http://www.malariagen.net/pf-crosses-2013

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P. falciparum genetic crosses data release 2013 - Introduction

Welcome to *Pf* Crosses 2013

This web application provides access to data released by the MalariaGEN P. falciparum Genetic Crosses Project, which is working to establish a shared resource of data on genetic variation in the three *P. falciparum* crosses 3D7 x HB3, HB3 x Dd2 and 7G8 x GB4.

If you use these data, please cite the following publication: **High density analysis of recombination in P. falciparum using deep sequencing** (in preparation)

To begin, please choose one of the options below.

Sample Metadata - view samples and download sequence data

Variant Call Sets - find SNPs & indels discovered in the crosses

Genotype Calls - browse genotypes & recombination patterns for individual samples

Genome Accessibility - explore the accessibility of different genome regions

Sequence Alignments - browse sequence alignments for individual samples

Downloads - download VCF and other data files

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P. falciparum genetic crosses data release 2013 - Sample Metadata

This page displays metadata about the samples that have been sequenced, with some summary statistics and links to the European Nucleotide Archive where the sequence data are held.

Sample set

3D7 x HB3 ▼
HB3 x Dd2
7G8 x GB4

Clone	Sample	Run	Coverage	%Mapped
HB3	PG0004-CW	ERR012788	80X	91.0
DD2	PG0008-CW	ERR012840	122X	92.3
...	...	...	...	...

Run links to ENA, e.g.: http://www.ebi.ac.uk/ena/data/view/ERR012788 (in new window)

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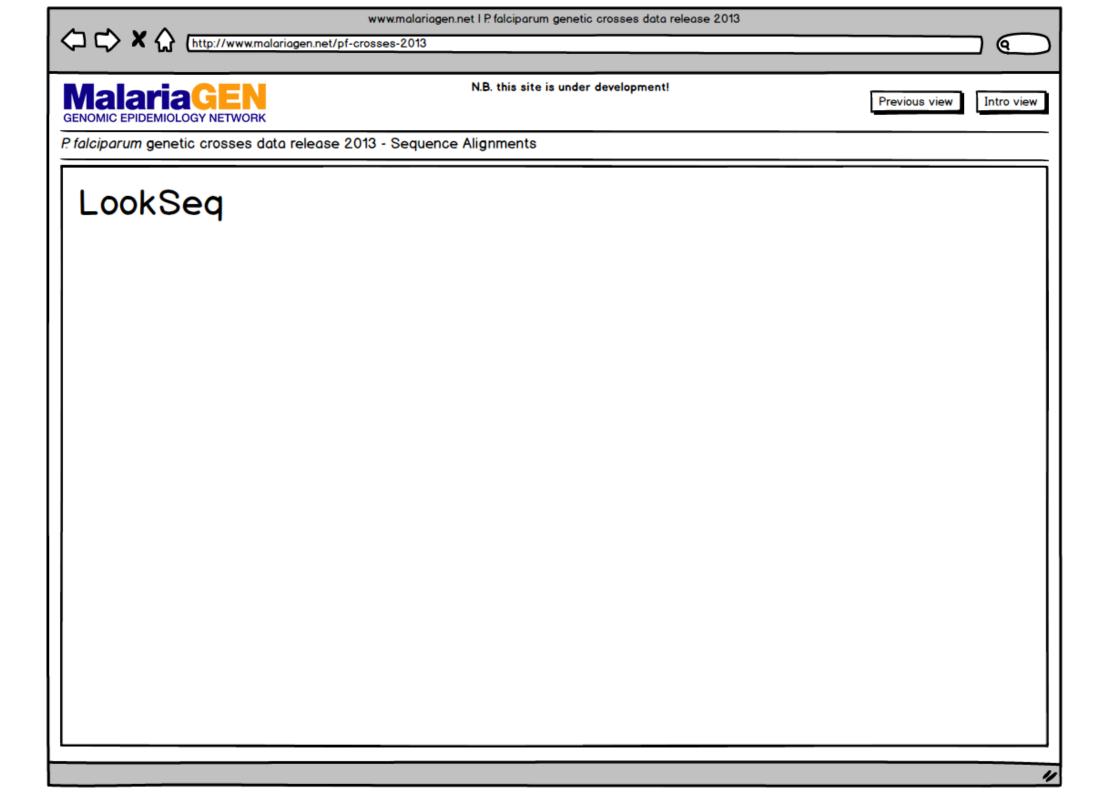**N.B. this site is under development!**

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P. falciparum genetic crosses data release 2013 - Variant Call Sets

The variant catalogues display basic properties of SNPs and indels discovered in the crosses. There are several catalogues for each cross, for variants discovered by different methods.

Variant call set

3D7 x HB3 - SNPs and indels (GATK) ▼

Search

Genome region

Chromosome: Pf3D7_01_v3 ▼

Start: [____] Stop: [____]

Go | Clear

Variant type
- ☑ SNP
- ☑ indel

Variant filters

apply all apply none

- ☑ LowQuality
- ☑ Centromere
- ☑ SubtelomericHypervariable
- ...

CHROM:POS	Gene	REF	ALT	FILTER	VQSLOD	DP	MQ	MQ0Fraction	UQ
Pf3D7_02_v3:100456	PF3D7_0206800 (MSP2)	A	G	PASS	2.4	1234	45	0.1	23
Pf3D7_02_v3:134555	-	A	AGG	LowQuality	0.1	1234	23	10.3	77
...	...	...	...	...					

Table columns for Cortex callsets:
- CHROM:POS
- Gene
- REF
- ALT
- FILTER
- SITE_CONF

Click on filter name to show description from VCF header

1-10 of 12000 | show 10 25 50 100 | < prev next >

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P. falciparum genetic crosses data release 2013 - Genotype Calls

Browse SNP and indel genotype calls for individual samples and view patterns of inheritance and recombination in the progeny.

Variant call set

3D7 x HB3 - SNPs and indels (GATK) ▼

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P. falciparum genetic crosses data release 2013 - Genome Accessibility

Browse properties of the sequence alignments and explore the accessibility of different genome regions.

Genome tracks

Reference genome
- ☑ Genes
- ☑ Sequence
- ☑ % GC
- ☑ Non-uniqueness
- ☑ Tandem repeats

Variants
- ☐ 3D7 x HB3 - SNPs & indels (GATK)
- ☐ 3D7 x HB3 - SNPs & indels (Cortex)
- ☐ HB3 x Dd2 - SNPs & indels (GATK)
- ☐ HB3 x Dd2 - SNPs & indels (Cortex)
- ☐ 7G8 x GB4 - SNPs & indels (GATK)
- ☐ 7G8 x GB4 - SNPs & indels (Cortex)

Alignment metrics
- ☐ 3D7 x HB3 coverage
- ☐ HB3 x Dd2 coverage
- ☐ 7G8 x GB4 coverage
- ☐ 3D7 x HB3 mapping quality
- ☐ HB3 x Dd2 mapping quality
- ☐ 7G8 x GB4 mapping quality

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P. falciparum genetic crosses data release 2013 - Sequence Alignments

LookSeq

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P. falciparum genetic crosses data release 2013 - Downloads

Sequence reads

To download sequence reads for an individual sample, go to the sample metadata page and click on the Run accession for a sample, which will take you to the European Nucleotide Archive page for that sequencing run.

Variant call files

The files below are VCF files containing details of SNPs and indels discovered and genotyped in the crosses.

- 3D7 x HB3 - SNPs & indels (GATK)
- 3D7 x HB3 - SNPs & indels (Cortex)
- HB3 x Dd2 - SNPs & indels (GATK)
- HB3 x Dd2 - SNPs & indels (Cortex)
- 7G8 x GB4 - SNPs & indels (GATK)
- 7G8 x GB4 - SNPs & indels (Cortex)

Genome region classification

The file below is a BED file containing the classification of genome regions into Core, SubtelomericHypervariable, InternalHypervariable, SubtelomericRepeat and Centromere.

- Genome region classification