Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 10:47:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238049.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_SRR6238049 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238049.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 10:47:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238049.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,150,139
Mapped reads	614,605 / 53.44%
Unmapped reads	535,534 / 46.56%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,141 / 0.53%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	59,253 / 5.15%
Duplication rate	8.37%
Clipped reads	428,531 / 37.26%

2.2. ACGT Content

Number/percentage of A's	9,647,167 / 26.1%
Number/percentage of C's	6,395,462 / 17.3%
Number/percentage of T's	12,012,352 / 32.5%
Number/percentage of G's	8,907,950 / 24.1%
Number/percentage of N's	1,517 / 0%
GC Percentage	41.4%

2.3. Coverage

Mean	0.0119

Standard Deviation	0.1632

2.4. Mapping Quality

Mean Mapping Quality	44.73

2.5. Mismatches and indels

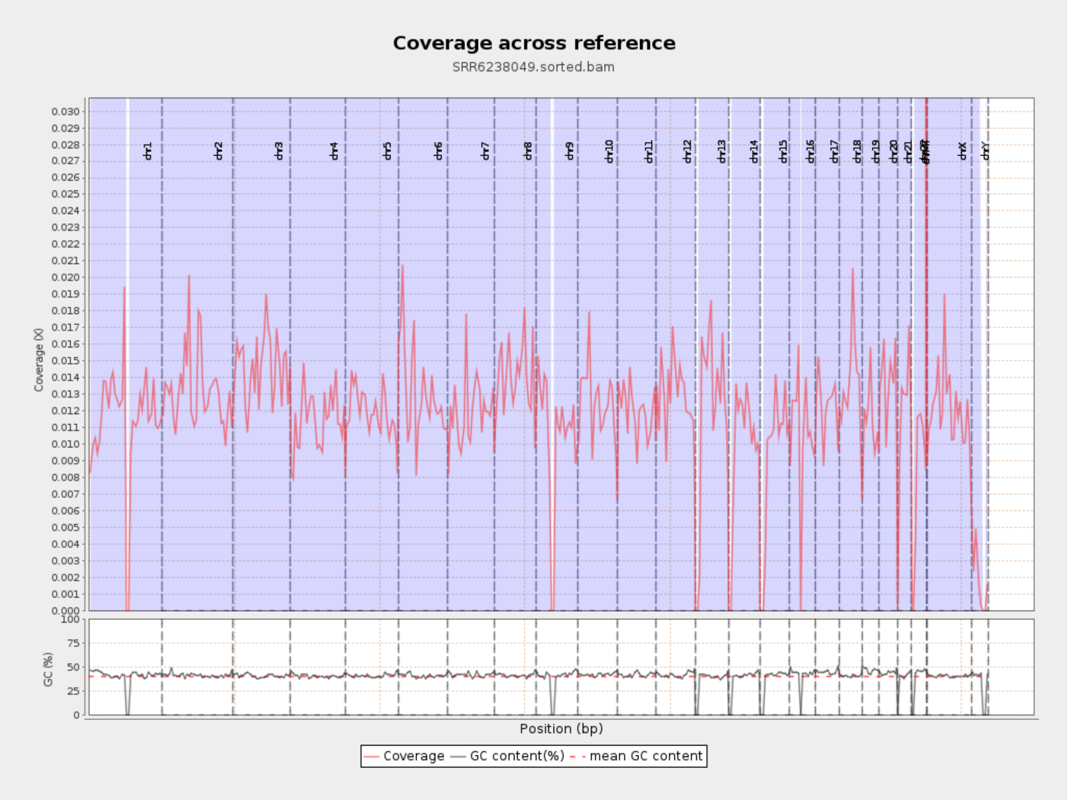
General error rate	0.83%
Mismatches	300,876
Insertions	2,807
Mapped reads with at least one insertion	0.45%
Deletions	11,756
Mapped reads with at least one deletion	1.89%
Homopolymer indels	45.47%

2.6. Chromosome stats

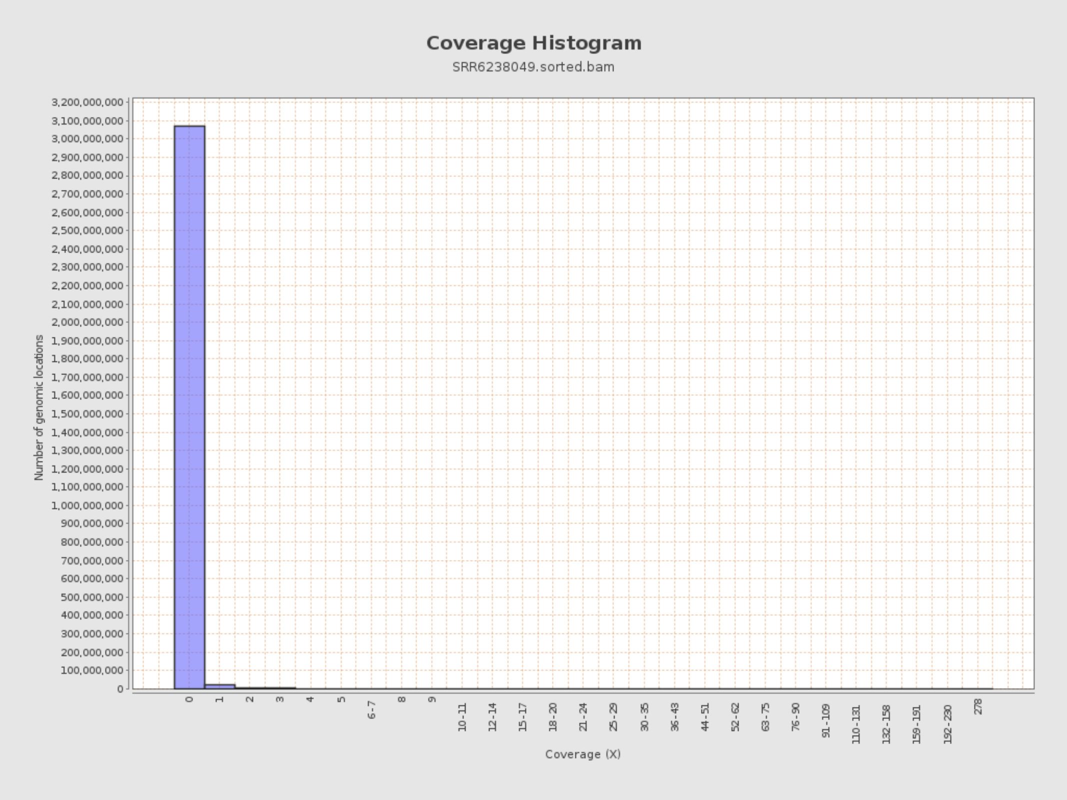
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2842167	0.0114	0.2298
chr2	243199373	3232569	0.0133	0.2065
chr3	198022430	2888432	0.0146	0.1572
chr4	191154276	2193144	0.0115	0.1404
chr5	180915260	2169721	0.012	0.1416
chr6	171115067	2249657	0.0131	0.1623
chr7	159138663	1914258	0.012	0.1623

chr8	146364022	2057350	0.0141	0.1756
chr9	141213431	1477155	0.0105	0.1413
chr10	135534747	1706414	0.0126	0.1587
chr11	135006516	1615827	0.012	0.1471
chr12	133851895	1745308	0.013	0.1475
chr13	115169878	1366173	0.0119	0.1437
chr14	107349540	1044218	0.0097	0.1325
chr15	102531392	936754	0.0091	0.1231
chr16	90354753	958908	0.0106	0.1348
chr17	81195210	992944	0.0122	0.1452
chr18	78077248	1088951	0.0139	0.221
chr19	59128983	680312	0.0115	0.1667
chr20	63025520	870206	0.0138	0.1535
chr21	48129895	564398	0.0117	0.143
chr22	51304566	389083	0.0076	0.1097
chrMT	16571	21048	1.2702	2.0174
chrX	155270560	1875831	0.0121	0.1461
chrY	59373566	102316	0.0017	0.0533

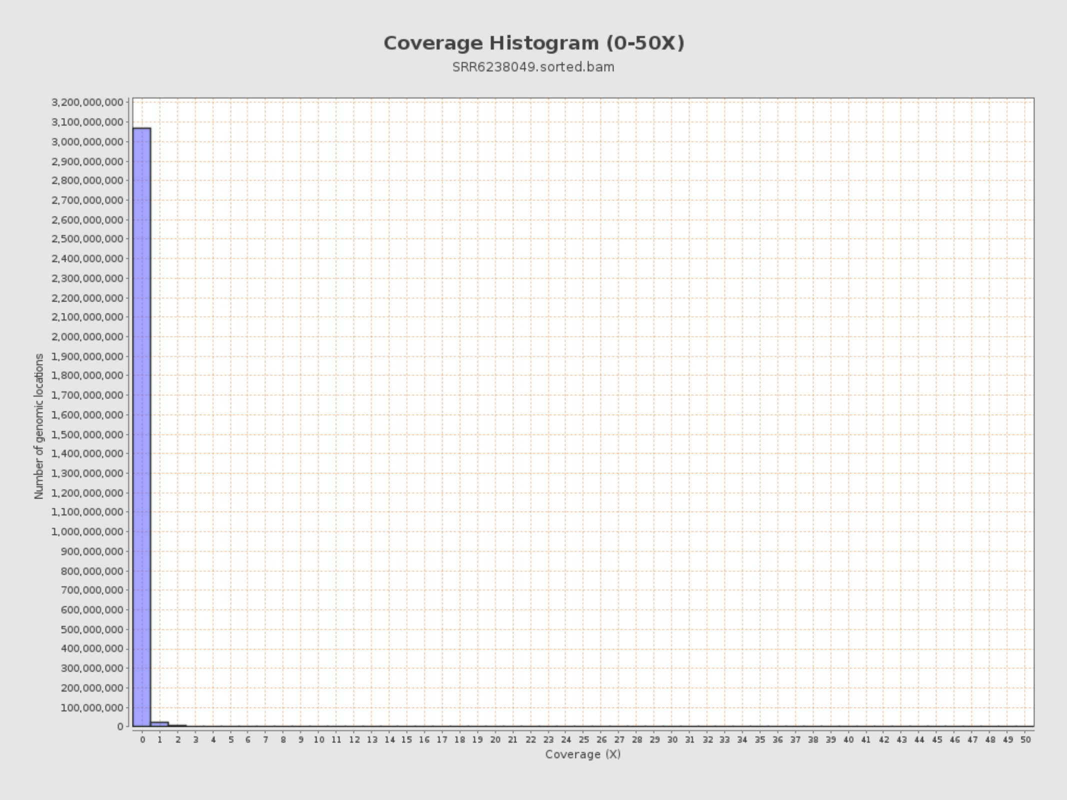
3. Results : Coverage across reference



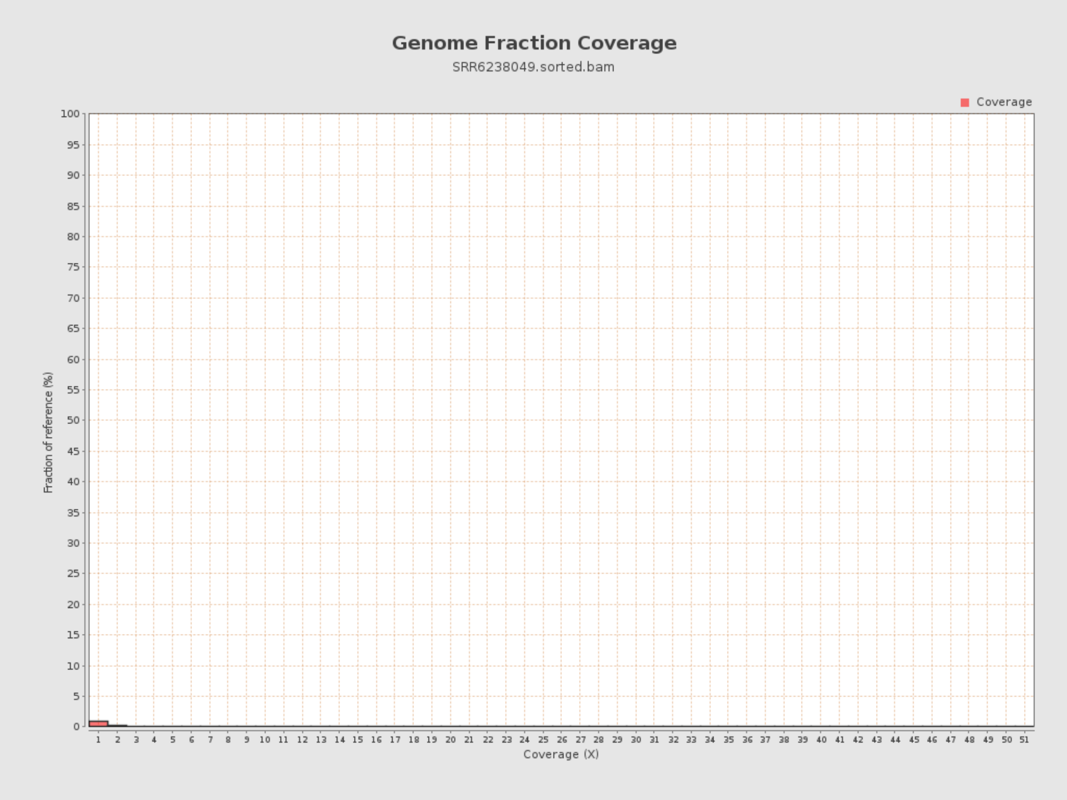
4. Results : Coverage Histogram



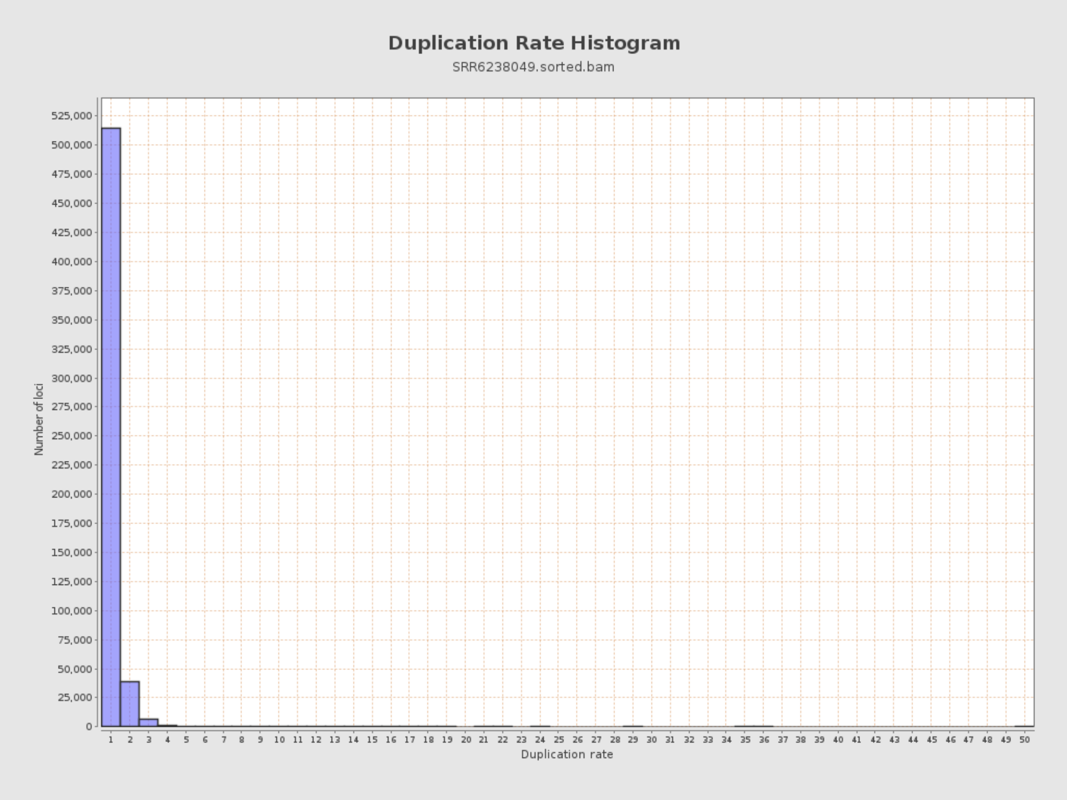
5. Results : Coverage Histogram (0-50X)



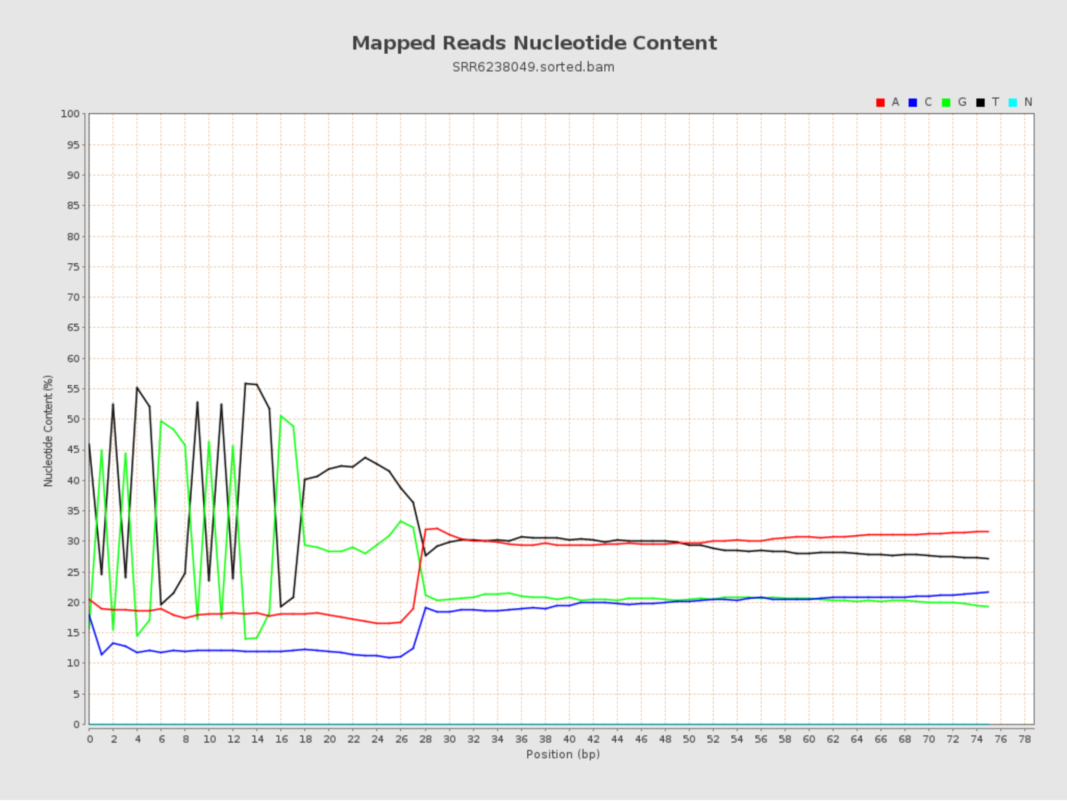
6. Results : Genome Fraction Coverage



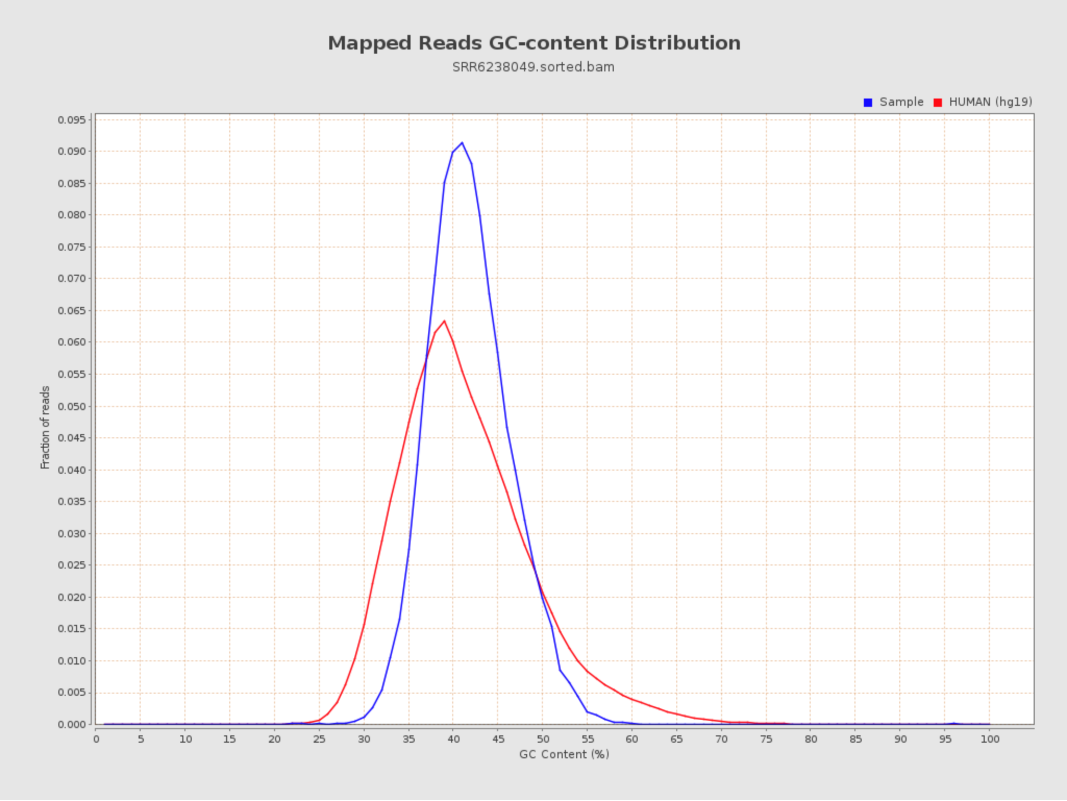
7. Results : Duplication Rate Histogram



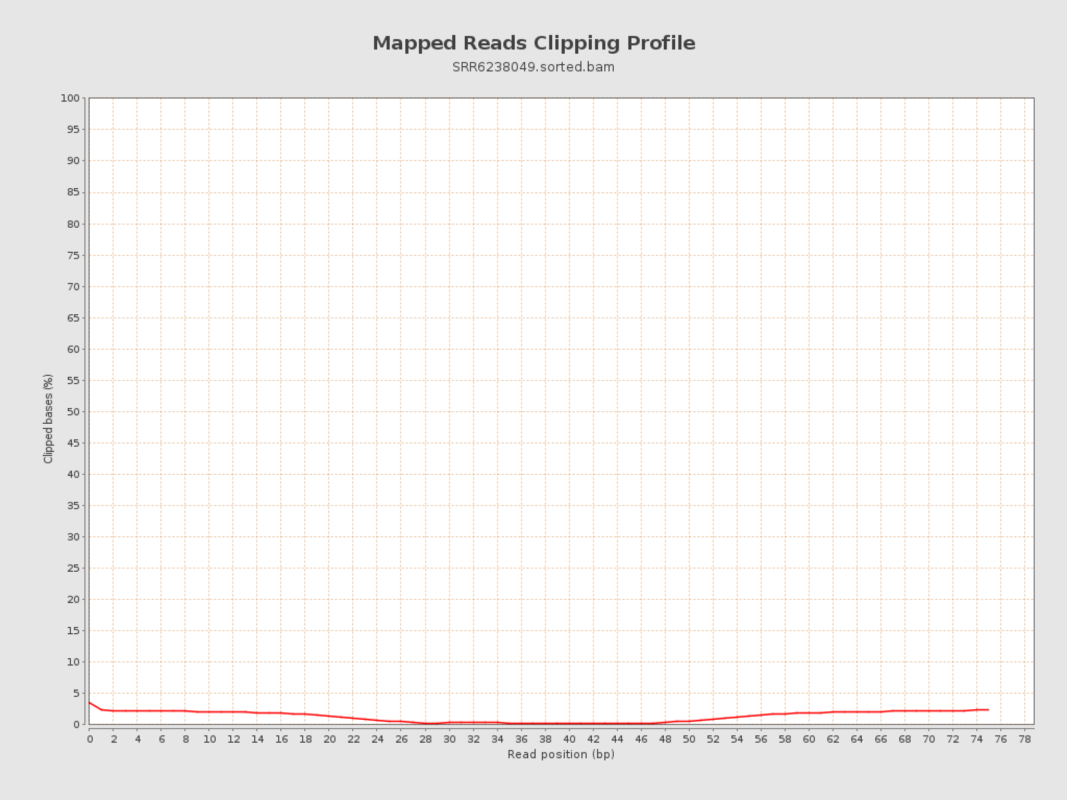
8. Results : Mapped Reads Nucleotide Content



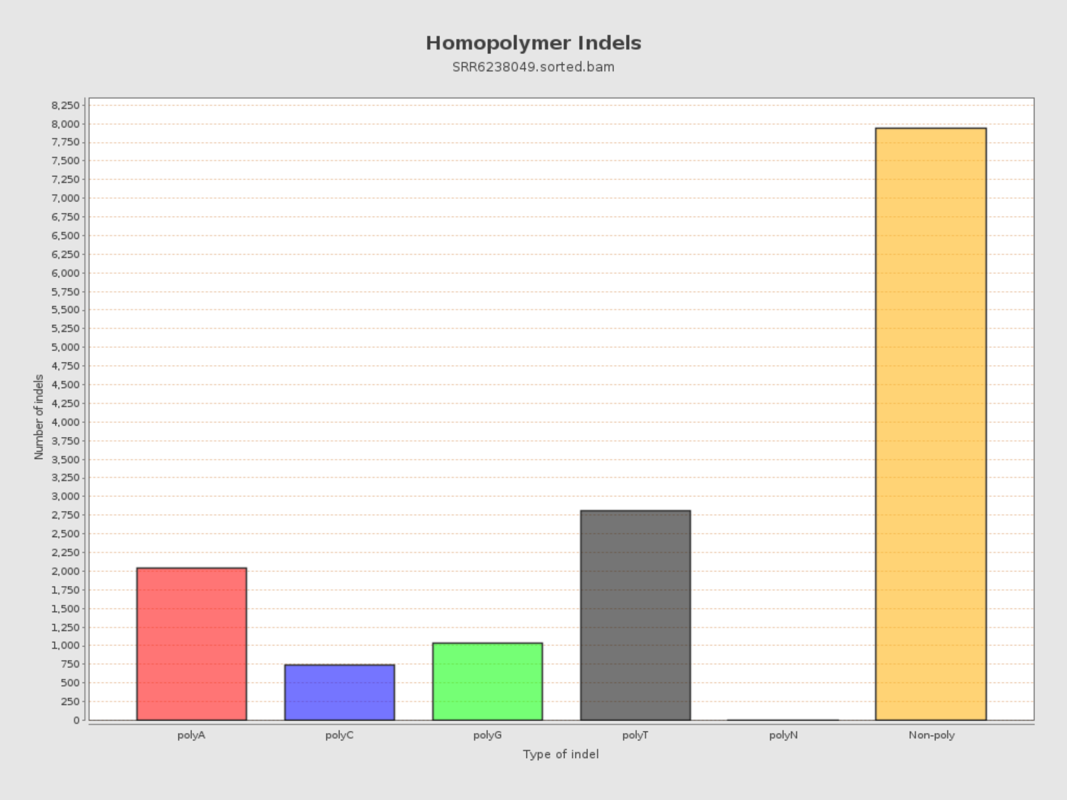
9. Results : Mapped Reads GC-content Distribution



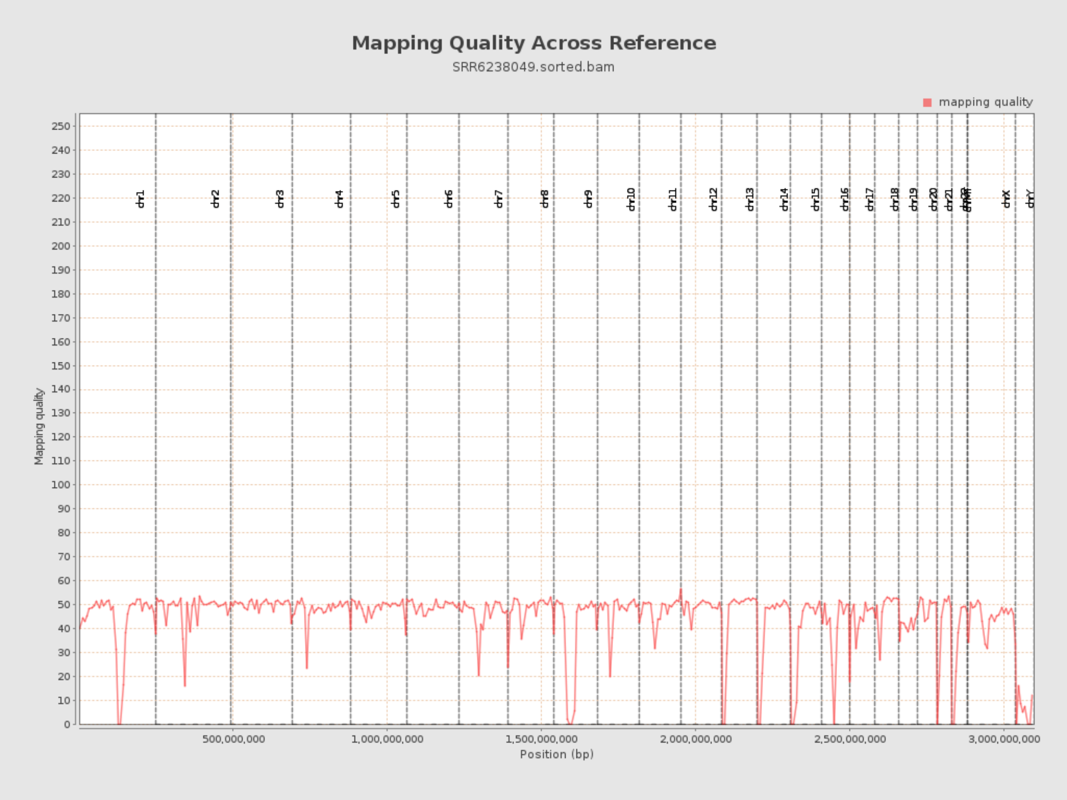
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram