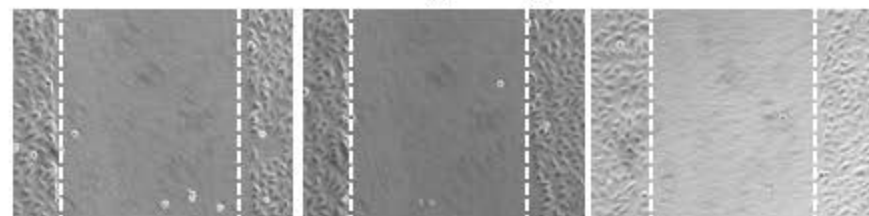
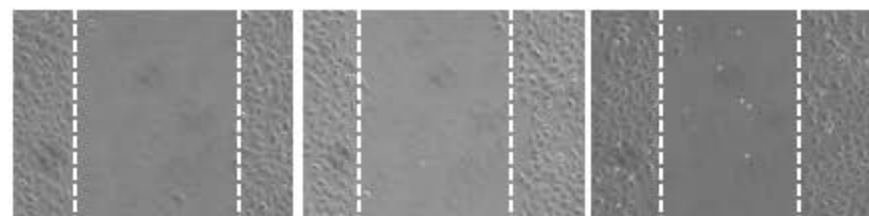
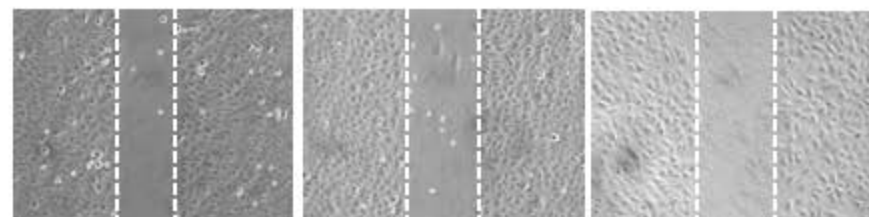
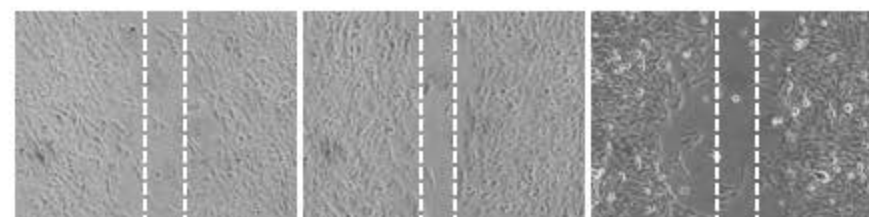
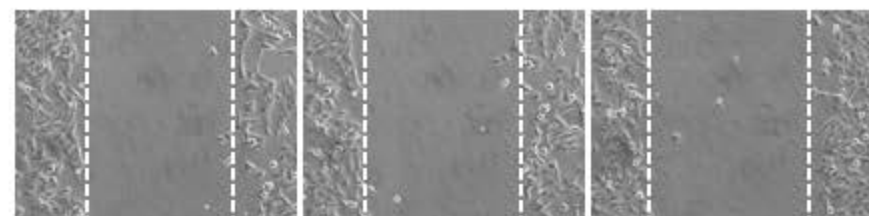
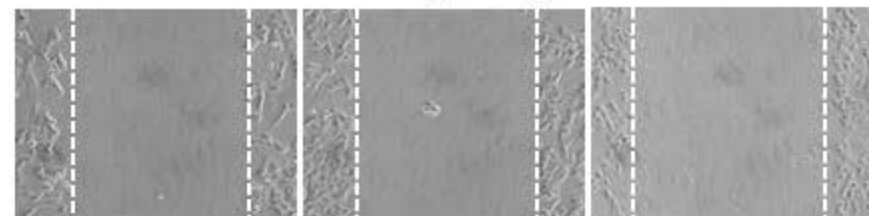


A**U-20S****control****Nonspecific
siRNA(40 nM)****AR siRNA(40 nM)****0h****8h****24h****B****MNNGHOS****control****Nonspecific
siRNA(40 nM)****AR siRNA(40 nM)**

**Androgen receptor is a potential novel prognostic marker and oncogenic target in
osteosarcoma with dependence on CDK11**

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Supplemental Figure 1. AR siRNA does not show the effects of the migratory in osteosarcoma cell lines. (A) Micrographs of osteosarcoma U-2OS cells at 0, 8, and 24 hours after wounding. (B) Micrographs of osteosarcoma MNNG/HOS cells at 0, 8, and 24 hours after wounding. Micrographs of osteosarcoma cells transfected with AR siRNA or nonspecific siRNA. The invading cells were stained with hematoxylin. * $P < 0.05$, ** $P < 0.01$ (compared with control cells).

Supplemental table 1

Gene_Symbol	KHOS_CDK11_siRNA	KHOS_control	KHOS_non-specific_siRNA	KHOS_Fold_Activation CDK11 vs. non-specific	U2OS_CDK11_siRNA	U2OS_control	U2OS_non-specific_siRNA	U2OS_Fold_Activation CDK11 vs. non-specific	Average_U2OS_KHOS_Activation
GNAS-A51	2.34	5.42	5.70	0.41	5.70	6.83	6.89	0.83	0.62
ACTR3	5.02	7.07	6.83	0.73	2.91	4.08	4.74	0.61	0.67
CDK11	6.45	8.35	8.55	0.75	4.97	7.81	7.61	0.65	0.70
TMEM19	5.22	7.76	7.51	0.69	4.84	7.45	6.80	0.71	0.70
LOC100505761	2.87	5.43	5.11	0.56	6.69	8.09	7.91	0.85	0.70
TBRG1	5.16	6.43	6.67	0.77	2.87	4.40	4.39	0.65	0.71
CBX5	3.74	5.53	5.53	0.68	5.56	6.26	6.99	0.80	0.74
UBE2K	5.98	9.42	9.14	0.65	6.21	8.49	7.50	0.83	0.74
RPRD1A	7.59	9.21	8.98	0.85	4.58	6.97	7.16	0.64	0.74
USP13	7.06	9.17	8.97	0.79	4.96	7.91	6.92	0.72	0.75
B9D1	4.75	6.84	7.23	0.66	6.18	7.06	7.28	0.85	0.75
CCDC15	5.77	7.33	7.14	0.81	3.55	4.82	5.01	0.71	0.76
TMEM68	6.91	9.16	8.80	0.78	5.25	6.96	6.82	0.77	0.78
SEC22C	5.17	6.57	7.02	0.74	6.78	8.04	8.16	0.83	0.78
HOTAIRM1	7.79	9.08	9.30	0.84	5.84	7.28	7.68	0.76	0.80
LEO1	8.87	10.19	10.28	0.86	6.07	8.12	8.13	0.75	0.81
CDC7	7.04	9.58	9.13	0.77	6.93	8.42	8.19	0.85	0.81
USP3	5.95	7.28	7.39	0.81	5.48	6.57	6.67	0.82	0.81
CDC27	5.75	7.31	7.12	0.81	5.91	7.76	7.13	0.83	0.82
ZFP62	7.98	10.13	10.04	0.79	8.16	10.12	9.66	0.84	0.82
GSTCD	6.93	8.78	8.82	0.79	7.47	8.54	8.57	0.87	0.83
RBFOX2	7.74	8.83	9.20	0.84	7.30	9.00	8.82	0.83	0.83
CBFB	9.59	11.64	11.74	0.82	9.22	10.95	10.77	0.86	0.84
NKAP	7.68	9.00	9.07	0.85	6.39	7.79	7.63	0.84	0.84
CTS2	7.25	8.49	8.62	0.84	7.16	8.86	8.50	0.84	0.84
CCDC82	7.07	8.48	8.60	0.82	7.70	8.58	8.87	0.87	0.85
MAP2K4	8.18	9.87	9.53	0.86	7.00	8.99	8.42	0.83	0.85
MCM3	9.22	10.87	10.81	0.85	9.39	11.46	11.05	0.85	0.85
HELLS	7.96	9.65	9.36	0.85	5.40	6.10	4.13	1.31	1.08
SMIM15	12.76	12.81	11.22	1.14	13.25	13.16	11.96	1.11	1.12
LCORL	9.43	8.86	7.94	1.19	8.60	8.53	7.49	1.15	1.17
CSGALNACT2	11.57	10.92	9.51	1.22	11.19	10.84	9.84	1.14	1.18
PTX3	9.78	10.41	8.29	1.18	9.81	9.90	8.27	1.19	1.18
TM2D1	8.27	6.90	6.78	1.22	7.73	6.31	6.35	1.22	1.22
PTHLH	9.80	8.21	7.98	1.23	7.18	5.49	5.78	1.24	1.23
ZNF367	9.25	8.94	7.49	1.23	9.51	9.16	7.69	1.24	1.24
SCUBE3	7.48	7.20	6.10	1.23	5.68	4.98	4.51	1.26	1.24
NHLRC3	8.51	7.50	6.42	1.33	8.45	7.90	7.23	1.17	1.25
CDADC1	6.97	6.33	5.58	1.25	6.05	5.83	4.82	1.25	1.25
RAB11FIP1	6.41	5.67	4.88	1.32	8.15	7.99	6.73	1.21	1.26
NACA	8.48	6.30	6.34	1.34	7.71	6.40	6.29	1.23	1.28
NEDD4	10.67	10.14	6.79	1.21	6.53	6.83	4.76	1.37	1.29
FAM73A	8.23	6.98	6.09	1.35	6.67	5.02	5.24	1.27	1.31
SLC16A6	10.24	7.01	7.66	1.34	5.04	4.07	3.66	1.38	1.36
SGMS2	5.37	4.75	3.40	1.58	8.63	7.96	7.39	1.17	1.37
DSC2	6.05	5.58	4.32	1.40	7.39	6.71	5.31	1.39	1.40
STC1	11.03	9.29	9.66	1.14	7.18	4.42	4.07	1.76	1.45
FAHD2CP	3.77	4.18	2.23	1.69	6.87	6.53	5.61	1.22	1.46

Supplemental Table 2. Multivariate Survival Analysis

Variable	5-Year survival			5-Year disease-free survival		
	Hazard Ratio	95 % CI	<i>P</i>	Hazard Ratio	95 % CI	<i>P</i>
Metastasis	2.877	1.840 - 4.262	0.013	3.15	2.076- 4.963	0.009
AR expression	1.836	1.259 - 2.738	0.128	1.961	1.465 - 2.798	0.067
Response to preoperative chemotherapy	2.095	1.446-3.204	0.084	2.332	1.811- 3.897	0.059