Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 21:24:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472525.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_SRR3472525 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472525_1.fastq.gz SRR3472525_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 21:24:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472525.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	17,095,520
Mapped reads	16,745,260 / 97.95%
Unmapped reads	350,260 / 2.05%
Mapped paired reads	16,745,260 / 97.95%
Mapped reads, first in pair	8,484,651 / 49.63%
Mapped reads, second in pair	8,260,609 / 48.32%
Mapped reads, both in pair	16,476,408 / 96.38%
Mapped reads, singletons	268,852 / 1.57%
Secondary alignments	0
Supplementary alignments	168,503 / 0.99%
Read min/max/mean length	30 / 100 / 100.38
Duplicated reads (estimated)	10,618,342 / 62.11%
Duplication rate	43.59%
Clipped reads	2,214,041 / 12.95%

2.2. ACGT Content

Number/percentage of A's	449,384,685 / 27.75%
Number/percentage of C's	347,035,816 / 21.43%
Number/percentage of T's	478,124,714 / 29.52%
Number/percentage of G's	344,640,094 / 21.28%
Number/percentage of N's	238,728 / 0.01%

GC Percentage	42.71%

2.3. Coverage

Mean	0.5232
Standard Deviation	21.2972

2.4. Mapping Quality

Mean Mapping Quality	51.83

2.5. Insert size

Mean	206,333.64
Standard Deviation	4,510,883.41
P25/Median/P75	170 / 240 / 327

2.6. Mismatches and indels

General error rate	0.7%
Mismatches	11,012,520
Insertions	129,176
Mapped reads with at least one insertion	0.76%
Deletions	96,900
Mapped reads with at least one deletion	0.57%
Homopolymer indels	43.36%

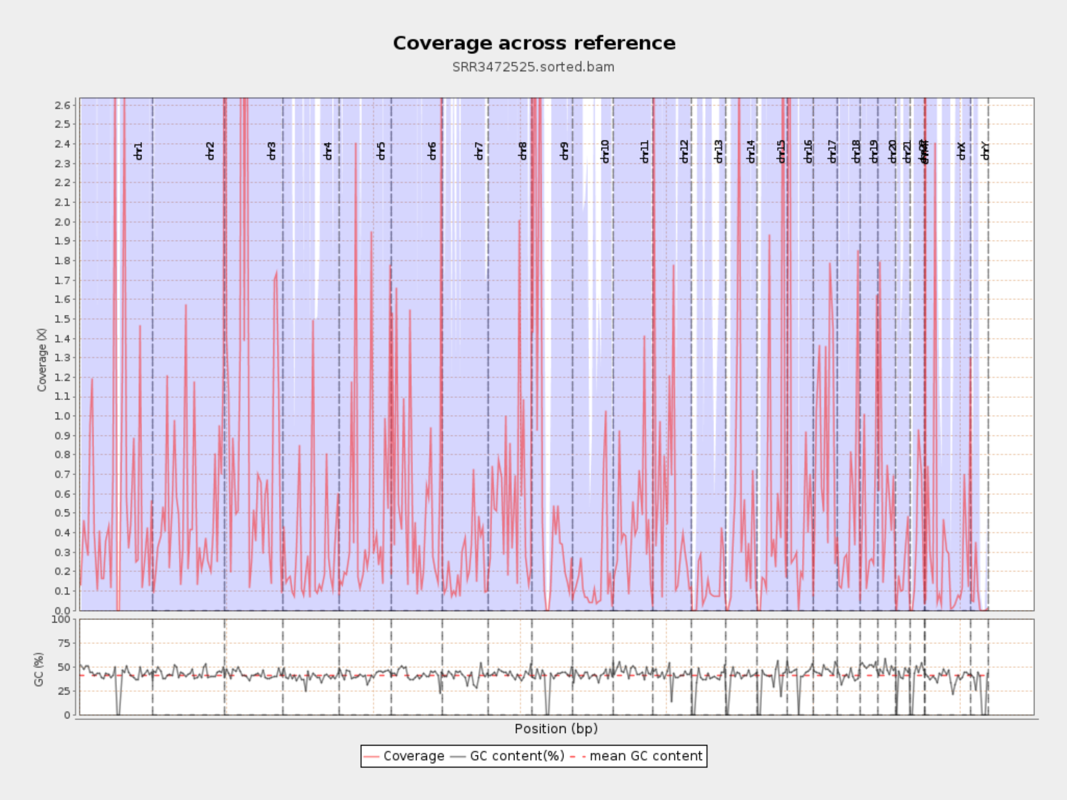
2.7. Chromosome stats

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

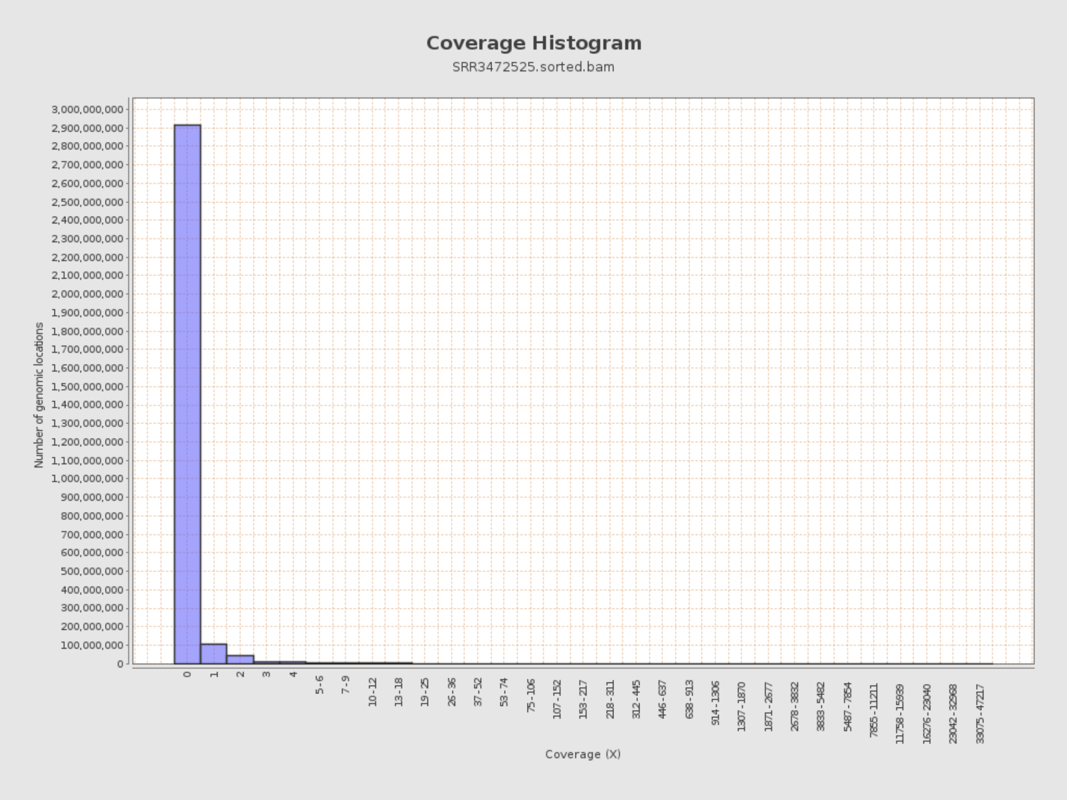
		bases	**coverage**	**deviation**
chr1	249250621	144804696	0.581	19.543
chr2	243199373	122906581	0.5054	15.972
chr3	198022430	224598161	1.1342	23.5212
chr4	191154276	55949068	0.2927	12.1543
chr5	180915260	99823054	0.5518	22.5672
chr6	171115067	103293480	0.6036	29.9182
chr7	159138663	37449089	0.2353	17.545
chr8	146364022	87333809	0.5967	19.0433
chr9	141213431	100924878	0.7147	18.5392
chr10	135534747	25515342	0.1883	11.3179
chr11	135006516	60371532	0.4472	18.9432
chr12	133851895	85713074	0.6404	40.1938
chr13	115169878	15239425	0.1323	6.5895
chr14	107349540	58853938	0.5482	21.177
chr15	102531392	63236207	0.6167	30.4075
chr16	90354753	66108698	0.7317	27.2787
chr17	81195210	71225871	0.8772	23.7566
chr18	78077248	39213965	0.5022	17.8575
chr19	59128983	28253626	0.4778	13.1255
chr20	63025520	40372275	0.6406	30.5305
chr21	48129895	9386827	0.195	7.683
chr22	51304566	17448055	0.3401	13.165
chrMT	16571	4956622	299.1142	904.3264
chrX	155270560	52446911	0.3378	16.143

chrY	59373566	4242420	0.0715	12.2393

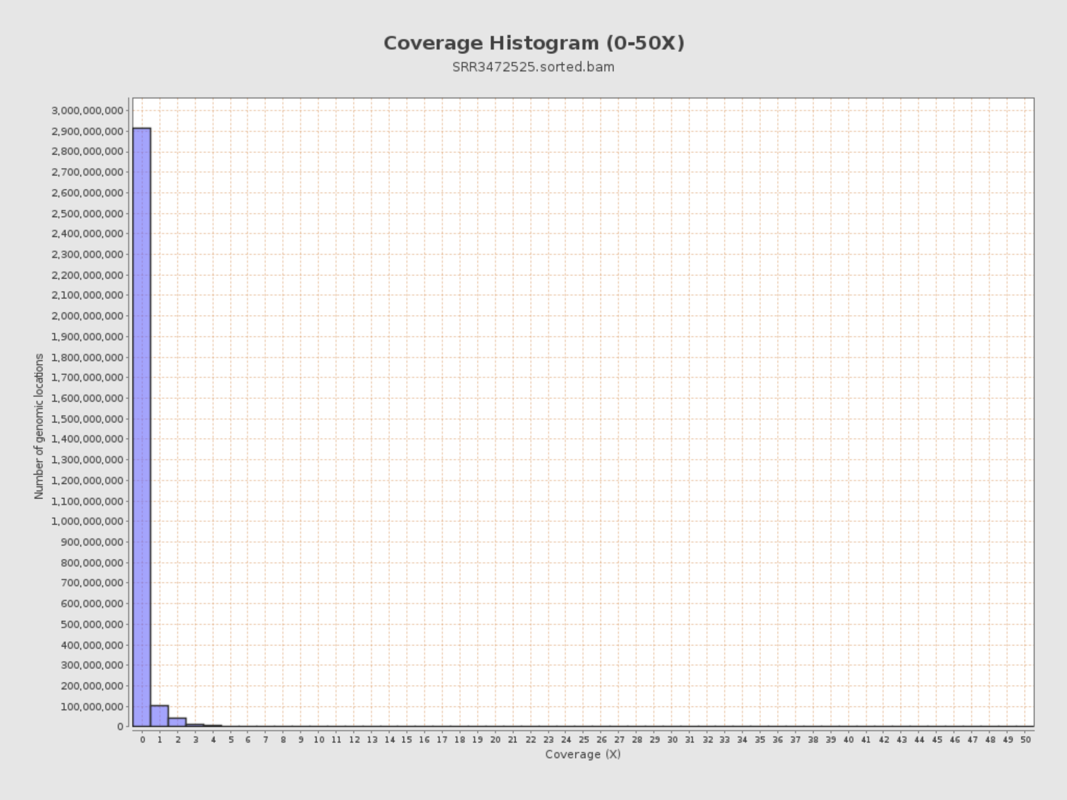
3. Results : Coverage across reference



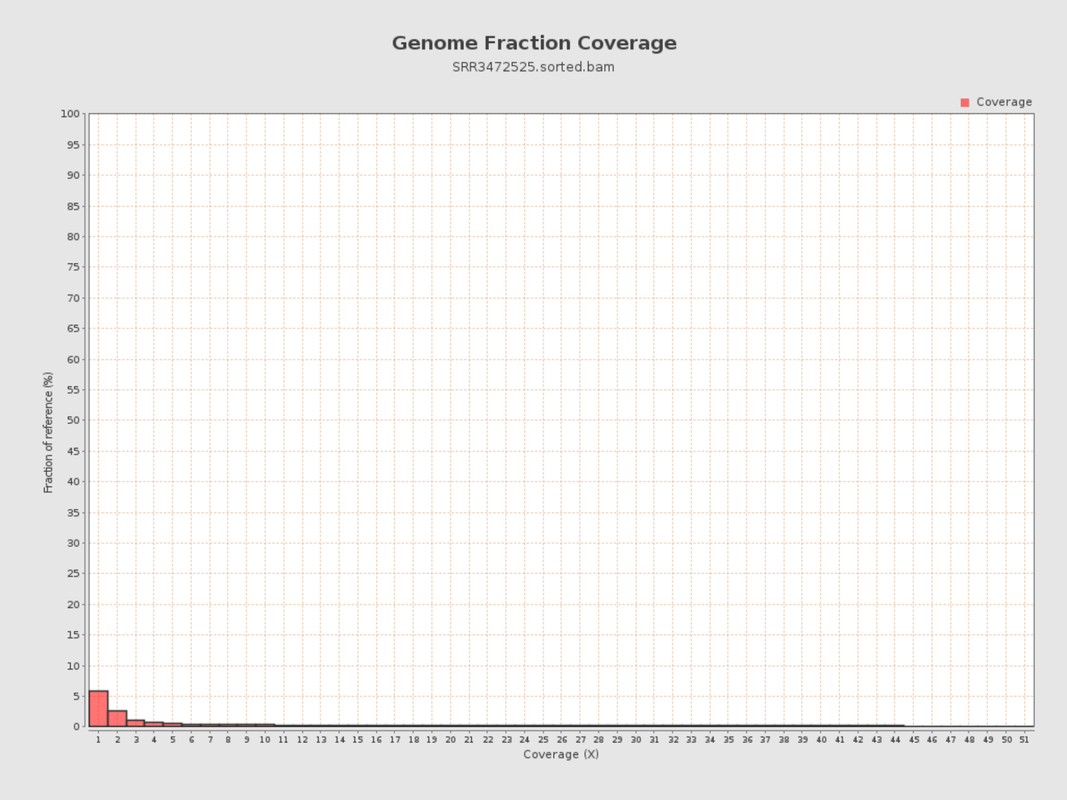
4. Results : Coverage Histogram



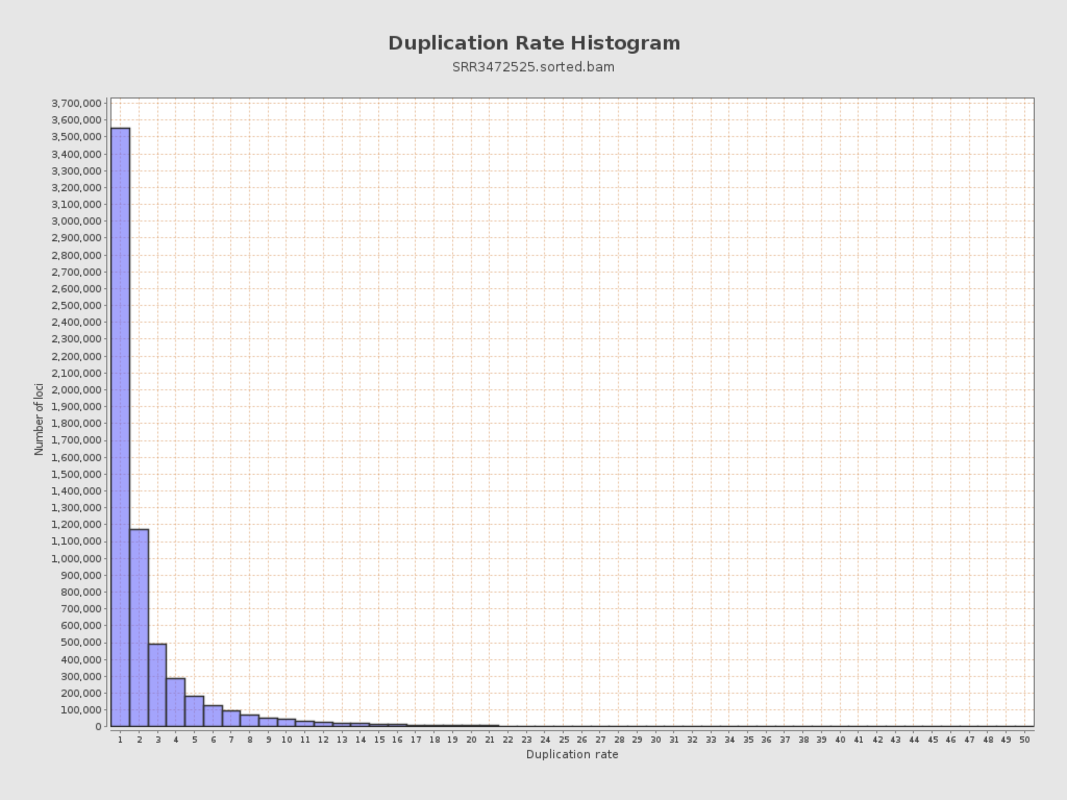
5. Results : Coverage Histogram (0-50X)



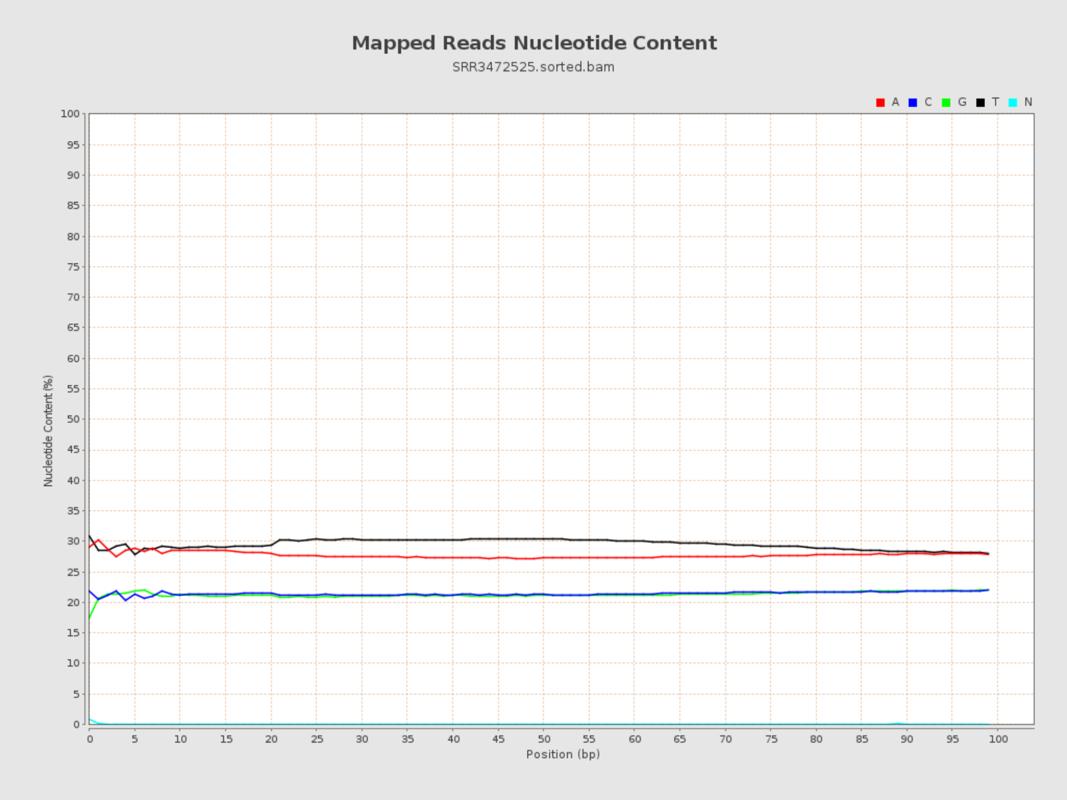
6. Results : Genome Fraction Coverage



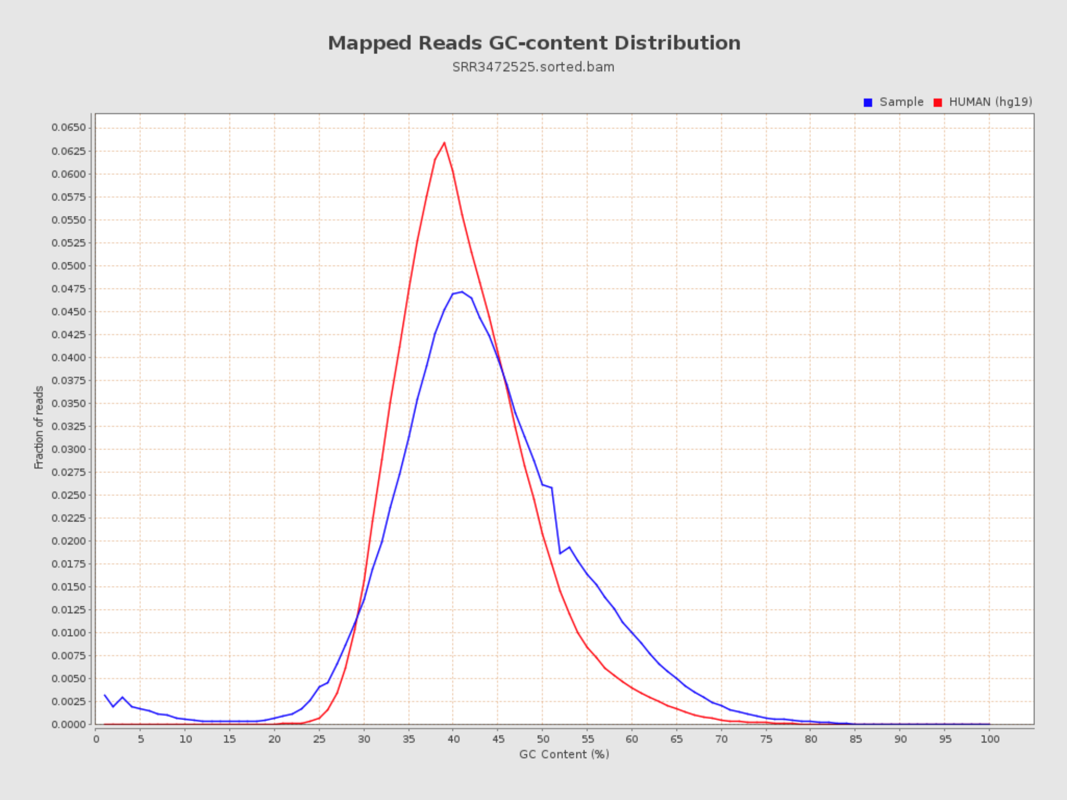
7. Results : Duplication Rate Histogram



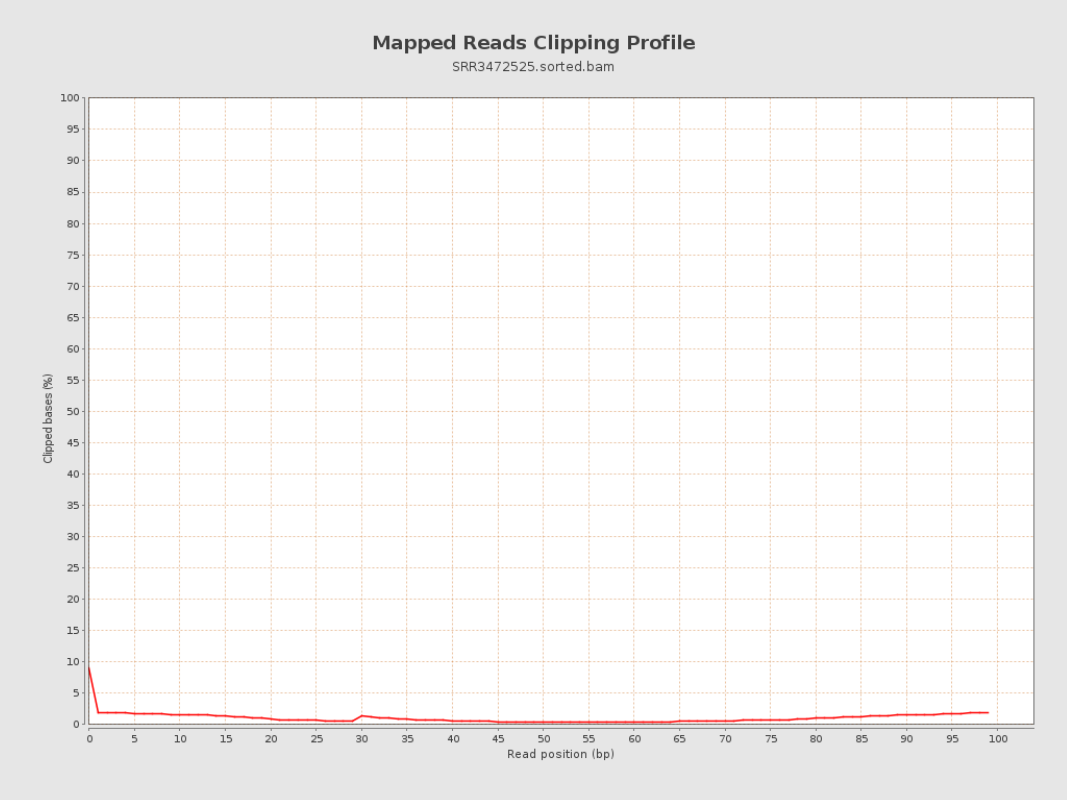
8. Results : Mapped Reads Nucleotide Content



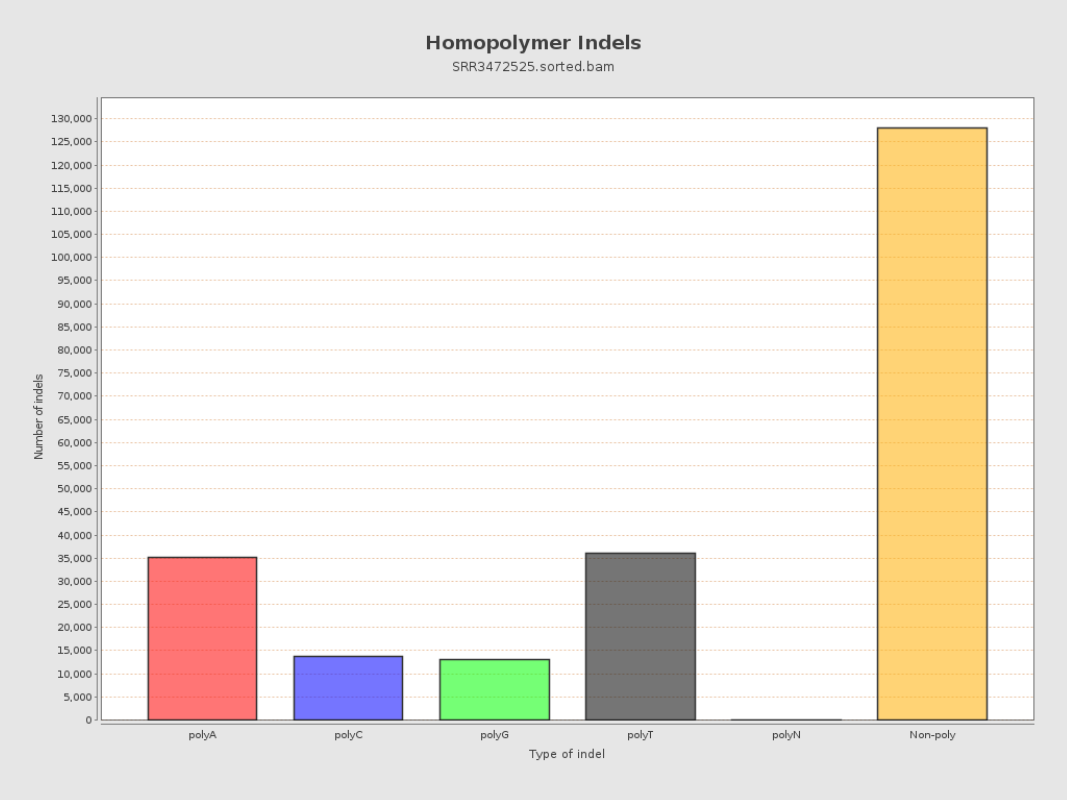
9. Results : Mapped Reads GC-content Distribution



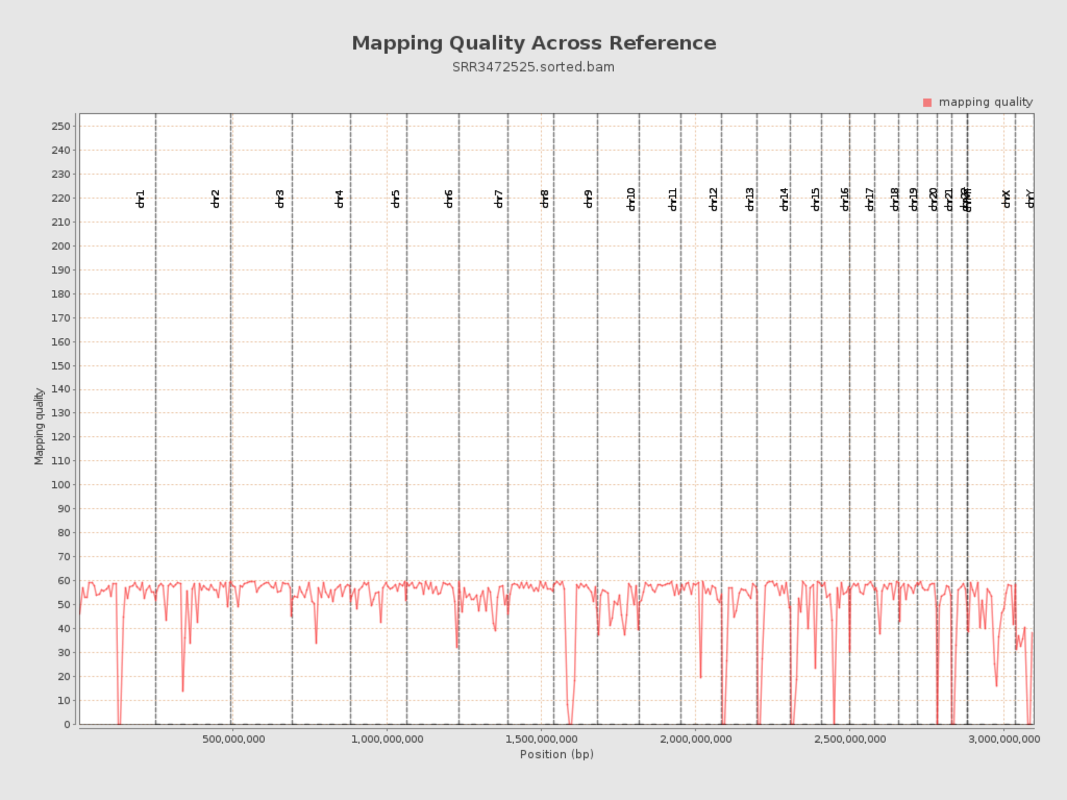
10. Results : Mapped Reads Clipping Profile



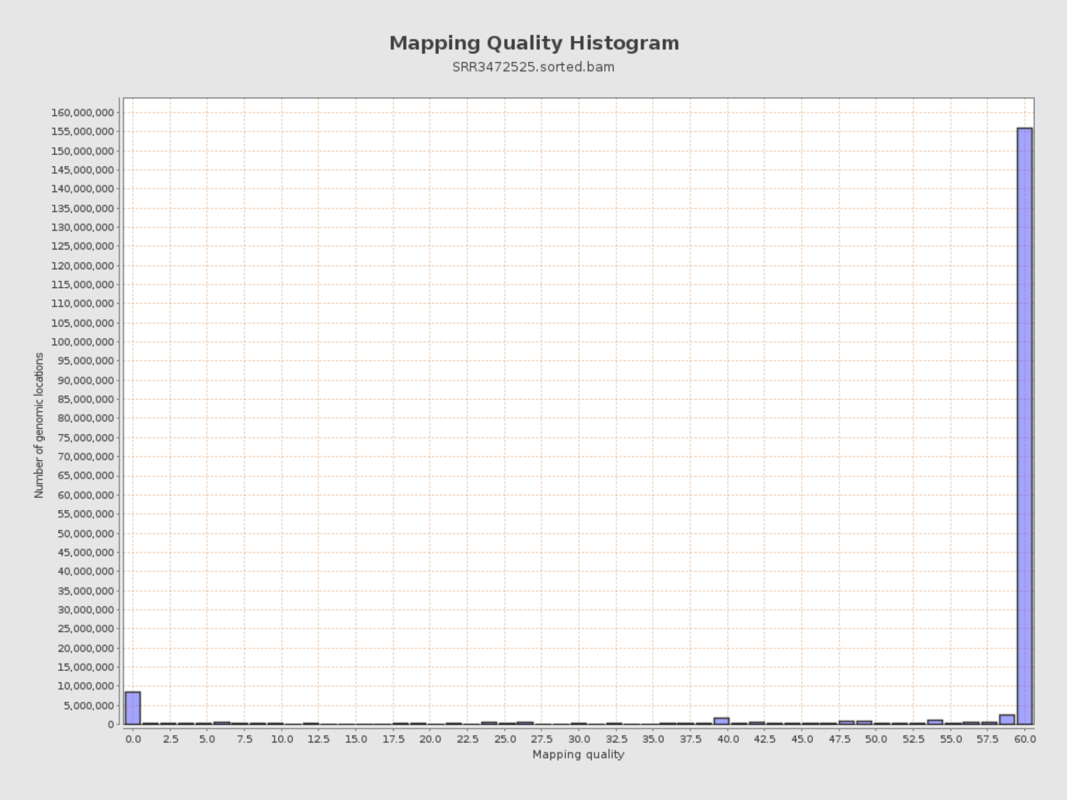
11. Results : Homopolymer Indels



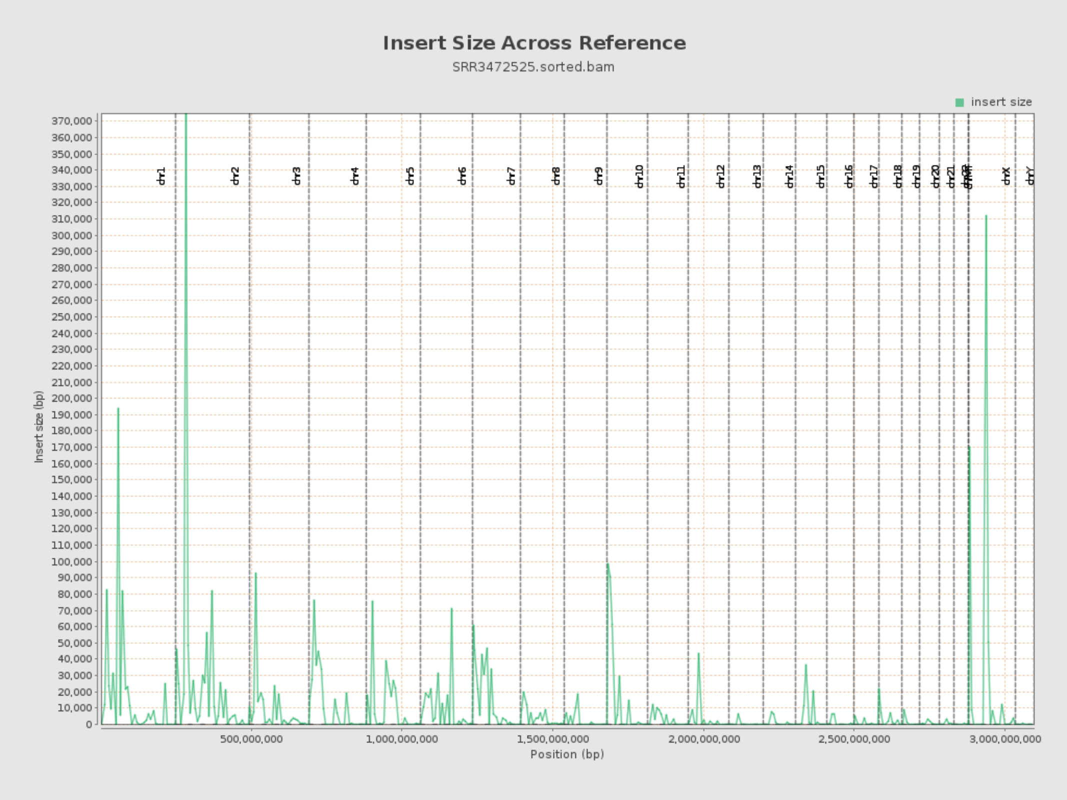
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram