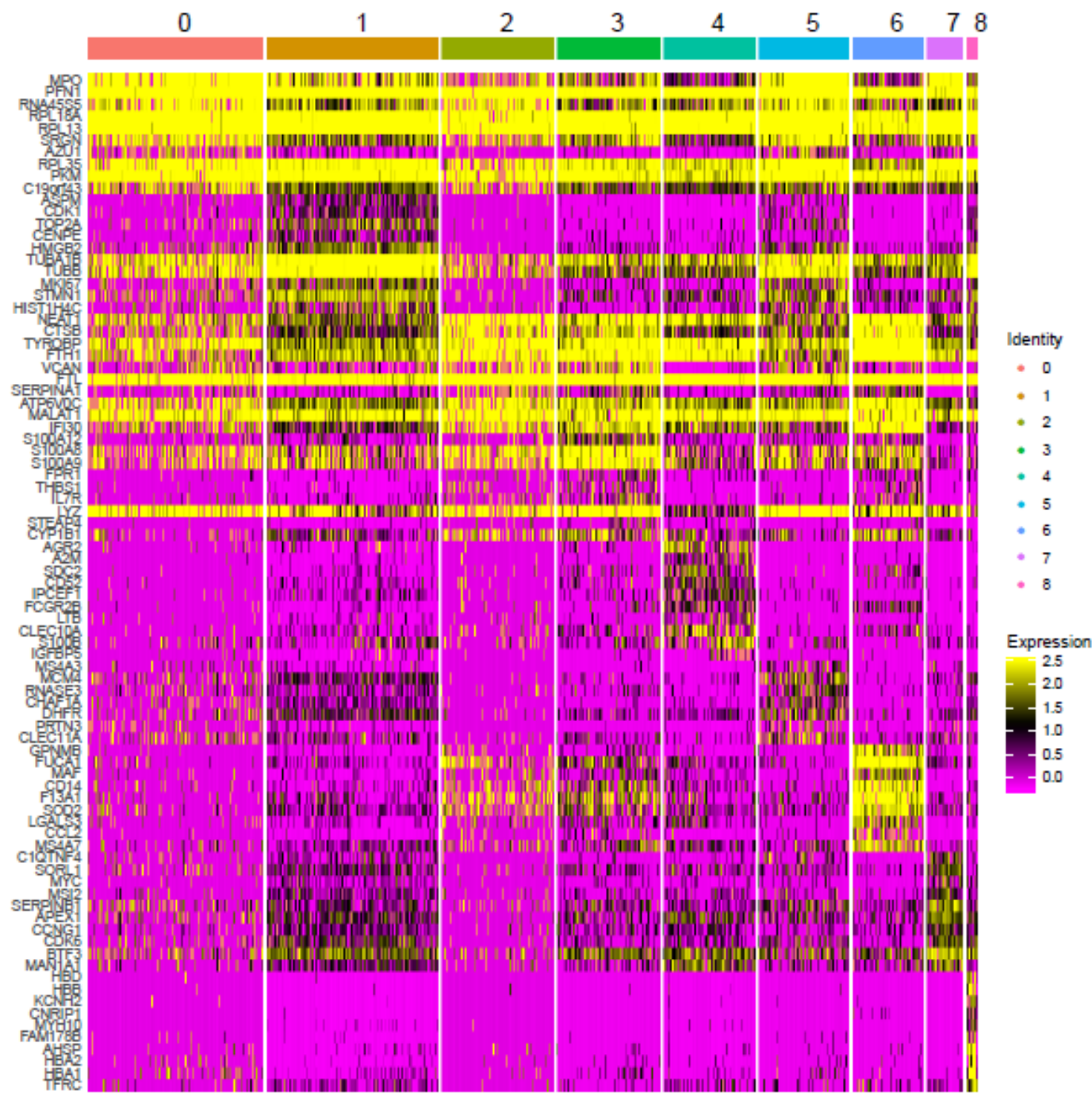


Supplementary Figure S1

cl 0		cl 5	
GO:0016071	mRNA metabolic process	GO:0006614	SRP-dependent cotranslational protein targeting to membrane
GO:0044265	cellular macromolecule catabolic process	GO:0006613	cotranslational protein targeting to membrane
GO:0008380	RNA splicing	GO:0000184	nuclear-transcribed mRNA catabolic process, nonsense-
GO:0006397	mRNA processing	GO:0045047	protein targeting to ER
GO:0034822	cellular protein-containing complex assembly	GO:0019080	viral gene expression
cl 1		cl 6	
GO:0000278	mitotic cell cycle	GO:0002274	myeloid leukocyte activation
GO:0140014	mitotic nuclear division	GO:0001775	cell activation
GO:1903047	mitotic cell cycle process	GO:0002252	immune effector process
GO:0007049	cell cycle	GO:0002444	myeloid leukocyte mediated immunity
GO:0000280	nuclear division	GO:0043299	leukocyte degranulation
cl 2		cl 7	
GO:0002444	myeloid leukocyte mediated immunity	GO:0006413	translational initiation
GO:0002274	myeloid leukocyte activation	GO:0006414	translational elongation
GO:0016050	vesicle organization	GO:0006412	translation
GO:0043299	leukocyte degranulation	GO:0043043	peptide biosynthetic process
GO:0002275	myeloid cell activation involved in immune response	GO:0000184	nuclear-transcribed mRNA catabolic process, nonsense-
cl 3		cl 8	
GO:0001775	cell activation	GO:0042254	ribosome biogenesis
GO:0002274	myeloid leukocyte activation	GO:0006364	rRNA processing
GO:0043299	leukocyte degranulation	GO:0016072	rRNA metabolic process
GO:0045321	leukocyte activation	GO:0022613	ribonucleoprotein complex biogenesis
GO:0002444	myeloid leukocyte mediated immunity	GO:0034660	ncRNA metabolic process
cl 4			
GO:0016032	viral process		
GO:0044403	symbiotic process		
GO:0044419	interspecies interaction between organisms		
GO:0002252	immune effector process		
GO:0016050	vesicle organization		

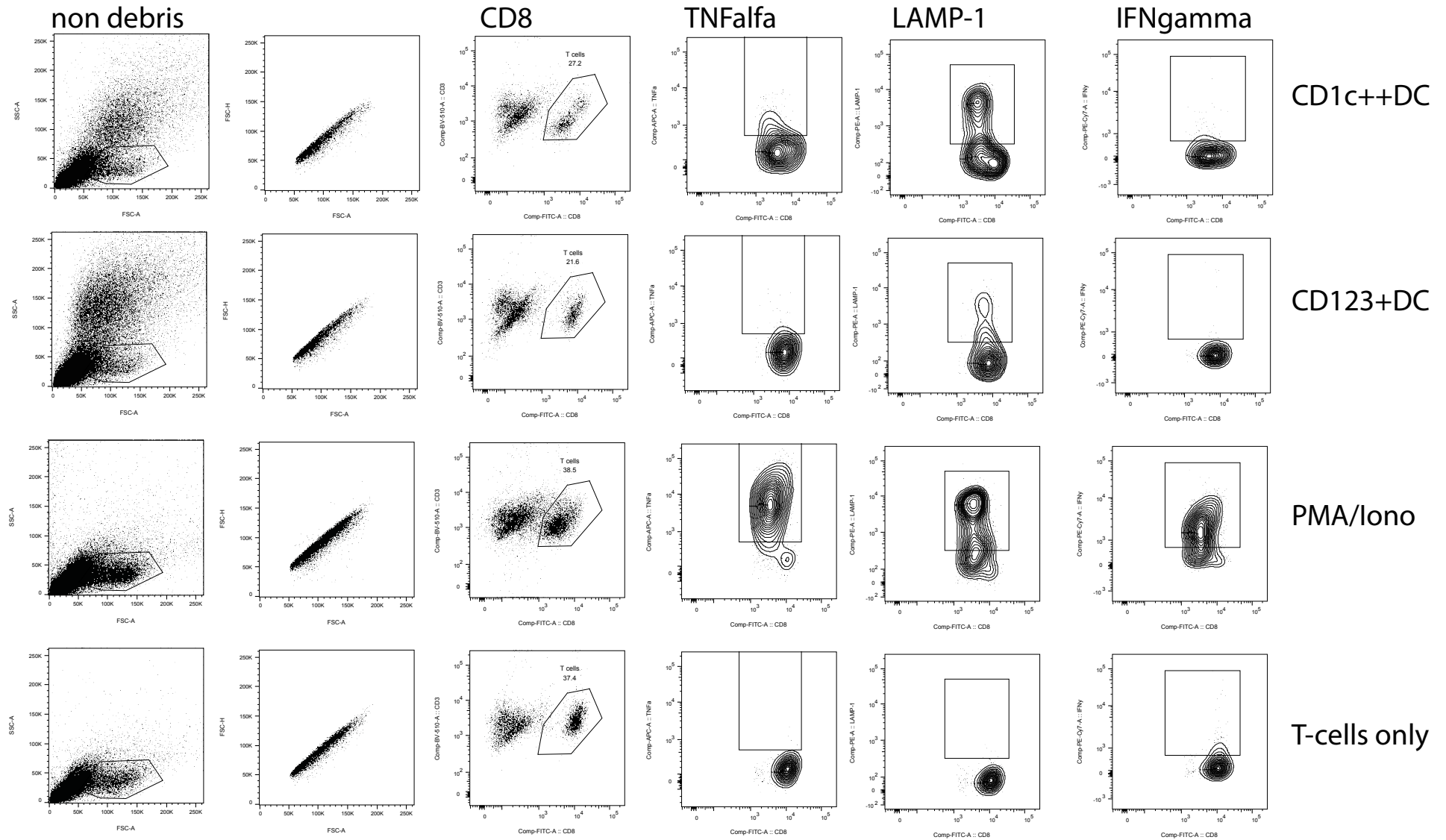
Supplementary Figure S1. Top 5 Gene ontology terms obtained from the differentially expressed genes (DEGs) of the clusters obtained from single cell RNA sequence data. The GO terms of candidate DEGs were analyzed using ToppGene.

Supplementary Figure S2



Supplementary Figure S2. Heatmap of the top 10 differentially expressed genes (DEGs) of the clusters obtained from single cell RNA sequence data.

Supplementary Figure S3



Supplementary Figure S3. Gating strategy for WT1-specific T-cell assay. One experiment is shown out of 5. Live lymphocytes are gated followed by CD8 and accordingly TNFalfa, LAMP-1 or IFNgamma.