

Supplementary information

Proteins that bind regulatory regions identified by histone-modification chromatin immunoprecipitations and mass spectrometry

Erik Engelen^{1*}, Johannes H. Brandsma^{1*}, Maaïke J. Moen¹, Luca Signorile¹, Dick H.W. Dekkers², Jeroen Demmers², Christel E.M. Kockx³, Zehila Ozgür³, Wilfred F. J. van IJcken³, Debbie L.C. van den Berg^{1,4}, Raymond A. Poot¹

¹ Department of Cell Biology, Erasmus MC, Wytemaweg 80, 3015 CN Rotterdam, The Netherlands

² Center for Proteomics, Erasmus MC, The Netherlands

³ Center for Biomics, Erasmus MC, The Netherlands

⁴ The Francis Crick Institute, Mill Hill Laboratory, The Ridgeway, London NW7 1AA, United Kingdom

* These authors contributed equally to this work

Correspondence to:

Raymond A. Poot

r.poot@erasmusmc.nl

Phone: +31-10-7043352

Fax: +31-10-7044743

Debbie L.C. van den Berg

debbie.vandenberg@crick.ac.uk

Phone: +44-20-88162574

Fax: + 44-20-89064477

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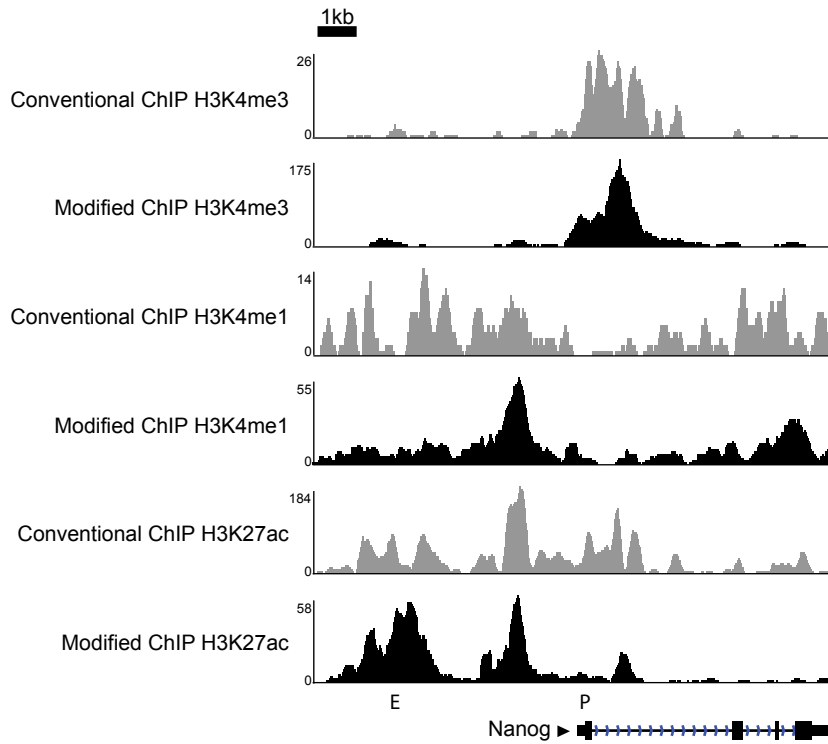
Supplementary Table 2: ChIP-MS identified proteins

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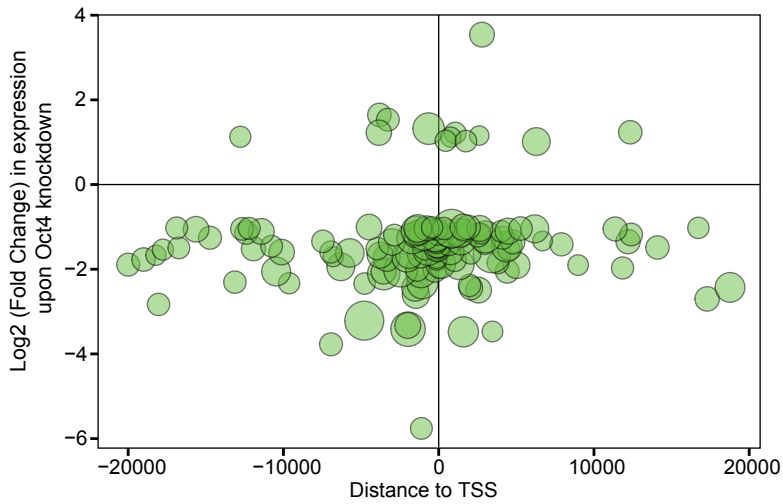
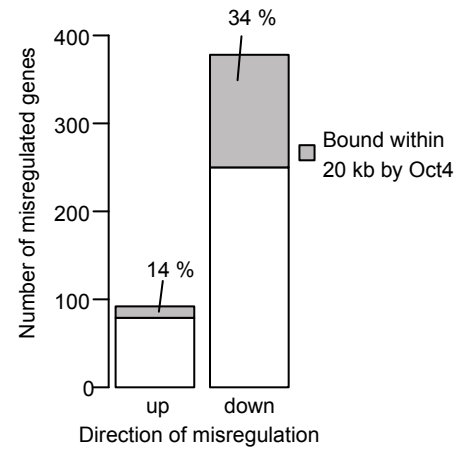
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References for pluripotency phenotypes of ChIP-MS identified factors (Supplementary Table 1)



Supplementary Figure 1. Modified ChIP-seq tracks around pluripotency gene *Nanog*.

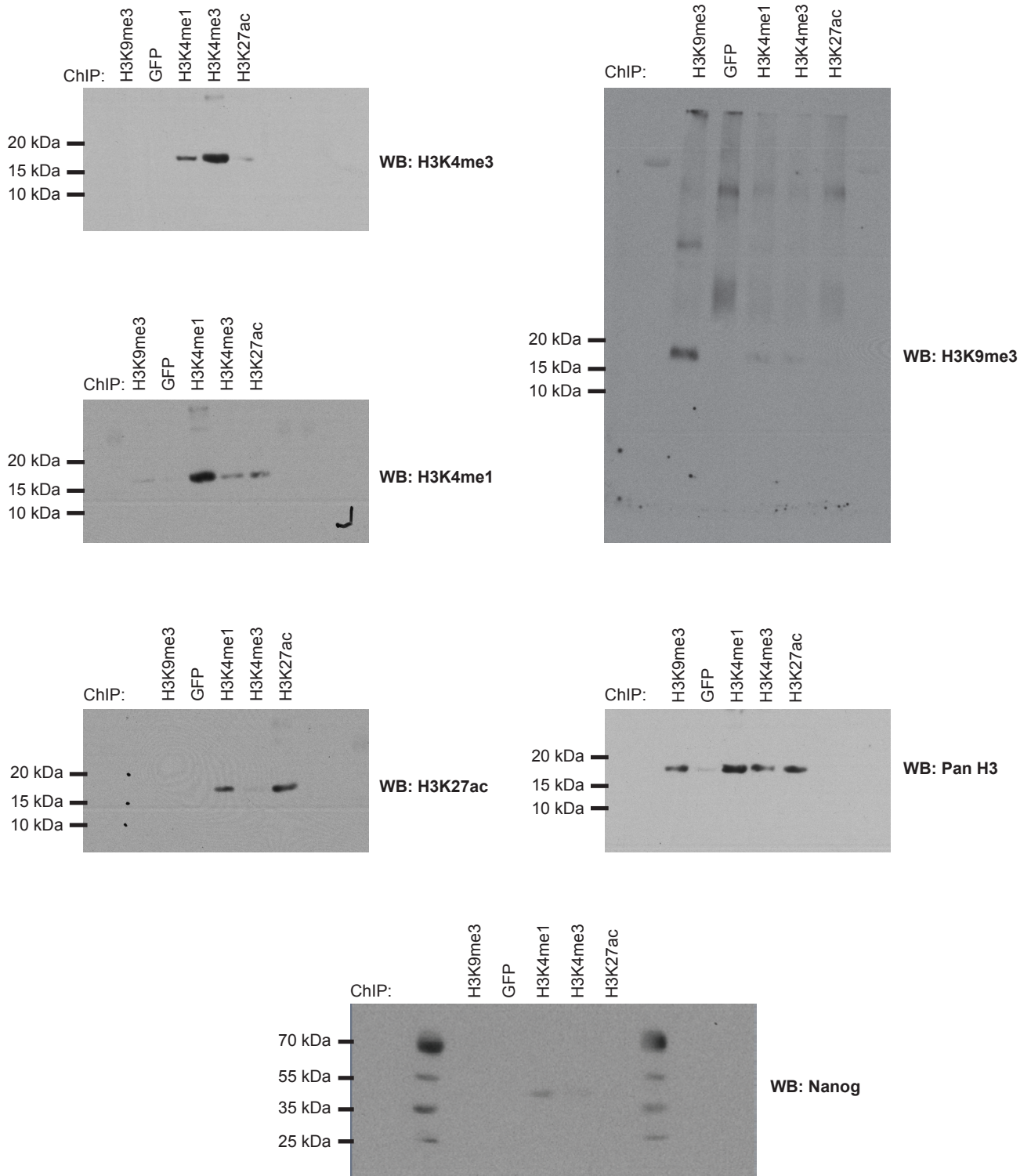
ChIP-seq tracks for modified ChIP or conventional ChIP for H3K4me3, H3K4me1 or H3K27ac around pluripotency gene *Nanog*. Sequence reads were plotted relative to chromosomal position. Genome location of *Nanog* is shown, scale bar indicates 1 kb of genome. P indicates promoter, E indicates putative enhancer.

a**b**

Supplementary Figure 2. Position of Oct4 binding sites on Oct4 target genes.

(a) Bubble plot indicating the positions of Oct4 binding sites relative to the transcription start site (TSS) on genes that are either up-regulated ≥ 2 fold (upper part) or down-regulated ≥ 2 fold (lower part) after 24 h of Oct4 depletion in mouse ESCs. Log₂ of the fold change in expression is indicated on the Y-axis, Oct4 binding distance from the TSS (in base pairs) is indicated on the X-axis. Size of the bubbles correlates with fold difference of Oct4 ChIP peak over control.

(b) Bar diagram showing the total number of up-regulated and down-regulated genes upon Oct4 depletion and the number of these genes bound by Oct4 within 20 kb from the TSS (grey areas). The number of Oct4-bound genes is also indicated as a percentage of the total number of up-regulated or down-regulated genes.



Supplementary Figure 3. Western Blots (full scans) for ChIP-MS samples (as in Figure 1d).

Western blots for histone modifications and Nanog for ChIP-MS samples. ChIP-MS samples (top), molecular weight markers (left) and antibody used for Western blot (right) are indicated.

Supplementary Table 1. ChIP-MS identified proteins, predictions and phenotypes

Protein	Complex ^a	H3K4me3 avrg emPAI	H3K27ac avrg emPAI	H3K4me1 avrg emPAI	H3K9me3 avrg emPAI	GFP avrg emPAI	H3K27ac ratio	Prediction ^b	Pluripotency phenotype ^c
Actl6a	BAF + INO80 + Trrap/Ep400	0,29	0,16	0,12	0,08		0,55	Promoter	-
Actr3	Arp2/3	0,04					0	Promoter	-
Actr5			0,03					Unclear	-
Adnp				0,03	0,02		0	Enhancer	-
Ankhd1				0,10			0	Enhancer	-
Anln					0,03			Heterochromatin	-
Anp32a	SET	0,17		0,18			0	Enhancer	-
Arid1a	BAF		0,07	0,06			1,17	Enhancer	yes
Arid4a	Sin3	0,12					0	Promoter	-
Ash2l	MLL	0,25					0	Promoter	yes
Atad2b			0,03	0,04	0,04		0,75	Enhancer	-
Atrx					0,09			Heterochromatin	-
Aurkb	Aurora K	0,22	0,10	0,10	0,65			Heterochromatin	yes
Banf1		0,66	0,47	0,63			0,71	Promoter	yes
Bap18	MLL	0,63					0	Promoter	-
Baz1a	ACF			0,01			0	Enhancer	-
Baz2a	NoRC	0,06	0,22	0,20	0,07		1,10	Enhancer	-
Bend3		0,24		0,04			0	Promoter	-
Bptf	NURF	0,08	0,02	0,02			0,25	Promoter	yes
Brd1	MOZ/MORF	0,03	0,05	0,10			0,50	Enhancer	-
Brd2		0,37	0,75	0,18			2,03	Promoter	-
Brd3		0,12	0,32				2,67	Promoter	-
Brd4		0,03	0,21	0,10			2,10	Enhancer	-
Brms1	Sin3	0,14					0	Promoter	-
Brms1l	Sin3	0,47					0	Promoter	-
Brpf1	MOZ/MORF	0,16					0	Promoter	-
Brpf3	MOZ/MORF	0,03					0	Promoter	-
Cad				0,04			0	Enhancer	-
Cald1		0,06					0	Promoter	-
Cbx7	PRC1	0,10		0,10			0	Promoter	yes
Cdc5l	Prp19			0,04			0	Enhancer	-
Cdc73	PAF1	0,10	0,10				1,00	Promoter	yes
Cdca7			0,09	0,09			1,00	Enhancer	-
Cdca8	Aurora K	0,28	0,13	0,24	1,17			Heterochromatin	-
Cdk7	TFIIH	0,05					0	Promoter	-
Cdk9	P-TEFb		0,09					Unclear	yes
Cep95			0,02	0,04			0,50	Enhancer	-
Chaf1b	CAF1		0,23	0,52			0,44	Enhancer	yes
Chd1		0,26	0,24	0,14	0,02		0,92	Promoter	yes
Chd2		0,05		0,03			0	Promoter	-
Chd8		0,15	0,03				0,20	Promoter	-
Ckb		0,14					0	Promoter	-
Coil					0,03			Heterochromatin	-
Cpsf6	CFIm	0,07	0,07				1,00	Promoter	-
Creb1		0,11					0	Promoter	-
Cse1l		0,04					0	Promoter	-
Csnk2a1		0,89	0,27	0,21			0,30	Promoter	-
Csnk2b		0,82	0,26	0,08			0,32	Promoter	-
Csrp2bp	ATAC	0,04					0	Promoter	-

Protein	Complex ^a	H3K4me3 avrg emPAI	H3K27ac avrg emPAI	H3K4me1 avrg emPAI	H3K9me3 avrg emPAI	GFP avrg emPAI	H3K27ac ratio	Prediction ^b	Pluripotency phenotype ^c
Ctbp2		0,46	0,30	0,43	0,04		0,65	Promoter	yes
Ctcf		0,07		0,05			0	Promoter	-
Ctr9	PAF1	0,03	0,03				1,00	Promoter	yes
Cul4b	DDB1/Cul4 ubiquitin ligase	0,17	0,18	0,18			1,00	Enhancer	-
Ddb1	DDB1/Cul4 ubiquitin ligase	0,19	0,24	0,29			0,83	Enhancer	-
Ddx47					0,15			Heterochromatin	-
Ddx54				0,04			0	Enhancer	-
Dido1		0,02					0	Promoter	-
Dis3			0,05	0,05			1,00	Enhancer	-
Dmap1	Trrap/Ep400	0,07		0,04			0	Promoter	yes
Dnajc9		0,07	0,14	0,14			1,00	Enhancer	-
Dpf2	BAF		0,22	0,12			1,83	Enhancer	-
Dppa2		0,61	0,06	0,29			0,10	Promoter	yes
Dppa4		0,58		0,39			0	Promoter	yes
Dpy30	MLL	0,18					0	Promoter	yes
Dut		0,41	0,18	0,18			0,44	Promoter	-
Emsy		0,02					0	Promoter	-
Ep300			0,05					Unclear	yes
Ep400	Trrap/Ep400		0,02					Unclear	yes
Erh		0,37					0	Promoter	-
Esrrb			0,08	0,20			0,40	Enhancer	yes
Ezh2	PRC2	0,07	0,04	0,09			0,44	Enhancer	yes
Fam60a	Sin3	0,24					0	Promoter	-
Fbx19	SCF ubiquitin ligase	0,05					0	Promoter	-
Fkbp4				0,07			0	Enhancer	-
Gltscr2				0,07			0	Enhancer	-
Glyr1		0,19	0,24	0,26	0,07		0,92	Enhancer	-
Gm53		0,19					0	Promoter	-
Gtf2e1	TFIIE			0,08			0	Enhancer	-
Gtf2i			0,04	0,07			0,57	Enhancer	-
Gtf3c1	TFIIIC	0,01	0,01	0,02			0,50	Enhancer	-
Hat1		0,11	0,04	0,04			0,36	Promoter	-
Hcfc1	MLL	0,05					0	Promoter	yes
Hdac1	NuRD + Sin3 + REST	1,02	0,30	0,38	0,11		0,29	Promoter	yes
Hdac2	NuRD + Sin3 + REST	0,40		0,10			0	Promoter	-
Hdgfrp2			0,05					Unclear	-
Hmga2		0,14	0,14		0,28			Heterochromatin	-
Hmgb3		0,11		0,1			0	Promoter	-
Hmgxb4		0,20					0	Promoter	-
Hp1bp3		0,26		0,38	0,23		0	Enhancer	-
Incenp	Aurora K	0,06			0,26			Heterochromatin	-
Ing1	Sin3	0,06					0	Promoter	-
Ing2	Sin3	0,11					0	Promoter	-
Ing3	Trrap/Ep400	0,04	0,04				1,00	Promoter	-
Ing4	Trrap/Ep400	0,14		0,07			0	Promoter	-
Ing5	MOZ/MORF	0,58	0,13	0,20			0,22	Promoter	yes
Ino80	INO80	0,05	0,05				1,00	Promoter	yes
Ints1	Integrator			0,02			0	Enhancer	-
Irgc				0,04			0	Enhancer	-
Jarid2	PRC2	0,16	0,05	0,21	0,04		0,24	Enhancer	yes
Kdm1a	BHC	0,06	0,02	0,02	0,02		0,33	Promoter	yes
Kdm2a	SCF ubiquitin ligase	0,16	0,03	0,03			0,19	Promoter	-

Protein	Complex ^a	H3K4me3 avrg emPAI	H3K27ac avrg emPAI	H3K4me1 avrg emPAI	H3K9me3 avrg emPAI	GFP avrg emPAI	H3K27ac ratio	Prediction ^b	Pluripotency phenotype ^c
Kdm2b	PRC1	0,09		0,01			0	Promoter	yes
Kdm4a		0,03					0	Promoter	-
Kdm4c		0,65	0,03	0,13			0,05	Promoter	yes
Kdm5a		0,02					0	Promoter	-
Kdm5b		0,25	0,02	0,12			0,08	Promoter	yes
Kif2c				0,05			0	Enhancer	-
Kif4				0,03			0	Enhancer	-
Kifc5b			0,07	0,15			0,47	Enhancer	-
Klf16		0,16					0	Promoter	-
Klf5			0,07	0,04			1,75	Enhancer	yes
L3mbtl2		0,08		0,07			0	Promoter	yes
Las1l	5FMC			0,06			0	Enhancer	-
Lasp1		0,29		0,13			0	Promoter	-
Lig1		0,08		0,02			0	Promoter	-
Lig3			0,02	0,05			0,40	Enhancer	-
Llph				0,13			0	Enhancer	-
Lmna		0,13	0,08	0,08	0,48			Heterochromatin	-
Lmnb1		0,99	1,60	1,83	3,15	0,37		Heterochromatin	-
Lmnb2		0,12	0,24	0,30	0,98			Heterochromatin	-
Lrwd1	ORC	0,14		0,11	0,35			Heterochromatin	-
Lsm2	U6 SnRNP		0,18					Unclear	-
Luc7l3				0,04			0	Enhancer	-
Max		0,11	0,11	0,10			1,00	Promoter	yes
Mbt1		0,06					0	Promoter	-
Mdc1			0,03	0,05			0,60	Enhancer	-
Meaf6	Trrap/Ep400	0,51	0,19	0,19			0,37	Promoter	-
Men1	MLL	0,32	0,03	0,15			0,09	Promoter	-
Mll2	MLL	0,21		0,02		0,01	0,00	Promoter	-
Morc2a			0,05					Unclear	-
Morc3		0,70	0,24	0,24	0,02		0,34	Promoter	-
Mta3	NuRD	0,24	0,14	0,27			0,52	Enhancer	-
Mtf2	PRC2	0,16	0,06	0,22	0,06		0,27	Enhancer	yes
Mycn		0,08	0,08				1,00	Promoter	yes
Myst2	HBO1	0,56	0,36	0,39	0,06		0,64	Promoter	yes
Myst3	MOZ	0,08					0	Promoter	yes
Myst4	MORF	0,04					0	Promoter	-
Nacc1		0,04	0,07	0,13			0,54	Enhancer	yes
Nasp			0,02	0,02			1,00	Enhancer	-
Nfkb			0,03					Unclear	yes
Nolc1				0,05			0	Enhancer	-
Nrf1		0,08					0	Promoter	-
Nsd1		0,01	0,04	0,05			0,80	Enhancer	-
Nudt13				0,10			0	Enhancer	-
Nudt21	CFIm	0,48					0	Promoter	-
Numa1		0,22	0,15	0,29	0,10		0,52	Enhancer	-
Oct4		0,16	0,10	0,21	0,05		0,48	Enhancer	yes
Ogt		0,15	0,02	0,05			0,13	Promoter	yes
Pak1ip1		0,19					0	Promoter	-
Parp2				0,03			0	Enhancer	-
Parp9					0,04			Heterochromatin	-
Patz1		0,05		0,05			0	Promoter	-
Pbrm1	BAF	0,02	0,11	0,11			1,00	Enhancer	-
Pds5a	Wapl		0,03	0,05			0,60	Enhancer	-

Protein	Complex ^a	H3K4me3 avrg emPAI	H3K27ac avrg emPAI	H3K4me1 avrg emPAI	H3K9me3 avrg emPAI	GFP avrg emPAI	H3K27ac ratio	Prediction ^b	Pluripotency phenotype ^c
Pds5b	Wapl	0,02	0,01	0,02			0,50	Enhancer	-
Phc1	PRC1			0,04			0	Enhancer	-
Phf16	HBO1	0,04					0	Promoter	-
Phf20				0,02			0	Enhancer	yes
Phf23		0,53		0,09			0	Promoter	yes
Phf8		0,23	0,02				0,09	Promoter	-
Phip		0,04	0,07	0,13			0,54	Enhancer	-
Pin1			0,11	0,11			1,00	Enhancer	yes
Pnp		0,20					0	Promoter	-
Polr1c	Pol I	0,3					0	Promoter	-
Polr2a	Pol II	0,15	0,13	0,06			0,87	Promoter	-
Polr2b	Pol II	0,43	0,33	0,07			0,77	Promoter	-
Polr2c	Pol II	0,57	0,16	0,11			0,28	Promoter	-
Polr2e	Pol II	0,85	0,24	0,08			0,28	Promoter	-
Polr2g	Pol II	0,22					0	Promoter	-
Ppp2cb				0,11			0	Enhancer	-
Prdm10		0,03	0,03				1,00	Promoter	-
Prdm2				0,02			0	Enhancer	-
Prrc2c				0,01			0	Enhancer	-
Psmc5	Proteasome	0,07		0,07			0	Promoter	-
Ptcd3				0,12			0	Enhancer	-
Qser1		0,03		0,01			0	Promoter	-
Rad21	Cohesin		0,03	0,03			1,00	Enhancer	yes
Rars		0,05					0	Promoter	-
Rbbp4	NuRD/CAF1	1,51	0,62	1,09	0,37	0,12	0,41	Promoter	-
Rbbp5	MLL	0,14					0	Promoter	yes
Rbl1				0,03			0	Enhancer	-
Rbpj		0,30		0,20	0,14		0	Promoter	-
Rfc3		0,05	0,10				2,00	Promoter	-
Rfc4		0,20	0,15	0,19			0,75	Promoter	-
Rnf2	PRC1	0,35		0,30			0	Promoter	yes
Rsf1	RSF	0,05	0,11	0,12			0,92	Enhancer	-
Ruvbl2	Trrap/Ep400	1,36	1,91	0,41	0,16		1,40	Promoter	yes
Samd1		0,26					0	Promoter	-
Sap130	Sin3	0,18					0	Promoter	-
Sap30	Sin3	0,29					0	Promoter	-
Sap30l	Sin3	0,09					0	Promoter	-
Sbno1				0,01			0	Enhancer	-
Sephs1		0,14	0,05				0,36	Promoter	-
Sf1		0,14					0	Promoter	-
Sf3b1				0,04			0	Enhancer	-
Shprh		0,04	0,01	0,03			0,25	Promoter	-
Sin3a	Sin3	1,34	0,15	0,30			0,11	Promoter	yes
Sin3b	Sin3	0,09					0	Promoter	-
Skp1a	SCF ubiquitin ligase	0,45	0,23	0,10			0,51	Promoter	-
Smarca4	BAF	0,14	0,28	0,22	0,03		1,27	Enhancer	yes
Smarcb1	BAF		0,09	0,05			1,80	Enhancer	yes
Smarcc1	BAF	0,10	0,46	0,31	0,07		1,48	Enhancer	yes
Smarcd1	BAF		0,50	0,35			1,43	Enhancer	-
Smc1a	Cohesin	0,08	0,12	0,22	0,06		0,55	Enhancer	yes
Smc6	Smc5/Smc6			0,03			0	Enhancer	yes
Smchd1			0,02	0,03	0,04			Heterochromatin	-
Spin1		0,72	0,13	0,13			0,18	Promoter	-

Protein	Complex ^a	H3K4me3 avrg emPAI	H3K27ac avrg emPAI	H3K4me1 avrg emPAI	H3K9me3 avrg emPAI	GFP avrg emPAI	H3K27ac ratio	Prediction ^b	Pluripotency phenotype ^c
Srrt		0,04	0,04	0,08			0,50	Enhancer	-
Ssrp1	FACT	0,68	0,93	0,73	0,29	0,13	1,27	Enhancer	-
Suds3	Sin3	0,41					0	Promoter	-
Supt4h2	DSIF	0,34					0	Promoter	yes
Supt5h	DSIF	0,22	0,16	0,06			0,73	Promoter	-
Supt6h		0,07	0,09				1,29	Promoter	-
Suv39h2					0,31			Heterochromatin	yes
Suz12	PRC2	0,31	0,12	0,40	0,07		0,30	Enhancer	yes
Taf1	TFIID	0,03					0	Promoter	yes
Taf2	TFIID	0,06	0,02				0,33	Promoter	yes
Taf3	TFIID	0,02	0,02				1,00	Promoter	yes
Taf4a	TFIID	0,11					0	Promoter	yes
Taf5	TFIID	0,05					0	Promoter	yes
Taf6	TFIID	0,20	0,14				0,70	Promoter	yes
Taf7	TFIID	0,16	0,11				0,69	Promoter	yes
Taldo1			0,05	0,11			0,45	Enhancer	-
Tbrg4				0,09			0	Enhancer	-
Tcea1	TFIIS	0,12	0,26	0,05			2,17	Promoter	-
Tcerg1		0,02	0,03	0,02			1,50	Enhancer	-
Tcof1					0,02			Heterochromatin	-
Tead1			0,04	0,04			1,00	Enhancer	-
Tlk2				0,06			0	Enhancer	-
Trim24			0,25	0,04			6,25	Enhancer	-
Trim33			0,08					Unclear	-
Trp53			0,06					Unclear	-
Trrap	Trrap/Ep400	0,05	0,05	0,01			1,00	Promoter	yes
Uba1			0,03	0,03			1,00	Enhancer	-
Ube2h				0,24			0	Enhancer	-
Ubtf		0,79	0,44	0,43			0,56	Promoter	-
Usp48		0,15	0,08	0,21	0,05		0,38	Enhancer	-
Utp14b				0,07			0	Enhancer	-
Vmn2r100		0,02		0,06			0	Enhancer	-
Wdr18	5FMC	0,04		0,12	0,08		0	Enhancer	-
Wdr5	MLL	0,60	0,27	0,17			0,45	Promoter	yes
Wdr55		0,05					0	Promoter	-
Zfp280c		0,05			0,22			Heterochromatin	-
Zfp281		0,04					0	Promoter	yes
Zfp462		0,01			0,02			Heterochromatin	-
Zic5		0,03					0	Promoter	-
Zmynd8	Integrator		0,05	0,04			1,25	Enhancer	-
Znf512		0,13		0,24	0,25			Heterochromatin	-
Zscan10		0,04		0,09			0	Enhancer	yes

^a Subunit of indicated protein complex

^b Prediction of genome localization based on our ChIP-MS criteria

^c ESC pluripotency phenotype (references in supplementary material)

Protein	H3K4me3								H3K27ac								H3K4me1								H3K9me3								GFP							
	Experiment 1				Experiment 2				Experiment 1				Experiment 2				Experiment 1				Experiment 2				Experiment 1				Experiment 2											
	Mascot	emPAI	Unique pept. ^a	Pept. count ^b	Mascot	emPAI	Unique pept. ^a	Pept. count ^b	Mascot	emPAI	Unique pept. ^a	Pept. count ^b	Mascot	emPAI	Unique pept. ^a	Pept. count ^b	Mascot	emPAI	Unique pept. ^a	Pept. count ^b	Mascot	emPAI	Unique pept. ^a	Pept. count ^b	Mascot	emPAI	Unique pept. ^a	Pept. count ^b	Mascot	emPAI	Unique pept. ^a	Pept. count ^b	Mascot	emPAI	Unique pept. ^a	Pept. count ^b				
Samd1	206	0.3	4	22	139	0.22	3	9																																
Sap130	215	0.22	5	14	183	0.14	4	5																																
Sap30	136	0.57	3	9																																				
Sap30l	53	0.18	1	2																																				
Sbno1																59	0.02	2	3																					
Sephs1	83	0.28	2	3								47	0.09	1	1																									
Sf1	62	0.27	2	2																																				
Sf3b1																150	0.07	3	4																					
Shprh	84	0.04	2	2	75	0.04	2	2				46	0.02	1	2					118	0.06	3	6																	
Sin3a	1717	1.85	36	143	1192	0.82	22	64	178	0.13	4	6	278	0.16	5	9	321	0.21	8	8	695	0.38	12	19																
Sin3b	115	0.09	3	4	118	0.09	3	4																																
Skp1a	110	0.45	2	11	71	0.45	2	5				61	0.45	2	3					61	0.2	1	2																	
Smarca4	430	0.22	9	15	106	0.06	3	5	530	0.25	11	18	742	0.3	12	33	510	0.16	8	13	580	0.27	11	29	56	0.02	1	1	57	0.04	2	2								
Smarcb1									72	0.18	2	2								63	0.09	1	3																	
Smarcc1	131	0.09	4	5	137	0.11	3	4	495	0.47	12	15	535	0.45	10	20	317	0.25	9	10	471	0.36	8	15	51	0.03	1	1	98	0.11	3	3								
Smarcd1									280	0.54	7	7	240	0.45	6	8	152	0.34	4	5	197	0.36	5	5																
Smc1a	126	0.11	4	4	56	0.05	2	2	240	0.19	7	7	66	0.05	2	2	452	0.3	11	12	180	0.13	4	6	141	0.11	4	4												
Smc6																	82	0.05	2	2																				
Smchd1									78	0.03	2	2					137	0.05	3	5					119	0.05	3	4	51	0.02	1	2								
Spin1	248	1.31	6	45	62	0.13	1	17	46	0.13	1	4	77	0.13	1	8	48	0.13	1	4	58	0.13	1	9																
Srrt	61	0.07	2	2					91	0.07	3	3					130	0.11	3	3	83	0.04	1	1																
Ssrp1	582	0.93	12	66	474	0.42	7	54	585	0.93	13	39	687	0.93	11	65	685	0.88	13	41	511	0.57	8	88	219	0.22	4	14	296	0.35	6	25	75	0.11	2	3	150	0.15	3	7
Suds3	234	0.6	6	8	105	0.21	2	2																																
Supt4h2	77	0.67	2	4																																				
Supt5h	386	0.31	10	13	265	0.13	4	9	191	0.16	5	5	281	0.16	5	13	72	0.06	2	2	155	0.06	2	4																
Supt6h	207	0.12	6	7	90	0.02	1	1	177	0.1	5	5	249	0.08	4	4																								
Suv39h2																									118	0.22	4	7	167	0.39	4	7								

Protein	H3K4me3				H3K27ac				H3K4me1				H3K9me3				GFP								
	Experiment 1		Experiment 2		Experiment 1		Experiment 2		Experiment 1		Experiment 2		Experiment 1		Experiment 2		Experiment 1		Experiment 2						
	Mascot	emPAI	Unique pept. ^a	Pept. count ^b	Mascot	emPAI	Unique pept. ^a	Pept. count ^b	Mascot	emPAI	Unique pept. ^a	Pept. count ^b	Mascot	emPAI	Unique pept. ^a	Pept. count ^b	Mascot	emPAI	Unique pept. ^a	Pept. count ^b	Mascot	emPAI	Unique pept. ^a	Pept. count ^b	
Wdr55					57	0.09	2	2																	
Zfp280c					116	0.09	4	5																	
Zfp281	74	0.08	2	2																					
Zfp462																									
Zic5	64	0.06	1	1																					
Zmynd8									57	0.03	2	2	101	0.06	2	6					55	0.07	1	7	
Znf512					153	0.25	4	10													160	0.3	5	7	91
Zscan10	60	0.08	2	2																	93	0.17	2	2	

^a Number of unique, non-redundant peptides identified for the specified protein

^b Number of peptide spectra counted for the specified protein

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Supplementary Table 3. CHIP-MS identified complex subunits and predictions

Complex / subunits	H3K4me3 avrg emPAI	H3K27ac avrg emPAI	H3K4me1 avrg emPAI	H3K9me3 avrg emPAI	GFP avrg emPAI	H3K27ac ratio	Prediction ^a
BAF complex	0,04	0,25	0,17	0,01		1,43	Enhancer
Arid1a (Baf250a)		0,07	0,06				Enhancer
Dpf2 (Baf45d)		0,22	0,12				Enhancer
Pbrm1 (Baf180)	0,02	0,11	0,11				Enhancer
Smarca4 (Brg1)	0,14	0,28	0,22	0,03			Enhancer
Smarca1 (Baf47)		0,09	0,05				Enhancer
Smarcc1 (Baf155)	0,10	0,46	0,31	0,07			Enhancer
Smarcd1 (Baf60a)		0,50	0,35				Enhancer
Sin3 complex	0,32	0,01	0,03			0,04	Promoter
Sin3a	1,34	0,15	0,30				Promoter
Sin3b	0,09						Promoter
Arid4a (Rbbp1)	0,12						Promoter
Brms1	0,14						Promoter
Brms1l	0,47						Promoter
Fam60a	0,24						Promoter
Ing1	0,06						Promoter
Ing2	0,11						Promoter
Sap130	0,18						Promoter
Sap30	0,29						Promoter
Sap30l	0,09						Promoter
Suds3	0,41						Promoter
PRC1 complex	0,15		0,14			0	Promoter
Cbx7	0,10		0,10				Promoter
Phc1			0,04				Enhancer
Rnf2	0,35		0,30				Promoter
PRC2 complex	0,17	0,07	0,23	0,04		0,29	Enhancer
Ezh2	0,07	0,04	0,09				Enhancer
Jarid2	0,16	0,05	0,21	0,04			Enhancer
Mtf2	0,16	0,06	0,22	0,06			Enhancer
Suz12	0,31	0,12	0,40	0,07			Enhancer
TFIID complex	0,09	0,04				0,47	Promoter
Taf1	0,03						Promoter
Taf2	0,06	0,02					Promoter
Taf3	0,02	0,02					Promoter
Taf4a	0,11						Promoter
Taf5	0,05						Promoter
Taf6	0,20	0,14					Promoter
Taf7	0,16	0,11					Promoter
Aurora Kinase complex	0,19	0,08	0,11	0,69			Heterochromatin
Aurkb	0,22	0,10	0,10	0,65			Heterochromatin
Cdca8	0,28	0,13	0,24	1,17			Heterochromatin
Incenp	0,06			0,26			Heterochromatin

Complex / subunits	H3K4me3 avrg emPAI	H3K27ac avrg emPAI	H3K4me1 avrg emPAI	H3K9me3 avrg emPAI	GFP avrg emPAI	H3K27ac ratio	Prediction ^a
Pol II complex	0,44	0,17	0,06			0,39	Promoter
Polr2a	0,15	0,13	0,06				Promoter
Polr2b	0,43	0,33	0,07				Promoter
Polr2c	0,57	0,16	0,11				Promoter
Polr2e	0,85	0,24	0,08				Promoter
Polr2g	0,22						Promoter
MLL complex	0,34	0,04	0,05			0,13	Promoter
Mll2	0,21		0,02		0,01		Promoter
Ash2l	0,25						Promoter
Bap18	0,63						Promoter
Dpy30	0,18						Promoter
Hcfc1	0,05						Promoter
Men1	0,32	0,03	0,15				Promoter
Rbbp5	0,14						Promoter
Wdr5	0,60	0,27	0,17				Promoter
Trrap/Ep400 complex	0,30	0,39	0,09	0,03	0,00	1,33	Promoter
Trrap	0,05	0,05	0,01				Promoter
Ep400		0,02					Unclear
Dmap1	0,07		0,04				Promoter
Ruvbl2	1,36	1,91	0,41	0,16			Promoter
HBO1/MOZ/MORF complex	0,20	0,07	0,09	0,01		0,34	Promoter
Myst2	0,56	0,36	0,39	0,06			Promoter
Myst3	0,08						Promoter
Myst4	0,04						Promoter
Brd1	0,03	0,05	0,10				Enhancer
Brpf1	0,16						Promoter
Brpf3	0,03						Promoter
Meaf6	0,51	0,19	0,19				Promoter
Ing4	0,14		0,07				Promoter
Ing5	0,58	0,13	0,20				Promoter
Phf16	0,04						Promoter
Cohesin complex	0,04	0,07	0,12	0,03		0,60	Enhancer
Rad21		0,03	0,03				Enhancer
Smc1a	0,08	0,12	0,22	0,06			Enhancer
DSIF complex	0,28	0,08	0,03			0,29	Promoter
Supt4h2	0,34						Promoter
Supt5h	0,22	0,16	0,06				Promoter

^a Prediction of genome localization based on our ChIP-MS criteria

Supplementary Table 4. Dppa2 target genes

Gene symbol	Ensembl gene ID	Tissue/cells with highest expression	FC over Embryonic stem cells
Pdgfb	ENSMUSG00000000489	Macrophage bone marrow 2hr LPS	83.7
Gnmt	ENSMUSG00000002769	Liver	3404.7
Gstm5	ENSMUSG00000004032	Testis	247.1
Taf7l	ENSMUSG00000009596	Placenta	633.1
Slc47a1	ENSMUSG00000010122	Kidney	64.5
Dazl	ENSMUSG00000010592	Testis	27.1
Mov10l1	ENSMUSG00000015365	Testis	26.4
Cd83	ENSMUSG00000015396	Macrophage peri LPS thio 1hrs	2432.4
Nkx2-5	ENSMUSG00000015579	Heart	26.8
Nuak1	ENSMUSG00000020032	MEF	46.2
Sycp3	ENSMUSG00000020059	Testis	19.2
Fgf22	ENSMUSG00000020327	Epidermis	1.8
Nipal4	ENSMUSG00000020411	Epidermis	56.4
Myocd	ENSMUSG00000020542	Umbilical cord	121.9
Cmpk2	ENSMUSG00000020638	Macrophage peri LPS thio 7hrs	2480.9
Rasgrf2	ENSMUSG00000021708	Hypothalamus	160.9
Ddx4	ENSMUSG00000021758	Testis	13.1
Galnt14	ENSMUSG00000024064	Kidney	11.1
Lipo1	ENSMUSG00000024766	Lacrimal gland	33.4
Rin1	ENSMUSG00000024883	Nucleus accumbens	19.1
Tdrd1	ENSMUSG00000025081	Testis	82.6
Syce1	ENSMUSG00000025480	Testis	24.4
150015O10Rik	ENSMUSG00000026051	Osteoblast day21	2756
Tnfrsf11a	ENSMUSG00000026321	RAW 264 7	79.7
Cybrd1	ENSMUSG00000027015	Stomach	58.2
Bfsp1	ENSMUSG00000027420	Lens	5785.3
Adad1	ENSMUSG00000027719	Testis	1618.9
Sycp1	ENSMUSG00000027855	Testis	108.1
Hormad1	ENSMUSG00000028109	Not Available	Not available
Spaca1	ENSMUSG00000028264	Testis	1382.4
Slc10a4	ENSMUSG00000029219	Not Available	Not available
Figla	ENSMUSG00000030001	Lens	1.7
Mesp2	ENSMUSG00000030543	Testis	3.3
Chst15	ENSMUSG00000030930	Mast cells IgE	73.9
Cryab	ENSMUSG00000032060	Lens	157.1
Itga11	ENSMUSG00000032243	Not Available	Not available
Kank1	ENSMUSG00000032702	Epidermis	61.2
Ptpm	ENSMUSG00000033278	Lung	118.1
Cdcp1	ENSMUSG00000035498	Cornea	36.9
C530008M17Rik	ENSMUSG00000036377	Testis	50.3
Kcna6	ENSMUSG00000038077	Cerebral cortex prefrontal	26.2
Spon1	ENSMUSG00000038156	Lens	391.8
Mpp6	ENSMUSG00000038388	Mast cells IgE	3.6
Tspyl5	ENSMUSG00000038984	Nucleus accumbens	98

Gene symbol	Ensembl gene ID	Tissue/cells with highest expression	FC over Embryonic stem cells
D1Pas1	ENSMUSG00000039224	Testis	6.5
Dusp26	ENSMUSG00000039661	Dorsal root ganglia	95.3
Fkbp6	ENSMUSG00000040013	Testis	12.6
Sec1	ENSMUSG00000040364	Testis	21.3
Mael	ENSMUSG00000040629	Testis	89.3
Rsph6a	ENSMUSG00000040866	Testis	262.4
Prima1	ENSMUSG00000041669	Neuro2a	9.9
Uggt2	ENSMUSG00000042104	Testis	9.2
Abcb4	ENSMUSG00000042476	Liver	190.9
Disc1	ENSMUSG00000043051	Not Available	Not available
Npy5r	ENSMUSG00000044014	Nucleus accumbens	11
Pcsk9	ENSMUSG00000044254	mIMCD.3	20.9
Mettl24	ENSMUSG00000045555	Lung	11.5
Olig3	ENSMUSG00000045591	Thymocyte DP CD4.CD8.	2
She	ENSMUSG00000046280	Lung	19.1
Gm11554	ENSMUSG00000048294	Embryonic stem cells Bruce4+ V26, average	1
Zfp697	ENSMUSG00000050064	Kidney	40.5
Tacstd2	ENSMUSG00000051397	Epidermis	640.2
Kcnf1	ENSMUSG00000051726	Olfactory bulb	263.7
Fes	ENSMUSG00000053158	Mast cells	99.2
Sh2d4a	ENSMUSG00000053886	Stomach	106.8
Kbtbd13	ENSMUSG00000054978	Skeletal muscle	29.6
H2-Q5	ENSMUSG00000055413	T.cells CD8.	783.5
Gulp1	ENSMUSG00000056870	Retinal pigment epithelium	87.5
Unc13d	ENSMUSG00000057948	Mast cells	73.8
Kl	ENSMUSG00000058488	Kidney	1051.7
Kcng2	ENSMUSG00000059852	Heart	80.1
Nkpd1	ENSMUSG00000060621	Stomach	8.2
Rnf217	ENSMUSG00000063760	C2C12	25.6
Zar1	ENSMUSG00000063935	Ovary	4.1
Dmrtc1c2	ENSMUSG00000067561	Not Available	Not available
4930444P10Rik	ENSMUSG00000067795	Testis	249.5
Slc25a31	ENSMUSG00000069041	Testis	27.1
Atxn1l	ENSMUSG00000069895	Ciliary bodies	3.9
Hsf5	ENSMUSG00000070345	Testis	303.5
Zfp783	ENSMUSG00000072653	Retinal pigment epithelium	22.4
Klhl40	ENSMUSG00000074001	Skeletal muscle	253
Tspyl3	ENSMUSG00000074671	T.cells CD8.	38.2
Chst14	ENSMUSG00000074916	X3T3.L1	9.7
Vgll3	ENSMUSG00000091243	Osteoblast day5	16.7

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Supplementary Table 5. Accession numbers of used ChIP-seq data sets

Histone modifications	GEO dataset accession number
H3K27ac	GSE24165
H3K4me1	GSE24165
H3K4me3	GSE24165
H3K9me3	GSE12241
Input	GSE24165

Protein	GEO dataset accession number
Atrx	GSE22162
Brd4	GSE36561
Cbx7	GSE42466
Ctcf	GSE49847
Ctr9	GSE20530
Esrrb	GSE11431
Ezh2	GSE49178
GFP	GSE11431
Hdac1	GSE27844
Hdac2	GSE27844
Jarid2	GSE19708
Kdm1a	GSE27844
Kdm2a	GSE21202
Kdm5b	GSE31968
Mtf2	GSE16526
Mycn	GSE11431
Nanog	GSE44286
Oct4	GSE44286
P300	GSE49847
Polr2a	GSE49847
Rad21	GSE33346
Rbbp5	GSE22934
Rnf2	GSE26680
Smarca4	GSE14344
Smc1a	GSE22557
Supt5h	GSE20485
Suz12	GSE48122
Taf1	GSE31270
Taf3	GSE30959
Wdr5	GSE22934

Protein	Bioproject accession number
Tcea1	PRJEB2674

References for pluripotency phenotype of factors identified by ChIP-MS

Arid1a¹, Ash2l², Aurkb³, Banf1⁴, Bptf1⁵, Cbx7⁶, Cdc73⁷, Cdk9⁸, Chaf1b⁹, Chd1¹⁰, Ctbp2¹¹, Ctr9^{8,12}, Dmap1¹³, Dppa2¹⁴, Dppa4¹⁴, Dpy30¹⁵, Ep300¹⁶, Ep400¹³, Esrrb¹⁷, Ezh2¹⁸, Hcfc1¹⁹, Hdac1²⁰, Ing5⁸, Ino80¹⁹, Jarid2²¹, Kdm1a²², Kdm2b²³, Kdm4c²⁴, Kdm5b²⁵, Klf5²⁶, L3mbtl2²⁷, Max²⁸, Mtf2²⁹, Mycn³⁰, Myst2³¹, Myst3³¹, Nacc1³², Nfrkb¹⁹, Oct4³³, Ogt³⁴, Phf20³⁵, Phf23¹², Pin1³⁶, Rad21³⁷, Rbbp5¹⁵, Rnf2^{8,13,37}, Ruvbl2¹³, Sin3a³⁸, Smarca4³⁹, Smarcb1⁴⁰, Smarcc1¹³, Smc1a^{8,13}, Smc6^{12,13}, Supt4h2¹³, Suv39h2¹⁹, Suz12⁴¹, Taf1⁴², Taf2⁴², Taf4a⁴², Taf5⁴², Taf6⁴², Taf3^{42,43}, Taf7¹⁹, Tpr^{13,19}, Trrap¹³, Wdr5⁴⁴, Zfp281^{32,45}, Zscan10⁴⁶.

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