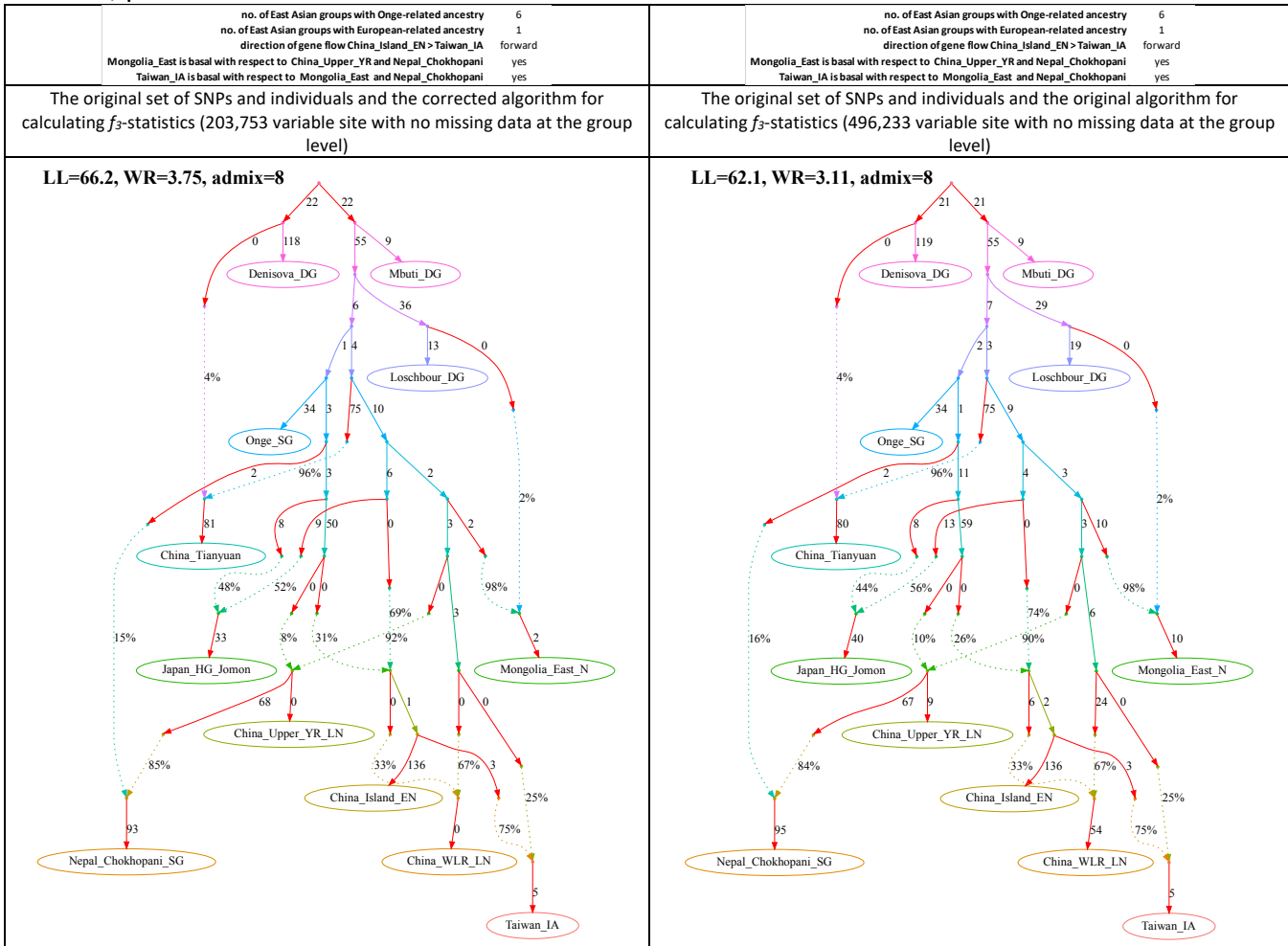
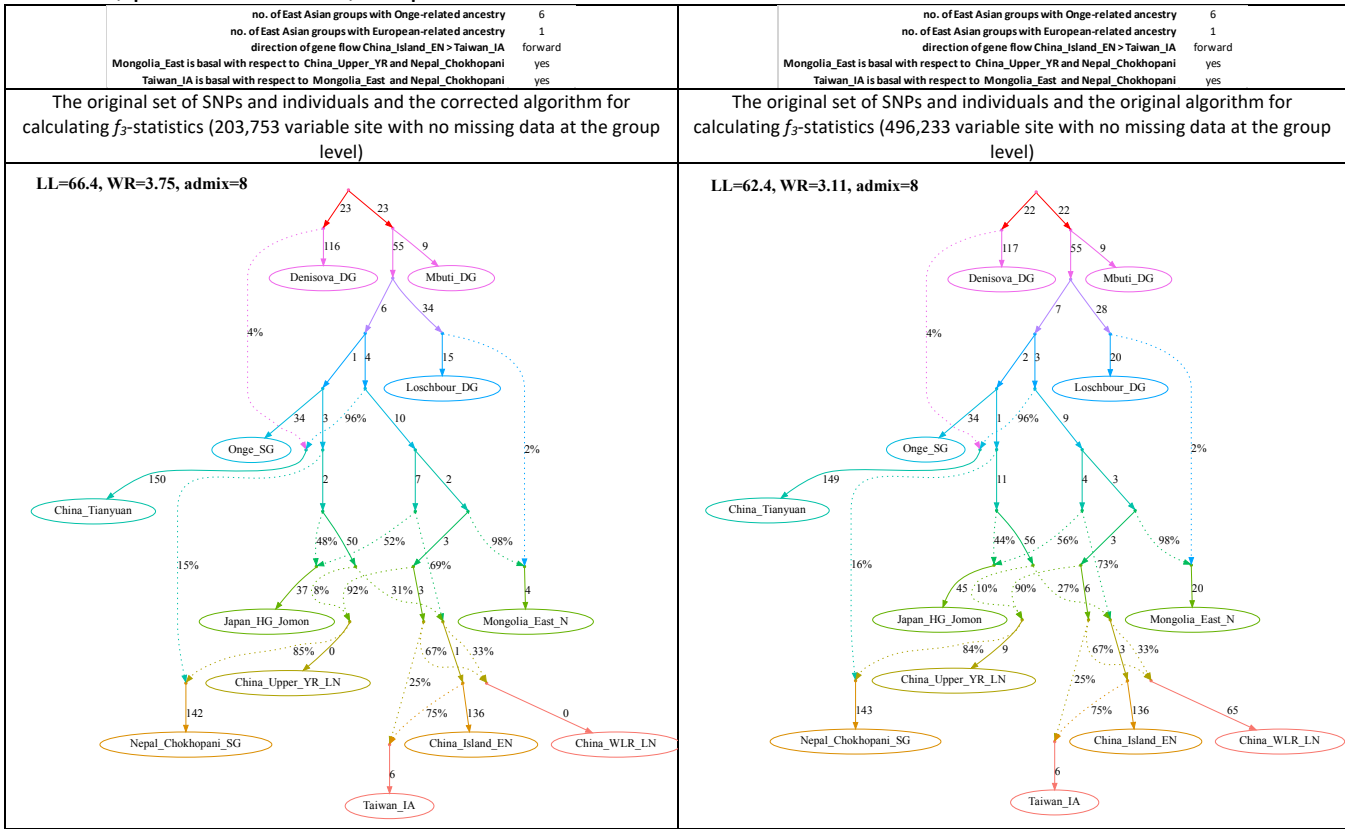


**Figure 4–source data 2.** Published admixture graph from Wang *et al.* (2021) and alternative graphs found with *findGraphs* (12 populations, 8 admixture events) using the updated algorithm for calculating  $f_3$ -statistics. The graphs were also re-fitted using the original algorithm for calculating  $f_3$ -statistics. Model parameters (graph edges) that were inferred to be unidentifiable are plotted in red.

**a, published model**



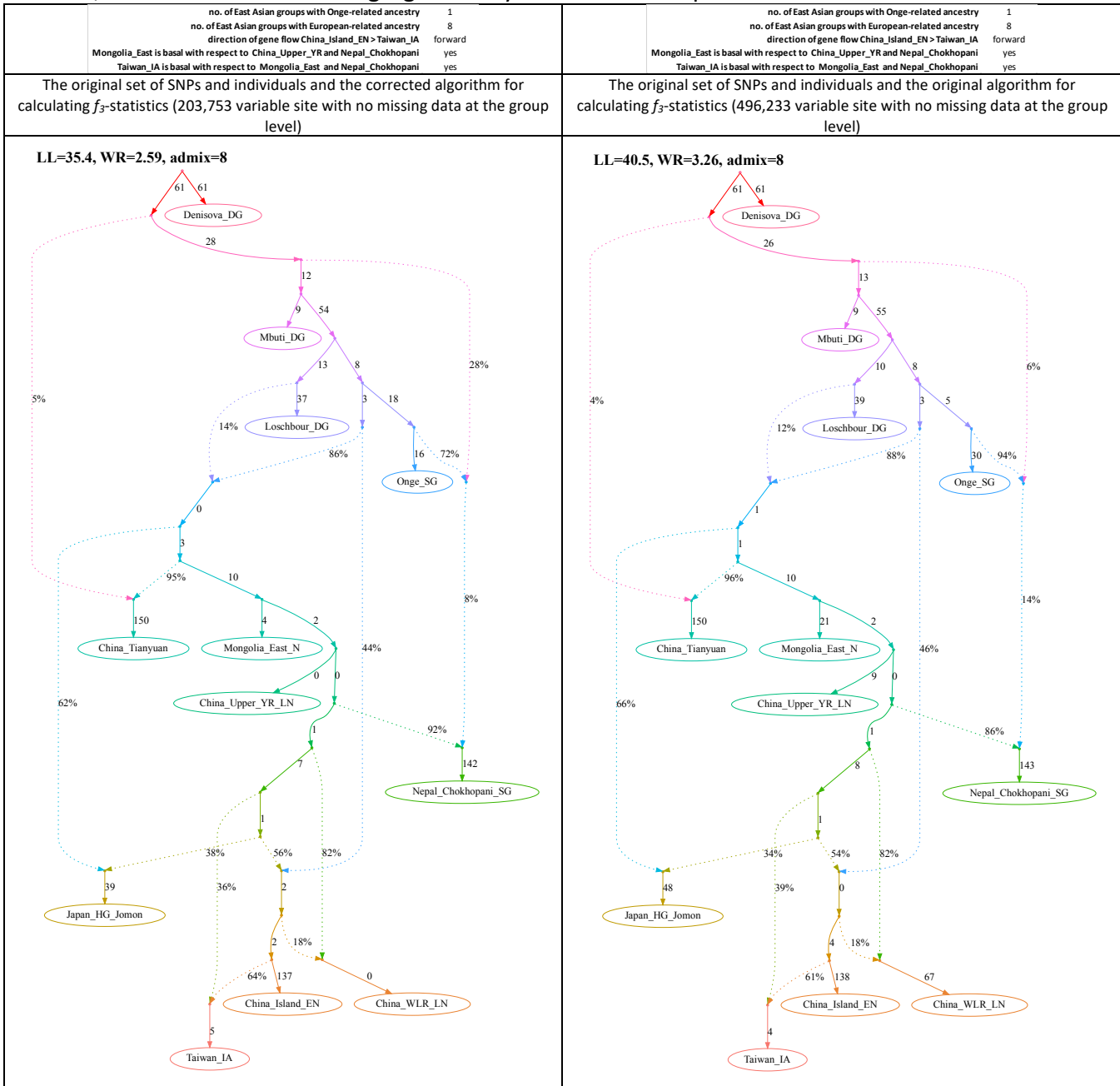
**b, published model, simplified**



A claim by Wang *et al.* 2021 relying on the admixture graph:

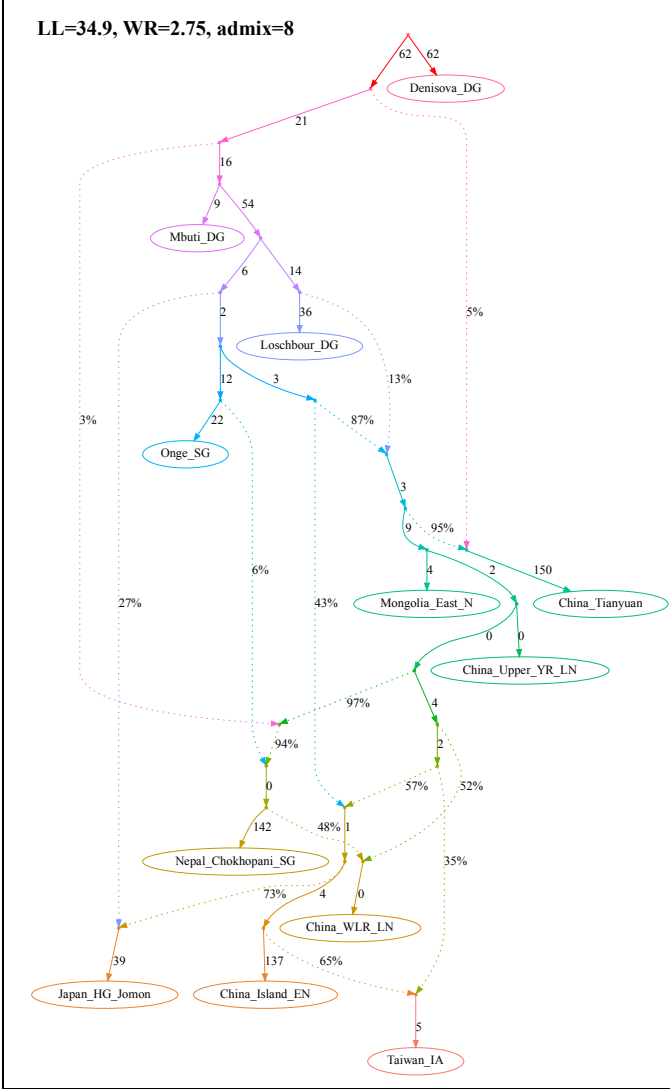
There is Onge-related admixture in the following lineages: Jomon (Japan\_HG\_Jomon), Tibetan (Nepal\_Chokhopani\_SG), Upper Yellow River Late Neolithic (China\_Upper\_YR\_LN), West Liao River Late Neolithic (China\_WLR\_LN), Taiwan Iron Age (Taiwan\_IA), China Island Early Neolithic (Liangdao, China\_Island\_EN).

**c, alternative models fitting significantly better than the published one**



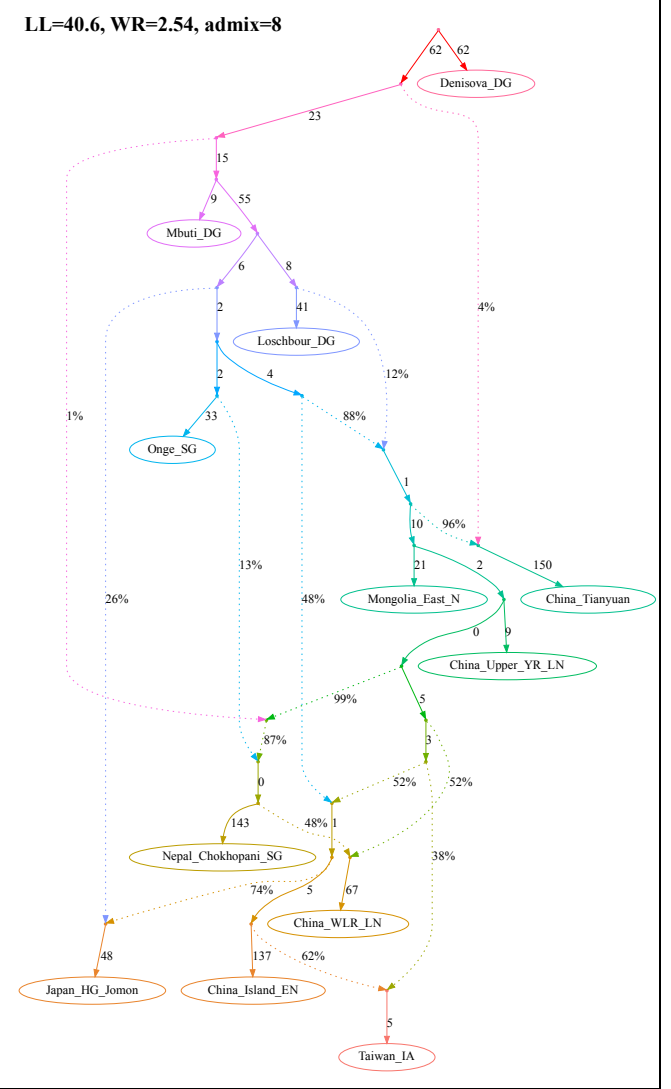
no. of East Asian groups with Onge-related ancestry 2  
 no. of East Asian groups with European-related ancestry 8  
 direction of gene flow China\_Island\_EN > Taiwan\_IA forward  
 Mongolia\_East is basal with respect to China\_Upper\_YR and Nepal\_Chokhopani yes  
 Taiwan\_IA is basal with respect to Mongolia\_East and Nepal\_Chokhopani yes

The original set of SNPs and individuals and the corrected algorithm for calculating  $f_3$ -statistics (203,753 variable site with no missing data at the group level)

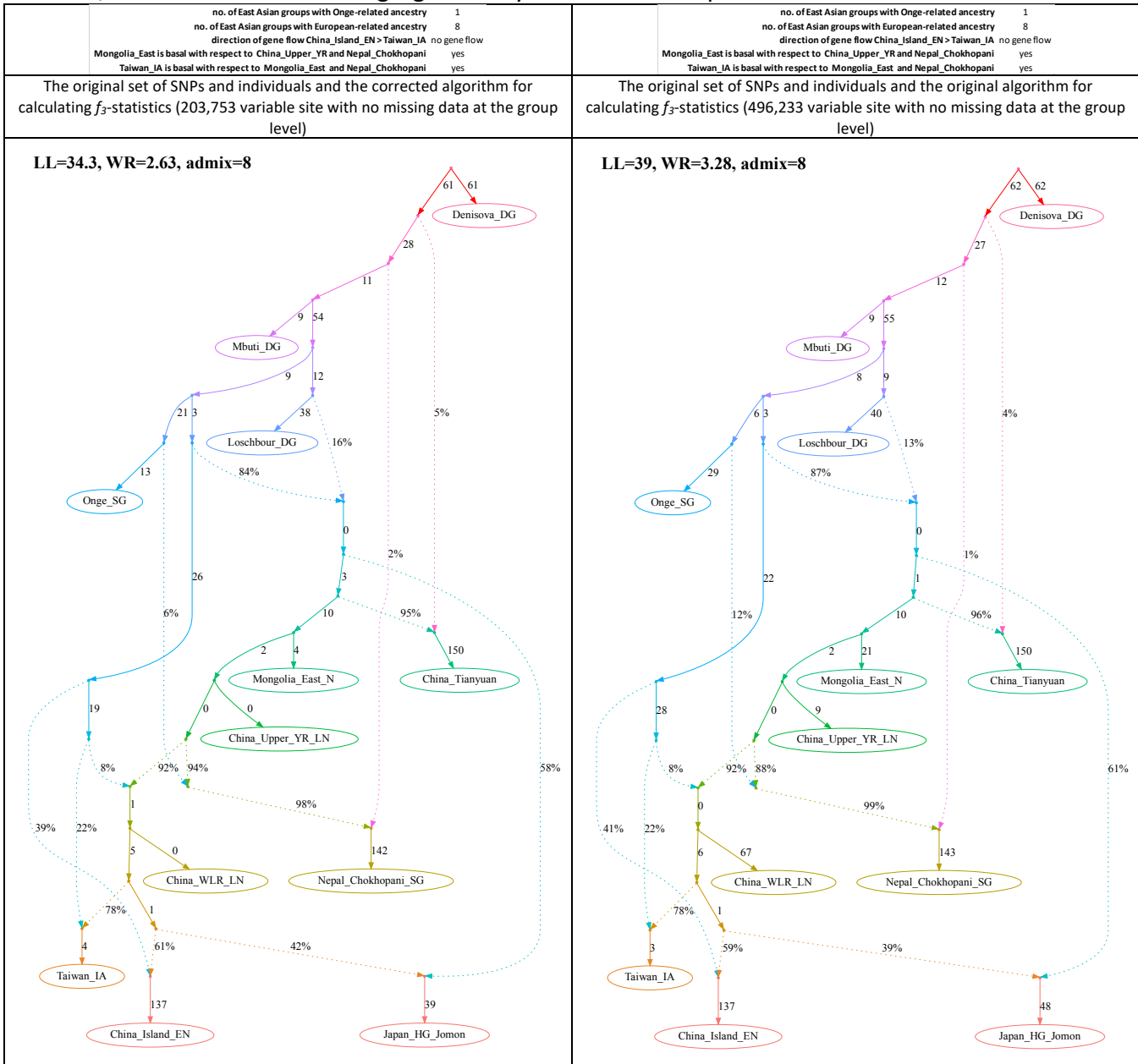


no. of East Asian groups with Onge-related ancestry 2  
 no. of East Asian groups with European-related ancestry 8  
 direction of gene flow China\_Island\_EN > Taiwan\_IA forward  
 Mongolia\_East is basal with respect to China\_Upper\_YR and Nepal\_Chokhopani yes  
 Taiwan\_IA is basal with respect to Mongolia\_East and Nepal\_Chokhopani yes

The original set of SNPs and individuals and the original algorithm for calculating  $f_3$ -statistics (496,233 variable site with no missing data at the group level)

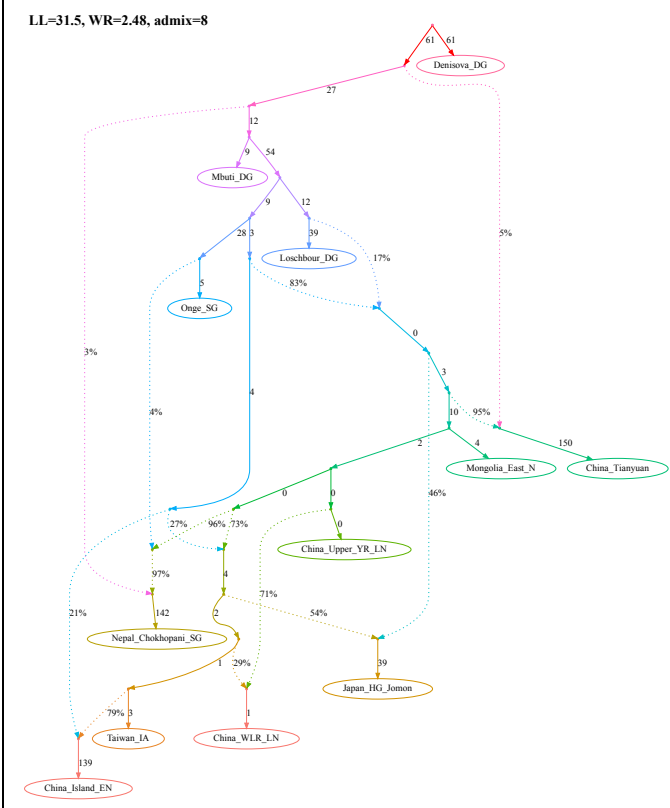


**d, alternative models fitting significantly better than the published one**



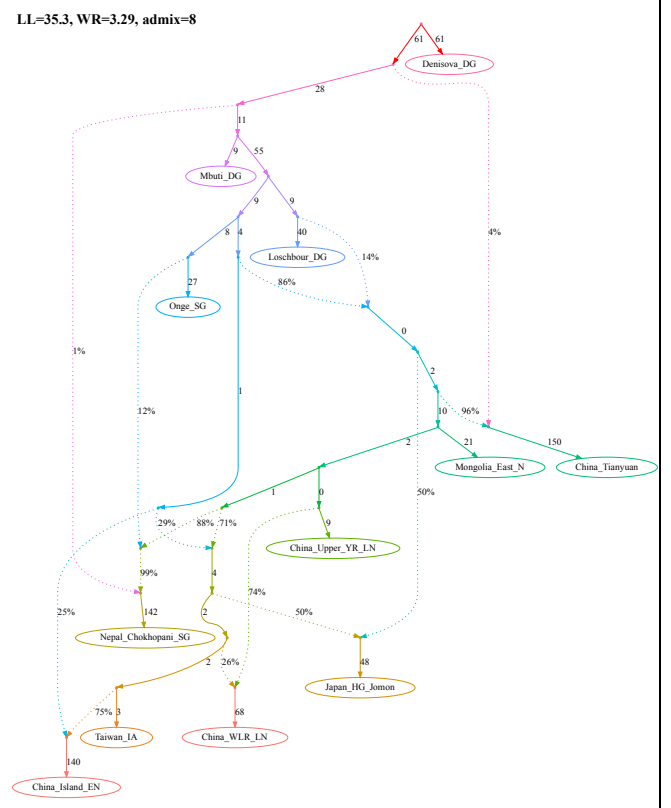
no. of East Asian groups with Onge-related ancestry 1  
 no. of East Asian groups with European-related ancestry 8  
 direction of gene flow China\_Island\_EN > Taiwan\_IA reverse  
 Mongolia\_East is basal with respect to China\_Upper\_YR and Nepal\_Chokhopani yes  
 Taiwan\_IA is basal with respect to Mongolia\_East and Nepal\_Chokhopani yes

The original set of SNPs and individuals and the corrected algorithm for calculating  $f_3$ -statistics (203,753 variable site with no missing data at the group level)

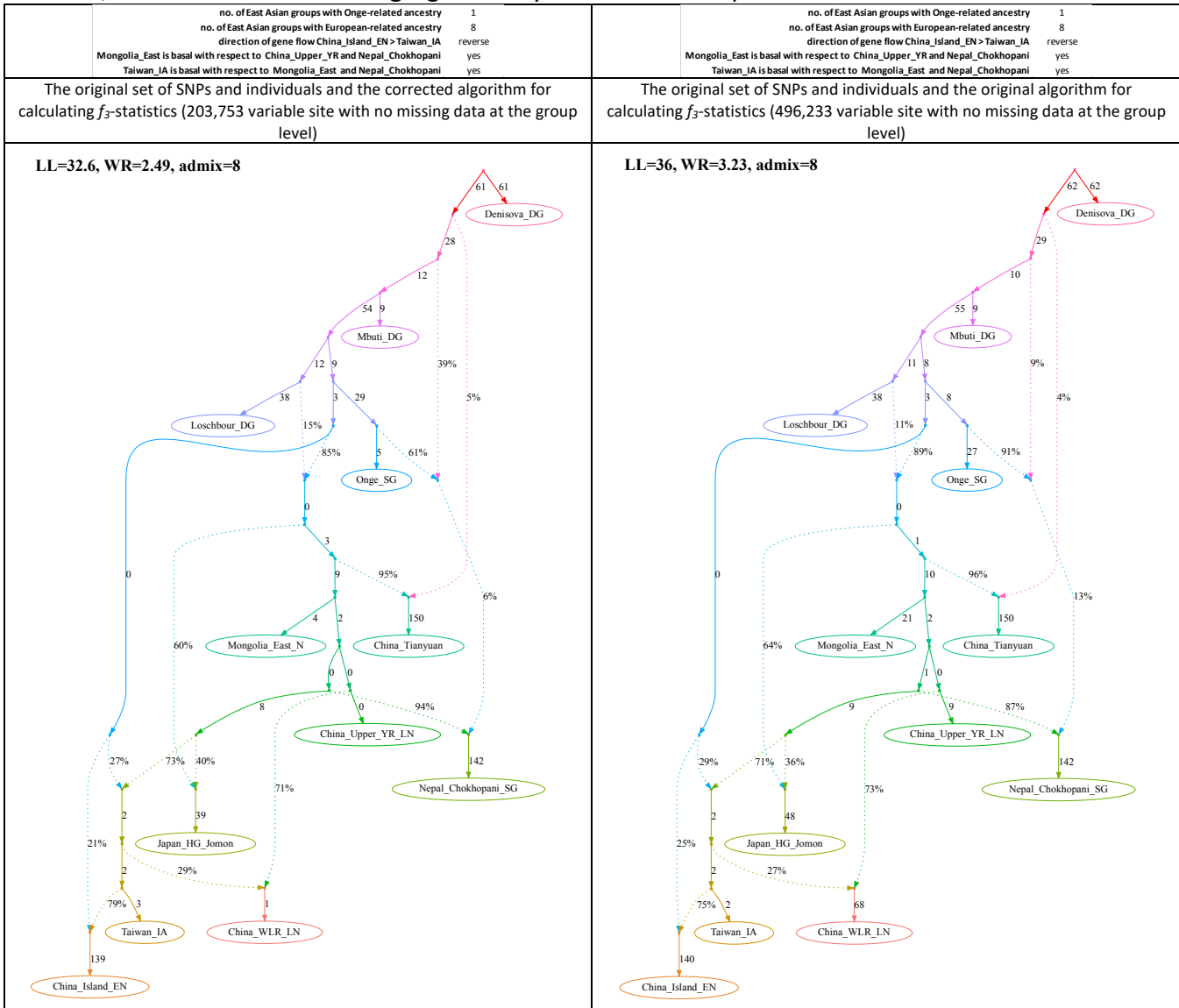


no. of East Asian groups with Onge-related ancestry 1  
 no. of East Asian groups with European-related ancestry 8  
 direction of gene flow China\_Island\_EN > Taiwan\_IA reverse  
 Mongolia\_East is basal with respect to China\_Upper\_YR and Nepal\_Chokhopani yes  
 Taiwan\_IA is basal with respect to Mongolia\_East and Nepal\_Chokhopani yes

The original set of SNPs and individuals and the original algorithm for calculating  $f_3$ -statistics (496,233 variable site with no missing data at the group level)

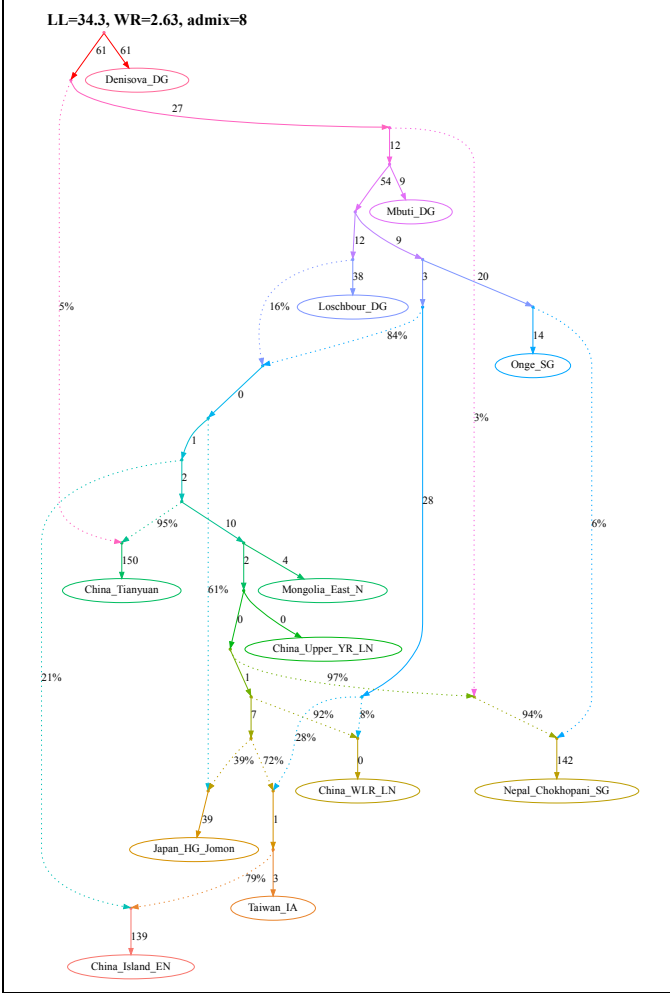


e, alternative models fitting significantly better than the published one



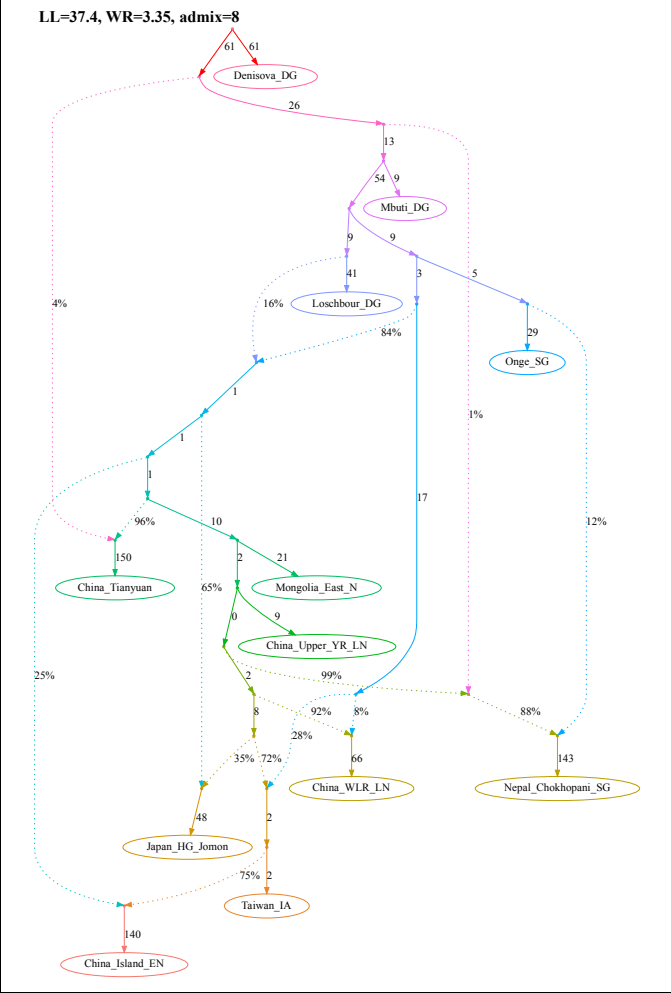
no. of East Asian groups with Onge-related ancestry	1
no. of East Asian groups with European-related ancestry	8
direction of gene flow China_Island_EN > Taiwan_IA	reverse
Mongolia_East is basal with respect to China_Upper_YR and Nepal_Chokhopani	yes
Taiwan_IA is basal with respect to Mongolia_East and Nepal_Chokhopani	yes

The original set of SNPs and individuals and the corrected algorithm for calculating  $f_3$ -statistics (203,753 variable site with no missing data at the group level)



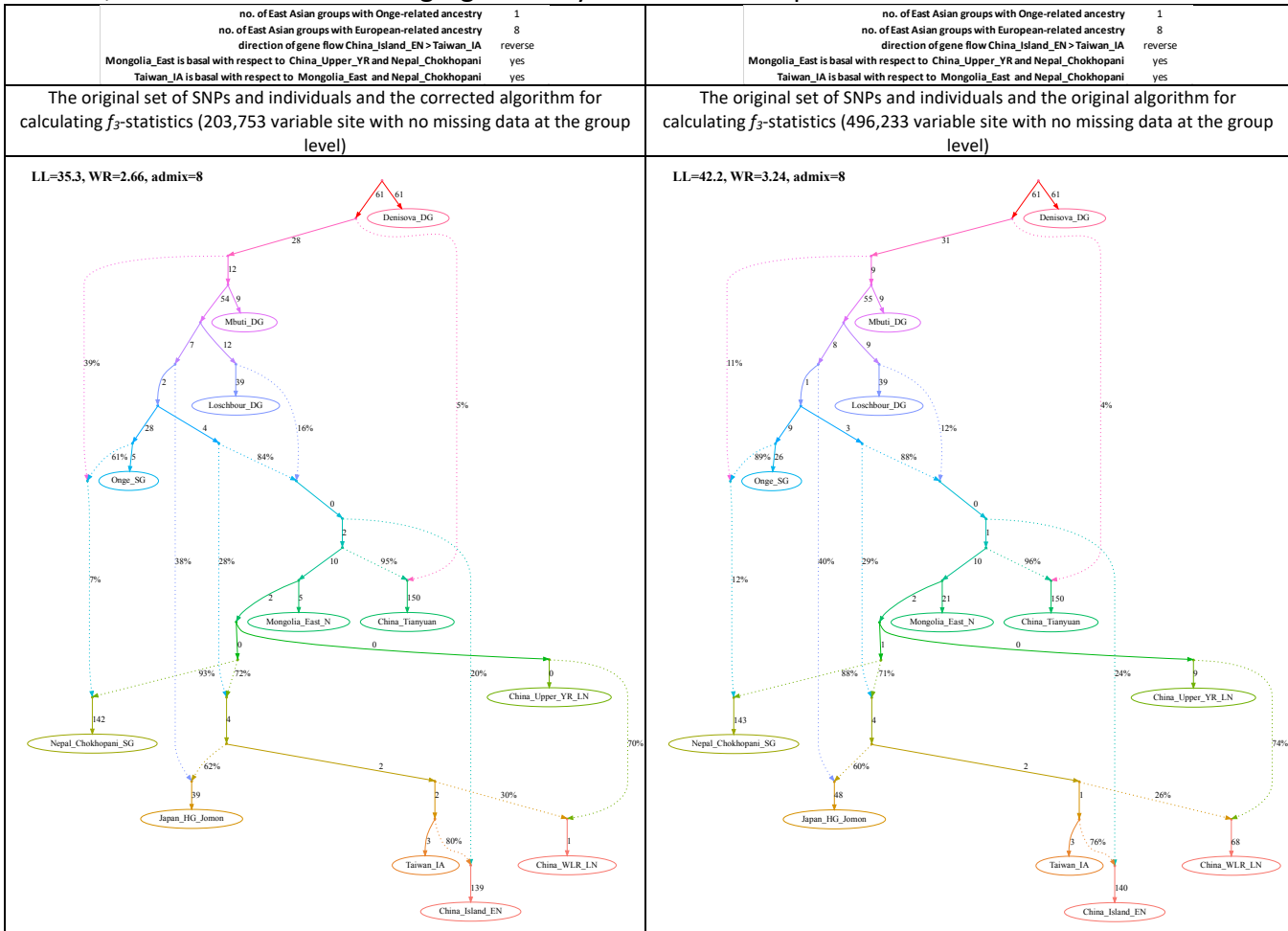
no. of East Asian groups with Onge-related ancestry	1
no. of East Asian groups with European-related ancestry	8
direction of gene flow China_Island_EN > Taiwan_IA	reverse
Mongolia_East is basal with respect to China_Upper_YR and Nepal_Chokhopani	yes
Taiwan_IA is basal with respect to Mongolia_East and Nepal_Chokhopani	yes

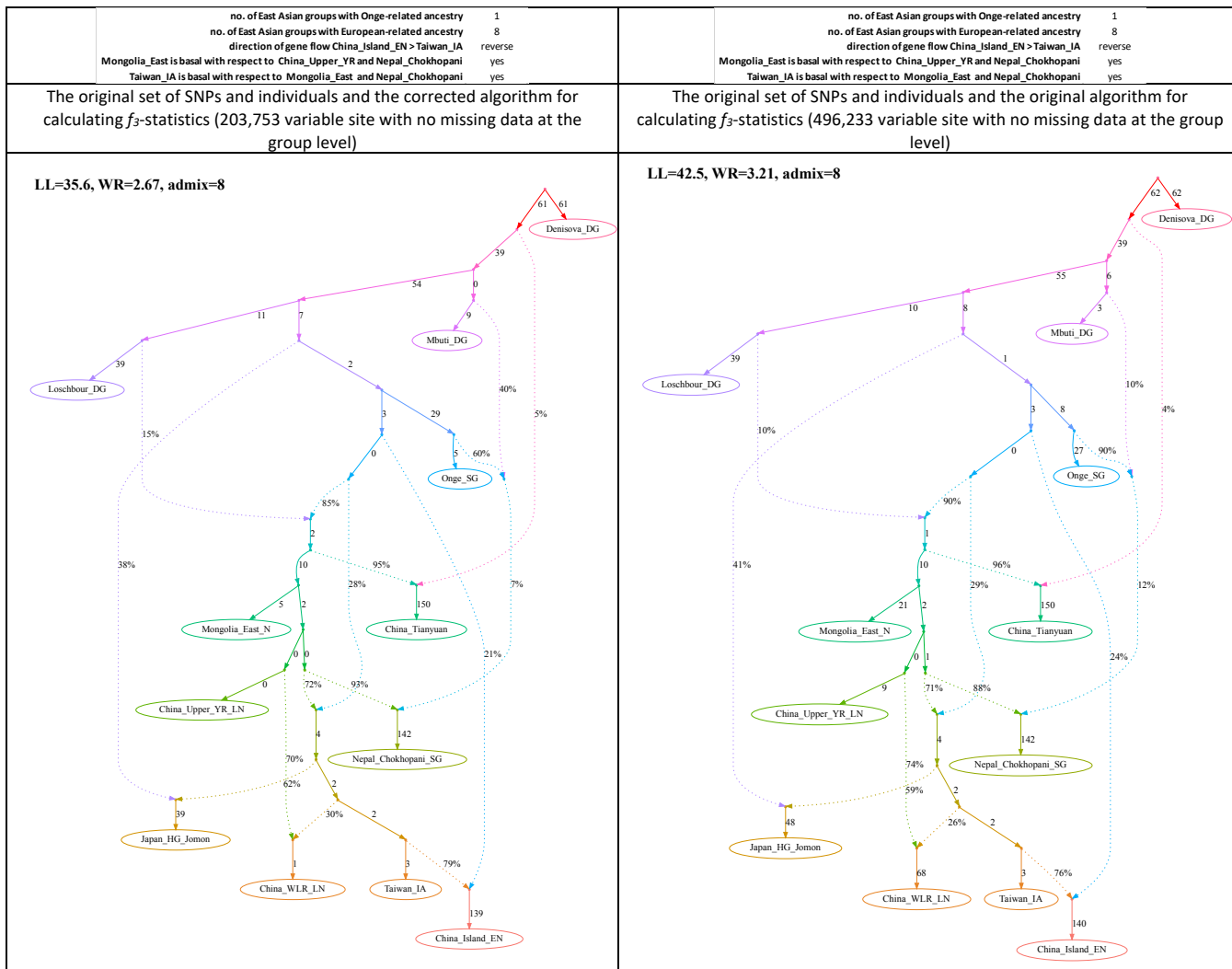
The original set of SNPs and individuals and the original algorithm for calculating  $f_3$ -statistics (496,233 variable site with no missing data at the group level)



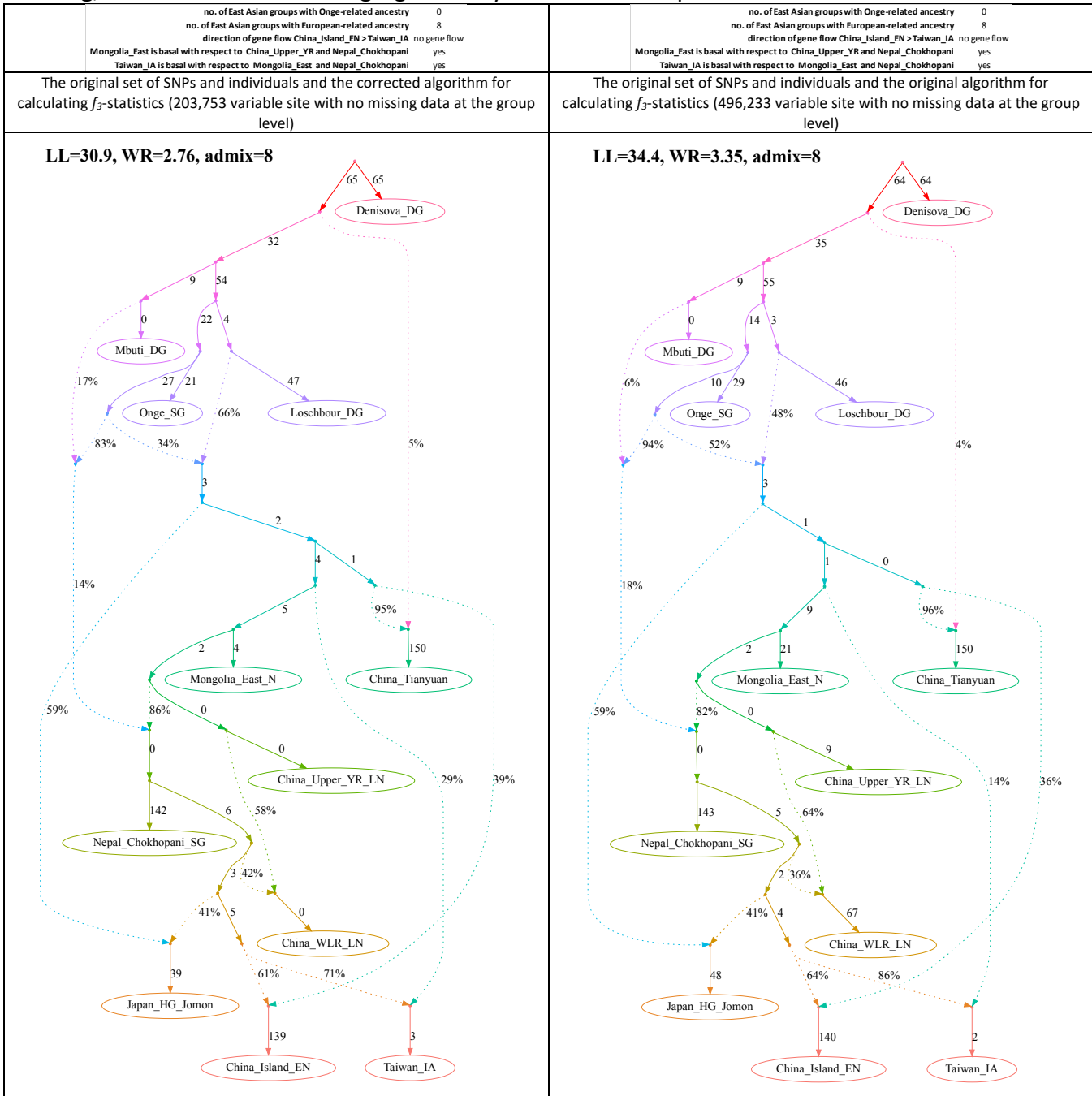


**f, alternative models fitting significantly better than the published one**



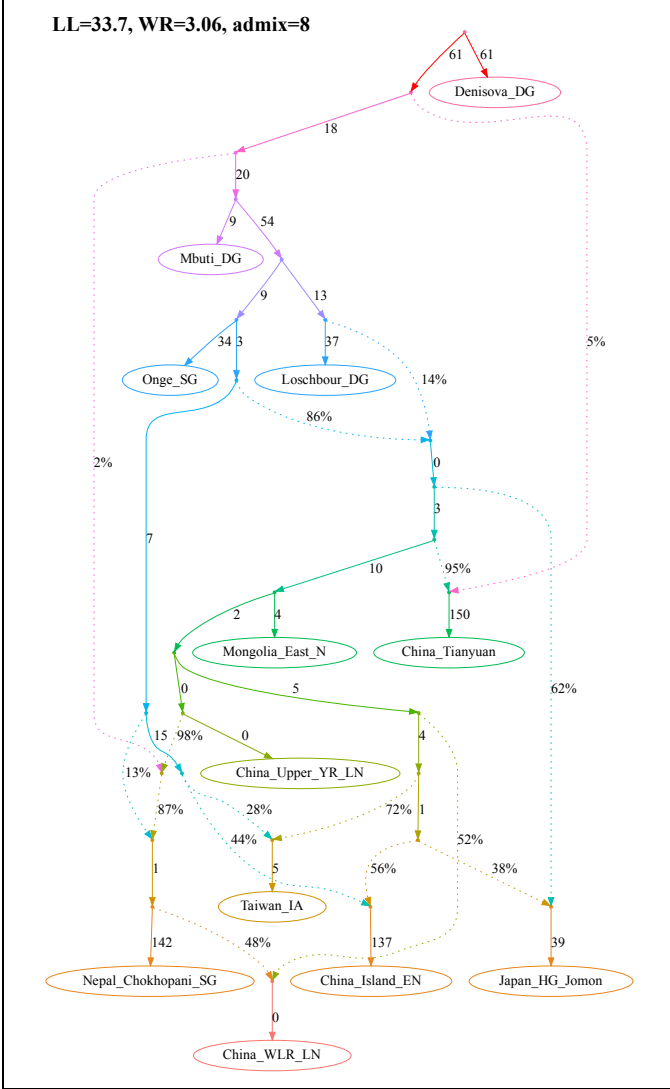


**g, alternative models fitting significantly better than the published one**



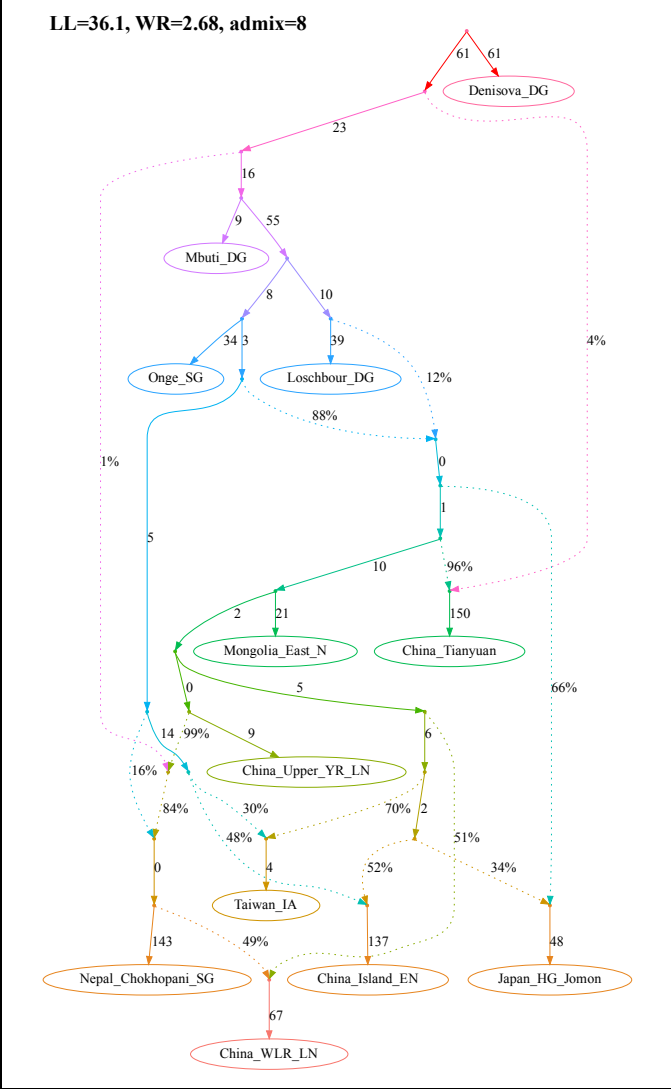
no. of East Asian groups with Onge-related ancestry 0  
 no. of East Asian groups with European-related ancestry 8  
 direction of gene flow China\_Island\_EN > Taiwan\_IA no gene flow  
 Mongolia\_East is basal with respect to China\_Upper\_YR and Nepal\_Chokhopani yes  
 Taiwan\_IA is basal with respect to Mongolia\_East and Nepal\_Chokhopani yes

The original set of SNPs and individuals and the corrected algorithm for calculating  $f_3$ -statistics (203,753 variable site with no missing data at the group level)

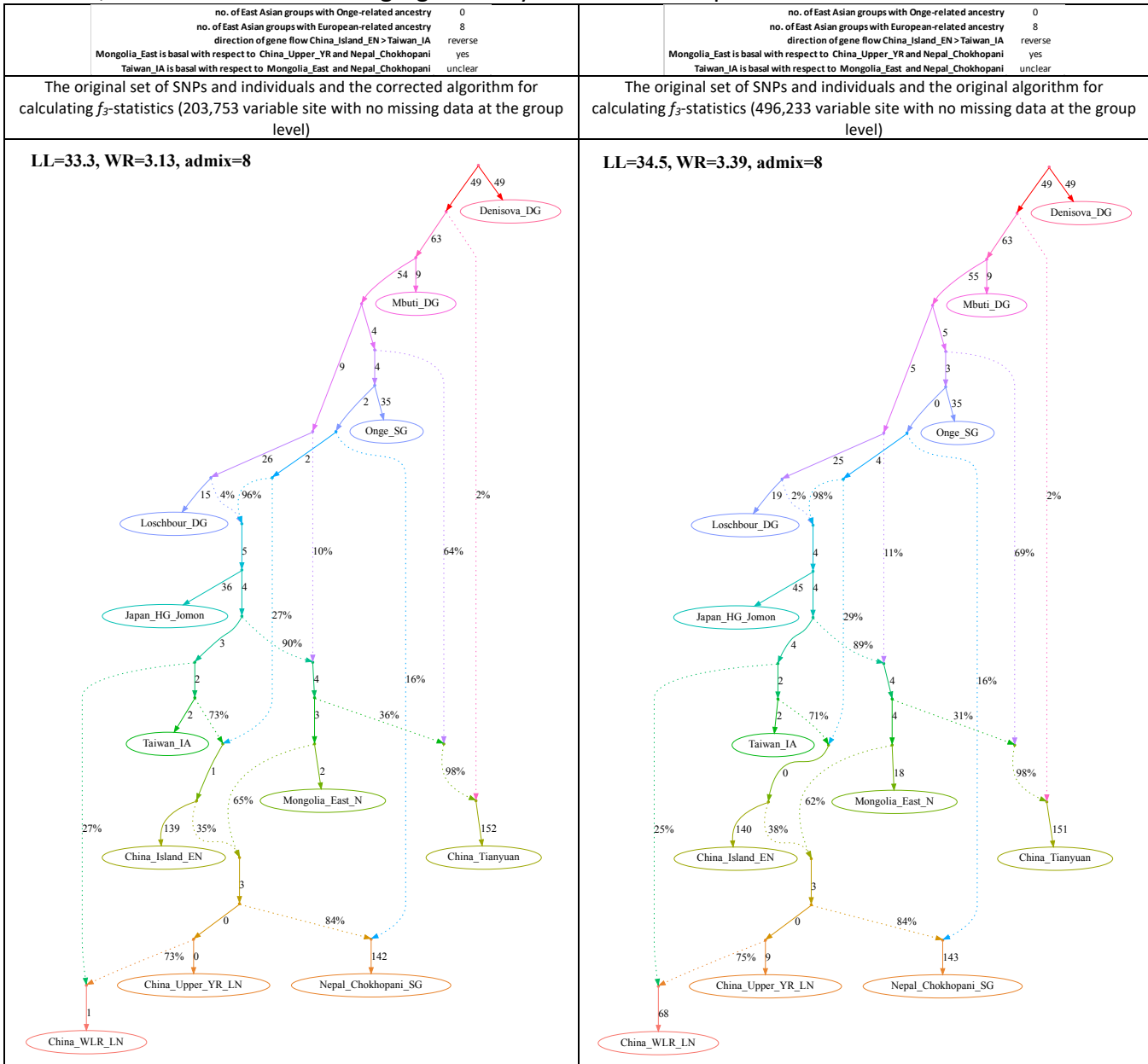


no. of East Asian groups with Onge-related ancestry 0  
 no. of East Asian groups with European-related ancestry 8  
 direction of gene flow China\_Island\_EN > Taiwan\_IA no gene flow  
 Mongolia\_East is basal with respect to China\_Upper\_YR and Nepal\_Chokhopani yes  
 Taiwan\_IA is basal with respect to Mongolia\_East and Nepal\_Chokhopani yes

The original set of SNPs and individuals and the original algorithm for calculating  $f_3$ -statistics (496,233 variable site with no missing data at the group level)



### h, alternative models fitting significantly better than the published one



no. of East Asian groups with Onge-related ancestry 0  
 no. of East Asian groups with European-related ancestry 8  
 direction of gene flow China\_Island\_EN > Taiwan\_IA reverse  
 Mongolia\_East is basal with respect to China\_Upper\_YR and Nepal\_Chokhopani yes  
 Taiwan\_IA is basal with respect to Mongolia\_East and Nepal\_Chokhopani yes

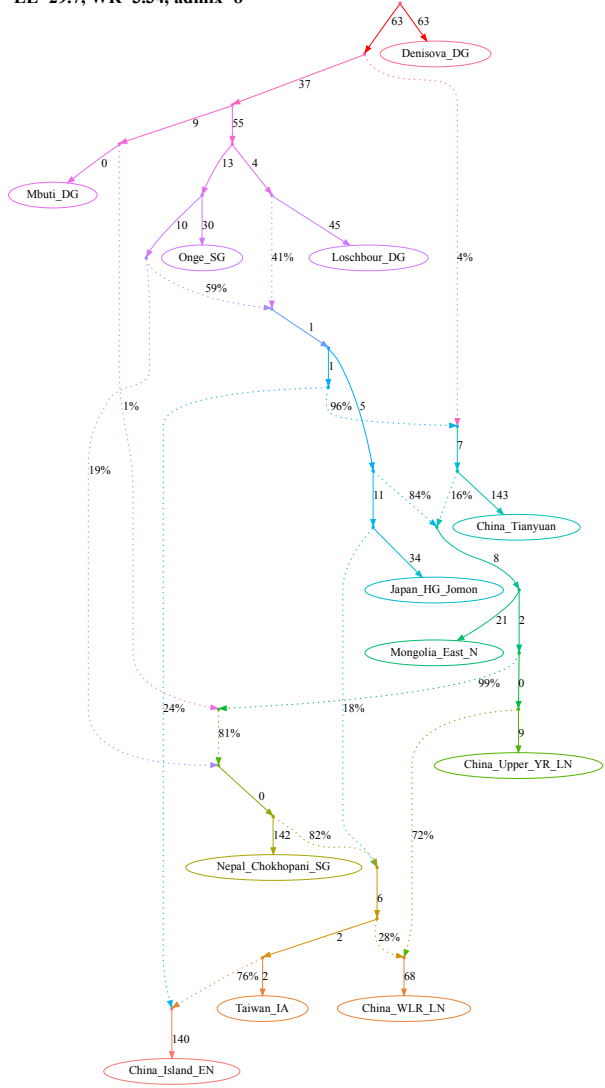
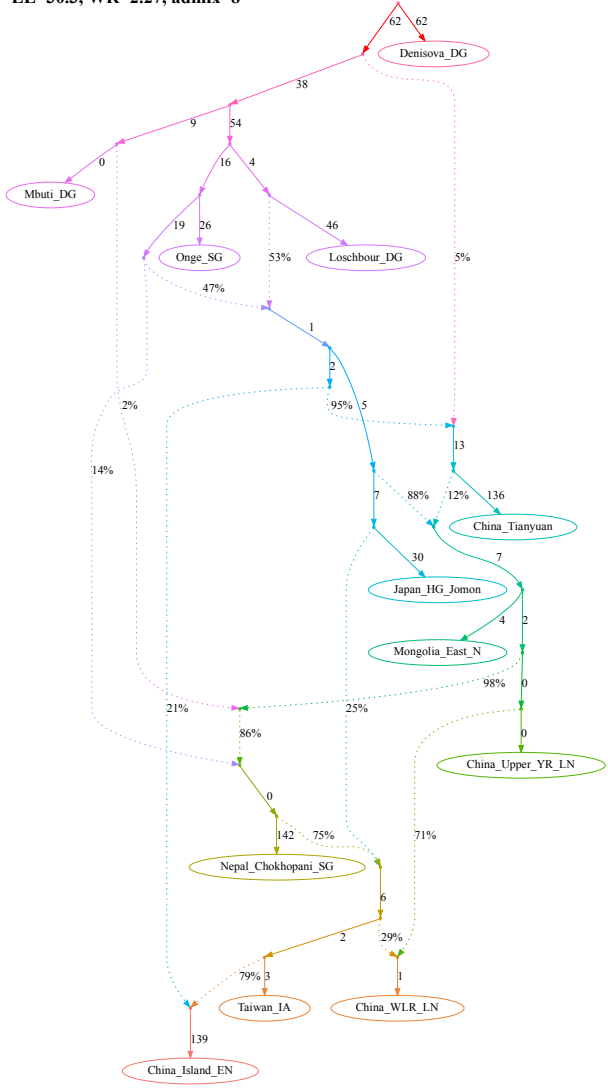
no. of East Asian groups with Onge-related ancestry 0  
 no. of East Asian groups with European-related ancestry 8  
 direction of gene flow China\_Island\_EN > Taiwan\_IA reverse  
 Mongolia\_East is basal with respect to China\_Upper\_YR and Nepal\_Chokhopani yes  
 Taiwan\_IA is basal with respect to Mongolia\_East and Nepal\_Chokhopani yes

The original set of SNPs and individuals and the corrected algorithm for calculating  $f_3$ -statistics (203,753 variable site with no missing data at the group level)

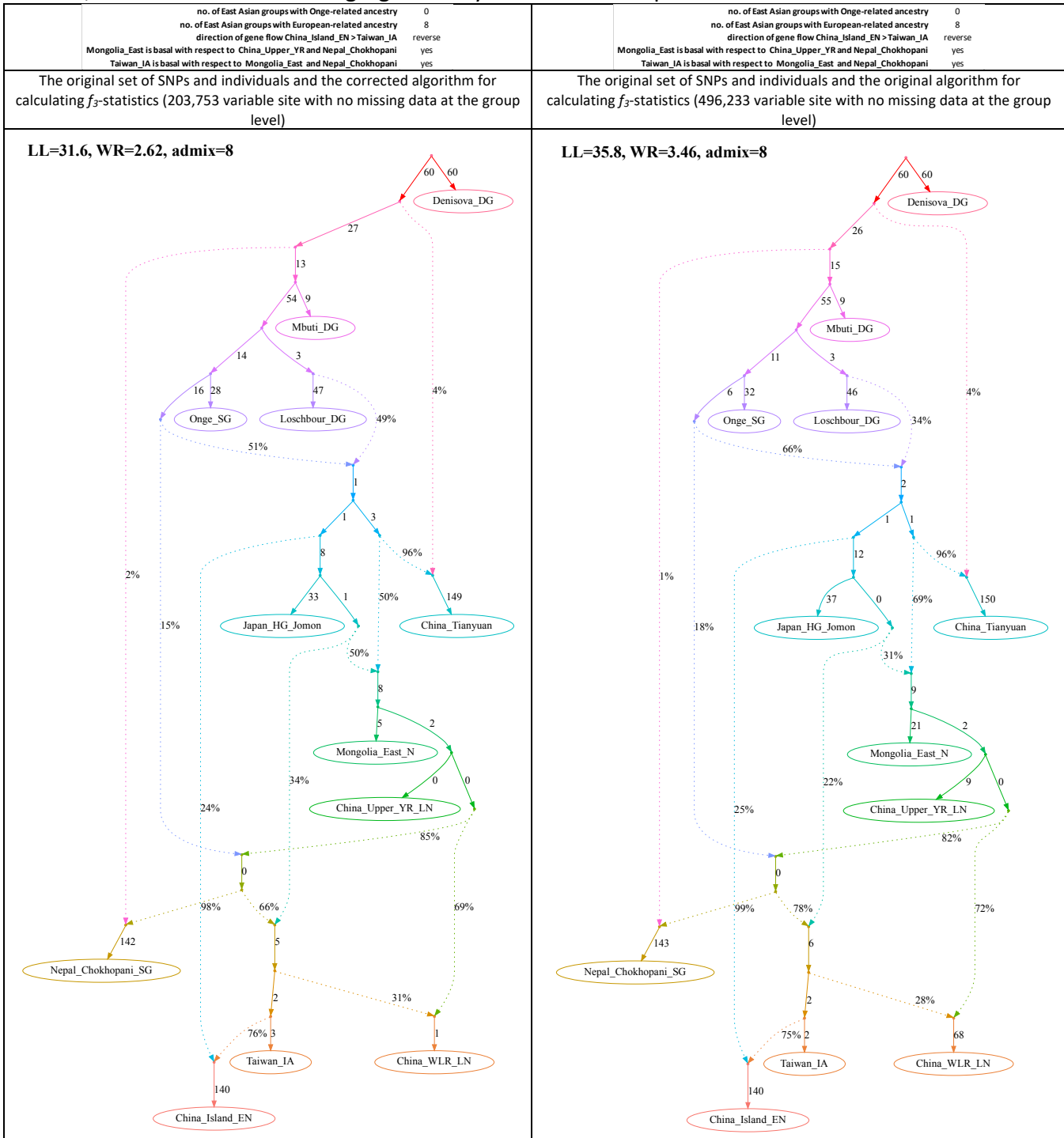
The original set of SNPs and individuals and the original algorithm for calculating  $f_3$ -statistics (496,233 variable site with no missing data at the group level)

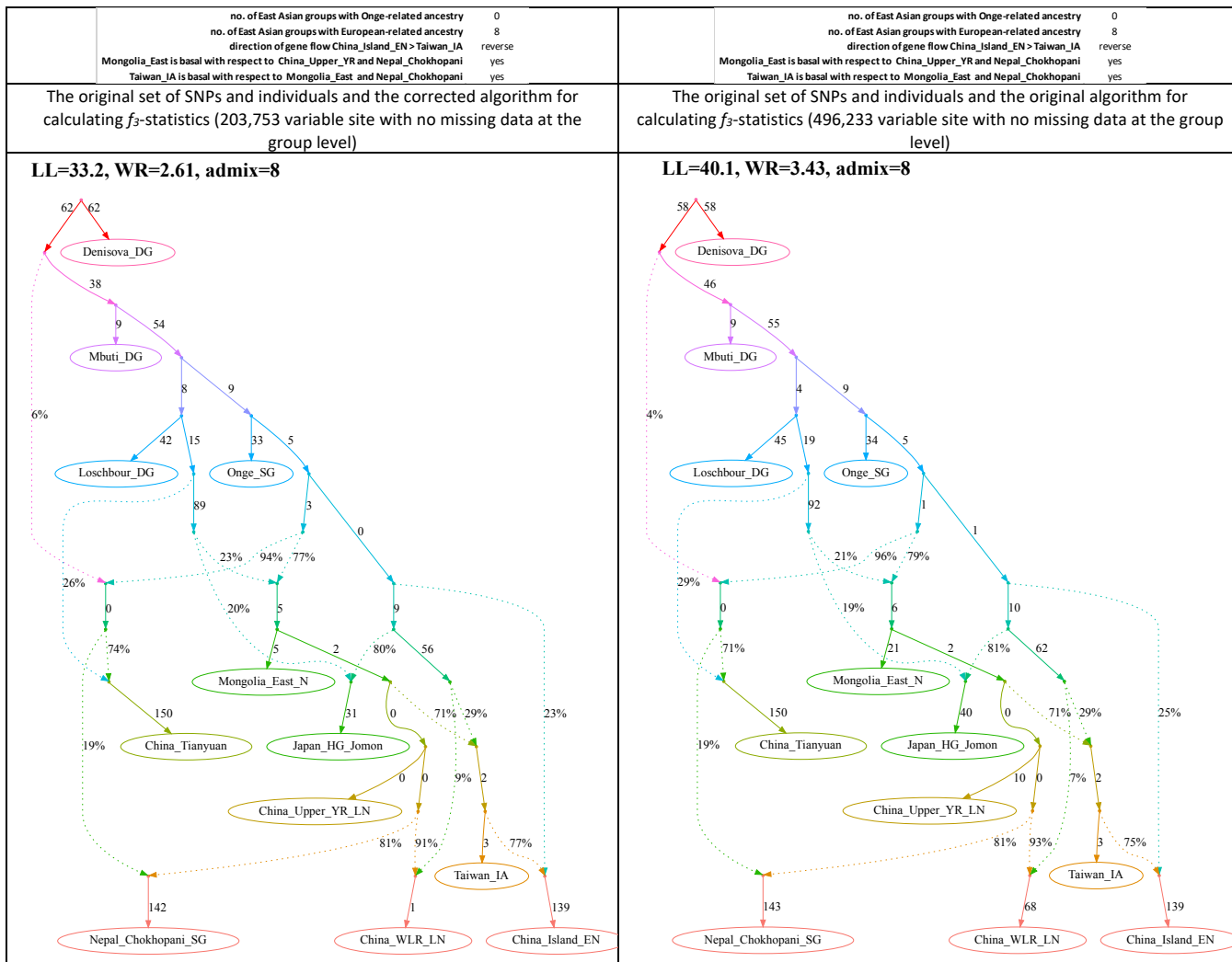
LL=30.3, WR=2.27, admix=8

LL=29.7, WR=3.34, admix=8



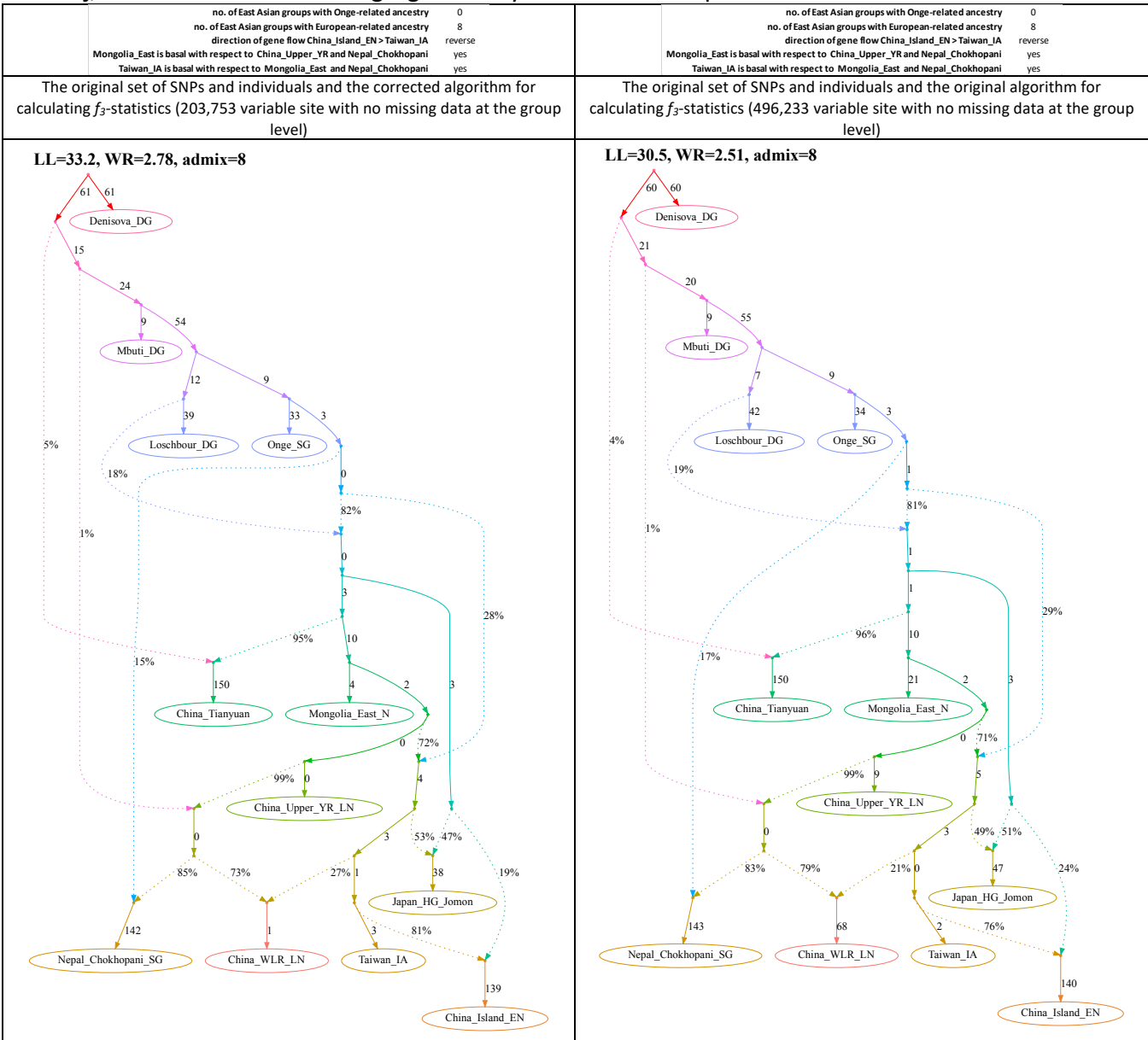
i, alternative models fitting significantly better than the published one

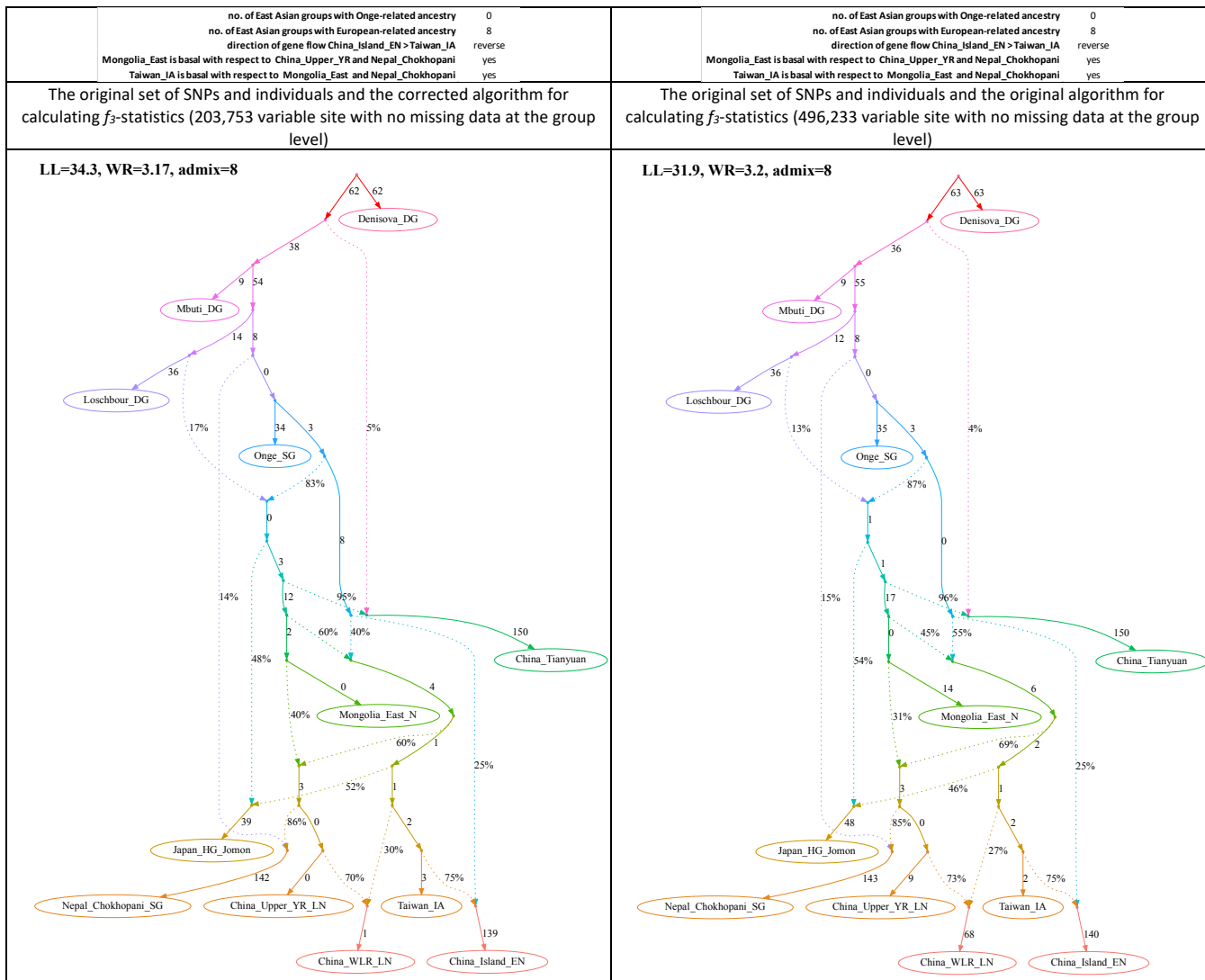




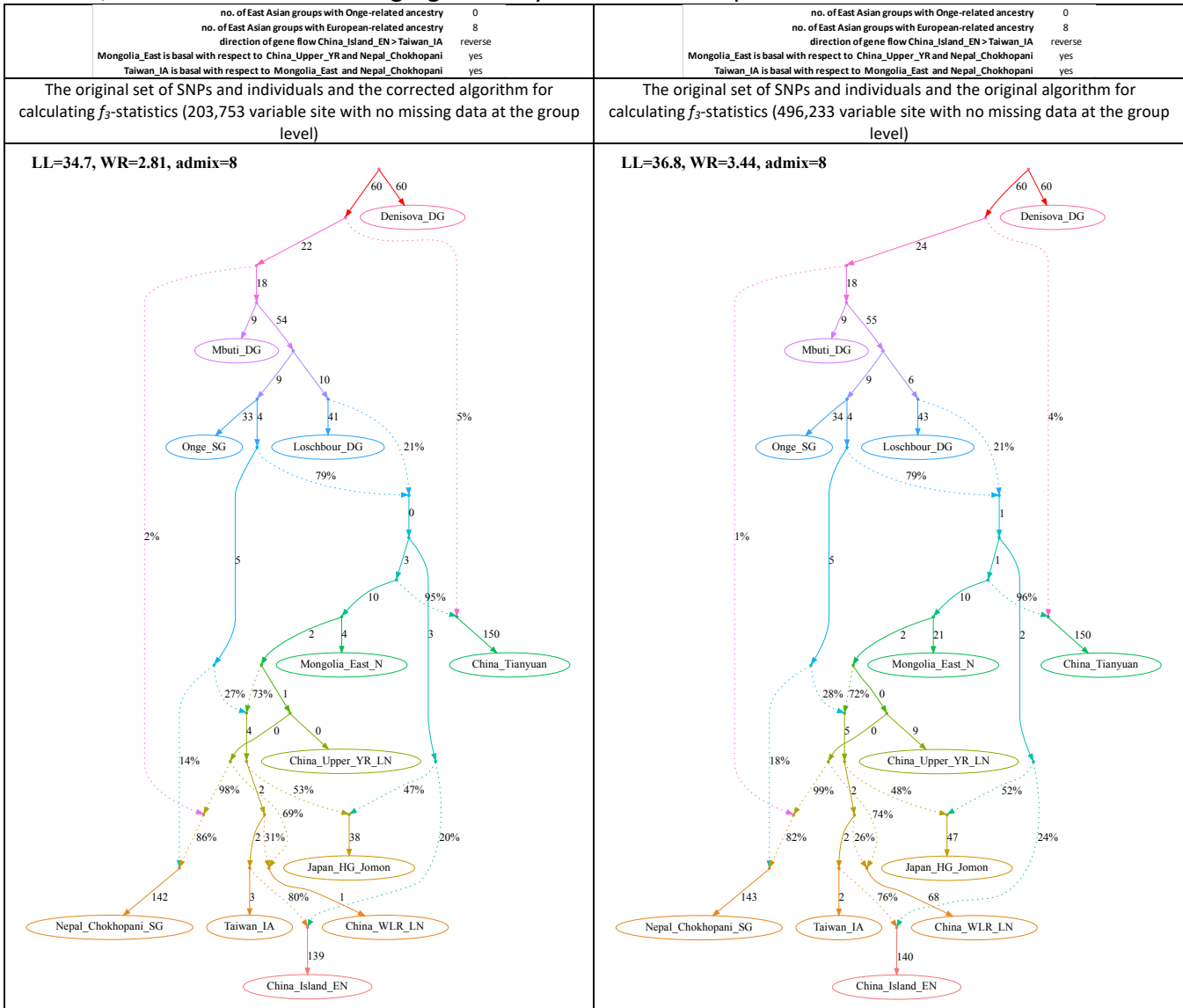


**j**, alternative models fitting significantly better than the published one



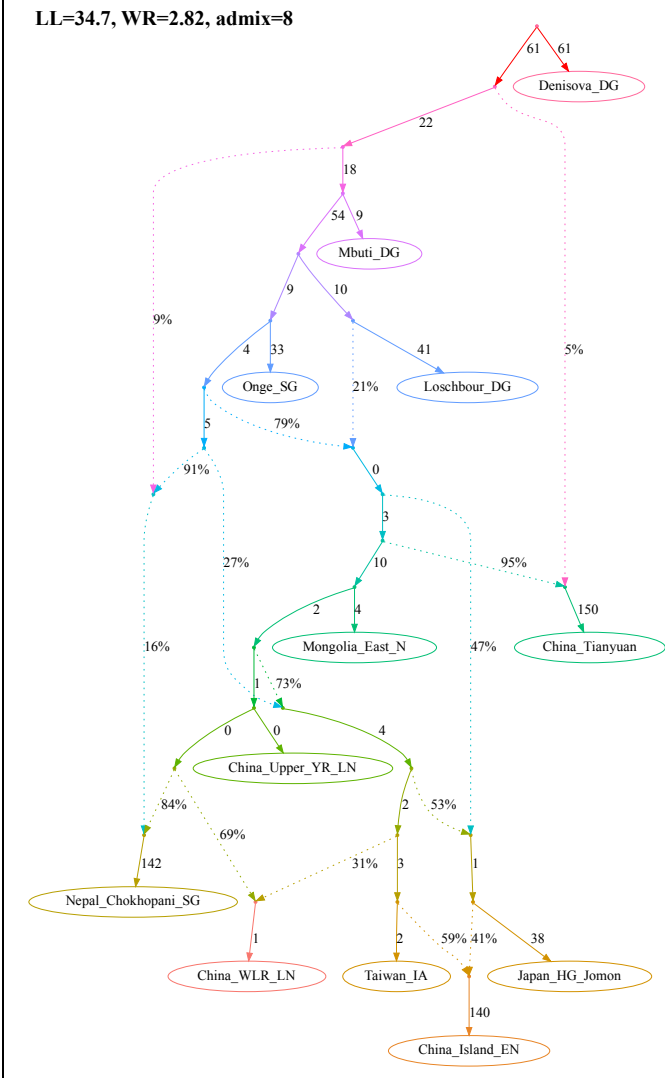


**k, alternative models fitting significantly better than the published one**



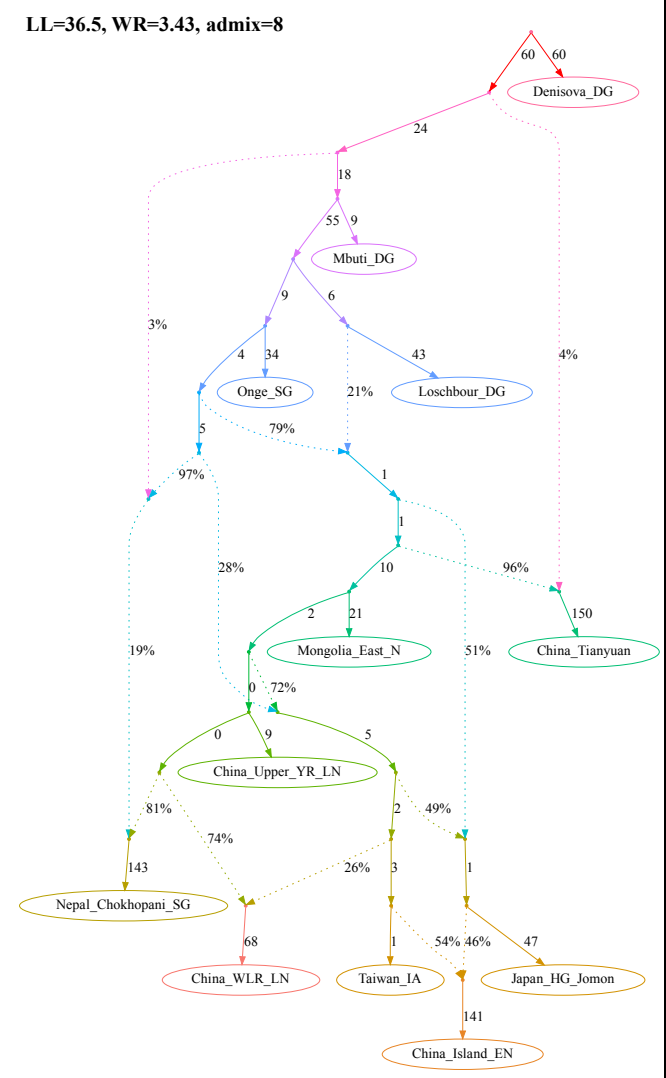
no. of East Asian groups with Onge-related ancestry	0
no. of East Asian groups with European-related ancestry	8
direction of gene flow China_Island_EN > Taiwan_IA	reverse
Mongolia_East is basal with respect to China_Upper_YR and Nepal_Chokhopani	yes
Taiwan_IA is basal with respect to Mongolia_East and Nepal_Chokhopani	yes

The original set of SNPs and individuals and the corrected algorithm for calculating  $f_3$ -statistics (203,753 variable site with no missing data at the group level)

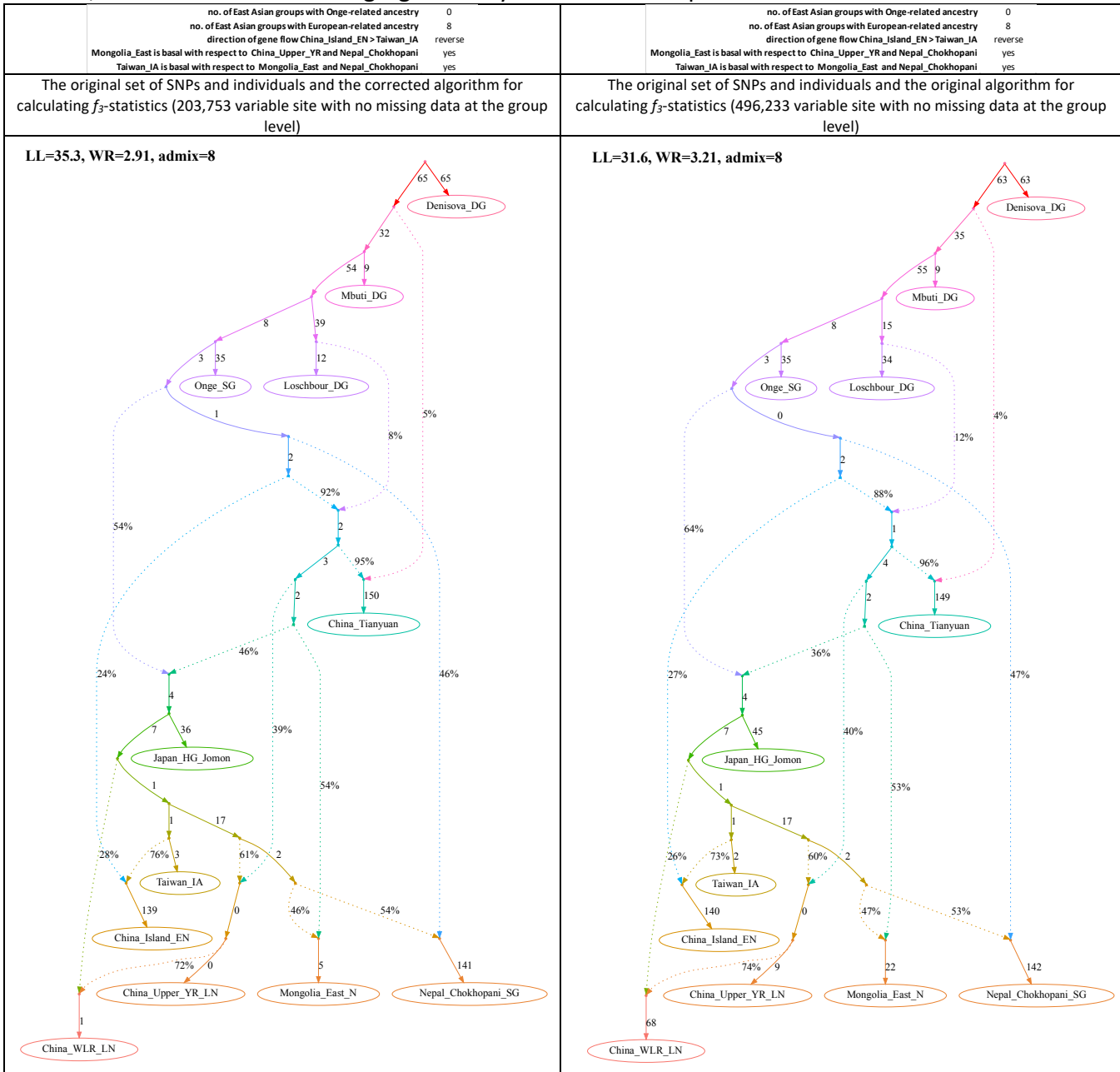


no. of East Asian groups with Onge-related ancestry	0
no. of East Asian groups with European-related ancestry	8
direction of gene flow China_Island_EN > Taiwan_IA	reverse
Mongolia_East is basal with respect to China_Upper_YR and Nepal_Chokhopani	yes
Taiwan_IA is basal with respect to Mongolia_East and Nepal_Chokhopani	yes

The original set of SNPs and individuals and the original algorithm for calculating  $f_3$ -statistics (496,233 variable site with no missing data at the group level)

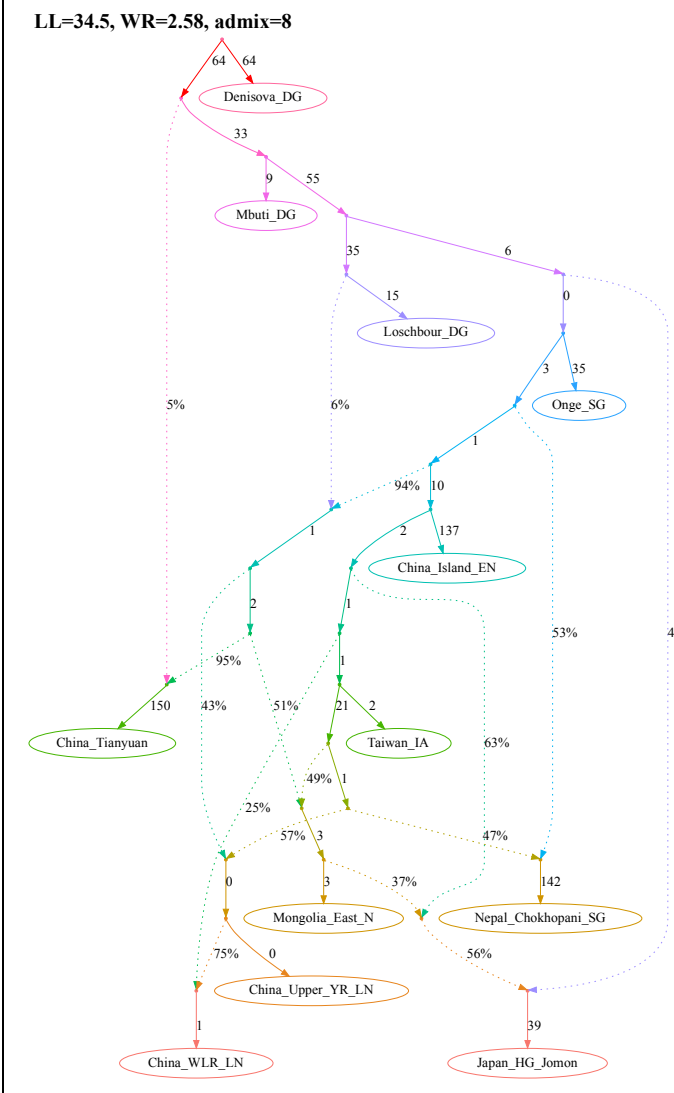


# I, alternative models fitting significantly better than the published one



no. of East Asian groups with Onge-related ancestry 0  
 no. of East Asian groups with European-related ancestry 5  
 direction of gene flow China\_Island\_EN>Taiwan\_IA no gene flow  
 Mongolia\_East is basal with respect to China\_Upper\_YR and Nepal\_Chokhopani yes  
 Taiwan\_IA is basal with respect to Mongolia\_East and Nepal\_Chokhopani unclear

The original set of SNPs and individuals and the corrected algorithm for calculating  $f_3$ -statistics (203,753 variable site with no missing data at the group level)



no. of East Asian groups with Onge-related ancestry 0  
 no. of East Asian groups with European-related ancestry 5  
 direction of gene flow China\_Island\_EN>Taiwan\_IA no gene flow  
 Mongolia\_East is basal with respect to China\_Upper\_YR and Nepal\_Chokhopani yes  
 Taiwan\_IA is basal with respect to Mongolia\_East and Nepal\_Chokhopani unclear

The original set of SNPs and individuals and the original algorithm for calculating  $f_3$ -statistics (496,233 variable site with no missing data at the group level)

