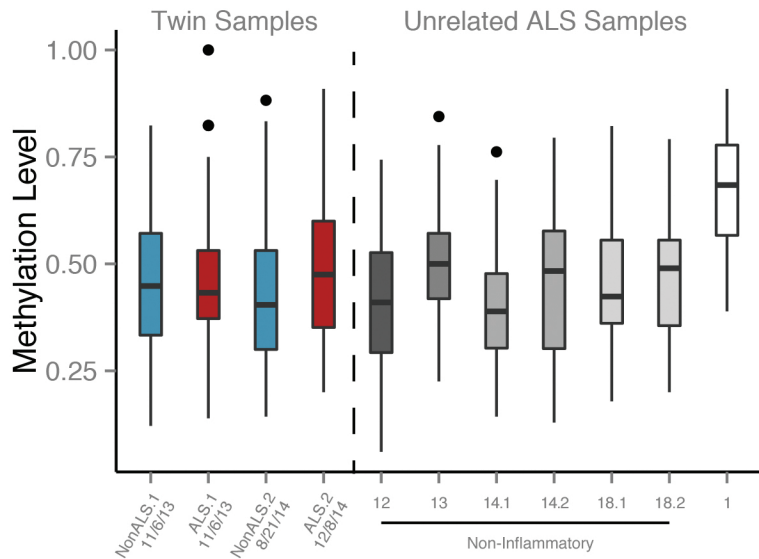


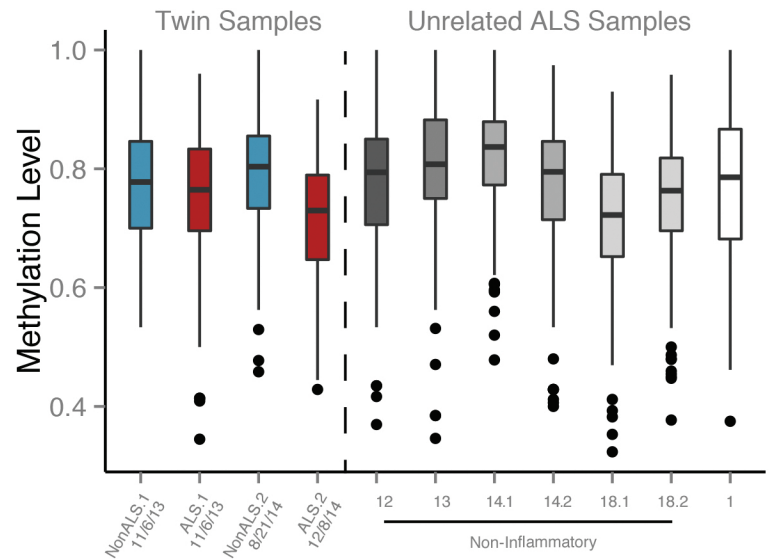
Suppl. Fig.2. Methylation distribution at cell type- specific CpG sites in PBMC samples from ALS-discordant twins and affected individuals

Methylation level distribution for the PBMC samples obtained in 2013 (Box 1 and Box 2) and 2014 (Box 3 and Box 4) at T cell, CD14- positive, natural killer, neutrophil, and B cell- specific CpG sites with the healthy twin's sample in blue and the ALS twin's sample in red. Methylation level distribution for PBMC sampled from unrelated non-inflammatory ALS patient samples 12, 13, 14.1, 14.2, 18.1, and 18.2 in grey (Box 5 - 10). The methylation level distribution from an unrelated inflammatory ALS patient in white (Box 11). A) T cell- specific CpG methylation distributions. B) CD14-specific CpG site methylation distributions. C) Natural killer-specific CpG site methylation distributions. D) Neutrophil- specific CpG site methylation distributions.

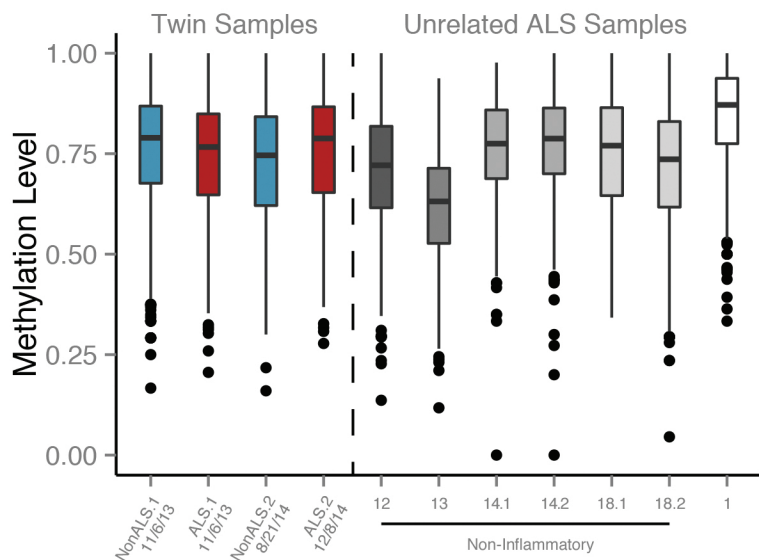
A) T Cell



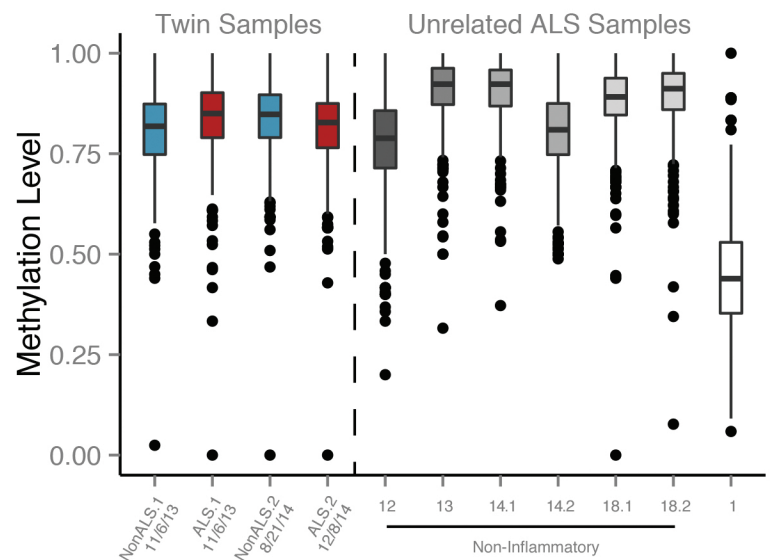
B) CD14



C) Natural Killer



D) Neutrophil



E) B Cell

