Scale chr3 ZIC	š:		128,000 RDVGLGI	N P F A D G N	147,128 (GAFK	UCS	147 C Genes (Re	AFTSQAPG	k, CCDS, Rfam YAAAAALG	47,128,150 , tRNAs & Compai HHHHPGHVG	rative Genom	147,128,20 ics)			128,250 ASAQHSL	FAASA
CTR147 CTR149	I	. •			•	C/D and H	H/ACA Box s	CTR147 (CpG merge met	RNAs from snoRN hylation level hylation level	IABase and n	niRBase 	I =			<u>-</u>
CTR150 CTR151	_ = =		 1	_ ==_	- -			CTR151 (CpG merge met	hylation level	_	_ _ _	- - -			-
CTR152 CTR153 CTR154	I	- -	■ = _ I	-	- -	- -		CTR153 (CpG merge meti CpG merge meti CpG merge meti	hylation level	•	_			-	_
CTR84	I		 -	_ 	-			CTR84 C	pG merge meth	nylation level	-	_	• • • -		_ _ _	_ !
CTR86 CTR97			8 - 8 - - 8		- 1	= -			pG merge meth		=	_	 		=	- ·
CTR98	-	• _ • _	 l b	U	-	= =		CTR101 C	pG merge meth	hylation level	- I	-				
CTR103 CTR104 CTR106	- - -		- -	_ = E	- I	= _ _ =		CTR104 0	CpG merge met	hylation level	-	<u>-</u>			_	- •
CTR107 CTR108		=		 E	-		- - -		CpG merge met		•	.			_	1
CTR110 CTR132			- -	_ III_ _ III_	_			CTR132 (CpG merge met	hylation level		_	-	11	-	
CTR134 CTR148 CTR111	=	I _		- E	-	■-		CTR148 (CpG merge met L CpG merge met	hylation level		_			-	_ ·
CTR113				_ 88_		-	_	CTR113 (DpG merge met	■ _■ hylation level	_	_	- -		_	
CTR117 CTR118	- - -	- -	- • • _					CTR118 0	CpG merge met	hylation level		_			_	
CTR126 CTR127								CTR127 (CpG merge met CpG merge met	hylation level						
CTR128 CTR129 CTR131				■_	_		_	CTR129 (CpG merge met	_ ■■ hylation level		-				
AT BS 03 AL BS 3 11			_		-			er Bisulfite-Seq		nor STL003 EA R		-	 		•	_ !
Aorta BS 03 Esophagus BS 03	_ = =		. i	_ 11.	•	•-				STL003 EA Releas	_	-		1-1-	•	_
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Gastric BS 03			- -	_ In-	•	: :	UCS	SD Gastric Bisul	Ifite-Seq Donor	STL003 EA Relea	se 9	-		- -		
LV BS 03			 - B				UCSDI	Left Ventricle B	isulfite-Seq Dor	nor STL003 EA Re	lease 9	-		- J.		
Lung BS 02 Ovary BS 02	- • •		• •	_ I.I		- -	UCS	SD Ovary Bisult	fite-Seq Donor S	STL002 EA Releas STL002 EA Releas T STL003 EA Rele	se 9	-				■: -:
Pancreas BS 03 PM BS 03	-		. .	- II.	-	••	UCSD F	Psoas Muscle B	Bisulfite-Seq Do	nor STL003 EA Re	elease 9	-	• - 		-	= ·
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SI BS 01 Spleen BS 03			- -	• 1-1	i	H	1	Small Intestine E	Bisulfite-Seq Do	nor STL001 EA Re		-		-41-		•
Thymus BS 01 Brain Methyl 2				_ ====	•	•-	UCS		llfite-Seq Donor	STL001 EA Relea	se 9	-		•	-	•
Kidney Methyl 2 Placenta1 Methyl 2		-	 •		-		DNA r		lation in kidney	tissue (bigWig) cal replicate 1) (bi	gWig)		 		-	- 1 1
Placenta2 Methyl 2 Placenta3 Methyl 2	1.	I	1	. 111 . 111	-	11				cal replicate 2) (bi		ıl		.1111 .1111.	I	11
Cerebellum Kidney		-		111-	-		11 1	Hun	nan_Cerebellum uman_Kidney_I		-	11	1 _	_ 11 1	I	_ 1
NKcells Sperm				<u> </u>				Н	uman_NKcells_ uman_Sperm_I	Meth						
NormalPancreas1 NormalPancreas2 93A								Human	_NormalPancre _NormalPancre _NormalPancre Human_93A_M	eas2_Meth				1111.		
93N Epidermis-old-sun-ex	×					-			Human_93N_M dermis-old-sun-		-		-			
Epidermis-old-sun-pi	n-							Human_Epide	ermis-young-su	protected_Meth						
Epidermis-young-sur Buccals Sperm	1· 					-	-	Hu	uman_Buccals_							
BloodHealthy CD4T-100yr			-			Distinct Hu	man DNA M		an_BloodHealth	ny_Meth , Heyn 2012 : Hum	nan_CD4T-10	00yr_Meth		-		
CD4T-Newborn PBMC										Heyn 2012 : Huma			n			
CD133HSC Macrophage	_		_			Change	in Human I	Roadmap 20		dges 2011 : Humar	n_CD133HSC	C_Meth	•		-	
NK BCell CD133HSC							1.		Human_BCell_N	leth	-					
HSPC Neut						•			luman_HSPC_N	leth						
H1 H1BMP4								Hu	Human_H1_Meman_H1BMP4H1-mesendod	_Meth						
H1-mesendoderm H1-NPC Mesenchymal			-					Hu	_H1-mesendod uman_H1-NPC_ an_Mesenchym	Meth						
IMR90 BS 1a	-				IMI	R90 Cell Line D	NA Methylat	H	uman_IMR90_I		brary:methylC		0_r1a)			
BloodALLL2								Hum	nan_BloodALLL	1_Meth			• -			
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ColonCancer ColonCancer HCC1954				fo			lation variat	tion in epigeneti	ic domains acro	ss cancer types. :	Human_Colo			eth		
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PancreaticCancer3								Human_ Human_	PancreaticCan PancreaticCan	cer3_Meth				11111		
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PancreaticCancer11 Layered H3K27Ac			• •					Found Near Ad		Elements) on 7 ce						
Layered H3K4Me1 Layered H3K4Me3							8K4Me3 Mai	rk (Often Found	Near Promote	ements) on 7 cell li	rom ENCODE					
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LNG.IMR90 LNG.IMR90 Restr Enzymes	s E							Restriction	on Enzymes fro	m REBASE Genes						
Mus Zic Danio zic Salmo zic Xenopus zic1. Gallus ZIC	1 1 6 1 >>>:			•>>>>>>	>>>>>	>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>		·····	•>>>>>>	>>>>>>>>>>>>		·	· · · · · · · · · · · · · · · · · · ·	**************************************	·····	>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>
Rattus Zicʻ ZICʻ CpG: 180	1 >>>:		**********	*****	>>>>>	>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>	UC >>>>>> C	CSC annotations >>>>>>> CpG Islands (Isla	s of RefSeq RN	As (NM_* and NR_ >>>>>>> es are Light Green	_*) >>>>>> n)	>>>>>>	>>>>>>	>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>	· · · · · · · · · · · · · · · · · · ·	>>>>>>
Mammal Cons -4_ Rhesue	s						Pla		al Basewise Cor	Nervation by Phylo) P				AMPAN A	
Mouse Dog Elephan Opossun Chicker	g at															
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