Kobor Lab

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Faculty of Medicine

Illumina BeadChip Arrays

Provide **end-to-end support** from sample collection to publication

DNA methylation arrays: EPICv2, MSA, Mouse, Mammalian
Genotyping arrays: GSAv3 and GSAv4

<u>sample types for BeadChip arrays:</u>

- whole blood
- buffy coat
- PBMCs
- dried blood spots
- saliva
- buccal
- FFPE

Other assay capabilities

- RNA-seq
- Olink Reveal panel (proteomics)
- Nanostring panels (targeted transcriptomics)

Bioinformatic expertise

Stratified array randomization design

Array data QC and pre-processing

Analysis (e.g Epigenetic clocks and EWAS)

Tool development (e.g CoMeBack, BECon, RAMEN)

Manuscript writing/publication

Cohort collaboration examples

- CLHNS
- CLSA
- CRELES
- CALERIE
- CANDLE
- CHILD
- GUSTO
- MLSFH
- PLUS
- SEED
- VHAS

Collaboration inquiries

Research Manager:
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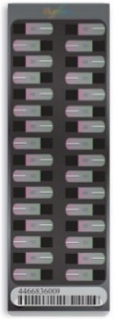
Illumina methylation arrays in human population epigenetic studies



GoldenGate (1.5K)

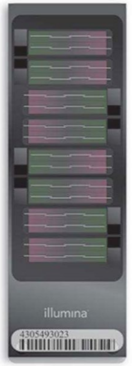
2006-2012

27K array

2008-2012

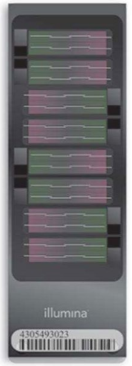
450K array

2011-2017



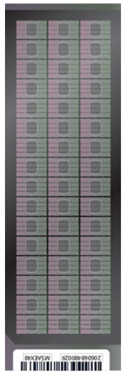
EPIC v1(850K)

2016-2023



EPIC v2 (930K)

2023-???



MSA (270K)

2024-???

1. **Standard assay within the field**
   - Established bioinformatic tools (i.e Epigenetic clocks and cell-type deconvolution)
   - Large public data repositories
2. **Cost and scalability**

1. **Limited coverage of genome (EPIC v2 = ~3%)**
   - Probes are primarily located in regulatory regions
   - Are not consistent between versions
2. **Higher DNA input** requirements (250 ng)
3. **Separate assay required for paired genetic information**

For some cohorts **5-base sequencing** may prove to be a viable alternative to BeadChip Arrays

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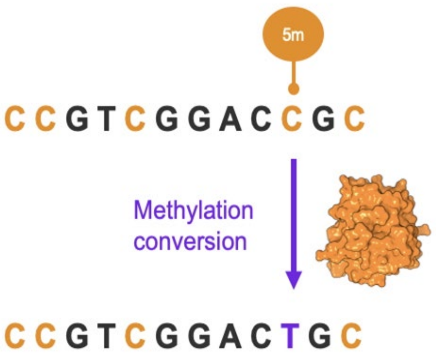
Illumina 5-base DNA prep (link)

- Released Oct 2025
- WGS + methylation calls for up to **28 million CpGs** in one assay
- 1-100 ng input



How it works:

- **Conversion of methylated cytosines**
  - Fewer conversions = reduced chance of error
  - Enzymatic conversion: gentler on the DNA than bisulfite conversion
- Standard NGS short-read sequencing

Why the Kobor lab is excited:

- **Low input** opens avenues for new sample types
  - Currently trialing cfDNA from CSF
- Get **genomic information** for every sample
- Simple, robust bench-top protocol that is **easy to scale**
- **Price** may become comparable to arrays in the next 5 years
  - currently ~$500 USD/sample for 35X coverage

Things to think about with sequencing data:

- Will we be able to use current analysis tools that are built for array data?
  - **Ageing clocks**
  - **Cell type deconvolution**
- Data harmonization between cohorts

Kobor Lab currently working on this question