

1 <Supplementary materials>

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3 **Transcriptional stratification of necrotizing enterocolitis identifies distinct**
4 **disease subtypes**

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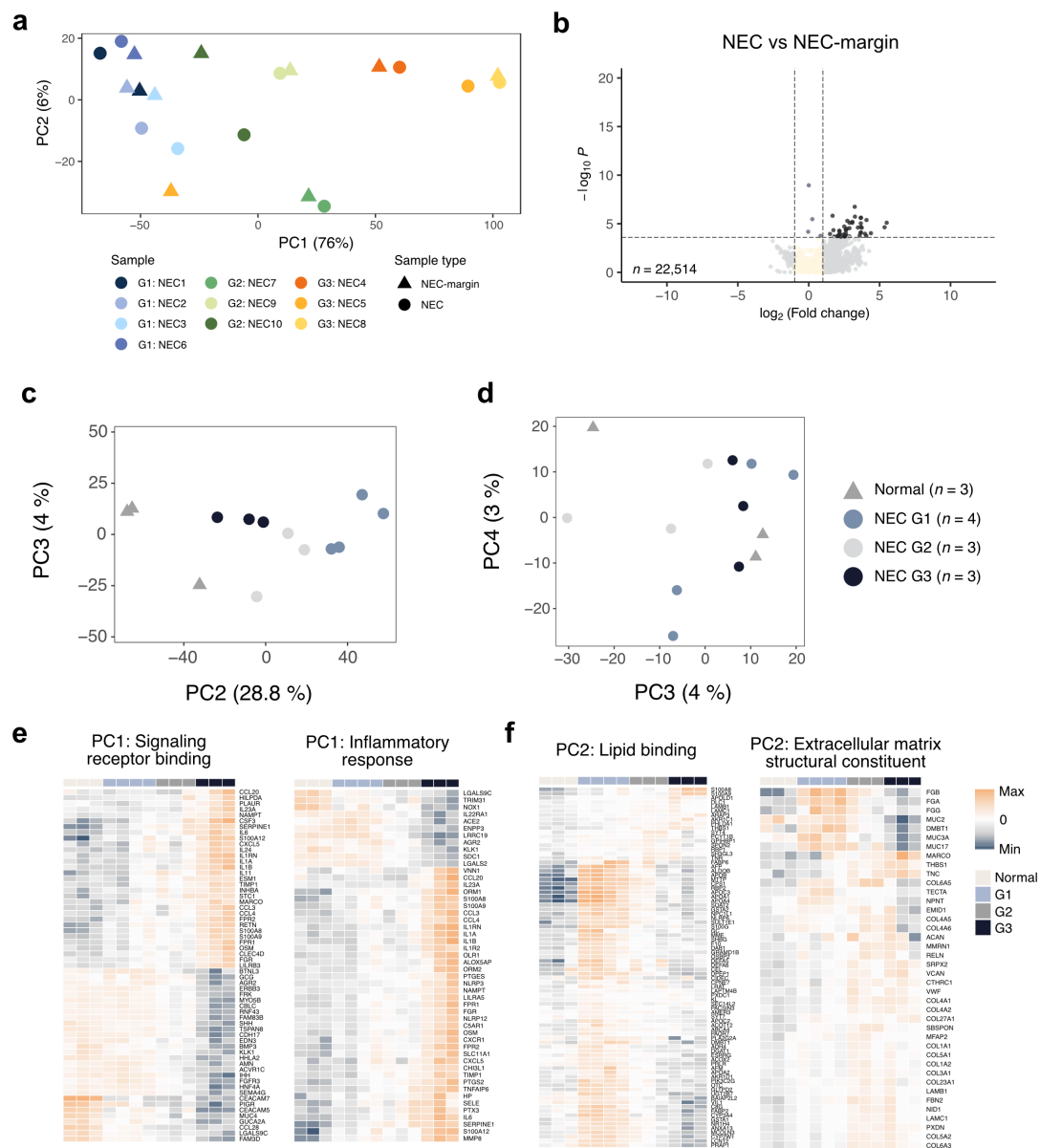


Fig S1. Comparative analysis of NEC vs. NEC-margin and NEC vs. normal samples (a) PCA plot of NEC and NEC-margin samples. (b) Volcano plot of DEGs of NEC and NEC-margin samples. (c-d) PCA plot of NEC and normal samples using PC2 and PC3 (c), PC3 and PC4 (d). (e-f) Heatmaps of GO positively correlated with PC1 (e) and PC2 (f).

17 **Table S1. Clinical characteristics by NEC subtype**

Subtype	Sample name	Gestational age (days)		PMA at surgery (days)		Weight at birth (kg)		Peak CRP (mg/dL)		WBC at surgery (cells/uL)		Hb at surgery (g/dL)		Histological characteristics
G1:Lipid	NEC1	173	173.25 (SD = 2.87)	200	186.0 (SD = 10.03)	0.73	0.685 (SD = 0.166)	0.08	1.19 (SD = 1.694)	19,310	26,280 (SD = 12,508)	10.7	10.47 (SD = 0.25)	Morphologic change
	NEC2	173		181		0.87		3.14		18,810		10.2		Morphologic change
	NEC3	177		186		0.47		-		-		-		-
	NEC6	170		177		0.67		0.35		40,720		10.5		Morphologic change
G2: Intermediate	NEC7	183	181.0 (SD = 8.19)	229	205.67 (SD = 20.23)	0.67	0.733 (SD = 0.183)	11.11	4.03 (SD = 6.142)	3,470	15,446 (SD = 12,378)	10.6	11.47 (SD = 0.85)	Morphologic change
	NEC9	172		193		0.59		0.13		28,190		12.3		Hemorrhage
	NEC10	188		195		0.94		0.85		14,680		11.5		Inflammation
G3: Inflammatory	NEC4	180	204.33 (SD = 30.83)	188	216.67 (SD = 28.02)	0.77	1.377 (SD = 0.790)	0.93	7.497 (SD = 8.949)	29,690	11,710 (SD = 15,571)	16	15.53 (SD = 3.03)	Morphologic change
	NEC5	194		219		1.09		17.69		2,660		12.3		Inflammation
	NEC8	239		244		2.27		3.87		2,780		18.3		Inflammation

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19 PMA: postnatal age; CRP: C-reactive protein; WBC: Whole blood cell count; Hb: Hemoglobin

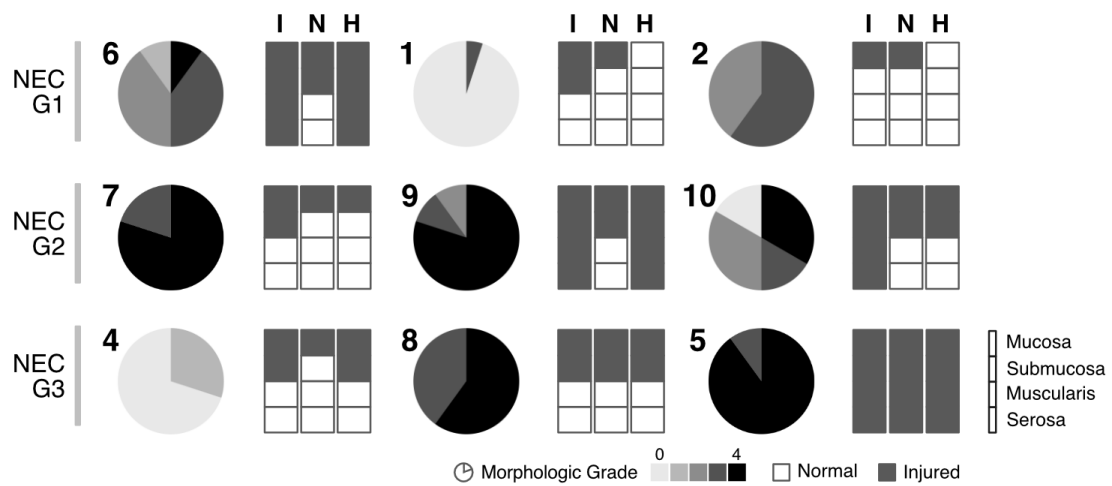
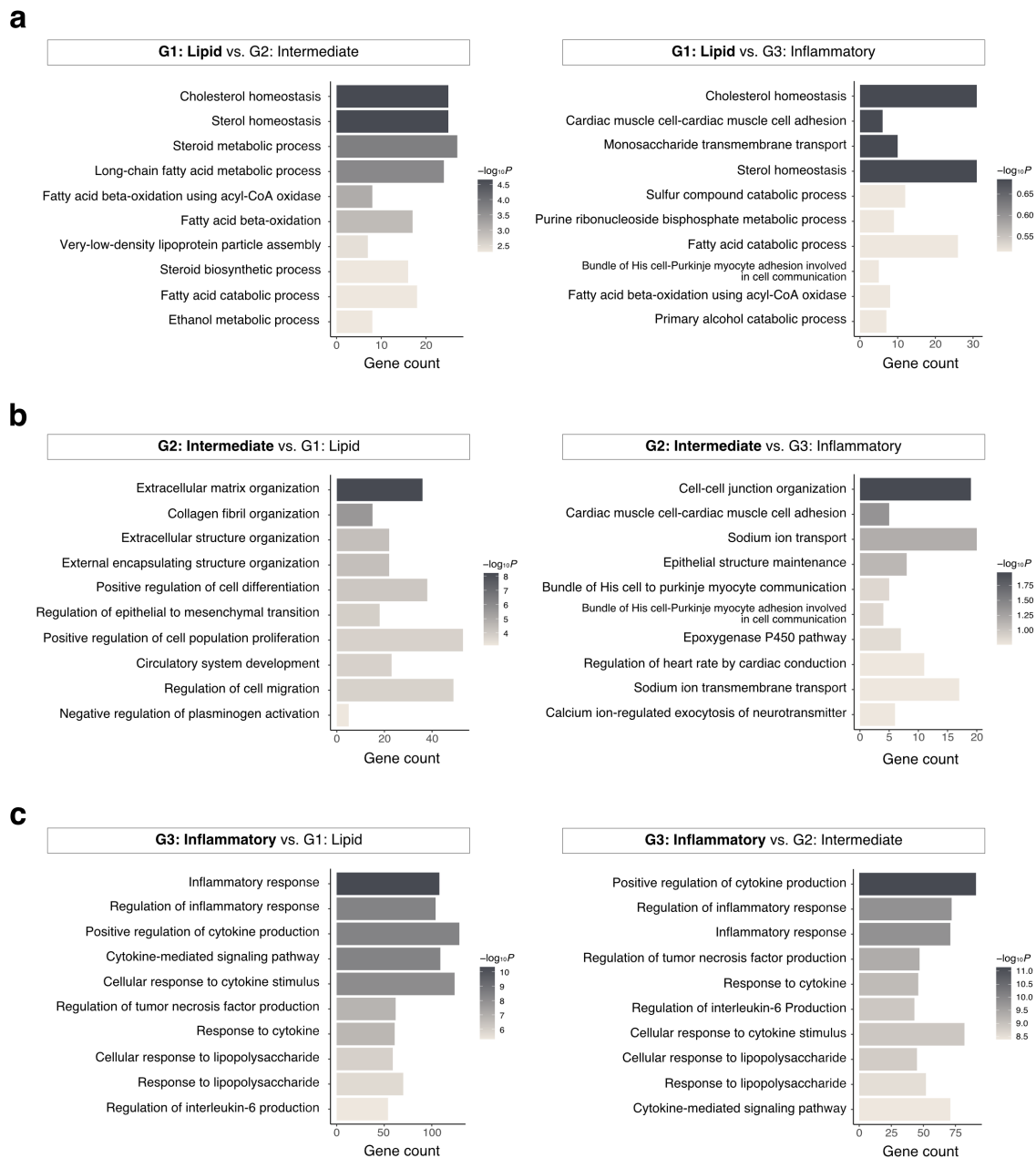


Fig S2. Phenotypic features of NEC samples

The numbers on the pie charts represent the sample ID. I: Inflammation; N: Necrosis; H: Hemorrhage



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27 **Fig S3. Comparative analysis of up-regulated gene ontologies across subtypes**

28 Biological process gene ontologies across subtypes. Up-regulated genes in the
 29 compared subtype ((**a**) G1, (**b**) G2, (**c**) G3; highlighted in bold) relative to their
 30 respective reference subtypes were analyzed.