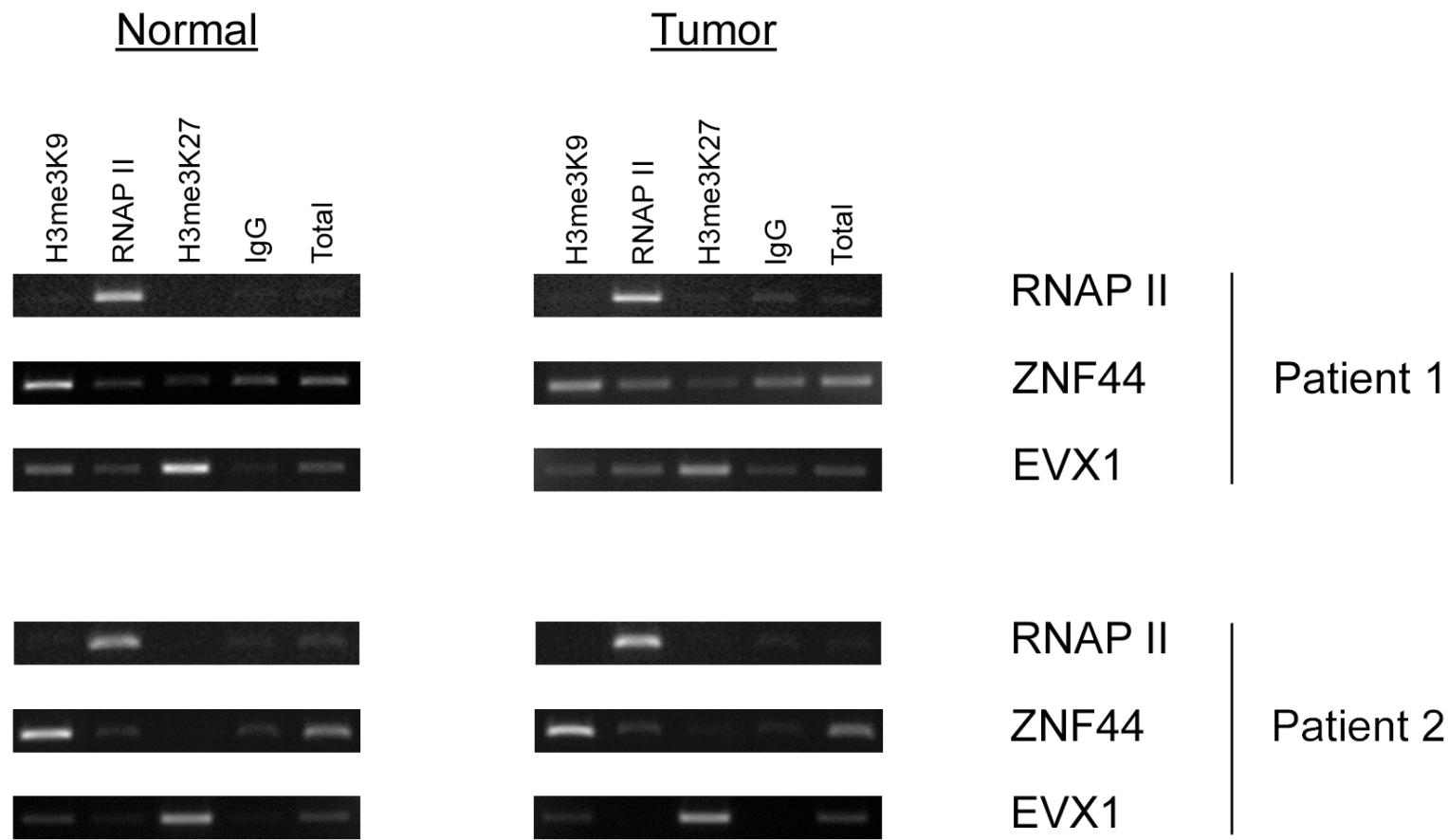


Figure S1



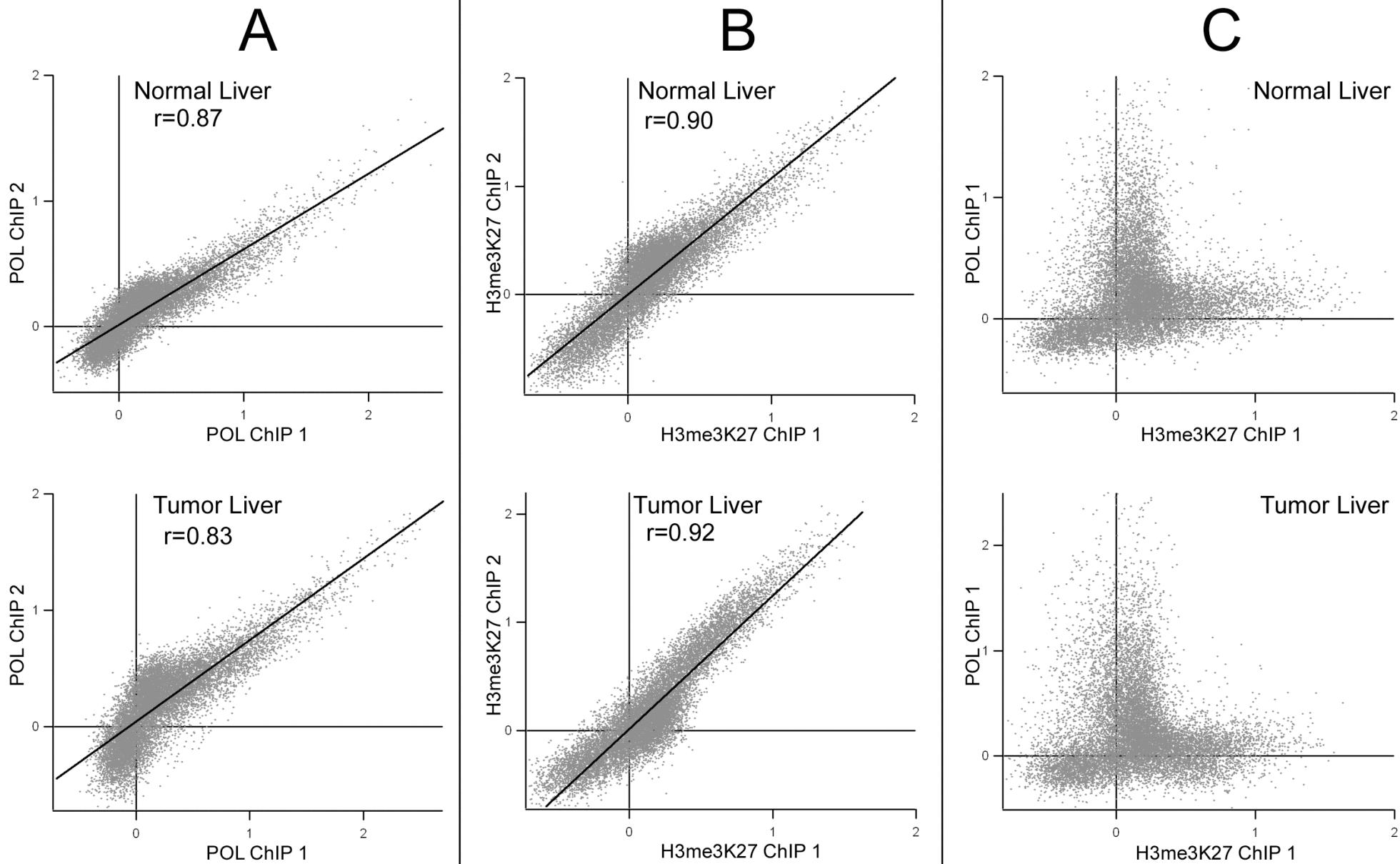


Figure S2. Reproducibility of the ChIP technique. RNAPII and H3me3K27 ChIP-chip experiments were performed in duplicate using normal and tumor liver samples. The Maxfour values for each promoter on the duplicate arrays are plotted for RNAPII (A) or H3me3K27 (B) to show reproducibility of the assay. For comparison, the values for each promoter in the RNAPII vs. the H3me3K27 arrays are also shown (C).

Acevedo_Figure_S3

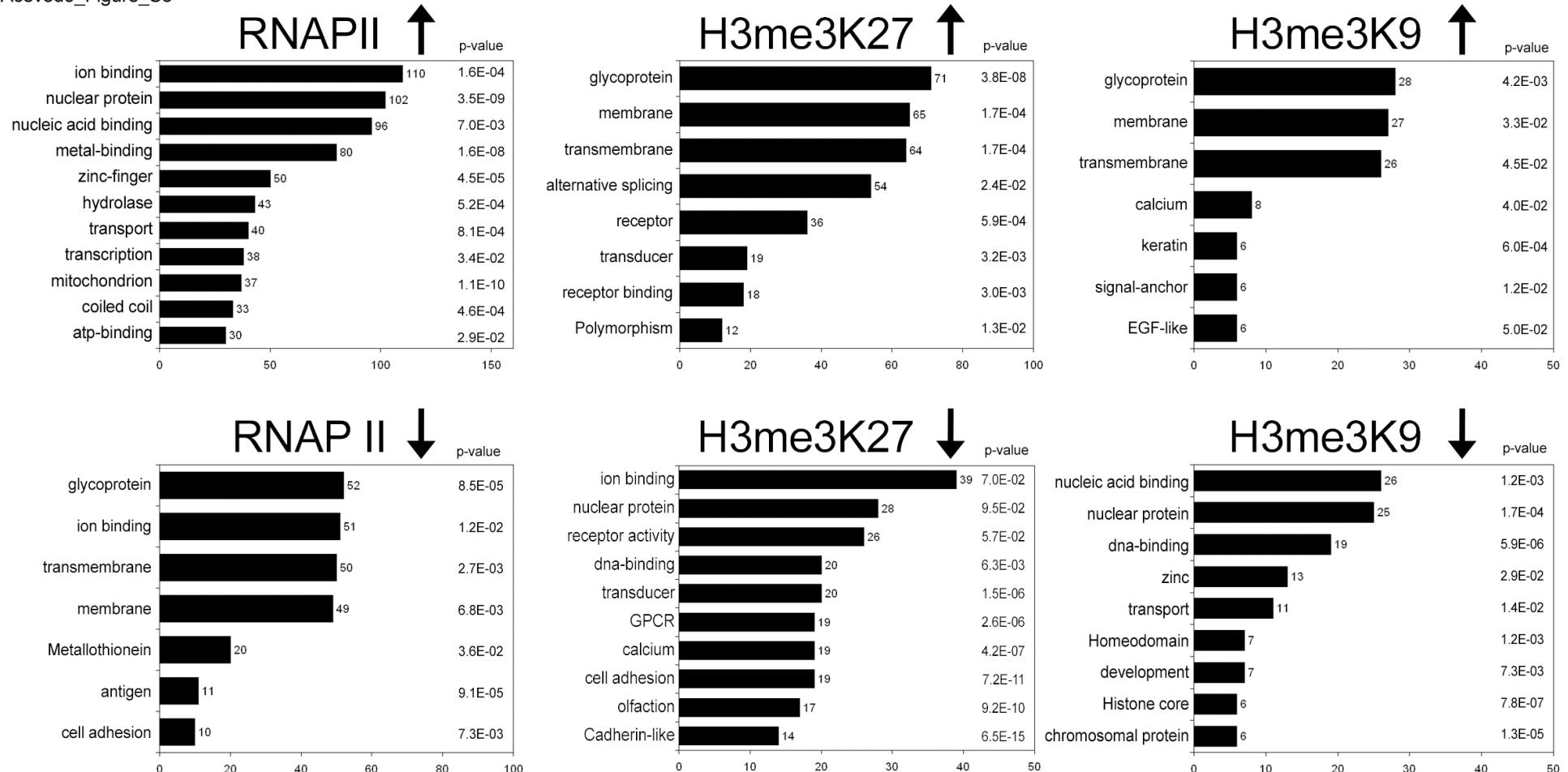


Figure S3. Gene ontology analysis of deregulated gene promoters using DAVID (<http://david.abcc.ncifcrf.gov/>) functional annotation from tables S23-S25. Up arrow indicates increased binding and down arrow indicates decreased binding by RNA Polymerase II (RNAPII), Histone H3me3K27 and H3me3K9. X axis indicates the number of genes in each category.

Acevedo_Figure_S4

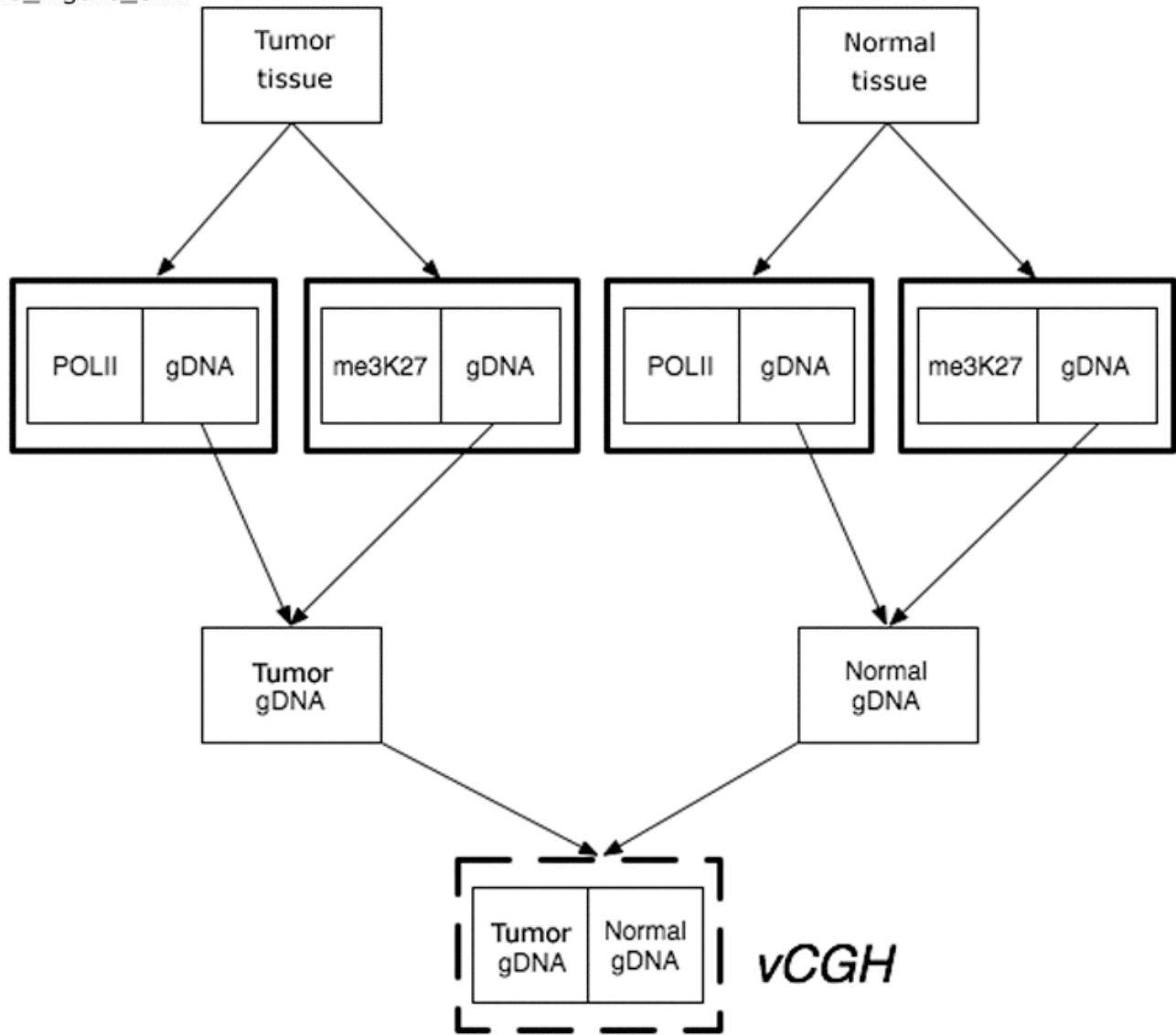


Figure S4. vCGH schematic. To perform a vCGH analysis, the data from the genomic (input) samples is extracted. For the analyses performed in this study, the input signals from two independent ChIP-chip experiments (POLII and me3K27) were used for both the tumor and normal samples. The genomic DNA channels of the "duplicate" arrays were quantile normalized (using the median values) to produce a single "merged" gDNA vector of values and then the average of all probes for a single promoter was calculated so that the promoter was represented by a single value. After calculation of the ratio of tumor/normal, the data was smoothed using a 21-point mean filter and displayed using the snapCGH package in R.

Acevedo_Figure_S5

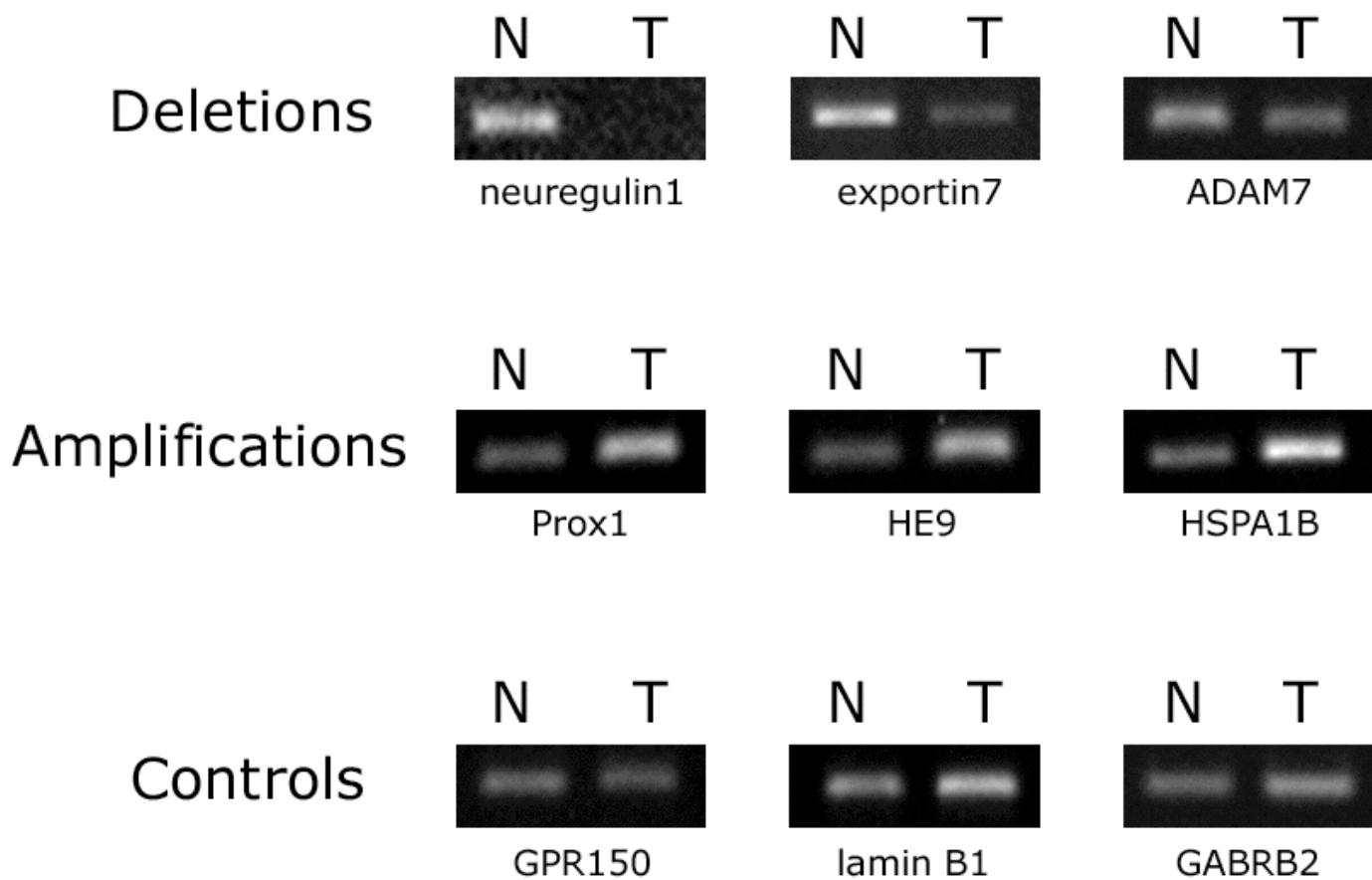
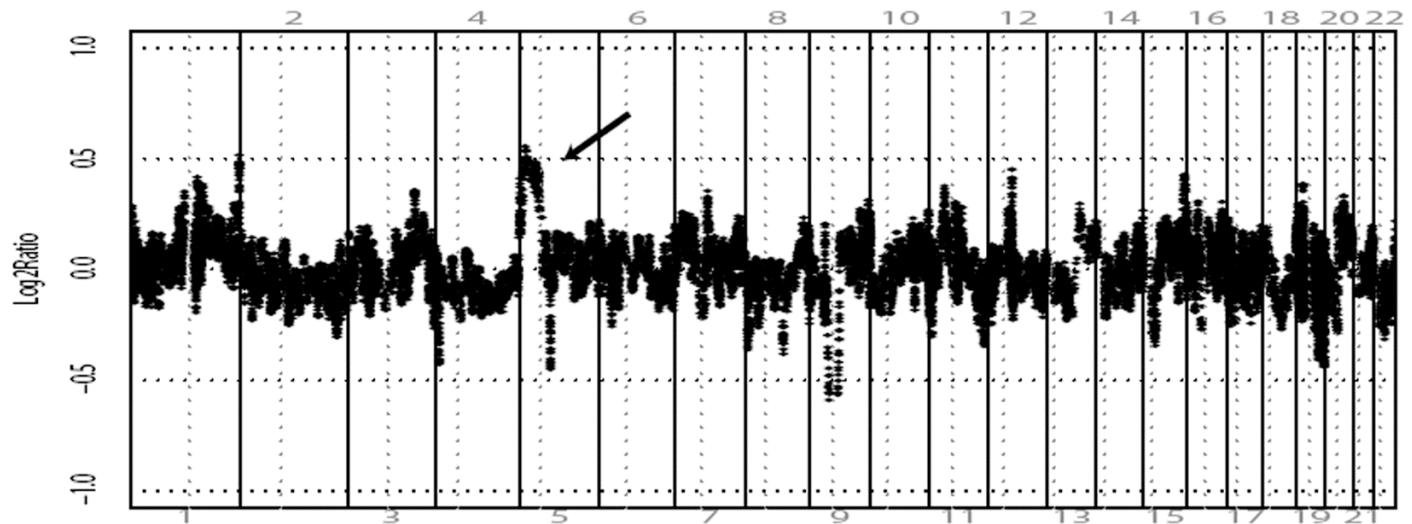


Figure S5. PCR confirmations of vCGH data. Semiquantitative PCR reactions were performed using specific primers for the promoter region of the indicated genes. Deletions represent loss of copy number in tumor. Amplifications depict gain of copy number in tumor. Controls represent regions with no change in copy number.

Acevedo_Figure_S6

A HeLa vs. Human ES



B Ntera2 vs. Human ES

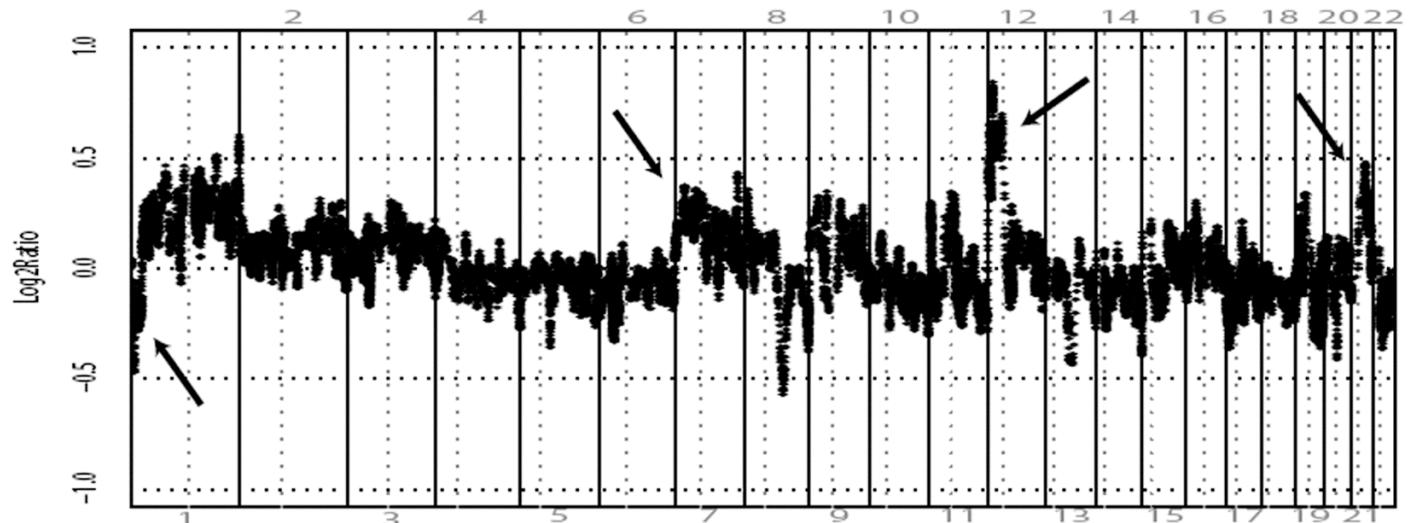


Figure S6. vCGH analysis of Hela and Ntera Cells across the 22 autosomal chromosomes. (A) The genomic DNA channels from Hela S3 ChIP-chip experiments was compared to genomic DNA channels from human ES cell (normal cell) ChIP-chip experiments. Same procedure was used as in main text, except that “cell line” was used in place of tumor (see RESULTS and METHODS for vCGH procedure description). Arrow indicates the large amplification in 5p, consistent with published studies using SKY and conventional CGH (see RESULTS). (B) Same procedure as A, except that genomic DNA channels from Ntera ChIP-chip experiments was used as “tumor” sample. Arrows indicate copy number changes observed in these experiments that are frequently observed in testicular carcinomas. Note that the patterns differ greatly between Ntera and Hela cells. The source of all of this data was 1.5 kb promoter array datasets, illustrating that the vCGH procedure can be used with both 5 kb array platforms (as in patient data in main text) and for other array designs.

chromosome organization and biogenesis (25)		zinc ion binding (38)	
86	actin-like 6a	ACTL6A	27301 apex nuclelease 2
8260	ard1 homolog a, n-acetyltransferase	ARD1	283481 kiaa1802 protein
23492	chromobox homolog 7	CBX7	10664 cctc-binding factor (zinc finger protein)
9126	chondroitin sulfate proteoglycan 6	CSPG6	1786 dna (cytosine-5'-)-methyltransferase 1
3014	h2a histone family, member x	H2AFX	163049 hypothetical protein loc163049
3015	h2a histone family, member z	H2AFZ	51621 kruppel-like factor 13
54145	h2b histone family, member s	H2BFS	28999 kruppel-like factor 15
440093	similar to h3 histone, family 3b	H3 3b-like	4005 lim domain only 2 (rhombotin-like 1)
8370	h4 histone, family 2	H4/O	55646 hypothetical protein fli20425
3006	histone 1, h1c	HIST1H1C	4520 metal-regulatory transcription factor 1
8334	histone 1, h2ac	HIST1H2AC	9972 nucleoporin 53kda
8349	histone 1, h2bb	HIST1H2BB	11097 nucleoporin like 2
85236	histone 1, h2bk	HIST1H2BK	142 poly (adp-ribose) polymerase family member 1
8337	histone 2, h2aa	HIST2H2AA	648 polycomb group ring finger 4
8338	histone 2, h2ac	HIST2H2AC	5437 polymerase (rna) ii (dna directed) polypeptide h
3148	high-mobility group box 2	HMG2B	83759 rna binding motif protein 4b
9643	mortality factor 4 like 2	MORF4L2	5987 ret finger protein
51203	nucleolar and spindle associated protein 1	NUSAP1	64326 ring finger and wd repeat domain 2
648	polycomb group ring finger 4	PCGF4	79102 ring finger protein 26
10856	ruvb-like 2	RUVBL2	6117 replication protein a1, 70kda
6418	set translocation (myeloid leukemia-associated)	SET	6631 small nuclear ribonucleoprotein polypeptide c
6599	swi/snft related, actin dependent regulator of chromatin, c1	SMARCC1	6666 sp2 transcription factor
6839	suppressor of variegation 3-9 homolog 1	SUV39H1	6827 suppressor of ty 4 homolog 1
7014	telomeric repeat binding factor 2	TERF2	6839 suppressor of variegation 3-9 homolog 1
26277	terf1 (trf1)-interacting nuclear factor 2	TINF2	57215 thp domain containing 11
nucleocytoplasmic transport (12)		WIG1	
79711	importin 4	IPO4	9235 zinc finger and btb domain containing 9
55705	importin 9	IPO9	51538 zinc finger, cch domain containing 17
3838	karyopherin alpha 2 (rag cohort 1, importin alpha 1)	KPN2A	285381 zinc finger, cst-type containing 2
4116	mao-nashi homolog, proliferation-associated	MAGOH	23051 zinc fingers and homeoboxes 3
22916	nuclear cap binding protein subunit 2, 20kda	NCBP2	153527 zinc finger, matrin type 2
7122	nucleoporin 107kda	NUP107	9204 zinc finger, mym-type 6
55746	nucleoporin 133kda	NUP133	57567 zinc finger protein 319
23165	nucleoporin 205kda	NUP205	79673 zinc finger protein 329
11097	nucleoporin like 2	NUPL2	80345 zinc finger protein 435
754	pituitary tumor-transforming 1 interacting protein	PTTG1IP	144348 zinc finger protein 664
6418	set translocation (myeloid leukemia-associated)	SFT	7553 zinc finger protein 7 (kox 4, clone hf.16)
7514	exportin 1 (crm1 homolog)	XPO1	ZNF7
transcription (67)		ZBTB9	
86	actin-like 6a	ACTL6A	221504 zinc finger and btb domain containing 9
328	apex nuclelease 1	APEX1	51538 zinc finger, cch domain containing 17
689	basic transcription factor 3	BTF3	285381 zinc finger, cst-type containing 2
23492	chromobox homolog 7	CBX7	23051 zinc fingers and homeoboxes 3
988	cdd5 cell division cycle 5-like (s. pombe)	CDC5L	153527 zinc finger, matrin type 2
85406	cytokine induced protein 29 kda	CIP29	9204 zinc finger, mym-type 6
79191	iroquois homeobox protein 3	CREB3L2	57567 zinc finger protein 319
9443	cofactor for sp1 transcriptional activation, subunit 9	CRSP9	79673 zinc finger protein 329
10664	cctc-binding factor (zinc finger protein)	CTCF	80345 zinc finger protein 435
1786	dna (cytosine-5')-methyltransferase 1	DNMT1	144348 zinc finger protein 664
163049	hypothetical protein loc163049	FLJ90396	7553 zinc finger protein 7 (kox 4, clone hf.16)
2296	forkhead box c1	FOXC1	ZNF7
94234	forkhead box a1	FOXO1	ZNF7
2958	general transcription factor iia, 2, 12kda	GTF2A2	ZNF7
2968	general transcription factor iih, polypeptide 4, 52kda	GTF2H4	ZNF7
2976	general transcription factor iiic, polypeptide 2, beta	GTF3C2	ZNF7
23462	hairy/enhancer-of-split related with yrpw motif 1	HEY1	ZNF7
3148	high-mobility group box 2	HMG2B	ZNF7
3608	interleukin enhancer binding factor 2, 45kda	ILF2	ZNF7
3664	interferon regulatory factor 6	IRF6	ZNF7
80345	zinc finger protein 435	JARID2	ZNF7
3720	jumonji, at rich interactive domain 2	KLF13	ZNF7
51621	kruppel-like factor 13	KLF15	ZNF7
28999	kruppel-like factor 15	MAFB	ZNF7
9935	v-maf oncogene homolog b	MCM3	ZNF7
4172	mcm3 minichromosome maintenance deficient 3	MCM4	ZNF7
4173	mcm3 minichromosome maintenance deficient 4	MCM5	ZNF7
4174	mcm5 minichromosome maintenance deficient 5	MORF4L2	ZNF7
9643	mortality factor 4 like 2	MTF1	ZNF7
4520	metal-regulatory transcription factor 1	NCOA6	ZNF7
23054	nuclear receptor coactivator 6	NUP62	ZNF7
23636	nucleoporin 62kda	PARP1	ZNF7
142	poly (adp-ribose) polymerase family, member 1	PCGF4	ZNF7
648	polycomb group ring finger 4	PIR	ZNF7
8544	prrn (iron-binding nuclear protein)	POGK	ZNF7
64764	camp responsive element binding protein 3-like 2	POLR2C	ZNF7
5432	polymerase (rna) ii (dna directed) polypeptide c, 33kda	POLR2H	ZNF7
5437	polymerase (rna) ii (dna directed) polypeptide h	POLR3E	ZNF7
55718	polymerase (rna) iii (dnase directed) polypeptide e (80kda)	PPP1R3E	ZNF7
57645	poop transposable element with krab domain	PURA	ZNF7
5813	purine-rich element binding protein a	RFP	ZNF7
5987	ret finger protein	RFX5	ZNF7
5993	regulatory factor x, 5 (influences hla class ii expression)	RUVBL2	ZNF7
10856	ruvb-like 2	SATB2	ZNF7
23314	sat family member 2	SEC14L2	ZNF7
23541	sec14-like 2 (s. cerevisiae)	SMARCC1	ZNF7
6599	swi/snft related, actin dependent regulator of chromatin, c1	SOX13	ZNF7
9580	sry (see determining region y)-box 13	SOX18	ZNF7
54345	sry (see determining region y)-box 18	SP2	ZNF7
6668	sp2 transcription factor	SREBF2	ZNF7
6721	sterol regulatory element binding transcription factor 2	SUPT4H1	ZNF7
6827	suppressor of ty 4 homolog 1	TAF12	ZNF7
6883	taf12 ma polymerase ii, (tbp)-associated factor, 20kda	TCEB1	ZNF7
6921	transcription elongation factor b (siii) (15kda, elonq c)	TCFL5	ZNF7
10732	transcription factor-like 5 (basic helix-loop-helix)	TEAD2	ZNF7
8463	tea domain family member 2	TEF	ZNF7
7008	thyrotrophic embryonic factor	TERF2	ZNF7
7014	telomeric repeat binding factor 2	TFDP1	ZNF7
7027	transcription factor dp-1	TIMELESS	ZNF7
8914	timeless homolog	TRIP4	ZNF7
9325	thyroid hormone receptor interactor 4	XRC6	ZNF7
2547	x-ray repair complementing defective repair (ku 70kda)	ZBTB9	ZNF7
221504	zinc finger and btb domain containing 9	ZHX3	ZNF7
23051	zinc fingers and homeoboxes 3	ZNF319	ZNF7
57567	zinc finger protein 319	ZNF435	ZNF7
84313	vacuolar protein sorting 25	ZNF7	ZNF7
7553	zinc finger protein 7 (kox 4, clone hf.16)	ZNF7	ZNF7
DNA repair and replication (24)		ZNF7	
328	apex nuclelease 1	27301	apex nuclelease 2
9126	chondroitin sulfate proteoglycan 6 (bamacan)	9216	chondroitin sulfate proteoglycan 6 (bamacan)
9521	eukaryotic translation elongation factor 1 epsilon 1	9264	general transcription factor ih, polypeptide 4, 52kda
2964	general transcription factor iih, polypeptide 1 epsilon 1	9264	general transcription factor iih, polypeptide 1 epsilon 1
3014	h2a histone family, member x	9264	general transcription factor iih, polypeptide 1 epsilon 1
3148	high-mobility group box 2	9264	general transcription factor iih, polypeptide 1 epsilon 1
4172	mcm3 minichromosome maintenance deficient 3	9264	general transcription factor iih, polypeptide 1 epsilon 1
4173	mcm4 minichromosome maintenance deficient 4	9264	general transcription factor iih, polypeptide 1 epsilon 1
4174	mcm5 minichromosome maintenance deficient 5	9264	general transcription factor iih, polypeptide 1 epsilon 1
9656	mediator of dna damage checkpoint 1	9264	general transcription factor iih, polypeptide 1 epsilon 1
4292	mutl homolog 1, colon cancer, nonpolyplosis type 2	9264	general transcription factor iih, polypeptide 1 epsilon 1
2956	mutl homolog 6 (e. coli)	9264	general transcription factor iih, polypeptide 1 epsilon 1
23054	nuclear receptor coactivator 6	9264	general transcription factor iih, polypeptide 1 epsilon 1
142	poly (adp-ribose) polymerase family, member 1	9264	general transcription factor iih, polypeptide 1 epsilon 1
143	poly (adp-ribose) polymerase family, member 4	9264	general transcription factor iih, polypeptide 1 epsilon 1
51659	dna replication complex gins protein psf2	9264	general transcription factor iih, polypeptide 1 epsilon 1
5813	purine-rich element binding protein a	9264	general transcription factor iih, polypeptide 1 epsilon 1
5984	replication factor c (activator 1) 4, 37kda	9264	general transcription factor iih, polypeptide 1 epsilon 1
6117	replication protein a1, 70kda	9264	general transcription factor iih, polypeptide 1 epsilon 1
6119	replication protein a3, 14kda	9264	general transcription factor iih, polypeptide 1 epsilon 1
10856	ruvb-like 2	9264	general transcription factor iih, polypeptide 1 epsilon 1
6418	set translocation (myeloid leukemia-associated)	SET	general transcription factor iih, polypeptide 1 epsilon 1
2547	x-ray repair complementing defective repair (ku 70)	XRCC6	general transcription factor iih, polypeptide 1 epsilon 1
RNA metabolism (32)		ZNF7	
988	cdd5 cell division cycle 5-like	CDC5L	ZNF7
1478	cleavage stimulation factor, 3' pre-rna, subunit 2	CSTF2	ZNF7
9775	dead (asp-alu-alu-asp) box polypeptide 48	DDX48	ZNF7
8449	dead (asp-alu-alu-his) box polypeptide 16	DHX16	ZNF7
51010	exosome component 3	EXOSC3	ZNF7
56915	exosome component 5	EXOSC5	ZNF7
79833	gem (nuclear organelle) associated protein 6	GEMIN6	ZNF7
10979	atp/gtp-binding protein	HEAB	ZNF7
10236	heterogeneous nuclear ribonucleoprotein r	HNRRP	ZNF7
84967	lsm10, u7 small nuclear rna associated	LSM10	ZNF7
27258	lsm3 homolog, u6 small nuclear rna associated	LSM3	ZNF7
25804	lsm4 homolog, u6 small nuclear rna associated	LSM4	ZNF7
4116	mao-nashi homolog, proliferation-associated	MAGOH	ZNF7
56339	methyltransferase like 3	METTL3	ZNF7
22916	nuclear cap binding protein subunit 2, 20kda	NCBP2	ZNF7
4809	nhp2 non-histone chromosome protein 2-like 1	NHP2L1	ZNF7
55651	nucelar protein family a, member 2	NOLA2	ZNF7
55505	nucelar protein family a, member 3	NOLA3	ZNF7
11097	nucleoporin like 2	NULP2	ZNF7
83759	rna binding motif protein 4b	RBM4B	ZNF7
29102	ribonuclease iii, nuclear	RNASEN	ZNF7
79897	ribonuclease p 21kda subunit	RPP21	ZNF7
8634	rna terminal phosphate cyclase domain 1	RTCD1	ZNF7
51630	splicing factor 3b, 14 kda subunit	SF3B14	ZNF7
10262	splicing factor 3b, subunit 4, 49kda	SF3B4	ZNF7
6732	srs protein kinase 1	sfrs	ZNF7
6427	splicing factor, arginine/serine-rich 2	SFRS2	ZNF7
6428	splicing factor, arginine/serine-rich 3	SFRS3	ZNF7
6628	small nuclear ribonucleoprotein polypeptides b and b1	SNRPB	ZNF7
6631	small nuclear ribonucleoprotein polypeptide c	SNRPC	ZNF7
6636	small nuclear ribonucleoprotein polypeptide f	SRPK1	ZNF7
7514	exportin 1 (crm1 homolog)	XPO1	ZNF7

Acevedo. **Supplementary Figure S7. Categories of nuclear proteins upregulated in tumors.**