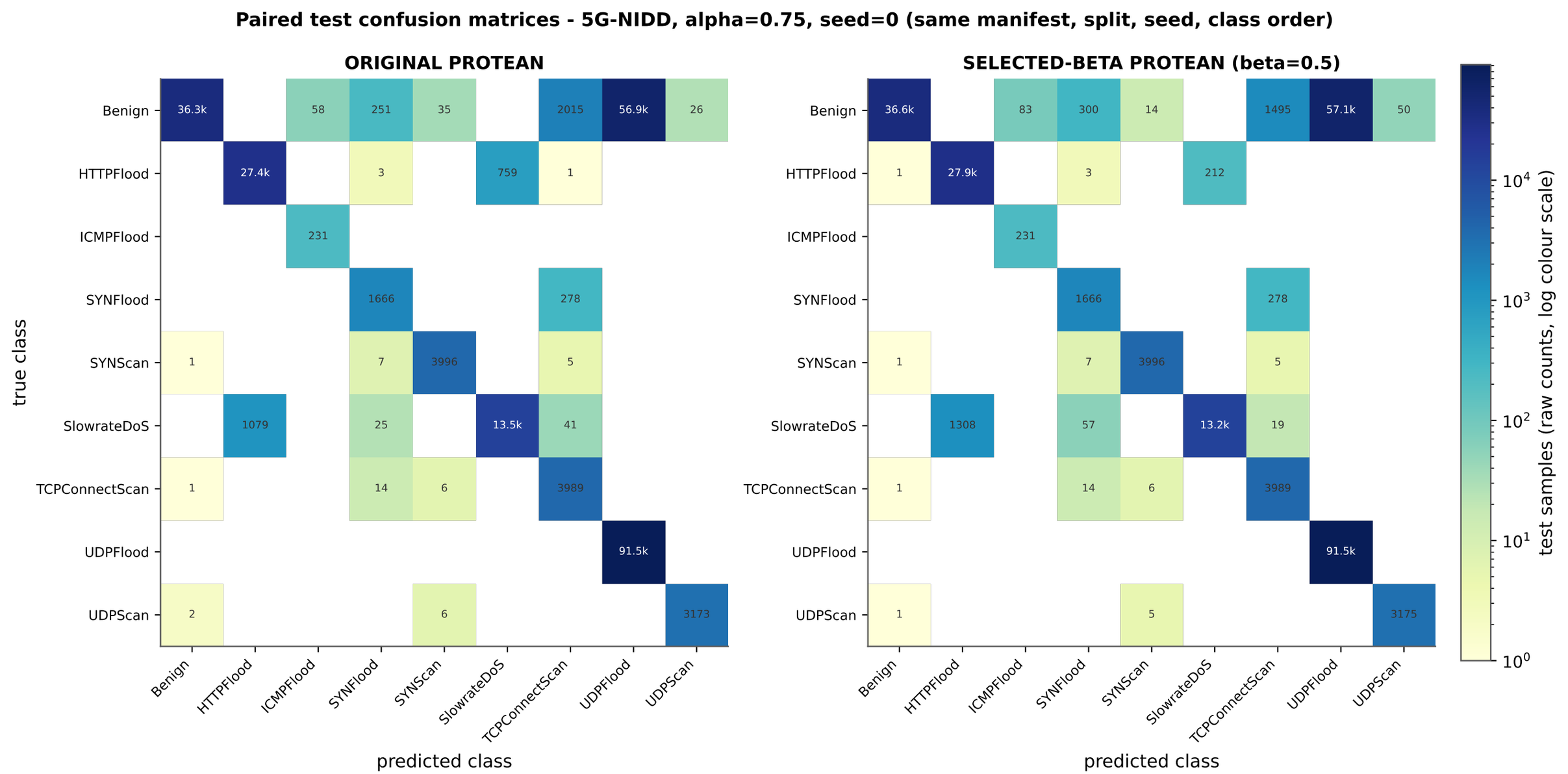


Left = original_protean; right = support_weighted at the validation-selected beta. Raw counts; identical class order and colour scale.
Dominant off-diagonal error: Benign predicted as UDPFlood, essentially unchanged by beta. No statistical significance is inferred.