Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 22:46:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472530.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_SRR3472530 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472530_1.fastq.gz SRR3472530_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 22:46:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472530.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	17,225,174
Mapped reads	17,060,387 / 99.04%
Unmapped reads	164,787 / 0.96%
Mapped paired reads	17,060,387 / 99.04%
Mapped reads, first in pair	8,549,831 / 49.64%
Mapped reads, second in pair	8,510,556 / 49.41%
Mapped reads, both in pair	16,977,148 / 98.56%
Mapped reads, singletons	83,239 / 0.48%
Secondary alignments	0
Supplementary alignments	63,550 / 0.37%
Read min/max/mean length	30 / 100 / 100.15
Duplicated reads (estimated)	11,022,638 / 63.99%
Duplication rate	45.35%
Clipped reads	1,542,040 / 8.95%

2.2. ACGT Content

Number/percentage of A's	454,505,620 / 27.12%
Number/percentage of C's	385,730,385 / 23.01%
Number/percentage of T's	451,779,420 / 26.95%
Number/percentage of G's	383,846,508 / 22.9%
Number/percentage of N's	262,761 / 0.02%

GC Percentage	45.91%

2.3. Coverage

Mean	0.5415
Standard Deviation	21.1661

2.4. Mapping Quality

Mean Mapping Quality	54.98

2.5. Insert size

Mean	27,194.73
Standard Deviation	1,617,429.95
P25/Median/P75	155 / 212 / 284

2.6. Mismatches and indels

General error rate	0.56%
Mismatches	9,150,553
Insertions	81,939
Mapped reads with at least one insertion	0.47%
Deletions	76,769
Mapped reads with at least one deletion	0.44%
Homopolymer indels	43.28%

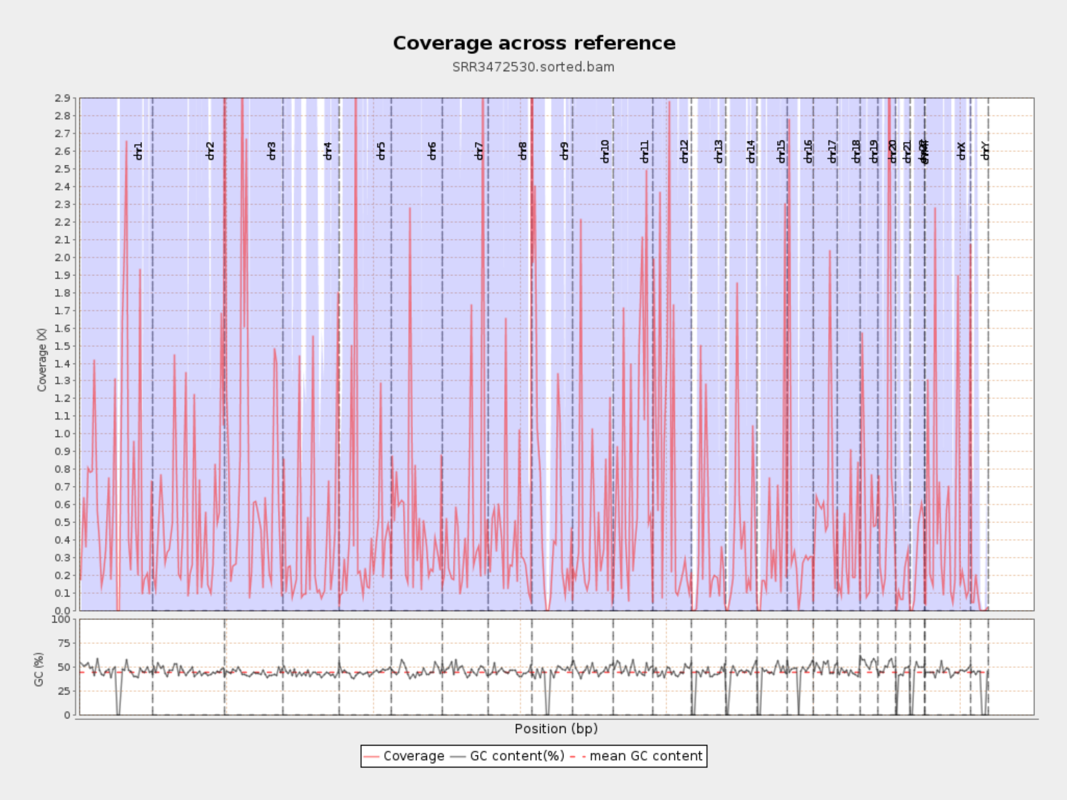
2.7. Chromosome stats

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

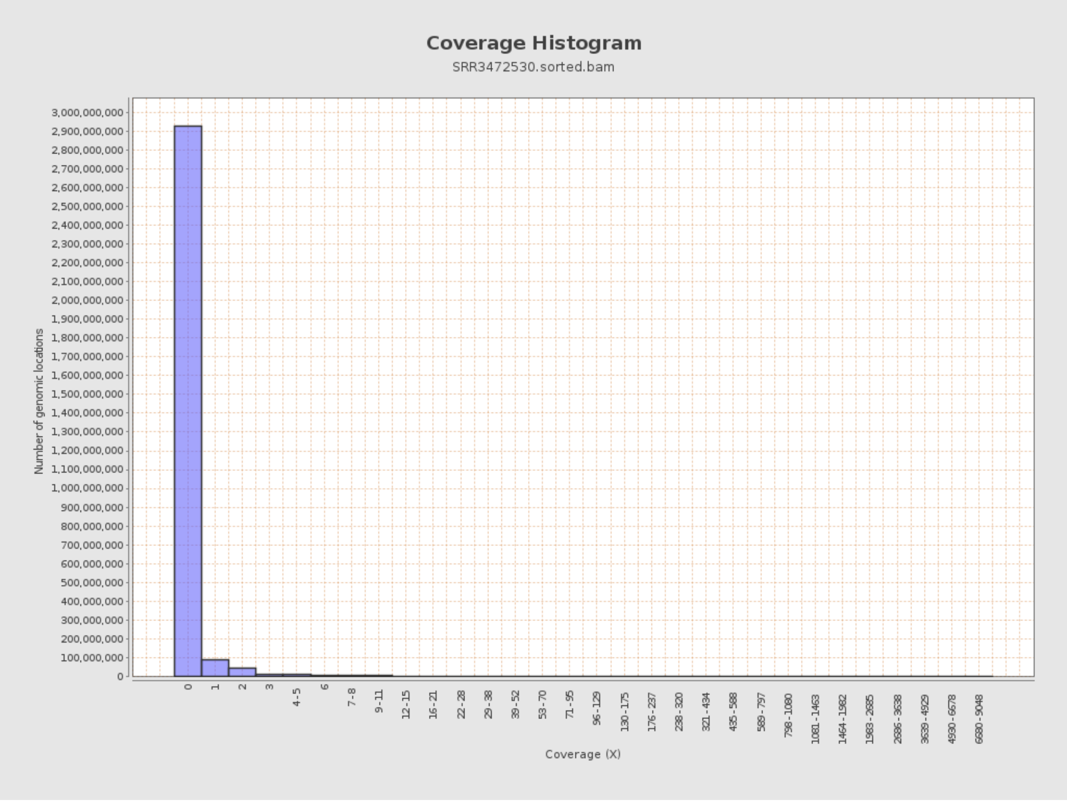
		bases	coverage	deviation
chr1	249250621	165273173	0.6631	21.6223
chr2	243199373	124832693	0.5133	17.6878
chr3	198022430	160826959	0.8122	21.14
chr4	191154276	75105002	0.3929	16.1666
chr5	180915260	89766058	0.4962	21.7627
chr6	171115067	85837053	0.5016	14.3507
chr7	159138663	84555244	0.5313	26.3003
chr8	146364022	60413272	0.4128	14.3623
chr9	141213431	91560100	0.6484	19.9042
chr10	135534747	67097386	0.4951	29.2218
chr11	135006516	114120537	0.8453	33.1434
chr12	133851895	111726032	0.8347	27.1504
chr13	115169878	40795345	0.3542	14.8719
chr14	107349540	46207159	0.4304	16.3304
chr15	102531392	44390235	0.4329	19.2139
chr16	90354753	41620956	0.4606	15.132
chr17	81195210	51650497	0.6361	16.9449
chr18	78077248	26844846	0.3438	18.5576
chr19	59128983	35338774	0.5977	17.2973
chr20	63025520	53694752	0.852	42.0886
chr21	48129895	6884048	0.143	4.7623
chr22	51304566	15241932	0.2971	13.1858
chrMT	16571	1061	0.064	0.3128
chrX	155270560	79510166	0.5121	21.7586

chrY	59373566	3035707	0.0511	1.6633

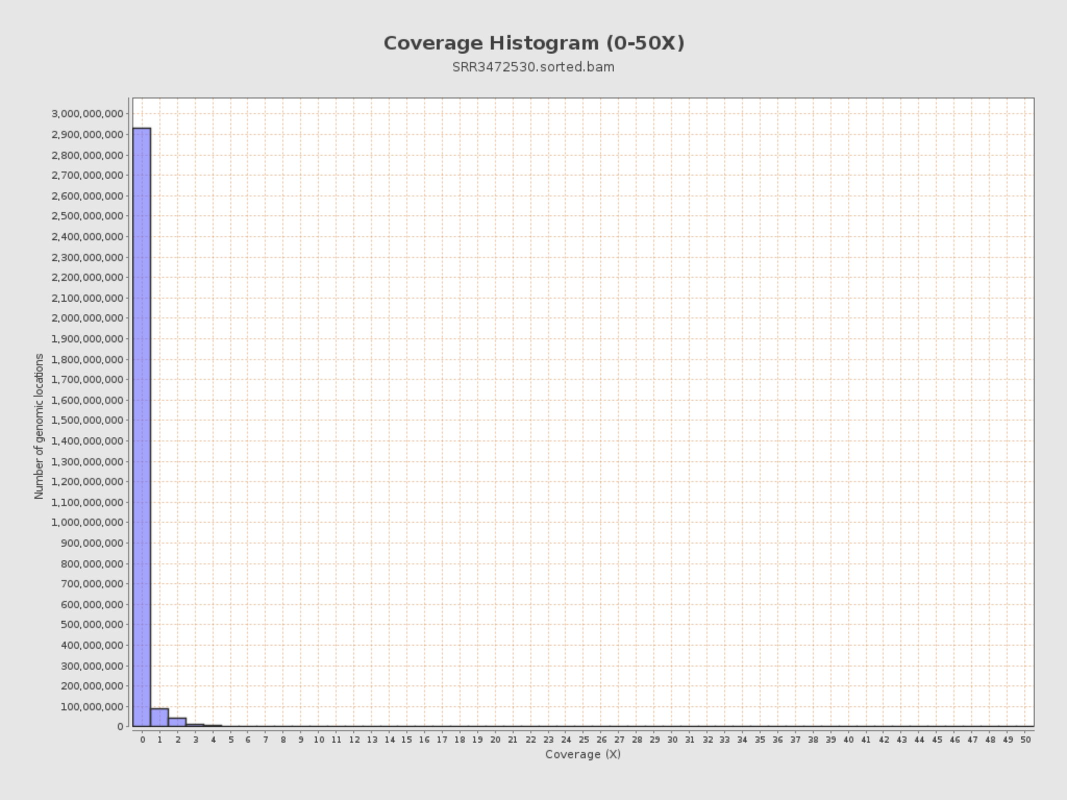
3. Results : Coverage across reference



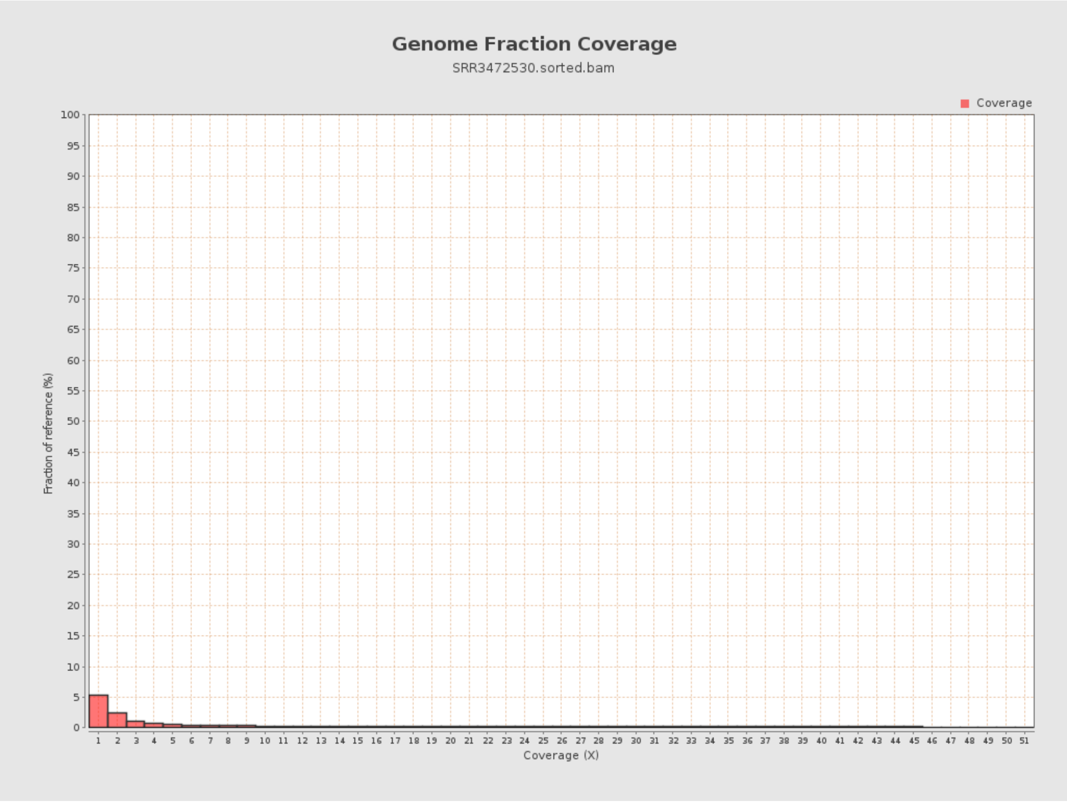
4. Results : Coverage Histogram



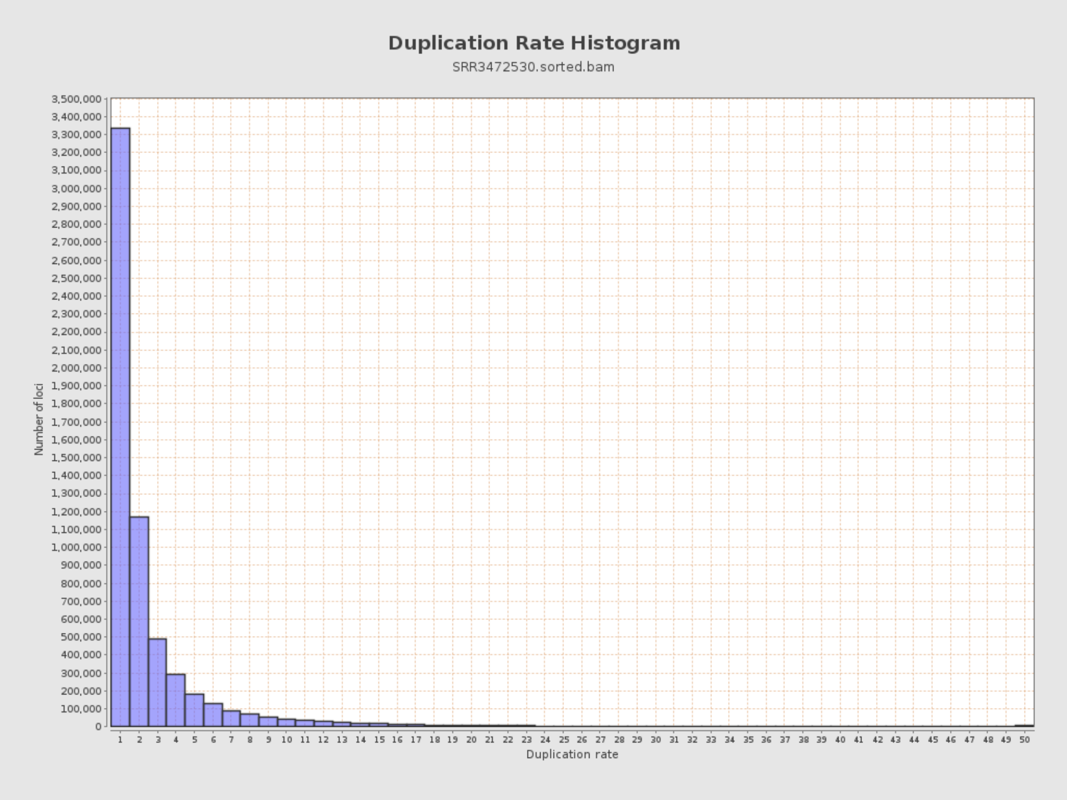
5. Results : Coverage Histogram (0-50X)



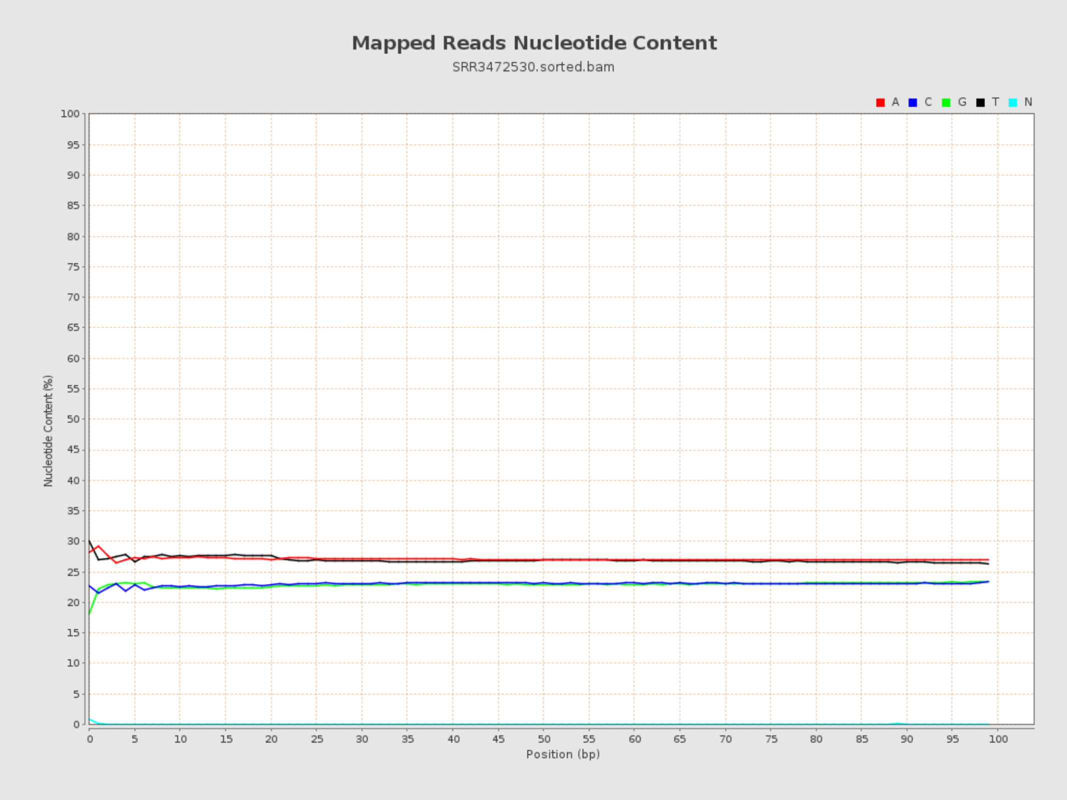
6. Results : Genome Fraction Coverage



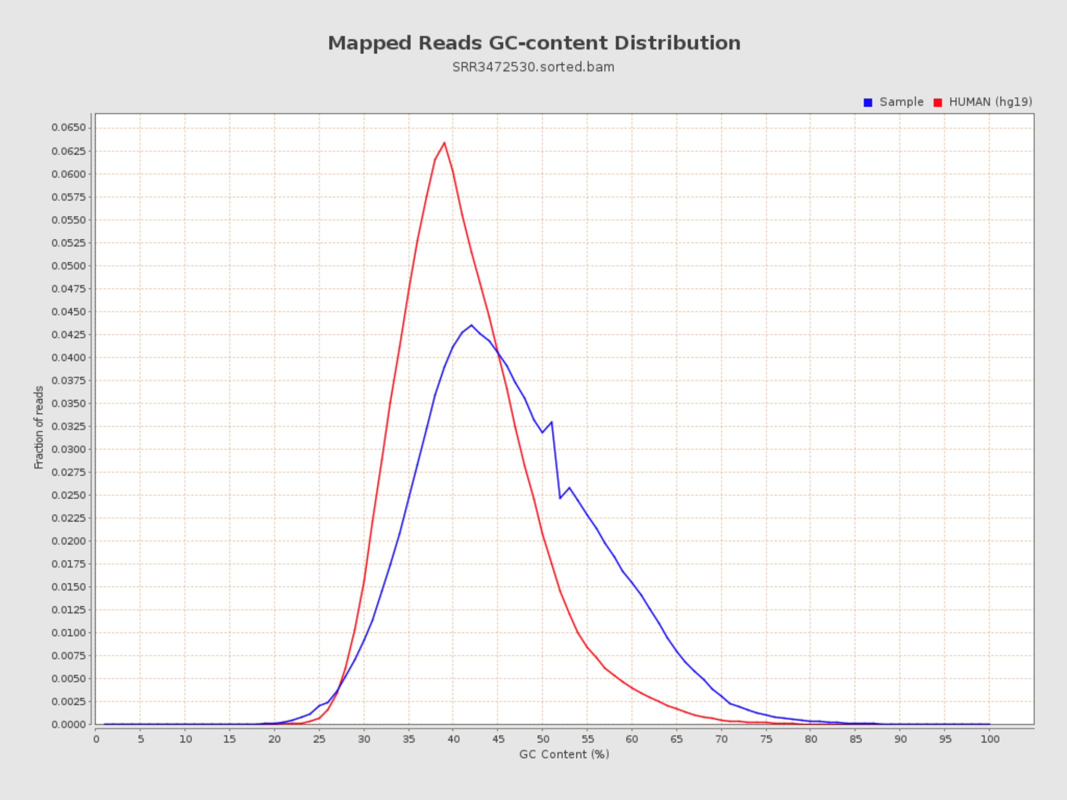
7. Results : Duplication Rate Histogram



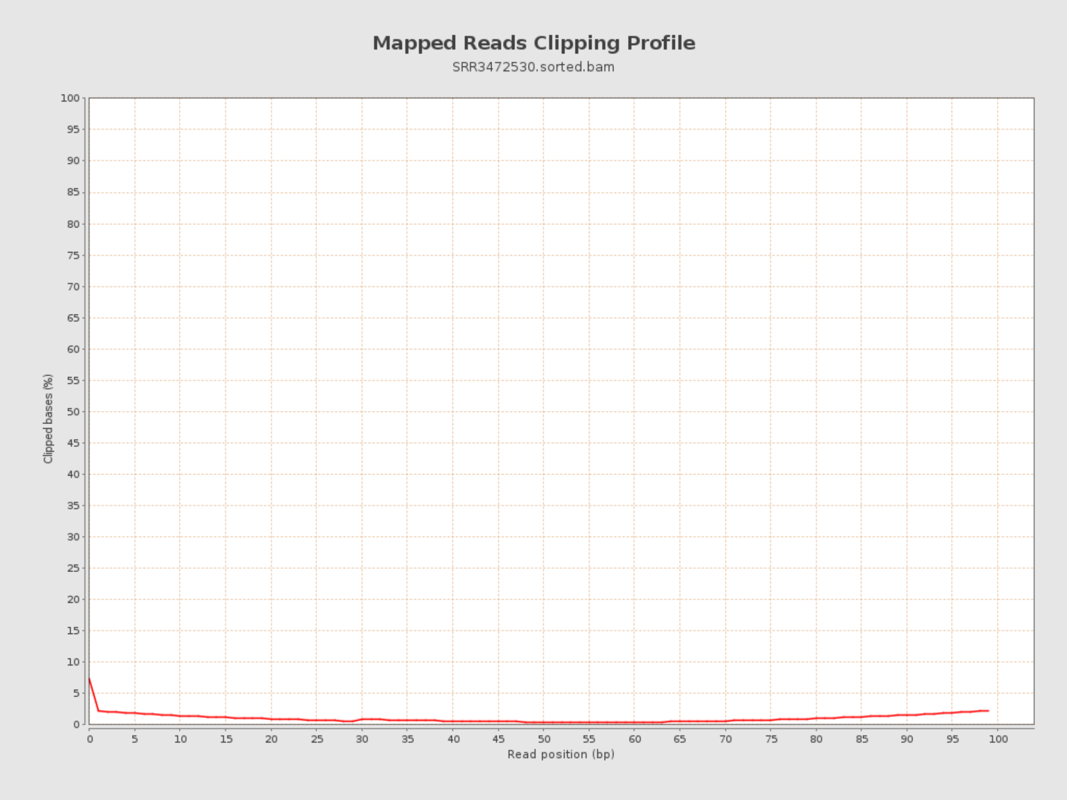
8. Results : Mapped Reads Nucleotide Content



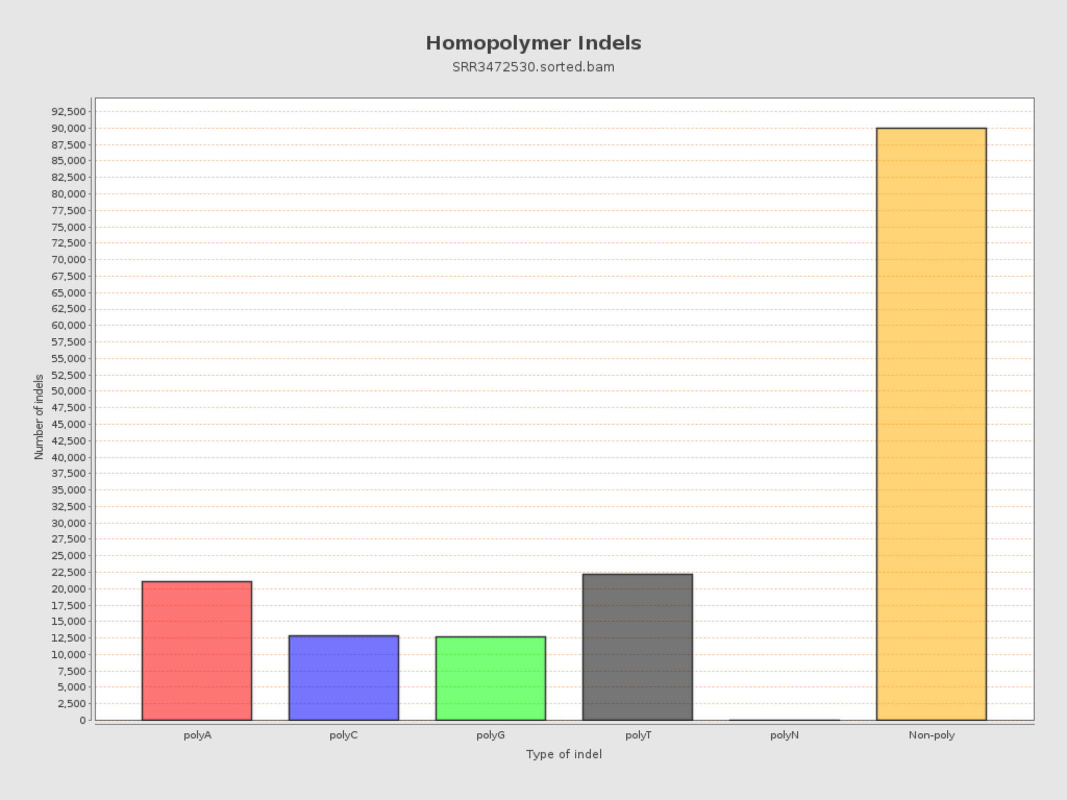
9. Results : Mapped Reads GC-content Distribution



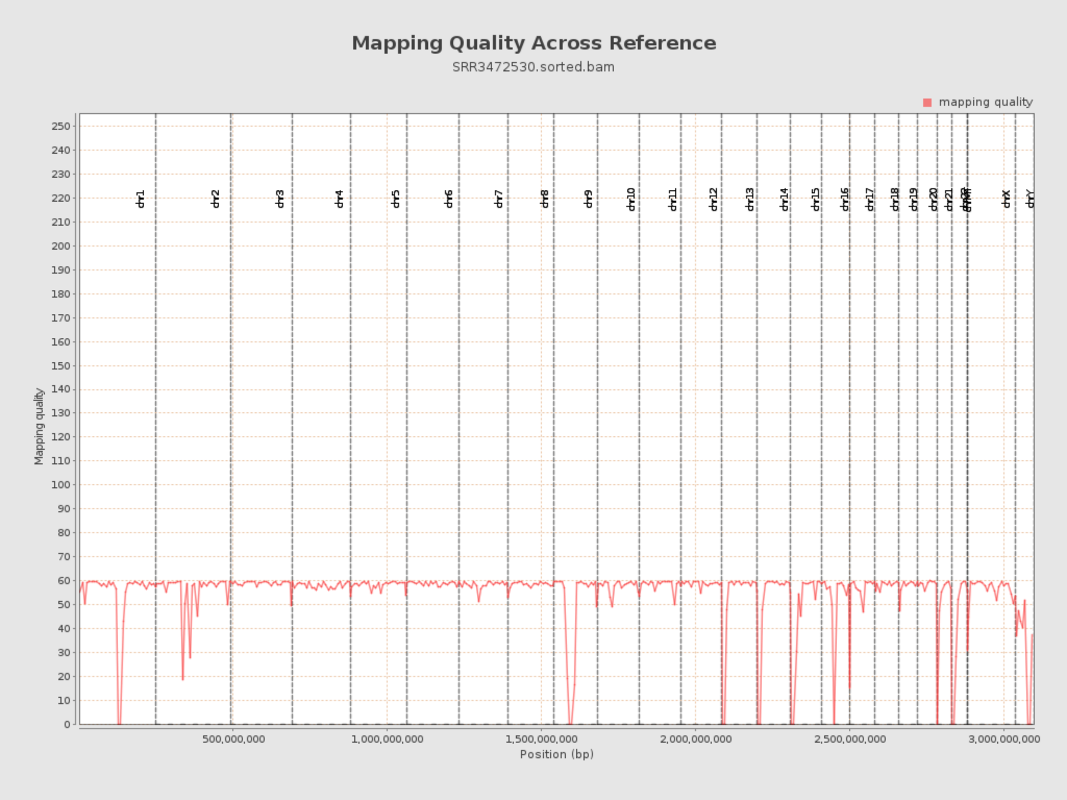
10. Results : Mapped Reads Clipping Profile



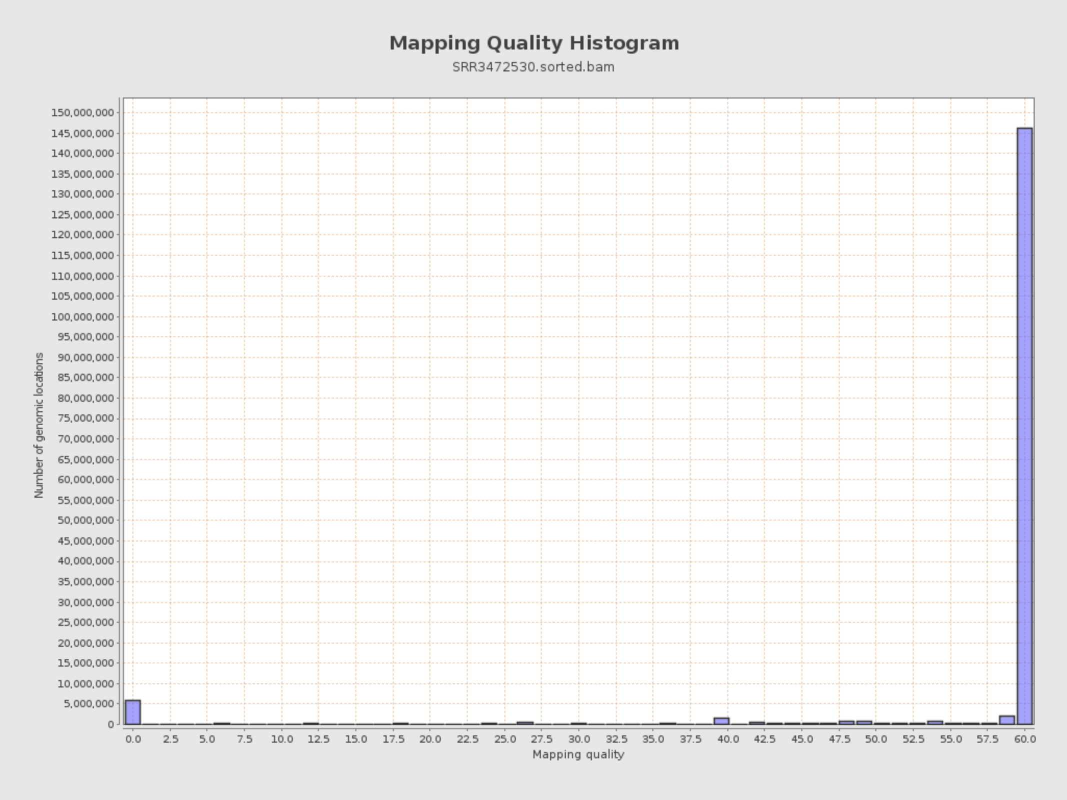
11. Results : Homopolymer Indels



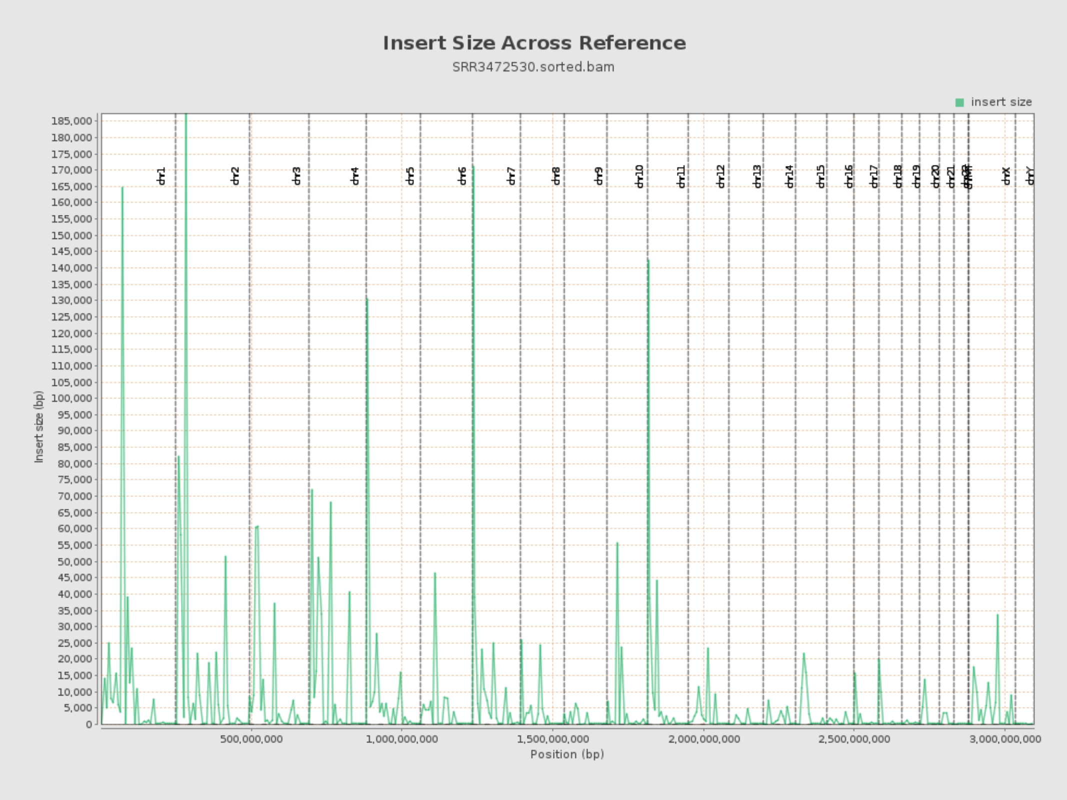
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram