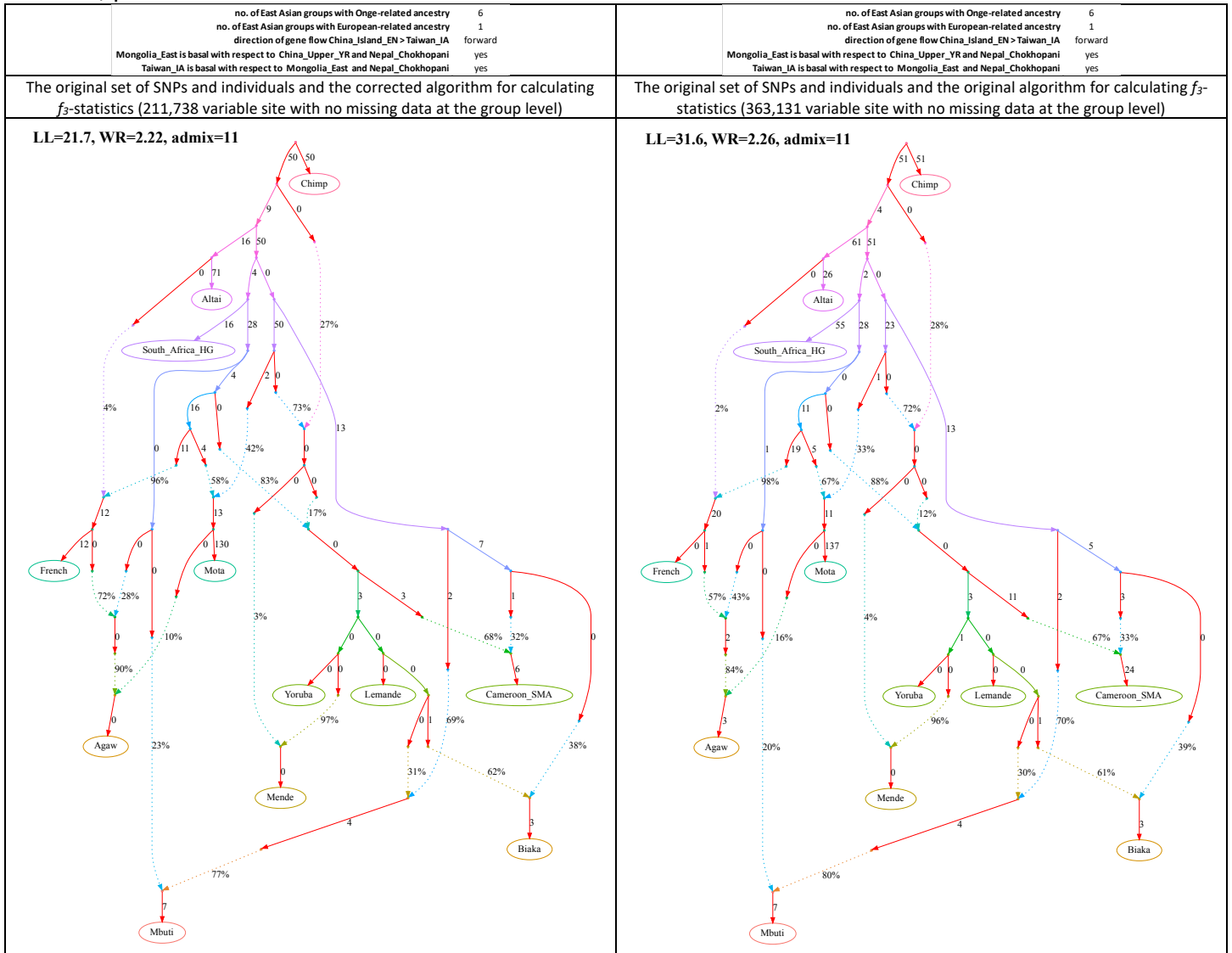
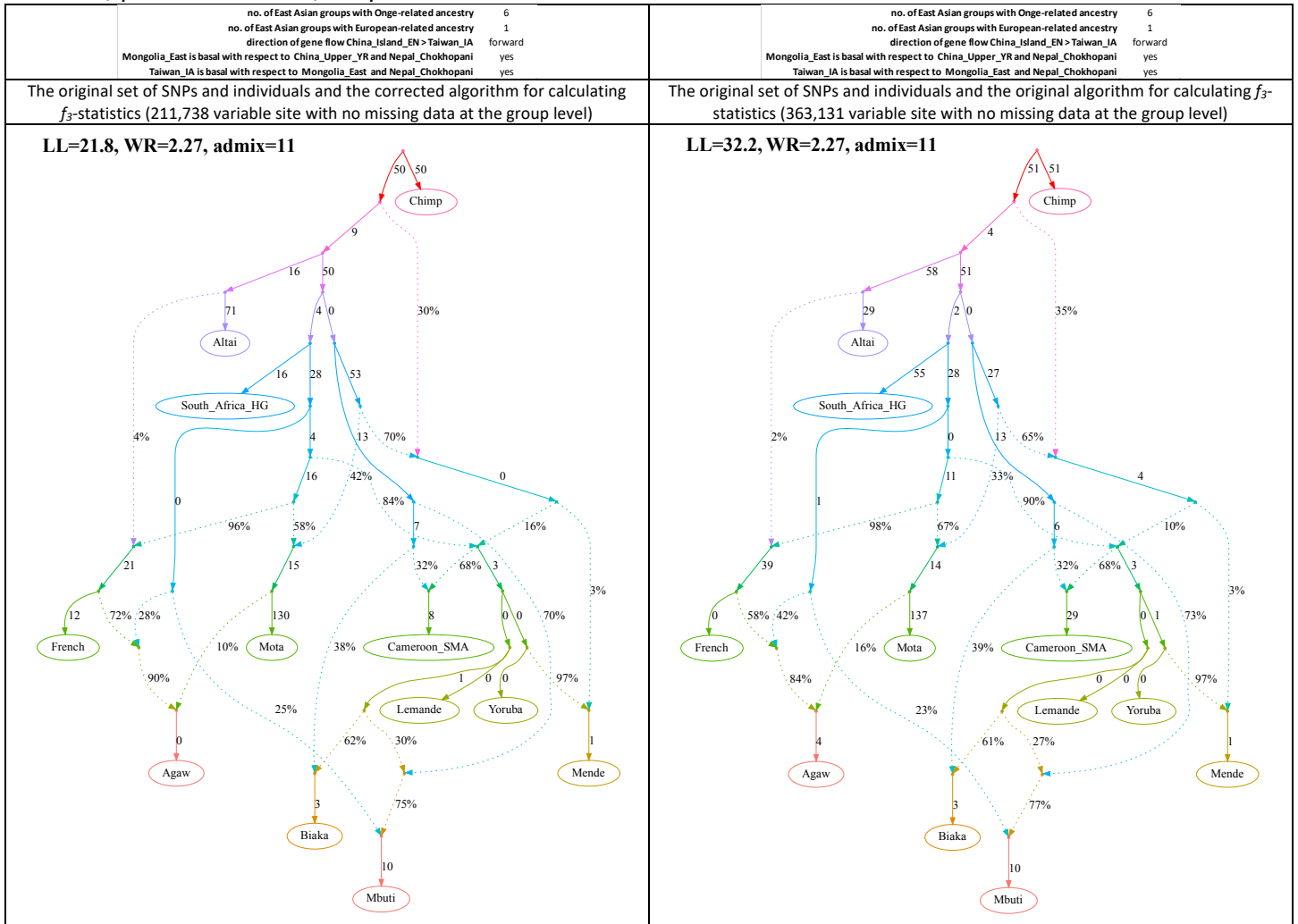


Figure 4–source data 1. Published admixture graph from Lipson *et al.* (2020) and alternative graphs found with *findGraphs* (12 populations, 11 admixture events) using the updated algorithm for calculating f_3 -statistics. The graphs were also re-fitted using the original algorithm for calculating f_3 -statistics. Model parameters (graph edges) that were inferred to be unidentifiable are plotted in red.

a, published model



b, published model, simplified



Selected claims by Lipson *et al.* 2020 relying on the admixture graph:

- 1) A lineage maximized in present-day West African groups (Lemande, Mende, and Yoruba) also contributed some ancestry to the ancient Shum Laka individual, and present-day Biaka and Mbuti;
- 2) another ancestry component in Shum Laka is a deep-branching lineage maximized in rainforest hunter-gatherers Biaka and Mbuti;
- 3) “super-archaic” ancestry (i.e., diverging at the modern human/Neanderthal split point or deeper) contributed to Biaka, Shum Laka, Mbuti, Lemande, Mende, and Yoruba;
- 4) a ghost modern human lineage (or lineages) contributed to Agaw, Mota, Biaka, Shum Laka, Mbuti, Lemande, Mende, and Yoruba.

c, selected alternative models fitting nominally better than the published one



support for claim 1 not supported
 support for claim 2 not supported
 support for claim 3 partial
 support for claim 4 not supported

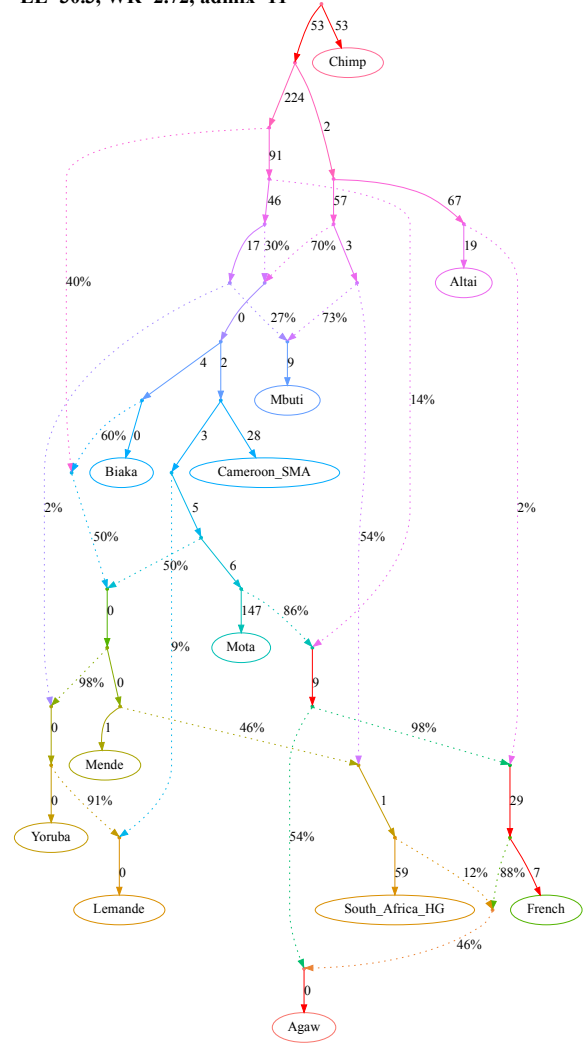
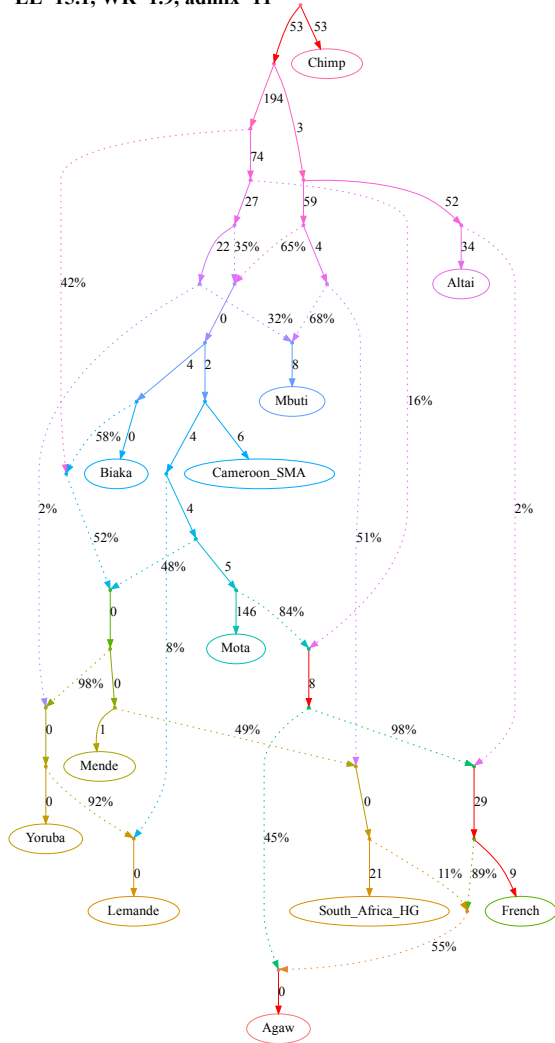
support for claim 1 not supported
 support for claim 2 not supported
 support for claim 3 partial
 support for claim 4 not supported

The original set of SNPs and individuals and the corrected algorithm for calculating f_3 -statistics (211,738 variable site with no missing data at the group level)

The original set of SNPs and individuals and the original algorithm for calculating f_3 -statistics (363,131 variable site with no missing data at the group level)

LL=15.1, WR=1.9, admix=11

LL=30.3, WR=2.72, admix=11



d, selected alternative models fitting nominally better than the published one



support for claim 1 partial
 support for claim 2 not supported
 support for claim 3 not supported
 support for claim 4 partial

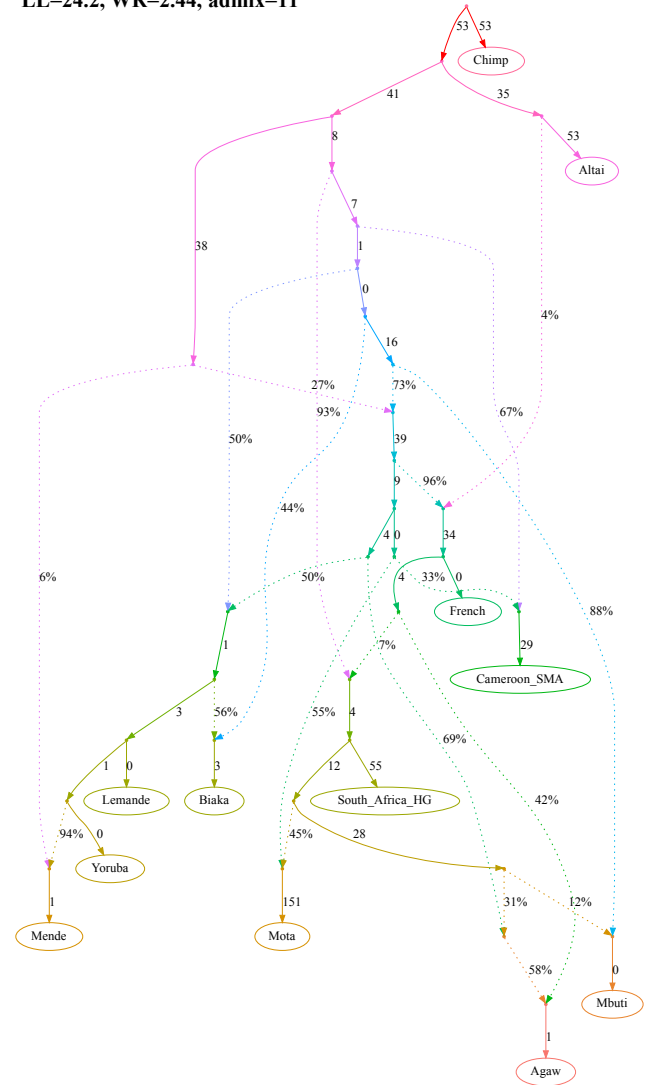
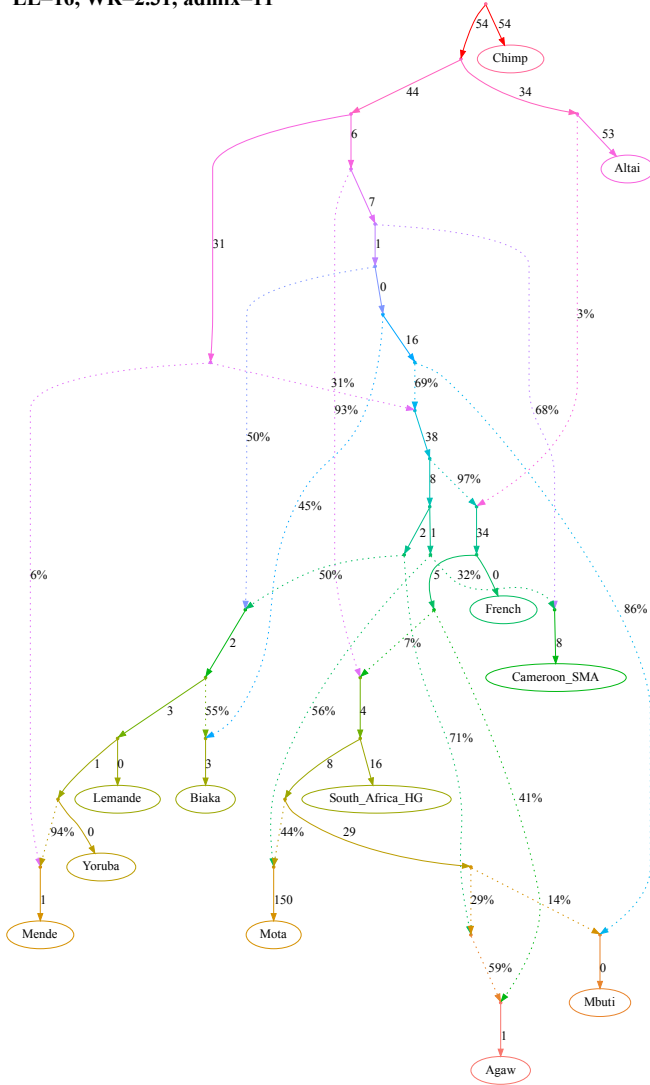
support for claim 1 partial
 support for claim 2 not supported
 support for claim 3 not supported
 support for claim 4 partial

The original set of SNPs and individuals and the corrected algorithm for calculating f_3 -statistics (211,738 variable site with no missing data at the group level)

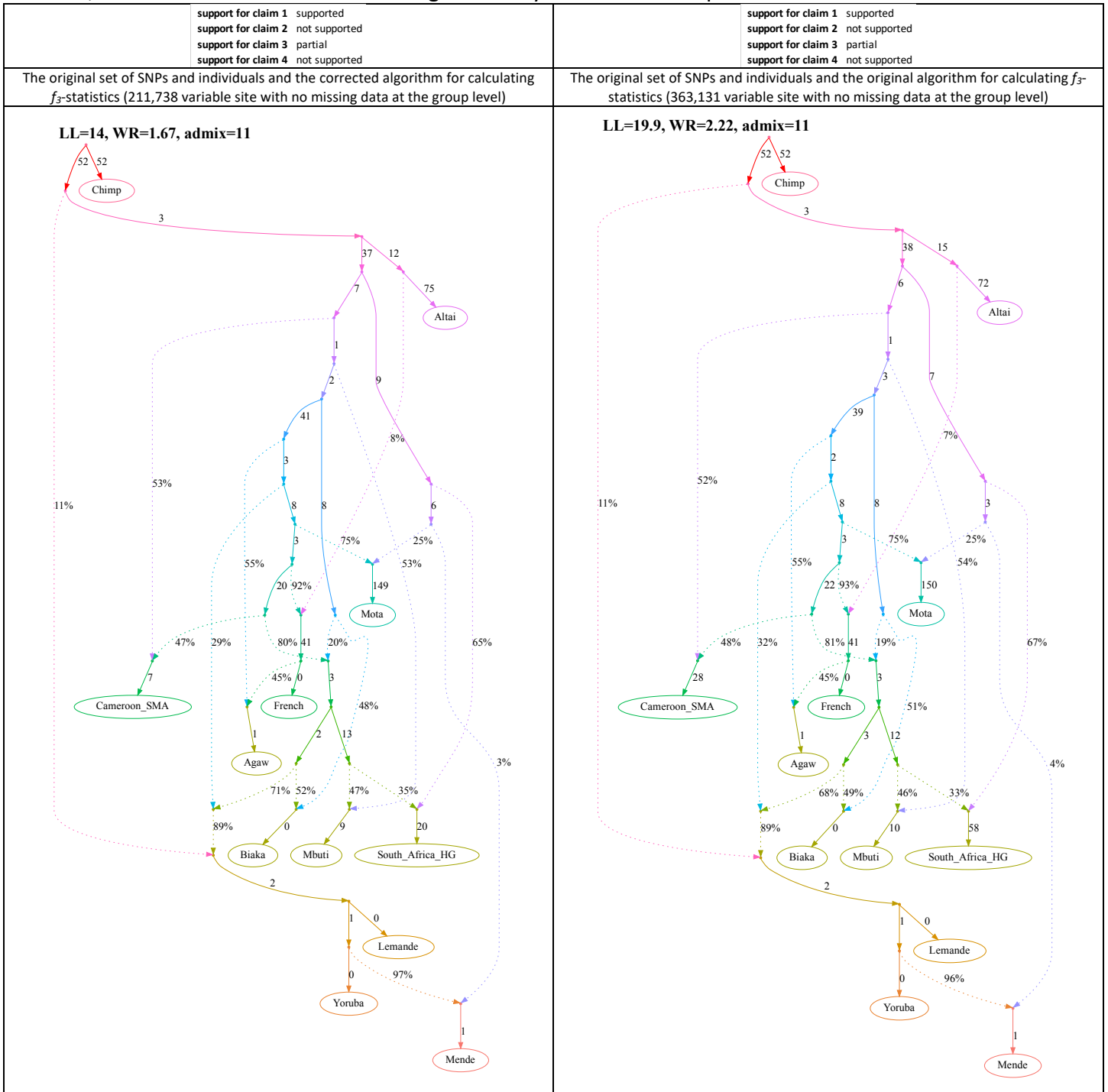
The original set of SNPs and individuals and the original algorithm for calculating f_3 -statistics (363,131 variable site with no missing data at the group level)

LL=16, WR=2.31, admix=11

LL=24.2, WR=2.44, admix=11



e, selected alternative models fitting nominally better than the published one



support for claim 1 not supported
 support for claim 2 partial
 support for claim 3 partial
 support for claim 4 partial

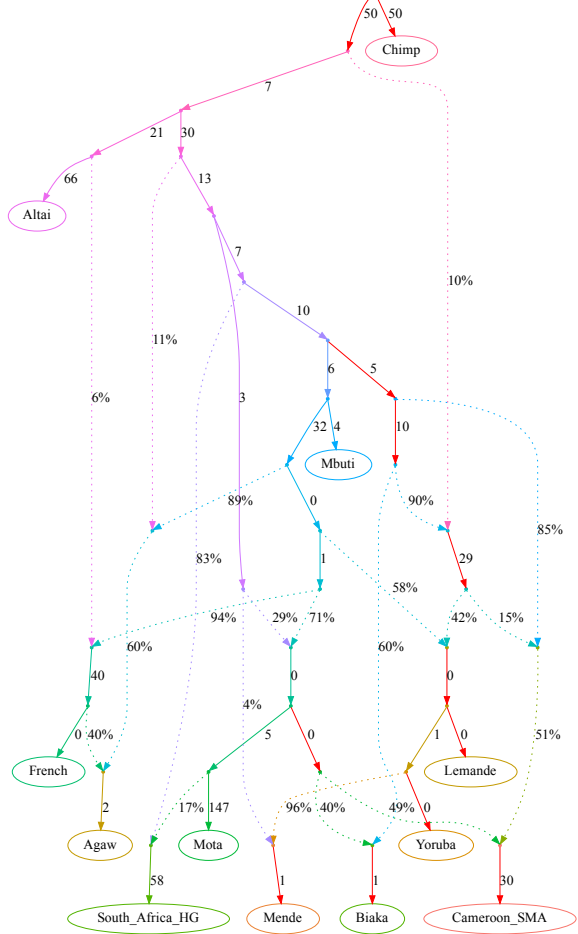
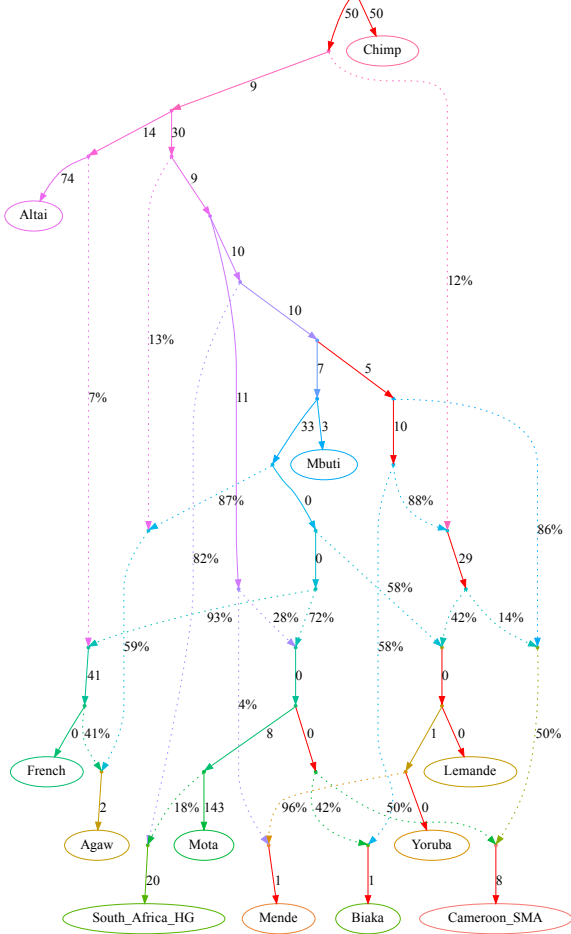
support for claim 1 not supported
 support for claim 2 partial
 support for claim 3 partial
 support for claim 4 partial

The original set of SNPs and individuals and the corrected algorithm for calculating f_3 -statistics (211,738 variable site with no missing data at the group level)

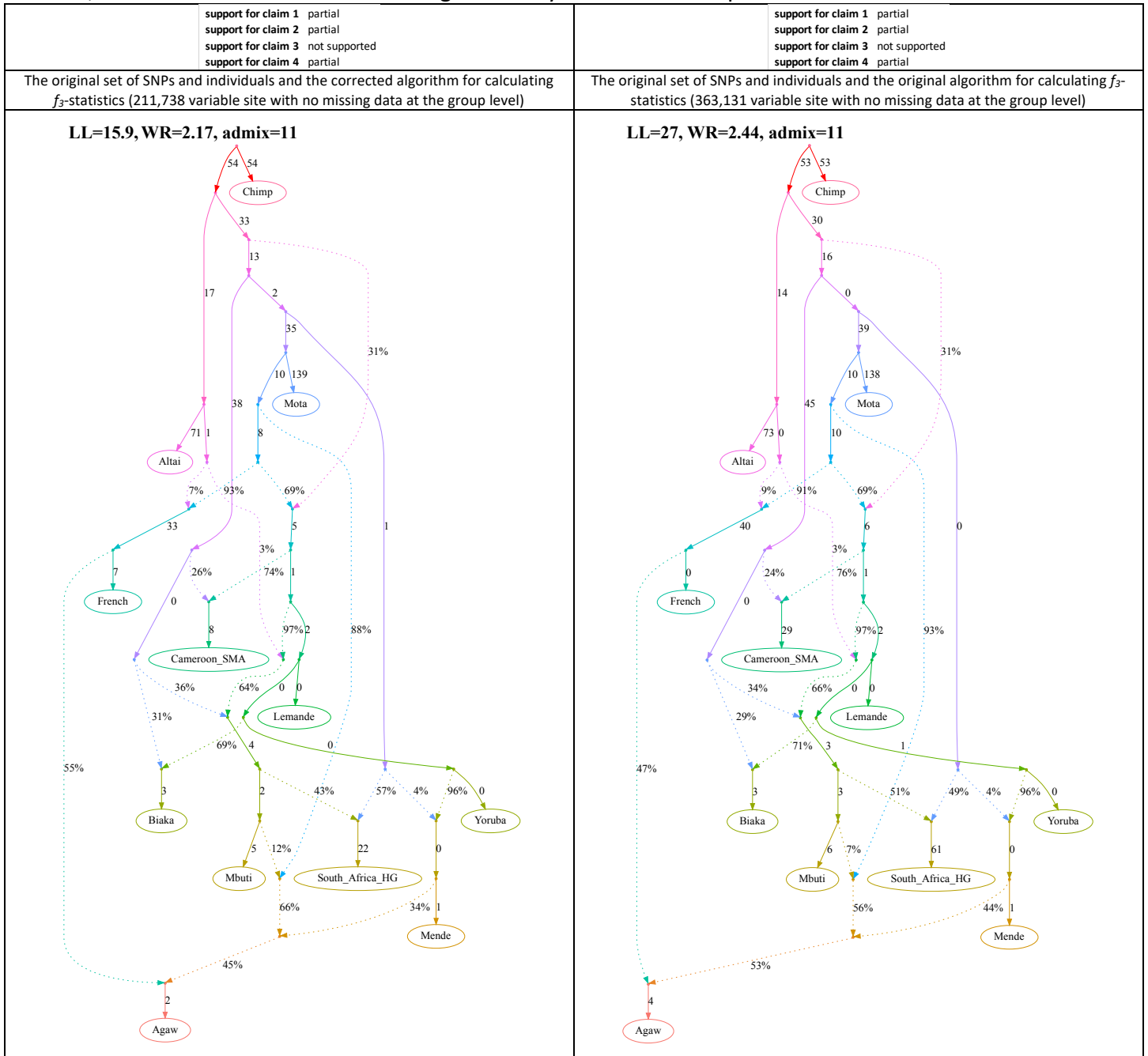
The original set of SNPs and individuals and the original algorithm for calculating f_3 -statistics (363,131 variable site with no missing data at the group level)

LL=14.6, WR=1.7, admix=11

LL=28.9, WR=2.45, admix=11



f, selected alternative models fitting nominally better than the published one



support for claim 1 partial
 support for claim 2 not supported
 support for claim 3 partial
 support for claim 4 partial

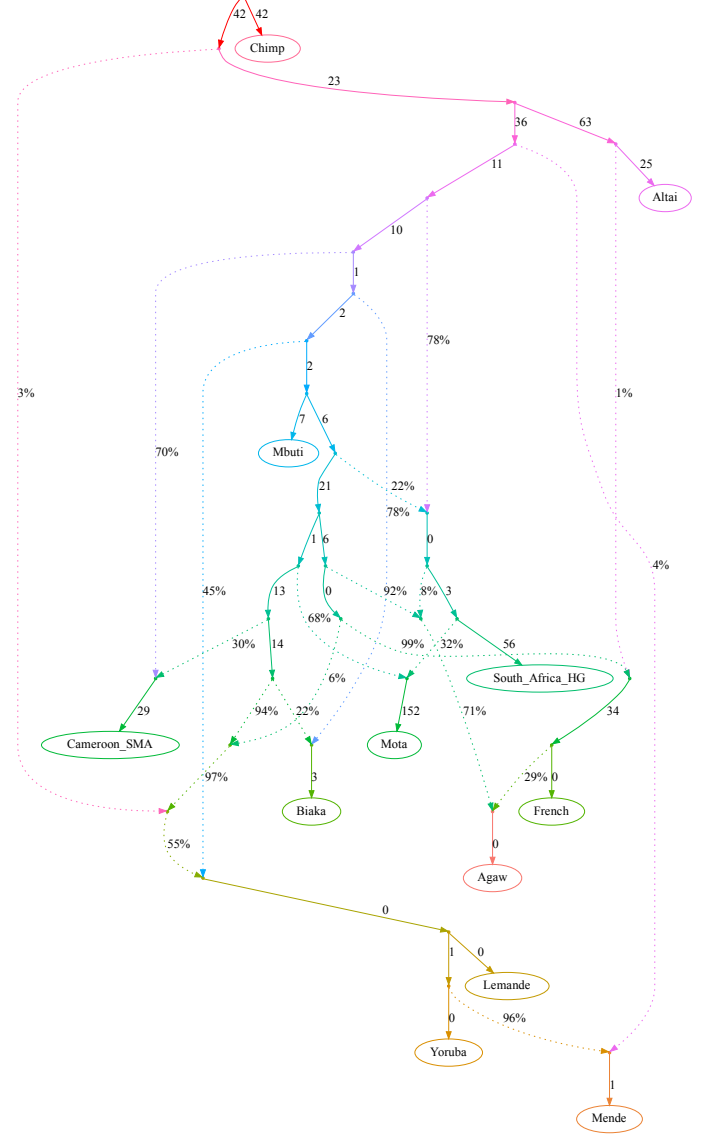
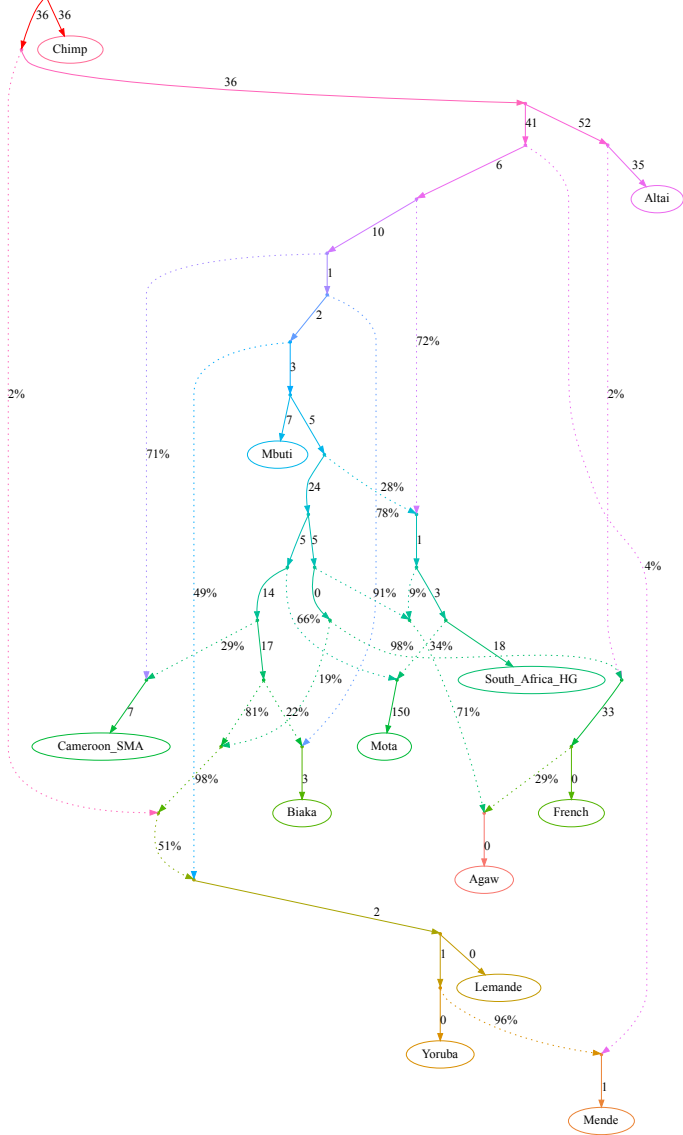
support for claim 1 partial
 support for claim 2 not supported
 support for claim 3 partial
 support for claim 4 partial

The original set of SNPs and individuals and the corrected algorithm for calculating f_3 -statistics (211,738 variable site with no missing data at the group level)

The original set of SNPs and individuals and the original algorithm for calculating f_3 -statistics (363,131 variable site with no missing data at the group level)

LL=16.1, WR=1.78, admix=11

LL=25, WR=2.08, admix=11



g, selected alternative models fitting nominally better than the published one



support for claim 1 partial
 support for claim 2 partial
 support for claim 3 supported
 support for claim 4 not supported

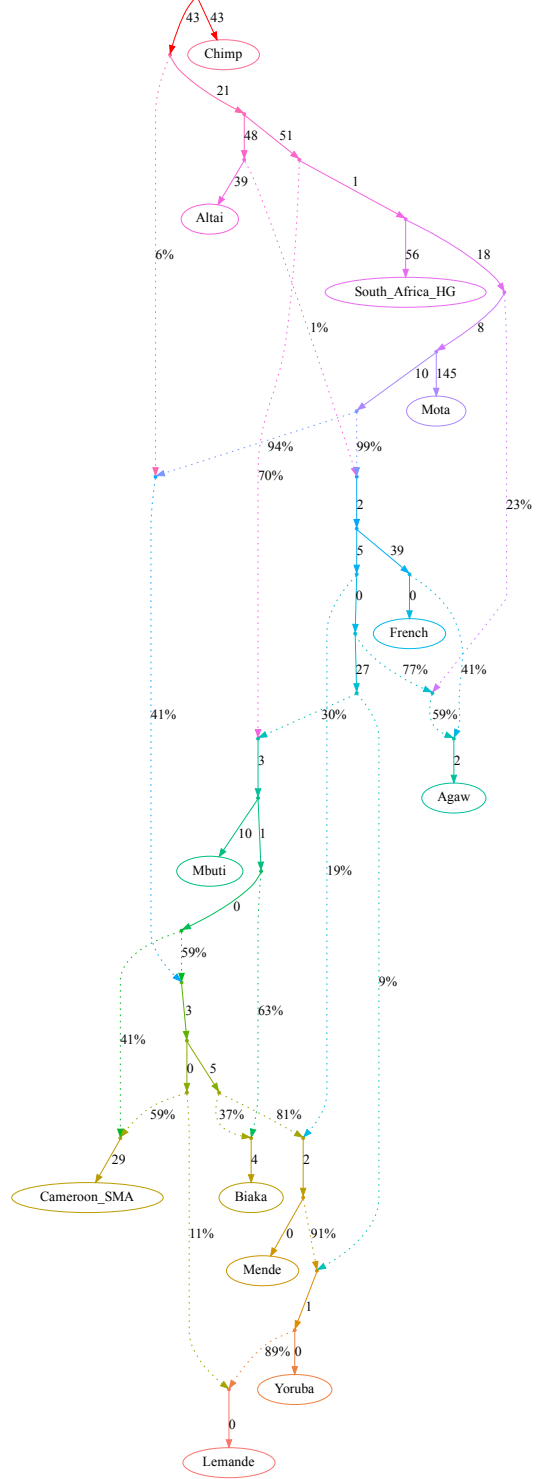
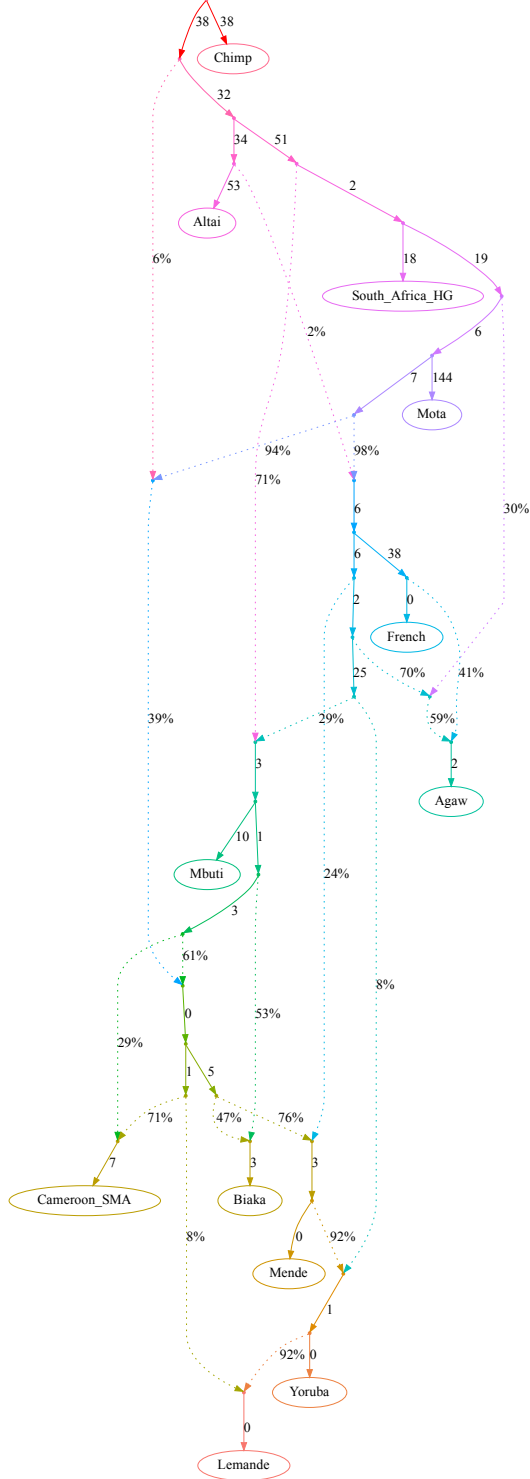
support for claim 1 partial
 support for claim 2 partial
 support for claim 3 supported
 support for claim 4 not supported

The original set of SNPs and individuals and the corrected algorithm for calculating f_3 -statistics (211,738 variable site with no missing data at the group level)

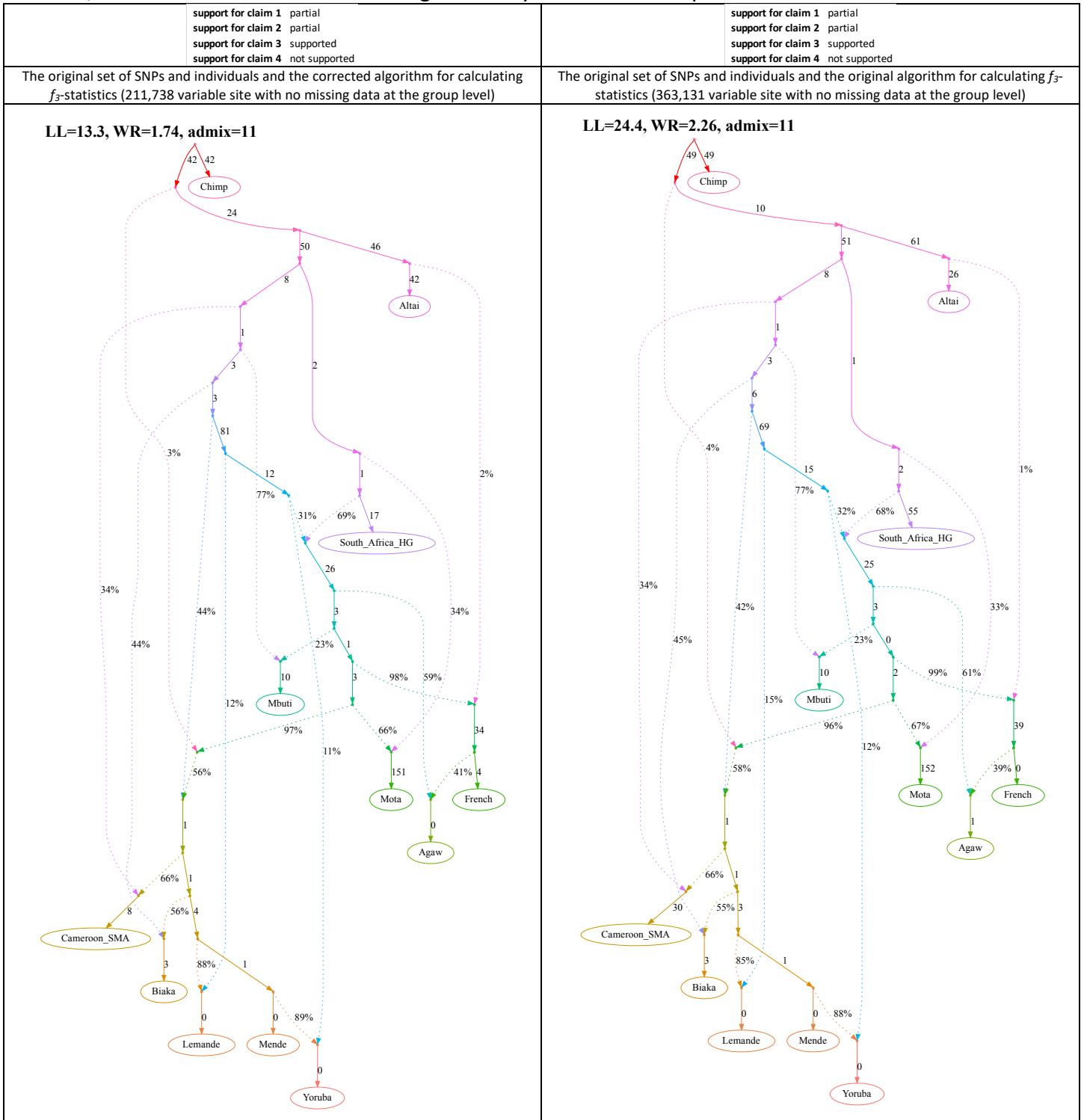
The original set of SNPs and individuals and the original algorithm for calculating f_3 -statistics (363,131 variable site with no missing data at the group level)

LL=13, WR=1.78, admix=11

LL=36.4, WR=3, admix=11

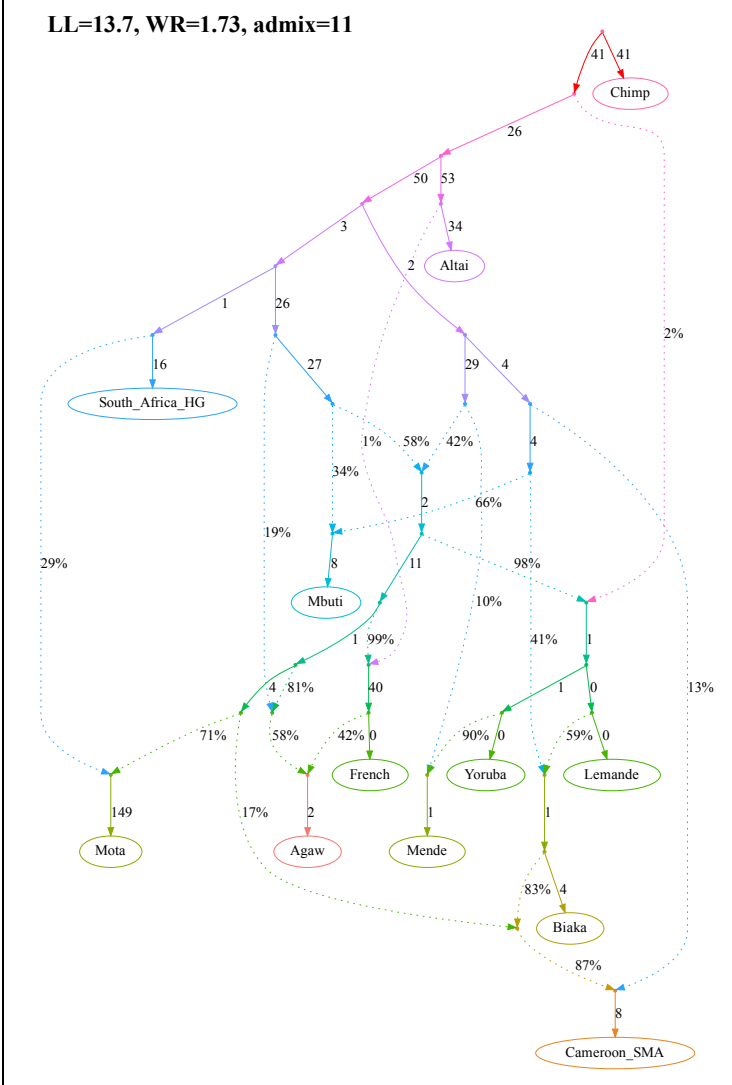


h, selected alternative models fitting nominally better than the published one



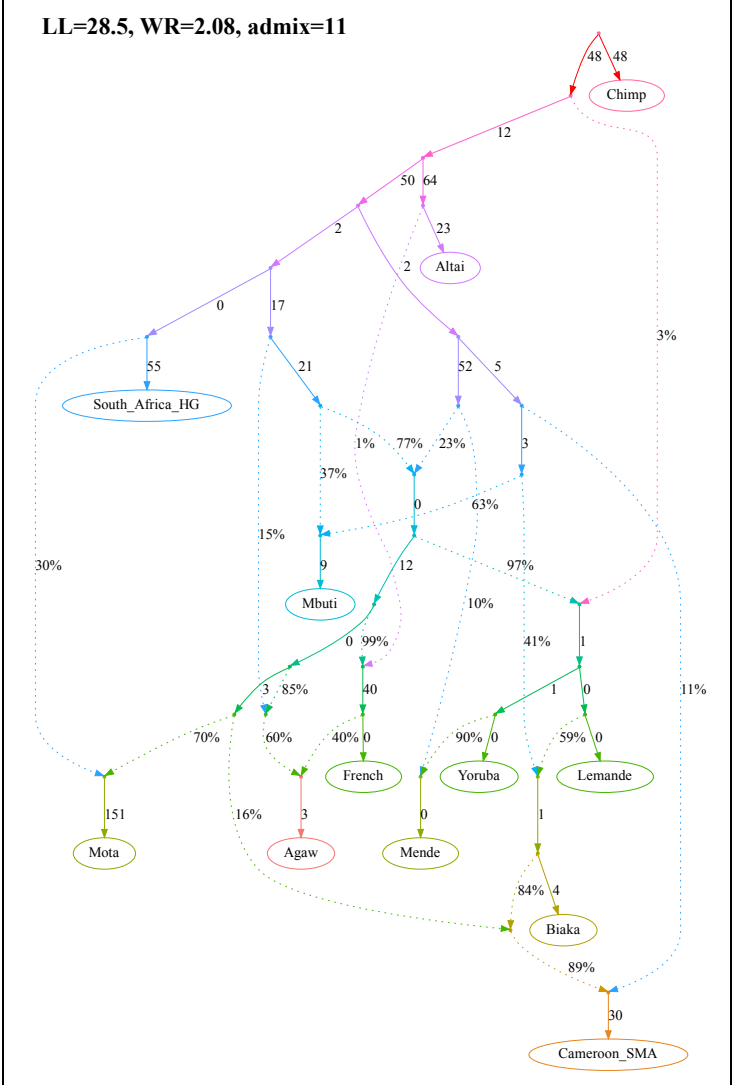
support for claim 1 partial
 support for claim 2 partial
 support for claim 3 supported
 support for claim 4 not supported

The original set of SNPs and individuals and the corrected algorithm for calculating f_3 -statistics (211,738 variable site with no missing data at the group level)

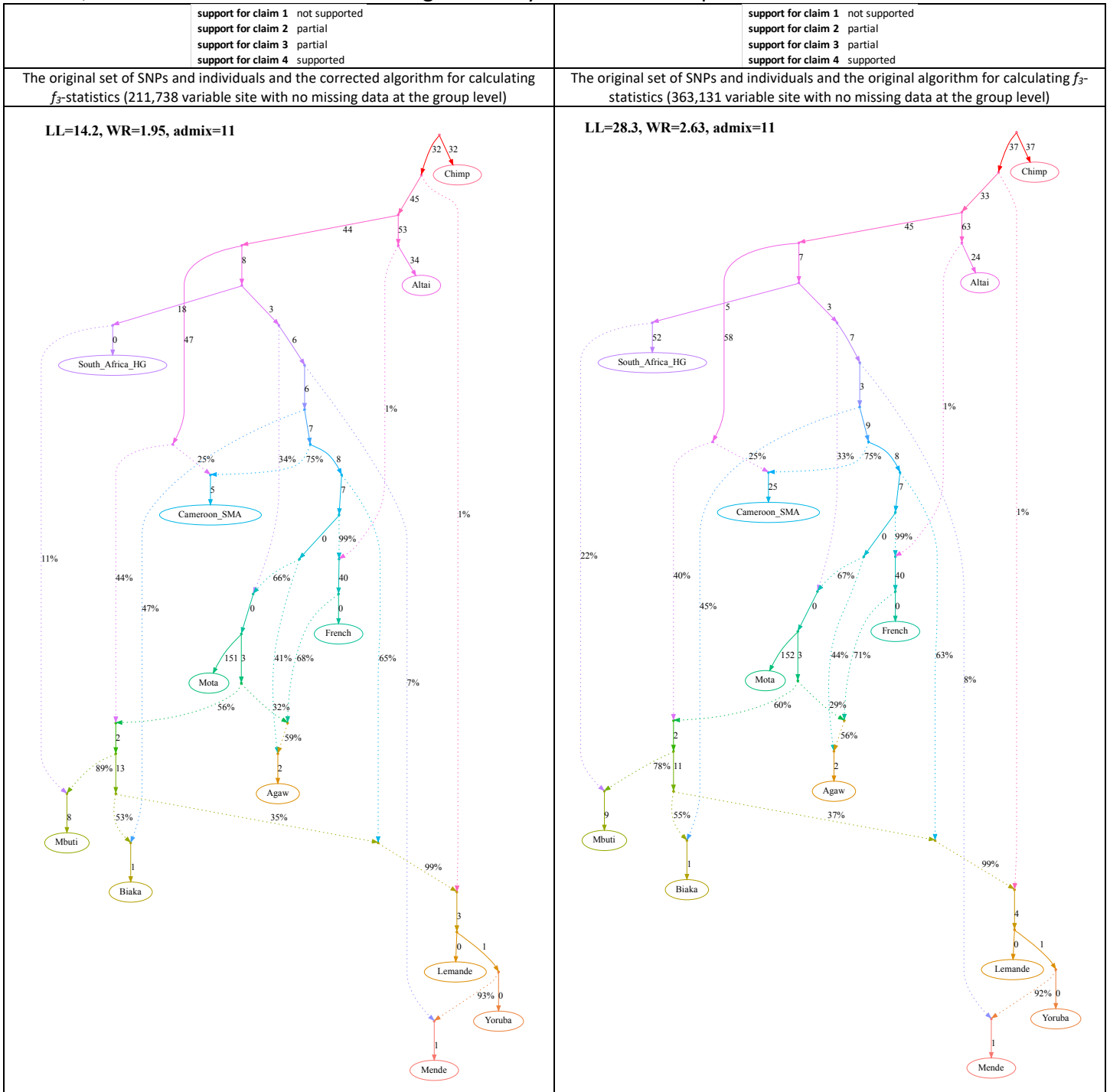


support for claim 1 partial
 support for claim 2 partial
 support for claim 3 supported
 support for claim 4 not supported

The original set of SNPs and individuals and the original algorithm for calculating f_3 -statistics (363,131 variable site with no missing data at the group level)



i, selected alternative models fitting nominally better than the published one



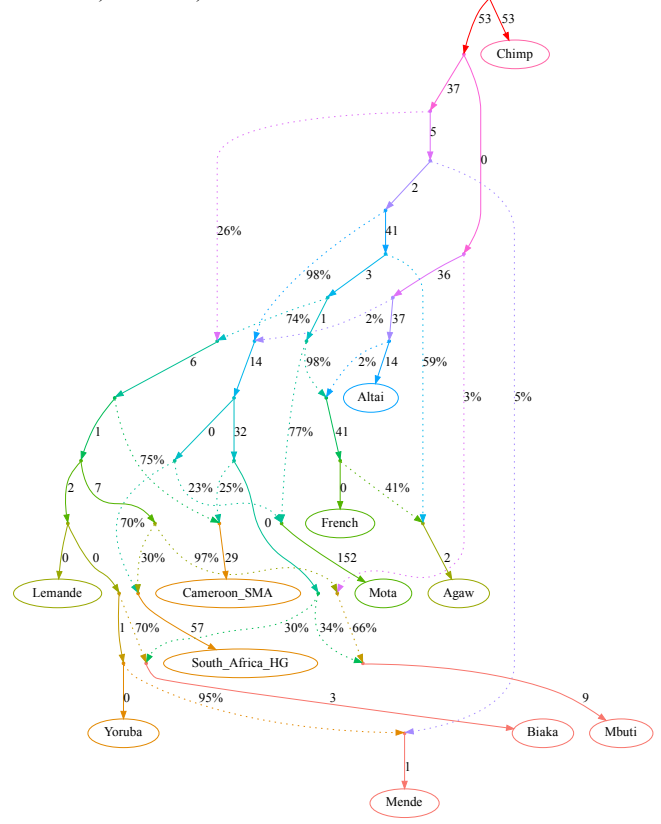
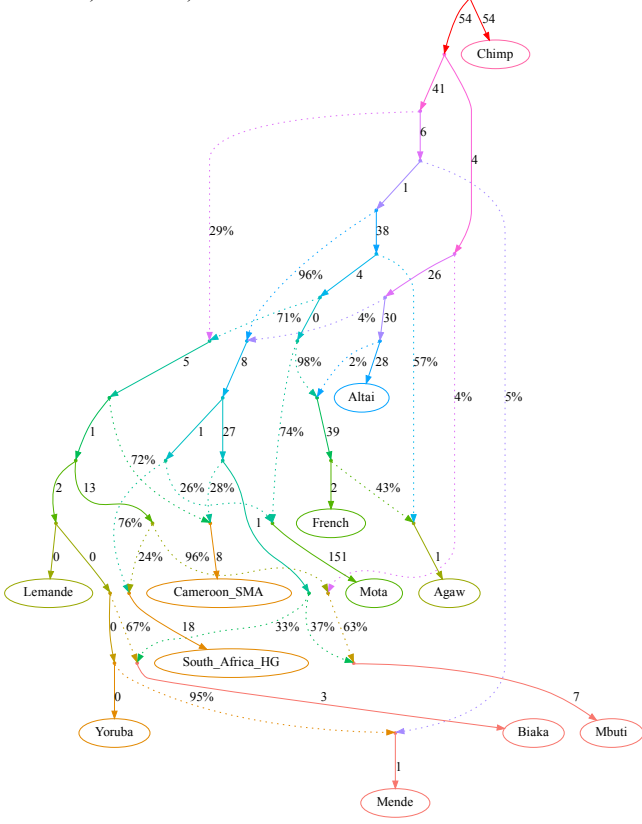
support for claim 1 supported support for claim 2 partial support for claim 3 not supported support for claim 4 partial	support for claim 1 supported support for claim 2 partial support for claim 3 not supported support for claim 4 partial
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The original set of SNPs and individuals and the corrected algorithm for calculating f_3 -statistics (211,738 variable site with no missing data at the group level)

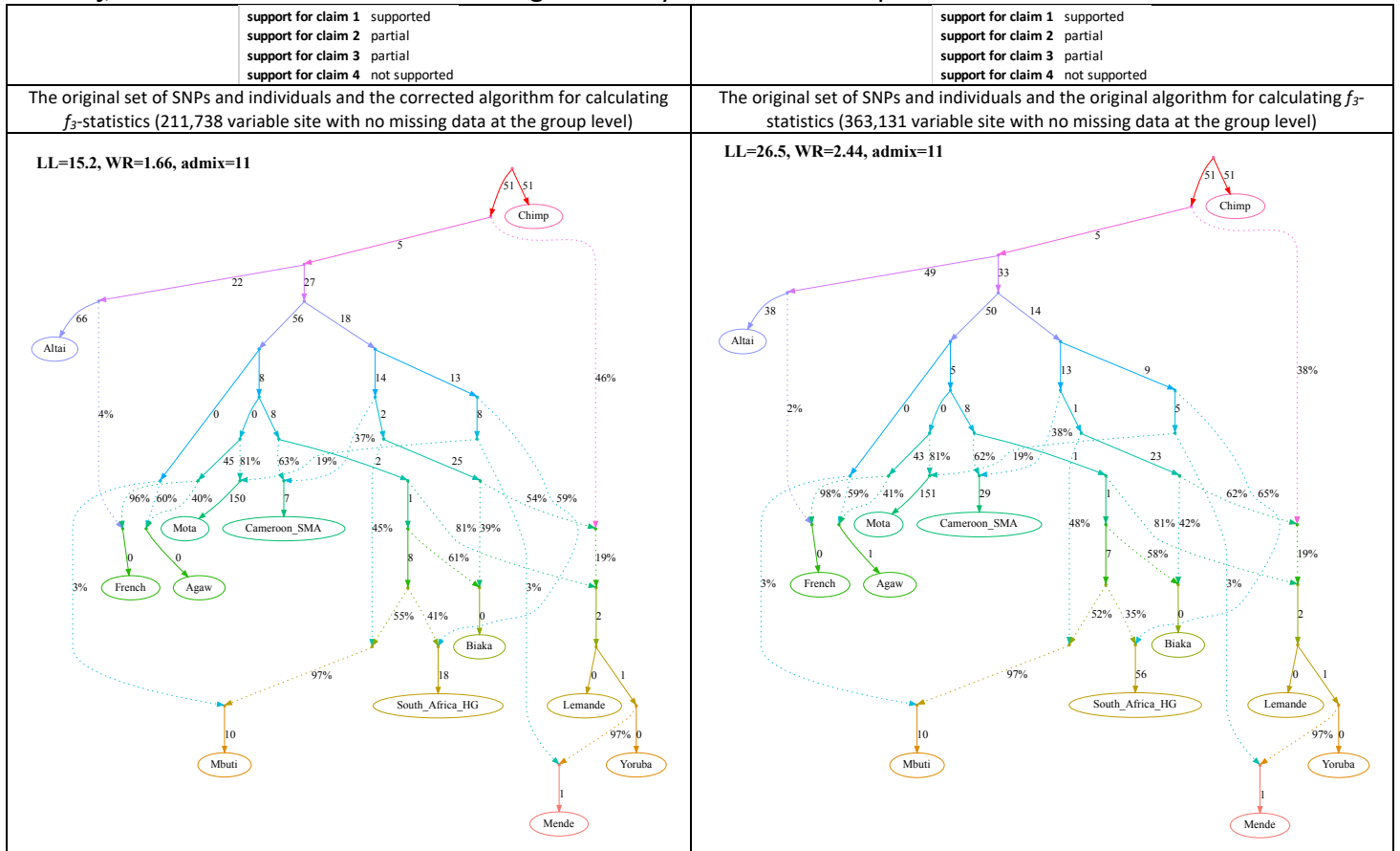
The original set of SNPs and individuals and the original algorithm for calculating f_3 -statistics (363,131 variable site with no missing data at the group level)

LL=14.9, WR=1.64, admix=11

LL=24.1, WR=2.08, admix=11



j, selected alternative models fitting nominally better than the published one



support for claim 1 supported
 support for claim 2 not supported
 support for claim 3 partial
 support for claim 4 partial

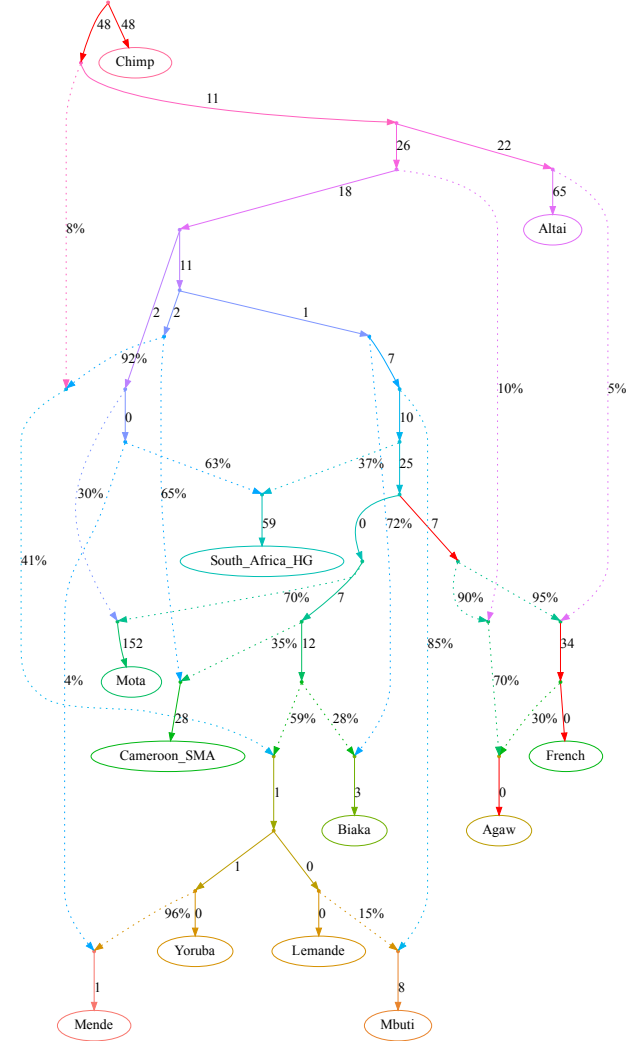
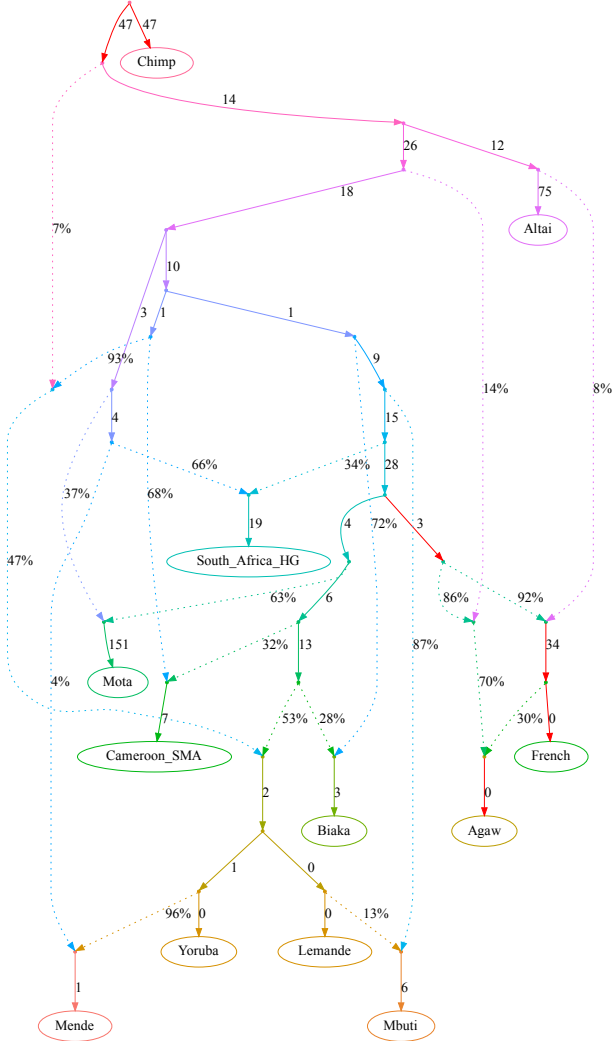
support for claim 1 supported
 support for claim 2 not supported
 support for claim 3 partial
 support for claim 4 partial

The original set of SNPs and individuals and the corrected algorithm for calculating f_3 -statistics (211,738 variable site with no missing data at the group level)

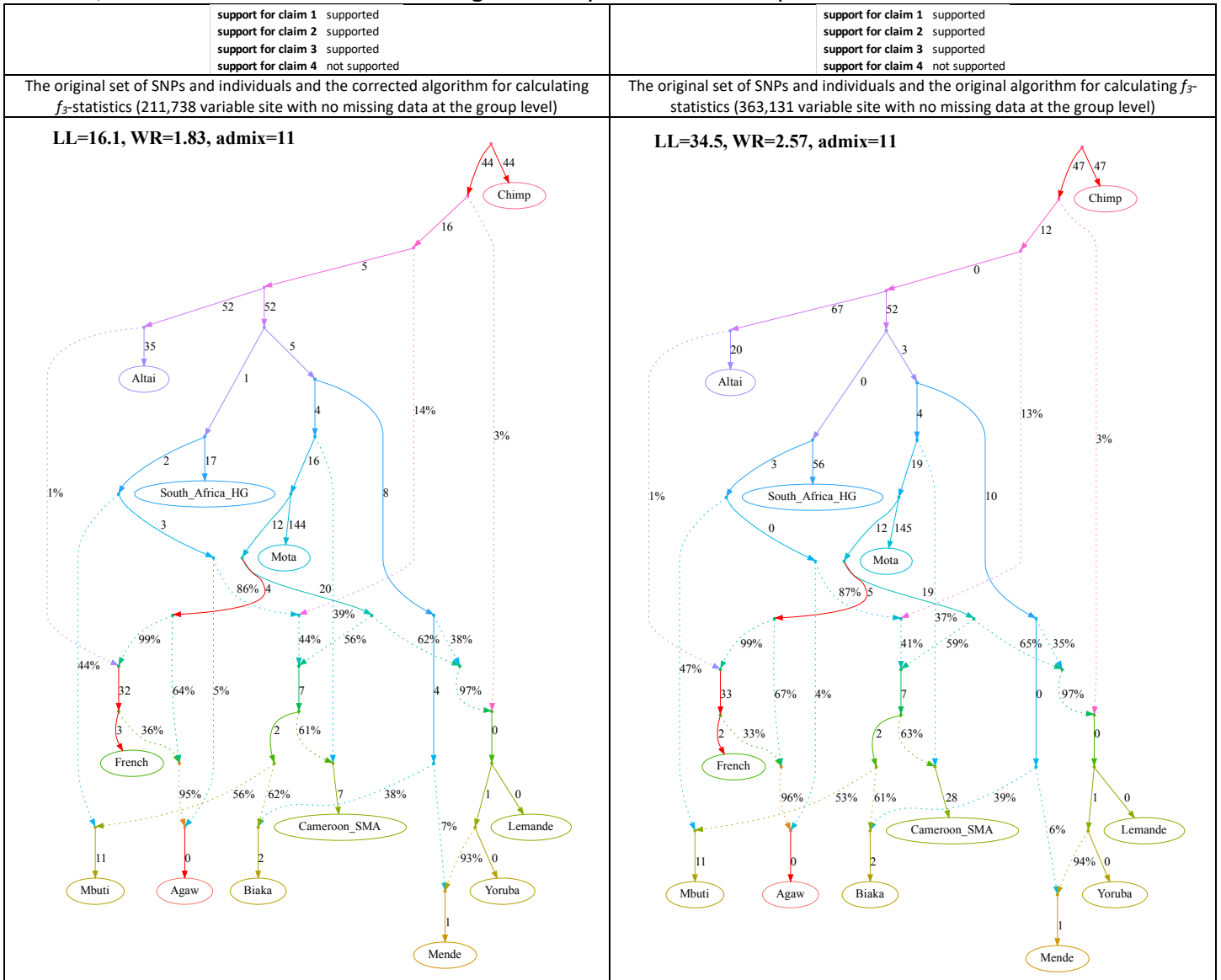
The original set of SNPs and individuals and the original algorithm for calculating f_3 -statistics (363,131 variable site with no missing data at the group level)

LL=15.8, WR=1.78, admix=11

LL=24.3, WR=2.49, admix=11



k, selected alternative models fitting nominally better than the published one



support for claim 1 partial
 support for claim 2 partial
 support for claim 3 partial
 support for claim 4 partial

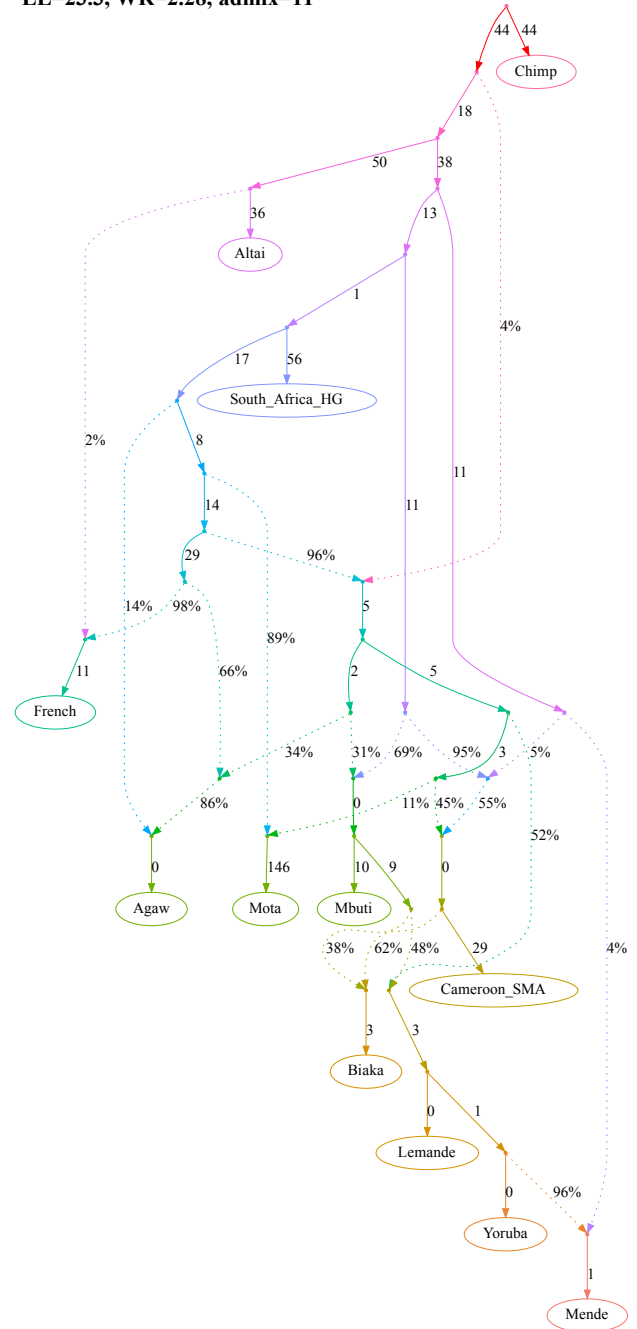
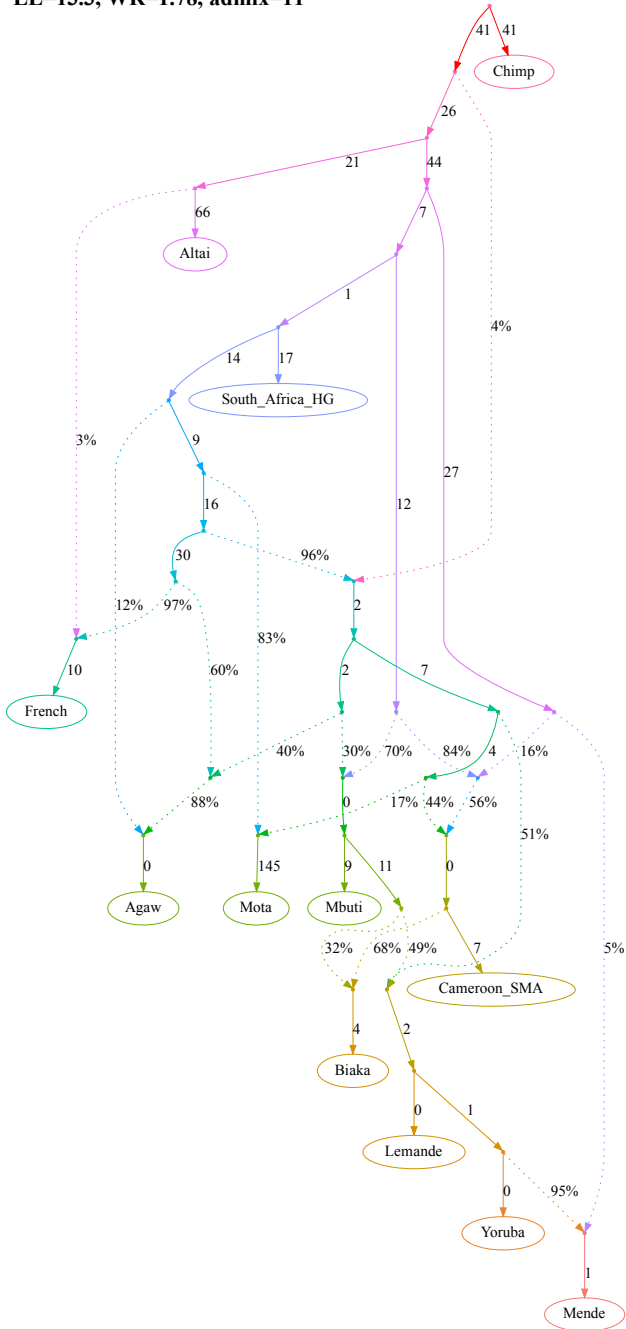
support for claim 1 partial
 support for claim 2 partial
 support for claim 3 partial
 support for claim 4 partial

The original set of SNPs and individuals and the corrected algorithm for calculating f_3 -statistics (211,738 variable site with no missing data at the group level)

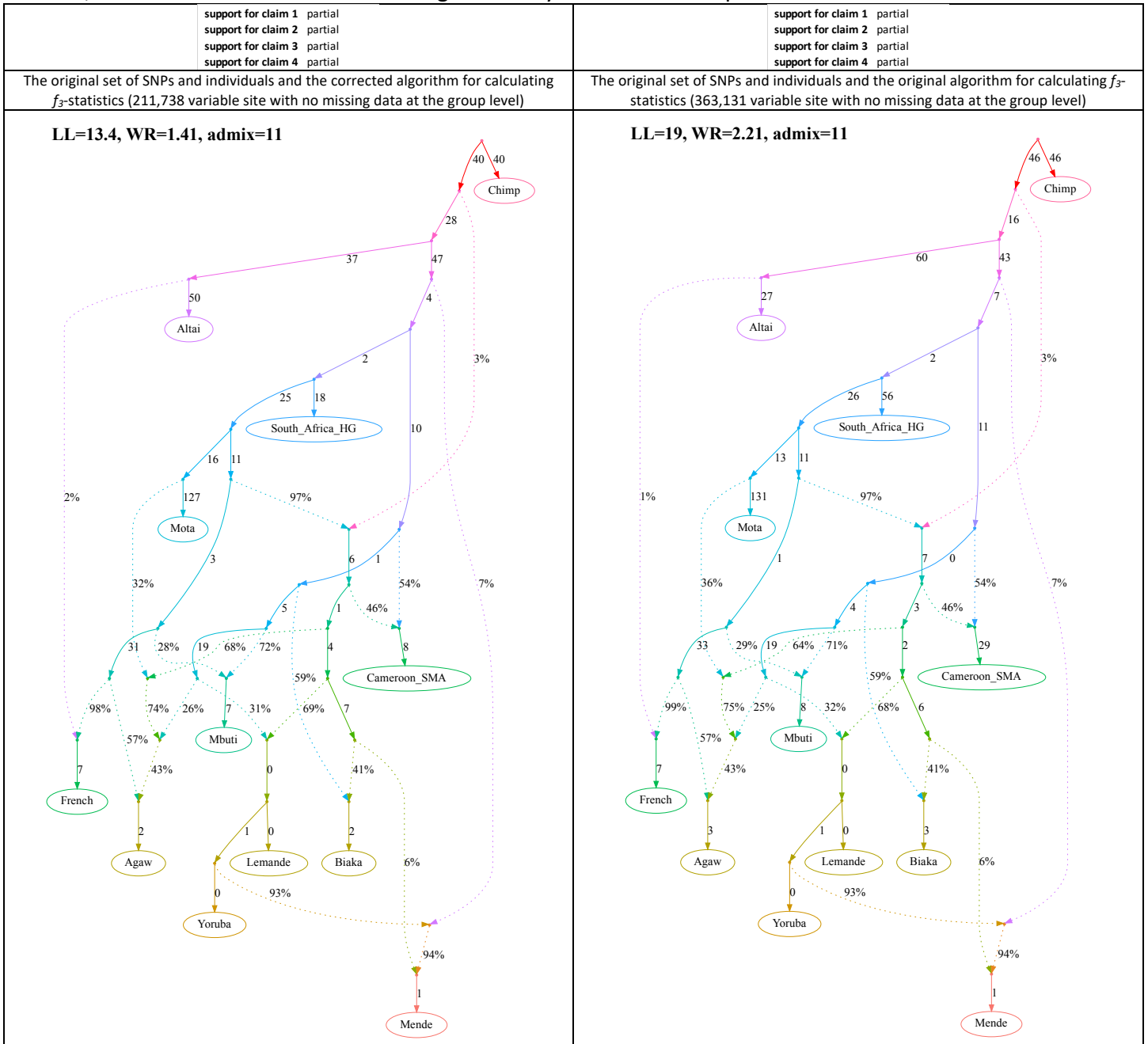
The original set of SNPs and individuals and the original algorithm for calculating f_3 -statistics (363,131 variable site with no missing data at the group level)

LL=13.3, WR=1.78, admix=11

LL=23.3, WR=2.28, admix=11



I, selected alternative models fitting nominally better than the published one



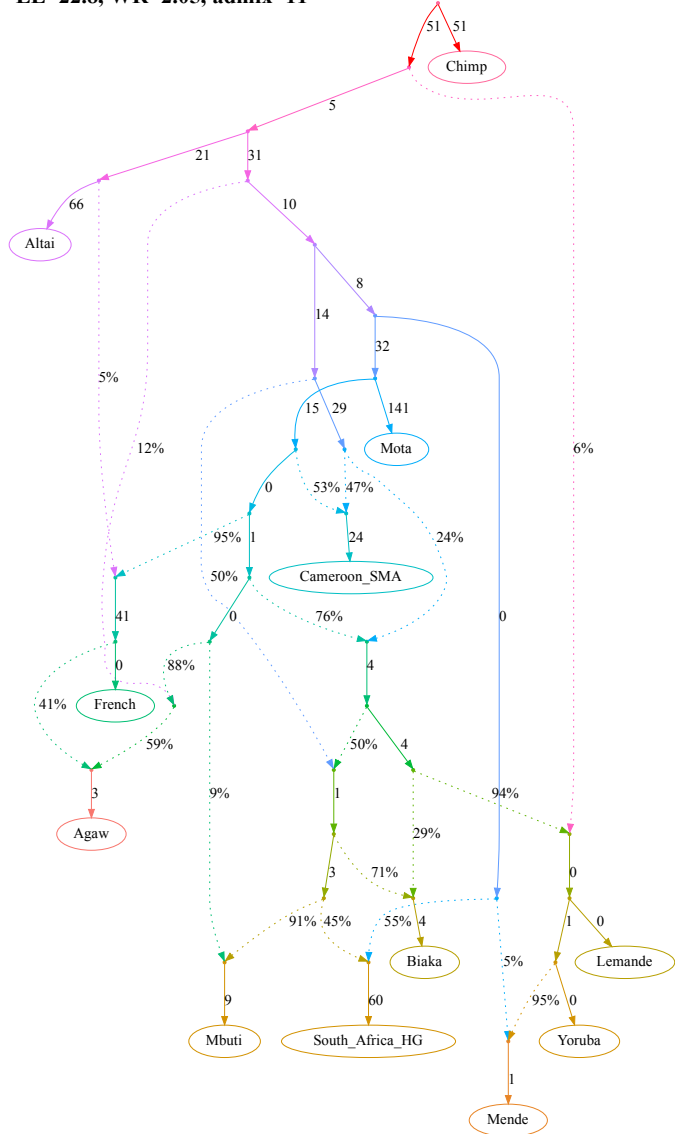
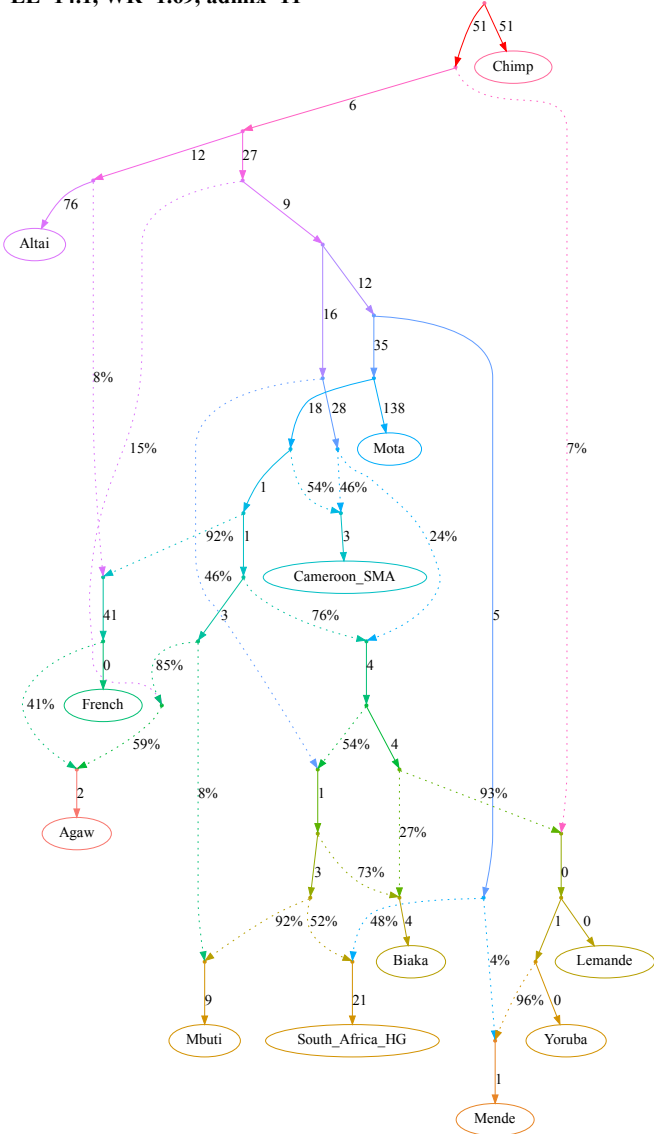
support for claim 1 partial support for claim 2 partial support for claim 3 partial support for claim 4 partial	support for claim 1 partial support for claim 2 partial support for claim 3 partial support for claim 4 partial
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The original set of SNPs and individuals and the corrected algorithm for calculating f_3 -statistics (211,738 variable site with no missing data at the group level)

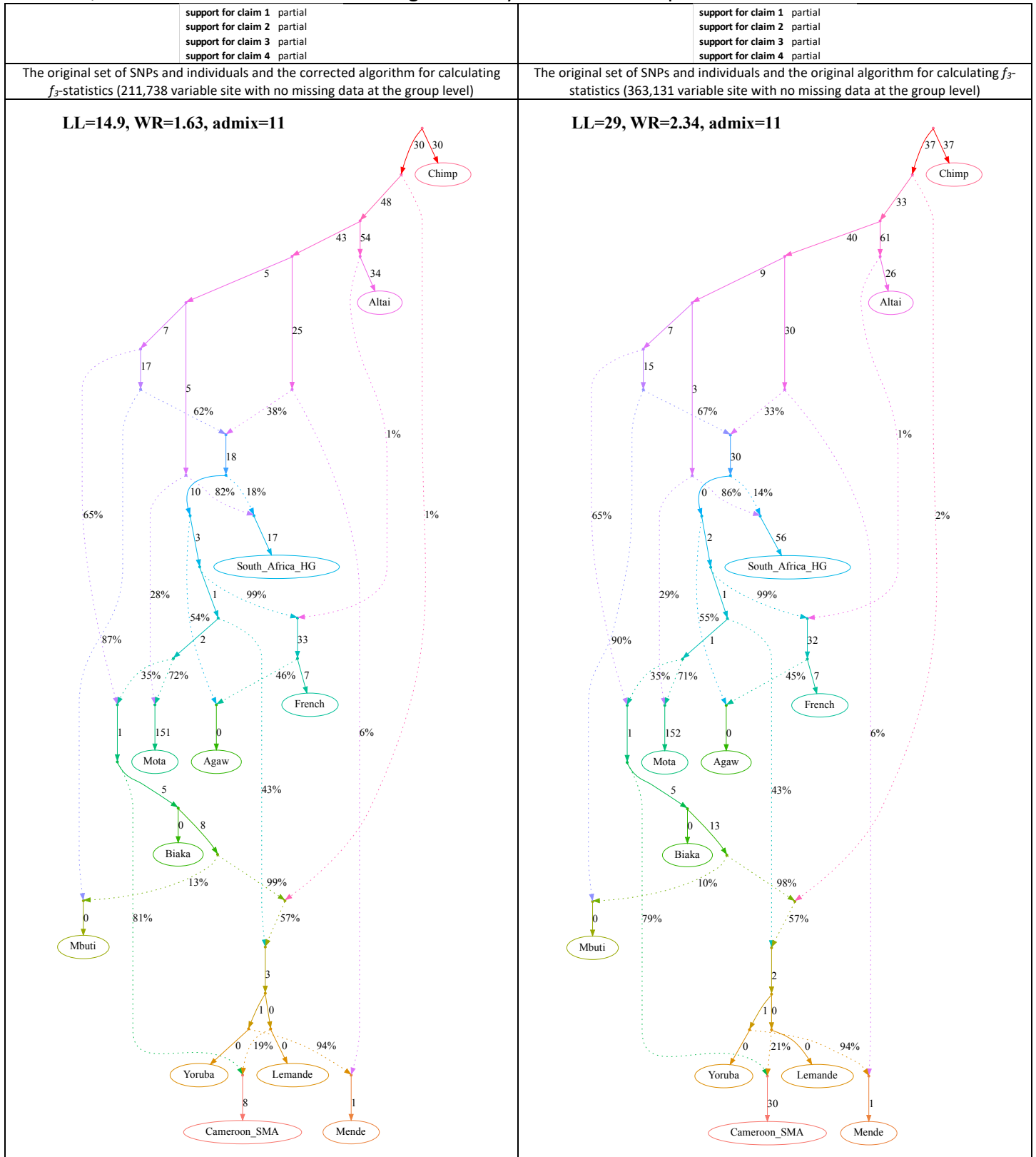
The original set of SNPs and individuals and the original algorithm for calculating f_3 -statistics (363,131 variable site with no missing data at the group level)

LL=14.1, WR=1.69, admix=11

LL=22.8, WR=2.05, admix=11



m, selected alternative models fitting nominally better than the published one



support for claim 1 partial
 support for claim 2 partial
 support for claim 3 partial
 support for claim 4 partial

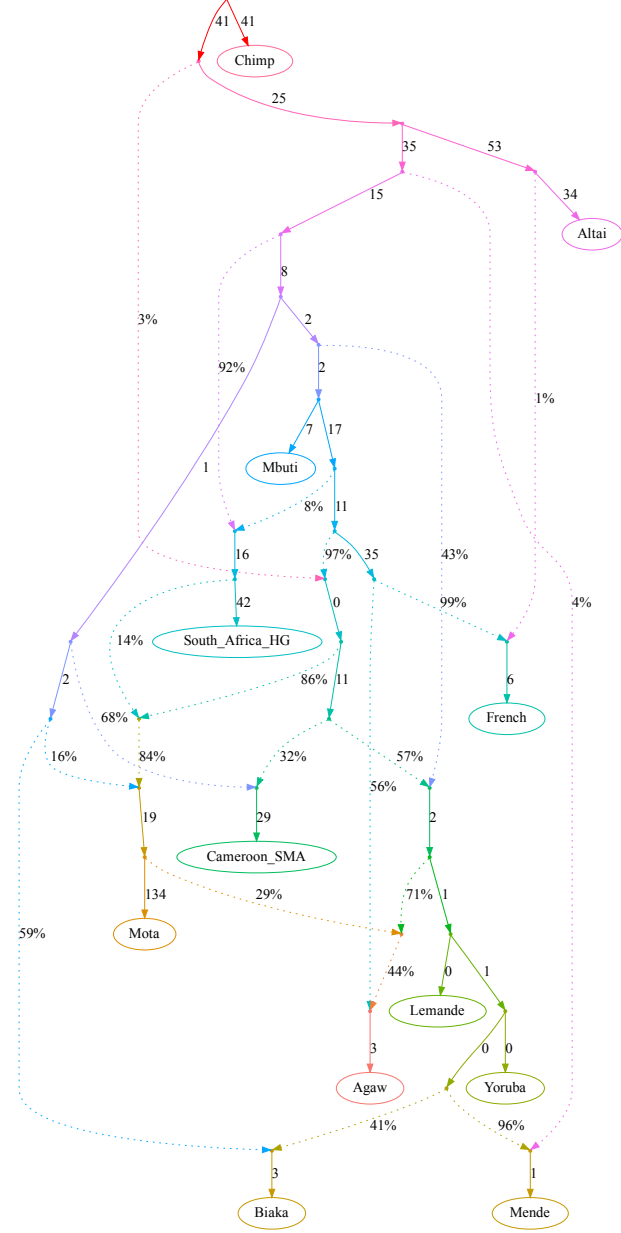
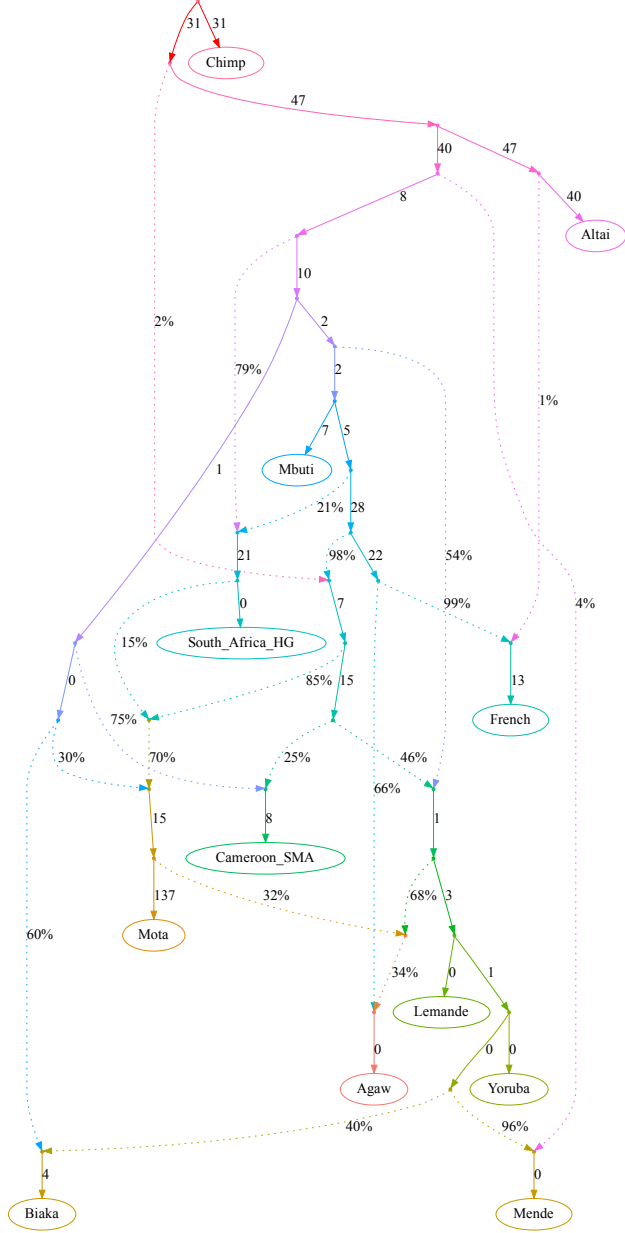
support for claim 1 partial
 support for claim 2 partial
 support for claim 3 partial
 support for claim 4 partial

The original set of SNPs and individuals and the corrected algorithm for calculating f_3 -statistics (211,738 variable site with no missing data at the group level)

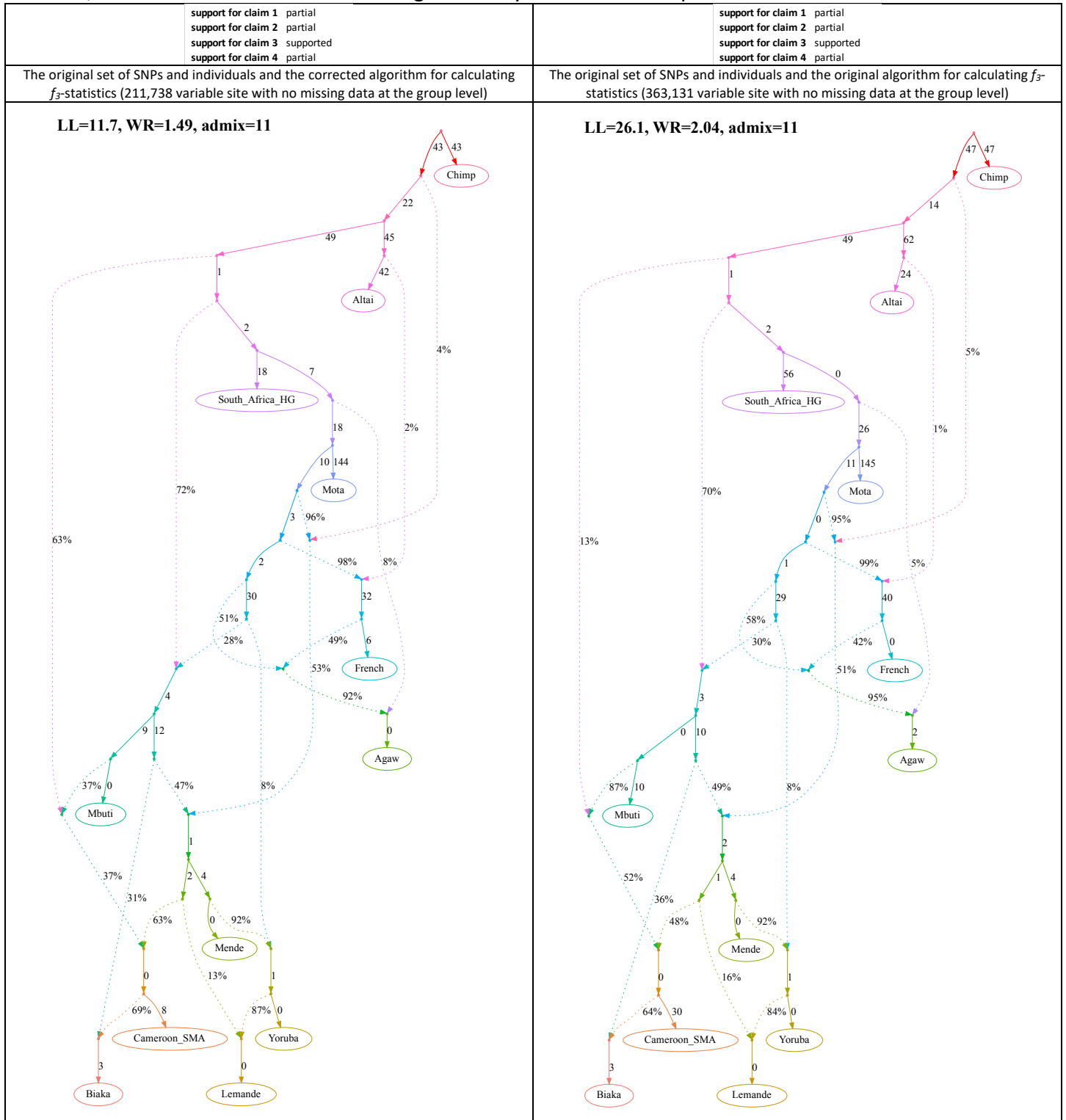
The original set of SNPs and individuals and the original algorithm for calculating f_3 -statistics (363,131 variable site with no missing data at the group level)

LL=15.6, WR=1.66, admix=11

LL=24.5, WR=2.61, admix=11



n, selected alternative models fitting nominally better than the published one



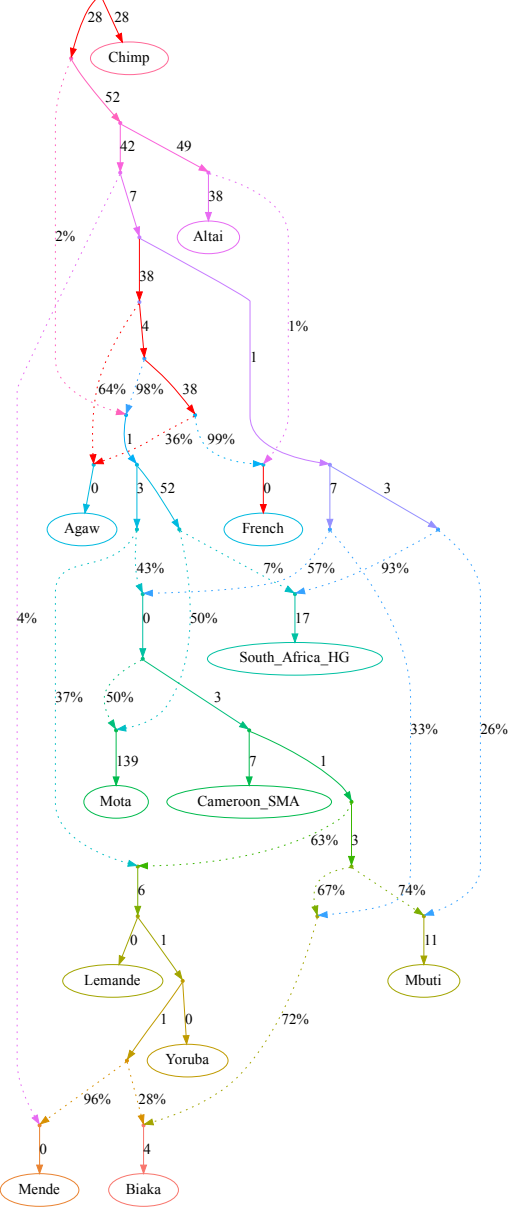
support for claim 1 supported
 support for claim 2 partial
 support for claim 3 partial
 support for claim 4 partial

support for claim 1 supported
 support for claim 2 partial
 support for claim 3 partial
 support for claim 4 partial

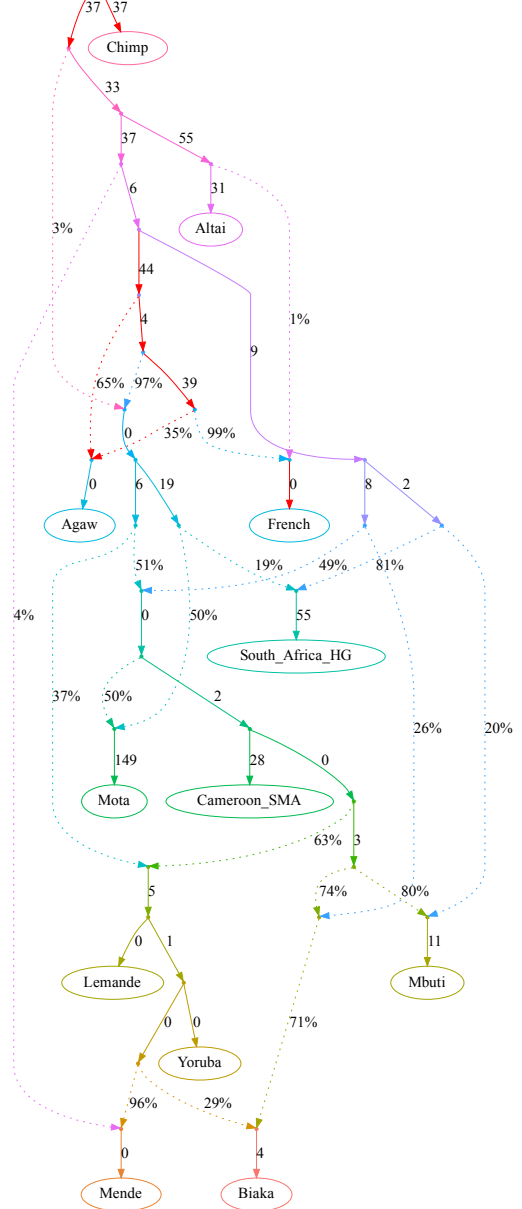
The original set of SNPs and individuals and the corrected algorithm for calculating f_3 -statistics (211,738 variable site with no missing data at the group level)

The original set of SNPs and individuals and the original algorithm for calculating f_3 -statistics (363,131 variable site with no missing data at the group level)

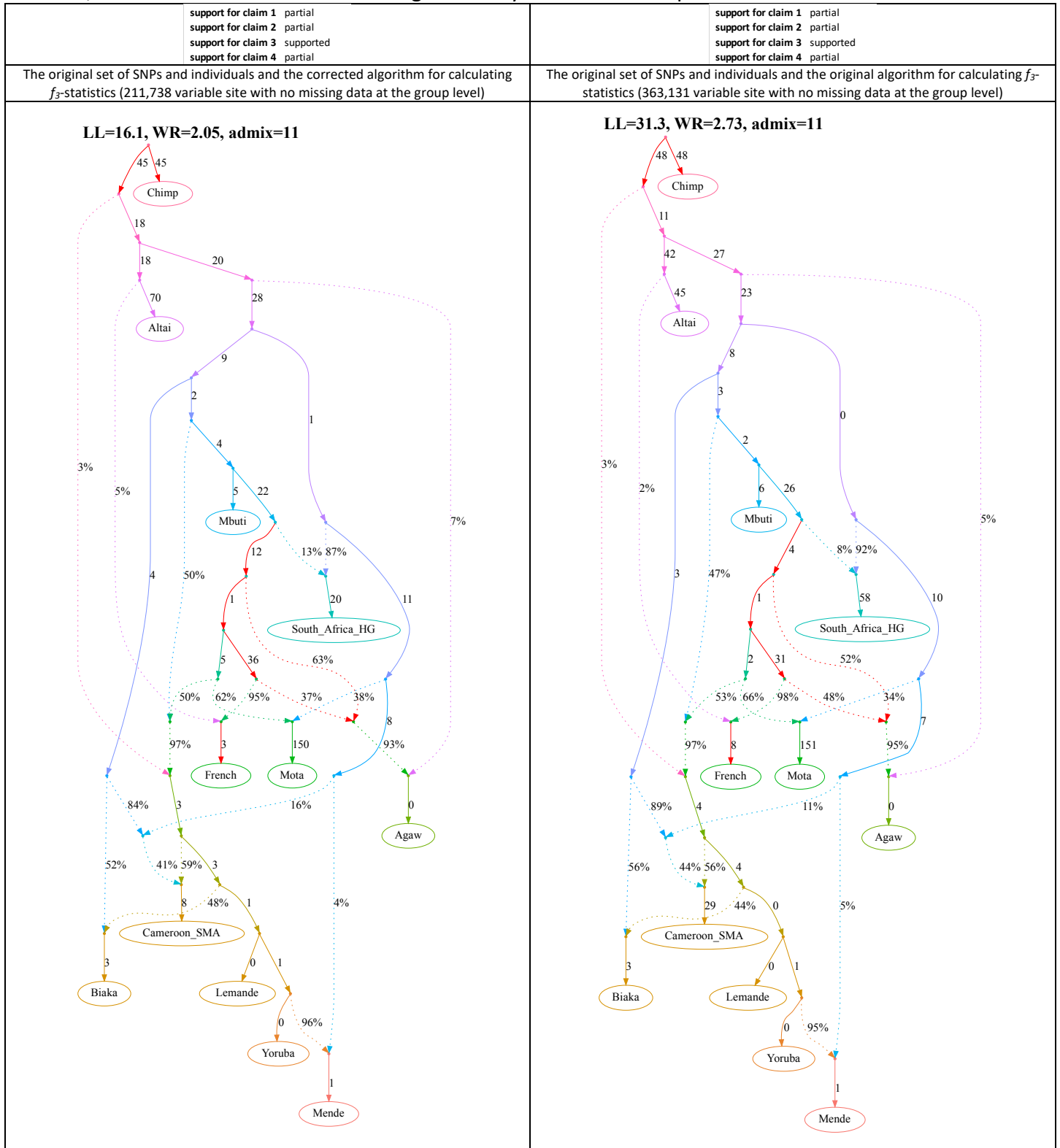
LL=14.4, WR=1.61, admix=11



LL=24.1, WR=2.28, admix=11



o, selected alternative models fitting nominally better than the published one



support for claim 1 supported
 support for claim 2 partial
 support for claim 3 supported
 support for claim 4 partial

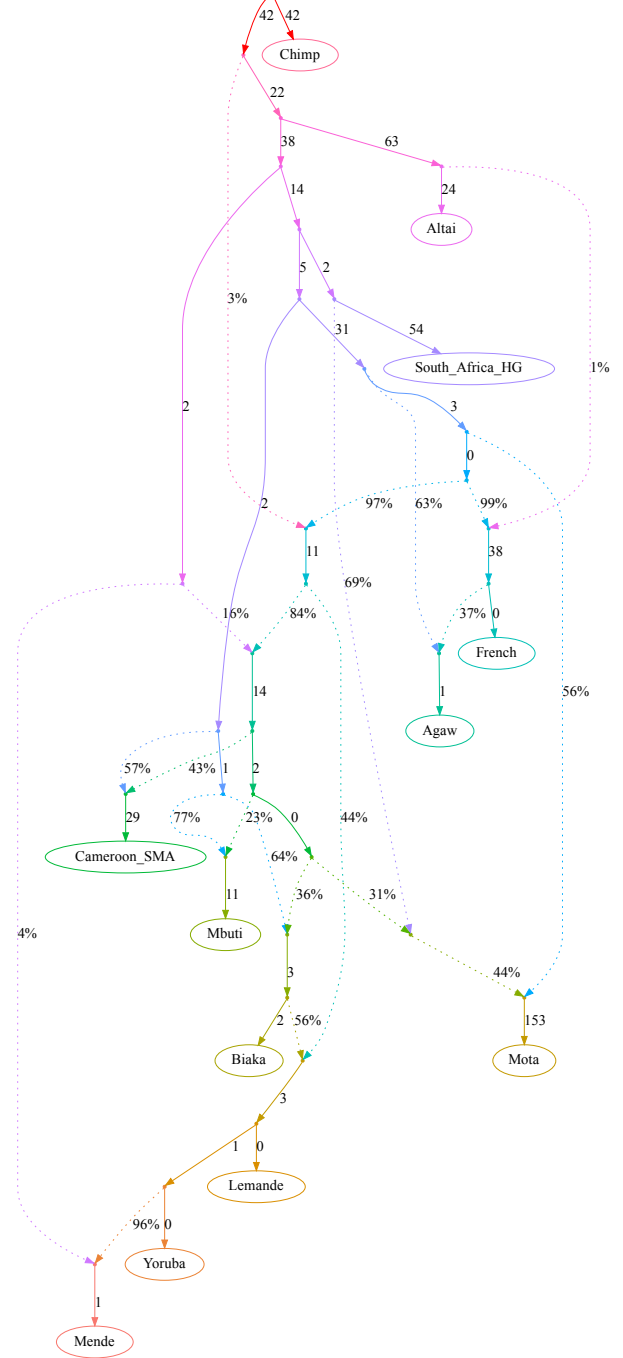
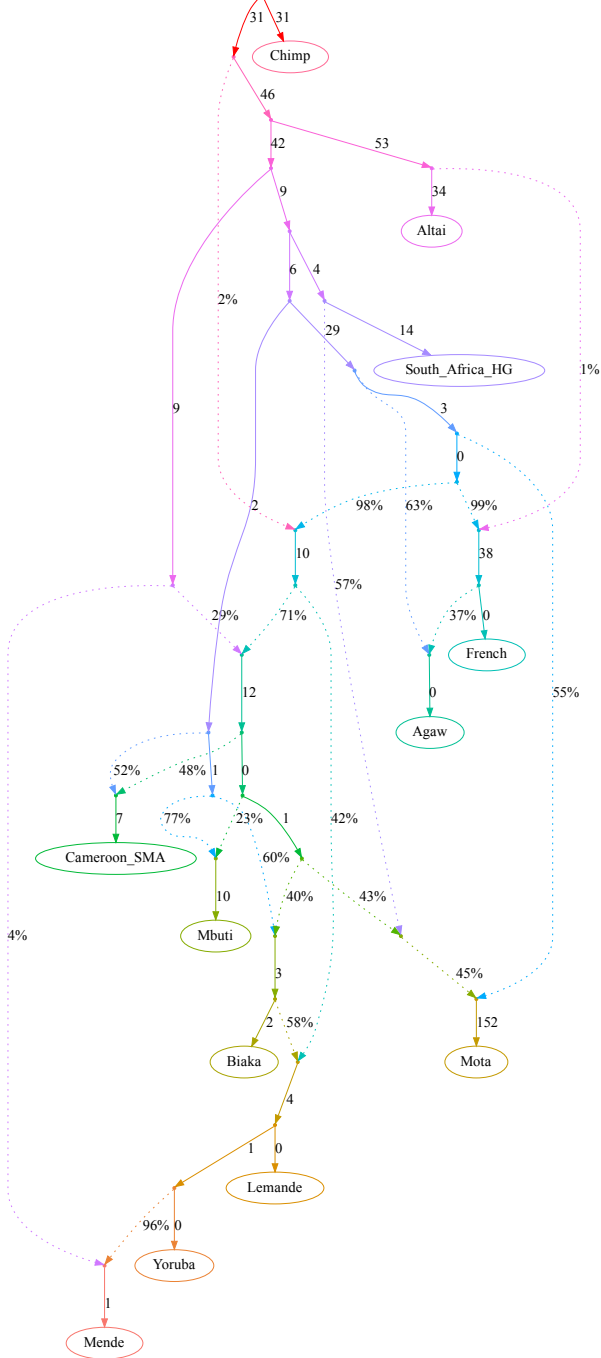
support for claim 1 supported
 support for claim 2 partial
 support for claim 3 supported
 support for claim 4 partial

The original set of SNPs and individuals and the corrected algorithm for calculating f_3 -statistics (211,738 variable site with no missing data at the group level)

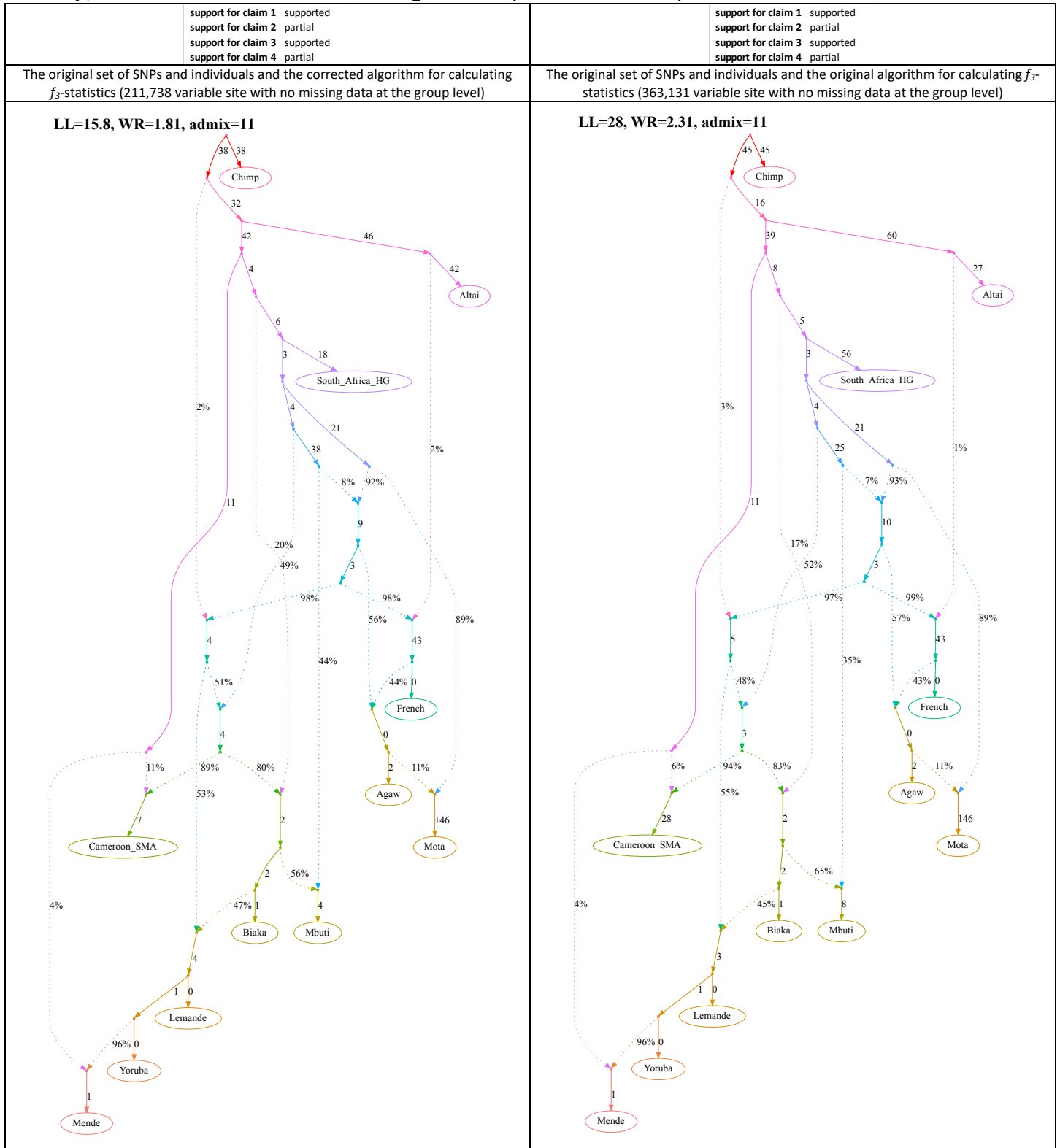
The original set of SNPs and individuals and the original algorithm for calculating f_3 -statistics (363,131 variable site with no missing data at the group level)

LL=15, WR=1.77, admix=11

LL=29, WR=2.19, admix=11

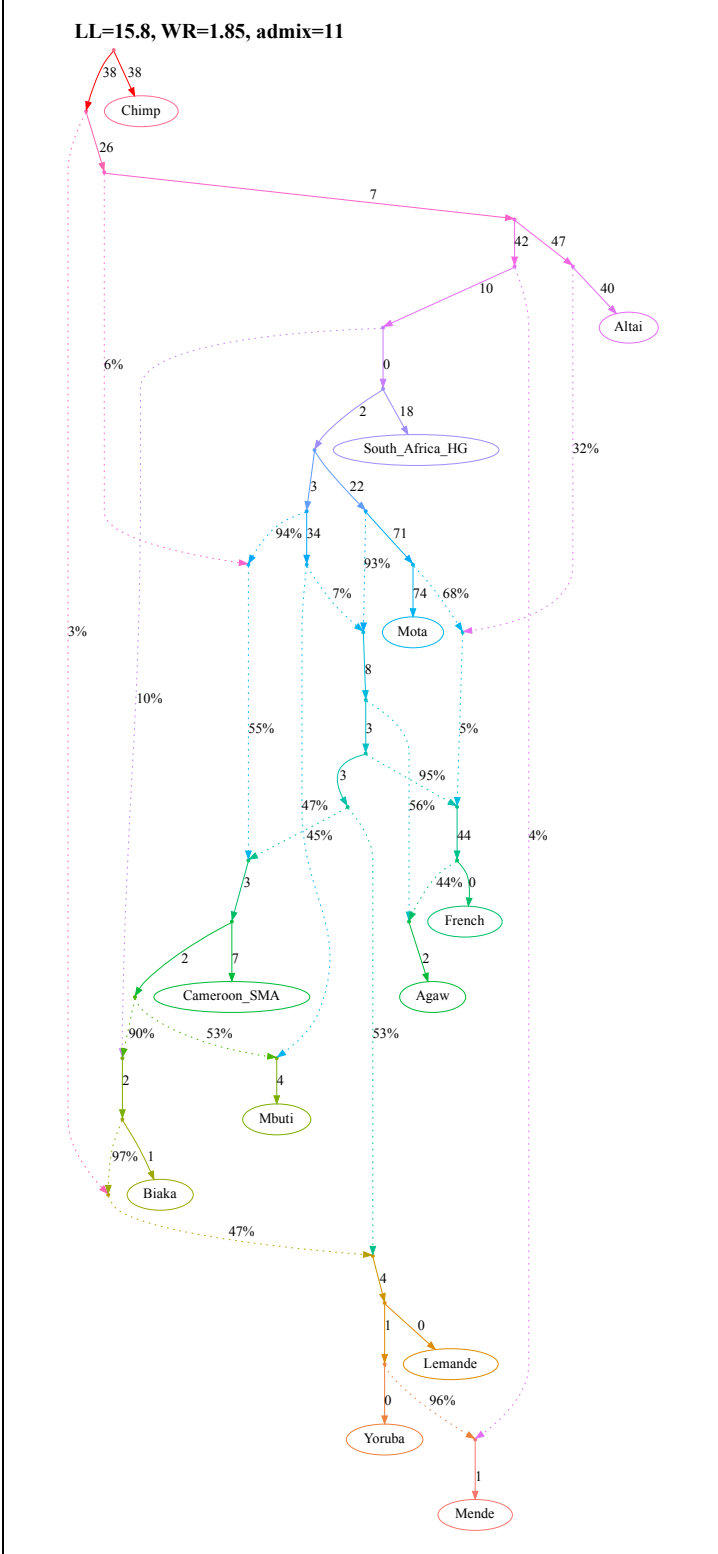


p, selected alternative models fitting nominally better than the published one

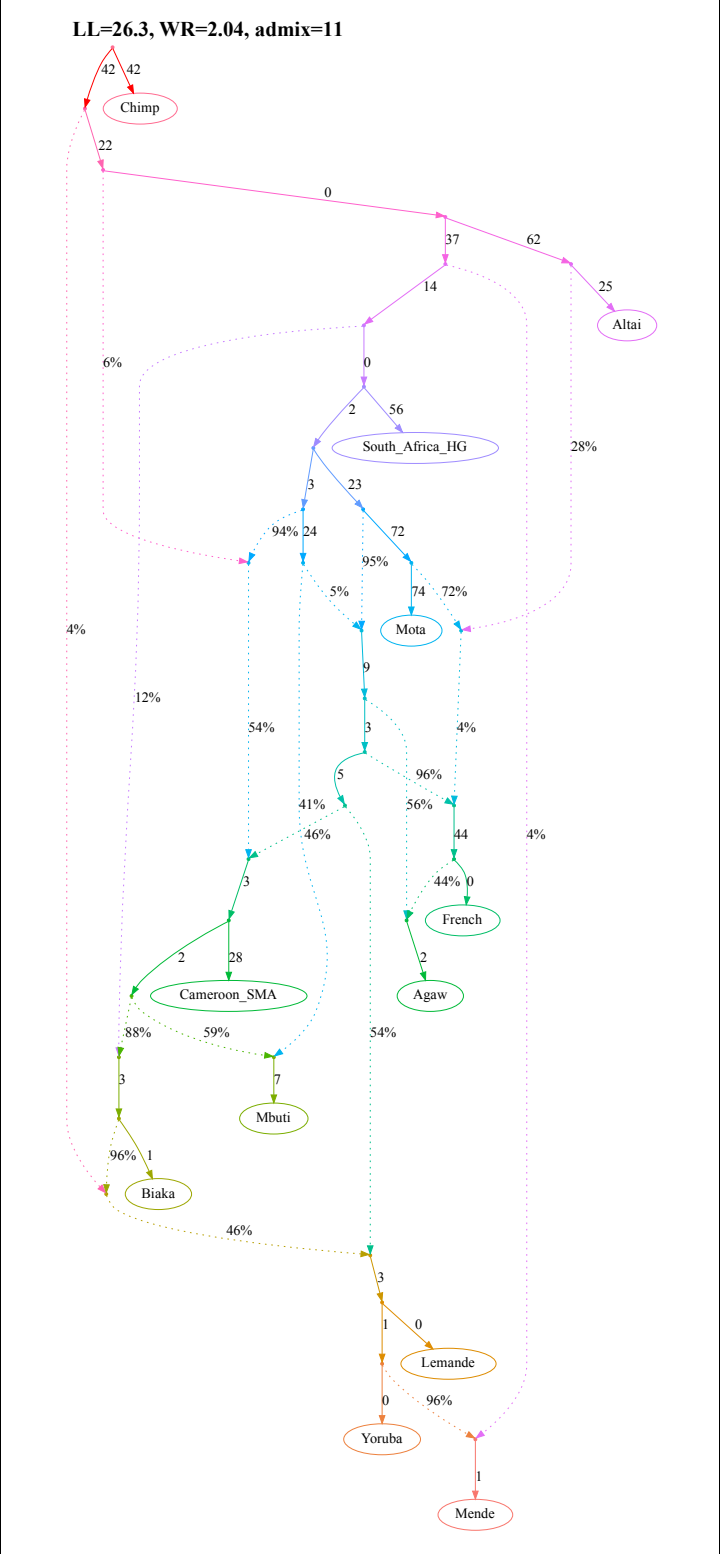


support for claim 1 supported support for claim 2 partial support for claim 3 supported support for claim 4 partial	support for claim 1 supported support for claim 2 partial support for claim 3 supported support for claim 4 partial
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The original set of SNPs and individuals and the corrected algorithm for calculating f_3 -statistics (211,738 variable site with no missing data at the group level)



The original set of SNPs and individuals and the original algorithm for calculating f_3 -statistics (363,131 variable site with no missing data at the group level)



q, selected alternative models fitting nominally better than the published one



support for claim 1 supported
 support for claim 2 supported
 support for claim 3 supported
 support for claim 4 supported

support for claim 1 supported
 support for claim 2 supported
 support for claim 3 supported
 support for claim 4 supported

The original set of SNPs and individuals and the corrected algorithm for calculating f_3 -statistics (211,738 variable site with no missing data at the group level)

The original set of SNPs and individuals and the original algorithm for calculating f_3 -statistics (363,131 variable site with no missing data at the group level)

LL=15.5, WR=1.93, admix=11

LL=30.8, WR=2.58, admix=11

