

SUPPLEMENTAL MATERIAL

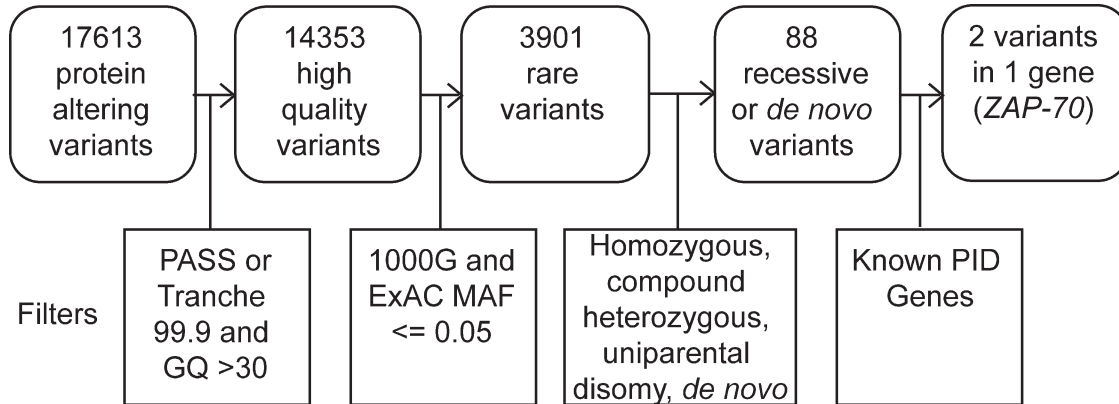
Chan et al., <http://www.jem.org/cgi/content/full/jem.20150888/DC1>

Figure S1. **Variant filtering on exome.** Data variant filtering for the affected siblings showing sequentially applied filters to yield a set of 3,901 variants that were further annotated based on the inheritance model. Highest priority was given to primary immunodeficiency genes; two shortlisted high quality variants were in *ZAP-70*.