Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 12:58:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238252.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_SRR6238252 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238252.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 12:58:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238252.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,432,833
Mapped reads	989,273 / 69.04%
Unmapped reads	443,560 / 30.96%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,570 / 0.81%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	100,224 / 6.99%
Duplication rate	7.81%
Clipped reads	647,215 / 45.17%

2.2. ACGT Content

Number/percentage of A's	17,286,826 / 28.31%
Number/percentage of C's	12,200,948 / 19.98%
Number/percentage of T's	18,289,340 / 29.95%
Number/percentage of G's	13,269,631 / 21.73%
Number/percentage of N's	16,839 / 0.03%
GC Percentage	41.71%

2.3. Coverage

Mean	0.0197

Standard Deviation	0.268

2.4. Mapping Quality

Mean Mapping Quality	44.04

2.5. Mismatches and indels

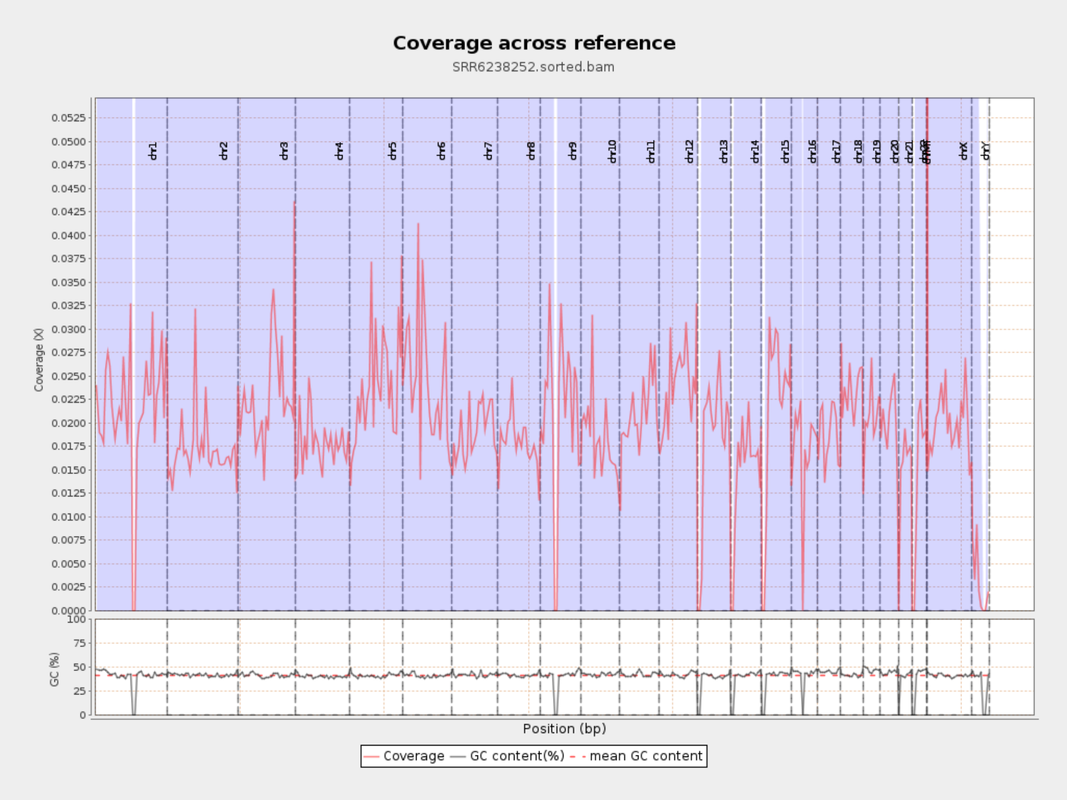
General error rate	0.95%
Mismatches	571,479
Insertions	5,051
Mapped reads with at least one insertion	0.51%
Deletions	15,432
Mapped reads with at least one deletion	1.55%
Homopolymer indels	46.12%

2.6. Chromosome stats

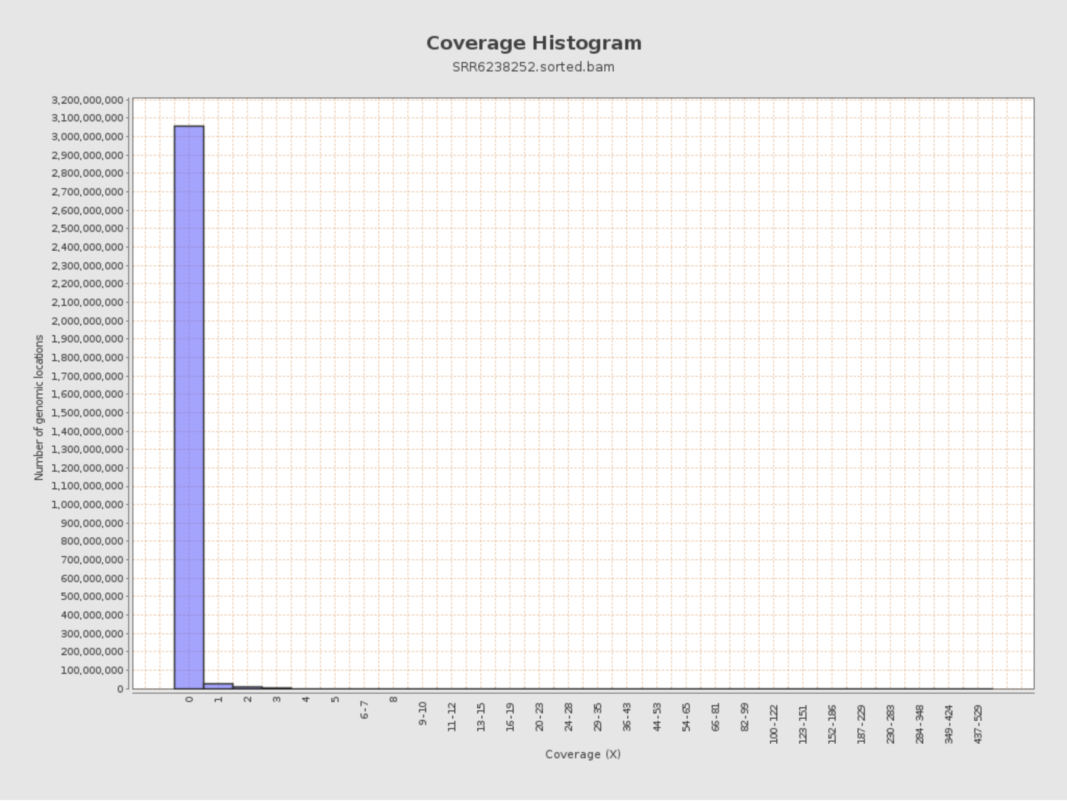
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5367956	0.0215	0.3928
chr2	243199373	4161808	0.0171	0.3386
chr3	198022430	4493131	0.0227	0.2253
chr4	191154276	3410591	0.0178	0.2103
chr5	180915260	4350021	0.024	0.2331
chr6	171115067	4181668	0.0244	0.2853
chr7	159138663	3038548	0.0191	0.2349

chr8	146364022	2623736	0.0179	0.2529
chr9	141213431	2988902	0.0212	0.2354
chr10	135534747	2484639	0.0183	0.2323
chr11	135006516	2857532	0.0212	0.2305
chr12	133851895	3211087	0.024	0.2348
chr13	115169878	2055829	0.0179	0.2167
chr14	107349540	1553458	0.0145	0.3423
chr15	102531392	2191661	0.0214	0.3726
chr16	90354753	1513456	0.0168	0.1924
chr17	81195210	1513447	0.0186	0.2052
chr18	78077248	1833564	0.0235	0.2918
chr19	59128983	1233617	0.0209	0.282
chr20	63025520	1266100	0.0201	0.2107
chr21	48129895	735319	0.0153	0.178
chr22	51304566	733961	0.0143	0.175
chrMT	16571	15157	0.9147	1.5134
chrX	155270560	3102419	0.02	0.2438
chrY	59373566	170485	0.0029	0.086

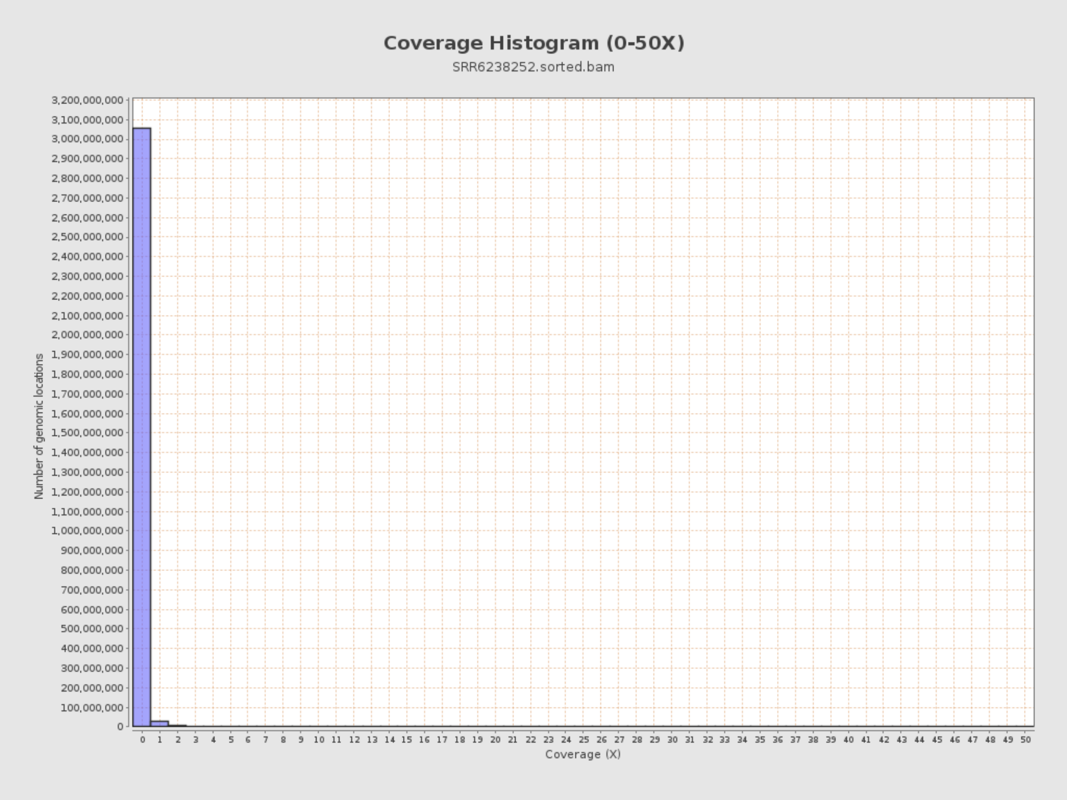
3. Results : Coverage across reference



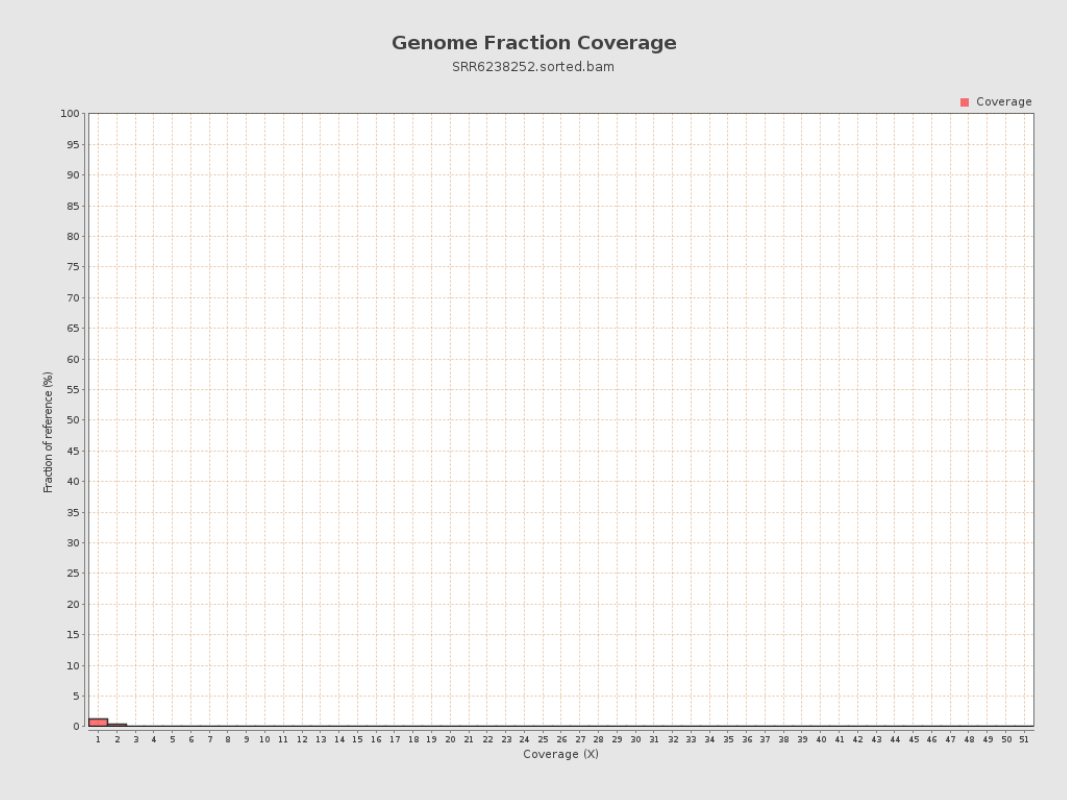
4. Results : Coverage Histogram



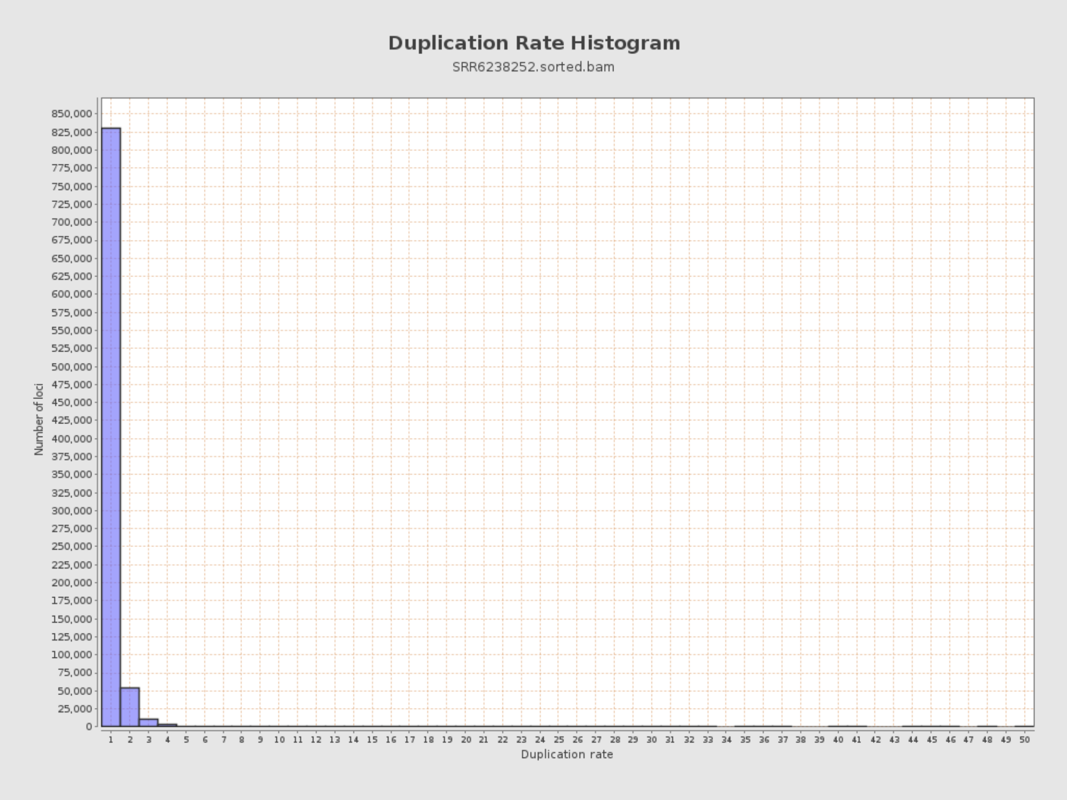
5. Results : Coverage Histogram (0-50X)



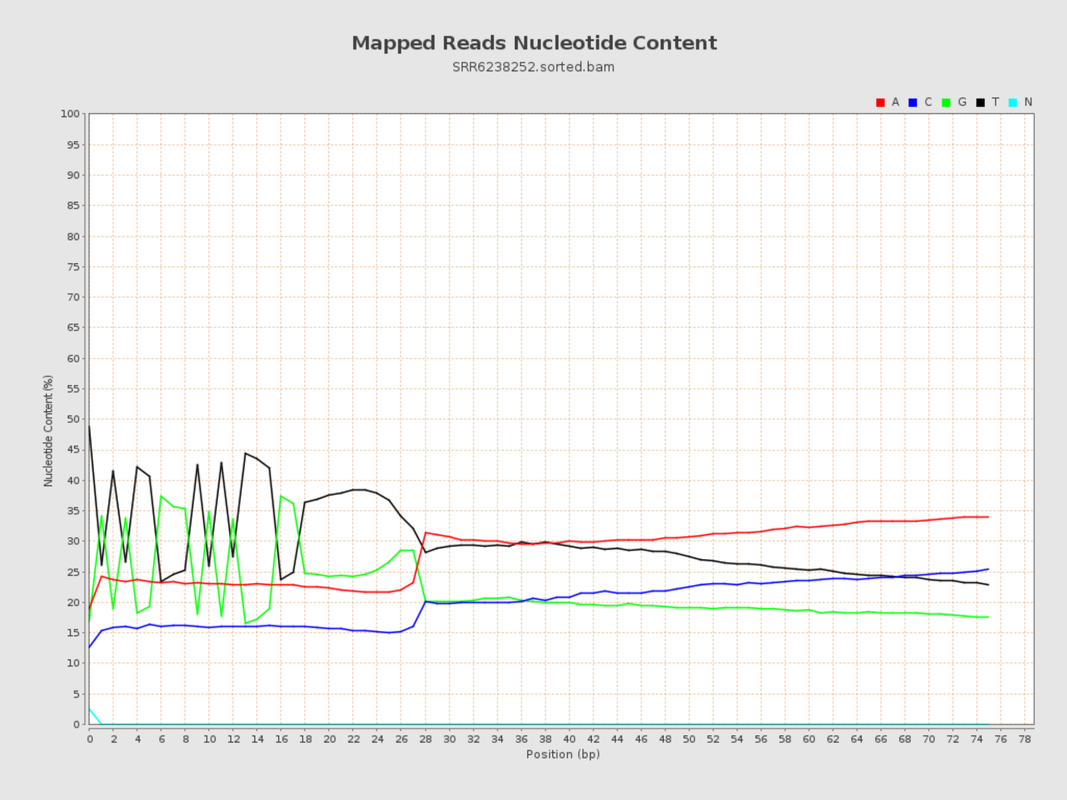
6. Results : Genome Fraction Coverage



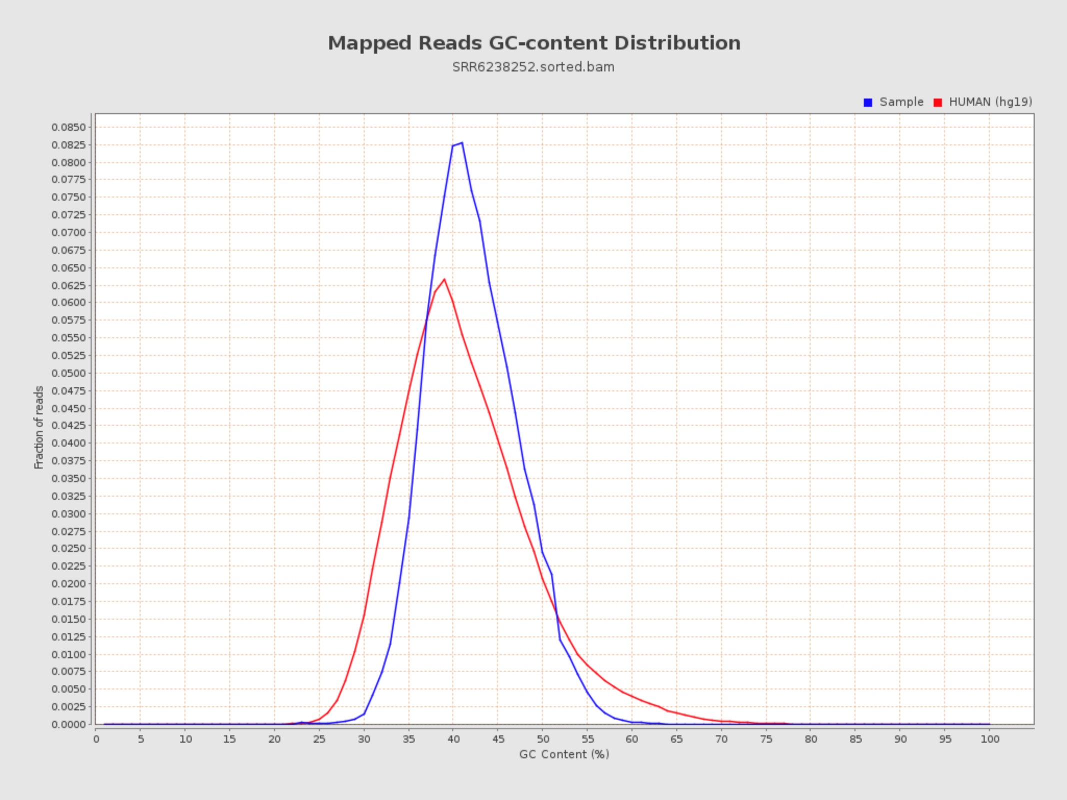
7. Results : Duplication Rate Histogram



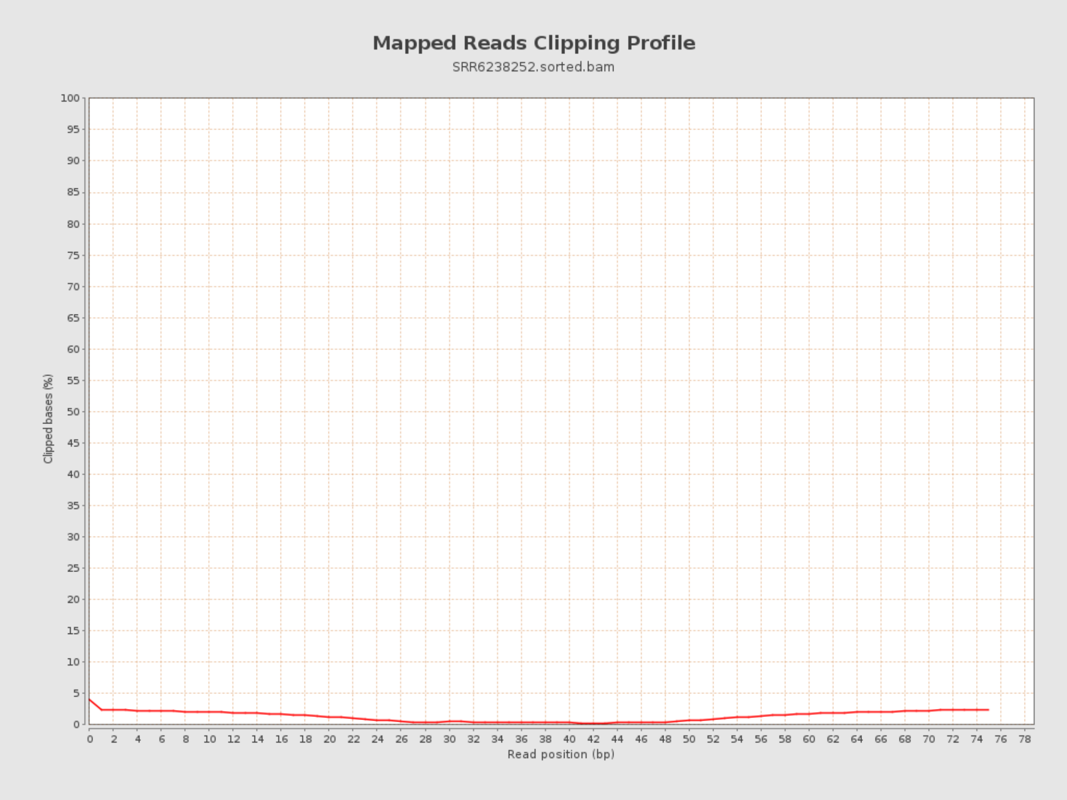
8. Results : Mapped Reads Nucleotide Content



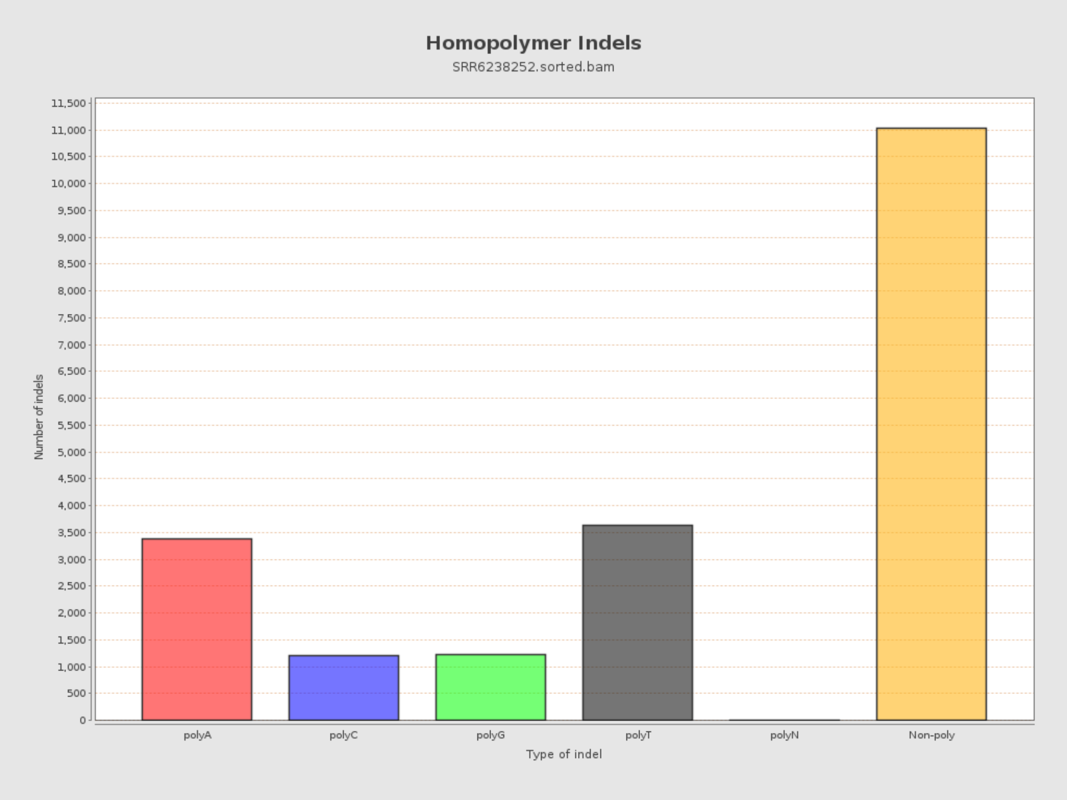
9. Results : Mapped Reads GC-content Distribution



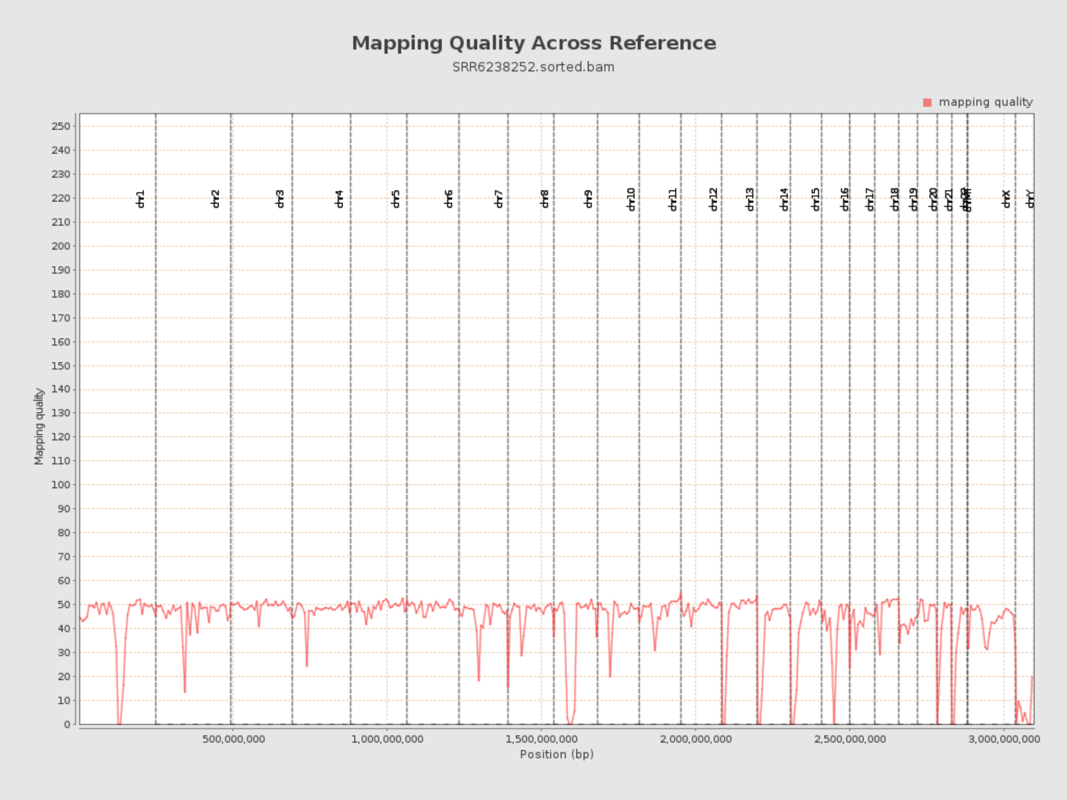
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram