

MLE for Individual Ancestries

Population Covariances and Selection

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Selection Study

$$\ln [P_1 (Q, F)] = \sum_i^I \sum_j^J \left\{ g_{ij} \cdot \ln \left[\sum_k^K q_{ik} \cdot f_{kj} \right] + (2 - g_{ij}) \cdot \ln \left[\sum_k^K q_{ik} \cdot (1 - f_{kj}) \right] \right\}$$

$$\ln [P_2 (F)]$$

$$= \ln \left\{ \prod_j^J \left[\frac{1}{\sqrt{|2\pi c_j \Omega'|}} \exp \left(-\frac{1}{2} \cdot f_j'^T \cdot (c_j \Omega')^{-1} \cdot f_j' \right) \right] \right\}$$

where $c_j = \mu_j (1 - \mu_j)$

$$f_j' = f_j - f_{j0}$$

SELECTION

Obtain the full genotype dataset G with N markers and M samples
Sample N' markers with respect to LD (N' > 100,000) to form G'

QPAS over $\ln(P_1)$ using G'

Produce admixture proportions Q' of size M by K

Produce allele frequencies F' of size K by N'

Nelder-Mead over $\ln(P_2)$ using F'

Produce variance covariance matrix Ω'

QPAS over $\ln(P_1)$ using G while fixing Q'

Produce allele frequencies F of size K by N

Repeat for each marker in F

Set l_{ratio} to zero

Repeat for each α in a range of an even interval starting from 1.0

Set l_{new} to $\ln(P_2)$ calculated for this marker using $\alpha \times \Omega'$

Set l_{old} to $\ln(P_2)$ calculated for this marker using Ω'

If $2 \times (l_{\text{new}} - l_{\text{old}})$ is greater than l_{ratio}

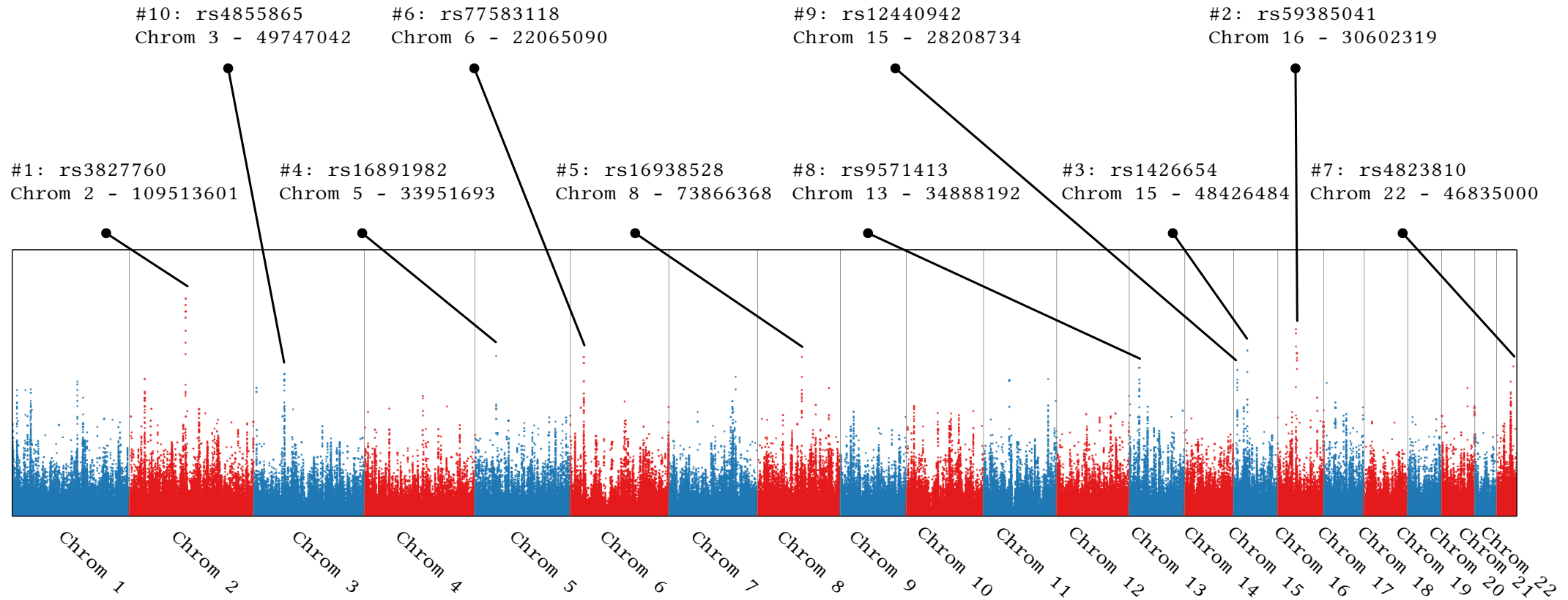
Set l_{ratio} to $2 \times (l_{\text{new}} - l_{\text{old}})$

End Repeat

Emit l_{ratio}

End Repeat

Selection Study



Covariance Scan: Australian, English, Han, and Yoruba

Selection Study

hair thickness
and curliness

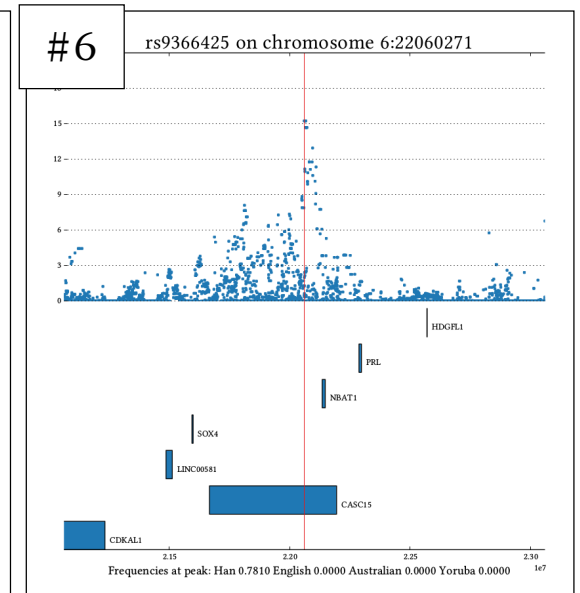
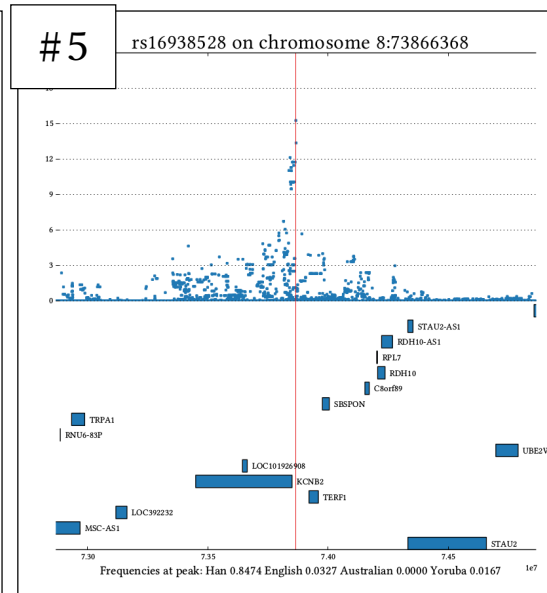
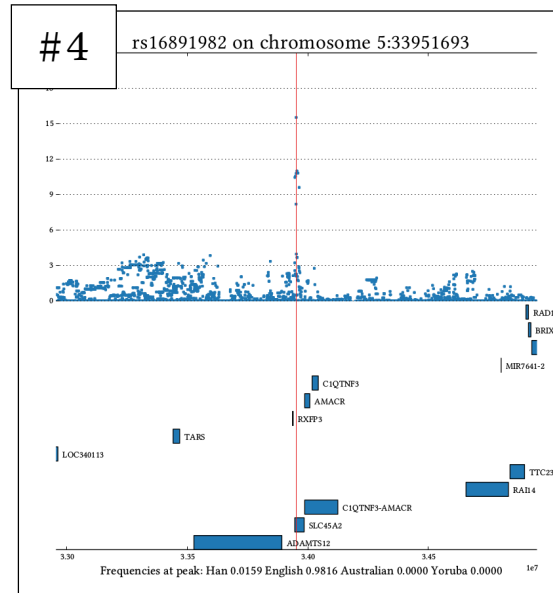
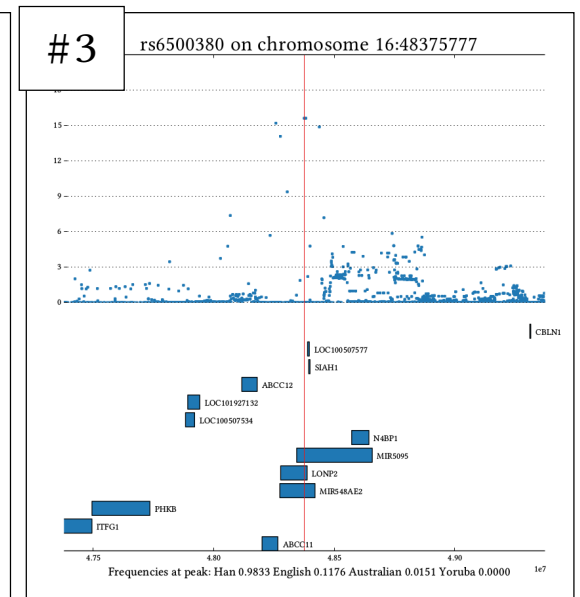
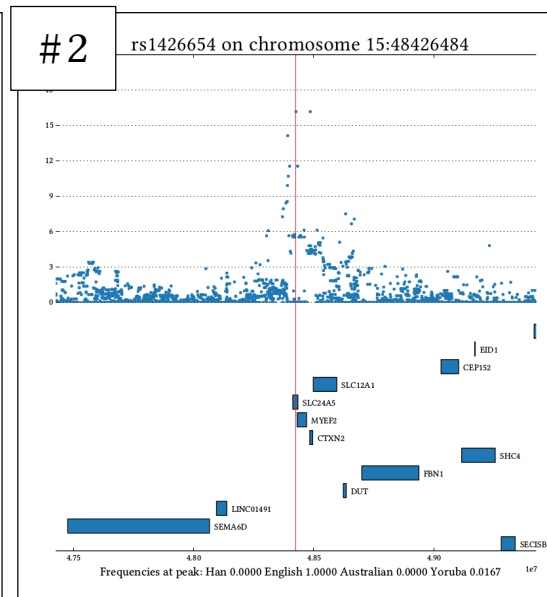
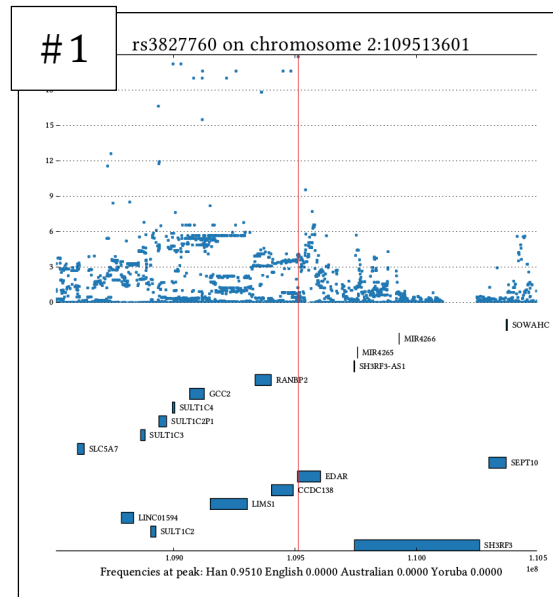
earwax moisture
underarm odor

skin
pigmentation

skin
pigmentation

‘maxDrinks’
alcohol
consumption
related

a melanoma
tumor repressor



Selection Study

neural tube
defect and
hair follicles

skin
pigmentation

Intergenic

Intergenic

insulin
dependent
regulation
of glucose

taste cells in
the mouth

