Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 13:37:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716821.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_SRR9716821 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716821.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 13:37:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716821.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	790,606
Mapped reads	659,625 / 83.43%
Unmapped reads	130,981 / 16.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,038 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	12,903 / 1.63%
Duplication rate	1.4%
Clipped reads	660,934 / 83.6%

2.2. ACGT Content

Number/percentage of A's	9,222,719 / 24.06%
Number/percentage of C's	6,937,012 / 18.1%
Number/percentage of T's	12,514,259 / 32.65%
Number/percentage of G's	9,659,095 / 25.2%
Number/percentage of N's	232 / 0%
GC Percentage	43.29%

2.3. Coverage

Mean	0.0124

Standard Deviation	0.1437

2.4. Mapping Quality

Mean Mapping Quality	44.65

2.5. Mismatches and indels

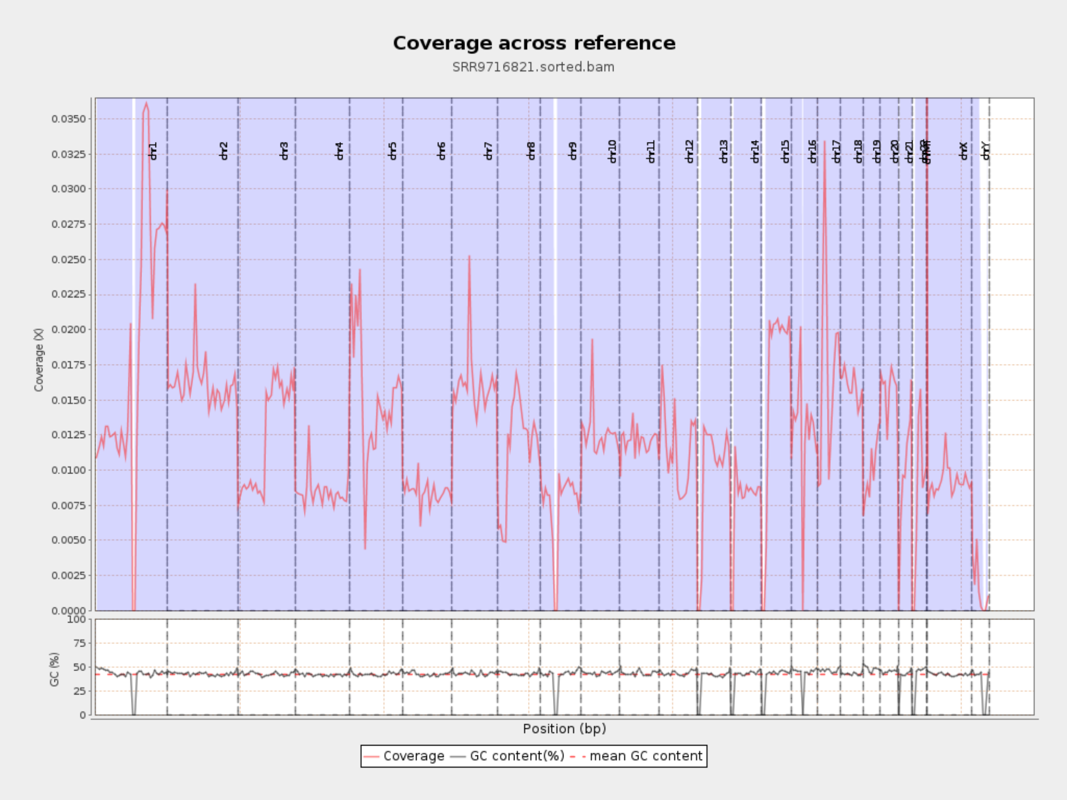
General error rate	0.53%
Mismatches	197,085
Insertions	2,549
Mapped reads with at least one insertion	0.38%
Deletions	7,450
Mapped reads with at least one deletion	1.12%
Homopolymer indels	42.25%

2.6. Chromosome stats

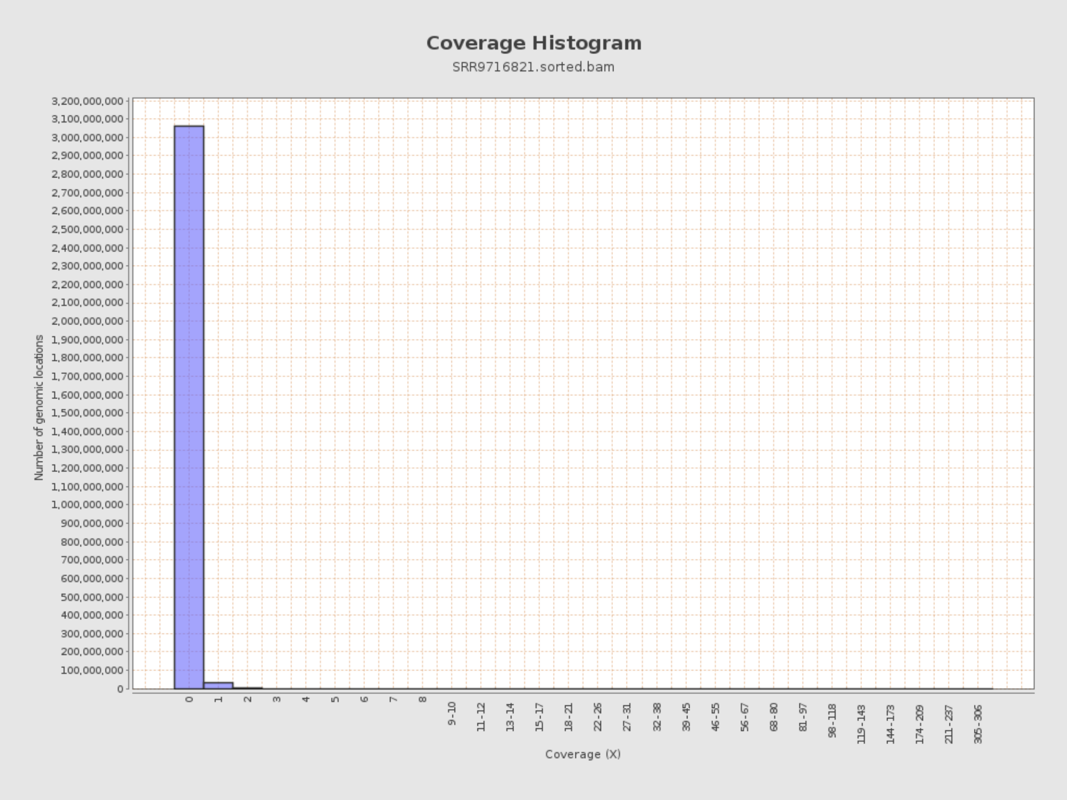
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4501824	0.0181	0.2216
chr2	243199373	3930085	0.0162	0.1901
chr3	198022430	2449263	0.0124	0.1155
chr4	191154276	1620005	0.0085	0.1004
chr5	180915260	2755115	0.0152	0.1283
chr6	171115067	1440726	0.0084	0.1004
chr7	159138663	2577592	0.0162	0.2063

chr8	146364022	1704505	0.0116	0.1293
chr9	141213431	1052553	0.0075	0.1086
chr10	135534747	1720219	0.0127	0.1333
chr11	135006516	1636367	0.0121	0.1353
chr12	133851895	1523946	0.0114	0.1112
chr13	115169878	1123455	0.0098	0.1023
chr14	107349540	824853	0.0077	0.0933
chr15	102531392	1660057	0.0162	0.133
chr16	90354753	1137036	0.0126	0.1194
chr17	81195210	1429596	0.0176	0.1427
chr18	78077248	1243436	0.0159	0.2218
chr19	59128983	593665	0.01	0.1568
chr20	63025520	987577	0.0157	0.1312
chr21	48129895	475708	0.0099	0.1051
chr22	51304566	435377	0.0085	0.0951
chrMT	16571	807	0.0487	0.2152
chrX	155270560	1426891	0.0092	0.1072
chrY	59373566	94456	0.0016	0.0483

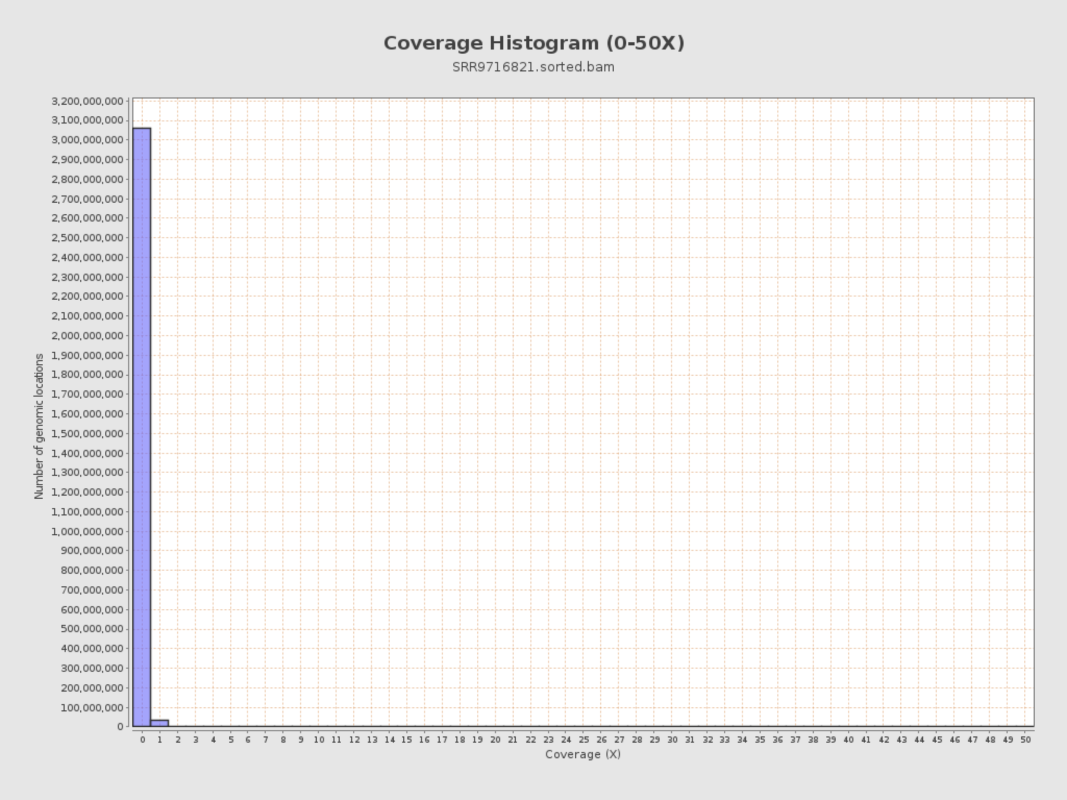
3. Results : Coverage across reference



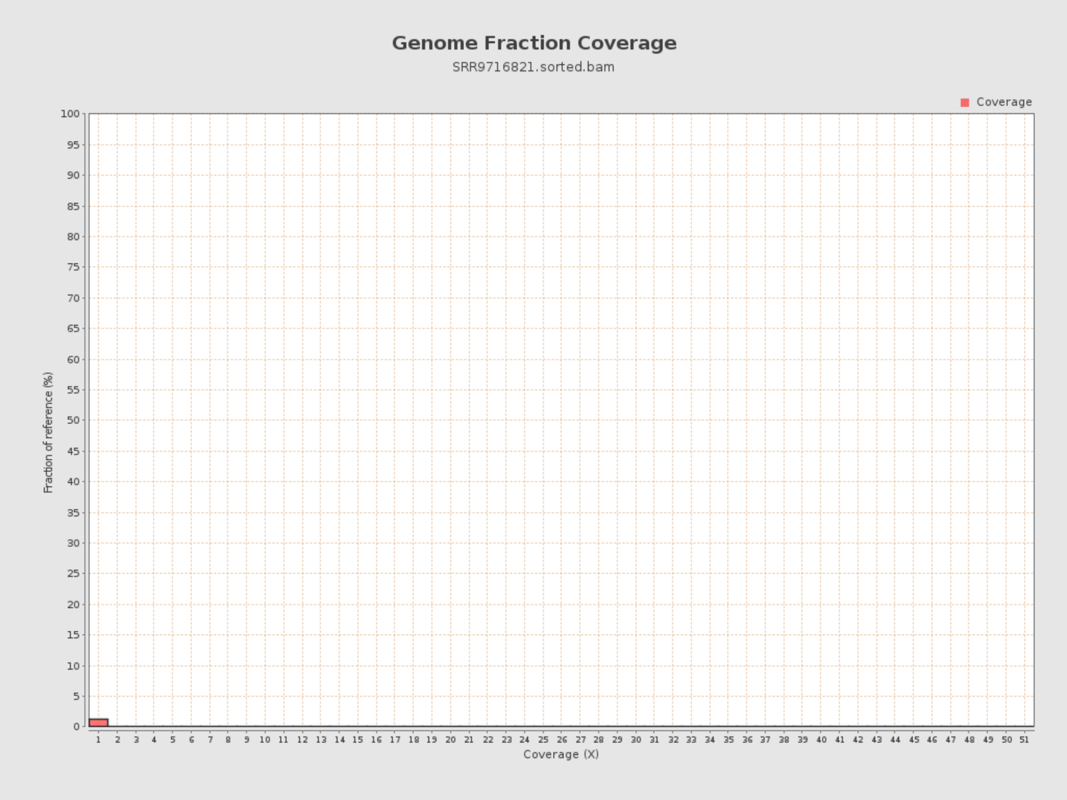
4. Results : Coverage Histogram



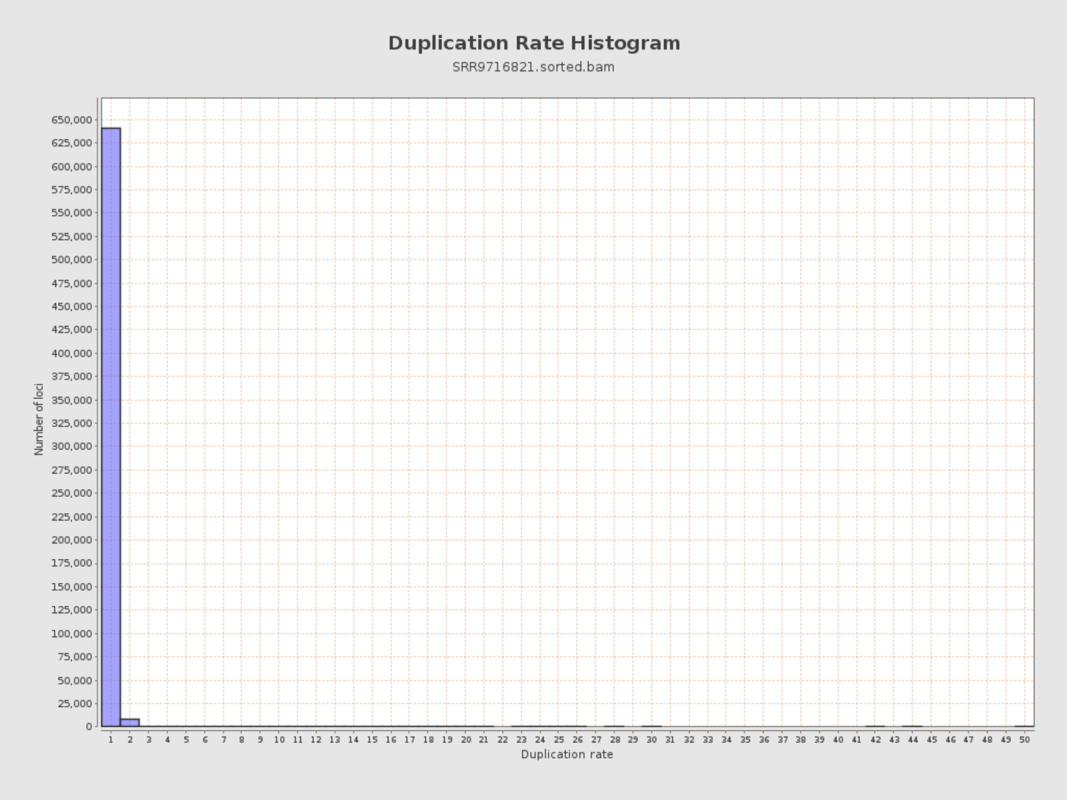
5. Results : Coverage Histogram (0-50X)



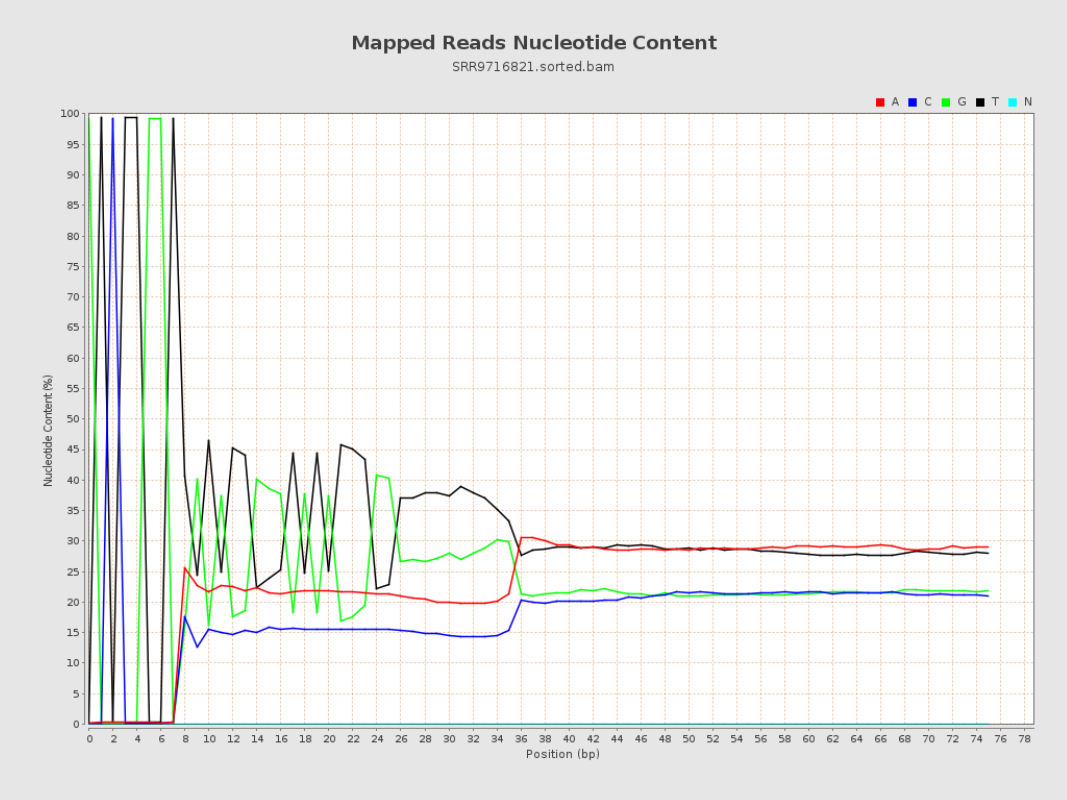
6. Results : Genome Fraction Coverage



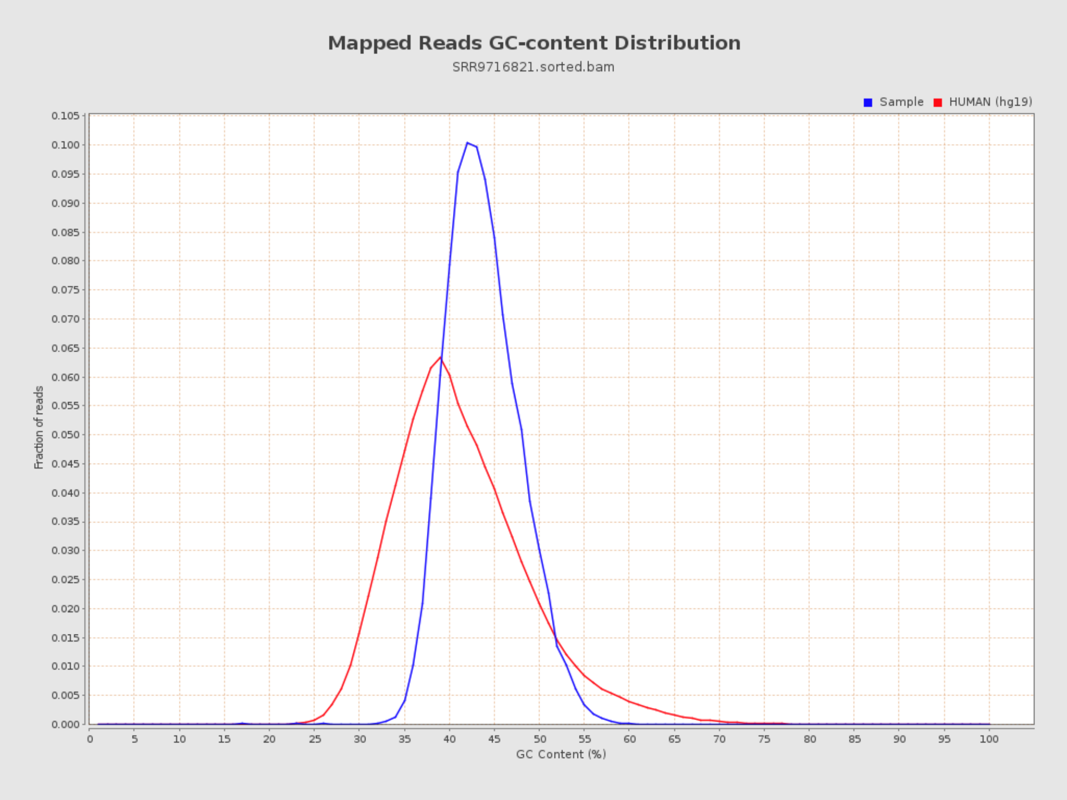
7. Results : Duplication Rate Histogram



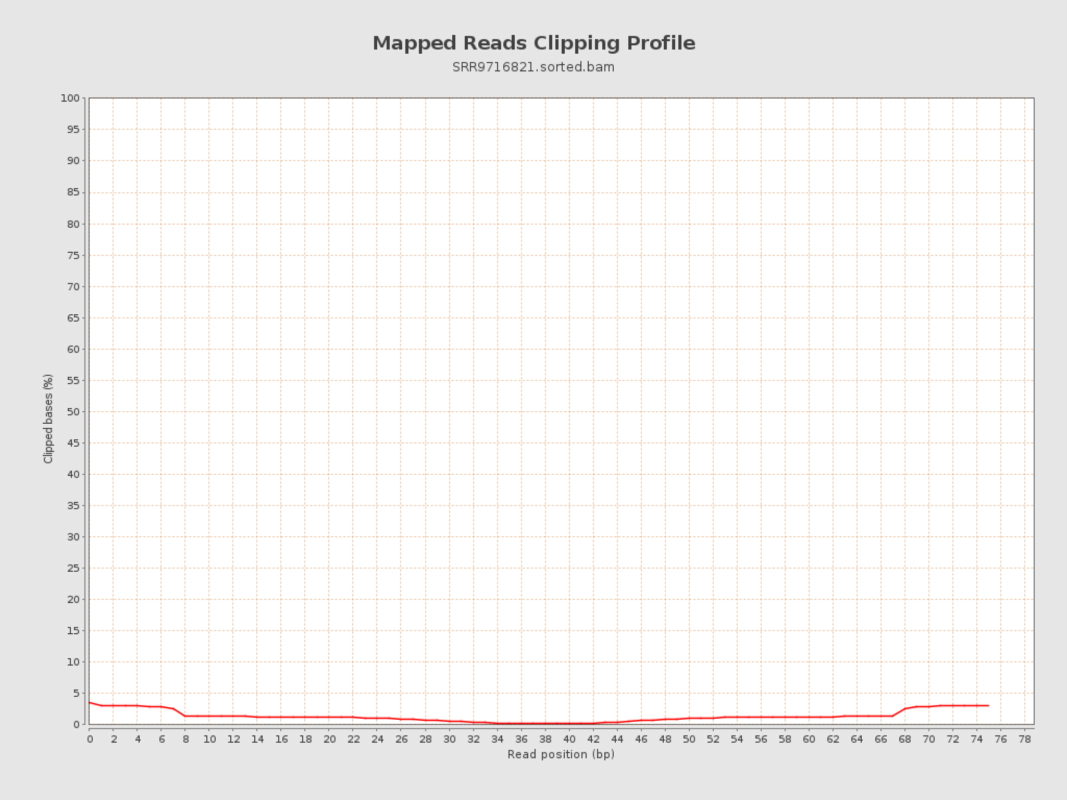
8. Results : Mapped Reads Nucleotide Content



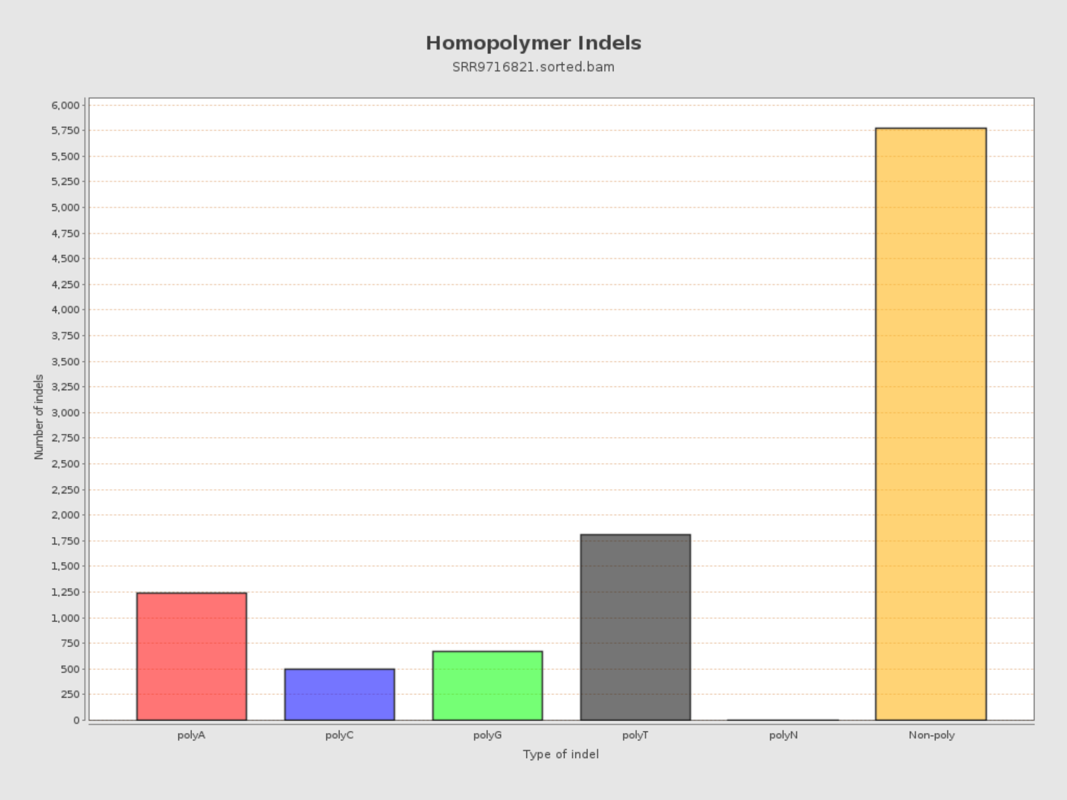
9. Results : Mapped Reads GC-content Distribution



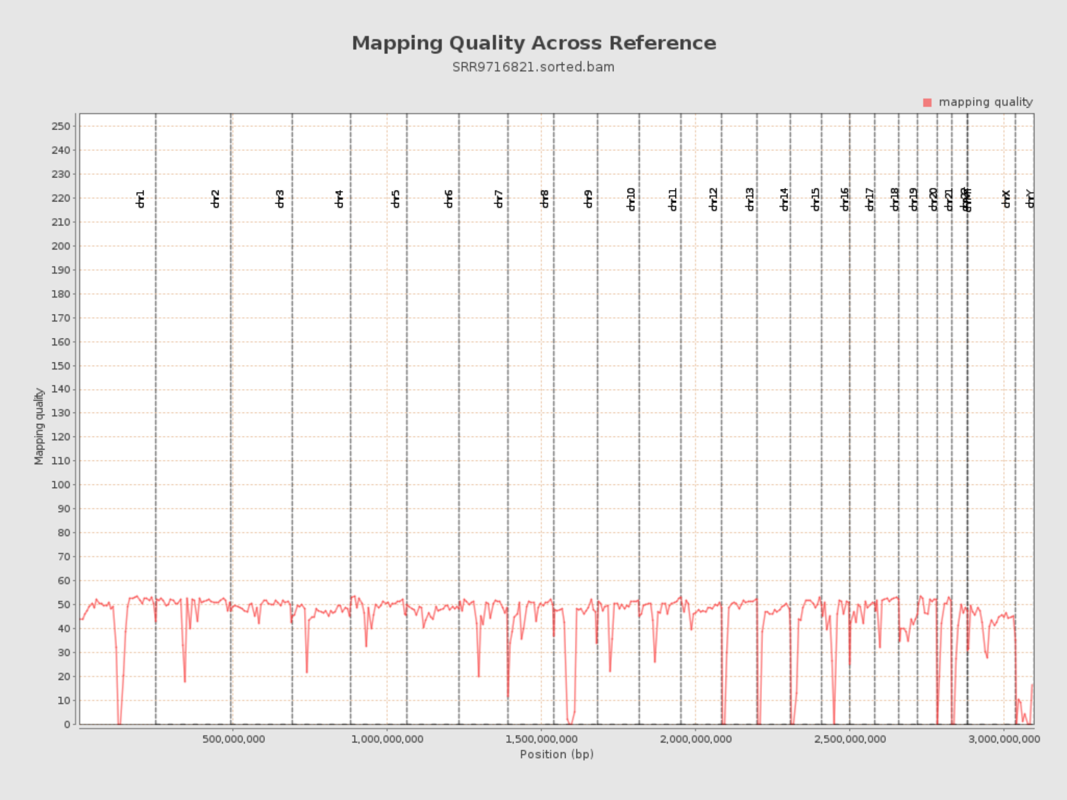
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram