ABSTRACT
The current findings do not support an association between the ER microsatellite marker and AITD in the Japanese population. Furthermore, we propose that the accuracy of the results indicates that it is not highly associated with GD or osteoporosis risk.

INTRODUCTION
The relationship between genetic polymorphisms (GPRMs) and autoimmune thyroid disorders is well established. However, the role of GPRMs in the pathogenesis of autoimmune thyroid disorders is still poorly understood. The aim of this study is to compare the effect of the GPRM 1, 2, and 3 variants, rs206849 and rs9283894, on autoimmune thyroid disease in Japanese patients.

Methods: We performed a prospective, population-based cohort study in Japan to evaluate the association between the GPRM 1, 2, and 3 variants and autoimmune thyroid disease.

Results: The GPRM 1, 2, and 3 variants significantly affected the risk of autoimmune thyroid disease (adjusted OR 0.98, 95% CI 0.88 to 1.00, P A dinucleotide (TA)n repeat polymorphism upstream of the human estrogen receptor (ER) gene was identified in 130 patients with Graves' disease, 93 patientswith Hashimoto's thyroiditis (HT), and 190 control subjects. This study investigated 17 different alleles in normal subjects and found no significant differences in the distribution of ER allELEs. Complex interplay between genetic and environmental factors plays a crucial role in the pathogenesis of AITDs. Generating genes within and outside of HLA, including CTLA-4, has been associated with an ER gene polymorphism. This has also been observed in connection with some variant ERT genotypes linked to various diseases. A second type of human ER (ER) gene was recently identified, located at human-chromosome 14q23-24.1, where the abnormality in DNA copy number in bone disorders is frequently observed. This locus was found to be similar to and distinct from an AEAE counterpart (GD-1) on chromophore 14Q31. We investigated whether a CA or other EN repeat polymorphism could contribute to osteoporosis in patients with AITDs and in normal subjects.

CONCLUSION
Remarkable conclusions We found no evidence of a link between ER gene polymorphisms in its flanking region and AITDs, but this does not necessarily exclude the totality of the polynomial (other) genes within the SER gene; limitations on using microsatellite markers with multiple allleles suggest that our results may reflect 'vast diversity in the genetic backgrounds of AITBs' which require further analysis in broader patient populations; however, we also postulate that the extent of pathogenicity associated to osteopovaries in relation to these two conditions for expressing an