Scale chr2: LBX2 <					74,72	6,800	< < < < <		s 26,850 Genes (RefSeq, 0		74,726,900 CCDS, Rfam, tl	RNAs & Com	74,726				74,727,	,ood	<del>&lt;&lt;&lt;&lt;</del>	***	***
CTR147 CTR149								C/D and H/A		ks, scaRNA FR147 CpG	and TUCP tran s, and microRt merge methy merge methy	NAs from sno lation level	RNABase a	and miRI	Base	-	_	_		1	
CTR150 CTR151			I	_		-	-		_ cı	TR150 CpG	merge methy	lation level	-			-	- -	-	<b>3</b> 3	=	
CTR152	=			_		-	<u>-</u>		_		merge methy						_	-	<b>-</b> -	=	1_ I 12 I
CTR154 CTR84						-					merge methyl			-			-	-			<b>-</b>
CTR85	=		 	_		-	_	<b>  • •</b>			merge methyla	_	_	-	 	-	- -	-		=	1. I 1. I
CTR97 CTR98	=			_		-					merge methyla merge methyla		- -	<b>.</b>		•	<b>-</b>	-	<b>-</b> -	- - -	
CTR101 CTR103	-		- - -						- c1	TR103 CpG	merge methy merge methy	lation level	_		-		- -	-	1.	•	11 I
CTR104 CTR106	-		 	-	 	-	-		СТ	TR106 CpG	merge methy	lation level	_		_	-	_	_		•	
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CTR110  CTR132						-			CT	TR132 CpG	merge methy	lation level	_	_# =		I	_	-		•	11 I -1 I
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CTR117						-	-	<b>-</b> -			merge methy				-		_	-	<b>88</b> - <b>8</b>	=	
CTR126 CTR127											merge methy						_	_	■-		•• I
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AL BS 3 11 Aorta BS 03	-			-	+   -			BI	Adult Liver Bisult  UCSD Aort		nor 3 Library V	_	_	e 8		·	-	-		-	
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Brain Methyl 2 Kidney Methyl 2							-				on in brain tiss										
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Kidney  NKcells											an_Kidney_Me ın_NKcells_Me										
Sperm - NormalPancreas1 - NormalPancreas2	•									Human_No	an_Sperm_Me  prmalPancreas  prmalPancreas	1_Meth					<u>-                                    </u>				
93A											nan_93A_Meti		-								11 1
Epidermis-old-sun-pro							•				mis-old-sun-ex						-		11	i	111
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Buccals - Sperm								-			n_Buccals_Mo		-					-			11 1
BloodHealthy – CD4T-100yr								Distinct Huma	an DNA Methylon		BloodHealthy_		uman_CD4	T-100yr	_Meth		-				11 1
CD4T-Newborn -								Distinct Hu	DNA Methylome	lomes from	Different Ages	s, Heyn 2012	: Human_P	BMC_M	leth						
CD133HSC  Macrophage								Changes in		map 2015 :	Human_Macr	ophage_Meth		BHSC_M	leth						
NK = BCell									F	Hum	015 : Human_I an_BCell_Met	th									
CD133HSC - HSPC -										Hum	_CD133HSC_I an_HSPC_Me nan_Neut_Met	th		-			-				1.
H1 H1BMP4							_			Hui	man_H1_Meth n_H1BMP4_M	1									1
H1-mesendoderm H1-NPC										Human_H	l-mesendoderi	m_Meth									-
Mesenchymal IMR90											Mesenchymal_ an_IMR90_Me			-							
IMR90 BS 1a	•			-			IMR90	Cell Line DNA	Methylation by E		Signal from R		(Library:me	thylC-se	eq_imr90	)_r1a)	-	-			11
BloodALLL1					-						BloodALLL1_ an_IMR90_Me						•			1	11 1
MCF7  ColonCancer						focal E			and long-range h	ypomethyla		tal cancer, Be					Meth				
ColonCancer  HCC1954							Incr	reased methyla	tion variation in e	st Cancer, I	omains across	man_HCC195			ancer_M	eth					<u>.</u>
HepG2 PancreaticCancer1								111		Human_Pa	ncreaticCance	r1_Meth									
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Restr Enzymes LBX2 ←							• • • • • • • • • • • • • • • • • • •		UCSC anr	Non-Hui notations of	man RefSeq G RefSeq RNAs	enes (NM_* and N	******	<del></del>	· · · · ·		<del>&lt; &lt; &lt; &lt; &lt;</del>	<<<	****	***	· · · · · · · · · · · · · · · · · · ·
CpG: 161 4 _ Mammal Cons -4 _		<b>.</b>	1, 5		Jih	1.244		- 444.0	Placental	Mammal Ba	asewise Conse	ervation by Ph		- <b>Q</b> -1-4,	( <b></b> - 1	ليبيي	الله ويوا		, 4 - 4 <sub>1</sub> 1	Ļ.	de, equa
Rhesus Mouse Dog Elephant					H					Multiz Alignr	ments of 46 Ve	ertebrates		7.							
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