Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 02:27:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240014.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_SRR6240014 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240014.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 02:27:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240014.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,373,852
Mapped reads	1,117,632 / 81.35%
Unmapped reads	256,220 / 18.65%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,811 / 0.42%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	75,506 / 5.5%
Duplication rate	5.84%
Clipped reads	698,203 / 50.82%

2.2. ACGT Content

Number/percentage of A's	19,212,269 / 27.58%
Number/percentage of C's	12,278,108 / 17.62%
Number/percentage of T's	22,602,886 / 32.44%
Number/percentage of G's	15,532,904 / 22.29%
Number/percentage of N's	45,051 / 0.06%
GC Percentage	39.92%

2.3. Coverage

Mean	0.0225

Standard Deviation	0.2268

2.4. Mapping Quality

Mean Mapping Quality	45.98

2.5. Mismatches and indels

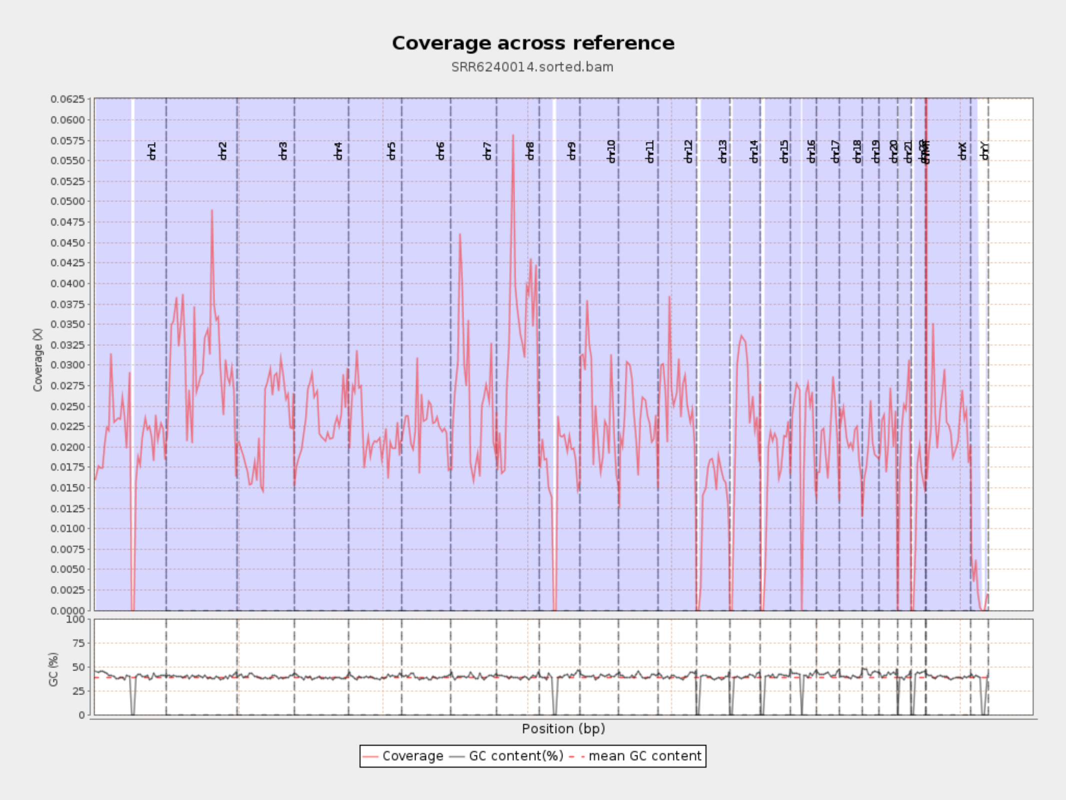
General error rate	0.97%
Mismatches	670,008
Insertions	4,948
Mapped reads with at least one insertion	0.44%
Deletions	21,939
Mapped reads with at least one deletion	1.94%
Homopolymer indels	48.88%

2.6. Chromosome stats

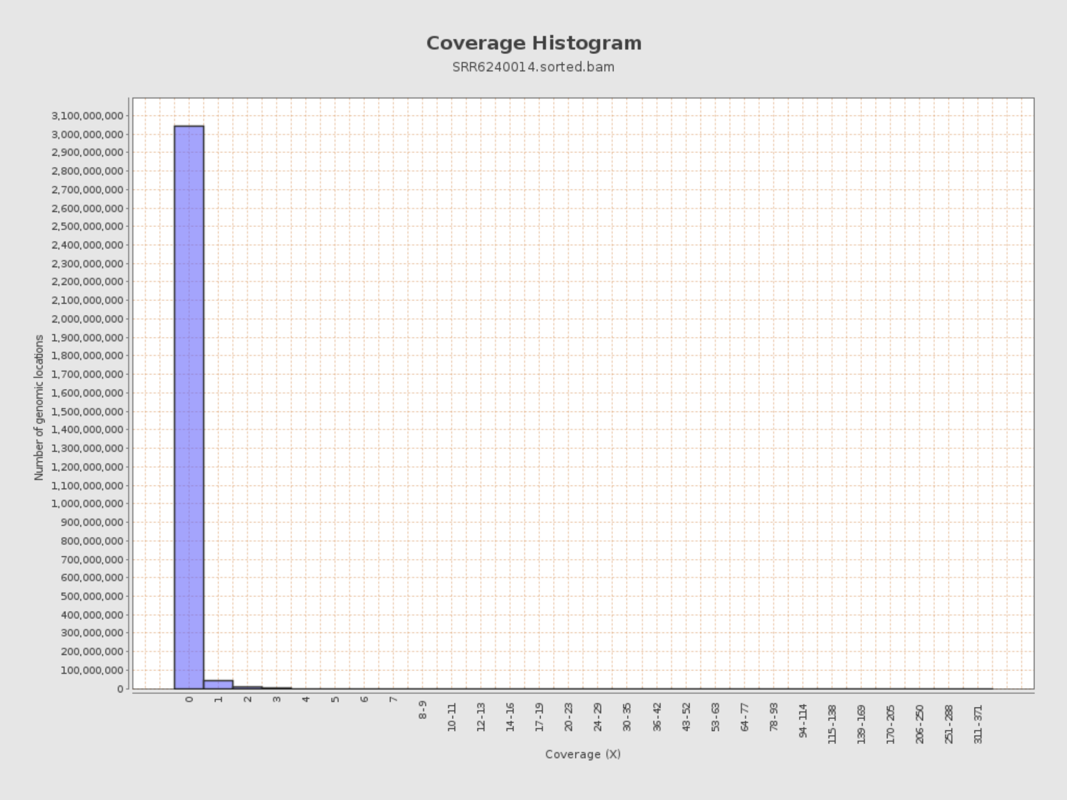
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5038633	0.0202	0.3153
chr2	243199373	7534433	0.031	0.2731
chr3	198022430	4456786	0.0225	0.1838
chr4	191154276	4431094	0.0232	0.1903
chr5	180915260	3953650	0.0219	0.1812
chr6	171115067	3875337	0.0226	0.2037
chr7	159138663	4123441	0.0259	0.3133

chr8	146364022	4889335	0.0334	0.317
chr9	141213431	2400435	0.017	0.1943
chr10	135534747	3336934	0.0246	0.2141
chr11	135006516	3163947	0.0234	0.215
chr12	133851895	3542787	0.0265	0.2017
chr13	115169878	1562135	0.0136	0.1417
chr14	107349540	2492195	0.0232	0.1936
chr15	102531392	1682529	0.0164	0.1646
chr16	90354753	1965101	0.0217	0.1821
chr17	81195210	1690443	0.0208	0.1873
chr18	78077248	1655148	0.0212	0.3046
chr19	59128983	1140428	0.0193	0.2294
chr20	63025520	1357415	0.0215	0.1814
chr21	48129895	1028180	0.0214	0.1827
chr22	51304566	632150	0.0123	0.1329
chrMT	16571	21218	1.2804	1.794
chrX	155270560	3591428	0.0231	0.1947
chrY	59373566	143803	0.0024	0.0589

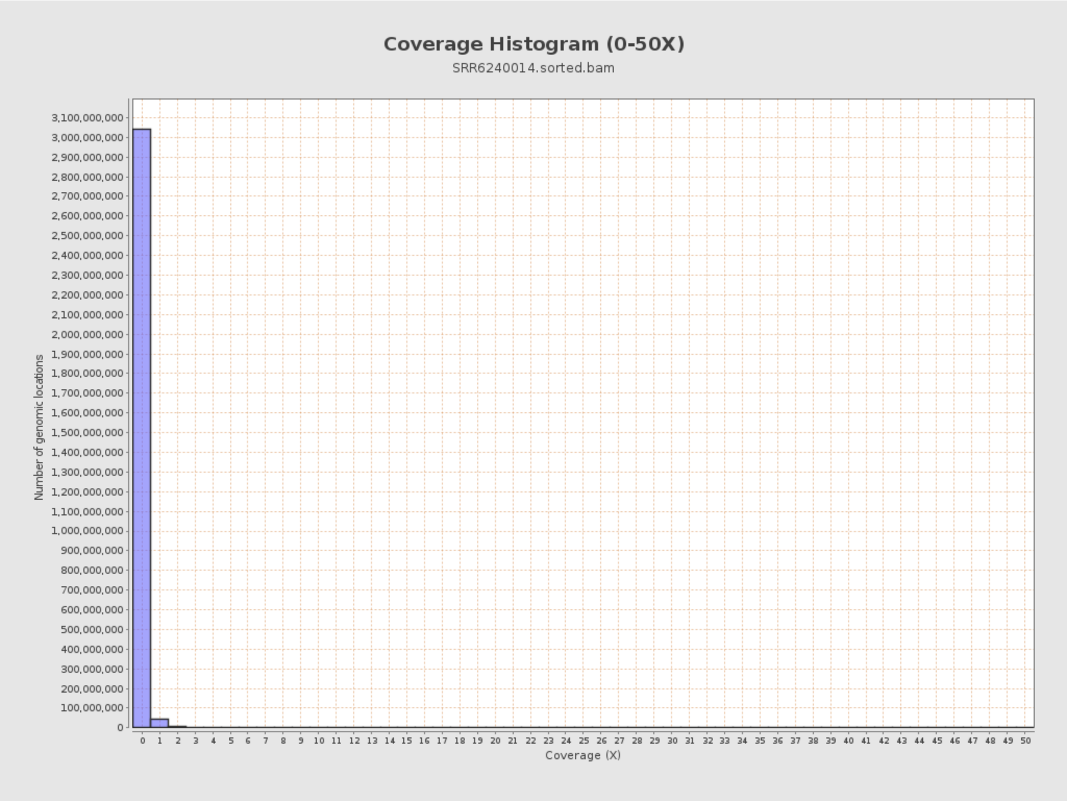
3. Results : Coverage across reference



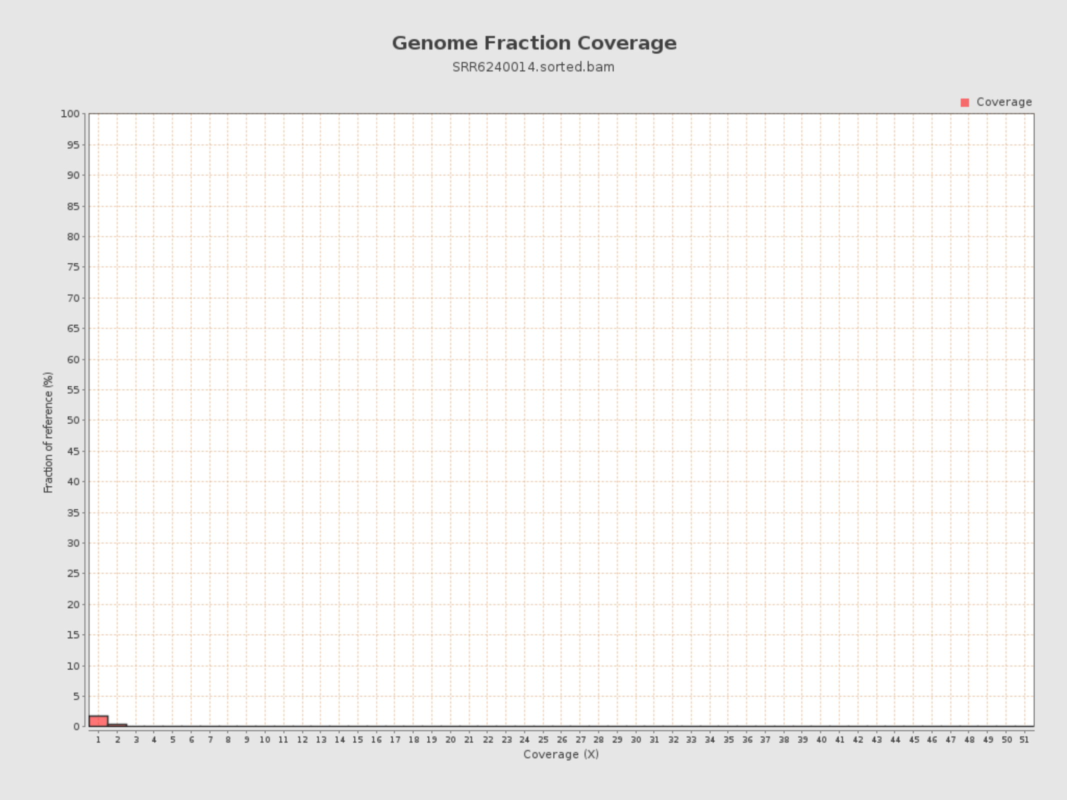
4. Results : Coverage Histogram



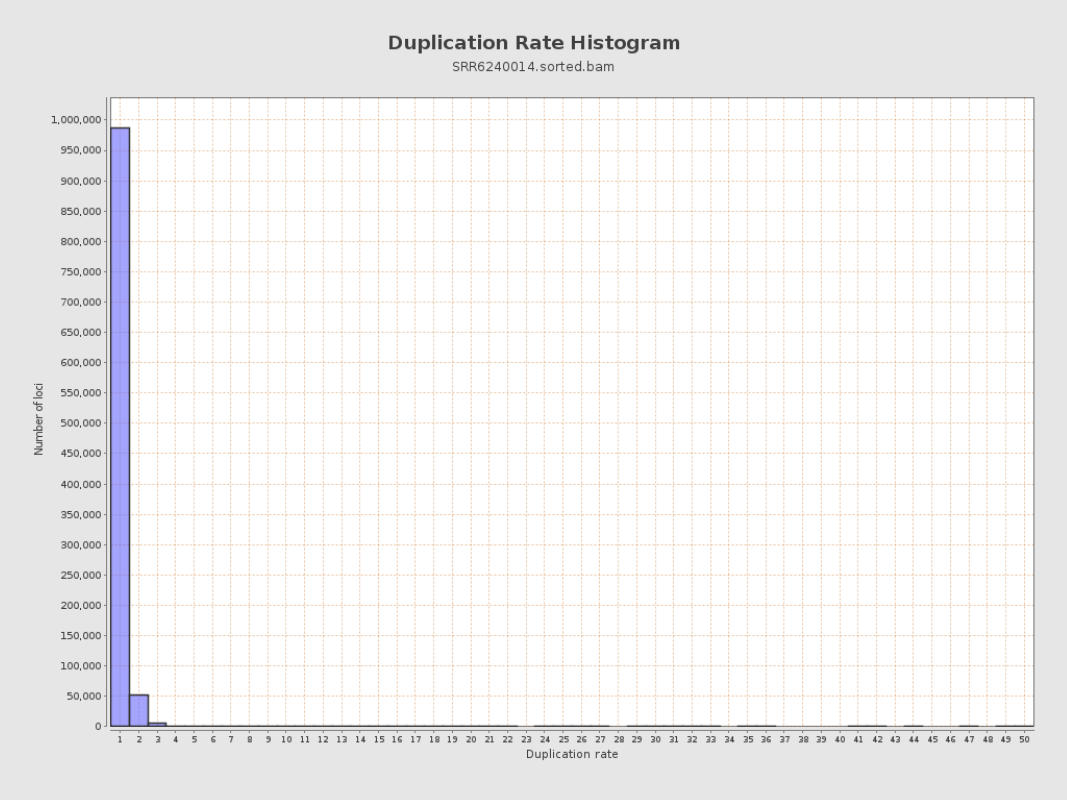
5. Results : Coverage Histogram (0-50X)



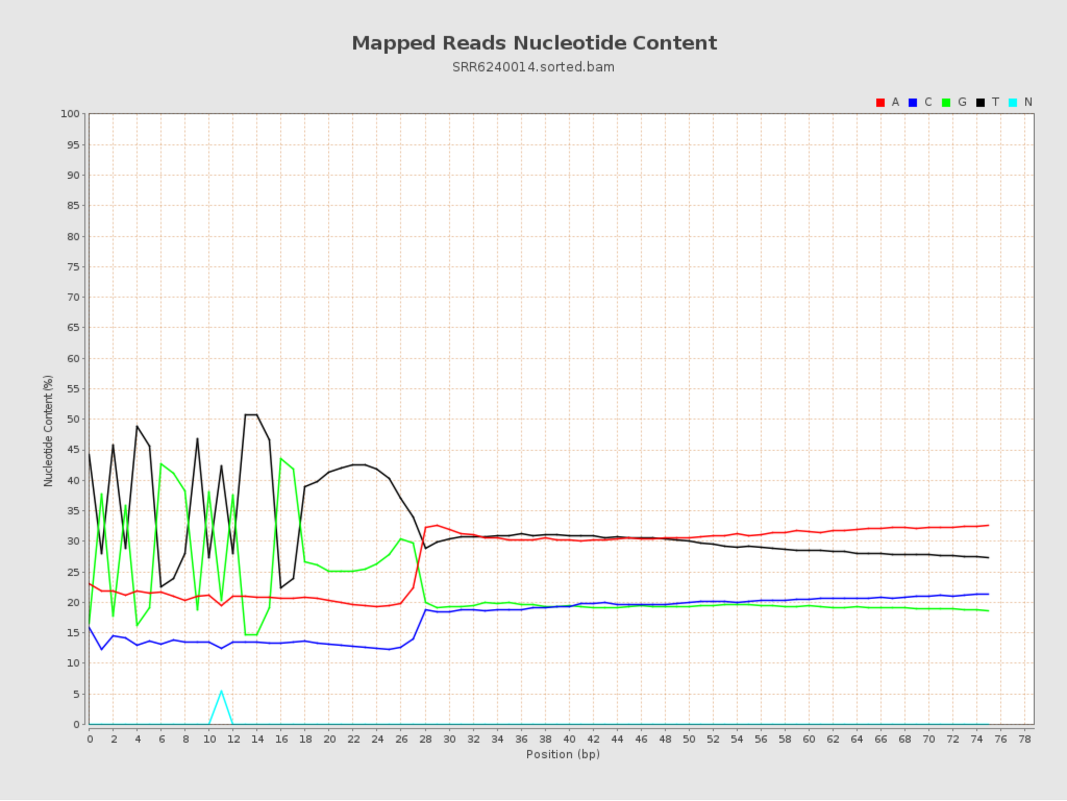
6. Results : Genome Fraction Coverage



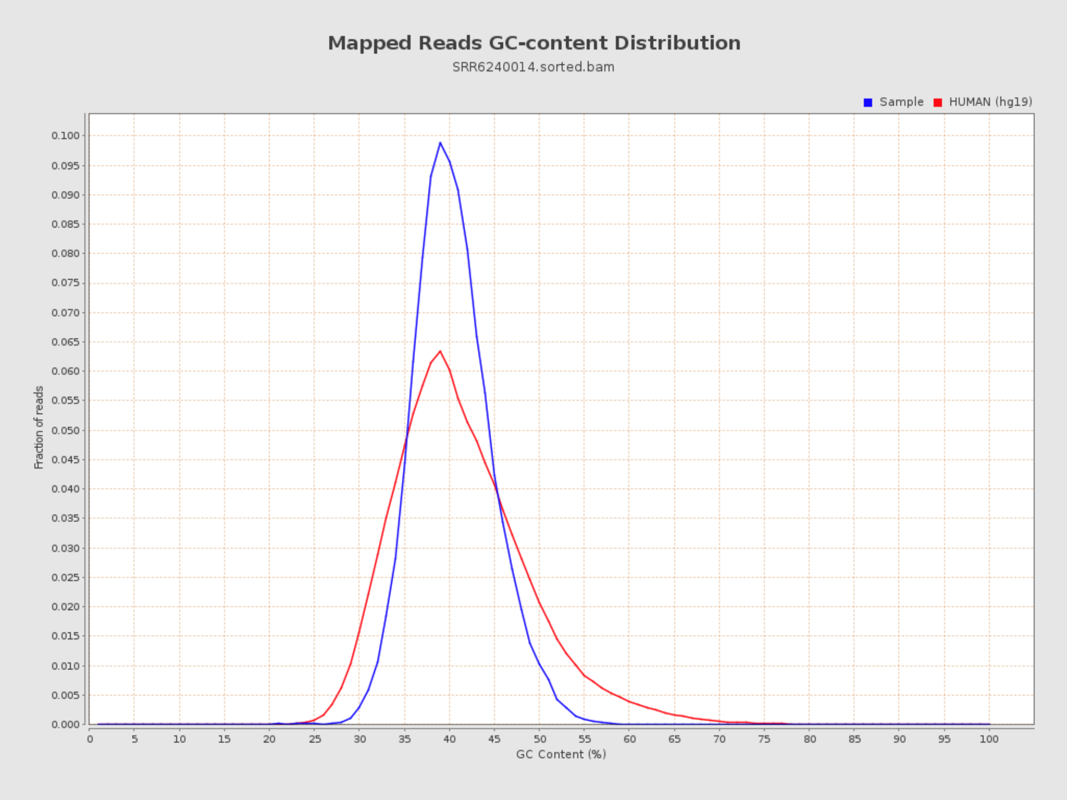
7. Results : Duplication Rate Histogram



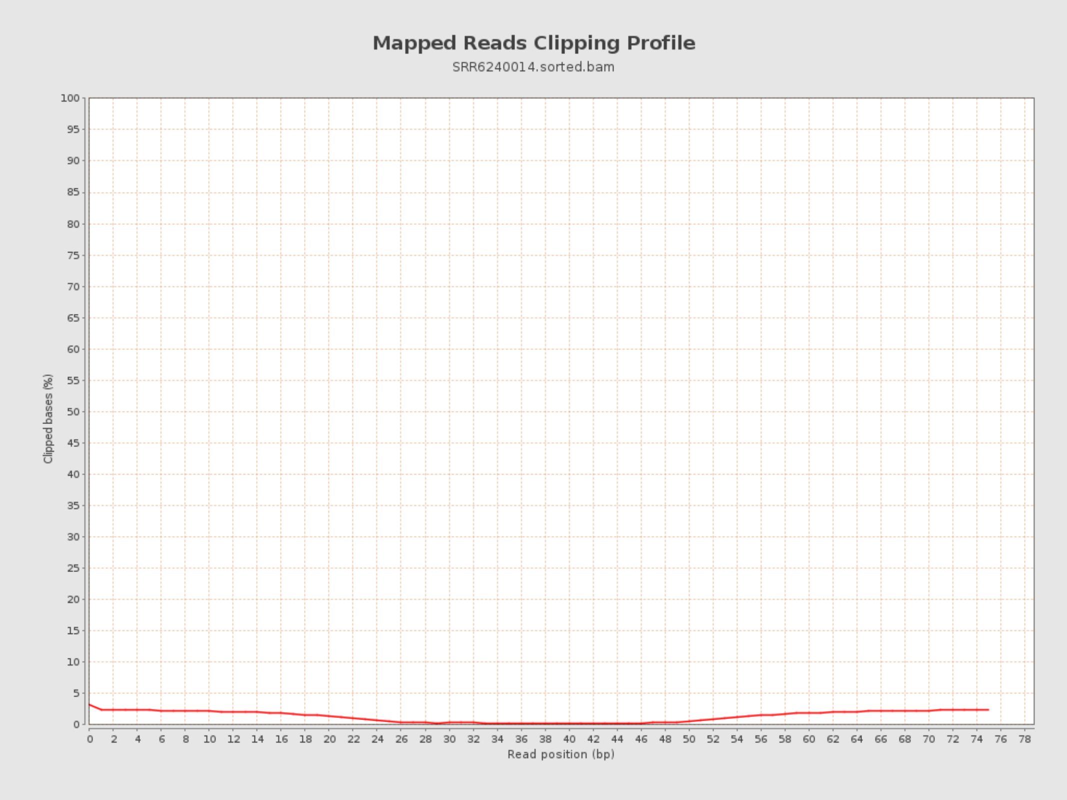
8. Results : Mapped Reads Nucleotide Content



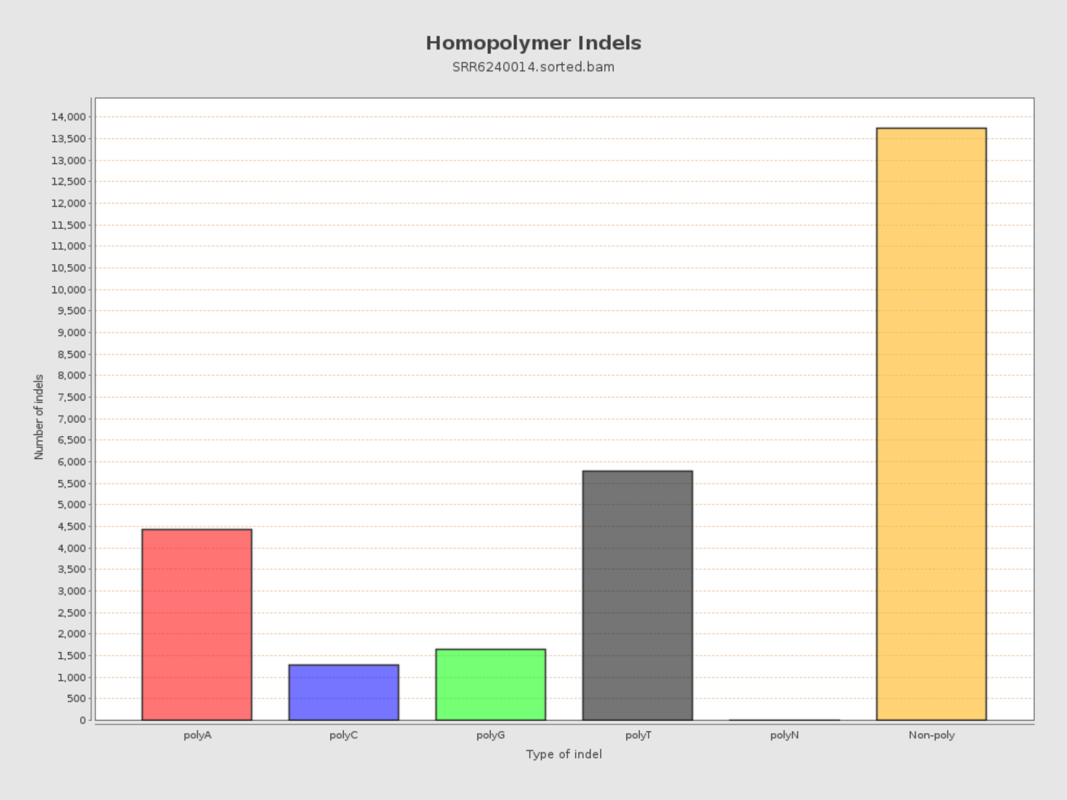
9. Results : Mapped Reads GC-content Distribution



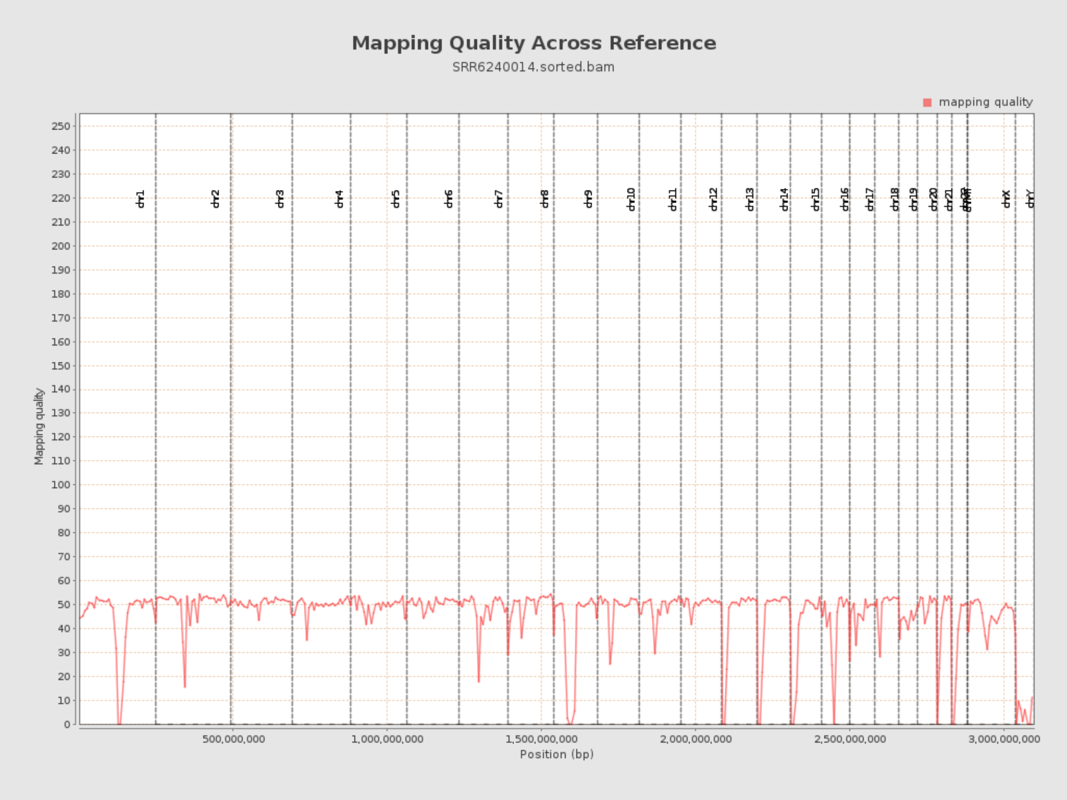
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram