

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 12:43:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716424.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_SRR9716424 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716424.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 12:43:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716424.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	836,720
Mapped reads	769,306 / 91.94%
Unmapped reads	67,414 / 8.06%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,622 / 0.31%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	17,809 / 2.13%
Duplication rate	1.52%
Clipped reads	771,075 / 92.15%

2.2. ACGT Content

Number/percentage of A's	10,687,264 / 23.92%
Number/percentage of C's	8,215,878 / 18.38%
Number/percentage of T's	14,593,570 / 32.66%
Number/percentage of G's	11,190,649 / 25.04%
Number/percentage of N's	857 / 0%
GC Percentage	43.43%

2.3. Coverage

Mean	0.0144

Standard Deviation	0.1712
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2.4. Mapping Quality

Mean Mapping Quality	43.85
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2.5. Mismatches and indels

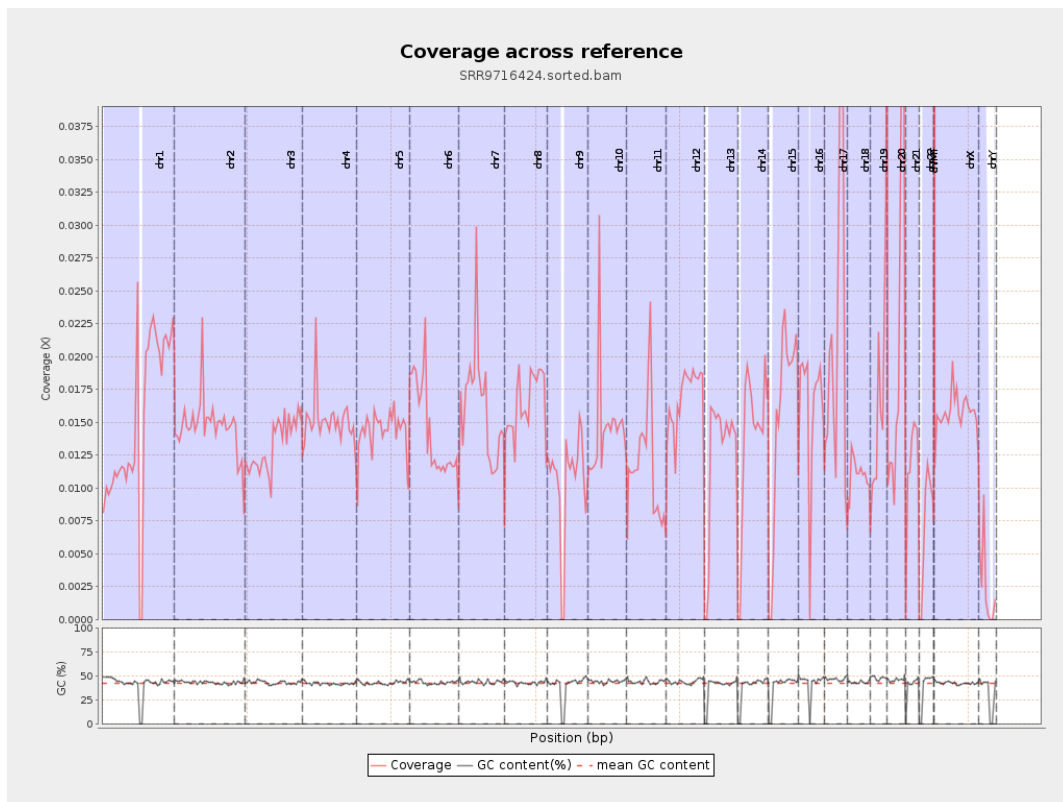
General error rate	0.52%
Mismatches	227,973
Insertions	2,588
Mapped reads with at least one insertion	0.34%
Deletions	8,567
Mapped reads with at least one deletion	1.11%
Homopolymer indels	43.74%

2.6. Chromosome stats

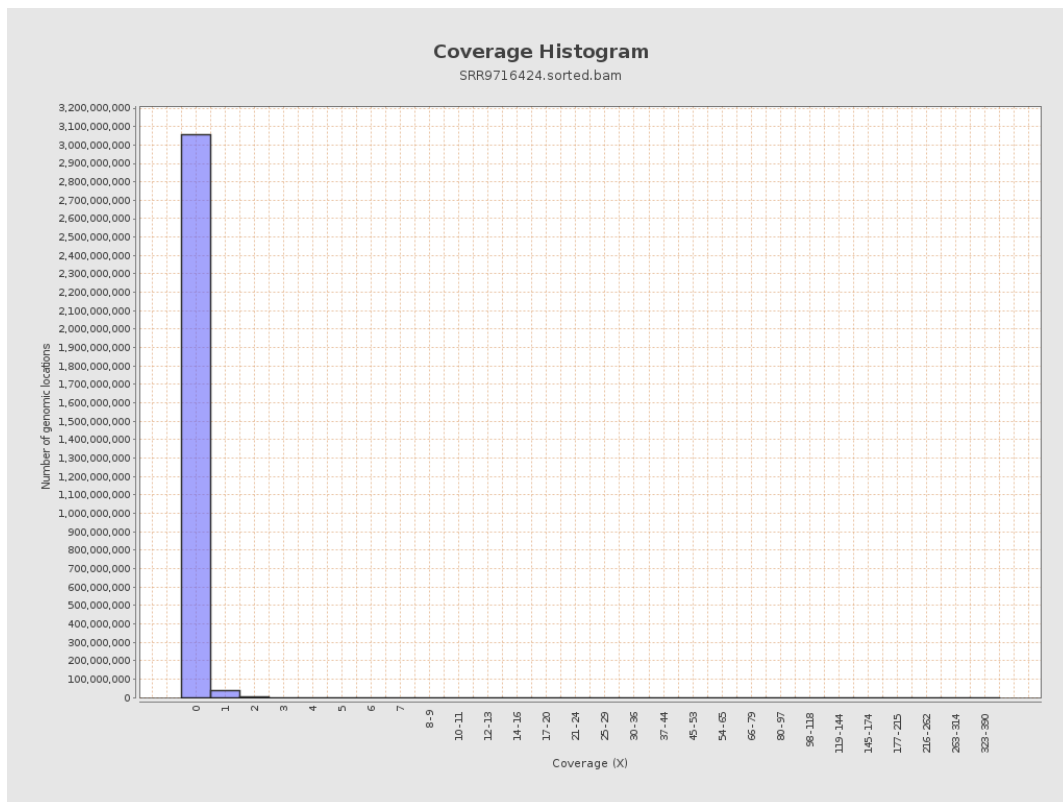
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	3743114	0.015	0.2837
chr2	243199373	3568528	0.0147	0.2079
chr3	198022430	2625286	0.0133	0.1206
chr4	191154276	2878081	0.0151	0.1353
chr5	180915260	2616070	0.0145	0.1254
chr6	171115067	2454407	0.0143	0.1427
chr7	159138663	2570460	0.0162	0.2317

chr8	146364022	2403933	0.0164	0.1983
chr9	141213431	1485865	0.0105	0.1279
chr10	135534747	1966959	0.0145	0.1761
chr11	135006516	1592593	0.0118	0.1386
chr12	133851895	2251746	0.0168	0.136
chr13	115169878	1417881	0.0123	0.1159
chr14	107349540	1487283	0.0139	0.1252
chr15	102531392	1603307	0.0156	0.1318
chr16	90354753	1431221	0.0158	0.1378
chr17	81195210	1811961	0.0223	0.1595
chr18	78077248	855657	0.011	0.2086
chr19	59128983	1021792	0.0173	0.2259
chr20	63025520	1356654	0.0215	0.1544
chr21	48129895	565098	0.0117	0.1208
chr22	51304566	371668	0.0072	0.0882
chrMT	16571	22870	1.3801	1.4754
chrX	155270560	2454058	0.0158	0.1383
chrY	59373566	145431	0.0024	0.1044

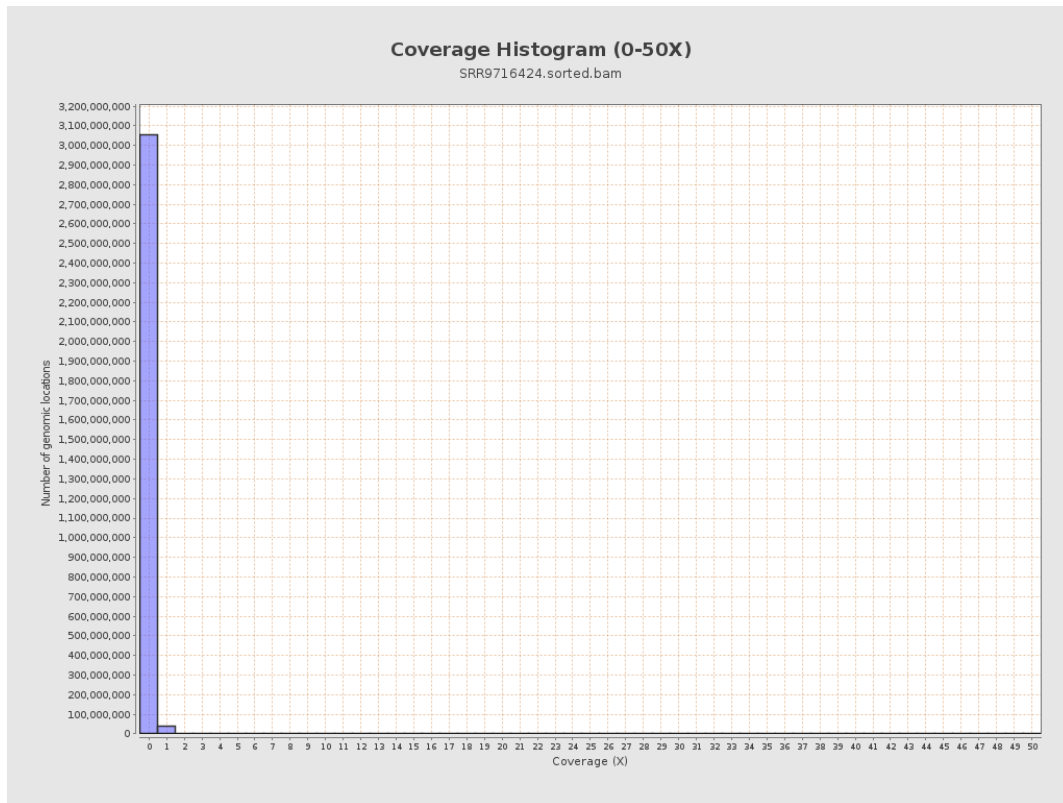
3. Results : Coverage across reference



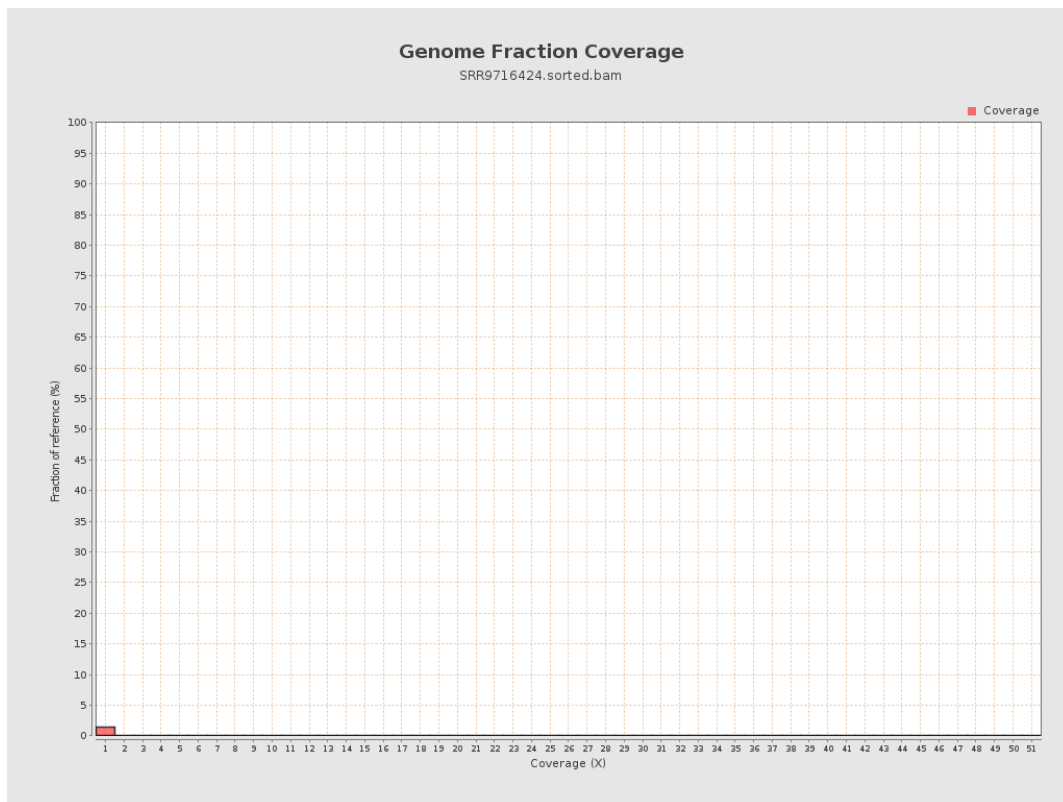
4. Results : Coverage Histogram



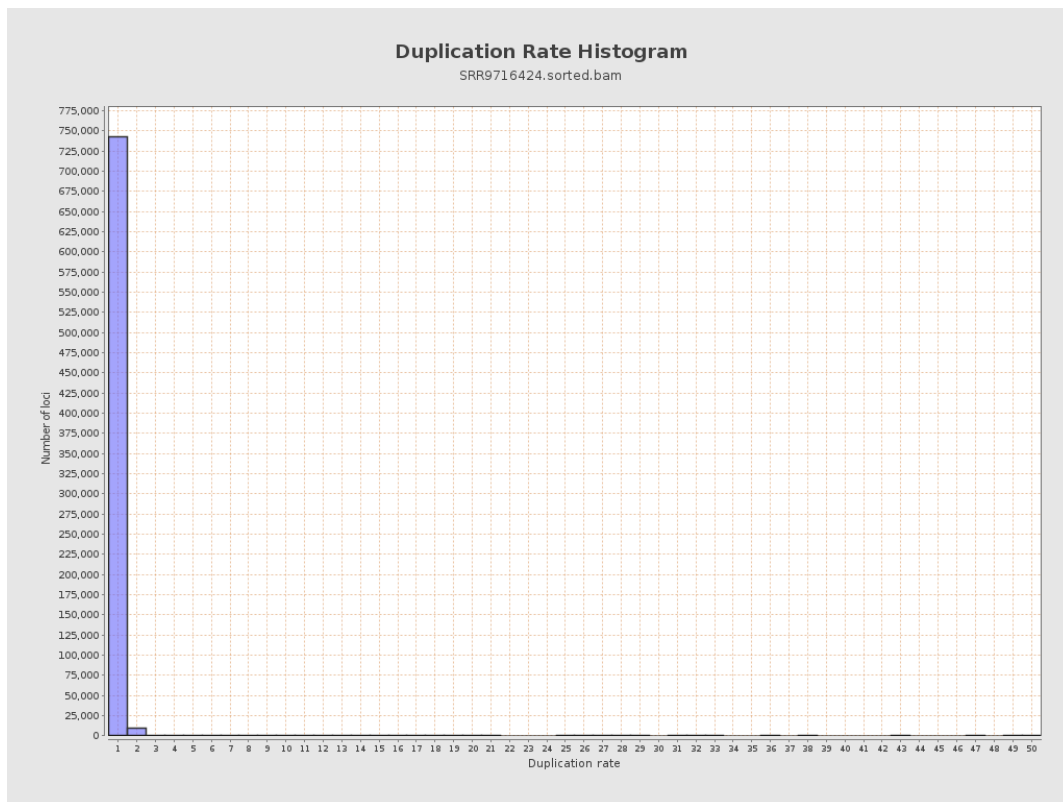
5. Results : Coverage Histogram (0-50X)



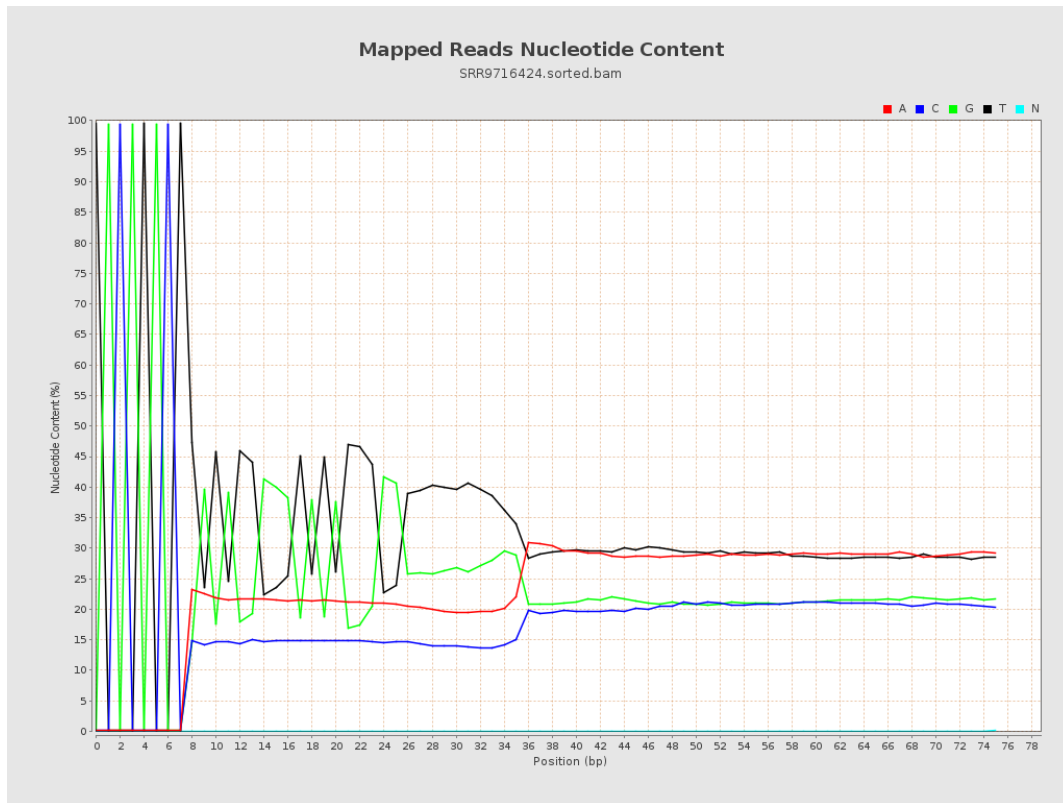
6. Results : Genome Fraction Coverage



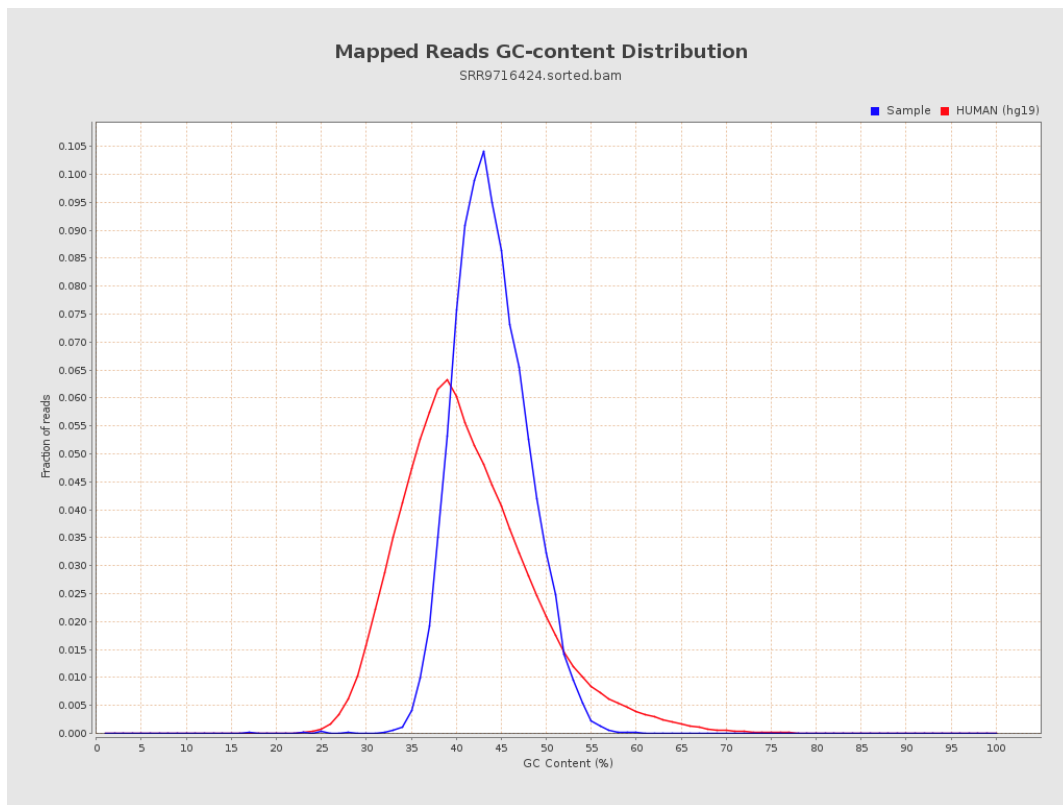
7. Results : Duplication Rate Histogram



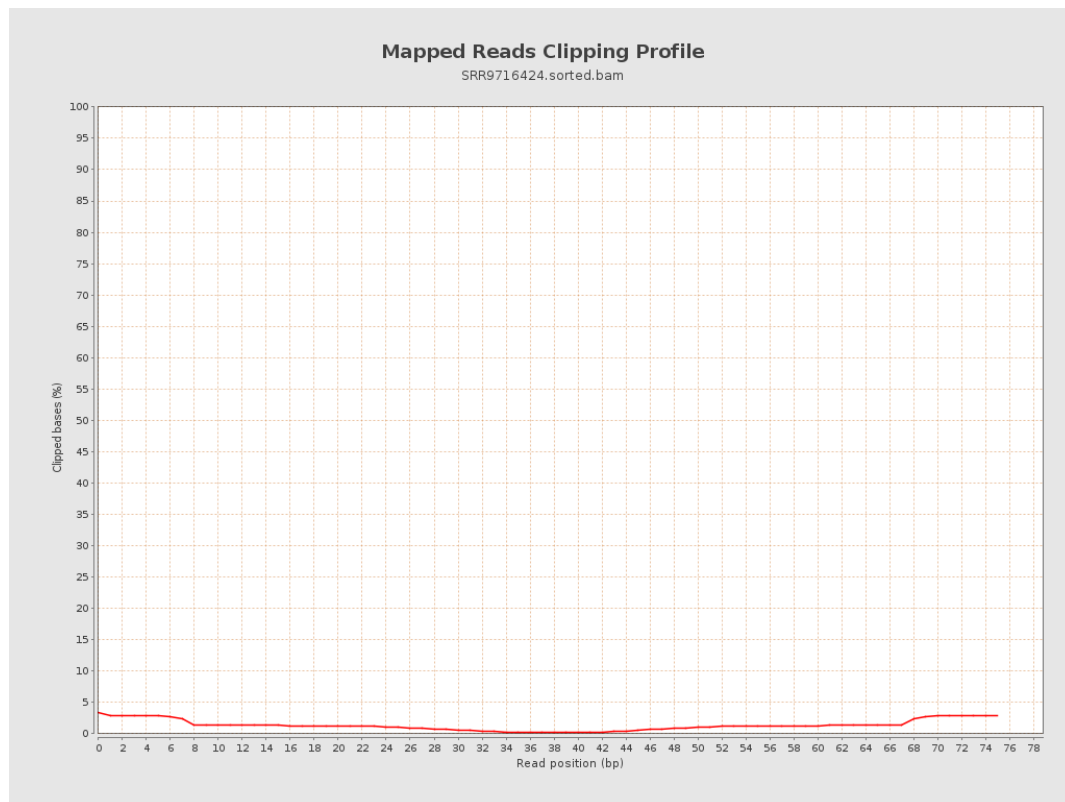
8. Results : Mapped Reads Nucleotide Content



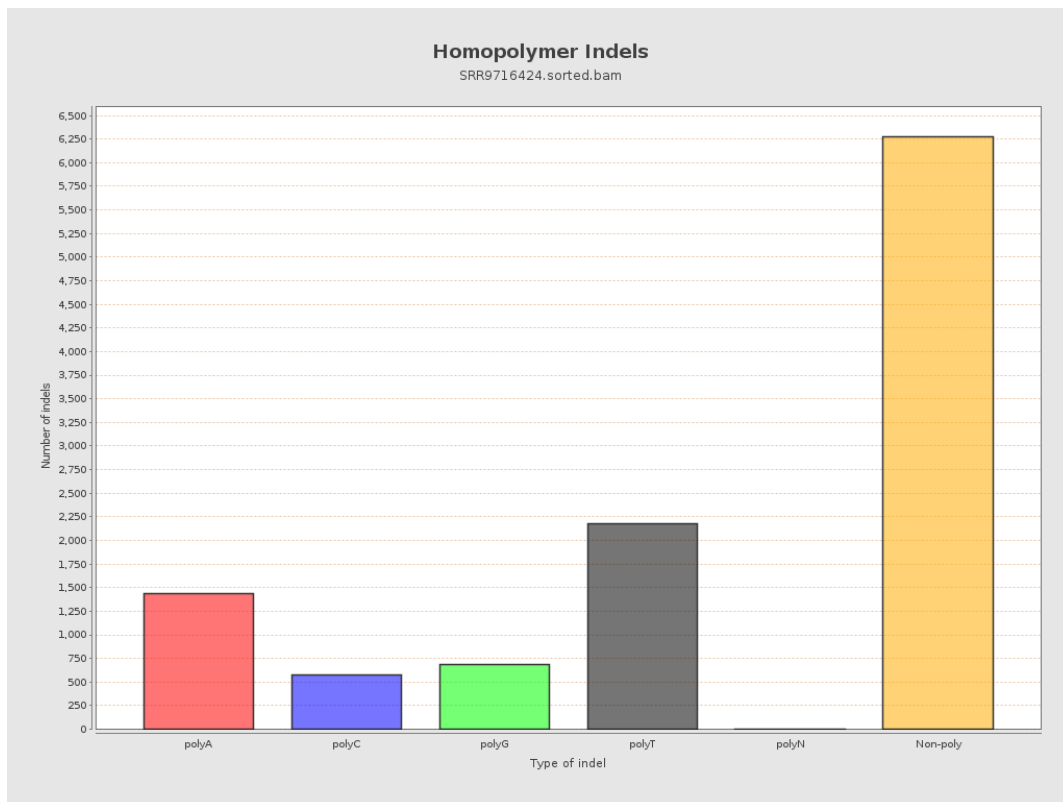
9. Results : Mapped Reads GC-content Distribution



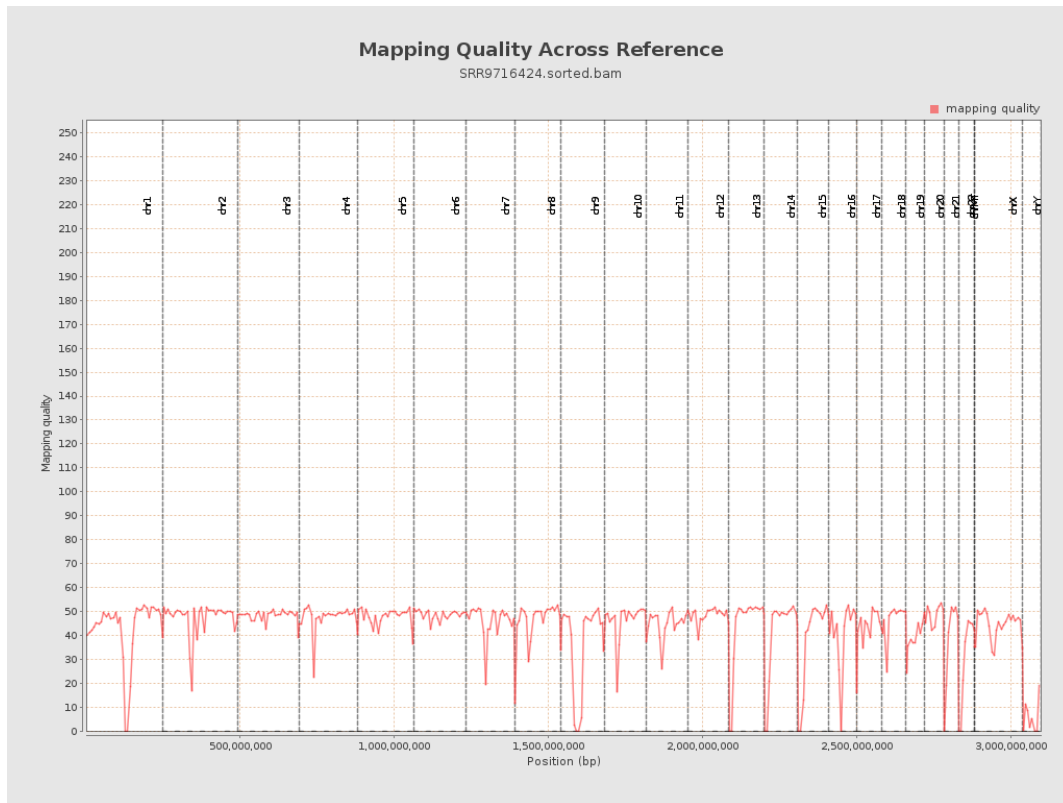
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

