

Table SI. Differentially expressed long non-coding RNAs between pazopanib-sensitive and pazopanib-resistant cells.

A, upregulated in pazopaib-sensitive cells		
lncRNA	Mean fold change	P-value ^a
<i>Gomafu</i>	17,581.59	0.08 ^b
<i>HULC</i>	7,457.82	0.08 ^b
<i>AK023948</i>	7,407.86	0.07 ^b
<i>HOTAIR</i>	360.69	0.08 ^b
<i>Jpx</i>	301.29	0.08 ^b
<i>HAR1B</i>	279.41	0.08 ^b
<i>H19</i>	32.79	0.04 ^b
<i>WT1-AS</i>	6.07	0.16
<i>Dio3os</i>	4.40	0.07 ^b
<i>ncR-uPAR</i>	3.07	0.17
<i>Y RNA-1</i>	2.58	0.07 ^b
<i>anti-NOS2A</i>	2.24	0.23
<i>NDM29</i>	2.21	0.19
<i>GAS5-family</i>	1.84	0.04 ^b
<i>HOXA6as</i>	1.71	0.17
<i>Alpha280</i>	1.64	0.24
<i>BACE1AS</i>	1.62	0.02 ^b
<i>E2F4 antisense</i>	1.56	0.31

B, downregulated in pazopanib-sensitive cells

lncRNA	Mean fold change	P-value ^a
<i>TncRNA</i>	0.58	0.26
<i>HOTAIRM1</i>	0.48	0.37
<i>Malat1</i>	0.40	0.40
<i>TUG1</i>	0.39	0.55
<i>NTT</i>	0.36	0.58
<i>Kcnq1ot1</i>	0.03	0.58
<i>Alpha250</i>	0.02	0.45
<i>Nespas</i>	<0.01	0.14
<i>L1PA16</i>	<0.01	0.52
<i>snaR</i>	<0.01	0.14
<i>SCA8</i>	<0.01	0.58
<i>MEG9</i>	<0.01	0.58
<i>PRINS</i>	<0.01	0.58
<i>Sox2ot</i>	<0.01	0.50
<i>UM9-5</i>	<0.01	0.58
<i>Zfx2as</i>	<0.01	0.51
<i>PR antisense</i>	<0.01	0.58
<i>NEAT1</i>	<0.01	0.16
<i>MER11C</i>	<0.01	0.03 ^b
<i>UCA1</i>	<0.01	0.44
<i>DHFR upstream</i>	<0.01	0.34
<i>ST7OT</i>	<0.01	0.57
<i>PTENP1</i>	<0.01	0.43
<i>Tmevpg1</i>	<0.01	0.58
<i>IPW</i>	<0.01	0.58
<i>SAF</i>	<0.01	0.58
<i>antiPeg11</i>	<0.01	0.58
<i>ANRIL</i>	<0.01	0.58
<i>LOC285194</i>	<0.01	0.58

Table SI. Continued.

B, downregulated in pazopanib-sensitive cells

lncRNA	Mean fold change	P-value ^a
<i>TEA ncRNAs</i>	<0.01	0.58
<i>HOXA3as</i>	<0.01	0.58

lncRNA >1.5 times highly or lowly expressed lncRNA in pazopanib-sensitive cells was compared with pazopanib-resistant cells. Mean fold change was calculated by dividing pazopanib-sensitive cell expression data by that of pazopanib-resistant cell. ^aCalculated using an unpaired t-test. ^bP<0.1.

Table SII. Gene enrichment analysis of 306 genes and long non-coding RNAs differentially expressed in both sarcoma cells and sarcoma tissues.

No.	Term	Count	%	P-value ^a	Source database ^b
1	VWC_out	5	1.7	0.0001	SMART
2	Cell adhesion	35	11.6	0.0001	Gene Ontology
3	Biological adhesion	35	11.6	0.0001	Gene Ontology
4	Cell membrane	53	17.5	0.0004	UniProt
5	Signal peptide	55	18.2	0.0004	UniProt
6	Cell-cell adhesion	26	8.6	0.0004	Gene Ontology
7	Single organism cell adhesion	20	6.6	0.0005	Gene Ontology
8	Single organismal cell-cell adhesion	19	6.3	0.0005	Gene Ontology
9	T Cytotoxic Cell Surface Molecules	4	1.3	0.0006	BIOCARTA
10	Inositol phosphate metabolic process	6	2	0.0007	Gene Ontology
11	Splice variant	104	34.4	0.0007	UniProt
12	VWFC	5	1.7	0.0008	InterPro
13	Polyol metabolic process	7	2.3	0.0009	Gene Ontology
14	Domain:VWFC 1	4	1.3	0.0009	UniProt
15	Domain:VWFC 2	4	1.3	0.0009	UniProt
16	EGF-like, conserved site	9	3	0.0010	InterPro
17	Signal	63	20.9	0.0010	UniProt
18	Regulation of cell adhesion	17	5.6	0.0010	Gene Ontology
19	Molecular transducer activity	31	10.3	0.0010	Gene Ontology
20	Signaling receptor activity	31	10.3	0.0010	Gene Ontology
21	Glycoprotein	67	22.2	0.0014	UniProt
22	Domain:TIL	3	1	0.0015	UniProt
23	EGF-like calcium-binding	7	2.3	0.0019	InterPro
24	Regulation of cell activation	14	4.6	0.0021	Gene Ontology
25	EGF-like domain	9	3	0.0025	InterPro
26	EGF_CA	7	2.3	0.0028	SMART
27	Domain:EGF-like 4	5	1.7	0.0032	UniProt
28	Disulfide bond	46	15.2	0.0033	UniProt
29	Regulation of leukocyte activation	13	4.3	0.0035	Gene Ontology
30	Alternative splicing	130	43	0.0035	UniProt
31	Neurogenesis	27	8.9	0.0038	Gene Ontology
32	Neuron differentiation	24	7.9	0.0039	Gene Ontology
33	Topological domain: extracellular	44	14.6	0.0041	UniProt
34	EGF-type aspartate/asparagine hydroxylation site	6	2	0.0043	InterPro
35	Signal transducer activity	30	9.9	0.0044	Gene Ontology
36	Domain:VWFD 2	3	1	0.0045	UniProt
37	Domain:VWFD 1	3	1	0.0045	UniProt
38	Domain:VWFD 3	3	1	0.0045	UniProt
39	EGF	8	2.6	0.0047	SMART
40	Gastric acid secretion	5	1.7	0.0049	Kegg Pathway
41	Intrinsic component of plasma membrane	30	9.9	0.0058	Gene Ontology
42	Disulfide bond	51	16.9	0.0059	UniProt
43	Cell activation	19	6.3	0.0062	Gene Ontology
44	EGF domain, merozoite surface protein 1-like	3	1	0.0063	InterPro
45	Positive regulation of multicellular organismal process	26	8.6	0.0065	Gene Ontology
46	Generation of neurons	25	8.3	0.0066	Gene Ontology
47	T cell activation	12	4	0.0067	Gene Ontology
48	T cell aggregation	12	4	0.0067	Gene Ontology
49	Lymphocyte aggregation	12	4	0.0068	Gene Ontology
50	Cell-cell signaling	27	8.9	0.0070	Gene Ontology
51	Regulation of hemopoiesis	10	3.3	0.0071	Gene Ontology
52	Leukocyte aggregation	12	4	0.0076	Gene Ontology
53	Positive regulation of interleukin-8 secretion	3	1	0.0077	Gene Ontology

Table SII. Continued.

No.	Term	Count	%	P-value ^a	Source database ^b
54	VWC	4	1.3	0.0077	SMART
55	Cell projection organization	24	7.9	0.0079	Gene Ontology
56	Cell projection	16	5.3	0.0080	UniProt
57	Domain:EGF-like 1	6	2	0.0082	UniProt
58	Uncharacterised domain, cysteine-rich	3	1	0.0086	InterPro
59	Trypsin inhibitor-like, cysteine rich domain	3	1	0.0086	InterPro
60	Salivary secretion	5	1.7	0.0086	KEGG pathway
61	Microtubule bundle formation	5	1.7	0.0087	Gene Ontology
62	Domain:VWFC 3	3	1	0.0089	UniProt
63	Alcohol metabolic process	9	3	0.0091	Gene Ontology
64	C2H2 zinc finger domain binding	3	1	0.0095	Gene Ontology
65	Positive regulation of myeloid cell differentiation	5	1.7	0.0099	Gene Ontology

Gene enrichment analysis was determined via DAVID pathways. Annotation terms with enrichment P-values <0.01 are listed above. ^aModified Fisher Exact P-values were generated for gene enrichment analysis. ^bEach database is available at the following URLs: SMART, <http://smart.embl-heidelberg.de>; Gene Ontology, <http://geneontology.org>; UniProt, <https://www.uniprot.org>; BIOCARTA, <http://www.biocarta.com>; InterPro, <https://www.ebi.ac.uk/interpro/>; KEGG pathway, <https://www.genome.jp/kegg/pathway.html>. vWF, von Willebrand factor; VWC, von Willebrand factor type C domain; VWFC, von Willebrand factor type C; EGF, epidermal growth factor; EGF_CA, Calcium-binding EGF-like domain; VWFD, von Willebrand factor type D; KEGG, Kyoto Encyclopedia of Genes and Genomes.