Supplemental Figures

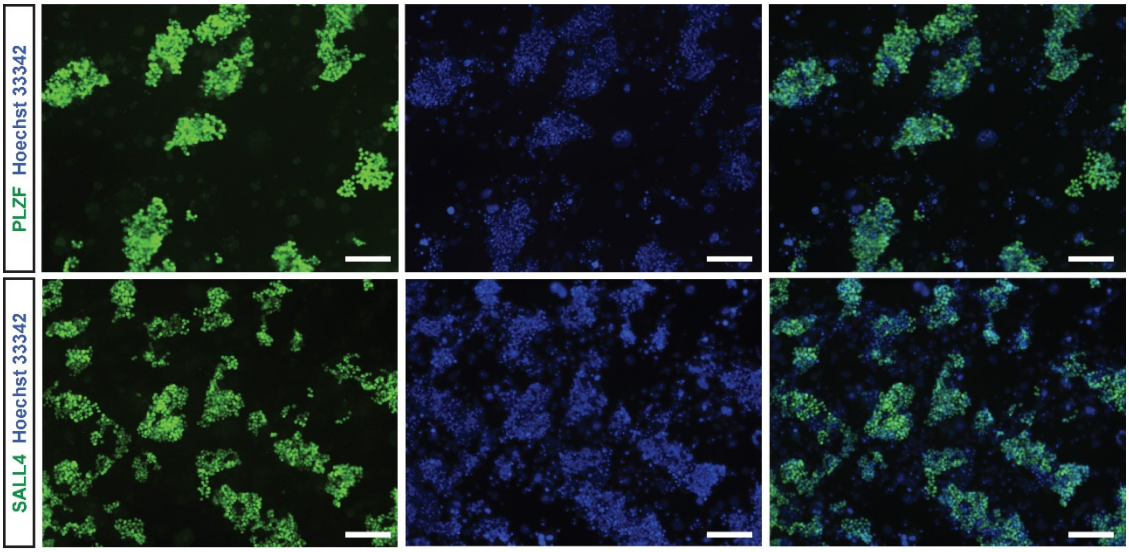


Figure S1: PLZF and SALL4 immunofluorescent staining in cultured THY1+ spermatogonia. Antibodies specific for PLZF (top row) and SALL4 (bottom row) were used to immunolocalize PLZF and SALL4 in cultured THY1+ spermatogonia. Hoechst 33342 staining was used to identify nuclei. Scale bar = 50μm.

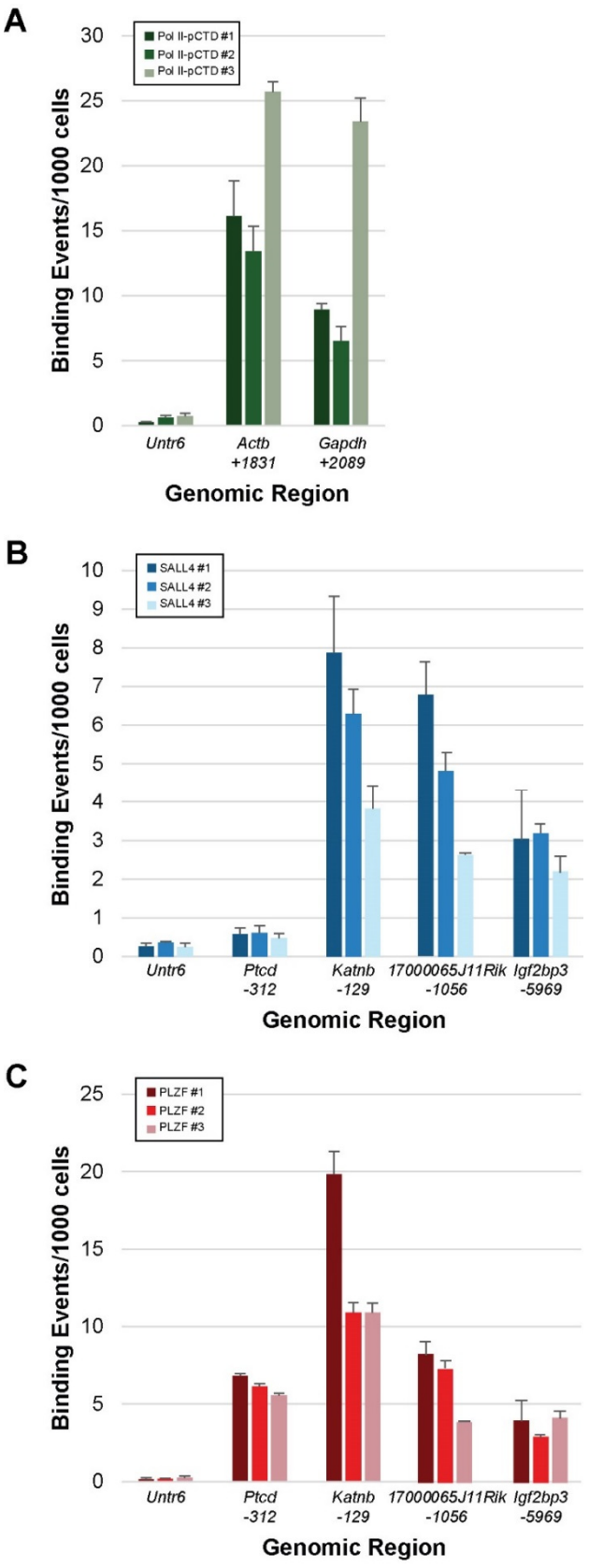


Figure S2: ChIP qPCR for Chromatin QC and ChIP-seq Validation. Three independent chromatin samples from THY1+ spermatogonia were used for ChIP. Prior to ChIP-seq, **(A)** ChIP qPCR for elongation phase specific RNA Polymerase II (phospho-C-terminal domain; Ser2) was used to measure chromatin quality by amplifying a non-expressed region on chromosome 6 (*Untr6*, negative control) and intron 1 segments of *Actb* (+1831) and *Gapdh* (+2089). After ChIP-seq, a panel of four randomly-selected binding sites were tested by ChIP-qPCR. **(B)** SALL4 ChIP DNA was examined for targets *Katnb -129*, *17000065J11Rik -1056*, *Igf2bp3 -5969*, non-target *Ptcd3-312*, and negative control *Untr6*. **(C)** PLZF ChIP DNA was examined for targets *Ptcd3-312*, *Katnb -129*, *17000065J11Rik -1056*, *Igf2bp3 -5969*, and negative control *Untr6*. All ChIP-qPCR data are normalized to input cell number (binding events per 1000 cells) and error bars are standard deviation.

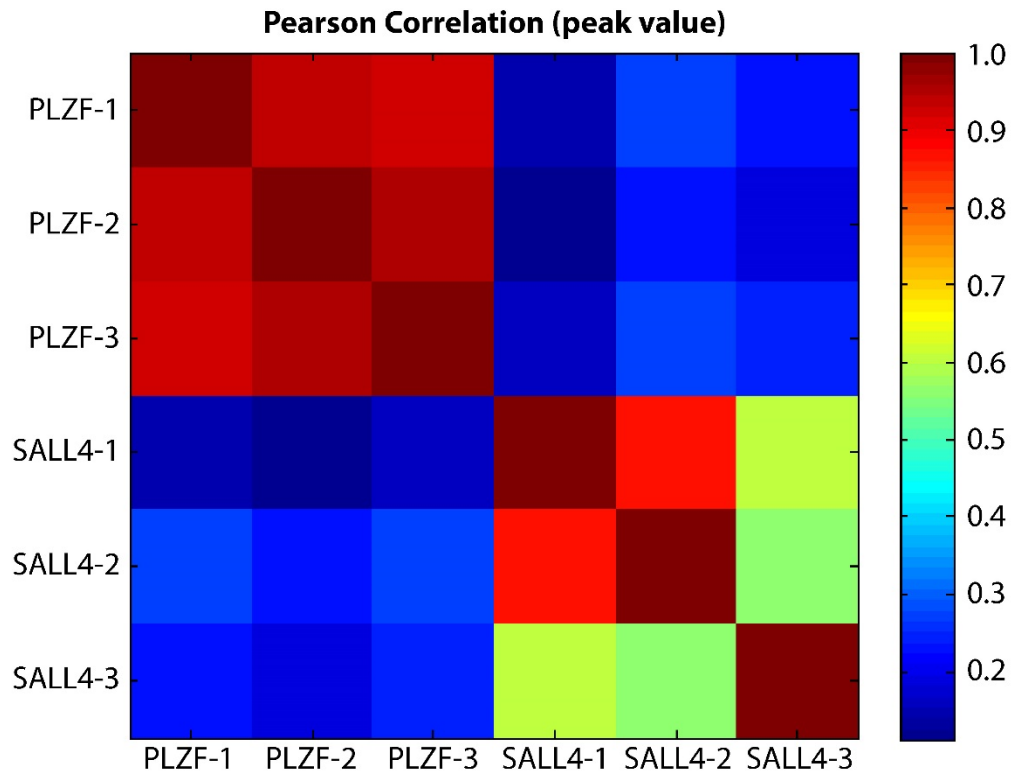


Figure S3 – Pairwise comparisons of ChIP-seq datasets. Linear correlation between individual PLZF and SALL4 samples was performed by Pearsons's method using the peak value for each identified genomic binding interval (the merged columns M-R of Tabs 3 & 4 in Table S2, with redundant rows removed). Shown is a heatmap of the pairwise Pearson correlation coefficients according to the scale shown at the right.

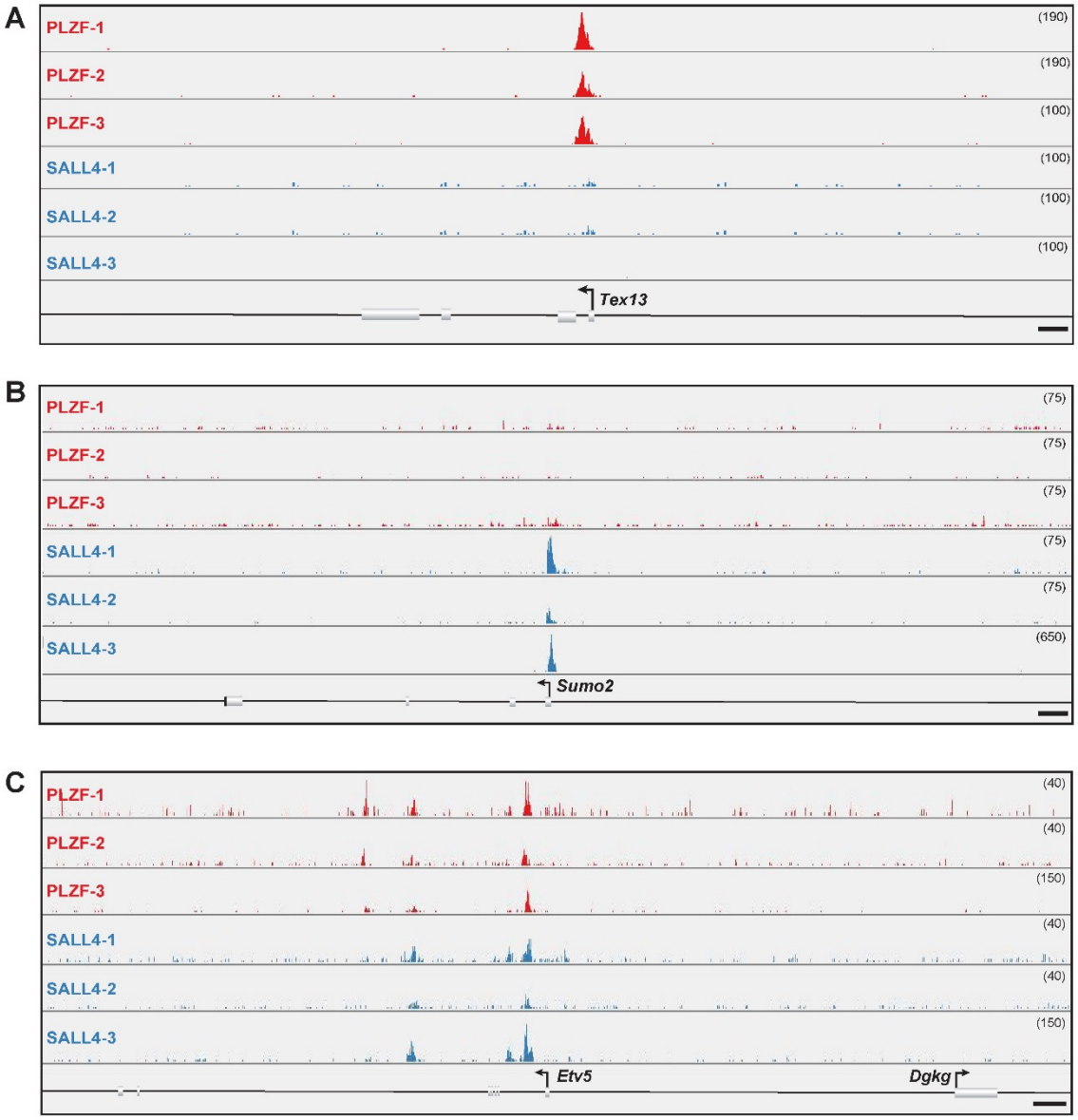


Figure S4: Biological replicates of example tracks for PLZF and SALL4 ChIP-seq. ChIP-seq was used to determine the locations of PLZF and SALL4 binding in mouse THY1+ spermatogonia. Shown are the three replicate histogram tracks showing abundance of ChIP DNA demonstrating some binding sites were unique to **(A)** PLZF (red curve, *Tex13)* or **(B)** SALL4 (blue curve, *Sumo2*), while others were **(C)** bound by both PLZF and SALL4 (shared, *Etv5*). Scale bar = 1kb. Track height is indicated at the upper right of each track in parentheses. These tracks correspond to the data shown in Figure 1.

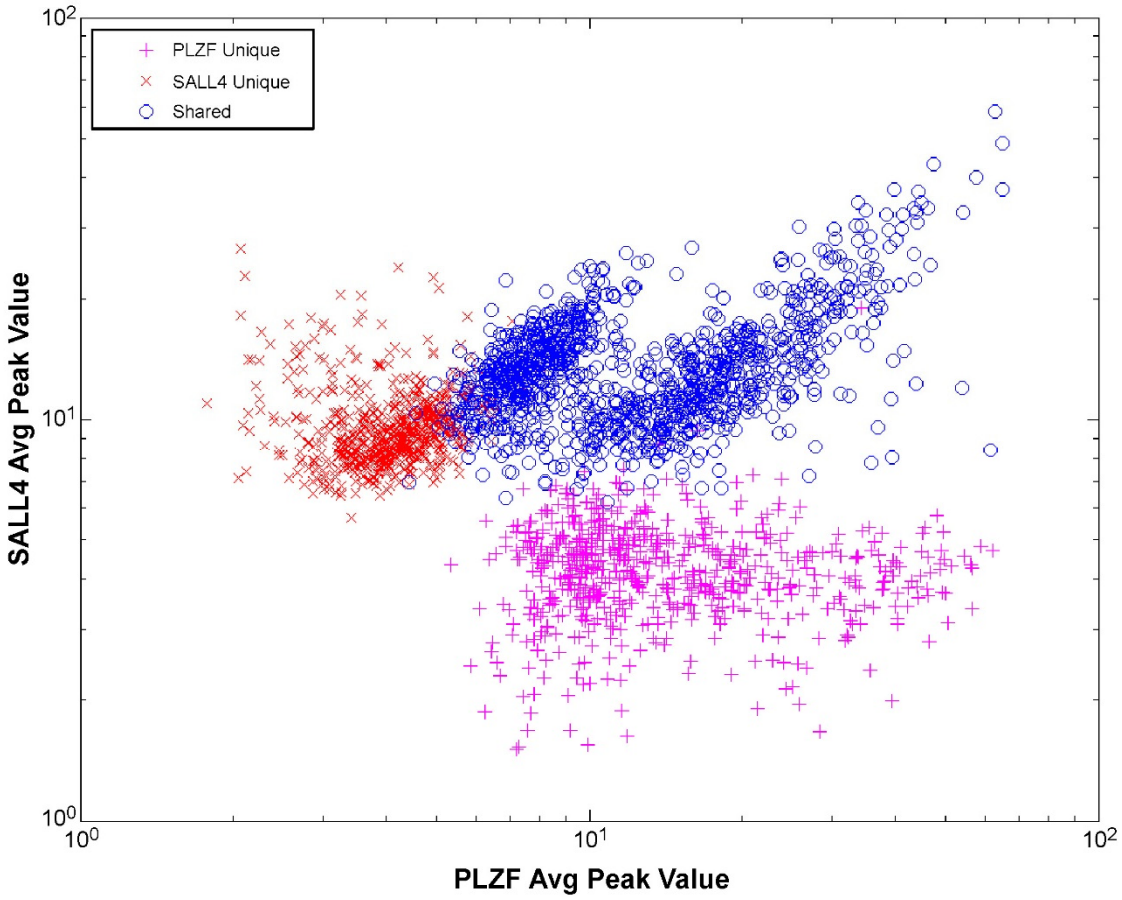


Figure S5 – Scatter plot showing relationship between PLZF unique, SALL4 unique and shared binding sites. Related to Figure 1A and B, average peak height is plotted for all PLZF unique, SALL4 unique and shared binding sites.

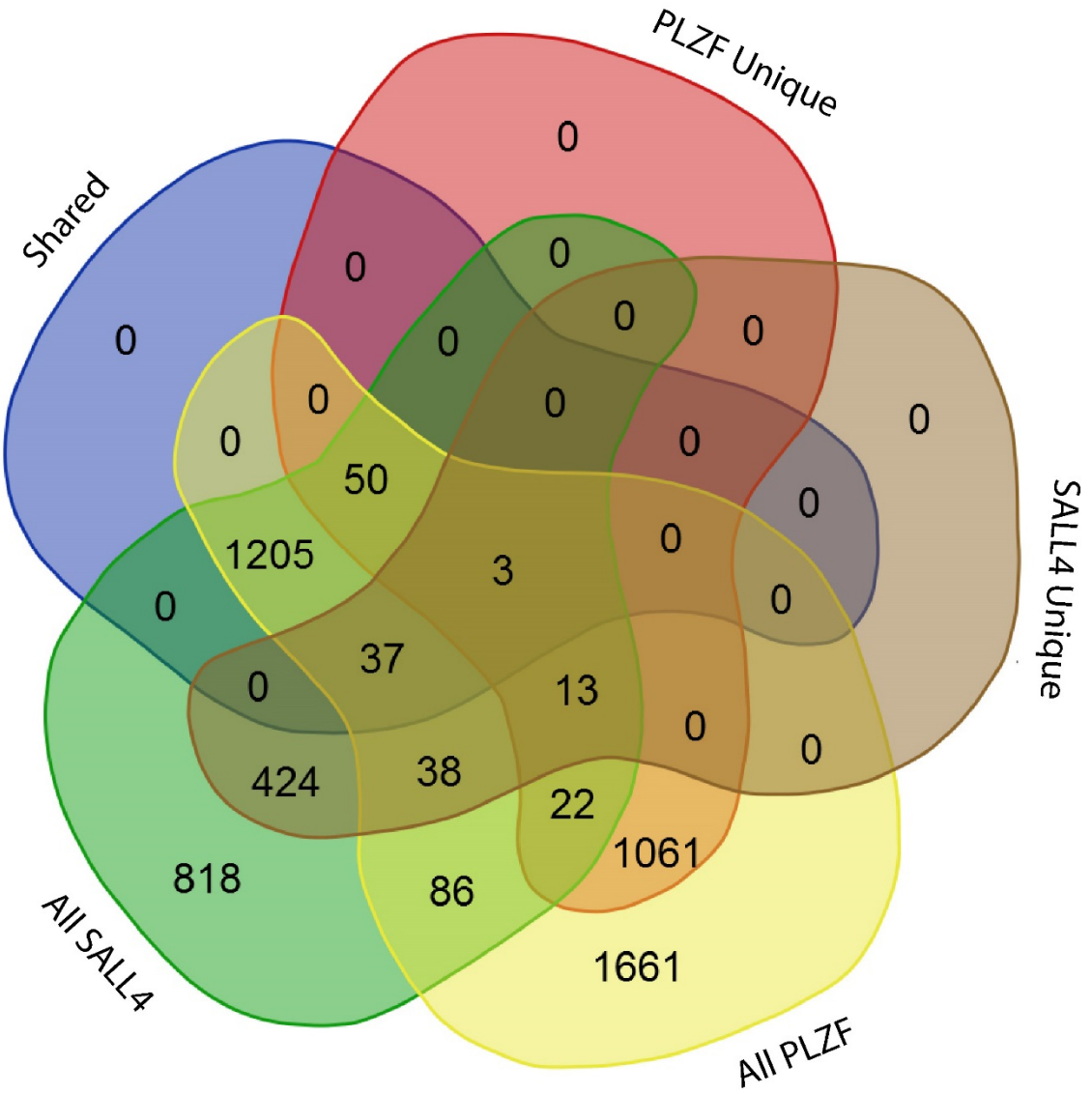


Figure S6 – Overlap between genes bound by PLZF and SALL4 sites. Related to Figure 1 D and E, overlap is shown between genes bound by all PLZF and SALL4 binding sites, including unique and shared subcategories, as well as those which were neither unique or shared. Note that some genes are associated with more than one binding site.

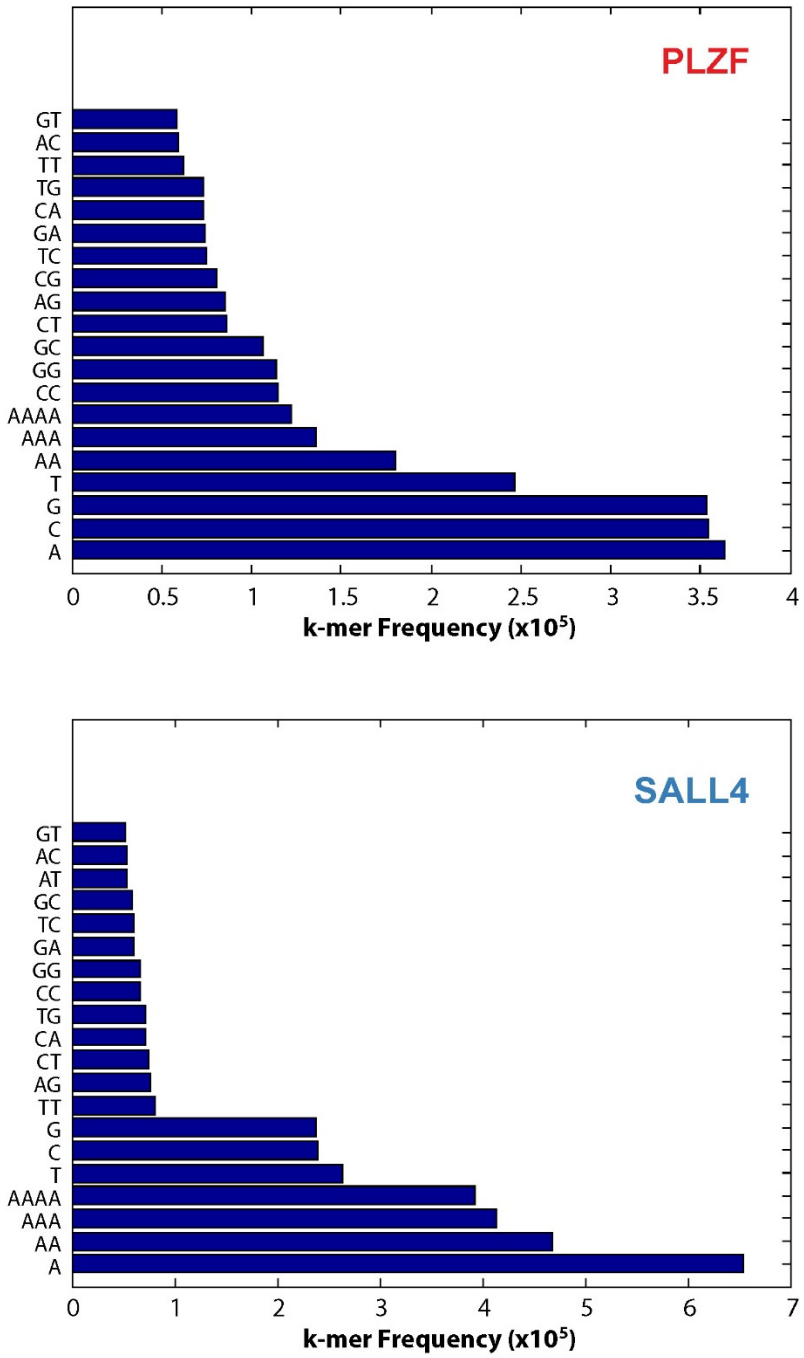


Figure S7 – k-mer frequency in PLZF and SALL4 bound-regions. Frequencies of sequence substrings of 'k' length (k-mers) up to a length of 4 bases were determined for the top 20 k-mers (sequence noted at the left of the chart).

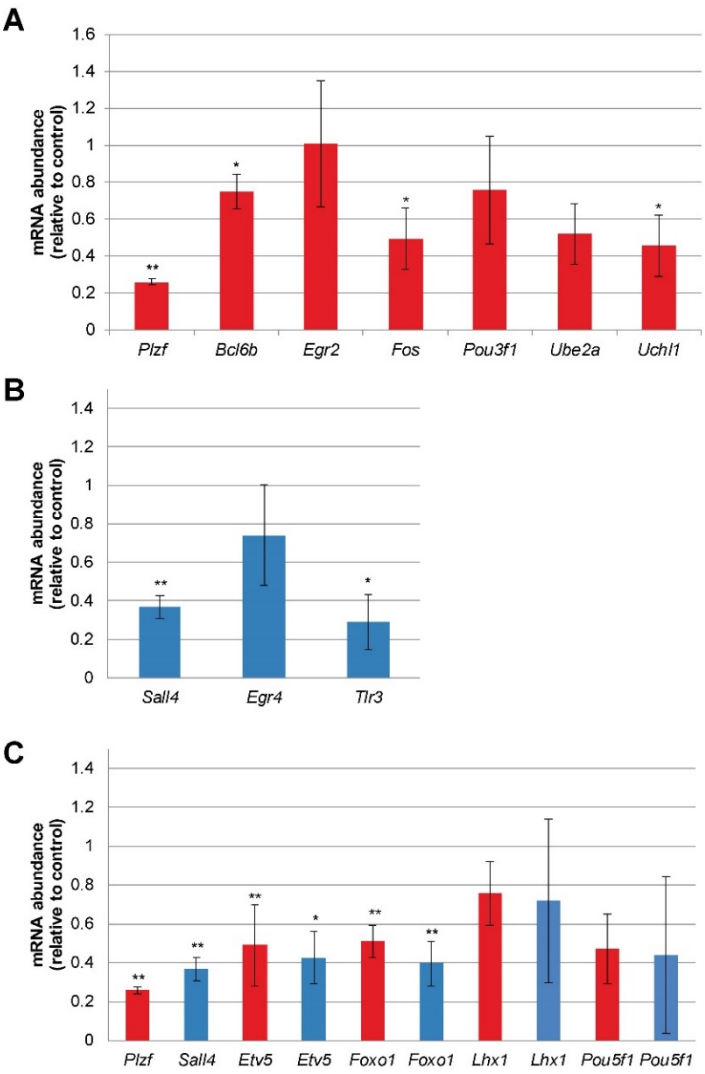


Figure S8: Analysis of target gene mRNA abundance after PLZF or SALL4 knockdown.

Graphs show mRNA abundance ($2^{\Delta\Delta Ct}$; mean ± standard error) for the noted genes following siRNA-mediated knockdown of PLZF (red bars) or SALL4 (blue bars) made relative to mRNA levels of negative control (transfected with non-targeting siRNAs), including **(A)** *Plzf* and target genes *Bcl6b, Egr2, Fos, Pou3f1,* and *Ube2a* and *Uchl1*, **(B)** *Sall4* and target genes *Egr4* and *Tlr3*, and **(C)** shared target genes *Etv5*, *Foxo1*, *Lhx1*, and *Pou5f1*. Data are from at least three replicate siRNA transfections and statistically significant reductions in mRNA levels (student's *t*-test) are noted above bars: ** $p<0.01$ and * $p<0.05$.

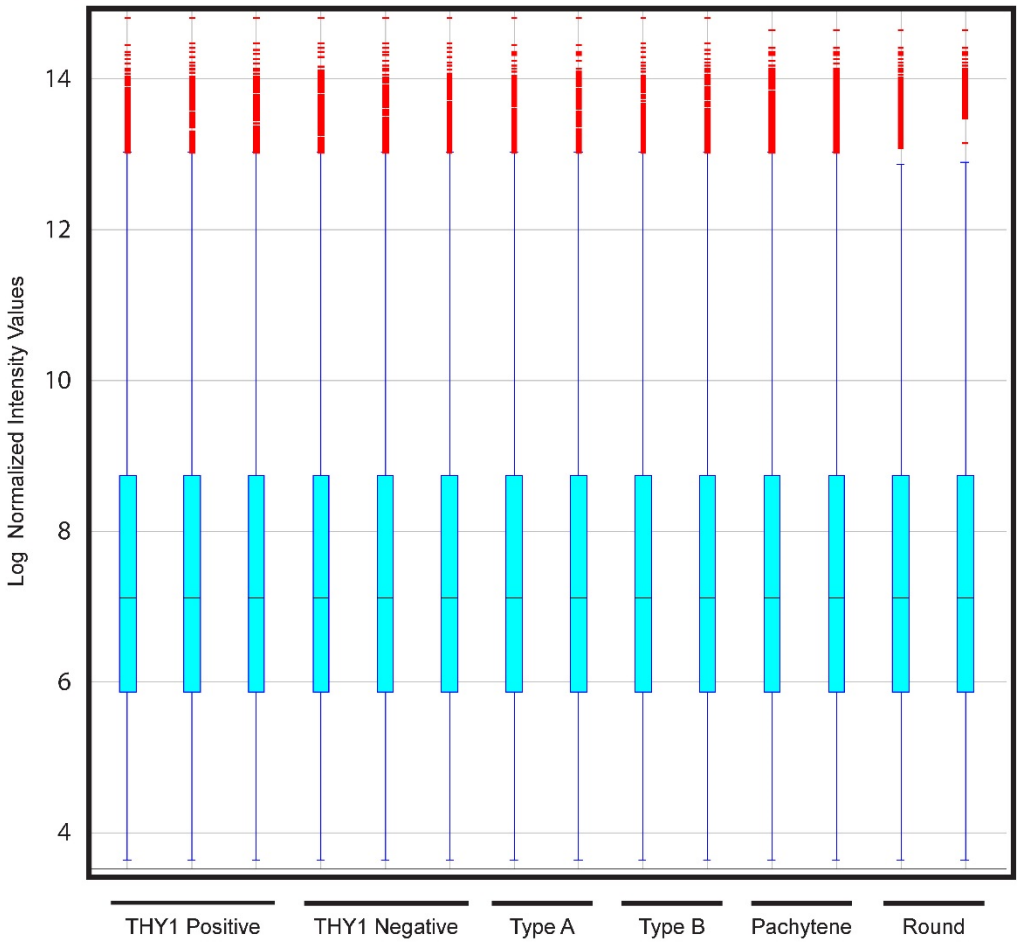


Figure S9: Microarray cross-normalization. Microarray datasets from two independent studies were analyzed together in Genespring GX (v13.0) following quantile normalization and RMA probe summarization, producing datasets with nearly identical distributions. Shown are box/whisker plots showing the median (red line), 25th and 75th percentiles (lower and upper edges of the box), 1.5 IQR (Inter Quantile Range) from box edges (whiskers) and measurements outside of the 1.5 IQR (red +).

Table S1: ChIP NGS reads per sample and MACS results (peaks and FDR).

*Sample**	**PLZF-1**	**PLZF-2**	**PLZF-3**	**SALL4-1**	**SALL4-2**	**SALL4-3**	**Input-1**	**Input-2**	**Input-3**
Total reads	58,820,501	35,641,470	33,071,774	51,180,431	33,079,073	34,672,766	65,649,306	33,349,409	37,603,521
Unique aligned reads	20,420,813	6,649,493	15,230,567	5,817,688	12,123,746	19,462,053	43,949,885	21,855,230	26,821,084
final peaks	7,199	6,891	4,274	13,843	14,246	6,270			
negative peaks	2	1	2	0	0	1			
FDR estimate (%)†	0.03%	0.01%	0.05%	0.00%	0.00%	0.02%			

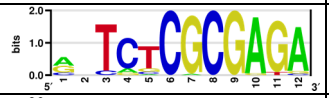
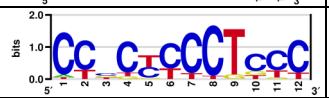
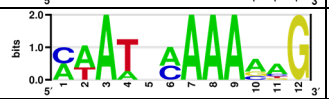
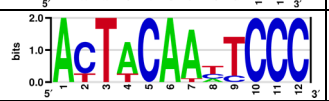
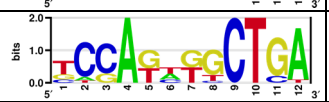
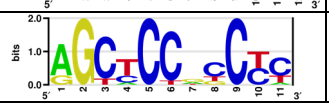
*Samples from three independent chromatin preparations -1/2/3 designations represent samples originating from the same chromatin.
†FDR= False Discovery Rate

Table S2: Excel spreadsheet will full ChIP-seq dataset.

Tab 1 – PLZF Intervals (all MACS-defined PLZF binding intervals identified in any PLZF ChIP sample).
Tab 2 – SALL4 Intervals (all MACS-defined SALL4 binding intervals identified in any SALL4 ChIP sample).
Tab 3 – All PLZF binding sites (any MACS-defined PLZF binding site identified in all three PLZF samples).
Tab 4 – All SALL4 binding sites (any MACS-defined SALL4 binding site identified in all three SALL4 samples).
Tab 5 – Shared PLZF-SALL4 binding sites (any MACS defined binding site found in all three PLZF and all three SALL4 samples).
Tab 6 – Binding site gene assignments (All genes assigned to active regions from Tab 3 based on 10kb proximity).
Tab 7 – PLZF-SALL4 bound gene lists (Six columns showing genes assigned to All PLZF, All SALL4, Shared, PLZF unique and SALL4 unique sites).

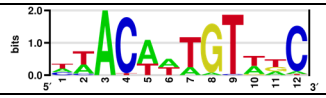
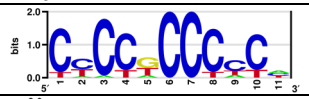
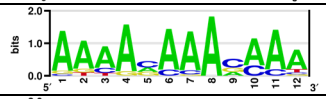
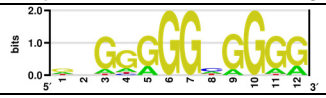
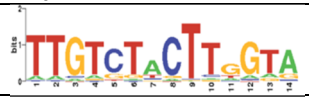
Click here to Download Table S2

Table S3: Top 10 PLZF motifs and hypergeometric p-value comparisons to 5 binding site sets.

PLZF Motif #	LOGO	*Hypergeometric p-value**				
		Shared	**PLZF unique**	**SALL4 unique**	**PLZF (all)**	**SALL4 (all)**
1		hygepdf(45:1116, 2232, 1116, 66) ≤ 1.867e-03	hygepdf(344:1387, 2774, 1387, 487) ≤ 2.635e-24	hygepdf(57:1625, 3250, 1625, 102) ≤ 1.342e-01	hygepdf(507:3075, 6150, 3075, 753) ≤ 9.326e-25	hygepdf(123:3490, 6980, 3490, 228) ≤ 1.261e-01
2		hygepdf(144:1116, 2232, 1116, 181) ≤ 1.286e-17	hygepdf(232:1387, 2774, 1387, 371) ≤ 1.272e-07	hygepdf(155:1625, 3250, 1625, 323) ≤ 7.941e-01	hygepdf(511:3075, 6150, 3075, 725) ≤ 9.911e-33	hygepdf(432:3490, 6980, 3490, 742) ≤ 1.252e-06
3		hygepdf(121:1116, 2232, 1116, 151) ≤ 2.564e-15	hygepdf(173:1387, 2774, 1387, 268) ≤ 3.194e-07	hygepdf(90:1625, 3250, 1625, 217) ≤ 9.963e-01	hygepdf(499:3075, 6150, 3075, 658) ≤ 1.244e-46	hygepdf(389:3490, 6980, 3490, 633) ≤ 8.431e-10
4		hygepdf(211:1116, 2232, 1116, 304) ≤ 1.435e-13	hygepdf(578:1387, 2774, 1387, 897) ≤ 3.222e-26	hygepdf(270:1625, 3250, 1625, 410) ≤ 3.318e-12	hygepdf(1089:3075, 6150, 3075, 1664) ≤ 5.696e-50	hygepdf(704:3490, 6980, 3490, 1118) ≤ 1.314e-21
5		hygepdf(237:1116, 2232, 1116, 346) ≤ 3.172e-14	hygepdf(518:1387, 2774, 1387, 873) ≤ 1.597e-11	hygepdf(495:1625, 3250, 1625, 806) ≤ 4.390e-14	hygepdf(1182:3075, 6150, 3075, 1939) ≤ 8.896e-32	hygepdf(1331:3490, 6980, 3490, 2151) ≤ 1.779e-40
6		hygepdf(58:1116, 2232, 1116, 393) ≤ 1.000e+00	hygepdf(106:1387, 2774, 1387, 513) ≤ 1.000e+00	hygepdf(258:1625, 3250, 1625, 1326) ≤ 1.000e+00	hygepdf(344:3075, 6150, 3075, 494) ≤ 2.460e-20	hygepdf(580:3490, 6980, 3490, 898) ≤ 3.025e-21
7		hygepdf(78:1116, 2232, 1116, 171) ≤ 8.986e-01	hygepdf(200:1387, 2774, 1387, 481) ≤ 1.000e+00	hygepdf(342:1625, 3250, 1625, 977) ≤ 1.000e+00	hygepdf(413:3075, 6150, 3075, 666) ≤ 2.836e-11	hygepdf(767:3490, 6980, 3490, 1205) ≤ 7.926e-26
8		hygepdf(58:1116, 2232, 1116, 94) ≤ 1.320e-02	hygepdf(188:1387, 2774, 1387, 272) ≤ 1.473e-11	hygepdf(135:1625, 3250, 1625, 323) ≤ 9.992e-01	hygepdf(266:3075, 6150, 3075, 415) ≤ 1.492e-09	hygepdf(283:3490, 6980, 3490, 571) ≤ 6.033e-01
9		hygepdf(71:1116, 2232, 1116, 112) ≤ 2.364e-03	hygepdf(189:1387, 2774, 1387, 309) ≤ 1.912e-05	hygepdf(198:1625, 3250, 1625, 318) ≤ 2.490e-06	hygepdf(357:3075, 6150, 3075, 637) ≤ 7.275e-04	hygepdf(480:3490, 6980, 3490, 884) ≤ 3.462e-03
10		hygepdf(128:1116, 2232, 1116, 212) ≤ 9.256e-04	hygepdf(374:1387, 2774, 1387, 675) ≤ 7.163e-04	hygepdf(307:1625, 3250, 1625, 534) ≤ 9.018e-05	hygepdf(786:3075, 6150, 3075, 1384) ≤ 5.431e-09	hygepdf(763:3490, 6980, 3490, 1360) ≤ 3.002e-07
Li et al. 1997	5'-A-T/G-G/C-T-A/C-A/C-A-G-T-3'	hygepdf(109:1116, 2232, 1116, 216) ≤ 4.715e-01	hygepdf(87:658, 1316, 658, 170) ≤ 4.027e-01	hygepdf(77:675, 1350, 675, 141) ≤ 1.428e-01	hygepdf(124:3075, 6150, 3075, 237) ≤ 2.539e-01	hygepdf(233:3490, 6980, 3490, 448) ≤ 2.032e-01

*p-values were calculated using the Matlab function 'p-value ≤ sum(hygepdf(X:K,M,K,N)), in which X= matches for motif in ChIP binding sites (true positives), K= # ChIP binding sites (actual positives) or negatives (actual negatives), M= # total sites (positives and negatives), N= predicted positives (based on appearance in negatives). Negative sequences were generated using a 1st-order Markov Chain model.

Table S4: Top 10 SALL4 motifs and hypergeometric p-value comparisons to 5 binding site sets.

SALL4 Motif #	LOGO	*Hypergeometric p-value**				
		Shared	**PLZF unique**	**SALL4 unique**	**PLZF (all)**	**SALL4 (all)**
1		hygepdf(90:1116, 2232, 1116, 122) ≤ 3.267e-08	hygepdf(64:1387, 2774, 1387, 103) ≤ 7.786e-03	hygepdf(353:1625, 3250, 1625, 418) ≤ 1.200e-55	hygepdf(267:3075, 6150, 3075, 342) ≤ 4.553e-28	hygepdf(963:3490, 6980, 3490, 1103) ≤ 5.955e-177
2		hygepdf(298:1116, 2232, 1116, 405) ≤ 1.392e-26	hygepdf(612:1387, 2774, 1387, 938) ≤ 6.160e-31	hygepdf(282:1625, 3250, 1625, 413) ≤ 7.394e-16	hygepdf(1388:3075, 6150, 3075, 2117) ≤ 6.046e-71	hygepdf(1161:3490, 6980, 3490, 1683) ≤ 5.836e-73
3		hygepdf(139:1116, 2232, 1116, 646) ≤ 1.000e+00	hygepdf(172:1387, 2774, 1387, 653) ≤ 1.000e+00	hygepdf(249:1625, 3250, 1625, 1325) ≤ 1.000e+00	hygepdf(614:3075, 6150, 3075, 764) ≤ 2.220e-76	hygepdf(980:3490, 6980, 3490, 1284) ≤ 6.369e-101
4		hygepdf(310:1116, 2232, 1116, 406) ≤ 3.979e-33	hygepdf(596:1387, 2774, 1387, 915) ≤ 1.806e-29	hygepdf(327:1625, 3250, 1625, 461) ≤ 6.835e-23	hygepdf(1416:3075, 6150, 3075, 2136) ≤ 1.141e-78	hygepdf(1141:3490, 6980, 3490, 1665) ≤ 1.380e-68
5		hygepdf(145:1116, 2232, 1116, 191)) ≤ 1.757e-14	hygepdf(217:1387, 2774, 1387, 301) ≤ 1.414e-16	hygepdf(303:1625, 3250, 1625, 421) ≤ 8.857e-23	hygepdf(665:3075, 6150, 3075, 841) ≤ 1.192e-77	hygepdf(1003:3490, 6980, 3490, 1419) ≤ 5.876e-70
6		hygepdf(55:1116, 2232, 1116, 91) ≤ 2.674e-02	hygepdf(232:1387, 2774, 1387, 429) ≤ 3.706e-02	hygepdf(143:1625, 3250, 1625, 255) ≤ 2.508e-02	hygepdf(484:3075, 6150, 3075, 844) ≤ 2.499e-06	hygepdf(592:3490, 6980, 3490, 987) ≤ 7.299e-12
7		hygepdf(101:1116, 2232, 1116, 170) ≤ 6.587e-03	hygepdf(296:1387, 2774, 1387, 543) ≤ 1.078e-02	hygepdf(175:1625, 3250, 1625, 287) ≤ 6.008e-05	hygepdf(551:3075, 6150, 3075, 990) ≤ 5.796e-05	hygepdf(648:3490, 6980, 3490, 1071) ≤ 4.254e-14
8		hygepdf(58:1116, 2232, 1116, 118) ≤ 6.116e-01	hygepdf(79:1387, 2774, 1387, 233) ≤ 1.000e+00	hygepdf(147:1625, 3250, 1625, 347) ≤ 9.989e-01	hygepdf(208:3075, 6150, 3075, 302) ≤ 7.679e-12	hygepdf(422:3490, 6980, 3490, 666) ≤ 2.084e-13
9		hygepdf(56:1116, 2232, 1116, 80) ≤ 1.777e-04	hygepdf(99:1387, 2774, 1387, 156) ≤ 3.416e-04	hygepdf(164:1625, 3250, 1625, 240) ≤ 1.864e-09	hygepdf(248:3075, 6150, 3075, 374) ≤ 3.761e-11	hygepdf(434:3490, 6980, 3490, 682) ≤ 3.205e-14
10		hygepdf(41:1116, 2232, 1116, 89) ≤ 8.065e-01	hygepdf(82:1387, 2774, 1387, 139) ≤ 1.820e-02	hygepdf(106:1625, 3250, 1625, 208) ≤ 4.149e-01	hygepdf(195:3075, 6150, 3075, 304) ≤ 2.442e-07	hygepdf(317:3490, 6980, 3490, 533) ≤ 3.110e-06
SALL4A Rao, 2010		hygepdf(220:1116, 2232, 1116, 360) ≤ 2.541e-06	hygepdf(116:658, 1316, 658, 203) ≤ 1.621e-02	hygepdf(99:675, 1350, 675, 167) ≤ 6.480e-03	hygepdf(421:3075, 6150, 3075, 743) ≤ 6.178e-05	hygepdf(637:3490, 6980, 3490, 1184) ≤ 2.260e-03
SALL4B Rao, 2010		hygepdf(152:1116, 2232, 1116, 285) ≤ 1.268e-01	hygepdf(84:658, 1316, 658, 166) ≤ 4.669e-01	hygepdf(80:675, 1350, 675, 165) ≤ 6.909e-01	hygepdf(286:3075, 6150, 3075, 461) ≤ 4.403e-08	hygepdf(510:3490, 6980, 3490, 854) ≤ 7.556e-10

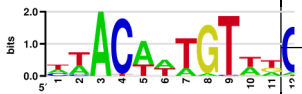
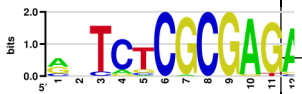
SALL4A/B Rao, 2010		hygepdf(159:1116, 2232, 1116, 307) ≤ 2.694e-01	hygepdf(71:658, 1316, 658, 139) ≤ 4.289e-01	hygepdf(76:675, 1350, 675, 154) ≤ 6.013e-01	hygepdf(305:3075, 6150, 3075, 482) ≤ 6.903e-10	hygepdf(554:3490, 6980, 3490, 929) ≤ 1.600e-10
SALL4 Kim, 2008		hygepdf(213:1116, 2232, 1116, 538) ≤ 1.000e+00	hygepdf(102:658, 1316, 658, 223) ≤ 9.292e-01	hygepdf(89:675, 1350, 675, 253) ≤ 1.000e+00	hygepdf(378:3075, 6150, 3075, 622) ≤ 8.315e-09	hygepdf(693:3490, 6980, 3490, 1234) ≤ 1.056e-06

*p-values were calculated using the Matlab function 'p-value ≤ sum(hygepdf(X:K,M,K,N)), in which X= matches for motif in ChIP binding sites (true positives), K= # ChIP binding sites (actual positives) or negatives (actual negatives), M= # total sites (positives and negatives), N= predicted positives (based on appearance in negatives). Negative sequences were generated using a 1st-order Markov Chain model.
**To perform the MAST validation using previously-published motifs, Position-specific weight matrices (PSWM) were converted to Position-specific scoring matrix (PSSM) prior to motif scanning.

Table S5 – Spreadsheet with hypergeometric p-values for appearance of top five PLZF and SALL4 motifs in gene promoters and Introns). *Separate file.*

Click here to Download Table S5

Table S6: PLZF motif 1 and SALL4 motif 1 co-occurrence in 5 binding site sets in promoters and introns.

Motif #	LOGO	*Hypergeometric p-value*					
		Shared	**PLZF unique**	**SALL4 unique**	**PLZF (all)**	**SALL4 (all)**	
SALL4 motif 1		hygepdf(3:136, 1116, 76, 136) ≤ 9.973e-01	hygepdf(7:26, 658, 155, 26) ≤ 4.152e-01	hygepdf(3:160, 675, 24, 160) ≤ 9.498e-01	hygepdf(12:267, 3075, 507, 267) ≤ 1.000e+00	hygepdf(11:963, 3490, 123, 963) ≤ 1.000e+00	**All sites**
		hygepdf(3:81, 732, 53, 81) ≤ 9.485e-01	hygepdf(7:25, 525, 131, 25) ≤ 4.366e-01	hygepdf(10:77, 366, 38, 77) ≤ 2.572e-01	hygepdf(7:267, 8745, 885, 267) ≤ 1.000e+00	hygepdf(5:983, 6516, 122, 983) ≤ 1.000e+00	**Introns**
PLZF motif 1		hygepdf(4:34, 576, 61, 34) ≤ 4.955e-01	hygepdf(11:34, 554, 149, 34) ≤ 2.879e-01	hygepdf(0:13, 136, 3, 13) ≤ 1.000e+00	hygepdf(19:75, 8686, 958, 75) ≤ 3.747e-04	hygepdf(8:173, 2983, 312, 173) ≤ 9.986e-01	**-1kb to TSS**
		hygepdf(6:42, 441, 40, 42) ≤ 1.673e-01	hygepdf(0:2, 361, 66, 2) ≤ 1.000e+00	hygepdf(0:34, 172, 0, 34) ≤ 1.000e+00	hygepdf(26:200, 4968, 694, 200) ≤ 6.880e-01	hygepdf(15:617, 2823, 131, 617) ≤ 9.995e-01	**-10kb -1kb**

*p-values were calculated using the Matlab function 'p-value ≤ sum(hygepdf(X:K,M,K,N)), in which X= matches for both motifs in ChIP binding sites (common predictions), K= matches for motif 1 in ChIP binding sites (true positives), M= # ChIP binding sites (actual positives) with equal number of negative sequences generated using a 1st-order Markov Chain model, N= matches to motif 1 in ChIP binding sites.

Table S7: Top canonical pathways and molecular/cellular functions.

	Canonical Pathway	*p-value ≤*	*Overlap*	*Molecular and Cellular Functions*	*p-value ≤*	*# Genes*
PLZF unique	EIF2 Signaling	4.43E-06	11.2% 21/187	Cell-to-Cell Signaling and Interaction	2.43E-02 – 7.82E-11	25
	Hereditary Breast Cancer Signaling	8.02E-05	11.5% 15/131	Cellular Assembly and Organization	3.16E-02 – 7.82E-11	106
	Oxidative Phosphorylation	1.02E-04	11.8% 14/119	RNA Post-Transcriptional Modification	3.29E-03 – 4.24E-06	32
	Mitochondrial Dysfunction	1.70E-04	9.6% 18/188	Cell Death and Survival	3.16E-02 – 2.77E-05	238
	Induction of Apoptosis by HIV1	2.86E-04	15.0% 9/60	Cell Morphology	2.88E-02 – 3.98E-05	153
SALL4 unique	Calcium-induced T Lymphocyte Apoptosis	9.81E-05	10.3% 7/68	Molecular Transport	4.76E-03 – 4.81E-08	84
	Nitric Oxide Signaling in the Cardiovascular System	4.35E-04	7.10% 8/113	Cellular Morphology	4.96E-03 – 7.30E-08	107
	Dopamine-Darpp32 Feedback in cAMP Signaling	4.88E-04	5.7% 10/175	Cell Function and Maintenance	4.30E-03 – 1.93E-07	114
	eNOS Signaling	8.25E-04	5.8% 9/155	Cellular Assembly and Organization	4.96E-03 – 2.66E-07	90
	Huntington's Disease Signaling	1.35E-03	4.7% 11/235	Cell Signaling	3.58E-03 – 1.34E-06	38
Shared	Unfolded protein response	2.32E-07	24.1% 13/54	Gene Expression	6.98E-03 – 2.60E-12	226
	IGF-1 Signaling	5.92E-05	14.1% 14/99	Cellular Assembly and Organization	9.86E-03 – 1.03E-08	217
	Protein Kinase A Signaling	1.41E-04	8.3% 33/398	Cellular Function and Maintenance	9.86E-03 – 1.03E-08	209
	Insulin Receptor Signaling	2.03E-04	11.6% 16/138	Cellular Growth and Proliferation	9.80E-03 – 1.19E-07	356
	Role of BRCA1 in DNA Damage Response	3.68E-04	14.1% 11/78	Post-Translational Modifications	9.20E-03 – 1.40E-07	130
All PLZF	Hereditary Breast Cancer Signaling	3.28E-14	39.7% 52/131	Gene Expression	1.80E-03 – 1.67E-34	700
	Protein Ubiquitination Pathway	7.58E-13	30.1% 78/259	Cell Cycle	1.87E-03 – 4.10E-19	528
	Role of BRCA1 in DNA Damage Response	2.09E-10	42.3% 33/78	Cellular Growth and Proliferation	1.38E-03 – 1.13E-17	1071
	ATM Signaling	1.09E-09	45.8% 27/59	DNA Replication, Recombination, and Repair	1.88E-03 - 5.84E-15	371
	Mitotic Roles of Polo like kinase	9.79E-08	39.4% 26/66	Molecular Transport	1.27E-03 - 2.29E-13	117
All SALL4	Protein Kinase A Signaling	3.69E-09	17.6% 70/398	Cellular Assembly and Organization	4.89E-04 – 3.02E-22	442
	Unfolded Protein Response	6.76E-09	37.0% 20/54	Cellular Function and Maintenance	4.89E-04 – 3.02E-22	572
	Renin-Angiotensin Signaling	4.75E-07	23.7% 28/118	Cellular Growth and Proliferation	4.85E-04 – 1.02E-21	771
	Axonal Guidance Signaling	5.07E-07	15.7% 69/440	Gene Expression	4.10E-04 – 4.76E-19	433
	Gap Junction Signaling	1.61E-06	20.2% 34/168	Cell Morphology	4.31E-04 – 5.98E-16	467

Table S8: Expression of PLZF/SALL4-bound genes in P6 THY1+ and THY1- testis cell populations.

Click here to Download Table S8

Table S9: Expression of PLZF/SALL4-bound genes (not differentially expressed in THY1+ and THY1-) in differentiating Type-A and Type-B spermatogonia.

Click here to Download Table S9

Table S10. Oligodeoxynucleotide primers and assays

Method	Site/gene	Forward primer 5′to 3′	Reverse primer 5′ to 3′
ChIP qPCR	*Untr6*	AATACCAATGTCCACCCTCTG	CAACATCCACACGTCCAGTG
ChIP qPCR	*Ptcd3-312*	TGGCTCTGCGCTACAAGACT	CCAGCATCTTCCGAGTCAGT
ChIP qPCR	*Katnb-129*	CGGGACTAAGAACGCAGAAG	CCTTTCCCCGACTCAGACTA
ChIP qPCR	*17000065J11Rik-1056*	TTGCGATTTTCCTGCTGTTA	TGCCATTTAGGTCAGGGTAT
ChIP qPCR	*Igf2bp3-5969*	AAACCTCGGAACGAATGATG	TACCTTTGTGGCTGCTGAGA
qRT-PCR	*Actb*	CACAGCTTCTTTGCAGCTCCTT	TGCCGGAGCCGTTGTC
qRT-PCR	*Egr4*	ATGCTCCACCTGAGCGACTT	TCCAGGAAGCAGGAGTCTGT
qRT-PCR	*Etv5*	CAGGAGCCCCGAGATTACTG	CCGCCTCTCATGTAGGATGAC
qRT-PCR	*Fos*	TTCCTGGCAATAGCGTGTTC	TTCAGACCACCTCGACAATG
qRT-PCR	*Foxo1*	ACGAGTGGATGGTGAAGAGC	TGCTGTGAAGGGACAGATTG
qRT-PCR	*Sall4*	GCAGATCCACGAGCGAACA	GGTTCTCTATGGCCAGCTTCCT
qRT-PCR	*Tlr3*	GAAGCAGGCGTCCTTGGACTT	TGTGCTGAATTCCGAGATCCA
qRT-PCR	*Uchl1*	Mm00495900_m1*	
qRT-PCR	*Plzf* (*Zbtb16*)	CGAGCTTCCGGACAACGA	TTGGCACCCGCTGAATG

*The noted TaqMan MGB probe assay (Life Technologies) was used for *Uchl1* qRT-PCR.