Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 09:12:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472609.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_SRR3472609 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472609_1.fastq.gz SRR3472609_2.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 09:12:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472609.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,115,858
Mapped reads	18,002,052 / 99.37%
Unmapped reads	113,806 / 0.63%
Mapped paired reads	18,002,052 / 99.37%
Mapped reads, first in pair	9,023,120 / 49.81%
Mapped reads, second in pair	8,978,932 / 49.56%
Mapped reads, both in pair	17,926,976 / 98.96%
Mapped reads, singletons	75,076 / 0.41%
Secondary alignments	0
Supplementary alignments	78,944 / 0.44%
Read min/max/mean length	30 / 101 / 99.62
Duplicated reads (estimated)	12,474,635 / 68.86%
Duplication rate	50.88%
Clipped reads	1,207,797 / 6.67%

2.2. ACGT Content

Number/percentage of A's	468,015,901 / 26.43%
Number/percentage of C's	419,234,646 / 23.68%
Number/percentage of T's	469,875,404 / 26.54%
Number/percentage of G's	413,261,703 / 23.34%
Number/percentage of N's	331,603 / 0.02%

GC Percentage	47.01%

2.3. Coverage

Mean	0.5721
Standard Deviation	23.8111

2.4. Mapping Quality

Mean Mapping Quality	54.71

2.5. Insert size

Mean	19,192.02
Standard Deviation	1,407,592.9
P25/Median/P75	148 / 203 / 272

2.6. Mismatches and indels

General error rate	0.57%
Mismatches	9,917,256
Insertions	99,768
Mapped reads with at least one insertion	0.55%
Deletions	91,783
Mapped reads with at least one deletion	0.5%
Homopolymer indels	46.5%

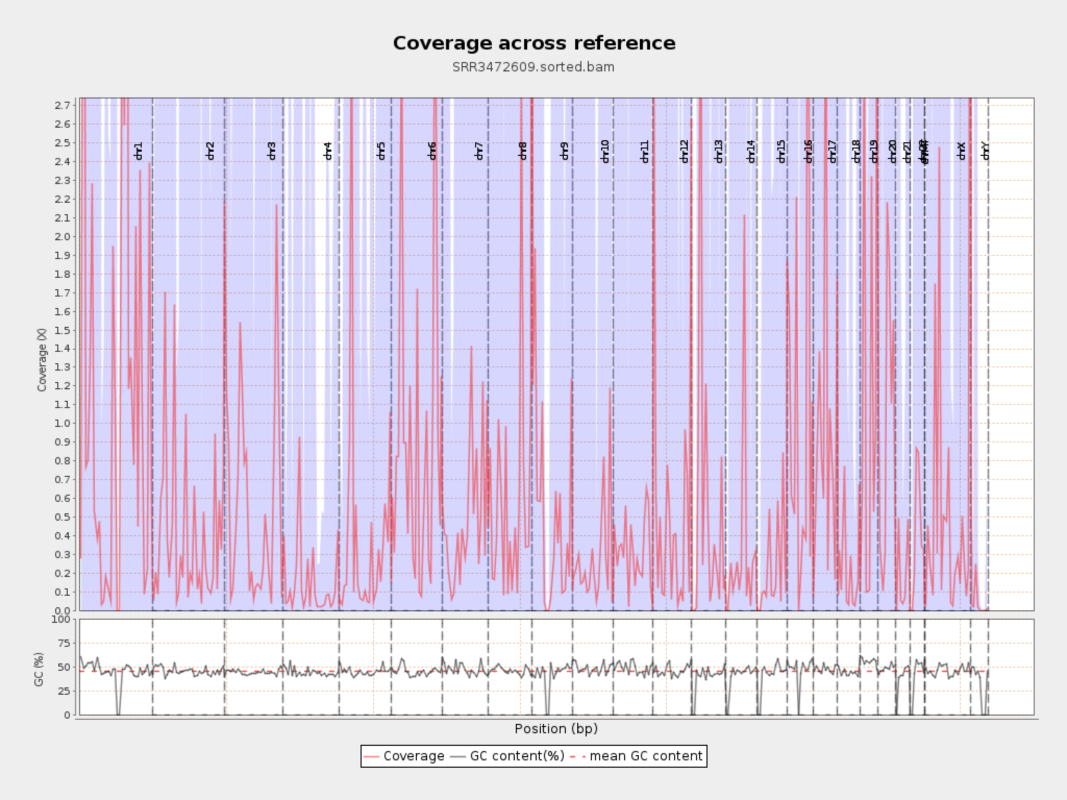
2.7. Chromosome stats

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

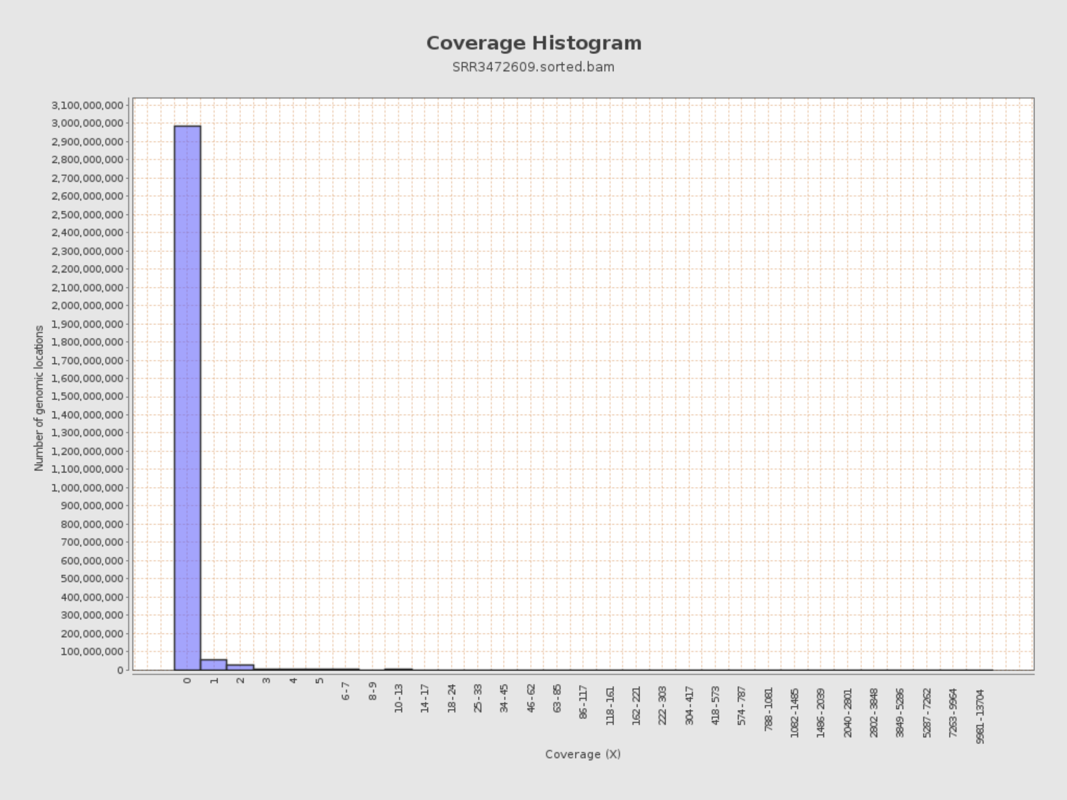
		bases	coverage	deviation
chr1	249250621	315455794	1.2656	42.3383
chr2	243199373	98462132	0.4049	16.3571
chr3	198022430	120119776	0.6066	18.6523
chr4	191154276	27131635	0.1419	6.6024
chr5	180915260	71995975	0.398	21.0304
chr6	171115067	155515991	0.9088	35.2966
chr7	159138663	80796655	0.5077	17.405
chr8	146364022	87420358	0.5973	19.737
chr9	141213431	81080277	0.5742	16.4336
chr10	135534747	37618746	0.2776	11.6995
chr11	135006516	44409322	0.3289	11.6346
chr12	133851895	72360643	0.5406	17.6236
chr13	115169878	68064655	0.591	25.7799
chr14	107349540	32132860	0.2993	12.686
chr15	102531392	22095860	0.2155	8.7525
chr16	90354753	104515114	1.1567	40.5485
chr17	81195210	82788705	1.0196	28.4676
chr18	78077248	17487175	0.224	11.3716
chr19	59128983	68003556	1.1501	46.2472
chr20	63025520	64077605	1.0167	26.6964
chr21	48129895	10045627	0.2087	10.2965
chr22	51304566	19876426	0.3874	11.5293
chrMT	16571	810	0.0489	0.2228
chrX	155270560	86990924	0.5603	30.0368

chrY	59373566	2486295	0.0419	4.5805

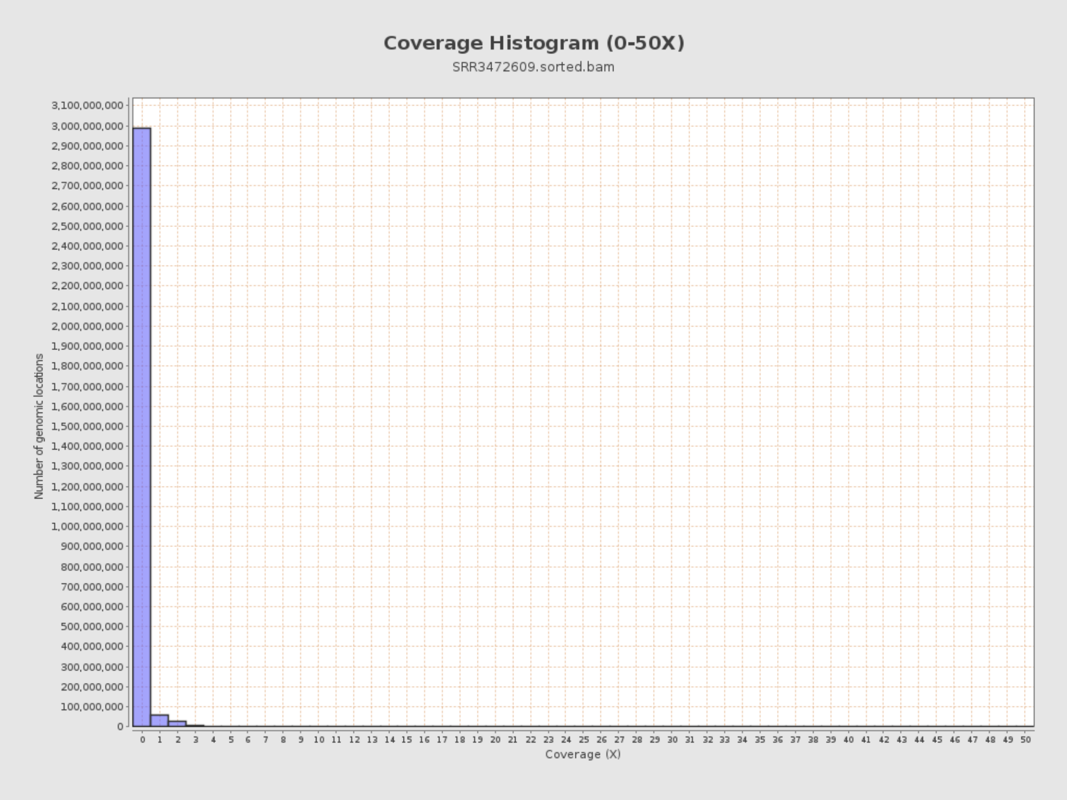
3. Results : Coverage across reference



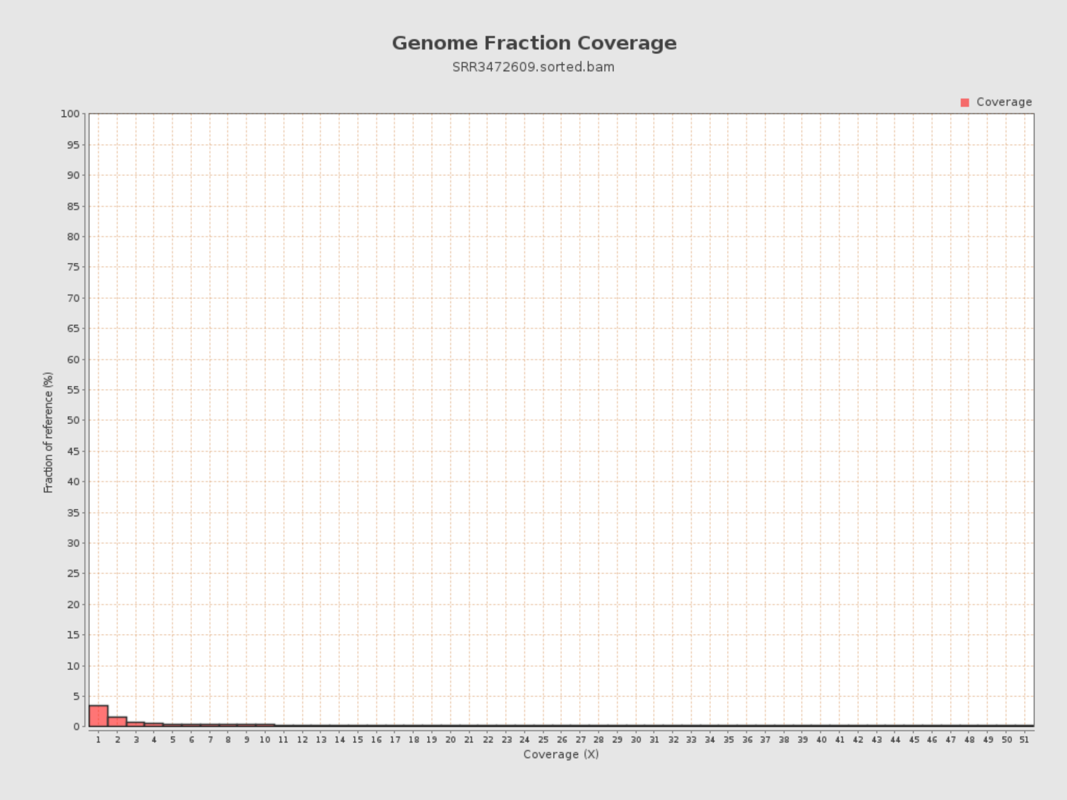
4. Results : Coverage Histogram



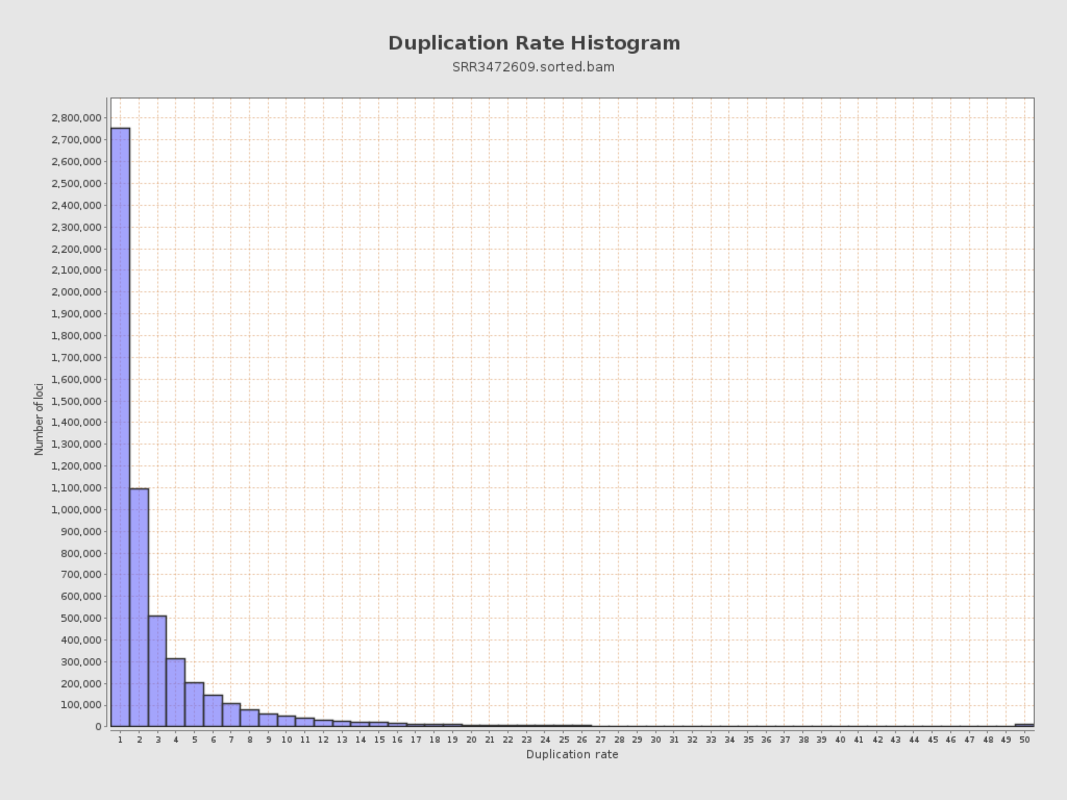
5. Results : Coverage Histogram (0-50X)



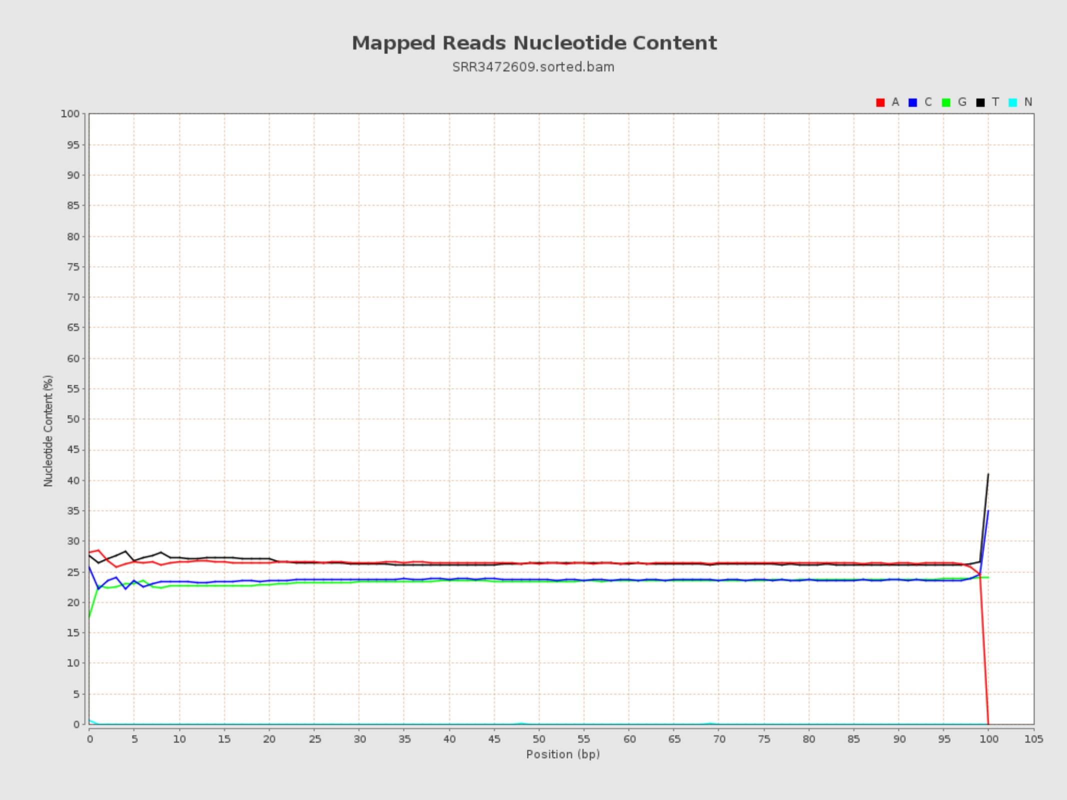
6. Results : Genome Fraction Coverage



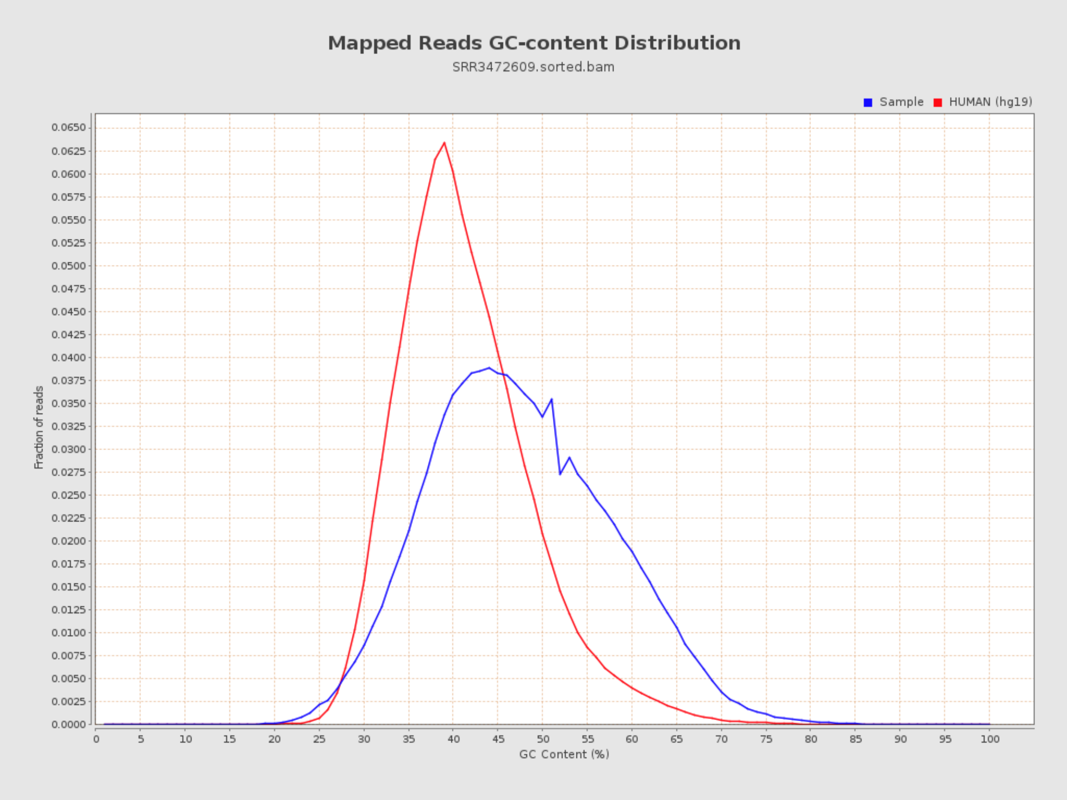
7. Results : Duplication Rate Histogram



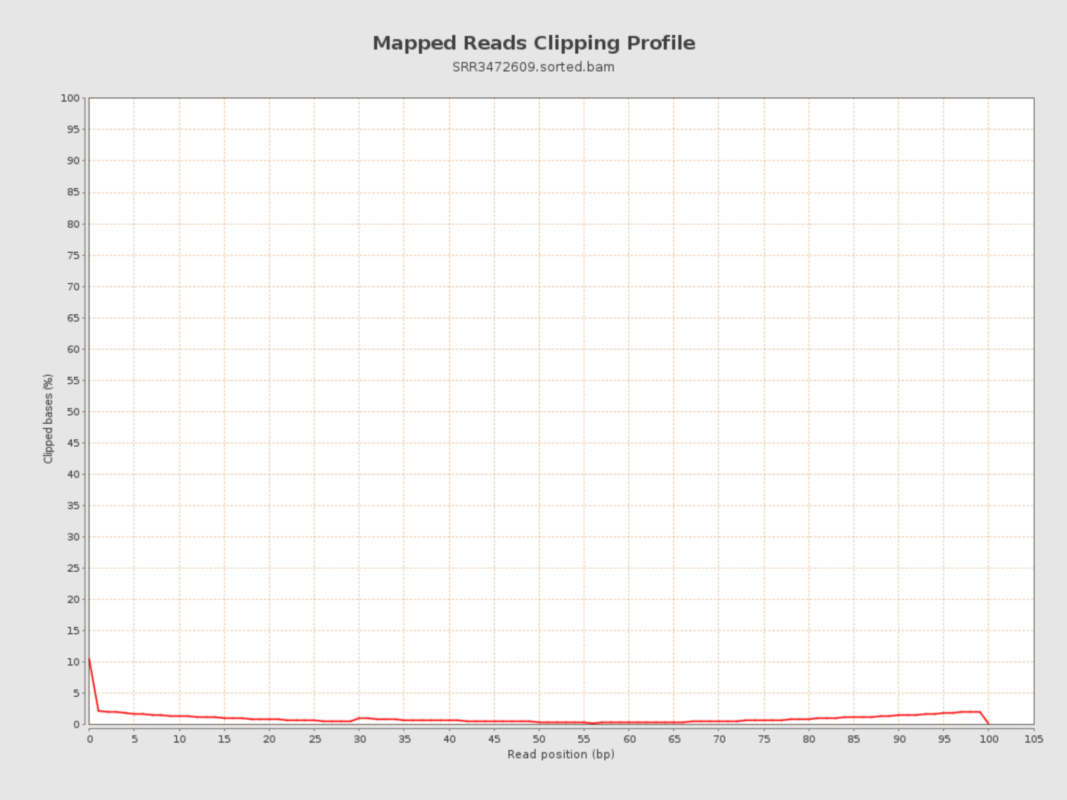
8. Results : Mapped Reads Nucleotide Content



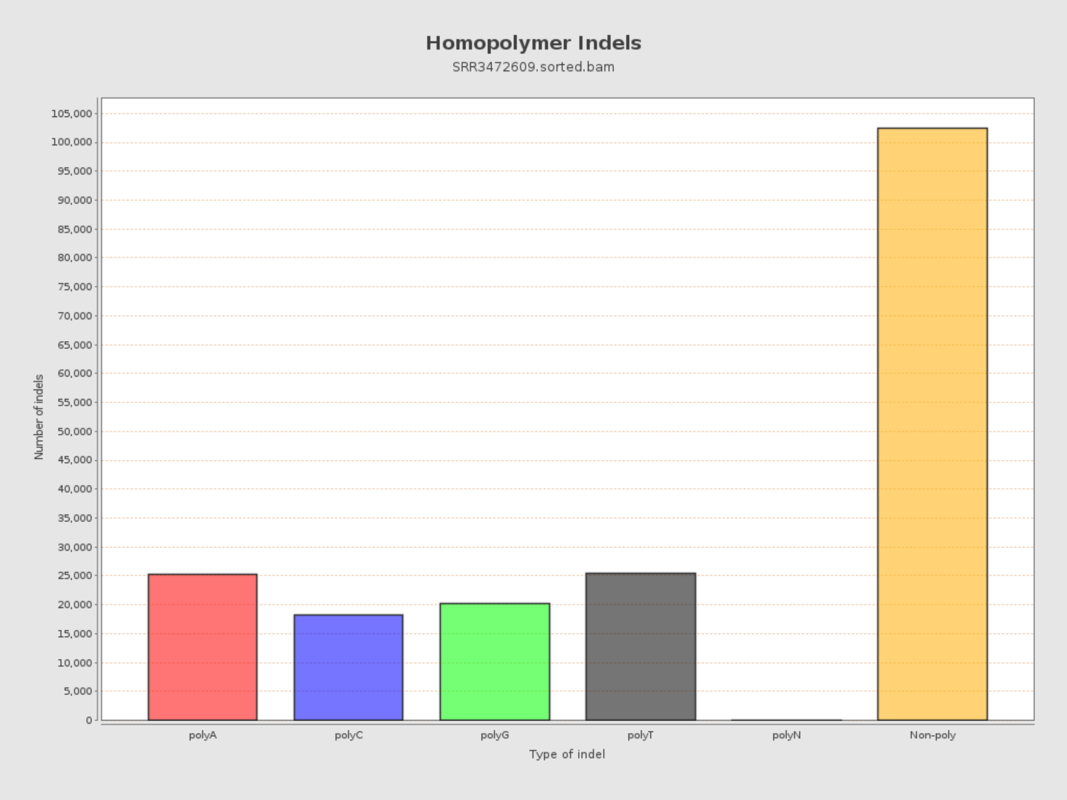
9. Results : Mapped Reads GC-content Distribution



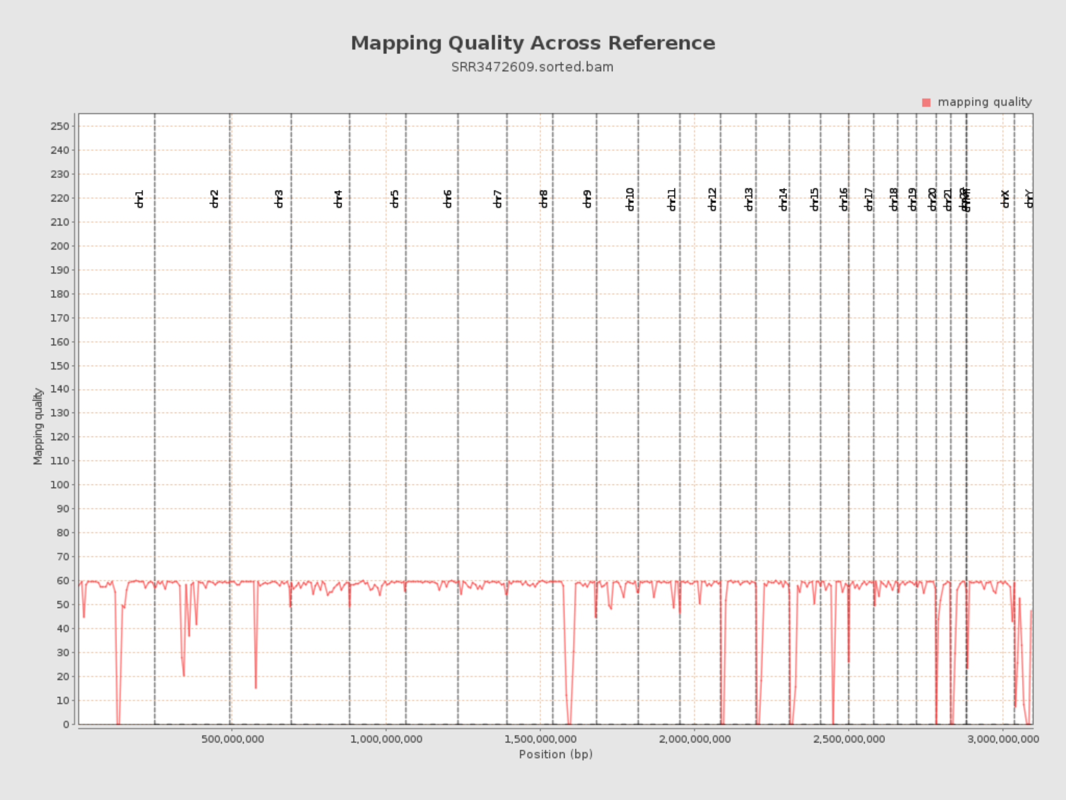
10. Results : Mapped Reads Clipping Profile



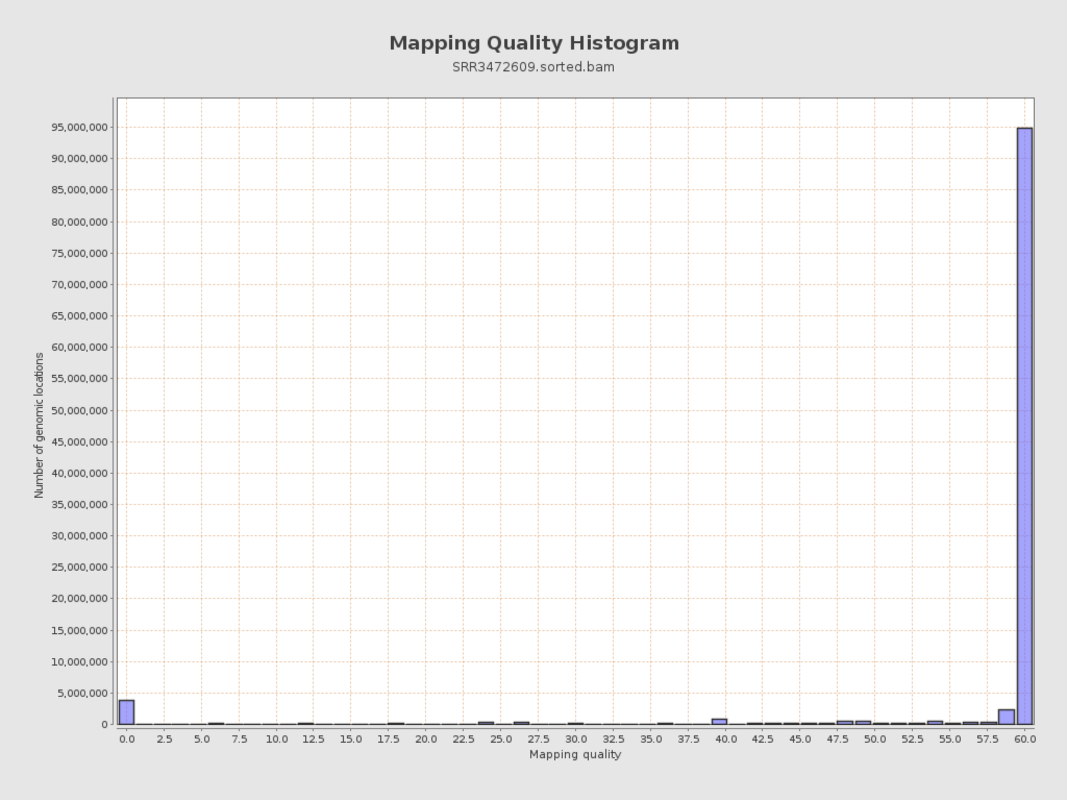
11. Results : Homopolymer Indels



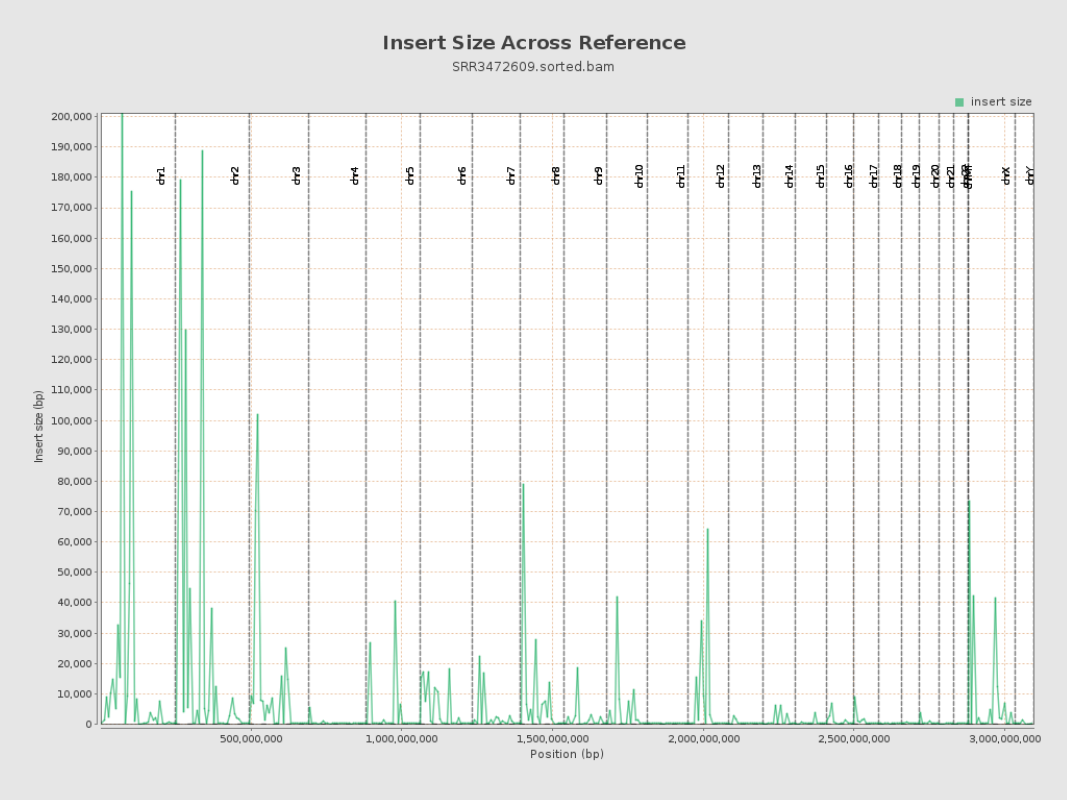
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram