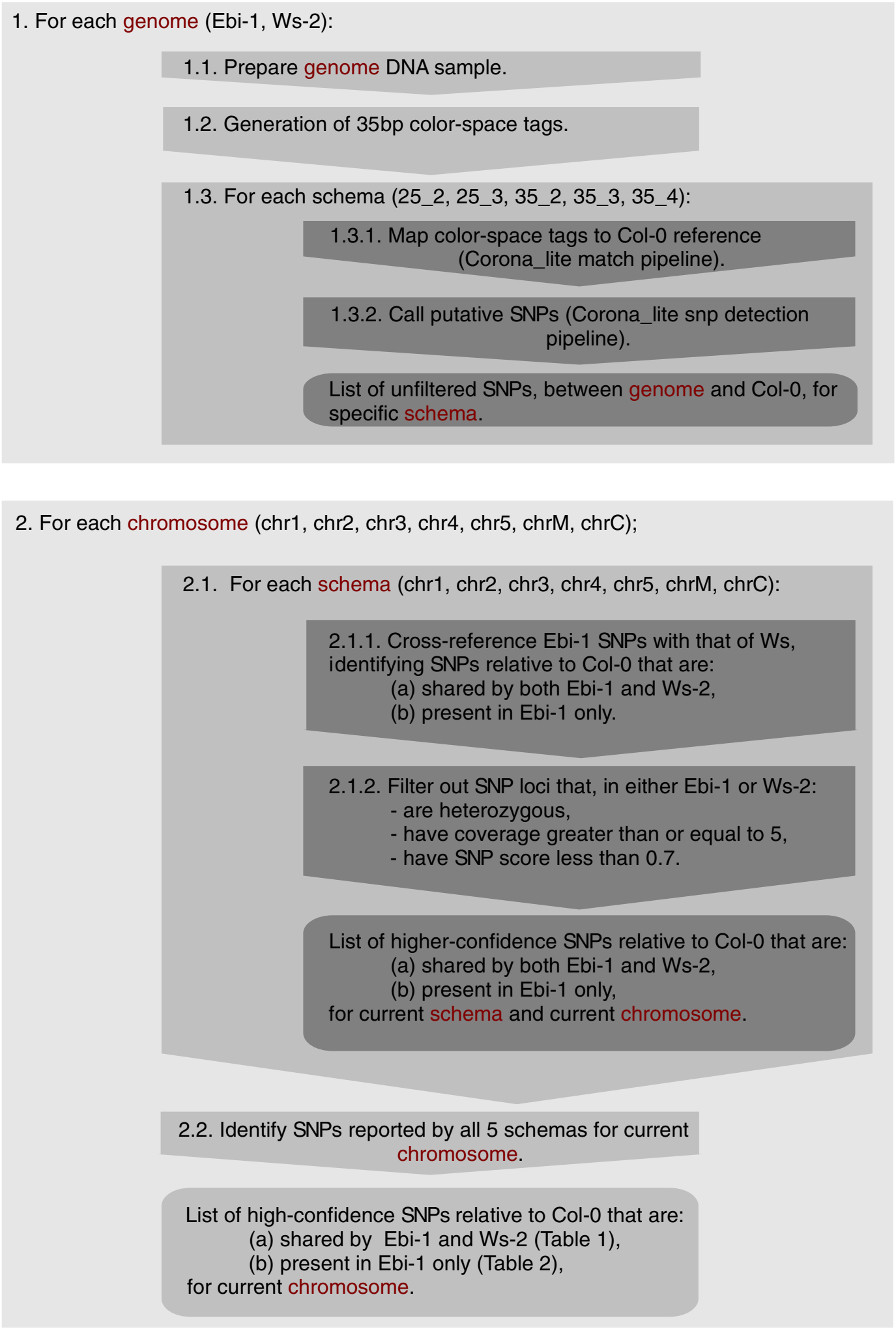
1. For each genome (Ebi-1, Ws-2):
1.1. Prepare genome DNA sample.
1.2. Generation of 35bp color-space tags.
1.3. For each schema (25_2, 25_3, 35_2, 35_3, 35_4):
1.3.1. Map color-space tags to Col-0 reference (Corona_lite match pipeline).
1.3.2. Call putative SNPs (Corona_lite snp detection pipeline).
List of unfiltered SNPs, between genome and Col-0, for specific schema.
2. For each chromosome (chr1, chr2, chr3, chr4, chr5, chrM, chrC);
2.1. For each schema (chr1, chr2, chr3, chr4, chr5, chrM, chrC):
2.1.1. Cross-reference Ebi-1 SNPs with that of Ws, identifying SNPs relative to Col-0 that are:
(a) shared by both Ebi-1 and Ws-2,
(b) present in Ebi-1 only.
2.1.2. Filter out SNP loci that, in either Ebi-1 or Ws-2:
- are heterozygous,
- have coverage greater than or equal to 5,
- have SNP score less than 0.7.
List of higher-confidence SNPs relative to Col-0 that are:
(a) shared by both Ebi-1 and Ws-2,
(b) present in Ebi-1 only,
for current schema and current chromosome.
2.2. Identify SNPs reported by all 5 schemas for current chromosome.
List of high-confidence SNPs relative to Col-0 that are:
(a) shared by Ebi-1 and Ws-2 (Table 1),
(b) present in Ebi-1 only (Table 2),
for current chromosome.