Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 03:17:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240033.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_SRR6240033 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240033.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 03:17:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240033.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,457,140
Mapped reads	1,813,616 / 73.81%
Unmapped reads	643,524 / 26.19%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,555 / 0.71%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	236,074 / 9.61%
Duplication rate	9.97%
Clipped reads	866,060 / 35.25%

2.2. ACGT Content

Number/percentage of A's	33,928,556 / 28.23%
Number/percentage of C's	22,157,099 / 18.44%
Number/percentage of T's	38,504,716 / 32.04%
Number/percentage of G's	25,586,168 / 21.29%
Number/percentage of N's	10,960 / 0.01%
GC Percentage	39.72%

2.3. Coverage

Mean	0.0388

Standard Deviation	0.4775

2.4. Mapping Quality

Mean Mapping Quality	46.73

2.5. Mismatches and indels

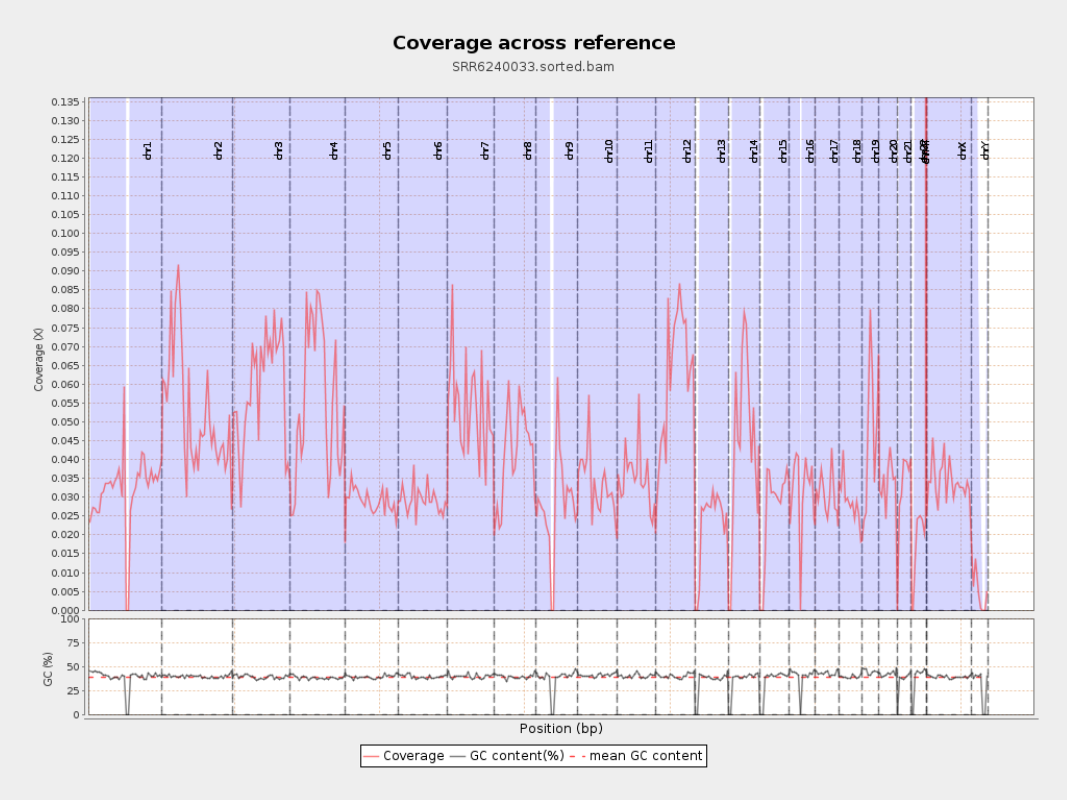
General error rate	0.87%
Mismatches	1,034,044
Insertions	8,615
Mapped reads with at least one insertion	0.47%
Deletions	36,576
Mapped reads with at least one deletion	1.99%
Homopolymer indels	47.44%

2.6. Chromosome stats

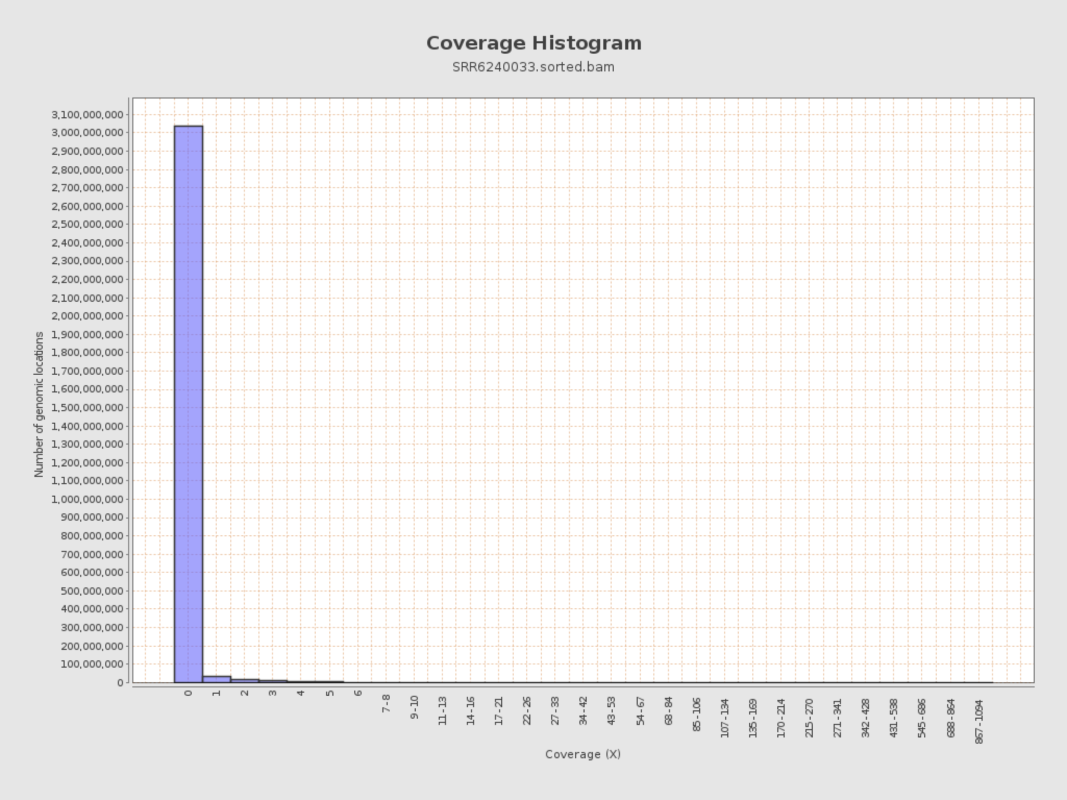
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7909619	0.0317	0.8476
chr2	243199373	12788939	0.0526	0.4934
chr3	198022430	11631044	0.0587	0.4212
chr4	191154276	10563663	0.0553	0.4162
chr5	180915260	5273348	0.0291	0.3013
chr6	171115067	5015124	0.0293	0.3214
chr7	159138663	8655157	0.0544	0.6565

chr8	146364022	6076498	0.0415	0.7382
chr9	141213431	3981211	0.0282	0.3548
chr10	135534747	4579854	0.0338	0.4065
chr11	135006516	4724278	0.035	0.3908
chr12	133851895	8408150	0.0628	0.4423
chr13	115169878	2611456	0.0227	0.2785
chr14	107349540	4754926	0.0443	0.3726
chr15	102531392	2758129	0.0269	0.2921
chr16	90354753	2849153	0.0315	0.3154
chr17	81195210	2473153	0.0305	0.3154
chr18	78077248	2281490	0.0292	0.578
chr19	59128983	2782832	0.0471	0.5901
chr20	63025520	2114618	0.0336	0.3289
chr21	48129895	1554341	0.0323	0.3238
chr22	51304566	873473	0.017	0.2182
chrMT	16571	19791	1.1943	1.8808
chrX	155270560	5280829	0.034	0.3386
chrY	59373566	290452	0.0049	0.1145

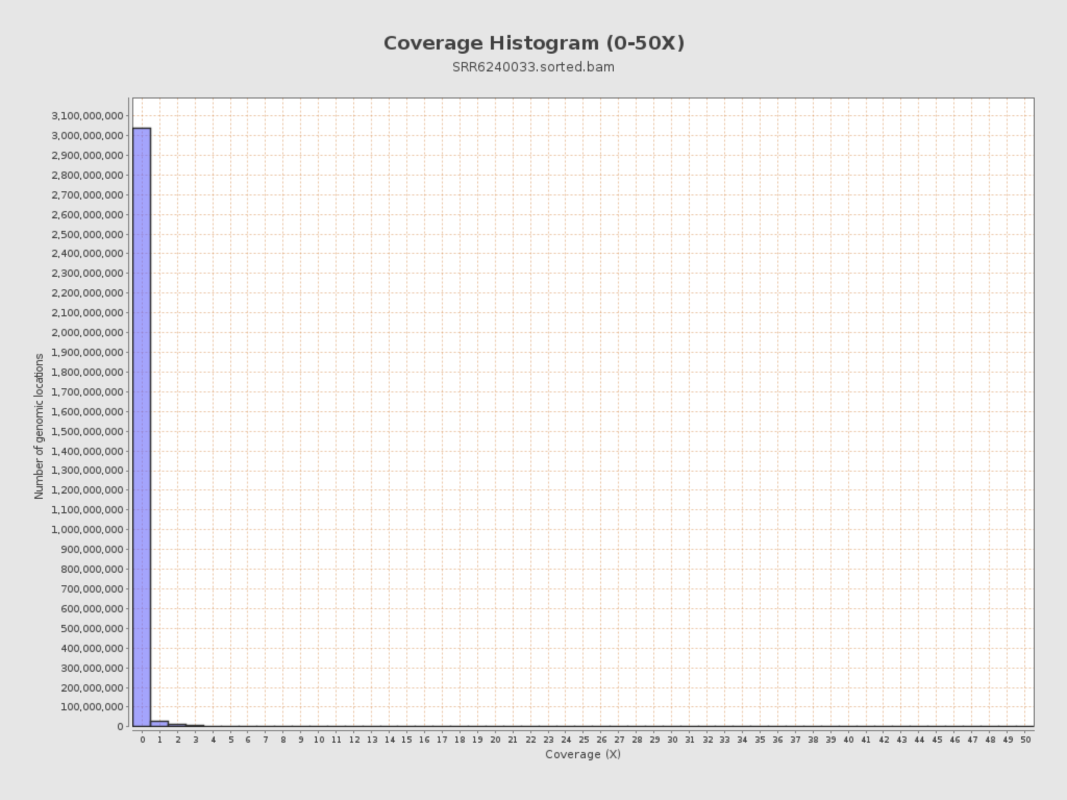
3. Results : Coverage across reference



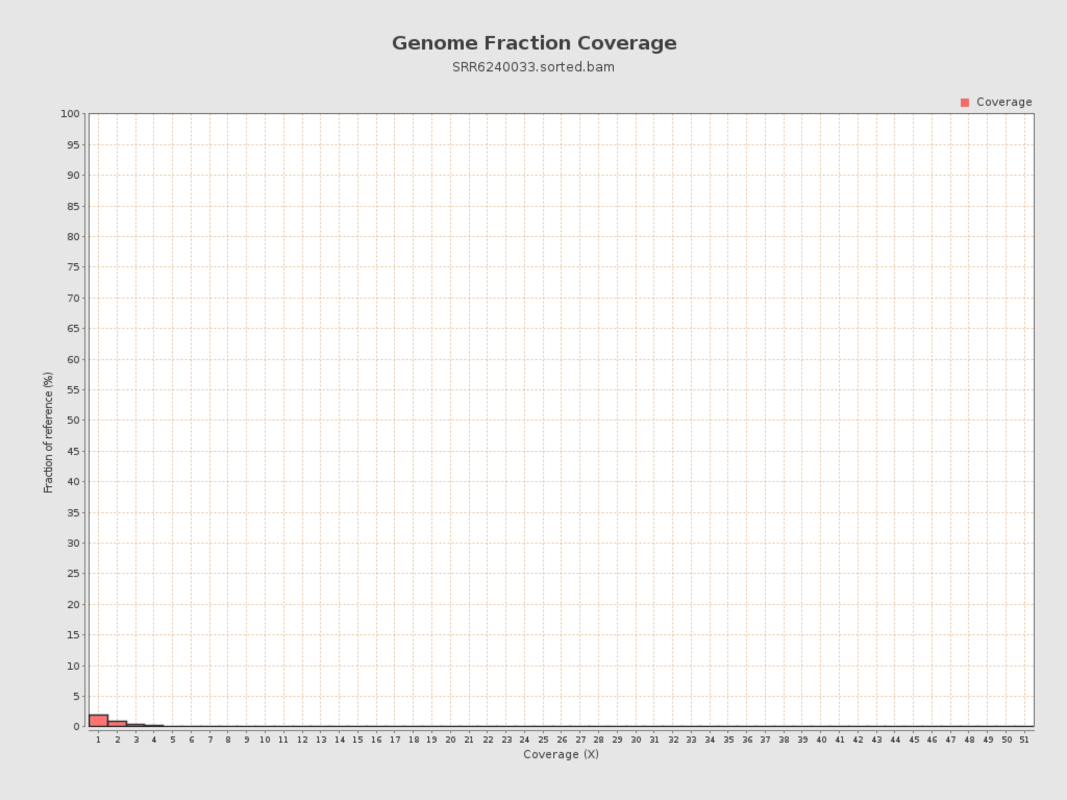
4. Results : Coverage Histogram



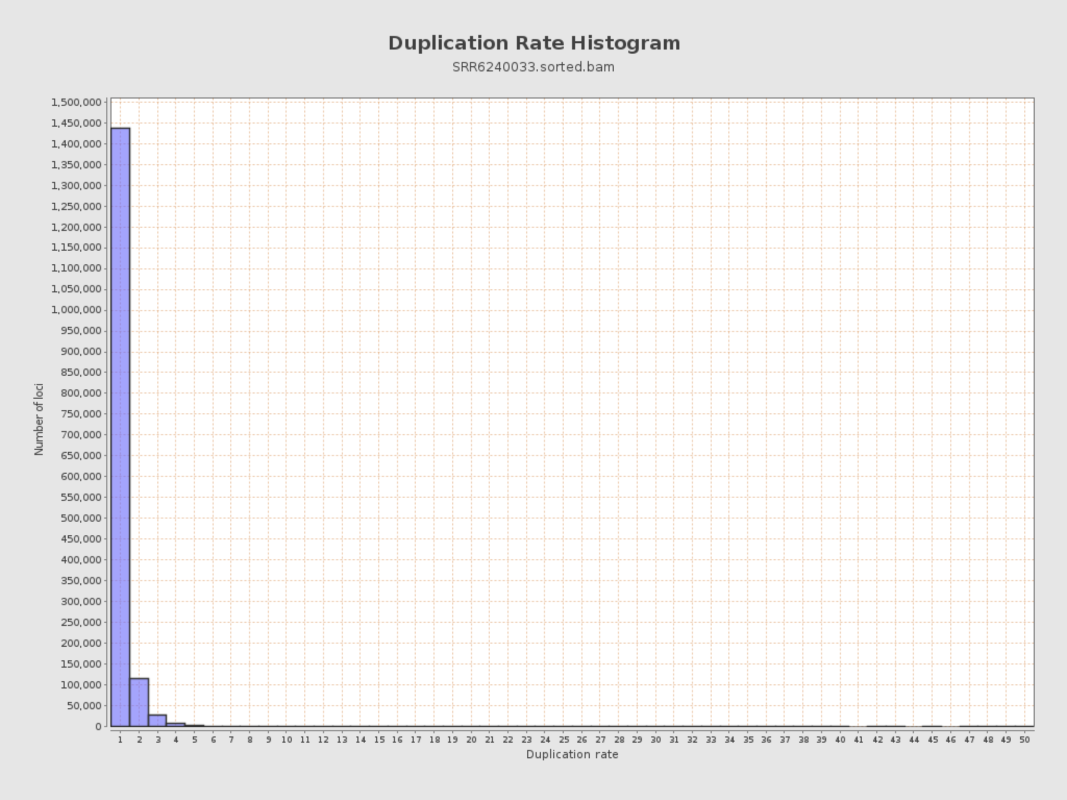
5. Results : Coverage Histogram (0-50X)



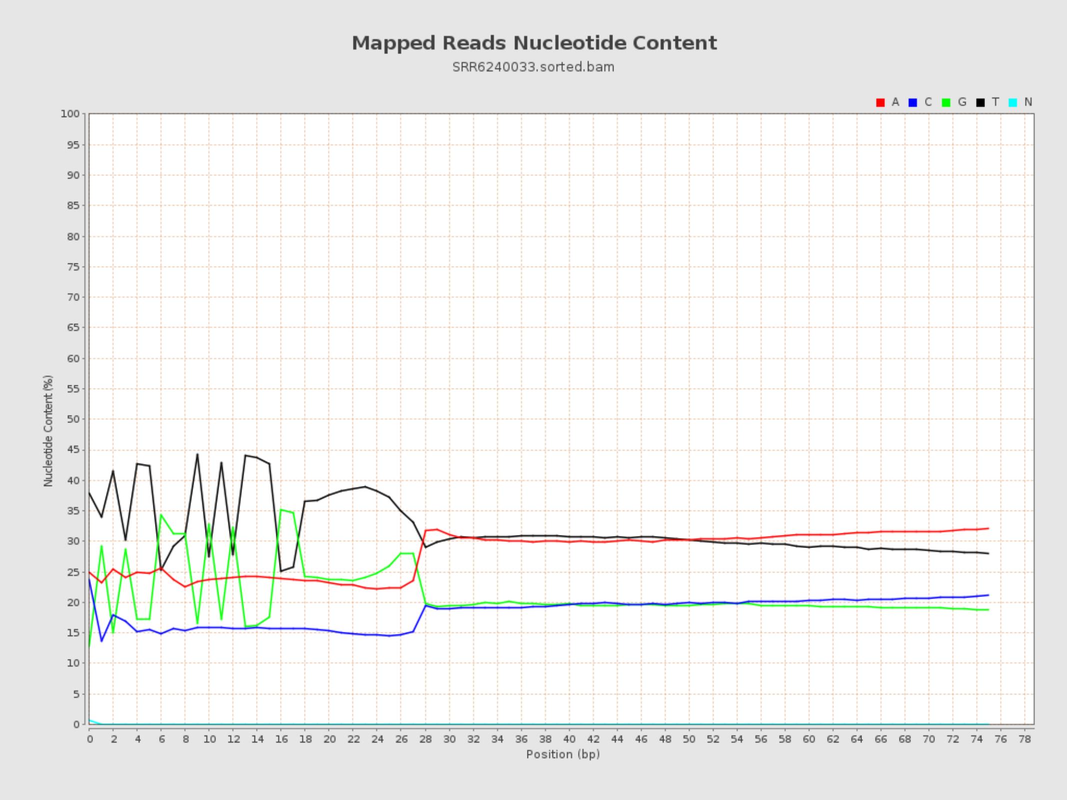
6. Results : Genome Fraction Coverage



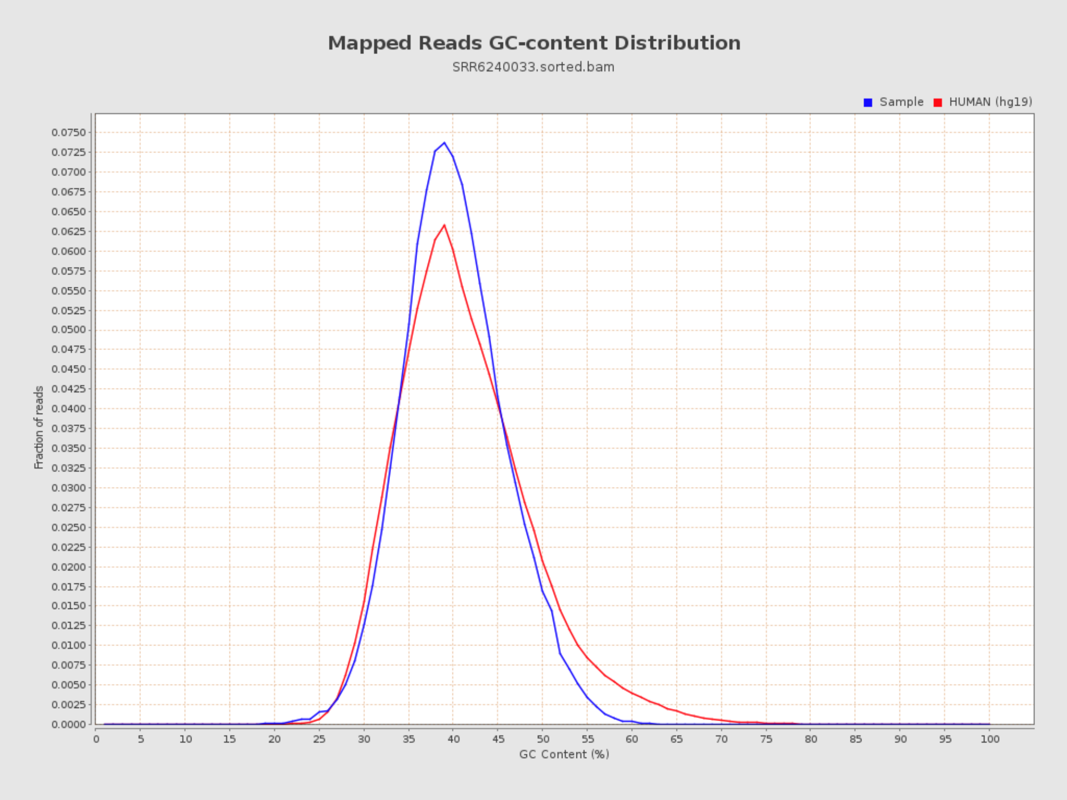
7. Results : Duplication Rate Histogram



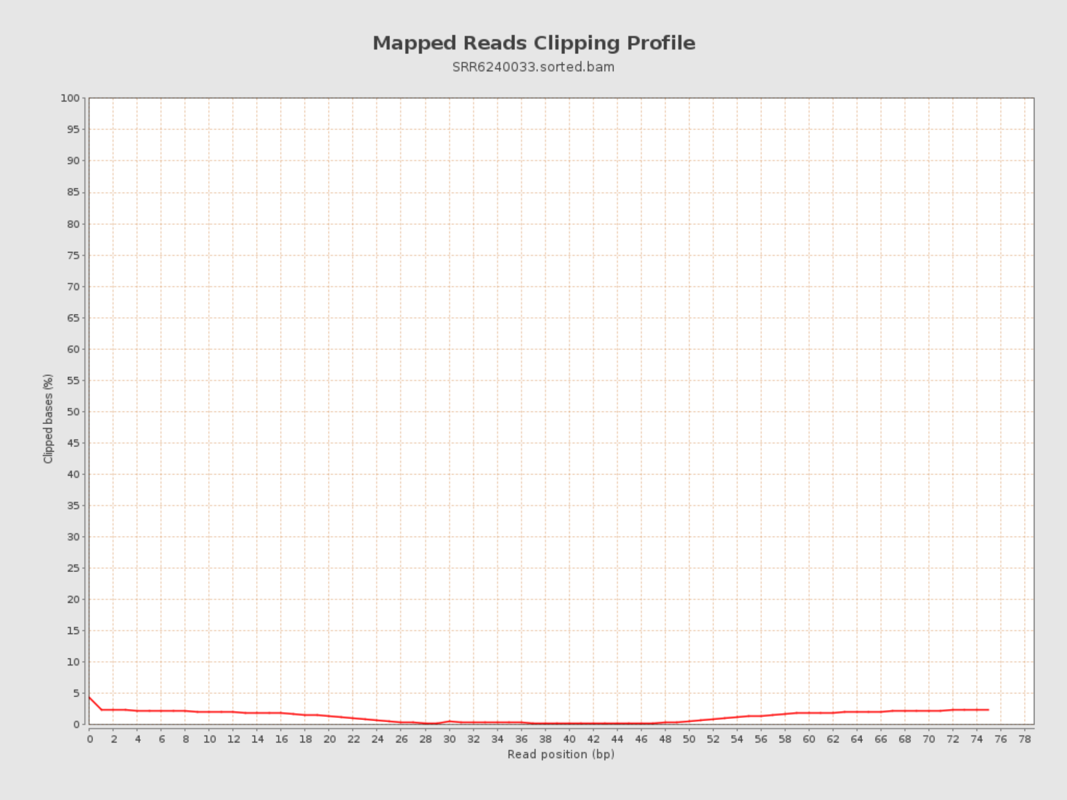
8. Results : Mapped Reads Nucleotide Content



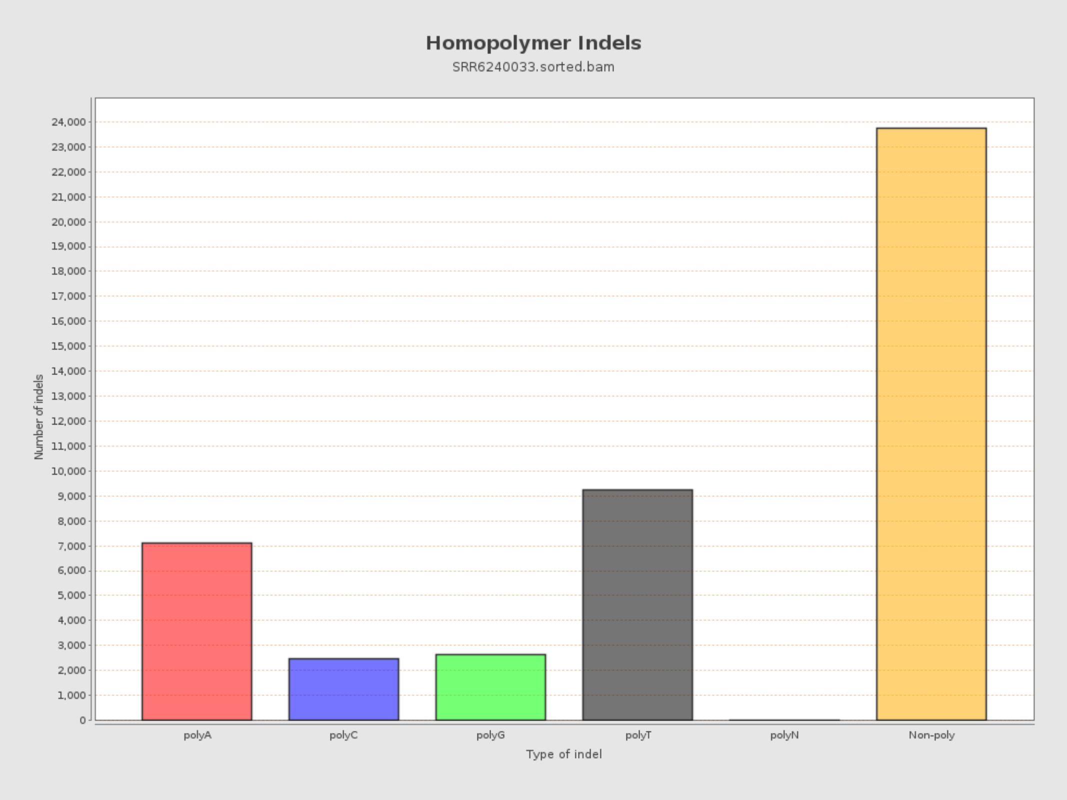
9. Results : Mapped Reads GC-content Distribution



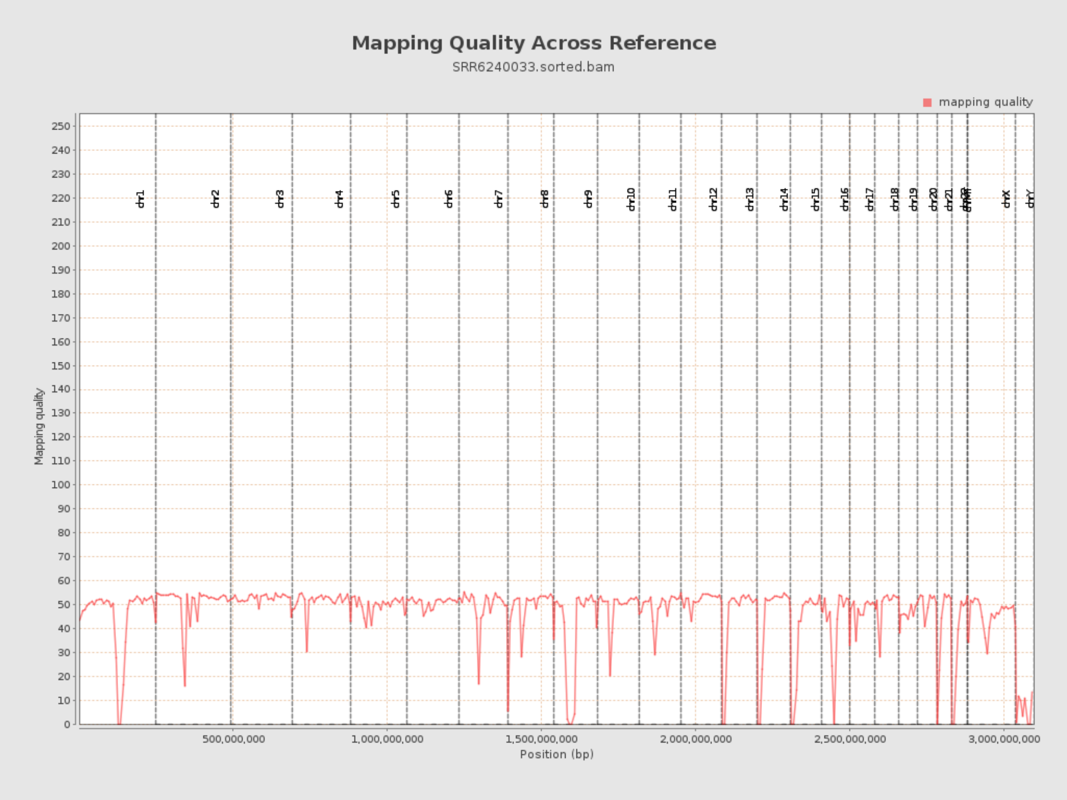
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram