

Analytics Report: LEggert_UMissouri_Bass_20180409–01669

September 04, 2018

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1. Introduction

Dear Floragenex Client,

Since 2008, the Floragenex genomics team has proudly provided end to end, full service commercial support for Restriction Site Associated DNA Sequencing (RAD-Seq) marker discovery, genotyping and analysis projects around the world. To date, we have completed over 200 projects in 75 plus species, and have facilitated a wide range of peer-reviewed publications in molecular genetics research.

Please find attached your customized project analysis report. This report was generated using a composite of software tools that have been optimized for bioinformatics analysis of RAD-Seq data. If you have any questions about this report or our analysis procedures, please do not hesitate to contact us. We look forward to helping advance your research.

Best regards,



Rick Nipper, Ph.D.
President and CEO
Floragenex, Inc.

2. Sequencing QA/QC

Section 2.1. FASTQ_Sequence_Files_QAQC_Report

Illumina Sequencing FASTQ Quality Control / Quality Assurance Report

Project: LEggert_UMissouri_Bass_20180409-01669

Directory: FASTQ_Sequence_Files

A) Information

Project Name: LEggert_UMissouri_Bass_20180409-01669

Sequence Directory: FASTQ_Sequence_Files

Analysis Date: 2018-08-31T21:02:23

Enzyme: PstI

Sequencing Chemistry: 1x95bp

Number of Samples in Project: 96

B) Statistics

Total Reads in Project: 1076117933

Mean Reads per Sample: 11209561.8

Median Reads per Sample: 11483651.5

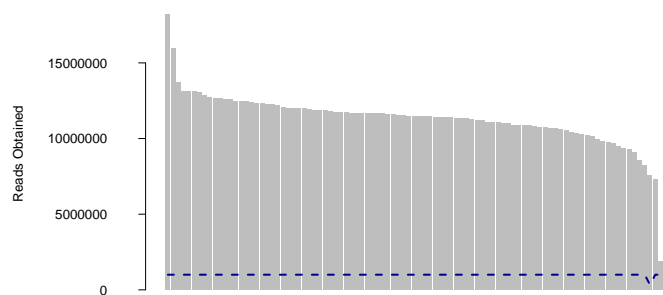
Read Goal per Sample: 1000000

Std. Dev of Reads per Sample: 2063521.9

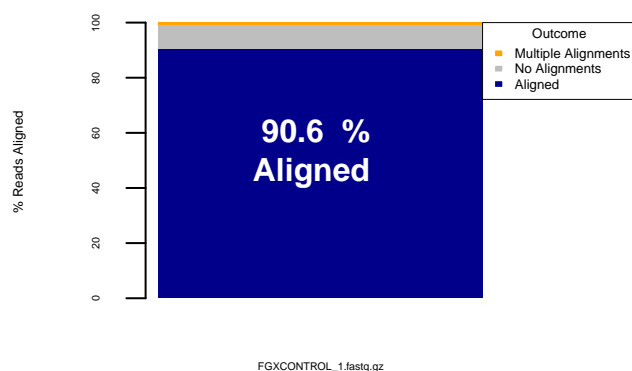
Number of Samples Meeting Read Goals: 94

Sequencing Coefficient of Variation: 0.18

C) Figure 1: Sequencing Distribution



D) Figure 2: S. bayanus (yeast) Sequence Control Performance



E) Individual Sample Sequencing Performance

| Sample Name | NGS Reads | Read Goal | RE | NGS Type | Sequencing Distribution | RAD Clusters (5x to 1000x) | Coverage Distribution | Coverages Low: Quantile Median: Upper: Quantile | Median Phred QScore vs Read Length |
|--------------------|-----------|-----------|------|----------|-------------------------|----------------------------|-----------------------|--|------------------------------------|
| | | | | | 0 % 100 % of goal | | 5x 15x 25x 100x 250x | | |
| GLVR11_1.fastq.gz | 18217476 | 1000000 | PstI | 1x95bp | | 501562 | | 9:20:40 | |
| SPRMO19_1.fastq.gz | 15992260 | 1000000 | PstI | 1x95bp | | 459332 | | 8:17:35 | |
| BFC06_1.fastq.gz | 13700609 | 1000000 | PstI | 1x95bp | | 410515 | | 9:18:34 | |
| GRSPB36_1.fastq.gz | 13118659 | 1000000 | PstI | 1x95bp | | 394579 | | 9:18:34 | |
| AR21_1.fastq.gz | 13117475 | 1000000 | PstI | 1x95bp | | 443463 | | 8:14:29 | |
| SKIA04_1.fastq.gz | 13102064 | 1000000 | PstI | 1x95bp | | 363280 | | 9:18:36 | |
| AT12_1.fastq.gz | 13078746 | 1000000 | PstI | 1x95bp | | 433319 | | 9:18:31 | |
| BC09_1.fastq.gz | 12882477 | 1000000 | PstI | 1x95bp | | 457298 | | 8:16:28 | |
| NOIS08_1.fastq.gz | 12754802 | 1000000 | PstI | 1x95bp | | 405543 | | 9:17:32 | |
| BFC02_1.fastq.gz | 12683495 | 1000000 | PstI | 1x95bp | | 419397 | | 9:17:31 | |
| BFORK02_1.fastq.gz | 12679586 | 1000000 | PstI | 1x95bp | | 421942 | | 8:15:30 | |
| BFC10_1.fastq.gz | 12609609 | 1000000 | PstI | 1x95bp | | 497601 | | 8:15:24 | |
| GRSPB50_1.fastq.gz | 12597697 | 1000000 | PstI | 1x95bp | | 432386 | | 8:16:29 | |
| ER17_1.fastq.gz | 12484195 | 1000000 | PstI | 1x95bp | | 433756 | | 9:17:29 | |
| SKIA09_1.fastq.gz | 12473333 | 1000000 | PstI | 1x95bp | | 416697 | | 9:16:30 | |
| HC44_1.fastq.gz | 12452292 | 1000000 | PstI | 1x95bp | | 417921 | | 8:16:30 | |
| BC14_1.fastq.gz | 12372444 | 1000000 | PstI | 1x95bp | | 419244 | | 9:16:29 | |
| ER20_1.fastq.gz | 12350664 | 1000000 | PstI | 1x95bp | | 449118 | | 9:16:28 | |
| AT02_1.fastq.gz | 12344293 | 1000000 | PstI | 1x95bp | | 433462 | | 9:17:29 | |
| AR18_1.fastq.gz | 12287384 | 1000000 | PstI | 1x95bp | | 418251 | | 8:16:30 | |
| AT09_1.fastq.gz | 12281374 | 1000000 | PstI | 1x95bp | | 403888 | | 9:17:31 | |
| NOIS18_1.fastq.gz | 12170181 | 1000000 | PstI | 1x95bp | | 402450 | | 9:17:31 | |
| MI421_1.fastq.gz | 12053883 | 1000000 | PstI | 1x95bp | | 388846 | | 10:19:32 | |
| ER33_1.fastq.gz | 12023608 | 1000000 | PstI | 1x95bp | | 407655 | | 9:16:30 | |
| HC43_1.fastq.gz | 12021025 | 1000000 | PstI | 1x95bp | | 402424 | | 9:18:31 | |
| AR16_1.fastq.gz | 12002934 | 1000000 | PstI | 1x95bp | | 403305 | | 8:15:30 | |
| MI425_1.fastq.gz | 11988170 | 1000000 | PstI | 1x95bp | | 408991 | | 9:17:30 | |
| BFC49_1.fastq.gz | 11899052 | 1000000 | PstI | 1x95bp | | 414379 | | 9:17:29 | |
| BC01_1.fastq.gz | 11868958 | 1000000 | PstI | 1x95bp | | 402893 | | 9:17:30 | |
| STOCK06_1.fastq.gz | 11841730 | 1000000 | PstI | 1x95bp | | 393467 | | 8:15:28 | |
| GRSPB41_1.fastq.gz | 11832689 | 1000000 | PstI | 1x95bp | | 398954 | | 8:16:30 | |
| SPVW07_1.fastq.gz | 11814887 | 1000000 | PstI | 1x95bp | | 371497 | | 8:16:31 | |
| SPVW05_1.fastq.gz | 11760746 | 1000000 | PstI | 1x95bp | | 391294 | | 8:15:30 | |
| AT08_1.fastq.gz | 11731028 | 1000000 | PstI | 1x95bp | | 428865 | | 8:15:28 | |
| GRSPB51_1.fastq.gz | 11730184 | 1000000 | PstI | 1x95bp | | 408032 | | 8:15:29 | |
| BC07_1.fastq.gz | 11693232 | 1000000 | PstI | 1x95bp | | 429869 | | 8:15:27 | |
| AT05_1.fastq.gz | 11686746 | 1000000 | PstI | 1x95bp | | 410440 | | 8:16:28 | |
| GRSPB39_1.fastq.gz | 11674383 | 1000000 | PstI | 1x95bp | | 379090 | | 8:14:29 | |
| BC08_1.fastq.gz | 11671727 | 1000000 | PstI | 1x95bp | | 437159 | | 8:14:26 | |
| GRSPB03_1.fastq.gz | 11665906 | 1000000 | PstI | 1x95bp | | 404952 | | 8:16:29 | |
| NOIS07_1.fastq.gz | 11653095 | 1000000 | PstI | 1x95bp | | 389238 | | 9:17:31 | |
| STOCK03_1.fastq.gz | 11648079 | 1000000 | PstI | 1x95bp | | 360428 | | 9:17:33 | |
| MI420_1.fastq.gz | 11619901 | 1000000 | PstI | 1x95bp | | 404812 | | 9:17:29 | |
| AR29_1.fastq.gz | 11592215 | 1000000 | PstI | 1x95bp | | 421544 | | 8:14:27 | |
| GRSPB35_1.fastq.gz | 11547795 | 1000000 | PstI | 1x95bp | | 401880 | | 8:15:29 | |
| GRSPB52_1.fastq.gz | 11546152 | 1000000 | PstI | 1x95bp | | 423773 | | 8:16:28 | |
| BFORK49_1.fastq.gz | 11486097 | 1000000 | PstI | 1x95bp | | 417428 | | 8:15:28 | |
| SPVW12_1.fastq.gz | 11484081 | 1000000 | PstI | 1x95bp | | 386707 | | 8:16:30 | |
| TBLR02_1.fastq.gz | 11483222 | 1000000 | PstI | 1x95bp | | 427529 | | 8:15:27 | |
| SPRMO11_1.fastq.gz | 11450594 | 1000000 | PstI | 1x95bp | | 414262 | | 7:13:26 | |
| ER35_1.fastq.gz | 11438869 | 1000000 | PstI | 1x95bp | | 419289 | | 8:15:27 | |
| MI422_1.fastq.gz | 11384414 | 1000000 | PstI | 1x95bp | | 375151 | | 9:17:31 | |
| GRSPB37_1.fastq.gz | 11380653 | 1000000 | PstI | 1x95bp | | 426393 | | 8:15:27 | |
| BP07_1.fastq.gz | 11376973 | 1000000 | PstI | 1x95bp | | 412819 | | 8:15:27 | |
| SPVW02_1.fastq.gz | 11370210 | 1000000 | PstI | 1x95bp | | 393795 | | 9:16:29 | |
| GLVR4_1.fastq.gz | 11352894 | 1000000 | PstI | 1x95bp | | 409009 | | 8:14:27 | |
| SPRMO49_1.fastq.gz | 11333848 | 1000000 | PstI | 1x95bp | | 421525 | | 8:15:27 | |
| BFORK24_1.fastq.gz | 11322723 | 1000000 | PstI | 1x95bp | | 421245 | | 8:14:26 | |
| MI419_1.fastq.gz | 11295066 | 1000000 | PstI | 1x95bp | | 413970 | | 9:16:28 | |
| BP17_1.fastq.gz | 11188566 | 1000000 | PstI | 1x95bp | | 422105 | | 8:15:27 | |

E) Individual Sample Sequencing Performance

| Sample Name | NGS Reads | Read Goal | RE | NGS Type | Sequencing Distribution | RAD Clusters (5x to 1000x) | Coverage Distribution | Coverages Low: Quantile Median: Upper: Quantile | Median Phred QScore vs Read Length |
|-----------------------|-----------|-----------|------|----------|-------------------------|----------------------------|-----------------------|--|------------------------------------|
| | | | | | 0 % 100 % of goal | | 5x 15x 25x 100x 250x | | |
| SPVW14_1.fastq.gz | 11187685 | 1000000 | PstI | 1x95bp | | 399425 | | 8:15:28 | |
| ER30_1.fastq.gz | 11102055 | 1000000 | PstI | 1x95bp | | 382156 | | 8:16:29 | |
| CANEY16_1.fastq.gz | 11084736 | 1000000 | PstI | 1x95bp | | 397863 | | 8:15:28 | |
| SC06_1.fastq.gz | 11038455 | 1000000 | PstI | 1x95bp | | 416619 | | 9:16:27 | |
| BP01_1.fastq.gz | 11015654 | 1000000 | PstI | 1x95bp | | 341451 | | 8:15:30 | |
| TBLR03_1.fastq.gz | 10975208 | 1000000 | PstI | 1x95bp | | 403458 | | 8:14:27 | |
| HC41_1.fastq.gz | 10900200 | 1000000 | PstI | 1x95bp | | 405850 | | 8:15:27 | |
| BP10_1.fastq.gz | 10899720 | 1000000 | PstI | 1x95bp | | 427223 | | 8:15:26 | |
| TBLR04_1.fastq.gz | 10869552 | 1000000 | PstI | 1x95bp | | 406214 | | 8:14:26 | |
| CANEY15_1.fastq.gz | 10849620 | 1000000 | PstI | 1x95bp | | 396071 | | 8:15:27 | |
| AR19_1.fastq.gz | 10818029 | 1000000 | PstI | 1x95bp | | 404294 | | 8:15:27 | |
| ER44_1.fastq.gz | 10757734 | 1000000 | PstI | 1x95bp | | 391406 | | 9:16:27 | |
| GRSPB02_1.fastq.gz | 10709036 | 1000000 | PstI | 1x95bp | | 398950 | | 8:14:26 | |
| BP02_1.fastq.gz | 10691523 | 1000000 | PstI | 1x95bp | | 404749 | | 8:15:26 | |
| NOIS12_1.fastq.gz | 10655620 | 1000000 | PstI | 1x95bp | | 393102 | | 8:13:26 | |
| BC12_1.fastq.gz | 10633483 | 1000000 | PstI | 1x95bp | | 391639 | | 8:15:26 | |
| HC40_1.fastq.gz | 10571344 | 1000000 | PstI | 1x95bp | | 412767 | | 8:14:25 | |
| STOCK04_1.fastq.gz | 10384320 | 1000000 | PstI | 1x95bp | | 316431 | | 8:16:32 | |
| AR30_1.fastq.gz | 10321742 | 1000000 | PstI | 1x95bp | | 382304 | | 8:14:26 | |
| SKIA05_1.fastq.gz | 10249968 | 1000000 | PstI | 1x95bp | | 360100 | | 8:15:29 | |
| GRSPB69_1.fastq.gz | 10210701 | 1000000 | PstI | 1x95bp | | 388053 | | 8:15:26 | |
| MI423_1.fastq.gz | 10135162 | 1000000 | PstI | 1x95bp | | 380758 | | 8:15:26 | |
| HC38_1.fastq.gz | 9961349 | 1000000 | PstI | 1x95bp | | 402480 | | 7:12:23 | |
| BFORK23_1.fastq.gz | 9836489 | 1000000 | PstI | 1x95bp | | 388978 | | 8:14:24 | |
| SKIA06_1.fastq.gz | 9764384 | 1000000 | PstI | 1x95bp | | 357052 | | 8:15:27 | |
| SPVW11_1.fastq.gz | 9659111 | 1000000 | PstI | 1x95bp | | 357142 | | 8:14:26 | |
| SC37_1.fastq.gz | 9483195 | 1000000 | PstI | 1x95bp | | 380912 | | 8:14:25 | |
| ER05_1.fastq.gz | 9384025 | 1000000 | PstI | 1x95bp | | 230408 | | 11:22:39 | |
| HC42_1.fastq.gz | 9279559 | 1000000 | PstI | 1x95bp | | 355806 | | 8:15:26 | |
| TBLR01_1.fastq.gz | 9098318 | 1000000 | PstI | 1x95bp | | 378475 | | 7:13:23 | |
| SKIA03_1.fastq.gz | 8559541 | 1000000 | PstI | 1x95bp | | 331928 | | 8:14:25 | |
| STOCK05_1.fastq.gz | 8204441 | 1000000 | PstI | 1x95bp | | 328770 | | 8:14:24 | |
| FGXCONTROL_1.fastq.gz | 7589235 | 330000 | PstI | 1x95bp | | 37528 | | 5:6:9 | |
| BFORK30_1.fastq.gz | 7291023 | 1000000 | PstI | 1x95bp | | 241816 | | 8:13:24 | |
| GRSPB34_1.fastq.gz | 1873661 | 1000000 | PstI | 1x95bp | | 23426 | | 10:29:75 | |
| BFORK32_1.fastq.gz | 404605 | 1000000 | PstI | 1x95bp | | 8122 | | 5:6:7 | |

3. Reference Assembly

Section 3.1. AR21_denovo_clusters_SR_denovo_Clustering_Report

RAD-Seq Single End Clustering Report

Project: LEggert_UMissouri_Bass_20180409-01669

FASTA Assembly: AR21_denovo_clusters.fasta

A) Information

Project: LEggert_UMissouri_Bass_20180409-01669

Date: 2018-08-31T18:15:45

FASTQ file used for Clustering: AR21_1.fastq.gz

FASTA genome directory: Genome_Assemblies

FASTA genome name: AR21_denovo_clusters.fasta

Clustering Options:

Min. Cluster Depth: 10 x
Max. Cluster Depth: 1000 x
5' Trimming: 0 bp
3' Trimming: 0 bp
Max. Variants / Cluster: 3
Max. Haplotypes / Cluster: 2

B) Statistics

Total Reads in Sample AR21_1.fastq.gz : 13117475

Reads Passing FASTQ Quality Filters: 12859536

Reads Failing FASTQ Quality Filters: 257939

Reads in Provisional Clusters: 8491818

Total Contigs in Provisional Clusters: 288336

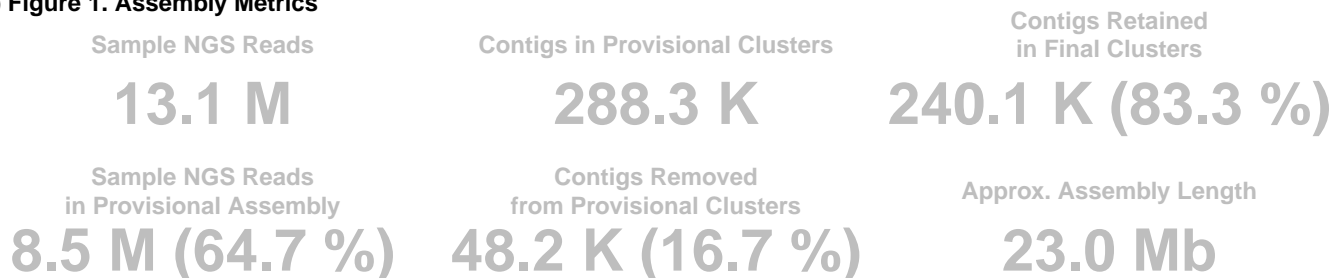
Contigs Extracted from Provisional Clusters: 48248

Total Contigs in Final Assembly: 240085

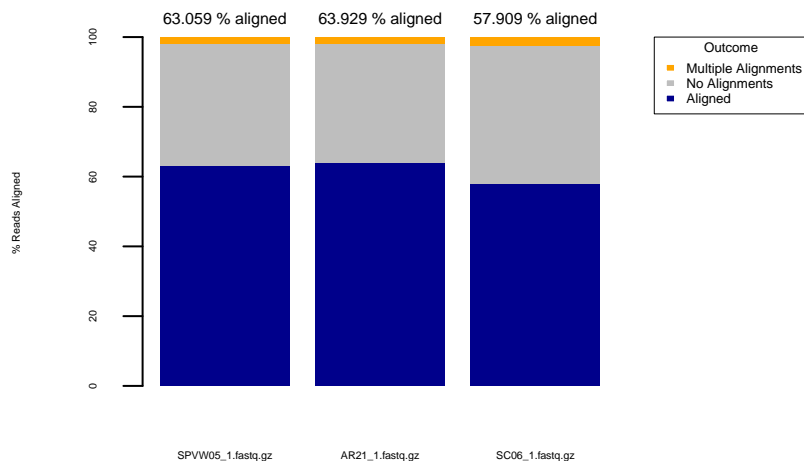
Contig Length: 96 bp

Total Cluster Length: 23048160 bp

C) Figure 1. Assembly Metrics



D) Figure 2. Test Alignment Performance of Clusters: AR21_denovo_clusters.fasta



4. Sequence Alignment

Section 4.1. BAM_mpileups_Alignment_Report

Alignment Summary: BAM_mpileups

A) Information and Statistics

Project Name: LEggert_UMissouri_Bass_20180409-01669

Analysis Date: 2018-09-01T19:15:59

Sequence Directory: FASTQ_Sequence_Files

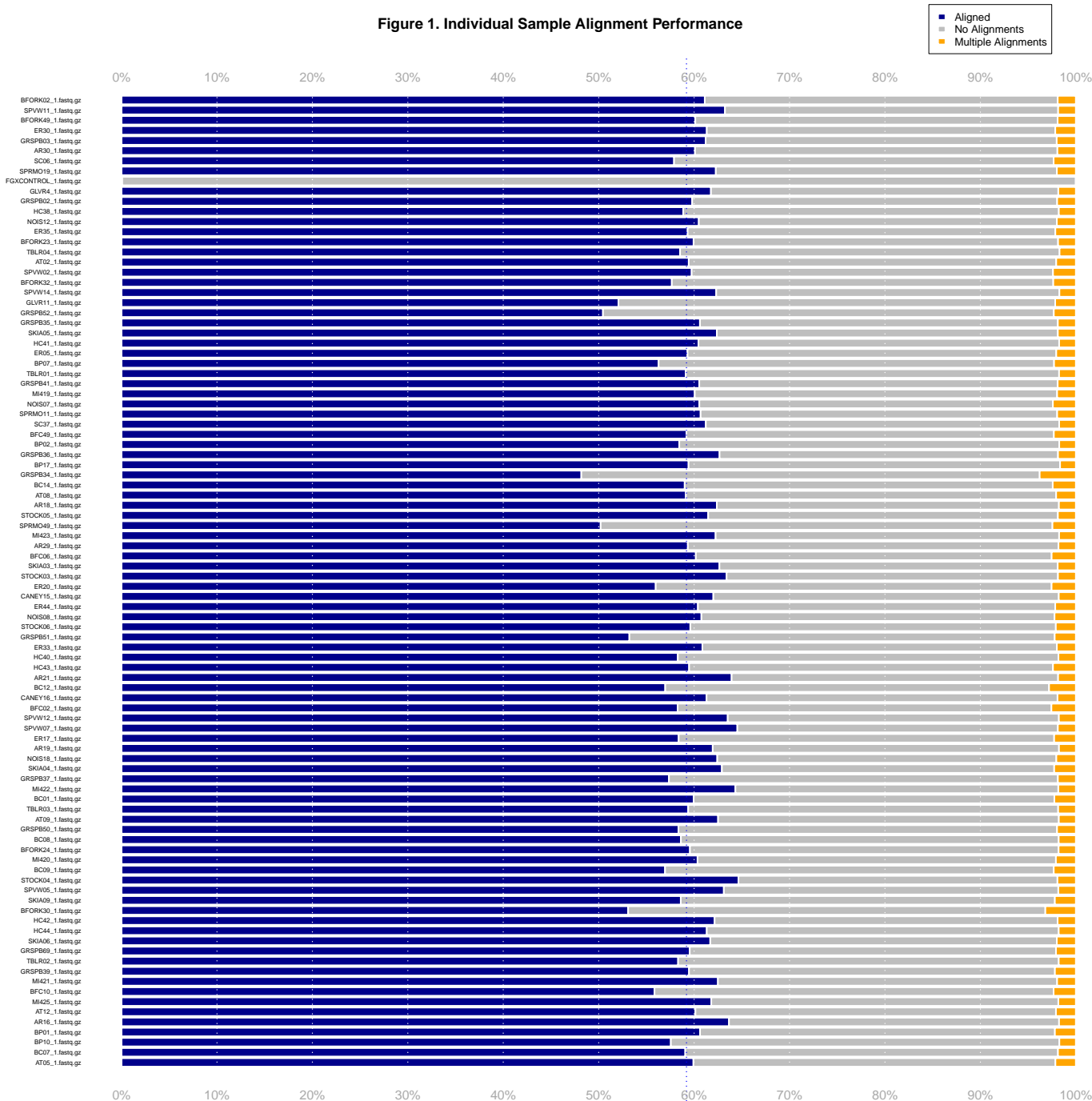
BAM Pileup Directory: BAM_mpileups

Reference Genome: AR21_denovo_clusters.fasta

Avg % Reads Aligning to Reference: 59.2

Avg % Reads Failing to Align: 38.8

Avg % Reads with Multiple Alignments: 2.0



5. Variant Calling (VCF)

Section 5.1. AR21_Aligned_Genotypes_VCF_Report

VCF File Summary: AR21_Aligned_Genotypes_relaxed.vcf

A) Information

VCF File: AR21_Aligned_Genotypes_relaxed.vcf
Date: 2018-09-02T03:39:11
Project: LEggert_UMissouri_Bass_20180409-01669
Reference Genome: AR21_denovo_clusters.fasta
BAM / mpileup Folder: BAM_mpileups
VCF Options:
Min. % Population Genotyped: 75
Min. Individual Sequencing Depth: 6 x
Min. Individual Genotype Quality: 10
Min. FASTQ Quality Score: 20
MAF to be Screened: 0.2
Min. Distance Free of Other Variants: 50
Genome Landscape Flanking SNP: 50

B) Variant Statistics

Number of Samples Screened: 95
Total Candidate Variants Detected: 357123
Candidate Variants Filtered (due to missing or low quality data): 77144
Candidate Variants with Low Probability: 2066
Candidate Variants Passing All Filters: 277913
Average Number of Polymorphisms within 200bp of Each Variant: 3
Sequencing Coverage Across Population for Each Variant: 3249.0 x
Variant Transition / Transversion Ratio: 1.43

Transitions: 167236
A→G: 61214
C→T: 106022
Transversions: 116934
G→T: 41133
A→C: 21860
A→T: 27627
C→G: 26314

C) Genotyping Statistics

Total Genotypes in VCF File: 26598005
Genotypes Scored: 25824119
Genotypes Missing: 773886
Average Individual Genotype Quality: 69.6 (Phred-scaled)
Average Individual Sequencing Coverage: 34.2 x
Homozygous Genotypes: 23202008
Heterozygous Genotypes: 2622111

D) Genotyping Design Statistics (if applicable)

Variants Screened: 0
Variants Passing Design Criteria: 0
Variants Failing Design Criteria: 0
Failed due to flanking polymorphism: 0
Failed due to lack of flanking sequence: 0

Figure 1. Variants Passing Filters

277.9 K

Filtering Criteria:

Minimum Sequencing Depth per Sample: 6 x
Minimum Phred Scaled Genotype Quality Per Sample: 10
Minimum Percent of Population Genotyped: 75 %

Figure 2. Histogram Plotting Number of Variations Over 200bp Genomic Interval

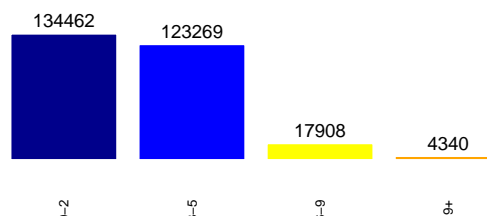


Figure 3. Variant Transition / Transversion Rates

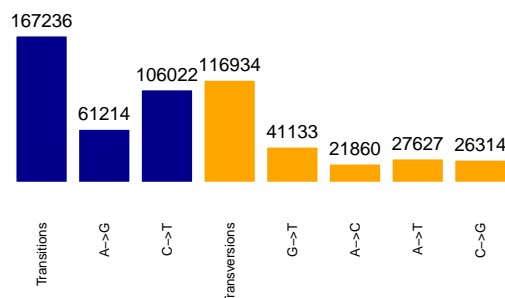


Figure 4. Percentage of Missing Genotype Data

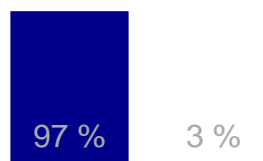
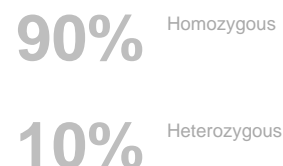


Figure 5. Percent Homozygous & Heterozygous Genotypes



Quality Genotype Missing Genotype

Figure 6. Individual Sequencing Coverage and Genotype Quality



VCF File Summary: AR21_Aligned_Genotypes_standard.vcf

A) Information

VCF File: AR21_Aligned_Genotypes_standard.vcf
Date: 2018-09-02T03:41:20
Project: LEggert_UMissouri_Bass_20180409-01669
Reference Genome: AR21_denovo_clusters.fasta
BAM / mpileup Folder: BAM_mpileups
VCF Options:
Min. % Population Genotyped: 82.5
Min. Individual Sequencing Depth: 10 x
Min. Individual Genotype Quality: 13
Min. FASTQ Quality Score: 20
MAF to be Screened: 0.2
Min. Distance Free of Other Variants: 50
Genome Landscape Flanking SNP: 50

B) Variant Statistics

Number of Samples Screened: 95
Total Candidate Variants Detected: 357124
Candidate Variants Filtered (due to missing or low quality data): 136885
Candidate Variants with Low Probability: 1167
Candidate Variants Passing All Filters: 219071
Average Number of Polymorphisms within 200bp of Each Variant: 2.9
Sequencing Coverage Across Population for Each Variant: 3705.0 x
Variant Transition / Transversion Ratio: 1.43

Transitions: 131051
A→G: 46085
C→T: 84966
Transversions: 91795
G→T: 32218
A→C: 16974
A→T: 21447
C→G: 21156

C) Genotyping Statistics

Total Genotypes in VCF File: 20922610
Genotypes Scored: 20403313
Genotypes Missing: 519297
Average Individual Genotype Quality: 79.9 (Phred-scaled)
Average Individual Sequencing Coverage: 39 x
Homozygous Genotypes: 18358647
Heterozygous Genotypes: 2044666

D) Genotyping Design Statistics (if applicable)

Variants Screened: 0
Variants Passing Design Criteria: 0
Variants Failing Design Criteria: 0
Failed due to flanking polymorphism: 0
Failed due to lack of flanking sequence: 0

Figure 1. Variants Passing Filters

219.1 K

Filtering Criteria:

Minimum Sequencing Depth per Sample: 10 x
Minimum Phred Scaled Genotype Quality Per Sample: 13
Minimum Percent of Population Genotyped: 82.5 %

Figure 2. Histogram Plotting Number of Variations Over 200bp Genomic Interval

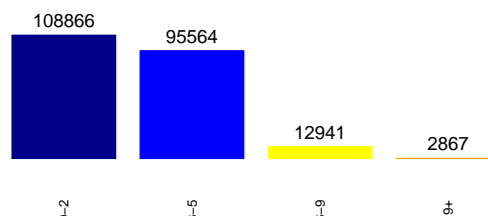


Figure 3. Variant Transition / Transversion Rates

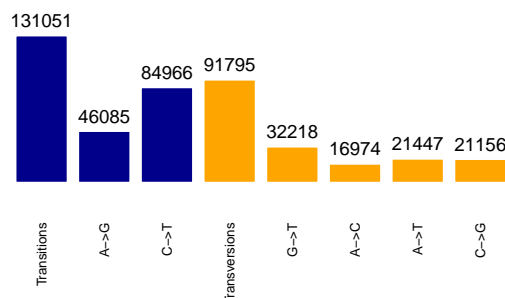


Figure 4. Percentage of Missing Genotype Data

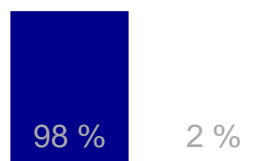
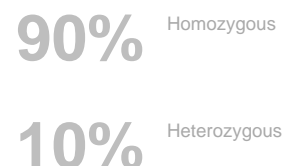


Figure 5. Percent Homozygous & Heterozygous Genotypes



Quality Genotype Missing Genotype

Figure 6. Individual Sequencing Coverage and Genotype Quality



VCF File Summary: AR21_Aligned_Genotypes_stringent.vcf

A) Information

VCF File: AR21_Aligned_Genotypes_stringent.vcf
Date: 2018-09-02T03:43:11
Project: LEggert_UMissouri_Bass_20180409-01669
Reference Genome: AR21_denovo_clusters.fasta
BAM / mpileup Folder: BAM_mpileups
VCF Options:
Min. % Population Genotyped: 90
Min. Individual Sequencing Depth: 15 x
Min. Individual Genotype Quality: 20
Min. FASTQ Quality Score: 20
MAF to be Screened: 0.2
Min. Distance Free of Other Variants: 50
Genome Landscape Flanking SNP: 50

B) Variant Statistics

Number of Samples Screened: 95
Total Candidate Variants Detected: 357124
Candidate Variants Filtered (due to missing or low quality data): 229694
Candidate Variants with Low Probability: 406
Candidate Variants Passing All Filters: 127023
Average Number of Polymorphisms within 200bp of Each Variant: 2.8
Sequencing Coverage Across Population for Each Variant: 4674.0 x
Variant Transition / Transversion Ratio: 1.45

Transitions: 76063
A→G: 25295
C→T: 50768
Transversions: 52544
G→T: 18522
A→C: 9550
A→T: 11868
C→G: 12604

C) Genotyping Statistics

Total Genotypes in VCF File: 12105755
Genotypes Scored: 11873918
Genotypes Missing: 231837
Average Individual Genotype Quality: 102.1 (Phred-scaled)
Average Individual Sequencing Coverage: 49.2 x
Homozygous Genotypes: 10699755
Heterozygous Genotypes: 1174163

D) Genotyping Design Statistics (if applicable)

Variants Screened: 0
Variants Passing Design Criteria: 0
Variants Failing Design Criteria: 0
Failed due to flanking polymorphism: 0
Failed due to lack of flanking sequence: 0

Figure 1. Variants Passing Filters

127.0 K

Filtering Criteria:

Minimum Sequencing Depth per Sample: 15 x
Minimum Phred Scaled Genotype Quality Per Sample: 20
Minimum Percent of Population Genotyped: 90 %

Figure 2. Histogram Plotting Number of Variations Over 200bp Genomic Interval

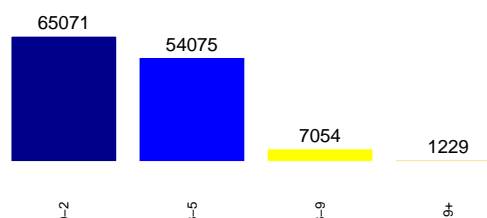


Figure 3. Variant Transition / Transversion Rates

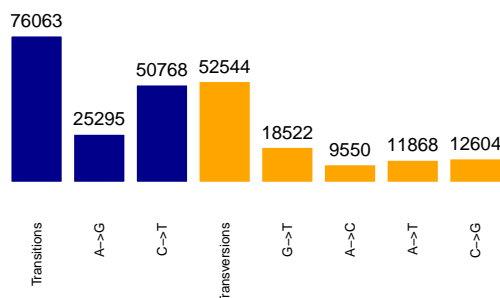


Figure 4. Percentage of Missing Genotype Data

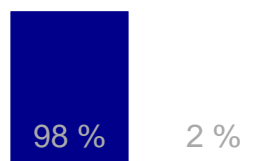


Figure 5. Percent Homozygous & Heterozygous Genotypes

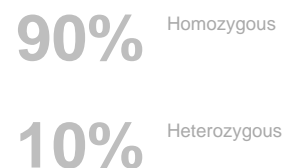


Figure 6. Individual Sequencing Coverage and Genotype Quality



6. Tools and Software

BOWTIE Version: bowtie-1.1.1

BWA Version: bwa-0.6.1

SAMTOOLS Version: samtools-0.1.16

VELVET Version: velvet_1.2.10
