

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_ 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	