

Supplementary materials

Table S1. The network topology analysis of the overlapped genes between liver cancer related genes and (20S)G-Rh2 target proteins. Three topological indicators including degree of distribution, betweenness centrality, and closeness centrality represent the importance of these 25 genes in the background network of human genes. “Ratio R/S” represents the propensity of these 25 potential targets to bind (20S)G-Rh2 based on the mass spectrometry data, with a smaller ratio value representing a greater tendency to bind (20S)G-Rh2.

Gene	Degree	Betweenness Centrality	Closeness Centrality	Ratio R/S
<i>STAT3</i>	108	0.17989041	0.42120344	0.943045
<i>HSP90AA1</i>	91	0.06761578	0.4091858	0.565545
<i>TRIP13</i>	83	0.15713539	0.37716485	0.726409
<i>HSPB1</i>	44	0.04918154	0.36865204	0.732591
<i>SFN</i>	42	0.05349587	0.37837838	0.905909
<i>ACTB</i>	40	0.03128229	0.38181818	0.956295
<i>KRT18</i>	34	0.02438184	0.37191651	0.791659
<i>NPM1</i>	33	0.04089923	0.34406085	0.684182
<i>HSPA5</i>	31	0.03642254	0.34690265	0.401864
<i>ITGB1</i>	20	0.02094208	0.32272228	0.681409
<i>KRT8</i>	15	0.00602339	0.33295583	0.742864
<i>HSPA9</i>	14	0.01784429	0.3442623	0.447409
<i>MSH2</i>	13	0.00579711	0.31160572	0.513909
<i>HSPA4</i>	12	0.00944665	0.34854772	0.553795
<i>PHB</i>	12	0.00667437	0.33220339	0.595886
<i>HSP90B1</i>	10	0.0028511	0.30561331	0.739227
<i>ANXA2</i>	6	0.0013638	0.30753138	0.577295
<i>IQGAP1</i>	6	0.00076746	0.30371901	0.605591
<i>COX5A</i>	6	0.00552004	0.28201439	0.918659
<i>CD44</i>	5	0.00379146	0.28543689	0.602045
<i>FASN</i>	4	0.00403451	0.27735849	0.355182
<i>MSH6</i>	4	0.00027764	0.28296439	0.837250
<i>BSG</i>	2	0.00010345	0.2527945	0.270114
<i>LRRC59</i>	2	0.00006077	0.26320501	0.996250
<i>PC</i>	0	0	0	0.766182

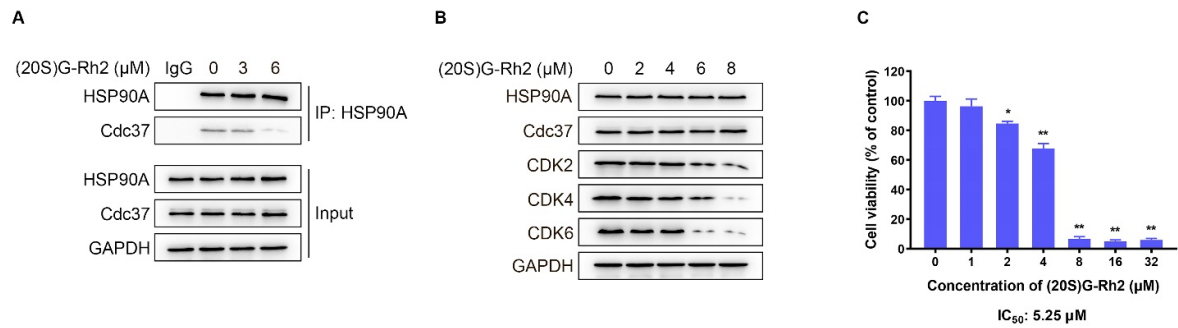


Figure S1. (20S)G-Rh2-induced interaction disruption of HSP90A and Cdc37, degradation of CDKs, and anti-proliferation effect of SK-HEP-1 cells. (A) Immunoprecipitation was performed with whole-cell lysate under treatment with the indicated concentrations of (20S)G-Rh2 for 24 h, and the interaction was analyzed by an immunoblot. (B) Protein levels of CDKs in SK-HEP-1 cells treated with (20S)G-Rh2 were determined by an immunoblot. (C) SK-HEP-1 cells were treated with the indicated concentrations of (20S)G-Rh2 for 48 h, and the cell viability was determined by MTT assay. All data are shown as the mean \pm SD of experiments performed in triplicate. A two-tail Student's *t*-test was used for statistical analyses (* p < 0.01, ** p < 0.001).

Table S2. Primers for vector construction.

Primer Description	Sequence
HSP90A_N-F	5'- CGGGATCCATGGAGGAGGAGGAGGTTGAGAC -3'
HSP90A_N-R	5'- GCCTCGAGATTTCAGGTTTGTCTTCCGACTCTTTC -3'
HSP90A_MC-F	5'- CGGGATCCGAAGAGCTCAACAAAACAAAGCCCCATC -3'
HSP90A_MC-R	5'- GCCTCGAGATAAGGGGTGGCATTCTTCAGTTACAG -3'
MC_R413V-F	5'- GCAAAATTTTGAAAGTTATCGTTAAGAATTTGGTCAAAAAATGC -3'
MC_R413V-R	5'- GCATTTTTTGACCAAATTCTTAACGATAACTTTCAAATTTTGC -3'
MC_Q454E-F	5'- CTTGGAATACACGAAGACTCTGAAAATCGGAAGAAG -3'
MC_Q454E-R	5'- CTCTTCCGATTTTCAGAGTCTTCGTGTATTCCAAG -3'

Table S3. Primers for qRT-PCR.

Gene Name	Sequence
CDK2-F	5'- ATGGATGCCTCTGCTCTCACTG -3'
CDK2-R	5'- CCCGATGAGAATGGCAGAAAGC -3'
CDK4-F	5'- CCATCAGCACAGTTCGTGAGGT -3'
CDK4-R	5'- TCAGTTCGGGATGTGGCACAGA -3'
CDK6-F	5'- GGATAAAGTTCCAGAGCCTGGAG -3'
CDK6-R	5'- GCGATGCACTACTCGGTGTGAA -3'
ACTB-F	5'- CACCATTGGCAATGAGCGGTTTC -3'
ACTB-R	5'- AGGTCTTTGCGGATGTCCACGT -3'