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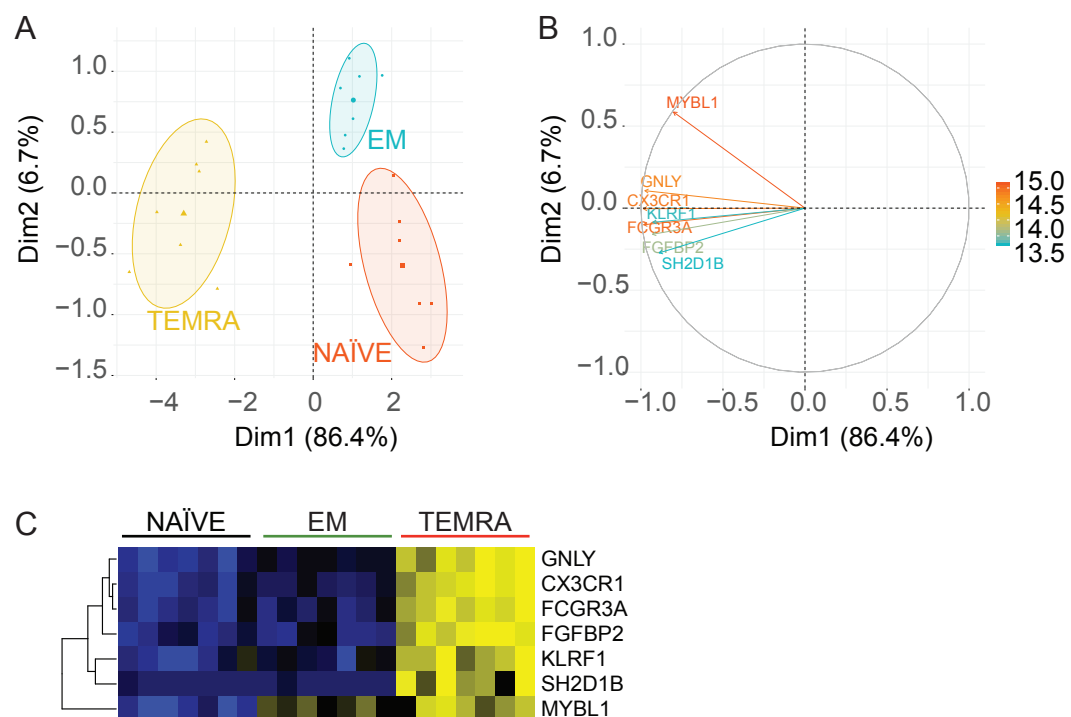
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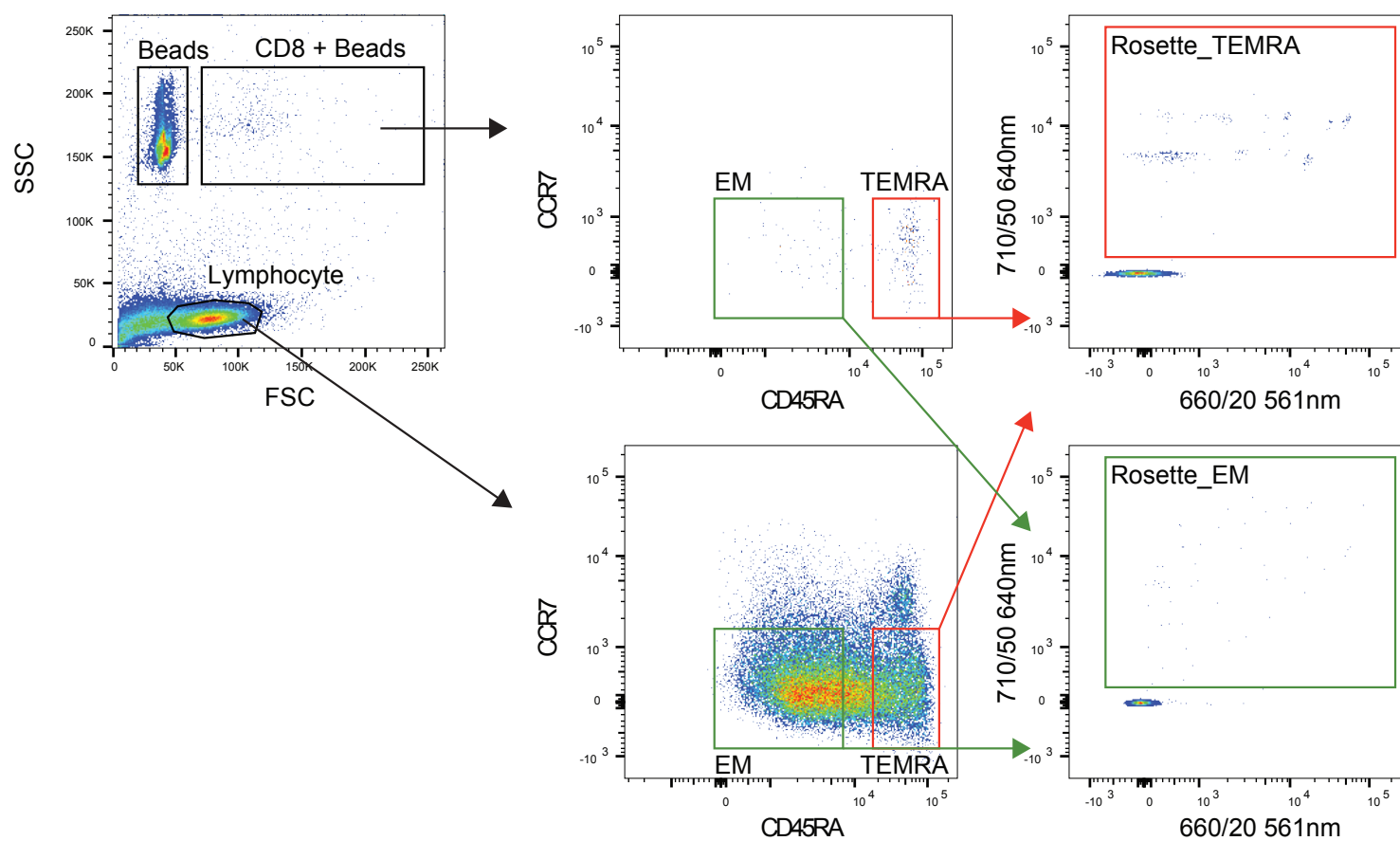
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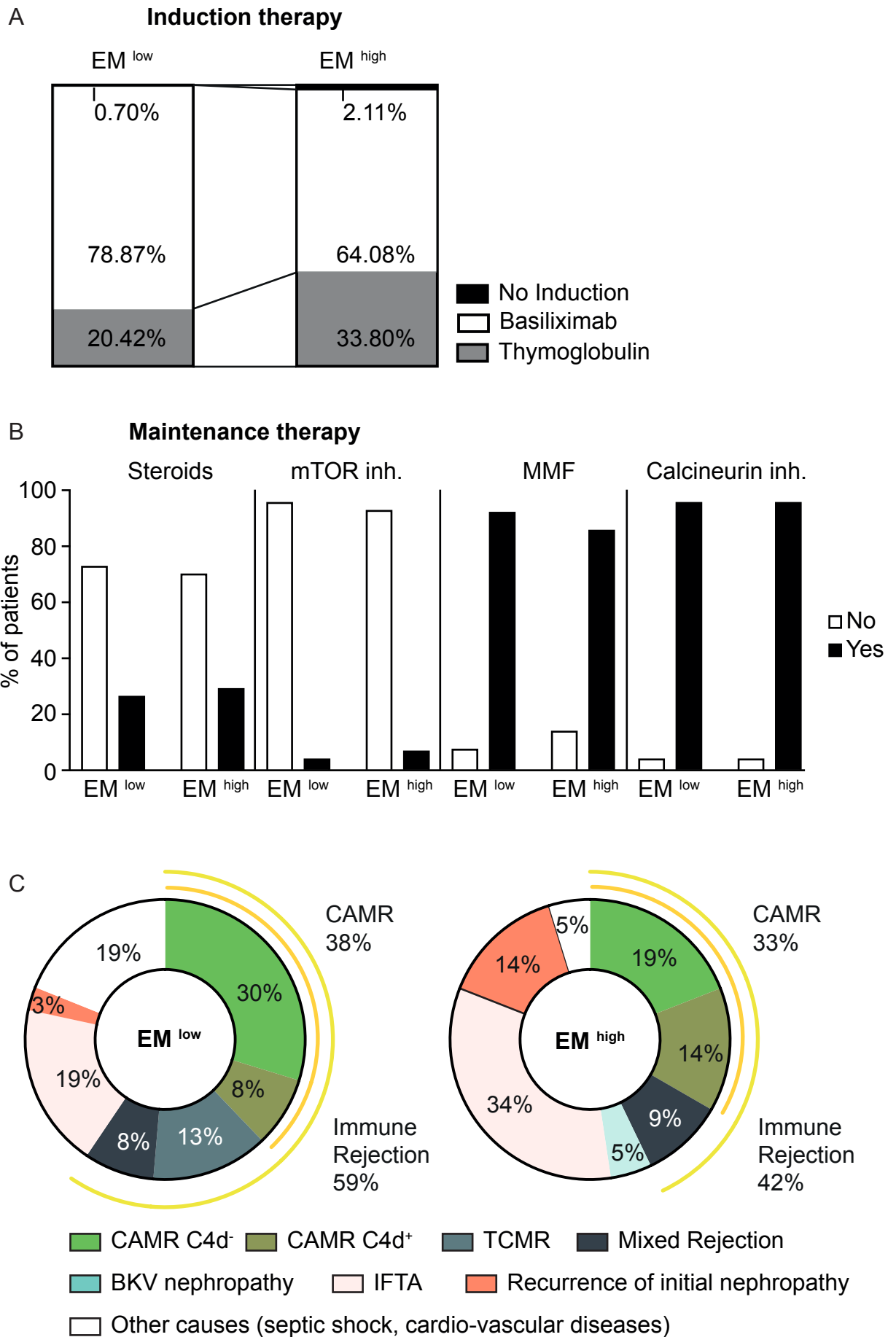
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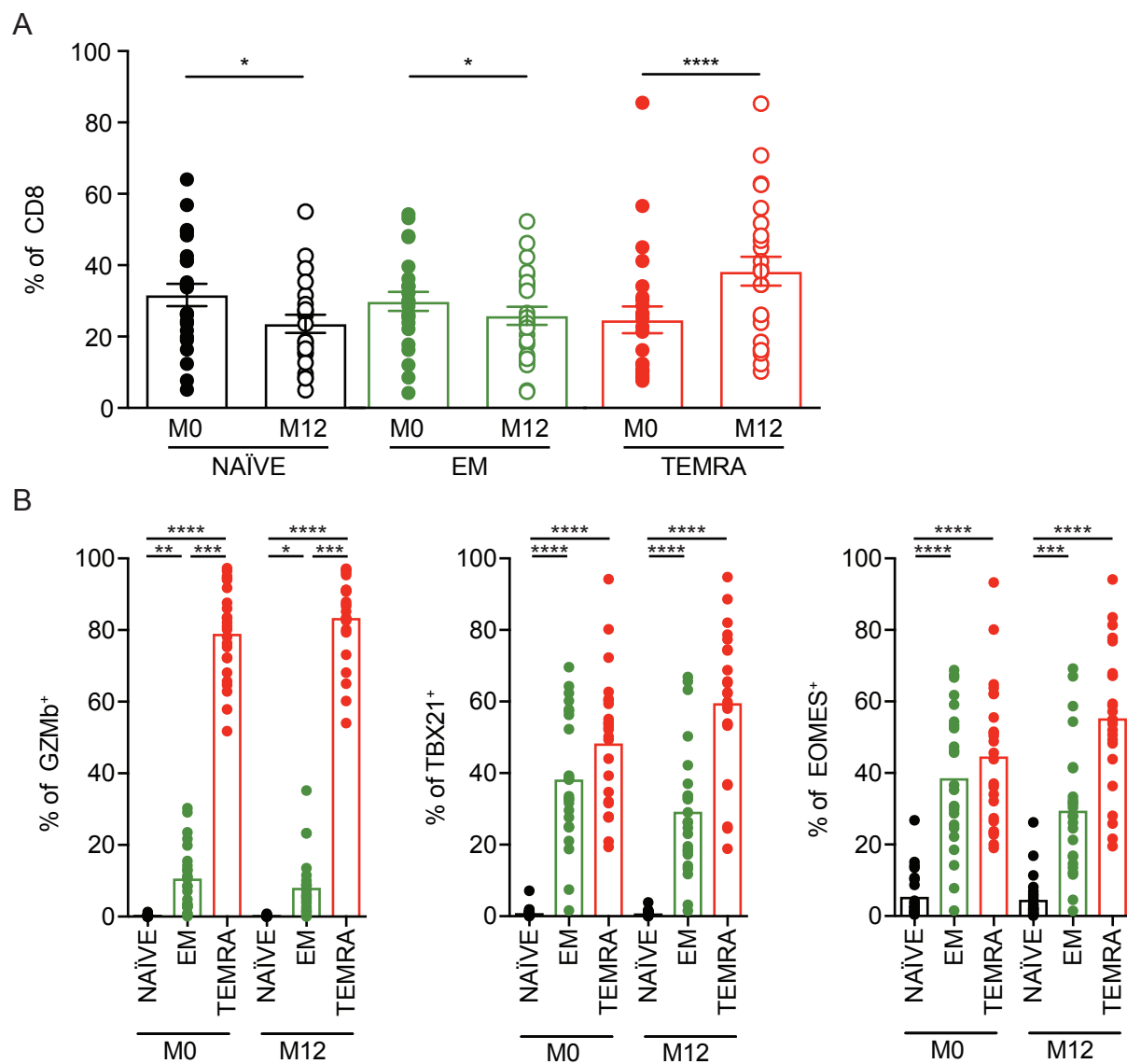
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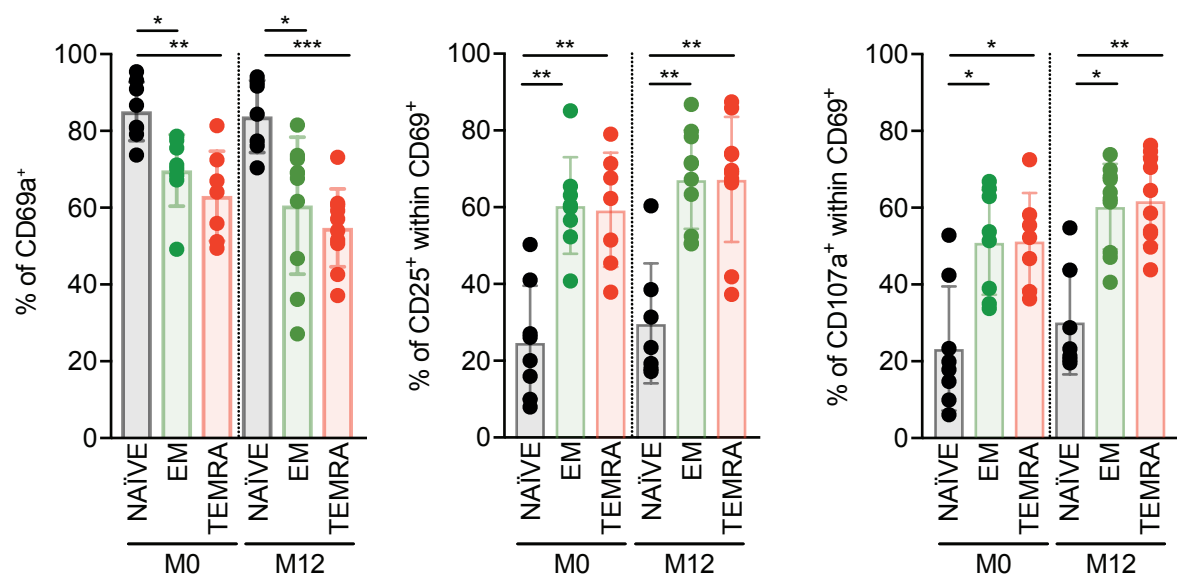
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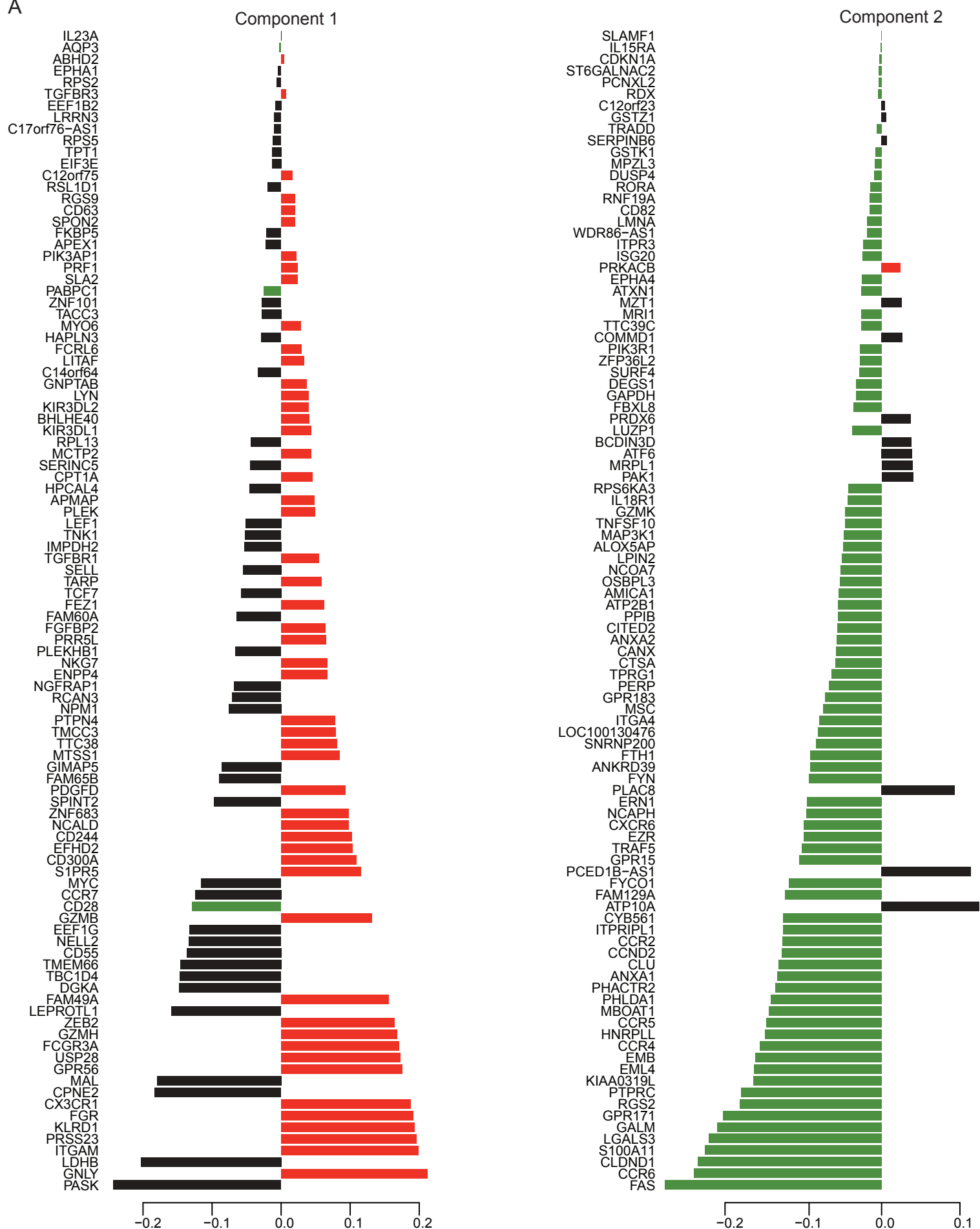


Supplementary Figure 4



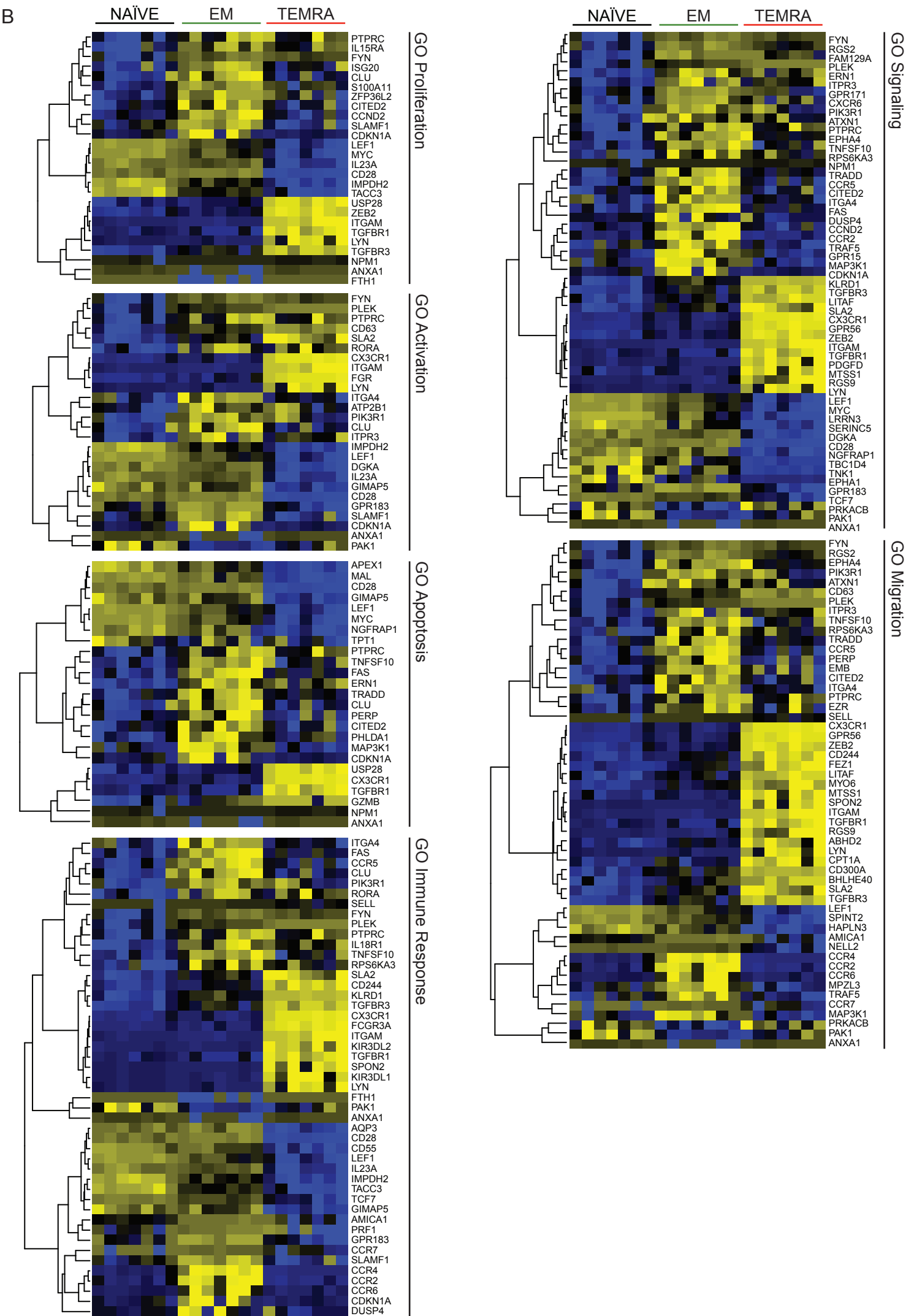
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A

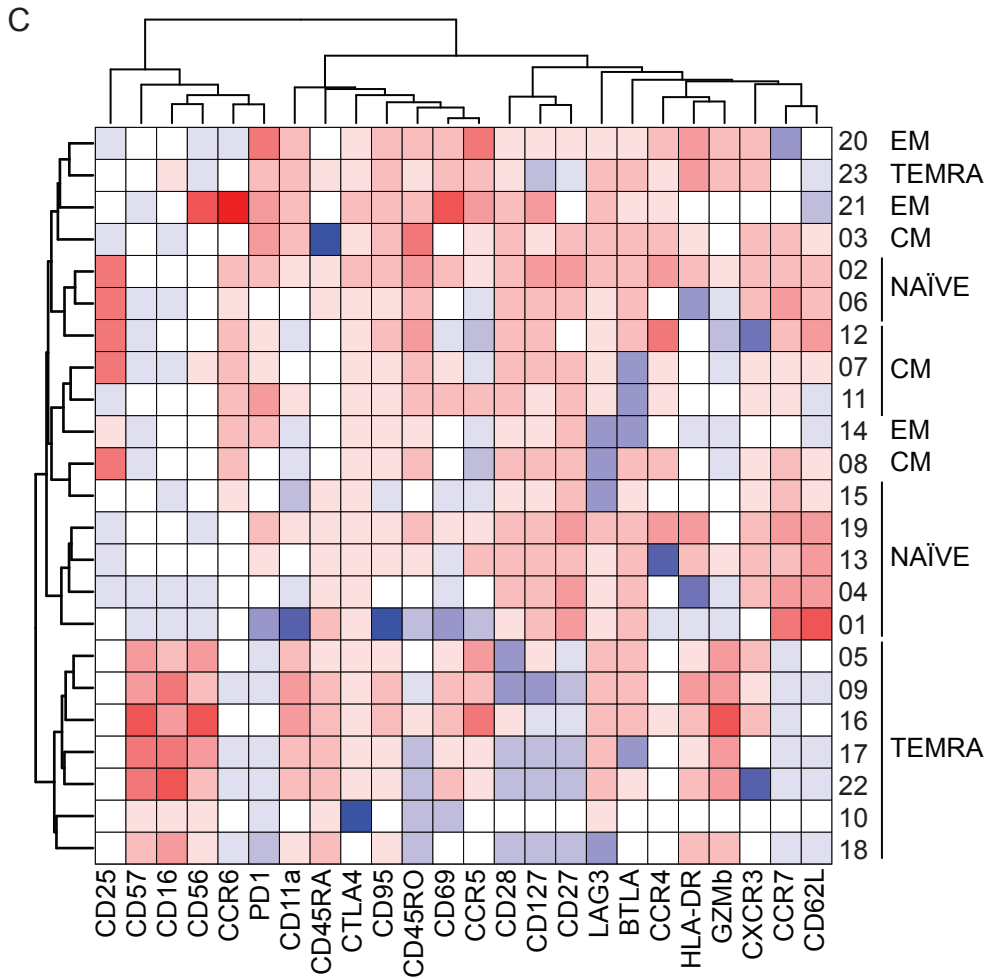
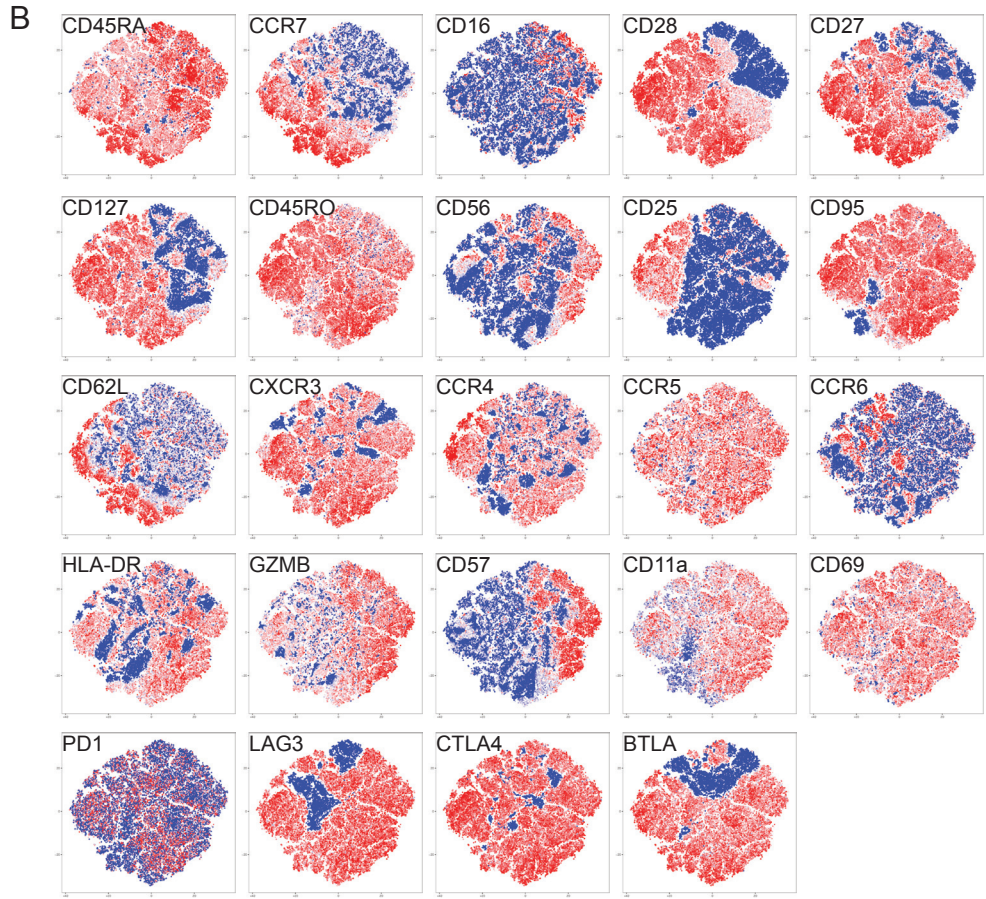
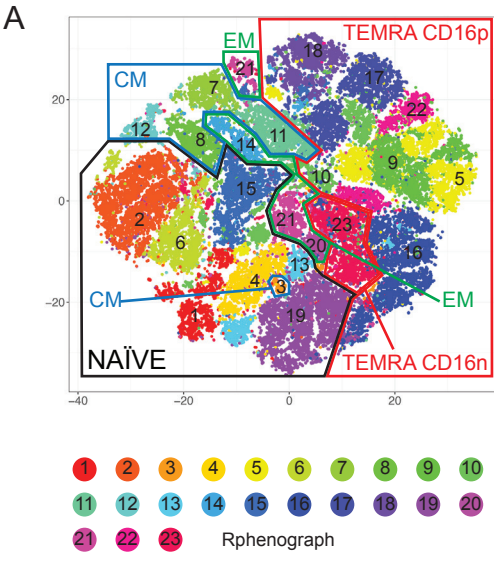


Supplementary Figure 6A

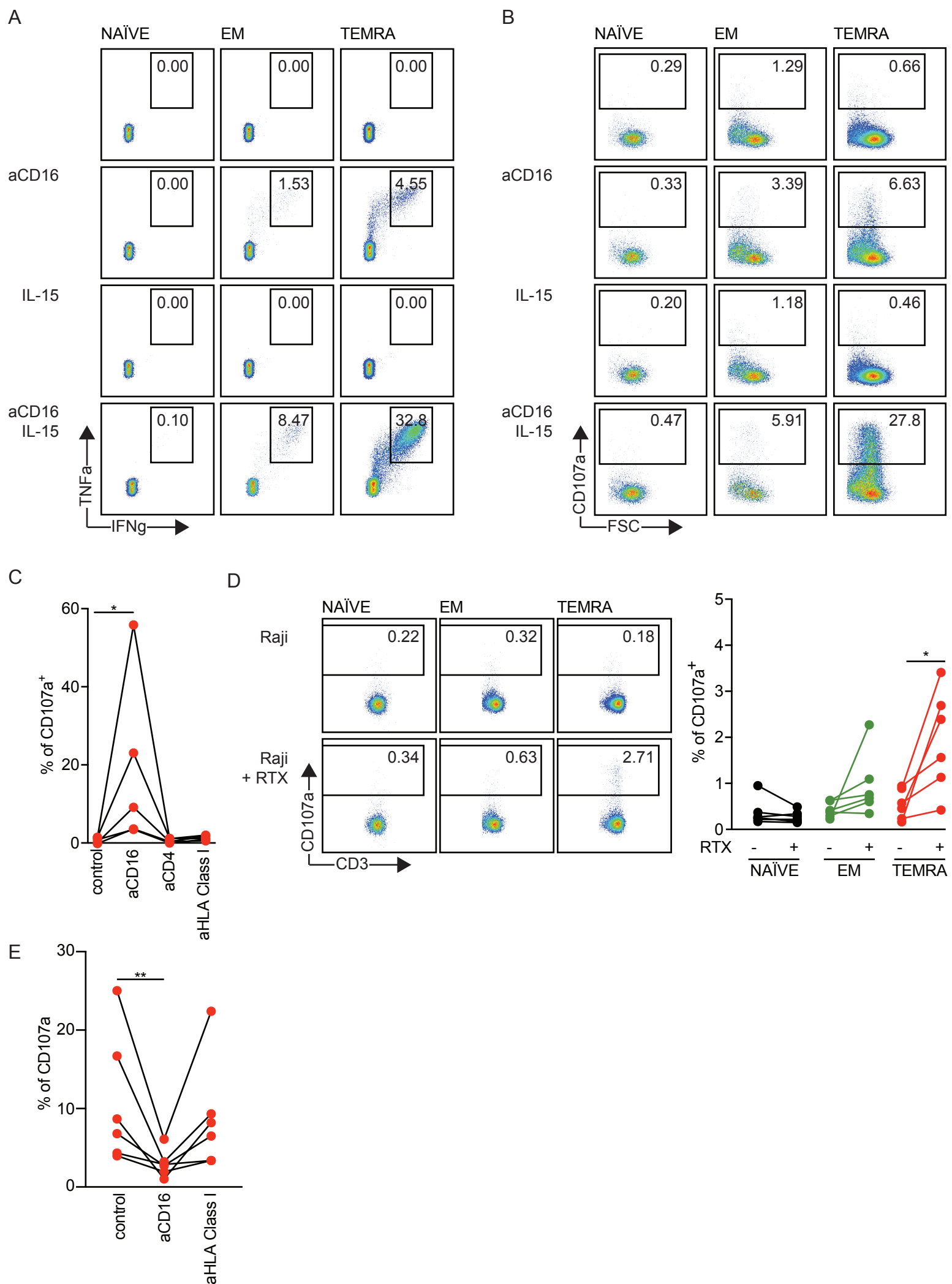
B



Supplementary Figure 6B



Supplementary Figure 7



Supplementary Figure 8

Target	Fluorochrome	Clone Name	Provider
CD3	VioGreen	BW264/56	Miltenyi
CD8	VioGreen	BW135/80	Miltenyi
CD27	VioBright FITC	M-T271	Miltenyi
CD45RA	APC-Vio770	T6D11	Miltenyi
CCR7	PE-Vio770	REA108	Miltenyi
TNF α	FITC	cA2	Miltenyi
PERF	VioBlue	Delta G9	Miltenyi
T-Bet	PE	REA102	Miltenyi
CD8	APC	RPA-T8	BD Biosciences
CD16	PE-Cy7	3G8	BD Biosciences
CD3	PE-CF594	UCHT1	BD Biosciences
CD3	FITC	UCHT1	BD Biosciences
CD25	FITC	M-A251	BD Biosciences
CD28	BV711	CD28.2	BD Biosciences
CD57	BV605	NK-1	BD Biosciences
CD69	PerCp-Cy5.5	FN50	BD Biosciences
CD107a	PE	H4A3	BD Biosciences
CCR7	BV421	150503	BD Biosciences
CCR7	V450	150503	BD Biosciences
IFN γ	V450	B27	BD Biosciences
GZMb	Alexa Fluor 700	GB11	BD Biosciences
EOMES	eFluor660	WD1928	Thermofisher

Supplementary Table 1. Listing of monoclonal antibodies

Main GO Category	GO CATEGORY	ENRICHMENT	FDR
Proliferation	GO:0008283_cell_proliferation	2.09	0.004091
	GO:0008284_positive_regulation_of_cell_proliferation	2.45	0.048677
	GO:0032943_mononuclear_cell_proliferation	3.95	0.020492
	GO:0046651_lymphocyte_proliferation	3.95	0.020492
	GO:0070661_leukocyte_proliferation	3.95	0.020492
Activation	GO:0001775_cell_activation	3.29	0.000000
	GO:0002694_regulation_of_leukocyte_activation	2.79	0.027771
	GO:0042110_T_cell_activation	2.84	0.014989
	GO:0045321_leukocyte_activation	3.16	0.000182
	GO:0046649_lymphocyte_activation	3.10	0.000679
	GO:0050865_regulation_of_cell_activation	3.03	0.014891
	GO:0050867_positive_regulation_of_cell_activation	3.22	0.020415
	GO:0051251_positive_regulation_of_lymphocyte_activation	3.01	0.039481
Apoptosis	GO:0006916_anti-apoptosis	3.21	0.009962
	GO:0006917_induction_of_apoptosis	2.57	0.011783
	GO:0008633_activation_of_pro-apoptotic_gene_products	7.66	0.008149
	GO:0010942_positive_regulation_of_cell_death	2.16	0.025574
	GO:0012502_induction_of_programmed_cell_death	2.57	0.011783
	GO:0043065_positive_regulation_of_apoptosis	2.18	0.024336
	GO:0043066_negative_regulation_of_apoptosis	2.45	0.018339

	GO:0043068_positive_regulation_of_programmed_cell_death	2.18	0.024336
	GO:0043069_negative_regulation_of_programmed_cell_death	2.43	0.020345
	GO:0060548_negative_regulation_of_cell_death	2.39	0.021040
Immune Response	GO:0002250_adaptive_immune_response	3.90	0.034490
	GO:0002252_immune_effector_process	3.15	0.011729
	GO:0002253_activation_of_immune_response	2.74	0.048390
	GO:0002376_immune_system_process	2.94	0.000000
	GO:0002460_adaptive_immune_response_based_on_somatic_recombination_of_immune_receptors_built_from_immunoglobulin_superfamily_domains	3.96	0.033440
	GO:0002520_immune_system_development	2.49	0.021085
	GO:0002682_regulation_of_immune_system_process	2.75	0.000178
	GO:0002684_positive_regulation_of_immune_system_process	2.49	0.017418
	GO:0006955_immune_response	3.48	0.000000
	GO:0006959_humoral_immune_response	10.73	0.000065
	GO:0050776_regulation_of_immune_response	3.16	0.000654
	GO:0050778_positive_regulation_of_immune_response	2.60	0.039376
Signaling	GO:0001932_regulation_of_protein_phosphorylation	3.45	0.015776
	GO:0007166_cell_surface_receptor_linked_signaling_pathway	2.44	0.000000
	GO:0007186_G-protein_coupled_receptor_protein_signaling_pathway	5.07	0.000000

	GO:0007243_intracellular_protein_kinase_cascade	2.19	0.017654
	GO:0023014_signal_transmission_via_phosphorylation_event	2.19	0.017654
	GO:0033674_positive_regulation_of_kinase_activity	3.37	0.007183
	GO:0042325_regulation_of_phosphorylation	2.33	0.016812
	GO:0043085_positive_regulation_of_catalytic_activity	2.55	0.002600
	GO:0045859_regulation_of_protein_kinase_activity	2.33	0.048429
	GO:0045860_positive_regulation_of_protein_kinase_activity	3.50	0.006353
	GO:0046777_protein_autophosphorylation	5.09	0.007014
	GO:0051336_regulation_of_hydrolase_activity	2.45	0.029788
	GO:0051338_regulation_of_transferase_activity	2.32	0.033336
	GO:0051345_positive_regulation_of_hydrolase_activity	3.36	0.017664
	GO:0051347_positive_regulation_of_transferase_activity	3.53	0.002594
Migration	GO:0006928_cellular_component_movement	3.47	0.000000
	GO:0006935_chemotaxis	3.94	0.000067
	GO:0007155_cell_adhesion	3.92	0.000000
	GO:0010646_regulation_of_cell_communication	2.14	0.014956
	GO:0016337_cell-cell_adhesion	4.29	0.015907
	GO:0016477_cell_migration	3.75	0.000000
	GO:0022610_biological_adhesion	3.92	0.000000
	GO:0040011_locomotion	3.72	0.000000
	GO:0048870_cell_motility	3.59	0.000037

	GO:0050900_leukocyte_migration	4.60	0.002540
	GO:0051270_regulation_of_cellular_component_movement	3.69	0.017639
	GO:0051674_localization_of_cell	3.59	0.000037
Other	GO:0006816_calcium_ion_transport	4.77	0.017221
	GO:0006873_cellular_ion_homeostasis	4.52	0.000040
	GO:0006874_cellular_calcium_ion_homeostasis	7.03	0.000000
	GO:0006875_cellular_metal_ion_homeostasis	6.86	0.000000
	GO:0007204_elevation_of_cytosolic_calcium_ion_concentration	10.16	0.000000
	GO:0030003_cellular_cation_homeostasis	5.54	0.000000
	GO:0050801_ion_homeostasis	4.26	0.000150
	GO:0051480_cytosolic_calcium_ion_homeostasis	9.19	0.000000
	GO:0055065_metal_ion_homeostasis	6.77	0.000000
	GO:0055074_calcium_ion_homeostasis	6.92	0.000000
	GO:0055080_cation_homeostasis	5.00	0.000154
	GO:0072503_cellular_divalent_inorganic_cation_homeostasis	6.60	0.000042
	GO:0072507_divalent_inorganic_cation_homeostasis	6.50	0.000071
	GO:0006952_defense_response	2.84	0.000143
	GO:0006968_cellular_defense_response	9.10	0.000174
	GO:0009605_response_to_external_stimulus	2.76	0.000186
	GO:0009615_response_to_virus	3.35	0.011942
	GO:0019724_B_cell_mediated_immunity	6.70	0.012011
	GO:0019725_cellular_homeostasis	3.72	0.000063
	GO:0030154_cell_differentiation	2.03	0.000852
	GO:0048583_regulation_of_response_to_stimulus	2.84	0.000000

GO:0048584_positive_regulation_of_respon se_to_stimulus	2.56	0.018216
GO:0051130_positive_regulation_of_cellular _component_organization	4.18	0.001232
GO:0051174_regulation_of_phosphorus_met abolic_process	2.37	0.011764
GO:0080134_regulation_of_response_to_str ess	2.29	0.035572

Supplementary Table 2. Gene ontology (GO) categories of CD8 subsets gene signature identified by sPLSDA