Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/29 22:48:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472731.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_SRR3472731 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472731_1.fastq.gz SRR3472731_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 29 22:47:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472731.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,705,414
Mapped reads	18,527,769 / 99.05%
Unmapped reads	177,645 / 0.95%
Mapped paired reads	18,527,769 / 99.05%
Mapped reads, first in pair	9,300,774 / 49.72%
Mapped reads, second in pair	9,226,995 / 49.33%
Mapped reads, both in pair	18,416,958 / 98.46%
Mapped reads, singletons	110,811 / 0.59%
Secondary alignments	0
Supplementary alignments	74,229 / 0.4%
Read min/max/mean length	30 / 100 / 100.16
Duplicated reads (estimated)	11,969,143 / 63.99%
Duplication rate	47.59%
Clipped reads	1,321,628 / 7.07%

2.2. ACGT Content

Number/percentage of A's	500,401,848 / 27.35%
Number/percentage of C's	417,162,678 / 22.8%
Number/percentage of T's	497,546,872 / 27.19%
Number/percentage of G's	414,099,728 / 22.63%
Number/percentage of N's	351,942 / 0.02%

GC Percentage	45.44%

2.3. Coverage

Mean	0.5911
Standard Deviation	20.1739

2.4. Mapping Quality

Mean Mapping Quality	55.17

2.5. Insert size

Mean	26,053.24
Standard Deviation	1,540,544.45
P25/Median/P75	180 / 248 / 333

2.6. Mismatches and indels

General error rate	0.65%
Mismatches	11,763,700
Insertions	103,571
Mapped reads with at least one insertion	0.55%
Deletions	101,445
Mapped reads with at least one deletion	0.54%
Homopolymer indels	45.72%

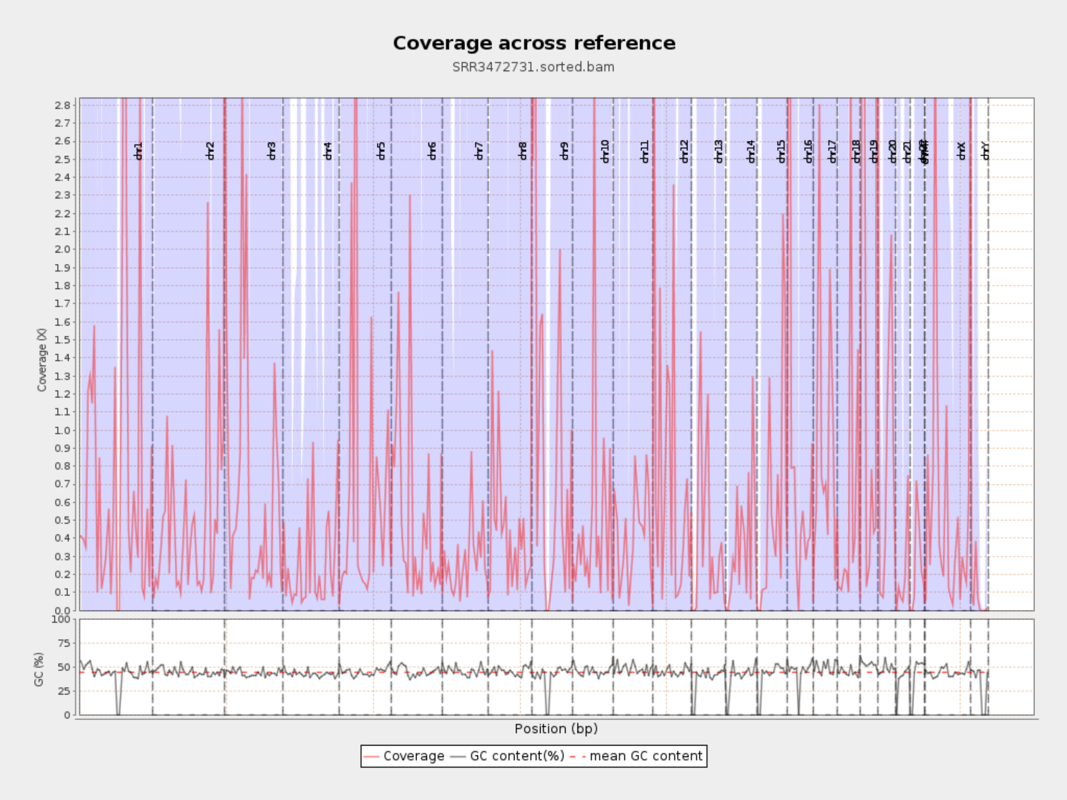
2.7. Chromosome stats

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

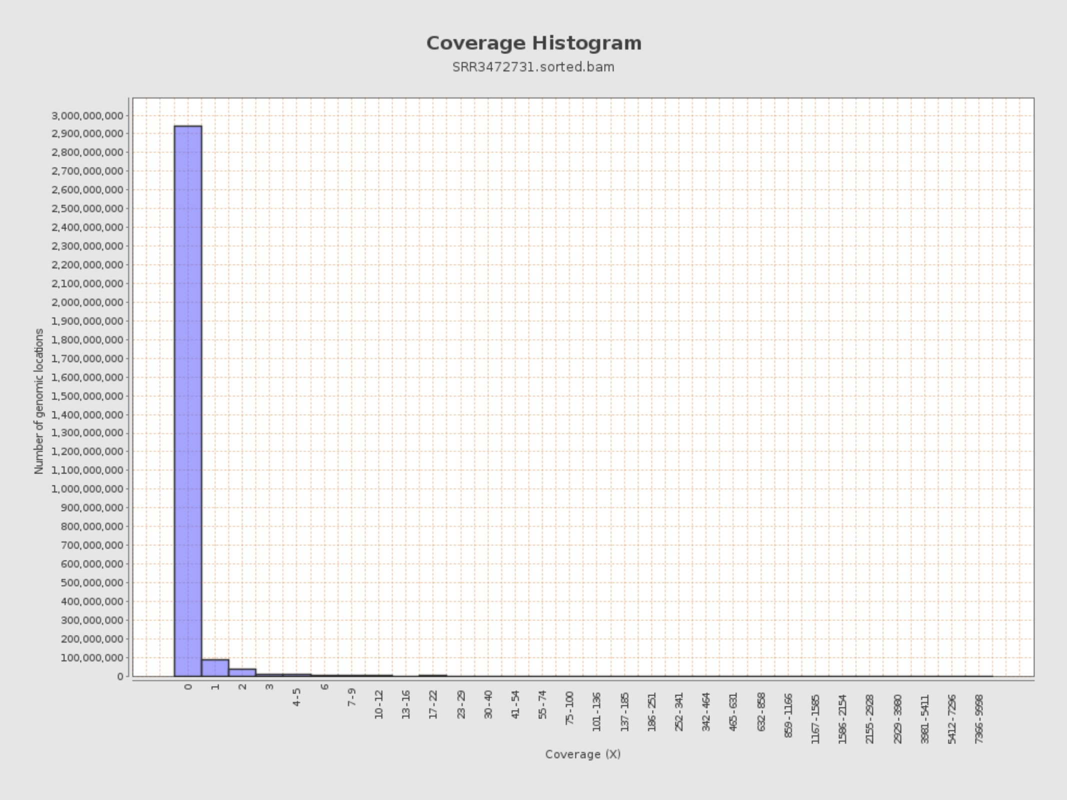
		bases	coverage	deviation
chr1	249250621	205727006	0.8254	26.2577
chr2	243199373	116407828	0.4787	16.0062
chr3	198022430	144527903	0.7299	14.9041
chr4	191154276	50032933	0.2617	10.7789
chr5	180915260	128152400	0.7084	23.0993
chr6	171115067	89658264	0.524	14.8015
chr7	159138663	44736857	0.2811	8.5049
chr8	146364022	64367129	0.4398	15.6942
chr9	141213431	137169283	0.9714	24.5152
chr10	135534747	70781458	0.5222	26.6111
chr11	135006516	57878280	0.4287	13.8142
chr12	133851895	109736813	0.8198	25.0245
chr13	115169878	48151221	0.4181	17.0882
chr14	107349540	38444221	0.3581	15.5065
chr15	102531392	61361266	0.5985	18.4934
chr16	90354753	81182329	0.8985	23.8547
chr17	81195210	74635634	0.9192	26.2045
chr18	78077248	47562880	0.6092	33.5968
chr19	59128983	86150733	1.457	40.0212
chr20	63025520	53465823	0.8483	30.3028
chr21	48129895	9315635	0.1936	7.4831
chr22	51304566	13288560	0.259	6.9416
chrMT	16571	4224	0.2549	0.6844
chrX	155270560	92715979	0.5971	15.8577

chrY	59373566	4366211	0.0735	3.5092

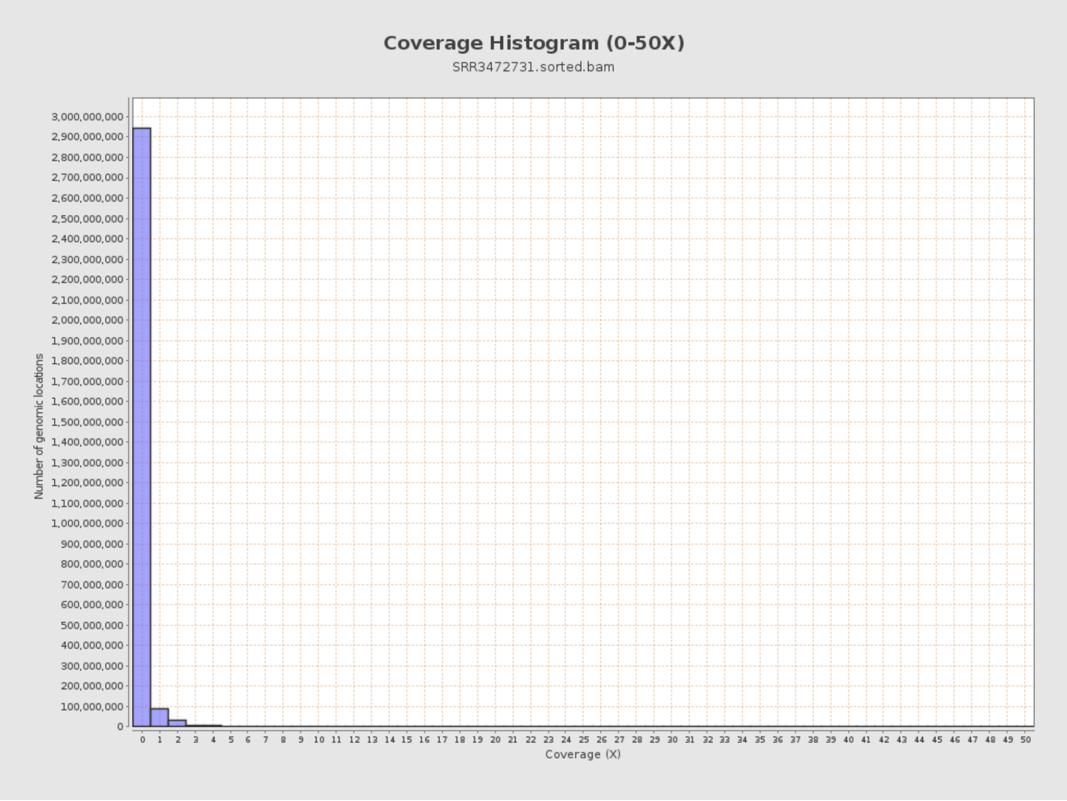
3. Results : Coverage across reference



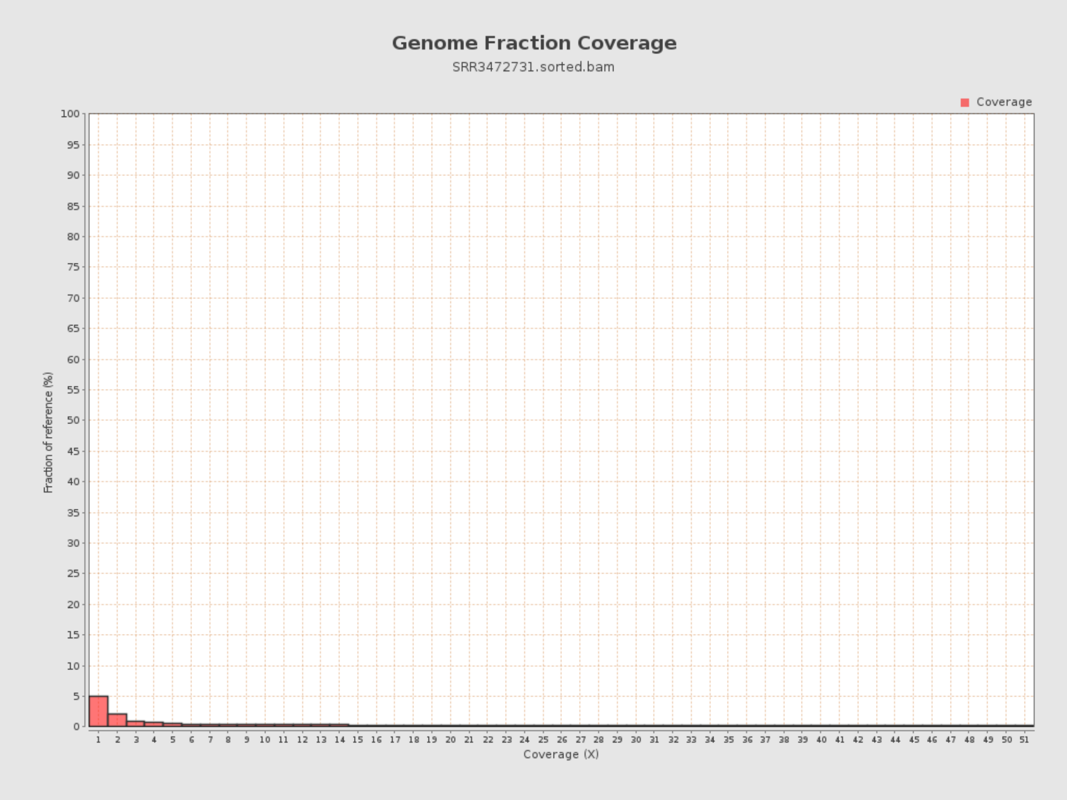
4. Results : Coverage Histogram



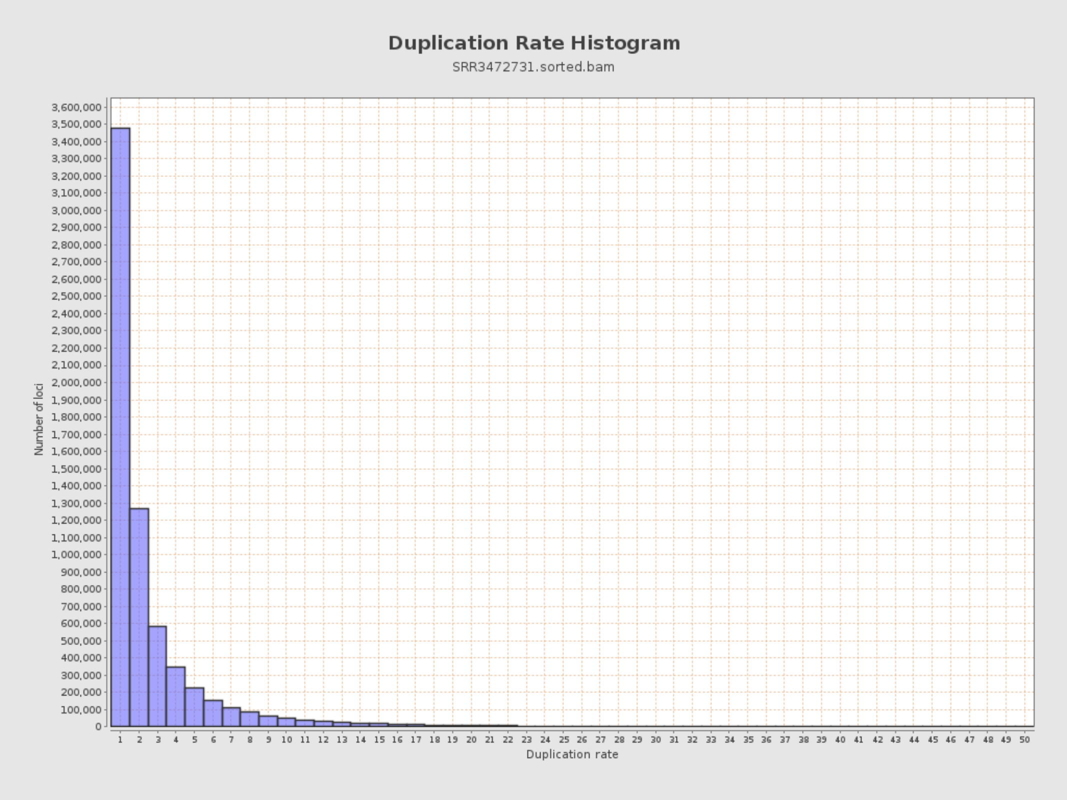
5. Results : Coverage Histogram (0-50X)



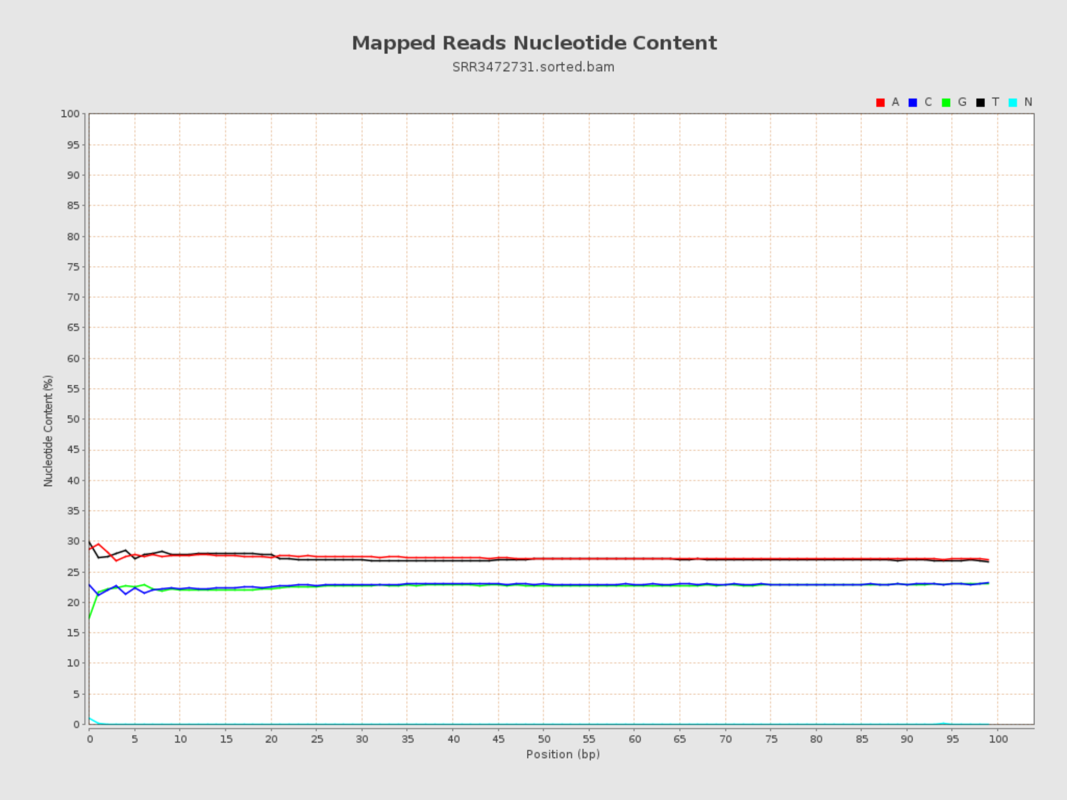
6. Results : Genome Fraction Coverage



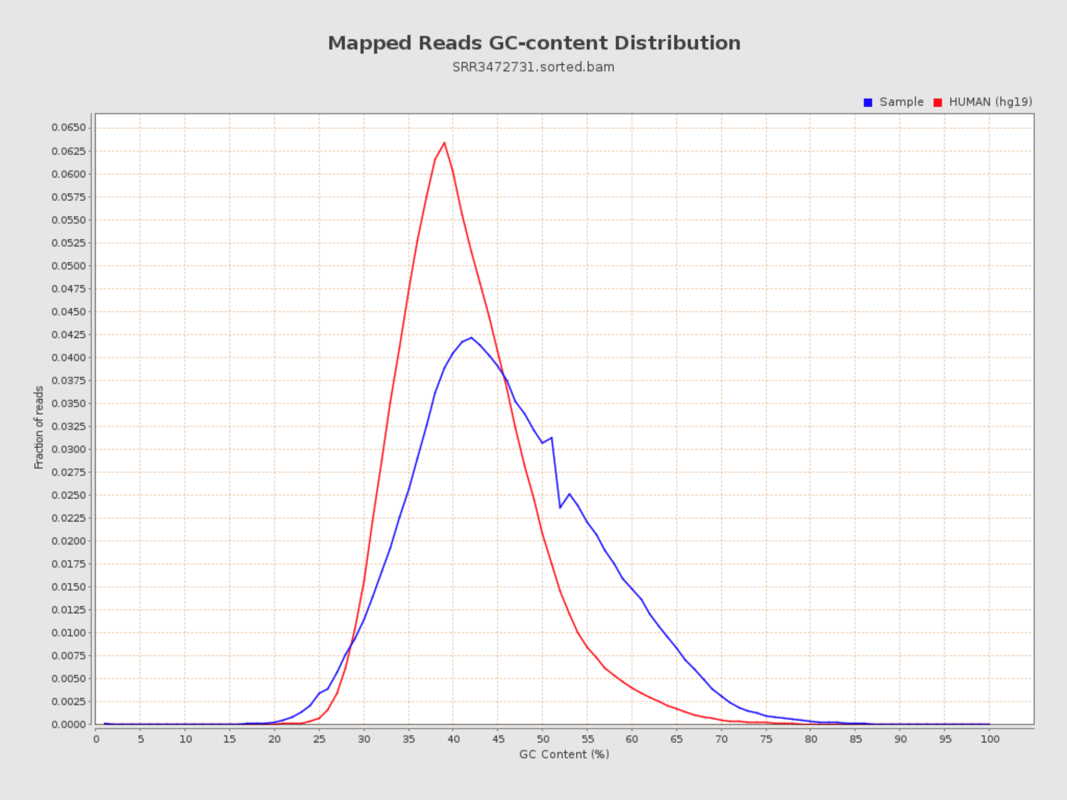
7. Results : Duplication Rate Histogram



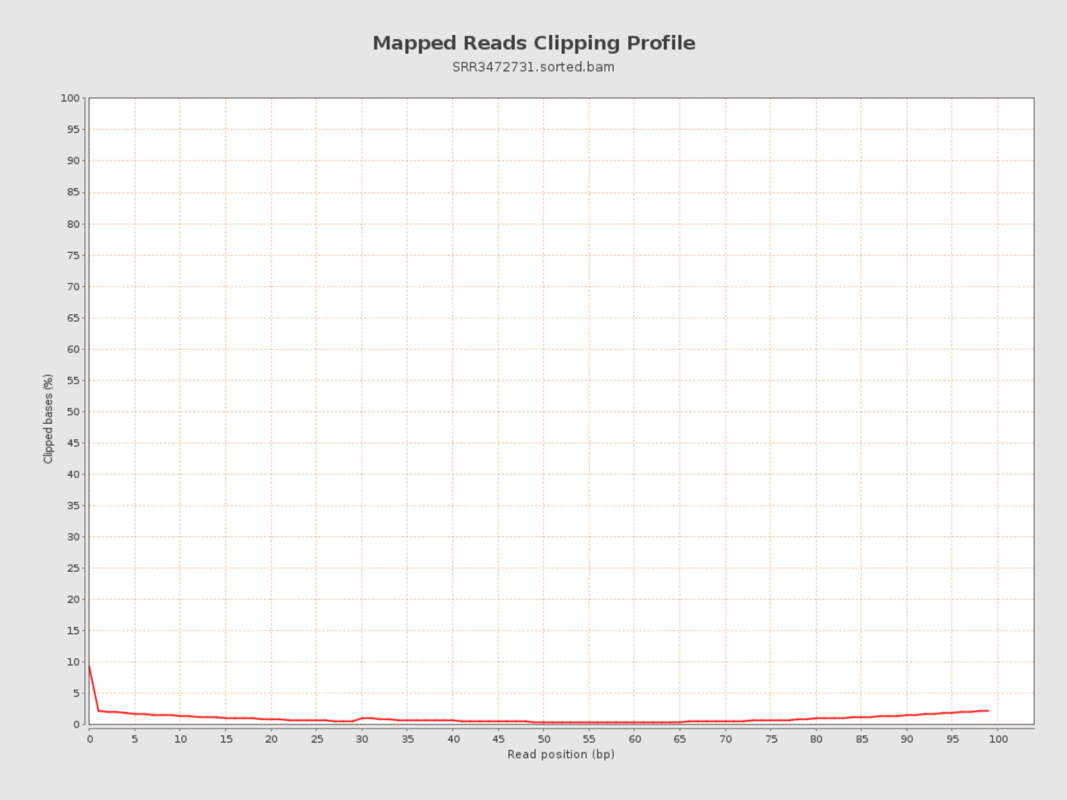
8. Results : Mapped Reads Nucleotide Content



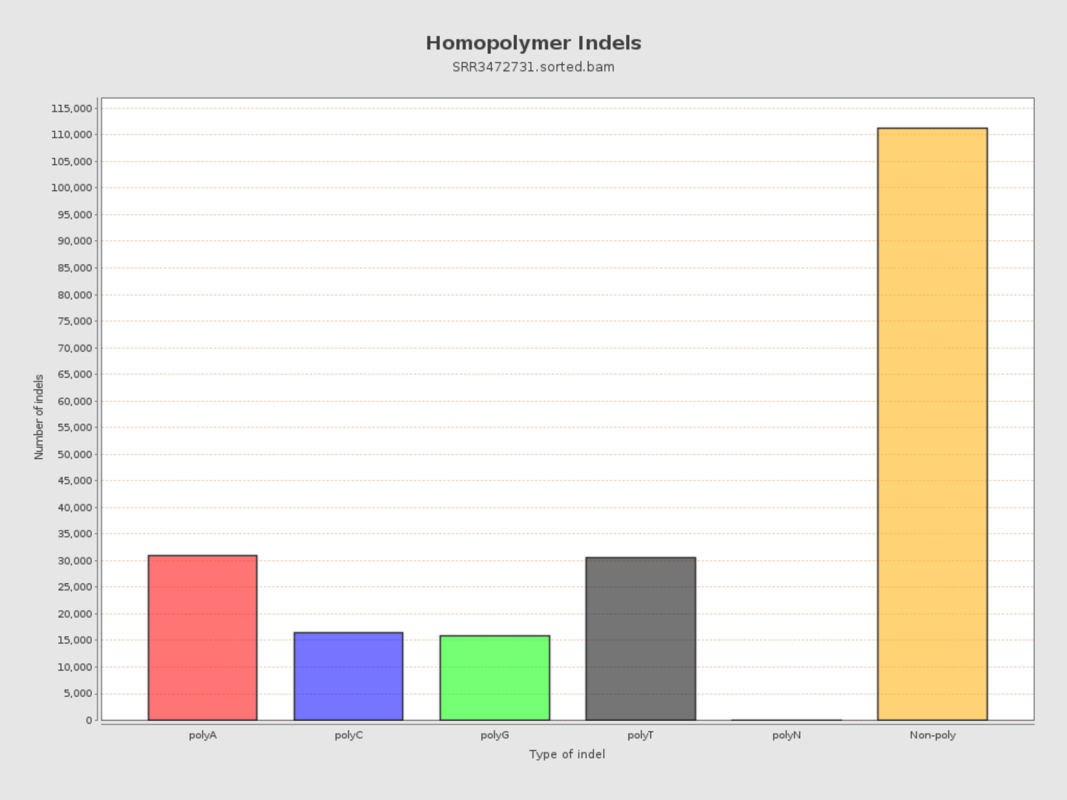
9. Results : Mapped Reads GC-content Distribution



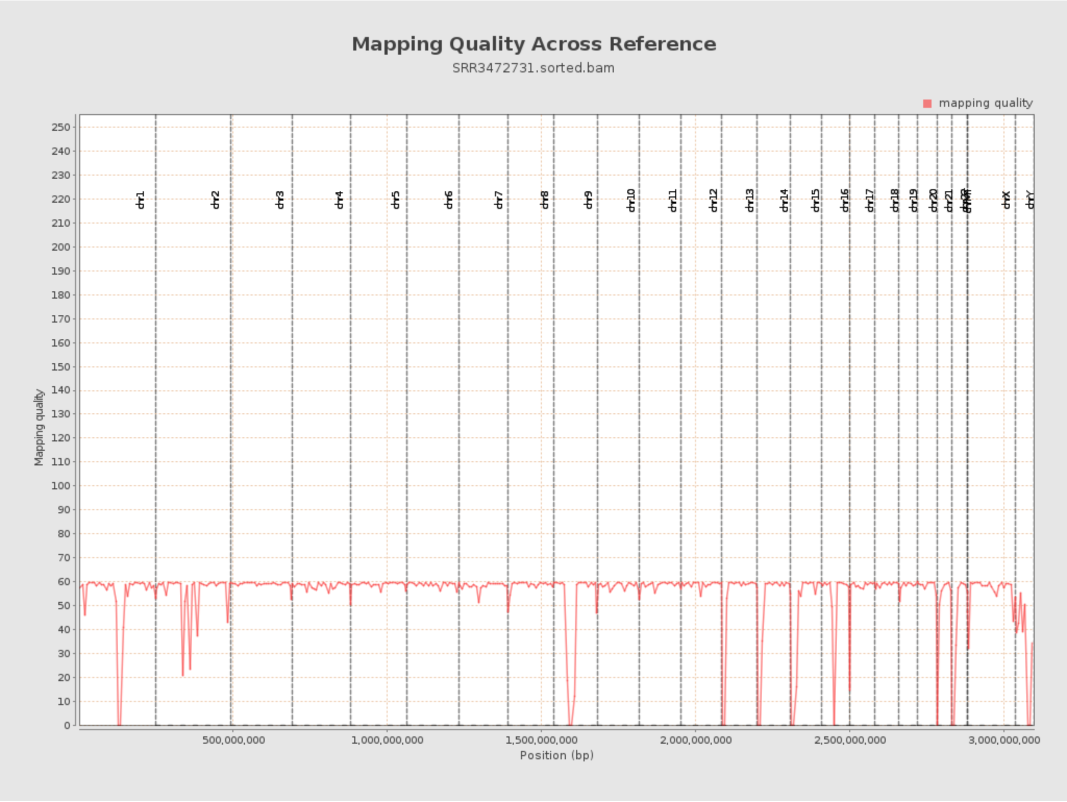
10. Results : Mapped Reads Clipping Profile



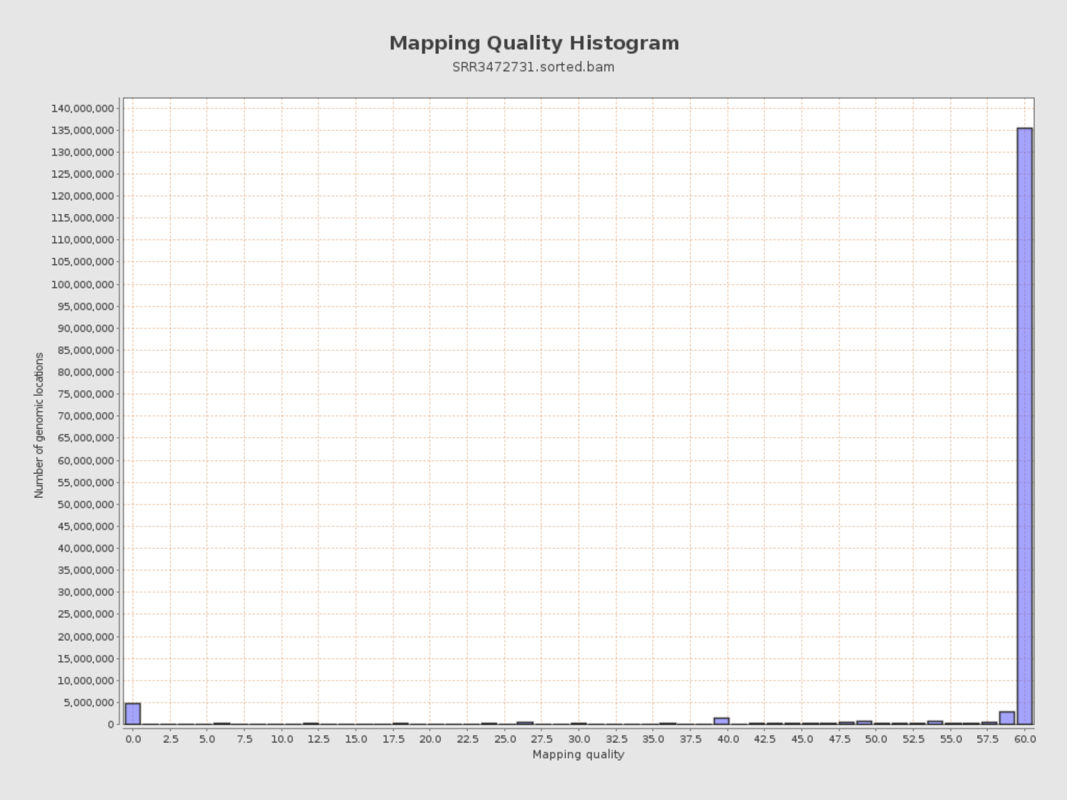
11. Results : Homopolymer Indels



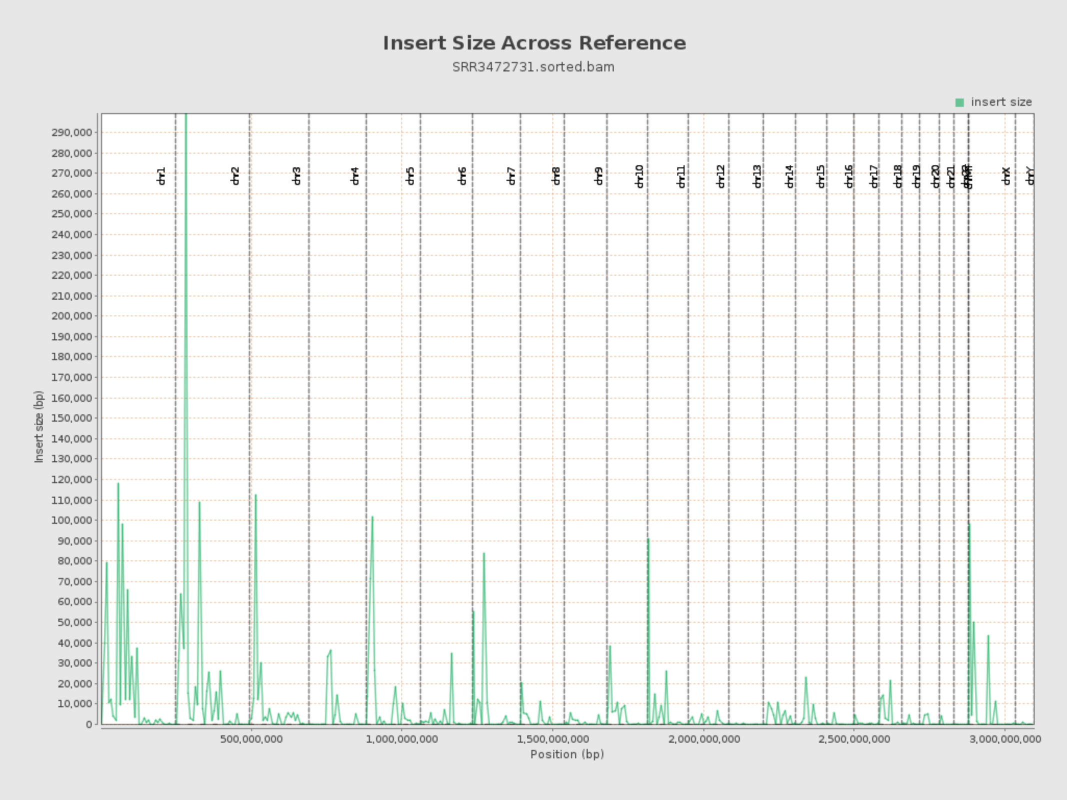
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram