Major Compulsory Revisions

1. The quality of the samples was not discussed. What percentage of tumor cells in each of the frozen tumors? The presence of normal cells in the tumors will greatly affect the expression profiles.

2. The authors failed to acknowledge other expression profile studies of ovarian tumor with BRCA1 such as by Tone et al., Clin Cancer Res 2008, 14:4067-4078 (raw data is available at GEO database as GSE10971) or Bellacosa et al., Cancer Prev Res 2010, 3:48-61. These prior studies did find genes with differential expression in normal ovarian epithelial cells with or without BRCA1 mutations. Microdissected tumor cells or low-passage ovarian epithelial cells were used for study. The authors should discuss their data.

3. The authors concluded that all ovarian high-grade serous carcinomas arise through oncogenic mechanism that result in chromosomal instability irrespective of BRCA status is questionable. Probably some ovarian high-grade serous carcinomas arise through a BRCA dependent pathway while other are not and may through p53 pathway. For those samples with wild type BRCA, do they carry another p53 mutation?

4. The number of samples is still small and should be addressed. The expression level of BRCA1 should be measured by real-time RT-PCR in all the samples as another indication of the mutation status and epigenic status before SAM analysis should be performed.

5. In the gene filtering, gene with less than 1.5 fold of signal to background will be removed. In such case, if the gene is not expressed in reference RNA and BRCA mutation but in wt type BRCA will be filtered out and not used for analysis. In other word, when genes with the signal for reference RNA and BRCA mutated sample are close to background signal, but with strong signal in the wild BRCA samples, those genes will be missed.

6. "Genes were filtered retaining only those whose expression levels differed by at least 4-fold in at least 3 samples" is not clear. Is the fold change between the tumor sample and the reference RNA?

7. The use of FDR of 5% is arbitrary. Have you tried to use higher FDR and
validate the differential gene expression by RT-PCR?

**Level of interest:** An article whose findings are important to those with closely related research interests

**Quality of written English:** Acceptable

**Statistical review:** Yes, but I do not feel adequately qualified to assess the statistics.

**Declaration of competing interests:**

I declare that I have no competing interests