Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 19:39:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716541.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_SRR9716541 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716541.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 19:39:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716541.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,365,078
Mapped reads	1,204,187 / 88.21%
Unmapped reads	160,891 / 11.79%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,042 / 0.37%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	40,705 / 2.98%
Duplication rate	2.57%
Clipped reads	1,207,230 / 88.44%

2.2. ACGT Content

Number/percentage of A's	17,288,994 / 24.9%
Number/percentage of C's	12,898,976 / 18.57%
Number/percentage of T's	22,447,449 / 32.32%
Number/percentage of G's	16,807,359 / 24.2%
Number/percentage of N's	2,110 / 0%
GC Percentage	42.78%

2.3. Coverage

Mean	0.0224

Standard Deviation	0.2238

2.4. Mapping Quality

Mean Mapping Quality	45.14

2.5. Mismatches and indels

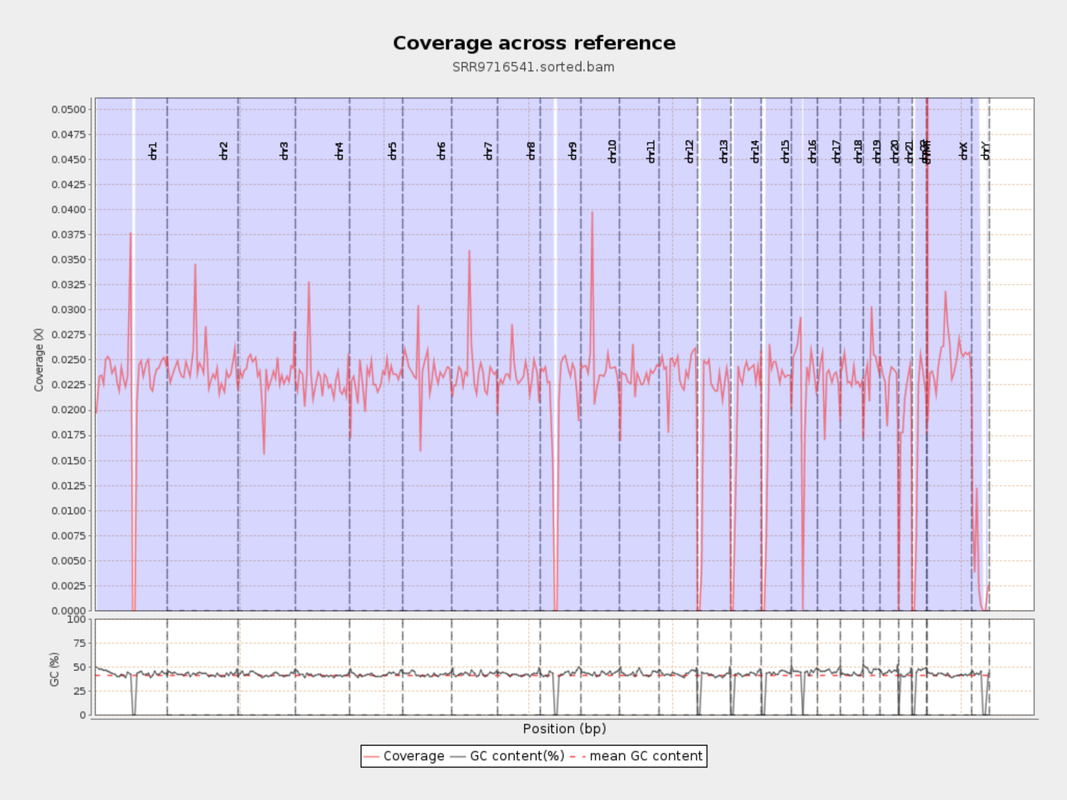
General error rate	0.52%
Mismatches	351,269
Insertions	4,471
Mapped reads with at least one insertion	0.37%
Deletions	13,517
Mapped reads with at least one deletion	1.11%
Homopolymer indels	41.7%

2.6. Chromosome stats

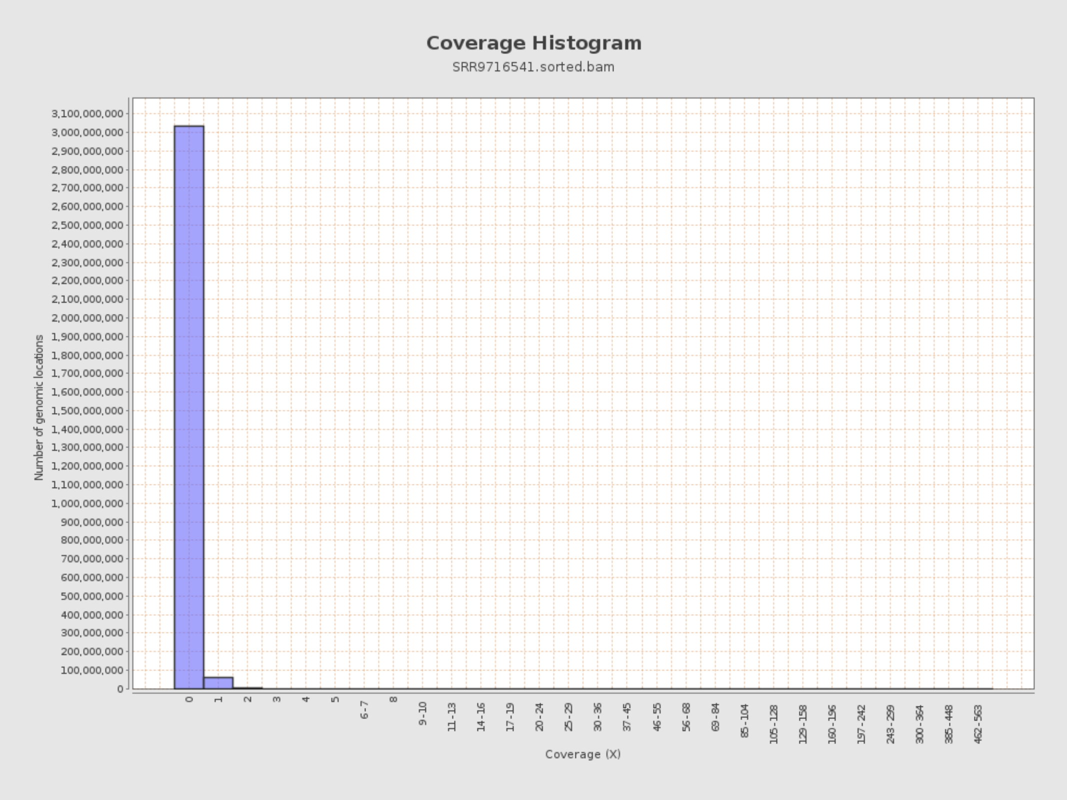
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5635165	0.0226	0.4022
chr2	243199373	5888810	0.0242	0.2904
chr3	198022430	4637461	0.0234	0.1655
chr4	191154276	4415035	0.0231	0.1726
chr5	180915260	4196280	0.0232	0.1644
chr6	171115067	4087744	0.0239	0.1918
chr7	159138663	3818015	0.024	0.259

chr8	146364022	3442187	0.0235	0.2124
chr9	141213431	2883688	0.0204	0.1882
chr10	135534747	3339501	0.0246	0.215
chr11	135006516	3149668	0.0233	0.1963
chr12	133851895	3206123	0.024	0.1686
chr13	115169878	2220152	0.0193	0.151
chr14	107349540	2119265	0.0197	0.1569
chr15	102531392	1991976	0.0194	0.151
chr16	90354753	1998549	0.0221	0.1685
chr17	81195210	1858055	0.0229	0.1707
chr18	78077248	1830007	0.0234	0.3009
chr19	59128983	1448248	0.0245	0.285
chr20	63025520	1437953	0.0228	0.1641
chr21	48129895	912439	0.019	0.1586
chr22	51304566	818996	0.016	0.1362
chrMT	16571	4475	0.2701	0.5337
chrX	155270560	3912156	0.0252	0.1861
chrY	59373566	214496	0.0036	0.1037

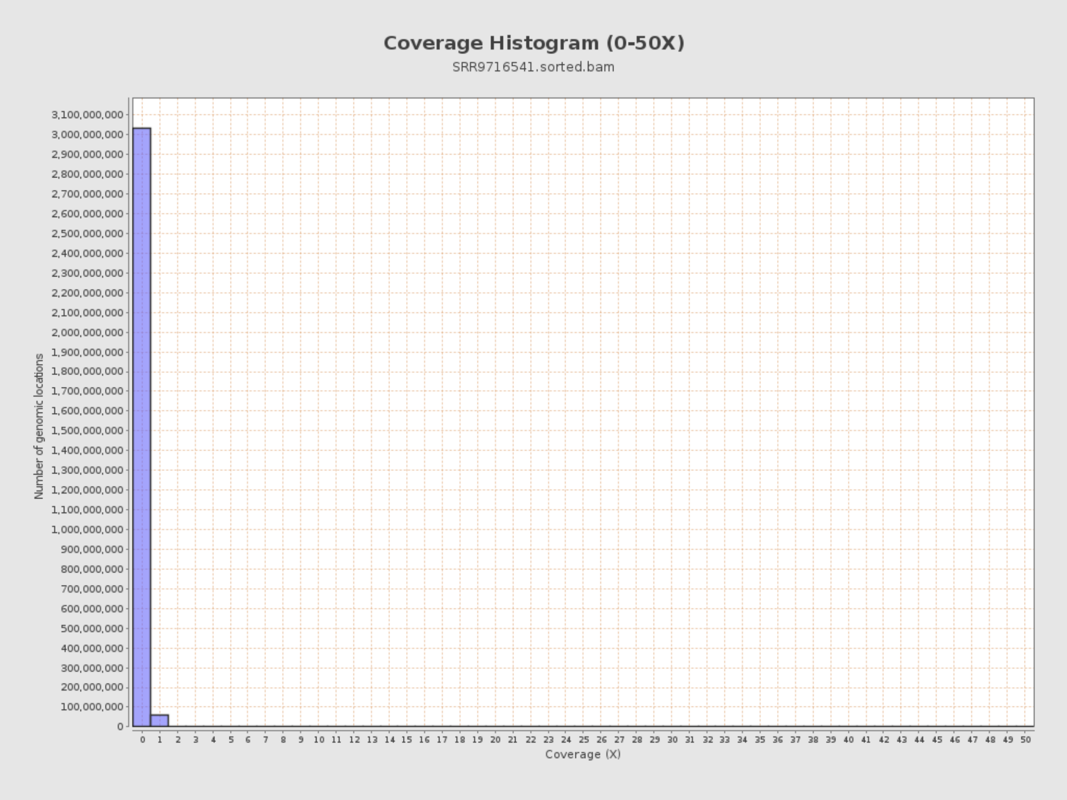
3. Results : Coverage across reference



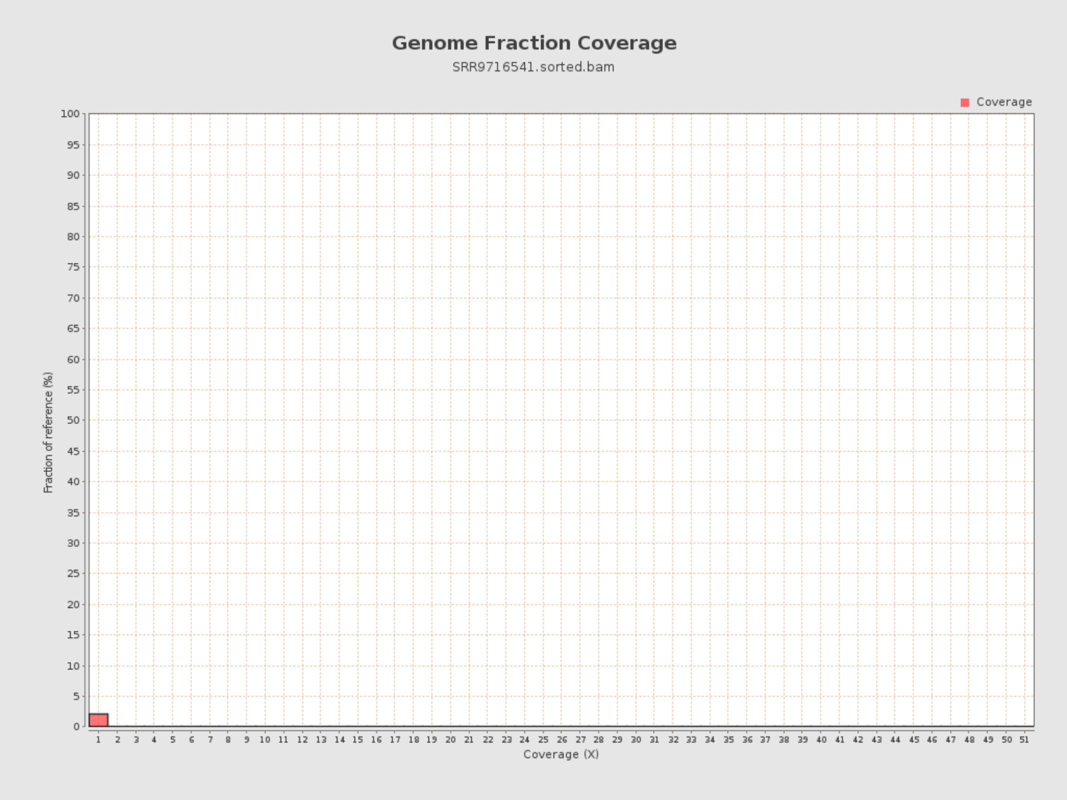
4. Results : Coverage Histogram



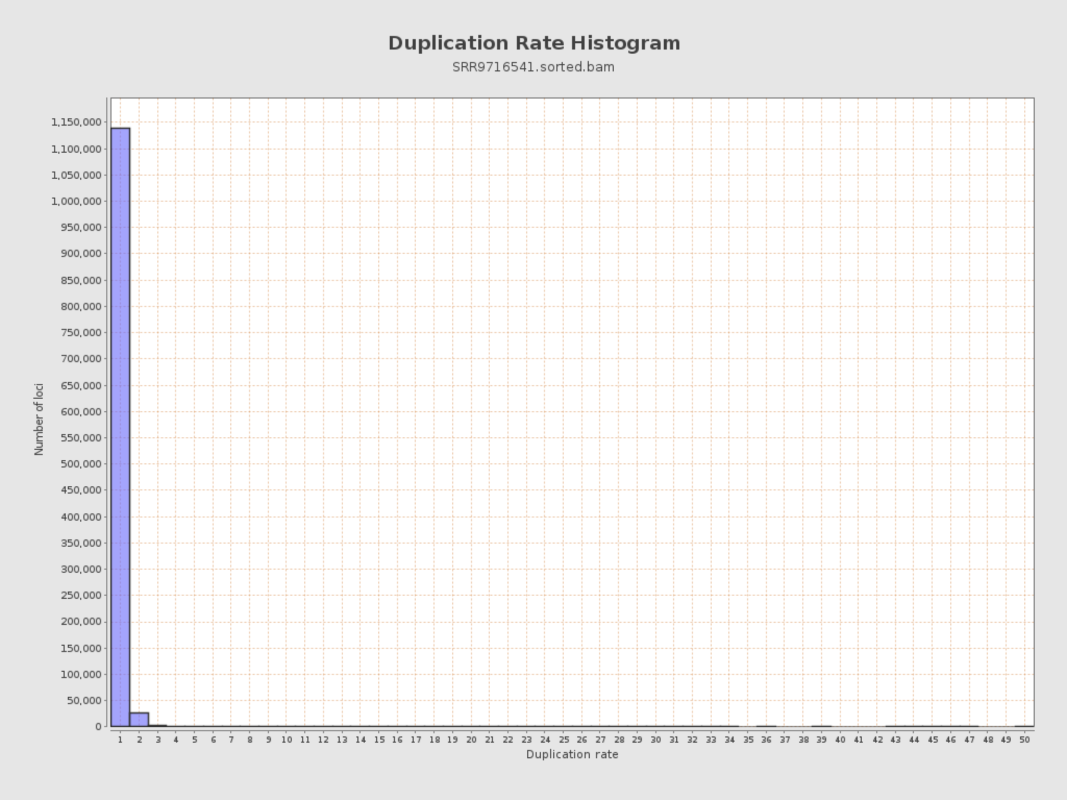
5. Results : Coverage Histogram (0-50X)



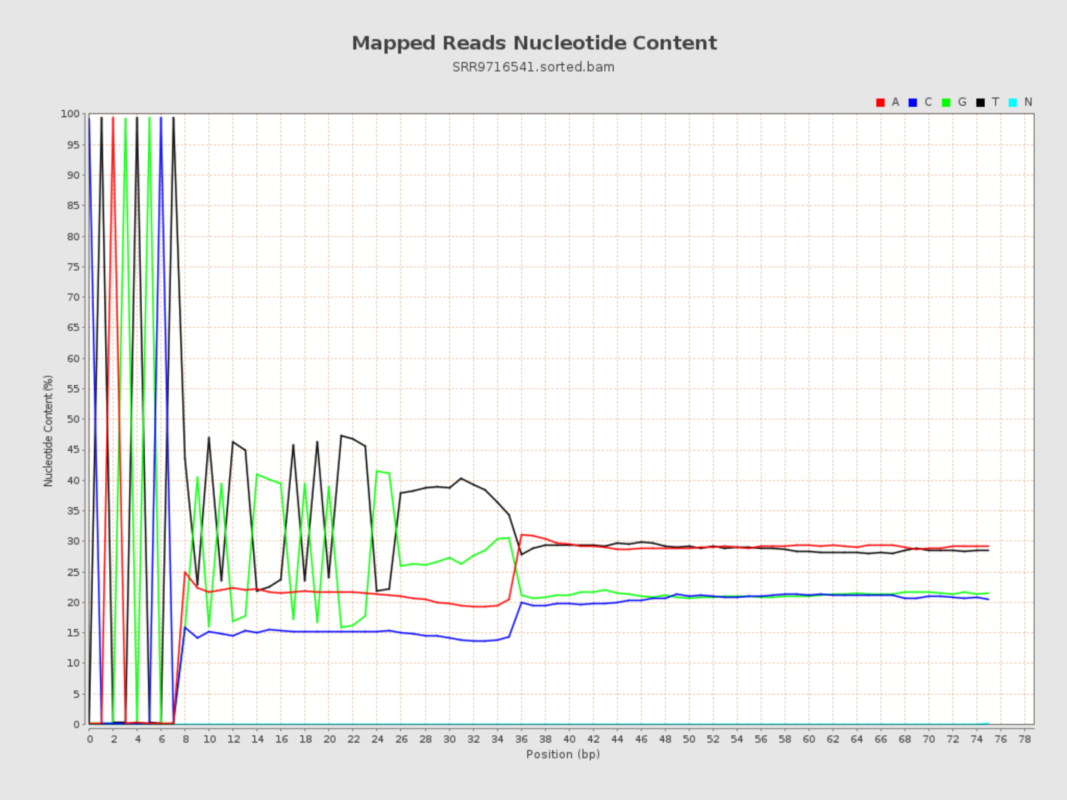
6. Results : Genome Fraction Coverage



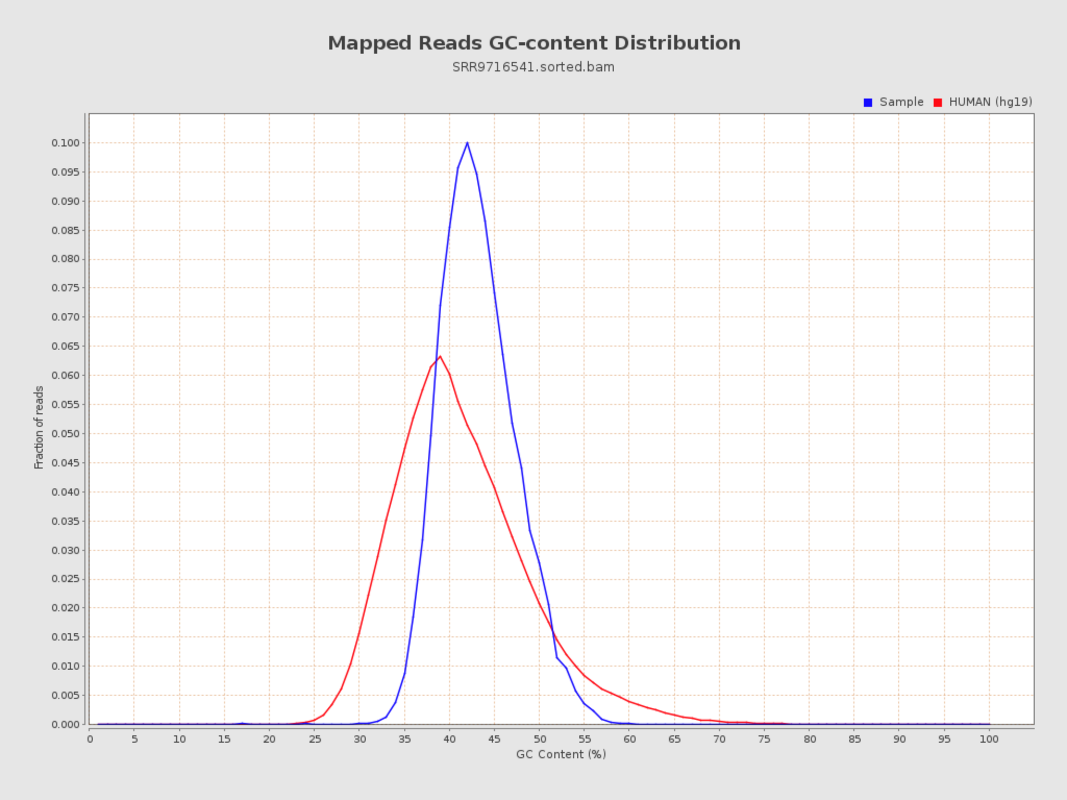
7. Results : Duplication Rate Histogram



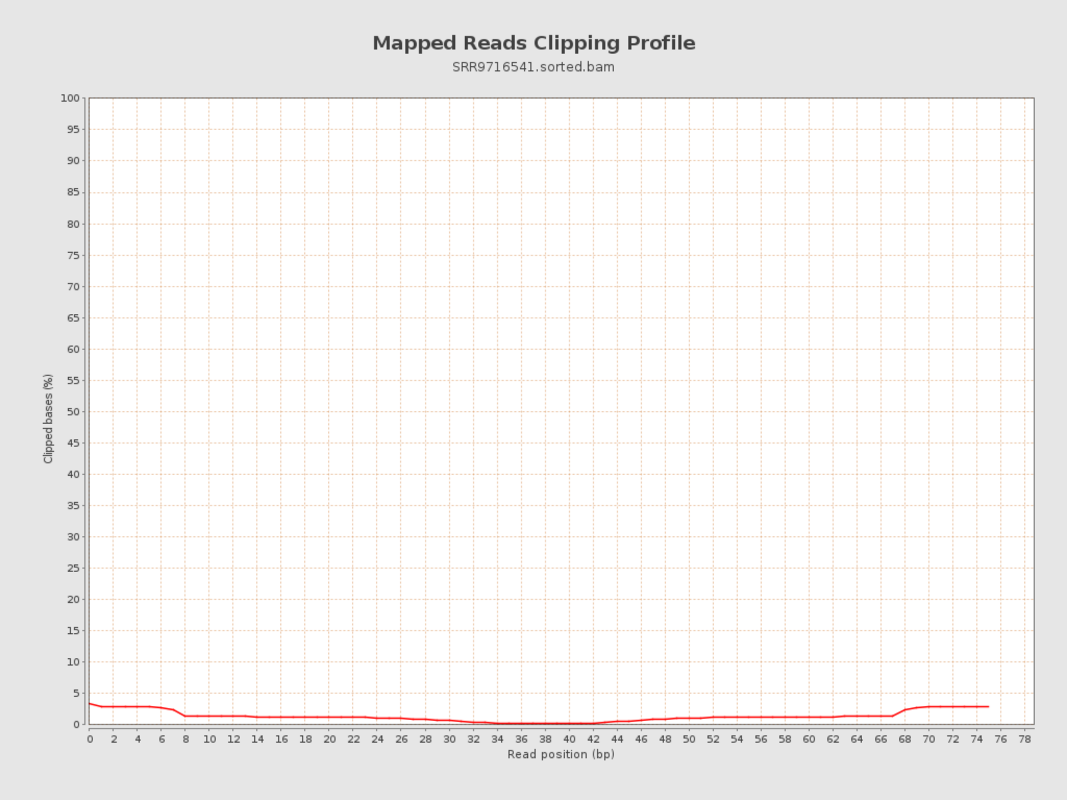
8. Results : Mapped Reads Nucleotide Content



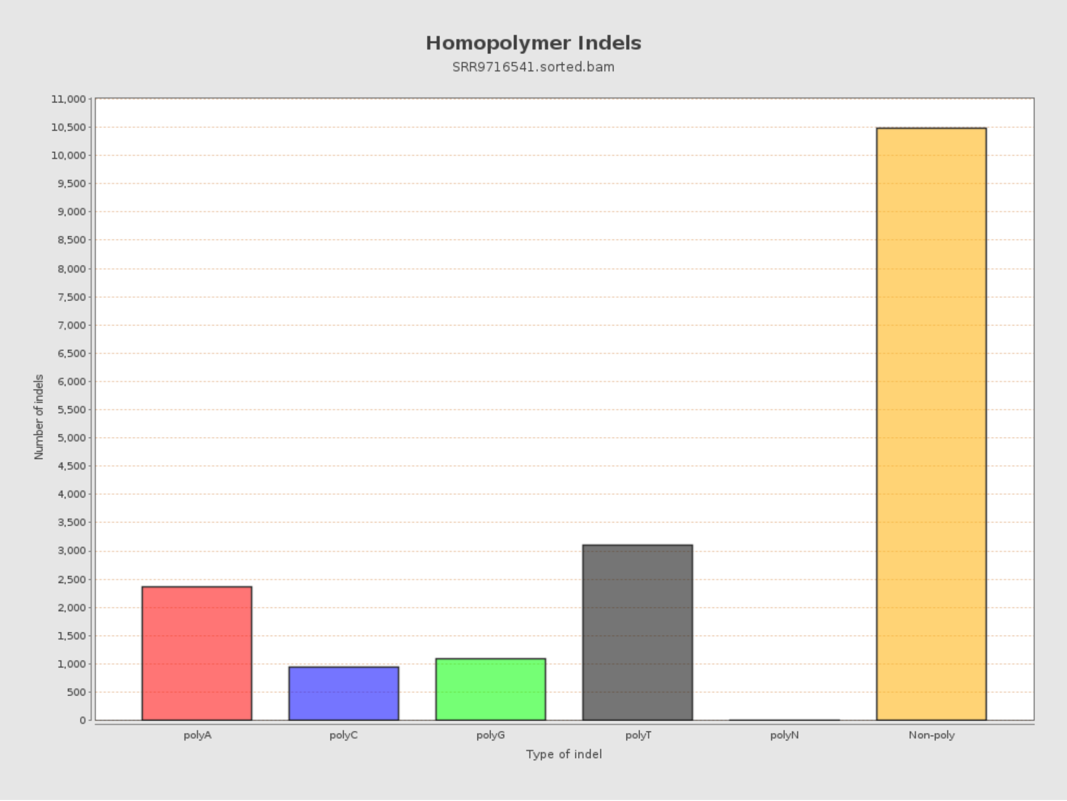
9. Results : Mapped Reads GC-content Distribution



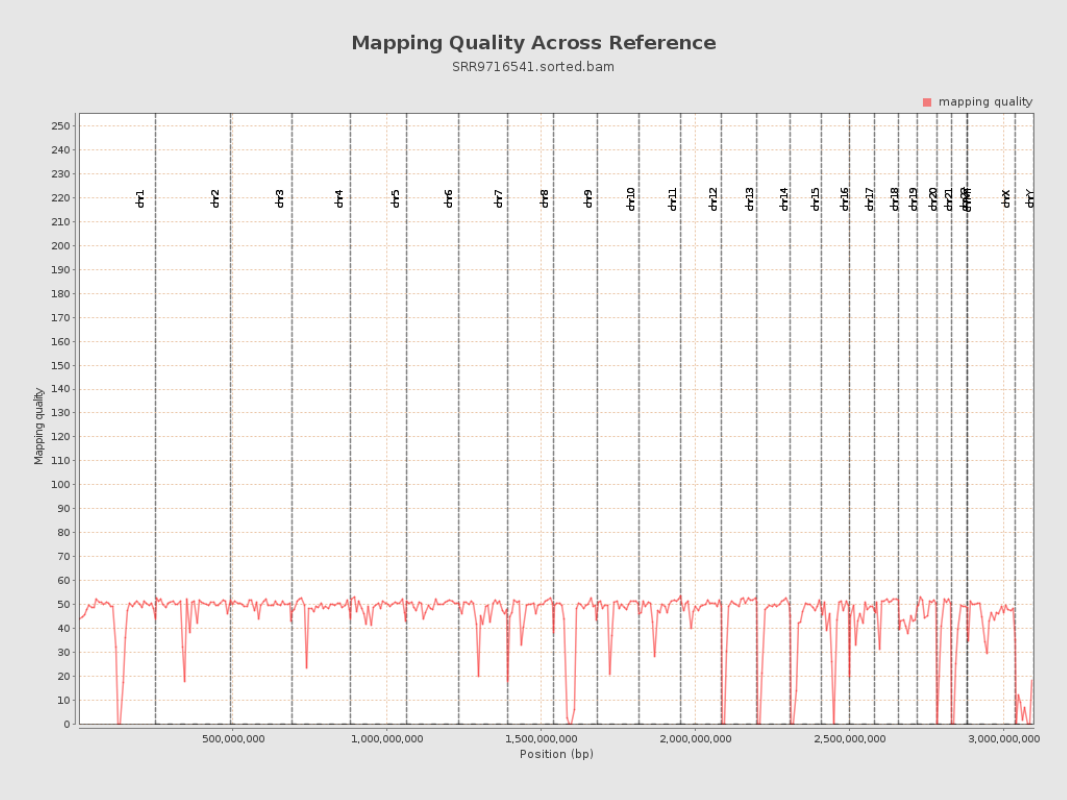
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram