Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 21:28:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472650.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_SRR3472650 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472650_1.fastq.gz SRR3472650_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 21:28:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472650.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,628,486
Mapped reads	5,555,390 / 98.7%
Unmapped reads	73,096 / 1.3%
Mapped paired reads	5,555,390 / 98.7%
Mapped reads, first in pair	2,797,920 / 49.71%
Mapped reads, second in pair	2,757,470 / 48.99%
Mapped reads, both in pair	5,512,212 / 97.93%
Mapped reads, singletons	43,178 / 0.77%
Secondary alignments	0
Supplementary alignments	11,834 / 0.21%
Read min/max/mean length	30 / 101 / 98.53
Duplicated reads (estimated)	3,154,480 / 56.04%
Duplication rate	49.88%
Clipped reads	196,063 / 3.48%

2.2. ACGT Content

Number/percentage of A's	150,392,560 / 27.65%
Number/percentage of C's	120,738,805 / 22.2%
Number/percentage of T's	154,684,514 / 28.44%
Number/percentage of G's	118,016,756 / 21.7%
Number/percentage of N's	99,022 / 0.02%

GC Percentage	43.89%

2.3. Coverage

Mean	0.1757
Standard Deviation	6.0158

2.4. Mapping Quality

Mean Mapping Quality	53.82

2.5. Insert size

Mean	24,643.34
Standard Deviation	1,557,654.35
P25/Median/P75	151 / 217 / 297

2.6. Mismatches and indels

General error rate	0.54%
Mismatches	2,879,396
Insertions	26,283
Mapped reads with at least one insertion	0.46%
Deletions	33,700
Mapped reads with at least one deletion	0.59%
Homopolymer indels	44.63%

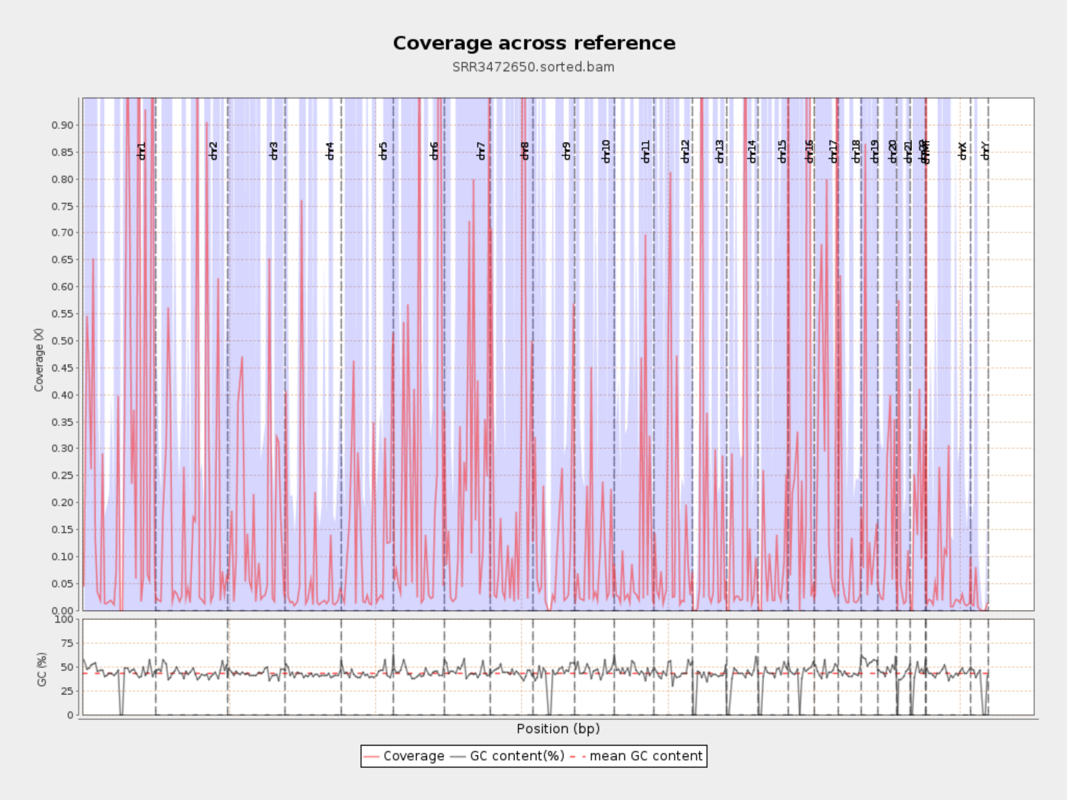
2.7. Chromosome stats

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

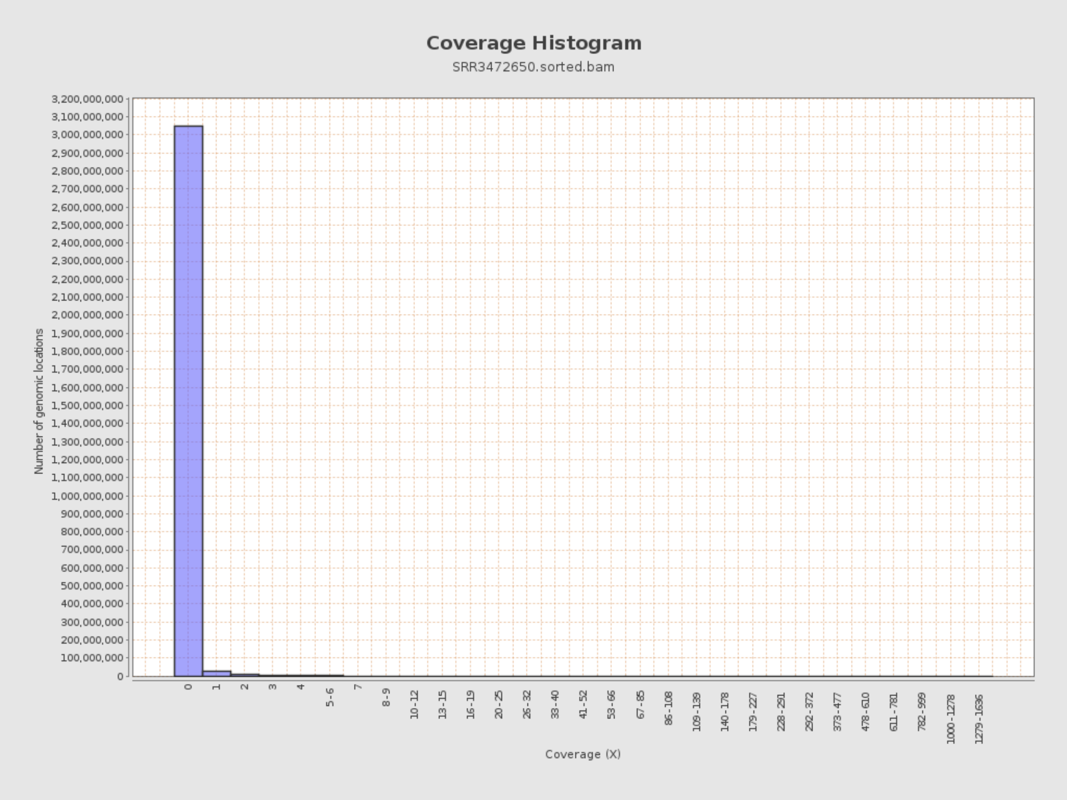
		bases	coverage	deviation
chr1	249250621	74060690	0.2971	8.1347
chr2	243199373	43537142	0.179	5.9419
chr3	198022430	30357515	0.1533	5.4072
chr4	191154276	16593047	0.0868	3.7052
chr5	180915260	25417730	0.1405	4.9855
chr6	171115067	47079414	0.2751	7.4796
chr7	159138663	41800536	0.2627	7.4895
chr8	146364022	39566354	0.2703	7.6075
chr9	141213431	15927337	0.1128	4.1628
chr10	135534747	13293675	0.0981	3.8269
chr11	135006516	15566119	0.1153	4.3744
chr12	133851895	19801527	0.1479	4.6115
chr13	115169878	20264982	0.176	6.7344
chr14	107349540	15581887	0.1452	5.21
chr15	102531392	8198869	0.08	3.292
chr16	90354753	34907785	0.3863	11.6729
chr17	81195210	28016270	0.345	8.1003
chr18	78077248	7375008	0.0945	3.79
chr19	59128983	11540073	0.1952	4.6092
chr20	63025520	9954009	0.1579	5.82
chr21	48129895	6010294	0.1249	8.0435
chr22	51304566	9624783	0.1876	6.0708
chrMT	16571	30304	1.8287	1.9729
chrX	155270560	8590505	0.0553	2.1953

chrY	59373566	920846	0.0155	0.7501

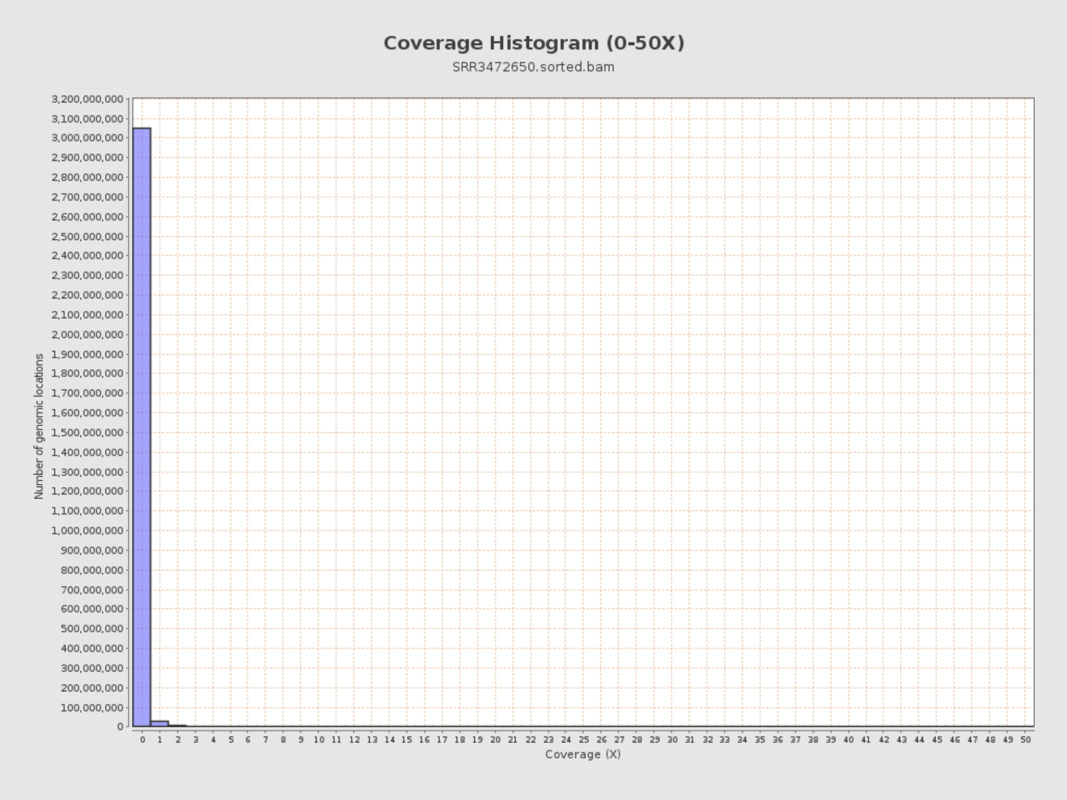
3. Results : Coverage across reference



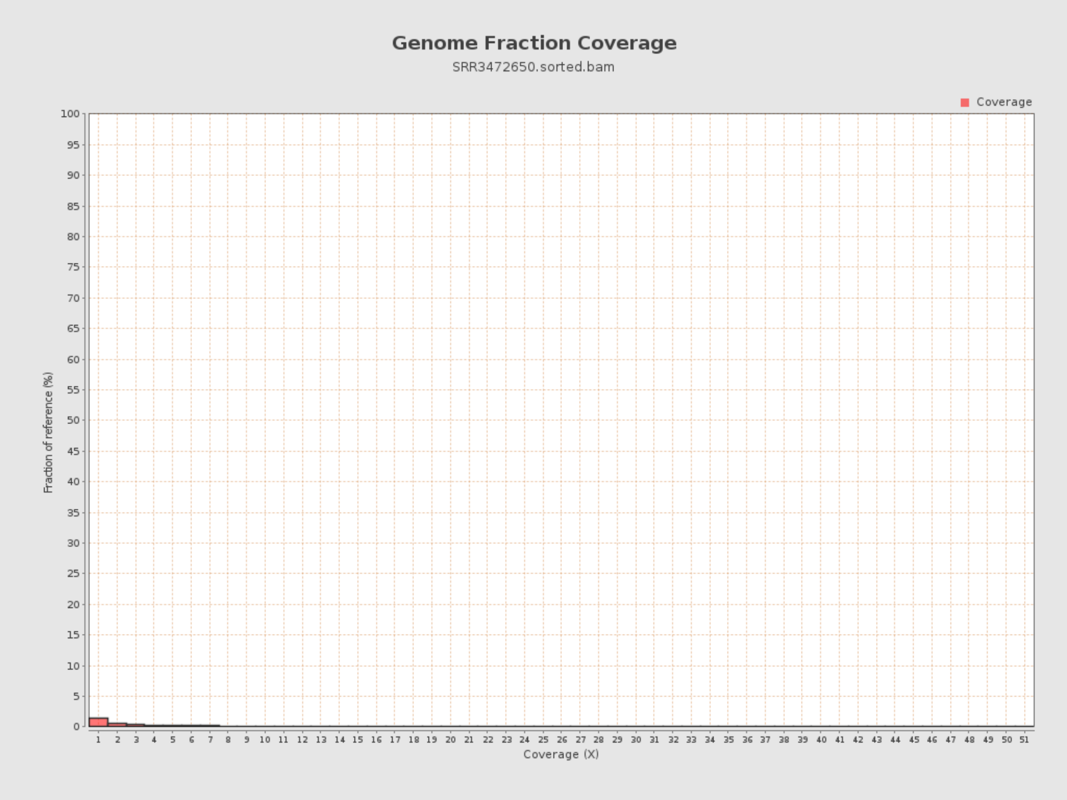
4. Results : Coverage Histogram



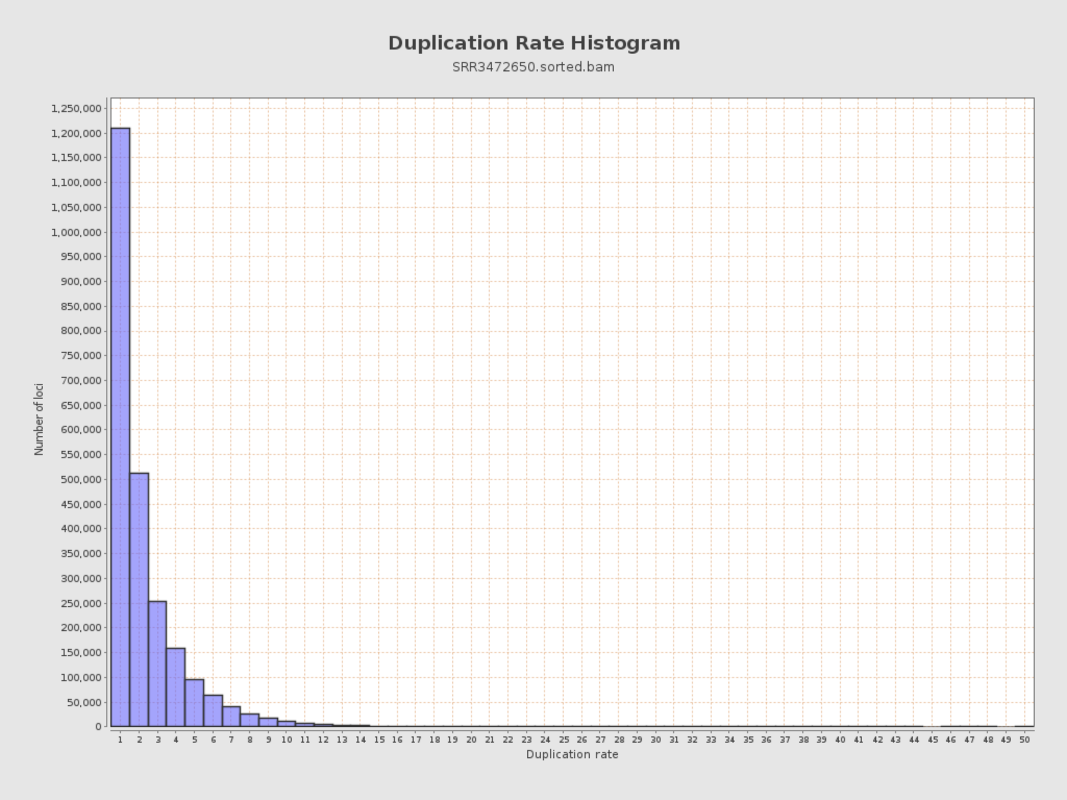
5. Results : Coverage Histogram (0-50X)



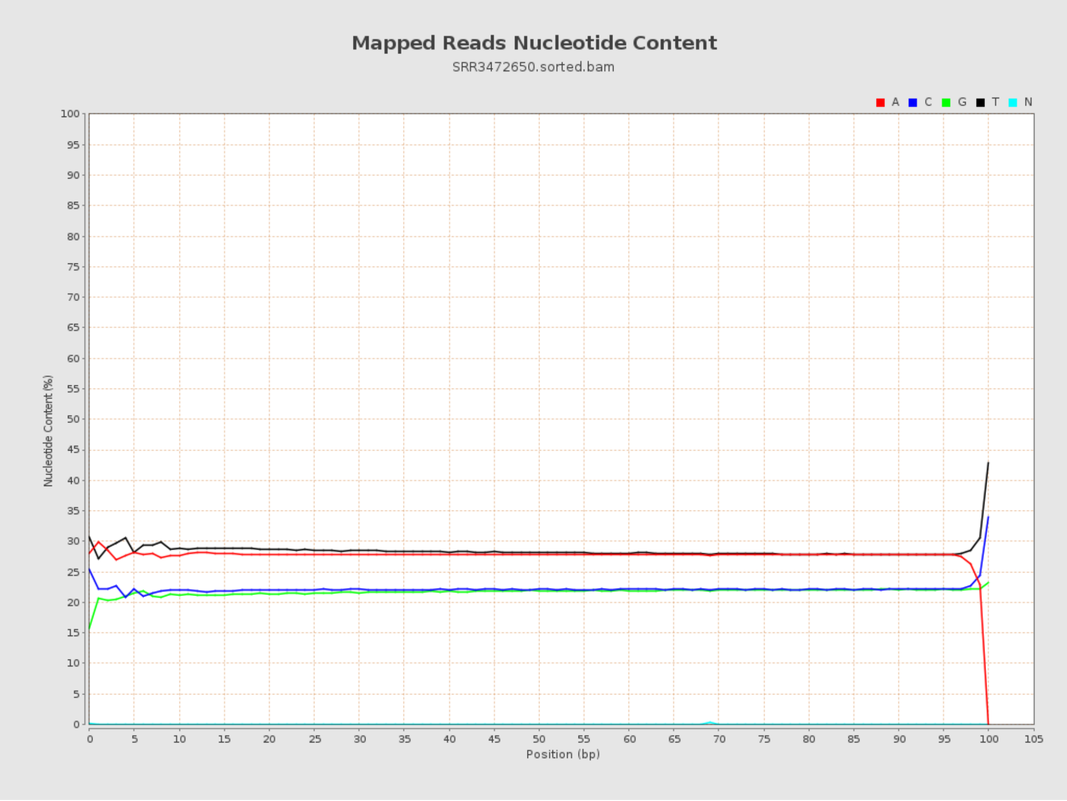
6. Results : Genome Fraction Coverage



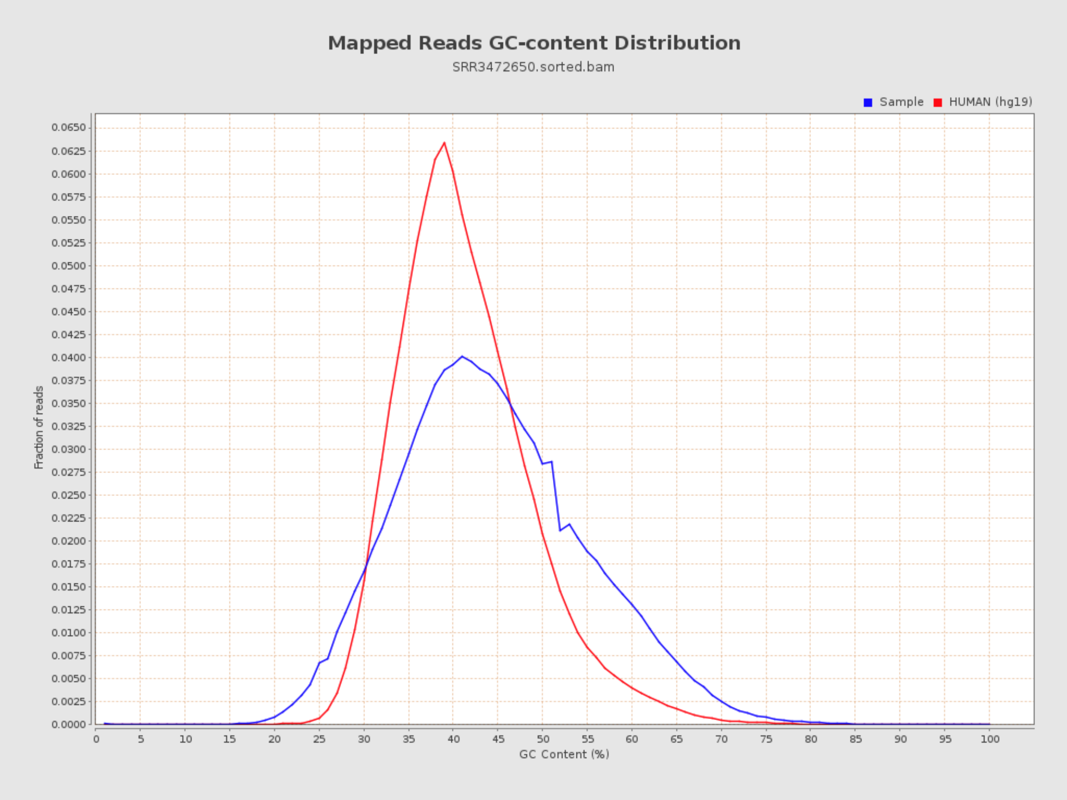
7. Results : Duplication Rate Histogram



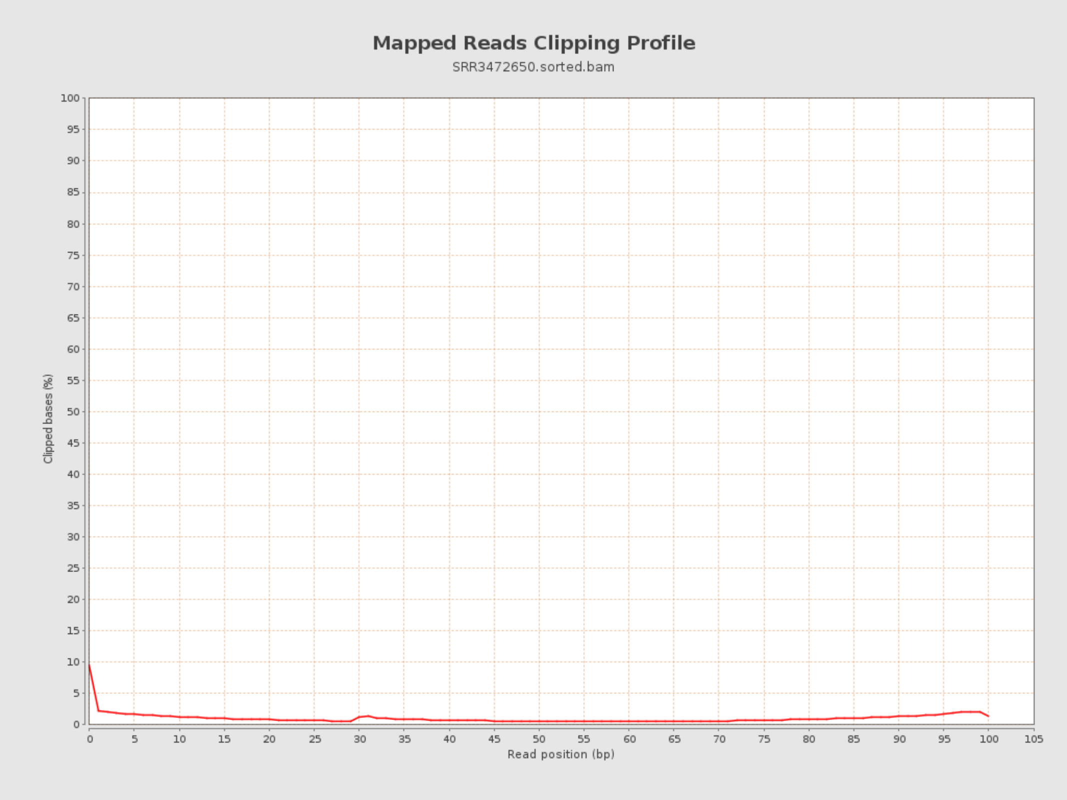
8. Results : Mapped Reads Nucleotide Content



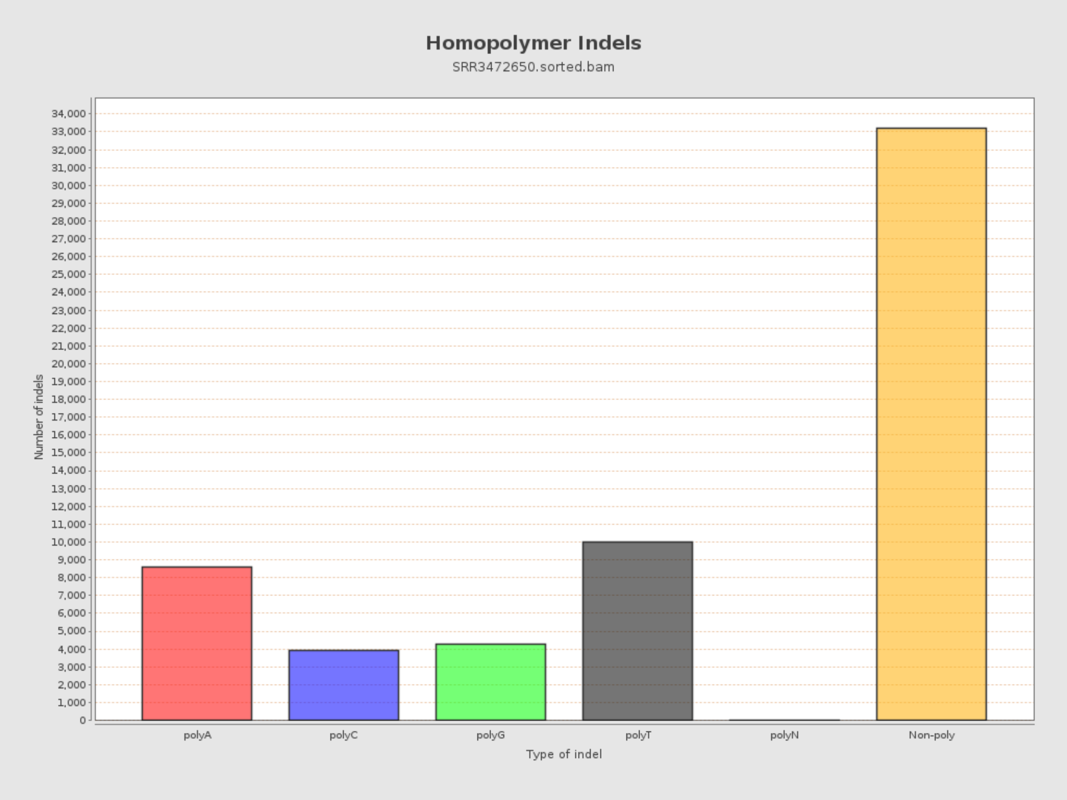
9. Results : Mapped Reads GC-content Distribution



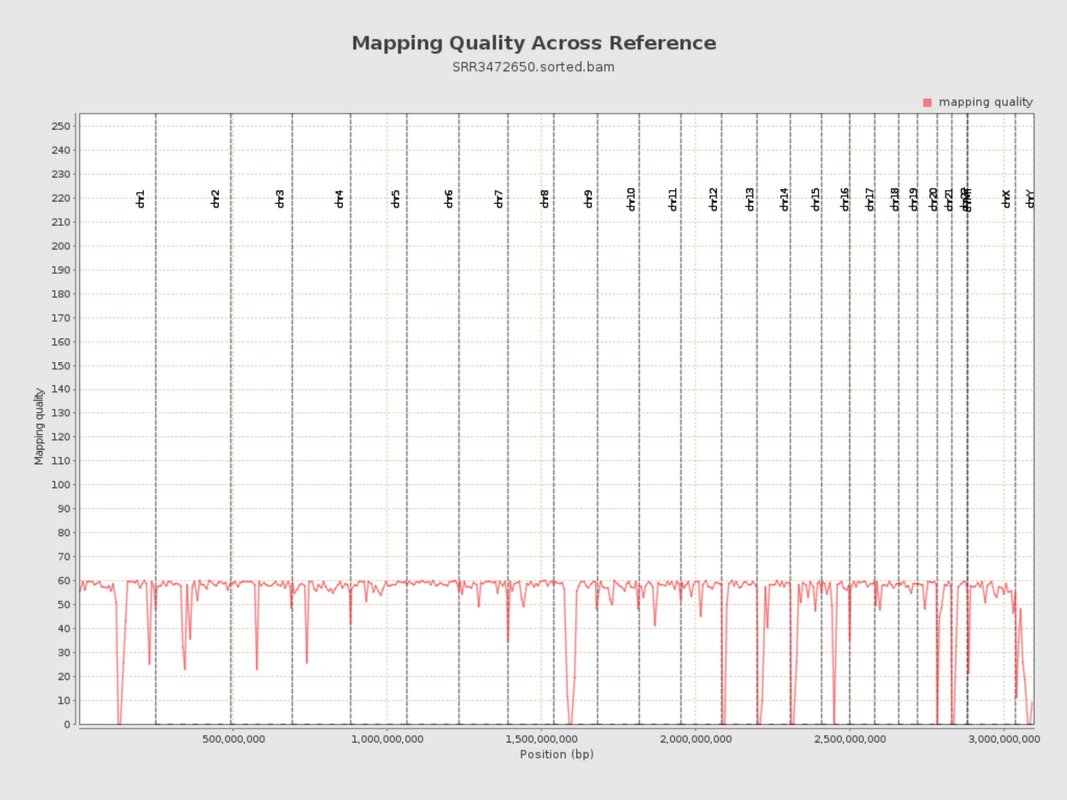
10. Results : Mapped Reads Clipping Profile



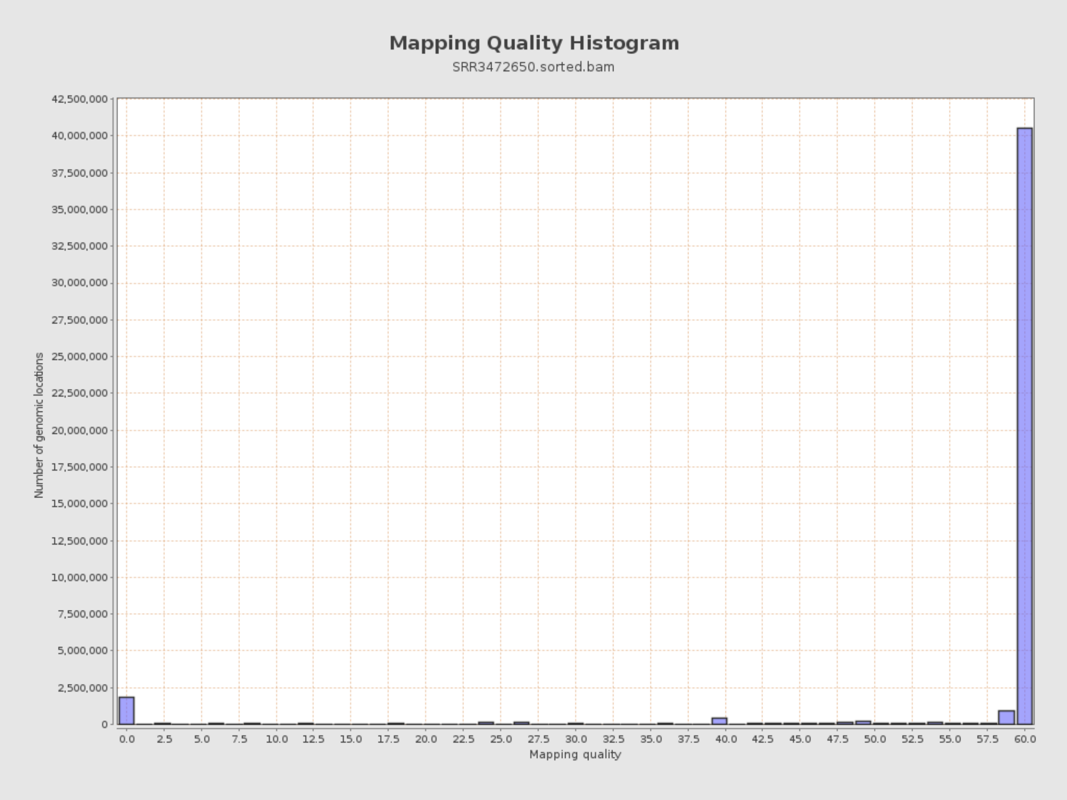
11. Results : Homopolymer Indels



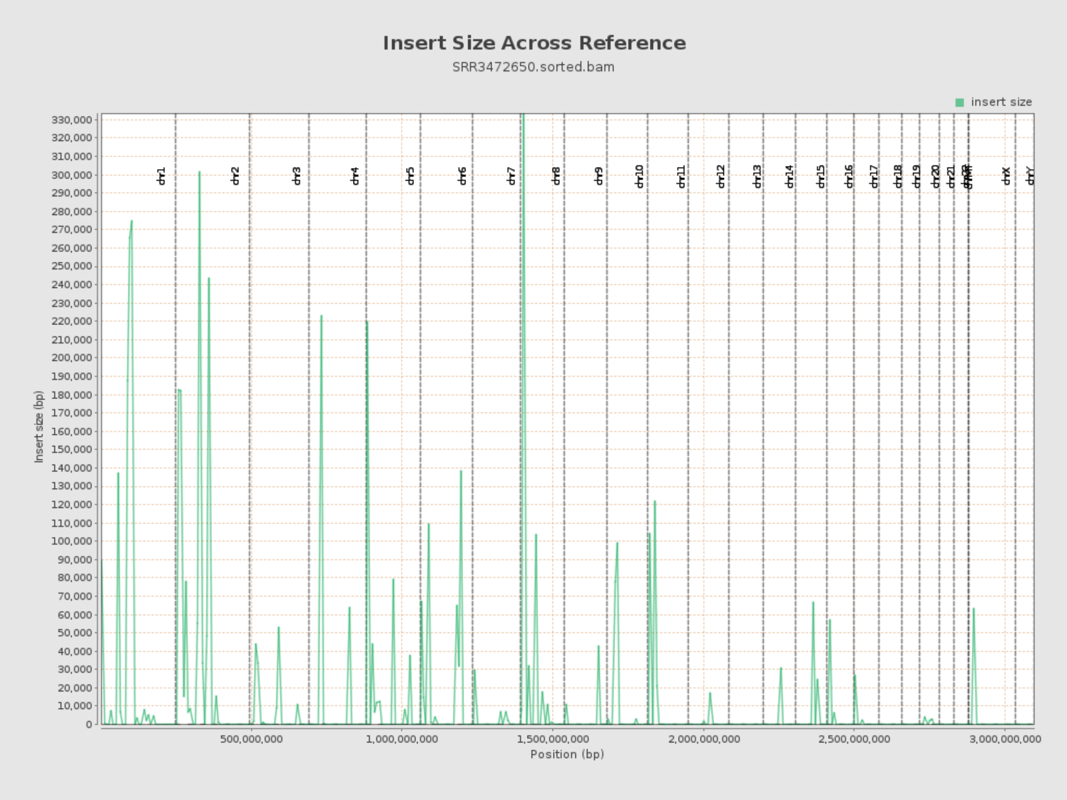
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram