Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 18:01:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013251.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_SRR6013251 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013251.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 18:01:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013251.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,387,093
Mapped reads	1,069,474 / 77.1%
Unmapped reads	317,619 / 22.9%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,692 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	30,153 / 2.17%
Duplication rate	2.48%
Clipped reads	554,887 / 40%

2.2. ACGT Content

Number/percentage of A's	21,054,106 / 30.43%
Number/percentage of C's	11,368,830 / 16.43%
Number/percentage of T's	21,749,851 / 31.44%
Number/percentage of G's	14,981,088 / 21.66%
Number/percentage of N's	25,646 / 0.04%
GC Percentage	38.09%

2.3. Coverage

Mean	0.0224

Standard Deviation	0.1866

2.4. Mapping Quality

Mean Mapping Quality	48.5

2.5. Mismatches and indels

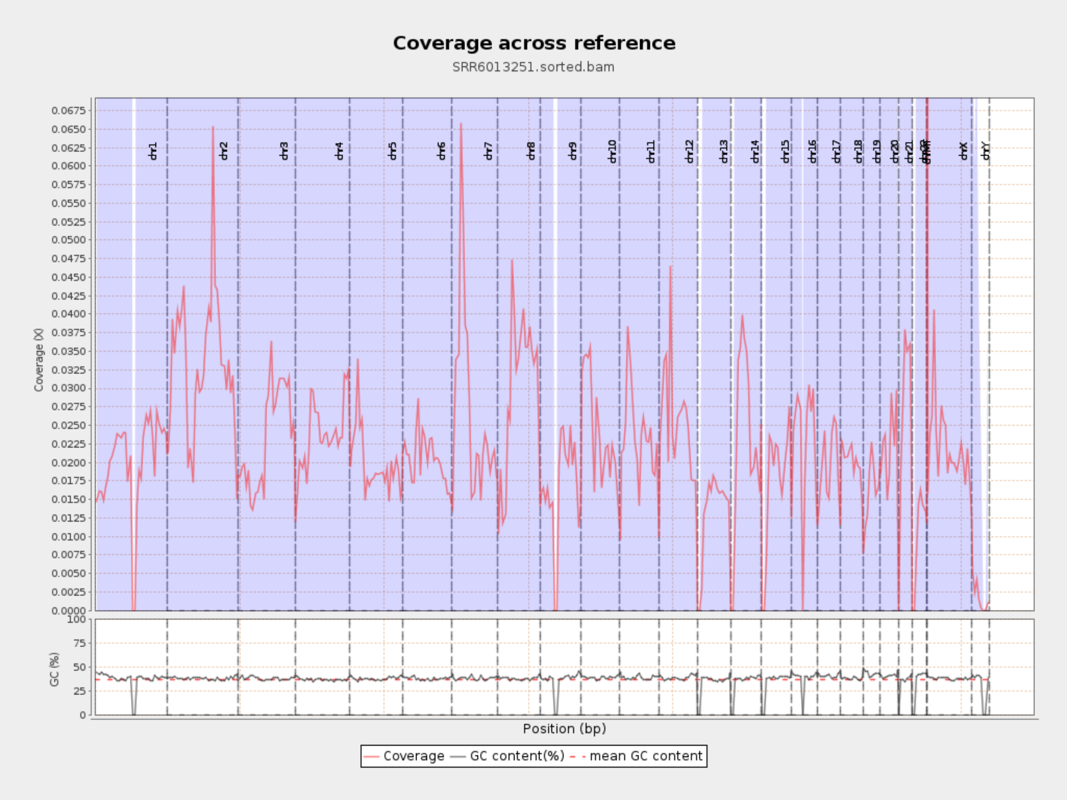
General error rate	1.06%
Mismatches	725,517
Insertions	4,335
Mapped reads with at least one insertion	0.4%
Deletions	19,945
Mapped reads with at least one deletion	1.85%
Homopolymer indels	49.76%

2.6. Chromosome stats

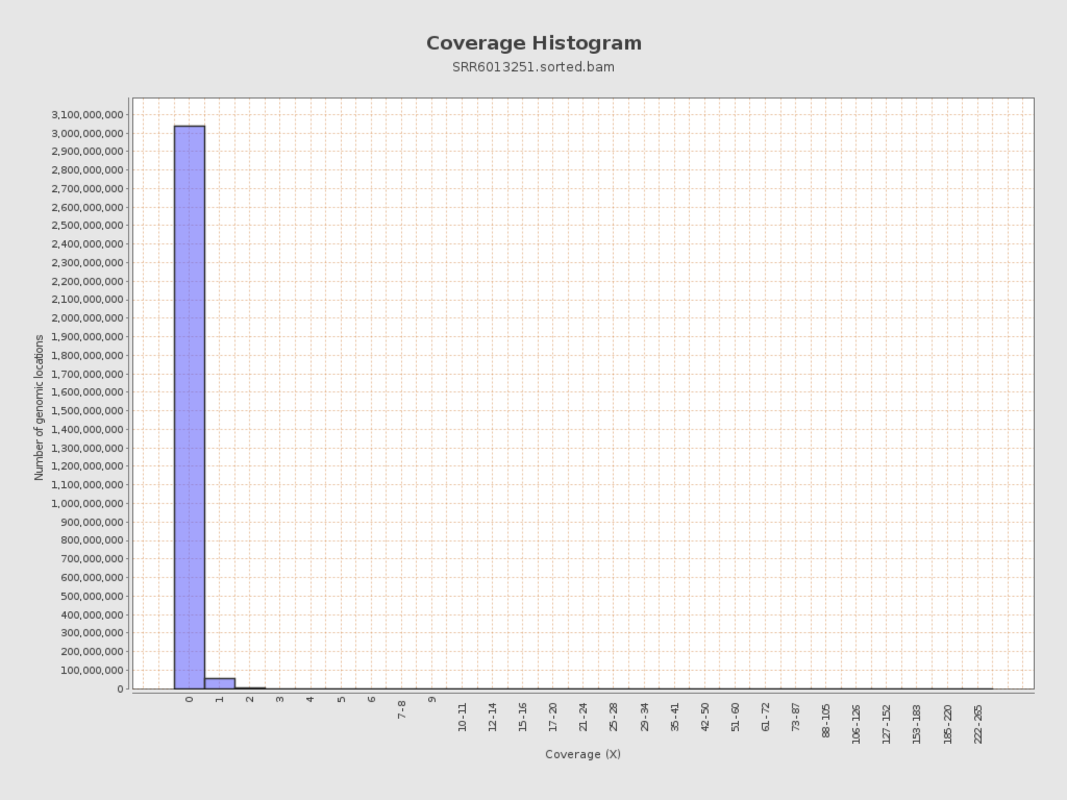
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4959532	0.0199	0.2346
chr2	243199373	8213253	0.0338	0.2185
chr3	198022430	4621300	0.0233	0.1703
chr4	191154276	4527757	0.0237	0.1732
chr5	180915260	3595681	0.0199	0.1579
chr6	171115067	3522583	0.0206	0.1717
chr7	159138663	4313700	0.0271	0.2375

chr8	146364022	4442238	0.0304	0.2531
chr9	141213431	2335029	0.0165	0.1529
chr10	135534747	3288202	0.0243	0.1873
chr11	135006516	3162145	0.0234	0.181
chr12	133851895	3452161	0.0258	0.1802
chr13	115169878	1513639	0.0131	0.1271
chr14	107349540	2491084	0.0232	0.172
chr15	102531392	1778641	0.0173	0.1475
chr16	90354753	2030516	0.0225	0.1698
chr17	81195210	1584379	0.0195	0.1611
chr18	78077248	1595888	0.0204	0.2163
chr19	59128983	975458	0.0165	0.1655
chr20	63025520	1398213	0.0222	0.1679
chr21	48129895	1316302	0.0273	0.1898
chr22	51304566	532163	0.0104	0.1128
chrMT	16571	9419	0.5684	0.9549
chrX	155270560	3450035	0.0222	0.1715
chrY	59373566	102779	0.0017	0.0456

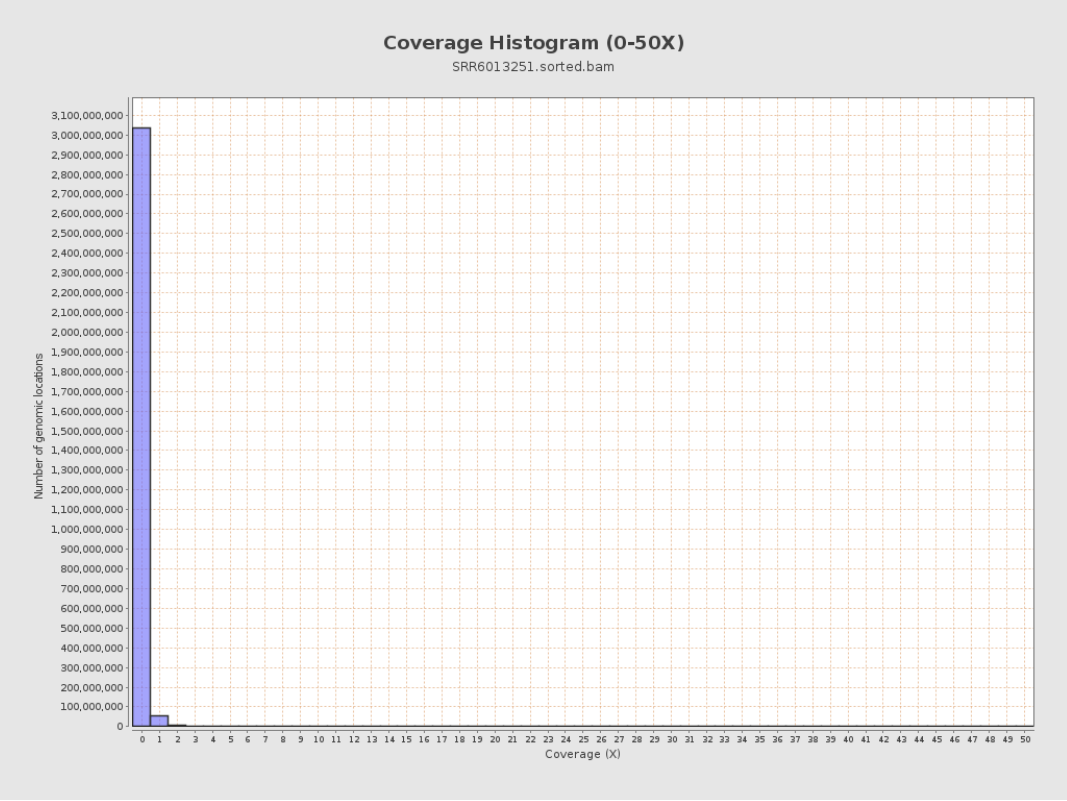
3. Results : Coverage across reference



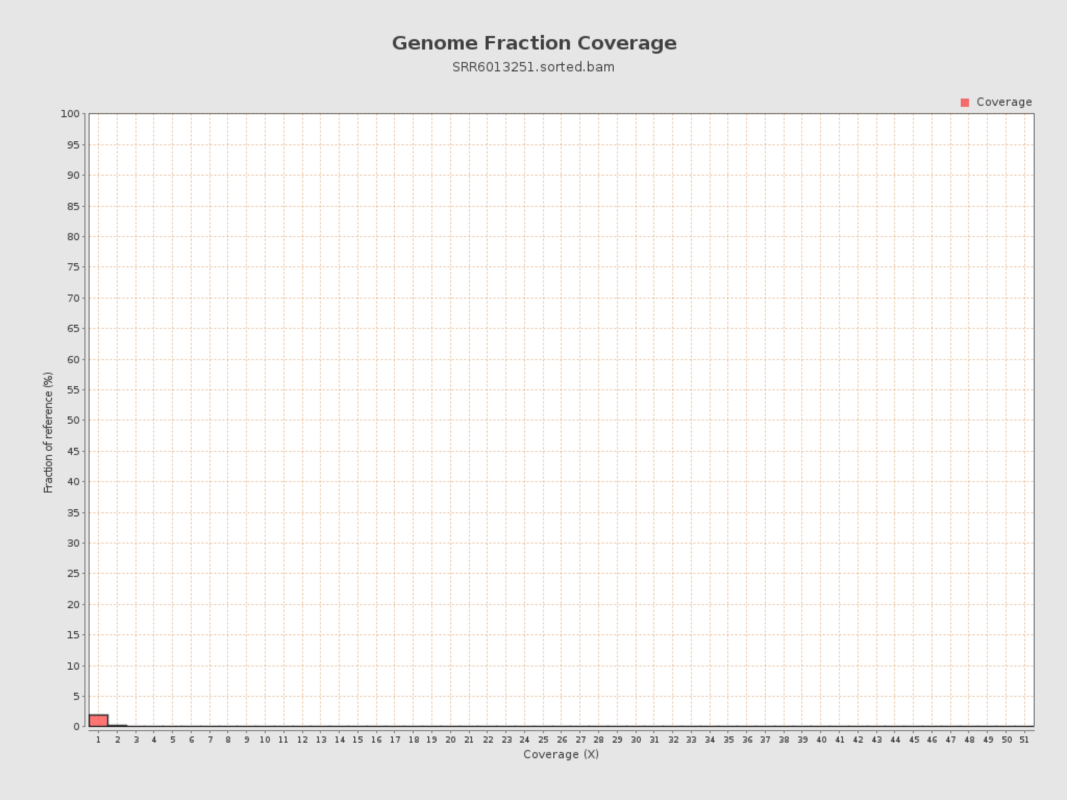
4. Results : Coverage Histogram



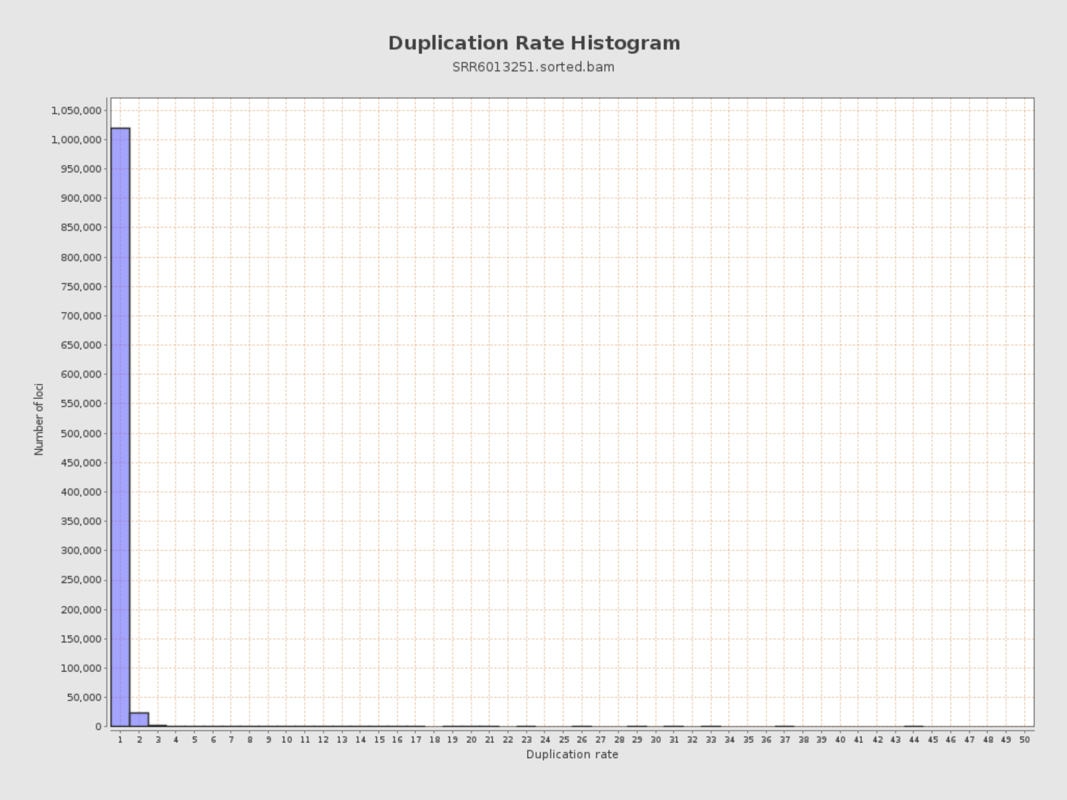
5. Results : Coverage Histogram (0-50X)



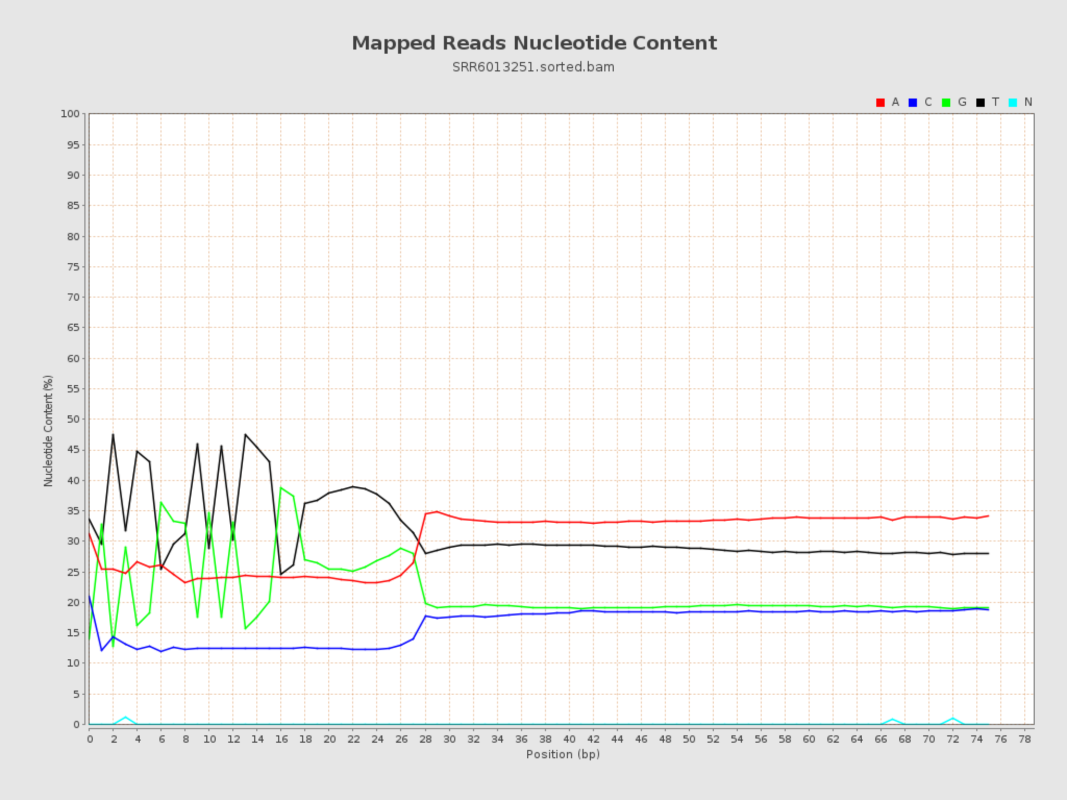
6. Results : Genome Fraction Coverage



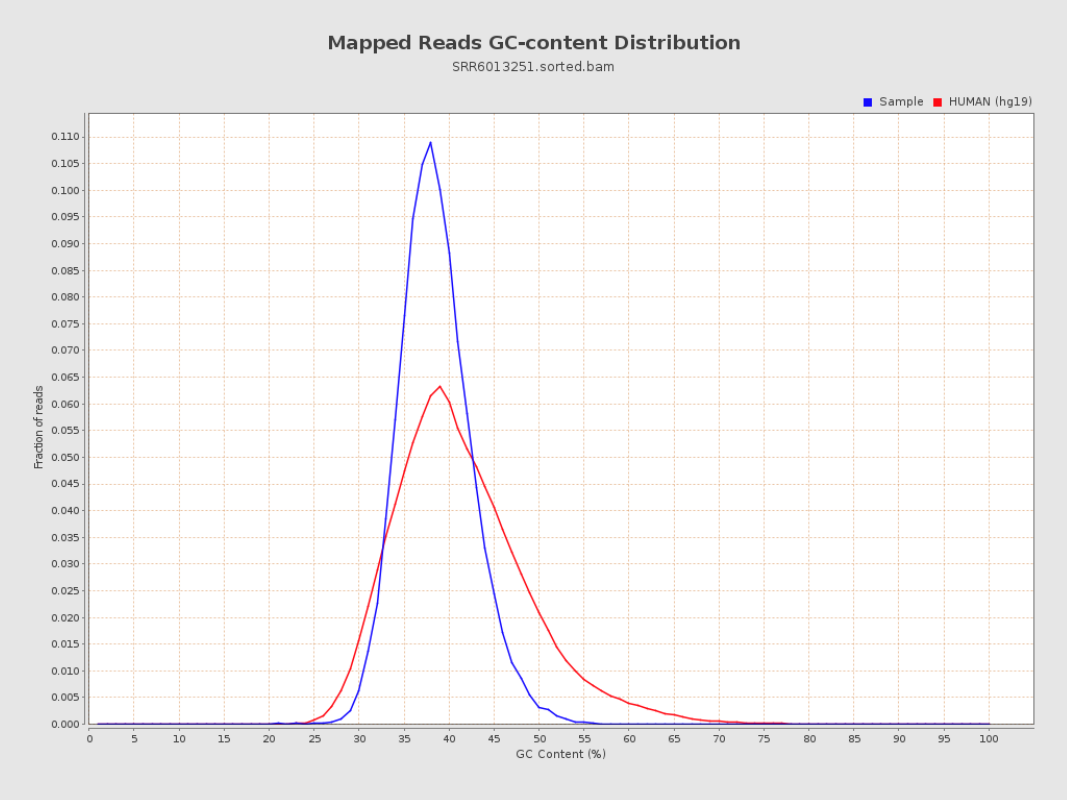
7. Results : Duplication Rate Histogram



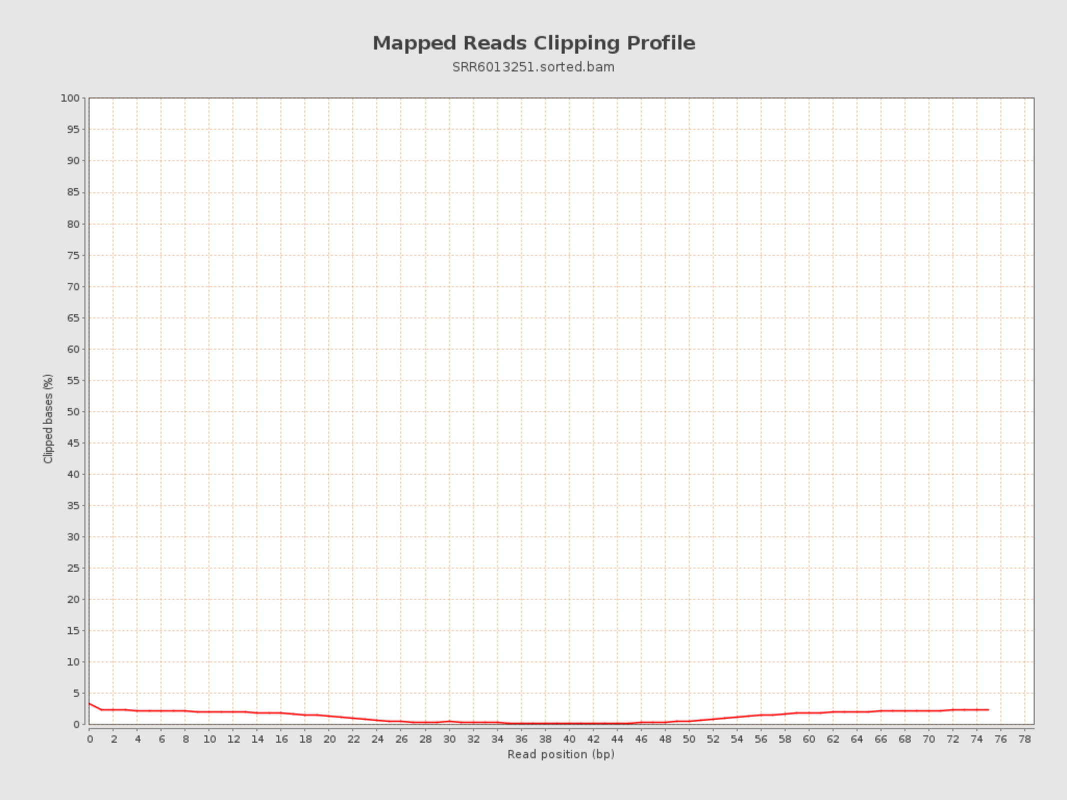
8. Results : Mapped Reads Nucleotide Content



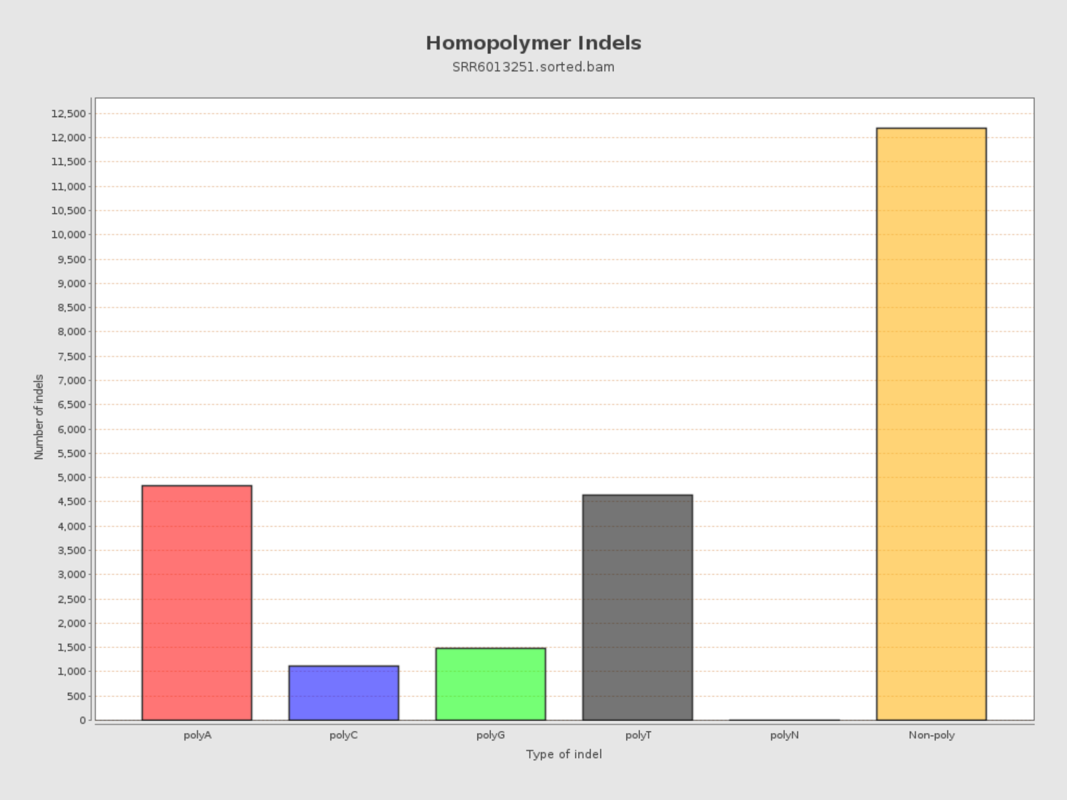
9. Results : Mapped Reads GC-content Distribution



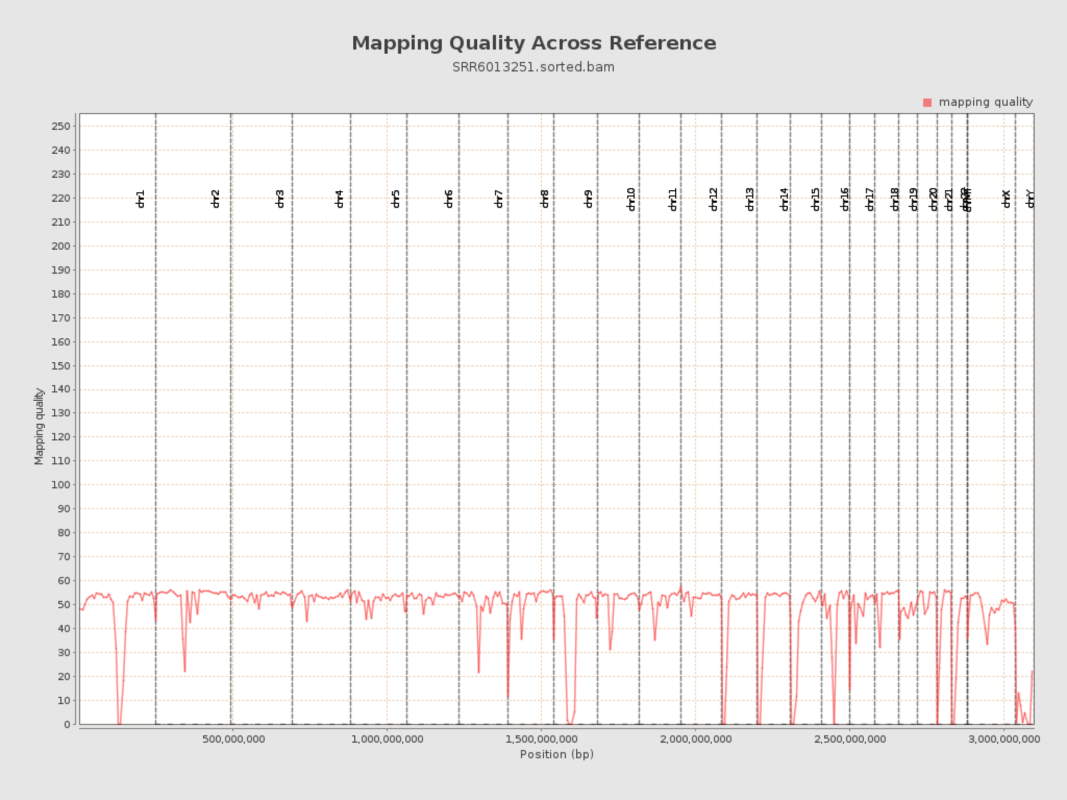
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram