Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 04:04:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240050.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_SRR6240050 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240050.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 04:04:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240050.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,477,187
Mapped reads	1,216,145 / 82.33%
Unmapped reads	261,042 / 17.67%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,529 / 0.37%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	61,728 / 4.18%
Duplication rate	4.26%
Clipped reads	733,760 / 49.67%

2.2. ACGT Content

Number/percentage of A's	20,851,564 / 27.3%
Number/percentage of C's	13,470,596 / 17.64%
Number/percentage of T's	24,702,347 / 32.35%
Number/percentage of G's	17,294,066 / 22.65%
Number/percentage of N's	51,436 / 0.07%
GC Percentage	40.28%

2.3. Coverage

Mean	0.0247

Standard Deviation	0.2466

2.4. Mapping Quality

Mean Mapping Quality	45.9

2.5. Mismatches and indels

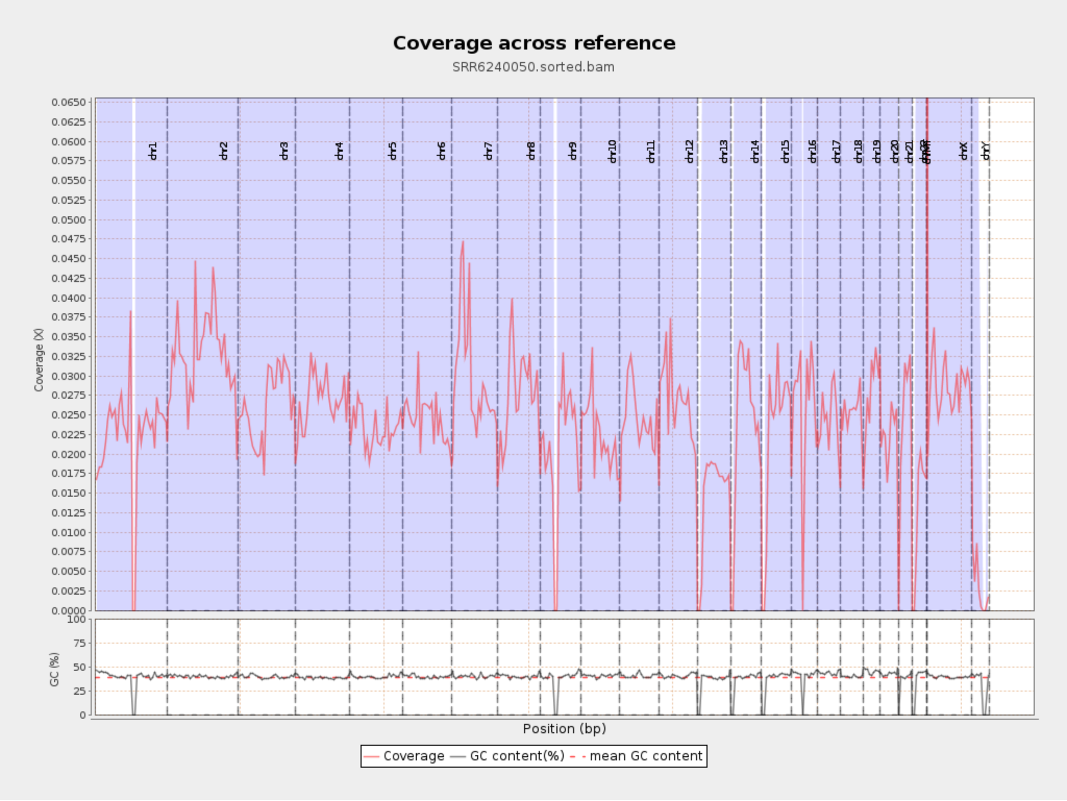
General error rate	0.93%
Mismatches	704,401
Insertions	5,379
Mapped reads with at least one insertion	0.44%
Deletions	22,302
Mapped reads with at least one deletion	1.81%
Homopolymer indels	49.18%

2.6. Chromosome stats

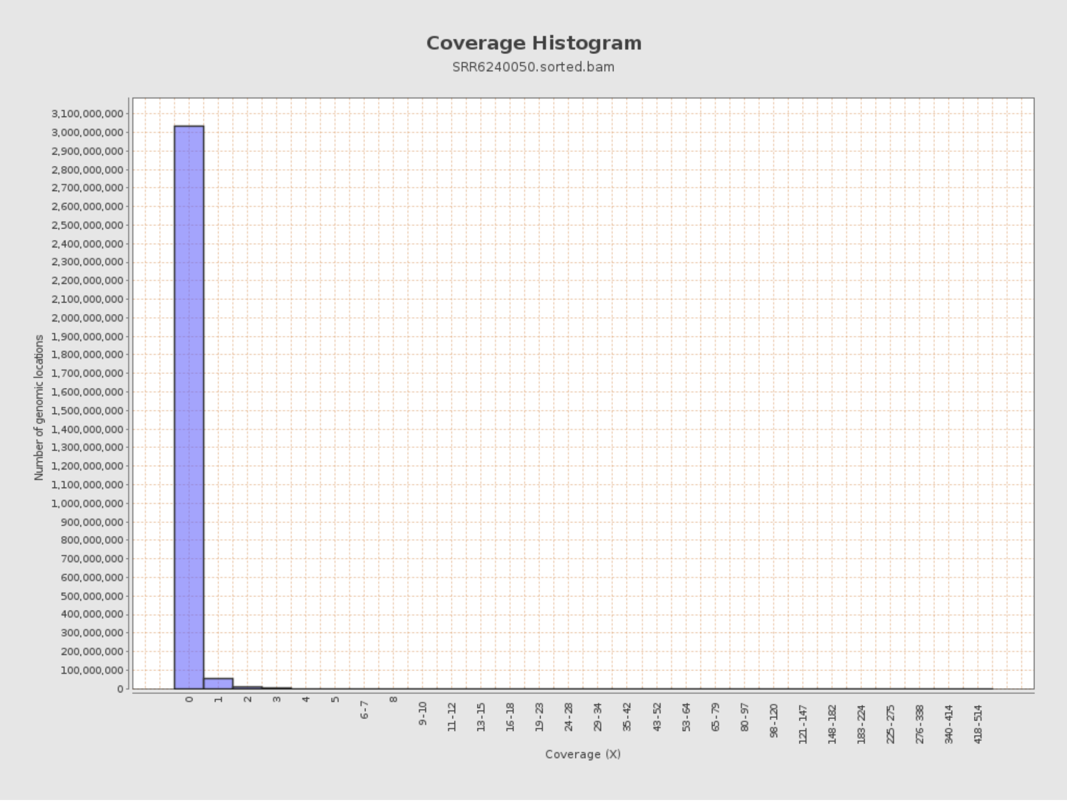
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5543610	0.0222	0.3784
chr2	243199373	7994726	0.0329	0.2815
chr3	198022430	5193229	0.0262	0.1873
chr4	191154276	5148948	0.0269	0.195
chr5	180915260	4215044	0.0233	0.1772
chr6	171115067	4193013	0.0245	0.2132
chr7	159138663	4763328	0.0299	0.3754

chr8	146364022	4086270	0.0279	0.3619
chr9	141213431	2915523	0.0206	0.2141
chr10	135534747	3054244	0.0225	0.2093
chr11	135006516	3318984	0.0246	0.2284
chr12	133851895	3627042	0.0271	0.1912
chr13	115169878	1700655	0.0148	0.1411
chr14	107349540	2561223	0.0239	0.1833
chr15	102531392	2292356	0.0224	0.179
chr16	90354753	2298462	0.0254	0.1894
chr17	81195210	1975819	0.0243	0.1902
chr18	78077248	1994814	0.0255	0.3211
chr19	59128983	1646447	0.0278	0.2797
chr20	63025520	1394387	0.0221	0.1754
chr21	48129895	1177896	0.0245	0.184
chr22	51304566	659728	0.0129	0.1289
chrMT	16571	21778	1.3142	1.7934
chrX	155270560	4455943	0.0287	0.2091
chrY	59373566	174992	0.0029	0.0689

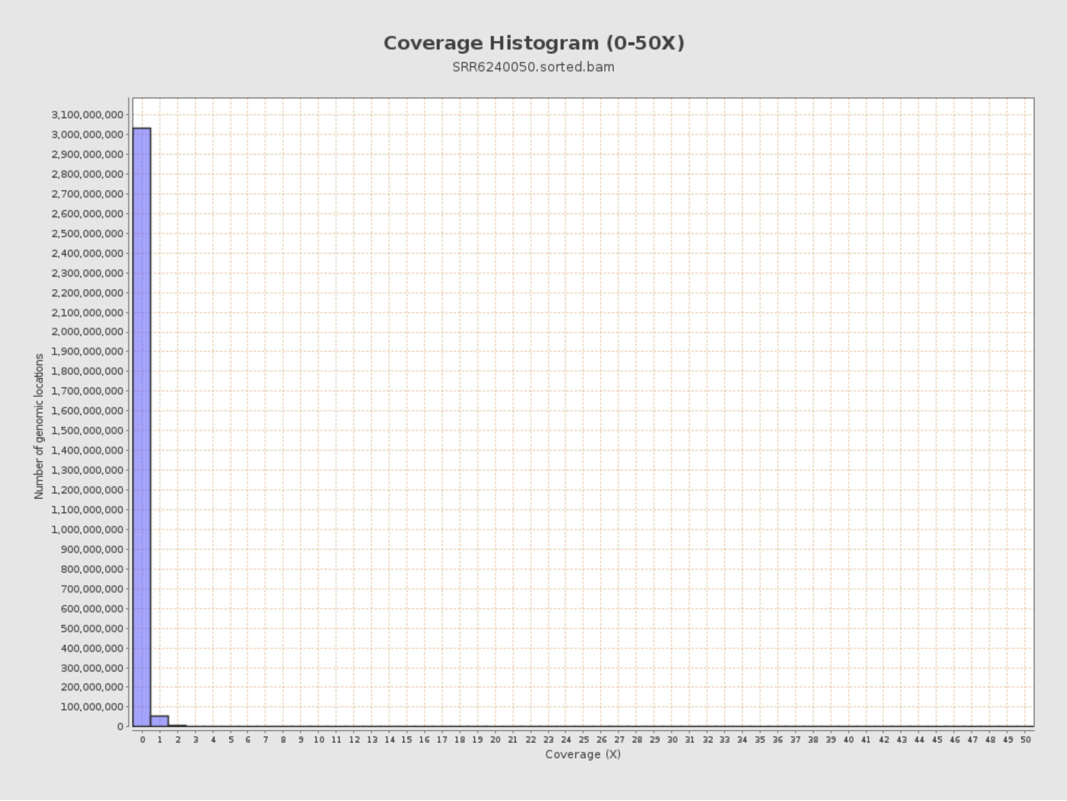
3. Results : Coverage across reference



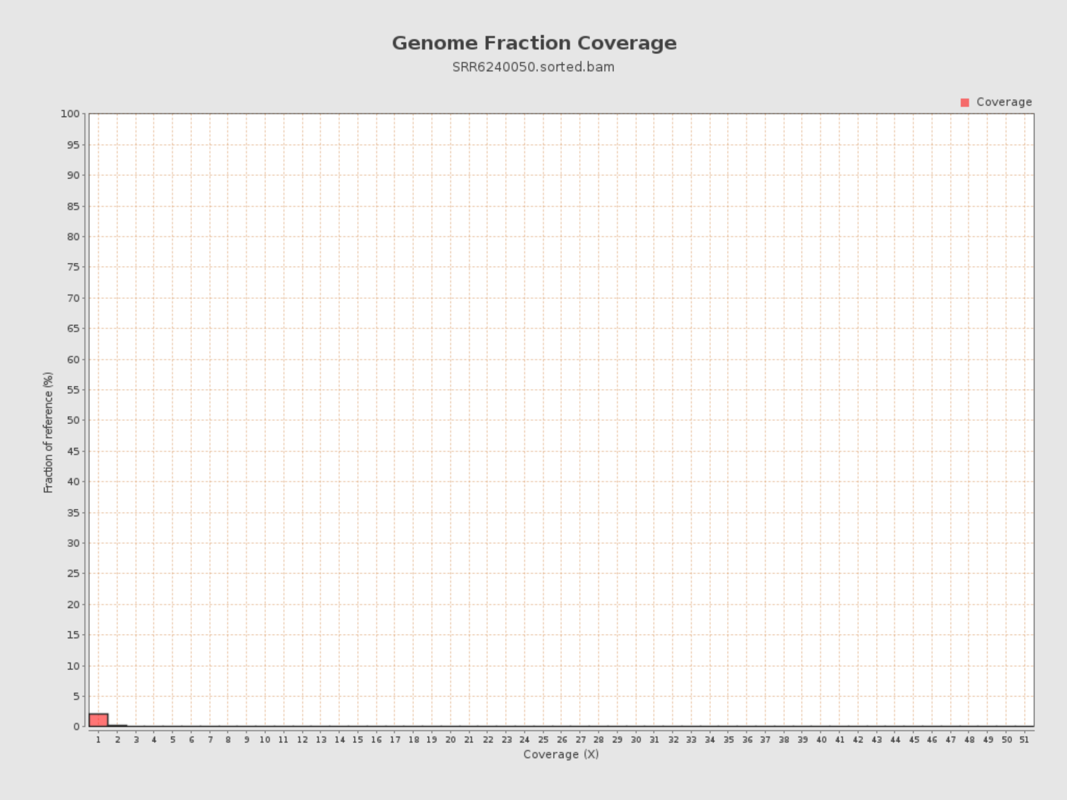
4. Results : Coverage Histogram



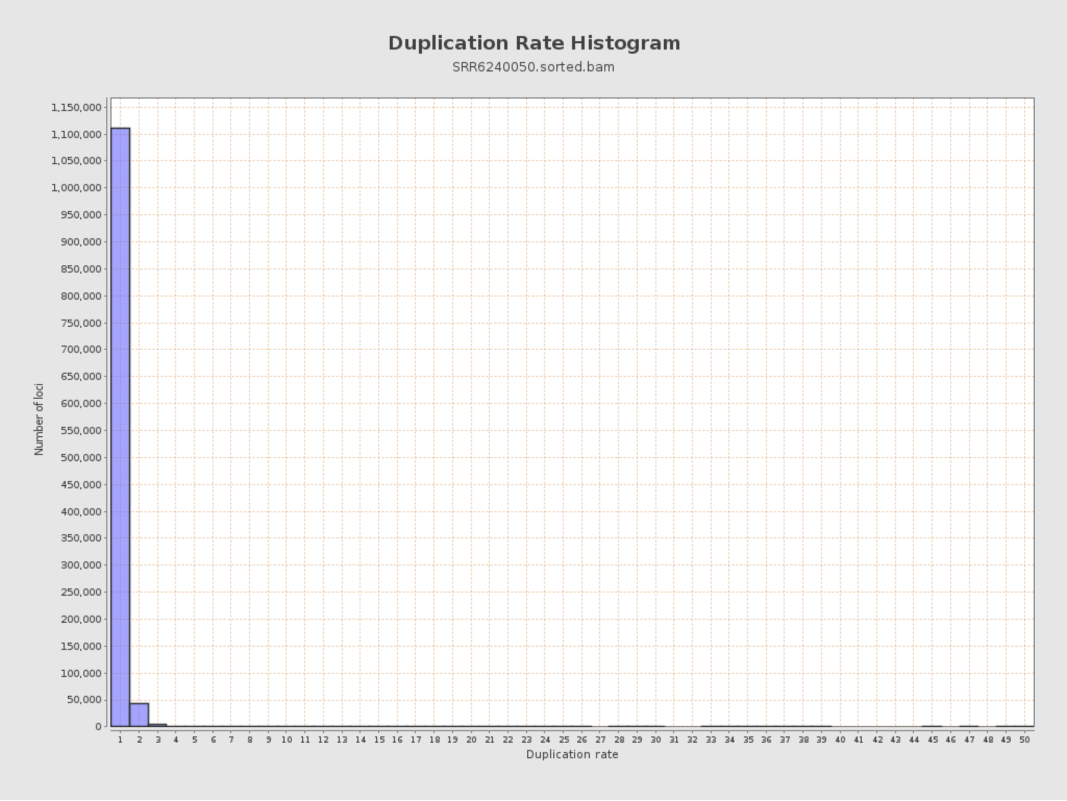
5. Results : Coverage Histogram (0-50X)



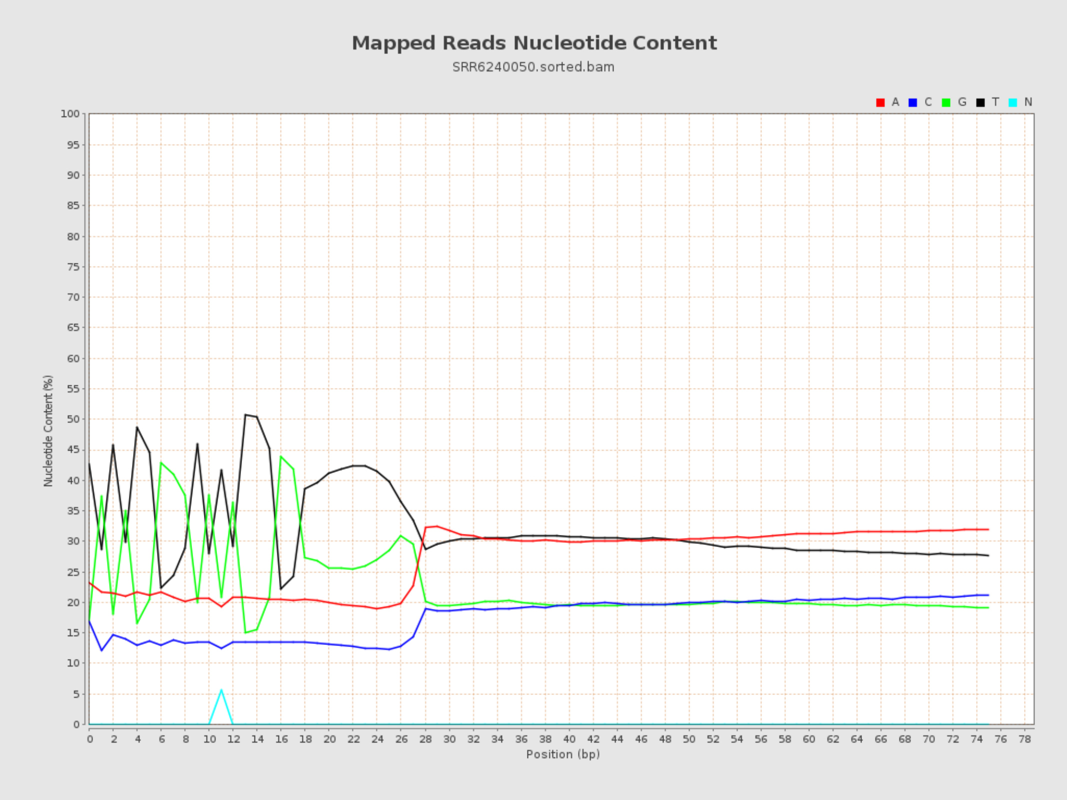
6. Results : Genome Fraction Coverage



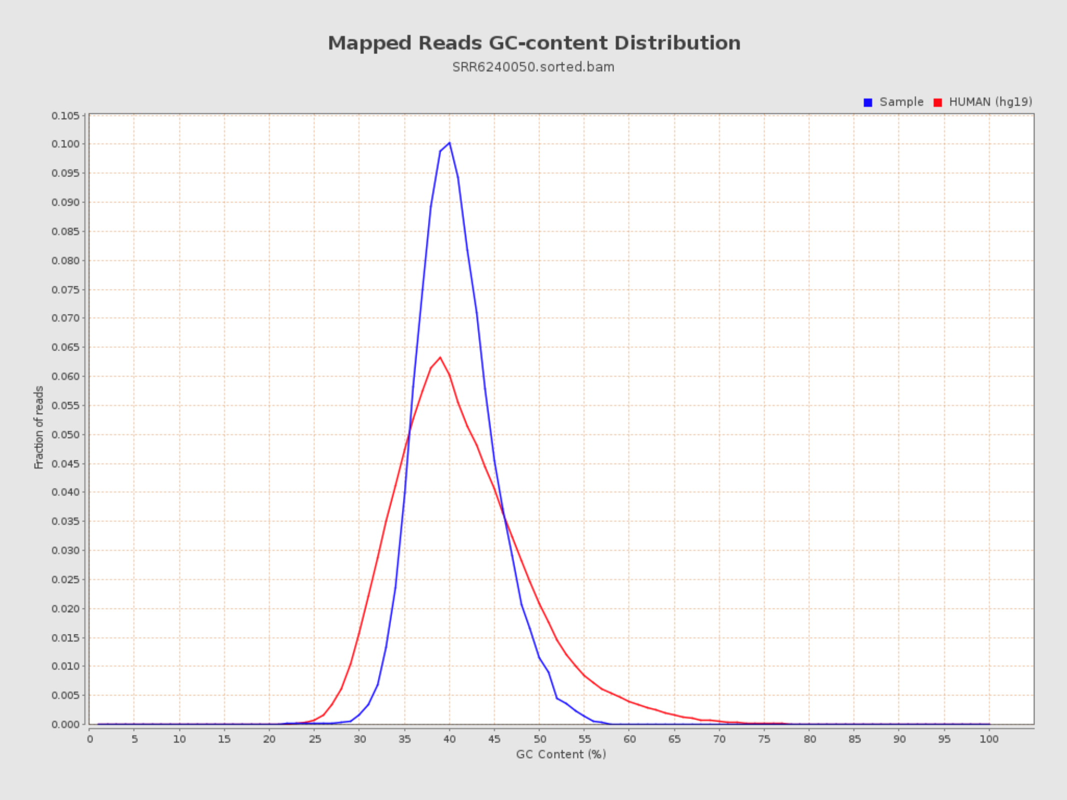
7. Results : Duplication Rate Histogram



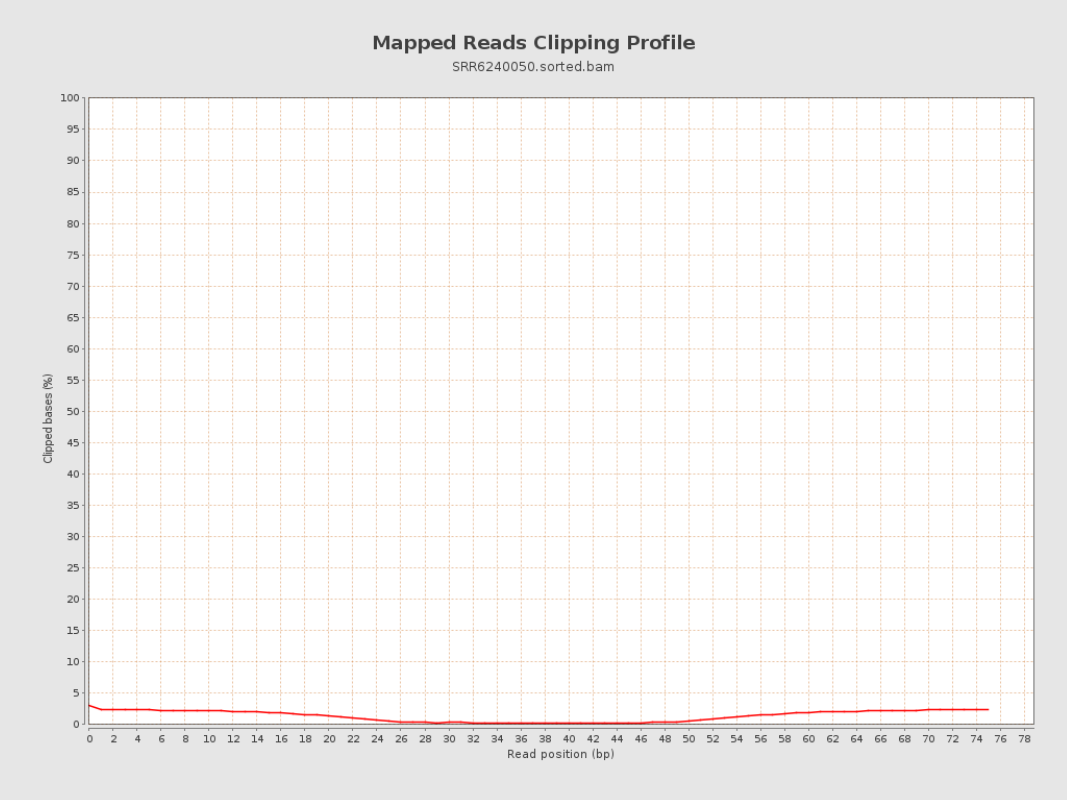
8. Results : Mapped Reads Nucleotide Content



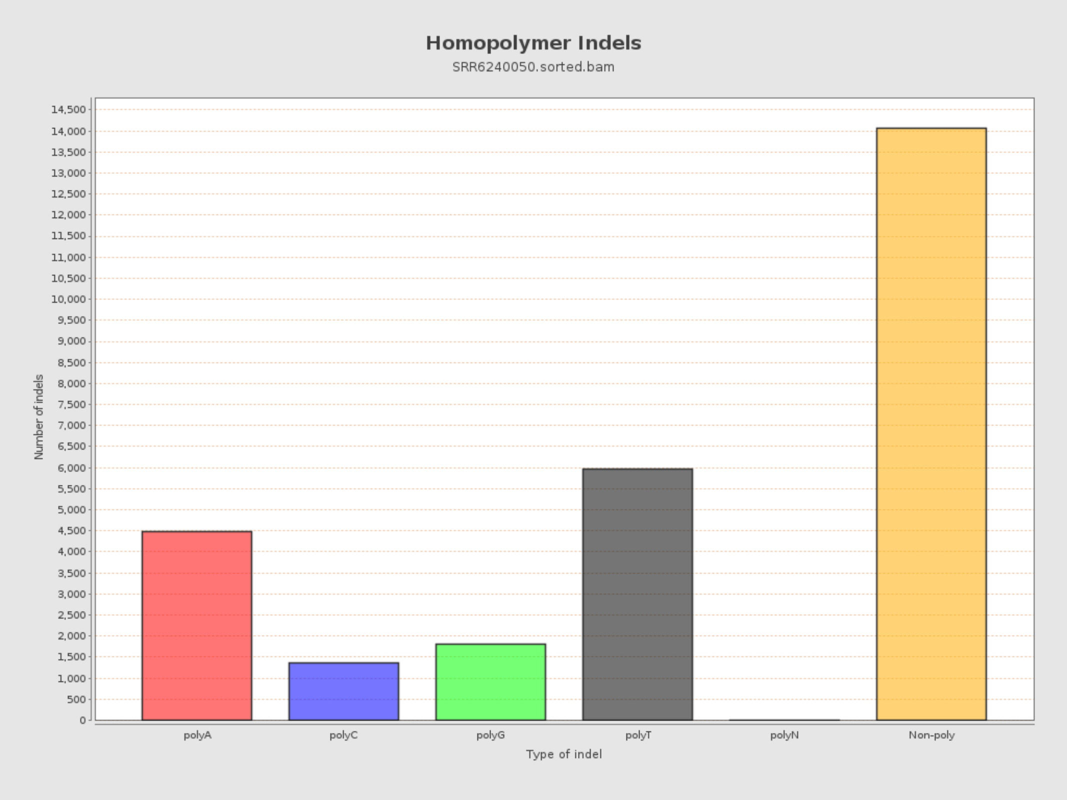
9. Results : Mapped Reads GC-content Distribution



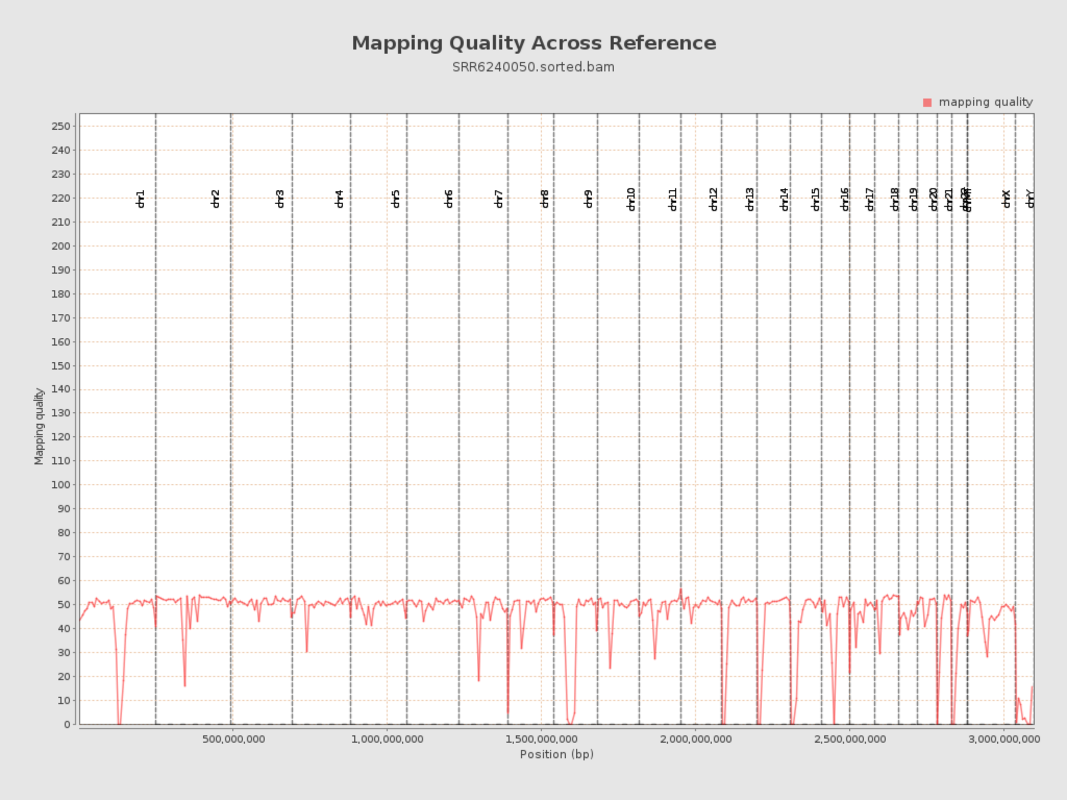
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram