Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 12:56:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234060.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_SRR6234060 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234060.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 12:56:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234060.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	903,467
Mapped reads	100,472 / 11.12%
Unmapped reads	802,995 / 88.88%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,463 / 0.16%
Read min/max/mean length	30 / 76 / 76.06
Duplicated reads (estimated)	12,027 / 1.33%
Duplication rate	9.07%
Clipped reads	71,523 / 7.92%

2.2. ACGT Content

Number/percentage of A's	1,506,652 / 26.12%
Number/percentage of C's	1,091,098 / 18.92%
Number/percentage of T's	1,799,996 / 31.21%
Number/percentage of G's	1,369,048 / 23.74%
Number/percentage of N's	1,239 / 0.02%
GC Percentage	42.65%

2.3. Coverage

Mean	0.0019

Standard Deviation	0.07

2.4. Mapping Quality

Mean Mapping Quality	30.57

2.5. Mismatches and indels

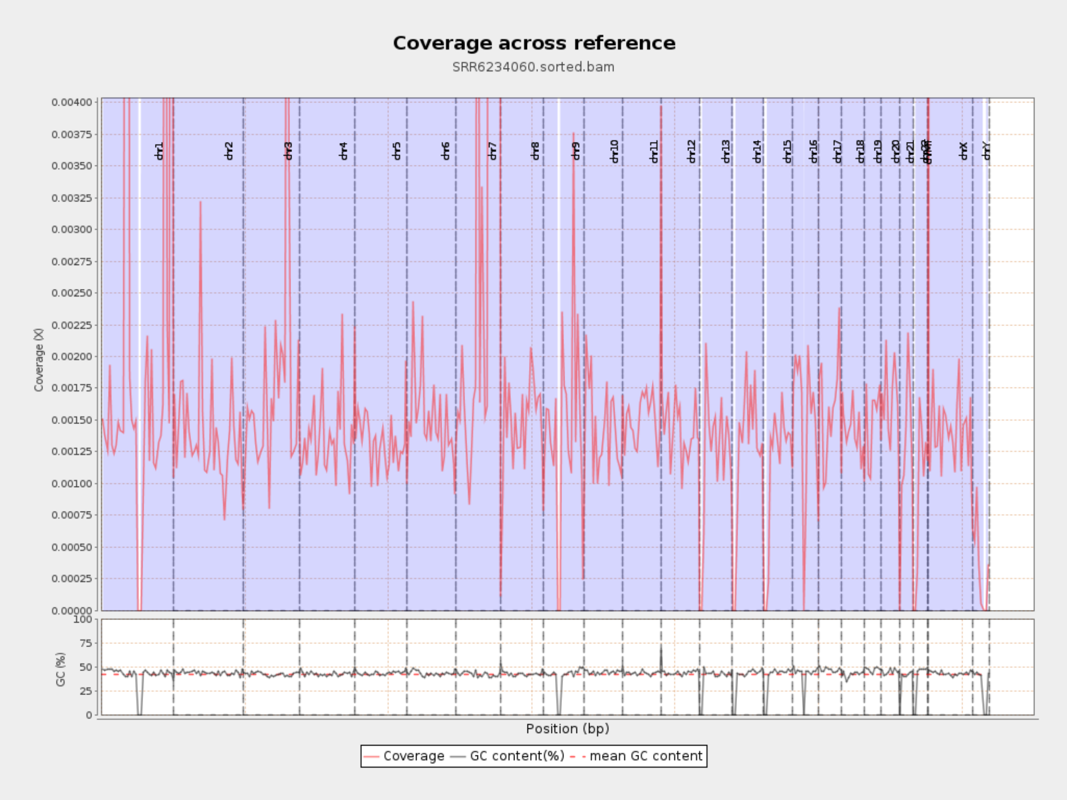
General error rate	1%
Mismatches	54,456
Insertions	1,151
Mapped reads with at least one insertion	1.11%
Deletions	1,738
Mapped reads with at least one deletion	1.7%
Homopolymer indels	33.51%

2.6. Chromosome stats

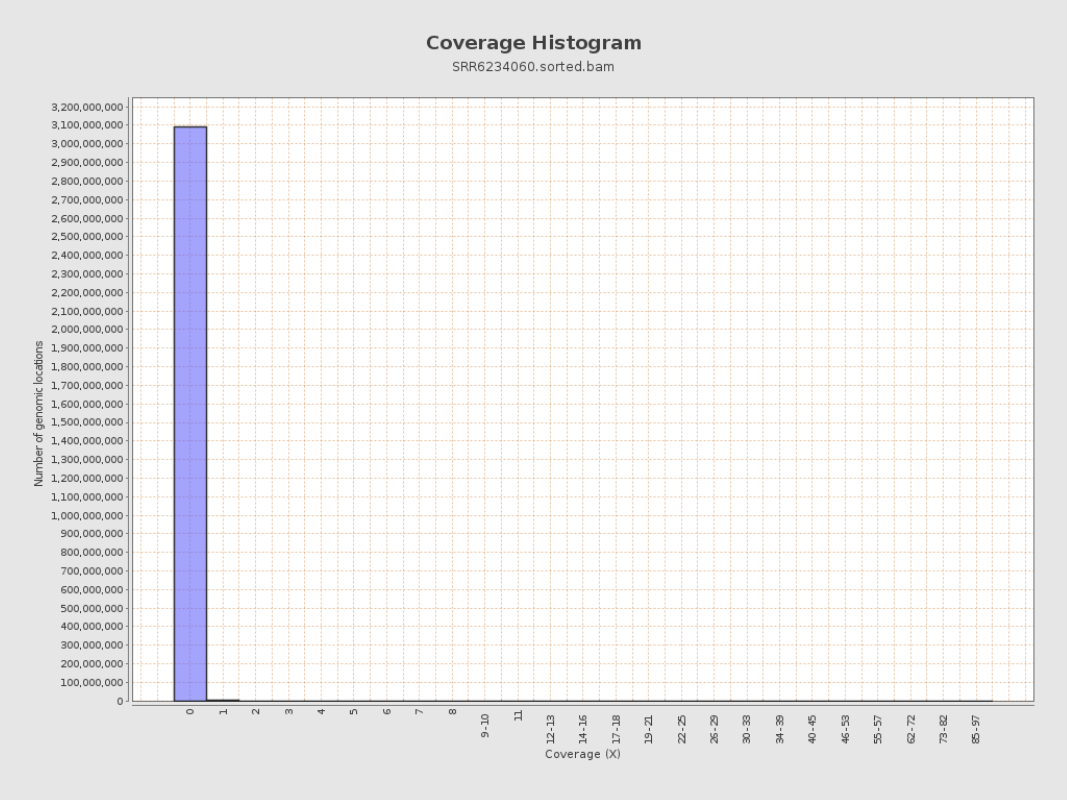
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	725814	0.0029	0.0859
chr2	243199373	343373	0.0014	0.0723
chr3	198022430	364348	0.0018	0.0638
chr4	191154276	259540	0.0014	0.0591
chr5	180915260	238832	0.0013	0.0582
chr6	171115067	257315	0.0015	0.0587
chr7	159138663	1249949	0.0079	0.1324

chr8	146364022	223493	0.0015	0.0608
chr9	141213431	207835	0.0015	0.058
chr10	135534747	194945	0.0014	0.0589
chr11	135006516	205675	0.0015	0.0624
chr12	133851895	191205	0.0014	0.0567
chr13	115169878	136970	0.0012	0.0981
chr14	107349540	135251	0.0013	0.0679
chr15	102531392	112996	0.0011	0.0524
chr16	90354753	135104	0.0015	0.0642
chr17	81195210	129134	0.0016	0.0612
chr18	78077248	111583	0.0014	0.0657
chr19	59128983	87524	0.0015	0.0573
chr20	63025520	104379	0.0017	0.0635
chr21	48129895	62538	0.0013	0.0528
chr22	51304566	47499	0.0009	0.0417
chrMT	16571	5774	0.3484	0.8785
chrX	155270560	218928	0.0014	0.0584
chrY	59373566	21015	0.0004	0.0284

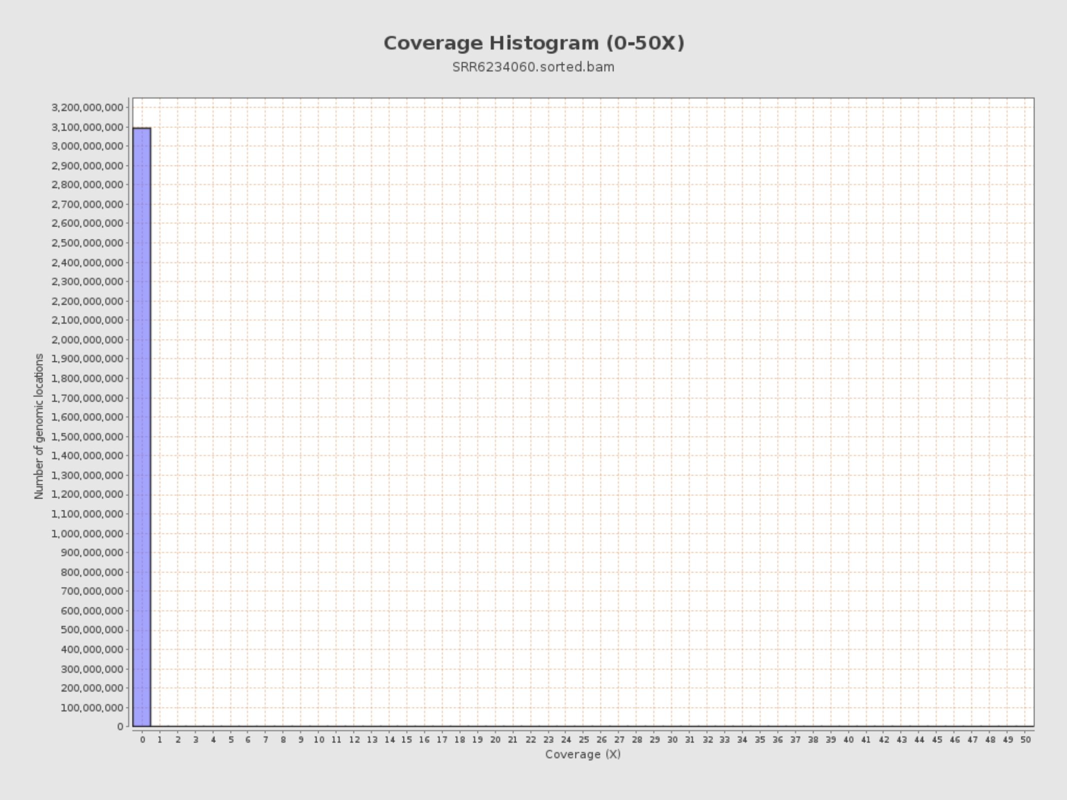
3. Results : Coverage across reference



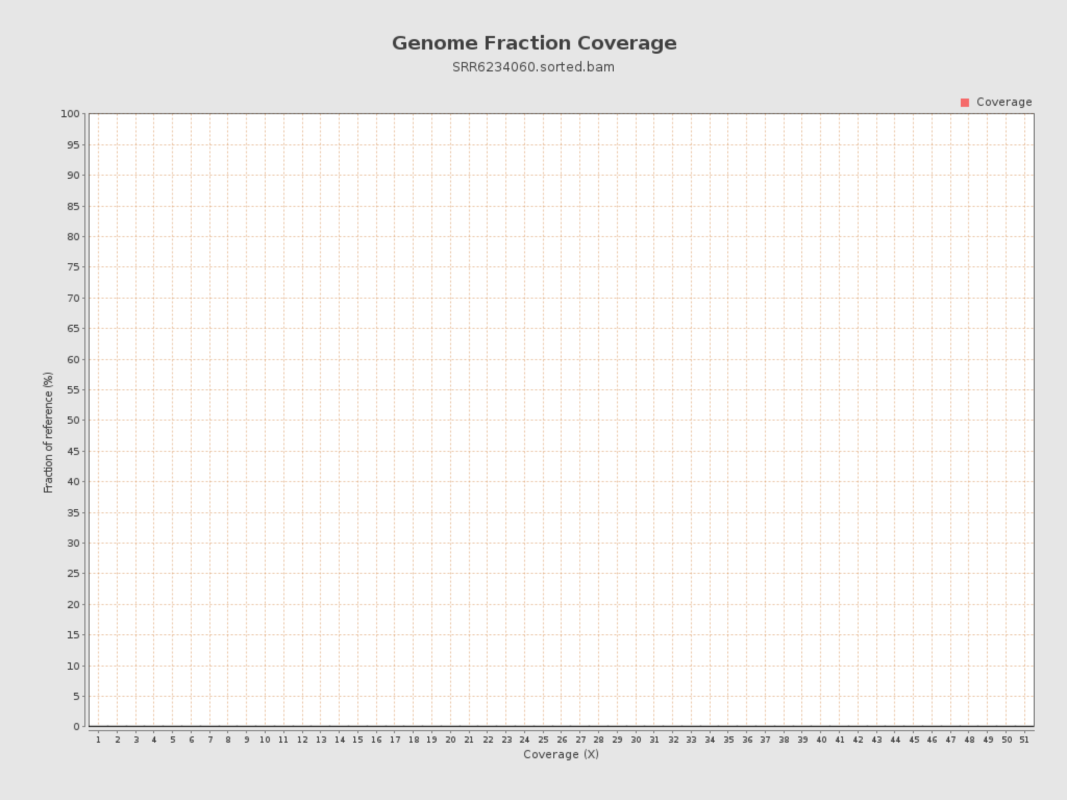
4. Results : Coverage Histogram



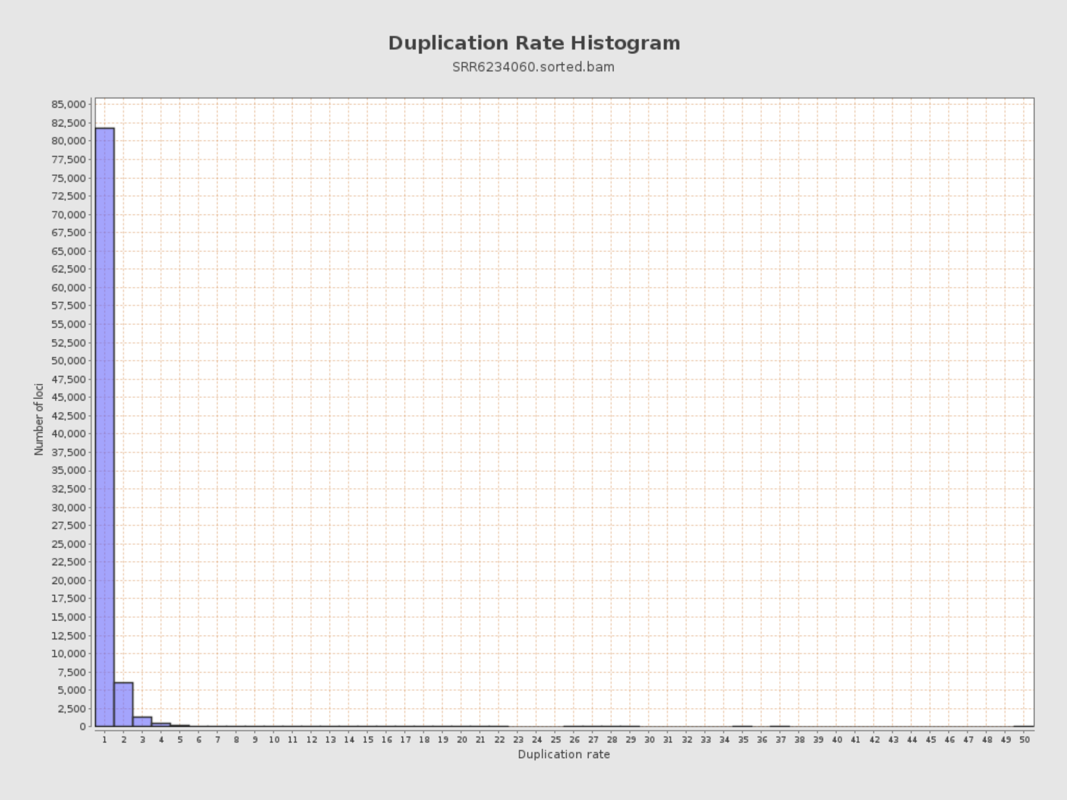
5. Results : Coverage Histogram (0-50X)



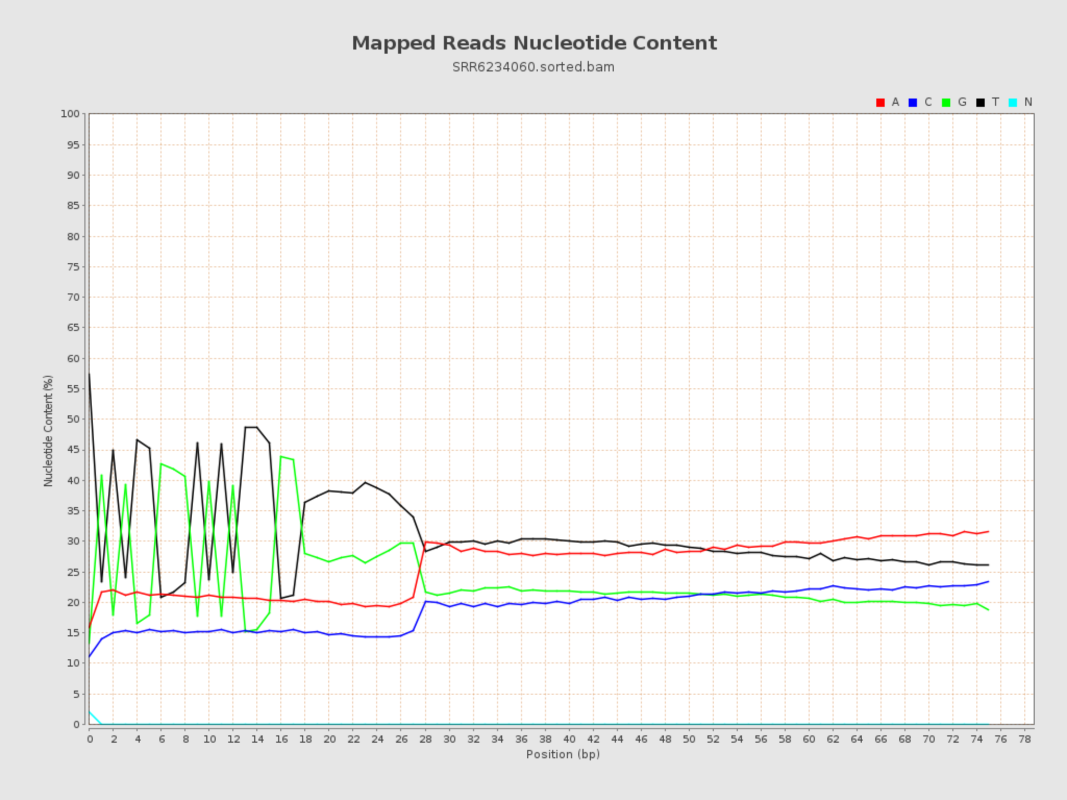
6. Results : Genome Fraction Coverage



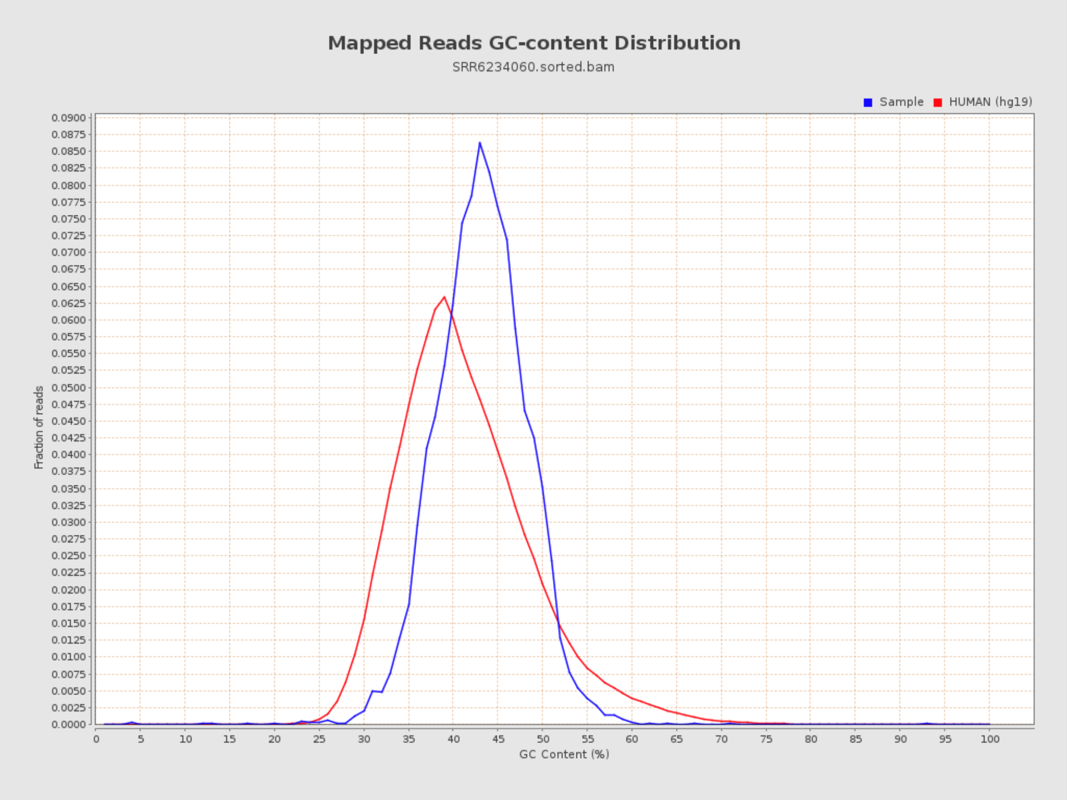
7. Results : Duplication Rate Histogram



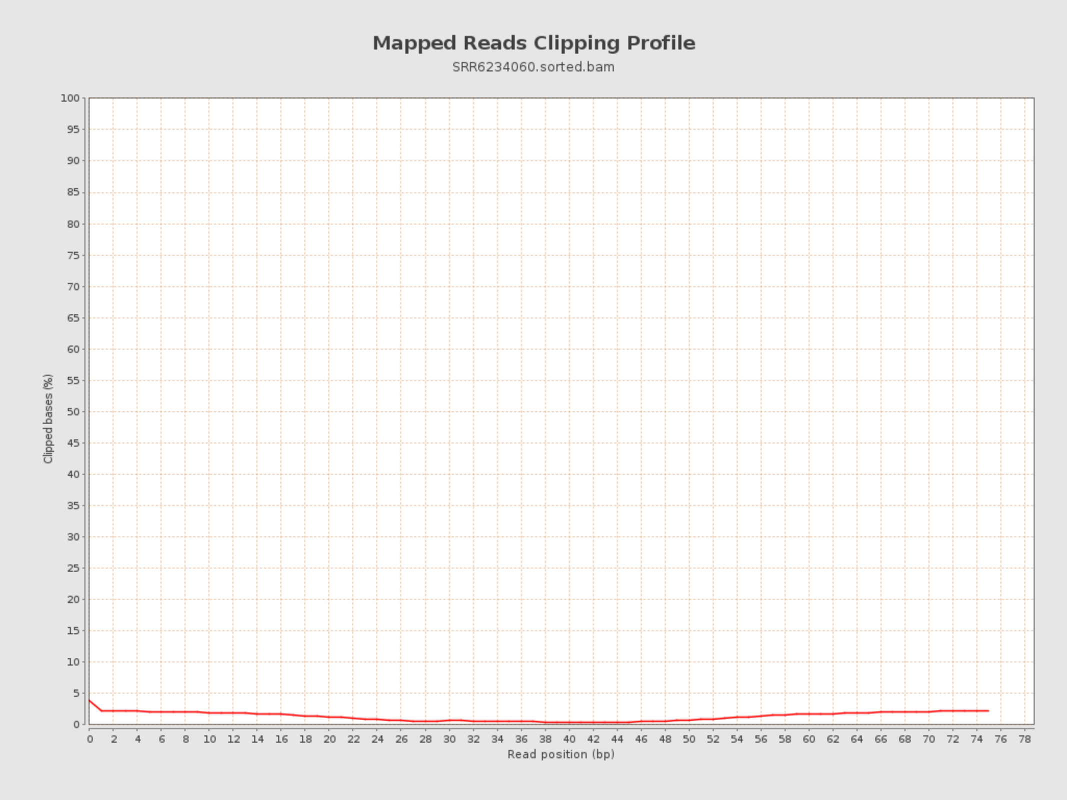
8. Results : Mapped Reads Nucleotide Content



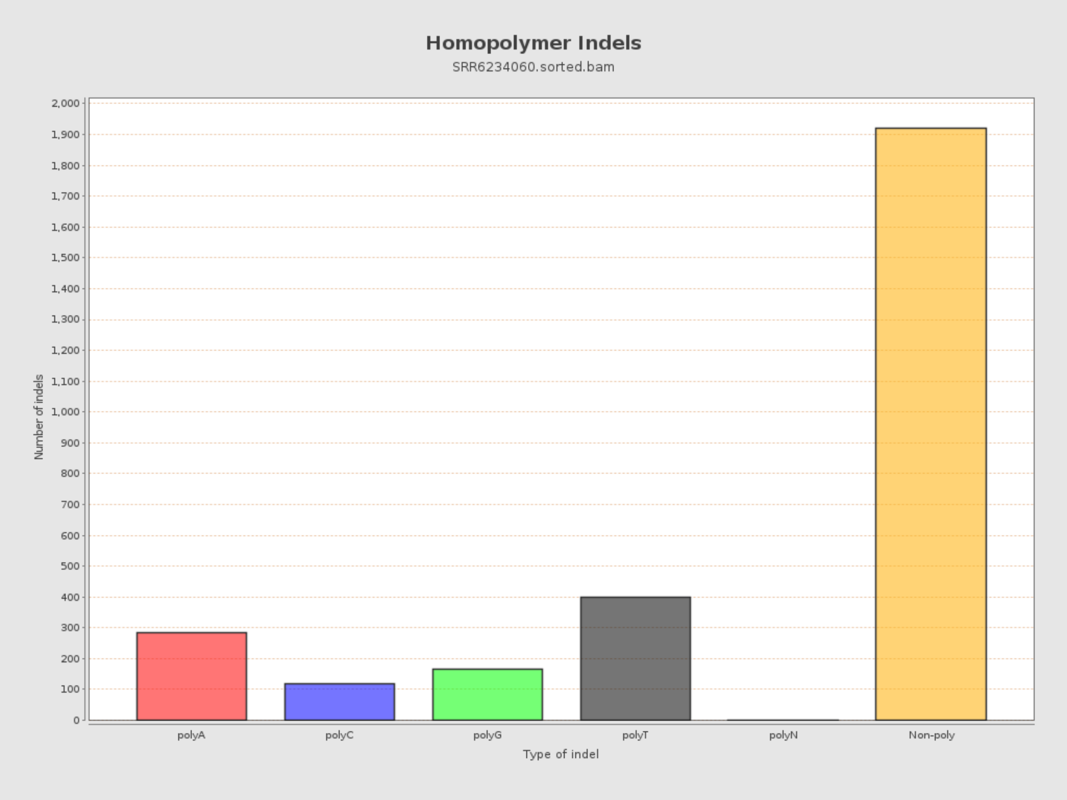
9. Results : Mapped Reads GC-content Distribution



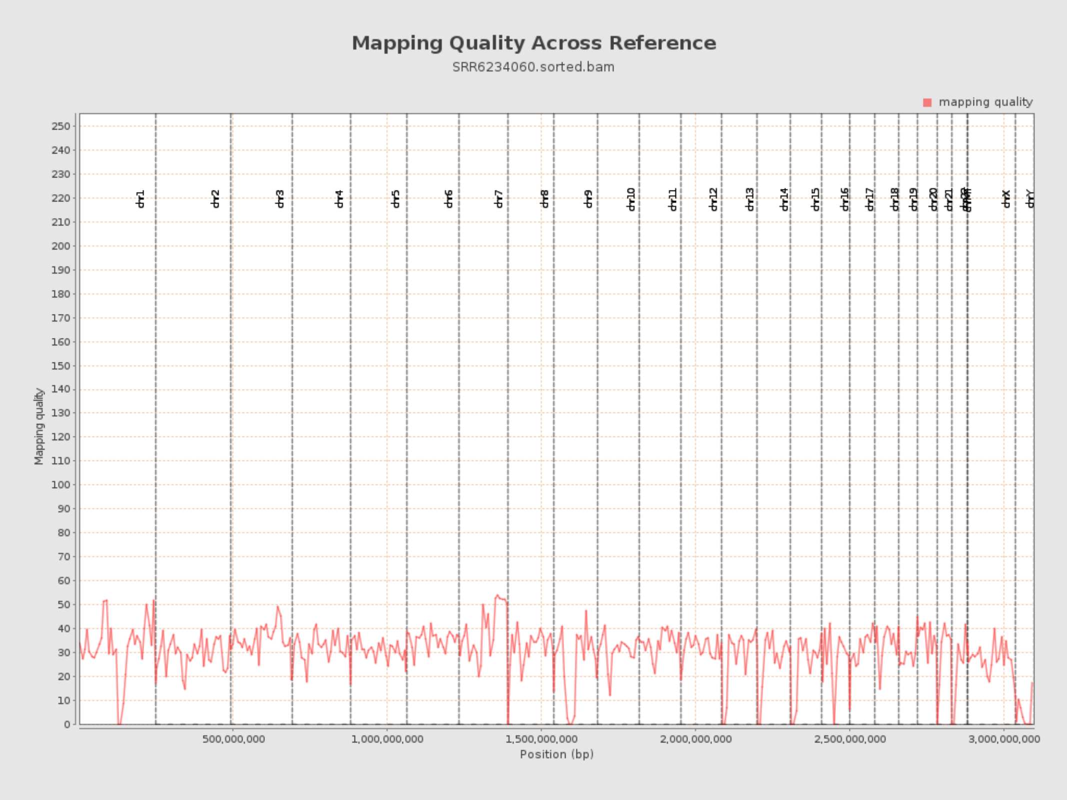
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram