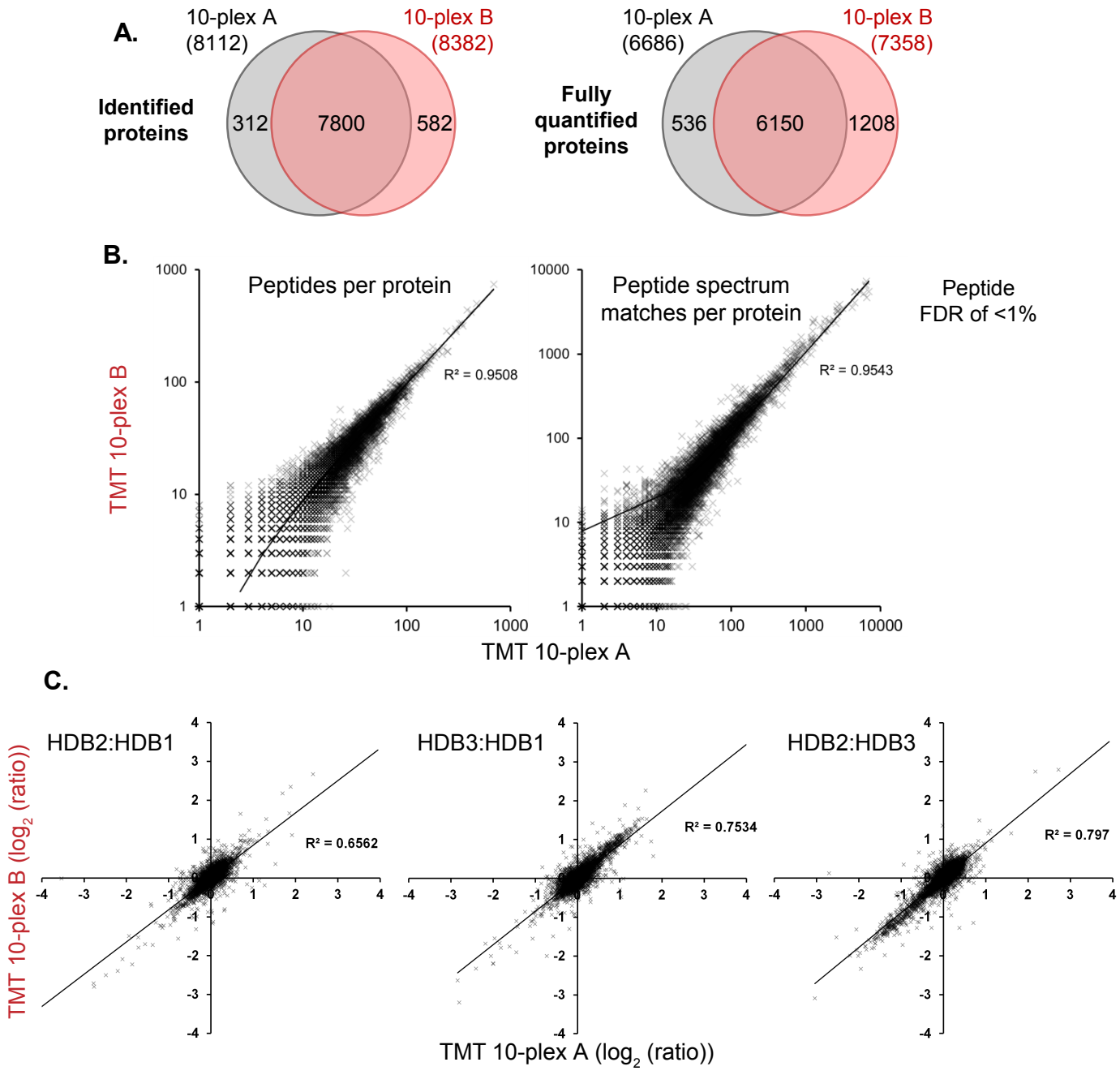
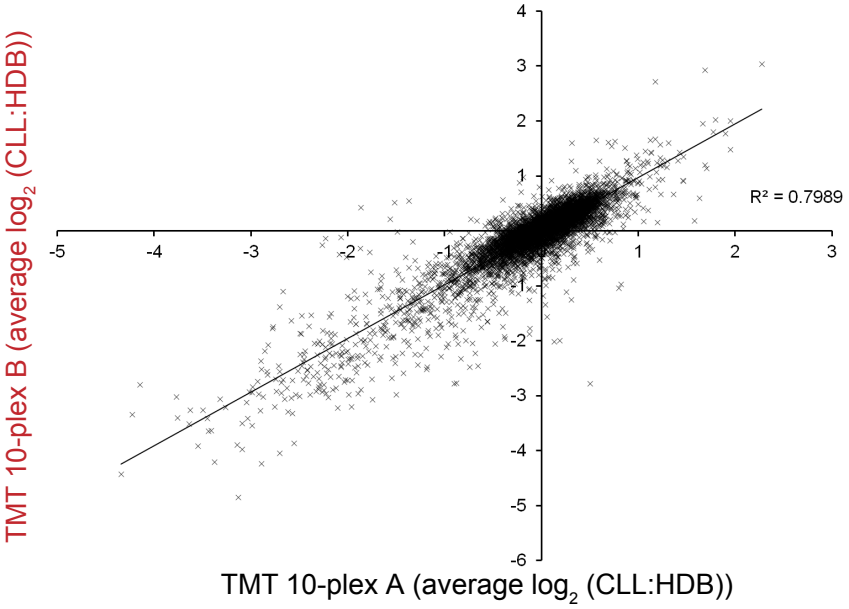
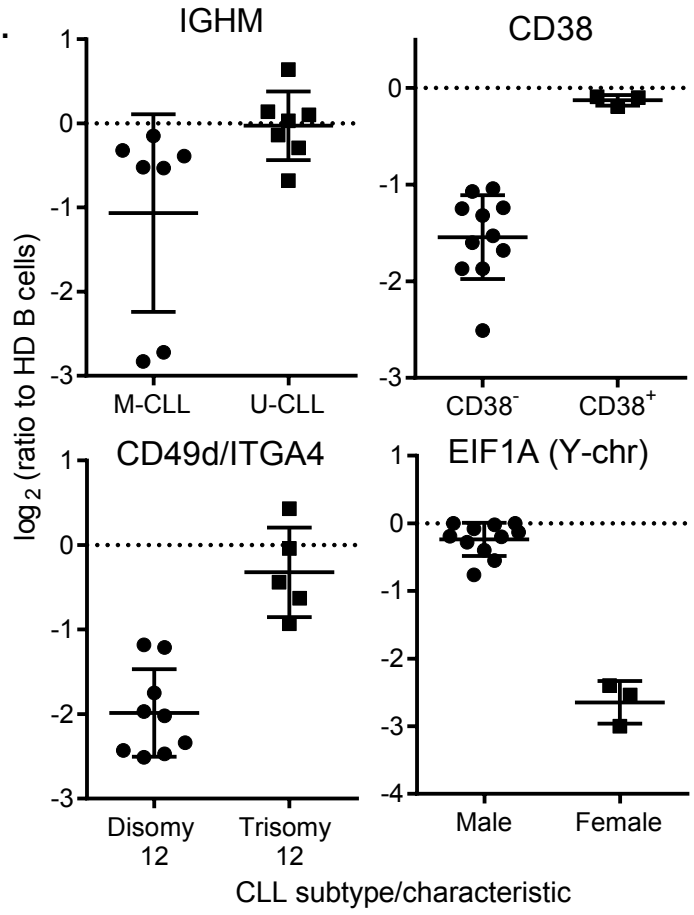
Figure S1. Evaluation of the qualitative and quantitative reproducibility between 10-plex A and B.
A. The numbers of identified and quantified proteins determined in experiments A and B and the c ommonly determined numbers for each of these.
B. The respective numbers of PSMs and peptides for each of the 7800 commonly identified proteins across experiments A and B.
C. The reproducibility of protein quantifications for the healthy donor B-cell (HDB) bridging controls characterised in each experiment. Log_2 (ratios) of the commonly quantified proteins comparing HD1, HD2 and HD3 derived from 10-plexes A and B.
D. The reproducibility of protein quantifications of CLL versus the healthy donor (HD) bridging controls characterised in each TMT 10-plex experiment. Log_2 (ratios) of the commonly quantified proteins comparing the average of the 7 log_2 (CLL:HDB ratios) derived from each of the 10-plexes A and B.
E. Proteomics-derived quantitations for characteristic markers and known phenotypes of CLL and CLL subtypes, relative to HDB.



D.


TMT 10-plex B (average log2 (CLL:HDB))
TMT 10-plex A (average log2 (CLL:HDB))
R² = 0.7989

E.


IGHM
CD38
CD49d/ITGA4
EIF1A (Y-chr)
log2 (ratio to HD B cells)
M-CLL
U-CLL
CD38-
CD38+
Disomy 12
Trisomy 12
Male
Female
CLL subtype/characteristic