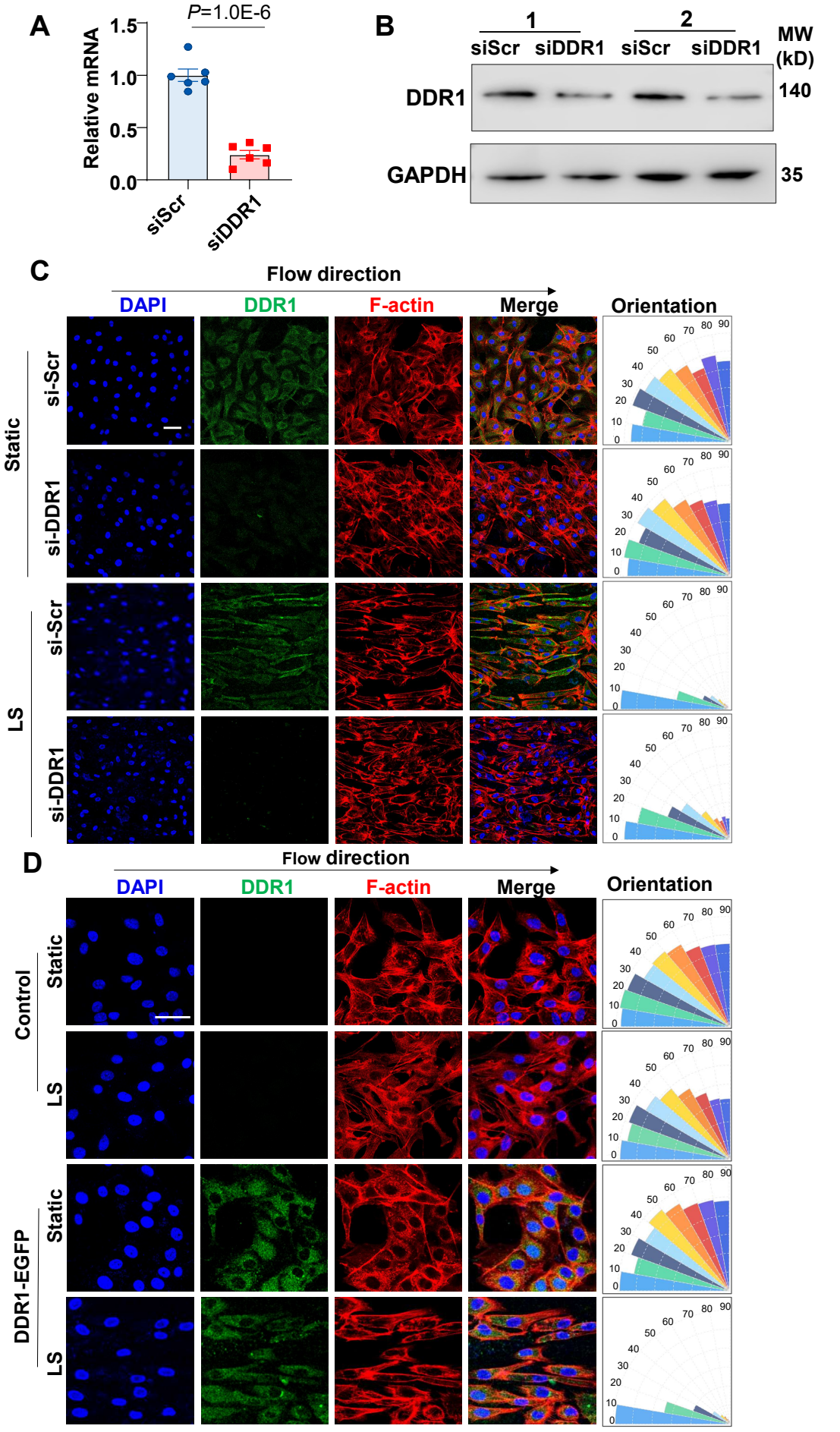

Figure S1. DDR1 is required for EC alignment with flow.

Figure S1. DDR1 is required for EC alignment with flow.
(A) The knockdown efficiency of DDR1 in HUVECs assessed by RT-qPCR. n=6 biological replicates. Data were expressed as the means ± SEM and analyzed by two-tailed unpaired t-test. (B)The knockdown efficiency of DDR1 confirmed by western blotting in HUVECs transfected with siRNAs specific for DDR1 or scrambled siRNA. Two biological replicates were showed. (C) Left: Immunofluorescence of F-actin and DDR1 in HUVECs transfected with DDR1-siRNA or scrambled control siRNA and subjected to static condition or laminar shear for 24h. Right: Quantification of alignment by measuring the orientation angle. n = 9 images from 3 biological replicates. (D) Left: Immunofluorescence of F-actin and DDR1 in NIH3T3 cells infected with DDR1-EGFP adenovirus and subjected to static condition or laminar shear for 24h. Right: Quantification of alignment by measuring the orientation angle. n = 9 images from 3 biological replicates. Scale bars, 50 μm.

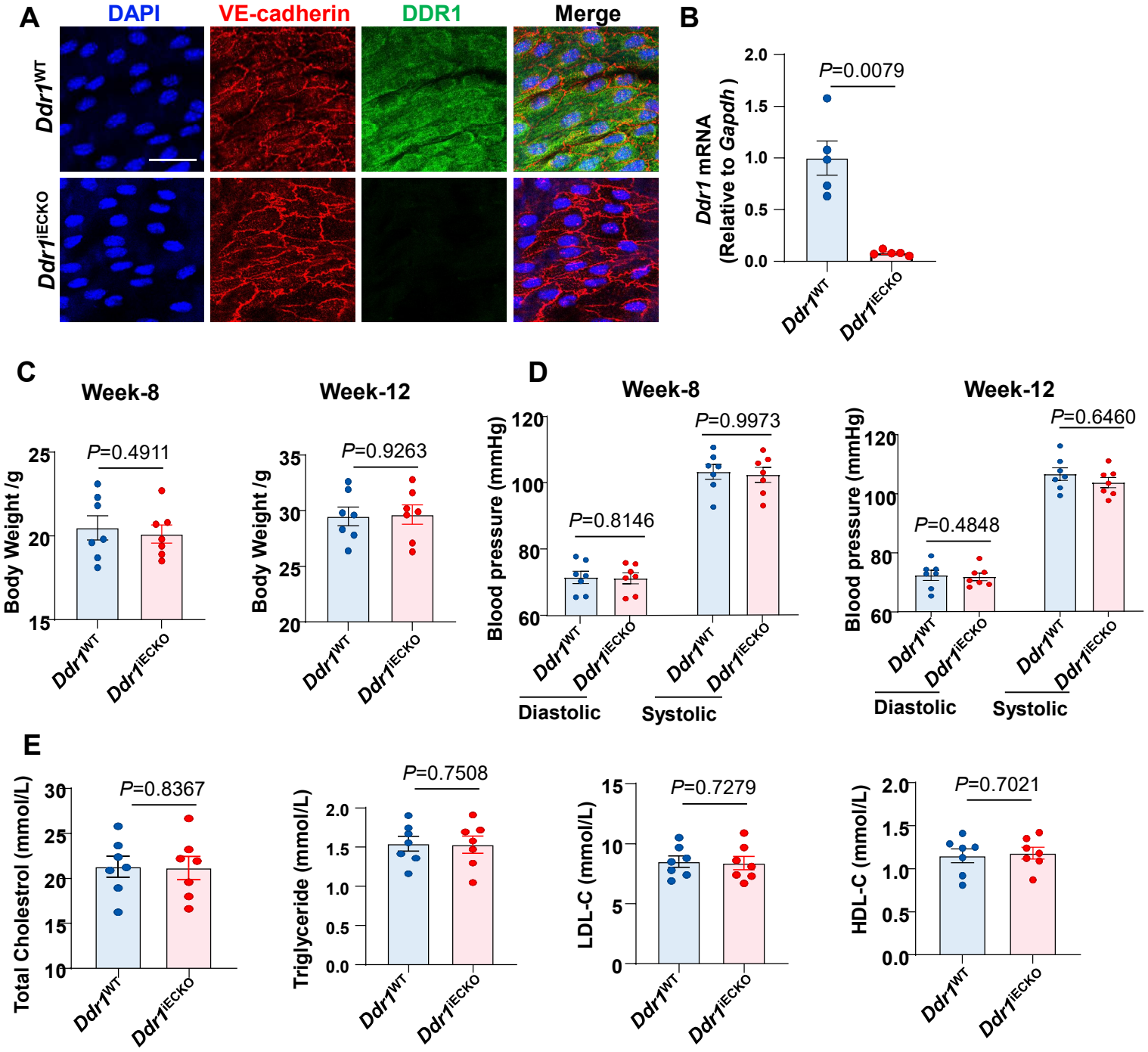

Figure S2. Bodyweights, blood pressures and lipid profile analysis of *Ddr1*^{WT} and *Ddr1*^{iECKO} mice.

(A) En-face staining to determine the expression of DDR1 in the aortas of *Ddr1* ^{WT} and *Ddr1*^{iECKO} mice at 1 week after tamoxifen injection. Scale bar, 50 μm. 3 biological replicates were conducted with similar results. (B) RT-qPCR to verify the efficiency of Ddr1 depletion in *Ddr1*^{iECKO} mice compared with *Ddr1* ^{WT} mice at 1 week after tamoxifen injection. n=5 mice. Data were expressed as the means ± SEM and analyzed by Mann-Whitney test. (C) Body weight of *Ddr1* ^{WT} and *Ddr1*^{iECKO} mice at week-8 (before surgery) and week-12 (4-wk postsurgery). (D) Systolic and diastolic blood pressures of *Ddr1* ^{WT} and *Ddr1*^{iECKO} mice at week-8 and week-12. (E) Total serum cholesterol, triglyceride, LDL-C, and HDL-C level in *Ddr1* ^{WT} and *Ddr1*^{iECKO} mice at 4-wk postsurgery. In (C-E), Data were expressed as the means ± SEM and analyzed by unpaired t-test, n=7 mice.

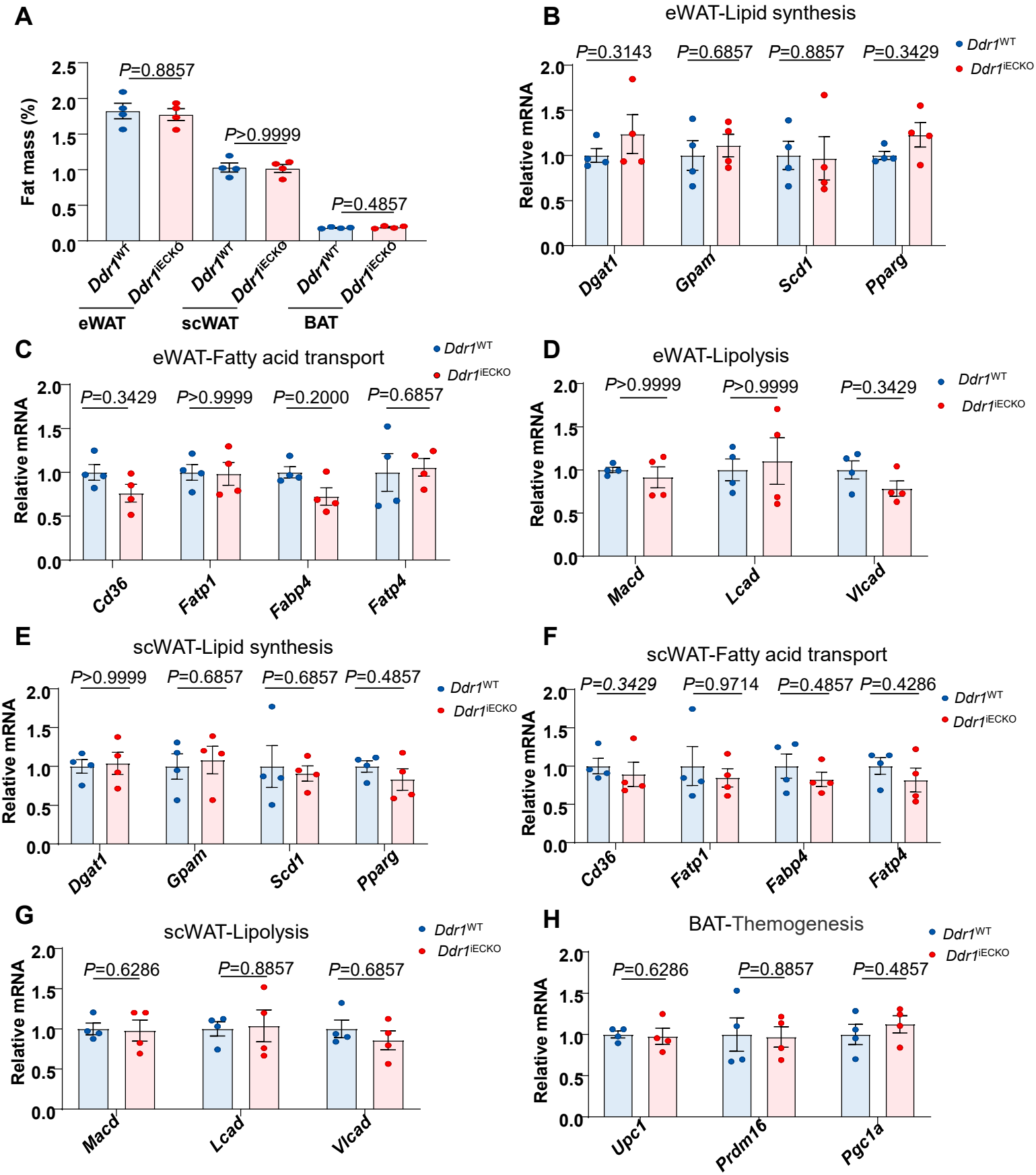

Figure S3. Cdh5-specific DDR1 knockout does not exert a discernible influence on lipid metabolism.

(A) The weight-to-body weight ratio of epididymal white adipose tissue (eWAT), subcutaneous white adipose tissue (scWAT) and brown adipose tissue (BAT) in western-diet-fed *Ddr1* ^{WT} and *Ddr1*^{iECKO} mice. (B-D) RT-qPCR to detect lipid synthesis (B), fatty acid transport (C) and lipolysis (D) of eWAT. n=4 mice. (E-G) RT-qPCR to detect lipid synthesis (E), fatty acid transport (F) and lipolysis (G) of scWAT. n=4 mice. (H) RT-qPCR to detect the themogenesis of BAT. n=4 mice. Data were all expressed as the means ± SEM and analyzed by Mann-Whitney test.

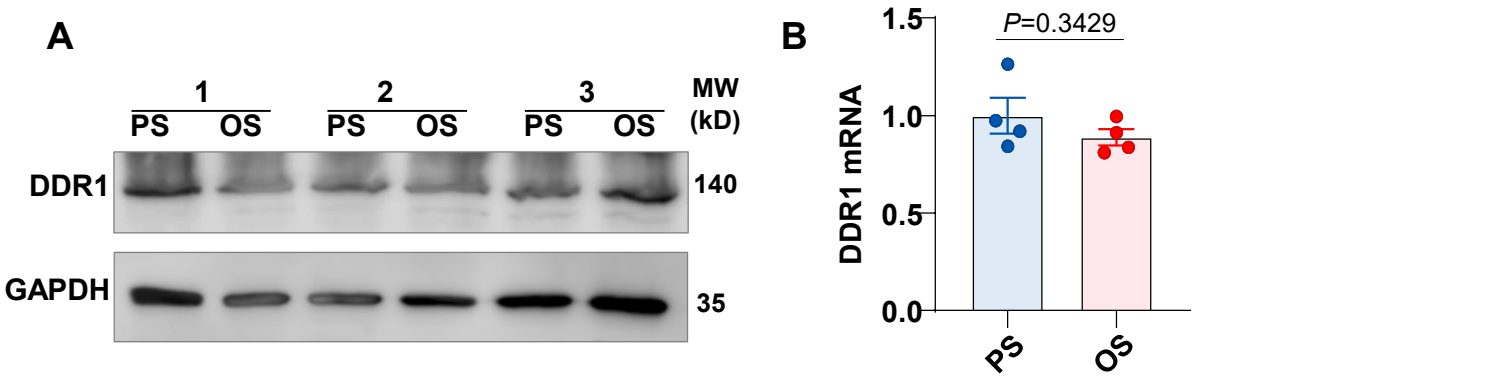

Figure S4. Shear stress does not affect the expression of DDR1 in endothelial cells. (A) Western blotting to detect DDR1 expression in HUVECs subjected to PS or OS for 24h. 3 biological replicates were presented. (B) Quantitative RT-PCR analysis of the expression of DDR1 in HUVECs treated as in (A). n=4 biological replicates. Data were expressed as the means ± SEM and analyzed by Mann-Whitney test.

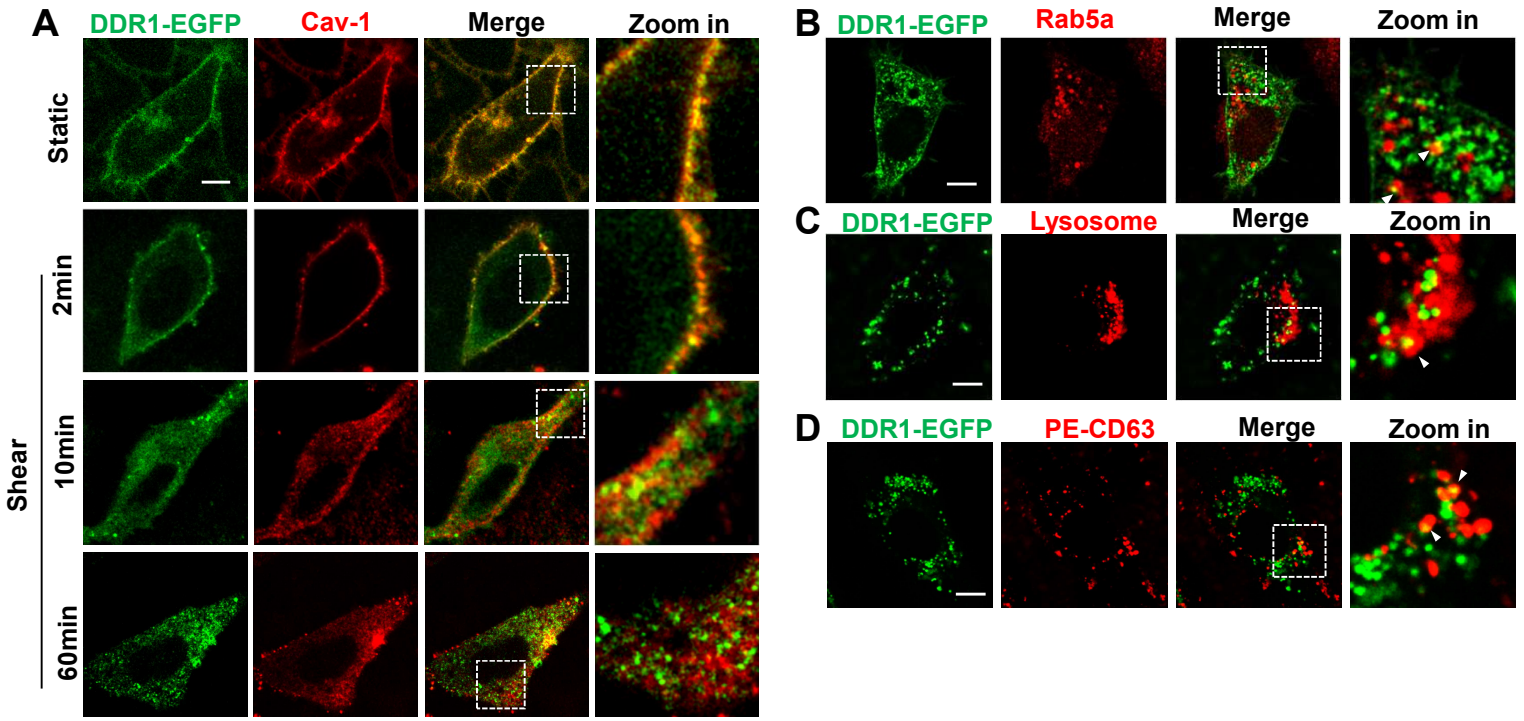

Figure S5. The relationship between DDR1 droplets and lipid rafts, endosomal or exocytotic vesicles.

(A) Immunofluorescence of DDR1-EGFP and lipid raft marker caveolin-1 (Cav-1) in HUVECs, which were infected with DDR1-EGFP adenovirus and subjected to laminar shear. (B) Immunofluorescence of DDR1-EGFP and early endosome marker Rab5A in HUVECs, which were infected with DDR1-EGFP adenovirus and subjected to laminar shear for 1h. (C) Immunofluorescence of DDR1-EGFP and Lyso-Tracker Red in HUVECs, which subjected to laminar shear for 1h. (D) Immunofluorescence of DDR1-EGFP and exosomes marker CD63 in HUVECs, which subjected to laminar shear for 1h. Scale bars, 10 μm. In A-D, experiments were repeated 3 times independently with similar results.

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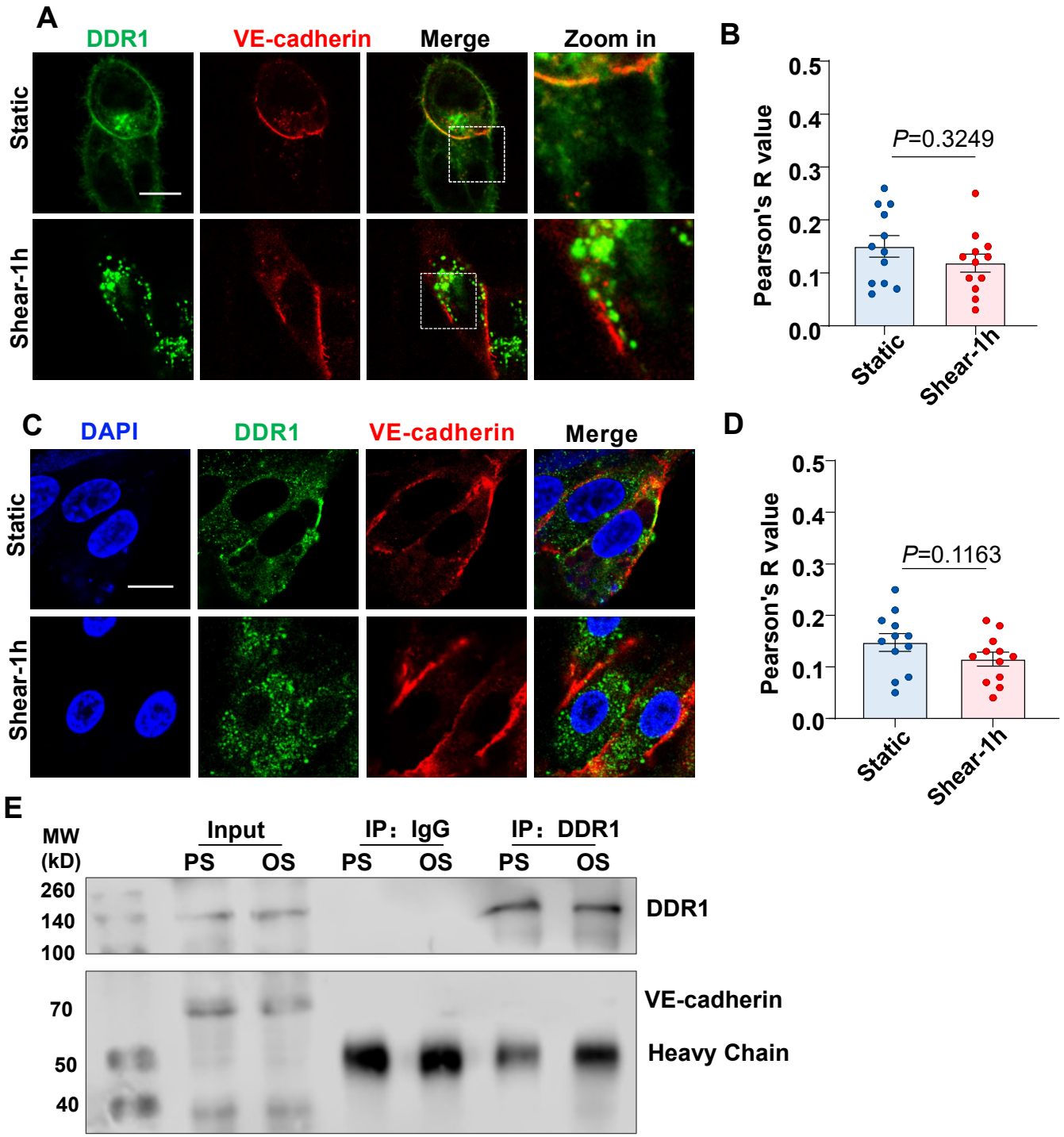

Figure S6. DDR1 has no interaction with VE-cadherin in endothelial cells.
(A) Live cell imaging of DDR1-EGFP and VE-cadherin-Cherry in ECs, which were grown in microfluidic chamber and subjected to laminar shear stress. (B) Colocalization analysis of DDR1-EGFP and VE-cadherin-Cherry in (A). Pearson‘s R value (above threshold) was calculated by ImageJ Fiji software (Analyze-colocalization-coloc2). n = 12 images from 3 biological replicates. (C) Immunofluorescence staining of DDR1 and VE-cadherin in HUVECs subjected to laminar shear stress for 1h or static. (D) Colocalization analysis of DDR1 and VE-cadherin in (C). n = 12 images from 3 biological replicates. Data were all expressed as the means ± SEM and analyzed by Mann-Whitney test. (E) Co-IP assay to detect the interaction between DDR1 and VE-cadherin in HUVECs subjected to PS or OS for 24h. Scale bars, 20 μm.

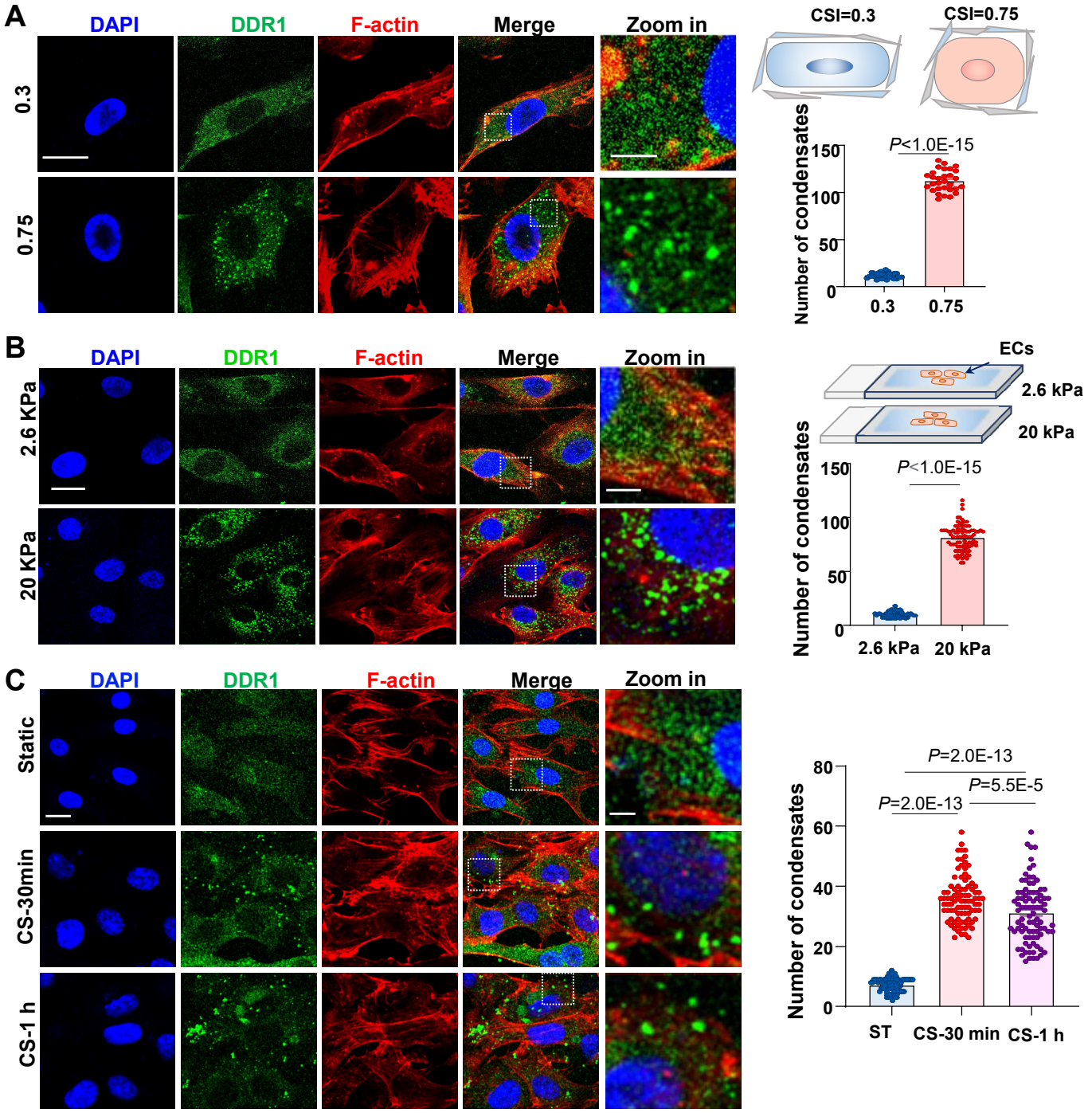

Figure S7. DDR1 can respond to various mechanical stimuli in endothelial cells.
(A) Immunofluorescence and quantification of DDR1 condensates in micropatterned (CSI = 0.30 or CSI = 0.75) HUVECs, PDMS stamp with micropatterned was coated with gelatin. CSI: cell shape index. n=30 cells from 3 biological replicates. Data were analyzed by unpaired t-test. (B) Immunofluorescence and quantification of DDR1 condensates in HUVECs seeded on gelatin-coated gels (2.6 and 20 kPa) for 24h. n=90 cells from 6 biological replicates. Data were analyzed by unpaired t-test. (C) Immunofluorescence and quantification of DDR1 condensates in HUVECs subjected to uniaxial cyclic stretch (15% deformation) or under the static condition. n=90 cells from 3 biological replicates. Data were analyzed by one-way ANOVA followed by Tukey's multiple comparisons test. Scale bars (overview), 20 μm. Data were all expressed as the means ± SEM. Scale bars (zoom in), 4 μm.

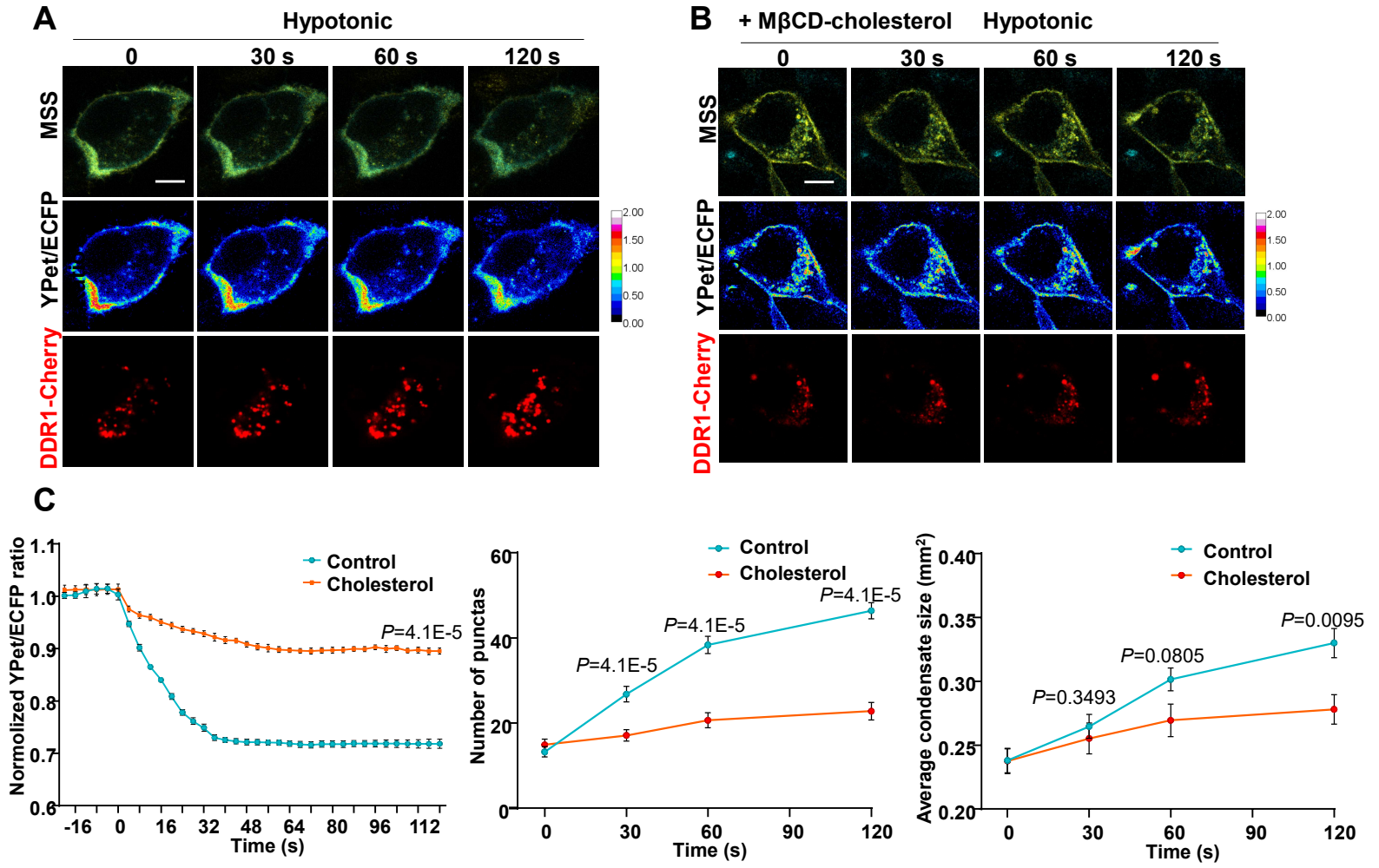

Figure S8. Elevate membrane tension by hypotonic stimulus can promote the DDR1 droplet formation.

(A) The representative living cell images of YPet/ECFP emission ratio and DDR1-Cherry in EA.hy926 ECs after exposure to hypotonic solution. (B) The representative living cell images of YPet/ECFP emission ratio and DDR1-Cherry in ECs pretreated with MβCD-cholesterol and then exposed to hypotonic solution. (C) The average time courses of FRET biosensors and quantification of number and size of DDR1 condensates in ECs exposed to hypotonic solution. n= 9 biological replicates. Data were expressed as the means ± SD, and analyzed by two-tailed Mann-Whitney test. Scale bars, 10 μm.

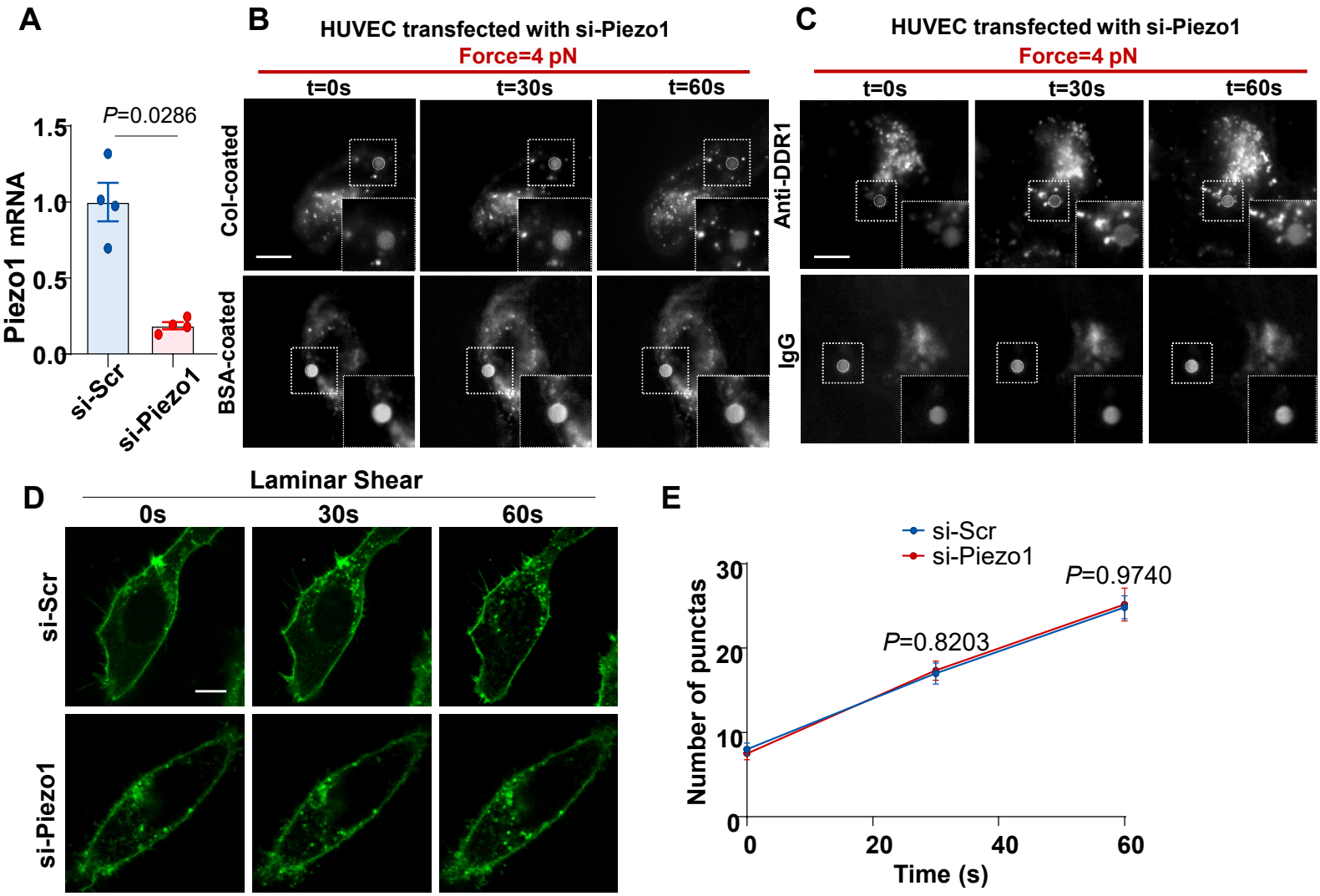

Figure S9. Knocking down piezo1 does not affect the activation of DDR1.
(A) The knockdown efficiency of DDR1 in HUVECs assessed by RT-qPCR. n=4 biological replicates. Data were expressed as the means ± SEM and analyzed by Mann-Whitney test. (B and C) Images of DDR1 condensates formation captured by total internal reflection fluorescence (TIRF) microscopy. HUVECs were transfected with Piezo1-specific siRNA and infected with DDR1 adenovirus. After 48 hours, cells were incubated with collagen/ BSA-coated beads (B) or anti-DDR1/IgG-coated beads (C). Scale bar, 5 μm. Experiments were repeated 3 times independently with similar results. (D) Time-lapse images of DDR1 in HUVECs infected with DDR1-EGFP adenovirus. Cell grown in gelatin-coated microfluidic chamber were subjected to laminar shear stress. (E) Quantification of DDR1 condensates number. Data were expressed as the means ± SEM. n=6 biological replicates. Data were analyzed by Mann-Whitney test. Scale bars, 10 μm.

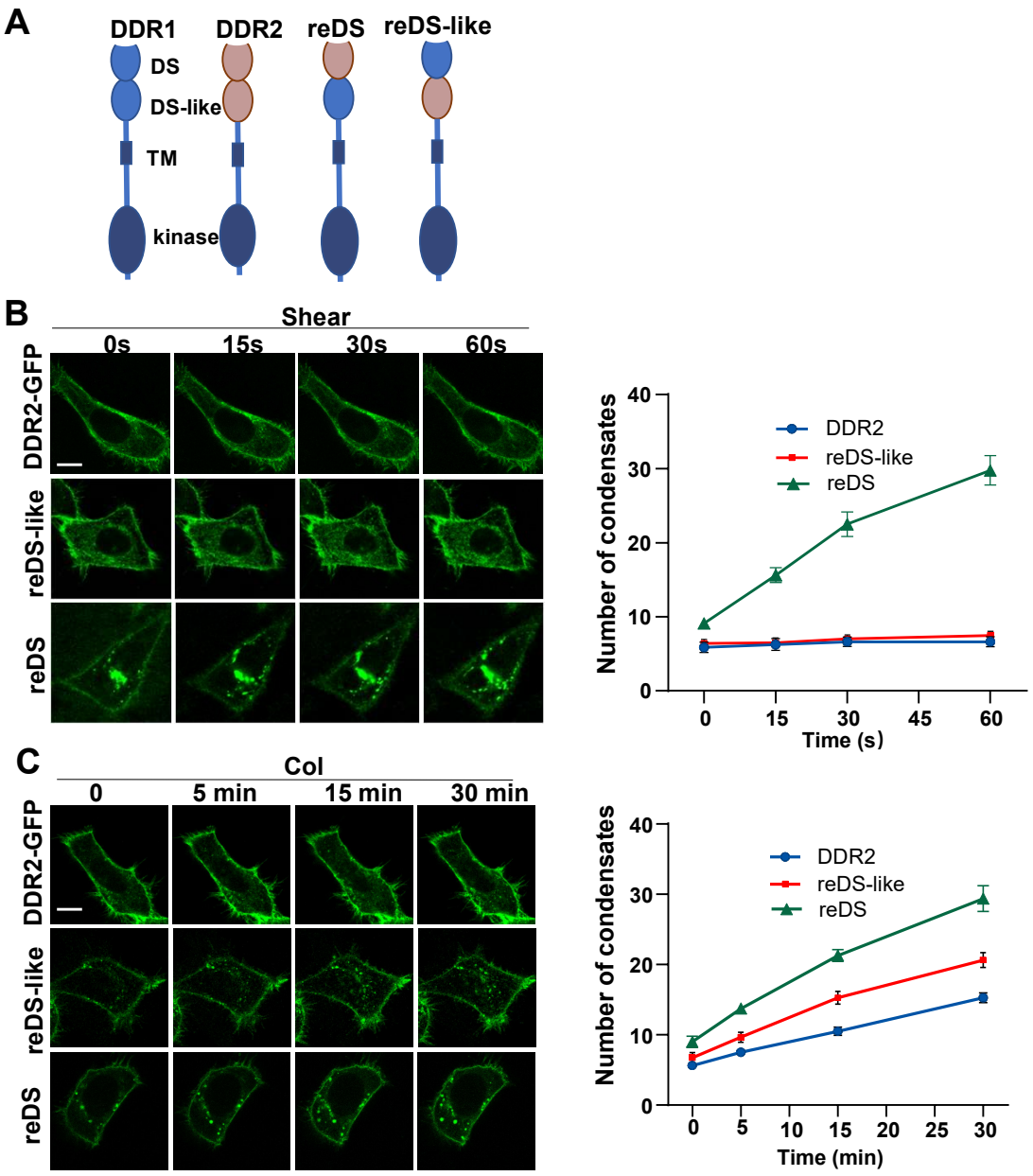

Figure S10. DS-like domain of DDR1 is crucial for shear stress-induced DDR1 droplets formation.

(A) Schematic diagram of DDR1, DDR2, reDS (the DS domain of DDR1 replaced by that of DDR2), reDS-like (the DS-like domain of DDR1 replaced by that of DDR2). (B) Left: live cell imaging of DDR2, reDS or reDS-like in EA.hy926 ECs exposed to laminar shear stress. Right: quantification of DDR1 condensates. n=8 biological replicates. Data were expressed as the means ± SEM. (C) Left: live cell imaging of DDR2, reDS or reDS-like in EA.hy926 ECs after 10μg/ml soluble collagen I stimulation. Right: quantification of DDR1 condensates. n=8 biological replicates. Data were expressed as the means±SEM. Scale bars, 10 μm.

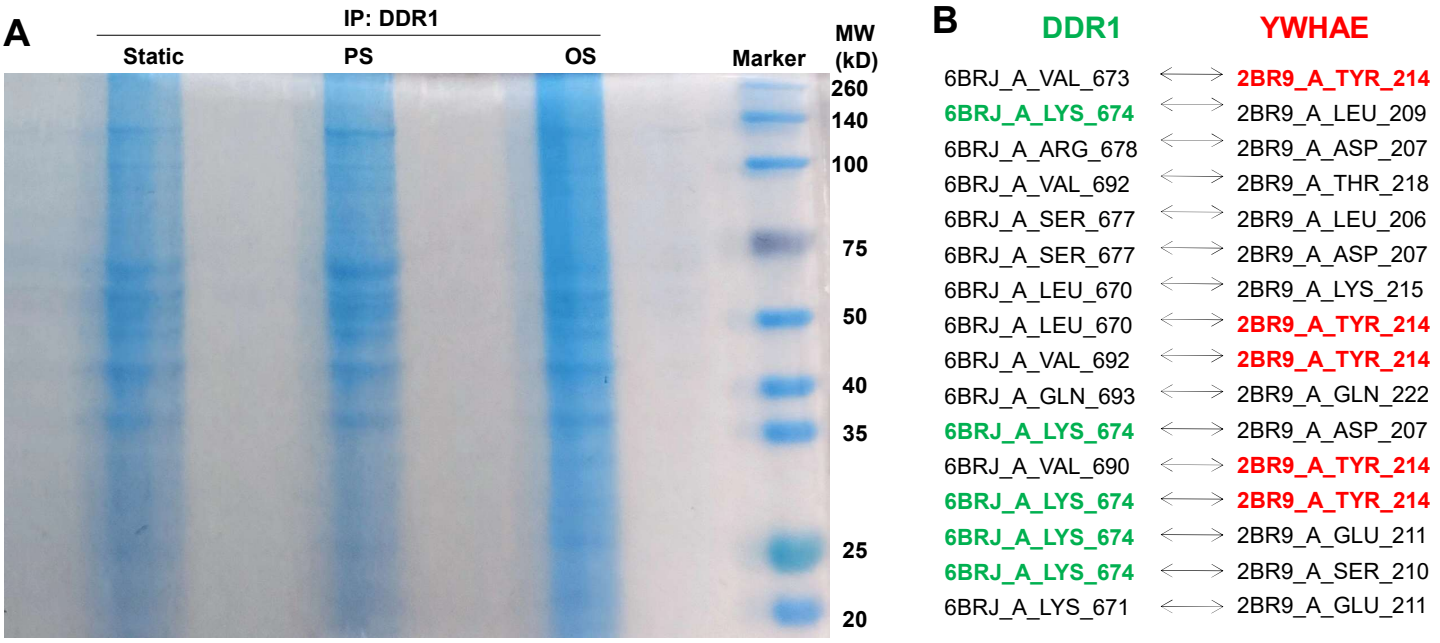

Figure S11. DDR1 can interact with YWHAE by C-terminal domain.
(A) Cellular extracts from HUVECs cultured under the static condition or subjected to PS or OS for 3h were subsequently immunoprecipitated with anti-DDR1 antibody. Eluted proteins were separated on SDS-PAGE and visualized by Coomassie blue staining. Eluted proteins were identified by mass spectrometry analysis. (B) Interface residues contacts of 6BRJ (605~913aa of DDR1) and 2BR9 (1~233aa of YWHAE) predicted by PRISM. The residues Lys674 of DDR1 and Tyr214 of YWHAE were highlighted in green and red, respectively.

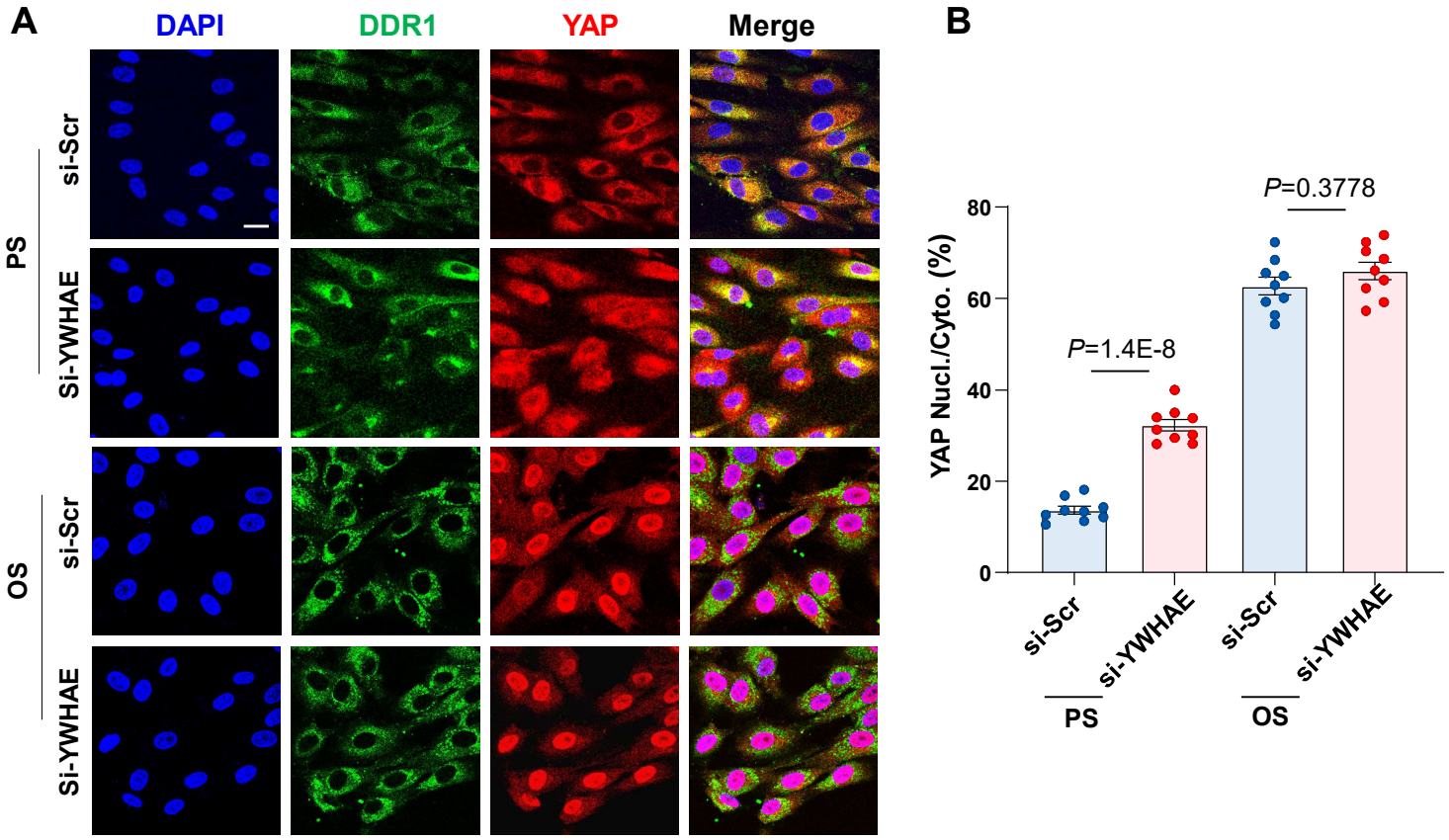

Figure S12. The elimination of YWAHE promotes the nuclear translocation of YAP.
(A) Representative Immunofluorescence staining of DDR1 and YAP1 in HUVECs subjected to PS or OS for 24 hours. (B) Quantification of YAP localization in (A). n= 9 images from 3 biological replicates. 10~15 cells per image. Data were expressed as the means ± SEM and analyzed by two-way ANOVA followed by Tukey's multiply test. Scale bar, 20 μm.

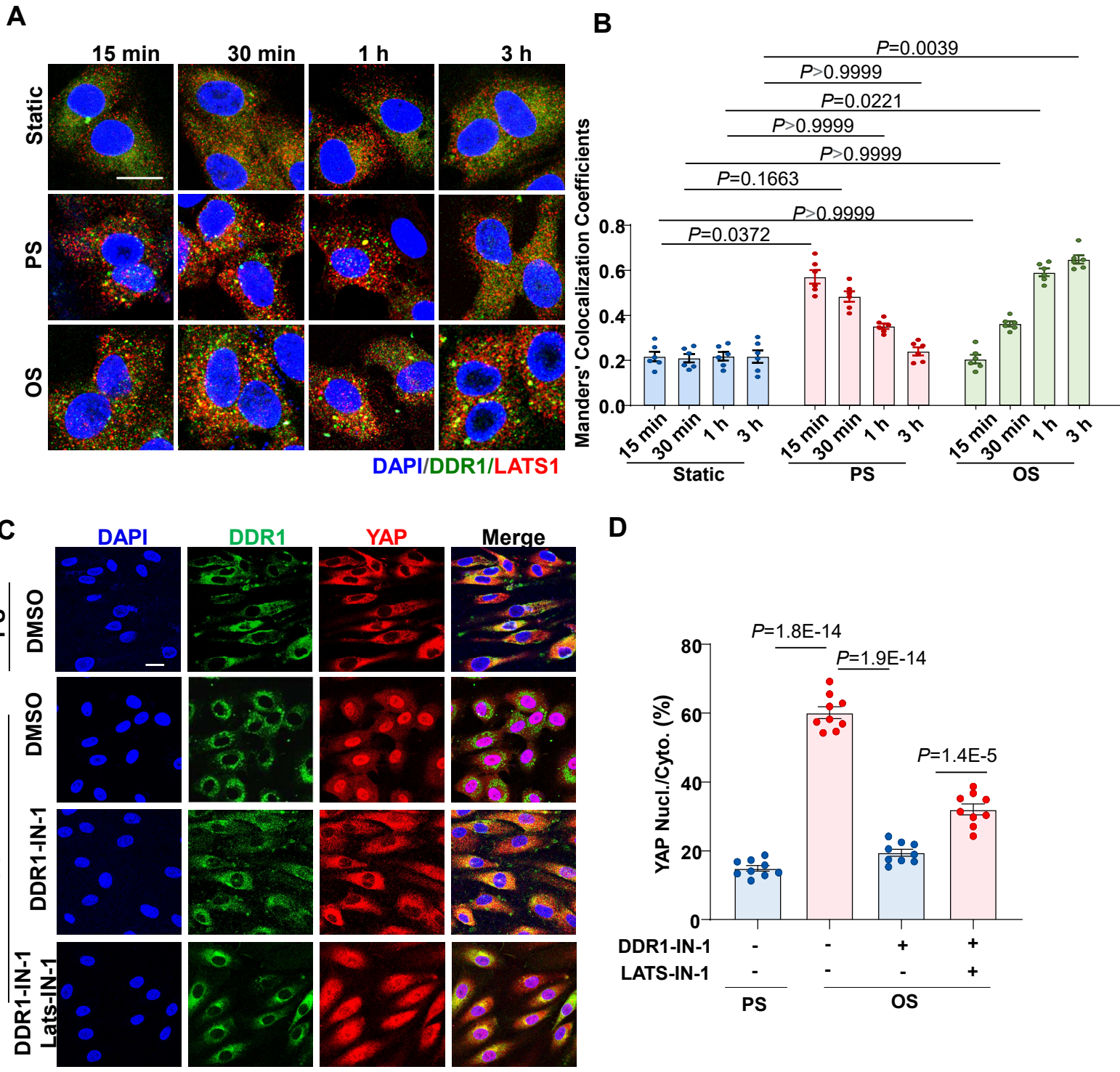

Figure S13. DDR1 can interact with LATS1 to regulate YAP nuclear translocation partially. (A) Representative Immunofluorescence staining of DDR1 and LATS1 in HUVECs subjected to PS or OS for four time periods (15 min, 30 min, 1 h and 3 h). (B) Co-location analysis of DDR1 and LATS1. Manders' colocalization coefficients was calculated by ImageJ Fiji software (Analyze-colocalization-coloc2), representing the proportion of LATS1 (co-located with DDR1) to the total LATS1. n=6 images from 3 biological replicates. Data were expressed as the means ± SEM and analyzed by Kruskal-Wallis test with Dunn's test. (C,D) Immunofluorescence and quantification of YAP localization in HUVECs. The cells were subjected to PS or OS for 24 hours, and treated wit hinhibitors or DMSO. n= 9 images from 3 biological replicates. 10~15 cells per image. Data were expressed as the means ± SEM and analyzed by two-way ANOVA followed by Tukey's multiply test. Scale bars, 20 μm.

SUPPLEMENTARY TABLES

Table S1: 64 proteins selected with a fold-change (OS/PS) > 1.25 or < 0.75 in Co-IP mass spectrometry.

Gene Name	Abundances (Normalized): OS	Abundances (Normalized): PS	Abundances (Normalized): Static	Fold Change (OS/PS)
HSPB1	414789.2388	Not detected	Not detected	∞
PIK3CB	226643.986	Not detected	71159.2542	∞
TPI	129236.2009	Not detected	152846.5244	∞
VCP	40654.493	Not detected	62338.88264	∞
VIM	49547078.08	19489685.16	127189802.8	2.542220547
CKB	737320.8495	307087.6719	326194.486	2.401010907
FUS	338556.8745	145159.7656	149319.4473	2.332305188
PIN1	143548.7231	63813.28125	97453.85217	2.249511705
SFPQ	385847.6719	210576.7344	135991.2527	1.832337618
APOB	241790.6156	136502.4551	200255.2553	1.771327963
YWHAE	381842.5701	219940.7813	57298.45542	1.736115367
FLNB	558885.0254	332616.5703	161435.1003	1.680268139
TXNDC5	2973484.988	1826692.203	2504556.567	1.627797493
LTF	633702.5845	392442.0234	512052.0581	1.614767397
PDIA6	2393447.301	1485056.578	1328970.061	1.61168762
SERPINB3	343245.1051	224773.1875	170386.8543	1.527073175
MBNL1	158607.7221	104213.3516	124500.33	1.521952031
DDX5	2623081.859	1759252.063	7904626.391	1.491021051
NONO	885605.9419	601472.6875	974922.5387	1.472395938
ALDOA	223297.2517	151961.4531	137943.8183	1.469433512
LDHB	956874.0026	662269.3125	559929.2751	1.444841222
EEF1G	658101.9341	473052.75	610593.9586	1.391180865
LYZ	310555.5012	227400.4063	214195.2739	1.365676985
RRBP1	184133.9759	138652.0469	186634.605	1.328029265
ANGPT2	491283.0894	371794.375	483650.0464	1.321383868
GNAI1	305754.1259	234926.125	217983.4941	1.301490526
PHB1	207892.6303	162256.2813	171568.332	1.281260909
PCNA	35264.14275	27803.61523	Not detected	1.268329404
TUFM	304427.1644	243535.5078	176575.4793	1.250031945
S100A8	500146.8482	683905.0625	273734.7413	0.731310346
PHB2	600543.7433	821629.8125	544927.6193	0.730917664
TUBB6	223063.0595	307143.4375	239724.5662	0.726250449
DSC1	841909.9922	1191202.516	1110858.381	0.706773182
RPN1	297375.6361	424372.625	206574.1289	0.700741798
FSCN1	356627.5862	510809.5		0.698161616
A2M	4455419.437	6428015.553	13474984.94	0.69312518
CCT2	83675.17322	121838.6797	95556.61598	0.68677019

FLNA	517993.8032	765010.0781	150108.7947	0.677107162
FLG2	628103.6432	939397.0625	706090.3212	0.668624236
CRIP2	195119.3378	293467.7813	150047.159	0.664874819
LRRC59	94290.24725	142262.3438	88410.98399	0.662791325
PXDN	205745.4913	310519.1875	123220.499	0.662585436
MIF	305178.9154	462720.7969	222825.7556	0.659531444
TUBB2C	2933402.05	4458585.703	1668500.896	0.657922096
NCL	277883.2042	423537.3125	276165.7562	0.656100882
GSR	534675.7329	821973.8125	494052.2251	0.650477819
SLC25A6	94502.69825	145730.6406	146630.8039	0.648475145
RPS4X	7967927.839	12363208.44	13703819.56	0.644487058
SET	51169.82559	82365.32813	42593.30066	0.621254437
RAN	782599.1111	1260666.75	746915.9318	0.620781909
LCN1	146154.2419	243398.125	140887.416	0.600473984
IBA57	106392.6437	182819.1094	183729.8119	0.581955814
TUBA1C	4782642.911	8434845.668	4590357.923	0.567010127
RACK1	346625.661	624345.4063	151372.8418	0.555182528
PTMAP7	306651.9555	557063.7813	522424.1056	0.550479076
DDX3X	146476.5173	277693.8125	363848.0347	0.527474905
DSG1	941016.4541	1937544.859	978878.5812	0.485674667
ERP70	105887.4437	225026.5313	59177.73485	0.470555375
CAPZA2	74534.69717	160005.4844	153121.4909	0.46582589
DDX6	131358.6917	290641.5313	213603.618	0.451961188
CLTC	85728.69801	219999.25	80074.51422	0.389677228
C1R	55129.98609	147060.9102	261390.9066	0.374878586
APOH	40771.90243	139749.0352	171549.7699	0.291750869
GAPDH	1226515.331	4847751.625	1103041.324	0.253007049

Table S2: 17 proteins predicted to be physically interacted with DDR1 by PRISM

Gene Name	Abundances (Normalized): OS	Abundances (Normalized): PS	Fold Change (OS/PS)	Identifier of protein	Binding energy predicted by PRISM
PIK3CB	226643.986	Not detected	∞	AF-P42338-F1	-16.58
PIN1	143548.7231	63813.28125	2.249511705	AF-Q13526-F1	-18.17
YWHAE	381842.5701	219940.7813	1.736115366	2BR9	-17.63
TXNDC5	2973484.988	1826692.203	1.627797493	3WGD	-22.92
LTF	633702.5845	392442.0234	1.614767397	AF-P02788-F1	-2.01
PDIA6	2393447.301	1485056.578	1.611687619	AF-Q15084-F1	-8.54
ANGPT2	491283.0894	371794.375	1.321383868	AF-O15123-F1	-56.2
YWHAQ	Not detected	136783.6563	0	AF-P27348-F1	-42.23
CLTC	85728.69801	219999.25	0.389677228	AF-Q00610-F1	-14.02

RACK1	346625.661	624345.4063	0.555182528	4AOW	-13.72
LCN1	146154.2419	243398.125	0.600473984	AF-P31025-F1	-35.63
SET	51169.82559	82365.32813	0.621254437	AF-Q01105-F1	-22.81
CRIP2	195119.3378	293467.7813	0.664874818	AF-P52943-F1	-3.58
CCT2	83675.17322	121838.6797	0.68677019	AF-P78371-F1	-6.91
FSCN1	356627.5862	510809.5	0.698161616	AF-Q16658-F1	-24.28
RPN1	297375.6361	424372.625	0.700741798	AF-P04843-F1	-14.4
PHB2	600543.7433	821629.8125	0.730917664	AF-Q99623-F1	-35.08

Table S3: Primers for qPCR

Primer name	Forward (5'-3')	Reverse (5'-3')
MCP1	CAGCCAGATGCAATCAATGCC	TGGAATCCTGAACCCACTTCT
E-selectin	TGGTGAGGTGTGCTCATTCC	TGATCTTTCCCGGAACTGCC
KLF4	ACCAGGCACTACCGTAAACACA	GGTCCGACCTGGAAAATGCT
KLF2	CTTCTCTCCCACCGGGTCTA	TAGCCCAAAAATGCCCACCT
CTGF	AGGAGTGGGTGTGTGACGA	CCAGGCAGTTGGCTCTAATC
CYR61	TGAAGCGGCTCCCTGTTTT	CGGGTTTCTTTCACAAGGCG
ANKRD1	AGTAGAGGAACTGGTCACTGG	TGGGCTAGAAGTGTCTTCAGAT
DDR1	CCGACTGGTTCGCTTCTACC	CGGTGTAAGACAGGAGTCCATC
YWHAE	GATTCGGGAATATCGGCAAATGG	GCTGGAATGAGGTGTTTGTCC
PIEZO1	GGCTGTCACTGAGAGGATGTTCA	AGCCACAGCGGATCTGGTA
GAPDH	AAGGTGAAGGTCGGAGTCAA	AATGAAGGGGTCATTGATGG
mGapdh	AGGTCGGTGTGAACGGATTTG	TGTAGACCATGTAGTTGAGGTCA
mDdr1	GCTCTCCAATCCGGCCTAC	CGGGCTCCATATAGTCCCCA
mDgat1	TTCCGCCTCTGGGCATT	AGAATCGGCCCACAATCCA
mGpam	CACACGAGCAGGAAAGATGA	GGACTGCATAGATGCTGCAA
mScd1	TTCTTGCGATACACTCTGGTGC	CGGGATTGAATGTTCTTGTCGT
mPparg	TCAGCTCTGTGGACCTCTCC	ACCCTTGCATCCTTCACAAG
mCd36	ACAGACGCAGCCTCCTTT	GTCGATTTCAGATCCGAACA
mFatp1	CAGTGCCACCAACAAGAAGA	CAGCTCGTCCATCACTAGCA
mFabp4	ACACCGAGATTTCCTTCAAACTG	CCATCTAGGGTTATGATGCTCTTCA
mFatp4	ACTGTTCTCCAAGCTAGTGCT	GATGAAGACCCGGATGAAACG
mMacd	TTACCGAAGAGTTGGCGTATGG	TGCGGAGGGCTCTGTCAC
mLcad	CTCCCTGCGCGTCCTGAG	AAAATGTCATGCTCCGAGGAAAAG
mVlcad	GCCCAGACACACAACCTTTG	CCGAGCCGACTGCATCTC
mUcp1	GTGAACCCGACAACTTCCGAA	TGCCAGGCAAGCTGAAACTC
mPrdm16	TGCTGACGGATACAGAGGTGT	CCACGCAGAACTTCTCGCTAC
mPgc1a	TGCGGGATGATGGAGACA	TCGTTCGACCTGCGTAAAG

Table S4: Primers for plasmid construction

Plasmids	Primer	sequence(5'to3')
DDR1 Point mutants	F-W53A	ATCTCTGCTTCCAGCTCCGCGTCAGATTCCA
	R-W53A	GCGGAGCTGGAAGCAGAGATGTCACTGTCTG

	F-K674A	GATTTCCTGAAAGAGGTGGCGATCATGTCG
	R-K674A	GCCACCTCTTTCAGGAAATCATTCCTGGC
	F-S677A	GAAAGAGGTGAAGATCATGGCGAGGCTCAAGG
	R-S677A	GCCATGATCTTCACCTCTTTCAGGAAATC
	F-C287A	CAGGTCCACGCTAACAACATGCACACG
	R-C287A	AGCGTGGACCTGCATAGCCTGGAAGGC
DDR1(1-669)-EGFP	F-DDR1-669	CTTGGTACCGAGCTCATGGGACCAGAGGCCCTGT
	R-DDR1-669	ACCAGAGCCGAAATCATTCCTGGCATTCTTGGTGG
	F-EGFP	TTCCTGGGCTCTGGTATGGTGAGCAAGG
	R-EGFP	GTGCTGGATATCTGCATTACTTGTACAGCTCGTCCATGCC
DDR1(1-693)-EGFP	F-DDR1-693	CTTGGTACCGAGCTCATGGGACCAGAGGCCCTGT
	R-DDR1-693	ACCAGAGCCCTGCACACACACGCCCAG
	F-EGFP	TGTGCAGGGCTCTGGTATGGTGAGCAAGG
	R-EGFP	GTGCTGGATATCTGCATTACTTGTACAGCTCGTCCATGCC
YWHAE-Cherry	F-YWHAE	CTTGGTACCGAGCTCATGGATGATCGAGAGGATCTGGTGTAC
	R-YWHAE	ACCAGAGCCCTGATTTTCGTCTTCCACGTCCTGC
	F-Cherry	AAATCAGGGCTCTGGTATGGAGGAGGACAA
	R-Cherry	GTGCTGGATATCTGCATTATCCGGATC
YWHAE-Y214A	F-Y214A	ACGCTGAGTGAAGAAAGCGCTAAGGACTCTA
	R-Y214A	GCGCTTTCTTCACTCAGCGTATCCAGTTC
DDR2-EGFP	F-DDR2	CTTGGTACCGAGCTCATGATCCTGATTCCCAGAATGCTC
	R-DDR2	ACCAGAGCCCTCGTCGCCTTGTTGAAGGAG
	F-EGFP	GCGACGAGGGCTCTGGTATGGTGAGCAAGG
	R-EGFP	GTGCTGGATATCTGCATTACTTGTACAGCTCGTCCATGCC
VE-Cadherin-Cherry	F-VE-Cadherin	CTTGGTACCGAGCTCATGCAGAGGCTCATGATGCTCC
	R-VE-Cadherin	ACCAGAGCCATACAGCAGCTCCTCCCGG
	F-Cherry	TGCTGTATGGCTCTGGTATGGAGGAGGACAACATGGCC
	R-Cherry	GTGCTGGATATCTGCATTATCCGGATCCACCACCGGTAC
Opto-YWHAE	F-opto	CTTGGTACCGAGCTCATGAAGATGGACAAAAAGACTATAGTTTGGTTTAGAAG
	R-opto	ACCAGAGCCTCCGGATCCACCA
	F-YWHAE	ATCCGGAGGCTCTGGTATGGATGATCGAGAGGATCTGGTGT
	R-YWHAE	GTGCTGGATATCTGCATTACTGATTTTCGTCTTCCACGTCCTG
reDS-DDR1	F-DS	GGTACCGAGCTCATGATCCTGATTC
	R-DS	CCAGACACAGCCGTAAAGCTC
	F-2	ACGGCTGTGTCTGGAGGGATGGACTCCTGTCTTACA
	R-2	GTGCTGGATATCTGCATTACTTGTACAGCTCGTCCATGCC

reDSlike-DDR1	F-DS	CTTGGTACCGAGCTCATGGGACCAGAGGCCCTGT
	R-DS	CCAGAGGCAGCCATAGAGCTC
	F-DSlike	TGGCTGCCTCTGGCTAGATGGCTTGGTGTCTTACAAT
	R-DSlike	ATCTGATTGGAAGGTGATCTCACTGAAC
	F-3	CCTTCCAATCAGATGTGGTGAACAATTCCTCTCCGG
	R-3	GTGCTGGATATCTGCATTACTTGTACAGCTCGTCCATGCC
DDR1-locked (D189C and F364C)	F-C1	CTTGGTACCGAGCTCATGGGACCAGAGGCCCTGT
	R-C1	ACACCTCCAGAGGCAGCCATAGAG
	F-C2	TGCCTCTGGAGGTGTGGACTCCTGTCTTACACC
	R-C2	GCAGGAGATTTCGCTGAAGAGTAACCAG
	F-3	GCGAAATCTCCTGCATCTCTGATGTGGTGAAC
	R-3	GTGCTGGATATCTGCATTACTTGTACAGCTCGTCCATGCC
mCherry-DDR1 (WT/locked)	F-mCherry	CTTGGTACCGAGCTCATGGTGAGCAAGGGCGAGGA
	R-mCherry	ACCAGAGCCCTTGTACAGCTCGTCCATGCC
	F-DDR1	GTACAAGGGCTCTGGTATGGGACCAGAGGCCCTG
	R-DDR1	GTGCTGGATATCTGCAttaCACCGTGTTGAGTGCATCCTC

Table S5: siRNAs specific for DDR1 and YWHAE

siRNA name	sense (5'-3')
si-DDR1	GAAUGUCGCUUCCGGCGUGUU
si-YWHAE	UGAAAAAGCCUCUAUGUAGUC
si-Piezo1	GCAAGUUCGUGCGCGGAUU

Table S6: Primers for mice genotyping

Primer name	sequence(5'to3')
F-DDR1 flox	TTAGGTAGGACCTGAAAGGACAGG
R-DDR1 flox	GAGTTCTGGATAGCCTGAAGGTTT
F-Cdh5-Cre	CCGGTCGATGCAACGAGTGATGAGG
R-Cdh5-Cre	GCCTCCAGCTTGCATGATCTCCGG

Legends of supplementary videos 1 and 2

Supplementary video 1. Three-dimensional reconstruction of DDR1 droplets in HUVECs under the static conditions. HUVECs were infected with DDR1-EGFP recombinant adenovirus and seeded on gelatin-coated microfluidic chamber.

Supplementary video 2. Three-dimensional reconstruction of DDR1 droplets in HUVECs subjected to laminar flow for 2 minutes. HUVECs were infected with DDR1-EGFP recombinant adenovirus, seeded on microfluidic chamber and then subjected to laminar flow for 2 minutes.