Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 13:30:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716817.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_SRR9716817 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716817.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 13:30:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716817.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	950,141
Mapped reads	863,235 / 90.85%
Unmapped reads	86,906 / 9.15%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,021 / 0.53%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	34,430 / 3.62%
Duplication rate	3.22%
Clipped reads	867,410 / 91.29%

2.2. ACGT Content

Number/percentage of A's	12,913,870 / 25.62%
Number/percentage of C's	10,175,006 / 20.19%
Number/percentage of T's	15,394,151 / 30.55%
Number/percentage of G's	11,914,401 / 23.64%
Number/percentage of N's	414 / 0%
GC Percentage	43.83%

2.3. Coverage

Mean	0.0163

Standard Deviation	0.1728

2.4. Mapping Quality

Mean Mapping Quality	45

2.5. Mismatches and indels

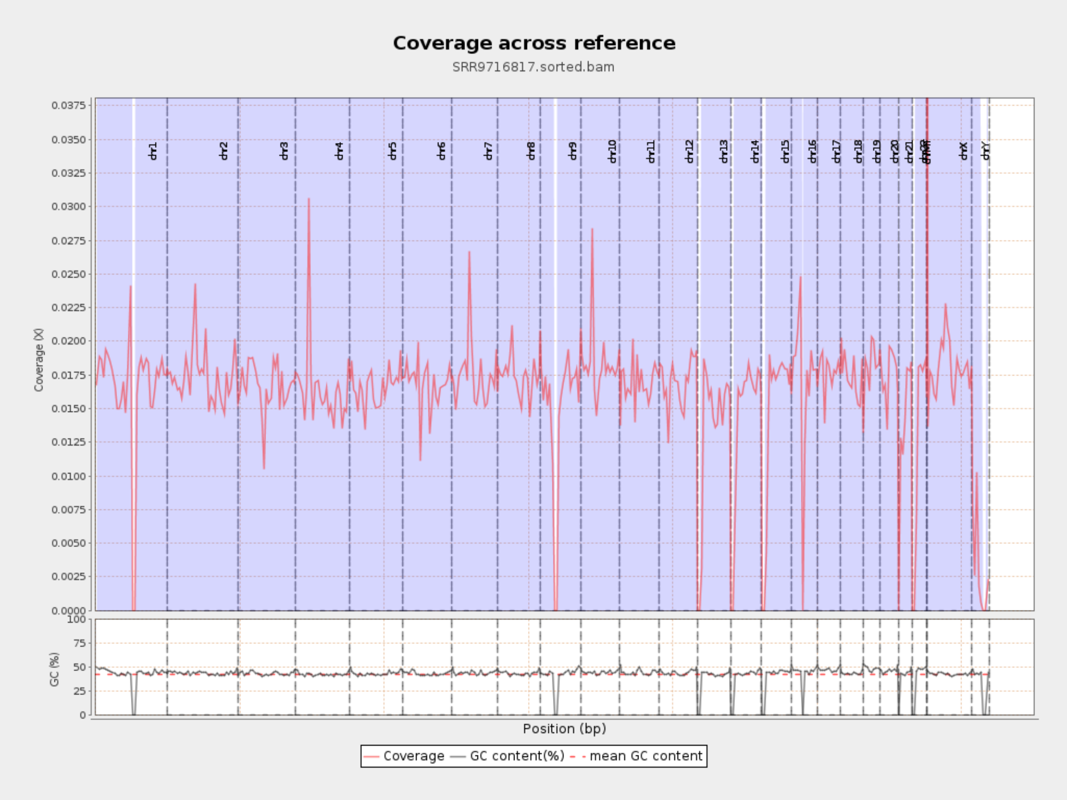
General error rate	0.51%
Mismatches	252,762
Insertions	3,119
Mapped reads with at least one insertion	0.36%
Deletions	9,066
Mapped reads with at least one deletion	1.04%
Homopolymer indels	43.32%

2.6. Chromosome stats

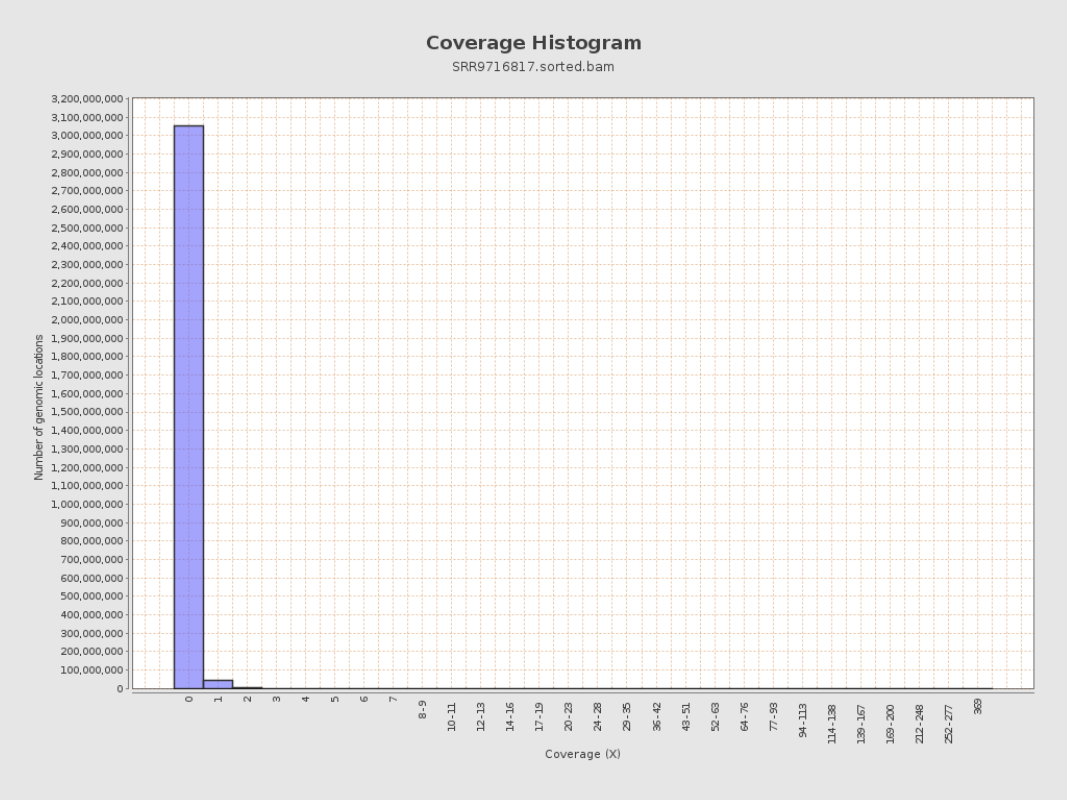
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4099478	0.0164	0.2395
chr2	243199373	4231914	0.0174	0.2216
chr3	198022430	3302116	0.0167	0.1407
chr4	191154276	3157684	0.0165	0.1584
chr5	180915260	3007301	0.0166	0.1406
chr6	171115067	2865072	0.0167	0.1499
chr7	159138663	2798002	0.0176	0.2072

chr8	146364022	2548496	0.0174	0.1922
chr9	141213431	2076332	0.0147	0.1471
chr10	135534747	2496677	0.0184	0.1925
chr11	135006516	2289213	0.017	0.165
chr12	133851895	2266923	0.0169	0.1432
chr13	115169878	1525559	0.0132	0.1251
chr14	107349540	1513485	0.0141	0.1324
chr15	102531392	1463551	0.0143	0.1313
chr16	90354753	1512834	0.0167	0.1469
chr17	81195210	1437443	0.0177	0.1514
chr18	78077248	1346982	0.0173	0.2372
chr19	59128983	1082562	0.0183	0.2002
chr20	63025520	1104666	0.0175	0.1472
chr21	48129895	665290	0.0138	0.14
chr22	51304566	644941	0.0126	0.1228
chrMT	16571	3960	0.239	0.5239
chrX	155270560	2795061	0.018	0.1519
chrY	59373566	176794	0.003	0.1011

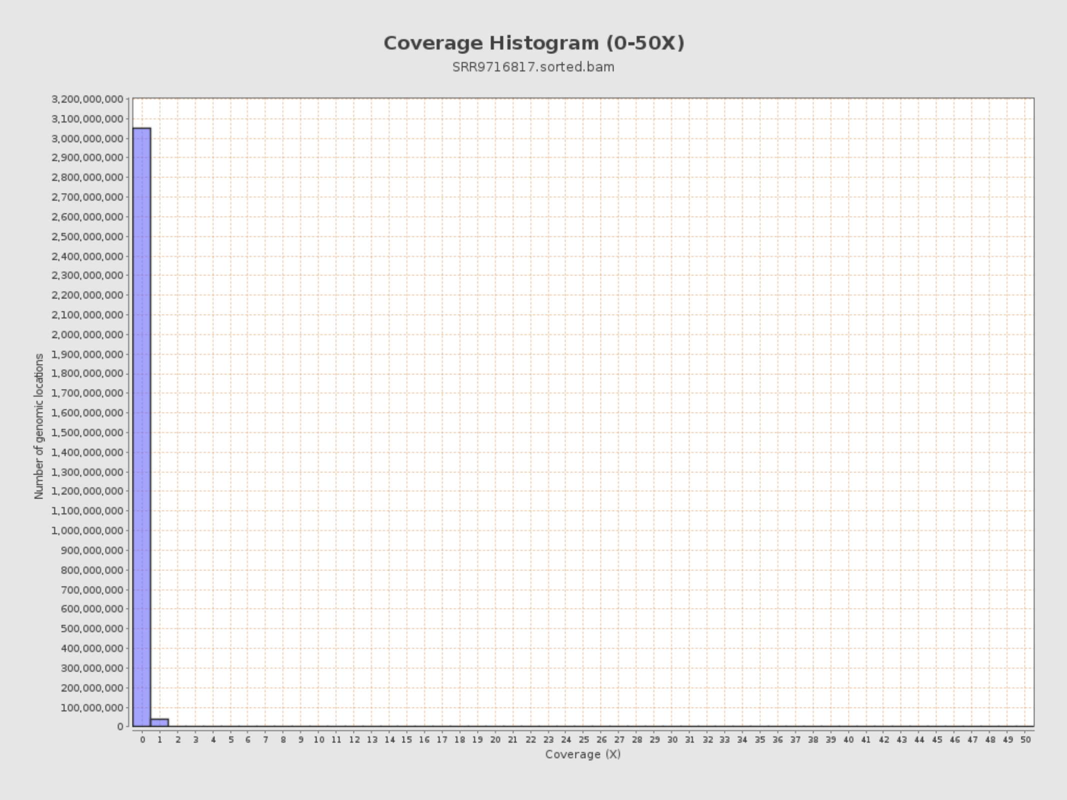
3. Results : Coverage across reference



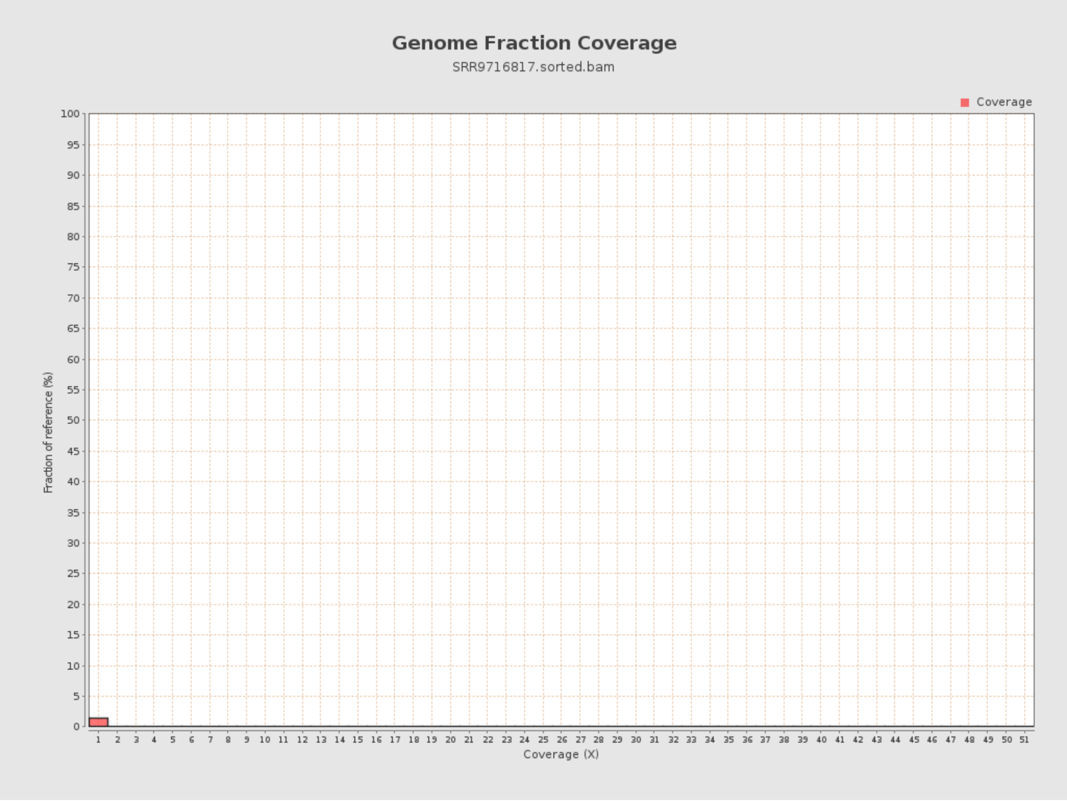
4. Results : Coverage Histogram



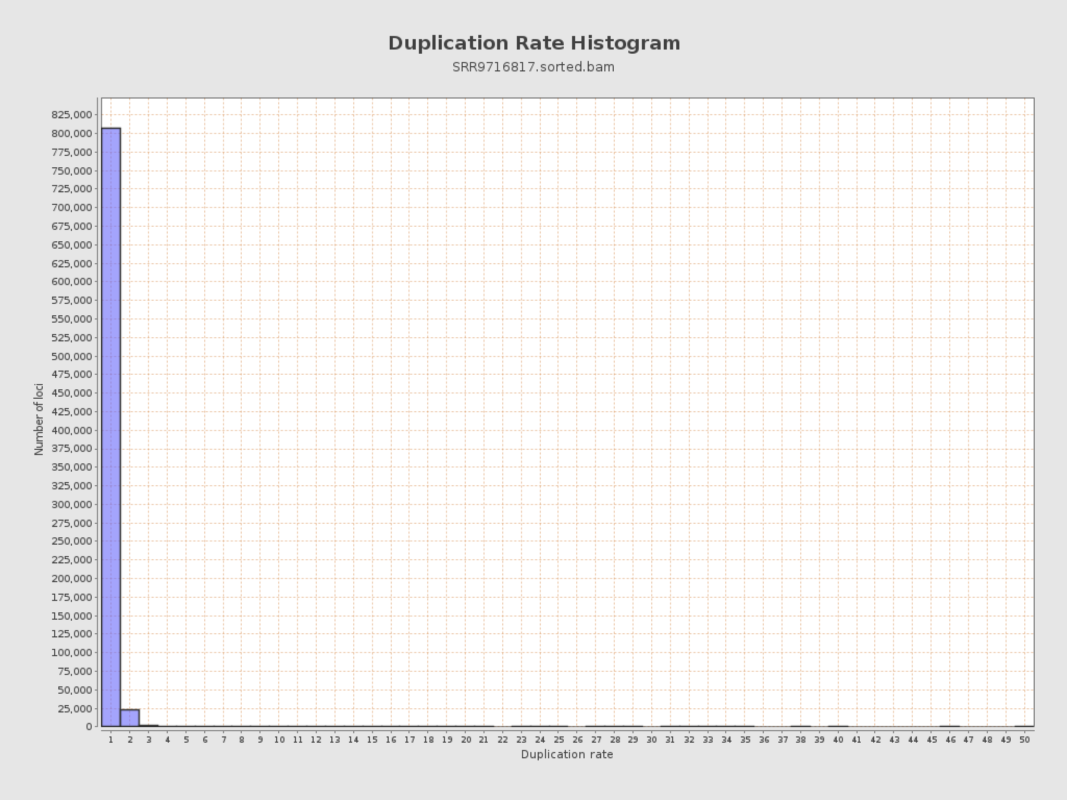
5. Results : Coverage Histogram (0-50X)



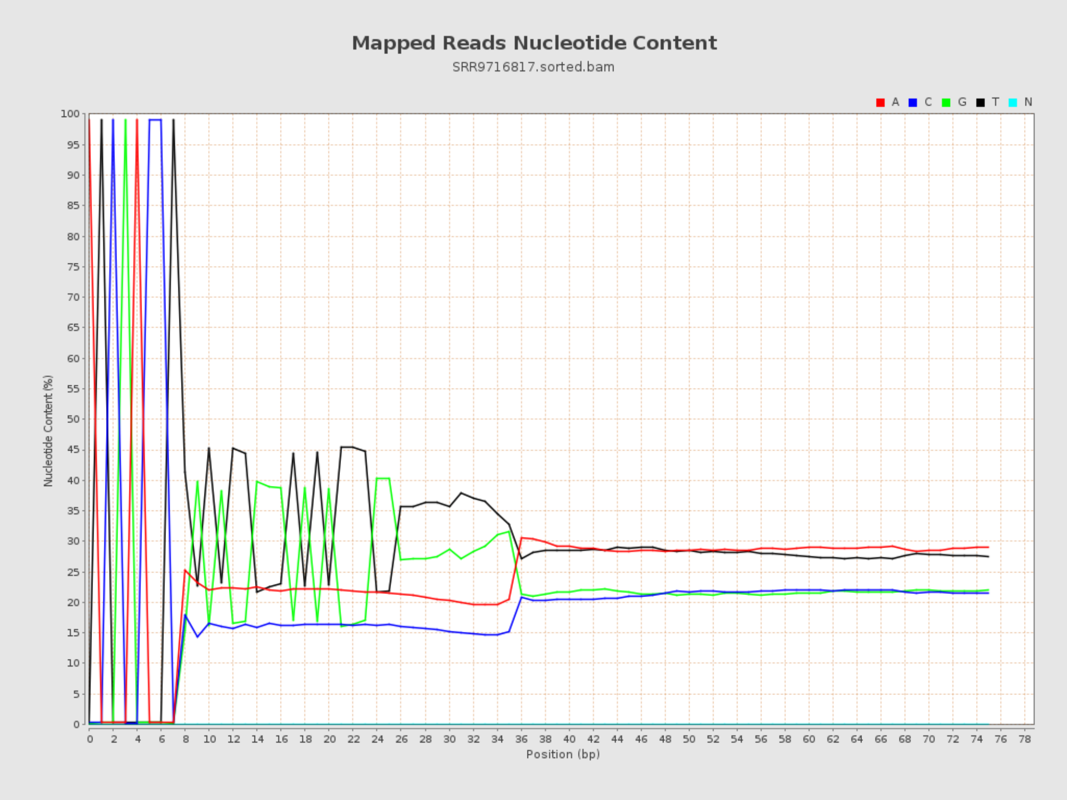
6. Results : Genome Fraction Coverage



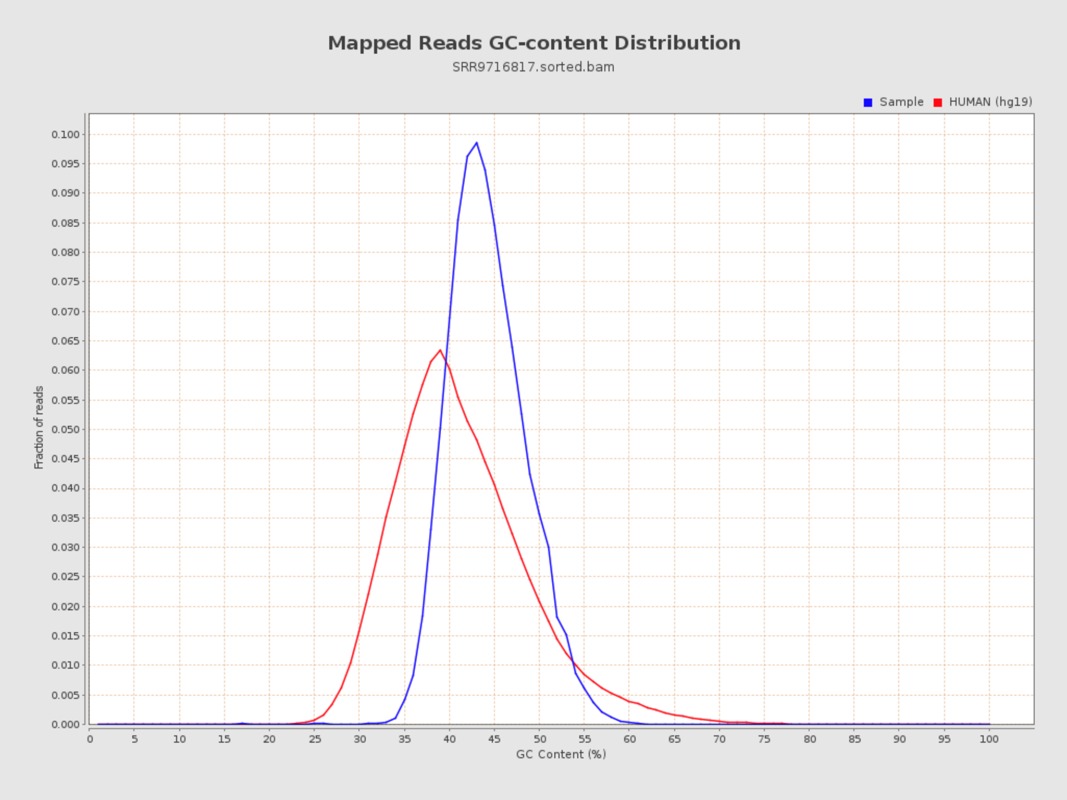
7. Results : Duplication Rate Histogram



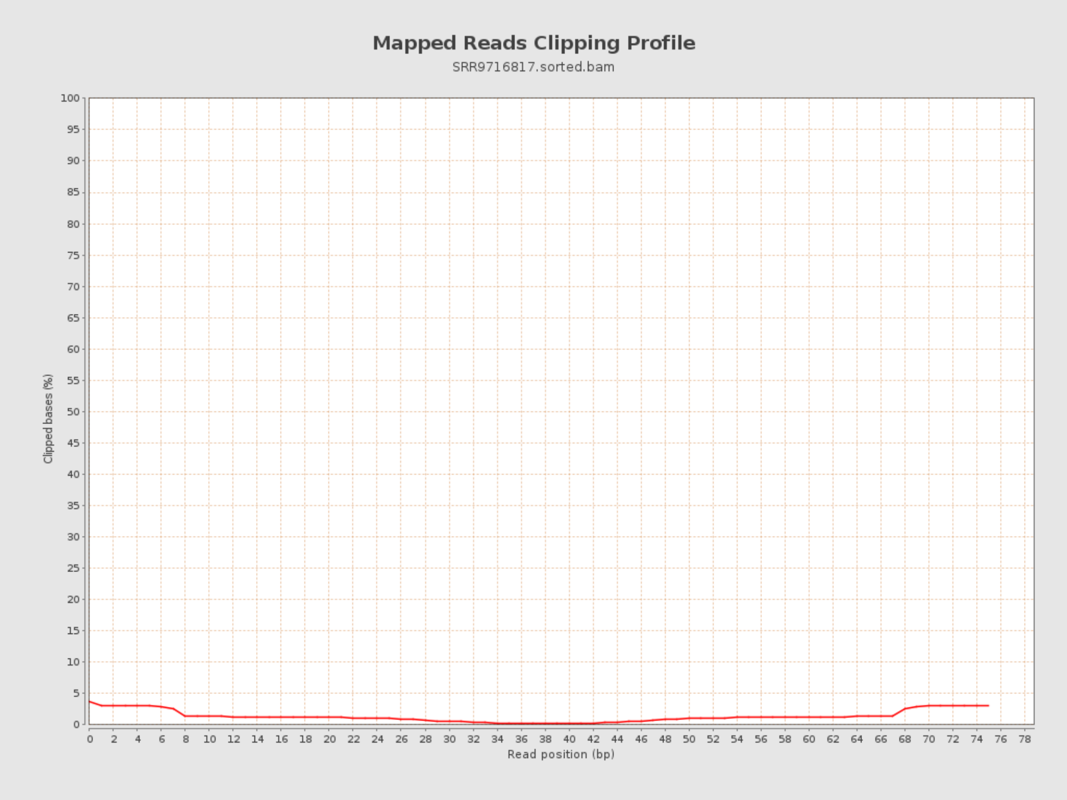
8. Results : Mapped Reads Nucleotide Content



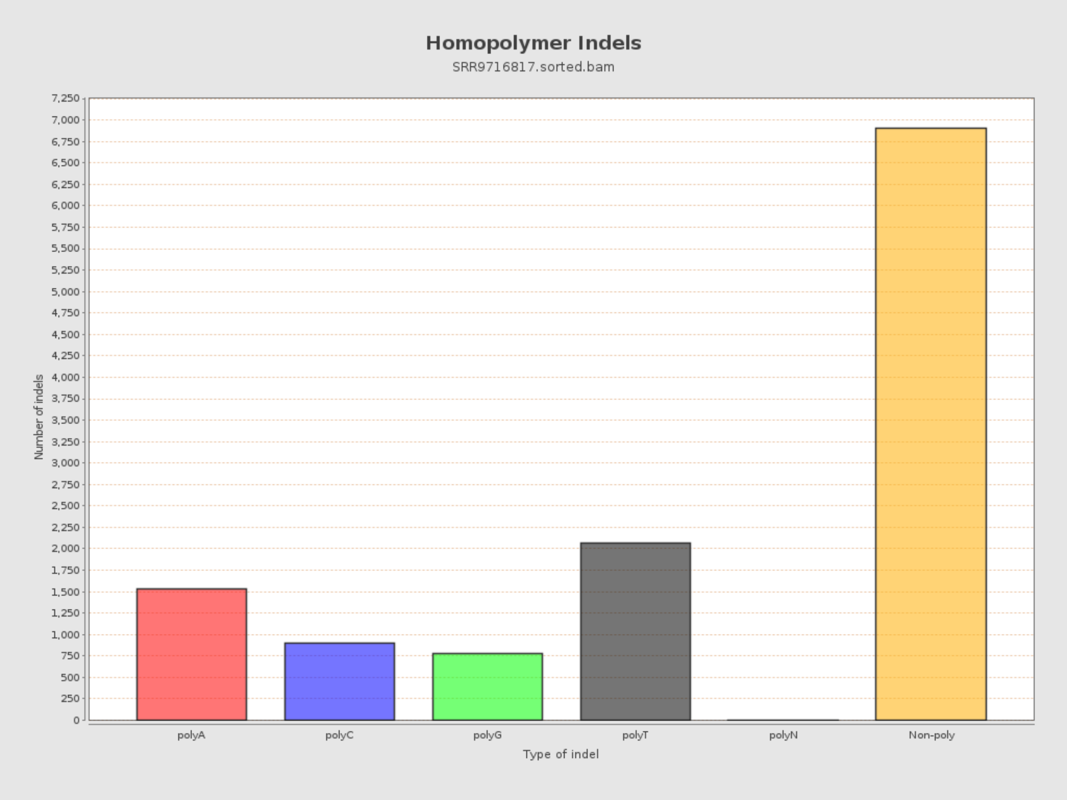
9. Results : Mapped Reads GC-content Distribution



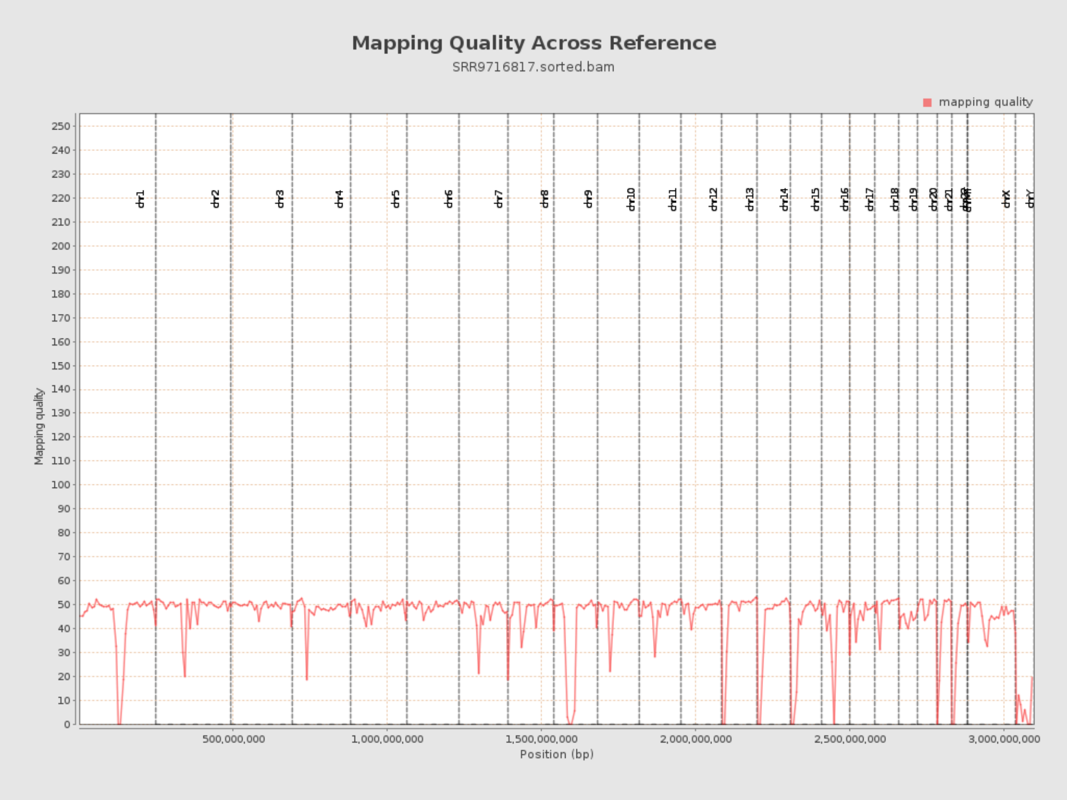
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram