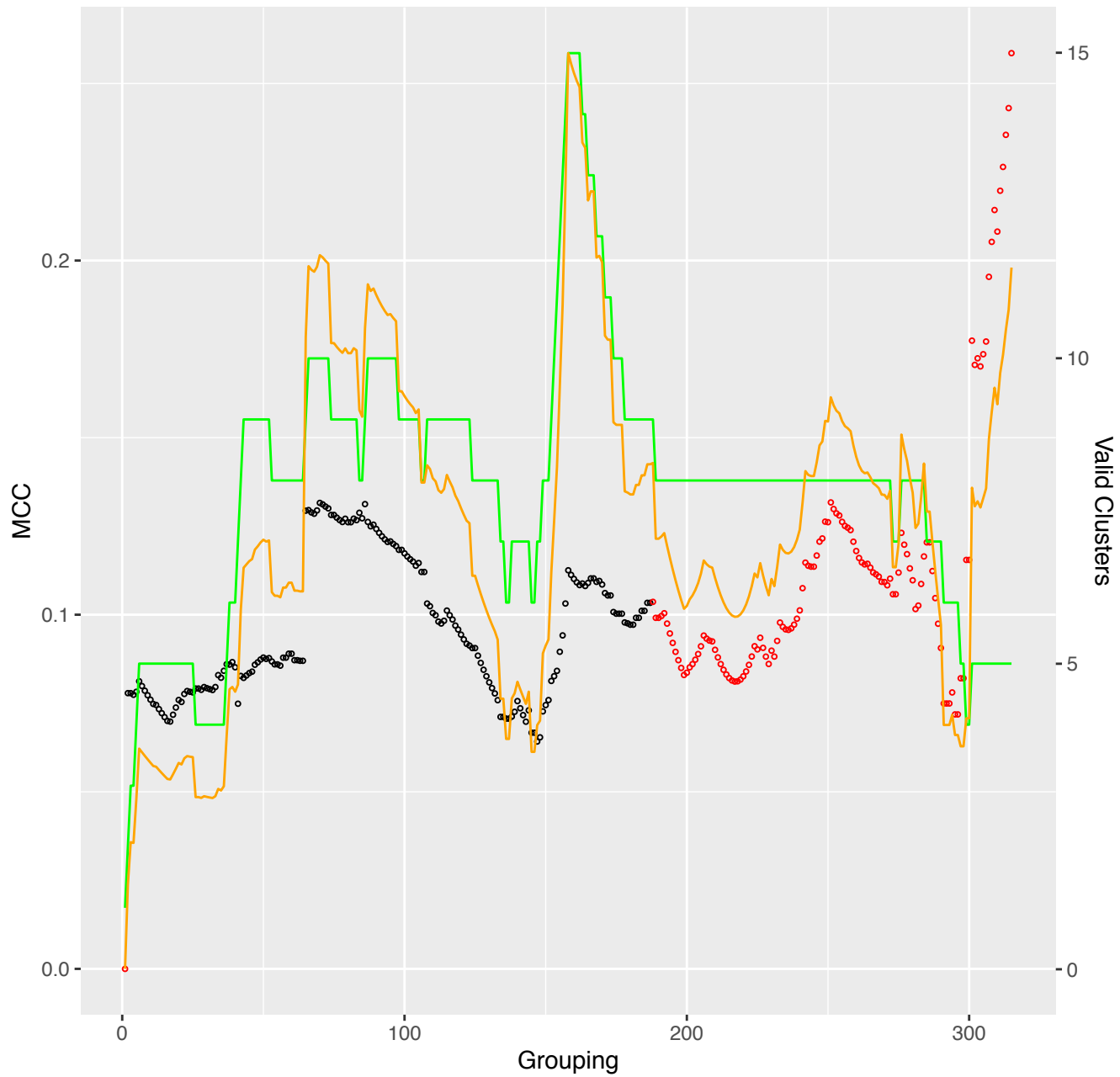


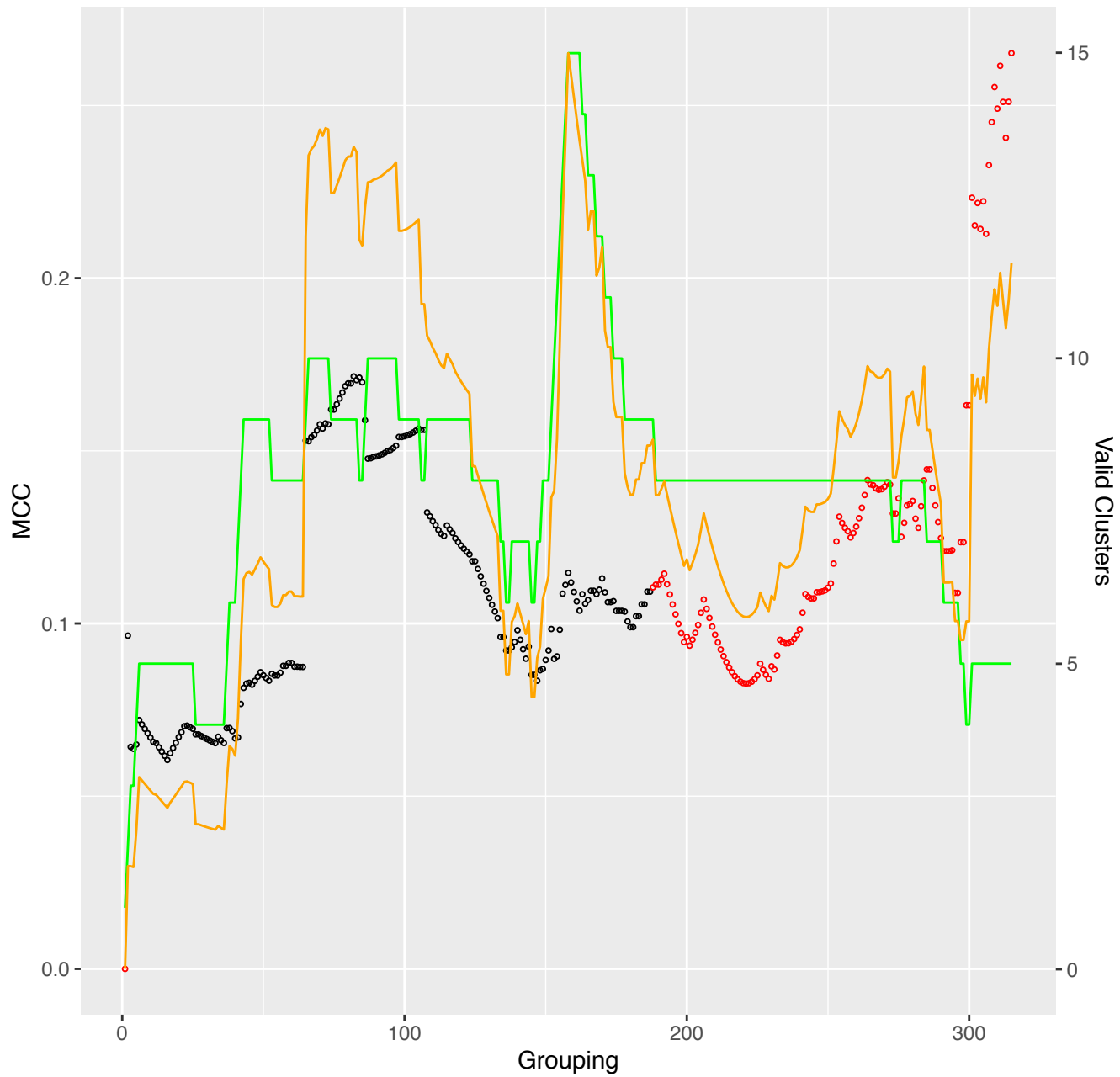
Supplementary Figure 6

Optimal grouping selection. Grouping statistics per gene. The dots represent the MCC value for each grouping; the black dots represent groupings for which the isolates inside valid clusters are above 50% of the total number of isolates for the gene, the red dots represent the ones that do not meet this criterion. The green line represents the number of valid clusters in each grouping (*i.e.* clusters formed by at least 3 isolates). The orange line represents the Clustering per Geography Score (CGS) given by the MCC value multiplied for the number of valid clusters. The grouping with the maximum point reached by the orange line where the isolates in valid clusters is more than 50% of the total (black dots), indicates the optimum grouping for the gene. A second grouping was chosen as the one with the maximum MCC score within those including at least 50% of the isolates in valid clusters (*i.e.* higher black dot).

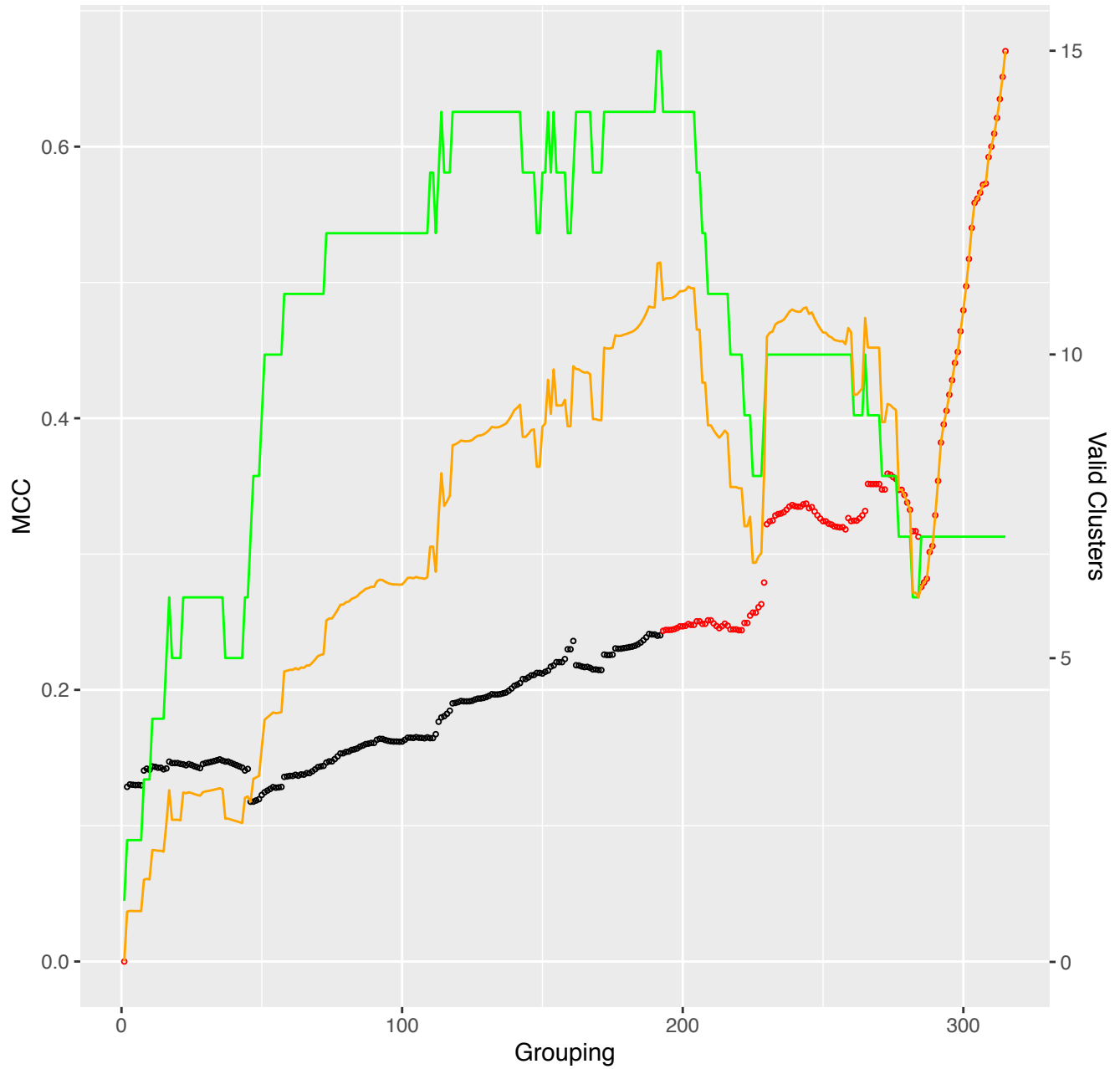
BDLF4 : grouping per country



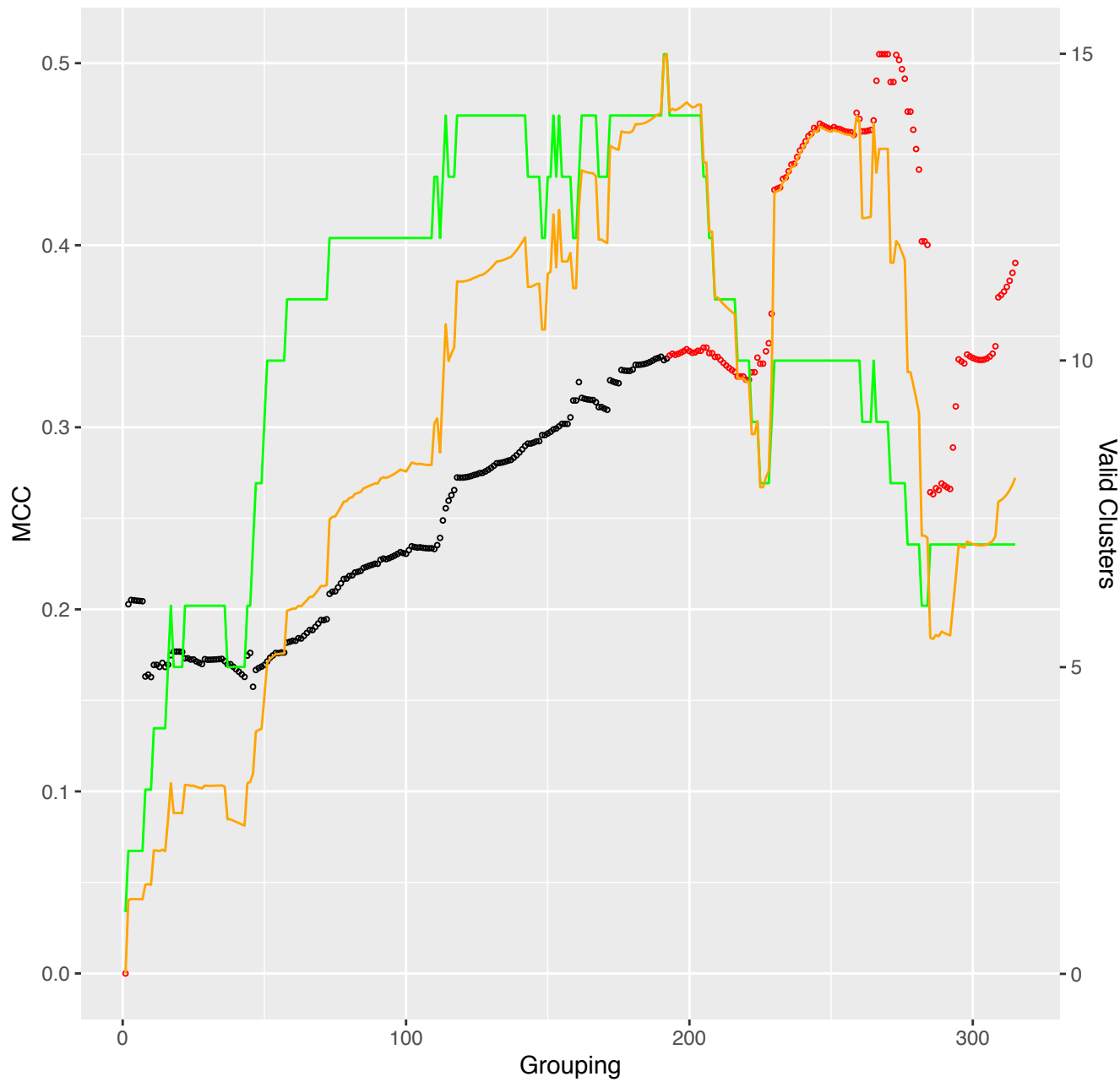
BDLF4 : grouping per continent



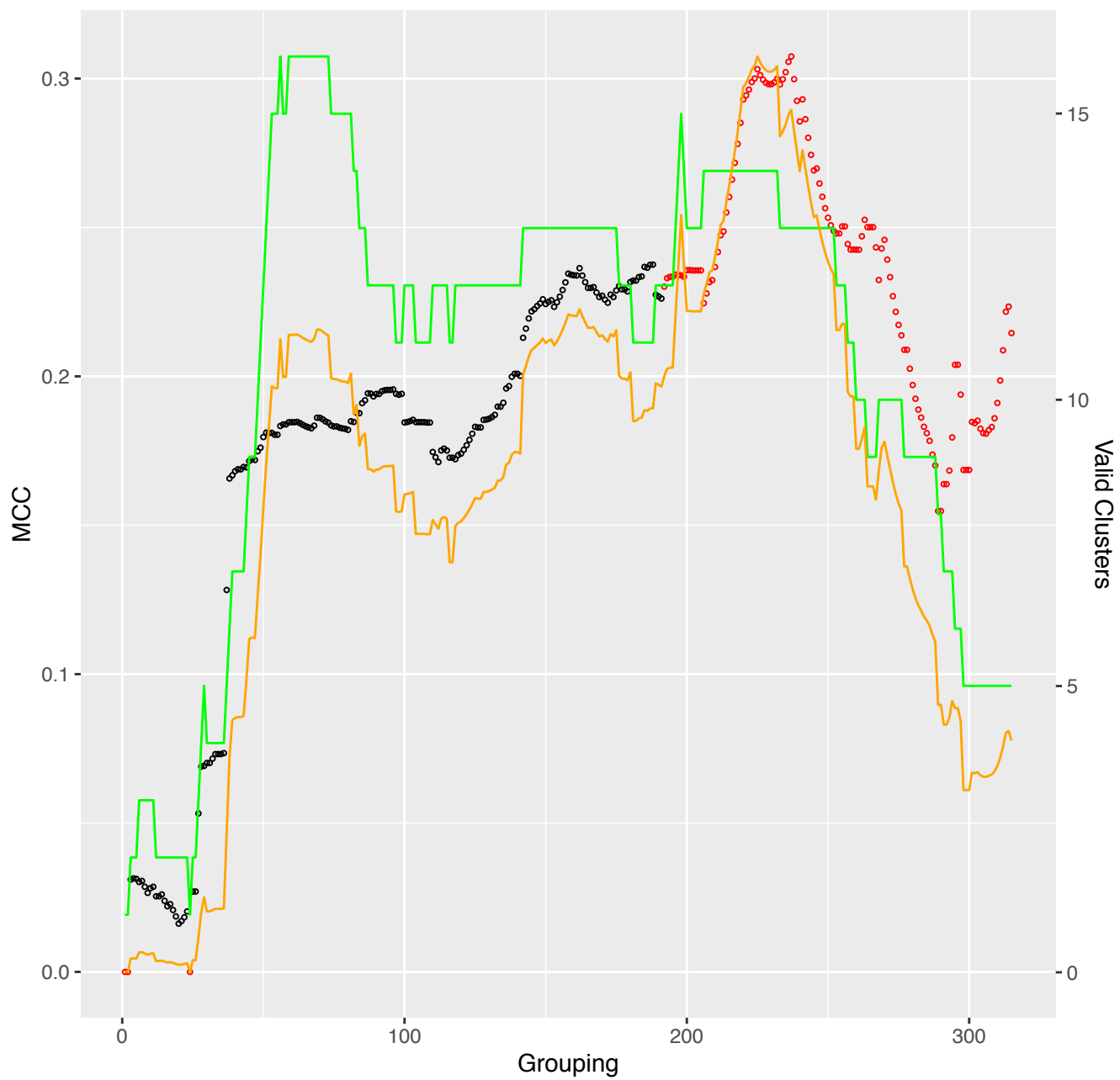
BGLF4 : grouping per country



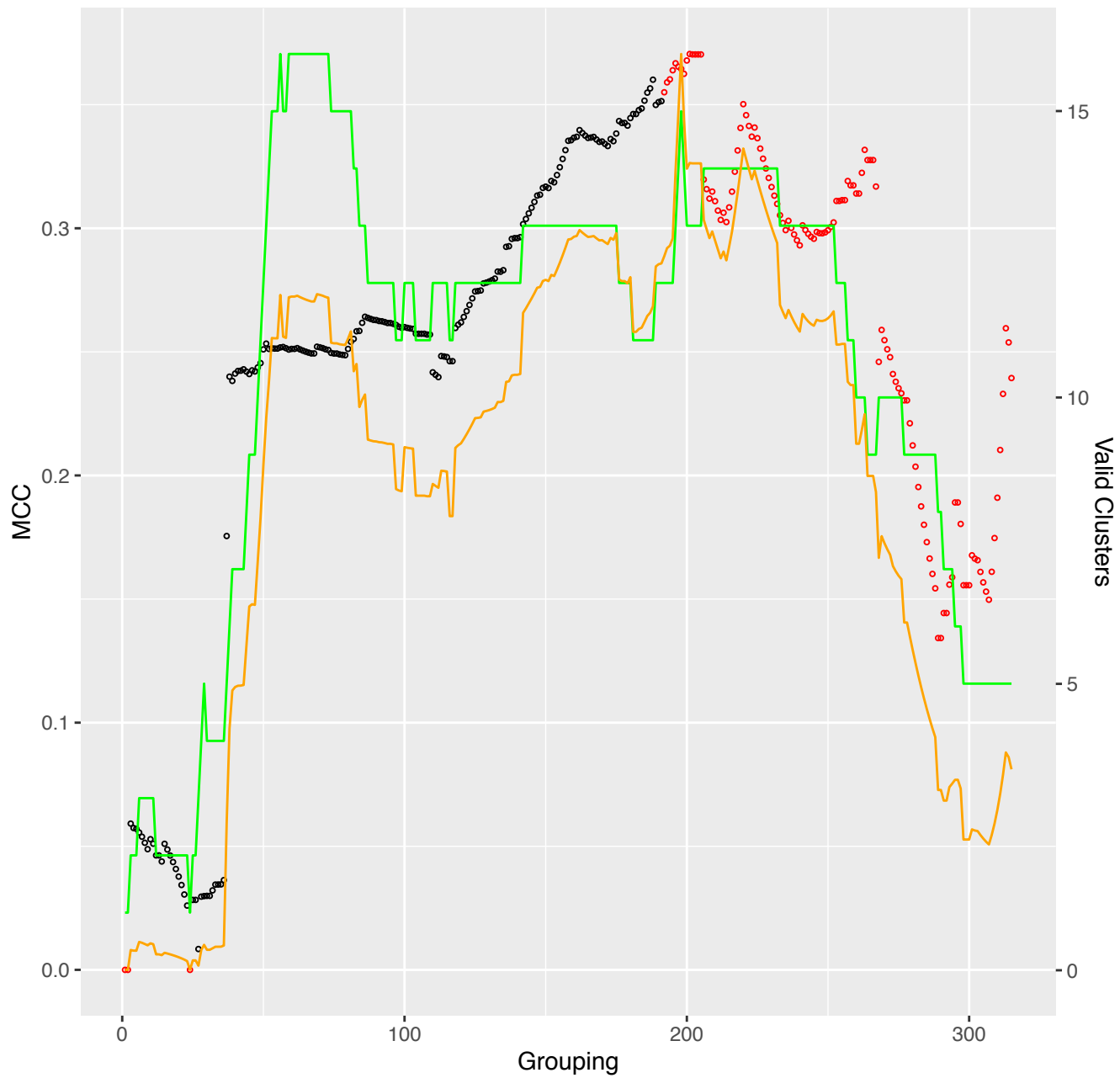
BGLF4 : grouping per continent



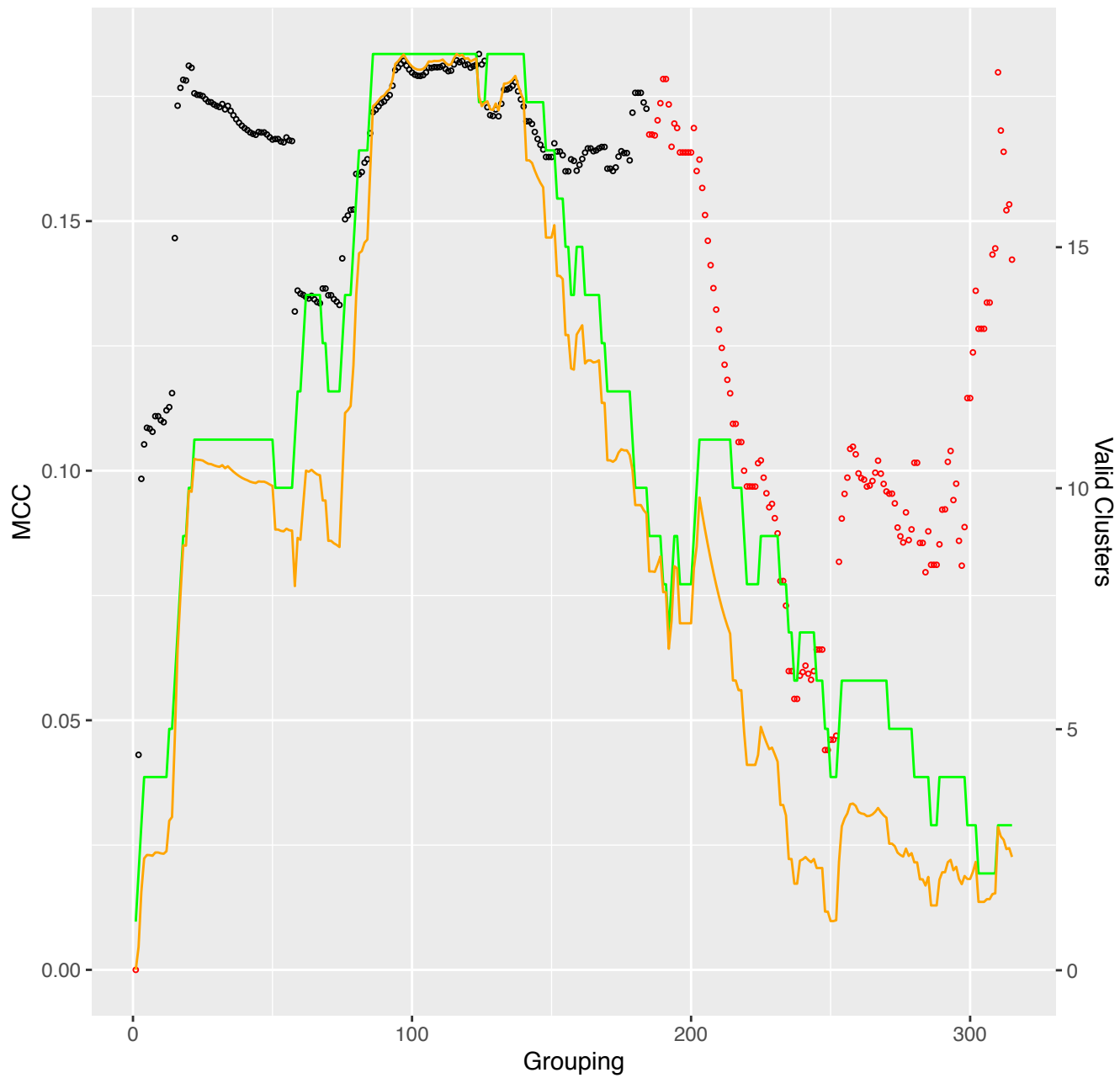
BHRF1 : grouping per country



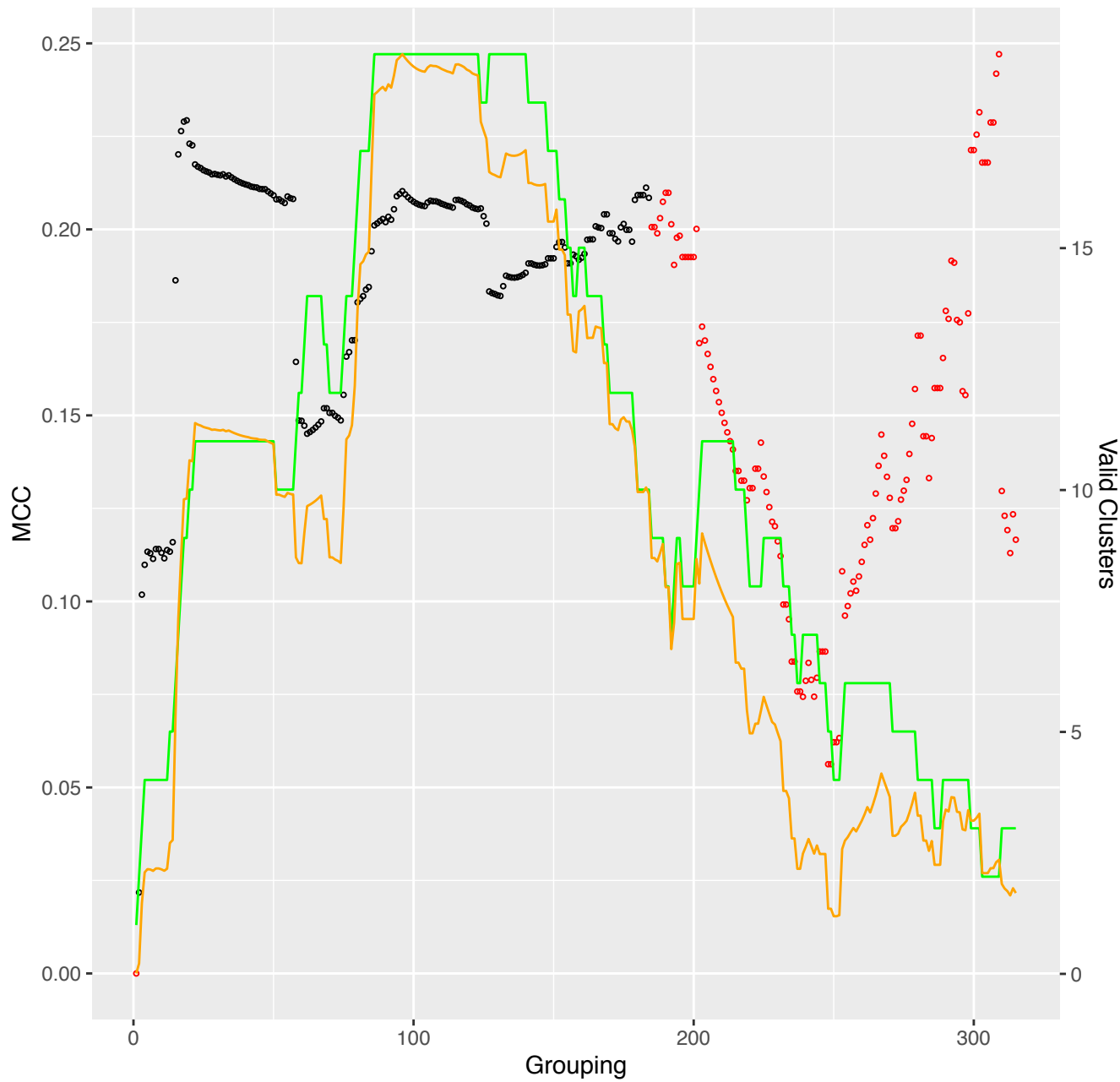
BHRF1 : grouping per continent



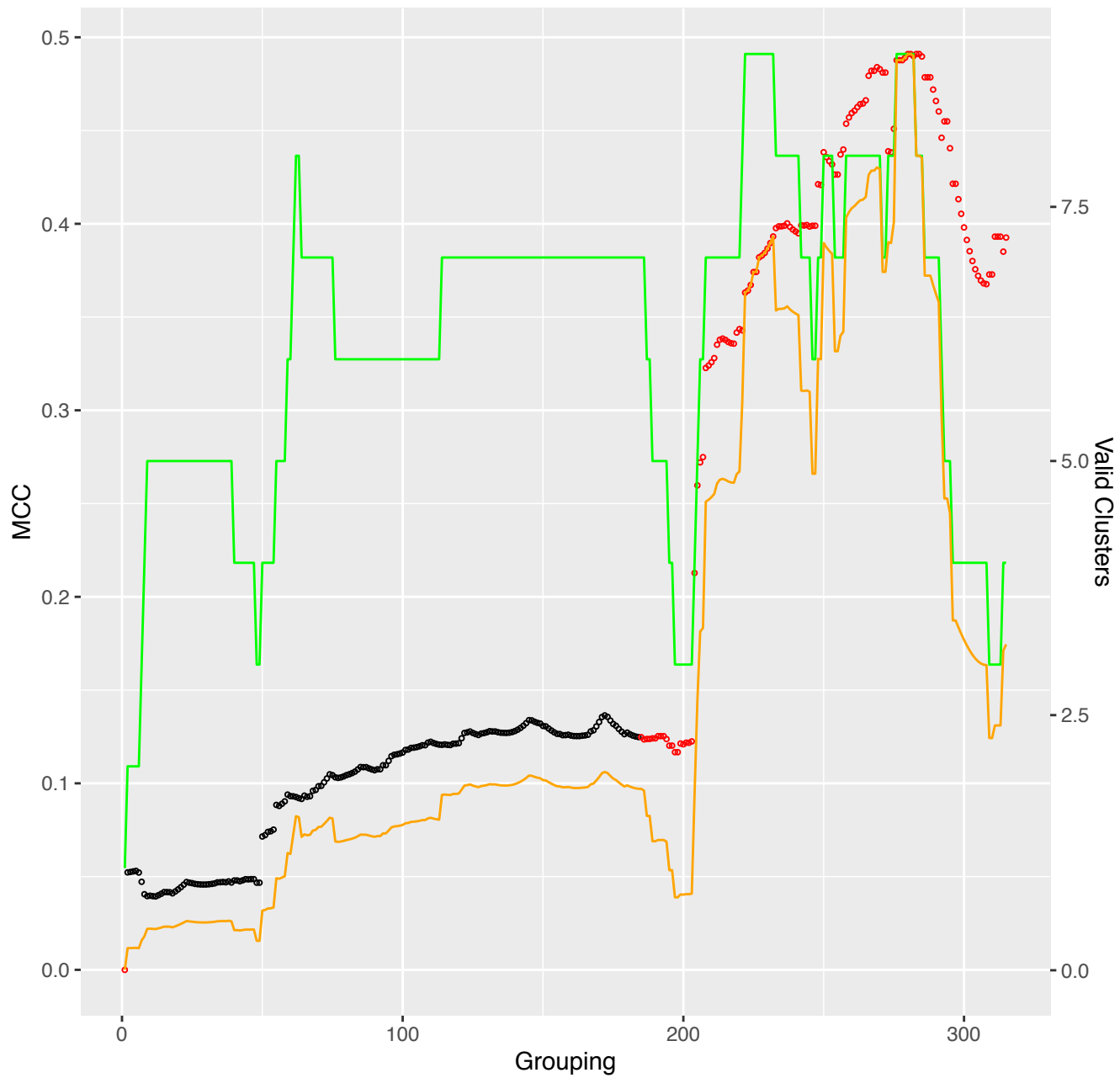
BRLF1 : grouping per country



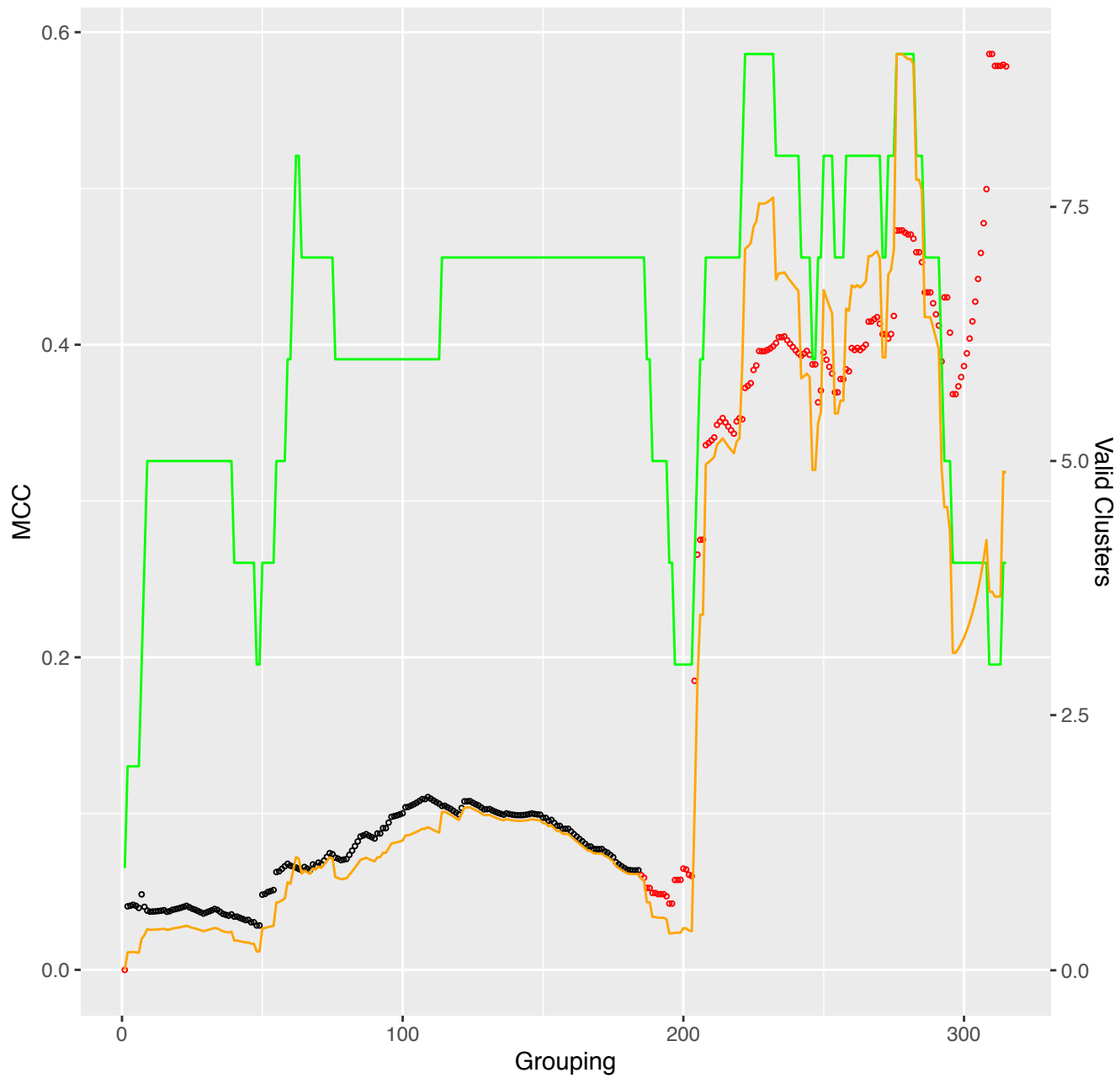
BRLF1 : grouping per continent



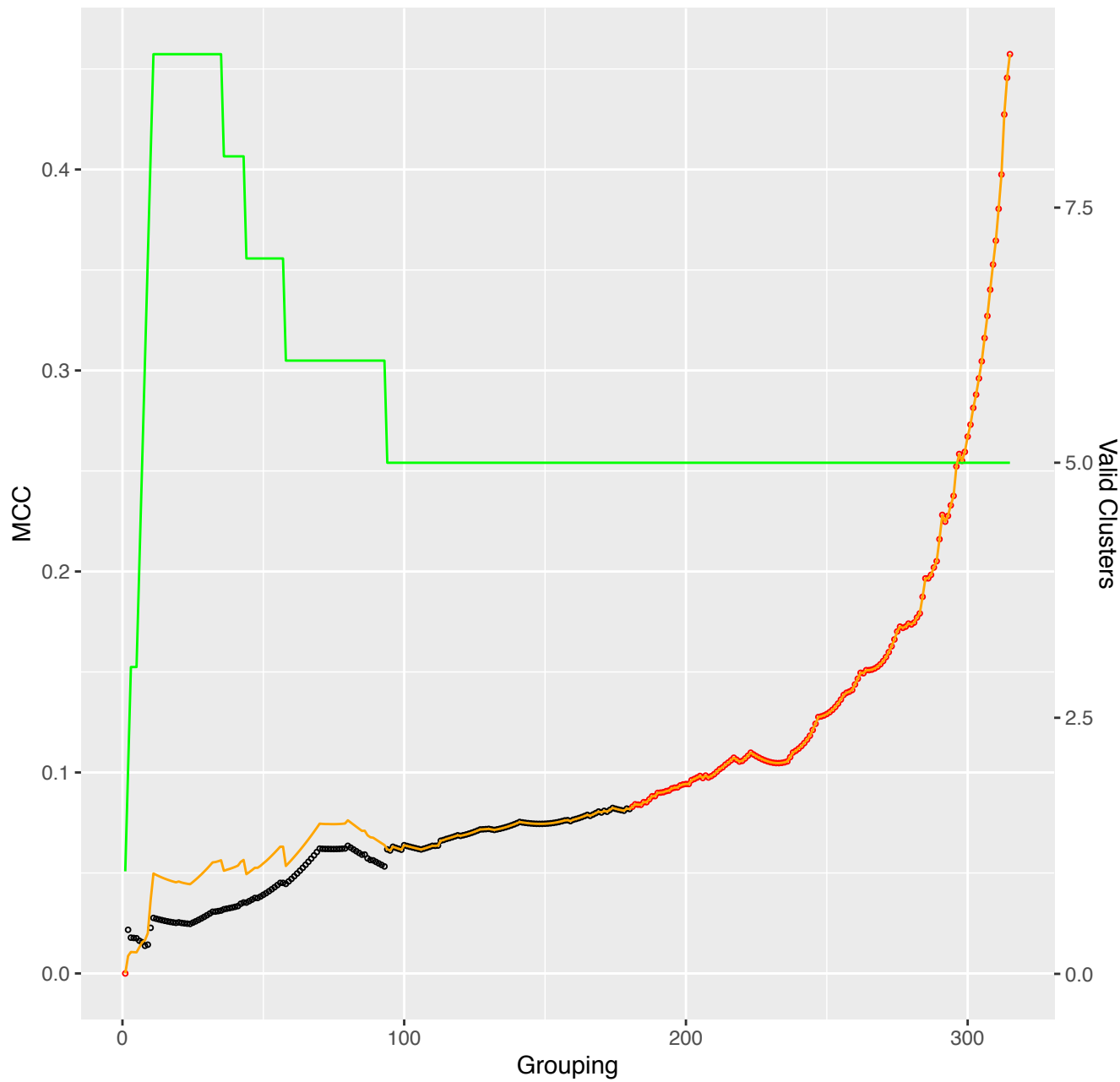
BZLF1 : grouping per country



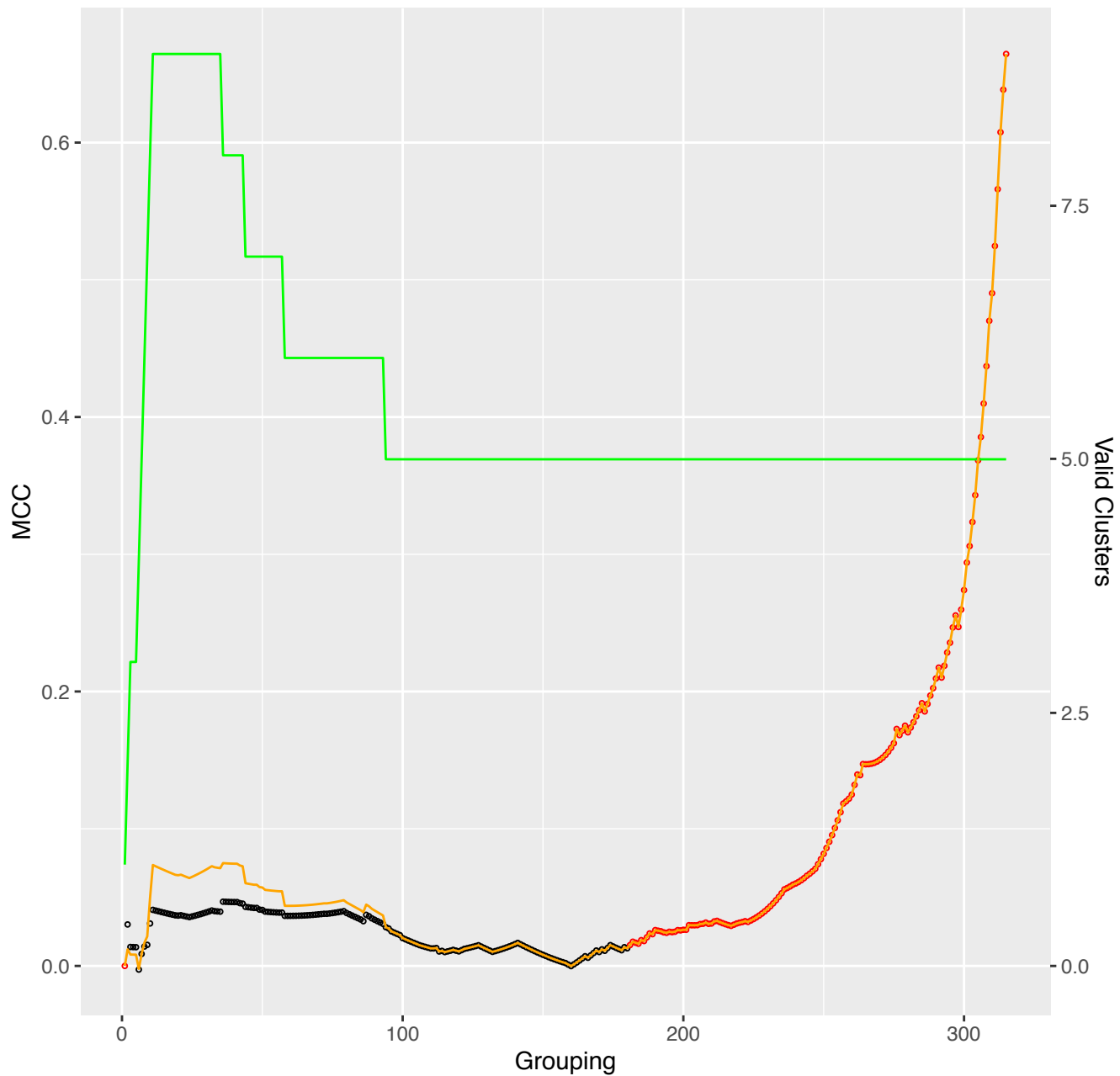
BZLF1 : grouping per continent



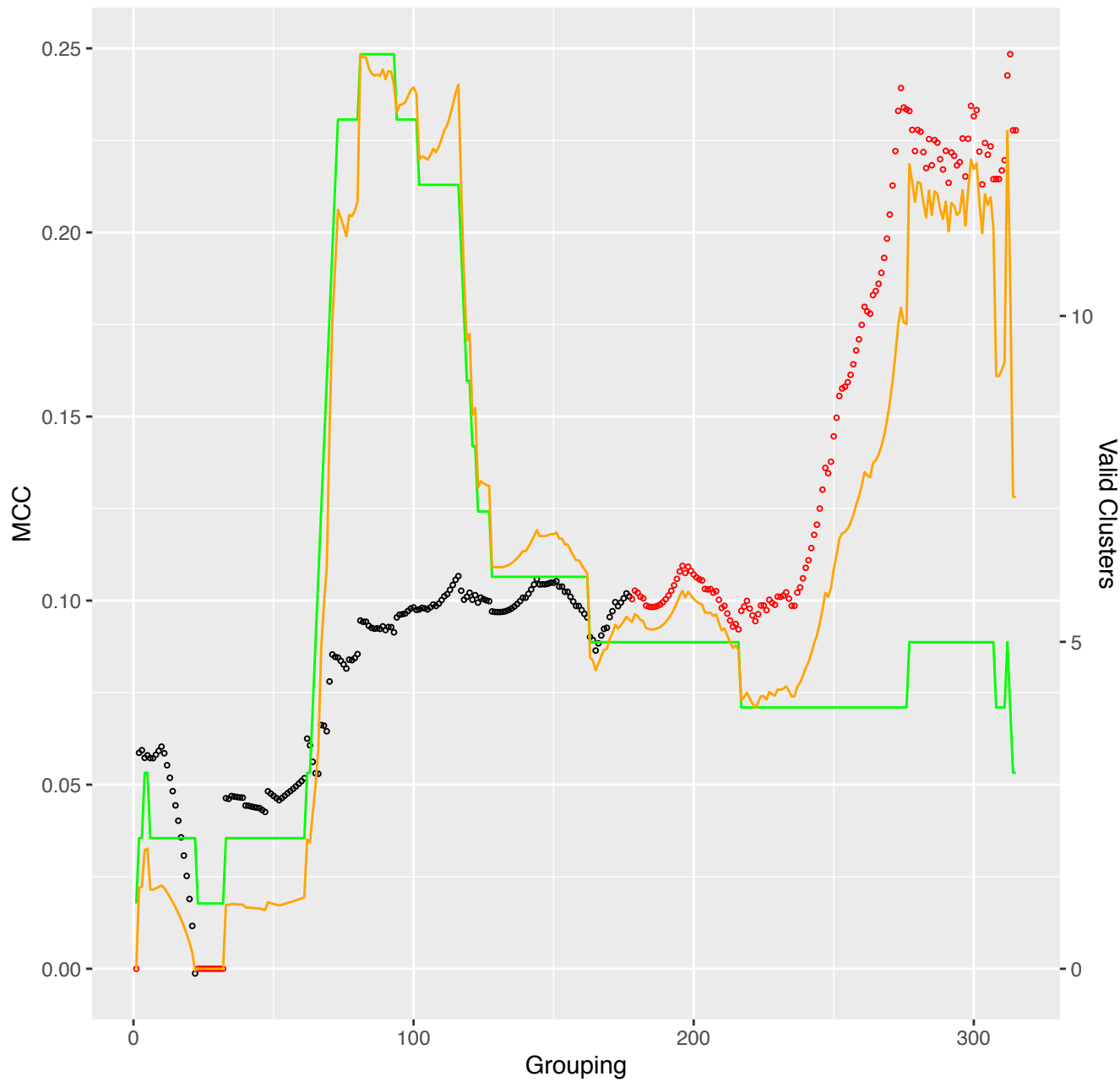
EBER-1 : grouping per country



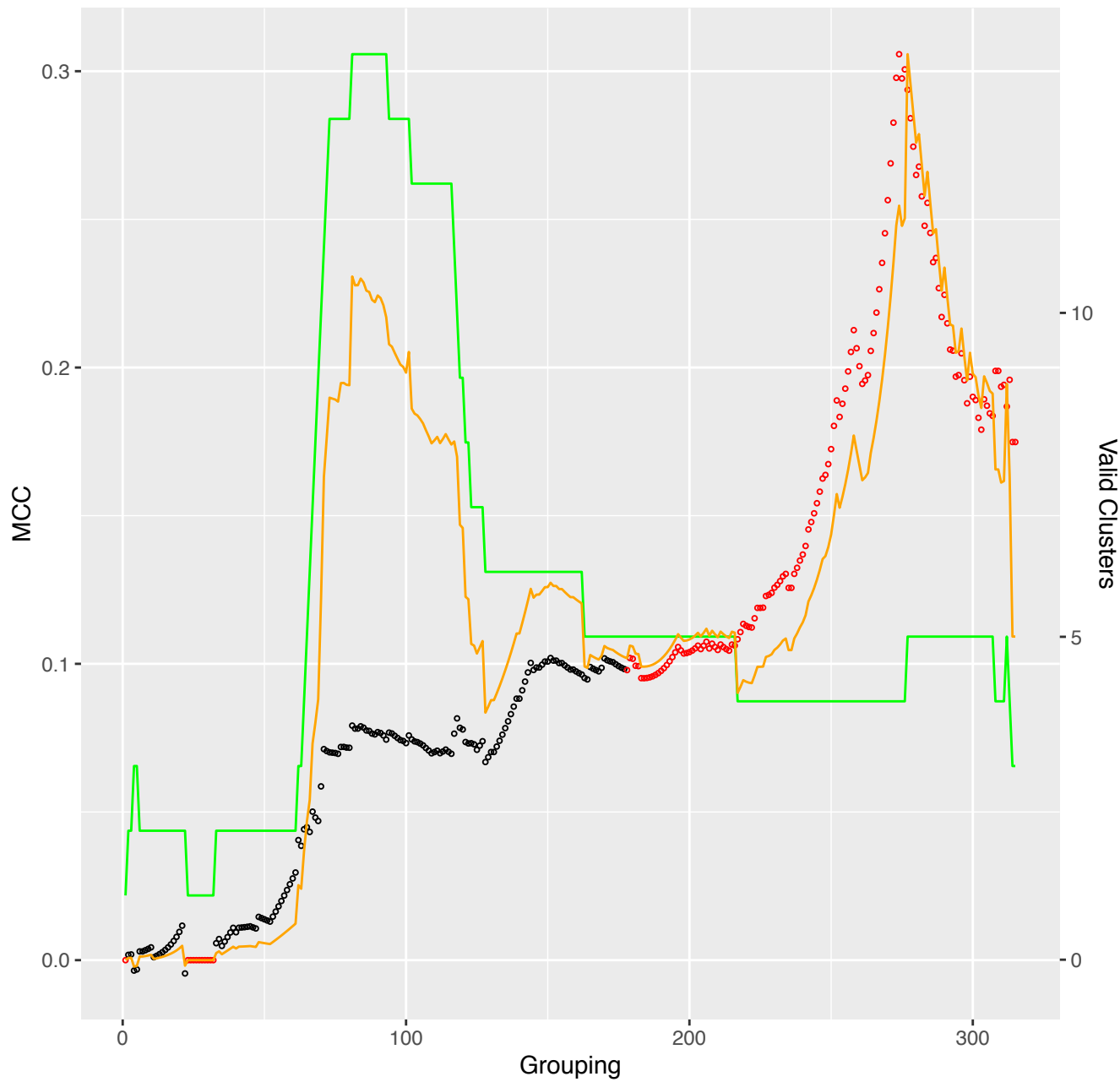
EBER-1 : grouping per continent



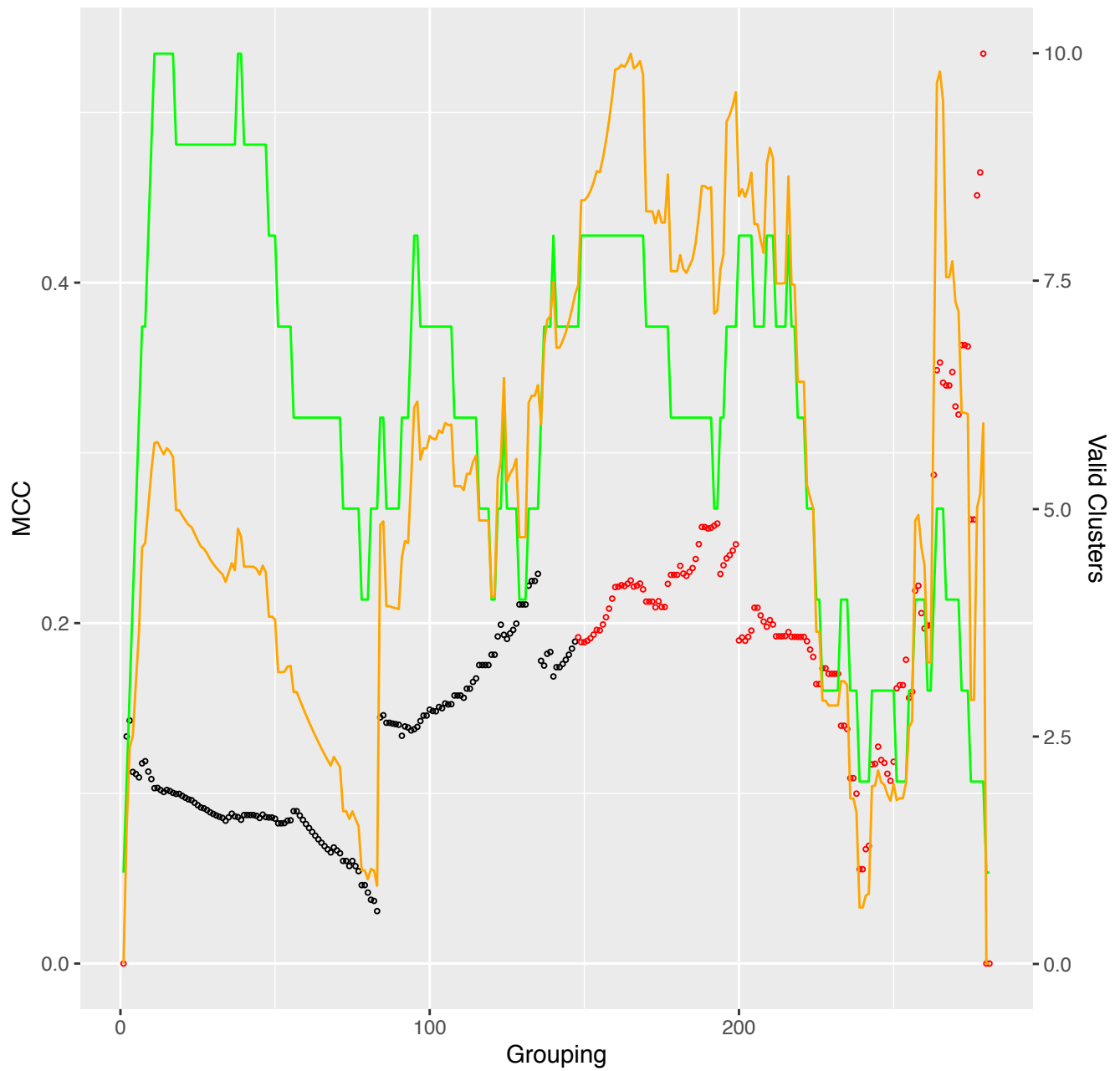
EBER-2 : grouping per country



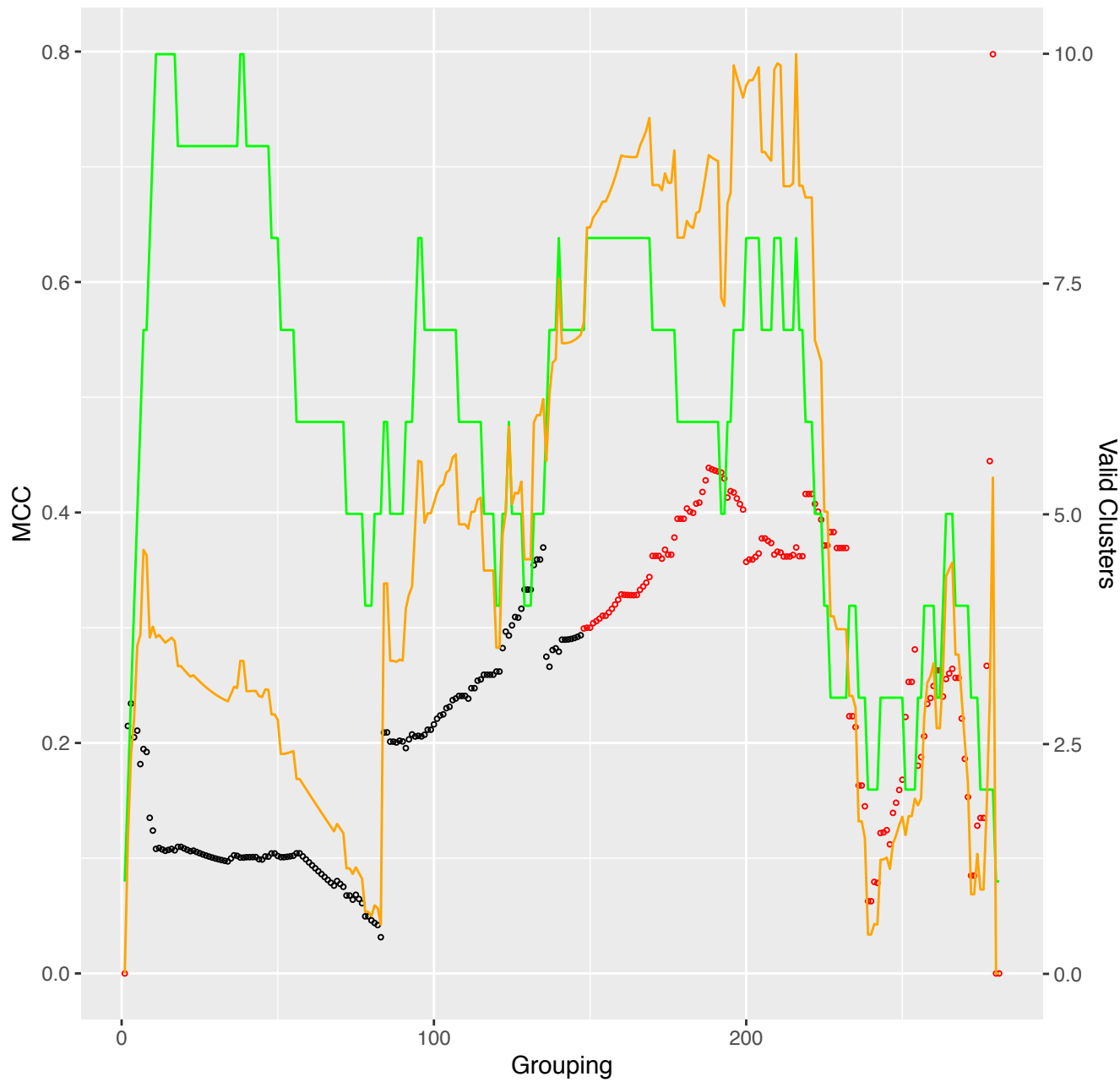
EBER-2 : grouping per continent



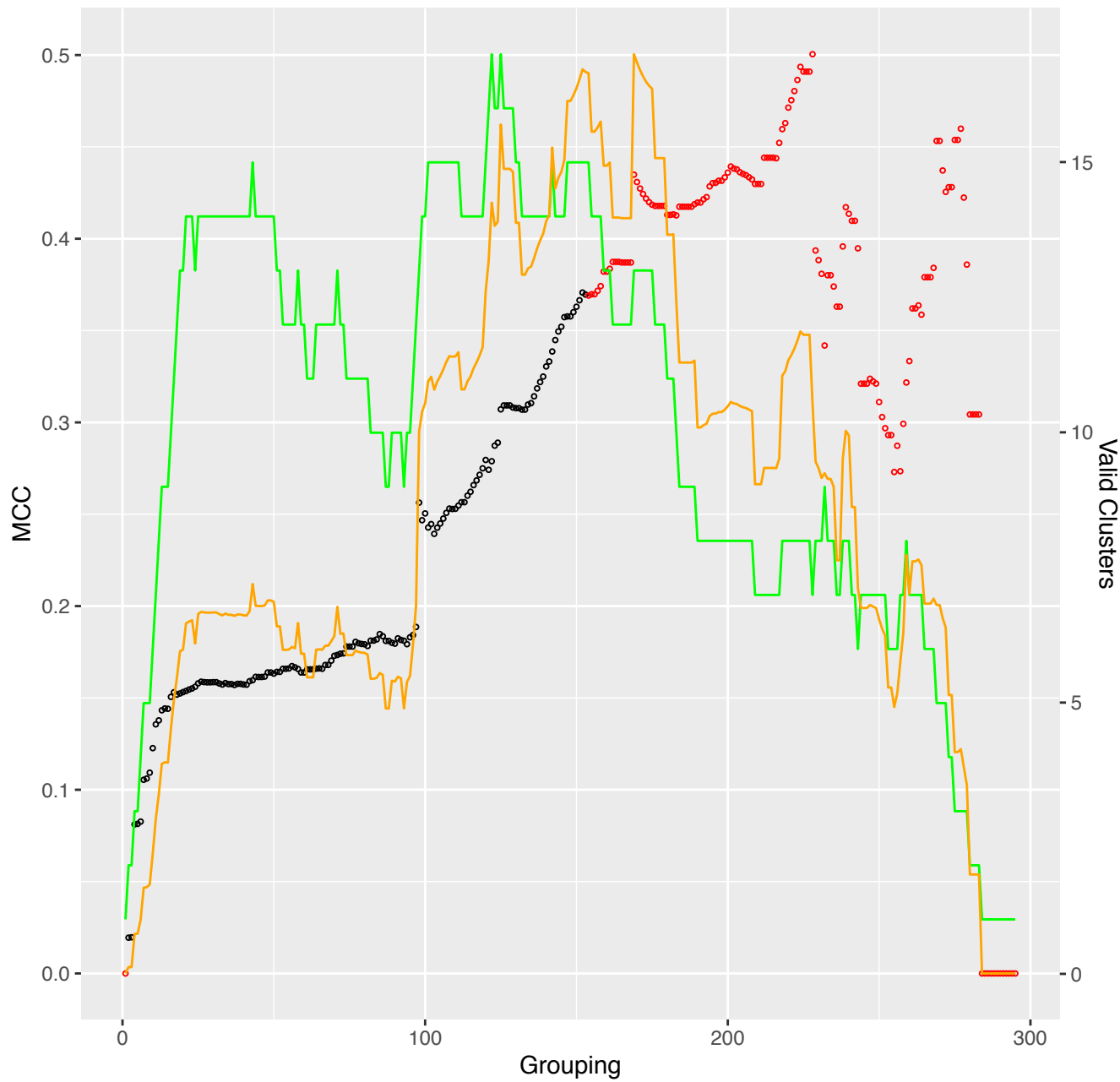
EBNA-1 : grouping per country



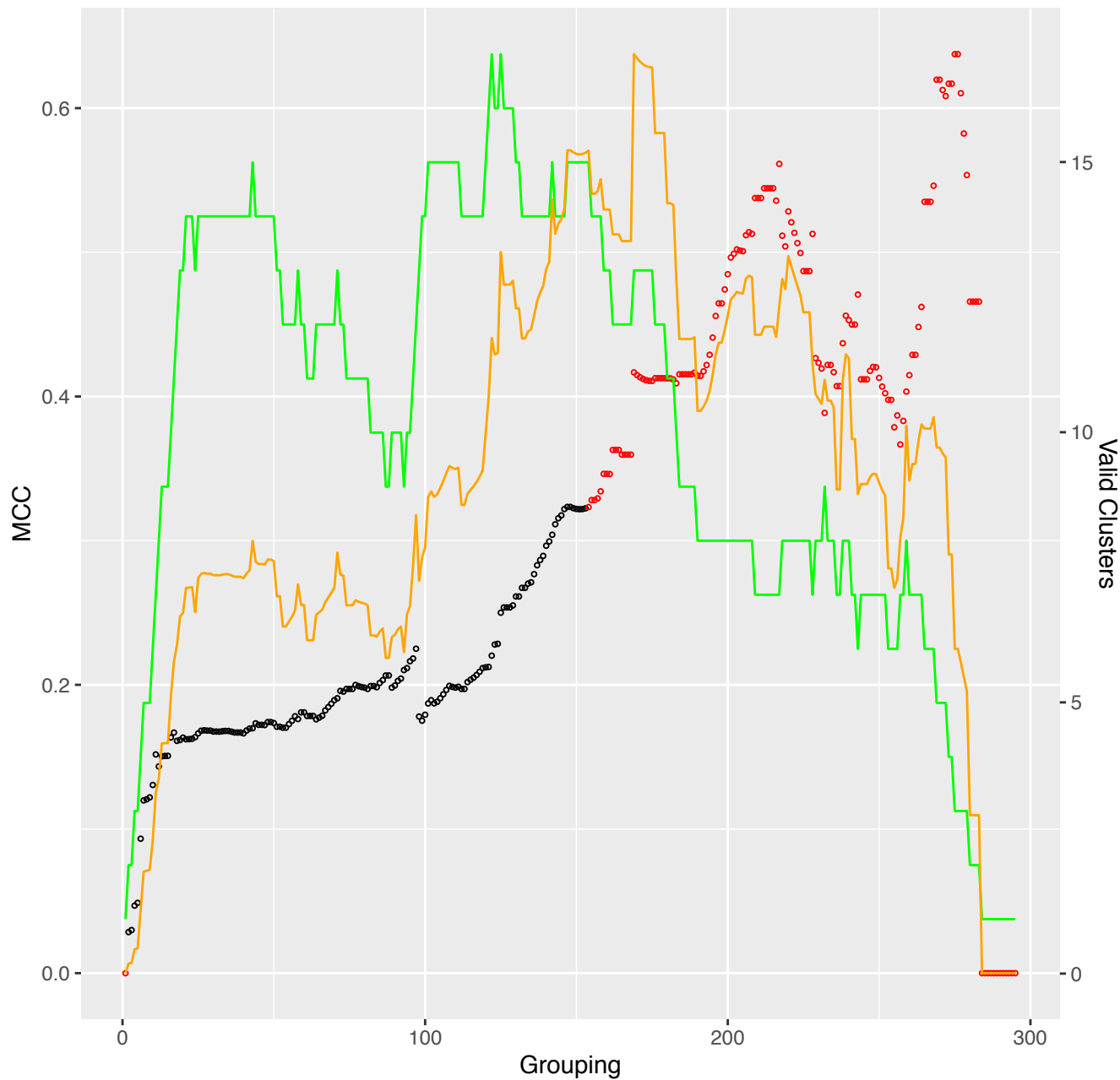
EBNA-1 : grouping per continent



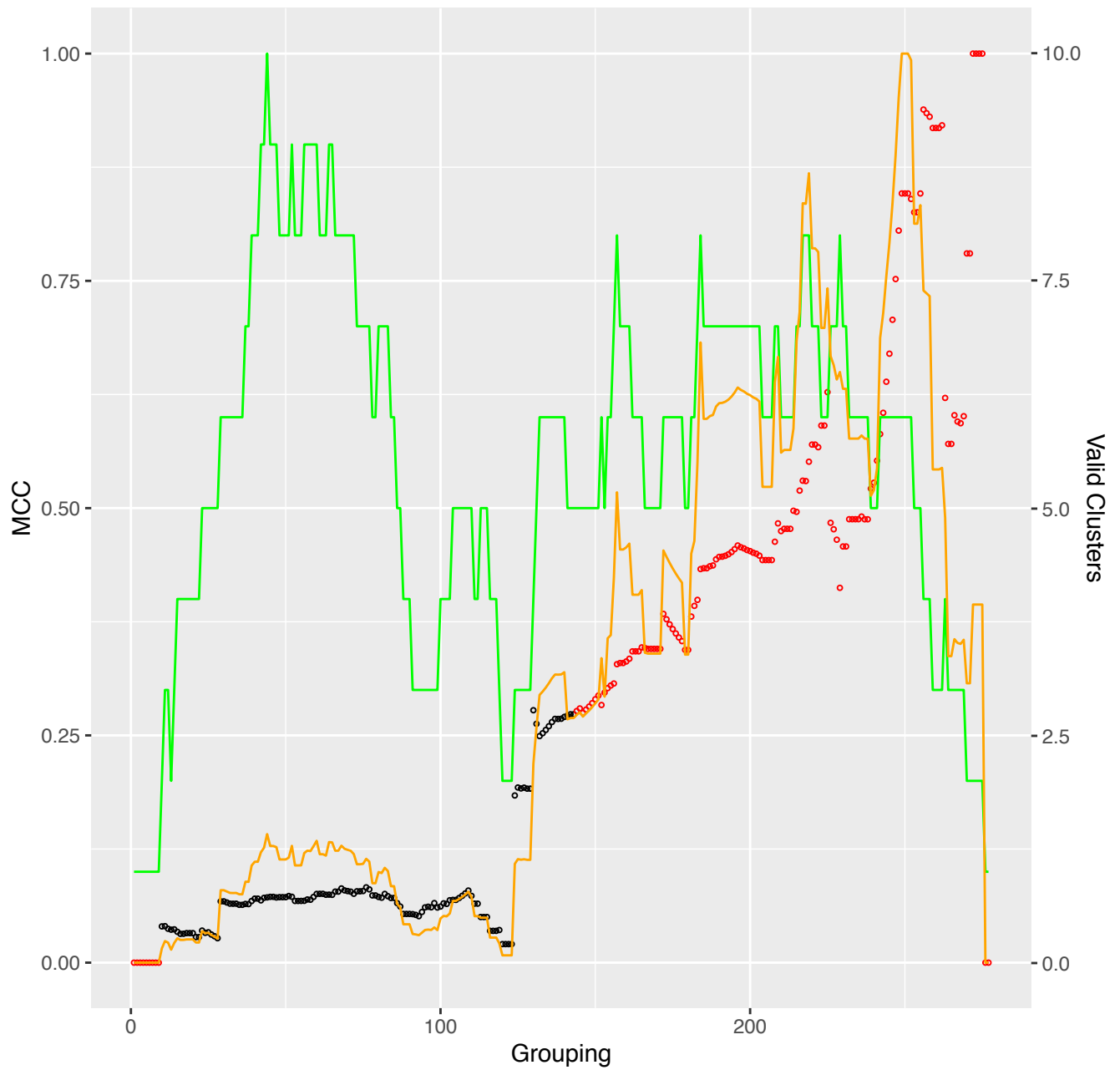
EBNA-2 : grouping per country



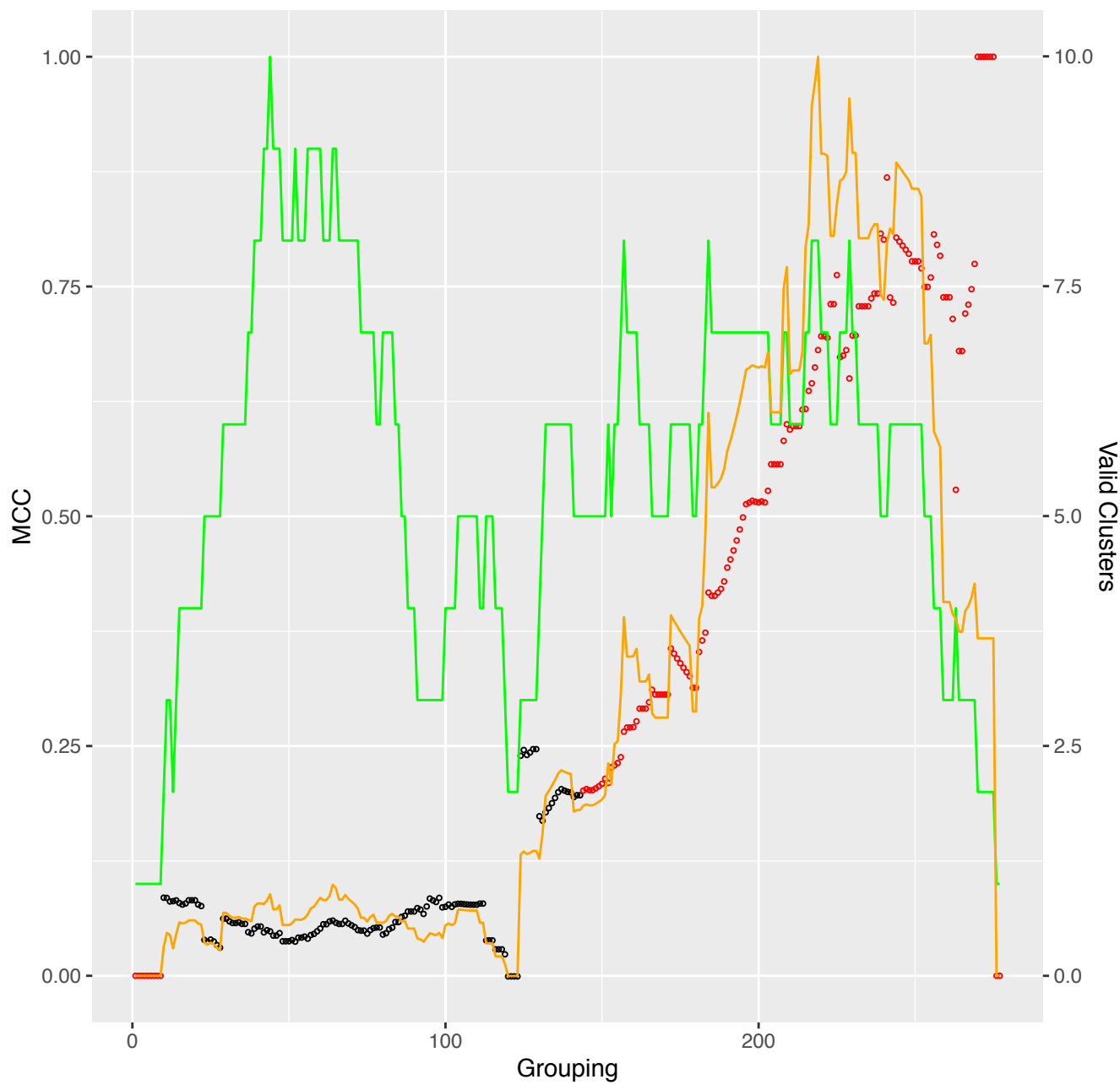
EBNA-2 : grouping per continent



EBNA-2_type1 : grouping per country



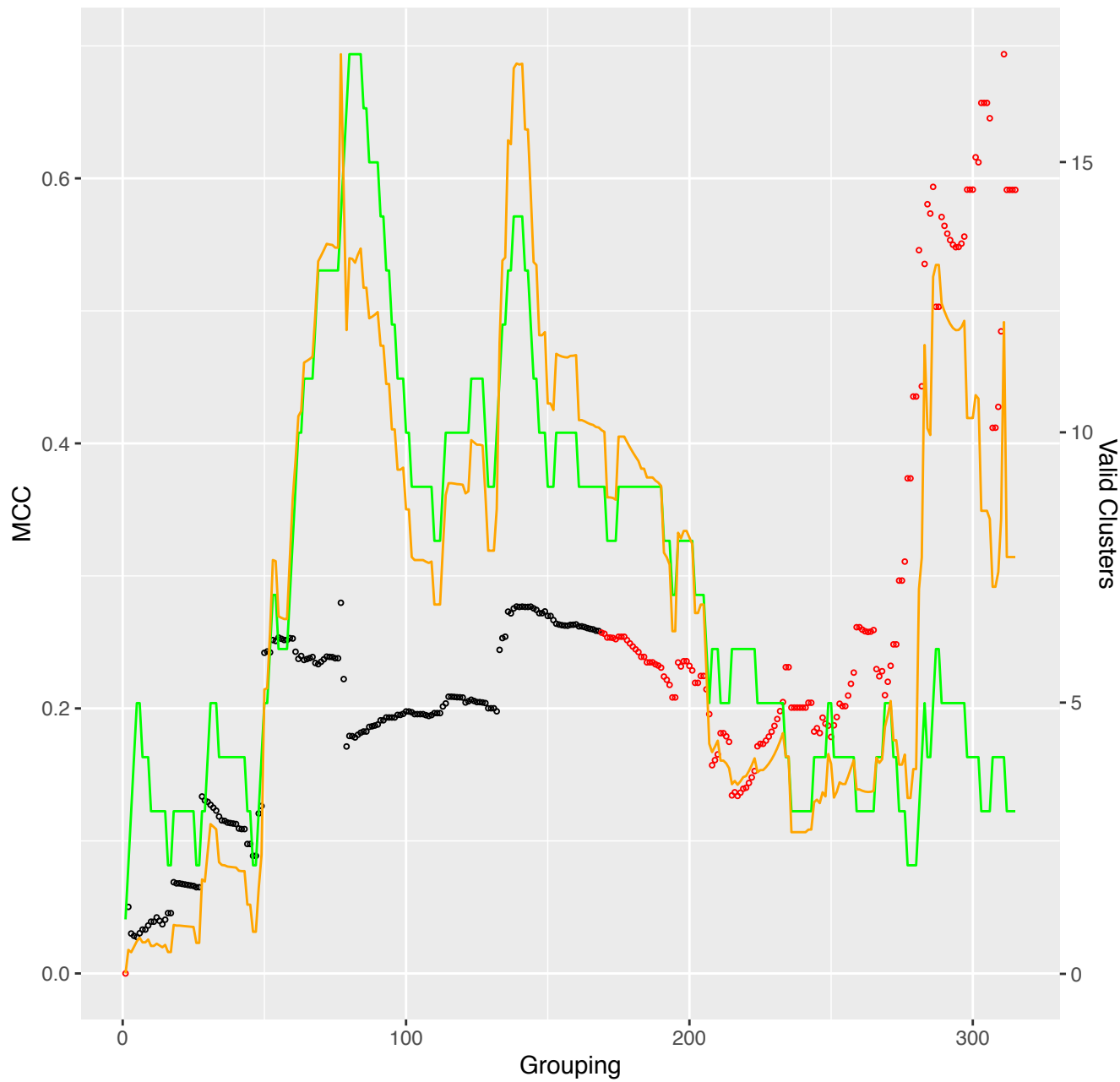
EBNA-2_type1 : grouping per continent



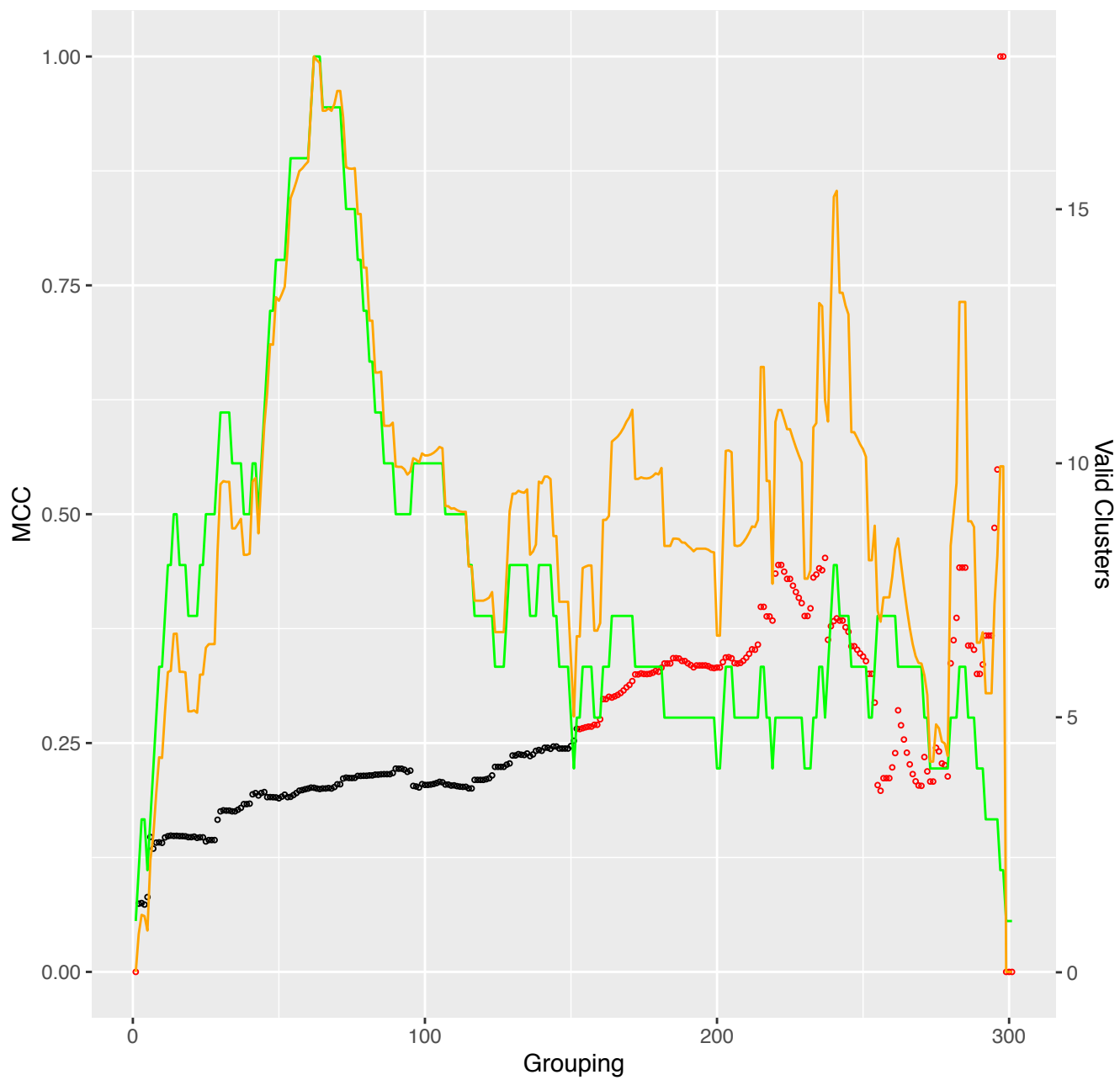
EBNA-3A : grouping per country



EBNA-3A : grouping per continent



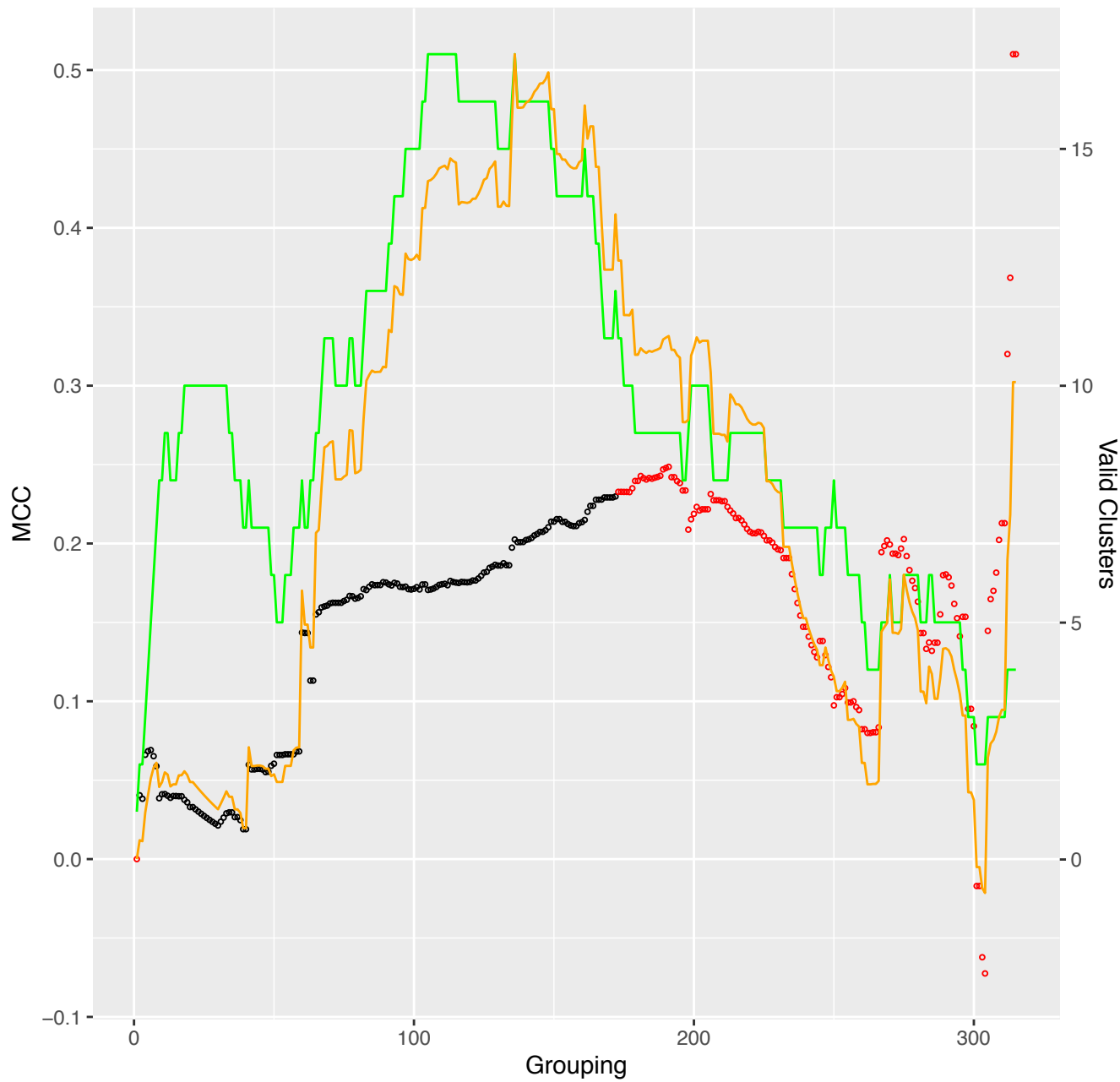
EBNA-3A_type1 : grouping per country



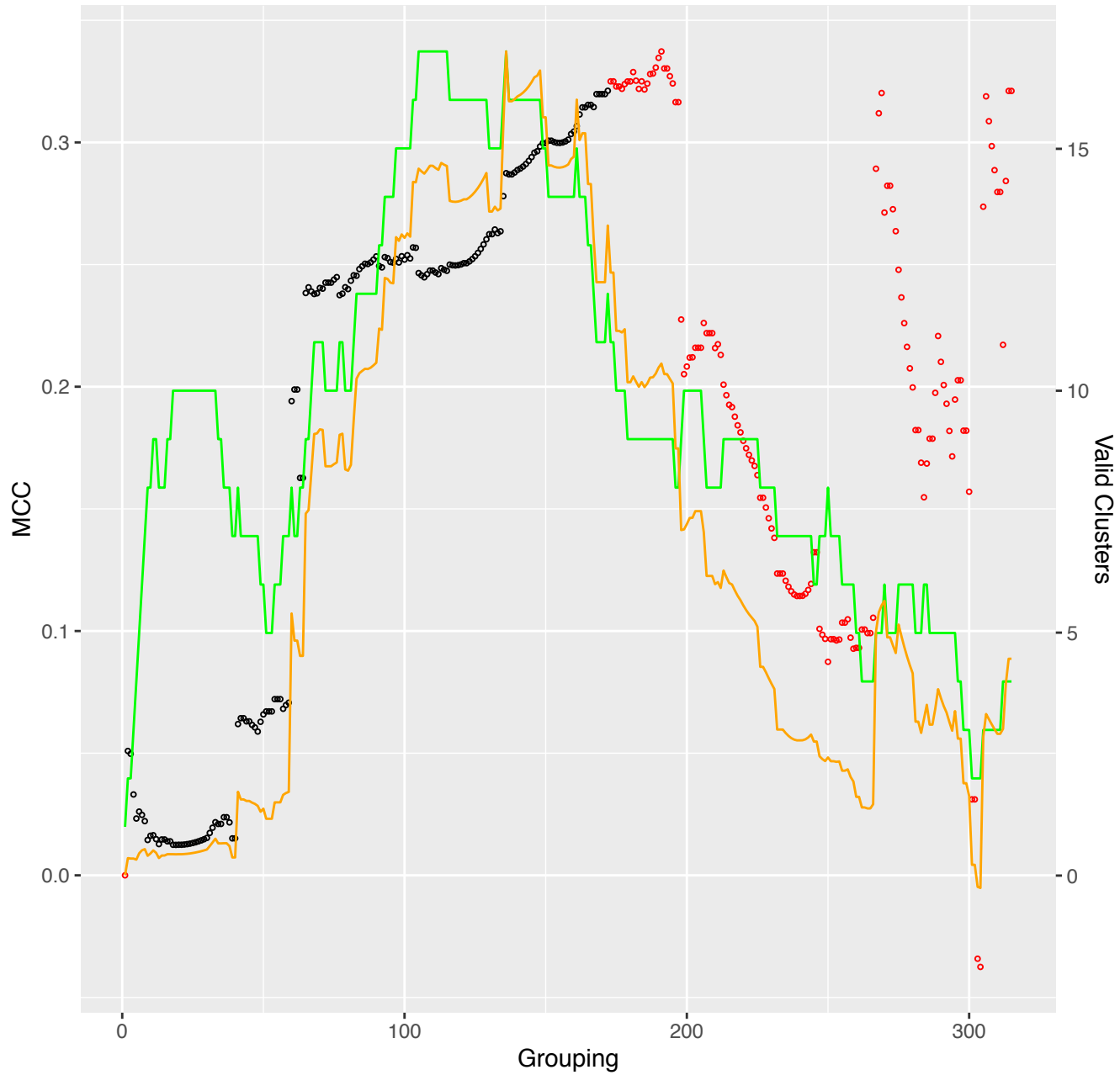
EBNA-3A_type1 : grouping per continent



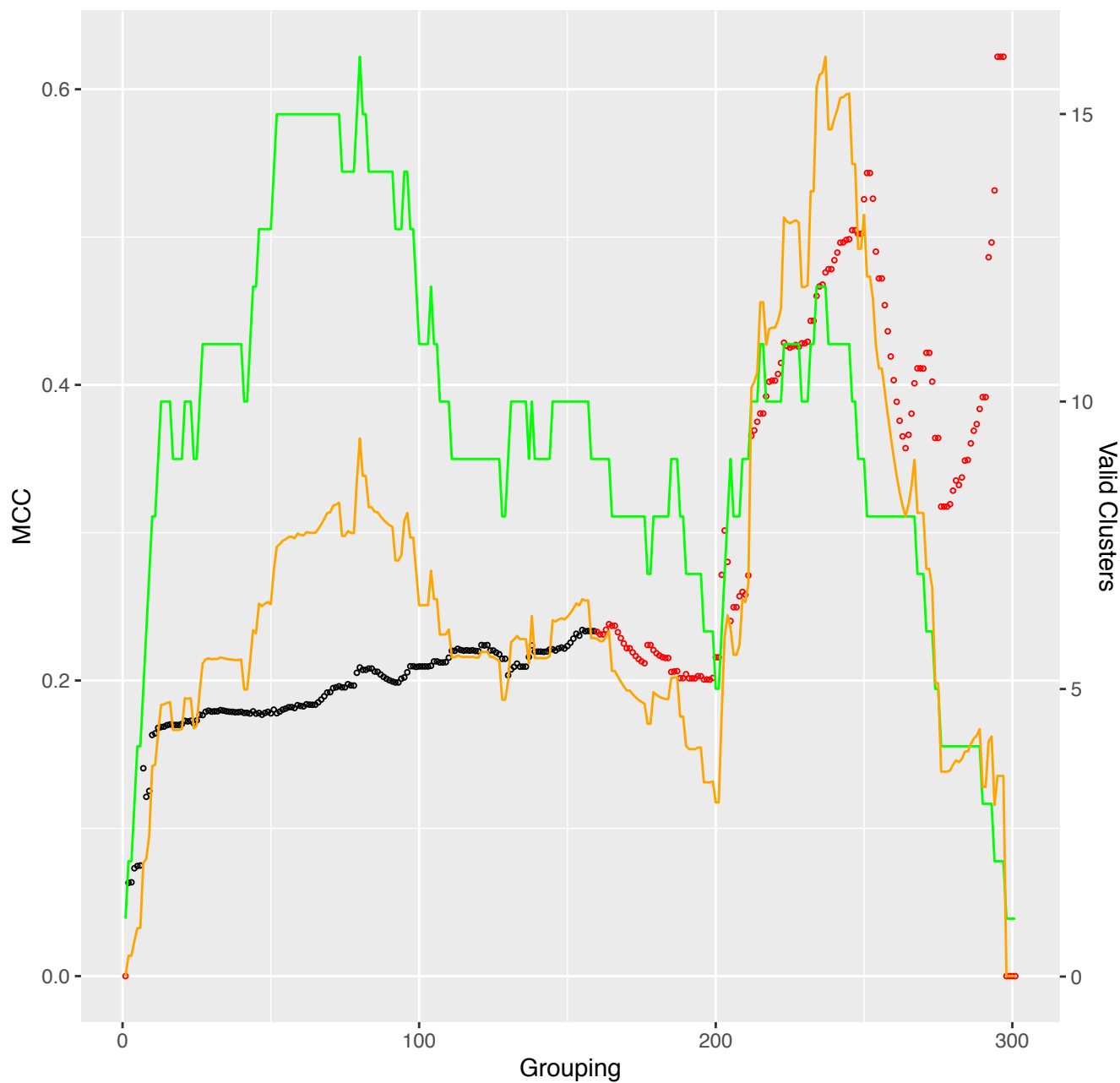
EBNA-3B : grouping per country



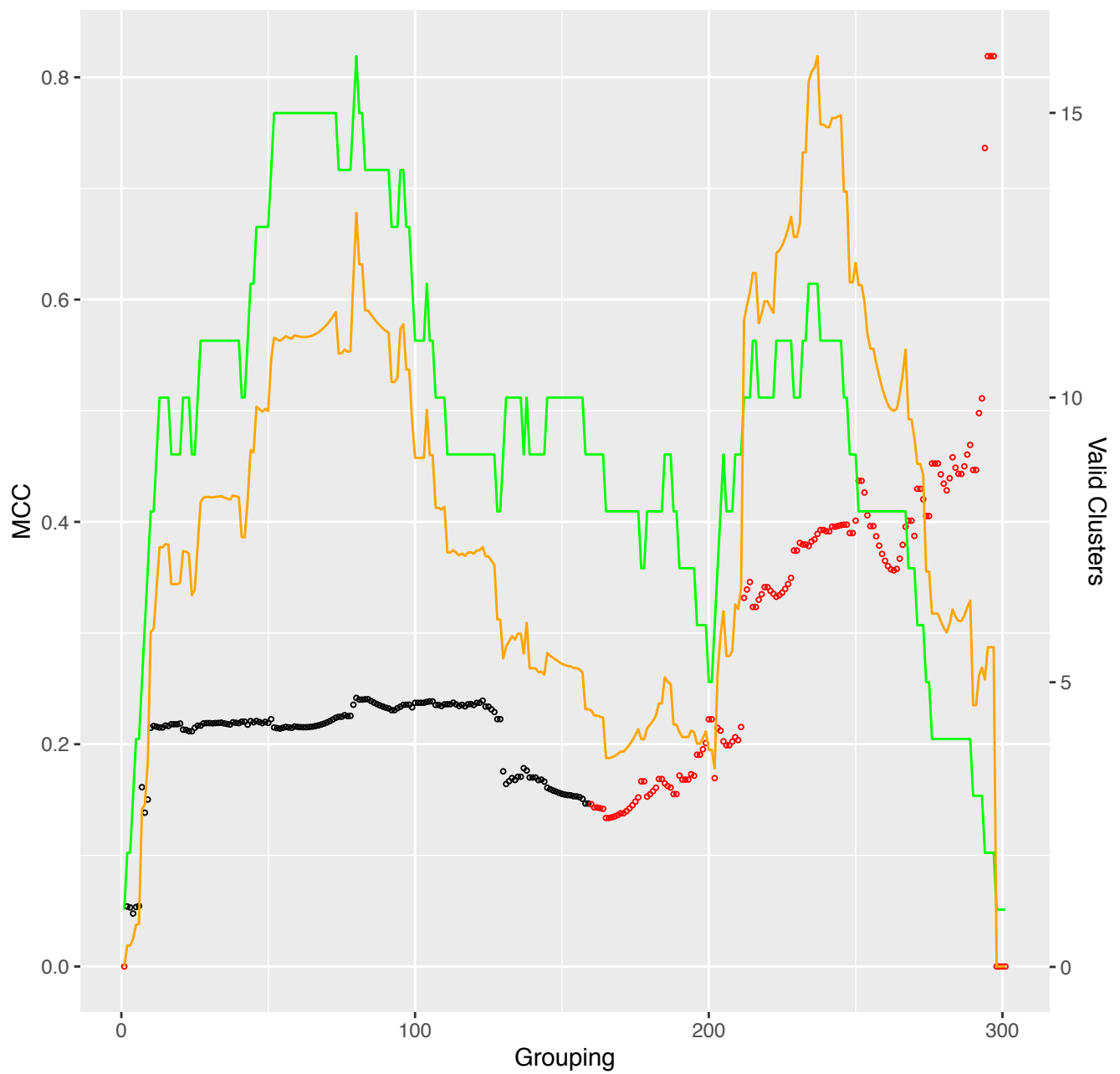
EBNA-3B : grouping per continent



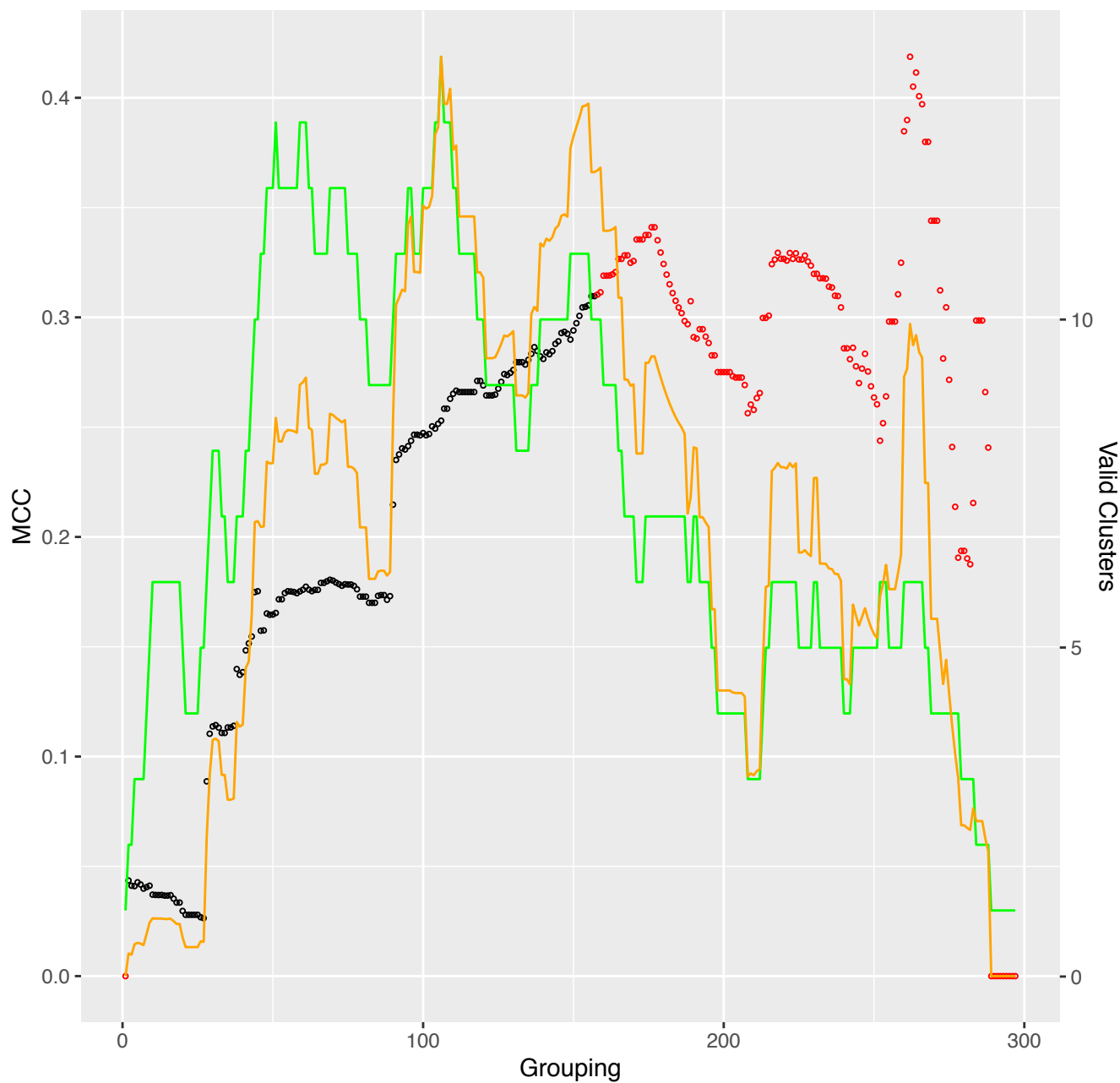
EBNA-3B_type1 : grouping per country



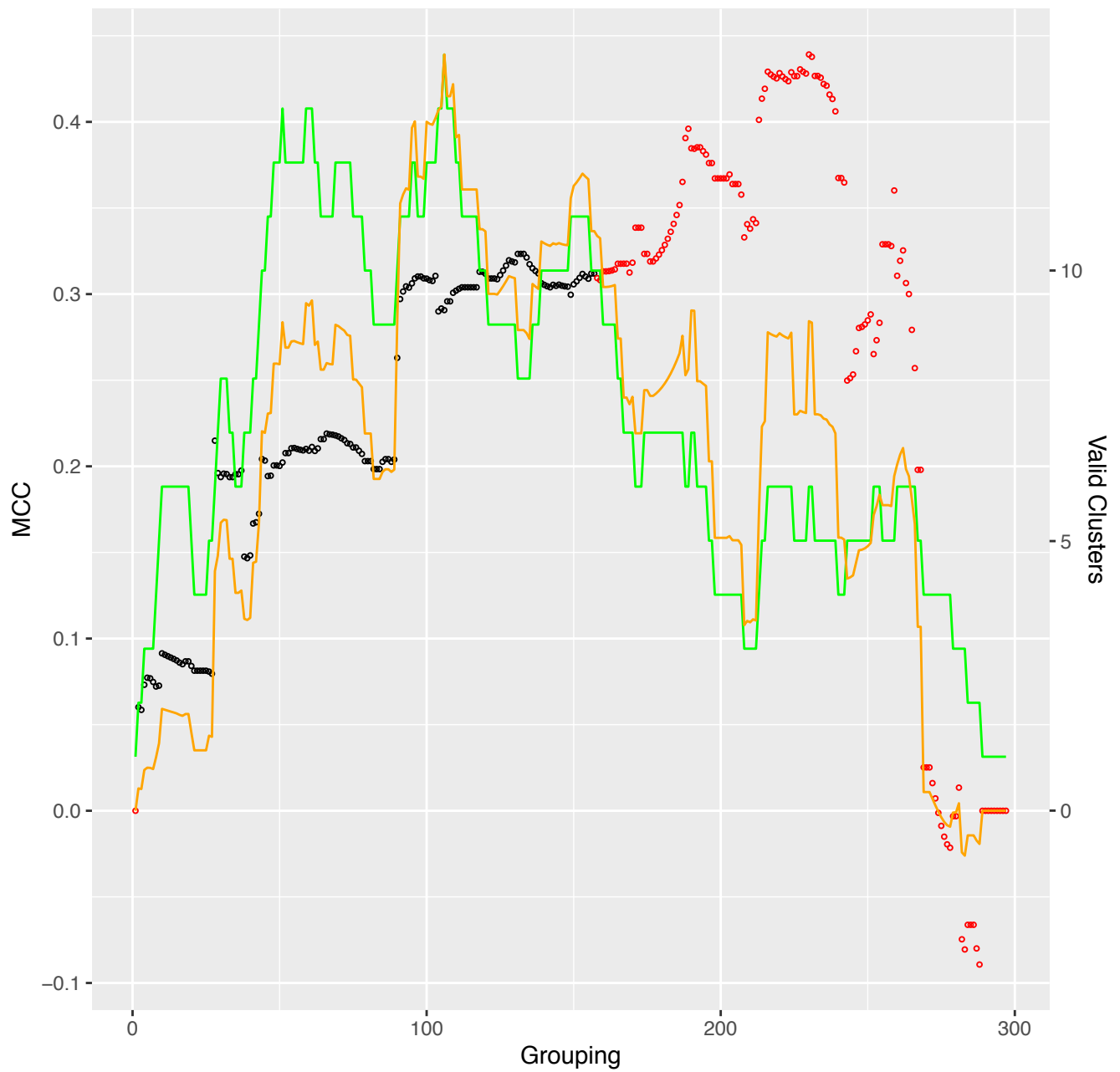
EBNA-3B_type1 : grouping per continent



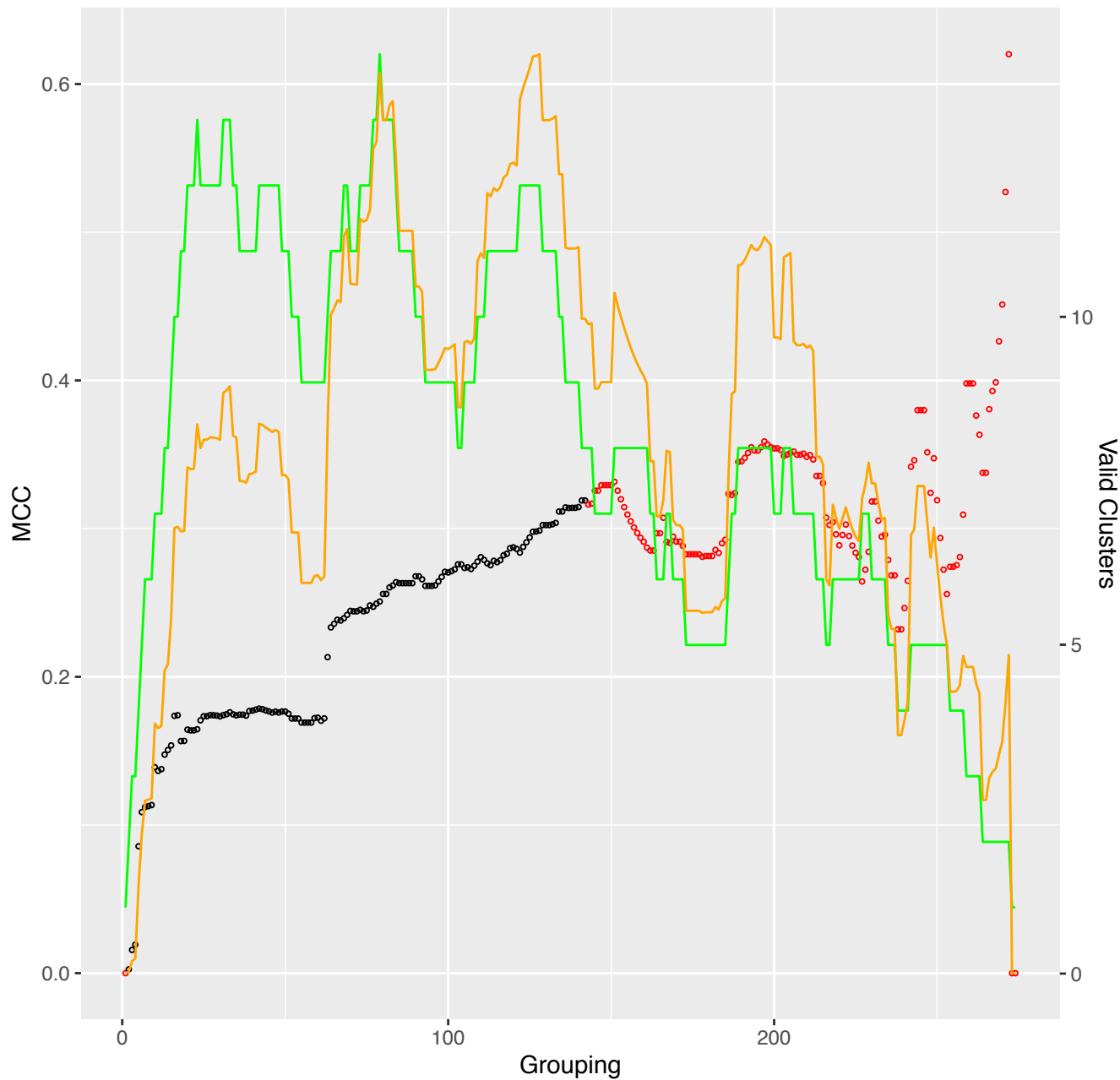
EBNA-3C : grouping per country



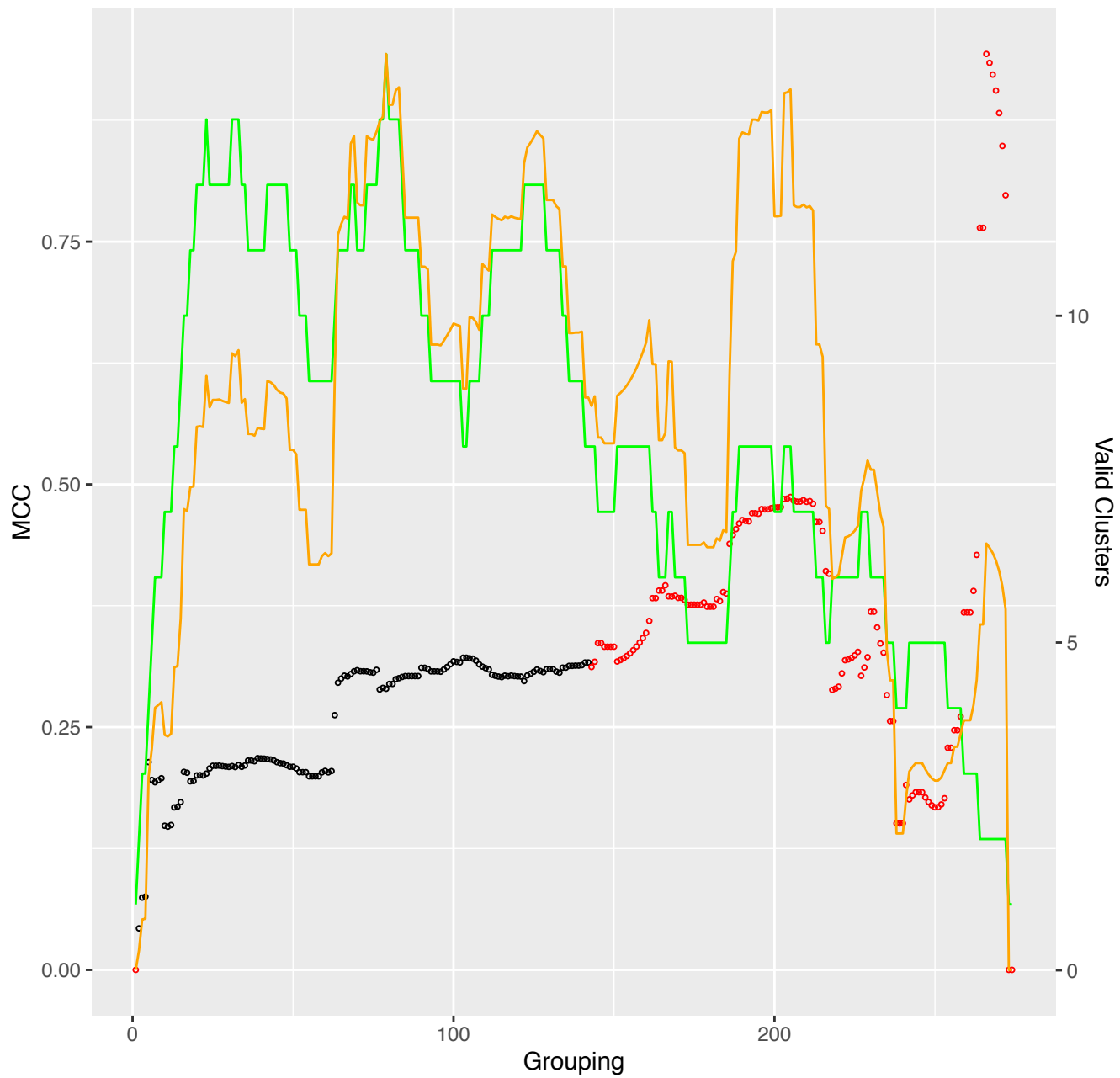
EBNA-3C : grouping per continent



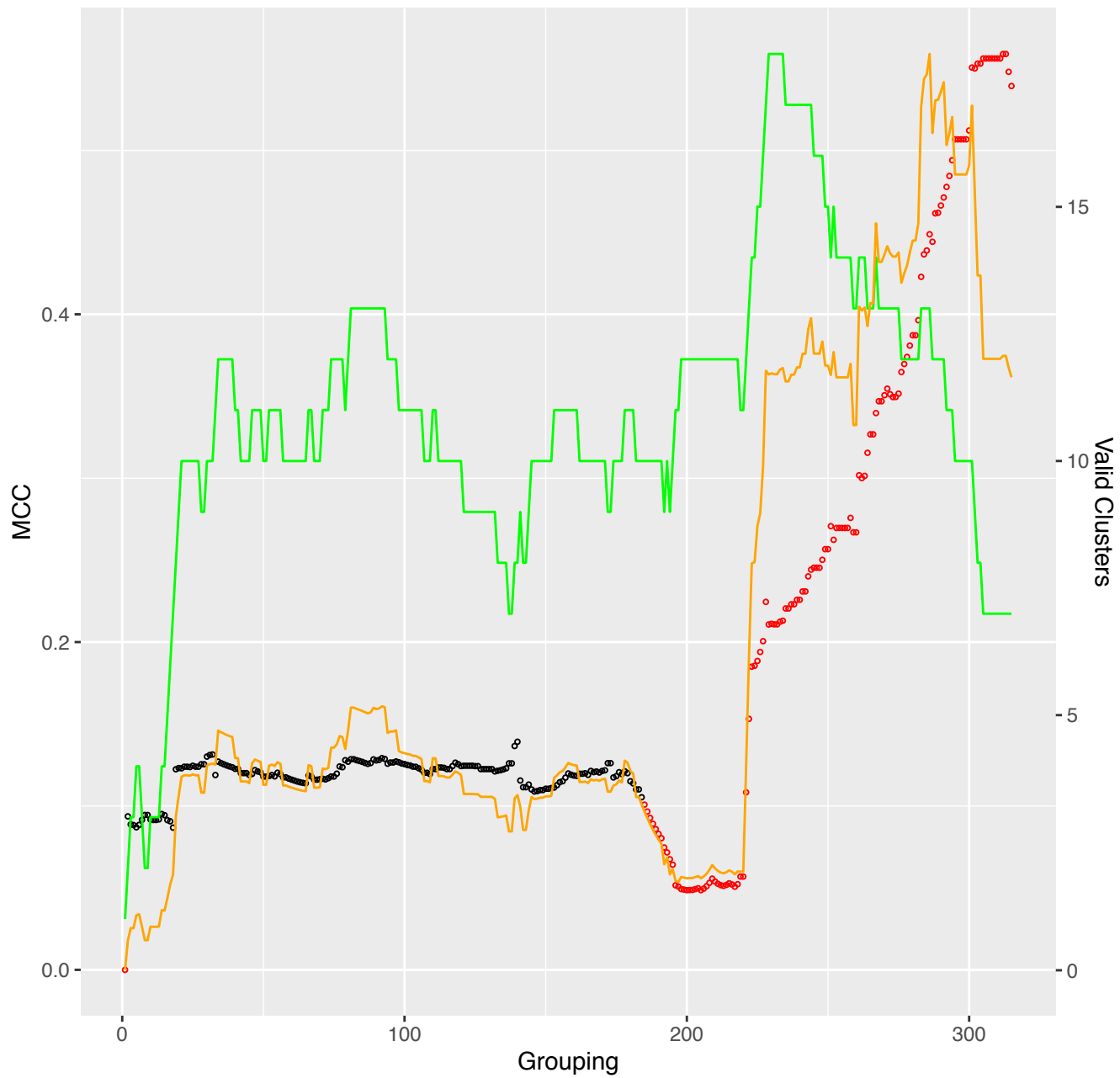
EBNA-3C_type1 : grouping per country



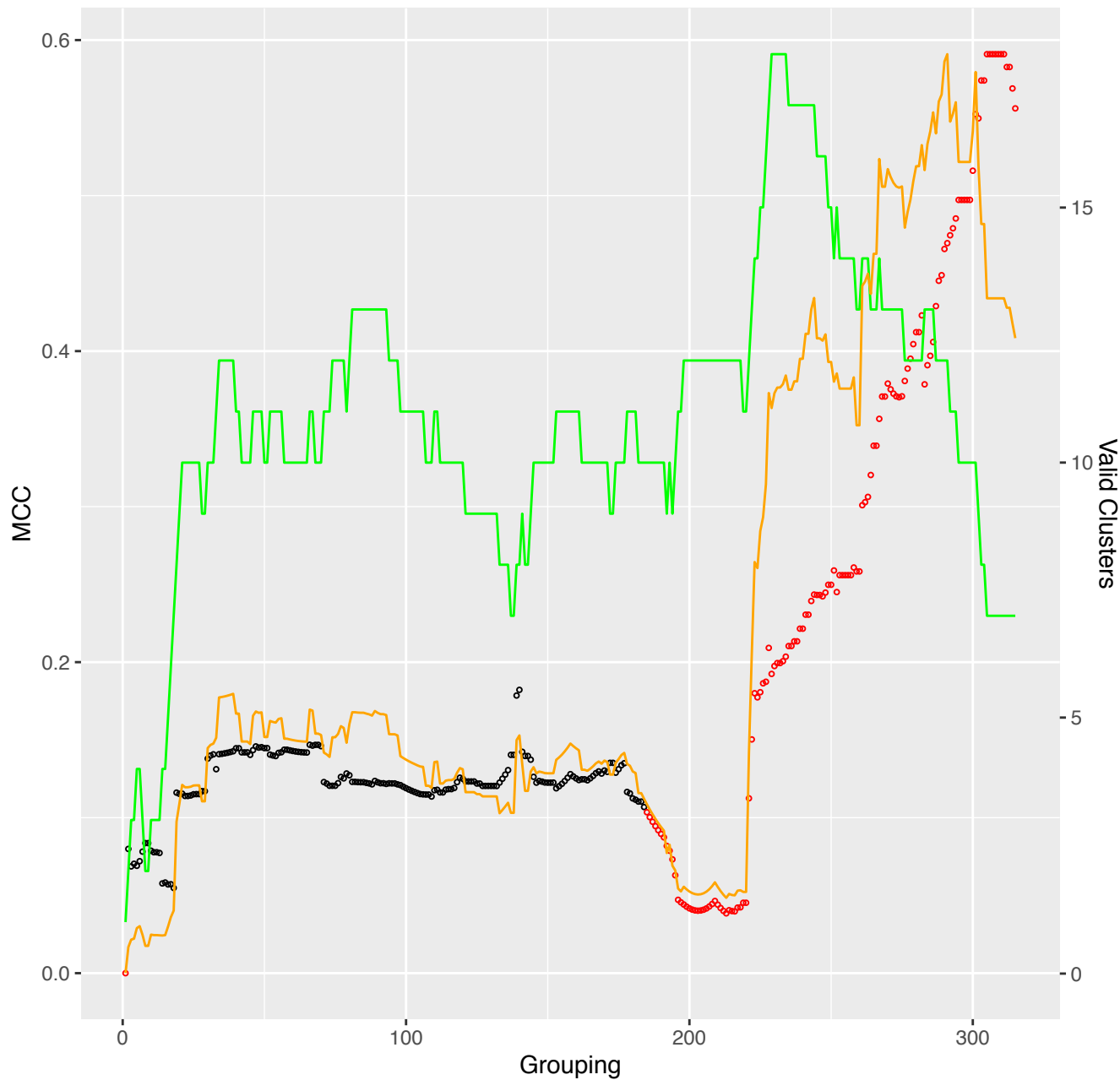
EBNA-3C_type1 : grouping per continent



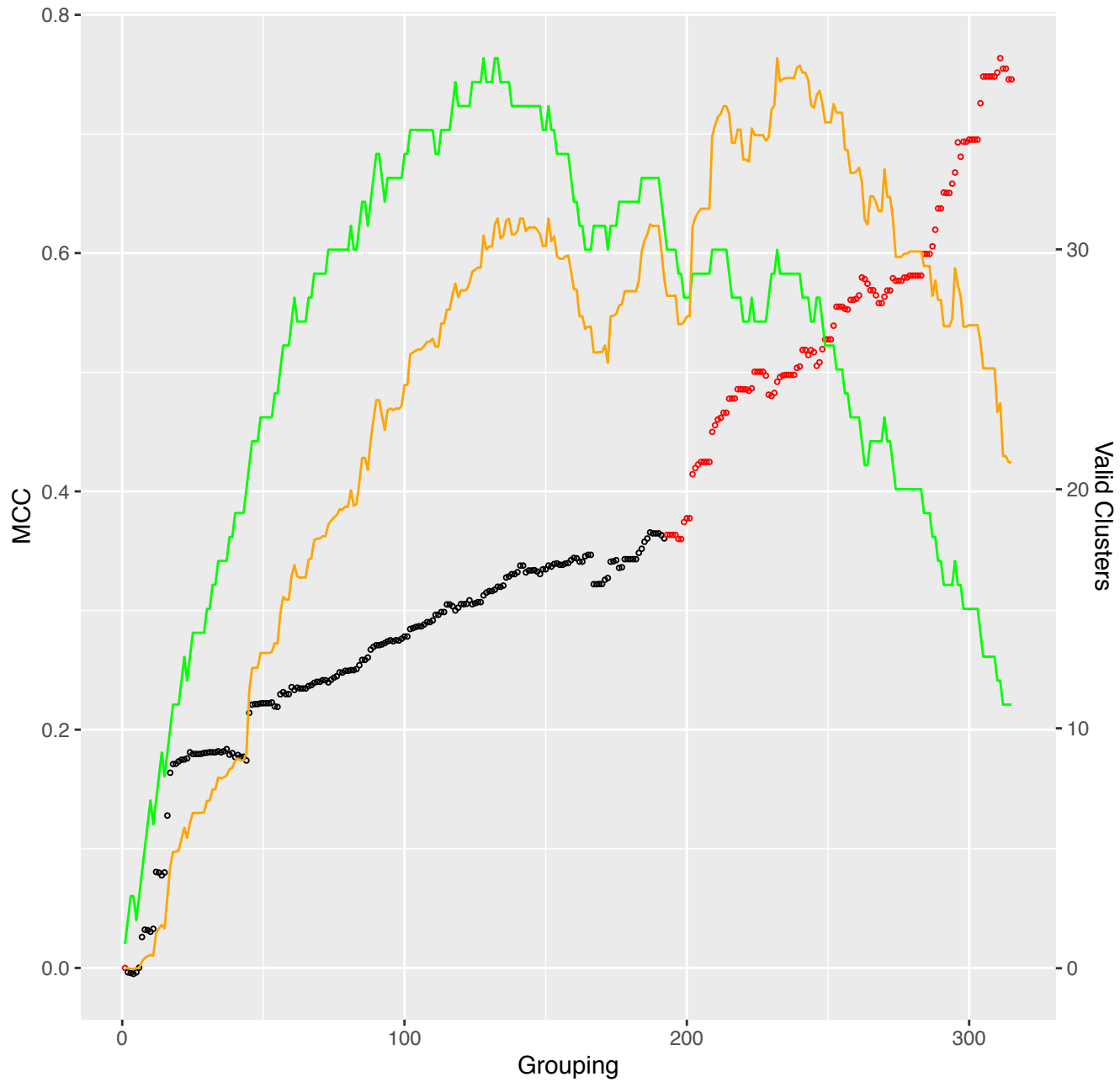
LMP-2A : grouping per country



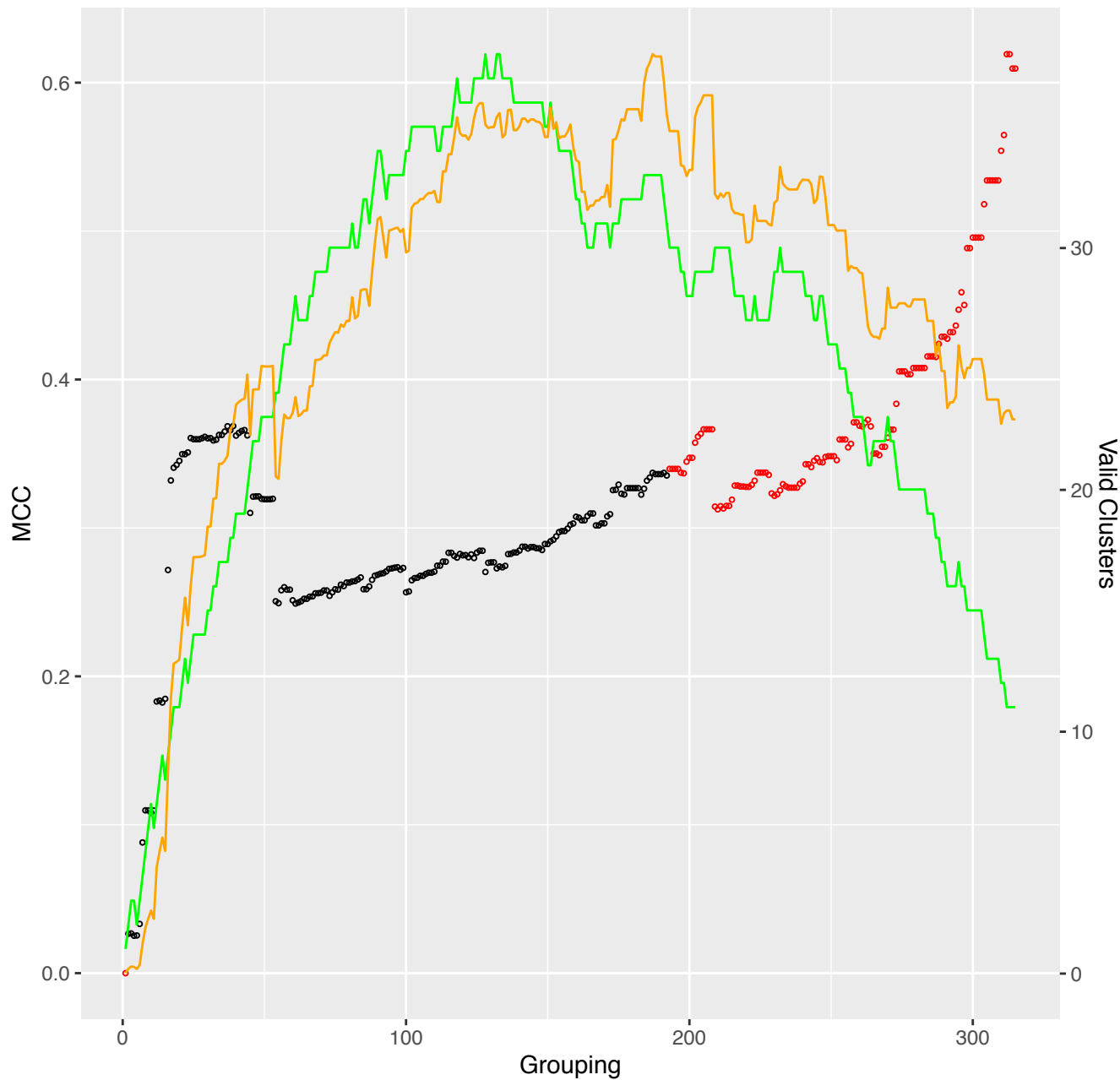
LMP-2A : grouping per continent



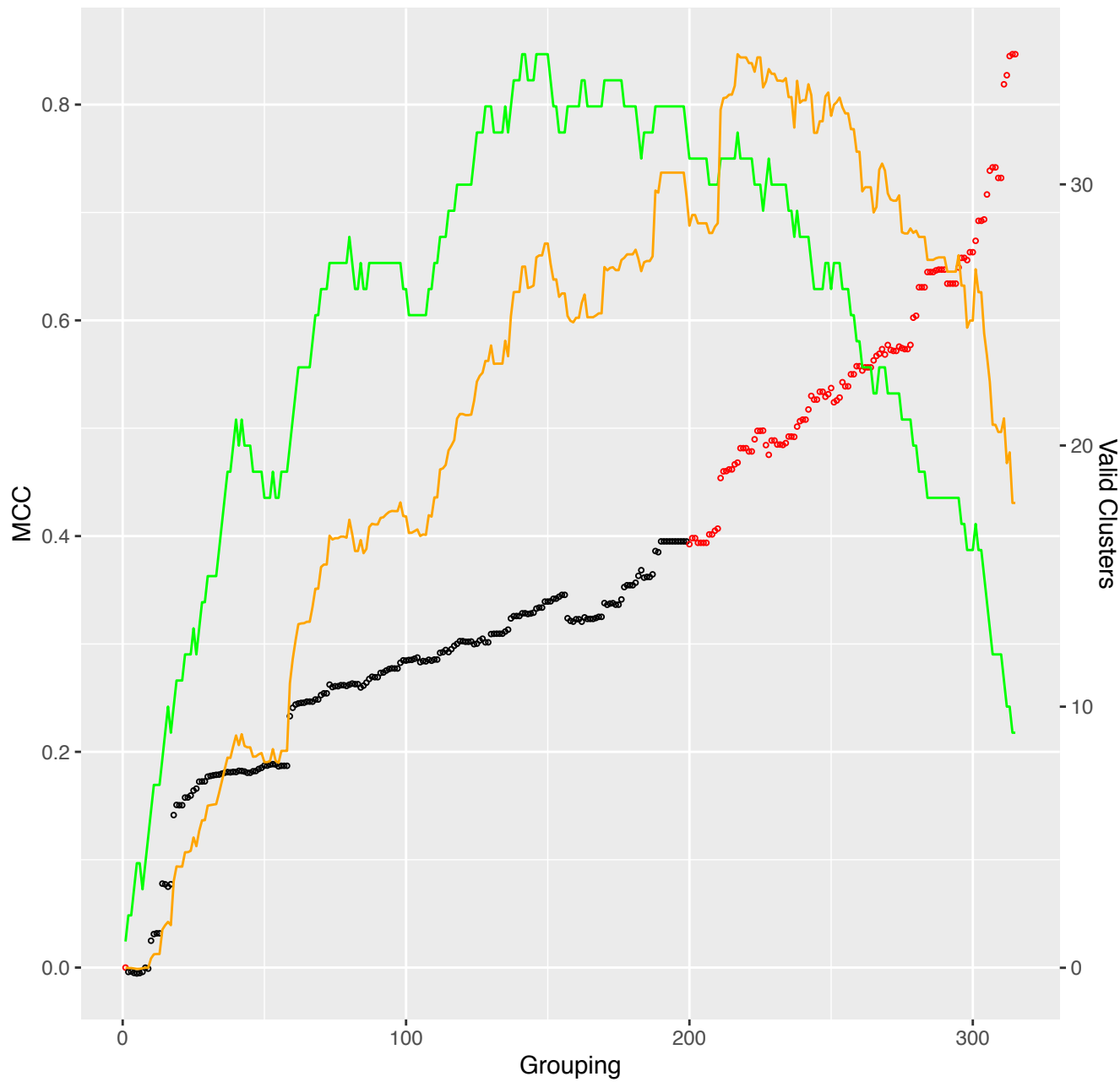
Supertree : grouping per country



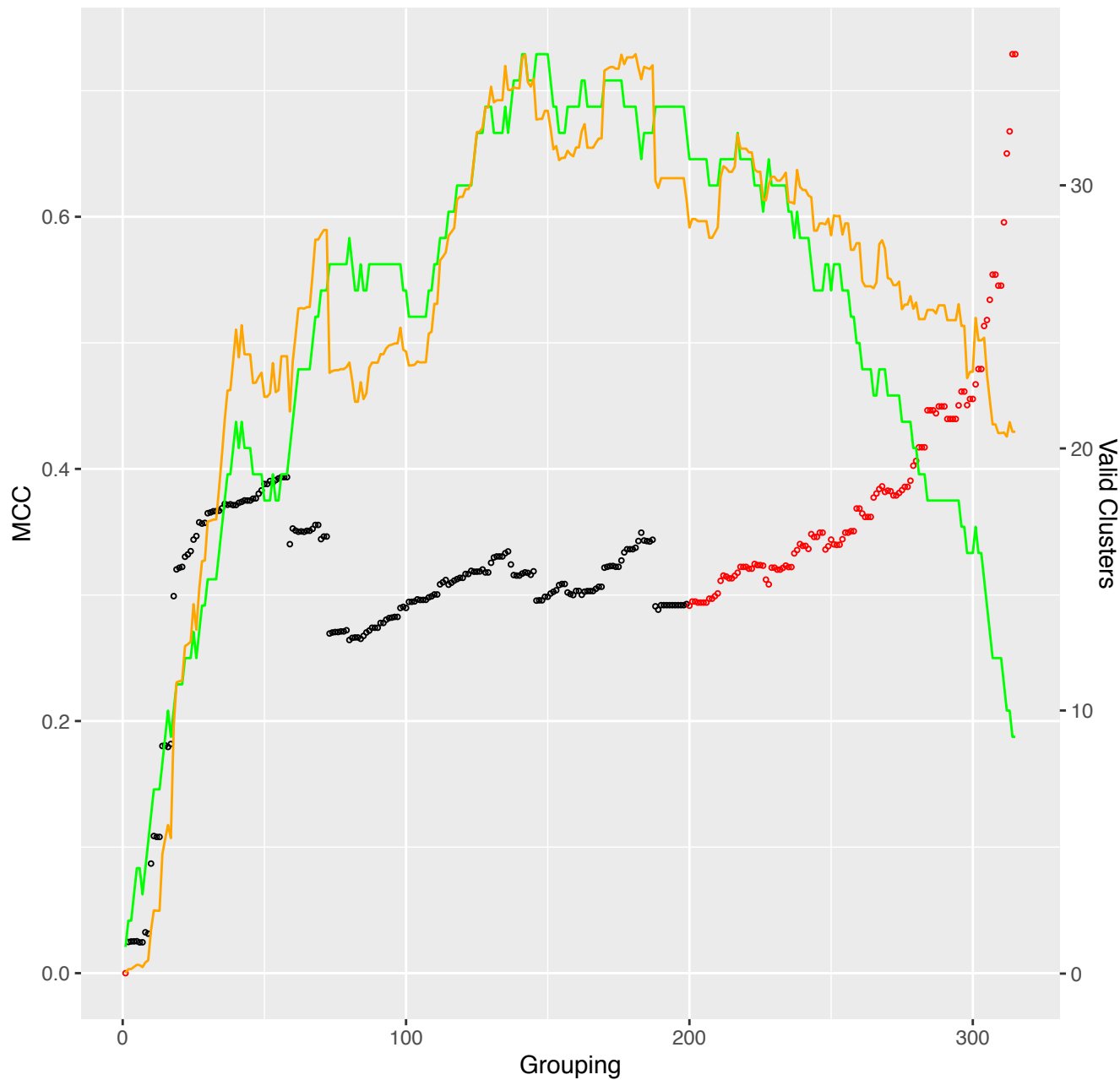
Supertree : grouping per continent



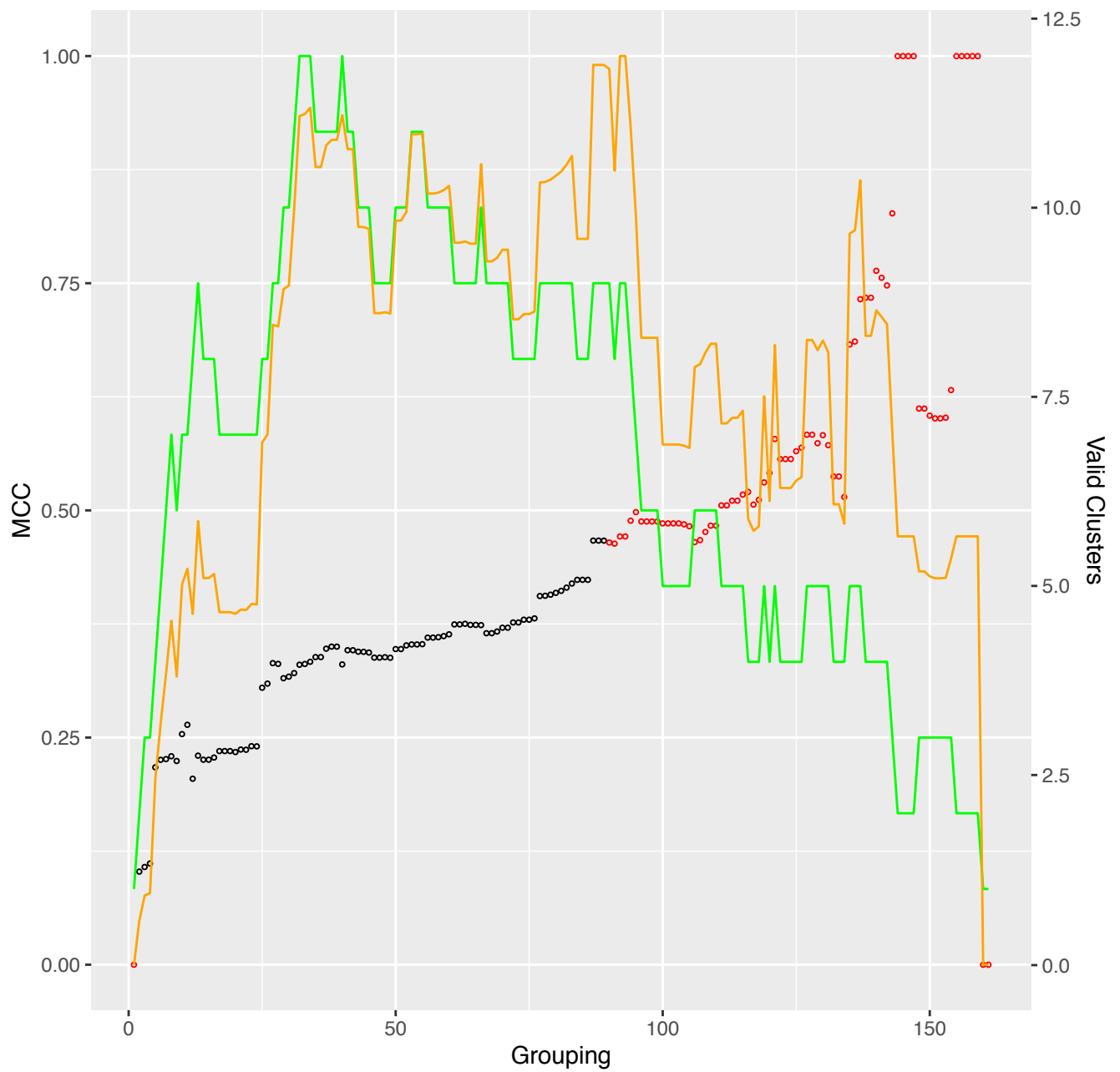
Supertree_type1 : grouping per country



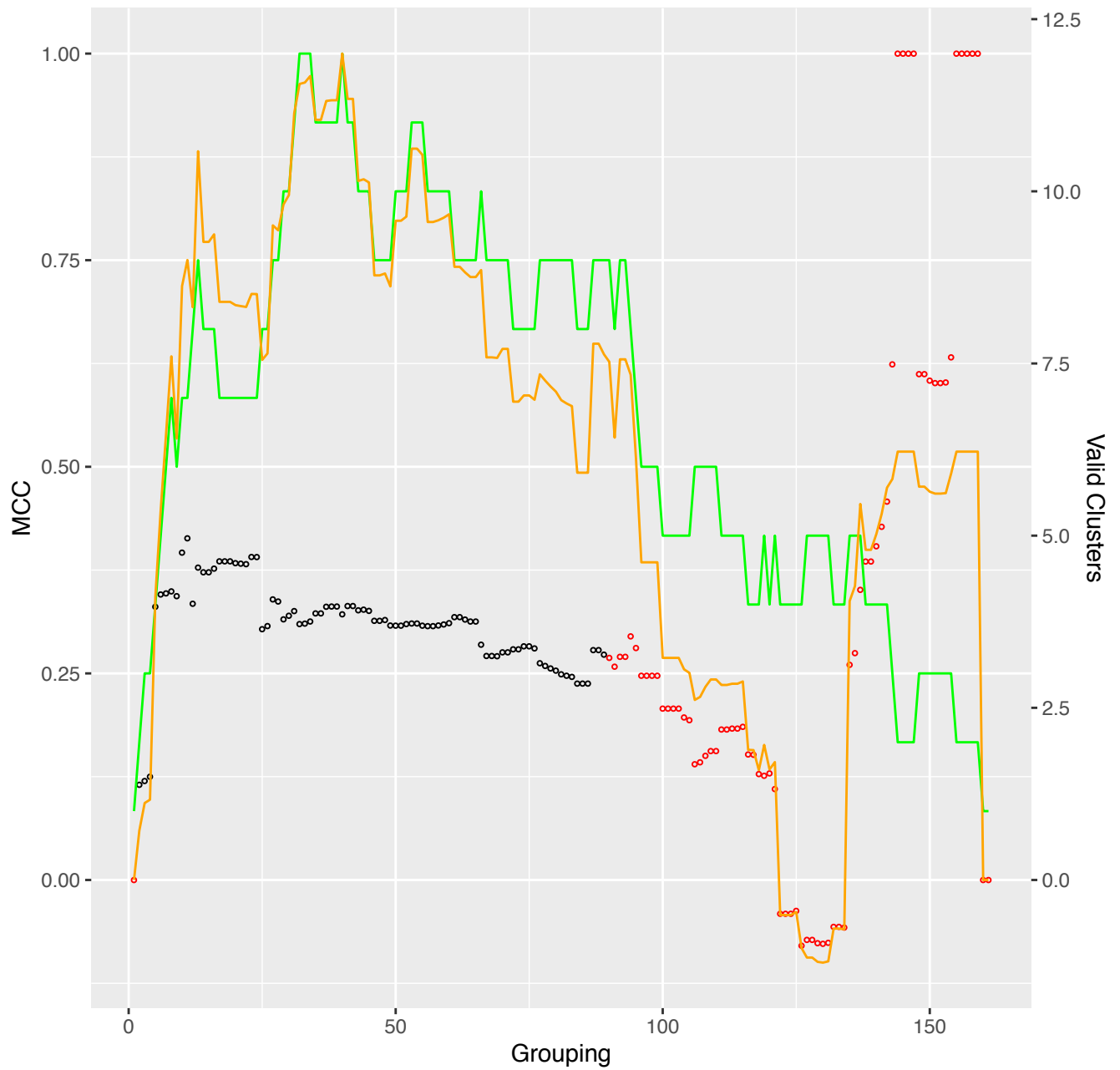
Supertree_type1 : grouping per continent



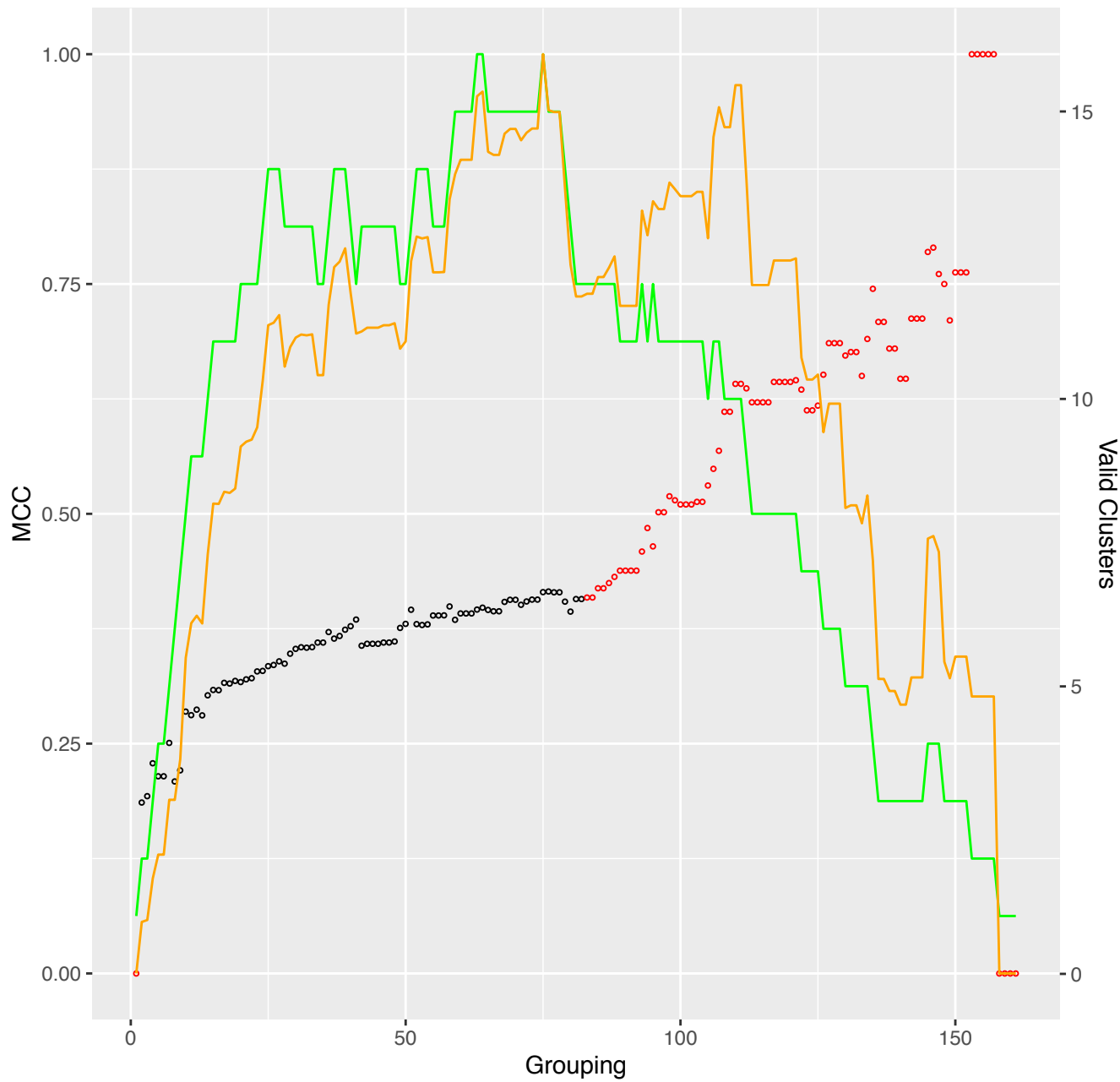
Concatenated tree : grouping per country



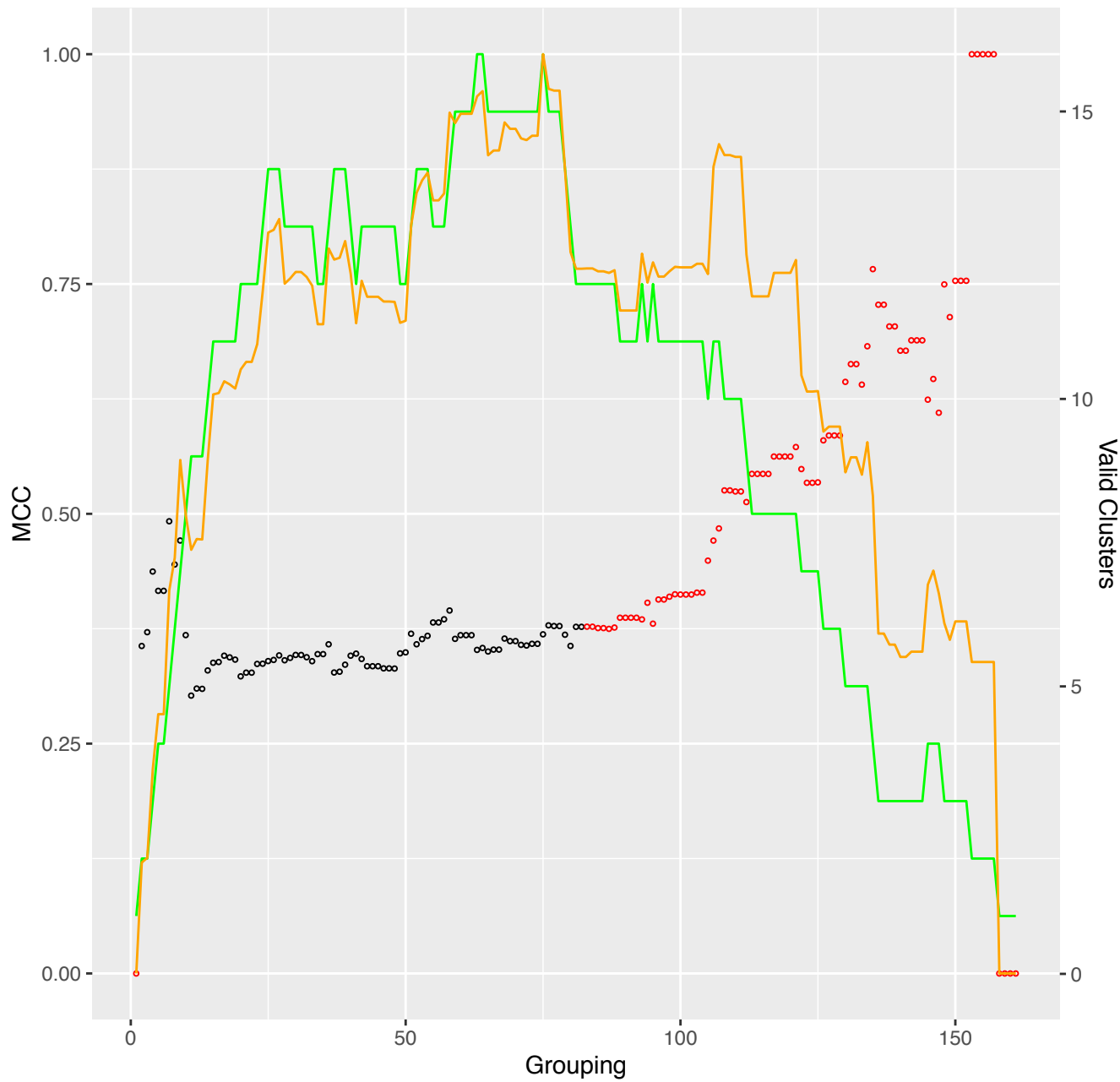
Concatenated tree : grouping per continent



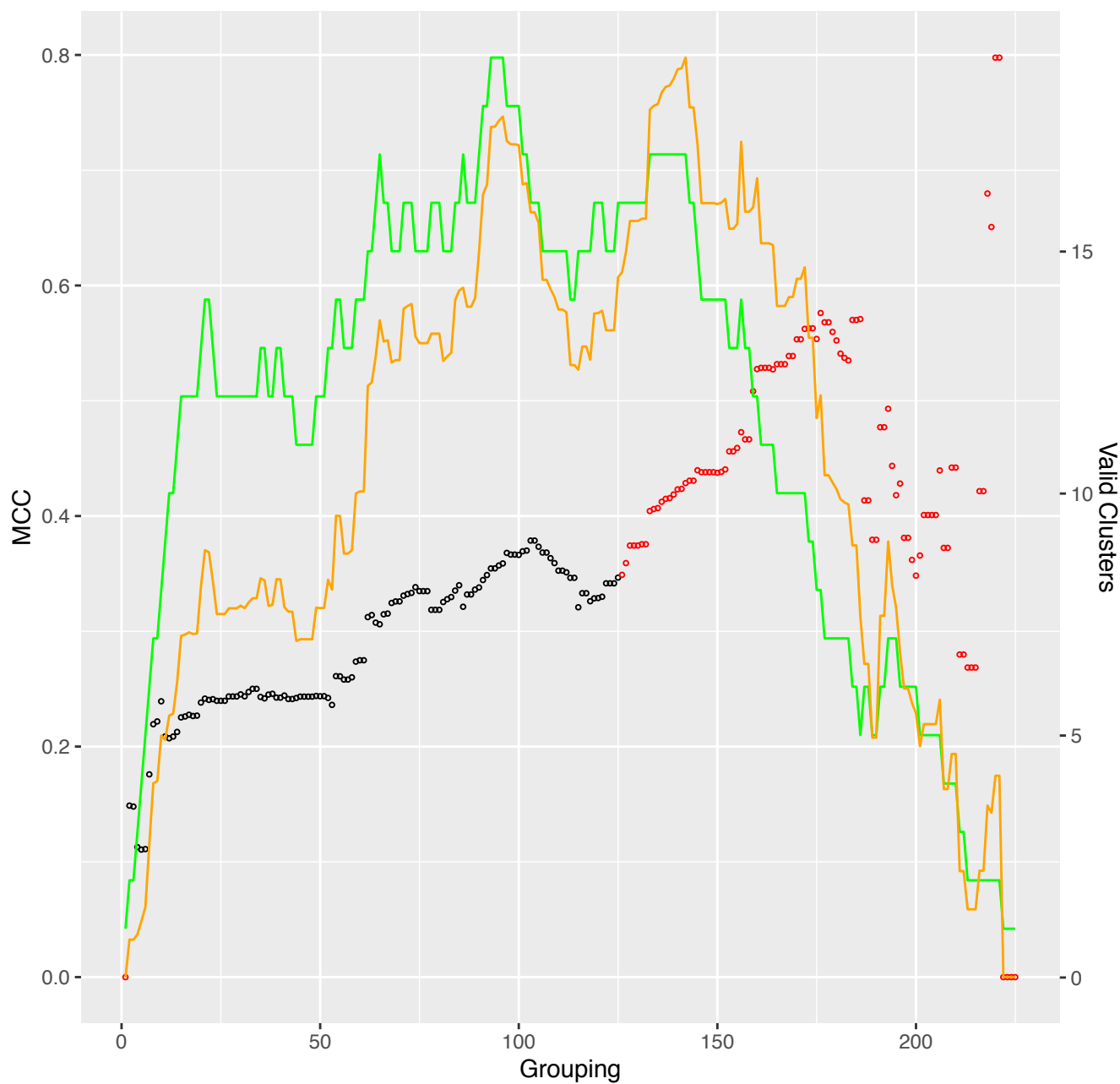
Supertree (conatenated tree isolates) : grouping per country



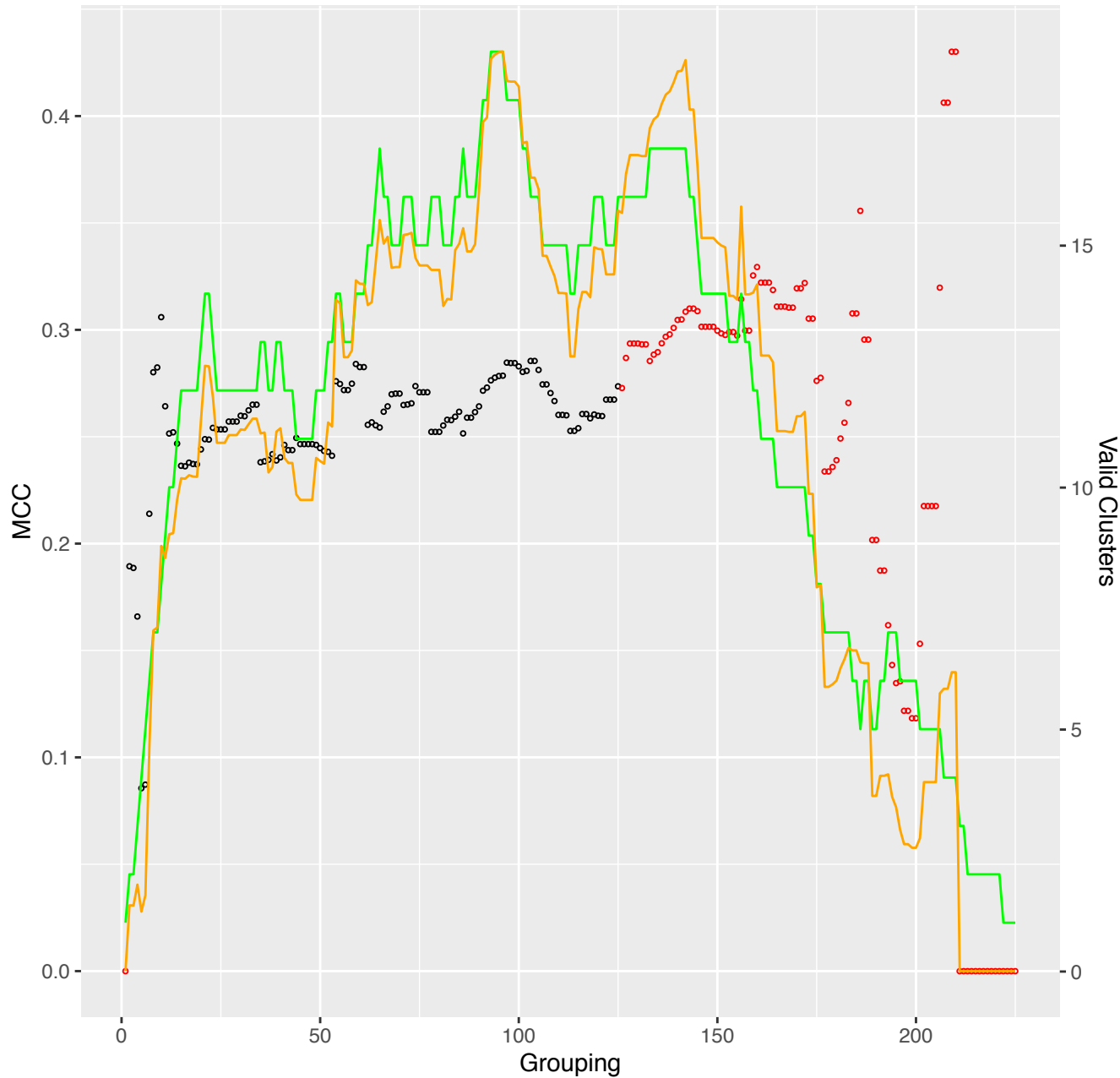
Supertree (conatenated tree isolates) : grouping per continent



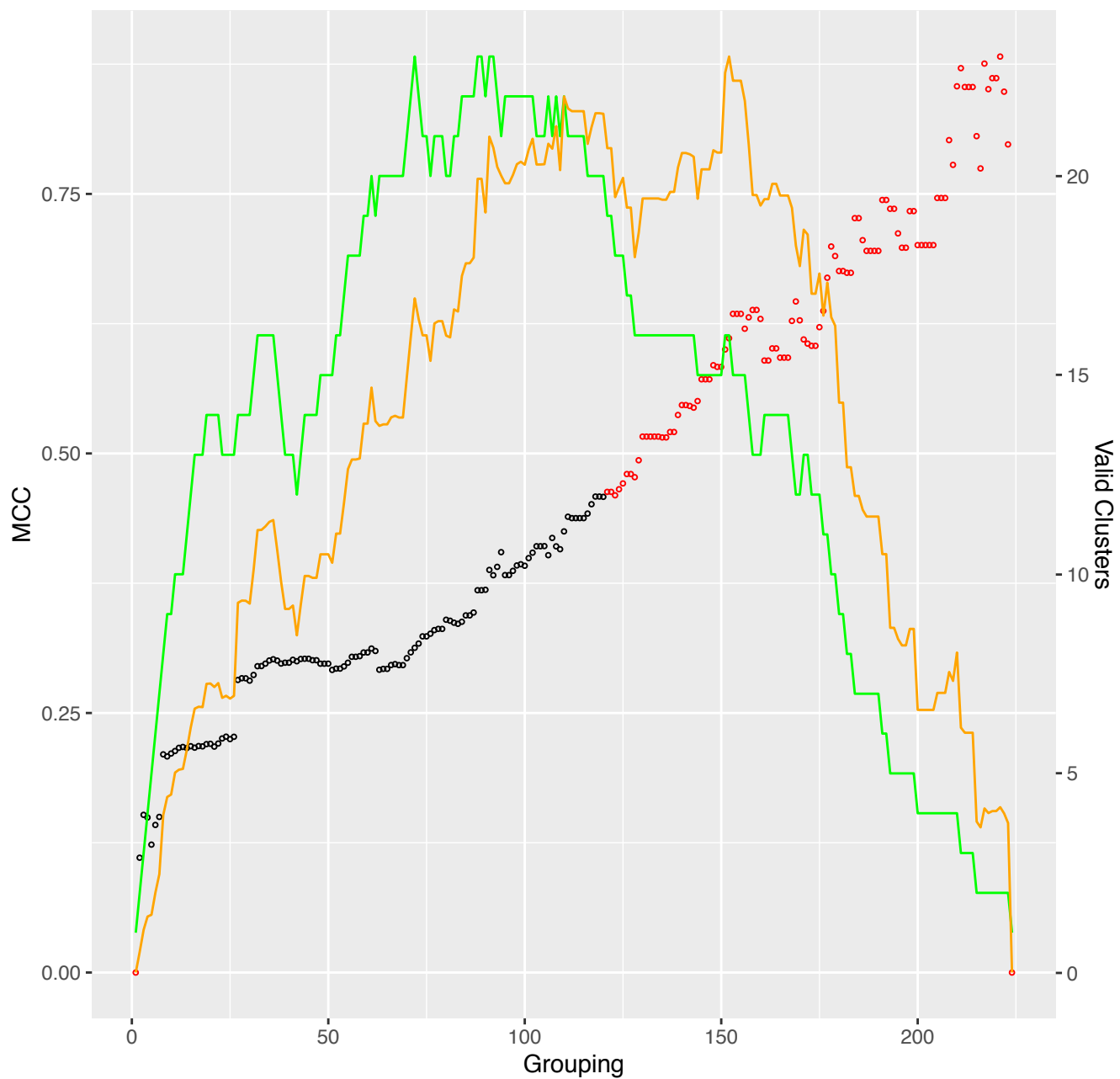
Concatenated tree (no EBNA-1) : grouping per country



Concatenated tree (no EBNA-1) : grouping per continent



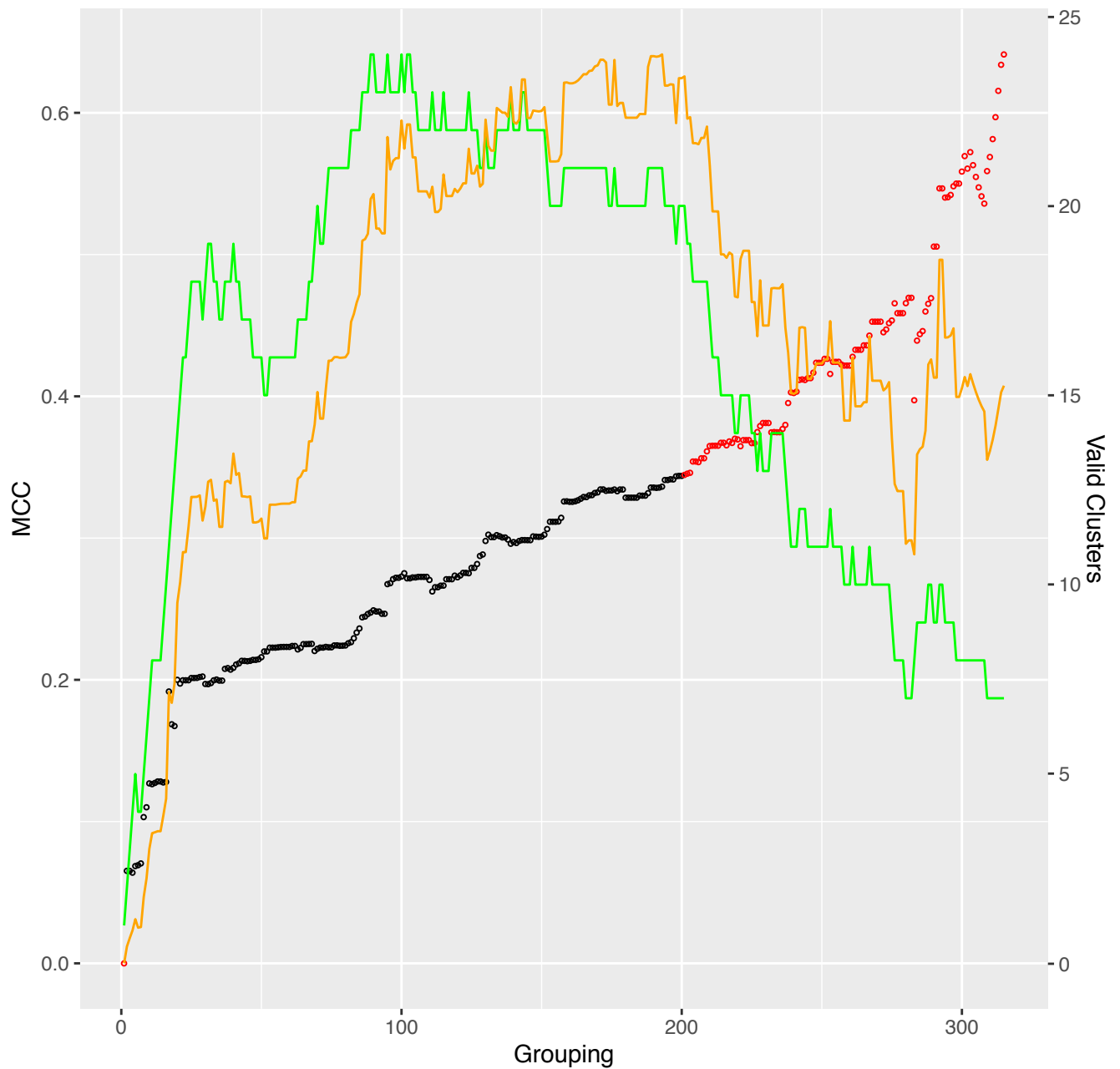
Supertree (conatenated tree isolates; no EBNA-1) : grouping per country



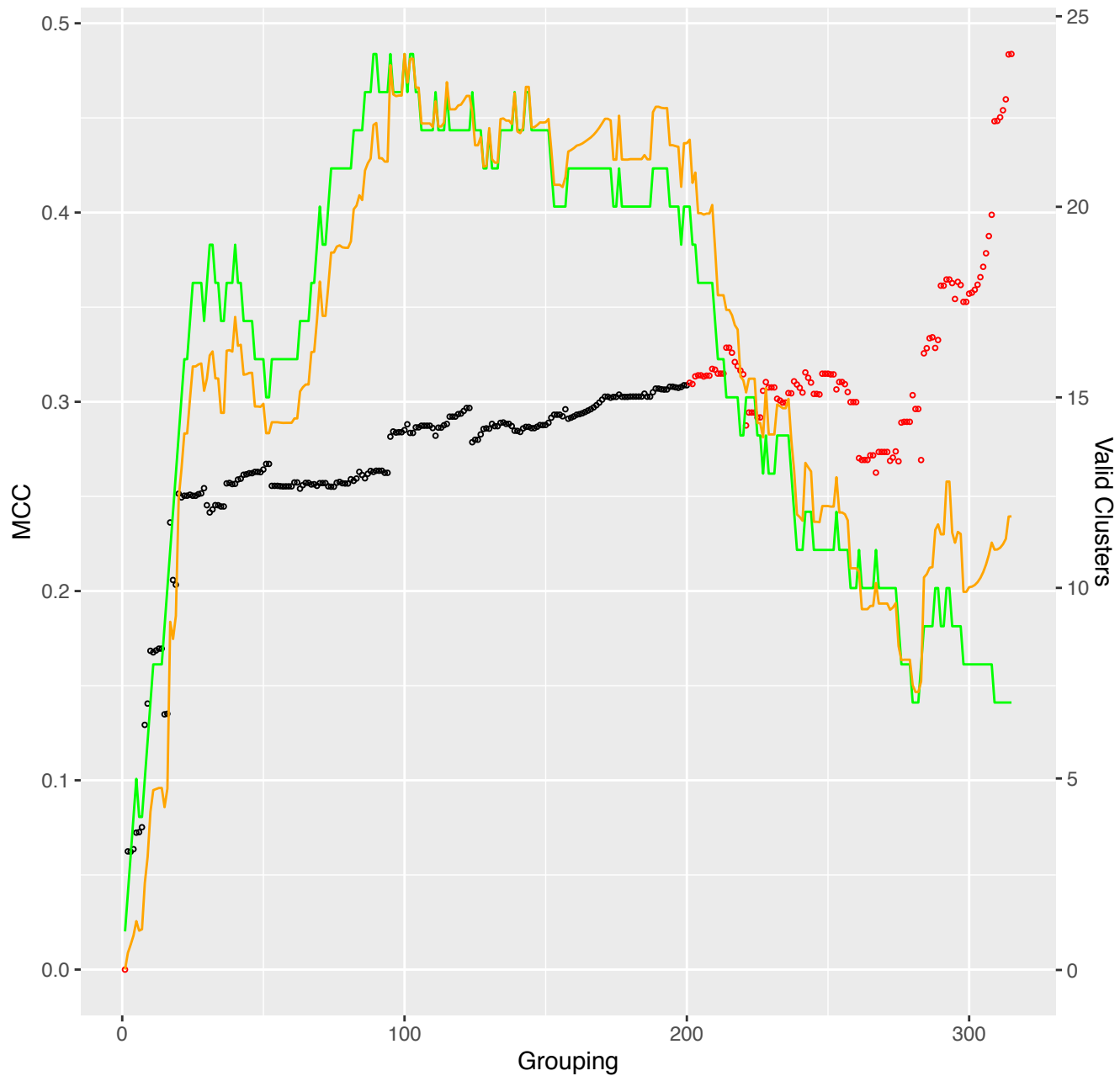
Supertree (conatenated tree isolates; no EBNA-1) : grouping per continent



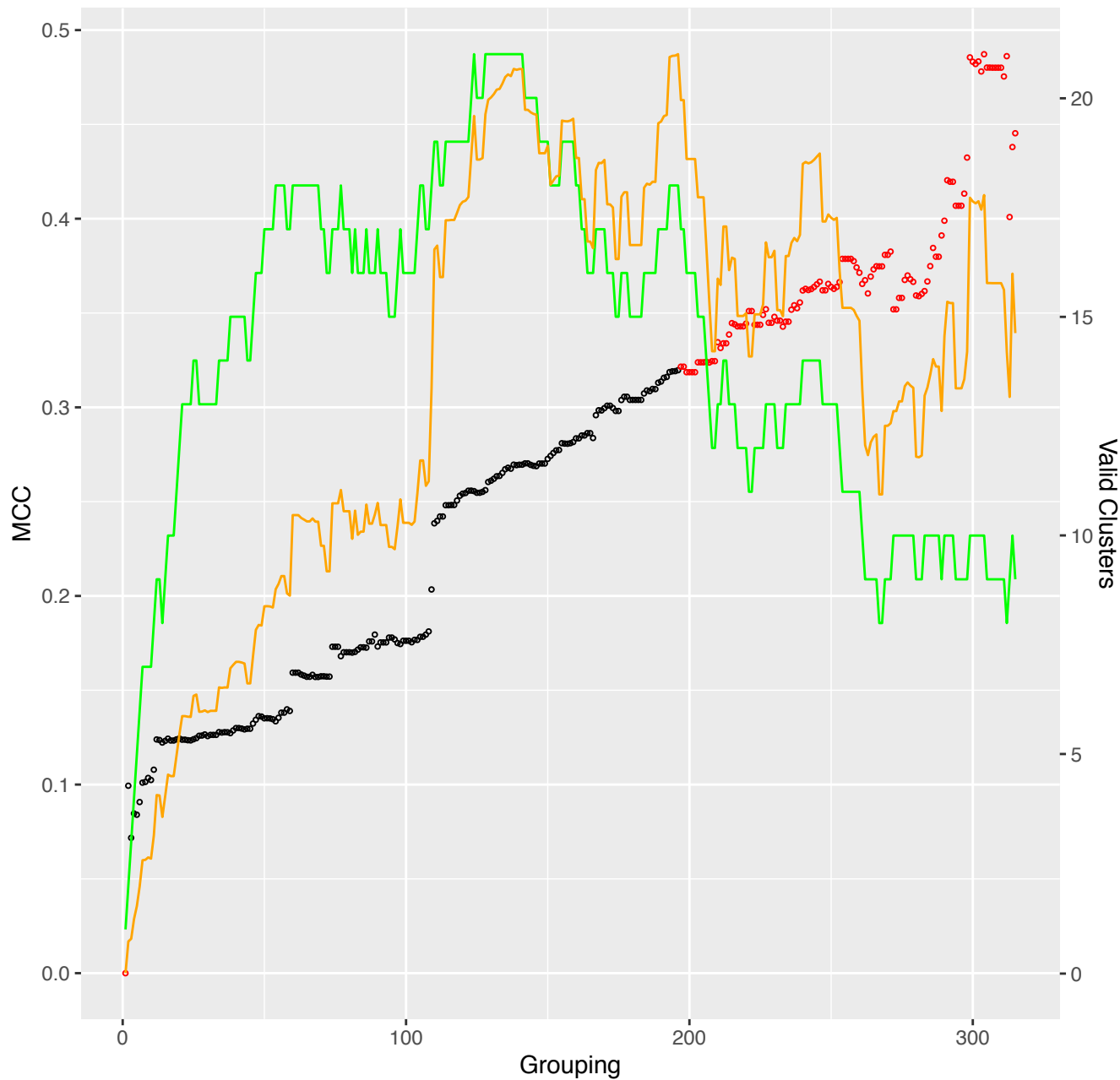
Concatenated tree (with Ns) : grouping per country



Concatenated tree (with Ns) : grouping per continent



Concatenated tree (with Ns; no EBNA-1) : grouping per country



Concatenated tree (with Ns; no EBNA-1) : grouping per continent

