

Supplementary Table 4. Putative androgen-related receptor binding sites in R1881-reponsive UC regions						
UC region	Binding Site	Start position	End position	Matrix Similarity	Sequence	Strand
uc.134	GRE.01	675	693	0.856	gagttattatatGTGCtta	+
uc.135	ARE.02	807	825	0.923	ctgccacttggtGTACTga	+
uc.135	GRE.02	807	825	0.851	tcaGTACaccaagtgccag	-
uc.135	GRE.02	2032	2050	0.842	aatGCACattgtgtattct	+
uc.204	GRE.03	1047	1065	0.893	ttcctcctgtaTGTTctga	-
uc.204	GRE.03	1460	1478	0.893	gcggtcacgtTGTTcaga	-
uc.204	ARE.03	1666	1684	0.892	tgtccacgggctGTCCtcc	+
uc.204	PRE.01	989	1007	0.885	tttggctttgtTGTTcttg	+
uc.204	GRE.02	1666	1684	0.849	ggaGGACagcccgtggaca	-
uc.204	GRE.02	1786	1804	0.839	gcgGGACagggcagtgcca	-
uc.240	ARE.03	578	596	0.891	gctgatccagatGTCCtta	+
uc.240	PRE.01	100	118	0.89	aggtgcccaacTGTTctga	+
uc.240	PRE.01	1226	1244	0.887	agagccgaggaTGTTcttt	-
uc.240	PRE.01	564	582	0.882	tcagcctcggTGTTcttg	-
uc.240	ARE.03	747	765	0.872	ttaggaaattgtGTACTtc	+
uc.240	ARE.03	1101	1119	0.871	ctgtctcagctGTGCtaa	-
uc.240	GRE.02	493	511	0.863	ctgGTACacgcggcatct	-
uc.240	GRE.02	455	473	0.848	tggGTACacatggtattta	-
uc.240	GRE.02	578	596	0.835	taaGGACatctggatcagc	-
uc.240	GRE.02	747	765	0.826	gaaGTACacaattcctaa	-
uc.249	ARE.02	1382	1400	0.895	tgatttcctctGTTcct	+
uc.249	GRE.03	2219	2237	0.889	acacctcactcTGTTccag	-
uc.249	PRE.01	86	104	0.879	catatatgtagTGTTctca	+
uc.249	ARE.03	2657	2675	0.871	ctcgcataaaatGTGCtta	+
uc.249	PRE.01	2298	2316	0.869	tgagaggctcaTGTTctgt	+
uc.283	GRE.01	1102	1120	0.869	aagtttgattttGTTccta	+
<b>uc.287</b>	<b>ARE.02</b>	<b>1259</b>	<b>1277</b>	<b>0.922</b>	<b>gtcttgctgctGTTccta</b>	-
<b>uc.287</b>	<b>GRE.03</b>	<b>1164</b>	<b>1182</b>	<b>0.914</b>	<b>aaagtgccaaaTGTTctgc</b>	-
<b>uc.287</b>	<b>GRE.03</b>	<b>1464</b>	<b>1482</b>	<b>0.892</b>	<b>tccttccagatTGTTccca</b>	-
<b>uc.287</b>	<b>GRE.03</b>	<b>152</b>	<b>170</b>	<b>0.886</b>	<b>ttgtcctccgTGTTcact</b>	+
<b>uc.287</b>	<b>GRE.01</b>	<b>143</b>	<b>161</b>	<b>0.862</b>	<b>gcagtaactttGTCCtcc</b>	+
<b>uc.287</b>	<b>ARE.01</b>	<b>2079</b>	<b>2097</b>	<b>0.834</b>	<b>ctagaacccaTGTTgtct</b>	+
<b>uc.287</b>	<b>GRE.02</b>	<b>1164</b>	<b>1182</b>	<b>0.822</b>	<b>gcaGAACattggcacttt</b>	+
uc.31	ARE.02	2214	2232	0.931	ttttgcctcctGTTctt	-
uc.31	GRE.03	265	283	0.899	tatgctcggcaTGTTccag	+
uc.344	GRE.01	2240	2258	0.853	aacgtcactctGTCCtgg	+
uc.349	PRE.01	503	521	0.852	ttatgtttaaTGTTctat	-
uc.410	GRE.01	2240	2258	0.853	aacgtcactctGTCCtgg	+
uc.445	ARE.03	279	297	0.899	ctgttcccactGTGCtga	-
uc.445	ARE.03	2842	2860	0.893	ggtgcacaggctGTGCact	+
uc.445	GRE.02	2842	2860	0.89	agtGCACagcctgtgcaac	-
uc.445	GRE.01	146	164	0.85	tgtgtggggtgtGTCCtgt	-
uc.445	GRE.02	279	297	0.821	tcaGCACagtggaacaag	+
uc.445	GRE.02	2514	2532	0.821	gttGCACagtggtctgtg	+

Note: Search included UC regions and corresponding 1kb flanking sequences of ucRNAs found to be altered in R1881-treated cells, using Genomatix software (München, Germany). Genomatix matrix family (V\$GREF) included the androgen receptor binding sites and related glucocorticoid responsive elements: ARE.01: RGNACRnngTGTTCT; ARE.02: DNWCWtnnTGTYCT; PRE.01: GNACNknTGTTCT; GRE.01: