ZYMO RESEARCH

The Beauty of Science is to Make Things Simple

Quote #in060

Services Performed:

The following checklist confirms the steps of the EpiQuest™ Service that we performed on your samples.

SERVICE	
Sample Received	✓
Sonication Efficiency Validation	✓
ChIP Assays	✓
ChIP-Seq Libraries Preparation	✓
ChIP-Seq Libraries QC and Quantification	✓
Next-Gen Sequencing	✓
Bioinoformatics Analysis	✓
Data/Result	✓

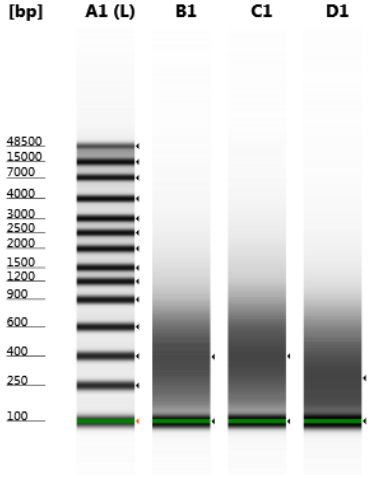
Sample Submission:

Samples were received on **XX/XX/20XX** and immediately stored in -80°C for long term storage.

Sonication Efficiency Validation:

Genomic DNA ScreenTape®

Gel Image



gDNA

Contrast: 0.50

A1: Ladder

B1: HeLa cells input DNA – 1st ChIP assay

C1: HeLa cells input DNA – 2nd ChIP assay

D1: HeLa cells input DNA – 3rd ChIP assay

The fragment size range from 100 – 900 bp with average fragment size ≤ 600 bp.

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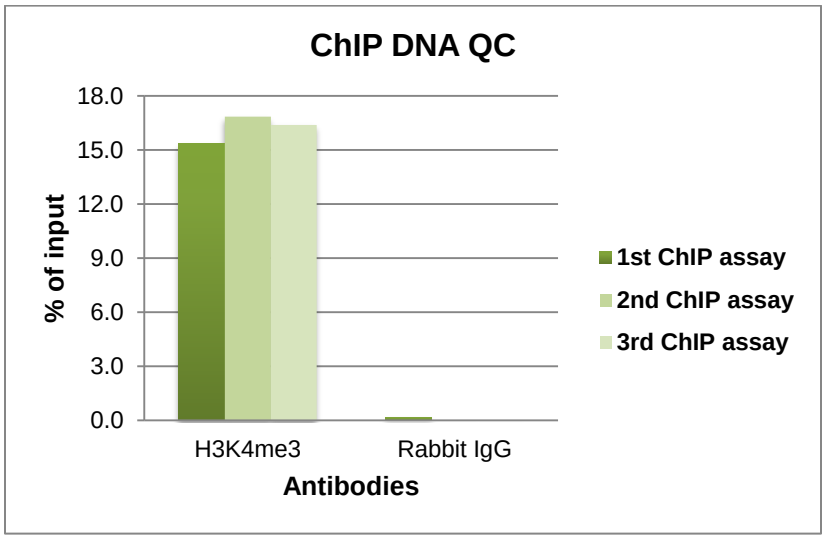
ChIP Assays:

Three independent ChIP pulldowns are prepared using cross-linked frozen HeLa samples from **XXX**. Antibodies used in ChIP assays included: Anti-H3K4me3 (Millipore, 07-473) and normal rabbit IgG (Millipore, 12-370).

ChIP DNA Verification using qPCR:

ChIP DNA from 3 independent ChIP assays are verified by qPCR using control primers specific for human GAPDH promoter.

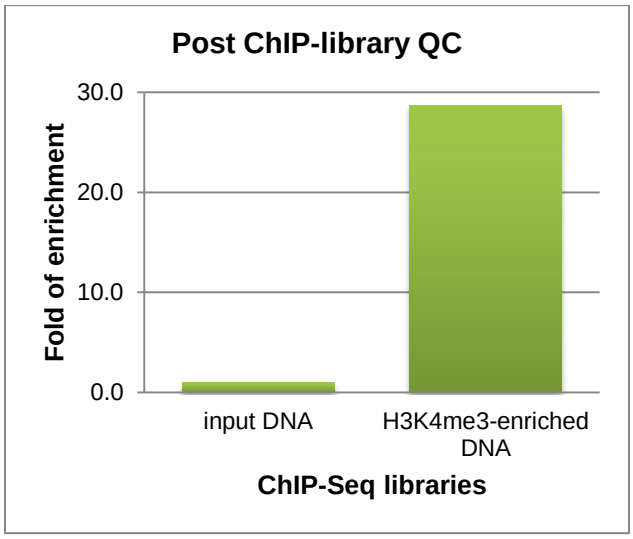


ChIP-Seq Libraries Preparation:

ChIP-Seq libraries are prepared from total input DNA or ChIP DNA enriched with anti-H3K4me3 pooled from 3 independent ChIP assays.

Post ChIP-Seq Libraries QC and Quantification:

ChIP-Seq libraries are verificated using qPCR and control primers specific for human GAPDH promoter.



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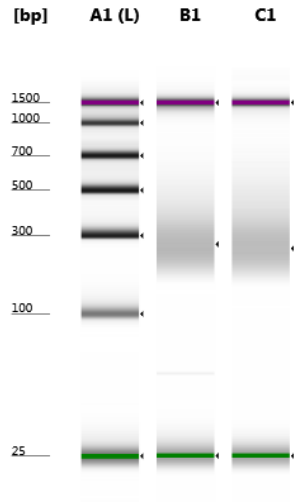
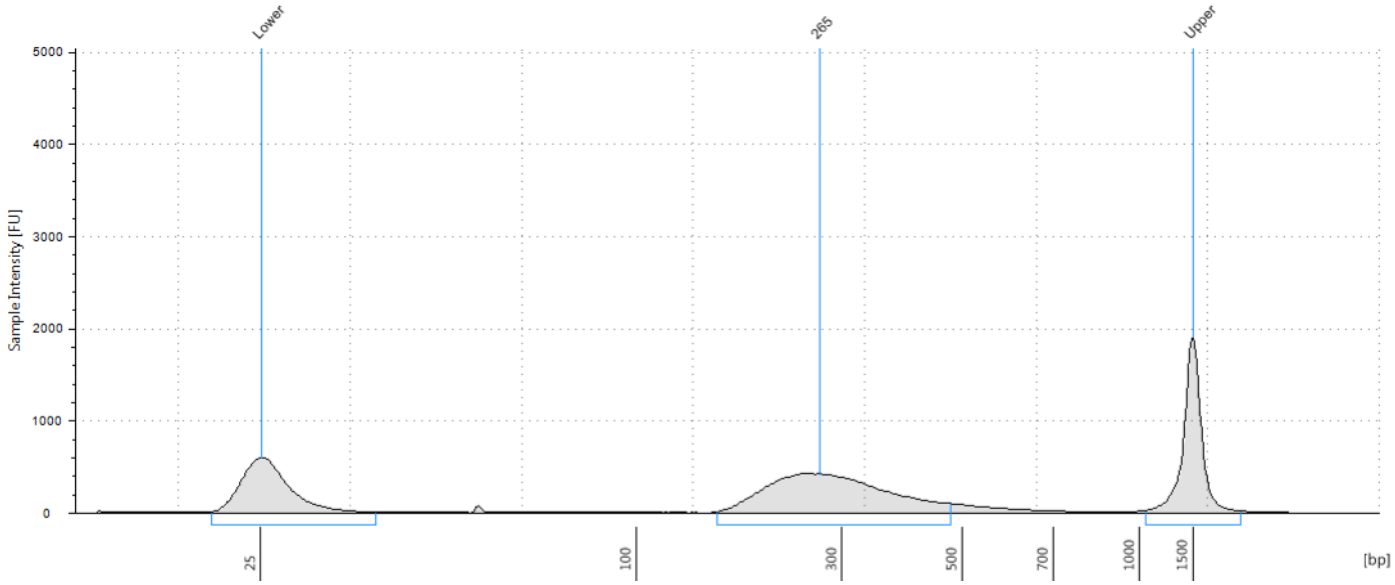
ChIP-Seq libraries are quantified using 2200 Tape Station before being run on Next-Gen Sequencing platform – HiSeq.

Gel Image



A1: Ladder
B1: HeLa cells input DNA
C1: HeLa cells H3K4me3 ChIP DNA

B1



B1: HeLa cells input DNA

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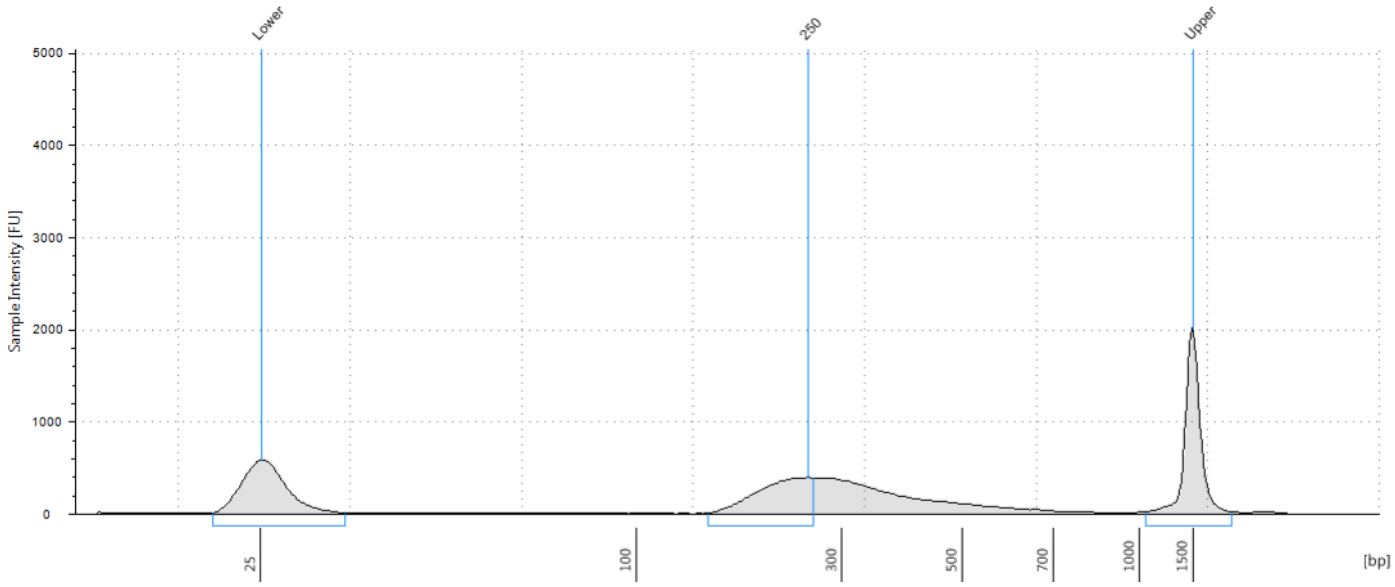
C1



C1: HeLa cells H3K4me3 ChIP DNA

Data/Result for ChIP-Seq Antibody Validation:

The following files are available on our website: http://epidata.zymoresearch.com:8000/#/sample_list/in060.
Username: **XXX**
Password: **XXX**

1. Excel data files containing peak regions location and gene annotations.
2. BED file for uploading as a custom track into the UCSC browser for visualization of intervals, active regions, and interval peaks.
3. WIG file for uploading into genome browser for visualization of probe signals and peaks.
4. BAM file containing genome aligned sequences.
5. FASTQ file containing the raw sequencing data.
6. PDF file containing the cis-regulatory element annotation system (CEAS) data.
7. Sample comparison data.

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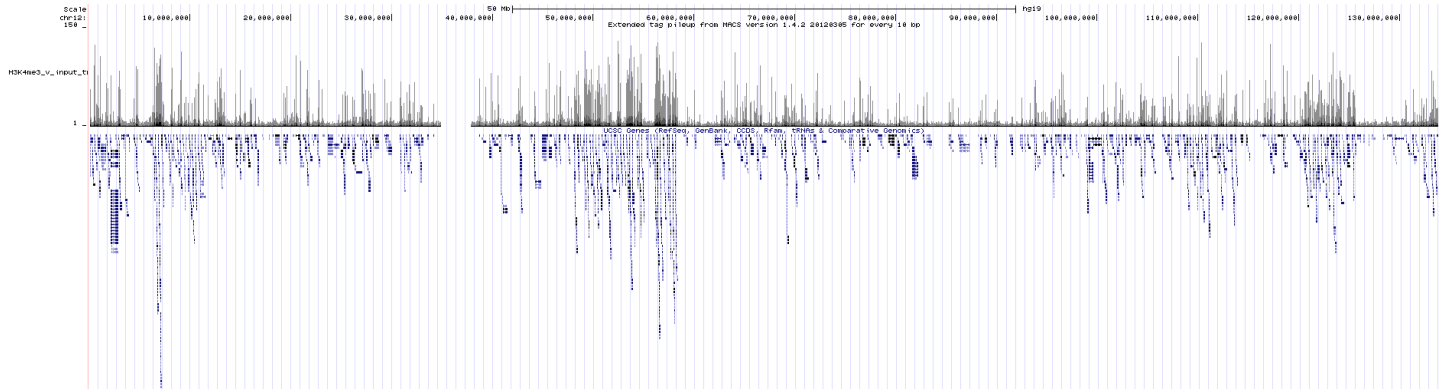
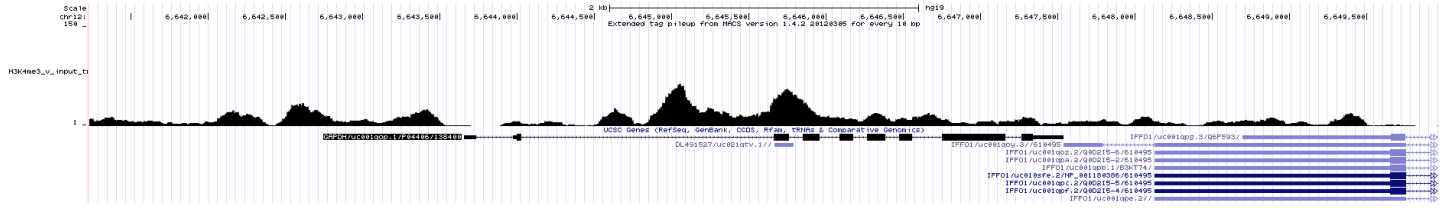
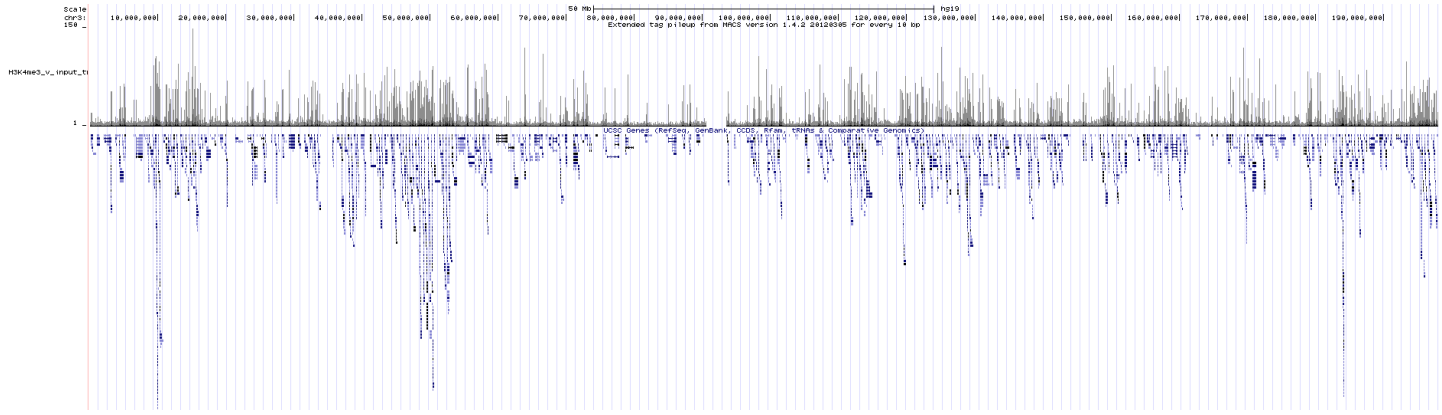
Example of Genome Browser:
Screenshot: chr12



Screenshot: chr12; Gene: GAPDH



Screenshot: chr3



Screenshot: chr3; Gene: EIF4A2