

The TMSB4 Pseudogene LncRNA Functions as a Competing Endogenous RNA to Promote Cartilage Degradation

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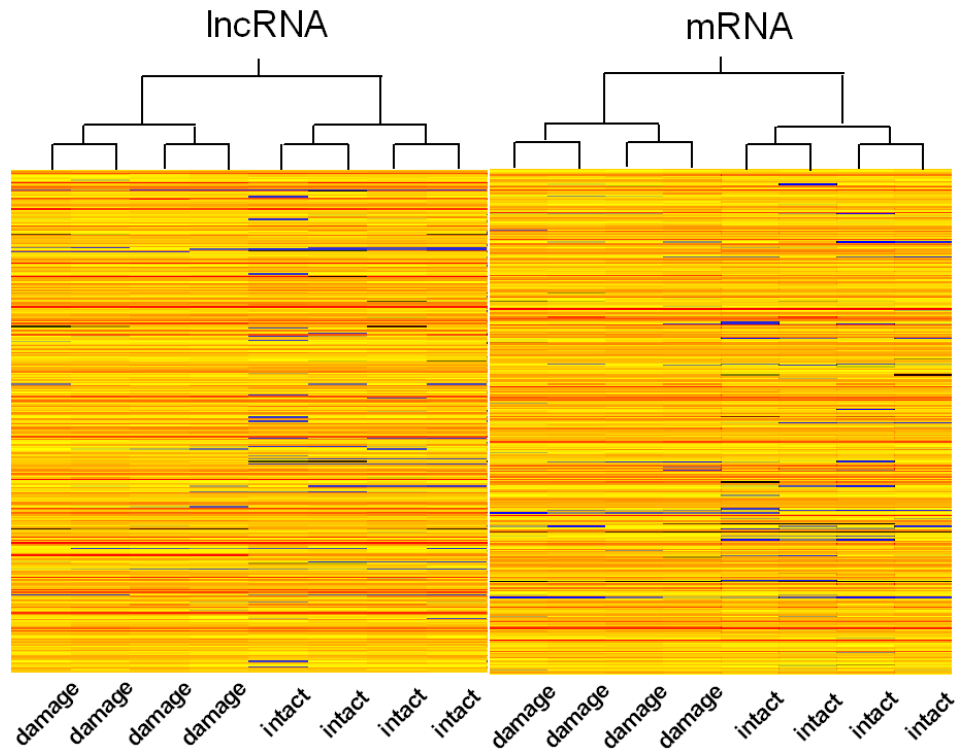
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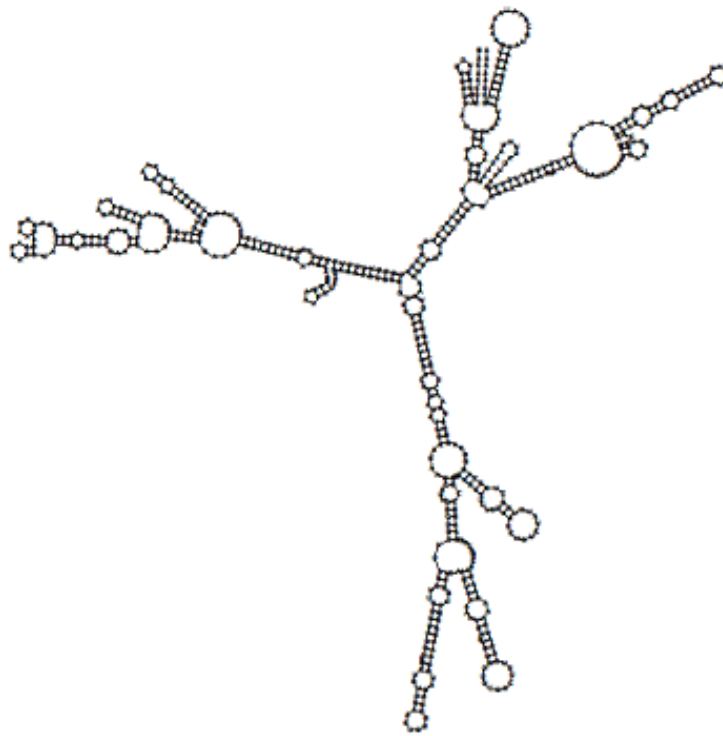
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Supplementary figure 1. The differential expression of lncRNAs in the different regions. A hierarchical clustering analysis of the lncRNAs and mRNAs that were differentially expressed between the intact and the damaged region of the cartilage samples. Each group contains 4 individuals (greater than two-fold; $p < 0.05$). The expression values are represented in different colors, which indicates expression above and below the median expression value across all samples.



Supplementary figure 2. The secondary structure of lncRNA-MSR was predicted using RNAFOLD.

Open-reading frames (ORFs) analysis

TMSB4X pseudogene lncRNA 144, 325, 469 (+)

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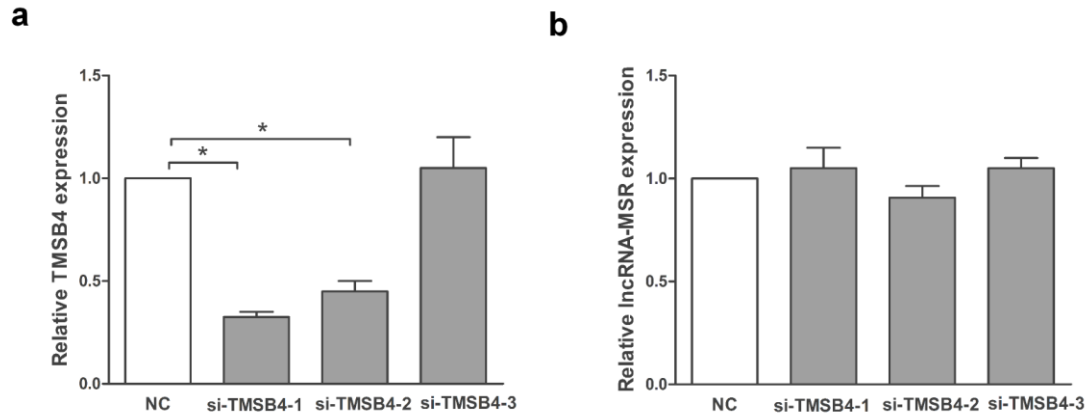
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TGCATGTTGGTGAAGGAAGAAGTGGGGTGGGACAACAGTGAAATCT

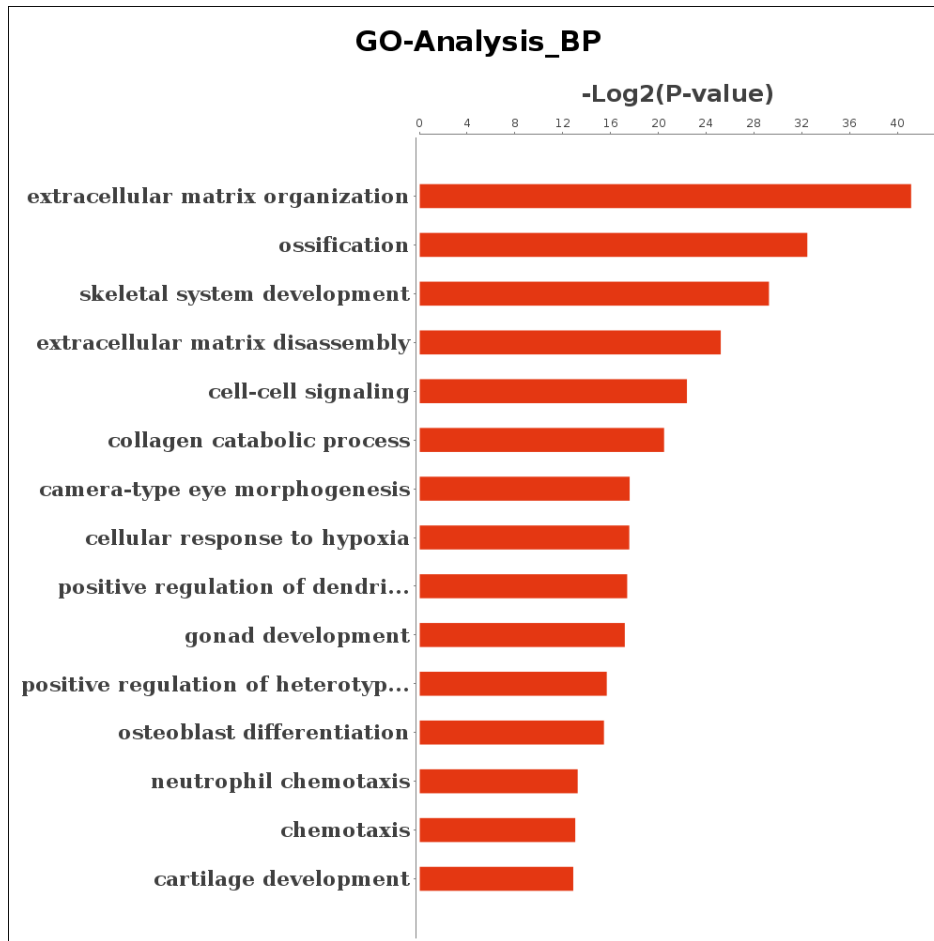
MTVLPLSHQRRTDNEGRDCLSHLSIWLKERTCMLVKEEVGWDNSEI

Coding potential calculator (CPC) analysis

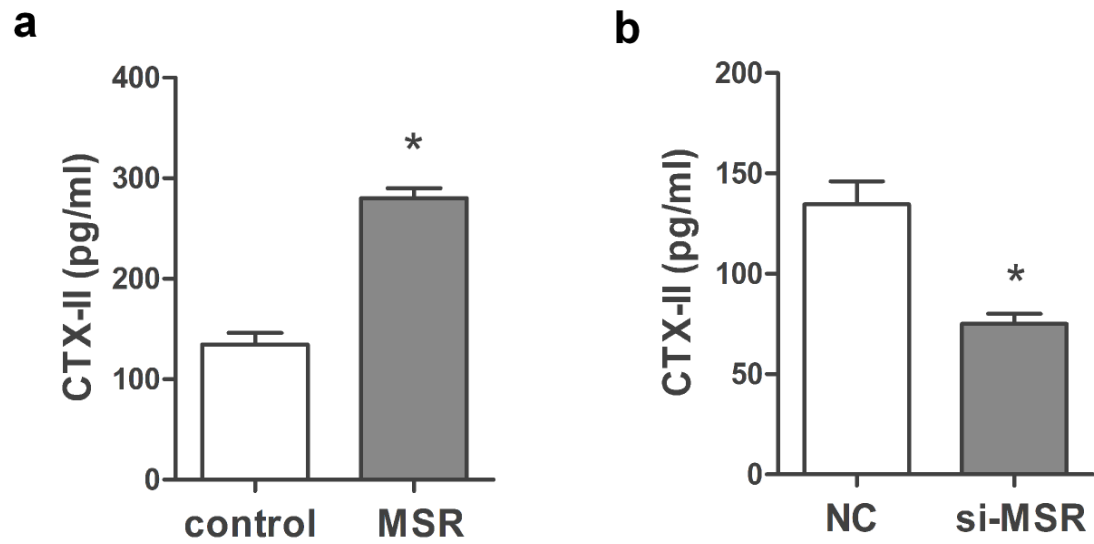
#ID	Length	C/NC	CODING POTENTIAL SCORE
ENST00000415187.1	617	NC	1.01895



Supplementary figure 3. The effect of 3 different small interfering RNAs (siRNAs) against TMSB4 (si-TMSB4) was analyzed using qPCR. The greatest inhibition was achieved using si-TMSB4-1. The results are shown as the mean \pm S.E.M. of at least three independent experiments (* $p < 0.05$, ** $p < 0.01$).



Supplementary figure 4. Gene ontology (GO) analysis of differentially expressed mRNAs.



Supplementary figure 5. Figure 3. The effects of lncRNA-MSR on COL2 degradation. The releases of CTX-II was detected by ELISA in chondrocyte supernates. (* $p < 0.05$, ** $p < 0.01$ MSR vs. control (treated with empty plasmid) and si-MSR vs. the negative control (NC) siR-Ribo™)

Supplementary Table 1 Differentially Expressed LncRNAs in damage versus intact Cartilage

seqname	FCAbsolute	regulation	p-value
AL359062	13.460988	up	4.409E-07
chr10:127700955-27703336	12.114503	up	3.513E-07
ENST00000424567	9.35231	up	5.604E-07
AK023660	9.072498	up	6.631E-05
ENST00000415187	8.803992	up	1.099E-07
AK001058	8.413234	up	1.02E-05
NR_026812	7.6083255	up	5.546E-08
ENST00000335179	7.2754674	up	1.297E-07
AK027294	6.239118	up	6.121E-05
uc003mjv.3	6.1100416	up	1.107E-06
ENST00000425396	6.046882	up	2.155E-05
CR612530	5.2172318	up	1.92E-06
ENST00000504601	5.1720085	up	1.704E-07
uc010bkj.1	4.987715	up	0.0095873
ENST00000402383	4.940405	up	0.0008607
ENST00000330974	4.880104	up	3.967E-08
uc.75-	4.753704	up	0.0001294
ENST00000444114	4.384677	up	0.0001165
BC012900	4.0893803	up	0.0001641
BC007804	4.0862594	up	4.148E-06

seqname	FCAbsolute	regulation	p-value
ENST00000507684	4.0651827	up	2.859E-05
M31164	4.0559654	up	5.449E-05
HIT000325634	3.962266	up	6.528E-06
ENST00000429872	3.9293466	up	1.899E-05
HIT000221810_03	3.9100006	up	0.0005118
ENST00000433189	3.794659	up	0.0004558
NR_024418	3.7814727	up	2.473E-06
ENST00000339991	3.717557	up	0.005656
uc003fdu.2	3.7065198	up	0.0025347
ENST00000420610	3.588953	up	0.0002368
NR_002734	3.5888178	up	1.769E-07
ENST00000405027	3.55626	up	0.002284
ENST00000447905	3.5138977	up	0.0010476
ENST00000441503	3.5125437	up	0.0024442
uc002uku.2	3.4596043	up	0.0001717
AK093691	3.396048	up	0.004957
ENST00000432950	3.3675792	up	0.0006702
AY927440	3.327262	up	1.791E-06
uc002kmd.1	3.2933195	up	0.0012249
AB007969	3.2462077	up	0.0007498
NR_002206	3.2148077	up	0.0033122

seqname	FCAbsolute	regulation	p-value
ENST00000505780	3.1980696	up	0.0008557
ENST00000415070	3.1871753	up	1.893E-06
NR_033397	3.1822324	up	0.0038331
CR602937	3.1793706	up	1.088E-05
nc-HOXD4-32+	3.1539834	up	0.0045857
NR_015421	3.1516075	up	0.0006931
ENST00000413496	3.1389694	up	3.895E-05
uc010fsr.1	3.0658016	up	0.0001031
ENST00000413189	3.0206683	up	0.0119237
ENST00000491506	3.005056	up	0.0007321
ENST00000441087	656.05615	down	8.402E-10
NR_001564	11.873753	down	3.834E-07
AK054860	7.9787536	down	2.317E-05
uc010mak.1	6.6142535	down	1.514E-06
AK091342	5.6048613	down	7.225E-06
nc-HOXA13-96-	5.374643	down	0.0002649
ENST00000502532	5.271958	down	4.591E-06
AK023939	5.136248	down	5.815E-06
BC015134	5.025621	down	1.327E-05
ENST00000418076	4.6331863	down	1.089E-05
AW086055	4.478261	down	2.331E-05

seqname	FCAbsolute	regulation	p-value
AK122798	4.3646903	down	4.607E-05
G43333	4.2439556	down	6.003E-05
uc011lrg.1	4.221657	down	0.0003047
ENST00000430908	4.2169766	down	4.371E-06
NR_023390	4.2151723	down	0.0001027
CR623725	4.134982	down	6.748E-07
ENST00000445028	4.024826	down	0.0011247
CR624187	3.9997923	down	0.0002249
uc002pez.1	3.9726923	down	0.0008609
CR625008	3.9617515	down	0.000142
uc.455-	3.9576786	down	0.0011496
BE244504	3.9407763	down	0.0037609
ENST00000472521	3.8614979	down	0.0024879
AK126122	3.7393925	down	6.355E-05
L38936	3.7110775	down	0.0001744
NR_003569	3.7005436	down	0.0004253
AK001910	3.674887	down	0.0002842
ENST00000504159	3.6549437	down	6.671E-05
AF086011	3.6325026	down	0.0001276
BC037328	3.6017063	down	0.0004227
uc002tzb.1	3.587518	down	4.994E-05

seqname	FCAbsolute	regulation	p-value
ENST00000466433	3.5284057	down	0.0075607
BC014215	3.4681048	down	0.0002933
CR624823	3.4392068	down	7.776E-07
ENST00000419236	3.408787	down	0.0003479
NR_027046	3.408307	down	0.0002762
uc003ijq.1	3.3813746	down	0.0001375
ENST00000434161	3.3780022	down	0.0007826
BC043279	3.2801988	down	0.0026941
NR_003191	3.2629626	down	9.356E-05
AK025239	3.2476842	down	0.0061064
AK096041	3.2438555	down	0.00013
ENST00000445125	3.2079	down	0.0038801
G43148	3.1514513	down	0.0008997
BC004287	3.146547	down	3.361E-05
BC071787	3.144896	down	0.0006328
HIT000067356	3.0885594	down	9.27E-05
NR_024368	3.085478	down	0.0001585
NR_003551	3.0842688	down	0.0001916
NR_026989	3.0833495	down	0.0003147
NR_024464	3.0403361	down	0.002204
NR_015392	3.0273528	down	1.259E-05

seqname	FCAbsolute	regulation	p-value
uc003hto.2	3.0184765	down	0.001565

Supplementary Table 2

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Sbjct 583 TAAATATGCAAATAAAAAGTTTAAAAACTTAAAA 617 TMSB4X pseudogene lncRNA
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The text in blue indicated the specific PCR probes, and the text in red indicated the specific siRNAs on the sequence alignment.