

Table S1 The parimifasor exhibited concentration-dependent inhibitory effects on 12 cell lines

Cells name	40 μ M	20 μ M	10 μ M	5 μ M	2.5 μ M	1.25 μ M	0.625 μ M	0.3125 μ M	0.15625 μ M
143B	97.76982%	96.33666%	67.25878%	70.39915%	33.77082%	24.32711%	7.20221%	4.56974%	0.98435%
HCT-116	95.57896%	94.29668%	89.72986%	88.70046%	56.06331%	15.78900%	6.76842%	5.49804%	3.86469%
KYSE140	64.82710%	45.48366%	65.36418%	54.09989%	15.50204%	-1.04974%	-13.44563%	-13.72422%	-6.33437%
H1299	94.88596%	85.73321%	79.72566%	88.14431%	45.09698%	9.74767%	5.84815%	-0.39287%	-2.01374%
786-O	89.88388%	78.08897%	66.68250%	55.68448%	33.53672%	10.53373%	2.05640%	1.27118%	-0.68269%
LN229	89.06612%	82.28857%	75.99439%	71.76643%	65.34412%	52.75225%	14.89162%	1.77679%	-3.42022%
Hela	91.50781%	38.78343%	35.83400%	44.16865%	45.84988%	25.18268%	2.47948%	0.94387%	-0.90680%
HCCC-9810	88.03560%	64.07881%	60.43128%	57.24319%	53.40793%	31.87679%	9.90762%	6.65530%	8.25758%
NCI-H460	96.89243%	48.46028%	-34.01697%	-25.04770%	-6.64441%	-6.67131%	-6.98684%	-10.60928%	-16.41107%
A375	97.83358%	-2.68133%	-1.02983%	-0.78418%	-1.91982%	0.45350%	-1.81023%	-0.41760%	-2.00486%
PANC-1	92.40518%	76.41509%	71.95302%	65.15152%	63.78883%	5.84858%	5.56032%	4.07852%	1.14113%
HepG2	37.10257%	23.05154%	-10.93556%	-46.28461%	-13.16970%	-11.62281%	-9.10440%	-5.69211%	-7.22302%

Table S2 IC50 values showed parimifasor inhibited tumor cell lines

Cell line	IC50 (μ M)	95% CI of IC50
LN229	0.06954	0.03816 to 0.1274
HCT-116	0.1864	0.08079 to 0.4288
H1299	0.2962	0.1311 to 0.6679
786-O	0.4287	0.2757 to 0.6733
143B	0.6794	0.3241 to 1.461
KYSE140	0.2345	0.06665 to 0.8492
PANC-1	0.2373	0.07518 to 0.8228
HCCC-9810	0.4067	0.1225 to 1.587
Hela	0.1434	0.002929 to ???
HepG2	1.666	0.06677 to ???
NCI-H460	3.236	0.2413 to ???
A375	0.2112	??? to 0.7718

Table S3 Statistical of RNA-seq base information

Sample name	Raw_reads	Clean_reads	Clean_bases	Error (%)	Q20 (%)	Q30 (%)	GC (%)
LD-3	63672122	63113644	9.46G	0.04	98.82	95.84	48.56
LC-2	61712118	61000982	9.14G	0.04	98.78	95.73	48.64
LC-3	56981304	56369318	8.44G	0.04	98.94	96.31	48.68
LD-1	53166716	52619158	7.88G	0.04	98.87	96.08	49.04
LD-2	50156196	49633914	7.44G	0.04	98.88	96.13	48.83
LC-1	62518242	61763366	9.26G	0.04	98.89	96.12	49.55
KD-3	59146488	58508646	8.77G	0.04	98.92	96.25	48.1
KC-2	48408516	47899982	7.18G	0.04	98.87	96.04	48.46
KC-3	58675788	58034208	8.7G	0.04	98.89	96.11	47.6
KD-1	45107652	44656408	6.69G	0.04	98.79	95.75	48.05
KD-2	61475686	60817494	9.12G	0.04	98.84	95.96	47.75
KC-1	59902820	59439324	8.9G	0.04	99.04	96.67	49.13

Table S4 The statistical of mapping the reference genome

Sample name	Total reads	Total mapped	Multiple mapped	Unique mapped	Reads map to '+'	Reads map to '-'	Non-splice reads	Splice reads
LD-3	63113644	62153551 (98.48%)	1899219 (3.01%)	60254332 (95.47%)	30115810 (47.72%)	30138522 (47.75%)	35218390 (55.80%)	25035942 (39.67%)
LC-2	61000982	60083533 (98.50%)	1799497 (2.95%)	58284036 (95.55%)	29131203 (47.76%)	29152833 (47.79%)	32774657 (53.73%)	25509379 (41.82%)
LC-3	56369318	54847196 (97.30%)	1739954 (3.09%)	53107242 (94.21%)	26543549 (47.09%)	26563693 (47.12%)	30330569 (53.81%)	22776673 (40.41%)
LD-1	52619158	51936837 (98.70%)	1590151 (3.02%)	50346686 (95.68%)	25162694 (47.82%)	25183992 (47.86%)	28980337 (55.08%)	21366349 (40.61%)
LD-2	49633914	48974550 (98.67%)	1422882 (2.87%)	47551668 (95.80%)	23766471 (47.88%)	23785197 (47.92%)	27310186 (55.02%)	20241482 (40.78%)
LC-1	61763366	60406897 (97.80%)	1863458 (3.02%)	58543439 (94.79%)	29258404 (47.37%)	29285035 (47.41%)	32427262 (52.50%)	26116177 (42.28%)
KD-3	58508646	57736061 (98.68%)	1737027 (2.97%)	55999034 (95.71%)	27988531 (47.84%)	28010503 (47.87%)	32790630 (56.04%)	23208404 (39.67%)
KC-2	47899982	47242930 (98.63%)	1432047 (2.99%)	45810883 (95.64%)	22897120 (47.80%)	22913763 (47.84%)	25970628 (54.22%)	19840255 (41.42%)
KC-3	58034208	52304528 (90.13%)	1563641 (2.69%)	50740887 (87.43%)	25360428 (43.70%)	25380459 (43.73%)	29290090 (50.47%)	21450797 (36.96%)
KD-1	44656408	44015782 (98.57%)	1261229 (2.82%)	42754553 (95.74%)	21369729 (47.85%)	21384824 (47.89%)	25857344 (57.90%)	16897209 (37.84%)
KD-2	60817494	59986194 (98.63%)	1771668 (2.91%)	58214526 (95.72%)	29095757 (47.84%)	29118769 (47.88%)	35070570 (57.67%)	23143956 (38.05%)
KC-1	59439324	53322540 (89.71%)	1731563 (2.91%)	51590977 (86.80%)	25784642 (43.38%)	25806335 (43.42%)	28394881 (47.77%)	23196096 (39.02%)

Table S5 The primers list for qRT-PCR

Gene_ID	Named	Forward Sequence (5'-3')	Reverse Sequence (5'-3')	PCR Products(bp)
	GAPDH	TCAAGAAGGTGGTGAAGCAGG	TCAAAGGTGGAGGAGTGGGT	115
ENSG00000178685	PARP10	CAGCTCTACCATGAGGACCTT	CGAAAGCCAGTCATATCCGGT	83
ENSG00000089127	OAS1	TGTCCAAGGTGGTAAAGGGTG	CCGGCGATTTAACTGATCCTG	112
ENSG00000111331	OAS3	GAAGGAGTTCGTAGAGAAGGCG	GAAGGAGTTCGTAGAGAAGGCG	114
ENSG00000111215	PRR4	CCAGATGTAGAGGACTCAAGTCA	GGAAATCGGGGTAGAGAGAGTT	227
ENSG00000124201	ZNFX1	AAATCAGGCCAATAACCCACC	GGCCCTAAATCTCTCTCCCT	121
ENSG00000130589	HELZ2	CAGGAGGAGCTGAAGGAGAA	CCTGAGAGGACAGTGCTTGA	108
ENSG00000135899	SP110	CCTATGCCATACACAAGCCATT	CCTCTCCAGTTGGGTGAGAAT	152
ENSG00000144655	CSRNP1	CCCCTGTCTATCCTGAAGCG	CCATACCCAGAGTACAGCCA	136
ENSG00000163840	DDX3X	AGCAGTTTTGGATCTCGTAGTG	ACTGTTTCCACCACGTTCAAAT	168
ENSG00000173193	PARP14	TGTTAGTGGAGAACATAAGTGGC	TGAATGGTGCTTGGTACAATCAT	140