Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 18:36:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013264.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_SRR6013264 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013264.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 18:36:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013264.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,173,721
Mapped reads	1,889,805 / 86.94%
Unmapped reads	283,916 / 13.06%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,245 / 0.52%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	94,746 / 4.36%
Duplication rate	3.91%
Clipped reads	815,369 / 37.51%

2.2. ACGT Content

Number/percentage of A's	34,628,514 / 27.32%
Number/percentage of C's	23,470,018 / 18.52%
Number/percentage of T's	40,361,252 / 31.85%
Number/percentage of G's	28,246,535 / 22.29%
Number/percentage of N's	27,196 / 0.02%
GC Percentage	40.81%

2.3. Coverage

Mean	0.041

Standard Deviation	0.4034

2.4. Mapping Quality

Mean Mapping Quality	44.74

2.5. Mismatches and indels

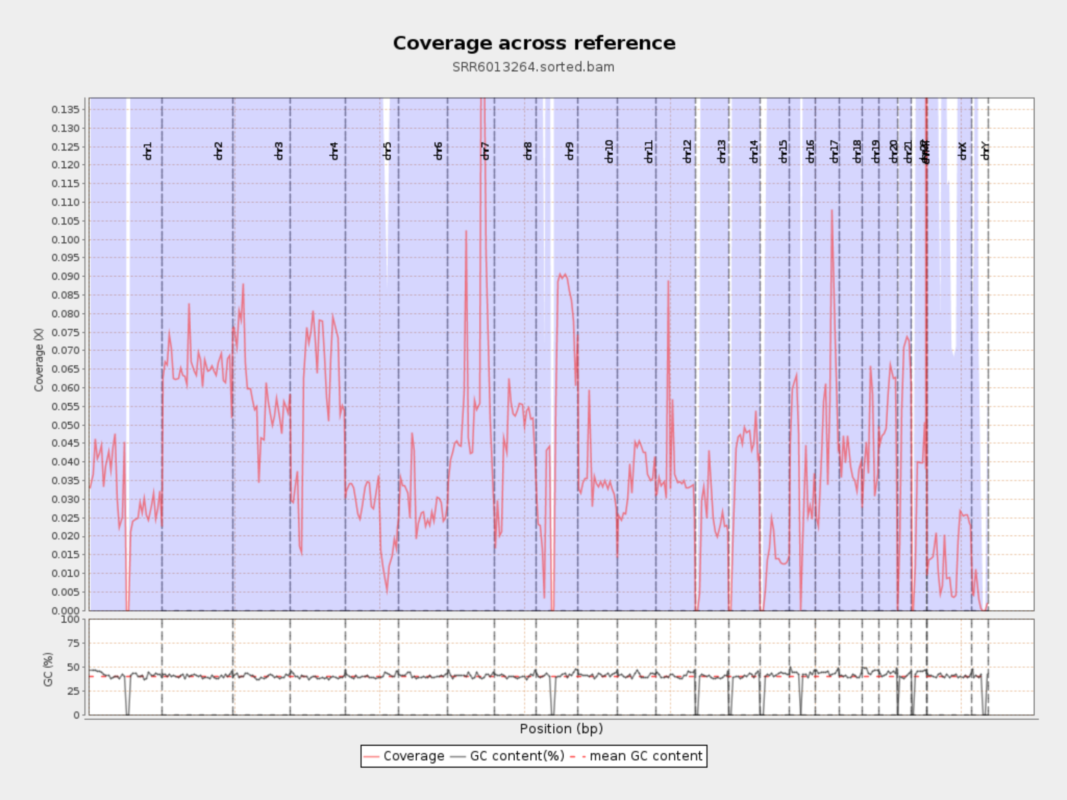
General error rate	0.84%
Mismatches	1,041,654
Insertions	9,522
Mapped reads with at least one insertion	0.5%
Deletions	32,543
Mapped reads with at least one deletion	1.7%
Homopolymer indels	45.98%

2.6. Chromosome stats

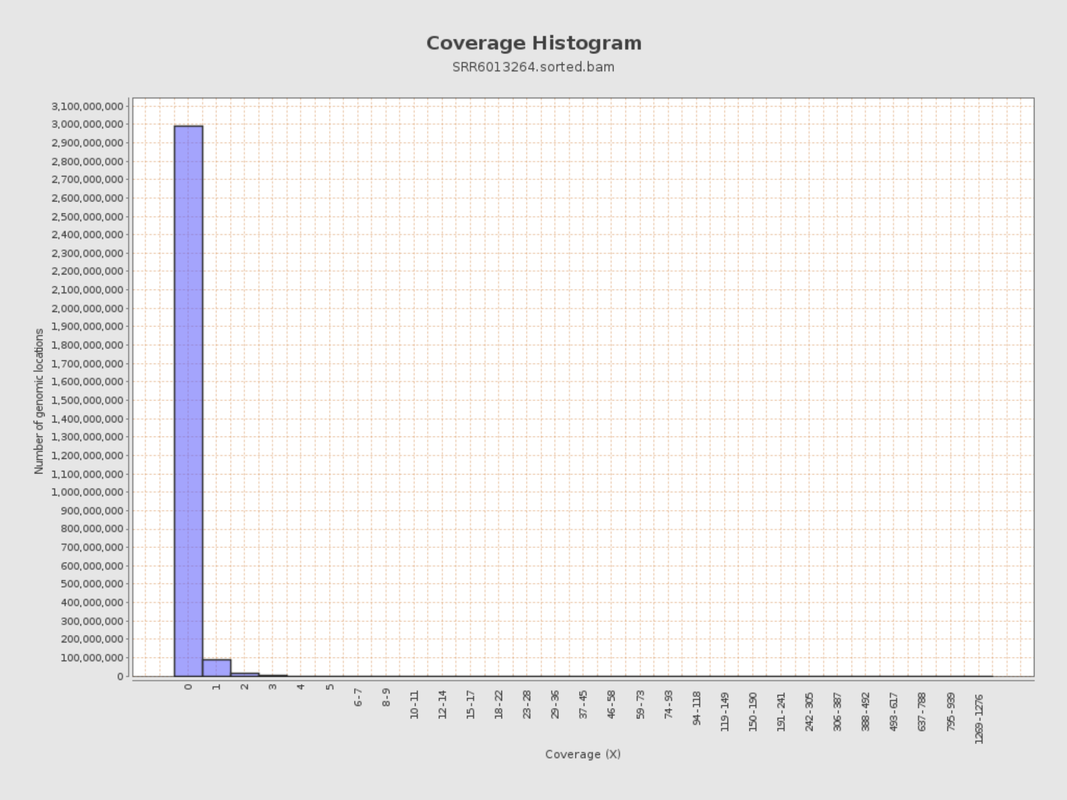
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7679770	0.0308	0.4735
chr2	243199373	15966306	0.0657	0.6319
chr3	198022430	11676416	0.059	0.2837
chr4	191154276	11213993	0.0587	0.2999
chr5	180915260	4493333	0.0248	0.1825
chr6	171115067	4914721	0.0287	0.2469
chr7	159138663	10463690	0.0658	0.9445

chr8	146364022	6691834	0.0457	0.4306
chr9	141213431	7583891	0.0537	0.3686
chr10	135534747	4713471	0.0348	0.3938
chr11	135006516	4839039	0.0358	0.2578
chr12	133851895	5110907	0.0382	0.2367
chr13	115169878	2607025	0.0226	0.179
chr14	107349540	4147153	0.0386	0.252
chr15	102531392	1291065	0.0126	0.1311
chr16	90354753	3420893	0.0379	0.2429
chr17	81195210	4302634	0.053	0.2785
chr18	78077248	3058326	0.0392	0.5394
chr19	59128983	2606757	0.0441	0.4421
chr20	63025520	3429920	0.0544	0.2807
chr21	48129895	2542581	0.0528	0.2861
chr22	51304566	1489027	0.029	0.199
chrMT	16571	84477	5.0979	4.1932
chrX	155270560	2277613	0.0147	0.1585
chrY	59373566	183441	0.0031	0.1165

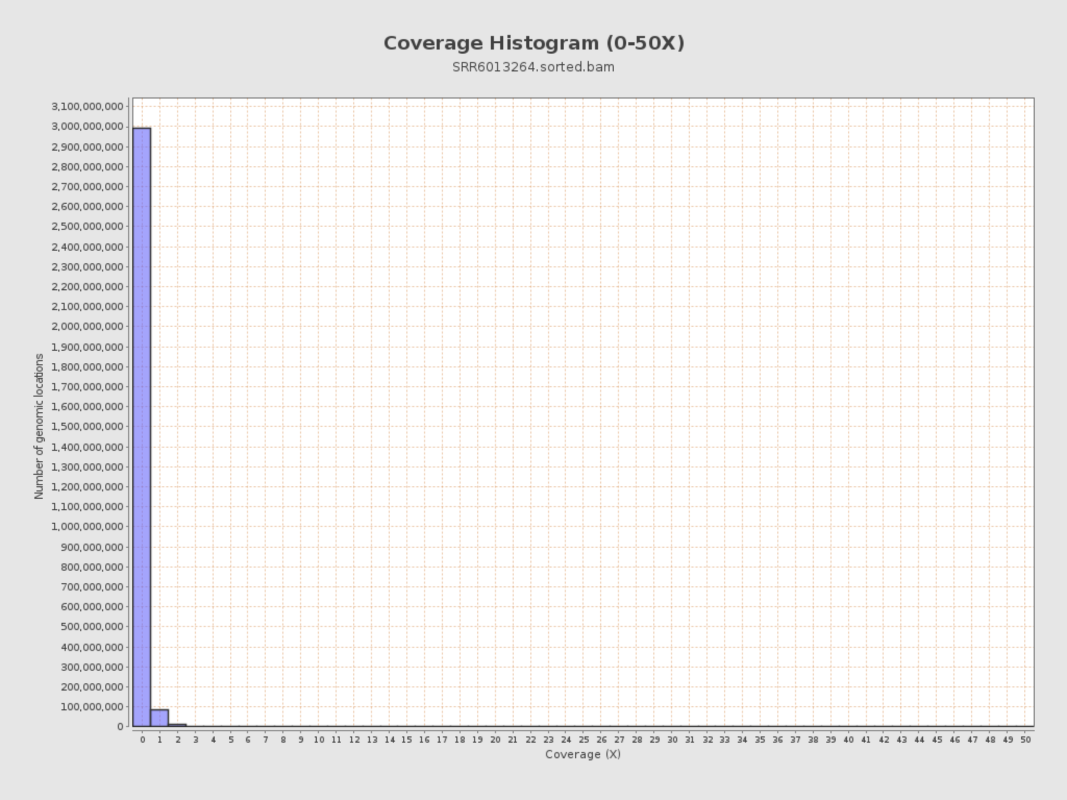
3. Results : Coverage across reference



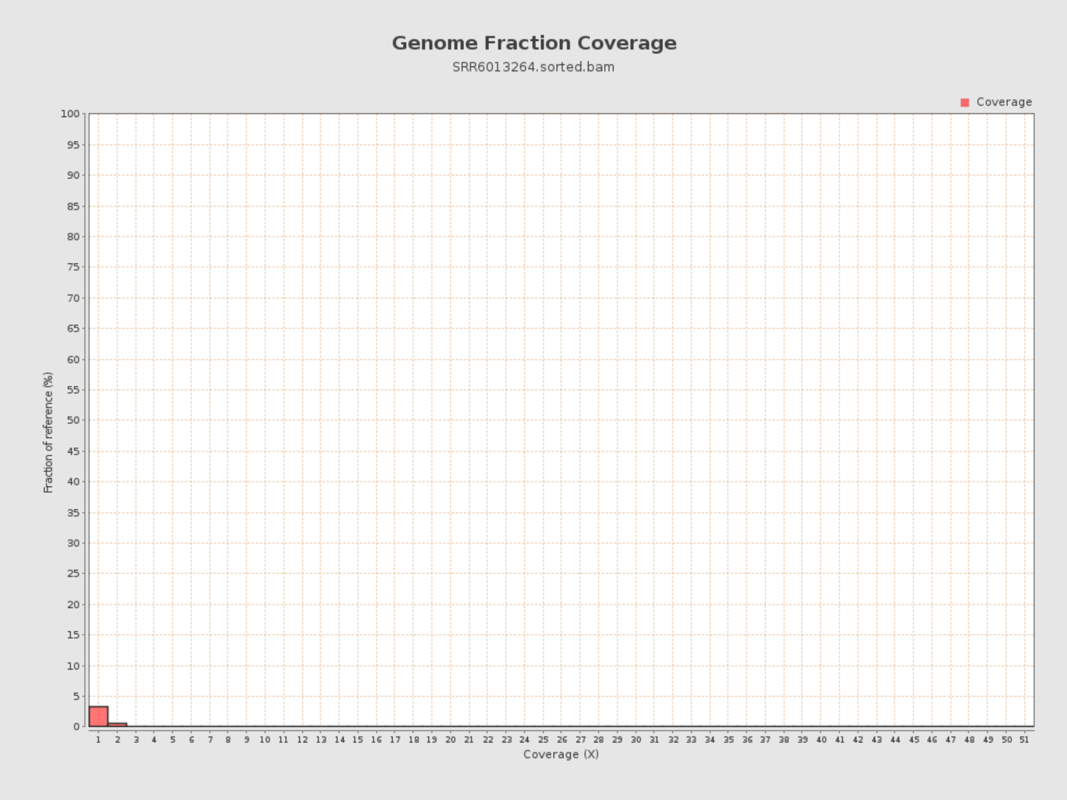
4. Results : Coverage Histogram



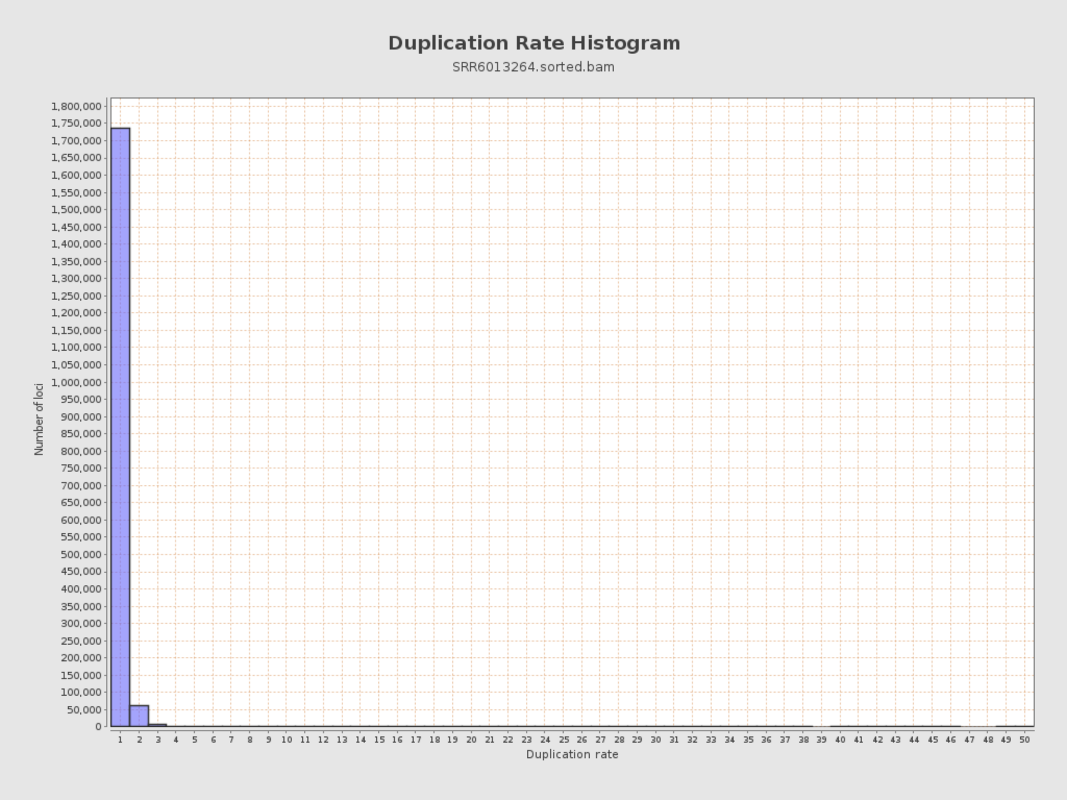
5. Results : Coverage Histogram (0-50X)



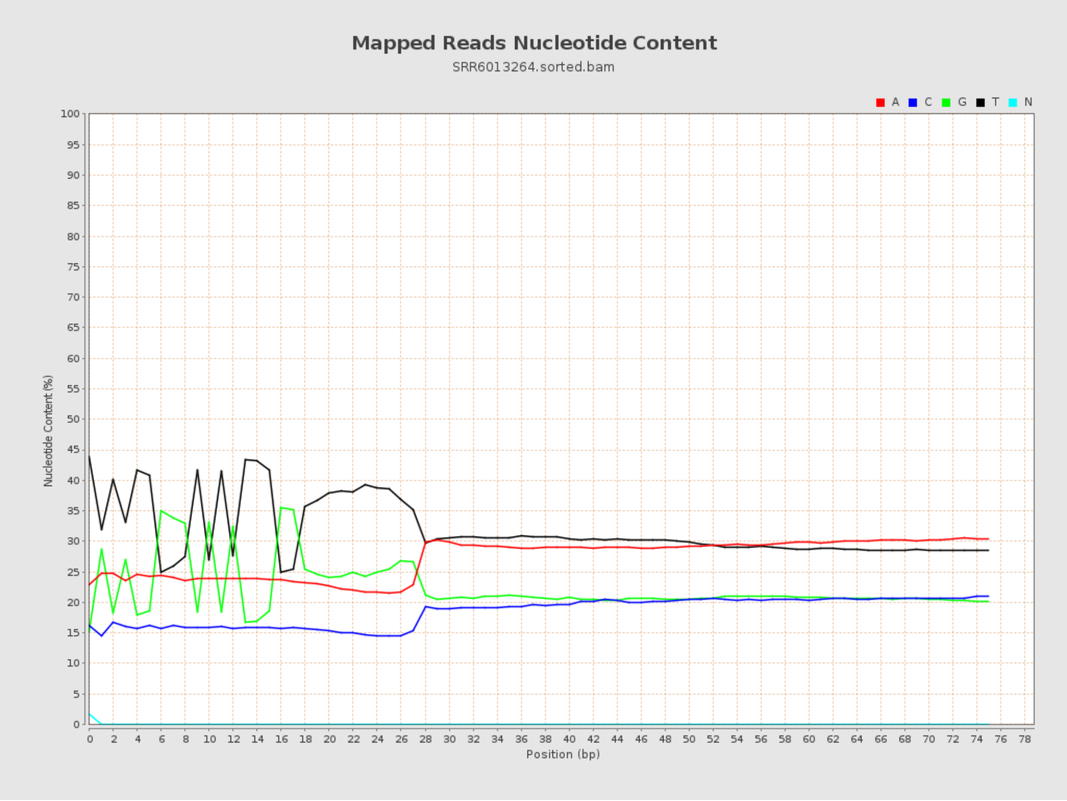
6. Results : Genome Fraction Coverage



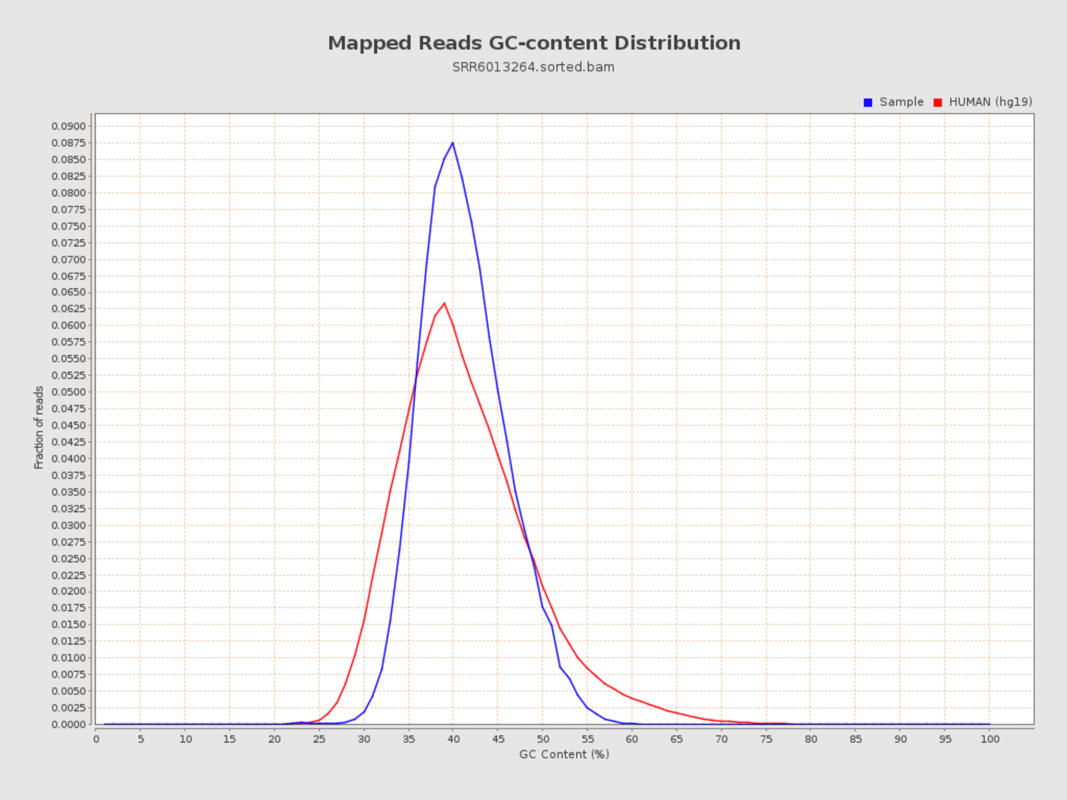
7. Results : Duplication Rate Histogram



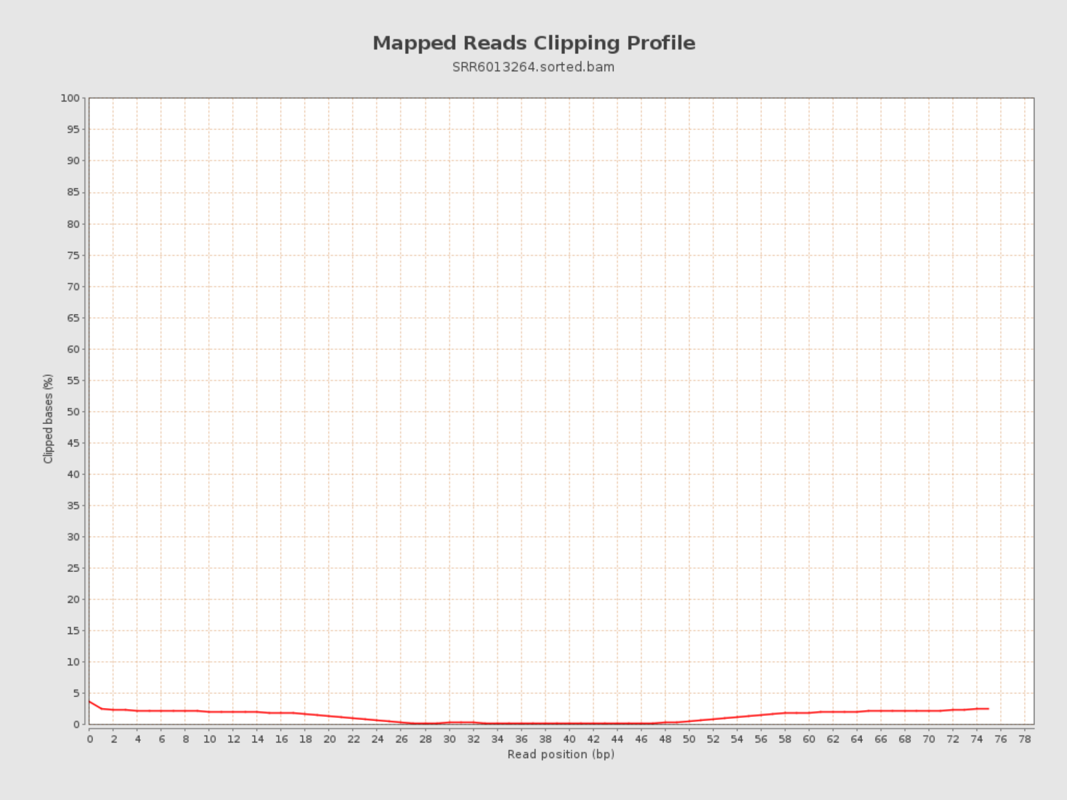
8. Results : Mapped Reads Nucleotide Content



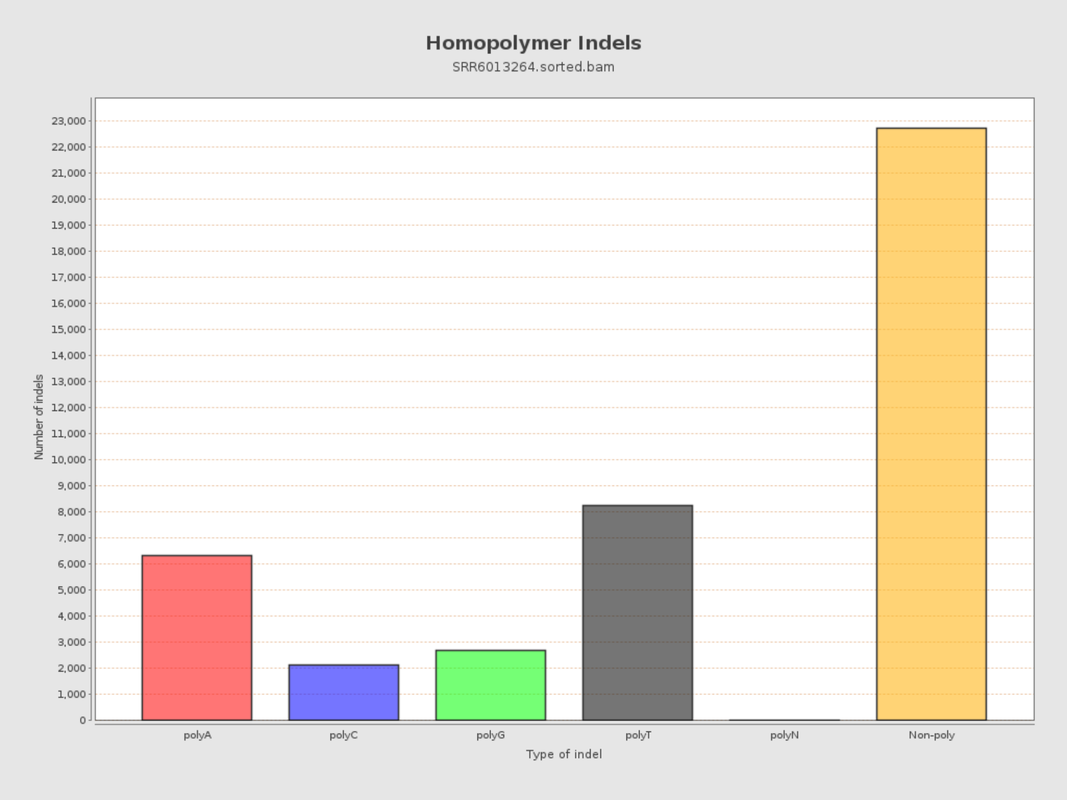
9. Results : Mapped Reads GC-content Distribution



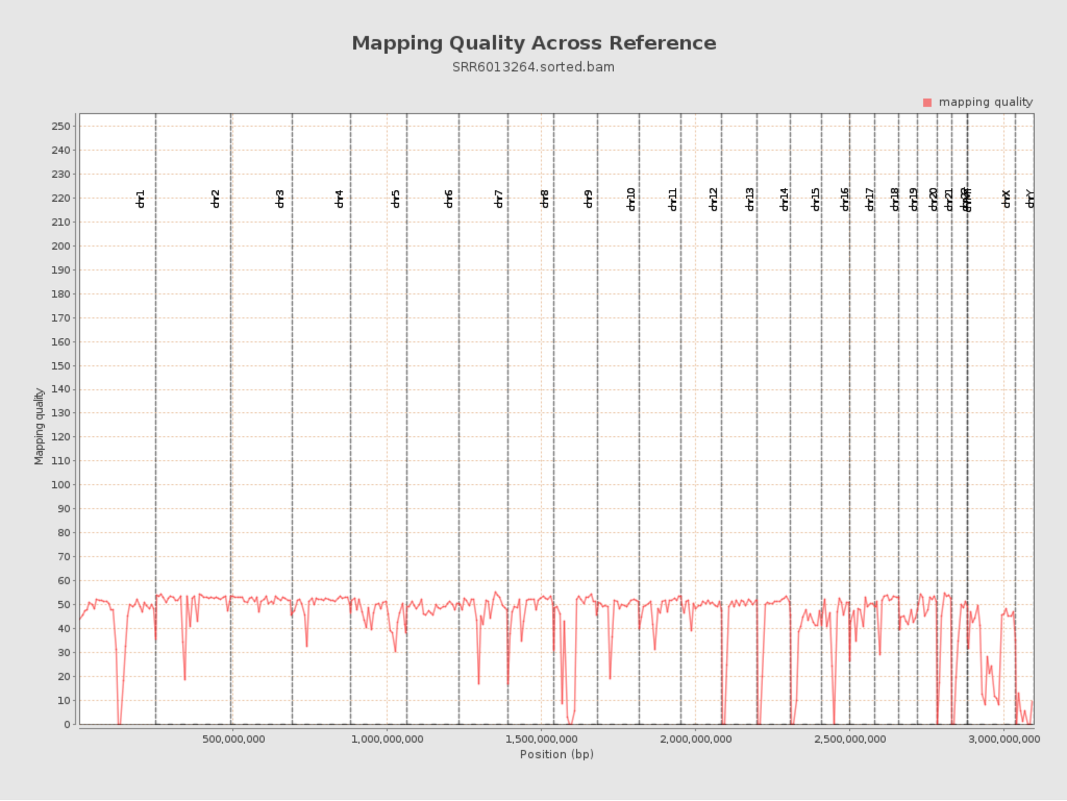
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram