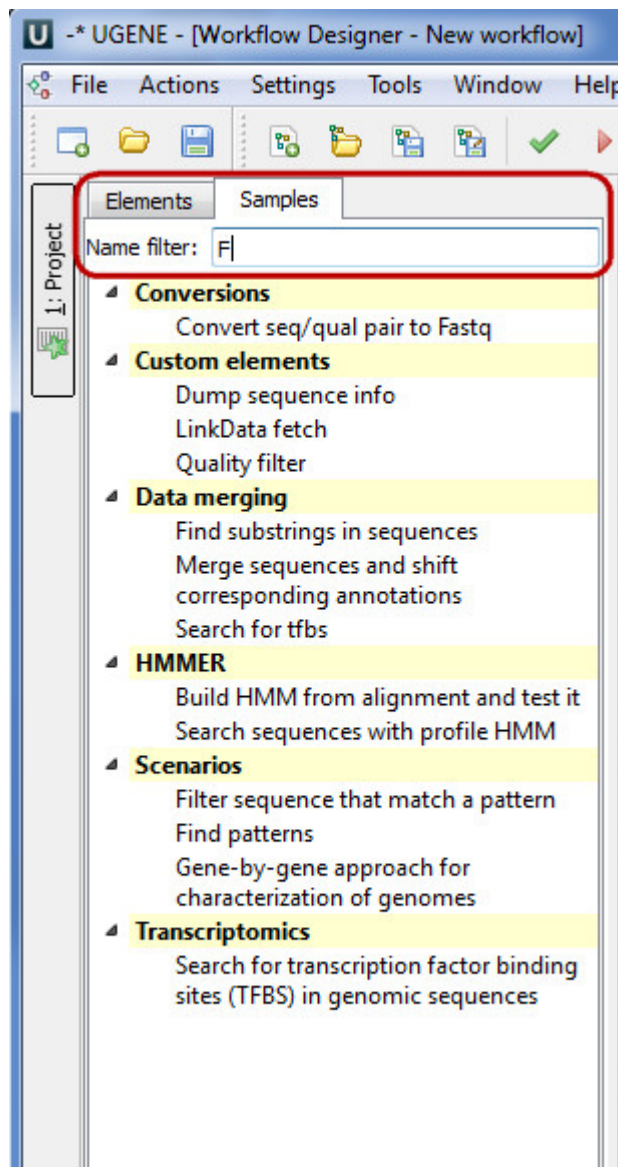


Workflow Samples

This section contains detailed description of workflow samples presented in the Workflow Designer. To search a sample use the name filter or press the *Ctrl+F* shortcut that moves you to the name filter also:



- Alignment
 - Align Sequences with MUSCLE
 - Extract Consensus as Sequence
 - Extract Consensus as Text
- Conversions
 - Convert "seq/qual" Pair to FASTQ
 - Convert Alignments to ClustalW
 - Convert UQL Schema Results to Alignment
 - Convert Sequence to Genbank
- Custom Elements
 - CASAVA FASTQ Filter
 - FASTQ Trimmer
 - Dump Sequence Info
 - LinkData Fetch
 - Quality Filter
- Data Marking
 - Marking Sequences by Annotation Number
 - Marking Sequences by Length
- Data Merging
 - Find Substrings at Sequences
 - Merge Sequences and Shift Corresponding Annotations
 - Search for TFBS
- HMMER
 - Build HMM from Alignment and test it
 - Search Sequences with Profile HMM
- NGS
 - De novo Assembly with Spades
 - Call Variants with SAMtools
 - ChIP-Seq Coverage
 - ChIP-seq Analysis with Cistrome Tools
 - Extract Consensus from Assembly
 - Extract Coverage from Assembly
 - Extract Transcript Sequences
 - Quality Control by FastQC
 - Raw ChIP-Seq Data Processing
 - Raw DNA-Seq Data Processing
 - Raw RNA-Seq Data Processing
 - RNA-seq Analysis with Tuxedo Tools
 - Get Unmapped Reads
 - Variation Annotation with SnpEff
- Sanger Sequencing
 - Trim and Align Sanger Reads
- Scenarios
 - Filter Sequence That Match a Pattern
 - Search for Inverted Repeats
 - Find Patterns
 - Gene-by-gene Approach for Characterization of Genomes
 - Group Primer Pairs
 - Intersect Annotations
 - Merge Sequences and Annotations
 - In Silico PCR
 - Remote BLASTing
 - Get Amino Translations of a Sequence
- Transcriptomics
 - Search for Transcription Factor Binding Sites (TFBS) in Genomic Sequences