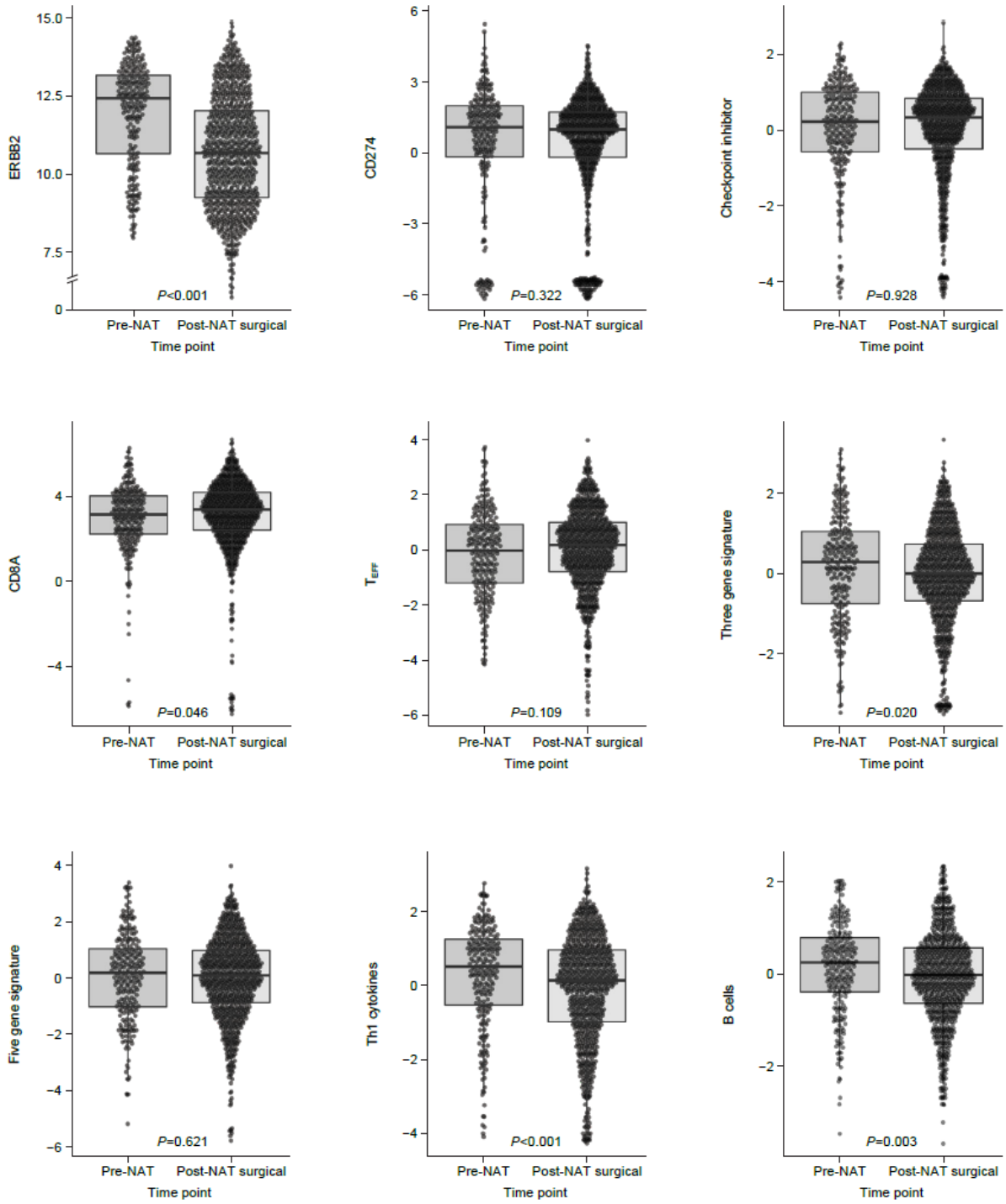
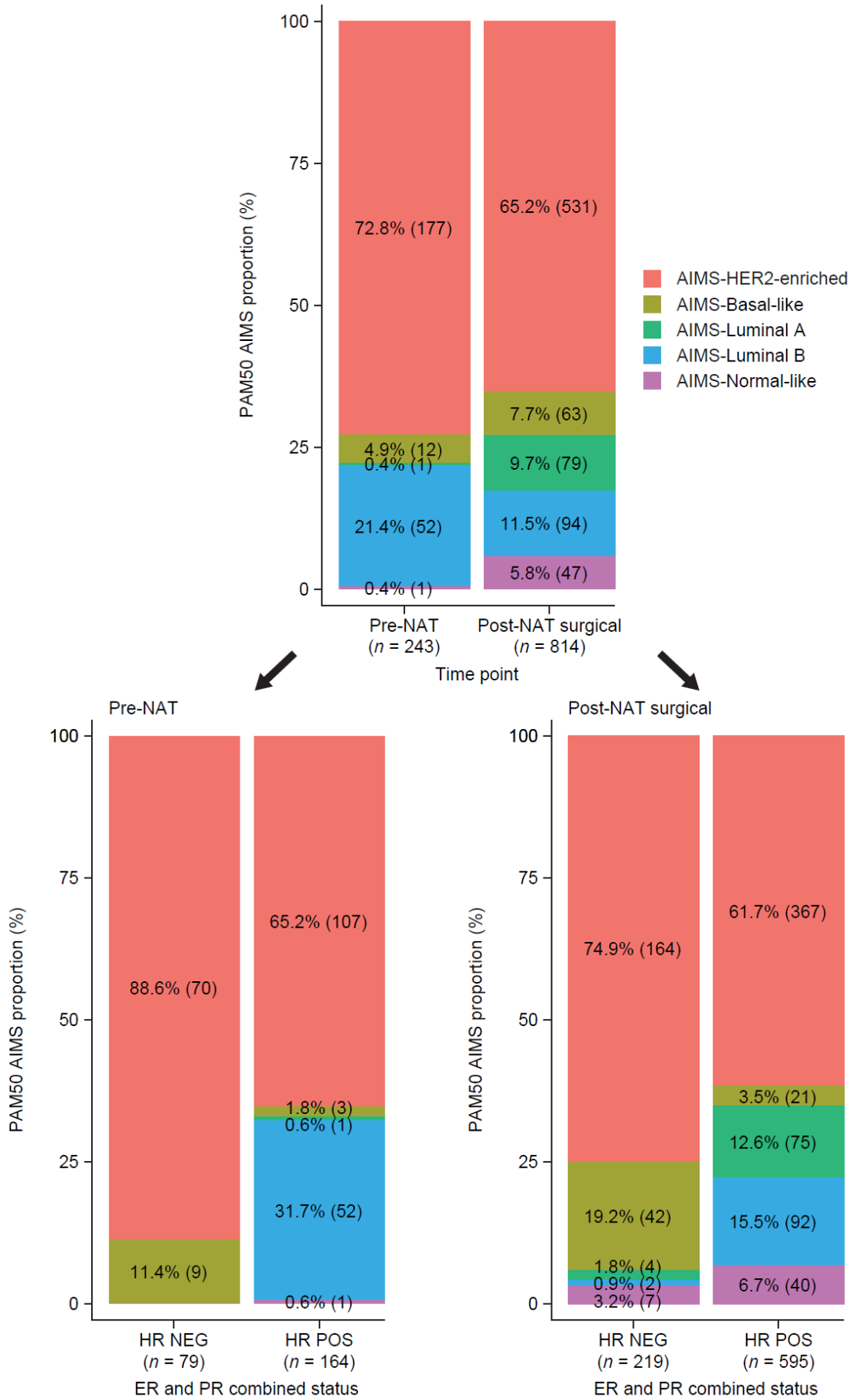


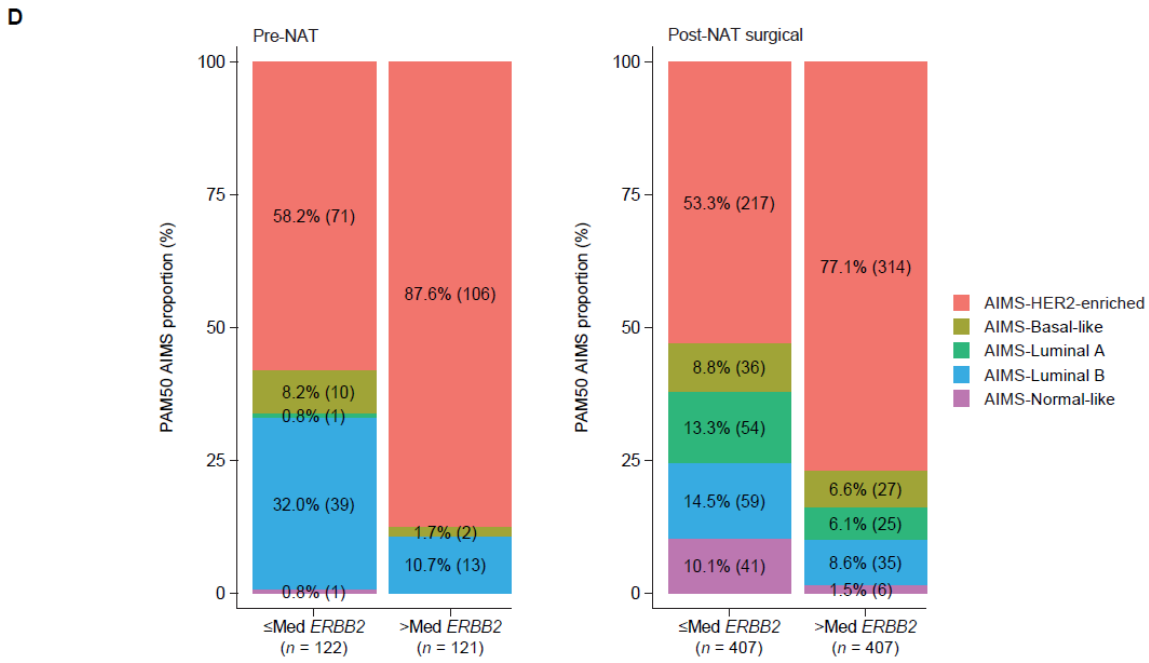
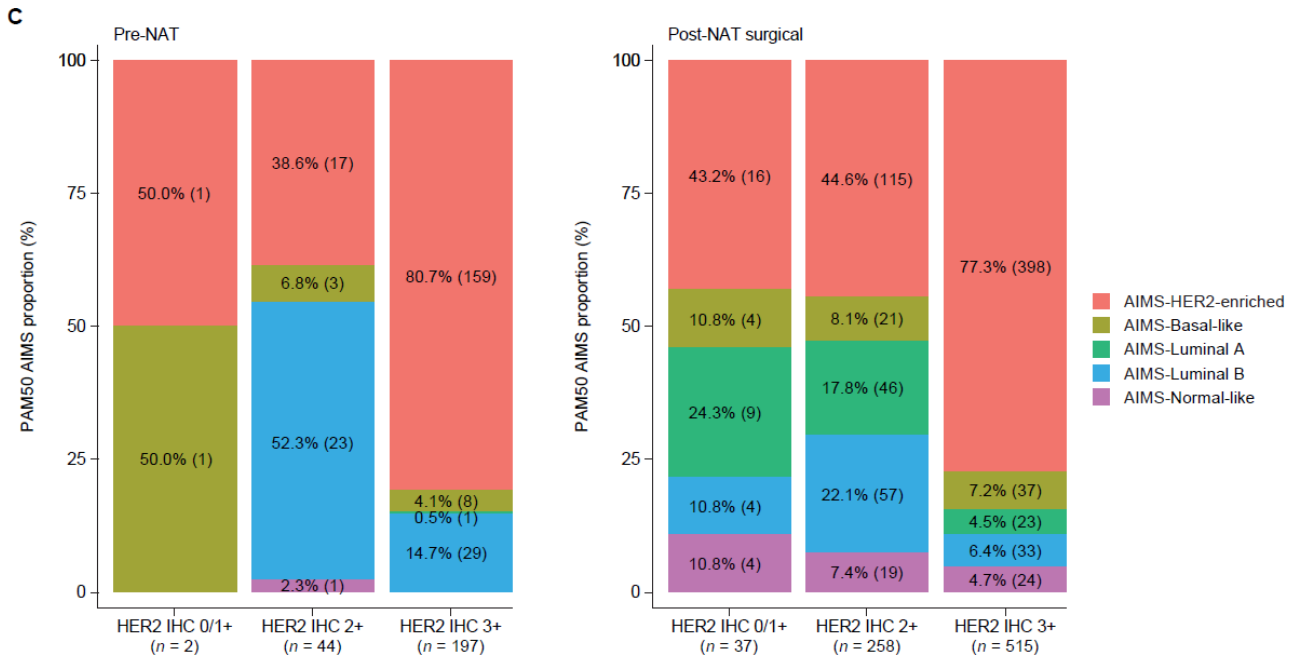
Supplementary Figure S5. Comparison of pre-NAT and post-NAT surgical RNA-evaluable samples. **(A)** ERBB2 (i.e., HER2), CD274 (i.e., PD-L1), checkpoint inhibitor signature (i.e., PD-L1/PD-L2/IDO), CD8A (i.e., CD8), TEFF signature CD8/granzymeA/granzymeB/perforin/IFN γ), three-gene signature (i.e., PD-L1/IFN γ /CXCL9), five-gene signature (i.e., PD-L1/granzymeB/CD8/IFN γ /CXCL9), Th1 cytokine signature (i.e., CXCL9/CXCL10/CXCL11), and B cell gene expression. **(B)** Frequency of AIMS PAM50 subtypes overall and by hormone receptor status. **(C)** Frequency of AIMS PAM50 subtypes by level of HER2 protein expression assessed by IHC in pre- and post-NAT samples. **(D)** Frequency of AIMS PAM50 subtypes by level of HER2 gene expression in pre- and post-NAT samples. **(E)** Hallmark gene sets enriched for genes upregulated in post-NAT surgical versus pre-NAT samples (adjusted $P < 0.05$). **(F)** Hallmark gene sets enriched for genes downregulated in post-NAT surgical versus pre-NAT samples (adjusted $P < 0.05$). Differential gene expression and pathway analyses were adjusted for tumor content. **(G)** Multidimensional scaling plot showing the differences in gene expression profiles between pre-NAT and post-NAT surgical samples. AIMS, Absolute Intrinsic Molecular Subtyping; ER, estrogen receptor; HER2, human epidermal growth factor receptor 2; HR, hormone receptor; IFN γ , interferon gamma; IHC, immunohistochemistry; MDS, multidimensional scaling; Med, median; NAT, neoadjuvant therapy; NEG, negative; NES, normalized enrichment score; PAM50, Prediction Analysis of Microarray 50; POS, positive; PR, progesterone receptor.

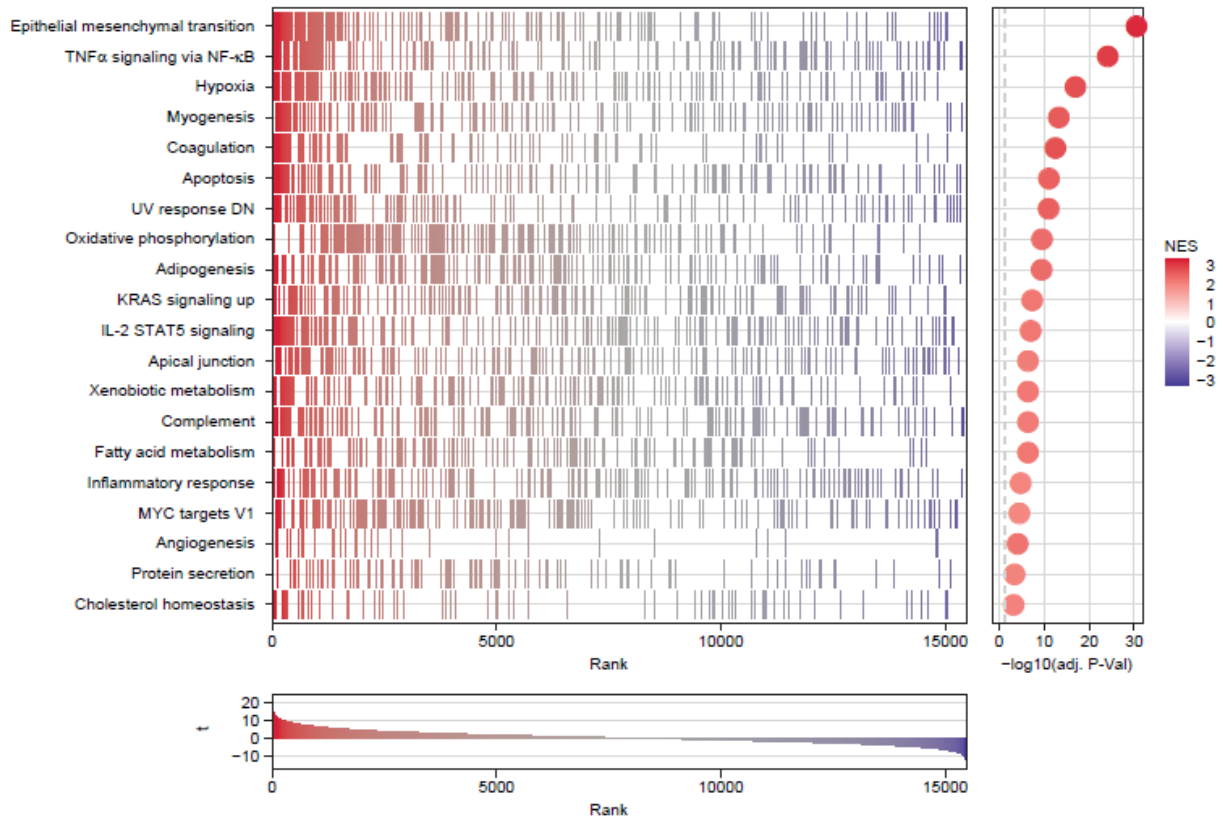
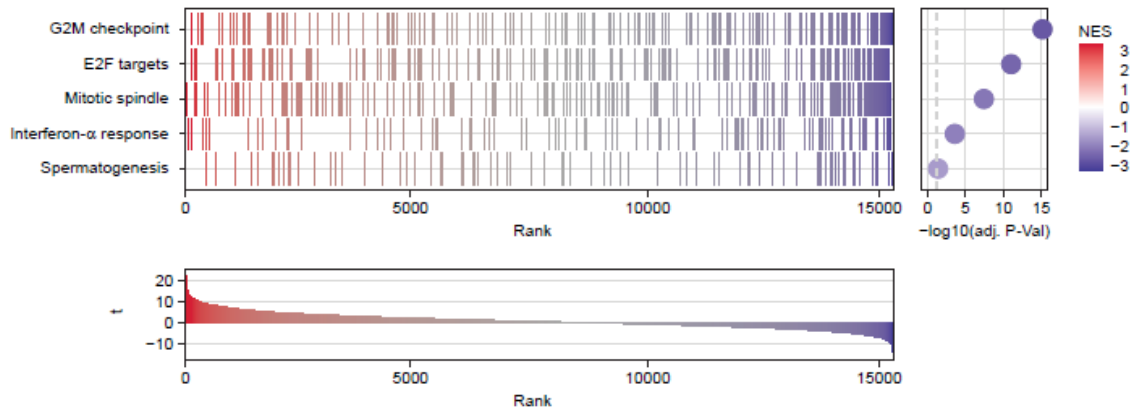
A



B





E**F**

G

