Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 07:40:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240232.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_SRR6240232 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240232.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 07:40:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240232.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,547,426
Mapped reads	1,805,896 / 70.89%
Unmapped reads	741,530 / 29.11%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,774 / 0.54%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	285,374 / 11.2%
Duplication rate	12.01%
Clipped reads	965,912 / 37.92%

2.2. ACGT Content

Number/percentage of A's	32,303,756 / 27.74%
Number/percentage of C's	20,856,823 / 17.91%
Number/percentage of T's	37,863,642 / 32.52%
Number/percentage of G's	25,380,692 / 21.8%
Number/percentage of N's	43,195 / 0.04%
GC Percentage	39.71%

2.3. Coverage

Mean	0.0376

Standard Deviation	0.4245

2.4. Mapping Quality

Mean Mapping Quality	46.71

2.5. Mismatches and indels

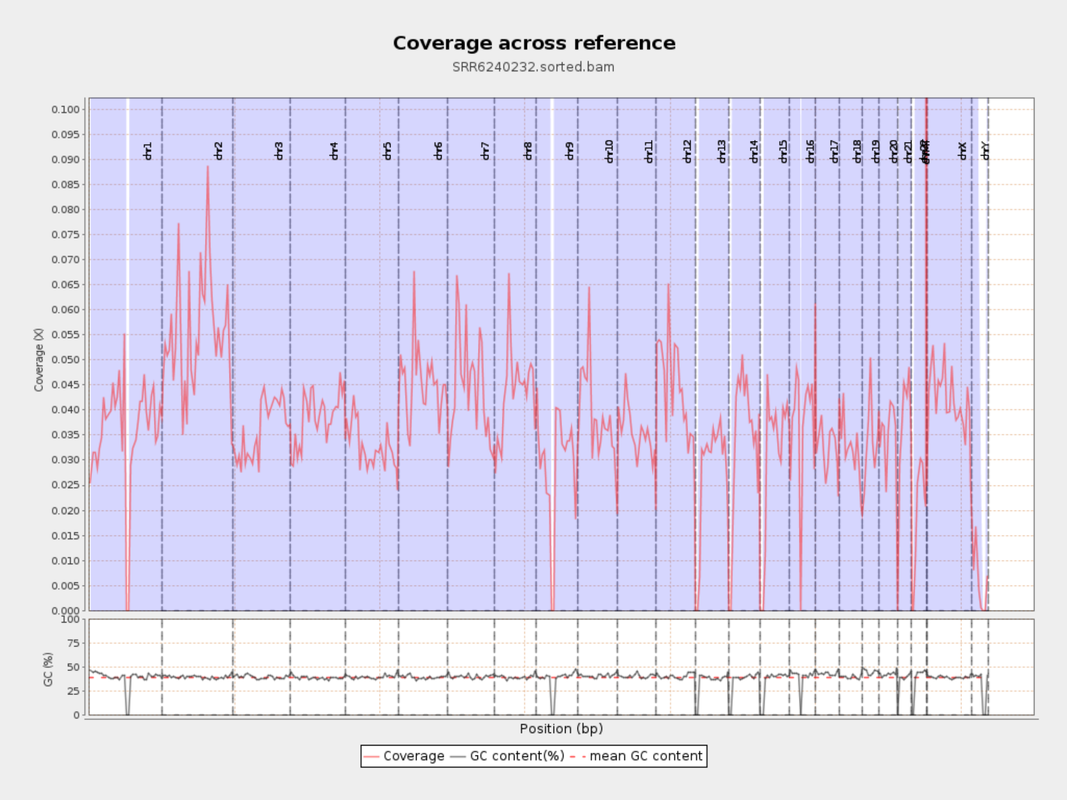
General error rate	0.9%
Mismatches	1,038,243
Insertions	8,304
Mapped reads with at least one insertion	0.46%
Deletions	32,696
Mapped reads with at least one deletion	1.79%
Homopolymer indels	48.01%

2.6. Chromosome stats

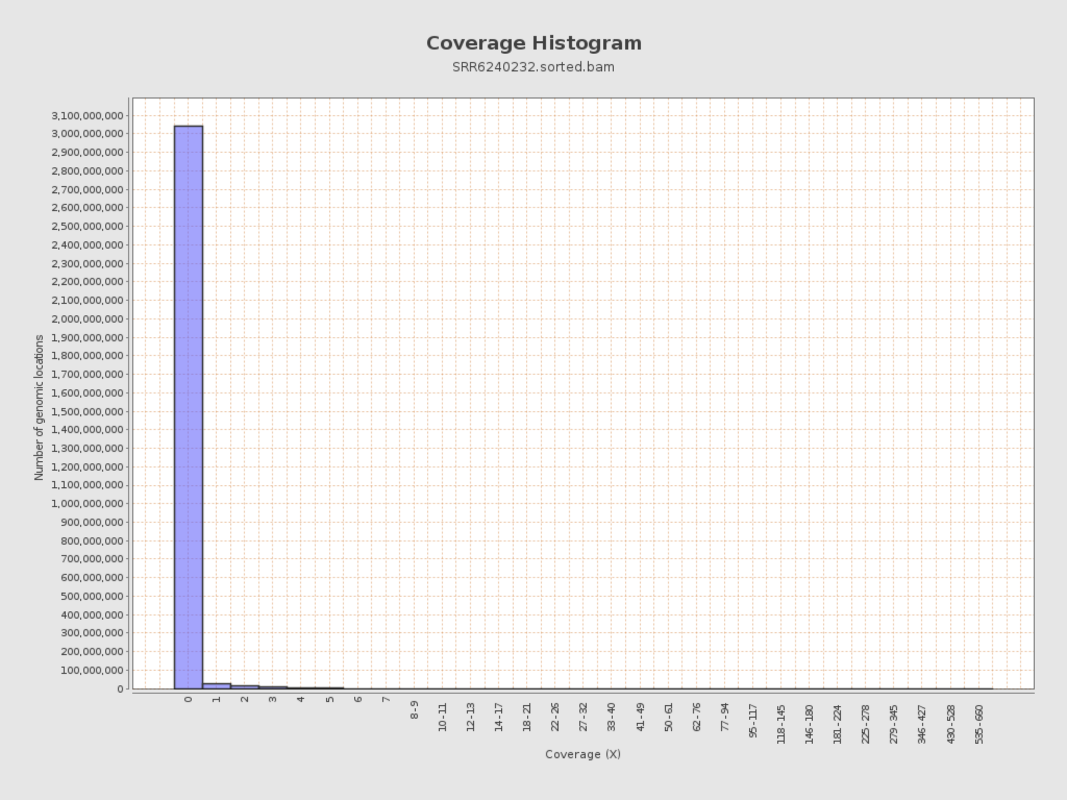
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8916164	0.0358	0.6165
chr2	243199373	13501648	0.0555	0.5066
chr3	198022430	7174509	0.0362	0.3475
chr4	191154276	7357227	0.0385	0.3817
chr5	180915260	5925422	0.0328	0.3249
chr6	171115067	7779490	0.0455	0.4208
chr7	159138663	7091602	0.0446	0.5157

chr8	146364022	6402531	0.0437	0.5471
chr9	141213431	4033111	0.0286	0.3666
chr10	135534747	5317355	0.0392	0.4233
chr11	135006516	4780570	0.0354	0.3866
chr12	133851895	6001721	0.0448	0.3819
chr13	115169878	3154228	0.0274	0.3067
chr14	107349540	3605897	0.0336	0.3415
chr15	102531392	3144772	0.0307	0.3628
chr16	90354753	3350219	0.0371	0.347
chr17	81195210	2608787	0.0321	0.327
chr18	78077248	2558548	0.0328	0.5318
chr19	59128983	1993816	0.0337	0.4284
chr20	63025520	2207827	0.035	0.3365
chr21	48129895	1738530	0.0361	0.3472
chr22	51304566	951119	0.0185	0.2375
chrMT	16571	34887	2.1053	2.3832
chrX	155270560	6523671	0.042	0.3888
chrY	59373566	351199	0.0059	0.1457

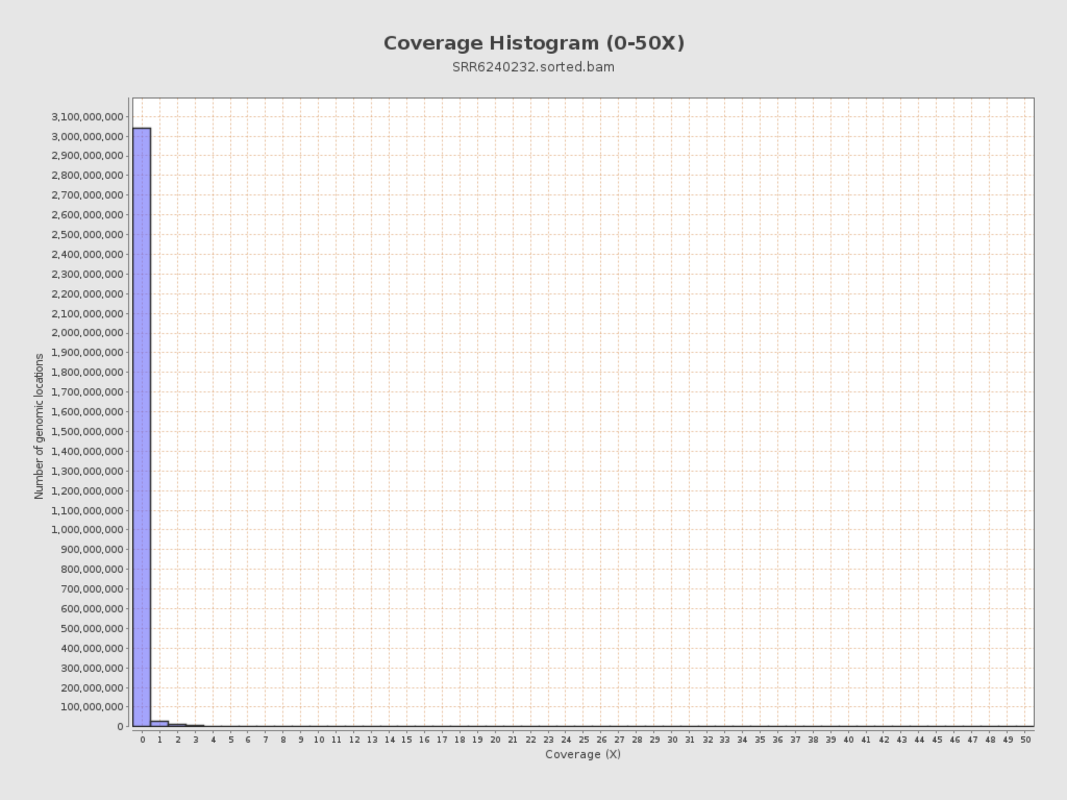
3. Results : Coverage across reference



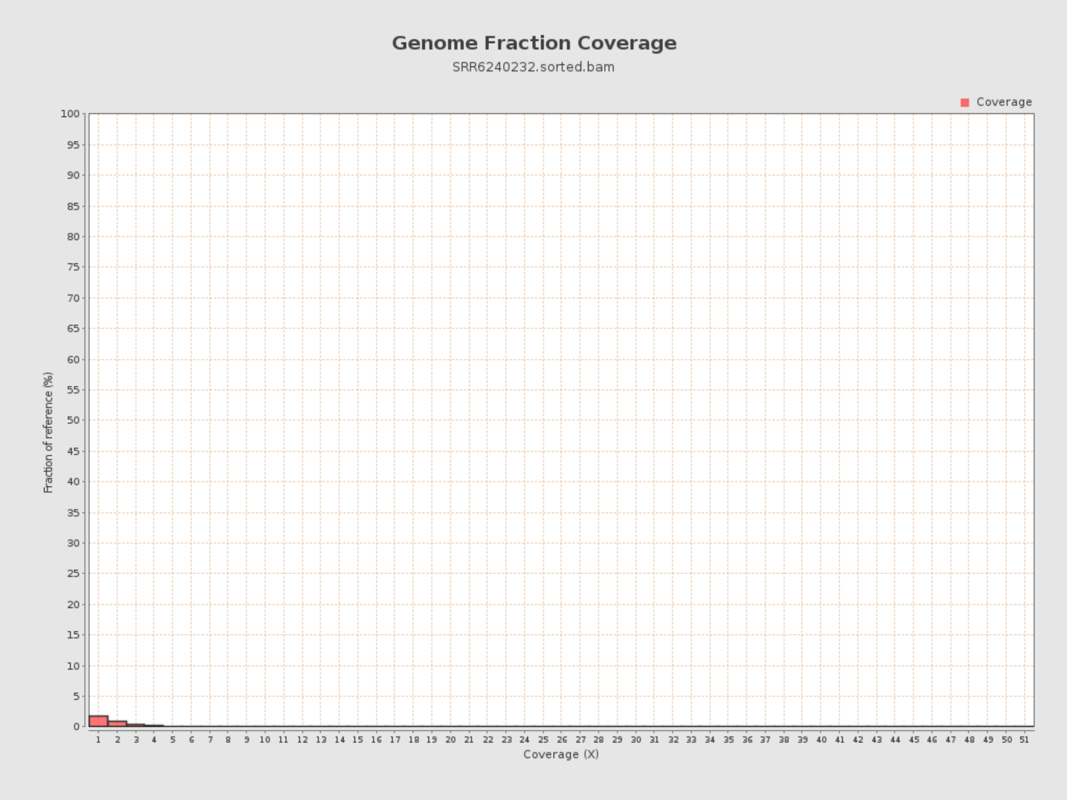
4. Results : Coverage Histogram



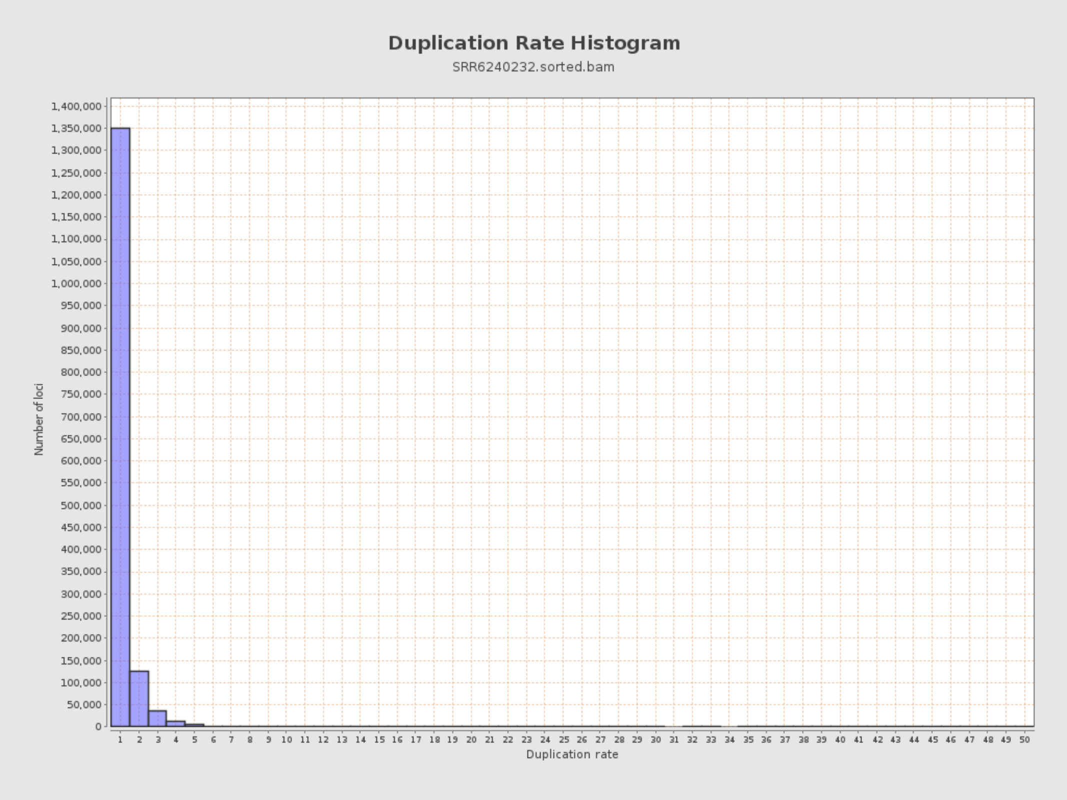
5. Results : Coverage Histogram (0-50X)



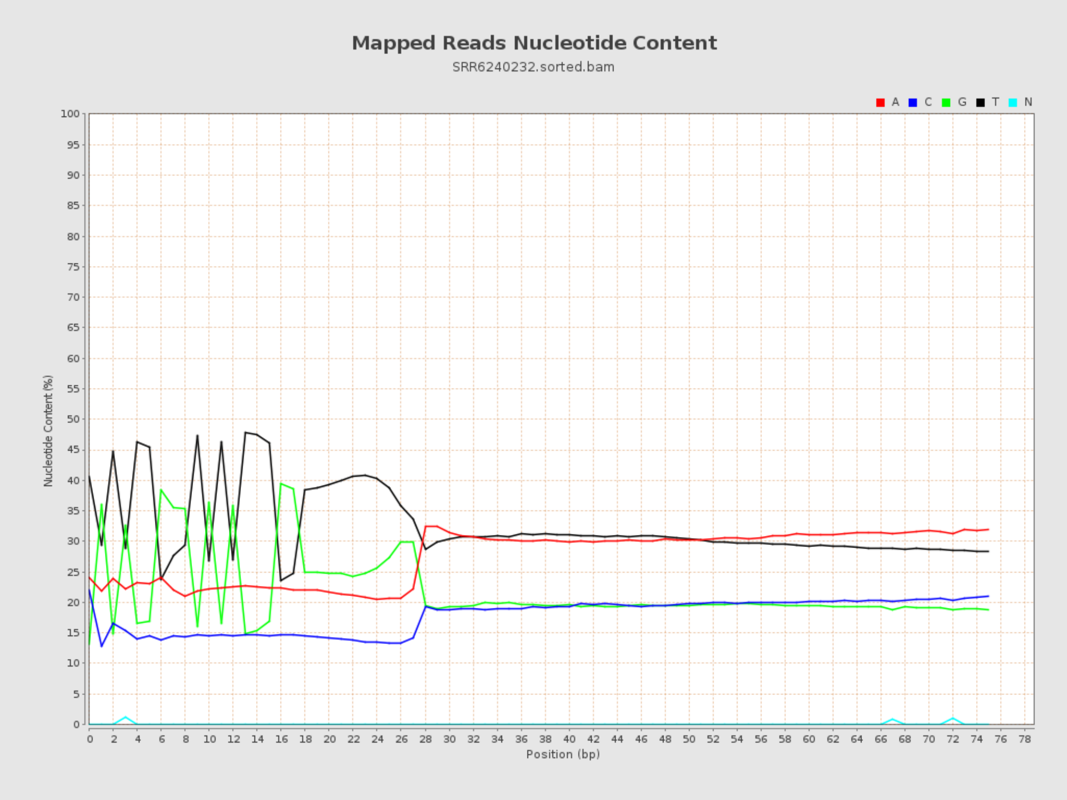
6. Results : Genome Fraction Coverage



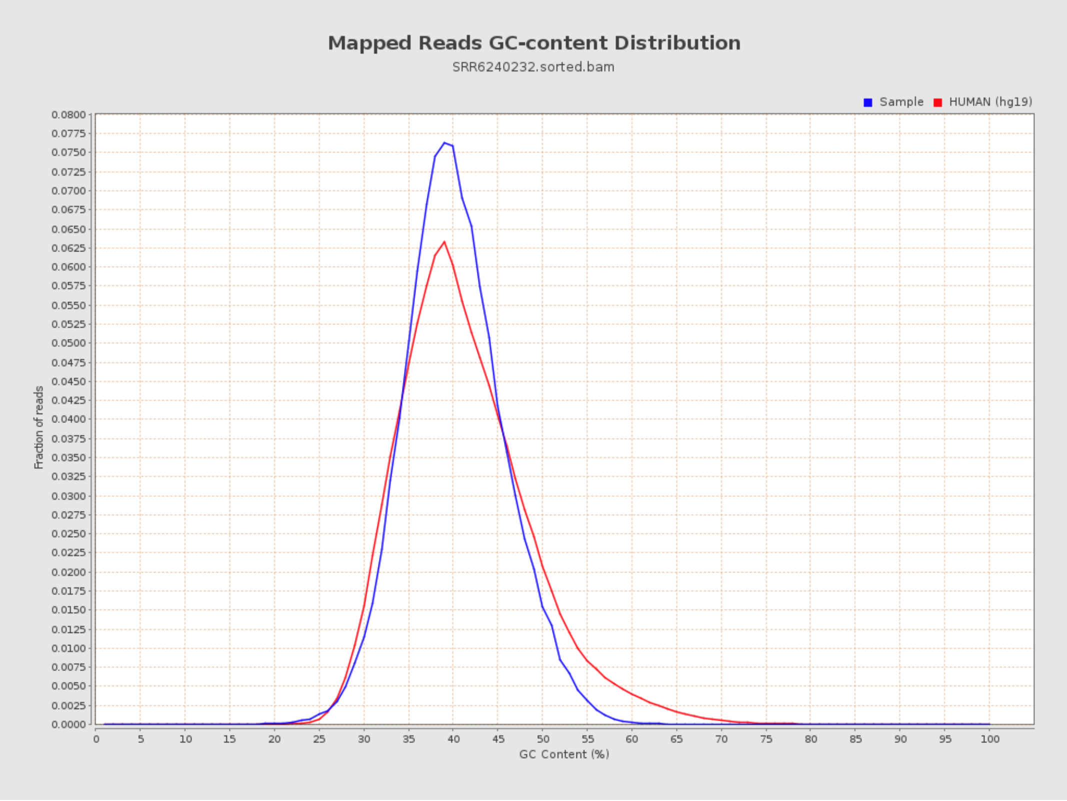
7. Results : Duplication Rate Histogram



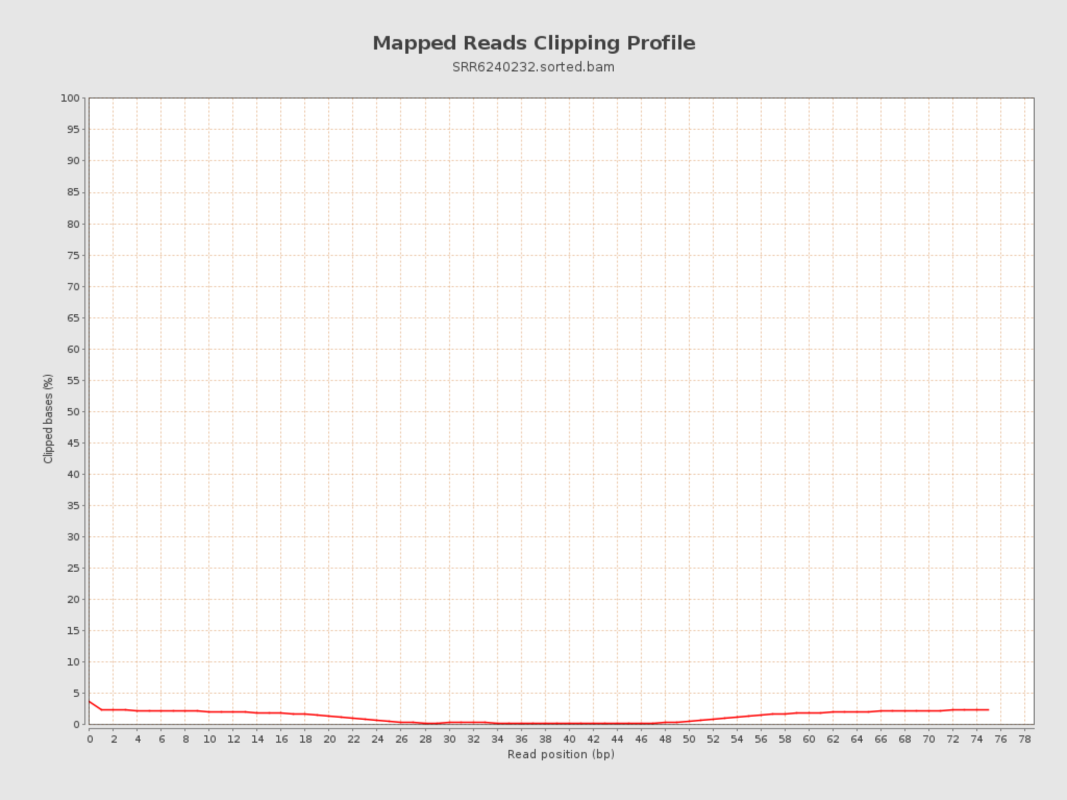
8. Results : Mapped Reads Nucleotide Content



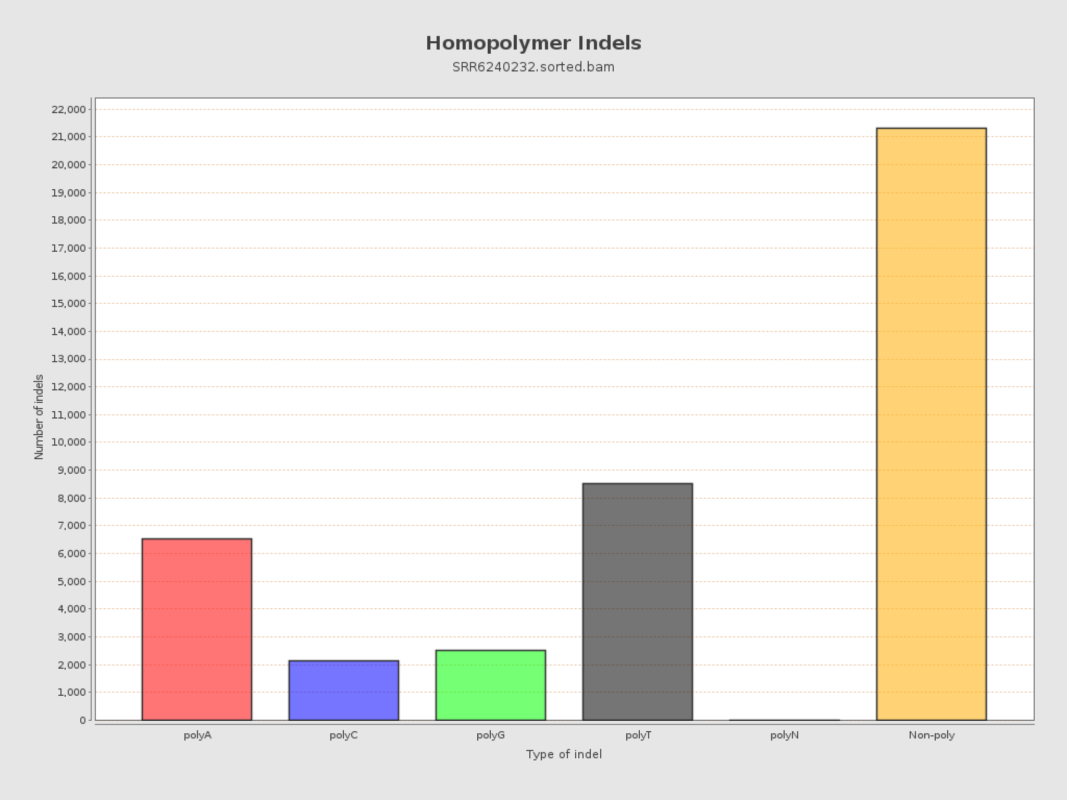
9. Results : Mapped Reads GC-content Distribution



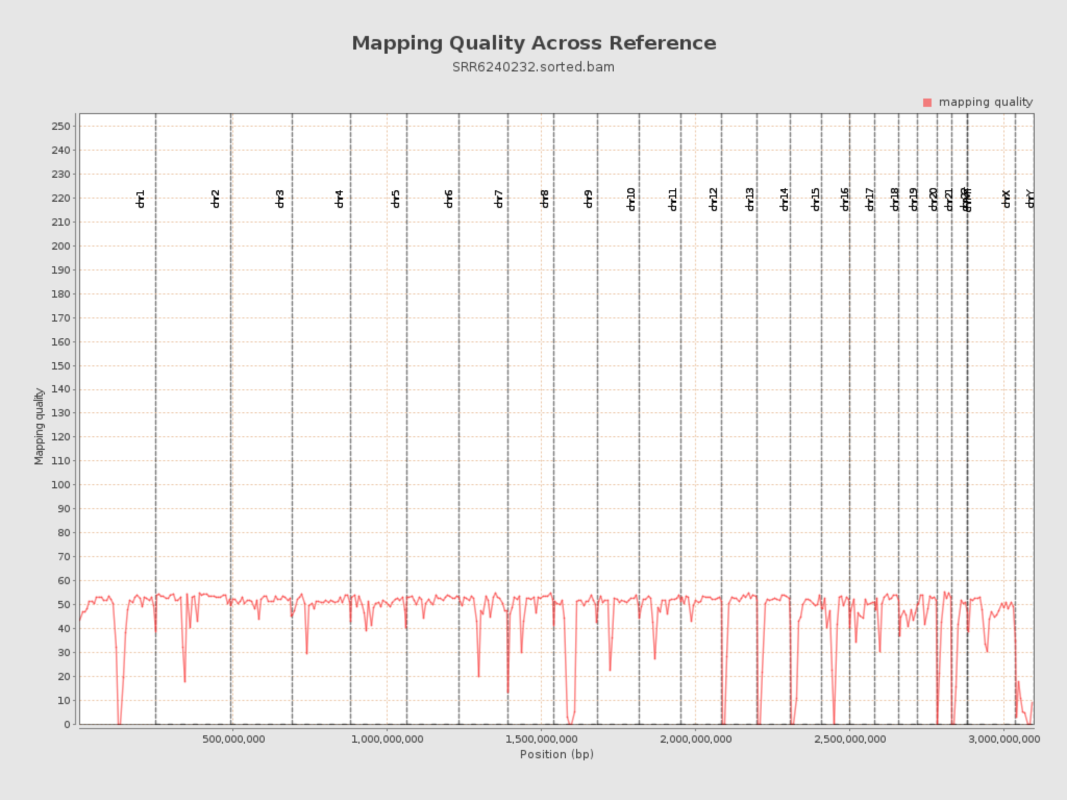
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram