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# Whole exome sequencing in families at high risk for Hodgkin lymphoma: identification of a predisposing mutation in the KDR gene

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Contributions: M.R., M.L.M, P.L.H., A.M.G., and L.R.G. performed and interpreted genetic analyses. M.L.M, M.A.T., L.F., and N.E.C. directed clinical work for the patients and families. J.B., S.B., X.Z, L.B., B.H., M.Y., S.J.C. and the NCI DCEG Cancer Genomics Research Laboratory conducted all whole-exome and targeting sequencing and associated bioinformatics. The NCI DCEG Cancer Sequencing Working Group examined and enrolled families for sequencing. S.R. and B.T.L. performed functional prediction analyses. M.R., M.L.M, and L.R.G. drafted the manuscript. All authors contributed to the final manuscript.