Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/01 00:19:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504633.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_SRR504633 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504633_1.fastq.gz SRR504633_2.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Jan 01 00:19:51 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504633.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	350,223,842
Mapped reads	304,502,143 / 86.95%
Unmapped reads	45,721,699 / 13.05%
Mapped paired reads	304,502,143 / 86.95%
Mapped reads, first in pair	152,701,854 / 43.6%
Mapped reads, second in pair	151,800,289 / 43.34%
Mapped reads, both in pair	302,253,704 / 86.3%
Mapped reads, singletons	2,248,439 / 0.64%
Secondary alignments	0
Supplementary alignments	3,343,341 / 0.95%
Read min/max/mean length	30 / 100 / 100.39
Duplicated reads (estimated)	95,519,427 / 27.27%
Duplication rate	25.51%
Clipped reads	26,365,089 / 7.53%

2.2. ACGT Content

Number/percentage of A's	7,553,589,296 / 25.15%
Number/percentage of C's	7,363,742,690 / 24.51%
Number/percentage of T's	7,590,137,043 / 25.27%
Number/percentage of G's	7,520,816,132 / 25.04%
Number/percentage of N's	11,077,573 / 0.04%

GC Percentage	49.55%

2.3. Coverage

Mean	9.706
Standard Deviation	38.2936

2.4. Mapping Quality

Mean Mapping Quality	53.63

2.5. Insert size

Mean	40,550.71
Standard Deviation	1,925,289.13
P25/Median/P75	329 / 366 / 411

2.6. Mismatches and indels

General error rate	0.66%
Mismatches	192,411,219
Insertions	2,391,107
Mapped reads with at least one insertion	0.76%
Deletions	2,930,340
Mapped reads with at least one deletion	0.93%
Homopolymer indels	38.8%

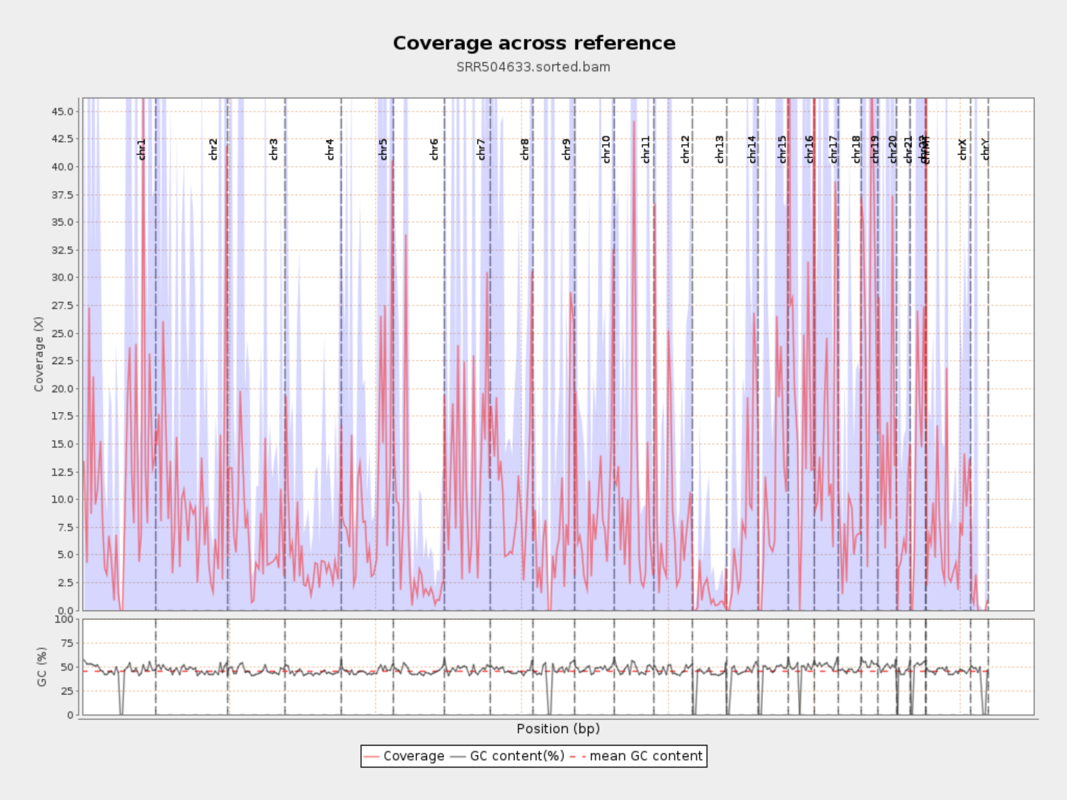
2.7. Chromosome stats

Name	**Length**	**Mapped**	**Mean**	**Standard**

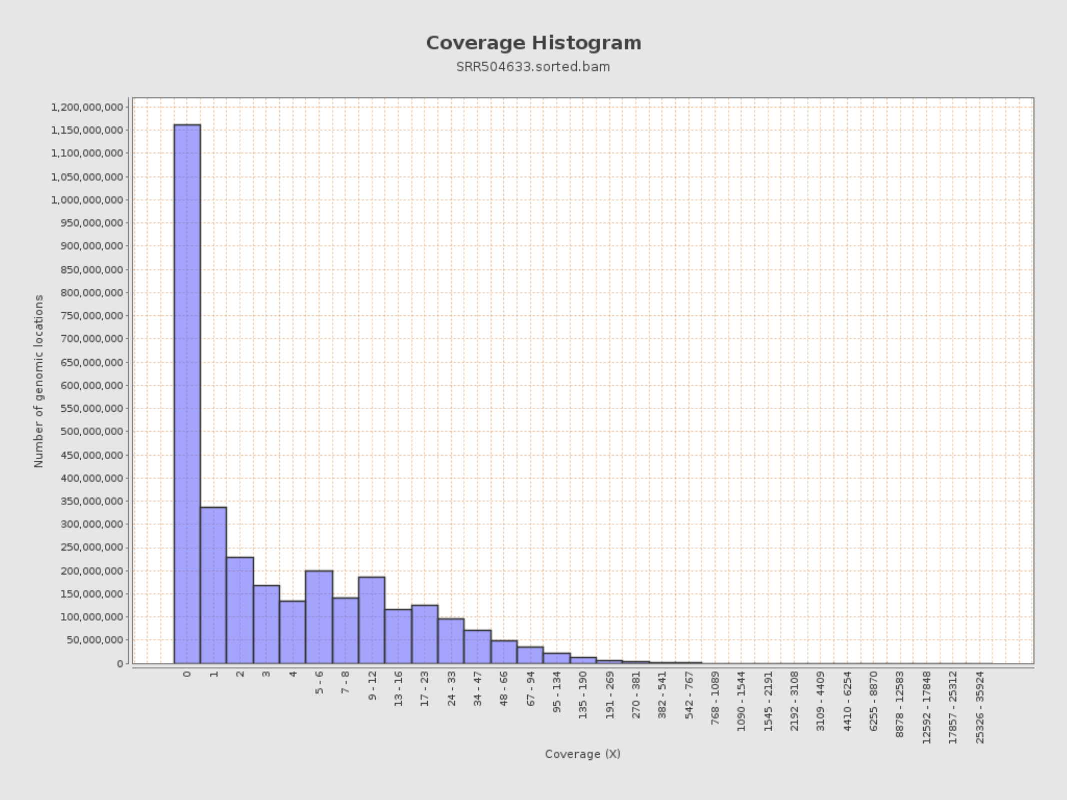
		bases	coverage	deviation
chr1	249250621	2886903936	11.5823	37.5124
chr2	243199373	2437120018	10.0211	29.374
chr3	198022430	1423821686	7.1902	24.4123
chr4	191154276	930073539	4.8656	15.1146
chr5	180915260	2023300846	11.1837	31.6778
chr6	171115067	864372104	5.0514	18.515
chr7	159138663	2067797618	12.9937	33.3409
chr8	146364022	1598957835	10.9245	28.6133
chr9	141213431	1041950074	7.3785	71.3583
chr10	135534747	1219216243	8.9956	28.5945
chr11	135006516	1404584563	10.4038	35.6856
chr12	133851895	1264968457	9.4505	28.0952
chr13	115169878	138710739	1.2044	5.6239
chr14	107349540	927015198	8.6355	23.3466
chr15	102531392	1094796533	10.6777	30.0003
chr16	90354753	1945638137	21.5333	53.7237
chr17	81195210	1299677480	16.0068	42.0198
chr18	78077248	516051836	6.6095	73.4366
chr19	59128983	1632083594	27.6021	113.4493
chr20	63025520	1026543366	16.2877	49.4656
chr21	48129895	321782128	6.6857	21.7122
chr22	51304566	752327236	14.6639	36.1234
chrMT	16571	2939366	177.3801	68.6894
chrX	155270560	1181346582	7.6083	18.345

chrY	59373566	44684187	0.7526	33.844

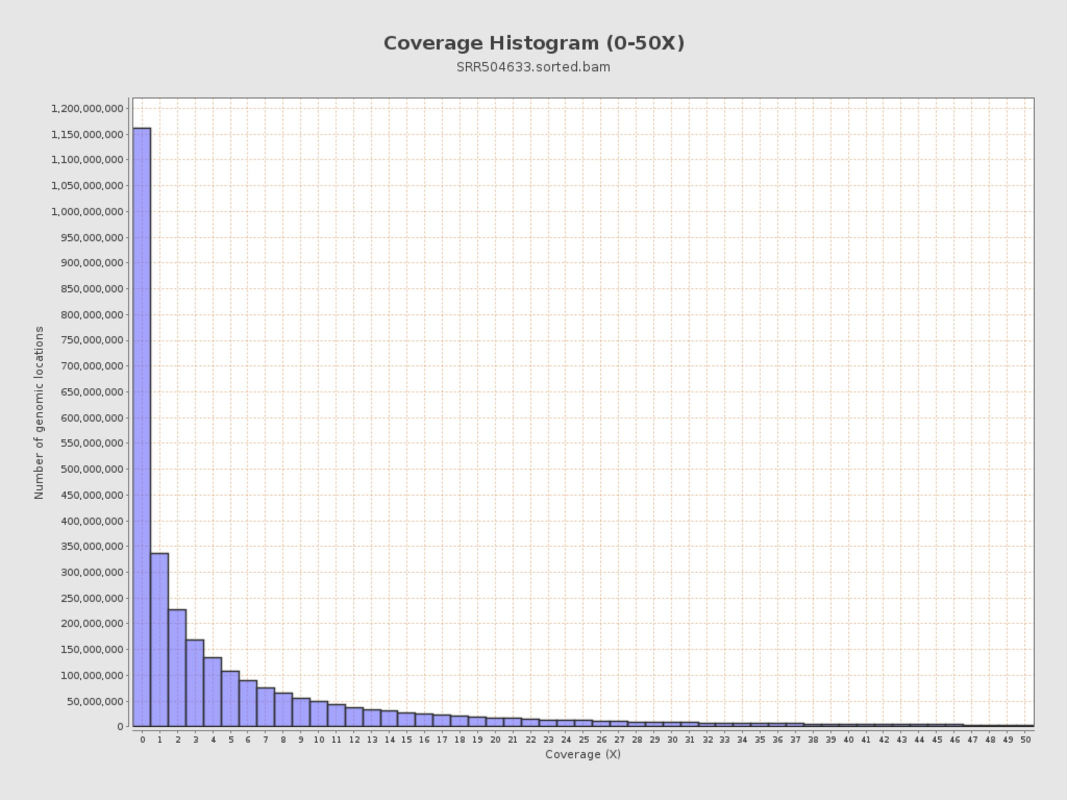
3. Results : Coverage across reference



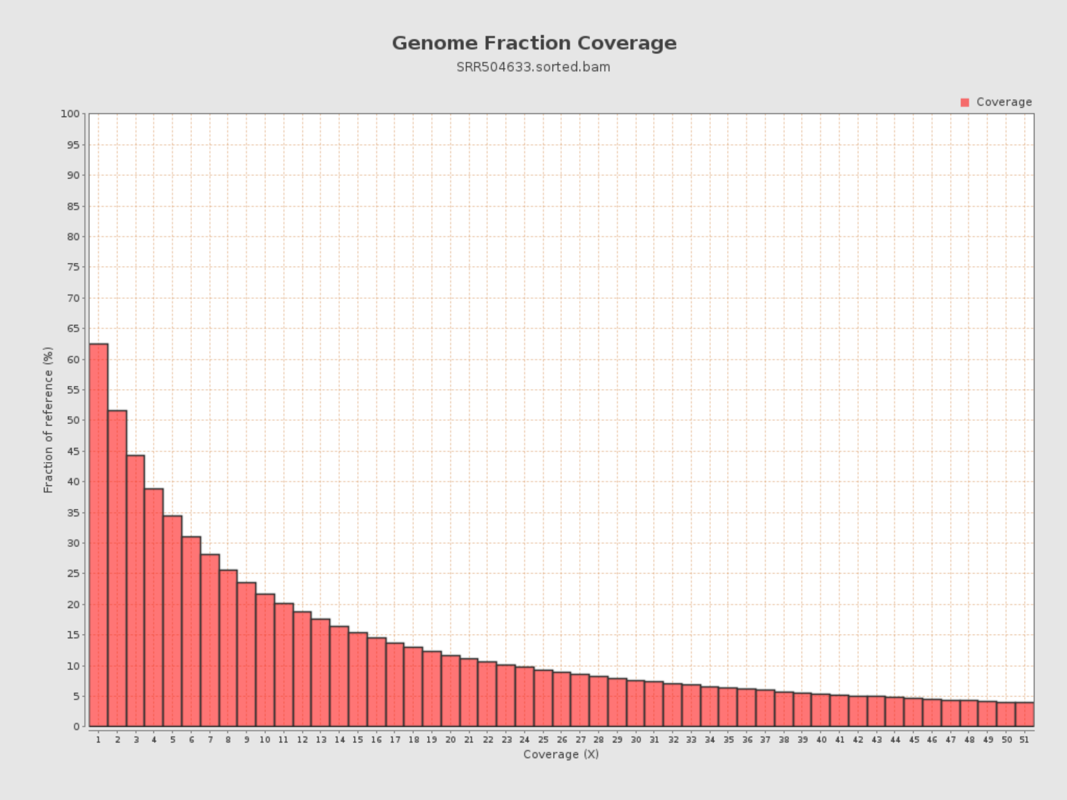
4. Results : Coverage Histogram



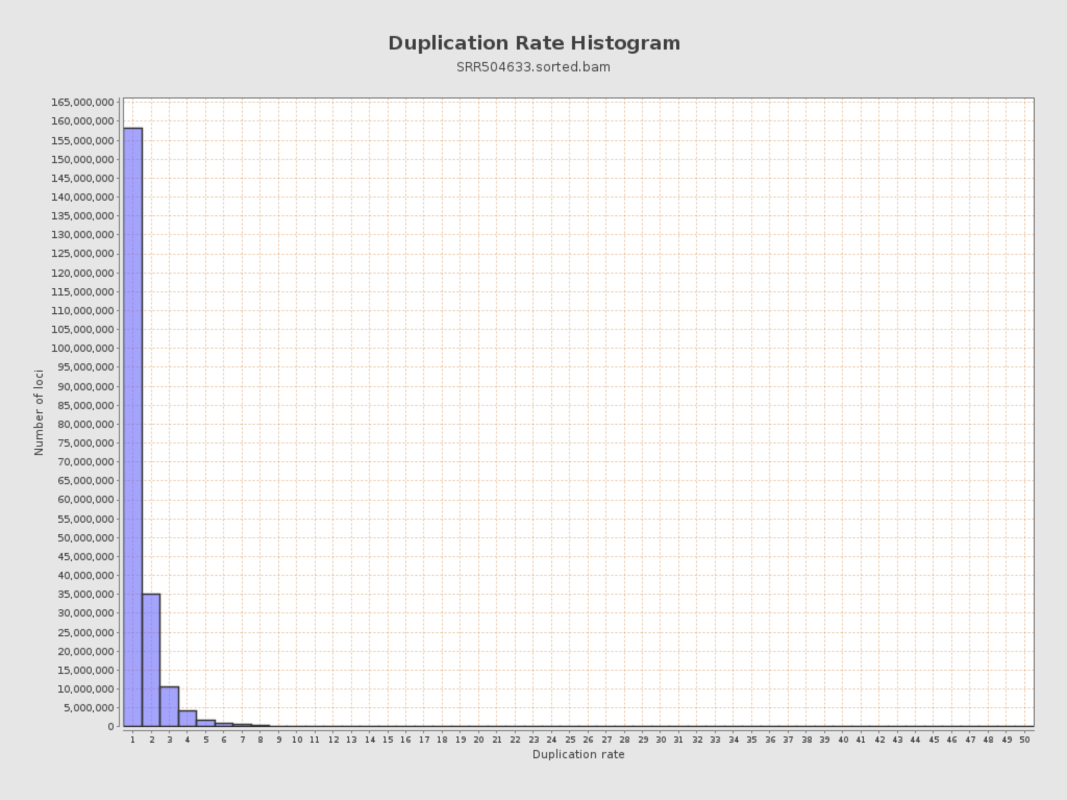
5. Results : Coverage Histogram (0-50X)



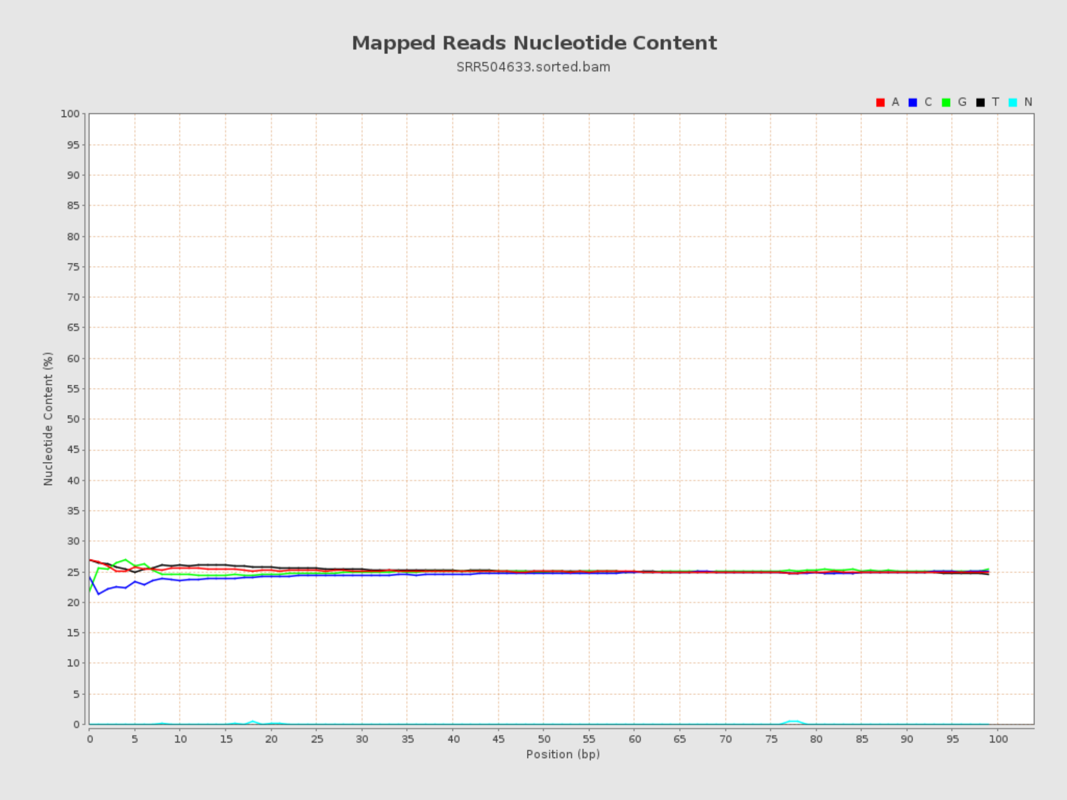
6. Results : Genome Fraction Coverage



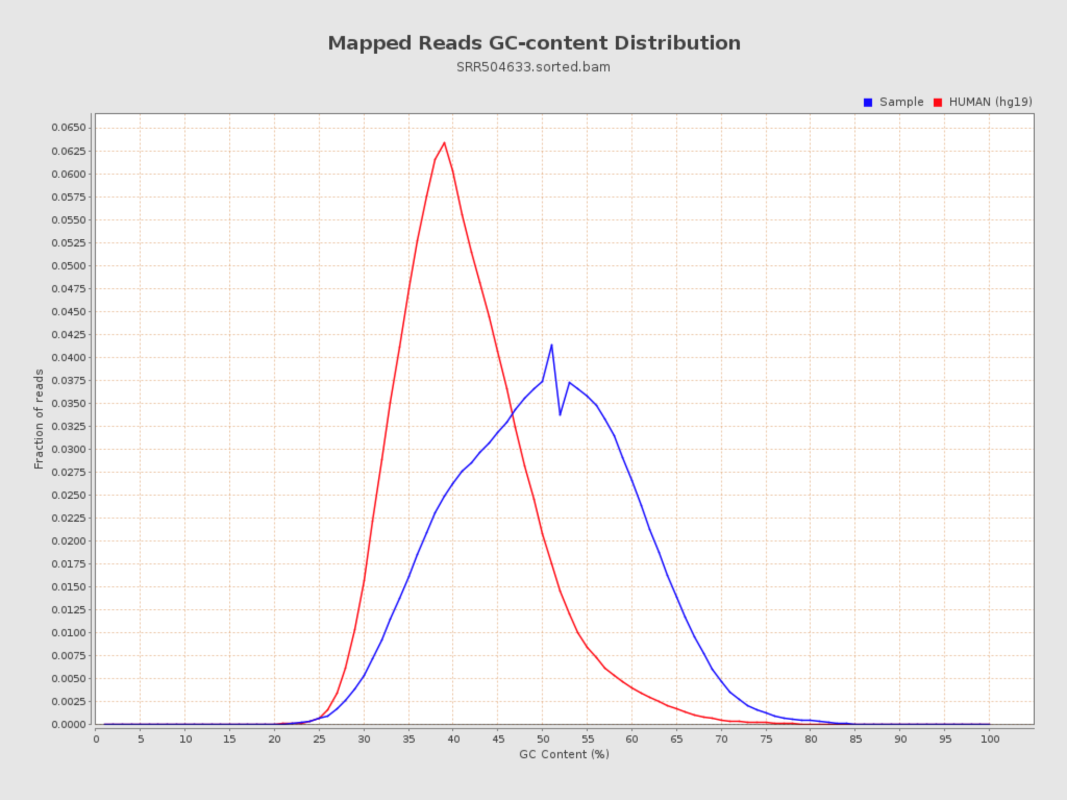
7. Results : Duplication Rate Histogram



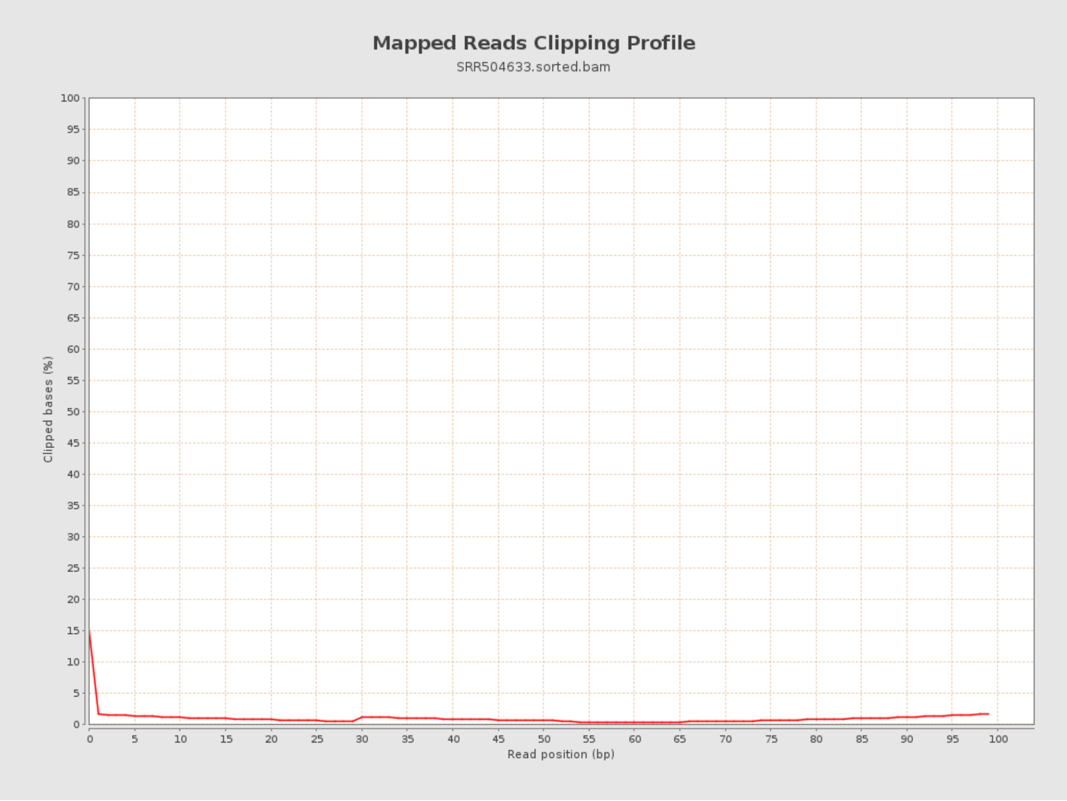
8. Results : Mapped Reads Nucleotide Content



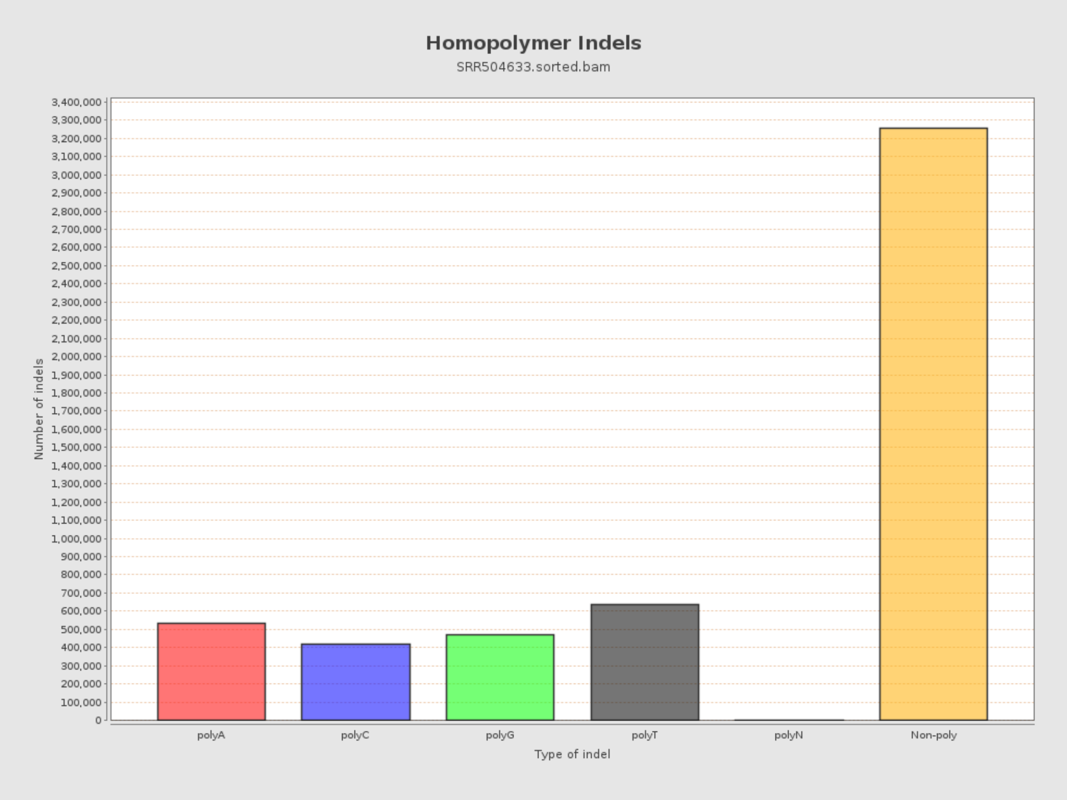
9. Results : Mapped Reads GC-content Distribution



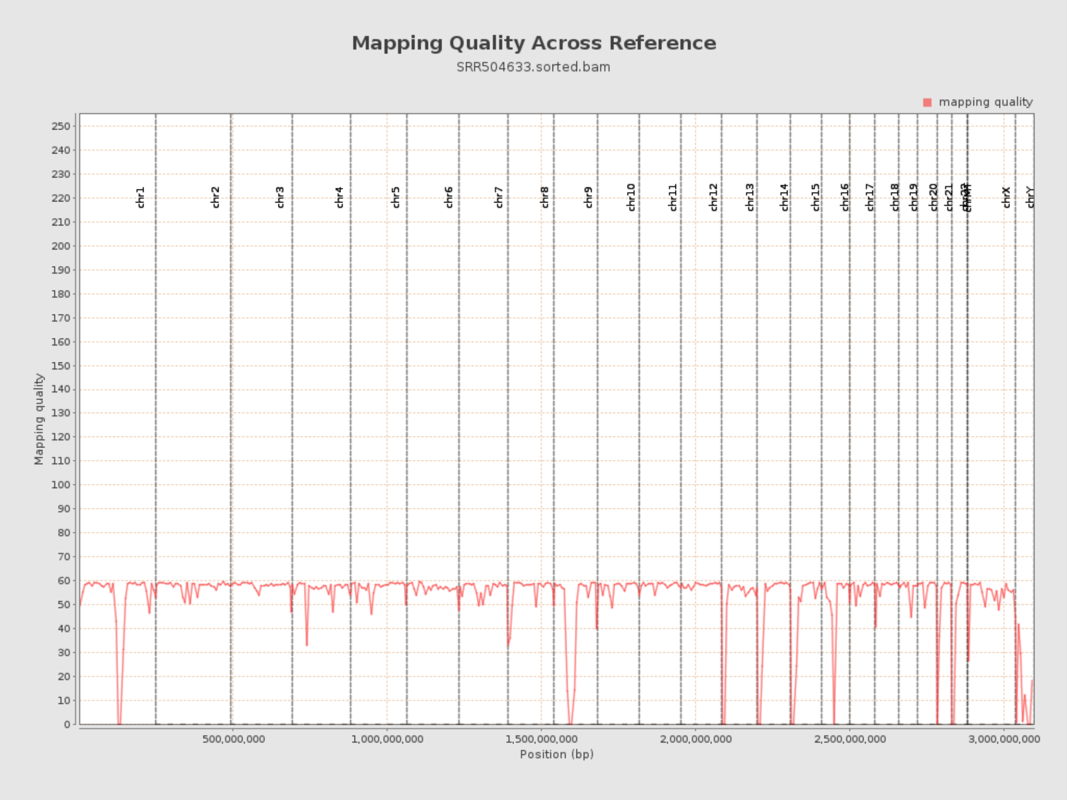
10. Results : Mapped Reads Clipping Profile



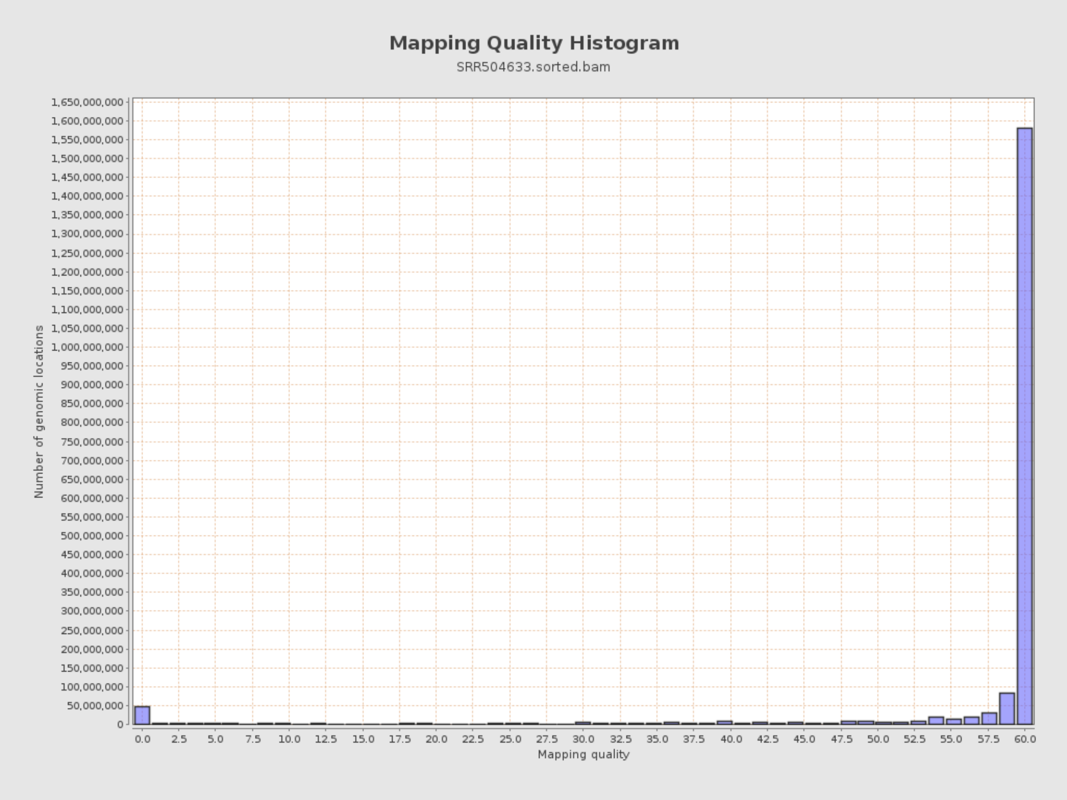
11. Results : Homopolymer Indels



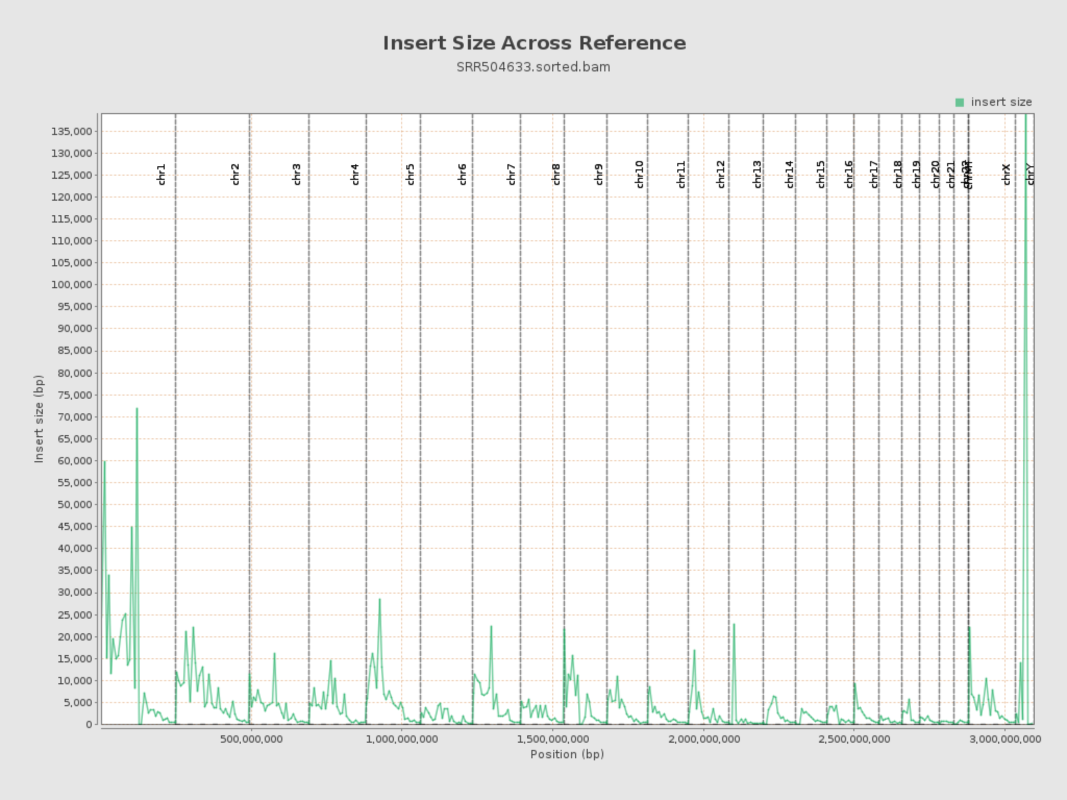
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram