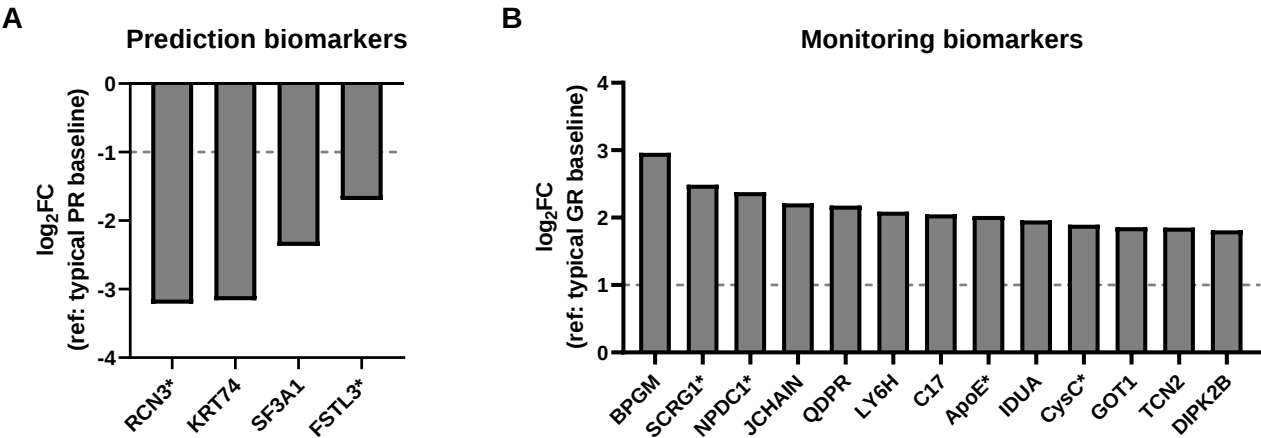
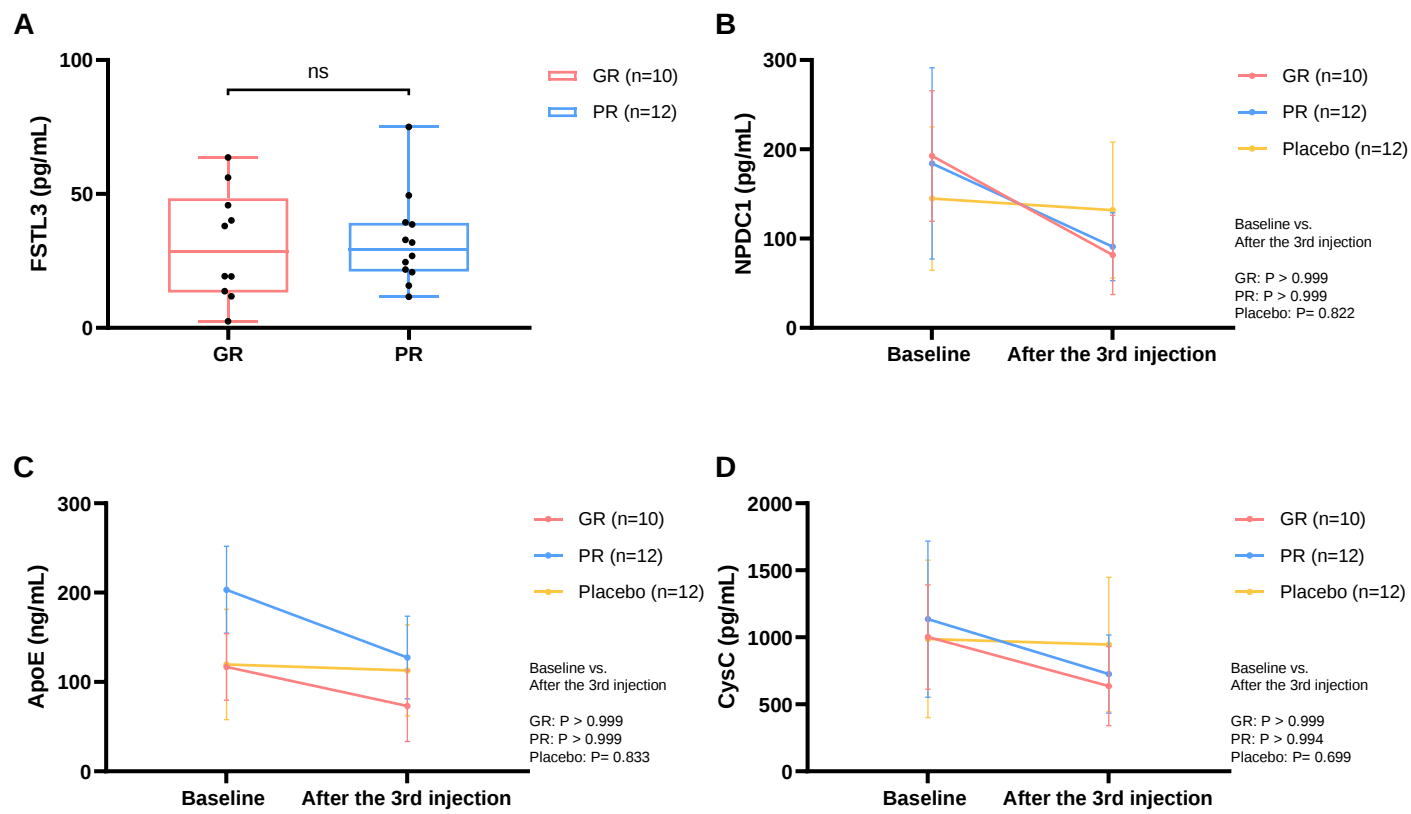


Supplementary Figure 1.



Supplementary Figure 1. (A) Four proteins were selected as prediction biomarker candidates that showed a significant difference in protein levels in baseline CSF between typical GR and typical PR (FDR $q < 0.05$, $|\log_2 FC| \geq 1.5$, unique peptide ≥ 2 , Fold change = baseline protein levels of typical GR/PR). (B) 13 proteins were selected as monitoring biomarker candidates that showed significant change after the third injection compared to the baseline exclusively in typical GR (FDR $q < 0.05$, $|\log_2 FC| \geq 1.8$, unique peptide ≥ 2 , Fold change = protein levels at one day after the third injection/baseline). *, Final selection of potential biomarkers based on their significance levels and known function. GR, Good Responder; PR, Poor Responder; FC, Fold change

Supplementary Figure 2.



Supplementary Figure 2. Validation of potential prediction (FSTL3) and monitoring (NPDC1, ApoE, and CysC) biomarkers in all participants (n=34) via ELISA. Student's t-test or paired t-test (one-tailed) was used. ns; not significant, GR; Good Responder, PR; Poor Responder.