

Species	Stage	Tissue/Cell	Experiment	Antibodies	Link	Reference
Human	Foetus (Week 16)	Heart	ChIP-seq	AcCBP/p300, RNAPolII	http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE32587	May D, Blow MJ, Kaplan T, McCulley DJ et al. Large-scale discovery of enhancers from human heart tissue. <i>Nat Genet</i> 2011 Dec 4;44(1):89-93. PMID: 22138689
Human	Adult (45 years)	Heart	ChIP-seq	AcCBP/p300	http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE32587	May D, Blow MJ, Kaplan T, McCulley DJ et al. Large-scale discovery of enhancers from human heart tissue. <i>Nat Genet</i> 2011 Dec 4;44(1):89-93. PMID: 22138689
Mouse	Postnatal day 2	Heart	ChIP-seq	AcCBP/p300	http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE32587	May D, Blow MJ, Kaplan T, McCulley DJ et al. Large-scale discovery of enhancers from human heart tissue. <i>Nat Genet</i> 2011 Dec 4;44(1):89-93. PMID: 22138689
Human	Foetus	Heart	ChIP-seq	H3K4me1, H3K4me3, H3K9ac	http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE17312	Bernstein BE, Stamatoyannopoulos JA, Costello JF, Ren B et al. The NIH Roadmap Epigenomics Mapping Consortium. <i>Nat Biotechnol</i> 2010 Oct;28(10):1045-8. PMID: 20944595
Human		Heart	ChIP-seq	p53 and NF-kB	http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE21356	Choy MK, Movassagh M, Siggins L, Vujic A et al. High-throughput sequencing identifies STAT3 as the DNA-associated factor for p53-NF-kappaB-complex-dependent gene expression in human heart failure. <i>Genome Med</i> 2010 Jun 14;2(6):37. PMID: 20546595
Human		Heart (End-Stage Cardiomyopathy)	ChIP-seq	p53 and NF-kB	http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE21356	Choy MK, Movassagh M, Siggins L, Vujic A et al. High-throughput sequencing identifies STAT3 as the DNA-associated factor for p53-NF-kappaB-complex-dependent gene expression in human heart failure. <i>Genome Med</i> 2010 Jun 14;2(6):37. PMID: 20546595
Human	Adult	Aorta	ChIP-seq	H3K27ac, H3K4me1, H3K4me3, H3K9me3, H3K27me3, H3K36me3	http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE16256	Lister R, Pelizzola M, Dowen RH, Hawkins RD et al. Human DNA methylomes at base resolution show widespread epigenomic differences. <i>Nature</i> 2009 Nov 19;462(7271):315-22. PMID: 19829295 Hawkins RD, Hon GC, Lee LK, Ngo Q et al. Distinct epigenomic landscapes of pluripotent and lineage-committed human cells. <i>Cell Stem Cell</i> 2010 May 7;6(5):479-91. PMID: 20452322 Bernstein BE, Stamatoyannopoulos JA, Costello JF, Ren B et al. The NIH Roadmap Epigenomics Mapping Consortium. <i>Nat Biotechnol</i> 2010 Oct;28(10):1045-8. PMID: 20944595 Lister R, Pelizzola M, Kida YS, Hawkins RD et al. Hotspots of aberrant epigenomic reprogramming in human induced pluripotent stem cells. <i>Nature</i> 2011 Mar 3;471(7336):68-73. PMID: 21289626
Human	Adult	Right Atrium	ChIP-seq	H3K27ac, H3K4me1, H3K4me3, H3K9me3, H3K27me3, H3K36me3	http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE16256	Lister R, Pelizzola M, Dowen RH, Hawkins RD et al. Human DNA methylomes at base resolution show widespread epigenomic differences. <i>Nature</i> 2009 Nov 19;462(7271):315-22. PMID: 19829295 Hawkins RD, Hon GC, Lee LK, Ngo Q et al. Distinct epigenomic landscapes of pluripotent and lineage-committed human cells. <i>Cell Stem Cell</i> 2010 May 7;6(5):479-91. PMID: 20452322 Bernstein BE, Stamatoyannopoulos JA, Costello JF, Ren B et al. The NIH Roadmap Epigenomics Mapping Consortium. <i>Nat Biotechnol</i> 2010 Oct;28(10):1045-8. PMID: 20944595 Lister R, Pelizzola M, Kida YS, Hawkins RD et al. Hotspots of aberrant epigenomic reprogramming in human induced pluripotent stem cells. <i>Nature</i> 2011 Mar 3;471(7336):68-73. PMID: 21289626
Human	Adult	Left Ventricle	ChIP-seq	H3K27ac, H3K4me1, H3K4me3, H3K9me3, H3K27me3, H3K36me3	http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE16256	Lister R, Pelizzola M, Dowen RH, Hawkins RD et al. Human DNA methylomes at base resolution show widespread epigenomic differences. <i>Nature</i> 2009 Nov 19;462(7271):315-22. PMID: 19829295 Hawkins RD, Hon GC, Lee LK, Ngo Q et al. Distinct epigenomic landscapes of pluripotent and lineage-committed human cells. <i>Cell Stem Cell</i> 2010 May 7;6(5):479-91. PMID: 20452322 Bernstein BE, Stamatoyannopoulos JA, Costello JF, Ren B et al. The NIH Roadmap Epigenomics Mapping Consortium. <i>Nat Biotechnol</i> 2010 Oct;28(10):1045-8. PMID: 20944595

						Lister R, Pelizzola M, Kida YS, Hawkins RD et al. Hotspots of aberrant epigenomic reprogramming in human induced pluripotent stem cells. <i>Nature</i> 2011 Mar 3;471(7336):68-73. PMID: 21289626
Mouse	HL-1 cells	ChIP-seq	Gata4, Mef2a, Nkx2-5, Srf, Tbx5, p300	http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE21529	He A, Kong SW, Ma Q, Pu WT. Co-occupancy by multiple cardiac transcription factors identifies transcriptional enhancers active in heart. <i>Proc Natl Acad Sci U S A</i> 2011 Apr 5;108(14):5632-7. PMID: 21415370	
Mouse	HL-1 cells	ChIP-seq	H3ac and Srf	http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE26397	Schlesinger J, Schueler M, Grunert M, Fischer JJ et al. The cardiac transcription network modulated by Gata4, Mef2a, Nkx2.5, Srf, histone modifications, and microRNAs. <i>PLoS Genet</i> 2011 Feb;7(2):e1001313. PMID: 21379568	
Mouse	Cardiac myocytes (sham control)	ChIP-seq	H3K9ac, H3K27ac, H3K4me3, H3K79me2, H3K9me2, H3K9me3, H3K27me3	https://www.ebi.ac.uk/arrayexpress/experiments/E-MTAB-1506/	Papaït R, Cattaneo P, Kunderfranco P, Greco C, Carullo P, Guffanti A, Vigano V, Stirparo GG, Latronico MV, Hasenfuss G, Chen J, Condorelli G. Genome-wide analysis of histone marks identifying an epigenetic signature of promoters and enhancers underlying cardiac hypertrophy. <i>Proc Natl Acad Sci U S A</i> (2013). PMID: 24284169	
Mouse	Cardiac myocytes (transverse aortic constriction)	ChIP-seq	H3K9ac, H3K27ac, H3K4me3, H3K79me2, H3K9me2, H3K9me3, H3K27me3	https://www.ebi.ac.uk/arrayexpress/experiments/E-MTAB-1506/	Papaït R, Cattaneo P, Kunderfranco P, Greco C, Carullo P, Guffanti A, Vigano V, Stirparo GG, Latronico MV, Hasenfuss G, Chen J, Condorelli G. Genome-wide analysis of histone marks identifying an epigenetic signature of promoters and enhancers underlying cardiac hypertrophy. <i>Proc Natl Acad Sci U S A</i> (2013). PMID: 24284169	
Mouse	Foetus (E11.5)	Heart	ChIP-seq	H3K27ac	http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE52386	Nord AS, Blow MJ, Attanasio C, Akiyama JA et al. Rapid and pervasive changes in genome-wide enhancer usage during mammalian development. <i>Cell</i> 2013 Dec 19;155(7):1521-31. PMID: 24360275
Mouse	Foetus (E14.5)	Heart	ChIP-seq	H3K27ac	http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE52386	Nord AS, Blow MJ, Attanasio C, Akiyama JA et al. Rapid and pervasive changes in genome-wide enhancer usage during mammalian development. <i>Cell</i> 2013 Dec 19;155(7):1521-31. PMID: 24360275
Mouse	Foetus (E17.5)	Heart	ChIP-seq	H3K27ac	http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE52386	Nord AS, Blow MJ, Attanasio C, Akiyama JA et al. Rapid and pervasive changes in genome-wide enhancer usage during mammalian development. <i>Cell</i> 2013 Dec 19;155(7):1521-31. PMID: 24360275
Mouse	Postnatal day 0	Heart	ChIP-seq	H3K27ac	http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE52386	Nord AS, Blow MJ, Attanasio C, Akiyama JA et al. Rapid and pervasive changes in genome-wide enhancer usage during mammalian development. <i>Cell</i> 2013 Dec 19;155(7):1521-31. PMID: 24360275
Mouse	Adult (1 week)	Heart	ChIP-seq	H3K27ac	http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE52386	Nord AS, Blow MJ, Attanasio C, Akiyama JA et al. Rapid and pervasive changes in genome-wide enhancer usage during mammalian development. <i>Cell</i> 2013 Dec 19;155(7):1521-31. PMID: 24360275
Mouse	Adult (3 weeks)	Heart	ChIP-seq	H3K27ac	http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE52386	Nord AS, Blow MJ, Attanasio C, Akiyama JA et al. Rapid and pervasive changes in genome-wide enhancer usage during mammalian development. <i>Cell</i> 2013 Dec 19;155(7):1521-31. PMID: 24360275
Mouse	Adult (8 weeks)	Heart	ChIP-seq	H3K27ac	http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE52386	Nord AS, Blow MJ, Attanasio C, Akiyama JA et al. Rapid and pervasive changes in genome-wide enhancer usage during mammalian development. <i>Cell</i> 2013 Dec 19;155(7):1521-31. PMID: 24360275
Mouse	Cardiac precursors (Differentiation day 5.3)	ChIP-seq	H3K4me1, H3K27ac, H3K27me3, H3K4me3, RNAPolIII Ser5P	http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE47949	Wamstad JA, Alexander JM, Truty RM, Shrikumar A et al. Dynamic and coordinated epigenetic regulation of developmental transitions in the cardiac lineage. <i>Cell</i> 2012 Sep 28;151(1):206-20. PMID: 22981692	
Mouse	Cardiomyocytes (Differentiation day 10)	ChIP-seq	H3K4me1, H3K27ac, H3K27me3, H3K4me3, RNAPolIII Ser5P	http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE47949	Wamstad JA, Alexander JM, Truty RM, Shrikumar A et al. Dynamic and coordinated epigenetic regulation of developmental transitions in the cardiac lineage. <i>Cell</i> 2012 Sep 28;151(1):206-20. PMID: 22981692	
Mouse	Adult	Heart	ChIP-seq	Tbx3, Gata4, Nkx2-5, p300	http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE35151	van den Boogaard M, Wong LY, Tessadori F, Bakker ML et al. Genetic variation in T-box binding element functionally affects SCN5A/SCN10A enhancer. <i>J Clin Invest</i> 2012 Jul 2;122(7):2519-30. PMID: 22706305
Mouse	Adult (8 weeks)	Heart	ChIP-seq	p300, RNAPolIII, CTCF	http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE36027	PRJNA63475 Mouse ENCODE functional genomics data
Mouse	Foetus (E11.5)	Heart	ChIP-seq	p300	http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE22549	Blow MJ, McCulley DJ, Li Z, Zhang T et al. ChIP-Seq identification of weakly conserved heart enhancers. <i>Nat Genet</i> 2010 Sep;42(9):806-10. PMID: 20729851

Mouse	Adult	Heart	ChIP-seq	Tbx3	http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE44821	de Boer BA, van Duijvenboden K, van den Boogaard M, Christoffels VM et al. OccuPeak: ChIP-Seq peak calling based on internal background modelling. <i>PLoS One</i> 2014;9(6):e99844. PMID: 24936875
Mouse	Adult (8 weeks)	Heart	ChIP-seq	CTCF, H3K4me1, H3K4me3, H3K27ac, p300, RNAPolII	http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE29218	Shen Y, Yue F, McCleary DF, Ye Z et al. A map of the cis-regulatory sequences in the mouse genome. <i>Nature</i> 2012 Aug 2;488(7409):116-20. PMID: 22763441
Mouse	Foetus (E14.5)	Heart	ChIP-seq	CTCF, H3K4me1, H3K4me3, H3K27ac, RNAPolII	http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE29218	Shen Y, Yue F, McCleary DF, Ye Z et al. A map of the cis-regulatory sequences in the mouse genome. <i>Nature</i> 2012 Aug 2;488(7409):116-20. PMID: 22763441
Mouse	Adult (12 weeks)	Heart	ChIP-seq	Pitx2	http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE47928	Tao Y, Zhang M, Li L, Bai Y et al. Pitx2, an atrial fibrillation predisposition gene, directly regulates ion transport and intercalated disc genes. <i>Circ Cardiovasc Genet</i> 2014 Feb;7(1):23-32. PMID: 24395921
Mouse	Adult (12 weeks)	Heart	ChIP-seq	H3K9ac, RNAPolII	http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE50637	Sayed D, He M, Yang Z, Lin L et al. Transcriptional regulation patterns revealed by high resolution chromatin immunoprecipitation during cardiac hypertrophy. <i>J Biol Chem</i> 2013 Jan 25;288(4):2546-58. PMID: 23229551
Mouse	Adult (12 weeks)	Heart (transverse aortic constriction)	ChIP-seq	H3K9ac, RNAPolII	http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE50637	Sayed D, He M, Yang Z, Lin L et al. Transcriptional regulation patterns revealed by high resolution chromatin immunoprecipitation during cardiac hypertrophy. <i>J Biol Chem</i> 2013 Jan 25;288(4):2546-58. PMID: 23229551
Mouse	Postnatal day 1-2	Heart	ChIP-seq	H3K9ac, RNAPolII	http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE50637	Sayed D, He M, Yang Z, Lin L et al. Transcriptional regulation patterns revealed by high resolution chromatin immunoprecipitation during cardiac hypertrophy. <i>J Biol Chem</i> 2013 Jan 25;288(4):2546-58. PMID: 23229551
Mouse		Heart (sham)	ChIP-seq	Brd4, RNAPolII	http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE46668	Anand P, Brown JD, Lin CY, Qi J et al. BET bromodomains mediate transcriptional pause release in heart failure. <i>Cell</i> 2013 Aug 1;154(3):569-82. PMID: 23911322
Mouse		Heart (transverse aortic constriction)	ChIP-seq	Brd4, RNAPolII	http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE46668	Anand P, Brown JD, Lin CY, Qi J et al. BET bromodomains mediate transcriptional pause release in heart failure. <i>Cell</i> 2013 Aug 1;154(3):569-82. PMID: 23911322
Mouse		Heart (transverse aortic constriction + treatment with JQ1)	ChIP-seq	Brd4, RNAPolII	http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE46668	Anand P, Brown JD, Lin CY, Qi J et al. BET bromodomains mediate transcriptional pause release in heart failure. <i>Cell</i> 2013 Aug 1;154(3):569-82. PMID: 23911322
Mouse	Foetus (E10.5)	Chamber myocardium	ChIP-seq	H3K27ac	http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE55611	Stefanovic S, Barnett P, van Duijvenboden K, Weber D et al. GATA-dependent regulatory switches establish atrioventricular canal specificity during heart development. <i>Nat Commun</i> 2014 Apr 28;5:3680. PMID: 24770533
Mouse	Foetus (E10.5)	Atrioventricular canal	ChIP-seq	H3K27ac	http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE55611	Stefanovic S, Barnett P, van Duijvenboden K, Weber D et al. GATA-dependent regulatory switches establish atrioventricular canal specificity during heart development. <i>Nat Commun</i> 2014 Apr 28;5:3680. PMID: 24770533
Human		Heart	DNase-seq		http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE32970	Thurman RE, Rynes E, Humbert R, Vierstra J et al. The accessible chromatin landscape of the human genome. <i>Nature</i> 2012 Sep 6;489(7414):75-82. PMID: 22955617
						Natarajan A, Yardimci GG, Sheffield NC, Crawford GE et al. Predicting cell-type-specific gene expression from regions of open chromatin. <i>Genome Res</i> 2012 Sep;22(9):1711-22. PMID: 22955983
Human	Adult (3 years)	Heart	DNase-seq		http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE18927	Bernstein BE, Stamatoyannopoulos JA, Costello JF, Ren B et al. The NIH Roadmap Epigenomics Mapping Consortium. <i>Nat Biotechnol</i> 2010 Oct;28(10):1045-8. PMID: 20944595
						Neph S, Vierstra J, Stergachis AB, Reynolds AP et al. An expansive human regulatory lexicon encoded in transcription factor footprints. <i>Nature</i> 2012 Sep 6;489(7414):83-90. PMID: 22955618
						Maurano MT, Humbert R, Rynes E, Thurman RE et al. Systematic localization of common disease-associated variation in regulatory DNA. <i>Science</i> 2012 Sep 7;337(6099):1190-5. PMID: 22955828
Human	Foetus (Various stages)	Heart	DNase-seq		http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE18927	Bernstein BE, Stamatoyannopoulos JA, Costello JF, Ren B et al. The NIH Roadmap Epigenomics Mapping Consortium. <i>Nat Biotechnol</i> 2010 Oct;28(10):1045-8. PMID: 20944595
						Neph S, Vierstra J, Stergachis AB, Reynolds AP et al. An expansive human regulatory lexicon encoded in transcription factor footprints. <i>Nature</i> 2012 Sep 6;489(7414):83-90. PMID: 22955618

					Maurano MT, Humbert R, Rynes E, Thurman RE et al. Systematic localization of common disease-associated variation in regulatory DNA. <i>Science</i> 2012 Sep 7;337(6099):1190-5. PMID: 22955828
Human		Cardiac Fibroblast (HCF) cell line	DNase-seq	http://www.ncbi.nlm.nih.gov/epigenomics/13920	ENCODE Project Consortium. The ENCODE (ENCyclopedia Of DNA Elements) Project. <i>Science</i> . 2004 Oct 22;306(5696):636-40. PMID: 15499007
Human		Cardiac Myocyte (HCM) cell line	DNase-seq	http://www.ncbi.nlm.nih.gov/epigenomics/13922	ENCODE Project Consortium. The ENCODE (ENCyclopedia Of DNA Elements) Project. <i>Science</i> . 2004 Oct 22;306(5696):636-40. PMID: 15499007
Human	Foetus (120 Days)	Heart	DNase-seq	http://www.ncbi.nlm.nih.gov/epigenomics/20608	Bernstein BE, Stamatoyannopoulos JA, Costello JF, Ren B et al. The NIH Roadmap Epigenomics Mapping Consortium. <i>Nat Biotechnol</i> 2010 Oct;28(10):1045-8. PMID: 20944595
Mouse	Adult (10 weeks)	Heart cells	FAIRE-seq	http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE33632	Pang B, Qiao X, Janssen L, Velds A et al. Drug-induced histone eviction from open chromatin contributes to the chemotherapeutic effects of doxorubicin. <i>Nat Commun</i> 2013;4:1908. PMID: 23715267
Mouse	Adult (10 weeks)	Heart cells (4 hours post treatment with doxorubicin)	FAIRE-seq	http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE33632	Pang B, Qiao X, Janssen L, Velds A et al. Drug-induced histone eviction from open chromatin contributes to the chemotherapeutic effects of doxorubicin. <i>Nat Commun</i> 2013;4:1908. PMID: 23715267
Mouse	Adult (10 weeks)	Heart cells (4 hours post treatment with etoposide)	FAIRE-seq	http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE33632	Pang B, Qiao X, Janssen L, Velds A et al. Drug-induced histone eviction from open chromatin contributes to the chemotherapeutic effects of doxorubicin. <i>Nat Commun</i> 2013;4:1908. PMID: 23715267
Human	Foetus (110 Days)	Heart	Bisulfite-Seq	http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE17312	Bernstein BE, Stamatoyannopoulos JA, Costello JF, Ren B et al. The NIH Roadmap Epigenomics Mapping Consortium. <i>Nat Biotechnol</i> 2010 Oct;28(10):1045-8. PMID: 20944595
Human	Foetus (101 Days)	Heart	Bisulfite-Seq	http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE17312	Bernstein BE, Stamatoyannopoulos JA, Costello JF, Ren B et al. The NIH Roadmap Epigenomics Mapping Consortium. <i>Nat Biotechnol</i> 2010 Oct;28(10):1045-8. PMID: 20944595
Human	Adult	Aorta	Bisulfite-Seq	http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE16256	Lister R, Pelizzola M, Dowen RH, Hawkins RD et al. Human DNA methylomes at base resolution show widespread epigenomic differences. <i>Nature</i> 2009 Nov 19;462(7271):315-22. PMID: 19829295 Hawkins RD, Hon GC, Lee LK, Ngo Q et al. Distinct epigenomic landscapes of pluripotent and lineage-committed human cells. <i>Cell Stem Cell</i> 2010 May 7;6(5):479-91. PMID: 20452322 Bernstein BE, Stamatoyannopoulos JA, Costello JF, Ren B et al. The NIH Roadmap Epigenomics Mapping Consortium. <i>Nat Biotechnol</i> 2010 Oct;28(10):1045-8. PMID: 20944595
Human	Adult	Right Atrium	Bisulfite-Seq	http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE16256	Lister R, Pelizzola M, Kida YS, Hawkins RD et al. Hotspots of aberrant epigenomic reprogramming in human induced pluripotent stem cells. <i>Nature</i> 2011 Mar 3;471(7336):68-73. PMID: 21289626
Human	Adult	Left Ventricle	Bisulfite-Seq	http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE16256	Lister R, Pelizzola M, Dowen RH, Hawkins RD et al. Human DNA methylomes at base resolution show widespread epigenomic differences. <i>Nature</i> 2009 Nov 19;462(7271):315-22. PMID: 19829295 Bernstein BE, Stamatoyannopoulos JA, Costello JF, Ren B et al. The NIH Roadmap Epigenomics Mapping Consortium. <i>Nat Biotechnol</i> 2010 Oct;28(10):1045-8. PMID: 20944595 Lister R, Pelizzola M, Kida YS, Hawkins RD et al. Hotspots of aberrant epigenomic reprogramming in human induced pluripotent stem cells. <i>Nature</i> 2011 Mar 3;471(7336):68-73. PMID: 21289626

Hawkins RD, Hon GC, Lee LK, Ngo Q et al. Distinct epigenomic landscapes of pluripotent and lineage-committed human cells. *Cell Stem Cell* 2010 May 7;6(5):479-91. PMID: 20452322

Bernstein BE, Stamatoyannopoulos JA, Costello JF, Ren B et al. The NIH Roadmap Epigenomics Mapping Consortium. *Nat Biotechnol* 2010 Oct;28(10):1045-8. PMID: 20944595

Lister R, Pelizzola M, Kida YS, Hawkins RD et al. Hotspots of aberrant epigenomic reprogramming in human induced pluripotent stem cells. *Nature* 2011 Mar 3;471(7336):68-73. PMID: 21289626

Mouse	Adult	Heart	Bisulfite-Seq	http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE42836	Hon GC, Rajagopal N, Shen Y, McCleary DF et al. Epigenetic memory at embryonic enhancers identified in DNA methylation maps from adult mouse tissues. <i>Nat Genet</i> 2013 Oct;45(10):1198-206. PMID: 23995138
Mouse	Foetus (E11.5, E14.5)	Heart	MRE-seq/MSFE/MPS	http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE55141	Chamberlain AA, Lin M, Lister RL, Maslov AA et al. DNA methylation is developmentally regulated for genes essential for cardiogenesis. <i>J Am Heart Assoc</i> 2014 Jun 19;3(3):e000976. PMID: 24947998
Human		Cardiac fibroblast cells	CAGE-seq	http://enhancer.binf.ku.dk/presets/CL:0002548_cardiac_fibroblast_differentially_expressed_enhancers.bed	Andersson R, Gebhard C, Miguel-Escalada I, Hoof I, Bornholdt J, Boyd M, Chen Y, Zhao X, Schmidl C, Suzuki T, Ntini E, Arner E, Valen E, Li K, Schwarzfischer L, Glatz D, Raithel J, Lilje B, Rapin N, Bagger FO, Jørgensen M, Andersen PR, Bertin N, Rackham O, Burroughs AM, Baillie JK, Ishizu Y, Shimizu Y, Furuhashi E, Maeda S, Negishi Y, Mungall CJ, Meehan TF, Lassmann T, Itoh M, Kawaji H, Kondo N, Kawai J, Lennartsson A, Daub CO, Heutink P, Hume DA, Jensen TH, Suzuki H, Hayashizaki Y, Müller F; FANTOM Consortium, Forrest AR, Carninci P, Rehli M, Sandelin A. An atlas of active enhancers across human cell types and tissues. <i>Nature</i> . 2014 Mar 27;507(7493):455-61. PMID: 24670763
Human		Cardiac myocyte cells	CAGE-seq	http://enhancer.binf.ku.dk/presets/CL:0000746_cardiac_myocyte_differentially_expressed_enhancers.bed	Andersson R, Gebhard C, Miguel-Escalada I, Hoof I, Bornholdt J, Boyd M, Chen Y, Zhao X, Schmidl C, Suzuki T, Ntini E, Arner E, Valen E, Li K, Schwarzfischer L, Glatz D, Raithel J, Lilje B, Rapin N, Bagger FO, Jørgensen M, Andersen PR, Bertin N, Rackham O, Burroughs AM, Baillie JK, Ishizu Y, Shimizu Y, Furuhashi E, Maeda S, Negishi Y, Mungall CJ, Meehan TF, Lassmann T, Itoh M, Kawaji H, Kondo N, Kawai J, Lennartsson A, Daub CO, Heutink P, Hume DA, Jensen TH, Suzuki H, Hayashizaki Y, Müller F; FANTOM Consortium, Forrest AR, Carninci P, Rehli M, Sandelin A. An atlas of active enhancers across human cell types and tissues. <i>Nature</i> . 2014 Mar 27;507(7493):455-61. PMID: 24670763
Human		Heart	CAGE-seq	http://enhancer.binf.ku.dk/presets/UBERON:000948_heart_differentially_expressed_enhancers.bed	Andersson R, Gebhard C, Miguel-Escalada I, Hoof I, Bornholdt J, Boyd M, Chen Y, Zhao X, Schmidl C, Suzuki T, Ntini E, Arner E, Valen E, Li K, Schwarzfischer L, Glatz D, Raithel J, Lilje B, Rapin N, Bagger FO, Jørgensen M, Andersen PR, Bertin N, Rackham O, Burroughs AM, Baillie JK, Ishizu Y, Shimizu Y, Furuhashi E, Maeda S, Negishi Y, Mungall CJ, Meehan TF, Lassmann T, Itoh M, Kawaji H, Kondo N, Kawai J, Lennartsson A, Daub CO, Heutink P, Hume DA, Jensen TH, Suzuki H, Hayashizaki Y, Müller F; FANTOM Consortium, Forrest AR, Carninci P, Rehli M, Sandelin A. An atlas of active enhancers across human cell types and tissues. <i>Nature</i> . 2014 Mar 27;507(7493):455-61. PMID: 24670763