

# Encode Cancer

## List of Encode Cancer Experiments

	ChIP-seq (TFs)	DNase-Seq (open chromatin)	FAIRE-seq (open chromatin)	Repli-Seq (replication timing)	RNA-Seq	RRBS (methylation)
<b>Encode 2 Released</b>	808	61	19	30	107	34
<b>Encode 3 Released</b>	218	13	0	0	60	0
<b>Revoked</b>	9	0	0	0	2	0
<b>Total</b>	1,035	74	19	30	169	34

***Last Updated: 12/8/2015***

- Curated w/ Shirley and Robert
- Total 73 human cancer cell line in Encode
- Most Encode 2 data is available to download, but very few Encode 3 data is released and available for download
- Plan on combining signal data to build covariate matrices -> publish and use for mutation rate correction

# Data Use

- Data use policy for internal users: [http://wiki.encodedcc.org/images/5/57/ENCODE-Internal Data Use Policy-Jun27-14-sent to Consortium.docx](http://wiki.encodedcc.org/images/5/57/ENCODE-Internal_Data_Use_Policy-Jun27-14-sent_to_Consortium.docx)

*“Any data or analysis that was produced by previous editions of ENCODE, or ENCODE 3 data or analyses that are published at the time when a Consortium member or group will be submitting a paper, may be used without restriction. However, if a group wants to publish results based in whole or in part on **unpublished** data or analyses generated by another ENCODE group, the authors are **required to consult with the PI** from the group that generated these data or analyses to establish a mutually agreeable path towards timely publication.”*

- Upcoming change: uniformly processed ChIP-Seq data

<http://www.encodeproject.org/experiments/ENCSR069XHI/>

<https://www.encodeproject.org/experiments/ENCSR932KWJ/>

- We need to think about how to combine replicates and normalize across cell lines for other experiments