

Supplementary Figures S50-S80

Peopling history of Tibet Plateau and multiple waves of admixture of Tibetans inferred from both ancient and modern genome-wide data

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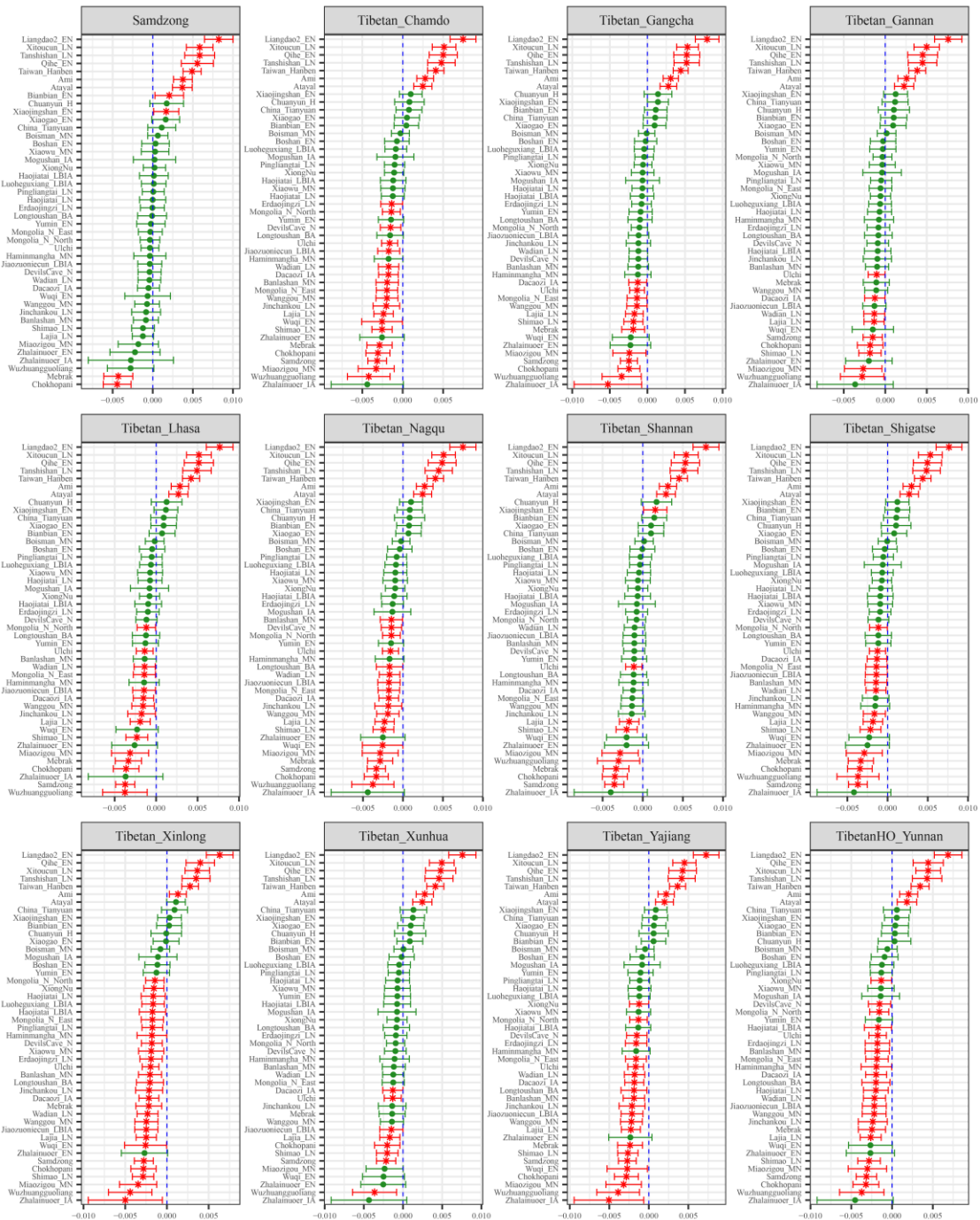


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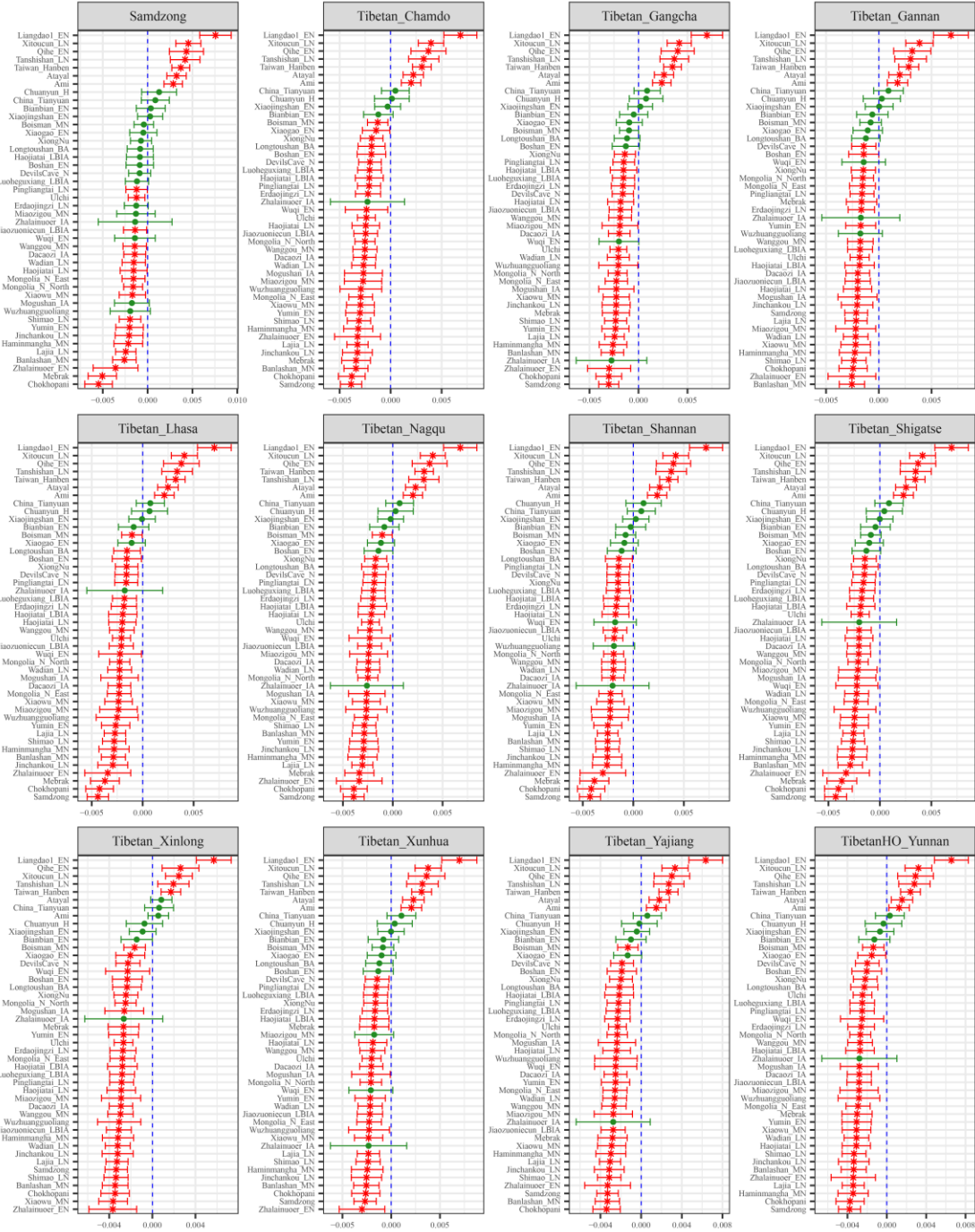


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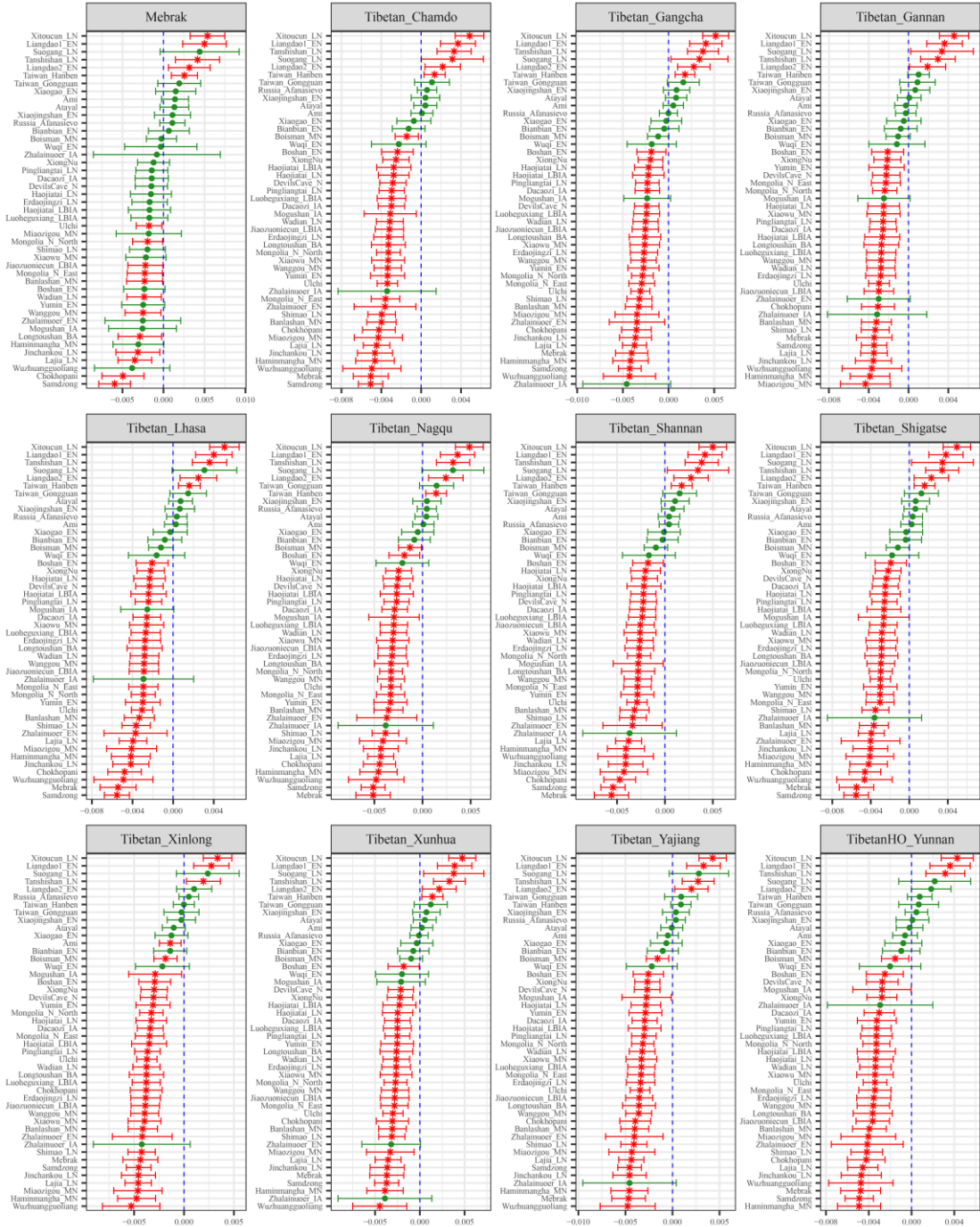


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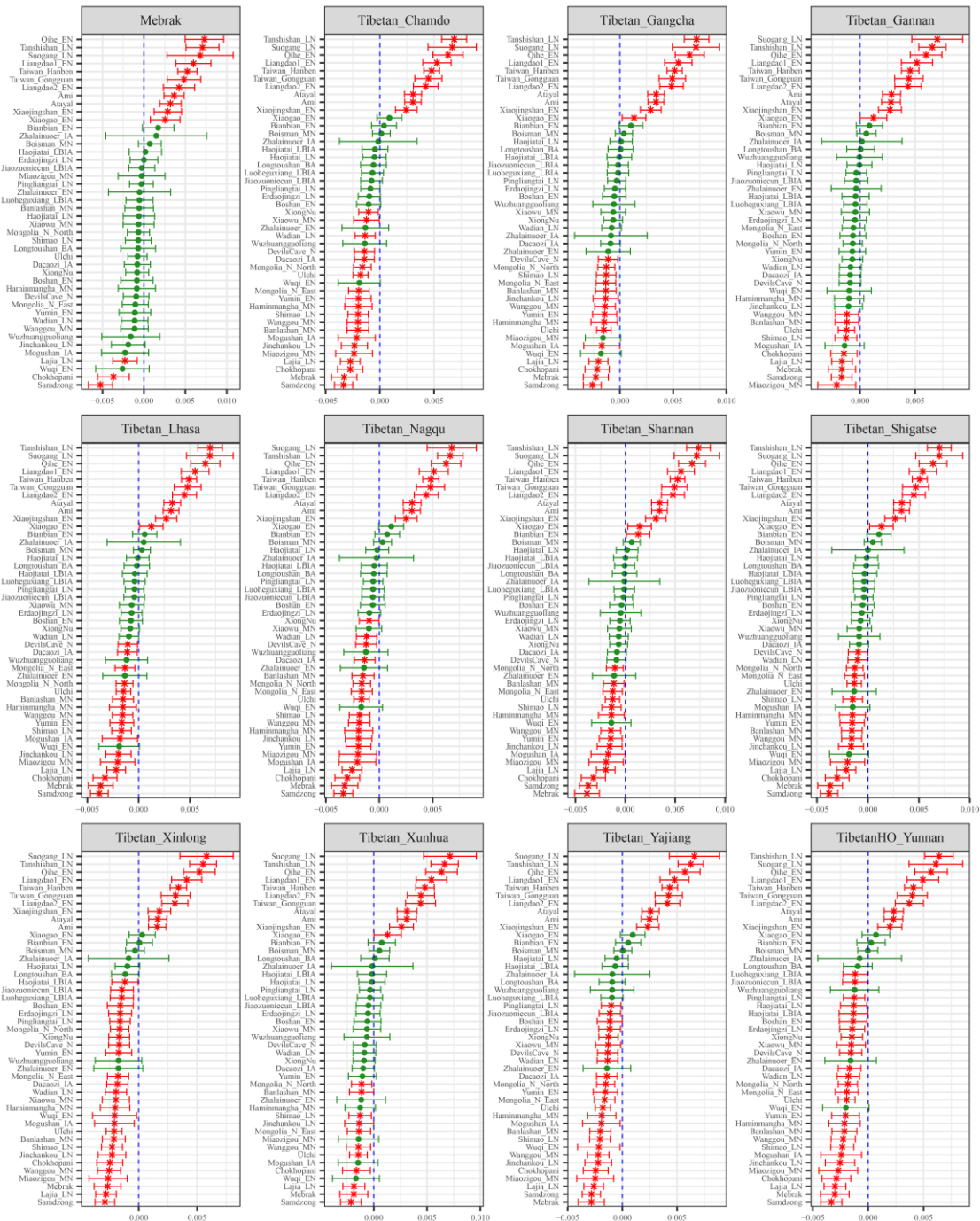


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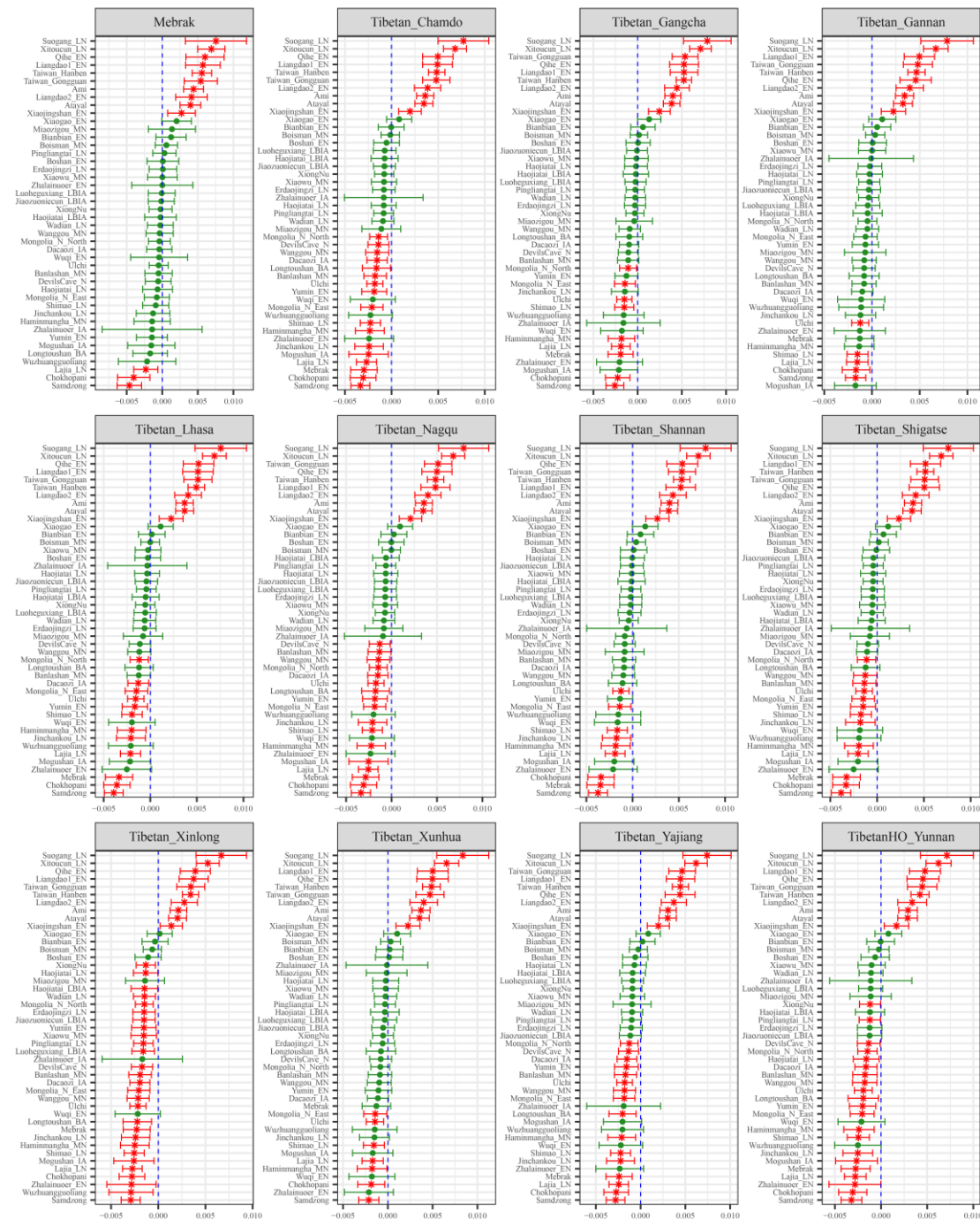


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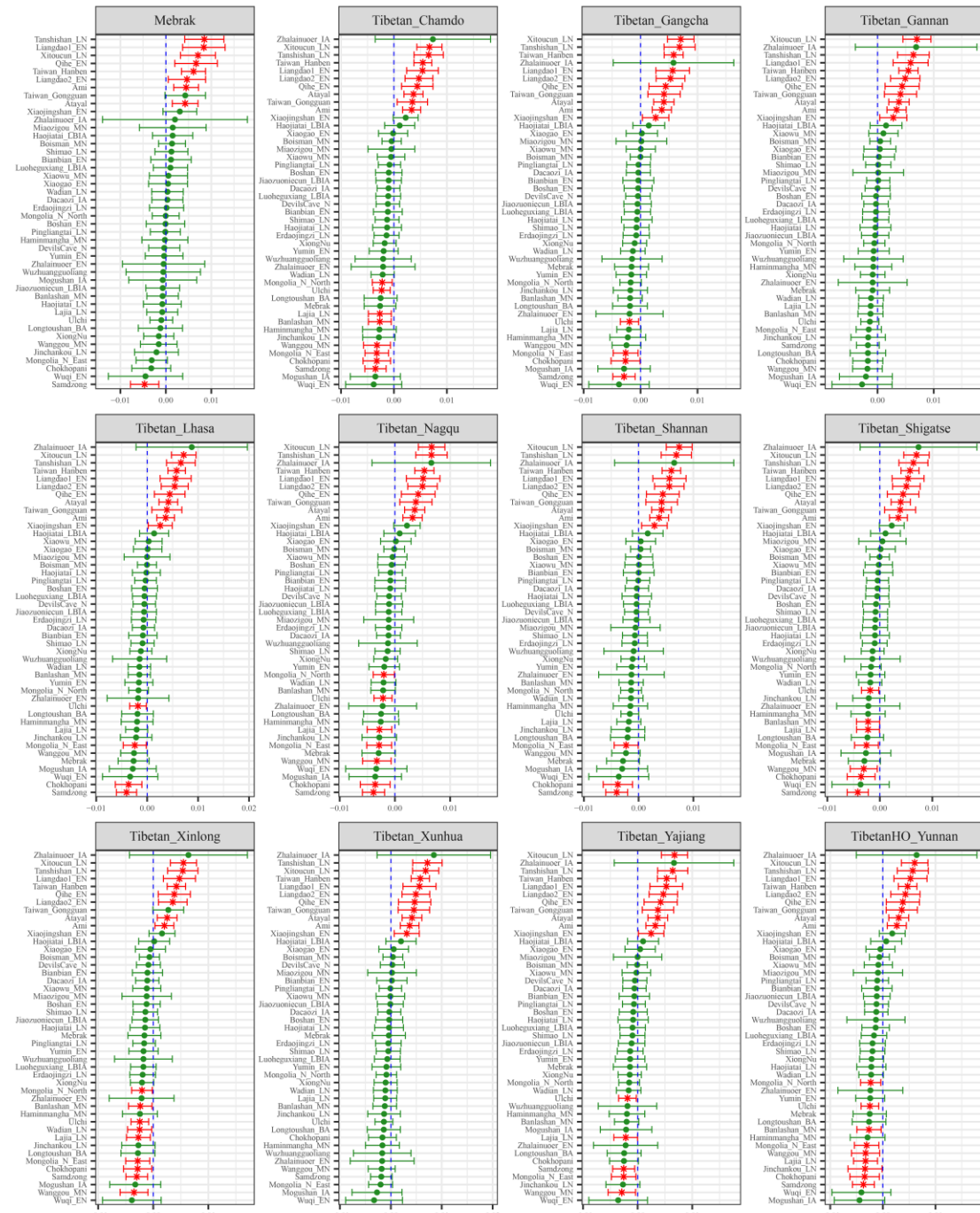


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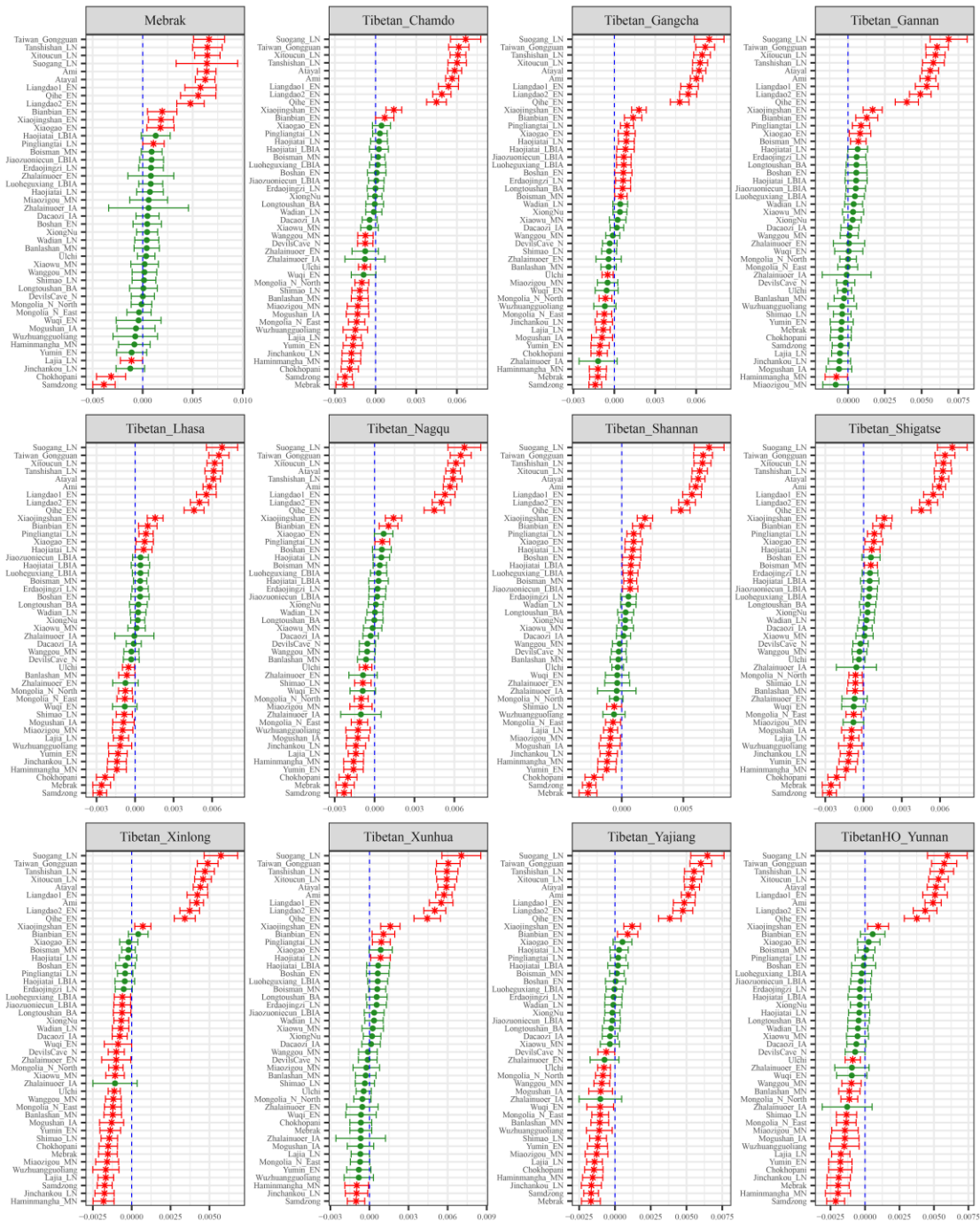


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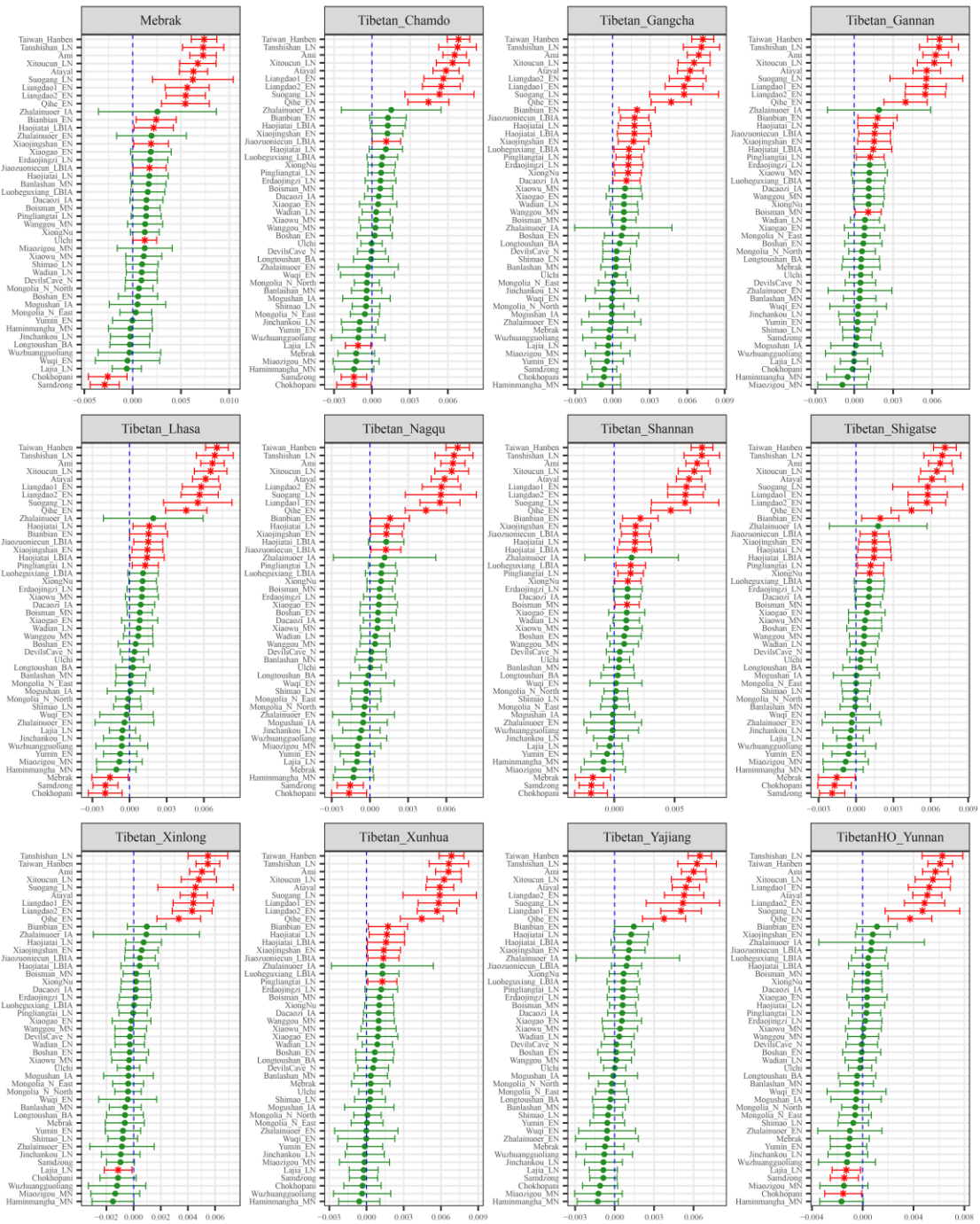


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Figure 1 displays 16 Manhattan plots arranged in a 4x4 grid, showing the results of a genome-wide association study (GWAS) for 12 traits across 16 populations. The traits are: Samdzong, Tibetan_Chamdo, Tibetan_Gangcha, Tibetan_Gannan, Tibetan_Lhasa, Tibetan_Naggu, Tibetan_Shannan, Tibetan_Shigatse, Tibetan_Xinlong, Tibetan_Xunhua, Tibetan_Yajiang, and TibetanHO_Yunnan. Each plot displays $-\log_{10}(p\text{-value})$ on the y-axis and genomic position on the x-axis. A vertical blue line indicates the position of the lead SNP. The plots show varying degrees of association across the genome, with some traits showing strong associations in specific populations.

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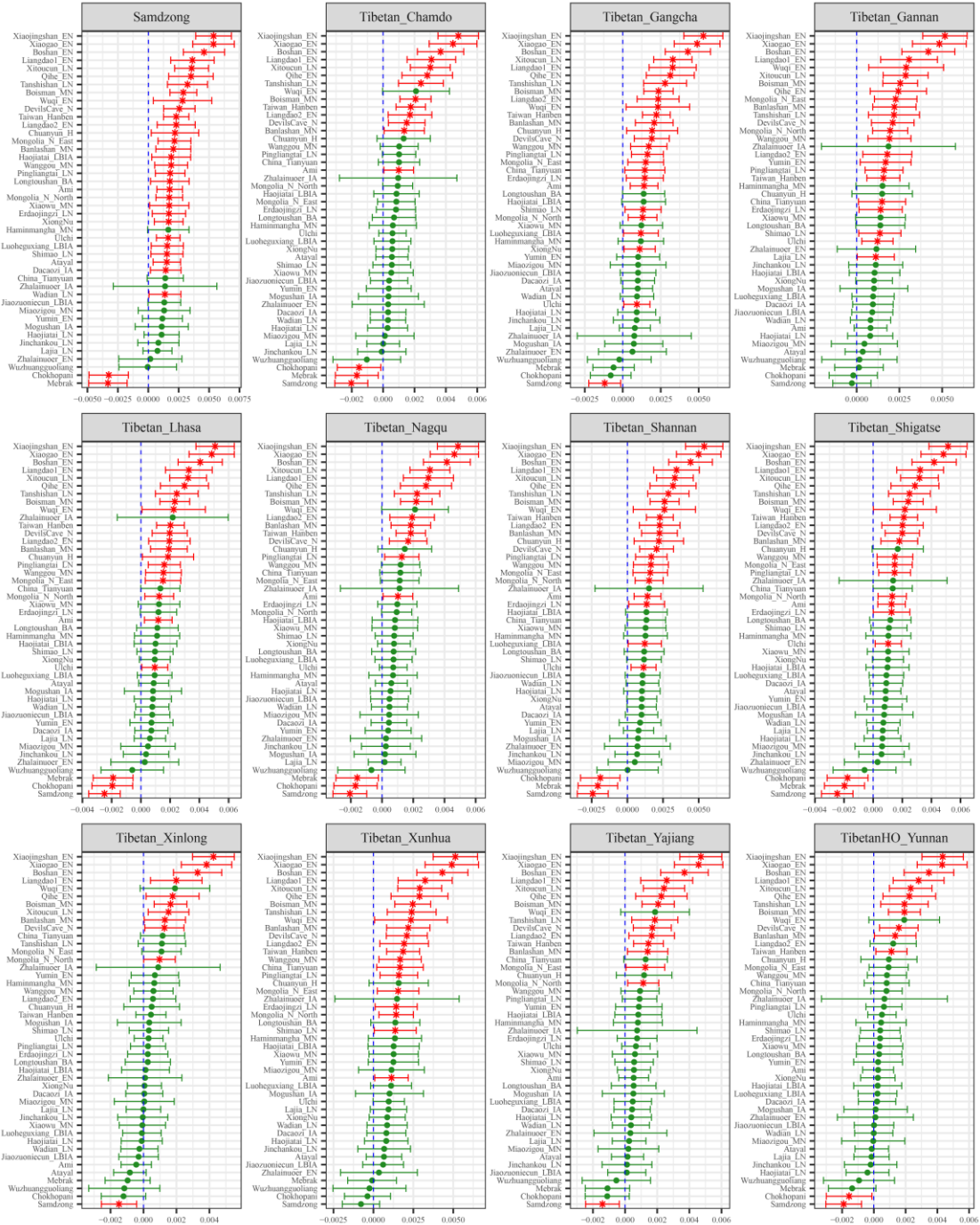


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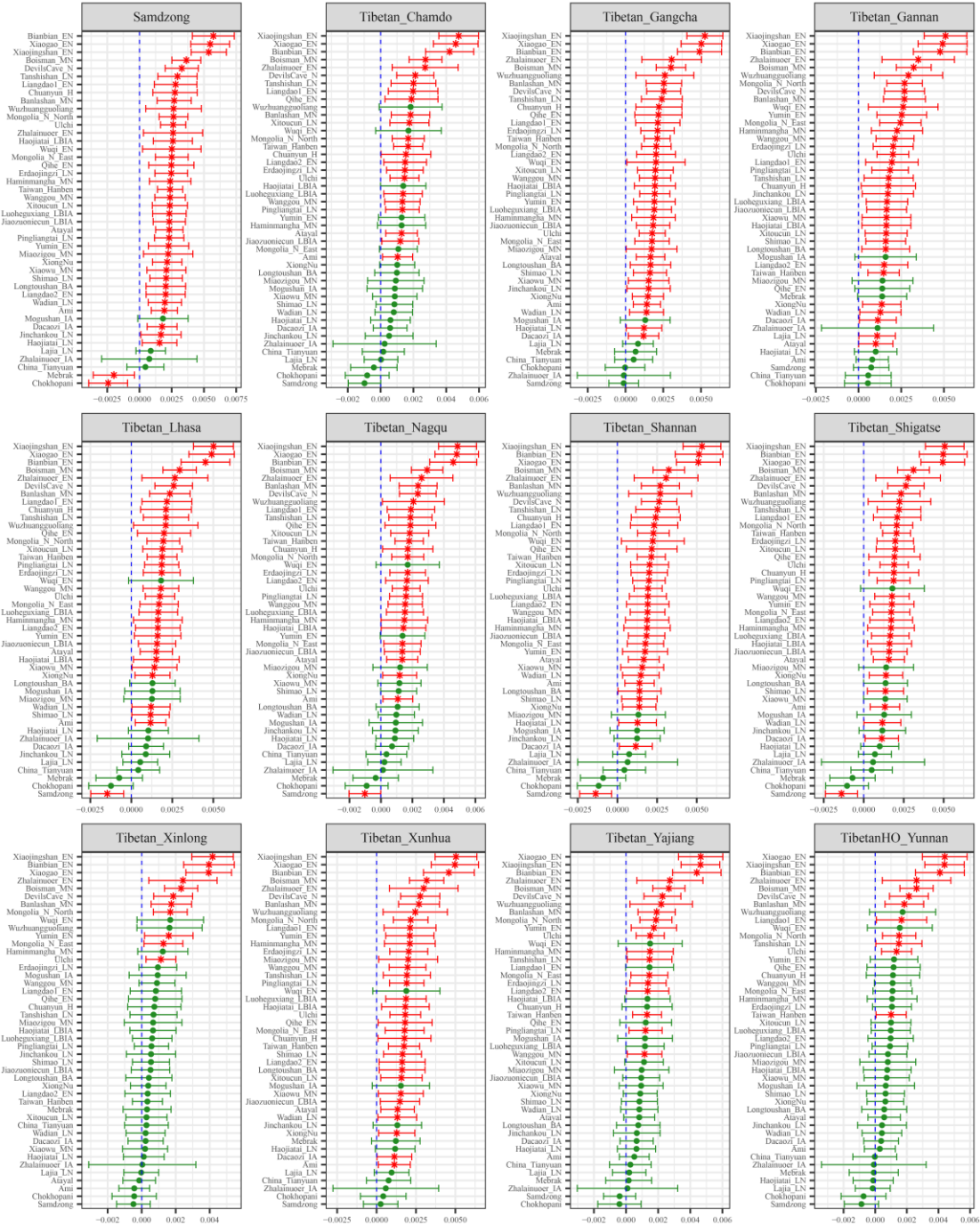


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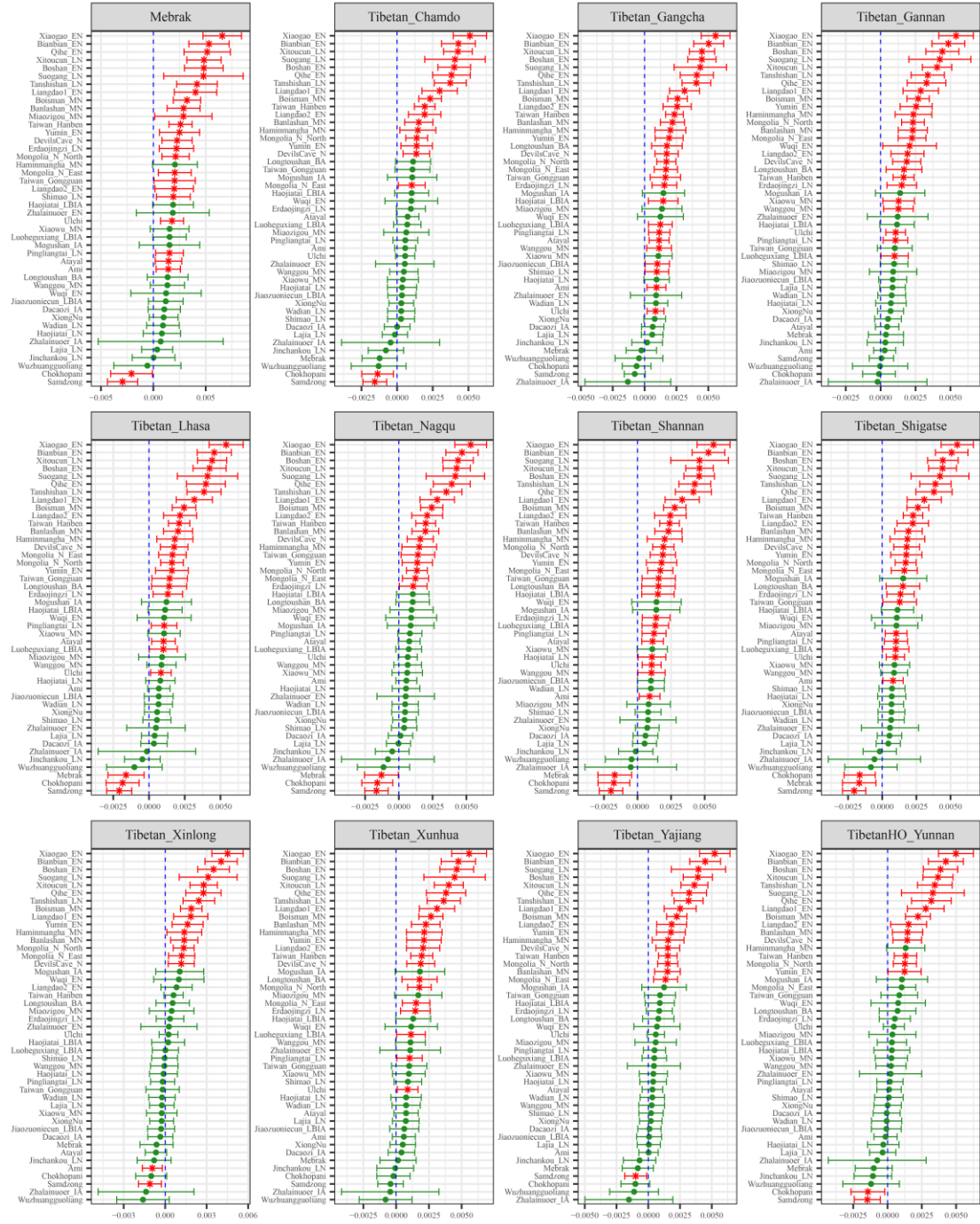
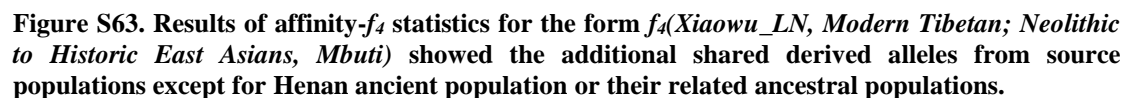


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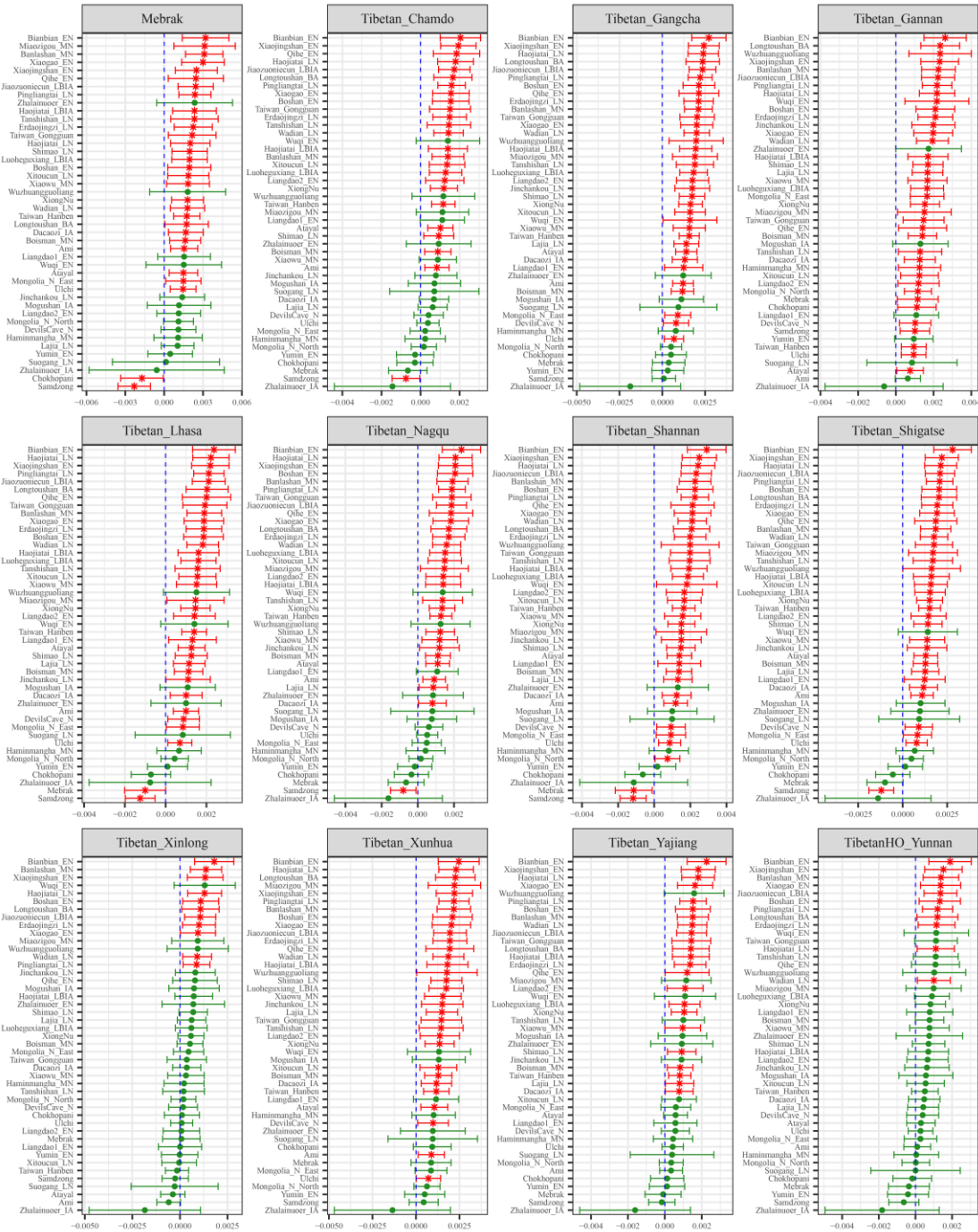


Figure S64. Results of affinity- f_4 statistics for the form $f_4(\text{Wanggou_LN}, \text{Modern Tibetan}; \text{Neolithic to Historic East Asians}, \text{Mbuti})$ showed the additional shared derived alleles from source populations except for Henan ancient population or their related ancestral populations.

Here, overlapping SNP loci included in the Affymetrix Human Origins platform among four analyzed populations were used. We used the genetic variation of Mbuti as the outgroup. Red asterisk point meant the significant value (Absolute value of Z-scores larger than three or equal to three) observed in the symmetry- f_4 statistics and green circle point denoted the non-significant f_4 -statistic values (Absolute value of Z-scores less than three). All ancient East Asians were listed along the Y-axis and f_4 values were labeled along the X-axis. All results were faceted or grouped via Tibetan populations. Significant negative f_4 values indicated that the third population shared more alleles with the second population, and

also means Tibetan obtained additional gene flow from the third source population (or related populations). And the significant positive f_4 value indicated that the third population shared more derived alleles with the first population. The value of f_4 -statistics equal to zero was marked as the blue dash line. The bar indicated three standard errors.

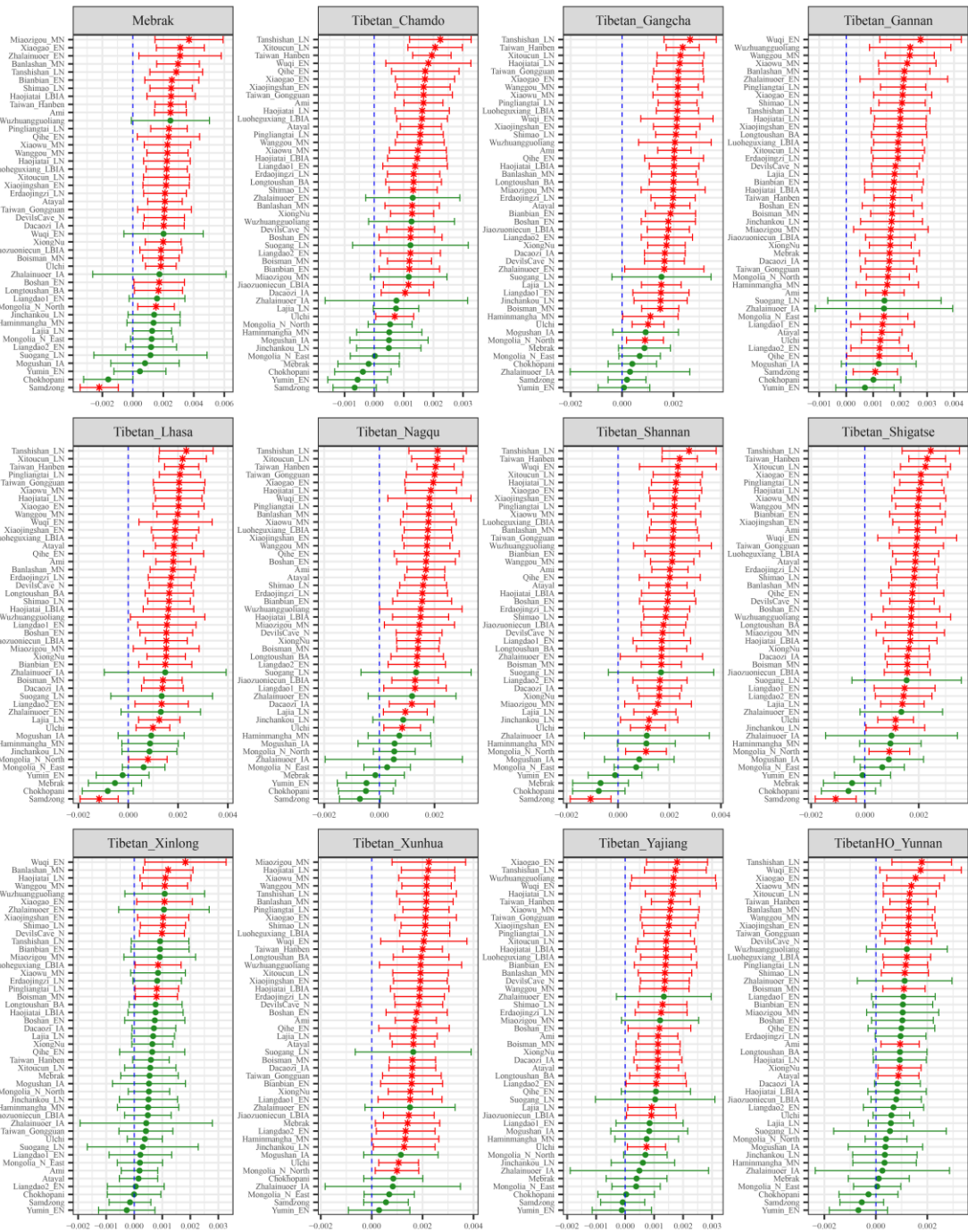


Figure S65. Results of affinity- f_4 statistics for the form $f_4(\text{Wadian_LN}, \text{Modern Tibetan}; \text{Neolithic to Historic East Asians}, \text{Mbuti})$ showed the additional shared derived alleles from source populations except for Henan ancient population or their related ancestral populations.

Here, overlapping SNP loci included in the Affymetrix Human Origins platform among four analyzed populations were used. We used the genetic variation of Mbuti as the outgroup. Red asterisk point meant the significant value (Absolute value of Z-scores larger than three or equal to three) observed in the symmetry- f_4 statistics and green circle point denoted the non-significant f_4 -statistic values (Absolute value of Z-scores less than three). All ancient East Asians were listed along the Y-axis and f_4 values were labeled along the X-axis. All results were faceted or grouped via Tibetan populations. Significant

negative f_4 values indicated that the third population shared more alleles with the second population, and also means Tibetan obtained additional gene flow from the third source population (or related populations). And the significant positive f_4 value indicated that the third population shared more derived alleles with the first population. The value of f_4 -statistics equal to zero was marked as the blue dash line. The bar indicated three standard errors.

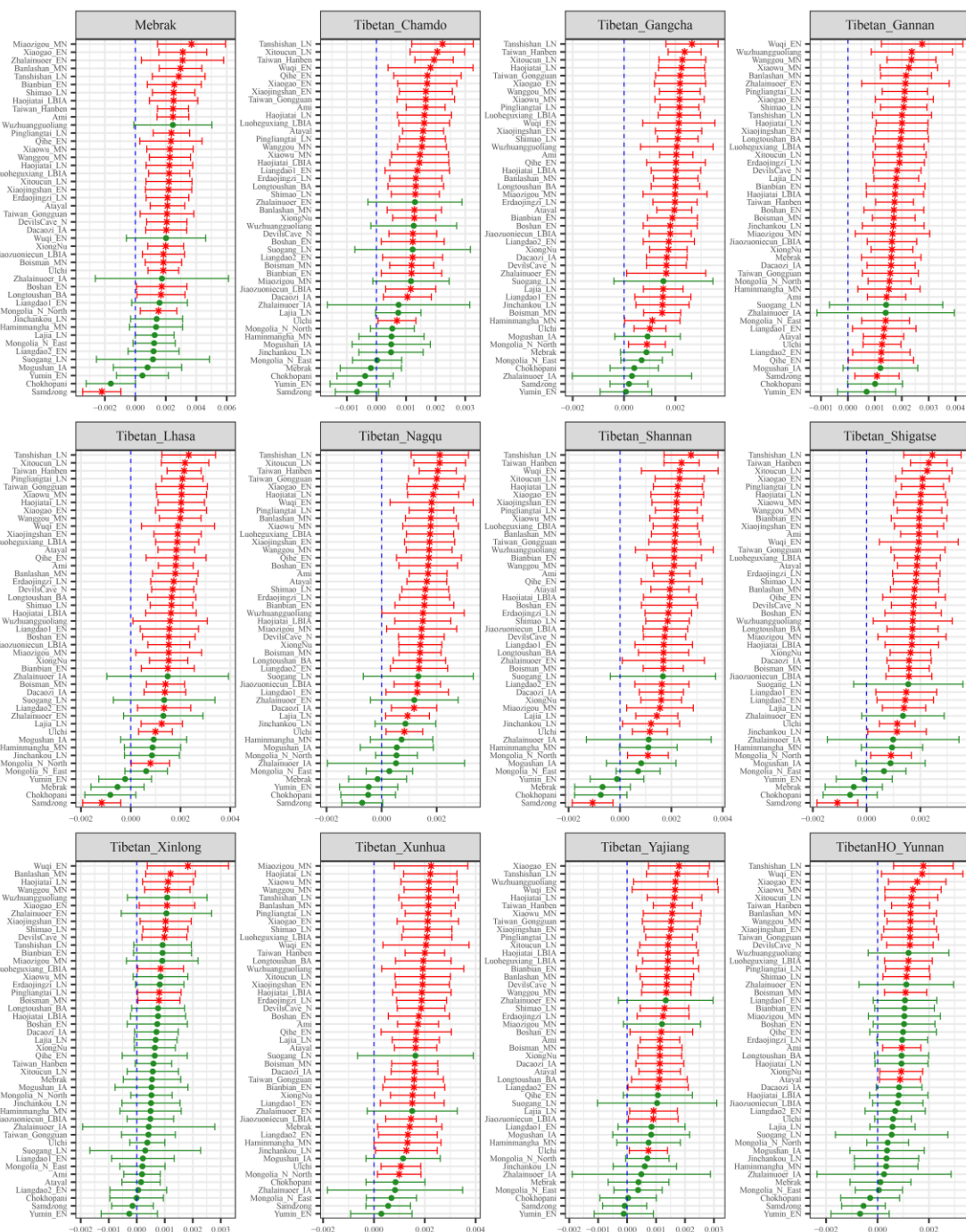


Figure S66. Results of affinity- f_4 statistics for the form $f_4(\text{Wadian_LN, Modern Tibetan; Neolithic to Historic East Asians, Mbuti})$ showed the additional shared derived alleles from source populations except for Henan ancient population or their related ancestral populations.

Here, overlapping SNP loci included in the Affymetrix Human Origins platform among four analyzed populations were used. We used the genetic variation of Mbuti as the outgroup. Red asterisk point meant the significant value (Absolute value of Z-scores larger than three or equal to three) observed in the symmetry- f_4 statistics and green circle point denoted the non-significant f_4 -statistic values (Absolute value of Z-scores less than three). All ancient East Asians were listed along the Y-axis and f_4 values were labeled along the X-axis. All results were faceted or grouped via Tibetan populations. Significant

negative f_4 values indicated that the third population shared more alleles with the second population, and also means Tibetan obtained additional gene flow from the third source population (or related populations). And the significant positive f_4 value indicated that the third population shared more derived alleles with the first population. The value of f_4 -statistics equal to zero was marked as the blue dash line. The bar indicated three standard errors.

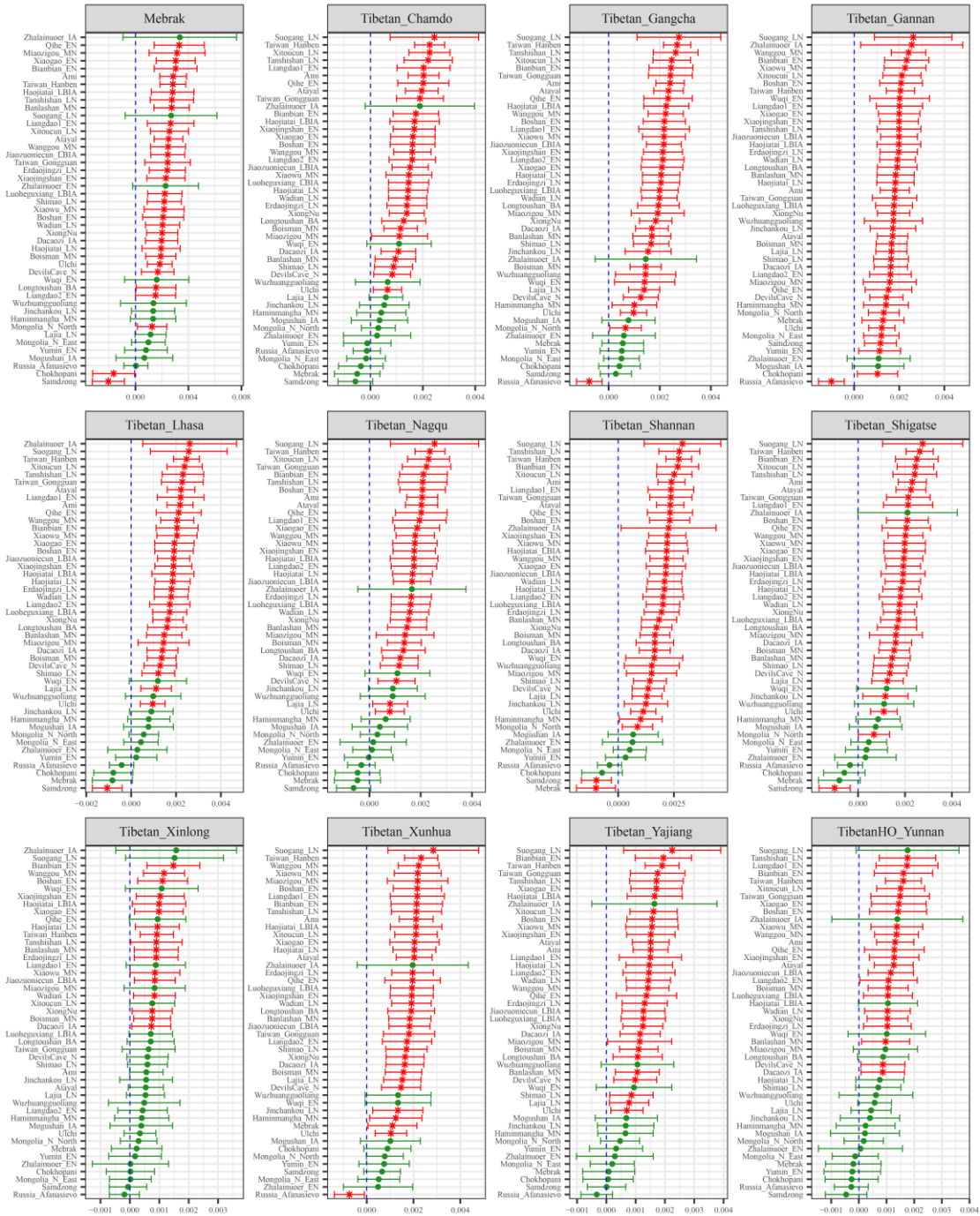


Figure S67. Results of affinity- f_4 statistics for the form $f_4(\text{Pingliangtai_LN}, \text{Modern Tibetan}; \text{Neolithic to Historic East Asians}, \text{Mbuti})$ showed the additional shared derived alleles from source populations except for Henan ancient population or their related ancestral populations.

Here, overlapping SNP loci included in the Affymetrix Human Origins platform among four analyzed populations were used. We used the genetic variation of Mbuti as the outgroup. Red asterisk point meant the significant value (Absolute value of Z-scores larger than three or equal to three) observed in the symmetry- f_4 statistics and green circle point denoted the non-significant f_4 -statistic values (Absolute value of Z-scores less than three). All ancient East Asians were listed along the Y-axis and f_4 values were labeled along the X-axis. All results were faceted or grouped via Tibetan populations. Significant

negative f_4 values indicated that the third population shared more alleles with the second population, and also means Tibetan obtained additional gene flow from the third source population (or related populations). And the significant positive f_4 value indicated that the third population shared more derived alleles with the first population. The value of f_4 -statistics equal to zero was marked as the blue dash line. The bar indicated three standard errors.

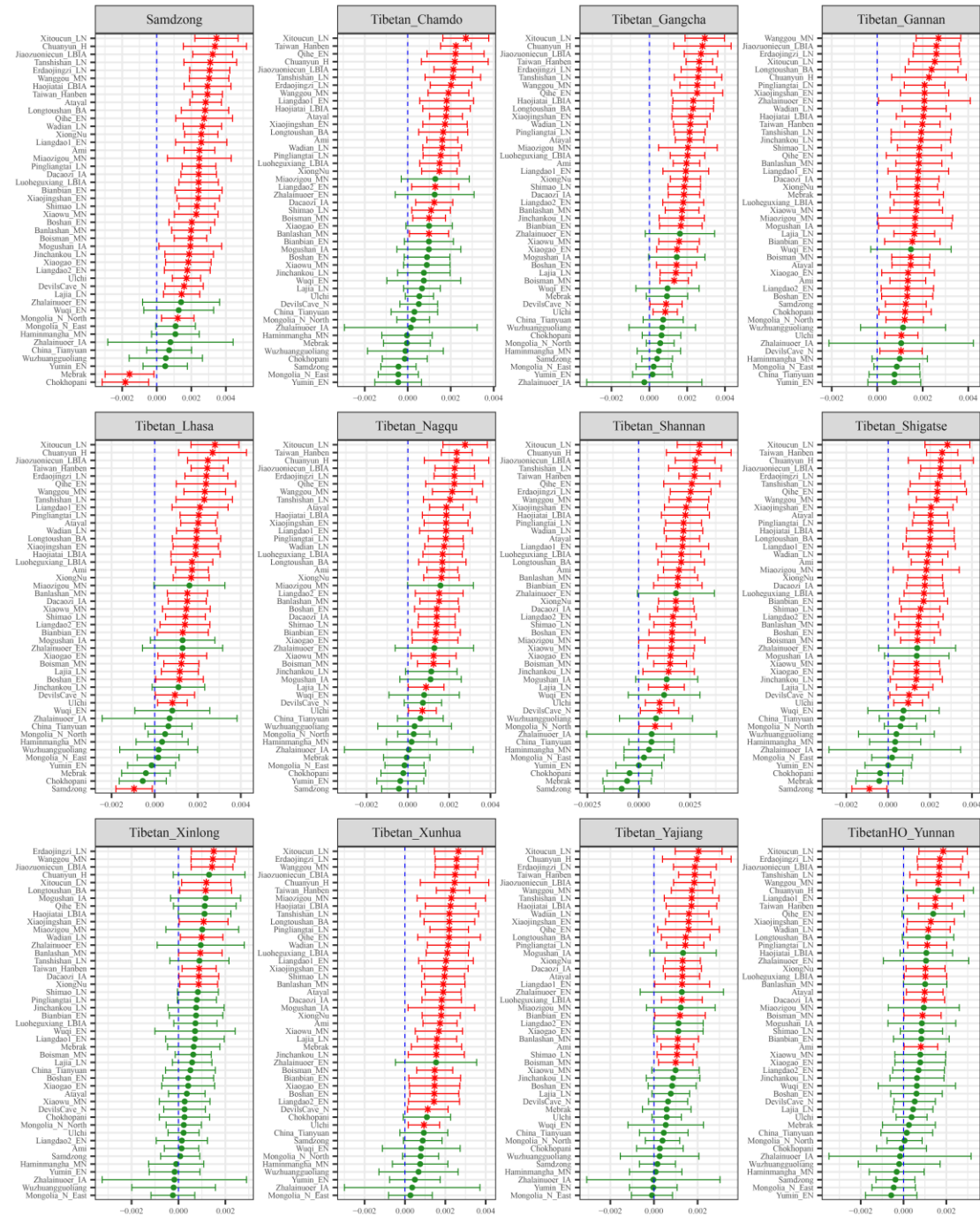


Figure S68. Results of affinity- f_4 statistics for the form $f_4(\text{Haojiatai_LN}, \text{Modern Tibetan}; \text{Neolithic to Historic East Asians}, \text{Mbuti})$ showed the additional shared derived alleles from source populations except for Henan ancient population or their related ancestral populations.

Here, overlapping SNP loci included in the Affymetrix Human Origins platform among four analyzed populations were used. We used the genetic variation of Mbuti as the outgroup. Red asterisk point meant the significant value (Absolute value of Z-scores larger than three or equal to three) observed in the symmetry- f_4 statistics and green circle point denoted the non-significant f_4 -statistic values (Absolute value of Z-scores less than three). All ancient East Asians were listed along the Y-axis and f_4 values were

labeled along the X-axis. All results were faceted or grouped via Tibetan populations. Significant negative f_4 values indicated that the third population shared more alleles with the second population, and also means Tibetan obtained additional gene flow from the third source population (or related populations). And the significant positive f_4 value indicated that the third population shared more derived alleles with the first population. The value of f_4 -statistics equal to zero was marked as the blue dash line. The bar indicated three standard errors.

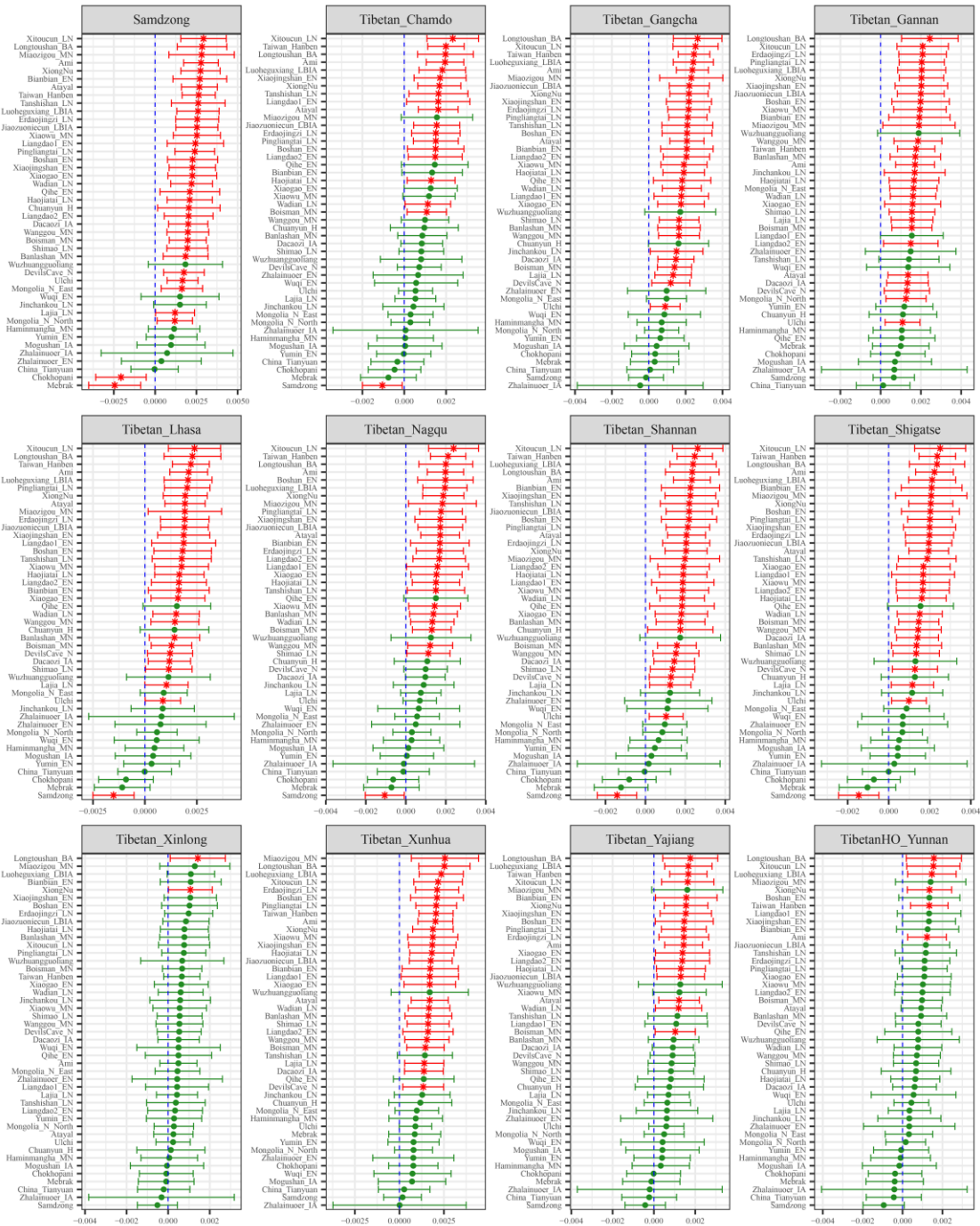


Figure S69. Results of affinity- f_4 statistics for the form $f_4(\text{Haojiatai_LBIA, Modern Tibetan; Neolithic to Historic East Asians, Mbuti})$ showed the additional shared derived alleles from source populations except for Henan ancient population or their related ancestral populations.

Here, overlapping SNP loci included in the Affymetrix Human Origins platform among four analyzed populations were used. We used the genetic variation of Mbuti as the outgroup. Red asterisk point meant the significant value (Absolute value of Z-scores larger than three or equal to three) observed in the symmetry- f_4 statistics and green circle point denoted the non-significant f_4 -statistic values (Absolute value of Z-scores less than three). All ancient East Asians were listed along the Y-axis and f_4 values were

labeled along the X-axis. All results were faceted or grouped via Tibetan populations. Significant negative f_4 values indicated that the third population shared more alleles with the second population, and also means Tibetan obtained additional gene flow from the third source population (or related populations). And the significant positive f_4 value indicated that the third population shared more derived alleles with the first population. The value of f_4 -statistics equal to zero was marked as the blue dash line. The bar indicated three standard errors.

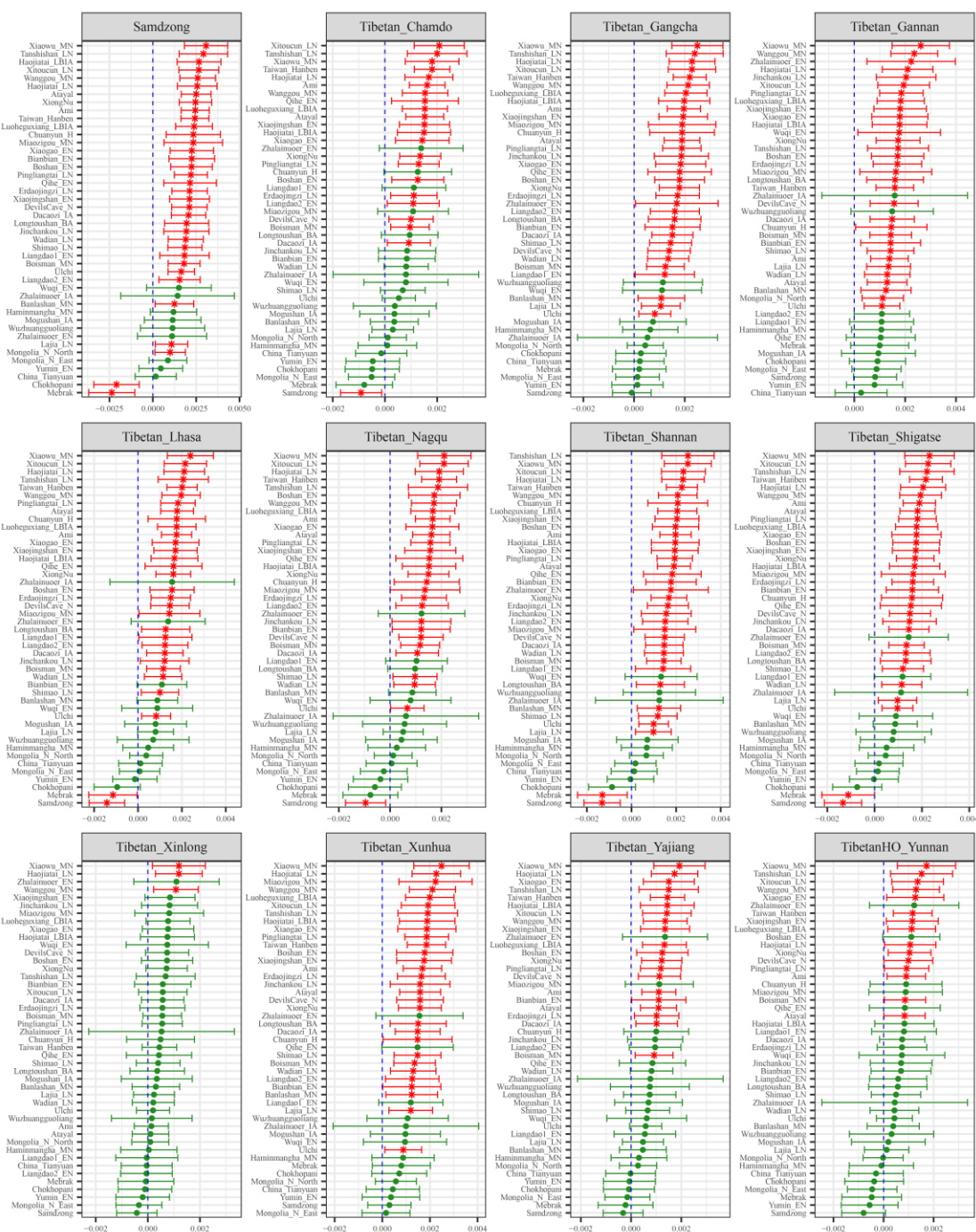


Figure S70. Results of affinity- f_4 statistics for the form $f_4(\text{Jiao zuo nie cu en_LBIA, Modern Tibetan; Neolithic to Historic East Asians, Mbuti})$ showed the additional shared derived alleles from source populations except for Henan ancient population or their related ancestral populations.

Here, overlapping SNP loci included in the Affymetrix Human Origins platform among four analyzed populations were used. We used the genetic variation of Mbuti as the outgroup. Red asterisk point meant the significant value (Absolute value of Z-scores larger than three or equal to three) observed in the symmetry- f_4 statistics and green circle point denoted the non-significant f_4 -statistic values (Absolute value of Z-scores less than three). All ancient East Asians were listed along the Y-axis and f_4 values were

labeled along the X-axis. All results were faceted or grouped via Tibetan populations. Significant negative f_4 values indicated that the third population shared more alleles with the second population, and also means Tibetan obtained additional gene flow from the third source population (or related populations). And the significant positive f_4 value indicated that the third population shared more derived alleles with the first population. The value of f_4 -statistics equal to zero was marked as the blue dash line. The bar indicated three standard errors.

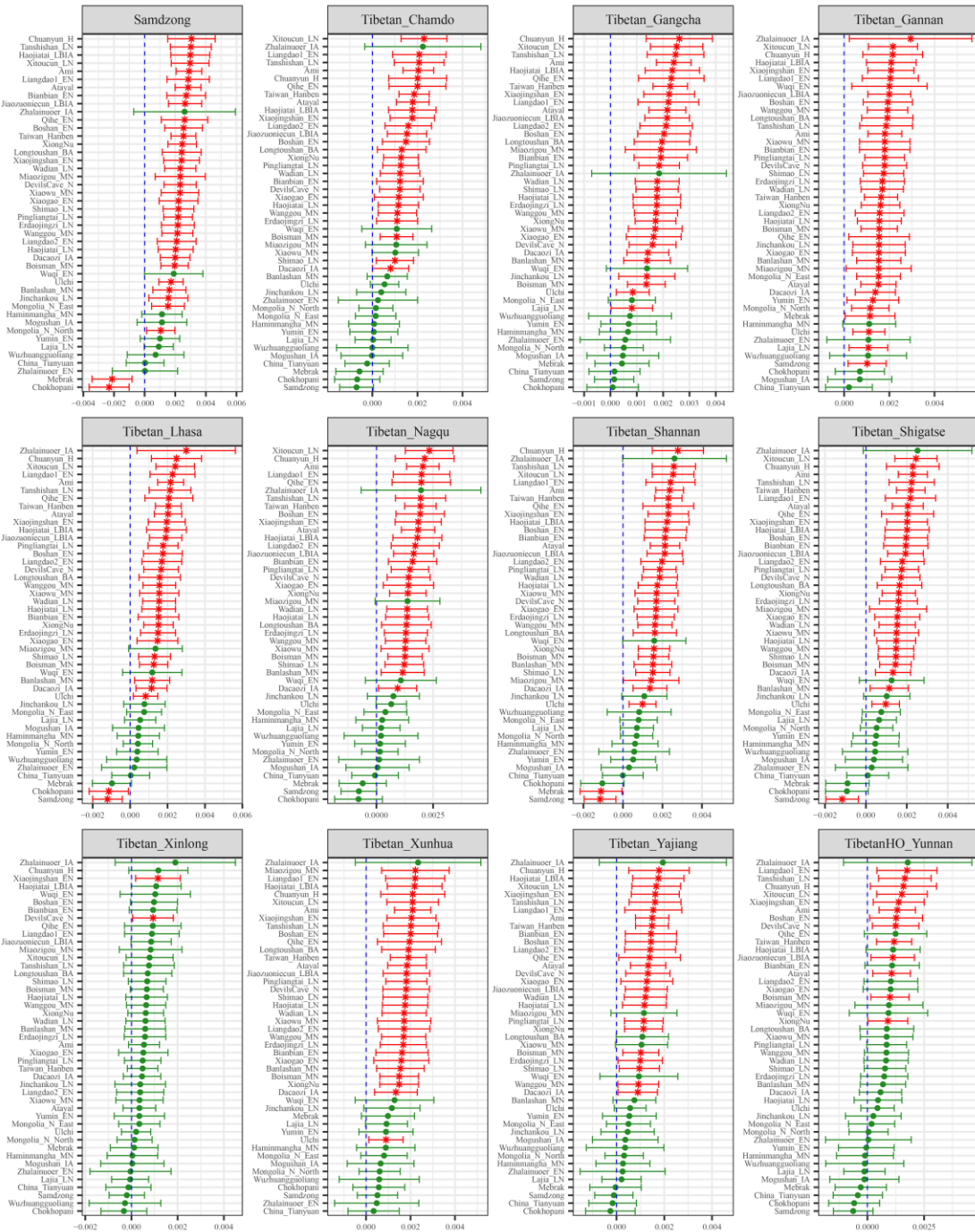


Figure S71. Results of affinity- f_4 statistics for the form $f_4(\text{Luoheguxiang_LBIA, Modern Tibetan; Neolithic to Historic East Asians, Mbuti})$ showed the additional shared derived alleles from source populations except for Henan ancient population or their related ancestral populations.

Here, overlapping SNP loci included in the Affymetrix Human Origins platform among four analyzed populations were used. We used the genetic variation of Mbuti as the outgroup. Red asterisk point meant the significant value (Absolute value of Z-scores larger than three or equal to three) observed in the symmetry- f_4 statistics and green circle point denoted the non-significant f_4 -statistic values (Absolute value of Z-scores less than three). All ancient East Asians were listed along the Y-axis and f_4 values were

labeled along the X-axis. All results were faceted or grouped via Tibetan populations. Significant negative f_4 values indicated that the third population shared more alleles with the second population, and also means Tibetan obtained additional gene flow from the third source population (or related populations). And the significant positive f_4 value indicated that the third population shared more derived alleles with the first population. The value of f_4 -statistics equal to zero was marked as the blue dash line. The bar indicated three standard errors.

Additional gene flow events when we assumed that Tibetans' direct ancestor is inland Neolithic northern East Asian from Shaanxi or Inner Mongolia or their related ancestral populations

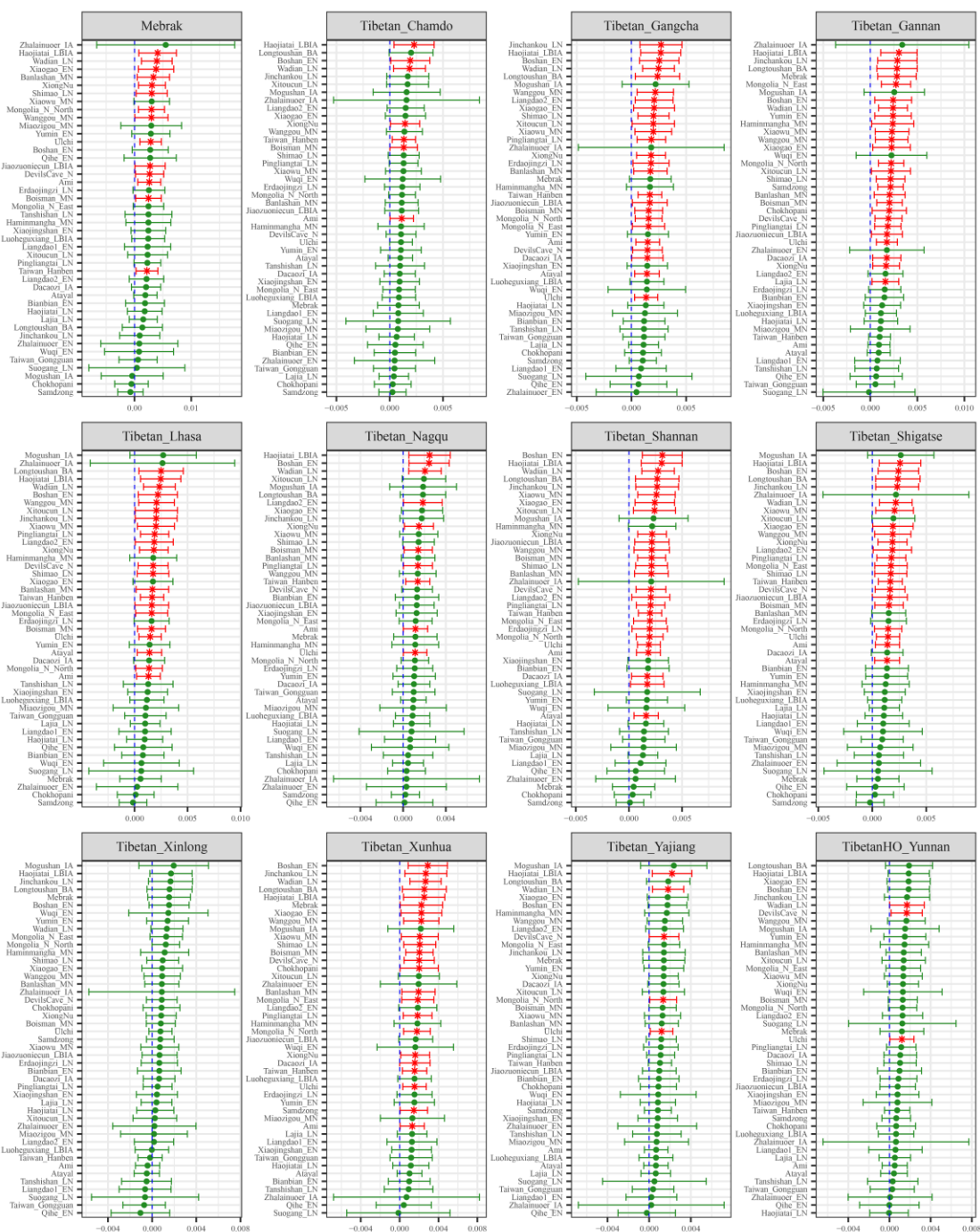


Figure S72. Results of affinity- f_4 statistics for the form $f_4(\text{Wuzhuangguoliang}, \text{Modern Tibetan}; \text{Neolithic to Historic East Asians}, \text{Mbuti})$ showed the additional shared derived alleles from source populations except for inland Neolithic northern East Asian from Shaanxi or Inner Mongolia or their related ancestral populations.

Here, overlapping SNP loci included in the Affymetrix Human Origins platform among four analyzed populations were used. We used the genetic variation of Mbuti as the outgroup. Red asterisk point meant the significant value (Absolute value of Z-scores larger than three or equal to three) observed in the symmetry- f_4 statistics and green circle point denoted the non-significant f_4 -statistic values (Absolute value of Z-scores less than three). All ancient East Asians were listed along the Y-axis and f_4 values were labeled along the X-axis. All results were faceted or grouped via Tibetan populations. Significant negative f_4 values indicated that the third population shared more alleles with the second population, and also means Tibetan obtained additional gene flow from the third source population (or related

populations). And the significant positive f_4 value indicated that the third population shared more derived alleles with the first population. The value of f_4 -statistics equal to zero was marked as the blue dash line. The bar indicated three standard errors.

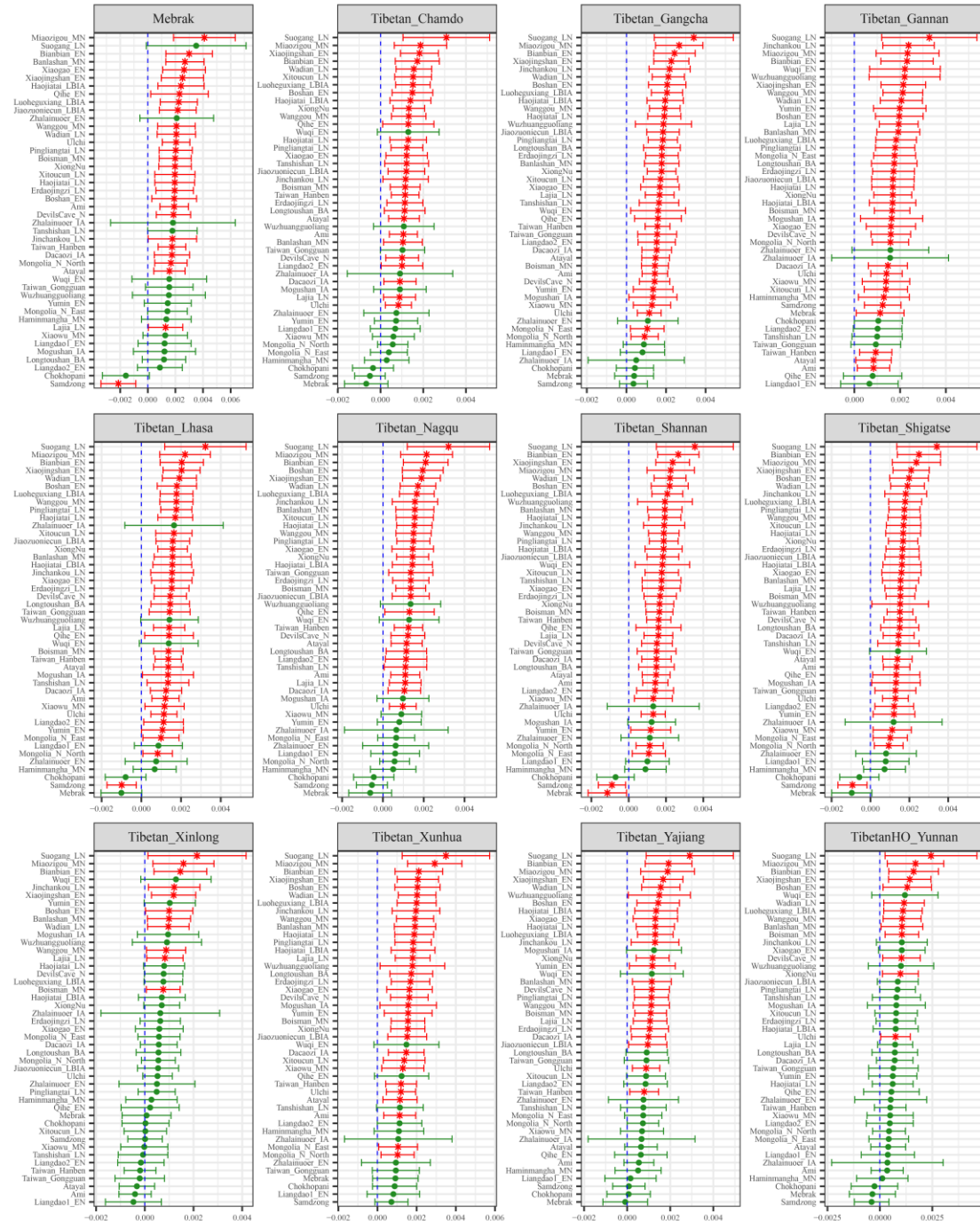


Figure S73. Results of affinity- f_4 statistics for the form $f_4(\text{Shimao_LN, Modern Tibetan; Neolithic to Historic East Asians, Mbuti})$ showed the additional shared derived alleles from source populations except for inland Neolithic northern East Asian from Shaanxi or Inner Mongolia or their related ancestral populations.

Here, overlapping SNP loci included in the Affymetrix Human Origins platform among four analyzed populations were used. We used the genetic variation of Mbuti as the outgroup. Red asterisk point meant the significant value (Absolute value of Z-scores larger than three or equal to three) observed in the symmetry- f_4 statistics and green circle point denoted the non-significant f_4 -statistic values (Absolute value of Z-scores less than three). All ancient East Asians were listed along the Y-axis and f_4 values were labeled along the X-axis. All results were faceted or grouped via Tibetan populations. Significant negative f_4 values indicated that the third population shared more alleles with the second population, and

also means Tibetan obtained additional gene flow from the third source population (or related populations). And the significant positive f_4 value indicated that the third population shared more derived alleles with the first population. The value of f_4 -statistics equal to zero was marked as the blue dash line. The bar indicated three standard errors.

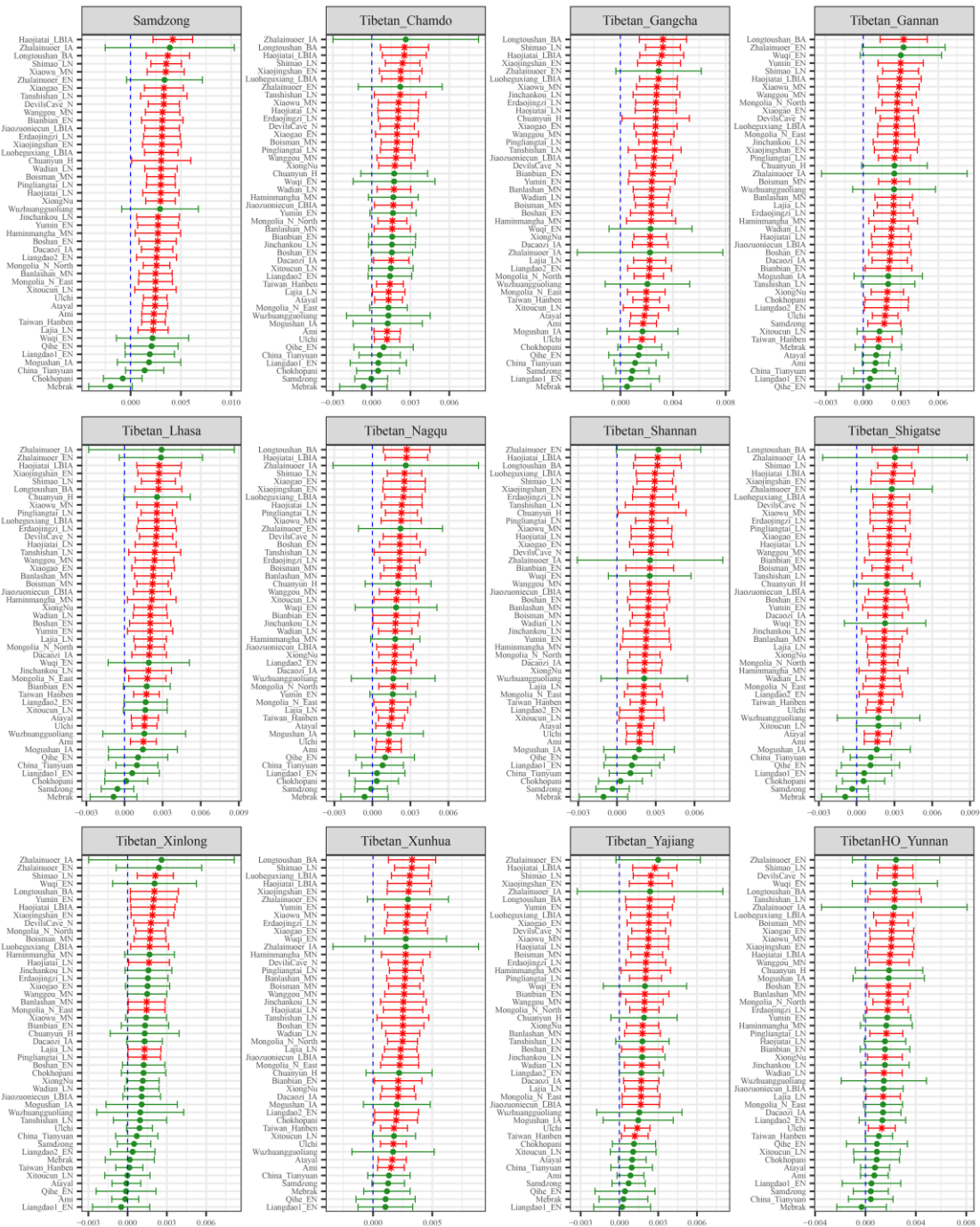


Figure S74. Results of affinity- f_4 statistics for the form $f_4(\text{Miaozigou_MN}, \text{Modern Tibetan}; \text{Neolithic to Historic East Asians}, \text{Mbuti})$ showed the additional shared derived alleles from source populations except for inland Neolithic northern East Asian from Shaanxi or Inner Mongolia or their related ancestral populations.

Here, overlapping SNP loci included in the Affymetrix Human Origins platform among four analyzed populations were used. We used the genetic variation of Mbuti as the outgroup. Red asterisk point meant the significant value (Absolute value of Z-scores larger than three or equal to three) observed in the symmetry- f_4 statistics and green circle point denoted the non-significant f_4 -statistic values (Absolute value of Z-scores less than three). All ancient East Asians were listed along the Y-axis and f_4 values were labeled along the X-axis. All results were faceted or grouped via Tibetan populations. Significant

negative f_4 values indicated that the third population shared more alleles with the second population, and also means Tibetan obtained additional gene flow from the third source population (or related populations). And the significant positive f_4 value indicated that the third population shared more derived alleles with the first population. The value of f_4 -statistics equal to zero was marked as the blue dash line. The bar indicated three standard errors.

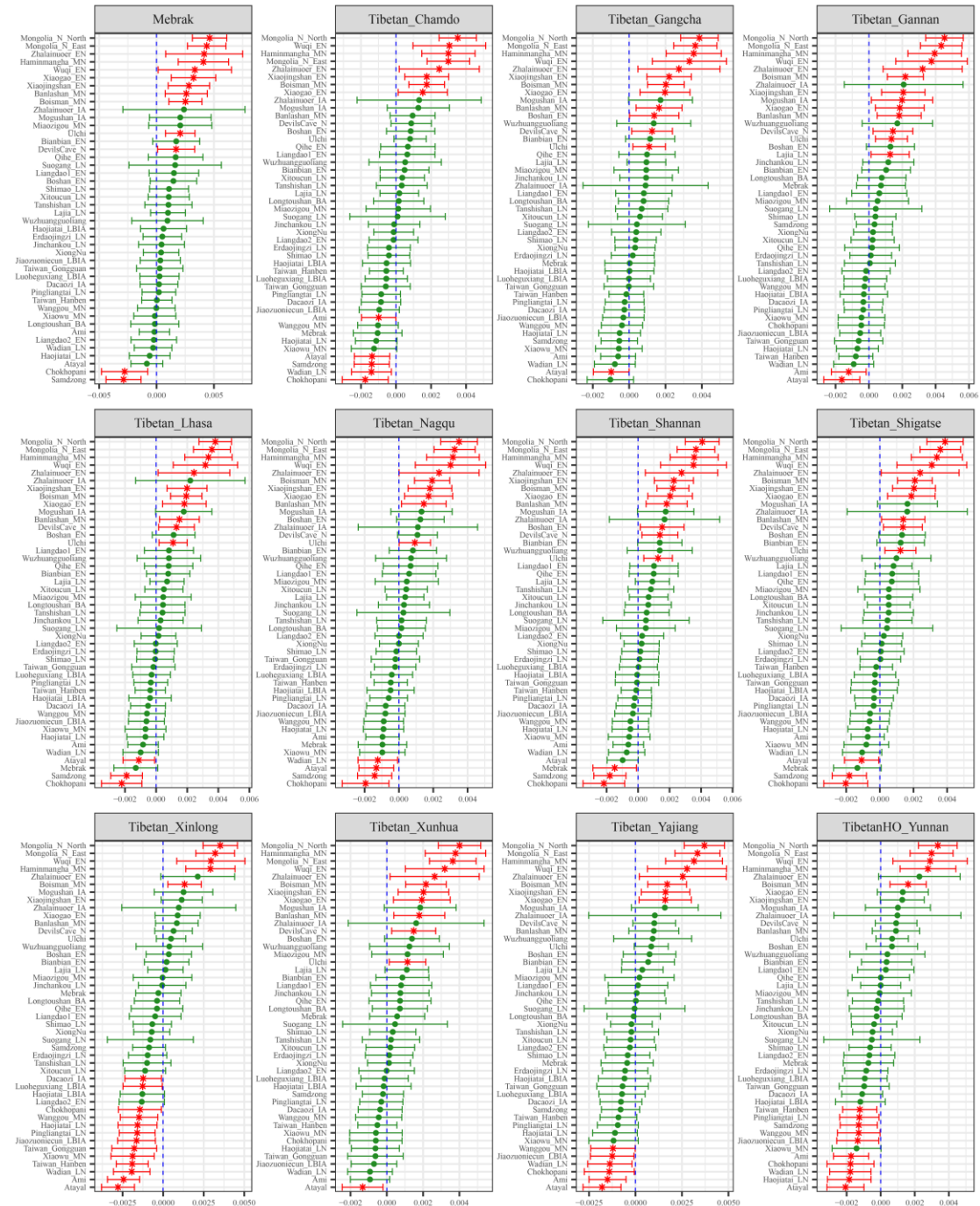


Figure S75. Results of affinity- f_4 statistics for the form $f_4(\text{Yumin_EN}, \text{Modern Tibetan}; \text{Neolithic to Historic East Asians}, \text{Mbuti})$ showed the additional shared derived alleles from source populations except for inland Neolithic northern East Asian from Shaanxi or Inner Mongolia or their related ancestral populations.

Here, overlapping SNP loci included in the Affymetrix Human Origins platform among four analyzed populations were used. We used the genetic variation of Mbuti as the outgroup. Red asterisk point meant the significant value (Absolute value of Z-scores larger than three or equal to three) observed in the symmetry- f_4 statistics and green circle point denoted the non-significant f_4 -statistic values (Absolute value of Z-scores less than three). All ancient East Asians were listed along the Y-axis and f_4 values were

labeled along the X-axis. All results were faceted or grouped via Tibetan populations. Significant negative f_4 values indicated that the third population shared more alleles with the second population, and also means Tibetan obtained additional gene flow from the third source population (or related populations). And the significant positive f_4 value indicated that the third population shared more derived alleles with the first population. The value of f_4 -statistics equal to zero was marked as the blue dash line. The bar indicated three standard errors.

Additional gene flow events when we assumed that Tibetans' direct ancestor is inland Neolithic to Iron Age northern East Asian from upper Yellow River Basin or their related ancestral populations

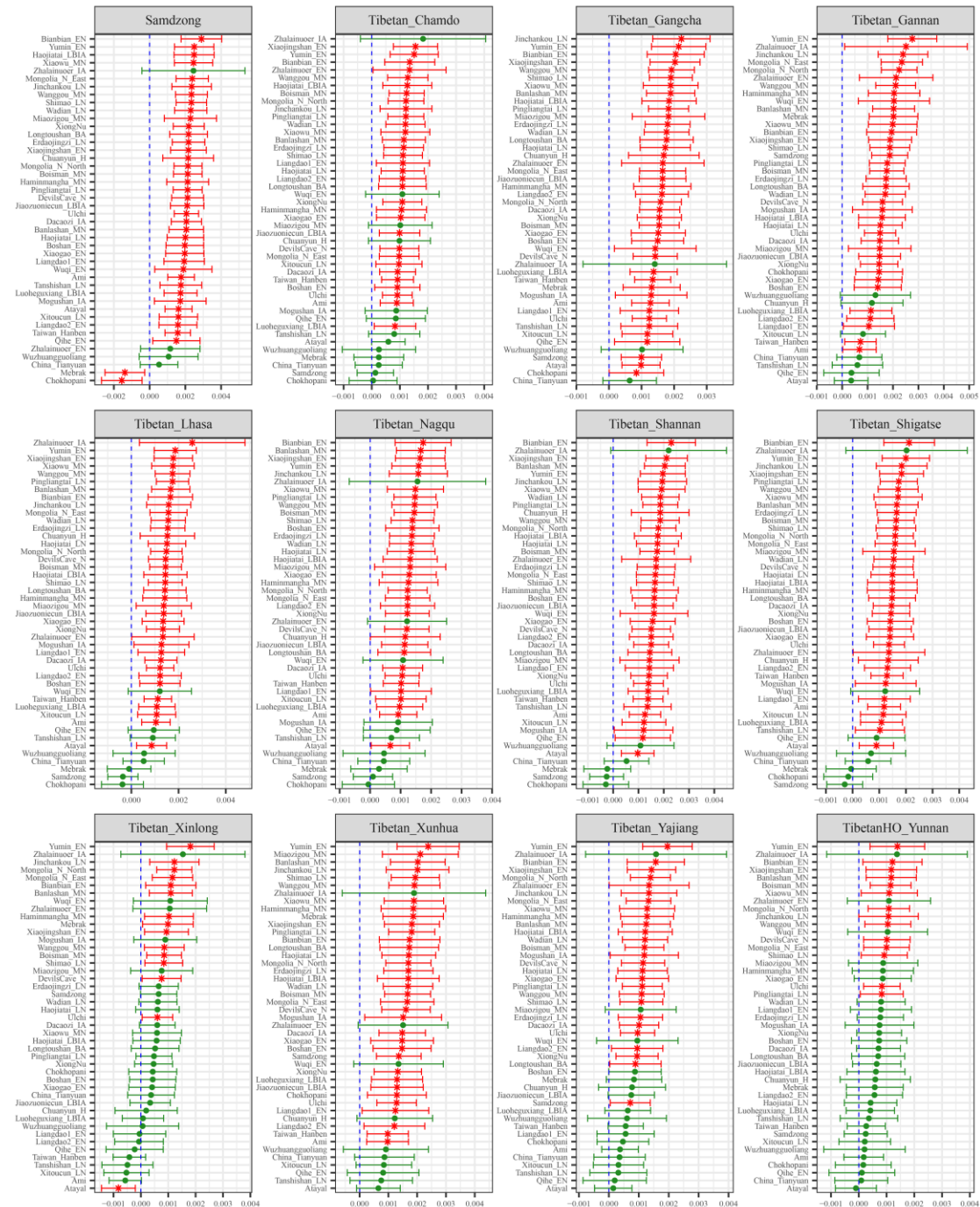


Figure S76. Results of affinity- f_4 statistics for the form $f_4(\text{Lajia_LN}, \text{Modern Tibetan}; \text{Neolithic to Historic East Asians}, \text{Mbuti})$ showed the additional shared derived alleles from source populations except for inland Neolithic northern East Asian from Shaanxi or Inner Mongolia or their related ancestral populations.

Here, overlapping SNP loci included in the Affymetrix Human Origins platform among four analyzed populations were used. We used the genetic variation of Mbuti as the outgroup. Red asterisk point meant the significant value (Absolute value of Z-scores larger than three or equal to three) observed in the symmetry- f_4 statistics and green circle point denoted the non-significant f_4 -statistic values (Absolute value of Z-scores less than three). All ancient East Asians were listed along the Y-axis and f_4 values were labeled along the X-axis. All results were faceted or grouped via Tibetan populations. Significant negative f_4 values indicated that the third population shared more alleles with the second population, and also means Tibetan obtained additional gene flow from the third source population (or related

populations). And the significant positive f_4 value indicated that the third population shared more derived alleles with the first population. The value of f_4 -statistics equal to zero was marked as the blue dash line. The bar indicated three standard errors.

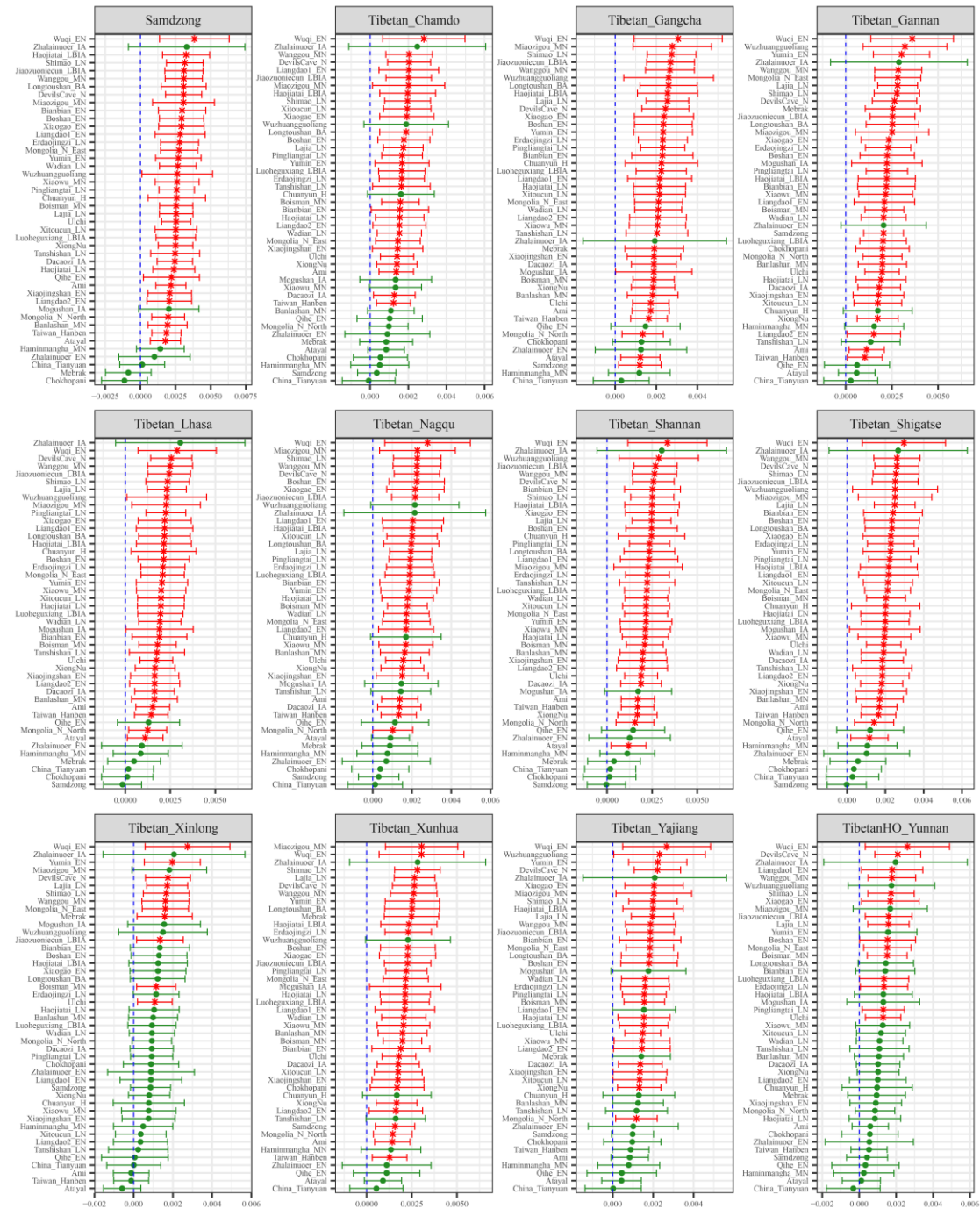


Figure S77. Results of affinity- f_4 statistics for the form $f_4(\text{Jinchankou LN, Modern Tibetan; Neolithic to Historic East Asians, Mbuti})$ showed the additional shared derived alleles from source populations except for inland Neolithic northern East Asian from Shaanxi or Inner Mongolia or their related ancestral populations.

Here, overlapping SNP loci included in the Affymetrix Human Origins platform among four analyzed populations were used. We used the genetic variation of Mbuti as the outgroup. Red asterisk point meant the significant value (Absolute value of Z-scores larger than three or equal to three) observed in the symmetry- f_4 statistics and green circle point denoted the non-significant f_4 -statistic values (Absolute value of Z-scores less than three). All ancient East Asians were listed along the Y-axis and f_4 values were labeled along the X-axis. All results were faceted or grouped via Tibetan populations. Significant negative f_4 values indicated that the third population shared more alleles with the second population, and also means Tibetan obtained additional gene flow from the third source population (or related

Here, overlapping SNP loci included in the Affymetrix Human Origins platform among four analyzed populations were used. We used the genetic variation of Mbuti as the outgroup. Red asterisk point meant the significant value (Absolute value of Z-scores larger than three or equal to three) observed in the symmetry- f_4 statistics and green circle point denoted the non-significant f_4 -statistic values (Absolute value of Z-scores less than three). All ancient East Asians were listed along the Y-axis and f_4 values were labeled along the X-axis. All results were faceted or grouped via Tibetan populations. Significant negative f_4 values indicated that the third population shared more alleles with the second population, and

also means Tibetan obtained additional gene flow from the third source population (or related populations). And the significant positive f_4 value indicated that the third population shared more derived alleles with the first population. The value of f_4 -statistics equal to zero was marked as the blue dash line. The bar indicated three standard errors.

Additional gene flow events when we assumed that Tibetans' direct ancestor is Liao River ancients or their related ancestral populations

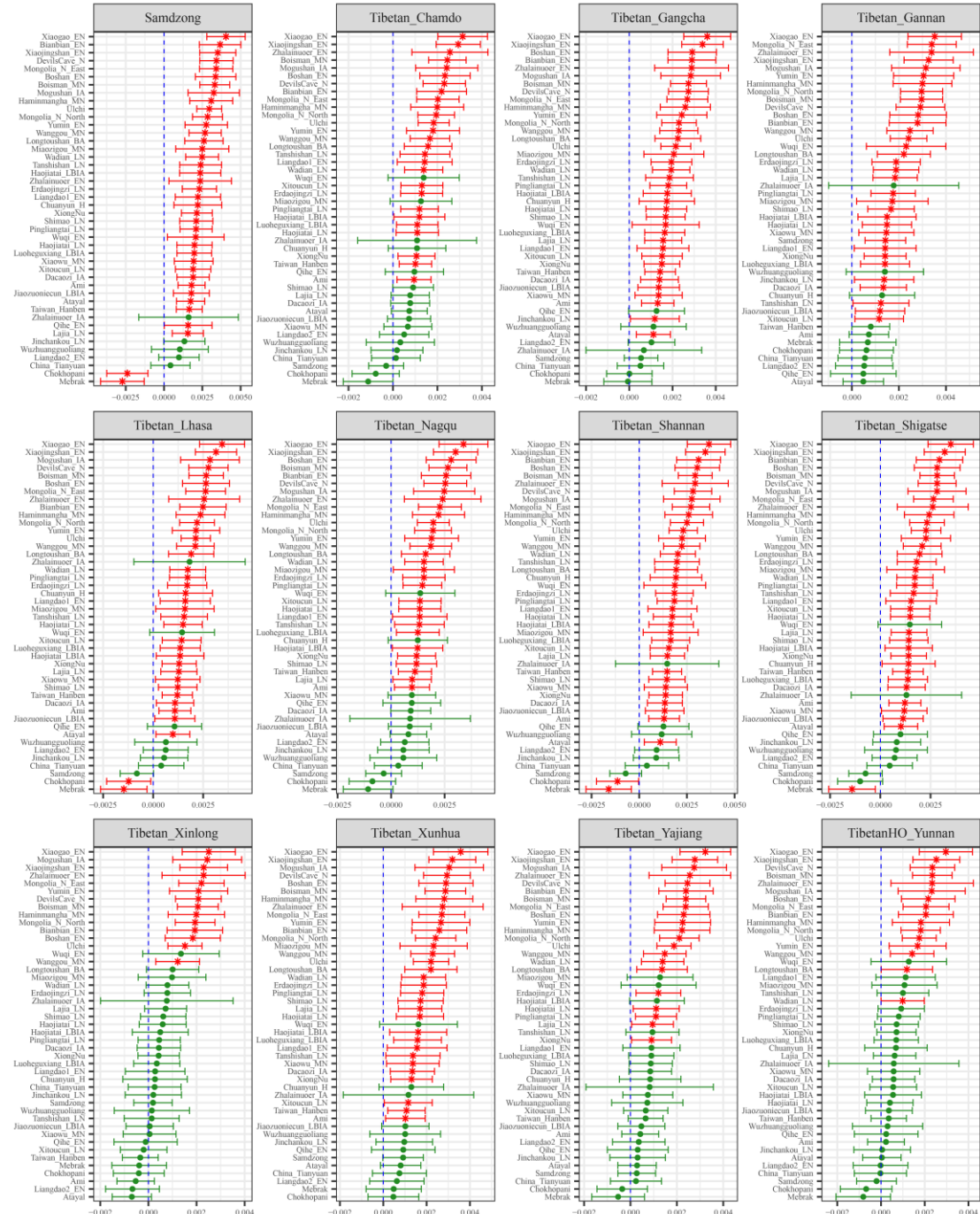


Figure S79. Results of affinity- f_4 statistics for the form $f_4(\text{Banhashan_MN}, \text{Modern Tibetan}; \text{Neolithic to Historic East Asians}, \text{Mbuti})$ showed the additional shared derived alleles from source populations except for ancestral populations from Liao River Basin.

Here, overlapping SNP loci included in the Affymetrix Human Origins platform among four analyzed populations were used. We used the genetic variation of Mbuti as the outgroup. Red asterisk point meant the significant value (Absolute value of Z-scores larger than three or equal to three) observed in the symmetry- f_4 statistics and green circle point denoted the non-significant f_4 -statistic values (Absolute

value of Z-scores less than three). All ancient East Asians were listed along the Y-axis and f_4 values were labeled along the X-axis. All results were faceted or grouped via Tibetan populations. Significant negative f_4 values indicated that the third population shared more alleles with the second population, and also means Tibetan obtained additional gene flow from the third source population (or related populations). And the significant positive f_4 value indicated that the third population shared more derived alleles with the first population. The value of f_4 -statistics equal to zero was marked as the blue dash line. The bar indicated three standard errors.

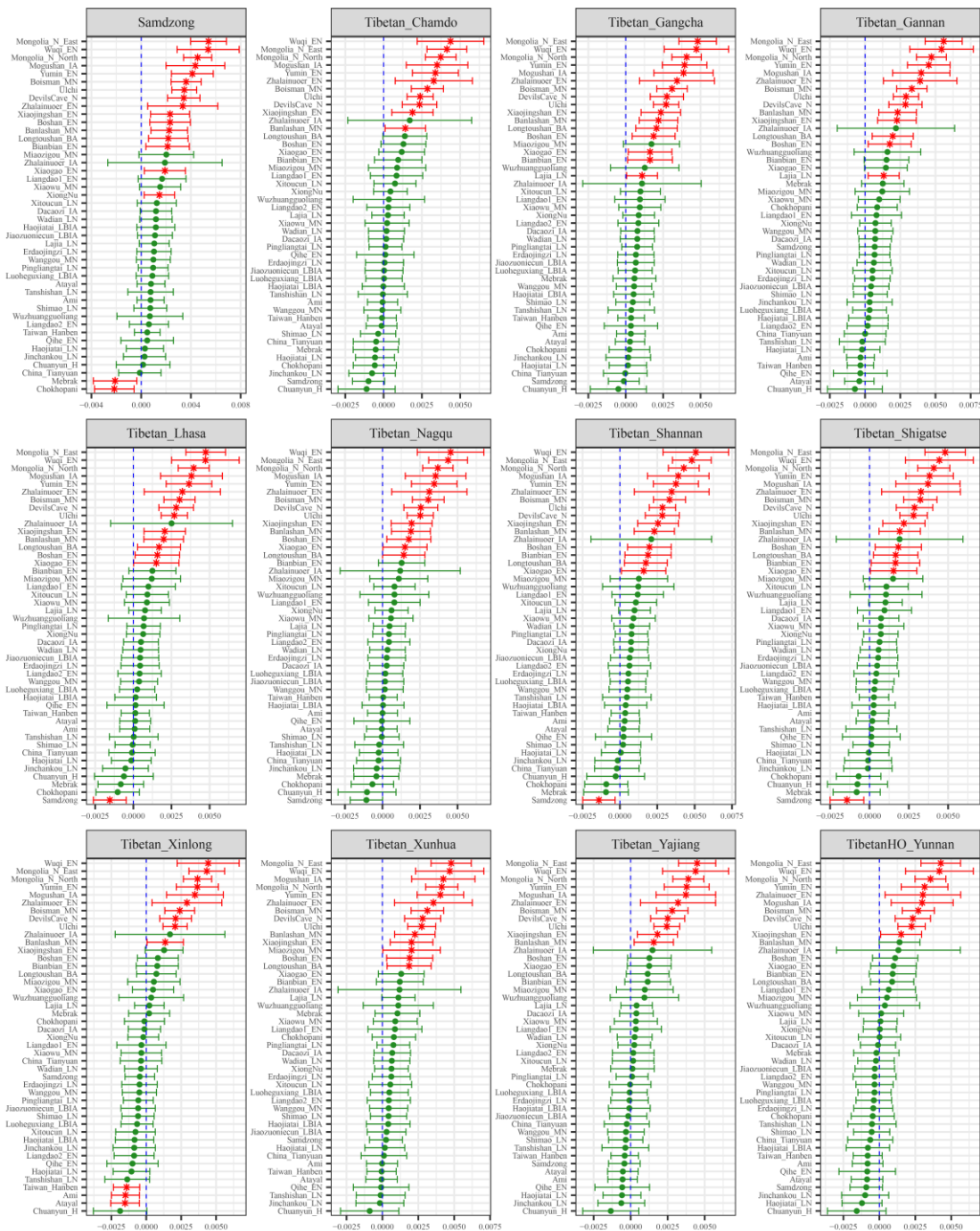


Figure S80. Results of affinity- f_4 statistics for the form $f_4(\text{Haminmangha_MN}, \text{Modern Tibetan}; \text{Neolithic to Historic East Asians}, \text{Mbuti})$ showed the additional shared derived alleles from source populations except for ancestral populations from Liao River Basin.

Here, overlapping SNP loci included in the Affymetrix Human Origins platform among four analyzed populations were used. We used the genetic variation of Mbuti as the outgroup. Red asterisk point meant the significant value (Absolute value of Z-scores larger than three or equal to three) observed in the symmetry- f_4 statistics and green circle point denoted the non-significant f_4 -statistic values (Absolute

value of Z-scores less than three). All ancient East Asians were listed along the Y-axis and f_4 values were labeled along the X-axis. All results were faceted or grouped via Tibetan populations. Significant negative f_4 values indicated that the third population shared more alleles with the second population, and also means Tibetan obtained additional gene flow from the third source population (or related populations). And the significant positive f_4 value indicated that the third population shared more derived alleles with the first population. The value of f_4 -statistics equal to zero was marked as the blue dash line. The bar indicated three standard errors.