

Figure 1

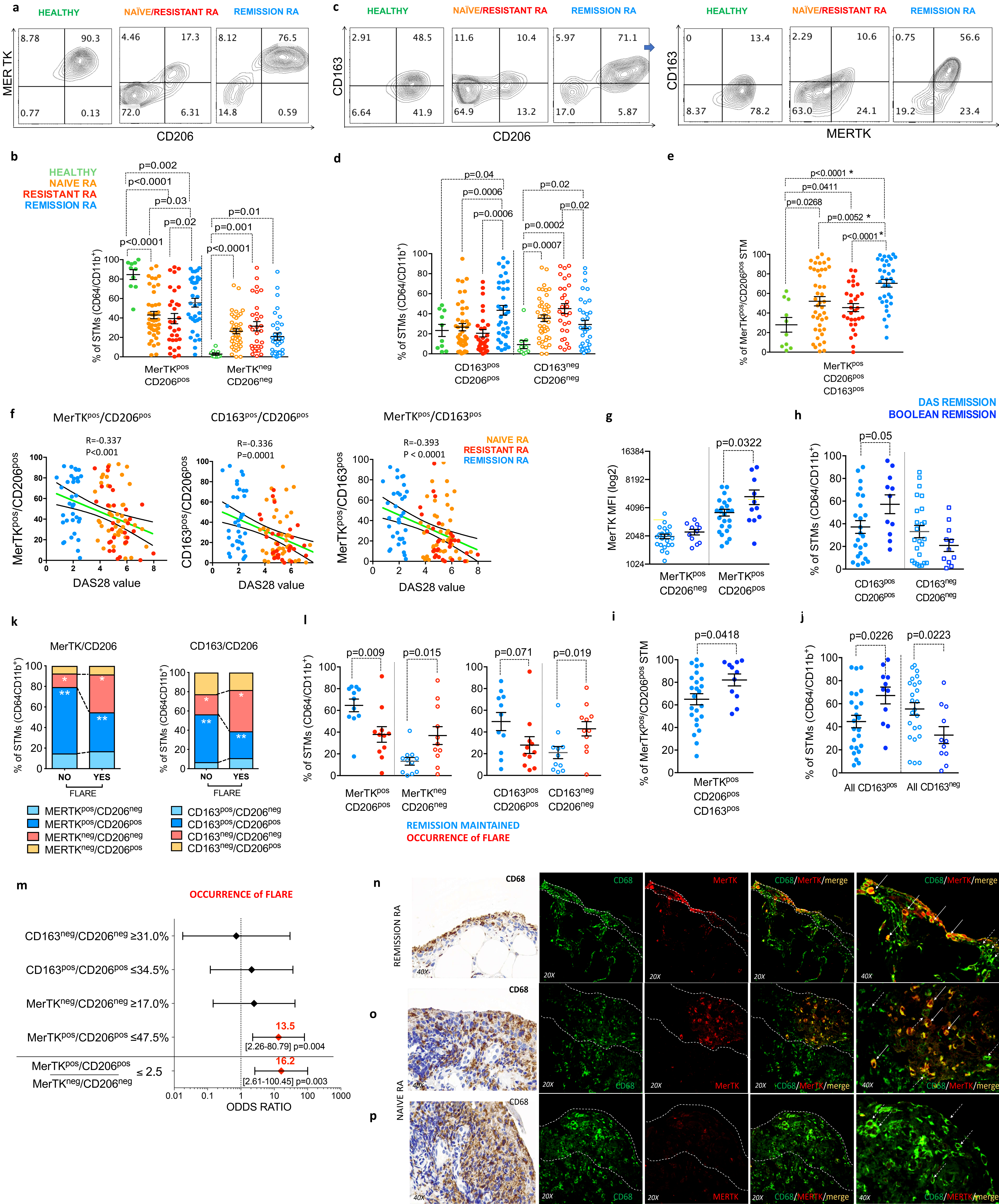


Figure 1. Synovial tissue of RA patients in sustained clinical and ultrasound remission is enriched in MerTK/CD206pos macrophages, with decline predictive of flare. (a) Representative expression of MerTK and CD206 on STMs distinguishes two mainpopulations of STMs. (b) Distribution of MerTK/CD206pos and MerTK/CD206neg STMs in healthy controls (n=10), RA treatment naïve (n=43), RA treatment resistant (n=30), and RA in remission (n=36). (c) CD163 expression is exclusively on CD206/MerTKpos STMs. (d-e) Distribution of CD163pos cells in healthy donors and RA patients as described in b. (f) Spearman correlation between DAS28 and the frequencies of MerTK/CD206pos, CD163/CD206pos and MerTK/CD206/CD163pos STMs in RA patients. (g) Comparison of the levels of MerTK expression, (h) distribution of CD163/CD206pos, (i) MerTK/CD163/CD206pos and (j) total CD163pos STMs in RA patients in sustained DAS-based remission (n=24) compared to RA patients in Boolean remission (n=11). (k) Comparison of the distribution of STM phenotypes in RA patients who maintained in remission (n=11) compared to those who flared (n=11) after treatment cessation (n=22, total number of patients who consented to treatment modification). (l) Relative proportions of MerTK/CD206 and CD163/CD206 positive and negative STMs in patients as in k showing that remission is associated with a higher proportion of MerTK/CD206pos compared to flare. (m) Odds Ratio (OR, 95% CI) showing the proportion of MerTK/CD206pos STMs 47.5%, or the MerTK/CD206pos to MerTK/CD206neg ratio 2.5 as independent factors predicting flare. (n-p) Representative IHC image of CD68 (brown) and IF staining of CD68 (green), MerTK (red) and nuclei (blue) in synovial tissue sections of RA patient in remission (n) and with active disease (o-p). MerTKpos STMs are mainly localized in the lining layer in remission (n). MerTKposCD68pos STMs are dispersed (o) or not present in tissues from RA patients with active disease (p), the dotted lines are reference edges of lining/sublining areas (20X), white arrows indicate CD68pos/MerTKpos STMs and white dotted arrows indicate CD68pos/MerTKneg STMs (40X). Data are mean ± sem; p values are provided on graphs or marked * (<0.05). Differences (a-l) in individual STM populations between different RA conditions evaluated by one-way ANOVA with Tukey correction, or two-tailed Mann-Whitney test.