

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/05 12:40:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR960898.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_SRR960898 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR960898_1.fastq.gz SRR960898_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Jan 05 12:40:17 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR960898.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	220,838,488
Mapped reads	217,442,821 / 98.46%
Unmapped reads	3,395,667 / 1.54%
Mapped paired reads	217,442,821 / 98.46%
Mapped reads, first in pair	108,962,232 / 49.34%
Mapped reads, second in pair	108,480,589 / 49.12%
Mapped reads, both in pair	216,229,764 / 97.91%
Mapped reads, singletons	1,213,057 / 0.55%
Secondary alignments	0
Supplementary alignments	380,611 / 0.17%
Read min/max/mean length	30 / 101 / 101.07
Duplicated reads (estimated)	30,968,539 / 14.02%
Duplication rate	9.56%
Clipped reads	32,551,928 / 14.74%

2.2. ACGT Content

Number/percentage of A's	6,516,674,455 / 30.54%
Number/percentage of C's	4,156,910,875 / 19.48%
Number/percentage of T's	6,508,460,477 / 30.5%
Number/percentage of G's	4,151,294,630 / 19.46%
Number/percentage of N's	4,186,813 / 0.02%

GC Percentage	38.94%
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2.3. Coverage

Mean	6.8947
Standard Deviation	93.5741

2.4. Mapping Quality

Mean Mapping Quality	53.63
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2.5. Insert size

Mean	15,351.54
Standard Deviation	1,164,539.29
P25/Median/P75	136 / 164 / 192

2.6. Mismatches and indels

General error rate	1.3%
Mismatches	271,198,620
Insertions	2,538,986
Mapped reads with at least one insertion	1.14%
Deletions	2,698,332
Mapped reads with at least one deletion	1.2%
Homopolymer indels	40.68%

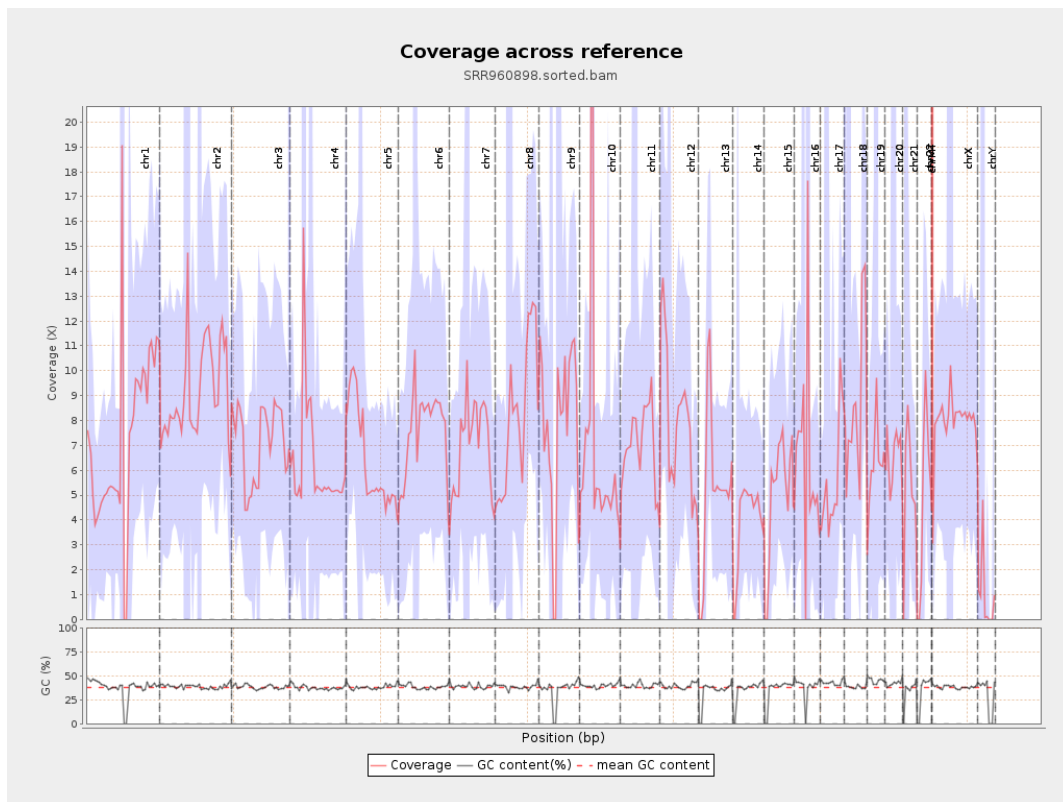
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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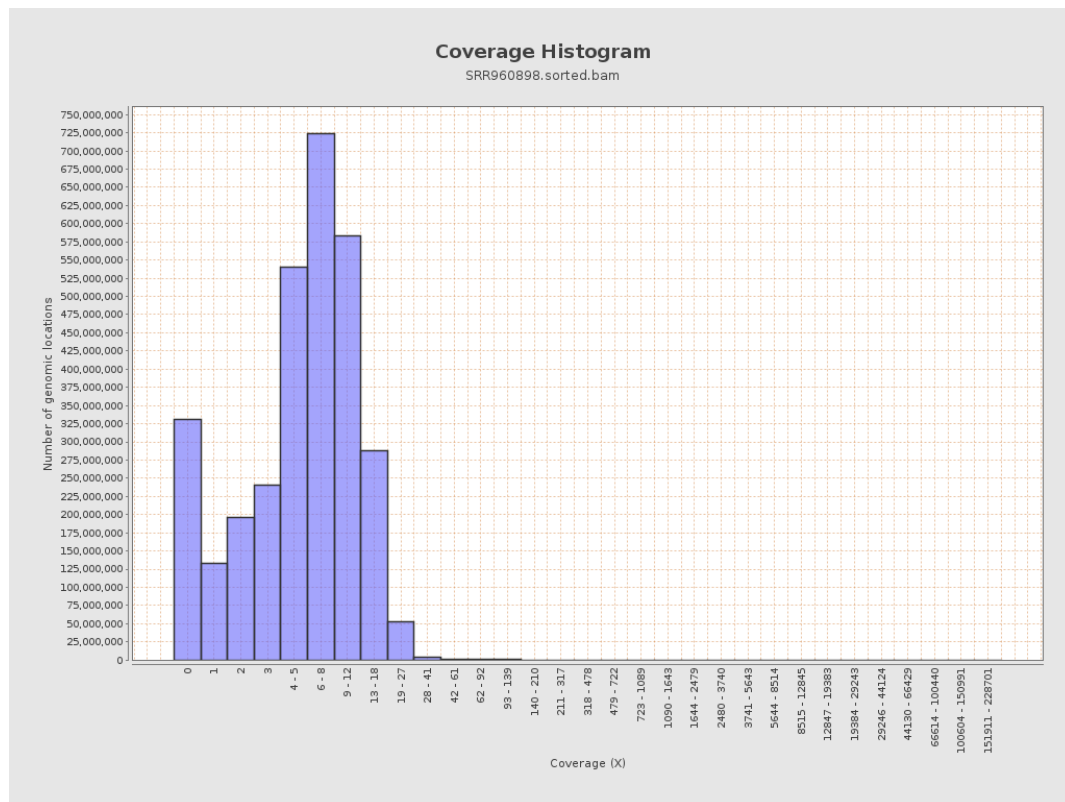
		bases	coverage	deviation
chr1	249250621	1809748850	7.2608	233.6208
chr2	243199373	2243782314	9.2261	49.7941
chr3	198022430	1402857261	7.0843	13.8485
chr4	191154276	1189352576	6.222	75.1289
chr5	180915260	1153627740	6.3766	8.1403
chr6	171115067	1308443041	7.6466	27.3763
chr7	159138663	1107055714	6.9565	59.0713
chr8	146364022	1219246803	8.3302	93.6915
chr9	141213431	1081118842	7.6559	75.9246
chr10	135534747	948310357	6.9968	219.753
chr11	135006516	944847591	6.9985	36.0016
chr12	133851895	1078880397	8.0603	7.8111
chr13	115169878	600697628	5.2158	4.6704
chr14	107349540	424114453	3.9508	6.7537
chr15	102531392	521260922	5.0839	4.575
chr16	90354753	578658959	6.4043	85.2596
chr17	81195210	454083186	5.5925	24.084
chr18	78077248	673060803	8.6204	79.2744
chr19	59128983	370829654	6.2715	102.1399
chr20	63025520	412809401	6.5499	21.9476
chr21	48129895	266833810	5.544	30.5772
chr22	51304566	245275510	4.7808	6.1407
chrMT	16571	8396851	506.7196	110.2812
chrX	155270560	1241224197	7.9939	25.4321

chrY	59373566	59216969	0.9974	64.8998
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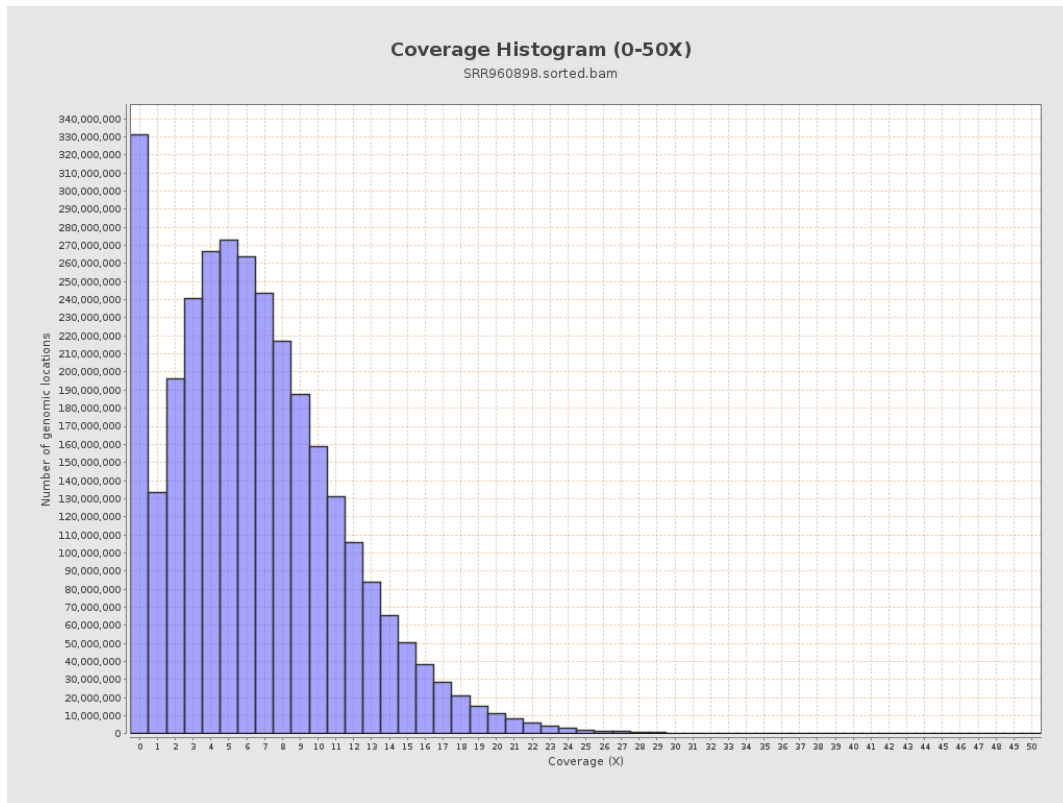
3. Results : Coverage across reference



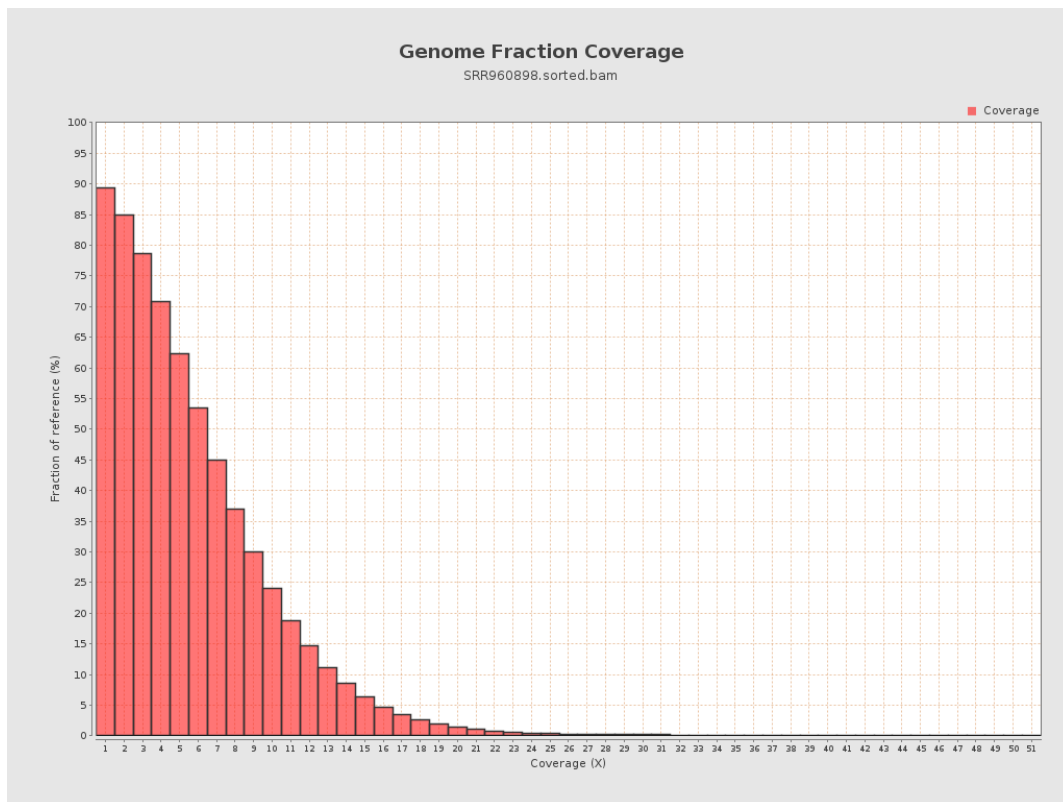
4. Results : Coverage Histogram



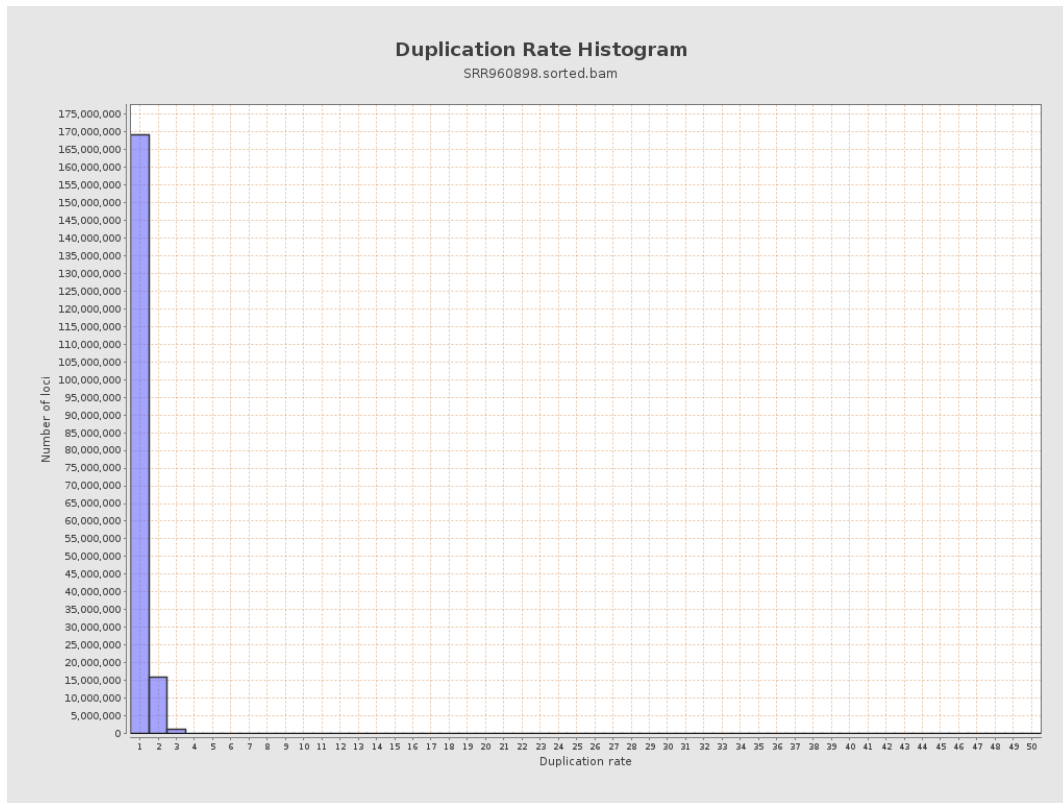
5. Results : Coverage Histogram (0-50X)



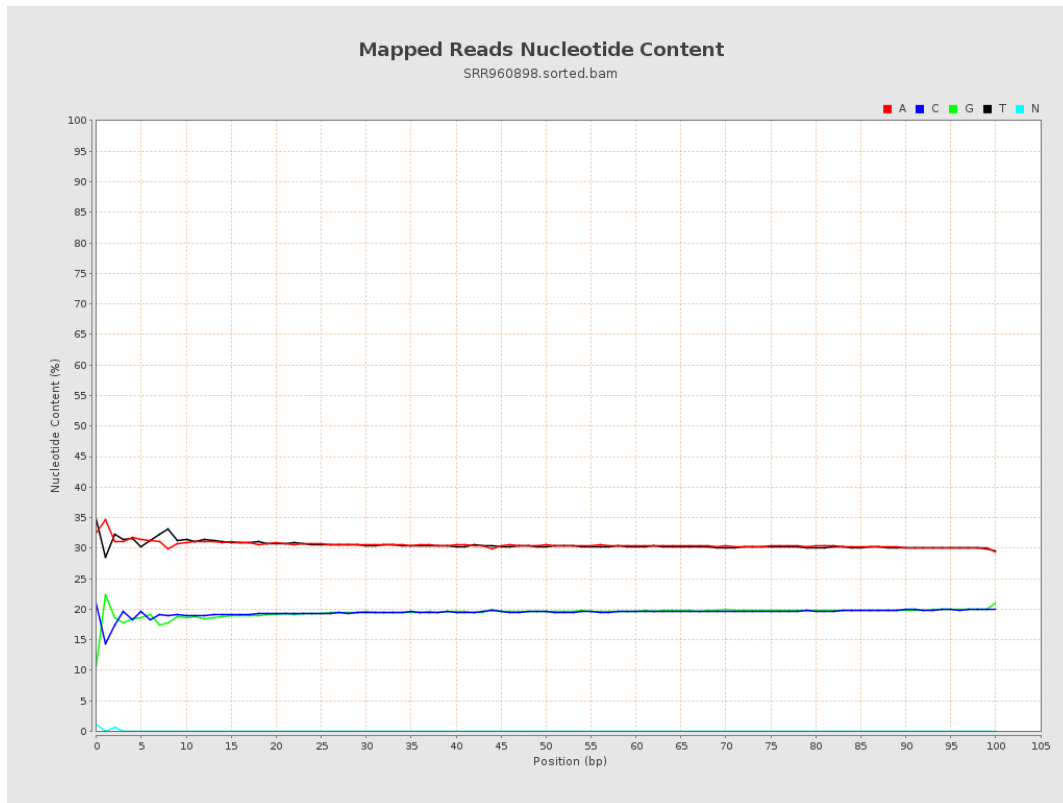
6. Results : Genome Fraction Coverage



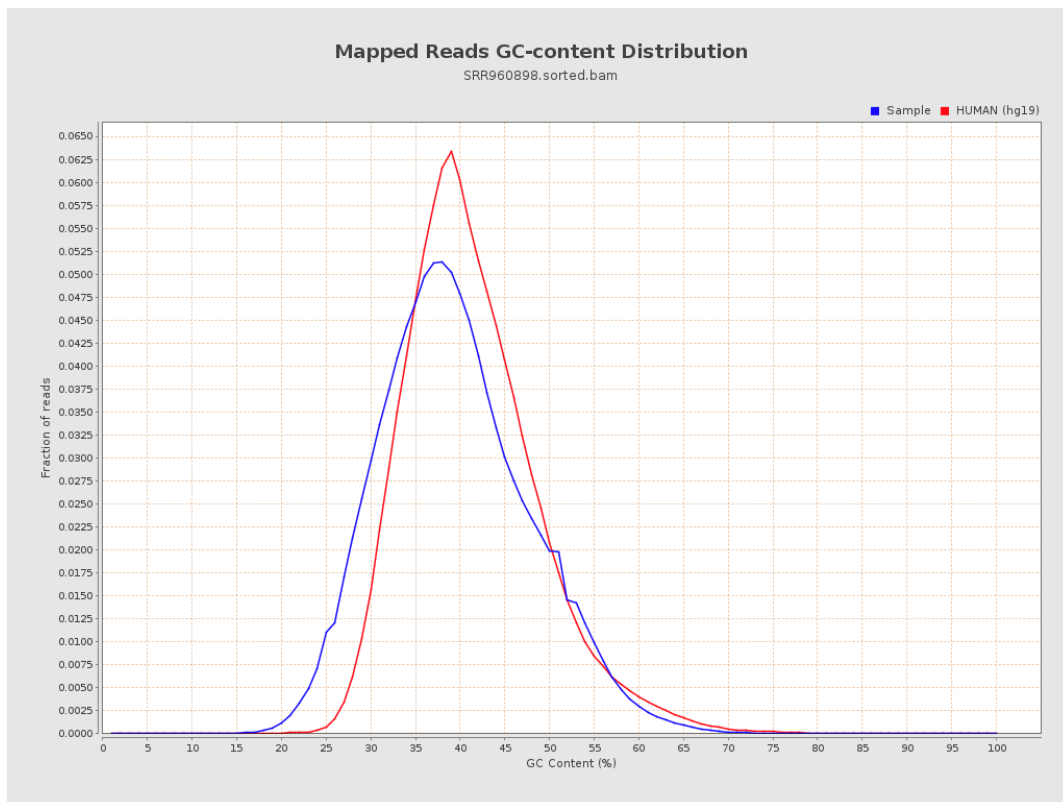
7. Results : Duplication Rate Histogram



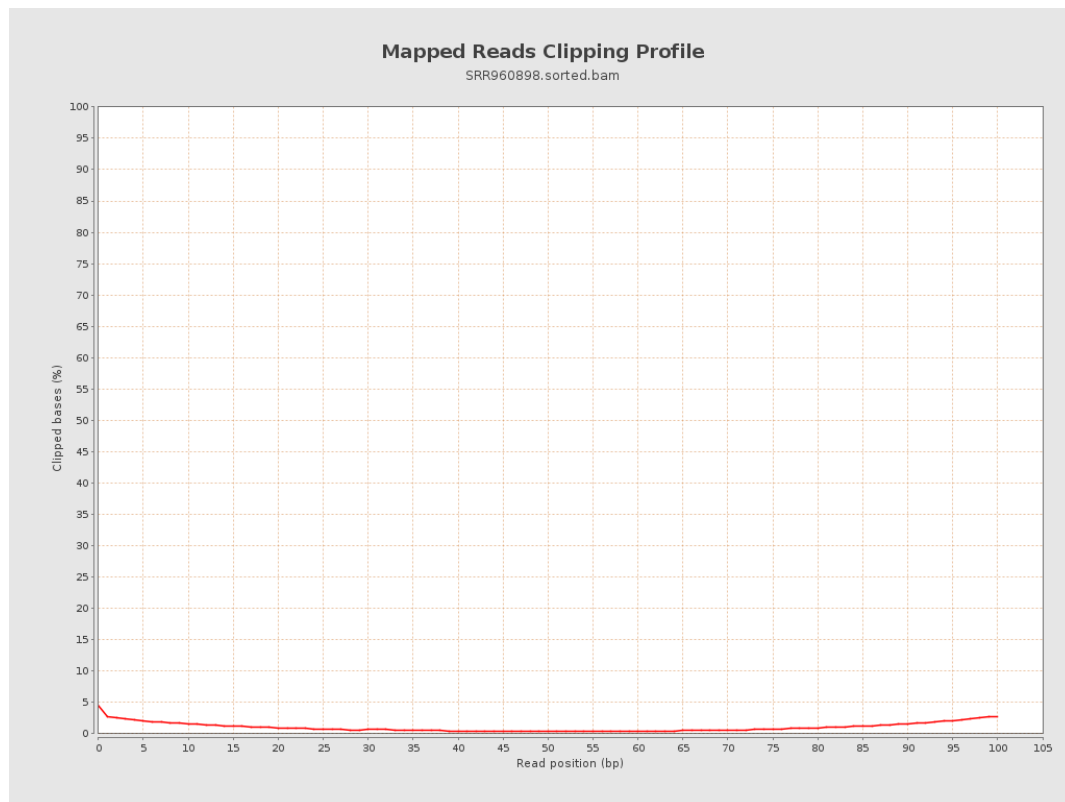
8. Results : Mapped Reads Nucleotide Content



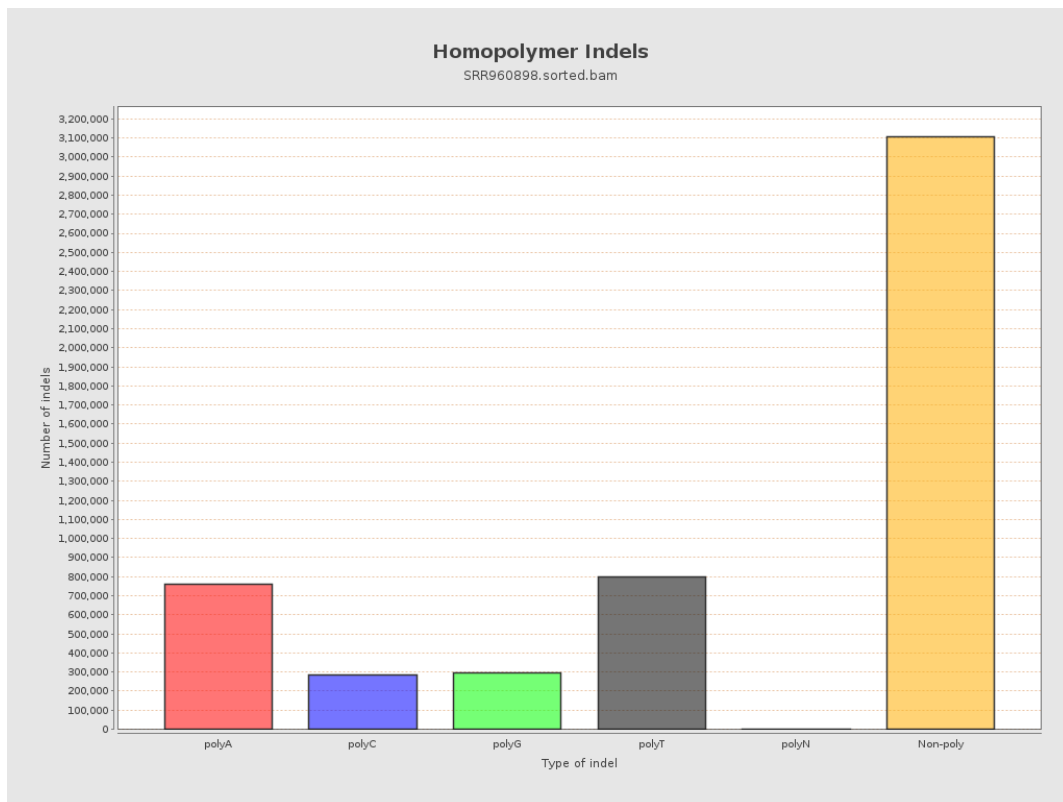
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



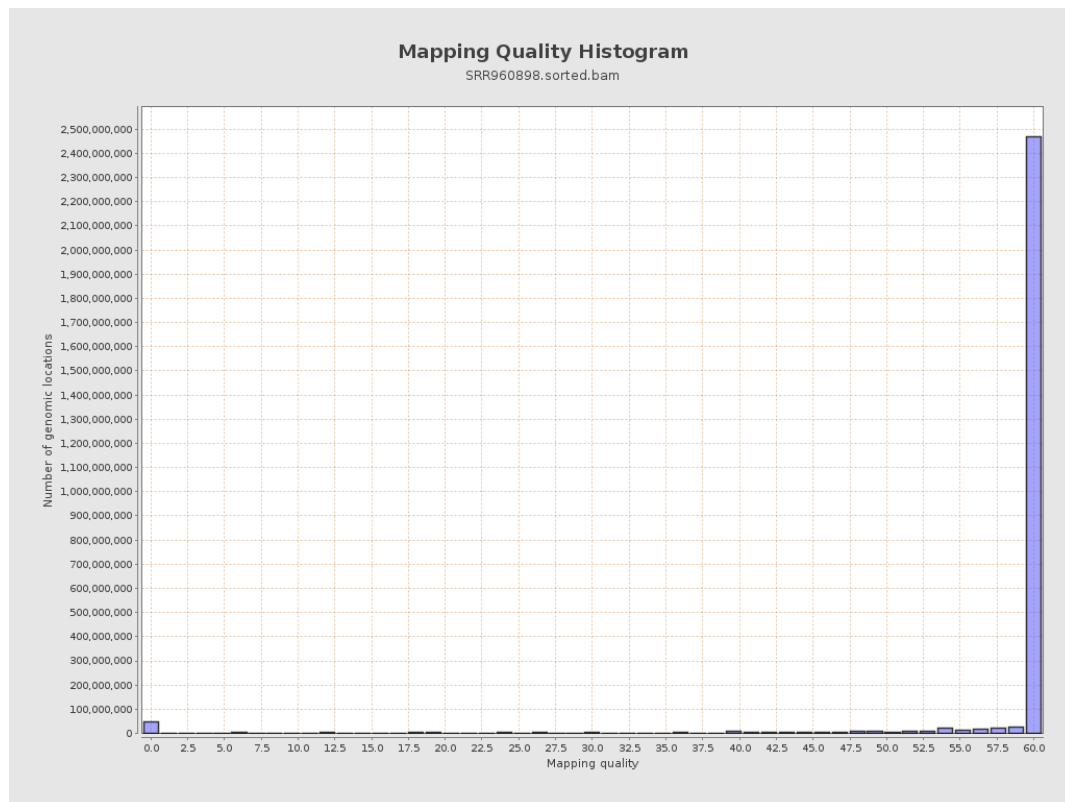
11. Results : Homopolymer Indels



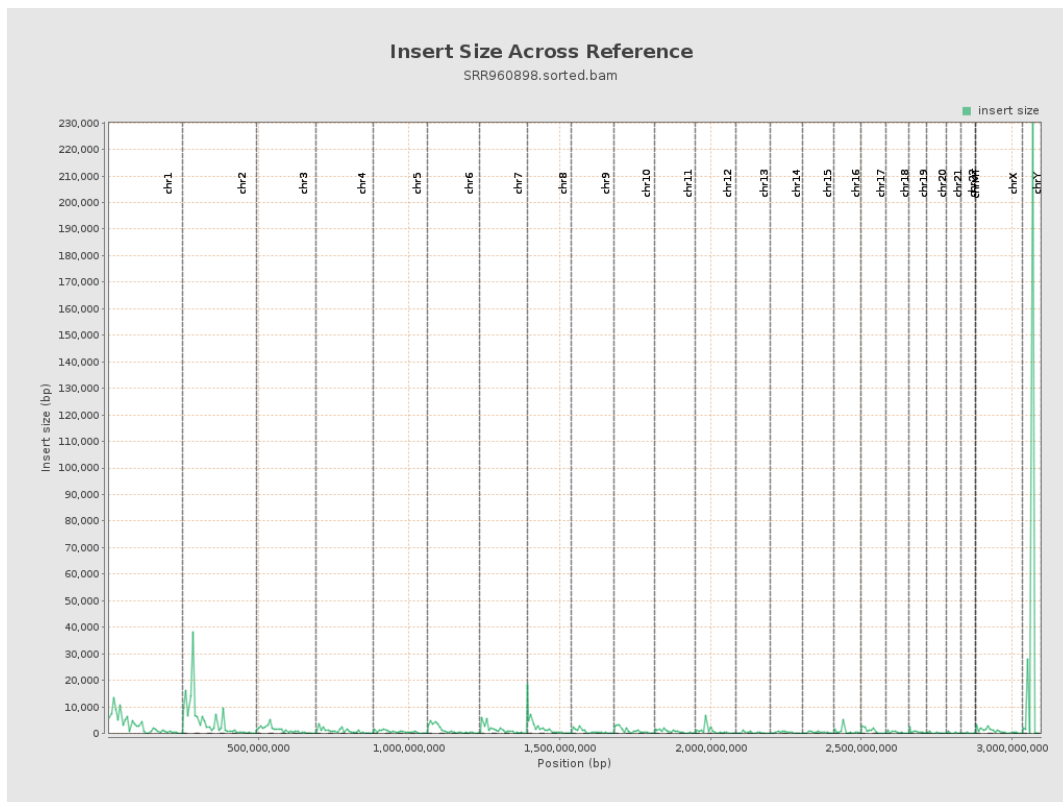
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

