Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 22:25:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716570.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_SRR9716570 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716570.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 22:25:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716570.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,878,491
Mapped reads	2,720,593 / 94.51%
Unmapped reads	157,898 / 5.49%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	66,437 / 2.31%
Read min/max/mean length	30 / 101 / 101.84
Duplicated reads (estimated)	189,833 / 6.59%
Duplication rate	5.17%
Clipped reads	2,786,468 / 96.8%

2.2. ACGT Content

Number/percentage of A's	50,749,160 / 24.12%
Number/percentage of C's	44,012,070 / 20.92%
Number/percentage of T's	61,790,739 / 29.36%
Number/percentage of G's	53,869,029 / 25.6%
Number/percentage of N's	8,441 / 0%
GC Percentage	46.51%

2.3. Coverage

Mean	0.068

Standard Deviation	0.5166

2.4. Mapping Quality

Mean Mapping Quality	46.49

2.5. Mismatches and indels

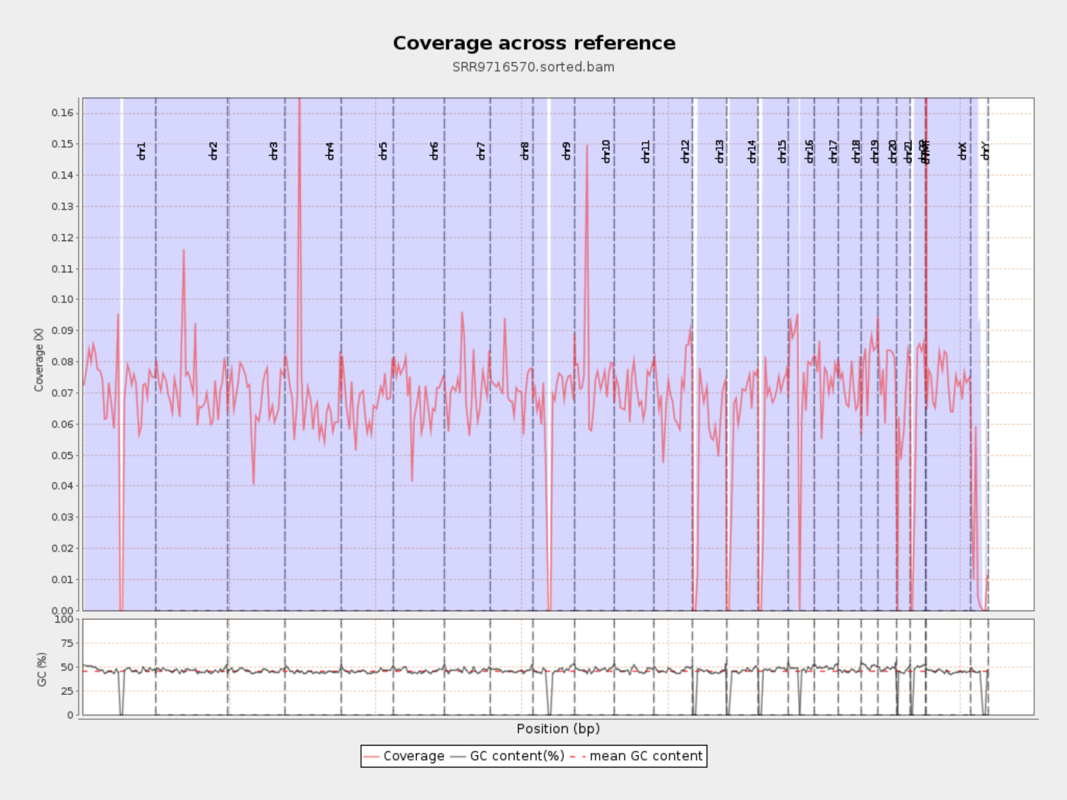
General error rate	0.68%
Mismatches	1,374,424
Insertions	17,787
Mapped reads with at least one insertion	0.64%
Deletions	38,782
Mapped reads with at least one deletion	1.4%
Homopolymer indels	38.94%

2.6. Chromosome stats

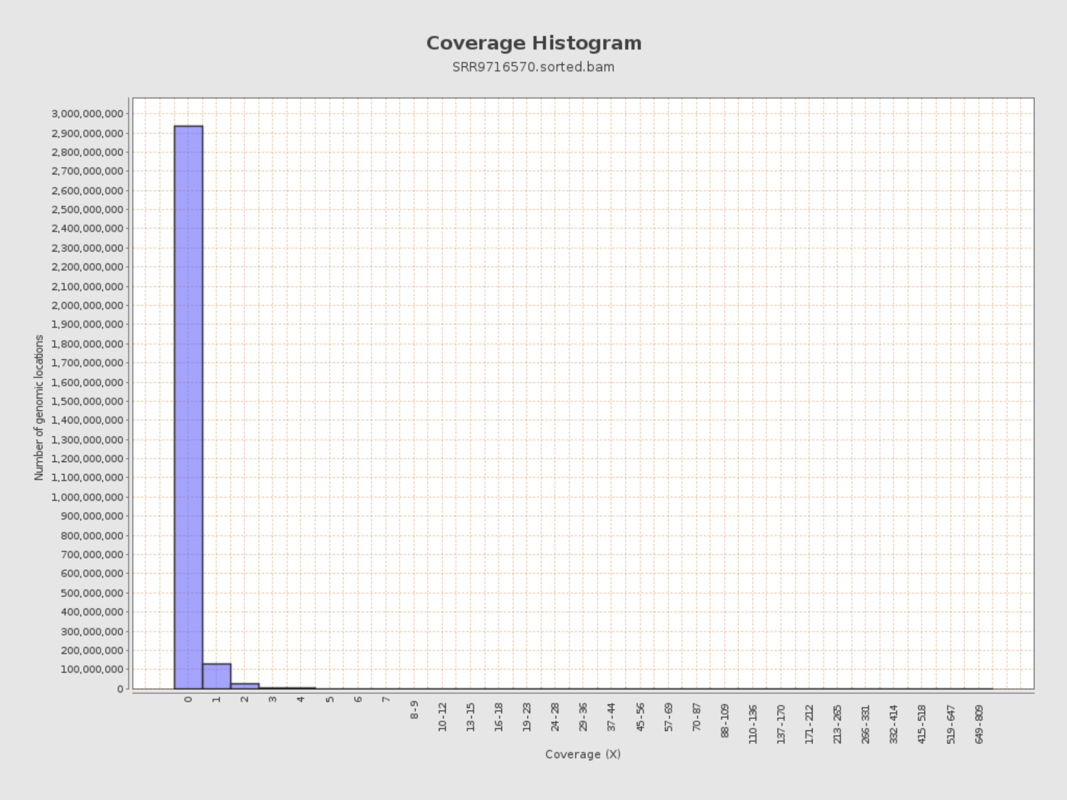
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17215585	0.0691	0.7533
chr2	243199373	17659385	0.0726	0.6076
chr3	198022430	13595262	0.0687	0.3267
chr4	191154276	13359912	0.0699	0.5898
chr5	180915260	12162765	0.0672	0.3253
chr6	171115067	11790226	0.0689	0.3514
chr7	159138663	11422947	0.0718	0.6397

chr8	146364022	10507401	0.0718	0.5095
chr9	141213431	8744109	0.0619	0.4625
chr10	135534747	10423609	0.0769	0.8167
chr11	135006516	9538293	0.0707	0.506
chr12	133851895	9472361	0.0708	0.3402
chr13	115169878	6218611	0.054	0.2886
chr14	107349540	6315898	0.0588	0.3478
chr15	102531392	6045529	0.059	0.3027
chr16	90354753	6628739	0.0734	0.3922
chr17	81195210	6094840	0.0751	0.4186
chr18	78077248	5599669	0.0717	0.7545
chr19	59128983	4748114	0.0803	0.5713
chr20	63025520	4863234	0.0772	0.3961
chr21	48129895	2894986	0.0601	0.5016
chr22	51304566	2984315	0.0582	0.3249
chrMT	16571	15742	0.95	1.275
chrX	155270560	11371435	0.0732	0.381
chrY	59373566	839481	0.0141	0.5702

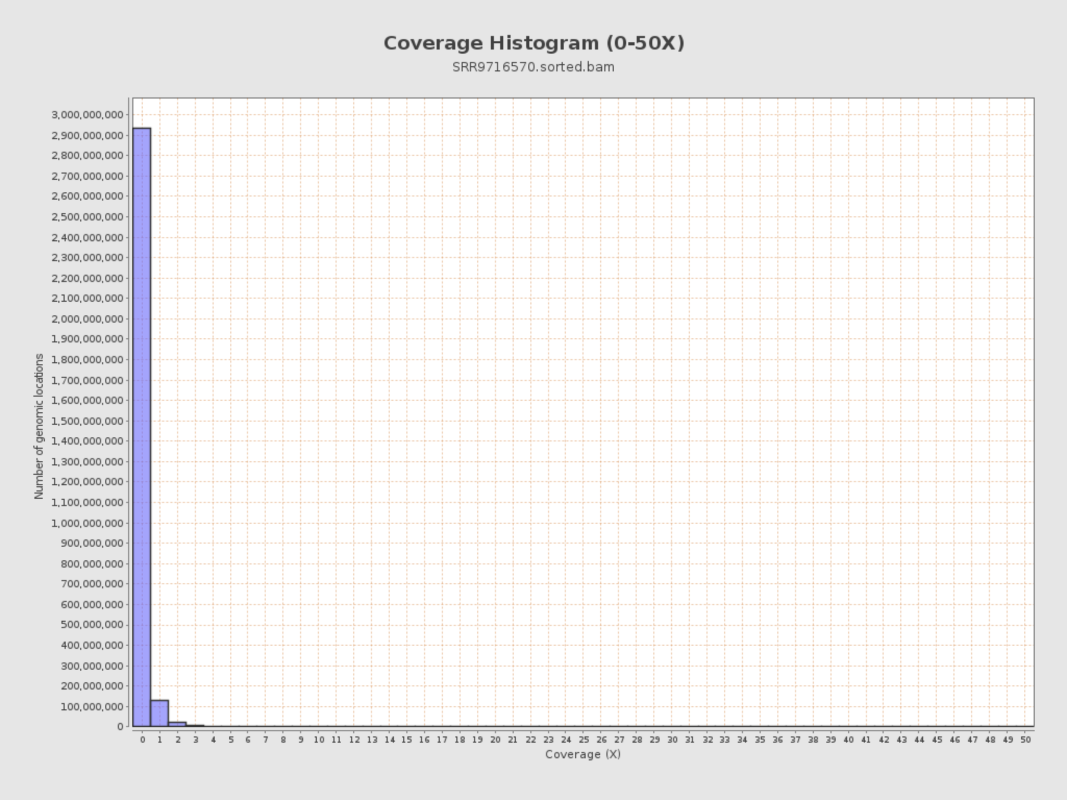
3. Results : Coverage across reference



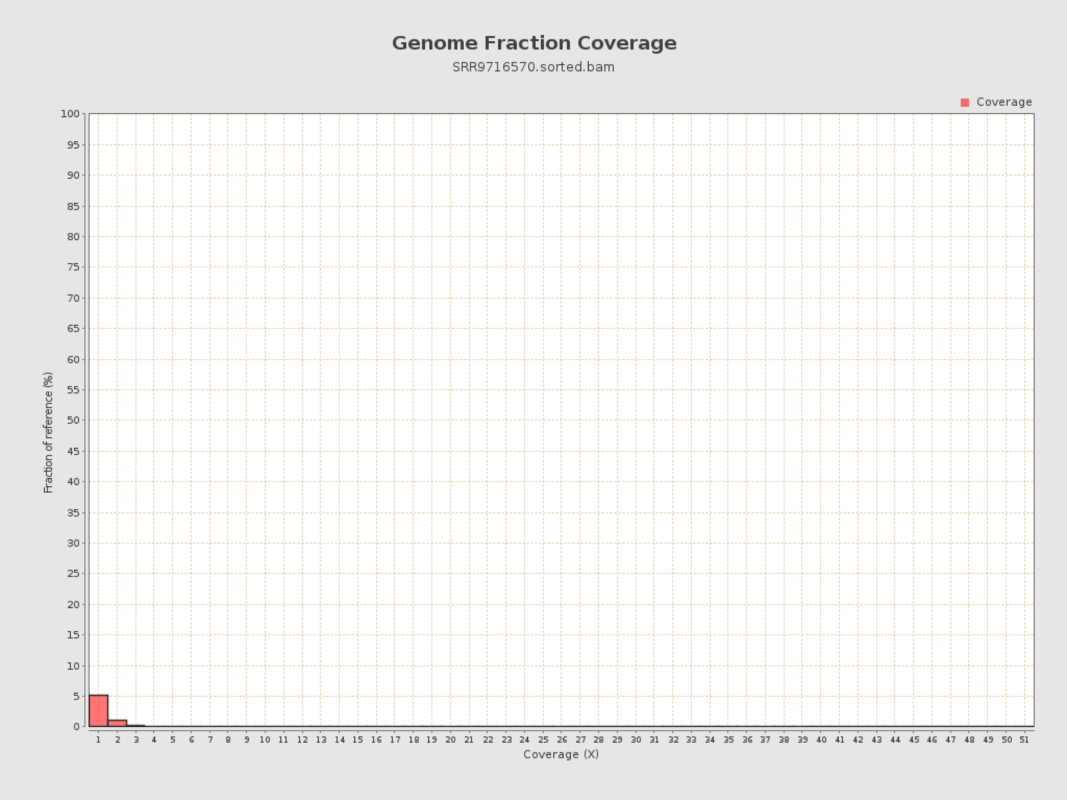
4. Results : Coverage Histogram



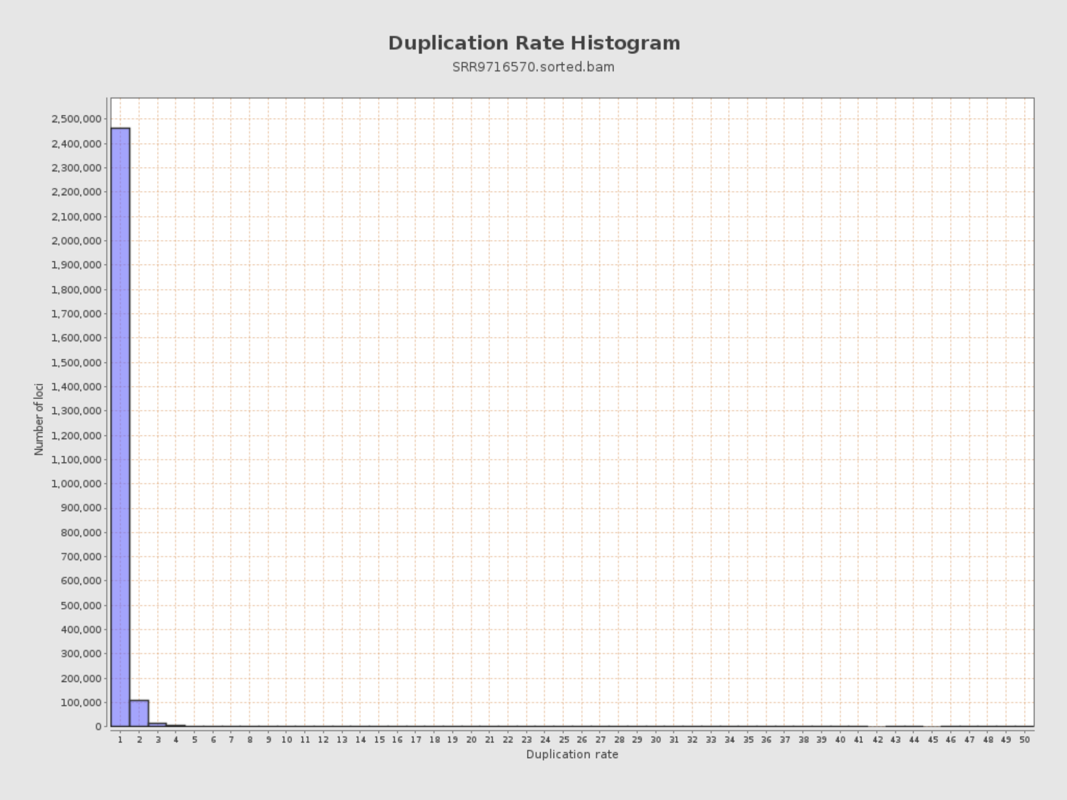
5. Results : Coverage Histogram (0-50X)



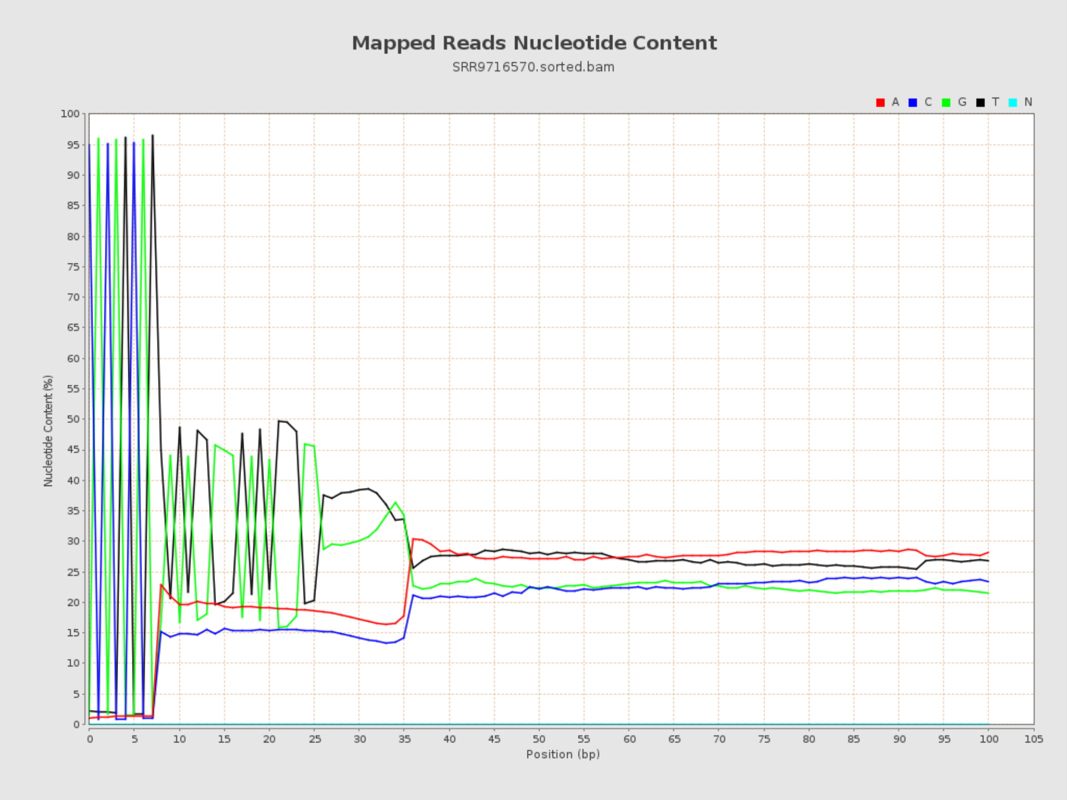
6. Results : Genome Fraction Coverage



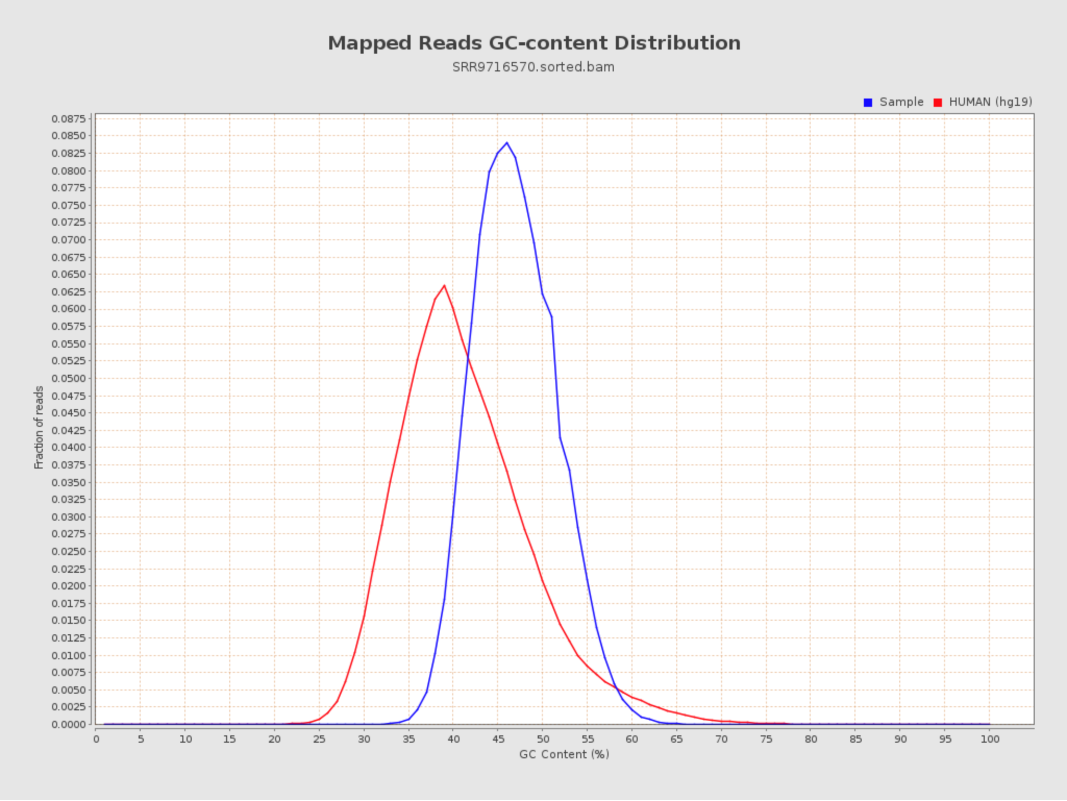
7. Results : Duplication Rate Histogram



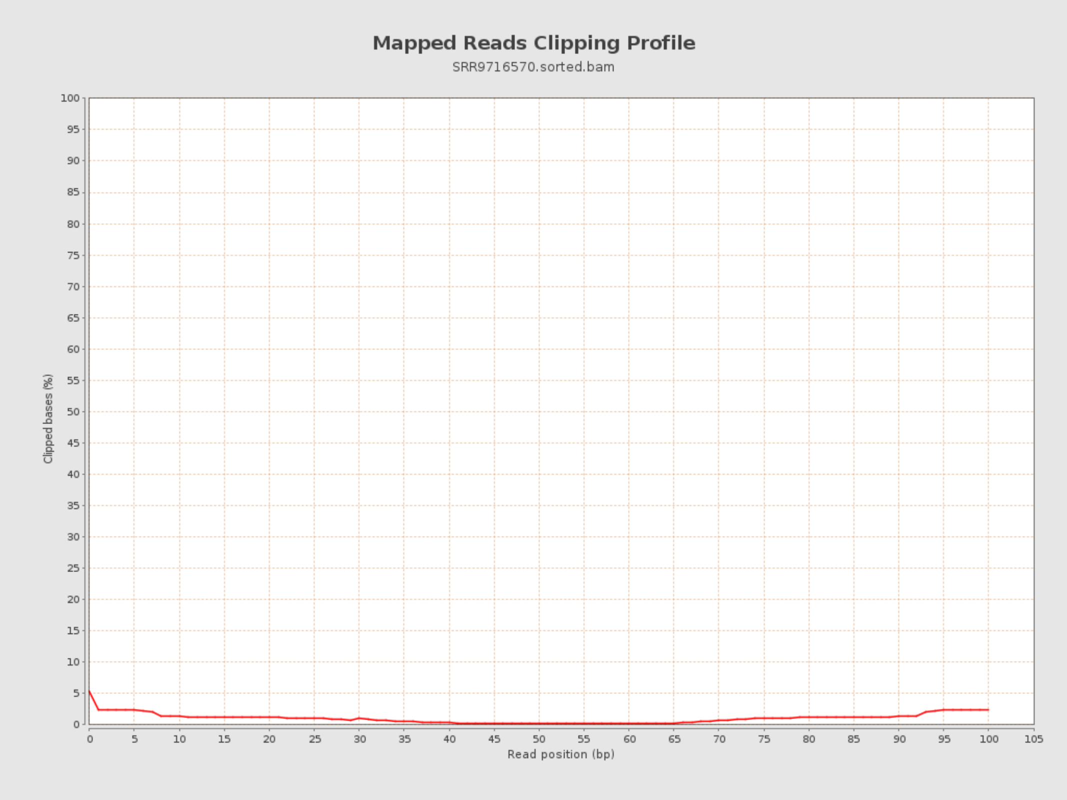
8. Results : Mapped Reads Nucleotide Content



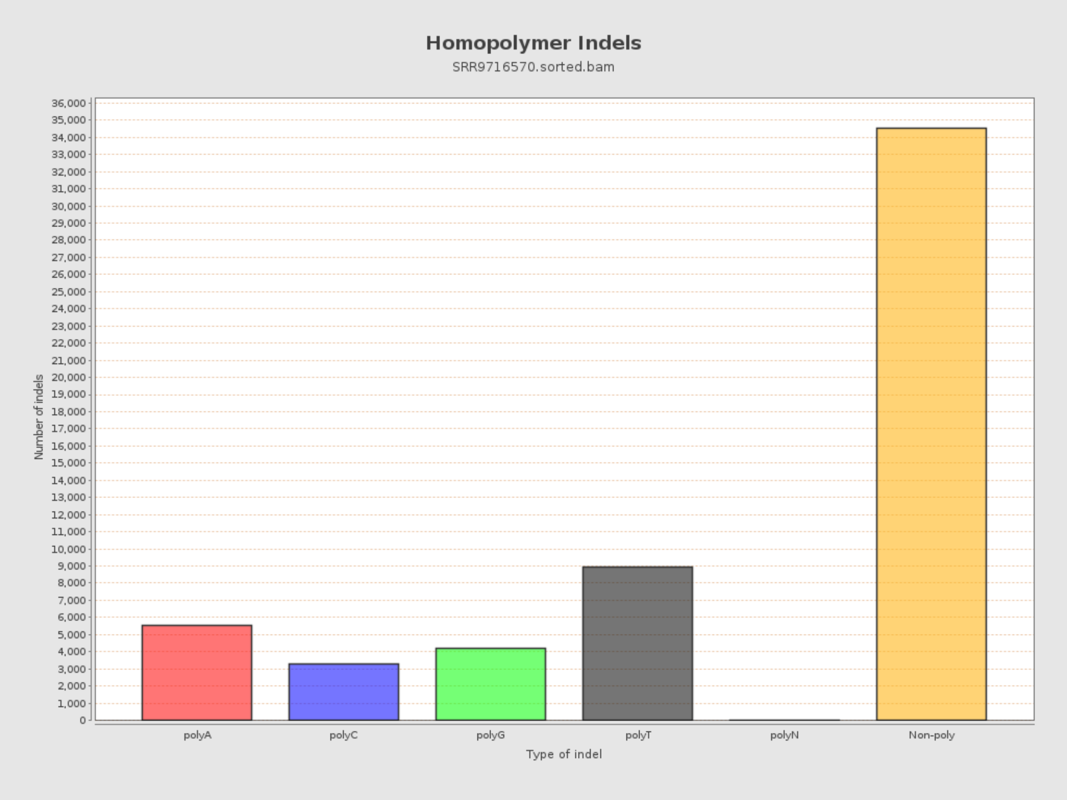
9. Results : Mapped Reads GC-content Distribution



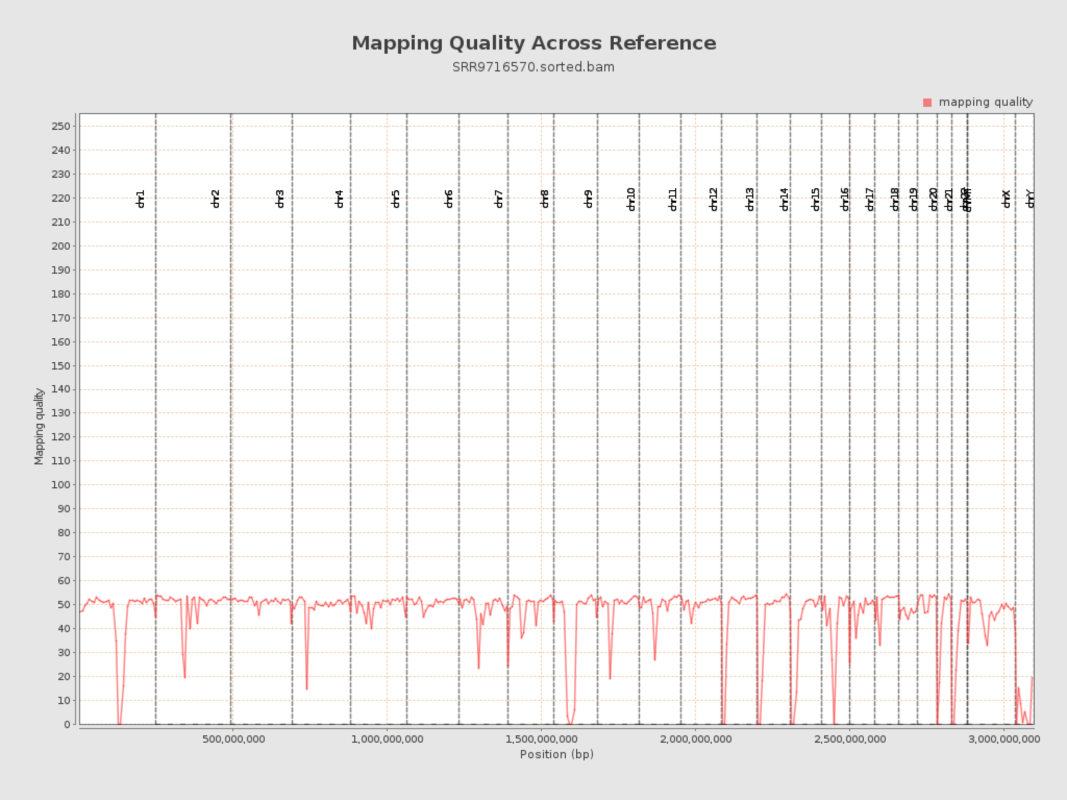
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram