Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 06:17:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240204.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_SRR6240204 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240204.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 06:17:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240204.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,829,546
Mapped reads	1,487,610 / 81.31%
Unmapped reads	341,936 / 18.69%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,835 / 0.37%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	164,626 / 9%
Duplication rate	9.2%
Clipped reads	959,247 / 52.43%

2.2. ACGT Content

Number/percentage of A's	25,190,737 / 27.39%
Number/percentage of C's	15,988,311 / 17.38%
Number/percentage of T's	30,140,024 / 32.77%
Number/percentage of G's	20,642,007 / 22.44%
Number/percentage of N's	23,079 / 0.03%
GC Percentage	39.82%

2.3. Coverage

Mean	0.0297

Standard Deviation	0.3096

2.4. Mapping Quality

Mean Mapping Quality	45.98

2.5. Mismatches and indels

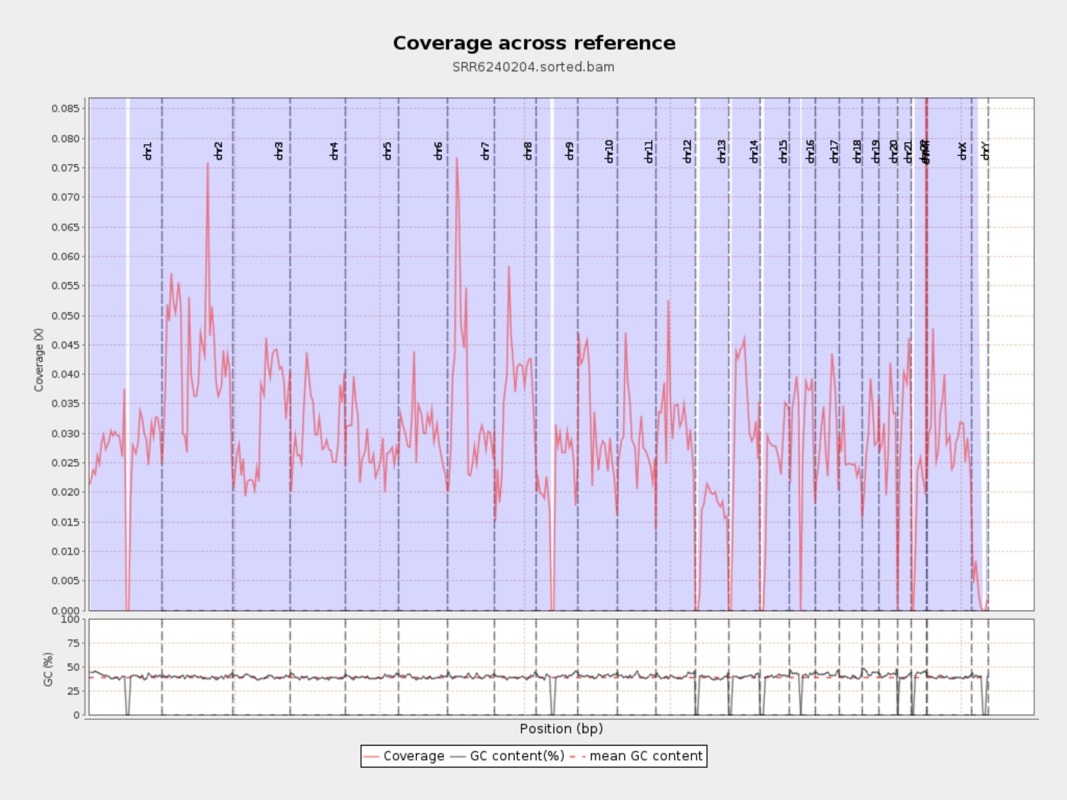
General error rate	0.97%
Mismatches	882,246
Insertions	6,381
Mapped reads with at least one insertion	0.43%
Deletions	32,223
Mapped reads with at least one deletion	2.14%
Homopolymer indels	50.67%

2.6. Chromosome stats

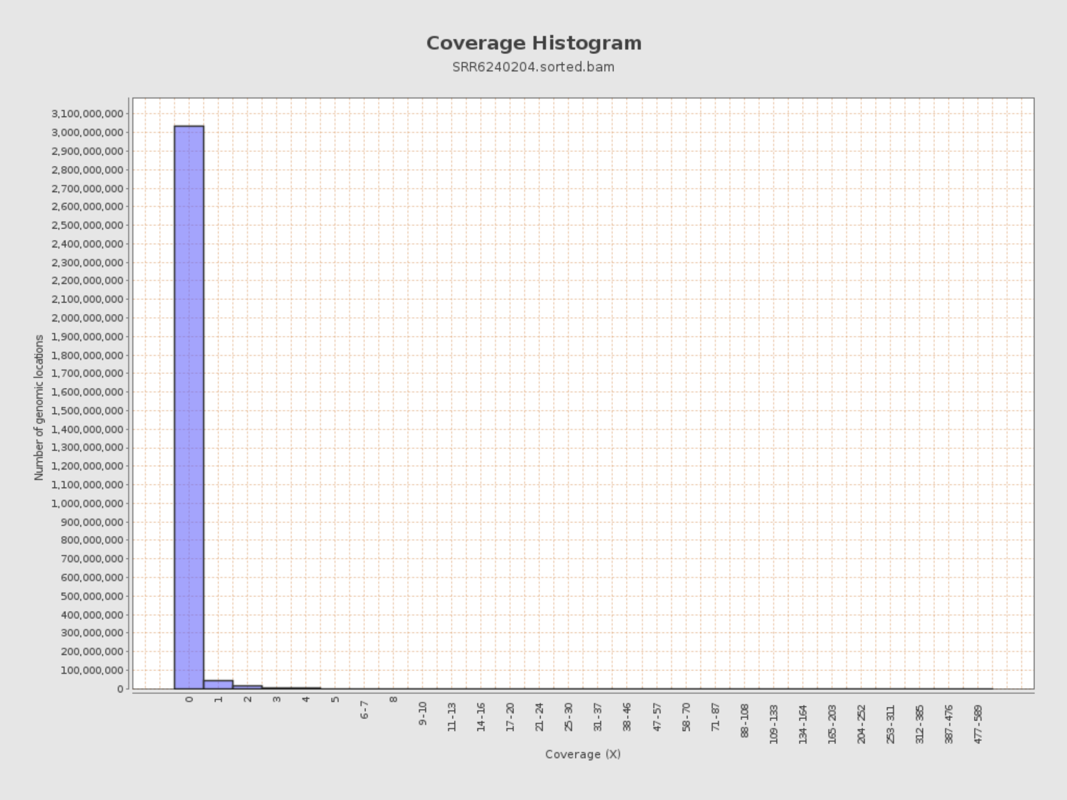
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6670085	0.0268	0.4274
chr2	243199373	10592187	0.0436	0.3618
chr3	198022430	6330800	0.032	0.2473
chr4	191154276	5859138	0.0307	0.2436
chr5	180915260	5024183	0.0278	0.2326
chr6	171115067	5172907	0.0302	0.2772
chr7	159138663	5747964	0.0361	0.5214

chr8	146364022	5346481	0.0365	0.4343
chr9	141213431	3096715	0.0219	0.2579
chr10	135534747	4334333	0.032	0.2776
chr11	135006516	3898131	0.0289	0.2767
chr12	133851895	4335870	0.0324	0.2488
chr13	115169878	1769371	0.0154	0.1672
chr14	107349540	3309335	0.0308	0.2484
chr15	102531392	2406706	0.0235	0.2153
chr16	90354753	2792744	0.0309	0.2424
chr17	81195210	2450666	0.0302	0.252
chr18	78077248	2010701	0.0258	0.4166
chr19	59128983	1729118	0.0292	0.327
chr20	63025520	1873181	0.0297	0.2397
chr21	48129895	1569609	0.0326	0.2567
chr22	51304566	833417	0.0162	0.1699
chrMT	16571	37390	2.2564	2.7639
chrX	155270560	4660114	0.03	0.2496
chrY	59373566	188588	0.0032	0.0774

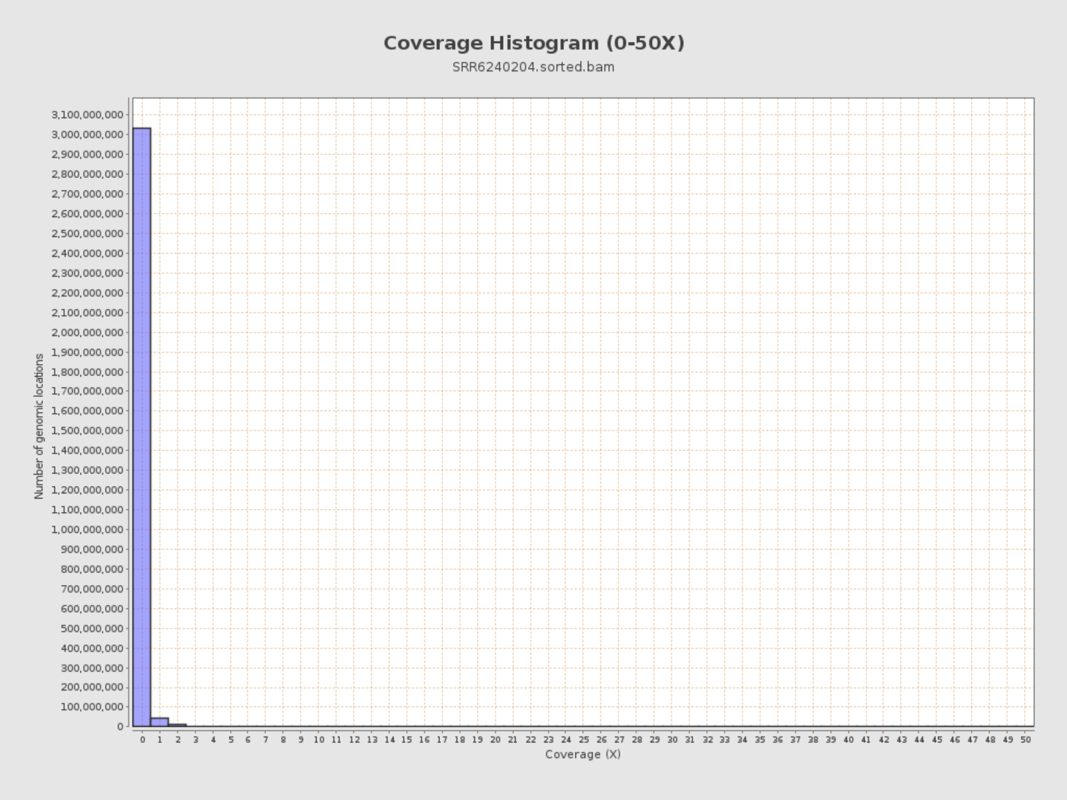
3. Results : Coverage across reference



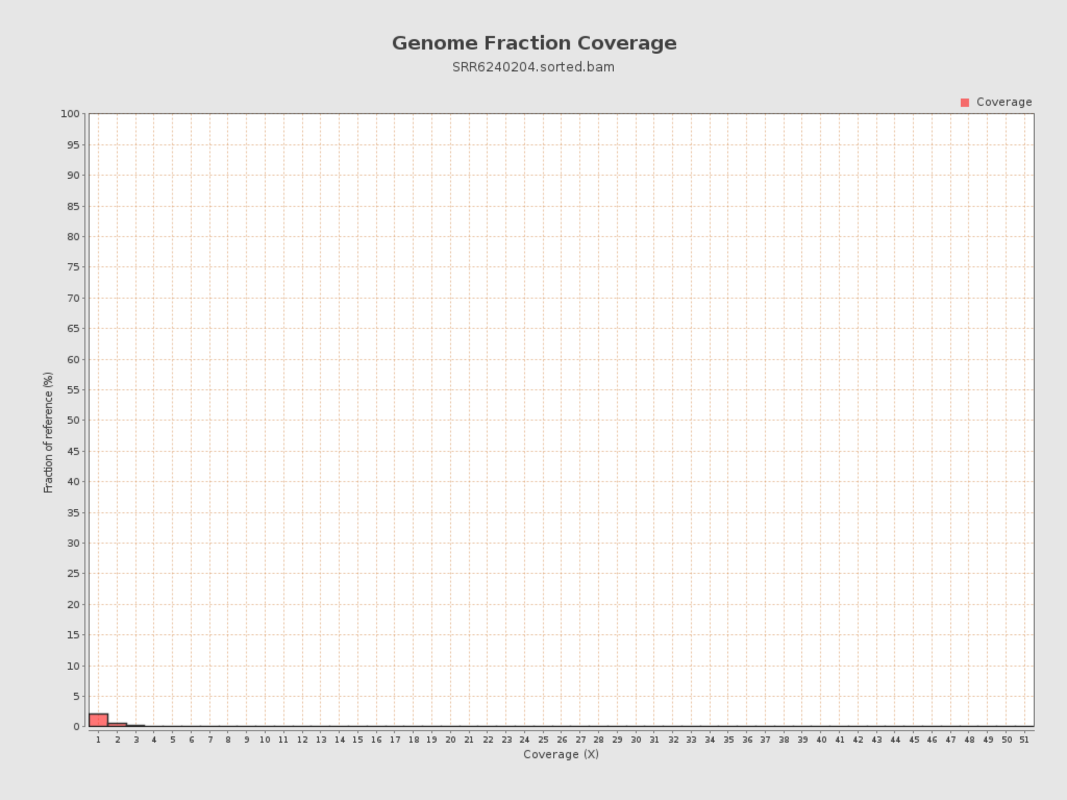
4. Results : Coverage Histogram



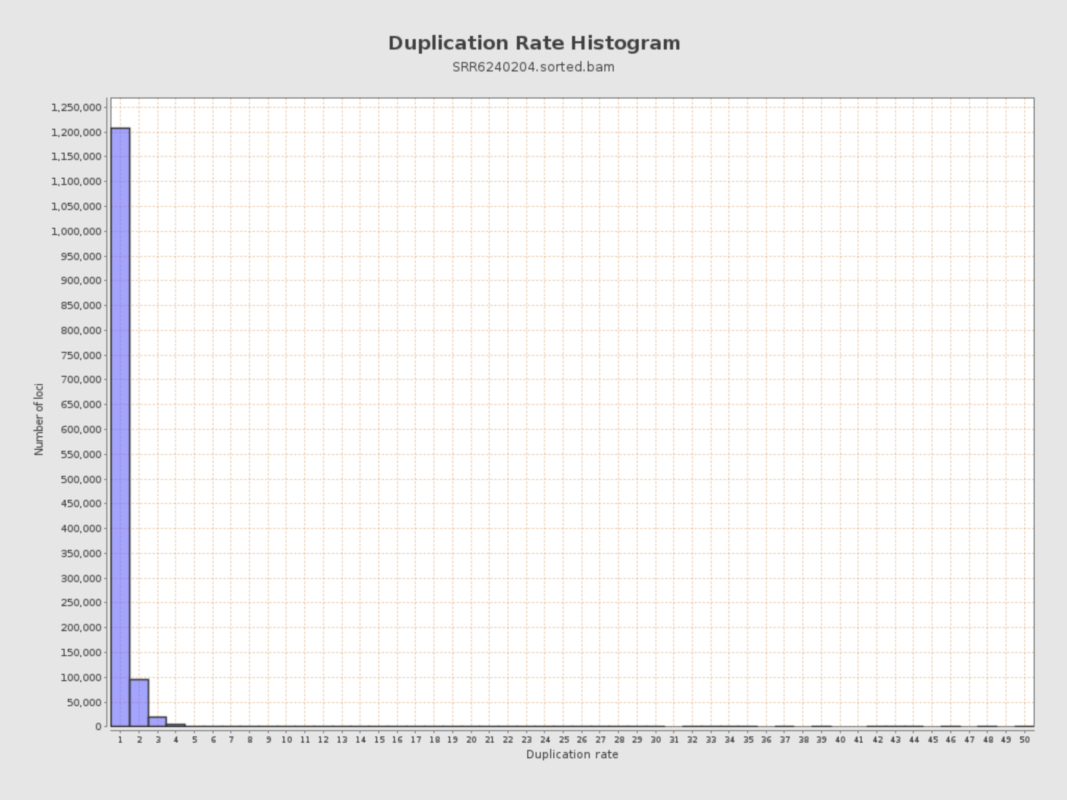
5. Results : Coverage Histogram (0-50X)



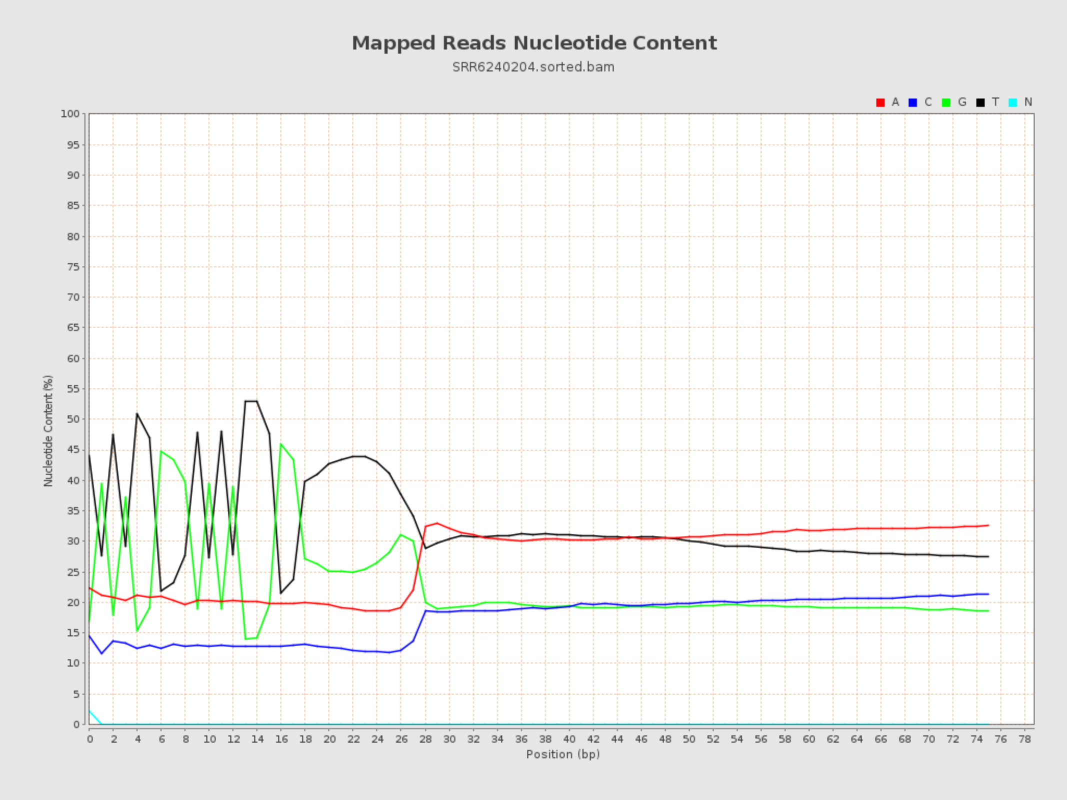
6. Results : Genome Fraction Coverage



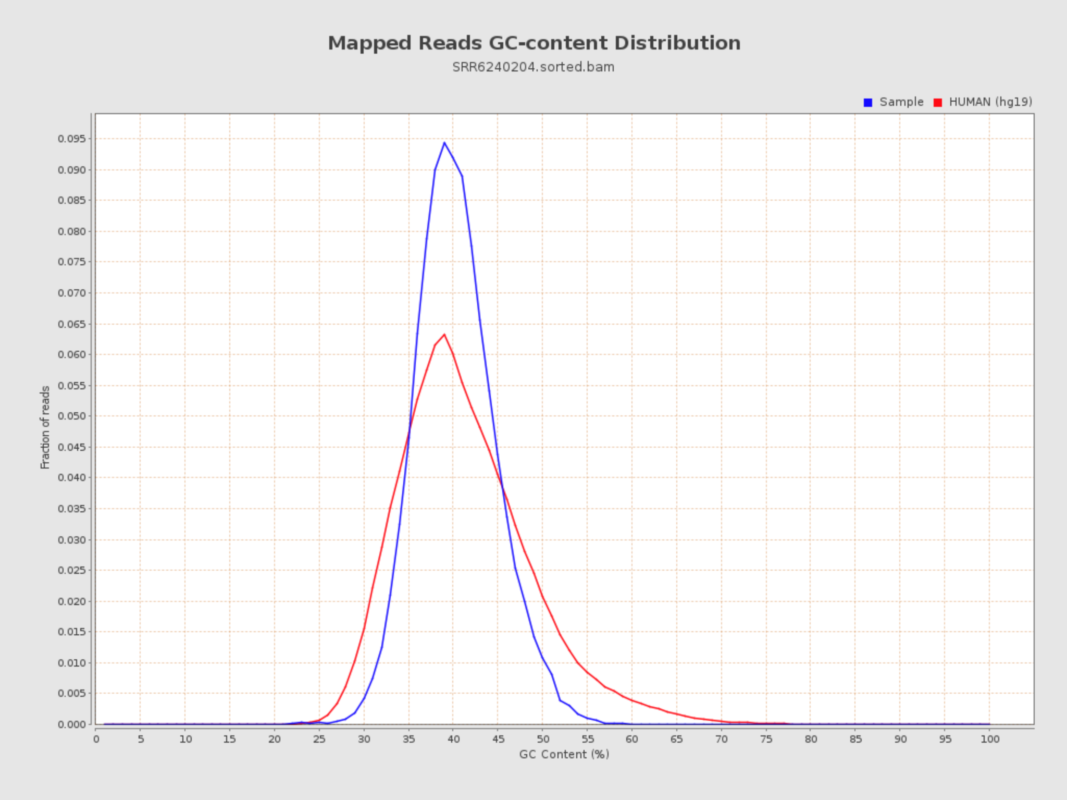
7. Results : Duplication Rate Histogram



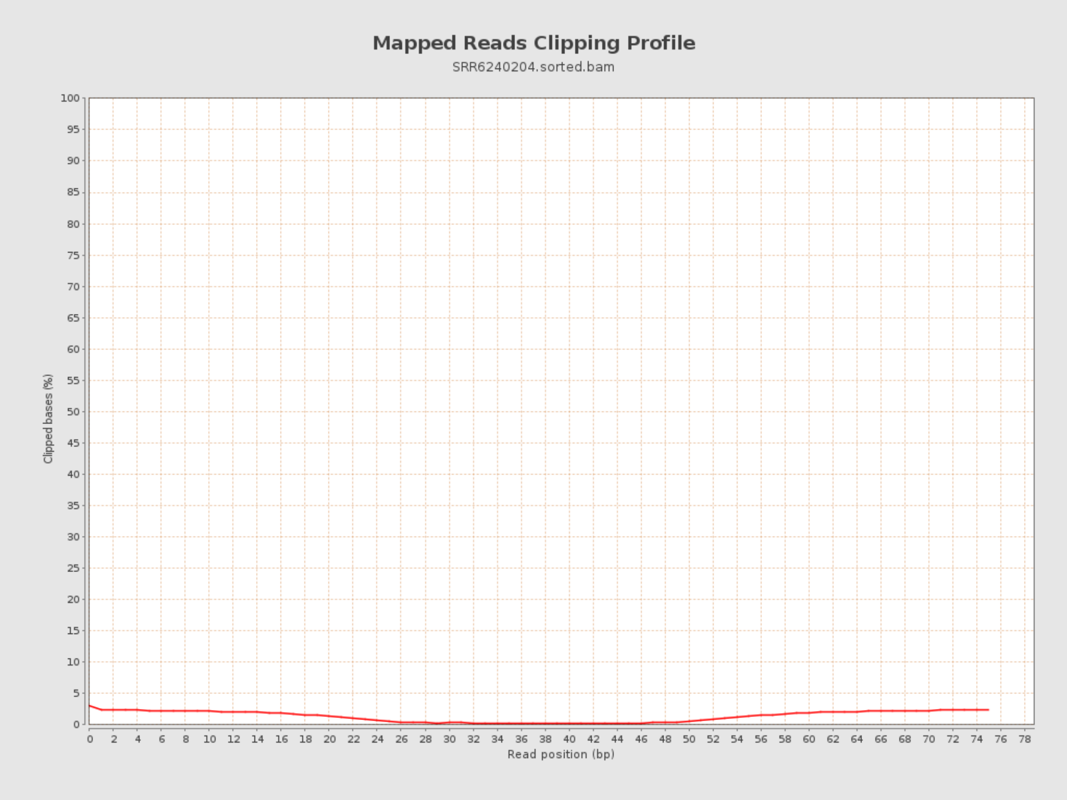
8. Results : Mapped Reads Nucleotide Content



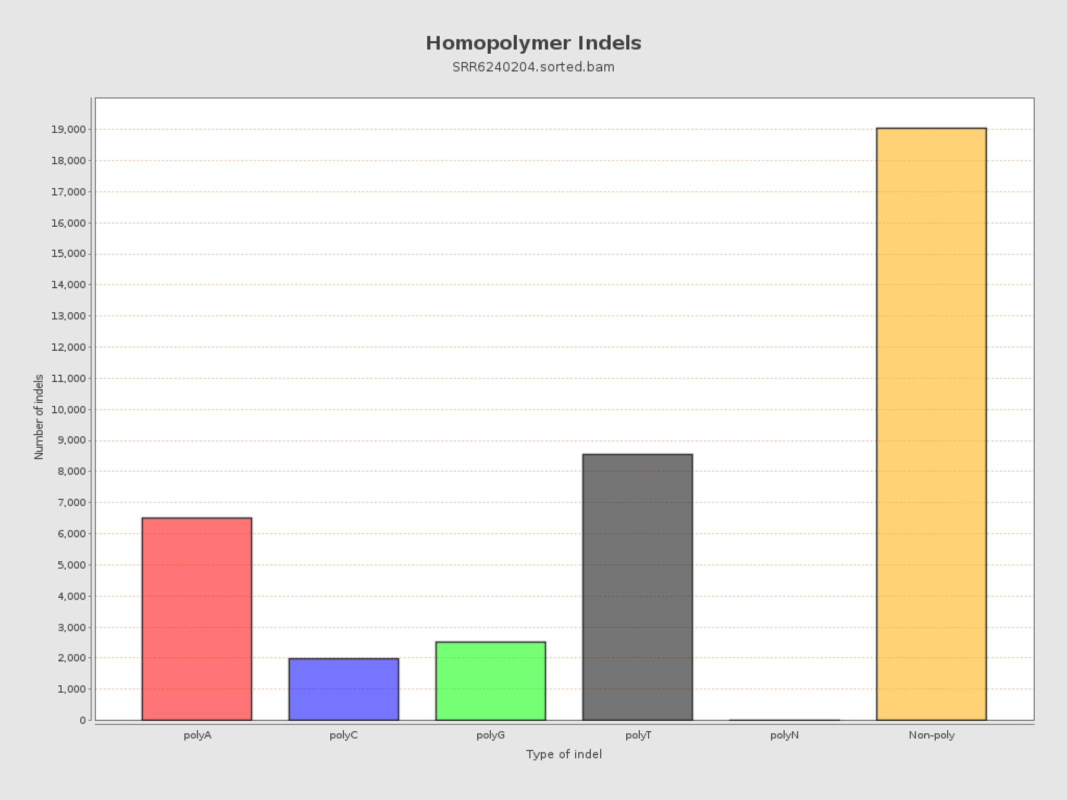
9. Results : Mapped Reads GC-content Distribution



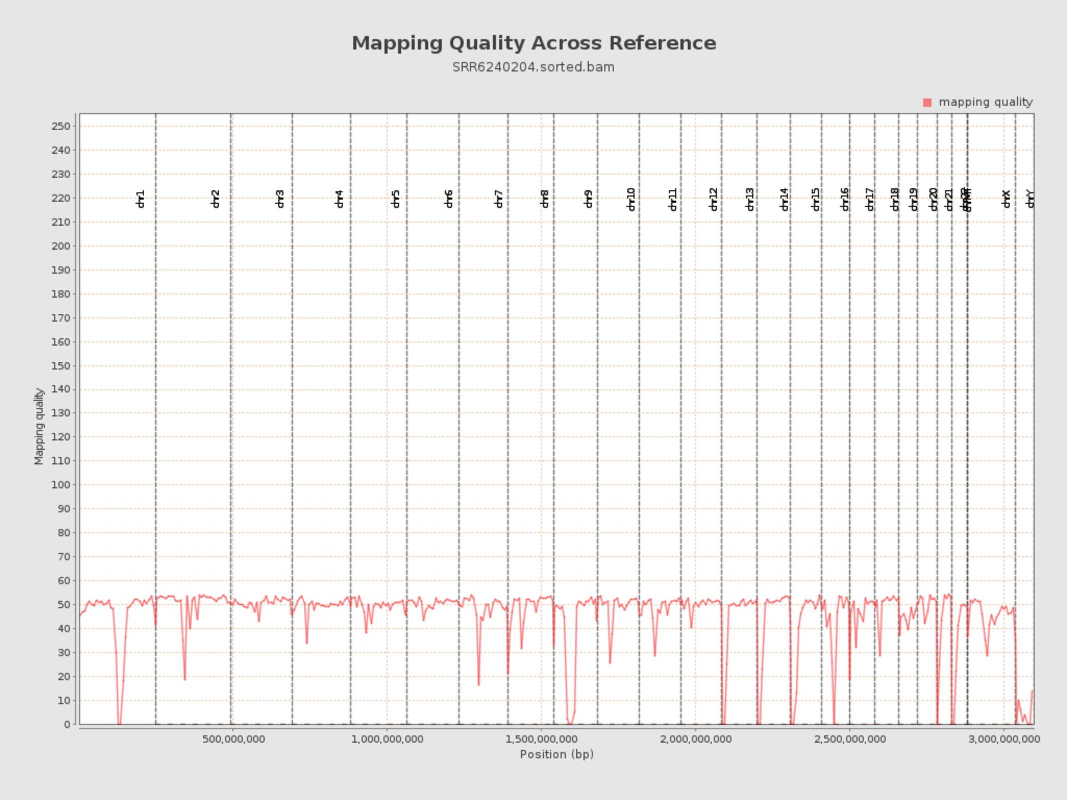
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram