Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 07:51:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716327.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_SRR9716327 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716327.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 07:51:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716327.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,452,107
Mapped reads	2,257,296 / 92.06%
Unmapped reads	194,811 / 7.94%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,219 / 0.54%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	91,665 / 3.74%
Duplication rate	3.04%
Clipped reads	2,266,356 / 92.42%

2.2. ACGT Content

Number/percentage of A's	31,705,283 / 24.2%
Number/percentage of C's	24,972,156 / 19.06%
Number/percentage of T's	41,506,667 / 31.69%
Number/percentage of G's	32,801,463 / 25.04%
Number/percentage of N's	3,777 / 0%
GC Percentage	44.11%

2.3. Coverage

Mean	0.0423

Standard Deviation	0.3516

2.4. Mapping Quality

Mean Mapping Quality	44.15

2.5. Mismatches and indels

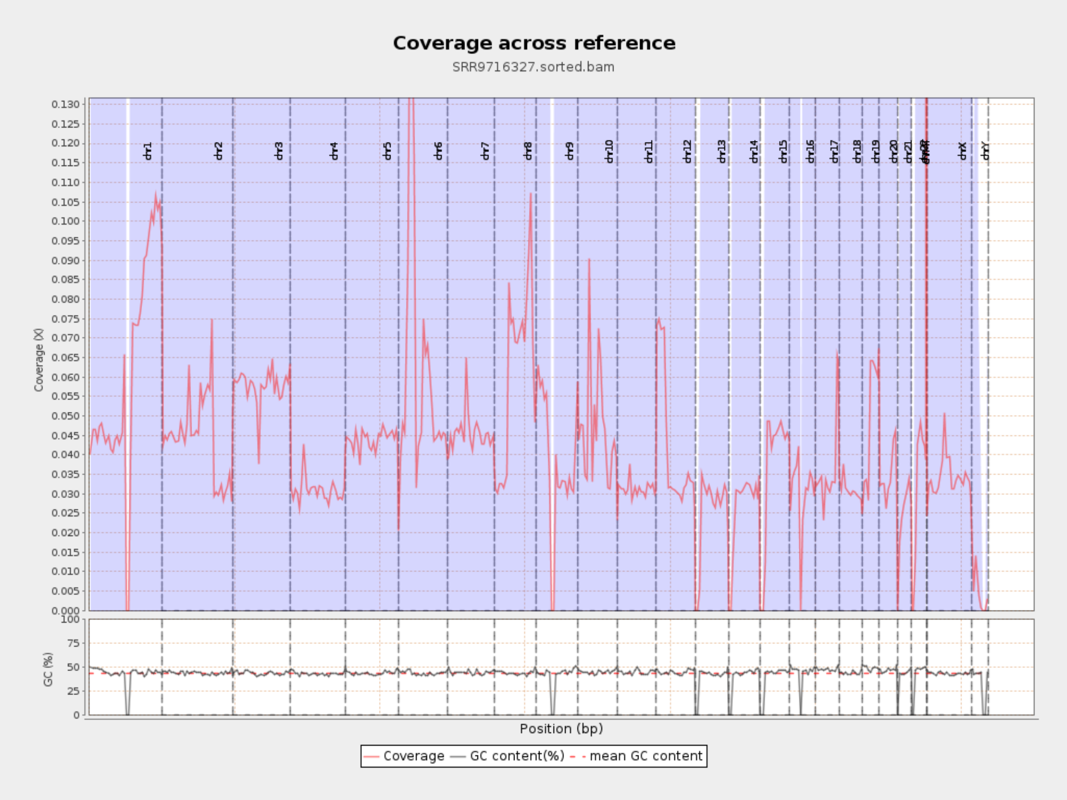
General error rate	0.5%
Mismatches	636,184
Insertions	7,871
Mapped reads with at least one insertion	0.35%
Deletions	22,181
Mapped reads with at least one deletion	0.98%
Homopolymer indels	42.26%

2.6. Chromosome stats

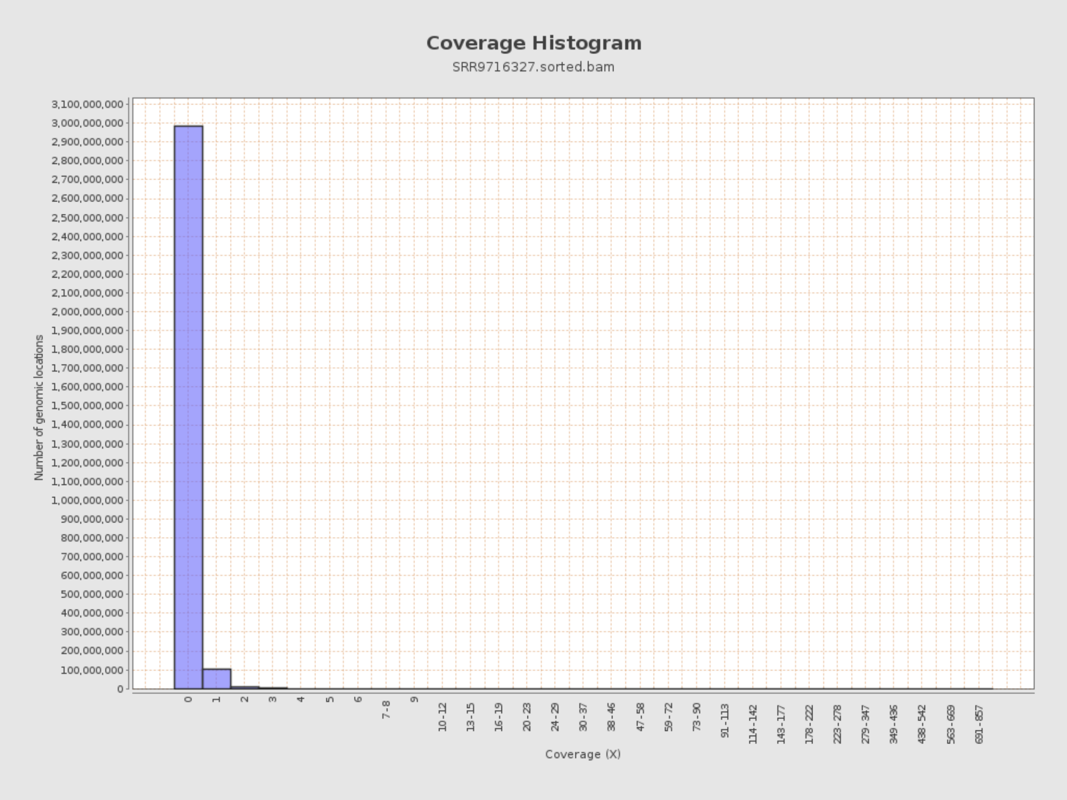
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15185220	0.0609	0.6192
chr2	243199373	10807001	0.0444	0.4364
chr3	198022430	11395601	0.0575	0.2745
chr4	191154276	5879865	0.0308	0.211
chr5	180915260	7962825	0.044	0.2368
chr6	171115067	10805954	0.0632	0.4245
chr7	159138663	7291568	0.0458	0.4365

chr8	146364022	9043858	0.0618	0.3169
chr9	141213431	5246420	0.0372	0.307
chr10	135534747	6416806	0.0473	0.4176
chr11	135006516	4200427	0.0311	0.2711
chr12	133851895	5605836	0.0419	0.2432
chr13	115169878	2898907	0.0252	0.1786
chr14	107349540	2776639	0.0259	0.2277
chr15	102531392	3789731	0.037	0.2195
chr16	90354753	2719574	0.0301	0.2307
chr17	81195210	2963457	0.0365	0.2262
chr18	78077248	2432159	0.0312	0.5098
chr19	59128983	2892223	0.0489	0.4538
chr20	63025520	2189455	0.0347	0.211
chr21	48129895	1173555	0.0244	0.2027
chr22	51304566	1549215	0.0302	0.1965
chrMT	16571	193384	11.67	6.63
chrX	155270560	5326510	0.0343	0.2537
chrY	59373566	277885	0.0047	0.1109

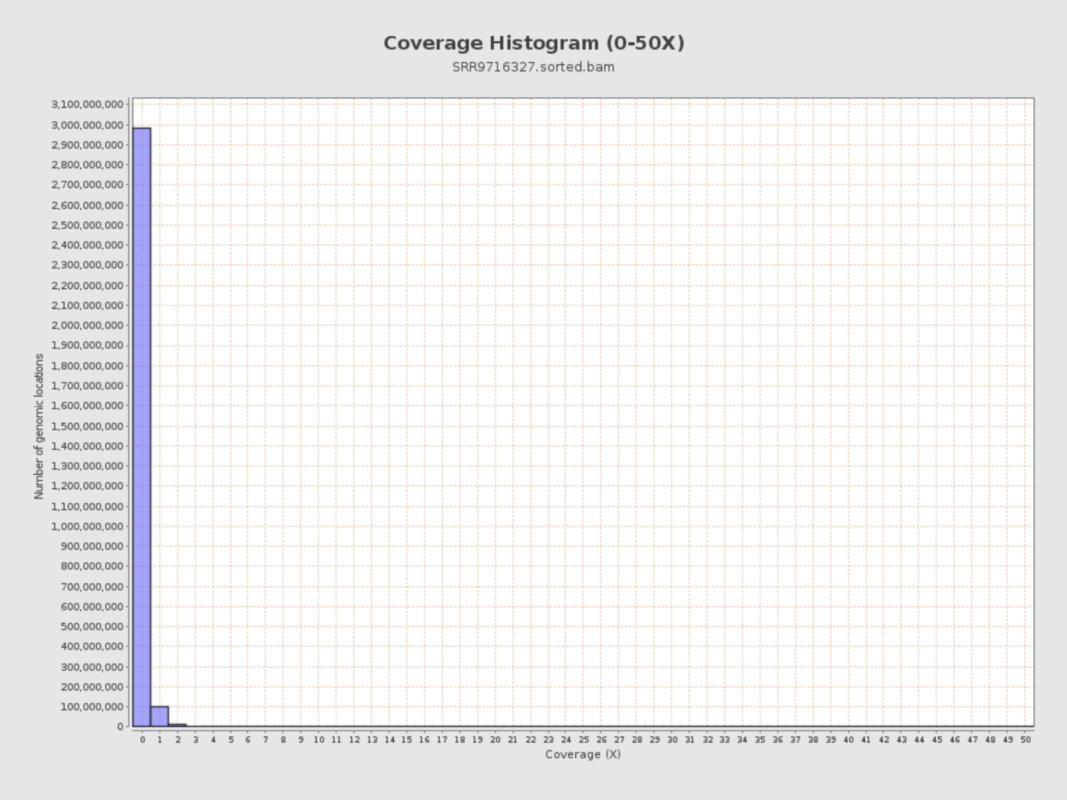
3. Results : Coverage across reference



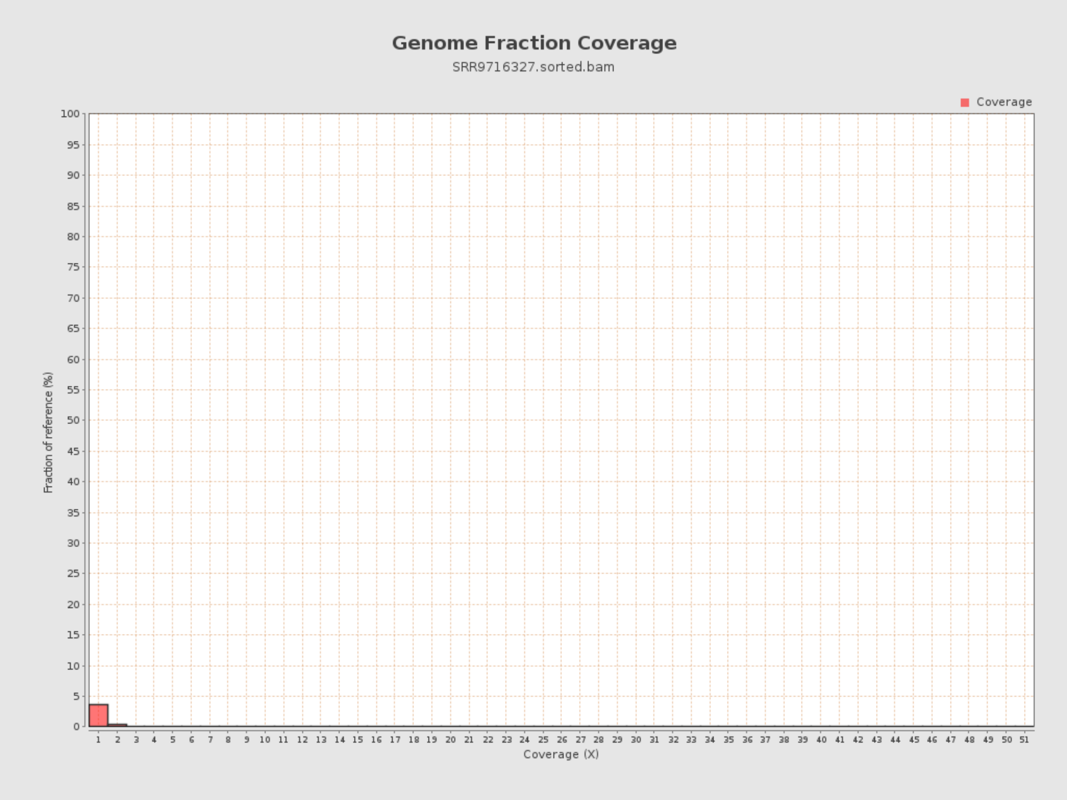
4. Results : Coverage Histogram



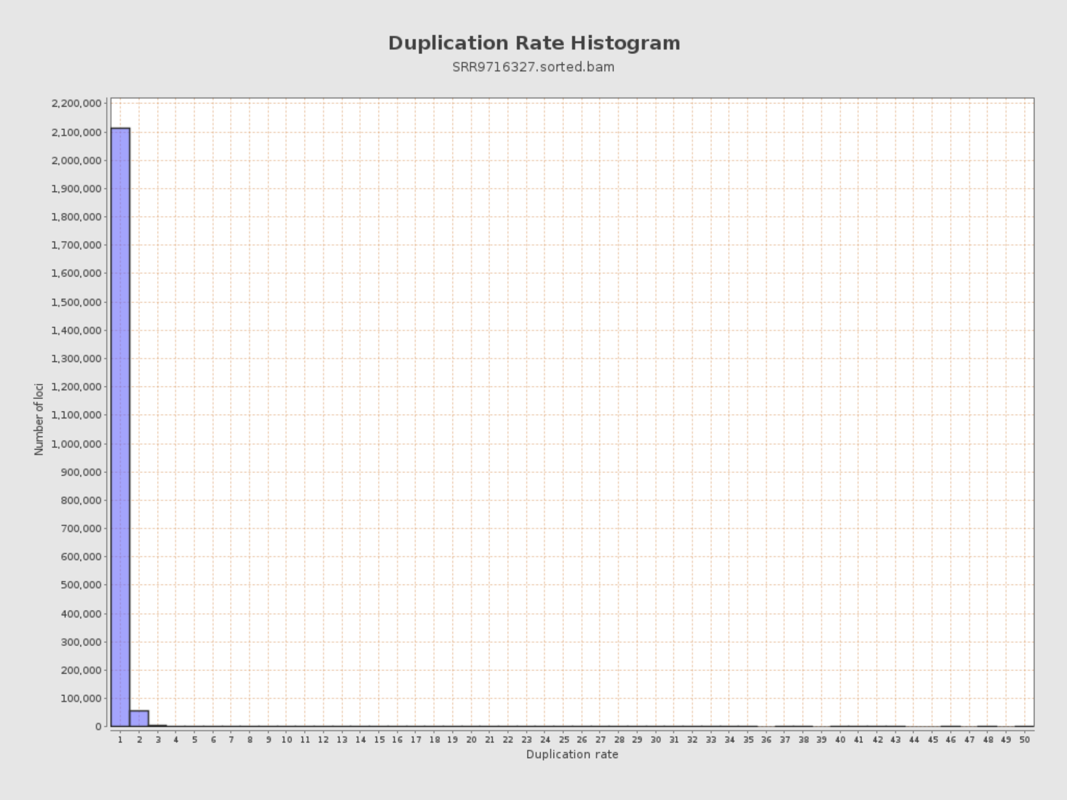
5. Results : Coverage Histogram (0-50X)



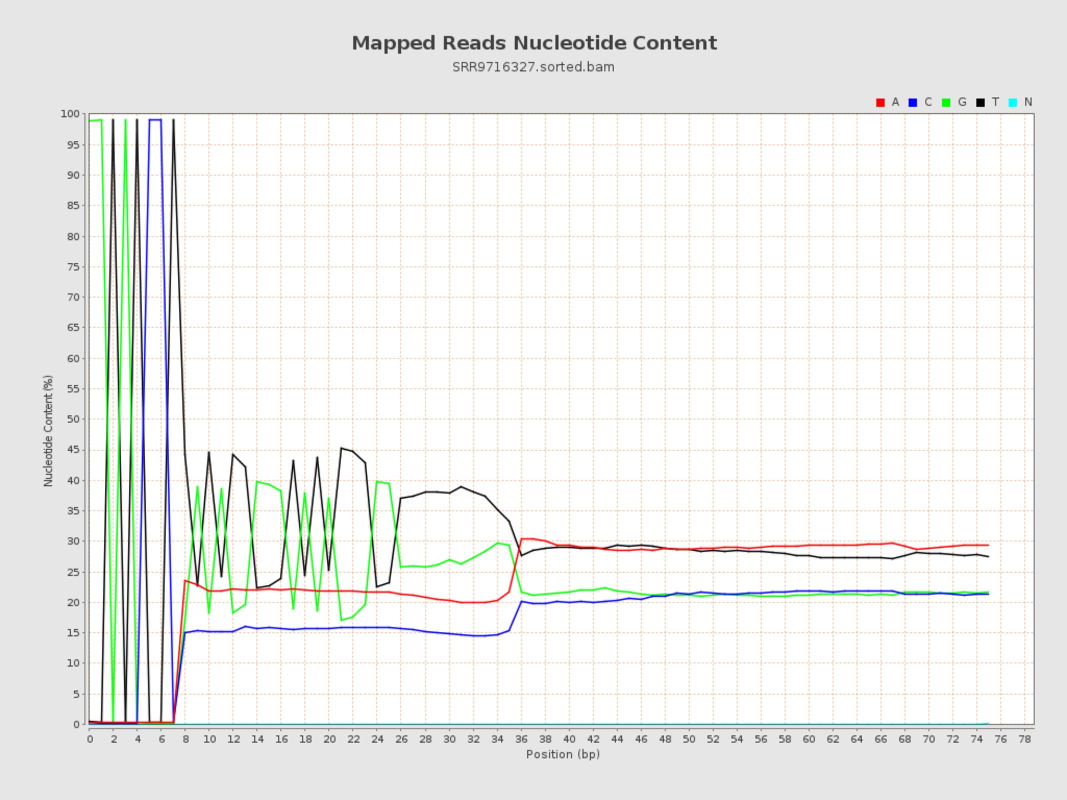
6. Results : Genome Fraction Coverage



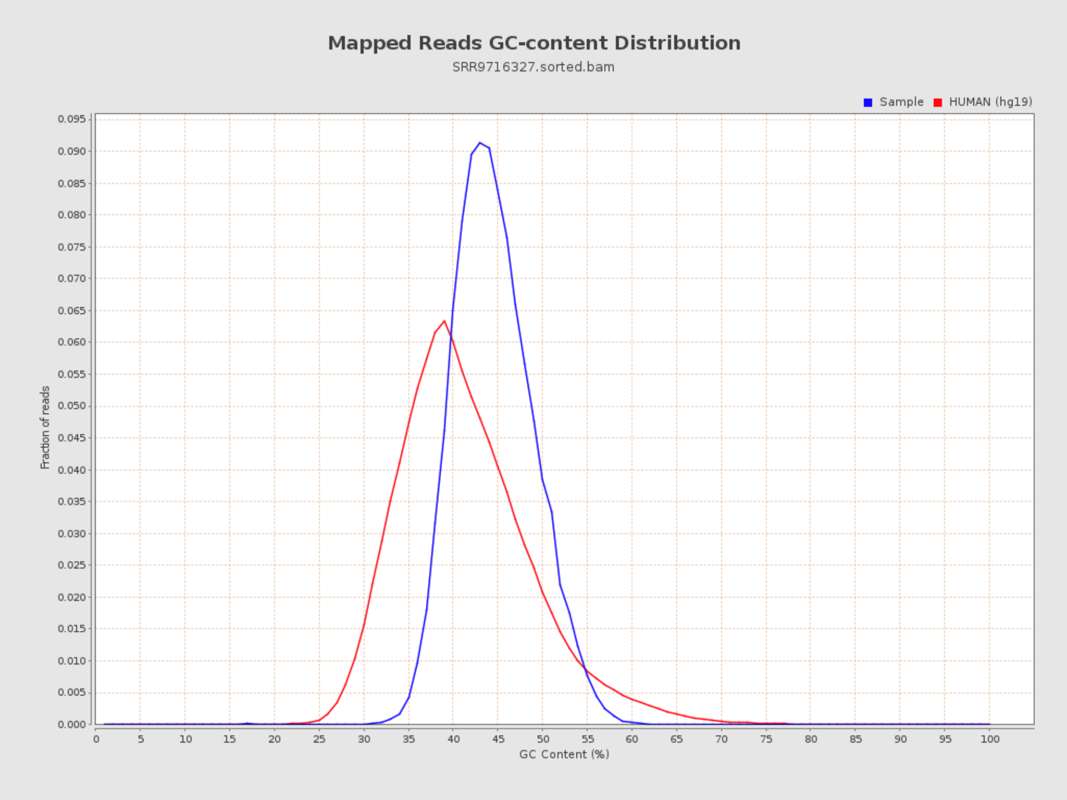
7. Results : Duplication Rate Histogram



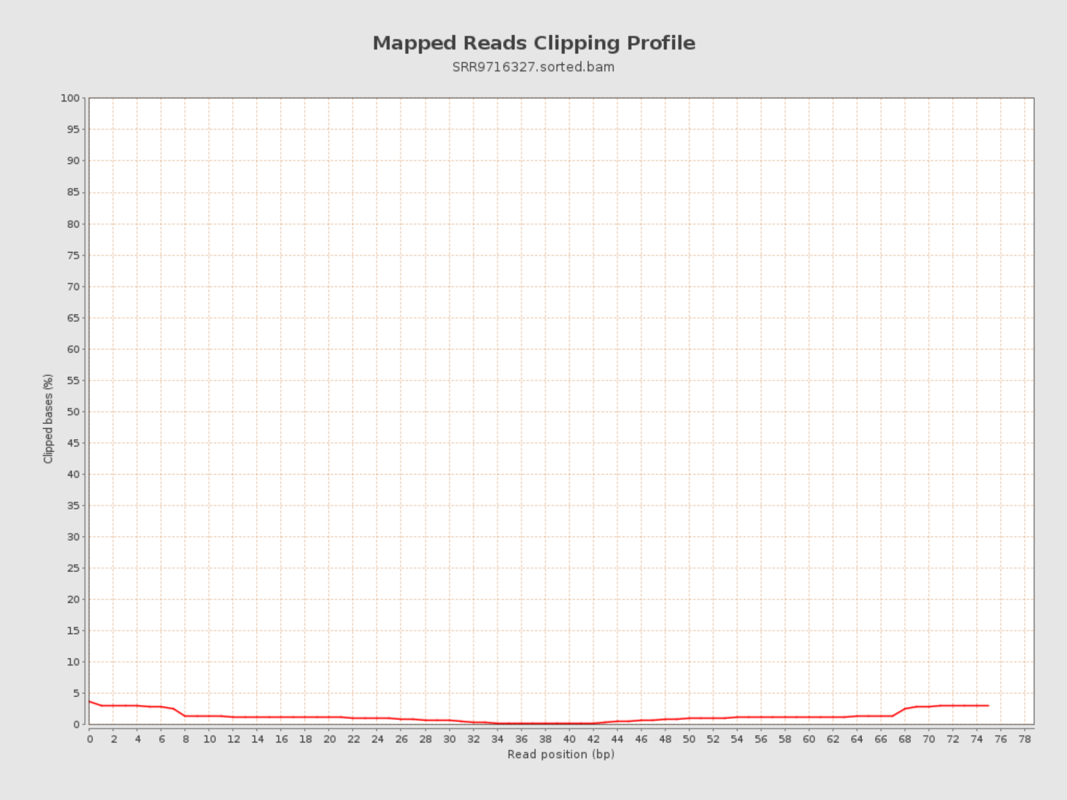
8. Results : Mapped Reads Nucleotide Content



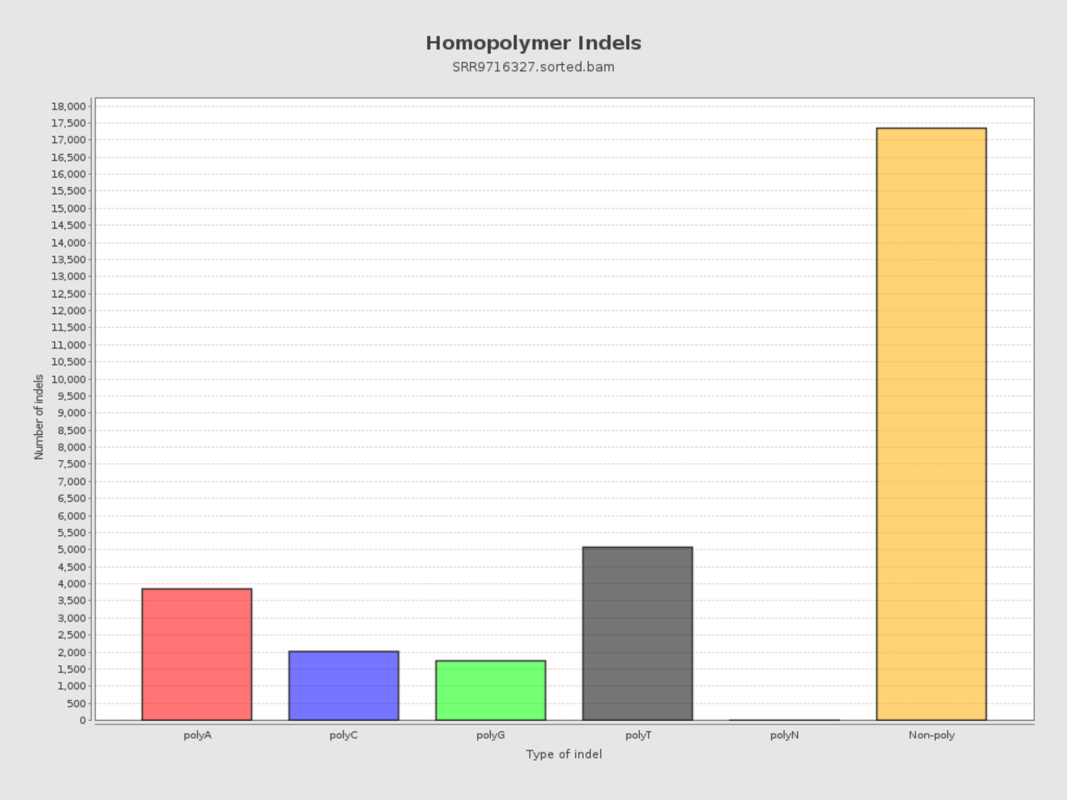
9. Results : Mapped Reads GC-content Distribution



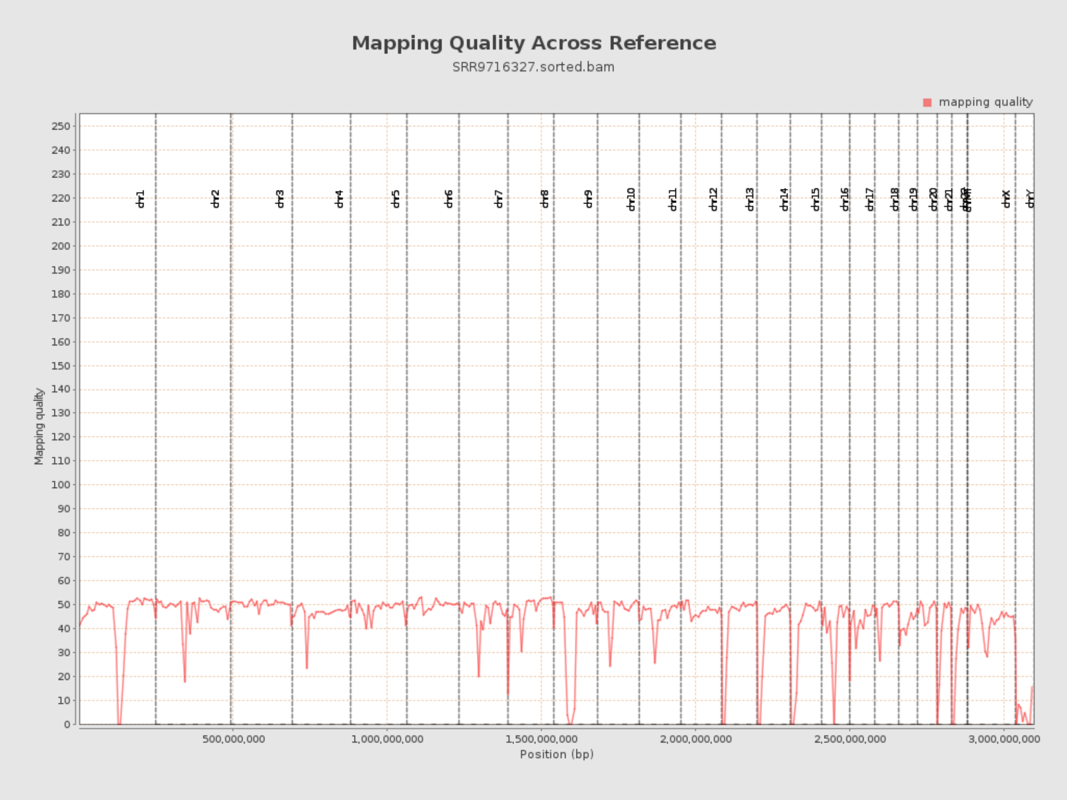
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram