Supplementary Material S2. Simulations for Mixed stock analysis (MSA)

For each baseline scenario and each prior, simulations were run to assess the accuracy of stock contribution estimates. 40 simulations with 200 individuals in the stock were performed with the leave-one-out cross-validation method (Anderson et al., 2008) implemented in the R package *rubias* (Moran and Anderson, 2019).

Anderson, E.C., Waples, R.S., Kalinowski, S.T., 2008. An improved method for predicting the accuracy of genetic stock identification. Can. J. Fish. Aquat. Sci. 65, 1475–1486. https://doi.org/10.1139/F08-049

Moran, B.M., Anderson, E.C., 2019. Bayesian inference from the conditional genetic stock identification model. Can. J. Fish. Aquat. Sci. 76, 551–560. https://doi.org/10.1139/cjfas-2018-0016

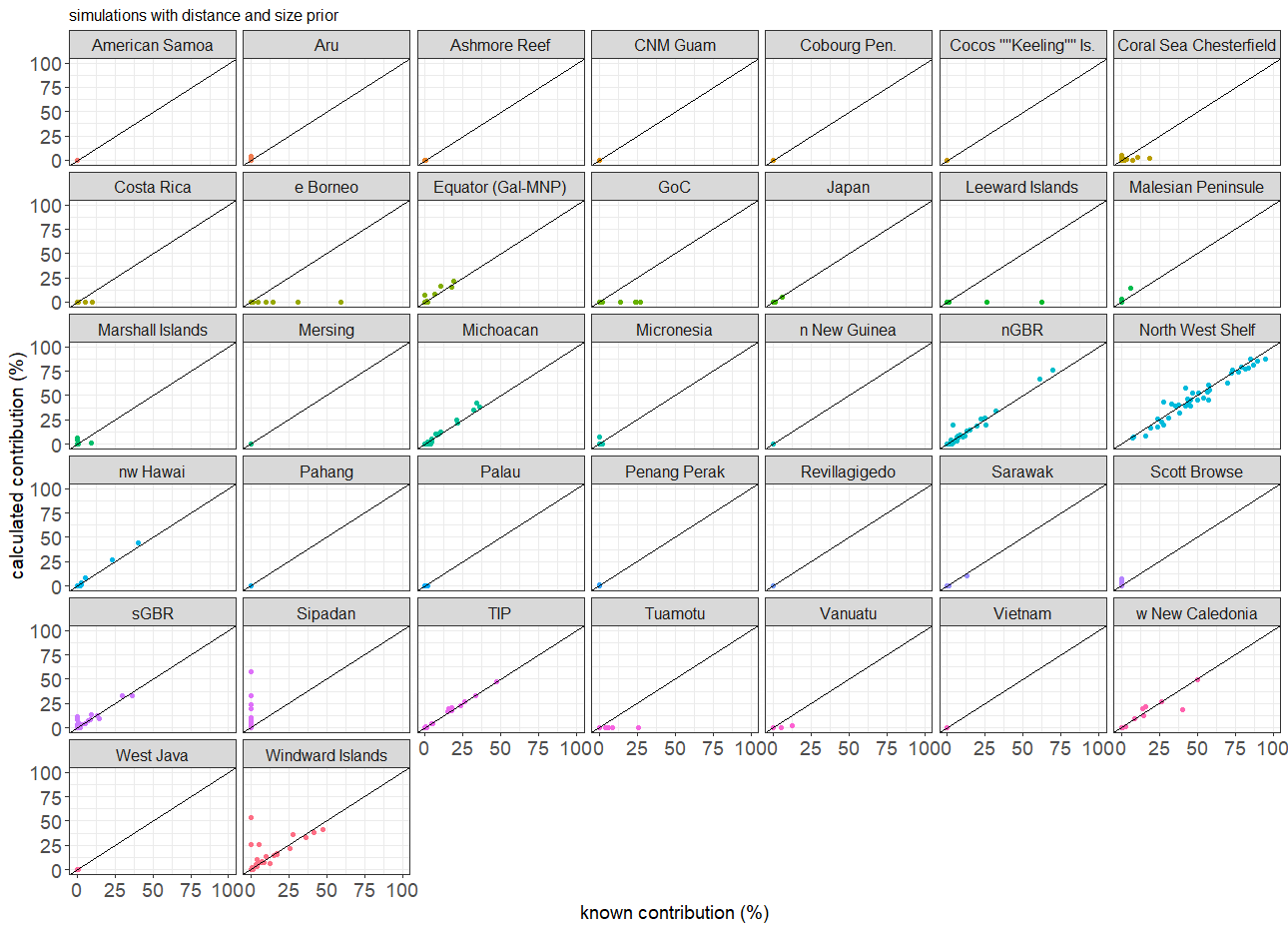
# Scenario 1: 3 MUs in French Polynesia: Leeward Islands, Winward Islands, Tuamotu

## Simulations with flat prior

## Simulations with distance prior

## Simulation with size prior

## Simulation with size and distance combined prior



# Scenario 2: 2 MUs in French Polynesia: Tetiaroa, other Islands

## Simulation with flat prior

## Simulation with distance prior

## Simulation with size prior

## Simulation with size and distance combined prior