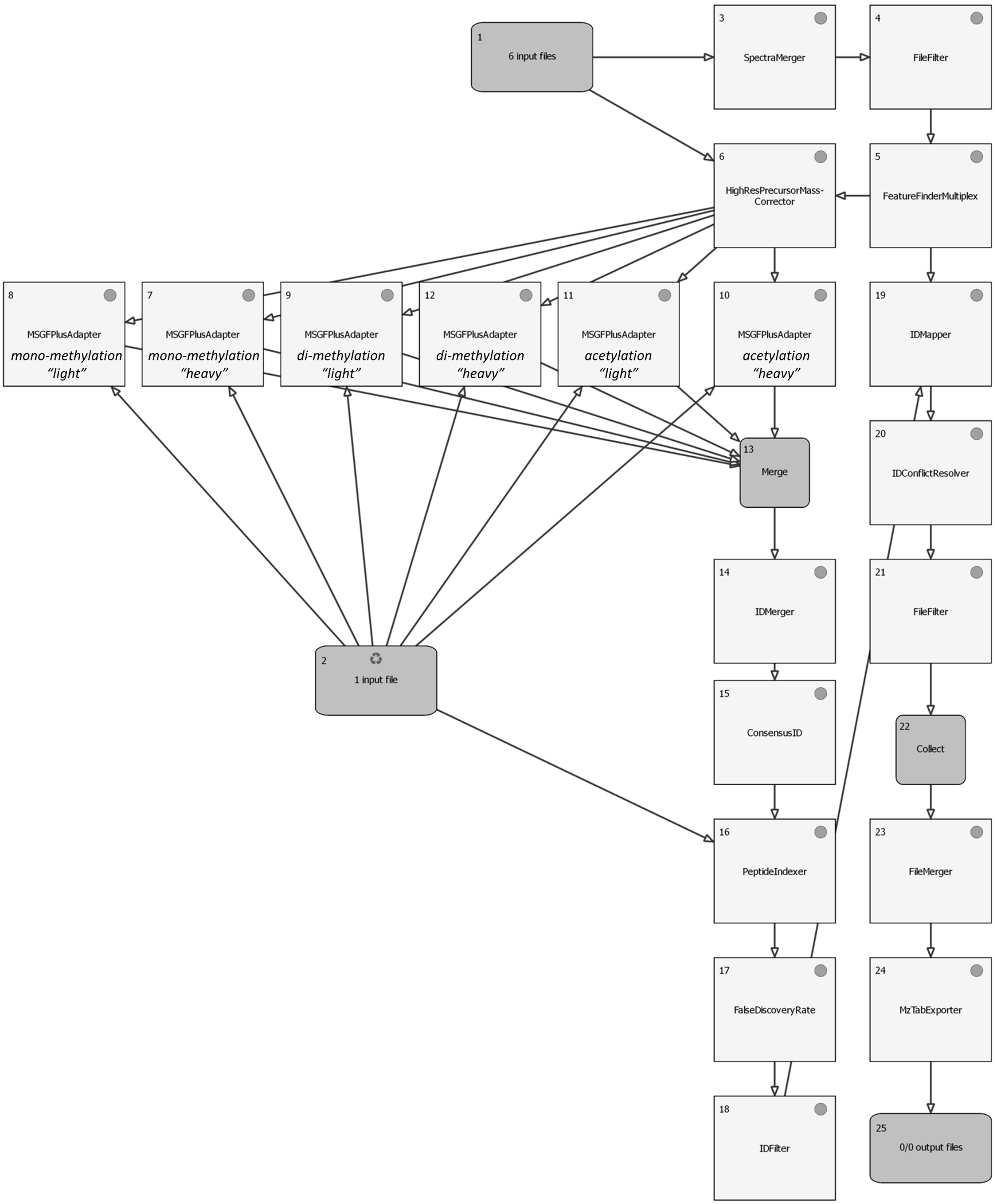
Supplementary Figure 1 (next page): OpenMS workflow for peptide identification and relative quantification. The workflow requires the MS data of six fractions in mzML format (1) and a protein search database (2) as input. In a first step, peptide features are detected and quantified (3-5). After a correction of the precursor masses (6), six MS-GF+ searches each with a different fixed modification (7-12) are performed. The results of the searches are combined and filtered for a 95% confidence level (13-18). The sequence information is mapped to the quantified peptide features (19-21), the fractions combined (22-23) and exported to mzTab (24-25).


1
6 input files
3
SpectraMerger
4
FileFilter
6
HighResPrecursorMass-Corrector
5
FeatureFinderMultiplex
8
MSGFPlusAdapter
mono-methylation
“light”
7
MSGFPlusAdapter
mono-methylation
“heavy”
9
MSGFPlusAdapter
di-methylation
“light”
12
MSGFPlusAdapter
di-methylation
“heavy”
11
MSGFPlusAdapter
acetylation
“light”
10
MSGFPlusAdapter
acetylation
“heavy”
19
IDMapper
13
Merge
20
IDConflictResolver
14
IDMerger
21
FileFilter
2
1 input file
15
ConsensusID
22
Collect
16
PeptideIndexer
23
FileMerger
17
FalseDiscoveryRate
24
MzTabExporter
18
IDFilter
25
0/0 output files