Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/29 04:03:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472672.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_SRR3472672 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472672_1.fastq.gz SRR3472672_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 29 04:03:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472672.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,426,340
Mapped reads	18,290,844 / 99.26%
Unmapped reads	135,496 / 0.74%
Mapped paired reads	18,290,844 / 99.26%
Mapped reads, first in pair	9,170,295 / 49.77%
Mapped reads, second in pair	9,120,549 / 49.5%
Mapped reads, both in pair	18,200,842 / 98.78%
Mapped reads, singletons	90,002 / 0.49%
Secondary alignments	0
Supplementary alignments	143,213 / 0.78%
Read min/max/mean length	30 / 101 / 99.83
Duplicated reads (estimated)	13,197,271 / 71.62%
Duplication rate	49.28%
Clipped reads	1,407,232 / 7.64%

2.2. ACGT Content

Number/percentage of A's	485,057,508 / 26.96%
Number/percentage of C's	417,384,689 / 23.2%
Number/percentage of T's	485,316,715 / 26.98%
Number/percentage of G's	410,766,015 / 22.83%
Number/percentage of N's	334,097 / 0.02%

GC Percentage	46.04%

2.3. Coverage

Mean	0.5812
Standard Deviation	30.6848

2.4. Mapping Quality

Mean Mapping Quality	54.77

2.5. Insert size

Mean	21,232.35
Standard Deviation	1,397,992.1
P25/Median/P75	160 / 219 / 292

2.6. Mismatches and indels

General error rate	0.63%
Mismatches	11,017,941
Insertions	133,659
Mapped reads with at least one insertion	0.72%
Deletions	101,199
Mapped reads with at least one deletion	0.54%
Homopolymer indels	46.36%

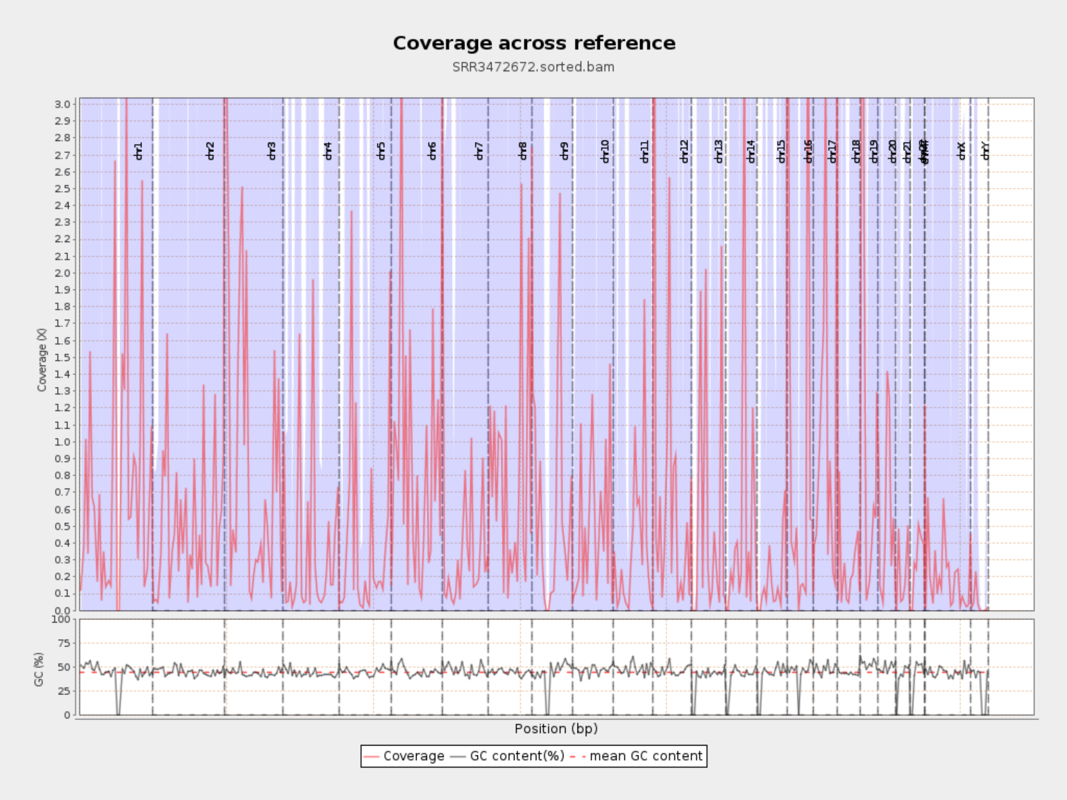
2.7. Chromosome stats

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

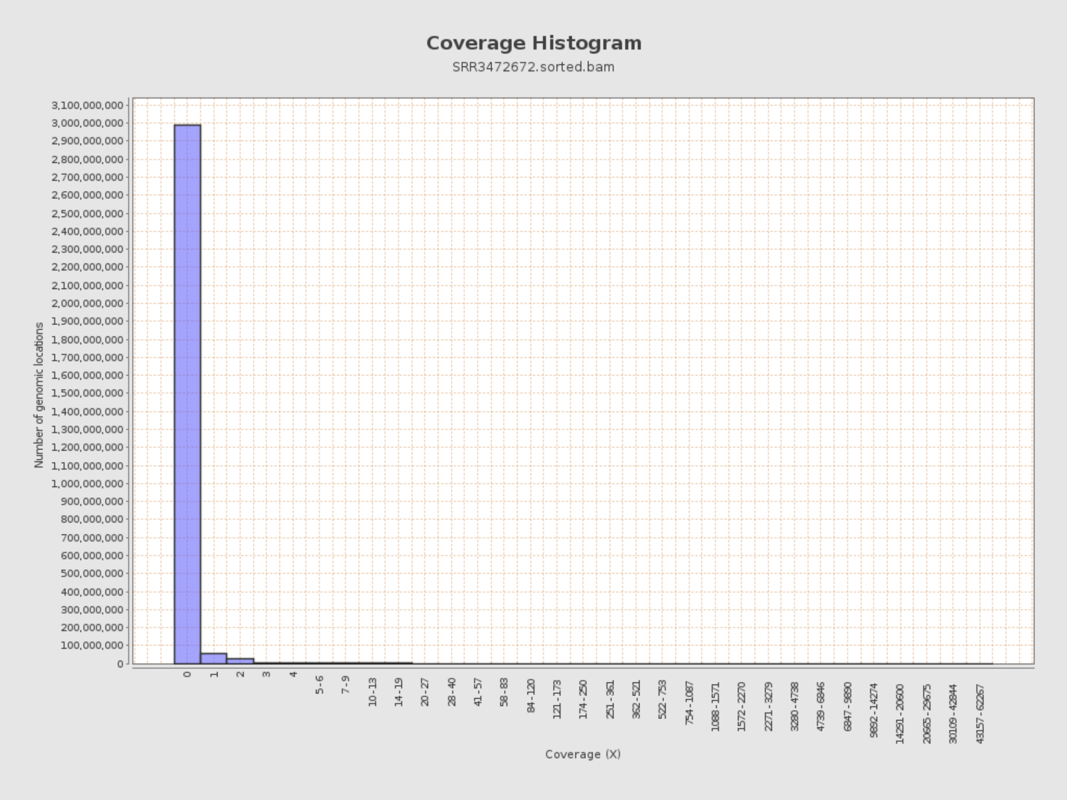
		bases	**coverage**	**deviation**
chr1	249250621	194034485	0.7785	28.5948
chr2	243199373	119944339	0.4932	24.4748
chr3	198022430	188063314	0.9497	29.9242
chr4	191154276	66425881	0.3475	19.4634
chr5	180915260	77666293	0.4293	23.8145
chr6	171115067	146424782	0.8557	33.4849
chr7	159138663	62459853	0.3925	23.5974
chr8	146364022	114583751	0.7829	33.0133
chr9	141213431	87799567	0.6218	25.0182
chr10	135534747	69034449	0.5093	30.2078
chr11	135006516	52634321	0.3899	29.3102
chr12	133851895	108994929	0.8143	32.6389
chr13	115169878	64077047	0.5564	32.0194
chr14	107349540	53459367	0.498	23.0362
chr15	102531392	18697195	0.1824	8.5413
chr16	90354753	97878423	1.0833	48.923
chr17	81195210	90920216	1.1198	79.091
chr18	78077248	20272441	0.2596	10.633
chr19	59128983	72202541	1.2211	67.61
chr20	63025520	36704267	0.5824	27.2584
chr21	48129895	10156780	0.211	10.1114
chr22	51304566	14521514	0.283	10.5427
chrMT	16571	20226	1.2206	1.432
chrX	155270560	29452441	0.1897	19.3687

chrY	59373566	2661390	0.0448	3.102

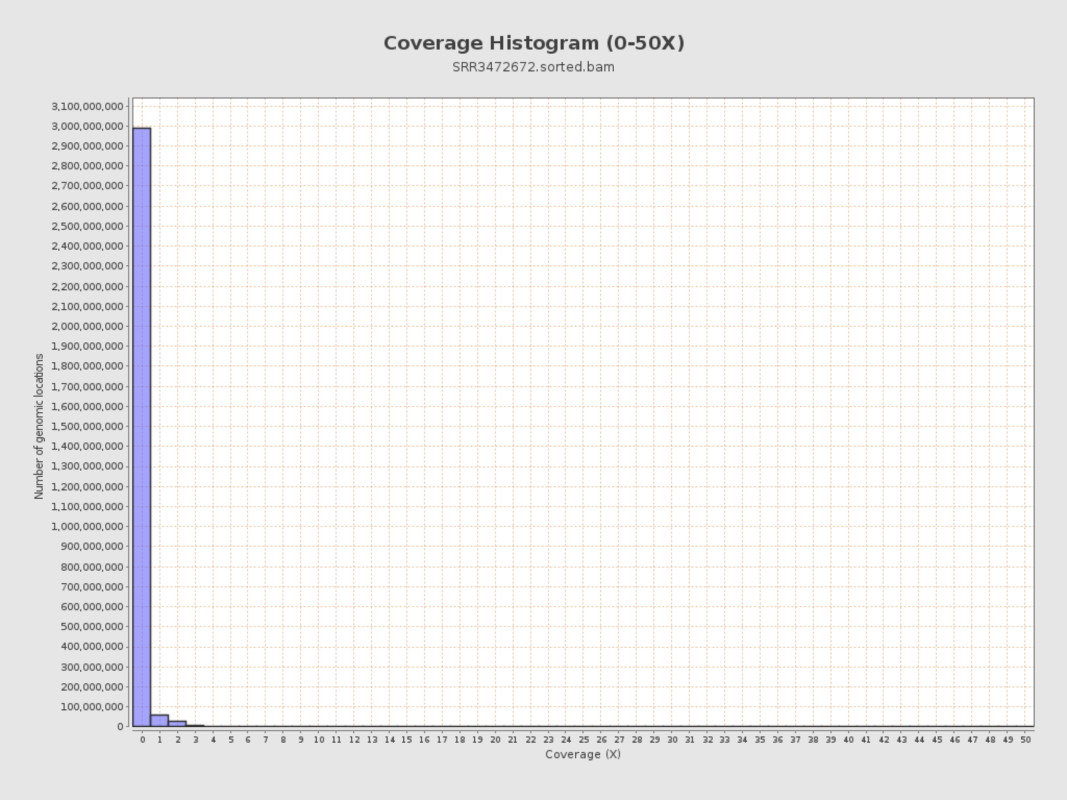
3. Results : Coverage across reference



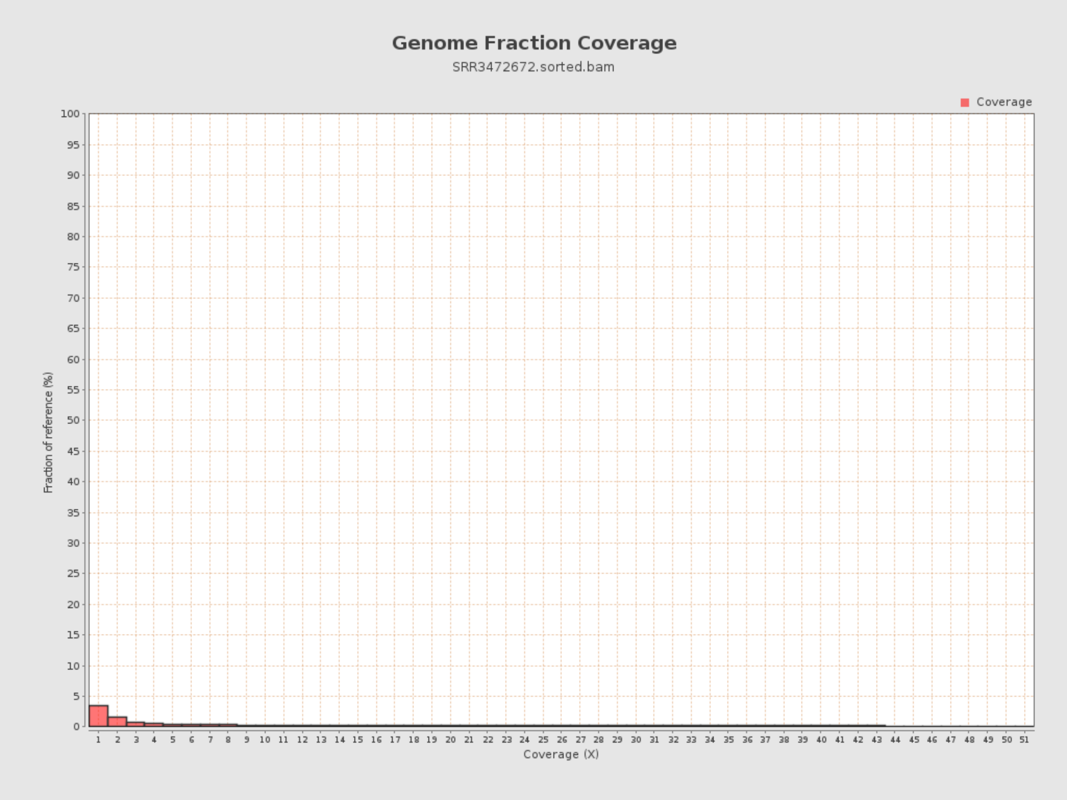
4. Results : Coverage Histogram



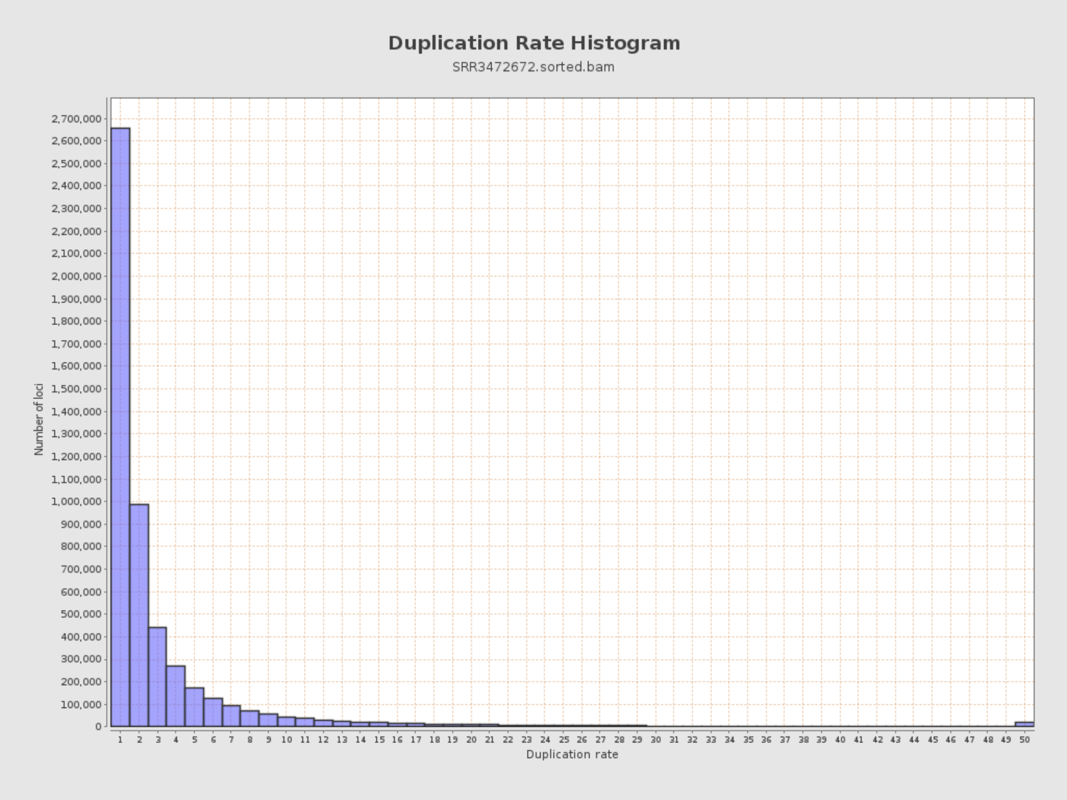
5. Results : Coverage Histogram (0-50X)



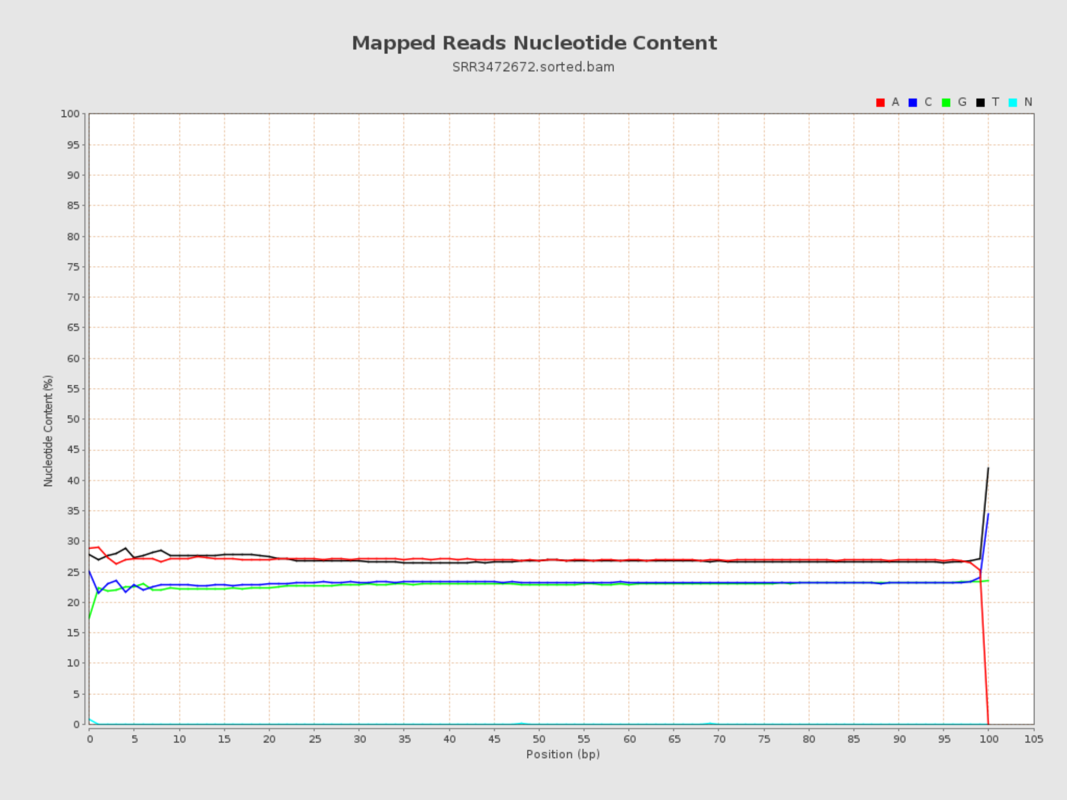
6. Results : Genome Fraction Coverage



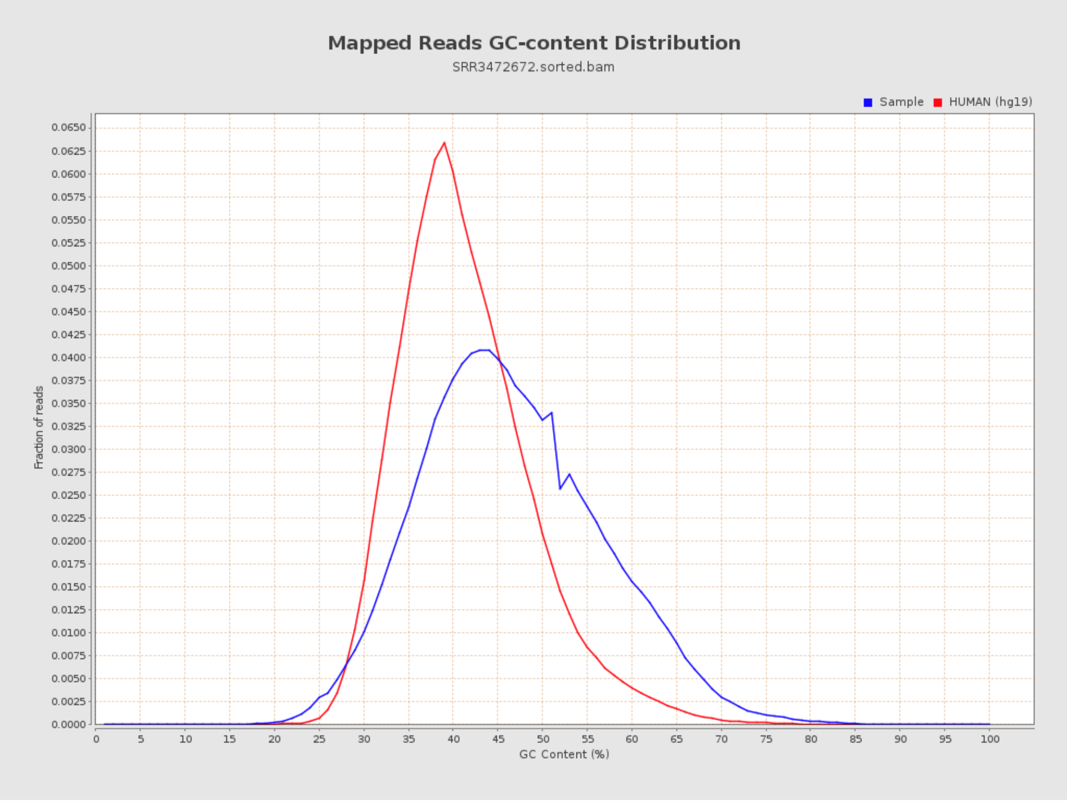
7. Results : Duplication Rate Histogram



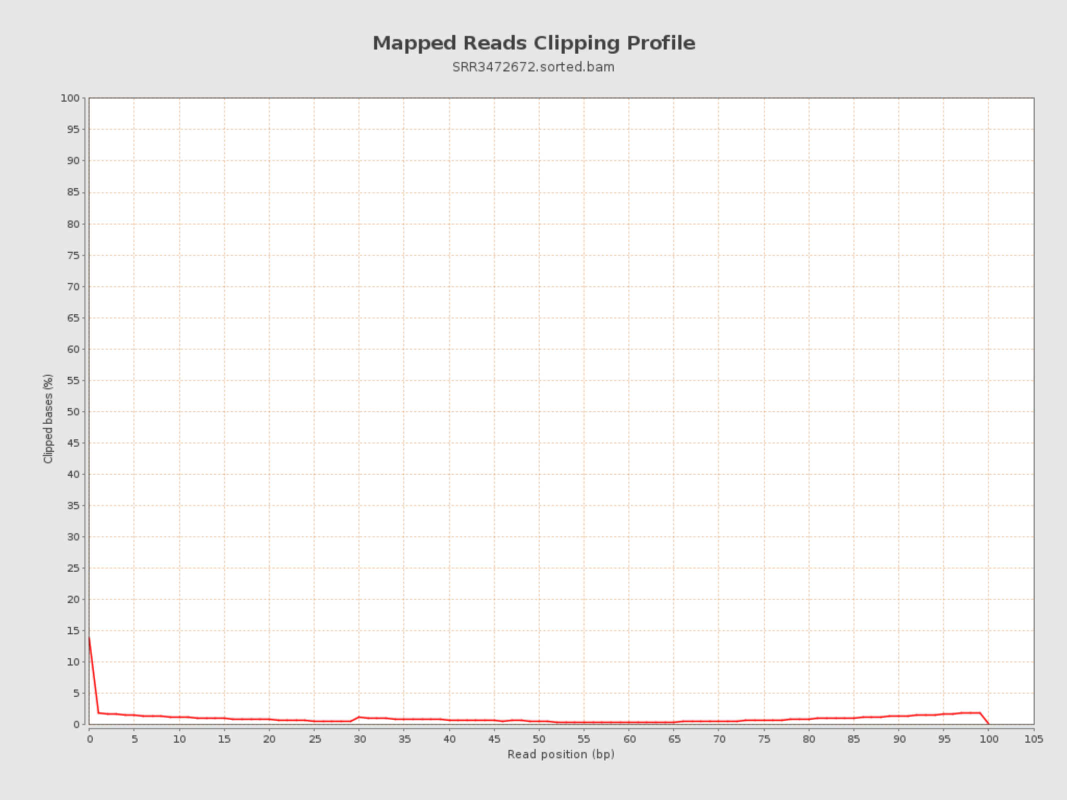
8. Results : Mapped Reads Nucleotide Content



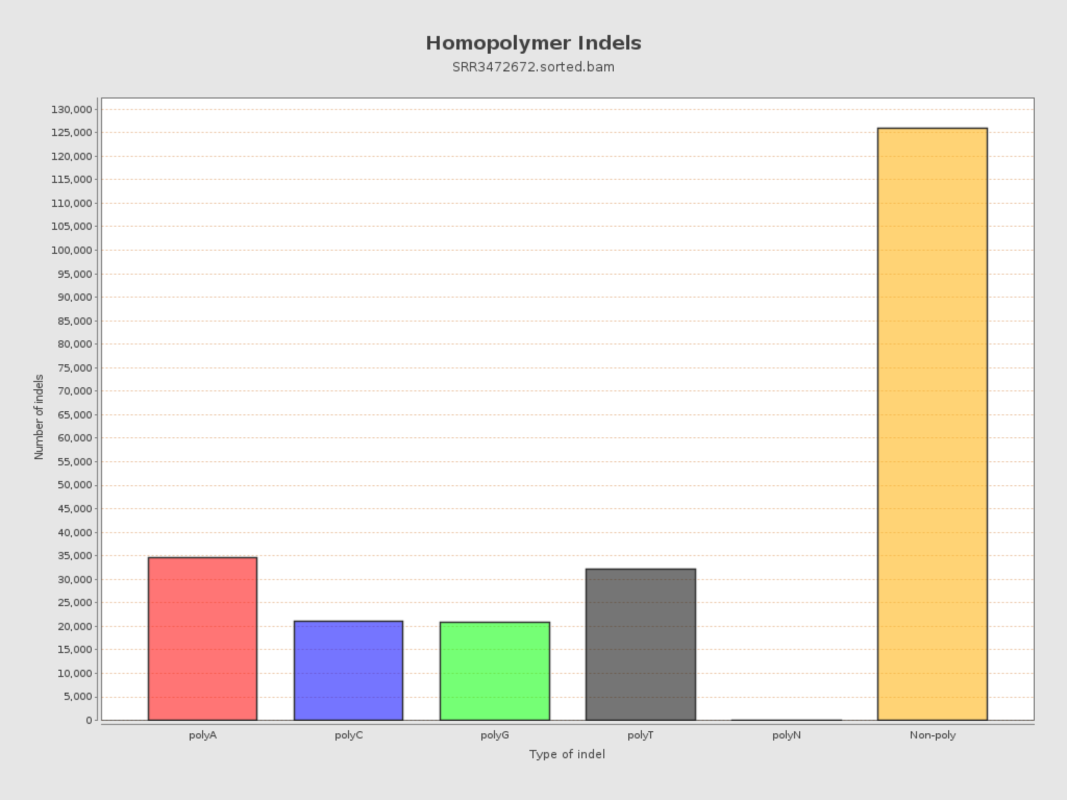
9. Results : Mapped Reads GC-content Distribution



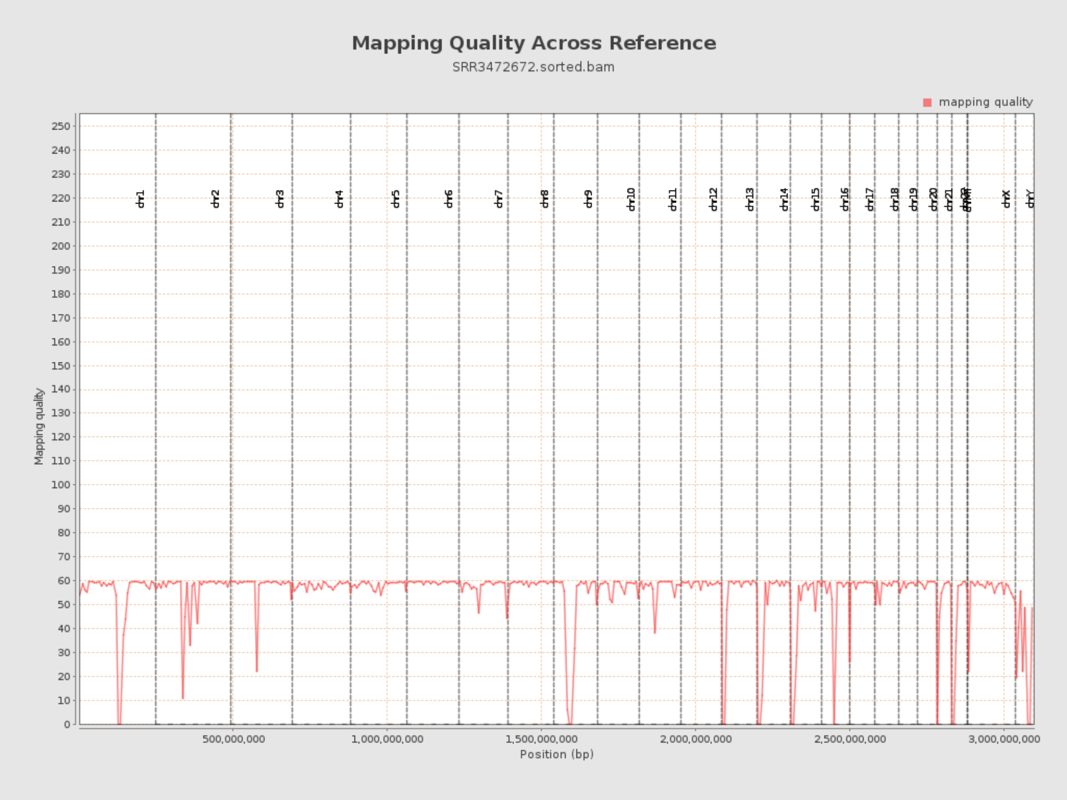
10. Results : Mapped Reads Clipping Profile



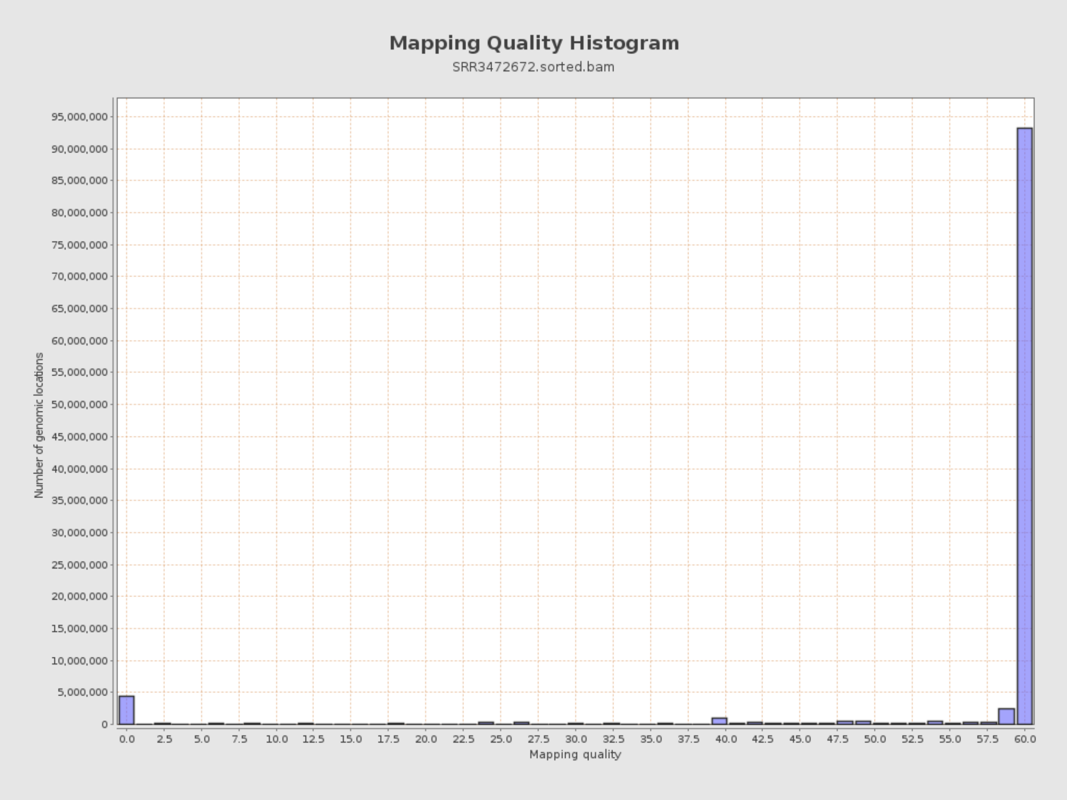
11. Results : Homopolymer Indels



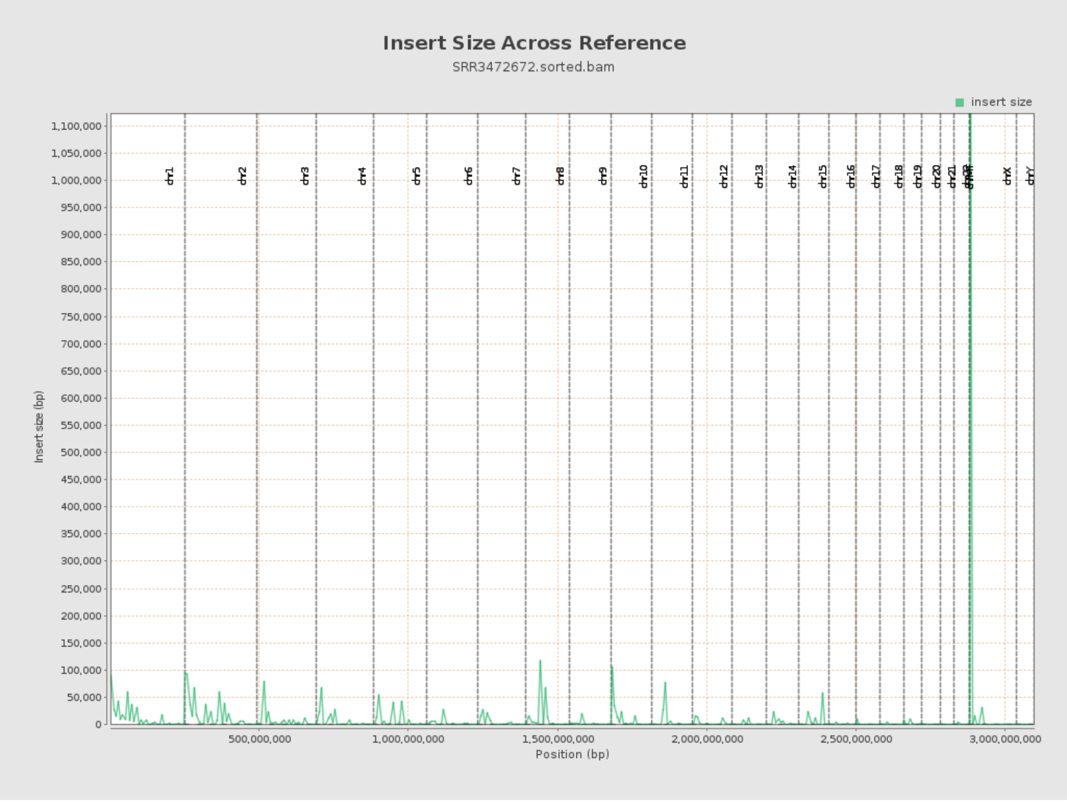
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram