Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 14:37:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472502.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_SRR3472502 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472502_1.fastq.gz SRR3472502_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 14:37:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472502.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,065,464
Mapped reads	15,904,160 / 99%
Unmapped reads	161,304 / 1%
Mapped paired reads	15,904,160 / 99%
Mapped reads, first in pair	7,973,171 / 49.63%
Mapped reads, second in pair	7,930,989 / 49.37%
Mapped reads, both in pair	15,818,054 / 98.46%
Mapped reads, singletons	86,106 / 0.54%
Secondary alignments	0
Supplementary alignments	71,321 / 0.44%
Read min/max/mean length	30 / 100 / 100.18
Duplicated reads (estimated)	10,276,196 / 63.96%
Duplication rate	45.98%
Clipped reads	1,363,850 / 8.49%

2.2. ACGT Content

Number/percentage of A's	435,011,312 / 27.8%
Number/percentage of C's	349,439,842 / 22.33%
Number/percentage of T's	433,492,475 / 27.7%
Number/percentage of G's	346,857,210 / 22.16%
Number/percentage of N's	243,532 / 0.02%

GC Percentage	44.49%

2.3. Coverage

Mean	0.5056
Standard Deviation	19.7378

2.4. Mapping Quality

Mean Mapping Quality	55

2.5. Insert size

Mean	37,353.31
Standard Deviation	1,887,497.17
P25/Median/P75	167 / 232 / 312

2.6. Mismatches and indels

General error rate	0.6%
Mismatches	9,175,015
Insertions	81,305
Mapped reads with at least one insertion	0.51%
Deletions	75,603
Mapped reads with at least one deletion	0.47%
Homopolymer indels	44.54%

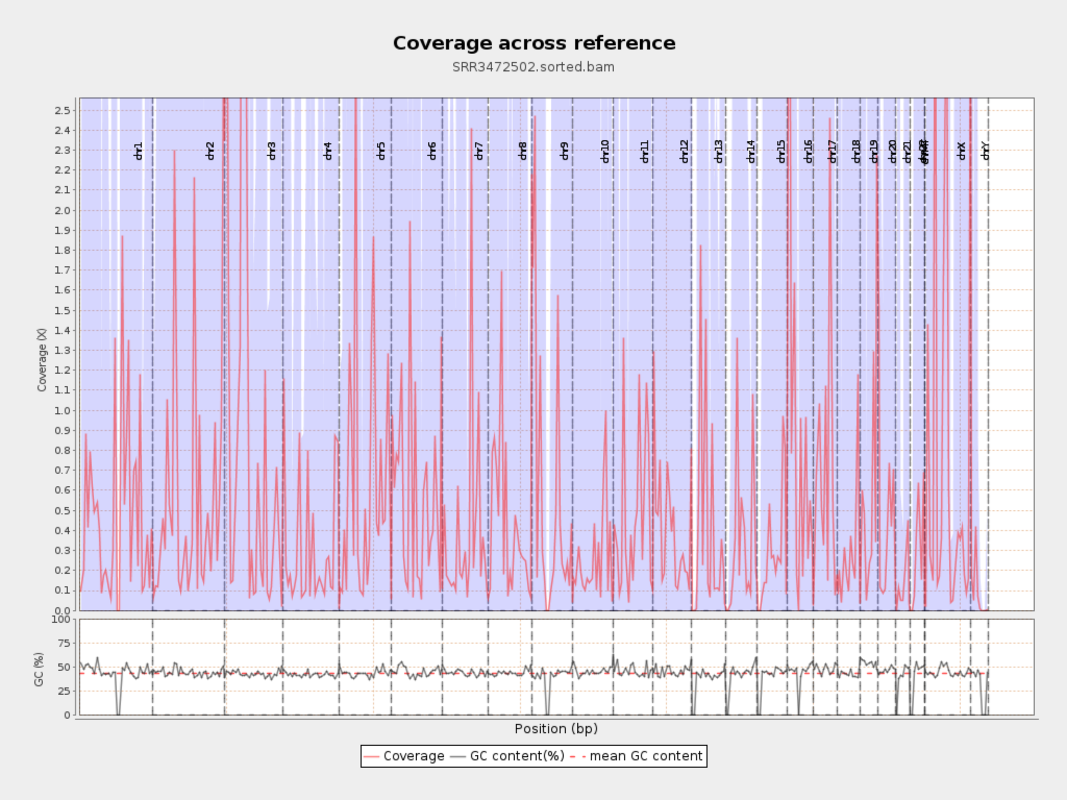
2.7. Chromosome stats

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

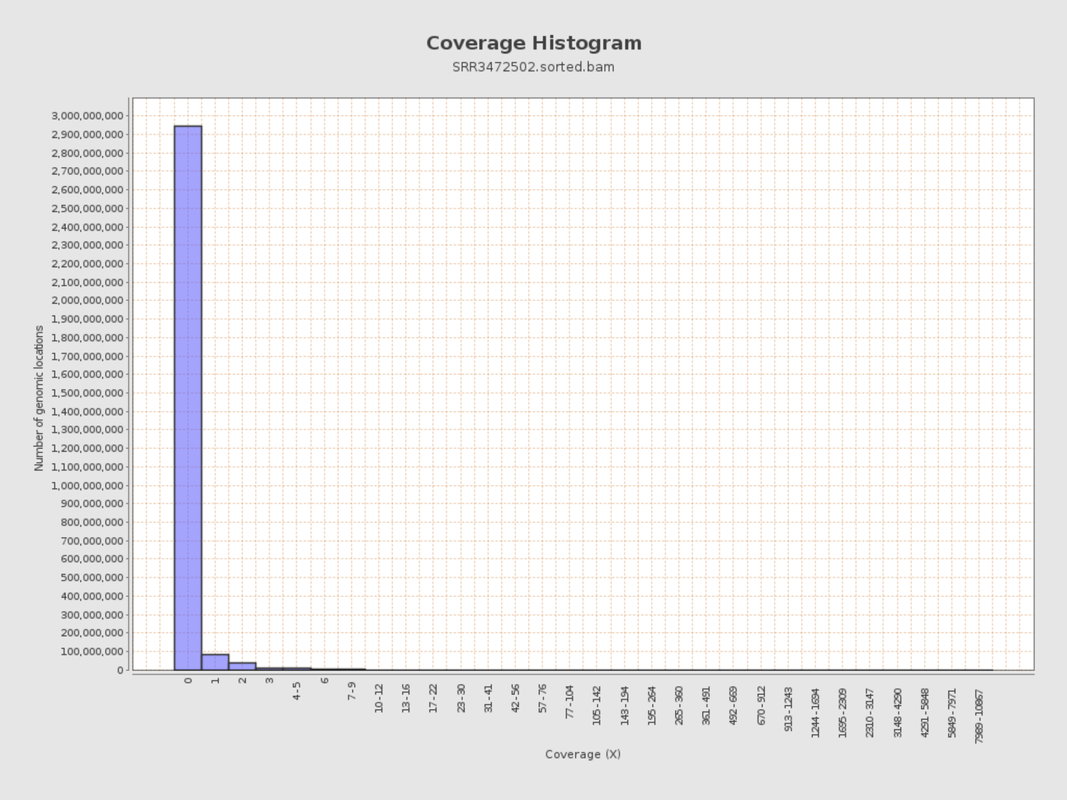
		bases	coverage	deviation
chr1	249250621	120453624	0.4833	18.5035
chr2	243199373	137737321	0.5664	23.2506
chr3	198022430	199092208	1.0054	30.7331
chr4	191154276	56175269	0.2939	11.3447
chr5	180915260	117360437	0.6487	22.6944
chr6	171115067	95218199	0.5565	20.8214
chr7	159138663	62353995	0.3918	15.1181
chr8	146364022	63181539	0.4317	15.3764
chr9	141213431	80013014	0.5666	15.5765
chr10	135534747	36363347	0.2683	9.5089
chr11	135006516	65123270	0.4824	20.8108
chr12	133851895	54555106	0.4076	12.8404
chr13	115169878	47384344	0.4114	22.3693
chr14	107349540	36299503	0.3381	17.3428
chr15	102531392	30498322	0.2975	9.4537
chr16	90354753	84065273	0.9304	29.3832
chr17	81195210	55137288	0.6791	17.1372
chr18	78077248	23815295	0.305	11.7754
chr19	59128983	30376548	0.5137	21.7357
chr20	63025520	28682812	0.4551	18.7069
chr21	48129895	6813060	0.1416	5.9491
chr22	51304566	15110466	0.2945	10.2699
chrMT	16571	1518	0.0916	0.4319
chrX	155270560	114213917	0.7356	30.1254

chrY	59373566	5207661	0.0877	6.1731

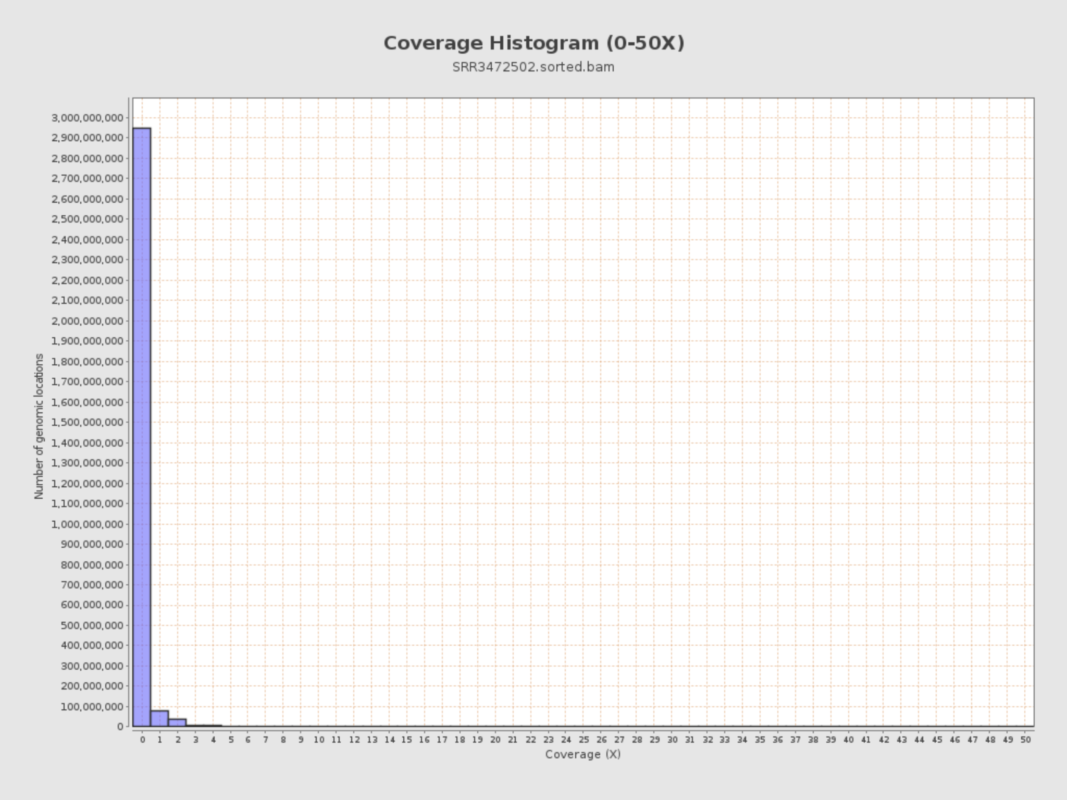
3. Results : Coverage across reference



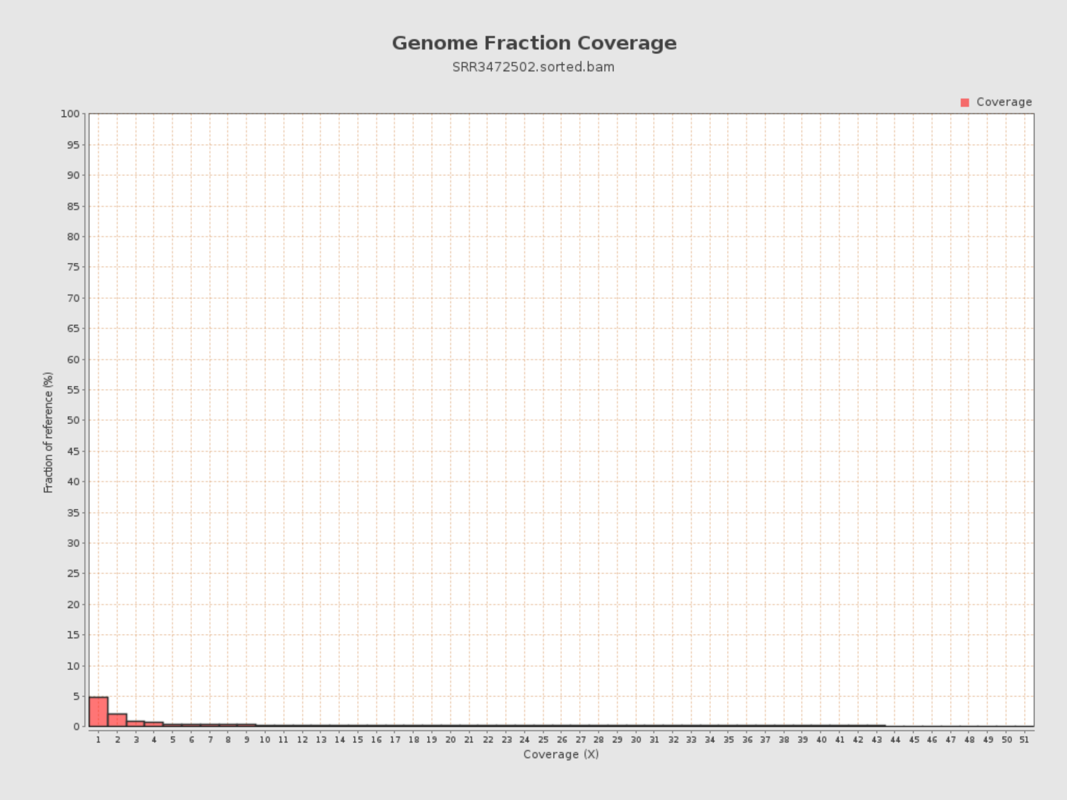
4. Results : Coverage Histogram



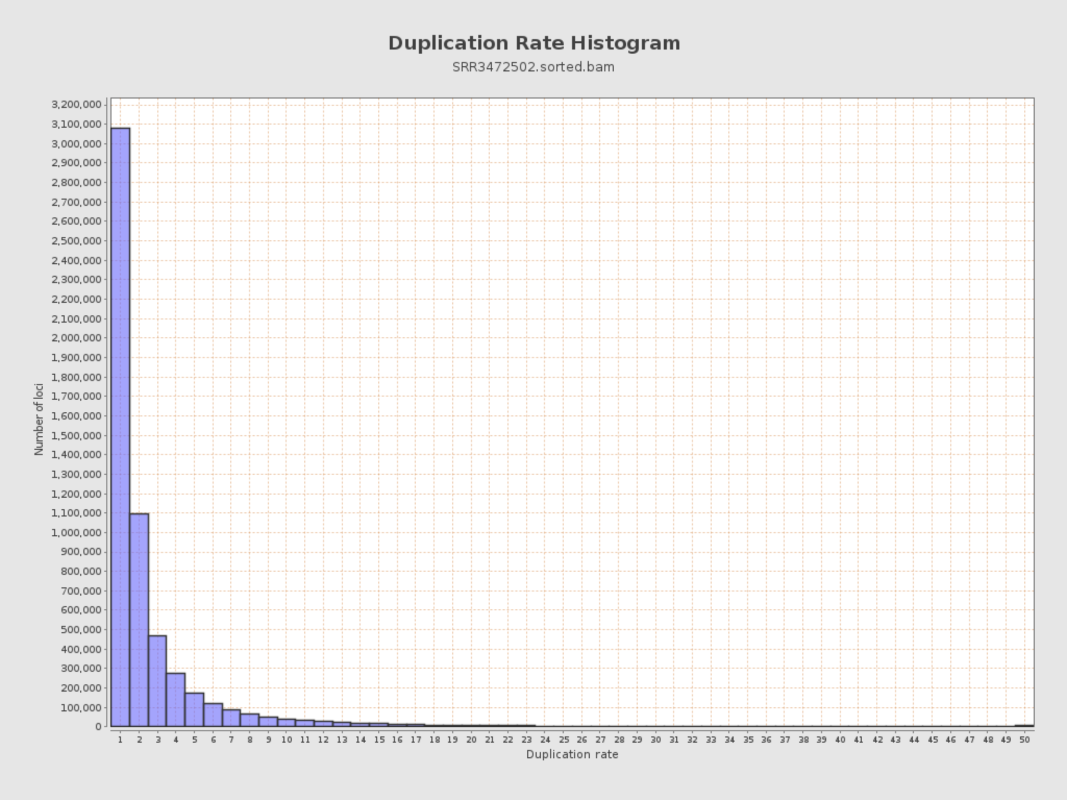
5. Results : Coverage Histogram (0-50X)



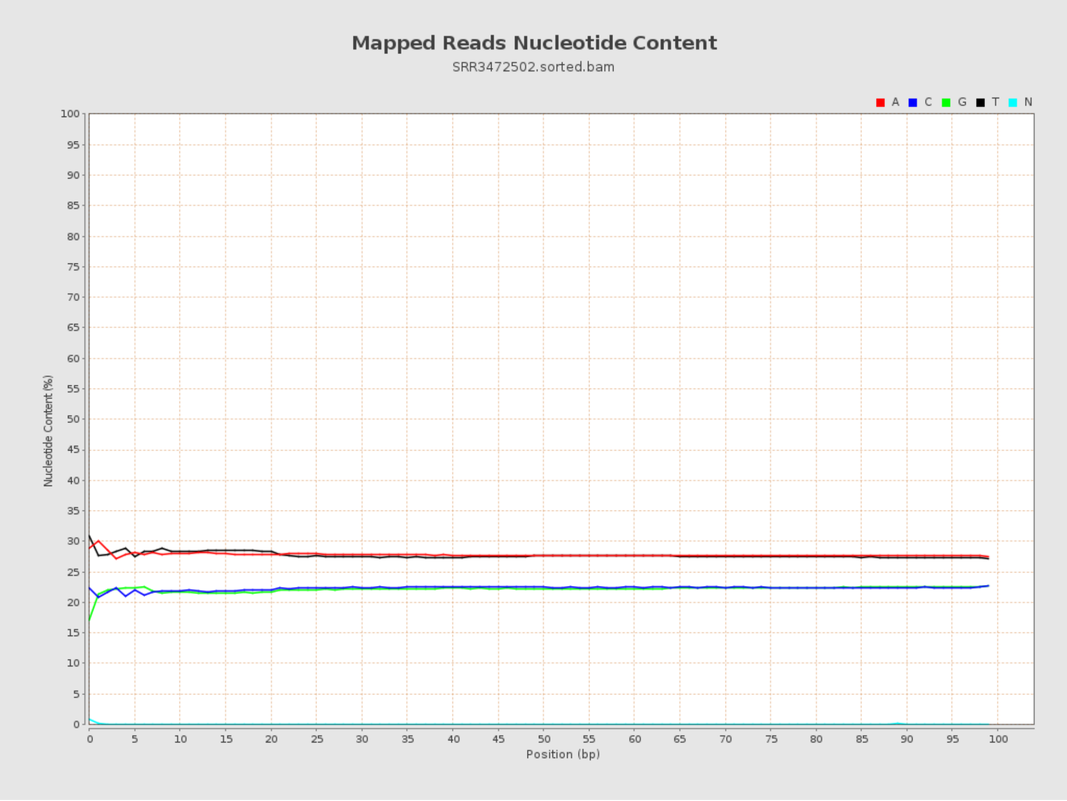
6. Results : Genome Fraction Coverage



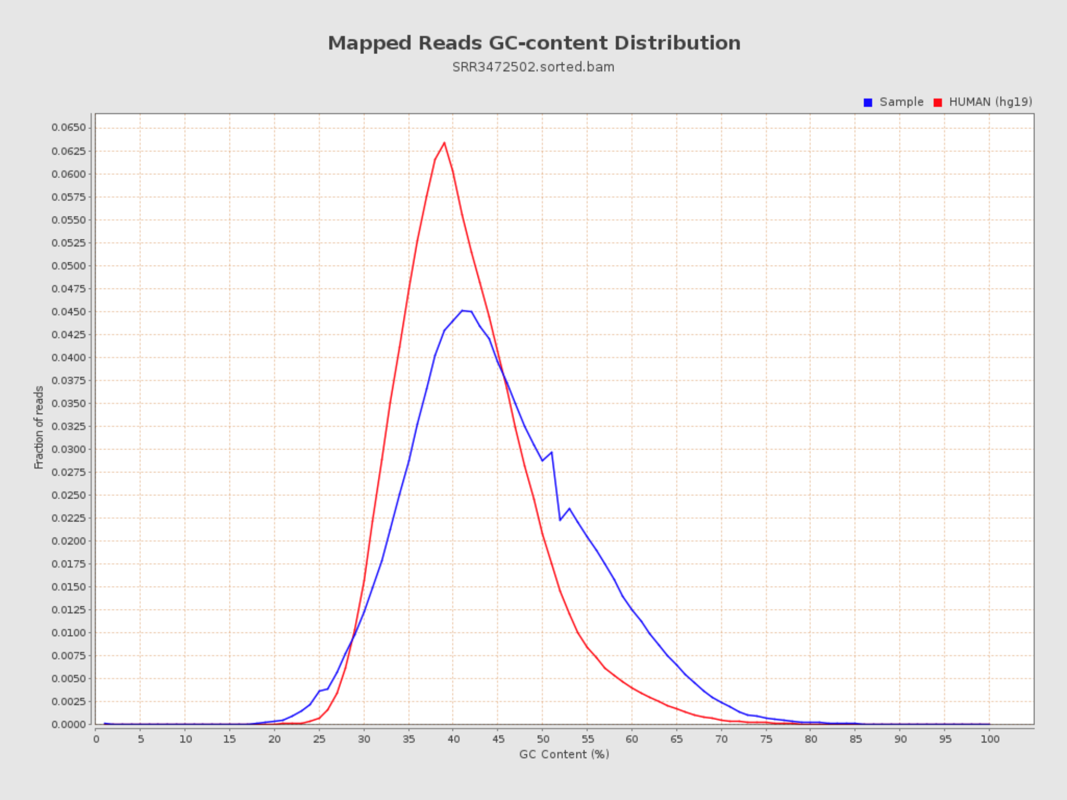
7. Results : Duplication Rate Histogram



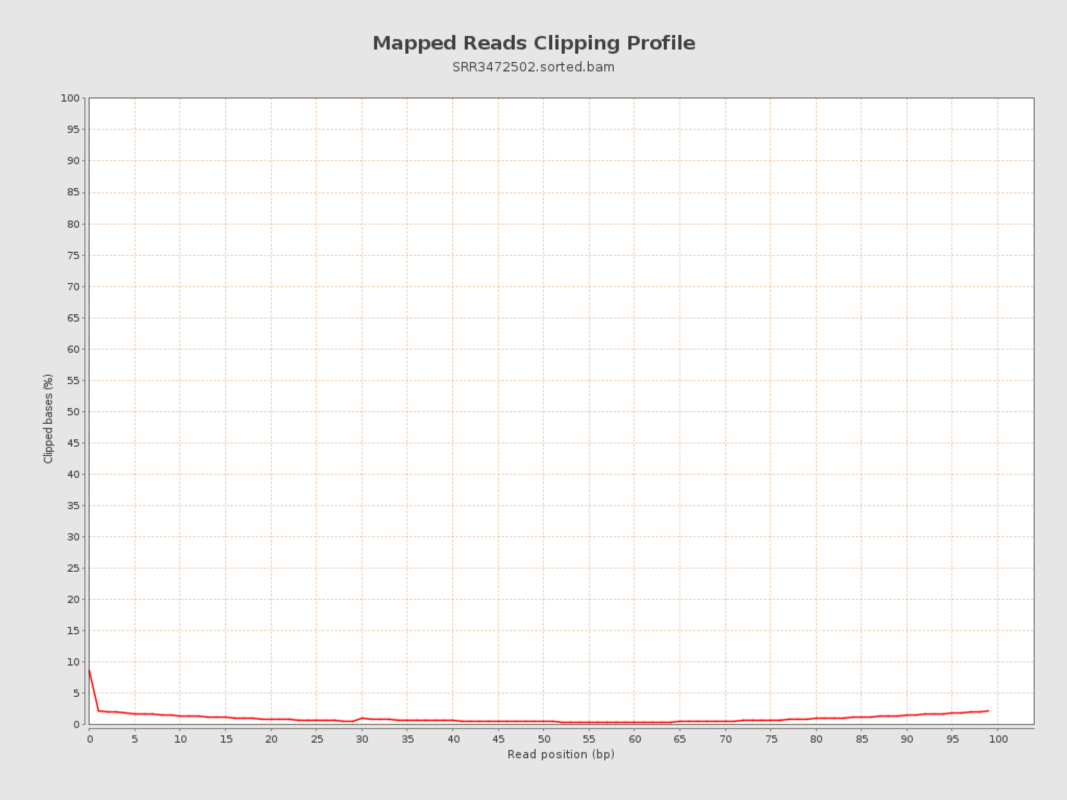
8. Results : Mapped Reads Nucleotide Content



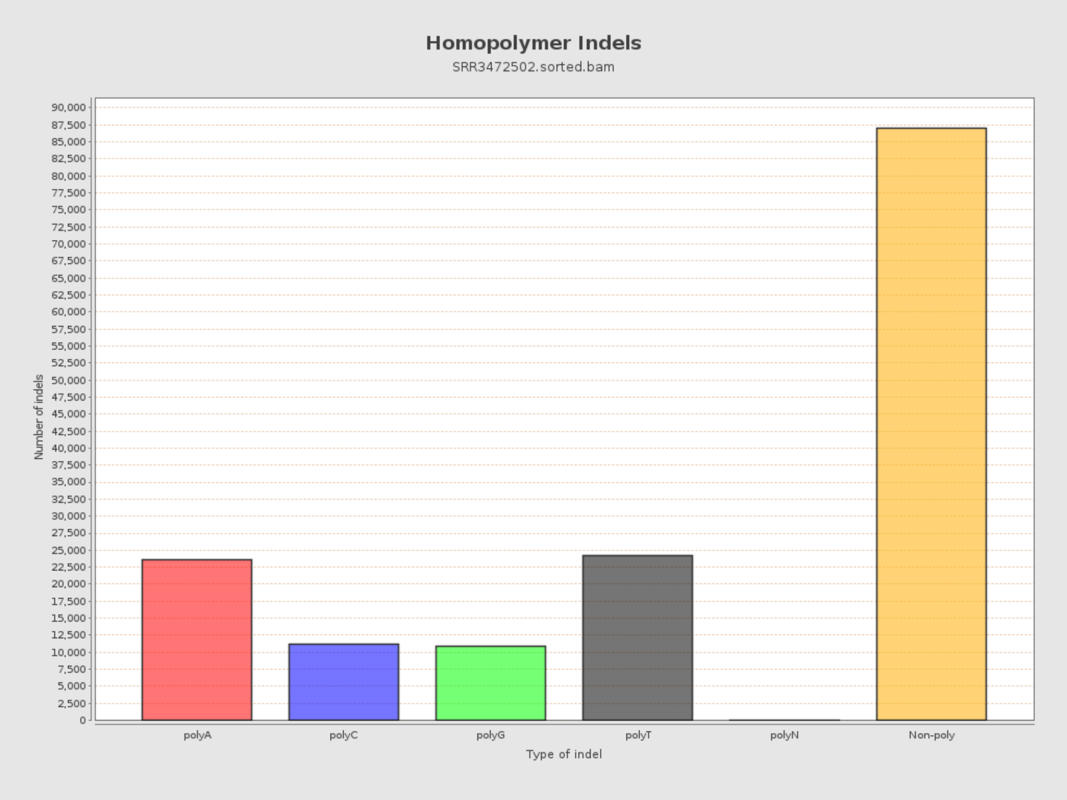
9. Results : Mapped Reads GC-content Distribution



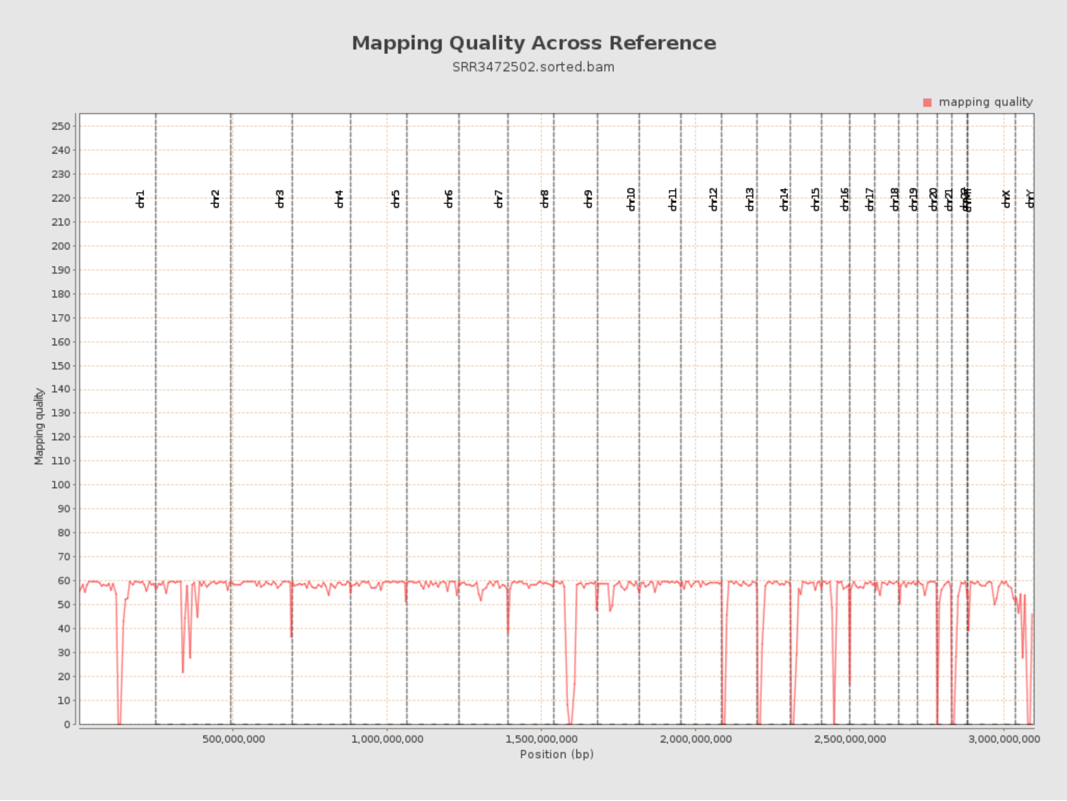
10. Results : Mapped Reads Clipping Profile



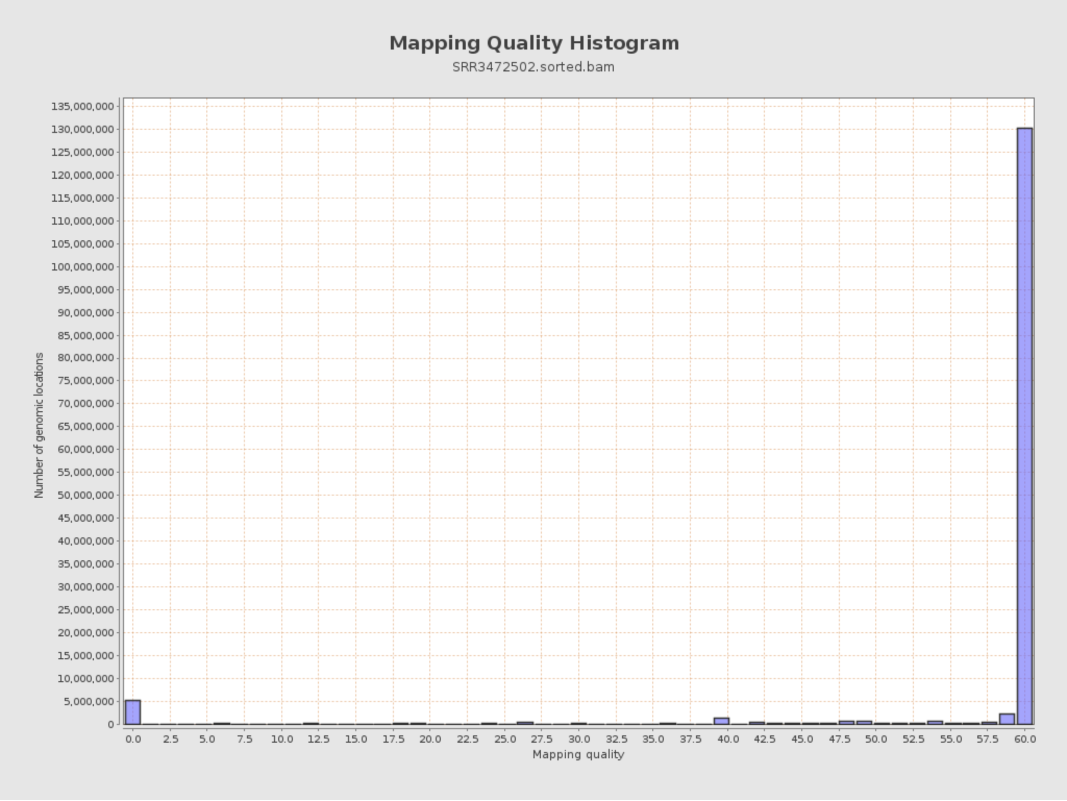
11. Results : Homopolymer Indels



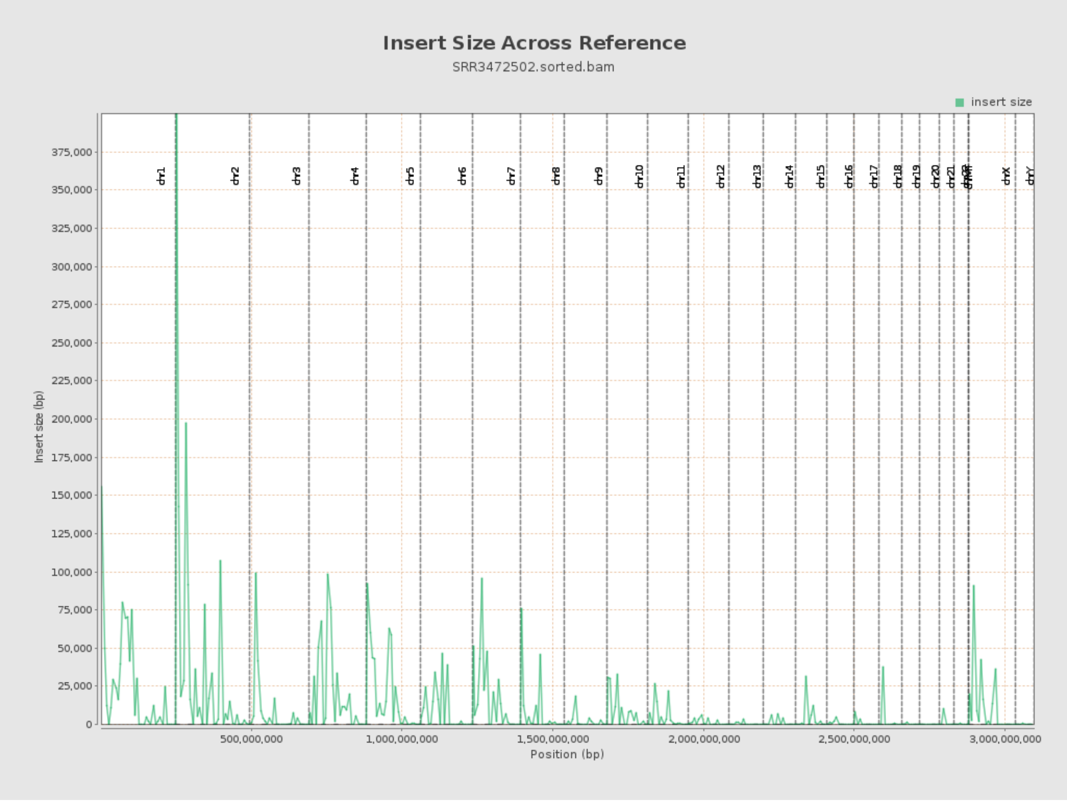
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram