Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 18:54:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472446.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_SRR3472446 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472446_1.fastq.gz SRR3472446_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 18:54:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472446.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	30,189,822
Mapped reads	27,393,709 / 90.74%
Unmapped reads	2,796,113 / 9.26%
Mapped paired reads	27,393,709 / 90.74%
Mapped reads, first in pair	13,748,144 / 45.54%
Mapped reads, second in pair	13,645,565 / 45.2%
Mapped reads, both in pair	27,244,204 / 90.24%
Mapped reads, singletons	149,505 / 0.5%
Secondary alignments	0
Supplementary alignments	171,964 / 0.57%
Read min/max/mean length	30 / 100 / 99.11
Duplicated reads (estimated)	25,370,037 / 84.04%
Duplication rate	33.62%
Clipped reads	1,916,287 / 6.35%

2.2. ACGT Content

Number/percentage of A's	704,014,877 / 26.25%
Number/percentage of C's	637,883,185 / 23.79%
Number/percentage of T's	705,063,516 / 26.29%
Number/percentage of G's	634,463,777 / 23.66%
Number/percentage of N's	314,295 / 0.01%

GC Percentage	47.44%

2.3. Coverage

Mean	0.8664
Standard Deviation	296.5479

2.4. Mapping Quality

Mean Mapping Quality	48.15

2.5. Insert size

Mean	16,069.13
Standard Deviation	1,093,052.51
P25/Median/P75	155 / 219 / 299

2.6. Mismatches and indels

General error rate	0.55%
Mismatches	14,694,796
Insertions	110,937
Mapped reads with at least one insertion	0.4%
Deletions	144,557
Mapped reads with at least one deletion	0.53%
Homopolymer indels	55.14%

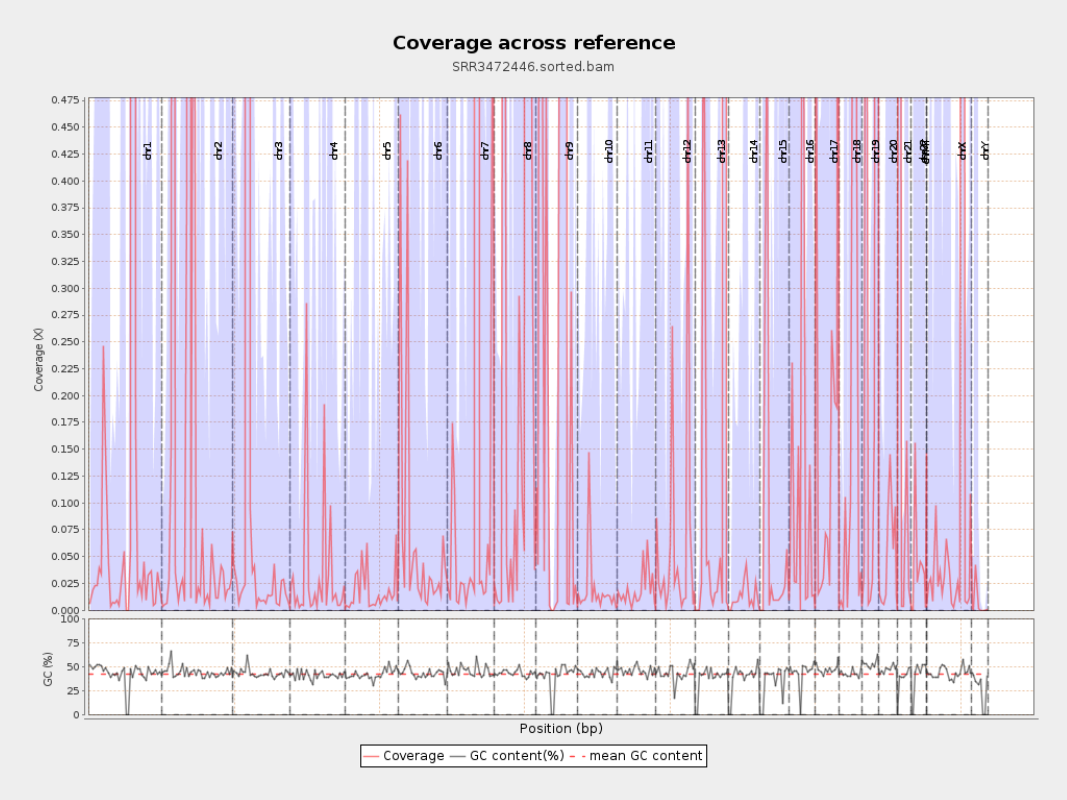
2.7. Chromosome stats

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

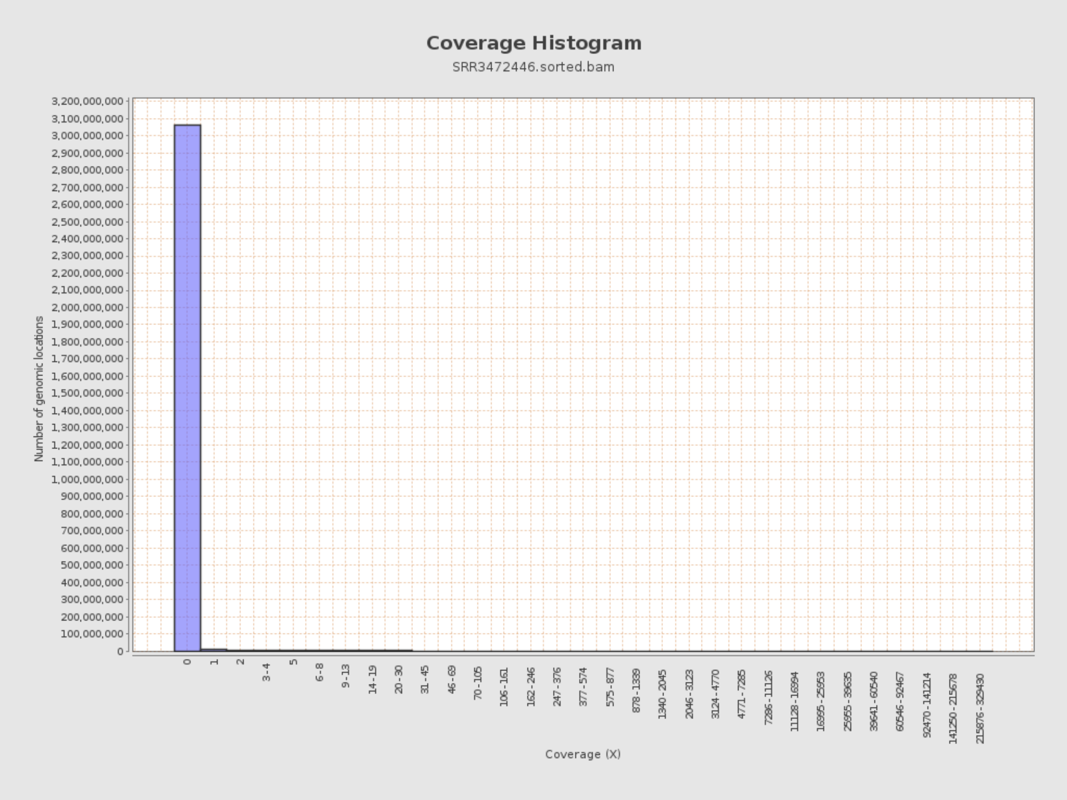
		bases	coverage	deviation
chr1	249250621	112061845	0.4496	131.3661
chr2	243199373	360120800	1.4808	298.3428
chr3	198022430	614043586	3.1009	761.9644
chr4	191154276	6505147	0.034	1.0811
chr5	180915260	3277258	0.0181	0.4895
chr6	171115067	11572568	0.0676	2.3194
chr7	159138663	145346112	0.9133	133.1508
chr8	146364022	332029630	2.2685	242.9117
chr9	141213431	139892642	0.9906	97.1069
chr10	135534747	2600896	0.0192	4.3521
chr11	135006516	2566470	0.019	0.5687
chr12	133851895	9267018	0.0692	1.742
chr13	115169878	778618663	6.7606	1,011.5197
chr14	107349540	1405019	0.0131	0.3873
chr15	102531392	8107562	0.0791	4.5971
chr16	90354753	11605724	0.1284	6.9483
chr17	81195210	18228042	0.2245	3.8413
chr18	78077248	31368980	0.4018	22.0975
chr19	59128983	40331020	0.6821	64.7911
chr20	63025520	3370086	0.0535	1.3573
chr21	48129895	17674510	0.3672	69.5373
chr22	51304566	2348518	0.0458	8.1953
chrMT	16571	2428	0.1465	0.463
chrX	155270560	29305451	0.1887	31.0889

chrY	59373566	353880	0.006	1.9638

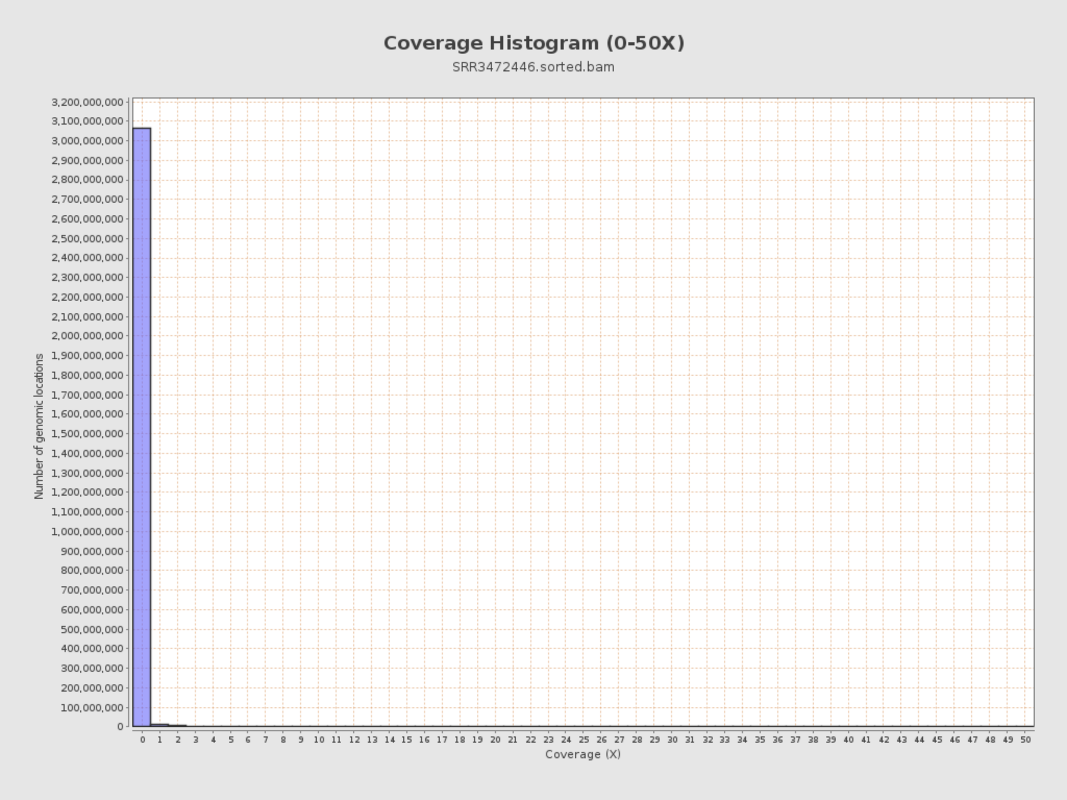
3. Results : Coverage across reference



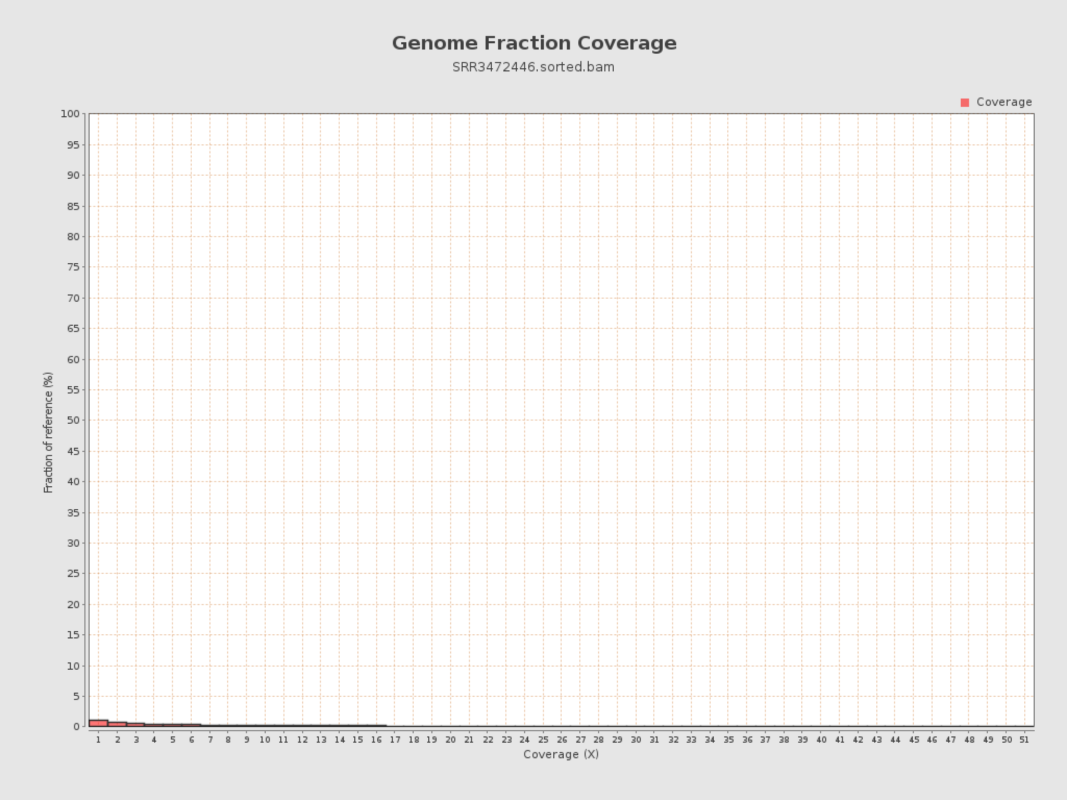
4. Results : Coverage Histogram



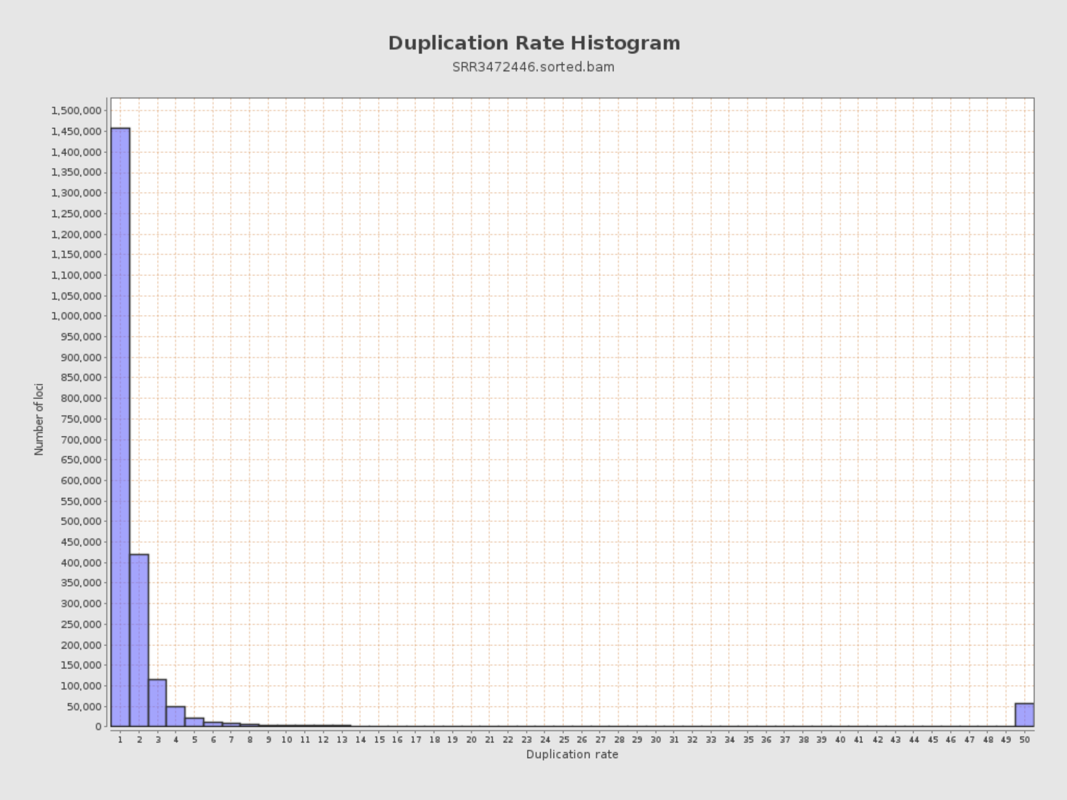
5. Results : Coverage Histogram (0-50X)



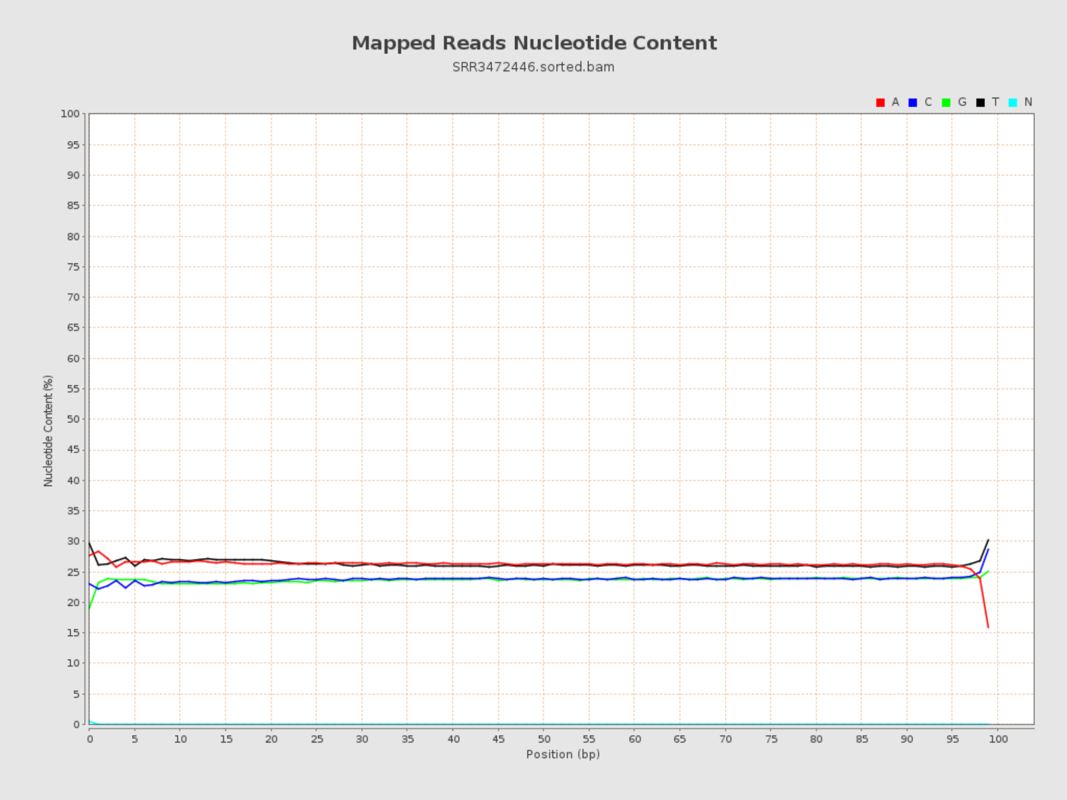
6. Results : Genome Fraction Coverage



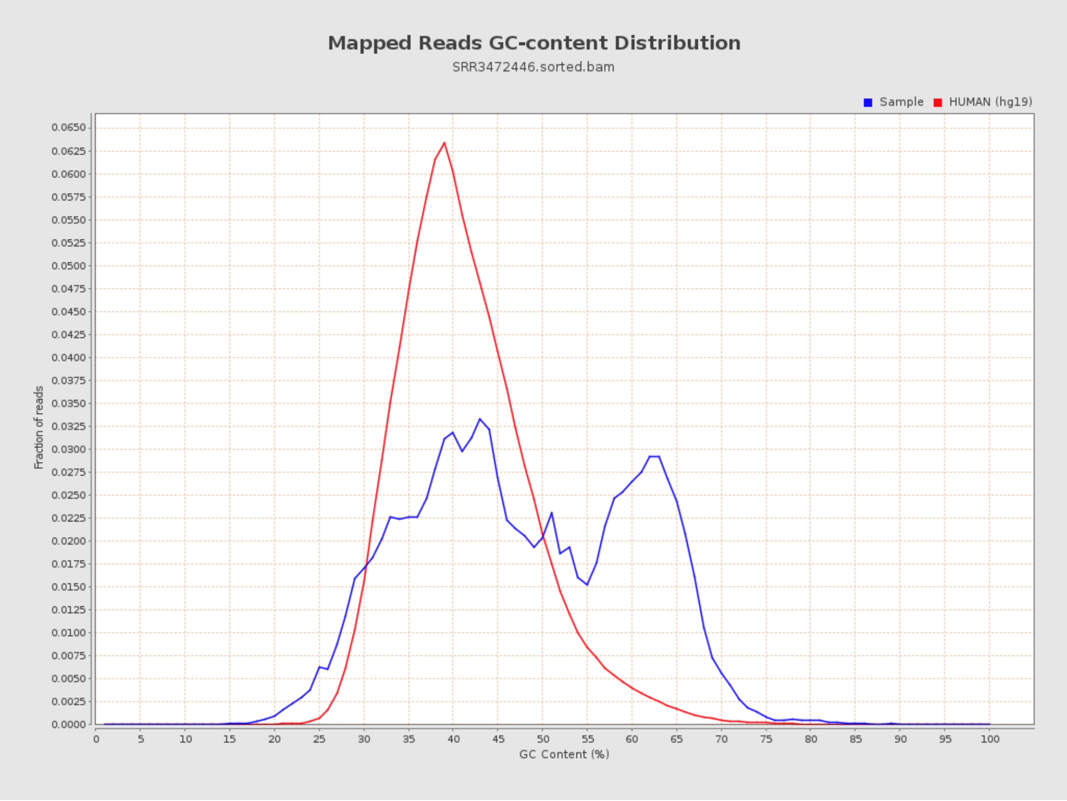
7. Results : Duplication Rate Histogram



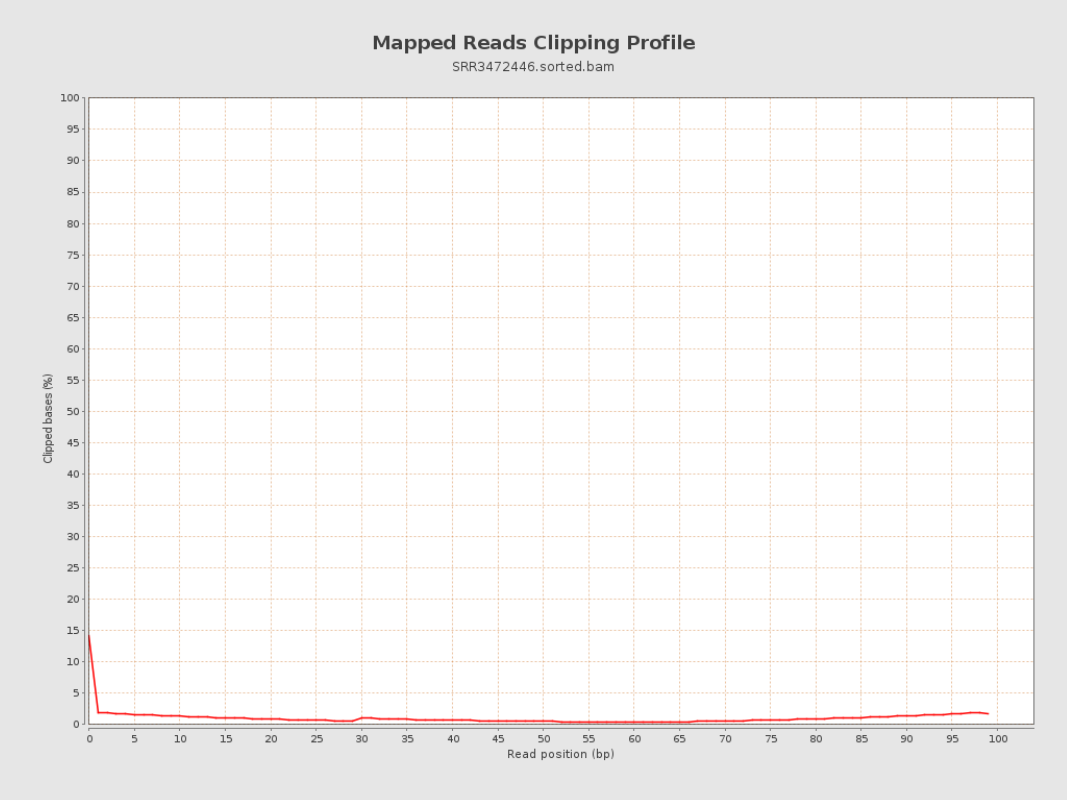
8. Results : Mapped Reads Nucleotide Content



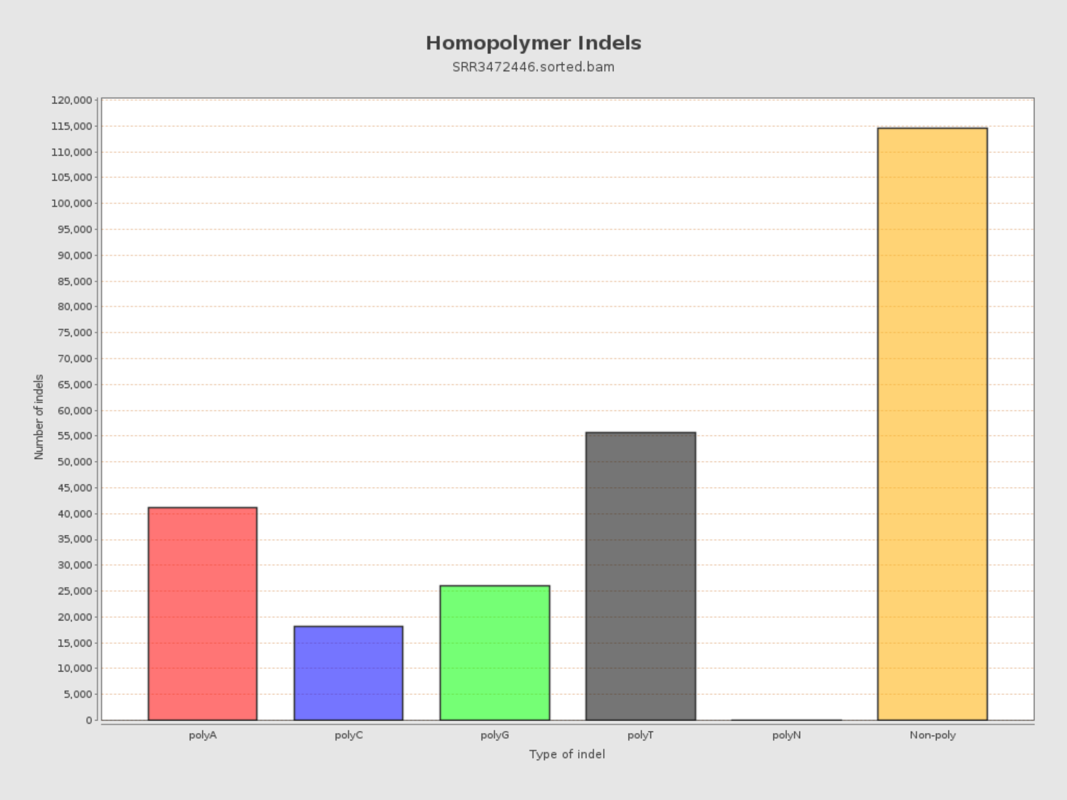
9. Results : Mapped Reads GC-content Distribution



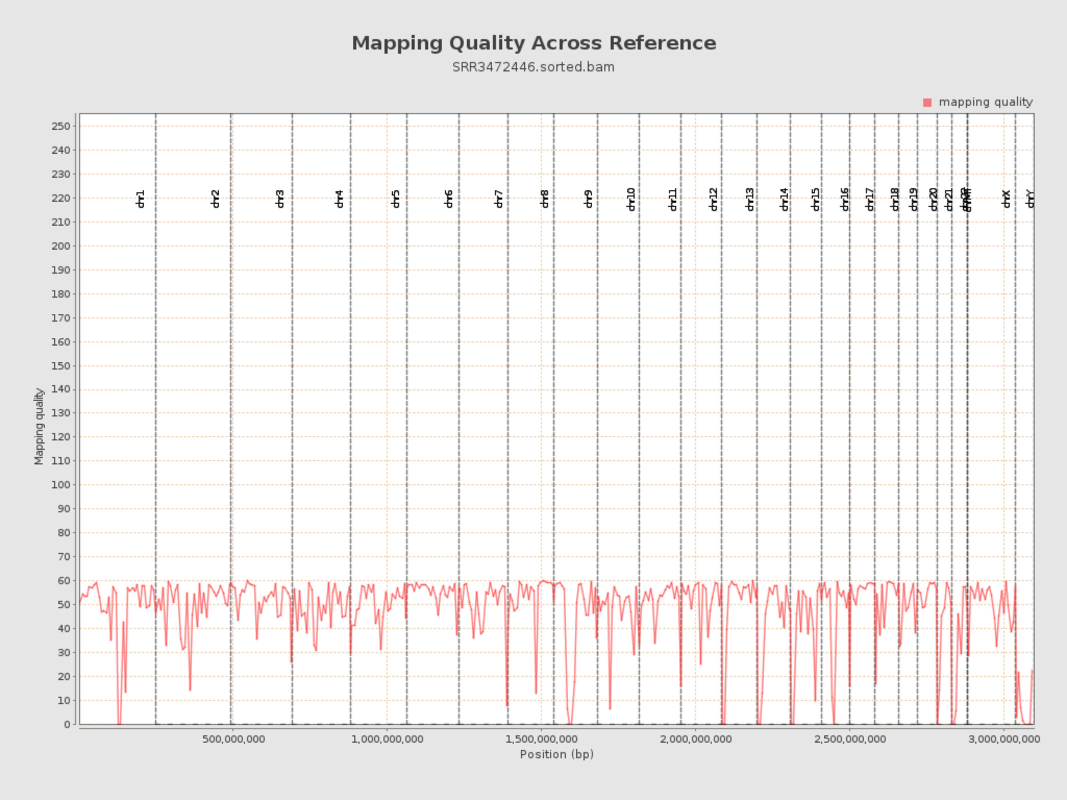
10. Results : Mapped Reads Clipping Profile



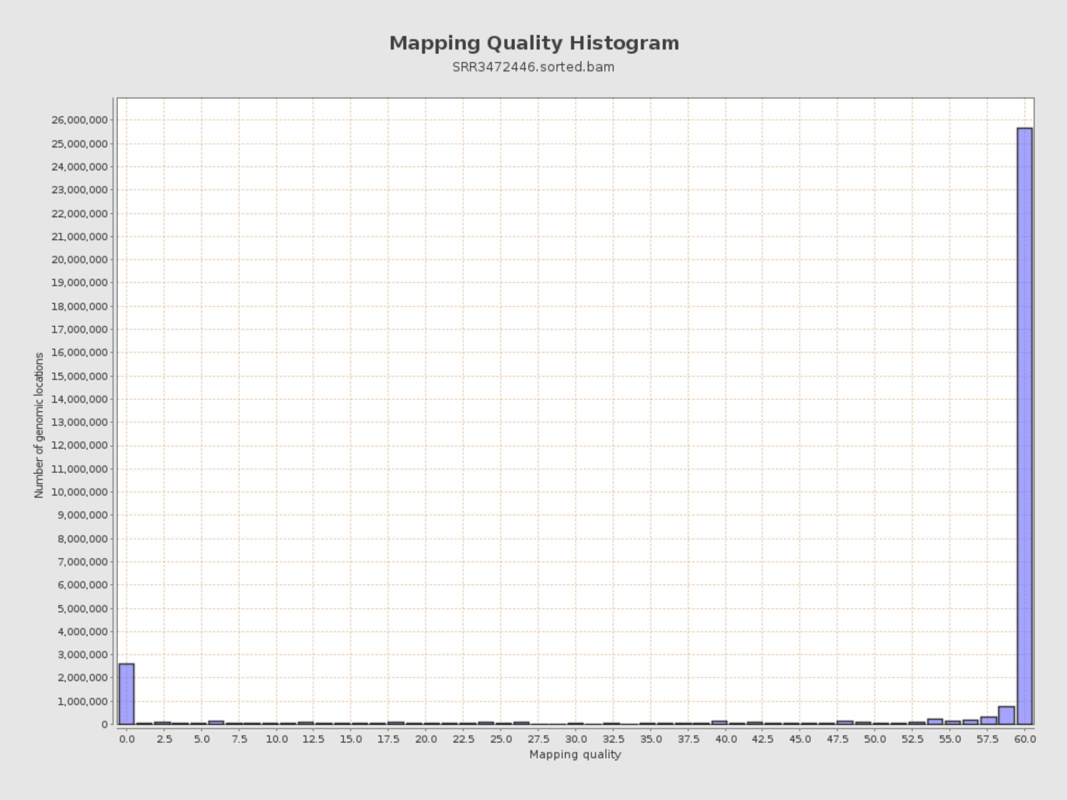
11. Results : Homopolymer Indels



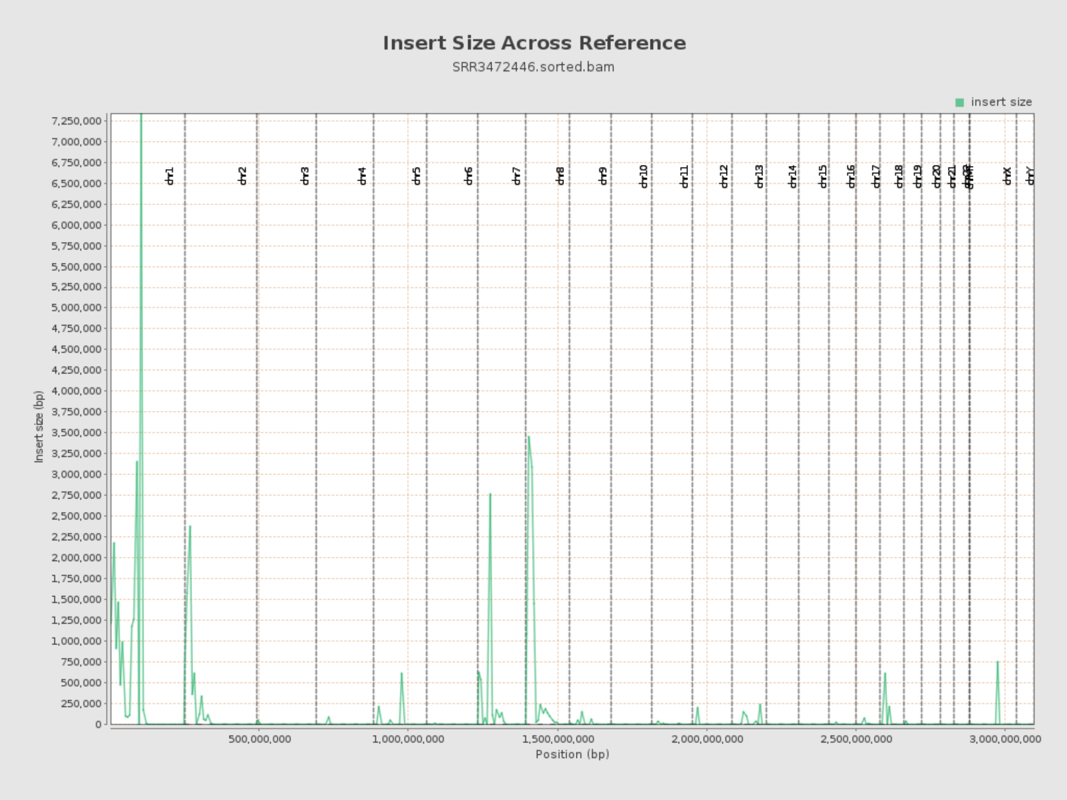
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram