Several moderate and high risk breast cancer susceptibility genes have been discovered, but more are likely to exist. To discover new breast cancer susceptibility genes, we used whole exome sequencing to study 195 familial breast cancer cases from founder populations from Poland and Quebec. Findings were validated using candidate gene sequencing and genotyping of recurrent mutations among 25,000 cases and controls. We identified recurrent RECQL mutations in breast cancer cases in both populations. These mutations increase the risk of breast cancer by 5-fold among unselected cases from Poland and by 16-fold among Quebec higher-risk cases. We found no association with age of onset. RECQL is implicated in resolving stalled DNA replication forks to prevent double-stranded DNA breaks (dsDNA), a function related to that of other known breast cancer susceptibility genes, many of which are involved in repairing dsDNA breaks. We conclude that RECQL is a new breast cancer susceptibility gene.