

The manuscript by Cheung *et al.* examined gene datasets up-regulated in esophageal carcinomas by microarray analysis. They confirmed HMGA2 overexpression in the carcinomas by quantitative real-time PCR and immunostaining. Although the data is straightforward to show the role of HMGA2 in carcinoma progression, several major concerns should be settled.

#### Major points

1. Approval for the ethical considerations to use carcinoma tissues by the institutional review boards must be mentioned in the materials and methods.
2. Figure legends were not provided.
3. In Fig. 1, fonts were too small. It is very hard to read.
4. Normal epithelium should be included in Fig. 2.
5. Expression of HMGA2 in esophageal carcinomas has been reported (Liu Q, *et al.*, Mol Biol Rep 39: 1239-46, 2012). Discussion with their data makes the manuscript in deep thought.

#### Minor points

1. N for microarray analysis has not been described.
2. In Fig. 2, scale bars should be used for each panel in substitution for magnification folds.

**Note: Anonymous Reviewer**