Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 00:41:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716615.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_SRR9716615 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716615.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 00:41:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716615.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,388,261
Mapped reads	2,185,475 / 91.51%
Unmapped reads	202,786 / 8.49%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,093 / 0.26%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	148,243 / 6.21%
Duplication rate	5.46%
Clipped reads	2,189,636 / 91.68%

2.2. ACGT Content

Number/percentage of A's	31,705,644 / 25.33%
Number/percentage of C's	23,931,151 / 19.12%
Number/percentage of T's	39,977,446 / 31.94%
Number/percentage of G's	29,532,669 / 23.6%
Number/percentage of N's	1,273 / 0%
GC Percentage	42.72%

2.3. Coverage

Mean	0.0404

Standard Deviation	0.3326

2.4. Mapping Quality

Mean Mapping Quality	45.5

2.5. Mismatches and indels

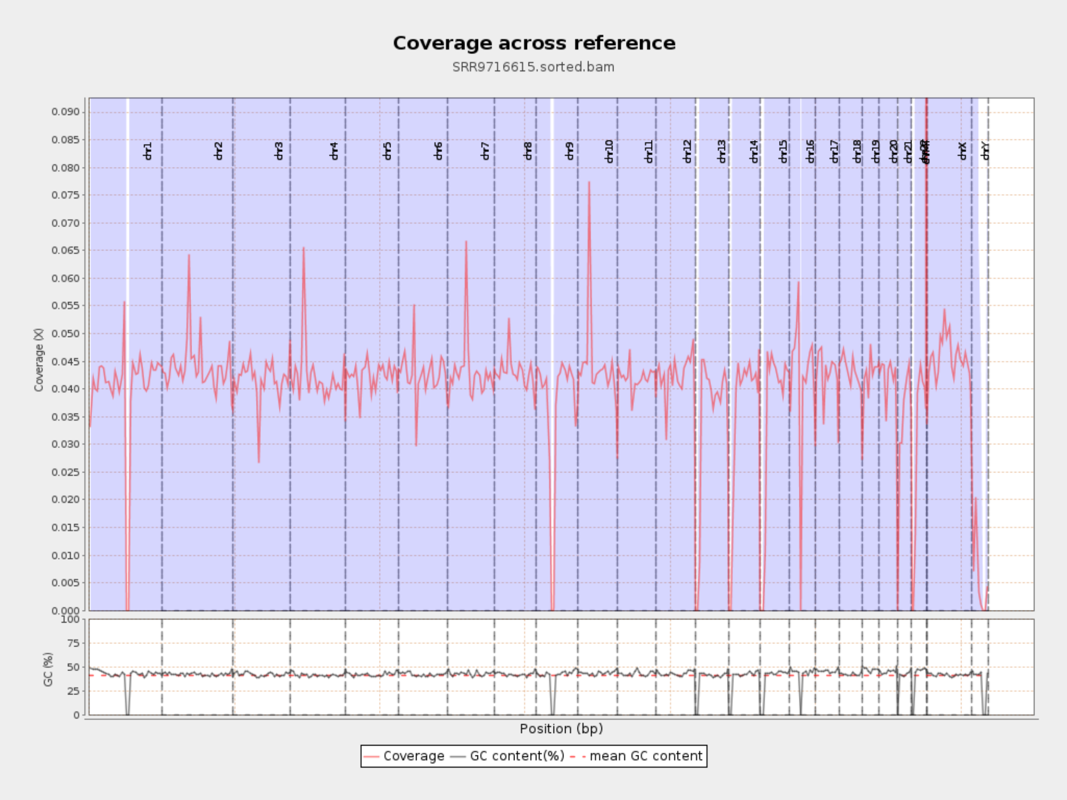
General error rate	0.49%
Mismatches	597,021
Insertions	7,529
Mapped reads with at least one insertion	0.34%
Deletions	24,012
Mapped reads with at least one deletion	1.09%
Homopolymer indels	44.18%

2.6. Chromosome stats

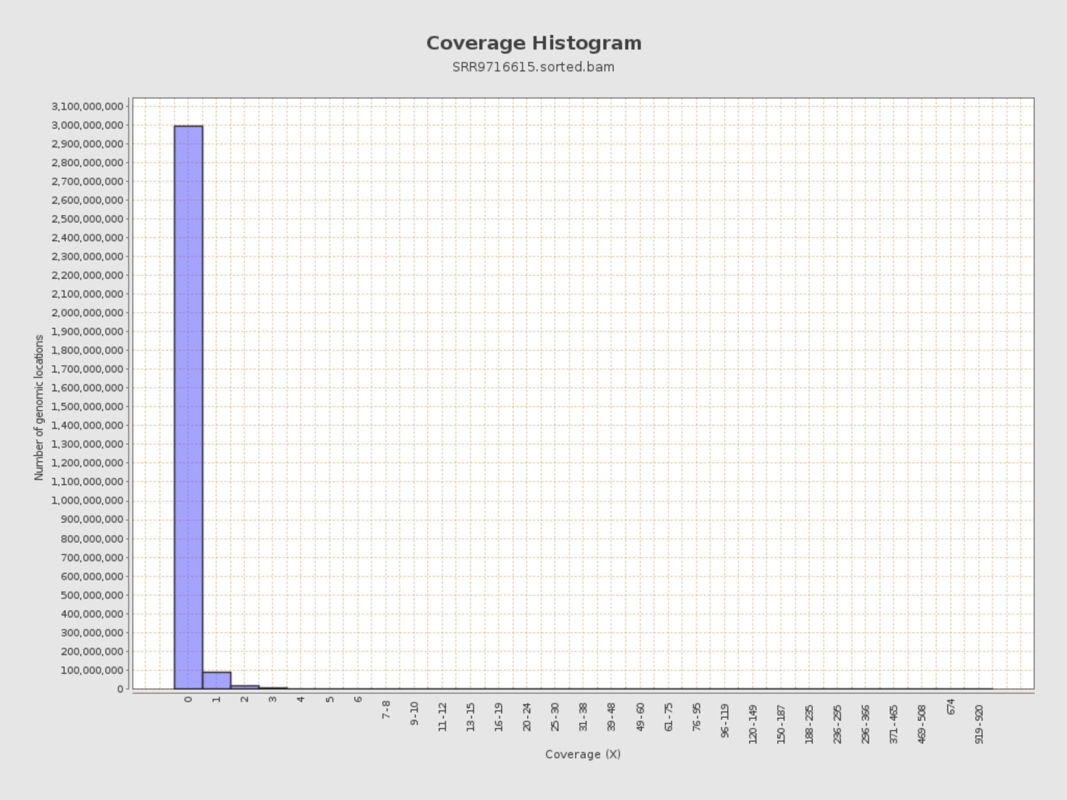
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9901979	0.0397	0.4567
chr2	243199373	10745160	0.0442	0.4812
chr3	198022430	8233074	0.0416	0.2444
chr4	191154276	8084033	0.0423	0.2649
chr5	180915260	7673882	0.0424	0.244
chr6	171115067	7318664	0.0428	0.3009
chr7	159138663	6860091	0.0431	0.4609

chr8	146364022	6296387	0.043	0.3371
chr9	141213431	5111136	0.0362	0.2843
chr10	135534747	6058730	0.0447	0.3813
chr11	135006516	5641936	0.0418	0.3097
chr12	133851895	5693547	0.0425	0.2465
chr13	115169878	3932062	0.0341	0.2185
chr14	107349540	3775998	0.0352	0.2291
chr15	102531392	3574886	0.0349	0.2238
chr16	90354753	3785966	0.0419	0.2756
chr17	81195210	3436281	0.0423	0.2643
chr18	78077248	3394627	0.0435	0.5163
chr19	59128983	2510675	0.0425	0.3655
chr20	63025520	2640922	0.0419	0.2498
chr21	48129895	1611981	0.0335	0.2401
chr22	51304566	1457845	0.0284	0.2014
chrMT	16571	7840	0.4731	0.8161
chrX	155270560	7073036	0.0456	0.2789
chrY	59373566	365594	0.0062	0.1598

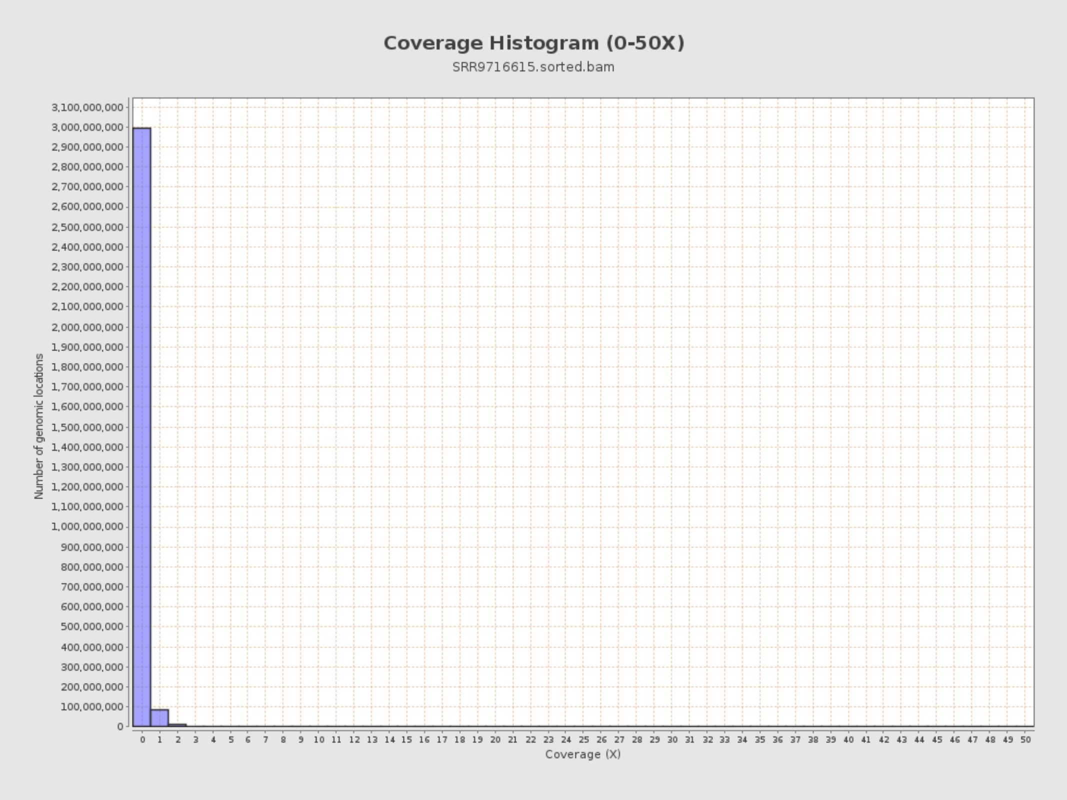
3. Results : Coverage across reference



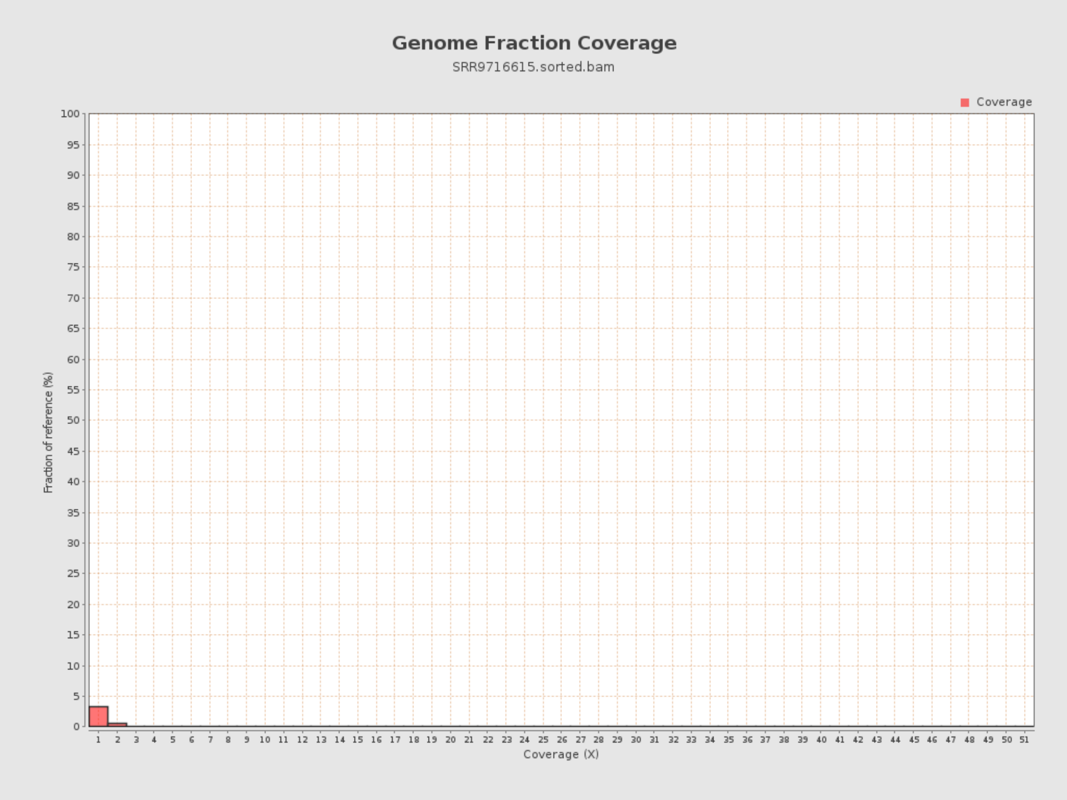
4. Results : Coverage Histogram



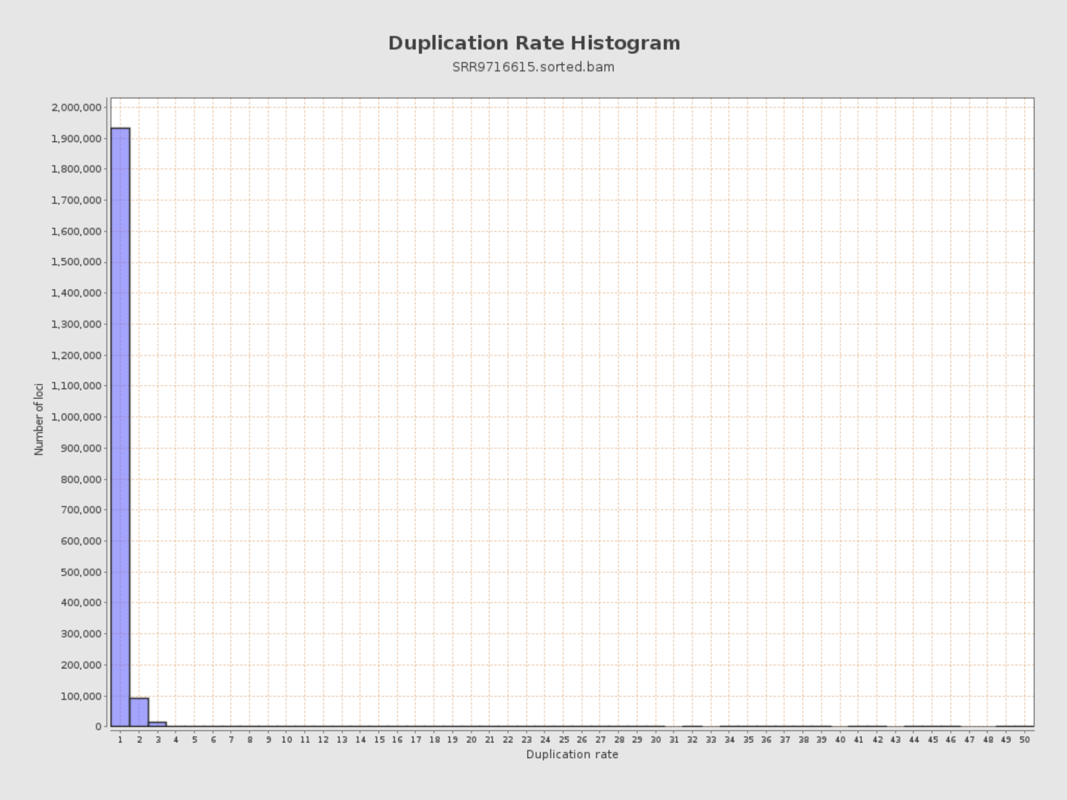
5. Results : Coverage Histogram (0-50X)



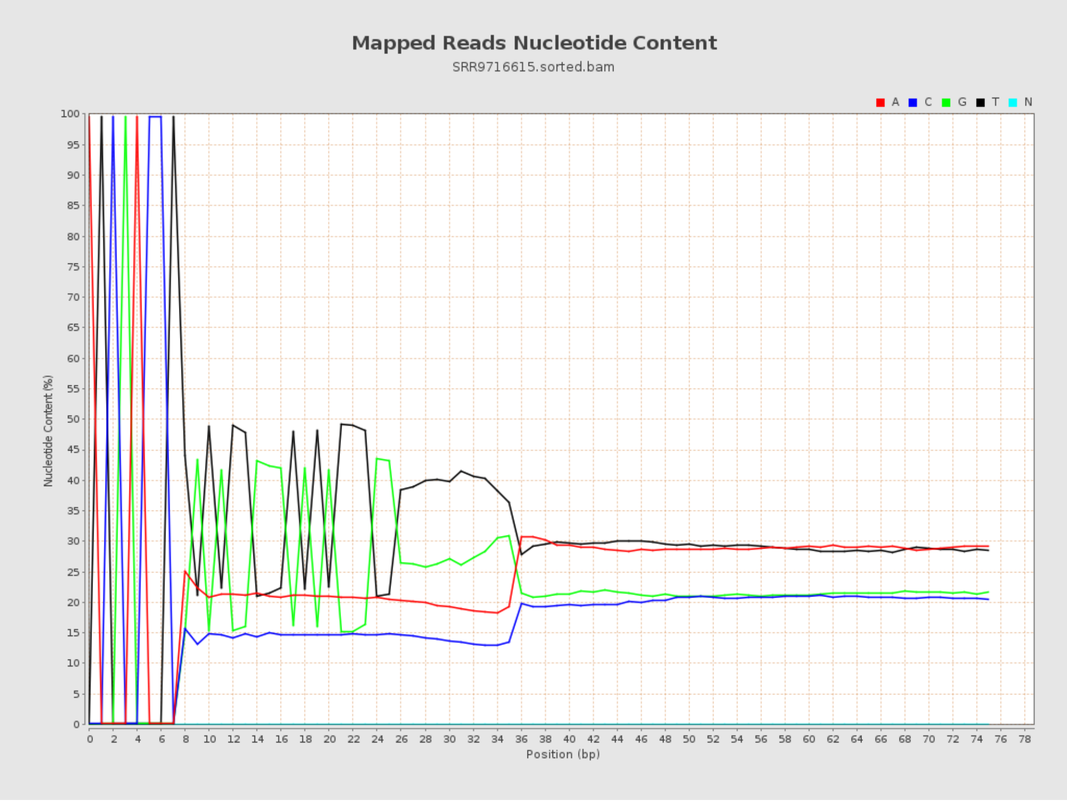
6. Results : Genome Fraction Coverage



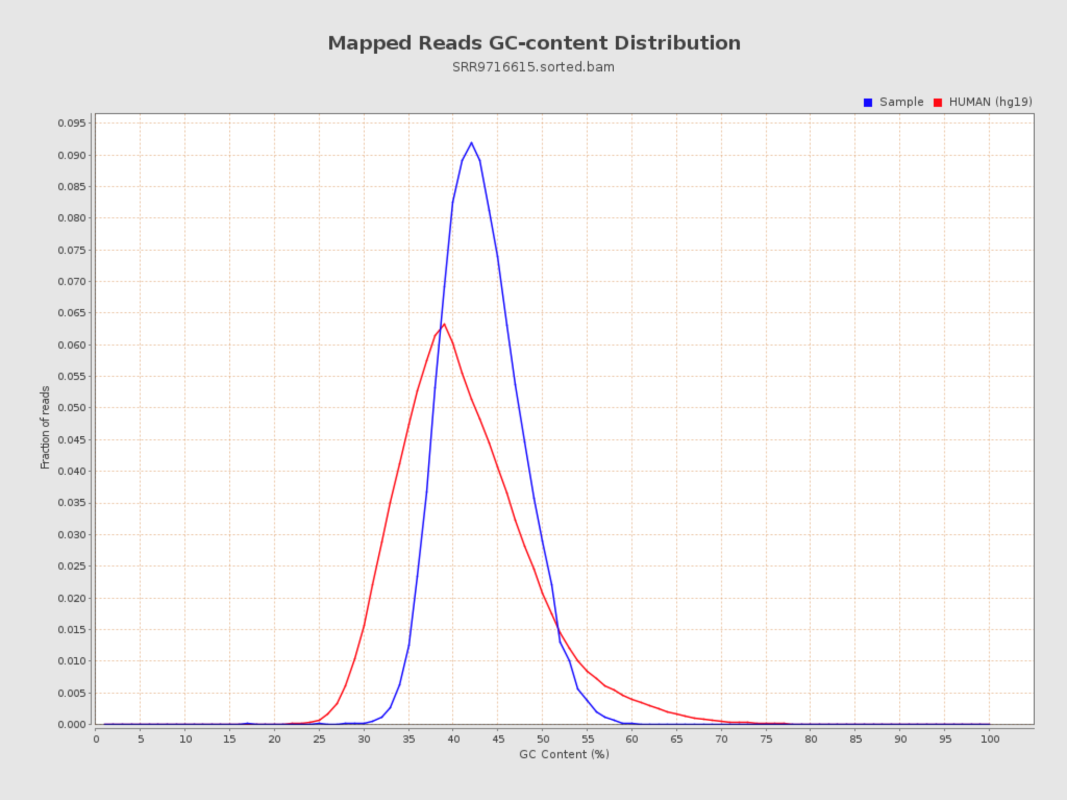
7. Results : Duplication Rate Histogram



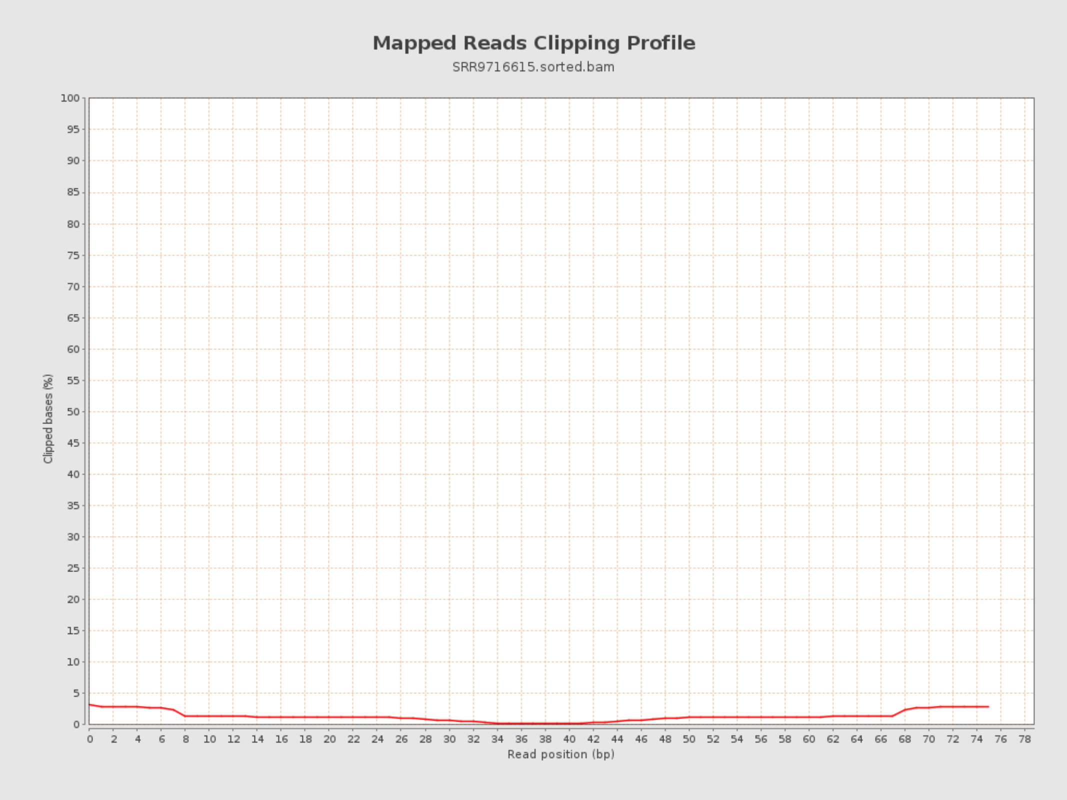
8. Results : Mapped Reads Nucleotide Content



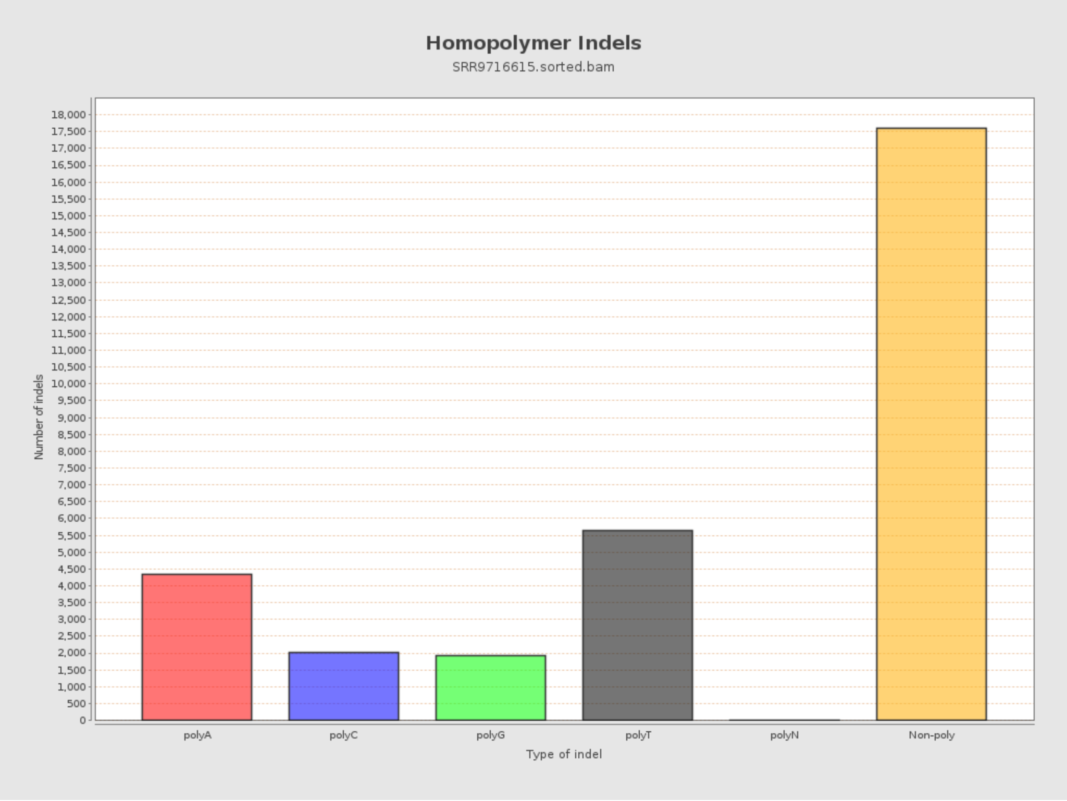
9. Results : Mapped Reads GC-content Distribution



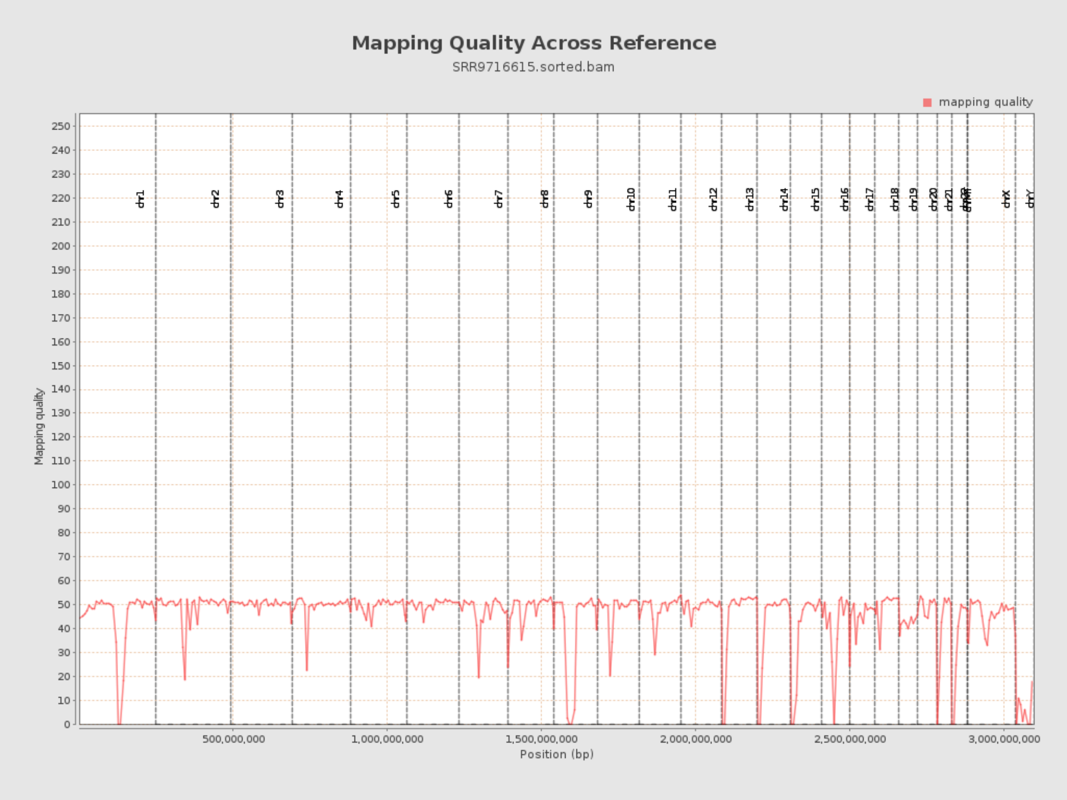
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram