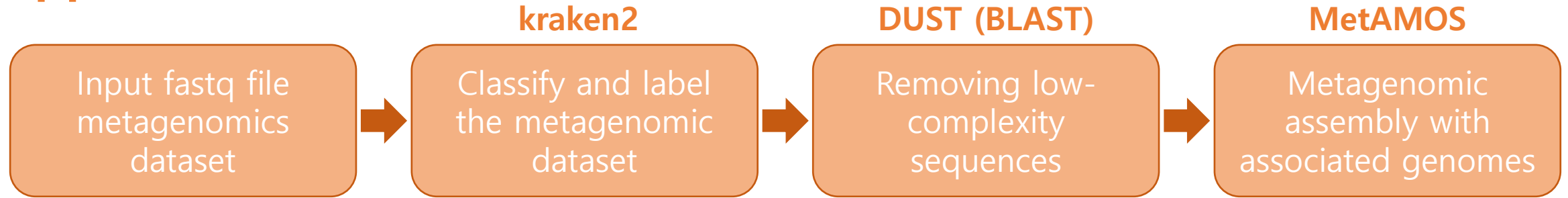
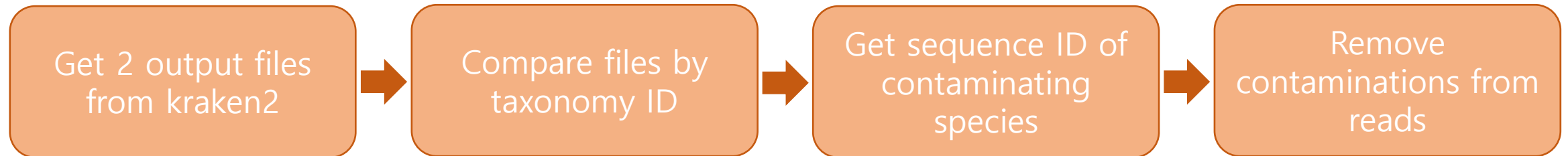


Approach 1



Approach 2



1. **Standard output file** contains taxonomy ID and sequence ID
2. **Report file** contains taxonomy ID and information about species