| Cell Line | Average Young's Modulus Pop \#1 <br> $\mathbf{( k P a )}$ | Average Young's Modulus Pop \#2 <br> $\mathbf{( k P a )}$ |
| :---: | :---: | :---: |
| SKOV3 | $0.23 \pm 0.17$ | $0.92 \pm 0.41$ |
| HEY | $0.24 \pm 0.20$ | $1.04 \pm 0.47$ |
| OVCAR8 | $0.3 \pm 0.13$ | $0.70 \pm 0.22$ |
| TYKNU <br> CpR | $0.24 \pm 0.12$ | $0.60 \pm 0.12$ |
| OVCAR4 | $0.41 \pm 0.26$ | $1.34 \pm 0.48$ |

Table S1: Average Young's Modulus (E) and standard deviation of the two populations in cell lines with bimodal distribution. Pop\#1: lowest-stiffness population, Pop\#2: highest stiffness population.

| Cell Line (Sample size) | Morphological <br> Classification (Circularity; <br> Aspect Ratio) |
| :---: | :---: |
| OAW42 (97) | $\mathrm{E}(0.89 \pm 0.03 ; 1.37 \pm 0.16)$ |
| IGROV1 (103) | $\mathrm{E}(0.94 \pm 0.01 ; 1.14 \pm 0.10)$ |
| SKOV3 (107) | $\mathrm{F}(0.46 \pm 0.13 ; 3.26 \pm 0.63)$ |
| TYKNU (100) | $\mathrm{F}(0.43 \pm 0.21 ; 3.44 \pm 1.49)$ |
| TYKNU CpR (102) | $\mathrm{F}(0.44 \pm 0.17 ; 3.11 \pm 1.07)$ |
| HEY (117) | $\mathrm{F}(0.27 \pm 0.03 ; 5.25 \pm 1.51)$ |
| OVCAR8 (103) | $\mathrm{E}(0.74 \pm 0.13 ; 1.91 \pm 0.42)$ |
| OVCAR4 (105) | $\mathrm{E}(0.81 \pm 0.15 ; 1.41 \pm 0.20)$ |

Table S2: Morphological classification of cell lines. For the morphological classification, the threshold values to discriminate between fibroblastic-like and epithelial-like morphology are 0.74 and 1.91 for circularity and aspect ratio respectively. E: Epithelial-like; F: Fibroblastic-like.


Figure S1: Scatterplot of the average number of invasive cells in function of the average Young's Modulus (a); Scatterplot of the average number of invasive cells in function of the average Young's Modulus, considering for cell lines with bimodal distribution only the lowest-stiffness population (b). Dotted lines represent the $95 \%$ confidence interval.
a

$$
R^{2}=0.3 ; p=0.2
$$


b

$$
R^{2}=0.55 ; p=0.03
$$



Figure S2: Scatterplot of the IC50 in function of the average Young's Modulus, considering for cell lines with bimodal distribution only the lowest-stiffness population (a); scatterplot of the IC50 in function of the average Young's Modulus, considering for cell lines with bimodal distribution only the highest-stiffness population (b). Dotted lines represent the $95 \%$ confidence interval.

| Cell Line | E Pop \#1 <br> before 2c <br> $\mathbf{( k P a )}$ | E Pop \#1 after <br> $\mathbf{2 c}(\mathbf{k P a})$ | $\mathbf{C V}$ \% Pop \#1 | E Pop \#2 <br> before 2c <br> $\mathbf{( k P a )}$ | E Pop \#2 <br> after 2c <br> $\mathbf{( k P a )}$ | CV\% Pop \#2 |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| HEY | $0.24 \pm 0.20$ | $0.21 \pm 0.19$ | 9.43 | $1.04 \pm 0.47$ | $0.96 \pm 0.26$ | 5.66 |
| OVCAR4 | $0.41 \pm 0.26$ | $0.19 \pm 0.13$ | 51.85 | $1.34 \pm 0.48$ | $0.98 \pm 0.28$ | 21.94 |
| TYKNU CpR | $0.24 \pm 0.12$ | $0.14 \pm 0.10$ | 37.22 | $0.60 \pm 0.12$ | $0.44 \pm 0.17$ | 21.76 |

Table S3: Effect of 2c on the Young modulus of the lowest (Pop \#1) and highest (Pop \#2) stiffness population in cell lines retaining a bimodal pattern after treatment. E Pop \#1: average Young modulus of the "softer" population; E Pop \#2: average Young modulus of the "stiffer" population; CV\% = coefficient of variation.


Figure S3: Fluorescent images of OVCAR4 after 2C-F2 treatment at 6 and 24 hours from treatment ( $3^{\text {rd }}$ column). In figure are reported the raw images ( $1^{\text {st }}$ column) and the DAPI-marked nuclei images ( 2 nd column). All images were taken at a magnification of 20x. The scale bar corresponds to $100 \mu \mathrm{~m}$.

| MMP1 | PPP2CA | AKT1 | MMP8 |
| :--- | :--- | :--- | :--- |
| TGFB1 | PIK3CB | MMP3 | WNT4 |
| MTOR | SMARCA2 | EEF1A2 | MMP2 |
| ABL2 | MMP11 | IGF1 | PDGFA |
| HRAS | CCNE1 | APC | SNAI1 |
| AKT3 | TGFBI | ITGB1 | MAPK1 |
| VIM | TUBG1 | SMAD2 | COL5A1 |
| TWIST2 | RHOT1 | INF2 | KRT8 |
| ZEB1 | MYD88 | CTNNB1 | E2F2 |
| TWIST1 | FN1 | MMP14 | AKT2 |
| E2F1 | TUBB3 | MUC1 | TGFND3 |
| CDH1 | TMSB4X | CDH2 | TUBB1 |
| SMARCAD1 | BRAF | EEF1A1 | FLNA |
| PIK3CA | CDC25C | FGFR1 | COL5A2 |
| ACTA2 | CLDN5 | DSP | PTEN |
| CFL1 | KRAS | KRT18 | RB1 |
| NRAS | ACTB | IGF2 | CDK2 |
| ZEB2 | MKI67 | NF1 | KRT9 |
| MMP13 | MMP9 | VTN | ITGB2 |
| SNAI2 |  |  |  |

Table S4: Panel of genes used for differential expression analysis. RNAseq data were extracted from CCLE Database.

