Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 07:17:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716703.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_SRR9716703 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716703.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 07:17:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716703.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,255,396
Mapped reads	2,879,299 / 88.45%
Unmapped reads	376,097 / 11.55%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,462 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	100,232 / 3.08%
Duplication rate	2.47%
Clipped reads	2,882,407 / 88.54%

2.2. ACGT Content

Number/percentage of A's	41,341,110 / 25.3%
Number/percentage of C's	30,873,483 / 18.89%
Number/percentage of T's	49,942,515 / 30.56%
Number/percentage of G's	41,245,627 / 25.24%
Number/percentage of N's	1,171 / 0%
GC Percentage	44.14%

2.3. Coverage

Mean	0.0528

Standard Deviation	0.3803

2.4. Mapping Quality

Mean Mapping Quality	42.32

2.5. Mismatches and indels

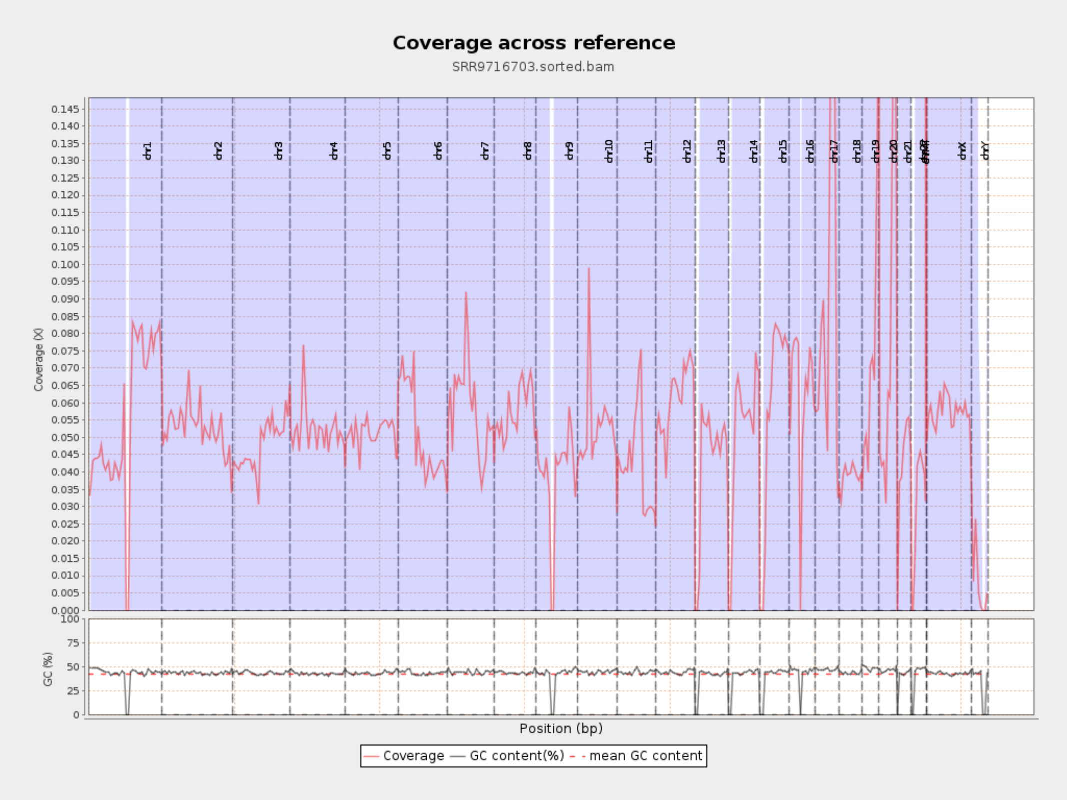
General error rate	0.53%
Mismatches	851,381
Insertions	11,584
Mapped reads with at least one insertion	0.4%
Deletions	29,847
Mapped reads with at least one deletion	1.03%
Homopolymer indels	40.2%

2.6. Chromosome stats

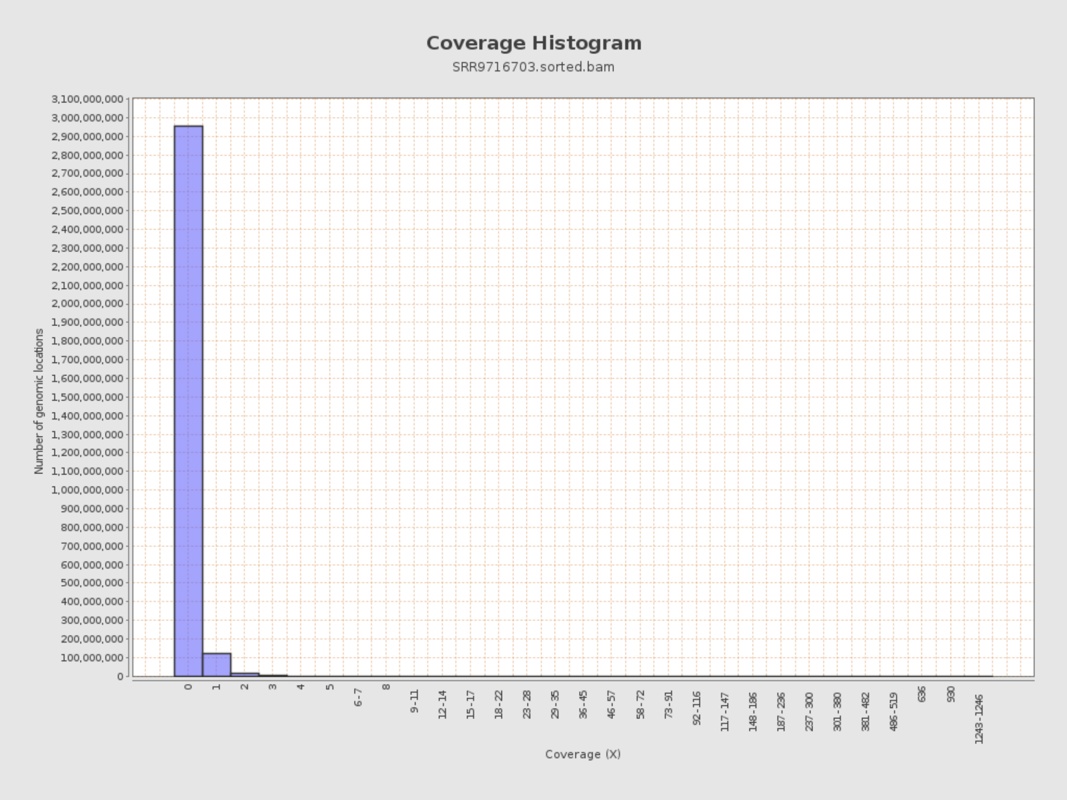
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13759726	0.0552	0.4841
chr2	243199373	12827914	0.0527	0.5754
chr3	198022430	9418664	0.0476	0.2546
chr4	191154276	9969906	0.0522	0.2918
chr5	180915260	9280674	0.0513	0.2571
chr6	171115067	8767264	0.0512	0.3277
chr7	159138663	9334638	0.0587	0.5933

chr8	146364022	8452592	0.0578	0.3566
chr9	141213431	5449717	0.0386	0.2843
chr10	135534747	7192470	0.0531	0.483
chr11	135006516	5725135	0.0424	0.322
chr12	133851895	8191352	0.0612	0.2874
chr13	115169878	4919831	0.0427	0.237
chr14	107349540	5485681	0.0511	0.2731
chr15	102531392	6006780	0.0586	0.2932
chr16	90354753	5655098	0.0626	0.3143
chr17	81195210	7313762	0.0901	0.3736
chr18	78077248	3038548	0.0389	0.4831
chr19	59128983	4375947	0.074	0.4866
chr20	63025520	5255676	0.0834	0.3578
chr21	48129895	2043592	0.0425	0.2627
chr22	51304566	1513200	0.0295	0.1985
chrMT	16571	63525	3.8335	3.2695
chrX	155270560	8935011	0.0575	0.3016
chrY	59373566	473850	0.008	0.205

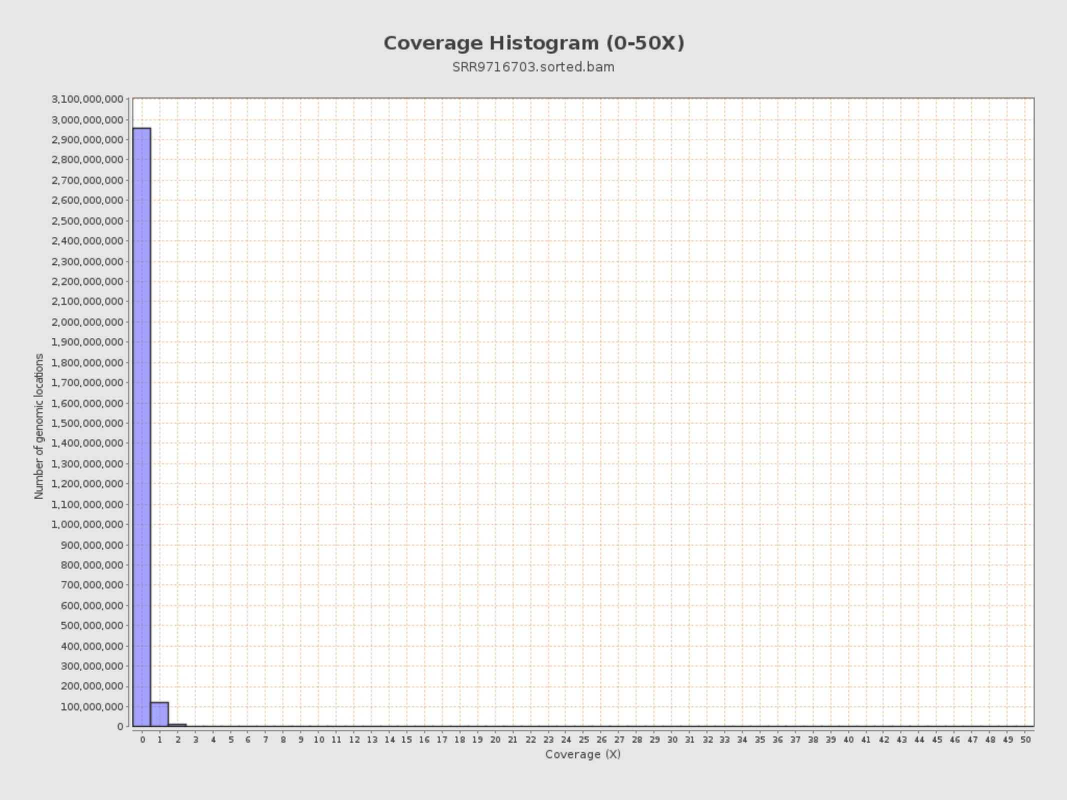
3. Results : Coverage across reference



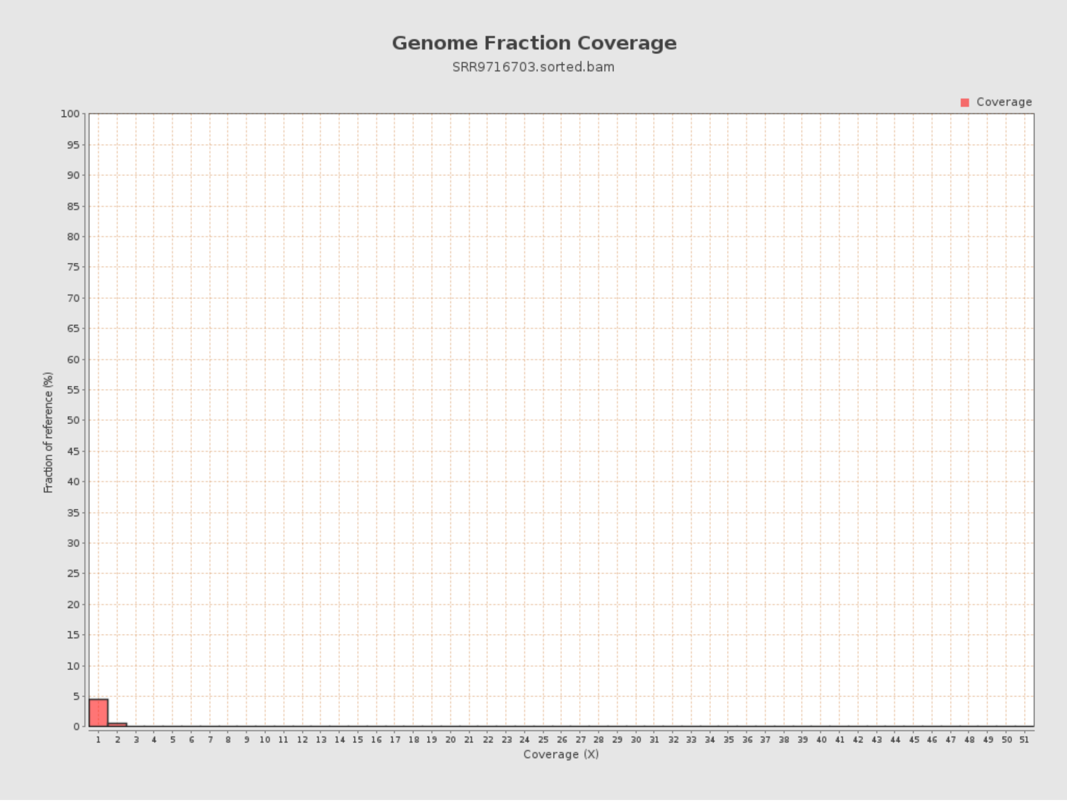
4. Results : Coverage Histogram



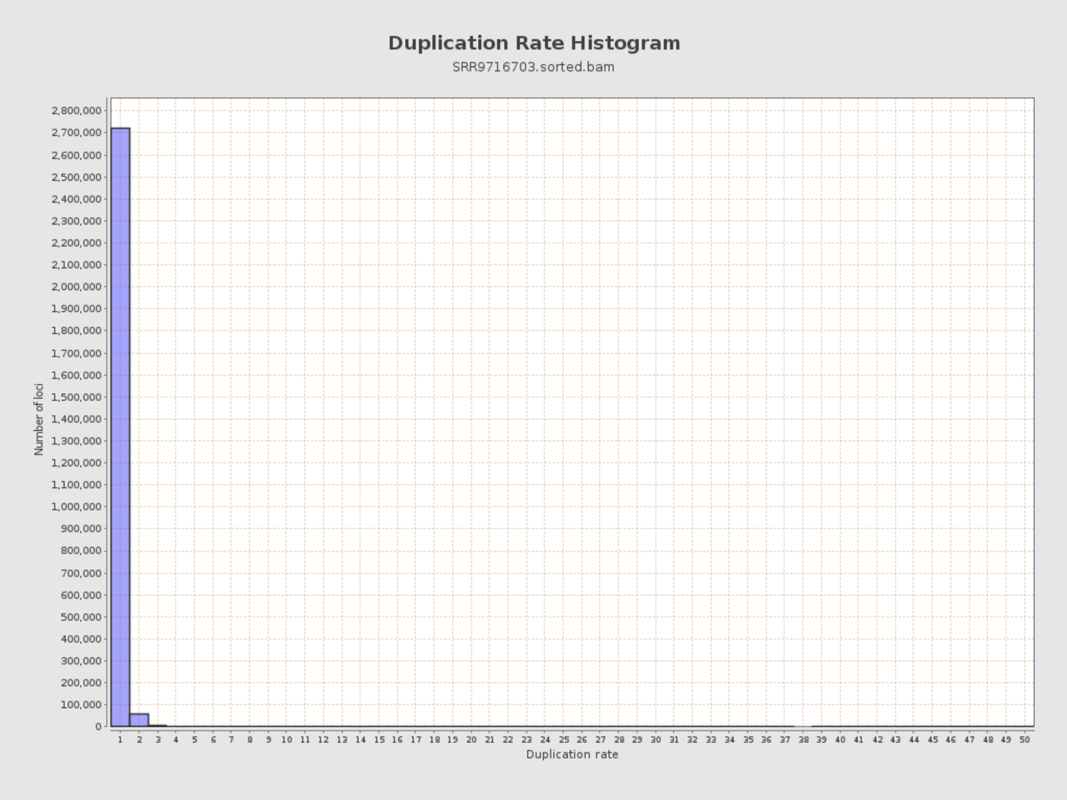
5. Results : Coverage Histogram (0-50X)



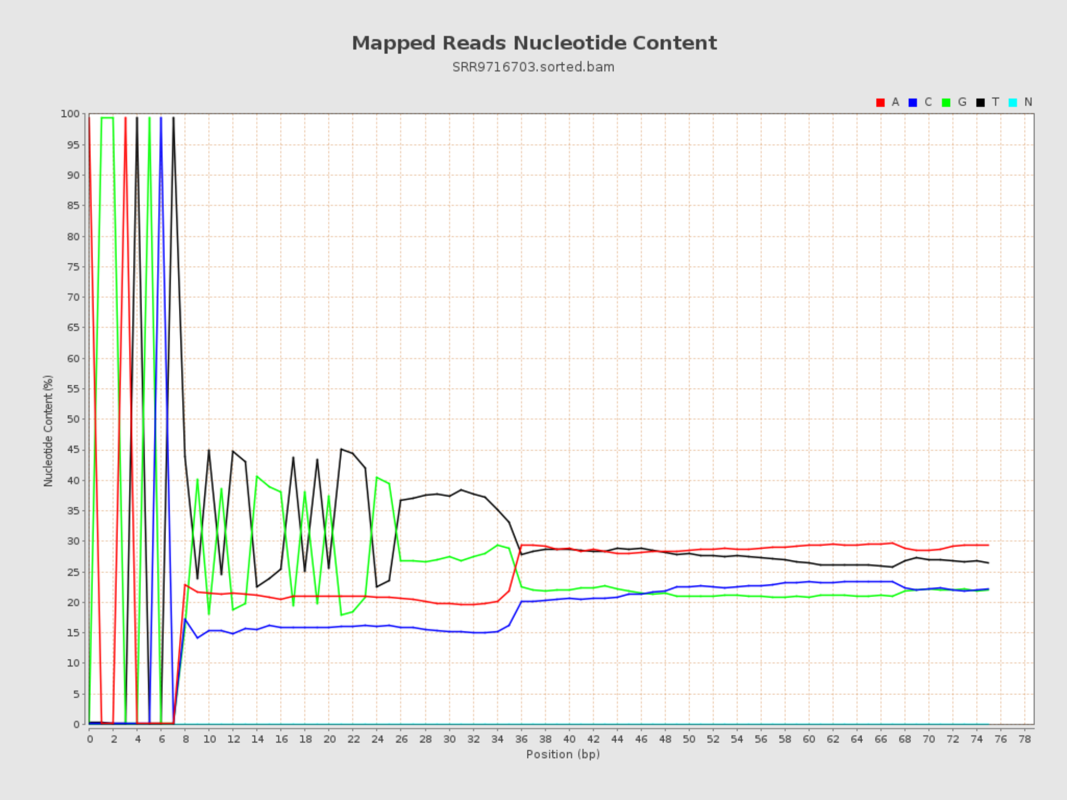
6. Results : Genome Fraction Coverage



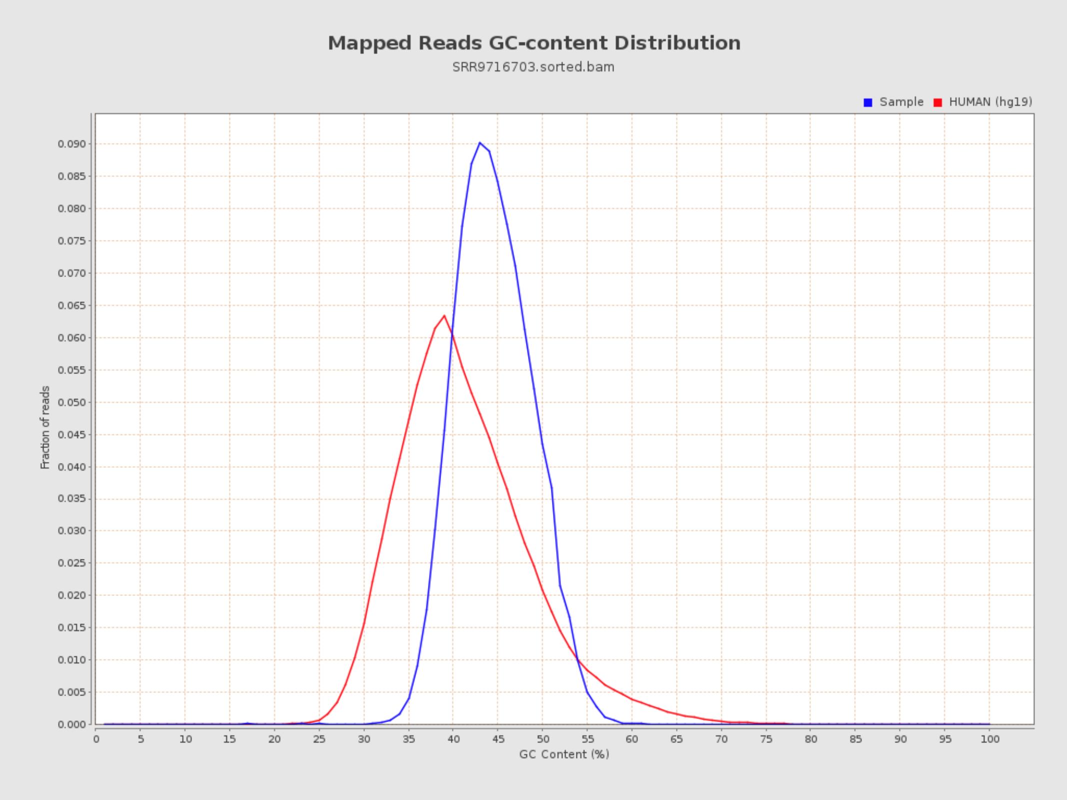
7. Results : Duplication Rate Histogram



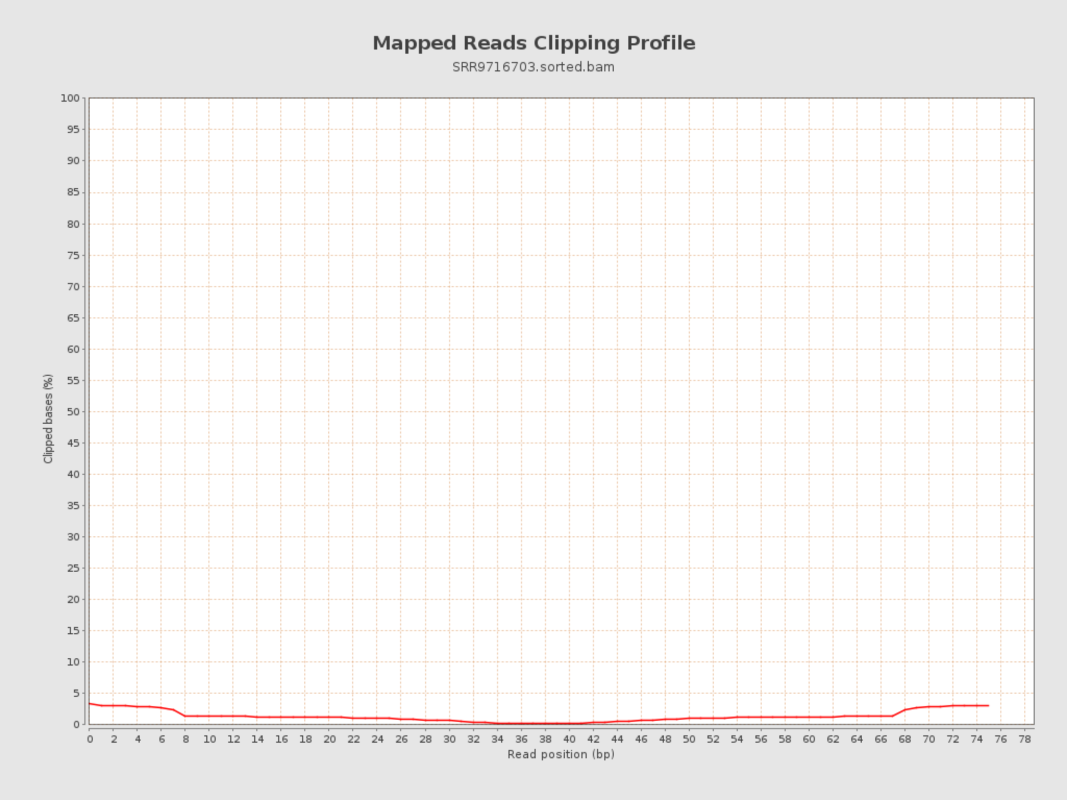
8. Results : Mapped Reads Nucleotide Content



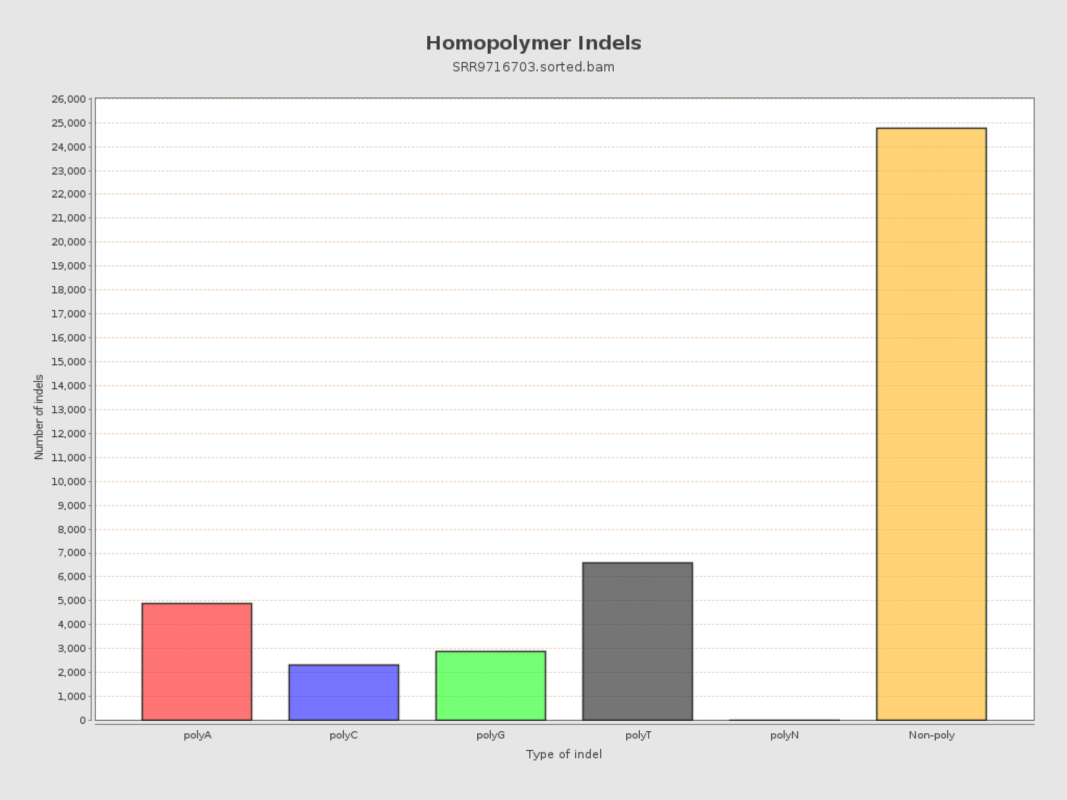
9. Results : Mapped Reads GC-content Distribution



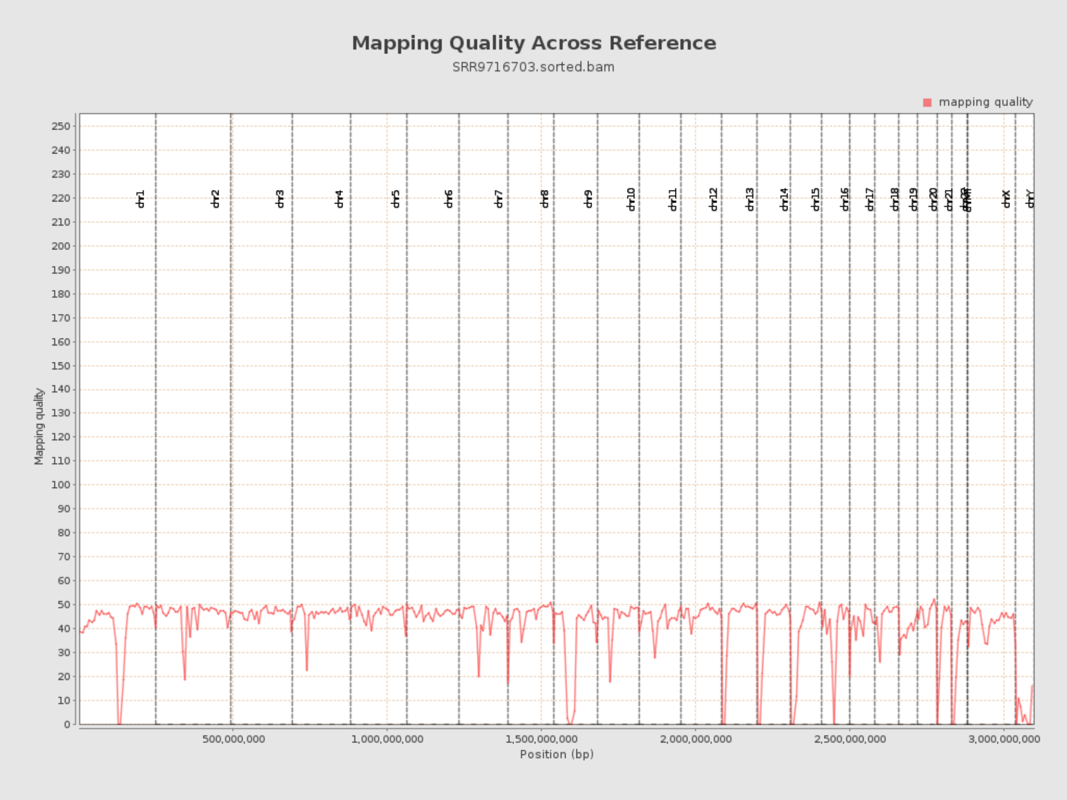
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram