Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 20:27:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238534.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_SRR6238534 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238534.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 20:27:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238534.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,882,268
Mapped reads	2,585,097 / 89.69%
Unmapped reads	297,171 / 10.31%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,726 / 0.72%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	923,135 / 32.03%
Duplication rate	20.15%
Clipped reads	1,474,639 / 51.16%

2.2. ACGT Content

Number/percentage of A's	40,856,792 / 25.04%
Number/percentage of C's	28,860,425 / 17.69%
Number/percentage of T's	54,632,479 / 33.48%
Number/percentage of G's	38,815,796 / 23.79%
Number/percentage of N's	11,506 / 0.01%
GC Percentage	41.47%

2.3. Coverage

Mean	0.0527

Standard Deviation	0.8685

2.4. Mapping Quality

Mean Mapping Quality	43.97

2.5. Mismatches and indels

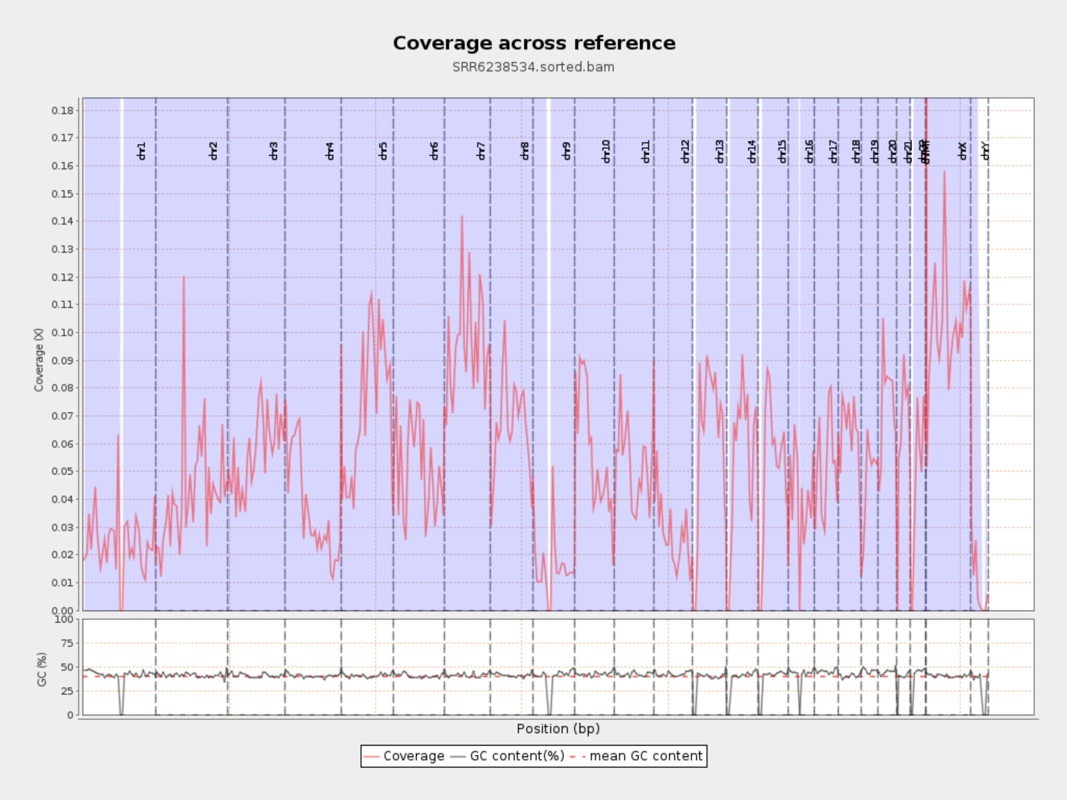
General error rate	0.56%
Mismatches	898,362
Insertions	11,100
Mapped reads with at least one insertion	0.43%
Deletions	38,984
Mapped reads with at least one deletion	1.5%
Homopolymer indels	42.85%

2.6. Chromosome stats

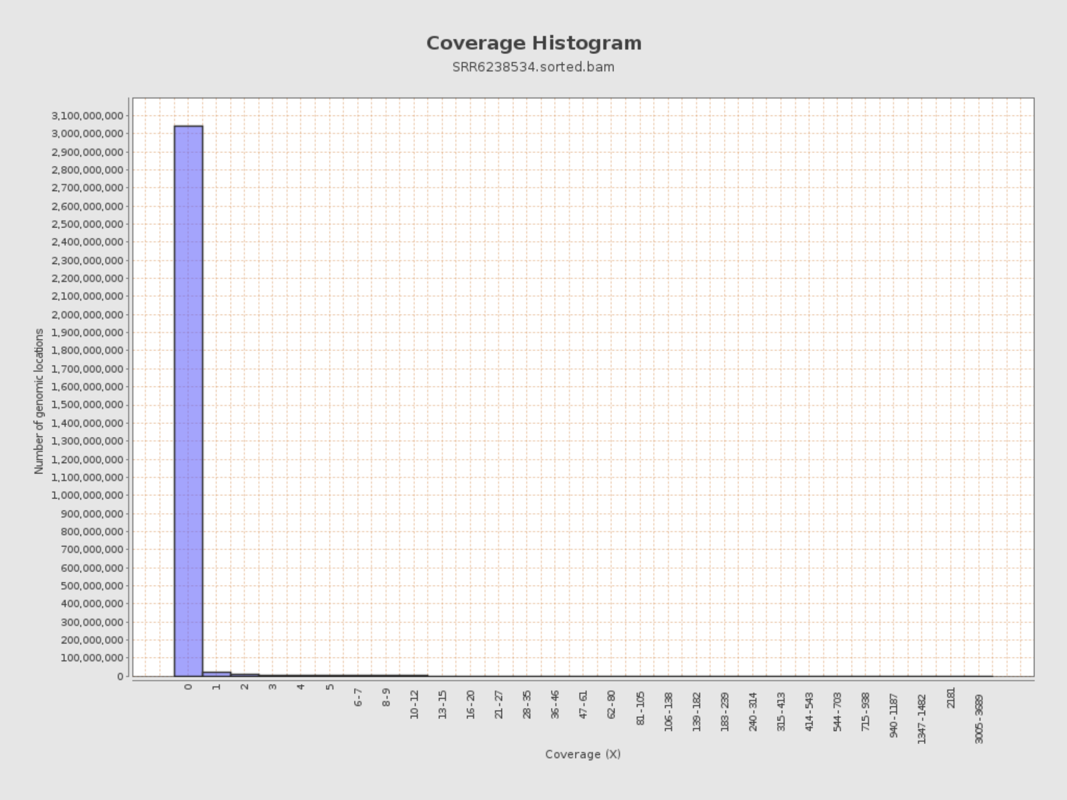
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6074167	0.0244	1.0143
chr2	243199373	10336359	0.0425	1.7103
chr3	198022430	11333205	0.0572	0.6135
chr4	191154276	6916957	0.0362	0.4817
chr5	180915260	13322082	0.0736	0.692
chr6	171115067	8894660	0.052	0.7599
chr7	159138663	15203600	0.0955	1.1741

chr8	146364022	9756768	0.0667	0.754
chr9	141213431	2207336	0.0156	0.4051
chr10	135534747	7777715	0.0574	0.6493
chr11	135006516	7079870	0.0524	0.6632
chr12	133851895	3689267	0.0276	0.414
chr13	115169878	7155055	0.0621	0.6907
chr14	107349540	5862988	0.0546	0.5947
chr15	102531392	5172834	0.0505	0.6473
chr16	90354753	3514423	0.0389	0.5333
chr17	81195210	4312314	0.0531	0.6035
chr18	78077248	5068878	0.0649	1.5246
chr19	59128983	2776944	0.047	0.8054
chr20	63025520	4741188	0.0752	0.7339
chr21	48129895	3075268	0.0639	0.6457
chr22	51304566	2372540	0.0462	0.5404
chrMT	16571	32092	1.9366	3.1554
chrX	155270560	16031826	0.1033	0.8463
chrY	59373566	534729	0.009	0.2864

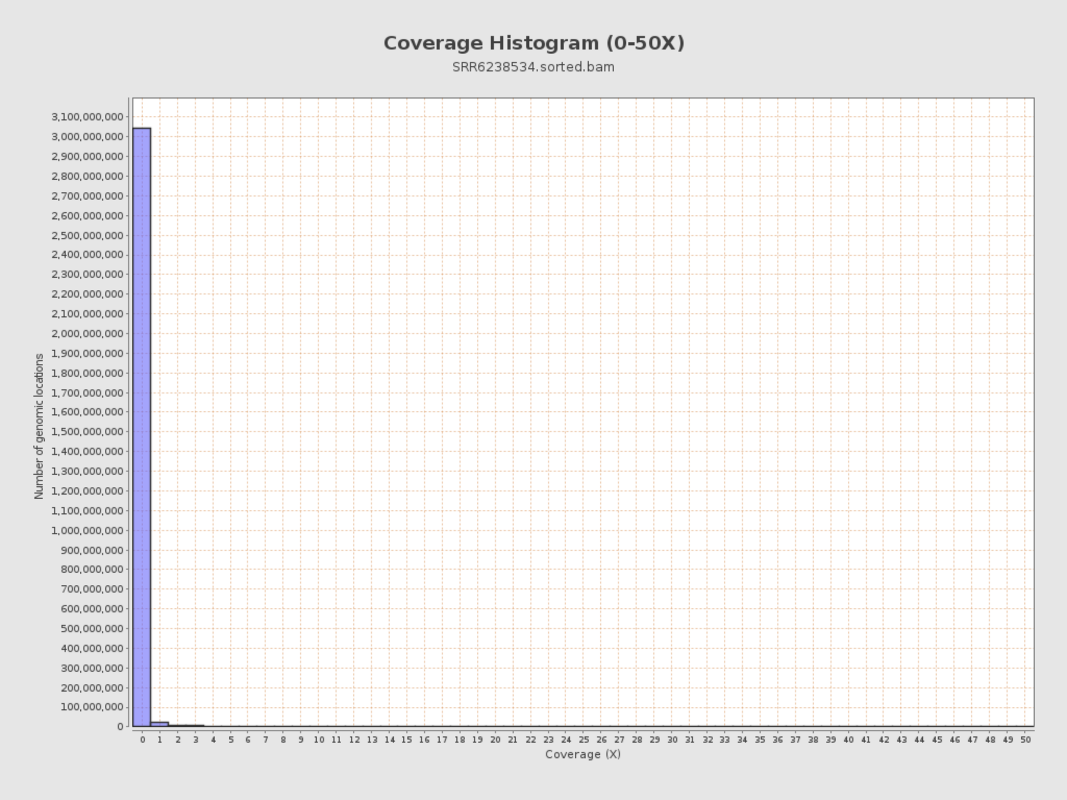
3. Results : Coverage across reference



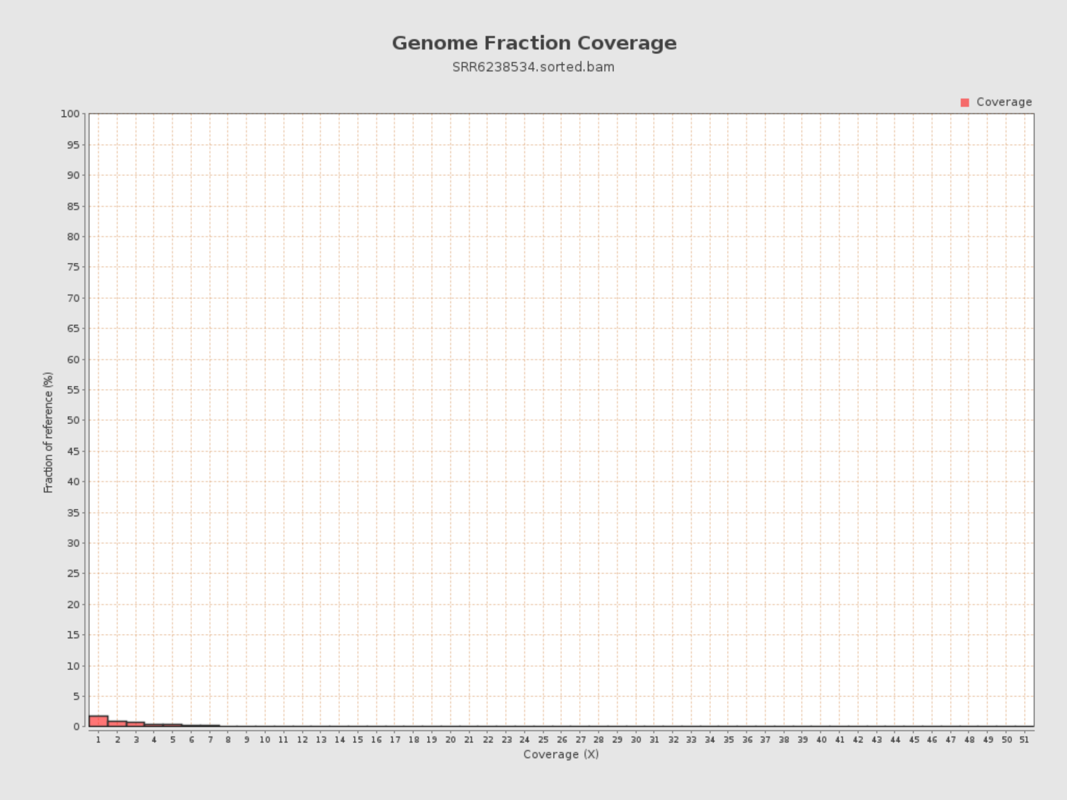
4. Results : Coverage Histogram



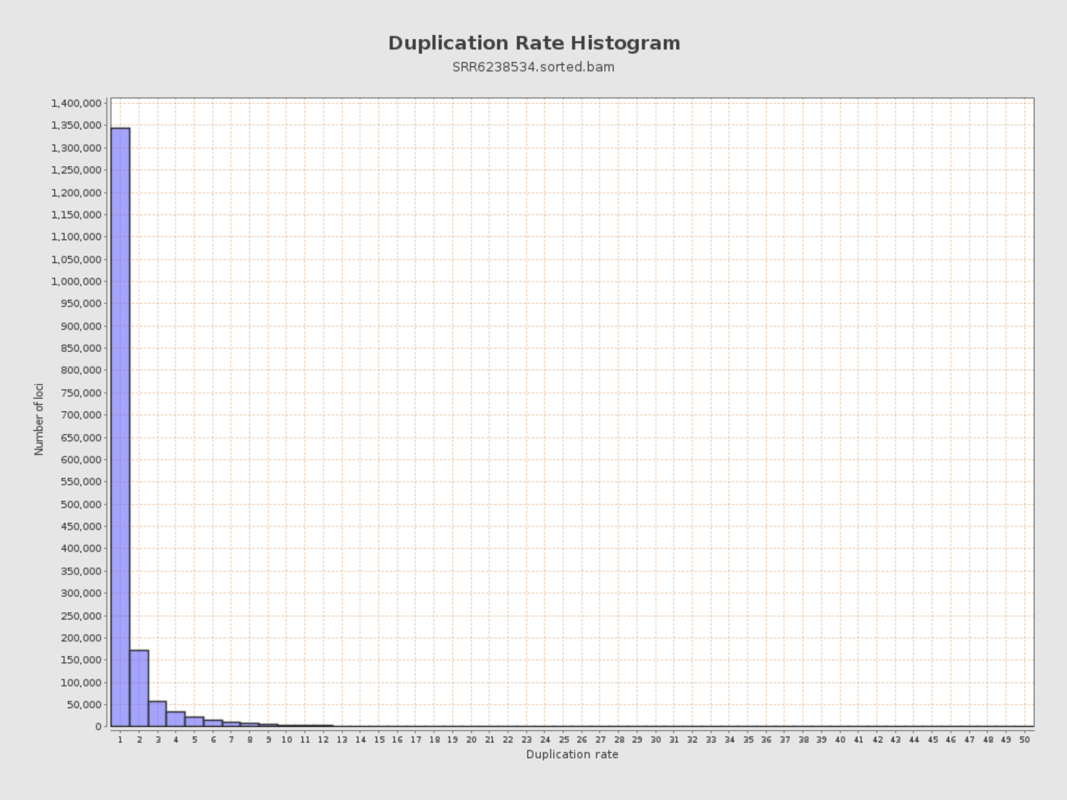
5. Results : Coverage Histogram (0-50X)



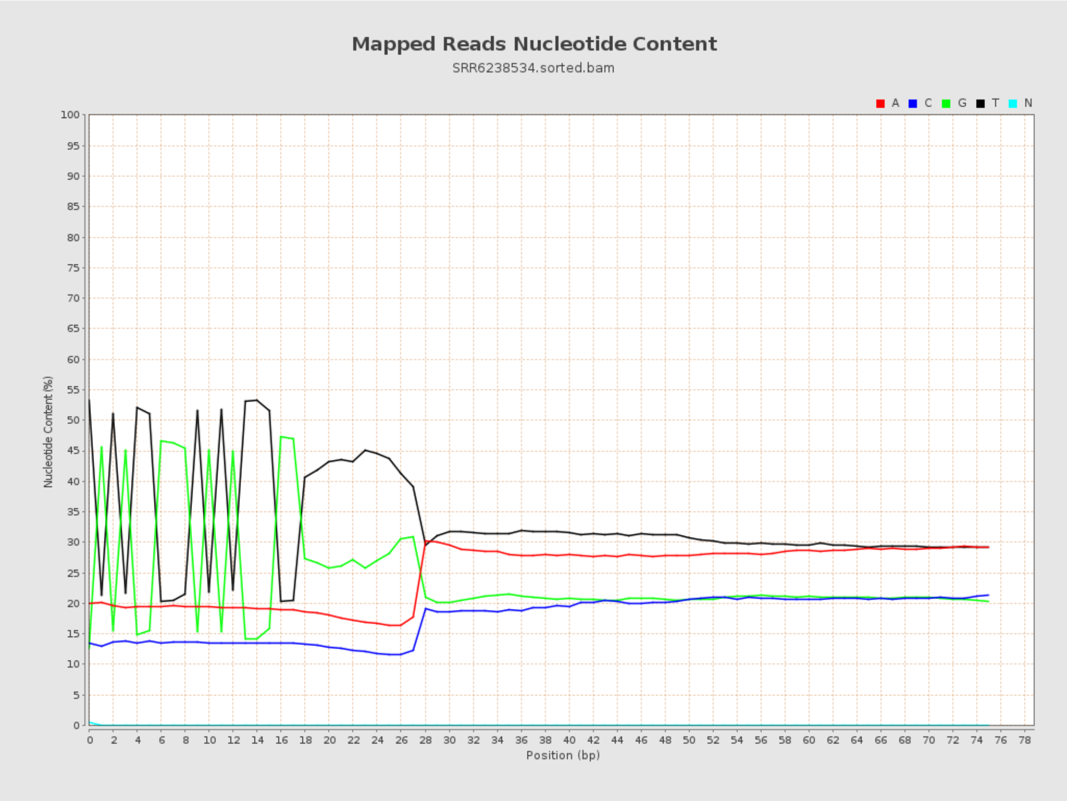
6. Results : Genome Fraction Coverage



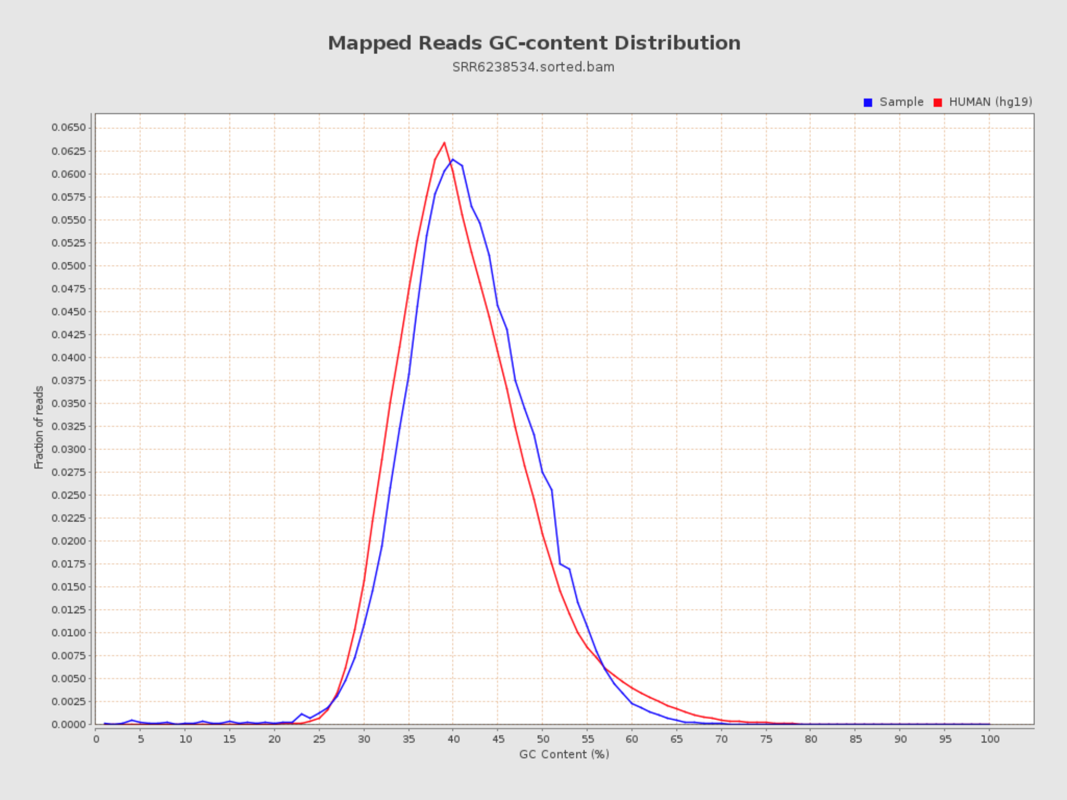
7. Results : Duplication Rate Histogram



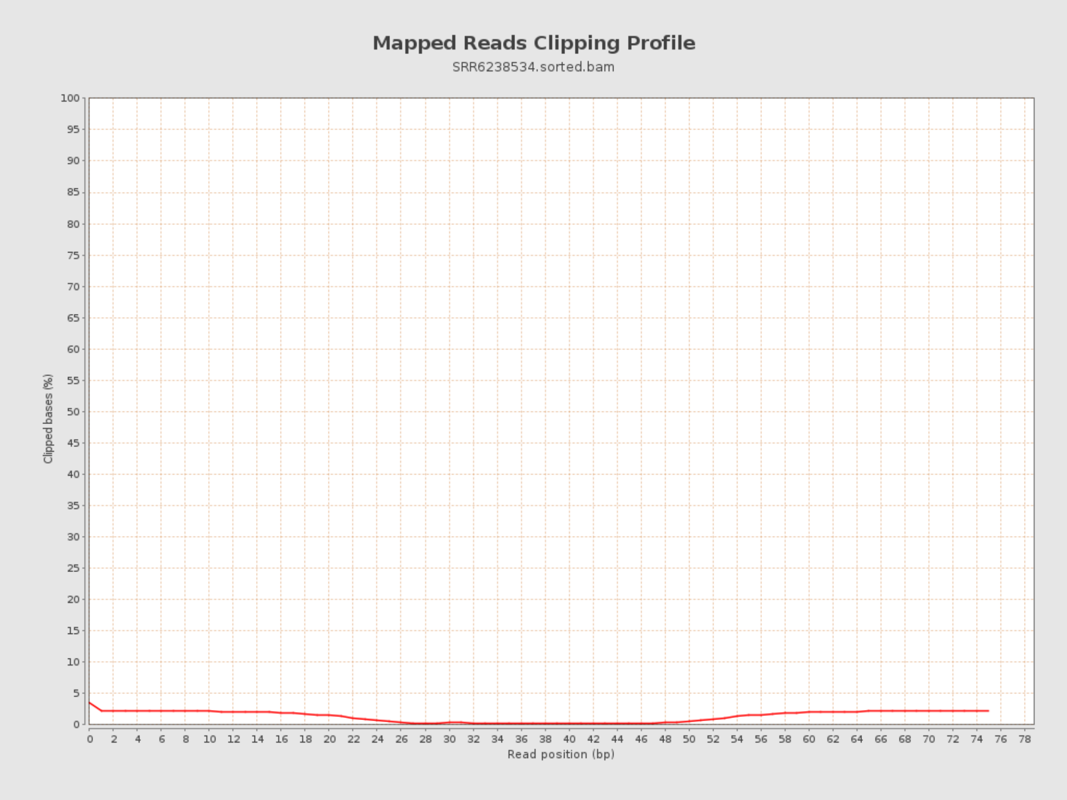
8. Results : Mapped Reads Nucleotide Content



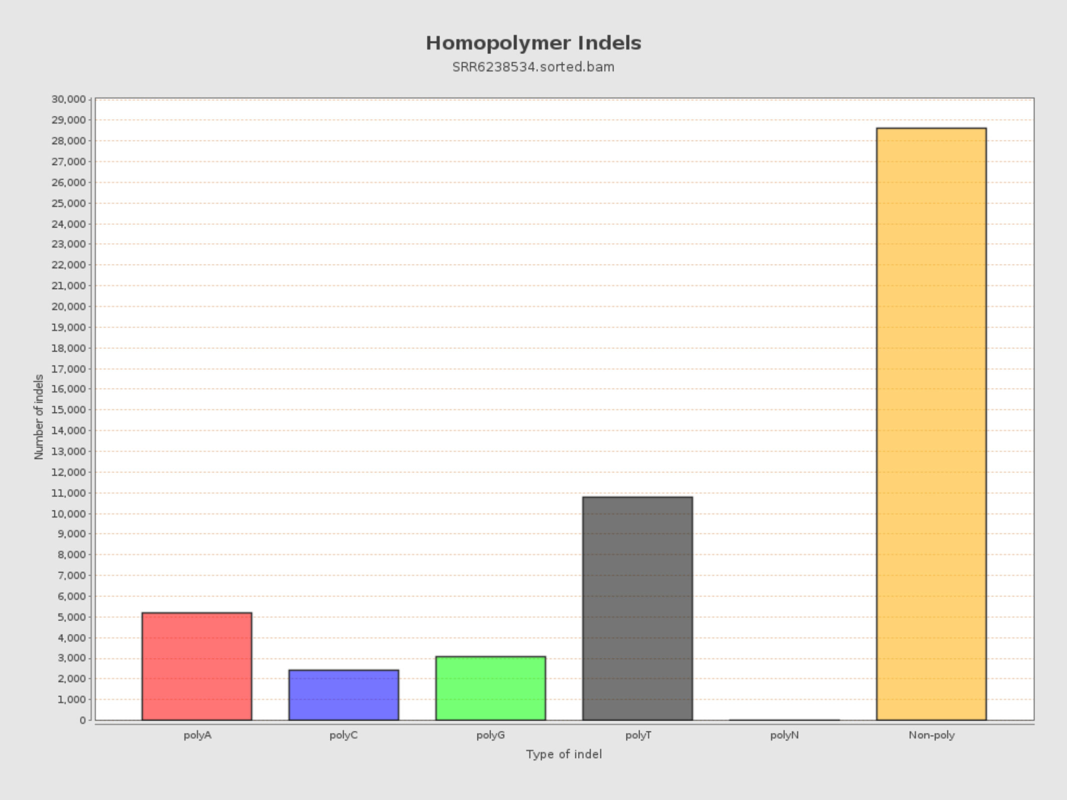
9. Results : Mapped Reads GC-content Distribution



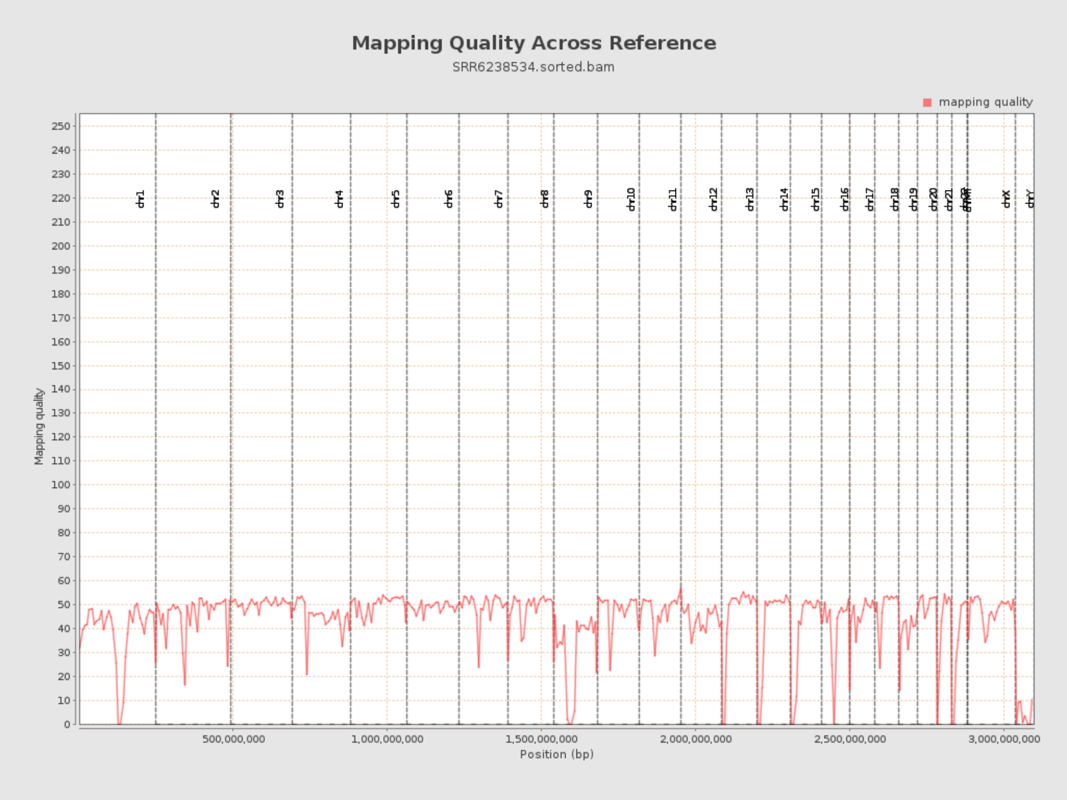
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram