SUPPLEMENTARY DATA:

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

(A) HES coloration of sections from *ras* and *ras* $junD^{-L}$ tumours. (B) Histological analysis of sections from *ras* and *ras* $junD^{-L}$ 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* $junD^{-L}$ 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 $junD^{-L}$ mice (c-h) did not exhibit any JunD staining. (D) CXCL12-staining detected in *ras* $junD^{-L}$ 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 $junD^{-L}$ mice (b,d). Scale bars = 40 μ m in (Aa-d;Ba-d;Da,b), 20 μ m in (Be-h;Dc,d) and 10 μ m 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 costained 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 following silencing of CXCL12 (siRNA CXCL12) or HIF-1 α (siRNA HIF-1 α) 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. β 2-microglobulin was used as an internal control. Right part: CXCL12 mRNA levels in *junD*^{-/-} fibroblasts following silencing of CXCL12 (siRNA CXCL12) or HIF-1 α (siRNA HIF-1 α) 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-1a protein levels modulates myofibroblast properties.

(A) Left part: Relative levels of HIF-1 α mRNA in *wt* and *junD*^{-/-} fibroblasts. β 2-microglobulin was used as an internal control. Right part: HIF-1 α mRNA levels in *junD*^{-/-} fibroblasts following silencing of CXCL12 (siRNA CXCL12) or HIF-1 α (siRNA HIF-1 α) 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-1 α -directed siRNA (+ si HIF-1 α). (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-1 α 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 (μ m) 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 \geq 3), orange, intermediate intensity (3> Int \geq 2); yellow, low intensity (2> Int \geq 1) and white, faint or no detected

signal (Int < 1). Percentage of positive cells was as follow: Yellow : $0 \le \% \le 49$, orange : $50 \le \% \le 79$, red : $\% \ge 80$. Finally, H score was calculated as follow: Intensity x % cells, and color code was as follow : yellow : $0 \le H \le 159$, orange : $160 \le H \le 269$, 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 ≤ 0.01), significant in orange (p ≤ 0.05) or non-significant (NS).

Figure S4: HER2 and BLC tumors are associated with high proliferation rate and proinflammatory 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 \pm 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 = 40 μ m.

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).

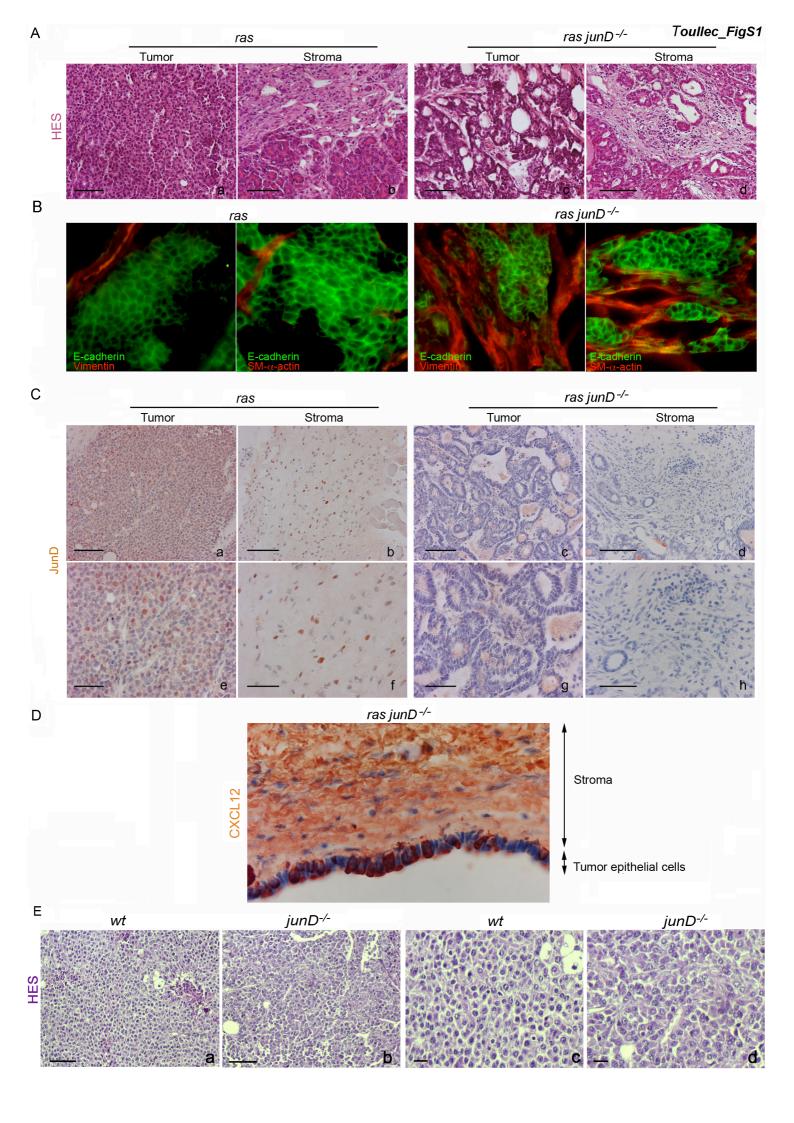
Figure S6: GO term oxido-reductase activity (GO:0016491) in HER2, BLC and Lum-A breast cancers. Same legend as in Figure S5.

 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.

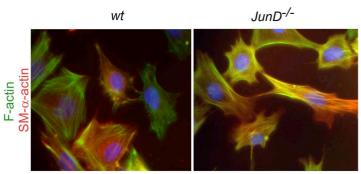
(A) Western blots showing CXCR4 or JunD protein in extracts from various human breast cancer cell lines. Ponceau coloration was used as an internal control for each protein loading; a representative gel is shown (B) Western blots showing HIF-1 α or CXCL12 protein in extracts from human breast cancer cell lines that have been treated with DFO (for detection of HIF-1 α) or DFO+Brefeldin (for detection of CXCL12). DFO is an iron chelator, which inhibits PHD and thus increases HIF-1 α ; Brefeldin (100yM) 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.



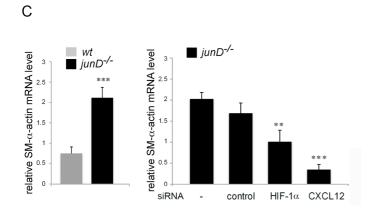
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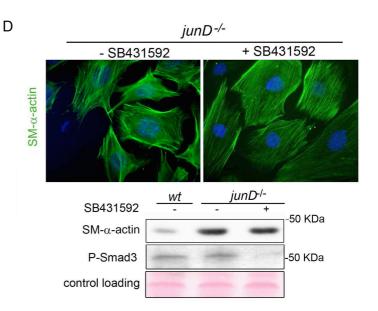


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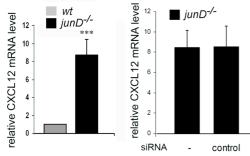


Staining	Quantified	Geno	p value	
Stanning	Parameter	wt	JunD-/-	p value
SM-α actin	Fluorescence intensity (A.U.)	3.6 ± 1.77	40.8 ± 9.28	4.E-11
F-actin	Fluorescence intensity (A.U.)	6.8 ± 3.34	37.5 ± 7.43	3.E-12
N-cadherin	Number of AJ / Cell	17.7 ± 1.96	42.1 ± 10.96	0.0014
Vinculin	Number of FA / Cell	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





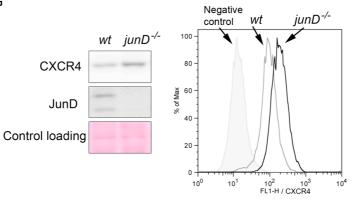
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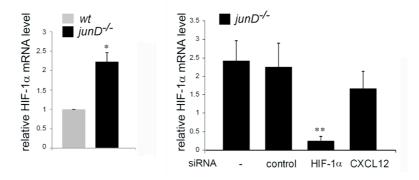
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RNA	-	control	HIF-10	x CXCL12	

Staining	Quantified	Jun	p value	
Stanning	Parameter	+ si control	+ si CXCL12	pvalue
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



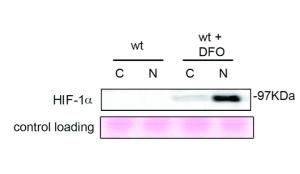
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В

Staining	Quantified	Juni	D-/-	p value
Stanning	Parameter	+ si control	+ si HIF	p value
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



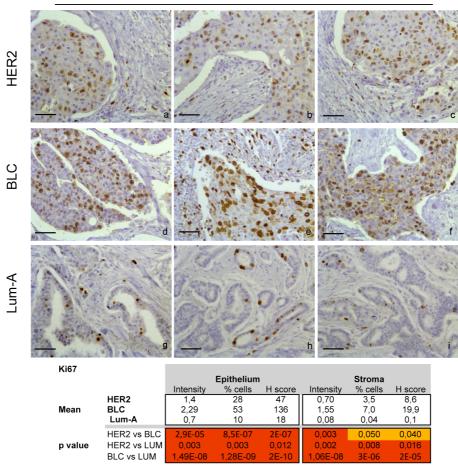


D)				
	Staining	Quantified	V	vt	p value
	otannig	Parameter	- DFO	+ DFO	pvalae
	SM-α-actin	Fluorescence intensity (A.U.)	5± 2.10	25.6 ± 6	2E-10
	F-actin	Fluorescence intensity (A.U.)	9.80 ± 2.90	21.9 ± 6.8	0.00004
	N-cadherin	Number of AJ / Cell	41.5 ± 8.80	51.2 ± 10.3	0.00025
	Vinculin	Number of FA / 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

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Staining	Quantified	jun	n voluo	
Staining	Parameter	- NAC	+ NAC	p value
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

	Tumor type	CXCR4	Epithelium		Intocsity	Stroma	Harris		Epitheliun		Intonsit	Stroma	Harris		Epitheliur			Stroma	Horac		Epithelium	ı	Interes'	Stroma	
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	Lum-A	0,3 1 1 0,5	100 100 100 100 100 100 100 100 100 100	30 100 100 50 80 20 80 100 20 80 80 100 30 50 50 50 50 50 50 100 20 20 80 50 20 80 80 100 100 100 80 80 100 10	0,5 1 1 2,5	80 25 60 70 70 50 20 30 0 0 0 0 0 0 0 0 50 5 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	40 25 60 175	2 0,5 1 0,5 1,3 0,8 0,8 0,8 1,5 3 5 0,4 1,5 0,5 0,5 0,5 0,5 0,5 0,5 0,5 0,5 0,5 0	100 100 100 100 100 100 100 100 100 100	200 50 100 50 130 64 250 80 80 150 250 40 75 40 250 40 75 250 40 75 150 250 40 300 50 130 50 130 50 130 50 130 350 350 350 350 30 30 30 30 30 30 30 30 30 30 30 30 30	3	90 100	120 45 300 160	2,5 2,5 1,5 0 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	60 50 50 70 0 5 0 0 5 0 0 0 0 0 0 0 0 0 0	60 150 100 75 210 0 5 0 0 0 0 0 0 0 0 0 0 0 0 0	3 2	5 20 5 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	7,5 60 10 0	4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0			4 4 3 3 3 3 3 3 3 3 3 5 2,5 2,5 2,5 2,5 0 3 3,5 0 3 3,5 0 2 2 3 3 3 3 5 5 0 2 2 3 3 3 5 5 2,5 2,5 2,5 2,5 2,5 2,5 2,5 2,5 2,5	80 30 55 40 70 80 35 60 10 40 20 0 70 20 20 20 20 40 70 20 40 70 20 40 70 0 90 80 80 80 80 80 80 80 80 80 8	220 90 110 120 140 165 180 30 105 50 0 210 270 270 270 270 270 270 270 270 270 27
0	HER2 BLC Lum-A HER2 vs BLC HER2 vs LUM BLC vs LUM		Epithelium % cells 99,2 100,0 95,6 NS NS NS NS	H score 120,0 113,9 40,8 NS 7,6E-05 1,5E-06	Intensity 2,20 1,39 0,20 0,0005 7,71E-14 1,44E-10	Stroma % cells 71,0 61,8 15,4 NS 2E-10 8,52E-09	H score 159,5 100,9 5,3 0,02645 5,1E-09 1,4E-07	Intensity 1,86 1,06 1,39 0,0005 0,05 NS	Epithelium % cells 98,2 98,4 96,1 NS NS NS	H score 182,431 104,352 129,125 0,00064 0,05 NS	Intensity 1,82 1,07 0,38 0,0007 1E-09 0,001	Stroma % cells 68,9 49,4 24,7 0,0026 3E-08 0,0008	H score 137,6 64,7 10,7 0,0008 6,28E-09 0,0002	Intensity 1,4 2,29 0,7 2,9E-05 0,003 1,5E-08	Epitheliun % cells 28 53,00 10 8,5E-07 0,003 1,3E-09	H score 47 136,00 18 2,2E-07	Intensity 0,70 1,55 0,08 0,00296 0,002 1,1E-08	Stroma % cells 3,5 7,0 0,04 0,050 0,008 3E-06	H score 8,6 19,9 0,1 0,040 0,016 2E-05	Intensity 0 0,56 0 0,008 NS 0,008	Epithelium % cells 0 8,49 0 0,016 NS 0,016	H score 0 0,30 0 0,020 NS 0,020	Intensity 3,19 3,03 2,63 NS 0,048 NS	Stroma % cells 54,9 61,5 45,4 NS NS 0,022	H score 178,8 193,0 128,0 NS 0,019 0,005





CD68

8,5E-0 0,003

2E-0 0,01

2,9E-0 0,003

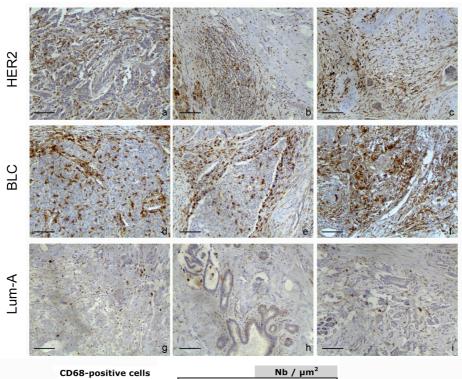
49E-0

p value

0,050 0,008 3E-06

0,000

0,040 0,016 2E-05



CD68-positive cells		Nb / µm ²
	HER2	0,0544 ± 8,6E-3 0,0435 ± 9,6E-3
Mean	BLC	0,0435 ± 9,6E-3
	Lum-A	0,0188 ± 4,1E-3
	HER2 vs BLC	NS
p value	HER2 vs LUM	0,002
	BLC VS LUM	0.03

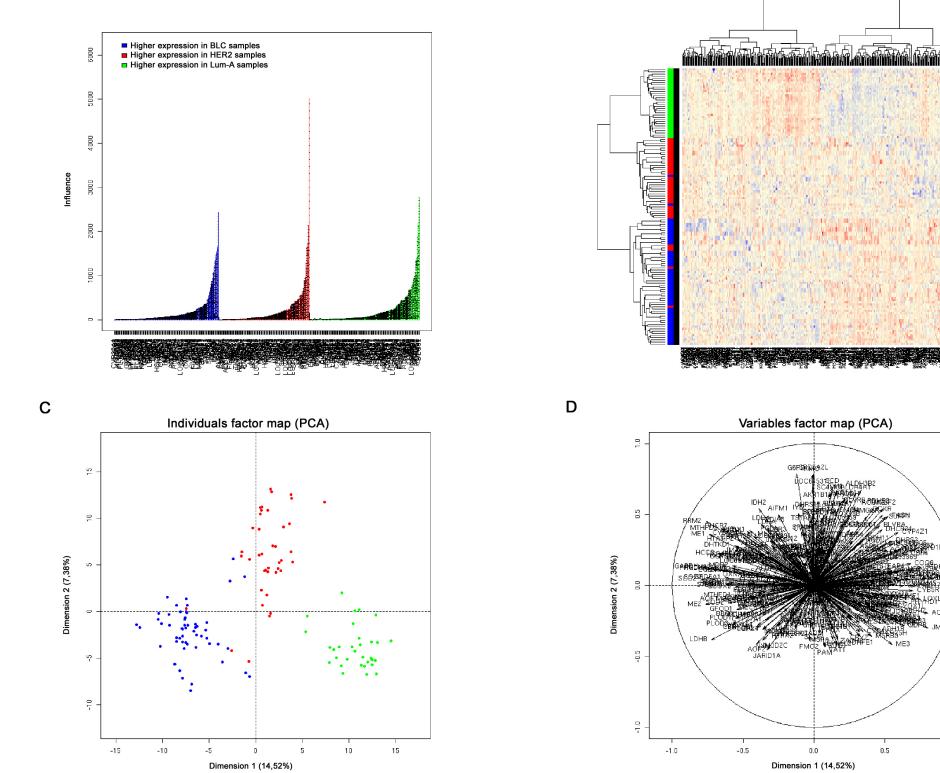


Contractor of the owner

ME3

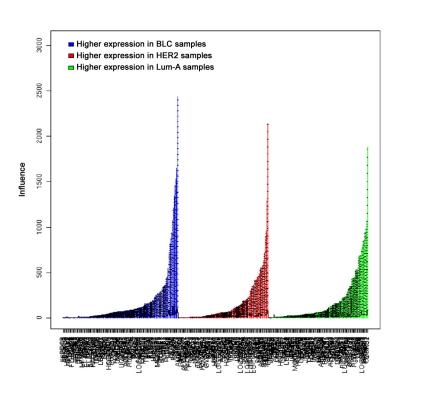
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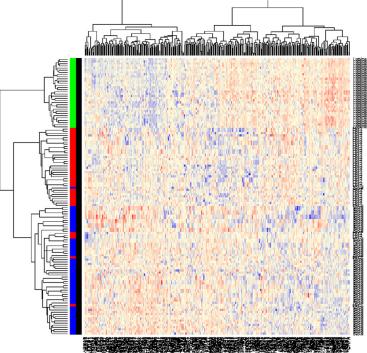
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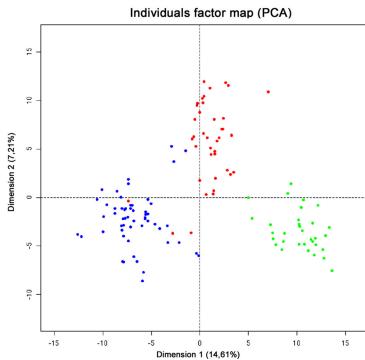
В

Α



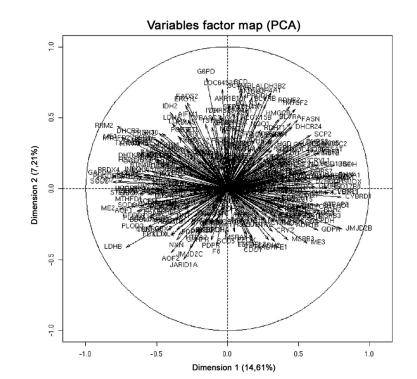


С



D

В



Symbol	Full Name	pValue	Symbol	Full Name
TM7SF2	Transmembrane 7 superfamily, member 2	8,41E-17	LOX	Lysyl oxidase
ALDH4A1	Aldehyde dehydrogenase, Family 4, subfamily A, member 1	5,72E-16	ALDH6A1	Aldehyde dehydrogenase 6 family, member A1
KMO	Kynurenine 3-monooxygenase	1,37E-15	SC5DL	Sterol-C5-desaturase
ALOX15B	Arachidonate-15-Lipoygenase, second type	1,49E-15	EGLN3	Egl9, C. elgans, Homolog of. PHD3
ALDH3B2	Aldehyde dehydrogenase 3 Family, member B2	1,68E-15	ASPH	Aspartate beta-hydroxylase
ACOX2	Acyl-Coenzyme A oxidase 2, branched chain	4,16E-15	IYD	lodotyrosine deiodinase
GPD1L	Glycerol-3-phosphate dehydrogenase	8,22E-15	CYP4X1	Cytochrome P450, family 4, subfamily X, polypepti
CYP4Z1	Cytochrome P450, family 4, subfamily Z, polypeptide 1	1,36E-14	LOXL1	Lysyl oxidase-like 1
RETSAT	Retinol saturase (all-trans-retinol 13,14-reductase)	1,82E-14	DHRS13	Dehydrogenase/reductase (SDR family) 13
G6PD	Glucose-6-phosphate dehydrogenase	2,03E-14	DHRS7	Dehydrogenase/reductase (SDR family) member 7
RDHE2	Short chain dehydrogenase/reductase family 16C, member 5	1,69E-13	STEAP4	Six-transmembrane epithelial antigen of prostate 4
UGDH	UDP-Glucose dehydrogenase	3,08E-13	HSD17B8	Hydroxysteroid (17-beta) dehydrogenase 8
PRODH	Proline dehydrogenase (oxidase) 1	8,51E-13	D2HGDH	D-2-hydroxyglutarate dehydrogenase
SCD	Stearoyl-CoA desaturase	1,16E-12	HSD17B4	Hydroxysteroid (17-beta) dehydrogenase 4
FASN	Fatty acid synthase	3,95E-12	FMO4	Flavin containing monooxygenase 4
SURF1	Surfeit 1	6,65E-12	NQO1	NADPH dehydrogenase, quinone 1
SC4MOL	sterol-C4-methyl oxidase-like	8,52E-12	ACOX1	Acyl-Coenzyme A oxidase 1, palmitoyl
IDH1	Isocitrate dehydrogenase 1 (NADP+), soluble	1,97E-11	GLUD1	Glutamate dehydrogenase 1
suox	Sulfite oxidase	4,97E-11	FADS2	Fatty acid desaturase 2
AKR1B10	Aldose reductase Family 1, member 10	1,36E-10	LOC653381	similar to Sorbitol dehydrogenase
SCP2	Sterol carrier protein 2	1,39E-10	AKR7A3	Aldo-keto reductase Family 7, member A3
LOC647305	similar to all-trans-13,14-dihydroretinol saturase	1,58E-10	CYB5R1	Cytochrome b reductase 1
DEGS2	Sphingolipid delta-4-Desaturase / C4-hydroxylase	1,64E-10	SQRDL	Sulfide quinone reductase-like (yeast)
CYP2J2	Cytochrome P450, family 2, subfamily J, polypeptide 2	2,79E-10	HGD	Homogentisate 1,2 dioxygenase
HMGCR	3-hydroxy-3-methylglutaryl-Coenzyme A reductase	4,51E-10	CRYL1	Crystallin, lambda 1
CBR4	Carbonyl reductase 4	4,59E-10	JMJD3	Lysine (K)-specific demethylase 6B
BLVRA	Biliverdin reductase A	5,23E-10	HSD17B11	Hydroxysteroid (17-beta) dehydrogenase 11
SRD5A2L	steroid 5 alpha-reductase 3	5,66E-10	AOC3	Amine oxidase, copper containing 3
MOSC2	MOCO sulphurase C-terminal domain containing 2	1,49E-09	JARID1B	Lysine (K)-specific demethylase 5B
LOC645313	similar to stearoyl-CoA desaturase	2,10E-09	FMO1	Flavin containing monooxygenase 1
NOX4	NADPH oxidase 4	2,19E-09	LOC493869	Glutathione peroxidase 8 (putative)
PH-4	prolyl 4-hydroxylase, transmembrane (endoplasmic reticulum)	8,99E-09	MSRB2	Methionine sulfoxide reductase B2
AKR1A1	Aldo-keto reductase family 1, member A1	1,35E-08	TXNRD2	Thioredoxin reductase 2
ACAD8	Acyl-CoA dehydrogenase family, member 8	1,57E-08	P4HA1	prolyl 4-hydroxylase, alpha polypeptide l
CYBRD1	Cytochrome b reductase 1	1,72E-08	RSAD1	Radical S-adenosyl methionine domain containing 1
DCXR	Dicarbonyl/L- L-xylulose reductase	3,64E-08	CYBASC3	Cytochrome b, ascorbate dependent 3
RDH11	Retinol dehydrogenase 11 (all-trans/9-cis/11-cis)	7,40E-08	C10orf59/RNLS	Renalase
DHRS2	Dehydrogenase/reductase (SDR family) 2	8,78E-08	SUMF1	Sulfatase modifying factor 1
ALOX15B	Arachidonate-15-Lipoygenase, type B	9,40E-08	UEVLD	Ubiquitin E2 lactamate/malate dehydrogenase
DIO2	Deiodinase, iodothyronine, type II	1,24E-07	P4HA3	prolyl 4-hydroxylase, alpha polypeptide III
DHCR24	24-dehydrocholesterol reductase (seladin-1)	1,31E-07	ALDH2	Aldehyde dehydrogenase 2 family (mitochondrial)
СМАН	cytidine monophosphate-N-acetylneuraminic acid hydroxylase	1,67E-07	MOSC1	MOCO sulphurase C-terminal domain containing 1
DHRS12	Dehydrogenase/reductase (SDR family) member 12	2,72E-07	PXDN	Peroxidasin homolog (Drosophila)
COQ6	Coenzyme Q6	3,30E-07	ALDH8A1	Aldehyde dehydrogenase 8 family, member A1
LOC652445	similar to NADPH oxidase 4	3,71E-07	PCYOX1	Prenylcysteine oxidase 1
BLVRB	Biliverdin reductase B	4,70E-07	RDH13	Retinol dehydrogenase 13 (all-trans/9-cis)
PRDX5	Peroxiredoxin 5	5,28E-07	GPX2	Glutathione peroxidase 2

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	0,005
SRXN1	Sulfiredoxin 1 homolog (S. cerevisiae)	0,006
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	0,008
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	0,012
ETFDH	Electron-transferring-flavoprotein dehydrogenase	0,0130
CYP51A1	Cytochrome P450, family 51, subfamily A, polypeptide 1	0,013
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	0,017
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	0,025
FBXL11	F-box and leucine-rich repeat protein 11	0,0299
ADH1C	ADH1C alcohol dehydrogenase 1C (class I), gamma polypeptide	0,031
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

pValue 5,763E-07 6,26E-07 1,06E-06 1,16E-06 1,19E-06 1,22E-06 1,39E-06 2,76E-06 4,96E-06 5,28E-06 5,83E-06 6,43E-06 1,25E-05 1,39E-05 1,85E-05 2,31E-05 2,73E-05 2,85E-05 2,91E-05 3,86E-05 4,43E-05 5,24E-05 5,83E-05 6,49E-05 7,23E-05 7,27E-05 7,58E-05 0,0001 0,0001 0,0002 0,0002 0,0002 0,0002 0,0003 0,0003 0,0003 0,0004 0,0005 0,0005 0,0006 0,0009 0,0010 0,0011 0,0011 0,0012 0,0013 0,0015

