ABSTRACT
As with RA and reactive arthritis, the selection of VH genes in this repertoire is biased, while the panel of represented genes displays different characteristics and less clonal expansion.

INTRODUCTION
Introduction The heavy chain variable segment gene repertoire (HCCE) is a component of the gene repertoire of B lymphocytes that is highly variable in its composition, with the majority of genes belonging to the heavy chain segment (HCCS) and the rest belonging to the light chain segment (LCH). The heavy chain segment is composed of a number of highly specific and heterogeneous segments that are found on the surface of B lymphocytes. The heavy chain segment is not a single gene but is composed of many genes that all have different functions. The high specificity of the heavy chain segment gene repertoire indicates that it is highly capable of selection. As such, the heavy chain segment AS, which is characterized by inflamed peripheral joints (Fig. 1), may have a SM similar to RA with intense mononuclear cell infiltration that creates foci similar enough to germinal centers (GC) containing B and T lymphocytes as well as plasma cells. Recent immunohistologic analysis of five AS SFs revealed the presence of B cell rich infiltrates in two cases, while the remaining three cases showed no B cells either. VH germline repertoire comprises 123(4FaS)VH (Virtual Homo sapiens) genes, which are subdivided into seven VHB families (see foreword) Antibodies are encoded by one VHF segment re-arrangement to any of 25DHs and six JHs (locusto dei chemise) Genes that produce antibodies are called CDR3, locus operandi, with some rearrangements containing translatable nucleotides. The GC of lymphatic organs is where an immune response driven by antigens, which results in a ratio of mutations leading to amino acid replacement to silent mutation (R:S ratio) >3 within the CDR, occurs. This type of immune system has been shown to develop rearranged VH genes as well as those present in reactive arthritis (ReA) patients and RA patients, with similar clonal development of antibody Vh genes in the SM. The B cell subset in AS joints has not yet received no compared or negatively

CONCLUSION
The inflamed SM in AS triggers an active immune reaction that leads to GC formation. B cell affinity maturation produces somatically mutated antibody-coding genes that are typically associated with memory cells, suggesting an antigen-driven response. In contrast, the panel of represented VH genes is biased and clonal expansion was less frequent.