Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/05 01:53:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124823.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_SRR3124823 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124823_1.fastq.gz SRR3124823_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Dec 05 01:53:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124823.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	30,761,518
Mapped reads	30,255,154 / 98.35%
Unmapped reads	506,364 / 1.65%
Mapped paired reads	30,255,154 / 98.35%
Mapped reads, first in pair	15,136,887 / 49.21%
Mapped reads, second in pair	15,118,267 / 49.15%
Mapped reads, both in pair	30,141,762 / 97.99%
Mapped reads, singletons	113,392 / 0.37%
Secondary alignments	0
Supplementary alignments	136,179 / 0.44%
Read min/max/mean length	30 / 101 / 101.18
Duplicated reads (estimated)	3,228,436 / 10.5%
Duplication rate	5.82%
Clipped reads	18,300,711 / 59.49%

2.2. ACGT Content

Number/percentage of A's	786,381,766 / 28.41%
Number/percentage of C's	561,663,431 / 20.29%
Number/percentage of T's	810,228,080 / 29.27%
Number/percentage of G's	610,131,024 / 22.04%
Number/percentage of N's	20,755 / 0%

GC Percentage	42.33%

2.3. Coverage

Mean	0.8948
Standard Deviation	8.5914

2.4. Mapping Quality

Mean Mapping Quality	52.69

2.5. Insert size

Mean	79,407.16
Standard Deviation	2,696,057.45
P25/Median/P75	140 / 174 / 222

2.6. Mismatches and indels

General error rate	0.77%
Mismatches	20,380,581
Insertions	393,208
Mapped reads with at least one insertion	1.27%
Deletions	927,201
Mapped reads with at least one deletion	3%
Homopolymer indels	47.54%

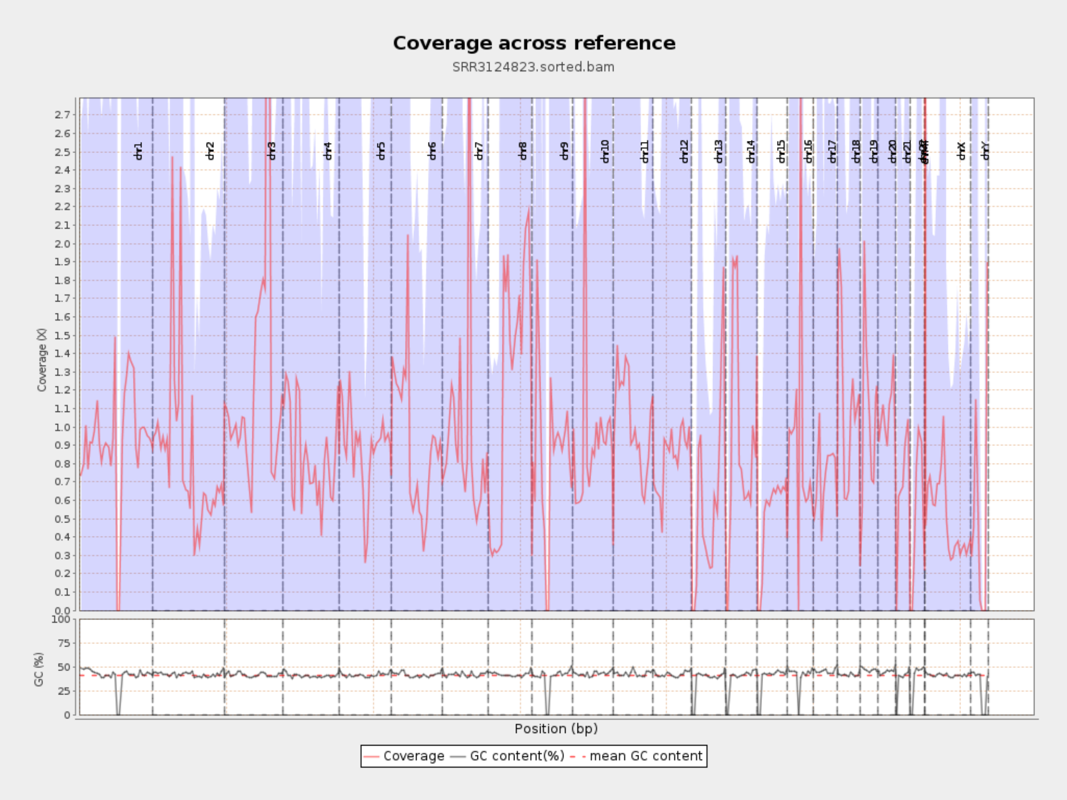
2.7. Chromosome stats

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

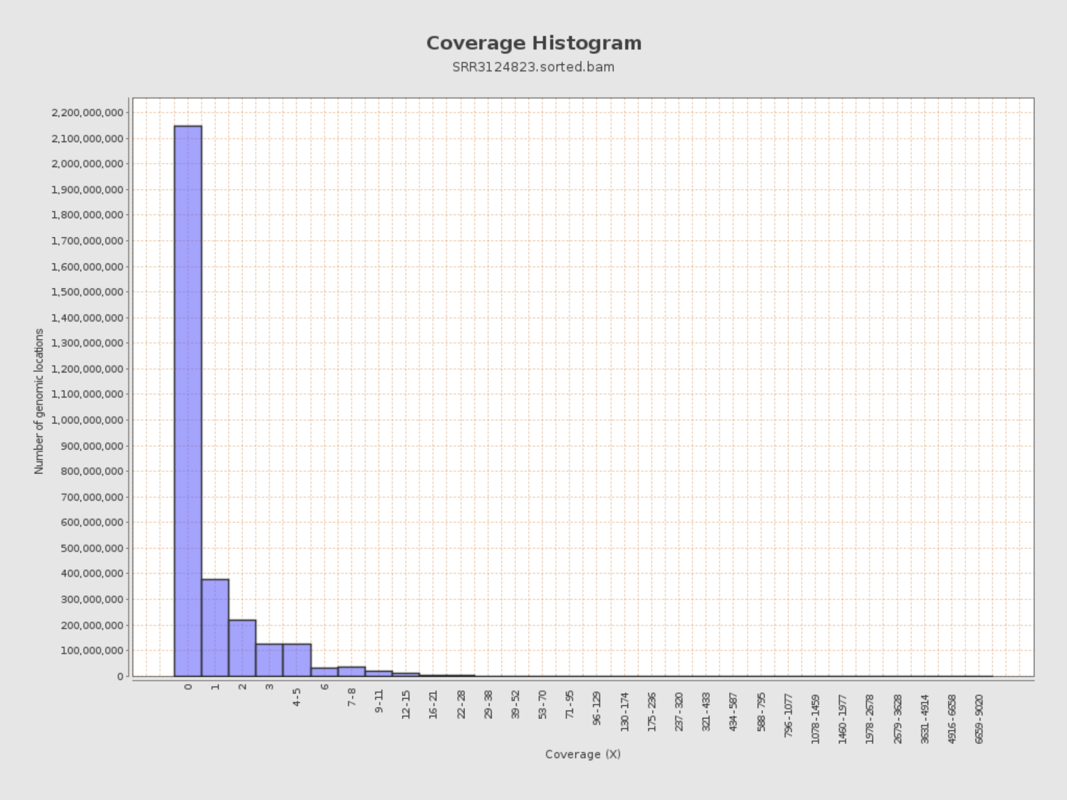
		bases	coverage	deviation
chr1	249250621	232220608	0.9317	9.3071
chr2	243199373	205772535	0.8461	10.1909
chr3	198022430	264541499	1.3359	3.138
chr4	191154276	161178266	0.8432	4.9354
chr5	180915260	160913138	0.8894	2.0037
chr6	171115067	157946985	0.923	10.5001
chr7	159138663	154967126	0.9738	11.9092
chr8	146364022	186371477	1.2733	3.6287
chr9	141213431	116955656	0.8282	12.4834
chr10	135534747	131200531	0.968	18.7
chr11	135006516	135679457	1.005	7.9963
chr12	133851895	110206418	0.8233	1.8366
chr13	115169878	70674789	0.6137	1.6859
chr14	107349540	95943374	0.8937	2.565
chr15	102531392	51898815	0.5062	1.3696
chr16	90354753	81413326	0.901	14.4353
chr17	81195210	58781229	0.7239	7.518
chr18	78077248	90753759	1.1624	13.6179
chr19	59128983	62388469	1.0551	5.9851
chr20	63025520	67190514	1.0661	2.4852
chr21	48129895	33844497	0.7032	2.7399
chr22	51304566	26915209	0.5246	1.711
chrMT	16571	685899	41.3915	20.9917
chrX	155270560	77800697	0.5011	3.7533

chrY	59373566	33759081	0.5686	11.5835

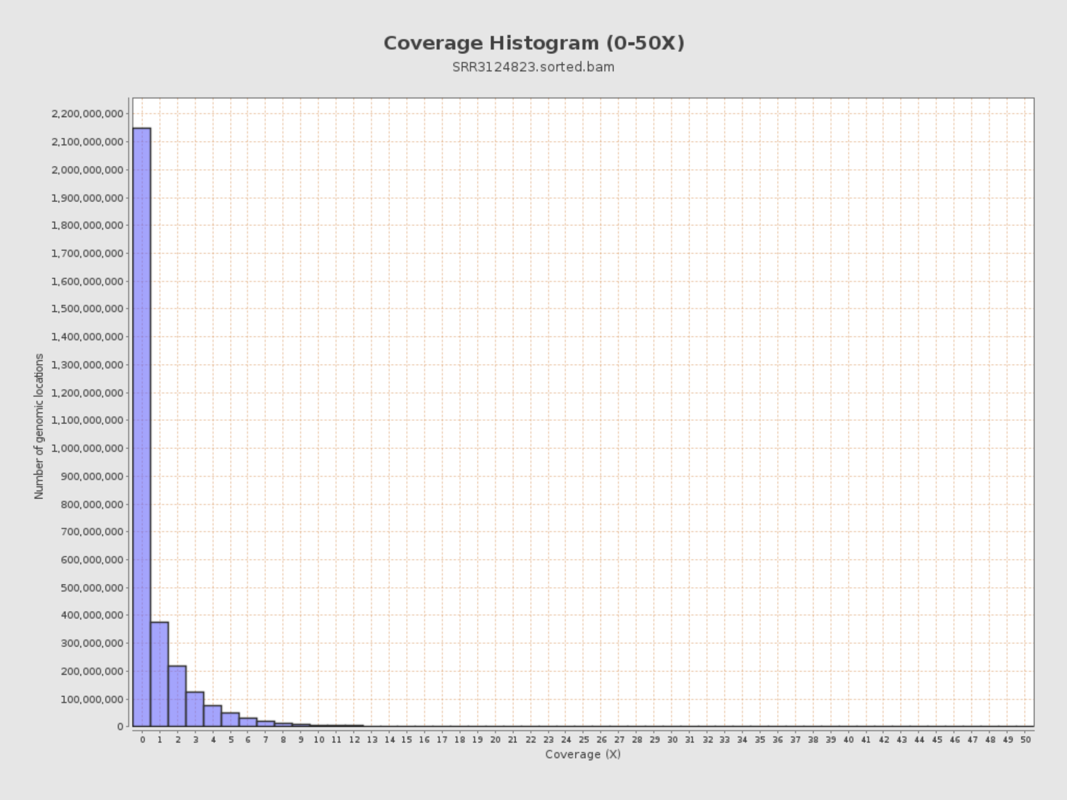
3. Results : Coverage across reference



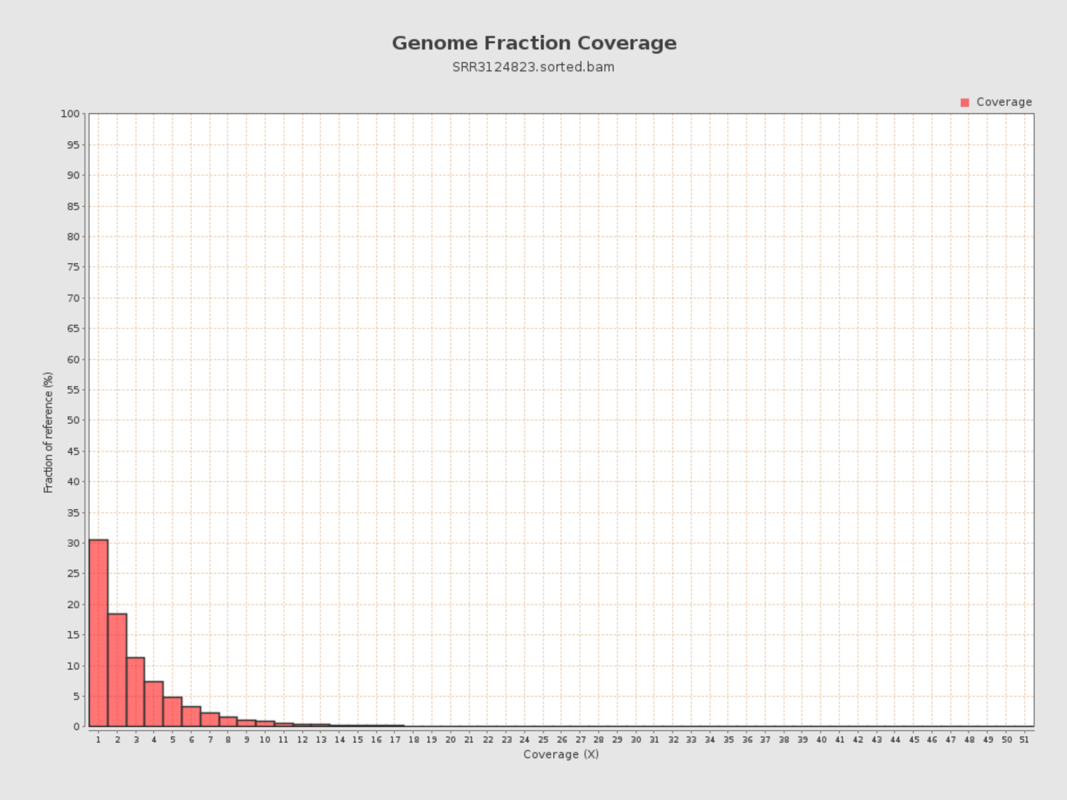
4. Results : Coverage Histogram



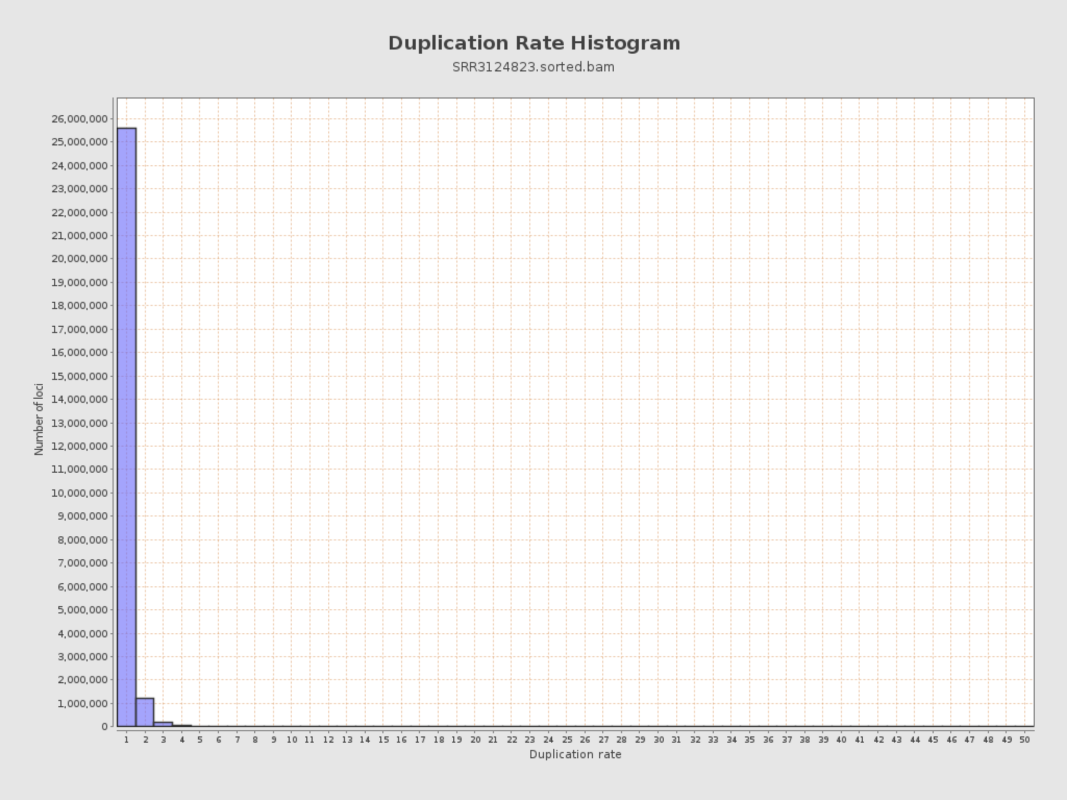
5. Results : Coverage Histogram (0-50X)



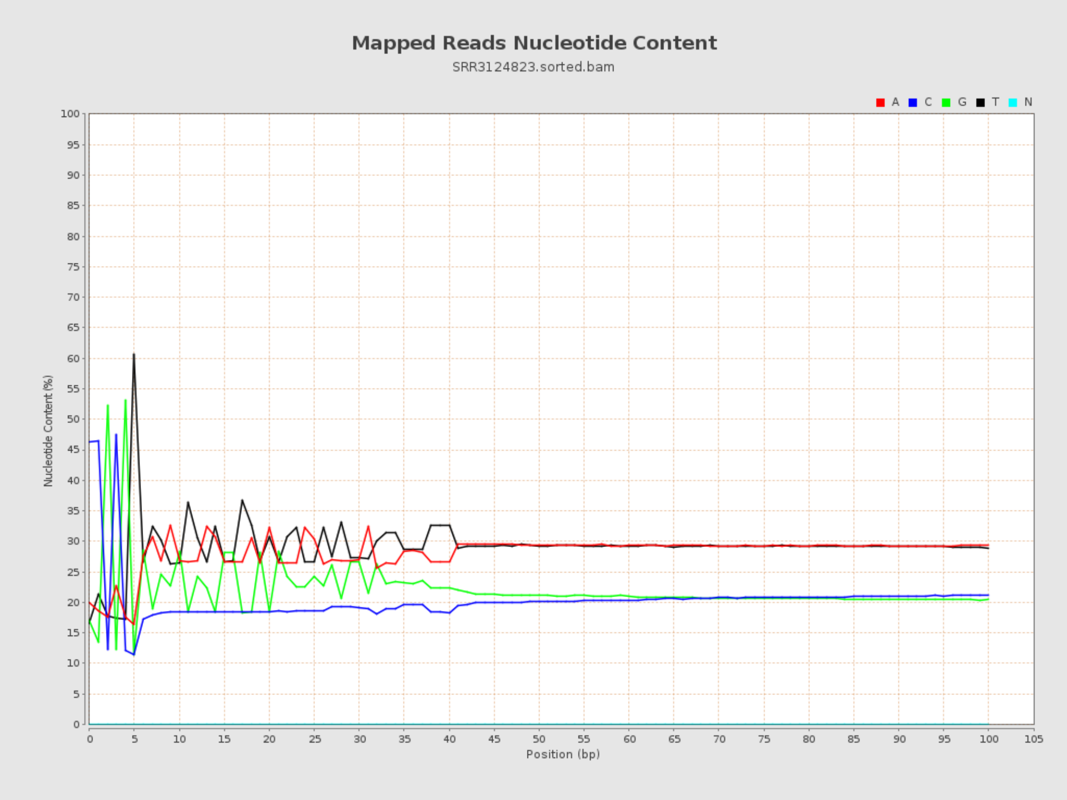
6. Results : Genome Fraction Coverage



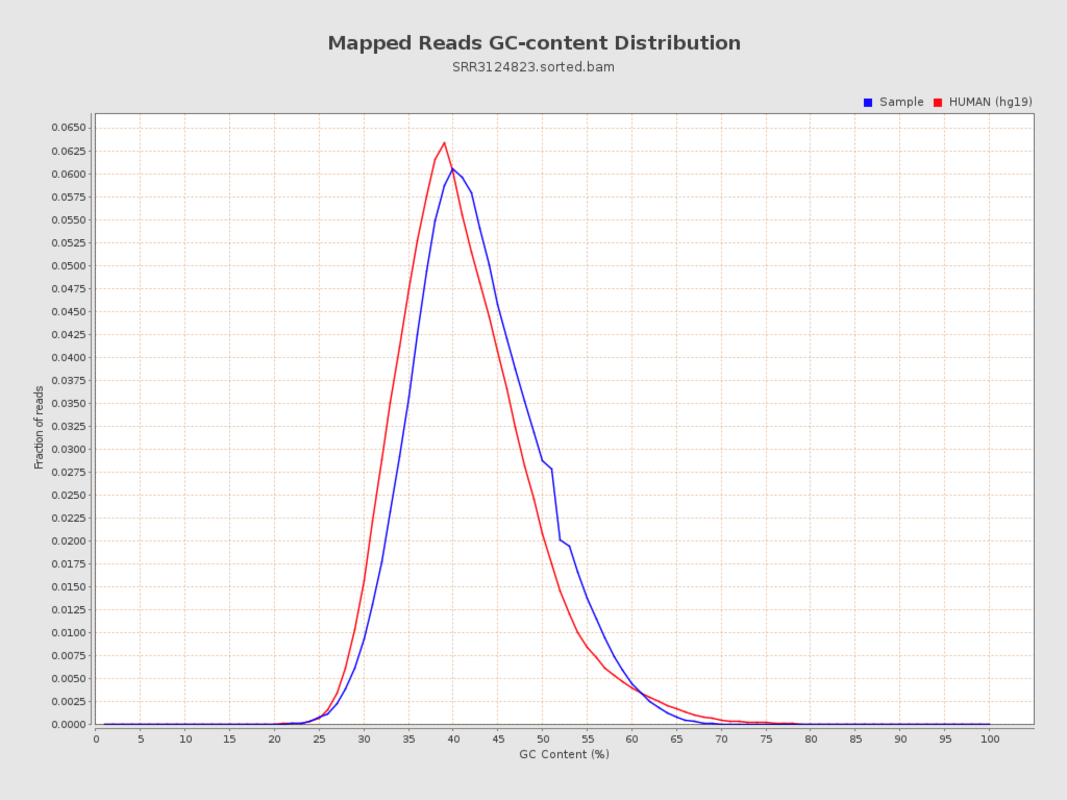
7. Results : Duplication Rate Histogram



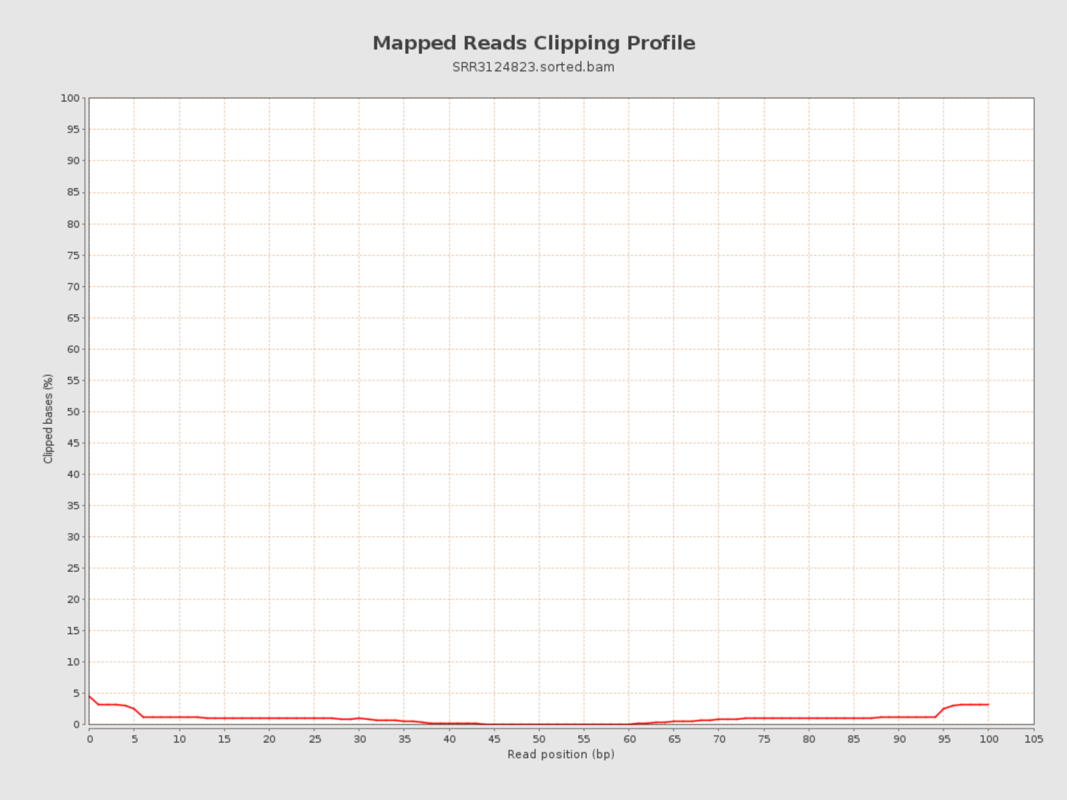
8. Results : Mapped Reads Nucleotide Content



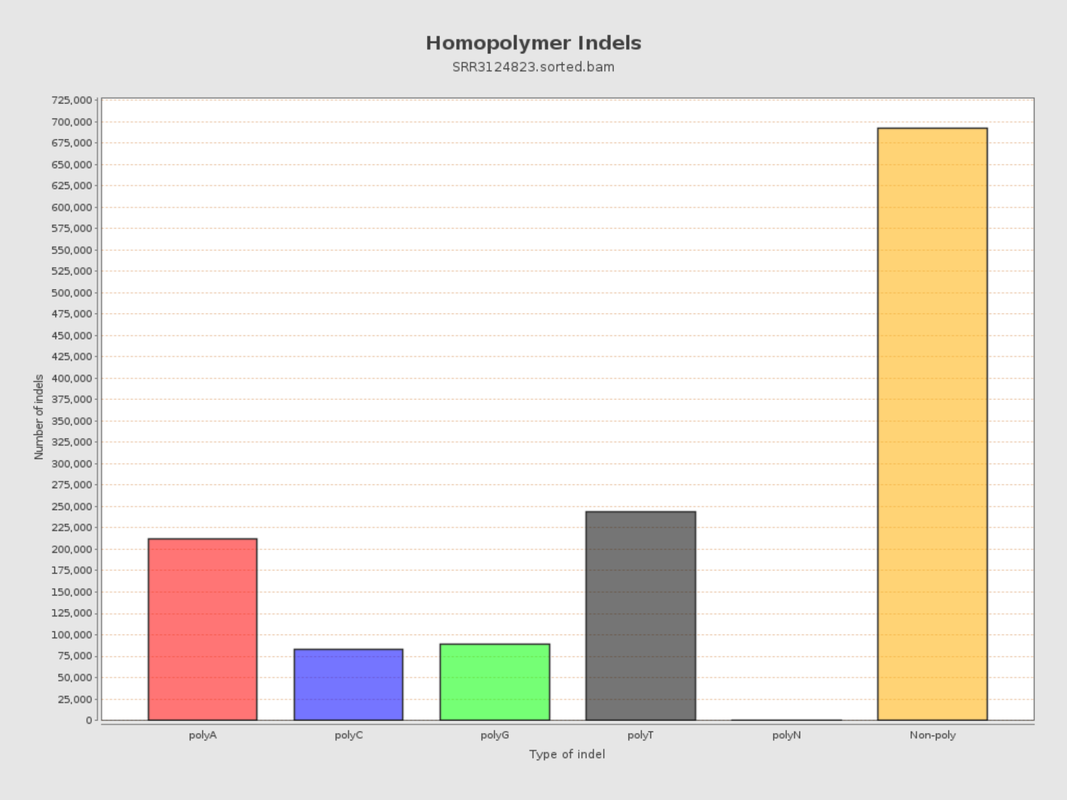
9. Results : Mapped Reads GC-content Distribution



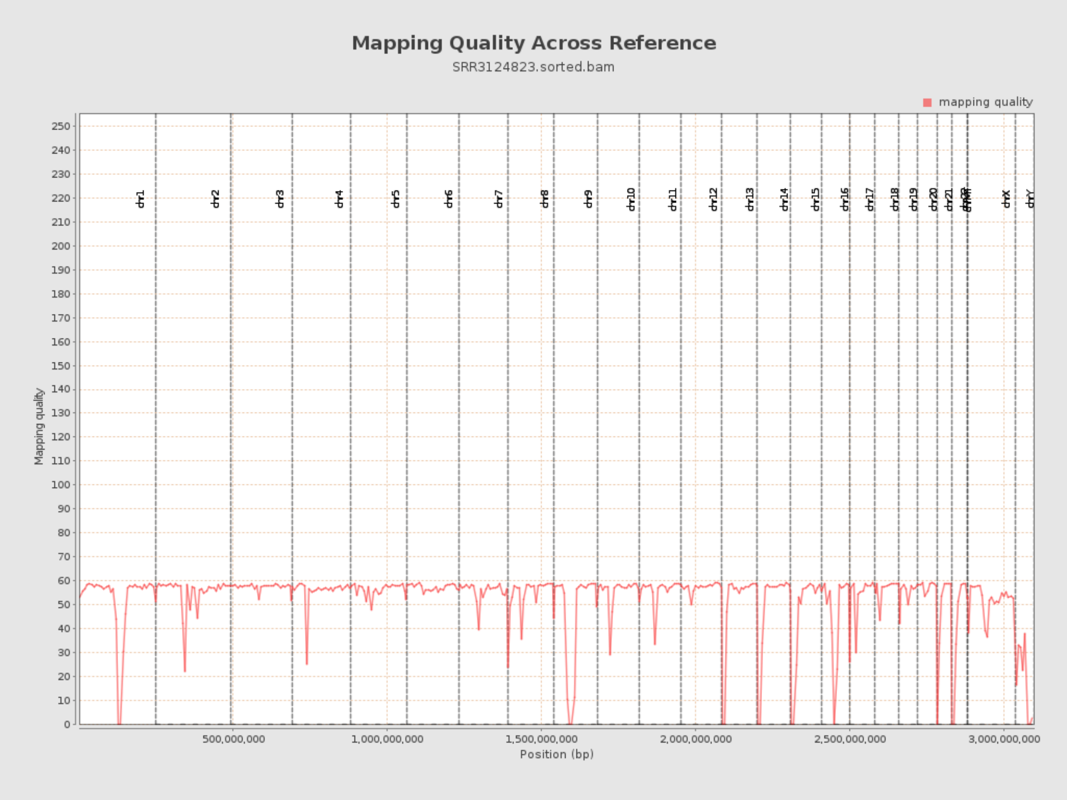
10. Results : Mapped Reads Clipping Profile



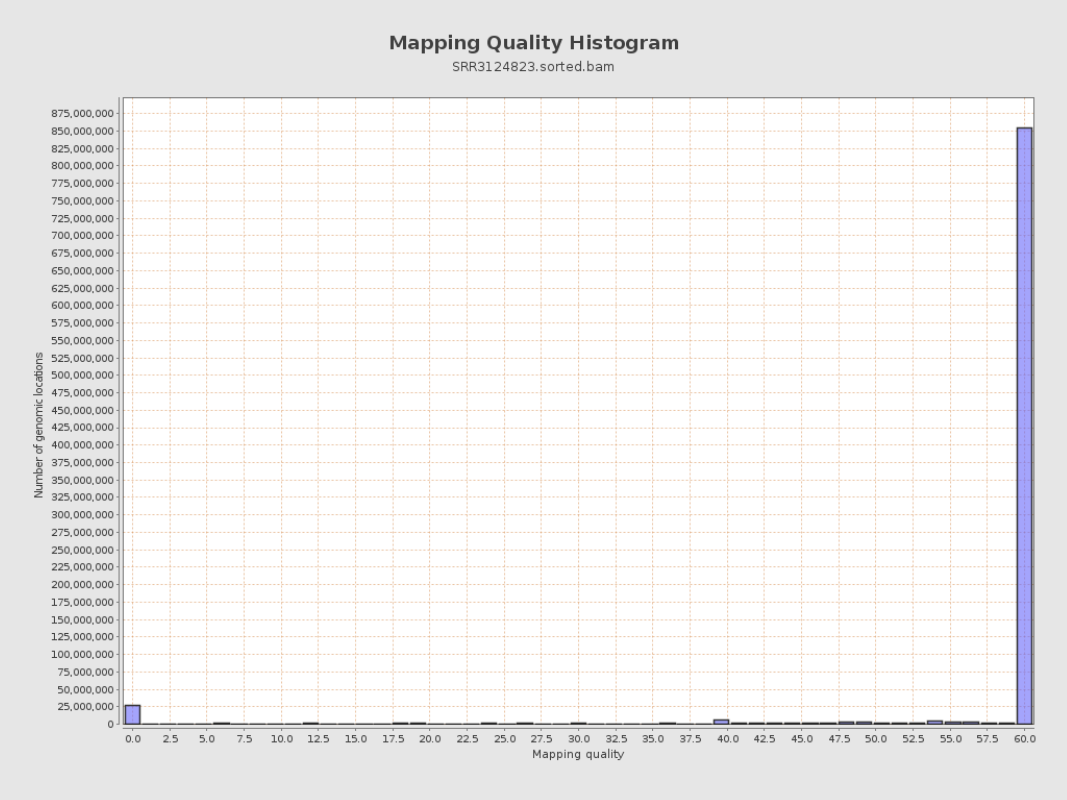
11. Results : Homopolymer Indels



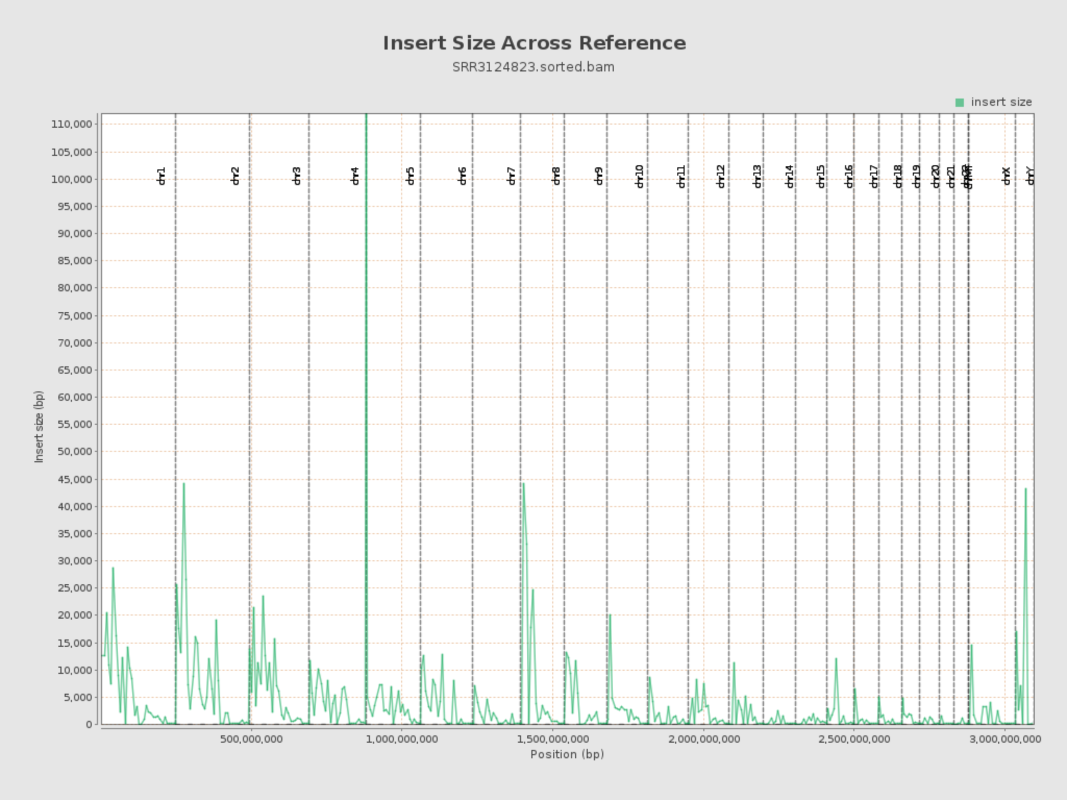
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram