Put all 16-mers from SBW25 that occur more often than the most abundant 16-mer in Pf0-1 into list X.

Pick the most abundant 16-mer from list X and search it against the genome of SBW25.

All occurrences plus 20bp of flanking DNA are concatenated, separated by a ‘|’

Search all 16-mers from list X against the concatenated string.

Remove all 16-mers that were found from list X and put them in a new group.

Is list X empty?

Yes

Terminate the program.

No