

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 01:46:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173885.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_SRR10173885 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173885_1.fastq.gz SRR10173885_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 01:46:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173885.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,267,908
Mapped reads	1,231,314 / 97.11%
Unmapped reads	36,594 / 2.89%
Mapped paired reads	1,231,314 / 97.11%
Mapped reads, first in pair	616,768 / 48.64%
Mapped reads, second in pair	614,546 / 48.47%
Mapped reads, both in pair	1,209,388 / 95.38%
Mapped reads, singletons	21,926 / 1.73%
Secondary alignments	0
Supplementary alignments	128,363 / 10.12%
Read min/max/mean length	30 / 133 / 128
Duplicated reads (estimated)	886,888 / 69.95%
Duplication rate	60.36%
Clipped reads	541,268 / 42.69%

2.2. ACGT Content

Number/percentage of A's	43,895,617 / 30.38%
Number/percentage of C's	27,976,687 / 19.37%
Number/percentage of T's	43,610,142 / 30.19%
Number/percentage of G's	28,981,095 / 20.06%
Number/percentage of N's	1,748 / 0%

GC Percentage	39.43%
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2.3. Coverage

Mean	0.0467
Standard Deviation	0.8647

2.4. Mapping Quality

Mean Mapping Quality	52.67
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2.5. Insert size

Mean	1,125,268.13
Standard Deviation	9,560,510.85
P25/Median/P75	139 / 196 / 288

2.6. Mismatches and indels

General error rate	1.13%
Mismatches	1,580,730
Insertions	18,043
Mapped reads with at least one insertion	1.41%
Deletions	36,359
Mapped reads with at least one deletion	2.87%
Homopolymer indels	41.7%

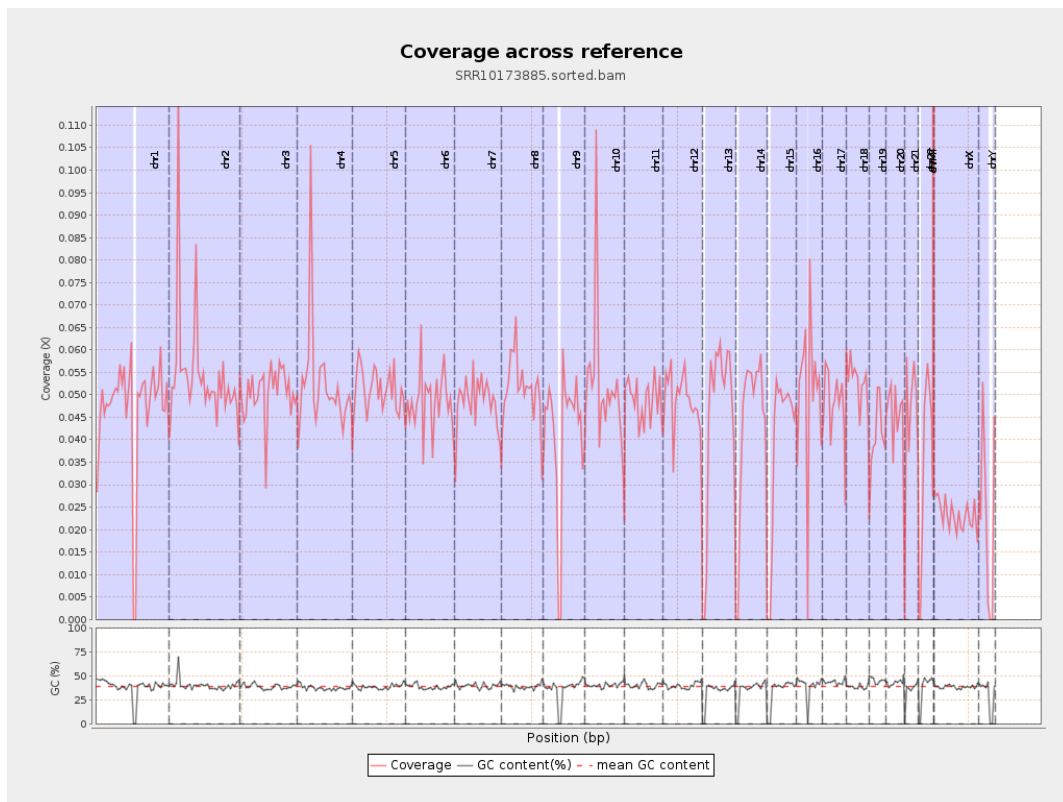
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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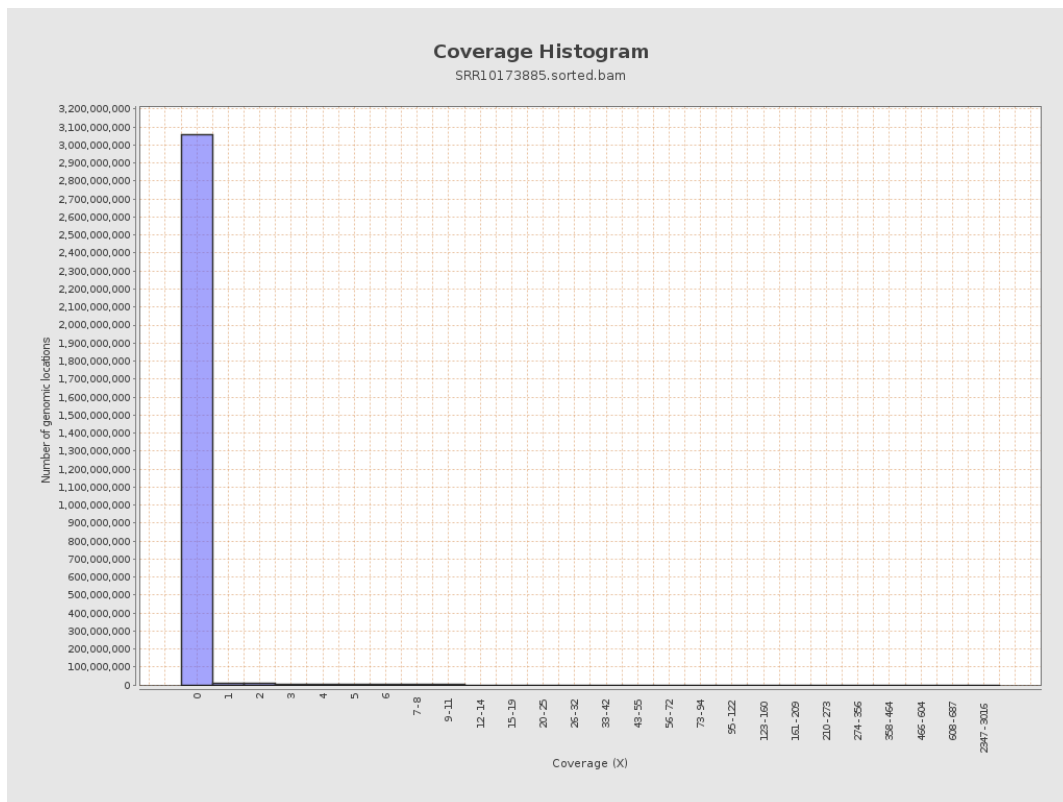
		bases	coverage	deviation
chr1	249250621	11710002	0.047	0.67
chr2	243199373	13289294	0.0546	2.178
chr3	198022430	10044861	0.0507	0.5984
chr4	191154276	9938241	0.052	0.7227
chr5	180915260	9307895	0.0514	0.6062
chr6	171115067	8255354	0.0482	0.6027
chr7	159138663	7756534	0.0487	0.6513
chr8	146364022	7515479	0.0513	0.8071
chr9	141213431	5879399	0.0416	0.6768
chr10	135534747	7038598	0.0519	0.819
chr11	135006516	6511504	0.0482	0.5842
chr12	133851895	6487663	0.0485	0.5733
chr13	115169878	5153296	0.0447	0.5636
chr14	107349540	4696980	0.0438	0.5562
chr15	102531392	4057604	0.0396	0.52
chr16	90354753	4538956	0.0502	0.6533
chr17	81195210	3861070	0.0476	0.5984
chr18	78077248	4143353	0.0531	0.8862
chr19	59128983	2455006	0.0415	0.5767
chr20	63025520	2888718	0.0458	0.5635
chr21	48129895	2128794	0.0442	0.6364
chr22	51304566	1764336	0.0344	0.494
chrMT	16571	185125	11.1716	10.5893
chrX	155270560	3640314	0.0234	0.4012

chrY	59373566	1308372	0.022	0.4825
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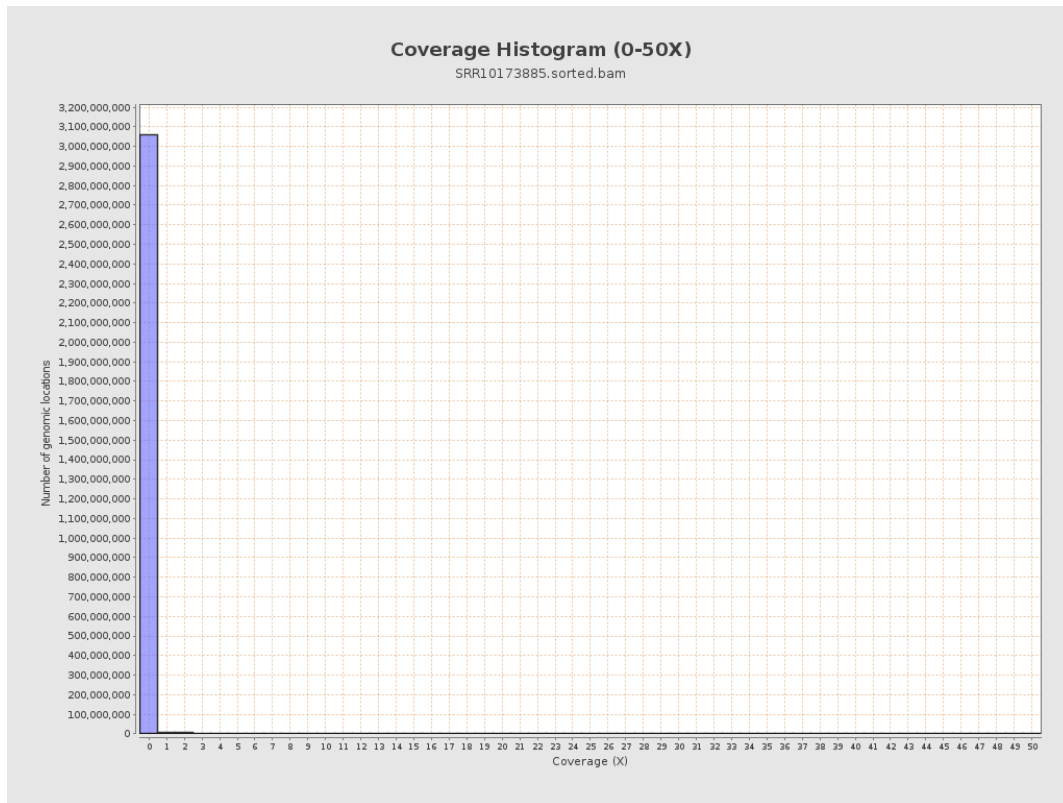
3. Results : Coverage across reference



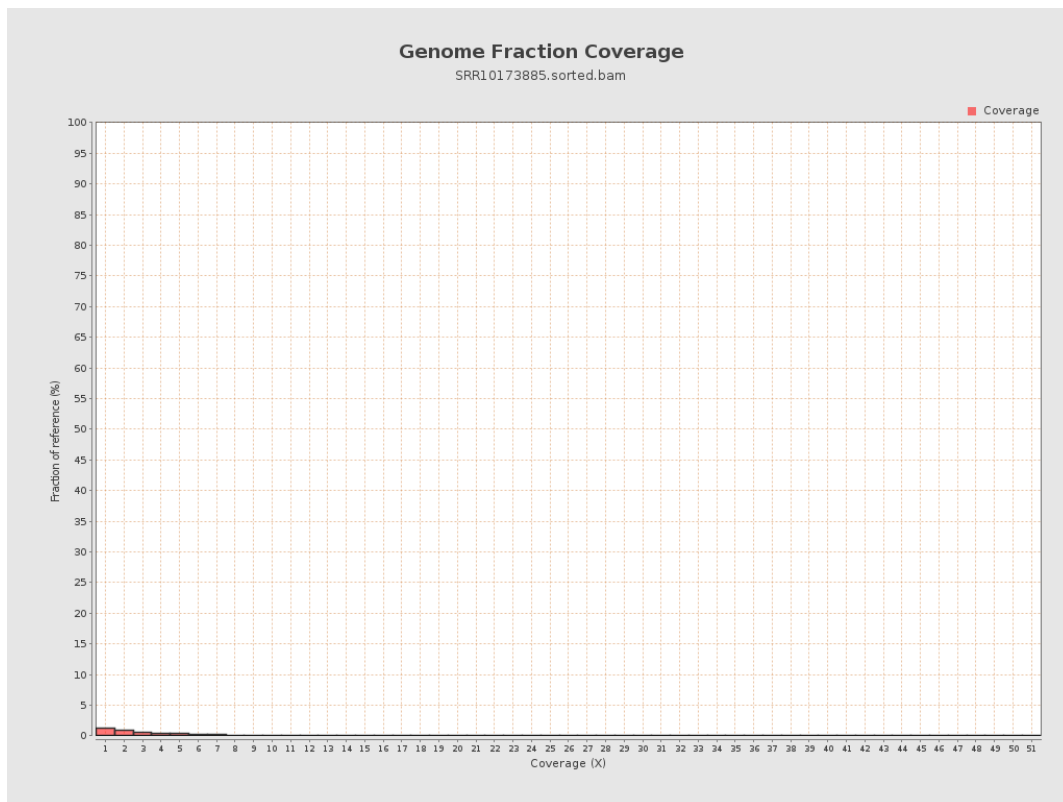
4. Results : Coverage Histogram



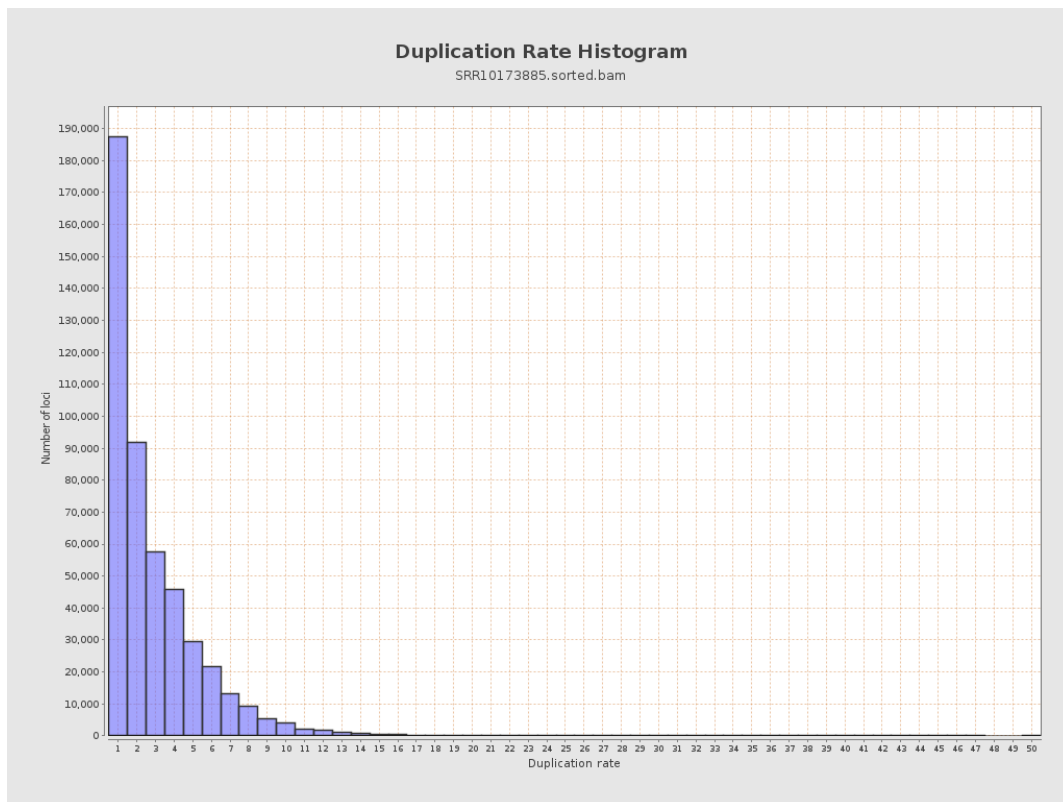
5. Results : Coverage Histogram (0-50X)



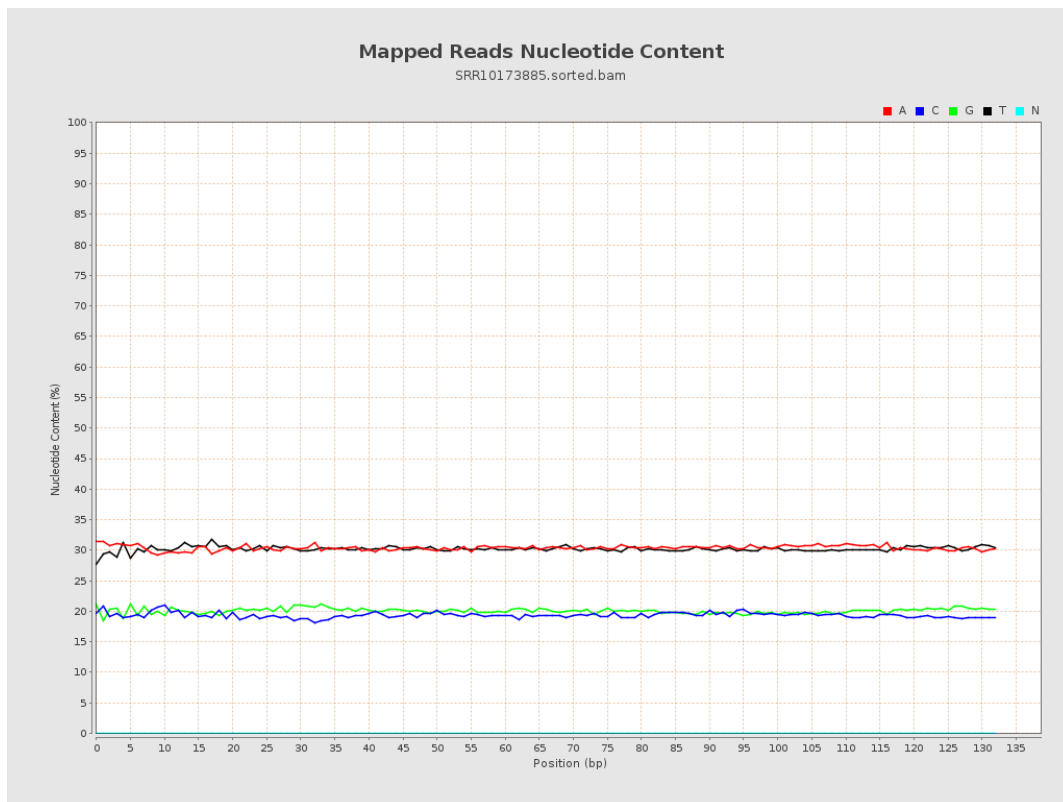
6. Results : Genome Fraction Coverage



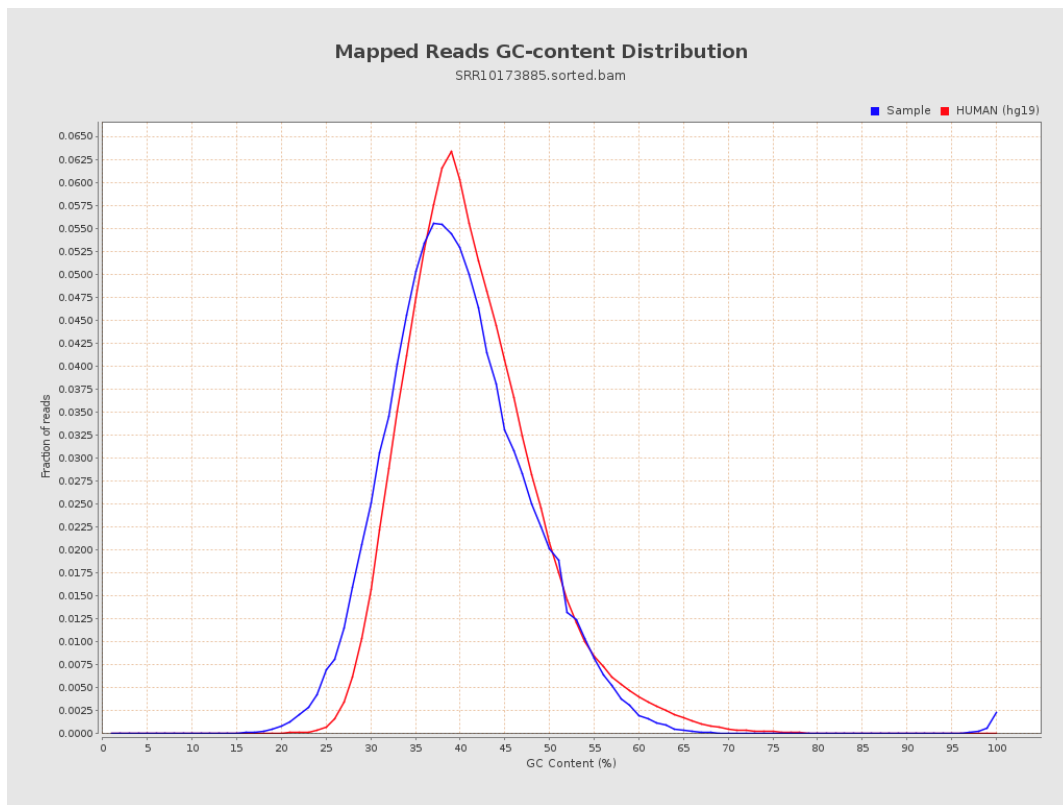
7. Results : Duplication Rate Histogram



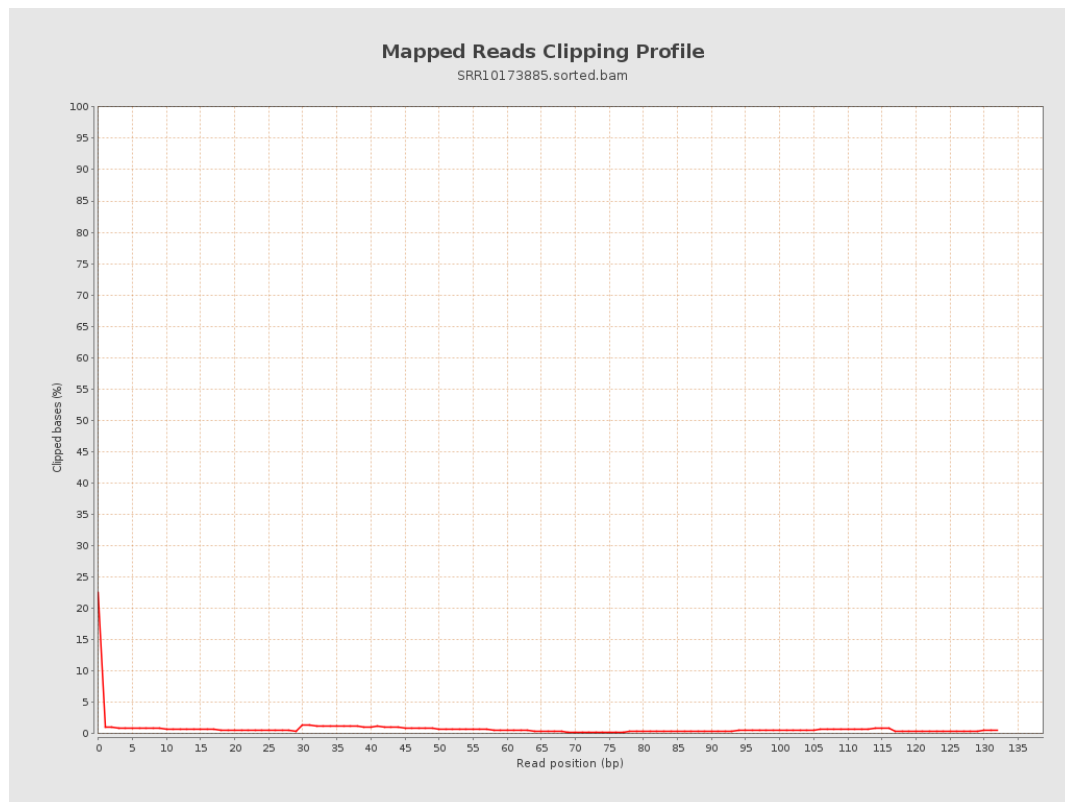
8. Results : Mapped Reads Nucleotide Content



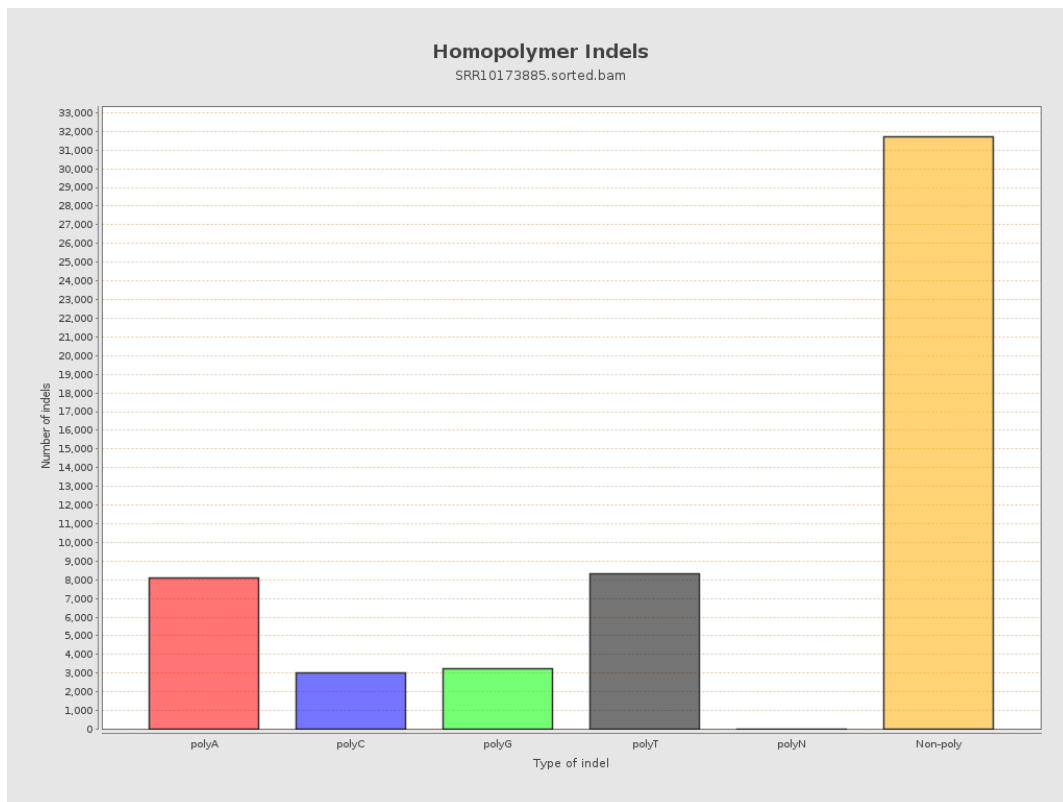
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



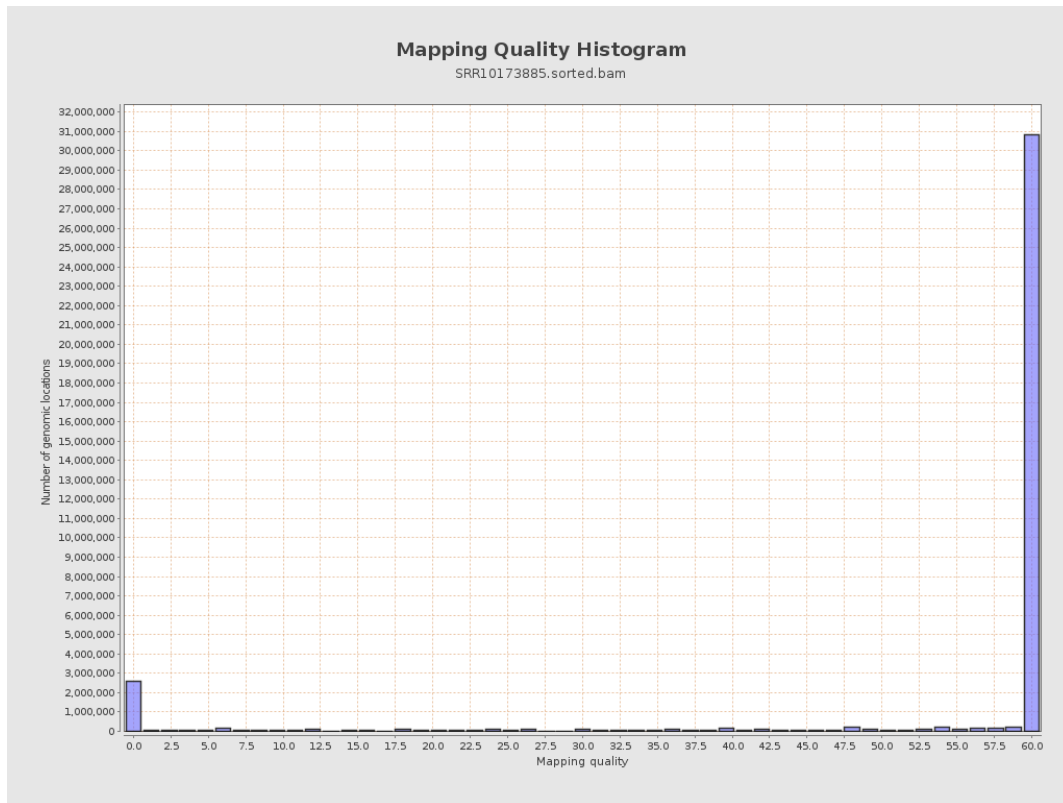
11. Results : Homopolymer Indels



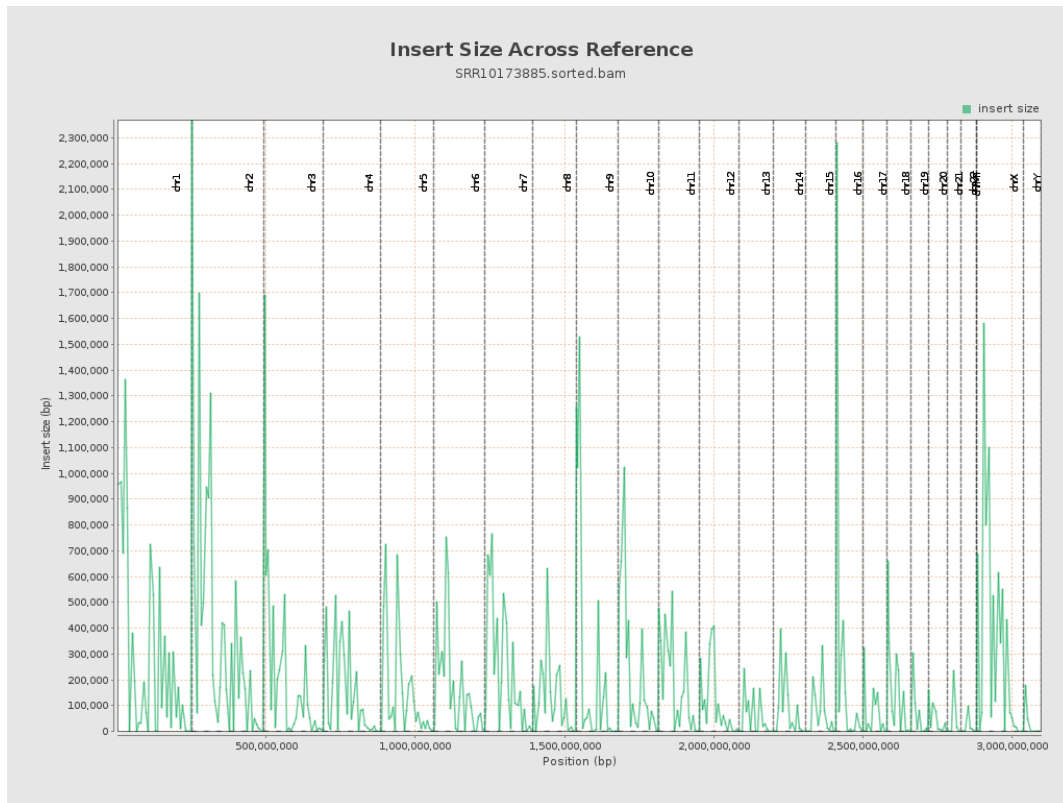
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

