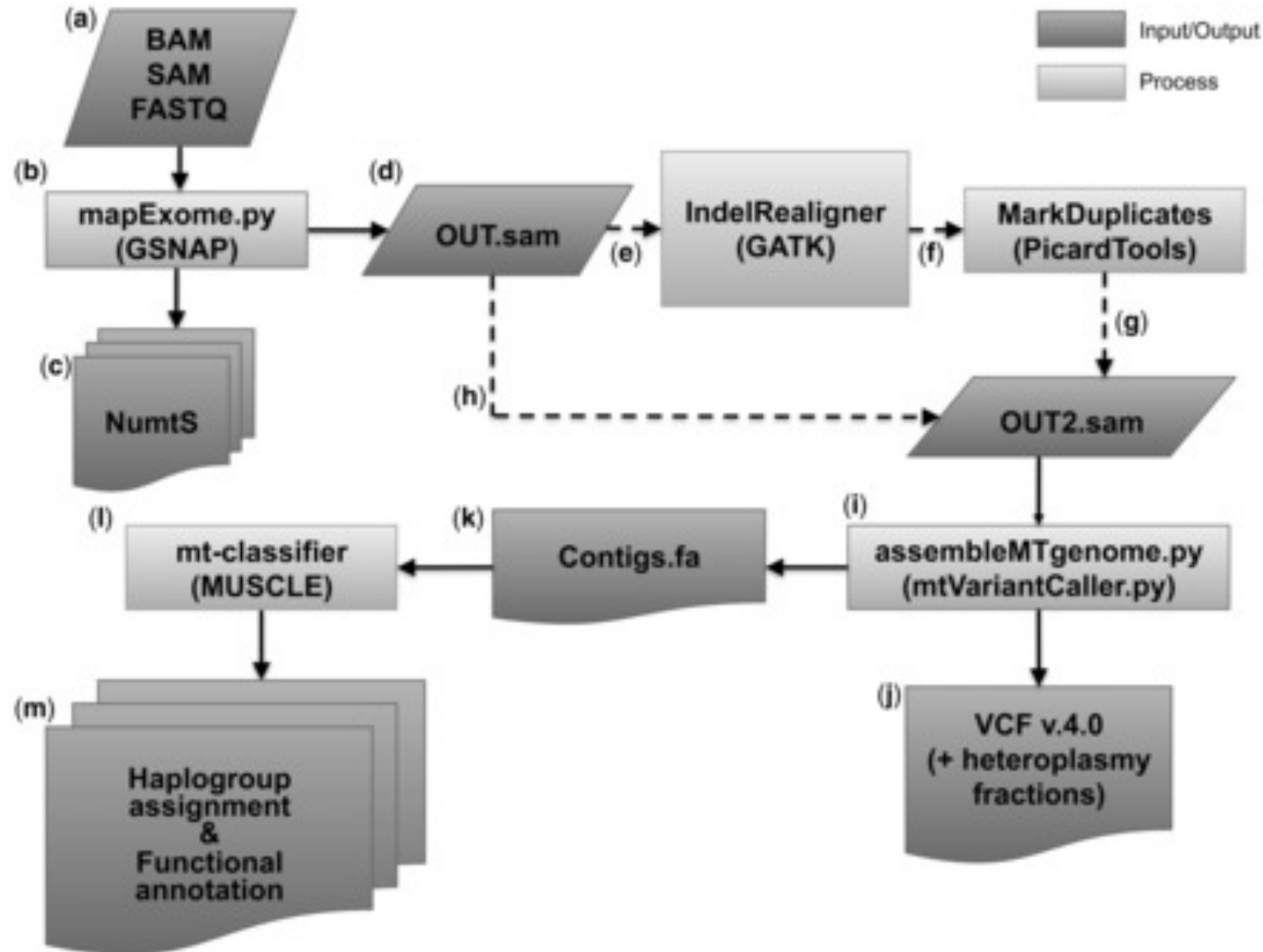


MToolBox workflow



(a–d) read mapping and NumtS filtering;

(e–h) post-mapping processing;

(i–m) genome assembly, haplogroup prediction and variant annotation.

(h) In brackets, programs or modules particularly important for the associated process. Solid connectors indicate mandatory pipeline steps; dashed connectors (e–g) indicate that the corresponding post-mapping steps can be optional, otherwise the OUT2.sam file directly undergoes the assembly process (h).

