

Table S1. Patients' tumors transplanted in mice and corresponding positivity of engraftment. For each patient with metastatic breast cancer (MBC) site of metastasis, year of surgery and molecular subtype (LB: Luminal B; TN: Triple Negative; HER2+: HER2 positive) is reported. For each Patient Derived Xenografts (PDXs) positivity (YES) or negativity (NO) to the engraftment and molecular subtype is reported.

	Patient			PDXs	
	Metastasis	Diagnosis	Subtype	Engraftment	Subtype
MBC4	liver	2012	LB	YES	LB
MBC7	liver	2012	TN	YES	TN
MBC12	liver	2012	LB	NO	-
MBC14	liver	2012	HER2+	NO	-
MBC18	liver	2012	LB	YES	LB
MBC19	liver	2012	LB	NO	-
MBC20	liver	2012	LB	NO	-
MBC21	liver	2012	HER2+	YES	HER2+
MBC22	liver	2012	LB	YES	LB
MBC24	liver	2012	LB	NO	-
MBC25	liver	2012	LB	NO	-
MBC26	liver	2012	LB	YES	LB
MBC28	node	2012	TN	NO	-
MBC1	lung	2013	TN	YES	TN
MBC2	lung	2013	TN	YES	TN
MBC3	lung	2013	LB	YES	LB
MBC16	lung	2013	LB	NO	-
MBC5	lung	2013	LB	YES	LB
MBC6	lung	2013	HER2+	NO	-
MBC8	node	2013	LB	NO	-
MBC9	node	2013	TN	NO	-
MBC10	lung	2014	LB	YES	LB
MBC11	lung	2014	LB	YES	LB

Table S2. Genomic and transcriptomic profiles reveal high heterogeneity among PDXs (see excel file). Exome sequencing analysis from 4 metastatic breast cancer Patient (PT) and corresponding Patient-derived xenograft (PDX) at different passages reveals high resemblance of mutational profile. Reference was obtained by normal blood samples. Chromosome (chr), start and end position, reference and alteration, variant allele frequency (>0.05 at least in one sample), gene name and variants classification are reported. For Insertions or Deletions, presence (YES) or absence (NO) of alterations is indicated for each sample.

Exome sequencing analysis from 12 metastatic breast cancer PDXs reveals mutation profiles of breast cancer tumors (see excel file). Gene name, chromosome (chr), start and end position, reference and alteration, type of annotated mutation and protein change are reported for each PDX.

RNA-seq analysis of PDXs highlighted a different expression pattern in each PDX (see excel file). Differential expression analysis for 4 metastatic breast cancer PDXs with respect to the normal breast tissue (n=3 samples) is reported. $FDR \leq 0.001$ and \log_2 fold change (FC) $\geq |2|$.