

Table S4: A linear regression model consisting of 11 CSF proteins could predict nARMSS. The coefficients of the combined model are compared to the predictive power of the individual proteins. For the individual protein models, the coefficient and Spearman correlation coefficient (SCC) between the true nARMSS and predicted nARMSS is stated. Age was included as a predictor in the models for all individual proteins. Last, the expression in CSF for four out of the 11 proteins were correlating with the expression in plasma. All values are marked for significance: * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$. The features are ordered on the significance of the coefficients.

Feature	Coefficient	Individual prediction power		SCC Replication	Correlation CSF vs Plasma
		Coefficient	SCC Discovery		
CXCL13	-0.490***	-0.026	0.38**	0.24	0.30*
Age	-0.067***	[-0.068, -0.076]**	0.38**	0.23	
LTA	0.741***	0.192	0.40***	0.26	0.21
FCN2	0.576**	0.153	0.39***	0.27	0.25*
ICAM3	-0.693**	0.052	0.38**	0.25	0.04
LY9	0.717**	0.23	0.42***	0.29	0.14
SLAMF7	0.705*	0.428*	0.48***	0.25	0.05
TYMP	-0.614*	-0.14	0.41***	0.21	-0.09
CHI3L1	-0.827*	0.161	0.37**	0.2	0.27*
FYB1	-0.346*	-0.047	0.38**	0.22	-0.16
TNFRSF1B	0.759*	0.325	0.40***	0.34	0.17
NfL	0.454*	0.369*	0.45***	0.14	0.45***
Intercept	-1.067	[-0.707, 0.111]			