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Supplemental information

lncRNA MELTF-AS1 facilitates osteosarcoma metastasis by modulating MMP14 expression

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Supplemental Information

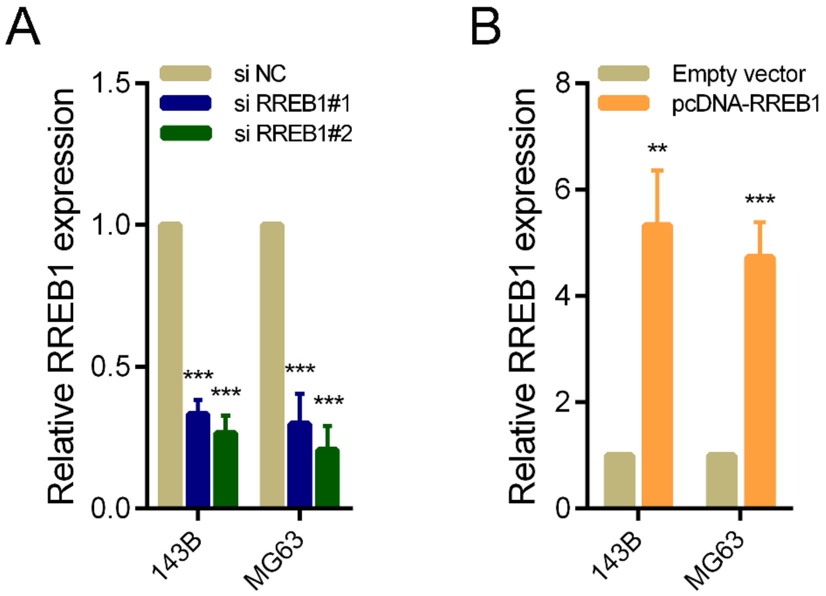

Figure S1. (A) QPCR analysis of RREB1 expression after knockdown of RREB1 in osteosarcoma cells. **(B)** QPCR analysis of RREB1 expression after overexpressing RREB1 in osteosarcoma cells. **P < 0.01 and ***P < 0.001.

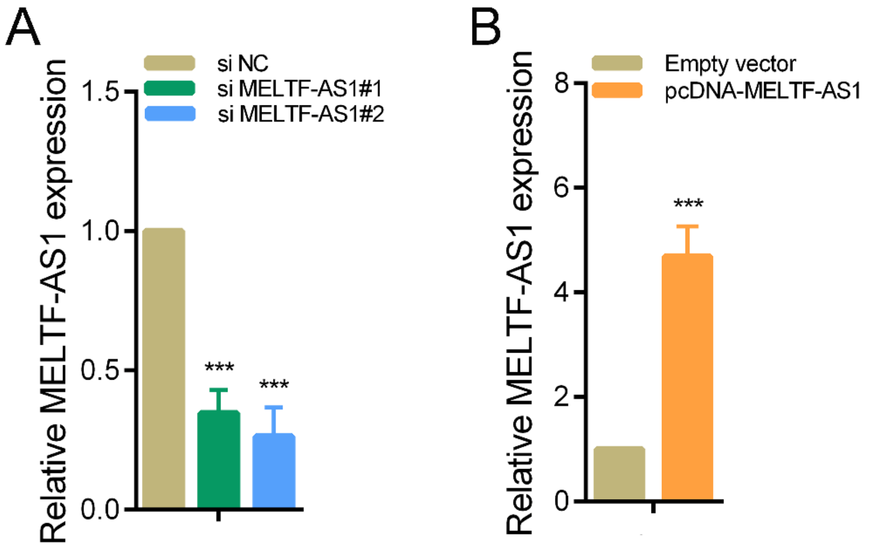

Figure S2. (A) QPCR analysis of MELTF-AS1 expression after knockdown of MELTF-AS1 in 143B cells. **(B)** QPCR analysis of MELTF-AS1 expression after overexpressing MELTF-AS1 in 143B cells. ***P < 0.001.

Table S1: The probability of each transcription factor binding to the MELTF-AS1 promoter region predicted by the JASPAR tool, the higher the score, the greater the probability.

Transcription factor	Score	Start	End	Strand	predicted site sequence
RREB1	18.844	312	331	-1	CCCCACACCACCACCCCTCG
Zfx	16.178	1491	1504	-1	CCGGCCGGGGCCTC
E2F3	16.047	1977	1991	1	CTCCCGCCGCCGCCA
PPARG::RXRA	16.039	548	562	1	GTGGGGCAGGGGGCA
TP63	15.596	856	875	1	CTGCATGTGCTGGCTTGTTT
EGR2	15.411	1721	1735	-1	CCCGCACCCACGCCC
Spi1	15.367	1404	1418	-1	ATGAAGAGGAAGAGA
Zfx	15.141	1867	1880	1	CCGGGCTCGGCCTC
EGR1	15.113	1977	1990	1	CTCCCGCCGCCGCC
SP2	14.648	1522	1536	-1	TGCCCGCCCCTCCGC
EGR1	14.636	413	426	1	GGCCCACCCCCACC
ZNF263	14.560	1394	1414	-1	AGAGGAAGAGAAGAAATGGGA
E2F3	14.381	1973	1987	1	CTCCCTCCCGCCGCC
Myod1	14.187	631	643	-1	TCCAGCTGCCTCC
Nkx2-5 (var.2)	14.170	795	805	-1	AGGCACTCAAA
HSF1	13.960	1437	1451	1	GTTCTGGAAACTTTT
ZNF263	13.959	1400	1420	-1	AAATGAAGAGGAAGAGAAGAA
E2F4	13.950	1975	1985	-1	CGGCGGGAGGG
RREB1	13.844	313	332	-1	CCCCCACACCACCACCCCTC
TP53	13.843	849	863	-1	ACATGCAGAGGCTTG
E2F6	13.669	1876	1886	-1	GGGAGGGAGGC
E2F6	13.669	1971	1981	-1	GGGAGGGAGGC
PRDM1	13.636	86	100	-1	TGGAAAGGAAAGTTA
KLF5	13.540	1915	1924	1	CCCCCACCCC
Zfx	13.392	1657	1670	1	GAGCCCGCGGCCTG
STAT3	13.347	94	104	-1	CTTCTGGAAAG
STAT2::STAT1	13.336	86	100	1	TAACTTTCCTTTCCA
Myog	13.329	634	644	1	GGCAGCTGGAA
TEAD1	13.305	637	648	-1	CACATTCCAGCT
POU2F2	13.293	1337	1349	-1	GCCATTTGCATTC
RFX2	13.191	1196	1214	1	GGTTGCATGGCTACAGCCG
TP53	13.147	858	872	1	GCATGTGCTGGCTTG
INSM1	13.033	551	562	1	GGGCAGGGGGCA
SP2	13.021	413	427	1	GGCCCACCCCCACCT
Tcf12	12.992	634	644	1	GGCAGCTGGAA
Zfx	12.906	1962	1975	1	CCCGGTCCGGCCTC
Bach1::Mafk	12.873	912	926	1	GCACTGACACAGCAG
Nfe2l2	12.862	911	925	1	AGCACTGACACAGCA
Spi1	12.795	108	122	1	AGGGTAGGGAAGTGG
ZEB1	12.786	1274	1282	-1	CCCCACCTG
NR2C2	12.757	548	562	1	GTGGGGCAGGGGGCA
ZNF263	12.735	550	570	1	GGGGCAGGGGGCAGCAGAGAA
Erg	12.604	1404	1414	-1	AGAGGAAGAGA
EGR2	12.599	1350	1364	1	TCCGCGCCCACGCGG
Nr1h3::Rxra	12.591	75	93	1	TGCCCAAAGGTTAACTTTC
Tcf3	12.445	148	158	-1	CTCAGCTGCAC
ESR1	12.424	1170	1189	-1	AGTCCCGGGCACCTTCACCC
SP1	12.418	413	423	1	GGCCCACCCCC
EGR2	12.410	413	427	1	GGCCCACCCCCACCT
INSM1	12.373	938	949	-1	TGTCAGGTGGCA
EGR2	12.343	966	980	1	ACTGCACCCACGCAG
STAT5	12.339	248	258	-1	TTTTCCATGAA

ZNF263	12.296	1397	1417	-1	TGAAGAGGAAGAGAAGAAATG
E2F6	12.239	349	359	1	GAGAGGGAAGC
Klf1	12.225	980	990	1	GGCCACACCTT
Zfx	12.178	1139	1152	-1	AGGACCTGGGCCTC
KLF5	12.124	477	486	1	CCCACGCCCC
STAT3	11.996	247	257	1	CTTCATGGAAA
Sox3	11.991	1120	1129	-1	GCTTTGTCCC
TLX1::NFIC	11.937	1346	1359	1	TGGCTCCGCGCCCA
SP1	11.891	1526	1536	-1	TGCCCGCCCCT
Tcf3	11.821	633	643	-1	TCCAGCTGCCT
YY1	11.821	1475	1486	1	CAAGATGGAGTA
RUNX2	11.813	433	447	-1	GTGCTCTGTGGTATC
RUNX1	11.773	434	444	-1	CTCTGTGGTAT
RREB1	11.722	315	334	-1	GGCCCCCACACCACCACCCC
EGR2	11.693	1723	1737	-1	CGCCCGCACCCACGC
Nfe2l2	11.682	489	503	1	TCCAGTGAGTTAGCA
SP1	11.679	1915	1925	1	CCCCCACCCCG
Nr2e3	11.665	1126	1132	-1	CAAGCTT
E2F1	11.654	1706	1716	-1	CTGGCGGCAGC
SREBF2	11.652	1167	1176	1	GTGGGGTGAA
E2F6	11.620	1975	1985	-1	CGGCGGGAGGG
Sox6	11.606	1120	1129	-1	GCTTTGTCCC
Spi1	11.597	1396	1410	-1	GAAGAGAAGAAATGG
TP63	11.594	846	865	-1	GCACATGCAGAGGCTTGGAC
ELF1	11.542	1405	1417	-1	TGAAGAGGAAGAG
EGR1	11.525	1276	1289	-1	GGCTCGCCCCCACC
Zfx	11.509	1219	1232	1	GCTGCCAGGGCCTC
Klf4	11.453	1915	1924	-1	GGGGTGGGGG
PLAG1	11.434	63	76	1	GAGGGGCTAGGGTG
RORA_2	11.416	180	193	1	ACAAAGTCGGTCAA
TP53	11.401	859	873	-1	ACAAGCCAGCACATG
Tcfcp2l1	11.364	213	226	-1	CCAGTCAATTCCTG
NFATC2	11.360	252	258	-1	TTTTCCA
Tcfcp2l1	11.316	665	678	1	CCTGCAAGAGCCAG
SP2	11.286	1840	1854	-1	GCCCTGCCTCGTCCC
Ddit3::Cebpa	11.285	1194	1205	-1	CCATGCAACCCC
Nfe2l2	11.279	138	152	1	TGGAGTGACTGTGCA
NHLH1	11.214	148	159	-1	TCTCAGCTGCAC
Klf4	11.207	477	486	-1	GGGGCGTGGG
SREBF1	11.106	1167	1176	-1	TTCACCCCAC
Tcfcp2l1	11.099	1812	1825	-1	CCAGCTCCATCCCG
ESR2	11.073	1664	1678	-1	AGGTGACCCAGGCCG
Rfx1	11.052	1196	1209	1	GGTTGCATGGCTAC
Zfx	11.052	1555	1568	-1	ACCCGCTGGGCCTG
EGR2	11.024	1561	1575	-1	GCCCCGCACCCGCTG
USF2	10.886	938	948	-1	GTCAGGTGGCA
EGR1	10.878	1980	1993	1	CCGCCGCCGCCAGC
Myc	10.867	858	867	1	GCATGTGCTG