

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/05 04:23:44

1. Input data & parameters

1.1. QualiMap command line

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qualimap bamqc -bam SRR10174068.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR10174068 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10174068_1.fastq.gz SRR10174068_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Sep 05 04:23:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10174068.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,201,592
Mapped reads	4,103,773 / 97.67%
Unmapped reads	97,819 / 2.33%
Mapped paired reads	4,103,773 / 97.67%
Mapped reads, first in pair	2,050,872 / 48.81%
Mapped reads, second in pair	2,052,901 / 48.86%
Mapped reads, both in pair	4,040,596 / 96.17%
Mapped reads, singletons	63,177 / 1.5%
Secondary alignments	0
Supplementary alignments	333,854 / 7.95%
Read min/max/mean length	30 / 133 / 126.92
Duplicated reads (estimated)	3,126,618 / 74.42%
Duplication rate	65.83%
Clipped reads	1,449,757 / 34.5%

2.2. ACGT Content

Number/percentage of A's	147,214,749 / 30.33%
Number/percentage of C's	94,211,501 / 19.41%
Number/percentage of T's	146,677,162 / 30.22%
Number/percentage of G's	97,235,151 / 20.03%
Number/percentage of N's	5,833 / 0%

GC Percentage	39.45%
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2.3. Coverage

Mean	0.1569
Standard Deviation	2.3539

2.4. Mapping Quality

Mean Mapping Quality	53.02
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2.5. Insert size

Mean	628,693.85
Standard Deviation	7,422,415.04
P25/Median/P75	142 / 198 / 285

2.6. Mismatches and indels

General error rate	1.04%
Mismatches	4,912,835
Insertions	50,888
Mapped reads with at least one insertion	1.2%
Deletions	110,549
Mapped reads with at least one deletion	2.62%
Homopolymer indels	43.21%

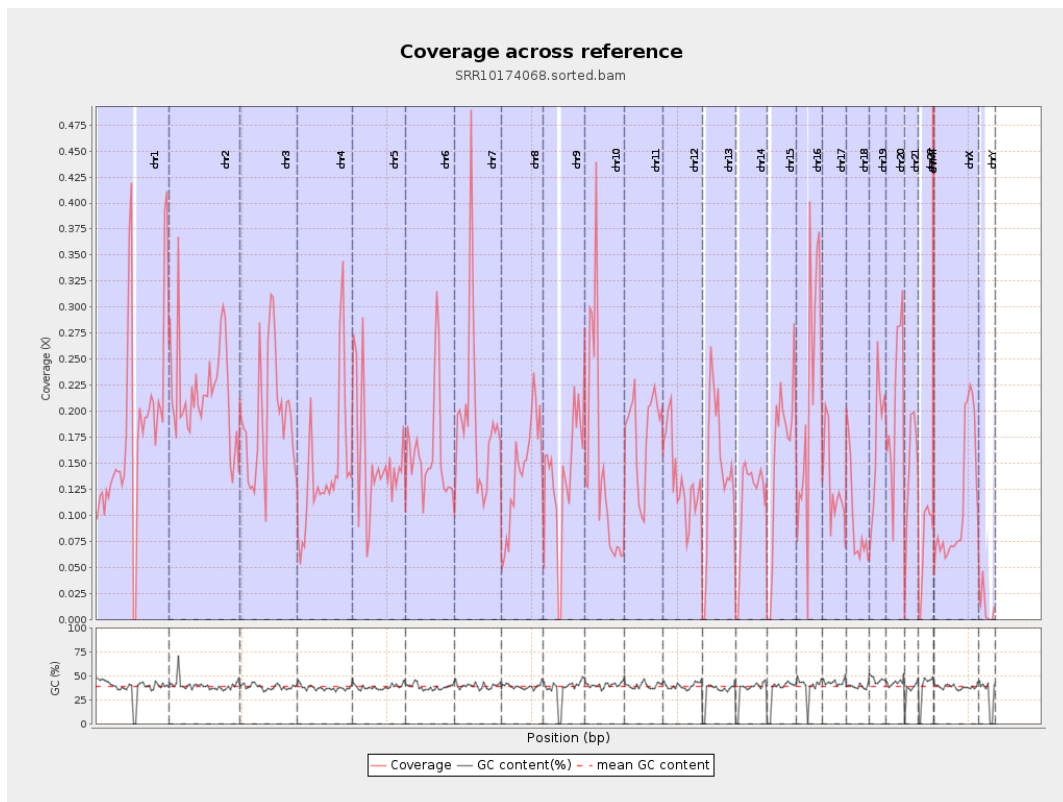
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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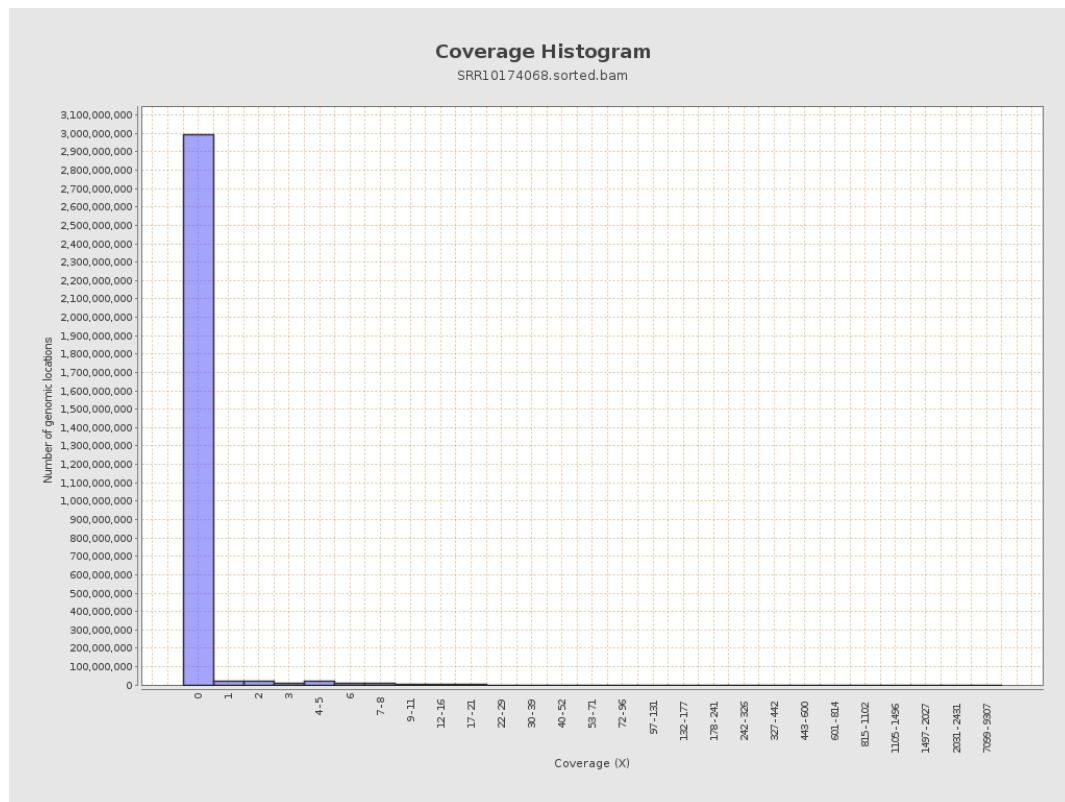
		bases	coverage	deviation
chr1	249250621	44926242	0.1802	1.9671
chr2	243199373	52834976	0.2172	6.5687
chr3	198022430	38323138	0.1935	1.2651
chr4	191154276	26868334	0.1406	1.3014
chr5	180915260	27780077	0.1536	1.116
chr6	171115067	27466799	0.1605	1.1889
chr7	159138663	30287971	0.1903	2.4198
chr8	146364022	21007591	0.1435	1.259
chr9	141213431	19791610	0.1402	1.2906
chr10	135534747	19778770	0.1459	2.8235
chr11	135006516	24254254	0.1797	1.2416
chr12	133851895	17861479	0.1334	1.0514
chr13	115169878	16407456	0.1425	1.0921
chr14	107349540	12142819	0.1131	0.9725
chr15	102531392	16180469	0.1578	1.1193
chr16	90354753	19178085	0.2123	1.865
chr17	81195210	10294163	0.1268	1.1005
chr18	78077248	7596525	0.0973	1.5901
chr19	59128983	10145619	0.1716	2.1939
chr20	63025520	13063326	0.2073	1.2916
chr21	48129895	6895646	0.1433	1.112
chr22	51304566	3714128	0.0724	0.7273
chrMT	16571	1144437	69.0626	58.69
chrX	155270560	16999932	0.1095	0.9488

chrY	59373566	677877	0.0114	0.5458
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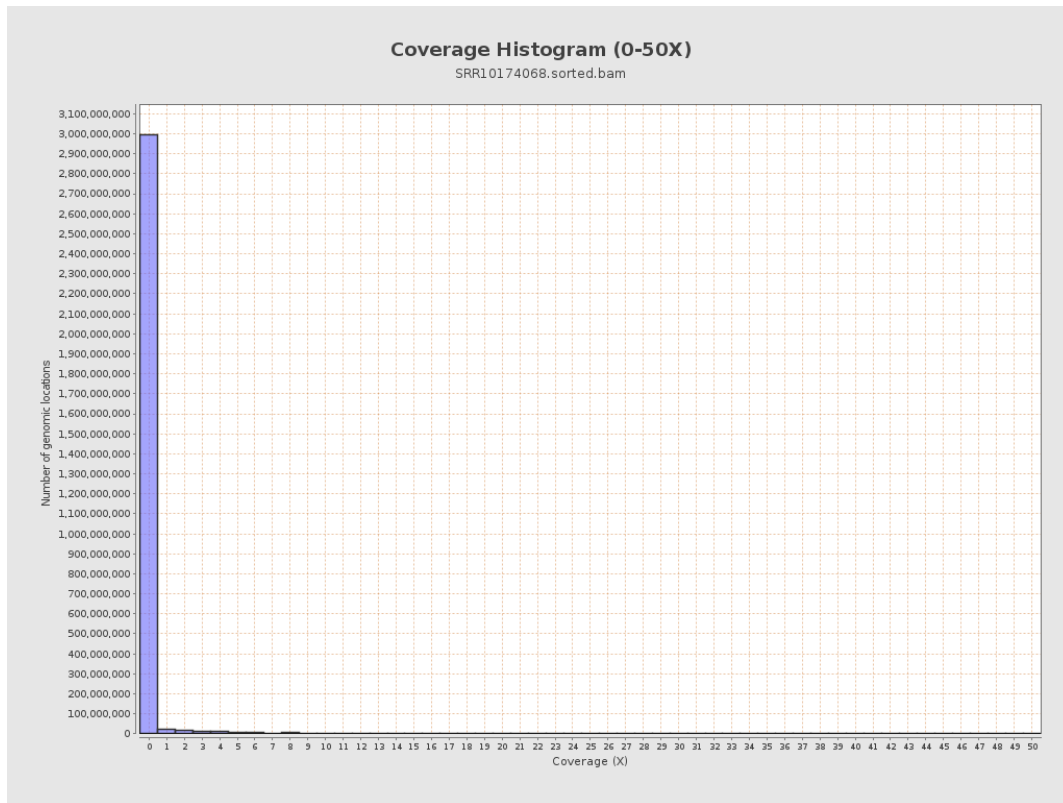
3. Results : Coverage across reference



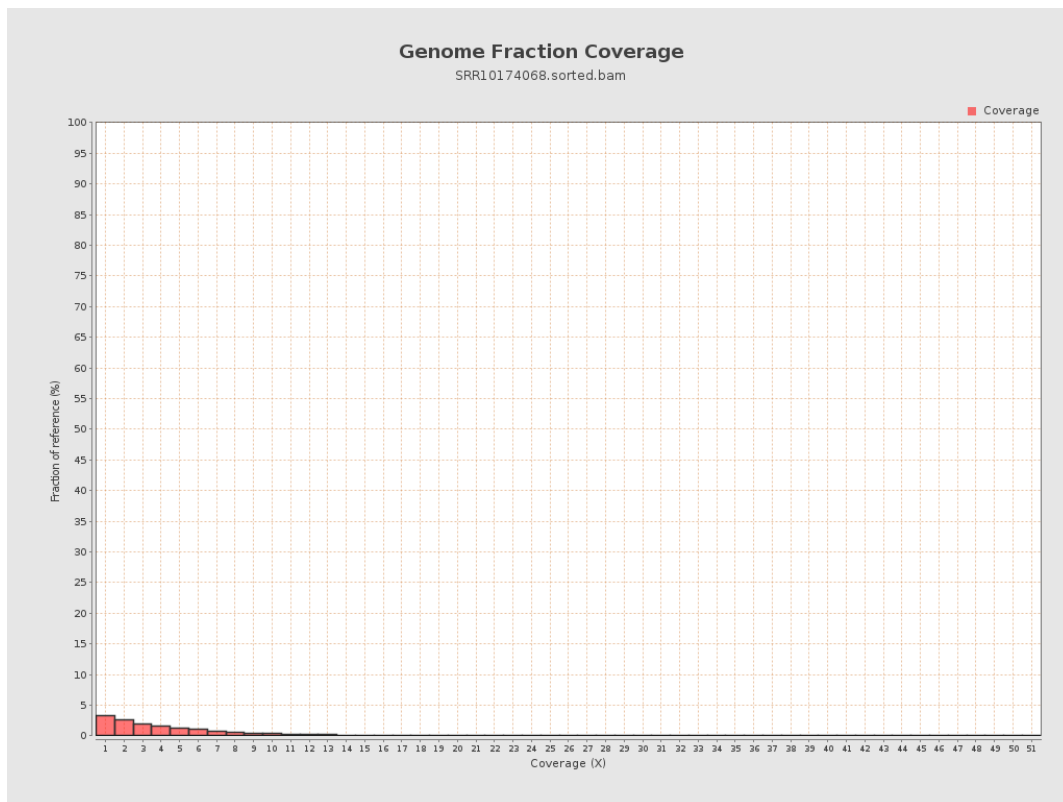
4. Results : Coverage Histogram



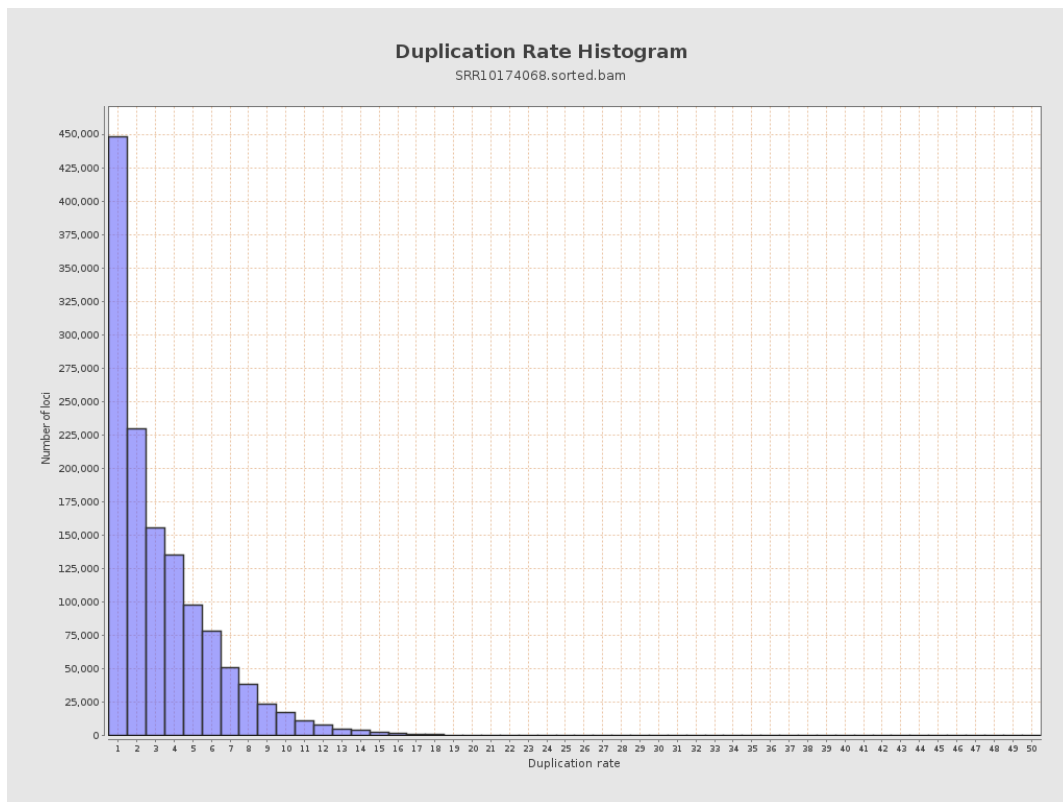
5. Results : Coverage Histogram (0-50X)



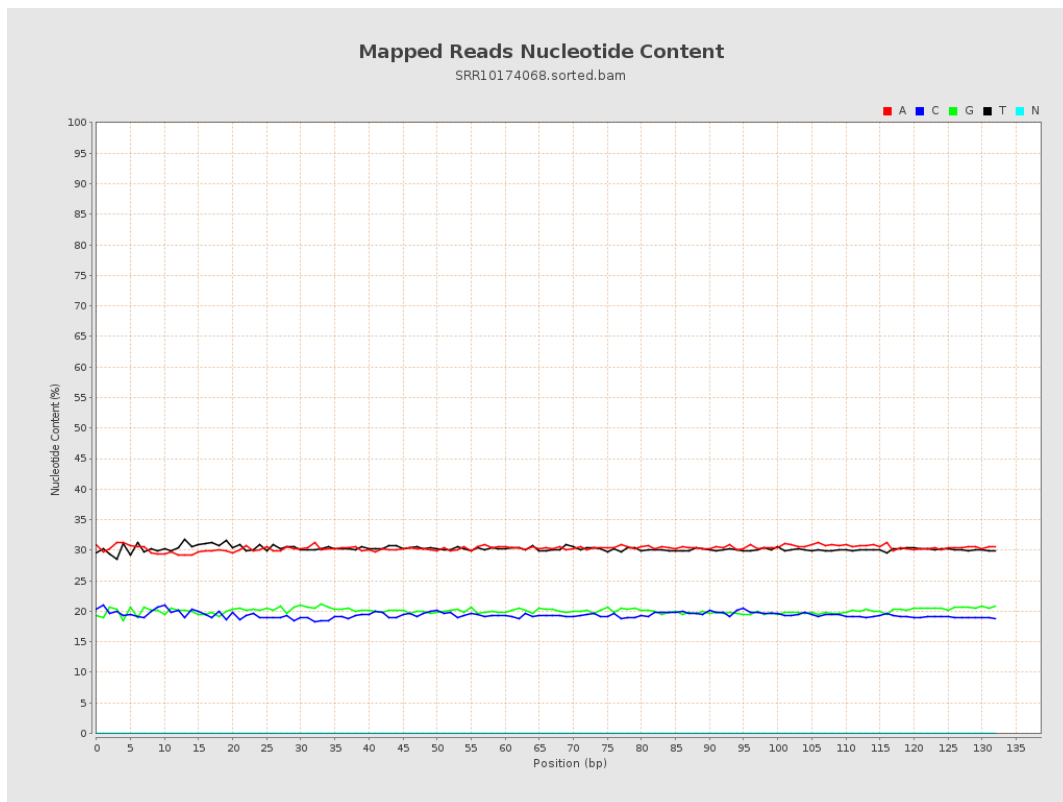
6. Results : Genome Fraction Coverage



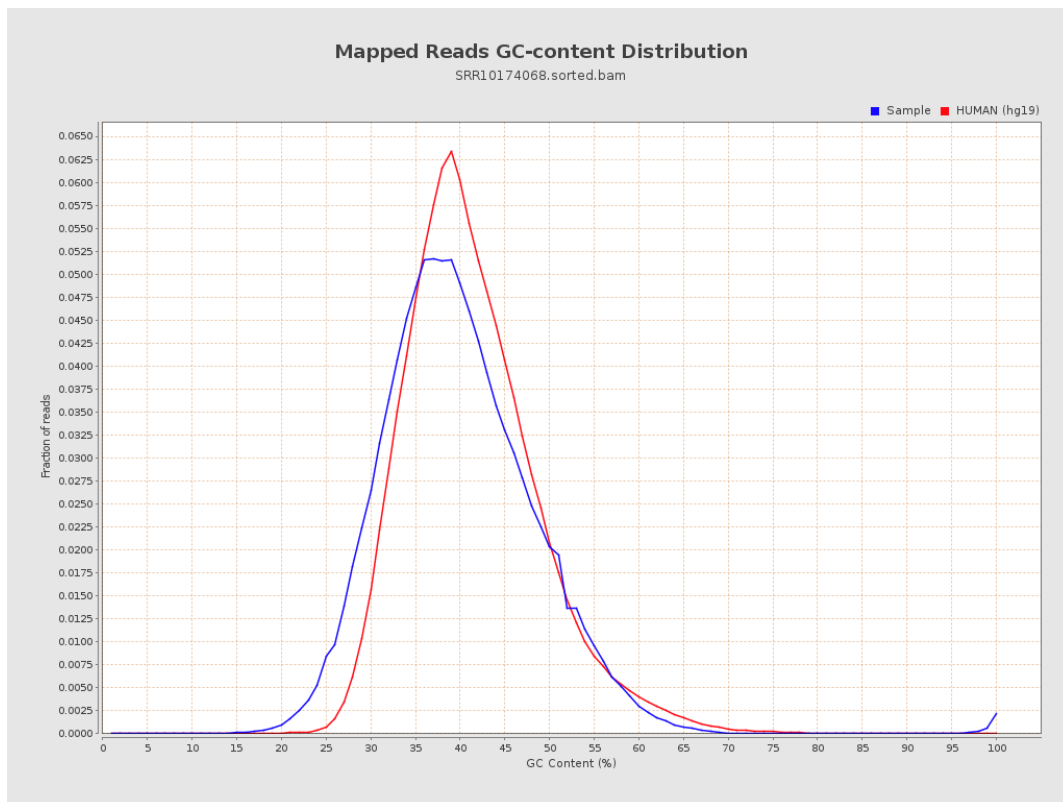
7. Results : Duplication Rate Histogram



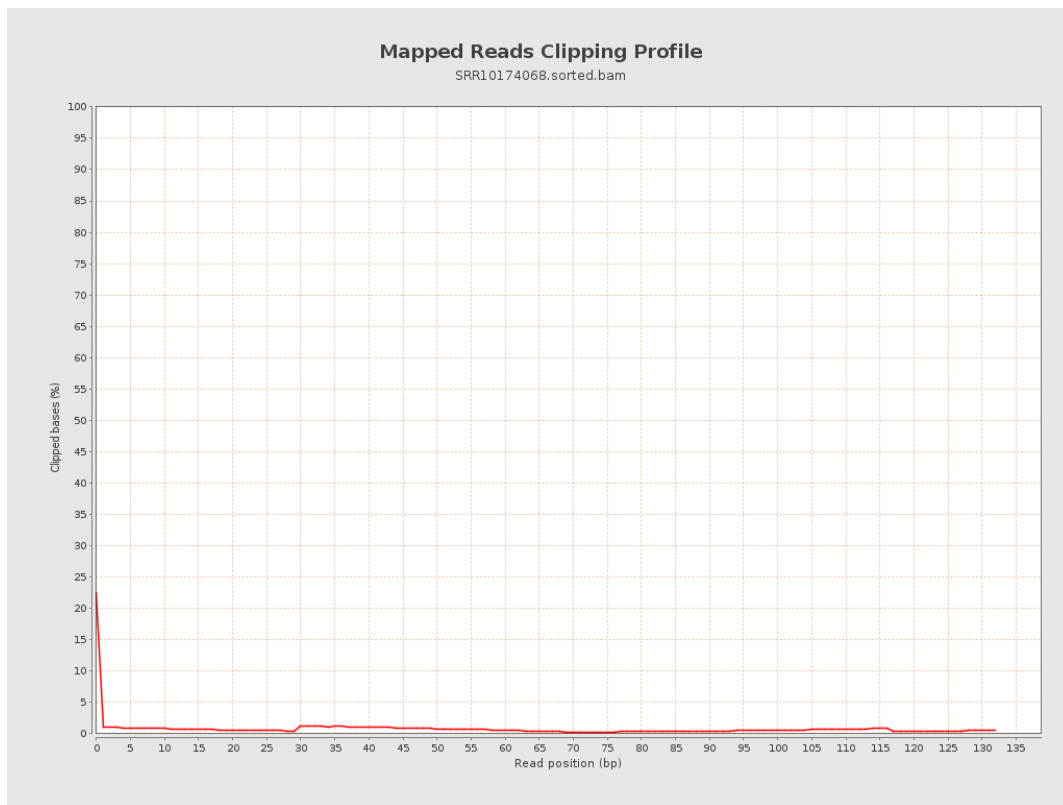
8. Results : Mapped Reads Nucleotide Content



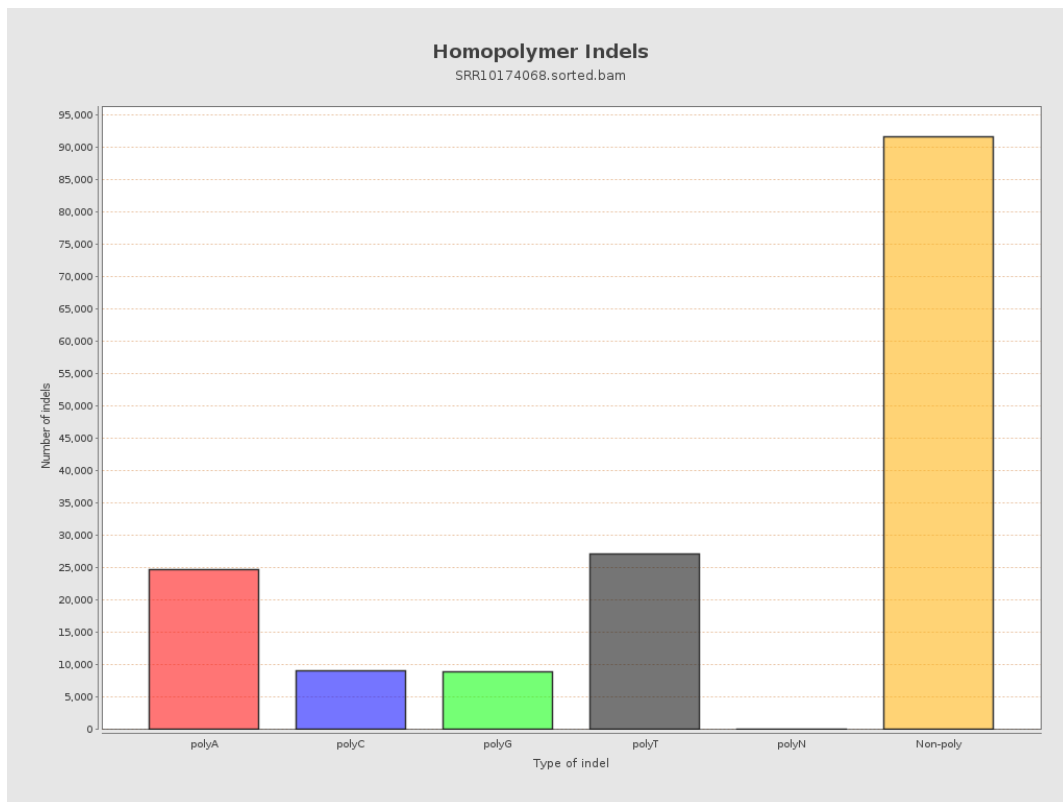
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



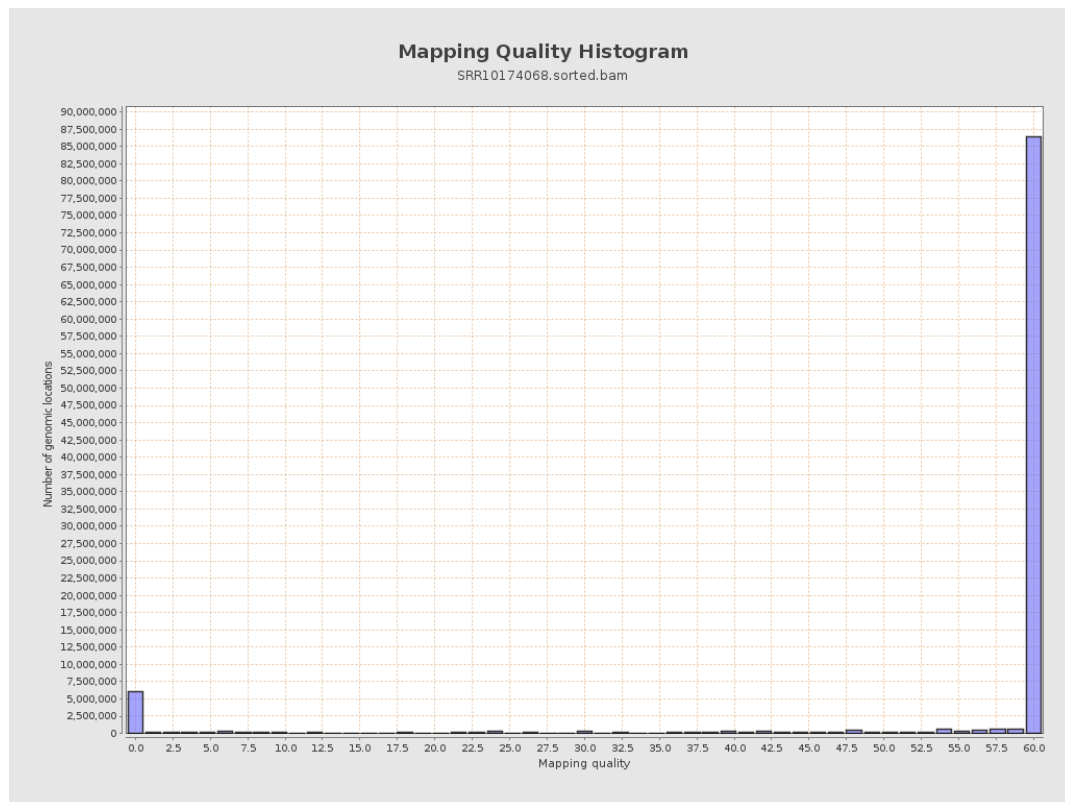
11. Results : Homopolymer Indels



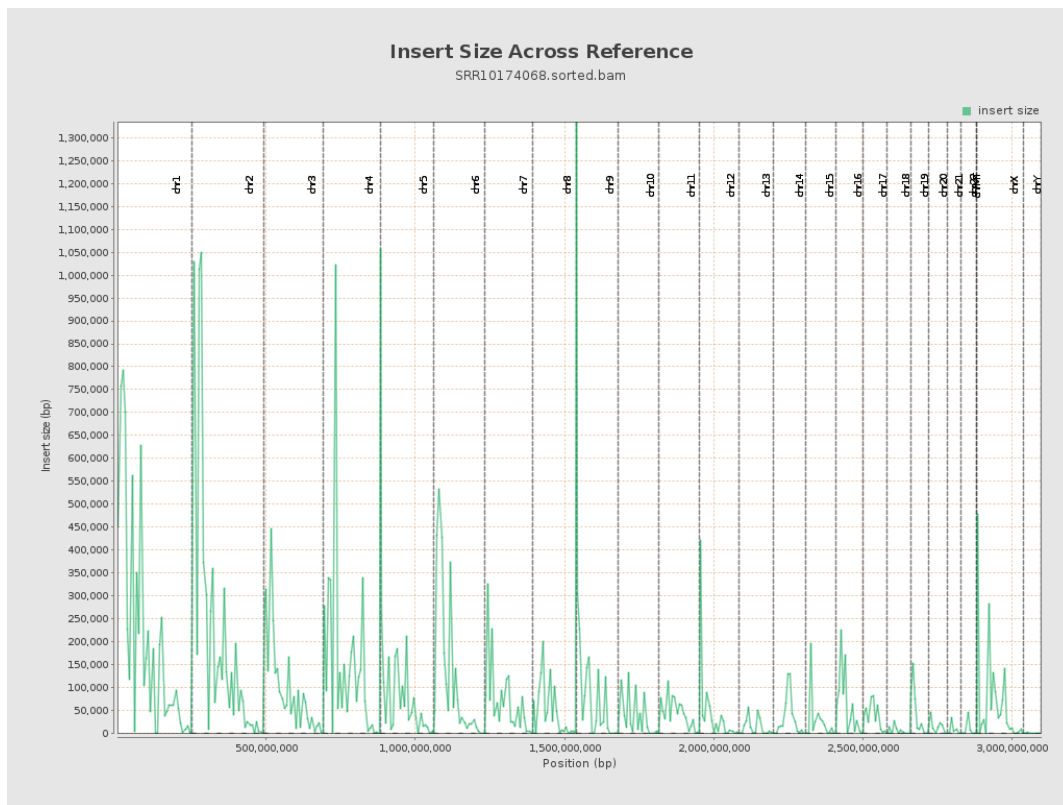
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

