

Table S1. Sensitivity to PARPi following siRNA silencing in U2OS cells. PARPi sensitivity was determined by calculating the viability ratio (treated/untreated) and the sensitivity index (SI) for each siRNA. P values were determined by comparison to the non-targeting control using an unpaired, two-tailed t-test. SI-sensitivity index (see methods). Highlighted values are sensitive to PARPi treatment (p<0.05, SI>0.1).

Eztrez ID	Gene Symbol	Oligo Name	Oligo Sequence	Mean Log Ratio	p Value	Mean SI
29882	ANAPC2	Hs_ANAPC2_6	CTCACTGGATCGTATCTACAA	0.0715	0.0417	-0.0496
29882	ANAPC2	Hs_ANAPC2_5	AAGGTTCTCTACCGCATCTA	0.2397	0.0014	-0.2096
51433	ANAPC5	Hs_ANAPC5_6	ACCCTTGATAAACCATCTCTA	-0.2435	0.0365	0.1531
51433	ANAPC5	Hs_ANAPC5_8	AGGAACGATTCCGCCTAATA	-0.0373	0.4558	0.0251
51433	ANAPC5	Hs_ANAPC5_7	CAGAACATCAAACGTGATGGCTGA	0.0435	0.5755	0.0000
51433	ANAPC5	Hs_ANAPC5_4	AGCGGTTGATTACAAGCTCA	0.0485	0.0313	-0.0475
648	BMI1	Hs_PCGF4_1	TTGGATCGGAAAGTAAACAAA	-0.0702	0.2935	0.0006
648	BMI1	Hs_PCGF4_3	CAGAGTTCGACCTACTTGTAA	0.1313	0.1403	-0.0465
672	BRCA1_15	Hs_BRCA1_15	ACCATACACGCTTCATAAATAA	-0.3111	0.0039	0.2134
9577	BRE	Hs_BRE_2	CCGCTCATGTTGAATACCA	-0.0116	0.9842	0.0260
9577	BRE	Hs_BRE_3	AAGGTGCACTACGTGATTCAA	-0.0225	0.8281	-0.0336
83990	BRIP1	Hs_BRIP1_2	AAGATAAACAGTCACCTCAA	-0.1982	0.0173	0.2312
83990	BRIP1	Hs_BRIP1_1	TAGCATGCCAACATCTCTA	-0.0529	0.2757	0.0544
7862	BRPF1	Hs_BRPF1_3	AAGGGAGACGATCAAGGTTCA	-0.0429	0.3203	0.0495
7862	BRPF1	Hs_BRPF1_2	CCGAAAGGTCATAAGAGTTA	-0.0332	0.7033	0.0219
55143	CDCA8	Hs_CDCA8_3	CTGGTACCTACTTTCAATAAA	0.0588	0.0932	-0.0933
55143	CDCA8	Hs_CDCA8_2	ACGAAAGTAACACAGGTAGA	0.1632	0.0117	-0.1496
9744	CENTB1	Hs_CENTB1_2	ACGGGCCAGCAACGCATTAA	-0.0491	0.2122	0.0652
9744	CENTB1	Hs_CENTB1_1	CACCTGTAGGCTGAACCAA	0.1137	0.0145	-0.0458
1111	CHEK1	Hs_CHEK1_7	AACTGAAGAACGAGTCGAGT	-0.2611	0.0013	0.3973
1111	CHEK1	Hs_CHEK1_7	AACTGAAGAACGAGTCGAGT	-0.3190	0.0034	0.2341
1111	CHEK1	Hs_CHEK1_8	CCCGCACAGGCTTTCCCTTAT	-0.1673	0.0573	0.0736
11200	CHEK2	Hs_CHEK2_9	ACGCCGCTCTTGAATAACAA	-0.1794	0.0266	0.2355
11200	CHEK2	Hs_CHEK2_10	AGGACTGTCTTATAAAGATTAA	0.1233	0.4648	0.0622
23122	CLASP2	Hs_CLASP2_3	AAGAACGAGTATTAAACATCAA	-0.1154	0.3003	0.2032
23122	CLASP2	Hs_CLASP2_1	CTGGGTTAACGATCTGCTTAA	-0.0852	0.2045	0.0667
152330	CNTN4	Hs_CNTN4_2	CACATCTGTCATTGAAACAAA	-0.0811	0.1748	0.0663
152330	CNTN4	Hs_CNTN4_1	CAGTTGGAATCAGACATCAA	0.0786	0.1851	-0.1030
22818	COPZ1	Hs_COPZ1_1	AGCGATTAAATTGTATTGAA	0.0220	0.6501	0.0314
22818	COPZ1	Hs_COPZ1_2	TTGGCTGTGGATGAAATTGTA	0.1973	0.4922	-0.0092
9077	DIRAS3	Hs_ARHI_2	ACAGCTTATTGACTTAAATAAA	-0.0982	0.2284	0.1266
9077	DIRAS3	Hs_ARHI_1	CAGAGAATTCAAATTGTTAA	-0.0634	0.1669	0.1075
1775	DNASE1L2	Hs_DNASE1L2_1	CCGGCAGATGTCGCTCAATA	-0.0569	0.2654	0.0819
1775	DNASE1L2	Hs_DNASE1L2_2	TCCAGTGGAGGTGACCTCAA	0.0669	0.1792	-0.0846
2074	ERCC6	Hs_ERCC6_2	ATGGATGGTACCACTACAAATA	-0.1405	0.0298	0.2227
2074	ERCC6	Hs_ERCC6_5	CAGAGCTTTAGAACGTGAAA	-0.0545	0.4185	0.0901
161829	EXDL1	Hs_MGC33637_2	AAGAAGTATAATTCTGATTA	0.1163	0.4555	0.0635
161829	EXDL1	Hs_MGC33637_1	TCAGATGACTAGAACGACAA	0.1018	0.1875	-0.0701
55120	FANCL	Hs_FANCL_1	CAGAATTGCTTGTAGGTTAA	0.0547	0.0469	-0.0163
55120	FANCL	Hs_FANCL_5	CACTCTCAAGTTGAAGGCAA	-0.0489	0.2231	-0.0438
6468	FBXW4	Hs_SHFM3_2	TGGGAAGATTGGCATTCTAA	-0.0763	0.1176	0.1054
6468	FBXW4	Hs_SHFM3_1	CAGCACCTTCACTGCAAGTA	0.1409	0.0559	-0.1097
56776	FMN2	Hs_FMNL_7	CTGATACATCTCAAAGACGA	-0.0813	0.2081	0.1012
56776	FMN2	Hs_FMNL_6	CCAGCGCTGTTCAAGCCCTA	-0.0181	0.8810	0.0371
26130	GAPVD1	Hs_DKFZP434C212_1	TTGATTGAATTGAACTTAA	-0.0568	0.2576	0.1780
26130	GAPVD1	Hs_DKFZP434C212_2	AAGCAATTAAATTACAAGATA	-0.1408	0.0461	0.1231
26354	GNL3	Hs_GNL3_3	CAGCATTATCAATAGCTAAA	0.1160	0.1638	-0.1380
26354	GNL3	Hs_GNL3_2	AAAGCTGGTACTTATTTAAA	0.2121	0.0040	-0.2213
51512	GTSE1	Hs_GTSE1_7	CAAGTTCTAACGCCAACAAA	0.0472	0.1436	-0.0590
51512	GTSE1	Hs_GTSE1_6	TTCCGGACCTTGGACATAAA	0.1038	0.0983	-0.0814
9555	H2AFY	Hs_H2AFY_1	AAGGCTTGGTTTCCAGGTTA	-0.2079	0.0308	0.2784
9555	H2AFY	Hs_H2AFY_6	ATGTCGCGGTACATCAAGAAA	-0.0138	0.8269	0.0289
9555	H2AFY	Hs_H2AFY_2	CTGGCTGTGGCCAATGATGAA	0.1305	0.0400	-0.0757
9555	H2AFY	Hs_H2AFY_3	CAAGTTGTTGATCCTACTGTA	0.0885	0.0037	-0.0937
57520	HECW2	Hs_HECW2_1	AAGCGGGATTCTGAAGCAAA	0.0141	0.4604	-0.0099
57520	HECW2	Hs_HECW2_2	ACGGTCTACTATCATCAGTAA	0.1362	0.0368	-0.1163
8924	HERC2	Hs_HERC2_3	CCAGAGGATATTAAACCAA	-0.0660	0.3411	0.1043
8924	HERC2	Hs_HERC2_2	CGGGATGATCATGAAGAGTTA	-0.0318	0.6785	0.0542
221613	HIST1H2AA	Hs_HIST1H2AA_3	CAGGCAATGCTCTGGCATA	-0.0927	0.0345	0.1352
221613	HIST1H2AA	Hs_HIST1H2AA_2	CTGCTTCGTAAGGGAAACTAT	-0.1049	0.0213	0.0796
221613	HIST1H2AA	Hs_HIST1H2AA_1	AAGCCAAAGCAAGTAACCTA	-0.0510	0.0171	0.0485
221613	HIST1H2AA	Hs_HIST1H2AA_5	TTAGAGTATCTCACAGCAGAA	-0.0178	0.7456	0.0239
3305	HSPA1L	Hs_HSPA1L_1	CTGGATGTCGAGAAATTTAA	-0.2210	0.0535	0.2808
3305	HSPA1L	Hs_HSPA1L_5	TCTGATCGGCAGGAAATTAA	-0.0845	0.0272	0.1314
3305	HSPA1L	Hs_HSPA1L_2	ATCAGTAAATTGTTGCTAA	-0.0151	0.9177	0.0628
3305	HSPA1L	Hs_HSPA1L_8	AAAGAATGCCCTAGAACCTTA	0.0147	0.4714	-0.0766
3306	HSPA2	Hs_HSPA2_3	TAGAACGTTGAAACAGTAA	-0.0534	0.3595	0.1918
3306	HSPA2	Hs_HSPA2_2	ATGCATAATGCAATGTA	-0.0577	0.3594	0.1341
3576	IL8	Hs_IL8_5	AAGAGGGCTGAGAACATTCAA	-0.0086	0.9645	0.0077
3576	IL8	Hs_IL8_6	ATCAGTGAAGATGCCAGTGAA	0.0478	0.1330	-0.0633
3659	IRF1	Hs_IRF1_1	CAGCCGAGATGCTAACAGGCAA	0.0732	0.1287	-0.0957
3659	IRF1	Hs_IRF1_2	AGCGCCTGGTATGACTTAA	0.0610	0.0661	-0.1153
51438	MAGEC2	Hs_MAGEC2_1	CAGGGTAGTGTGGTATTGTTAA	-0.0872	0.0553	0.1110
51438	MAGEC2	Hs_MAGEC2_2	TAGCTTCAGAGTGTGTTAA	-0.0522	0.4916	0.1041
23389	MED13L	Hs_THRAP2_5	ATGGCTTAAGTGGACGCTAA	0.0304	0.7820	0.2164
23389	MED13L	Hs_THRAP2_6	CAGCCTATTGATACCACCTAA	0.0263	0.5926	-0.0469
284382	MGC33407	Hs_MGC33407_1	CAGGAATTCTCCGTATGGT	-0.1158	0.0155	0.1518

284382	MGC33407	Hs_MGC33407_5	TGGACCTAGTGGAGAACATTA	0.0787	0.0525	-0.0851
284382	MGC33407	Hs_MGC33407_2	TCCCTATATCGTGTACCGCAA	0.1287	0.0760	-0.1234
284382	MGC33407	Hs_MGC33407_3	CCGGCCGGAGCAGGAGTACAA	0.1391	0.0073	-0.1816
9221	NOLC1	Hs_NOLC1_7	CAGGTCAATTCTATAAGTTT	-0.0801	0.0134	0.0852
9221	NOLC1	Hs_NOLC1_6	CTGCGCGATAACCAACTCTCA	-0.0293	0.5711	0.0282
9221	NOLC1	Hs_NOLC1_9	AAGGTGGATTCACAGATAA	0.0247	0.2905	-0.0404
9221	NOLC1	Hs_NOLC1_8	CACCAAGAATTCTCAAATAA	0.0276	0.4466	-0.0428
4897	NRCAM	Hs_NRCAM_5	AGCCGGCTGAAGGAAACGAAA	-0.1201	0.1361	0.1972
4897	NRCAM	Hs_NRCAM_6	AGCCTAGTTGACTATGGAGAA	-0.0840	0.1663	0.1207
9381	OTOF	Hs_OTOF_1	CAGGATTGAAGCTTAGTGAA	-0.0992	0.1300	0.1519
9381	OTOF	Hs_OTOF_2	CCGGTACAAGTGGCTCATCAT	0.0182	0.4314	-0.0035
80301	PLEKHO2	Hs_pp9099_3	GACGGAGAAAATGTTGAACAA	-0.0188	0.8417	0.0558
80301	PLEKHO2	Hs_pp9099_2	AACAAAGTCAGCGACATCAA	-0.0040	0.8562	0.0204
5422	POLA	Hs_POLA_1	CAGGTGAGAGTACAGAAGAA	0.1761	0.0081	-0.1241
5422	POLA	Hs_POLA_2	CAGGATCTAACACTGAGACA	0.1961	0.0029	-0.1987
5423	POLB	Hs_POLB_7	TACGAGTTCATCCATCAATT	-0.1483	0.1391	0.2427
5423	POLB	Hs_POLB_2	CCGGAGCGAATGAGCTGTA	-0.1043	0.0732	0.0825
5423	POLB	Hs_POLB_9	CAGGTTGAGGAGCTAACAA	0.0292	0.2087	-0.0519
5423	POLB	Hs_POLB_5	CAAGATATTGACTAAATGAA	0.0290	0.4304	-0.0604
5424	POLD1	Hs_POLD1_5	CCGAGAGAGCATGTTGGTA	-0.0090	0.9679	-0.0061
5424	POLD1	Hs_POLD1_2	CGGGACCAAGGAGAAATTATA	0.0367	0.3320	-0.0634
5426	POLE	Hs_POLE_3	CTGGATGGATCCATCTAACTA	0.0622	0.1187	-0.0800
5426	POLE	Hs_POLE_2	CCGCATCATCCTCTGTACAAA	0.0147	0.5693	-1.2337
5427	POLE2	Hs_POLE2_2	CCGTGAAGACTTAGTAAATAA	-0.0746	0.2135	0.0359
5427	POLE2	Hs_POLE2_1	CAGTCTGTGATGAAACTATA	0.0243	0.5083	-0.0218
54776	PPP1R12C	Hs PPP1R12C_2	CAGCGGGAGCTCAACCCAGAA	-0.0715	0.1746	0.0615
54776	PPP1R12C	Hs PPP1R12C_5	CAGGAGCACCTTCGGAAACAA	0.0767	0.0085	-0.0994
5518	PPP2R1A	Hs PPP2R1A_5	CTGGTGTCCGATGCCAACCAA	-0.0809	0.0238	0.0870
5518	PPP2R1A	Hs PPP2R1A_6	ACGGCTAACATCATCTCAA	-0.0282	0.4891	0.0225
5518	PPP2R1A	Hs PPP2R1A_7	GACCAGGATGTGGACGTCAAA	-0.0111	0.9824	0.0117
5518	PPP2R1A	Hs PPP2R1A_8	ATCGCGTGTCTCATAGACGAA	0.0387	0.1303	-0.0345
5557	PRIM1	Hs_PRIM1_2	AAGGGTGGTCAAGACGTTAA	0.0053	0.6884	-0.0034
5557	PRIM1	Hs_PRIM1_3	CTGGGATAGTTGAGTATTGA	0.0046	0.4386	-0.0332
5714	PSMD8	Hs_PSMD8_1	TCCAACTGACATGTTCAATTAA	-0.0377	0.2561	0.0450
5714	PSMD8	Hs_PSMD8_2	AAGGGCGAGTGGAAACCGAAA	0.3116	0.0671	-0.0221
5929	RBBP5	Hs_RBBP5_3	ACGGCAGATCGAATAATCAGA	-0.0748	0.1205	0.0546
5929	RBBP5	Hs_RBBP5_1	CAGGTGCTCTCAACAAAGCTA	0.1002	0.3621	0.0133
5937	RBMS1	Hs_RBMS1_1	AACGAAACAAATGCAAAGGTTA	-0.1384	0.2624	0.1370
5937	RBMS1	Hs_RBMS1_2	CTGGTCTTATTAGCCTGTTAA	0.0429	0.3561	-0.0340
23186	RCOR1	Hs_RCOR1_1	CCCAATAATGGCCAGAAAAAA	-0.0263	0.7485	0.0653
23186	RCOR1	Hs_RCOR1_3	AACGACAGATCCAGAAATATA	0.0050	0.7532	0.0583
5985	RFC5	Hs RFC5_3	TAGCACAAGGACAATATTTAA	-0.0675	0.2906	0.0889
5985	RFC5	Hs RFC5_1	ACAGAAGACTTTCAATTTAA	-0.0043	0.9259	0.0259
117584	RRFL	Hs_RFFL_1	ATCGGTTCTTCAGTGCCTTA	-0.1153	0.0932	0.0747
117584	RRFL	Hs_RFFL_5	CTCCATGACATCTACCGAA	0.0204	0.4269	-0.0350
117584	RRFL	Hs_RFFL_3	TCGCAACTTGTCAACTACAA	0.0548	0.1411	-0.0672
117584	RRFL	Hs_RFFL_4	CCGGCTATACAAGGATCAGAA	0.0998	0.0590	-0.1203
6240	RRM1	Hs_RRM1_5	ATGCCCTGAATTCTGCTTAA	0.2992	0.0253	-0.1014
6240	RRM1	Hs_RRM1_1	AACGGATATTTGAGAAATCAA	0.3348	0.0075	-0.1498
6282	S100A11	Hs_S100A11_1	CTGCCAATAGTAAATAAGCAA	-0.0233	0.8014	0.0878
6282	S100A11	Hs_S100A11_3	ACCAACAGTGTGGTCAGCTA	-0.0365	0.6095	0.0326
23256	SCFD1	Hs_SCFD1_1	CAGAACTTGTGACTACATA	-0.0595	0.4162	0.0248
23256	SCFD1	Hs_SCFD1_3	CTGGAAGATATTGCAAATGCA	0.0977	0.2302	-0.0482
4735	SEPT2	Hs_SEPT2_2	GAGATATATTTATACTTAA	-0.0410	0.4629	0.0548
4735	SEPT2	Hs_SEPT2_3	ACCCAGGACCTTCATTATGAA	-0.0500	0.5411	0.0280
83852	SETDB2	Hs_SETDB2_3	TACCAGGTTAGAATGGTATA	-0.0585	0.1357	0.0692
83852	SETDB2	Hs_SETDB2_2	CCAGTGTATTCTGCAATCAA	0.0124	0.4114	-0.0127
50485	SMARCAL1	Hs_SMARCAL1_3	TTGAGTTATGAGTTAGGTCAA	-0.0710	0.1360	0.0690
50485	SMARCAL1	Hs_SMARCAL1_1	CAGCTTGACCTTCTTAGCAA	0.0972	0.0382	-0.1352
258010	SVIP	Hs_DKFZp313A2432_1	ATGGACATGAACTTGAATT	-0.0293	0.5862	0.0344
258010	SVIP	Hs_DKFZp313A2432_2	GAGGCTGAGAGAGAACCAA	-0.0013	0.9091	-0.0103
50945	TBX22	Hs_TBX22_1	CTGGAAGAGAAAGATATCAA	-0.0996	0.1016	0.1561
50945	TBX22	Hs_TBX22_2	ATGGATGTATTCTCATGAAA	-0.0436	0.5093	0.0733
221400	TDRD6	Hs_TDRD6_1	AAACACTGATTATGAACTATA	-0.0493	0.3772	0.0941
221400	TDRD6	Hs_TDRD6_3	TTGAATAAAGTTTATCCTTAA	-0.0243	0.8258	0.0165
7283	TUBG1	Hs_TUBG1_5	CCGAGGGAAATCATCACCTTA	-0.0299	0.3780	0.0274
7283	TUBG1	Hs_TUBG1_6	CTCCTTATGAGACTATTTA	0.1178	0.0165	-0.1208
7398	USP1	Hs_USP1_5	AGCAGATTATGAGCTATACAA	-0.0676	0.2132	0.0879
7398	USP1	Hs_USP1_6	ATGTTGAGAATTACCTACTA	0.1021	0.0353	-0.0889
8237	USP11	Hs_USP11_6	ACCGATTCTATTGGCCTAGTA	-0.1562	0.0221	0.1460
8237	USP11	Hs_USP11_10	AAGCGTTACTATGACGAGGTA	-0.0893	0.1628	0.1371
8237	USP11	Hs_USP11_4	CCCATTGAACGCAAGGTATA	-0.0177	0.8350	0.0419
8237	USP11	Hs_USP11_5	CTGCGTGGCTACGTGATGAA	-0.0366	0.7081	0.0214
151525	WDSAM1	Hs_WDSAM1_3	TCGCATCAGATGGCTATTAT	-0.2023	0.0061	0.2633
151525	WDSAM1	Hs_WDSAM1_1	TCCATTGAAGTTCTACCTA	-0.0195	0.8656	0.0045
151525	WDSAM1	Hs_WDSAM1_4	AAACATCAGCTGAAGCAATT	0.0828	0.0016	-0.2199
151525	WDSUB1	Hs_WDSUB1_1	TCGCCTGACTCGTTACGTGA	-0.0384	0.5100	0.0722
7465	WEE1	Hs_WEE1_8	CAAGACCTGTAAGAGAATT	0.0537	0.7580	-0.0087
7465	WEE1	Hs_WEE1_5	CACTGGTAAGCATTCACTGAT	0.0246	0.4803	-0.0142
7486	WRN	Hs_WRN_7	CCACGGAGGGTTCTATCTTA	-0.0414	0.5516	0.1131
7486	WRN	Hs_WRN_6	CGGATTGTATACGTAACCTCA	0.0434	0.1313	-0.0709

56897	WRNIP1	Hs_WRNIP1_1	CGCCATGTTCATAGAGGATAA	-0.1027	0.1173	0.0575
56897	WRNIP1	Hs_WRNIP1_5	ATGAATTAAATGTTATAAGGAA	-0.0085	0.9415	0.0066
56949	XAB2	Hs_XAB2_6	CCGCGTGTACAAGTCACGTGAA	0.2216	0.1349	-0.0060
56949	XAB2	Hs_XAB2_5	CACGTACAAACACGCAGGTCAA	0.2419	0.0643	-0.0371
7507	XPA	Hs_XPA_5	AGGGAGACGATTGTTCATCAA	-0.0066	0.9263	0.0065
7507	XPA	Hs_XPA_6	CTGCAGAGATGCTGATGATAA	0.0328	0.5365	-0.1634
7709	ZBTB17	Hs_ZBTB17_1	CCCTTCTGACTGTTATTAA	-0.0447	0.2756	0.0622
7709	ZBTB17	Hs_ZBTB17_2	CCGCCTCATCAGCCTGCTGAA	0.0586	0.3144	-0.0441

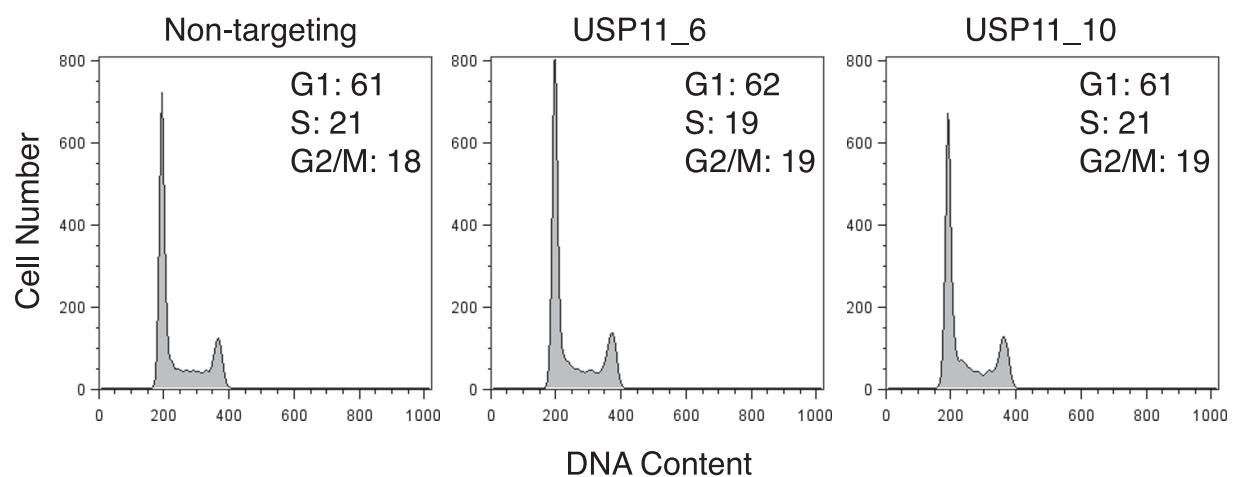


Fig S1. USP11 silencing does not alter cell proliferation. U2OS cells were analyzed for DNA content by flow cytometry 72h after transfection with non-targeting, USP11_6, or USP11_10 siRNAs.