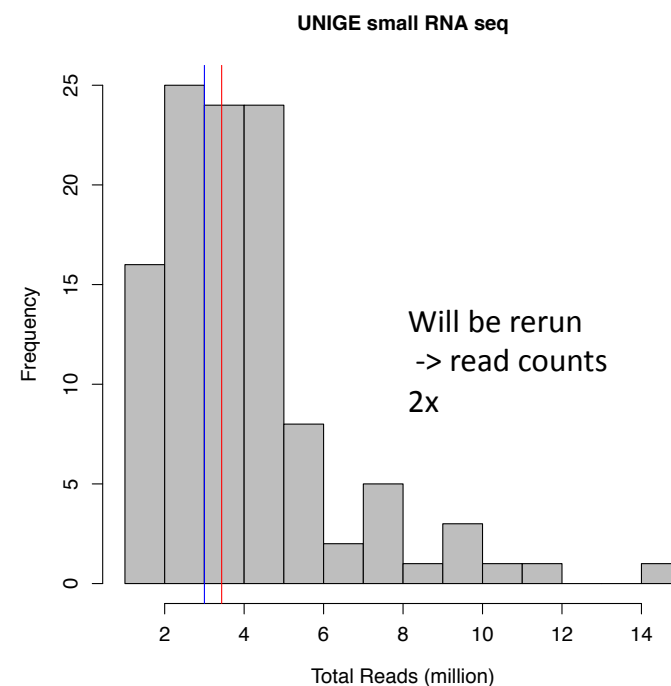
Suggestion:
- Per sample total reads >3 M **or** median total reads across the samples 6M
    - a few drop offs don't matter
- How to make sure that the reads are of normal quality for these samples:
    - trim reads to 36 bp if you have sequenced more
    - remove adaptors
        - 3 bp minimum overlap, 10% error rate, keep reads of length 14-36 bp
    - map to human mature miRNA sequences; about 2.5-5% should map, aim for >=100 000