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Genome-wide distribution of histone trimethylation reveals a global impact of bisphenol A on telomeric binding proteins and histone acetyltransferase factors: A pilot study with human and *in vitro* data.

Supplementary information

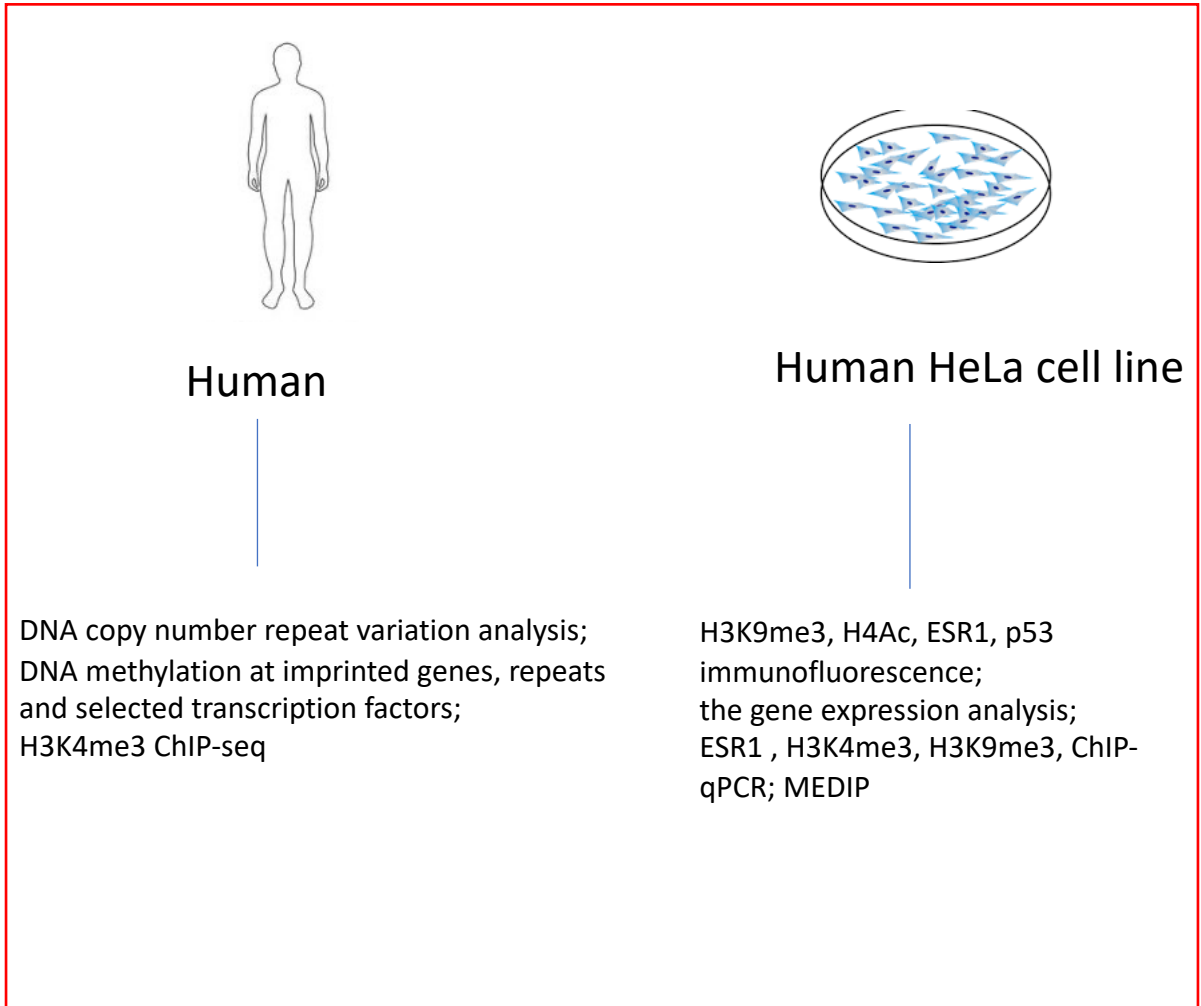
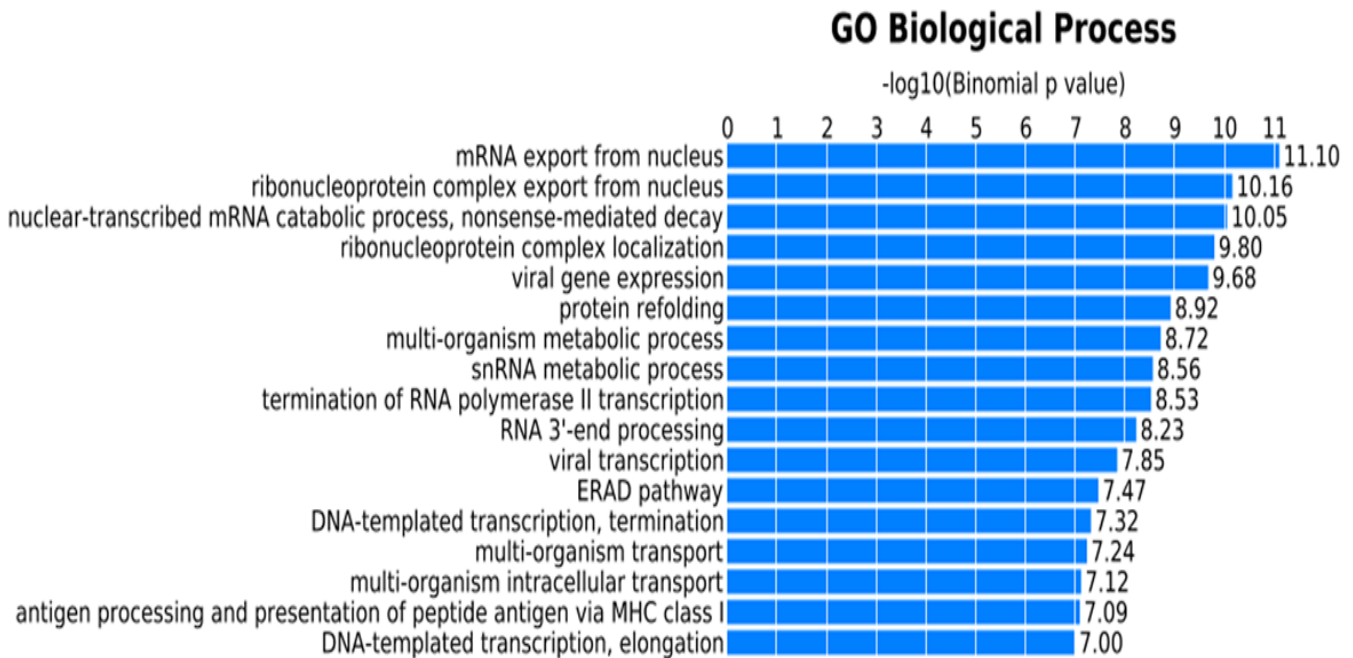


Figure S1. Schematic presentation of the experiments performed in this study in human samples and HeLa cells.

A



B

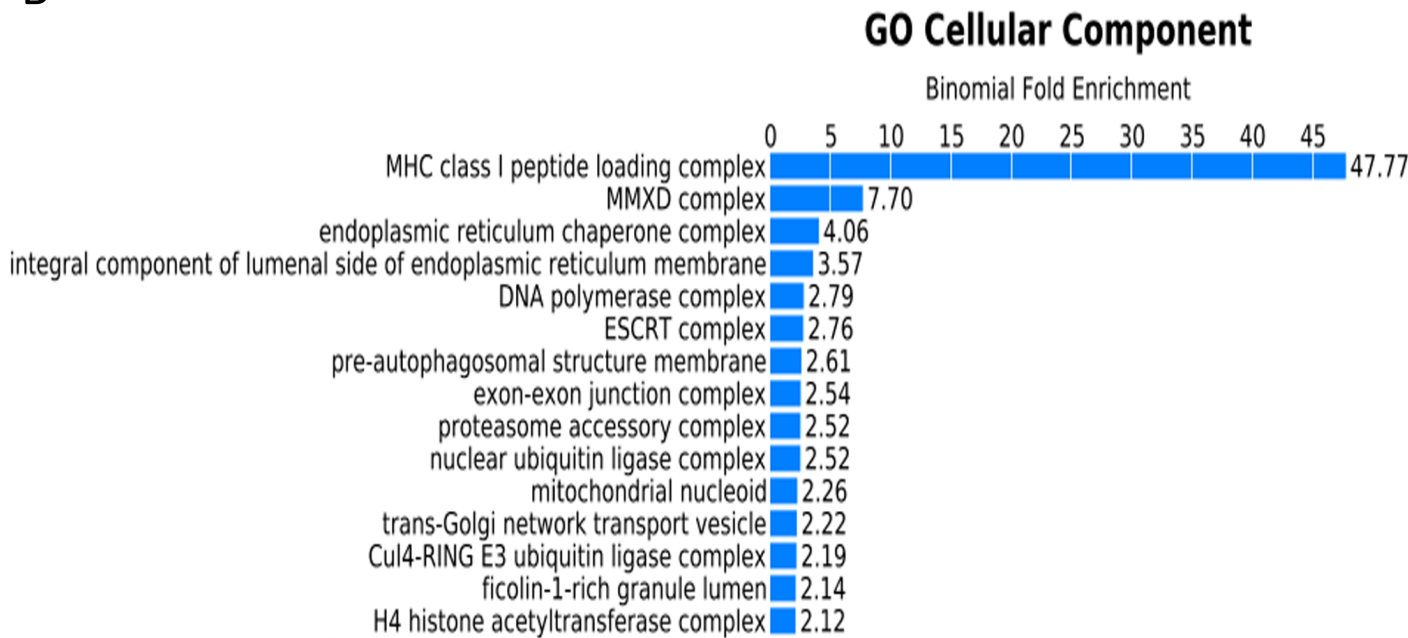


Figure S2. Gene Ontology generated by GREAT. A) Gene Ontology “Biological process”, B) Gene Ontology “Cellular component”.

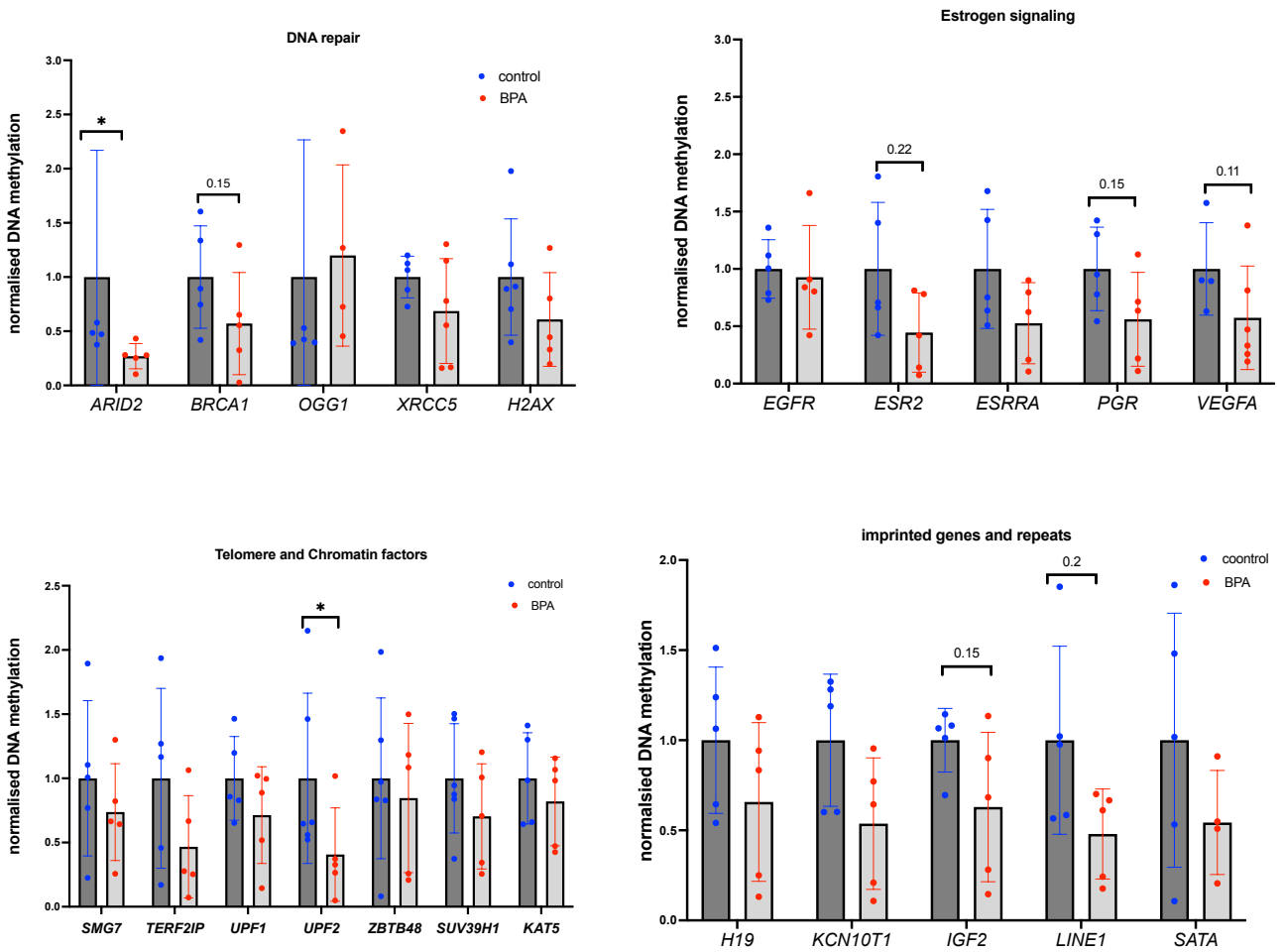


Figure S3. DNA methylation analysis at the promoters: A) DNA repair genes, B) oestrogen signalling pathway genes, C) telomere maintenance and chromatin factors genes D) of imprinted genes and repeat regions. * $p < 0.05$, Mann–Whitney test.

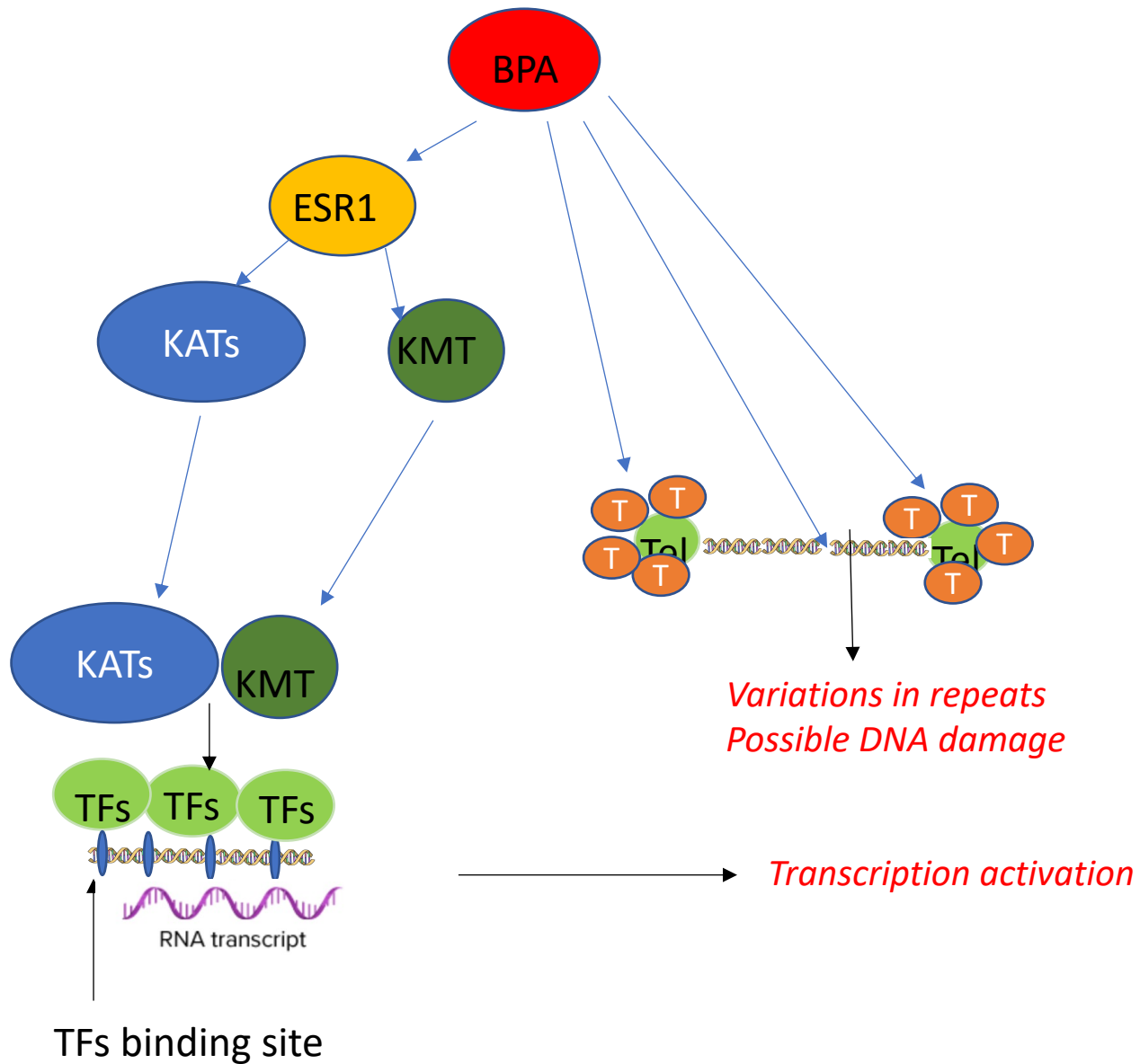


Figure S4. A proposed mechanism of BPA action. BPA stabilizes ESR1, which in turn activates histone acetyltransferases and methyltransferases and thereby increases access to chromatin. This complex activates the gene expression at several regions. In addition, the genotoxic effect of BPA induces the expression of telomere maintenance genes and DNA repair factors.

Table S1. The human samples used for the DNA repeat analysis

N	BPA (microg/gram Creat)	BPA group
1	0,66	low
2	0,73	low
3	1,1	low
4	1,12	low
5	1,28	low
6	2,13	low
7	2,31	low
8	2,35	low
9	2,43	low
10	2,55	low
11	3,1	low
12	3,94	low
13	4,47	low
14	4,55	low
15	4,57	low
16	4,67	low
17	4,85	high
18	5,1	high
19	6,28	high
20	7,46	high
21	8,14	high
22	8,98	high
23	9,44	high
24	10,07	high
25	10,55	high
26	12,24	high
27	15,87	high
28	17,11	high
29	19,57	high
30	39,34	high
31	42,64	high

Note, Creat., creatinine, microg., microgram

Table S2. The human samples used for DNA methylation analysis

	BPA (microg/gram Creatinine)	BPA group
1	0,66	low
2	0,73	low
3	1,1	low
4	1,12	low
5	1,28	low
6	2,13	low
7	2,31	low
8	2,35	low
9	2,43	low
10	2,55	low
11	3,1	low
12	3,94	low
13	9,44	high
14	10,07	high
15	10,55	high
16	12,24	high
17	15,87	high
18	17,11	high
19	19,57	high
20	39,34	high
21	42,64	high

Note, Creat., creatinine, microg., microgram

Table S3. The human samples used for Chip-seq analysis

N	BPA (microg/gram Creat)	BPA gpoup
1	0,66	low
2	0,73	low
3	1,1	low
4	1,12	low
5	1,28	low
6	2,13	low
7	2,31	low
8	2,35	low
9	2,43	low
10	2,55	low
11	10,07	high
12	10,55	high
13	12,24	high
14	17,11	high
15	19,57	high
16	39,34	high
17	42,64	high

Note, Creat., creatinine, microg., microgram

Table S4. Genes encoding telomeric DNA binding proteins located in differential peaks

Gene	distance to TSS	description
ACD	(+344)	ACD shelterin complex subunit and telomerase recruitment factor
CTC1	(+25,553)	CST telomere replication complex component 1
HNRNPA2B1	(+95)	heterogeneous nuclear ribonucleoprotein A2/B1
HNRNPD	(+570)	heterogeneous nuclear ribonucleoprotein D
KDM1A	(+228), (+148,773)	lysine demethylase 1A
NABP2	(-2,573)	nucleic acid binding protein 2
NCL	(+178)	nucleolin
PURA	(-6,082), (+8)	purine rich element binding protein A
RPA1	(-43)	replication protein A1
SMG1	(+218)	SMG1 nonsense mediated mRNA decay associated PI3K related kinase
SMG5	(+149)	SMG5 nonsense mediated mRNA decay factor
SMG6	(+145)	SMG6 nonsense mediated mRNA decay factor
SMG7	(-527)	SMG7 nonsense mediated mRNA decay factor
TEN1	(+101)	TEN1 subunit of CST complex
TERF2IP	(+830)	TERF2 interacting protein
TERT	(+96)	telomerase reverse transcriptase
TP53BP1	(+190)	tumor protein p53 binding protein 1
UPF1	(+815)	UPF1 RNA helicase and ATPase
UPF2	(-6,794)	UPF2 regulator of nonsense mediated mRNA decay
UPF3A	(+282)	UPF3A regulator of nonsense mediated mRNA decay
XRCC6	(-234)	X-ray repair cross complementing 6
ZBTB48	(+288), (+21,528)	zinc finger and BTB domain containing 48

Table S5. Genes encoding ESR1-interacting proteins located in differential H3K4me3 peaks

Gene	description		
1AHR	aryl hydrocarbon receptor	61CALM1	calmodulin 1
2ESRRA	estrogen related receptor alpha	62CALM2	calmodulin 2
3NCOR1	nuclear receptor corepressor 1	63CALM2	calmodulin 3
4NCOR2	nuclear receptor corepressor 2	64CALM2	calmodulin 1
5NR2F6	nuclear receptor subfamily 2 group F member 6	65CALM3	calmodulin 3
6PSMD2	proteasome 26S subunit ubiquitin receptor, non-ATPase 2	66CAND1	cullin associated and neddylation dissociated 1
7RARA	retinoic acid receptor alpha	67CAPRIN1	cell cycle associated protein 1
8RXRA	retinoid X receptor alpha	68CAPZB	capping actin protein of muscle Z-line subunit beta
9TFRC	transferrin receptor	69CCDC110	coiled-coil domain containing 110
10ABCC5	ATP binding cassette subfamily C member 5	70CCT7	chaperonin containing TCP1 subunit 7
11ABCF1	ATP binding cassette subfamily F member 1	71CD47	CD47 molecule
12ABL1	ABL proto-oncogene 1, non-receptor tyrosine kinase	72CDC25B	cell division cycle 25B
13ACAA1	acetyl-CoA acyltransferase 1	73CDK11B	cyclin dependent kinase 11B
14ACLY	ATP citrate lyase	74CDK5	cyclin dependent kinase 5
15ACO2	aconitase 2	75CDK8	cyclin dependent kinase 8
16ACTB	actin beta	76CEBPA	CCAAT enhancer binding protein alpha
17ACTN1	actinin alpha 1	77CEBPB	CCAAT enhancer binding protein beta
18ACTN4	actinin alpha 4	78CFL1	cofilin 1
19ACTR2	actin related protein 2	79CHD3	chromodomain helicase DNA binding protein 3
20ACTR3	actin related protein 3	80CHD4	chromodomain helicase DNA binding protein 4
21AHNAK	AHNAK nucleoprotein	81CHD9	chromodomain helicase DNA binding protein 9
22AIFM1	apoptosis inducing factor mitochondria associated 1	82CHUK	component of inhibitor of nuclear factor kappa B kinase complex
23AKAP13	A-kinase anchoring protein 13	83CLTC	clathrin heavy chain
24AKAP8	A-kinase anchoring protein 8	84CNDP2	carnosine dipeptidase 2
25AKT2	AKT serine/threonine kinase 2	85CNOT1	CCR4-NOT transcription complex subunit 1
26ALDH18A1	aldehyde dehydrogenase 18 family member A1	86COPA	COP1 coat complex subunit alpha
27ALDOA	aldolase, fructose-bisphosphate A	87COPB1	COP1 coat complex subunit beta 1
28ALKBH7	alkB homolog 7	88COP55	COP9 signalosome subunit 5
29ANP32A	acidic nuclear phosphoprotein 32 family member A	89CSE1L	chromosome segregation 1 like
30ANP32B	acidic nuclear phosphoprotein 32 family member B	90CSNK2A1	casein kinase 2 alpha 1
31ANXA2	annexin A2	91CSNK2B	casein kinase 2 beta
32AP2M1	adaptor related protein complex 2 subunit mu 1	92CSNK2B	novel protein
33APOD	apolipoprotein D	93CTNNB1	catenin beta 1
34ARF1	ADP ribosylation factor 1	94CTSD	cathepsin D
35ARFGAP2	ADP ribosylation factor GTPase activating protein 2	95CUL4B	cullin 4B
36ARHGDI2	Rho GDP dissociation inhibitor alpha	96DAGLB	diacylglycerol lipase beta
37ARID5A	AT-rich interaction domain 5A	97DAP3	death associated protein 3
38ARNT	aryl hydrocarbon receptor nuclear translocator	98DBN1	drebrin 1
39ARPC4	actin related protein 2/3 complex subunit 4	99DDOST	dolichyl-diphosphooligosaccharide--protein glycosyltransferase non-catalytic subunit
40ARSB	arylsulfatase B	100DDX17	DEAD-box helicase 17
41ASF1A	anti-silencing function 1A histone chaperone	101DDX18	DEAD-box helicase 18
42ASH2L	ASH2 like, histone lysine methyltransferase complex subunit	102DDX21	DEAD-box helicase 21
43ASXL1	ASXL transcriptional regulator 1	103DDX3X	DEAD-box helicase 3 X-linked
44ATAD2	ATPase family AAA domain containing 2	104DDX5	DEAD-box helicase 5
45ATAD3A	ATPase family AAA domain containing 3A	105DDX54	DEAD-box helicase 54
46ATF1	activating transcription factor 1	106DECR1	2,4-dienoyl-CoA reductase 1
47ATP1A1	ATPase Na ⁺ /K ⁺ transporting subunit alpha 1	107DEK	DEK proto-oncogene
48ATP2A2	ATPase sarcoplasmic/endoplasmic reticulum Ca ²⁺ transporting 2	108DHX15	DEAH-box helicase 15
49ATP2B1	ATPase plasma membrane Ca ²⁺ transporting 1	109DHX30	DEXH-box helicase 30
50ATP5B	None	110DHX9	DEXH-box helicase 9
51ATP5F1	None	111DKC1	dyskerin pseudouridine synthase 1
52BAG1	BAG cochaperone 1	112DNAJB11	DnaJ heat shock protein family (Hsp40) member B11
53BARD1	BRCA1 associated RING domain 1	113DNM1L	dynamamin 1 like
54BAZ1B	bromodomain adjacent to zinc finger domain 1B	114DTD1	D-aminoacyl-tRNA deacylase 1
55BCL3	BCL3 transcription coactivator	115DYNC1H1	dynein cytoplasmic 1 heavy chain 1
56BCLAF1	BCL2 associated transcription factor 1	116EDF1	endothelial differentiation related factor 1
57BLCAP	BLCAP apoptosis inducing factor	117EEF1A1	eukaryotic translation elongation factor 1 alpha 1
58BTF3	basic transcription factor 3	118EEF2	eukaryotic translation elongation factor 2
59BZW1	basic leucine zipper and W2 domains 1	119EHMT2	euchromatic histone lysine methyltransferase 2
60CALM1	calmodulin 3	120EIF3F	eukaryotic translation initiation factor 3 subunit F

Table S5. Genes encoding ESR1-interacting proteins located in differential H3K4me3 peaks

121 EIF4A1	eukaryotic translation initiation factor 4A1	181 HNRNPAB	heterogeneous nuclear ribonucleoprotein A/B
122 EIF4G1	eukaryotic translation initiation factor 4 gamma 1	182 HNRNPD	heterogeneous nuclear ribonucleoprotein D
123 ELMSAN1	None	183 HNRNPF	heterogeneous nuclear ribonucleoprotein F
124 EMD	emerin	184 HNRNPK	heterogeneous nuclear ribonucleoprotein K
125 ENO1	enolase 1	185 HNRNPL	heterogeneous nuclear ribonucleoprotein L
126 EP300	E1A binding protein p300	186 HNRNPM	heterogeneous nuclear ribonucleoprotein M
127 EP400	E1A binding protein p400	187 HNRNPR	heterogeneous nuclear ribonucleoprotein R
128 EPPK1	epiplakin 1	188 HNRNPU	heterogeneous nuclear ribonucleoprotein U
129 ESYT1	extended synaptotagmin 1	189 HNRNPUL1	heterogeneous nuclear ribonucleoprotein U like 1
130 EWSR1	EWS RNA binding protein 1	190 HPCAL1	hippocalcin like 1
131 EXOSC10	exosome component 10	191 HSP90AA1	heat shock protein 90 alpha family class A member 1
132 EXOSC4	exosome component 4	192 HSP90AB1	heat shock protein 90 alpha family class B member 1
133 EZH2	enhancer of zeste 2 polycomb repressive complex 2 subunit	193 HSP90B1	heat shock protein 90 beta family member 1
134 EZR	ezrin	194 HSPA1B	heat shock protein family A (Hsp70) member 1B
135 FAF2	Fas associated factor family member 2	195 HSPA1L	heat shock protein family A (Hsp70) member 1 like
136 FAM120A	family with sequence similarity 120A	196 HSPA4	heat shock protein family A (Hsp70) member 4
137 FAM213A	None	197 HSPA5	heat shock protein family A (Hsp70) member 5
138 FASN	fatty acid synthase	198 HSPA8	heat shock protein family A (Hsp70) member 8
139 FIS1	fission, mitochondrial 1	199 HSPA9	heat shock protein family A (Hsp70) member 9
140 FKBP1A	FKBP prolyl isomerase 1A	200 HSPD1	heat shock protein family D (Hsp60) member 1
141 FKBP5	FKBP prolyl isomerase 5	201 HSP E1	heat shock protein family E (Hsp10) member 1
142 FLII	FLII actin remodeling protein	202 HSPH1	heat shock protein family H (Hsp110) member 1
143 FLNA	filamin A	203 HUWE1	HECT, UBA and WWE domain containing E3 ubiquitin protein ligase 1
144 FMR1	FMRP translational regulator 1	204 HYOU1	hypoxia up-regulated 1
145 FOS	Fos proto-oncogene, AP-1 transcription factor subunit	205 IDH2	isocitrate dehydrogenase (NADP(+)) 2
146 FOXL2	forkhead box L2	206 ILF3	interleukin enhancer binding factor 3
147 FOXO1	forkhead box O1	207 IMMT	inner membrane mitochondrial protein
148 FOXO3	forkhead box O3	208 INGI1	inhibitor of growth family member 1
149 FTSJ3	FtsJ RNA 2'-O-methyltransferase 3	209 INTS1	integrator complex subunit 1
150 FUS	FUS RNA binding protein	210 IPO7	importin 7
151 G3BP2	G3BP stress granule assembly factor 2	211 IQGAP1	IQ motif containing GTPase activating protein 1
152 GADD45A	growth arrest and DNA damage inducible alpha	212 IRS2	insulin receptor substrate 2
153 GADD45B	growth arrest and DNA damage inducible beta	213 JUNB	JunB proto-oncogene, AP-1 transcription factor subunit
154 GAK	cyclin G associated kinase	214 JUND	JunD proto-oncogene, AP-1 transcription factor subunit
155 GAPDH	glyceraldehyde-3-phosphate dehydrogenase	215 KAT2A	lysine acetyltransferase 2A
156 GARS	None	216 KAT5	lysine acetyltransferase 5
157 GLYR1	glyoxylate reductase 1 homolog	217 KAT6A	lysine acetyltransferase 6A
158 GNB1	G protein subunit beta 1	218 KDM1A	lysine demethylase 1A
159 GNB2	G protein subunit beta 2	219 KDM4A	lysine demethylase 4A
160 GNL3	G protein nucleolar 3	220 KDM4C	lysine demethylase 4C
161 GOLGA2	golgin A2	221 KHDRBS1	KH RNA binding domain containing, signal transduction associated 1
162 GRB2	growth factor receptor bound protein 2	222 KPNB1	karyopherin subunit beta 1
163 GSK3B	glycogen synthase kinase 3 beta	223 LACTB	lactamase beta
164 GTF3C4	general transcription factor IIIC subunit 4	224 LARP1	La ribonucleoprotein 1, translational regulator
165 H2AFX	None	225 LCK	LCK proto-oncogene, Src family tyrosine kinase
166 H3F3A	None	226 LCOR	ligand dependent nuclear receptor corepressor
167 HAX1	HCLS1 associated protein X-1	227 LDB1	LIM domain binding 1
168 HDAC1	histone deacetylase 1	228 LGALS7B	galectin 7B
169 HDAC2	histone deacetylase 2	229 LGALS7B	galectin 7
170 HDAC3	histone deacetylase 3	230 LMNB1	lamin B1
171 HDAC4	histone deacetylase 4	231 LUC7L3	LUC7 like 3 pre-mRNA splicing factor
172 HDAC5	histone deacetylase 5	232 LYAR	Ly1 antibody reactive
173 HEBP2	heme binding protein 2	233 MAP3K1	mitogen-activated protein kinase kinase 1
174 HIF1A	hypoxia inducible factor 1 subunit alpha	234 MAPK14	mitogen-activated protein kinase 14
175 HIST4H4	None	235 MAPK3	mitogen-activated protein kinase 3
176 HM13	histocompatibility minor 13	236 MARK2	microtubule affinity regulating kinase 2
177 HMGB2	high mobility group box 2	237 MBD2	methyl-CpG binding domain protein 2
178 HNRNPA0	heterogeneous nuclear ribonucleoprotein A0	238 MCM5	minichromosome maintenance complex component 5
179 HNRNPA2B1	heterogeneous nuclear ribonucleoprotein A2/B1	239 MDH2	malate dehydrogenase 2
180 HNRNPA3	heterogeneous nuclear ribonucleoprotein A3	240 MDM2	MDM2 proto-oncogene

Table S5. Genes encoding ESR1-interacting proteins located in differential H3K4me3 peaks

241 MED12	mediator complex subunit 12	301 PIK3R1	phosphoinositide-3-kinase regulatory subunit 1
242 MED14	mediator complex subunit 14	302 PIK3R2	phosphoinositide-3-kinase regulatory subunit 2
243 MED16	mediator complex subunit 16	303 PLEC	plectin
244 MED17	mediator complex subunit 17	304 PNRC2	proline rich nuclear receptor coactivator 2
245 MED20	mediator complex subunit 20	305 POLR1B	RNA polymerase I subunit B
246 MED25	mediator complex subunit 25	306 POLR2D	RNA polymerase II subunit D
247 MEN1	menin 1	307 POR	cytochrome p450 oxidoreductase
248 MGMT	O-6-methylguanine-DNA methyltransferase	308 POU2F1	POU class 2 homeobox 1
249 MKI67	marker of proliferation Ki-67	309 POU2F2	POU class 2 homeobox 2
250 MKNK2	MAPK interacting serine/threonine kinase 2	310 PPARGC1B	PPARG coactivator 1 beta
251 MMS19	MMS19 homolog, cytosolic iron-sulfur assembly component	311 PPP1CA	protein phosphatase 1 catalytic subunit alpha
252 MOGS	mannosyl-oligosaccharide glucosidase	312 PPP1CC	protein phosphatase 1 catalytic subunit gamma
253 MPG	N-methylpurine DNA glycosylase	313 PPP5C	protein phosphatase 5 catalytic subunit
254 MRPS2	mitochondrial ribosomal protein S2	314 PRDM2	PR/SET domain 2
255 MRPS27	mitochondrial ribosomal protein S27	315 PRDX2	peroxiredoxin 2
256 MRPS6	mitochondrial ribosomal protein S6	316 PRDX3	peroxiredoxin 3
257 MSH2	mutS homolog 2	317 PRDX6	peroxiredoxin 6
258 MSH6	mutS homolog 6	318 PRKAR2A	protein kinase cAMP-dependent type II regulatory subunit alpha
259 MTA2	metastasis associated 1 family member 2	319 PRKCA	protein kinase C alpha
260 MTA3	metastasis associated 1 family member 3	320 PRKCB	protein kinase C zeta
261 MTCH2	mitochondrial carrier 2	321 PRKDC	protein kinase, DNA-activated, catalytic subunit
262 MTDH	metadherin	322 PRMT1	protein arginine methyltransferase 1
263 MVP	major vault protein	323 PRMT2	protein arginine methyltransferase 2
264 MYH9	myosin heavy chain 9	324 PRPF4B	pre-mRNA processing factor 4B
265 MYL6	myosin light chain 6	325 PSIP1	PC4 and SFRS1 interacting protein 1
266 NCL	nucleolin	326 PSMAS5	proteasome 20S subunit alpha 5
267 NCOA2	nuclear receptor coactivator 2	327 PSMB9	proteasome 20S subunit beta 9
268 NCOA3	nuclear receptor coactivator 3	328 PSMC5	proteasome 26S subunit, ATPase 5
269 NCOA4	nuclear receptor coactivator 4	329 PSMC1	proteasome 26S subunit, non-ATPase 1
270 NCOA5	nuclear receptor coactivator 5	330 PSMC6	proteasome 26S subunit, non-ATPase 6
271 NCOA6	nuclear receptor coactivator 6	331 PTGES3	prostaglandin E synthase 3
272 NCOA7	nuclear receptor coactivator 7	332 PTMA	prothymosin alpha
273 NME2	NME/NM23 nucleoside diphosphate kinase 2	333 PTPN1	protein tyrosine phosphatase non-receptor type 1
274 NOP2	NOP2 nucleolar protein	334 PTPN6	protein tyrosine phosphatase non-receptor type 6
275 NOP56	NOP56 ribonucleoprotein	335 PUS1	pseudouridine synthase 1
276 NOP58	NOP58 ribonucleoprotein	336 PYGB	glycogen phosphorylase B
277 NPEPPS	aminopeptidase puromycin sensitive	337 RAB10	RAB10, member RAS oncogene family
278 NR2C2	nuclear receptor subfamily 2 group C member 2	338 RAB1A	RAB1A, member RAS oncogene family
279 NSD1	nuclear receptor binding SET domain protein 1	339 RAB1B	RAB1B, member RAS oncogene family
280 NSDHL	NAD(P) dependent steroid dehydrogenase-like	340 RAB7A	RAB7A, member RAS oncogene family
281 NUP153	nucleoporin 153	341 RABGEF1	RAB guanine nucleotide exchange factor 1
282 OTUB1	OTU deubiquitinase, ubiquitin aldehyde binding 1	342 RAP1A	RAP1A, member of RAS oncogene family
283 OXSR1	oxidative stress responsive kinase 1	343 RAP2C	RAP2C, member of RAS oncogene family
284 P4HB	prolyl 4-hydroxylase subunit beta	344 RBBP4	RB binding protein 4, chromatin remodeling factor
285 PABPC1	poly(A) binding protein cytoplasmic 1	345 RBBP6	RB binding protein 6, ubiquitin ligase
286 PAK1	p21 (RAC1) activated kinase 1	346 RBCK1	RANBP2-type and C3HC4-type zinc finger containing 1
287 PCBP1	poly(rC) binding protein 1	347 RBM14	RNA binding motif protein 14
288 PCK2	phosphoenolpyruvate carboxykinase 2, mitochondrial	348 RBMX	RNA binding motif protein X-linked
289 PDIA3	protein disulfide isomerase family A member 3	349 RCN2	reticulocalbin 2
290 PDIA4	protein disulfide isomerase family A member 4	350 REEP6	receptor accessory protein 6
291 PELP1	proline, glutamate and leucine rich protein 1	351 RELA	RELA proto-oncogene, NF-kB subunit
292 PFKL	phosphofructokinase, liver type	352 REXO4	REX4 homolog, 3'-5' exonuclease
293 PFKP	phosphofructokinase, platelet	353 RNF14	ring finger protein 14
294 PFN1	profilin 1	354 RNF4	ring finger protein 4
295 PGM2	phosphoglucomutase 2	355 RPL10	ribosomal protein L10
296 PHB2	prohibitin 2	356 RPL10A	ribosomal protein L10a
297 PHGDH	phosphoglycerate dehydrogenase	357 RPL13	ribosomal protein L13
298 PIAS1	protein inhibitor of activated STAT 1	358 RPL14	ribosomal protein L14
299 PIAS3	protein inhibitor of activated STAT 3	359 RPL15	ribosomal protein L15
300 PIK3CA	phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit alpha	360 RPL18A	ribosomal protein L18a

Table S5. Genes encoding ESR1-interacting proteins located in differential H3K4me3 peaks

361RPL19	ribosomal protein L19	421SP3	Sp3 transcription factor
362RPL22	ribosomal protein L22	422SPOP	speckle type BTB/POZ protein
363RPL28	ribosomal protein L28	423SPTAN1	spectrin alpha, non-erythrocytic 1
364RPL36AL	ribosomal protein L36a like	424SREBF1	sterol regulatory element binding transcription factor 1
365RPL5	ribosomal protein L5	425SRPK1	SRSF protein kinase 1
366RPL7	ribosomal protein L7	426SRRM1	serine and arginine repetitive matrix 1
367RPL7A	ribosomal protein L7a	427SRRM2	serine/arginine repetitive matrix 2
368RPL8	ribosomal protein L8	428SRSF1	serine and arginine rich splicing factor 1
369RPLP0	ribosomal protein lateral stalk subunit P0	429SRSF2	serine and arginine rich splicing factor 2
370RPN1	ribophorin I	430SRSF5	serine and arginine rich splicing factor 5
371RPN2	ribophorin II	431SRSF6	serine and arginine rich splicing factor 6
372RPS11	ribosomal protein S11	432SRSF7	serine and arginine rich splicing factor 7
373RPS14	ribosomal protein S14	433STAT3	signal transducer and activator of transcription 3
374RPS15A	ribosomal protein S15a	434STAT5A	signal transducer and activator of transcription 5A
375RPS19	ribosomal protein S19	435STAU1	staufen double-stranded RNA binding protein 1
376RPS2	ribosomal protein S2	436STRN	striatin
377RPS20	ribosomal protein S20	437STUB1	STIP1 homology and U-box containing protein 1
378RPS23	ribosomal protein S23	438SUMO1	small ubiquitin like modifier 1
379RPS24	ribosomal protein S24		
380RPS25	ribosomal protein S25	439SYNCRIP	synaptotagmin binding cytoplasmic RNA interacting protein
381RPS3A	ribosomal protein S3A	440TAB2	TGF-beta activated kinase 1 (MAP3K7) binding protein 2
382RPS6KA1	ribosomal protein S6 kinase A1	441TADA3	transcriptional adaptor 3
383RPS6KA3	ribosomal protein S6 kinase A3		
384RPS6KB1	ribosomal protein S6 kinase B1	442TAF1B	TATA-box binding protein associated factor, RNA polymerase I subunit B
385RPS7	ribosomal protein S7		
386RPS8	ribosomal protein S8	443TAGLN2	transgelin 2
387RRP1B	ribosomal RNA processing 1B	444TAP1	transporter 1, ATP binding cassette subfamily B member
388RRS1	ribosome biogenesis regulator 1 homolog	445TBL2	transducin beta like 2
389RSL1D1	ribosomal L1 domain containing 1	446TBP	TATA-box binding protein
390SAFB	scaffold attachment factor B	447TCF20	transcription factor 20
391SAFB2	scaffold attachment factor B2	448TCF7L1	transcription factor 7 like 1
392SCYL2	SCY1 like pseudokinase 2	449THEM6	thioesterase superfamily member 6
393SEC11A	SEC11 homolog A, signal peptidase complex subunit	450THRAP3	thyroid hormone receptor associated protein 3
394SEC22B	SEC22 homolog B, vesicle trafficking protein	451TKT	transketolase
395SEC23A	SEC23 homolog A, COPII coat complex component	452TMED10	transmembrane p24 trafficking protein 10
396SEC61B	SEC61 translocon subunit beta	453TMED2	transmembrane p24 trafficking protein 2
397SENP5	SUMO specific peptidase 5	454TMOD3	tropomodulin 3
398SETD7	SET domain containing 7, histone lysine methyltransferase	455TMX1	thioredoxin related transmembrane protein 1
399SF1	splicing factor 1	456TNFRSF14	TNF receptor superfamily member 14
400SIN3A	SIN3 transcription regulator family member A	457TNPO2	transportin 2
401SIN3B	SIN3 transcription regulator family member B	458TOP1	DNA topoisomerase I
402SIRT1	sirtuin 1	459TOP2B	DNA topoisomerase II beta
403SKI	SKI proto-oncogene	460TOR1AIP1	torsin 1A interacting protein 1
404SKIL	SKI like proto-oncogene	461TPM1	tropomyosin 1
405SLC25A5	solute carrier family 25 member 5	462TRAF6	TNF receptor associated factor 6
406SLC30A9	solute carrier family 30 member 9	463TRAM1	translocation associated membrane protein 1
407SLC3A2	solute carrier family 3 member 2	464TRAP1	TNF receptor associated protein 1
408SLC9A3R1	SLC9A3 regulator 1	465TRIM24	tripartite motif containing 24
409SMAD2	SMAD family member 2	466TRIM25	tripartite motif containing 25
410SMARCA2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	467TRIM59	tripartite motif containing 59
411SMARCB1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily b, member 1	468TRIP12	thyroid hormone receptor interactor 12
412SMARCC2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin subfamily c member 2	469TRIP4	thyroid hormone receptor interactor 4
413SMARCD1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 1	470TRRAP	transformation/transcription domain associated protein
414SMARCD3	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3	471TSC2	TSC complex subunit 2
415SMURF1	SMAD specific E3 ubiquitin protein ligase 1	472TUBA1A	tubulin alpha 1a
416SNRPD1	small nuclear ribonucleoprotein D1 polypeptide	473TUBA1C	tubulin alpha 1c
417SOS1	SOS Ras/Rac guanine nucleotide exchange factor 1	474TUBB	tubulin beta class I
418SOS2	SOS Ras/Rho guanine nucleotide exchange factor 2	475TUBB2A	tubulin beta 2A class IIa
419SP1	Sp1 transcription factor	476TUBB4B	tubulin beta 4B class IVb
420SP2	Sp2 transcription factor	477U2AF2	U2 small nuclear RNA auxiliary factor 2
		478UBA3	ubiquitin like modifier activating enzyme 3
		479UBAP2L	ubiquitin associated protein 2 like
		480UBC	ubiquitin C

Table S5. Genes encoding ESR1-interacting proteins located in differential H3K4me3 peaks

481	UBE2I	ubiquitin conjugating enzyme E2 I
482	UBE3A	ubiquitin protein ligase E3A
483	UBTF	upstream binding transcription factor
484	UGDH	UDP-glucose 6-dehydrogenase
485	UIMC1	ubiquitin interaction motif containing 1
486	UNC45A	unc-45 myosin chaperone A
487	UPF1	UPF1 RNA helicase and ATPase
488	USF1	upstream transcription factor 1
489	UTP14A	UTP14A small subunit processome component
490	UTP3	UTP3 small subunit processome component
491	VAPA	VAMP associated protein A
492	VAPB	VAMP associated protein B and C
493	VCL	vinculin
494	VCP	valosin containing protein
495	VDAC1	voltage dependent anion channel 1
496	VDAC3	voltage dependent anion channel 3
497	WDR1	WD repeat domain 1
498	WDR18	WD repeat domain 18
499	WDR5	WD repeat domain 5
500	WIPI1	WD repeat domain, phosphoinositide interacting 1
501	XBP1	X-box binding protein 1
502	XPO1	exportin 1
503	XPO5	exportin 5
504	XRCC6	X-ray repair cross complementing 6
505	YBX1	Y-box binding protein 1
506	YTHDF2	YTH N6-methyladenosine RNA binding protein 2
507	YWHAB	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein beta
508	YWHAE	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein epsilon
509	YWHAQ	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein theta
510	YWHAZ	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein zeta
511	ZBTB17	zinc finger and BTB domain containing 17
512	ZC3HAV1	zinc finger CCCH-type containing, antiviral 1
513	ZNF398	zinc finger protein 398
514	ZNFX1	zinc finger NFX1-type containing 1
515	ZNHIT3	zinc finger HIT-type containing 3

Table S6. Genes encoding DNA repair proteins located in differential H3K4me3 peaks

gene	Description
1 ABL1	ABL proto-oncogene 1, non-receptor tyrosine kinase
2 ATM	ATM serine/threonine kinase
3 ATR	ATR serine/threonine kinase
4 ATRIP	ATR interacting protein
5 BACH1	BTB domain and CNC homolog 1
6 BARD1	BRCA1 associated RING domain 1
7 BLM	BLM RecQ like helicase
8 BRCC3	BRCA1/BRCA2-containing complex subunit 3
9 CDK9	cyclin dependent kinase 9
10 CHEK2	checkpoint kinase 2
11 FANCA	FA complementation group A
12 MDC1	mediator of DNA damage checkpoint 1
13 MLH1	mutL homolog 1
14 MORF4L1	mortality factor 4 like 1
15 MSH2	mutS homolog 2
16 MSH3	mutS homolog 3
17 MSH6	mutS homolog 6
18 NBN	nibrin
19 PIAS4	protein inhibitor of activated STAT 4
20 POLR2I	RNA polymerase II subunit I
21 PRKDC	protein kinase, DNA-activated, catalytic subunit
22 RAD23B	RAD23 homolog B, nucleotide excision repair protein
23 RAD51	RAD51 recombinase
24 RBX1	ring-box 1
25 RFC2	replication factor C subunit 2
26 RPA1	replication protein A1
27 SIRT1	sirtuin 1
28 SMC1A	structural maintenance of chromosomes 1A
29 SUMO1	small ubiquitin like modifier 1
30 TP53BP1	tumor protein p53 binding protein 1
31 TRRAP	transformation/transcription domain associated protein
32 UBE2D3	ubiquitin conjugating enzyme E2 D3
33 UBE2N	ubiquitin conjugating enzyme E2 N
34 UBE2W	ubiquitin conjugating enzyme E2 W
35 UIMC1	ubiquitin interaction motif containing 1
36 VCP	valosin containing protein
37 WDR48	WD repeat domain 48
38 XRCC6	X-ray repair cross complementing 6
39 YY1	YY1 transcription factor

Table S7. Primers used for repeat, Chip-qPCR and Medip-qPCR analysis

CNV			
LINE L1 ORF2-1	TGCGGAGAAATAGGAACACTTTT	TGAGGAATCGCCACTGACT	[1]
LINE L1 ORF2-2	CAAACCCGCATATCTCACTCA	CTTCTGTGCCATGTGATCTCA	[1]
SAT2	CATCGAATGGAAATGAAAGGAGTC	ACCATTGGATGATTGCAGTCAA	[2]
SATA	CTGCACTACCTGAAGAGGAC	GATGGTTCAACTCTTACA	[2]
ALU	CCAGAAAAATTACCAATTAGTTC	GGGCCTATTGACTATGCTTAC	[3]
Telomere length	CGGTTTGGTTGGGTTTGGGTTTGGGTTTGGGTTTGGGTT	GGCTTCCCTTACCCTTACCCTTACCCTTACCCTTACCCT	
RPLP0	CAGCAAGTGGGAAGGTGTAATCC	CCCATTCTATCATCAACGGGTACAA	
DNA methylation			
ARID2	GGCCGAAATACACGCTGTCA	CGATGGTGAAGGGTCTGGG	*
ATM	CTGCGTGGCTAACGGAGAAA	TACCACTGCACCTCGGAAGGT	*
EGFR	GCCCAGACCGGACGACA	ATACTGGACGAGTCAGGGG	*
ESR2	CAGTGTGGACGCTACGAG	GATTTTGTACCCGCACGTC	*
ESRRA	GCAACTTCCAAAGGTGTGC	AGCCTGCAGGTCCACTTTA	*
H19	CTCCTTGTCTGCCAATGTCC	GGAAAGACAGCAGTGTCTG	*
H2AFX	ACGGTGGCGCTGTCTTC	CCATCCGCAACGACGAGG	*
IGF2	TCGTCTGATTGTCCAGGGAGGA	CTGACCTCATTCCCAGTACCTTT	*
KAT5	GCGGAACCAAGGACAACGAA	GGGATTTCACTGACTCCCGC	*
KCNQ1	AACCACGATGACTGACGCAC	GCGATTCTGCCGGGGTG	*
LINE1	TCTGAGCCAGGTGTGGGATA	TCACTAGGAGTGCCAGACA	[4]
OGG1	CCTACACCTCAGGAAAGCCG	GTGCTGTTTAAACACCTTCCCTG	*
PGR	TTATCTTTAGAGCGGGCGGC	GGAGTTCACCTGTGCTTC	*
RPLP0	CAGCAAGTGGGAAGGTGTAATCC	CCCATTCTATCATCAACGGGTACAA	*
SAT2	CATCGAATGGAAATGAAAGGAGTC	ACCATTGGATGATTGCAGTCAA	*
SINEB1	TGGTGGTGCATGCCTTTAAT	CCTGGTGTCTGGAACTCACT	[3]
SMG7	GTGGACTTCACCACCGGGGA	AACCGATGTGTCGGACAGG	*
SUV39H1	AAAGTGAAGCAGTGGAGGC	CCTATCCTTCCGCGCC	*
TERF2IP	GACACCGGCTCGGAAGCAAA	ATGGCTACGTCTCCGCATC	*
TERT	CAGGGCCGCACGAA	CACCCCGCGATGCC	*
UPF1	TACGCCAGCTGGGTTTGTC	GACCAGGGCAGGTCAACCCTA	*
UPF2	CTGAGGAGAACGACGCCGGA	GCTCCAACGATCGGGAGGAA	*
VEGFA	CAGCTACCACCTCTCCCC	CAGCCAGAAGTTGGACGAA	*
XRCC5	GCCTGAGGACCGCAACAT	TTCCTGCTCCGAACCCCC	*
ZBTB48	GCCGCTCGGACCTGTG	ATGAGAGCGAACGGACTGGC	*
ChIP			
STAT2	TCAGGGCCCGTACCTGATTA	GGGGCGCGAGTTCTAGT	[4]
5'UTR LINE	GCCAAGATGGCCGAATAGG	AAATCACCCGTCTTCTGCGT	[6]
BRCA1	TTCCCTCGGACCTACAAAC	CGTGGGAGAGTGGATTTCCG	
ESR1	ACTCAACAGCGTGTCTCCGA	GGGCTGTTCTCCAGGTAGT	
KMT2E	GGGGTCGAGCACATAACGG	ACACAAGTACCCCAACCCCG	[4]
RARA	CGGGTAAAGTTTCAGCTCCG	GCGTCTGCCCTAACCCG	

* used for DNA methylation and ChIP-qPCR analysis

- Coufal NG, Garcia-Perez JL, Peng GE, Yeo GW, Mu Y, Lovci MT, et al. L1 retrotransposition in human neural progenitor cells. *Nature*. 2009;460:1127–31.
- Alexiadis V, Ballestas ME, Sanchez C, Winokur S, Vedanarayanan V, Warren M, et al. RNAPol-ChIP analysis of transcription from FSHD-linked tandem repeats and satellite DNA. *Biochim Biophys Acta*. 2007;1769:29–40.
- Varshney D, Vavrova-Anderson J, Oler AJ, Cowling VH, Cairns BR, White RJ. SINE transcription by RNA polymerase III is suppressed by histone methylation but not by DNA methylation. *Nat Commun*. 2015;6:6569.
- Legoff L, D'Cruz SC, Bouchehkhouchka K, Monfort C, Jaulin C, Multigner L, et al. In utero exposure to chlordecone affects histone modifications and activates LINE-1 in cord blood. *Life Sci Alliance*. 2021;4:e202000944.
- Dessain SK, Yu H, Reddel RR, Beijersbergen RL, Weinberg RA. Methylation of the human telomerase gene CpG island. *Cancer Res*. 2000;60:537–41.
- De Cecco M, Ito T, Petrashen AP, Elias AE, Skvir NJ, Criscione SW, et al. L1 drives IFN in senescent cells and promotes age-associated inflammation. *Nature*. 2019;566:73–8.

Table S8. ChIP-seq reads

Group	Sample name	BPA (microg/gram Creat)	number of reads
low	FMSV217	2,55	4,64E+07
low	FMSV218	1,12	6,22E+07
low	FMSV219	2.13	4,94E+07
low	FMSV220	2,43	4,46E+07
low	FMSV221	0,66	4,24E+07
low	FMSV222	1,10	6,40E+07
low	FMSV223	0,73	4,97E+07
low	FMSV224	2,31	4,62E+07
low	FMSV225	2,35	5,27E+07
low	FMSV226	1,28	6,70E+07
high	FMSV167	19,57	4,37E+07
high	FMSV170	17,11	5,20E+07
high	FMSV173	10,55	6,20E+07
high	FMSV175	39,34	4,89E+07
high	FMSV177	42,64	5,47E+07
high	FMSV233	10,07	5,49E+07
high	FMSV234	12.24	6,41E+07
input	FMSV 178	input	6,38E+07

Table S9. Primers used for RT-qPCR in this work

	forward	reverse
<i>ARID2</i>	GGAGCAGATCCAAGCACTGT	TGGCATAGGAGTGTCTCGC
<i>ATM</i>	CCGAGTGCAGTGACAGTGAT	CATGTTCTAGTTGACGGCAGCA
<i>BRCA1</i>	TCAGGAGGCCTTCAACCTC	TTGATCAACTCCAGACAGATGGG
<i>CDC45</i>	ATAAGAGCCTGAAGGAGGGAGCC	TCTTGGCTGTTGTCTCCCTGAGC
<i>DNMT1</i>	ACAGAAAAGGAATGTGTGAAGGAGA	CCAGGTAGCCCTCCTCGGAT
<i>EGFR</i>	ACACCTTCTCCCACTGCCT	CCCCCTCTGGAGATGCTGGA
<i>ESR1</i>	CCCAGGGAAGCTACTGTTTGC	TGATGTAGCCAGCAGCATGTC
<i>ESR2</i>	CAAACCAAAGCATCGGTCACG	AGGCCATGATCCTGCTCAATTC
<i>ESRRA</i>	AGAGGACCATCCAGGGGAGC	CTCCTGAGCATGCCACCC
<i>EZH2</i>	GACACCCGGTGGGACTCAGA	AGTCTGGCCCATGATTATCTTCGT
<i>FOS</i>	CACTCCAAGCGGAGACAGAC	GTGAGCTGCCAGGATGAA
<i>HDAC1</i>	CCTGGGTCGGACGCTGAG	AATTTCCAACATCCCCGTCGT
<i>HDAC2</i>	GTCTGCTACTACTACGACGGTGATA	TTAACAGCAAGTTATGGGTCATGCG
<i>HDAC5</i>	ACGAGTCGGCAGATGGGATG	ACCGGCTTCACCTCCACTGT
<i>HDAC6</i>	AGTCGCGGGGAAAAGGTCG	GGTGGAATCTGGCCGGTTG
<i>IGF2</i>	CTGGCAGAGGAGTGTCGGC	GGGATTCCCATTTGGTGTCTGGAAG
<i>KAT5</i>	GAGGTGGGTAGAGCCCGAGG	GATCTCGGCCAGGGGCCA
<i>KDM1A</i>	AGCGAATCCCCAAGTGATGT	AGAGAGTTGAGAGAGGTGTGGCA
<i>KMT2E</i>	GGTCGAGCACTGTGGCTG	CTCATGACGTTCCGCTCTGG
<i>NAPBL</i>	GGCTGGCTTGGTGGGGTG	CGGCCTGTCTCCAGACAAT
<i>NUDT1</i>	CCGACGACAGCTACTGGTTT	CGCGGAGTGTGTAGTCCAG
<i>OGG1</i>	TTTCTGCGCTTTGCTGGTGG	CTGTGGGGACCTTATGCTGG
<i>PGR</i>	GGCATGGTCCTTGGAGGTCG	ATTTGGAACGCCCACTGGCT
<i>POT1</i>	GGCGGAGAACAAGCGACTAT	ATCTGACAACCTGTGCCGT
<i>RAD18</i>	ATCCTCTTCTCTGTGTCAGTTCCA	CTATCTTCTGTATGCATGGGACAGG
<i>RAD21</i>	GCTTCATGGTCTTCAGCGTGC	AGAACTTTGCGGCAGCTTGT
<i>RPL37A</i>	GAGACGAGCTGTGGGGATCT	CTGATGGCGGACTTACCGT
<i>SETDB1</i>	TGGAAGACGGGAGAGGACAA	GTTCTCAACCACTGCCTGT
<i>SMG1</i>	TGACTGGCAACCCAGAACTGA	GCCGAGACACCACAGCTGAA
<i>SMG7</i>	GAGCCTGAGAGACCCACGGA	GGACCCAGCTTAGAATCGGAGG
<i>STAT2</i>	CGTGACGGTTGCACAGAGT	GGCACCTTTCTACTGCGCTT
<i>TEN1</i>	GACGCCTAGAACAGGAGCCC	ATGTTCTCAGCGTGCTCCCA
<i>TERF2IP</i>	GCGGATAGCGGGGAACCCAC	CCTCAAACCTCCCGGTGGC
<i>TERT</i>	TGGGGTCTTCCAAACTTGCT	GACGGTGTGACCAACATCT
<i>TP53BP1</i>	TCGTGCCTCCATGGGAGTTCT	AACTCTCTGCCCTACAGGTT
<i>UPF1</i>	AGGTCCTGATAATTATGGCGATG	TGCGCTCTGCATCCTGTCAA
<i>UPF2</i>	CAACAGGCTCGAGATTGCTCT	TTGGCCTCTCCTTGCTGCTC
<i>VEGFA</i>	GGTGCCCGCTGCTGTCTAAT	CCTTGCAACGCGAGTCTGTG
<i>XRCC5</i>	ACCATGTTGTACAGCGACAGG	CCCCACCAGAAAGGGGATTG
<i>XRCC6</i>	CGCTTCGCTCGTGAGCAGT	AGTCTCCACTTGCTTCAAGTTCT
<i>XRCC6</i>	CGCTTCGCTCGTGAGCAGT	AGTCTCCACTTGCTTCAAGTTCT
<i>ZBTB48</i>	CTGTGCGGGGGAGCTTT	CCTTCTCCCGCTGCTGTTGA