SUPPLEMENTARY DATA:

Figure S1: Histological properties of tumors developed in *junD*$^{-/-}$ mice

(A) HES coloration of sections from *ras* and *ras junD*$^{-/-}$ tumours. (B) Histological analysis of sections from *ras* and *ras junD*$^{-/-}$ tumours co-stained with specific antibodies against E-cadherin (in green, anti-E-cadherin antibody : 4065, Cell signalling ; 2nd antibody : anti-rabbit-Alexa, A-11070 Molecular probes) and Vimentin (in red, anti-Vimentin antibody : RV202, abcam ; 2nd antibody :anti-mouse-Cy3, 715-165-151, Jackson ImmunoResearch) or E-cadherin (in green) and SM-α-actin (in red, anti- SM-α-actin antibody : A2547, clone1A4, Sigma; 2nd antibody : anti-mouse-Cy3, 715-165-151, Jackson ImmunoResearch), as indicated. (C) Histological analysis of sections from *ras* and *ras junD*$^{-/-}$ tumours specifically stained with JunD-specific antibody (sc-74, tebu-bio). Arrows indicate typical nuclear staining in epithelial cells (e) or surrounding fibroblasts (f). As expected, tumors from *junD*$^{-/-}$ mice (c-h) did not exhibit any JunD staining. (D) CXCL12-staining detected in *ras junD*$^{-/-}$ tumours showing high fibroblastic expression as well as staining at the surface of epithelial cells, most probably reflecting fixation of the CXCL12 ligand on CXCR4-receptor. (E) Typical HES views of grafted tumours after cell injection in *wt* (a,c) and *junD*$^{-/-}$ mice (b,d). Scale bars = 40μm in (Aa-d;Ba-d;Da,b), 20μm in (Be-h;Dc,d) and 10μm in (C).

Table S1: *junD*$^{-/-}$ fibroblasts exhibit gene expression profiling similar to CAFs

List of CAF-specific genes up-regulated in *junD*$^{-/-}$ fibroblasts compared to *wt* cells. Genes are classified according to their function and/or sub-cellular localization. Fold changes correspond to the differential expression levels in *junD*$^{-/-}$ fibroblasts versus *wt* cells. Genes in bold were found in studies of reference (Allinen et al. 2004; Farmer et al. 2009).

Figure S2: CXCL12-pathway is involved in the myofibroblastic properties of *junD*$^{-/-}$ fibroblasts

(A) Phase contrast images showing representative immunofluorescence from *wt* and *junD*$^{-/-}$ cells co-stained with fluorescent phalloidin (F-actin, in green) and immunofluorescence using a specific SM-α-actin antibody (in red). Merged images reveal co-localization (in yellow) in *junD*$^{-/-}$ but not in *wt* cells. (B) Quantification using ImageJ software of myofibroblast markers in *wt* and *junD*$^{-/-}$ fibroblasts. The intensity of SM-α-actin and F-actin stainings, the number of adherens junctions (AJ) or focal adhesions (FA) per cell, and the size of FA (µm) are listed. Values are presented as means ± SEM. *p* values by student's test are indicated for each measure. A.U. stems for arbitrary units. (C) Left part: Relative levels of SM-α-actin mRNA in *wt* and *junD*$^{-/-}$ fibroblasts. β2-microglobulin was used as an internal control. Right part: SM-α-actin mRNA levels in *junD*$^{-/-}$ fibroblasts following silencing of CXCL12 (siRNA CXCL12) or HIF-1α (siRNA HIF-1α) and compared to untreated cells (-) or to cells transfected with an untargeted siRNA (sicontrol). (D) Upper part: Representative immunofluorescence of SM-α-actin staining from *junD*$^{-/-}$ fibroblasts. Cells were either untreated (-SB431592) or incubated for 12 hours with a specific inhibitor of TGF-β pathway (+SB431592). Lower part: Western blot analysis of whole cell extracts from *junD*$^{-/-}$ fibroblasts incubated or not with SB431592. Analyses were performed using specific antibodies for SM-α-actin and the phosphorylated form of Smad3, as an internal control for inhibition of the TGF-β pathway. Ponceau coloration was used as an internal control for each protein loading; a representative gel is shown. (E) Left part: Relative levels of CXCL12 mRNA in *wt* and *junD*$^{-/-}$ fibroblasts. β2-microglobulin was used as an internal control. Right part: CXCL12 mRNA levels in *junD*$^{-/-}$ fibroblasts following silencing of CXCL12 (siRNA CXCL12) or HIF-1α (siRNA HIF-1α) and compared to untreated cells (-) or to cells transfected with an untargeted siRNA (si control). (F) Quantification of myofibroblast markers in *junD*$^{-/-}$ fibroblasts after transfection with an untargeted siRNA (+ si control) or with a CXCL12-directed siRNA (+ si CXCL12). (G) Western blot (left) and FACS (right) analysis showing expression of the CXCR4 receptor at the surface of the fibroblasts.

Figure S3: Variation of HIF-1α protein levels modulates myofibroblast properties.

(A) Left part: Relative levels of HIF-1α mRNA in *wt* and *junD*$^{-/-}$ fibroblasts. β2-microglobulin was used as an internal control. Right part: HIF-1α mRNA levels in *junD*$^{-/-}$ fibroblasts following silencing of CXCL12 (siRNA CXCL12) or HIF-1α (siRNA HIF-1α) and compared to untreated cells (-) or to cells transfected with an untargeted siRNA (si control). (B) Quantification of myofibroblast markers in *junD*$^{-/-}$ fibroblasts after transfection with an untargeted siRNA (+ si control) or with a HIF-1α-directed siRNA (+ si HIF-1α). (C) Western blot analysis of cytosolic (C) or nuclear (N) extracts from *wt* fibroblasts incubated or not with DFO. Analysis was performed using a specific HIF-1α antibody, a kind gift of J. Pouysségur. Ponceau staining was used as an internal control for protein loading. (D) Quantification of myofibroblast markers in *wt* fibroblasts incubated with (+DFO) or without (-DFO) desferrioxamine (E) Quantification of myofibroblast markers in *junD*$^{-/-}$ fibroblasts incubated with (+NAC) or without (-NAC) N-acetyl-cysteine. The intensity of SM-α-actin and F-actin stainings, the number of AJ or FA per cell and the size of FA (μm) are listed. Values are presented as means ± SEM. *p* values by student's test are indicated for each measure. A.U. stems for arbitrary units.

Table S2: Quantitative analysis of HER2, BLC and Lum-A human breast cancers

Table showing quantitative data of intensity staining, percentage of positive cells and H score (Intensity x % cells) in the epithelium and the stroma of HER2 (n=36), BLC (n=44) or Lum-A (n=23) human breast cancers. Each line represents one tumor. Analyses were performed using CXCR4-, CXCL12-, Ki67- and SM-α actin-specific antibodies. Color code was as the following: maximal intensity value was arbitrarily defined as 4; red represents high signal intensity (Int ≥3), orange, intermediate intensity (3> Int ≥ 2); yellow, low intensity (2> Int ≥ 1) and white, faint or no detected signal (Int < 1). Percentage of positive cells was as follow: Yellow : 0≤ % ≤ 49, orange : 50 ≤ % ≤ 79, red : % ≥ 80. Finally, H score was calculated as follow: Intensity x % cells, and color code was as follow : yellow : 0 ≤ H ≤ 159, orange : 160 ≤ H ≤ 269, red : ≥ 270. Both epithelium and stroma have been separately analyzed. Means of each measure are indicated below, as well as p values corresponding to t-test from comparative analysis of HER2 vs BLC, HER2 vs Lum-A and BLC vs Lum-A. p values are represented as highly significant in red ($p \leq 0.01$), significant in orange ($p \leq 0.05$) or non-significant (NS).

Figure S4: HER2 and BLC tumors are associated with high proliferation rate and pro-inflammatory response when compared to Lum-A

Sections and histological analysis of HER2 (a-c), BLC (d-f) and Lum-A (g-i) human breast tumors. (A) Representative staining of Ki67 (A) in each tumour type. Below are the tables summarizing the quantitative means of staining intensity (Intensity), percentage of positive cells (% cells) and scoring (Intensity x % cells) in the epithelium and in the stroma, respectively. (B) Representative staining of CD68 in each tumour type. Data are presented below as number of CD68-positive macrophages (mean ± SEM). p values by student test are represented as highly significant in red ($p \leq 0.01$), significant in orange ($p \leq 0.05$) or non-significant (NS). Scale bars = 40μm.

Figure S5: GO term Oxido-reduction (GO:0055114) in HER2, BLC and Lum-A breast cancers

(A) Pathway analysis plot: each bar of the X-axis represents each gene found in the GO:0055114 pathway. The height of the bar indicates the influence of each gene in the pathway according to the tumor subtype. Horizontal markers in a bar indicate one SD away from the reference point; two or more horizontal markers in a bar indicate a statistically significant association of the corresponding gene with the tumor subtype. (B) Hierarchical clustering of breast tumors based on the GO:0055114 pathway genes. (C / D) Principal component analysis of the GO:0055114 pathway genes. (C) Representation of the tumor using the first two principal components: each dot corresponds to a tumor. The x and y axes represent the coordinates of the tumor on the first and second principal components (respectively). (D) Representation of the genes using the first two principal components: each arrow corresponds to a gene. The x and y coordinates are the correlation of the gene with the first and second principal components (respectively).

Figure S6: GO term oxido-reductase activity (GO:0016491) in HER2, BLC and Lum-A breast cancers. Same legend as in Figure S5.

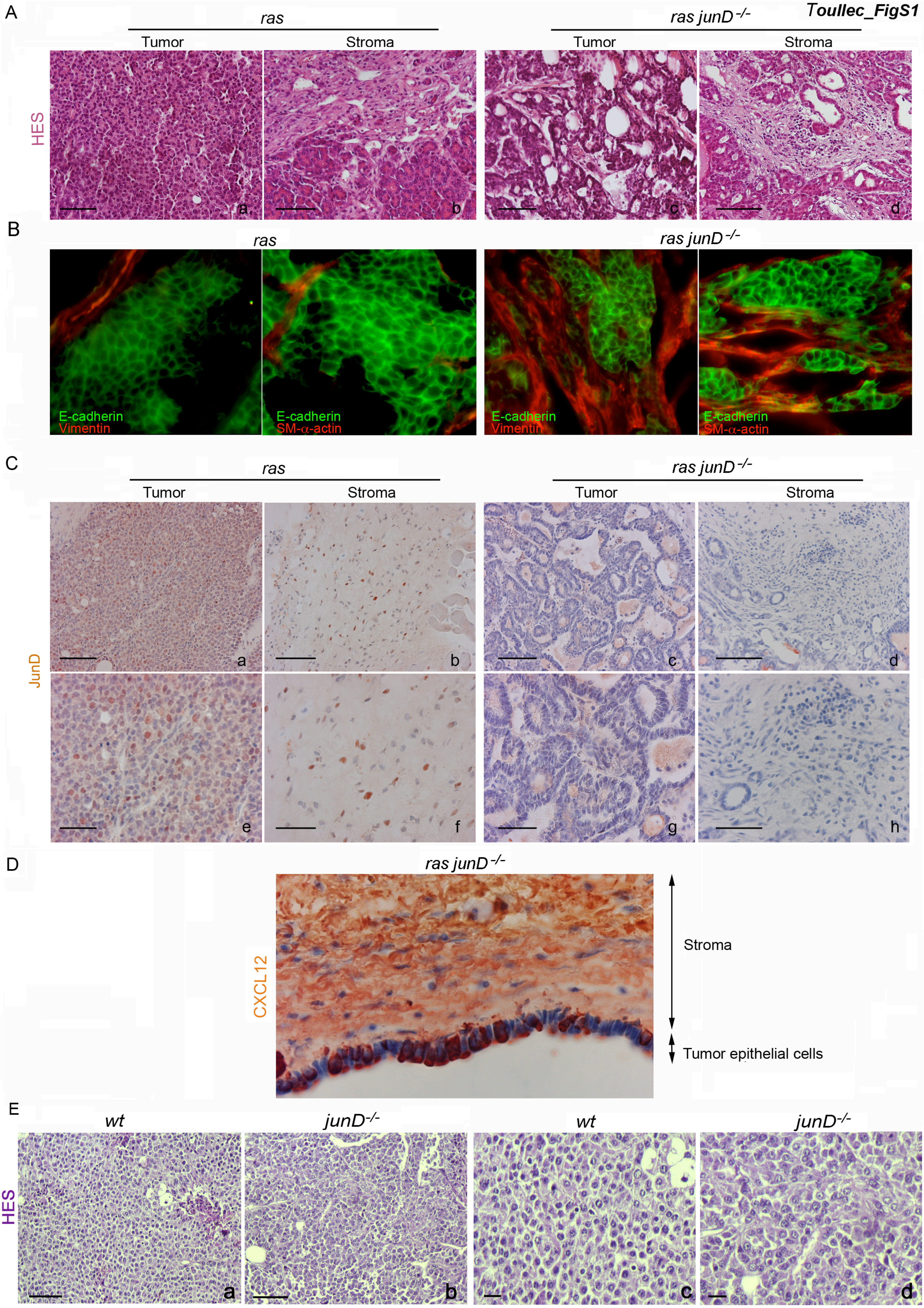
Table S3: List of genes involved in oxido-reduction that are up-regulated in HER2 vs BLC

Are indicated in bold the genes that have been cited in the text.

Figure S7: Specificity of the antibodies used on human samples.

(A) Western blots showing CXCR4 or JunD protein in extracts from various human breast cancer cell lines. Ponceau coloration was used as an internal control for each protein loading; a representative gel is shown (B) Western blots showing HIF-1α or CXCL12 protein in extracts from human breast cancer cell lines that have been treated with DFO (for detection of HIF-1α) or DFO+Brefeldin (for detection of CXCL12). DFO is an iron chelator, which inhibits PHD and thus increases HIF-1α; Brefeldin (100γM) interferes with retrograde transport and avoid secretion of CXCL12 in the medium. (C) Relative levels of CXCR4 (left part) or CXCL12 (right part) mRNA in various breast epithelial cell lines. GAPDH was used as an internal control. (D) The specificity of the human CXCL12-recognizing antibody has been evaluated by performing a competitive assay using 2-fold molecular excess of human CXCL12 ligand. In that aim, since CXCL12 molecular mass is 8kD, we incubated 1300ng of CXCL12 antibody (ab9797 AbCam) with 100ng of human recombinant CXCL12 (350NS R&Dsystem) per reaction. By this method, we depleted the pool of antibody that specifically recognizes CXCL12. We performed IHC on HER2-amplified breast adenocarcinomas following this treatment. The same areas of 3 different tumors are shown with or without human recombinant CXCL12, as indicated. This competitive depletion severely decreased the staining in both fibroblasts and epithelial cells (arrows), further arguing that the antibody we used is specific and the detected staining did not result from unspecific background.

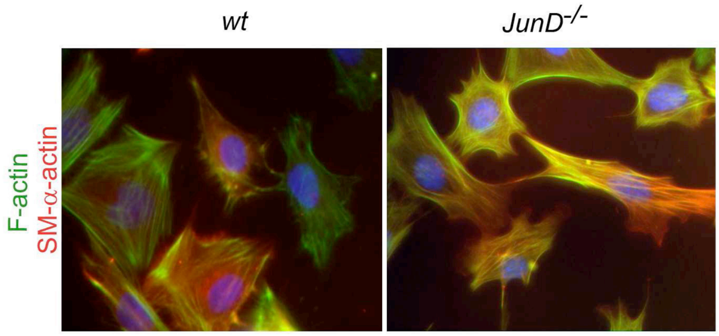
Toullec_FigS1



GeneID	Name	Gene description	Fold
Extracellular matrix proteins			
23794	**Adamts5**	**A disintegrin-like and metallopeptidase with thrombospondin type 1 motif,**	**3.18**
12842	**Col1a1**	**Collagen, type I, alpha 1**	**1.48**
12843	**Col1a2**	**Collagen, type I, alpha 2**	**36.45**
12825	**Col3a1**	**Collagen, type III, alpha 1**	**17.75**
12826	Col4a1	Collagen, type IV, alpha 1	1.92
12835	**Col6a3**	**Collagen, type VI, alpha 3**	**5.92**
12837	Col8a1	Collagen, type VIII, alpha 1	1.87
68588	**Cthrc1**	**Collagen triple helix repeat containing 1**	**5.63**
14268	**Fn1**	**Fibronectin 1**	**1.46**
16948	Lox	Lysyl oxidase	1.94
268977	Ltpb1	Latent transforming growth factor beta binding protein 1	1.64
17181	**Matn2**	**Matrilin 2**	**1.44**
50530	Mfap5	Microfibrillar associated protein 5	1.83
17390	**Mmp2**	**Matrix metalloproteinase 2**	**1.66**
17387	**Mmp14**	**Matrix metalloproteinase 14 (membrane-inserted)**	**1.51**
17389	Mmp16	Matrix metallopeptidase 16	3.25
18073	**Nid1**	**Nidogen 1**	**4.42**
19242	**Ptn**	**Pleiotrophin**	**3.82**
116847	Prelp	Proline arginine-rich end leucine-rich repeat	2.18
13602	**Sparcl1**	**SPARC-like 1 (mast9, hevin)**	**1.30**
Cytoskeleton			
11461	Actb	Actin, beta, cytoplasmic	7.25
11468	**Actg2**	**Actin, gamma 2, smooth muscle, enteric**	**3.90**
56456	Actl6A	Actin-like 6A	1.25
60595	Actn4	Actinin alpha 4	1.47
109676	Ank2	Ankyrin 2, neuronal	3.38
12798	Cnn2	Calponin 2	1.75
18163	Ctnnd2	Catenin delta 2	2.87
13043	Cttn	Cortactin	1.71
208846	Daam1	Dishevelled associated activator of morphogenesis 1	2.02
109619	Dctn2	Dynactin 2	1.26
140579	Elmo2	Engulfment and cell motility 2	1.39
223254	Farp1	FERM, RhoGEF (Arhgef) and pleckstrin domain protein 1 (chondrocyte-derived)	1.46
14609	**Gja1**	**Gap junction protein, alpha 1, 43kDa (Connexin 43)**	**1.25**
17886	Myh9	Myosin, heavy polypeptide 9, non-muscle	1.55
98932	**Myl9**	**Myosin, light polypeptide 9, regulatory**	**1.63**
213019	Pdlim2	PDZ and LIM domain 2	2.32
227937	Pkp4	Plakophilin 4	1.39
27205	Podxl	Podocalyxin-like	1.85
19684	Rdx	Radixin	2.66
20259	Scin	Scinderin	1.30
21345	**Tagln**	**Transgelin**	**1.74**
21894	Tln1	Talin 1	1.38
22004	**Tpm2**	**Tropomyosin 2, beta**	**1.36**
74237	Tubgcp2	Tubulin, gamma complex associated protein 2	1.80
Cell adhesion			
76709	Arpc2	Actin related protein 2/3 complex, subunit 2	1.42
14618	Gjb1	Gap junction membrane channel protein beta 1	1.37
84004	Mcam	Melanoma cell adhesion molecule	2.61
17967	Ncam1	Neural cell adhesion molecule 1	1.89
75599	Pcdh1	Protocadherin 1	2.52
93701	Pcdhgb4	Protocadherin gamma subfamily B, 4	1.92
20692	**Sparc**	**Secreted protein, acidic, cysteine-rich**	**9.98**
21826	**Thbs2**	**Thrombospondin 2**	**2.24**
81877	**Tnxb**	**Tenascin XB**	**1.30**
Chemokines			
12769	Ccr9	Chemokine (C-C motif) receptor 9	1.44
20315	**Cxcl12**	**Chemokine (C-X-C motif) ligand 12**	**1.99**
57266	**Cxcl14**	**Chemokine (C-X-C motif) ligand 14**	1.89
Ribosomal proteins			
110954	**Rpl10**	**Ribosomal protein L10**	**1.14**
58988	**Rps6kb2**	**Ribosomal protein S6 kinase, 70kDa, polypeptide 2**	**2.07**
20116	**Rps8**	**Ribosomal protein S8**	**1.22**
Growth factor / Receptor			
69538	**Antxr1**	**Anthrax toxin receptor 1**	2.28
12033	Bcap29	B-cell receptor-associated protein 29	1.42
235505	Cd109	CD109 antigen	2.15
54219	Cd320	CD320 antigen	1.36
12520	**Cd81**	**CD 81 antigen**	**1.82**
26364	Cd97	CD97 antigen	1.28
12801	Cnr1	Cannabinoid receptor 1 (brain)	2.00
12982	Csf2ra	Colony stimulating factor 2 receptor, alpha, low-affinity (granulocyte-macrophage)	2.18
14219	**Ctgf**	**Connective tissue growth factor**	**2.06**
12305	Ddr1	Discoidin domain receptor family, member 1	1.43
14062	**F2r**	**coagulation factor II (thrombin) receptor**	**1.21**
14167	Fgf12	Fibroblast growth factor 12	1.44
14184	Fgfr3	Fibroblast growth factor receptor 3	1.43
233575	Frag1	FGF receptor activating protein 1	1.40
14600	Ghr	Growth hormone receptor	1.37
14694	**Gnb2l1**	**Guanine nucleotide binding protein (G protein), beta polypeptide 2 like 1**	**1.36**
93695	**Gpnmb**	**Glycoprotein (transmembrane) nmb**	**4.15**
14783	Grb10	Growth factor receptor bound protein 10	2.00
15200	Hbegf	heparin-binding EGF-like growth factor	1.57
16004	Igf2r	Insulin-like growth factor 2 receptor	1.68
16008	Igfbp2	Insulin-like growth factor binding protein 2	2.15
16411	Itgax	Integrin alpha X	2.10
16635	Klra4	Killer cell lectin-like receptor, subfamily A, member 4	4.00
56873	Lmbr1	Limb region 1	1.37
16971	**Lrp1**	**Low density lipoprotein-related protein 1**	**1.60**
17000	Ltbr	Lymphotoxin B receptor	2.22
80509	Med8	Mediator of RNA polymerase II transcription, subunit 8	1.70
18049	Ngf	Nerve growth factor	1.63
18442	P2ry2	Purinergic receptor P2Y, G-protein coupled 2	1.60
12034	Phb2	Prohibitin 2	1.42
19263	Ptprb	Protein tyrosine phosphatase, receptor type, B	10.00
387341	Tas2r106	Taste receptor, type 2, member 106	5.00
22403	Wisp2	WNT1 inducible signaling pathway protein 2	1.50
22415	Wnt3	Wingless-related MMTV integration site 3	1.60
22420	Wnt6	wingless-related MMTV integration site 6	1.20
Rho GTP-ases			
260409	Cdc42ep3	CDC42 effector protein (Rho GTPase binding) 3	1.58
303634	**Gna13**	**Guanine nucleotide binding protein, alpha 13**	**2.17**
19353	Rac1	RAS-related C3 botulinum substrate 1	1.48
56044	Rala	v-ral simian leukemia viral oncogene homolog A	2.24
11852	Rhob	ras homolog gene family, member B	2.05
19877	**Rock1**	**Rho-associated, coiled-coil containing protein kinase 1**	**1.43**

Toullec_FigS2

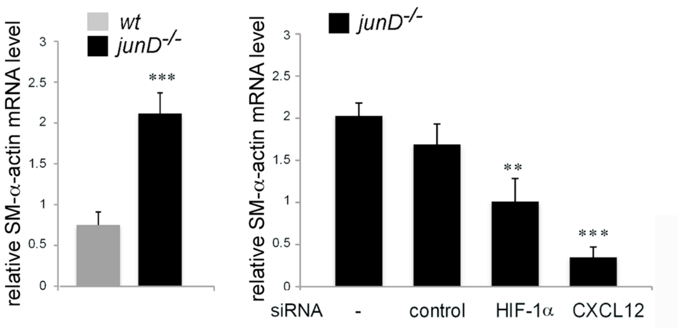
A



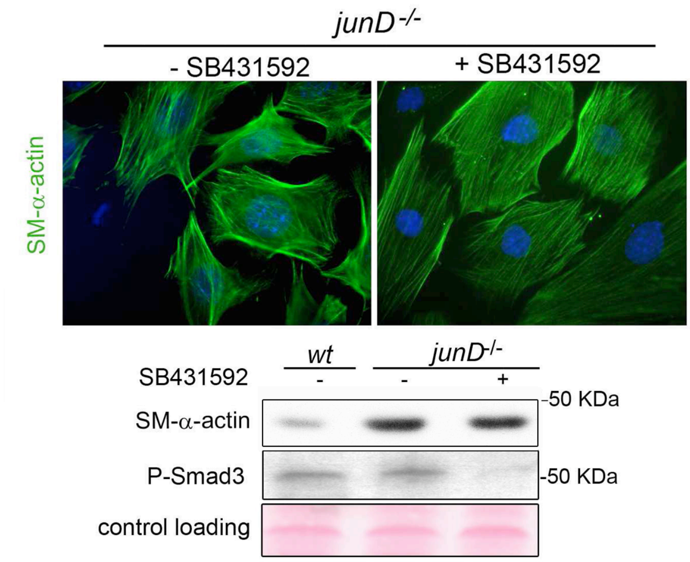
B

Staining	Quantified Parameter	Genotype		p value
		wt	JunD-/-	
SM-α actin	Fluorescence intensity (A.U.)	3.6 ± 1.77	40.8 ± 9.28	4.E-11
F-actin	Fluorescence intensity (A.U.)	6.8 ± 3.34	37.5 ± 7.43	3.E-12
N-cadherin	Number of AJ / Cell	17.7 ± 1.96	42.1 ± 10.96	0.0014
Vinculin	Number of FA / Cell	24.2 ± 5.04	98.4 ± 17.92	0.00095
	Size of FA (µm)	4.1 ± 1.82	7.3 ± 1.87	2.64E-10

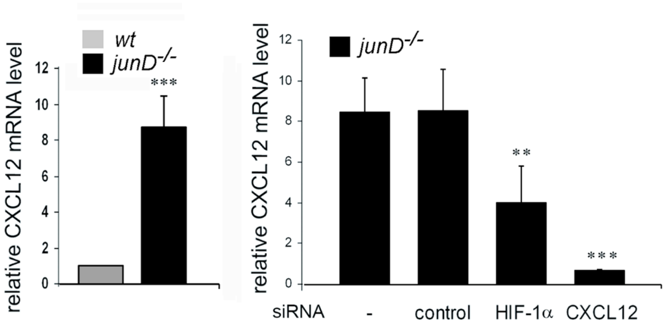
C



D



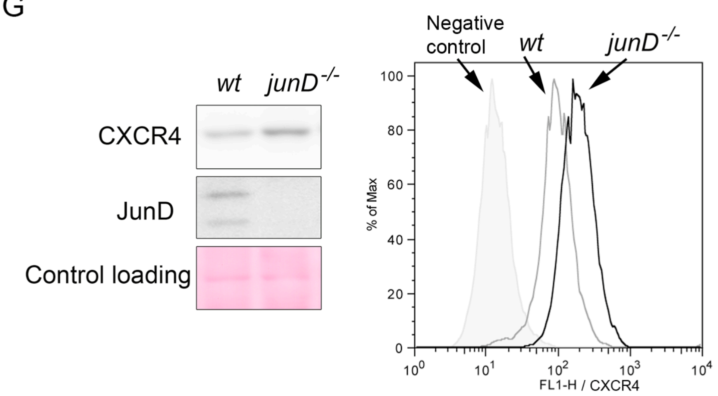
E



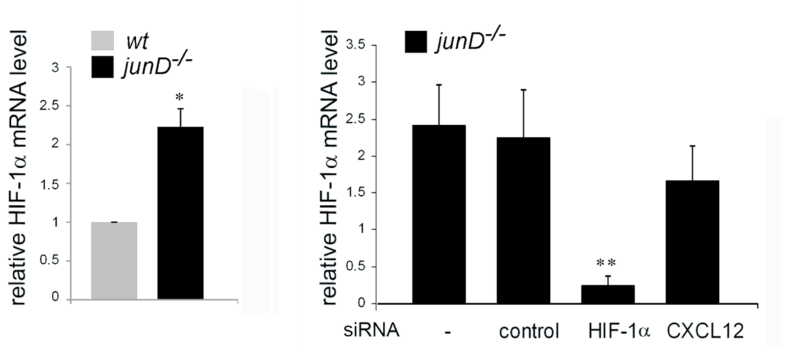
F

Staining	Quantified Parameter	*JunD-/-*		p value
		+ si control	+ si CXCL12	
SM-α actin	Fluorescence intensity (A.U.)	49.3 ± 7.88	15.3 ± 3.68	1.E-12
F-actin	Fluorescence intensity (A.U.)	55.4 ± 13.79	16.8 ± 4.54	6.E-10
N-cadherin	Number of AJ / Cell	50.7 ± 12.10	17.6 ± 3.88	0.00003
Vinculin	Number of FA / Cell	92.5 ± 33.60	33.7 ± 9.90	0.001
	Size of FA (µm)	6.57 ± 2.55	3.17 ± 1.9	4.50E-15

G



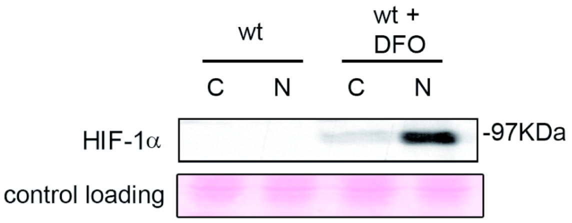
A



B

Staining	Quantified Parameter	*JunD-/-*		p value
		+ si control	+ si HIF	
SM-α-actin	Fluorescence intensity (A.U.)	45.6 ± 14.32	12.4 ± 4.40	2.E-08
F-actin	Fluorescence intensity (A.U.)	48.3 ± 10.40	16.6 ± 5.44	1.E-10
N-cadherin	Number of AJ / Cell	41.5 ± 8.80	21.5 ± 5.50	0.00025
Vinculin	Number of FA / Cell	91.7 ± 23.60	33.2 ± 9.40	0.000178
	Size of FA (µm)	7.7 ± 0.38	3.4 ± 0.16	5.17E-31

C



D

Staining	Quantified Parameter	*wt*		p value
		- DFO	+ DFO	
SM-α-actin	Fluorescence intensity (A.U.)	5 ± 2.10	25.6 ± 6	2E-10
F-actin	Fluorescence intensity (A.U.)	9.80 ± 2.90	21.9 ± 6.8	0.00004
N-cadherin	Number of AJ / Cell	41.5 ± 8.80	51.2 ± 10.3	0.00025
Vinculin	Number of FA / Cell	30.14 ± 8.60	65.03 ± 5.75	0.00068
	Size of FA (µm)	3.88 ± 1.9	6.68 ± 3.44	3.20E-09

E

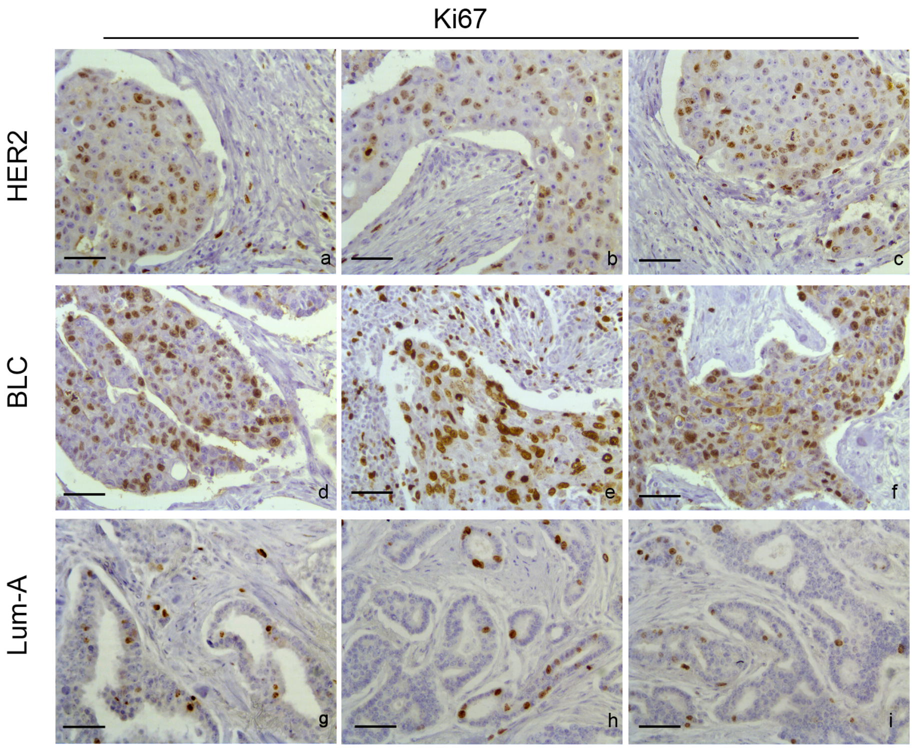
Staining	Quantified Parameter	*junD-/-*		p value
		- NAC	+ NAC	
SM-α-actin	Fluorescence intensity (A.U.)	27 ± 4.20	3.8 ±1.5	9.90E-07
F-actin	Fluorescence intensity (A.U.)	31.8 ± 11	17.9 ± 5.8	0.01333
N-cadherin	Number of AJ / Cell	75.5 ± 30.9	25.9 ± 7.3	0.00227
Vinculin	Number of FA / Cell	159.3 ± 65.5	57.5 ± 15.2	0.00188
	Size of FA (µm)	6.3 ± 4.44	2.7 ± 1.73	2.70E-07

Toullec-Table S2

Tumor type	CXCR4						CXCL12						Ki67						Smooth muscle actin					
	Epithelium			Stroma			Epithelium			Stroma			Epithelium			Stroma			Epithelium			Stroma		
	Intensity	% cells	H score	Intensity	% cells	H score	Intensity	% cells	H score	Intensity	% cells	H score	Intensity	% cells	H score	Intensity	% cells	H score	Intensity	% cells	H score	Intensity	% cells	H score
HER2	0,5	100	50	2	50	100	2,5	95	237,5	2	70	140	0,5	40	20	0	0	0	0	0	0	2,5	40	100
	0,2	100	20	1	100	100	1,5	100	150	1,5	90	135	0,5	20	10	0	0	0	0	0	0	3	70	210
	0,2	100	20	0,5	60	30	1	100	100	0,5	50	25	1	20	20	0	0	0	0	0	0	2,5	20	50
	1	100	100	1	70	70	2	100	200	1	40	40	0,5	20	10	0	0	0	0	0	0	4	40	160
	0,5	100	50	2	20	40	1,5	60	90	1	40	40	0,5	1	0,5	0	0	0	0	0	0	4	30	120
	0,3	100	30	2	20	40	2	80	160	1,5	20	30	1	1	1	0	0	0	0	0	0	3	25	75
	0,8	100	80	3,5	20	70	0,5	100	50	2	80	160	2	5	10	0	0	0	0	0	0	3	60	180
	1,2	70	84	1,5	30	45	1	100	100	1	20	20	2	30	60	0	0	0	0	0	0	3	50	150
	0,5	100	50	2	30	60	1	100	100	1,5	80	120	2	15	30	0	0	0	0	0	0	4	40	160
	0,5	100	50	1	90	90	1,5	100	150	1,5	80	120	0	0	0	0	0	0	0	0	0	2	50	100
	1	100	100	2,5	100	250	2,5	100	250	2	80	160	0,5	10	5	0	0	0	0	0	0	4	50	200
	0,5	100	50	3,5	100	350	2	100	200	3	70	210	0,5	5	2,5	0	0	0	0	0	0	3	95	285
	0,2	100	20	0,5	80	40	0,3	100	30	0,3	50	15	1	50	50	0	0	0	0	0	0	2	30	60
	0,5	100	50	1	80	80	1	100	100	0,3	40	12	3,5	50	175	3	10	30	0	0	0	4	50	200
	0,3	100	30	2	90	180	2,5	100	250	2,5	100	250	1	50	50	1	5	5	0	0	0	3,5	60	210
	2	100	200	2	15	30	2	100	200	1,5	60	90	1,5	20	30	0	0	0	0	0	0	1,5	30	45
	3	100	300	3	60	180	2,5	100	250	2	70	140	2,5	60	150	0	0	0	0	0	0	2,5	30	75
	2	100	200	2,5	70	175	3,5	100	350	3	60	180	2	20	40	2	5	10	0	0	0	3	60	180
	1	100	100	0,8	80	64	4	100	400	1,5	80	120	3	10	30	2	1	2	0	0	0	3	50	150
	3	100	300	4	100	400	4	100	400	3	100	300	1,5	45	67,5	2	10	20	0	0	0	4	90	360
	2,5	100	250	4	100	400	2,5	100	250	2,5	100	250	1,5	25	37,5	3	30	90	0	0	0	2,5	70	175
	0,3	100	30	3,5	80	280	1,5	100	150	1,5	60	90	2	50	100	0	0	0	0	0	0	4	90	360
	2	100	200	2	80	160	3	100	300	2,5	60	150	1,5	50	75	2	1,5	3	0	0	0	3,5	80	280
	2,5	100	250	2,5	80	200	2,5	100	250	1,5	60	90	1	60	60	2	10	20	0	0	0	4	40	160
	3	100	300	2,5	100	250	4	100	400	3,5	100	350	1,5	20	30	0	0	0	0	0	0	4	60	240
	1,3	100	130	4	100	400	3	100	300	3,5	100	350	1	10	10	0	0	0	0	0	0	3	90	270
	3	100	300	3,5	100	350	1	100	100	3	80	240	1,5	30	45	0	0	0	0	0	0	3	60	180
	0,5	100	50	3	80	240	0,7	100	70	3	100	300	1,5	20	30	0	0	0	0	0	0	2,5	60	150
	0,5	100	50	3	80	240	2	100	200	3	100	300	1,5	30	45	2	20	40	0	0	0	4	75	300
	0,5	100	50	1	100	100	2,5	100	250	0,5	60	30	2,5	45	112,5	0	0	0	0	0	0	4	60	240
	2	100	200	1,5	90	135	0,5	100	50	0,5	20	10	2	20	40	2	5	10	0	0	0	2	30	60
	0,5	100	50	3	100	300	1	100	100	2	70	140	1,5	50	75	3	25	75	0	0	0	4	70	280
	0,3	100	30	3	15	45	2	100	200	2	60	120	2,5	50	125	2	3,5	7	0	0	0	4	40	160
	1	100	100	1,5	30	45	0,5	100	50	2,5	30	75	0,5	10	5	0	0	0	0	0	0	4	30	120
	1,5	100	150	1	100	100	0,5	100	50	1	100	100	2,5	60	150	0	0	0	0	0	0	3	90	270
	0,8	100	80	2	35	70	0,8	100	80	0,5	100	50	0,5	15	7,5	0	0	0	0	0	0	2	60	120
BLC	2,5	100	250	4	100	400	1,5	80	120	0,5	60	30	1	10	10	0	0	0	0	0	0	3	90	270
	1,5	100	150	4	100	400	2,5	100	250	3	50	150	0,5	1	0,5	0	0	0	0	0	0	4	75	300
	2,5	100	250	0,5	50	25	0,5	80	40	0,5	20	10	3	70	210	0	0	0	0	0	0	3	40	120
	1	100	100	2,5	100	250	1	90	90	1	60	60	3	50	150	0	0	0	0	0	0	4	100	400
	3	100	300	1,5	50	75	0,5	100	50	1	30	30	4	95	380	0	0	0	0	0	0	3,5	70	245
	3,5	100	350	2	70	140	2,5	100	250	0,5	20	10	2	30	60	0	0	0	0	0	0	2	60	120
	2,5	100	250	0,5	5	2,5	2	100	200	0	0	0	2	25	50	0	0	0	0	0	0	2	40	80
	2,5	100	250	2	80	160	2,5	100	250	1	50	50	3	50	150	3	20	60	0	0	0	4	50	200
	0,8	100	80	2	100	200	0,3	100	30	0,5	40	20	3	100	300	3	10	30	0	0	0	2,5	60	150
	0,8	100	80	2	70	140	0,3	95	28,5	0,1	60	6	1	20	20	0	0	0	0	0	0	2,5	60	150
	2	100	200	3	100	300	2	95	190	0,3	20	6	4	50	200	3	5	15	0	0	0	3,5	25	87,5
	2,5	100	250	2	100	200	1,5	100	150	0,2	15	3	1,5	80	120	2	5	10	3	80	2,4	3	70	210
	0,8	100	80	0,8	100	80	0,2	100	20	0,5	70	35	2	70	140	2	10	20	0	0	0	3	80	240
	1	100	100	2	100	200	1,7	90	153	2	80	160	3	90	270	3	15	45	0	0	0	4	95	380
	0,5	100	50	2	100	200	1	100	100	1	80	80	4	80	320	4	20	80	4	70	2,8	4	80	320
	0,2	100	20	0,5	100	50	0,3	100	30	0,2	30	6	2	65	130	2,5	10	25	0	0	0	2	100	200
	0,8	100	80	1	40	40	0,5	100	50	0,2	50	10	3	50	150	3	10	30	0	0	0	2,5	20	50
	0,2	100	20	1	10	10	0,2	100	20	0,2	30	6	2,5	70	175	2,5	1	2,5	0	0	0	3	70	210
	0,8	100	80	1	15	15	0,3	100	30	0,2	20	4	2	70	140	1	2,5	2,5	0	0	0	2	40	80
	0,8	100	80	0,8	100	80	1	100	100	0,2	20	4	2	10	20	2	5	10	4	50	2	4	90	360
	0,5	100	50	1	5	5	0,5	100	50	2	5	10	2	50	100	2	15	30	0	0	0	1,5	20	30
	0,2	100	20	0,2	20	4	0,1	100	10	1	2	2	0,5	30	15	0	0	0	0	0	0	4	50	200
	1	100	100	1,5	50	75	1	100	100	0,5	3	1,5	2,5	70	175	2,5	20	50	0	0	0	4	100	400
	1,5	100	150	1,5	30	45	1	100	100	1,5	30	45	3	80	240	3	35	105	0	0	0	4	85	340
	1,5	100	150	1	60	60	1	100	100	1,5	60	90	0,5	15	7,5	0	0	0	0	0	0	3,5	70	245
	1,5	100	150	1	60	60	0,5	100	50	0,5	50	25	3	50	150	2	1	2	0	0	0	3,5	60	210
	0,3	100	30	0,2	10	2	0,2	100	20	0,1	2	0,2	2,5	20	50	0	0	0	0	0	0	1,5	60	90
	0,5	100	50	2,5	90	225	0,8	100	80	0,5	40	20	2	60	120	0	0	0	0	0	0	2,5	90	225
	1,5	100	150	1,5	60	90	0,5	100	50	1	50	50	3,5	70	245	3,5	30	105	0	0	0	3	70	210
	1	100	100	0,2	20	4	0,5	100	50	0,2	50	10	2	40	80	0	0	0	0	0	0	4	40	160
	0,8	100	80	1,5	40	60	1	100	100	1	80	80	2	70	140	2	2	4	0	0	0	2	50	100
	0,2	100	20	0,5	30	15	4	100	400	3	50	150	3	70	210	3	10	30	3	50	1,5	3	50	150
	0,5	100	50	2	20	40	0,5	100	50	1,5	10	15	2	60	120	0	0	0	0	0	0	0,5	40	20
	1,5	100	150	0,3	50	15	2,5	100	250	2,5	65	162,5	2,5	50	125	3	15	45	0	0	0	3,5	60	210
	1	100	100	1,5	80	120	1,5	100	150	4	100	400	1	40	40	0	0	0	0	0	0	4	70	280
	1	100	100	1,5	90	135	1	100	100	2	80	160	2	50	100	2,5	10	25	0	0	0	2	60	120
	0,8	100	80	0,5	80	40	1,5	100	150	1,5	50	75	3	70	210	2	10	20	2	30	0,6	2	70	140
	0,8	100	80	1	100	100	0,5	100	50	0,5	90	45	3	60	180	0	0	0	4	5	0,2	3,5	20	70
	0,2	100	20	0,5	50	25	0,5	100	50	1	100	100	2	45	90	2,5	15	37,5	0	0	0	4	80	320
	0,3	100	30	0,5	80	40	2	100	200	2	60	120	1,5	40	60	1,5	5	7,5	4	80	3,2	4	40	160
	1	100	100	1	25	25	0,5	100	50	0,5	90	45	2,5	60	150	3	20	60	0	0	0	4	80	320
	1	100	100	1	60	60	1	100	100	3	100	300	2	50	100	2	5	10	0	0	0	3	30	90
	0,5	100	50	2,5	70	175	0,5	100	50	1,6	100	160	1,5	50	75	0	0	0	0	0	0	2	55	110
	0,8	100	80	1	50	50	1,3	100	130	1	100	100	3	70	210	3	5	15	0	0	0	3	40	120
Lum-A	0,2	100	20	0,1	20	2	0,8	80	64	0,3	40	12	0	0	0	0	0	0	0	0	0	2	70	140
	0,3	100	30	0,2	30	6	2,5	100	250	0,2	20	4	1	5	5	0	0	0	0	0	0	2	80	160
	0,8	100	80	0	0	0	0,8	100	80	0	0	0	0	0	0	0	0	0	0	0	0	3	35	105
	0,1	100	10	0	0	0	0,8	100	80	0,1	20	2	0	0	0	0	0	0	0	0	0	3	60	180
	0,2	100	20	0	0	0	1,5	100	150	0,1	5	0,5	2,5	30	75	0	0	0	0	0	0	3	10	30
	0,8	100	80	0,3	50	15	1,5	100	150	0,2	60	12	0	0	0	0	0	0	0	0	0	2,5	40	100
	0,8	100	80	1	40	40	3	100	300	0,2	60	12	0	0	0	0	0	0	0	0	0	2,5	30	75
	0,5	100	50	0	0	0	2,5	100	250	0	0	0	0	0	0	0	0	0	0	0	0	2,5	20	50
	1	100	100	1	10	10	0,4	100	40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	0,3	100	30	0,2	20	4	1,5	50	75	0,1	5	0,5	2	1	2	0	0	0	0	0	0	3	70	210
	0,2	100	20	0,2	90	18	0,5	80	40	0,1	2	0,2	1,5	1	1,5	0	0	0	0	0	0	3,5	50	175
	0,5	100	50	0,5	5	2,5	1,5	100	150	0,3	50	15	0	0	0	0	0	0	0	0	0	2,5	25	62,5
	0,5	100	50	0,2	5	1	2	100	200	0,2	10	2	0	0	0	0	0	0	0	0	0	4	70	280
	0,5	100	50	0	0	0	0,5	100	50	0	0	0	3	30	90	0	0	0	0	0	0	4	20	80
	0,5	100	50	0,3	20	6	1,3	100	130	1,5	75	112,5	1	10	10	0	0	0	0	0	0	2	40	80
	0,1	100	10	0	0	0	0,5	100	50	0,2	50	10	0	0	0	0	0	0	0	0	0	3	70	210
	0,5	100	50	0	0	0	3,5	100	350	2	15	30	1	0,5	0,5	0	0	0	0	0	0	4	50	200
	0	0	0	0,3	10	3	0,5	100	50	0,2	10	2	0	0	0	0	0	0	0	0	0	3,5	30	105
	0	0	0	0	0	0	0,1	100	10	0,1	5	0,5	0	0	0	0	0	0	0	0	0	0	0	0
	0,2	100	20	0	0	0	0,8	100	80	0,2	10	2	1	15	15	0	0	0	0	0	0	2	80	160
	0,2	100	20	0	0	0	0,8	100	80	2	2	4	0,5	0,5	0,25	0	0	0	0	0	0	2	50	100
	0,8	100	80	0	0	0	1,5	100	150	0,5	30	15	1	75	75	0	0	0	0	0	0	3	40	120
	0,5	100	50	0,2	20	4	3	100	300	0,2	35	7	2	80	160	2	1	2	0	0	0	3	60	180
	0,3	100	30	0,3	50	15	0,3	100	30	0,2	70	14	1	5	5	0	0	0	0	0	0	3	90	270

		CXCR4						CXCL12						Ki67						SM-actin					
		Epithelium			Stroma			Epithelium			Stroma			Epithelium			Stroma			Epithelium			Stroma		
		Intensity	% cells	H score	Intensity	% cells	H score	Intensity	% cells	H score	Intensity	% cells	H score	Intensity	% cells	H score	Intensity	% cells	H score	Intensity	% cells	H score	Intensity	% cells	H score
Mean	**HER2**	1,15	99,2	120,0	2,20	71,0	159,5	1,86	98,2	182,431	1,82	68,9	137,6	1,4	28	47	0,70	3,5	8,6	0	0	0	3,19	54,9	178,8
	BLC	1,14	100,0	113,9	1,39	61,8	100,9	1,06	98,4	104,352	1,07	49,4	64,7	2,29	53,00	136,00	1,55	7,0	19,9	0,56	8,49	0,30	3,03	61,5	193,0
	Lum-A	0,41	95,6	40,8	0,20	15,4	5,3	1,39	96,1	129,125	0,38	24,7	10,7	0,7	10	18	0,08	0,04	0,1	0	0	0	2,63	45,4	128,0
p value	HER2 vs BLC	NS	NS	NS	0,0005	NS	0,02645	0,0005	NS	0,00064	0,0007	0,0026	0,0008	2,9E-05	8,5E-07	2,2E-07	0,00296	0,050	0,040	0,008	0,016	0,020	NS	NS	NS
	HER2 vs LUM	7,6E-05	NS	7,6E-05	7,71E-14	2E-10	5,1E-09	0,05	NS	0,05	1E-09	3E-08	6,28E-09	0,003	0,003	0,012	0,002	0,008	0,016	NS	NS	NS	0,048	NS	0,019
	BLC vs LUM	2,4E-06	NS	1,5E-06	1,44E-10	8,52E-09	1,4E-07	NS	NS	NS	0,001	0,0008	0,0002	1,5E-08	1,3E-09	2E-10	1,1E-08	3E-06	2E-05	0,008	0,016	0,020	NS	0,022	0,005

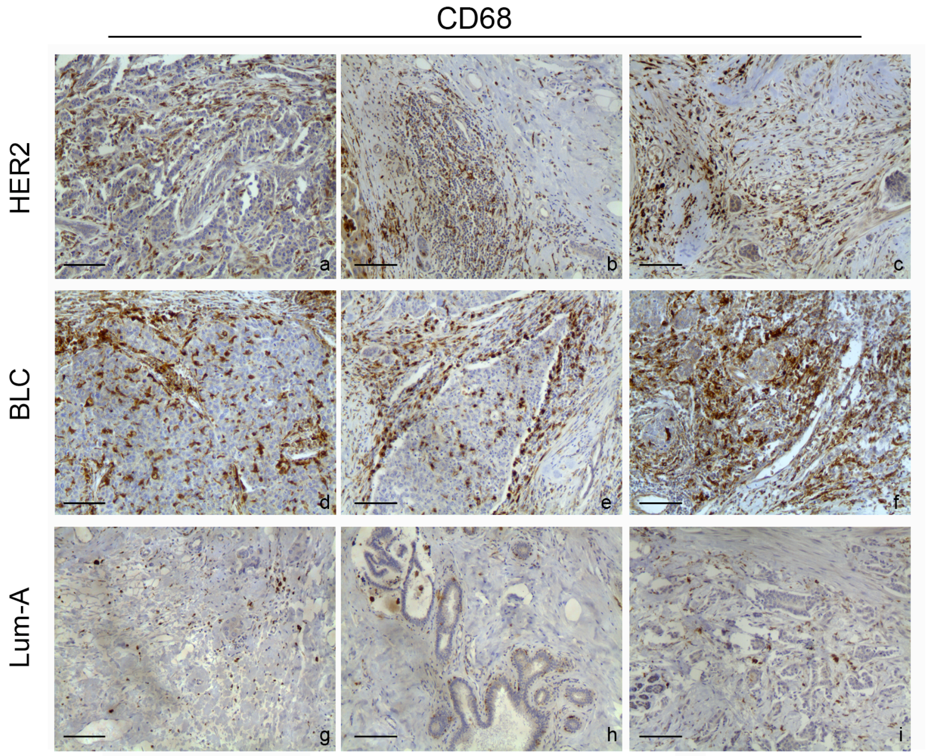
A



Ki67

		Epithelium			Stroma		
		Intensity	% cells	H score	Intensity	% cells	H score
Mean	**HER2**	1,4	28	47	0,70	3,5	8,6
	BLC	2,29	53	136	1,55	7,0	19,9
	Lum-A	0,7	10	18	0,08	0,04	0,1
p value	HER2 vs BLC	2,9E-05	8,5E-07	2E-07	0,003	0,050	0,040
	HER2 vs LUM	0,003	0,003	0,012	0,002	0,008	0,016
	BLC vs LUM	1,49E-08	1,28E-09	2E-10	1,06E-08	3E-06	2E-05

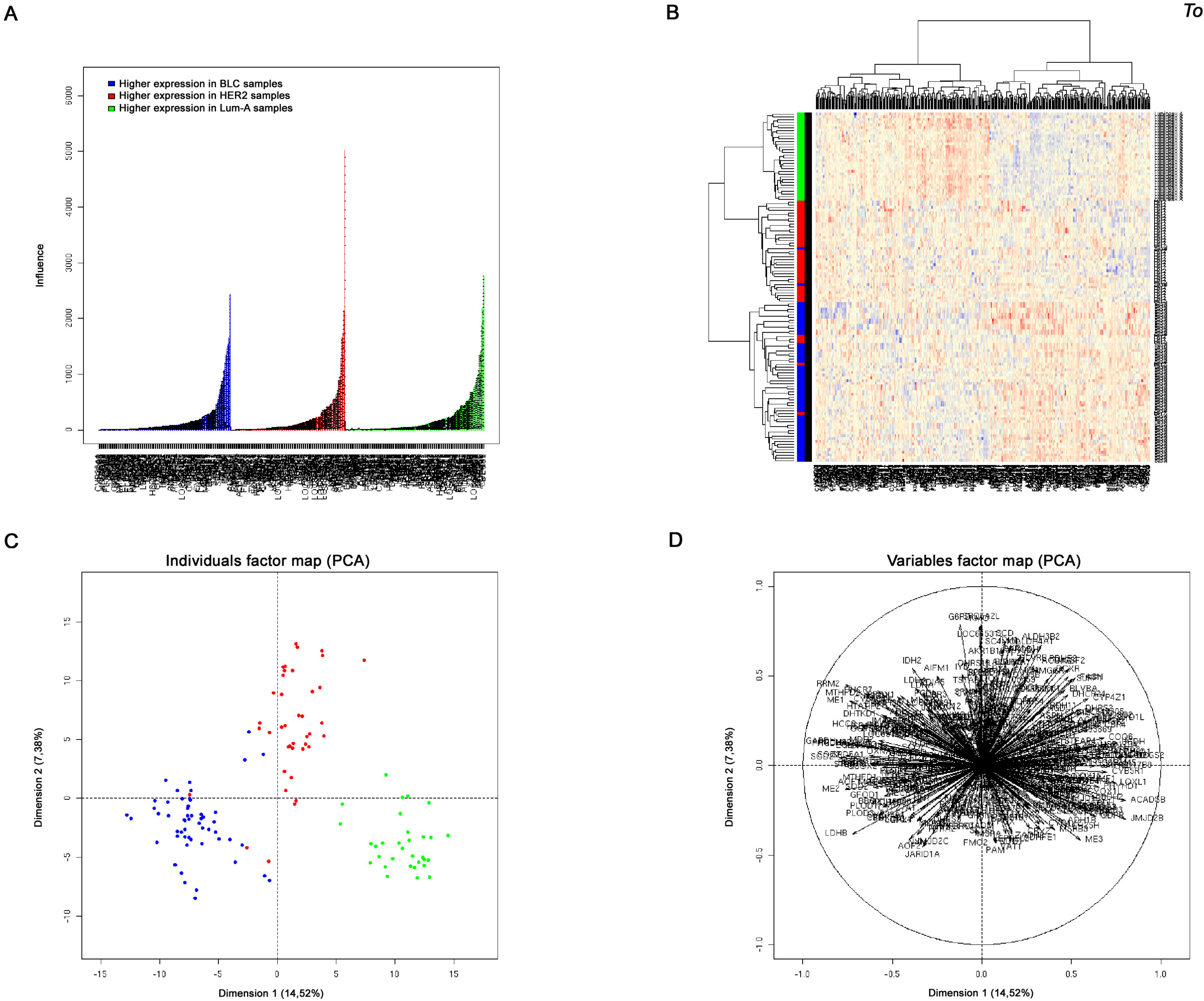
B



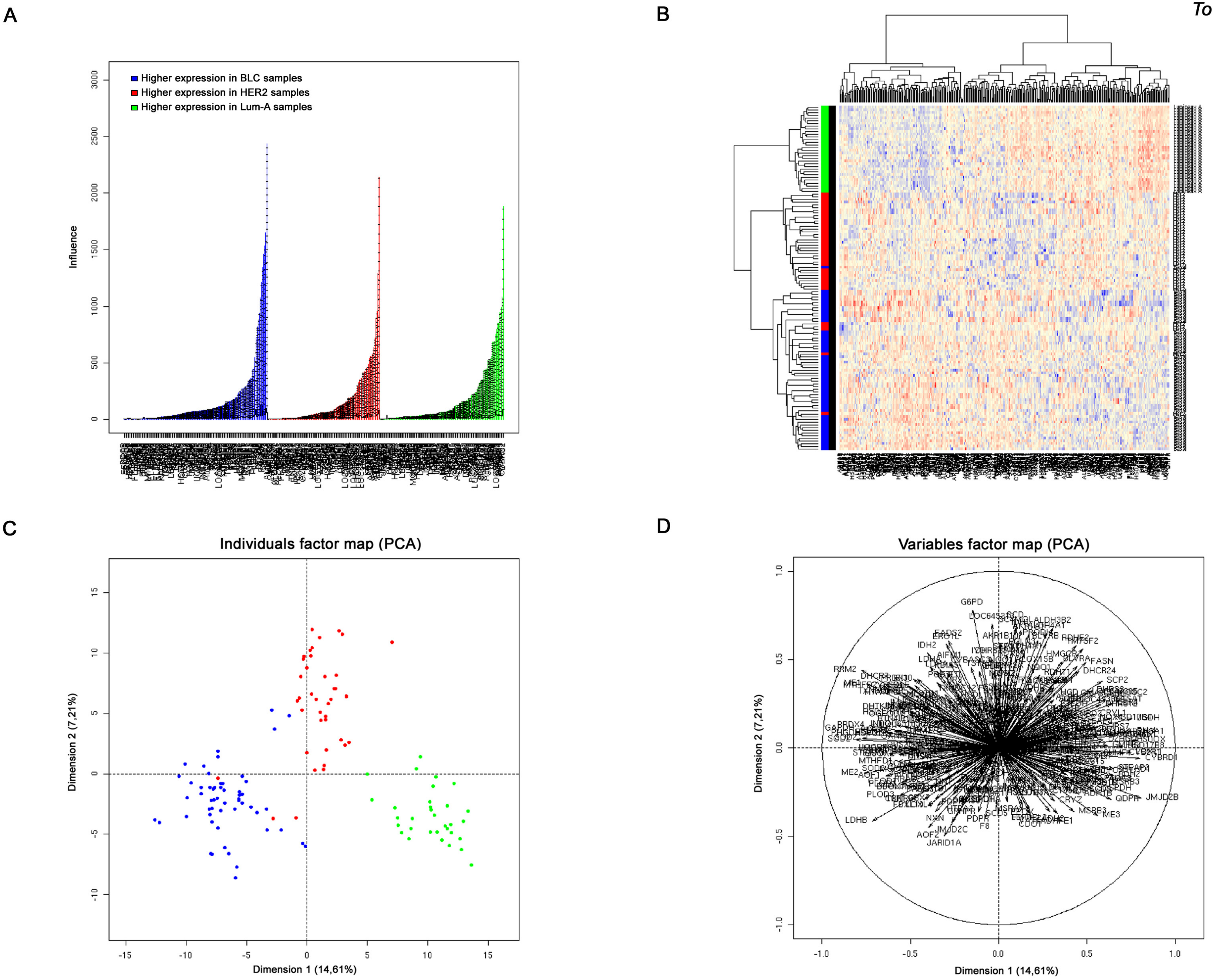
CD68-positive cells

		Nb / µm^2
Mean	**HER2**	0,0544 ± 8,6E-3
	BLC	0,0435 ± 9,6E-3
	Lum-A	0,0188 ± 4,1E-3
p value	HER2 vs BLC	NS
	HER2 vs LUM	0,002
	BLC vs LUM	0,03

Toullec_FigS5



Toullec_FigS6



Symbol	Full Name	pValue
TM7SF2	Transmembrane 7 superfamily, member 2	8,41E-17
ALDH4A1	Aldehyde dehydrogenase, Family 4, subfamily A, member 1	5,72E-16
KMO	**Kynurenine 3-monooxygenase**	**1,37E-15**
ALOX15B	**Arachidonate-15-Lipoygenase, second type**	**1,49E-15**
ALDH3B2	Aldehyde dehydrogenase 3 Family, member B2	1,68E-15
ACOX2	Acyl-Coenzyme A oxidase 2, branched chain	4,16E-15
GPD1L	Glycerol-3-phosphate dehydrogenase	8,22E-15
CYP4Z1	**Cytochrome P450, family 4, subfamily Z, polypeptide 1**	**1,36E-14**
RETSAT	Retinol saturase (all-trans-retinol 13,14-reductase)	1,82E-14
G6PD	Glucose-6-phosphate dehydrogenase	2,03E-14
RDHE2	Short chain dehydrogenase/reductase family 16C, member 5	1,69E-13
UGDH	UDP-Glucose dehydrogenase	3,08E-13
PRODH	**Proline dehydrogenase (oxidase) 1**	**8,51E-13**
SCD	Stearoyl-CoA desaturase	1,16E-12
FASN	Fatty acid synthase	3,95E-12
SURF1	Surfeit 1	6,65E-12
SC4MOL	**sterol-C4-methyl oxidase-like**	**8,52E-12**
IDH1	Isocitrate dehydrogenase 1 (NADP+), soluble	1,97E-11
SUOX	**Sulfite oxidase**	**4,97E-11**
AKR1B10	Aldose reductase Family 1, member 10	1,36E-10
SCP2	Sterol carrier protein 2	1,39E-10
LOC647305	similar to all-trans-13,14-dihydroretinol saturase	1,58E-10
DEGS2	Sphingolipid delta-4-Desaturase / C4-hydroxylase	1,64E-10
CYP2J2	**Cytochrome P450, family 2, subfamily J, polypeptide 2**	**2,79E-10**
HMGCR	3-hydroxy-3-methylglutaryl-Coenzyme A reductase	4,51E-10
CBR4	Carbonyl reductase 4	4,59E-10
BLVRA	Biliverdin reductase A	5,23E-10
SRD5A2L	steroid 5 alpha-reductase 3	5,66E-10
MOSC2	MOCO sulphurase C-terminal domain containing 2	1,49E-09
LOC645313	similar to stearoyl-CoA desaturase	2,10E-09
NOX4	**NADPH oxidase 4**	**2,19E-09**
PH-4	prolyl 4-hydroxylase, transmembrane (endoplasmic reticulum)	8,99E-09
AKR1A1	Aldo-keto reductase family 1, member A1	1,35E-08
ACAD8	Acyl-CoA dehydrogenase family, member 8	1,57E-08
CYBRD1	Cytochrome b reductase 1	1,72E-08
DCXR	Dicarbonyl/L- L-xylulose reductase	3,64E-08
RDH11	Retinol dehydrogenase 11 (all-trans/9-cis/11-cis)	7,40E-08
DHRS2	Dehydrogenase/reductase (SDR family) 2	8,78E-08
ALOX15B	**Arachidonate-15-Lipoygenase, type B**	**9,40E-08**
DIO2	Deiodinase, iodothyronine, type II	1,24E-07
DHCR24	24-dehydrocholesterol reductase (seladin-1)	1,31E-07
CMAH	cytidine monophosphate-N-acetylneuraminic acid hydroxylase	1,67E-07
DHRS12	Dehydrogenase/reductase (SDR family) member 12	2,72E-07
COQ6	Coenzyme Q6	3,30E-07
LOC652445	similar to NADPH oxidase 4	3,71E-07
BLVRB	Biliverdin reductase B	4,70E-07
PRDX5	Peroxiredoxin 5	5,28E-07

Symbol	Full Name	pValue
LOX	**Lysyl oxidase**	**5,763E-07**
ALDH6A1	Aldehyde dehydrogenase 6 family, member A1	6,26E-07
SC5DL	Sterol-C5-desaturase	1,06E-06
EGLN3	Egl9, C. elgans, Homolog of. PHD3	1,16E-06
ASPH	Aspartate beta-hydroxylase	1,19E-06
IYD	Iodotyrosine deiodinase	1,22E-06
CYP4X1	**Cytochrome P450, family 4, subfamily X, polypeptide 1**	**1,39E-06**
LOXL1	**Lysyl oxidase-like 1**	**2,76E-06**
DHRS13	Dehydrogenase/reductase (SDR family) 13	4,96E-06
DHRS7	Dehydrogenase/reductase (SDR family) member 7	5,28E-06
STEAP4	Six-transmembrane epithelial antigen of prostate 4	5,83E-06
HSD17B8	Hydroxysteroid (17-beta) dehydrogenase 8	6,43E-06
D2HGDH	D-2-hydroxyglutarate dehydrogenase	1,25E-05
HSD17B4	Hydroxysteroid (17-beta) dehydrogenase 4	1,39E-05
FMO4	**Flavin containing monooxygenase 4**	**1,85E-05**
NQO1	**NADPH dehydrogenase, quinone 1**	**2,31E-05**
ACOX1	Acyl-Coenzyme A oxidase 1, palmitoyl	2,73E-05
GLUD1	Glutamate dehydrogenase 1	2,85E-05
FADS2	Fatty acid desaturase 2	2,91E-05
LOC653381	similar to Sorbitol dehydrogenase	3,86E-05
AKR7A3	Aldo-keto reductase Family 7, member A3	4,43E-05
CYB5R1	Cytochrome b reductase 1	5,24E-05
SQRDL	Sulfide quinone reductase-like (yeast)	5,83E-05
HGD	**Homogentisate 1,2 dioxygenase**	**6,49E-05**
CRYL1	Crystallin, lambda 1	7,23E-05
JMJD3	Lysine (K)-specific demethylase 6B	7,27E-05
HSD17B11	Hydroxysteroid (17-beta) dehydrogenase 11	7,58E-05
AOC3	Amine oxidase, copper containing 3	0,0001
JARID1B	Lysine (K)-specific demethylase 5B	0,0001
FMO1	**Flavin containing monooxygenase 1**	**0,0002**
LOC493869	Glutathione peroxidase 8 (putative)	0,0002
MSRB2	Methionine sulfoxide reductase B2	0,0002
TXNRD2	Thioredoxin reductase 2	0,0002
P4HA1	prolyl 4-hydroxylase, alpha polypeptide I	0,0003
RSAD1	Radical S-adenosyl methionine domain containing 1	0,0003
CYBASC3	Cytochrome b, ascorbate dependent 3	0,0003
C10orf59/RNLS	Renalase	0,0004
SUMF1	Sulfatase modifying factor 1	0,0005
UEVLD	Ubiquitin E2 lactamate/malate dehydrogenase	0,0005
P4HA3	prolyl 4-hydroxylase, alpha polypeptide III	0,0006
ALDH2	Aldehyde dehydrogenase 2 family (mitochondrial)	0,0009
MOSC1	MOCO sulphurase C-terminal domain containing 1	0,0010
PXDN	Peroxidasin homolog (Drosophila)	0,0011
ALDH8A1	Aldehyde dehydrogenase 8 family, member A1	0,0011
PCYOX1	Prenylcysteine oxidase 1	0,0012
RDH13	Retinol dehydrogenase 13 (all-trans/9-cis)	0,0013
GPX2	Glutathione peroxidase 2	0,0015

Symbol	Full Name	pValue
MTRR	5-methyltetrahydrofolate-homocysteine methyltransferase reductase	0,0016
DHRSX	Dehydrogenase/reductase (SDR family) X-linked	0,0029
HSD17B6	Hydroxysteroid (17-beta) dehydrogenase 6	0,0032
FMO5	Flavin-containing monooxygenase 5	0,0033
BDH1	3-hydroxybutyrate dehydrogenase, type 1	0,0040
STEAP2	Six transmembrane epithelial antigen of the prostate 2	0,0043
TSTA3	Tissue specific transplantation antigen P35B	0,0057
SRXN1	Sulfiredoxin 1 homolog (S. cerevisiae)	0,0065
SEPX1	Selenoprotein X, 1	0,0066
STEAP1	Six transmembrane epithelial antigen of the prostate 1	0,0072
P4HA2	prolyl 4-hydroxylase, alpha polypeptide II	0,0072
MSRB3	Methionine sulfoxide reductase B3	0,0081
BDH2	3-hydroxybutyrate dehydrogenase, type 2	0,0083
APBA2BP	N-terminal EF-hand calcium binding protein 3	0,0088
PDIA5	Protein disulfide isomerase family A, member 5	0,0102
NDUFV2	NADH dehydrogenase (ubiquinone) flavoprotein 2	0,0125
ETFDH	Electron-transferring-flavoprotein dehydrogenase	0,0130
CYP51A1	**Cytochrome P450, family 51, subfamily A, polypeptide 1**	**0,0131**
GPD2	Glycerol-3-phosphate dehydrogenase 2 (mitochondrial)	0,0142
COX15	**Cytochrome c oxidase assembly protein**	**0,0155**
FTL	Ferritin, light polypeptide	0,0169
ERO1L	Thioredoxin domain containing protein 4	0,0171
NMRAL1	NmrA-like family domain containing 1	0,0180
BEST1	Bestrophin 1	0,0181
GPX4	Glutathione peroxidase 4 (phospholipid hydroperoxidase)	0,0199
CTBP2	C-terminal binding protein 2	0,0205
PDHB	Pyruvate dehydrogenase (lipoamide) beta	0,0206
GSR	Glutathione reductase	0,0212
OGDH	Oxoglutarate (alpha-ketoglutarate) dehydrogenase (lipoamide)	0,0224
TP53I3	Tumor protein p53 inducible protein 3	0,0225
DHRS7B	Dehydrogenase/reductase (SDR family) member 7B	0,0232
CYP4F8	**Cytochrome P450, family 4, subfamily F, polypeptide 8**	**0,0236**
GMPR2	Guanosine monophosphate reductase 2	0,0246
DECR2	2,4-dienoyl CoA reductase 2, peroxisomal	0,0249
JMJD2B	Jumonji domain-containing protein 2A	0,0252
FDFT1	Farnesyl-diphosphate farnesyltransferase 1	0,0255
FBXL11	F-box and leucine-rich repeat protein 11	0,0299
ADH1C	ADH1C alcohol dehydrogenase 1C (class I), gamma polypeptide	0,0311
ACADVL	Acyl-Coenzyme A dehydrogenase, very long chain	0,0316
ACADSB	Acyl-Coenzyme A dehydrogenase, short/branched chain	0,0356
QSOX1	Quiescin Q6 sulfhydryl oxidase 1	0,0364
PRDX3	Peroxiredoxin 3	0,0366
IDH2	Isocitrate dehydrogenase 1 (NAD+)/ oxidoreductase	0,0375
CYP27B1	**Cytochrome P450, family 27, subfamily B, polypeptide 1**	**0,0396**
PNPO	Pyridoxamine 5'-phosphate oxidase	0,0430
DPYD	Dihydropyrimidine dehydrogenase	0,0514

Toullec_FigS7