Table S1 Blood transcriptional modules (BTM) identified by NonLoss and the overlap comparison to MAST method

BTM Module	DIS	log(FDR)	MAST
type I interferon response (M127)	1.78	29.68	No
suppression of MAPK signaling (M56)	1.57	29.68	Yes
AP-1 transcription factor network (M20)	1.50	38.37	Yes
signaling in T cells (I) (M35.0)	1.26	29.68	No
complement activation (I) (M112.0)	1.07	29.68	No
enriched in B cells (V) (M47.4)	1.07	29.68	No
spliceosome (M250)	0.94	29.68	Yes
phosphatidylinositol signaling system (M101)	0.87	29.68	No
myeloid, dendritic cell activation via NFkB (II) (M43.1)	0.72	29.68	No
enriched for TF motif TNCATNTCCYR (M232)	0.71	29.68	No
enriched in T cells (II) (M223)	0.68	29.68	No
proteasome (M226)	0.63	29.68	Yes
cell cycle and growth arrest (M31)	0.62	29.68	Yes
leukocyte activation and migration (M45)	0.56	29.68	No
transcription elongation, RNA polymerase II (M234)	0.56	29.68	Yes
respiratory electron transport chain (mitochondrion) (M238)	0.54	29.68	Yes
myeloid, dendritic cell activation via NFkB (I) (M43.0)	0.54	29.68	No
translation initiation factor 3 complex (M245)	0.53	29.68	Yes
respiratory electron transport chain (mitochondrion) (M219)	0.52	29.68	Yes
respiratory electron transport chain (mitochondrion) (M216)	0.49	29.68	Yes
cell cycle, ATP binding (M144)	0.47	29.68	Yes
leukocyte differentiation (M160)	0.44	29.68	No
T cell differentiation (Th2) (M19)	0.43	38.37	No
mitotic cell cycle in stimulated CD4 T cells (M4.9)	0.42	38.37	No

BTM, Blood transcriptional modules; DIS, difference of IScore; FDR, false discovery rate.

https://dx.doi.org/10.21037/atm-21-6401

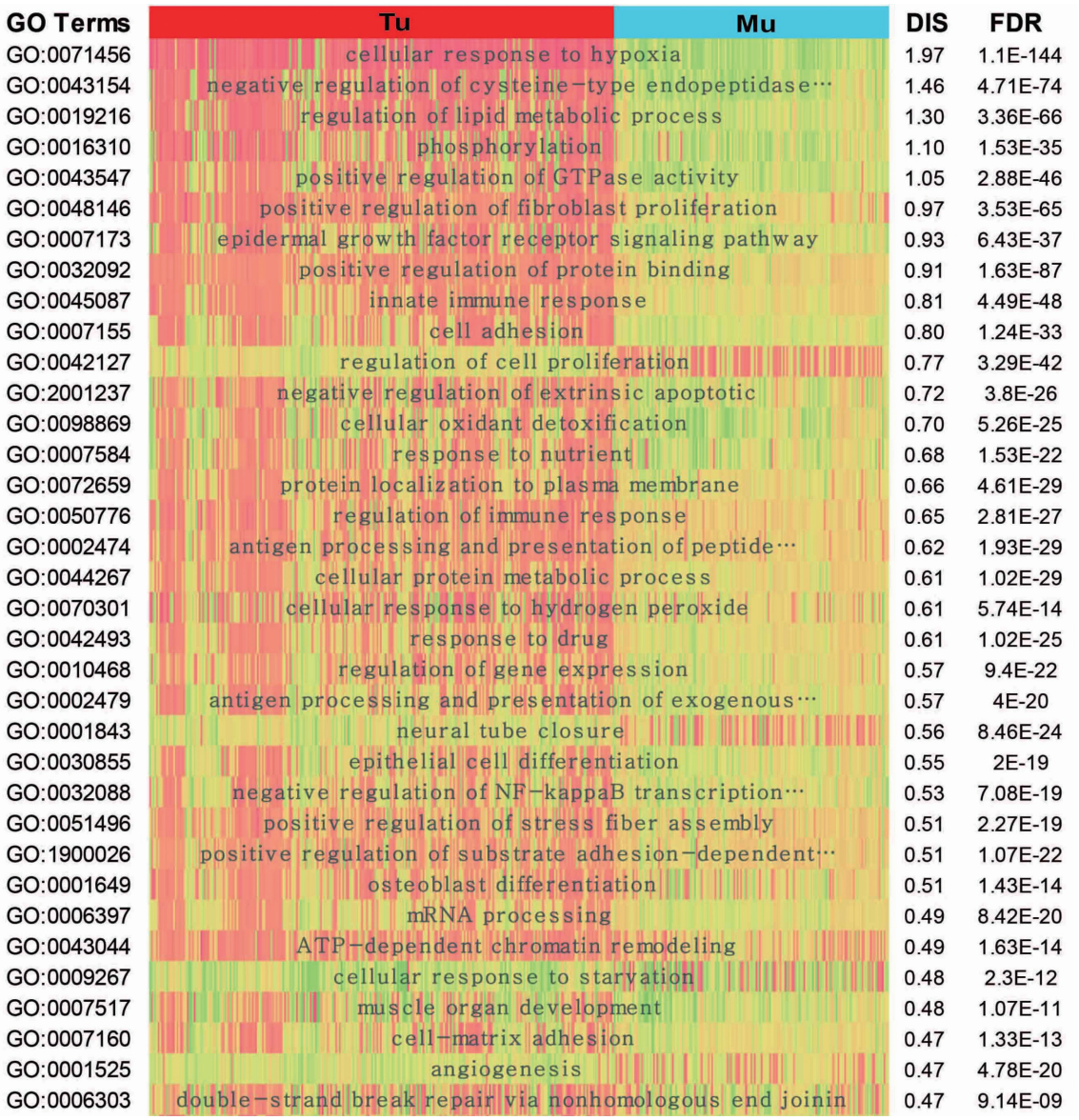

Figure S1 Heatmap shows IScore difference of GO BP category between Tumor and Normal mucosa. Furthermore, 28/386 (7.2%) BP GO terms were identified as DBMs by setting DIS threshold to 0.5. IScore, integrated scores; DBMs, differential biological modules; GO, Gene Ontology; BP, biological process; DIS, difference of IScore.

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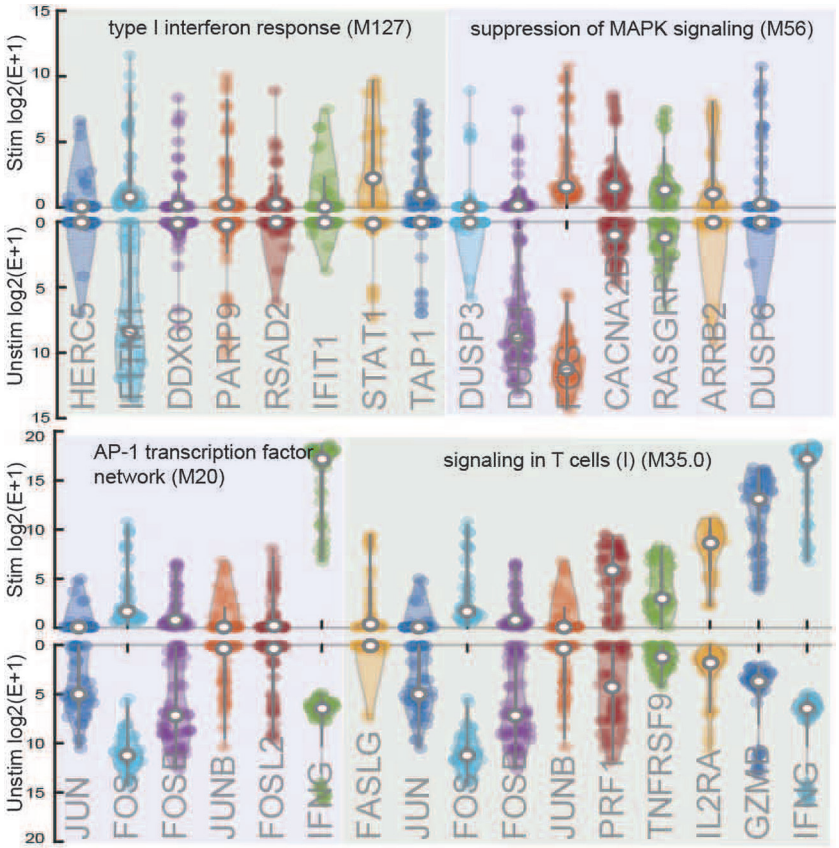

Figure S2 The violin plot shows gene expression patterns in non-stimulated (Unstim) and cytokine-stimulated (Stim) MAST cell. The genes displayed in the graph are annotated in "type I interferon response (M127)", "suppression of MAPK signaling (M56)", "AP-1 transcription factor network (M20)" and "signaling in T cells (I) (M35.0)". The letter (E) indicates FPKM value.

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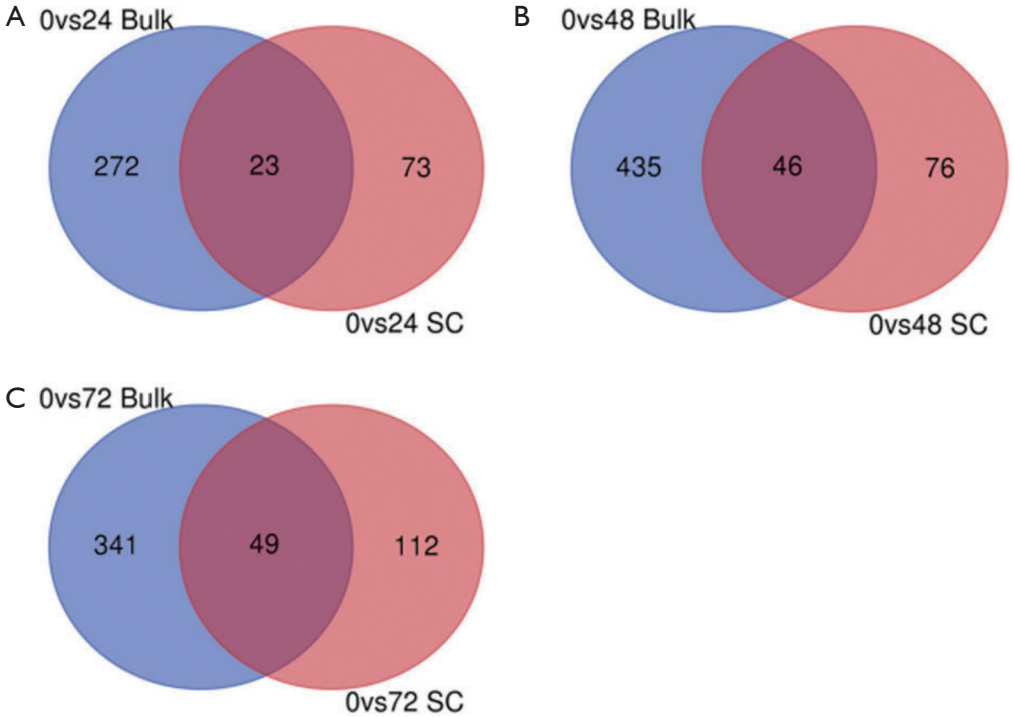

Figure S3 The venn diagram shows the number of DBMs overlap between scRNA-seq and Bulk RNA-seq data which were collected at different time points. DBMs identified by NonLoss between any pair of time points using bulk RNA-seq and single cell RNA-seq data respectively. (A) Calculated by cells of DM and cells collected 24h after serum switch. (B) Calculated by cells of DM and cells collected 48h after serum switch. (C) Calculated by cells of DM and cells collected 72h after serum switch.

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