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BRC1      -----NHSFGG-SFRTASNKEIKLSEHNIKKSKMFFKDIEEQY 37
BRC2      ---NEVGFRFG--FYSAHGTKLNVSTEALKAVK-LFSDIEN-- 35
BRC3      EQNIKDFETSDTFFQTASGKNISVAKESFNKIVNFFDKQPEEL 43
BRC4      ----KEPTLLG--FHTASGKKVKIAKESLDKVKNLFDKEQ-- 35
BRC5      ----IENSALA--FYTSCSRKTSVSQTSLEAKKWLREGIF-- 35
BRC6      -----VGPPAFRIASGKIVCVSHETIKKVKDIFTDS---- 31
BRC7      -----TCG-IFSTASGKSVQVSDASLQARQVFSEIED-- 32
BRC8      -----AFSG--FSTASGKQVSILESSLHKVKGVLLEFDLI- 33
BRC4T08A  ----KEPTLLG--FHAASGKKVKIAKESLDKVKNLFDKEQ-- 35
          *   :   .       :       :       :       :

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Figure S8. Sequence alignment of the eight human BRC repeats and a BRC4T08A mutation used in our FP assays, generated with ClustalW. The symbols on the bottom row denote the degree of conservation observed in each column: '' denotes that the residues in that column are identical in all sequences in the alignment, ':' denotes that conserved substitutions have been observed and '.' denotes that semi-conserved substitutions are observed.*