Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 11:22:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234032.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_SRR6234032 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234032.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 11:22:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234032.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,303,936
Mapped reads	2,009,818 / 87.23%
Unmapped reads	294,118 / 12.77%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,257 / 0.45%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	77,304 / 3.36%
Duplication rate	2.86%
Clipped reads	895,327 / 38.86%

2.2. ACGT Content

Number/percentage of A's	36,507,637 / 27.53%
Number/percentage of C's	24,499,492 / 18.47%
Number/percentage of T's	41,579,221 / 31.35%
Number/percentage of G's	30,021,422 / 22.64%
Number/percentage of N's	23,791 / 0.02%
GC Percentage	41.11%

2.3. Coverage

Mean	0.0429

Standard Deviation	0.4085

2.4. Mapping Quality

Mean Mapping Quality	45.61

2.5. Mismatches and indels

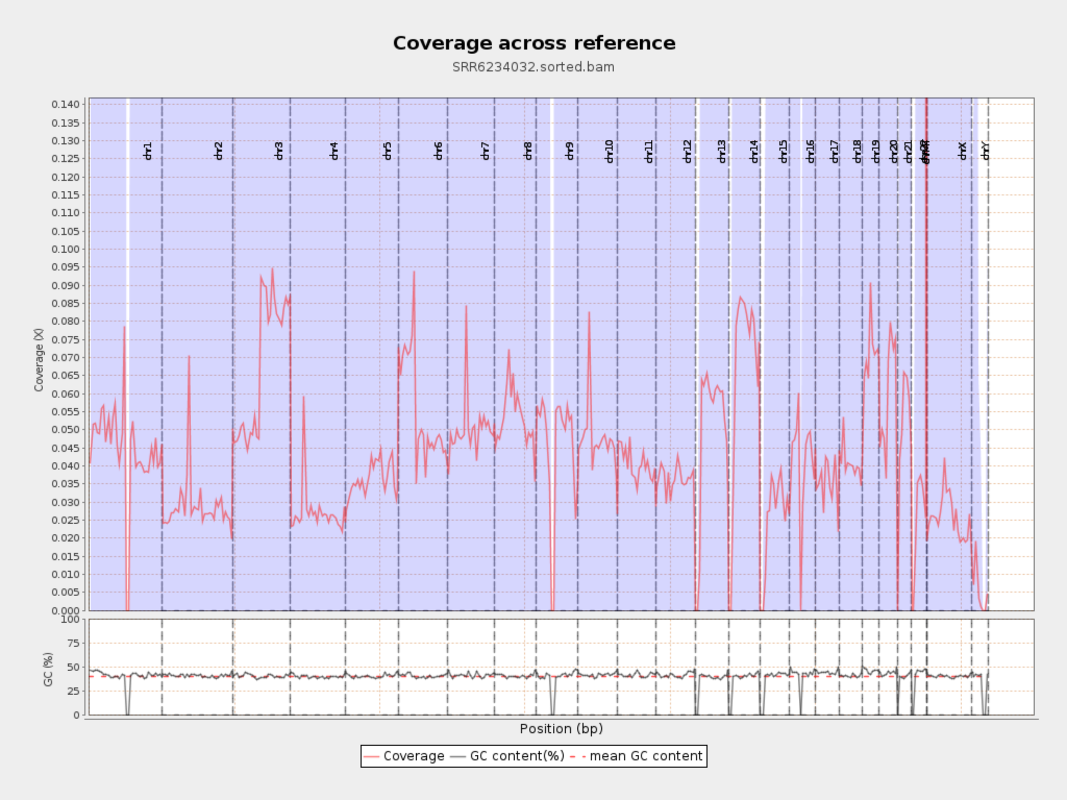
General error rate	0.78%
Mismatches	1,017,535
Insertions	9,634
Mapped reads with at least one insertion	0.47%
Deletions	38,210
Mapped reads with at least one deletion	1.88%
Homopolymer indels	45.27%

2.6. Chromosome stats

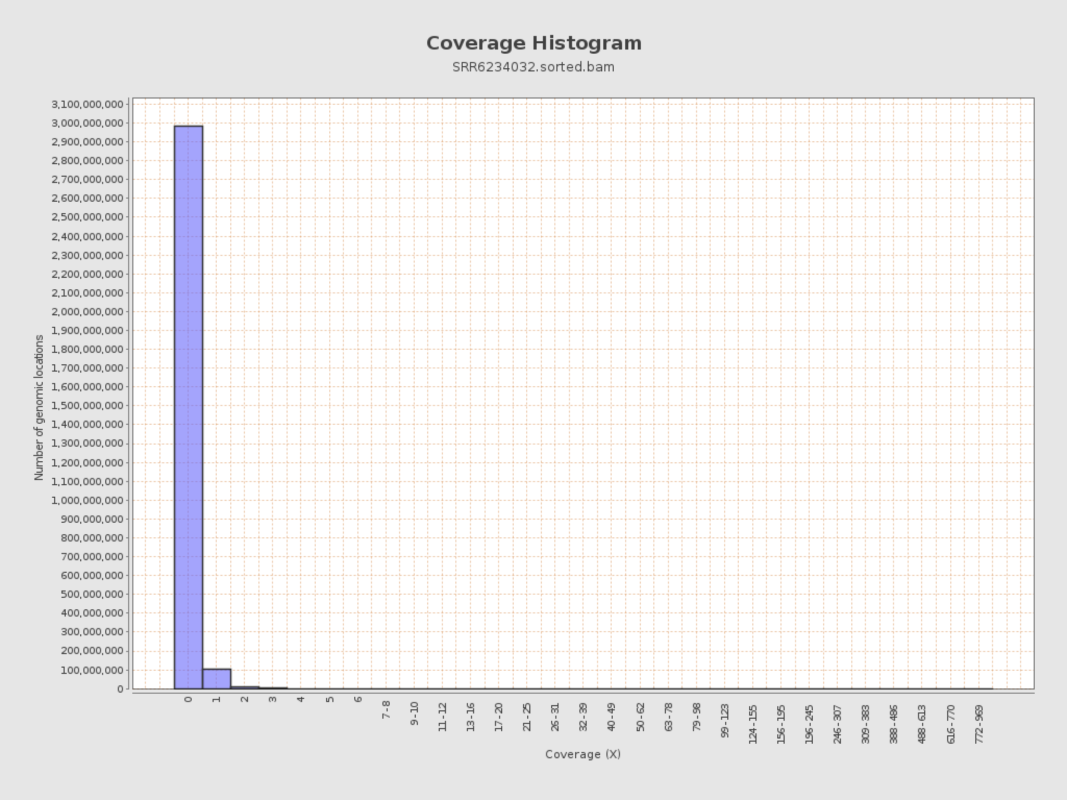
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11039460	0.0443	0.8381
chr2	243199373	7053987	0.029	0.421
chr3	198022430	13402806	0.0677	0.2933
chr4	191154276	5188673	0.0271	0.2119
chr5	180915260	6595931	0.0365	0.217
chr6	171115067	9466842	0.0553	0.3648
chr7	159138663	8042400	0.0505	0.5775

chr8	146364022	7786190	0.0532	0.4393
chr9	141213431	6339206	0.0449	0.3524
chr10	135534747	6509759	0.048	0.4043
chr11	135006516	5448861	0.0404	0.3127
chr12	133851895	4847242	0.0362	0.2184
chr13	115169878	5674846	0.0493	0.248
chr14	107349540	7079963	0.066	0.3093
chr15	102531392	2602370	0.0254	0.1793
chr16	90354753	3701490	0.041	0.2709
chr17	81195210	2837634	0.0349	0.2263
chr18	78077248	3196546	0.0409	0.684
chr19	59128983	4173438	0.0706	0.4974
chr20	63025520	3725496	0.0591	0.2834
chr21	48129895	2387756	0.0496	0.2698
chr22	51304566	1228269	0.0239	0.1716
chrMT	16571	20847	1.258	1.3603
chrX	155270560	4026714	0.0259	0.207
chrY	59373566	322533	0.0054	0.1326

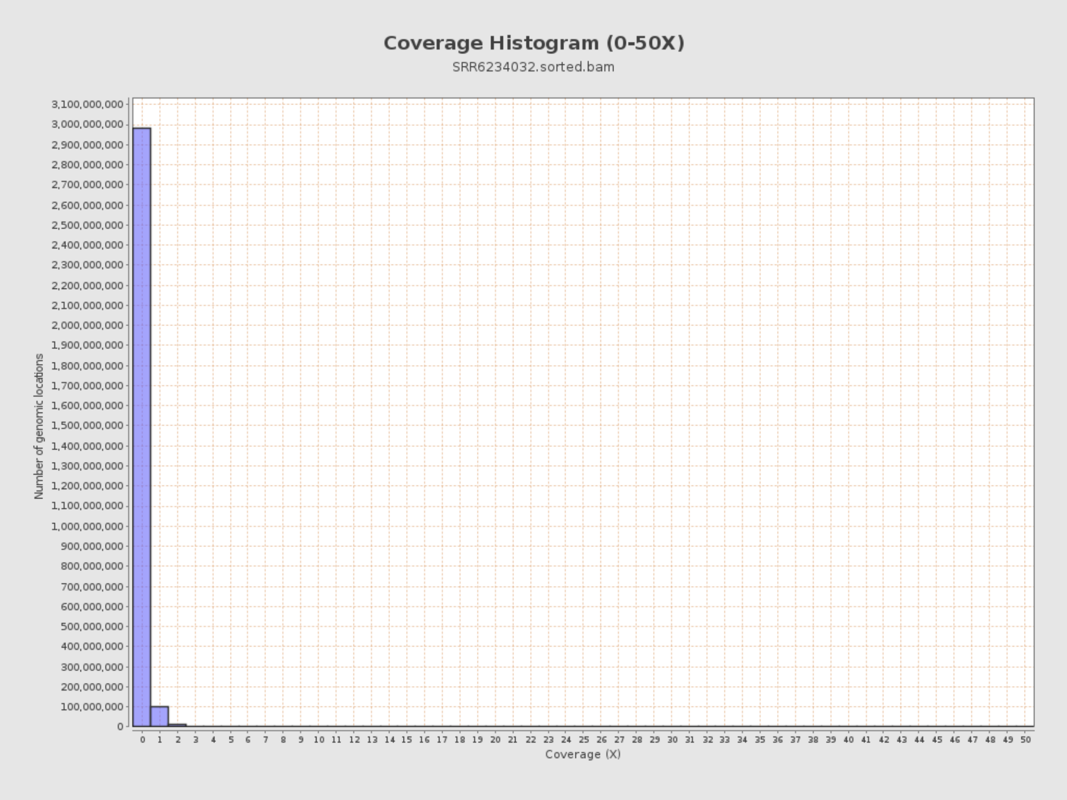
3. Results : Coverage across reference



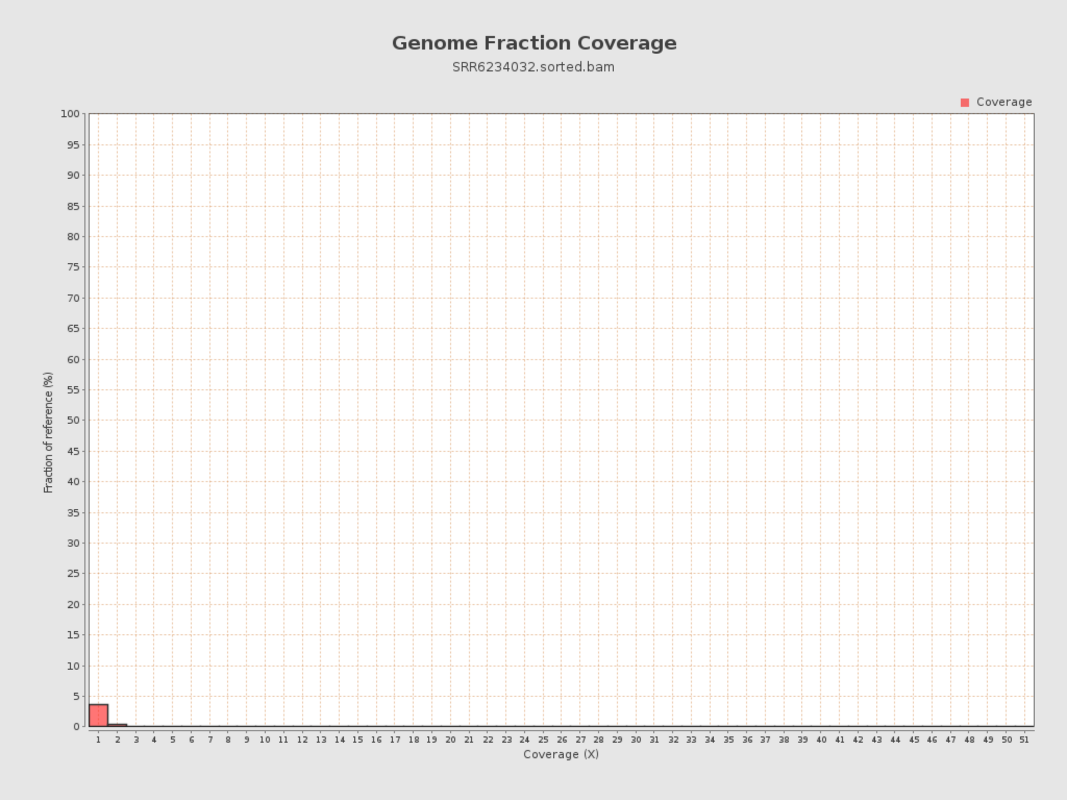
4. Results : Coverage Histogram



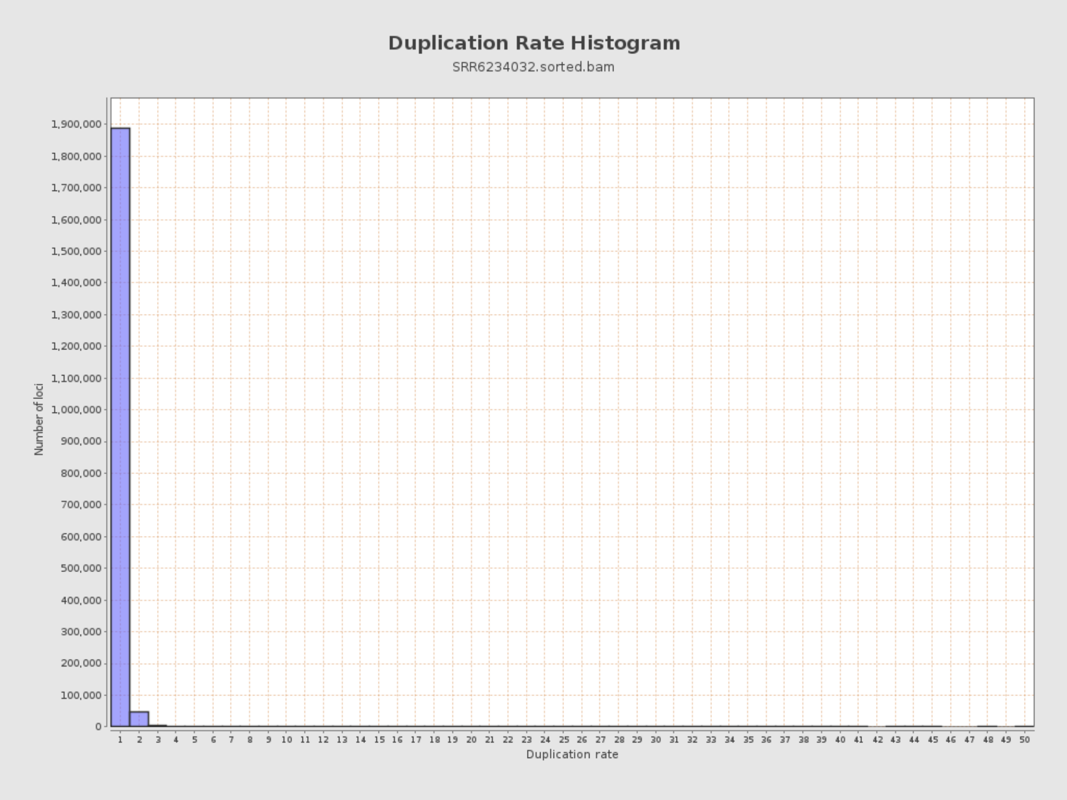
5. Results : Coverage Histogram (0-50X)



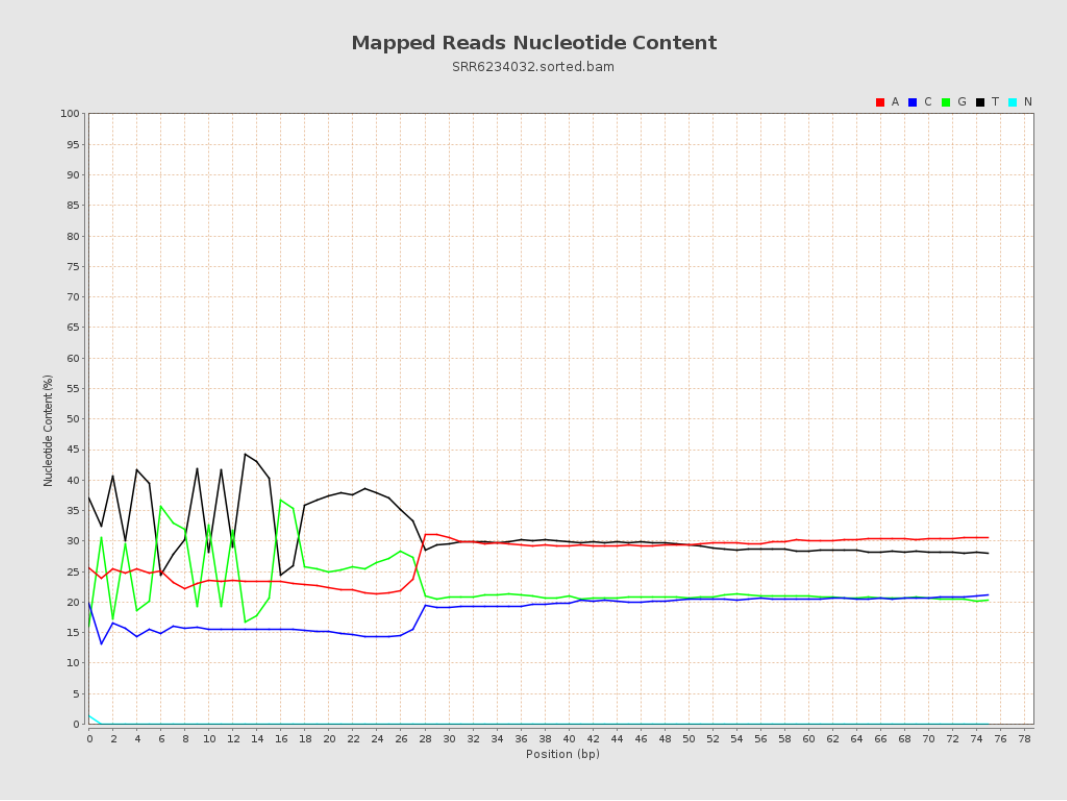
6. Results : Genome Fraction Coverage



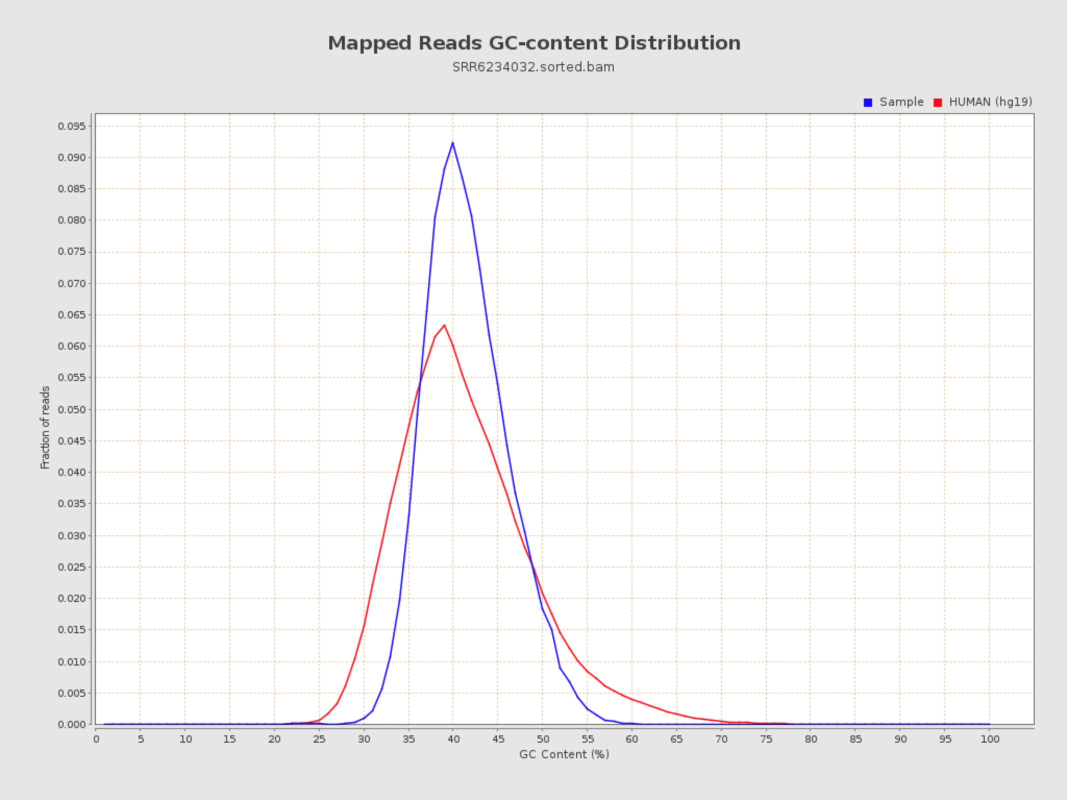
7. Results : Duplication Rate Histogram



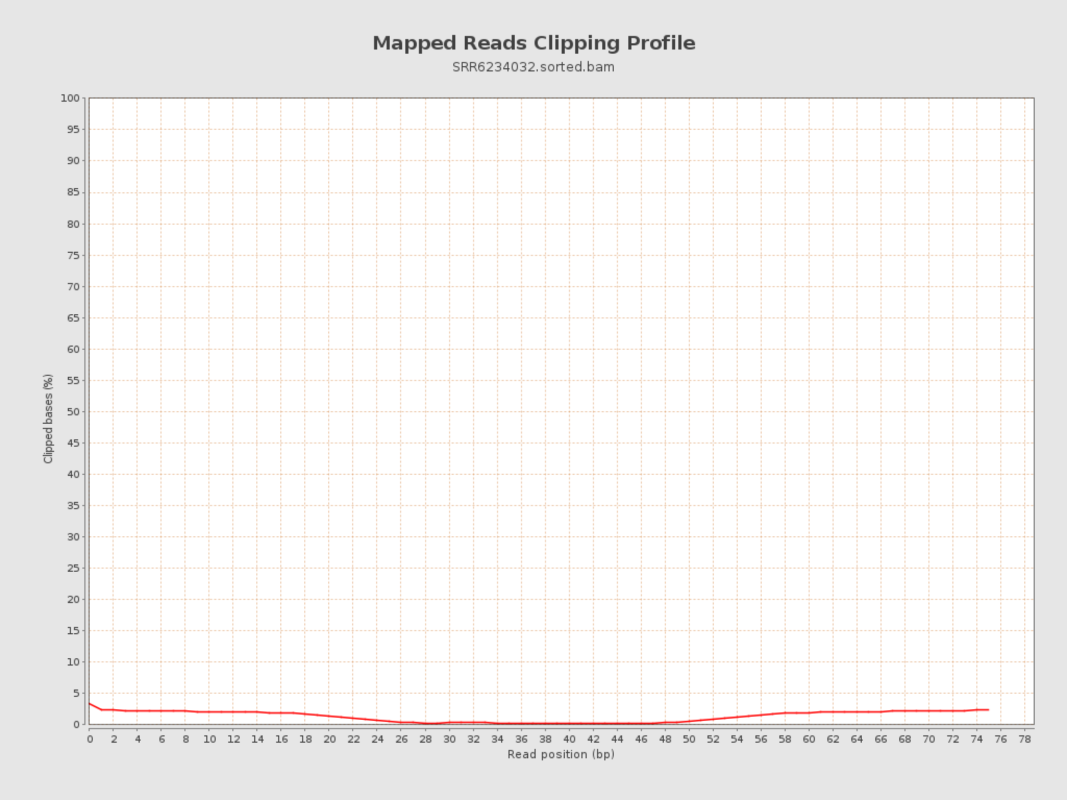
8. Results : Mapped Reads Nucleotide Content



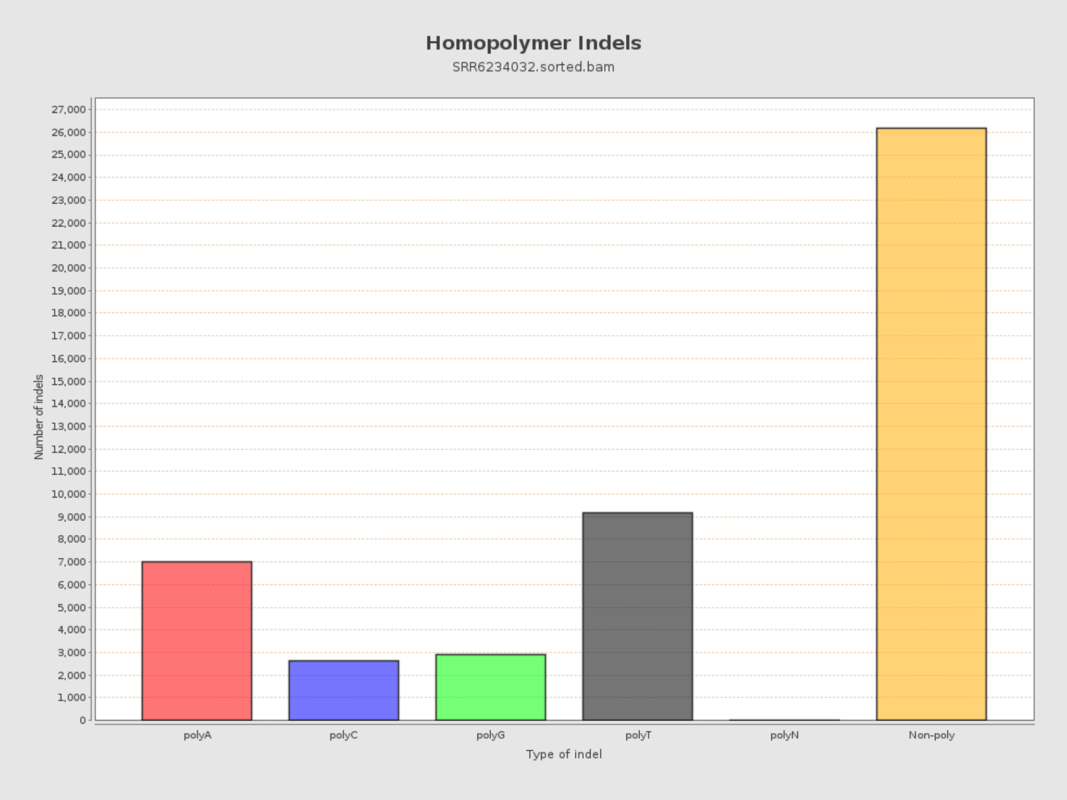
9. Results : Mapped Reads GC-content Distribution



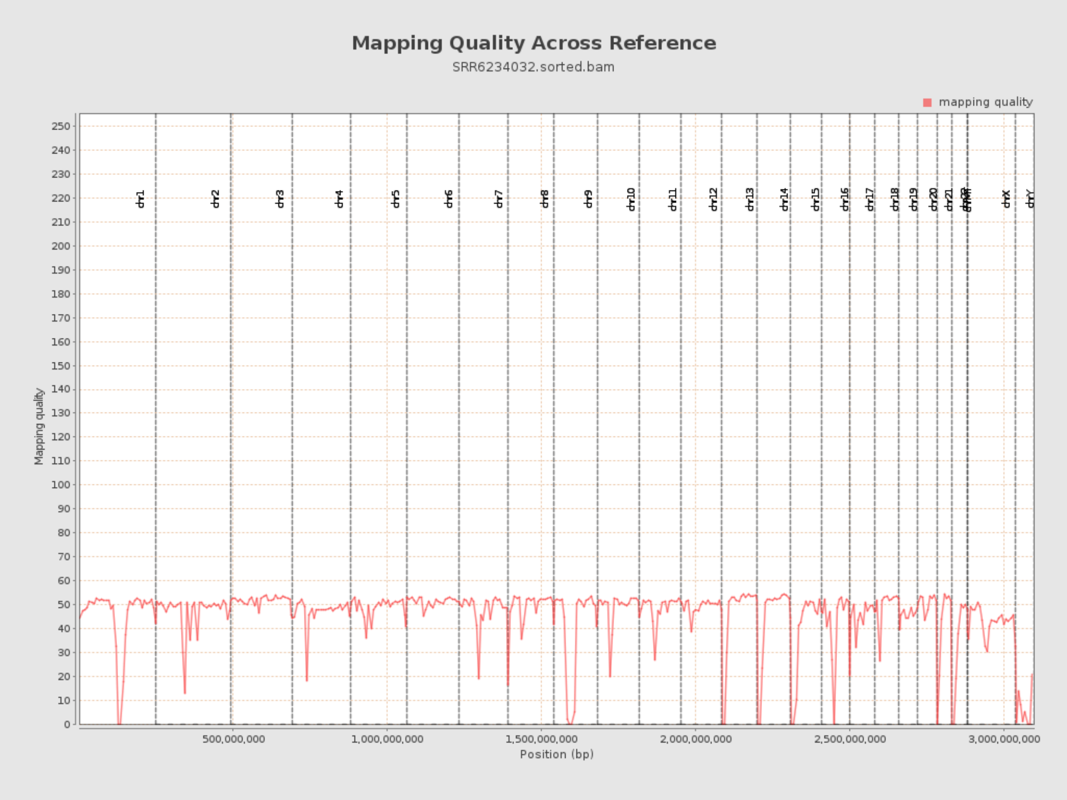
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram