Assembly Report

Experiment Details

| ExperimentID: | Experiment 67 |
|-----------------------------------|---------------|
| Sequencing Coverage: | 23 |
| Number of Partitions: | 2 |
| Allowed Mismatch Count in (Base): | 0 |
| Length of Sliding Window: | 101 |

Reads Dataset Details

| reads Dataset Details | T |
|-------------------------------|--------|
| Total Reads Count: | 1212 |
| Total Dataset Size in (Base): | 241272 |
| Valid Read Count: | 1212 |
| Rejected Read Count: | 0 |
| Maximum Read Length: | 201 |
| Minimum Read Length: | 162 |

Reference Genome Details

| Length of Reference Genome (Base): | 10080 |
|------------------------------------|-------|
| Number of K-mers: | 9880 |
| Length of K-mer | 419 |

Assembly Details

| Number of Contigs: | 28 |
|---------------------|-------|
| Contig N50: | 911 |
| Contig N90: | 826 |
| Number of Scaffold | 5 |
| Scaffold N50: | 2695 |
| Scaffold N90: | 2150 |
| Mis-assembly Count: | 0 |
| TotalAssembly Size: | 11208 |

Repeat Details

| Total Reads Count(Non-Repeat) : | 341 |
|---|-----|
| Total Reads Count(Repeat): | 47 |
| Retetitve Read Count based on (Partitions Identifier): | 40 |
| Retetitve Read Count (Entire Read Frequency Identifier): | 4 |
| Retetitve Read Count (Contained Read Frequency Identifier): | 3 |
| Total Repetitive Sequences Count | 81 |
| Total Unique Repetitive Sequences Count | 3 |

| Total Repeat | Total Repeat Size (Base) | | 7000 | | | |
|--------------|--------------------------|--|--------------|--------|--------------------------------------|---|
| Starting | Ending | Repetitive Sequences | Repeat Count | Length | Positions | |
| 1 | 4348 | CGGTCGAAAA ACTGCTGGCA GTGGGGCATT ACCTCGAATCT ACCGTCGATAT TGCTGAGTCC ACCCGCCGTA TTGCGGCAAG TCGTATTCCGG CTGATCACATG GTGCTGATGG CAGGTTTCACC GCCGGTAATG AAAAAGGCGA ACTGGTGGTG CTTGGACGCA ACGGTTCCGA CTACTCTGCTG CGGTGCTGGC TGCCTGTTTAC GCGCCGATTG TTGCGAGATTT GGACGCATTG TTGCGAGATTT GGACGCATTG TTGCGAGATTT GGACGCATTG TTGCGAGATTT GGACGCGTCAG GTGCCCGATTG TTGCGAGTTTT GAAGTCGATG TCCTACCAGG AAGCGATGGA CCTACCAGG AAGCGATGGA GCTTTCCTACT TCGGCGCTCT AGGTCAGGCC | 3 | 350 | Positio F n r 1756 2 3561 3 | End Position 2105 3910 4313 |

| GATTCATTCGG GATGGTCTGT GTGGATTAAAA AAAGAGTGTCT GATAGCAGCTT CTGAACTGGTT ACCTGCCGTG AGTAAATTAAA ATTTTATTGAC TTAGGTCACTA AATACTTTAAC CAATATAGGCA TAGCGCACAG ACAGATAAAAA TTACAGAGTAC ACAACATCCTC AAAACCCTCC AAAACCCTGC GGGTTTTTT TTCGACCAAAAG GTAACGAGGT AACAACATCGC GAGTGTTGAA GTCAAGGAGT ACACAACGC TAGCGCACTT GGCATTAAC CTAAAGCC TGTACCCGTTA CCTAAAGCC TGTACCCGTTA CCTAACGCAC GTATACGGTAC CTAGCCATGA | | | | <u> </u> | - | | 1 |
|--|---|------|-------------|----------|-----|---------|---------|
| GTGGATTAAAA AAAGAGTGTCT GATAGCAGCTT CTGAACTGGTT ACCTGCCGTG AGTAAATTAAA ATTITATTGAC TTAGGTCACTA AATACTITAAC CAATATAGGCA TAGCGCACAG ACAGATAAAAA TTACAGAGTAC ACAACATCCTC GGTGACAGTG CGGGCTTTTTT TTCGACCAAAG GTAACGAGGT AACAACCATGC GAGTGTTGAA GTCAGGAGAT CCTAAAGGCC TGTACCCGTTA CCTAAAGGCC TGTACCCGTTA CCTAGCCAGTT GGCATTAAAC GTATACGGTAC CTAGGCATGTA CCTAGCCAGTT GGCATTAAAC GTATACGGTAC CTAGGCATGTA | | | GATTCATTCGG | | | | |
| AAAGAGTGTCT GATAGCAGCTT CTGAACTGGTT ACCTGCCGTG AGTAAATTAAA ATTITATTGAC TTAGGTCACTA AATACTITAAC CAATATAGGCA TAGCGCACAG ACAGATAAAAA TTTACAGAGTAC AAAGCCTACC GGTGACAGTG CGGCTTTTT TTCGACCAAAG GTAACGAGT AACAACATCC GATGACAGGT CGGGCTTTTTT TTCGACCAAAG GTAACGAGAT CCTAAAGGCC TGTACCCGTTA CCTAGCAGTT GGCATTAAAC GTATACGGTAC CTAGCCAGTT GGCATTAAAC GTATACGGTAC CTAGGCATGTA | | | GATGGTCTGT | | | | |
| GATAGCAGCTT CTGAACTGGTT ACCTGCCGTG AGTAAATTAAA ATTTTATTGAC TTAGGTCACTA AATACTTTAAC CAATATAGGCA TAGCGCACAG ACAGATAAAAA TTTACAGAGTAC AAAGCCTACC GGTGACAGTG CGGGCTTTTTT TTCGACCAAAG GTAACGAGAT GACACCC GATGACGAGAT AACAACCATCC GATGACGAGAT CCTAAAGGCC TGTACCGGTTA CCTAAAGGCC TGTACCGGTTA CCTAACGCACT GCATTAAAC GTATACGGTAC CTAGGCATGTA | | | GTGGATTAAAA | | | | |
| CTGAACTGGTT ACCTGCCGTG AGTAAATTAAA ATTTTATTGAC TTAGGTCACTA AATACTTTAAC CAATATAGGCA TAGCGCACAG ACAGATAAAAA TTTACAGAGTAC ACAACATCCTC AAAACACTCCTC AAAACACTCTC GGTGACAGTG CGGGCTTTTTT TTCGACCAAAG GTAACGAGT AACAACACTCC GAGTGACAGT ACAACACTCC GGTGACAGT CCGGGCTTTTT TCGACCAAAG GTAACGAGT AACAACCATGC GAGTGTGAA GTCAGGAGAT CCTAAAGGCC TGTACCCGTTA CCTAGCCAGTT GGCATTAAAC GTATACGGTAC CTAGGCATGTA | | | AAAGAGTGTCT | | | | |
| ACCTGCCGTG AGTAAATTAAA ATTTTATTGAC TTAGGTCACTA AATACTTTAAC CAATATAGGCA TAGCGCACAG ACAGATAAAAA TTACAGAGTAC ACAACATCCTC AAAGCCTACC GGTGACAGTG CGGGCTTTTT TTCGACCAAAG GTAACGAGGT AACACCATGC GAGTGTTGAA GTCAGGAGAT CCTAAAGGCC TGTACCCGTTA CCTAGCCAGTAC CTAGGCATGAC GTATACGGTAC CTAGGCATGTA CCTAGGCATGTA | | | GATAGCAGCTT | | | | |
| AGTAAATTAAA ATTTTATTGAC TTAGGTCACTA AATACTTTAAC CAATATAGGCA TAGCGCACAG ACAGATAAAAA TTACAGAGTAC ACAACATCCTC ACAACATCCTC GGTGACAGTG CGGGCTTTTTT TTCGACCAAAG GTAACGAGGT AACAACCATGC GAGTGTTGAA GTCAGGAGAT CCTAAAGGCC TGTACCCGTTA CCTAGCCAGTT GGCATTAAAC GTATACGGTAC CTAGGCATGAC CTAGGCATGTA | | | CTGAACTGGTT | | | | |
| ATTITATTGAC TTAGGTCACTA AATACTITAAC CAATATAGGCA TAGCGCACAG ACAGATAAAAA TTACAGAGTAC ACAACATCCTC ACAACATCCTC GGTGACAGTG CGGGCTTTTTT TTCGACCAAAG GTAACGAGGT AACAACCATGC GAGTGTTGAA GTCAGGAGAT CCTAAAGGCC TGTACCCGTTA CCTAGCCAGTT GGCATTAAAC GTATACGGTAC CTAGGCATGTA | | | ACCTGCCGTG | | | | |
| TTAGGTCACTA AATACTTTAAC CAATATAGGCA TAGCGCACAG ACAGATAAAAA TTACAGAGTAC ACAACATCCTC ACAACATCCTC GGTGACAGTG CGGGCTTTTTT TTCGACCAAAG GTAACGAGGT AACAACCATGC GAGTGTGAA GTCAGGAGAT CCTAAAGGCC TGTACCCGTTA CCTAGCCAGTT GGCATTAAC GTATACGGTAC CTAGGCATGTA | | | AGTAAATTAAA | | | | |
| AATACTTTAAC CAATATAGGCA TAGCGCACAG ACAGATAAAAA TTACAGAGTAC ACAACATCCTC ACAACACTCCTC GGTGACAGTG CGGCTTTTTT TTCGACCAAAG GTAACGAGGT AACAACCATGC GAGTGTGAA GTCAGGAGAT CCTAAAGGCC TGTACCCGTTA CCTAGCCAGTA CCTAGGCATGTA CCTAGGCATGTA CCTAGGCATGTA CCTAGGCATGTA CCTAGGCATGTA CCTAGGCATGTA CCTAGGCATGTA | | | ATTTTATTGAC | | | | |
| CAATATAGGCA TAGCGCACAG ACAGATAAAAA TTACAGAGTAC ACAACATCCTC ACAACATCCTC GGTGACAGTG CGGGCTTTTTT TTCGACCAAAG GTAACGAGGT AACAACCATGC GAGTGTTGAA GTCAGGAGAT CCTAAAGGCC TGTACCCGTTA CCTAGCCAGTC GGTATACGGTAC CTAGGCATGTA CCTAGGCATGTA CCTAGGCATGTA CCTAGGCATGTA CCTAGGCATGTA CCTAGGCATGTA CCTAGGCATGTA | | | TTAGGTCACTA | | | | |
| TAGCGCACAG ACAGATAAAAA TTACAGAGTAC ACAACATCCTC ACAACATCCTC GGTGACAGTG CGGGCTTTTTT TTCGACCAAAG GTAACGAGGT AACAACCATGC GAGTGTTGAA GTCAGGAGAT CCTAAAGGCC TGTACCCGTTA CCTAGCCAGTT GGCATTAAAC GTATACGGTAC CTAGGCATGTA | | | AATACTTTAAC | | | | |
| ACAGATAAAAA TTACAGAGTAC ACAACATCCTC AAAGCCTACC GGTGACAGTG CGGGCTTTTTT TTCGACCAAAG GTAACGAGGT AACAACCATGC GAGTGTTGAA GTCAGGAGAT CCTAAAGGCC TGTACCCGTTA CCTAGCCAGTT GGCATTAAAC GTATACGGTAC CTAGGCATGTA CCTAGGCATGTA CCTAGGCATGTA CCTAGGCATGTA CCTAGGCATGTA CCTAGGCATGTA CCTAGGCATGTA CCTAGGCATGTA | | | CAATATAGGCA | | | | |
| TTACAGAGTAC ACAACATCCTC ACAACATCCTC ACAACATCCTC AAAAGCCTACC GGTGACAGTG CGGGCTTTTTT TTCGACCAAAG GTAACGAGGT AACAACCATGC GAGTGTTGAA GTCAGGAGAT CCTAAAGGCC TGTACCCGTTA CCTAGCCAGTT GGCATTAAAC GTATACGGTAC CTAGGCATGTA | | | TAGCGCACAG | | | | |
| ACAACATCCTC AAAGCCTACC GGTGACAGTG CGGGCTTTTTT TTCGACCAAAG GTAACGAGGT AACAACCATGC GAGTGTTGAA GTCAGGAGAT CCTAAAGGCC TGTACCCGTTA CCTAGCCAGTT GGCATTAAAC GTATACGGTAC CTAGGCATGTA | | | ACAGATAAAAA | | | Start | End |
| 1 4348 AAAGCCTACC GGTGACAGTG CGGGCTTTTTT TTCGACCAAAG GTAACGAGGT AACAACCATGC GAGTGTTGAA GTCAGGAGAT CCTAAAGGCC TGTACCCGTTA CCTAGCCAGTT GGCATTAAAC GTATACGGTAC CTAGGCATGTA | | | TTACAGAGTAC | | | Positio | Positio |
| GGTGACAGTG CGGGCTTTTTT TTCGACCAAAG GTAACGAGGT AACAACCATGC GAGTGTTGAA GTCAGGAGAT CCTAAAGGCC TGTACCCGTTA CCTAGCCAGTT GGCATTAAAC GTATACGGTAC CTAGCCATGTA | | | ACAACATCCTC | | | n | n |
| GGTGACAGTG CGGGCTTTTTT TTCGACCAAAG GTAACGAGGT AACAACCATGC GAGTGTTGAA GTCAGGAGAT CCTAAAGGCC TGTACCCGTTA CCTAGCCAGTT GGCATTAAAC GTATACGGTAC CTAGGCATGTA | 1 | 4348 | AAAGCCTACC | 3 | 350 | 409 | 758 |
| TTCGACCAAAG GTAACGAGGT AACAACCATGC GAGTGTTGAA GTCAGGAGAT CCTAAAGGCC TGTACCCGTTA CCTAGCCAGTT GGCATTAAAC GTATACGGTAC CTAGGCATGTA | | | GGTGACAGTG | | | | |
| GTAACGAGGT AACAACCATGC GAGTGTTGAA GTCAGGAGAT CCTAAAGGCC TGTACCCGTTA CCTAGCCAGTT GGCATTAAAC GTATACGGTAC CTAGGCATGTA | | | CGGGCTTTTTT | | | 2228 | 2577 |
| AACAACCATGC GAGTGTTGAA GTCAGGAGAT CCTAAAGGCC TGTACCCGTTA CCTAGCCAGTT GGCATTAAAC GTATACGGTAC CTAGGCATGTA | | | TTCGACCAAAG | | | 3182 | 3531 |
| GAGTGTTGAA GTCAGGAGAT CCTAAAGGCC TGTACCCGTTA CCTAGCCAGTT GGCATTAAAC GTATACGGTAC CTAGGCATGTA | | | GTAACGAGGT | | | | |
| GTCAGGAGAT CCTAAAGGCC TGTACCCGTTA CCTAGCCAGTT GGCATTAAAC GTATACGGTAC CTAGGCATGTA | | | AACAACCATGC | | | | |
| CCTAAAGGCC TGTACCCGTTA CCTAGCCAGTT GGCATTAAAC GTATACGGTAC CTAGGCATGTA | | | GAGTGTTGAA | | | | |
| TGTACCCGTTA CCTAGCCAGTT GGCATTAAAC GTATACGGTAC CTAGGCATGTA | | | GTCAGGAGAT | | | | |
| CCTAGCCAGTT GGCATTAAAC GTATACGGTAC CTAGGCATGTA | | | CCTAAAGGCC | | | | |
| GGCATTAAAC GTATACGGTAC CTAGGCATGTA | | | TGTACCCGTTA | | | | |
| GTATACGGTAC CTAGGCATGTA | | | CCTAGCCAGTT | | | | |
| CTAGGCATGTA | | | GGCATTAAAC | | | | |
| | | | GTATACGGTAC | | | | |
| | | | CTAGGCATGTA | | | | |
| CGTAATCGTAG | | | CGTAATCGTAG | | | | |
| CCTTAGCAATC | | | CCTTAGCAATC | | | | |
| TCCAGTCC | | | TCCAGTCC | | | | |

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|---|------|--------------|--------------|-----|---------|---------|
| | | GCTTTTCATTC | | | | |
| | | TGACTGCAAC | | | | |
| | | GGGCAATATG | | | | |
| | | TCTCTGTGTGG | | | | |
| | | ATTAAAAAAAAG | | | | |
| | | AGTGTCTGATA | | | | |
| | | GCAGCTTCTG | | | | |
| | | AACTGGTTACC | | | | |
| | | TGCCGTGAGT | | | | |
| | | AAATTAAAATT | | | | |
| | | TTATTGACTTA | | | | |
| | | GGTCACTAAAT | | | | |
| | | ACTTTAACCAA | | | Start | End |
| | | TATAGGCATAG | | | Positio | Positio |
| | | CGCACAGACA | | | n | n |
| | | GATAAAAATTA | | | | |
| 1 | 4348 | CAGAGTACAC | 4 | 350 | 1 | 350 |
| | | AACATCCATGA | | | 854 | 1203 |
| | | AACGCATTAGC | | | 1295 | 1644 |
| | | ACCACCATTAC | | | | |
| | | CACCACCATCA | | | 2705 | 3054 |
| | | CCATTACCACA | | | | |
| | | GGTAACGGTG | | | | |
| | | CGGGCTGACG | | | | |
| | | CGTACAGGAA | | | | |
| | | ACACAGAAAAA | | | | |
| | | AGCCCGCACC | | | | |
| | | TGACAGTGCG | | | | |
| | | GGCTTTTTTTT | | | | |
| | | CGACCAAAGG | | | | |
| | | TAACGAGGTAA | | | | |
| | | CAACCATGCG | | | | |
| | | AGTGTTGAAGT | | | | |

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|------|------|--|---|-----|---------|---------|
| | | CGGTCGAAAA | | | | |
| | | ACTGCTGGCA | | | | |
| | | GTGGGGCATT | | | | |
| | | ACCTCGAATCT | | | | |
| | | ACCGTCGATAT | | | | |
| | | TGCTGAGTCC | | | | |
| | | ACCCGCCGTA | | | | |
| | | TTGCGGCAAG | | | | |
| | | TCGTATTCCGG | | | | |
| | | CTGATCACATG | | | | |
| | | GTGCTGATGG | | | | |
| | | CAGGTTTCACC | | | | |
| | | GCCGGTAATG | | | | |
| | | AAAAAGGCGA | | | | 1 |
| | | ACTGGTGGTG | | | Start | End |
| | | CTTGGACGCA | | | Positio | Positio |
| 4113 | 6262 | ACGGTTCCGA | 0 | 050 | n | n |
| 4113 | 6262 | CTACTCTGCTG | 2 | 350 | 5117 | 5466 |
| | | CGGTGCTGGC | | | 3117 | 3400 |
| | | TGCCTGTTTAC | | | 5910 | 6259 |
| | | GCGCCGATTG | | | | |
| | | TTGCGAGATTT | | | | |
| | | GGACGGACGT | | | | |
| | | TGACGGGGTC | | | | |
| | | TATACCTGCGA | | | | |
| | | CCCGCGTCAG | | | | |
| | | GTGCCCGATG | | | | |
| | | CGAGGTTGTT | | | | |
| | | GAAGTCGATG | | | | |
| | | TCCTACCAGG | | | | |
| | | AAGCGATGGA | | | | |
| | | GCTTTCCTACT | | | | |
| | | TCGGCGCTCT | | | | |
| | | AGGTCAGGCC | | | | |

| | | CATTCATTCCC | | | | |
|------|------|-------------|---|-----|---------|---------|
| | | GATTCATTCGG | | | | |
| | | GATGGTCTGT | | | | |
| | | GTGGATTAAAA | | | | |
| | | AAAGAGTGTCT | | | | |
| | | GATAGCAGCTT | | | | |
| | | CTGAACTGGTT | | | | |
| | | ACCTGCCGTG | | | | |
| | | AGTAAATTAAA | | | | |
| | | ATTTTATTGAC | | | | |
| | | TTAGGTCACTA | | | | |
| | | AATACTTTAAC | | | | |
| | | CAATATAGGCA | | | | |
| | | TAGCGCACAG | | | | |
| | | ACAGATAAAA | | | Start | End |
| | | TTACAGAGTAC | | | Positio | Positio |
| | | ACAACATCCTC | | 0=0 | n | n |
| 4113 | 6262 | | 2 | 350 | | |
| | | GGTGACAGTG | | | 4730 | 5079 |
| | | CGGGCTTTTTT | | | 5529 | 5878 |
| | | TTCGACCAAAG | | | | |
| | | GTAACGAGGT | | | | |
| | | AACAACCATGC | | | | |
| | | GAGTGTTGAA | | | | |
| | | GTCAGGAGAT | | | | |
| | | CCTAAAGGCC | | | | |
| | | TGTACCCGTTA | | | | |
| | | CCTAGCCAGTT | | | | |
| | | GGCATTAAAC | | | | |
| | | GTATACGGTAC | | | | |
| | | CTAGGCATGTA | | | | |
| | | CGTAATCGTAG | | | | |
| | | CCTTAGCAATC | | | | |
| | | TCCAGTCC | | | | |

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|------|------|---------------|---|------|---------|---------|
| | | CGGTCGAAAA | | | | |
| | | ACTGCTGGCA | | | | |
| | | GTGGGGCATT | | | | |
| | | ACCTCGAATCT | | | | |
| | | ACCGTCGATAT | | | | |
| | | TGCTGAGTCC | | | | |
| | | ACCCGCCGTA | | | | |
| | | TTGCGGCAAG | | | | |
| | | TCGTATTCCGG | | | | |
| | | CTGATCACATG | | | | |
| | | GTGCTGATGG | | | | |
| | | CAGGTTTCACC | | | | |
| | | GCCGGTAATG | | | | |
| | | AAAAAGGCGA | | | | |
| | | ACTGGTGGTG | | | Start | End |
| | | CTTGGACGCA | | 350 | Positio | Positio |
| 6076 | 8770 | ACGGTTCCGA | 0 | | n | n |
| 0070 | 0770 | CTACTCTGCTG 2 | | 7138 | 7487 | |
| | | CGGTGCTGGC | | | | |
| | | TGCCTGTTTAC | | | 8386 | 8735 |
| | | GCGCCGATTG | | | | |
| | | TTGCGAGATTT | | | | |
| | | GGACGGACGT | | | | |
| | | TGACGGGGTC | | | | |
| | | TATACCTGCGA | | | | |
| | | CCCGCGTCAG | | | | |
| | | GTGCCCGATG | | | | |
| | | CGAGGTTGTT | | | | |
| | | GAAGTCGATG | | | | |
| | | TCCTACCAGG | | | | |
| | | AAGCGATGGA | | | | |
| | | GCTTTCCTACT | | | | |
| | | TCGGCGCTCT | | | | |
| | | AGGTCAGGCC | | | | |

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|------|------|-------------|---|-----|---------|---------|
| | | GATTCATTCGG | | | | |
| | | GATGGTCTGT | | | | |
| | | GTGGATTAAAA | | | | |
| | | AAAGAGTGTCT | | | | |
| | | GATAGCAGCTT | | | | |
| | | CTGAACTGGTT | | | | |
| | | ACCTGCCGTG | | | | |
| | | AGTAAATTAAA | | | | |
| | | ATTTTATTGAC | | | | |
| | | TTAGGTCACTA | | | | |
| | | AATACTTTAAC | | | | |
| | | CAATATAGGCA | | | | |
| | | TAGCGCACAG | | | | |
| | | ACAGATAAAAA | | | | |
| | | TTACAGAGTAC | | | Start | End |
| | | ACAACATCCTC | | | Positio | Positio |
| 6076 | 8770 | AAAGCCTACC | 2 | 350 | n | n |
| | | GGTGACAGTG | | | 6730 | 7079 |
| | | CGGGCTTTTTT | | | 8014 | 8363 |
| | | TTCGACCAAAG | | | 0011 | |
| | | GTAACGAGGT | | | | |
| | | AACAACCATGC | | | | |
| | | GAGTGTTGAA | | | | |
| | | GTCAGGAGAT | | | | |
| | | CCTAAAGGCC | | | | |
| | | TGTACCCGTTA | | | | |
| | | CCTAGCCAGTT | | | | |
| | | GGCATTAAAC | | | | |
| | | GTATACGGTAC | | | | |
| | | CTAGGCATGTA | | | | |
| | | CGTAATCGTAG | | | | |
| | | CCTTAGCAATC | | | | |
| | | TCCAGTCC | | | | |

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|------|------|--------------|---|-----|---------|----------|
| | | GCTTTTCATTC | | | | |
| | | TGACTGCAAC | | | | |
| | | GGGCAATATG | | | | |
| | | TCTCTGTGTGG | | | | |
| | | ATTAAAAAAAAG | | | | |
| | | AGTGTCTGATA | | | | |
| | | GCAGCTTCTG | | | | |
| | | AACTGGTTACC | | | | |
| | | TGCCGTGAGT | | | | |
| | | AAATTAAAATT | | | | |
| | | TTATTGACTTA | | | | |
| | | GGTCACTAAAT | | | | |
| | | ACTTTAACCAA | | | | |
| | | TATAGGCATAG | | | G | <u> </u> |
| | | CGCACAGACA | | | Start | End |
| | | GATAAAAATTA | | | Positio | Positio |
| 6076 | 8770 | CAGAGTACAC | 2 | 350 | n | n |
| | | AACATCCATGA | | | 6359 | 6708 |
| | | AACGCATTAGC | | | 7574 | 7923 |
| | | ACCACCATTAC | | | 1011 | 7 020 |
| | | CACCACCATCA | | | | |
| | | CCATTACCACA | | | | |
| | | GGTAACGGTG | | | | |
| | | CGGGCTGACG | | | | |
| | | CGTACAGGAA | | | | |
| | | ACACAGAAAAA | | | | |
| | | AGCCCGCACC | | | | |
| | | TGACAGTGCG | | | | |
| | | GGCTTTTTTTT | | | | |
| | | CGACCAAAGG | | | | |
| | | TAACGAGGTAA | | | | |
| | | CAACCATGCG | | | | |
| | | AGTGTTGAAGT | | | | |

SRGD Performance Metrics

| Initial Reads Count: | 1212 |
|---|------|
| Reads Count after Removing Duplication: | 388 |

| Reads Count after Overlapping: | | 158 | | | | |
|---|--------------------------|-------------------|-------------------|---------------------------|----|--|
| Initial Dataset Size in (Base): | | | 241272 | | | |
| Dataset Sizet after Removing Duplication: | | | 99165 | | | |
| Dataset Size after Overlapping: | | | 35306 | | | |
| Overlapping Metri | CS | | | | | |
| Repeat Identification Time: | | | 00h:00m:08s:000ms | | | |
| Overlapping Time: | | | 00h:03m:14s:000ms | | | |
| Reads Alignment Time: | | | 00h:00m:19s:000ms | | | |
| Total Hybrid Assembly Time: | | | 00h:03m:33s:000ms | | | |
| Repeat Annotation Time: | | 00h:00m:10s:000ms | | | | |
| Overlapping Length | O(N)2 Time Complexity | Hit Index Count | | Overlapping Matched Count | RI | |
| 200 | 116281 | 158 | | 31 | 0 | |
| 199 | 96100 | 140 | | 20 | 0 | |
| 198 | 84100 | 124 | | 13 | 0 | |
| 197 | 76729 | 109 | | 20 | 0 | |
| 196 | 66049 | 88 | | 6 | 0 | |
| 195 | 63001 | 64 | | 1 | 0 | |
| 194 | 62500 | 107 | | 8 | 0 | |
| 193 | 58564 | 56 | | 4 | 0 | |
| 191 | 56644 | 56 | | 1 | 0 | |
| 190 | 56169 | 68 | | 2 | 0 | |
| 188 | 55225 | 64 | | 5 | 0 | |
| 187 | 52900 | 73 | | 1 | 0 | |

| 186 | 52441 | 53 | 1 | 0 |
|-----|-------|-----|----|---|
| 183 | 51984 | 82 | 1 | 0 |
| 181 | 51529 | 66 | 1 | 0 |
| 180 | 51076 | 81 | 1 | 0 |
| 179 | 50625 | 80 | 2 | 0 |
| 178 | 49729 | 68 | 1 | 0 |
| 177 | 49284 | 77 | 1 | 0 |
| 176 | 48841 | 242 | 96 | 0 |
| 174 | 15625 | 30 | 2 | 0 |
| 172 | 15129 | 26 | 1 | 0 |
| 171 | 14884 | 17 | 1 | 0 |
| 170 | 14641 | 13 | 1 | 0 |
| 169 | 14400 | 27 | 3 | 0 |
| 155 | 13689 | 18 | 1 | 0 |
| 151 | 13456 | 16 | 2 | 0 |
| 146 | 12996 | 26 | 1 | 0 |
| 144 | 12769 | 19 | 1 | 0 |
| 141 | 12544 | 19 | 1 | 0 |
| L | l | | | |