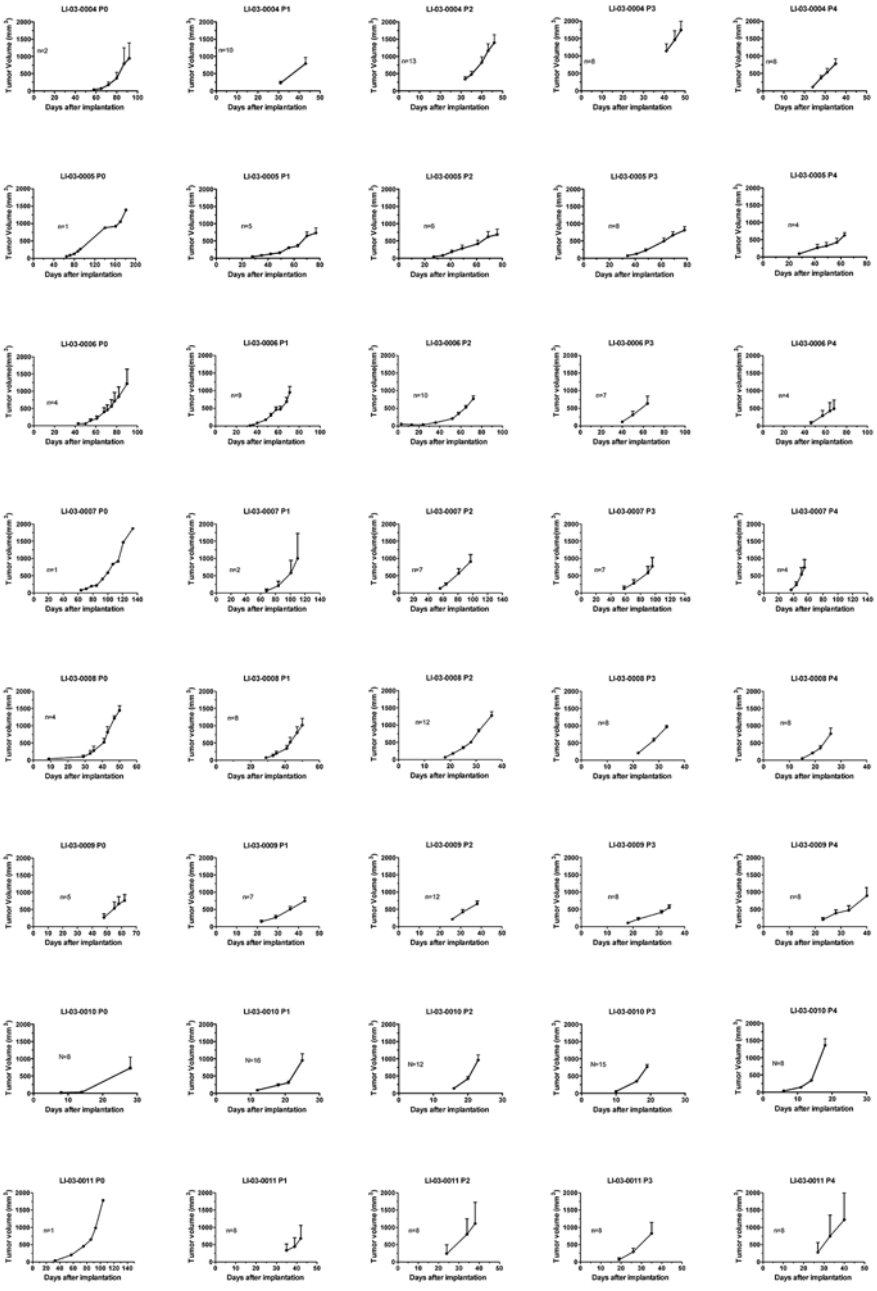
SUPPLEMENTARY FIGURES AND TABLES



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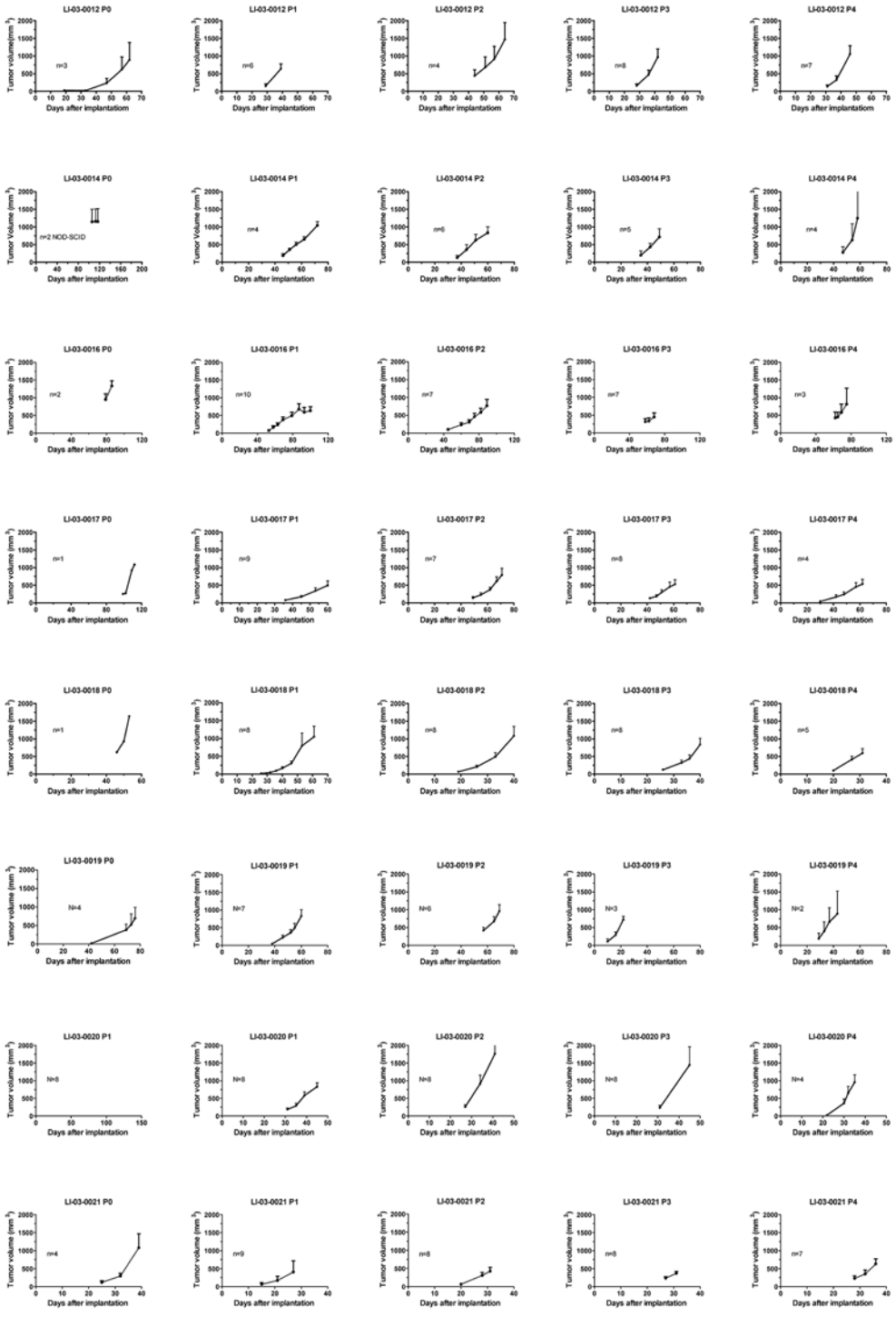
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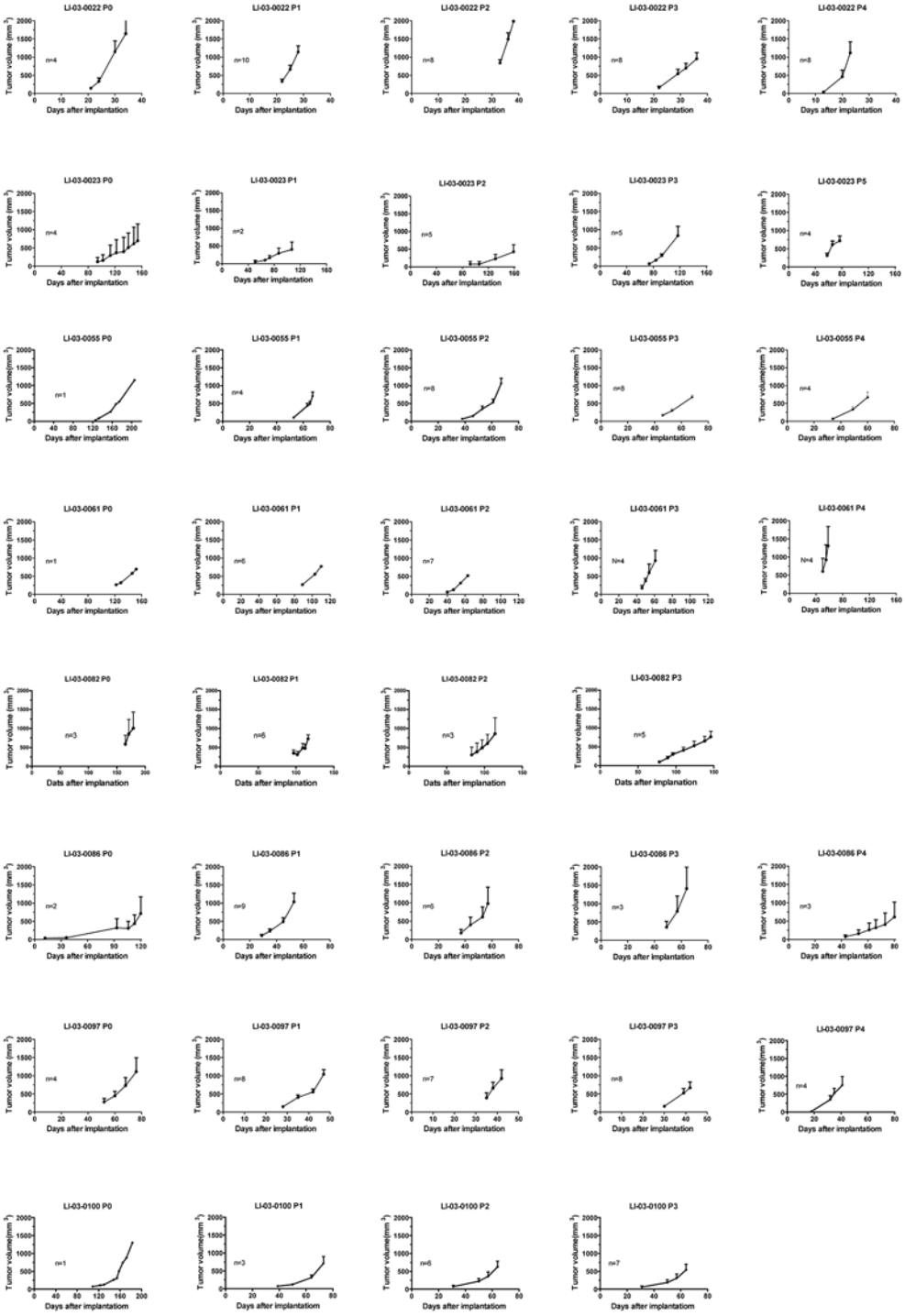
Days after implantation

(*Continued*)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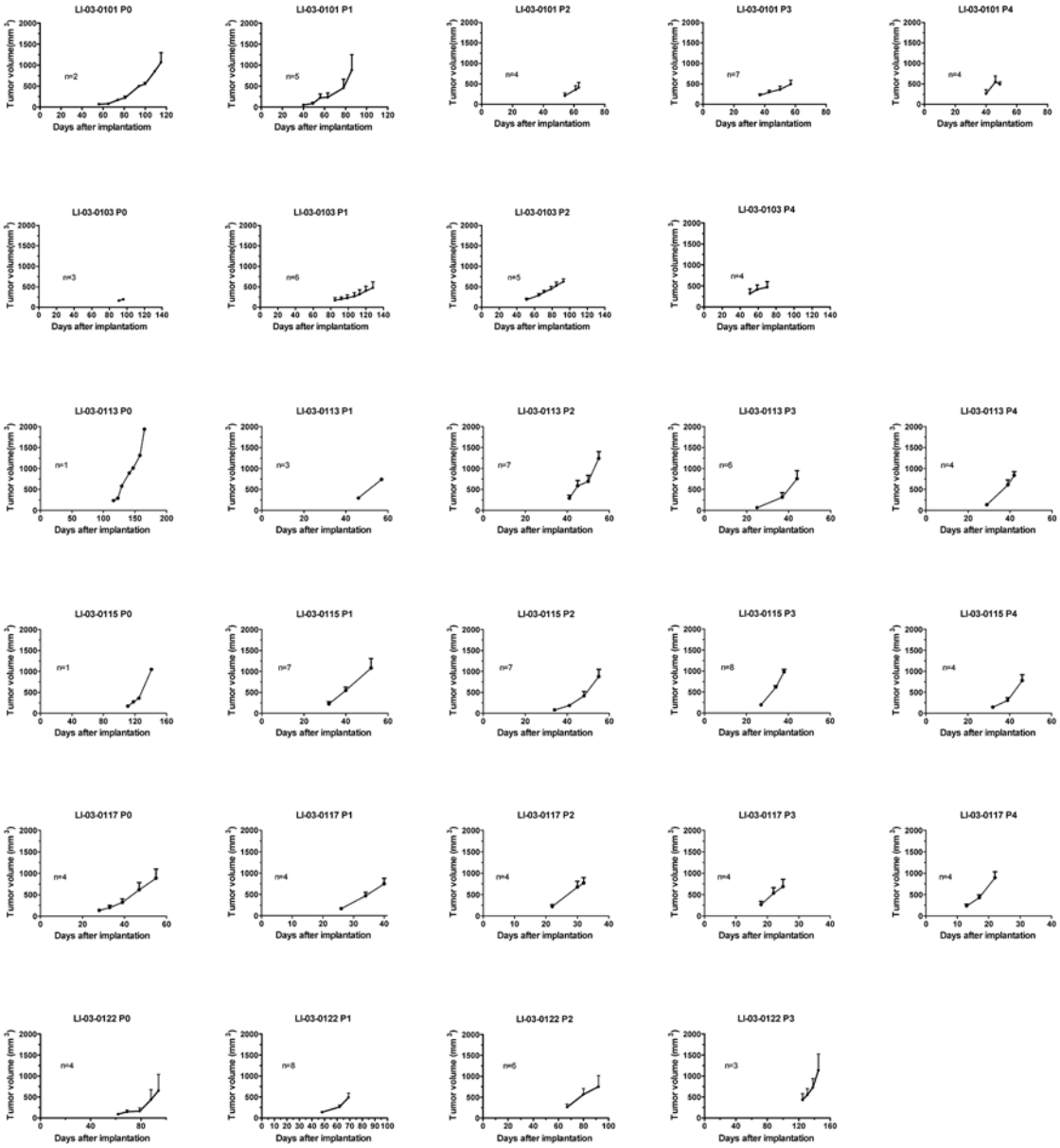
Tumor volume (mm3)
Days after implantation

(*Continued*)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Tumor volume(mm3)
Days after implantation

(*Continued*)


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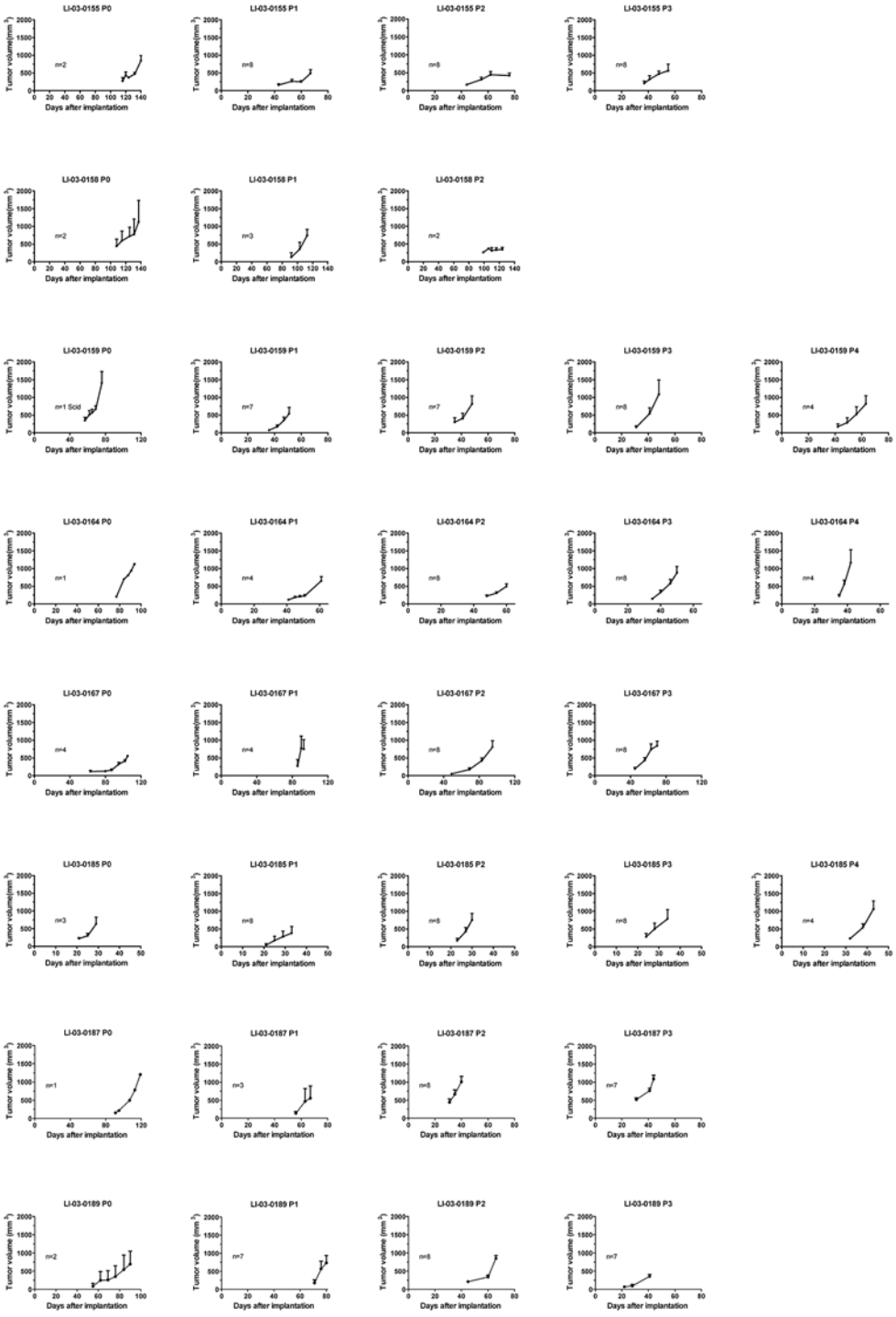
Tumor volume (mm3)
Days after implantation

(*Continued*)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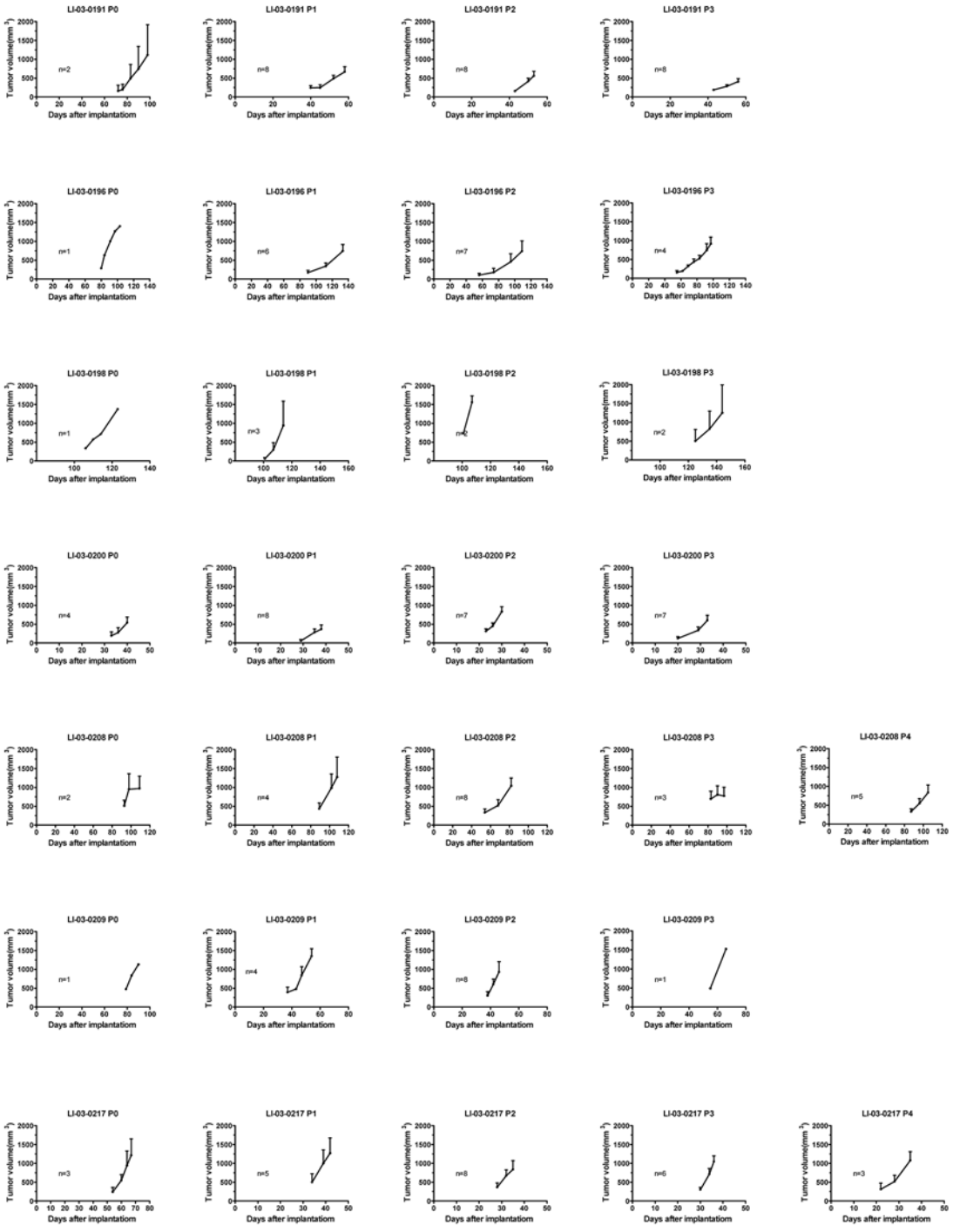
Tumor volume(mm3)
Days after implantation

(*Continued*)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Tumor volume(mm 3)
Days after implantatiom

(*Continued*)


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LI-03-0243 P3
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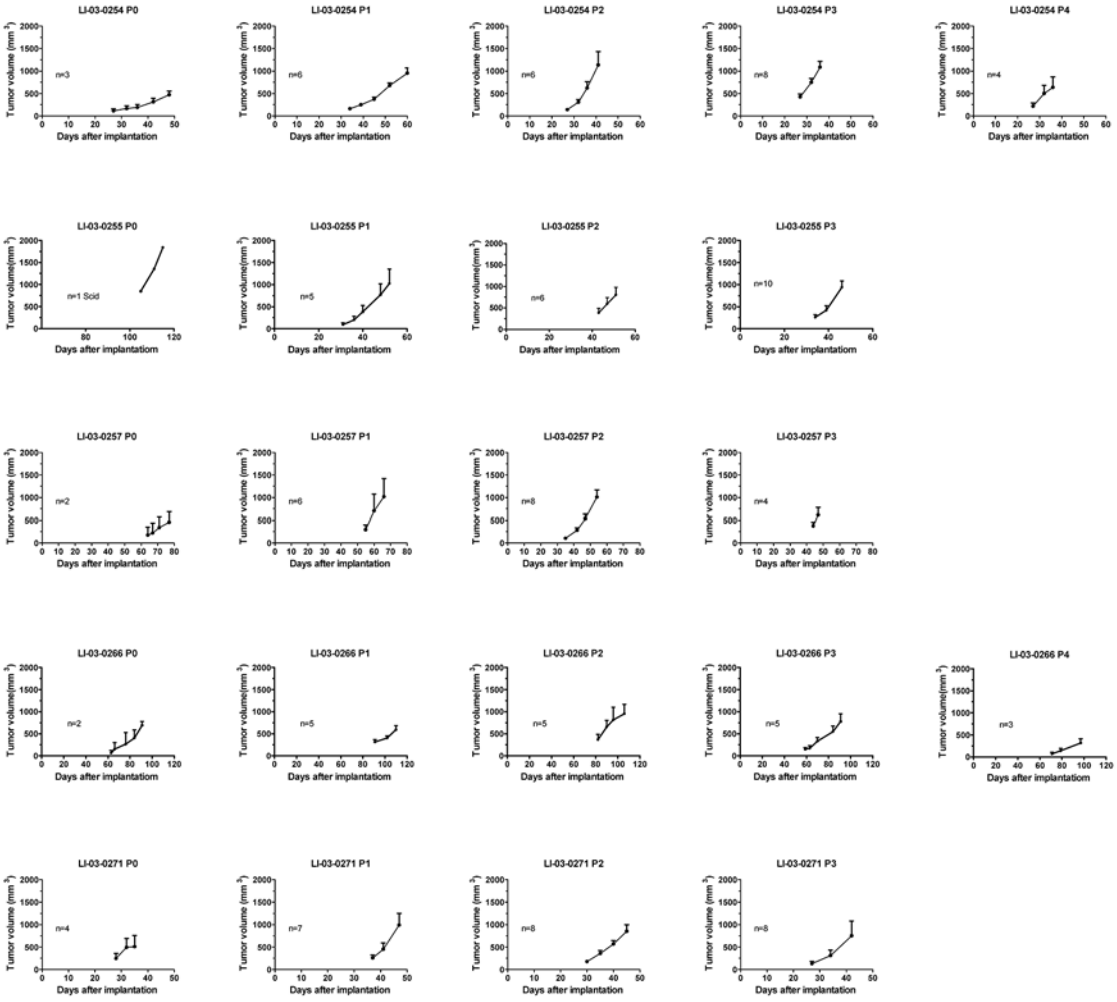
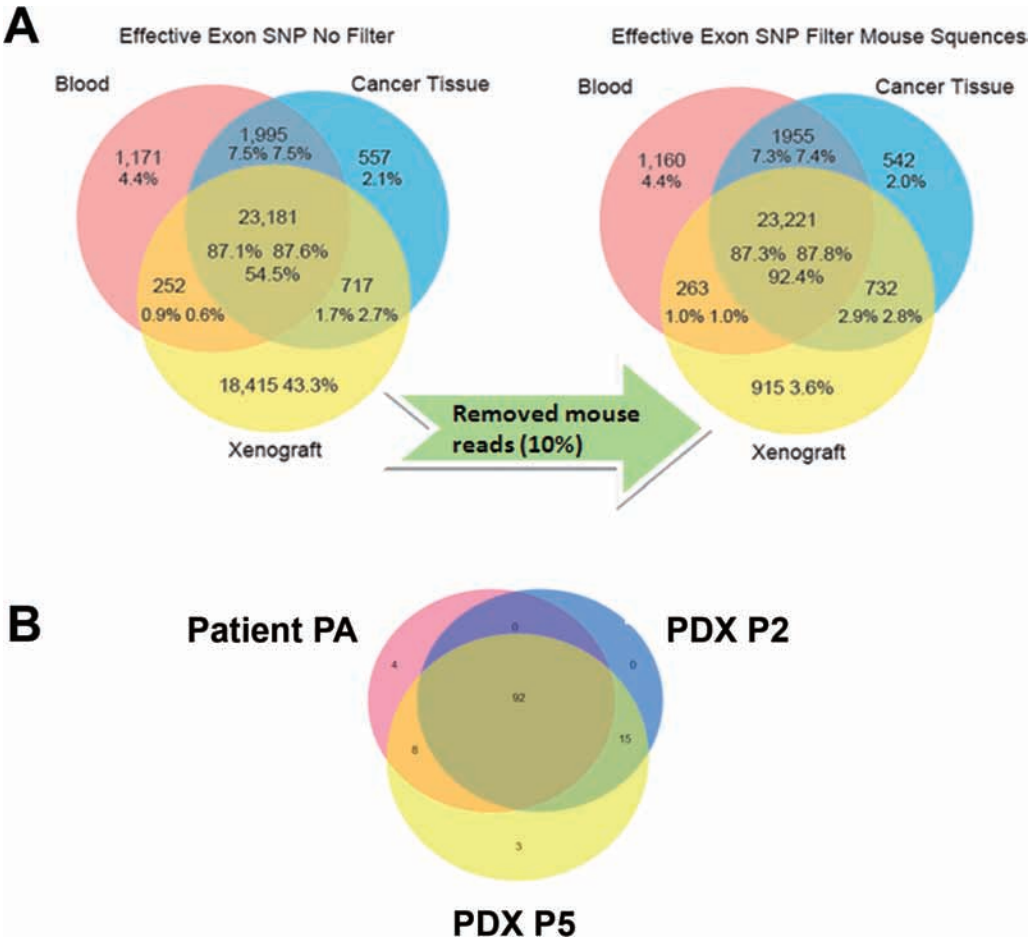
Tumor volume(mm3)
Days after implantation

(*Continued*)



Supplementary Figure S1: The growth curves of 65 transplantable PDX models at various passages in the present study. The data shown are mean ± standard error mean (SEM).



Supplementary Figure S2: A. An example of exonic, amino-acid changing SNPs detection in esophageal cancer before (left) and after (right) filtering mouse sequences during the data analysis of whole exome sequencing of PDX tumor tissues. More than 40% of amino-acid changing SNPs detected in xenograft samples were due to mouse sequence contaminations (yellow circle on the left panel). Removal of mouse reads significantly reduced the false positive SNP calls but did not affect the capability to detect real mutations/SNPs in the human compartment. Pink circle, amino-acid changing alterations detected in human blood samples. Blue circle, amino-acid changing alterations detected in case-matched original tumor samples. Yellow circle, amino-acid changing alterations detected in derived PDX samples. The numbers and percentages present genetic alterations, as well as their percentages, in individual or overlapped populations. **B.** A case study was shown to demonstrate the consistence of amino-acid changing alterations detected by WES between the original patient tumor and its PDX at various passages. Color-coded circles present the alterations detected in patient, P2 and P5 PDX samples. The numbers represent the alterations in each or overlapped populations**.**

Supplementary Table S1 (part I). Analysis of gene expression levels between PDX and primary tumors.
Differential expression of genes in patient and PDX tissues assessed by gene expression array in case-matched 9 paired samples. Genes up-regulated in PDXs relevant to the original tumors were summarized on the sheet entitled 'UP in PDX' and genes down-regulated in PDXs were summarized on the sheet entitled 'DOWN in PDX'. The data analysis process and detailed descriptions were outlined on a separate sheet entitled 'Summary'.

1	Item Name	Description
	Probeset ID	Affymetrix PrimeView Probeset ID
	Gene Symbol	HGNC gene symbol
	Description	Gene description
	logFC (i.e., log fold change)	Log(2) of gene expression in PDXs minus Log(2) of gene expression in the original tumors. A positive logFC indicates an upregulation in PDXs and a downregulation in the original tumors. A negative logFC indicates a downregulation in PDXs and upregulation in the original tumors. (logFC = 1) suggests a 2-fold increase in PDXs when compared to the original tumors. (logFC = −1) suggests a 2-fold decrease in PDXs when compared to the original tumors
	adj.*P*.Val	Adjusted *P* value. Usually confident threshold is set as 0.05.
2	**Criteria of genes selection**	**Threshold**
	adj.*P*.Val	0.05
3	**Differential Expression Genes**	**Top Related Pathways in KEGG (www.genome.jp/kegg/pathway.html)**
	UP_in_PDX_DOWN_in_Tumor	Cell cycle, DNA replication
	DOWN_in_PDX_UP_in_Tumor	Cell adhesion molecules, Systemic lupus erythematosus, Allograft rejection, Graft-versus-host disease, Intestinal immune network for IgA production, Type I diabetes mellitus, Viral myocarditis, Autoimmune thyroid disease, Cytokine-cytokine receptor interaction

Supplementary Table S2. A list of nonsynonymous SNPs and indels identified in the exonic regions by WES in PDXs. The detailed information includes frequency, total variations detected in 56 models, specific models, chromosome numbers, locations of genes, reference (i.e., normal) and altered nucleotide bases, type of variations (i.e., SNP and indel), reference and altered amino acids, and the related information on the dbSNP (http://www.ncbi.nlm.nih.gov/SNP/) and COSMIC databases (http://cancer.sanger.ac.uk/cancergenome/projects/cosmic/; N/A, not available).

Supplementary Table S3. A summary of CNA in 42 PDX models assessed by SNP 6.0 arrays. Copy number status of each sample (sheet 1), frequencies of amplifications (A), deletions (D) and normal copy number states (N) were shown in sheet 2.