Reviewer's report

Title: TP53 mutations in ovarian carcinomas from sporadic cases and carriers of two distinct BRCA1 founder mutations; relation to age at diagnosis and survival

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Reviewer: richard buller

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The authors still have not really acknowledged the importance of the two "minor essential" revisions I listed in my earlier review. The reader is asked to accept that fully 8 out of 24 BRCA1 tumors with abnormal bands could not be sequenced. This rate is very high and compromises the ability to determine statistical significance. Two neutral mutations were sequenced and the potential for intron abnormalities not leading to sequence abnormality exists as well. Furthermore, how the data is handled seems to vary. On page 8, 24/38 familial cancers are inferred to contain a mutation - counting the unsequenceable tumors as mutant. Yet in Table 3, 17 (shouldn't it be 16?) cases are listed as having a mutation and 21 (now includes the tumor with abnormal bands, not sequenced) are listed as no TP53 mutation. Table 1 states that 55.3% of the 38 tumors contain TP53 mutations (that works out to 21 cases with mutations). So I'm very confused. This issue must be resolved and consistent. I would offer that the 8 cases in question be dropped from the analysis. I suspect this will change the conclusions, but at least the authors can be consistent and the reader can be certain that a "mutation" is a mutation that has real potential to impact P53 function.