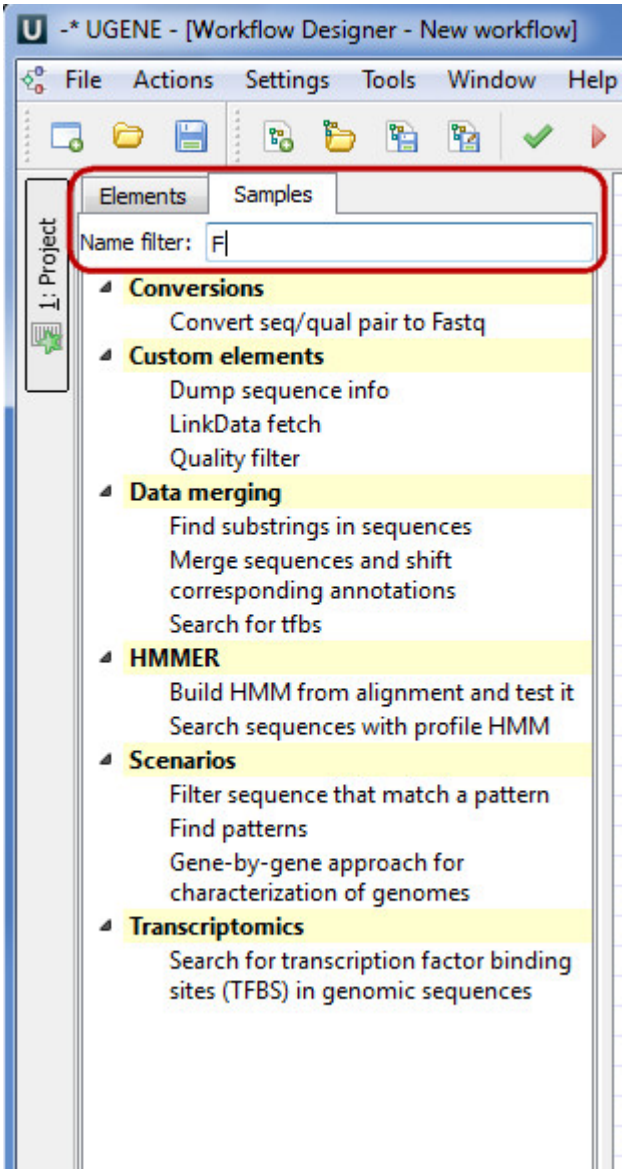
Workflow Samples

This section contains detailed description of workflow samples presented in the Workflow Designer. To search a sample use the name filter or press the *Ctr l+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 by Annotation Number
  - Marking by Length
- Data Merging
  - Find Substrings in Sequences
  - Merge Sequences and Shift Corresponding Annotations
  - Search for TFBS
- HMMER
  - Build HMM from Alignment and test it
  - Search Sequences with Profile HMM
- NGS
  - ChIP-Seq Coverage
  - ChIP-seq Analysis with Cistrome Tools
  - Extract Consensus from Assembly
  - Extract Coverage from Assembly
  - Extract Transcript Sequences
  - Quality Control by FastQC
  - De novo Assemble Illumina PE Reads
  - De novo Assemble Illumina PE and Nanopore Reads
  - De novo Assemble Illumina SE Reads
  - De Novo Assembly and Contigs Classification
  - Parallel NGS Reads Classification
  - Serial NGS Reads Classification
  - RNA-Seq Analysis with TopHat and StringTie
  - RNA-seq Analysis with Tuxedo Tools
  - Variation Annotation with SnpEff
  - Call Variants with SAMtools
  - Variant Calling and Effect Prediction
  - Raw ChIP-Seq Data Processing
  - Raw DNA-Seq Data Processing
  - Raw RNA-Seq Data Processing
  - Get Unmappet Reads
- 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
  - Filter out Short Sequences
  - 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