Transcriptome Comparison Between Tiling Arrays and Next Generation Sequencing on Matched Worm Samples, Towards Making Optimal Use of Arrays

ENCODE/modENCODE Meeting 2009

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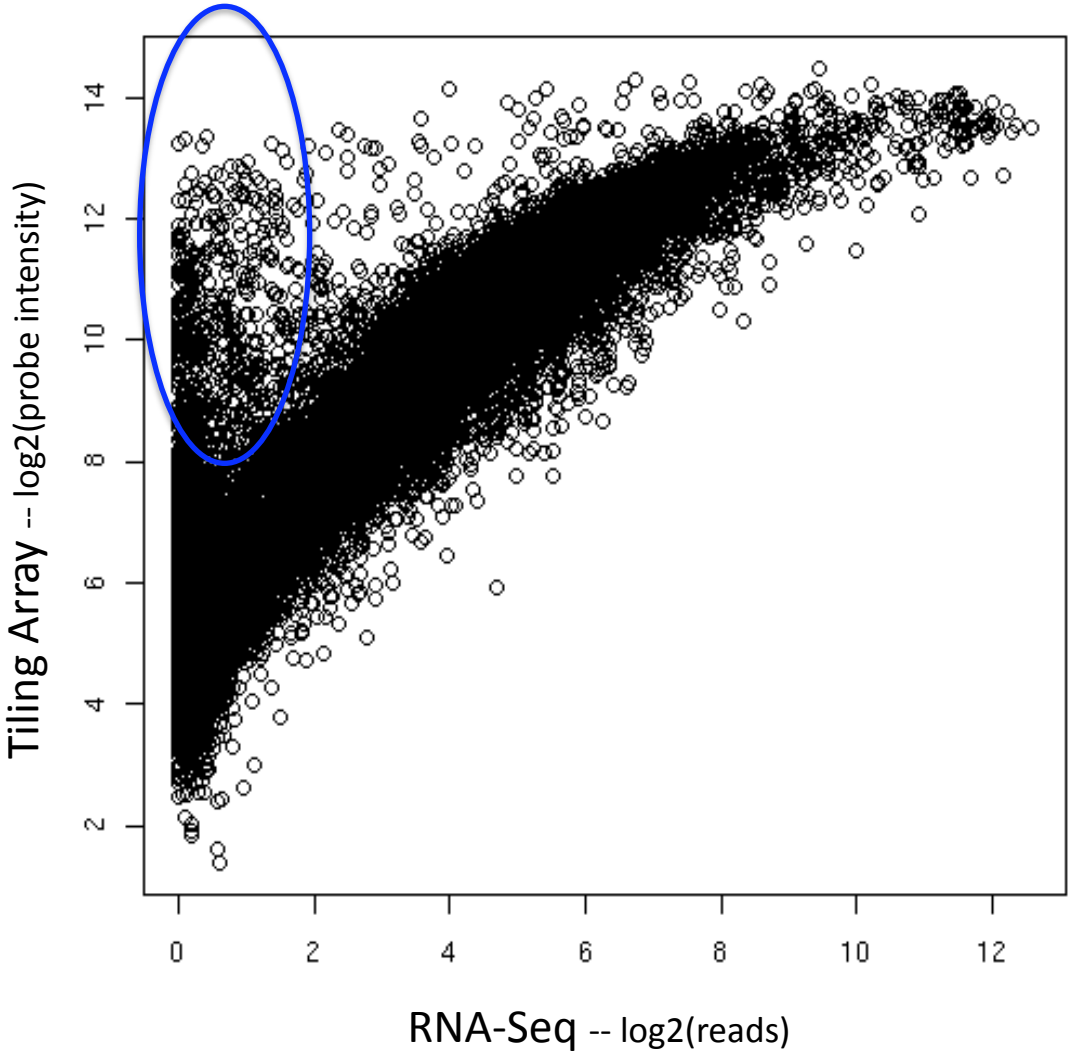
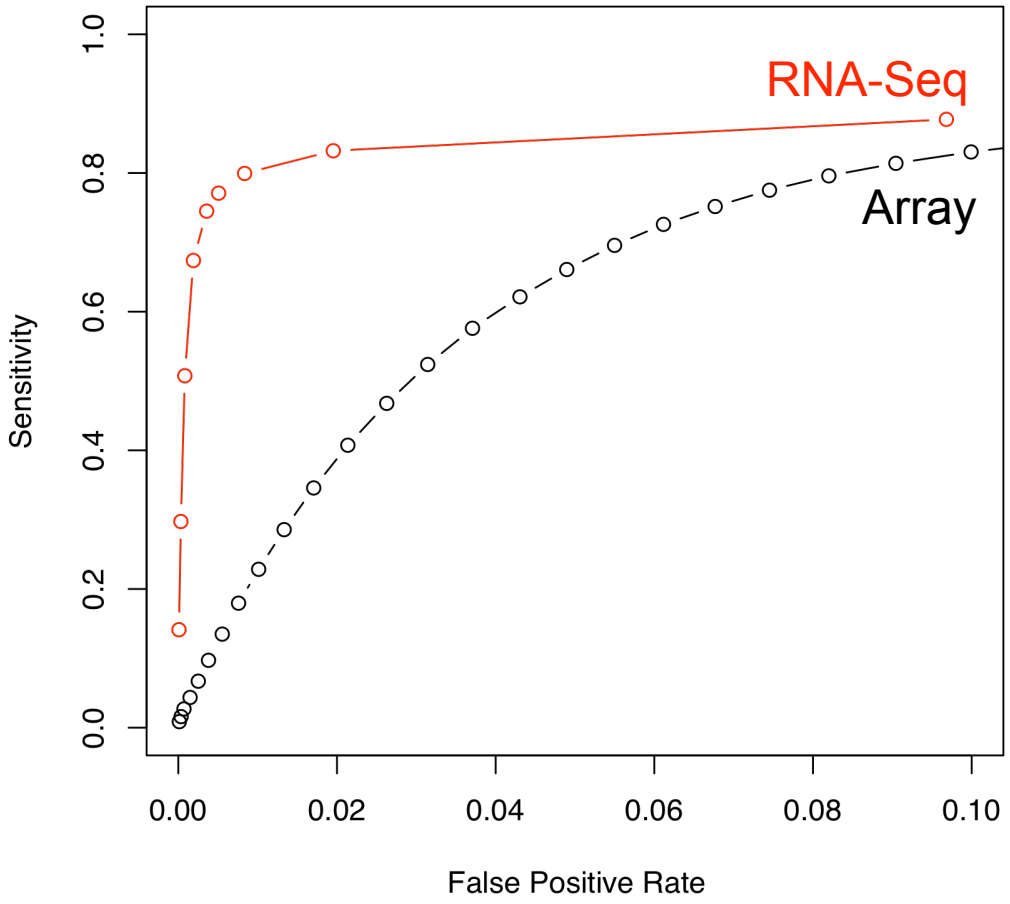
Signal Correlation of Transcribed Regions (TARs) on Matched Samples



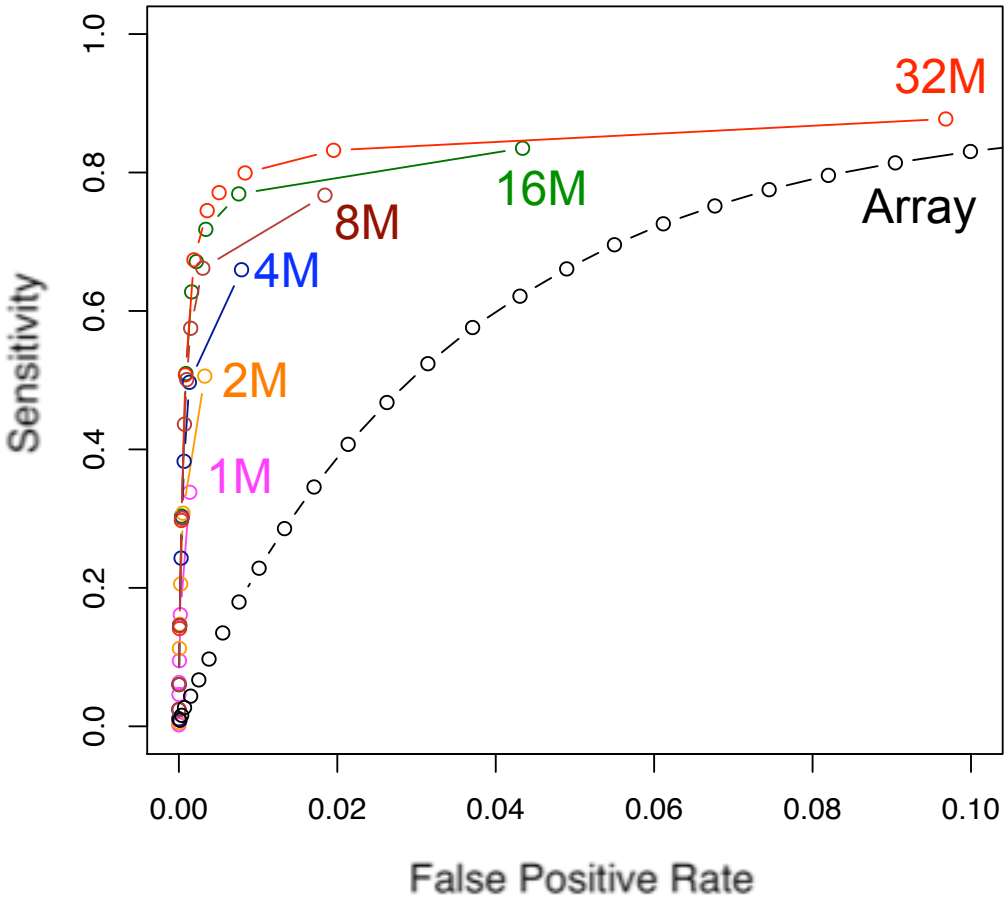
- *C. elegans* L2 larval stage
  - similar results for L3, L4, and young adult
- polyA enriched RNA
- raw signal correlation
  Spearman = 0.90
- Regions potentially affected by cross-hybridization evident

Seq vs Array: Annotation as Gold Standard

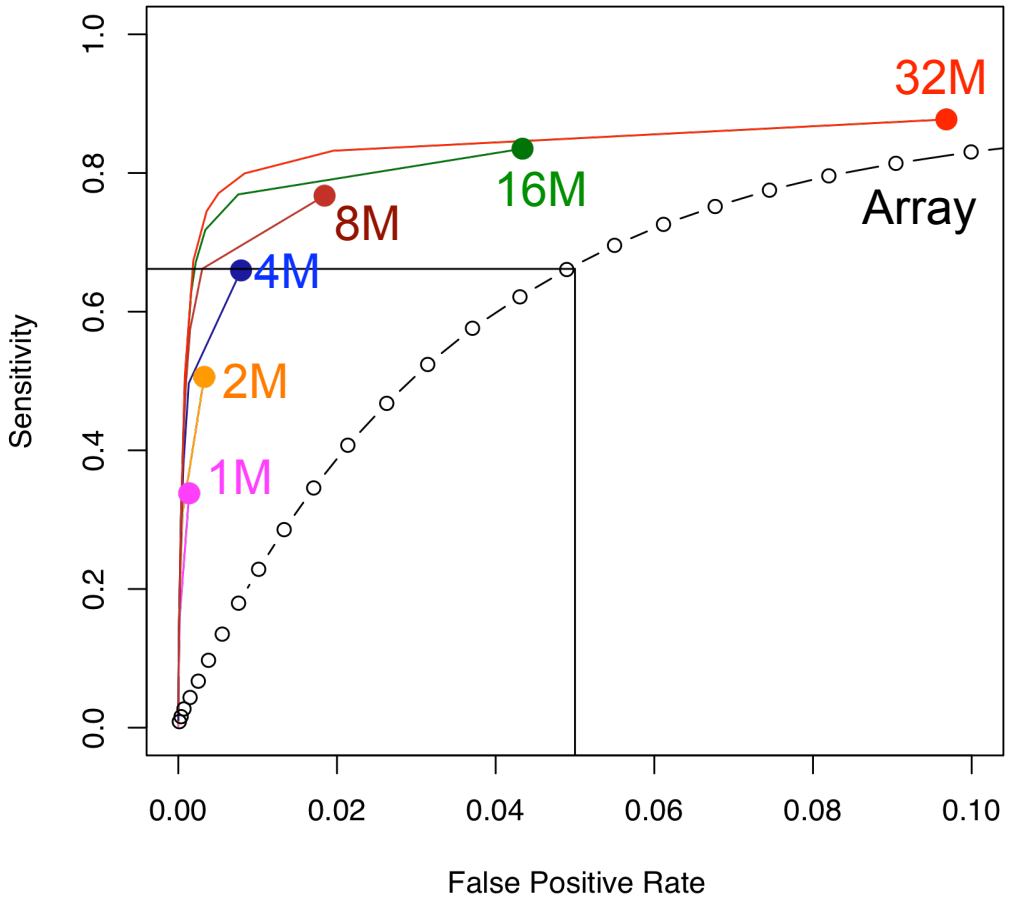


- Sensitivity and FPR substantially improved in RNA-Seq

Seq vs Array: Effect of Sequencing Depth

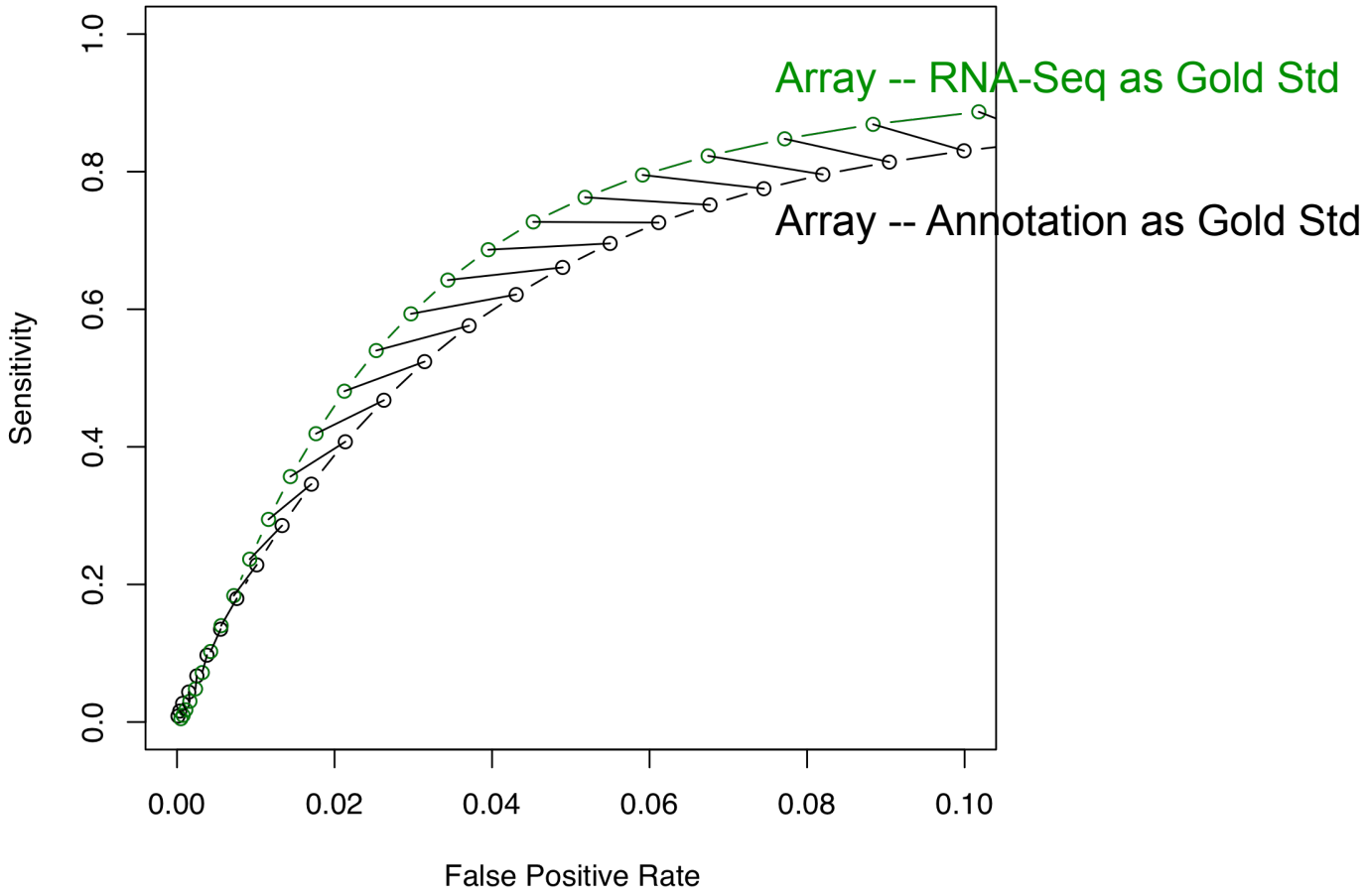


Seq vs Array: Sequencing Depth Required to Match Array



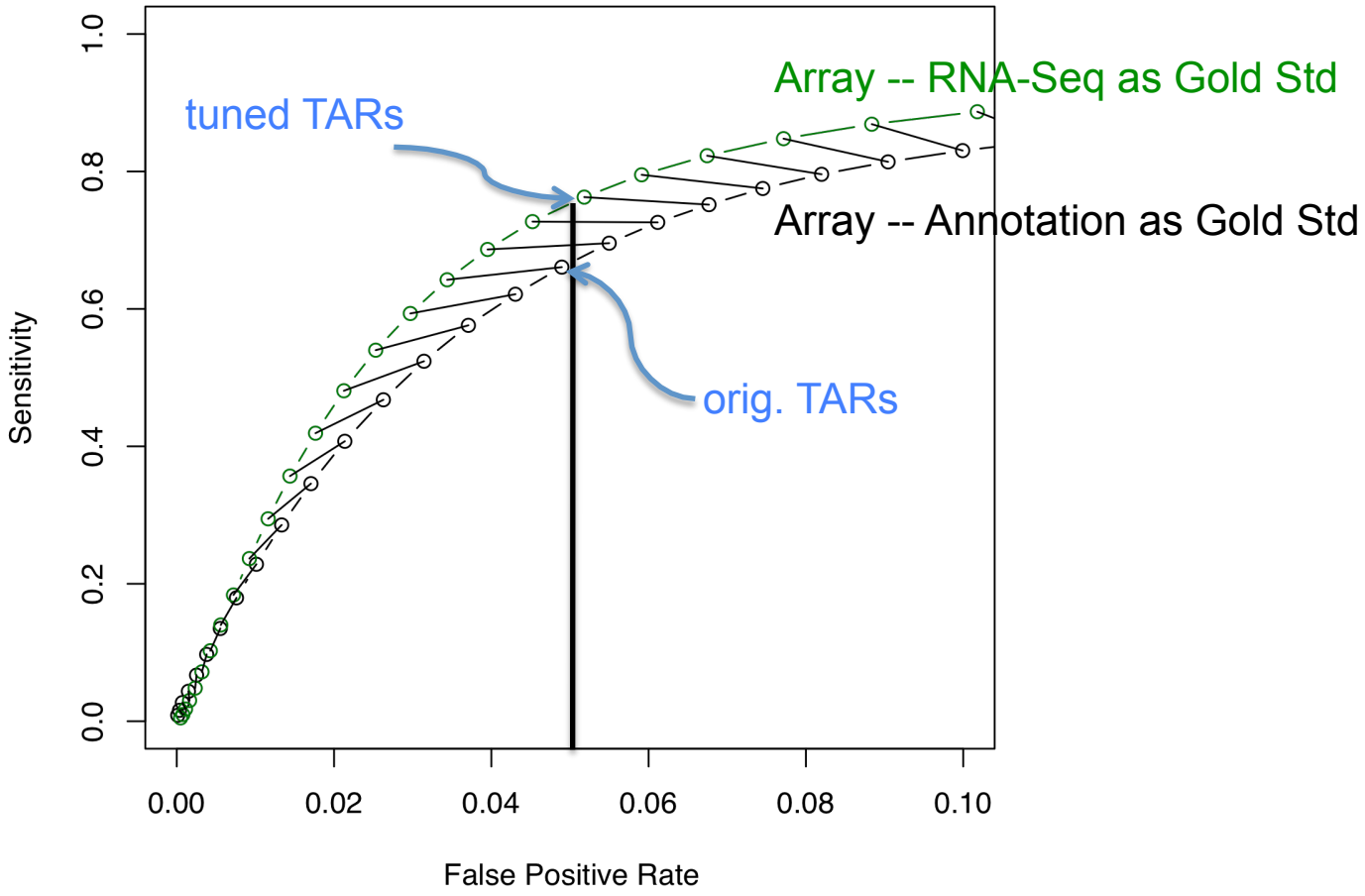
- At desired FPR of 0.05, RNA-Seq matches tiling array with 4M reads, about 1/2 lane

Array Tuning: Using RNA-Seq as Gold Std.



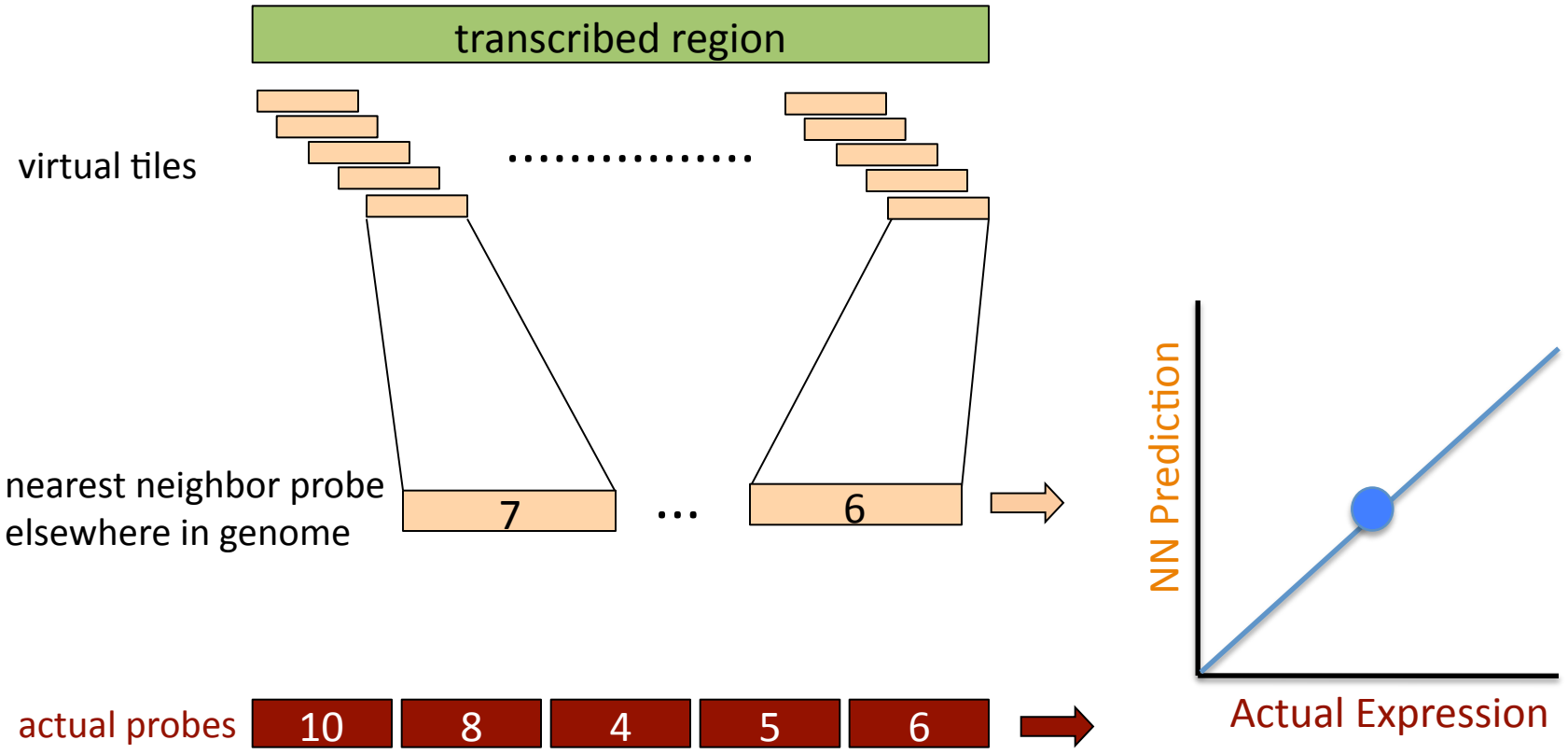
- Matched RNA-Seq data serves as a better gold standard

Array Tuning: Developing an Optimized Array Scoring System

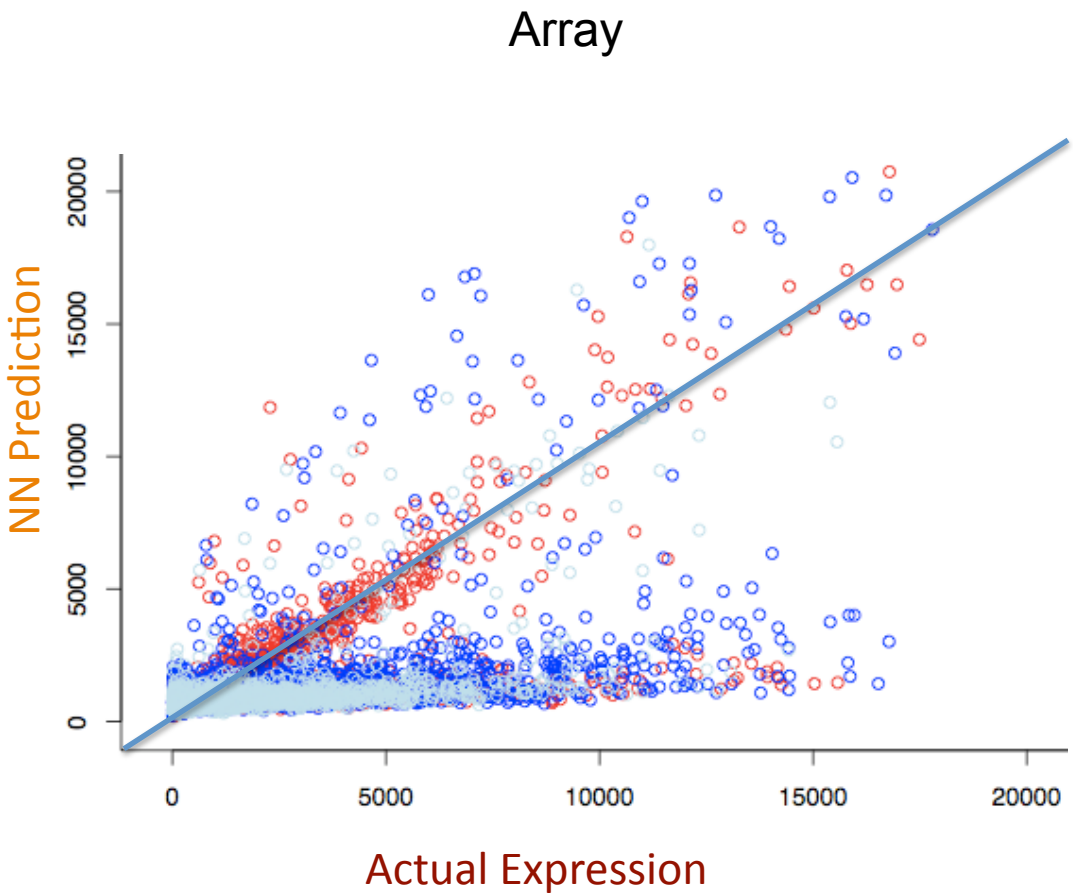


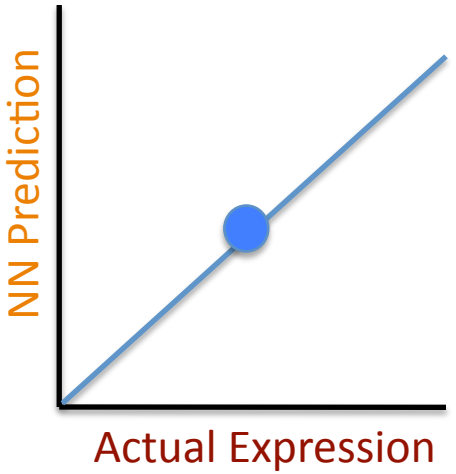
- Parameters can be tuned with knowledge of better gold standard
- This can be used to calibrate an optimal threshold and p-value for array analysis

Cross-Hyb: Developing Nearest-Neighbor Predictor



Cross-Hyb: Flagging Regions of Spurious Signal





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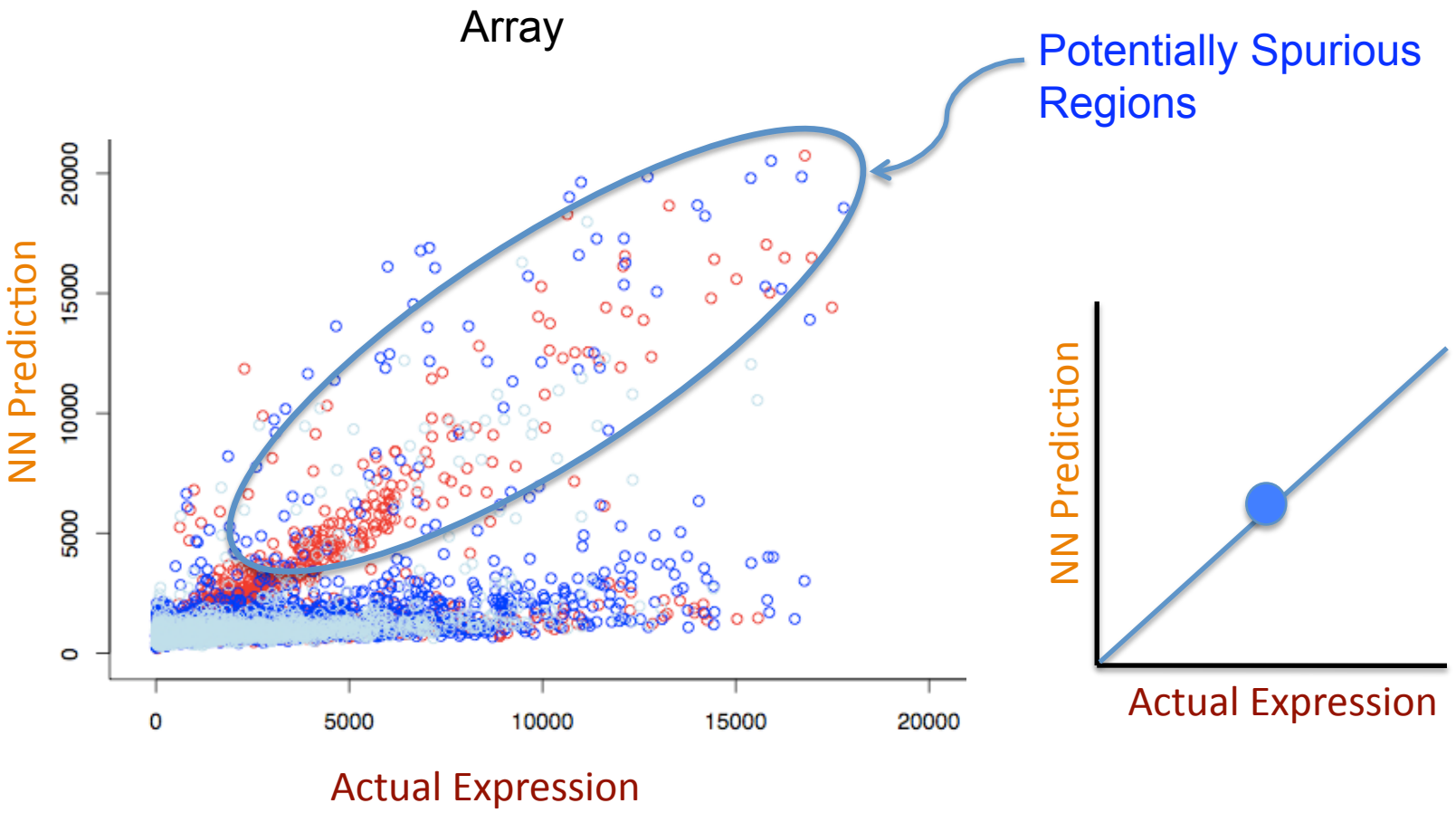

Cross-Hyb: No Spurious Signal in RNA-Seq