McColl et al. Vol. 198, No. 6, September 15, 2003. Pages 863–868.

Typographical errors were made in the Results section under the subheading Assay for VEGF-D Processing. In each case, kD was used instead of the unit D, implying that the value being quoted was 1,000-fold greater than in reality. The corrected paragraph appears below:

A range of proteases were tested in this assay, including plasmin, thrombin, and MMP-2 and MMP-9. These proteases were chosen because of their involvement in angiogenesis or tumor formation. MMP-2 and MMP-9 had no effect on the counts detected in the SPA, however, plasmin caused a >90% reduction of signal, indicating substantial cleavage of the peptide (Fig. 1 c). Thrombin caused a small reduction of signal. To identify the site at which plasmin hydrolyzed the peptide, samples were analyzed by mass spectrometry. Undigested peptide consisted of a single peak of a molecular mass of 2,282.15 D, as expected (Fig. 1 d, top). After plasmin treatment, a predominant peak of a molecular mass of 1,267.68 D was observed, corresponding to Biotin-HPYSIIRR (Fig. 1 d, bottom). This molecular species is an expected product of cleavage of the peptide at the same site as observed in VEGF-D expressed in 293EBNA cells (i.e., between R205 and S206) (Fig. 1 a; reference 18). An alternative cleavage event generating Biotin-HPYSIIR (molecular mass 1,111.59 D) was also detected.