

### Supplementary Table 1

ENCODE, Roadmap Epigenomics, and EnhancerAtlas data sets used to define the functional regions employed in our workflows. The GEO accessions for the alignment files are provided only for the marks where these were needed during ChromHMM binarization. For the Human Cardiomyocytes and HCF H3K4me3 narrow peaks, we used the overlapping regions between replicates. UCSC1=<http://genome.ucsc.edu/cgi-bin/hgFileUi?db=hg19&g=wgEncodeOpenChromDnase>; UCSC2=<http://genome.ucsc.edu/cgi-bin/hgFileUi?db=hg19&g=wgEncodeUwHistone>.

Tissue	Project	Region Type	Source	GEO Accessions
LV	Epigenome Roadmap	H3K27me3 broad peaks	E095	GSM908952, GSM910562
LV	Epigenome Roadmap	H3K36me3 broad peaks	E095	GSM906402, GSM910569
LV	Epigenome Roadmap	H3K4me1 broad peaks	E095	GSM906404, GSM910575
LV	Epigenome Roadmap	H3K9me3 broad peaks	E095	GSM906409, GSM906412
LV	Epigenome Roadmap	H3K4me3 narrow peaks	E095	
LV	Epigenome Roadmap	H3K27ac narrow peaks	E095	
LV	EnhancerAtlas	enhancers		
Heart	ENCODE	DNase narrow peaks	UCSC1	
Human cardiac myocytes	ENCODE	H3K4me3 narrow peaks	UCSC2	
HCF	ENCODE	H3K4me3 narrow peaks	UCSC2	