PPP1I	1R13L ←	<<<	< < <	45,88				45,888	11111	45,888 UCSC	1 kb hg19 50¢ 45,889,00¢ 45,889,50¢ 45,890,00¢ 45,890,50¢ 45,8 Genes (RefSeq, GenBank, CCDS, Rfam, tRNAs & Comparative Genomics)	391,0	000	< < < 	<<<
PPP1I	IR13L ÷			11		***	· · · · ·		<u> </u>	C/D and H//	lincRNA and TUCP transcripts ICA Box snoRNAs, scaRNAs, and microRNAs from snoRNABase and miRBase CTR147 CpG merge methylation level CTR149 CpG merge methylation level		***		***
CTR149 CTR150 CTR151				11	 					il di H di	CTR150 CpG merge methylation level		1		
CTR152 CTR153		l	 	11			1		1 		CTR152 CpG merge methylation level			I	
CTR154		 	 							11 III 1 11 IJ.	CTR154 CpG merge methylation level CTR84 CpG merge methylation level CTR854 CpG merge methylation level CTR85 CpG merge methylation level			 	1 1
CTR85 CTR86 CTR97						ĺ			 	11 111	CTR85 CpG merge methylation level CTR86 CpG merge methylation level CTR86 CpG merge methylation level CTR97 CpG merge methylation level	 			ı
CTR98				1	1	 	 	İ	1	11 ih ih 1 16	CTR98 CpG merge methylation level			 	
CTR103 CTR104				! []	 		1 II 1 II				CTR103 CpG merge methylation level		i l		 -
CTR106 CTR107			11 11	ĺ	l	ı	 		l	1 , 1h	CTR106 CpG merge methylation level CTR107 CpG merge methylation level CTR108 CpG merge methylation level	II	li I	 	
CTR108 CTR110 CTR132		1] [1	11				ıl	ıl 11 11	CTR100 CpC integer interly auton level i i.i. CTR110 CpG merge methylation level ii. CTR132 CpG merge methylation level			 - -	
CTR134 CTR148		hı] d n	ij		ı	1				CTR134 CpG merge methylation level CTR148 CpG merge methylation level		1	l [- -
CTR111 CTR113				((ļ			1		CTR113 CpG merge methylation level			 	.
CTR114 CTR117			I	I			III		l		CTR114 CpG merge methylation level I				ı
CTR118 CTR126 CTR127							111			11 1 11	CTR126 CpG merge methylation level . IIII				
CTR128 CTR129		11]]		I		Ì	lh 1 ili	CTR128 CpG merge methylation level		ı 1] 	
CTR131 AT BS 03		a1		1						.1.4	CTR131 CpG merge methylation level		(l 		
AL BS 3 11 Aorta BS 03										¦¦ <mark>∥</mark> ві 	Adult Liver Bisulfite-Seq Donor 3 Library WGBS_Lib 11 EA Release 8	, " 			
Esophagus BS (03	 	- 1 1	11 11 11					, , , , , , , , , , , , , , , , , , ,	- 1 1 11 da 1	UCSD Esophagus Bisulfite-Seq Donor STL003 EA Release 9				
FT BS 43 65 Gastric BS 03		 	44 	11		, 			(hymus Bisulfite-Seq Donor UW H24943 Library WGBS_Lib 65 EA Release 9 UCSD Gastric Bisulfite-Seq Donor STL003 EA Release 9	. (1) - -			
LV BS 01 LV BS 03		a 61 		#1]]]1		,			r 		UCSD Left Ventricle Bisulfite-Seq Donor STL001 EA Release 9	#	a 		
Lung BS 02 Ovary BS 02				#1 		;			(UCSD Lung Bisulfite-Seq Donor STL002 EA Release 9 UCSD Ovary Bisulfite-Seq Donor STL002 EA Release 9				
Pancreas BS 03	3			11 11					1 		UCSD Pancreas Bisulfite-Seq Donor STL003 EA Release 9 UCSD Psoas Muscle Bisulfite-Seq Donor STL003 EA Release 9				
RA BS 03				11 11					(UCSD Right Atrium Bisulfite-Seq Donor STL003 EA Release 9 UCSD Right Ventricle Bisulfite-Seq Donor STL003 EA Release 9				
RV BS 03 SC BS 01				11 11						 	UCSD Sigmoid Colon Bisulfite-Seq Donor STL001 EA Release 9 UCSD Sigmoid Colon Bisulfite-Seq Donor STL001 EA Release 9 UCSD Sigmoid Colon Bisulfite-Seq Donor STL003 EA Release 9				
SC BS 03 SI BS 01				11 11						11 di 11 di					
Spleen BS 03 Thymus BS 01				11						th th	UCSD Spleen Bisulfite-Seq Donor STL003 EA Release 9 UCSD Thymus Bisulfite-Seq Donor STL001 EA Release 9 UCSD Thymus Bisulfite-Seq Donor STL001 EA Release 9 DNA methylation in brain tissue (bigWig)	1 			
Brain Methyl 2 Kidney Methyl 2	2										DNA methylation in kidney tissue (bigWig)				
Placenta1 Methy											DNA methylation in placenta (biological replicate 1) (bigWig)				
Placenta3 Methy	ıyl 2										DNA methylation in placenta (biological replicate 3) (bigWig) Human_Cerebellum_Meth				
Kidney NKcells Sperm	-										Human_Kidney_Meth Human_NKcells_Meth Human_Sperm_Meth				
Sperm NormalPancreas NormalPancreas	_] b]							Human_NormalPancreas1_Meth Laut Laut Human_NormalPancreas2_Meth				
93A 93N	_			11			111				Human_93N_Meth Human_93N_Meth				
Epidermis-old-su	sun-pro			11							Human_Epidermis-old-sun-exposed_Meth Human_Epidermis-old-sun-protected_Meth Human_Epidermis-old-sun-protected_Meth				
Epidermis-young Epidermis-young Buccals	_			11							Human_Epidermis-young-sun-protected_Meth Human_Buccals_Meth				
Sperm BloodHealthy	_			11			1				Human_BloodHealthy_Meth				
CD4T-100yr CD4T-Newborn	_									Distinct Humar	in DNA Methylomes from Different Ages, Heyn 2012 : Human_CD4T-100yr_Meth DNA Methylomes from Different Ages, Heyn 2012 : Human_CD4T-Newborn_Meth				
PBMC CD133HSC Macrophage	_									<u> </u>	man DNA Methylomes from Different Ages, Heyn 2012 : Human_PBMC_Meth I Human Hematopoietic Stem Cells, Hodges 2011 : Human_CD133HSC_Meth Roadmap 2015 : Human_Macrophage_Meth				
Macrophage NK BCell	-			11							Roadmap 2015 : Human_NK_Meth Roadmap 2015 : Human_NK_Meth Human_BCell_Meth				
CD133HSC	_										Human_CD133HSC_Meth Human_HSPC_Meth				
Neut H1	-			11							Human_Neut_Meth Human_H1_Meth Human_H1_Meth				
H1BMP4 H1-mesendoden H1-NPC	rm _			11							Human_H1BMP4_Meth				
Mesenchymal IMR90	_						111 111 110				Human_MR80_Meth Human_MR90_Meth				
IMR90 BS 1a							1		IMR90	Cell Line DNA	Methylation by Bisulfite-seq Signal from REMC/UCSD (Library:methylC-seq_imr90_r1a)				
BloodALLL1	-						111				Human_BloodALLL1_Meth Human_IMR90_Meth				
MCF7 ColonCancer ColonCancer	_							focal I			Human MCF7_Meth and long-range hypomethylation in colorectal cancer, Berman 2012 : Human_ColonCancer_Meth tion variation in epigenetic domains across cancer types. : Human_ColonCancer_Meth				
HCC1954 HepG2	_			11			1				Human Breast Cancer, Hon 2012 : Human HCC1954_Meth Human Breast Cancer, Hon 2012 : Human HCC1954_Meth Human HepG2_Meth				11
PancreaticCance	_			11						11 11	Human_PancreaticCancer2_Meth Human_PancreaticCancer2_Meth				
PancreaticCance	cer4										Human_PancreaticCancer3_Meth Human_PancreaticCancer4_Meth Human_PancreaticCancer5_Meth				
PancreaticCance PancreaticCance PancreaticCance	cer6						110				Jilin				
PancreaticCance PancreaticCance	cer8										Human_PancreaticCancer8_Meth Human_PancreaticCancer9_Meth Human_PancreaticCancer9_Meth				
PancreaticCance	_			1						Lie	Human_PancreaticCancer10_Meth				
Layered H3K27/	_									H3K4Me ²	Mark (Often Found Near Regulatory Elements) on 7 cell lines from ENCODE Mark (Often Found Near Regulatory Elements) on 7 cell lines from ENCODE				
Layered H3K4M DNase Clu	_										4Me3 Mark (Often Found Near Promoters) on 7 cell lines from ENCODE Nasel Hypersensitivity Clusters in 125 cell types from ENCODE (V3) n Factor ChIP-seq Clusters (161 factors) from ENCODE with Factorbook Motifs				
Txn Factor LNG.IN LNG.IN	MR90									. ranscriptio	n Factor ChIP-seq Clusters (161 factors) from ENCODE with Factorbook Motifs chromHMM tracks from Roadmap Restriction Enzymes from REBASE				
Restr Enzy Bos NH Bos PPP1I Mus Ppp	KPD1 +		 	■ ■	I	 	· · · · · · · · · · · · · · · · · · ·	## I	· · · · · · · · · · · · · · · · · · ·		Restriction Enzymes from REBASE Non-Human RefSeq Genes	<	I		I I
Mus Ppp PPP1I PPP1I	IR13L ÷	· · · · · · · · · · · · · · · · · · ·	· · · · · · · · · · · · · · · · · · ·	***	· · · · ·	***	· · · · · ·				UCSC annotations of RefSeq RNAs (NM_* and NR_*) CpG Islands (Islands < 300 Bases are Light Green)	· · · ·	· · · · · · · · · · · · · · · · · · ·	. 	***
Mammal Cons	4_							-11		······································	CpG: 72 Placental Mammal Basewise Conservation by PhyloP Multiz Alignments of 46 Vertebrates	h dipersona		~~~***********************************	or-hear-mely
M Elep Opos	hesus Mouse = Dog = ephant = ossum =										Multiz Alignments of 46 Vertebrates				
	nicken picalis = orafish =										Repeating Elements by RepeatMasker				