Supplementary Material

Genome-wide DNA-binding profile of SRY-box transcription factor 3 (SOX3) in mouse testes

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Table S1. GO term summary and associated gene

Figure S1. Comparison of P7 testes SOX3 ChIP-seq with PLZF and SALL4 SSC ChIP-seq peaks

File S1. Gene symbol definitions

BonfP, Bonferroni P value; FdrQ, False discovery rate Q value; Exp, Expected value; Obs, Observed value; GO, Gene Ontology

			Binomia	l	Regions		Genes		
Rank	GO #: Description	Р	BonfP	FdrQ	Exp	Obs	Obs	Total	Genes
1	GO:0006335: DNA replication-dependent nucleosome assembly	6.16E- 47	7.91E- 43	7.91E- 43	0.306	29	16	27	Hist1h3a, Hist1h3b, Hist1h3c, Hist1h4a, Hist1h4b, Hist1h4c, Hist1h4f, Hist1h4h, Hist1h4i, Hist1h4j, Hist1h4k, Hist1h4m, Hist1h4n, Hist2h3b, Hist2h3c1, Hist2h3c2
2	GO:0045653: negative regulation of megakaryocyte differentiation	5.10E- 41	6.55E- 37	3.28E- 37	0.107	21	10	15	Histlh4a, Histlh4b, Histlh4c, Histlh4f, Histlh4h, Histlh4i, Histlh4j, Histlh4k, Histlh4m, Histlh4n
3	GO:0031497: chromatin assembly	2.12E- 31	2.72E- 27	6.80E- 28	5.41	50	44	119	Bahcc1, Brd2, H1fx, H2afy, H3f3b, Hist1h1a, Hist1h1b, Hist1h1c, Hist1h1d, Hist1h1e, Hist1h2ba, Hist1h2bb, Hist1h2bc, Hist1h2be, Hist1h2bf, Hist1h2bj, Hist1h2bk, Hist1h2bp, Hist1h2bq, Hist1h2br, Hist1h3a, Hist1h3b, Hist1h3c, Hist1h4a, Hist1h4b, Hist1h4c, Hist1h4f, Hist1h4h, Hist1h4i, Hist1h4j, Hist1h4k, Hist1h4m, Hist1h4n, Hist2h2aa1, Hist2h2aa2, Hist2h2be, Hist2h3b, Hist2h3c1, Hist2h3c2, Hmgb1, Nap113, Smarca5, Tnrc18, Zfp469

			Binomia		Regions		Genes		
Rank	GO #: Description	Р	BonfP	FdrQ	Exp	Obs	Obs	Total	Genes
4	GO:0006333: chromatin assembly or disassembly	5.85E- 30	7.51E- 26	1.50E- 26	6.42	52	46	137	Bahcc1, Brd2, Chd1, H1fx, H2afy, H3f3b, Hist1h1a, Hist1h1b, Hist1h1c, Hist1h1d, Hist1h1e, Hist1h2ba, Hist1h2bb, Hist1h2bc, Hist1h2be, Hist1h2bf, Hist1h2bj, Hist1h2bk, Hist1h2bp, Hist1h2bq,
									Hist1h2br, Hist1h3a, Hist1h3b, Hist1h3c, Hist1h4a, Hist1h4b, Hist1h4c, Hist1h4f, Hist1h4h, Hist1h4i, Hist1h4j, Hist1h4k, Hist1h4m, Hist1h4n, Hist2h2aa1, Hist2h2aa2, Hist2h2be, Hist2h3b, Hist2h3c1, Hist2h3c2, Hmgb1, Nap113, Smarca5, Suv39h2, Tnrc18, Zfp469
5	GO:0006334: nucleosome assembly	1.56E- 28	2.00E- 24	3.34E- 25	4.56	44	40	101	Brd2, H1fx, H2afy, H3f3b, Hist1h1a, Hist1h1b, Hist1h1c, Hist1h1d, Hist1h1e, Hist1h2ba, Hist1h2bb, Hist1h2bc, Hist1h2be, Hist1h2bf, Hist1h2bj, Hist1h2bk, Hist1h2bp, Hist1h2bq, Hist1h2br, Hist1h3a, Hist1h3b, Hist1h3c, Hist1h4a, Hist1h4b, Hist1h4c, Hist1h4f, Hist1h4h, Hist1h4i, Hist1h4j, Hist1h4k, Hist1h4m, Hist1h4n, Hist2h2aa1, Hist2h2aa2, Hist2h2be, Hist2h3b, Hist2h3c1, Hist2h3c2, Nap113, Smarca5



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Figure S1. Comparison of P7 testes SOX3 ChIP-seq with PLZF and SALL4 SSC ChIP-seq peaks. Comparison of testes and SSC ChIP-seq datasets for SOX3, PLZF and SALL4 show 20 peaks common to all three datasets. GO analysis of the genes neighbouring the 20 common peaks identified a single enriched GO term, "chromatin organisation". Almost all histone neighbouring peaks do not overlap with SALL4. GO enrichment identified "chromatin assembly" as the only enriched term for the 32 peaks common to SOX3 and PLZF datasets. The peaks associated with the two GO terms identified were almost exclusively found within 5kb of a transcriptional start site.

Gene symbol	Definition
1700008P02Rik	RIKEN cDNA 1700008P02 gene
AK016178	RIKEN cDNA 4930558J22 gene
Ap1g1	Adaptor protein complex AP-1, gamma 1 subunit
Axin2	Axin 2
BC107364	cDNA sequence BC107364
Cmss1	Cms small ribosomal subunit 1
E030025P04Rik	RIKEN cDNA E030025P04 gene
Fcgr1	Fc receptor, IgG, high affinity I
Fgfr1op2	FGFR1 oncogene partner 2
Filip11	Filamin A interacting protein 1-like
Gapvd1	GTPase activating protein and VPS9 domains 1
Gm11492	Predicted gene 11492
H3f4	H3.4 histone
Histlhla	H1.1 linker histone, cluster member
Hist1h1b	H1.5 linker histone, cluster member
Hist1h1c	H1.2 linker histone, cluster member
Hist1h2aa	H2A clustered histone 1
Hist1h2ab	H2A clustered histone 4
Hist1h2ac	H2A clustered histone 6
Hist1h2ad	H2A clustered histone 7
Hist1h2ae	H2A clustered histone 8
Hist1h2ag	H2A clustered histone 11
Hist1h2ai	H2A clustered histone 13
Hist1h2an	H2A clustered histone 22
Hist1h2ba	H2B clustered histone 1
Hist1h2bb	H2B clustered histone 3
Hist1h2bc	H2B clustered histone 4
Hist1h2bf	H2B clustered histone 7
Hist1h2bj	H2B clustered histone 11
Hist1h2bp	H2B clustered histone 22
Hist1h3a	H3 clustered histone 1
Hist1h3b	H3 clustered histone 2
Hist1h3c	H3 clustered histone 3
Hist1h4a	H4 clustered histone 1
Hist1h4b	H4 clustered histone 2

File S1. Gene symbol definitions

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Gene symbol	Definition						
Hist1h4c	H4 clustered histone 3						
Hist1h4i	H4 clustered histone 9						
Hist1h4j	H4 clustered histone 11						
HIst2h2aa2	H2A clustered histone 19						
Hist2h2ab	H2A clustered histone 21						
Hist2h2ac	H2A clustered histone 20						
Hist2h2bb	H2B clustered histone 18						
Hist2h2be	H2B clustered histone 21						
Hist2h3b	H3 clustered histone 13						
Hist2h3c1	H3 clustered histone 14						
Hist2h4	H4 clustered histone 14						
Hist3h2a	H2A.W histone						
Hist3h2ba	H2B.U histone 2						
Hist3h2bb-ps	H2B.U histone 1, pseudogene						
Hmgb1	High mobility group box 1						
Hnrnpu	Heterogeneous nuclear ribonucleoprotein U						
Hspa5	Heat shock protein 5						
Ints13	Integrator complex subunit 13						
Mreg	Melanoregulin						
Pecr	Peroxisomal trans-2-enoyl-CoA reductase						
Pex2	Peroxisomal biogenesis factor 2						
Pgk2	Phosphoglycerate kinase 2						
Pik3r3	Phosphoinositide-3-kinase regulatory subunit 3						
Ptma	Prothymosin alpha						
Pxn	Paxillin						
Samd9l	Sterile alpha motif domain containing 9-like						
Sirt4	Sirtuin 4						
Taf12	TATA-box binding protein associated factor 12						
Tex14	Testis expressed gene 14						
Tnrc18	Trinucleotide repeat containing 18						
Trim17	Tripartite motif-containing 17						