Molecule Osteoblast cell	#
I <sub>d</sub>	500
I <sub>f act</sub>	0
$I_{f act} + FAK_{act}$	0
I <sub>act</sub>	0
FAK <sub>act</sub>	1000
If act + FAKact	1
$I_{f act} + FAK_{act} + RAS_{d}$	ī
FAK <sub>d</sub>	1
RAS <sub>d</sub>	1000
$I_{f act} + FAK_{act} + RAS_{d}$	0
RASact	0
RAS <sub>act</sub> + RAF <sub>d</sub>	0
$RAF_d$	32
$RAS_{act} + RAF_{d}$	0
RAFact	0
$RAF_{act} + MEK_{d}$	0
MEK <sub>d</sub>	3400
$RAF_{act} + MEK_{d}$	0
MEKact	0
$MEK_{act} + ERK_{d}$	0
ERK <sub>d</sub>	2300
$MEK_{act} + ERK_{d}$	0
ERKact	0
ERK <sub>act</sub> + RUNX2 <sub>d</sub>	0
$ERK_{act} + OTHER$	0
RUNX2 <sub>d</sub>	24
$ERK_{act} + RUNX2_{d}$	0
RUNX2 <sub>act</sub>	0
$RUNX2_{act} + DNA$	0
$OSX_{mon}$	8
$RUNX2_{act} + OSX_{mon}$	0
$OSX_{mon} + DNA$	5
$RUNX2_{act} + OSX_{mon} + DNA$	0
$RUNX2_{act} + OSX_{mon} + DNA + AP1$	0
$OSX_{mul}$	5
$RUNX2_{act} + OSX_{mul}$	0
$OSX_{mul} + DNA$	6
$RUNX2_{act} + OSX_{mul} + DNA$	0
AP1	0
$RUNX2_{act} + OSX_{mon} + DNA + AP1$	0
OPN <sub>RNA</sub>	0
$Rib_{av} + OPN_{RNA}$	0
Rib <sub>n av</sub> + OPN <sub>RNA</sub>	0
OCN <sub>RNA</sub>	0
Rib <sub>av</sub> + OCN <sub>RNA</sub>	0
$Rib_{n \text{ av}} + OCN_{RNA}$	0
ALPRNA	0
$Rib_{av} + ALP_{RNA}$	0
Rib <sub>n av</sub> + ALP <sub>RNA</sub>	0
BSP <sub>RNA</sub>	0
Rib <sub>av</sub> + BSP <sub>RNA</sub>	0
Rib <sub>n av</sub> + BSP <sub>RNA</sub>	0
Rib <sub>n comp</sub>	299
$Rib_{n \text{ comp}} + RNA$ $Rib_{c}$	0
KID	301
Rib <sub>c</sub> + RNA	0

2 Supplementary table 1: Number of molecules at t<sub>0</sub>

Parameter	Symbol	Value	Unit of measure
Mechanical min. magnitude	m	100	$\mu Pa$
Mechanical phase	$\phi$	0	rad
Integrin activation delay	T <sub>Id</sub> →I <sub>f act</sub>	0	S
$I_d$ dissoc. time from $I + FAK$ comp.	T <sub>If act</sub> +FAK <sub>act</sub> →I <sub>d</sub>	U[0, 80]	S
FAK <sub>act</sub> activation delay	TFAKd → FAKact	5	S
FAK <sub>d</sub> dissoc. time from I + FAK comp.	T <sub>If act</sub> +FAK <sub>act</sub> →FAK <sub>d</sub>	30	S
$I_{act} + FAK$ dissoc. time	TI <sub>f act</sub> +FAK <sub>act</sub> +RAS <sub>d</sub> →I <sub>f act</sub> +FAK <sub>act</sub>	7	S
RAS <sub>act</sub> dissoc. time from I+ FAK+ RAS comp.	T <sub>If act</sub> +FAK <sub>act</sub> +RAS <sub>d</sub> →RAS <sub>act</sub>	7	S
RAS <sub>act</sub> dissoc. form RAS + RAF comp.	$T_{\mathrm{RAS_{act}}+\mathrm{RAF_{d}} \to \mathrm{RAS_{act}}}$	14	S
RAS <sub>act</sub> relaxation time	T <sub>RAS<sub>act</sub>→RAS<sub>d</sub></sub>	60	S
RAF <sub>act</sub> dissoc. time	T <sub>RAS<sub>act</sub>+RAF<sub>d</sub>→RAF<sub>act</sub></sub>	14	S
RAFact dissoc. time from RAF + MEK	TRAFact+MEK <sub>d</sub> →RAFact	10	S
Relaxation of RAFact	T <sub>RAFact</sub> →RAF <sub>d</sub>	60	S
MEKact dissoc. time from RAF + MEK comp.	TRAFact+MEK <sub>d</sub> →MEK <sub>act</sub>	10	S
MEK <sub>act</sub> dissoc. time from MEK + ERK comp.	TMEK <sub>act</sub> +ERK <sub>d</sub> →MEK <sub>act</sub>	8	S
MEK relaxation time	T <sub>MEKact</sub> →MEK <sub>d</sub> →MEK <sub>act</sub>	88	S
ERK activation time	TMEKact - MEKd	8	S
ERK relaxation time	T <sub>MEK<sub>act</sub>+ERK<sub>d</sub>→ERK<sub>act</sub></sub>	50	S
ERK <sub>d</sub> dissoc. time from RUNX2 + ERK comp.	$T_{\text{ERK}_{\text{act}} \to \text{ERK}_{\text{d}}}$	10	S
	$T_{\text{ERK}_{\text{act}}+\text{RUNX2}_{\text{d}} \to \text{ERK}_{\text{act}}}$	6	S
ERK <sub>act</sub> dissoc time from ERK <sub>act</sub> + OTHER comp.	Terk <sub>act</sub> +Other→erk <sub>act</sub>	10	S
RUNX2 <sub>act</sub> dissoc. time from ERK <sub>act</sub> + RUNX2 <sub>d</sub> comp.	$T_{\text{ERK}_{\text{act}}+\text{RUNX2}_{\text{d}}\rightarrow\text{RUNX2}_{\text{act}}}$	30	
RUNX2 <sub>act</sub> dissoc. time from RUNX2 <sub>act</sub> + DNA comp.	$T_{\text{RUNX2}_{\text{act}}}$ +DNA $\rightarrow$ RUNX2 <sub>act</sub>	10	S
RUNX2 relaxation time	$T_{\text{RUNX2}_{\text{act}} \to \text{RUNX2}_{\text{d}}}$	60	S
OSX <sub>mon</sub> dissoc. time from RUNX2 <sub>act</sub> + OSX <sub>mon</sub> comp.	$T_{\text{RUNX2}_{\text{act}} + \text{OSX}_{\text{mon}} \to \text{OSX}_{\text{mon}}}$	20	S
OSX <sub>mon</sub> + DNA dissoc. time from RUNX2 <sub>act</sub>	$T_{\text{RUNX2}_{\text{act}} + \text{OSX}_{\text{mon}} + \text{DNA} \rightarrow \text{OSX}_{\text{mon}} + \text{DNA}}$	30	S
OSX <sub>mon</sub> + DNA dissoc. time from AP1	T <sub>RUNX2<sub>act</sub>+OSX<sub>mon</sub>+DNA+AP1→OSX<sub>mon</sub>+DNA</sub>	0	S
OSX <sub>mul</sub> dissoc. time from RUNX2 <sub>act</sub> + OSX <sub>mul</sub> comp.	T <sub>RUNX2<sub>act</sub>+OSX<sub>mul</sub>→OSX<sub>mul</sub></sub>	40	S
OSX <sub>mul</sub> + DNA dissoc. time from RUNX2 <sub>act</sub>	TRUNX2 <sub>act</sub> +OSX <sub>mul</sub> +DNA→OSX <sub>mul</sub> +DNA	50	S
ribosome availability time from Rib <sub>n av</sub> + OPN <sub>RNA</sub>	TRibn av+OPNRNA→Ribav+OPNRNA	20	S
OPN <sub>RNA</sub> dissociation time from available ribosome	$T_{\text{Rib}_{av}} + \text{OPN}_{RNA} \rightarrow \text{OPN}_{RNA}$	75	S
ribosome availability time from $\mathrm{Rib}_{\mathrm{n}\ \mathrm{av}} + \mathrm{OCN}_{\mathrm{RNA}}$	IRib <sub>n av</sub> +OCN <sub>RNA</sub> →Rib <sub>av</sub> +OCN <sub>RNA</sub>	20	S
OCN <sub>RNA</sub> dissociation time from available ribosome	$T_{\text{Rib}_{av}} + \text{OCN}_{RNA} \rightarrow \text{OCN}_{RNA}$	75	S
ribosome availability time from $Rib_{n av} + ALP_{RNA}$	$T_{\text{Rib}_{n \text{ av}}} + \text{ALP}_{\text{RNA}} \rightarrow \text{Rib}_{\text{av}} + \text{ALP}_{\text{RNA}}$	20	S
ALP <sub>RNA</sub> dissociation time from available ribosome	$T_{\text{Rib}_{av}} + \text{ALP}_{\text{RNA}} \rightarrow \text{ALP}_{\text{RNA}}$	75	S
ribosome availability time from $Rib_{n av} + BSP_{RNA}$	$T_{\text{Rib}_{\text{n av}} + \text{BSP}_{\text{RNA}} \to \text{Rib}_{\text{av}} + \text{BSP}_{\text{RNA}}}$	20	S
BSP <sub>RNA</sub> dissociation time from available ribosome	$T_{\text{Rib}_{av}} + \text{BSP}_{\text{RNA}} \rightarrow \text{BSP}_{\text{RNA}}$	75	S
RNA dissociation time from Rib <sub>n comp</sub>	T <sub>Rib<sub>n comp</sub>+RNA→Rib<sub>n comp</sub></sub>	100	S
RNA dissociation time from complete ribosome	$T_{\mathrm{Rib_c}+\mathrm{RNA} \to \mathrm{Rib_c}}$	100	S
force tag probability	$F_{ m tag}$	$P_{\{01,02\}} = \{0.9, 0.1\}$	
I <sub>d</sub> interaction radius	$R_{ m I_d}$	50	nm
FAK <sub>act</sub> interaction radius	R <sub>FAK<sub>act</sub></sub>	50	nm
RAS <sub>d</sub> interaction radius	$R_{ m RAS_d}$	80	nm
RAF <sub>d</sub> interaction radius	$R_{\mathrm{RAF_d}}$	70	nm
MEK <sub>d</sub> interaction radius	$R_{\text{MEK}_d}$	50	nm
ERK <sub>d</sub> interaction radius	R <sub>ERKd</sub>	30	nm
RUNX2 <sub>d</sub> interaction radius	R <sub>RUNX2d</sub>	30	nm
OSX <sub>mon</sub> interaction radius	ROSX <sub>mon</sub>	30	nm
Rib <sub>n comp</sub> interaction radius	Rp:	30	nm
cell radius	R <sub>Rib<sub>n</sub> comp</sub>	1000	nm
nucleus radius	$R_{\rm cell}$	400	nm
	R <sub>nucl</sub>		The second second
protein's average velocity	$\frac{\overline{v}_p}{\Delta}$	2	nm/s
protein's velocity variation	$\frac{\Delta v_p}{\Delta v_p}$	1	nm/s
protein's direction variation	$\Delta \varphi_p = \Delta \theta_p$	$\pi/10$	rad
protein translation delay	$T_p$	95	S
transcription delay per mRNA	$T_{ m RNA}$	600	S
Integrins $\theta$ angle on cell membrane distribution	$I_{\theta}$	$U[0,\pi]$	1/rad
Integrins $\phi$ angle on cell membrane distribution	$I_{\phi}$	$U[0,2\pi]$	1/rad

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5 Supplementary table 2: Parameters' name, symbols and values.

Parameter	Symbol	List of values	Unit of measure
Mechanical max. magnitude	M	{1000, 10000}	$\mu Pa$
Mechanical period	P	{10000, 50000, 2000000}	s
$MEK_{act}$ dissoc. time from $RAF_{act} + MEK_d$ comp.	TRAFact+MEKd - MEKact	{10, 90, 300, 480, 1320}	s
$MEK_{act}$ dissoc. time from $MEK_{act} + ERK_{d}$ comp.	TMEKact+ERKd→MEKact	{8, 90, 300, 480, 1320}	S
MEK <sub>d</sub> relaxation time	TMEKact - MEKA	{60, 90, 300, 480, 1320}	S
ERK <sub>act</sub> activation time	T <sub>MEKact</sub> +ERK <sub>d</sub> →ERK <sub>act</sub>	{8, 90, 300, 480, 1320}	S
ERK <sub>d</sub> relaxation time	$T_{\text{ERK}_{\text{act}} \to \text{ERK}_{\text{d}}}$	{90, 300, 480, 600, 1320}	S
$ERK_{act}$ dissoc. time from $ERK_{act} + RUNX2_d$ comp.	TERKact+RUNX2d → ERKact	{10, 90, 300, 480, 1320}	S

## 7

## 8 Supplementary table 3: Parameter ranges

- 9 Names, symbols, unit of measures and list of values simulated. Bold quantities represent the
- baseline values. Where no baseline is present, then all possible combinations has been considered.
- 11 Each set of parameters has been independently repeated 10 times.