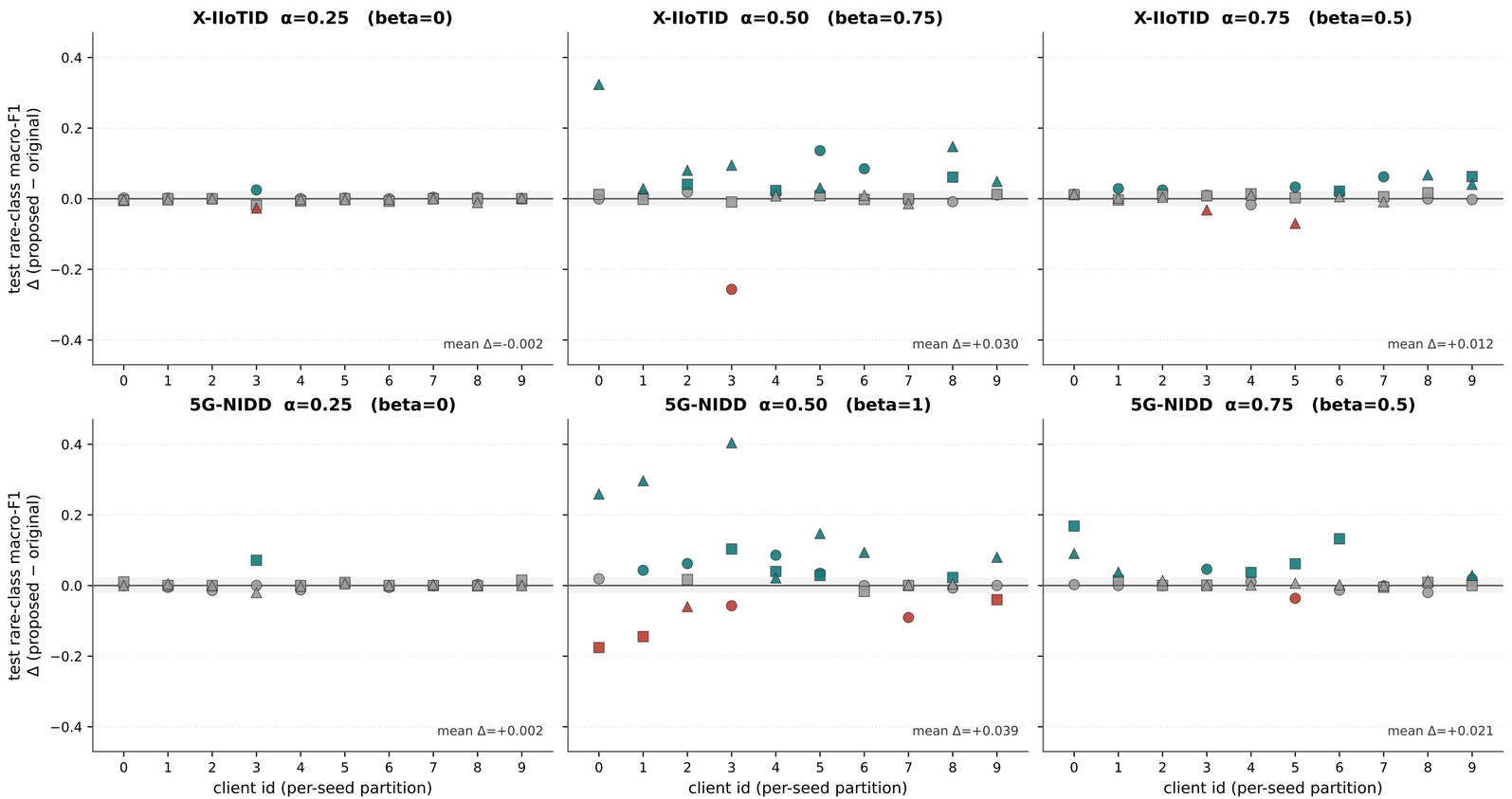


Each point is one (client, seed) test observation; x = client id, marker = seed. Points compare the support_weighted run at the validation-selected beta against original_protean on the same partition. At α=0.25 the selected beta is 0, so the residual spread is numerical (equal-weight equivalence), not a weighting effect. Do not treat client id across seeds as the same real-world client.