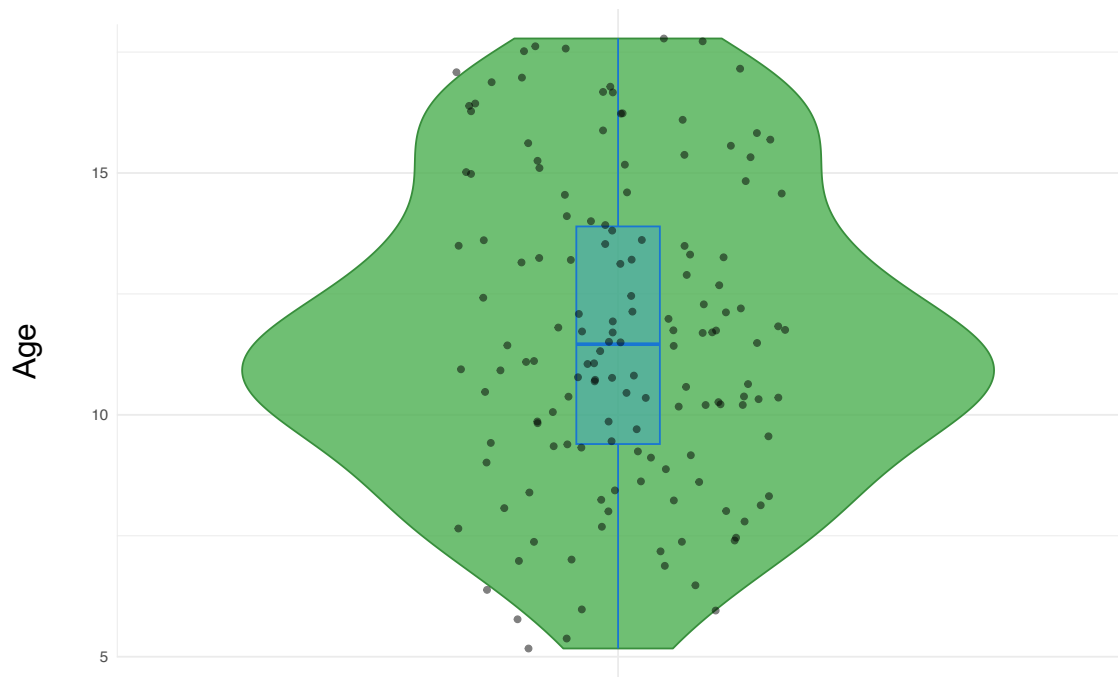


SUPPLEMENTARY MATERIAL

Population	N	Median	Interquartile range
IgM-low naive B cells	131	53.57	47.95-57.79
Naive B cells	131	25.03	21.76-30.39
Unswitched memory B cells	131	2.37	1.33-4.12
Transitional B cells	131	5.15	4.13-6.36
Early plasmablasts	131	0.17	0.07-0.33
Plasmablasts	131	0.63	0.28-1.18
Switched memory B cells	131	7.38	4.80-11.44
Double-negative-1 B cells	131	1.59	0.90-2.59
Double-negative-2 B cells	131	0.23	0.10-0.45
IgD only switched memory B cells	131	0.86	0.46-1.47
Plasmacytoid DCs	132	3.94	2.18-5.72
CD1c myeloid DCs	132	1.99	1.26-2.84
CD16 myeloid DCs	132	5.52	3.64-7.63
Classical monocytes	132	68.95	57.08-76.20
Intermediate monocytes	132	3.70	1.90-7.48
Non-classical monocytes	132	6.84	4.64-8.90
Double positive CD4 CD8 T cells	134	0.26	0.18-0.35
CD4- CD8- CD3 T cells	134	6.34	4.76-8.24
CD27+ CD28+ CD4 T cells	134	38.60	32.75-43.55
CD27- CD28+ CD4 T cells	134	1.44	0.98-2.00
CD27- CD28- CD4 T cells	134	0.02	0.01-0.16
Naive CD4 T cells	133	41.00	34.24-45.42
Effector memory CD4 T cells	133	11.25	9.39-14.10
Central memory CD4 T cells	133	6.53	5.24-8.25
PD1+ effector memory CD4 T cells	133	1.92	1.27-2.43
PD1+ CD57+ effector memory CD4 T cells	133	0.16	0.10-0.26
CD127+ CD45RA- CD4 T cells	128	26.31	21.23-32.88
CD127+ CD45RA+ CD4 T cells	128	68.36	62.13-74.04
CD127- CD45RA+ CD4 T cells	128	1.59	0.93-2.64
CD27+ CD28+ CD8 T cells	134	18.14	16.00-21.13
CD27- CD28+ CD8 T cells	134	0.33	0.14-0.64
CD27- CD28- CD8 T cells	134	0.66	0.29-2.89
CD27+ CD28- CD8 T cells	134	3.06	2.07-4.50
CD69+ CD27+ CD28+ CD8 T cells	134	0.71	0.40-1.34
Naive CD8 T cells	133	14.85	12.46-17.84
Effector memory CD8 T cells	133	5.78	4.43-7.09
CD57+ terminally differentiated effector memory CD8 T cells	133	0.93	0.53-2.31
CD57+ effector memory CD8 T cells	133	0.54	0.35-0.94
PD1+ CD57+ effector memory CD8 T cells	133	0.11	0.06-0.23
CD56dim NK cells	134	6.40	4.78-9.14
CD56bright NK cells	134	0.59	0.42-0.86
CD8+ NKT cells	134	1.04	0.56-1.57
CD69+ CD56dim NK cells	134	0.29	0.16-0.51
CD45RA+ FoxP3lo resting Tregs	128	3.23	2.01-4.12
CD45RA- FoxP3lo non Tregs	128	1.78	1.11-2.49
CD45RA- FoxP3hi activated Tregs	128	1.56	1.07-2.25

Supplementary Table 1. Immune cell subset frequencies in T1D patients.

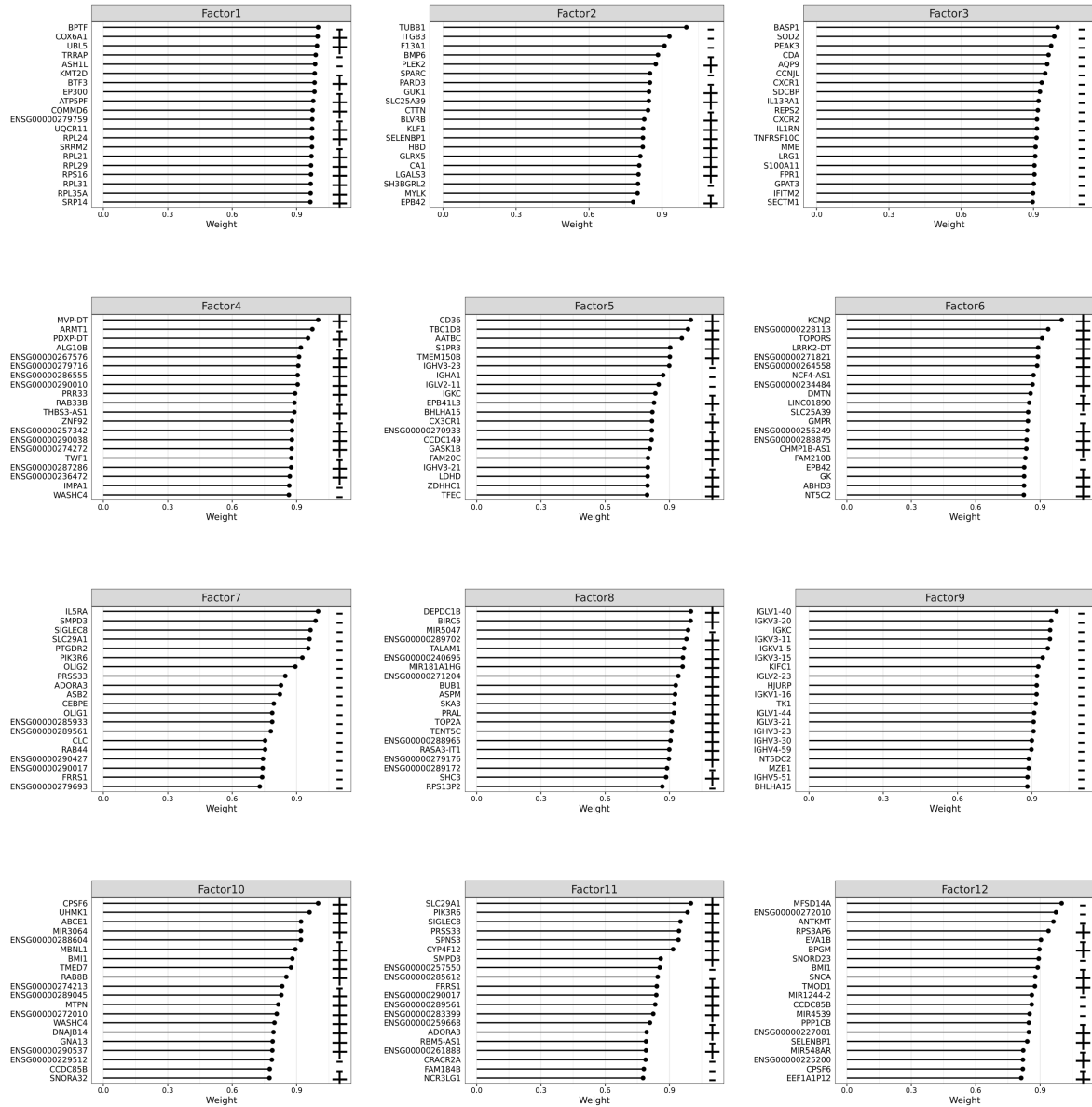


Supplementary Figure 1. Age distribution of the study cohort. The violin plot depicts the distribution of patient ages using density curves. The boxplot shows the median, lower and upper quartiles, and distribution extremes. Dots indicate the position of each data point representing patients.



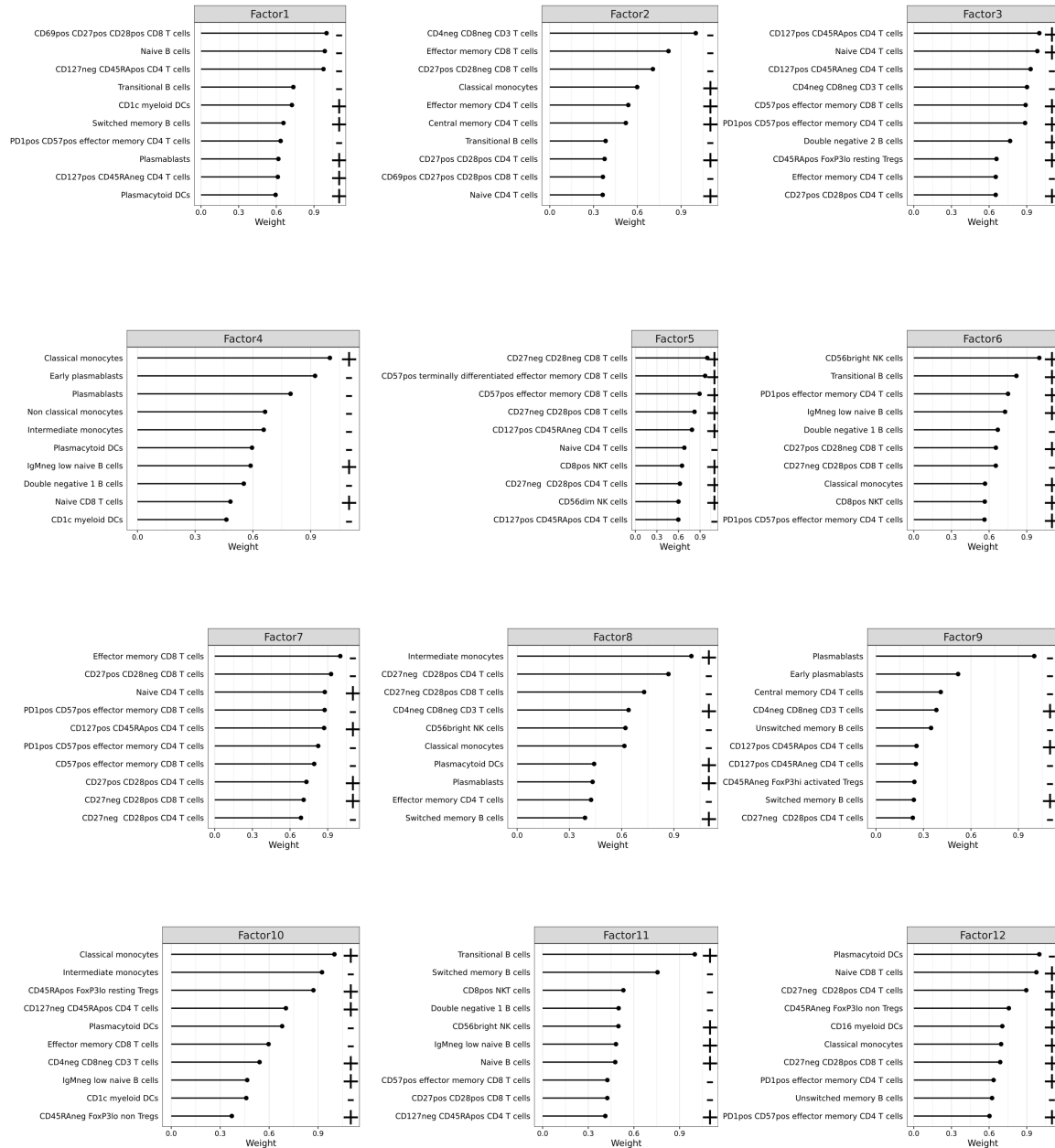
Supplementary Figure 2. Scatterplots of MOFA scores for different MOFA models. Each dot represents a patient, and patient coordinates are determined by the scores in the respective pair of factors. MOFA models ranged from 5 to 15 factors.

RNA



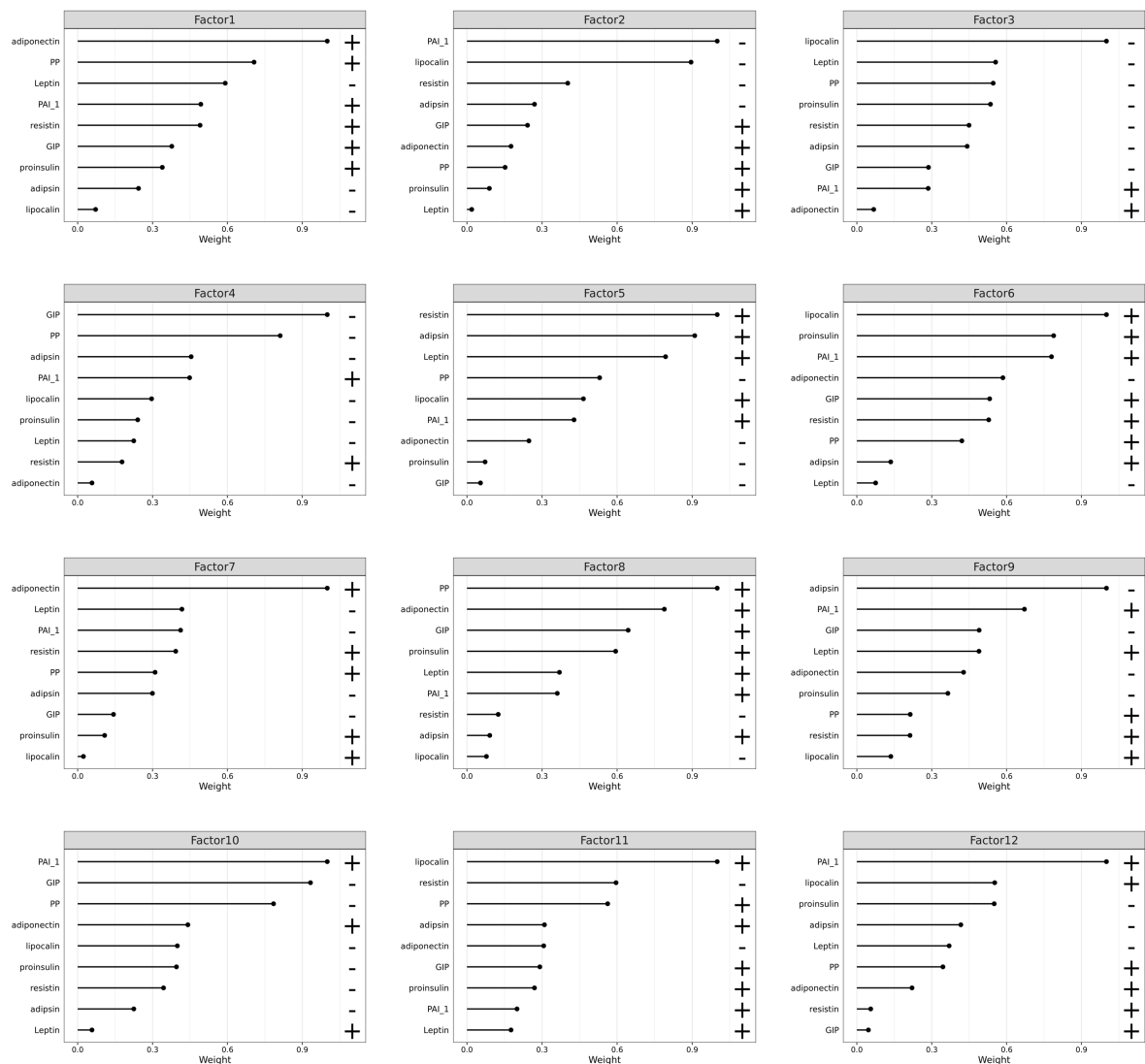
Supplementary Fig. 3. Weights of the top 20 RNA genes in each factor. Illustration of the top 20 genes for each factor that are accountable for the variability observed among factors. The x axis reported the weight of each gene on the factor while the sign (+ or -) indicates the direction of the association.

IMM

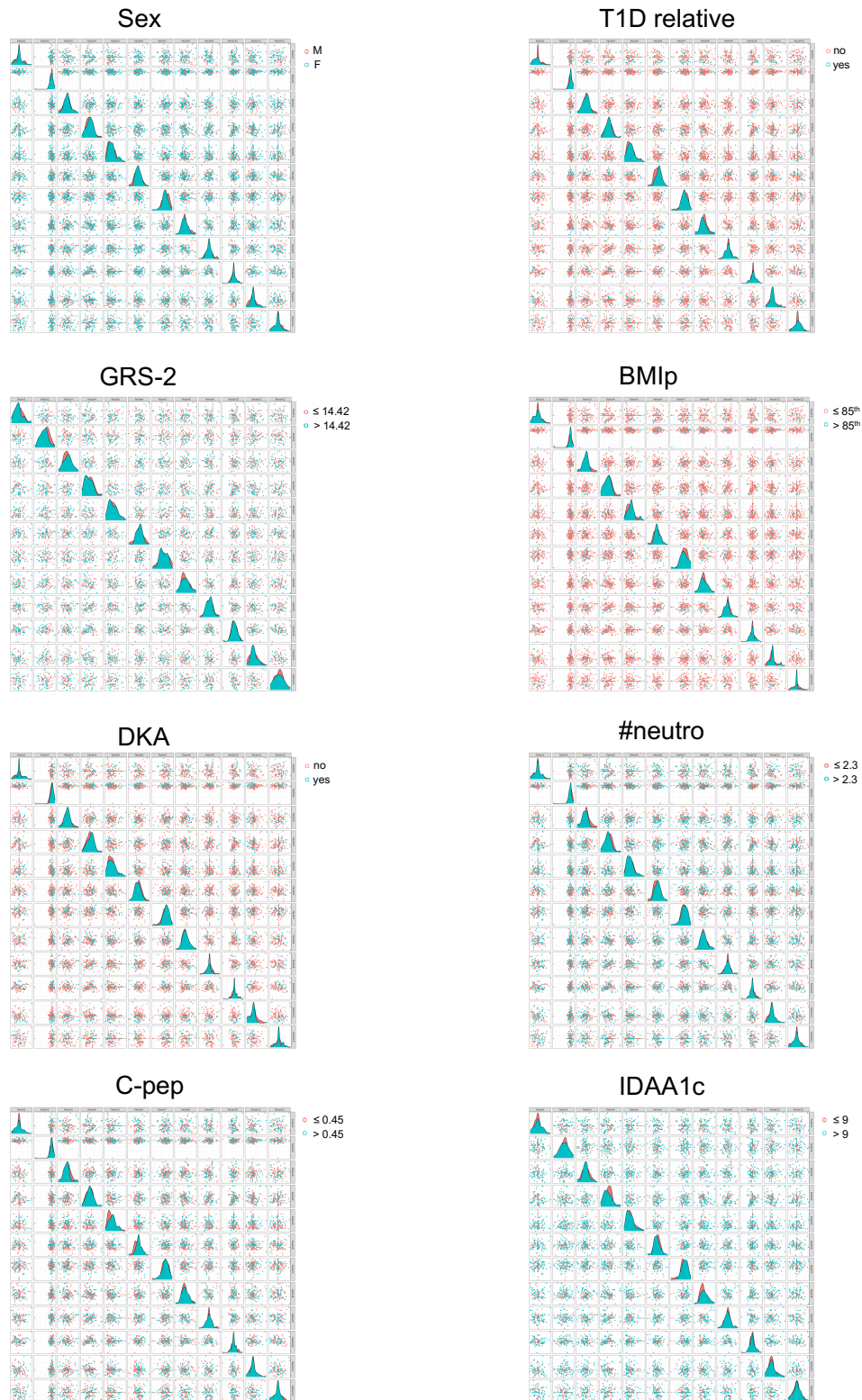


Supplementary Fig. 4. Weights of the top 10 immune cell subsets in each factor. Illustration of the top 10 immune cell subsets for each factor that are accountable for the variability observed among factors. The x axis reported the weight of each cell population on the factor while the sign (+ or -) indicates the direction of the association.

Meth

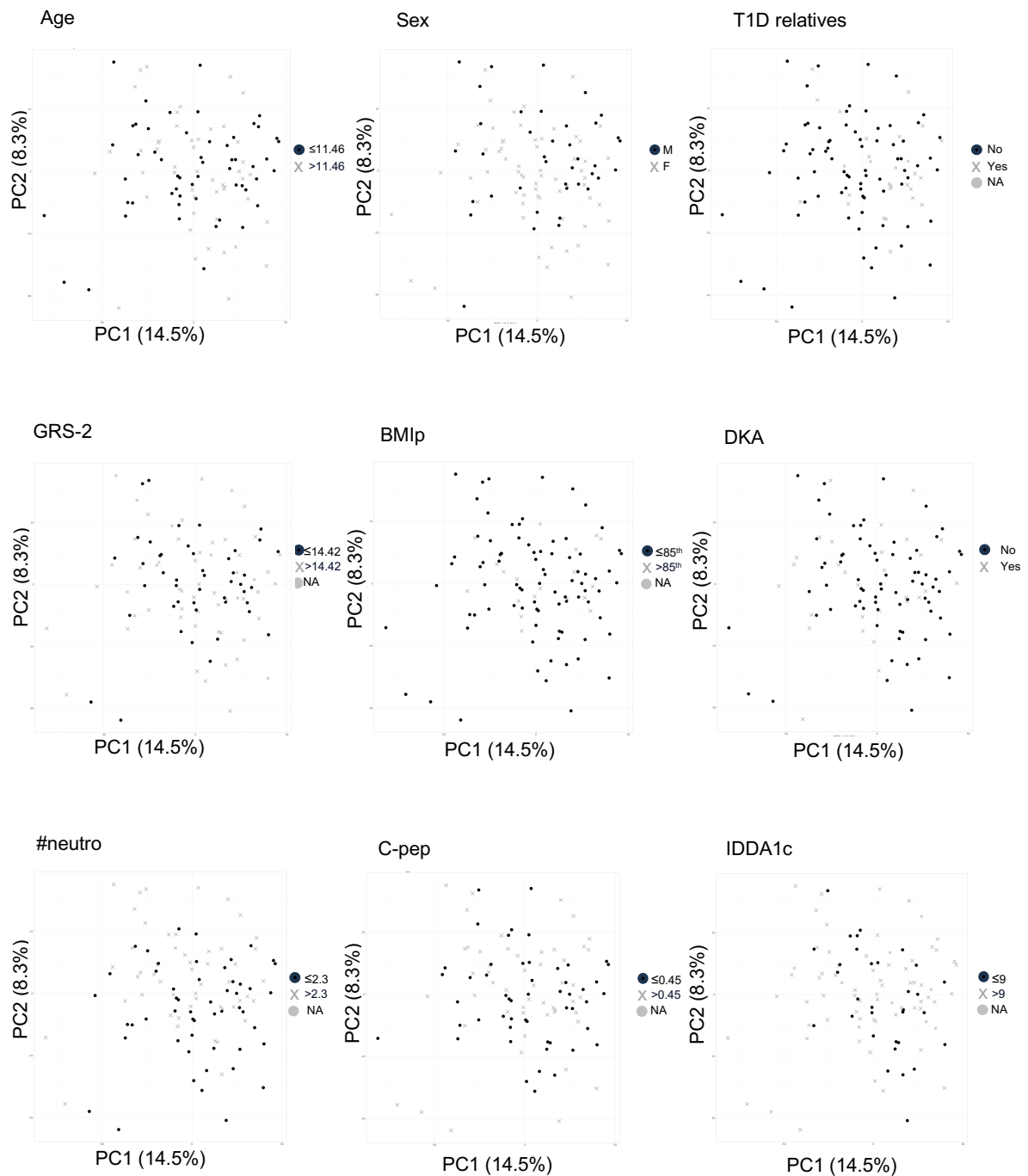


Supplementary Fig. 5. Weights of the metabolic hormones in each factor. Illustration of the 9 metabolic hormones weight for each factor. The x axis reported the weight of each cell population on the factor while the sign (+ or -) indicates the direction of the association.



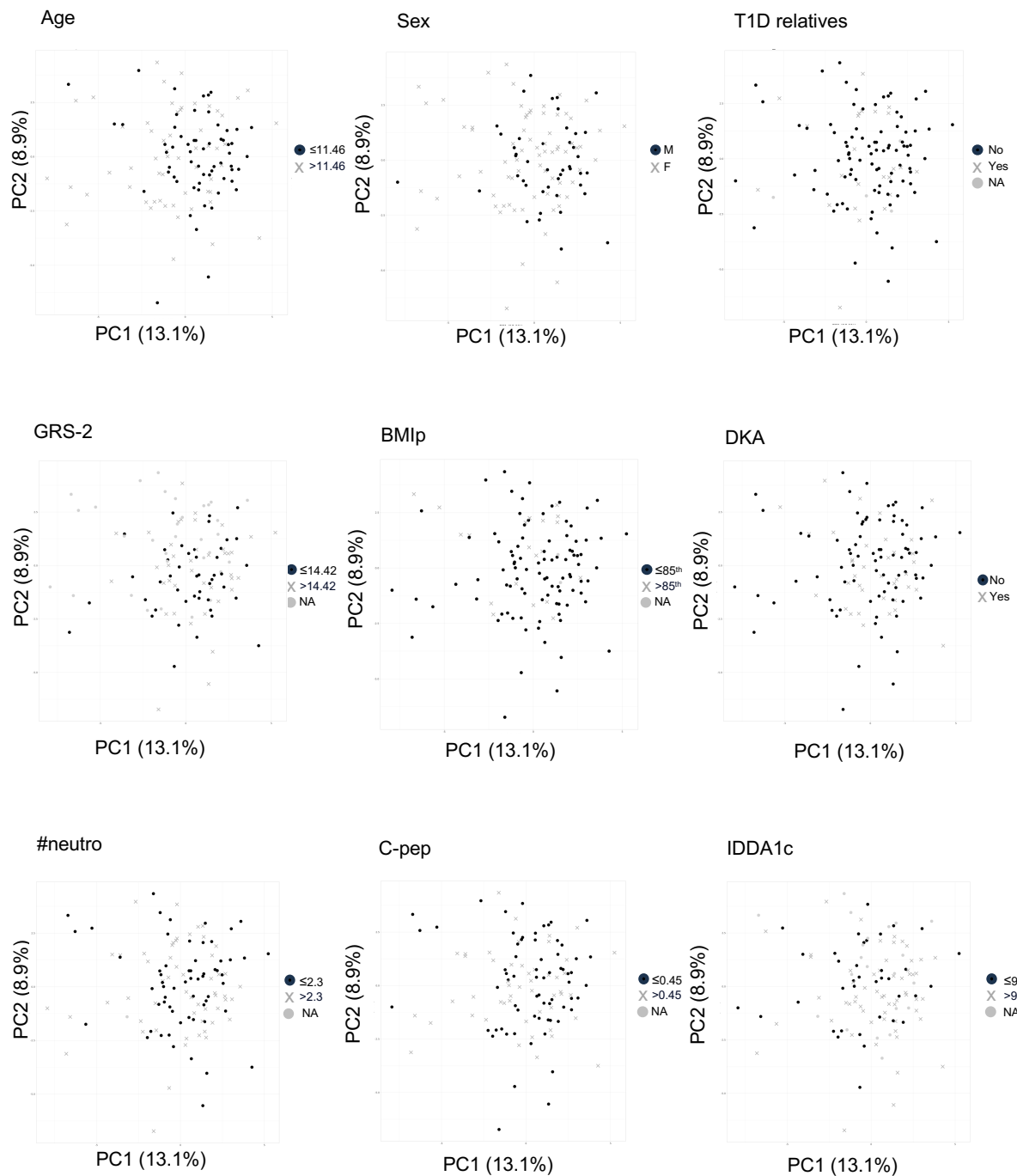
Supplementary Fig. 6. MOFA scoreplots of patient distribution for clinical phenotypes. MOFA scoreplots show patient distribution for clinical phenotypes including sex, family history of T1D, genetic predisposition (GRS-2), percentile of body mass index (BMIp), presence of diabetic ketoacidosis (DKA), neutrophil count, C-peptide levels and disease outcome (IDAA1c). Each dot represents a patient, and it is coloured according to the patient's clinical features.

RNA



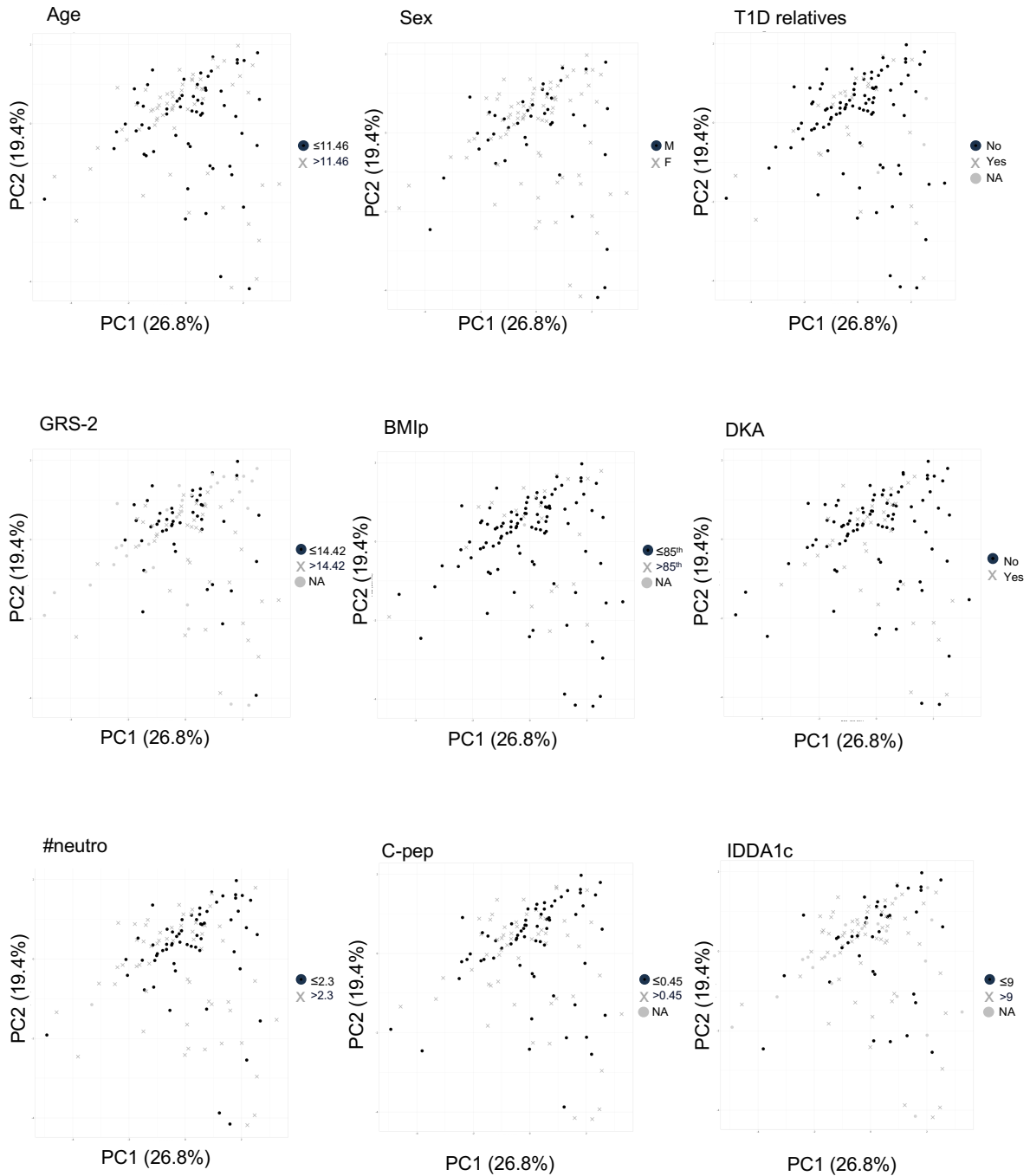
Supplementary Fig. 7. Principal component analysis for RNA genes based on phenotypes. Transcriptome-principal component analysis show patient distribution based on age, sex, family history of T1D, genetic predisposition (GRS-2), percentile of body mass index (BMIp), presence of diabetic ketoacidosis (DKA), neutrophil count, C-peptide levels and disease outcome (IDAA1c).

IMM



Supplementary Fig. 8. Principal component analysis for immune cell populations based on phenotypes. Immunome-principal component analysis show patient distribution based on age, sex, family history of T1D, genetic predisposition (GRS-2), percentile of body mass index (BMIp), presence of diabetic ketoacidosis (DKA), neutrophil count, C-peptide levels and disease outcome (IDAA1c).

Meth



Supplementary Fig. 9. Principal component analysis for metabolic hormones based on phenotypes. Metabolic hormones-principal component analysis show patient distribution based on age, sex, family history of T1D, genetic predisposition (GRS-2), percentile of body mass index (BMIp), presence of diabetic ketoacidosis (DKA), neutrophil count, C-peptide levels and disease outcome (IDAA1c).