Projects With Similarities To ENCODE

Project Title	Project Acronym	URL	Funding Agencies	Sample Types	Assays/Data Types	Project Summary	Similarities with ENCODE	Distinctions from ENCODE	Status	Coordination with ENCODE	Program Contacts
International Human Epigenome Consortium	IHEC	http://www.ihec-epigenomes.org/	Consortium of projects funded by member nations	Healthy and diseased; generally purified cells	Transcriptomic; epigenomic	Data collection and reference maps of human epigenomes for key cellular states relevant to health and diseases	Chromatin and gene expression profiling of numerous samples; provides resources for interpretation of variant data	Disease samples	Active	ENCODE is IHEC associate member	Eric Marcotte (lead); Mike Pazin
Reference Epigenome Mapping Centers	REMC	http://www.roadmapepigenomics.org/	NIH Common Fund	Healthy tissues	Transcriptomic; epigenomic	Data collection, integrative analysis and a resource of human epigenomic data	Chromatin and gene expression profiling of numerous samples; provides resources for interpretation of variant data	Human only; producing reference epigenomes; limited number of assay types	Completed 2008-2013	REMC metadata hosted at ENCODE DCC; both IHEC members	Fred Tyson, Lisa Chadwick, John Satterlee (leads); Elise Feingold, Mike Pazin, Dan Gilchrist
BLUEPRINT	BLUEPRINT	http://www.blueprint-epigenome.eu/	EU	Normal and malignant haematopoietic cells	Transcriptomic; epigenomic	Data collection and analysis of normal and malignant blood cells	Chromatin and gene expression profiling of numerous samples; provides resources for interpretation of variant data	Disease samples; limited to haematopoietic cells; limited number of assay types	Active 2011-2016	Through IHEC membership	Henk Stunnenberg (lead); Mike Pazin
PsychENCODE	PsychENCODE	http://grants.nih.gov/grants/guide/rfa-files/RFA-MH-14-020.html	NIMH	Normal and diseased neural tissues and cell types from human brain, and iPSC and CNON-derived neurons	Transcriptomic; epigenomic; genomic; proteomic	Data collection and integrative analysis of human neural epigenomic, genomic, transcriptomic and proteomic data	Cataloguing of functional elements; chromatin and gene expression profiling of numerous samples; provides resources for interpretation of variant data	Emphasis on normal and diseased neural tissues and cell types from adult and developing human brain, and comparison to non-human primates	Active 2014-present		Geetha Senthil
Functional Annotation of the Mammalian Genome	FANTOM	http://fantom.gsc.riken.jp	RIKEN	Human and mouse primary cells, tissues and cell lines	Transcriptomic; CAGE	Data collection of CAGE transcriptomic data and data analysis to annotate human and mouse functional elements	Gene expression profiling of numerous samples; focus on functional element annotation; provides resources for interpretation of variant data	No chromatin data	Active 2000-present	Includes four cell lines used in ENCODE	Yoshihide Hayashizaki, Piero Carninci
4D Nucleome	4DN	http://commonfund.nih.gov/4Dnucleome/index	NIH Common Fund	TBD	Imaging; genomic	Nuclear architecture; technology development and mapping projects; data integration and coordination center	Global interactions between gene loci and regulatory elements	Emphasis on tech dev; Imaging; nuclear dynamics; modeling of structure/function relationships; investigation of poorly characterized nuclear features	Beginning 2015	Program Officer Overlap	Olivier Blondell, Judy Meitz (leads); Mike Pazin

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Genomics of Gene Regulation	GGR	http://grants.nih.gov/grants/guide/rfa-files/RFA-HG-13-012.html	NHGRI	Skin, immune system, nuclear hormone response	Transcriptomic; epigenomic	Determine how to develop predictive gene regulatory network models from genomic data	Chromatin and gene expression profiling of numerous samples	Goal is network modeling, based on data from cell transitions	Active 2015-2018	GGR data and metadata hosted at ENCODE DCC; Program Officer Overlap	Mike Pazin (lead)
Genotype-Tissue Expression Project	GTEx	http://www.gtexportal.org/home/	NIH Common Fund	post-mortem, non-diseased human tissues	WGS and WES; transcriptomic; additional data types in eGTEx (proteomic, epigenomic, ASE)	Data collection and analysis of variation in human gene expression, across individuals, and across >30 tissues from the same subjects	Provides resources for interpretation of variant data; gene expression profiling of numerous samples	Large population data-set; no chromatin data; not focused on identification of functional elements	Active 2010-present	Collaboration to perform ENCODE assays on GTEx samples	Simona Volpi, Jeff Struewing
Library of Integrated Network-based Cellular Signatures	LINCS	https://commonfund.nih.gov/LINCS/	NIH Common Fund	Primary cells; cell lines; iPS cells, differentiated neurons and cardiomyocytes	Transcriptomic; phosphoproteomic; imaging; epigenomic	Data collection and analysis of molecular signatures describing how different cell types respond to perturbing agents	Gene expression profiling of numerous samples	Emphasis on cataloguing responses to perturbations (small molecule, genetic, disease); not focused on identification of functional elements	Phase 1 2010-2013; Phase 2 2014-present		Ajay Pillai
International Cancer Genome Consortium	ICGC	http://www.icgc.org/	Consortium of projects funded by member nations	Tumor and normal	WGS and WES; transcriptomic; epigenomic	Data collection and analysis of genomic, transcriptomic and epigenomic changes in 50 different tumor types (includes TCGA samples)	Chromatin and gene expression profiling of numerous samples; provides resources for interpretation of somatic mutation data	Emphasis on cataloguing somatic genomic abnormalities; limited to tumors; not focused on identification of functional elements	Active 2008-present		Carolyn Hutter, Heidi Sofia
The Cancer Genome Atlas	TCGA	http://cancergenome.nih.gov/	NHGRI, NCI	Tumor and normal	WGS and WES; transcriptomic; epigenomic; proteomic	Data collection and analysis of genomic, transcriptomic, and epigenomic changes in ~30 different tumor types, and repository for DNA and RNA sequence data	Chromatin and gene expression profiling of numerous samples; provides resources for interpretation of somatic mutation data	Human only; tumors only; no chromatin data beyond DNAme; not focused on identification of functional elements	Active 2005-2016	Through ENCODE AWG Cancer working group	Carolyn Hutter, Heidi Sofia
Interpreting Variation in Human Non-Coding Genomic Regions Using Computational Approaches and Experimental Assessment	FunVar (will be updated)	http://grants.nih.gov/grants/guide/rfa-files/RFA-HG-13-013.html	NHGRI, NCI, NIDA	Various	TBD; functional tests of prediction specificity/sensitivity	Development of computational approaches to interpret sequence variation in non-coding regions, and assessment of approaches through targeted data collection	Develops approaches for interpreting variant data	Goal is developing computational approaches to infer causal variants; limited data generation	Active 2015-2019	Program Officer Overlap	Lisa Brooks (Lead), Mike Pazin, Stefanie Nelson (NCI), Joni Rutter (NIDA)
Knockout Mouse Phenotyping Program	KOMP2	https://commonfund.nih.gov/KOMP2/	NIH Common Fund	Mice	Phenotypic	Data collection for standardized phenotyping of a genome-wide collection of mouse knockouts; member of International Mouse Phenotyping Consortium (IMPC)			Active 2011-2021		Colin Fletcher