remodelling, its influence on bone stability and development of osteoporosis is not known.

**Objectives:** The objective of this project is the analysis of the role of miR-146a in bone metabolism.

**Methods:** Systemic bone, tibiae and femur, of wt and miR-146a deficient animals was assessed histologically and via μCT analysis, over a period of 3 to 18 months of age. Serum cytokine levels were analysed by Elisa. qRNA expression levels in bone were analysed by qPCR. To induce osteoporosis, ovariectomy (OVX) induced bone loss was performed.

**Results:** When we analysed bone volume of long bones histologically as well as with μCT analysis we detected significantly increased trabecular bone mass in miR-146a deficient compared to wt animals, starting at an age of 6 months. However, cortical thickness of systemic bones from miR-146a knock out animals was significantly reduced compared to control mice. Analysis of serum in aged miR-146a deficient animals displayed elevated expression of signature molecules of both cell types in aged miR-146a deficient mice, suggesting a regulatory role of miR-146a in both osteoclasts as well as osteoblast marker genes in bones ex vivo displayed elevated expression of signature molecules of both cell types in aged miR-146a deficient mice.

**Conclusions:** miR-146a seems to control bone turnover and miR-146a deficient mice accrue bone over time. Moreover this miRNA has a negative influence on bone loss occurring during oestrogen loss induced osteoporosis. Therefore miR-146a could be possibly used as a therapeutic target in the treatment of osteoporosis.

**Disclosure of Interest:** None declared

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**Abstract SAT0073 – Figure 1. Cumulative incidence of first sustained remission by ACPA/RF status**

**Conclusions:** These results suggest that anti-CCP but not RF positivity may be associated with a higher chance of remission, possibly due to an improved treatment response.

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**Rheumatoid arthritis – prognosis, predictors and outcome**

**SAT0074**

**IDENTIFICATION OF A PROTEIN PANEL USEFUL FOR THE PREDICTION OF RESPONSE TO METHOTREXATE IN RHEUMATOID ARTHRITIS PATIENTS**

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**Background:** The treatment of rheumatoid arthritis (RA) aims to control a patient’s signs and symptoms, prevent joint damage, and maintain his/her quality of life. Among the best known disease-modifying antirheumatic drugs, Methotrexate (MTX) is one of the most effective and widely used medications. It is used as a general first-choice drug, although some patients will not respond to this treatment and it is not free from side-effects.

**Objectives:** To identify circulating proteins that could be useful as predictors of the patient’s response to MTX.

**Disclosure of Interest:** None declared

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