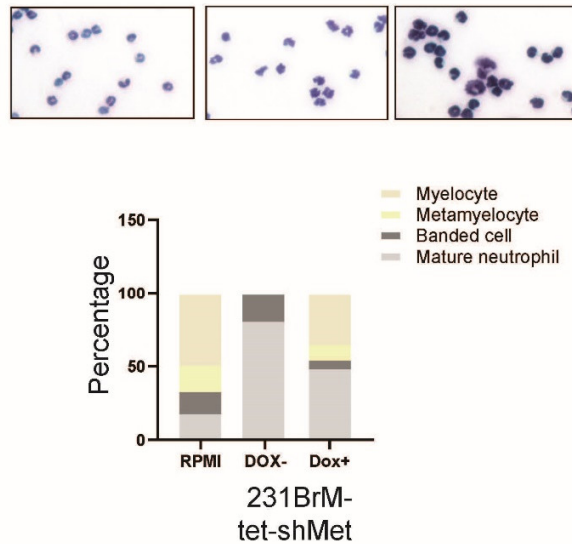
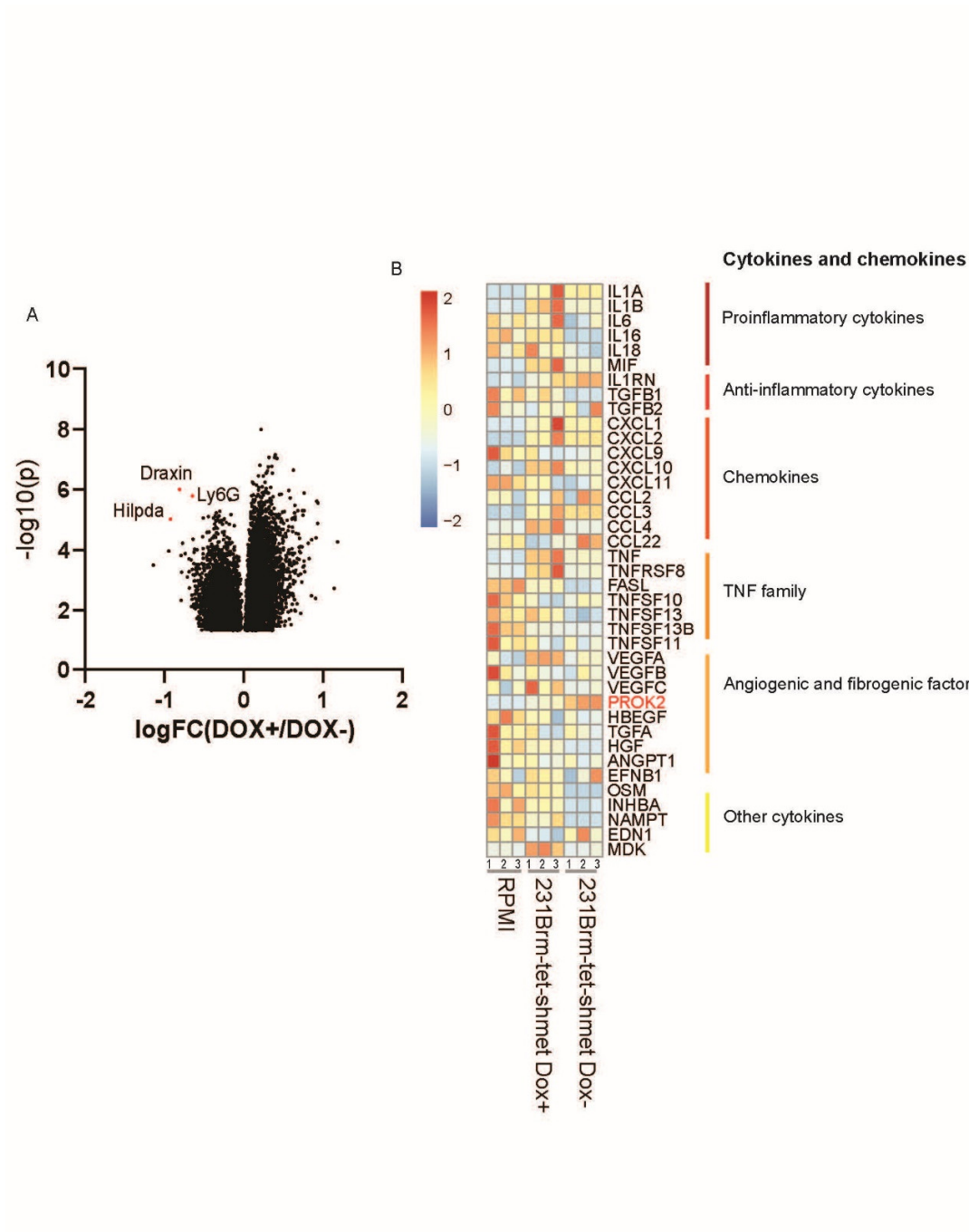


**Supplementary Figure S1. c-Met pathway regulate key granulopoiesis regulators expression.**

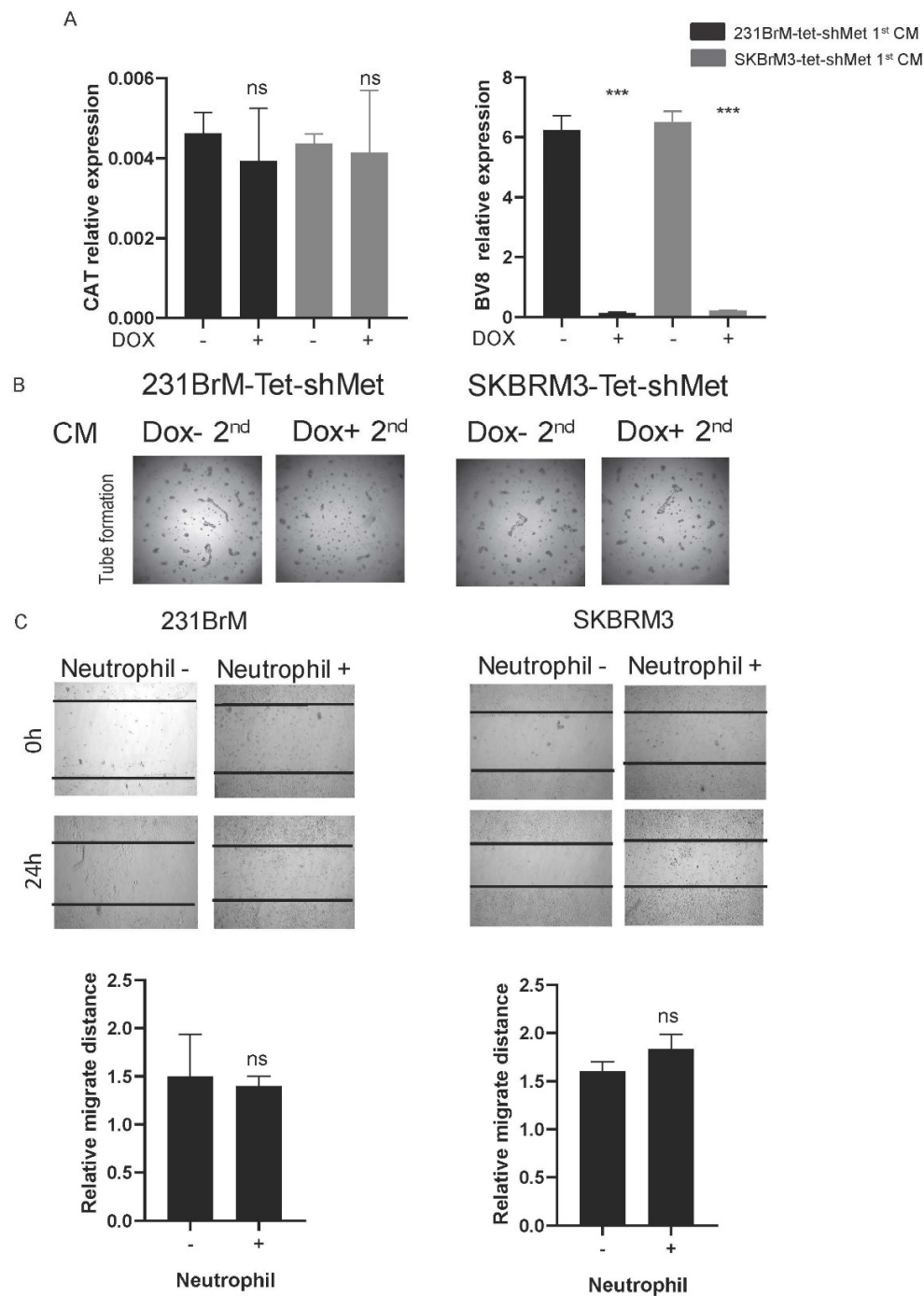
**A.** Correlation between cMet and CXCL1/2 or G-CSF/GM-CSF using the combined GEO databases (GSE12276, GSE2034, GSE2603, GSE5327, and GSE14020). (Pearson correlation). **B.** Brain metastasis-free survival analyses of GM-CSF and CXCL2. **C.** ELISA of GMCSF in MCF7, MCF7-cMet, MDA-MB-453 and MDA-MB-453-cMet CM.



**Supplementary Figure S2. c-Met pathway in cancer cells significantly promote neutrophil maturation.** Upper, representative of nuclear morphology of neutrophils treated by indicated CM. Lower, quantification of percentage of different stage of neutrophil treated by indicated CM.



**Supplementary Figure S3. c-Met pathway in cancer significantly reshape neutrophil transcriptome.** **A.** Volcano plot of RNA sequencing of neutrophils treated by CM. Only significantly differentiated genes were shown on plot. Fold change and p value between DOX+ group and DOX- group was calculated. **B.** Heatmap of key cytokines and chemokines expression from RNA sequencing after treated by indicated CM or RPMI.



**Supplementary Figure S4. N2 neutrophil does not regulate invasiveness and angiogenesis. A.** Expression of CAT and BV8 was examined by qPCR. **B.** Tube formation assay of endothelial cells treated by indicated CM. **C.** Cancer cells were co-cultured with neutrophils for 48 hours before wound healing assay. Upper, representative picture of wound healing at 0 and 24 hours. Lower, quantification of migrated distance.