Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 21:45:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716162.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_SRR9716162 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716162.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 21:45:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716162.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,432,314
Mapped reads	3,950,624 / 89.13%
Unmapped reads	481,690 / 10.87%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,725 / 0.51%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	205,122 / 4.63%
Duplication rate	3.63%
Clipped reads	3,966,208 / 89.48%

2.2. ACGT Content

Number/percentage of A's	57,270,364 / 25.51%
Number/percentage of C's	44,962,963 / 20.03%
Number/percentage of T's	68,064,335 / 30.32%
Number/percentage of G's	54,183,948 / 24.14%
Number/percentage of N's	3,428 / 0%
GC Percentage	44.17%

2.3. Coverage

Mean	0.0725

Standard Deviation	0.6233

2.4. Mapping Quality

Mean Mapping Quality	42.89

2.5. Mismatches and indels

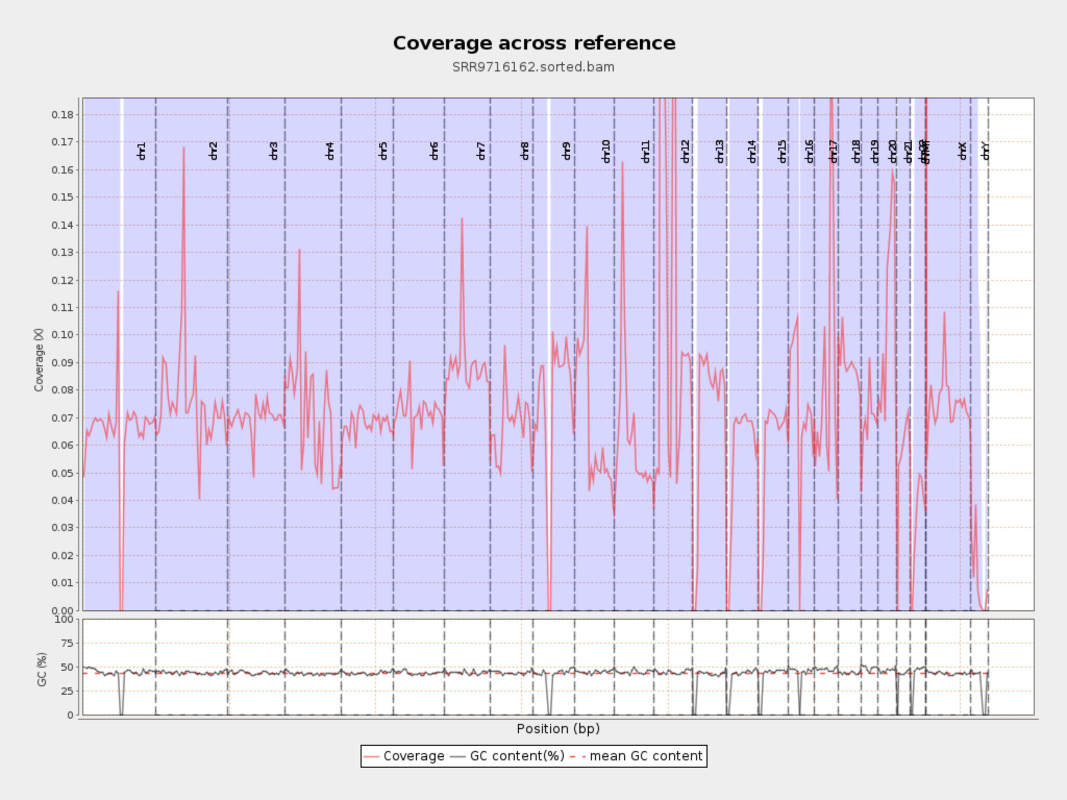
General error rate	0.57%
Mismatches	1,244,105
Insertions	14,725
Mapped reads with at least one insertion	0.37%
Deletions	36,899
Mapped reads with at least one deletion	0.93%
Homopolymer indels	40.61%

2.6. Chromosome stats

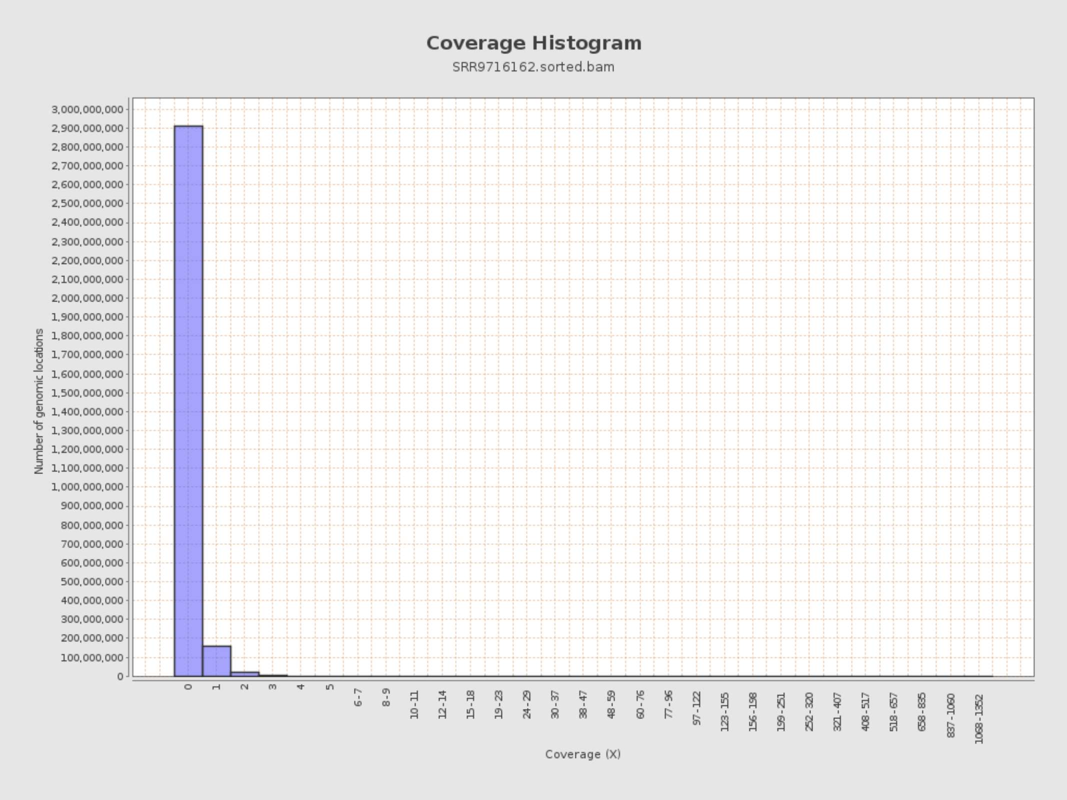
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16013630	0.0642	1.115
chr2	243199373	18612611	0.0765	0.7772
chr3	198022430	13826087	0.0698	0.3083
chr4	191154276	13677960	0.0716	0.3996
chr5	180915260	12236672	0.0676	0.3123
chr6	171115067	12324549	0.072	0.3883
chr7	159138663	14259746	0.0896	0.8607

chr8	146364022	9838180	0.0672	0.5464
chr9	141213431	10603939	0.0751	0.7147
chr10	135534747	9135135	0.0674	0.6801
chr11	135006516	8741194	0.0647	0.4707
chr12	133851895	16662609	0.1245	0.5154
chr13	115169878	8233985	0.0715	0.3083
chr14	107349540	6103865	0.0569	0.4145
chr15	102531392	5730779	0.0559	0.281
chr16	90354753	6501049	0.072	0.4
chr17	81195210	7173002	0.0883	0.3797
chr18	78077248	7007646	0.0898	1.2335
chr19	59128983	4144436	0.0701	0.9129
chr20	63025520	6983575	0.1108	0.4225
chr21	48129895	2682242	0.0557	0.3699
chr22	51304566	1628471	0.0317	0.2028
chrMT	16571	32854	1.9826	1.9306
chrX	155270560	11732616	0.0756	0.47
chrY	59373566	659545	0.0111	0.2613

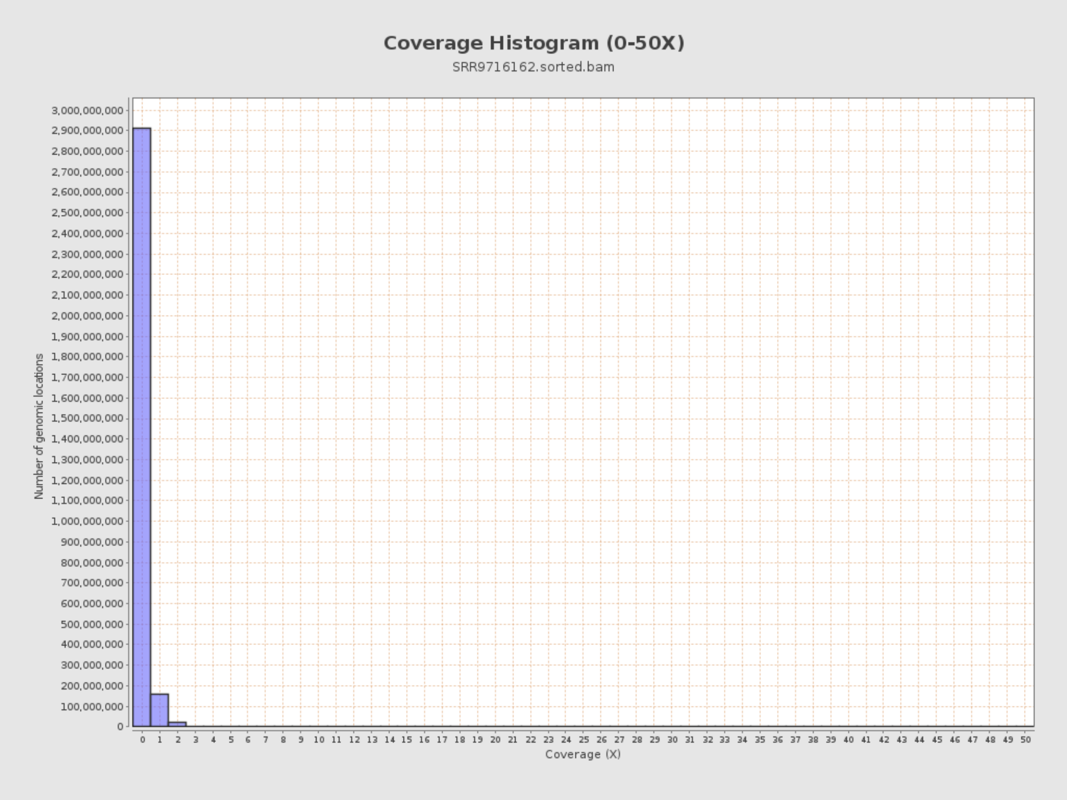
3. Results : Coverage across reference



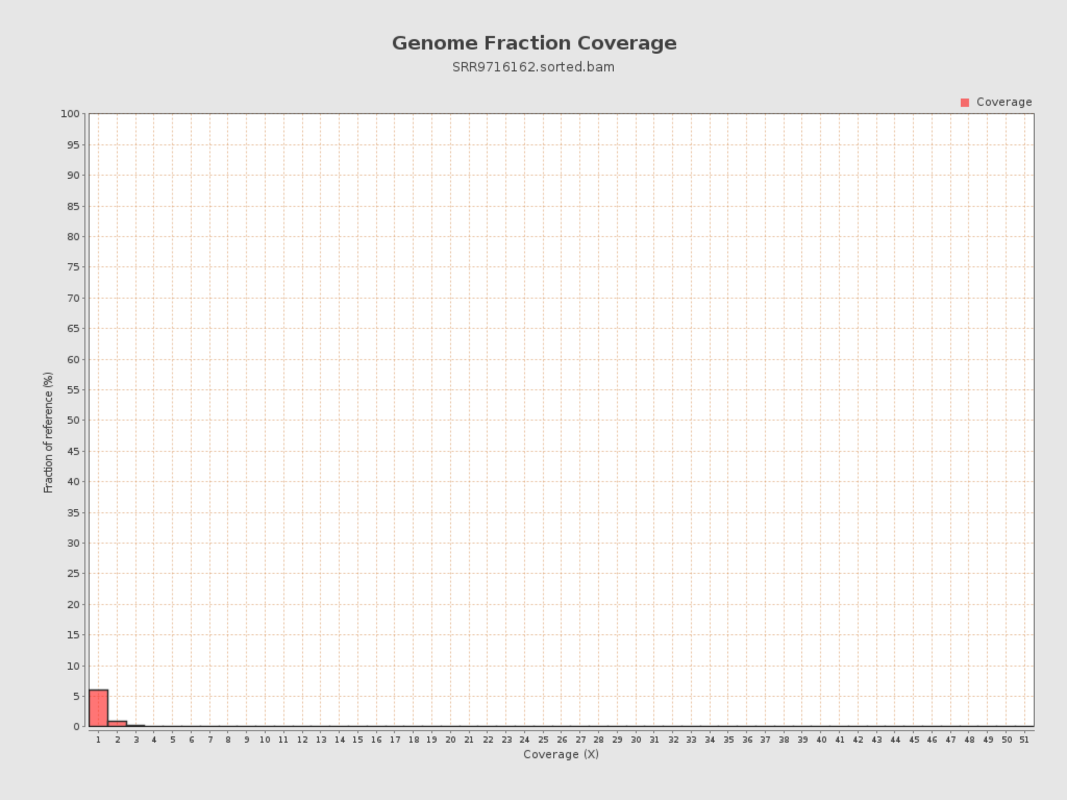
4. Results : Coverage Histogram



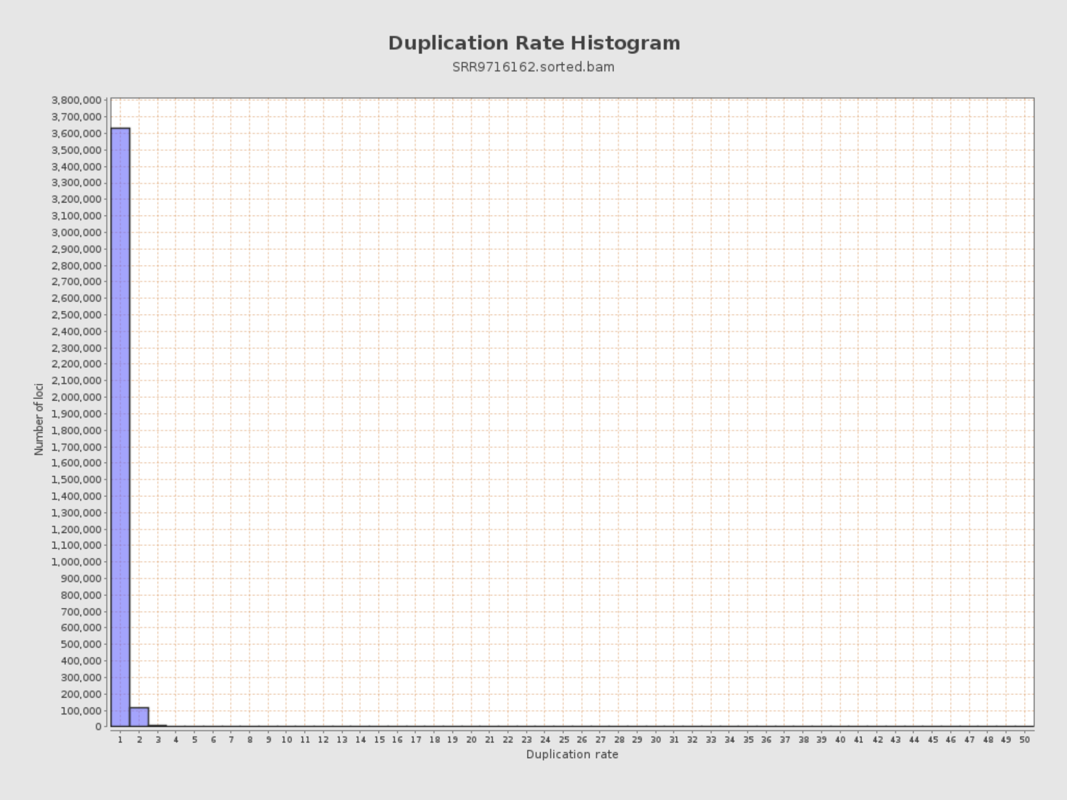
5. Results : Coverage Histogram (0-50X)



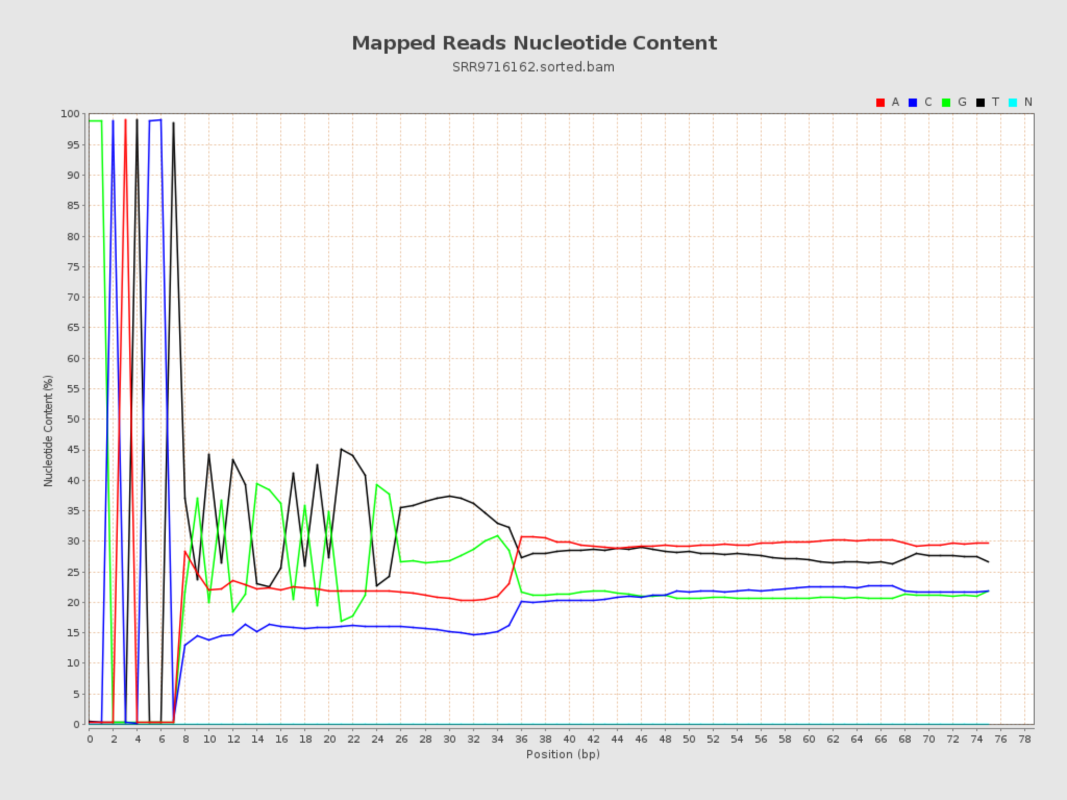
6. Results : Genome Fraction Coverage



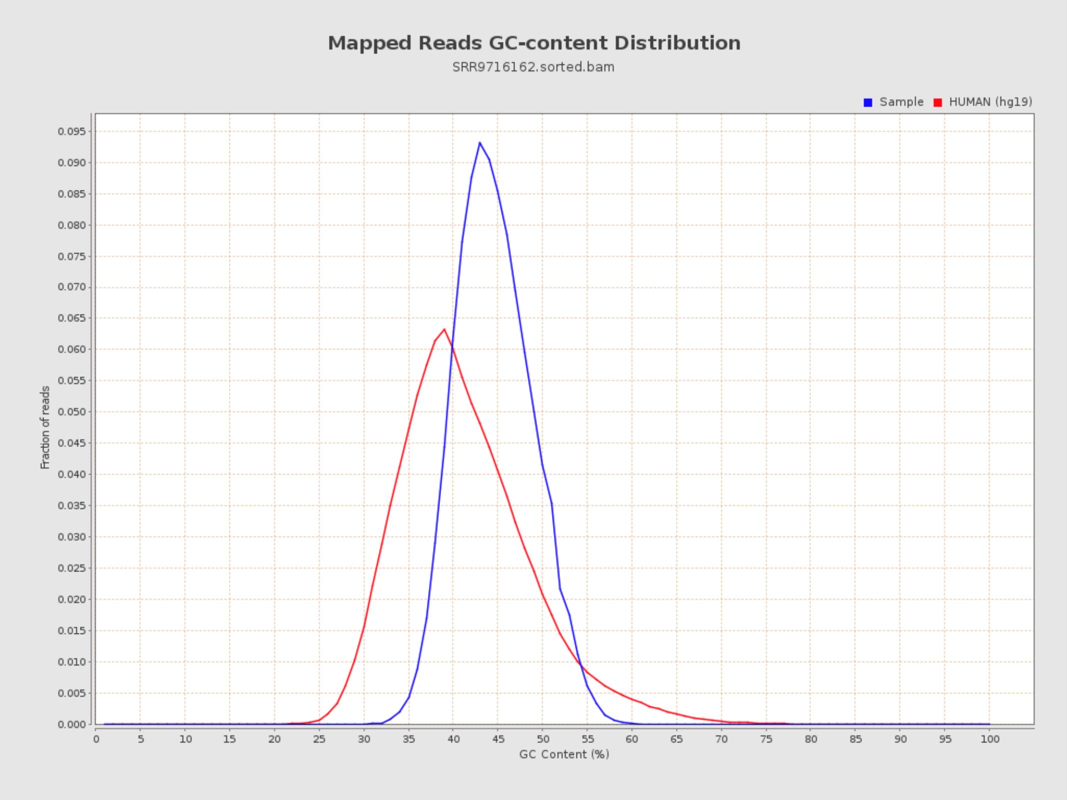
7. Results : Duplication Rate Histogram



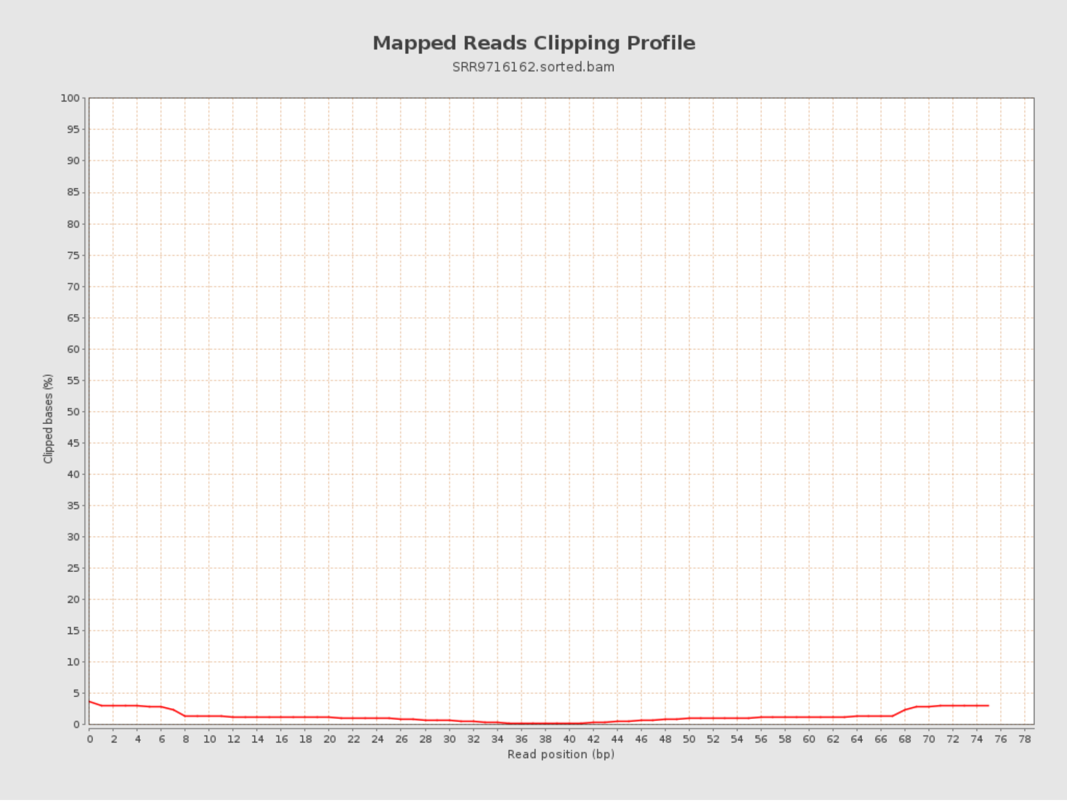
8. Results : Mapped Reads Nucleotide Content



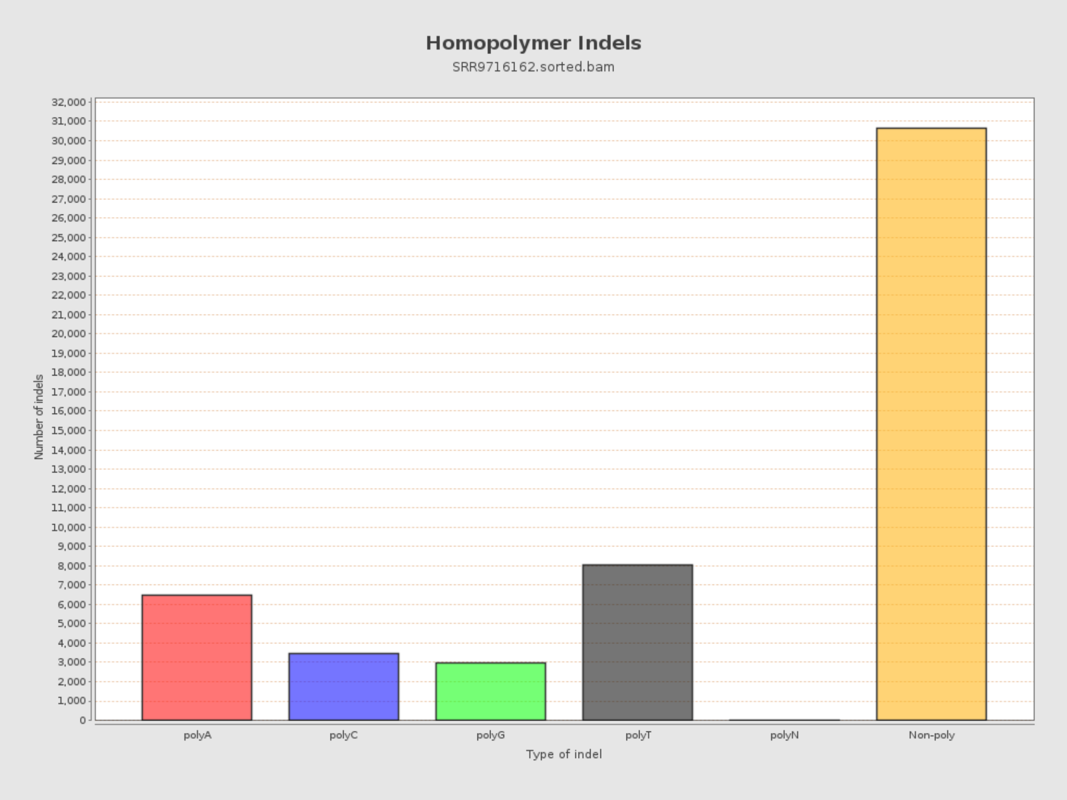
9. Results : Mapped Reads GC-content Distribution



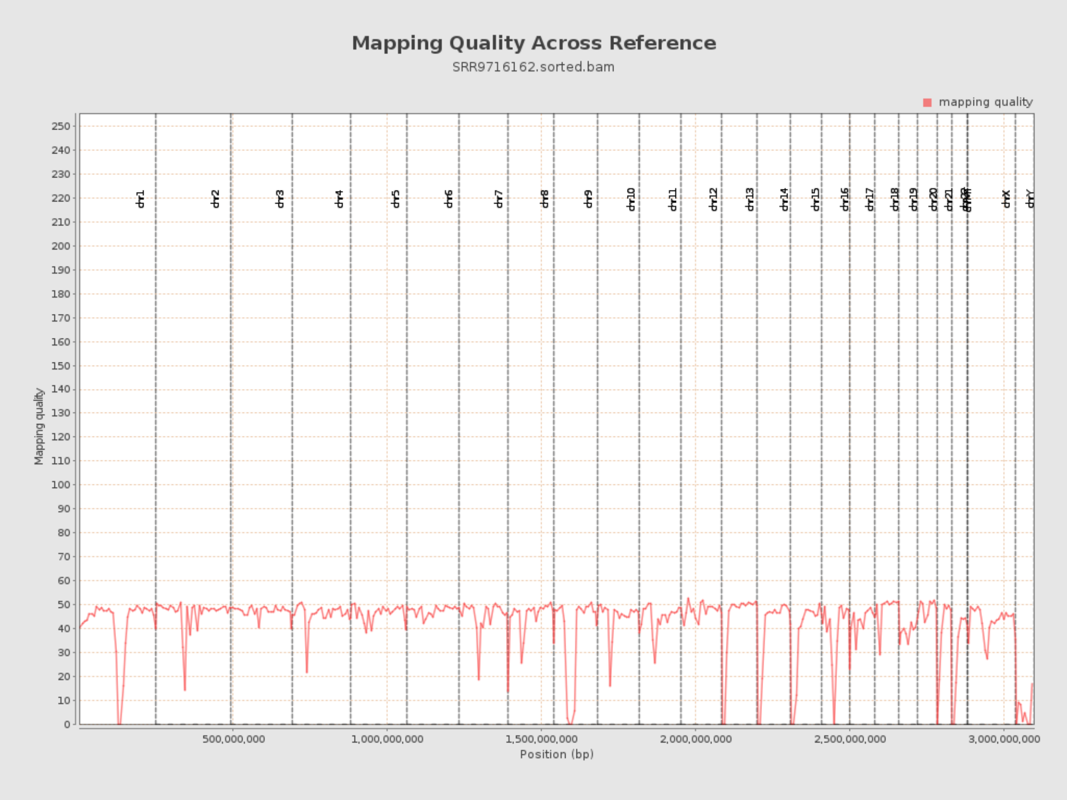
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram