

SUPPLEMENTAL:

Figure S1. Structure of the updated database.

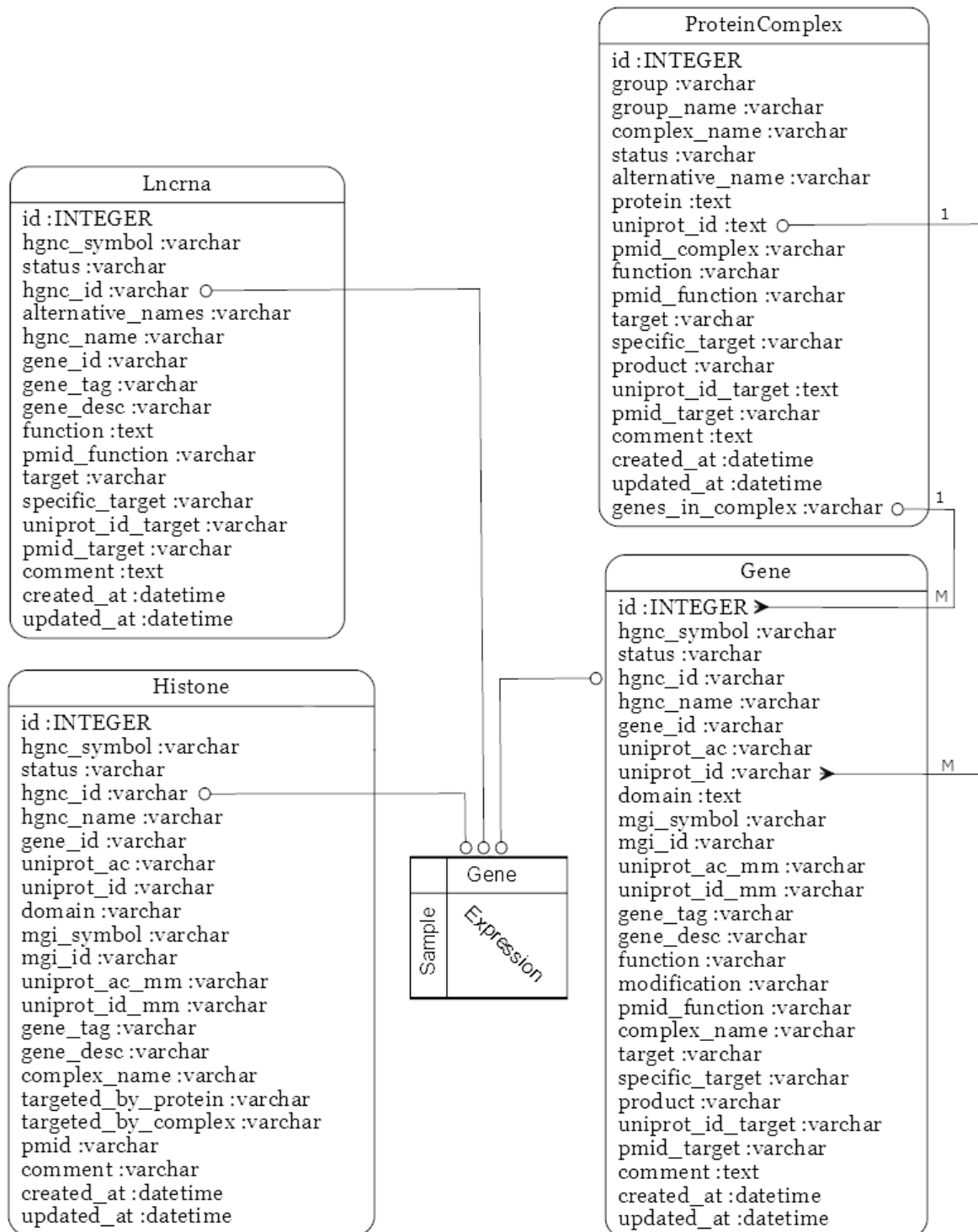


Table S1. lncRNAs added to the database according to their functions.

Function	lncRNAs
Chromatin remodeler recruitment	CDKN2B-AS1, DGCR5, LINC00163, HAND2-AS1, KDM2B-DT, DLEU1, NEXN-AS1, BAALC-AS1, WSPAR, MANTIS, lincRNA-Cox2, NMR, BlackMamba, lincRNA-Cox2, KCNQ1OT1
Histone modifier recruitment	TARID, UMLILO, COR1, RASSF1-AS1, CCAT1, MAGI2-AS3, LINC00968, MEG3, LINC00511, DANCR, PVT1, XIST, HOTAIR, CDKN2B-AS1, AIRN, HOTTIP, NEAT1, MALAT1, FIRRE, IL-7-AS, Khps1, ecCEBPA, SWINGN, PARTICL, DN3OS, TUG1, BLACAT1, LINC00702, MEG3, KCNQ1OT1
DNA modifier recruitment	KCNQ1OT1, DALIR, ecCEBPA, MEG3, TARID, TP53, COR1
TF recruitment	DN3OS, MEG3, MTA2TR, Braveheart
Splicing factor recruitment	FAS-AS1, MEG3, CircSMARCA5, Lnc-Spry1, AC091729, sno-lncRNAs (1-5) from the PWS critical region of chr15
Protein sequestration	LNCPRESS1, LINC01133, FOXD3-AS1, PANDAR, NORAD, Linc-YY1, SPAs from the imprinted region 15q11-q13
Modulation of protein functions	NKILA, SAMMSON, DINOL, DDX11-AS1, MIAT, LASTR, HELLPAR, DSCAM-AS1, ZNF674-AS1, JPX, PTCSC3, LNCBRM, MANTIS, LCTS5, lncAKHE, CCAT1, uc.291
miRNA sponging	GNAS-AS1, DN3OS, PPP1R10, RMRP, TUG1, SNHG14, BLACAT1, LINC00702, MAGI2-AS3, LINC00968, MEG3, LINC00511, NR2F1-AS1, SBF2-AS1, NORAD, MAPKAPK5-AS1, FGD5-AS1, A1BG-AS1, PVT1, LINC00963, CD27-AS1, EMX2OS, ZNF674-AS1, JPX, CASC15,

	SPAG5-AS1, LINC00899, LINC00668, MATN1-AS1, LINC01410, SNHG15, ARAP1-AS1
RNA binding	UCHL1-DT, PCGEM1, FAS-AS1, ZEB2-AS1, uc.57, NCYM NAT, 51A, 17A
Chromatin looping	NRIP1e eRNA, CCAT1, HPSE eRNA
Promoter switching	Antisense transcript at each Pcdha first exon
Transcription machinery interference	AIRN, transcript from DHFR minor promoter
Protein binding	TINCR, EMX2OS, DRAIC, MVIH, TP53COR1
Undefined	CHASERR, SCHLAP1, LUCAT1, TMCC1-DT, BOLA3-DT, RAB30-DT, LINC00862, LINC01503, SERTAD4-AS1, AC005592.2, RP11-395B7.4, RP11-221N13.3, RP6-99M1.2, RP11-660L16.2, RP11-539L10.3, RP6-109B7.3, AC016747.3, RP11-137L10.6, RP11-38L15

Table S2. lncRNAs added to the database according to the functions of their targets.

lncRNAs	Target proteins	Function of target proteins
BlackMamba, DDX11-AS1	HELLS, DDX11	DNA helicases
DALIR, MEG3, TP53COR1, KCNQ1OT1, ecCEBPA	DNMT1	DNA methylation
TARID	GADD45A	DNA demethylation
AIRN, BLACAT1, CDKN2B-AS1, DANCR, HOTAIR, HOTTIP, Linc-YY1, LINC00511, LINC00702, LINC00968, MALAT1, MEG3, NEAT1, PVT1, RASSF1-AS1, TUG1, UMLILO, KCNQ1OT1	PRC (EZH2, EHMT2, YY1, SUZ12), KMT2A	Histone methylation
HOTTIP, UMLILO	WDR5	Histone methylation reader
DNM3OS, MAGI2-AS3, LINC00511	KDM1A, KDM6B	Histone demethylation
IL-7-AS, Khps1, lncAKHE, NEAT1	EP300, CREBBP, EP400, TRRAP, YETS4	Histone acetylation
LNCPRESS1	SIRT6	Histone deacetylation

DRAIC, HAND2-AS1, LCTS5	UCHL5, INO80	Ino80 compounds
DLEU1, KDM2B-DT, NEXN-AS1, NMR	SMARCA1, SRCAP, SATB1, BAZ1A, BPTF	ISWI compounds
BAALC-AS1, DGCR5, DLEU1, LINC00163, lincRNA-Cox2, LNCBRM, MANTIS, MVIH, SWINGN, uc.291, WSPAR	SMARCA4, ARID1A, SMARCA1, MyBBP1A, SMARCA2, SMARCA4, ACTL6A, SMARCA4, SMARCC2, SNF5	SWI/SNF compounds
Braveheart, CCAT1, DINOL, FIRRE, LINC00968, MEG3, MTA2TR, PANDAR, MIAT	CNBP, CTCF, TP53, HEY1, KLF4, ATF3, NF-YA, SF1	TF
FIRRE, HPSE eRNA, NRIP1e eRNA, MEG3	hnRNPU, STAG1, STAG2, PTBP3	Looping factors
AC091729, CIrcSMARCA5, EMX2OS, FAS-AS1, HELLPAR, LASTR, LINC01133, Lnc-Spry1, MEG3, MIAT, sno-lncRNAs (1-5) from the PWS critical region of chr15, SPAs from the imprinted region 15q11-q13, TINCR	SRSF2, SRSF1, FUS, SPF45, YBX1, PCBP1, PCBP2, RPS6, RPL7, SART3, SRSF6, U2AF65, PTBP3, CELF3, QKI, FOX2, hnRNPM, RBFOX2, TDP43, STAU1	Splicing factors

Table S3. Proteins added to the database according to their functions.

Function	Modification	Proteins
Chromatin remodeling	#	MIS18A, MIS18BP1, OIP5
TF	#	HSFX3, KLF18
Histone modification eraser	Histone deubiquitination	MPND
Histone modification writer	Histone methylation	NTMT1, METTL11B
Protein modification	Protein methylation	METTL21A, EEF1AKMT3, EEF1AKMT4, EEF1AKNMT
DNA modification	DNA demethylation	ALKBH4
RNA modification	RNA demethylation	ALKBH1, ALKBH5, FTO
	RNA methylation	CBLL1, METTL14, METTL16, METTL3, METTL4, NSUN2, NSUN6, RBM15, RBM15B, VIRMA, WTAP, ZC3H13
	RNA acetylation	NAT10
	RNA degradation	THRAP3, RBM7
	RNA pseudouridination	RPUSD3, TRUB2
	Alternative splicing	ACINU, CELF1, CELF2, CELF3, CELF4, CELF5, CELF6, DDX17, DDX5, DHX9, EIF4A3, HNRNPU, HNRPL, HNRPM, KHDRBS1, MAGOH, MBNL1, MBNL3, NSRP1, NUP98, PQBP1, PTBP1, PUF60, RBFOX1, RBM11, RBM17, RBM24, RBM25, RBM4, RBM5, RBM8A, RBMY1A1, RFOX1, RNPS1, RSRC1, SFSWAP, SLU7, SRRM4, SRSF10, SRSF12, SRSF6, TRA2B, U2AF2, YTHDC1, ZBTB7A

Table S4. Protein complexes added to the database.

Complex name	Protein	Function	Target (modification)	Comment
MSL histone acetyltransferase complex	MSL1, MSL2, MSL3, KAT8 (hMOF)	histone acetylation complex	Histone H4 (H4K16Ac)	Responsible for genome-wide H4K16 acetylation. Affects chromatin organization and regulates transcription. Involved in regulation of cell cycle progression, DNA damage repair and apoptosis.
WMM (WTAP-METTTL3-METTTL14) methyltransferase complex	METTTL3, METTTL14, WTAP, ZC3H13, CBL1, VIRMA	RNA methylation	Adenosines of RNA and DNA (m6A)	Regulates processes dependent on RNA stability as m6A methylation leads to RNA degradation. Controls cell differentiation of embryonic and hematopoietic stem cells by destabilization of transcripts. Involved in response to DNA-damage. Mediates random X-inactivation by methylation of Xist-RNA. Marks primary microRNAs for processing. Promotes translation.
Mis18	MIS18A, OIP5, MIS18BP1	Chromatin remodeling	Histone variant CENPA	Regulates CENPA recruitment to centromeres and thereby normal chromosome segregation during mitosis. Interacts with DNMT3A/3B and provides its centromeric localization regulating epigenetic states of centromeric chromatin. Provides access of CENPA-specific chaperone HJURP to centromeres.
CUL4-DDB-ROC1 (CUL4-DDB-RBX1)	DDB2, DDB1, RBX1, CUL4B, CUL4A	Histone ubiquitination complex	Histones	Recognises UV-induced cyclobutane pyrimidine dimers in chromatin and ubiquitinates histones and other chromatin-associated proteins located around the DNA lesion. Promotes the removal of ubiquitinated histones from the nucleosome and subsequent DNA repair.