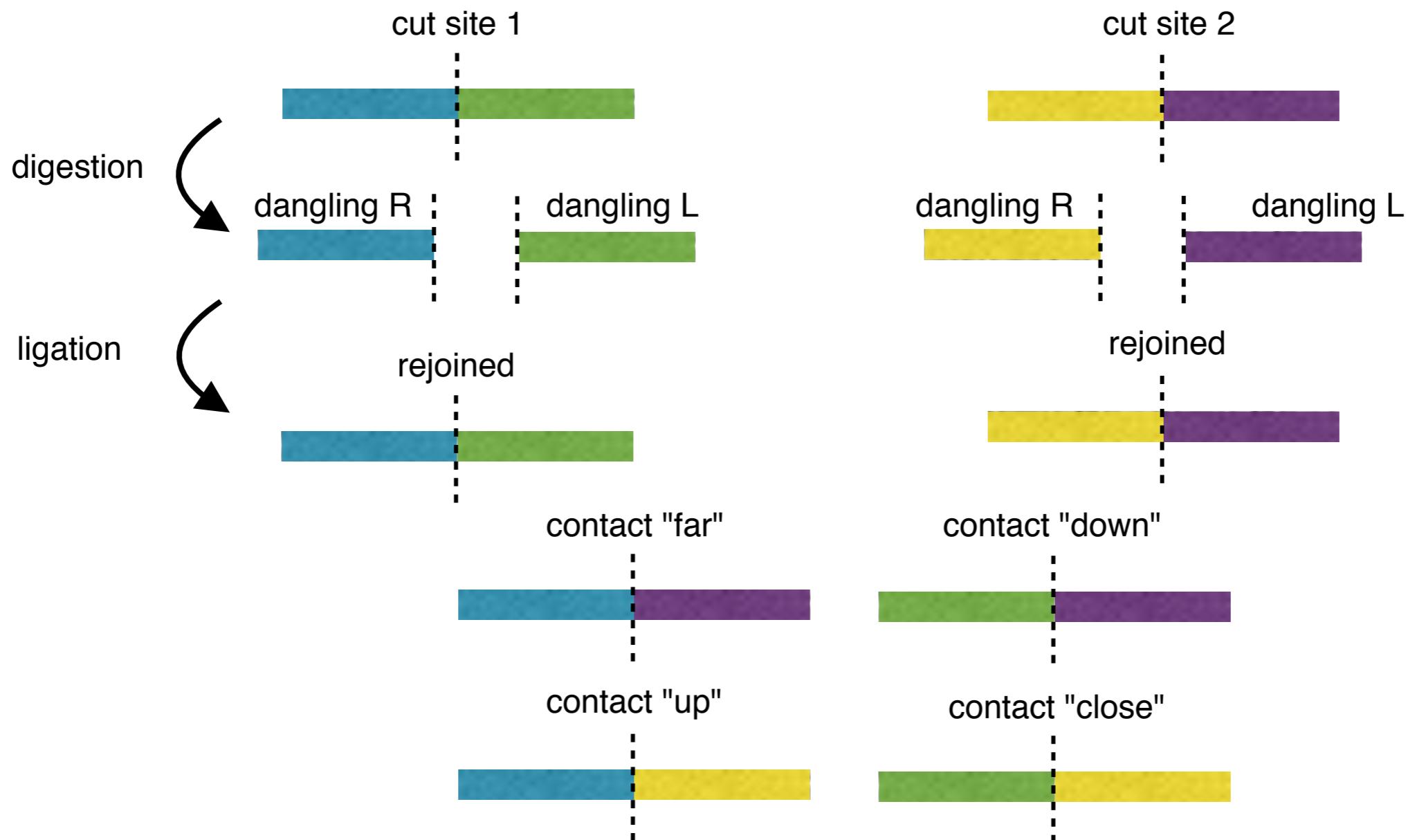


How do we normalize this?



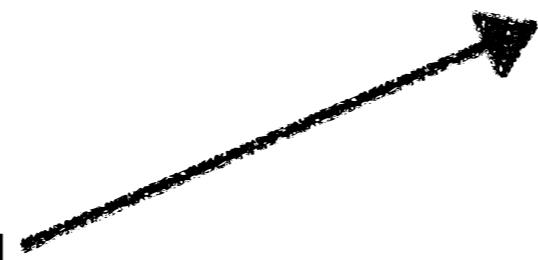
Cut-site normalization

$$c_{ij} \sim NB(e_C \iota_i \rho_j f_{ij}, \alpha)$$

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$$c_{ij} \sim NB(e_C \ell_i \rho_j f_{ij}, \alpha)$$

Sequencing
depth

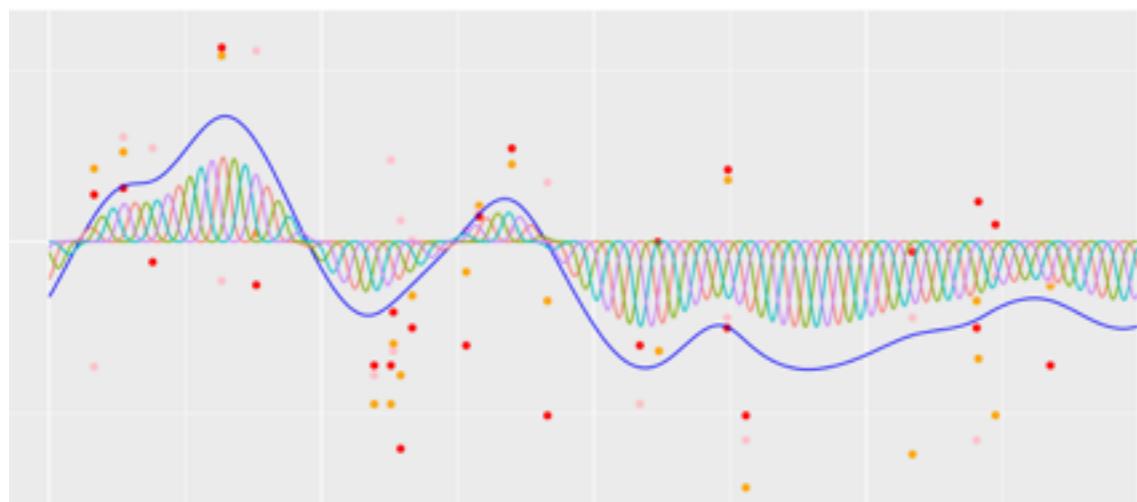


Cut-site normalization

$$c_{ij} \sim NB(e_C \ell_i \rho_j f_{ij}, \alpha)$$

Sequencing
depth

Genomic biases

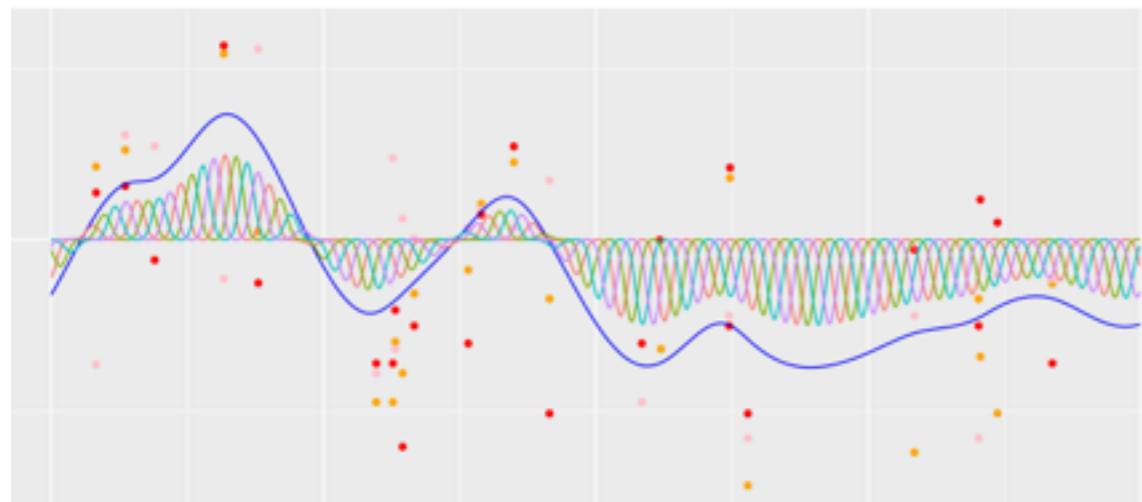


Cut-site normalization

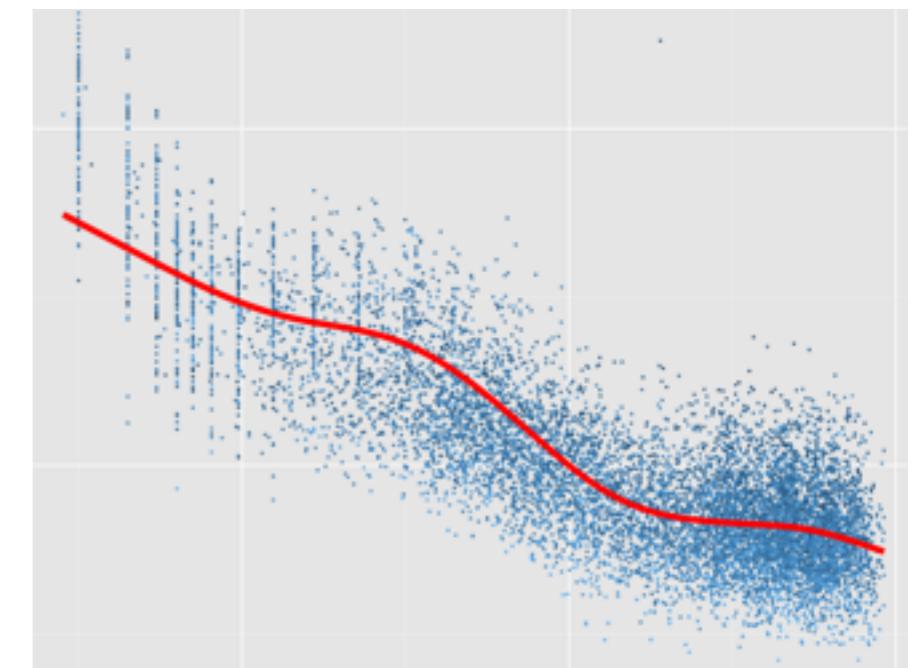
$$c_{ij} \sim NB(e_C \ell_i \rho_j f_{ij}, \alpha)$$

Sequencing
depth

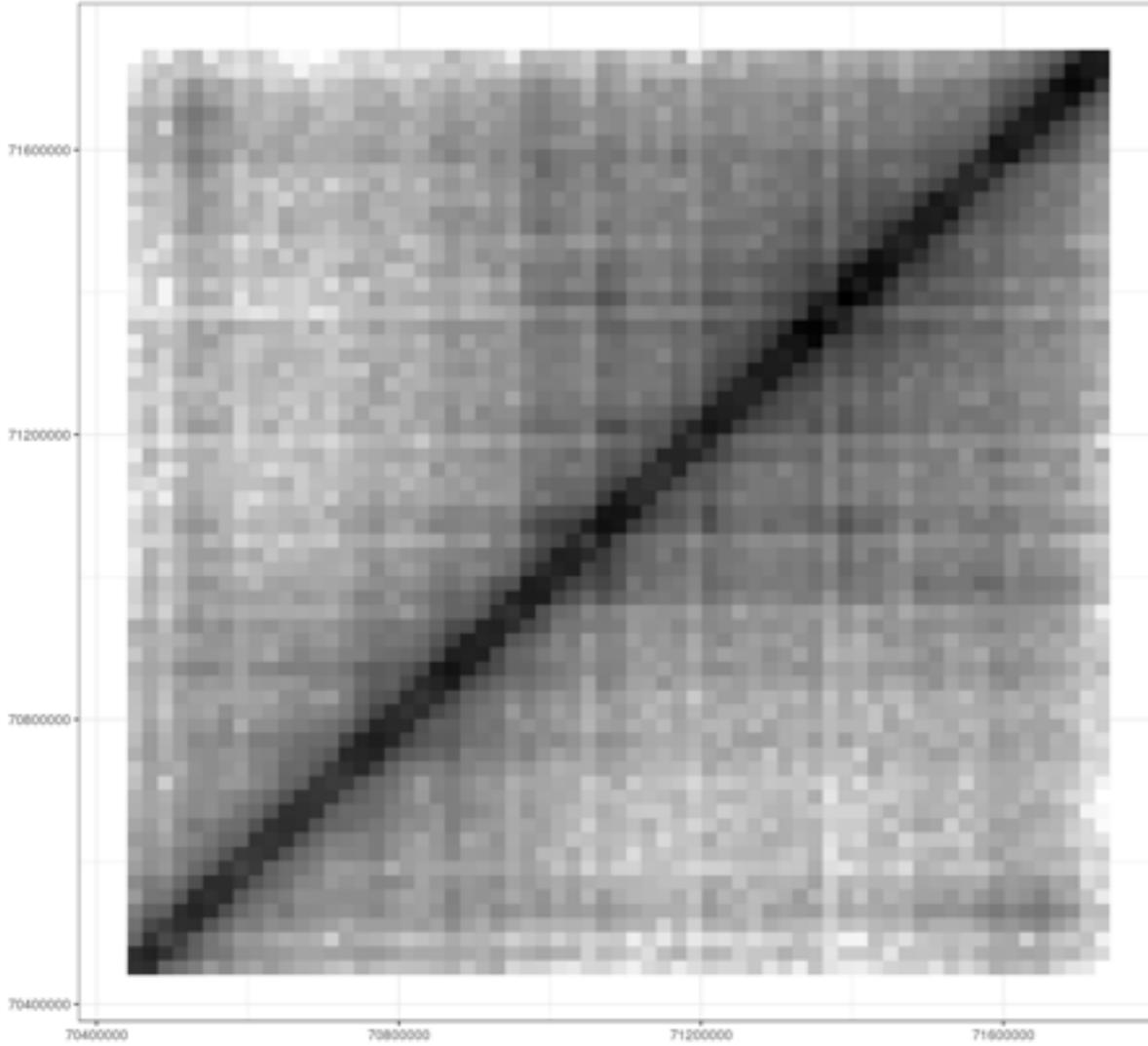
Genomic biases



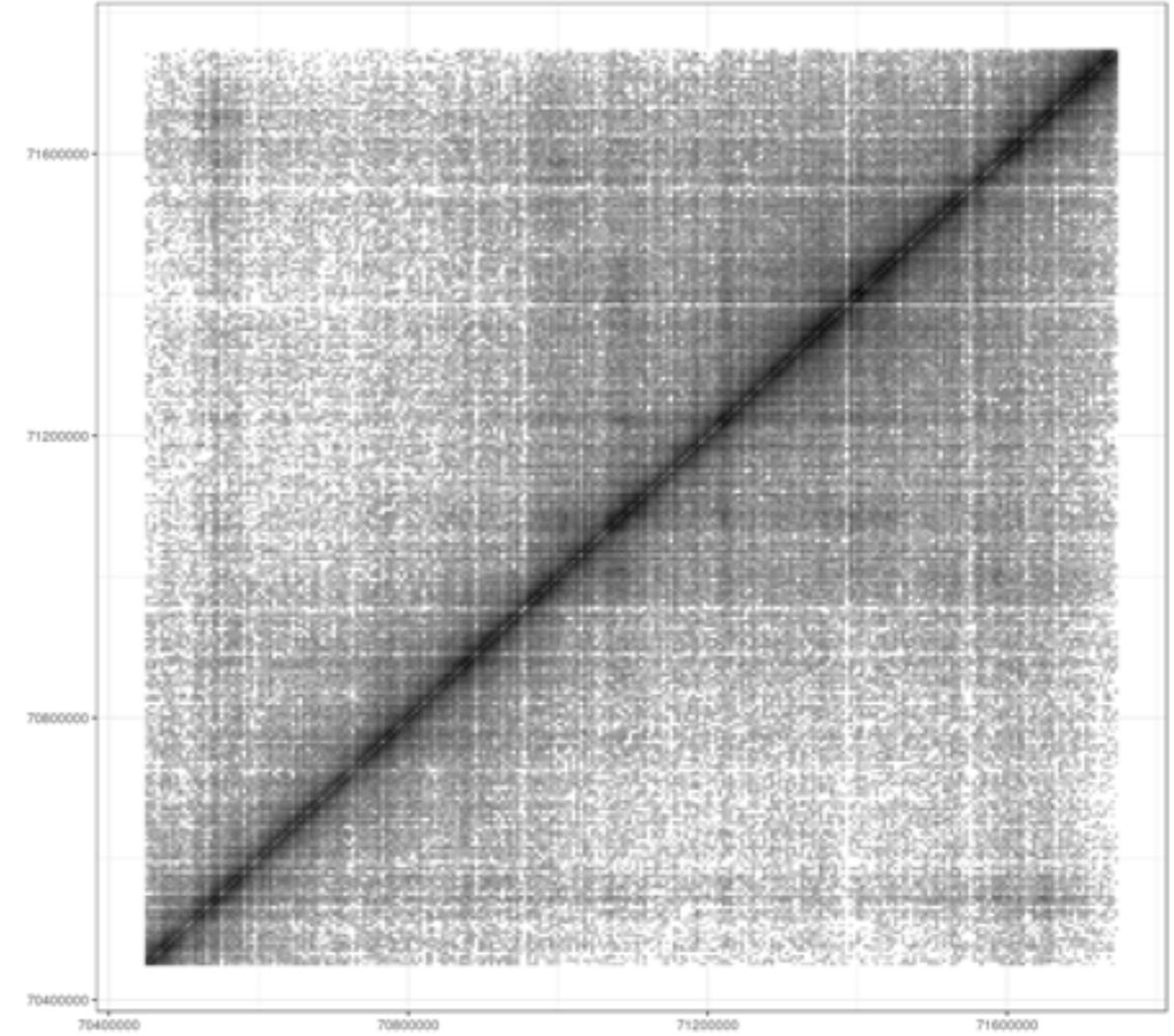
Distance decay



Observed

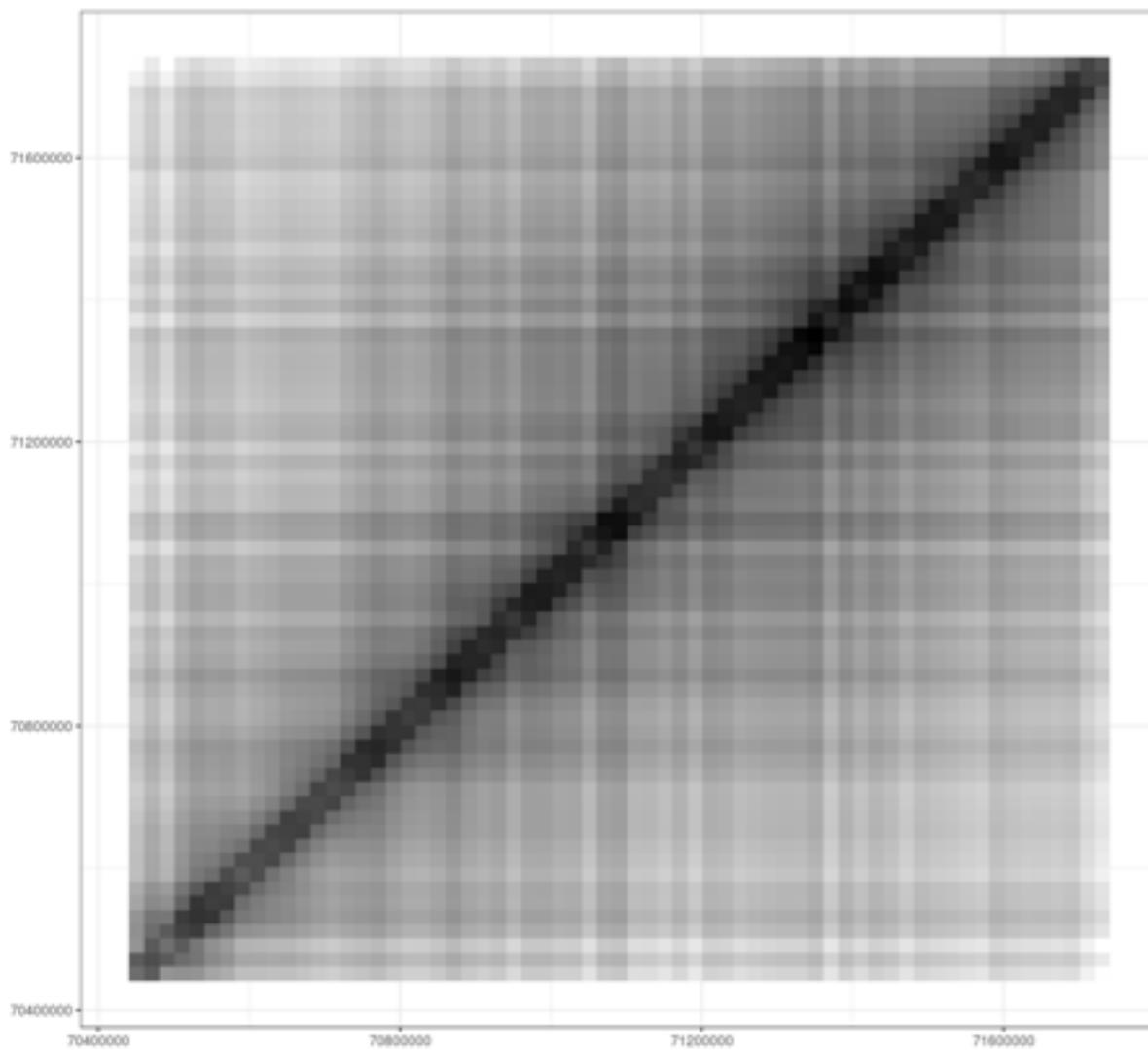


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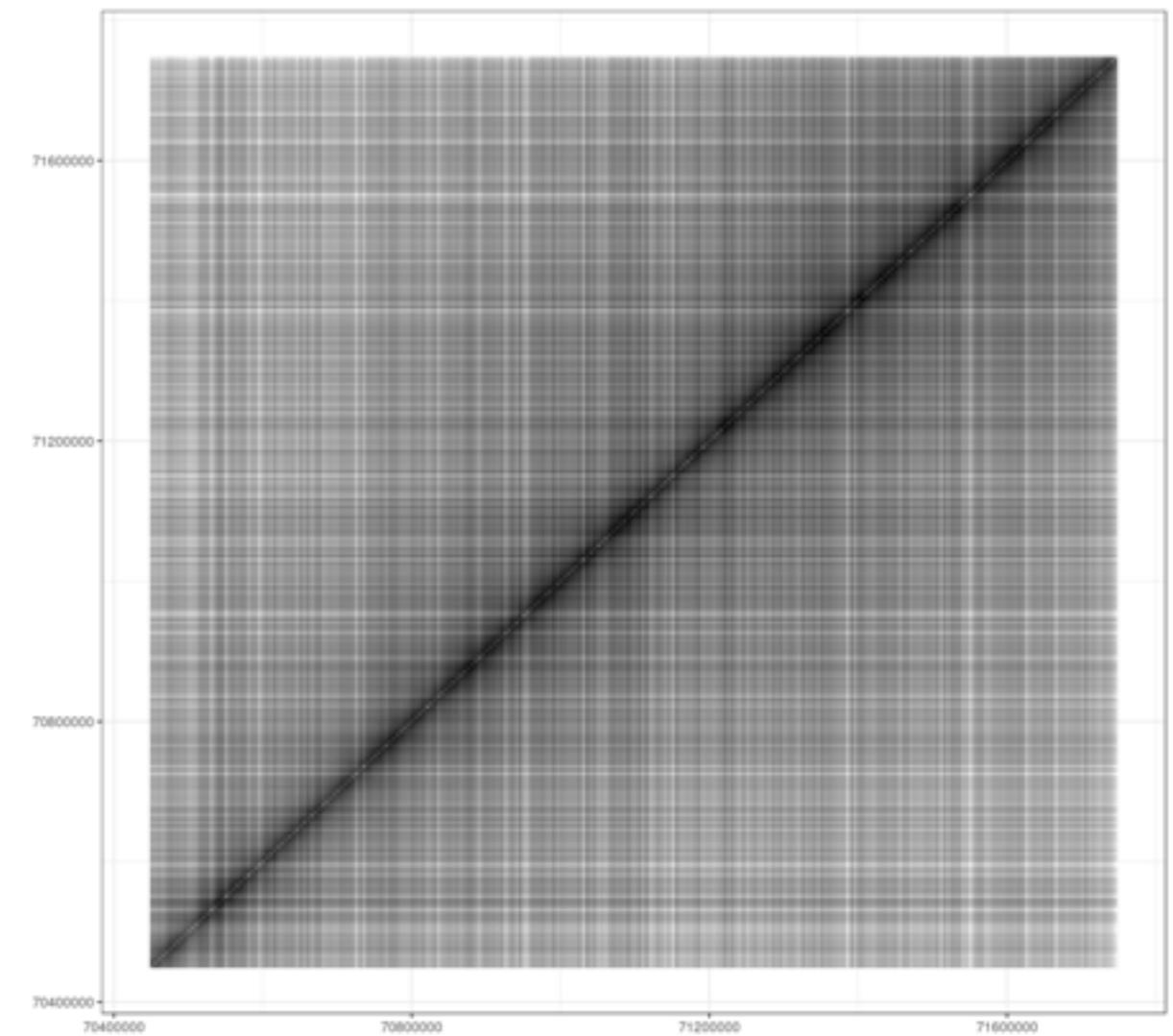


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Expected

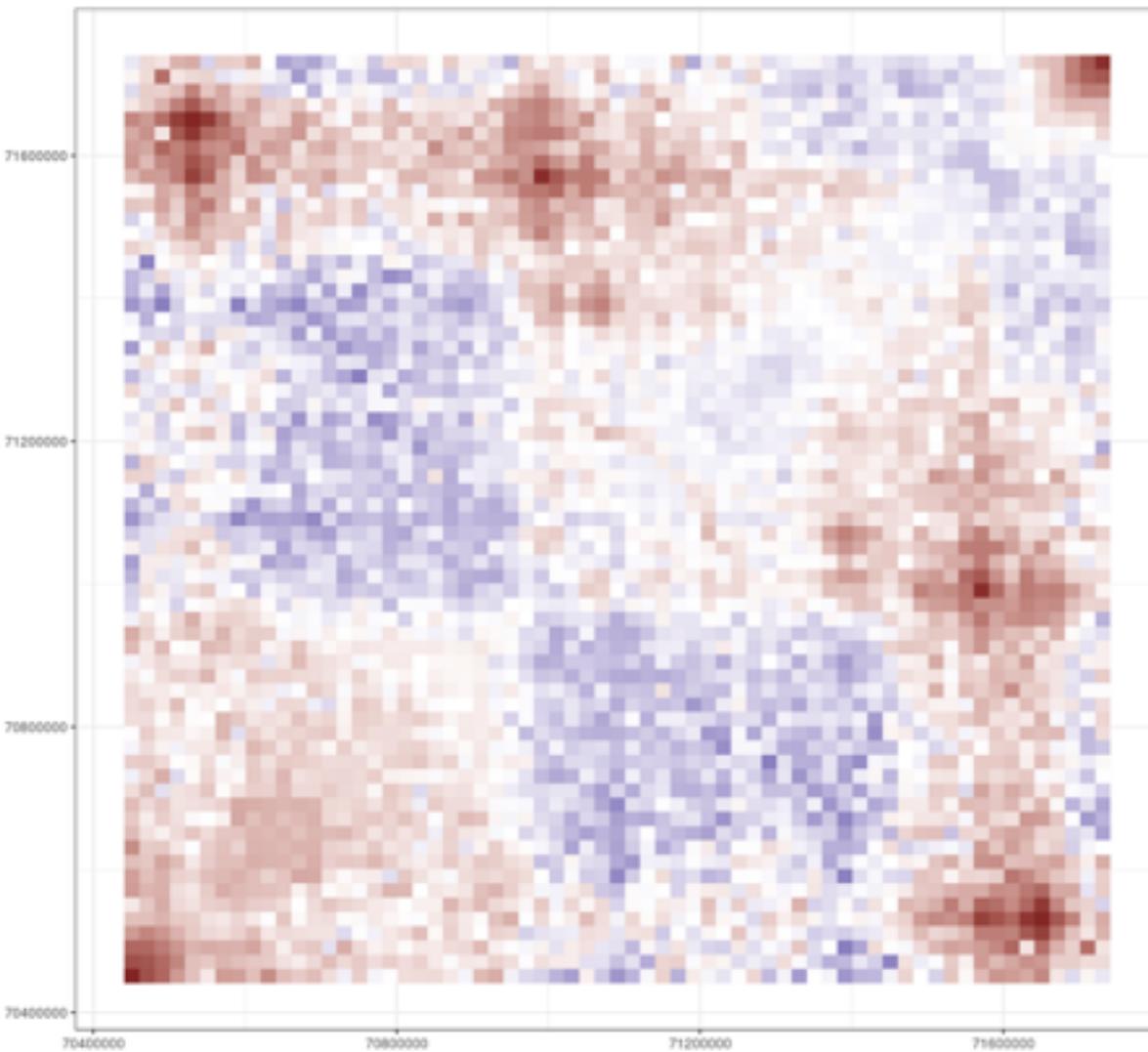


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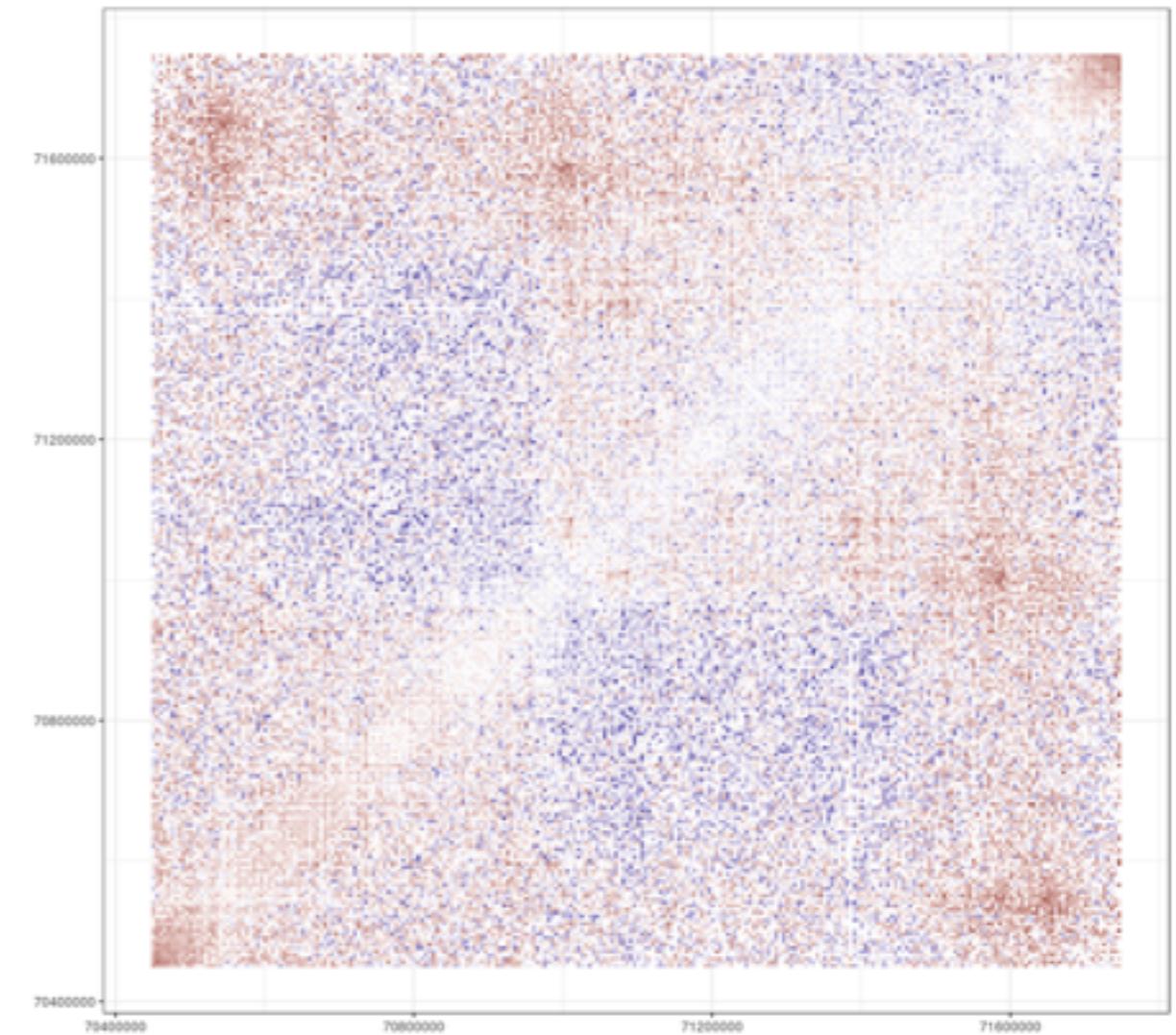
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Signal



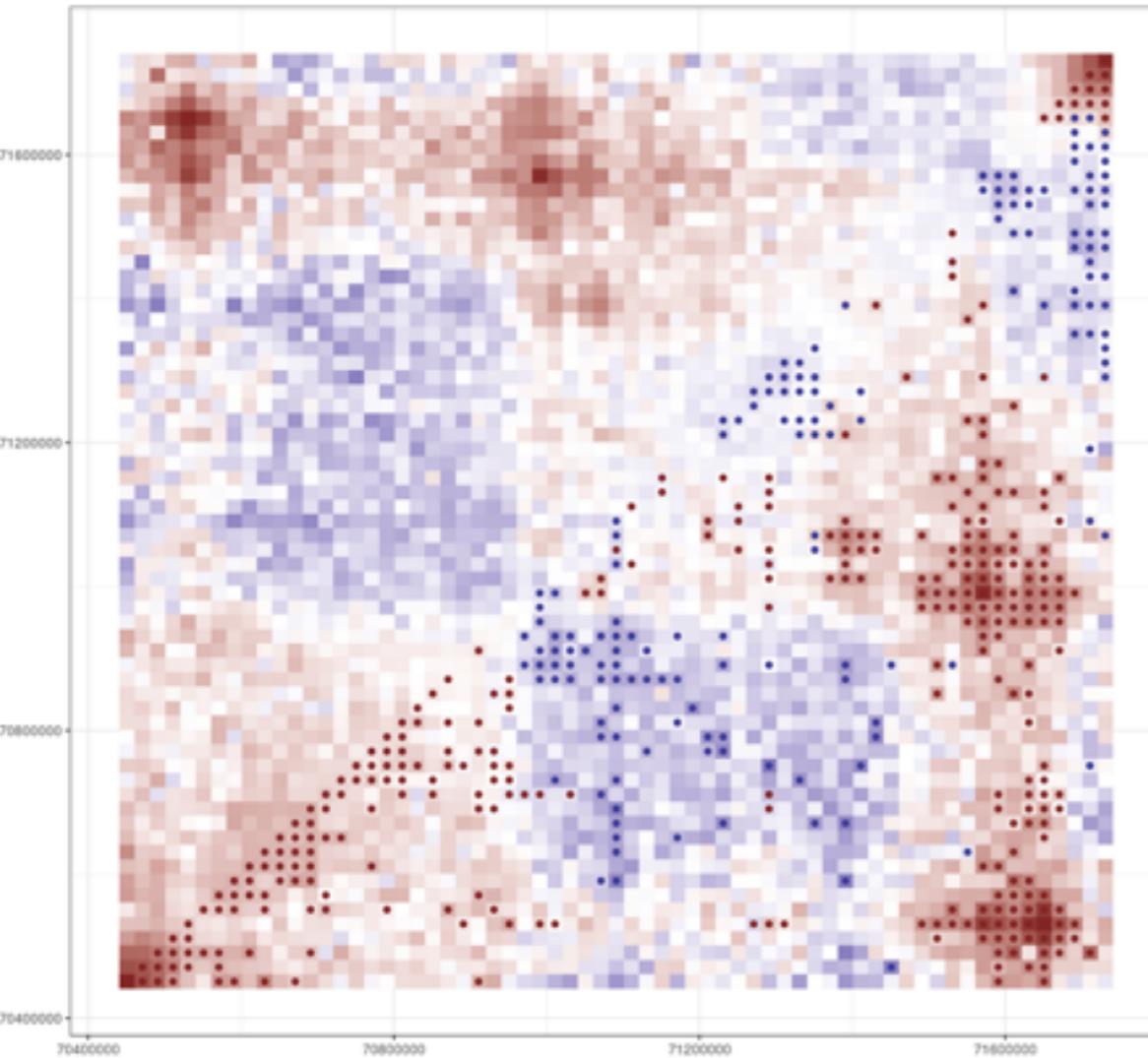
@20kb

Enriched
Depleted



@5kb

Interaction detection

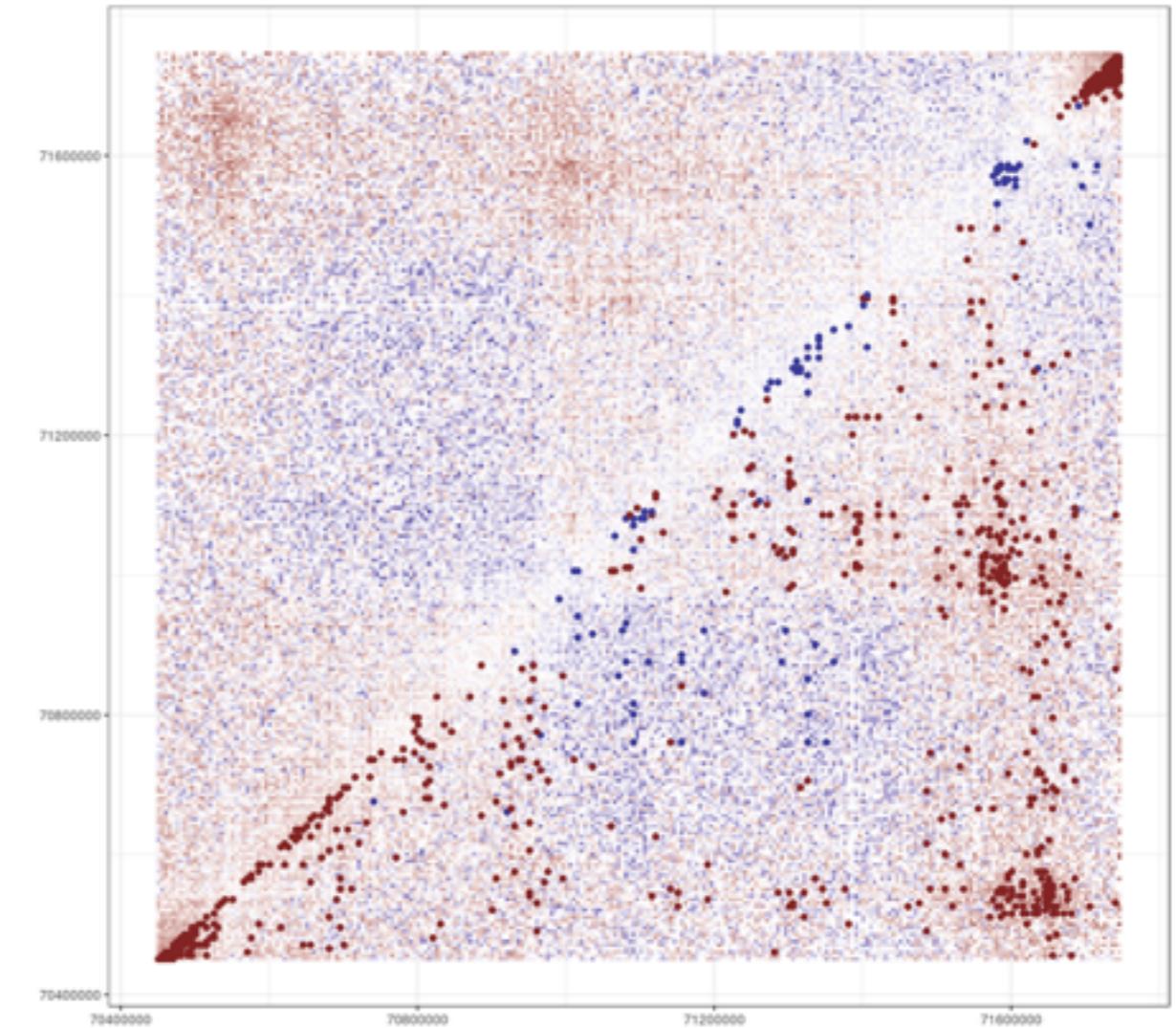


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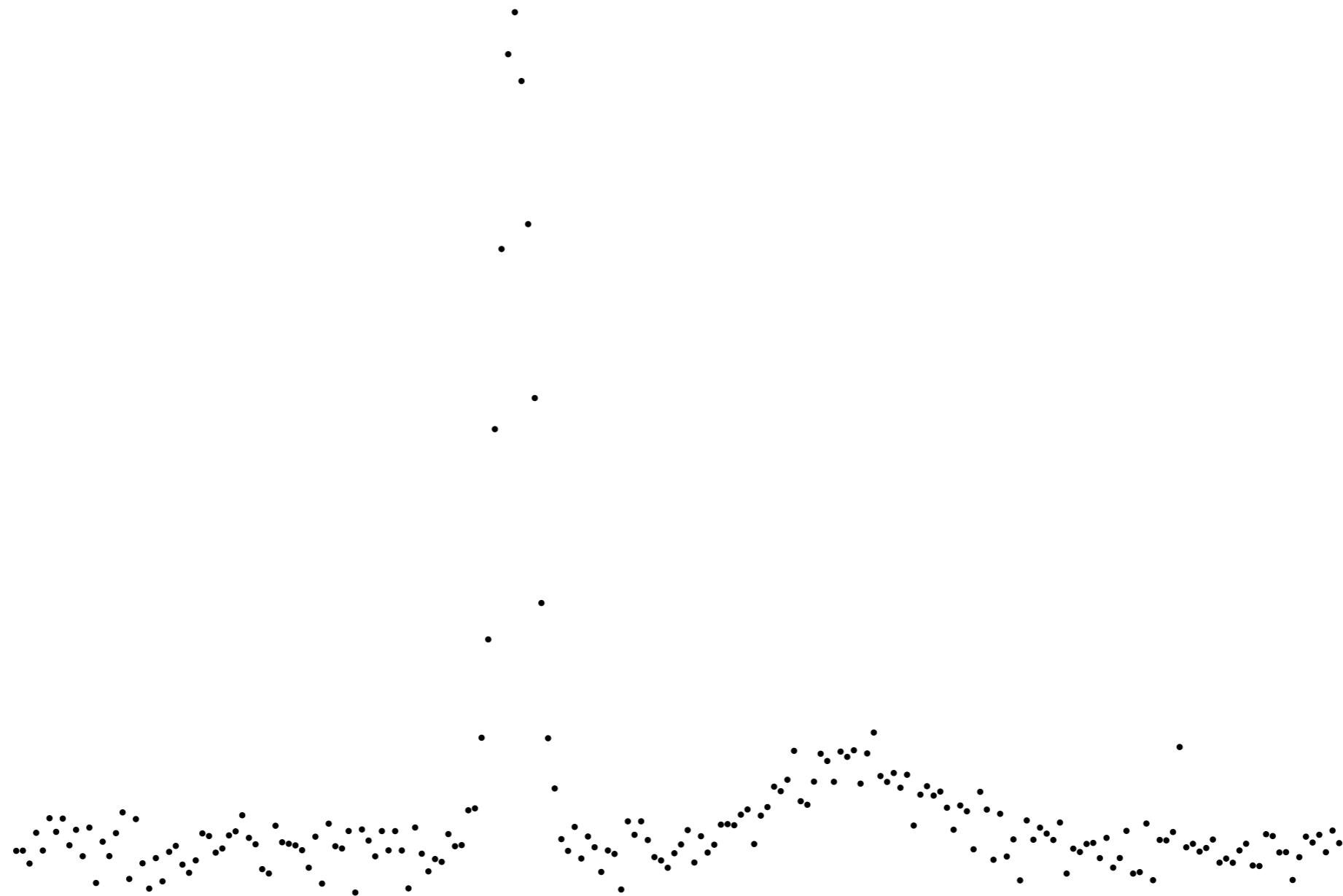
Enriched

Depleted

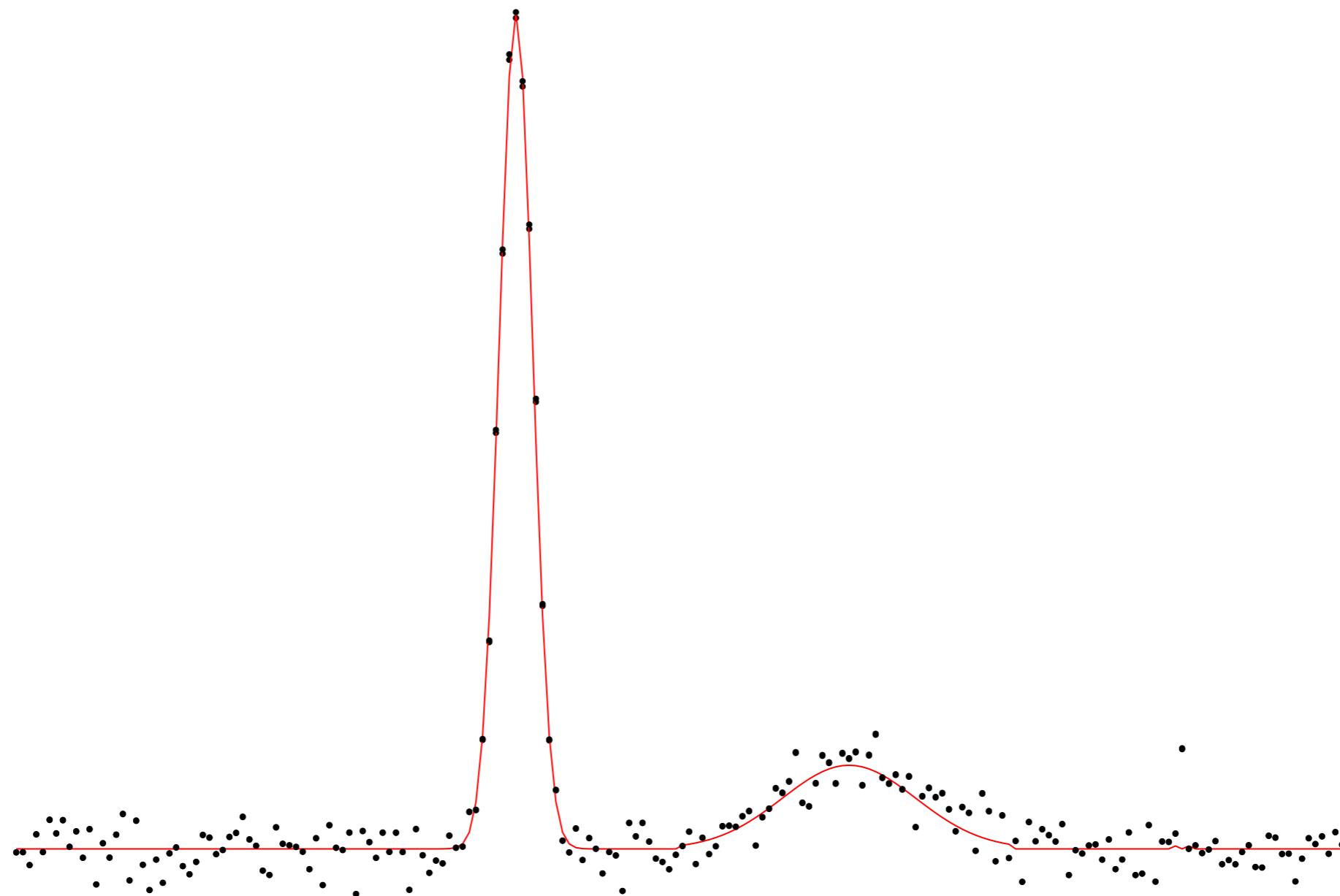
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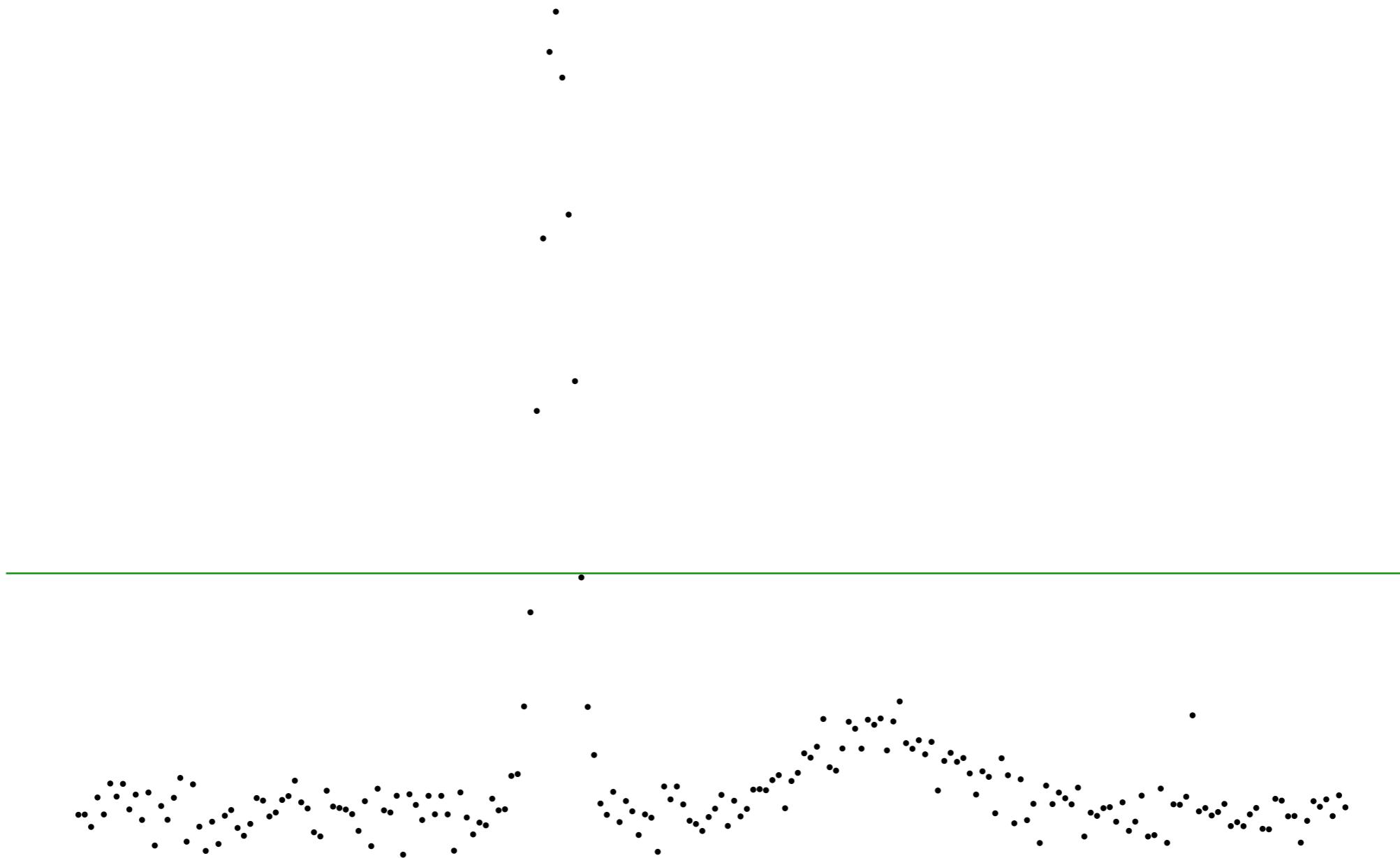
Where is the signal?



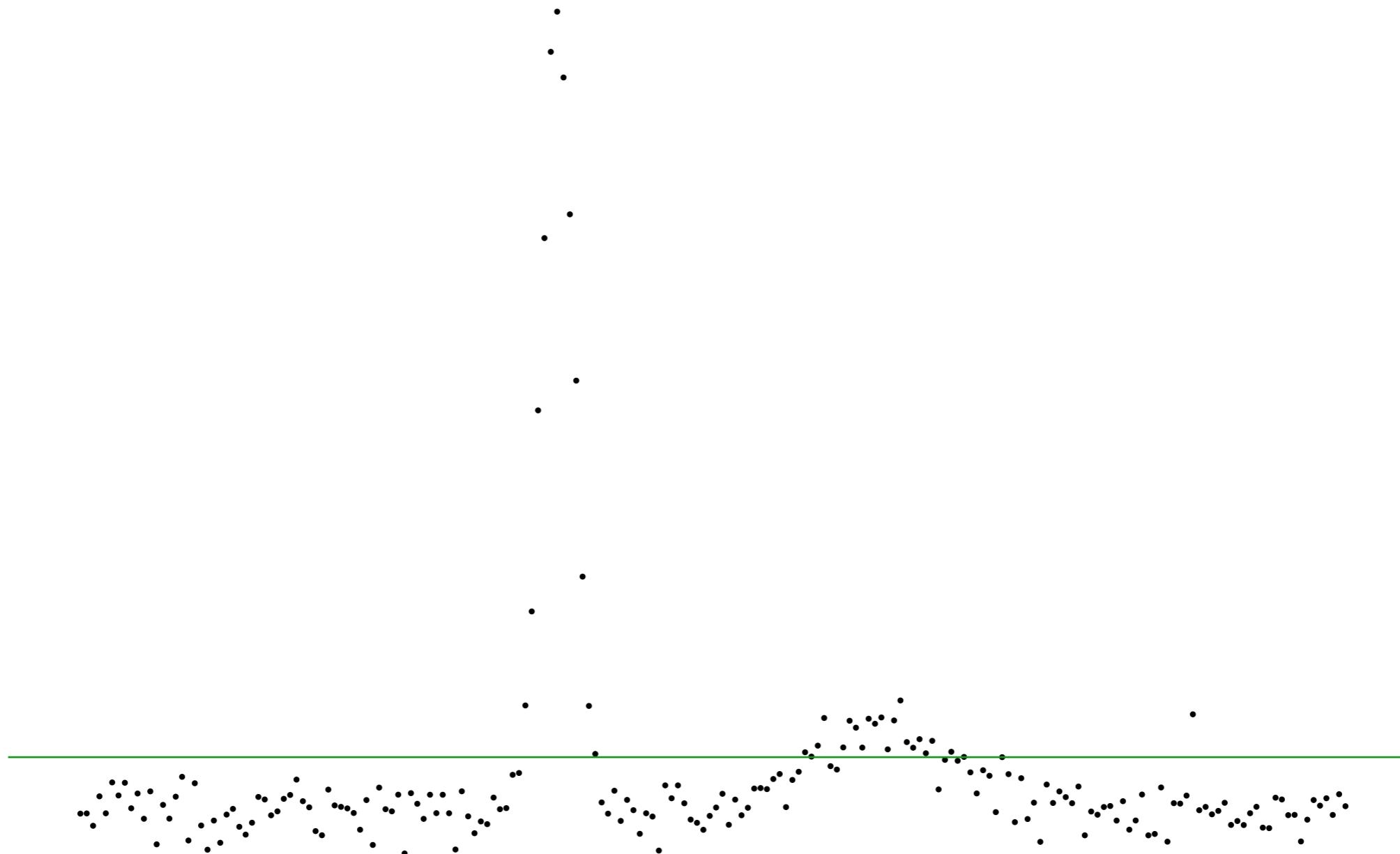
Where is the signal?



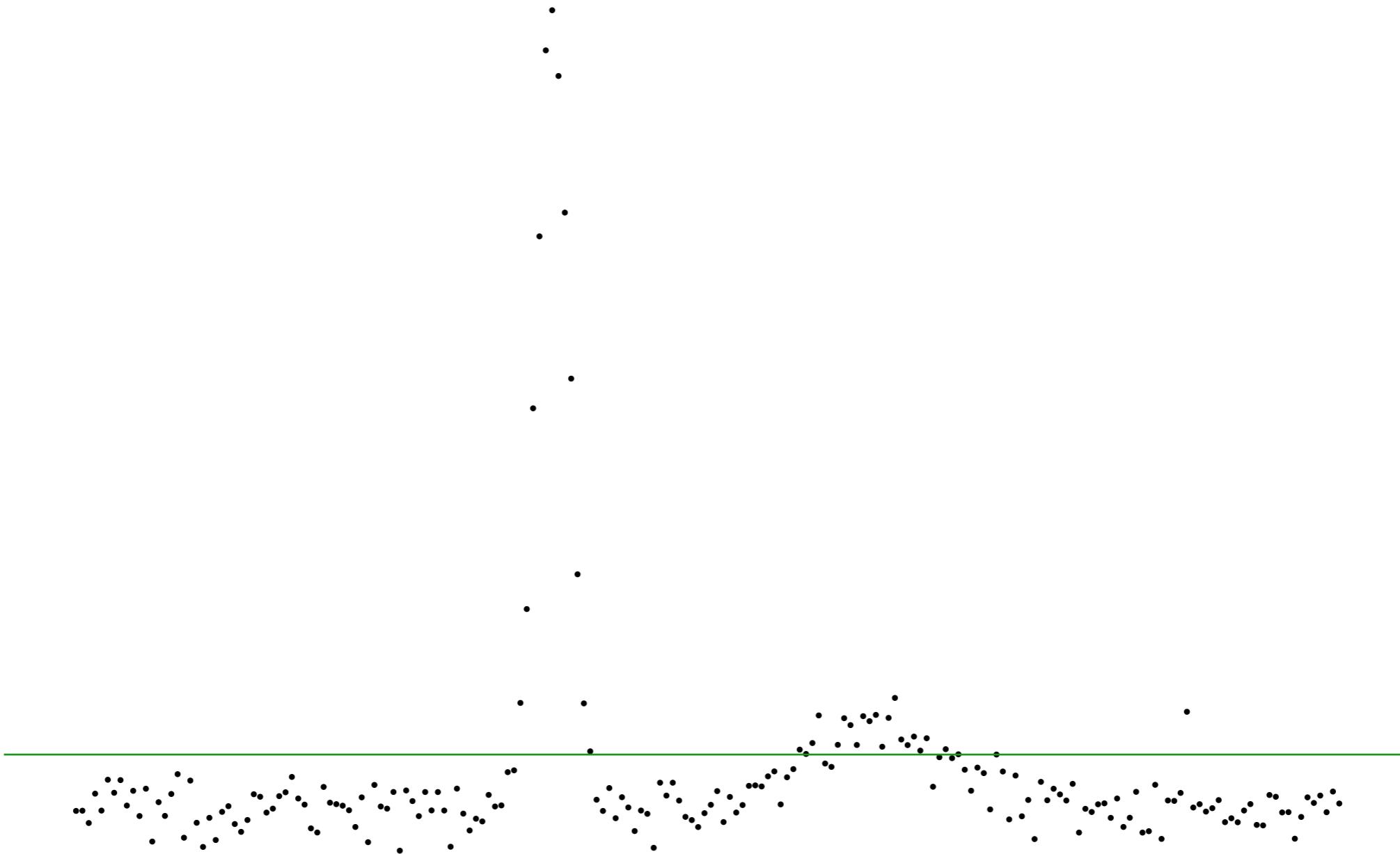
Where is the signal?



Where is the signal?

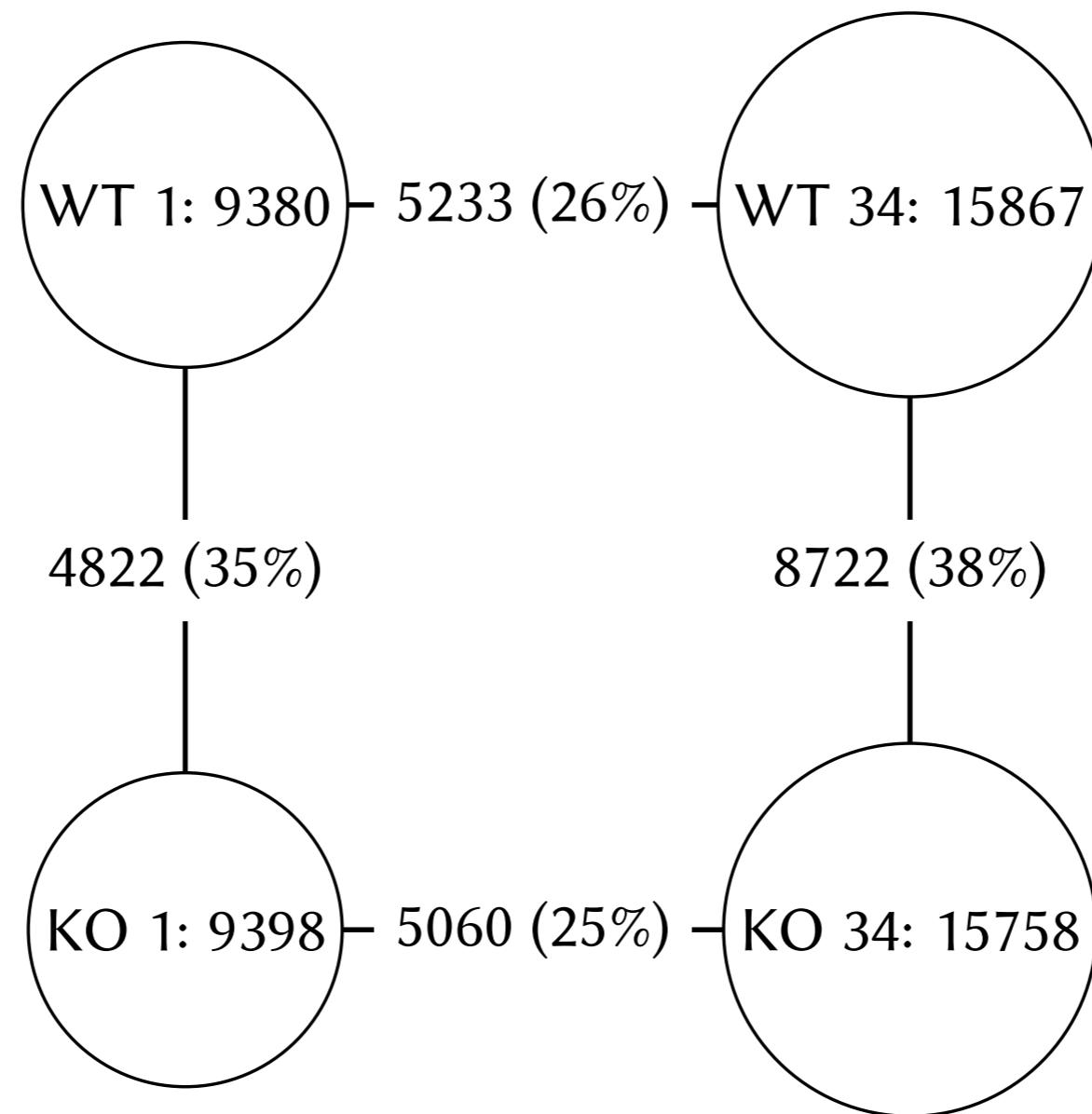


Where is the signal?



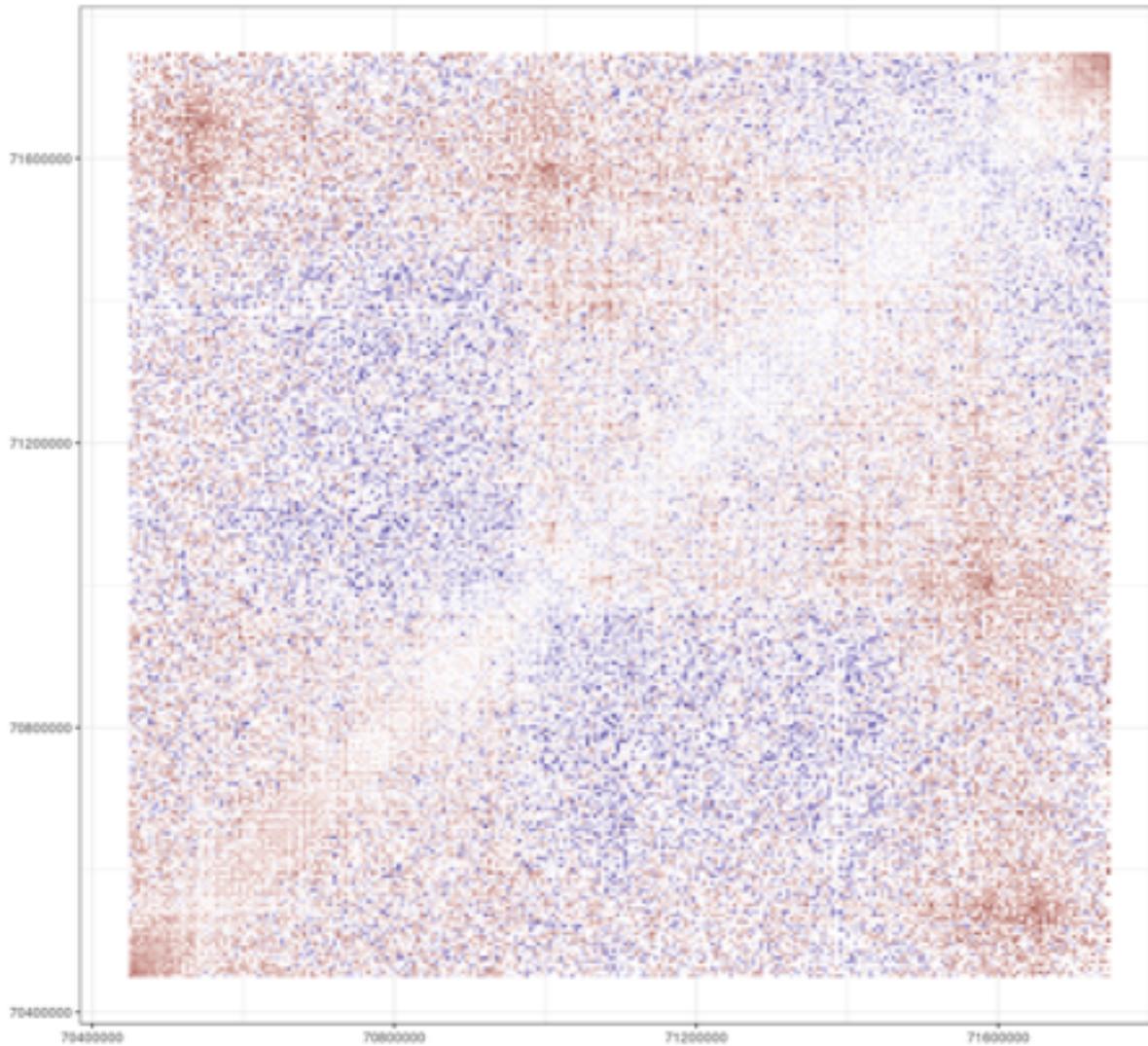
Statistical significance

Peak calling methods inconsistent

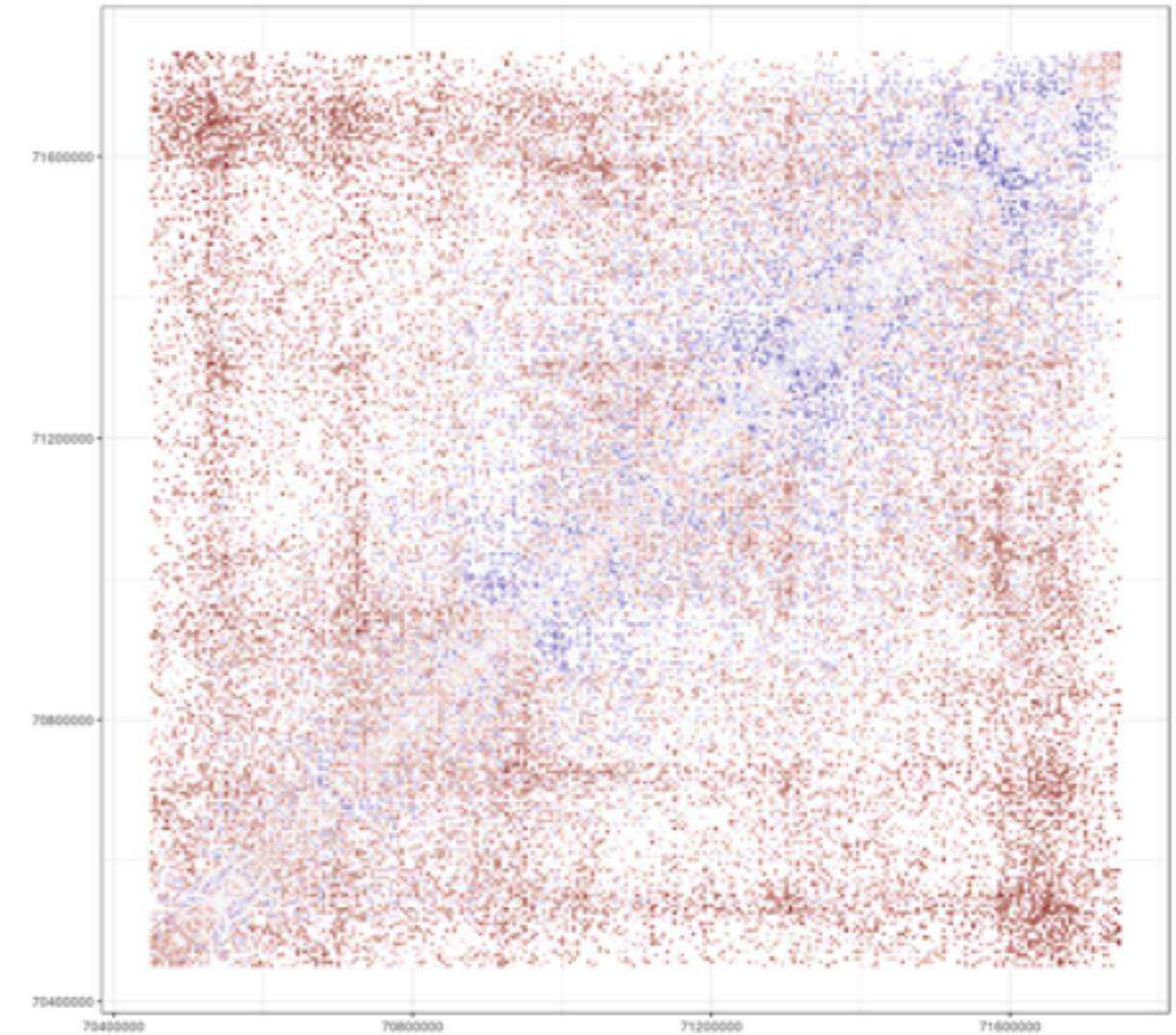


collab. with G. Mas, L. Di Croce

Signal



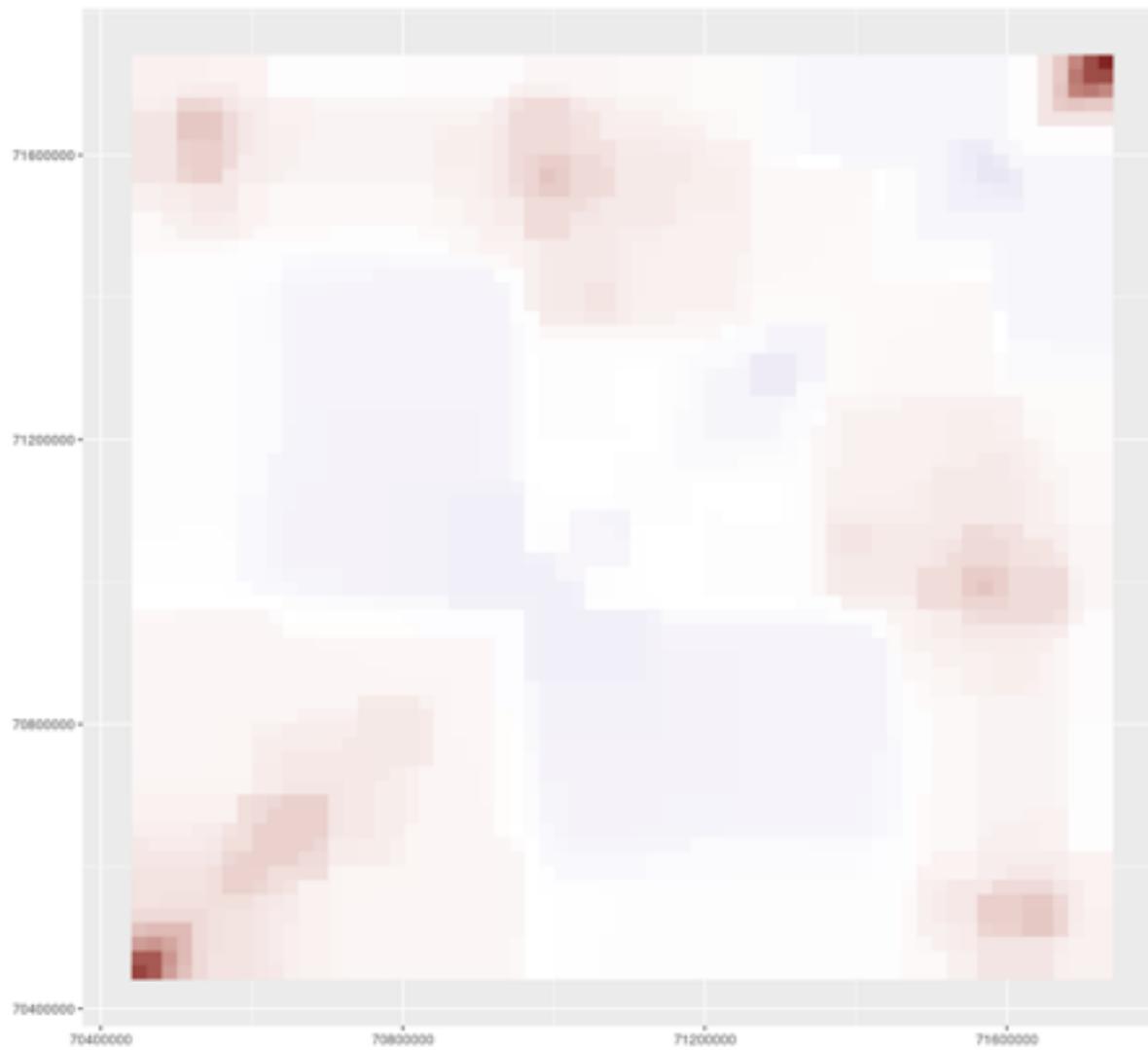
GM12878



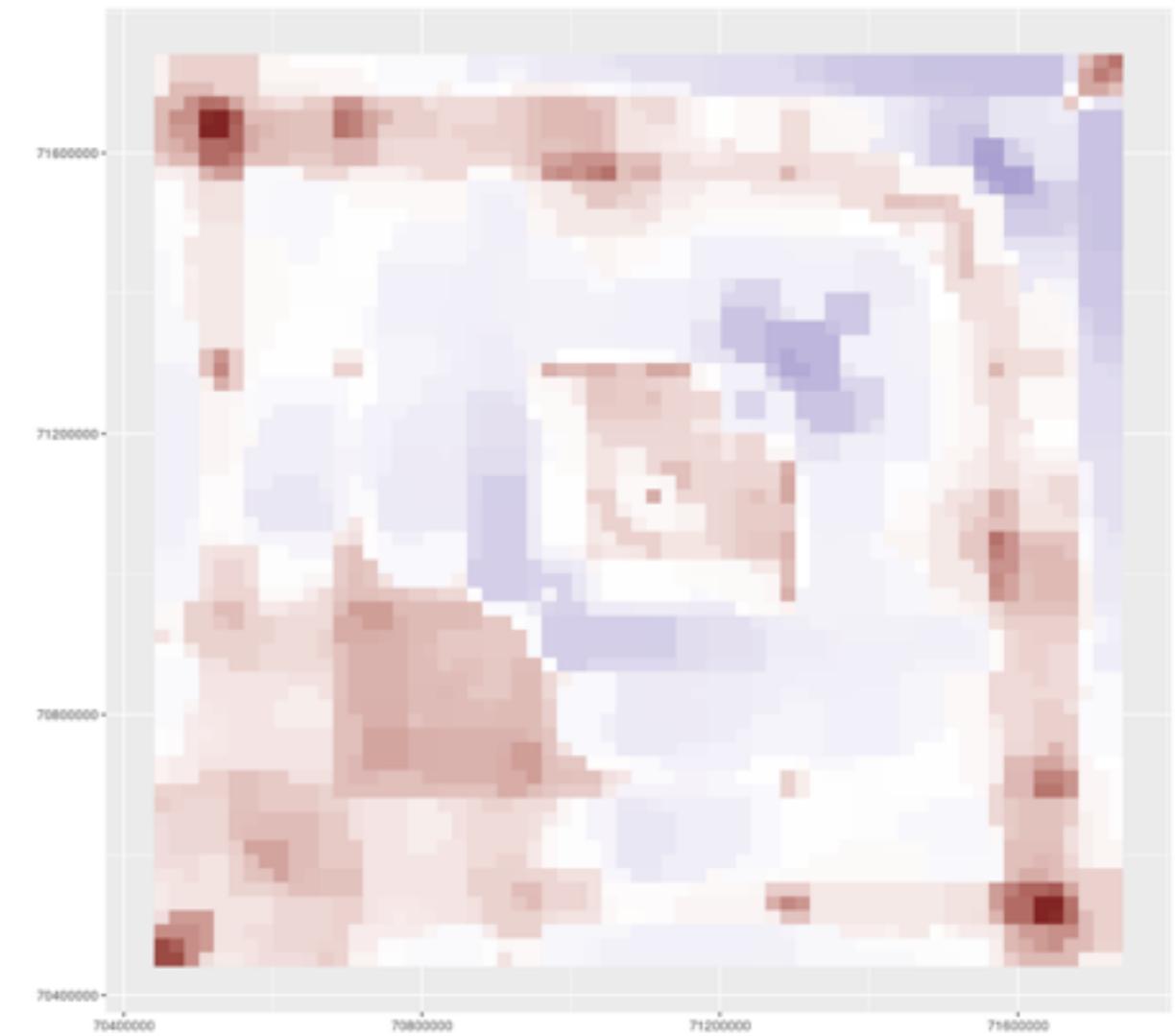
IMR90

@5kb

Binless matrices



GM12878



IMR90