

## Data supporting chr1:2488607 (rs1886730)

Score: 1b

Likely to affect binding and linked to expression of a gene target

Protein BindingProtein Binding
Filter:

Protein Binding
Filter:

Method	Location	<b>Bound Protein</b>	Cell Type	<b>Additional Info</b>	Reference
ChIP-seq	chr1:24885682488992	CTCF	K562		<b>ENCODE</b>
ChIP-seq	chr1:24881352488659	POLR2A	GM18505		<b>ENCODE</b>
ChIP-seq	chr1:24884582488894	MXI1	GM12878		<b>ENCODE</b>
ChIP-seq	chr1:24883222488658	RFX5	GM12878		<b>ENCODE</b>

ChIP-seq ch ChIP-seq ch ChIP-seq ch ChIP-seq ch ChIP-seq ch ChIP-seq ch MotifsMotifs Filter: Motifs	r1:24883702488640 US r1:24884072488627 PE r1:24884282488628 US r1:24869132488922 PC r1:24869132488922 PC	ATA2 SF1 BX3 SF1 DLR2A DLR2A DLR2A	K562 GM12878 GM12878 HepG2 GM12878 GM12878		ENCODE ENCODE ENCODE ENCODE ENCODE ENCODE ENCODE
Filter: <b>Method</b>	Location	Motif	Cell Type	PWM	Reference
Footprinting	chr1:24885972488609	Pax-4	Huh7	EGGG GE	<u>21106904</u>
Footprinting	chr1:24885972488609	Pax-4	Huh75	EGGG GE	<u>21106904</u>
Footprinting	chr1:24885972488609	Pax-4	Hsmm	EGGG GE	<u>21106904</u>
Footprinting	chr1:24885972488609	Pax-4	Hmec	EGGG GE	<u>21106904</u>
Footprinting	chr1:24885972488609	Pax-4	Hepg2	EGGG GE	<u>21106904</u>
Footprinting	chr1:24885972488609	Pax-4	H1hesc	EGGG GE	<u>21106904</u>
Footprinting	chr1:24885972488609	Pax-4	Gm19239	EGGG GE	<u>21106904</u>
Footprinting	chr1:24885972488609	Pax-4	Gm19238	EGGG GE	<u>21106904</u>
Footprinting	chr1:24885972488609	Pax-4	Gm18507	EGGG GE	<u>21106904</u>
Footprinting	chr1:24885972488609	Pax-4	Gm12892	EGGG GE	<u>21106904</u>
Footprinting	chr1:24885972488609	Pax-4	K562	EGGG GE	<u>21106904</u>
Footprinting	chr1:24885972488609	Pax-4	LncapAndro	EGGG GE	21106904
Footprinting	chr1:24885972488609	Pax-4	Lncap	EGGG GE	<u>21106904</u>

Footprinting	chr1:24885972488609	Pax-4	Myometr	ggg Gg	<u>21106904</u>
Footprinting	chr1:24885972488609	Pax-4	Panisd	EGGG GE	21106904
Footprinting	chr1:24885972488609	Pax-4	Phte	eggG Ge	21106904
Footprinting	chr1:24885932488619		GM12892	***************************************	21106903
Footprinting	chr1:24885972488609	Pax-4	8988t	EGGG GE	21106904
Footprinting	chr1:24885972488609	Pax-4	Chorion	EGGG GE	21106904
Footprinting	chr1:24885972488609	Pax-4	Fibrop	EGGG GE	21106904
Footprinting	chr1:24885972488609	Pax-4	Gm12891	EGGG GE	21106904
PWM	chr1:24885922488608	Bcl6b		<u> </u>	<u>19443739</u>
PWM	chr1:24885952488608	FOXO6		G-CGTGTGGGAA	23332764
PWM	chr1:24885972488609	Pax-4		EGGG GE	<u>16381825</u>
PWM	chr1:24885942488610	Ascl2		çç <mark>ç ççç</mark> ç	<u>19443739</u>
Single nucleoti Filter: Single nucleoti Filter:	desSingle nucleotides des				
Method	Location	Affected G	Gene Cell Typ	oe Additional Ir	nfo Reference
eQTL chr	:1:24886072488608 TN		Lymphoblas		<u>18846210</u>
Chromatin stru Filter:	ctureChromatin structure				
Chromatin stru	ecture				
Filter:					
Method	Location		J 1	Additional Info	Reference
DNase-seq	chr1:24813982489775	Psoasmuse	cleoc		ENCODE
DNase-seq DNase-seq	chr1:24814322489203 chr1:24814592495175	Heartoc H7es			ENCODE ENCODE
DNase-seq	chr1:24814772489257		frontaloc		ENCODE
DNase-seq	chr1:24814952490659	K562			ENCODE

ENCODE

DNase-seg chr1:2482568...2489067 8988t

DNase-seq	chr1:24829702490065	Frontalcortexoc		ENCODE
DNase-seq	chr1:24830282489148	K562	Sahactrl	ENCODE
DNase-seq	chr1:24830442489147	Ips		ENCODE
DNase-seq	chr1:24830612490251	K562	Nabut	ENCODE
DNase-seq	chr1:24830792492113	Lncap		ENCODE
DNase-seq	chr1:24831682493728	Chorion		ENCODE
DNase-seq	chr1:24839212489977	Gm12892		ENCODE
DNase-seq	chr1:24839412489963	H1hesc		ENCODE
DNase-seq	chr1:24839532489132	Cd20ro01794		ENCODE
DNase-seq	chr1:24839062489243	Imr90		ENCODE
DNase-seq	chr1:24842932488855	Huvec		ENCODE
DNase-seq	chr1:24852842489230	Hepatocytes		ENCODE
DNase-seq	chr1:24857922489098	Gm12891		ENCODE
DNase-seq	chr1:24858122489362	Medullo		ENCODE
DNase-seq	chr1:24859412489362	Medullod341		ENCODE
DNase-seq	chr1:24860932489171	Gm19239		ENCODE
DNase-seq	chr1:24861322489053	K562	Saha1u72hr	ENCODE
DNase-seq	chr1:24861662489011	Sknsh		ENCODE
DNase-seq	chr1:24861902488887	Gm20000		ENCODE
DNase-seq	chr1:24861972489119	Huh75		ENCODE
DNase-seq	chr1:24861972489131	Huh7		ENCODE
DNase-seq	chr1:24862252488902	Gm10266		ENCODE
DNase-seq	chr1:24862542489043	Hsmm		ENCODE
DNase-seq	chr1:24862572489177	Hmec		ENCODE
DNase-seq	chr1:24862572489195	Helas3		ENCODE
DNase-seq	chr1:24862602489174	Gm13976		ENCODE
DNase-seq	chr1:24862882489241	Mel2183		ENCODE
DNase-seq	chr1:24863012489086	Hepg2		ENCODE
DNase-seq	chr1:24863102489364	Osteobl		ENCODE
DNase-seq	chr1:24869032489238	Lncap	Andro	ENCODE
DNase-seq	chr1:24869132489047	Olfneurosphere		ENCODE
DNase-seq	chr1:24869562489114	K562G2mphase		ENCODE
DNase-seq	chr1:24870012489164	Phte		ENCODE
DNase-seq	chr1:24876032489101	K562G1phase		ENCODE
DNase-seq	chr1:24868192488895	Fibrop		ENCODE
DNase-seq	chr1:24868192488895	Fibropag08396		ENCODE
DNase-seq	chr1:24869222488859	Progfib		ENCODE
DNase-seq	chr1:24869422488897	Fibrobl		ENCODE
DNase-seq	chr1:24869512488676	Fibropag20443		ENCODE
DNase-seq	chr1:24869522488634	Myometr		ENCODE
DNase-seq	chr1:24869822488652	Panisd		ENCODE
DNase-seq	chr1:24870822488817	Fibroblgm03348	Lenticon	ENCODE
DNase-seq	chr1:24870822488897	Fibroblgm03348		ENCODE
DNase-seq	chr1:24870842488897	Fibroblgm03348	Lentimyod	ENCODE
DNase-seq	chr1:24872262488784	Helas3	Ifna4h	ENCODE
DNase-seq	chr1:24873512488757	Gliobla		ENCODE
DNase-seq	chr1:24884002488630	Th1		<b>ENCODE</b>
DNase-seq	chr1:24884202488650	K562	Znff41b2	<b>ENCODE</b>
DNase-seq	chr1:24884202488690	K562	Znf4c50c4	<b>ENCODE</b>
DNase-seq	chr1:24884602488610	Th17		ENCODE
DNase-seq	chr1:24884602488610	Gm12864		ENCODE
DMagaza	al. 1.0400500 0400700	II		ENCODE
DNase-seg	chr1:24885802488730	Hmvecdlvneo		ENCODE

DNase-seq	chr1:24886002488750	Tregwb78495824		ENCODE
DNase-seq	chr1:24886002488750	Gm06990		<b>ENCODE</b>
DNase-seq	chr1:24883802488650	K562	Znfe103c6	<b>ENCODE</b>
DNase-seq	chr1:24858122488664	Panislets		<b>ENCODE</b>
DNase-seq	chr1:24858342488873	Adultcd4th1		<b>ENCODE</b>
DNase-seq	chr1:24860402488871	Gm19238		<b>ENCODE</b>
DNase-seq	chr1:24862272488823	Gm13977		<b>ENCODE</b>
DNase-seq	chr1:24862472488830	Gm12878		<b>ENCODE</b>
DNase-seq	chr1:24862522488872	Gm10248		<b>ENCODE</b>
DNase-seq	chr1:24862562488656	Gcbcell		<b>ENCODE</b>
DNase-seq	chr1:24862662488977	Adultcd4th0		<b>ENCODE</b>
DNase-seq	chr1:24862732488711	Naivebcell		<b>ENCODE</b>
DNase-seq	chr1:24862752488925	Monocd14		<b>ENCODE</b>
DNase-seq	chr1:24863052488703	Hsmmt		<b>ENCODE</b>
DNase-seq	chr1:24863052488745	Hsmmfshd		<b>ENCODE</b>
DNase-seq	chr1:24863262488637	Cll		<b>ENCODE</b>
DNase-seq	chr1:24863262488863	Stellate		<b>ENCODE</b>
DNase-seq	chr1:24863802488931	Gm19240		<b>ENCODE</b>
DNase-seq	chr1:24863912488733	Gm18507		<b>ENCODE</b>
DNase-seq	chr1:24864142488609	Cerebellumoc		<b>ENCODE</b>
DNase-seq	chr1:24869462488973	Nhek		<b>ENCODE</b>
FAIRE	chr1:24869822488642	Gm18507		<b>ENCODE</b>
FAIRE	chr1:24884522488727	Gm12892		<b>ENCODE</b>
FAIRE	chr1:24864212488751	Gm12891		<b>ENCODE</b>
Histone modi	ficationsHistone modificati	ions		
Filter:				
TT:	<u> </u>			

**Chromatin State** 

Histone modifications

Filter: Location Method

Method	Location	<b>Chromatin State</b>	Group	Tissue	Reference
ChromHMM chr	1:24794002516400	Quiescent/Low	ES-deriv	H1 BMP4 Derived Mesendoderm Cultured Cells	REMC
ChromHMM chr	1:24796002509600	Quiescent/Low	ESC	H9 Cell Line	<b>REMC</b>
ChromHMM chr	1:24796002514800	Quiescent/Low	iPSC	iPS-15b Cell Line	<b>REMC</b>
ChromHMM chr	1:24806002503000	Weak transcription	niPSC	iPS DF 6.9 Cell Line	<b>REMC</b>
ChromHMM chr	1:24806002503200	Weak Repressed PolyComb	ESC	ES-I3 Cell Line	<u>REMC</u>
ChromHMM chr	1:24806002509600	Quiescent/Low	ESC	ES-WA7 Cell Line	<b>REMC</b>
ChromHMM chr	1:24808002504800	Quiescent/Low	iPSC	iPS-20b Cell Line	<b>REMC</b>
ChromHMM chr	1:24880002516800	Quiescent/Low	ENCODE	A549 EtOH 0.02pct Lung Carcinoma Cell Line	<u>REMC</u>
ChromHMM chr	1:24880002516800	Weak Repressed PolyComb	ENCODE	HeLa-S3 Cervical Carcinoma Cell Line	<u>REMC</u>
ChromHMM chr	1:24884002515000	Quiescent/Low	ESC	HUES48 Cell Line	<b>REMC</b>
ChromHMM chr	1:24882002509600	Quiescent/Low	ESC	HUES64 Cell Line	<b>REMC</b>
ChromHMM chr	1:24884002509400	Quiescent/Low	Other	Fetal Kidney	<b>REMC</b>
ChromHMM chr	1:24884002507600	Quiescent/Low	Heart	Fetal Heart	<b>REMC</b>
				Ganglion Eminence derived	
ChromHMM chr	1:24884002494800	Quiescent/Low	Neurosph	primary cultured	<b>REMC</b>
			_	neurospheres	
ChromHMM chr	1:24886002495000	Weak transcription	<sup>1</sup> Myosat	Muscle Satellite Cultured Cells	<u>REMC</u>

Tissue

Tissue

Reference

ChromHMM chr1:24884002494600	Weak transcription	nENCODE	HUVEC Umbilical Vein Endothelial Primary Cells	<u>REMC</u>
ChromHMM chr1:24886002494400	Weak transcription	nENCODE	NHDF-Ad Adult Dermal Fibroblast Primary Cells	<u>REMC</u>
ChromHMM chr1:24874002498800	Quiescent/Low	ES-deriv	H1 BMP4 Derived Trophoblast Cultured Cells	<u>REMC</u>
ChromHMM chr1:24882002496400 ChromHMM chr1:24882002497600		Brain ESC	Fetal Brain Male HUES6 Cell Line	REMC REMC
ChromHMM chr1:24882002497600	Quiescent/Low	ES-deriv	hESC Derived CD56+	<u>REMC</u>
ChromHMM chr1:24882002504600	Quiescent/Low	iPSC	Mesoderm Cultured Cells iPS-18 Cell Line	REMC
ChromHMM chr1:24884002494600	Weak transcription	nES-deriv	hESC Derived CD56+ Ectoderm Cultured Cells	REMC
ChromHMM chr1:24884002496400	Weak Repressed PolyComb	Neurosph	Cortex derived primary cultured neurospheres	<u>REMC</u>
ChromHMM chr1:24884002497600	Quiescent/Low	ES-deriv	H1 Derived Neuronal Progenitor Cultured Cells	<u>REMC</u>
ChromHMM chr1:24884002501400	_	Heart	Aorta	REMC
ChromHMM chr1:24884002504400		ESC	H1 Cell Line HSMM Skeletal Muscle	REMC
ChromHMM chr1:24886002504400	Quiescent/Low	ENCODE	Myoblasts Cell Line	REMC
ChromHMM chr1:24866002489600	Flanking Active TSS	HSC & B-cell	Primary hematopoietic stem cells G-CSF-mobilized Female	<u>REMC</u>
ChromHMM chr1:24862002489400	Flanking Active TSS	HSC & B-cell	Primary hematopoietic stem cells G-CSF-mobilized Male	<u>REMC</u>
ChromHMM chr1:24866002489600	Flanking Active TSS	Adipose	Adipose Nuclei	<u>REMC</u>
ChromHMM chr1:24884002493400 ChromHMM chr1:24884002493400	1	nBrain Brain	Brain Angular Gyrus Brain Germinal Matrix	REMC REMC
ChromHMM chr1:24866002492600	Transcr. at gene 5' and 3'	Digestive	Fetal Intestine Small	<u>REMC</u>
ChromHMM chr1:24870002489000	Flanking Active TSS	HSC & B-cell	Primary B cells from cord blood	<u>REMC</u>
ChromHMM chr1:24872002489000	Flanking Active TSS	HSC & B-cell	Primary hematopoietic stem cells	<u>REMC</u>
ChromHMM chr1:24860002489200	Flanking Active TSS	HSC & B-cell	Primary hematopoietic stem cells short term culture	<u>REMC</u>
ChromHMM chr1:24864002489200	Flanking Active TSS	Blood & T-cell	Primary T helper cells fromÃÂ peripheralÃÂ blood	REMC
ChromHMM chr1:24876002489000	Active TSS	Blood & T-cell	Primary T CD8+ memory cells from peripheral blood	<u>REMC</u>
ChromHMM chr1:24872002489200	Flanking Active TSS	Epithelial	Foreskin Keratinocyte Primary Cells skin02	<u>REMC</u>
ChromHMM chr1:24870002489200	Flanking Active TSS	Epithelial	Foreskin Keratinocyte Primary Cells skin03	<u>REMC</u>
ChromHMM chr1:24868002489200	Active TSS	Epithelial	Foreskin Melanocyte Primary Cells skin01	<u>REMC</u>
ChromHMM chr1:24870002489200	Flanking Active TSS	Blood & T-cell	Primary mononuclear cells fromÃÂ peripheralÃÂ blood	REMC
ChromHMM chr1:24872002489000	Flanking Bivalent	Other	Fetal Adrenal Gland	<u>REMC</u>

	TSS/Enh			
ChromHMM chr1:24874002489000 ChromHMM chr1:24872002489200		Digestive Other	Fetal Intestine Large Pancreatic Islets	REMC REMC
ChromHMM chr1:24876002489000	Flanking Active TSS	Muscle	Fetal Muscle Leg	<u>REMC</u>
ChromHMM chr1:24866002489200	Flanking Active TSS	Thymus	Fetal Thymus	<u>REMC</u>
ChromHMM chr1:24872002489000 ChromHMM chr1:24872002489200		Digestive Heart	Gastric Left Ventricle	REMC REMC
ChromHMM chr1:24874002489000	Active TSS	Other	Lung	REMC
ChromHMM chr1:24874002489200		Digestive	Sigmoid Colon	<u>REMC</u>
ChromHMM chr1:24868002489200	Flanking Active TSS	Sm. Muscle	Stomach Smooth Muscle	REMC
ChromHMM chr1:24868002489000	Flanking Active TSS	ENCODE	Dnd41 TCell Leukemia Cell Line	<u>REMC</u>
ChromHMM chr1:24870002489000	Flanking Active TSS	ENCODE	HMEC Mammary Epithelial Primary Cells	<u>REMC</u>
ChromHMM chr1:24878002489000	Active TSS	Mesench	Mesenchymal Stem Cell Derived Adipocyte Cultured Cells	<u>REMC</u>
ChromHMM chr1:24868002491200	Genic enhancers	iPSC	iPS DF 19.11 Cell Line	REMC
ChromHMM chr1:24870002489400		Brain	Brain Anterior Caudate	REMC
ChromHMM chr1:24870002489600	Flanking Bivalent TSS/Enh	Muscle	Skeletal Muscle Male	<u>REMC</u>
ChromHMM chr1:24870002489600	Flanking Active TSS	Muscle	Skeletal Muscle Female	<u>REMC</u>
ChromHMM chr1:24874002489400 ChromHMM chr1:24876002489400		Other Sm. Muscle	Placenta Amnion Rectal Smooth Muscle	REMC REMC
ChromHMM chr1:24882002492600	Quiescent/Low	ENCODE	NH-A Astrocytes Primary Cells	<u>REMC</u>
ChromHMM chr1:24886002489800	Flanking Active TSS	Digestive	Colonic Mucosa	REMC
ChromHMM chr1:24886002489800	Flanking Active TSS	Digestive	Duodenum Mucosa	<u>REMC</u>
ChromHMM chr1:24886002490400	Weak transcription	Other	Ovary	<b>REMC</b>
ChromHMM chr1:24886002491200	Quiescent/Low	ENCODE	HSMM cell derived Skeletal Muscle Myotubes Cell Line	<b>REMC</b>
ChromHMM chr1:24886002492400	Weak Repressed PolyComb	IMR90	IMR90 fetal lung fibroblasts	<u>REMC</u>
ChromHMM chr1:24886002493000	Repressed PolyComb	ES-deriv	H9 Derived Neuron Cultured Cells	REMC
ChromHMM chr1:24872002488800	•	Epithelial	Foreskin Melanocyte Primary Cells skin03	<u>REMC</u>
ChromHMM chr1:24872002488800	Enhancers	ESC	ES-UCSF4 Cell Line	<b>REMC</b>
ChromHMM chr1:24872002488800	Flanking Active TSS	ES-deriv	H1 Derived Mesenchymal Stem Cells	<u>REMC</u>
ChromHMM chr1:24872002488800	Flanking Active TSS	Other	Placenta	<u>REMC</u>
ChromHMM chr1:24872002488800		Muscle	Psoas Muscle	<u>REMC</u>
ChromHMM chr1:24872002488800	Active TSS	Digestive	Small Intestine	<b>REMC</b>
ChromHMM chr1:24874002488800	Active TSS	Blood & T- cell	Primary T helper naive cells from peripheral blood	<u>REMC</u>

ChromHMM chr1:24874002488800	Active TSS	Digestive	Stomach Mucosa	<u>REMC</u>
ChromHMM chr1:24876002488800	Active TSS	Blood & T-	Primary T helper memory	<u>REMC</u>
		cell Blood & T-	cells from peripheral blood 1 Primary T helper memory	
ChromHMM chr1:24876002488800	Active TSS	cell	cells from peripheral blood 2	REMC
ChromHMM chr1:24876002488800	Active TSS	Digestive	Rectal Mucosa Donor 31	<u>REMC</u>
ChromHMM chr1:24876002488800	Active TSS	ENCODE	GM12878 Lymphoblastoid Cell Line	<u>REMC</u>
ChromHMM chr1:24878002488800	Active TSS	ENCODE	Osteoblast Primary Cells	<u>REMC</u>
ChromHMM chr1:24880002488800		Brain	Brain Cingulate Gyrus	<b>REMC</b>
ChromHMM chr1:24880002488800		Digestive	Rectal Mucosa Donor 29	<u>REMC</u>
ChromHMM chr1:24882002488800	Flanking Active TSS	Brain	Brain Inferior Temporal Lobe	<u>REMC</u>
ChromHMM chr1:24882002489000	Flanking Active TSS	Epithelial	Foreskin Fibroblast Primary Cells skin01	<u>REMC</u>
ChromHMM chr1:24882002489000	Flanking Active TSS	Digestive	Fetal Stomach	<u>REMC</u>
ChromHMM chr1:24882002489200	Flanking Active TSS	Epithelial	Foreskin Fibroblast Primary Cells skin02	<u>REMC</u>
ChromHMM chr1:24882002489200	Flanking Active TSS	Brain	Brain Dorsolateral Prefrontal Cortex	REMC
	Flanking Active	Blood & T-	Primary T cells	
ChromHMM chr1:24882002489600	TSS	cell	effector/memory enriched from peripheral blood	REMC
ChromHMM chr1:24884002489000	Flanking Active TSS	Digestive	Esophagus	<u>REMC</u>
ChromHMM chr1:24884002489000	Flanking Active TSS	Other	Pancreas	<u>REMC</u>
ChromHMM chr1:24884002489200	Flanking Active TSS	Blood & T-cell	Primary T regulatory cells fromÃÂ peripheralÃÂ blood	REMC
ChromHMM chr1:24884002489200	Flanking Active TSS	Blood & T-cell	Primary T helper cells PMA-I stimulated	REMC
ChromHMM chr1:24884002489200	Flanking Active TSS	HSC & B-cell	Primary monocytes from peripheral blood	<u>REMC</u>
ChromHMM chr1:24884002489200		Other	Fetal Lung	<b>REMC</b>
ChromHMM chr1:24884002489200	Flanking Active	ENCODE	Monocytes-CD14+ RO01740	REMC
Cin cin 11.2 100 100 1.2 10.2 200	155		I Illiary Cells	TTETTE
ChromHMM chr1:24884002489400	Flanking Active TSS	Blood & T-cell	Primary T helper naive cells fromÃÂ peripheralÃÂ blood	<b>REMC</b>
ChromHMM chr1:24884002489400	Flanking Active TSS	HSC & B-cell	Primary neutrophils fromÃÂ peripheralÃÂ blood	REMC
ChromHMM chr1:24884002489600	Flanking Active	Blood & T-cell	Primary T helper 17 cells PMA-I stimulated	REMC
ChromHMM chr1:24884002489600			hESC Derived CD184+ Endoderm Cultured Cells	<u>REMC</u>
ChromHMM chr1:24884002489600	Flanking Active TSS	Blood & T-cell	Primary T cells fromÃÂ peripheralÃÂ blood	REMC
ChromHMM chr1:24886002489000	Flanking Active TSS	HSC & B-cell	Primary B cells from peripheral blood	REMC
ChromHMM chr1:24886002489000	Enhancers	Epithelial	Breast variant Human Mammary Epithelial Cells (vHMEC)	REMC

ChromHMM chr1:24886002489000	Flanking Active TSS	Epithelial	Breast Myoepithelial Primary Cells	REMC
			Adipose Derived	
ChromHMM chr1:24886002489000	Flanking Active TSS	Mesench	Mesenchymal Stem Cell Cultured Cells	REMC
ChromHMM chr1:24886002489000	1	nBrain	Fetal Brain Female	<b>REMC</b>
ChromHMM chr1:24886002489000	Flanking Active TSS	Heart	Right Atrium	<u>REMC</u>
ChromHMM chr1:24886002489000	Flanking Active TSS	Thymus	Thymus	<u>REMC</u>
ChromHMM chr1:24886002489000	Flanking Active TSS	Other	Spleen	<u>REMC</u>
ChromHMM chr1:24886002489000	Flanking Active TSS	ENCODE	NHLF Lung Fibroblast Primary Cells	<u>REMC</u>
ChromHMM chr1:24886002489200	Flanking Active TSS	HSC & B- cell	Primary Natural Killer cells fromÃÂ peripheralÃÂ blood	l <u>REMC</u>
ChromHMM chr1:24886002489200	Flanking Active TSS	Other	Liver	<u>REMC</u>
ChromHMM chr1:24886002489400	Flanking Active TSS	Blood & T-cell	Primary T CD8+ naive cells from peripheral blood	REMC
ChromHMM chr1:24886002489400	Repressed PolyComb	ES-deriv	H9 Derived Neuronal Progenitor Cultured Cells	REMC
ChromHMM chr1:24886002489400	•	Brain	Brain Substantia Nigra	<b>REMC</b>
ChromHMM chr1:24886002489400	Flanking Active TSS	Sm. Muscle	Colon Smooth Muscle	<u>REMC</u>
ChromHMM chr1:24886002489600	Bivalent Enhancer	r Muscle	Fetal Muscle Trunk	<b>REMC</b>
ChromHMM chr1:24886002489600	Flanking Active TSS	ENCODE	HepG2 Hepatocellular Carcinoma Cell Line	<u>REMC</u>
ChromHMM chr1:24884002488800	Active TSS	ENCODE	NHEK-Epidermal Keratinocyte Primary Cells	<u>REMC</u>
ChromHMM chr1:24884002488800	Enhancers	ENCODE	K562 Leukemia Cell Line Mesenchymal Stem Cell	<u>REMC</u>
ChromHMM chr1:24884002488800	Active TSS	Mesench	Derived Chondrocyte Cultured Cells	REMC
ChromHMM chr1:24886002488800	Flanking Active TSS	Heart	Right Ventricle	<u>REMC</u>
ChromHMM chr1:24886002488800	Active TSS	Sm. Muscle	Duodenum Smooth Muscle	<b>REMC</b>
ChromHMM chr1:24886002488800	Active TSS	Brain	Brain Hippocampus Middle	<u>REMC</u>
ChromHMM chr1:24886002488800	Active TSS	Blood & T-cell	Primary T cells from cord blood	REMC
ChromHMM chr1:24886002488800	Active TSS	Mesench	Bone Marrow Derived Cultured Mesenchymal Stem Cells	n <u>REMC</u>
			2005	

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