

Supporting Information

Title

Covalent inhibitors allosterically block the activation of Rho family proteins and suppress cancer cell invasion

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Supplementary figures and legends

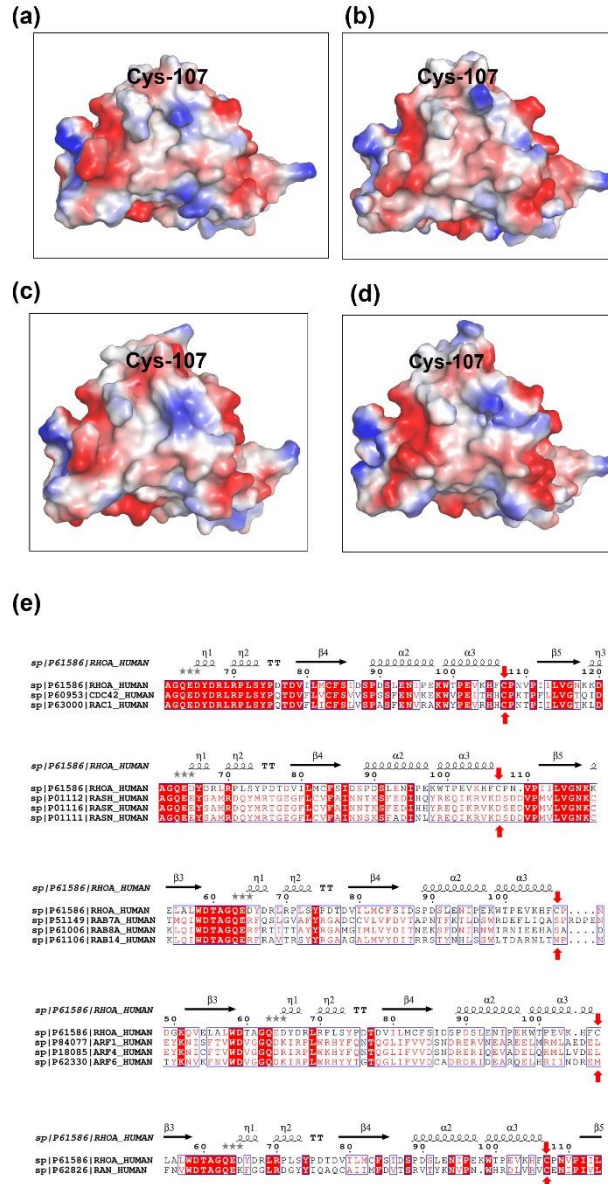


Figure S1. The relative conservative binding pockets around Cys107 among Rho family proteins revealed by molecular dynamics simulation. a-d) The structural dynamics of the potential binding pocket around the Cys-107 residue, revealed by the representative structures from the most principal (four out of ten) clusters. e) Sequence alignment of five small GTPases, which represents the five families of Ras. The conserved Cys107 among Rho GTPases is pointed by red arrows.

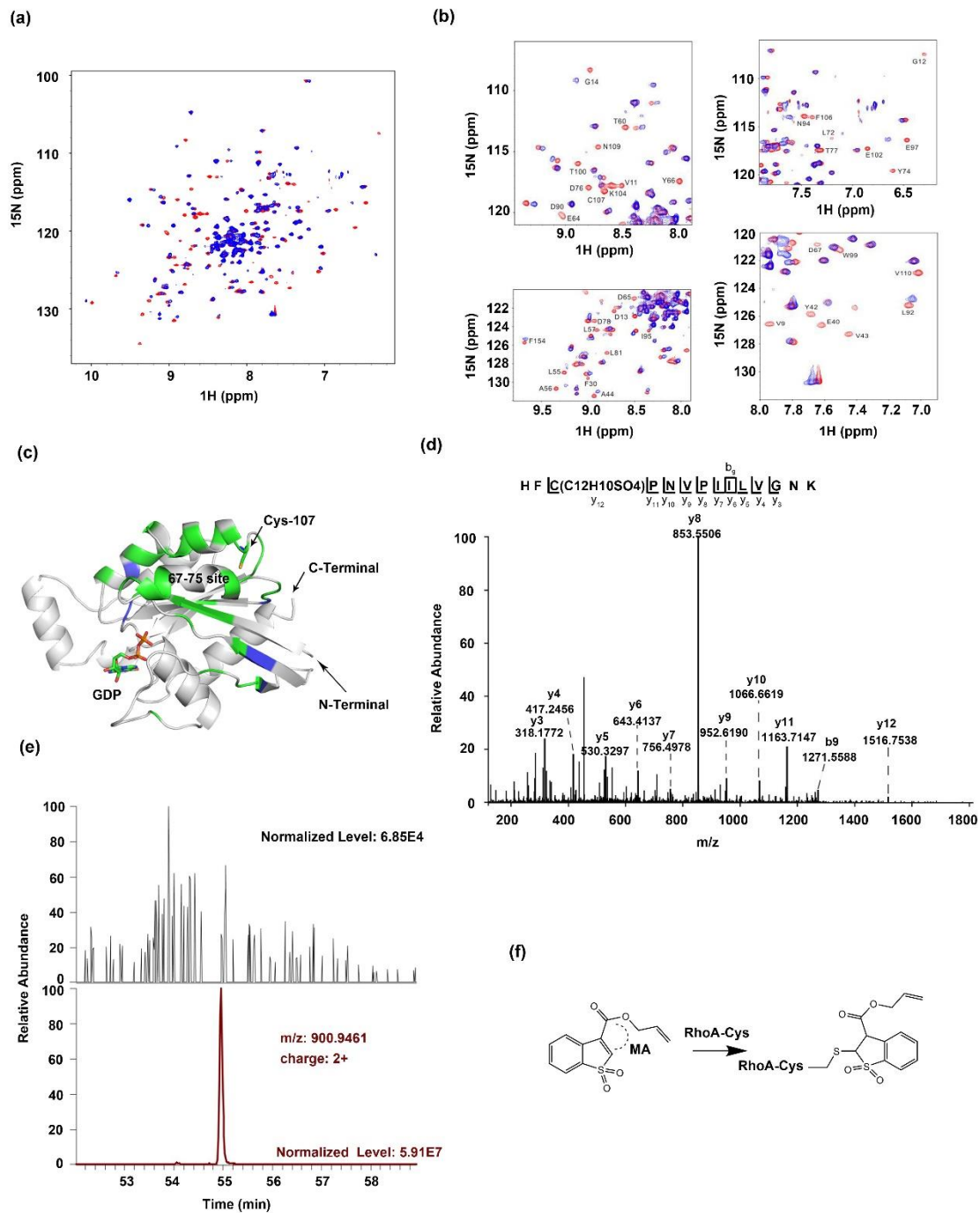


Figure S2. DC-RhoA covalently binds to Cys107 of RhoA. a) Overlapped 1H-15N HSQC spectra for RhoA in the absence (red) and presence (blue) of compound DC-RhoA at the ratio 1:1. b) The residues with attenuating peaks or with their CSP values bigger than 0.05 upon the addition of DC-RhoA are labeled. c) The residues with significant chemical shift changes observed in response to DC-RhoA modification are highlighted on the 3D cartoon structure of RhoA-GDP complex (PDB: 1FTN). The

residues with attenuating peaks upon the addition of DC-Rhoins are highlighted in green, and the residues with their CSP values bigger than 0.05 upon the addition of DC-Rhoins are colored in blue. d) Extracted ion chromatograms (XIC) for peptide HFC(C12H10SO4)PNVPILVGNK in DMSO treatment versus compound treatment. e) ESI-MS/MS tandem mass spectra results showed the modified peptide HFC(C12H10SO4)PNVPILVGNK by compound DC-Rhoins. f) Proposed reaction mechanism between compound DC-Rhoins and the Cys-107 residue of RhoA (MA represents Michael acceptor).

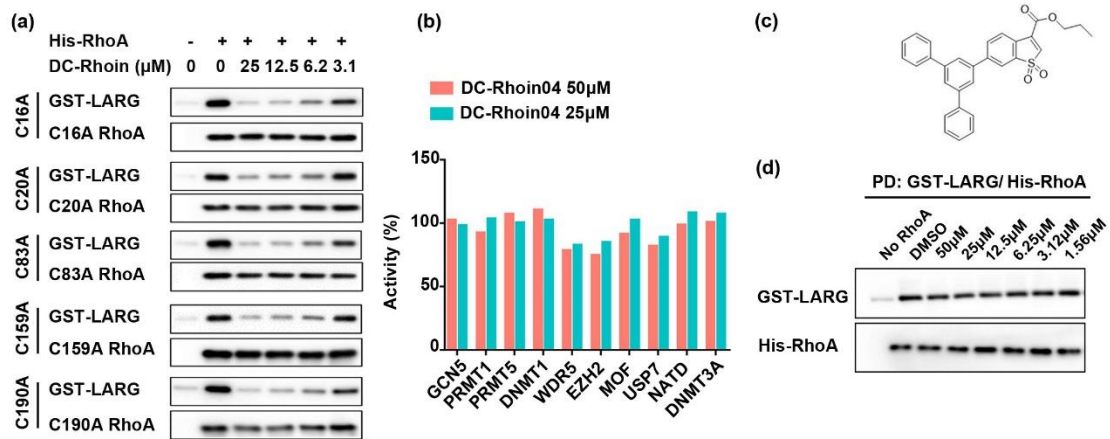


Figure S3. DC-Rhoins are selective Rho family inhibitors. a) The interactions of RhoA^{C16A}, RhoA^{C20A}, RhoA^{C83A}, RhoA^{C159A} and RhoA^{C190A} with LARG were blocked by DC-Rhoins at the concentration around 3.1 μM. b) DC-Rhoins04 shows minimal inhibition on several epigenetic targets containing exposed cysteine. c) The chemical structure of inactive compound DC-Rhoins10. d) DC-Rhoins10 did not block the interaction between RhoA and LARG.

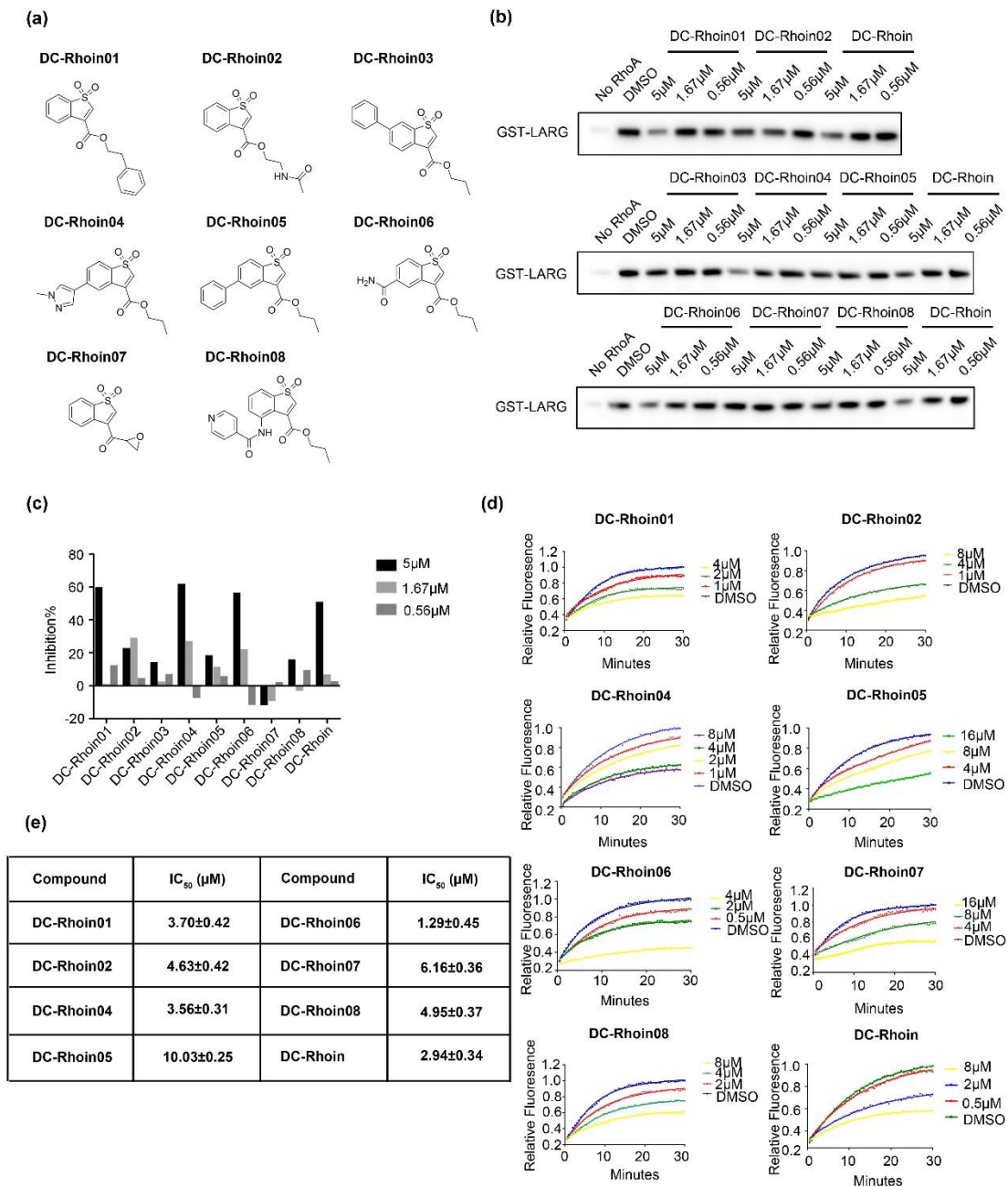


Figure S4. Screening of active derivatives of DC-Rhoi *in vitro*. a) The chemical structures of DC-Rhoi's derivative compounds. b) The inhibitory effect of a panel of derivatives of DC-Rhoi were tested in a complex formation assay. c) The inhibition ratio of the derivatives at the concentration of 5 μ M; 1.7 μ M and 0.56 μ M in pull down assay. d) The inhibitory effect of a panel of derivatives of DC-Rhoi were tested in the GDP/GTP exchange assay of RhoA. e) The half maximal inhibitory concentrations of several inhibitors in the GDP/GTP exchange assay.

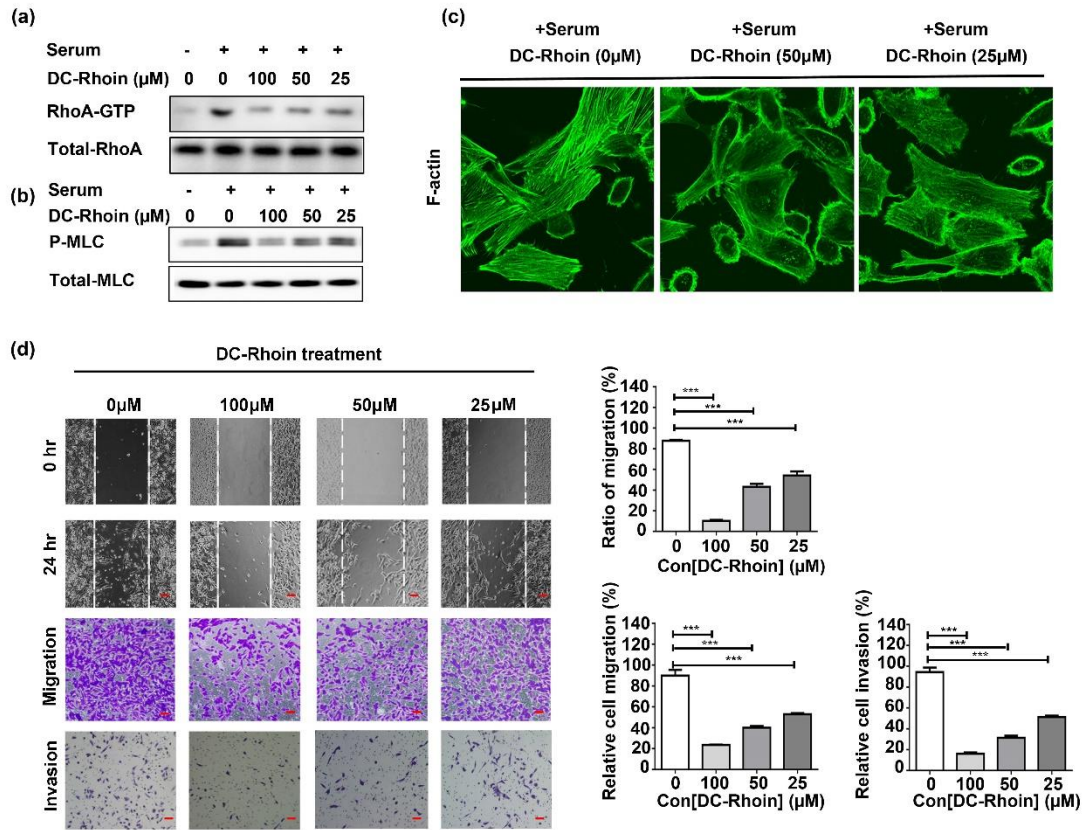


Figure S5. Compound DC-Rhoin inhibited cellular activity of Rho family proteins, and suppressed the migration and invasion of breast cancer MDA-MB-231 cells. a) DC-Rhoin inhibited the activation of RhoA at 25 μM in MDA-MB-231 cells. b) DC-Rhoin decreased the level of p-MLC at the dose of 25 μM in MDA-MB-231 cells. c) DC-Rhoin suppressed the formation of stress fiber in MDA-MB-231 cells d) The migration and invasion ability of MDA-MB-231 cells was inhibited by DC-Rhoin. Data are shown as mean \pm SD of three independent experiments, *** $p < 0.001$ (Student's t -test). Scale bars, 1mm.

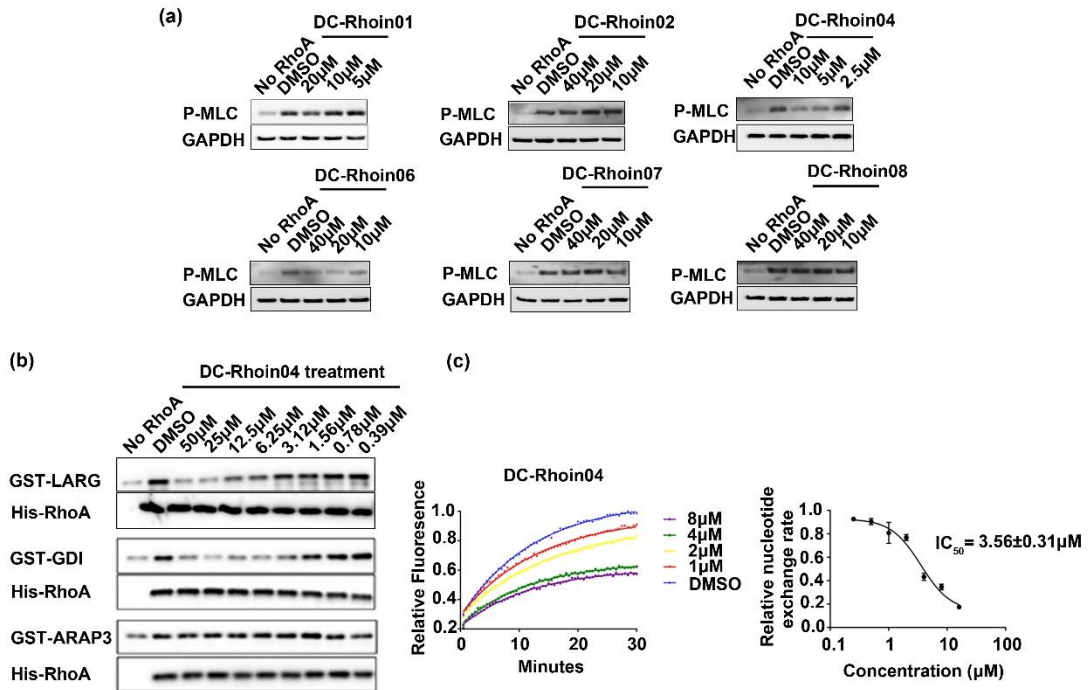


Figure S6. Identification of DC-Rhoin04 as the most potent inhibitor of RhoA in cell. a) DC-Rhoin04 inhibited the phosphorylation of MLC protein at the concentration of 5 μM , it has more potent cellular activity than other derivatives. b) Consistent with DC-Rhoins, DC-Rhoin04 inhibits the interaction of RhoA with LARG and GDI. c) DC-Rhoin04 exhibited inhibition against the GDP/GTP exchange rate of RhoA, with an IC_{50} value of $3.56 \pm 0.31 \mu\text{M}$.

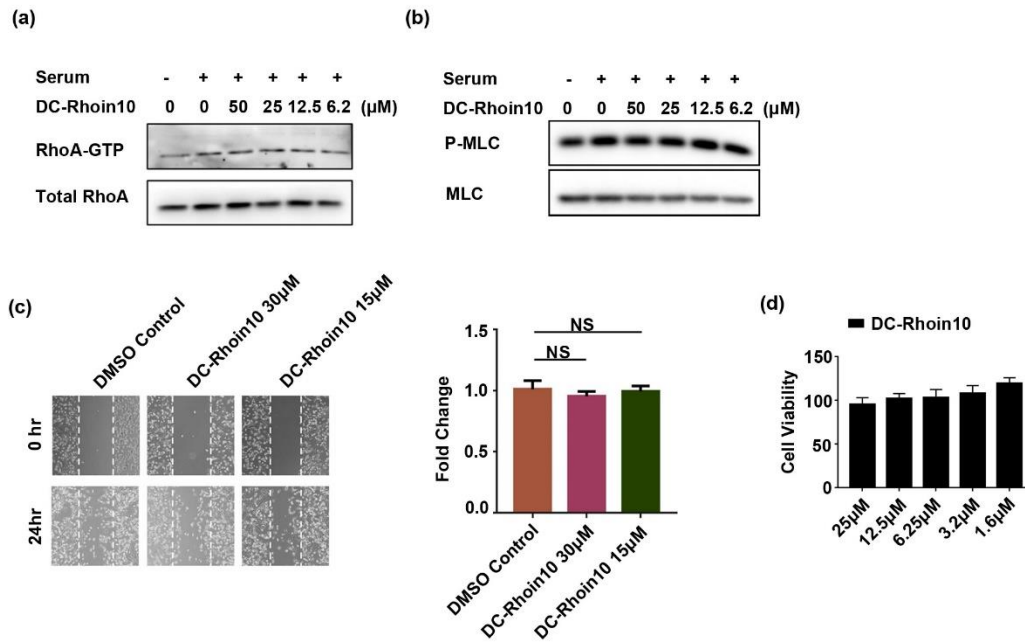


Figure S7. The negative molecule has no effect on the RhoA related pathway. a) DC-Rhoi10 did not inhibit the activation of RhoA in MDA-MB-231 cells. b) DC-Rhoi10 did not inhibit the serum induced phospho-MLC activities in MDA-MB-231 cells. c) DC-Rhoi10 has no effect on the migration of MDA-MB-231 cells. d) DC-Rhoi10 showed minimal anti-proliferative effect on MDA-MB-231 cells.

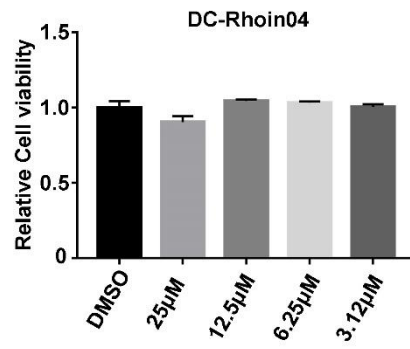


Figure S8. Under the condition of cell migration or invasion assays, DC-Rhoi04 has weak effect on the proliferation of MDA-MB-231 cells.

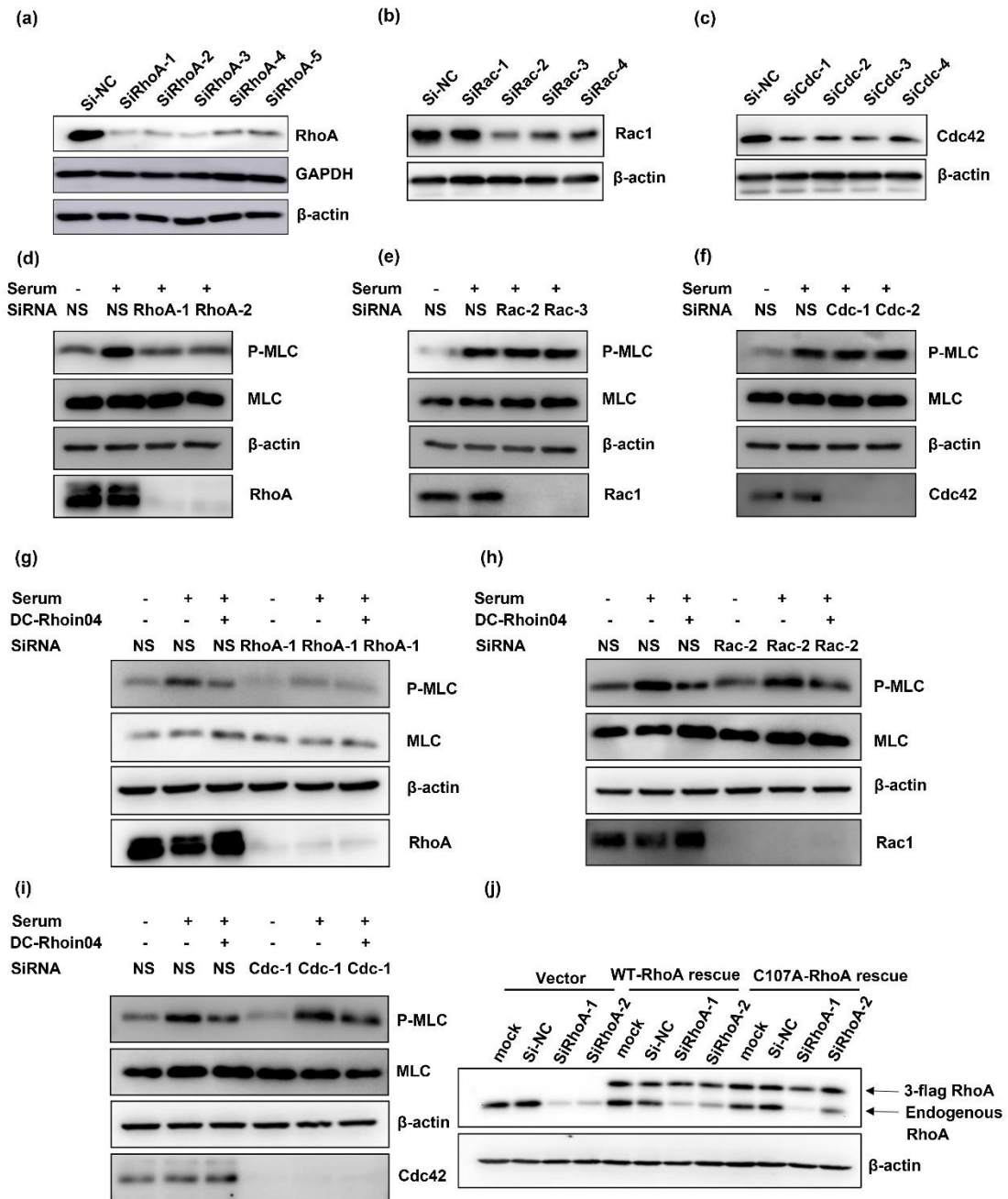


Figure S9. The evaluation of the pMLC level in the RhoA/Rac1/Cdc42 knockdown cells with DC-Rhoin treatment, and the establishment of RhoA^{C107A} rescued model in MDA-MB-231 cells. a-c) MDA-MB-231 cells transduced with control (si-NC) or RhoA/Rac1/Cdc42 targeting siRNAs, and assessed for knockdown selection. d-f) Knock down of RhoA blocked the phosphorylation of MLC activated by serum, while deletion of Rac1 or Cdc42 has minimal effect. g-i) In the MDA-MB-231 cell line with

RhoA stably knocked down, the inhibition of DC-RhoA on p-MLC was weak, while deletion of RAC1 or CDC42 had little effect. j) Rescue of RhoA knockdown cells by expression of 3×flag fusion RhoA protein.

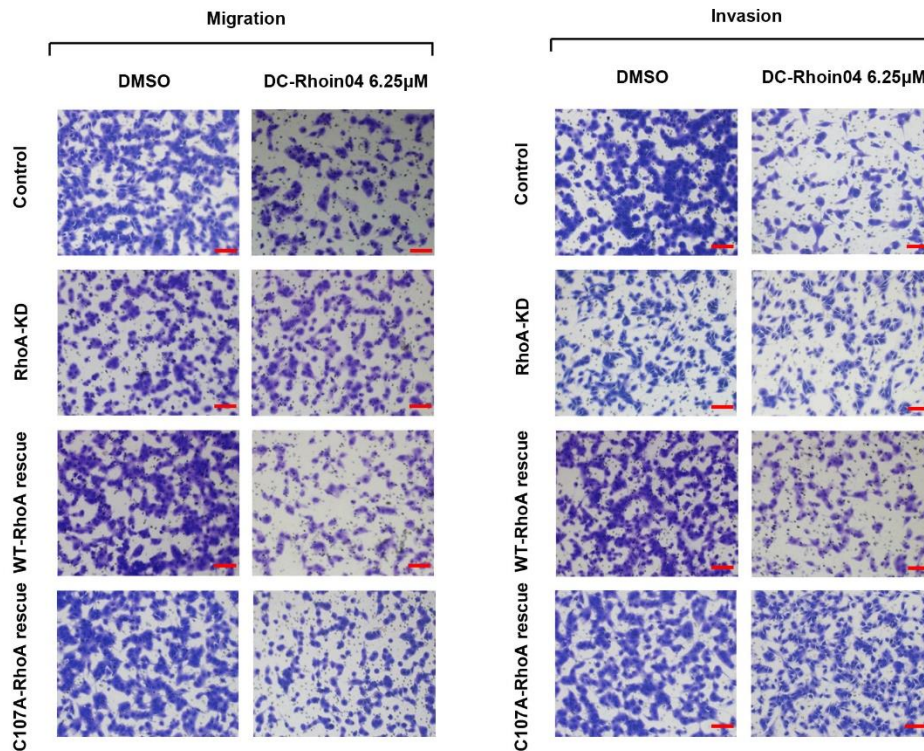


Figure S10. The images of the transwell assay for testing the inhibition ability of DC-RhoA on the migration or invasion in the normal MDA-MB-231 cell; RhoA-KD cell; RhoA^{WT} rescued cell and RhoA^{C107A} rescued cell. DC-RhoA has weak inhibition on cell migration and invasion when endogenous RhoA expression was knocked down, while, the inhibition effect of DC-RhoA was partially restored by re-expressing WT RhoA in RhoA knockdown cells, by contrast, RhoA^{C107A} did not restore this effect. Shown are representative images of migrated cells.

Supplementary tables and legends

Table S1. Structural clustering of molecular dynamics simulation.

Cluster	Frames	Occurrence*
1	8	0.000
2	2984	0.149
3	6006	0.300
4	11	0.001
5	2	0.000
6	3	0.000
7	443	0.022
8	10540	0.527
9	1	0.000
10	1	0.000

* 19999 frames from 1000 nano-seconds trajectory were divided into 10 clusters, using the C-alpha RMSD values between frames. Occurrence is calculated by dividing the frame numbers of each cluster by the total frame number 19999.

Table S2. Full list of the covalent docking.

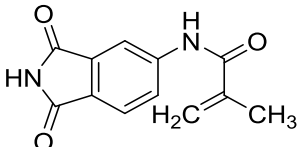
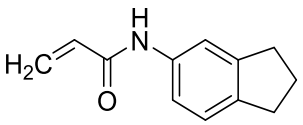
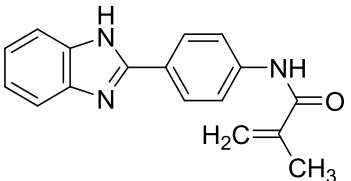
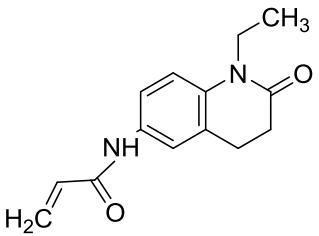
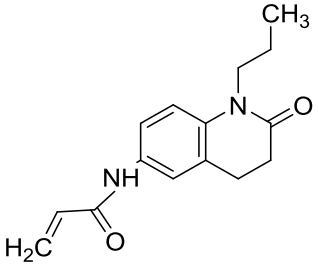
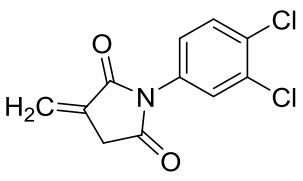
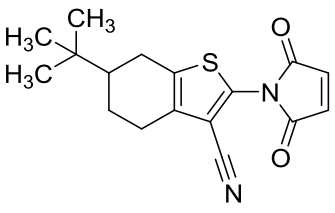
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2	DC-RC-039	AN-919/15183007	Specs	-4.730
3	DC-RC-022	M074-0694	ChemDiv	-3.637
4	DC-RC-072	AK-968/41922636	Specs	-3.556
5	DC-RC-008	1037-1122	ChemDiv	-3.376
6	DC-RC-021	M074-0516	ChemDiv	-3.195
7	DC-RC-061	AB-337/13036006	Specs	-2.806
8	DC-RC-011	4238-0006	ChemDiv	-2.360
9	DC-RC-068	AG-205/14231021	Specs	-2.210
10	DC-RC-103	AB-337/13036263	Specs	-1.704
11	DC-RC-023	Y021-0860	ChemDiv	-0.984
12	DC-RC-067	AN-970/40920551	Specs	-0.901
13	DC-RC-077	AA-516/12432384	Specs	0.611
14	DC-RC-034	AK-968/37173253	Specs	0.655
15	DC-RC-028	AQ-360/42595901	Specs	0.667
16	DC-RC-057	AH-262/34334028	Specs	0.706
17	DC-RC-026	AS-871/34823013	Specs	0.802
18	DC-RC-025	M381-2881	ChemDiv	1.651
19	DC-RC-043	AE-848/11827160	Specs	1.704
20	DC-RC-038	AK-968/15611698	Specs	1.724
21	DC-RC-083	AI-204/31701043	Specs	1.858
22	DC-RC-081	AR-360/42760396	Specs	1.898
23	DC-RC-066	AE-848/32762024	Specs	2.216
24	DC-RC-003	5511490	ChemBridge	2.224
25	DC-RC-014	0933-0015	ChemDiv	2.354
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27	DC-RC-080	AN-970/40920625	Specs	2.556
28	DC-RC-091	AO-365/15162219	Specs	2.618
29	DC-RC-005	1831-7638	ChemDiv	2.679
30	DC-RC-019	8019-9525	ChemDiv	2.721
31	DC-RC-010	1000-0138	ChemDiv	2.908
32	DC-RC-006	2188-1675	ChemDiv	2.970
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35	DC-RC-073	AH-262/01728005	Specs	3.619
36	DC-RC-017	1831-6582	ChemDiv	3.786
37	DC-RC-020	F517-0048	ChemDiv	3.886
38	DC-RC-030	AS-871/43118758	Specs	3.892
39	DC-RC-069	AG-690/40124728	Specs	4.073
40	DC-RC-002	5331004	ChemBridge	4.131

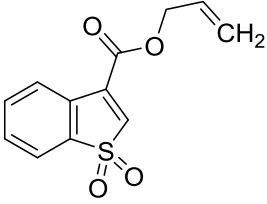
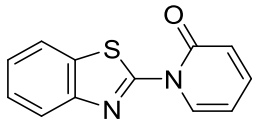
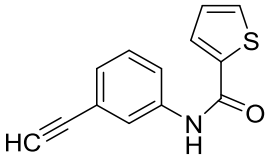
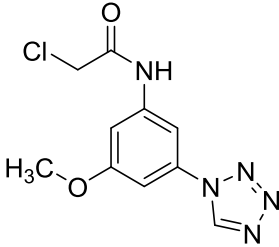
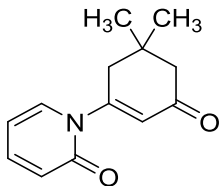
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44	DC-RC-036	AJ-264/34032056	Specs	4.773
45	DC-RC-071	AK-968/37173229	Specs	4.773
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47	DC-RC-094	AC-907/34123034	Specs	5.133
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51	DC-RC-118	AK-968/11532043	Specs	6.452
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87	DC-RC-012	8004-7004	ChemDiv	25.938
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116	DC-RC-085	AN-648/15240030	Specs	87.025
117	DC-RC-070	AH-487/41801493	Specs	89.209
118	DC-RC-119	AC-907/15498023	Specs	92.765
119	DC-RC-105	AN-056/25013017	Specs	97.320
120	DC-RC-047	AG-205/06782028	Specs	104.124

The DC-Rho is the lead compound with identifier DC-RC-063.

Table S3. The structures of twelve top-score compounds, and their inhibitory activities against the nucleotide exchange rate of RhoA.

Compound ID	Compound structure	Inhibition% at 100 μ M	Inhibition% at 50 μ M
DC-RC-008		6.31 \pm 3.24	13.50 \pm 2.79
DC-RC-012		9.58 \pm 2.60	7.91 \pm 1.06
DC-RC-014		15.27 \pm 2.78	14.13 \pm 3.18
DC-RC-022		8.16 \pm 2.81	4.59 \pm 6.69
DC-RC-023		11.19 \pm 4.80	6.52 \pm 1.60
DC-RC-024		11.18 \pm 2.68	7.11 \pm 2.75
DC-RC-040		20.94 \pm 4.77	18.63 \pm 1.67

DC-RC-063		99.97±0.01	98.87±0.01
DC-RC-069		22.62±6.84	20.55±3.07
DC-RC-070		9.12±1.20	11.08±1.12
DC-RC-077		16.89±3.32	16.98±4.58
DC-RC-108		17.17±7.47	18.99±2.62

Quantification was calculated from three independent assays and the error bars represent \pm SD for triplicate experiments. The DC-Rhoin is the lead compound with identifier DC-RC-063.

Table S4. Effect of DC-Rhoi04 on the activity of 180 human kinases.

Kinase Target	Protein activity% (50 μM)	Kinase Target	Protein activity% (50 μM)
Abl(h)	83	JAK1(h)	88
ACK1(h)	82	JAK2(h)	90
ACTR2(h)	101	JAK3(h)	89
ALK(h)	100	JNK3(h)	101
Arg(h)	71	KDR(h)	94
AMPK α 1(h)	85	Lck(h)	94
AMPK α 2(h)	85	LIMK1(h)	97
A-Raf(h)	115	LIMK2(h)	110
ARK5(h)	91	LKB1(h)	85
ASK1(h)	93	LOK(h)	129
Aurora-A(h)	93	Lyn(h)	89
Aurora-C(h)	127	LRRK2(h)	99
Bmx(h)	80	LTK(h)	92
BRK(h)	103	MAK(h)	105
BTK(h)	75	MAPK1(h)	114
B-Raf(h)	96	MAPK2(h)	109
CaMKI(h)	90	MAP4K3(h)	84
Cdc7/cyclinB1(h)	90	MAP4K4(h)	103
CDK1/cyclinB(h)	88	MAP4K5(h)	93
CDK2/cyclinA(h)	92	MAPKAP-K2(h)	109
CDK2/cyclinE(h)	111	MEK1(h)	97
CDK3/cyclinE(h)	98	MEK2(h)	107
CDK4/cyclinD3(h)	89	Mer(h)	89
CDK5/p25(h)	100	Met(h)	78
CDK5/p35(h)	98	MLCK(h)	82
CDK6/cyclinD3(h)	115	MLK2(h)	84
CDK7/cyclinH/MAT1(h)	113	MSK2(h)	78
CDK9/cyclin T1(h)	99	MST1(h)	88
CDK12/cyclinK(h)	76	MST2(h)	101
CDK13/cyclinK(h)	125	MST3(h)	97
CDK14/cyclinY(h)	93	MST4(h)	111
CDK18/cyclinY(h)	95	MuSK(h)	110
CDKL1(h)	110	MYLK2(h)	90
CHK1(h)	99	MYO3B(h)	98
CHK2(h)	108	NDR2(h)	90
CK1 δ (h)	82	NEK1(h)	73
CK1(y)	89	NEK2(h)	111
CK2(h)	82	NEK3(h)	83

CSK(h)	99	NIM1(h)	100
c-RAF(h)	93	NLK(h)	90
cSRC(h)	105	NUAK2(h)	108
DAPK1(h)	94	p70S6K(h)	85
DAPK2(h)	85	PAK1(h)	93
DRAK1(h)	87	PAK2(h)	100
DRAK2(h)	121	PAR-1B α (h)	114
eEF-2K(h)	118	PEK(h)	95
EGFR(h)	80	PDGFR α (h)	84
EphA5(h)	77	PDK1(h)	107
EphB2(h)	85	PhK γ 1(h)	86
EphB4(h)	91	PhK γ 2(h)	85
ErbB4(h)	82	Pim-1(h)	74
FAK(h)	93	Pim-2(h)	88
Fer(h)	92	PKA(h)	89
Fes(h)	81	PKB α (h)	93
FGFR1(h)	141	PKB β (h)	92
FGFR2(h)	106	PKB γ (h)	97
FGFR4(h)	98	PKD3(h)	85
Fgr(h)	80	PKG1 α (h)	94
Flt1(h)	99	PKR(h)	97
Flt3(h)	130	Plk1(h)	106
Flt4(h)	81	Plk3(h)	108
Fms(h)	102	Plk4(h)	90
Fyn(h)	139	PRAK(h)	119
GCK(h)	111	PRK1(h)	97
GCN2(h)	100	PRK2(h)	104
GRK1(h)	94	RIPK2(h)	89
GRK2(h)	107	ROCK-I(h)	87
GRK5(h)	91	ROCK-II(h)	96
GRK7(h)	89	Rse(h)	101
GSK3 β (h)	93	Rsk1(h)	74
Hck(h)	85	Rsk2(h)	104
Hck(h) activated	91	Rsk3(h)	80
IGF-1R(h)	113	Rsk4(h)	133
IGF-1R(h), activated	97	SAPK2a(h)	87
IKK α (h)	95	SGK(h)	88
IKK β (h)	76	Src(1-530)(h)	77
IKK ϵ (h)	97	SRPK1(h)	90
IR(h)	125	Syk(h)	110
IR(h), activated	92	TAK1(h)	102
IRE1(h)	93	TAO1(h)	99
IRR(h)	97	TAO2(h)	75

IRAK1(h)	99	Tec(h) activated	82
IRAK4(h)	83	TGFBR1(h)	103
Itk(h)	72	TGFBR2(h)	95
ULK1(h)	88	ZAK(h)	115
ULK2(h)	101	ZAP-70(h)	105
VRK1(h)	91	ATM(h)	92
Wee1(h)	111	ATR/ATRIP(h)	91
WNK1(h)	104	PI3 Kinase (p120□)(h)	95
Yes(h)	95	PIP5K1□(h)	98

Table S5. The sequences of siRNA used in the experiments.

	sense (5'-3')	antisense (5'-3')
siRhoA-1	CUAUGAUUAUUAACGAUGUTT	ACAUCGUUAAUAAUCAUAGTT
siRhoA-2	GGCUUUACUCCGUAACAGATT	UCUGUUACGGAGUAAAGCCCT
siRhoA-3	GUACAUGGAGUGUUCAGCAAAC	GUUUGCUGAACACUCCAUGUAC
siRhoA-4	GGAAAGACAUGCUUGCUCauc	GAUGAGCAAGCAUGUCUUUCCA
siRhoA-5	GAAAGCAGGUAGAGUUGGCUU	GAAGCCAACUCUACCUGCUUU
siRac1-1	UGUAGGUAAAACUUGCCUACU	AGUAGGCAAGUUUUACCUACA
siRac1-2	UGCAUUUCCUGGAGAAUAUUAU	AUAUAUUCUCCAGGAAAUGCA
siRac1-3	UCGUUCUUGGUCCUGUCCCUU	AAGGGACAGGACCAAGAACGA
siRac1-4	AGUUCAGACUCACAUUCUAUU	AAUAGAAUGUGAGUCUGAACU
siCdc42-1	UCAAGUAUGUGGAGUGUUCUG	CAGAACACUCCACAUACUUGA
siCdc42-2	UGCCUGAGAUAAACUCACCACU	AGUGGUGAGUUUAUCUCAGGCA
siCdc42-3	UACUGCAGGGCAAGAGGAUUUAU	AUAAUCCUCUUGCCCUGCAGUA
siCdc42-4	UGACGUCAGGUGCGUGCCCUU	AGGGGCACGCACCUGACGUCA
NC-siRNA	UUCUCCGAACGUGUCACGUdTdT	ACGUGACACGUUCGGAGAAAdTdT