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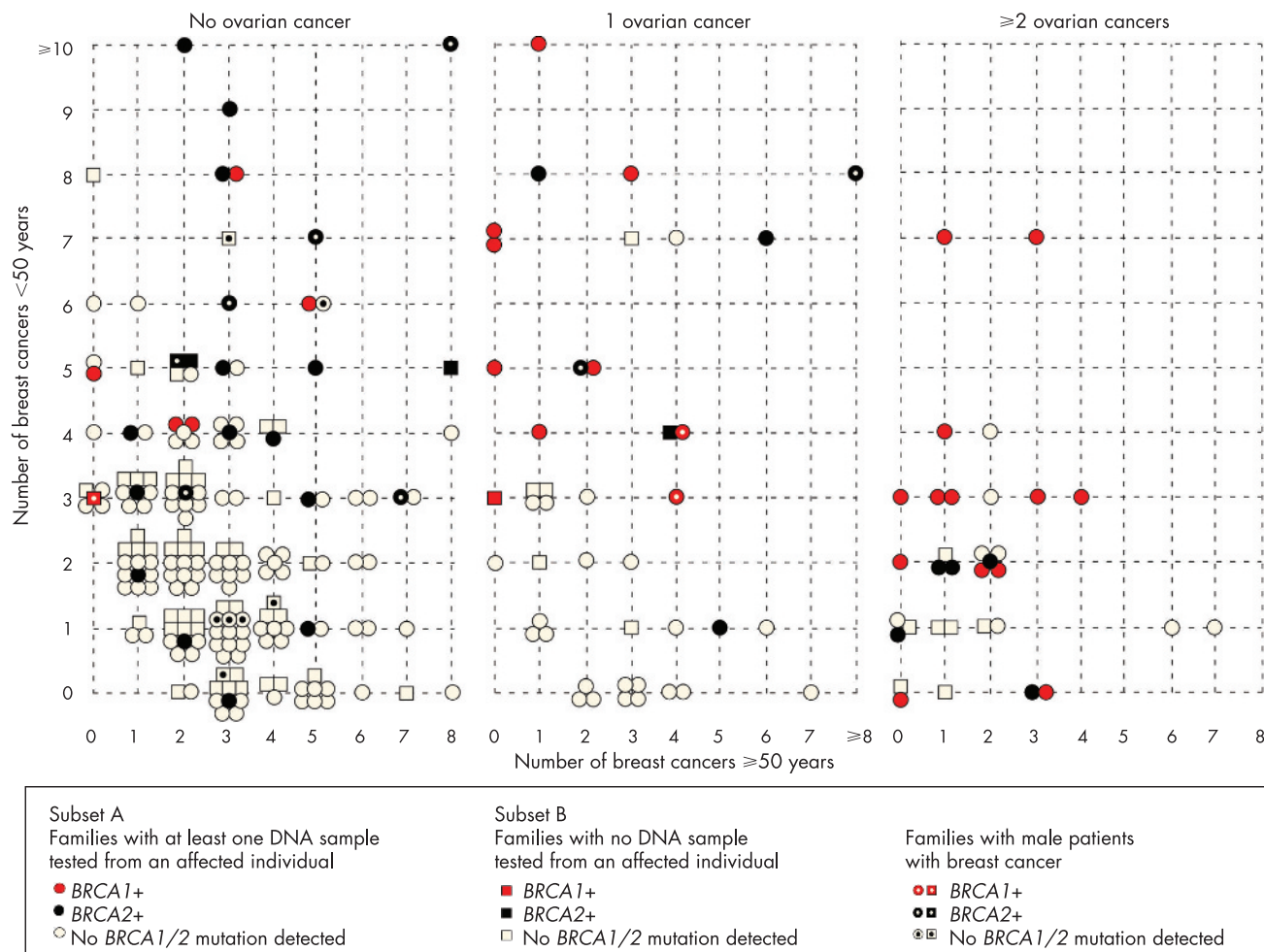
CORRECTION

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Jacques Simard, Martine Dumont, Anne-Marie Moisan, Valérie Gaborieau, Hélène Vézina, Francine Durocher, Jocelyne Chiquette, Marie Plante, Denise Avard, Paul Bessette, Claire Brousseau, Michel Dorval, Béatrice Godard, Louis Houde, Yann Joly, Marie-Andrée Lajoie, Gilles Leblanc, Jean Lépine, Bernard Lespérance, Hélène Malouin, Jillian Parboosingh, Roxane Pichette, Louise Provencher, Josée Rhéaume, Daniel Sinnett, Carolle Samson, Jean-Claude Simard, Martine Tranchant, Patricia Voyer, INHERIT BRCAs, Douglas Easton, Sean V Tavtigian, Bartha-Maria Knoppers, Rachel Laframboise, Peter Bridge, and David Goldgar. Evaluation of *BRCA1* and *BRCA2* mutation prevalence, risk prediction models and a multistep testing approach in French-Canadian families with high risk of breast and ovarian cancer. *J Med Genet* 2007;**44**: 107–21.

The journal apologises for an error that has occurred in this paper in figure 4 on page 116, where the numbers 0 to ⩾10 on the vertical axis of the graph should align with the horizontal dotted lines, starting with zero at the bottom. The correct figure is printed here.

Figure 4 Distribution of the 256 families according to the presence of ovarian cancer, the number of breast cancer cases diagnosed before (<) or after (⩾) 50 years and their mutation status. *BRCA1*-positive (+) families are represented by either a red circle (families of subset A) or a red square (families of subset B). *BRCA2*-positive families are represented by either a black circle (families of subset A) or a black square (families of subset B). Families with no *BRCA1/BRCA2* mutation detected are represented by either an open circle (families of subset A) or an open square (families of subset B). Female breast and ovarian cancer cases were at most third-degree relatives from the proband, whereas the presence of a male patient with breast cancer was considered at any degree from the proband. A dot in each form indicates the presence of male patients with breast cancer in the family.