Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 18:07:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472513.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_SRR3472513 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472513_1.fastq.gz SRR3472513_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 18:07:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472513.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,363,566
Mapped reads	13,244,904 / 99.11%
Unmapped reads	118,662 / 0.89%
Mapped paired reads	13,244,904 / 99.11%
Mapped reads, first in pair	6,640,749 / 49.69%
Mapped reads, second in pair	6,604,155 / 49.42%
Mapped reads, both in pair	13,178,256 / 98.61%
Mapped reads, singletons	66,648 / 0.5%
Secondary alignments	0
Supplementary alignments	55,184 / 0.41%
Read min/max/mean length	30 / 100 / 100.17
Duplicated reads (estimated)	7,909,134 / 59.18%
Duplication rate	45.69%
Clipped reads	1,160,857 / 8.69%

2.2. ACGT Content

Number/percentage of A's	359,226,775 / 27.57%
Number/percentage of C's	294,361,697 / 22.59%
Number/percentage of T's	357,004,258 / 27.4%
Number/percentage of G's	292,146,836 / 22.42%
Number/percentage of N's	203,860 / 0.02%

GC Percentage	45.01%

2.3. Coverage

Mean	0.4209
Standard Deviation	14.4735

2.4. Mapping Quality

Mean Mapping Quality	55.18

2.5. Insert size

Mean	32,199.31
Standard Deviation	1,788,827.14
P25/Median/P75	164 / 229 / 309

2.6. Mismatches and indels

General error rate	0.6%
Mismatches	7,728,255
Insertions	69,142
Mapped reads with at least one insertion	0.52%
Deletions	67,358
Mapped reads with at least one deletion	0.5%
Homopolymer indels	44.56%

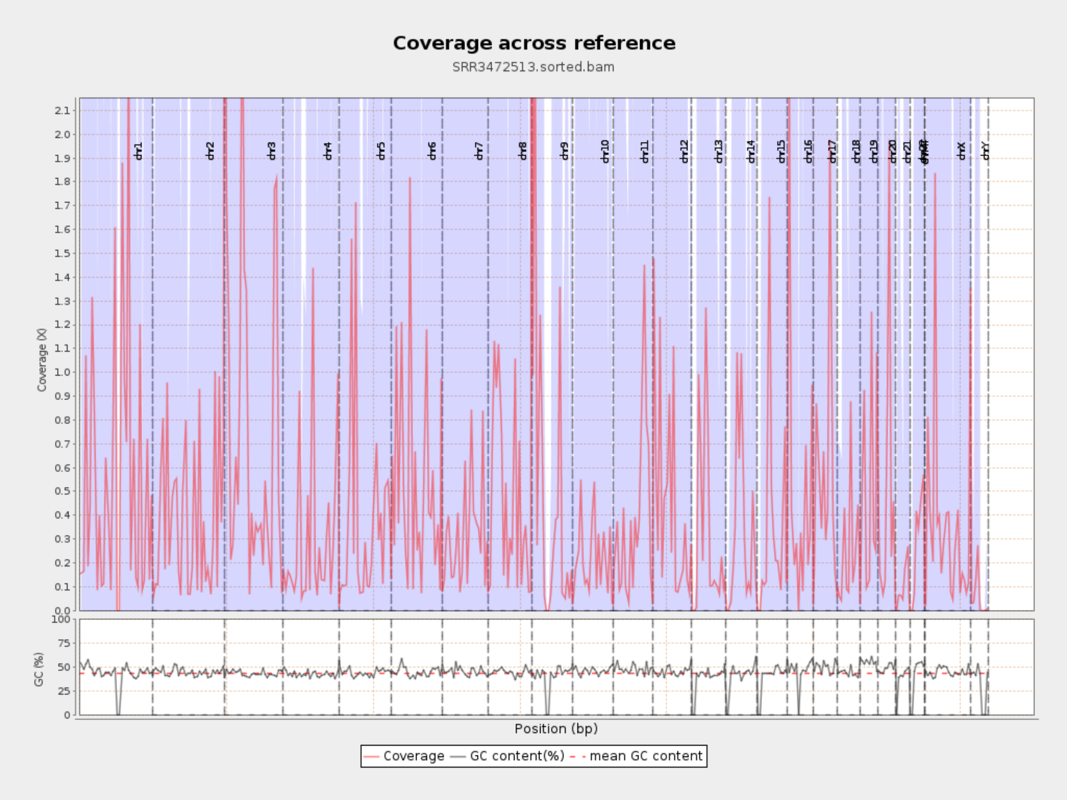
2.7. Chromosome stats

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

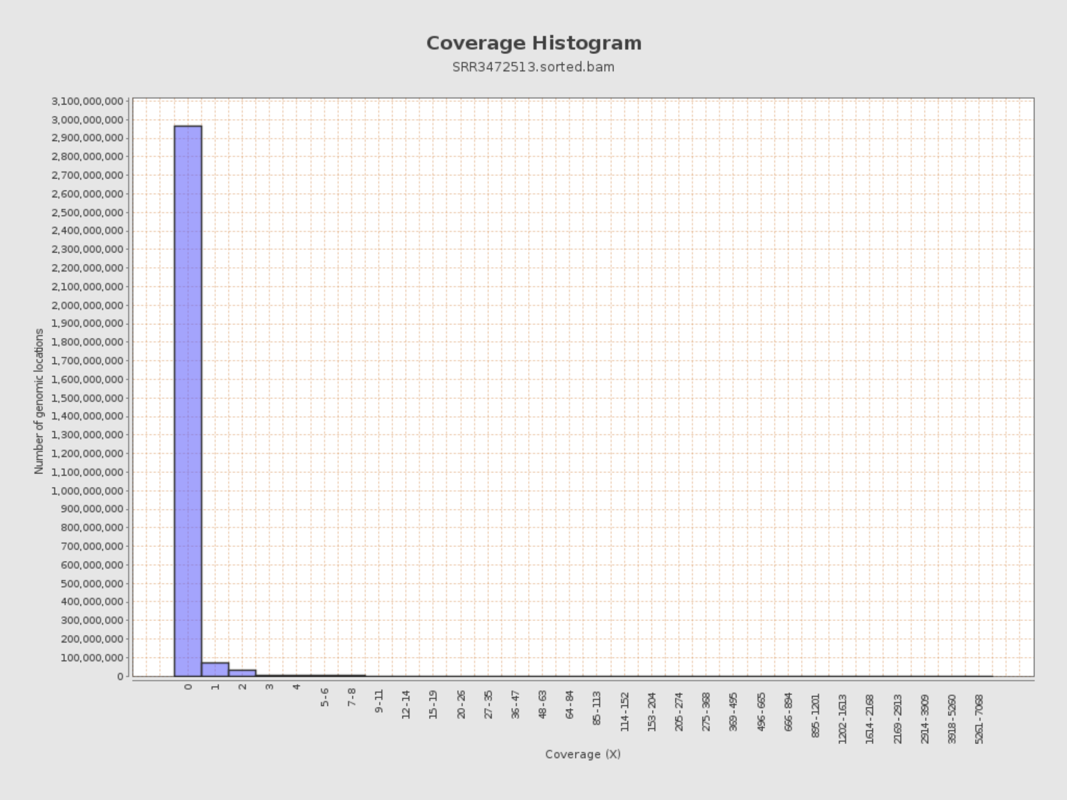
		bases	**coverage**	**deviation**
chr1	249250621	141449152	0.5675	23.2366
chr2	243199373	94242264	0.3875	13.0217
chr3	198022430	154294149	0.7792	17.6566
chr4	191154276	56057708	0.2933	11.8793
chr5	180915260	69019784	0.3815	14.1575
chr6	171115067	89909246	0.5254	13.0955
chr7	159138663	51418721	0.3231	10.6616
chr8	146364022	68291383	0.4666	15.3192
chr9	141213431	74172249	0.5252	13.6473
chr10	135534747	30919128	0.2281	7.4595
chr11	135006516	53559188	0.3967	16.3166
chr12	133851895	61849077	0.4621	13.2678
chr13	115169878	37222468	0.3232	16.7251
chr14	107349540	35032312	0.3263	10.4125
chr15	102531392	36012823	0.3512	13.2205
chr16	90354753	45318241	0.5016	15.4516
chr17	81195210	45441110	0.5597	15.7736
chr18	78077248	19821668	0.2539	10.8333
chr19	59128983	29320443	0.4959	16.8823
chr20	63025520	31522558	0.5002	18.8629
chr21	48129895	5083619	0.1056	4.0786
chr22	51304566	14706609	0.2867	8.9637
chrMT	16571	1764	0.1065	0.4289
chrX	155270560	54883855	0.3535	9.6599

chrY	59373566	3573627	0.0602	4.3046

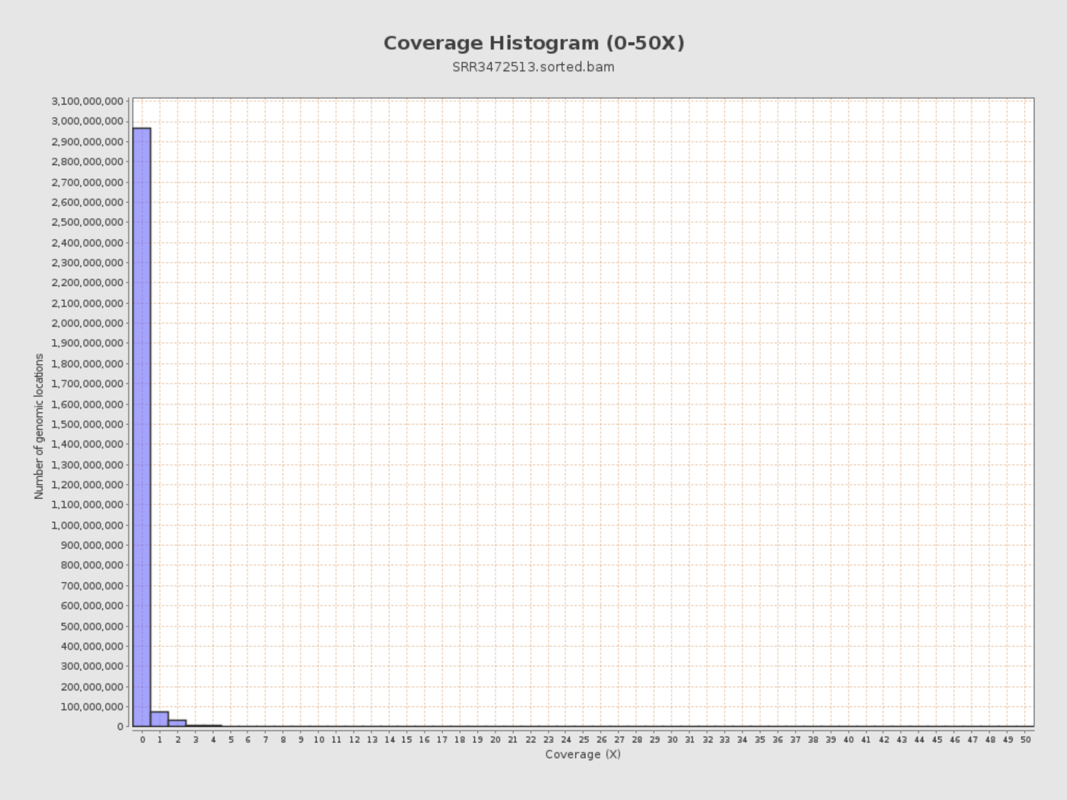
3. Results : Coverage across reference



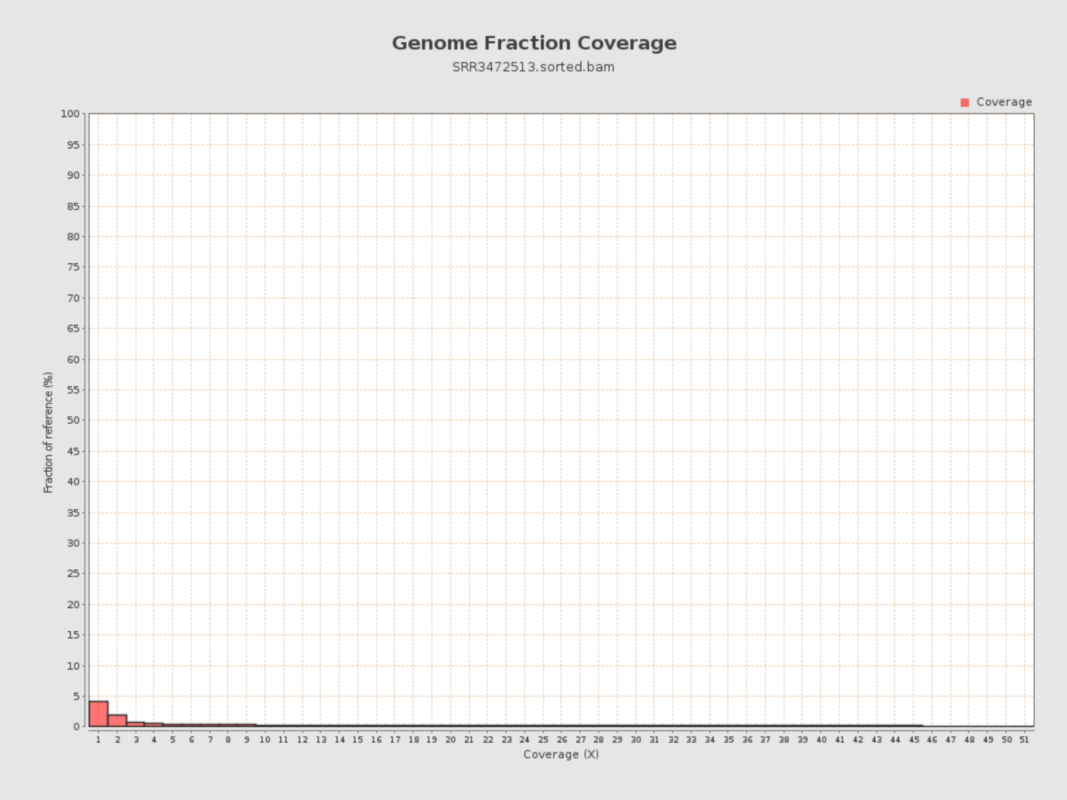
4. Results : Coverage Histogram



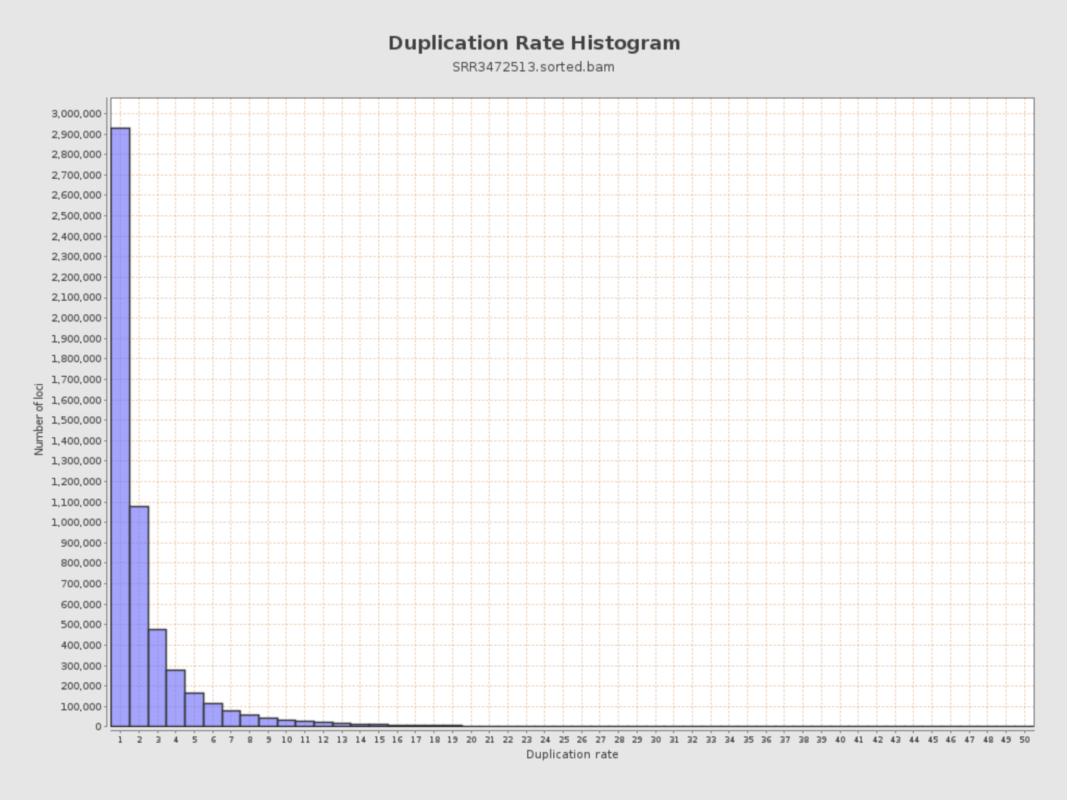
5. Results : Coverage Histogram (0-50X)



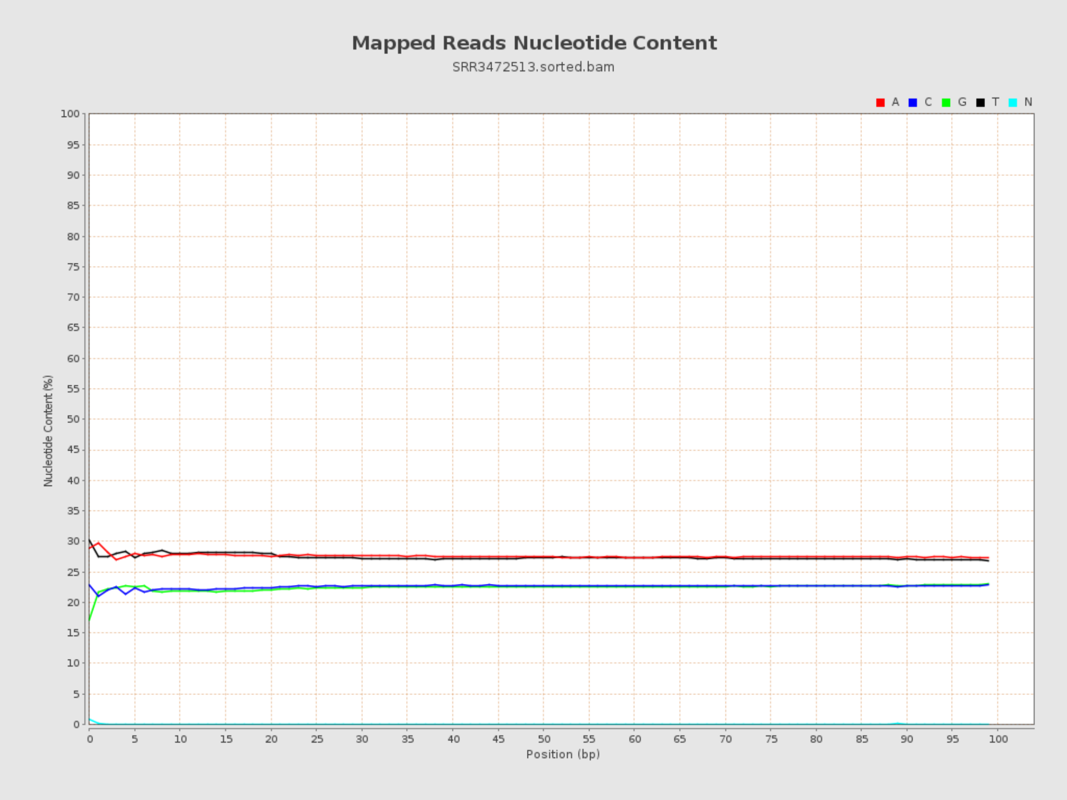
6. Results : Genome Fraction Coverage



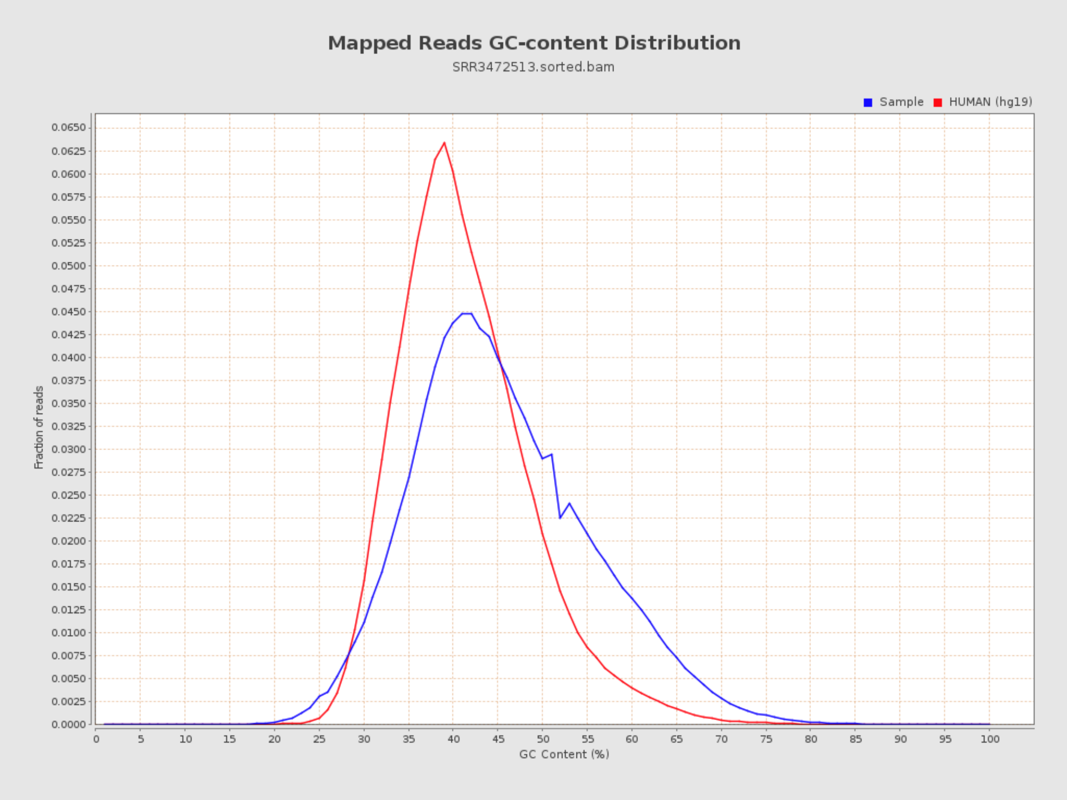
7. Results : Duplication Rate Histogram



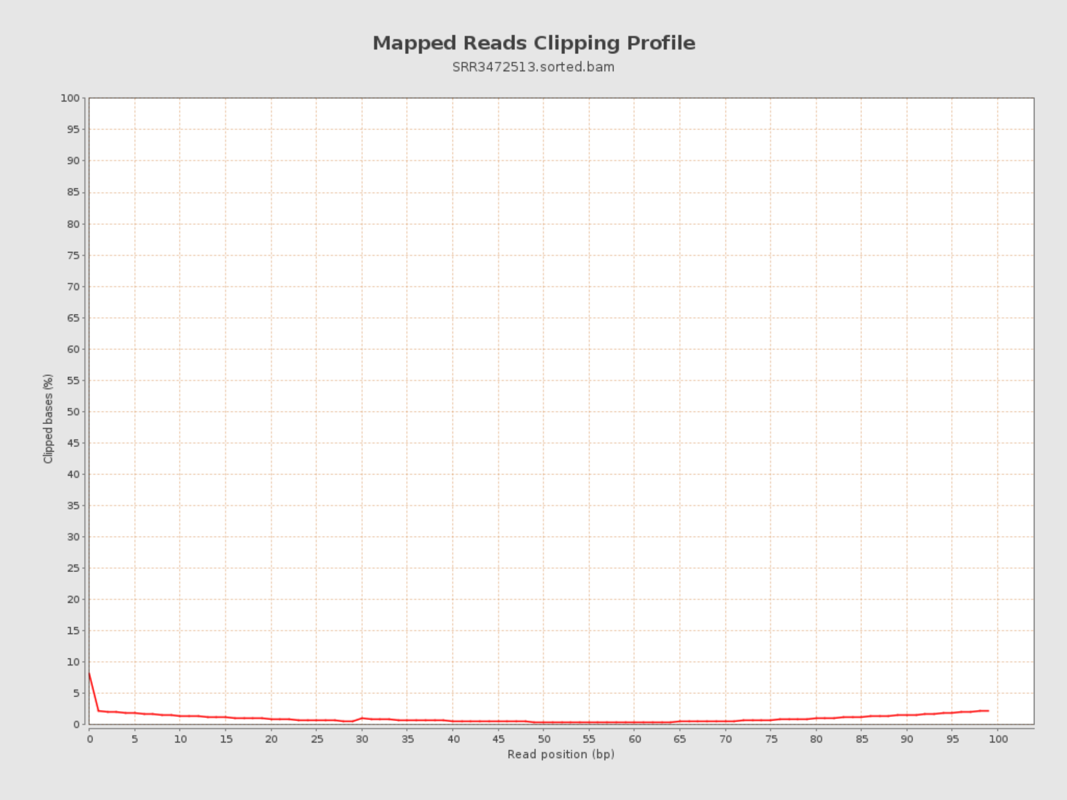
8. Results : Mapped Reads Nucleotide Content



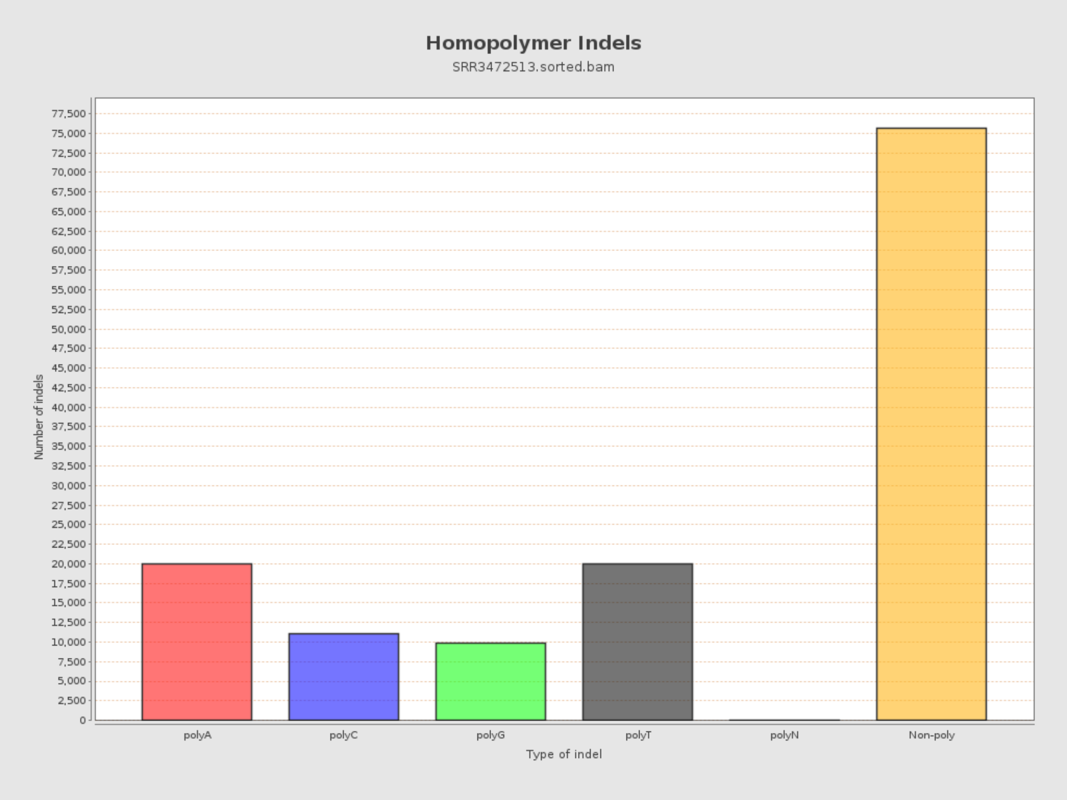
9. Results : Mapped Reads GC-content Distribution



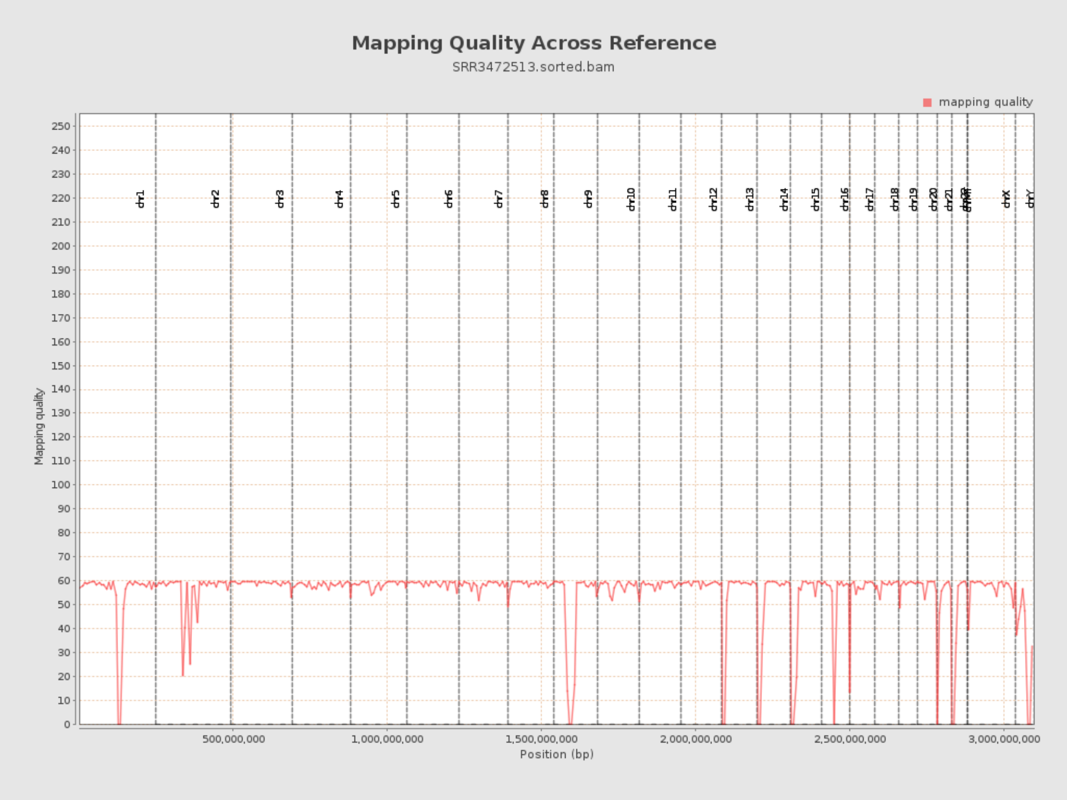
10. Results : Mapped Reads Clipping Profile



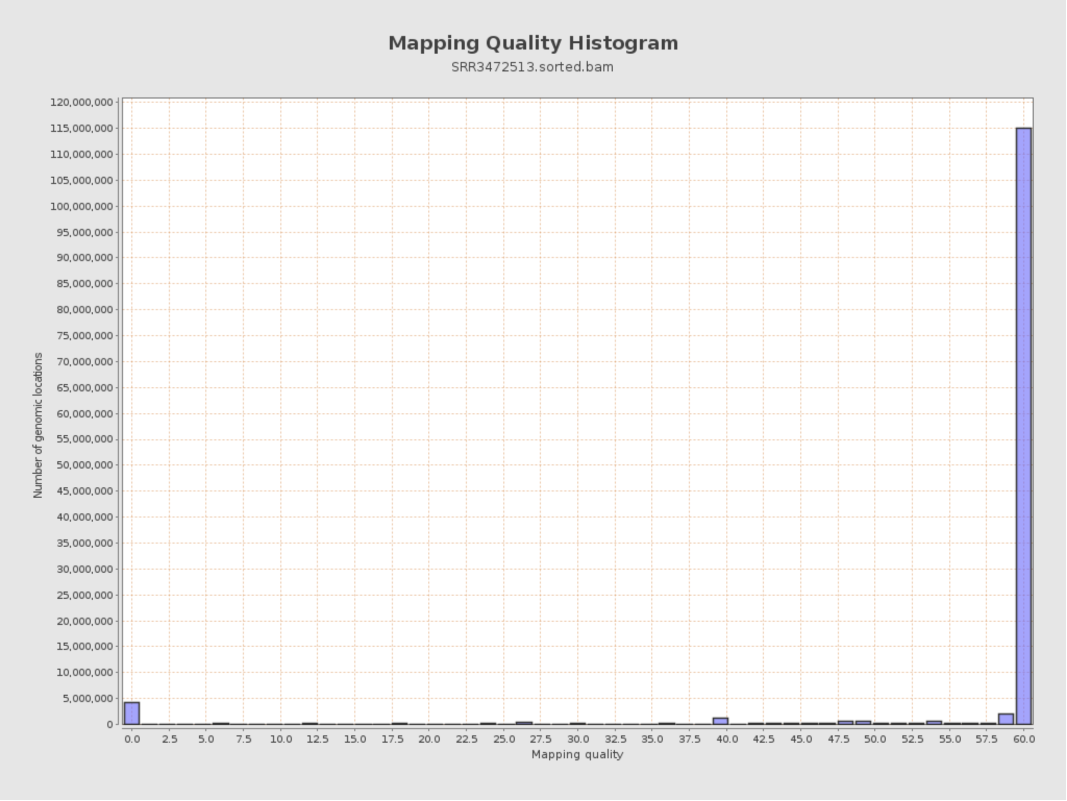
11. Results : Homopolymer Indels



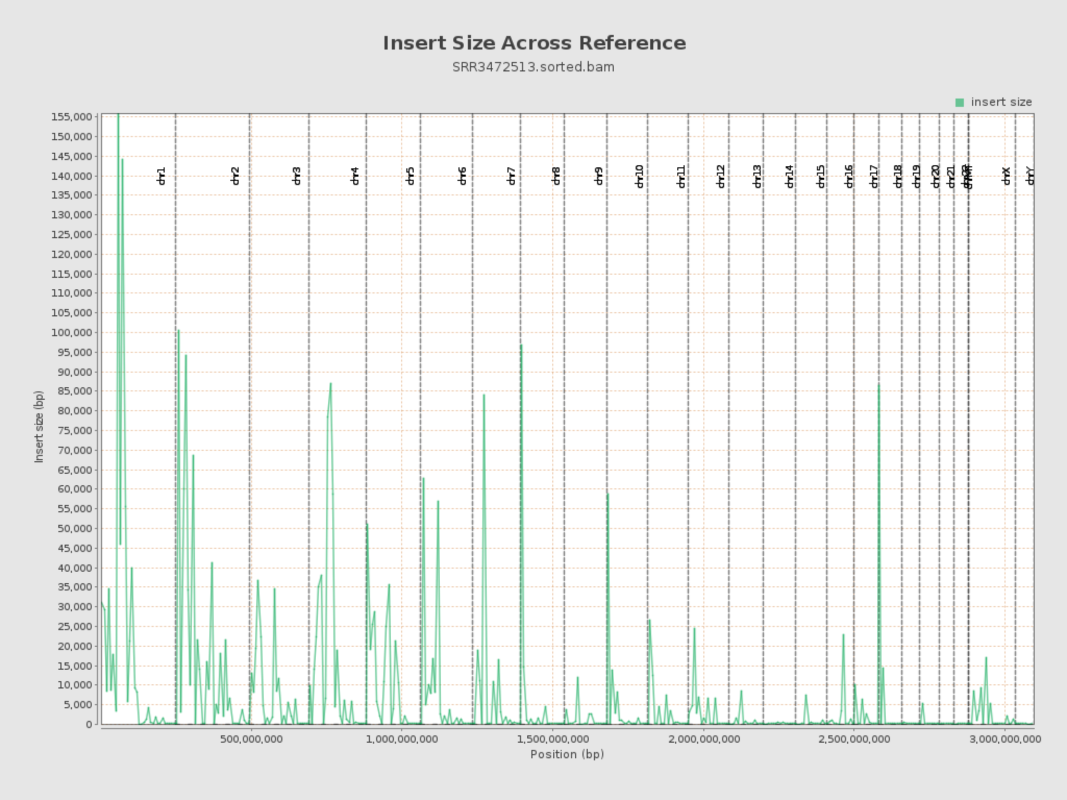
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram