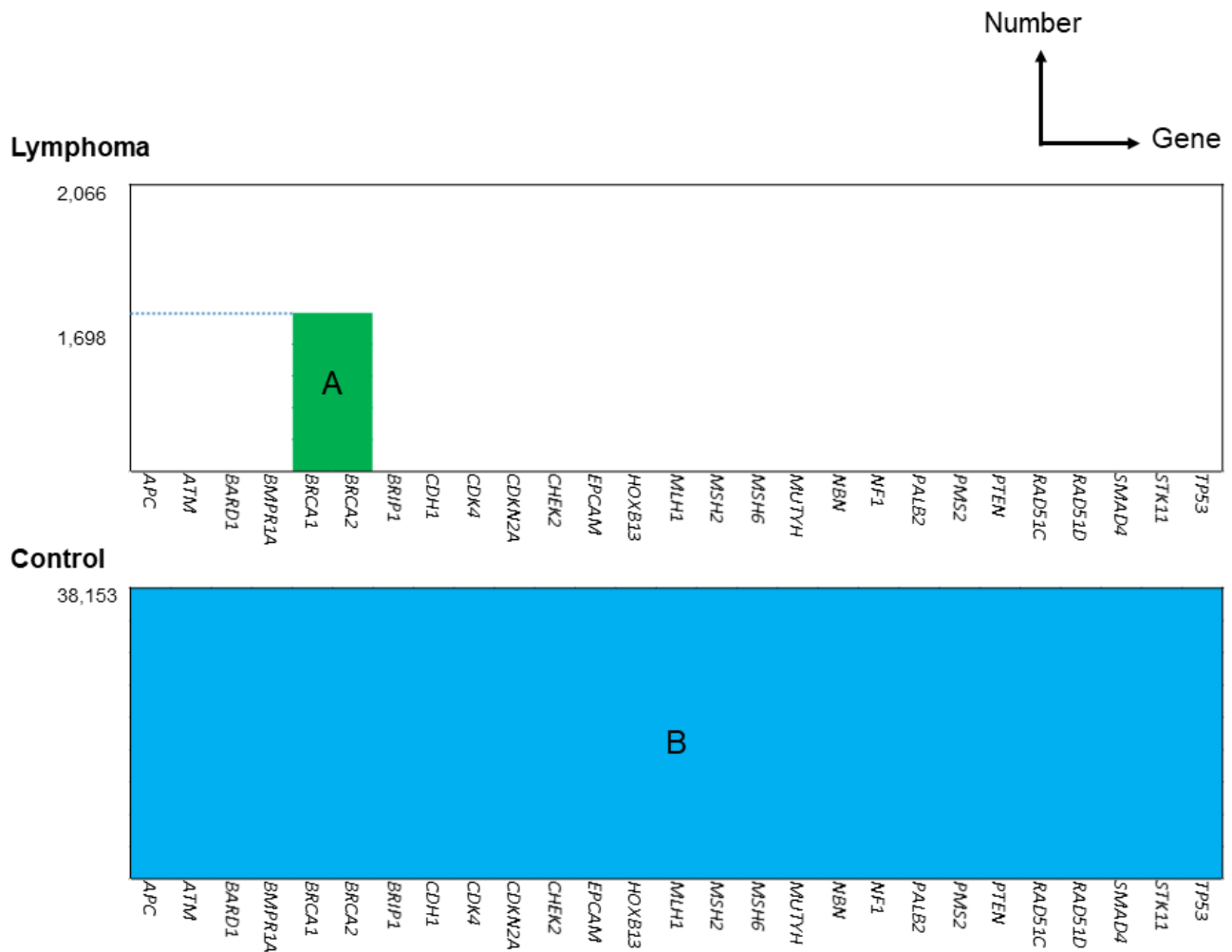


**Figure S1. Use of sequence data from our other studies**



In this study, we analyzed 2,066 lymphoma patients and 38,153 cancer-free controls. (A) Concerning *BRCA1/2*, 82% (1,698/2,066) of sequence data of the lymphoma patients were included in our previous study.<sup>1</sup> Other sequencing data of lymphoma patients were analyzed for the present study. (B) Sequence data of all controls for 27 cancer-predisposing genes were obtained from our previous study (in submission).

1. Momozawa Y, Sasai R, Usui Y, et al. Expansion of Cancer Risk Profile for BRCA1 and BRCA2 Pathogenic Variants. *JAMA Oncol.* 2022; 8: 871-878.