

Figure 1: growth kinetics of established breast PDXs. The average duration of the 3 first passage was calculated for each PDX and used as an estimate of their growth rate. Time is presented in days. Each bar represents a PDX. Color of the bar indicates the molecular subtype to which the PDX was assigned. As shown in Figure 2 red=Bas-L, light blue=Lum-B, pink=Lum-C, orange=m-Apo.

		Molecular subgroups						Steroid receptor status				TP53 status
		CIT	Hu	PAM50	Sorlie	Neve		ER status	PR status	HER2 status		Mut.
B2164	Primary	basL	Basal	Basal	Basal	BasalA		ER-	PR-	0		no
B2164_P2_353	Xenograft	basL	Basal	Basal	Basal	BasalA		ER-	PR-	0		no
B3467	Primary	basL	Basal	Basal	Basal	BasalA		ER-	PR-	0		yes
B3467_P2_548	Xenograft	basL	Basal	Basal	Basal	BasalA		ER-	PR-	0		yes
B3977	Primary	basL	Basal	Basal	Basal	BasalA		ER-	PR-	0		yes
B3977_P3_538	Xenograft	basL	Basal	Basal	Basal	BasalA		ER-	PR-	0		yes
B4122	Primary	basL	Basal	Basal	Basal	BasalA		ER-	PR-	0		no
B4122_P2_1048	Xenograft	basL	Basal	Basal	Basal	BasalA		ER-	PR-	0		no
B0444	Primary	basL	Basal	Basal	Basal	BasalA		ER-	PR-	1+		yes
B0444_P2_916	Xenograft	basL	Basal	Basal	Basal	BasalA		ER-	PR-	1+		yes
B0460	Primary	basL	Basal	Basal	Basal	BasalA		ER-	PR-	1+		yes
B0460_P3_1255	Xenograft	basL	Basal	Basal	Basal	BasalA		ER-	PR-	1+		yes
B1915	Primary	basL	Basal	Basal	Basal	BasalA		ER-	PR-	1+		yes
B1915_P2_887	Xenograft	basL	Basal	Basal	Basal	BasalA		ER-	PR-	1+		yes
B1995	Primary	basL	Basal	Basal	Basal	BasalA		ER-	PR-	0		yes
B1995_P3_896	Xenograft	basL	Basal	Basal	Basal	BasalA		ER-	PR-	0		yes
B0523	Primary	basL	Basal	Basal	Basal	BasalA		ER-	PR-	0		yes
B3029	Primary	basL	Basal	Basal	Basal	BasalA		ER-	PR-	0		yes
B3029_P3_1078	Xenograft	basL	Basal	Basal	Basal	BasalA		ER-	PR-	0		yes
B1240	Primary	basL	Basal	Basal	Basal	BasalA		ER-	PR-	0		yes
B1240_P2_1036	Xenograft	basL	HER2	Basal	Basal	BasalA		ER-	PR-	0		yes
B2412	Primary	basL	Basal	Basal	Basal	BasalB		ER-	PR-	0		yes
B2412_P2_339	Xenograft	basL	Basal	Basal	LuminalB	BasalB		ER-	PR-	0		yes
B3160	Primary	basL	Basal	Normal	Basal	BasalA		ER-	PR-	0		no
B3160_P2_746	Xenograft	basL	Basal	Basal	Basal	BasalA		ER-	PR-	0		no
B3804	Primary	basL	HER2	LuminalB	HER2	BasalB		ER-	PR-	0		yes
B3804_P3_1177	Xenograft	basL	HER2	LuminalB	Basal	BasalB		ER-	PR-	0		yes
B3499	Primary	тАро	HER2	HER2	HER2	Luminal		ER-	PR-	1+		yes
B3499_P2_606	Xenograft	тАро	HER2	HER2	LuminalB	Luminal		ER-	PR-	1+		yes
B3925	Primary	тАро	HER2	LuminalB	LuminalB	Luminal		ER-	PR-	3+		no
B3925_P2_1295	Xenograft	тАро	HER2	LuminalB	LuminalB	Luminal		ER-	PR-	3+		no
B3921	Primary	lumC	LuminalA	LuminalB	LuminalB	Luminal		ER+	PR-	3+		yes
B3921_P2_1369	Xenograft	тАро	HER2	LuminalB	LuminalB	Luminal		ER+	PR-	3+		yes
B3828	Primary	lumB	LuminalA	LuminalB	LuminalB	Luminal		ER+	PR+	0		yes
B3828_P2_777	Xenograft	lumB	LuminalA	LuminalB	LuminalB	Luminal		ER+	PR+	0		yes
B0627	Primary	lumB	LuminalA	LuminalB	LuminalB	Luminal		ER+	PR+	2+		no
B0627_P2_1033	Xenograft	lumB	LuminalA	LuminalB	LuminalB	Luminal		ER+	PR+	2+		no
B2115	Primary	lumC	LuminalA	LuminalB	LuminalB	Luminal		ER+	PR-	3+		no
B2115_P2_703	Xenograft	lumB	LuminalB	LuminalB	LuminalB	Luminal		ER+	PR-	3+		no
B3034	Primary	lumC	LuminalA	LuminalA	LuminalB	Luminal		ER+	PR-	0		no
B3034_P2_814	Xenograft	lumB	LuminalA	LuminalB	LuminalB	Luminal		ER+	PR-	0		no

Figure 2: Molecular classification of PDX and tumors of origin are highly concordant. Identical assignment were found in 87 % of the cases with at least 3/5 identical classifications for each PDX. Divergences were restricted to the luminal subtypes. Transcriptome PDX and corresponding tumor of origin were classified using the Guedj, Hu, PAM 50, Sorlie and Neve breast cancer classifiers and assignments were indicated by a color code. Red: Basal or Bas-L, Orange: M-Apo (ER-/HER2+), Pink: Lum-C (ER+/PR-), light blue: Lum-B (ER+/PR+/HER2-), dark blue: Luminal A. ER, PR status determined by IHC is presented in red for ER-, in green for ER+. HER2 status was noted negative in green when scored <2+, positive in red score = 3+. TP53 mutation status determined by DNA sequencing, mutated in red, wt in green.



Figure 3: Breast tumors of origin and corresponding PDXs show elevated similarity at the genomic level. CNC profiles of all PDXs (* indicates corrected profiles) and breast tumors of origin were determined by array-CGH and convergence tested by clustering analysis. Breast tumors and their cognate PDXs were systematically clustered together (pairs, triplet or quadriplet according to profile availability).



Figure 4: CNC profiles of different grafts from the same primary tumor remain remarkably stable .

A: Graft tree indicating the position of the analyzed PDXs which have been highlighted by a color code.

B: Histograms showing the fraction of overlapping events in the tumor of origin and the corresponding PDX which are identified by color codes indicated in the graft tree. **C**: whole genome CNC profiles, gains are shown in blue, losses in red, chromosomes by alternating light blue and white bars. Samples are identified as shown in the tree



Figure 5: quantification of CNC specifically found in primary tumors (A) or specific of the PDX (B). Events specific to the tumors give an insight on tumor heteroclonality, whereas those found only in the PDX represent events acquired *de novo* during propagation in the mice. A: Each bar represents the percentage of the genome interrogated by the array involved in primary tumor specific CNC. B: the fraction of the genome corresponding to CNC occurring *de novo* in the PDX. CGH profiles of the PDXs and cognate primary tumors were analyzed after correction for the contamination by normal stromal cells.



Figure 6: Expression differences between primary tumors that give rise to PDX (Take) and those that did not (No Take). We analyzed 3 expression signatures with known prognostic impact and two further signatures (*VEGF, IL8*). The tumor set was stratified according to molecular subgroups to verify whether these differences were not due to differences in composition of the Take and the No Take groups. GGI identifies the molecular grade signature (ref), Wound healing (ref) and proliferation signature (ref).