Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/29 02:33:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472667.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_SRR3472667 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472667_1.fastq.gz SRR3472667_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 29 02:33:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472667.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	20,902,604
Mapped reads	20,707,747 / 99.07%
Unmapped reads	194,857 / 0.93%
Mapped paired reads	20,707,747 / 99.07%
Mapped reads, first in pair	10,393,047 / 49.72%
Mapped reads, second in pair	10,314,700 / 49.35%
Mapped reads, both in pair	20,575,526 / 98.44%
Mapped reads, singletons	132,221 / 0.63%
Secondary alignments	0
Supplementary alignments	135,128 / 0.65%
Read min/max/mean length	30 / 101 / 99.79
Duplicated reads (estimated)	15,597,122 / 74.62%
Duplication rate	49.36%
Clipped reads	1,462,422 / 7%

2.2. ACGT Content

Number/percentage of A's	540,063,304 / 26.49%
Number/percentage of C's	482,707,154 / 23.68%
Number/percentage of T's	541,339,240 / 26.55%
Number/percentage of G's	474,201,381 / 23.26%
Number/percentage of N's	383,665 / 0.02%

GC Percentage	46.94%

2.3. Coverage

Mean	0.6586
Standard Deviation	47.1823

2.4. Mapping Quality

Mean Mapping Quality	54.86

2.5. Insert size

Mean	21,076.24
Standard Deviation	1,419,135.75
P25/Median/P75	160 / 218 / 289

2.6. Mismatches and indels

General error rate	0.6%
Mismatches	11,979,213
Insertions	127,399
Mapped reads with at least one insertion	0.61%
Deletions	103,738
Mapped reads with at least one deletion	0.5%
Homopolymer indels	46.48%

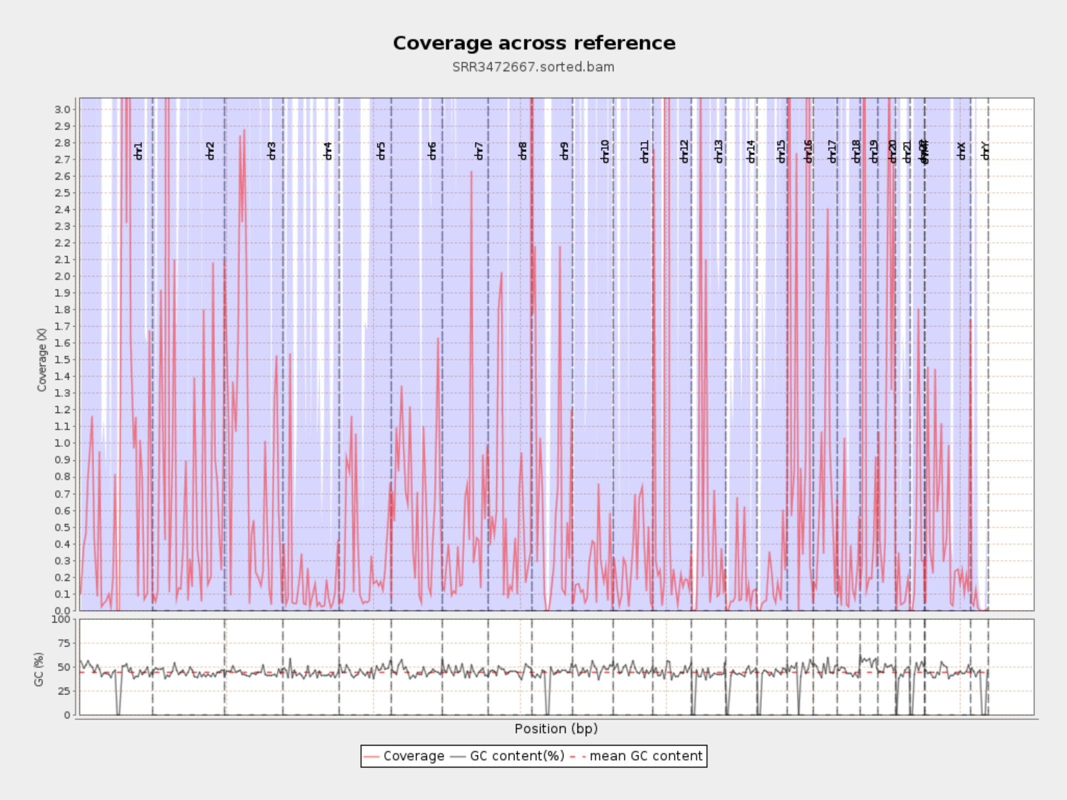
2.7. Chromosome stats

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

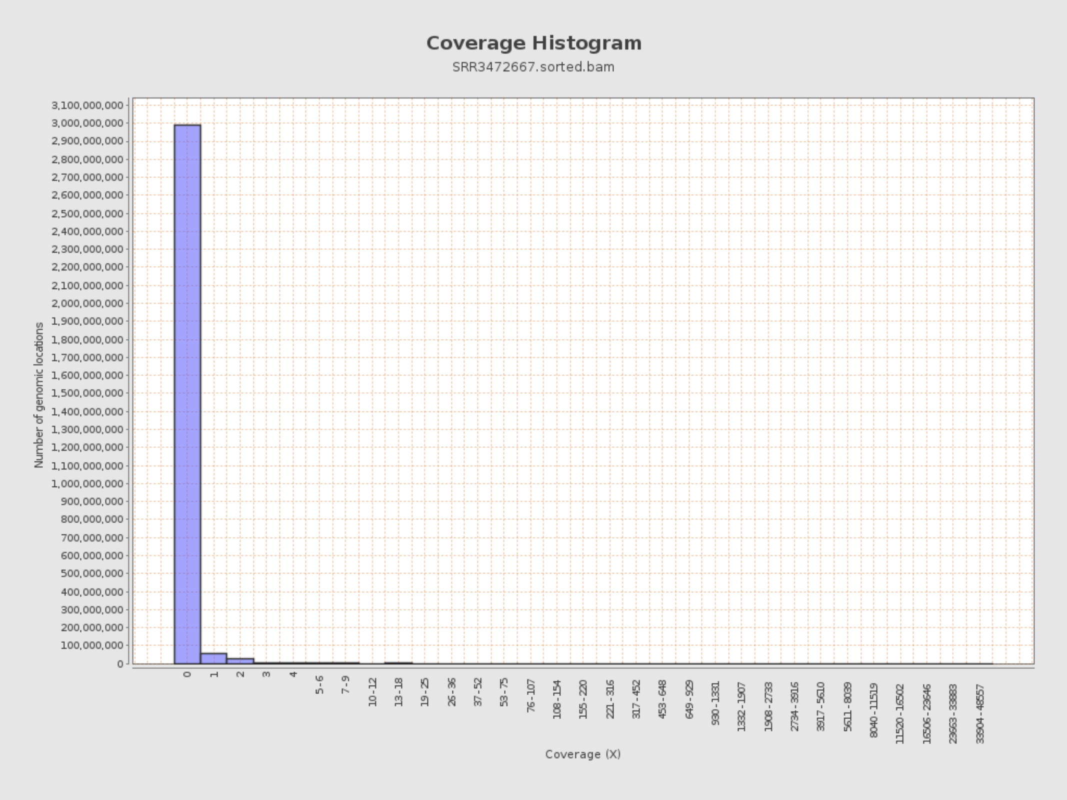
		bases	coverage	deviation
chr1	249250621	242793301	0.9741	62.596
chr2	243199373	219466067	0.9024	66.4027
chr3	198022430	193715439	0.9782	35.4945
chr4	191154276	32440969	0.1697	23.6976
chr5	180915260	59695677	0.33	16.7051
chr6	171115067	113772389	0.6649	23.7857
chr7	159138663	77833096	0.4891	18.1506
chr8	146364022	80493916	0.55	19.2469
chr9	141213431	123582208	0.8751	38.1161
chr10	135534747	31046865	0.2291	13.0683
chr11	135006516	39566099	0.2931	17.4049
chr12	133851895	248962819	1.86	153.6984
chr13	115169878	63905841	0.5549	24.1452
chr14	107349540	16208580	0.151	7.1074
chr15	102531392	16057932	0.1566	6.6684
chr16	90354753	148443447	1.6429	65.129
chr17	81195210	63493068	0.782	32.9362
chr18	78077248	20254239	0.2594	16.5909
chr19	59128983	53680594	0.9079	29.4117
chr20	63025520	87288369	1.385	41.3274
chr21	48129895	5815313	0.1208	5.6144
chr22	51304566	23894062	0.4657	23.8897
chrMT	16571	5063	0.3055	0.6666
chrX	155270560	74912185	0.4825	16.1107

chrY	59373566	1629299	0.0274	1.4745

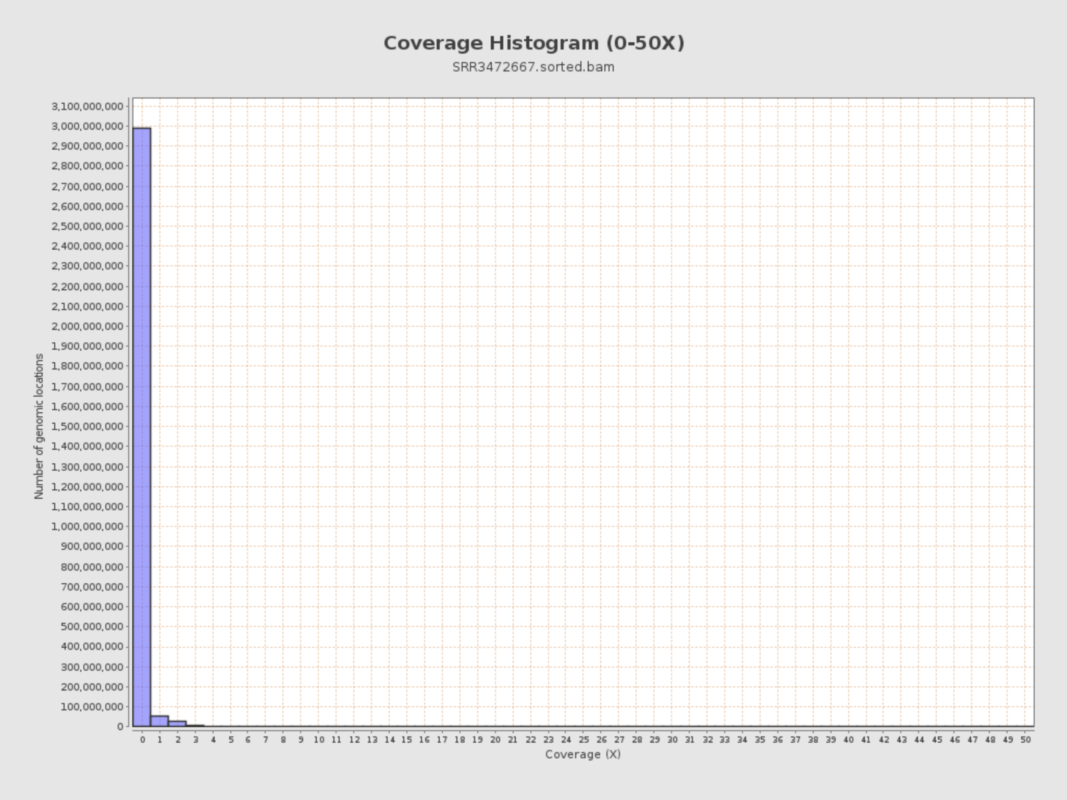
3. Results : Coverage across reference



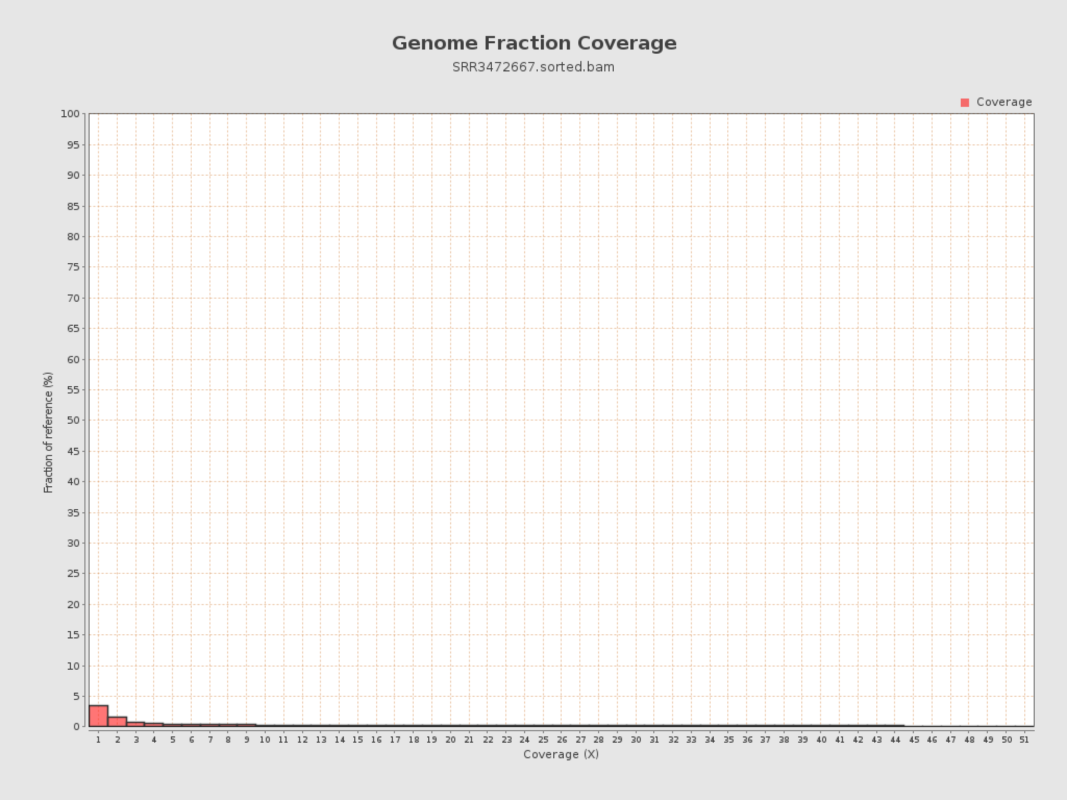
4. Results : Coverage Histogram



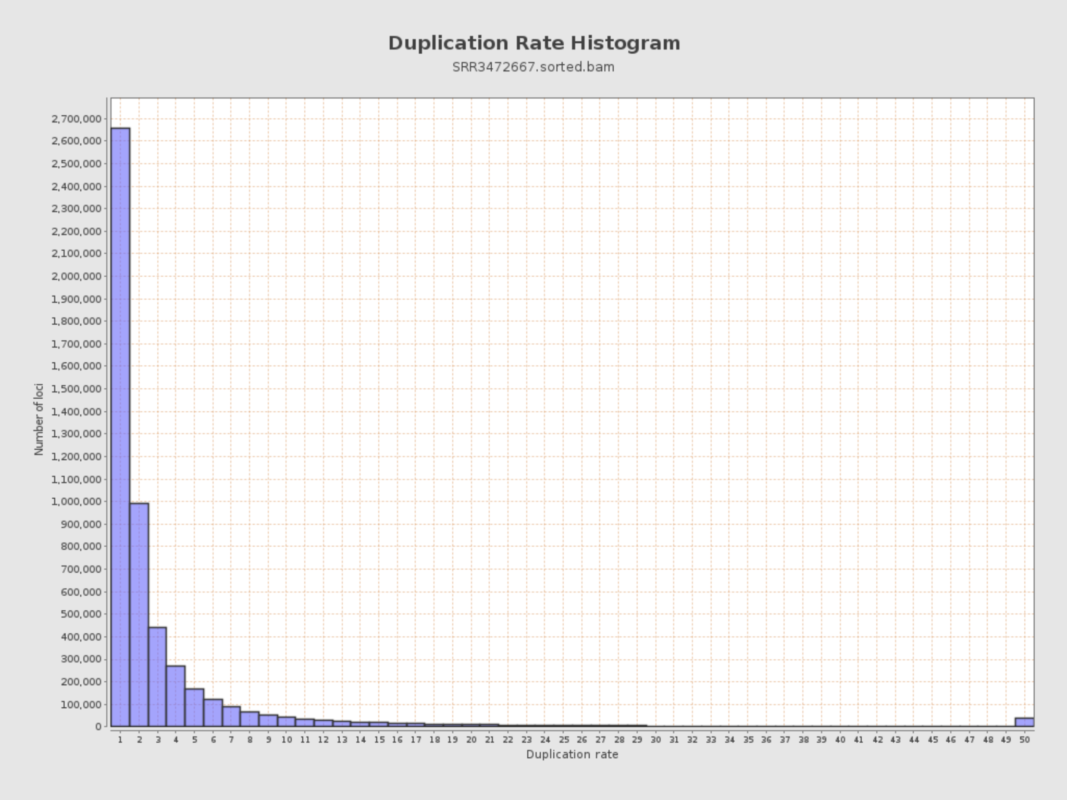
5. Results : Coverage Histogram (0-50X)



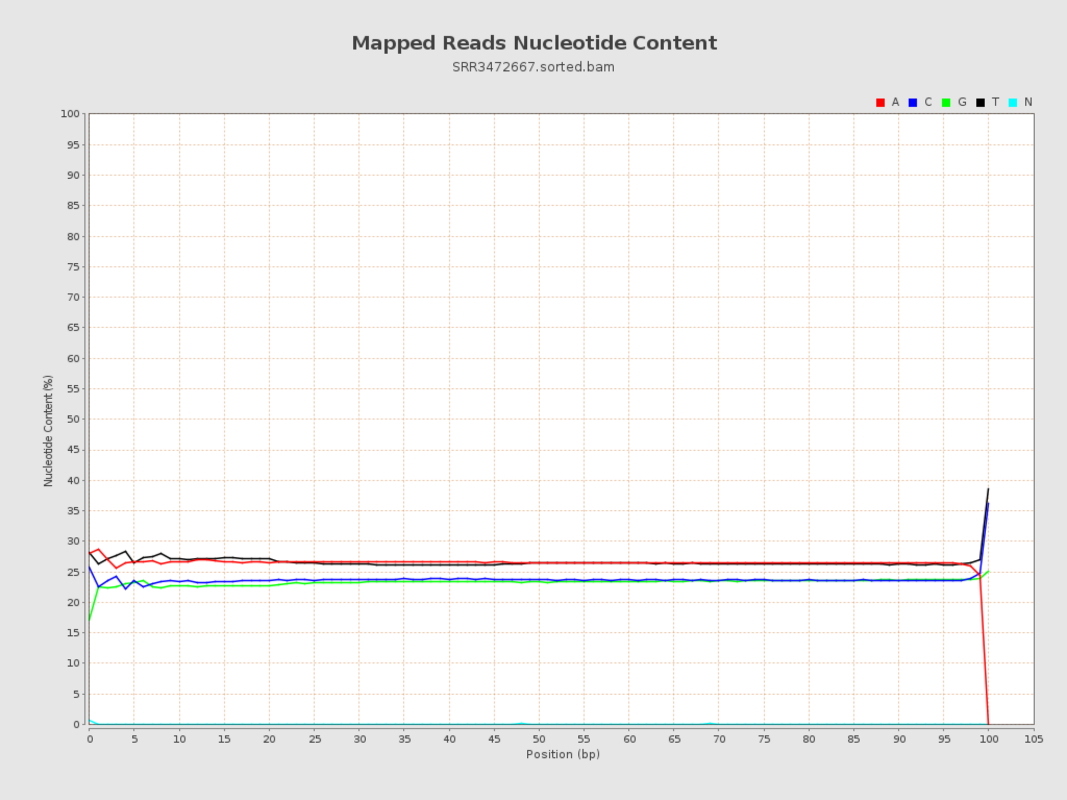
6. Results : Genome Fraction Coverage



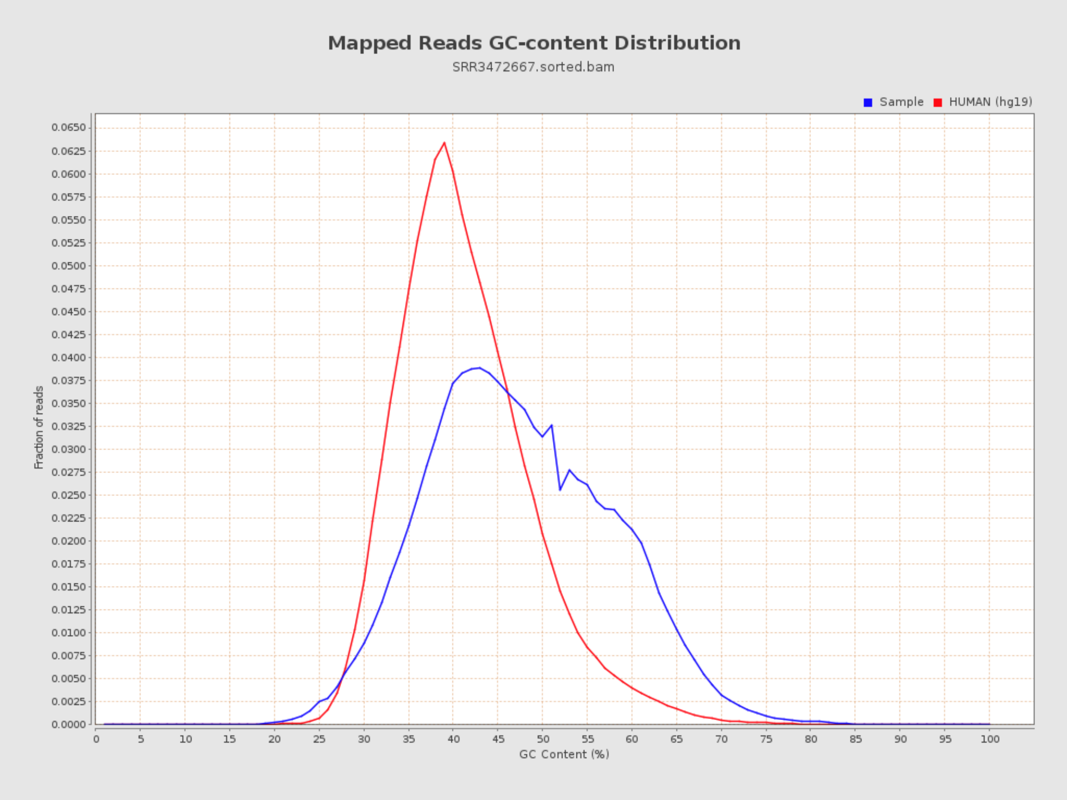
7. Results : Duplication Rate Histogram



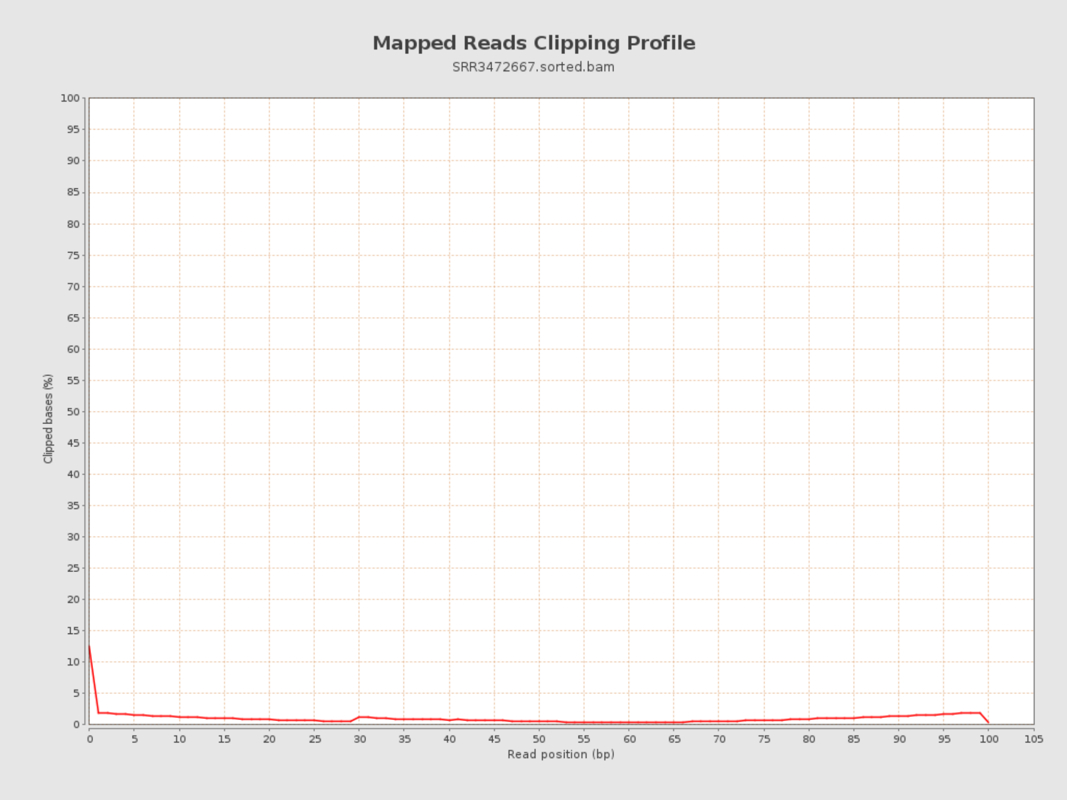
8. Results : Mapped Reads Nucleotide Content



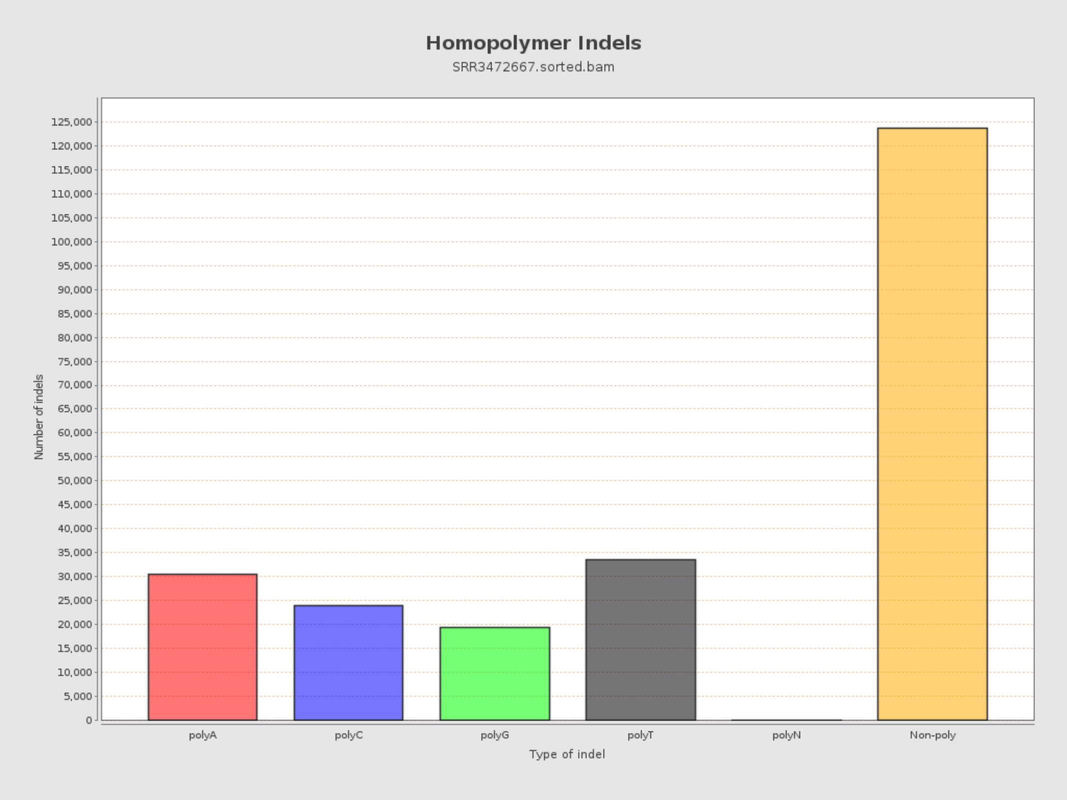
9. Results : Mapped Reads GC-content Distribution



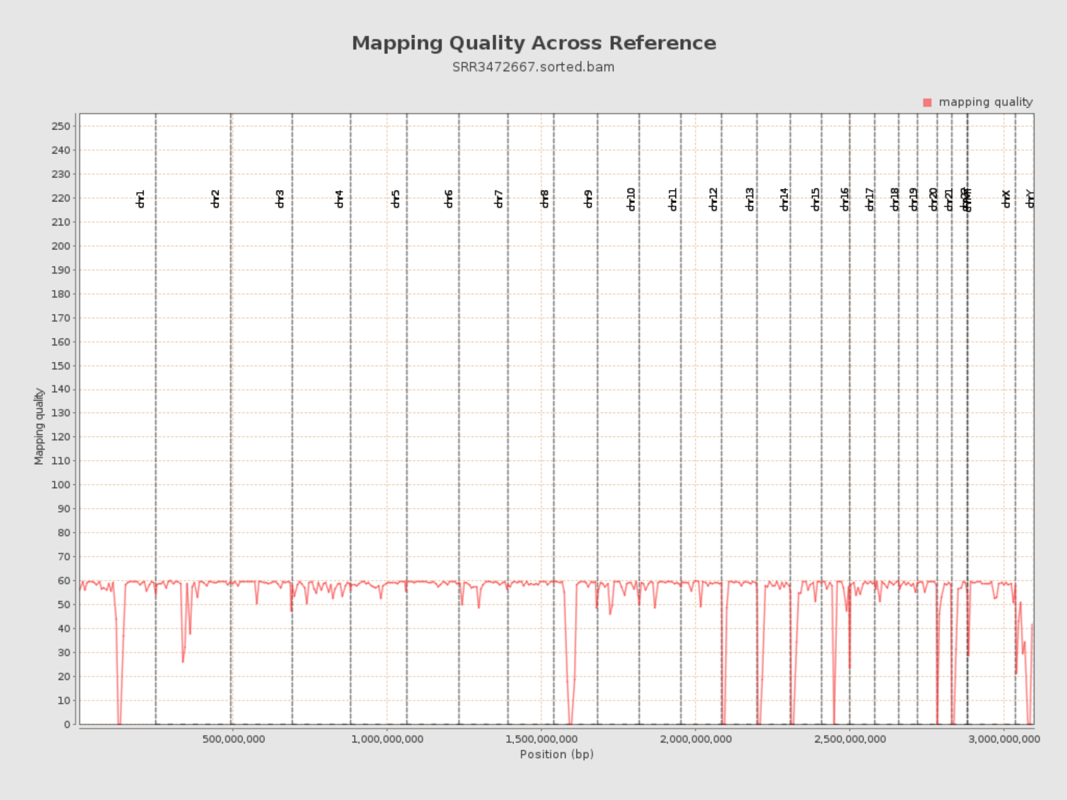
10. Results : Mapped Reads Clipping Profile



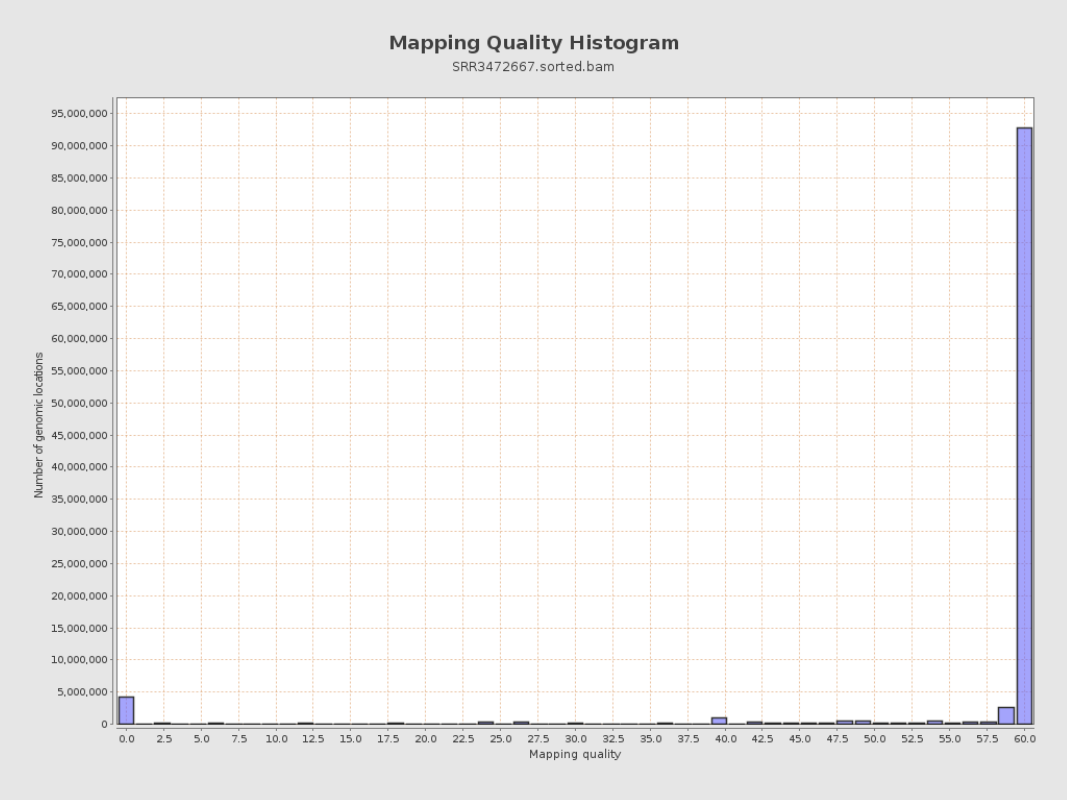
11. Results : Homopolymer Indels



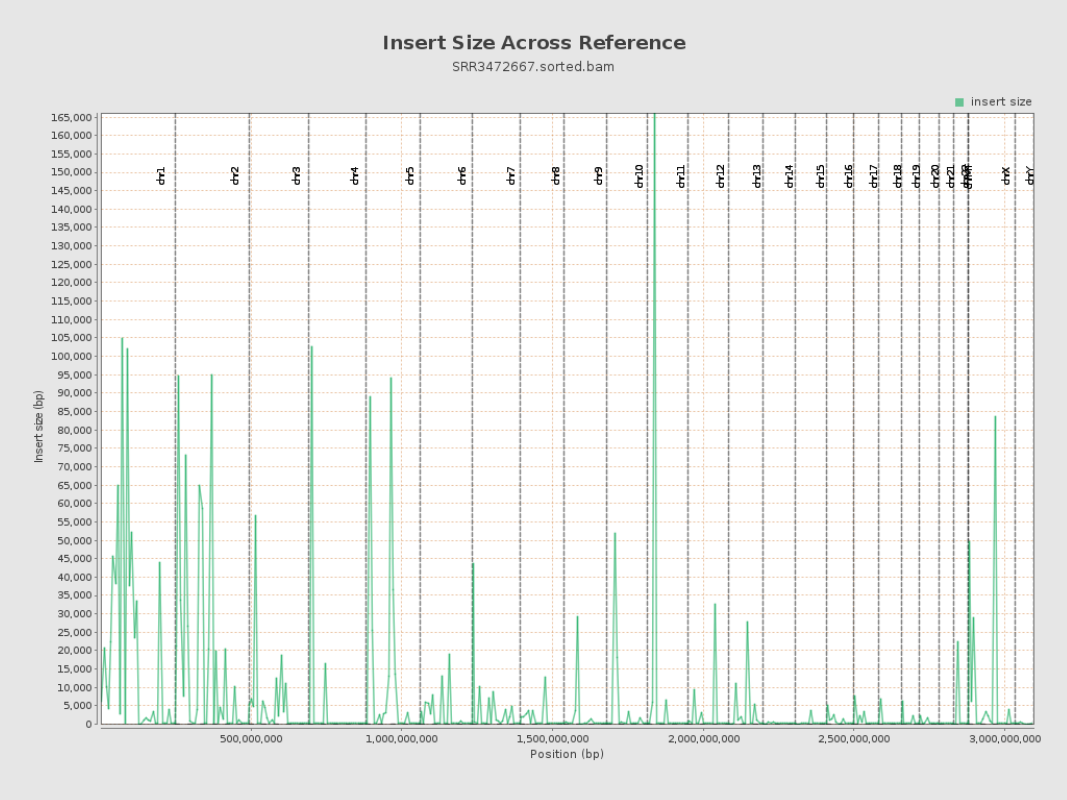
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram