

Supplementary Materials for

**Th17 and effector CD8 T cells relate to disease progression in amyotrophic lateral sclerosis:
a case control study**

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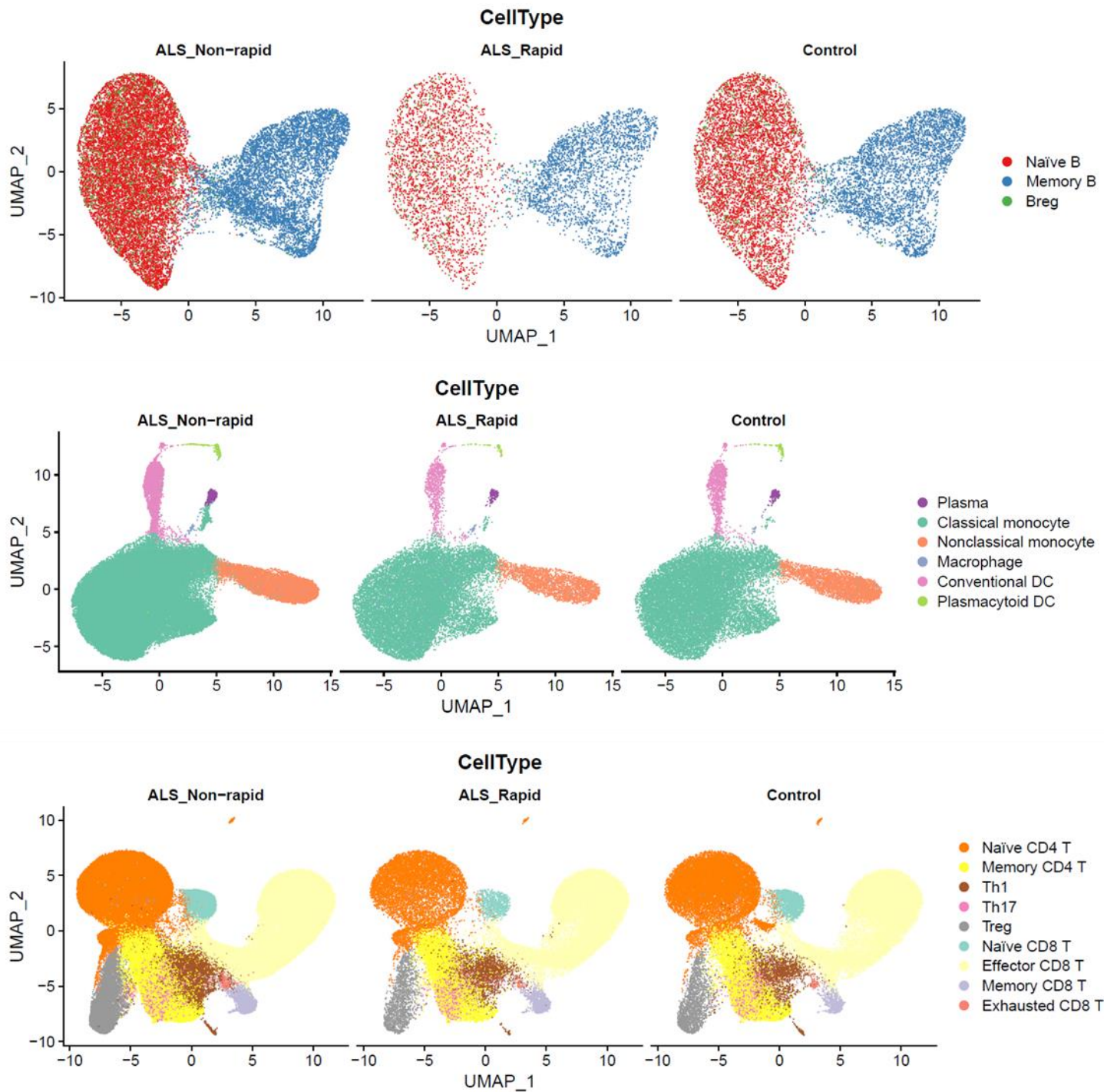


Fig. S1. Visualization of cell subsets. (A) B cells. (B) Monocytes/Macrophages/Dendritic cells. (C) T cells. UMAP: uniform manifold approximation and projection. In the principal component analysis (PCA) of B cells alone (top), Breg overlapped with naïve B cells. The data used in UMAP (the top principal components in PCA) are different between Fig. 1B and Fig. S1, which highlights the differences between naïve B and memory B cells, thereby obscuring the characteristics of Breg cells.

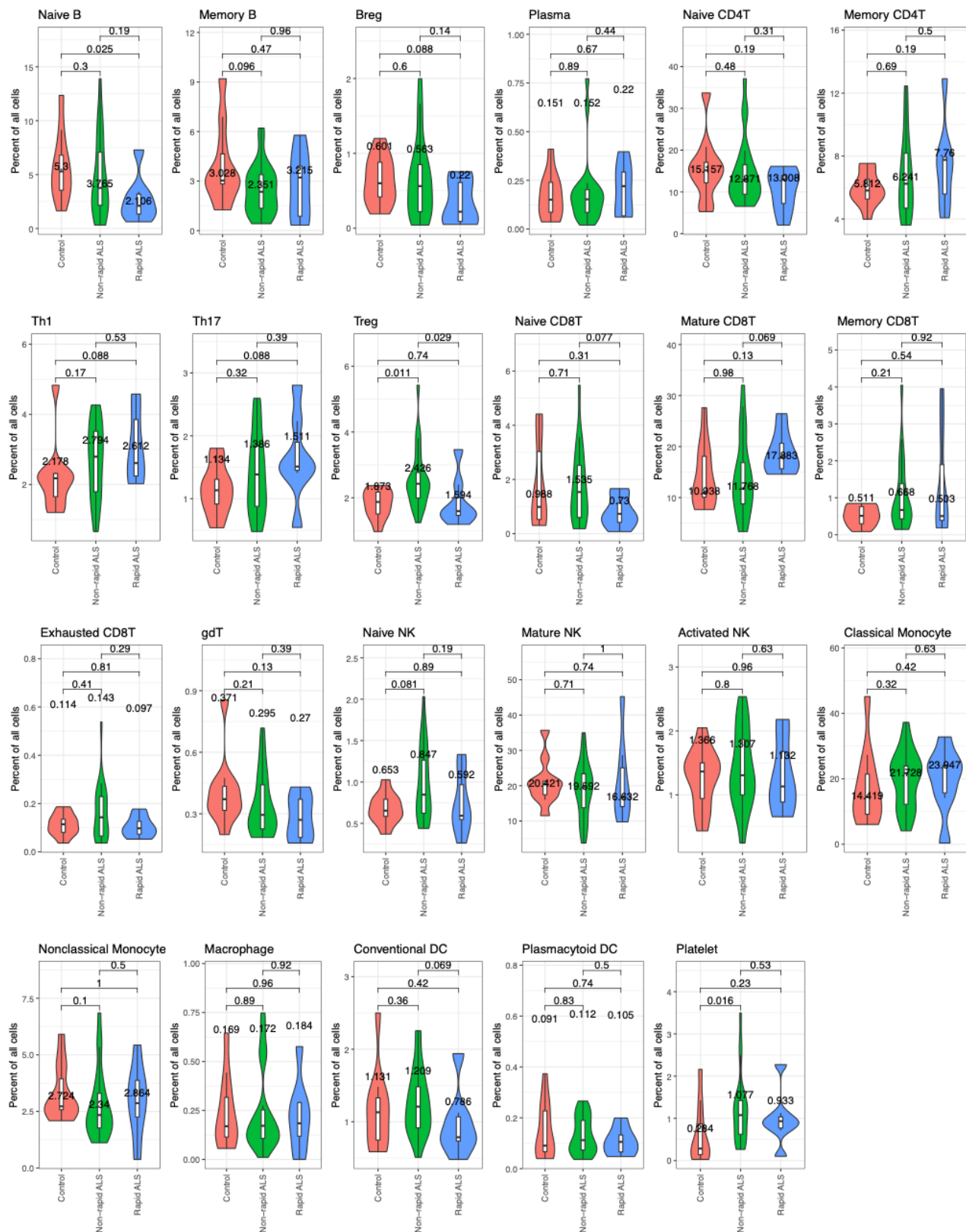


Fig. S2. Frequencies of cell types in all cells in healthy control, non-rapid ALS, and rapid ALS.

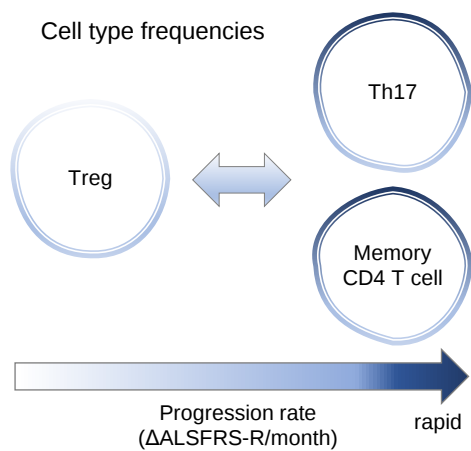
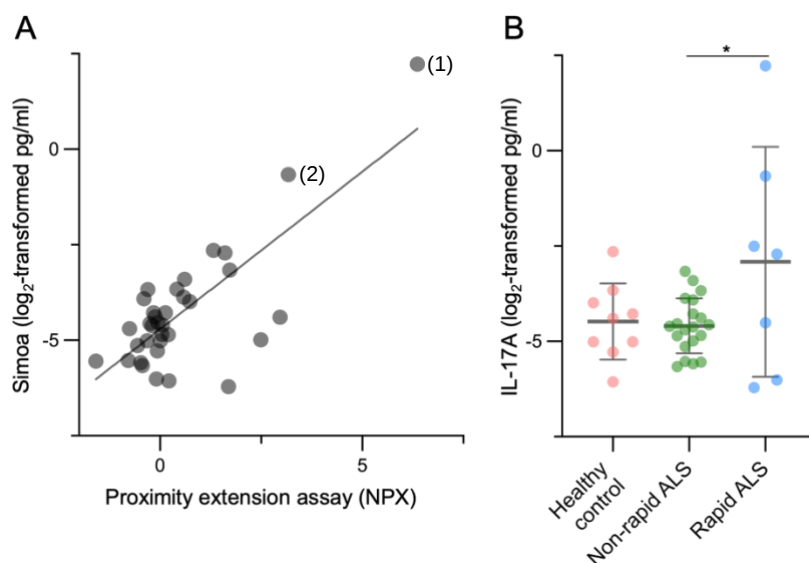


Fig. S3. Illustrative presentation of the relationship between cell type frequencies and progression rate. ALSFRS-R: Revised Amyotrophic Lateral Sclerosis Functional Scale; Th17: T helper 17 cell; Treg: regulatory T cell.



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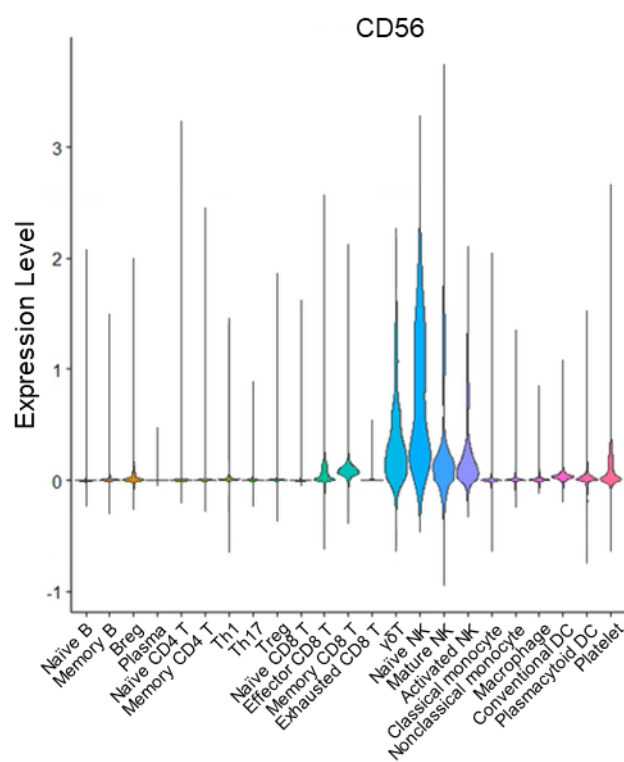
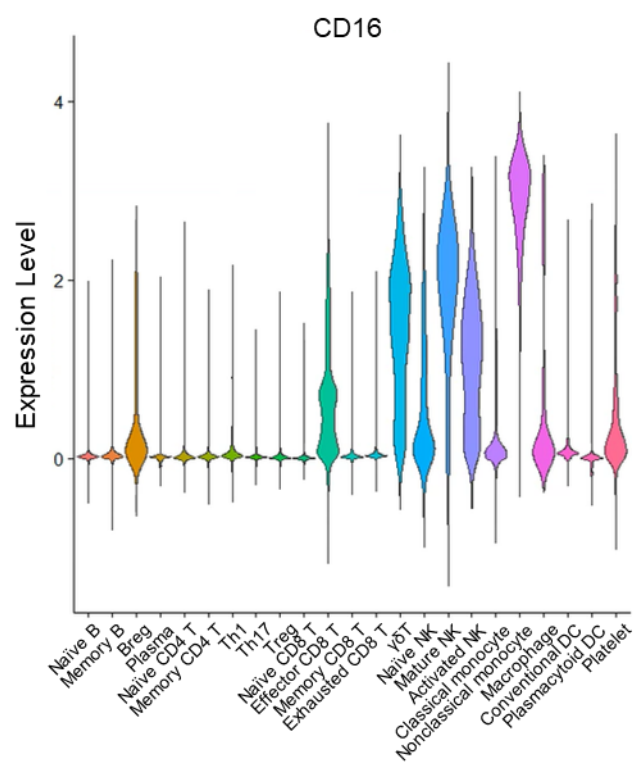
40 **Fig. S4. Serum interleukin-17 values measured by Simoa. (A)** Interleukin-17A (IL-17A)
 41 values obtained with proximity extension assay (PEA) were significantly correlated with those
 42 obtained with Simoa (Pearson's correlation coefficient = 0.764, $p < 0.0001$) in the samples where
 43 data were quantifiable with both methods. **(B)** While IL-17A values did not differ between
 44 healthy control and rapid ALS ($p = 0.105$, Tukey's HSD test), they were significantly higher in
 45 rapid ALS than in non-rapid ALS ($p = 0.0379$, Tukey's HSD test; $p = 0.0425$, one-way ANOVA).

46 (1) The patient with the highest titer of IL-17A (PEA and Simoa) was a non-demented 79-year-
 47 old woman with limb-onset ALS. The duration from symptom onset to blood sampling was 6
 48 months. ALSFRS-R at the first visit was 25, which was the second lowest among all the patients.
 49 The Δ ALSFRS-R was 3.83, which was the second highest in the patients.

50 (2) The patient with the second-highest titer of IL-17A (PEA and Simoa) was a demented 88-
 51 year-old man with limb-onset ALS. The duration from symptom onset to blood sampling was 5
 52 months. ALSFRS-R at the first visit was 25, which was the second lowest among all the patients.
 53 The Δ ALSFRS-R was 4.60, which was the highest in the patients.

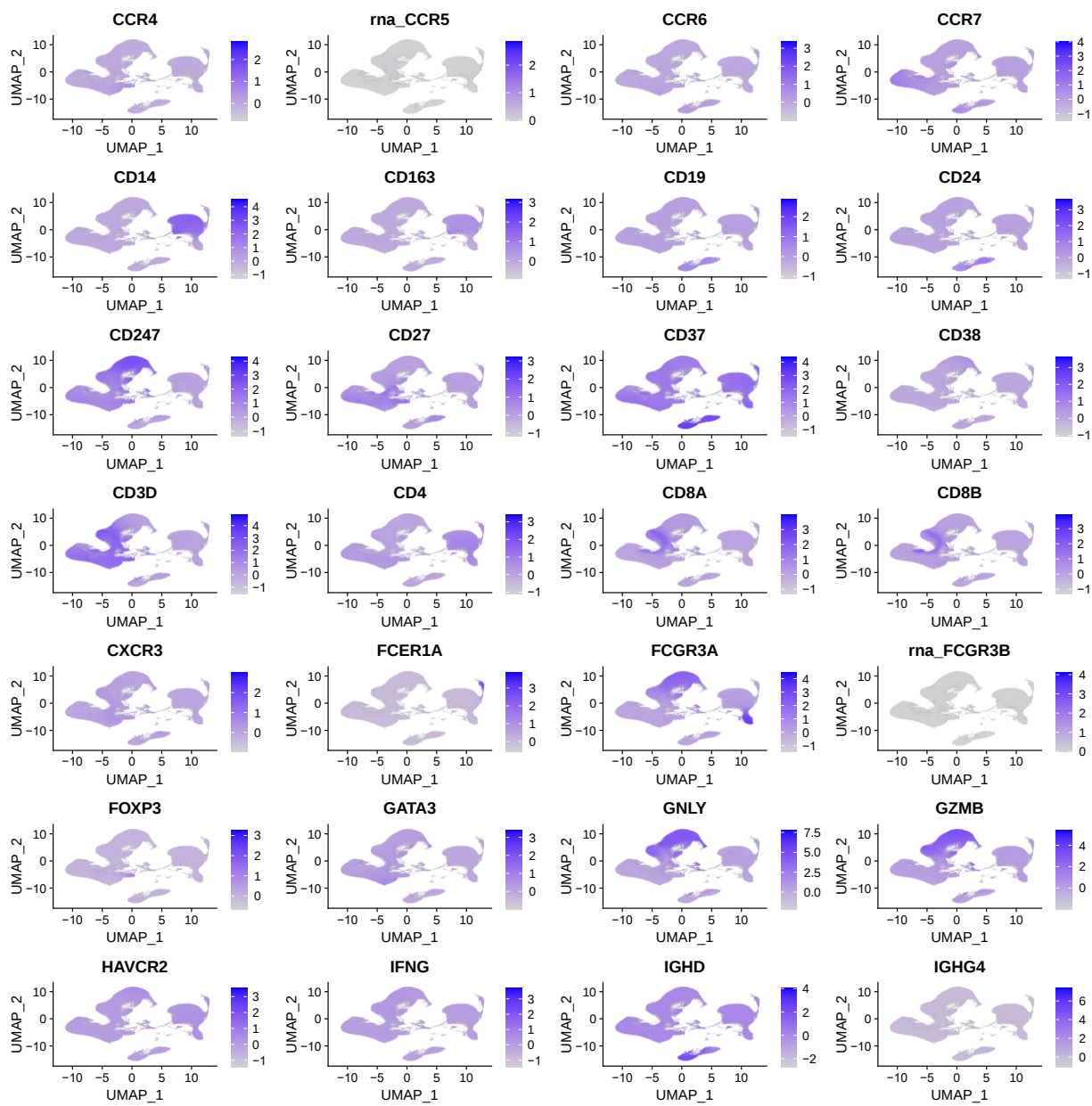
54 Error bars indicate the standard deviation of the mean. ALS: amyotrophic lateral sclerosis; NPX:
 55 normalized protein expression.

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58 **Fig. S5. CD16 and CD56 expression levels in each cell subtype.**



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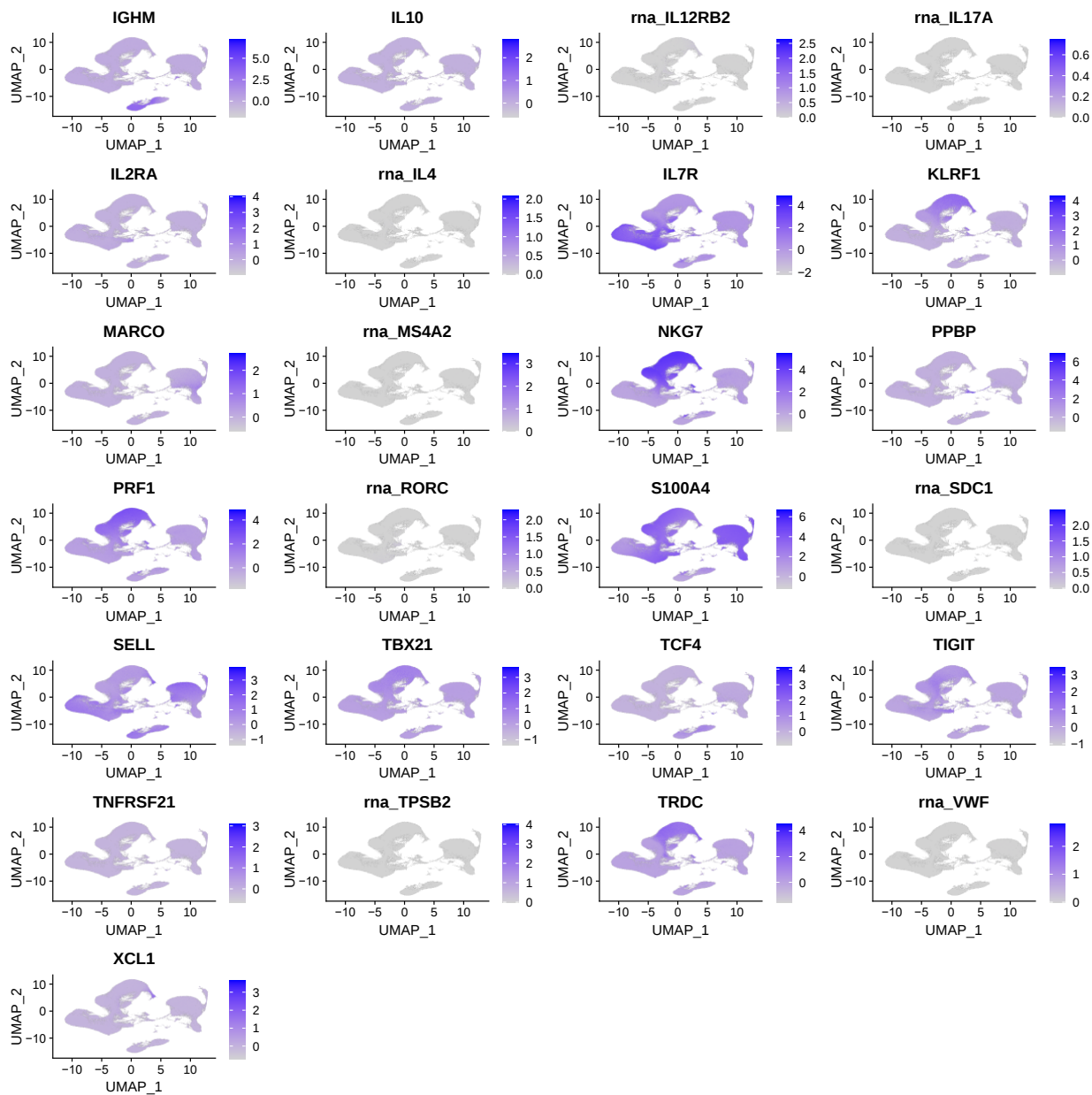


Fig. S6. Uniform manifold approximation and projection (UMAP) of cell-type marker genes for identification of cell types.

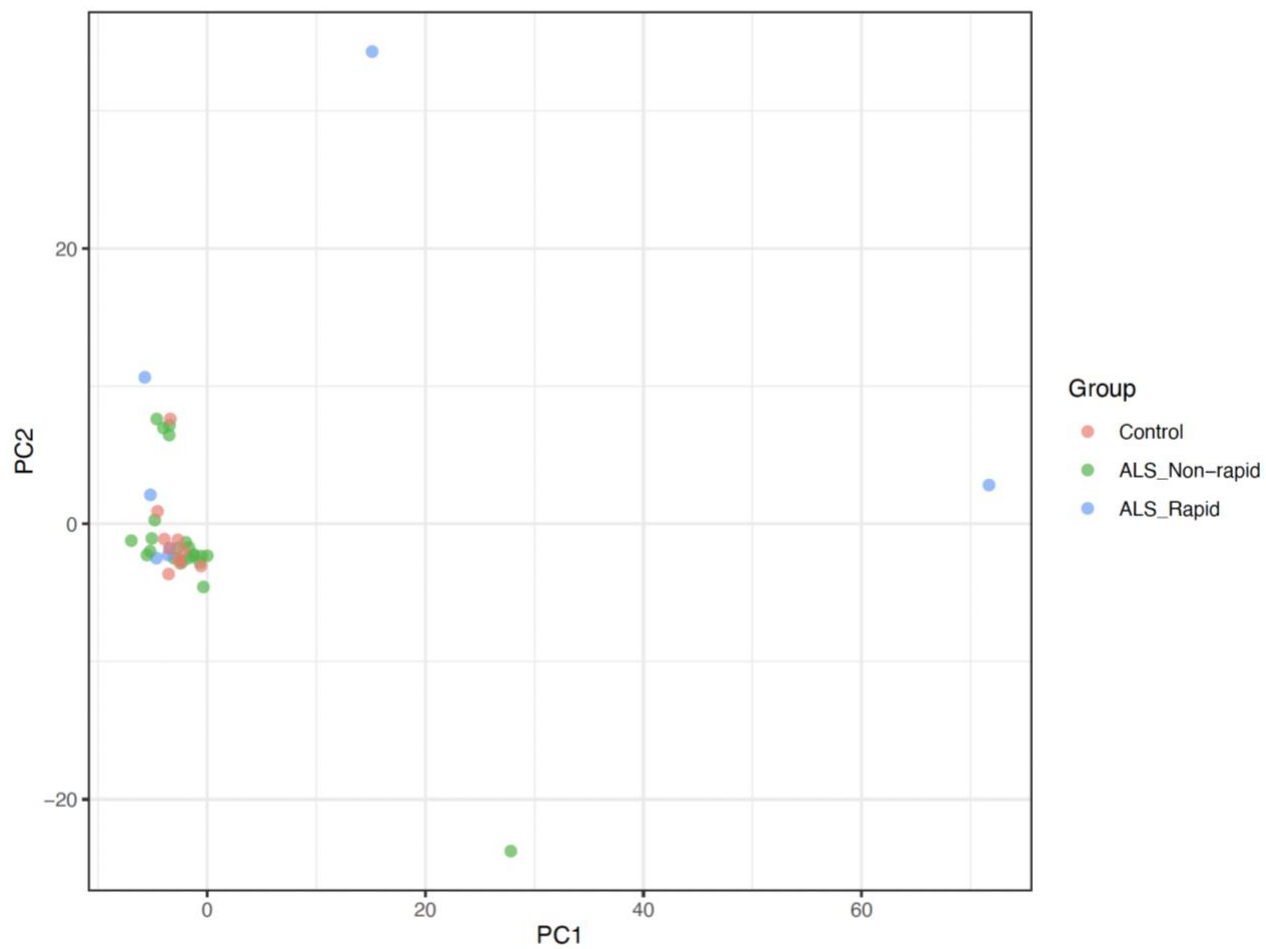


Fig. S8. Principal component analysis of the serum proteome samples. ALS: amyotrophic lateral sclerosis.

72 **Table S1.** The number of cells in each cell subset.

Cell type	Number
Naïve B cell	18656
Memory B cell	12537
Regulatory B cell	2532
Plasma cell	763
Naïve CD4 T cell	59269
Memory CD4 T cell	28779
T helper 1 cell	11217
T helper 17 cell	5833
Regulatory T cell	9575
Naïve CD8 T cell	6569
Effector CD8 T cell	62578
Memory CD8 T cell	4104
Exhausted CD8 T cell	596
γδT cell	1463
Naïve natural killer cell	3580
Mature natural killer cell	82634
Activated natural killer cell	6005
Classical monocyte	81546
Nonclassical monocyte	12765
Macrophage	1050
Conventional dendritic cell	5074
Plasmacytoid dendritic cell	555
Platelet	4455

74 **Table S2.** Partial correlation analysis between the frequency of each cell type in all cells and
75 Δ ALSFRS-R/month.

Cell type	Partial correlation coefficient	P-value
Regulatory T cell	−0.351	0.062
Conventional dendritic cell	−0.249	0.193
T helper 17 cell	0.246	0.198
Effector CD8 T cell	0.235	0.220
Naïve natural killer cell	−0.188	0.329
Naïve B cell	−0.177	0.358
Naïve CD4 T cell	−0.176	0.362
Exhausted CD8 T cell	−0.166	0.390
Plasmacytoid dendritic cell	−0.163	0.400
Regulatory B cell	−0.157	0.416
T helper 1 cell	0.145	0.453
Memory CD8 T cell	0.144	0.456
Macrophage	−0.126	0.516
$\gamma\delta$T cell	−0.118	0.541
Classical monocyte	0.115	0.553
Memory CD4 T cell	0.100	0.606
Mature natural killer cell	−0.084	0.667
Memory B cell	−0.073	0.707
Nonclassical monocyte	0.056	0.771
Activated natural killer cell	−0.053	0.787
Plasma cell	0.046	0.814
Naïve CD8 T cell	−0.018	0.925
Platelet	0.011	0.956

77 **Table S3.** Partial correlation analysis between cell type frequencies in each immune cell and
78 Δ ALSFRS-R/month.

Population	Cell type	Partial correlation coefficient	P-value
CD4 T cell	T helper 17	0.3898	0.0366
CD4 T cell	Memory CD4 T cell	0.3338	0.0768
T cell	CD8 T cell	0.3061	0.1063
T cell	CD4 T cell	-0.3051	0.1075
CD4 T cell	Naïve CD4 T cell	-0.2689	0.1584
CD8 T cell	Exhausted CD8 T cell	-0.2459	0.1984
B cell	Regulatory B cell	-0.2291	0.2319
CD4 T cell	T helper 1 cell	0.2169	0.2585
CD4 T cell	Regulatory T cell	-0.2012	0.2952
B cell	Memory B cell	0.1948	0.3112
Natural killer cell	Naïve natural killer cell	-0.1636	0.3966
B cell	Naïve B cell	-0.1565	0.4177
T cell	$\gamma\delta$ T cell	-0.1080	0.5772
CD8 T cell	Effector CD8 T cell	0.1079	0.5775
Natural killer cell	Activated natural killer cell	0.0971	0.6165
CD8 T cell	Naïve CD8 T cell	-0.0921	0.6348
Monocyte	Classical monocyte	0.0694	0.7207
Monocyte	Nonclassical monocyte	-0.0694	0.7207
NK cell	Mature natural killer cell	0.0326	0.8666
Dendritic cell	Conventional dendritic cell	-0.0058	0.9760
Dendritic cell	Plasmacytoid dendritic cell	0.0058	0.9760
CD8 T cell	Memory CD8 T cell	-0.0002	0.9991

83 **Table S5.** Differentially expressed genes.

Cell type	ALS vs. control	Non-rapid ALS vs. Control	Rapid ALS vs. control	Rapid ALS vs. Non-rapid ALS
Naïve B cell	-	-	-	-
Memory B cell	-	-	HBA2*	-
Regulatory B cell	-	-	-	-
Plasma cell	-	-	-	-
Naïve CD4 T cell	SERPINA1	SERPINA1	SERPINA1	-
Memory CD4 T cell	-	-	-	-
T helper 1 cell	-	-	AC103591.3	-
T helper 17 cell	-	-	-	-
Regulatory T cell	-	-	-	-
Naïve CD8 T cell	-	-	-	-
Effector CD8 T cell	-	-	-	-
Memory CD8 T cell	-	-	-	-
Exhausted CD8 T cell	-	-	-	-
$\gamma\delta$ T cell	-	-	IGHA1*	-
Naïve natural killer cell	-	-	-	-
Mature natural killer cell	-	-	-	-
Activated natural killer cell	-	-	-	-
Classical monocyte	AC103591.3	AC103591.3	AC103591.3	-
Nonclassical monocyte	-	-	-	-
Macrophage	MS4A1	MS4A1	CD52	-
Conventional dendritic cell	-	-	-	-
Plasmacytoid dendritic cell	-	-	GNG11	-
Platelet	CA2 CAVIN2 CLEC1B CMTM5 ENKUR GSTO1 HEMGN LYL1 NEXN	CA2 ENKUR GSTO1 HEMGN LYL1 NEXN	CA2 CLEC1B CMTM5 ENKUR HEMGN LIMS1 PLEKHO1 PRKAR2B RUFY1 SNCA	-

84 *Upregulated in ALS; the other genes were downregulated in ALS. ALS: amyotrophic lateral
85 sclerosis.
86

Table S6. Correlation between serum proteome and Δ ALSFRS-R/month.

Protein	Gene	Partial correlation coefficient	P-value
Killer cell lectin-like receptor D1 (CD94)*	KLRD1	0.745	<0.0001
Centrosomal protein of 164 kDa	CEP164	0.697	<0.0001
CD160 antigen	CD160	0.665	0.0001
Keratin, type I cytoskeletal 19*	KRT19	0.658	0.0002
Tumor necrosis factor receptor superfamily member 11A	TNFRSF11A	0.644	0.0002
B cell antigen receptor complex-associated protein beta chain	CD79B	0.610	0.001
C-type lectin domain family 7 member A	CLEC7A	0.594	0.001
Trefoil factor 2*	TFF2	0.584	0.001
Cytoskeleton-associated protein 4	CKAP4	0.585	0.001
Macrophage colony-stimulating factor 1	CSF1	0.554	0.002
Proteinase-activated receptor 1	F2R	0.550	0.002
Butyrophilin subfamily 3 member A2	BTN3A2	0.563	0.002
Interleukin-17A*	IL17A	0.556	0.003
Leukocyte-associated immunoglobulin-like receptor 1	LAIR1	0.536	0.003
NF-kappa-B essential modulator	IKBKG	0.548	0.003
T cell surface glycoprotein CD4	CD4	0.541	0.004
C-type natriuretic peptide	NPPC	0.540	0.004
Collagen alpha-1(IX) chain	COL9A1	0.538	0.004
Fc receptor-like protein 6	FCRL6	0.533	0.004
Carcinoembryonic antigen-related cell adhesion molecule 21	CEACAM21	0.531	0.004
C-C motif chemokine 23	CCL23	0.512	0.004
Serpin B8	SERPINB8	0.518	0.005
Follistatin-related protein 3	FSTL3	0.504	0.005
Transcription regulator protein BACH1	BACH1	0.518	0.006
Galanin peptides	GAL	-0.492	0.007
Endothelial cell-specific molecule 1	ESM1	0.491	0.007
Fms-related tyrosine kinase 3 ligand	FLT3LG	-0.498	0.007
Agrin	AGRN	0.490	0.007
Killer cell lectin-like receptor subfamily B member 1	KLRB1	0.497	0.007
Beta-1,4-galactosyltransferase 1	B4GALT1	0.483	0.008
Urokinase plasminogen activator surface receptor	PLAUR	0.483	0.008
Interleukin-2	IL2	0.498	0.008
Neutrophil cytosol factor 2*	NCF2	0.498	0.008
Interferon gamma receptor 1	IFNGR1	0.478	0.009
Tumor necrosis factor receptor superfamily member 13B	TNFRSF13B	0.477	0.009
YTH domain-containing family protein 3*	YTHDF3	0.492	0.009

Proteins with p-values < 0.01 are shown. *Significantly elevated in rapid versus non-rapid amyotrophic lateral sclerosis. ALSFRS-R: Revised Amyotrophic Lateral Sclerosis Functional Rating Scale.

Table S7. Correlation between serum proteome and cell types.

Protein	Gene	Cell type	Coefficient
<i>In all cells</i>			
Hepatocyte growth factor	HGF	Classical monocyte	0.756
Oncostatin-M	OSM	Classical monocyte	0.641
Transforming growth factor alpha	TGFalpha	Classical monocyte	0.628
Protransforming growth factor alpha	TGFA	Classical monocyte	0.606
5'-AMP-activated protein kinase subunit beta-1	PRKAB1	Naïve NK	0.597
Neutrophil cytosol factor 2*	NCF2	Classical monocyte	0.591
Interleukin-1 receptor antagonist protein	IL1RN	Classical monocyte	0.580
C-type lectin domain family 4 member D	CLEC4D	Classical monocyte	0.563
Caspase-8	CASP8	Macrophage	0.548
Egl nine homolog 1	EGLN1	Classical monocyte	0.542
SRSF protein kinase 2	SRPK2	Classical monocyte	0.532
Tumor necrosis factor ligand superfamily member 14	TNFSF14	Classical monocyte	0.524
Lymphotoxin-alpha	LTA	$\gamma\delta$ T	0.524
CCN family member 2	CCN2	Platelet	0.524
Transcription regulator protein BACH1	BACH1	Classical monocyte	0.516
Nibrin	NBN	Classical monocyte	0.513
Linker for activation of T cells family member 1	LAT	Breg	0.511
Urokinase plasminogen activator surface receptor	PLAUR	Classical monocyte	0.509
Hematopoietic lineage cell-specific protein	HCLS1	Classical monocyte	0.507
Lymphocyte-specific protein 1	LSP1	Classical monocyte	0.505
<i>In cell subsets</i>			
Butyrophilin subfamily 3 member A2	BTN3A2	Memory CD4 T	0.620
Interleukin-2 receptor subunit beta	IL2RB	Th17	0.601
Kynureninase	KYNU	Treg	0.570
C-type lectin domain family 4 member C	CLEC4C	$\gamma\delta$ T	0.567
Interleukin-17A*	IL17A	Memory CD4 T	0.559
Fibroblast growth factor 21	FGF21	Treg	0.557
Trefoil factor 2*	TFF2	Effector CD8 T	0.556
Tumor necrosis factor receptor superfamily member 11B	TNFRSF11B	Effector CD8 T	0.556
Urokinase plasminogen activator surface receptor	PLAUR	Memory CD4 T	0.555
Granulocyte colony-stimulating factor	CSF3	Th17	0.551
Tumor necrosis factor receptor superfamily member 14	TNFRSF14	Memory CD4 T	0.547
Protein sprouty homolog 2	SPRY2	$\gamma\delta$ T	0.545
Leukocyte immunoglobulin-like receptor subfamily B member 4	LILRB4	Memory CD4 T	0.542
Follistatin-related protein 3	FSTL3	Memory CD4 T	0.537
Proteinase-activated receptor 1	F2R	Memory CD4 T	0.536
Protransforming growth factor alpha	TGFA	$\gamma\delta$ T	0.536
Interleukin-18	IL18	$\gamma\delta$ T	0.535

Granzyme B	GZMB	Treg	0.532
Oncostatin-M	OSM	Memory CD4 T	0.530
Hepatocyte growth factor	HGF	Classical monocyte	0.528
Interleukin-17A*	IL17A	Th17	0.527
Tumor necrosis factor receptor superfamily member 9	TNFRSF9	$\gamma\delta$ T	0.527
Interleukin-18	IL18	Treg	0.525
Carcinoembryonic antigen-related cell adhesion molecule 21	CEACAM21	Memory CD4 T	0.517
CUB domain-containing protein 1	CDCP1	Effector CD8 T	0.515
Cysteine-rich motor neuron 1 protein	CRIM1	Memory CD4 T	0.514
Killer cell lectin-like receptor D1 (CD94)*	KLRD1	Effector CD8 T	0.513
Interferon gamma	IFNgamma	Nonclassical monocyte	0.511
Bile salt sulfotransferase	SULT2A1	Treg	0.509
Interleukin-1 receptor antagonist protein	IL1RN	Treg	0.508
Interleukin-4 receptor subunit alpha	IL4R	Memory CD4 T	0.504
<i>Ratio of subsets</i>			
Protocadherin-1	PCDH1	Memory CD4 T / Treg	0.584
Protocadherin-1	PCDH1	Th17 / Treg	0.578
Interferon gamma receptor 1	IFNGR1	Memory CD4 T / Treg	0.547
Killer cell lectin-like receptor D1 (CD94)*	KLRD1	Effector CD8T / exhausted CD8 T	0.546
Cell surface glycoprotein CD200 receptor 1	CD200	Memory CD4 T / Treg	0.532
2,4-dienoyl-CoA reductase, mitochondrial	DECR1	Naïve NK / activated NK	0.527
Macrophage colony-stimulating factor 1	CSF1	Effector CD8 T / memory CD8 T	0.525
Leukemia inhibitory factor receptor	LIFR	Naïve B / Breg	0.518
Hepatocyte growth factor	HGF	Classical monocyte / nonclassical monocyte	0.512
Protocadherin-1	PCDH1	Th1 / Treg	0.509

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93 *Significantly elevated in rapid versus non-rapid amyotrophic lateral sclerosis. Breg: regulatory B
94 cell; DC: dendritic cell; NK: natural killer cell; Th1: T helper 1 cell; Th17: T helper 17 cell; Treg:
95 regulatory T cell.

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97	Table S8. Exclusion criteria.
98	(1) Persons with a tracheostomy.
99	(2) Persons with chronic obstructive pulmonary disease.
100	(3) Persons who used edaravone within 4 weeks before obtaining consent.
101	(4) Persons who used immune-modifying drugs (e.g., steroids, immunoglobulin agents) within 4
102	weeks before obtaining consent.
103	(5) Persons who were (possibly) pregnant or breast-feeding.
104	(6) Persons with serious respiratory, cardiovascular, hepatic, or renal diseases.
105	(7) Persons with malignant tumors.
106	(8) Persons with diseases in which immune abnormality is involved in the onset of the disease
107	(e.g., autoimmune diseases).
108	(9) Persons who participated in a clinical trial within 12 weeks before obtaining consent.
109	(10) Persons who could not obtain consent.
110	

111 **Table S9.** Genetic markers for each cluster.

Cell type	Marker genes
Naïve B cell	CD19, CD37, IGHD
Memory B cell	CD19, CD27, IGHM, IGHG4
Regulatory B cell	CD19, CD24, CD38, IL10
Plasma cell	SDC1
Naïve CD4 T cell	CD3D, CD4, IL7R, CCR7
Memory CD4 T cell	CD3D, CD4, IL7R, S100A4
T helper 1 cell	CD3D, CD4, CXCR3, CCR5, IL12RB2, IFNG, TBX21
T helper 2 cell	CD3D, CCR4, IL4, GATA3
T helper 17 cell	CD3D, CCR6, CCR4, IL17A, RORC
Regulatory T cell	CD3D, FOXP3, IL2RA
Naïve CD8 T cell	CD3D, CD8A, CD8B, CCR7
Effector CD8 T cell	CD3D, CD8A, CD8B, PRF1, GZMB, NKG7
Memory CD8 T cell	CD3D, CD8A, CD8B, IL7R, S100A4
Exhausted CD8 T cell	CD3D, CD8A, CD8B, HAVCR2, TIGIT
$\gamma\delta$ T cell	CD3D, TRDC
Naïve natural killer cell	NKG7, GNLY, SELL, XCL1
Mature natural killer cell	NKG7, GNLY, FCGR3A, PRF1
Activated natural killer cell	NKG7, GNLY, KLRF1, GZMB, CD247
Classical monocyte	CD14
Nonclassical monocyte	CD14, FCGR3A
Macrophage	MARCO, CD163
Conventional dendritic cell	FCER1A
Plasmacytoid dendritic cell	FCER1A, TCF4, TNFRSF21
Platelet	PPBP, VWF
Neutrophil	FCGR3B
Mast cell	TPSB2, MS4A2

113 **Table S10.** Measured inflammation proteins by gene names.

114	4EBP1, ACTN4, ADA, ADAM23, ADGRE2, AGER, AGRN, AGRP, ALDH3A1, AMBN,
115	AMN, ANGPT1, ANGPTL2, ANGPTL4, ANXA11, AOC1, ARHGEF12, ARNT, ARTN,
116	ATP5IF1, AXIN1, B4GALT1, BACH1, BANK1, BCR, BSG, BTN2A1, BTN3A2, C1QA,
117	CASP2, CASP8, CCL11, CCL17, CCL19, CCL20, CCL21, CCL22, CCL23, CCL24, CCL25,
118	CCL26, CCL28, CCL3, CCL4, CCL7, CCN2, CD160, CD200, CD200R1, CD22, CD244,
119	CD276, CD4, CD40, CD40LG, CD48, CD5, CD58, CD6, CD70, CD79B, CD83, CD84, CD8A,
120	CDCP1, CDON, CDSN, CEACAM21, CEP164, CHRDL1, CKAP4, CKMT1A_CKMT1B,
121	CLEC4A, CLEC4C, CLEC4D, CLEC4G, CLEC7A, CLIP2, CLSTN2, CNTNAP2, COL9A1,
122	COLEC12, CRELD2, CRHBP, CRIM1, CRKL, CRLF1, CSF1, CSF3, CST5, CST7, CTRC,
123	CTSC, CTSO, CX3CL1, CXADR, CXCL1, CXCL10, CXCL11, CXCL12, CXCL14, CXCL17,
124	CXCL3, CXCL5, CXCL6, CXCL8, CXCL9, DAG1, DAPP1, DBNL, DECR1, DFFA, DGKZ,
125	DNER, DNPH1, DPP10, EDAR, EGF, EGLN1, EIF4G1, EIF5A, ENAH, ENPP5, ENPP7,
126	ENRAGE, EPCAM, EPHA1, EPO, ERBB3, ESM1, F2R, FABP1, FABP9, FASLG, FCAR,
127	FCRL2, FCRL3, FCRL6, FGF19, FGF2, FGF21, FGF23, FGF5, FIS1, FKBP1B, Flt3L,
128	FLT3LG, FOXO1, FST, FSTL3, FXYD5, GAL, GALNT3, GBP2, GDNF, GLOD4, GMPR,
129	GOPC, GZMA, GZMB, HCLS1, HEXIM1, HGF, HLADRA, HLAE, HPCAL1, HSD11B1,
130	HSPA1A, ICA1, ICAM4, IDS, IFNG, IFNgamma, IFNGR1, IFNLR1, IKBKG, IL10, IL10RA,
131	IL10RB, IL11, IL12B, IL12RB1, IL13, IL15, IL15RA, IL16, IL17A, IL17C, IL17D, IL17F,
132	IL17RB, IL18, IL18R1, IL1A, IL1B, IL1R2, IL1RL2, IL1RN, IL2, IL20, IL20RA, IL24, IL2RB,
133	IL32, IL33, IL3RA, IL4, IL4R, IL5, IL5RA, IL6, IL7, IL8, IRAK1, IRAK4, ISM1, ITGA11,
134	ITGA6, ITGB6, ITM2A, JCHAIN, JUN, KLRB1, KLRD1, KRT19, KYNU, LAIR1, LAMA4,
135	LAMP3, LAP.TGFbeta1, LAP3, LAT, LGALS4, LGALS9, LGMN, LHPP, LIFR, LILRB4,
136	LRRN1, LSP1, LTA, LTBR, LTO1, LY6D, LY75, LY9, MANF, MAP2K6, MAPK9, MATN2,
137	MCP1, MCP2, MCP3, MCP4, MEGF10, MEPE, MERTK, METAP1D, MGMT, MICB_MICA,
138	MILR1, MLN, MMP1, MMP10, MPIG6B, MVK, MYO9B, MZB1, NBN, NCF2, NCK2, NCLN,
139	NCR1, NELL2, NFASC, NFATC1, NFATC3, NME3, NPPC, NRTN, NT3, NT5C3A, NTF3,
140	NUB1, NUDC, OMD, OPG, OSCAR, OSM, PADI2, PAPPA, PARP1, PCDH1, PDGFB, PDL1,
141	PDLIM7, PGF, PIK3AP1, PKLR, PLA2G4A, PLAUR, PLXNA4, PNLIPRP2, PNPT1, PON3,
142	PPP1R9B, PRDX3, PRDX5, PREB, PRELP, PRKAB1, PRKCQ, PROK1, PRSS8, PSIP1,
143	PSMG3, PSPN, PTH1R, PTPN6, PTPRM, PTX3, RAB37, RAB6A, RABGAP1L, REG4, RGS8,
144	ROBO1, SAMD9L, SCF, SCG3, SCGB1A1, SCGB3A2, SCGN, SCRIN1, SELPLG, SERPINB8,
145	SH2D1A, SHMT1, SIGLEC1, SIGLEC10, SIRPB1, SIRT2, SIT1, SKAP2, SLAMF1, SLAMF7,
146	SLC39A5, SMOC2, SMPDL3A, SPINK4, SPINT2, SPON1, SPRY2, SRPK2, ST1A1, STAMBP,
147	STX8, SULT2A1, TANK, TBC1D5, TFF2, TGFA, TGFalpha, TGFB1, TIMP3, TLR3, TNF,
148	TNFAIP8, TNFB, TNFRSF11A, TNFRSF11B, TNFRSF13B, TNFRSF13C, TNFRSF14,
149	TNFRSF4, TNFRSF9, TNFSF10, TNFSF11, TNFSF12, TNFSF13, TNFSF14, TPP1, TPSAB1,
150	TPT1, TRAF2, TRAIL, TRANCE, TREM2, TRIM21, TRIM5, TWEAK, uPA, VASH1, VEGFA,
151	VEGFD, WAS, WFIKKN2, WNT9A, YTHDF3

152
153 The proteins are included in the Olink Target 96 Inflammation and Olink Explore 384
154 Inflammation panels (<https://olink.com>).