Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 12:06:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472425.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_SRR3472425 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472425_1.fastq.gz SRR3472425_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 12:06:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472425.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,795,582
Mapped reads	14,654,636 / 99.05%
Unmapped reads	140,946 / 0.95%
Mapped paired reads	14,654,636 / 99.05%
Mapped reads, first in pair	7,346,022 / 49.65%
Mapped reads, second in pair	7,308,614 / 49.4%
Mapped reads, both in pair	14,580,540 / 98.55%
Mapped reads, singletons	74,096 / 0.5%
Secondary alignments	0
Supplementary alignments	56,629 / 0.38%
Read min/max/mean length	30 / 100 / 99.26
Duplicated reads (estimated)	8,934,307 / 60.38%
Duplication rate	45.95%
Clipped reads	1,034,732 / 6.99%

2.2. ACGT Content

Number/percentage of A's	387,881,094 / 27.01%
Number/percentage of C's	331,251,312 / 23.07%
Number/percentage of T's	388,381,778 / 27.05%
Number/percentage of G's	328,131,352 / 22.85%
Number/percentage of N's	176,048 / 0.01%

GC Percentage	45.92%

2.3. Coverage

Mean	0.4639
Standard Deviation	15.8831

2.4. Mapping Quality

Mean Mapping Quality	54.78

2.5. Insert size

Mean	16,727.26
Standard Deviation	1,280,256.63
P25/Median/P75	150 / 206 / 276

2.6. Mismatches and indels

General error rate	0.54%
Mismatches	7,593,072
Insertions	87,993
Mapped reads with at least one insertion	0.59%
Deletions	69,368
Mapped reads with at least one deletion	0.47%
Homopolymer indels	46.62%

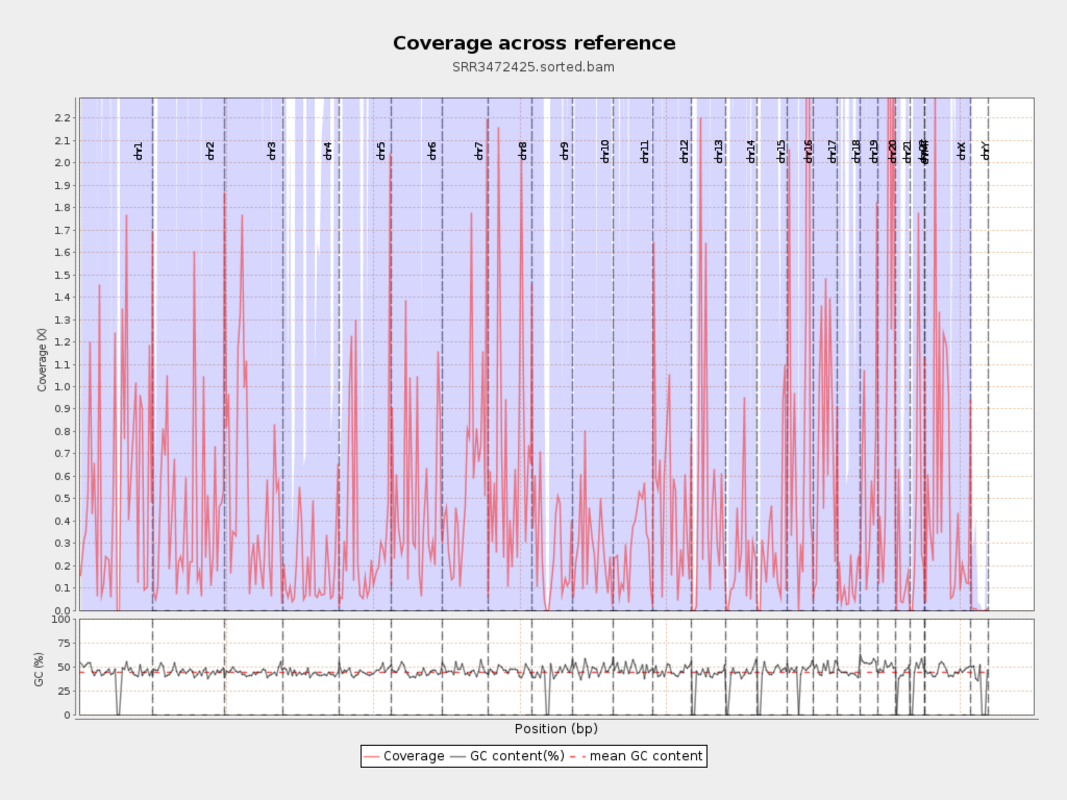
2.7. Chromosome stats

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

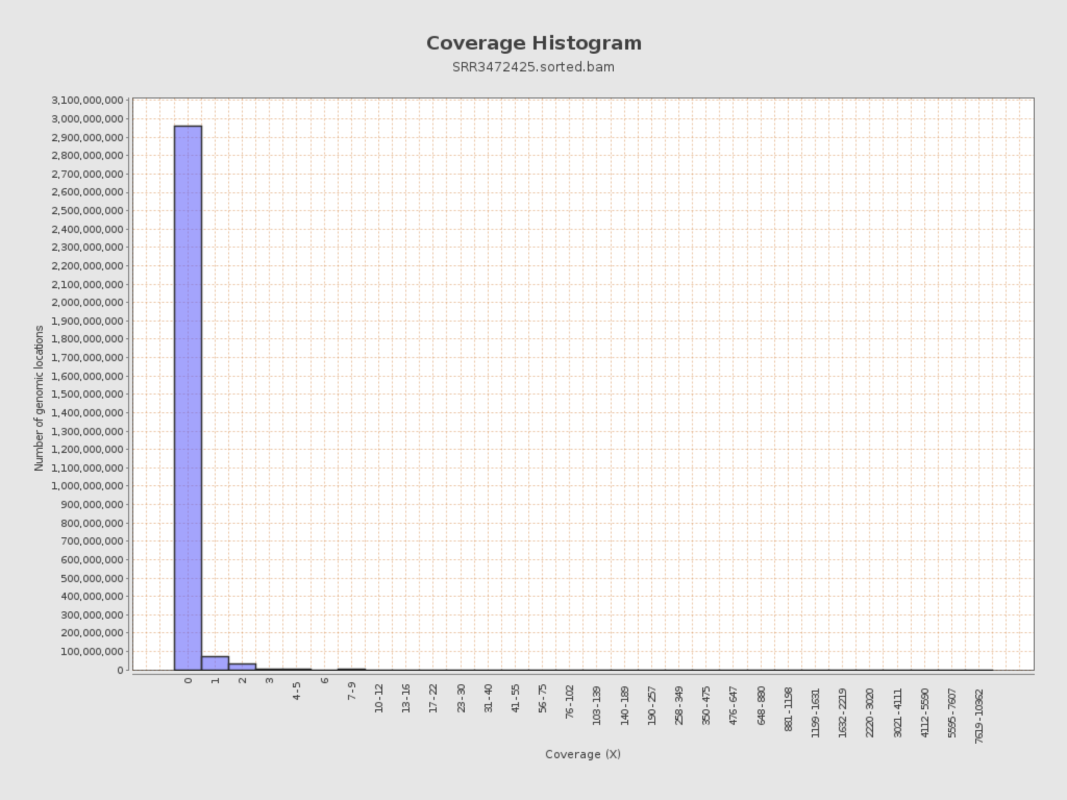
		bases	coverage	deviation
chr1	249250621	143290576	0.5749	17.8248
chr2	243199373	99663935	0.4098	13.6389
chr3	198022430	111747571	0.5643	13.0057
chr4	191154276	34234540	0.1791	5.9499
chr5	180915260	69555950	0.3845	15.7871
chr6	171115067	85422844	0.4992	18.222
chr7	159138663	102411229	0.6435	16.4781
chr8	146364022	100183029	0.6845	20.0429
chr9	141213431	37387582	0.2648	7.361
chr10	135534747	37723339	0.2783	10.8821
chr11	135006516	38623662	0.2861	8.2836
chr12	133851895	69746667	0.5211	13.3806
chr13	115169878	59590952	0.5174	15.0585
chr14	107349540	24344168	0.2268	6.6183
chr15	102531392	32454512	0.3165	10.7158
chr16	90354753	95948472	1.0619	35.8198
chr17	81195210	62204735	0.7661	18.1575
chr18	78077248	9202839	0.1179	4.3151
chr19	59128983	34305764	0.5802	13.7935
chr20	63025520	74712198	1.1854	34.3663
chr21	48129895	7710512	0.1602	10.5002
chr22	51304566	22748153	0.4434	23.1214
chrMT	16571	18760	1.1321	1.4234
chrX	155270560	82499567	0.5313	17.9615

chrY	59373566	257940	0.0043	0.266

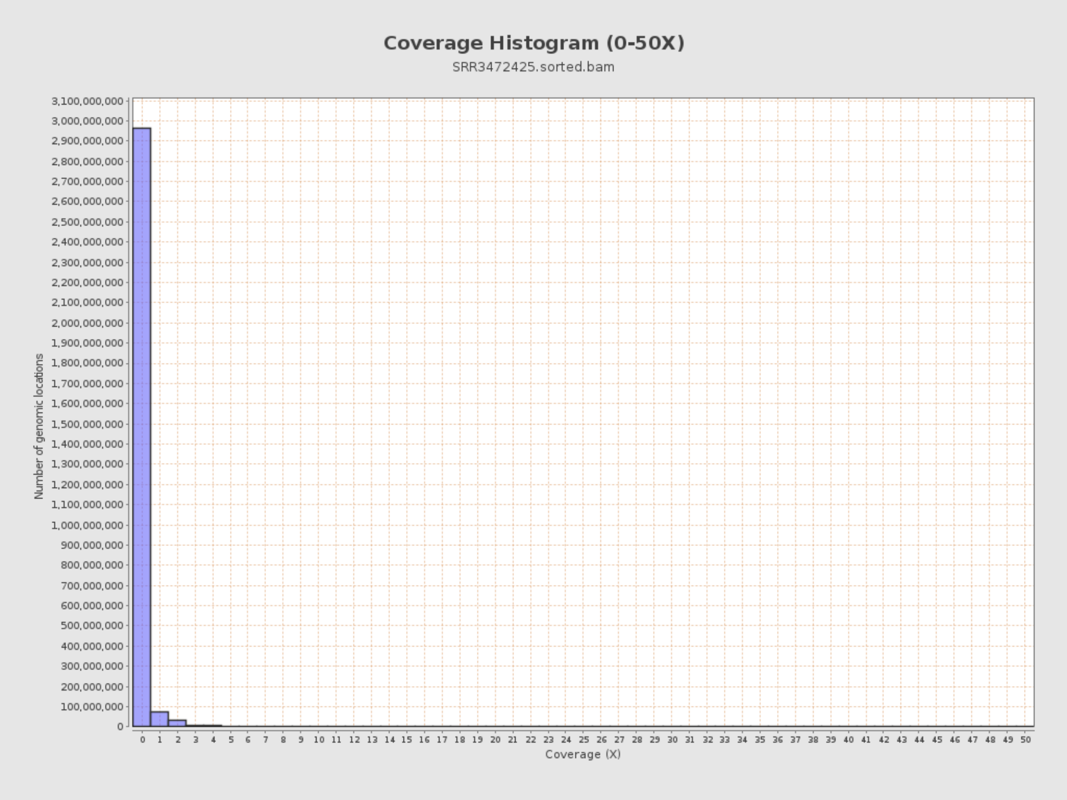
3. Results : Coverage across reference



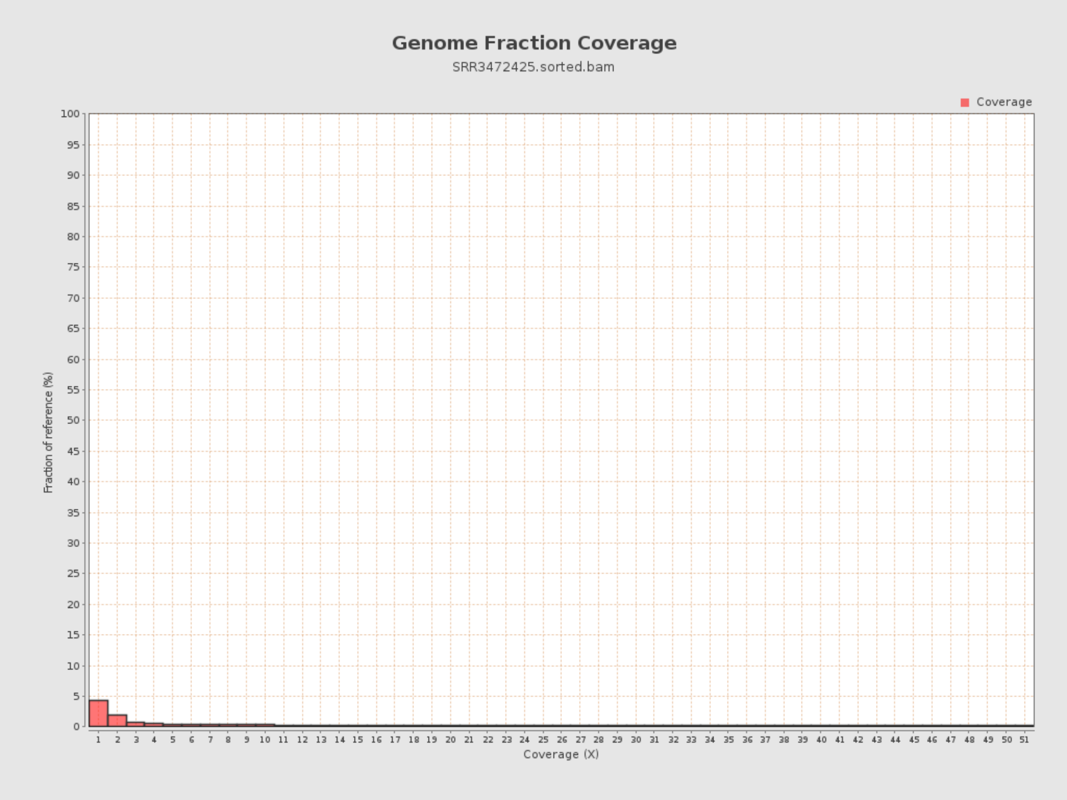
4. Results : Coverage Histogram



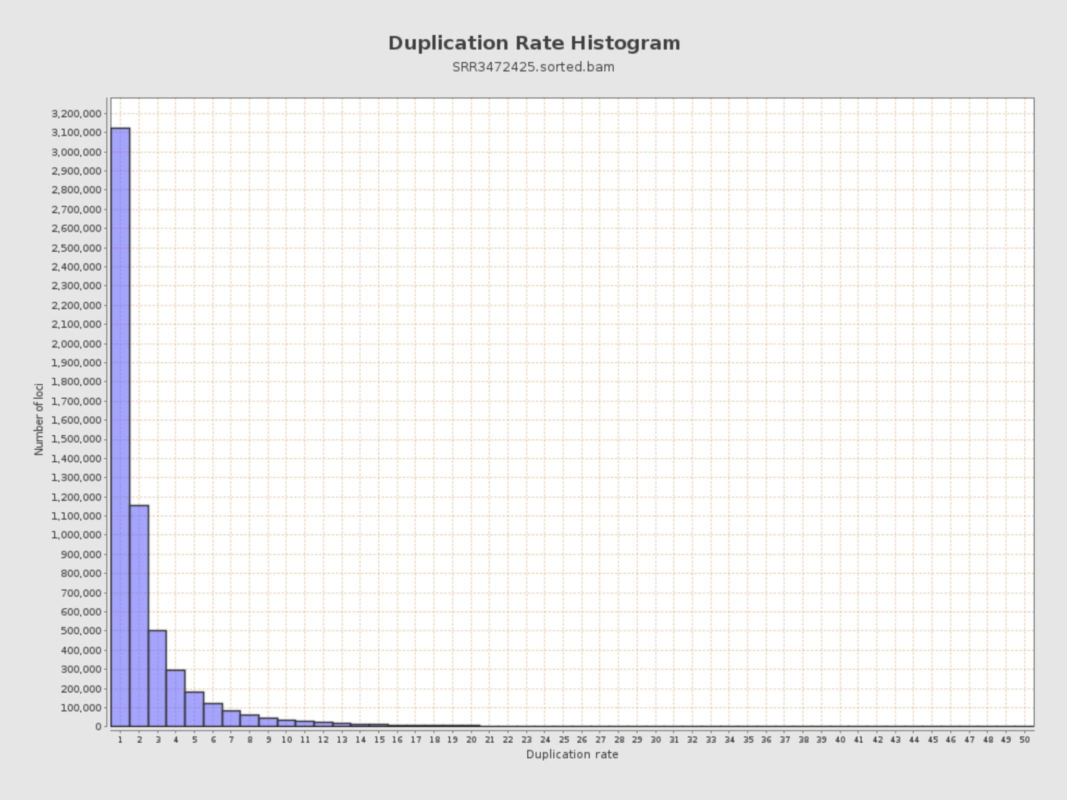
5. Results : Coverage Histogram (0-50X)



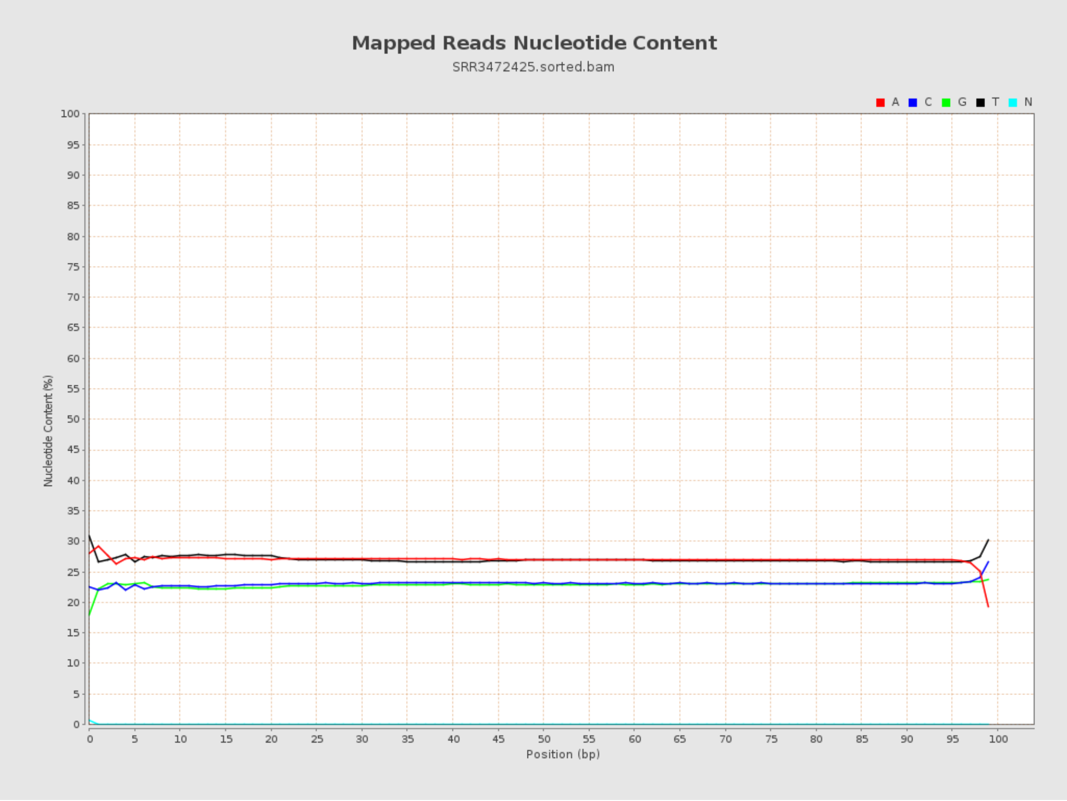
6. Results : Genome Fraction Coverage



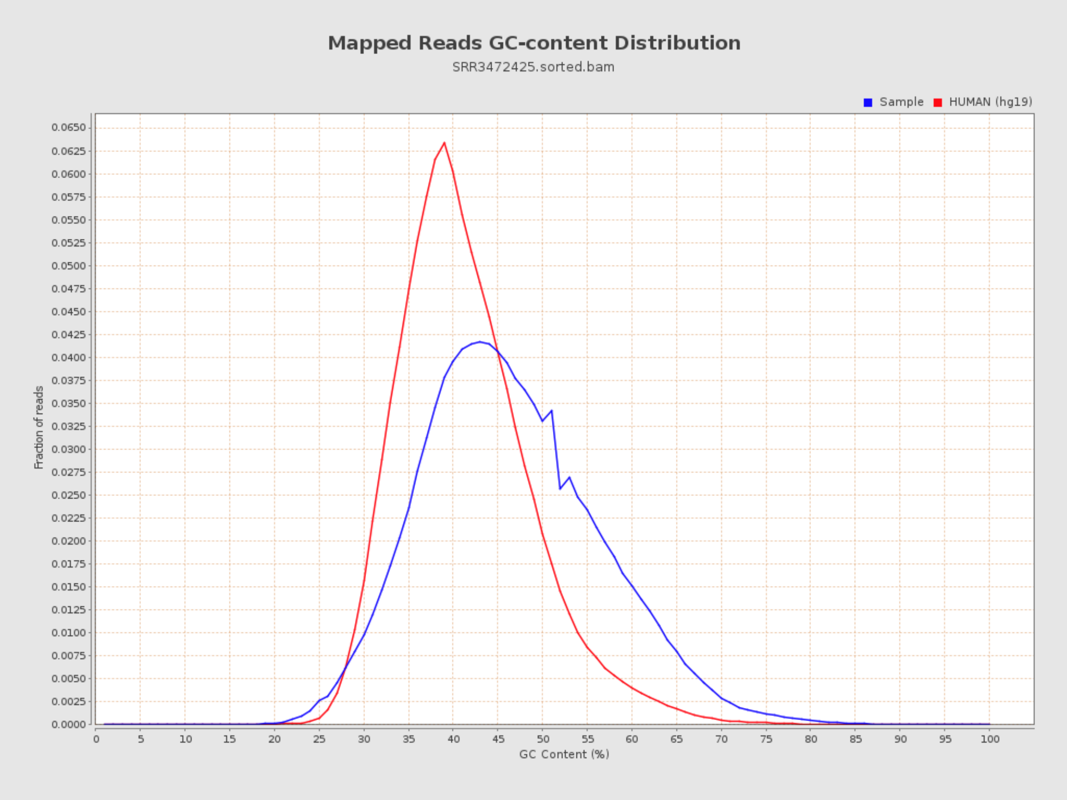
7. Results : Duplication Rate Histogram



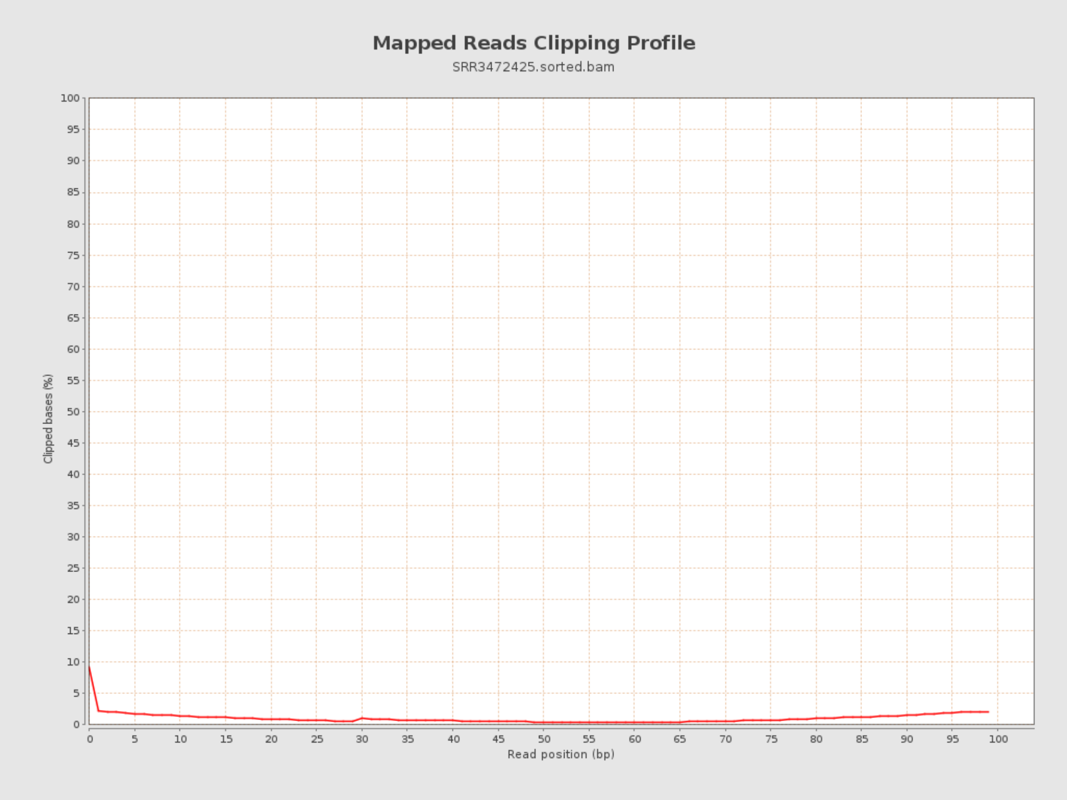
8. Results : Mapped Reads Nucleotide Content



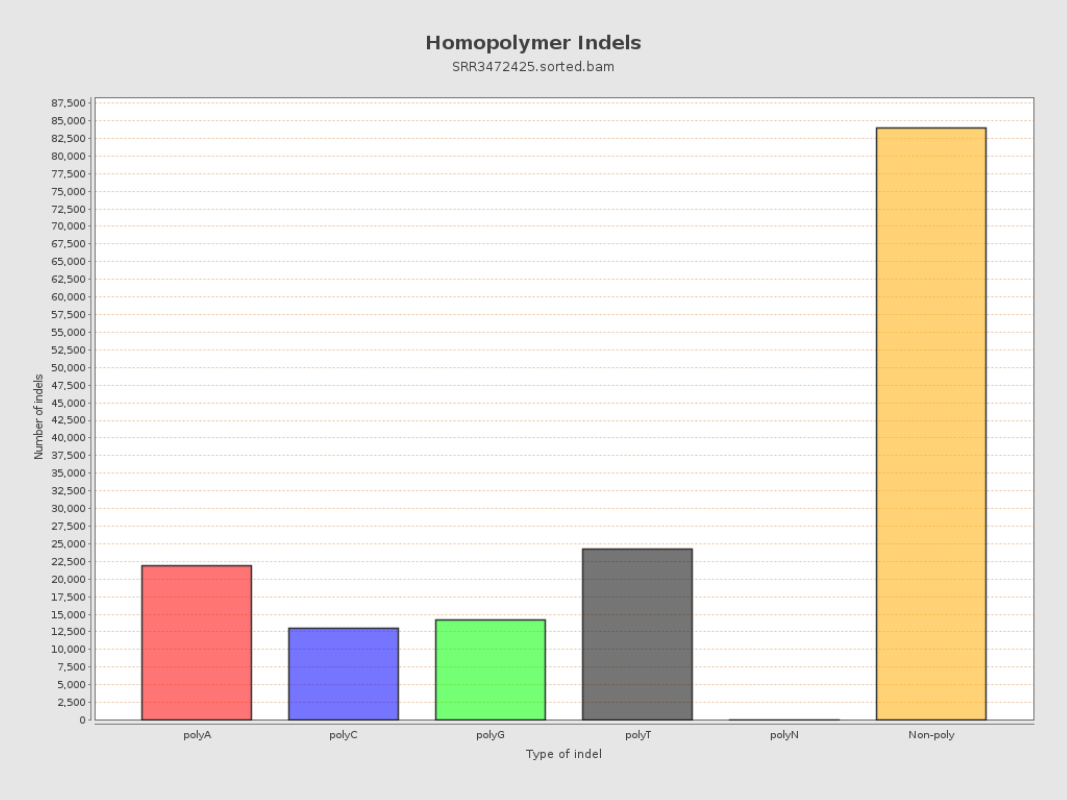
9. Results : Mapped Reads GC-content Distribution



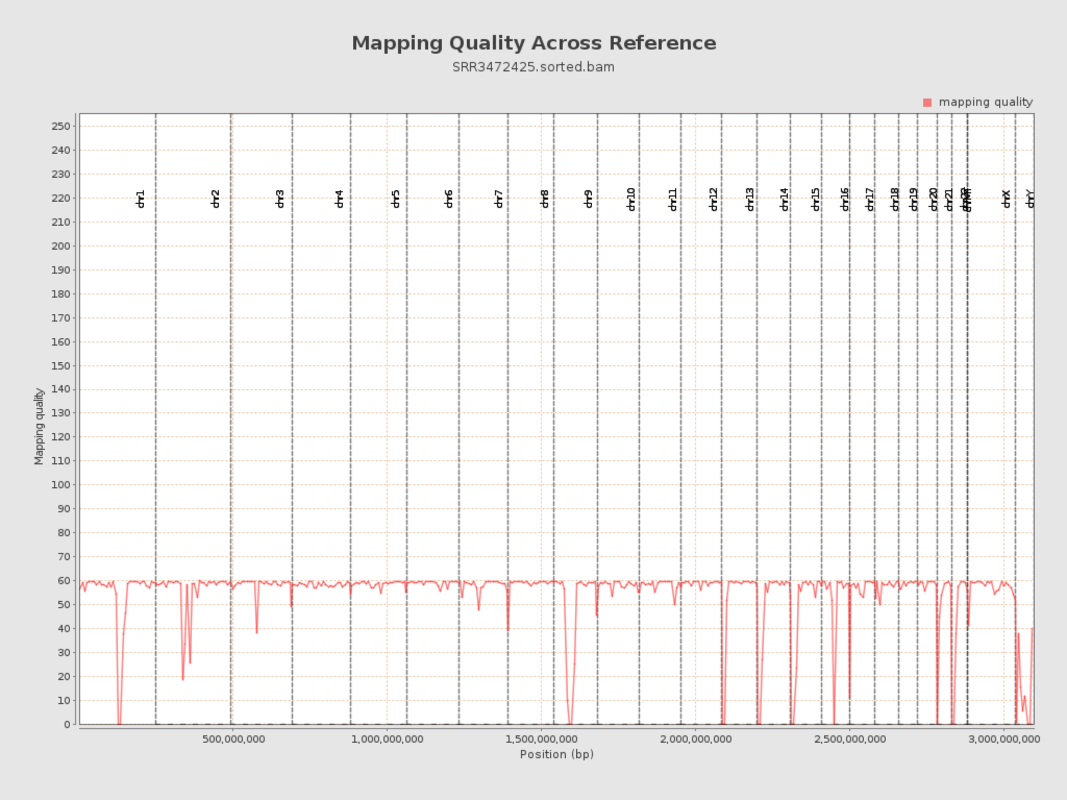
10. Results : Mapped Reads Clipping Profile



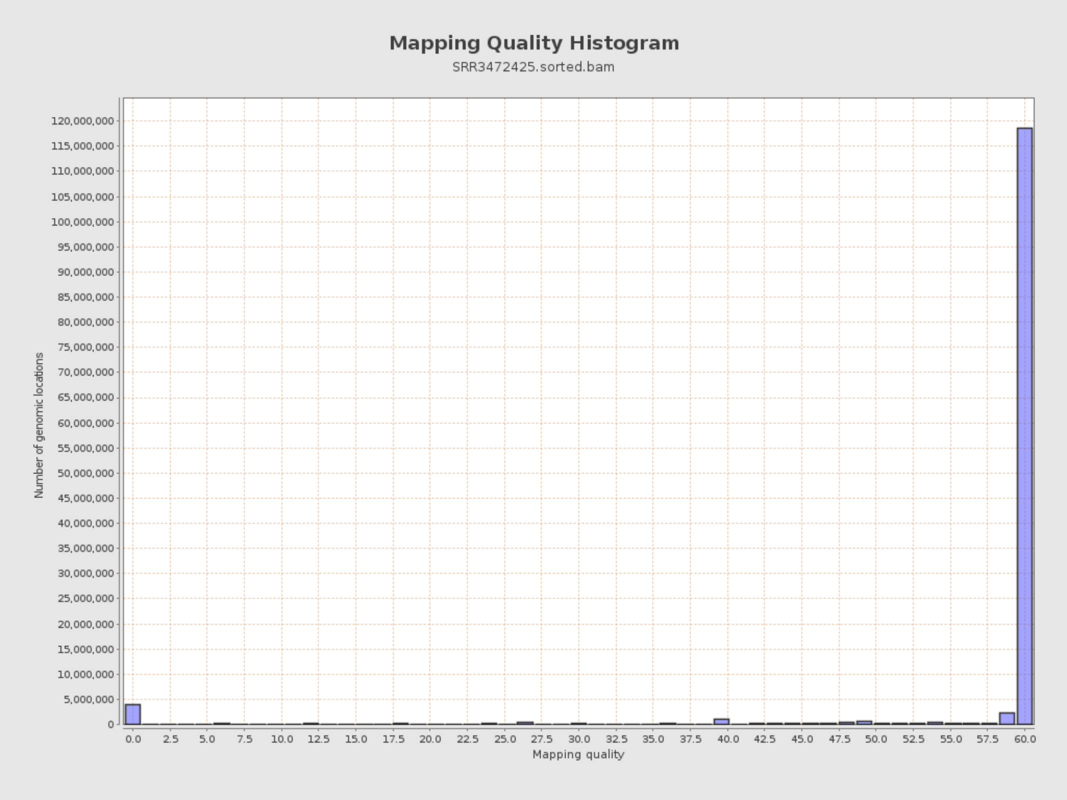
11. Results : Homopolymer Indels



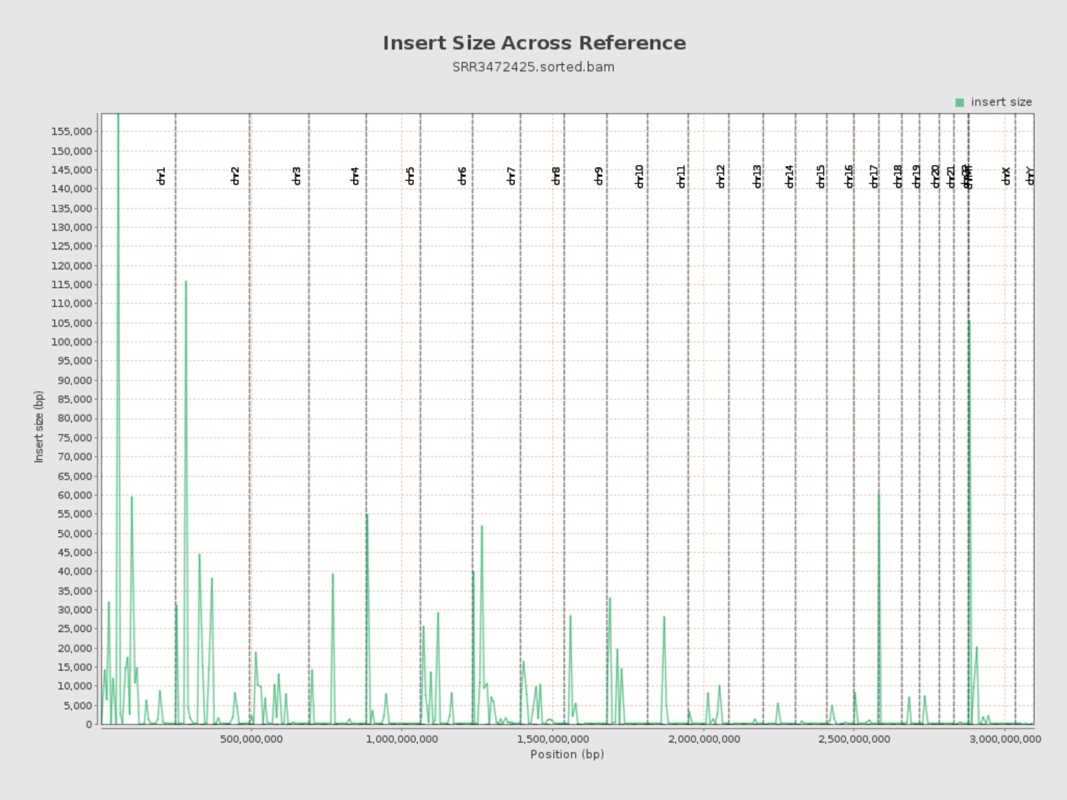
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram