Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 04:35:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004148.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_SRR6004148 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004148.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 04:35:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004148.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,947,200
Mapped reads	4,366,729 / 88.27%
Unmapped reads	580,471 / 11.73%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	36,001 / 0.73%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	289,462 / 5.85%
Duplication rate	4.91%
Clipped reads	1,659,224 / 33.54%

2.2. ACGT Content

Number/percentage of A's	85,473,940 / 28.62%
Number/percentage of C's	54,464,169 / 18.24%
Number/percentage of T's	96,536,561 / 32.33%
Number/percentage of G's	62,096,207 / 20.8%
Number/percentage of N's	33,422 / 0.01%
GC Percentage	39.04%

2.3. Coverage

Mean	0.0965

Standard Deviation	0.9319

2.4. Mapping Quality

Mean Mapping Quality	46.99

2.5. Mismatches and indels

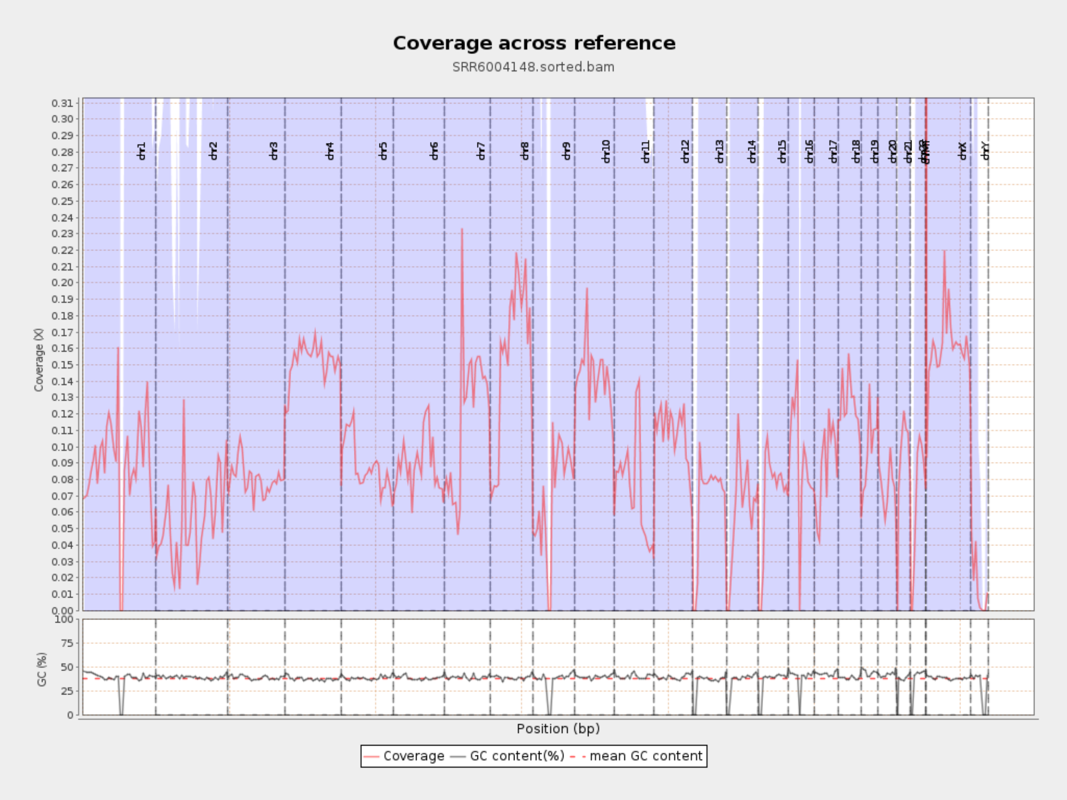
General error rate	0.93%
Mismatches	2,718,292
Insertions	26,245
Mapped reads with at least one insertion	0.6%
Deletions	79,452
Mapped reads with at least one deletion	1.8%
Homopolymer indels	47.08%

2.6. Chromosome stats

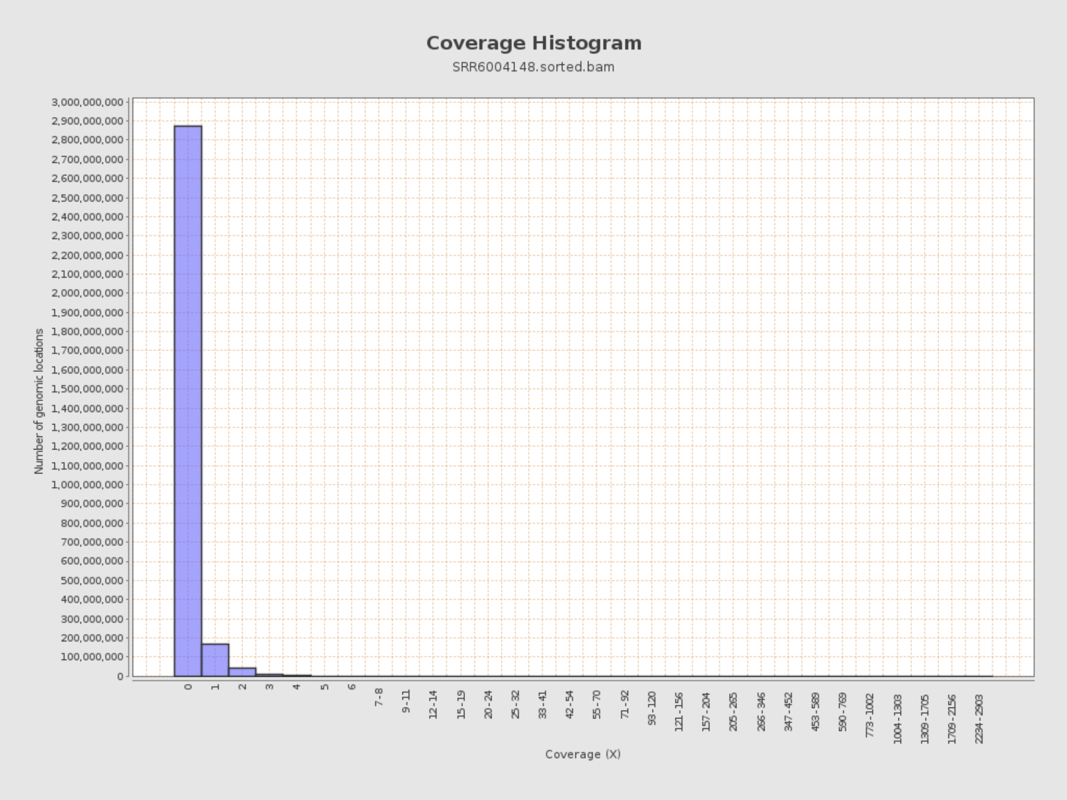
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	21931339	0.088	1.7216
chr2	243199373	13474206	0.0554	0.7912
chr3	198022430	15988381	0.0807	0.3602
chr4	191154276	29248601	0.153	0.546
chr5	180915260	15964422	0.0882	0.3904
chr6	171115067	15282038	0.0893	0.4255
chr7	159138663	18904899	0.1188	1.612

chr8	146364022	22984749	0.157	1.7838
chr9	141213431	9860366	0.0698	0.8559
chr10	135534747	19472608	0.1437	0.8516
chr11	135006516	9990154	0.074	0.5225
chr12	133851895	14578150	0.1089	0.4566
chr13	115169878	7696429	0.0668	0.3244
chr14	107349540	6624506	0.0617	0.414
chr15	102531392	6967680	0.068	0.3285
chr16	90354753	8174275	0.0905	0.5337
chr17	81195210	7084761	0.0873	0.401
chr18	78077248	9867931	0.1264	1.7881
chr19	59128983	5855177	0.099	1.1231
chr20	63025520	4760326	0.0755	0.3725
chr21	48129895	4358412	0.0906	0.4828
chr22	51304566	3445212	0.0672	0.318
chrMT	16571	378676	22.8517	13.139
chrX	155270560	24981440	0.1609	0.6193
chrY	59373566	862859	0.0145	0.322

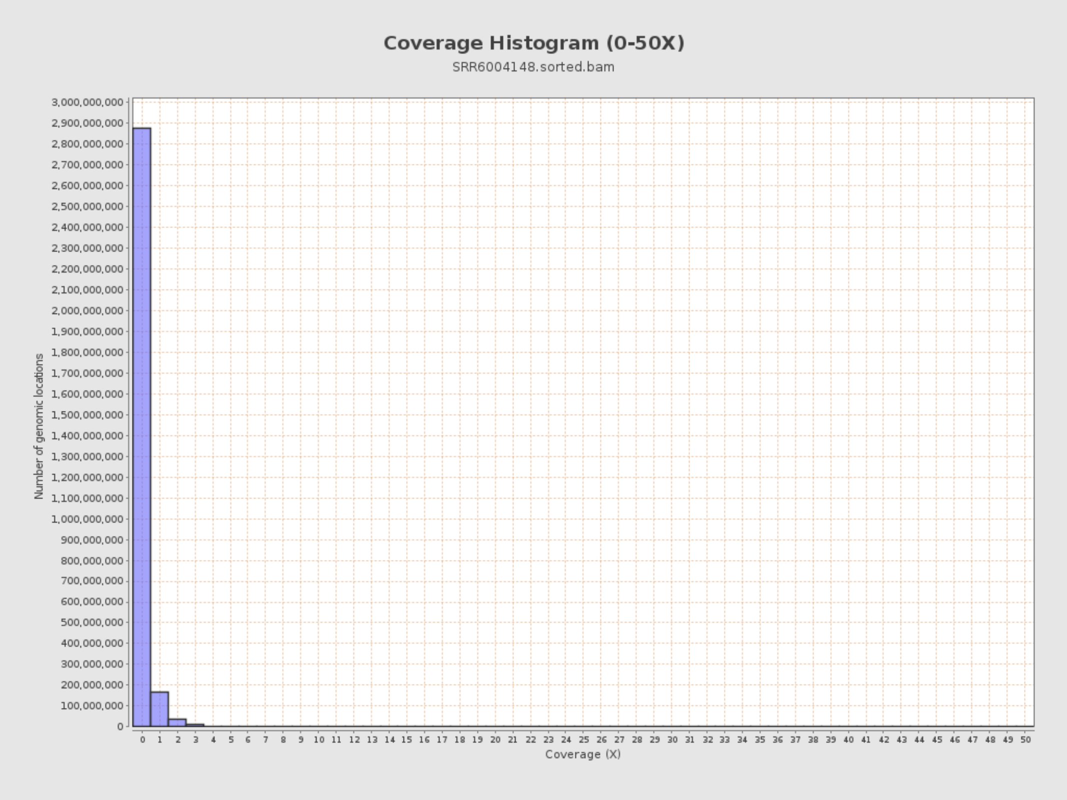
3. Results : Coverage across reference



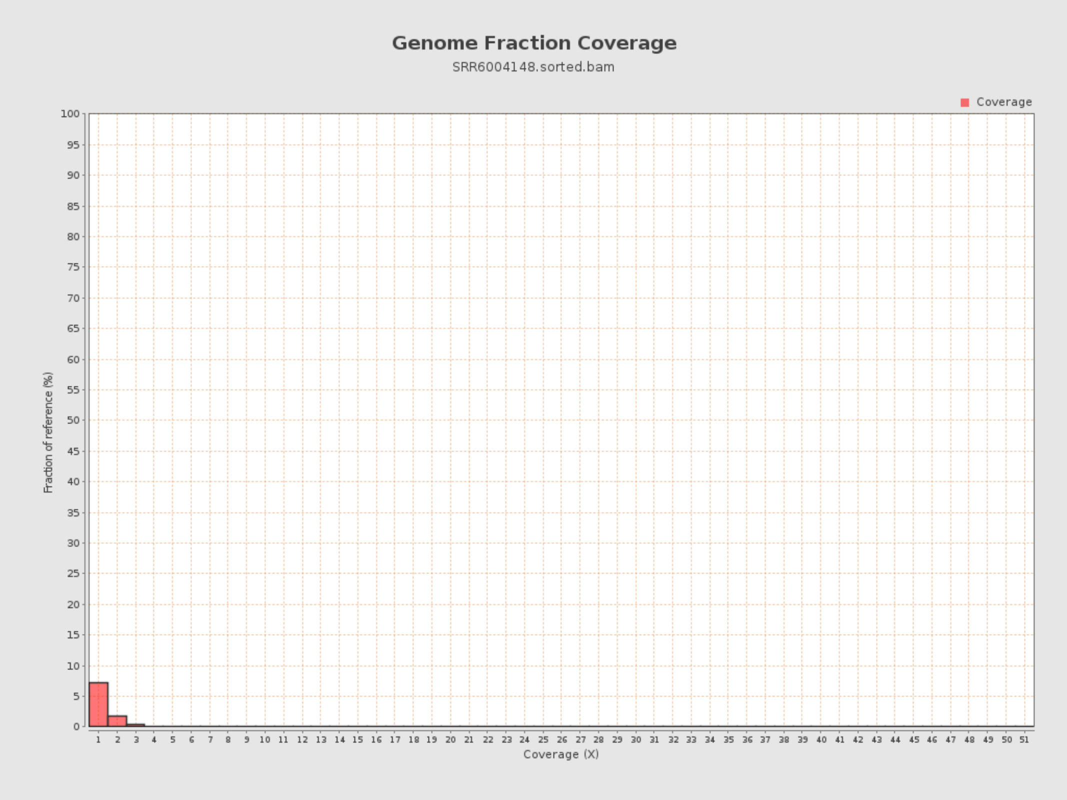
4. Results : Coverage Histogram



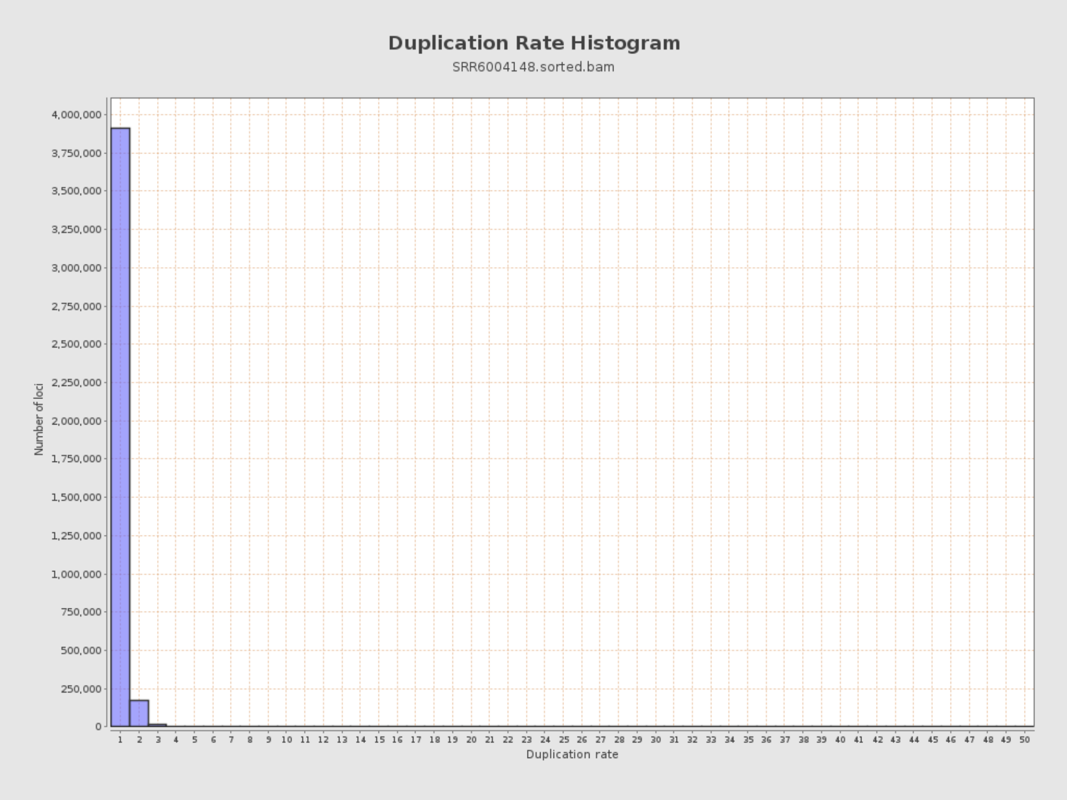
5. Results : Coverage Histogram (0-50X)



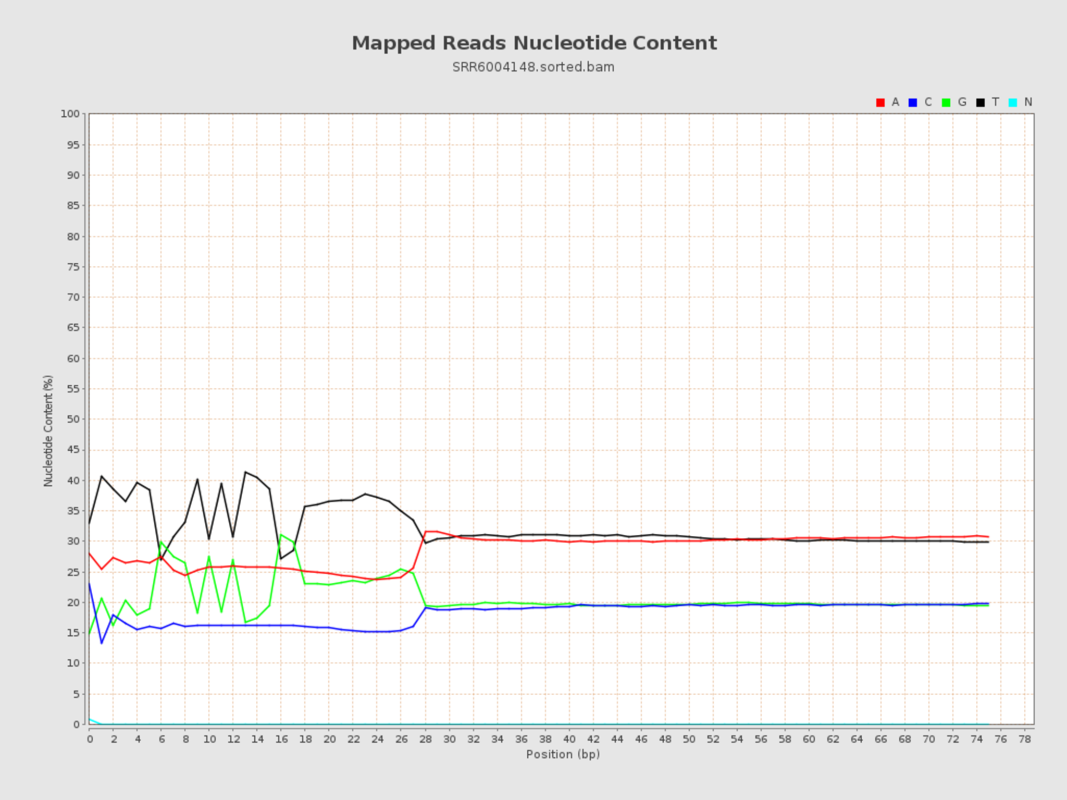
6. Results : Genome Fraction Coverage



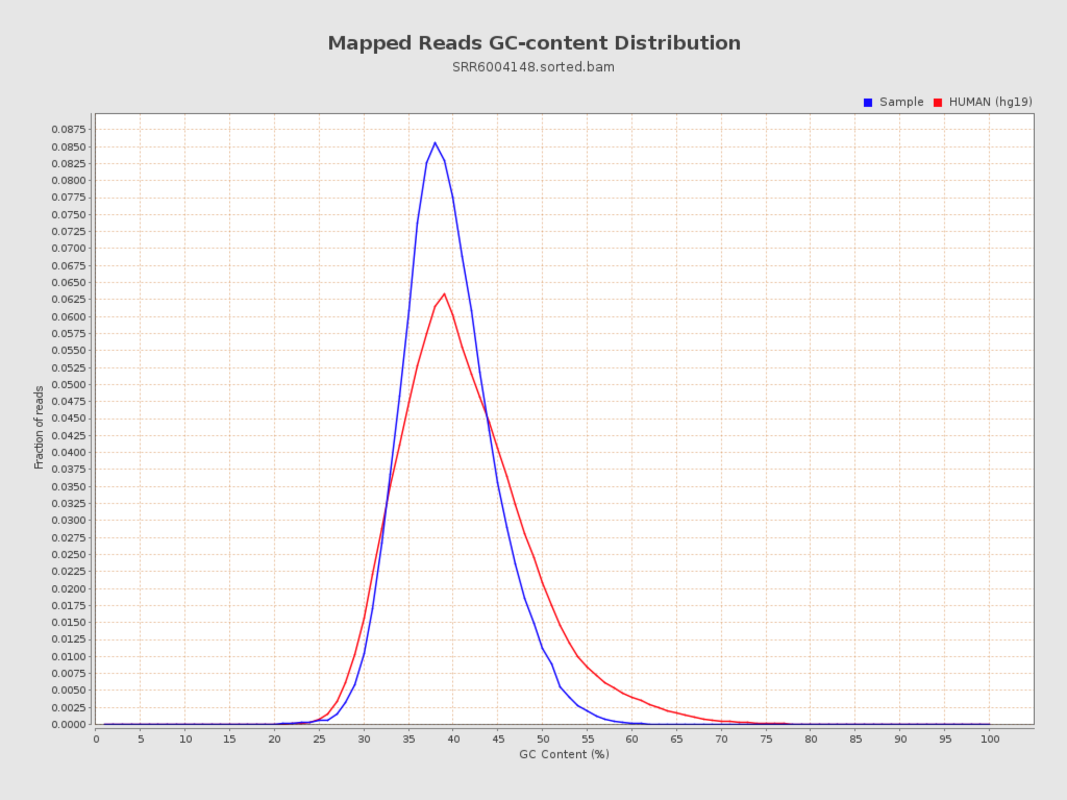
7. Results : Duplication Rate Histogram



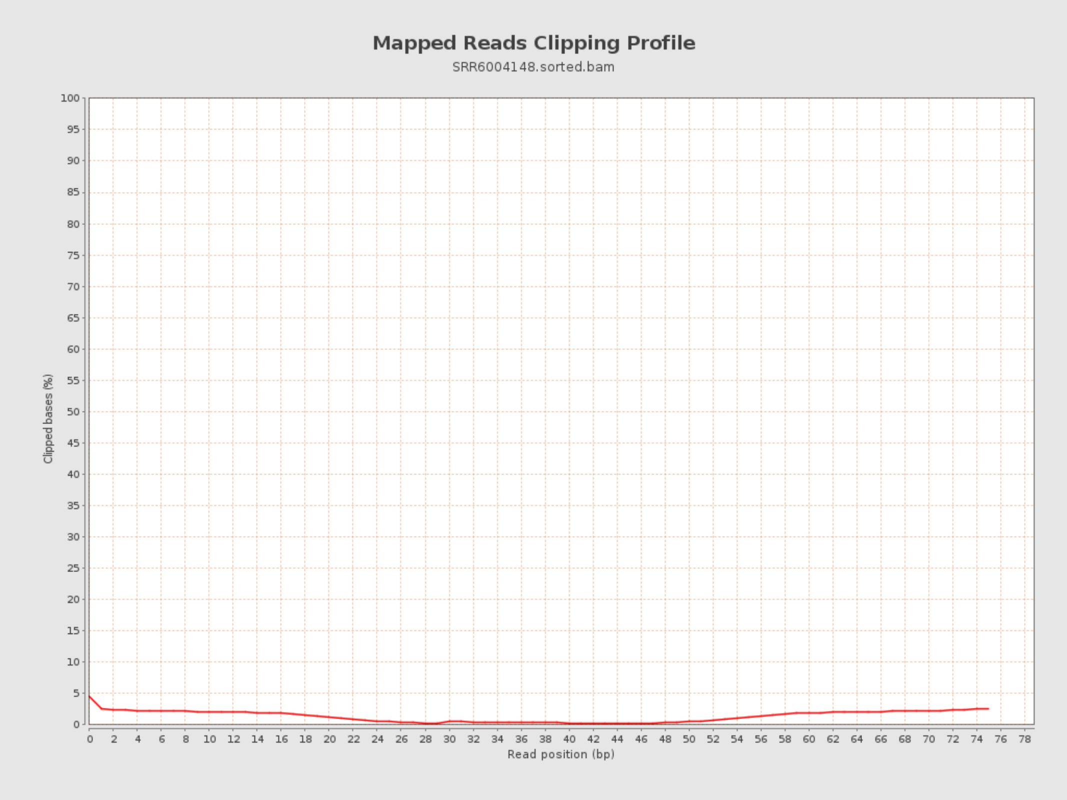
8. Results : Mapped Reads Nucleotide Content



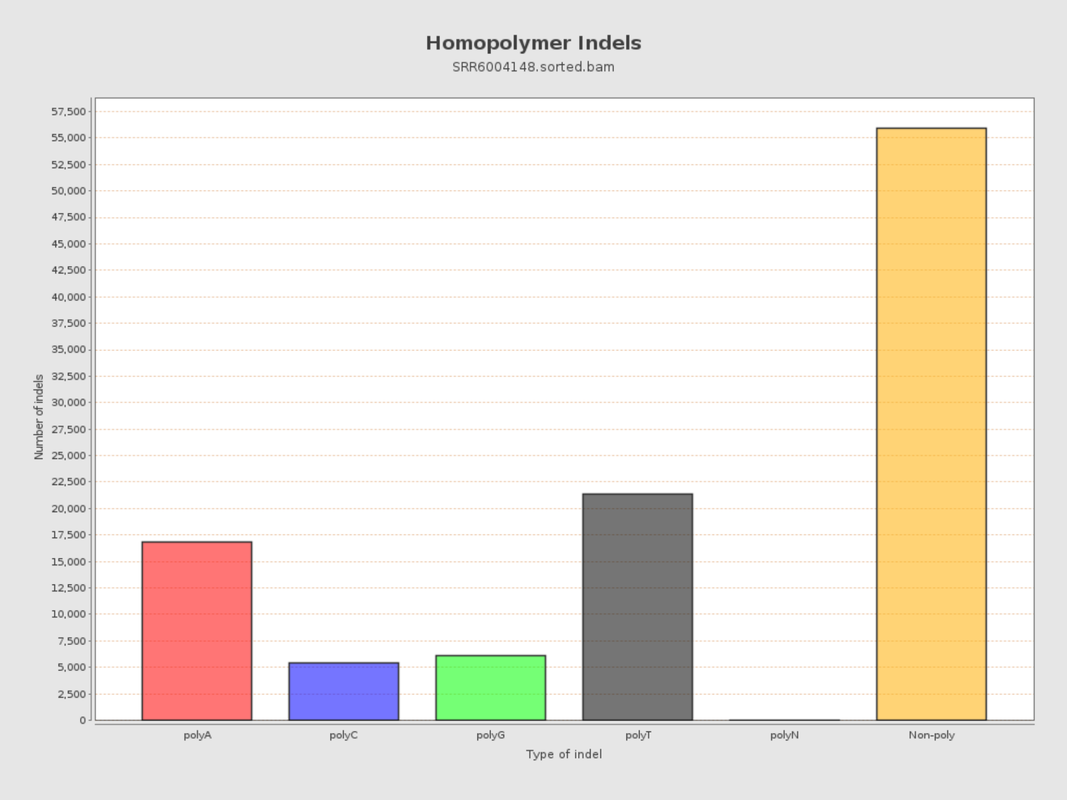
9. Results : Mapped Reads GC-content Distribution



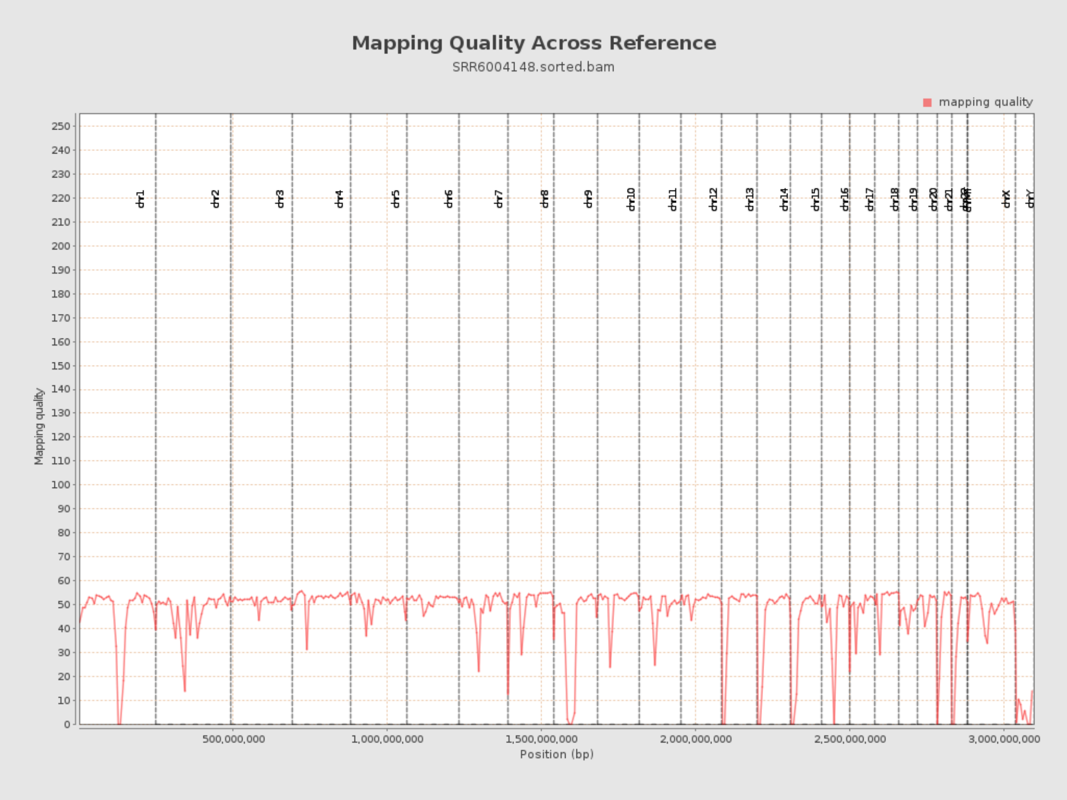
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram