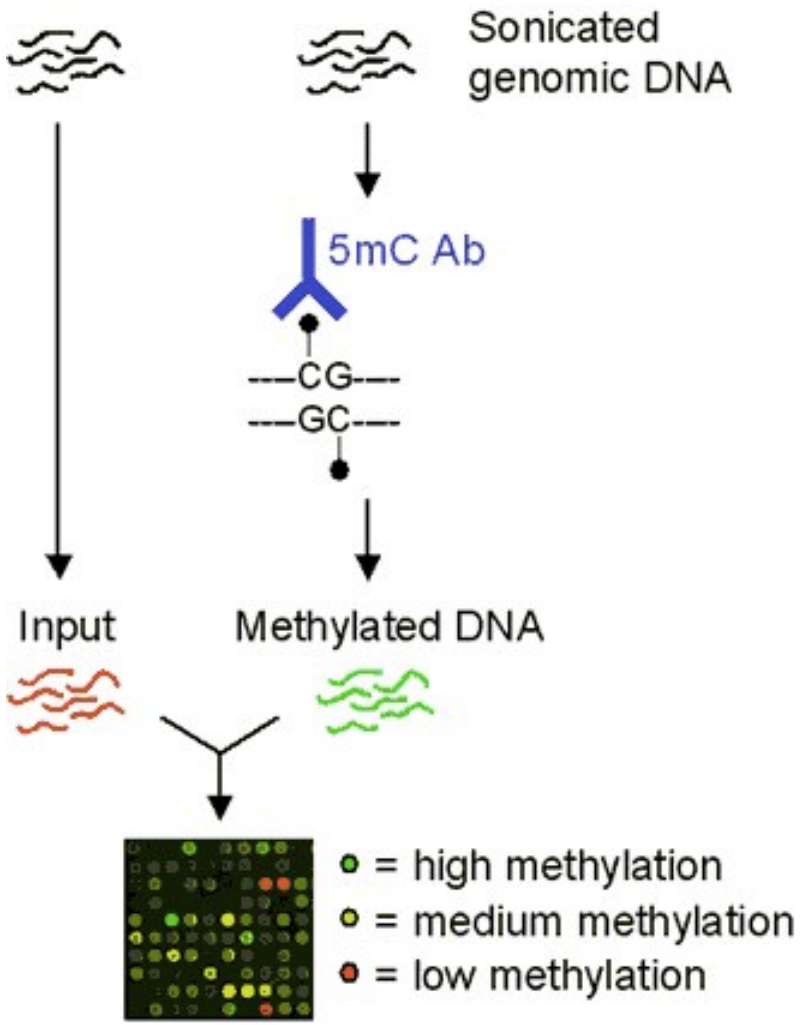
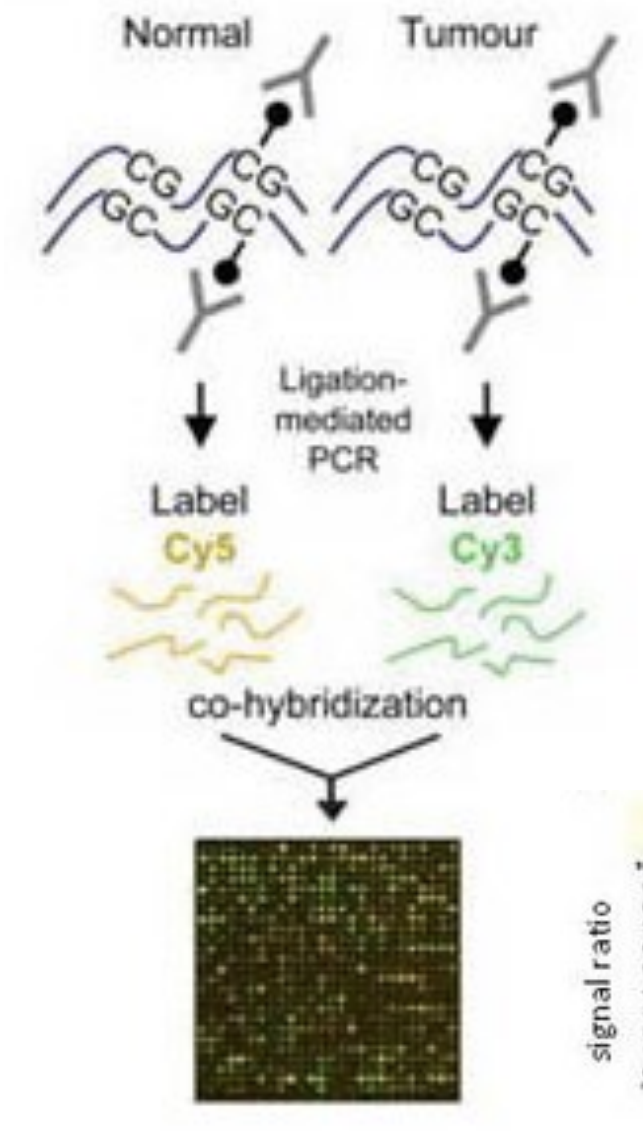
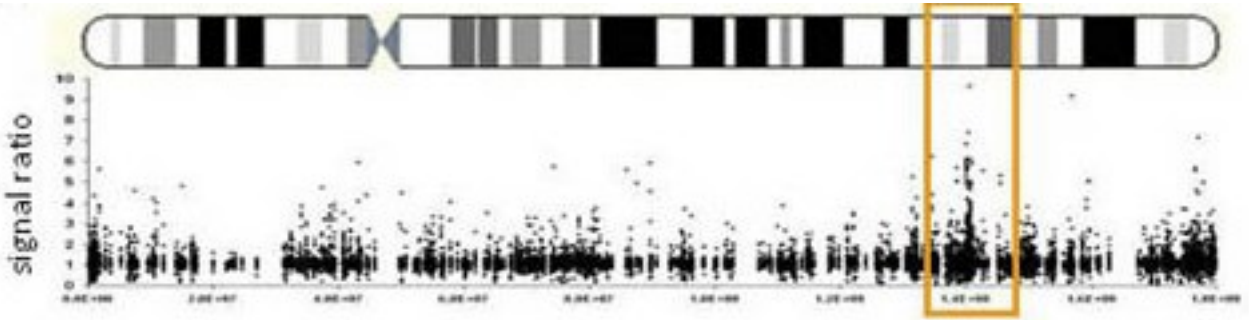
MBD-Chip

Workflow: Identify methylated regions



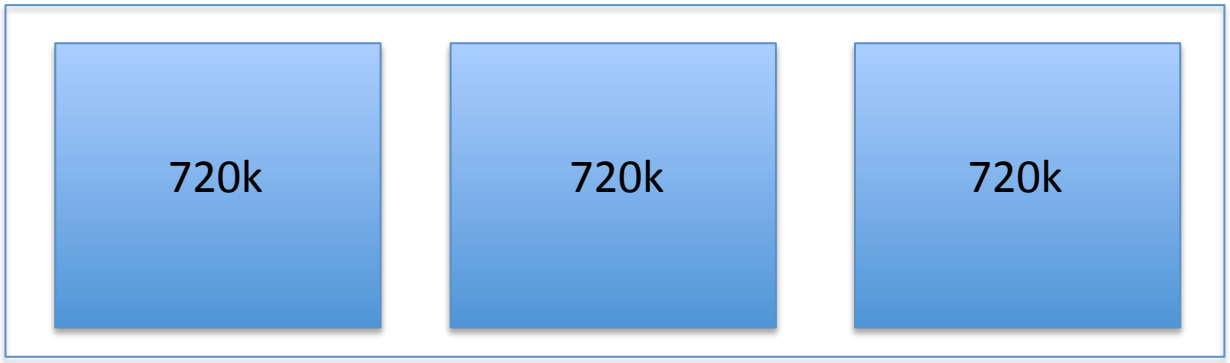
Workflow: differential methylation





Oyster DNA Tiling Array

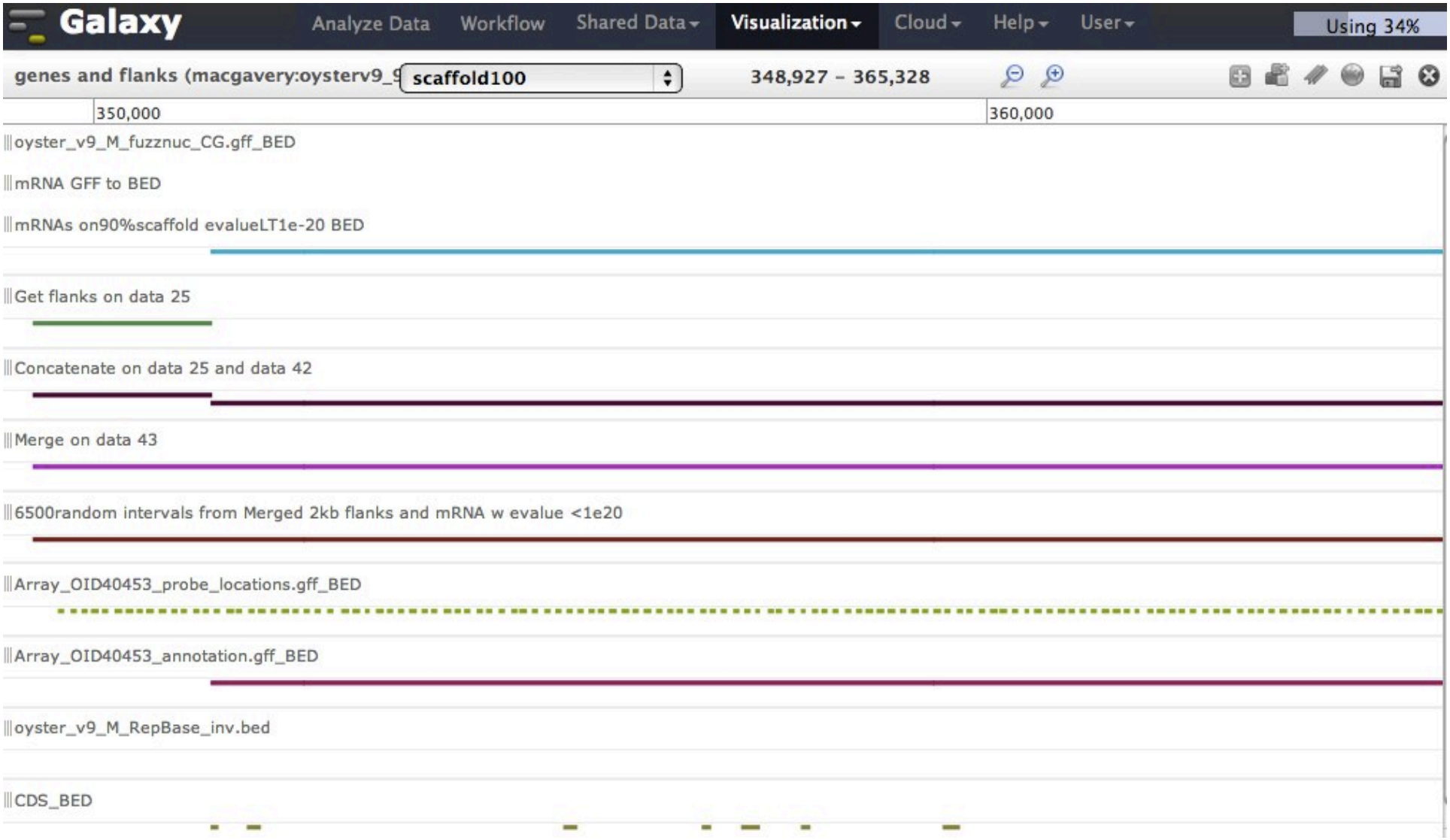
- 3 x 720k design



- Each feature ~100bp x 720k feature =72Mb for the microarray

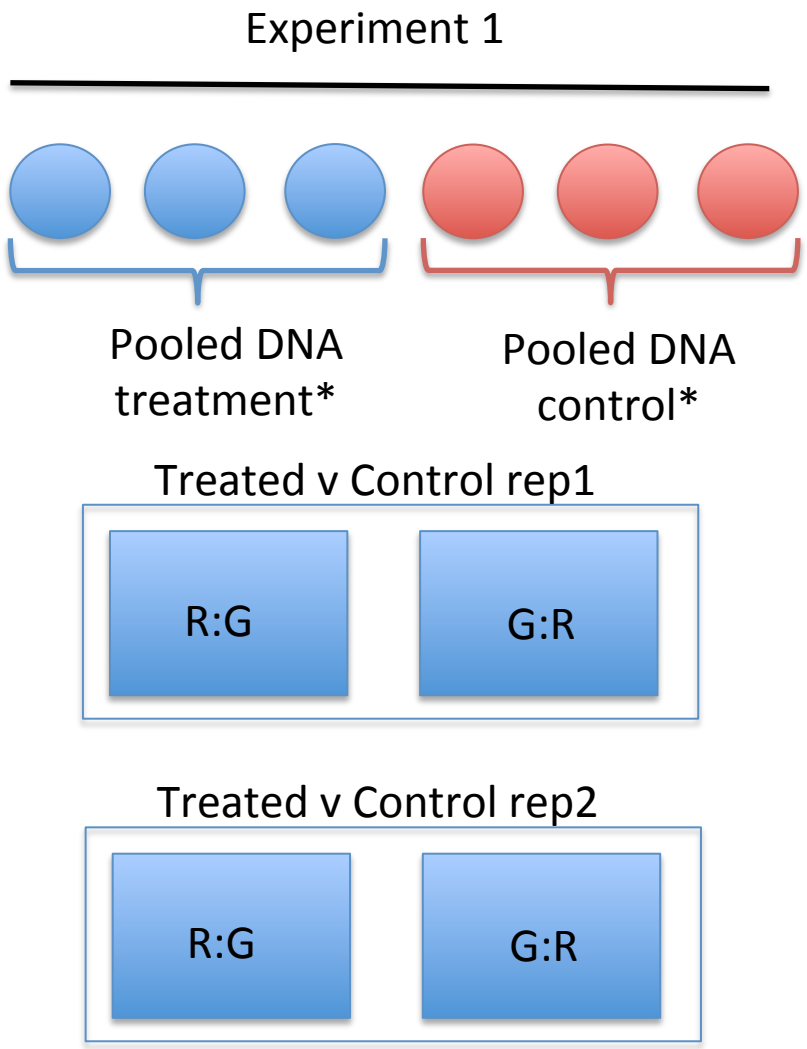
Oyster DNA Tiling Array

- Reducing the genome to most 'informative' parts (100Mb)
  - 28k oyster genes (227Mb)
  - 13k with evalue <1e-20 (total: 138Mb)
  - 12k on scaffolds that cover 90% of genome (132kb)
- Generate intervals that include the gene and 2kb upstream (promoter)
  - Randomly select 6500 (of the ~12k) intervals =100Mb

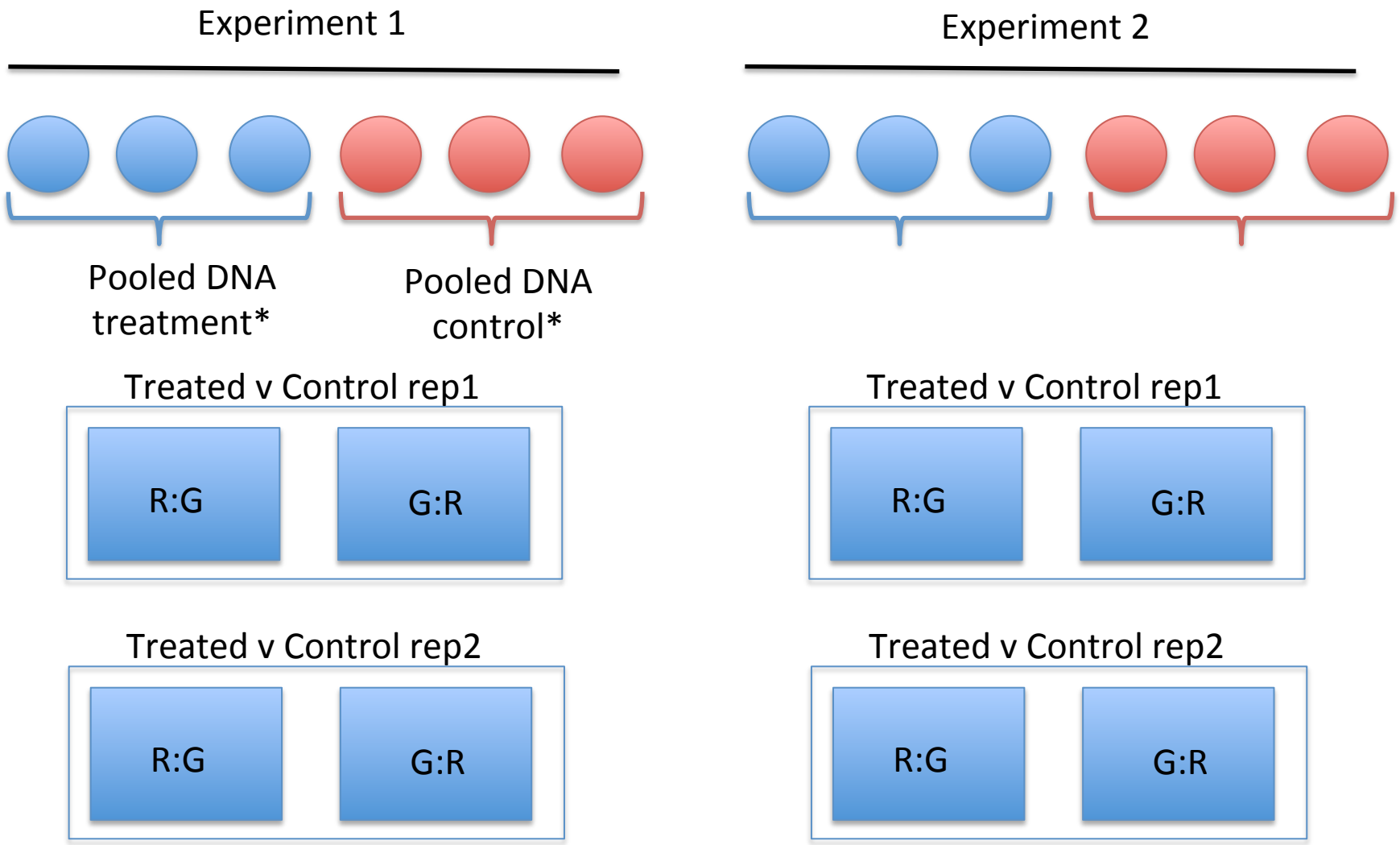

Galaxy
Analyze Data
Workflow
Shared Data
Visualization
Cloud
Help
User
Using 34%
genes and flanks (macgavery:oysterv9_9
scaffold100
348,927 - 365,328
350,000
360,000
oyster_v9_M_fuzznuc_CG.gff_BED
mRNA GFF to BED
mRNAs on90%scaffold evalueLT1e-20 BED
Get flanks on data 25
Concatenate on data 25 and data 42
Merge on data 43
6500random intervals from Merged 2kb flanks and mRNA w evalue <1e20
Array_OID40453_probe_locations.gff_BED
Array_OID40453_annotation.gff_BED
oyster_v9_M_RepBase_inv.bed
CDS_BED

- QC:
  - Dye swap
  - Input v. Input (CNV)
- Validation
  - MBD-PCR
  - pyrosequencing
- Example..

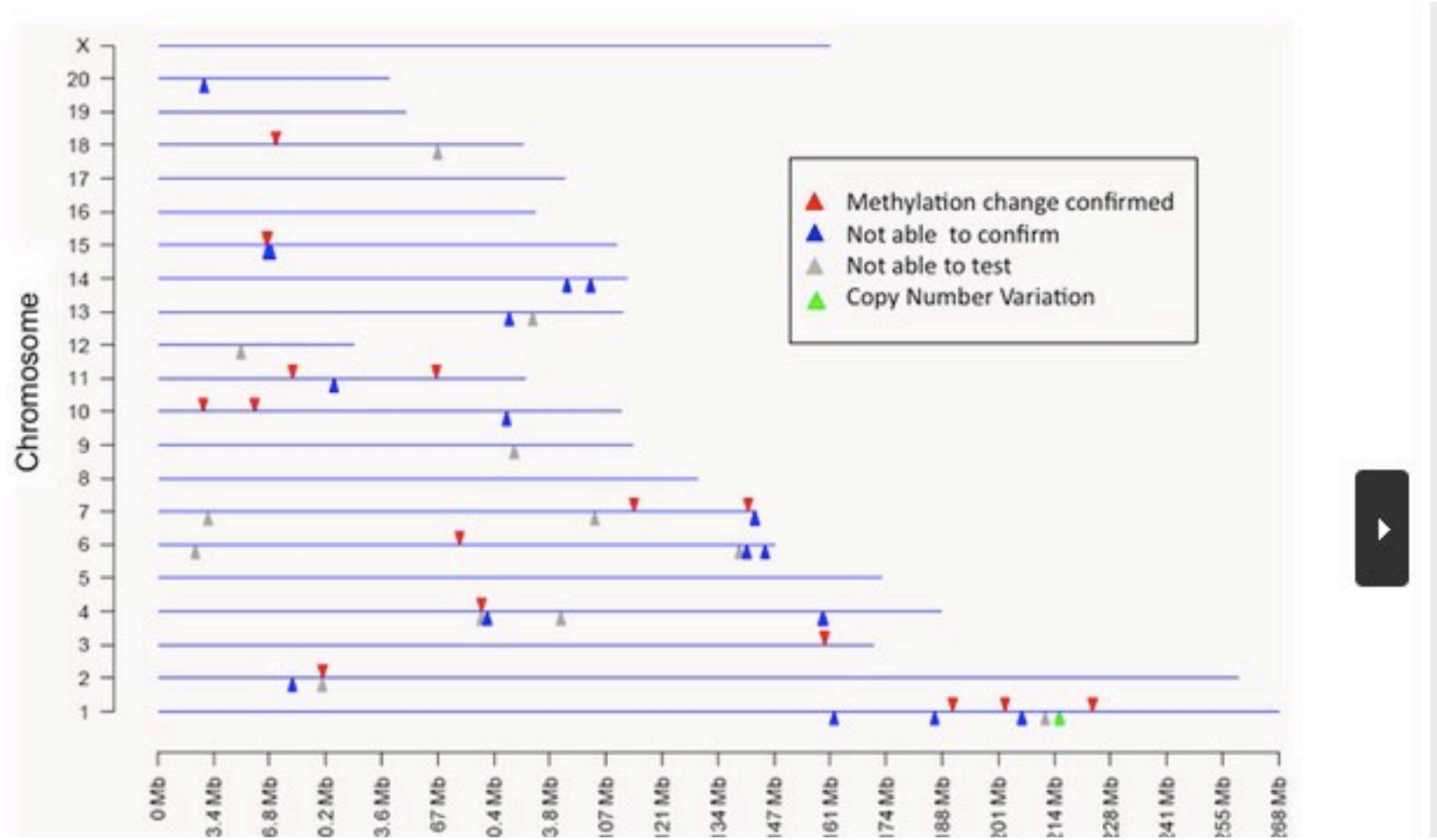
Guerrero-Bosagna et al 2010 (vinclozolin treated sperm F3 gen)



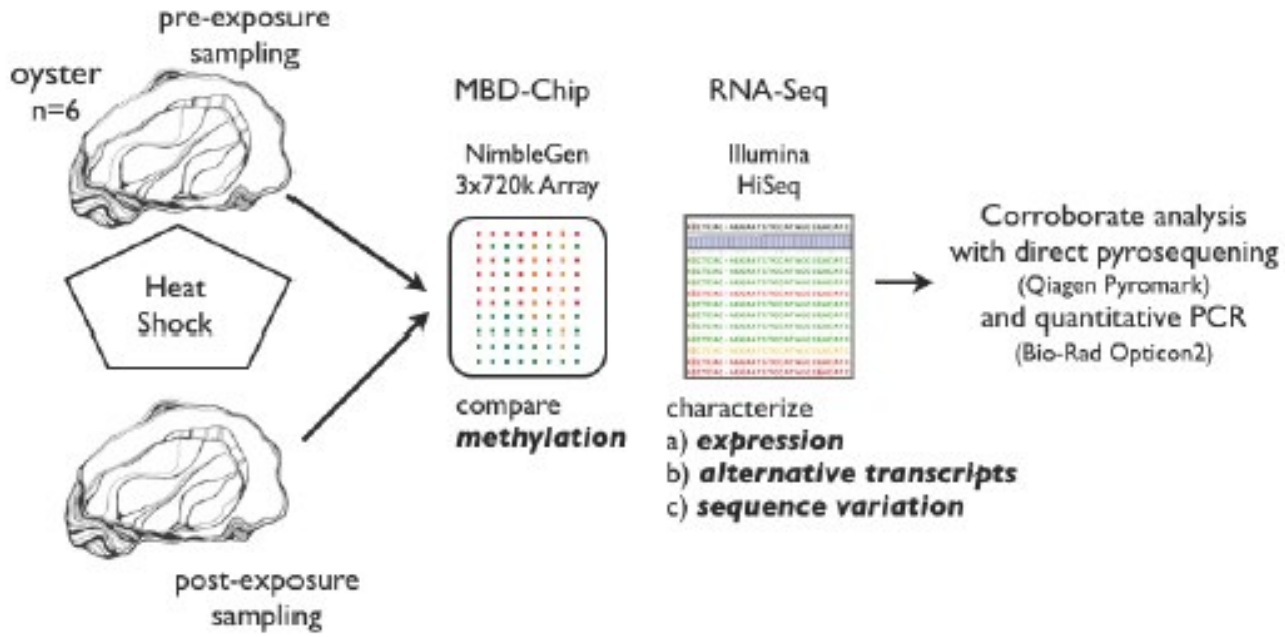
Guerrero-Bosagna et al 2010 (vinclozolin treated sperm F3 gen)



Skinner paper



- Chip #1: methylation changes after heat shock



- Chip #1: methylation changes after heat shock

- Chip #2: methylation changes in response to EE2
  - Day 7
    - Control Pool: 4 females (across 3 tanks)
    - EE2 Pool: 8 females (select 4 across 3 tanks)