Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 04:36:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240061.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_SRR6240061 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240061.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 04:36:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240061.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,311,323
Mapped reads	1,878,506 / 81.27%
Unmapped reads	432,817 / 18.73%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,704 / 0.64%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	292,167 / 12.64%
Duplication rate	11.3%
Clipped reads	976,545 / 42.25%

2.2. ACGT Content

Number/percentage of A's	35,615,067 / 28.92%
Number/percentage of C's	23,589,192 / 19.16%
Number/percentage of T's	38,250,408 / 31.06%
Number/percentage of G's	25,680,570 / 20.85%
Number/percentage of N's	10,966 / 0.01%
GC Percentage	40.01%

2.3. Coverage

Mean	0.0398

Standard Deviation	0.4751

2.4. Mapping Quality

Mean Mapping Quality	46.8

2.5. Mismatches and indels

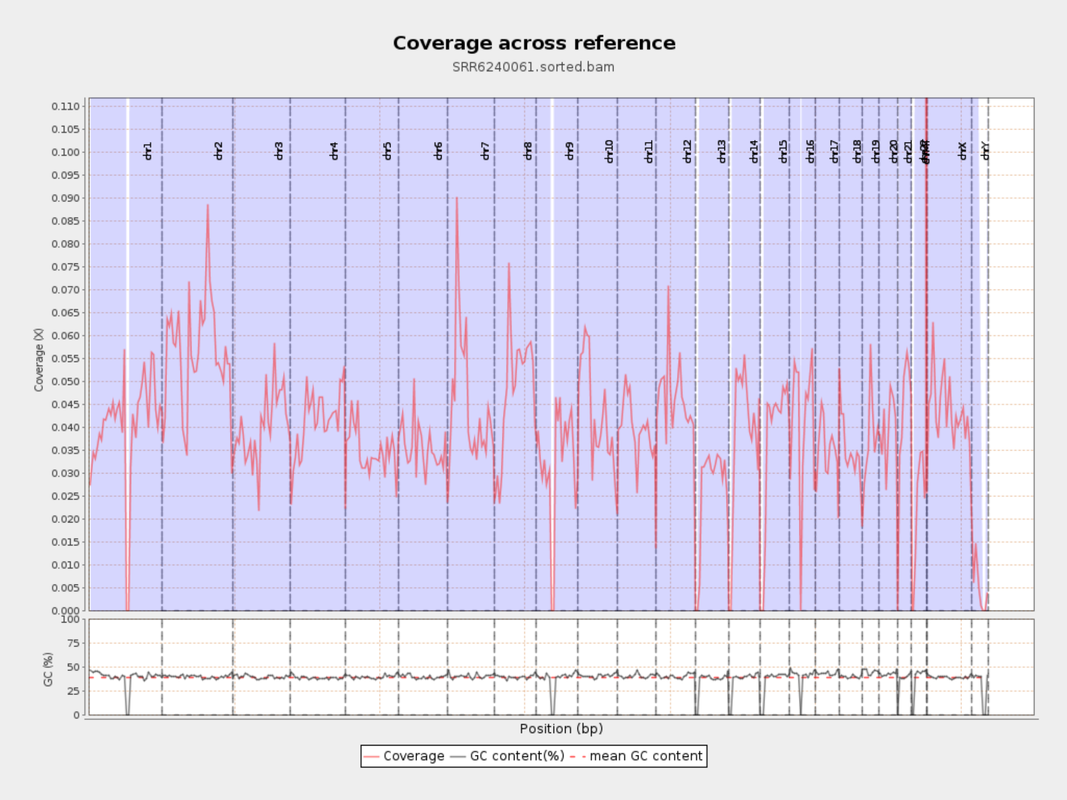
General error rate	0.86%
Mismatches	1,039,549
Insertions	9,014
Mapped reads with at least one insertion	0.48%
Deletions	34,293
Mapped reads with at least one deletion	1.81%
Homopolymer indels	47.81%

2.6. Chromosome stats

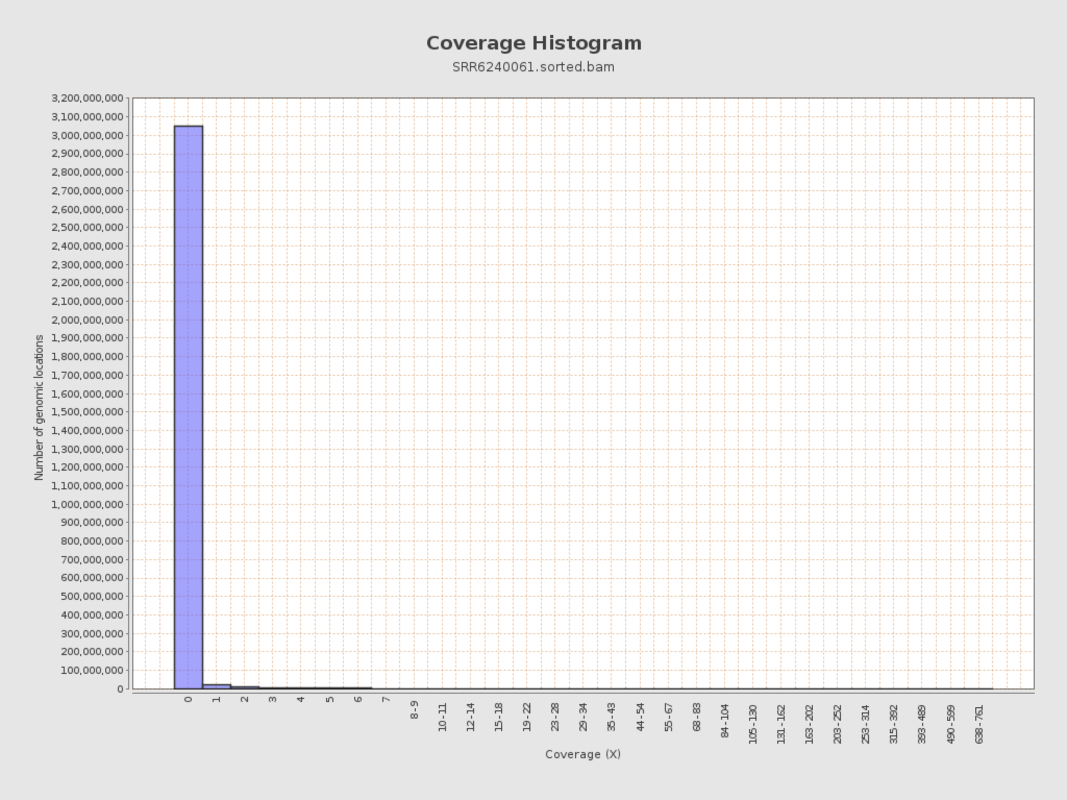
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10010176	0.0402	0.6327
chr2	243199373	13737955	0.0565	0.5613
chr3	198022430	7936379	0.0401	0.4149
chr4	191154276	7907373	0.0414	0.4221
chr5	180915260	6304529	0.0348	0.3813
chr6	171115067	6072281	0.0355	0.4026
chr7	159138663	7252483	0.0456	0.6155

chr8	146364022	7089018	0.0484	0.6527
chr9	141213431	4538644	0.0321	0.413
chr10	135534747	5871512	0.0433	0.4723
chr11	135006516	5335809	0.0395	0.4601
chr12	133851895	6212522	0.0464	0.4406
chr13	115169878	2993834	0.026	0.3354
chr14	107349540	4051737	0.0377	0.4129
chr15	102531392	3738027	0.0365	0.4051
chr16	90354753	3724075	0.0412	0.4095
chr17	81195210	2801462	0.0345	0.3861
chr18	78077248	2754931	0.0353	0.5606
chr19	59128983	2230985	0.0377	0.4708
chr20	63025520	2484559	0.0394	0.4078
chr21	48129895	2026499	0.0421	0.4286
chr22	51304566	1088928	0.0212	0.2901
chrMT	16571	26047	1.5718	2.8655
chrX	155270560	6708785	0.0432	0.4437
chrY	59373566	307294	0.0052	0.135

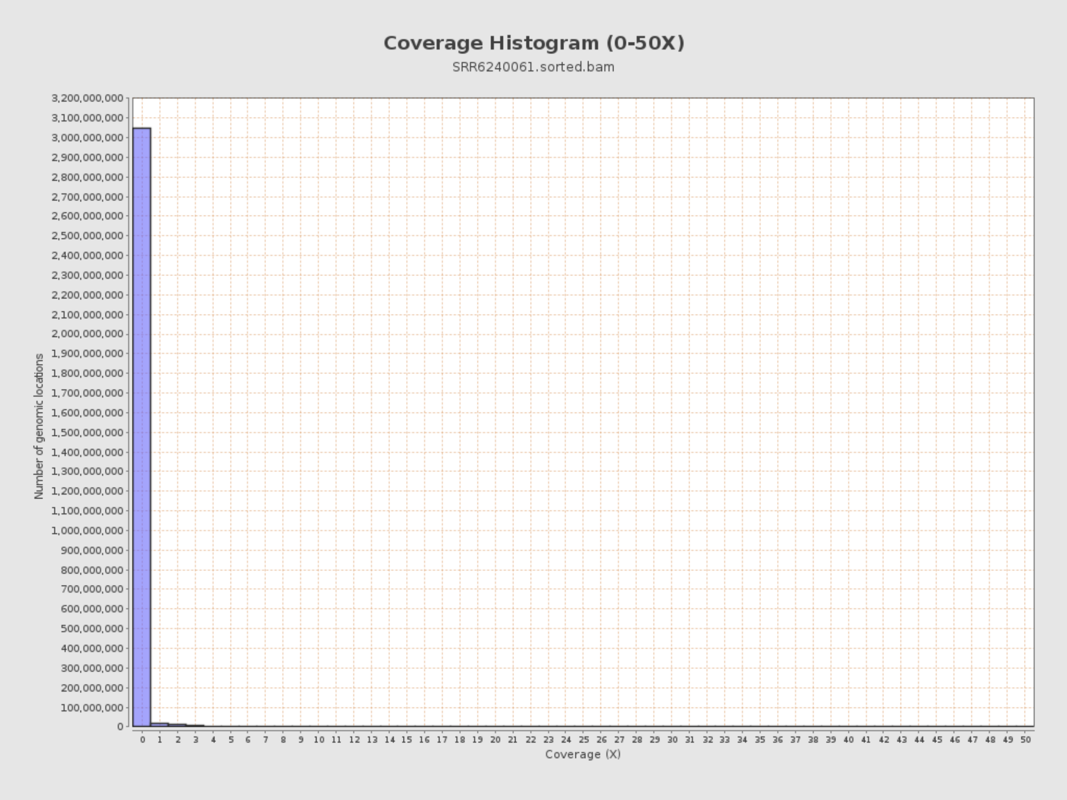
3. Results : Coverage across reference



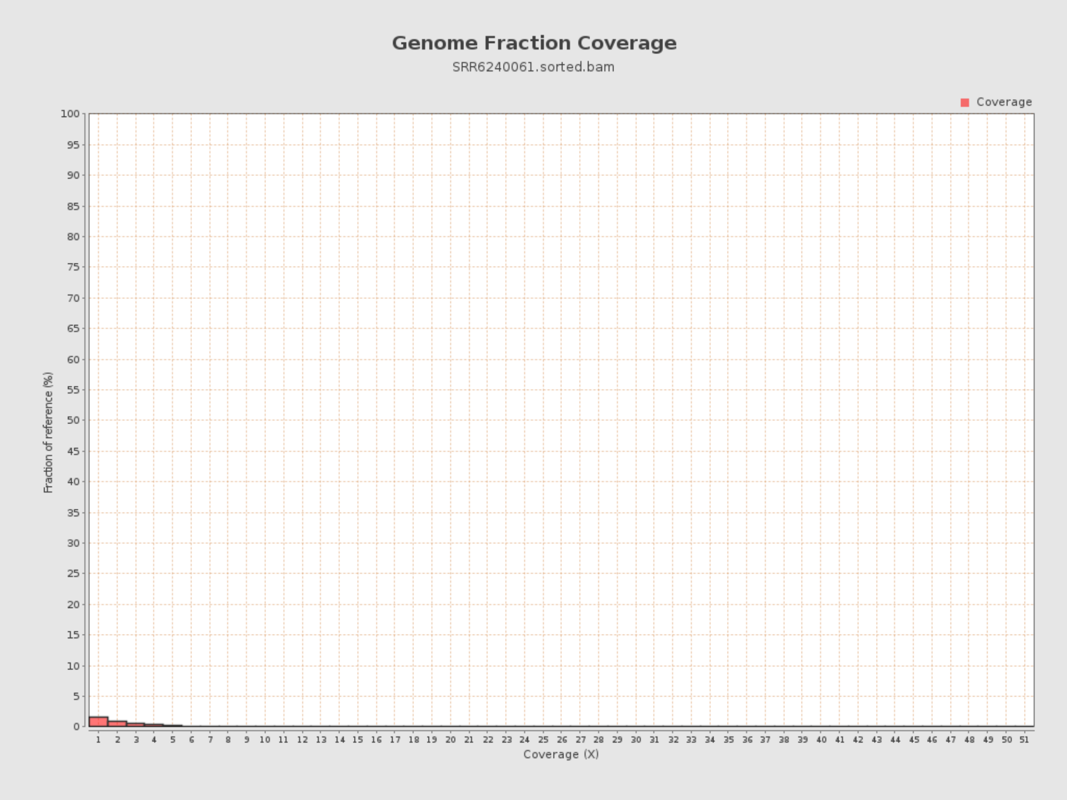
4. Results : Coverage Histogram



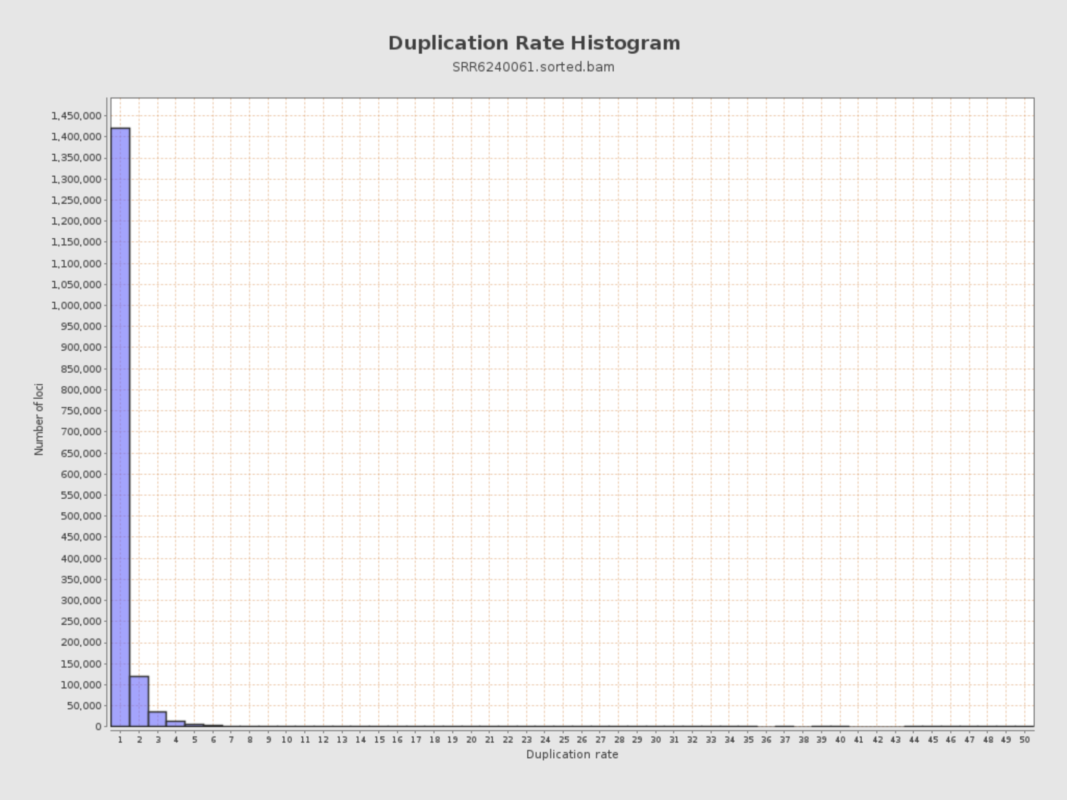
5. Results : Coverage Histogram (0-50X)



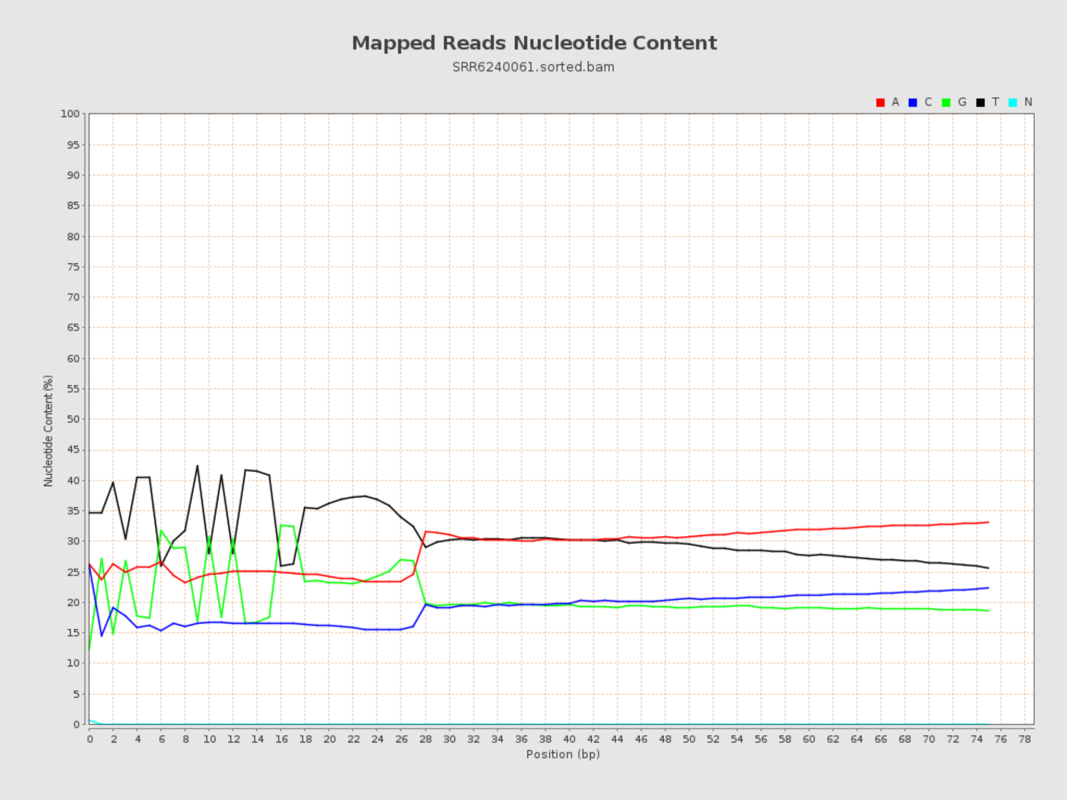
6. Results : Genome Fraction Coverage



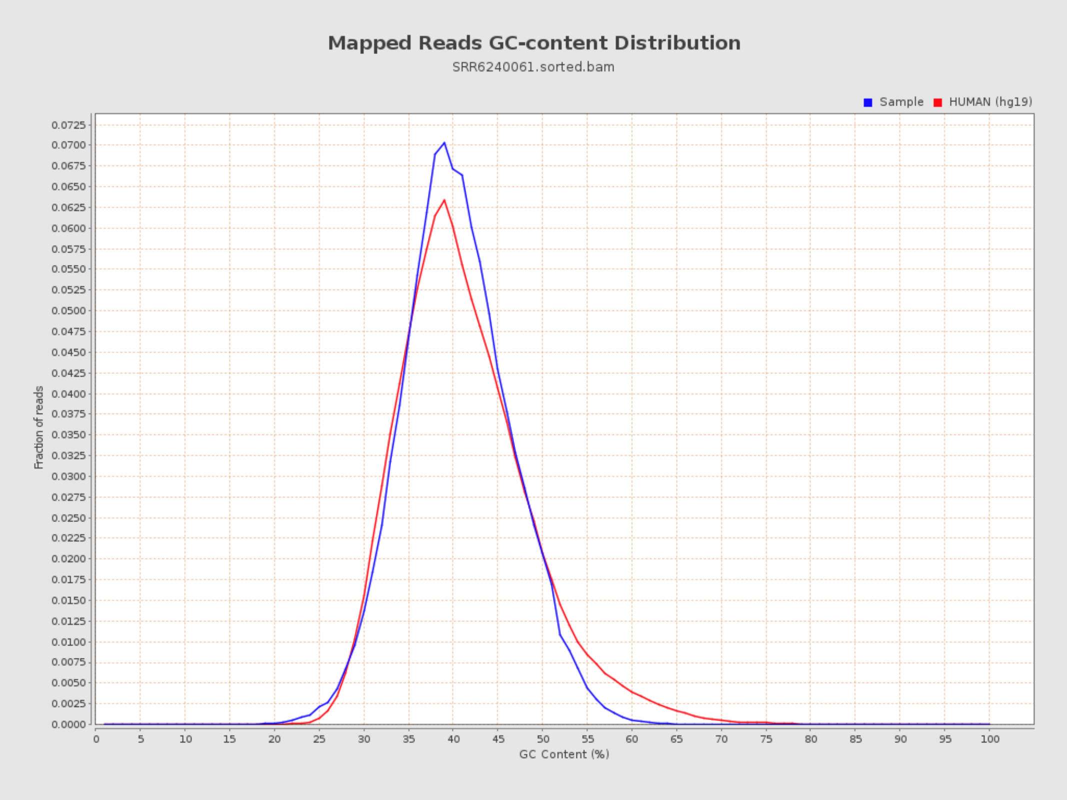
7. Results : Duplication Rate Histogram



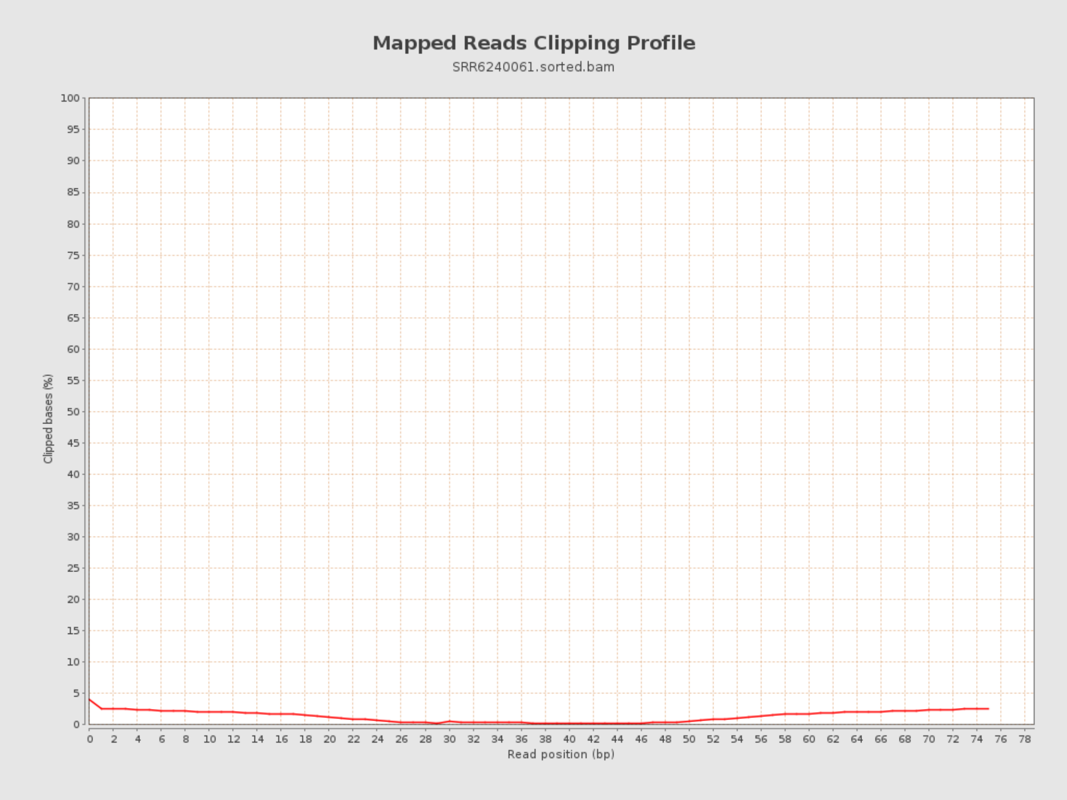
8. Results : Mapped Reads Nucleotide Content



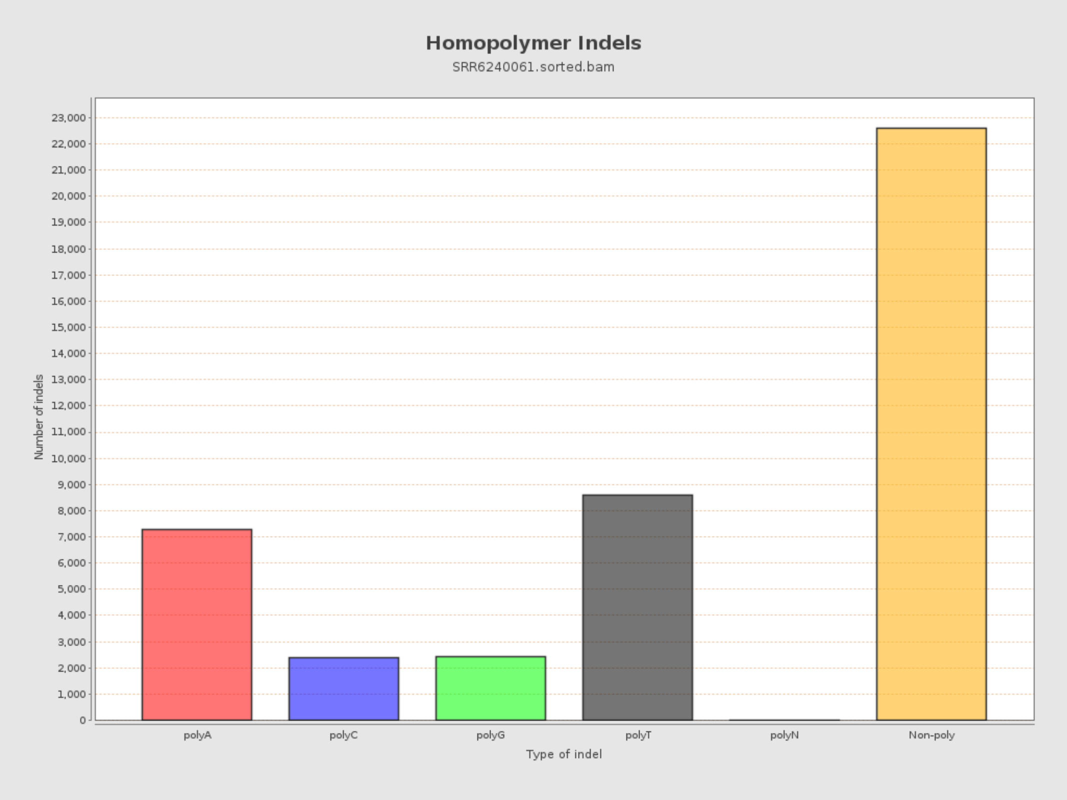
9. Results : Mapped Reads GC-content Distribution



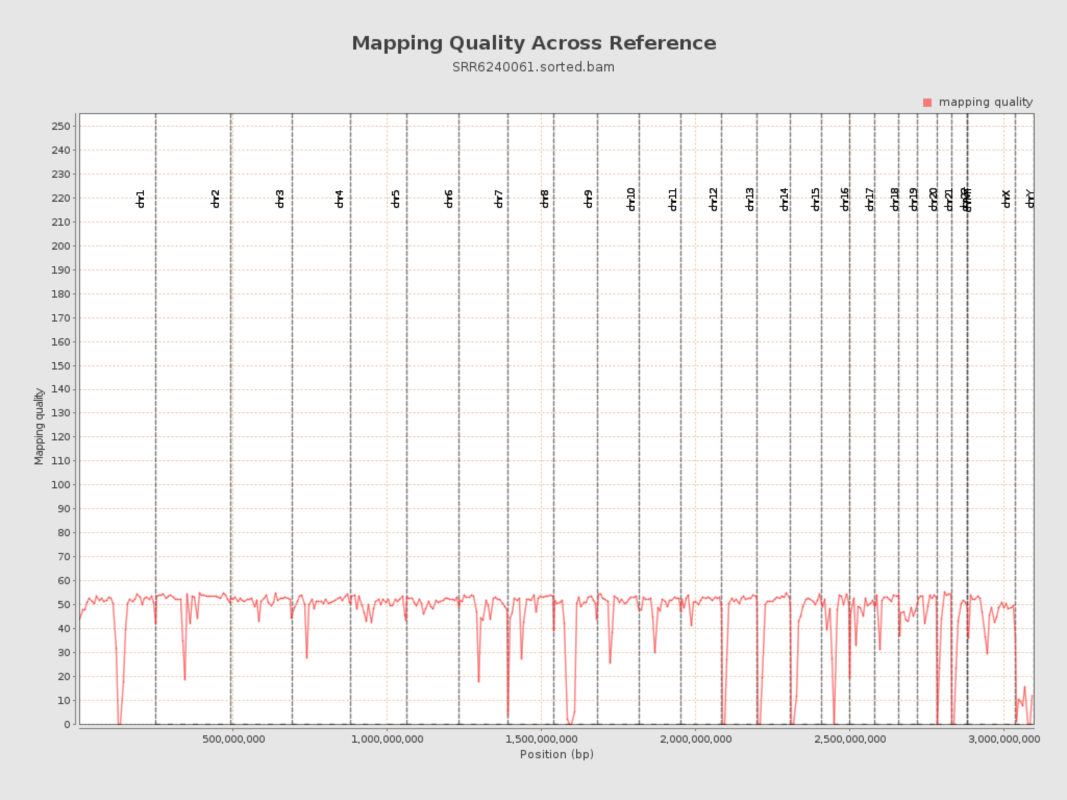
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram