We wish to thank Cremolini and colleagues for their interesting letter that highlights their previous finding that VEGFR-2 may be a predictive marker for benefit from bevacizumab therapy. Their data are derived from the setting of postprogression bevacizumab in advanced colorectal cancer, and there are other supportive data in the breast cancer settings of first-line metastatic HER2-negative disease and adjuvant triple-negative disease.

In our study of patients with high-risk early- and advanced-stage ovarian cancer treated with bevacizumab, VEGFR-2 was not detected in the patient samples used in the initial discovery cohort. This may be due to its absence or alternatively its concentration being below the detection level of our proteomic techniques. We acknowledge this as a limitation in our selection of potentially relevant markers, along with the limited size of the discovery cohort, as further discussed in the original article (1).

VEGFR-2 has, however, already been investigated further in a separate ICON7 translational study (currently submitted for publication) that used the same samples as the validation cohorts I and II from our study. This parallel study specifically investigated the predictive value of a large number of angiogenic-related cytokines, including VEGFR-2, by immunoassay. Although a small number of angiogenic markers were found to have some evidence of predictive value, VEGFR-2 did not seem to be predictive of benefit from bevacizumab in the ovarian cancer setting (G. Jayson; personal communication). This lack of predictive value for VEGFR2 was also seen in the advanced gastric cancer setting in the context of the AVAGAST trial (2). Whether these differences between different studies for VEGFR2, and indeed for other potential predictive markers, reflect different cancer types or trial settings and size remains to be determined.

Disclosure of Potential Conflicts of Interest
No potential conflicts of interest were disclosed.

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