Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 07:35:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472603.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_SRR3472603 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472603_1.fastq.gz SRR3472603_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 07:35:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472603.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,288,864
Mapped reads	8,576,519 / 92.33%
Unmapped reads	712,345 / 7.67%
Mapped paired reads	8,576,519 / 92.33%
Mapped reads, first in pair	4,329,697 / 46.61%
Mapped reads, second in pair	4,246,822 / 45.72%
Mapped reads, both in pair	8,382,052 / 90.24%
Mapped reads, singletons	194,467 / 2.09%
Secondary alignments	0
Supplementary alignments	279,097 / 3%
Read min/max/mean length	30 / 100 / 101.17
Duplicated reads (estimated)	1,310,537 / 14.11%
Duplication rate	13.56%
Clipped reads	6,531,849 / 70.32%

2.2. ACGT Content

Number/percentage of A's	180,959,542 / 25.94%
Number/percentage of C's	140,813,190 / 20.18%
Number/percentage of T's	205,948,415 / 29.52%
Number/percentage of G's	169,569,505 / 24.3%
Number/percentage of N's	442,268 / 0.06%

GC Percentage	44.48%

2.3. Coverage

Mean	0.2255
Standard Deviation	1.9015

2.4. Mapping Quality

Mean Mapping Quality	50.46

2.5. Insert size

Mean	238,825.81
Standard Deviation	4,674,047.45
P25/Median/P75	88 / 126 / 173

2.6. Mismatches and indels

General error rate	1.17%
Mismatches	8,021,461
Insertions	65,212
Mapped reads with at least one insertion	0.75%
Deletions	156,265
Mapped reads with at least one deletion	1.79%
Homopolymer indels	42.8%

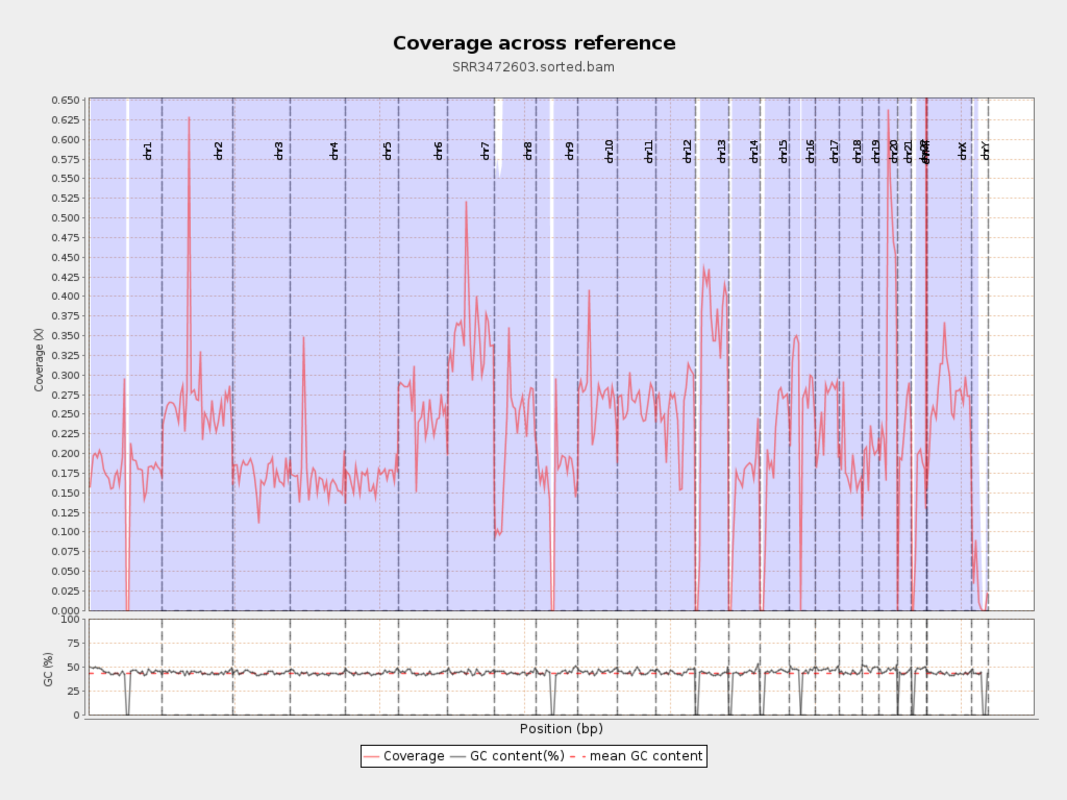
2.7. Chromosome stats

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

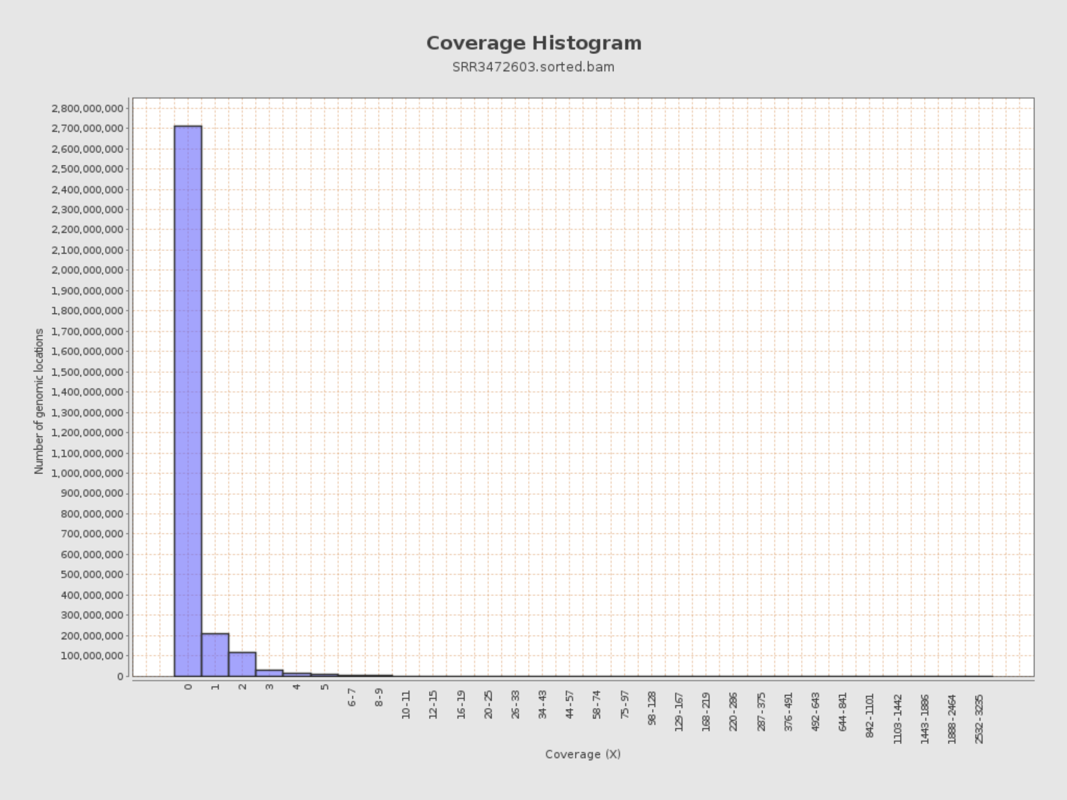
		bases	coverage	deviation
chr1	249250621	42929842	0.1722	2.1491
chr2	243199373	65896235	0.271	2.9182
chr3	198022430	34312634	0.1733	0.6189
chr4	191154276	32830531	0.1717	1.1209
chr5	180915260	30641406	0.1694	0.6449
chr6	171115067	43703109	0.2554	1.1626
chr7	159138663	56486519	0.355	3.6145
chr8	146364022	32585801	0.2226	1.69
chr9	141213431	23169309	0.1641	2.1758
chr10	135534747	37549525	0.277	1.967
chr11	135006516	35568578	0.2635	2.1714
chr12	133851895	34016669	0.2541	0.7945
chr13	115169878	36914533	0.3205	0.9186
chr14	107349540	16409383	0.1529	3.0081
chr15	102531392	19592276	0.1911	0.675
chr16	90354753	24446110	0.2706	1.1448
chr17	81195210	20448689	0.2518	1.407
chr18	78077248	14425114	0.1848	3.5357
chr19	59128983	11755747	0.1988	1.5776
chr20	63025520	23354294	0.3706	1.1761
chr21	48129895	10220387	0.2124	0.984
chr22	51304566	6730564	0.1312	0.5484
chrMT	16571	39156	2.3629	2.5424
chrX	155270560	42413286	0.2732	1.1681

chrY	59373566	1585337	0.0267	0.8719

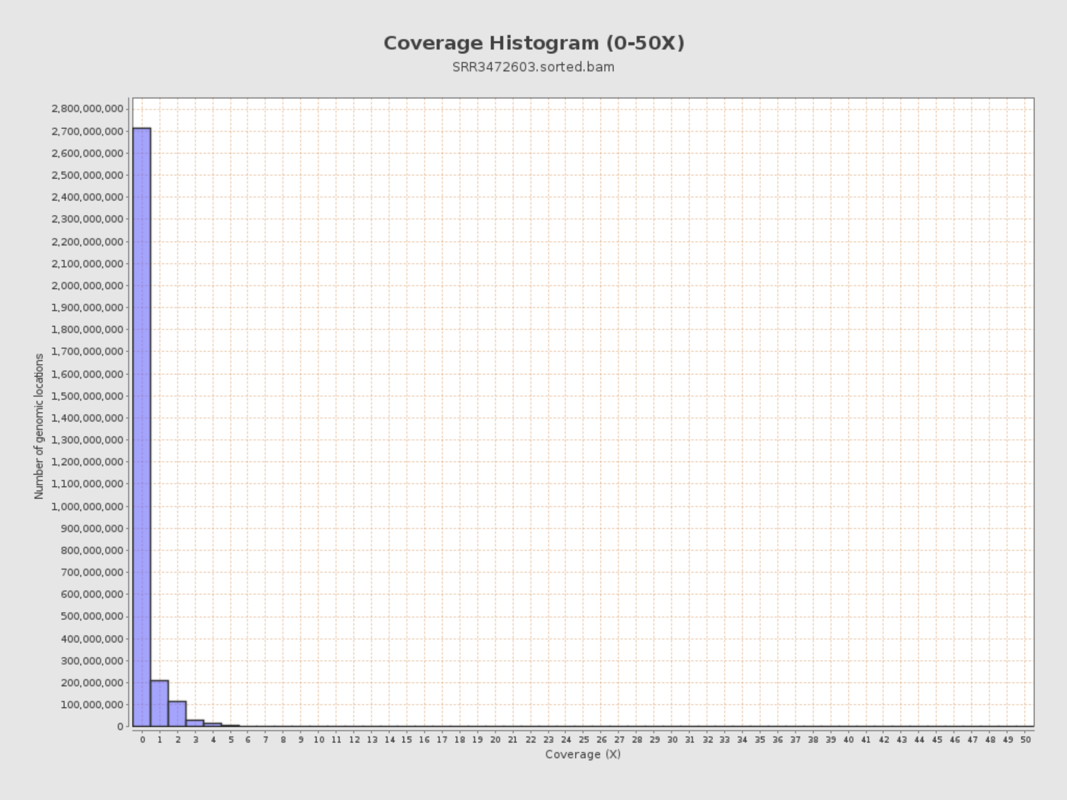
3. Results : Coverage across reference



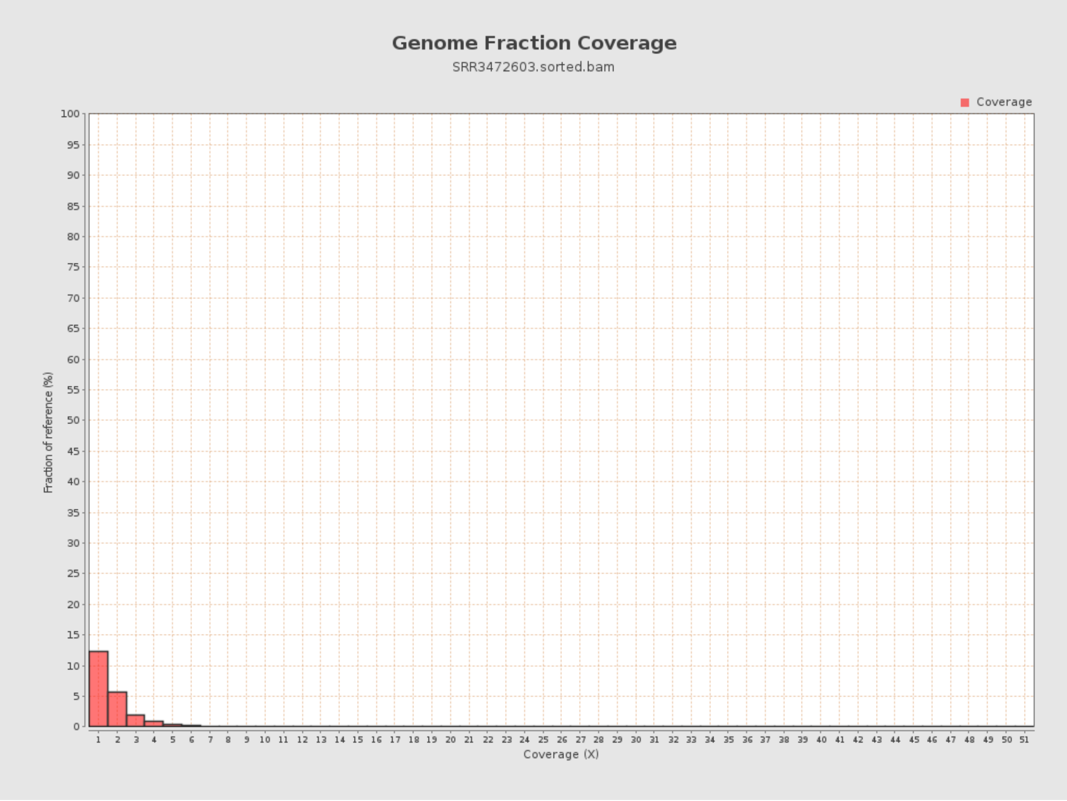
4. Results : Coverage Histogram



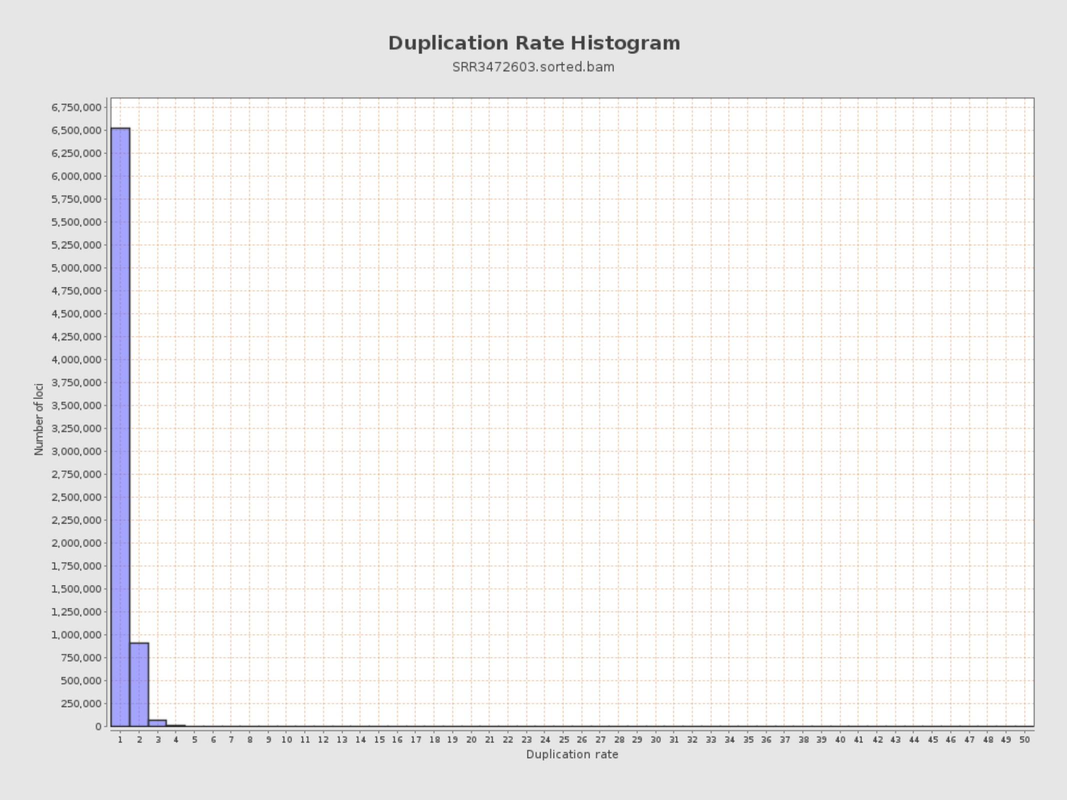
5. Results : Coverage Histogram (0-50X)



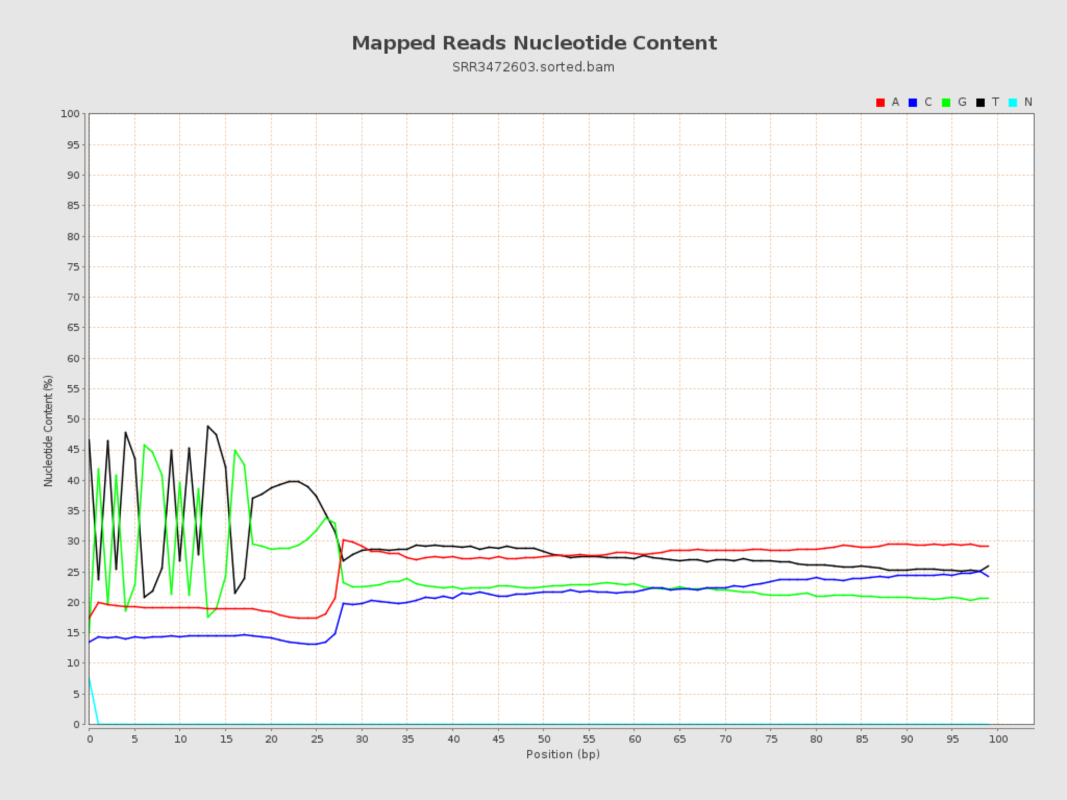
6. Results : Genome Fraction Coverage



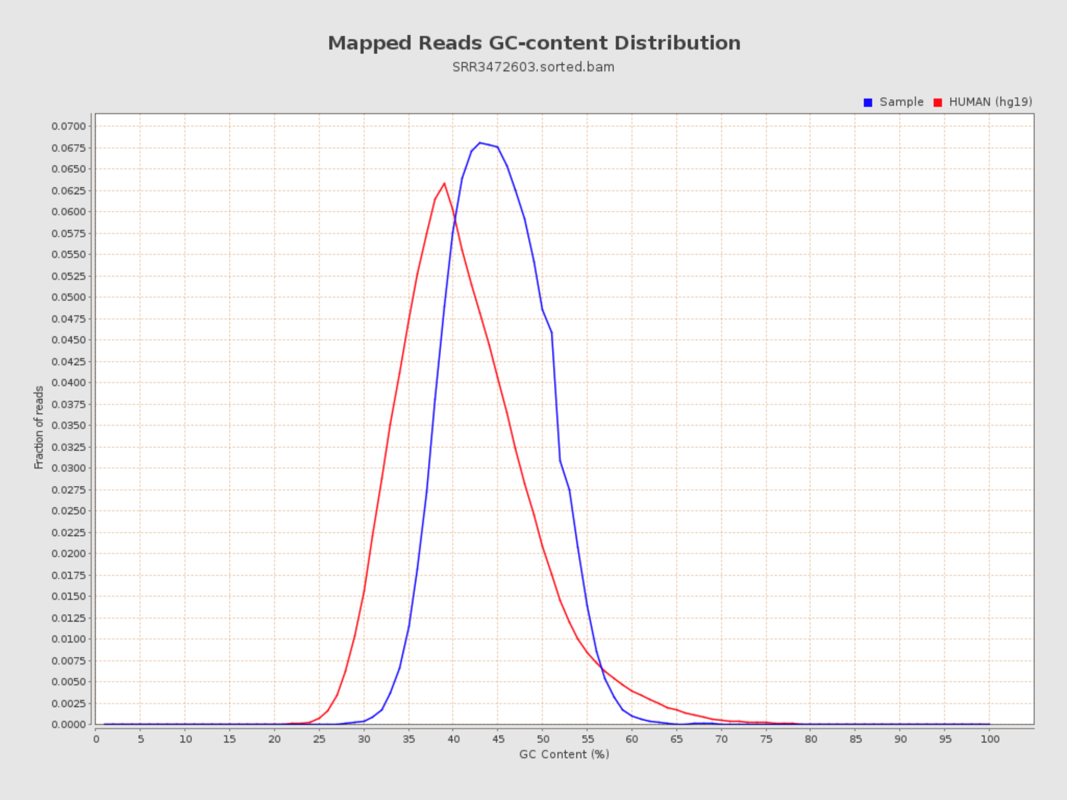
7. Results : Duplication Rate Histogram



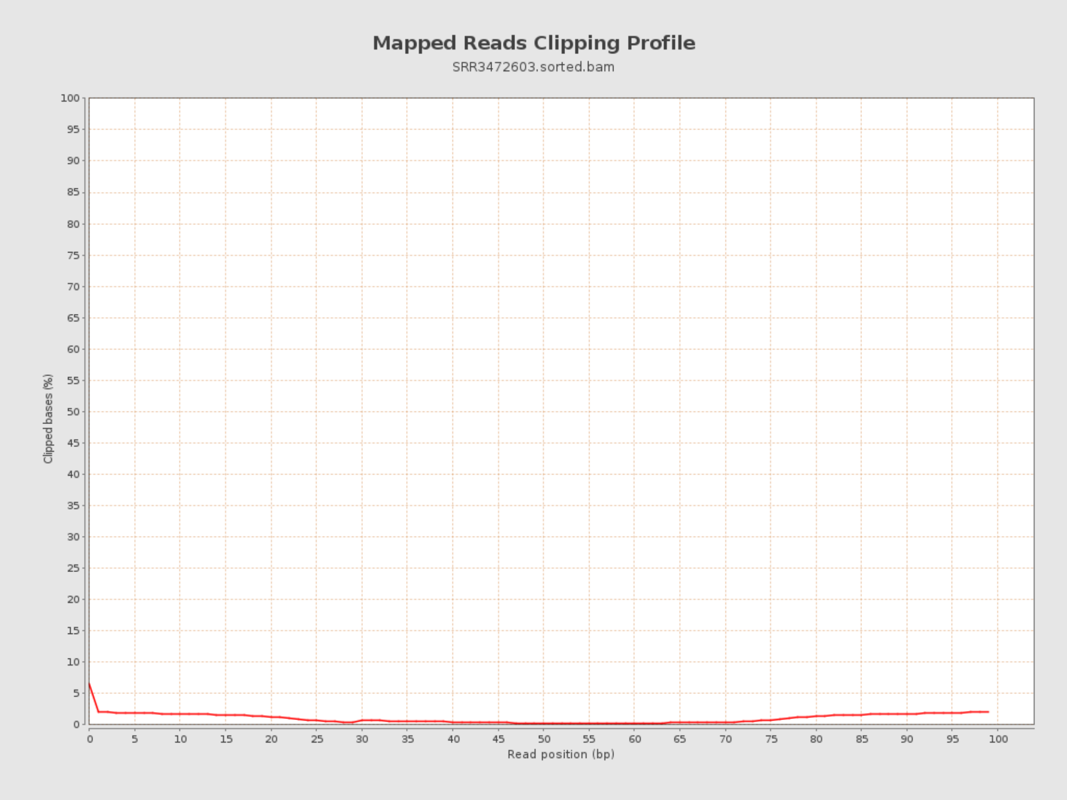
8. Results : Mapped Reads Nucleotide Content



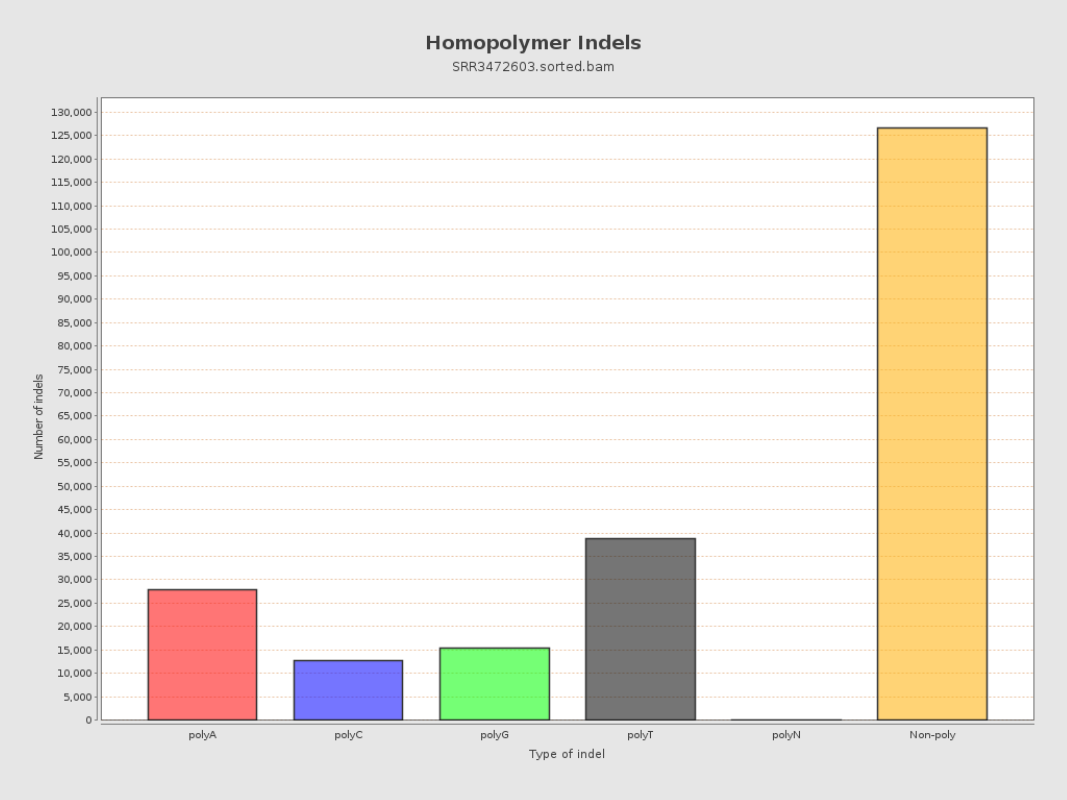
9. Results : Mapped Reads GC-content Distribution



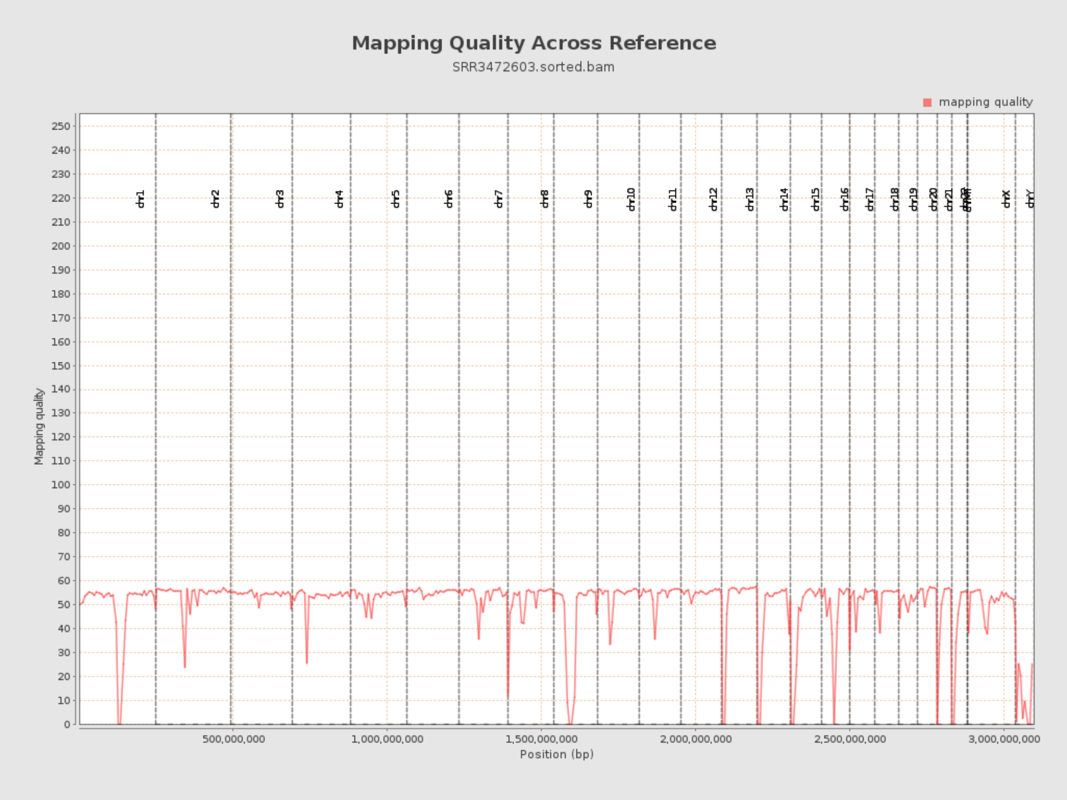
10. Results : Mapped Reads Clipping Profile



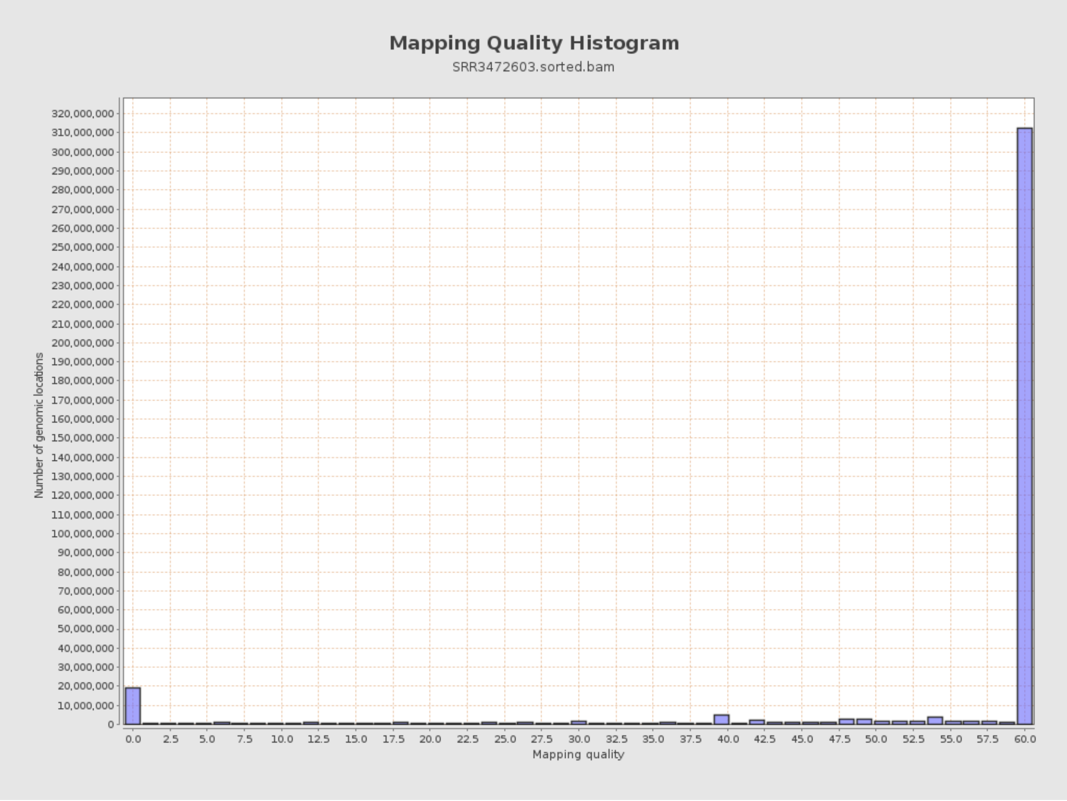
11. Results : Homopolymer Indels



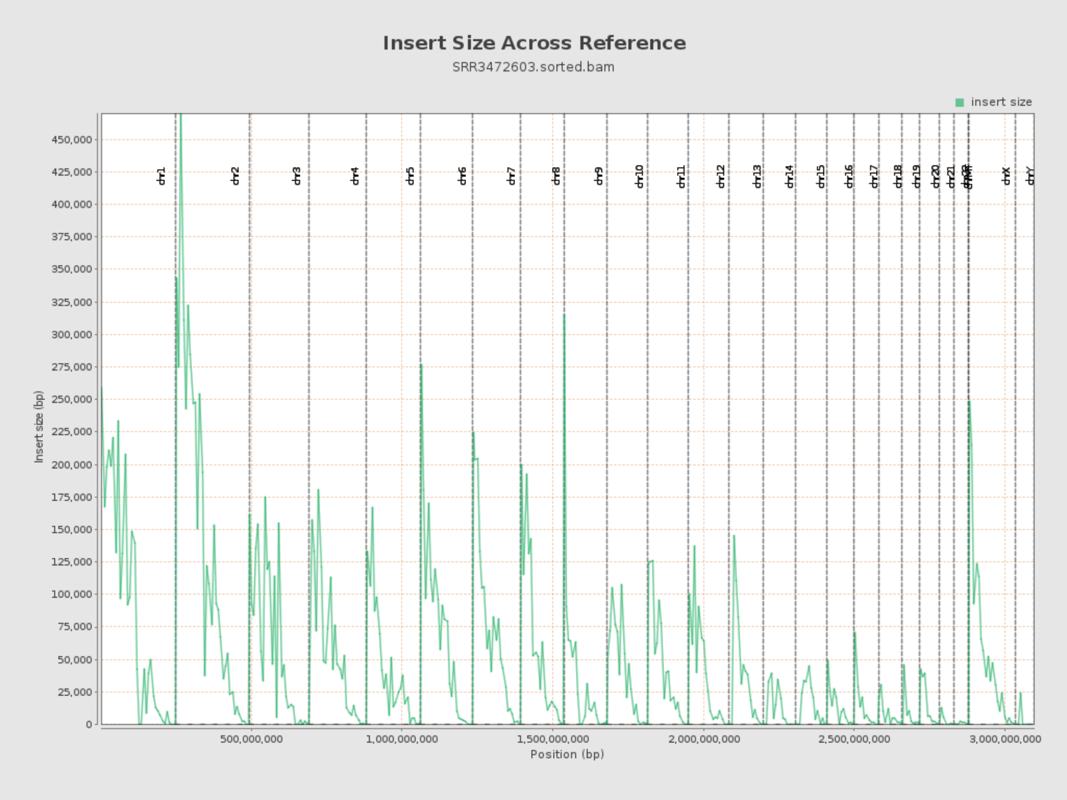
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



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15. Results : Insert Size Histogram