

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/22 18:53:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR630574.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_SRR630574 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR630574_1.fastq.gz SRR630574_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Jan 22 18:53:19 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR630574.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	34,830,550
Mapped reads	34,486,687 / 99.01%
Unmapped reads	343,863 / 0.99%
Mapped paired reads	34,486,687 / 99.01%
Mapped reads, first in pair	17,299,724 / 49.67%
Mapped reads, second in pair	17,186,963 / 49.34%
Mapped reads, both in pair	34,308,218 / 98.5%
Mapped reads, singletons	178,469 / 0.51%
Secondary alignments	0
Supplementary alignments	71,438 / 0.21%
Read min/max/mean length	30 / 101 / 101.08
Duplicated reads (estimated)	4,312,702 / 12.38%
Duplication rate	10.26%
Clipped reads	4,712,373 / 13.53%

2.2. ACGT Content

Number/percentage of A's	987,775,292 / 29.45%
Number/percentage of C's	663,321,339 / 19.77%
Number/percentage of T's	997,845,598 / 29.75%
Number/percentage of G's	705,083,803 / 21.02%
Number/percentage of N's	501,827 / 0.01%

GC Percentage	40.79%
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2.3. Coverage

Mean	1.0844
Standard Deviation	5.0715

2.4. Mapping Quality

Mean Mapping Quality	53.94
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2.5. Insert size

Mean	26,082
Standard Deviation	1,571,199.33
P25/Median/P75	163 / 208 / 276

2.6. Mismatches and indels

General error rate	0.94%
Mismatches	30,417,731
Insertions	607,198
Mapped reads with at least one insertion	1.73%
Deletions	1,749,774
Mapped reads with at least one deletion	4.94%
Homopolymer indels	54.21%

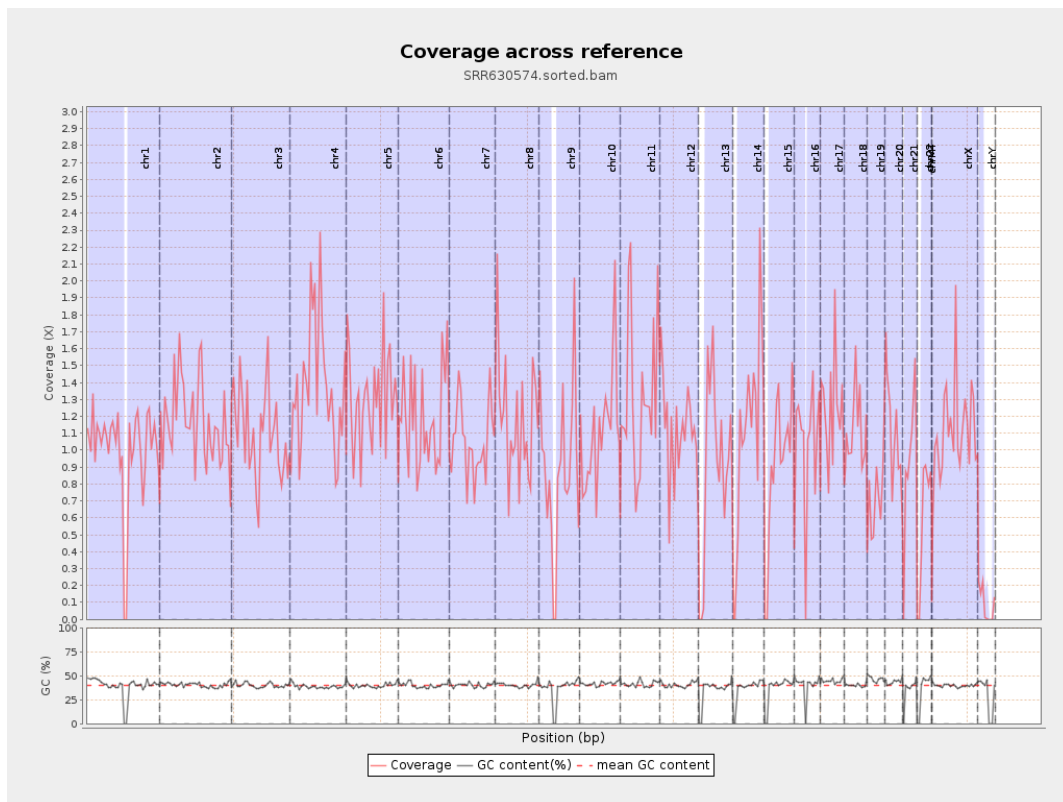
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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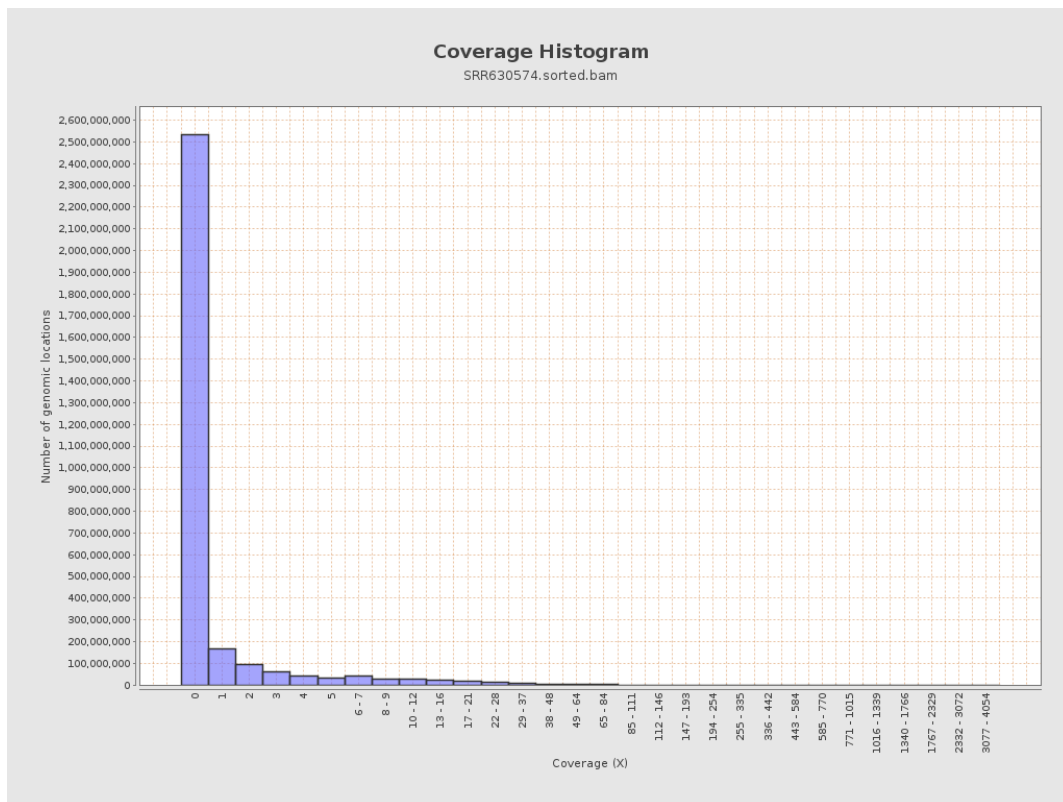
		bases	coverage	deviation
chr1	249250621	247955363	0.9948	6.2472
chr2	243199373	283220746	1.1646	5.7425
chr3	198022430	216302012	1.0923	4.4633
chr4	191154276	261983161	1.3705	5.6167
chr5	180915260	235404487	1.3012	4.8207
chr6	171115067	204700626	1.1963	4.8728
chr7	159138663	166598865	1.0469	4.2746
chr8	146364022	171056976	1.1687	4.7489
chr9	141213431	123872860	0.8772	5.6398
chr10	135534747	153388247	1.1317	5.0278
chr11	135006516	176424233	1.3068	5.3114
chr12	133851895	149826168	1.1193	4.517
chr13	115169878	104959713	0.9113	3.9607
chr14	107349540	117444016	1.094	4.5088
chr15	102531392	93383428	0.9108	4.0272
chr16	90354753	91947337	1.0176	5.9095
chr17	81195210	100971156	1.2436	5.0008
chr18	78077248	89134163	1.1416	6.6707
chr19	59128983	41230452	0.6973	4.1426
chr20	63025520	69249342	1.0988	4.7682
chr21	48129895	46611787	0.9685	5.7364
chr22	51304566	31154072	0.6072	3.3477
chrMT	16571	1703	0.1028	0.5683
chrX	155270560	174899451	1.1264	4.7052

chrY	59373566	5194328	0.0875	2.8302
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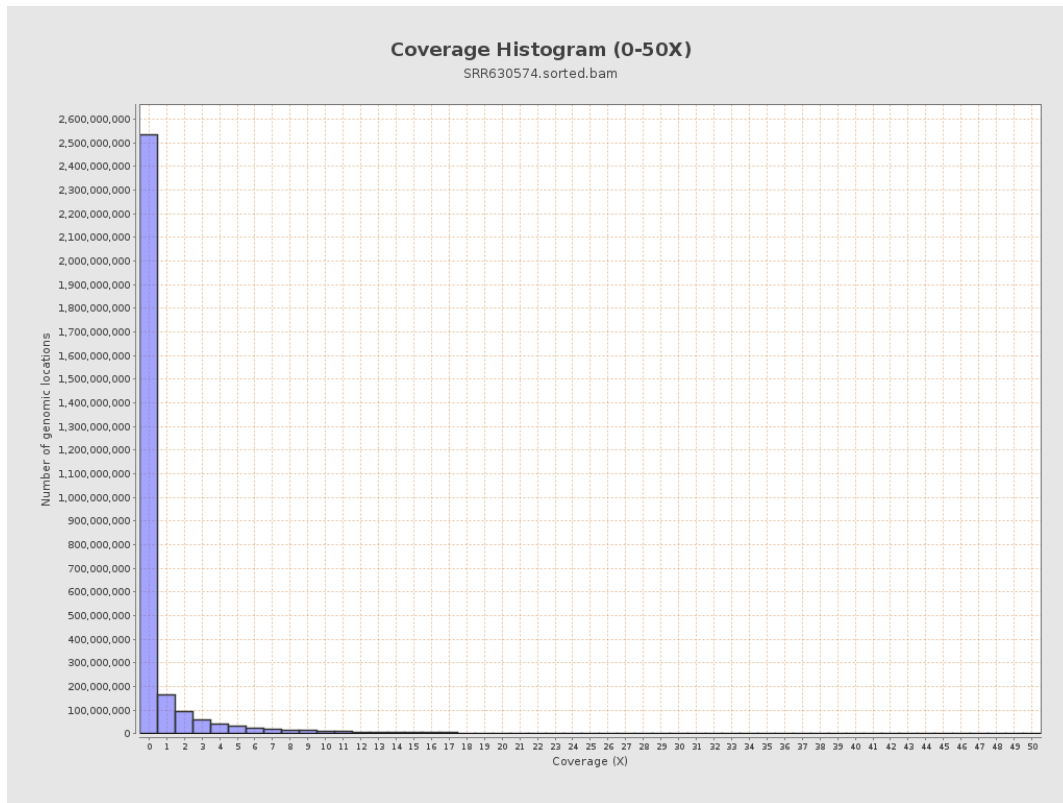
3. Results : Coverage across reference



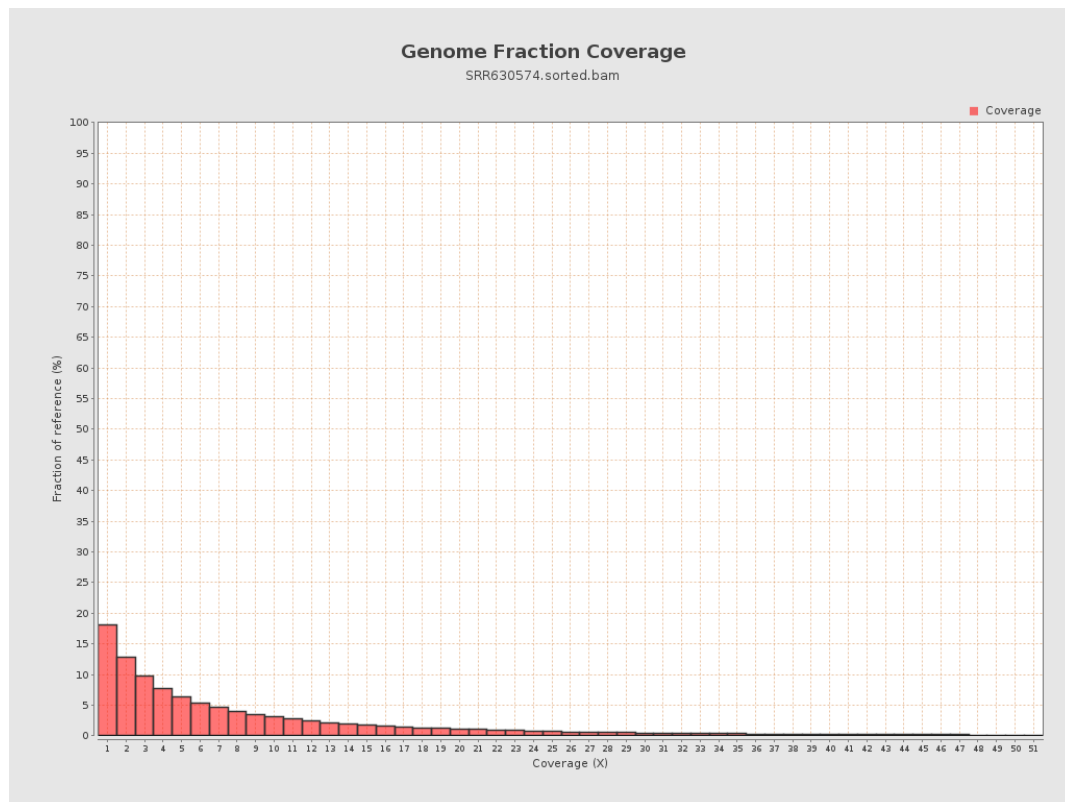
4. Results : Coverage Histogram



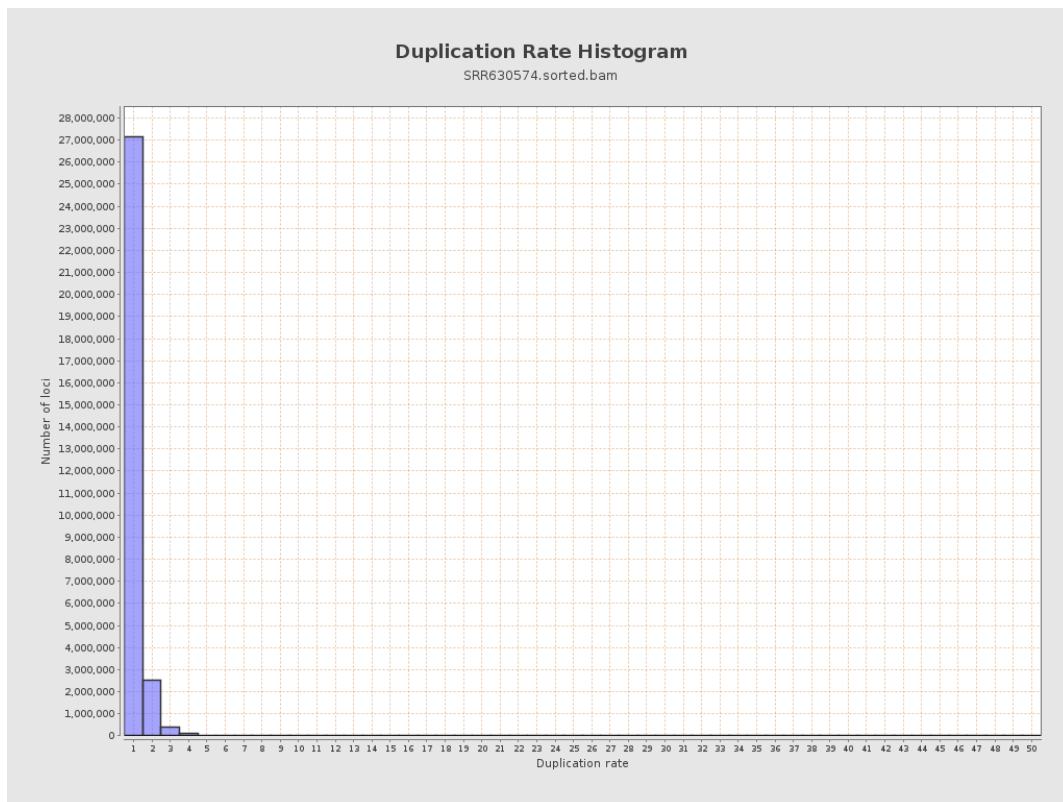
5. Results : Coverage Histogram (0-50X)



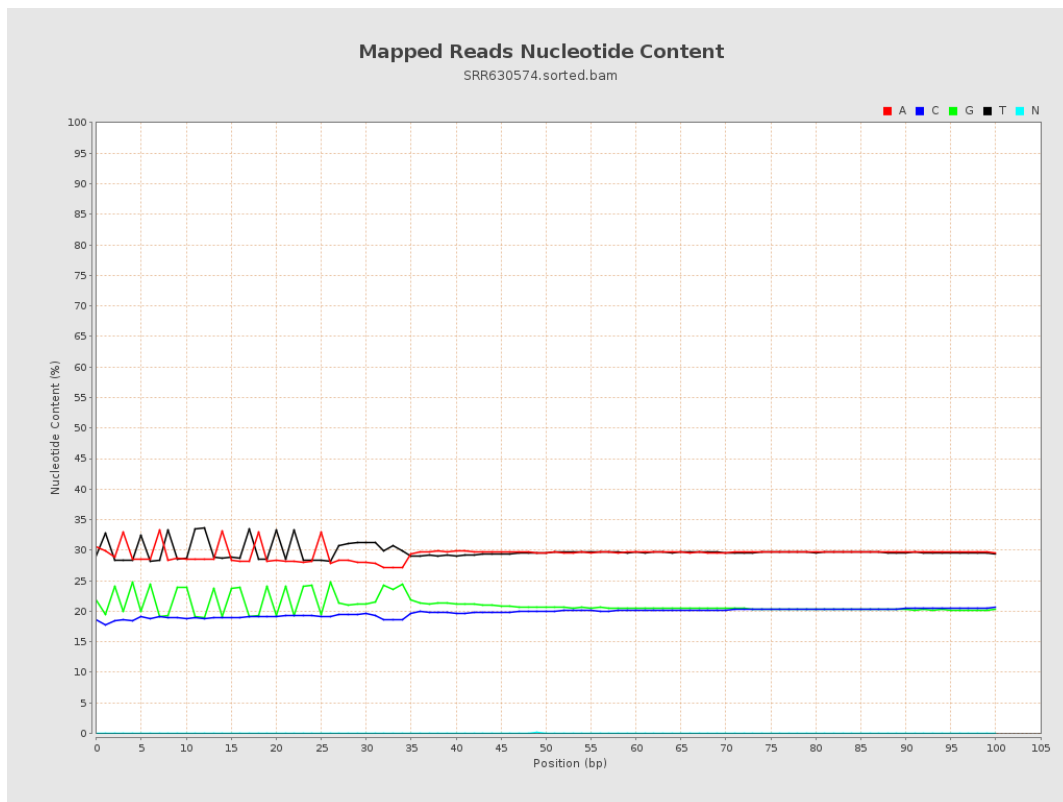
6. Results : Genome Fraction Coverage



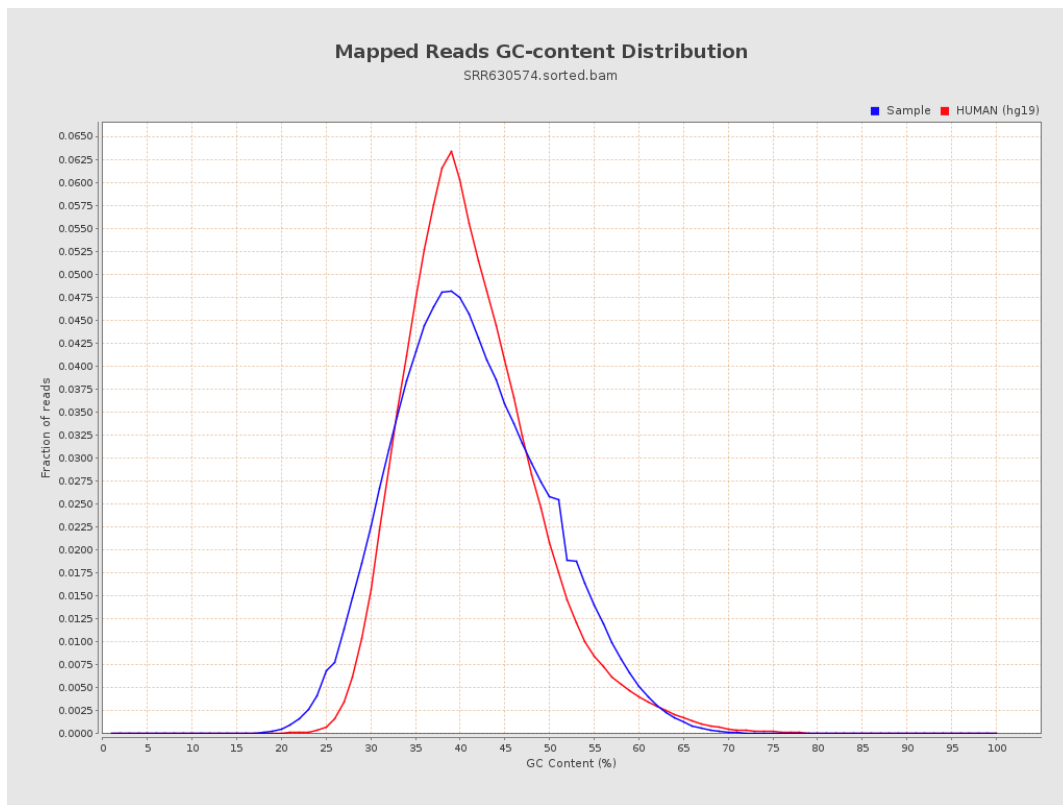
7. Results : Duplication Rate Histogram



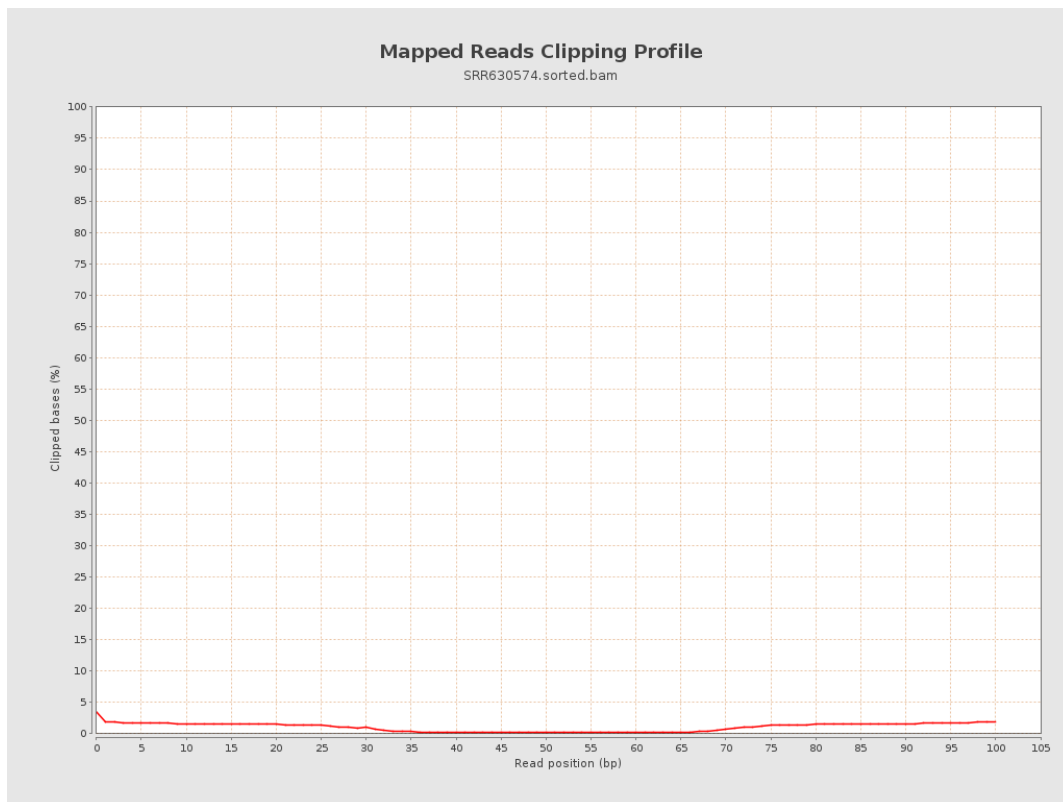
8. Results : Mapped Reads Nucleotide Content



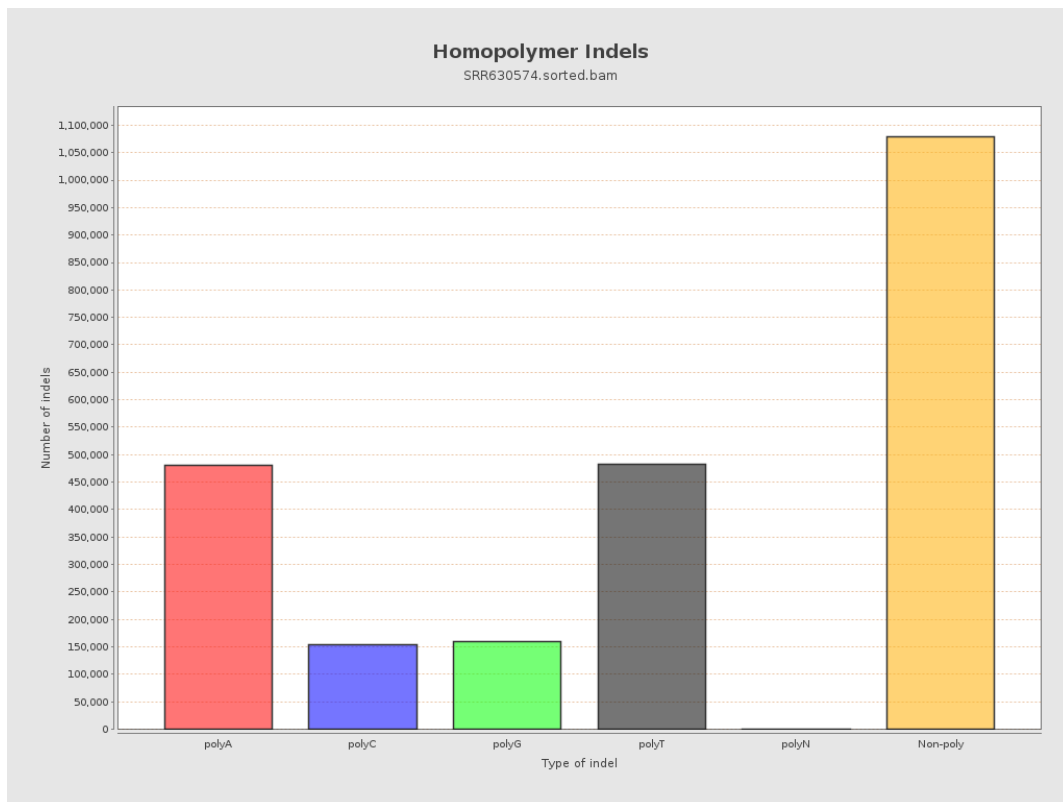
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



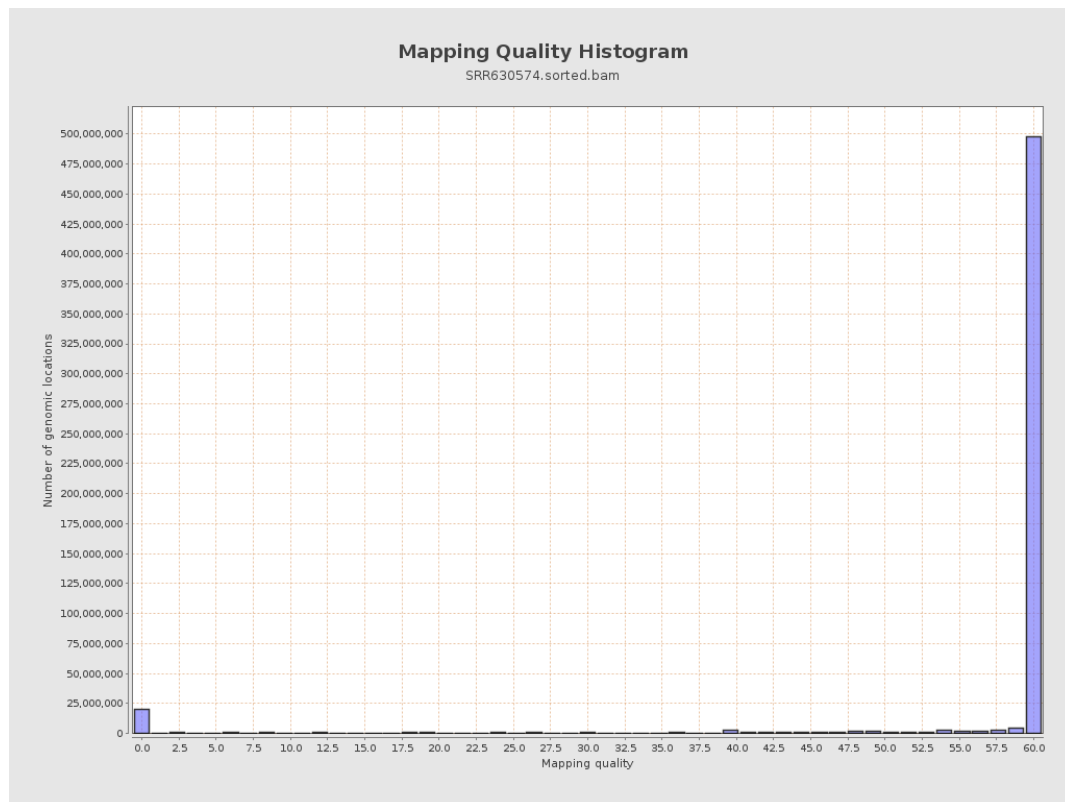
11. Results : Homopolymer Indels



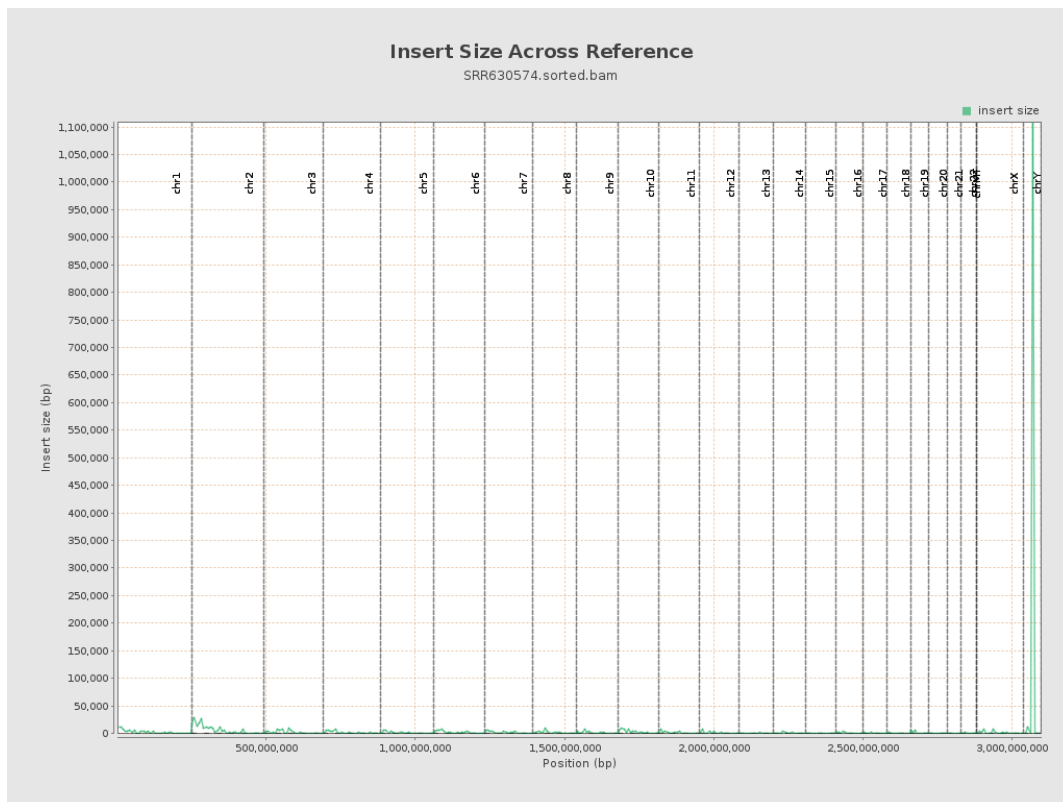
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

