Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/07 11:28:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124841.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_SRR3124841 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124841_1.fastq.gz SRR3124841_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Dec 07 11:28:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124841.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	128,349,802
Mapped reads	124,524,057 / 97.02%
Unmapped reads	3,825,745 / 2.98%
Mapped paired reads	124,524,057 / 97.02%
Mapped reads, first in pair	63,792,344 / 49.7%
Mapped reads, second in pair	60,731,713 / 47.32%
Mapped reads, both in pair	121,315,110 / 94.52%
Mapped reads, singletons	3,208,947 / 2.5%
Secondary alignments	0
Supplementary alignments	2,313,105 / 1.8%
Read min/max/mean length	30 / 150 / 150.83
Duplicated reads (estimated)	43,058,229 / 33.55%
Duplication rate	21.14%
Clipped reads	58,196,738 / 45.34%

2.2. ACGT Content

Number/percentage of A's	4,725,546,503 / 28.15%
Number/percentage of C's	3,410,406,466 / 20.32%
Number/percentage of T's	4,843,475,349 / 28.86%
Number/percentage of G's	3,804,619,549 / 22.67%
Number/percentage of N's	305,004 / 0%

GC Percentage	42.99%

2.3. Coverage

Mean	5.426
Standard Deviation	47.0831

2.4. Mapping Quality

Mean Mapping Quality	53.59

2.5. Insert size

Mean	105,022.72
Standard Deviation	3,153,497.5
P25/Median/P75	207 / 266 / 334

2.6. Mismatches and indels

General error rate	1.26%
Mismatches	203,305,605
Insertions	2,937,229
Mapped reads with at least one insertion	2.2%
Deletions	6,341,624
Mapped reads with at least one deletion	4.87%
Homopolymer indels	45.14%

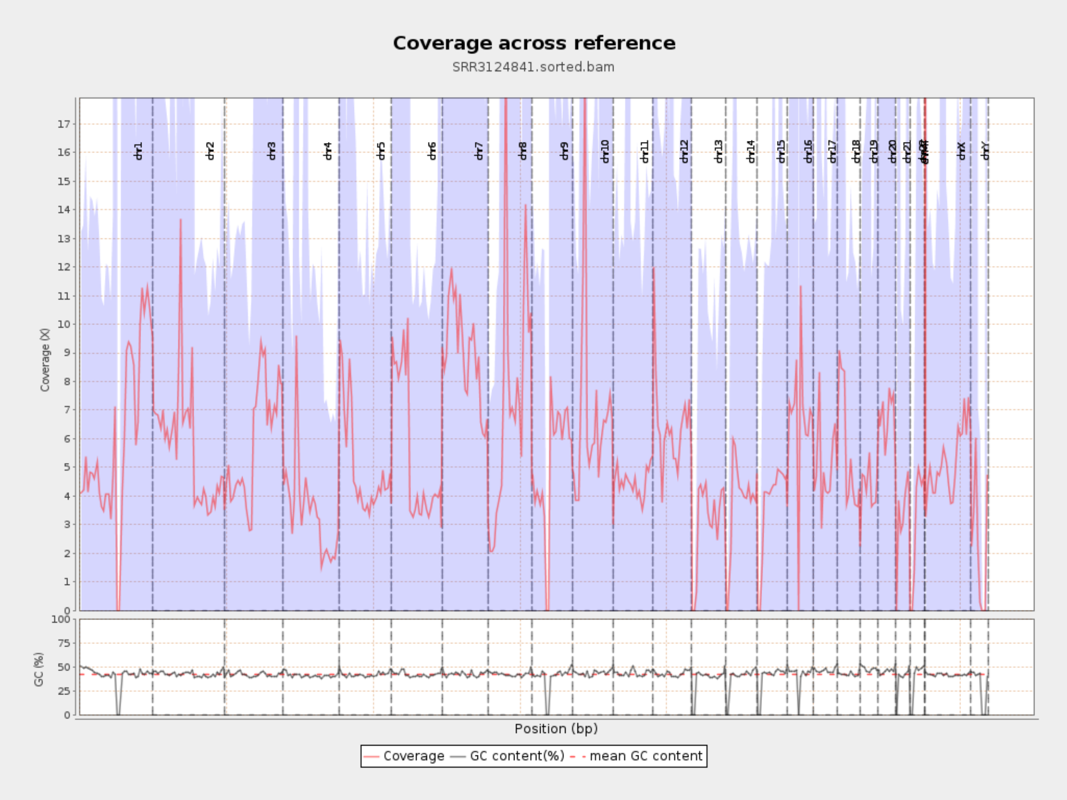
2.7. Chromosome stats

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

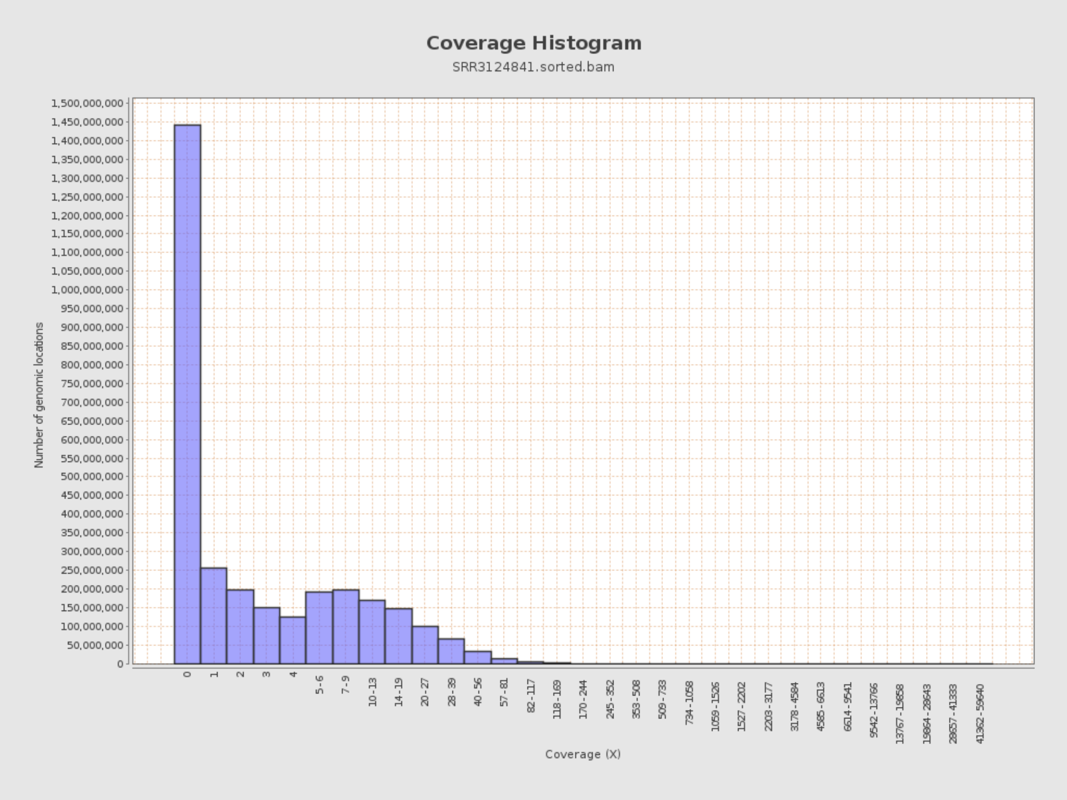
		bases	coverage	deviation
chr1	249250621	1517076155	6.0865	50.2618
chr2	243199373	1403286711	5.7701	67.1453
chr3	198022430	1176997748	5.9438	10.8628
chr4	191154276	660823668	3.457	40.9388
chr5	180915260	914959511	5.0574	11.1822
chr6	171115067	944107943	5.5174	33.4927
chr7	159138663	1425878884	8.96	72.7359
chr8	146364022	1092168609	7.462	19.1447
chr9	141213431	706129186	5.0004	76.2132
chr10	135534747	952419603	7.0271	101.5065
chr11	135006516	599287187	4.439	27.7282
chr12	133851895	868568225	6.489	20.0851
chr13	115169878	359767463	3.1238	7.0578
chr14	107349540	401544685	3.7405	9.9403
chr15	102531392	371000140	3.6184	11.3256
chr16	90354753	598361253	6.6224	55.6177
chr17	81195210	405225506	4.9908	66.1354
chr18	78077248	437730113	5.6064	57.0212
chr19	59128983	250081512	4.2294	33.8601
chr20	63025520	427392786	6.7813	16.7453
chr21	48129895	162951106	3.3857	22.2878
chr22	51304566	160107606	3.1207	10.0687
chrMT	16571	16769185	1,011.9597	428.1417
chrX	155270560	803862518	5.1772	15.8225

chrY	59373566	140724074	2.3701	59.4694

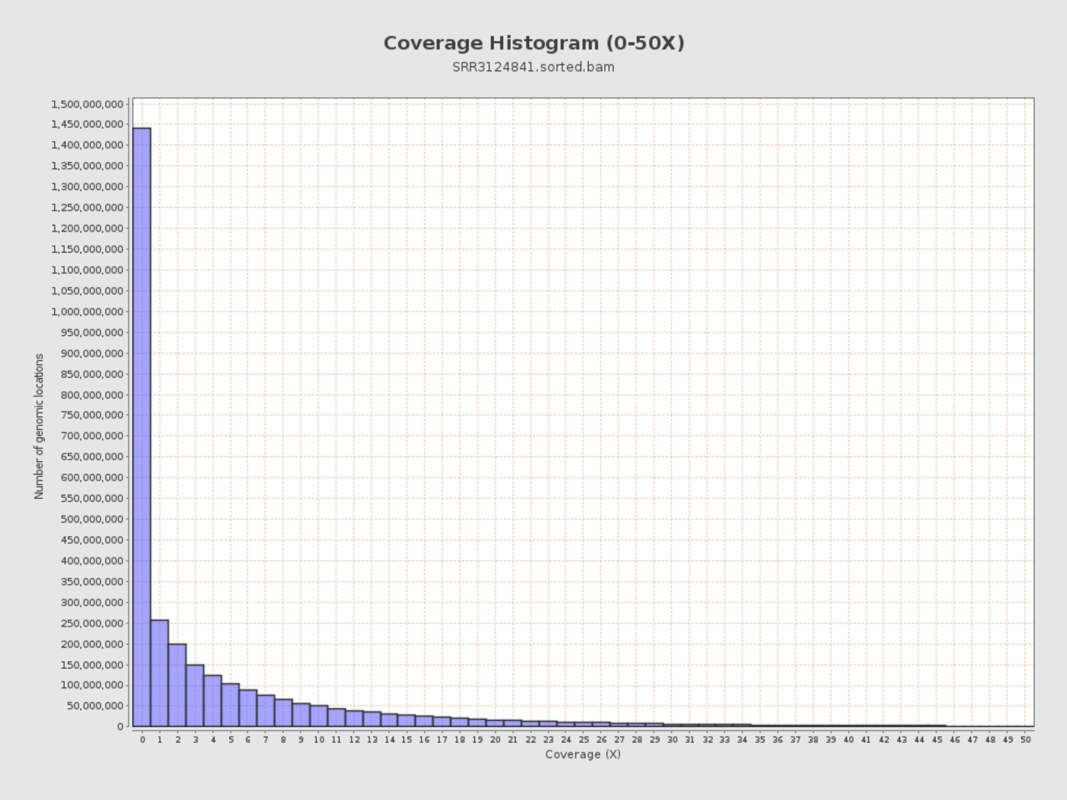
3. Results : Coverage across reference



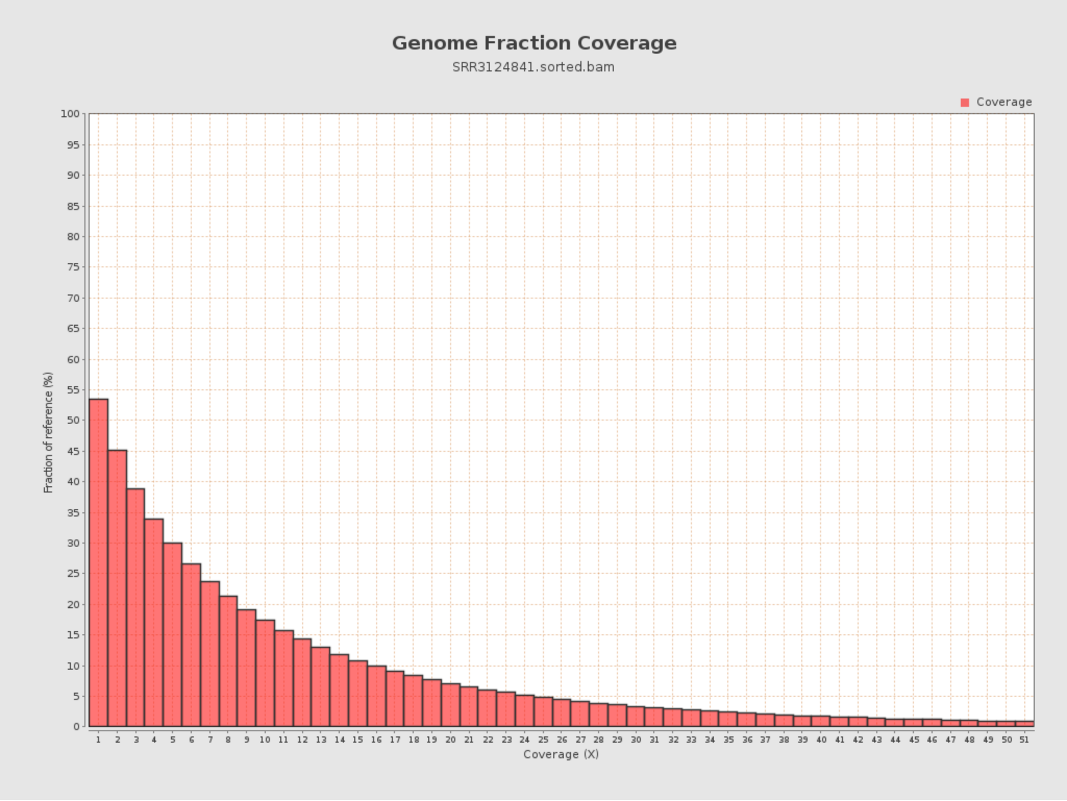
4. Results : Coverage Histogram



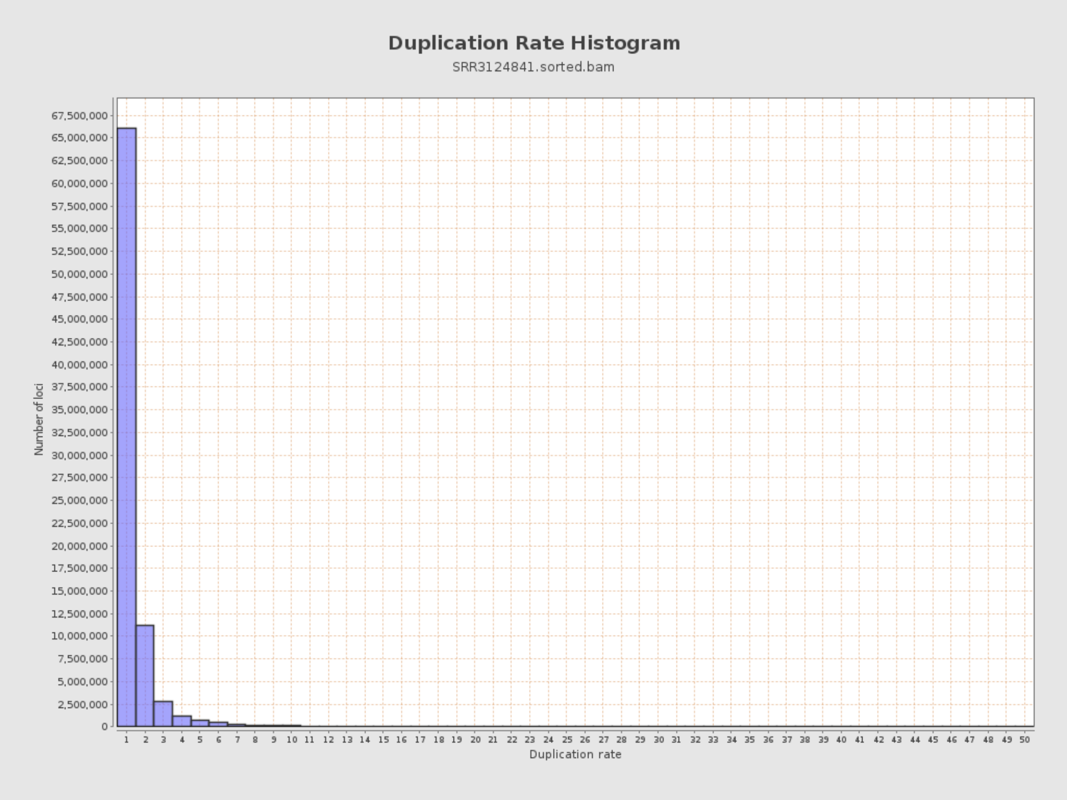
5. Results : Coverage Histogram (0-50X)



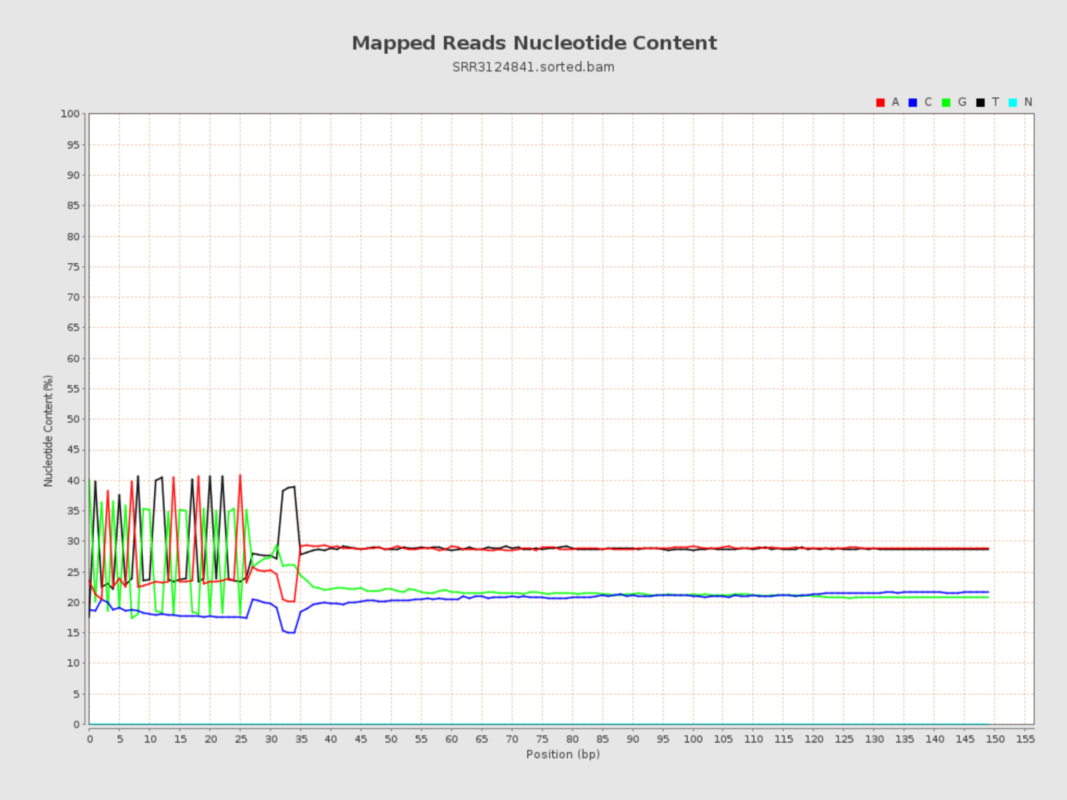
6. Results : Genome Fraction Coverage



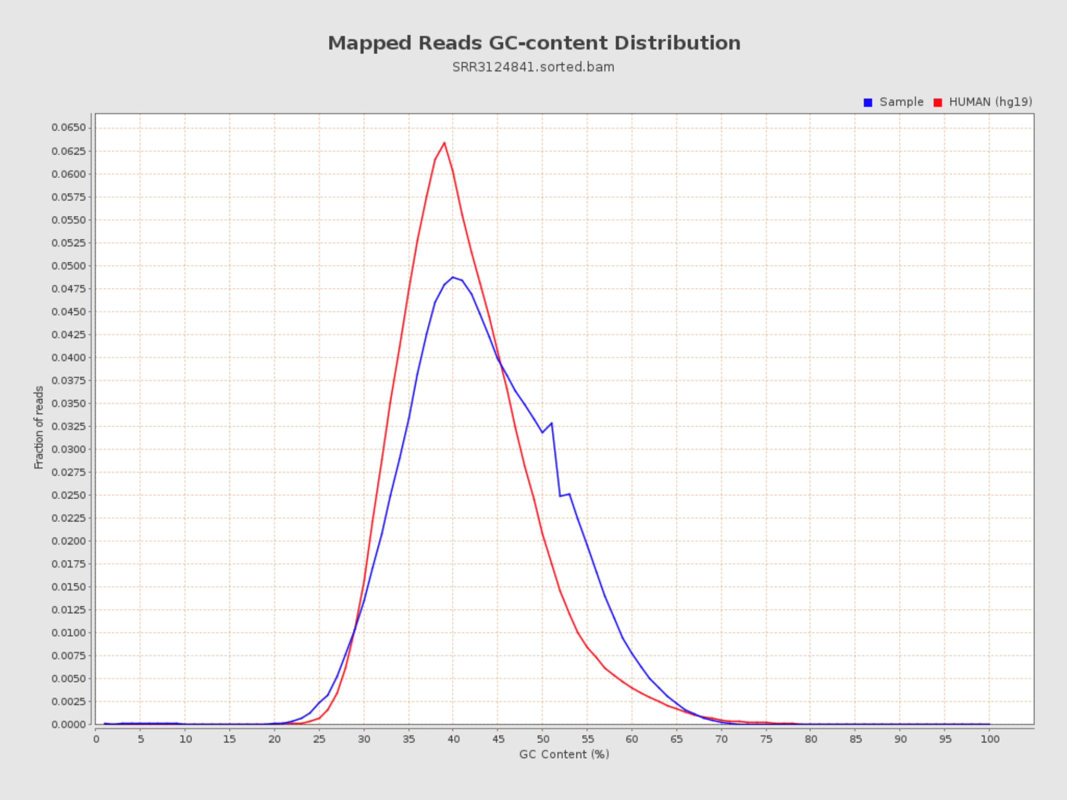
7. Results : Duplication Rate Histogram



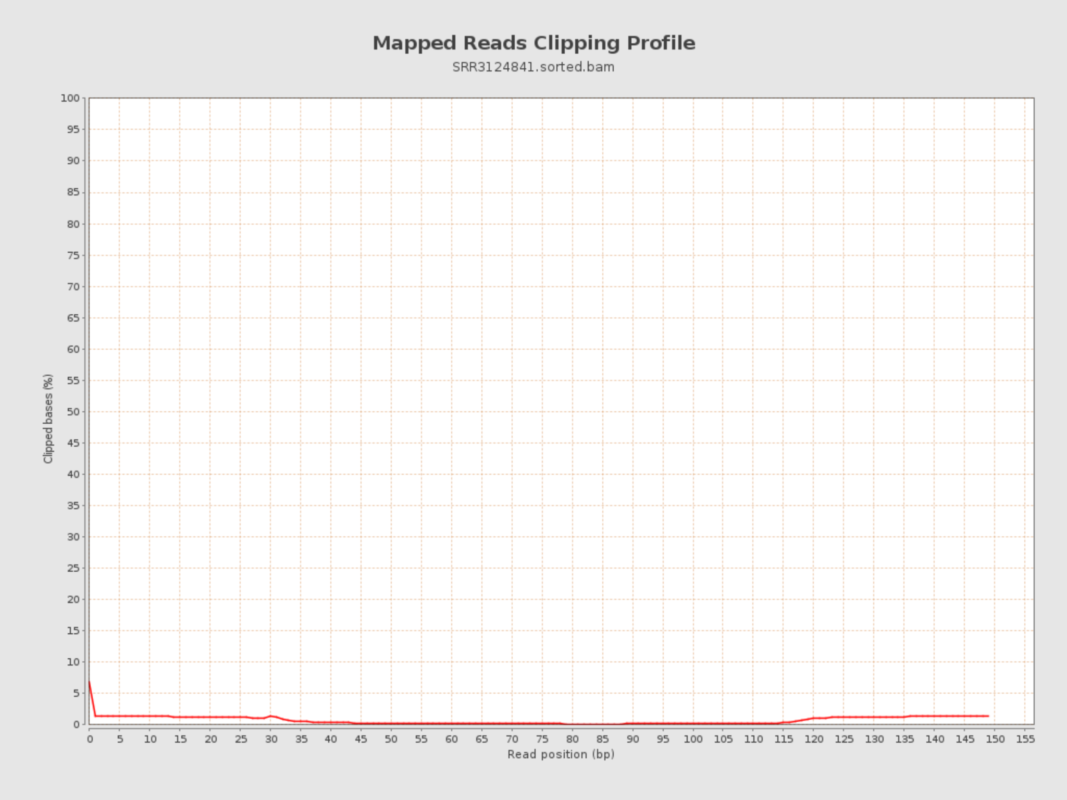
8. Results : Mapped Reads Nucleotide Content



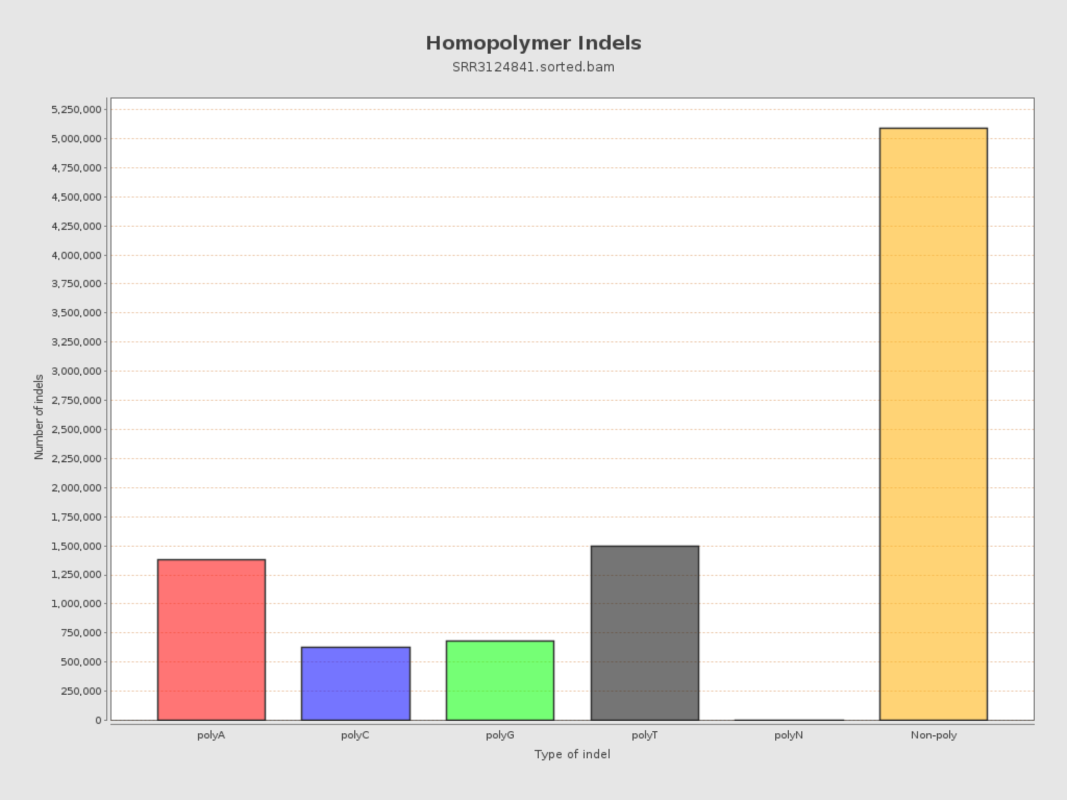
9. Results : Mapped Reads GC-content Distribution



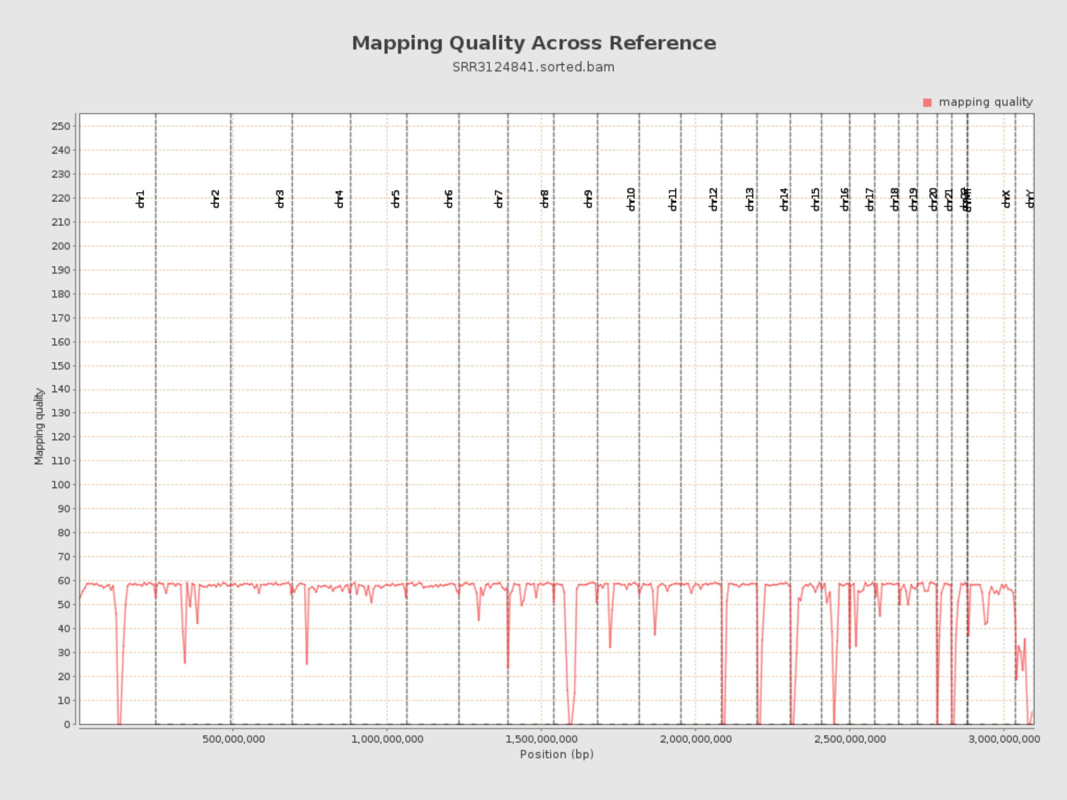
10. Results : Mapped Reads Clipping Profile



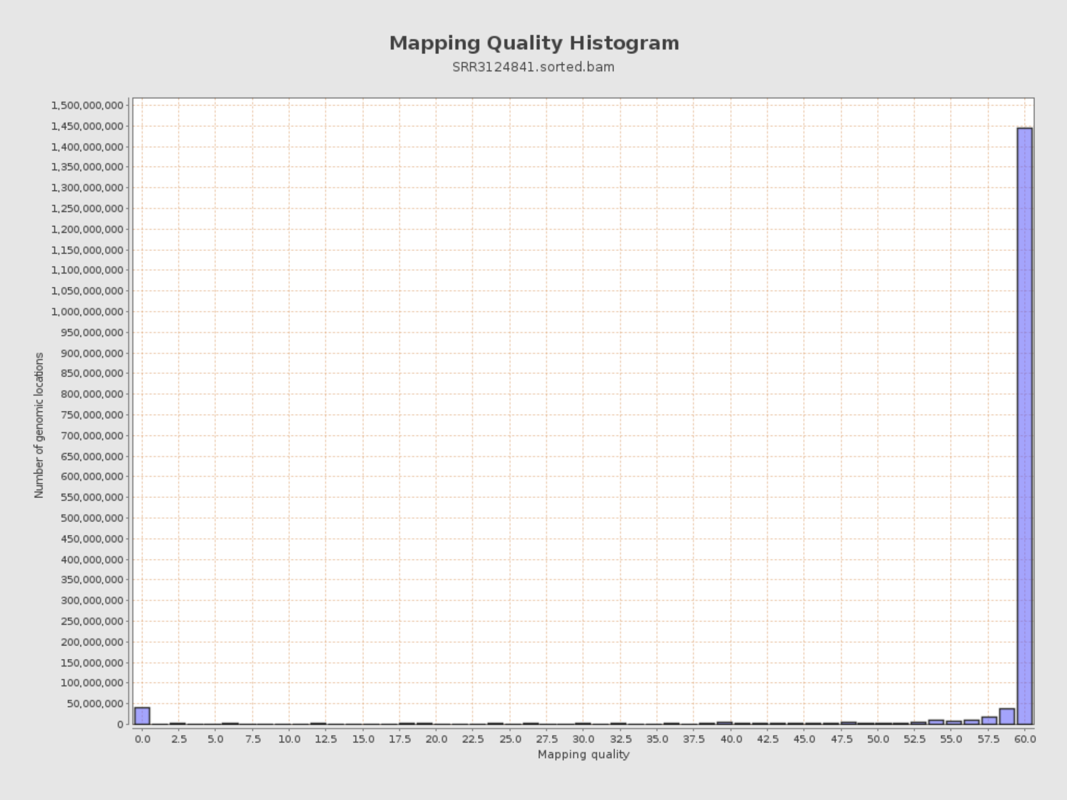
11. Results : Homopolymer Indels



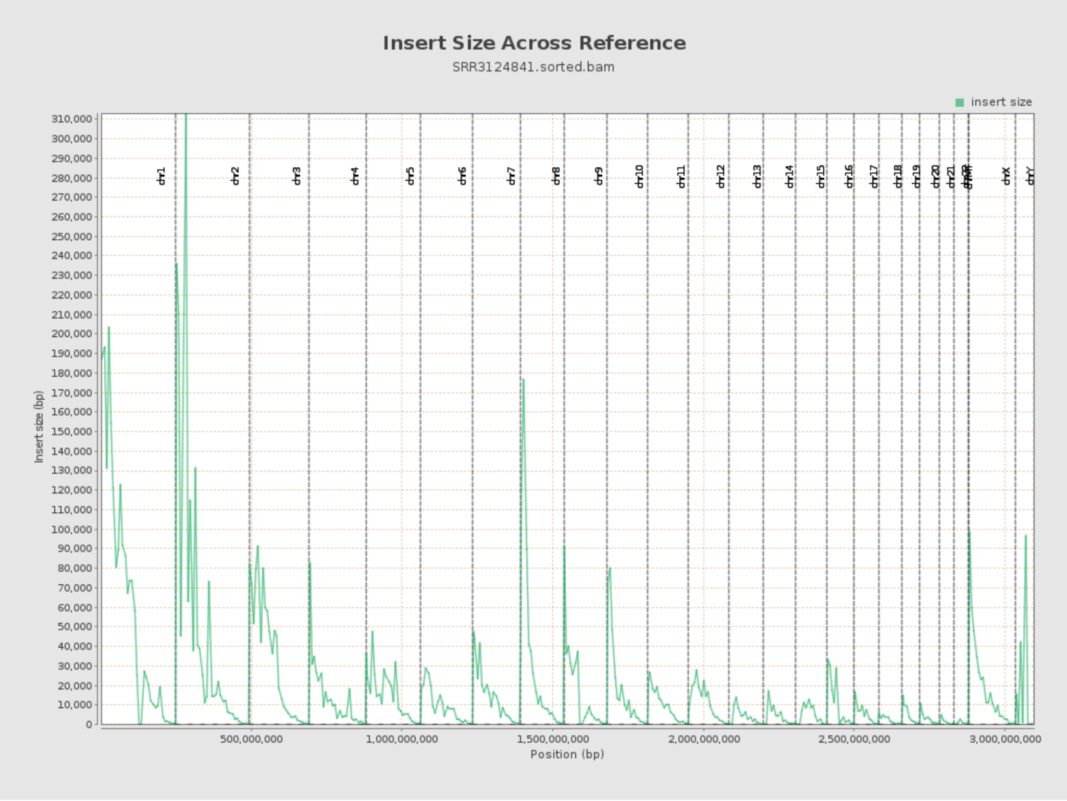
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram