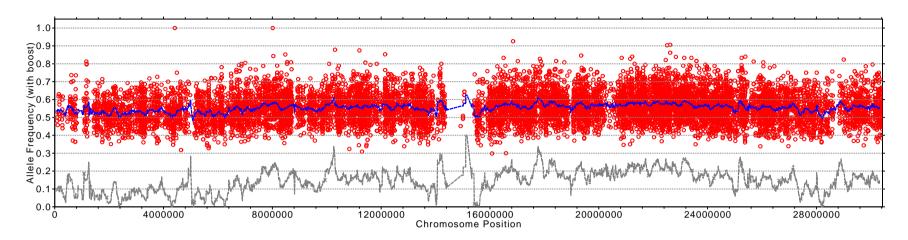
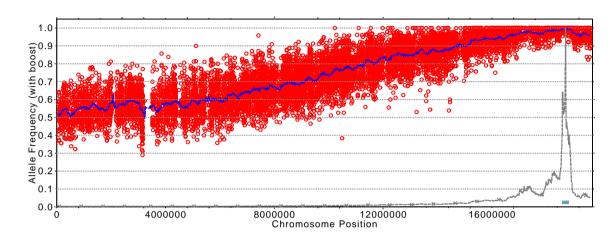
## Chromosome 1: 30427671bp



\*Parameter settings:

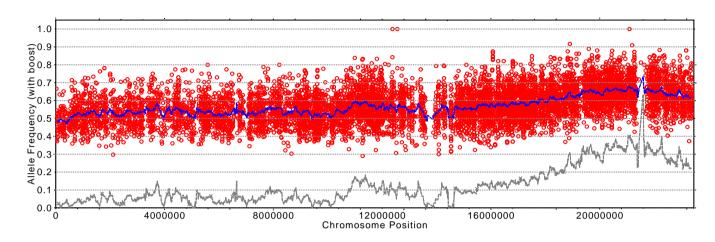
- \*Points in colors: AF (=alt divided by (alt+ref)) at markers. alt or ref: coverage of non-reference or reference allele
- \*Dashed line in blue: window-based AF (= summation-of-single-marker-AF divided by number-of-markers with min quality score involved).
- \*Dashed line in gray: window-based boost value

## Chromosome 2: 19698289bp



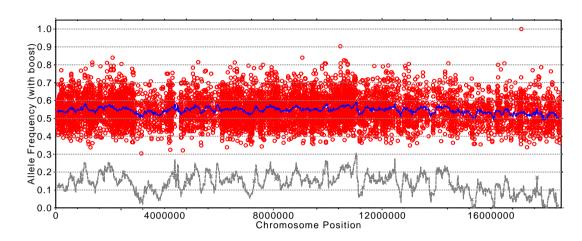
\*Parameter settings:

- \*Points in colors: AF (=alt divided by (alt+ref)) at markers. alt or ref: coverage of non-reference or reference allele
- \*Dashed line in blue: window-based AF (= summation-of-single-marker-AF divided by number-of-markers with min quality score involved).
- \*Dashed line in gray: window-based boost value
- \*Predicted mapping interval of size 215.00 Kbp (normal): 18595000 ~ 18809999



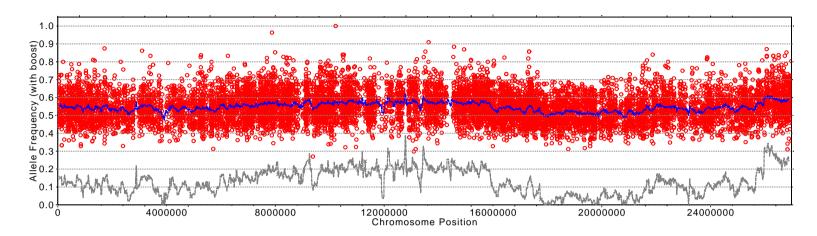
\*Parameter settings:

- \*Points in colors: AF (=alt divided by (alt+ref)) at markers. alt or ref: coverage of non-reference or reference allele
- \*Dashed line in blue: window-based AF (= summation-of-single-marker-AF divided by number-of-markers with min quality score involved).
- \*Dashed line in gray: window-based boost value



\*Parameter settings:

- \*Points in colors: AF (=alt divided by (alt+ref)) at markers. alt or ref: coverage of non-reference or reference allele
- \*Dashed line in blue: window-based AF (= summation-of-single-marker-AF divided by number-of-markers with min quality score involved).
- \*Dashed line in gray: window-based boost value



\*Parameter settings:

- \*Points in colors: AF (=alt divided by (alt+ref)) at markers. alt or ref: coverage of non-reference or reference allele
- \*Dashed line in blue: window-based AF (= summation-of-single-marker-AF divided by number-of-markers with min quality score involved).
- \*Dashed line in gray: window-based boost value