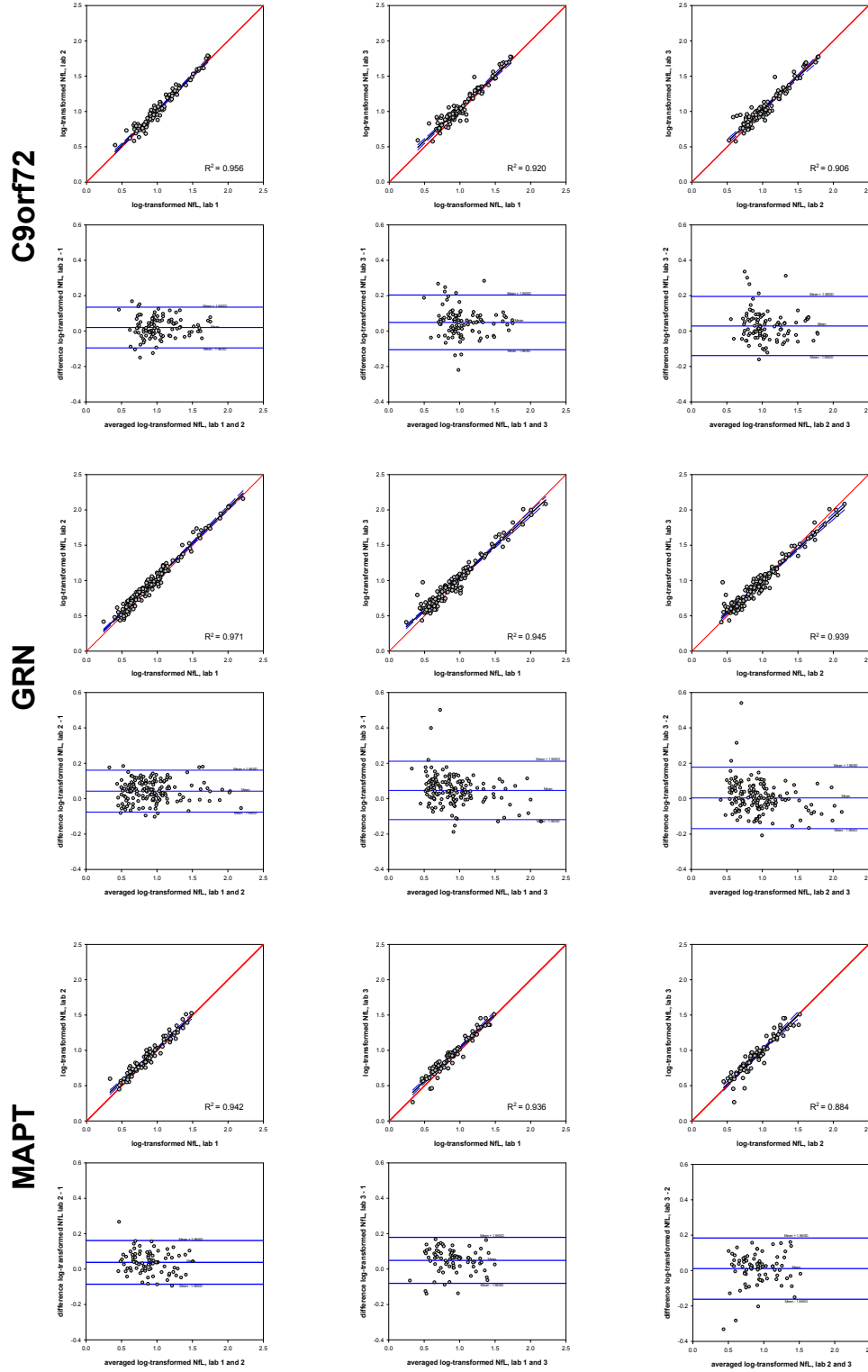
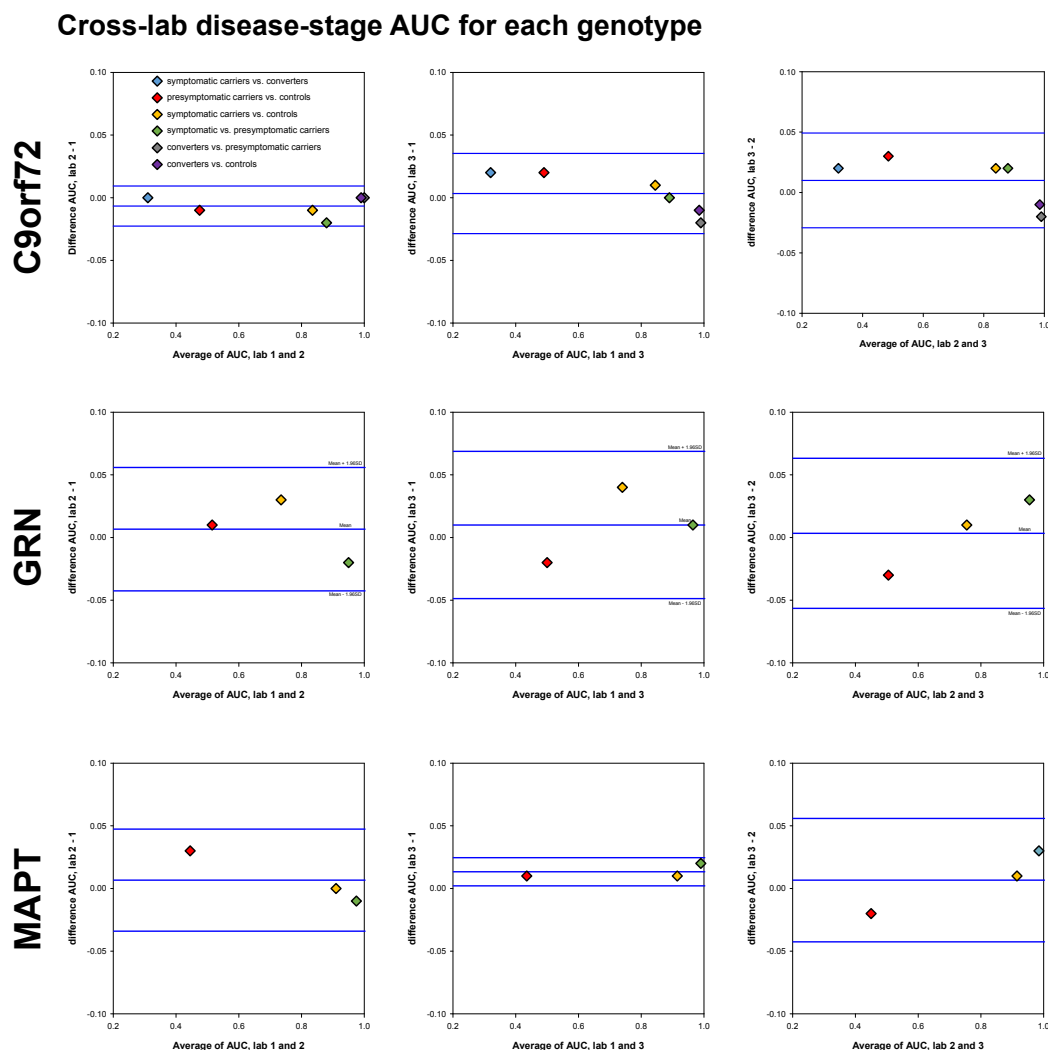


Supplementary Figures

Cross-lab reliability for each genotype



Supplementary Figure 1: Cross-lab reliability for each genotype (*C9orf72*, *GRN*, and *MAPT*) of blood NfL measurements in genetic FTD (gFTD) across three labs (lab 1 and 2 serum, lab 3 plasma) - linear regressions and Bland-Altman analyses of log-transformed NfL values. For detailed statistics see Supplementary Table 3.



Supplementary Figure 2: Cross-lab disease stage AUC for each genotype (*C9orf72*, *GRN*, and *MAPT*) of blood NfL measurements in genetic FTD (gFTD) across three labs - Bland-Altman analyses of disease stage AUC. For detailed statistics see Supplementary Table 4. An analysis for the converters was performed for *C9orf72*, but not for *GRN* and *MAPT* due to the sample size (see cohort characteristics in Supplementary Table 1).

## Supplementary Tables

Group	Subjects	Subjects with longitudinal samples	Male sex	Age (years)	Disease onset (years)
Presymptomatic	66	57	42	41 (34.00 – 49.38)	n.a.
– C9orf72	22	17	14	42 (35.04 – 48.88)	n.a.
– GRN	29	28	16	43 (34.97 – 52.62)	n.a.
– MAPT	15	12	12	36 (32.17 – 46.44)	n.a.
Converter	4	4	1	65 (59.72 – 67.53)	n.a.
– C9orf72	3	3	1	63 (56.89 – 65.00)	n.a.
– GRN	1	1	0	68	n.a.
Symptomatic	21	18	8	63 (59.29 – 66.23)	56 (53.00 – 60.00)
– C9orf72	7	6	1	66 (64.17 – 71.66)	57 (51.50 – 61.50)
– GRN	8	7	4	61 (59.67 – 66.03)	58 (54.75 – 58.50)
– MAPT	6	5	3	61 (58.30 – 64.51)	54 (52.25 – 55.50)
Controls (non-carriers)	60	53	34	45 (37.52 – 55.74)	

Supplementary Table 1. Cohort characteristics at baseline. Data are reported as median and interquartile range. N.a.: not applicable.

A.				
	Lab 1 vs. lab 2	Lab 1 vs. lab 3	Lab 2 vs. lab 3	
Bias	1.08	1.12	1.03	
Std Dev	1.15	1.20	1.22	
Limits of Agreement	0.82, 1.43	0.78, 1.59	0.69, 1.53	
Bias CI 95% CI	1.07 to 1.10	1.10 to 1.14	1.01 to 1.05	
Lower Limit of Agreement CI 95% CI	0.80 to 0.84	0.76 to 0.81	0.67 to 0.72	
Upper Limit of Agreement CI 95% CI	1.39 to 1.47	1.54 to 1.64	1.48 to 1.59	
B.				
Bias	-0.1	0.00	0.01	
Std Dev	0.01	0.01	0.01	
Limits of Agreement	-0.21, to 0.01	-0.07, to 0.01	-0.01, to 0.03	
Bias CI 95% CI	-0.01 to 0.00	-0.00 to 0.01	-0.00 to 0.02	
Lower Limit of Agreement CI 95% CI	-0.04 to -0.01	-0.02 to 0.00	-0.03 to 0.01	
Upper Limit of Agreement CI 95% CI	-0.01 to 0.03	0.00 to 0.02	0.01 to 0.05	

Supplementary Table 2. Numerical results of the Bland-Altman analysis comparing blood NfL measurements in genetic FTD across three labs (lab 1 and 2 serum, lab 3 plasma) (A: see Figure 1A; B: see Figure 1C). Data are given as pg/ml.

C9orf72				
		Lab 1 vs. lab 2	Lab 1 vs. lab 3	Lab 2 vs. lab 3
	Bias	1.58	1.12	1.07
	Std Dev	1.15	1.20	1.23
	Limits of Agreement	0.11, 1.38	0.78, 1.58	0.72, 1.58
	Bias CI 95% CI	1.02 to 1.07	1.07 to 1.15	1.02 to 1.12
	Lower Limit of Agreement CI 95% CI	0.76 to 0.83	0.74 to 0.83	0.68 to 0.78
	Upper Limit of Agreement CI 95% CI	1.32 to 1.45	1.51 to 1.70	1.48 to 1.70
GRN				
	Bias	1.10	1.12	1.00
	Std Dev	1.15	1.20	1.23
	Limits of Agreement	0.83, 1.45	0.76, 1.62	0.68, 1.51
	Bias CI 95% CI	1.07 to 1.12	1.07, to 1.14	0.98 to 1.05
	Lower Limit of Agreement CI 95% CI	0.81 to 0.87	0.72 to 0.79	0.63 to 0.71
	Upper Limit of Agreement CI 95% CI	1.38 to 1.51	1.55 to 1.70	1.41 to 1.58
MAPT				
	Bias	1.10	1.12	1.02
	Std Dev	1.15	1.17	1.23
	Limits of Agreement	0.81, 1.45	0.83, 1.51	0.69, 1.55
	Bias CI 95% CI	1.05 to 1.12	1.07 to 1.15	0.98 to 1.07
	Lower Limit of Agreement CI 95% CI	0.78 to 0.87	0.78 to 0.87	0.63 to 0.74
	Upper Limit of Agreement CI 95% CI	1.38 to 1.55	1.41 to 1.62	1.41 to 1.66

Supplementary Table 3. Numerical values of Bland-Altman analysis for cross-lab reliability for each genotype (see supplementary figure 1). Data are given as pg/ml.

C9orf72				
		Lab 1 vs. lab 2	Lab 1 vs. lab 3	Lab 2 vs. lab 3
	Bias	-0.07	0.03	0.01
	Std Dev	0.01	0.02	0.02
	Limits of Agreement	-0.02, 0.01	-0.03, 0.04	-0.03, 0.05
	Bias CI 95% CI	-0.02 to 0.00	-0.02 to 0.02	-0.01 to 0.03
	Lower Limit of Agreement CI 95% CI	-0.04 to -0.01	-0.06 to 0.00	-0.07 to 0.01
	Upper Limit of Agreement CI 95% CI	-0.01 to 0.03	0.00 to 0.07	0.01 to 0.09
GRN				
	Bias	0.01	0.01	0.00
	Std Dev	0.03	0.03	0.03
	Limits of Agreement	-0.04, 0.06	-0.05, 0.07	-0.06, 0.06
	Bias CI 95% CI	-0.18 to 0.20	-0.21, to 0.23	-0.22 to 0.23
	Lower Limit of Agreement CI 95% CI	-0.36 to 0.28	-0.43 to 0.33	-0.44 to 0.33
	Upper Limit of Agreement CI 95% CI	-0.26 to 0.38	-0.31 to 0.45	-0.33 to 0.45
MAPT				
	Bias	0.01	0.01	0.01
	Std Dev	0.02	0.06	0.03
	Limits of Agreement	-0.03, 0.05	0.00, 0.02	-0.04, 0.06
	Bias CI 95% CI	-0.15 to 0.16	-0.03 to 0.06	-0.18 to 0.20
	Lower Limit of Agreement CI 95% CI	-0.30 to 0.23	-0.07 to 0.08	-0.36 to 0.28
	Upper Limit of Agreement CI 95% CI	-0.22 to 0.31	-0.05 to 0.10	-0.26 to 0.38

Supplementary Table 4. Numerical values of Bland-Altman analysis for cross-lab disease-stage AUC for each genotype (see supplementary figure 2). Data are given as pg/ml.