Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 07:19:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472602.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_SRR3472602 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472602_1.fastq.gz SRR3472602_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 07:19:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472602.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,610,040
Mapped reads	7,992,276 / 92.83%
Unmapped reads	617,764 / 7.17%
Mapped paired reads	7,992,276 / 92.83%
Mapped reads, first in pair	4,034,606 / 46.86%
Mapped reads, second in pair	3,957,670 / 45.97%
Mapped reads, both in pair	7,809,648 / 90.7%
Mapped reads, singletons	182,628 / 2.12%
Secondary alignments	0
Supplementary alignments	233,412 / 2.71%
Read min/max/mean length	30 / 100 / 101.06
Duplicated reads (estimated)	1,136,339 / 13.2%
Duplication rate	12.18%
Clipped reads	5,852,407 / 67.97%

2.2. ACGT Content

Number/percentage of A's	168,584,029 / 25.56%
Number/percentage of C's	132,520,756 / 20.09%
Number/percentage of T's	195,950,770 / 29.71%
Number/percentage of G's	162,105,116 / 24.58%
Number/percentage of N's	429,303 / 0.07%

GC Percentage	44.67%

2.3. Coverage

Mean	0.2132
Standard Deviation	1.74

2.4. Mapping Quality

Mean Mapping Quality	50.74

2.5. Insert size

Mean	229,186.41
Standard Deviation	4,570,488.15
P25/Median/P75	98 / 135 / 183

2.6. Mismatches and indels

General error rate	1.17%
Mismatches	7,603,117
Insertions	60,035
Mapped reads with at least one insertion	0.74%
Deletions	149,736
Mapped reads with at least one deletion	1.84%
Homopolymer indels	42.99%

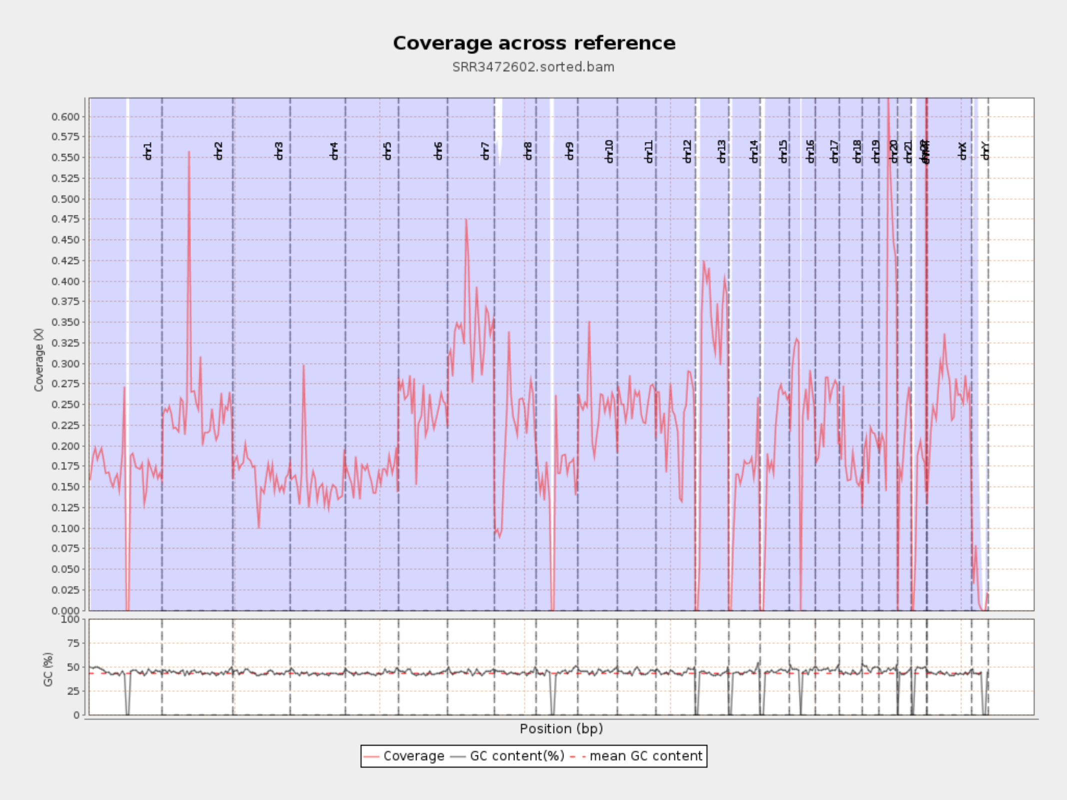
2.7. Chromosome stats

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

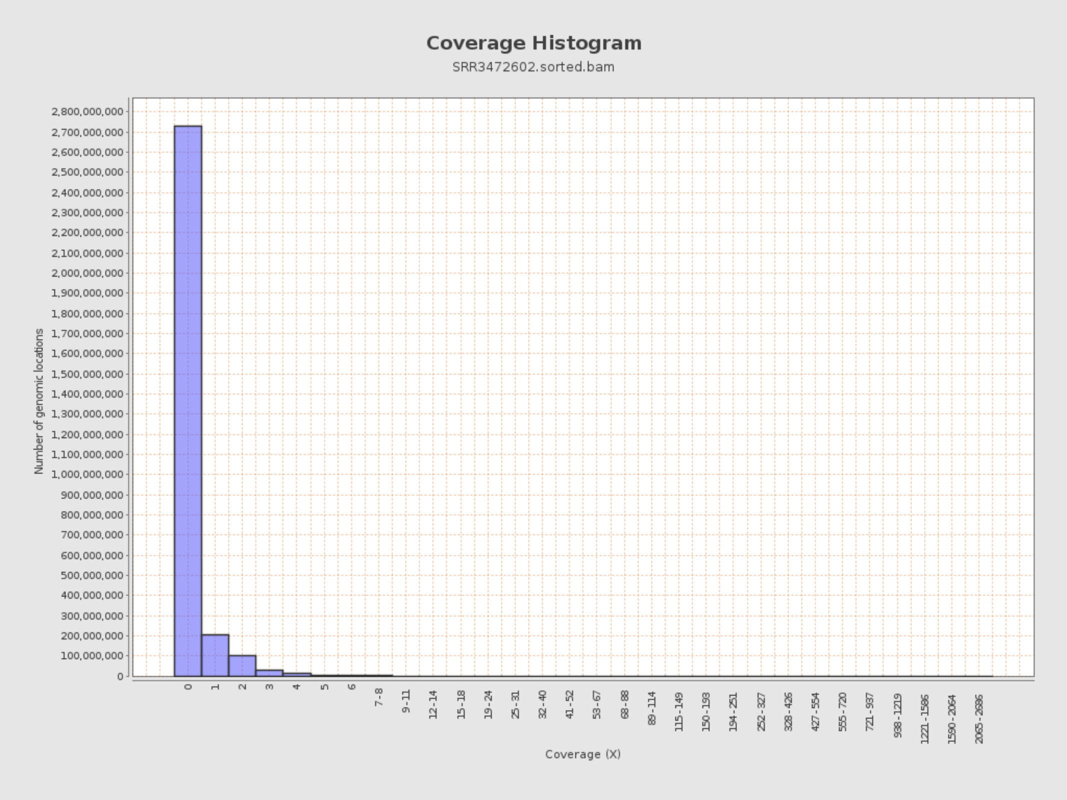
		bases	coverage	deviation
chr1	249250621	40816782	0.1638	2.1511
chr2	243199373	60590081	0.2491	2.5283
chr3	198022430	32413157	0.1637	0.6118
chr4	191154276	29666426	0.1552	0.9464
chr5	180915260	29862335	0.1651	0.6366
chr6	171115067	42269823	0.247	1.0868
chr7	159138663	54583158	0.343	3.1462
chr8	146364022	31123875	0.2126	1.5223
chr9	141213431	21604007	0.153	1.8806
chr10	135534747	33493726	0.2471	1.6658
chr11	135006516	34092829	0.2525	1.8505
chr12	133851895	31137805	0.2326	0.7611
chr13	115169878	35338968	0.3068	0.9043
chr14	107349540	16068053	0.1497	3.4327
chr15	102531392	18826858	0.1836	0.6682
chr16	90354753	22913705	0.2536	1.0533
chr17	81195210	19628927	0.2417	1.2035
chr18	78077248	14096581	0.1805	2.9446
chr19	59128983	11731206	0.1984	1.5909
chr20	63025520	22475866	0.3566	1.1716
chr21	48129895	9295902	0.1931	0.886
chr22	51304566	6617555	0.129	0.5604
chrMT	16571	52026	3.1396	3.1694
chrX	155270560	39774386	0.2562	1.0803

chrY	59373566	1398169	0.0235	0.7205

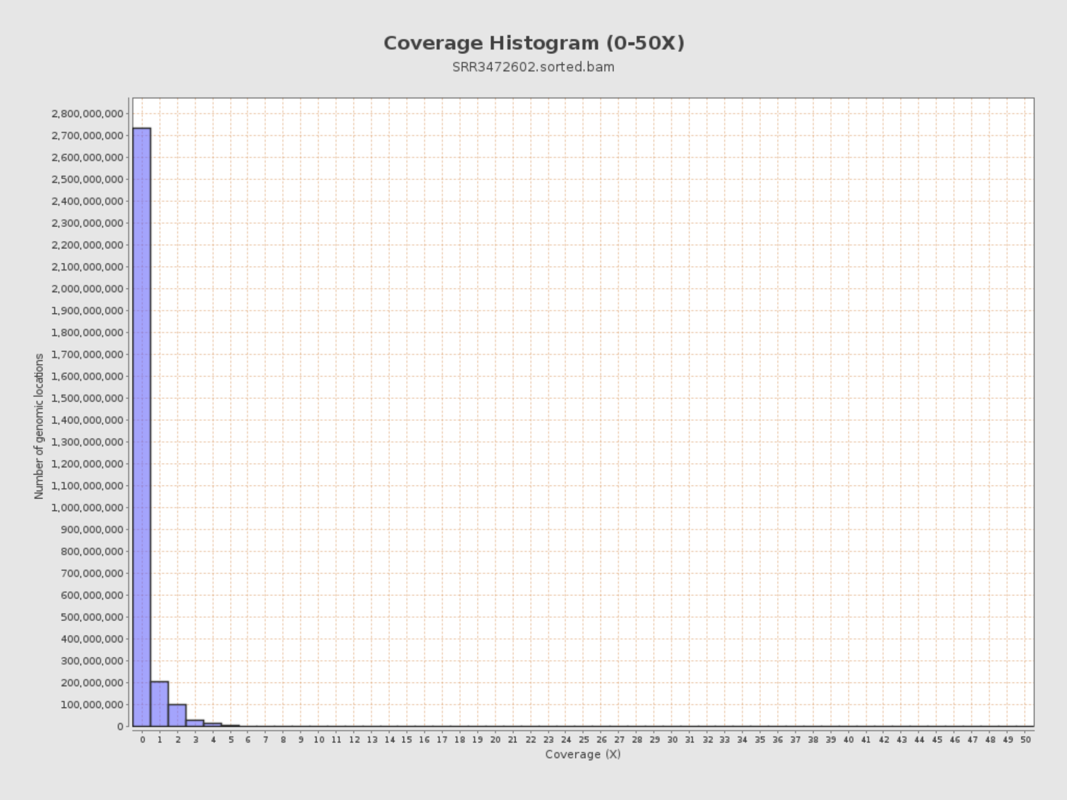
3. Results : Coverage across reference



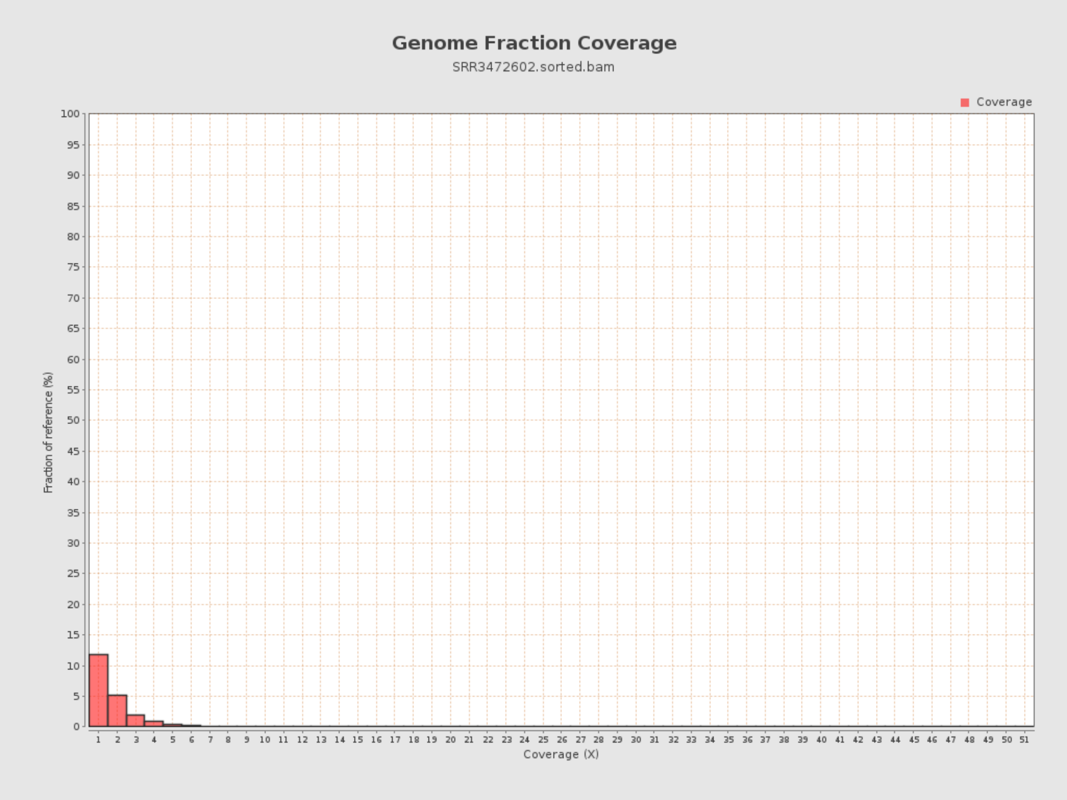
4. Results : Coverage Histogram



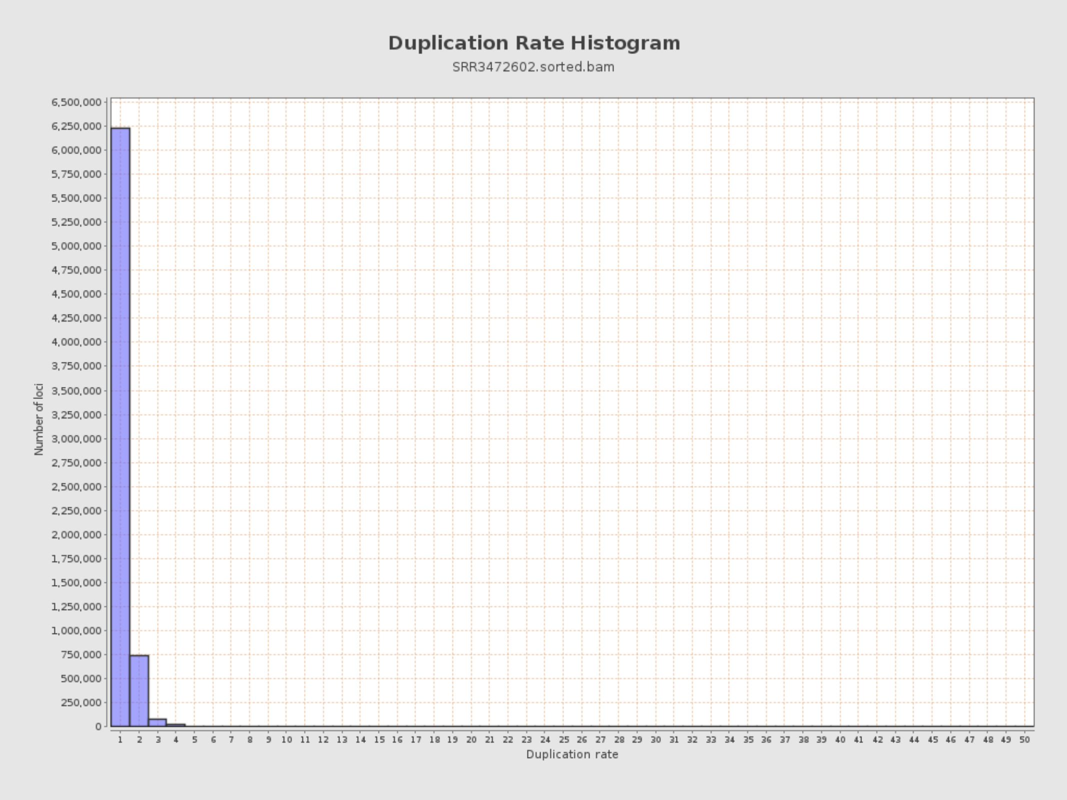
5. Results : Coverage Histogram (0-50X)



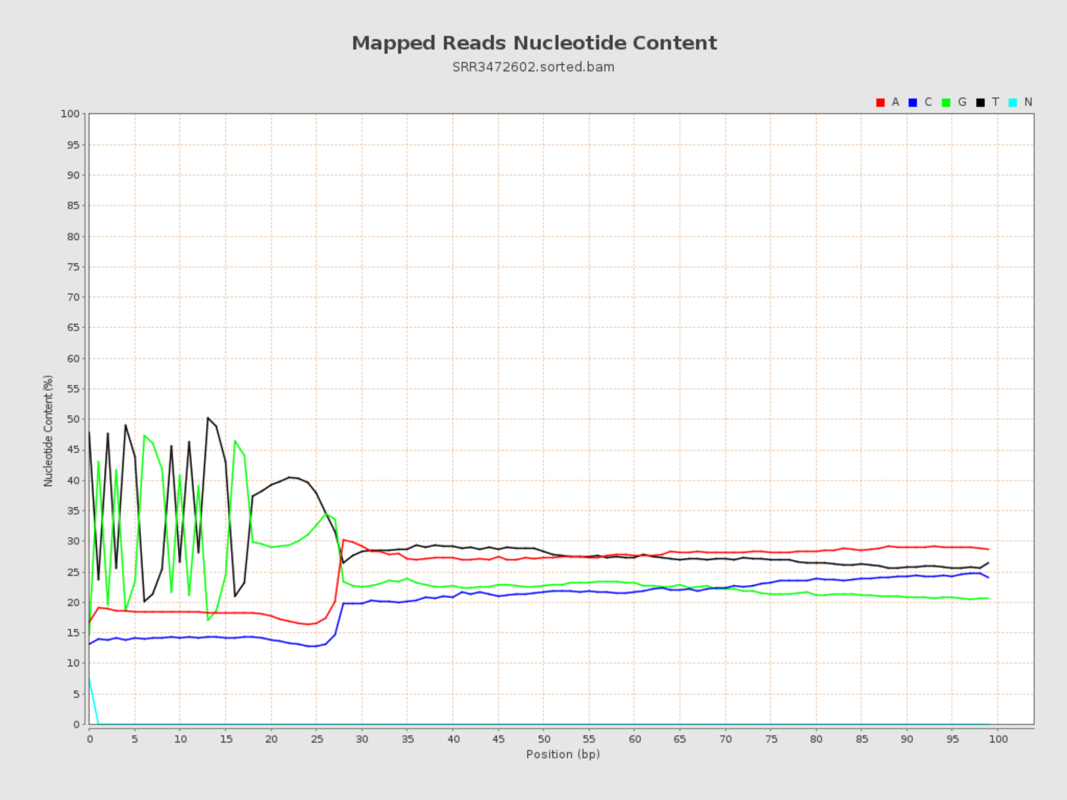
6. Results : Genome Fraction Coverage



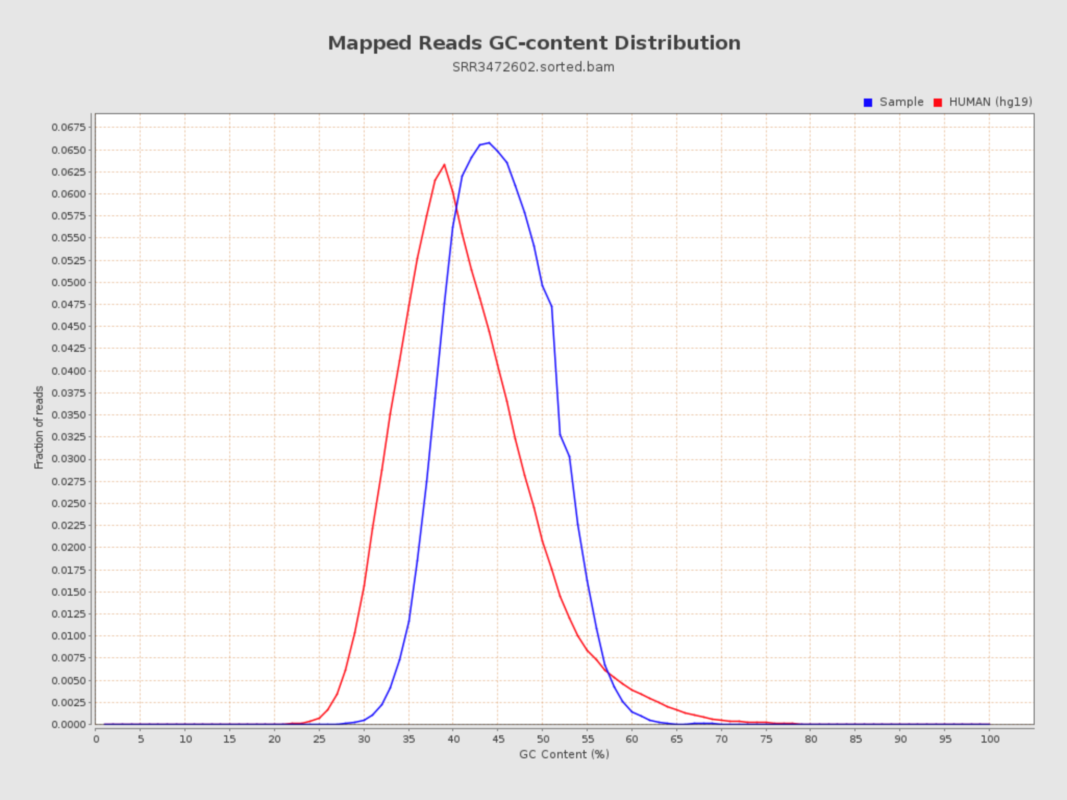
7. Results : Duplication Rate Histogram



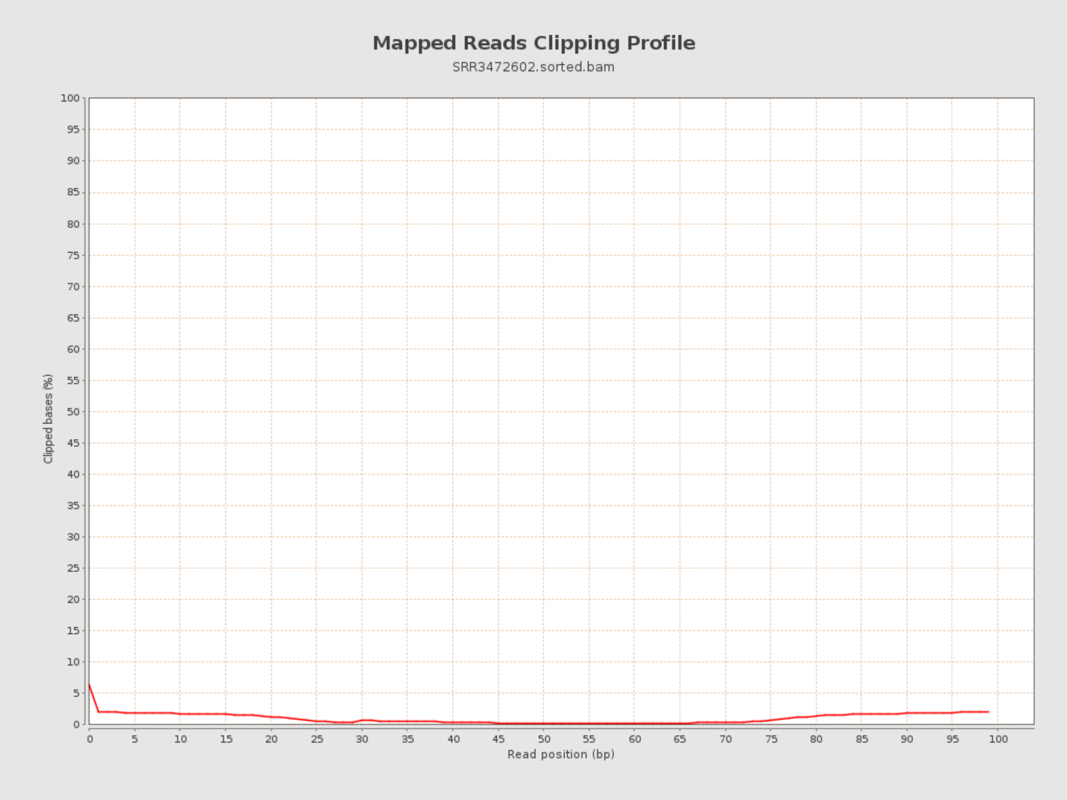
8. Results : Mapped Reads Nucleotide Content



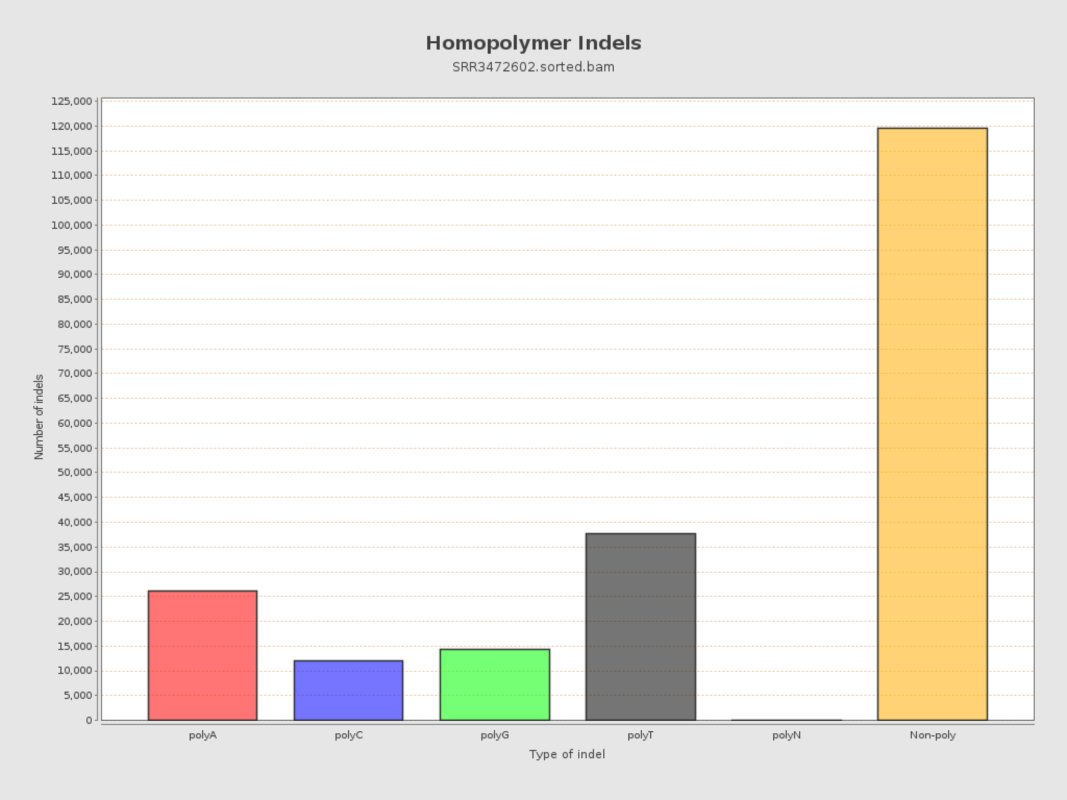
9. Results : Mapped Reads GC-content Distribution



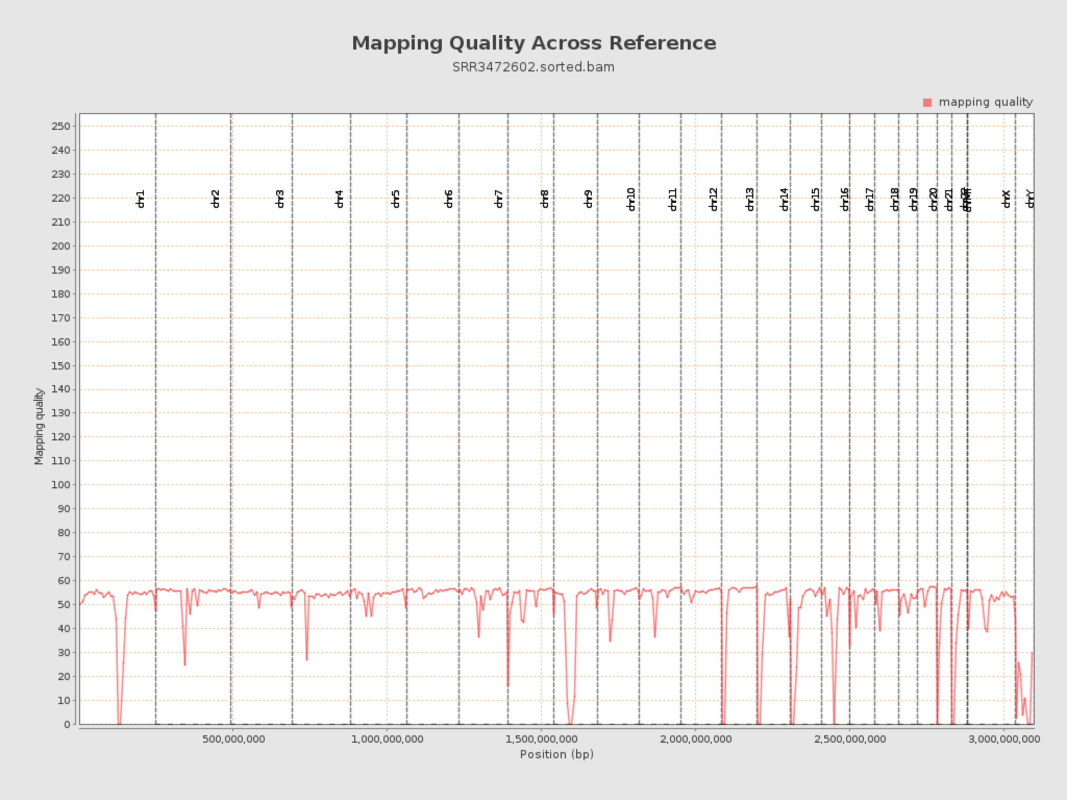
10. Results : Mapped Reads Clipping Profile



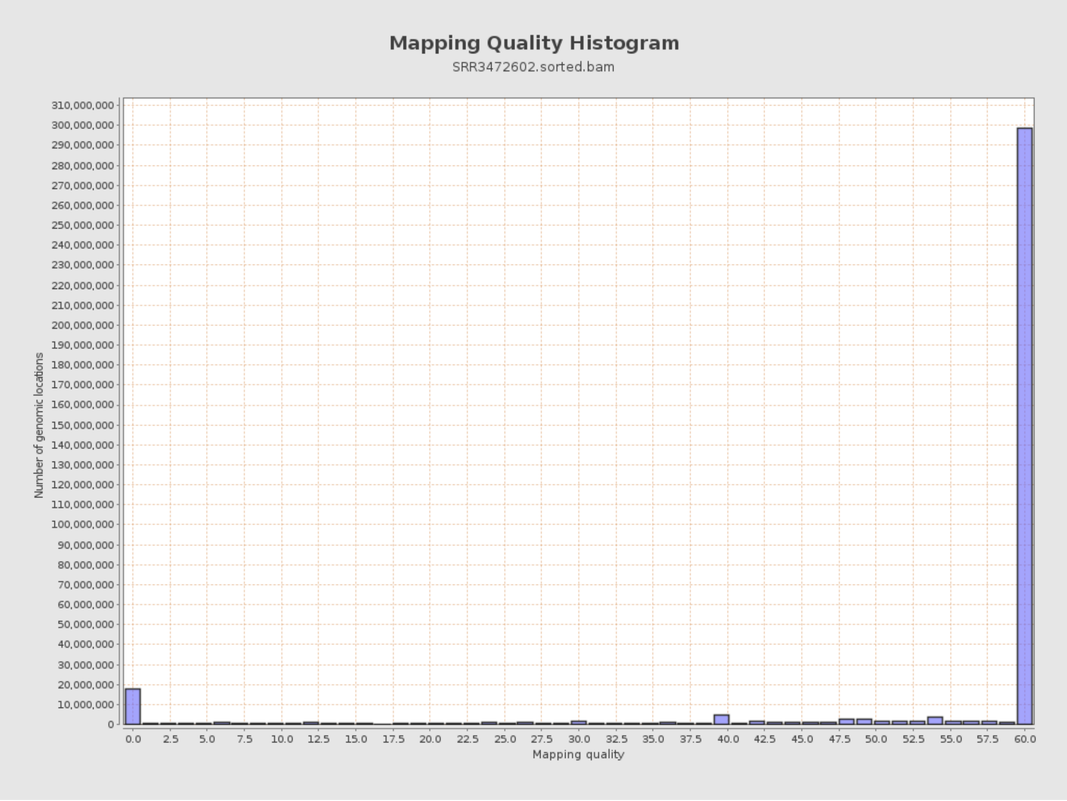
11. Results : Homopolymer Indels



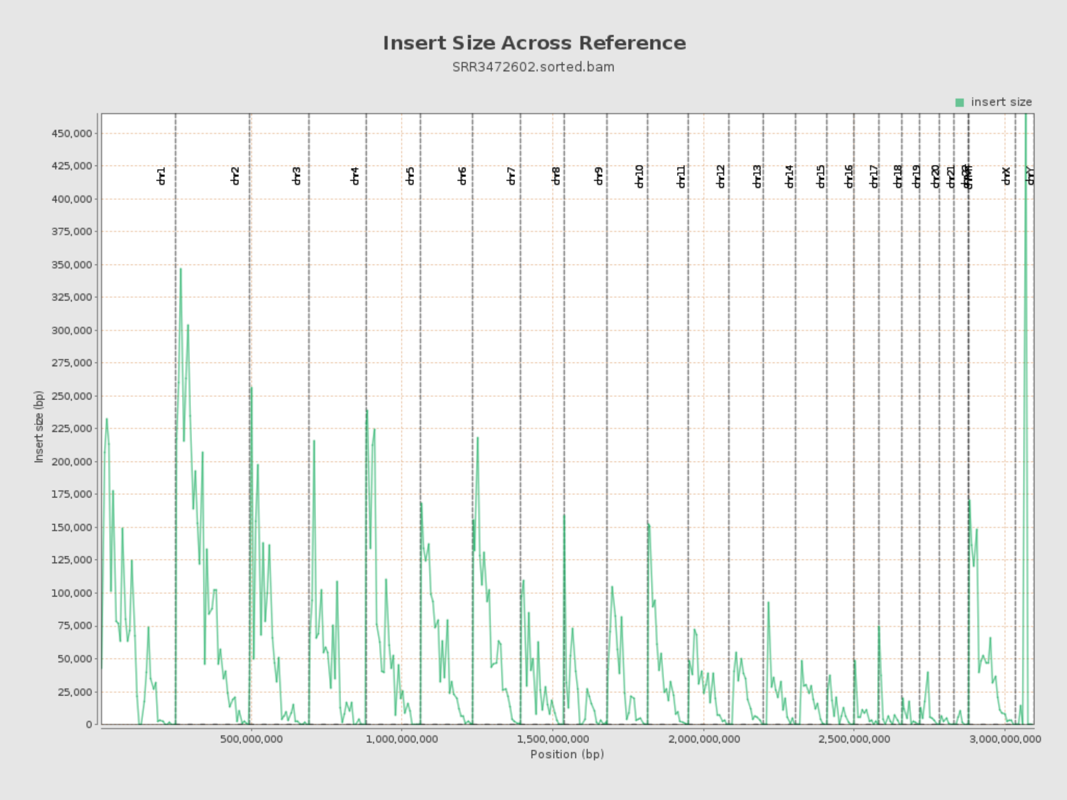
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram