Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 12:40:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238246.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_SRR6238246 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238246.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 12:40:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238246.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,230,242
Mapped reads	582,672 / 47.36%
Unmapped reads	647,570 / 52.64%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,272 / 0.43%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	79,549 / 6.47%
Duplication rate	9.04%
Clipped reads	382,147 / 31.06%

2.2. ACGT Content

Number/percentage of A's	9,894,627 / 27.83%
Number/percentage of C's	7,122,215 / 20.03%
Number/percentage of T's	10,643,158 / 29.94%
Number/percentage of G's	7,886,510 / 22.18%
Number/percentage of N's	7,665 / 0.02%
GC Percentage	42.21%

2.3. Coverage

Mean	0.0115

Standard Deviation	0.2986

2.4. Mapping Quality

Mean Mapping Quality	43.58

2.5. Mismatches and indels

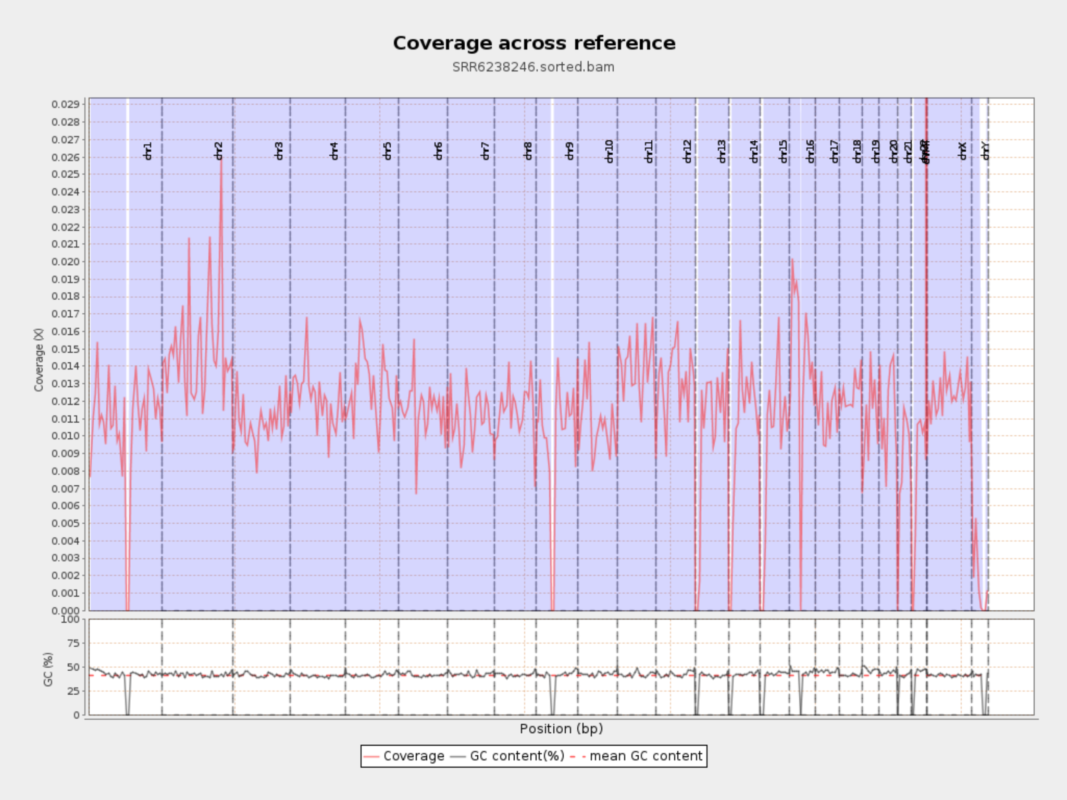
General error rate	1.01%
Mismatches	355,717
Insertions	2,895
Mapped reads with at least one insertion	0.49%
Deletions	9,568
Mapped reads with at least one deletion	1.63%
Homopolymer indels	45.94%

2.6. Chromosome stats

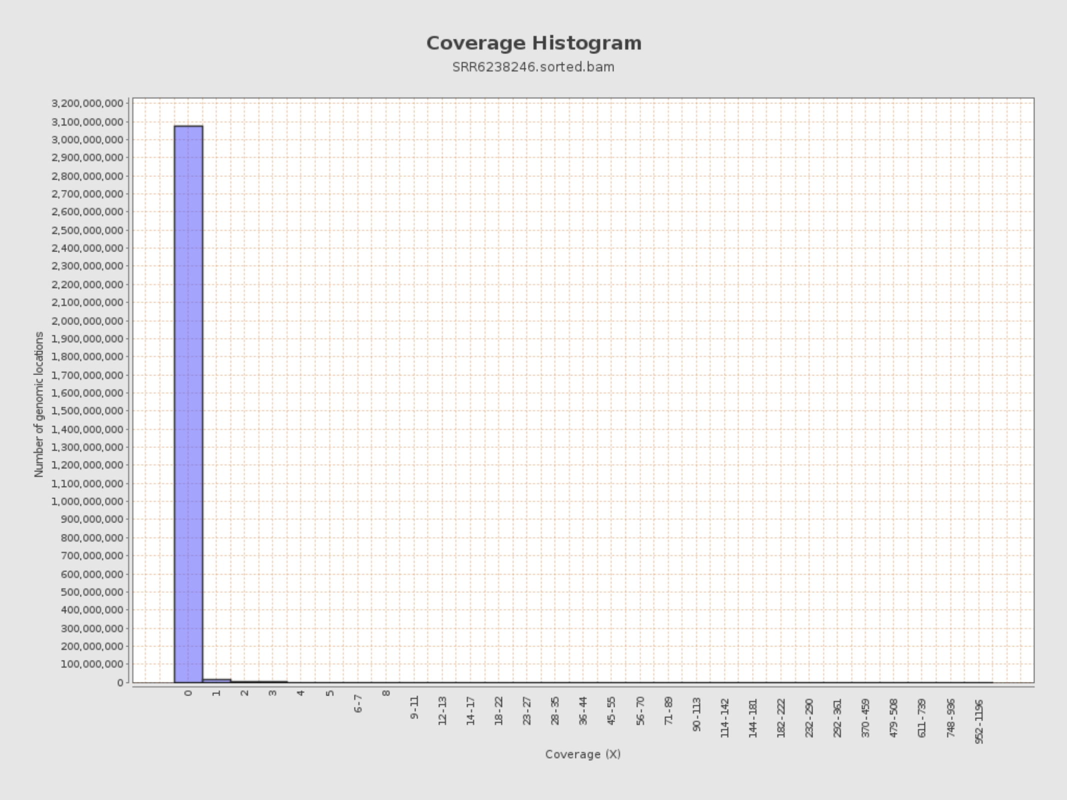
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2643532	0.0106	0.297
chr2	243199373	3663261	0.0151	0.4357
chr3	198022430	2125326	0.0107	0.192
chr4	191154276	2330408	0.0122	0.2531
chr5	180915260	2317763	0.0128	0.2274
chr6	171115067	1974789	0.0115	0.2903
chr7	159138663	1753639	0.011	0.2111

chr8	146364022	1689120	0.0115	0.2341
chr9	141213431	1396603	0.0099	0.1854
chr10	135534747	1459943	0.0108	0.2037
chr11	135006516	1882313	0.0139	0.2049
chr12	133851895	1760373	0.0132	0.2332
chr13	115169878	1153456	0.01	0.2626
chr14	107349540	1100719	0.0103	0.5649
chr15	102531392	971560	0.0095	0.7083
chr16	90354753	1296029	0.0143	0.2129
chr17	81195210	910816	0.0112	0.2064
chr18	78077248	973186	0.0125	0.2078
chr19	59128983	655850	0.0111	0.1917
chr20	63025520	719033	0.0114	0.1962
chr21	48129895	395484	0.0082	0.1431
chr22	51304566	379242	0.0074	0.1365
chrMT	16571	8709	0.5256	1.3279
chrX	155270560	1911027	0.0123	0.3031
chrY	59373566	97628	0.0016	0.0993

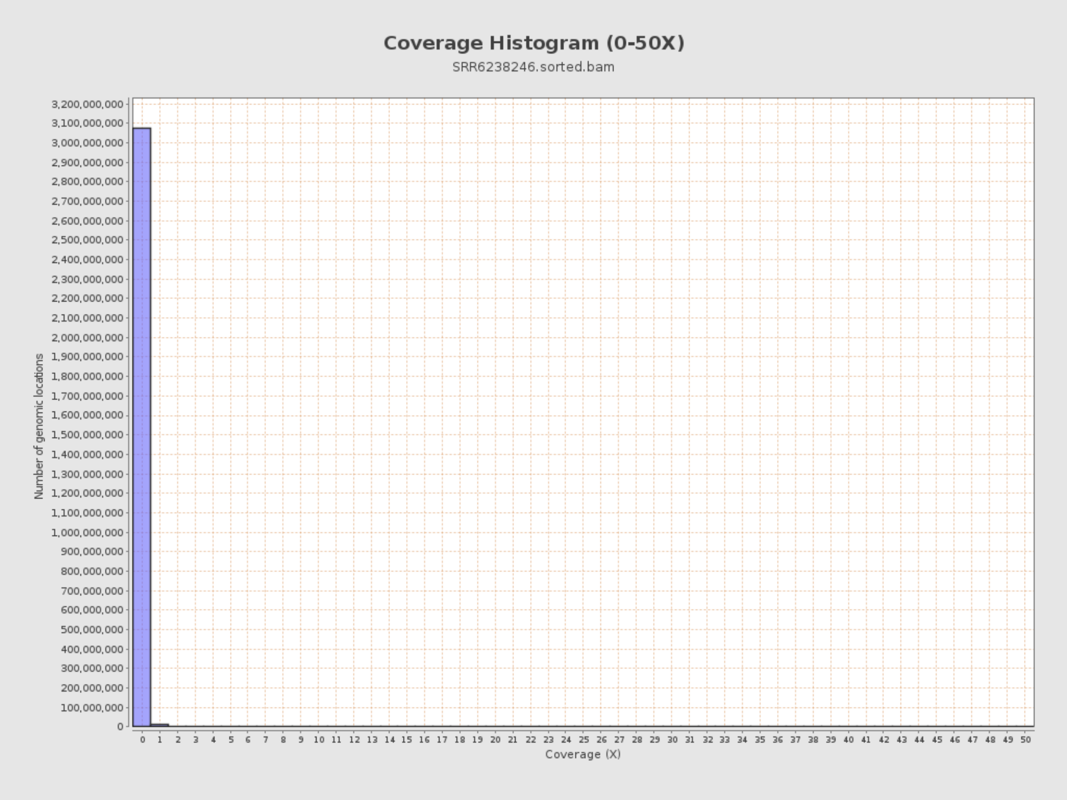
3. Results : Coverage across reference



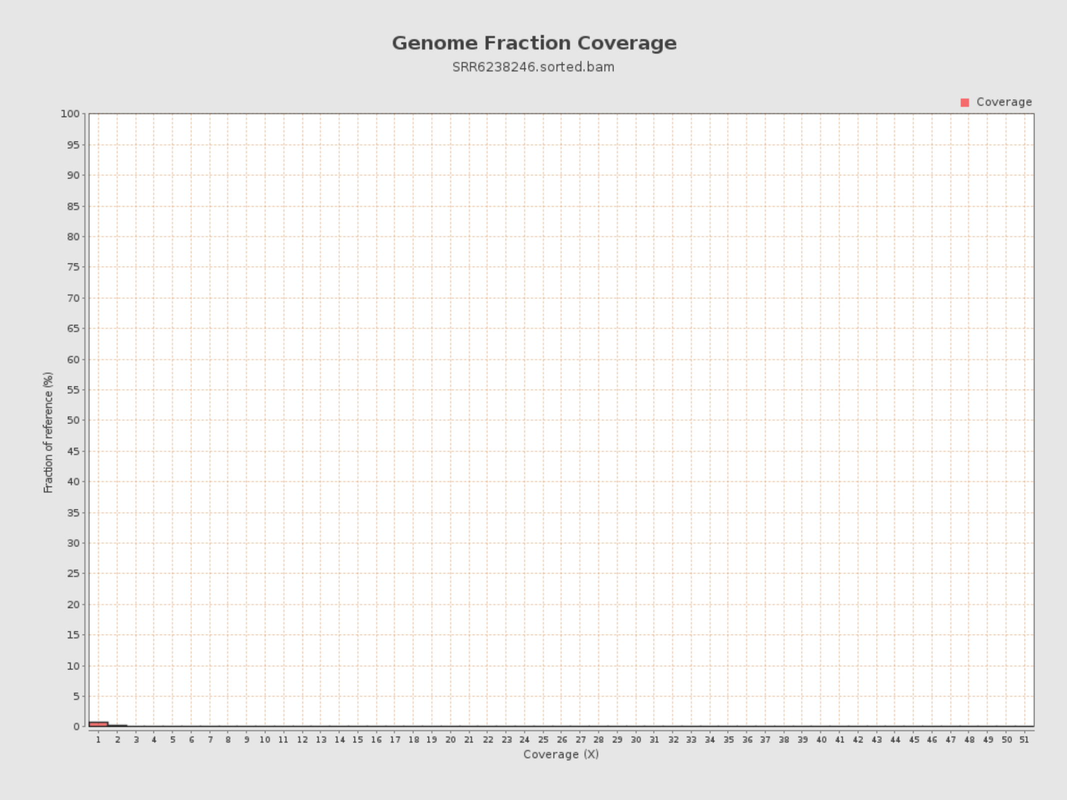
4. Results : Coverage Histogram



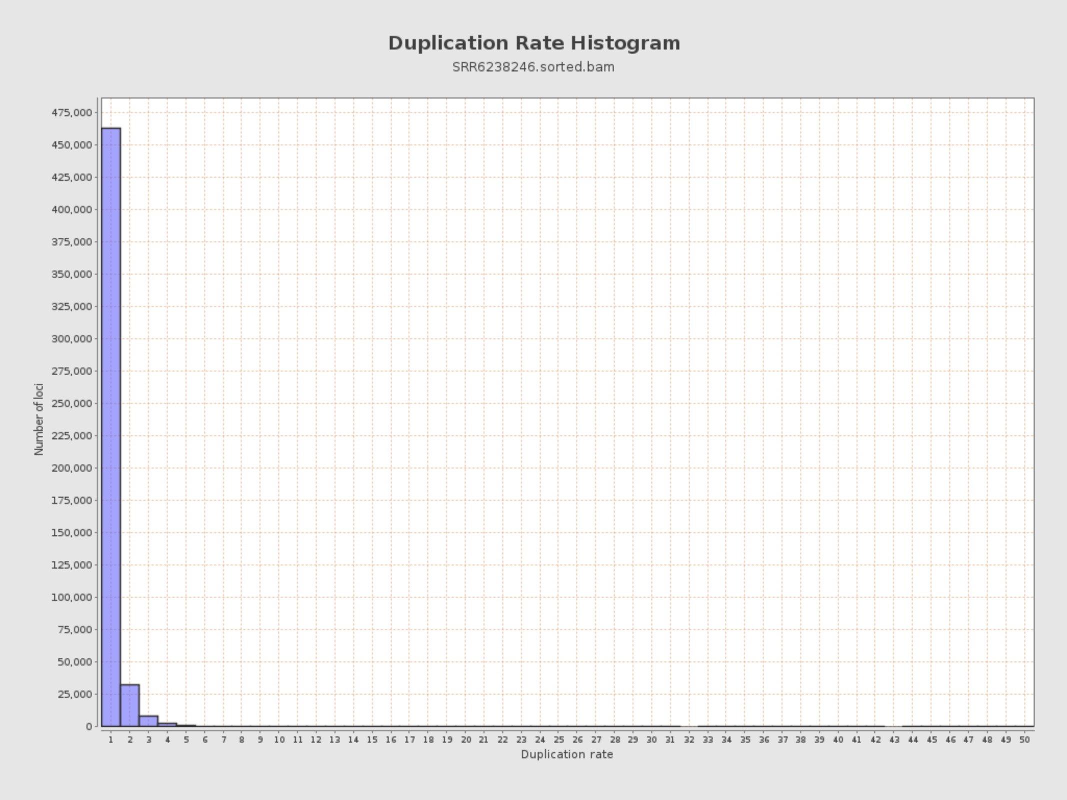
5. Results : Coverage Histogram (0-50X)



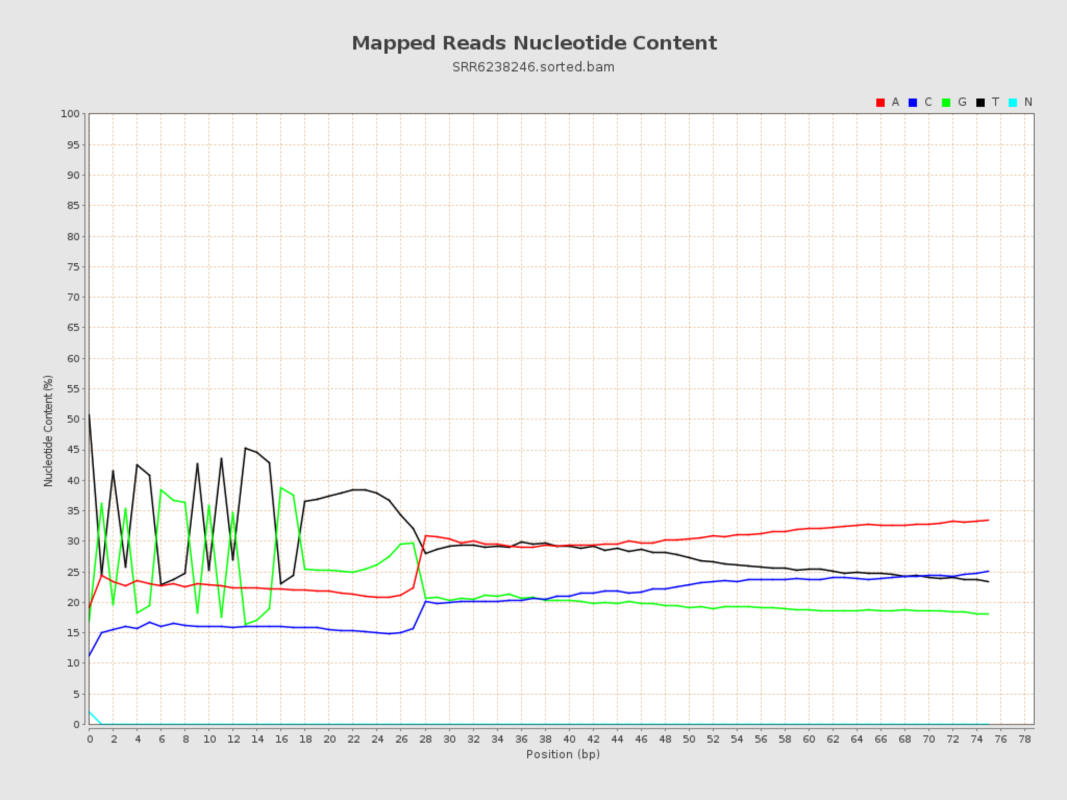
6. Results : Genome Fraction Coverage



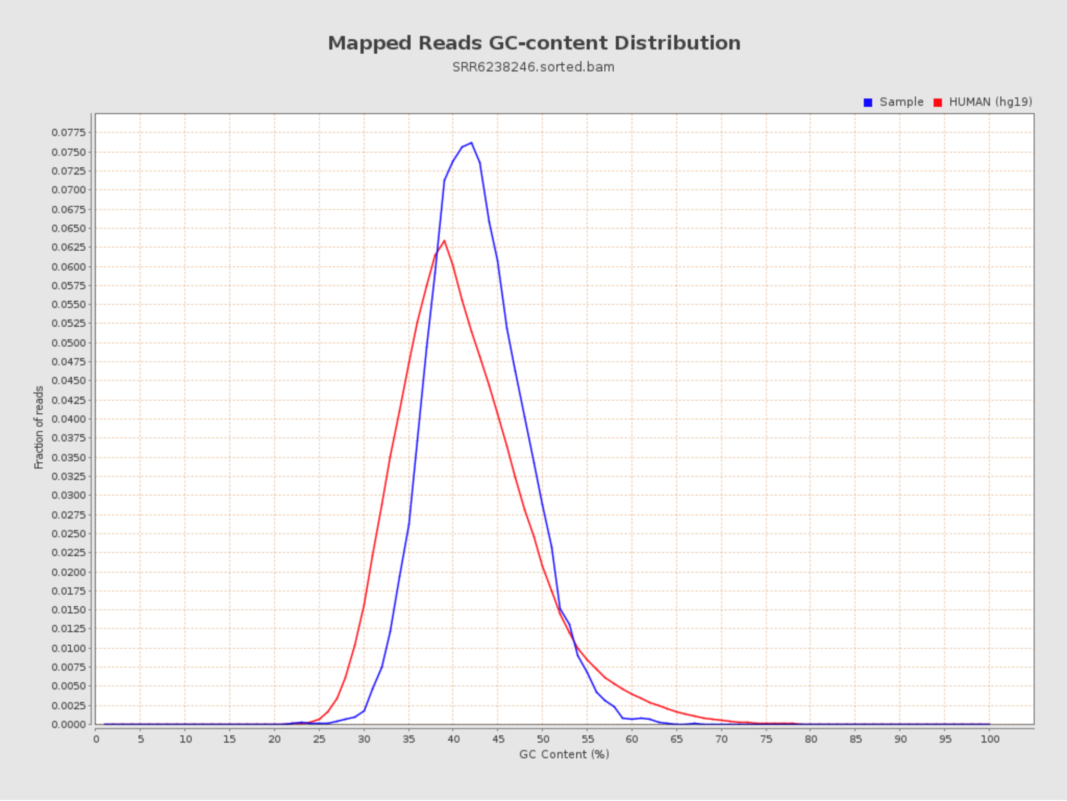
7. Results : Duplication Rate Histogram



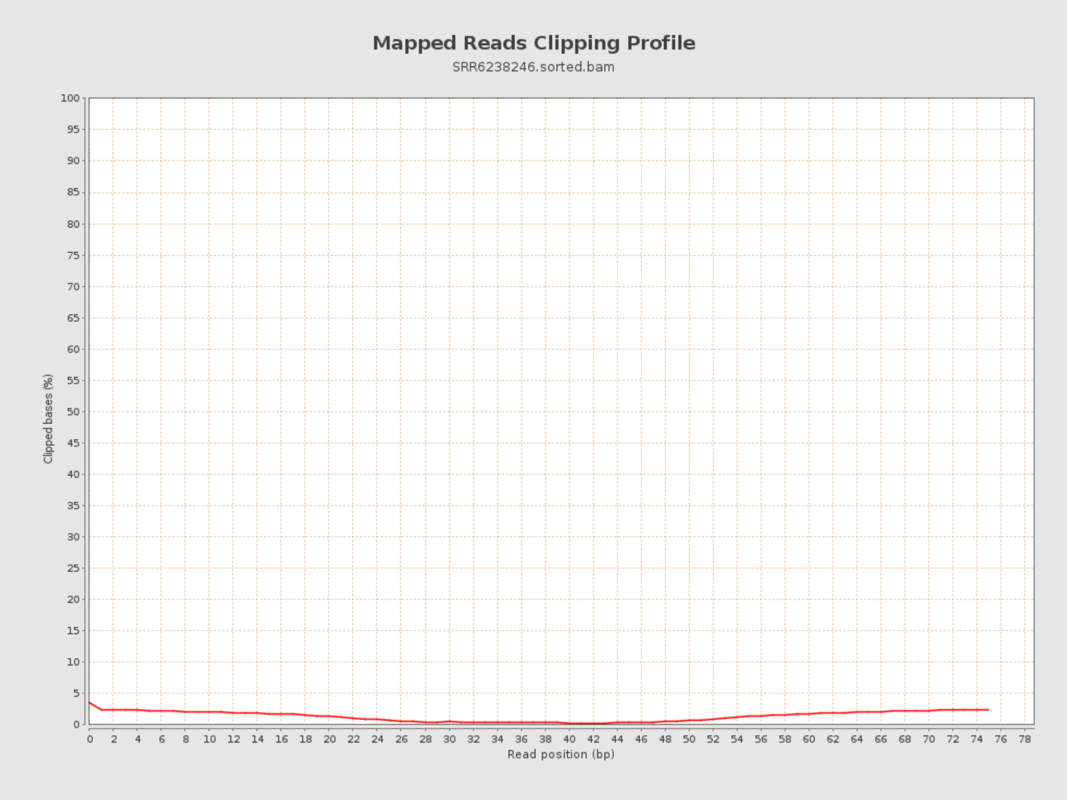
8. Results : Mapped Reads Nucleotide Content



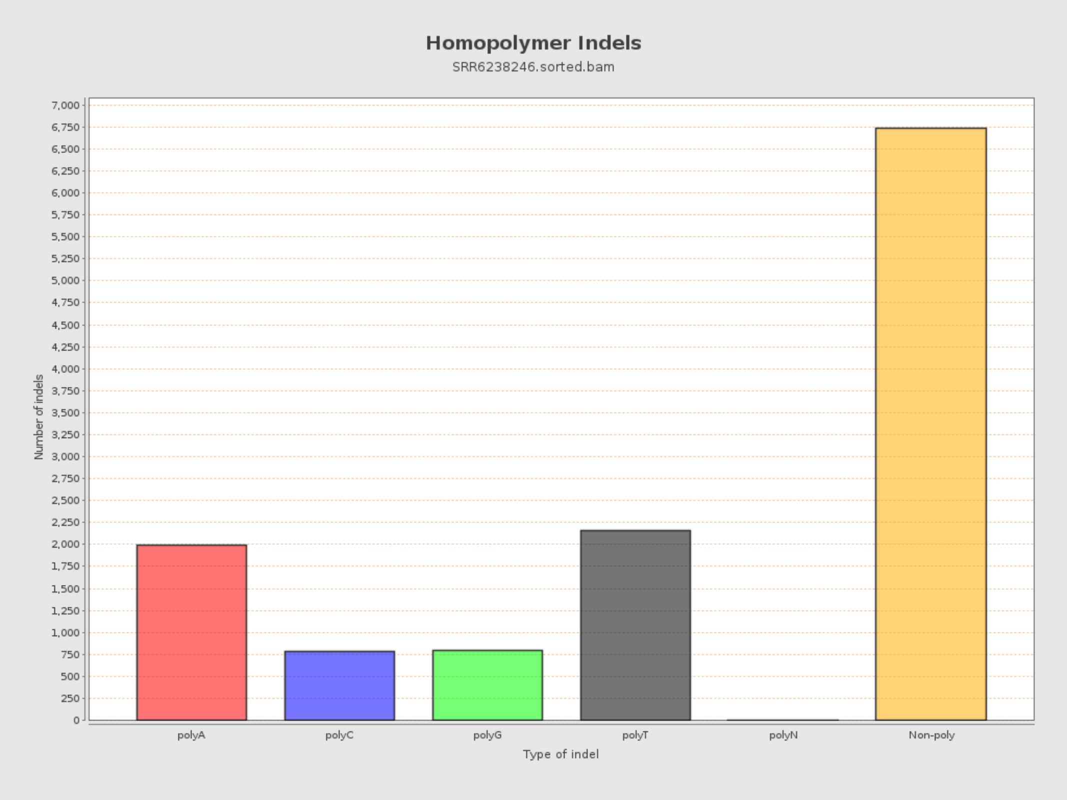
9. Results : Mapped Reads GC-content Distribution



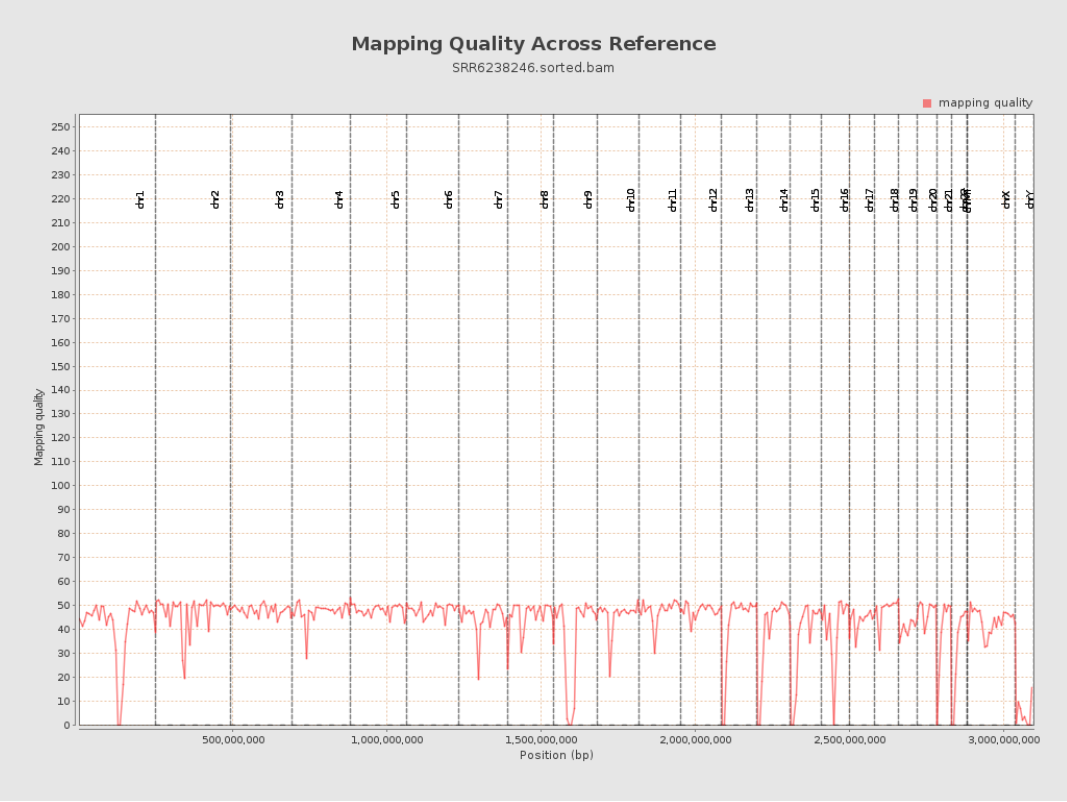
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram