



GWAS: Step-by-step (green) methodological pipeline developed to identify genomic variation in association with a trait

Citation for this pipeline:

Batley K, Sandoval-Castillo J, Kemper C, Attard C, Zanardo N, Tomo I, Beheregaray LB, Möller LM (2019) Genome-wide association study of an unusual dolphin mortality event reveals candidate genes for susceptibility and resistance to cetacean morbillivirus. *Evolutionary Applications* In press

