Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 17:37:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013241.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_SRR6013241 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013241.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 17:37:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013241.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,123,519
Mapped reads	1,882,663 / 88.66%
Unmapped reads	240,856 / 11.34%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,804 / 1.03%
Read min/max/mean length	30 / 76 / 76.36
Duplicated reads (estimated)	104,034 / 4.9%
Duplication rate	4.3%
Clipped reads	940,499 / 44.29%

2.2. ACGT Content

Number/percentage of A's	33,635,753 / 27.28%
Number/percentage of C's	23,200,927 / 18.81%
Number/percentage of T's	38,629,883 / 31.33%
Number/percentage of G's	27,836,423 / 22.57%
Number/percentage of N's	14,377 / 0.01%
GC Percentage	41.39%

2.3. Coverage

Mean	0.0399

Standard Deviation	0.4053

2.4. Mapping Quality

Mean Mapping Quality	43.81

2.5. Mismatches and indels

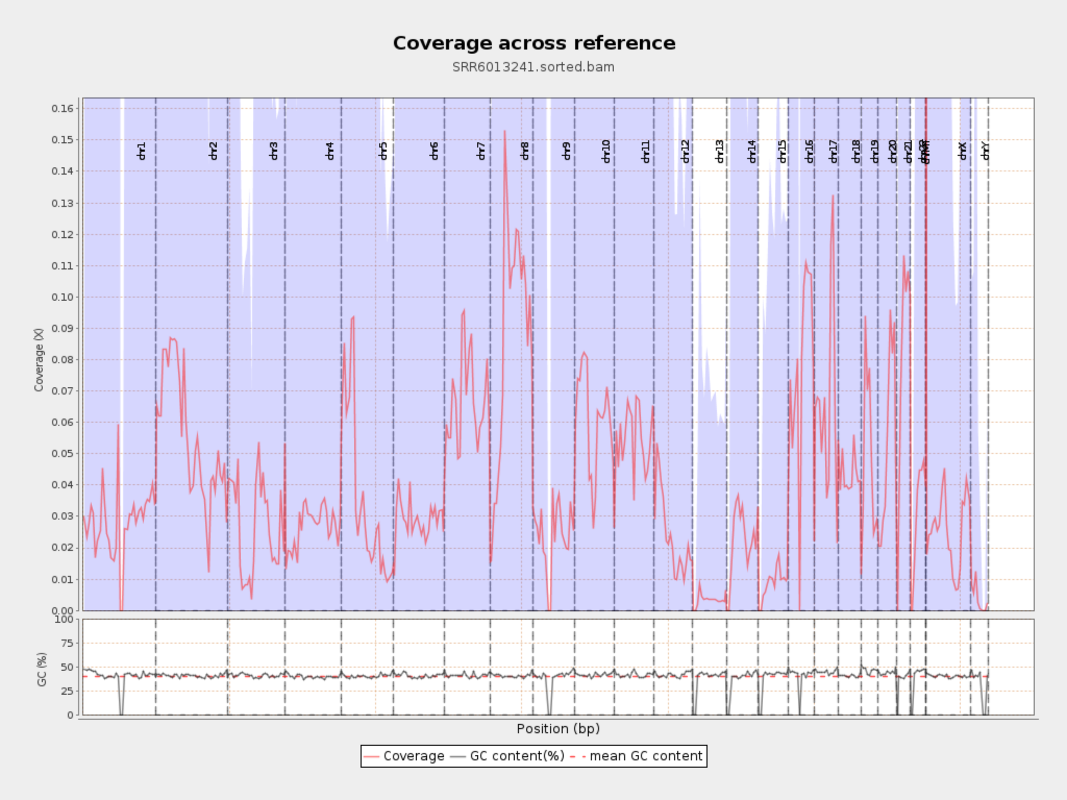
General error rate	0.81%
Mismatches	989,298
Insertions	8,424
Mapped reads with at least one insertion	0.44%
Deletions	38,411
Mapped reads with at least one deletion	2.01%
Homopolymer indels	44.3%

2.6. Chromosome stats

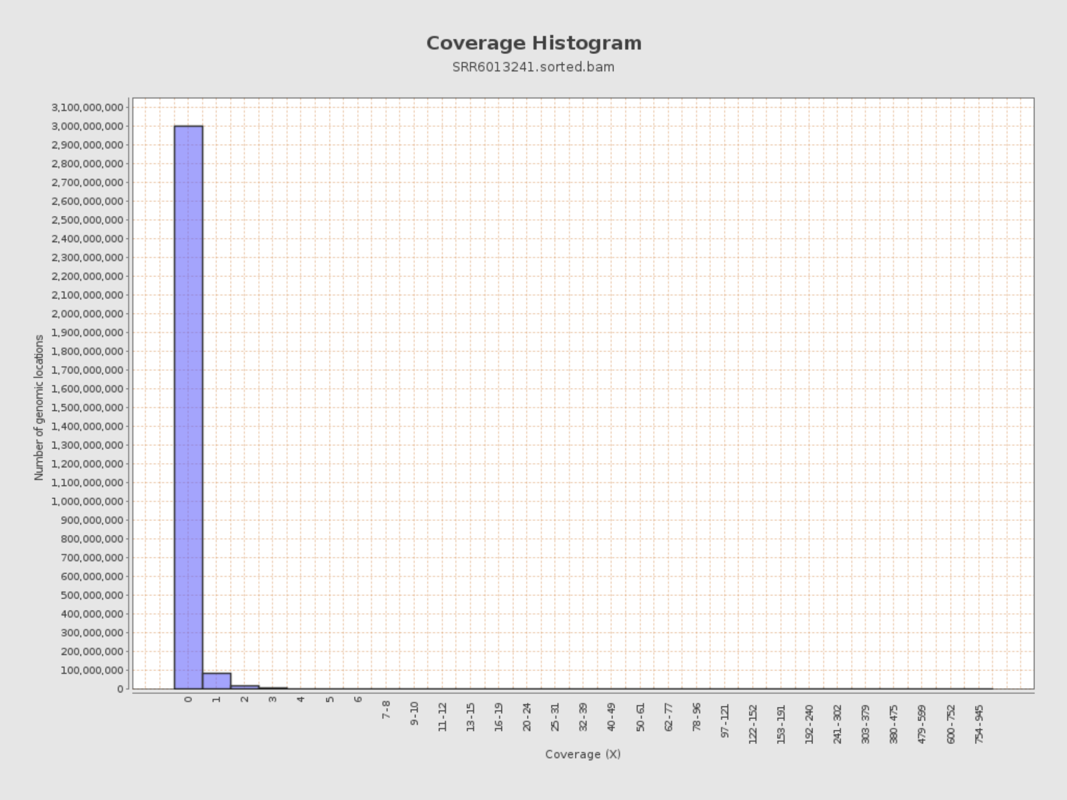
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6990628	0.028	0.7867
chr2	243199373	13579479	0.0558	0.5071
chr3	198022430	5320149	0.0269	0.1941
chr4	191154276	5118476	0.0268	0.2083
chr5	180915260	6386318	0.0353	0.2309
chr6	171115067	5000548	0.0292	0.239
chr7	159138663	10579304	0.0665	0.5432

chr8	146364022	12923041	0.0883	0.5361
chr9	141213431	3355467	0.0238	0.2988
chr10	135534747	8240144	0.0608	0.4387
chr11	135006516	7343338	0.0544	0.3905
chr12	133851895	3193837	0.0239	0.1892
chr13	115169878	388760	0.0034	0.0677
chr14	107349540	2377558	0.0221	0.1846
chr15	102531392	887295	0.0087	0.1094
chr16	90354753	6840060	0.0757	0.3522
chr17	81195210	5509181	0.0679	0.4066
chr18	78077248	3416988	0.0438	0.4814
chr19	59128983	2995349	0.0507	0.7254
chr20	63025520	3430946	0.0544	0.2887
chr21	48129895	3753112	0.078	0.3485
chr22	51304566	1550908	0.0302	0.2068
chrMT	16571	9298	0.5611	0.8858
chrX	155270560	3969810	0.0256	0.2365
chrY	59373566	223025	0.0038	0.1044

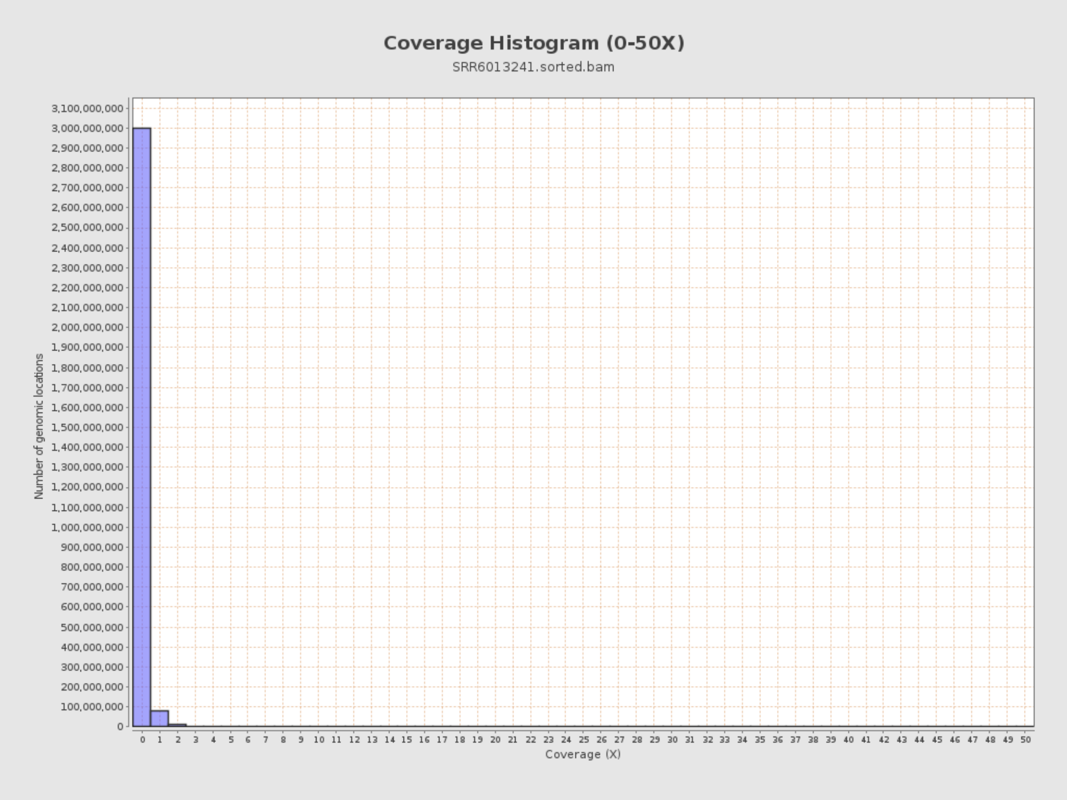
3. Results : Coverage across reference



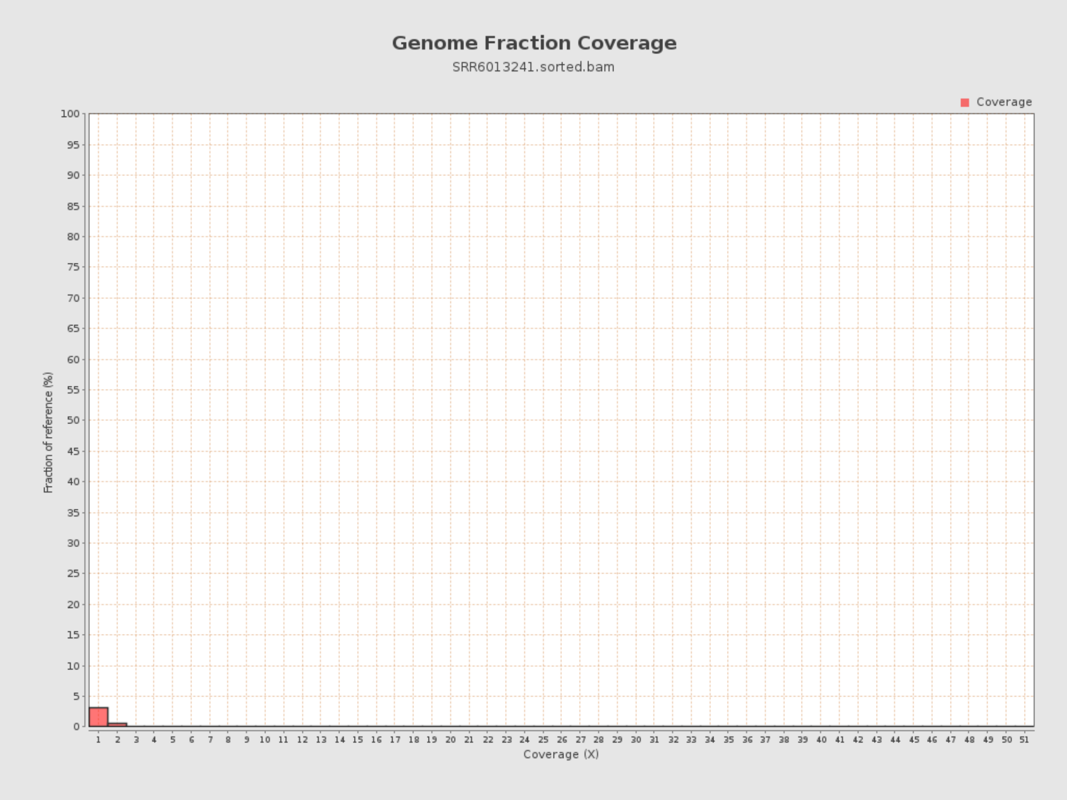
4. Results : Coverage Histogram



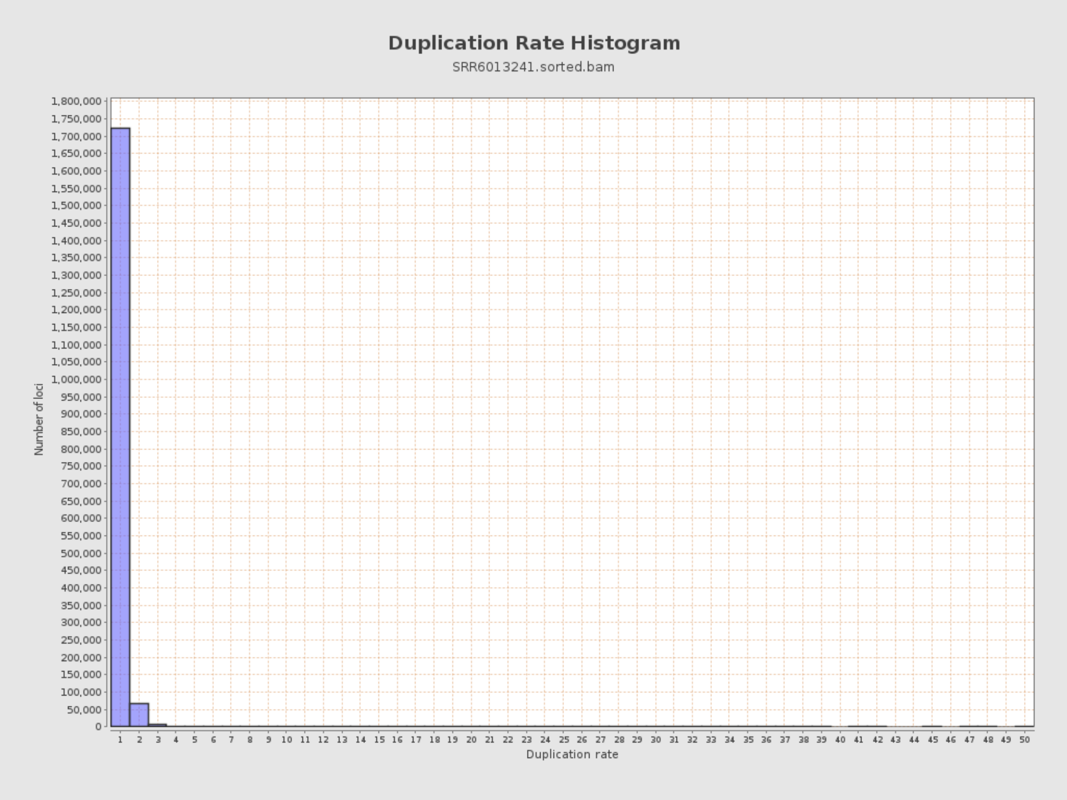
5. Results : Coverage Histogram (0-50X)



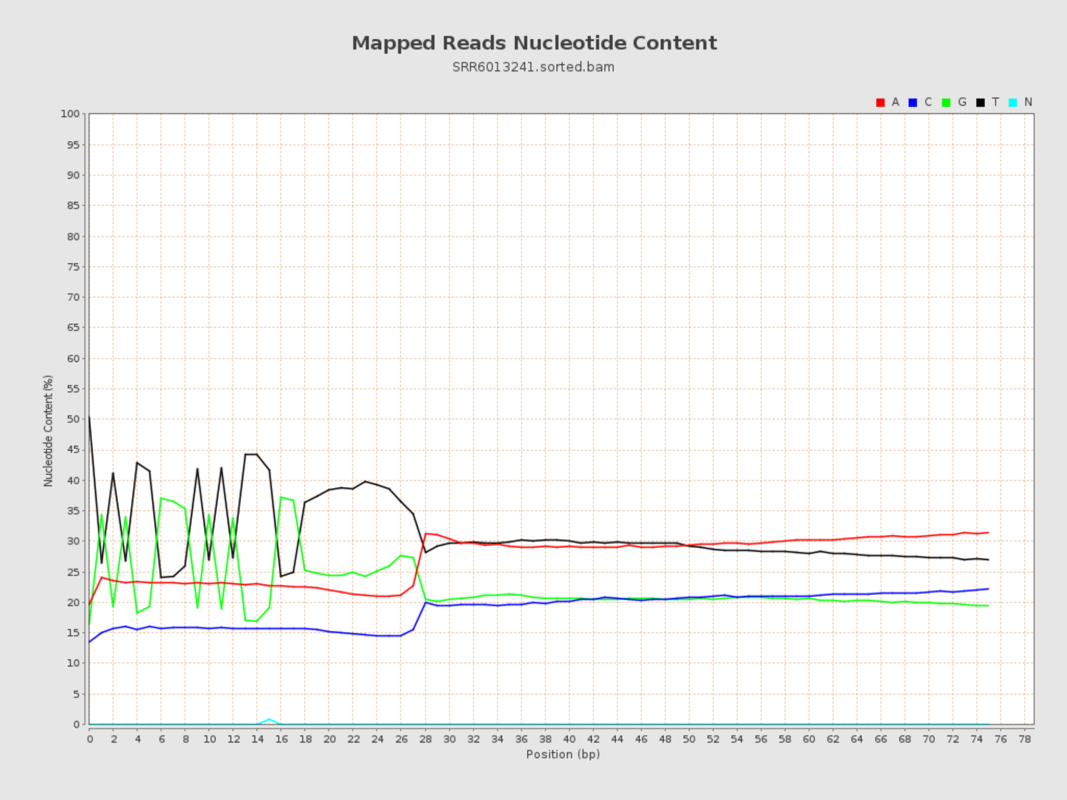
6. Results : Genome Fraction Coverage



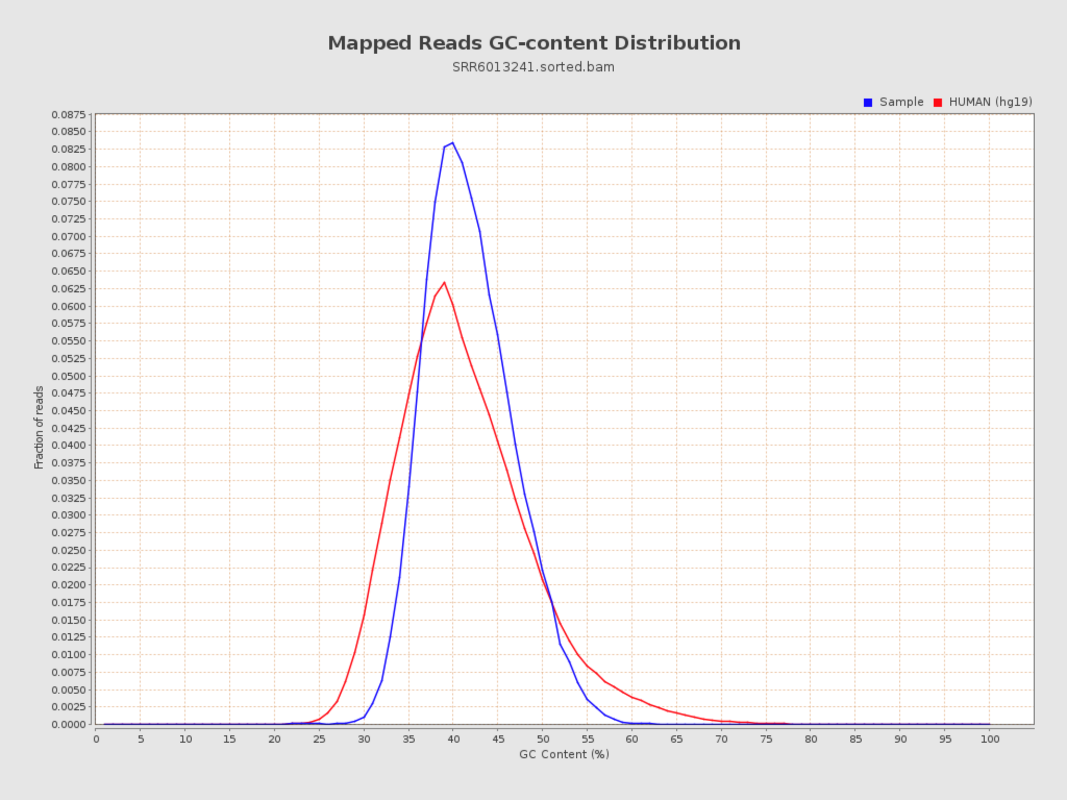
7. Results : Duplication Rate Histogram



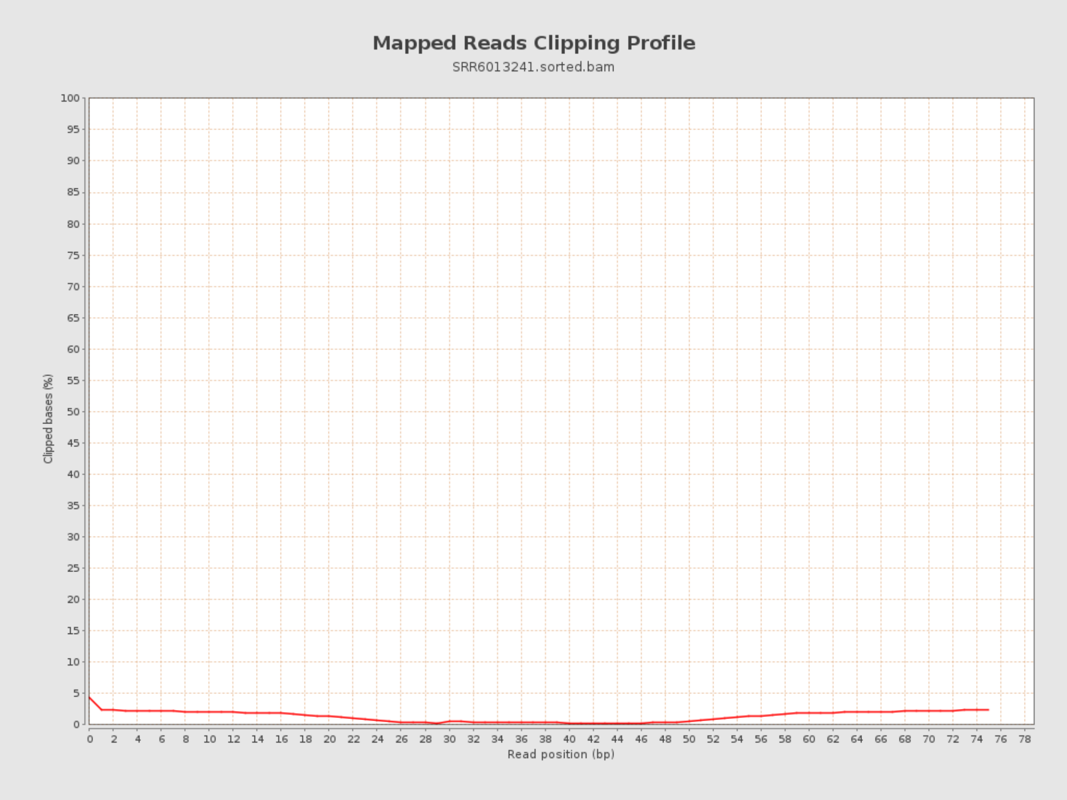
8. Results : Mapped Reads Nucleotide Content



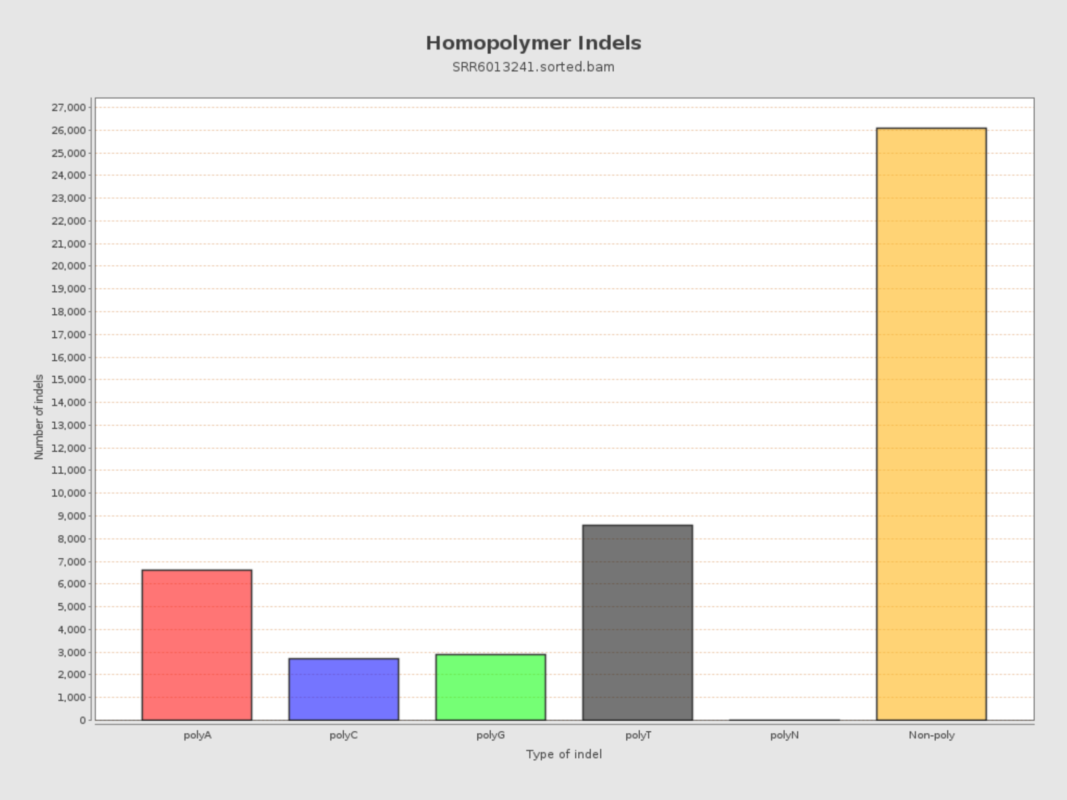
9. Results : Mapped Reads GC-content Distribution



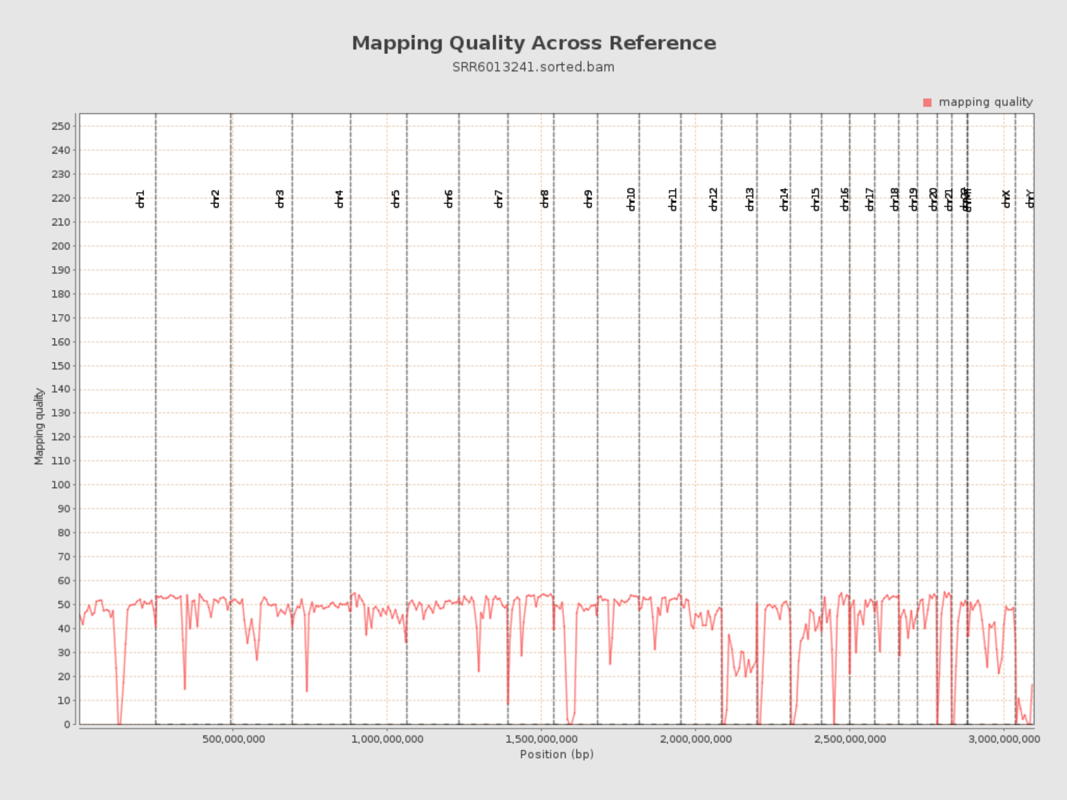
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram