Table S1. Mitral valve interstitial cell deformation (snapshots with strain). Mi, minor axis (micrometres); Ma, major axis (micrometres); AR, aspect ratio; C, cytoplasmic; N, nuclear; AVG, average; s.d., standard deviation.

MVIC deformation		0%			10%			20%			30%		
		Ma	Mi	AR	Ma	Mi	AR	Ma	Mi	AR	Ma	Mi	AR
C	AVG	11.46	4.68	2.46	15.09	4.07	3.68	14.18	2.56	5.68	27.50	2.45	11.10[a]
	s.d.	1.70	0.89	0.11	2.67	0.46	0.22	1.91	0.38	0.26	3.62	0.35	0.52
N	AVG	7.46	3.19	2.32	8.81	2.68	3.47	8.21	1.69	5.05	10.93	1.54	7.43[a]
	s.d.	1.86	0.46	0.20	1.44	0.54	0.46	1.09	0.17	0.43	2.37	0.21	0.55

[a] Cytoplasmic AR is significantly higher than nuclear AR ($p < 0.001$) at hyper-physiological strain levels.

Table S2. Fold regulation for static (0%) group. Only samples that are above or below the fold regulation threshold of 2 are shown.

gene symbol	gene name	fold regulation
SELE	Selectin E	3.12
MMP3	MMP 13	2.73
SELP	Selectin P	2.73
ICAM1	Intracellular CAM 1	2.51
MMP1	MMP 1	2.21
VCAM1	Vascular CAM 1	2.21
ITGA2	Integrin, alpha 2	2.08
ADAMTS5	ADAM metallopeptidase with thrombospondin type 1, motif 5	−11.43
MMP12	MMP 12	−5.49
MMP9	MMP 9	−3.42
ITGA8	Integrin, alpha 8	−3.32
TNC	Tenascin C	−2.59
LOC397571	Collagen, type I, alpha 1	−2.48
COL11A1	Collagen, type XI, alpha 1	−2.25
LAMB3	Laminin, Beta 1	−2.25
MMP16	MMP 16	−2.19

Table S3. Fold regulation for the 20% strain group. Only samples that are above or below the fold regulation threshold of 2 are shown.

gene symbol	gene name	fold regulation
SELL	Selectin L	8.24
LOC100156689	Collagen, alpha-1 (XII) chain-like	4.24
SELP	Selectin P	3.79
MMP8	MMP 8	3.73
ITGA8	Integrin, alpha 8	3.36
MMP15	MMP 15	3.05
VCAN	Versican	2.90
THBS2	Thrombospondin-2-like	2.78
VCAM1	Vascular cell adhesion molecule 1	2.64
CNTN1	Contactin-1-like	2.46
LOC397571	Collagen, type I, alpha 1	2.46
SPP1	Secreted phosphoprotein 1	2.34
ICAM1	Intracellular adhesion molecule-1	2.31
VTN	Vitronectin	2.31
ITGA5	Integrin, alpha 5	2.24
LOC397459	Integrin, alpha M	2.21
THBS1	Thrombospondin 1	2.19
LOC100517053	Integrin, alpha 3	2.15
CTNND1	Catenin, delta 1	2.14
CTGF	Connective tissue growth factor	2.14
SGCE	Sarcoglycan, epsilon	2.06
HAPLN1	Hyaluronan synthase 1	2.06
COL5A1	Collagen, type V, alpha 1	2.06
ITGB2	Integrin, beta 2	2.02
MMP14	MMP 14	−10.99
LAMA1	Laminin, alpha 1	−2.28

Table S4. Fold regulation for the 30% strain group. Only samples that are above or below the fold regulation threshold of 2 are shown.

gene symbol	gene name	fold regulation
CTNND2	Catenin (Cadherin-associated protein), delta 2	6.62
LOC100156689	Collagen alpha-1 (XII) chain-like	5.90
SELL	Selectin L	5.51
VCAN	Versican	4.43
ITGB5	Integrin, beta 5	3.76
ICAM1	Intracellular adhesion molecule-1	3.60
COL8A1	Collagen, type VIII, alpha 1	3.54
VCAM1	Vascular cell adhesion molecule 1	3.39
ITGB2	Integrin, beta 2	3.36
B2M	Beta-2-microglobulin	3.24
THBS1	Thrombospondin 1	3.16
CNTN1	Contactin-1-like	3.00
ADAMTS5	ADAM metallopeptidase with thrombospondin type 1 motif, 5	2.98
MMP15	MMP 15	2.96
LAMB1	Laminin, beta 1	2.86
CTGF	Connective tissue growth factor	2.73
ITGA5	Integrin, alpha 5	2.66
CTNND1	Catenin, delta 1	2.61
THBS2	Thrombospondin-2-like	2.59
COL5A1	Collagen, type V, alpha 1	2.58
MMP2	MMP 2	2.39
FBLN1	Fibulin 1	2.37
ITGA4	Integrin, alpha 4	2.33
ITGB1	Integrin, beta 1	2.32
TIMP2	TIMP metallopeptidase inhibitor 1	2.28
MMP9	MMP 9	2.26
MMP14	MMP 14	2.24
CTNNB1	Catenin, beta 1, 88 kDa	2.22
LOC397571	Collagen, type I, alpha 1	2.20
VTN	Vitronectin	2.16
SGCE	Sarcoglycan, epsilon	2.10
COL3A1	Collagen, type III, alpha 1	2.05
LAMB3	Laminin, Beta 1	−3.24