ovitrap\_results.csv

* trap = oviposition trap identifier
* time\_point = epiweek of trap collection
* month = month of trap collection
* n\_larvae = number of hatched larvae
* n\_larvae\_tested = number of hatched larvae tested for *Wolbachia* detection
* n\_wmel = number of hatched larvae tested that tested positive for *w*Mel *Wolbachia* infection
* n\_wt = number of hatched larvae tested that tested negative for *w*Mel *Wolbachia* infection
* n\_alb = number of hatched larvae tested that were molecularly identified as *Aedes albopictus*
* n\_aeg = number of hatched larvae tested that were molecularly identified as *Aedes aegypti*
* cluster = EVITA Dengue Trial cluster blinded name
* n\_eggs = number of eggs collected by the oviposition trap

bgtrap\_results.csv

* collected\_at = date of trap collection
* year\_week = epiweek of trap collection
* total\_aegypti\_caught = number of *Aedes aegypti* adults collected in trap
* total\_albopictus\_caught = number of *Aedes albopictusi* adults collected in trap
* screening\_total\_aeg = number of adults tested that were molecularly identified as *Aedes aegypti*
* screening\_wmel\_aeg = number of adults tested that tested positive for *w*Mel *Wolbachia* infection
* month = month of trap collection
* cluster = EVITA Dengue Trial cluster blinded name