Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 11:43:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234040.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_SRR6234040 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234040.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 11:43:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234040.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,125,681
Mapped reads	147,235 / 3.57%
Unmapped reads	3,978,446 / 96.43%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,165 / 0.03%
Read min/max/mean length	30 / 76 / 76.01
Duplicated reads (estimated)	16,952 / 0.41%
Duplication rate	6.7%
Clipped reads	76,099 / 1.84%

2.2. ACGT Content

Number/percentage of A's	2,468,726 / 26.2%
Number/percentage of C's	1,764,147 / 18.73%
Number/percentage of T's	3,053,479 / 32.41%
Number/percentage of G's	2,134,223 / 22.65%
Number/percentage of N's	554 / 0.01%
GC Percentage	41.38%

2.3. Coverage

Mean	0.003

Standard Deviation	0.1783

2.4. Mapping Quality

Mean Mapping Quality	43.31

2.5. Mismatches and indels

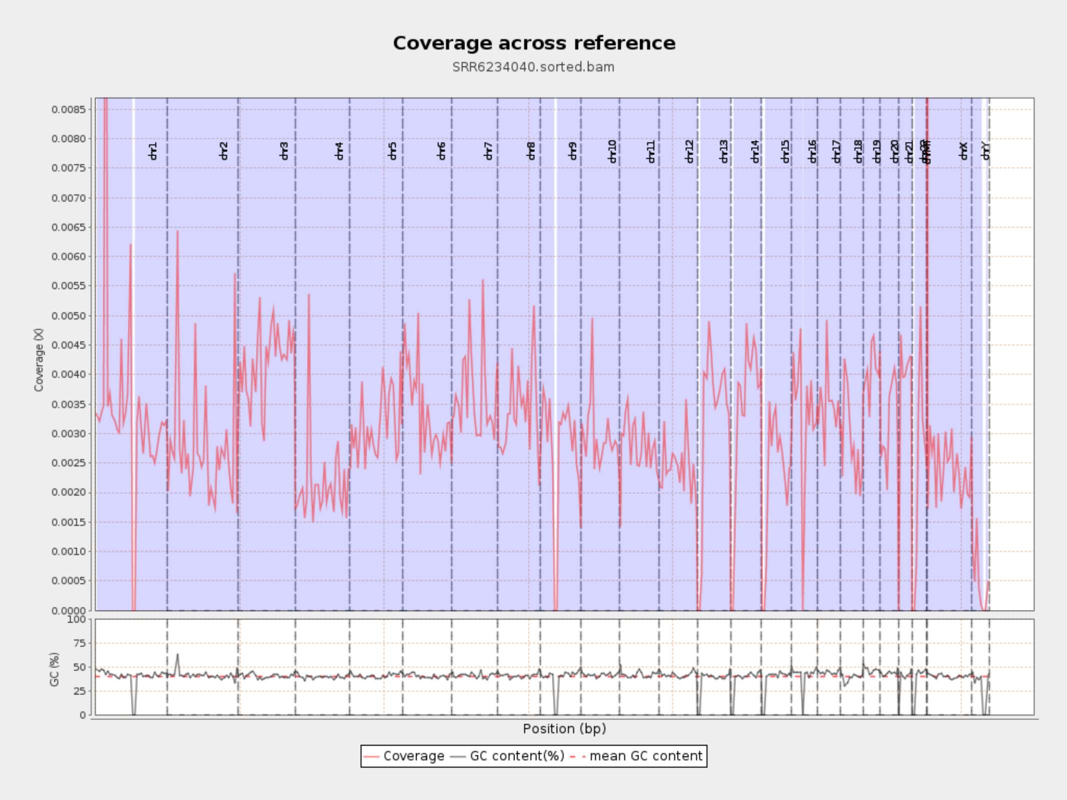
General error rate	1.06%
Mismatches	97,757
Insertions	948
Mapped reads with at least one insertion	0.63%
Deletions	2,570
Mapped reads with at least one deletion	1.72%
Homopolymer indels	39.74%

2.6. Chromosome stats

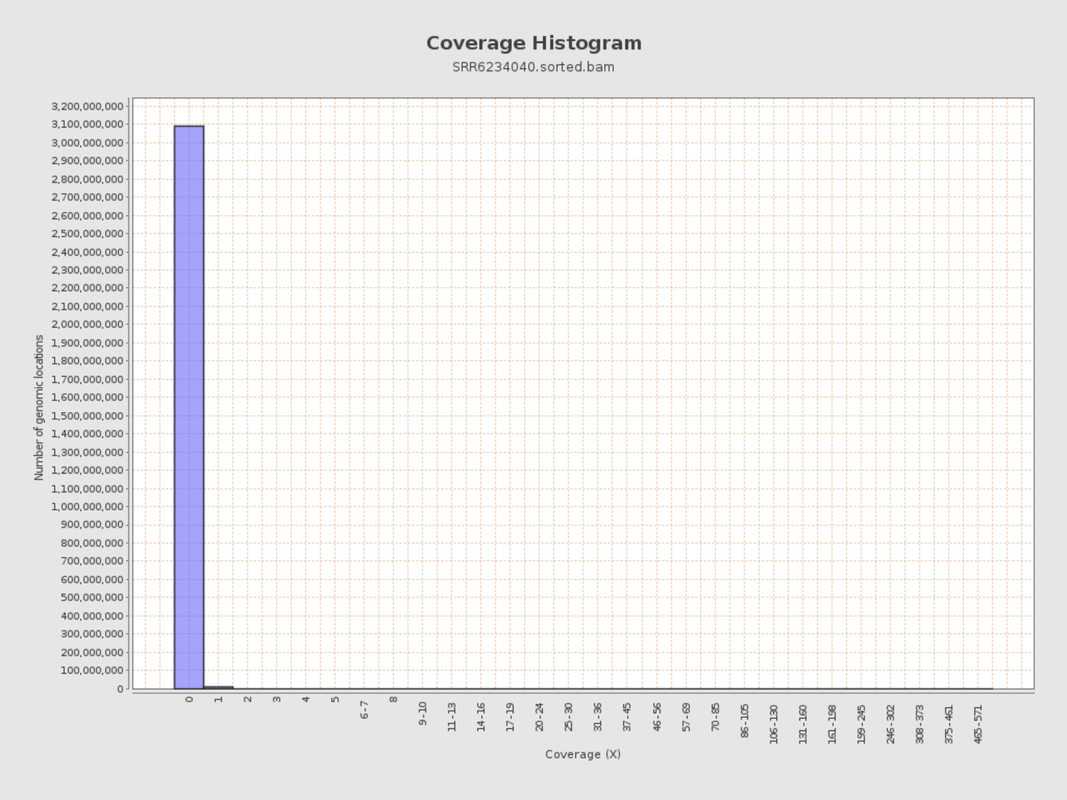
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	858902	0.0034	0.4108
chr2	243199373	674109	0.0028	0.2664
chr3	198022430	837138	0.0042	0.2356
chr4	191154276	410612	0.0021	0.1273
chr5	180915260	573671	0.0032	0.0748
chr6	171115067	578567	0.0034	0.0896
chr7	159138663	580582	0.0036	0.1643

chr8	146364022	497321	0.0034	0.0895
chr9	141213431	385348	0.0027	0.0839
chr10	135534747	402859	0.003	0.0736
chr11	135006516	381285	0.0028	0.0708
chr12	133851895	326917	0.0024	0.1544
chr13	115169878	371850	0.0032	0.0736
chr14	107349540	357539	0.0033	0.0731
chr15	102531392	228030	0.0022	0.0638
chr16	90354753	292051	0.0032	0.0955
chr17	81195210	282190	0.0035	0.1153
chr18	78077248	220811	0.0028	0.1988
chr19	59128983	241046	0.0041	0.0859
chr20	63025520	201379	0.0032	0.067
chr21	48129895	184228	0.0038	0.1596
chr22	51304566	122351	0.0024	0.1819
chrMT	16571	13838	0.8351	1.292
chrX	155270560	373720	0.0024	0.0889
chrY	59373566	29003	0.0005	0.0306

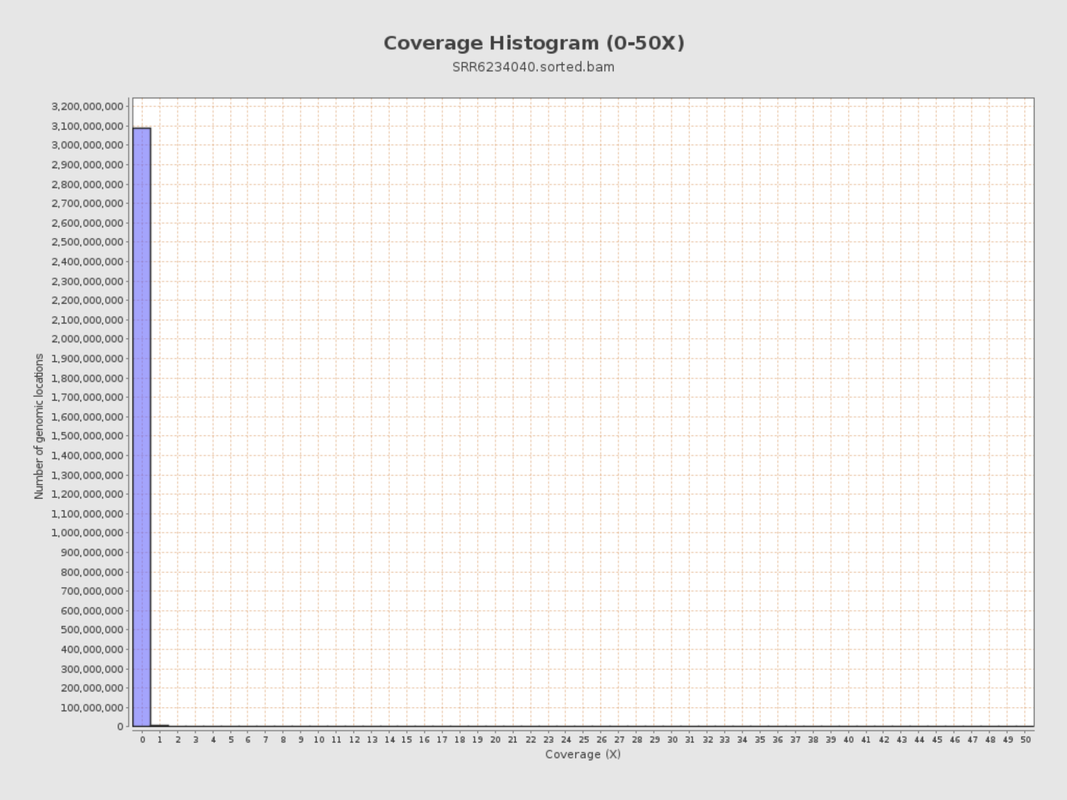
3. Results : Coverage across reference



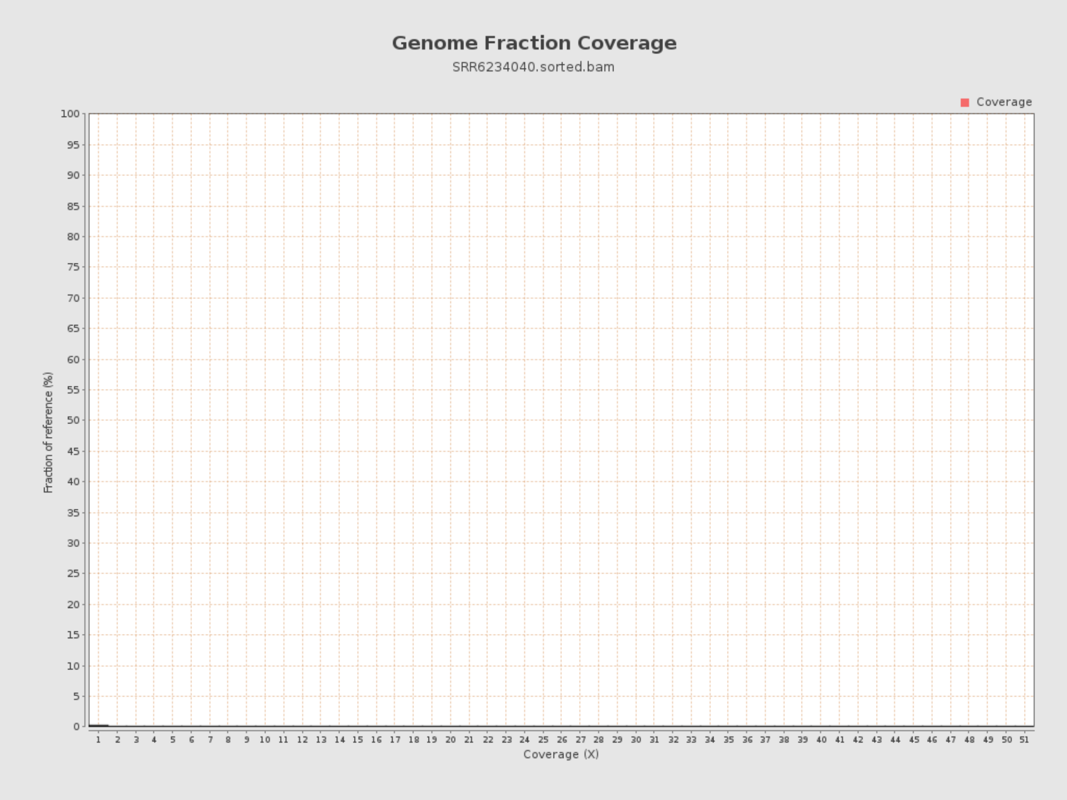
4. Results : Coverage Histogram



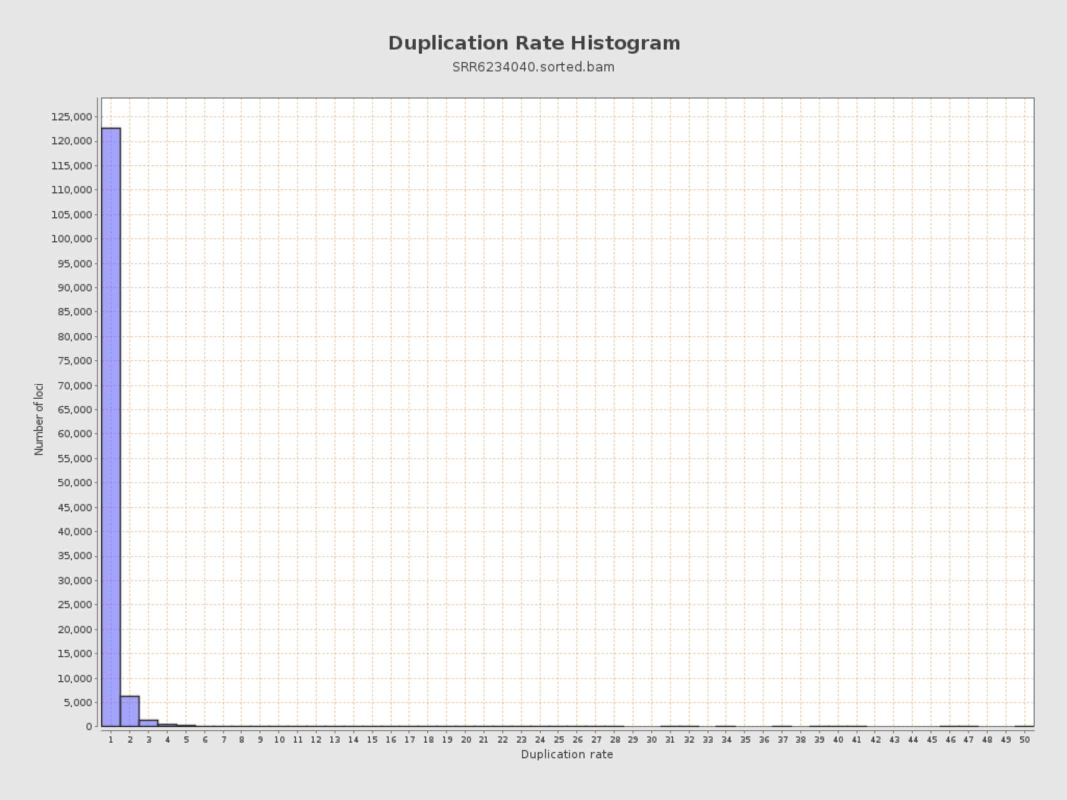
5. Results : Coverage Histogram (0-50X)



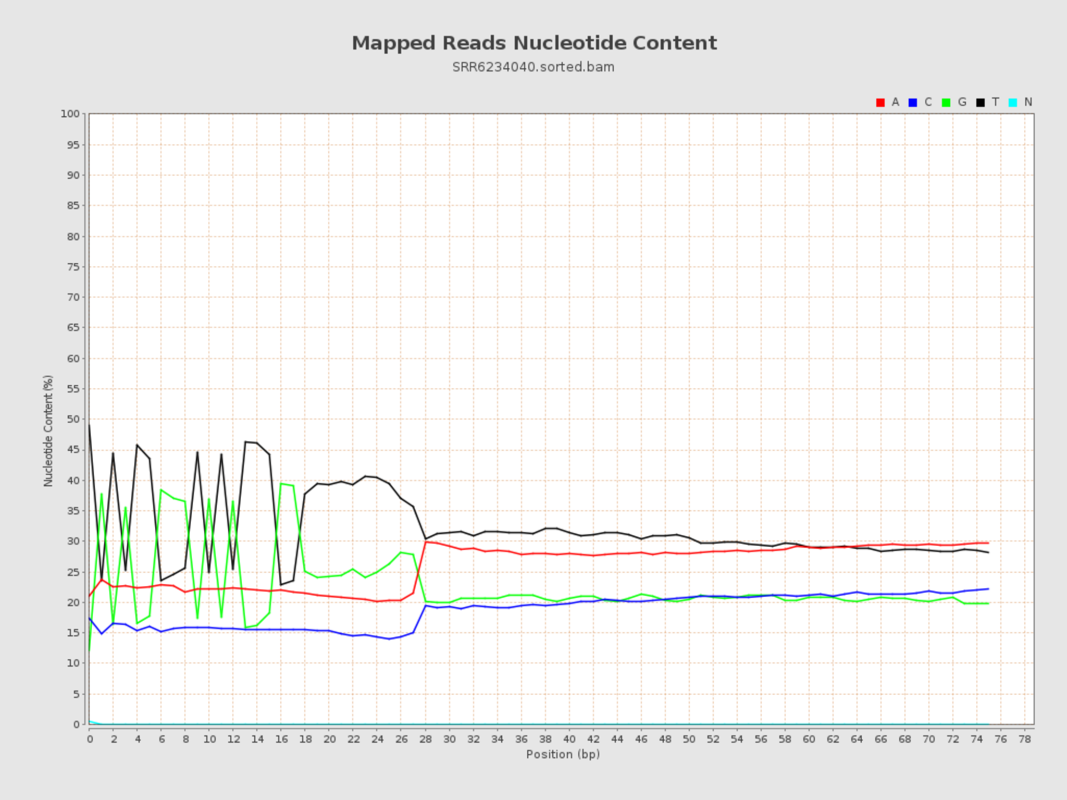
6. Results : Genome Fraction Coverage



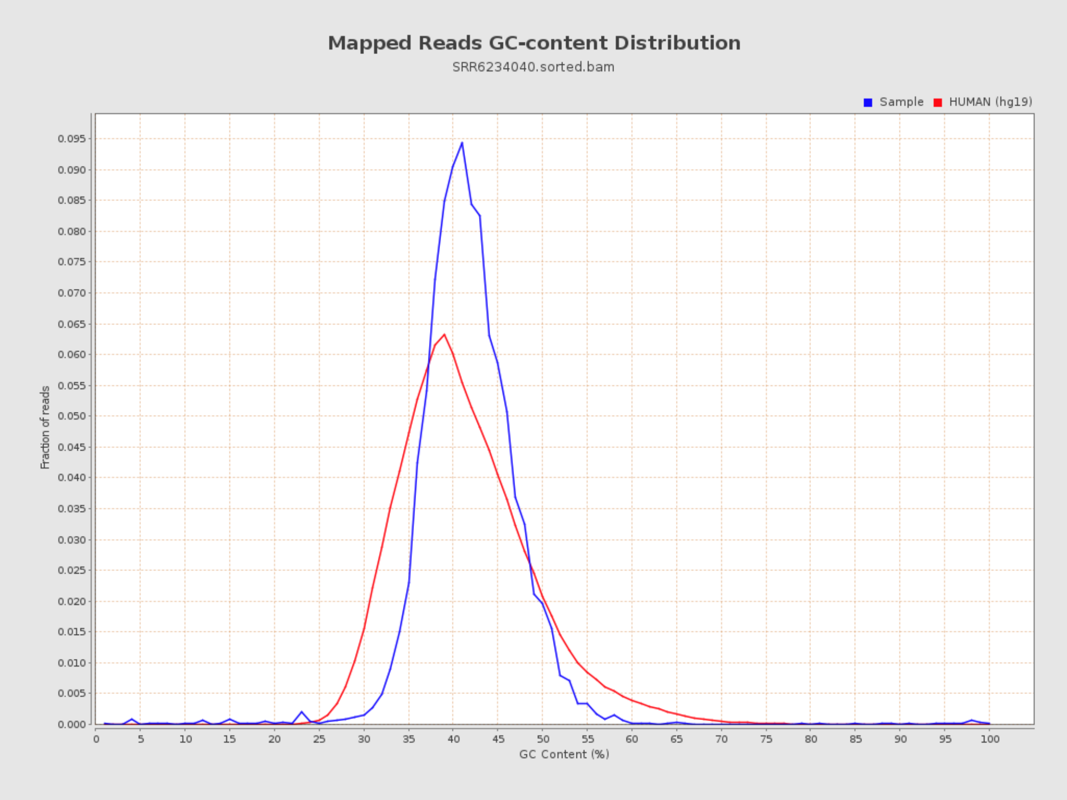
7. Results : Duplication Rate Histogram



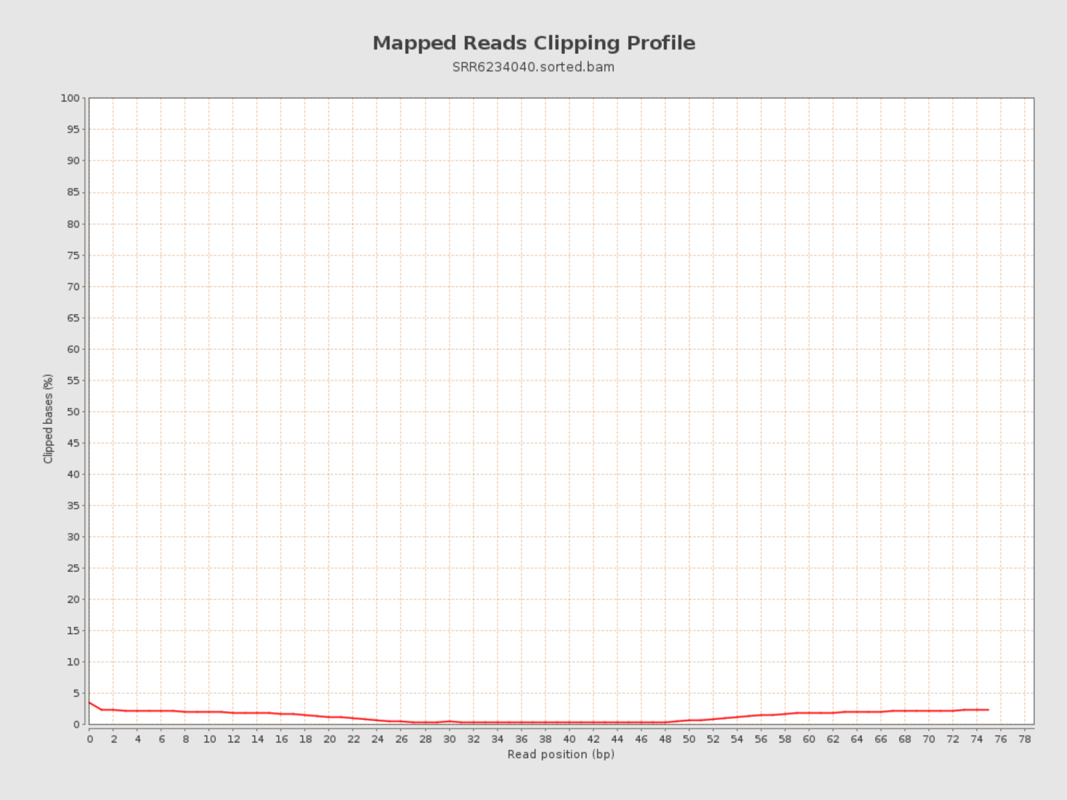
8. Results : Mapped Reads Nucleotide Content



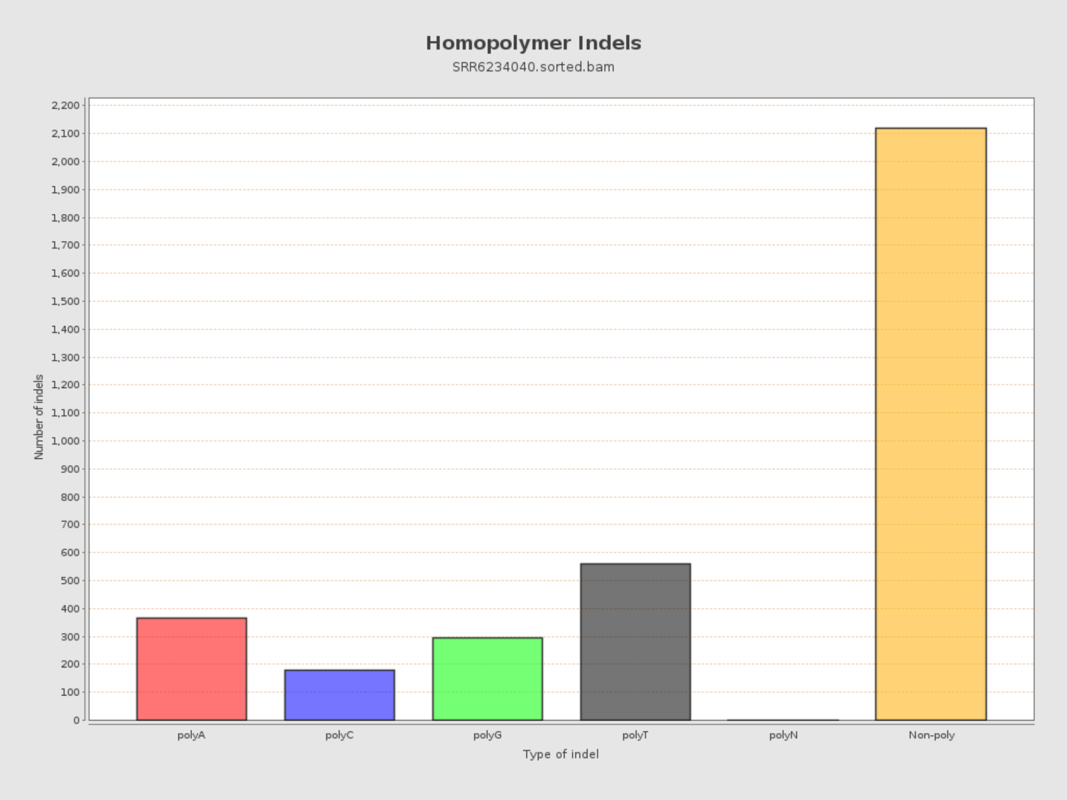
9. Results : Mapped Reads GC-content Distribution



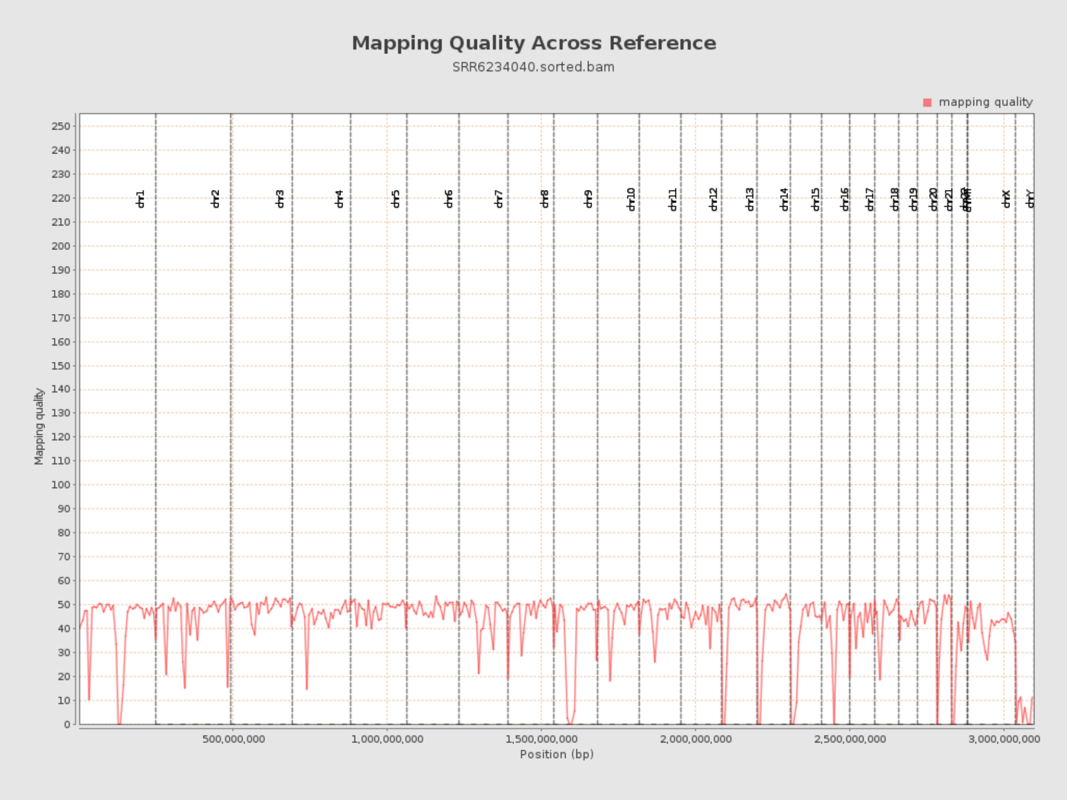
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram