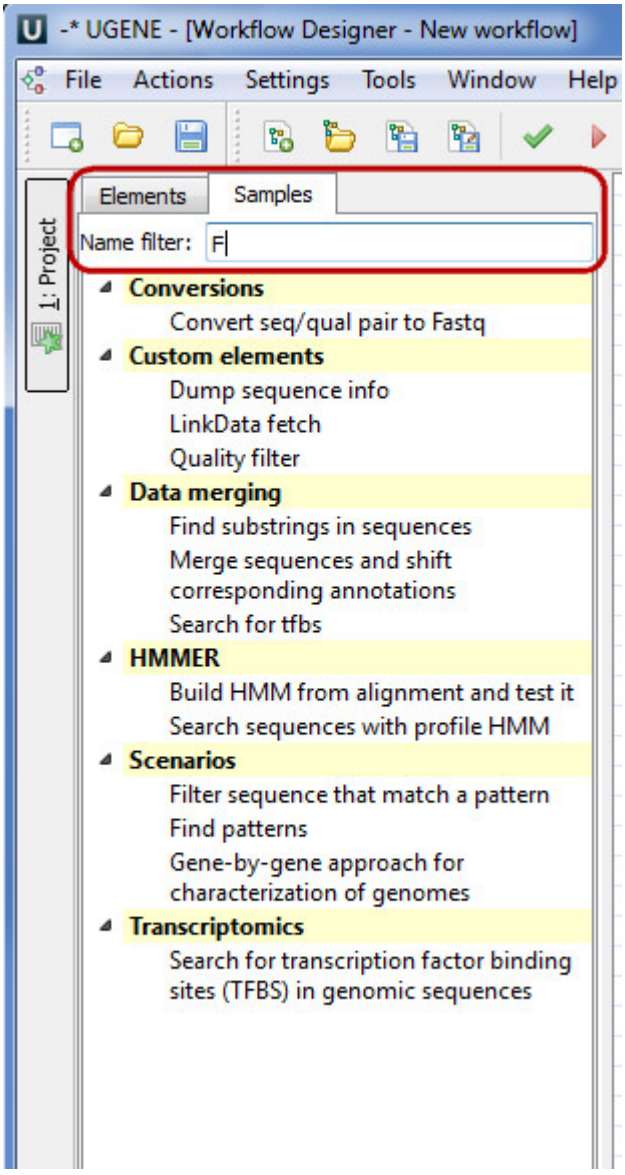
Workflow Samples

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
- 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
  - Call Variants with SAMtools
  - ChIP-seq Analysis with Cistrome Tools
  - Extract Consensus
  - Extract transcript sequences
  - RNA-seq Analysis with Tuxedo Tools
- Scenarios
  - Filter sequence that match a pattern
  - Find patterns
  - Gene-by-gene approach for characterization of genomes
  - Merge sequences and annotations
- Transcriptomics
  - Search for transcription factor binding sites (TFBS) in genomic sequences