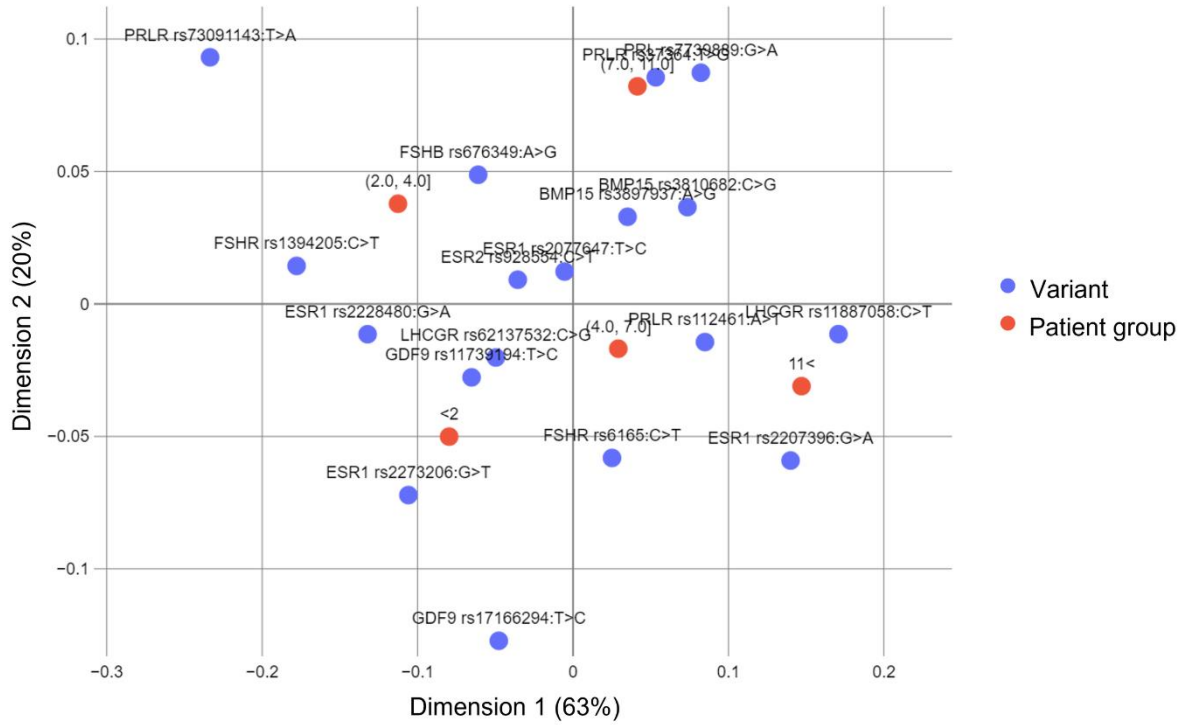

S1 Fig. Identification of sequence variants characteristic of MII groups by correspondence analysis (CA). The x- and y-axes show vertical and horizontal dimensions, respectively. Sequence variants on the chart are described with the gene symbol, variant name, and type of nucleotide change. Correspondence analysis allows the visualization of multidimensional datasets. In this study, it was used to present both patient groups and sequence variants on the same figure. The location of dots denoting the groups and variants shows dependencies in the dataset. The more the sequence variant is characteristic of a given MII group, the closer it is located on the visualization. The dependencies between variants and patient groups are stronger with increased distance from the origin of the coordinate system. Inertia covered $I \in [0,1]$ shows the goodness of the model's representation of the dataset, where 1 is the perfect representation. Here, the first two dimensions explain 83% of the inertia (x—0.63, y—0.20). Sequence variants *LHCGR* rs11887058 (NC_000002.12:g.48729336:C>T), *PRLR* rs112461 (NC_000005.10:g.35063190:A>T), and *ESR1* rs2207396 (NC_000006.12:g.152061247:G>A) are located closest to the MII group >11.