

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/18 01:51:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006409.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_SRR1006409 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006409_1.fastq.gz SRR1006409_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 18 01:51:43 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006409.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,467,772
Mapped reads	6,513,801 / 87.23%
Unmapped reads	953,971 / 12.77%
Mapped paired reads	6,513,801 / 87.23%
Mapped reads, first in pair	3,289,991 / 44.06%
Mapped reads, second in pair	3,223,810 / 43.17%
Mapped reads, both in pair	5,906,364 / 79.09%
Mapped reads, singletons	607,437 / 8.13%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	266,325 / 3.57%
Duplication rate	3.43%
Clipped reads	376,726 / 5.04%

2.2. ACGT Content

Number/percentage of A's	70,173,123 / 27.84%
Number/percentage of C's	54,371,070 / 21.57%
Number/percentage of T's	71,468,158 / 28.36%
Number/percentage of G's	56,011,575 / 22.22%
Number/percentage of N's	10,730 / 0%
GC Percentage	43.8%

2.3. Coverage

Mean	0.0814
Standard Deviation	0.4697

2.4. Mapping Quality

Mean Mapping Quality	47.91
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2.5. Insert size

Mean	85,581.19
Standard Deviation	2,781,376.39
P25/Median/P75	118 / 158 / 215

2.6. Mismatches and indels

General error rate	0.35%
Mismatches	866,368
Insertions	6,705
Mapped reads with at least one insertion	0.1%
Deletions	21,807
Mapped reads with at least one deletion	0.33%
Homopolymer indels	43.73%

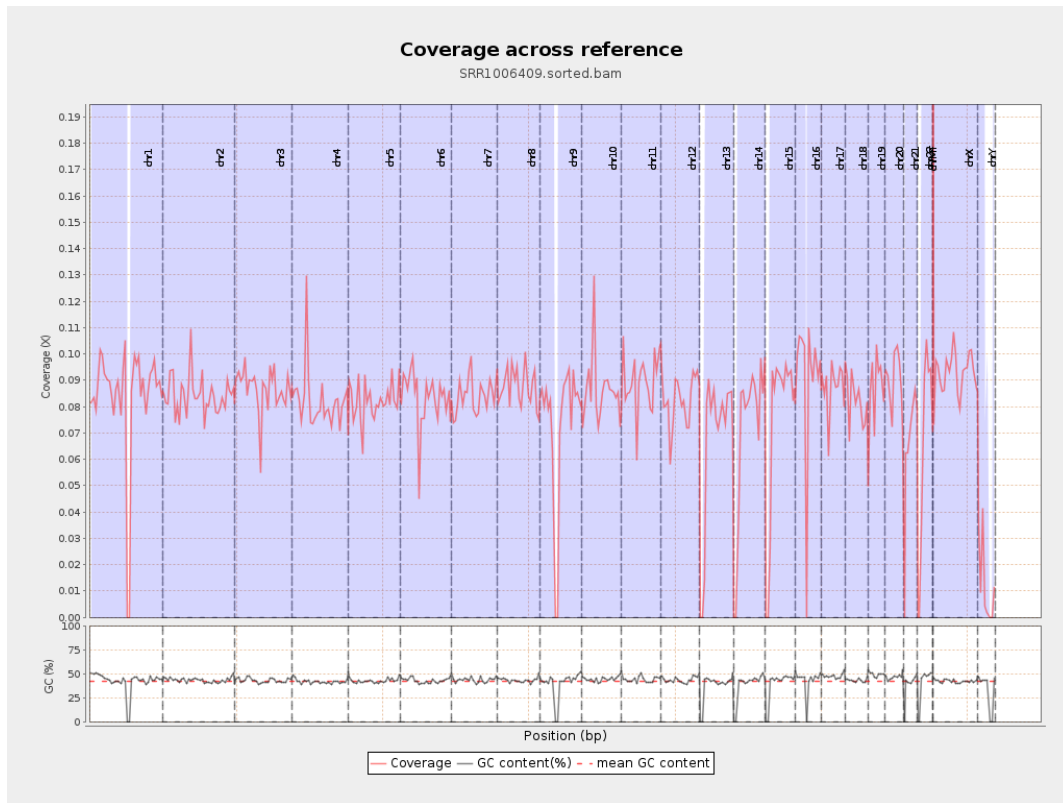
2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

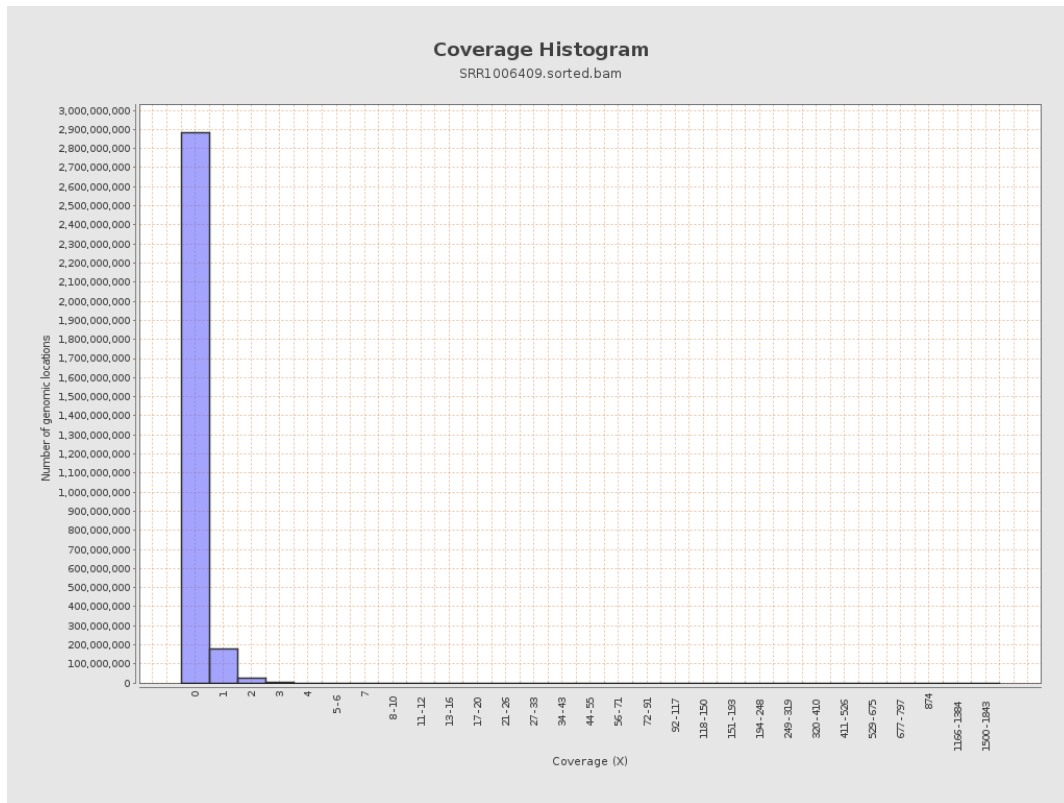
chr1	249250621	20934266	0.084	0.7022
chr2	243199373	20484433	0.0842	0.4231
chr3	198022430	17146332	0.0866	0.3334
chr4	191154276	15741430	0.0823	0.3871
chr5	180915260	14889727	0.0823	0.3261
chr6	171115067	14333965	0.0838	0.3588
chr7	159138663	13403896	0.0842	0.5237
chr8	146364022	12805644	0.0875	0.9596
chr9	141213431	10354963	0.0733	0.3552
chr10	135534747	11662192	0.086	0.5354
chr11	135006516	12023362	0.0891	0.4058
chr12	133851895	11090002	0.0829	0.3294
chr13	115169878	7764053	0.0674	0.2948
chr14	107349540	7616146	0.0709	0.3427
chr15	102531392	7496339	0.0731	0.307
chr16	90354753	8184354	0.0906	0.4377
chr17	81195210	7114622	0.0876	0.3544
chr18	78077248	6415665	0.0822	0.6096
chr19	59128983	5178866	0.0876	0.5347
chr20	63025520	5660198	0.0898	0.3552
chr21	48129895	3225147	0.067	0.3424
chr22	51304566	3373809	0.0658	0.2997
chrMT	16571	7822	0.472	0.821
chrX	155270560	14436808	0.093	0.3801

chrY	59373566	719424	0.0121	0.3187
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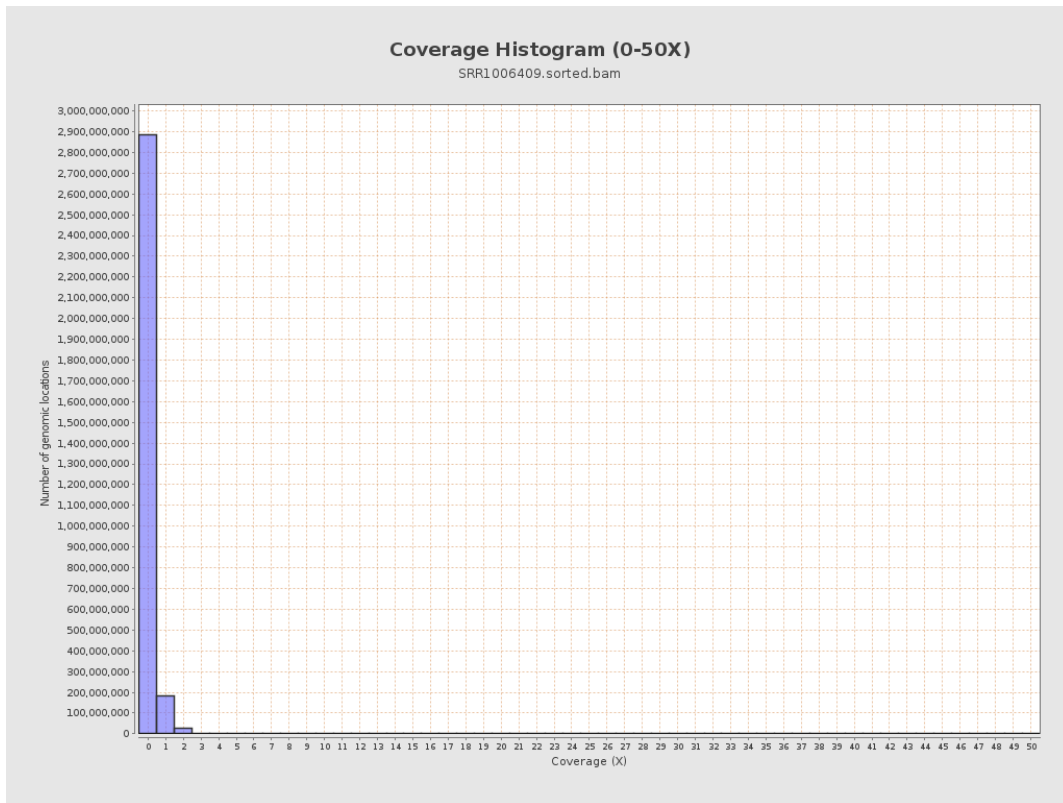
3. Results : Coverage across reference



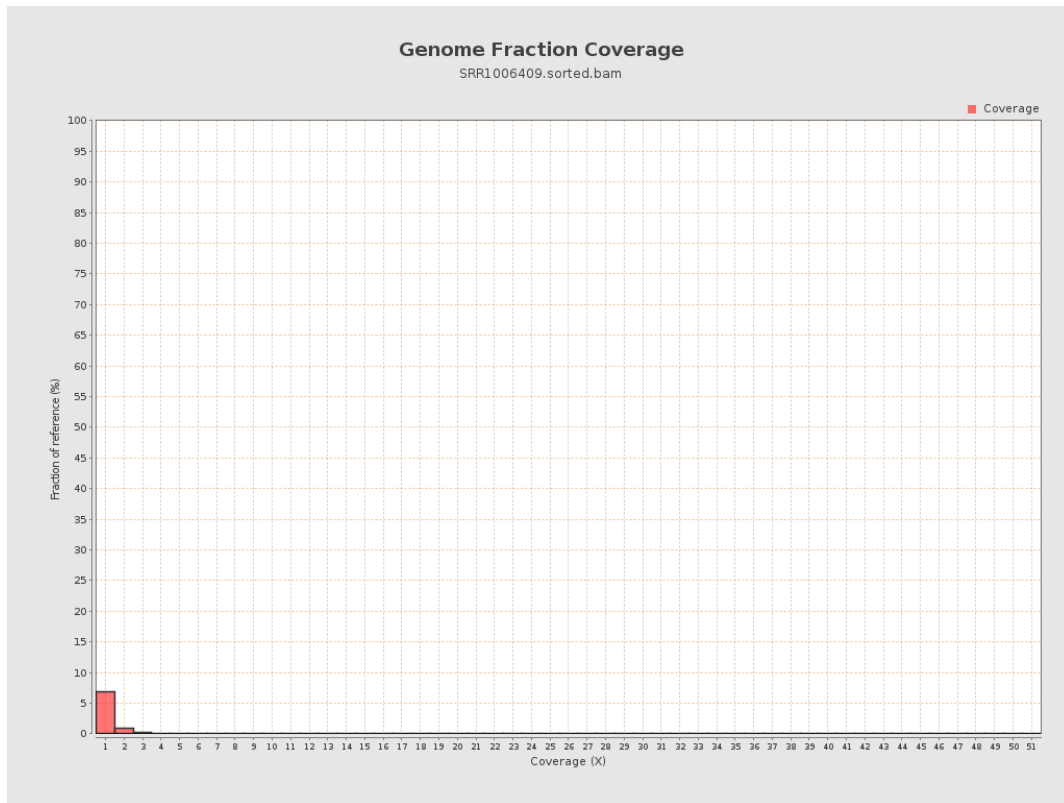
4. Results : Coverage Histogram



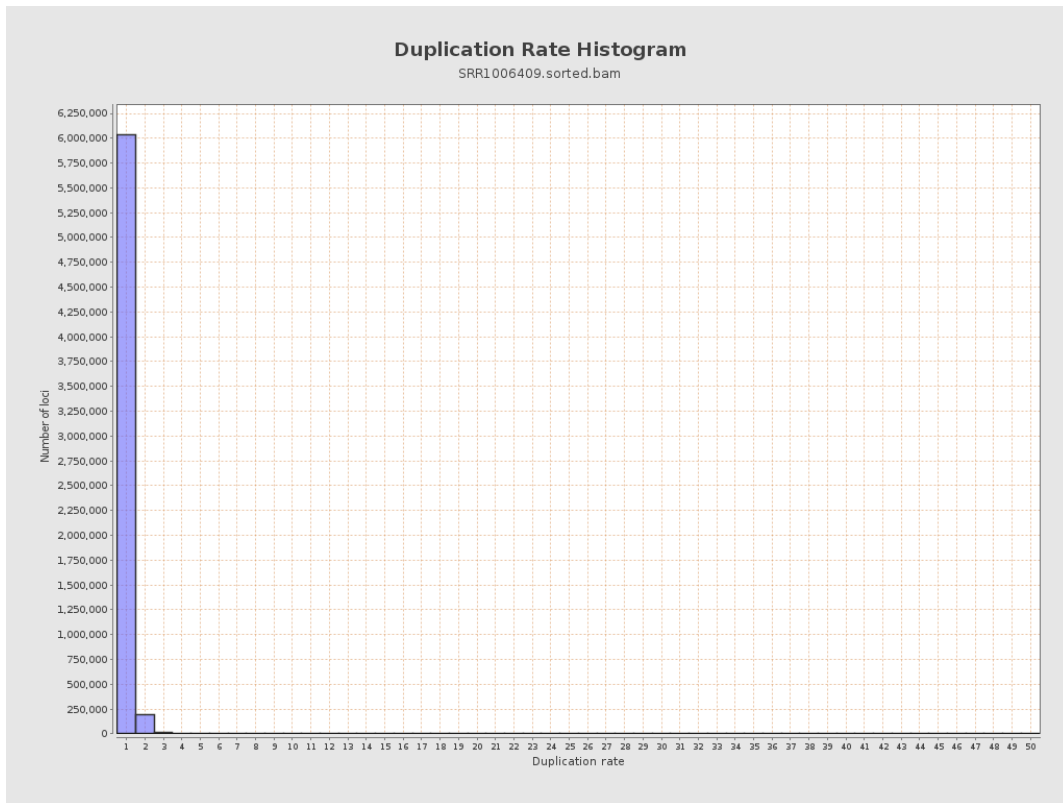
5. Results : Coverage Histogram (0-50X)



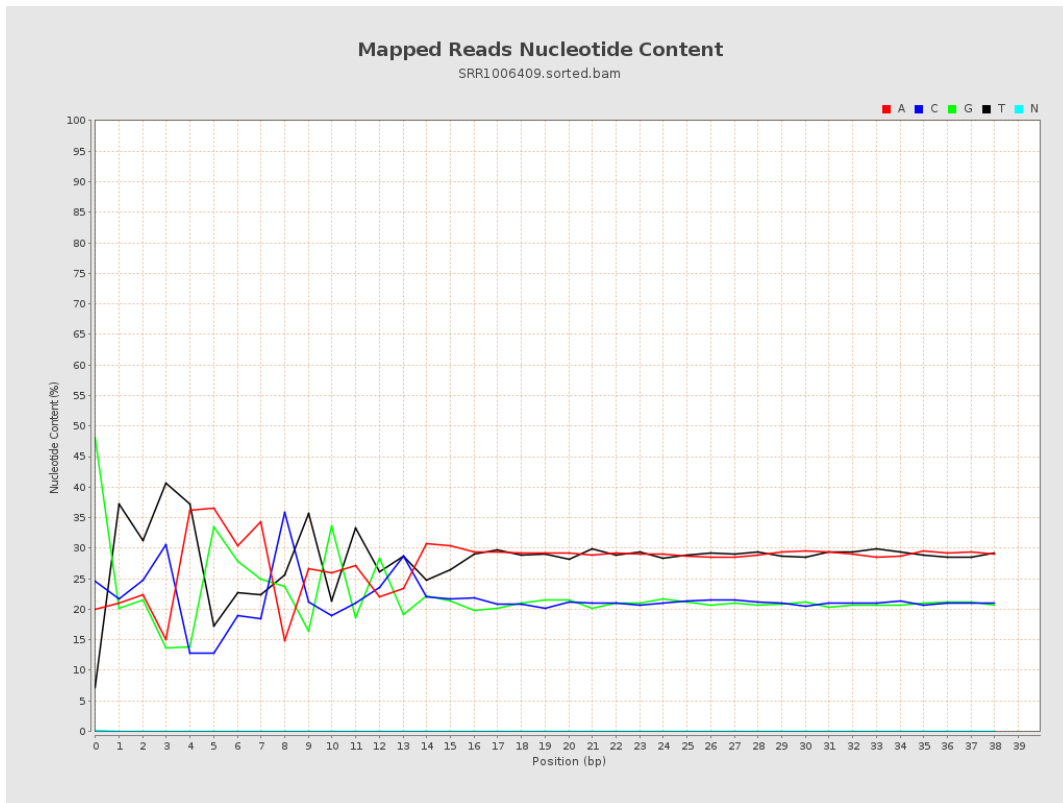
6. Results : Genome Fraction Coverage



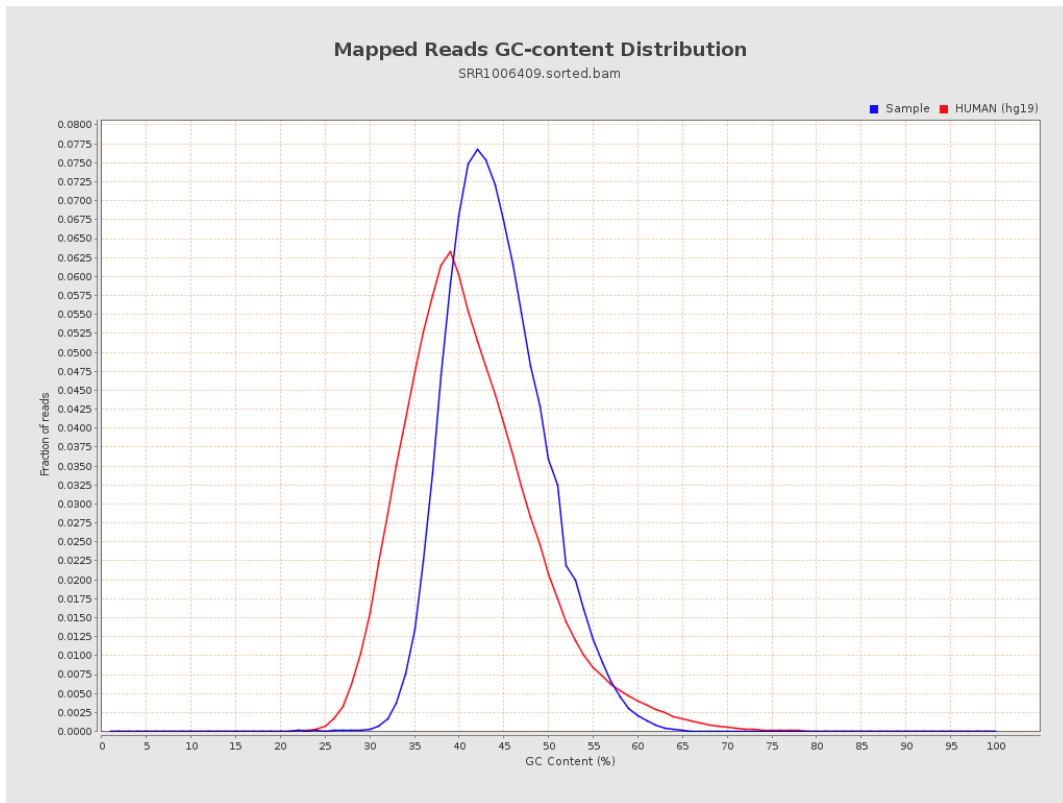
7. Results : Duplication Rate Histogram



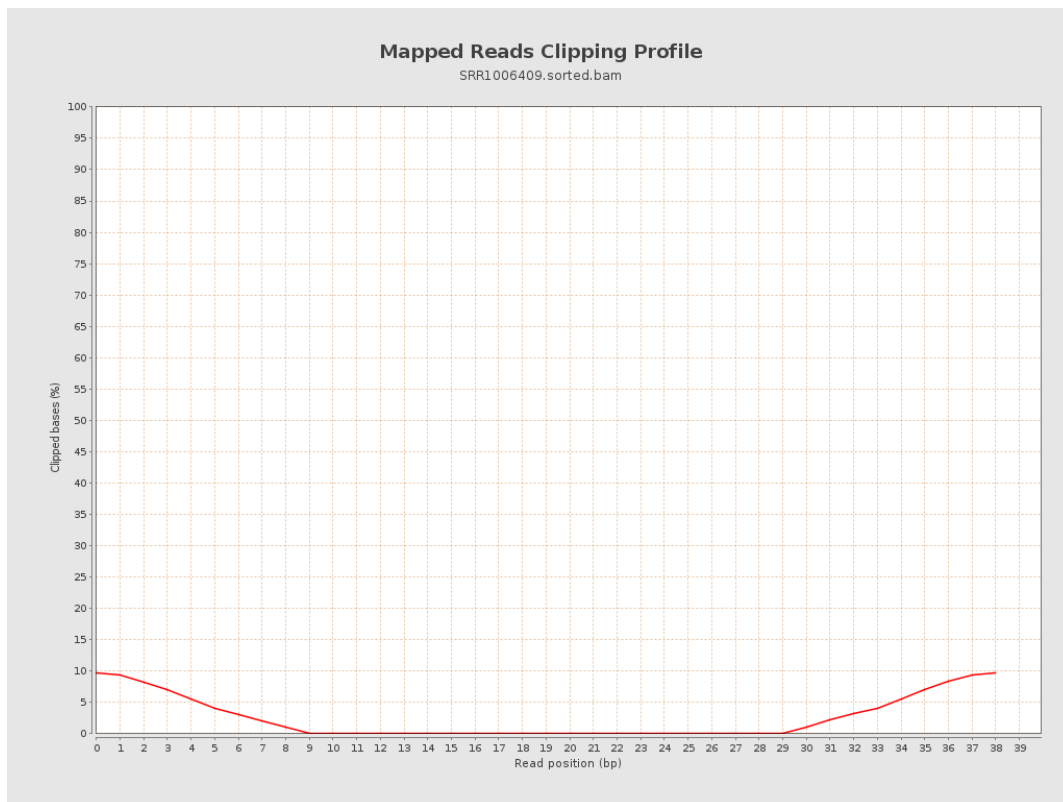
8. Results : Mapped Reads Nucleotide Content



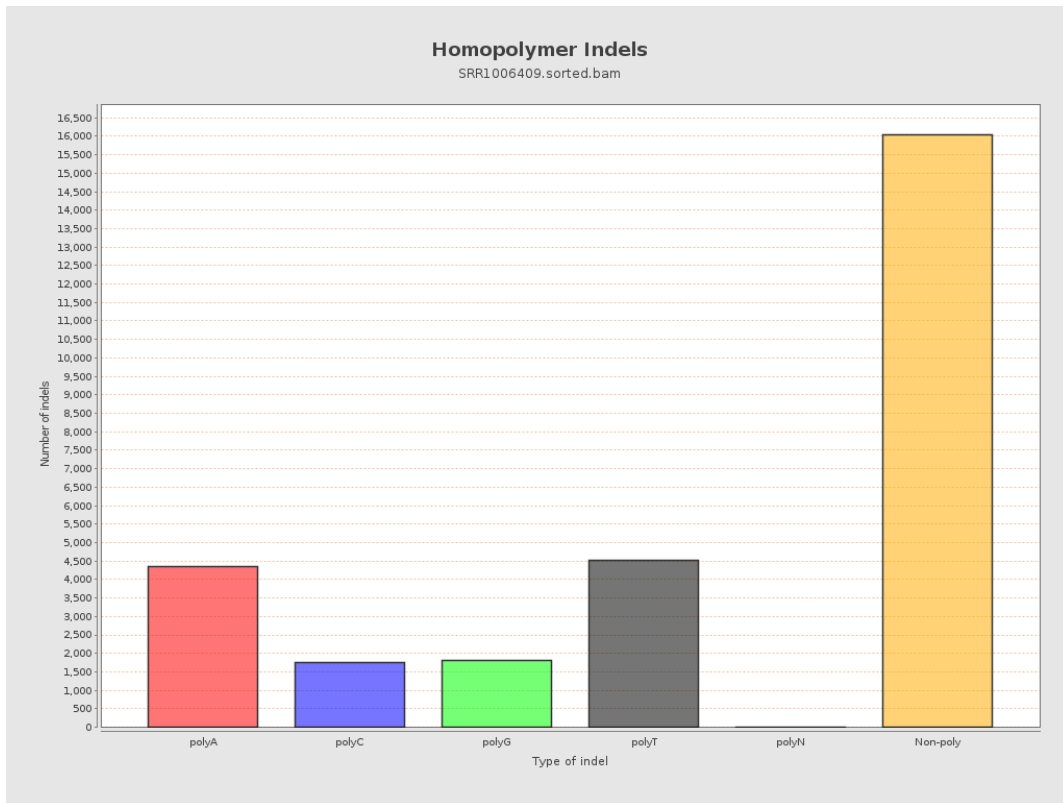
9. Results : Mapped Reads GC-content Distribution



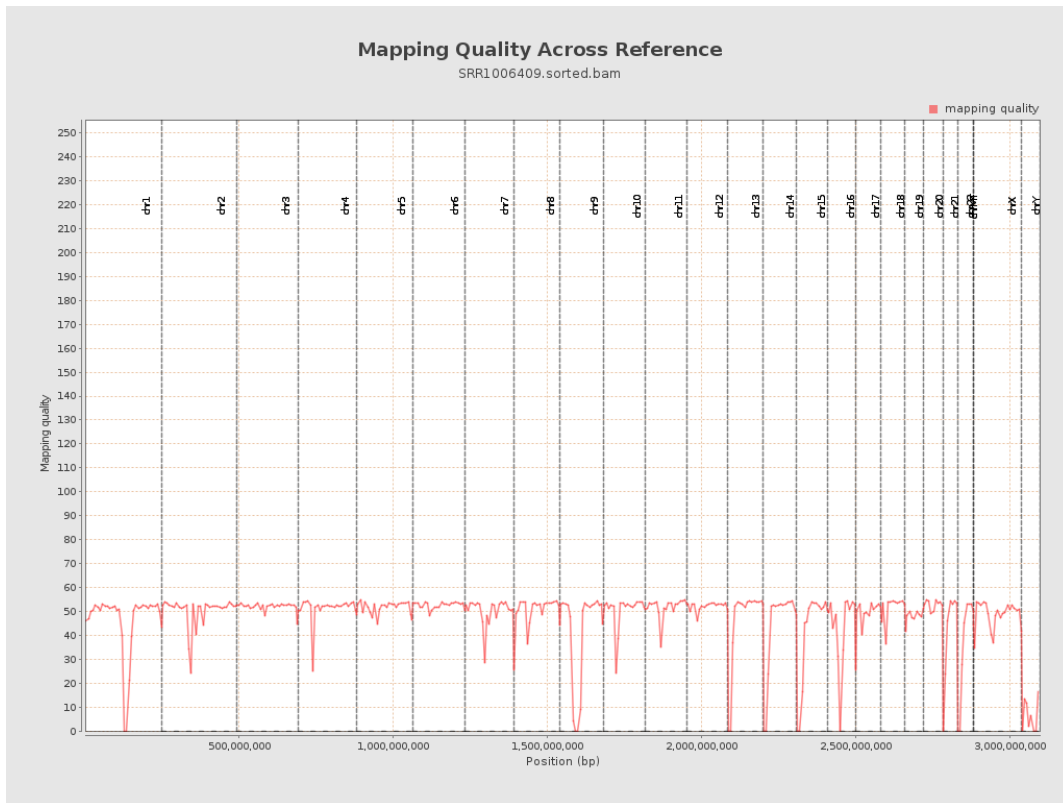
10. Results : Mapped Reads Clipping Profile



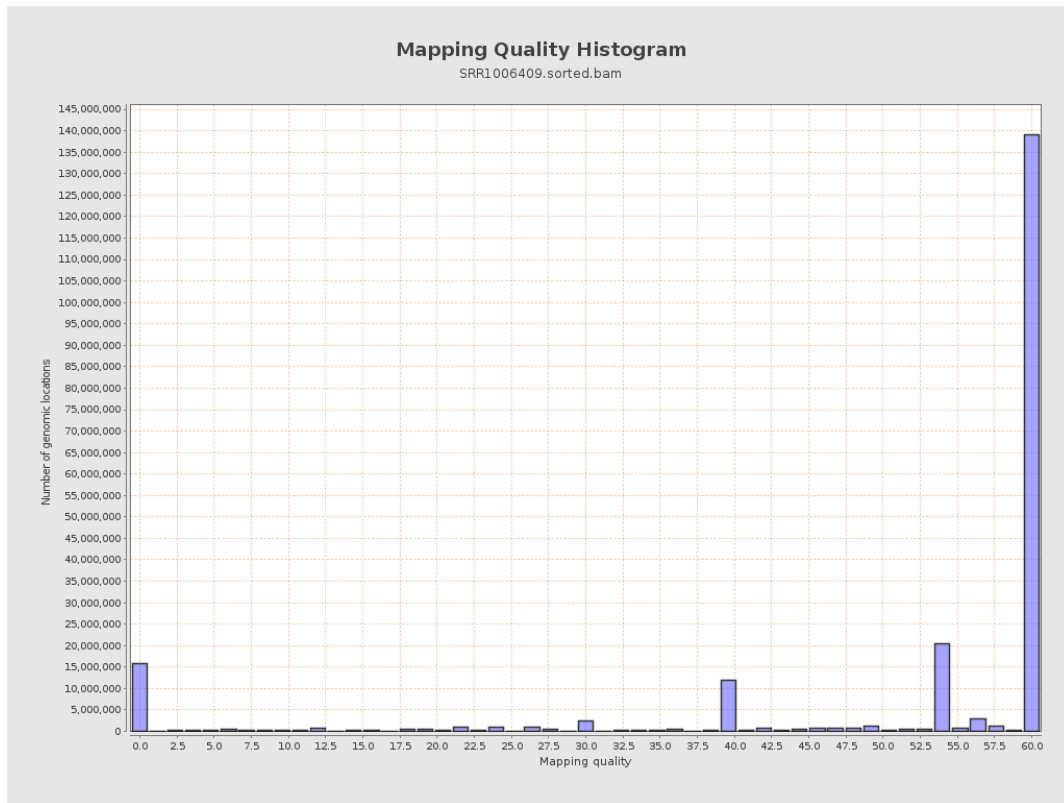
11. Results : Homopolymer Indels



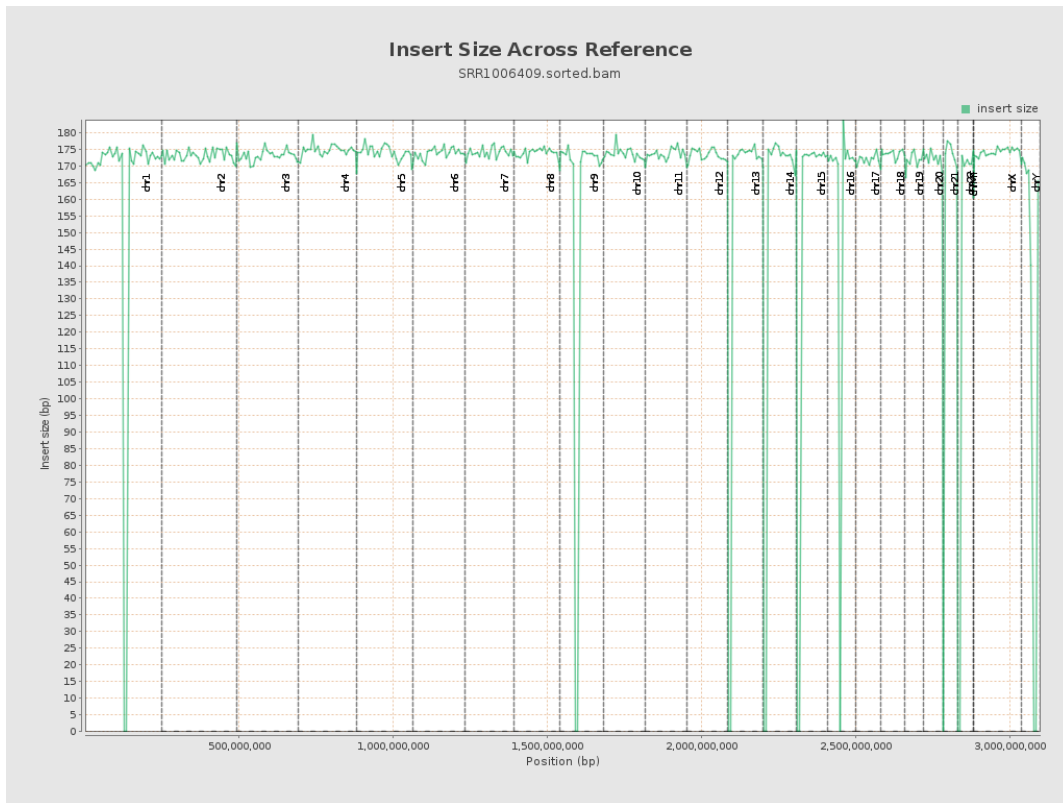
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

