Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 20:35:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013304.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_SRR6013304 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013304.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 20:35:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013304.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,097,614
Mapped reads	349,509 / 16.66%
Unmapped reads	1,748,105 / 83.34%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,433 / 0.21%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	66,262 / 3.16%
Duplication rate	12.79%
Clipped reads	218,368 / 10.41%

2.2. ACGT Content

Number/percentage of A's	5,819,495 / 26.78%
Number/percentage of C's	3,947,103 / 18.16%
Number/percentage of T's	6,965,706 / 32.05%
Number/percentage of G's	4,997,039 / 22.99%
Number/percentage of N's	2,290 / 0.01%
GC Percentage	41.16%

2.3. Coverage

Mean	0.007

Standard Deviation	0.1707

2.4. Mapping Quality

Mean Mapping Quality	43.59

2.5. Mismatches and indels

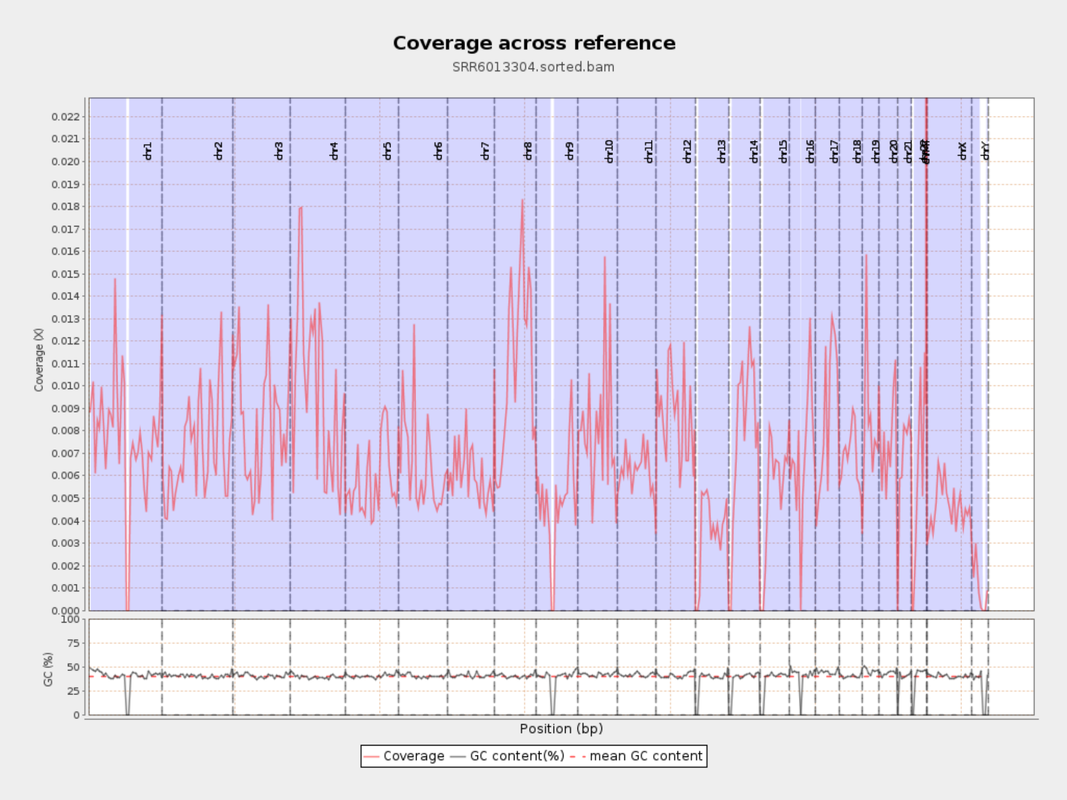
General error rate	0.91%
Mismatches	194,193
Insertions	1,462
Mapped reads with at least one insertion	0.42%
Deletions	7,397
Mapped reads with at least one deletion	2.09%
Homopolymer indels	42.93%

2.6. Chromosome stats

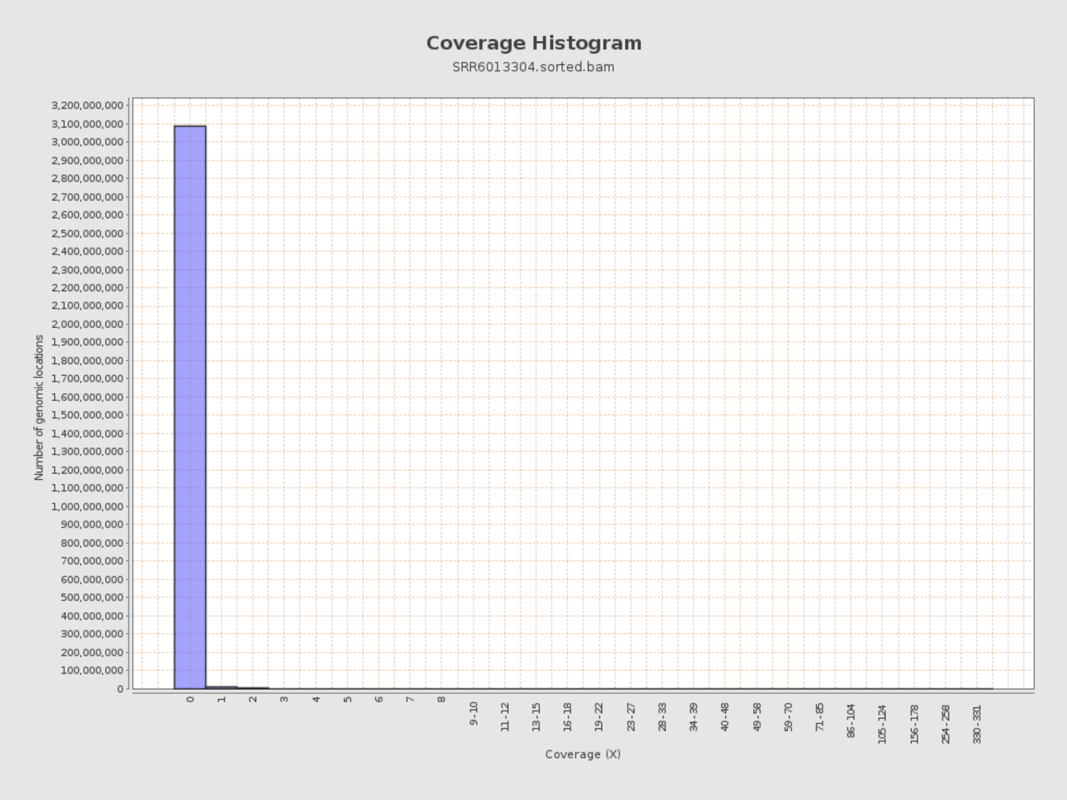
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1912799	0.0077	0.1994
chr2	243199373	1738893	0.0072	0.209
chr3	198022430	1655552	0.0084	0.1737
chr4	191154276	1893049	0.0099	0.192
chr5	180915260	1059408	0.0059	0.1395
chr6	171115067	1114078	0.0065	0.1658
chr7	159138663	958693	0.006	0.1495

chr8	146364022	1599025	0.0109	0.2048
chr9	141213431	675540	0.0048	0.1289
chr10	135534747	1097750	0.0081	0.1827
chr11	135006516	840085	0.0062	0.1584
chr12	133851895	1167580	0.0087	0.1863
chr13	115169878	398659	0.0035	0.1136
chr14	107349540	847942	0.0079	0.1897
chr15	102531392	527621	0.0051	0.1451
chr16	90354753	630296	0.007	0.1678
chr17	81195210	706965	0.0087	0.1711
chr18	78077248	540393	0.0069	0.1865
chr19	59128983	502859	0.0085	0.1763
chr20	63025520	474840	0.0075	0.1596
chr21	48129895	320361	0.0067	0.1844
chr22	51304566	293902	0.0057	0.1422
chrMT	16571	8511	0.5136	1.1973
chrX	155270560	720268	0.0046	0.1242
chrY	59373566	59191	0.001	0.0472

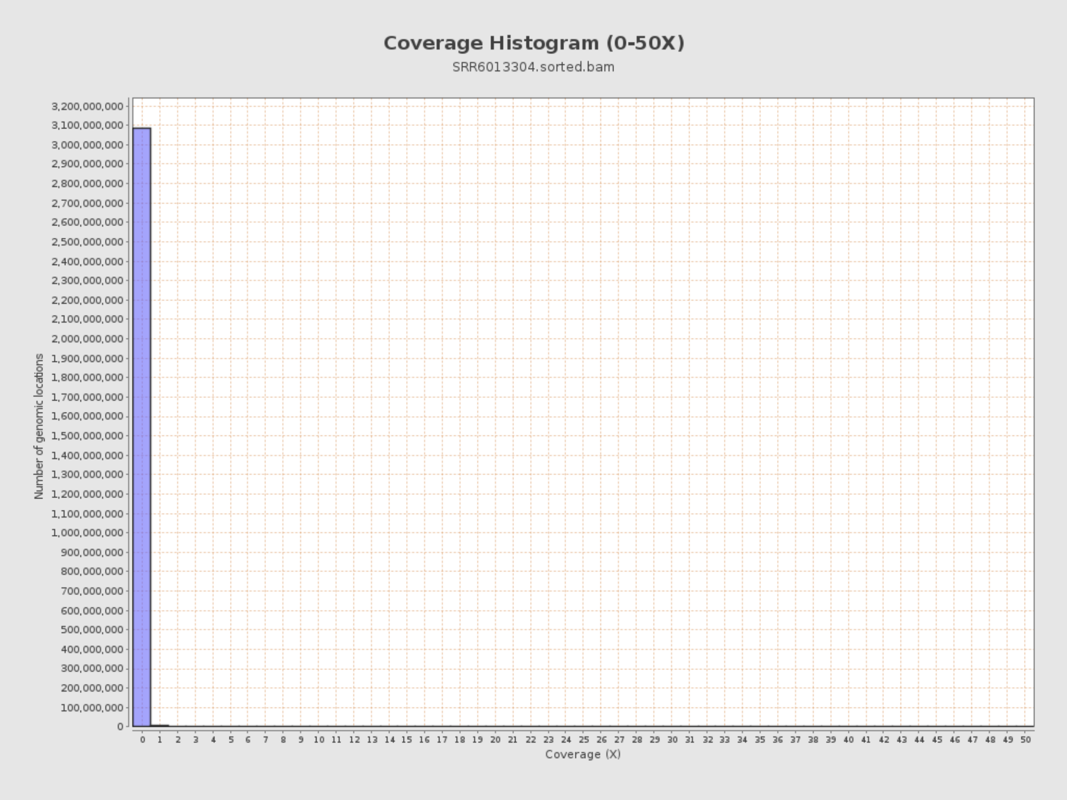
3. Results : Coverage across reference



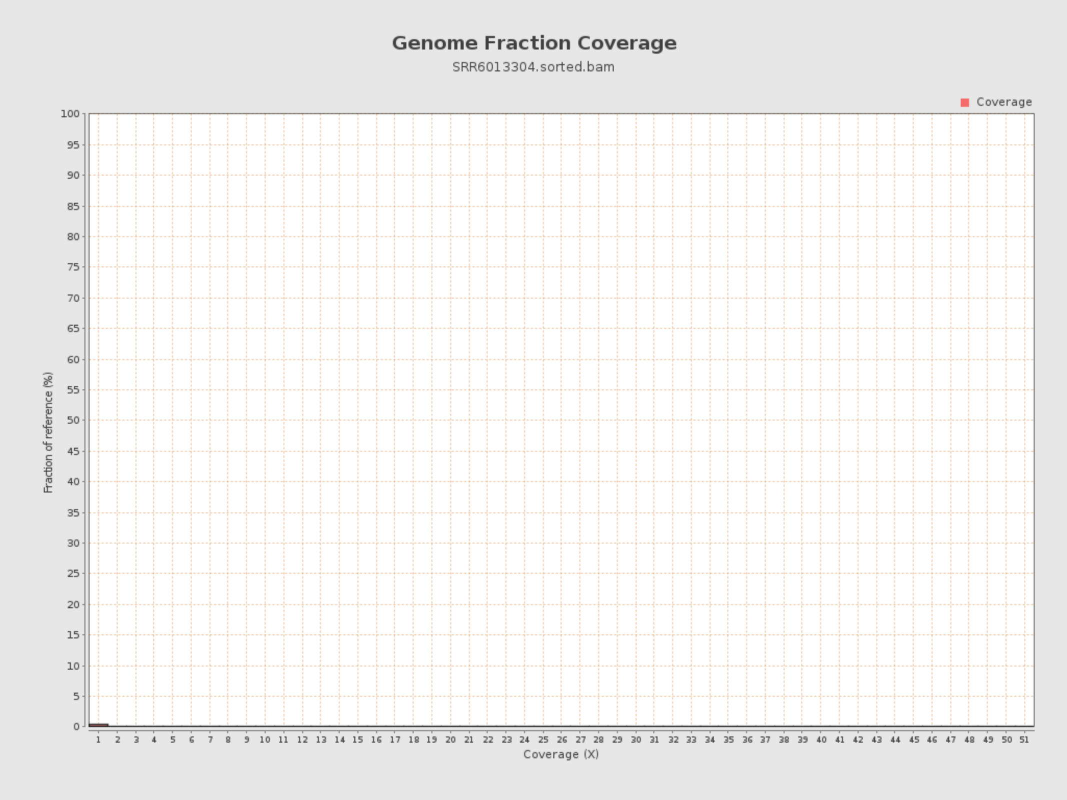
4. Results : Coverage Histogram



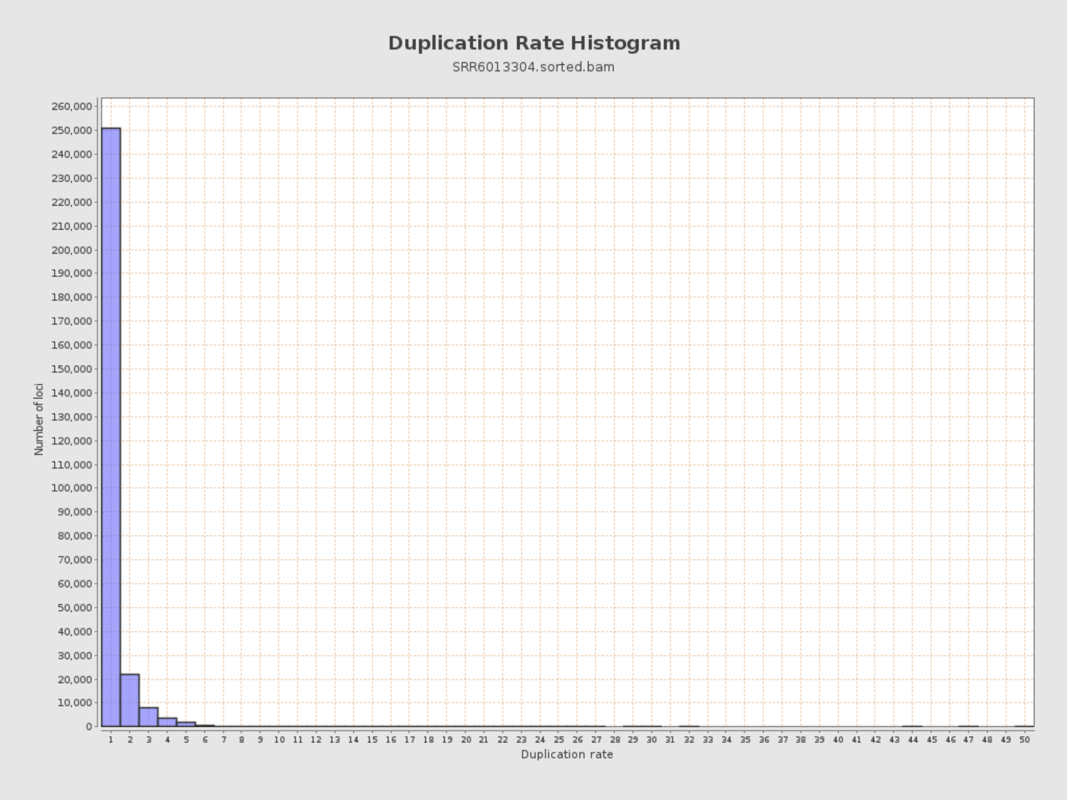
5. Results : Coverage Histogram (0-50X)



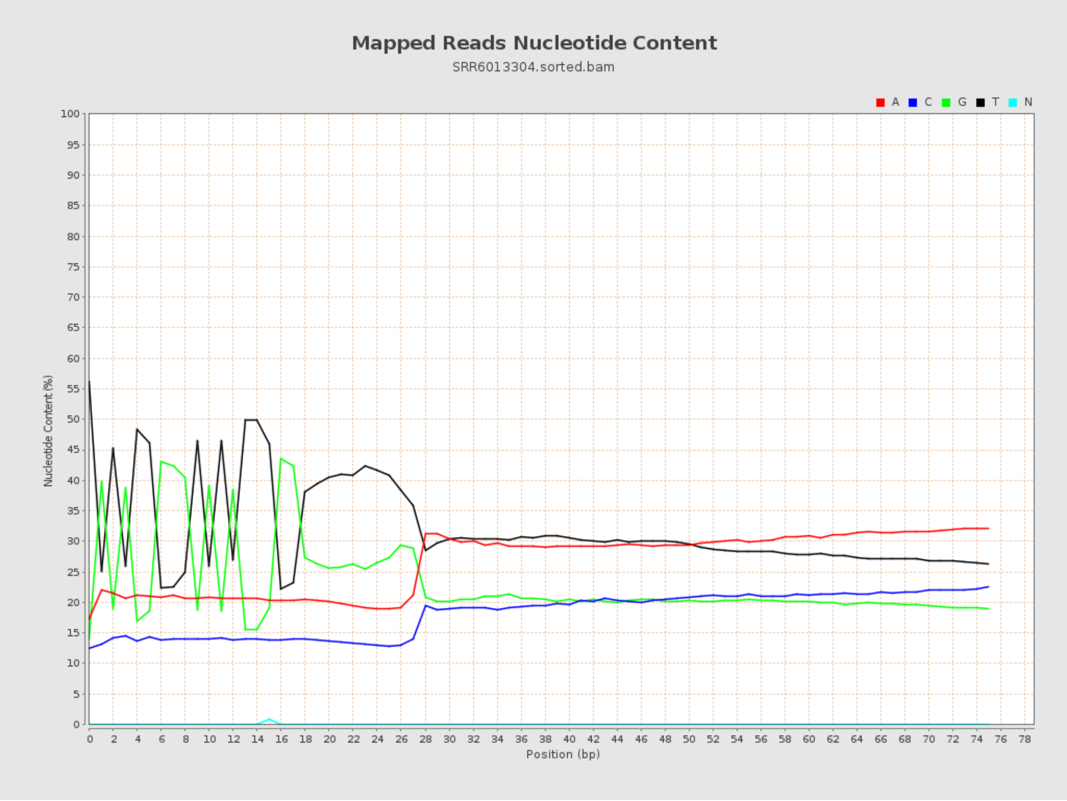
6. Results : Genome Fraction Coverage



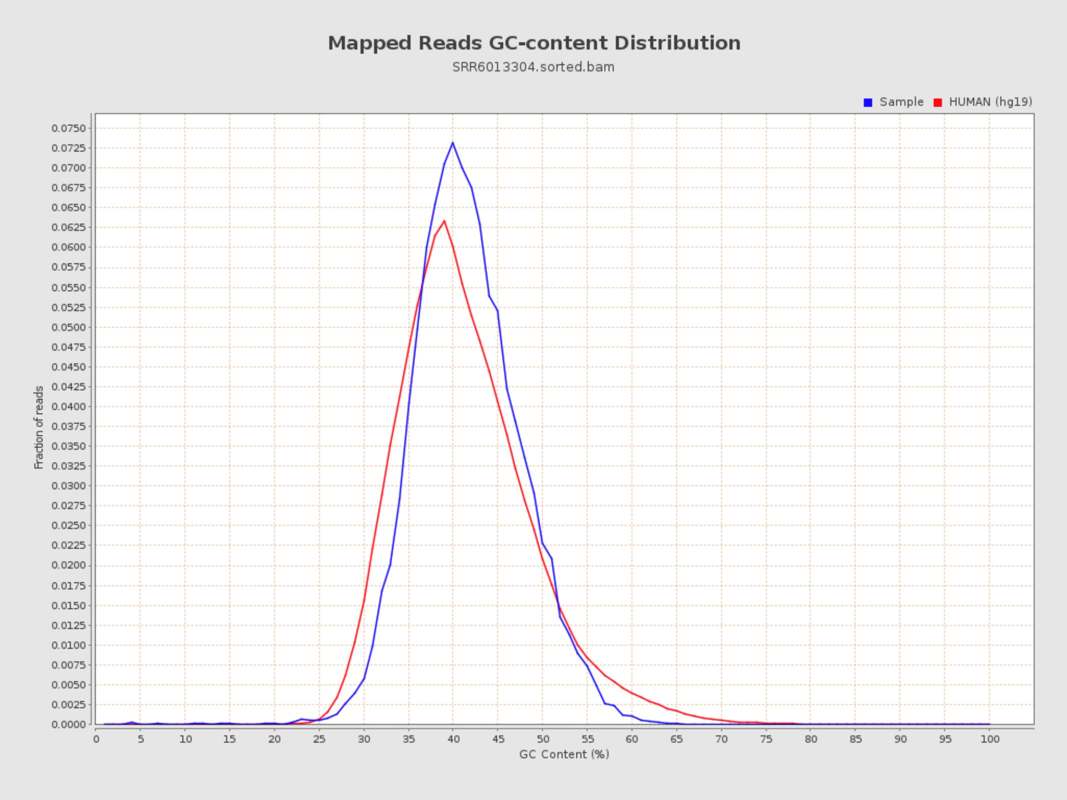
7. Results : Duplication Rate Histogram



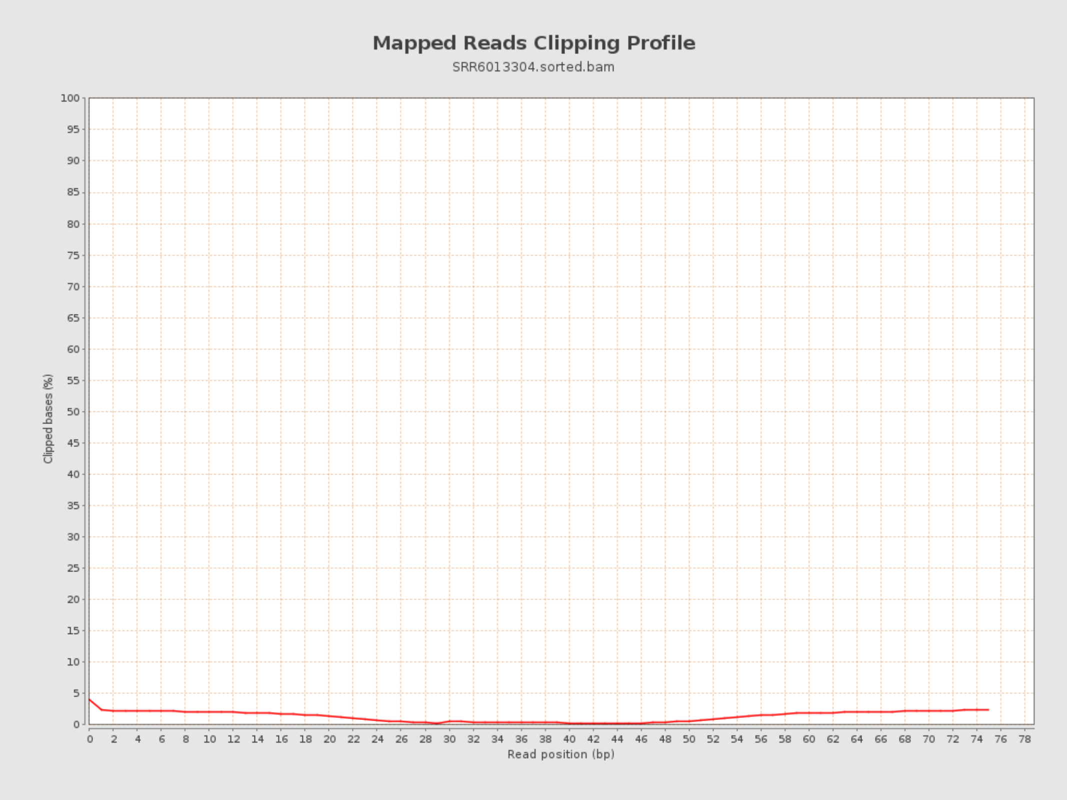
8. Results : Mapped Reads Nucleotide Content



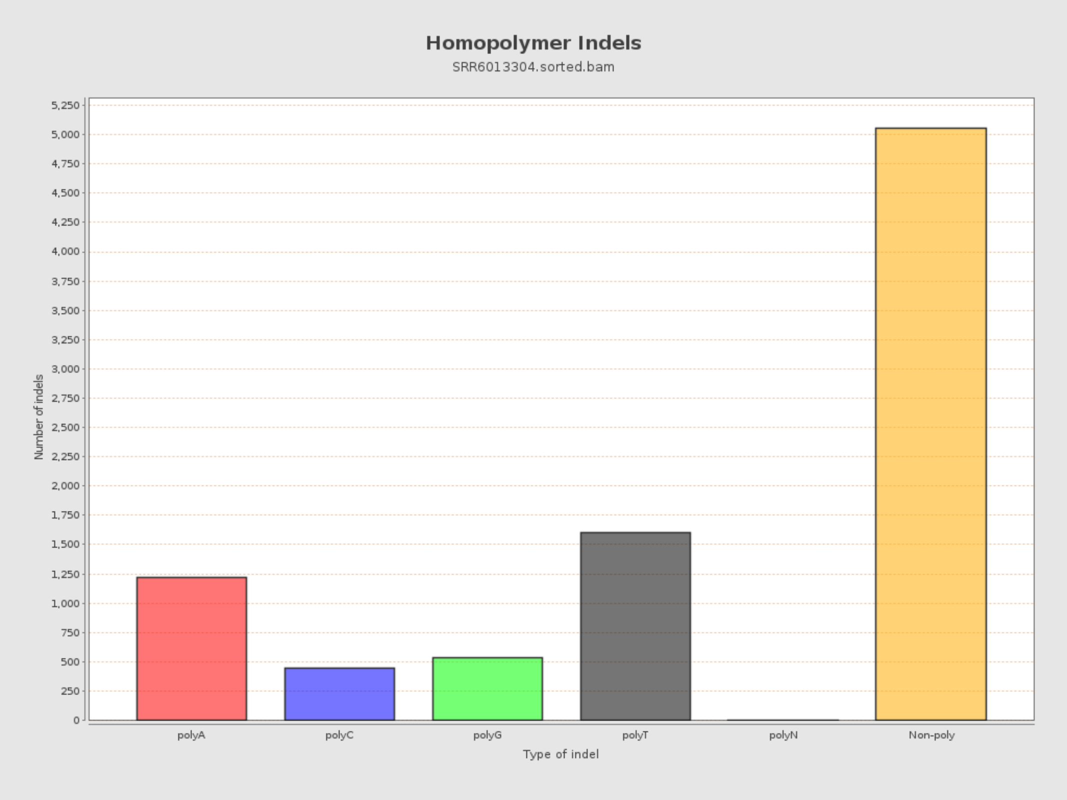
9. Results : Mapped Reads GC-content Distribution



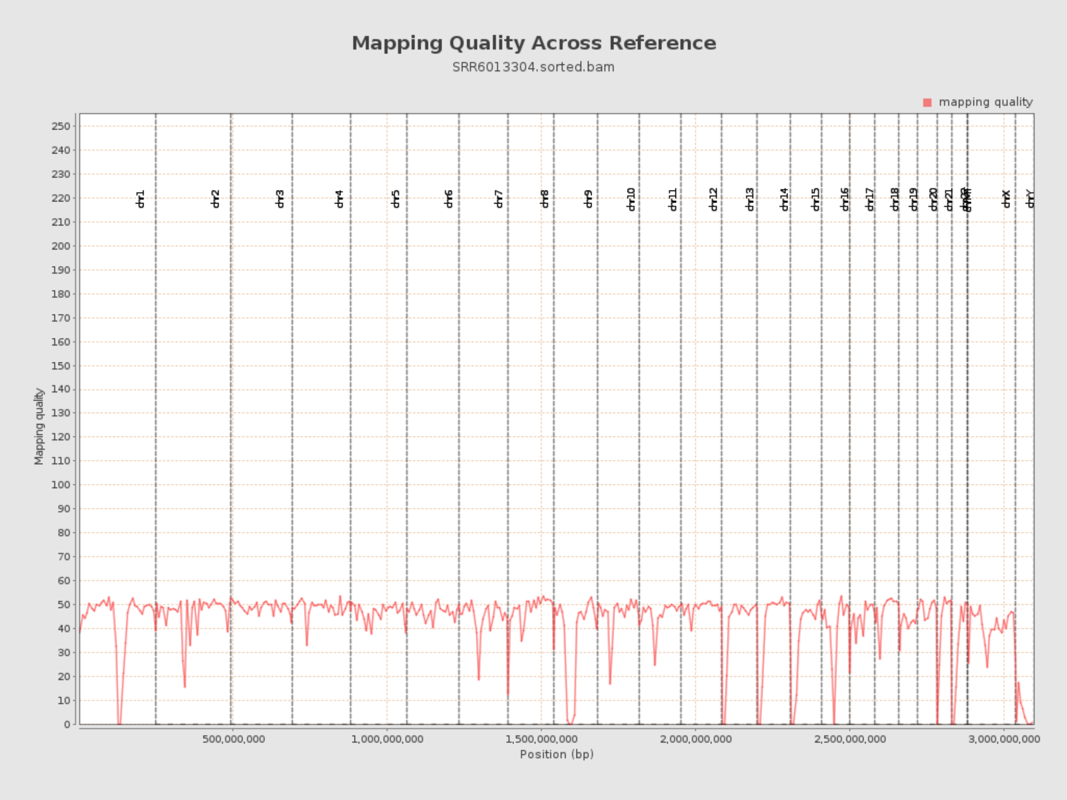
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram