Figure 1. Characteristics of the absolute numbers and proportions of Th1 cells, Th2 cells, Th17 cells and CD4 Treg cells in the PB of patients with TA. (A-C) The levels of Th17 cells and the ratio of Th1/Treg, Th2/Treg, Th17/Treg in PB were significantly increased in patients with TA ($n=46$). The absolute number and the proportion of CD4 Treg cells were significantly decreased in TA ($n=46$). (D-F) The absolute number and ratio of Th2 cells and ratio of Th1/Treg in PB were significantly decreased in active patients with TA ($n=30$). Neither the absolute number nor proportion of Th1, Th17 and Treg cells was altered significantly between active TA patients ($n=30$) and inactive TA patients ($n=16$). * $P<0.05$; ** $P<0.001$. $P<0.05$ was considered statistically significant. TA, Takayasu arteritis; PB, peripheral blood; Tregs, regulatory T cells.

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Figure 2. Characteristics of serum concentrations of cytokine (including IL-6, IL-10, IL-17 and TNF- α) between active TA patients ($n=30$) and inactive TA patients ($n=16$). (A, D) In terms of cytokines, the concentration of IL-6 and TNF- α was significantly up-regulated (B, C) but no significant changes in IL-10, and IL-17 were found. * $P<0.05$; ** $P<0.001$. $P<0.05$ was considered statistically significant.

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AB0491 ELEVATED COMPLEMENT 3 INDICATES DISEASE ACTIVITY IN TAKAYASU ARTERITIS

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Background: The disease activity evaluation of Takayasu arteritis (TA) is a critical issue for disease monitoring and treatment. But the previous markers such as Kerr score or ITAS 2010 are not convenient enough.

Objectives: We aim to explore novel biomarkers to assess TA disease activity. **Methods:** This cross-sectional study was based on the East China TA (ECTA) cohort. Demographic characteristics, clinical features, laboratory and imaging results were collected. Complements and their combination with other biomarkers in identifying active disease (Kerr ≥ 2) group were analyzed. Internal and external validation were employed to confirm the accuracy and stability of the results.

Results: 519 patients were enrolled, among which 406 cases (72.2%) were identified as active disease. Higher ESR, CRP, platelet, globulin, IgG, IL-6, complement 3 (C3), complement 4 (C4) and median haemolytic complement (CH50) levels were observed in the active disease group. Logistic regression analysis demonstrated that C3 levels [odds ratio (OR) (95%CI): 10.710 (1.825 – 62.835), $P=0.009$] and CRP [OR (95%CI): 1.041 (1.009 – 1.073), $P=0.011$] were independently associated with active disease. The cut-off of C3 to identify active TA was 1.085 g/L, with 69.9% sensitivity, 66.7% specificity. Combining the CRP (cut-off, 10.65 g/L; sensitivity, 50.7%; specificity, 82.4%) and C3, the sensitivity and specificity to identify the active disease were 85.1% and 55.0% (parallel test), and 35.4% and 94.1% (serial test), respectively. C3 could significantly improve the diagnostic ability of CRP [net reclassification index: OR (95%CI): 1.728 (1.556–1.990), $P=0.000$; integrated discrimination index: OR (95%CI): 0.328 (0.224–0.431), $P=0.000$]. The accuracy of the 10-fold cross validation of combining CRP with C3 was over 75%, and the accuracy of the external validation with 53 TA cases was 72.73%.

Conclusion: C3 could reflect the disease activity of TA, and combining CRP with C3 could significantly improve the disease activity evaluation in TA.

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AB0492 INTESTINAL MICROBIOTA COMPOSITION OF PATIENT'S WITH BEHCET'S DISEASE: DIFFERENCES BETWEEN EYE, MUCOCUTANEOUS AND VASCULAR INVOLVEMENT (RHEUMA-BIOTA STUDY)

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Background: Recently, it has been shown that changes in microbiota composition play a role in the etiology and pathogenesis of chronic diseases. Changes in oral and intestinal microbiota diversity and composition are suggested in Behcet disease (BD), however there are no study available about the potential gut microbiota changes among different clinical forms of BD.

Objectives: The aim of this study was to evaluate the intestinal microbiota composition of patient with BD and healthy controls, and also compare BD patients regarding to their eye, mucocutaneous and vascular involvement.

Methods: In this prospective cohort study, 27 patients diagnosed with BD and 10 aged and sex matched healthy controls were included. Patients with a body mass index > 35 , who have used antibiotics or probiotics in the last 4 weeks, patients with chronic gastrointestinal or other systemic diseases, and those with acute / severe gastrointestinal symptoms requiring medical treatment were excluded from the study. For the intestinal microbiota analysis, gene amplification, library formation, sequence analysis and bioinformatic evaluation of the results were performed with 16S rRNA next generation sequencing methods with Illumina MiSeq.

Results: There was no difference between the BD group and the control group in terms of alpha (Chao-1 and Shannon) and beta (Bray-Curtis) microbiota diversity indices ($p>0.05$). *Actinomyces*, *Libanibacter*, *Collinsella*, *Eggerthella*, *Enetrohabdus*, *Catenibacterium* and *Enterobacter* were significantly higher in BD group compared to the