Reviewer's report

Title: Expression profiling identifies genes involved in neoplastic transformation of serous ovarian cancer

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Reviewer: Teri Longacre

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Major Revisions:
1. The percent epithelial content needs to be correlated with the array data. The authors suggest that similar expression profiles in benign tumors and normal tissue may reflect stromal content as opposed to epithelial expression, but they should be able to correlate to stromal content in these cases.
2. The Venn diagrams in Figure 1c needs more explanation. For example, does the 44 entry reflect co-clustering of SLP1 and GLTSCR2? If so, what does 43 represent? WNT7A is differentially expressed in invasive vs normal as well as vs benign, but it appears to be represented only in the benign vs invasive group in the Venn diagram.
3. The discovery that a small gene set distinguishes LMP and invasive cancer is not new. This was reported in the Gilks et al study. The authors are not citing the latter study correctly.
4. Representative images of the frozen tissue sections of benign, cancer and LMP tumors should be presented.

Minor Revisions:
1. Abstract, Results, 47 should be 46.
2. This study was conducted in Australia. Why use US cancer statistics? Australian statistics would be more relevant to their data.
3. "Positive staining" for SLPI should be described more fully: cytoplasmic, nuclear, both??? The figure depicting staining for SLPI suggests it is cytoplasmic. Was there stromal staining in any of the tumors? Also, the figures that are depicted are a bit deceptive, since the data in Figure 1d indicates that LMP tumors were more frequently positive than invasive cancers.

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

Quality of written English: Acceptable

Statistical review: No, the manuscript does not need to be seen by a statistician.
Declaration of competing interests:

I declare that I have no competing interests.