

Minimum required track files:

This document aims at describing a minimum set of analysis tracks that should be provided for any dataset, for IHEC Core Assays. Other non-core assays are also described at the end of the document.

Please refer to the [tracks generation standards](#) for information on how to generate each track types.

IHEC Core Assays

ChIP-Seq Histone (H3K*):

| Track Type | Data Hub Identifier | Format | Mandatory | Notes |
|-----------------|--------------------------------|--------|-----------|-------|
| Signal/Coverage | <code>signal_unstranded</code> | bigWig | Y | |
| Peak calls | <code>peak_calls</code> | bigBed | Y | |

ChIP-Seq Input:

| Track Type | Data Hub Identifier | Format | Mandatory | Notes |
|-----------------|--------------------------------|--------|-----------|-------|
| Signal/Coverage | <code>signal_unstranded</code> | bigWig | Y | |

DNA Methylation:

| Track Type | Data Hub Identifier | Format | Mandatory | Notes |
|------------------------------|--|--------|-----------|--|
| Fractional Methylation Calls | <code>methylation_profile</code> | bigWig | Y | Needs to be formally specified, reports #Cs vs #Ts at each CpG site. See current proposal here . |
| Signal/Coverage | <code>signal_unstranded</code> OR <code>signal_forward</code> , <code>signal_reverse</code> | bigWig | Y | Raw coverage over CpGs as a measure of confidence in Fractional Methylation Calls. See current proposal here . |

mRNA / total RNA :

For strand specific signal:

| Track Type | Data Hub Identifier | Format | Mandatory | Notes |
|--------------------------------|---------------------|--------|-----------|---|
| Signal/Coverage forward strand | signal_forward | bigWig | Y | |
| Signal/Coverage reverse strand | signal_reverse | bigWig | Y | |
| RPKM on positive strand | rpkm_forward | bigWig | | Computation needs to be standardized. Proposal available here . |
| RPKM on negative strand | rpkm_reverse | bigWig | | Computation needs to be standardized. Proposal available here . |

For single stranded signal:

| Track Type | Data Hub Identifier | Format | Mandatory | Notes |
|-----------------|---------------------|--------|-----------|---|
| Signal/Coverage | signal_unstranded | bigWig | Y | |
| RPKM | rpkm_unstranded | bigWig | | Computation needs to be standardized. Proposal available here . |

Non-core Assays

smRNA-Seq signal:

| Track Type | Data Hub Identifier | Format | Mandatory | Notes |
|-----------------|---------------------|--------|-----------|-------|
| Signal/Coverage | signal_unstranded | bigWig | Y | |

| Track Type | Data Hub Identifier | Format | Mandatory | Notes |
|-----------------------------------|--|--------|-----------|--|
| Reads per million miRNA mapped | <code>reads_per_million_</code> <code>miRNA_mapped</code> | bigWig | | Computation needs to be standardized |

Whole Genome Sequencing:

| Track Type | Data Hub Identifier | Format | Mandatory | Notes |
|-----------------------|------------------------------------|--------|-----------|-------|
| Copy Number Variation | <code>copy_number_variation</code> | bigWig | Y | |

ATAC-Seq:

| Track Type | Data Hub Identifier | Format | Mandatory | Notes |
|-----------------|--------------------------------|--------|-----------|-------|
| Signal/Coverage | <code>signal_unstranded</code> | bigWig | Y | |
| Peak calls | <code>peak_calls</code> | bigBed | Y | |