EpiSwitch® Explorer Array Kit

OXFORD BIODYNAMICS

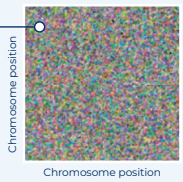
Enabling turnkey precision 3D Genomics for high-throughput biomarker discovery

- **Practical:** EpiSwitch Explorer Array Kit **facilitates 3D genomic biomarker discovery** and profiling for **academic and clinical R&D**
- **Informative:** EpiSwitch Analytical and Data Portal provide advanced data analytics and biological context of the assay microarray readouts, layering on Oxford BioDynamics (OBD) deep knowledgebase of 3D regulation **built on tens of thousands of real patient data across numerous disease indications**
- **Unbiased:** EpiSwitch Explorer Array Kit **enables turnkey high resolution 3D genome screening**—bypassing the need for expensive and lengthy deep sequencing of Hi-C products—thereby unlocking a vast resource critical for better understanding of genomic regulation and its link to clinical outcomes
- **Powerful: Chromosome conformation signatures (CCSs)**, —are reproducibly captured from peripheral blood, delivering practical biomarkers which inform on systemic, stable 3D gene regulatory conformations which are correlated to biological relevance in complex disease applications[1-5]

Current paradigm

Costly deep-sequencing readouts for chromosome conformation capture methods, like Hi-C, are typically limited to only delivering 10,000's of usable data points.

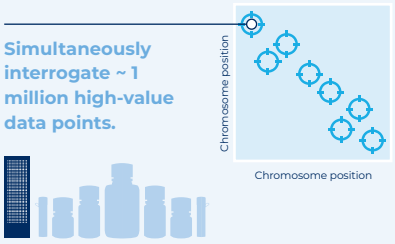
Only a small fraction of that output data is, in fact, relevant to disease or is even reproducible.



EpiSwitch Explorer Array

Probes select reproducible, regulatory 3D architecture, delivering sample-to-results in a rapid, mature workflow with minimal analytical overhead.

Simultaneously interrogate ~ 1 million high-value data points.



We know where to find the drivers of 3D gene regulation

WHOLE-GENOME AT THE HIGHEST RESOLUTION

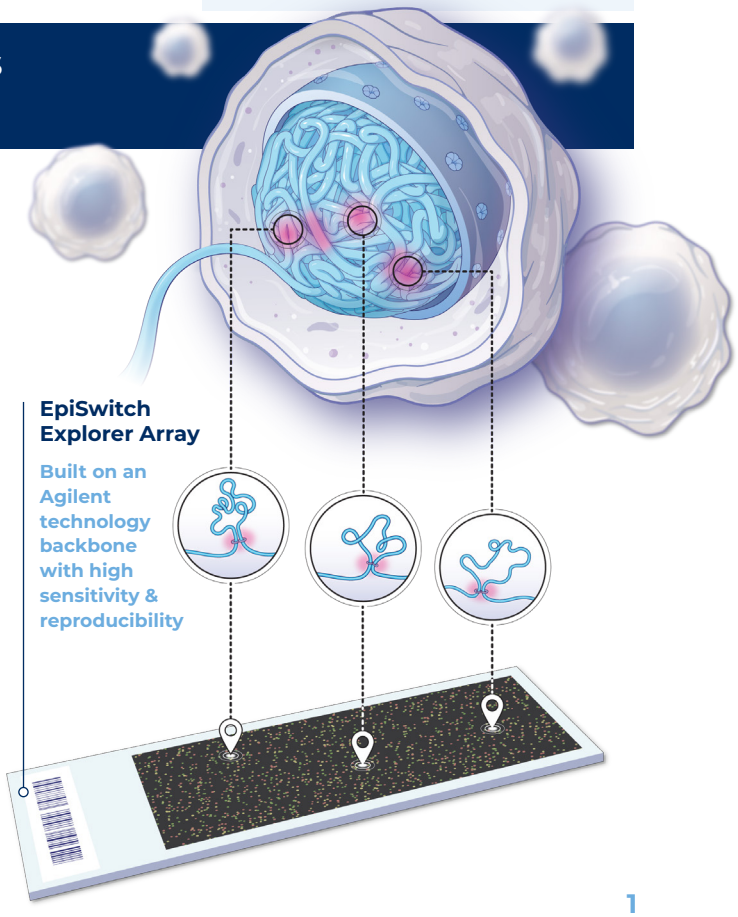
Knowing where to look dramatically simplifies the task. Oxford BioDynamics encoded the Explorer Array to simultaneously interrogate ~ 1 million high-value data points — radically richer complexity than conventional methods.

HIGHEST SENSITIVITY — CUTS THROUGH THE NOISE

EpiSwitch probes select for regulatory 3D architecture that shows high reproducibility, thereby filtering stochastic interactions and giving complex, biologically relevant data with a high signal-to-noise ratio.

THE ANSWER IS IN BLOOD

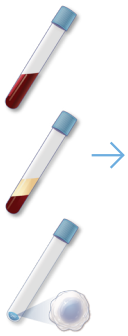
Systemic, early-stage 3D regulatory changes can be captured from peripheral blood long before the results of these epigenetic events manifest as apparent abnormalities. EpiSwitch blood markers have delivered accurate, robust predictive, prognostic and diagnostic assays in oncological, inflammatory, neurological & other complex disease applications[1-5].



Mature, end-to-end reproducible workflow

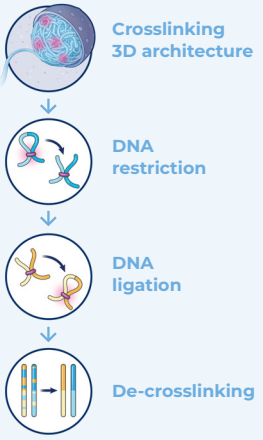
EpiSwitch® Explorer Array Kit

Sample



Analyse blood, PBMCs or cell samples with Kit reagents

1 EpiSwitch sample prep (~4hr)



Proprietary EpiSwitch extraction reagents

2 EpiSwitch Explorer Array

Adaptable to 1- or 2-color approach based on experimental needs

3 EpiSwitch Portal

EpiSwitch Analytical Portal (EAP) → Biomarker development

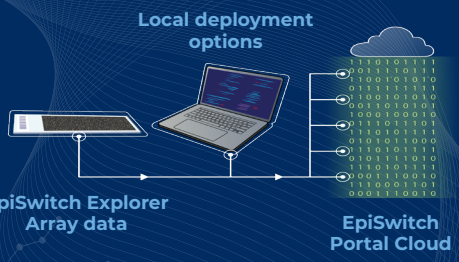
Tool suite for statistical analyses of 3DG array data

EpiSwitch Data Portal (EDP) → Enrichment analyses of regulated pathways

Tool suite maps data to the annotated genome for:

- integrating other multi-omic data
- biological interpretation

Turnkey tools for statistical analyses + genome mapping of Explorer Array data



EpiSwitch Analytical Portal

Array Processing

- Load EpiSwitch arrays 1- or 2-color
- Normalize & QC arrays

Core Statistical Analyses

- Linear regression
- Rank based analysis

Additional Analyses + Visualization

- PCA, LDA
- Hierarchical clustering
- VENN diagrams

EpiSwitch Data Portal

Multi-Omic Integration

- Load EpiSwitch or other CCS data
- Layer other epigenetic/genetic data (SNPs, Hi-C, ATAC-Seq, Chip, RNA-Seq...)

Layer Episwitch Databases

- Query EpiSwitch CCS databases

Genomic Rendering + Mapping Analyses

- Multi-omic genomic rendering of array data
- Circos plots
- Bedtool functionality

Other Biological Interpretation

- Map CCS data to SNP & TF binding sites
- CCS mapping to TSS for enrichment analysis
- GSEA of saved CCS/Genes/TF list

Whole-Genome At High Resolution

Simultaneously interrogate ~1 million high-confidence chromosome conformations across the whole genome

Design includes positive and negative control probes

Highest Sensitivity—Cut Through Noise

EpiSwitch probes select regulatory 3D conformations with high reproducibility, filtering stochastic interactions

Built on an Agilent technology backbone

Scalable, Economic, Rapid Results

Sample-to-results in a few days, with a mature workflow

Small fraction of the cost & time of sequencing-based methods

Turnkey Analytics

Low analytical overhead

Ready-to-use analytic tools & contextual integrations with no coding

Analyse Many Sample Types

Analyse blood, PBMCs or cell lines with the Kit protocol

References

1: Hunter, et al. *Classification of DLBCL*. doi:10.1186/s41231-020-00054-1
2: Hunter, et al. *Response to PD-(L)-1 ICIs*. doi:10.1101/2021.12.21.21268094
3: Carini, et al. *Response to MTX in RA*. doi:10.1186/s12967-018-1387-9
4: Hunter, et al. *Severity of COVID*. doi:10.1101/2021.06.21.21259145
5: Alshaker, et al. *Detect prostate cancer*. doi:10.1186/s12967-021-02710-y

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