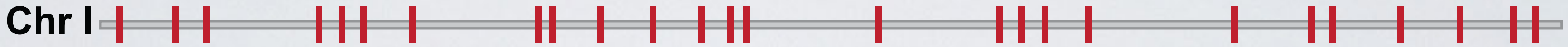
What is RAD-seq?

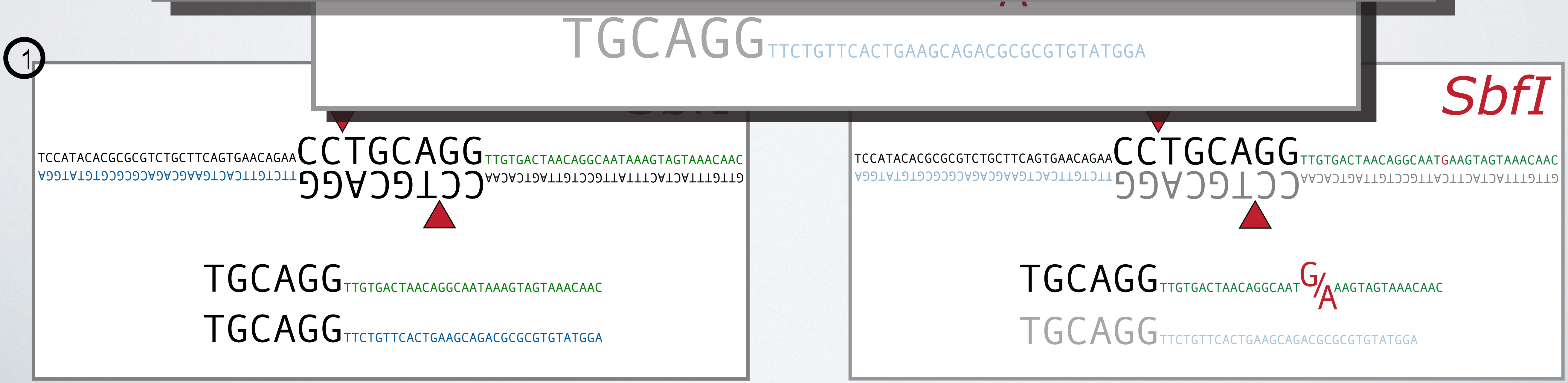
(Restriction-site Associated DNA)



22,830 *SbfI* sites in Stickleback

~ 45,000 RAD-Tags

HiSeq Illumina Lane:
150 million reads, 96 barcoded individuals



Stacks

1. Stacks is implemented in C++ with Perl wrappers
2. Core programs are shared-memory parallelized
3. Data visualization provided by MySQL / PHP web interface

30,000 Lines of C++

6,500 Lines of PHP

8,000 Lines of Perl

Angel Amores

Bill Cresko

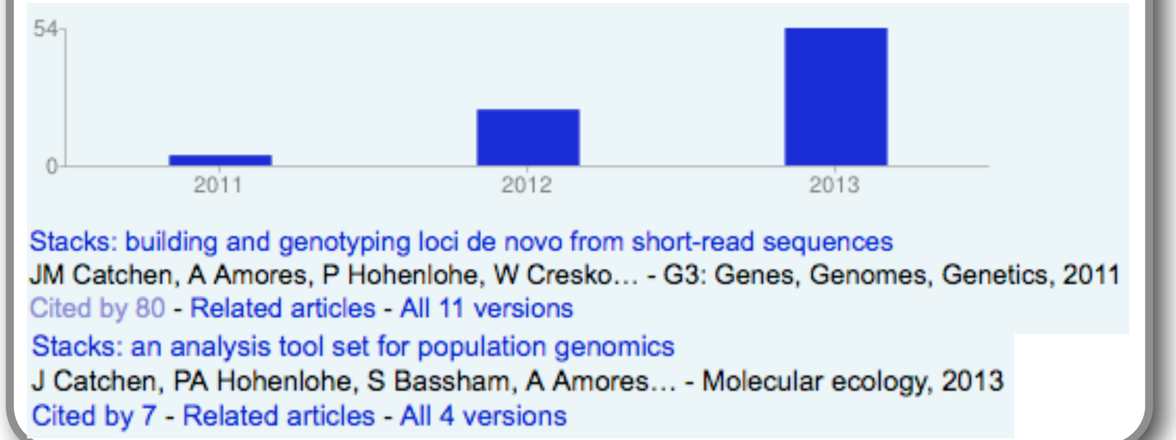
Paul Hohenlohe

Dec. 2012 - Dec. 2013

13,254 visitors

42,084 visits

87 Citations



Stacks: building and genotyping loci de novo from short-read sequences

JM Catchen, A Amores, P Hohenlohe, W Cresko… - G3: Genes, Genomes, Genetics, 2011

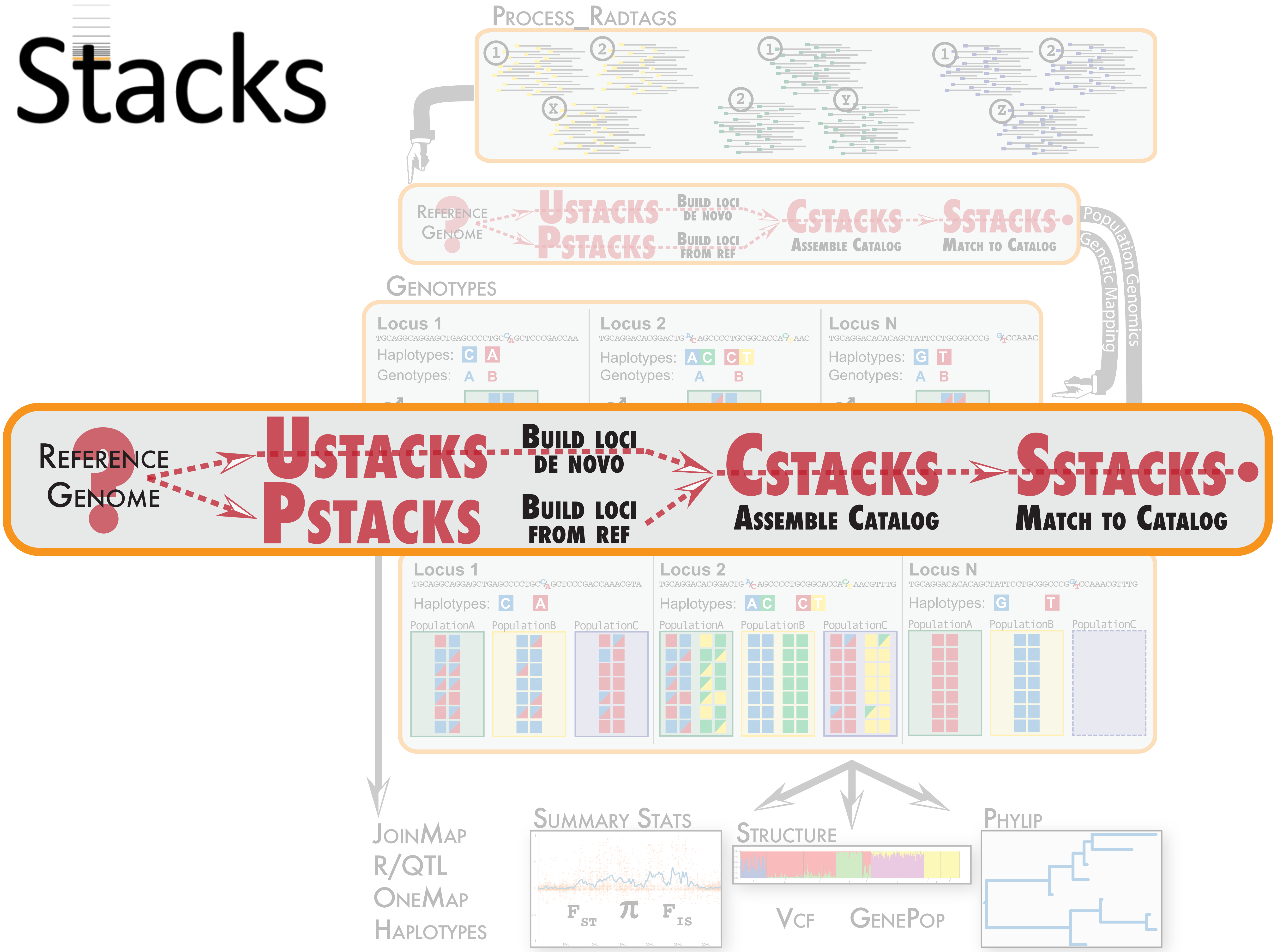
Cited by 80 - Related articles - All 11 versions

Stacks: an analysis tool set for population genomics

J Catchen, PA Hohenlohe, S Bassham, A Amores… - Molecular ecology, 2013

Cited by 7 - Related articles - All 4 versions

Stacks



REFERENCE GENOME ?

USTACKS — BUILD LOCI DE NOVO

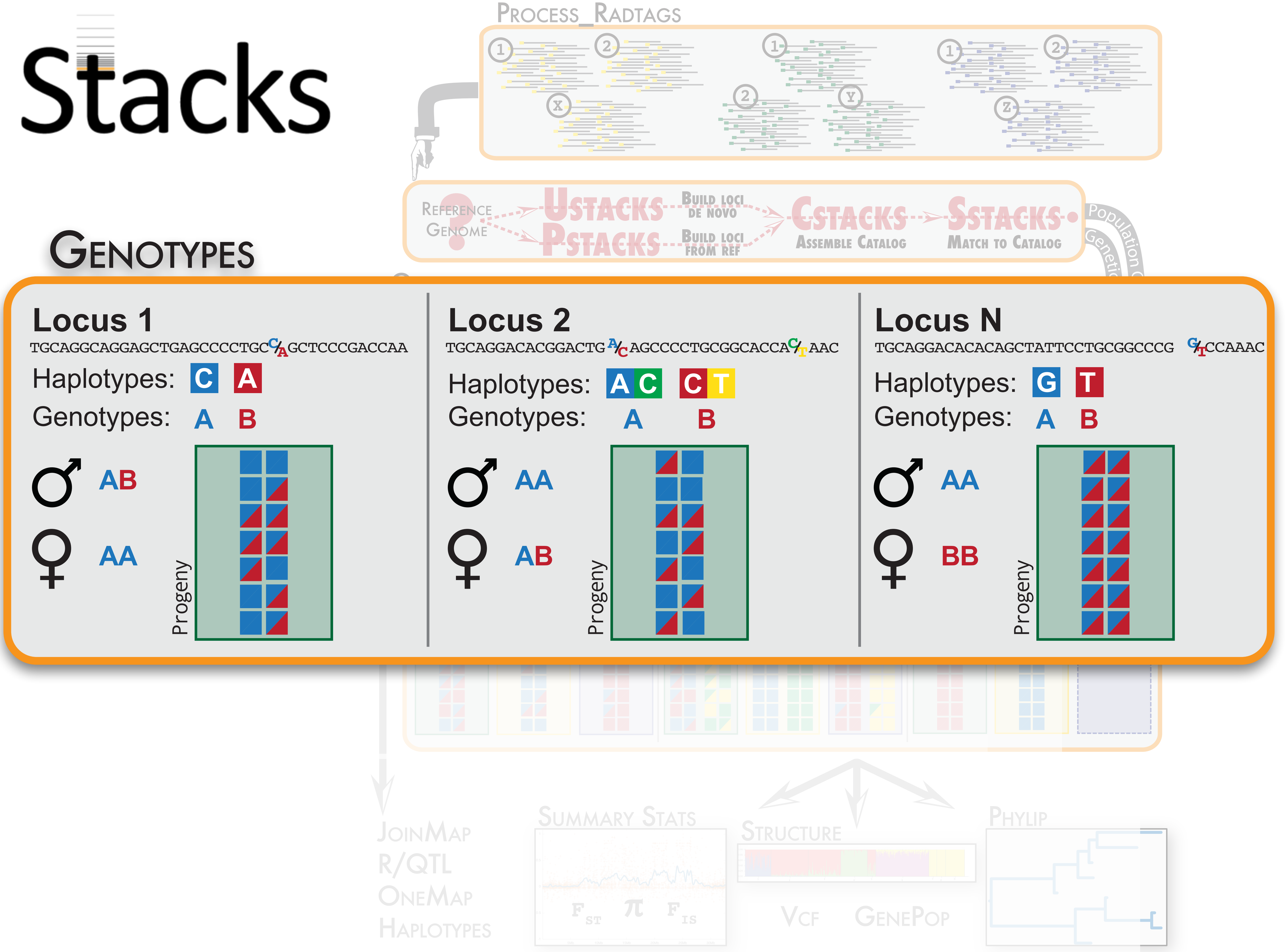
PSTACKS — BUILD LOCI FROM REF

CSTACKS — ASSEMBLE CATALOG

SSTACKS — MATCH TO CATALOG

Stacks

GENOTYPES



Locus 1

TGCAGGCAGGAGCTGAGCCCCTGC C/A GCTCCCGACCAA

Haplotypes: C A

Genotypes: A B

♂ AB

♀ AA

Locus 2

TGCAGGACACGGACTG A/C AGCCCCTGCGGCACCA C/T AAC

Haplotypes: AC CT

Genotypes: A B

♂ AA

♀ AB

Locus N

TGCAGGACACACAGCTATTCCTGCGGCCCG G/T CCAAAC

Haplotypes: G T

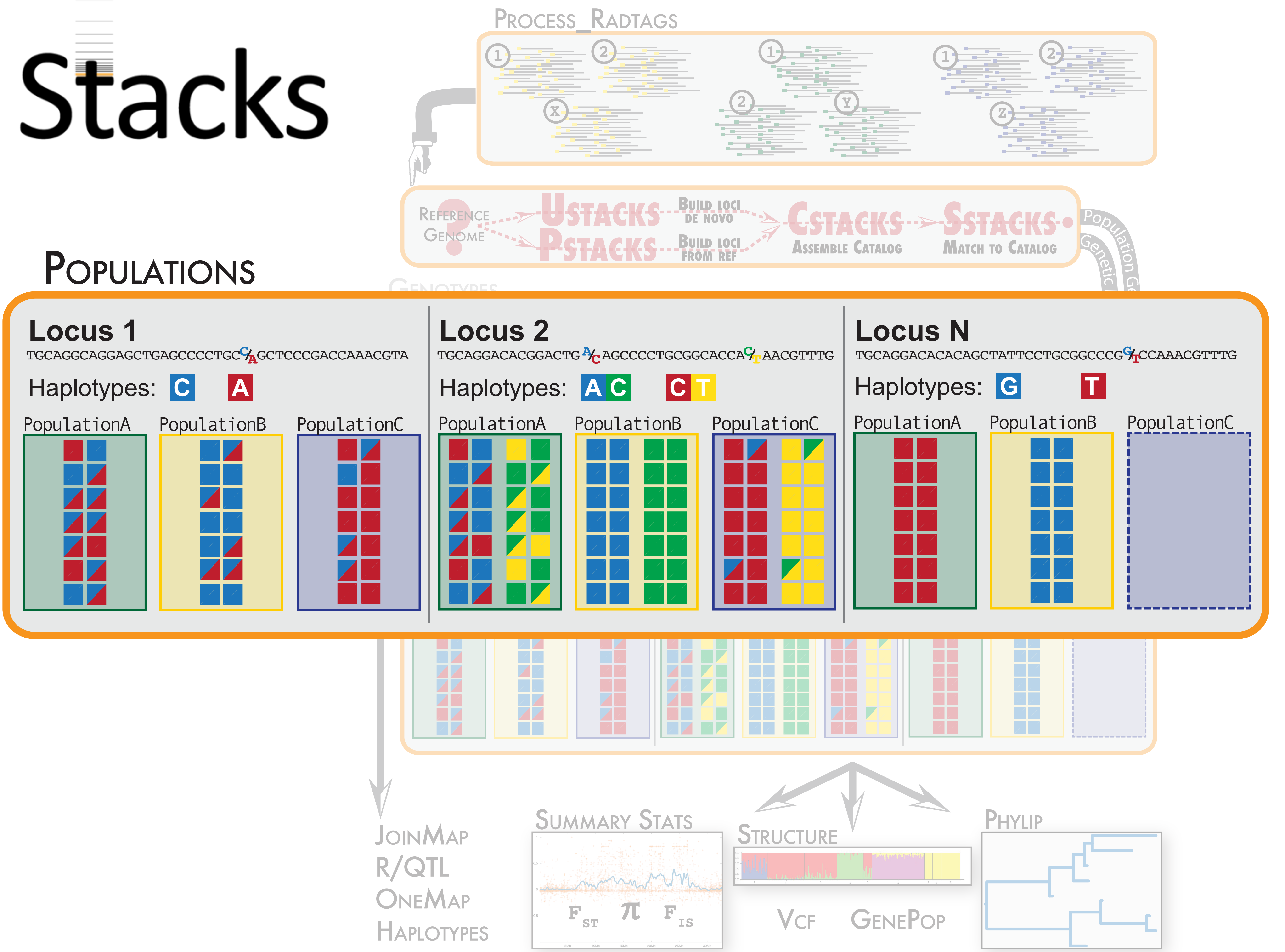
Genotypes: A B

♂ AA

♀ BB

Stacks

POPULATIONS



PROCESS_RADTAGS

REFERENCE GENOME

USTACKS Build loci de novo

PSTACKS Build loci from ref

CSTACKS Assemble Catalog

SSTACKS Match to Catalog

Population Genetic

GENOTYPES

Locus 1

TGCAGGCAGGAGCTGAGCCCCTGC C/A GCTCCCGACCAAACGTA

Haplotypes: C A

PopulationA PopulationB PopulationC

Locus 2

TGCAGGACACGGACTG A/C AGCCCCTGCGGCACCA C/T AACGTTTG

Haplotypes: AC CT

PopulationA PopulationB PopulationC

Locus N

TGCAGGACACACAGCTATTCCTGCGGCCCCG G/T CCAAACGTTTG

Haplotypes: G T

PopulationA PopulationB PopulationC

JOINMAP
R/QTL
ONEMAP
HAPLOTYPES

SUMMARY STATS

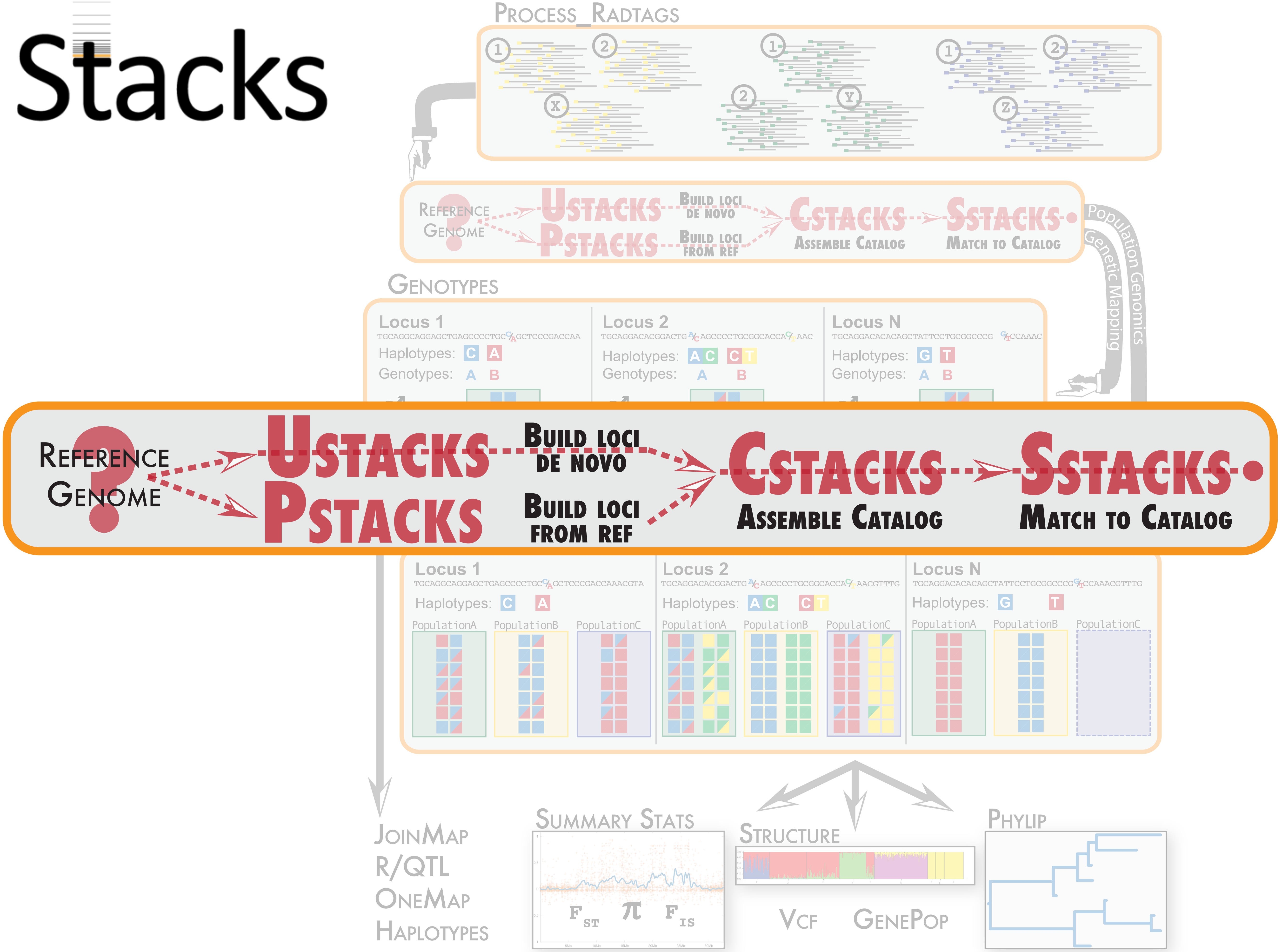
F_{ST} π F_{IS}

STRUCTURE

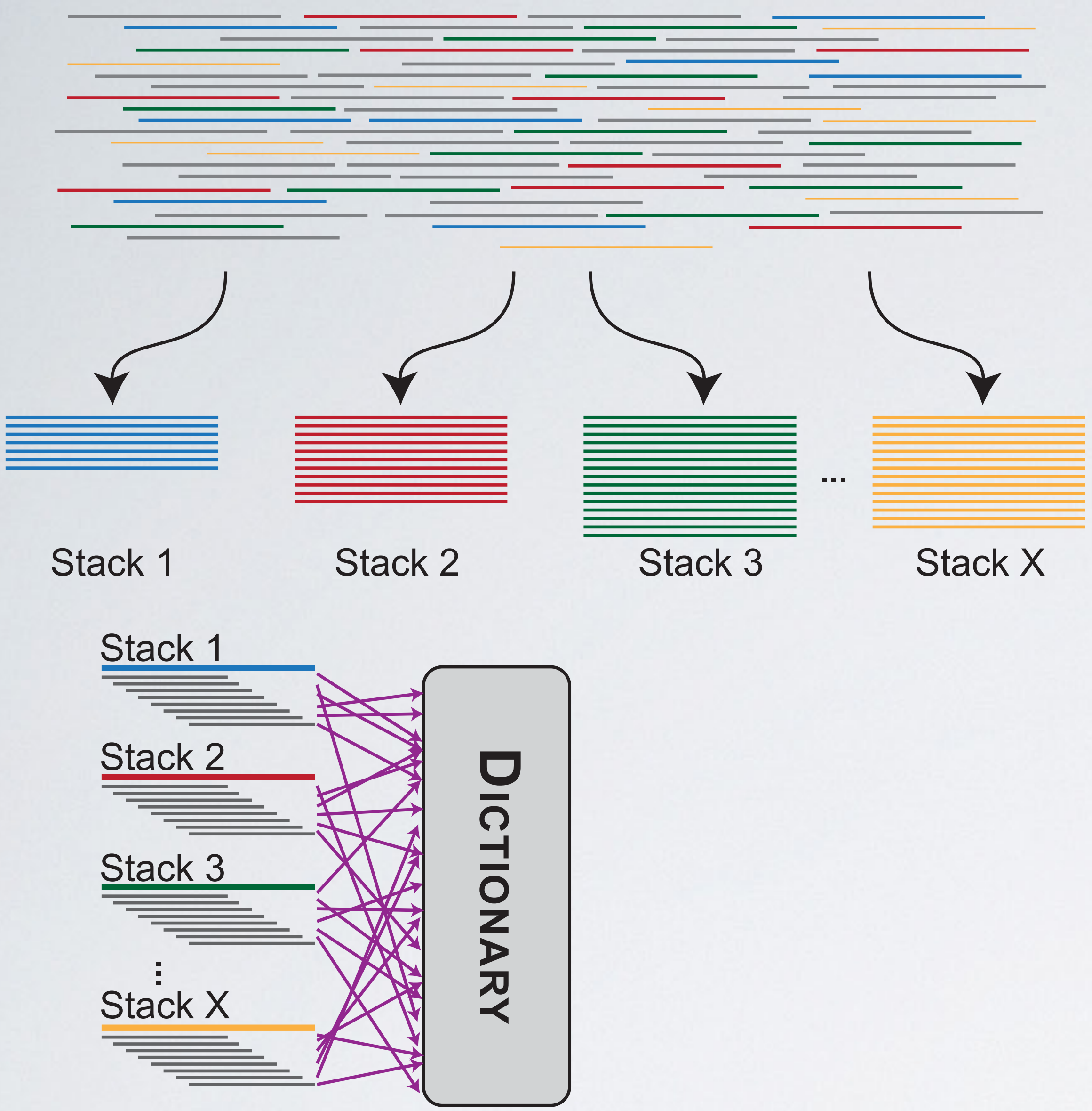
VCF GENEPOP

PHYLIP

Stacks



REFERENCE GENOME → USTACKS (BUILD LOCI DE NOVO) / PSTACKS (BUILD LOCI FROM REF) → CSTACKS (ASSEMBLE CATALOG) → SSTACKS (MATCH TO CATALOG)


Stack 1
Stack 2
Stack 3
...
Stack X
Stack 1
Stack 2
Stack 3
⋮
Stack X
DICTIONARY

C

CT

Matching stacks using k-mers

A string ca

TACCACAT
TACCACAT
ACCACAT
CCACAT
CACAT
ACAT
CAT
AT
T

AATCCTTT
AATCCTTT

1. Replace an n^2 algorithm with linear hash table lookup
2. Further reduce the search space:
    1. Given a number of allowed mismatches calculate the maximum useful k-mer size
    2. For each sequence: lookup matching k-mers and record associated reads
    3. For pairs of sequences with minimum number of k-mers, align reads.

A
AA
AAA
AAAT
AAATC

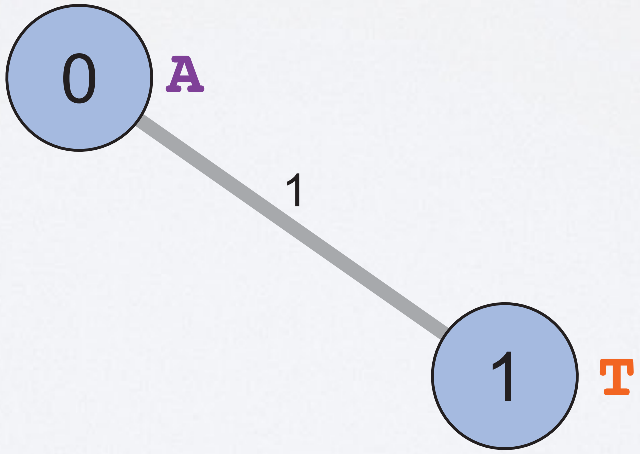
ACGTGTGAAAAATCC
CGTGTGAAAAATCCT
GTGTGAAAAATCCTT
TGTGAAAAATCCTTT

ACGTGTGAAAAATCC
CGTGTGAAAAATCCT
GTGTGAAAAATCCTT
TGTGAAAAATCCTTT

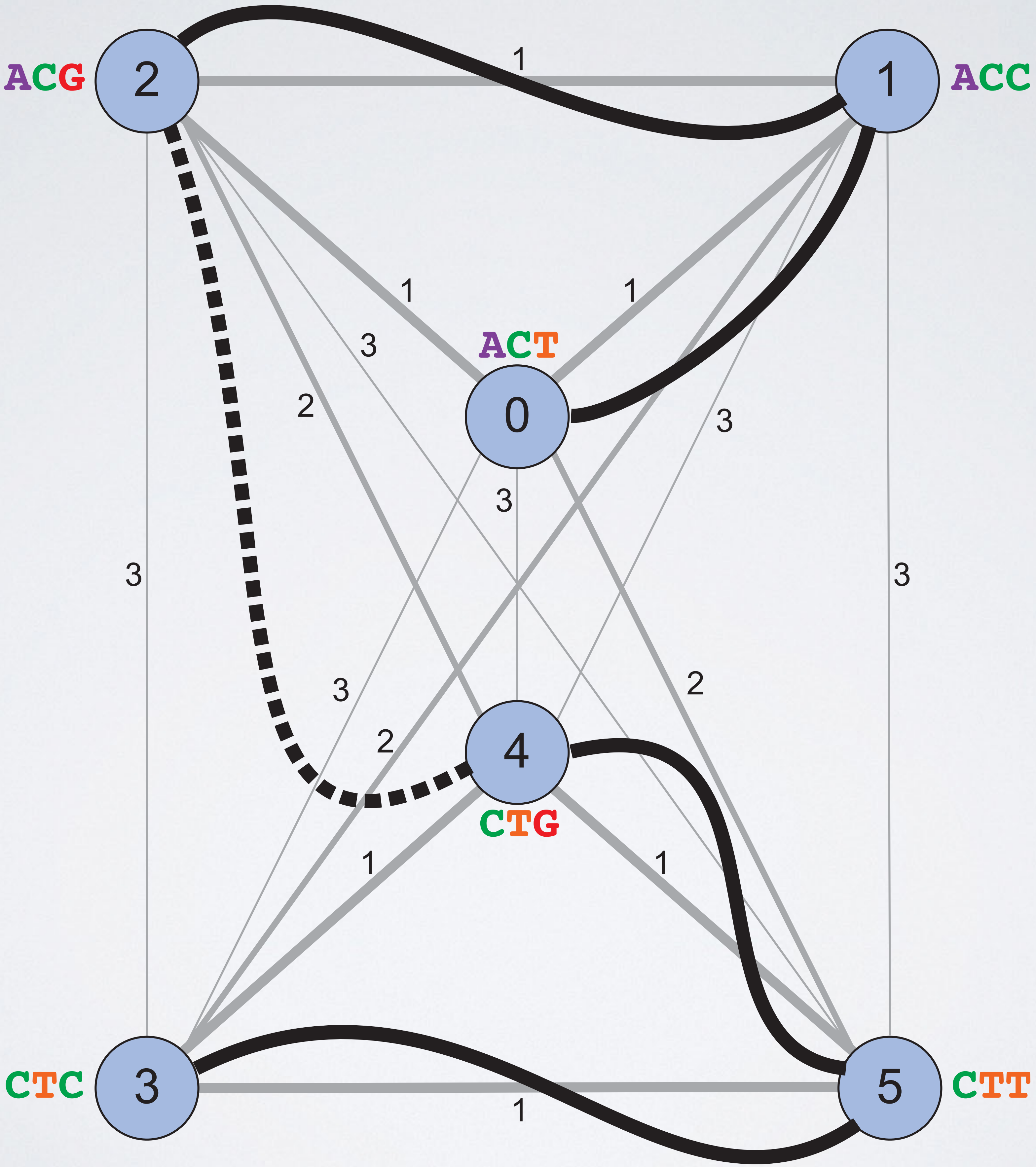
Building loci using minimum spanning trees

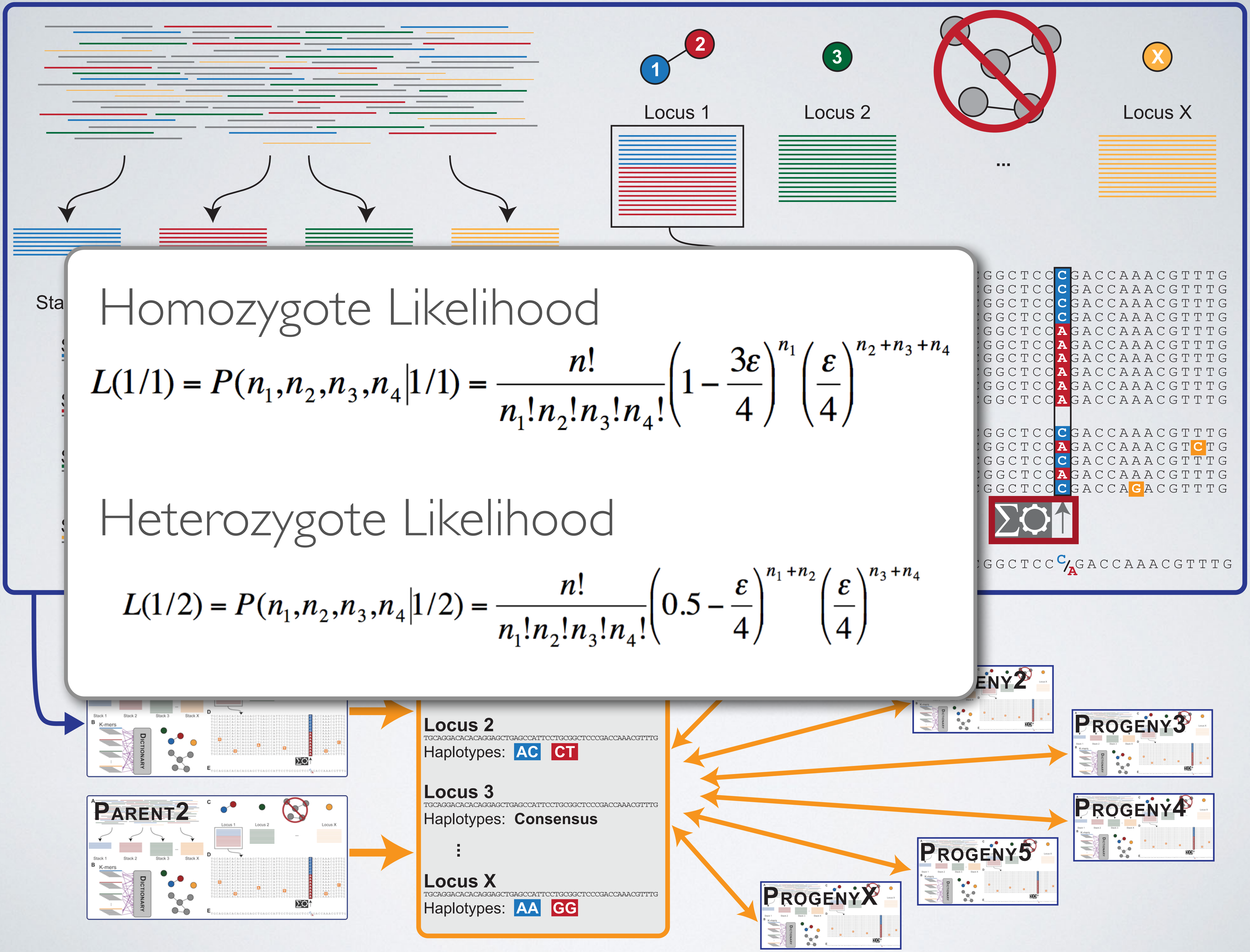
TGCAGGTACCCCGTCCCC**A**GCGGAGGACCTGTTACC
TGCAGGTACCCCGTCCCC**A**GCGGAGGACCTGTTACC
TGCAGGTACCCCGTCCCC**A**GCGGAGGACCTGTTACC
TGCAGGTACCCCGTCCCC**A**GCGGAGGACCTGTTACC
TGCAGGTACCCCGTCCCC**A**GCGGAGGACCTGTTACC

TGCAGGTACCCCGTCCCC**T**GCGGAGGACCTGTTACC
TGCAGGTACCCCGTCCCC**T**GCGGAGGACCTGTTACC
TGCAGGTACCCCGTCCCC**T**GCGGAGGACCTGTTACC
TGCAGGTACCCCGTCCCC**T**GCGGAGGACCTGTTACC
TGCAGGTACCCCGTCCCC**T**GCGGAGGACCTGTTACC



Building loci using minimum spanning trees





Locus 2
TGCAGGACACACAGGAGCTGAGCCATTCCTGCGGCTCCCGACCAAACGTTTG
Haplotypes: AC CT

Locus 3
TGCAGGACACACAGGAGCTGAGCCATTCCTGCGGCTCCCGACCAAACGTTTG
Haplotypes: **Consensus**

⋮

Locus X
TGCAGGACACACAGGAGCTGAGCCATTCCTGCGGCTCCCGACCAAACGTTTG
Haplotypes: AA GG

Homozygote Likelihood

$$L(1/1) = P(n_1,n_2,n_3,n_4|1/1) = \frac{n!}{n_1!n_2!n_3!n_4!}\left(1-\frac{3\varepsilon}{4}\right)^{n_1}\left(\frac{\varepsilon}{4}\right)^{n_2+n_3+n_4}$$

Heterozygote Likelihood

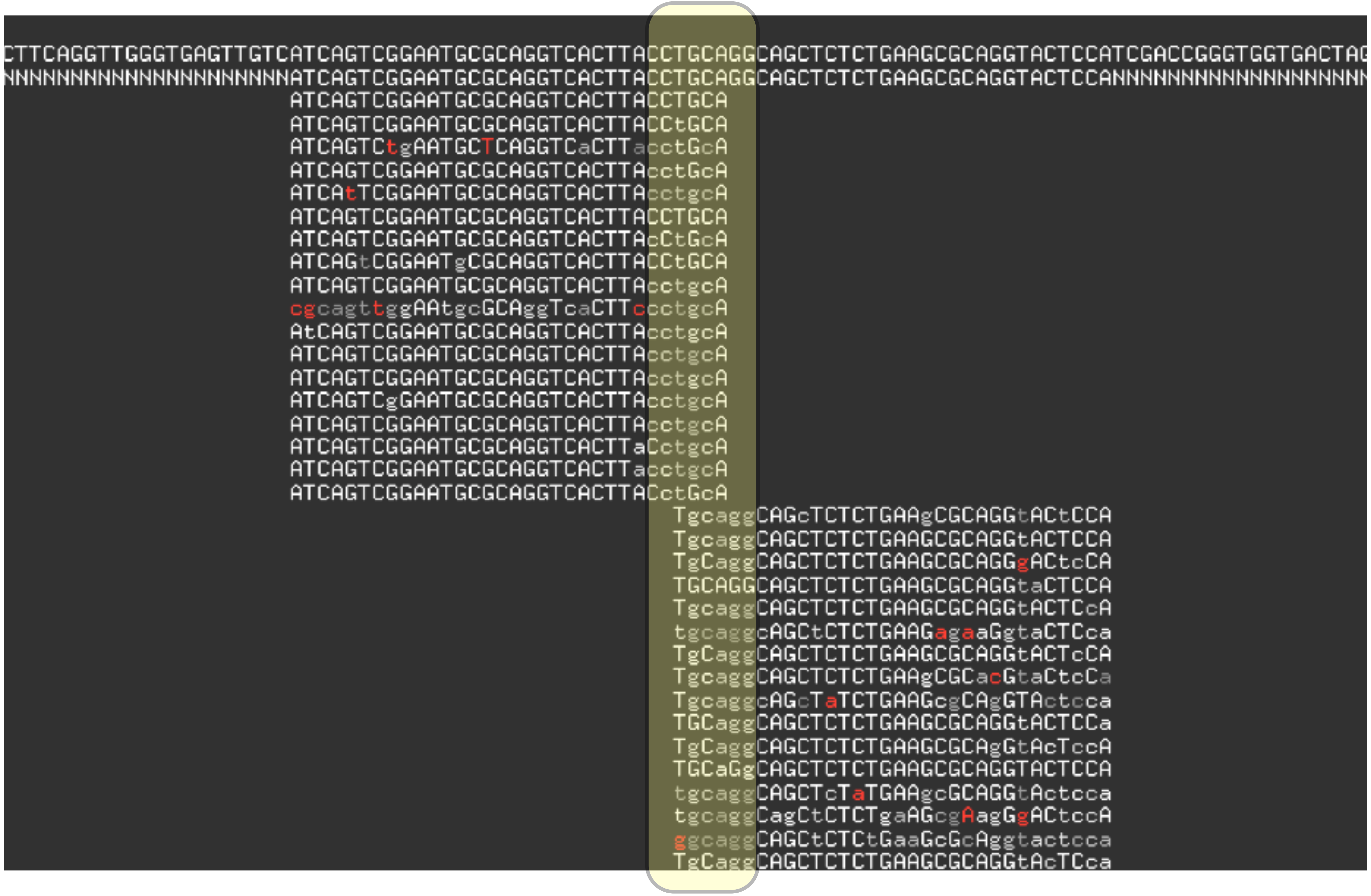
$$L(1/2) = P(n_1,n_2,n_3,n_4|1/2) = \frac{n!}{n_1!n_2!n_3!n_4!}\left(0.5-\frac{\varepsilon}{4}\right)^{n_1+n_2}\left(\frac{\varepsilon}{4}\right)^{n_3+n_4}$$

Differentiating SNPs from error

Restriction enzyme recognition site

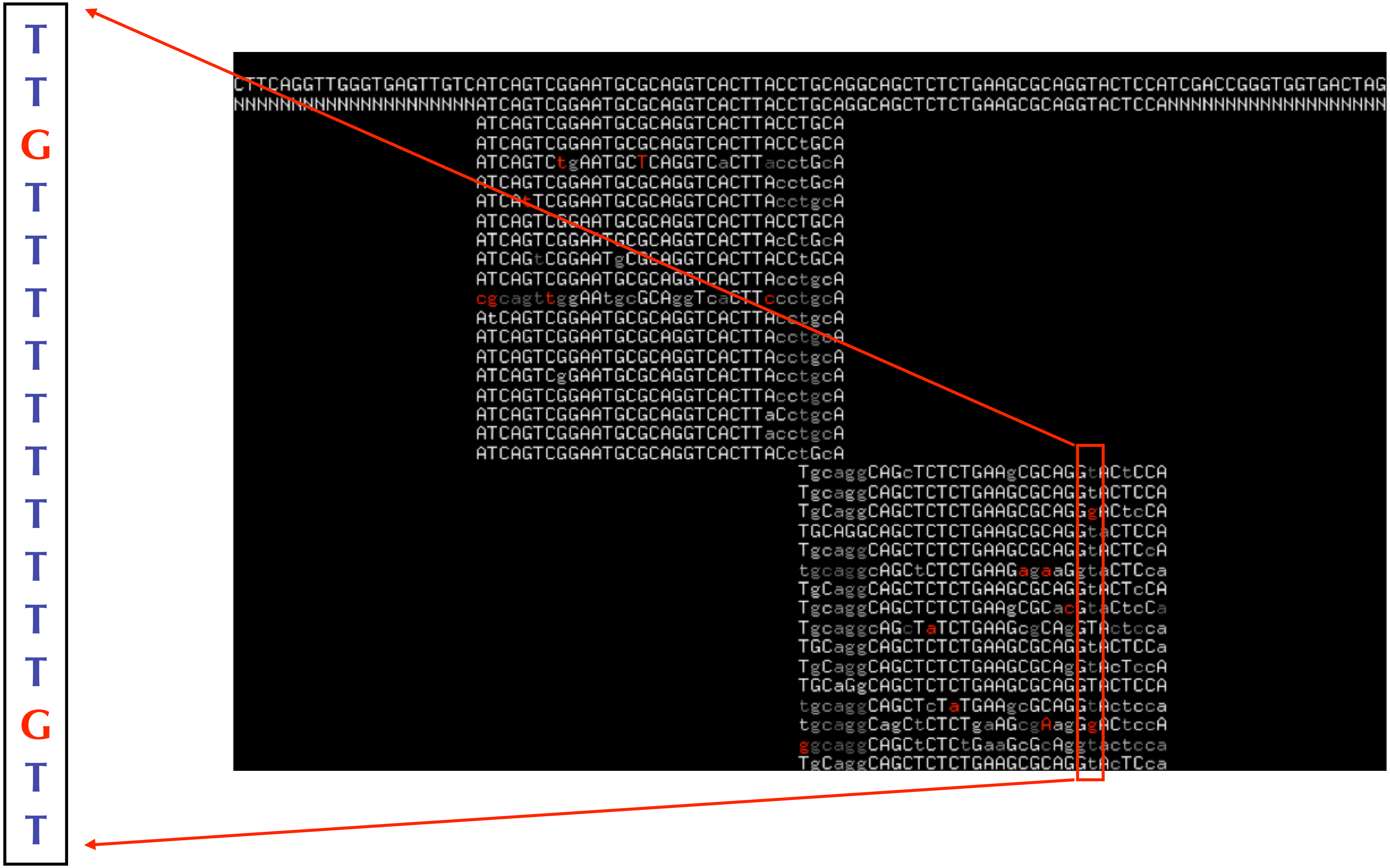
Reference genome sequence

sequence reads



```
CTTCAGGTTGGGTGAGTTGTCATCAGTCGGAATGCGCAGGTCACTTACCTGCAGGCAGCTCTCTGAAGCGCAGGTACTCCATCGACCGGGTGGTGACTAG
NNNNNNNNNNNNNNNNNNNNNATCAGTCGGAATGCGCAGGTCACTTACCTGCAGGCAGCTCTCTGAAGCGCAGGTACTCCANNNNNNNNNNNNNNNNNNN
                     ATCAGTCGGAATGCGCAGGTCACTTACCTGCA
                     ATCAGTCGGAATGCGCAGGTCACTTACCtGCA
                     ATCAGTCtgAATGCTCAGGTCaCTTacctGcA
                     ATCAGTCGGAATGCGCAGGTCACTTAcctGcA
                     ATCAtTCGGAATGCGCAGGTCACTTAcctgcA
                     ATCAGTCGGAATGCGCAGGTCACTTACCTGCA
                     ATCAGTCGGAATGCGCAGGTCACTTAcCtGcA
                     ATCAGtCGGAATgCGCAGGTCACTTACCtGCA
                     ATCAGTCGGAATGCGCAGGTCACTTAcctgcA
                     cgcagttggAAtgcGCAggTcaCTTccctgcA
                     AtCAGTCGGAATGCGCAGGTCACTTAcctgcA
                     ATCAGTCGGAATGCGCAGGTCACTTAcctgcA
                     ATCAGTCGGAATGCGCAGGTCACTTAcctgcA
                     ATCAGTCgGAATGCGCAGGTCACTTAcctgcA
                     ATCAGTCGGAATGCGCAGGTCACTTAcctgcA
                     ATCAGTCGGAATGCGCAGGTCACTTaCctgcA
                     ATCAGTCGGAATGCGCAGGTCACTTacctgcA
                     ATCAGTCGGAATGCGCAGGTCACTTACctGcA
                                                 TgcaggCAGcTCTCTGAAgCGCAGGtACtCCA
                                                 TgcaggCAGCTCTCTGAAGCGCAGGtACTCCA
                                                 TgCaggCAGCTCTCTGAAGCGCAGGgACtcCA
                                                 TGCAGGCAGCTCTCTGAAGCGCAGGtaCTCCA
                                                 TgcaggCAGCTCTCTGAAGCGCAGGtACTCcA
                                                 tgcaggcAGCtCTCTGAAGagaaGgtaCTCca
                                                 TgCaggCAGCTCTCTGAAGCGCAGGtACTcCA
                                                 TgcaggCAGCTCTCTGAAgCGCacGtaCtcCa
                                                 TgcaggcAGcTaTCTGAAGcgCAgGTActcca
                                                 TGCaggCAGCTCTCTGAAGCGCAGGtACTCCa
                                                 TgCaggCAGCTCTCTGAAGCGCAgGtAcTccA
                                                 TGCaGgCAGCTCTCTGAAGCGCAGGTACTCCA
                                                 tgcaggCAGCTcTaTGAAgcGCAGGtActcca
                                                 tgcaggCagCtCTCTgaAGcgAagGgACtccA
                                                 ggcaggCAGCtCTCtGaaGcGcAggtactcca
                                                 TgCaggCAGCTCTCTGAAGCGCAGGtAcTCca
```

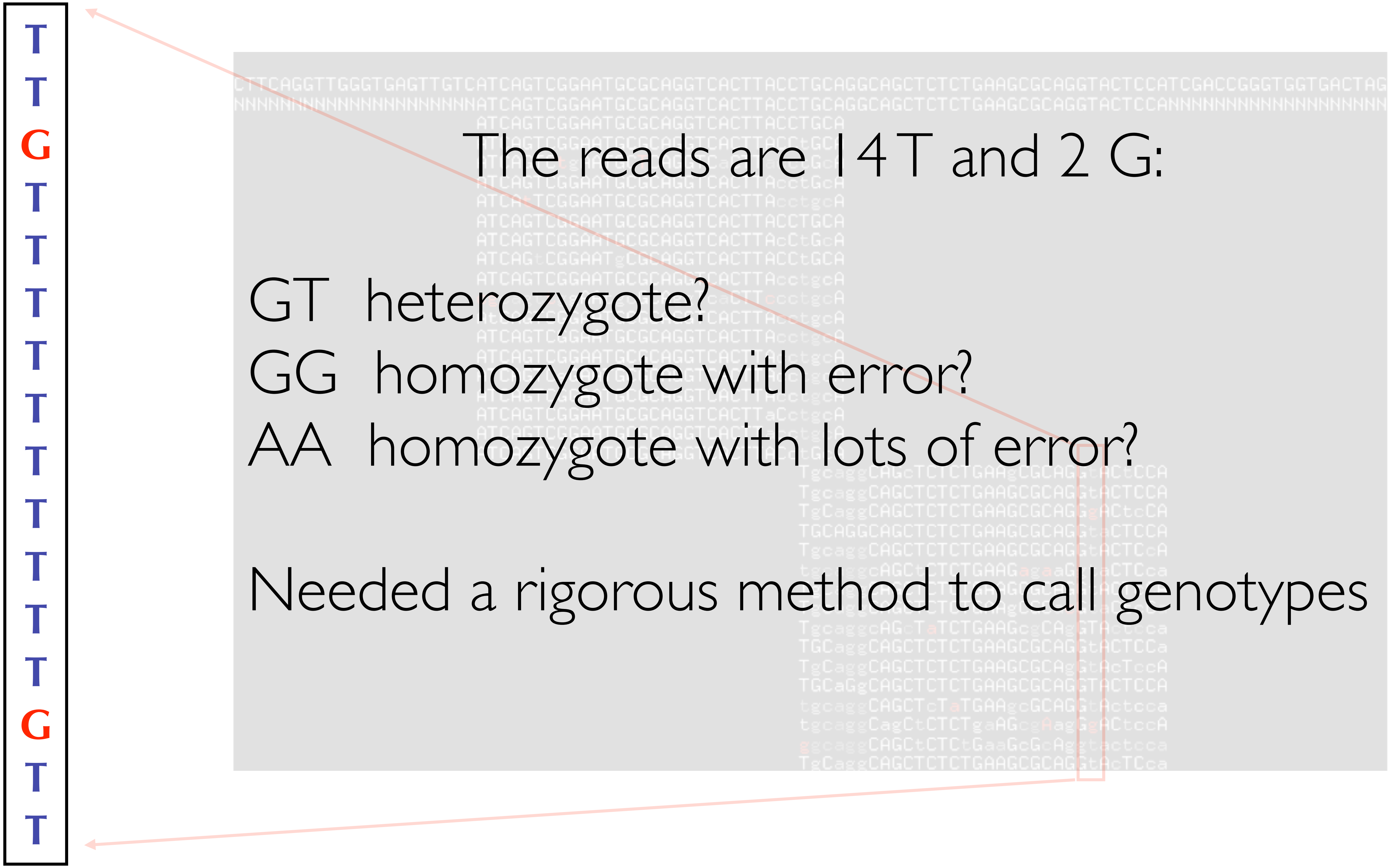
Differentiating SNPs from error



T
T
G
T
T
T
T
T
T
T
T
T
T
G
T
T

```
CTTCAGGTTGGGTGAGTTGTCATCAGTCGGAATGCGCAGGTCACTTACCTGCAGGCAGCTCTCTGAAGCGCAGGTACTCCATCGACCGGGTGGTGACTAG
NNNNNNNNNNNNNNNNNNNNNATCAGTCGGAATGCGCAGGTCACTTACCTGCAGGCAGCTCTCTGAAGCGCAGGTACTCCANNNNNNNNNNNNNNNNNNN
                     ATCAGTCGGAATGCGCAGGTCACTTACCTGCA
                     ATCAGTCGGAATGCGCAGGTCACTTACCtGCA
                     ATCAGTCtgAATGCTCAGGTCaCTTacctGcA
                     ATCAGTCGGAATGCGCAGGTCACTTAcctGcA
                     ATCAtTCGGAATGCGCAGGTCACTTAcctgcA
                     ATCAGTCGGAATGCGCAGGTCACTTACCTGCA
                     ATCAGTCGGAATGCGCAGGTCACTTAcCtGcA
                     ATCAGtCGGAATgCGCAGGTCACTTACCtGCA
                     ATCAGTCGGAATGCGCAGGTCACTTAcctgcA
                     cgcagttggAAtgcGCAggTcaCTTcсctgcA
                     AtCAGTCGGAATGCGCAGGTCACTTAcctgcA
                     ATCAGTCGGAATGCGCAGGTCACTTAcctgcA
                     ATCAGTCGGAATGCGCAGGTCACTTAcctgcA
                     ATCAGTCgGAATGCGCAGGTCACTTAcctgcA
                     ATCAGTCGGAATGCGCAGGTCACTTAcctgcA
                     ATCAGTCGGAATGCGCAGGTCACTTaCctgcA
                     ATCAGTCGGAATGCGCAGGTCACTTacctgcA
                     ATCAGTCGGAATGCGCAGGTCACTTACctGcA
                                                 TgcaggCAGcTCTCTGAAgCGCAGGtACtCCA
                                                 TgcaggCAGCTCTCTGAAGCGCAGGtACTCCA
                                                 TgCaggCAGCTCTCTGAAGCGCAGGgACtcCA
                                                 TGCAGGCAGCTCTCTGAAGCGCAGGtaCTCCA
                                                 TgcaggCAGCTCTCTGAAGCGCAGGtACTCcA
                                                 tgcaggcAGCtCTCTGAAGagaaGgtaCTCca
                                                 TgCaggCAGCTCTCTGAAGCGCAGGtACTcCA
                                                 TgcaggCAGCTCTCTGAAgCGCacGtaCtcCa
                                                 TgcaggcAGcTaTCTGAAGcgCAgGTActcca
                                                 TGCaggCAGCTCTCTGAAGCGCAGGtACTCCa
                                                 TgCaggCAGCTCTCTGAAGCGCAgGtAcTccA
                                                 TGCaGgCAGCTCTCTGAAGCGCAGGTACTCCA
                                                 tgcaggCAGCTcTaTGAAgcGCAGGtActcca
                                                 tgcaggCagCtCTCTgaAGcgAagGgACtccA
                                                 ggcaggCAGCtCTCtGaaGcGcAggtactcca
                                                 TgCaggCAGCTCTCTGAAGCGCAGGtAcTCca
```

Differentiating SNPs from error



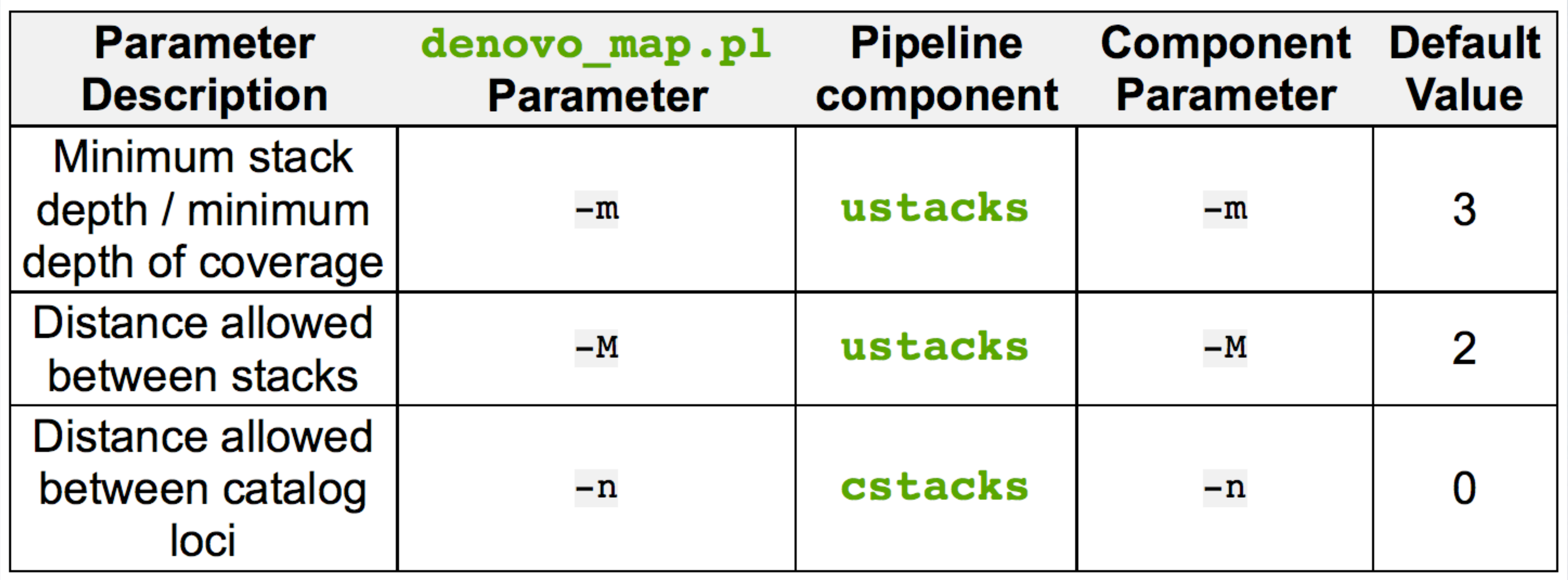
T
T
G
T
T
T
T
T
T
T
T
T
T
G
T
T

The reads are 14 T and 2 G:

GT heterozygote?
GG homozygote with error?
AA homozygote with lots of error?

Needed a rigorous method to call genotypes

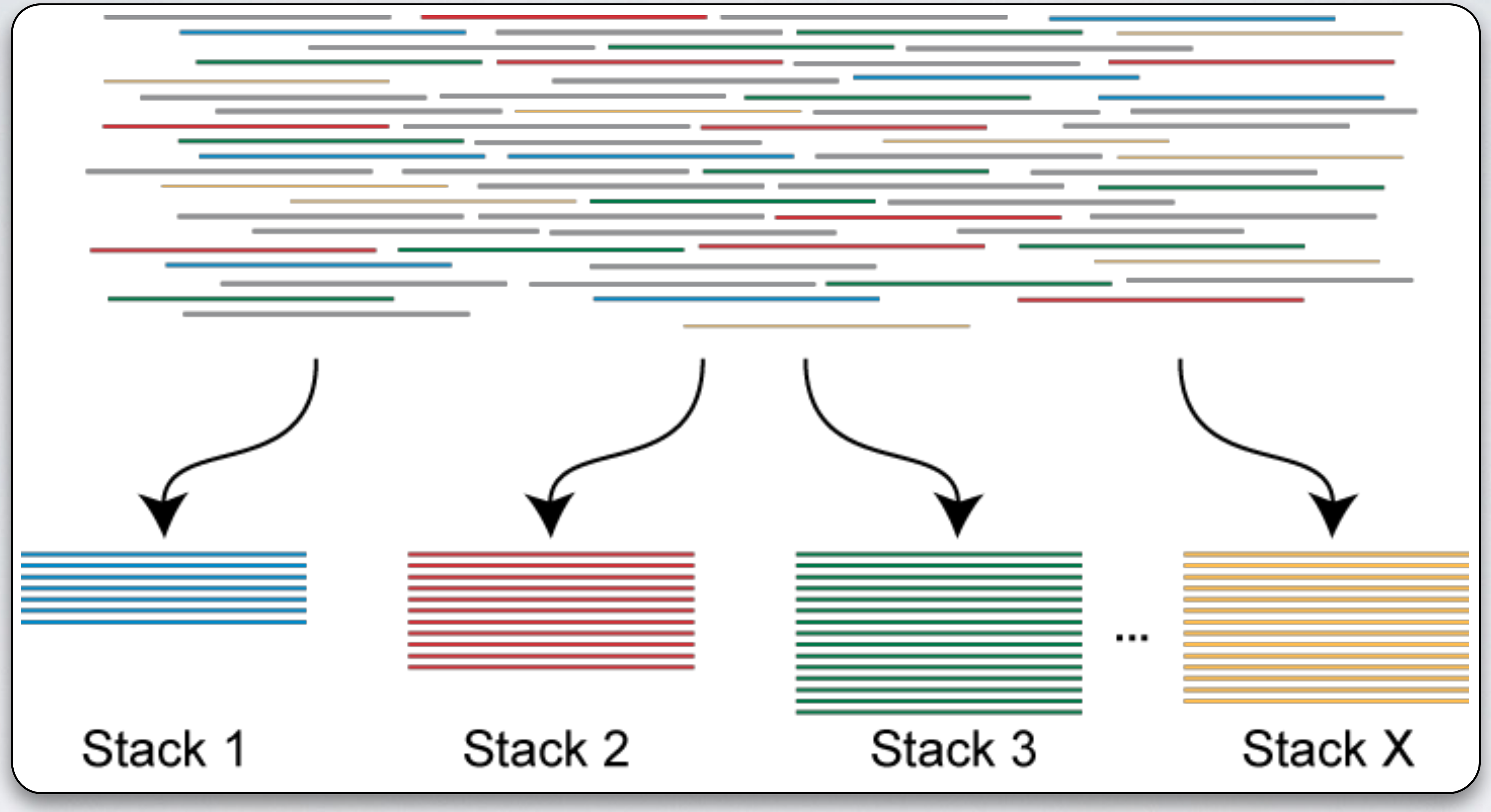
Parameters to control stack formation



Parameter Description	**`denovo_map.pl` Parameter**	**Pipeline component**	**Component Parameter**	**Default Value**
Minimum stack depth / minimum depth of coverage	`-m`	**`ustacks`**	`-m`	3
Distance allowed between stacks	`-M`	**`ustacks`**	`-M`	2
Distance allowed between catalog loci	`-n`	**`cstacks`**	`-n`	0

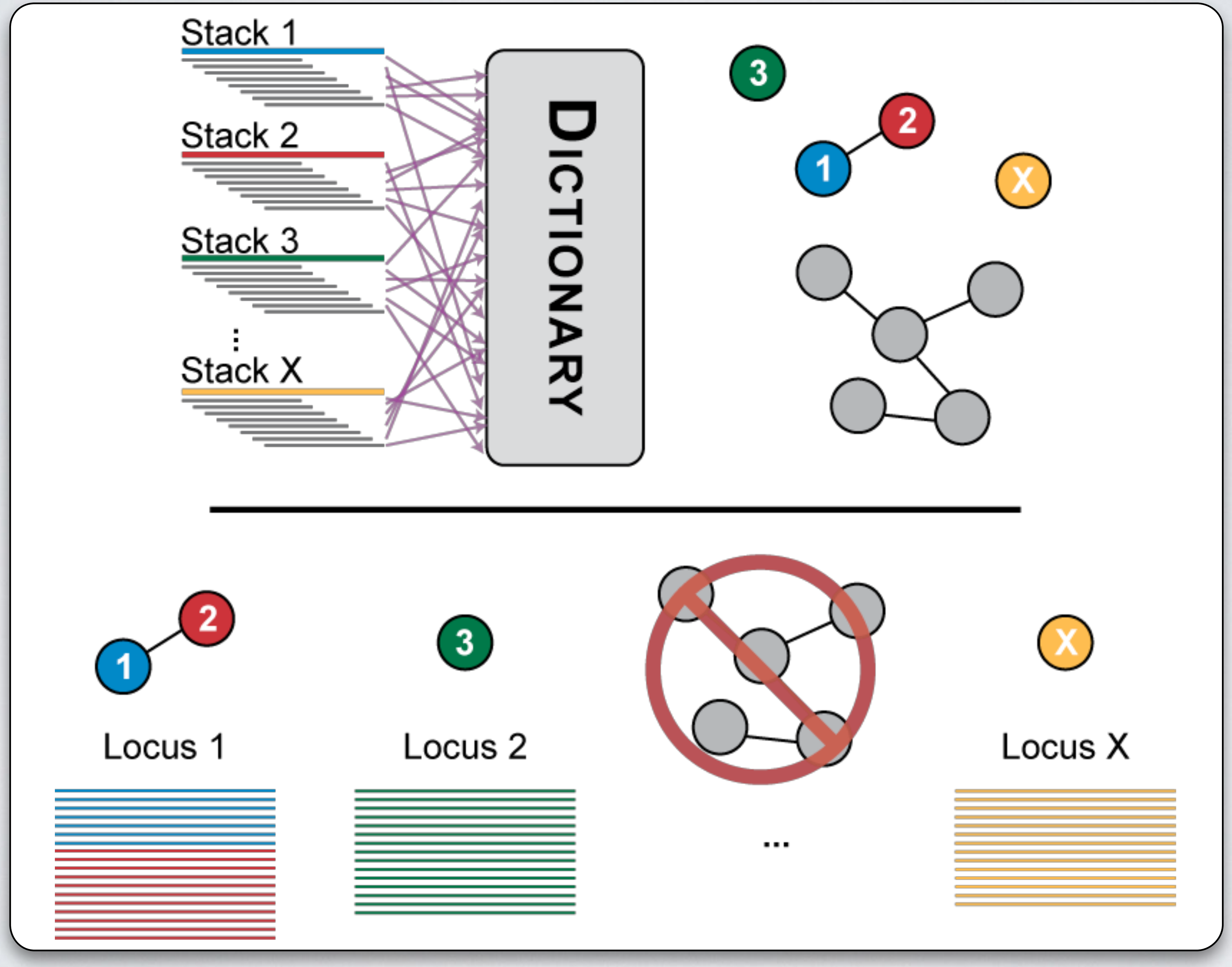
Parameters to control stack formation, ctd.

`-m <min stack depth>`



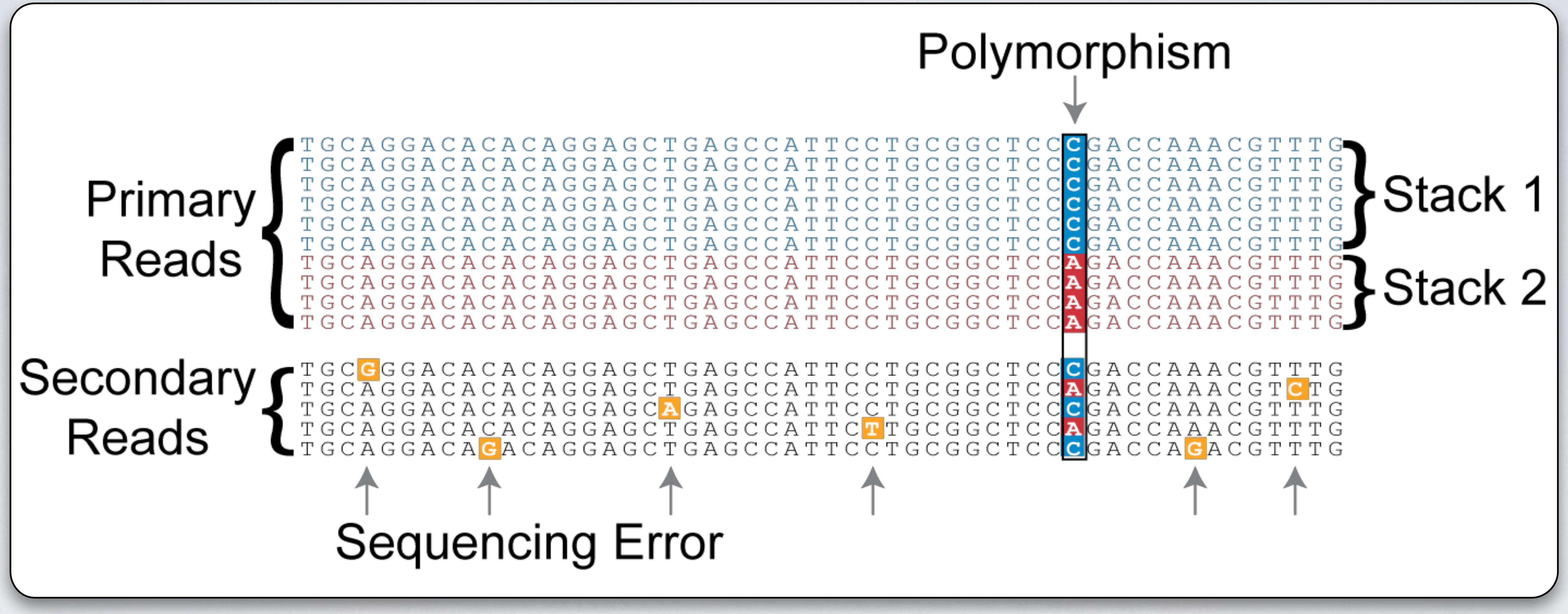
Parameters to control stack formation, ctd.

`-M <distance allowed between stacks>`



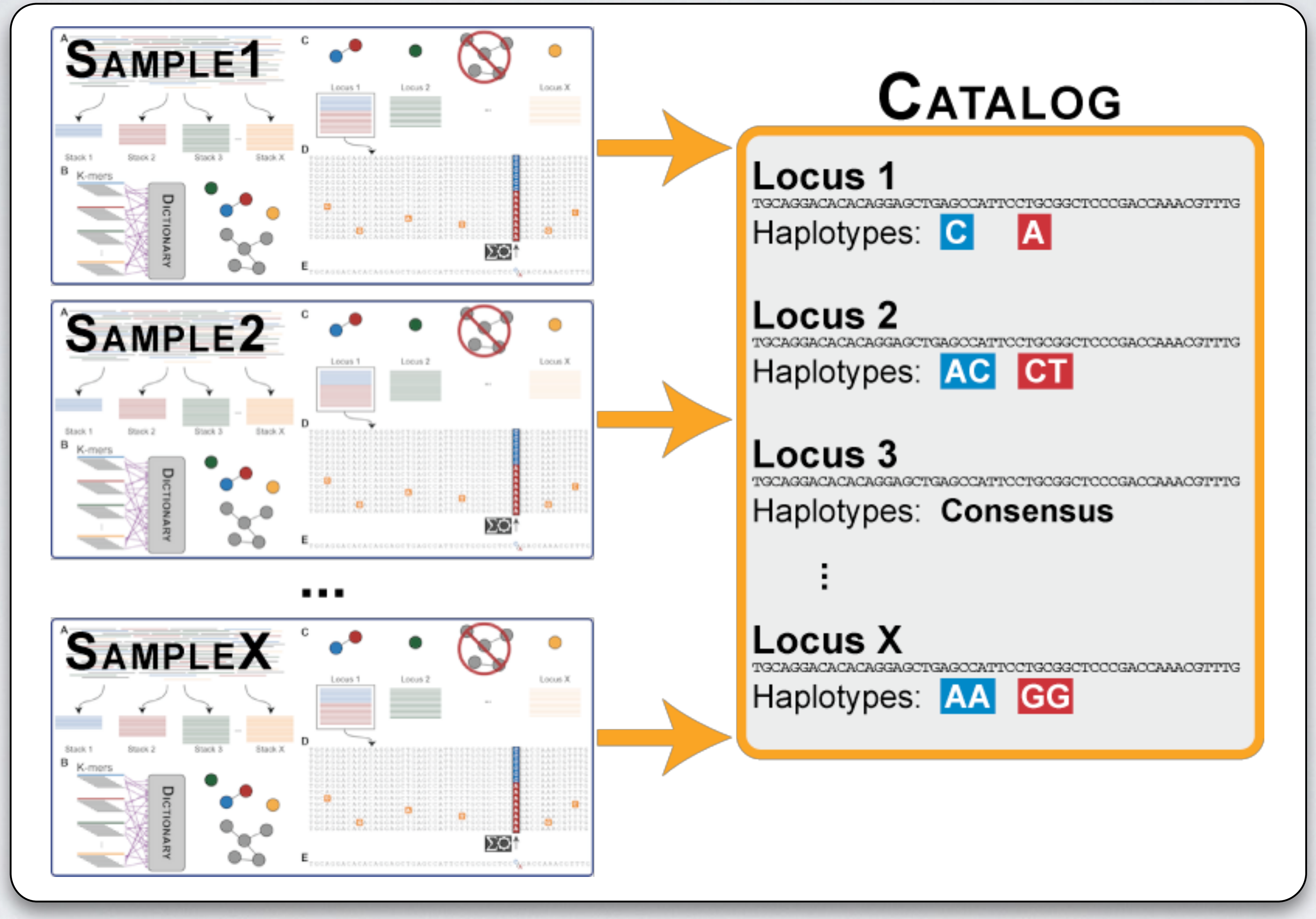
Parameters to control stack formation, ctd.

`-N <secondary read distance>`



Parameters to control stack formation, ctd.

`-n <distance between catalog loci>`



Locus 1
TGCAGGACACACAGGAGCTGAGCCATTCCTGCGGCTCCCGACCAAACGTTTG
Haplotypes: C A

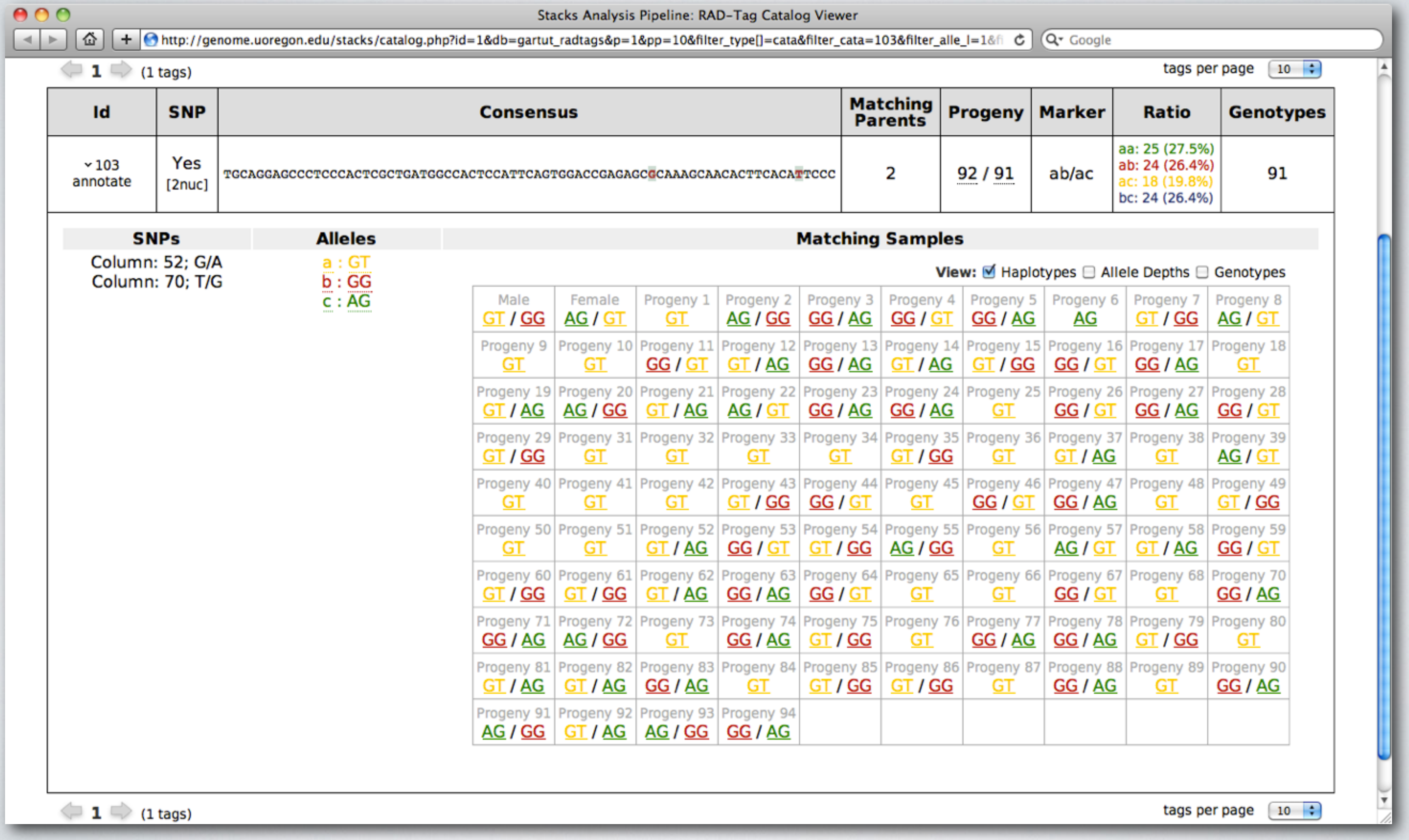
Locus 2
TGCAGGACACACAGGAGCTGAGCCATTCCTGCGGCTCCCGACCAAACGTTTG
Haplotypes: AC CT

Locus 3
TGCAGGACACACAGGAGCTGAGCCATTCCTGCGGCTCCCGACCAAACGTTTG
Haplotypes: **Consensus**

⋮

Locus X
TGCAGGACACACAGGAGCTGAGCCATTCCTGCGGCTCCCGACCAAACGTTTG
Haplotypes: AA GG

Stacks



Id	SNP	Consensus	Matching Parents	Progeny	Marker	Ratio	Genotypes
103 annotate	Yes [2nuc]	TGCAGGAGCCCTCCCACTCGCTGATGGCCACTCCATTCAGTGGACCGAGAGCGCAAAGCAACACTTCACATTCCC	2	92 / 91	ab/ac	aa: 25 (27.5%) ab: 24 (26.4%) ac: 18 (19.8%) bc: 24 (26.4%)	91

SNPs

Column: 52; G/A
Column: 70; T/G

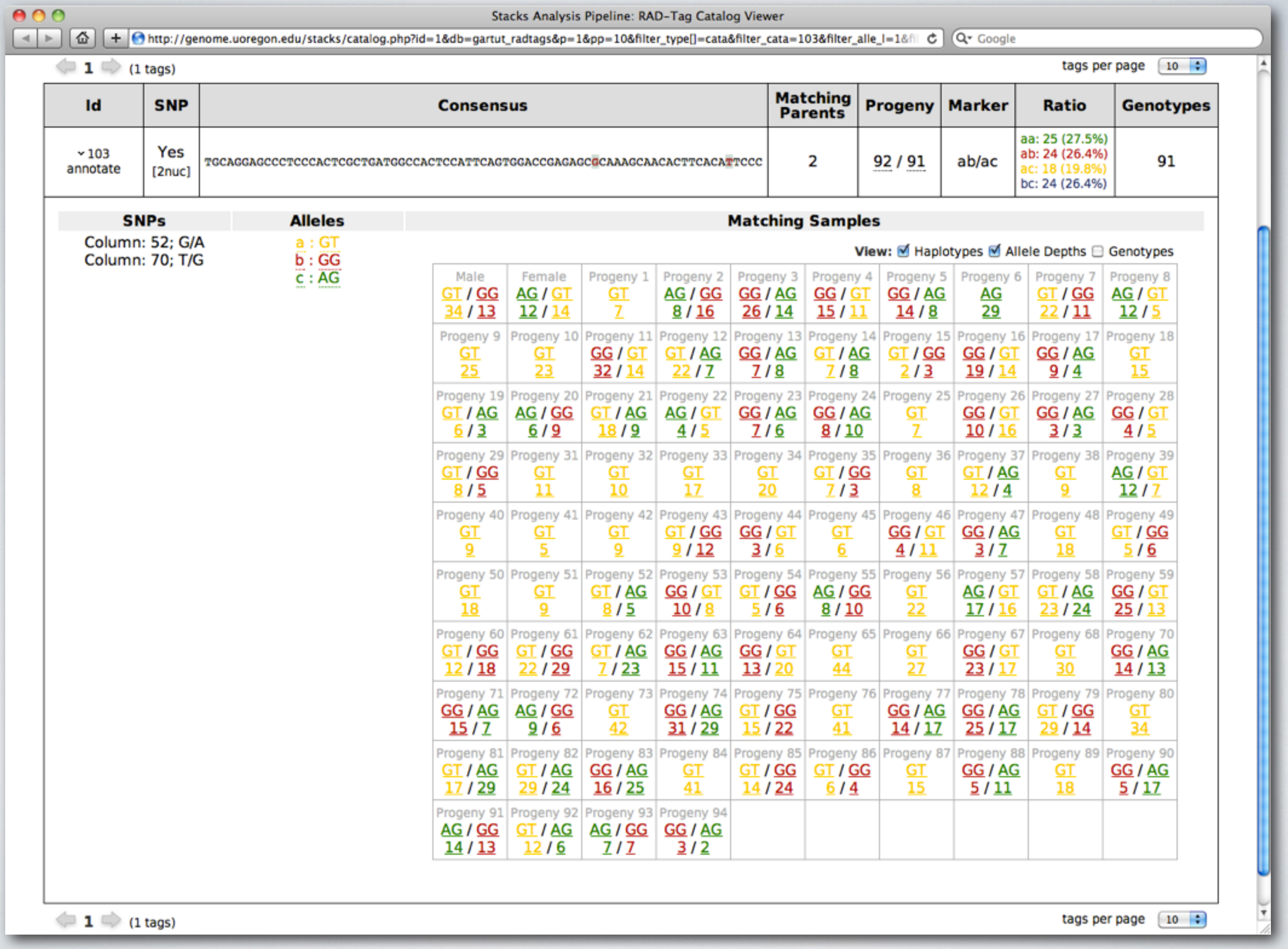
Alleles

a : GT
b : GG
c : AG

Matching Samples

View: ☑ Haplotypes ☐ Allele Depths ☐ Genotypes

Male GT / GG	Female AG / GT	Progeny 1 GT	Progeny 2 AG / GG	Progeny 3 GG / AG	Progeny 4 GG / GT	Progeny 5 GG / AG	Progeny 6 AG	Progeny 7 GT / GG	Progeny 8 AG / GT
Progeny 9 GT	Progeny 10 GT	Progeny 11 GG / GT	Progeny 12 GT / AG	Progeny 13 GG / AG	Progeny 14 GT / AG	Progeny 15 GT / GG	Progeny 16 GG / GT	Progeny 17 GG / AG	Progeny 18 GT
Progeny 19 GT / AG	Progeny 20 AG / GG	Progeny 21 GT / AG	Progeny 22 AG / GT	Progeny 23 GG / AG	Progeny 24 GG / AG	Progeny 25 GT	Progeny 26 GG / GT	Progeny 27 GG / AG	Progeny 28 GG / GT
Progeny 29 GT / GG	Progeny 31 GT	Progeny 32 GT	Progeny 33 GT	Progeny 34 GT	Progeny 35 GT / GG	Progeny 36 GT	Progeny 37 GT / AG	Progeny 38 GT	Progeny 39 AG / GT
Progeny 40 GT	Progeny 41 GT	Progeny 42 GT	Progeny 43 GT / GG	Progeny 44 GG / GT	Progeny 45 GT	Progeny 46 GG / GT	Progeny 47 GG / AG	Progeny 48 GT	Progeny 49 GT / GG
Progeny 50 GT	Progeny 51 GT	Progeny 52 GT / AG	Progeny 53 GG / GT	Progeny 54 GT / GG	Progeny 55 AG / GG	Progeny 56 GT	Progeny 57 AG / GT	Progeny 58 GT / AG	Progeny 59 GG / GT
Progeny 60 GT / GG	Progeny 61 GT / GG	Progeny 62 GT / AG	Progeny 63 GG / AG	Progeny 64 GG / GT	Progeny 65 GT	Progeny 66 GT	Progeny 67 GG / GT	Progeny 68 GT	Progeny 70 GG / AG
Progeny 71 GG / AG	Progeny 72 AG / GG	Progeny 73 GT	Progeny 74 GG / AG	Progeny 75 GT / GG	Progeny 76 GT	Progeny 77 GG / AG	Progeny 78 GG / AG	Progeny 79 GT / GG	Progeny 80 GT
Progeny 81 GT / AG	Progeny 82 GT / AG	Progeny 83 GG / AG	Progeny 84 GT	Progeny 85 GT / GG	Progeny 86 GT / GG	Progeny 87 GT	Progeny 88 GG / AG	Progeny 89 GT	Progeny 90 GG / AG
Progeny 91 AG / GG	Progeny 92 GT / AG	Progeny 93 AG / GG	Progeny 94 GG / AG						



1 (1 tags)

tags per page 10

Id	SNP	Consensus	Matching Parents	Progeny	Marker	Ratio	Genotypes
103 annotate	Yes [2nuc]	TGCAGGAGCCCTCCCACTCGCTGATGGCCACTCCATTCAGTGGACCGAGAGCGCAAAGCAACACTTCACATTCCC	2	92 / 91	ab/ac	aa: 25 (27.5%) ab: 24 (26.4%) ac: 18 (19.8%) bc: 24 (26.4%)	91

SNPs	Alleles
Column: 52; G/A	a : GT
Column: 70; T/G	b : GG
	c : AG

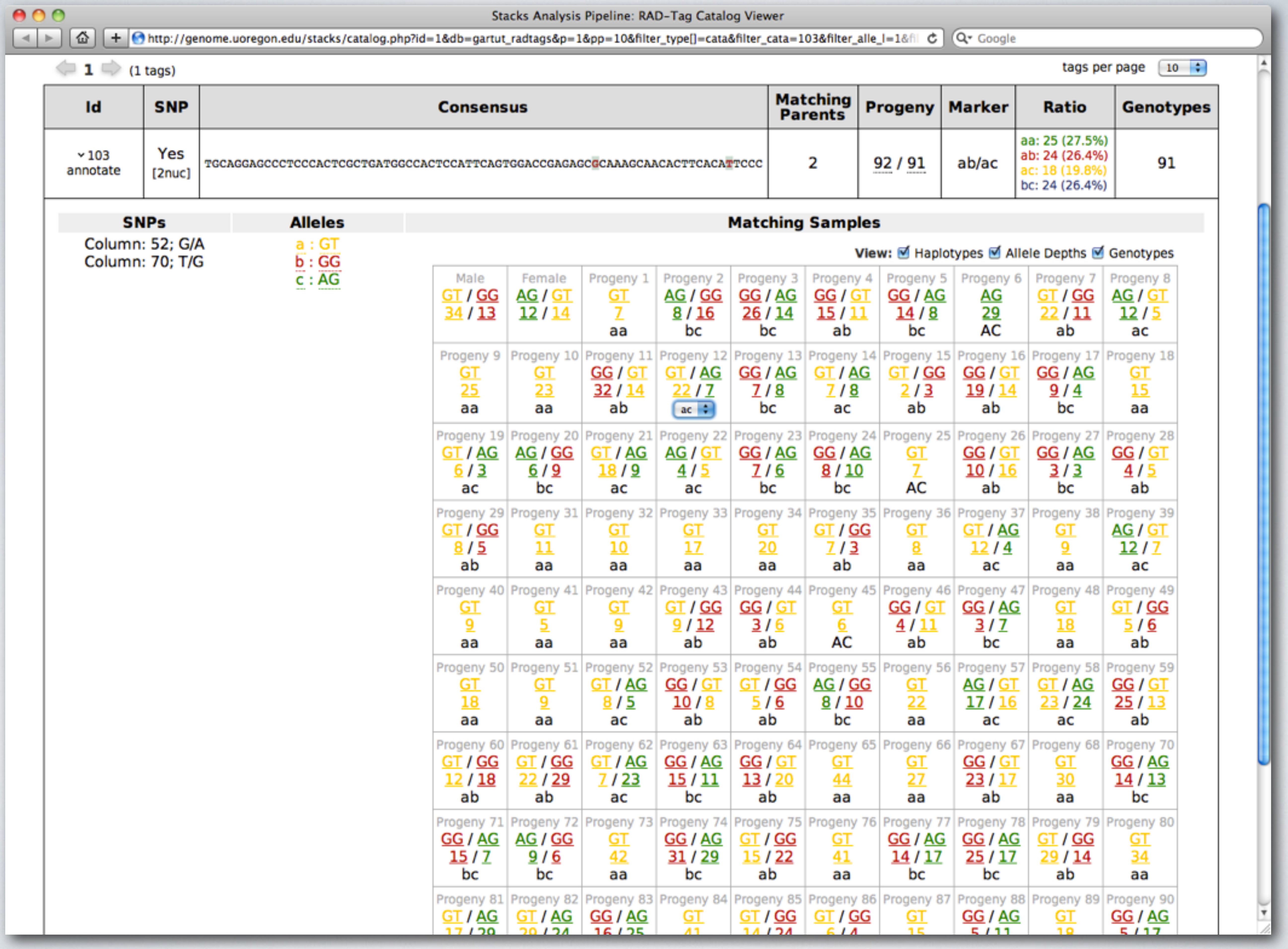
Matching Samples

View: ☑ Haplotypes ☑ Allele Depths ☐ Genotypes

Male GT / GG 34 / 13	Female AG / GT 12 / 14	Progeny 1 GT 7	Progeny 2 AG / GG 8 / 16	Progeny 3 GG / AG 26 / 14	Progeny 4 GG / GT 15 / 11	Progeny 5 GG / AG 14 / 8	Progeny 6 AG 29	Progeny 7 GT / GG 22 / 11	Progeny 8 AG / GT 12 / 5
Progeny 9 GT 25	Progeny 10 GT 23	Progeny 11 GG / GT 32 / 14	Progeny 12 GT / AG 22 / 7	Progeny 13 GG / AG 7 / 8	Progeny 14 GT / AG 7 / 8	Progeny 15 GT / GG 2 / 3	Progeny 16 GG / GT 19 / 14	Progeny 17 GG / AG 9 / 4	Progeny 18 GT 15
Progeny 19 GT / AG 6 / 3	Progeny 20 AG / GG 6 / 9	Progeny 21 GT / AG 18 / 9	Progeny 22 AG / GT 4 / 5	Progeny 23 GG / AG 7 / 6	Progeny 24 GG / AG 8 / 10	Progeny 25 GT 7	Progeny 26 GG / GT 10 / 16	Progeny 27 GG / AG 3 / 3	Progeny 28 GG / GT 4 / 5
Progeny 29 GT / GG 8 / 5	Progeny 31 GT 11	Progeny 32 GT 10	Progeny 33 GT 17	Progeny 34 GT 20	Progeny 35 GT / GG 7 / 3	Progeny 36 GT 8	Progeny 37 GT / AG 12 / 4	Progeny 38 GT 9	Progeny 39 AG / GT 12 / 7
Progeny 40 GT 9	Progeny 41 GT 5	Progeny 42 GT 9	Progeny 43 GT / GG 9 / 12	Progeny 44 GG / GT 3 / 6	Progeny 45 GT 6	Progeny 46 GG / GT 4 / 11	Progeny 47 GG / AG 3 / 7	Progeny 48 GT 18	Progeny 49 GT / GG 5 / 6
Progeny 50 GT 18	Progeny 51 GT 9	Progeny 52 GT / AG 8 / 5	Progeny 53 GG / GT 10 / 8	Progeny 54 GT / GG 5 / 6	Progeny 55 AG / GG 8 / 10	Progeny 56 GT 22	Progeny 57 AG / GT 17 / 16	Progeny 58 GT / AG 23 / 24	Progeny 59 GG / GT 25 / 13
Progeny 60 GT / GG 12 / 18	Progeny 61 GT / GG 22 / 29	Progeny 62 GT / AG 7 / 23	Progeny 63 GG / AG 15 / 11	Progeny 64 GG / GT 13 / 20	Progeny 65 GT 44	Progeny 66 GT 27	Progeny 67 GG / GT 23 / 17	Progeny 68 GT 30	Progeny 70 GG / AG 14 / 13
Progeny 71 GG / AG 15 / 7	Progeny 72 AG / GG 9 / 6	Progeny 73 GT 42	Progeny 74 GG / AG 31 / 29	Progeny 75 GT / GG 15 / 22	Progeny 76 GT 41	Progeny 77 GG / AG 14 / 17	Progeny 78 GG / AG 25 / 17	Progeny 79 GT / GG 29 / 14	Progeny 80 GT 34
Progeny 81 GT / AG 17 / 29	Progeny 82 GT / AG 29 / 24	Progeny 83 GG / AG 16 / 25	Progeny 84 GT 41	Progeny 85 GT / GG 14 / 24	Progeny 86 GT / GG 6 / 4	Progeny 87 GT 15	Progeny 88 GG / AG 5 / 11	Progeny 89 GT 18	Progeny 90 GG / AG 5 / 17
Progeny 91 AG / GG 14 / 13	Progeny 92 GT / AG 12 / 6	Progeny 93 AG / GG 7 / 7	Progeny 94 GG / AG 3 / 2						

1 (1 tags)

tags per page 10



Id	SNP	Consensus	Matching Parents	Progeny	Marker	Ratio	Genotypes
103 annotate	Yes [2nuc]	TGCAGGAGCCCTCCCACTCGCTGATGGCCACTCCATTCAGTGGACCGAGAGCGCAAAGCAACACTTCACATTCCC	2	92 / 91	ab/ac	aa: 25 (27.5%) ab: 24 (26.4%) ac: 18 (19.8%) bc: 24 (26.4%)	91

SNPs

Column: 52; G/A
Column: 70; T/G

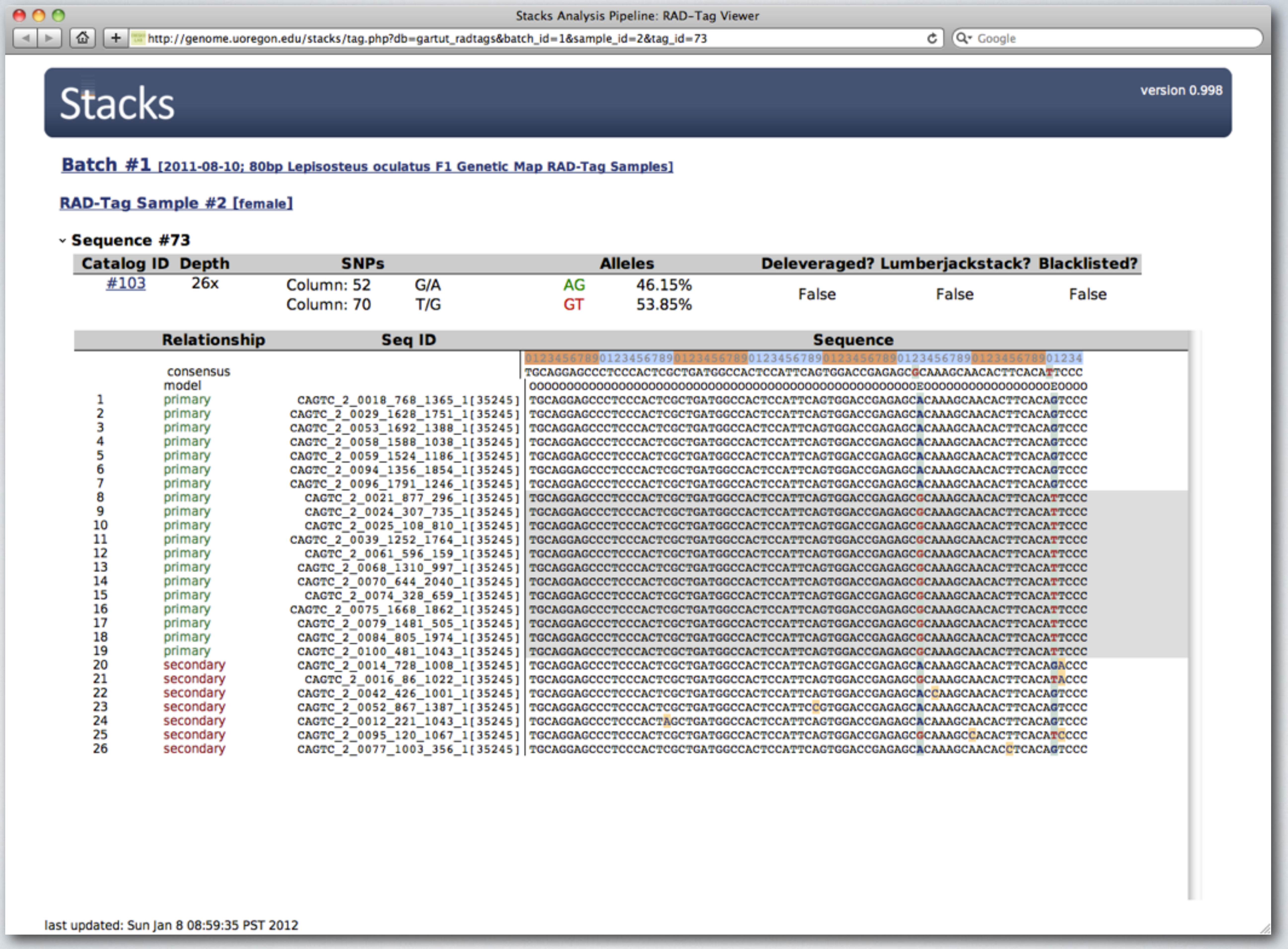
Alleles

a : GT
b : GG
c : AG

Matching Samples

View: ☑ Haplotypes ☑ Allele Depths ☑ Genotypes

Male GT / GG 34 / 13	Female AG / GT 12 / 14	Progeny 1 GT 7 aa	Progeny 2 AG / GG 8 / 16 bc	Progeny 3 GG / AG 26 / 14 bc	Progeny 4 GG / GT 15 / 11 ab	Progeny 5 GG / AG 14 / 8 bc	Progeny 6 AG 29 AC	Progeny 7 GT / GG 22 / 11 ab	Progeny 8 AG / GT 12 / 5 ac
Progeny 9 GT 25 aa	Progeny 10 GT 23 aa	Progeny 11 GG / GT 32 / 14 ab	Progeny 12 GT / AG 22 / 7 ac	Progeny 13 GG / AG 7 / 8 bc	Progeny 14 GT / AG 7 / 8 ac	Progeny 15 GT / GG 2 / 3 ab	Progeny 16 GG / GT 19 / 14 ab	Progeny 17 GG / AG 9 / 4 bc	Progeny 18 GT 15 aa
Progeny 19 GT / AG 6 / 3 ac	Progeny 20 AG / GG 6 / 9 bc	Progeny 21 GT / AG 18 / 9 ac	Progeny 22 AG / GT 4 / 5 ac	Progeny 23 GG / AG 7 / 6 bc	Progeny 24 GG / AG 8 / 10 bc	Progeny 25 GT 7 AC	Progeny 26 GG / GT 10 / 16 ab	Progeny 27 GG / AG 3 / 3 bc	Progeny 28 GG / GT 4 / 5 ab
Progeny 29 GT / GG 8 / 5 ab	Progeny 31 GT 11 aa	Progeny 32 GT 10 aa	Progeny 33 GT 17 aa	Progeny 34 GT 20 aa	Progeny 35 GT / GG 7 / 3 ab	Progeny 36 GT 8 aa	Progeny 37 GT / AG 12 / 4 ac	Progeny 38 GT 9 aa	Progeny 39 AG / GT 12 / 7 ac
Progeny 40 GT 9 aa	Progeny 41 GT 5 aa	Progeny 42 GT 9 aa	Progeny 43 GT / GG 9 / 12 ab	Progeny 44 GG / GT 3 / 6 ab	Progeny 45 GT 6 AC	Progeny 46 GG / GT 4 / 11 ab	Progeny 47 GG / AG 3 / 7 bc	Progeny 48 GT 18 aa	Progeny 49 GT / GG 5 / 6 ab
Progeny 50 GT 18 aa	Progeny 51 GT 9 aa	Progeny 52 GT / AG 8 / 5 ac	Progeny 53 GG / GT 10 / 8 ab	Progeny 54 GT / GG 5 / 6 ab	Progeny 55 AG / GG 8 / 10 bc	Progeny 56 GT 22 aa	Progeny 57 AG / GT 17 / 16 ac	Progeny 58 GT / AG 23 / 24 ac	Progeny 59 GG / GT 25 / 13 ab
Progeny 60 GT / GG 12 / 18 ab	Progeny 61 GT / GG 22 / 29 ab	Progeny 62 GT / AG 7 / 23 ac	Progeny 63 GG / AG 15 / 11 bc	Progeny 64 GG / GT 13 / 20 ab	Progeny 65 GT 44 aa	Progeny 66 GT 27 aa	Progeny 67 GG / GT 23 / 17 ab	Progeny 68 GT 30 aa	Progeny 70 GG / AG 14 / 13 bc
Progeny 71 GG / AG 15 / 7 bc	Progeny 72 AG / GG 9 / 6 bc	Progeny 73 GT 42 aa	Progeny 74 GG / AG 31 / 29 bc	Progeny 75 GT / GG 15 / 22 ab	Progeny 76 GT 41 aa	Progeny 77 GG / AG 14 / 17 bc	Progeny 78 GG / AG 25 / 17 bc	Progeny 79 GT / GG 29 / 14 ab	Progeny 80 GT 34 aa
Progeny 81 GT / AG 17 / 29	Progeny 82 GT / AG 29 / 24	Progeny 83 GG / AG 16 / 25	Progeny 84 GT 41	Progeny 85 GT / GG 14 / 24	Progeny 86 GT / GG 6 / 4	Progeny 87 GT 15	Progeny 88 GG / AG 5 / 11	Progeny 89 GT 18	Progeny 90 GG / AG 5 / 17



Stacks Analysis Pipeline: RAD-Tag Viewer

http://genome.uoregon.edu/stacks/tag.php?db=gartut_radtags&batch_id=1&sample_id=2&tag_id=73

Stacks

version 0.998

Batch #1 [2011-08-10; 80bp Lepisosteus oculatus F1 Genetic Map RAD-Tag Samples]

RAD-Tag Sample #2 [female]

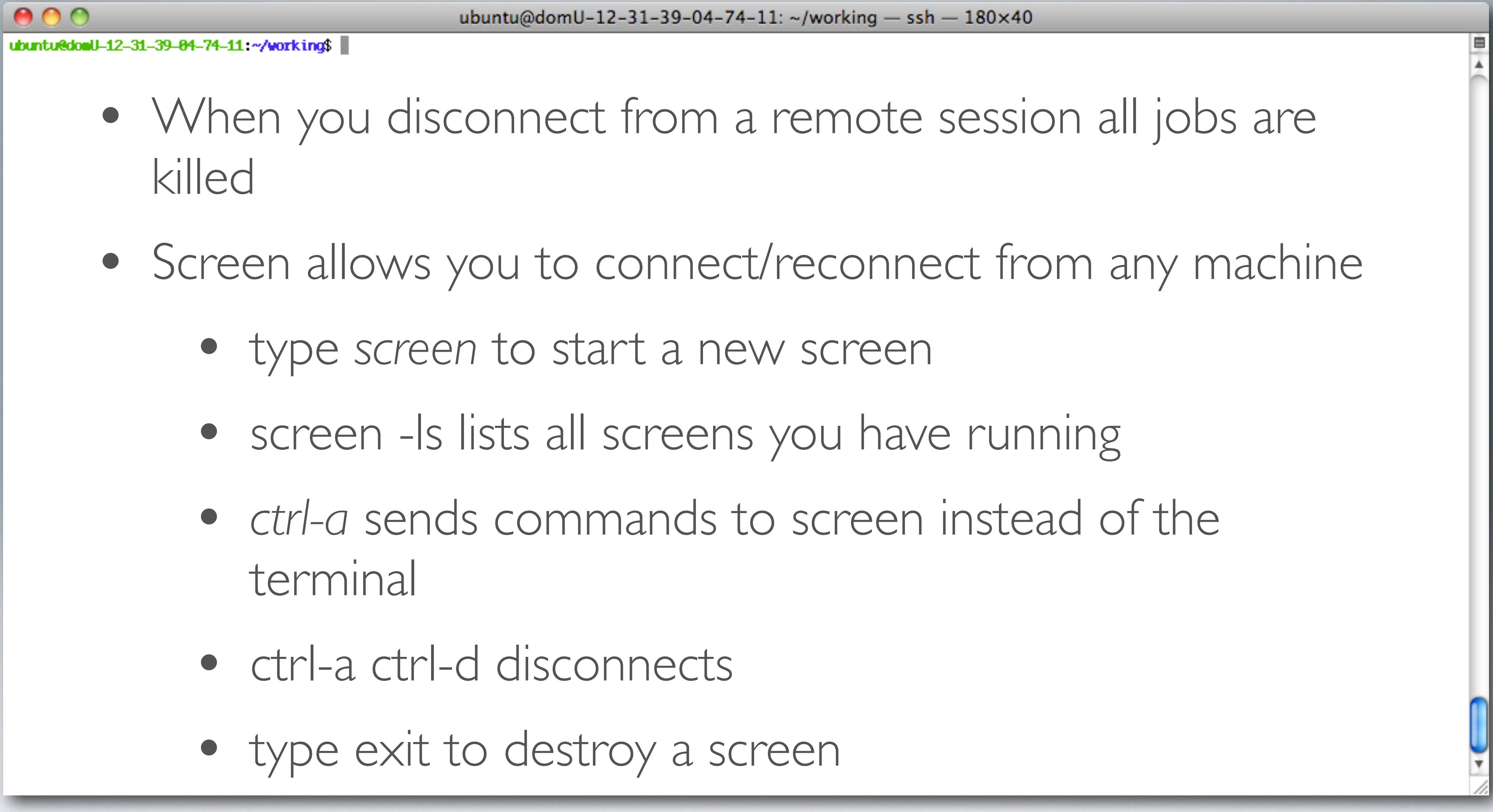
Sequence #73

Catalog ID	Depth	SNPs		Alleles		Deleveraged?	Lumberjackstack?	Blacklisted?
#103	26x	Column: 52	G/A	AG	46.15%	False	False	False
		Column: 70	T/G	GT	53.85%			

	Relationship	Seq ID	Sequence
			012345678901234567890123456789012345678901234567890123456789012345678901234
	consensus		TGCAGGAGCCCTCCCACTCGCTGATGGCCACTCCATTCAGTGGACCGAGAGCGCAAAGCAACACTTCACATTCCC
	model		OOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOEOOOOOOOOOOOOOOOOOEOOOO
1	primary	CAGTC_2_0018_768_1365_1[35245]	TGCAGGAGCCCTCCCACTCGCTGATGGCCACTCCATTCAGTGGACCGAGAGCACAAAGCAACACTTCACAGTCCC
2	primary	CAGTC_2_0029_1628_1751_1[35245]	TGCAGGAGCCCTCCCACTCGCTGATGGCCACTCCATTCAGTGGACCGAGAGCACAAAGCAACACTTCACAGTCCC
3	primary	CAGTC_2_0053_1692_1388_1[35245]	TGCAGGAGCCCTCCCACTCGCTGATGGCCACTCCATTCAGTGGACCGAGAGCACAAAGCAACACTTCACAGTCCC
4	primary	CAGTC_2_0058_1588_1038_1[35245]	TGCAGGAGCCCTCCCACTCGCTGATGGCCACTCCATTCAGTGGACCGAGAGCACAAAGCAACACTTCACAGTCCC
5	primary	CAGTC_2_0059_1524_1186_1[35245]	TGCAGGAGCCCTCCCACTCGCTGATGGCCACTCCATTCAGTGGACCGAGAGCACAAAGCAACACTTCACAGTCCC
6	primary	CAGTC_2_0094_1356_1854_1[35245]	TGCAGGAGCCCTCCCACTCGCTGATGGCCACTCCATTCAGTGGACCGAGAGCACAAAGCAACACTTCACAGTCCC
7	primary	CAGTC_2_0096_1791_1246_1[35245]	TGCAGGAGCCCTCCCACTCGCTGATGGCCACTCCATTCAGTGGACCGAGAGCACAAAGCAACACTTCACAGTCCC
8	primary	CAGTC_2_0021_877_296_1[35245]	TGCAGGAGCCCTCCCACTCGCTGATGGCCACTCCATTCAGTGGACCGAGAGCGCAAAGCAACACTTCACATTCCC
9	primary	CAGTC_2_0024_307_735_1[35245]	TGCAGGAGCCCTCCCACTCGCTGATGGCCACTCCATTCAGTGGACCGAGAGCGCAAAGCAACACTTCACATTCCC
10	primary	CAGTC_2_0025_108_810_1[35245]	TGCAGGAGCCCTCCCACTCGCTGATGGCCACTCCATTCAGTGGACCGAGAGCGCAAAGCAACACTTCACATTCCC
11	primary	CAGTC_2_0039_1252_1764_1[35245]	TGCAGGAGCCCTCCCACTCGCTGATGGCCACTCCATTCAGTGGACCGAGAGCGCAAAGCAACACTTCACATTCCC
12	primary	CAGTC_2_0061_596_159_1[35245]	TGCAGGAGCCCTCCCACTCGCTGATGGCCACTCCATTCAGTGGACCGAGAGCGCAAAGCAACACTTCACATTCCC
13	primary	CAGTC_2_0068_1310_997_1[35245]	TGCAGGAGCCCTCCCACTCGCTGATGGCCACTCCATTCAGTGGACCGAGAGCGCAAAGCAACACTTCACATTCCC
14	primary	CAGTC_2_0070_644_2040_1[35245]	TGCAGGAGCCCTCCCACTCGCTGATGGCCACTCCATTCAGTGGACCGAGAGCGCAAAGCAACACTTCACATTCCC
15	primary	CAGTC_2_0074_328_659_1[35245]	TGCAGGAGCCCTCCCACTCGCTGATGGCCACTCCATTCAGTGGACCGAGAGCGCAAAGCAACACTTCACATTCCC
16	primary	CAGTC_2_0075_1668_1862_1[35245]	TGCAGGAGCCCTCCCACTCGCTGATGGCCACTCCATTCAGTGGACCGAGAGCGCAAAGCAACACTTCACATTCCC
17	primary	CAGTC_2_0079_1481_505_1[35245]	TGCAGGAGCCCTCCCACTCGCTGATGGCCACTCCATTCAGTGGACCGAGAGCGCAAAGCAACACTTCACATTCCC
18	primary	CAGTC_2_0084_805_1974_1[35245]	TGCAGGAGCCCTCCCACTCGCTGATGGCCACTCCATTCAGTGGACCGAGAGCGCAAAGCAACACTTCACATTCCC
19	primary	CAGTC_2_0100_481_1043_1[35245]	TGCAGGAGCCCTCCCACTCGCTGATGGCCACTCCATTCAGTGGACCGAGAGCGCAAAGCAACACTTCACATTCCC
20	secondary	CAGTC_2_0014_728_1008_1[35245]	TGCAGGAGCCCTCCCACTCGCTGATGGCCACTCCATTCAGTGGACCGAGAGCACAAAGCAACACTTCACAGACCC
21	secondary	CAGTC_2_0016_86_1022_1[35245]	TGCAGGAGCCCTCCCACTCGCTGATGGCCACTCCATTCAGTGGACCGAGAGCGCAAAGCAACACTTCACATACCC
22	secondary	CAGTC_2_0042_426_1001_1[35245]	TGCAGGAGCCCTCCCACTCGCTGATGGCCACTCCATTCAGTGGACCGAGAGCACCAAGCAACACTTCACAGTCCC
23	secondary	CAGTC_2_0052_867_1387_1[35245]	TGCAGGAGCCCTCCCACTCGCTGATGGCCACTCCATTCCGTGGACCGAGAGCACAAAGCAACACTTCACAGTCCC
24	secondary	CAGTC_2_0012_221_1043_1[35245]	TGCAGGAGCCCTCCCACTAGCTGATGGCCACTCCATTCAGTGGACCGAGAGCACAAAGCAACACTTCACAGTCCC
25	secondary	CAGTC_2_0095_120_1067_1[35245]	TGCAGGAGCCCTCCCACTCGCTGATGGCCACTCCATTCAGTGGACCGAGAGCGCAAAGCCACACTTCACATCCCC
26	secondary	CAGTC_2_0077_1003_356_1[35245]	TGCAGGAGCCCTCCCACTCGCTGATGGCCACTCCATTCAGTGGACCGAGAGCACAAAGCAACACCTCACAGTCCC

last updated: Sun Jan 8 08:59:35 PST 2012

Screen



```
ubuntu@domU-12-31-39-04-74-11:~/working$
```

- When you disconnect from a remote session all jobs are killed
- Screen allows you to connect/reconnect from any machine
    - type *screen* to start a new screen
    - screen -ls lists all screens you have running
    - *ctrl-a* sends commands to screen instead of the terminal
    - ctrl-a ctrl-d disconnects
    - type exit to destroy a screen