Scale chr5:			170,735,	250		100 bas 170,735 UCSC	5,300		170,735,400 Comparative Gen	omics)	170,735,45¢	DGSG	SVPRO	GRTGL	LGAA
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BloodHealthy CD4T-100yr						Distinct Hum	nan DNA Me	Human_BloodHealthy_Meth	2 : Human_CD4T	-100yr_Meth					
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CD133HSC Macrophage						Changes	in Human H	ematopoietic Stem Cells, Hodges 2011 : Roadmap 2015 : Human_Macrophage_l		HSC_Meth				-	
NK BCell			1.					Roadmap 2015 : Human_NK_Meth Human_BCell_Meth							
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H1-mesendoderm								Human_H1BMP4_Meth Human_H1-mesendoderm_Meth							
H1-NPC Mesenchymal								Human_H1-NPC_Meth Human_Mesenchymal_Meth Human_IMR90_Meth					-		
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Layered H3K4Me1								ound Near Active Regulatory Elements)							
Layered H3K4Me1 Layered H3K4Me3						НЗ	K4Me3 Mark	(Often Found Near Promoters) on 7 cell	lines from ENCC	DDE					
DNase Clusters Txn Factor ChIP								ersensitivity Clusters in 125 cell types from IP-seq Clusters (161 factors) from ENConchromHMM tracks from Roadmap							
LNG.IMR90 LNG.IMR90 Restr Enzymes								Restriction Enzymes from REBASE Non-Human RefSeq Genes							
CpG: 411							Ср	Non-Human Refised Genes C annotations of RefSeq RNAs (NM_* a G Islands (Islands < 300 Bases are Light cental Mammal Basewise Conservation b	Green)						
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