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Microhomology-mediated end joining drives complex rearrangements and over expression of MYC and PVT1 in multiple myeloma

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Contributions: AM, CA, FED, GJM and BAW conceived and designed the study; AM, CA PQ, AR, AH and AT collected clinical data, sequencing data and performed statistical testing; JK, DA and AT were responsible for collection and availability of CoMMpass study related data; JAD, KRR, SY and FED developed and maintained mouse models; RGT, SD and ET processed the samples and performed laboratory protocols; AM, CA, ET, JK, DA, GHJ, GJM and BAW analyzed and interpreted data; CA, MAB, CPW, KM and MT performed the bioinformatics of the sequencing data; All authors discussed the results, wrote, reviewed and approved the manuscript.