Supplementary material

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Supplementary Table 1. Differentially expressed genes in two statistical tests

	Log$_2$(FC)[1][*]	Odds ratio	P value in logistic regression	P value in Kolmogorov–Smirnov test
RPL15	0.331	1.479	0.022	0.005
BACE1-AS	0.271	1.384	0.034	0.013
CEPT1	0.105	1.416	0.022	0.030
EIF4G1	0.573	1.702	0.015	0.044
TMEM91	0.357	1.419	0.027	0.044
TBCK	0.519	1.344	0.036	0.044
ARG2	0.135	2.137	0.161	0.010
DIS3	0.280	1.904	0.063	0.020
TMEM 129	0.181	2.368	0.101	0.028
PRPF40B	0.270	2.763	0.115	0.030
PCCB	0.225	1.279	0.105	0.030
PASK	0.278	2.054	0.214	0.030
KCNQ5	0.316	1.428	0.093	0.030
ATP1A1-AS1	0.053	2.798	0.230	0.040
FAM120AOS	0.238	1.182	0.157	0.044

Abbreviation: Log$_2$(FC) = log$_2$(fold-change)

[*] Value >0 indicates higher mean expression in the severe group

**Supplementary Table 2. Differentially expressed genes in the 46-65 age group[*]**

	Severe group log$_2$(FPM) values			Non-severe group log$_2$(FPM) values		Log$_2$(FC)	P value in *t* tests
	Case 1	Case 2	Case 3	Control 1	Control 2		
RPL15	7.79	8.6	7.94	6.95	7.14	0.20	0.039
TBCK	7.79	8.77	8.94	7.27	6.92	0.26	0.044
EIF4G1	6.57	6.96	8.11	5.27	5.27[†]	0.45	0.052
TMEM91	8.3	7.71	8.11	5.56	6.51	0.41	0.115
BACE1-AS	9.78	9.03	9.11	6.28	7.91	0.39	0.202
CEPT1	9.5	9.46	8.26	6.54	9.11	0.21	0.502

Abbreviations: Log$_2$(FC) = log$_2$(fold-change); log$_2$(FPM) = log$_2$(fragments per million reads mapped)

[*]Among the 24 patients, three did not pass the quality control requirement for RNA sequencing data. One patient without age information was excluded. Among the remaining 23 patients, there were zero severe cases in the 0-18 age group, zero severe cases in the >65 age group, and one severe case in the 19-45 age group; these values were insufficient for statistical analyses. Among the remaining six patients in the 46-65 age group, one control patient (in the non-severe group) had zero counts for these genes and was excluded. Thus, *t* tests on log$_2$ values were performed between the three patients with severe disease and the two patients with non-severe disease

[†] Missing value imputed using the mean expression level for this gene in the 16-65 age group

Supplementary Figure. Differentially expressed genes in the 46-65 age group. Horizontal lines indicate group mean. P values in *t* tests are shown above the groups
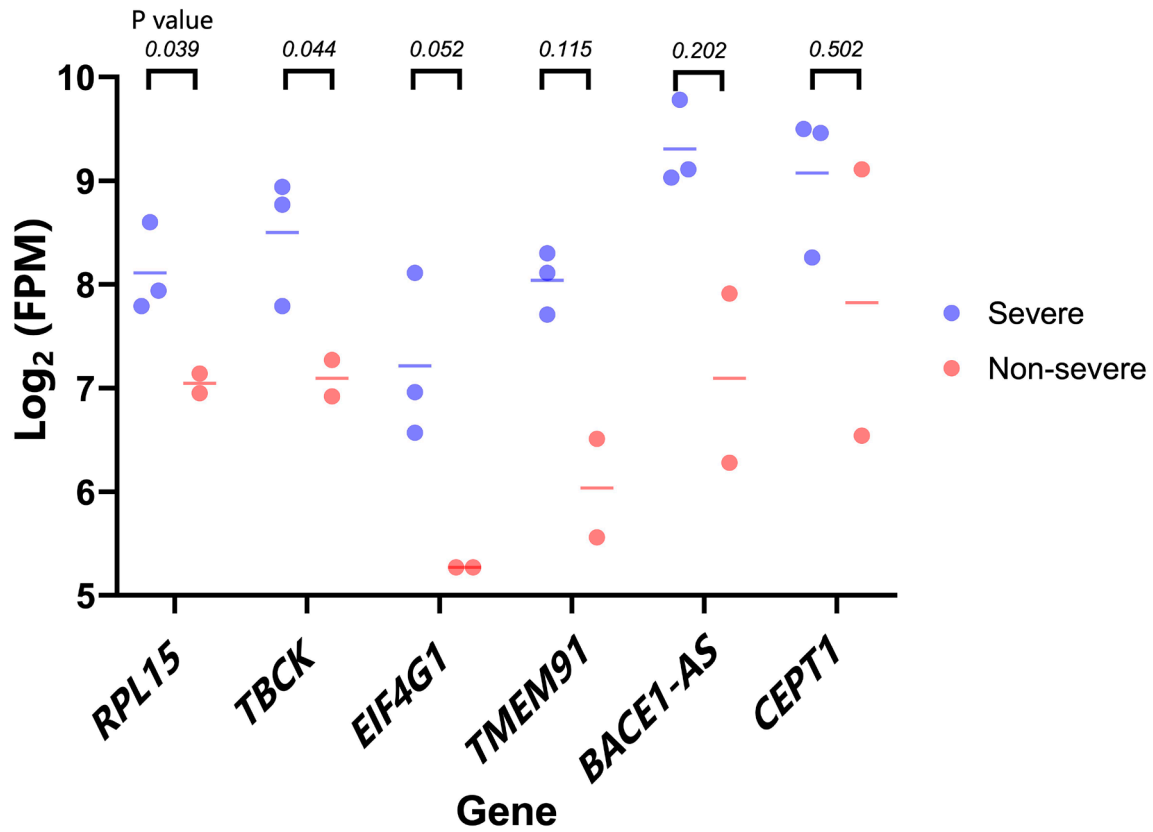
References

1. Mortazavi A, Williams BA, McCue K, Schaeffer L, Wold B. Mapping and quantifying mammalian transcriptomes by RNA-Seq. Nat Methods 2008;5:621-8.