Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 15:19:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716462.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_SRR9716462 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716462.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 15:18:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716462.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,204,356
Mapped reads	1,027,218 / 85.29%
Unmapped reads	177,138 / 14.71%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,914 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	22,692 / 1.88%
Duplication rate	1.55%
Clipped reads	1,027,972 / 85.35%

2.2. ACGT Content

Number/percentage of A's	14,165,316 / 24.47%
Number/percentage of C's	11,127,753 / 19.22%
Number/percentage of T's	18,309,179 / 31.63%
Number/percentage of G's	14,282,876 / 24.67%
Number/percentage of N's	870 / 0%
GC Percentage	43.9%

2.3. Coverage

Mean	0.0187

Standard Deviation	0.1874

2.4. Mapping Quality

Mean Mapping Quality	42.22

2.5. Mismatches and indels

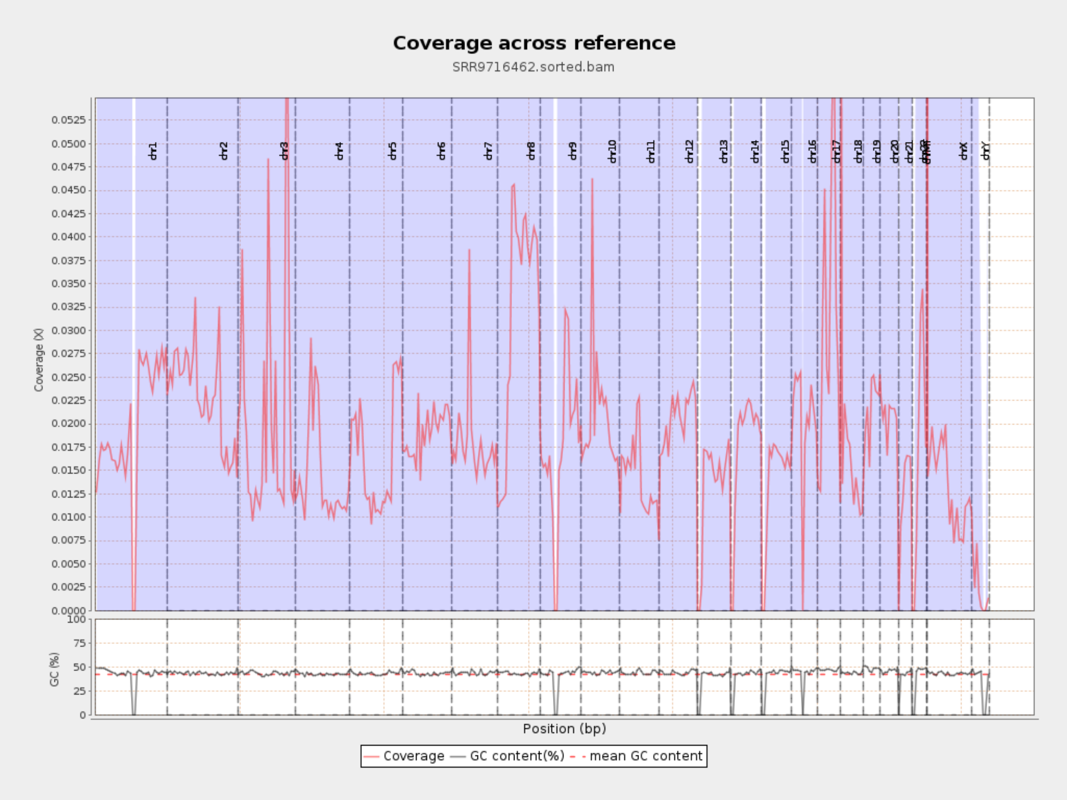
General error rate	0.54%
Mismatches	302,542
Insertions	4,640
Mapped reads with at least one insertion	0.45%
Deletions	11,117
Mapped reads with at least one deletion	1.07%
Homopolymer indels	39.07%

2.6. Chromosome stats

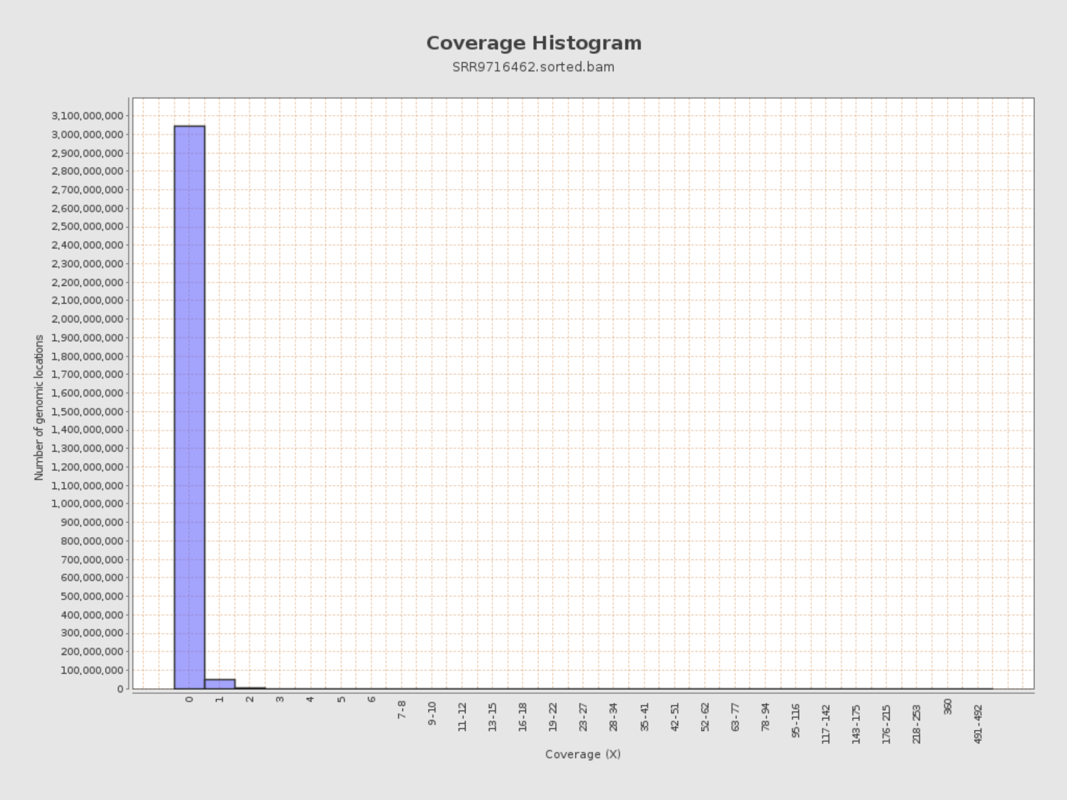
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4876979	0.0196	0.2127
chr2	243199373	5576469	0.0229	0.264
chr3	198022430	4086614	0.0206	0.166
chr4	191154276	2739590	0.0143	0.1337
chr5	180915260	2988640	0.0165	0.1356
chr6	171115067	3253420	0.019	0.1566
chr7	159138663	2876649	0.0181	0.3281

chr8	146364022	4752134	0.0325	0.2092
chr9	141213431	2411547	0.0171	0.153
chr10	135534747	2820419	0.0208	0.2361
chr11	135006516	1964995	0.0146	0.1458
chr12	133851895	2752874	0.0206	0.1578
chr13	115169878	1516150	0.0132	0.1213
chr14	107349540	1881536	0.0175	0.1441
chr15	102531392	1388548	0.0135	0.1265
chr16	90354753	1808302	0.02	0.1556
chr17	81195210	2563098	0.0316	0.1945
chr18	78077248	1332844	0.0171	0.2038
chr19	59128983	1275641	0.0216	0.2156
chr20	63025520	1297917	0.0206	0.1542
chr21	48129895	606818	0.0126	0.1236
chr22	51304566	887177	0.0173	0.1397
chrMT	16571	44144	2.6639	2.2974
chrX	155270560	2062005	0.0133	0.1368
chrY	59373566	139132	0.0023	0.0705

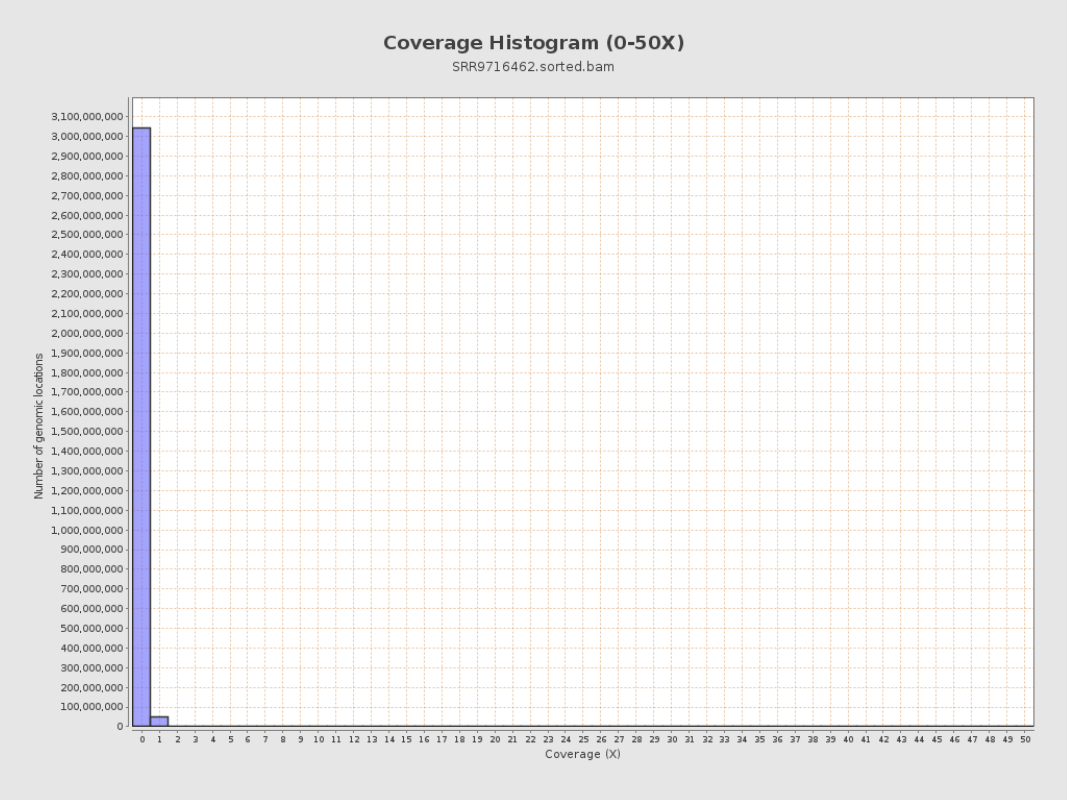
3. Results : Coverage across reference



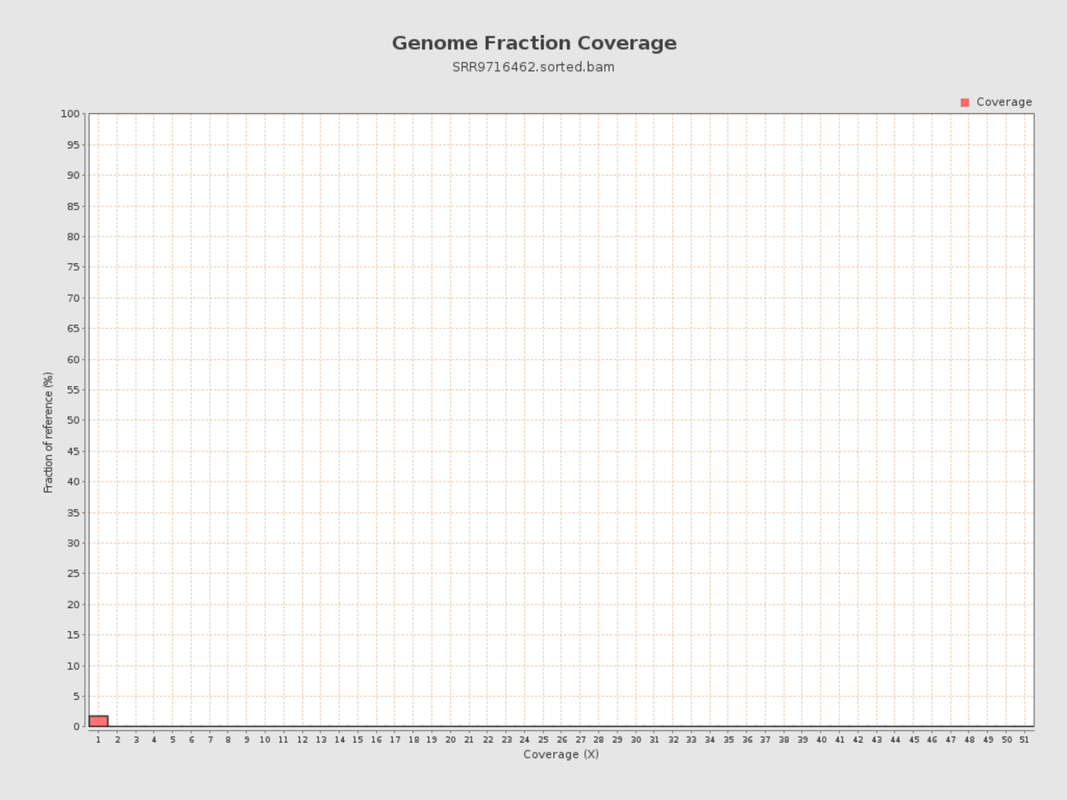
4. Results : Coverage Histogram



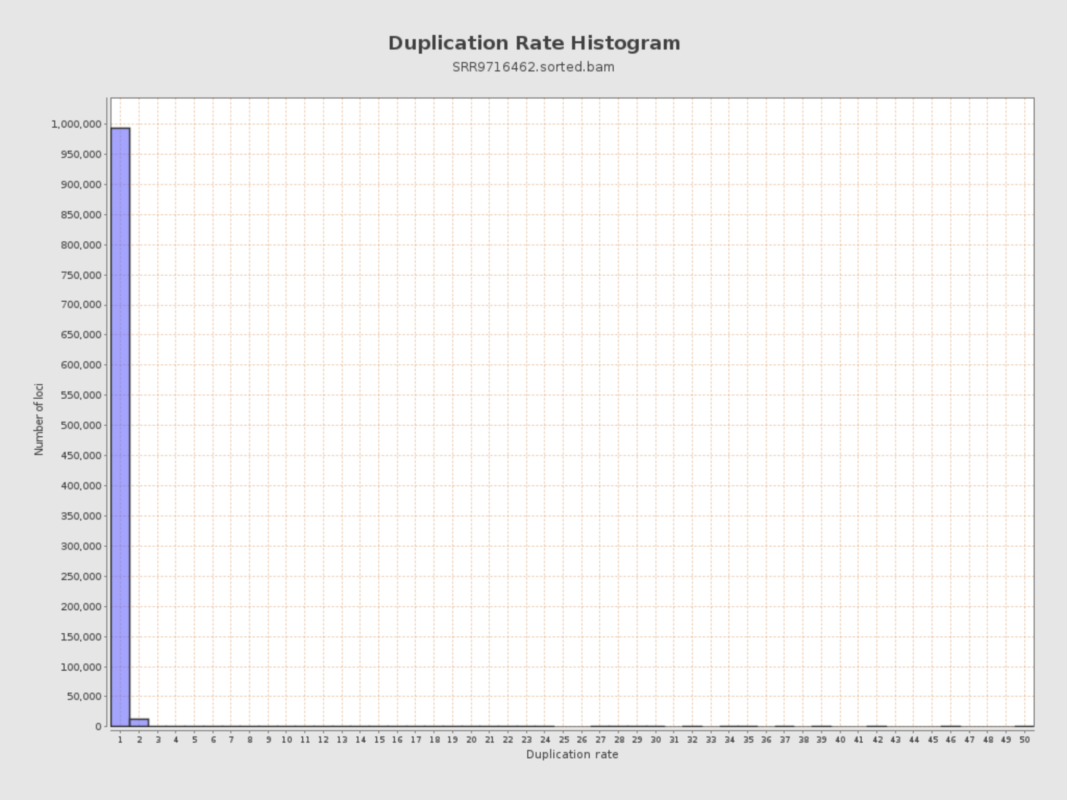
5. Results : Coverage Histogram (0-50X)



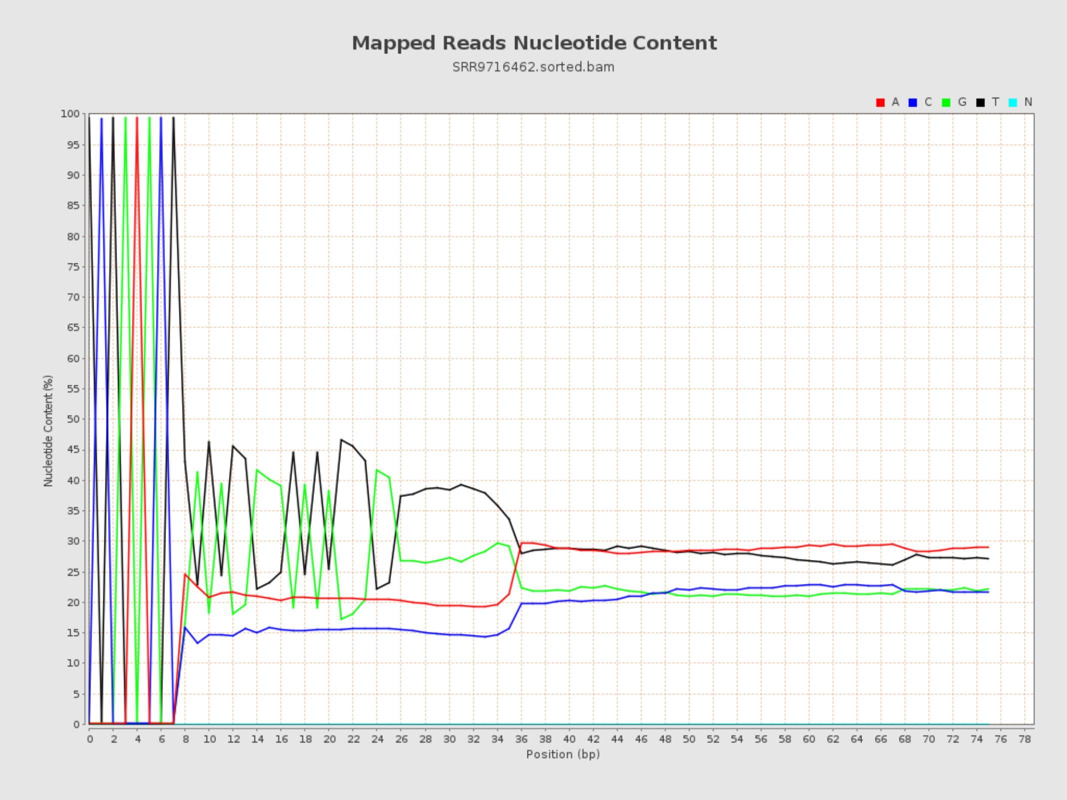
6. Results : Genome Fraction Coverage



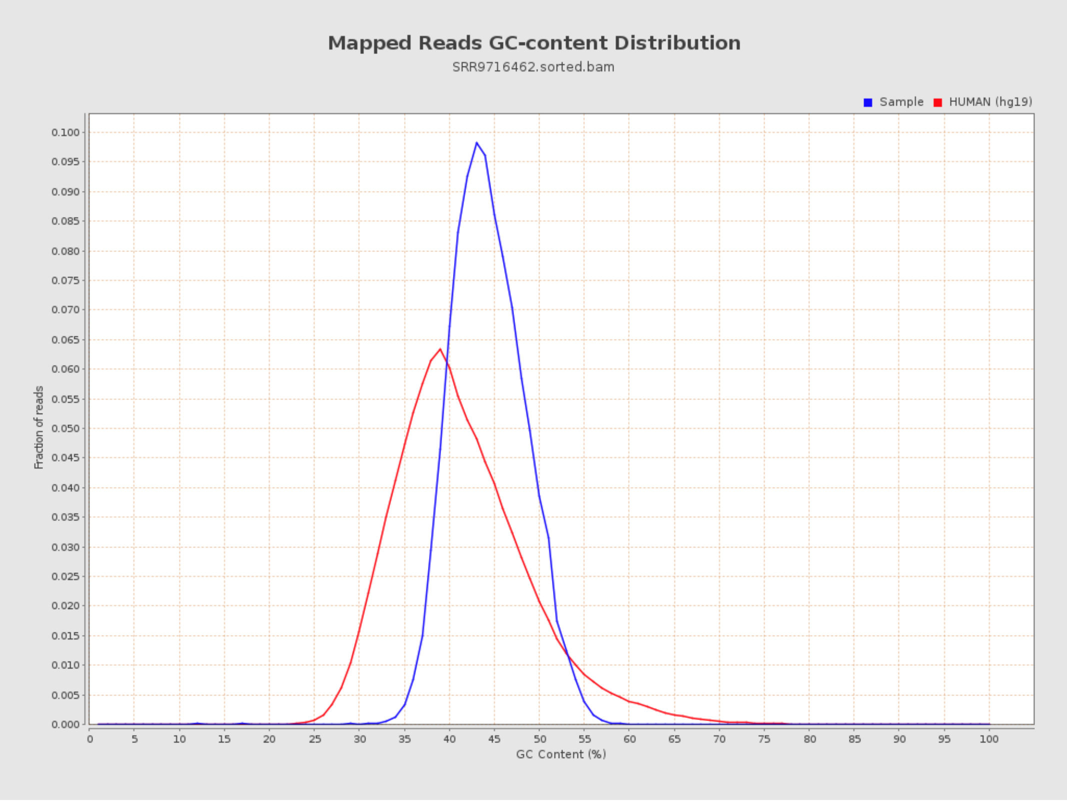
7. Results : Duplication Rate Histogram



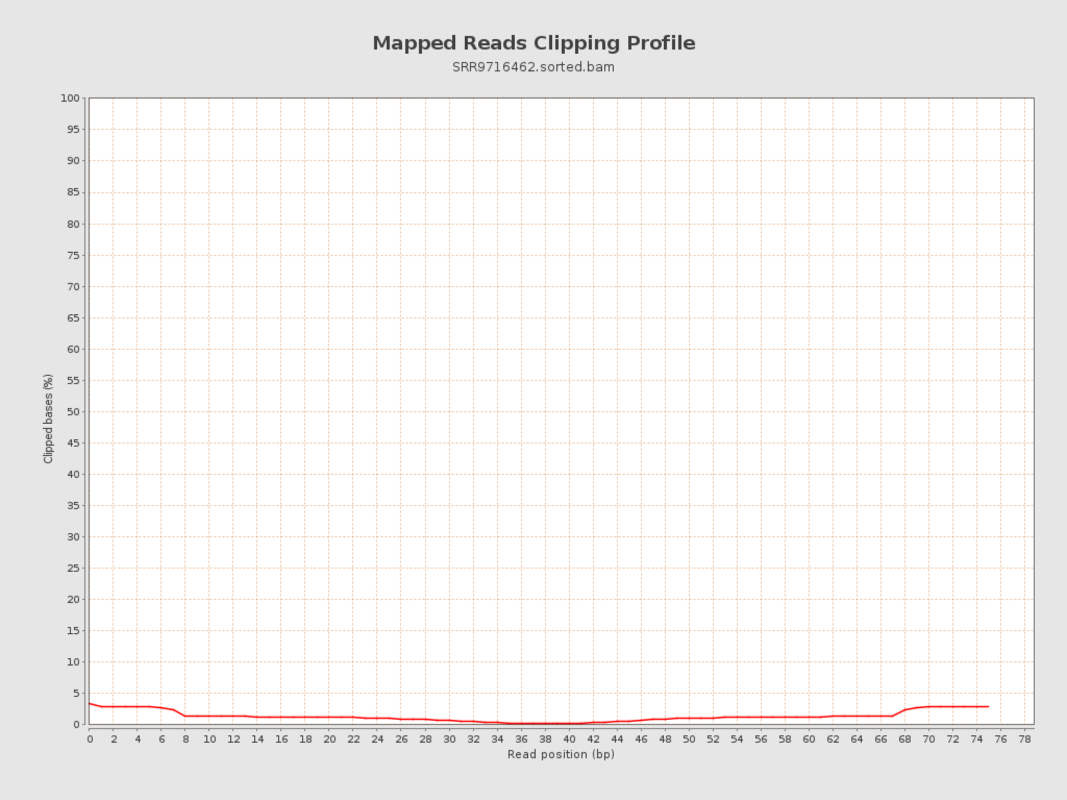
8. Results : Mapped Reads Nucleotide Content



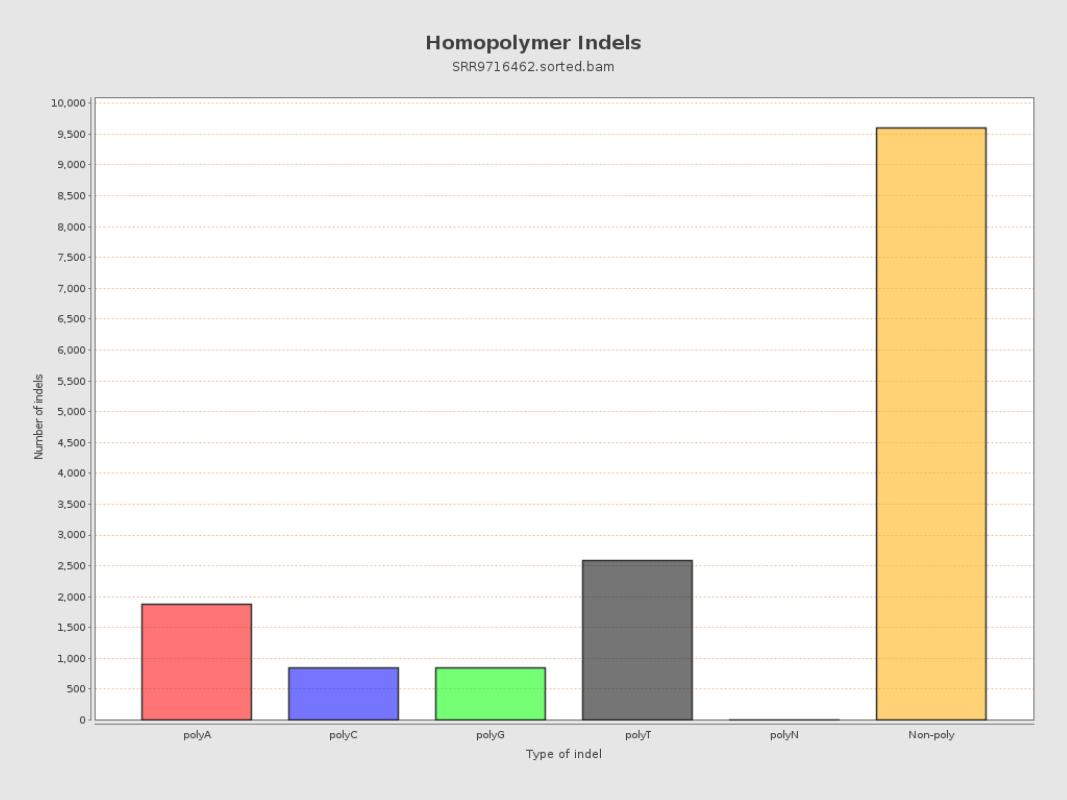
9. Results : Mapped Reads GC-content Distribution



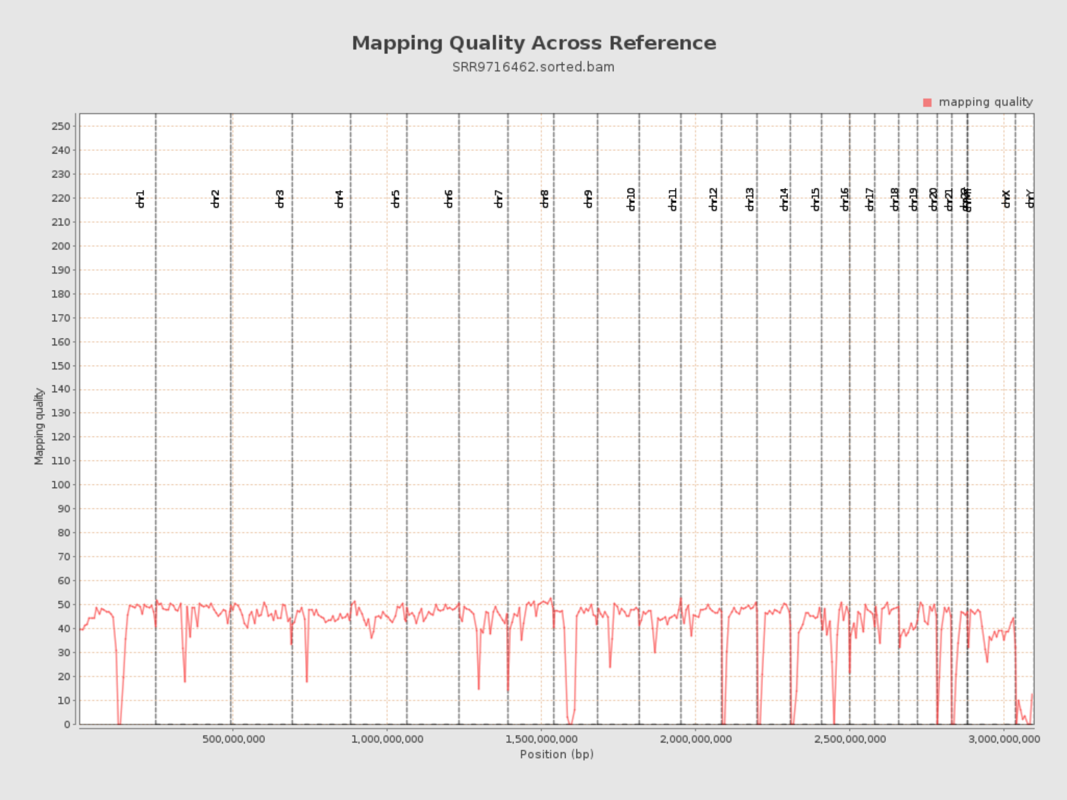
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram