

Figure W1. Mouse gDNA cross-hybridization on aCGH arrays. (A) Evaluation of cross-hybridization of mouse gDNA on human aCGH arrays. Equal amounts of human reference gDNA ($1 \mu\text{g}$) were labeled with Cy3 and Cy5, hybridized to the aCGH arrays (right bar, 0% mouse), and compared to 75% human/25% mouse mixture (left bar, 25% mouse). Selected chromosomes are displayed above. Additional red bands in the bars on the left side are indicative of gains (cross-hybridization). (B) Comparison of original tumor (right bar) *versus* xenograft passage 4 with high mouse component (47%, left bar). Two selected chromosomes are shown, with evidence of greater amounts of gains/amplifications in the xenograft passage with high mouse component.

Pearson correlation coefficient (specimen comparisons)

<u>Model</u>	<u>Xenograft passage</u>	<u>Pearson Correlation</u>
AG-Panc2	p6	0.90
AG-Panc2	p17	0.90
	p6 vs. p17	0.975
AG-Panc3	p6	NA
AG-Panc3	p18	NA
	p6 vs. p18	0.98
AG-Panc4	p5	0.9
AG-Panc4	p16	0.9
	p5 vs. p16	0.98
AG-Panc5	p6	0.875
AG-Panc5	p12	0.875
	p6 vs. p12	0.98
AG-Panc6	p1	0.91
AG-Panc6	p7	0.91
	p1 vs. p7	0.98
AG-Panc8	p3	0.89
AG-Panc8	p5	0.9
	p3 vs. p5	0.99
AG-Panc9	p2	0.89
	p4	0.89
	p2 vs. p4	0.98
AG-Panc10	p4	0.92

Orthotopic comparisons

<u>Model</u>	<u>Orthotopic passage</u>	<u>Pearson Correlation</u>
AG-Panc2 p6	from SQ P10	0.93-0.96
	from SQ P39	0.93
AG-Panc2 p17	from SQ P10	0.92-0.95
	from SQ P39	0.95
AG-Panc10 p4	OT P1	0.97
	OT P2	0.98
AG-Panc13 p0	OT P0	0.97
	OT P1	0.98

Figure W2. Comparison of genome-wide gene expression profiles among samples.

Variable	AG-Panc2-T	AG-Panc2-T	AG-Panc2-T	AG-Panc2-P1	AG-Panc2-P1	AG-Panc2-P1	AG-Panc2-P1	AG-Panc2-P1	AG-Panc2-P1	AG-Panc2-P1	AG-Panc2-P1	AG-Panc2-P1	AG-Panc2-P1	AG-Panc2-P1	AG-Panc2-P1	AG-Panc2-P1	AG-Panc2-P1	AG-Panc2-P1	AG-Panc2-P1	AG-Panc2-P1	
AG-Panc2-T	1.00	0.99	0.98	0.90	0.89	0.89	0.91	0.90	0.90	0.87	0.89	0.88	0.89	0.94	0.89	0.89	0.89	0.88	0.88	0.88	0.88
AG-Panc2-T	0.99	1.00	0.99	0.89	0.90	0.90	0.90	0.90	0.90	0.86	0.88	0.87	0.88	0.94	0.89	0.88	0.88	0.88	0.87	0.88	0.88
AG-Panc2-T	0.98	0.99	1.00	0.89	0.90	0.90	0.90	0.90	0.90	0.86	0.88	0.87	0.88	0.93	0.88	0.88	0.88	0.88	0.87	0.88	0.88
AG-Panc2-P17	0.90	0.89	0.89	1.00	0.99	0.99	0.98	0.97	0.97	0.93	0.95	0.95	0.95	0.90	0.94	0.94	0.94	0.93	0.93	0.93	0.94
AG-Panc2-P17	0.89	0.90	0.90	0.99	1.00	0.99	0.97	0.98	0.97	0.92	0.95	0.95	0.95	0.90	0.94	0.94	0.94	0.93	0.93	0.94	0.94
AG-Panc2-P17	0.89	0.90	0.90	0.99	0.99	1.00	0.97	0.97	0.98	0.92	0.95	0.95	0.95	0.89	0.94	0.94	0.94	0.93	0.93	0.93	0.94
AG-Panc2-P6	0.91	0.90	0.90	0.98	0.97	0.97	1.00	0.99	0.99	0.94	0.96	0.93	0.93	0.89	0.95	0.94	0.94	0.93	0.93	0.93	0.94
AG-Panc2-P6	0.90	0.90	0.90	0.97	0.98	0.97	0.99	1.00	0.99	0.93	0.96	0.93	0.93	0.90	0.95	0.94	0.94	0.93	0.93	0.93	0.94
AG-Panc2-P6	0.90	0.90	0.90	0.97	0.97	0.98	0.99	0.99	1.00	0.93	0.96	0.93	0.93	0.89	0.94	0.94	0.94	0.93	0.93	0.93	0.94
AG-Panc2 OT (from SQ P10)	0.87	0.86	0.86	0.93	0.92	0.92	0.94	0.93	0.93	1.00	0.97	0.93	0.92	0.86	0.90	0.92	0.91	0.89	0.91	0.90	0.91
AG-Panc2 OT (from SQ P10)	0.89	0.88	0.88	0.95	0.95	0.95	0.96	0.96	0.96	0.97	1.00	0.94	0.93	0.88	0.92	0.94	0.93	0.92	0.93	0.92	0.93
AG-Panc2 OT (from SQ P39)	0.88	0.87	0.87	0.95	0.95	0.95	0.93	0.93	0.93	0.93	0.94	1.00	0.98	0.89	0.92	0.93	0.93	0.91	0.92	0.91	0.93
AG-Panc2 OT (from SQ P39)	0.89	0.88	0.88	0.95	0.95	0.95	0.93	0.93	0.93	0.92	0.93	0.98	1.00	0.90	0.93	0.93	0.93	0.91	0.92	0.91	0.93
AG-Panc10-T	0.94	0.94	0.93	0.90	0.90	0.89	0.89	0.90	0.89	0.86	0.88	0.89	0.90	1.00	0.92	0.91	0.91	0.89	0.89	0.89	0.90
AG-Panc10-P4	0.89	0.89	0.88	0.94	0.94	0.94	0.95	0.95	0.94	0.90	0.92	0.92	0.93	0.92	1.00	0.97	0.98	0.94	0.94	0.94	0.95
AG-Panc10 OT-P1	0.89	0.88	0.88	0.94	0.94	0.94	0.94	0.94	0.94	0.92	0.94	0.93	0.93	0.91	0.97	1.00	0.99	0.94	0.95	0.94	0.95
AG-Panc10 OT-P2	0.89	0.88	0.88	0.94	0.94	0.94	0.94	0.94	0.94	0.91	0.93	0.93	0.93	0.91	0.98	0.99	1.00	0.94	0.95	0.94	0.95
AG-Panc13-P0	0.88	0.88	0.88	0.93	0.93	0.93	0.93	0.93	0.93	0.89	0.92	0.91	0.91	0.89	0.94	0.94	0.94	1.00	0.97	0.98	0.98
AG-Panc13 OT-P0	0.88	0.87	0.87	0.93	0.93	0.93	0.93	0.93	0.93	0.91	0.93	0.92	0.92	0.89	0.94	0.95	0.95	0.97	1.00	0.97	0.99
AG-Panc13 OT-P1	0.88	0.88	0.88	0.93	0.94	0.93	0.93	0.93	0.93	0.90	0.92	0.91	0.91	0.89	0.94	0.94	0.94	0.98	0.97	1.00	0.98
AG-Panc13 OT-P1	0.88	0.88	0.88	0.94	0.94	0.94	0.94	0.94	0.94	0.91	0.93	0.93	0.93	0.90	0.95	0.95	0.95	0.98	0.99	0.98	1.00

Figure W2. (continued).

Regulated Genes

- FC was calculated compared to normal Pancreas
- FC ≥ 2.0 , FDR < 0.05

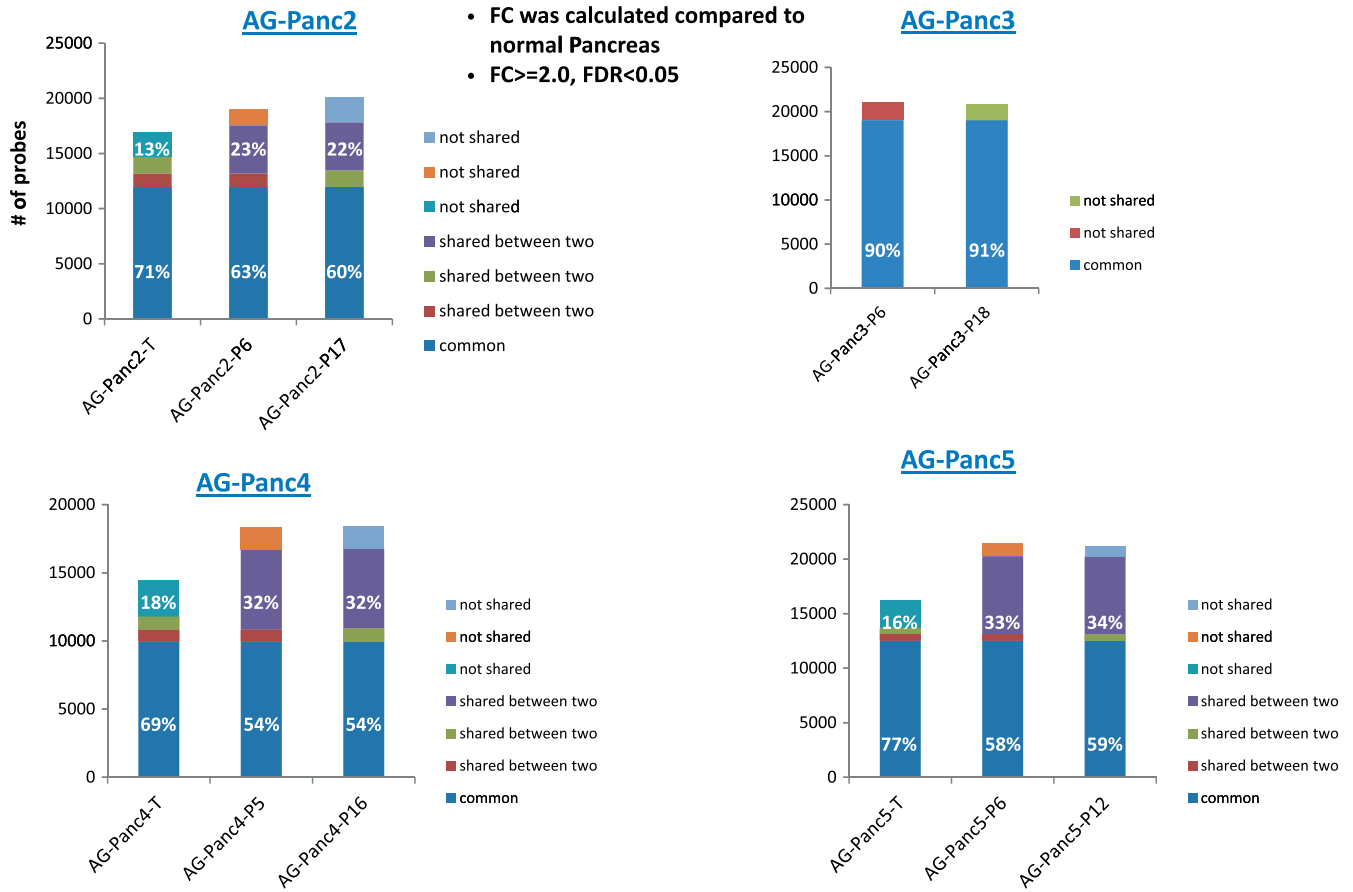


Figure W3. Comparison of the number of significantly-regulated probes and number of shared probes between samples.

Regulated Genes

- FC was calculated compared to normal Pancreas
- FC >= 2.0, FDR < 0.05

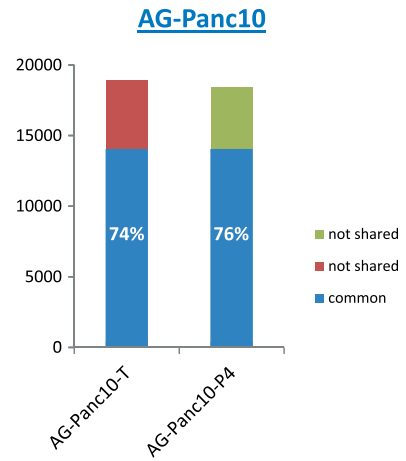
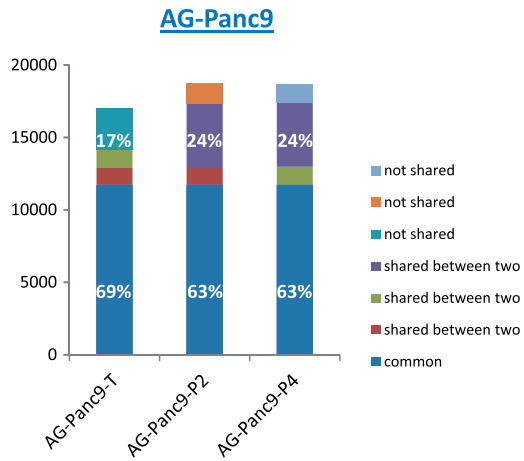
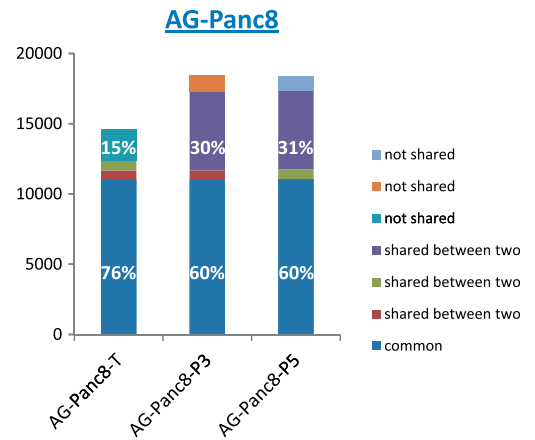
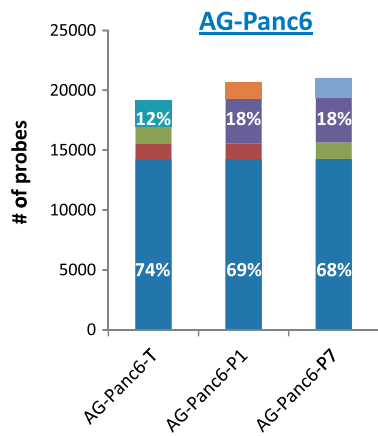


Figure W3. (continued).

Regulated Genes: AG-Panc2 OT

- FC was calculated compared to normal Pancreas
- $FC \geq 2.0$, $FDR < 0.05$

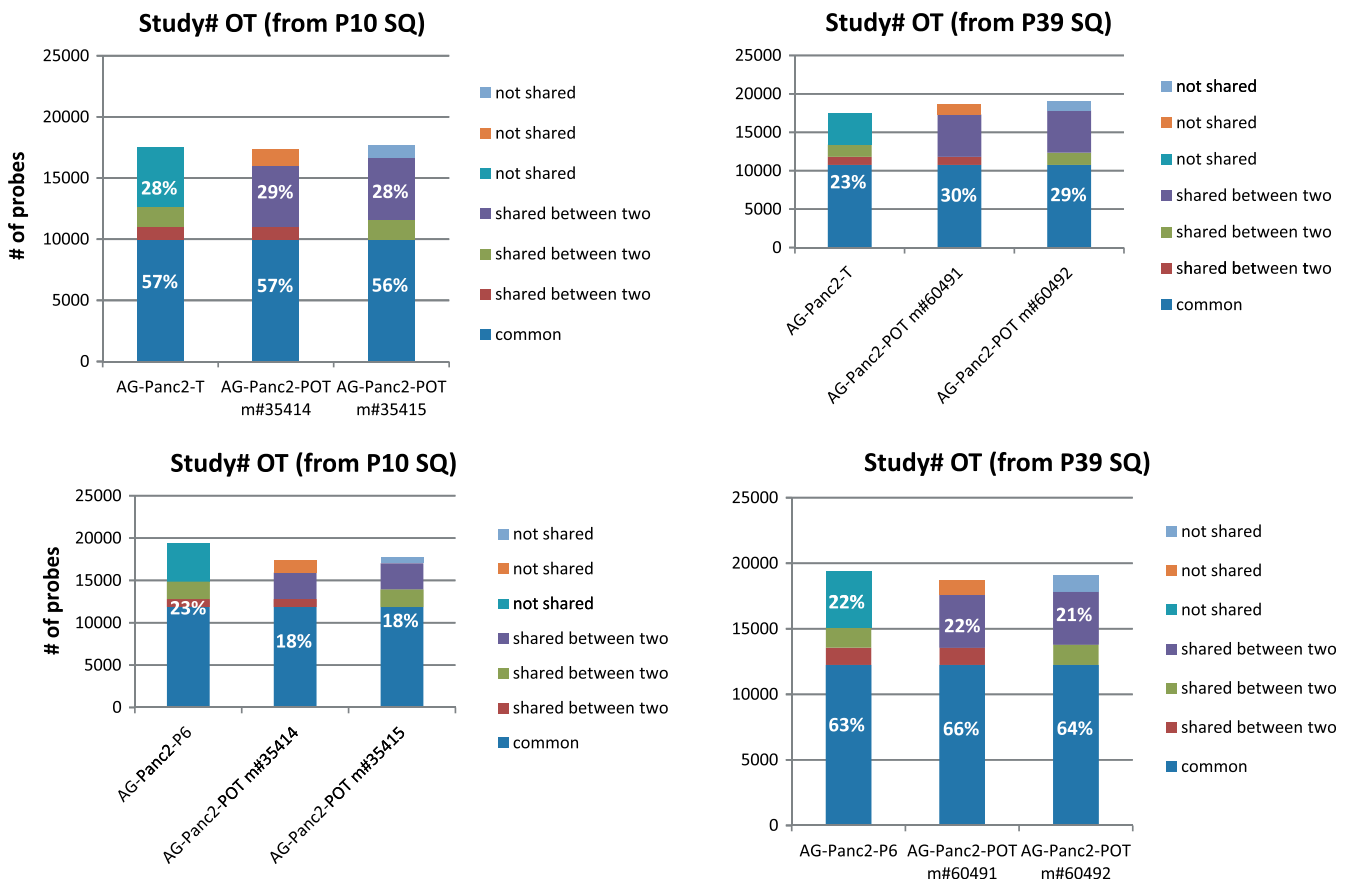
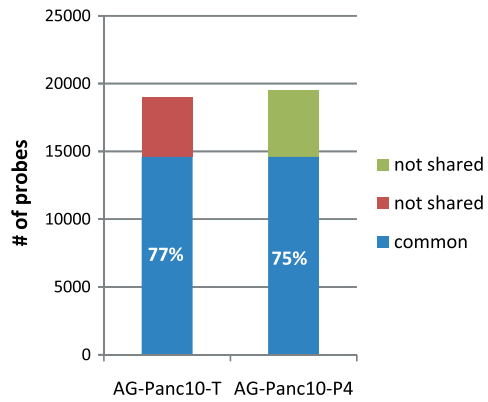
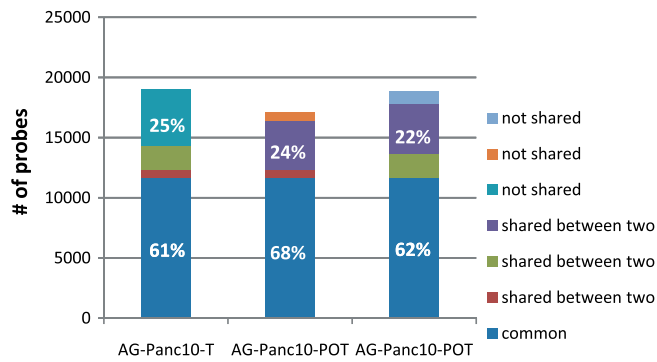
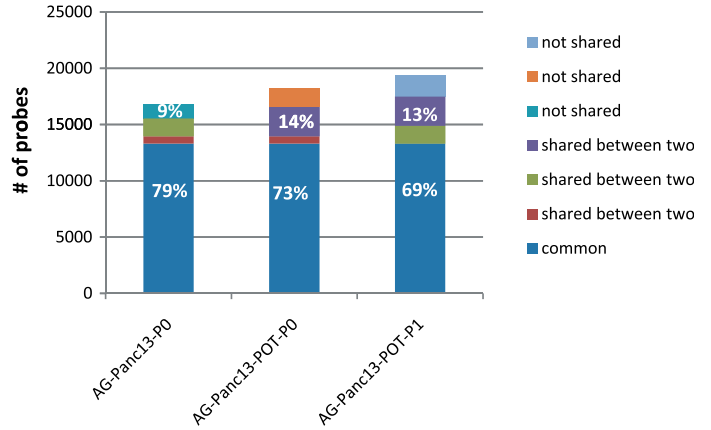


Figure W3. (continued).

Regulated Genes: AG-Panc10 OT



Regulated Genes: AG-Panc13 OT



- FC was calculated compared to normal Pancreas
- FC >= 2.0, FDR < 0.05

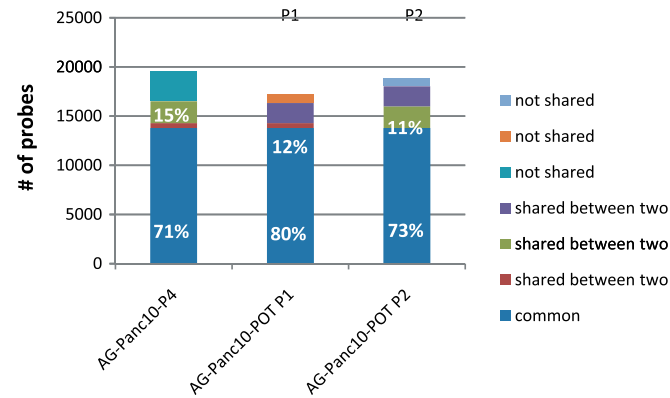


Figure W3. (continued).