

Figure S1. Reverse transcription-quantitative PCR-based expression of long non-coding RNAs detected in >50% of samples.

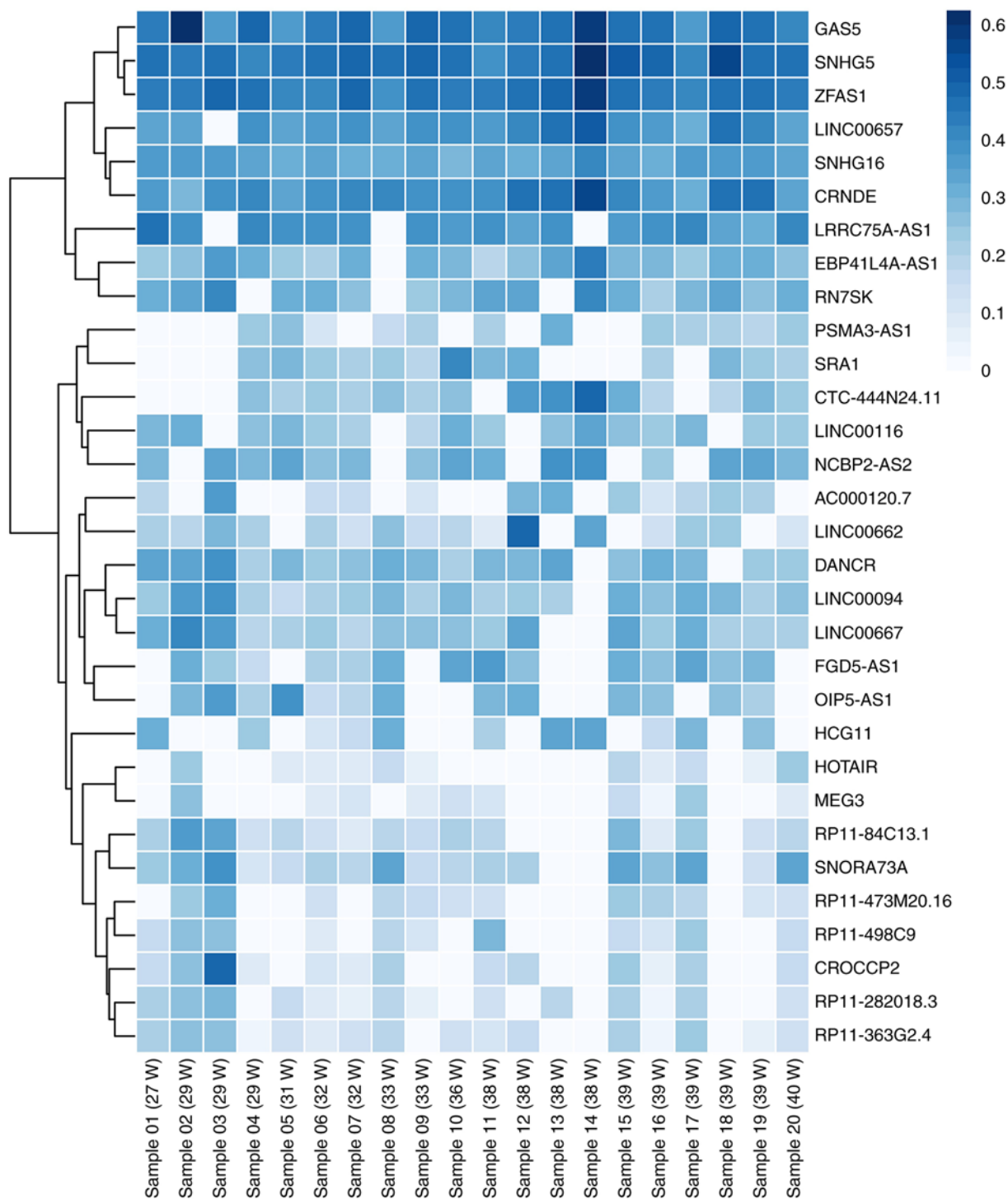


Table SI. Biological function of lncRNAs detected in more than 85% breastmilk samples.

lncRNA ID	Function	(Refs.)	
EBP41L4A-AS1	Metabolic programming (glycolysis and glutaminolysis)	(1)	
	P-53 regulated	(1)	
GAS5	Riborepressor regulating glucocorticoid receptor (GR)	(2)	
	Normal growth arrest of T cells and non-transformed lymphocytes	(3)	
	Macrophage polarization	(4)	
LINC00094	BBB permeability	(5)	
	Lies in promoter of BRD3 gene	(6)	
	Related with a high risk of spontaneous preterm delivery	(7)	
	Oncogenic (cancer hallmarks)	(8)	
	Cell growth	(9)	
LINC00657	Maintaining genome stability (guardian of the human genome)	(10)	
	Regulates DNA repair and replication, mitosis and mitochondrial homeostasis	(11-14)	
	Regulates nuclear translocation and signal transduction	(15)	
LINC00667	Apoptosis	(16)	
	Renal fibrosis	(16)	
	Upregulation of FOXQ1	(1)	
SNHG16	Wnt-regulated	(17)	
	Associated with polysomes	(17)	
	Lipid metabolism	(17)	
SNHG5	Activates wnt/ β -catenin and GSK3 β pathway	(18)	
	ceRNA	(18)	
ZFAS1	Differentiation	(19)	
	Inhibitor of Ca ²⁺ ATPase and Ca ²⁺ overload	(19)	
	Mitochondria mediated apoptosis	(19)	
	Regulation NOTCH3 (neural development)	(20)	
	Regulation of Wnt/ β -catenin pathway	(21)	
CRNDE	IL-6R activation	(22)	
	NOTCH1 upregulation	(23)	
	Cyclin D1 regulation	(24)	
	Glucose and lipid metabolism	(25)	
	Regulated by insulin and insulin-like growth factors	(25)	
	Multiple splice variants	(26)	
	Normal developmental properties	(26)	
	Cellular multipotency	(26)	
	DANCR	Negative regulator of cell differentiation	(27)
		Competing endogenous RNA	(27)
IL-6 and TNF- α expression regulation in blood mononuclear		(27)	
mTOR regulation		(28)	
Stem cell differentiation and cell proliferation		(29)	
mRNA stabilization		(29)	
IL-11-mediated activation of Jak/STAT3 signaling		(29)	
Wnt/ β -catenin activation		(30)	
LRRC75A-AS1		Regulated by oxidative stress	(31)
		Accelerates cellular senescence and triggers pro-inflammatory cytokine release from senescent cells	(31)
	Upregulated in in placentas of women with preterm labor	(31)	
RN7SK	Neuronal differentiation	(32)	
	Cellular senescence	(33)	
	Macrophage polarization and innate immune responses	(4)	
SNORA73A	Steroid synthesis	(34)	
	The most enriched small nucleolar RNA in the cytoplasm of granulosa cells	(34)	

lncRNA, long non-coding RNA.

Table SII. Upregulated lncRNAs detected in >50% of samples.

LncRNA ID	Mean Δ cq preterm (\pm SD)	Mean Δ cq full-term (\pm SD)	Sample no.	Log ₂ fold change	P-value
LRRC37BP1	5.80 (\pm 2.64)	6.87 (\pm 0.57)	5/20	1.076	0.333
LL22NC03-N27C7.1	6.23 (\pm 0.39)	7.00 (\pm 0.83)	7/20	0.777	0.081
CROCCP2	7.47 (\pm 3.31)	8.22 (\pm 1.32)	13/20	0.755	0.297
LRRC75A-AS1	2.90 (\pm 0.65)	3.62 (\pm 0.95)	17/20	0.713	0.045
RP11-363G2.4	8.54 (\pm 1.46)	9.00 (\pm 1.57)	16/20	0.466	0.277
SRA1	5.81 (\pm 1.74)	6.19 (\pm 0.82)	13/20	0.376	0.312
DANCR	5.51 (\pm 1.17)	5.77 (\pm 0.85)	18/20	0.256	0.299
RP11-84C13.1	7.56 (\pm 1.90)	7.79 (\pm 1.40)	16/20	0.228	0.394
LINC00667	5.84 (\pm 1.55)	6.06 (\pm 1.30)	18/20	0.221	0.373
MEG3	9.01 (\pm 1.30)	9.19 (\pm 1.45)	10/20	0.184	0.419
LINC00094	6.17 (\pm 1.42)	6.25 (\pm 0.94)	19/20	0.080	0.443
RP1-239B22.5	8.20 (\pm 1.96)	8.27 (\pm 2.30)	9/20	0.066	0.484
OIP5-AS1	5.93 (\pm 1.80)	5.93 (\pm 0.61)	13/20	0.003	0.498

lncRNA, long non-coding RNA.

Table SIII. Downregulated lncRNAs detected in >50% of samples.

lncRNA ID	Mean Δ cq preterm (\pm SD)	Mean Δ cq full-term (\pm SD)	Sample no.	Log ₂ fold change	P-value
JPX	7.78 (\pm 1.96)	5.53 (\pm 1.90)	8/20	-2.247	0.089
NEAT1	6.88 (\pm 3.18)	5.21 (\pm 0.96)	5/20	-1.665	0.234
CTC-444N24.11	6.61 (\pm 0.57)	5.09 (\pm 2.21)	15/20	-1.521	0.048
HCG18	6.58 (\pm 1.36)	5.35 (\pm 0.71)	9/20	-1.234	0.086
AC000120.7	8.27 (\pm 2.50)	7.06 (\pm 1.21)	13/20	-1.213	0.157
NUTM2A-AS1	7.66 (\pm 1.76)	6.47 (\pm 0.91)	8/20	-1.183	0.128
MZF1-AS1	8.09 (\pm 1.40)	6.92 (\pm 1.59)	7/20	-1.164	0.217
CRNDE	3.35 (\pm 1.00)	2.20 (\pm 1.83)	20/20	-1.144	0.052
LINC00657	3.78 (\pm 0.61)	2.79 (\pm 1.44)	19/20	-0.996	0.034
FGD5-AS1	6.30 (\pm 1.27)	5.32 (\pm 0.96)	14/20	-0.981	0.065
RP11-498C9	8.74 (\pm 1.82)	7.84 (\pm 1.64)	12/20	-0.892	0.199
CTD-3185P2.1	9.39 (\pm 0.93)	8.53 (\pm 2.12)	5/20	-0.860	0.334
HCG11	6.80 (\pm 1.94)	5.99 (\pm 1.34)	11/20	-0.807	0.229
RP11-399K21.11	10.77 (\pm 0.38)	10.01 (\pm 1.27)	5/20	-0.759	0.208
HOTAIR	9.52 (\pm 1.27)	8.77 (\pm 1.55)	11/20	-0.746	0.208
TUG1	7.33 (\pm 1.59)	6.65 (\pm 0.74)	5/20	-0.686	0.282
SNHG5	1.49 (\pm 0.57)	0.86 (\pm 1.79)	20/20	-0.629	0.156
SNORA73A	6.73 (\pm 1.88)	6.12 (\pm 1.77)	17/20	-0.617	0.251
LINC00662	7.51 (\pm 1.07)	6.90 (\pm 3.26)	16/20	-0.610	0.324
ZFAS1	1.78 (\pm 0.76)	1.24 (\pm 1.09)	20/20	-0.541	0.108
PSMA3-AS1	7.45 (\pm 1.42)	6.93 (\pm 0.97)	12/20	-0.526	0.249
NCBP2-AS2	5.16 (\pm 0.61)	4.68 (\pm 1.10)	15/20	-0.477	0.167
SNHG16	4.55 (\pm 0.60)	4.13 (\pm 0.78)	20/20	-0.413	0.102
ABCA11P	7.68 (\pm 0.35)	7.27 (\pm 1.10)	7/20	-0.409	0.295
RP11-819C21.1	8.14 (\pm 1.92)	7.88 (\pm 2.77)	9/20	-0.259	0.437
GAS5	1.64 (\pm 1.92)	1.39 (\pm 1.55)	20/20	-0.251	0.376
EBP41L4A-AS1	5.61 (\pm 0.99)	5.44 (\pm 1.63)	19/20	-0.169	0.393
RP11-282018.3	8.75 (\pm 1.95)	8.67 (\pm 1.22)	15/20	-0.076	0.464
RP11-473M20.16	8.34 (\pm 1.93)	8.27 (\pm 1.21)	13/20	-0.075	0.467
RN7SK	4.89 (\pm 1.24)	4.84 (\pm 1.12)	17/20	-0.047	0.468
LINC00116	6.14 (\pm 0.88)	6.13 (\pm 0.73)	16/20	-0.016	0.485

Table SIV. lncRNAs positively and negatively correlated with *NORAD* levels in breastmilk-derived exosomes.

LncRNA ID	R value	P-value
CTC-444N24.11	0.654	1.77E-03
GAS5	0.524	1.77E-02
CRNDE	0.477	3.36E-02
SNHG5	0.386	9.27E-02
ZFAS1	0.295	2.07E-01
HCG11	0.293	2.09E-01
SNHG16	0.094	6.92E-01
NCBP2-AS2	0.066	7.83E-01
MEG3	-0.065	7.87E-01
HOTAIR	-0.073	7.60E-01
DANCR	-0.572	8.39E-03
LINC00667	-0.583	7.00E-03
RP11-498C9	-0.605	4.73E-03
RP11-282018.3	-0.615	3.93E-03
RP11-473M20.16	-0.616	3.86E-03
LINC00094	-0.617	3.77E-03
RP11-84C13.1	-0.665	1.39E-03
SNORA73A	-0.693	7.04E-04
CROCCP2	-0.790	3.40E-05

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