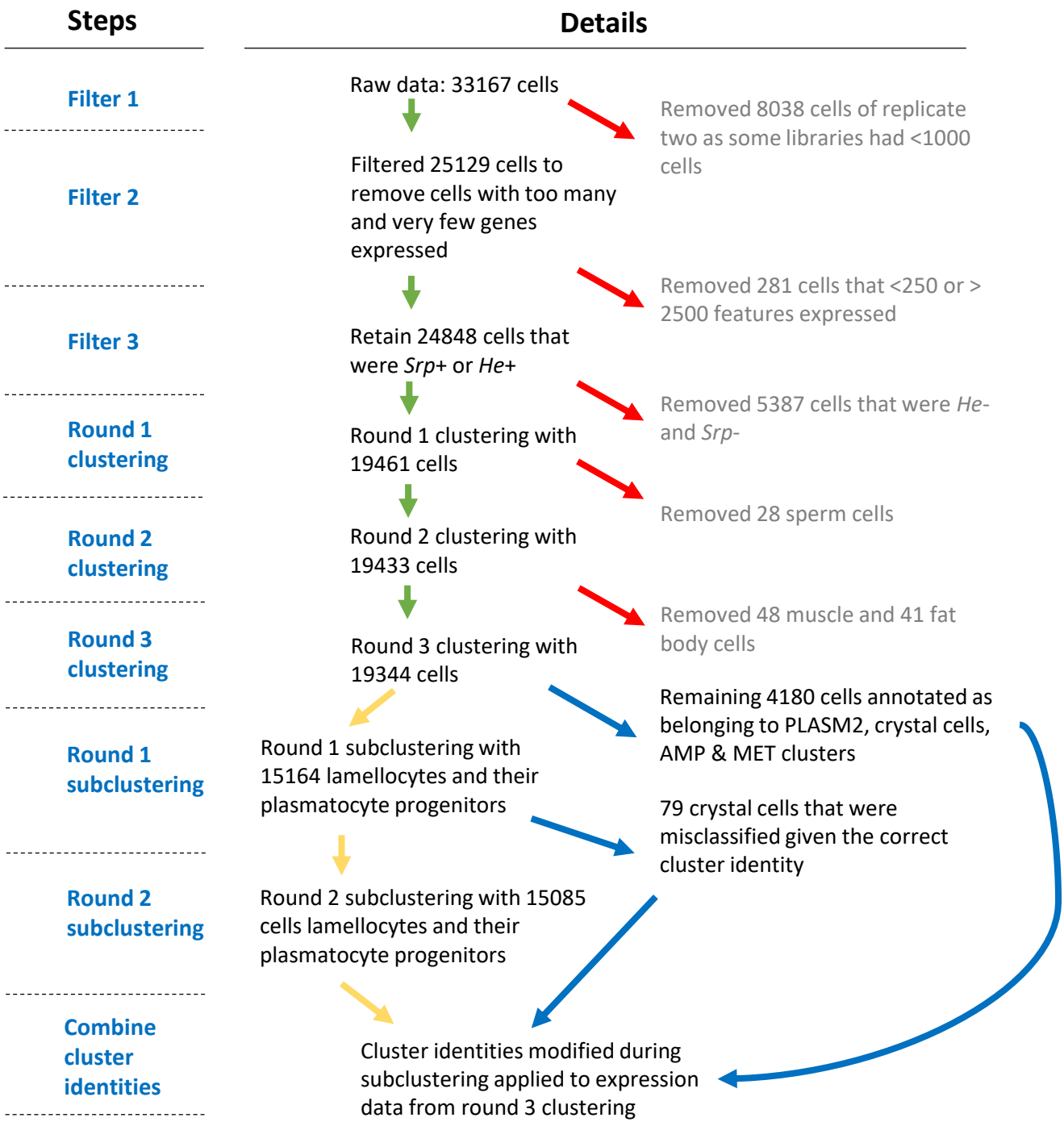
Steps
Details
Filter 1
Raw data: 33167 cells
Removed 8038 cells of replicate two as some libraries had <1000 cells
Filter 2
Filtered 25129 cells to remove cells with too many and very few genes expressed
Removed 281 cells that <250 or > 2500 features expressed
Filter 3
Retain 24848 cells that were *Srp*+ or *He*+
Removed 5387 cells that were *He*- and *Srp*-
Round 1 clustering
Round 1 clustering with 19461 cells
Removed 28 sperm cells
Round 2 clustering
Round 2 clustering with 19433 cells
Removed 48 muscle and 41 fat body cells
Round 3 clustering
Round 3 clustering with 19344 cells
Remaining 4180 cells annotated as belonging to PLASM2, crystal cells, AMP & MET clusters
Round 1 subclustering
Round 1 subclustering with 15164 lamellocytes and their plasmatocyte progenitors
79 crystal cells that were misclassified given the correct cluster identity
Round 2 subclustering
Round 2 subclustering with 15085 cells lamellocytes and their plasmatocyte progenitors
Combine cluster identities
Cluster identities modified during subclustering applied to expression data from round 3 clustering