



Tilapia SkimSEEK™

Low-pass skim sequencing & imputation from Neogen® Genomics

The Next Advancement in Genomic Technology

Leverage low-pass sequence data with SkimSEEK™ and explore deeper into the Nile Tilapia genome. Powered by Neogen and the Center for Aquaculture Technologies (CAT).

Advantages of SkimSEEK

- Reduce dependence on linkage disequilibrium between fixed arrays and Quantitative Trait Loci (QTL) that are impacting the phenotypes of interest
- Lower cost than population-specific genotyping panels
- Complete genotyping of Nile Tilapia (*Oreochromis niloticus*) populations, which reduces bias due to selective genotyping
- Data report contains millions of SNP variants (22 million), small indels (6 million), and multi-allelic sites (1.6 million) to help discover novel, population-specific causative variants
- Same cost and effort to sequence many individuals at low coverage when compared to sequencing a few individuals at high coverage
- Imputation – match low-coverage reads to well-characterized reference haplotypes
- SNP content covers 96% of the ~65K Open Access SNP Array for Nile Tilapia (*Oreochromis niloticus*)¹

96% overlap of the ~65K Open Access SNP Array content¹