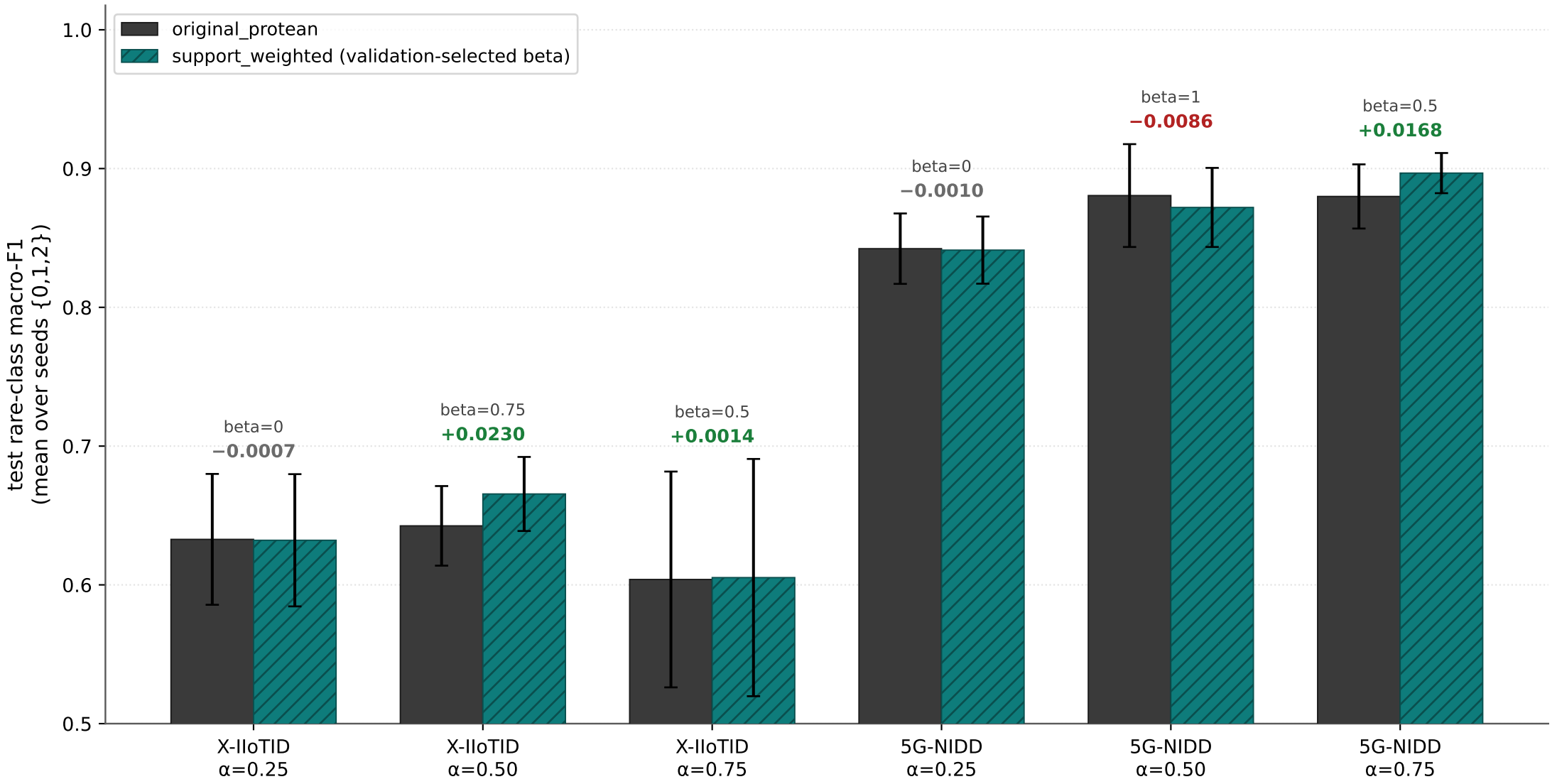


Bar height = mean test rare-class macro-F1 over seeds {0,1,2}; error bars = ±1 sample std across seeds.
Delta (top) = selected-beta minus original_protean; green = positive, red = negative, grey = selected beta 0
(floating-point ~0). No statistical significance test is applied (3 seeds). Gains are condition-dependent;
the proposed weighting does NOT consistently outperform original PROTEAN.