### Agilent microarrays containing 1205 mature human miRNAs



### 104 CpG-island associated miRNA genes (126 mature miRNAs)

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#### Selection of potentially methylated miRNAs

- 1) Ranking analysis (fold change between + and DAC) per cell line
  - A) top-25 greatest DAC effect over all timepoints
  - B) top-25 greatest difference between anchorage dependent and independent cells
- 2) Identified in at least 2 out of 4 cell lines



## 45 miRNA genes (57 mature miRNAs)



40 genes

5 genes

# Infinium HumanMethylation450 BeadChip

- 1) <25% methylation in HFKs
- 2) >50% methylation in HPV-transformed cells
- 3) At least 30% increase from HFK to HPV-transformed cells



nr	miRNA gene	mature miRNA
		(identified in DAC screen)
1	hsa-mir-129-2	hsa-miR-129-2-3p
		hsa-miR-129-5p
2	hsa-mir-137	hsa-miR-137
3	hsa-mir-615	hsa-miR-615-3p
		hsa-miR-615-5p
4	hsa-mir-675	hsa-miR-675-3p
		hsa-miR-675-5p
5	hsa-mir-935	hsa-miR-935
6	hsa-mir-2277	hsa-miR-2277-3p
7	hsa-mir-3663	hsa-miR-3663-3p
8	hsa-mir-3665	hsa-miR-3665
9	hsa-mir-4281	hsa-miR-4281
10	hsa-mir-4323	hsa-miR-4323