Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 17:12:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013232.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_SRR6013232 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013232.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 17:12:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013232.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,018,210
Mapped reads	905,053 / 88.89%
Unmapped reads	113,157 / 11.11%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,537 / 0.54%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	29,781 / 2.92%
Duplication rate	2.41%
Clipped reads	328,530 / 32.27%

2.2. ACGT Content

Number/percentage of A's	18,037,675 / 29.03%
Number/percentage of C's	11,237,892 / 18.08%
Number/percentage of T's	19,976,515 / 32.15%
Number/percentage of G's	12,877,981 / 20.72%
Number/percentage of N's	14,096 / 0.02%
GC Percentage	38.81%

2.3. Coverage

Mean	0.0201

Standard Deviation	0.2473

2.4. Mapping Quality

Mean Mapping Quality	46.77

2.5. Mismatches and indels

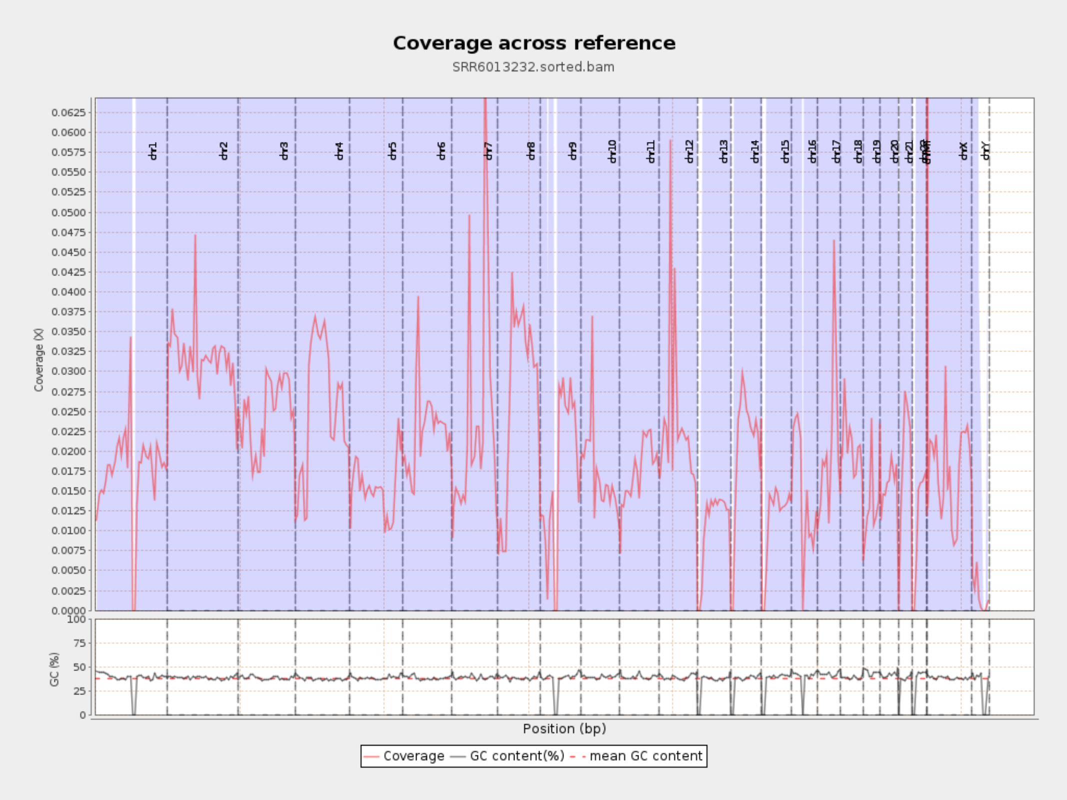
General error rate	0.83%
Mismatches	506,991
Insertions	4,924
Mapped reads with at least one insertion	0.54%
Deletions	15,274
Mapped reads with at least one deletion	1.67%
Homopolymer indels	47.64%

2.6. Chromosome stats

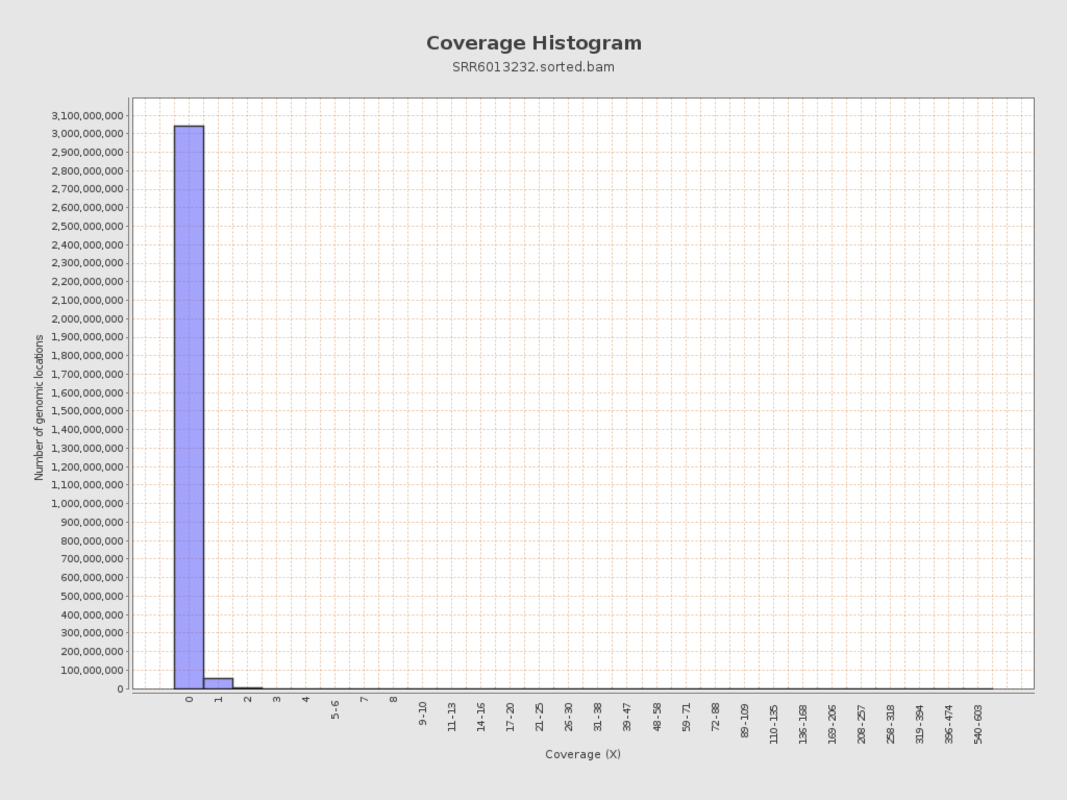
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4355059	0.0175	0.3921
chr2	243199373	7743289	0.0318	0.2767
chr3	198022430	4899368	0.0247	0.1669
chr4	191154276	4920904	0.0257	0.1791
chr5	180915260	2807286	0.0155	0.1323
chr6	171115067	3884165	0.0227	0.1987
chr7	159138663	3825029	0.024	0.4364

chr8	146364022	4039506	0.0276	0.3974
chr9	141213431	2431382	0.0172	0.2165
chr10	135534747	2356650	0.0174	0.254
chr11	135006516	2380804	0.0176	0.1713
chr12	133851895	3157589	0.0236	0.1668
chr13	115169878	1234791	0.0107	0.11
chr14	107349540	2177695	0.0203	0.1569
chr15	102531392	1151556	0.0112	0.1128
chr16	90354753	1281542	0.0142	0.1435
chr17	81195210	1705622	0.021	0.1621
chr18	78077248	1610714	0.0206	0.4104
chr19	59128983	794262	0.0134	0.2807
chr20	63025520	991104	0.0157	0.1384
chr21	48129895	919637	0.0191	0.1558
chr22	51304566	573058	0.0112	0.1113
chrMT	16571	22559	1.3614	1.45
chrX	155270560	2794173	0.018	0.1548
chrY	59373566	113022	0.0019	0.0664

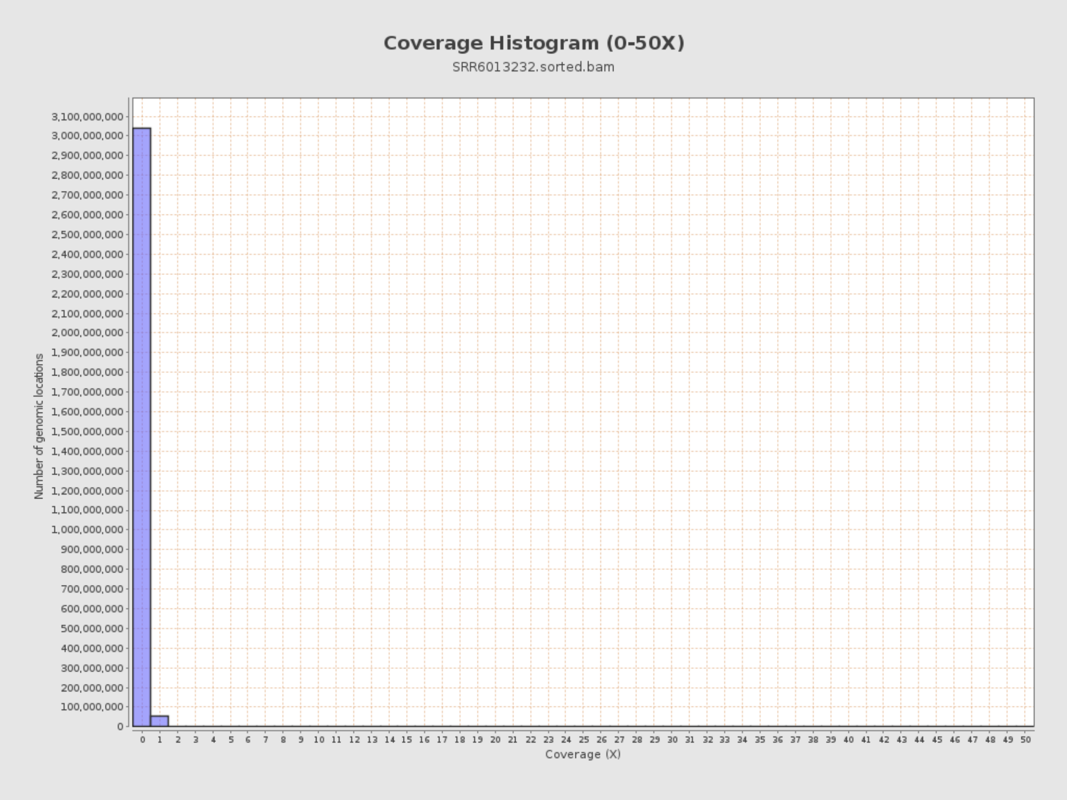
3. Results : Coverage across reference



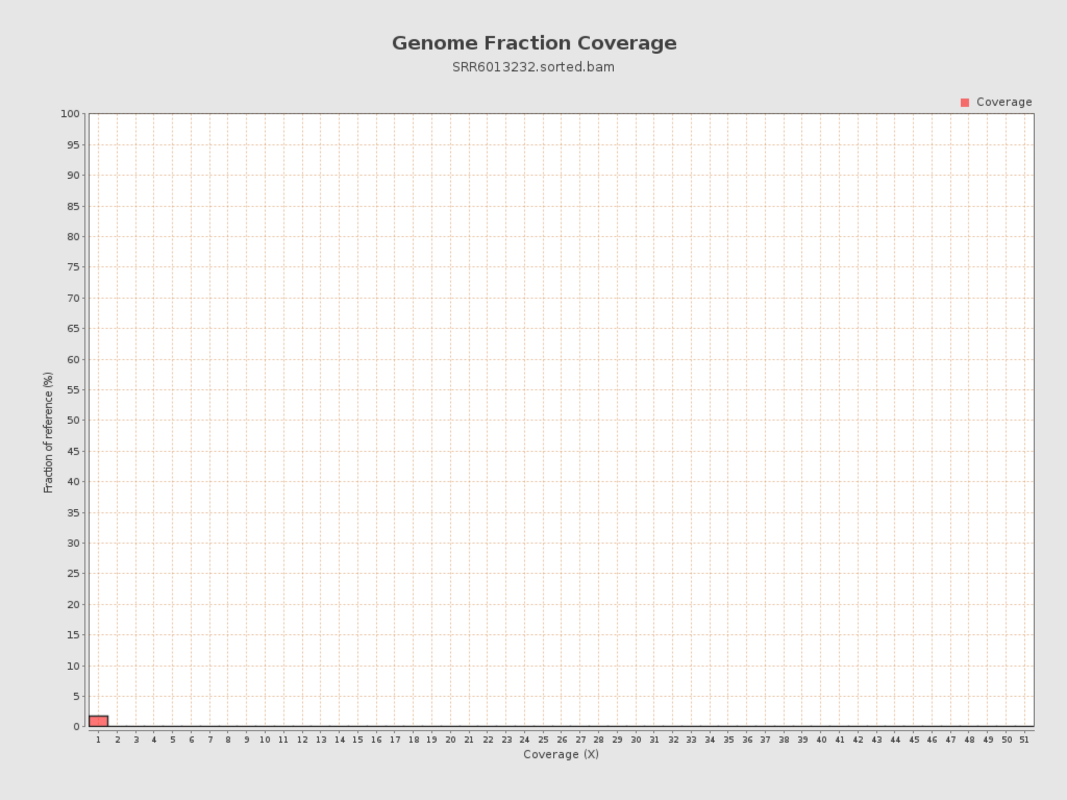
4. Results : Coverage Histogram



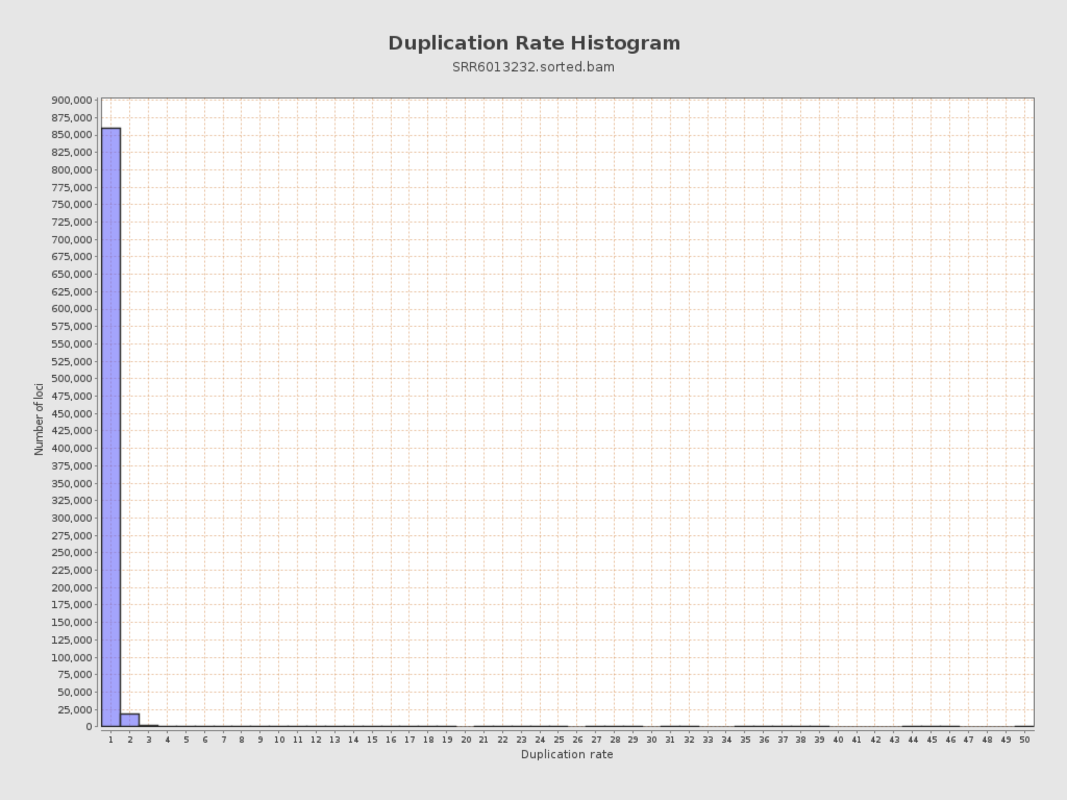
5. Results : Coverage Histogram (0-50X)



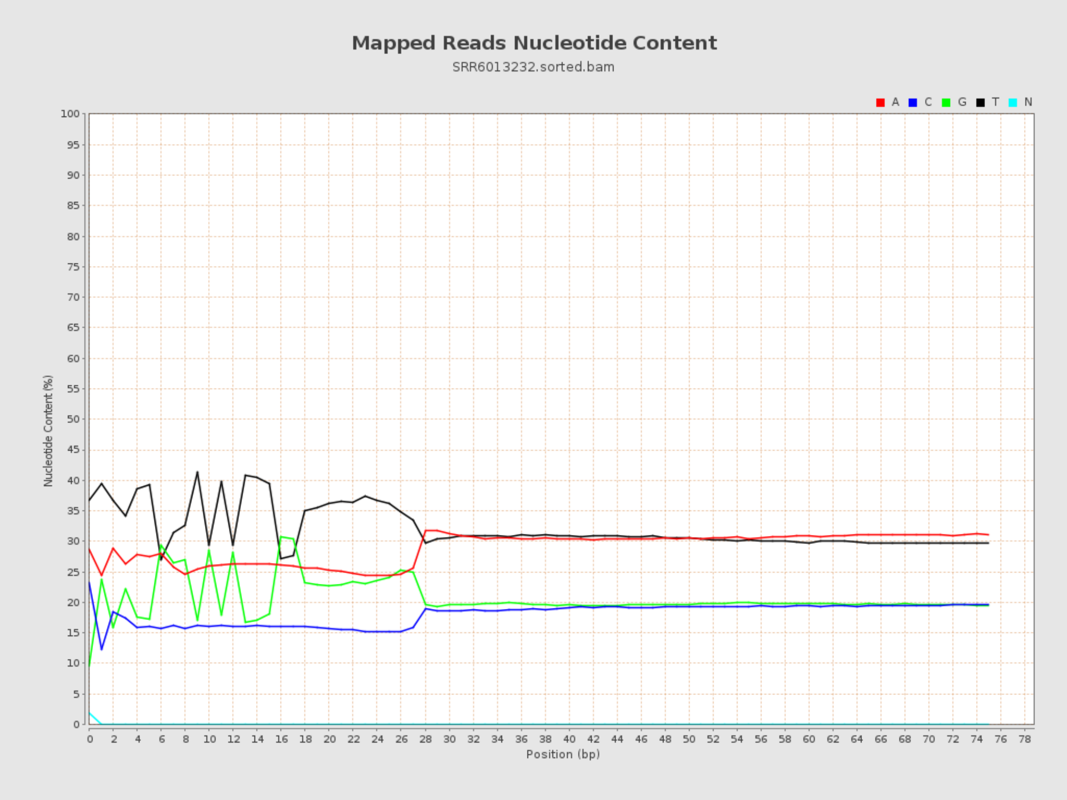
6. Results : Genome Fraction Coverage



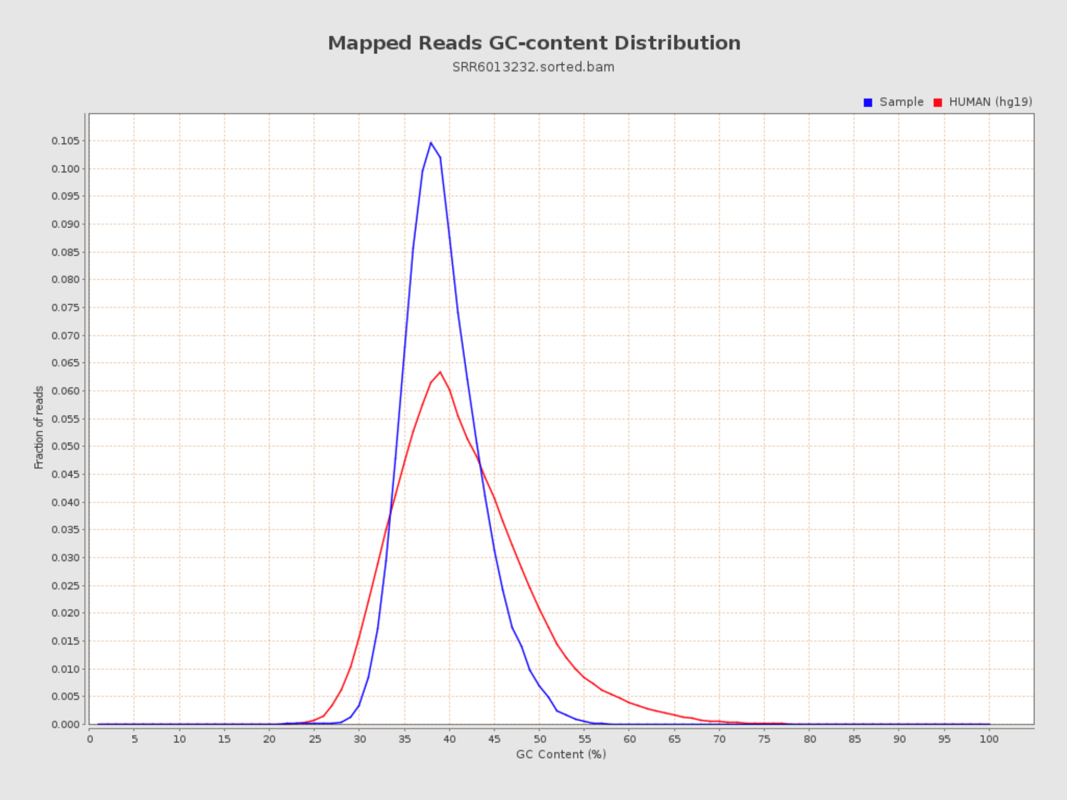
7. Results : Duplication Rate Histogram



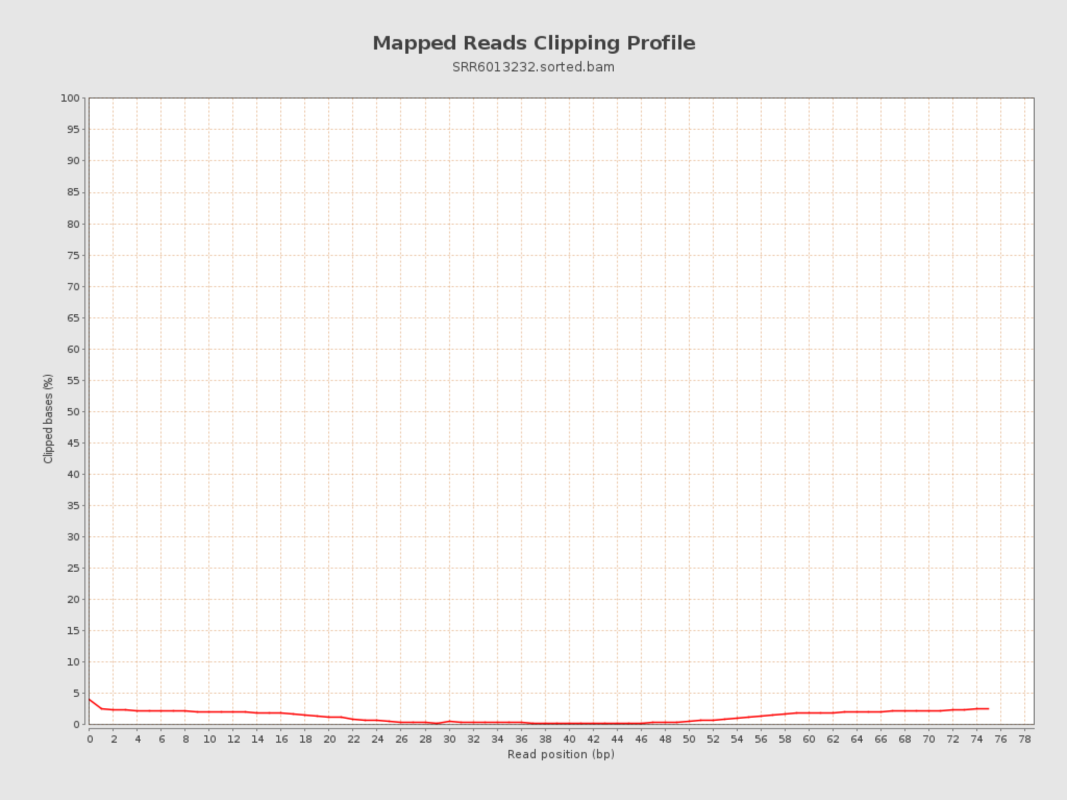
8. Results : Mapped Reads Nucleotide Content



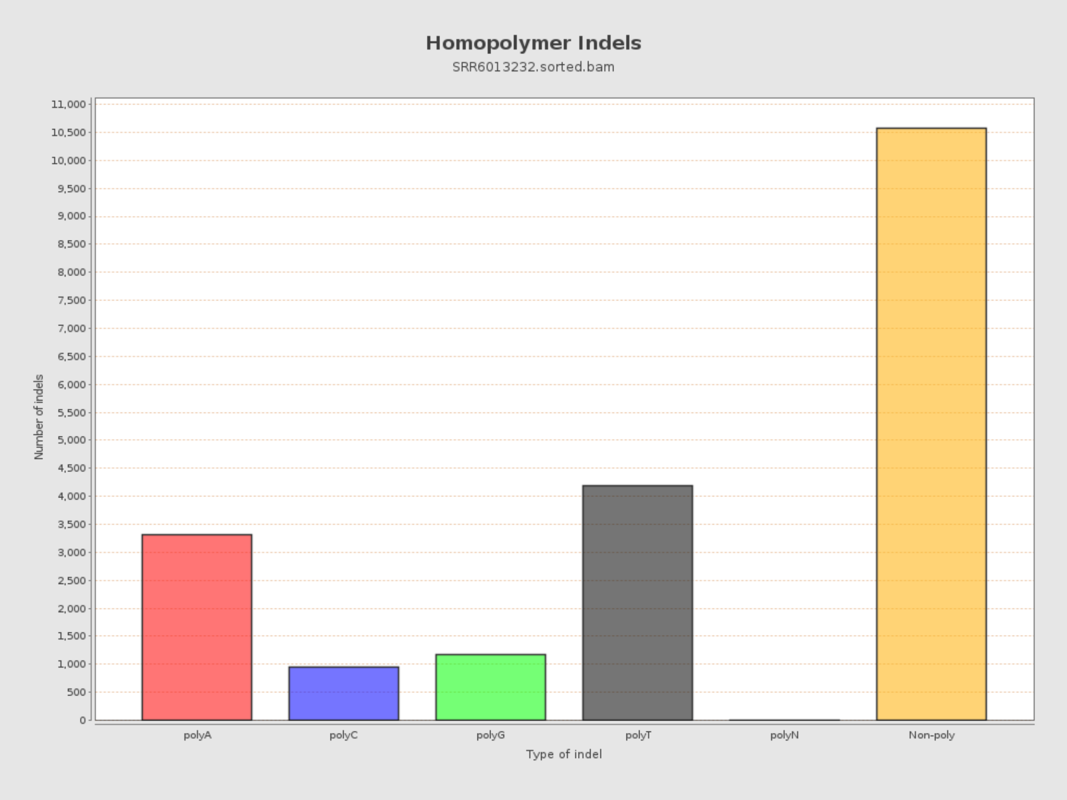
9. Results : Mapped Reads GC-content Distribution



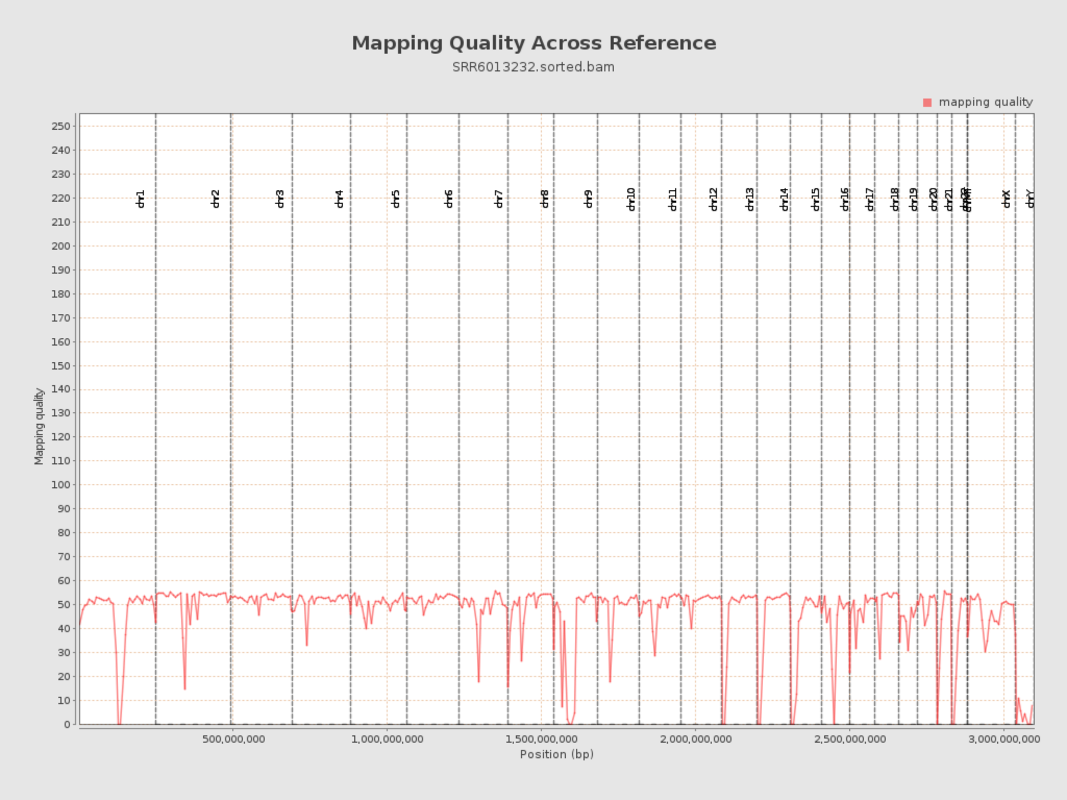
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram