Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 16:35:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013219.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_SRR6013219 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013219.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 16:35:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013219.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,009,324
Mapped reads	884,820 / 87.66%
Unmapped reads	124,504 / 12.34%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,395 / 0.53%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	26,984 / 2.67%
Duplication rate	1.84%
Clipped reads	335,450 / 33.24%

2.2. ACGT Content

Number/percentage of A's	17,365,940 / 28.83%
Number/percentage of C's	10,997,649 / 18.26%
Number/percentage of T's	19,007,641 / 31.56%
Number/percentage of G's	12,863,459 / 21.36%
Number/percentage of N's	897 / 0%
GC Percentage	39.61%

2.3. Coverage

Mean	0.0195

Standard Deviation	0.2926

2.4. Mapping Quality

Mean Mapping Quality	46.21

2.5. Mismatches and indels

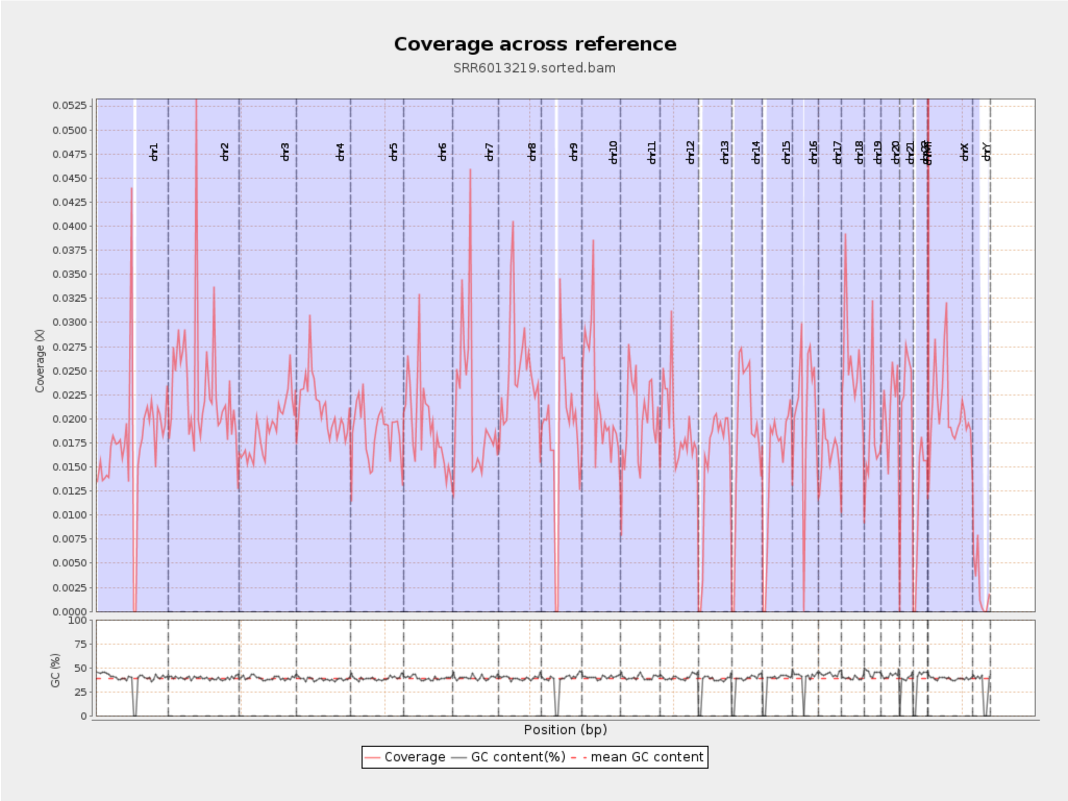
General error rate	0.79%
Mismatches	466,274
Insertions	4,926
Mapped reads with at least one insertion	0.55%
Deletions	14,497
Mapped reads with at least one deletion	1.62%
Homopolymer indels	46.94%

2.6. Chromosome stats

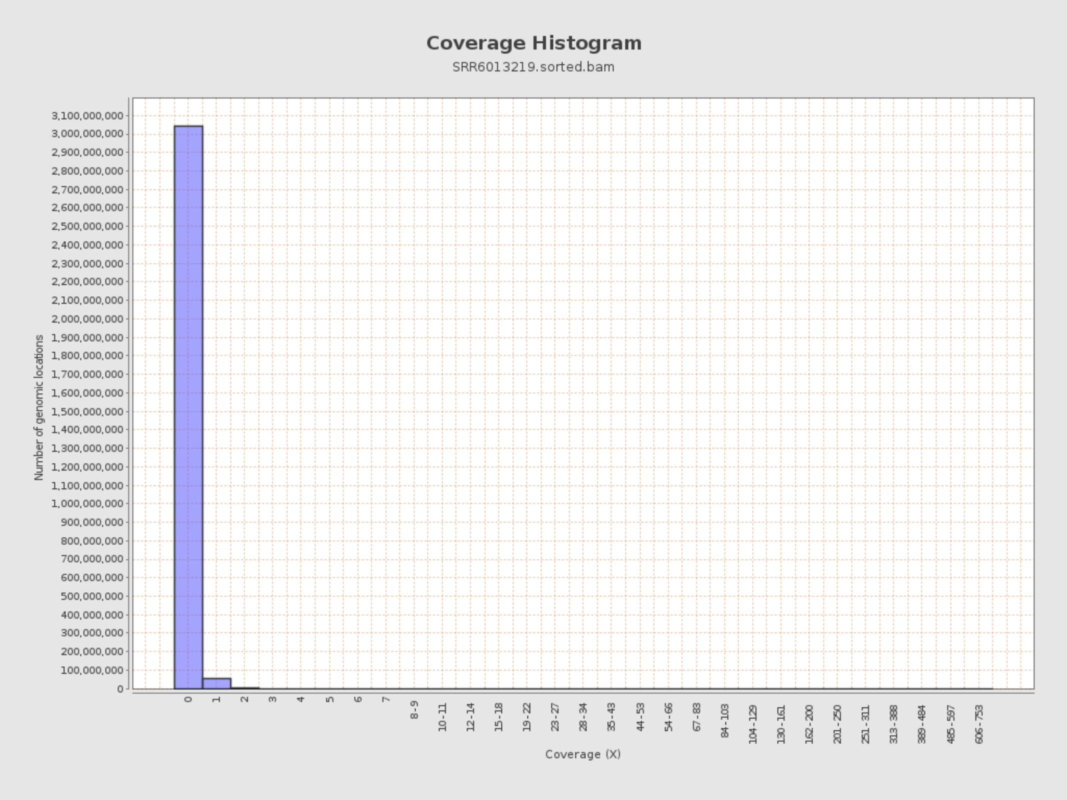
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4318830	0.0173	0.6414
chr2	243199373	5629085	0.0231	0.3055
chr3	198022430	3744676	0.0189	0.1442
chr4	191154276	4038792	0.0211	0.1607
chr5	180915260	3388828	0.0187	0.1469
chr6	171115067	3307906	0.0193	0.1795
chr7	159138663	3331930	0.0209	0.3801

chr8	146364022	3632328	0.0248	0.3734
chr9	141213431	2629447	0.0186	0.2674
chr10	135534747	2990057	0.0221	0.2273
chr11	135006516	2709006	0.0201	0.2152
chr12	133851895	2587817	0.0193	0.1525
chr13	115169878	1767630	0.0153	0.129
chr14	107349540	1998794	0.0186	0.1582
chr15	102531392	1572551	0.0153	0.1319
chr16	90354753	1838727	0.0204	0.1782
chr17	81195210	1322317	0.0163	0.1541
chr18	78077248	1996613	0.0256	0.532
chr19	59128983	1090762	0.0184	0.3966
chr20	63025520	1321208	0.021	0.1605
chr21	48129895	1034692	0.0215	0.1644
chr22	51304566	587420	0.0114	0.1113
chrMT	16571	4427	0.2672	0.5269
chrX	155270560	3269478	0.0211	0.1789
chrY	59373566	147690	0.0025	0.073

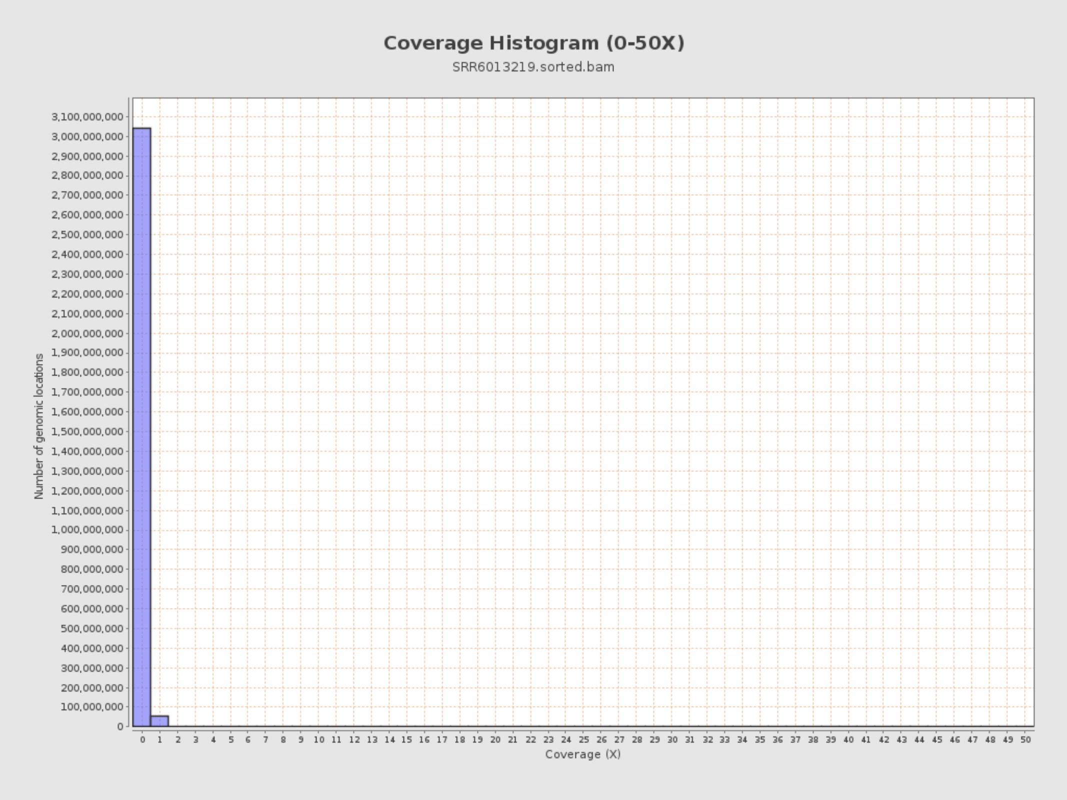
3. Results : Coverage across reference



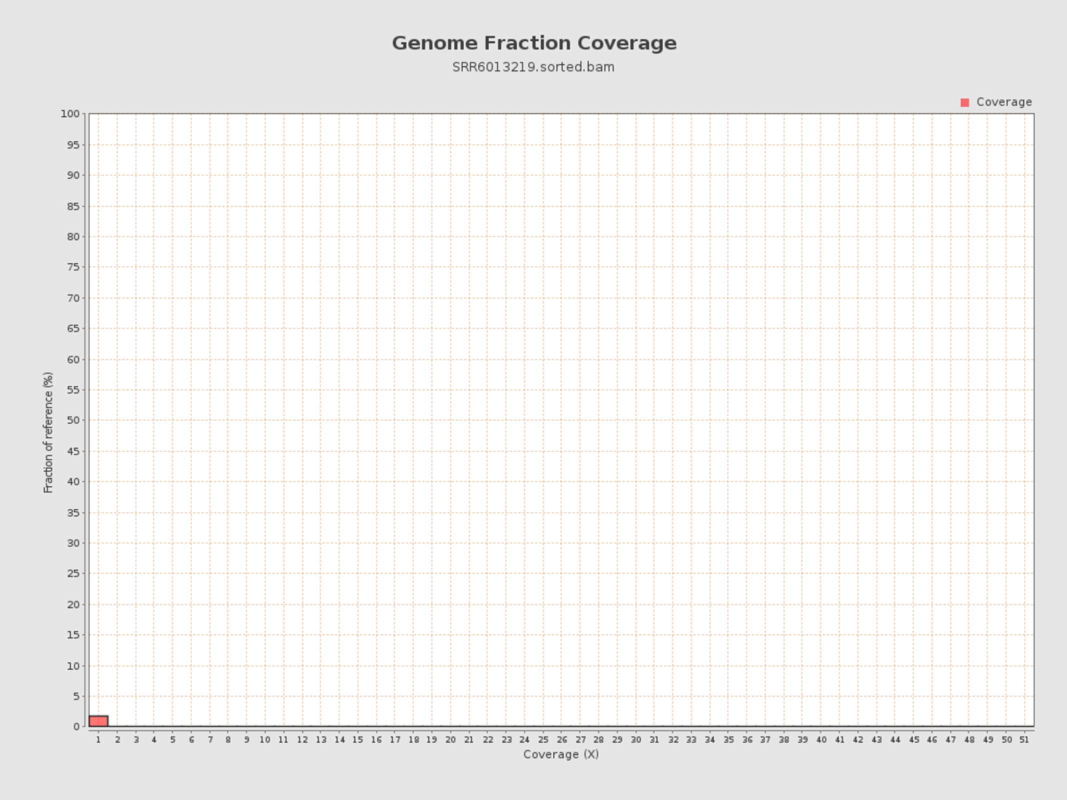
4. Results : Coverage Histogram



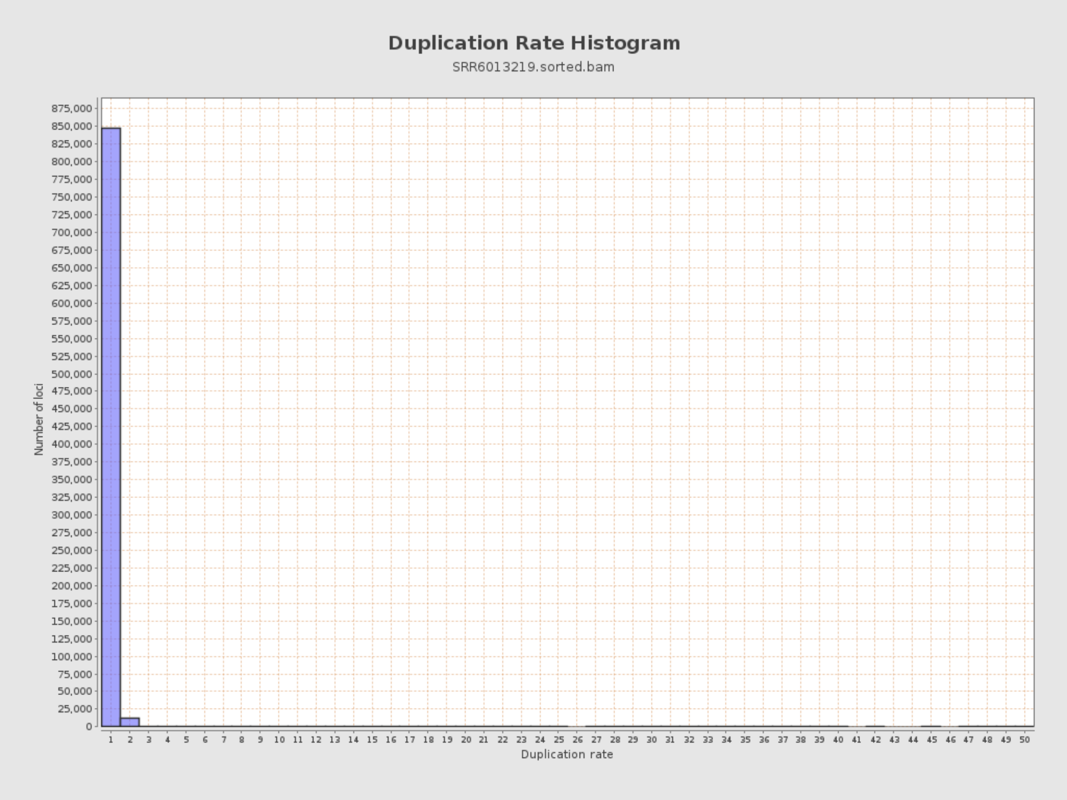
5. Results : Coverage Histogram (0-50X)



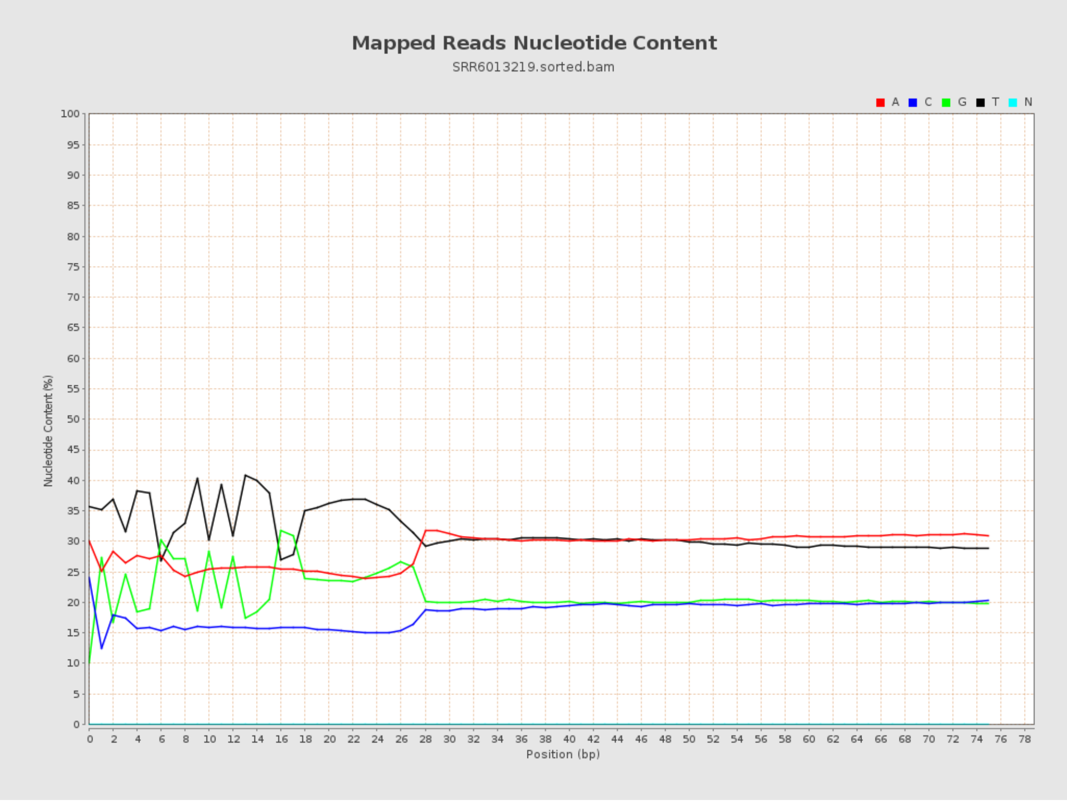
6. Results : Genome Fraction Coverage



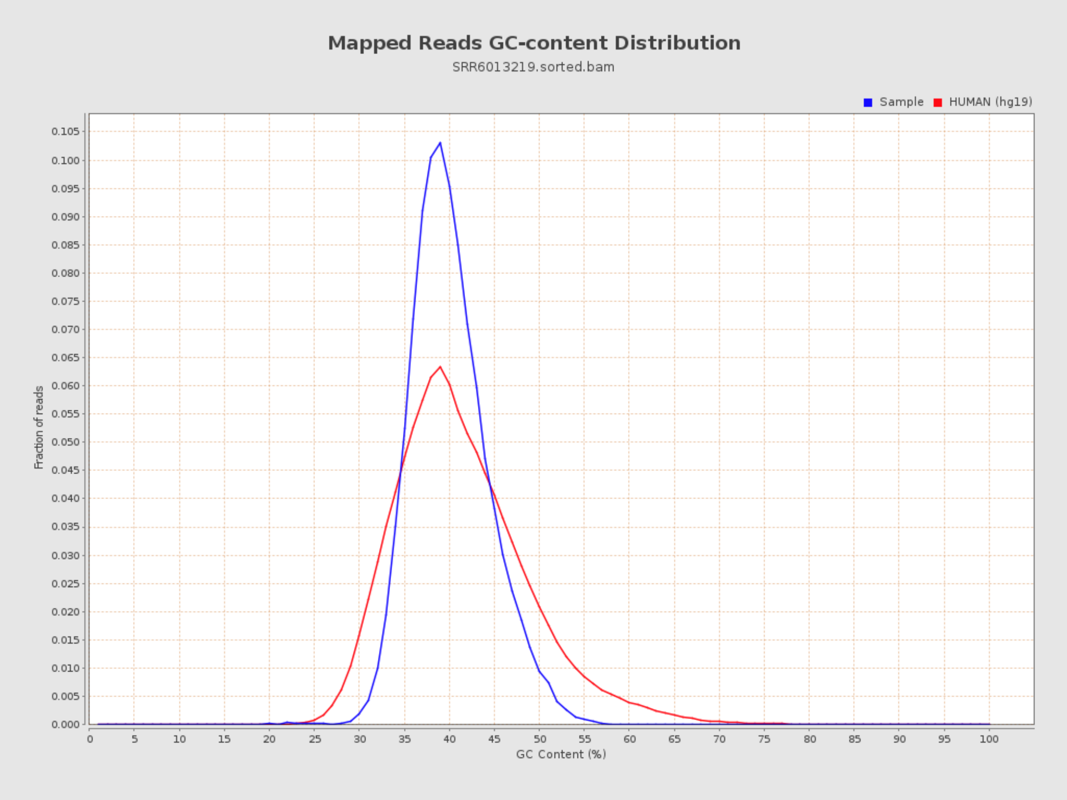
7. Results : Duplication Rate Histogram



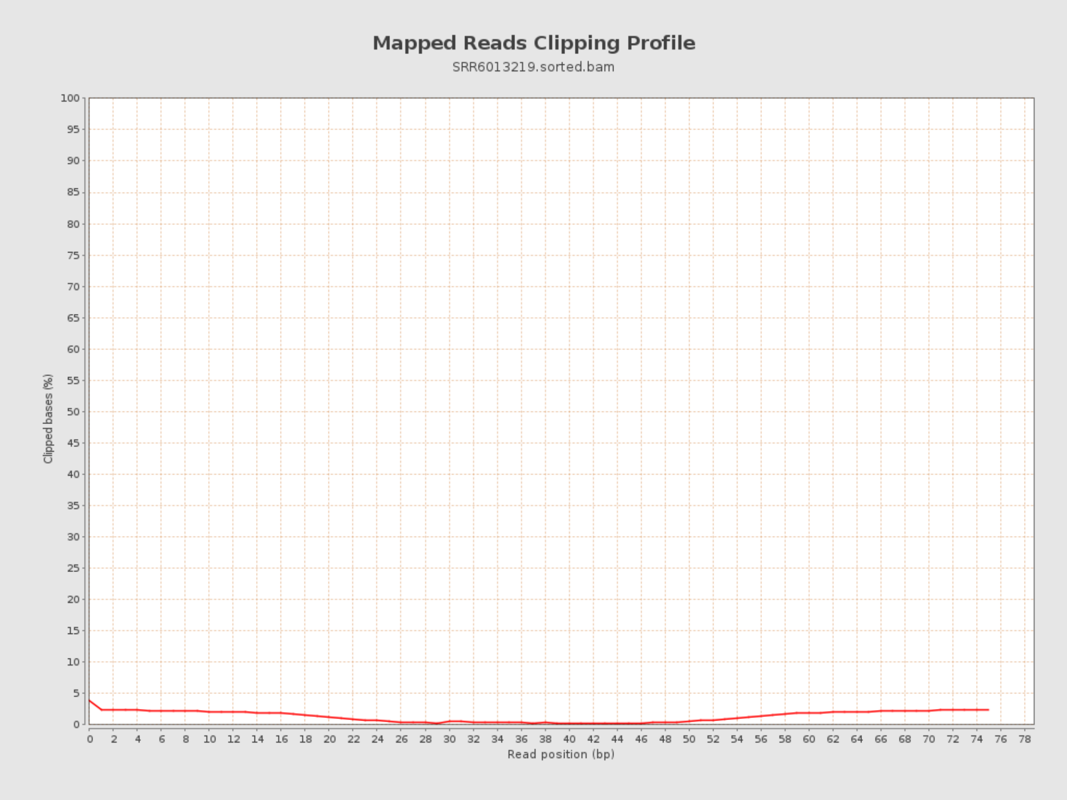
8. Results : Mapped Reads Nucleotide Content



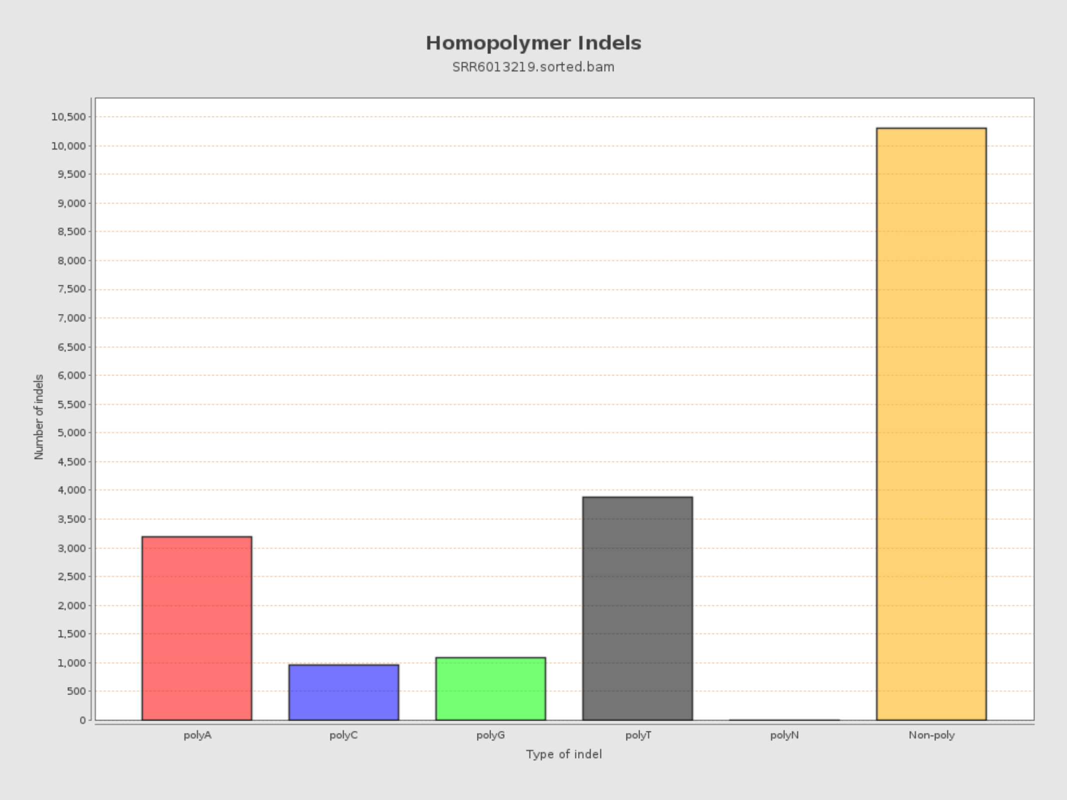
9. Results : Mapped Reads GC-content Distribution



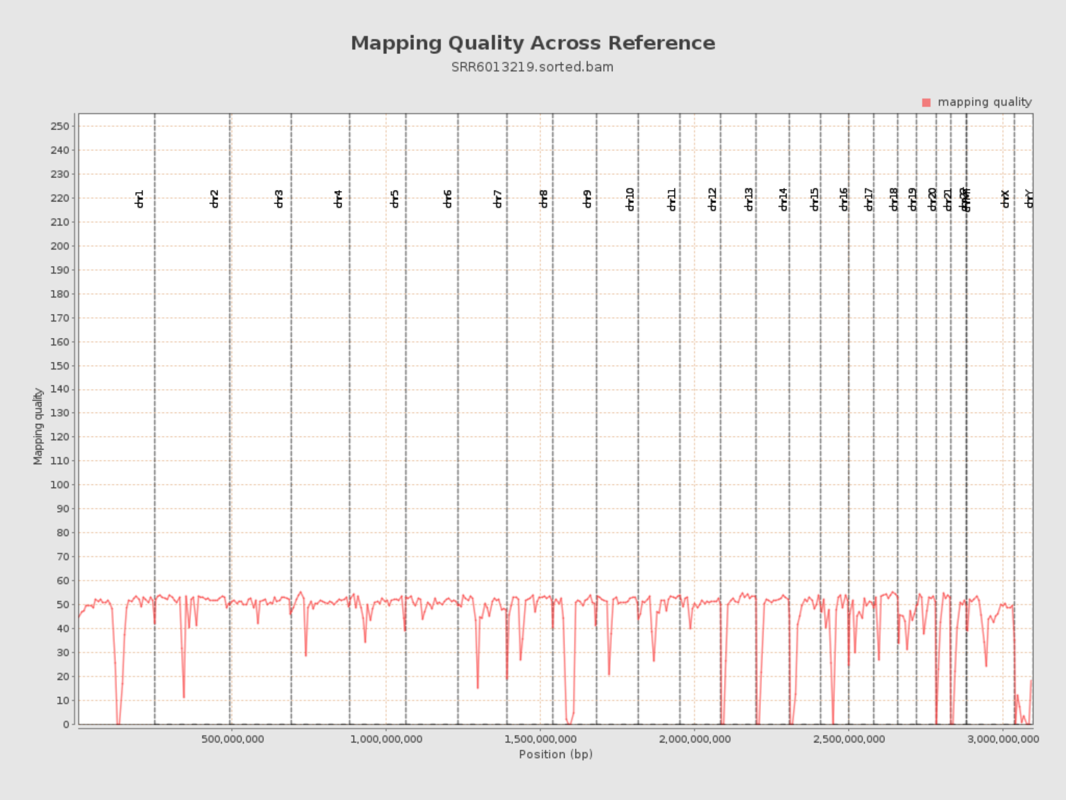
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram