Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 23:17:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237266.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_SRR6237266 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237266.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 23:17:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237266.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,353,043
Mapped reads	437,471 / 18.59%
Unmapped reads	1,915,572 / 81.41%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,259 / 0.14%
Read min/max/mean length	30 / 76 / 76.05
Duplicated reads (estimated)	32,728 / 1.39%
Duplication rate	6.09%
Clipped reads	233,343 / 9.92%

2.2. ACGT Content

Number/percentage of A's	7,598,907 / 26.95%
Number/percentage of C's	5,164,198 / 18.32%
Number/percentage of T's	9,017,997 / 31.99%
Number/percentage of G's	6,410,522 / 22.74%
Number/percentage of N's	383 / 0%
GC Percentage	41.06%

2.3. Coverage

Mean	0.0091

Standard Deviation	0.1436

2.4. Mapping Quality

Mean Mapping Quality	45.14

2.5. Mismatches and indels

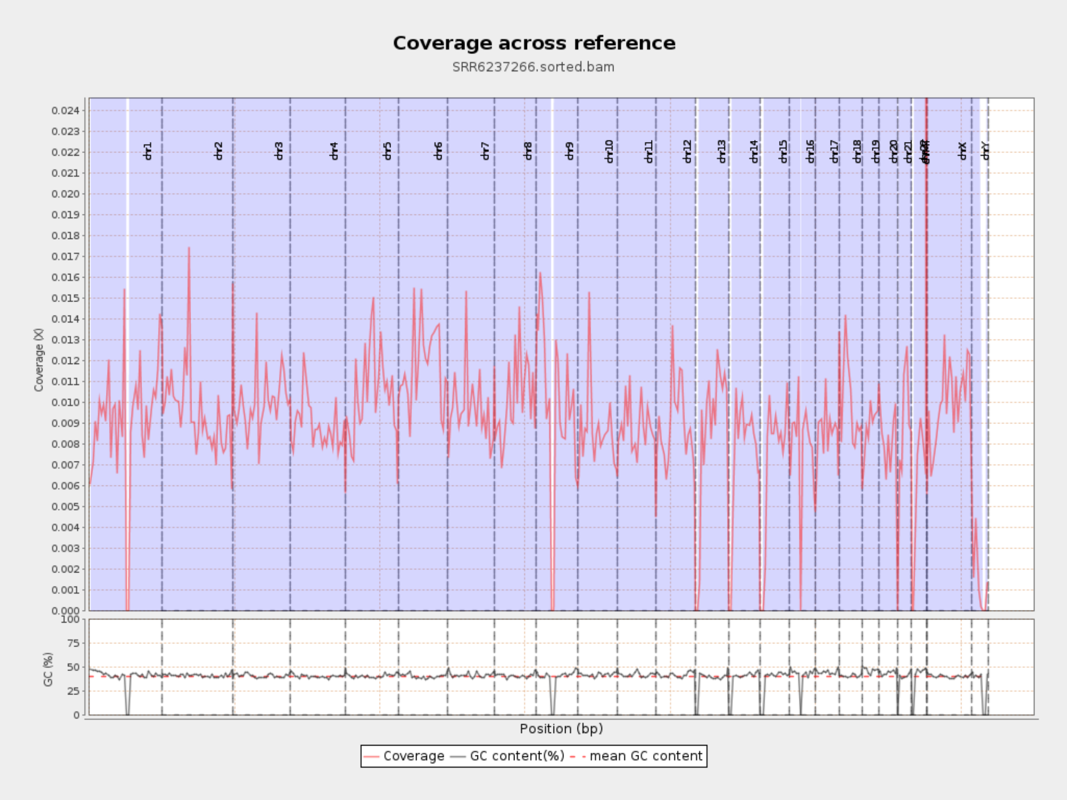
General error rate	0.94%
Mismatches	259,829
Insertions	2,029
Mapped reads with at least one insertion	0.46%
Deletions	6,987
Mapped reads with at least one deletion	1.58%
Homopolymer indels	45.69%

2.6. Chromosome stats

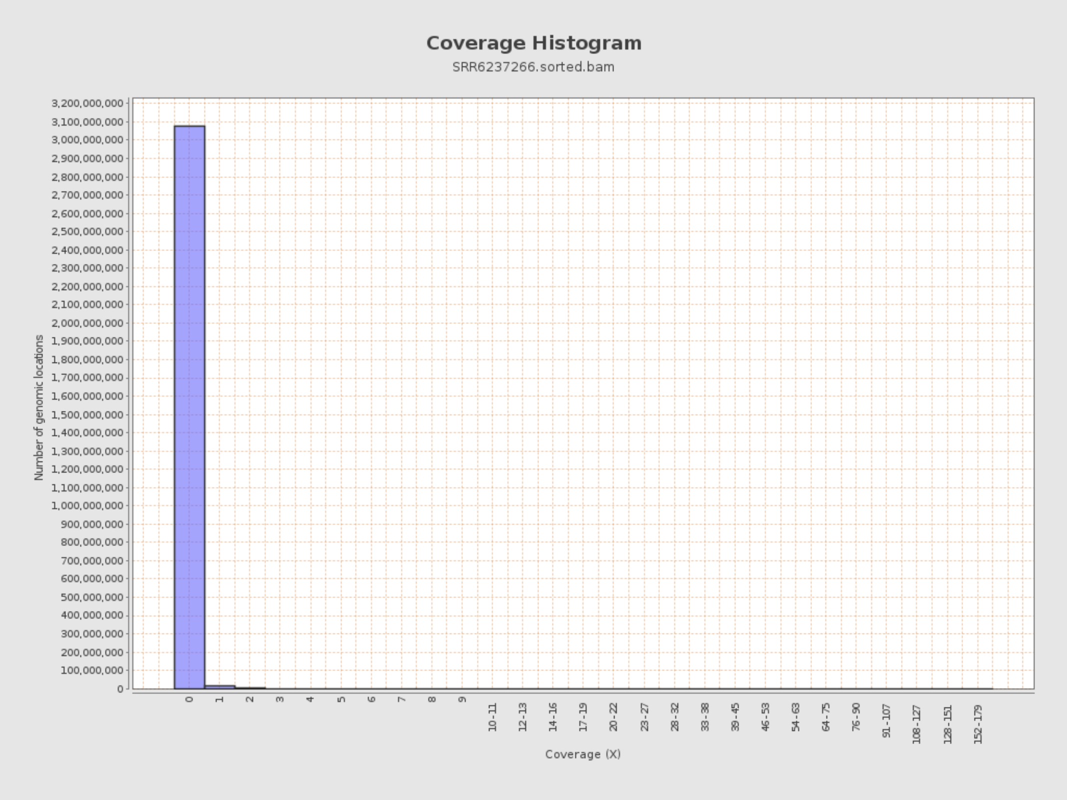
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2262660	0.0091	0.1921
chr2	243199373	2320794	0.0095	0.1596
chr3	198022430	2004052	0.0101	0.134
chr4	191154276	1695703	0.0089	0.1313
chr5	180915260	1898415	0.0105	0.1375
chr6	171115067	2010047	0.0117	0.147
chr7	159138663	1544999	0.0097	0.1523

chr8	146364022	1483554	0.0101	0.1511
chr9	141213431	1381761	0.0098	0.1478
chr10	135534747	1171752	0.0086	0.1391
chr11	135006516	1185276	0.0088	0.1304
chr12	133851895	1194437	0.0089	0.1287
chr13	115169878	963037	0.0084	0.1195
chr14	107349540	796179	0.0074	0.1166
chr15	102531392	726079	0.0071	0.1269
chr16	90354753	697242	0.0077	0.1208
chr17	81195210	689707	0.0085	0.1284
chr18	78077248	787133	0.0101	0.2035
chr19	59128983	522383	0.0088	0.1447
chr20	63025520	509668	0.0081	0.1194
chr21	48129895	404666	0.0084	0.1246
chr22	51304566	292894	0.0057	0.0978
chrMT	16571	39199	2.3655	2.1242
chrX	155270560	1540039	0.0099	0.1358
chrY	59373566	82734	0.0014	0.0498

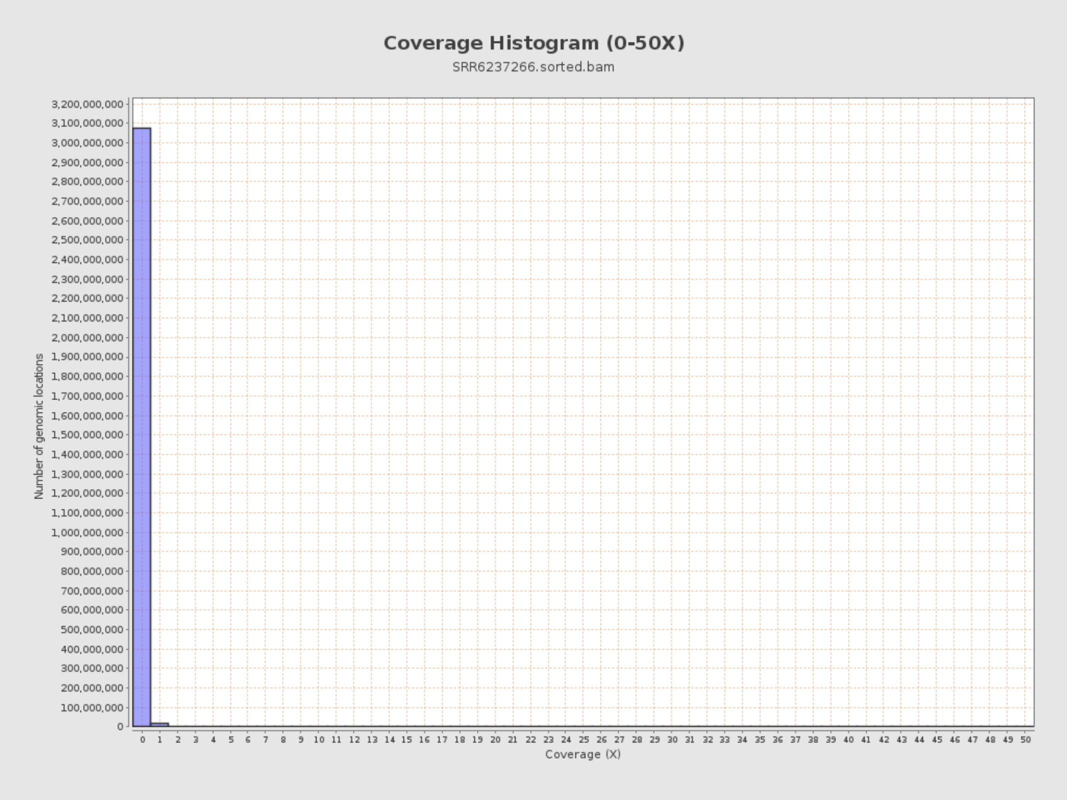
3. Results : Coverage across reference



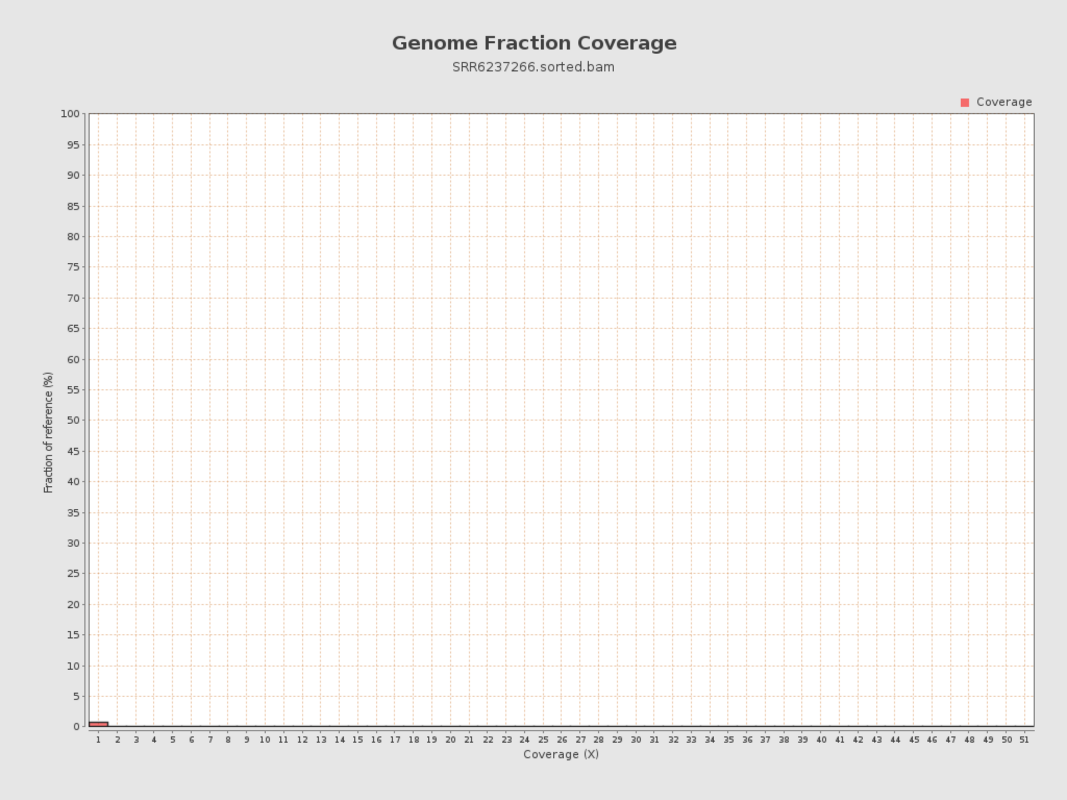
4. Results : Coverage Histogram



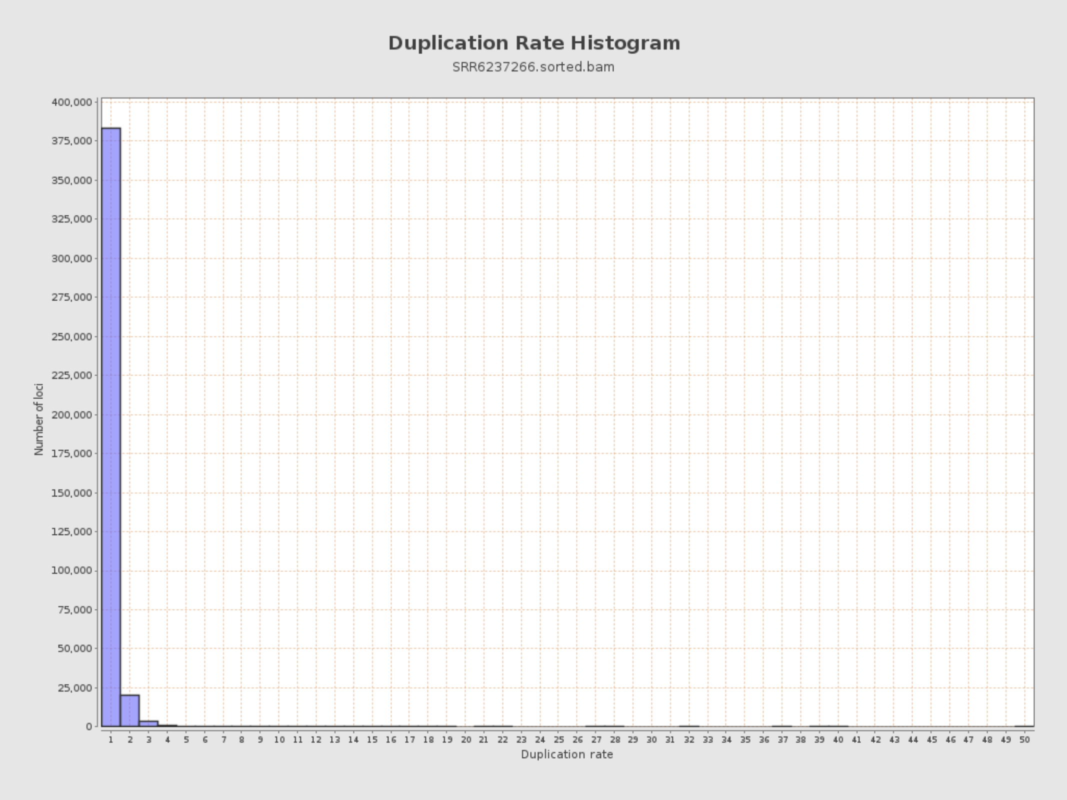
5. Results : Coverage Histogram (0-50X)



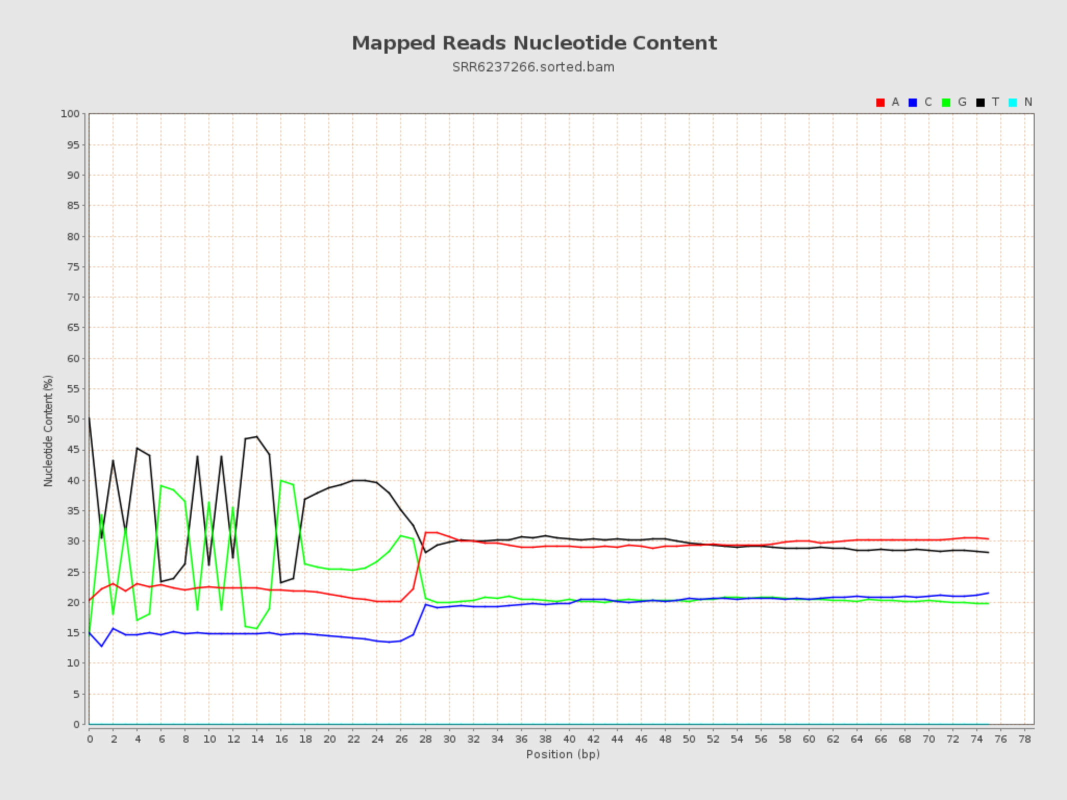
6. Results : Genome Fraction Coverage



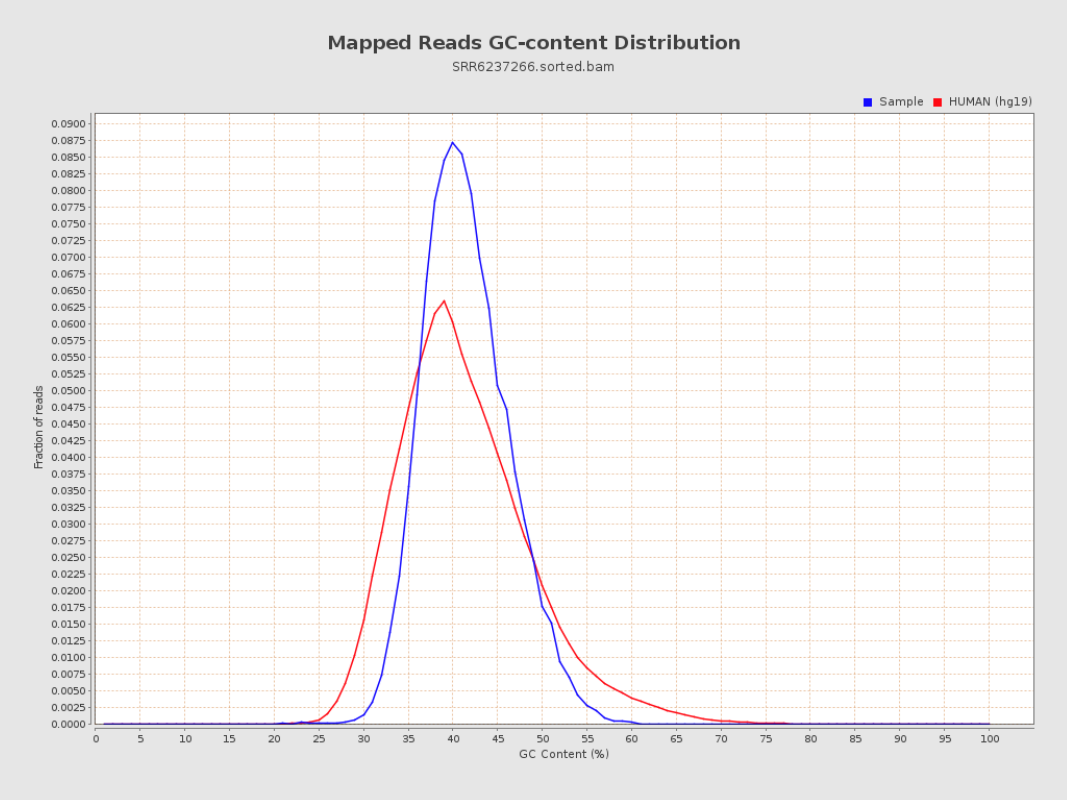
7. Results : Duplication Rate Histogram



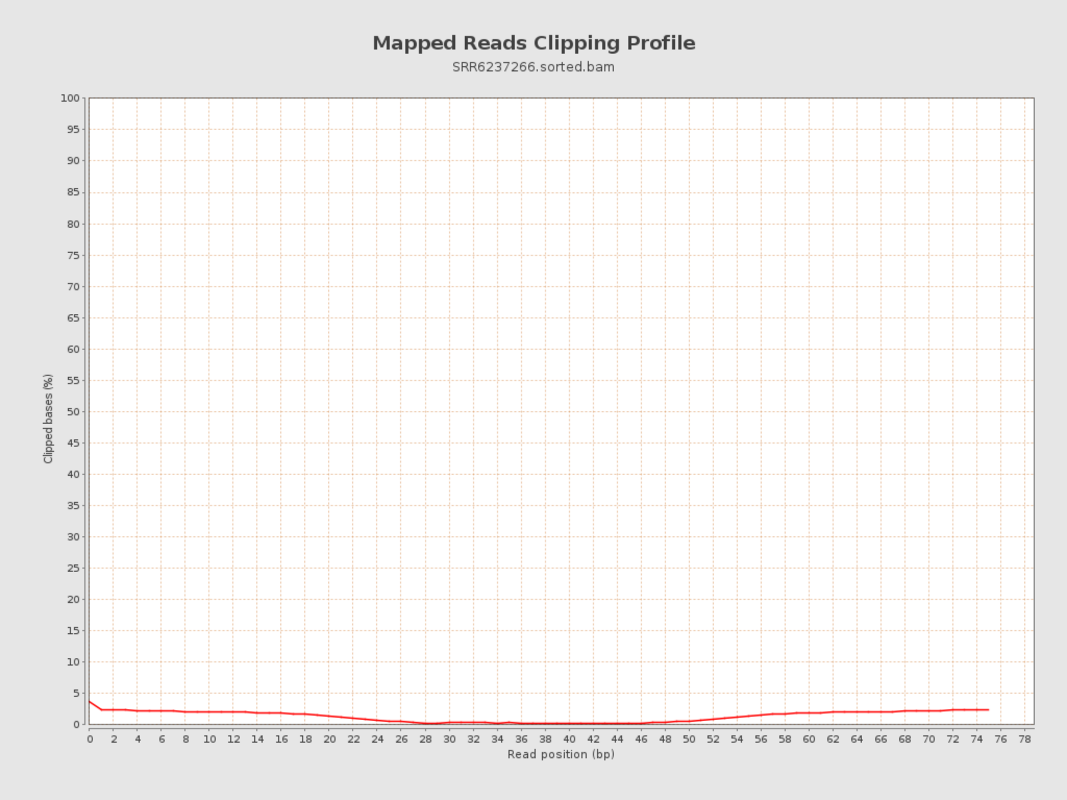
8. Results : Mapped Reads Nucleotide Content



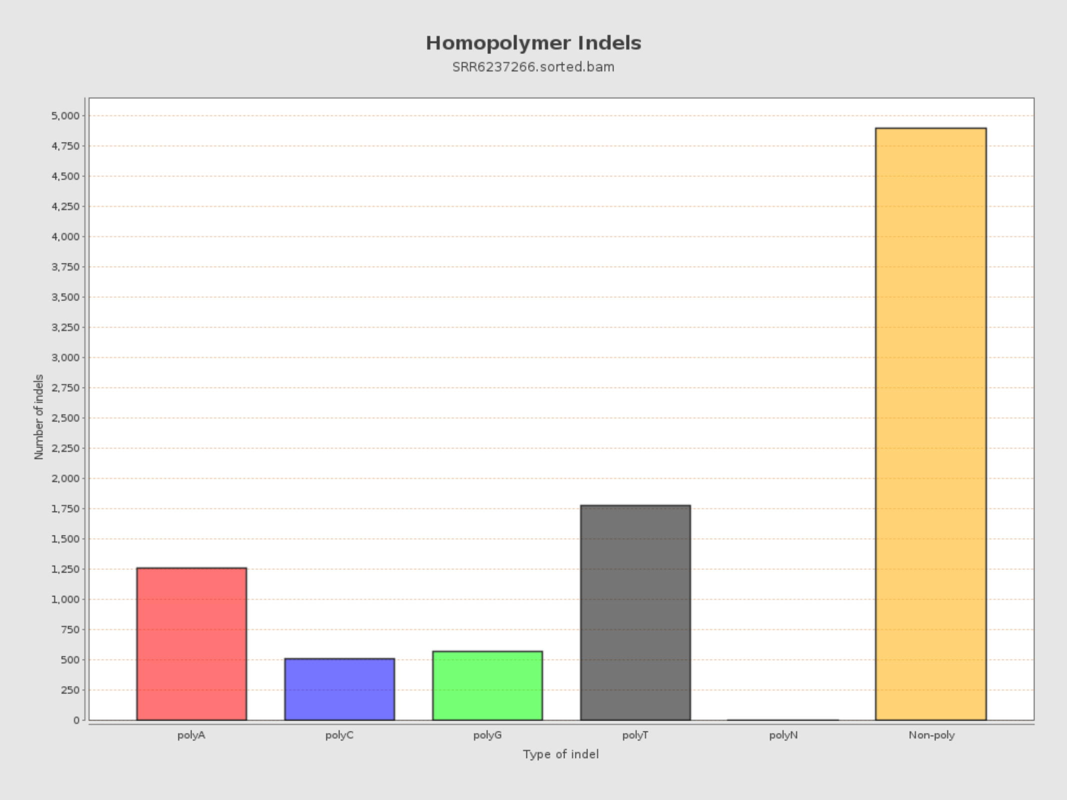
9. Results : Mapped Reads GC-content Distribution



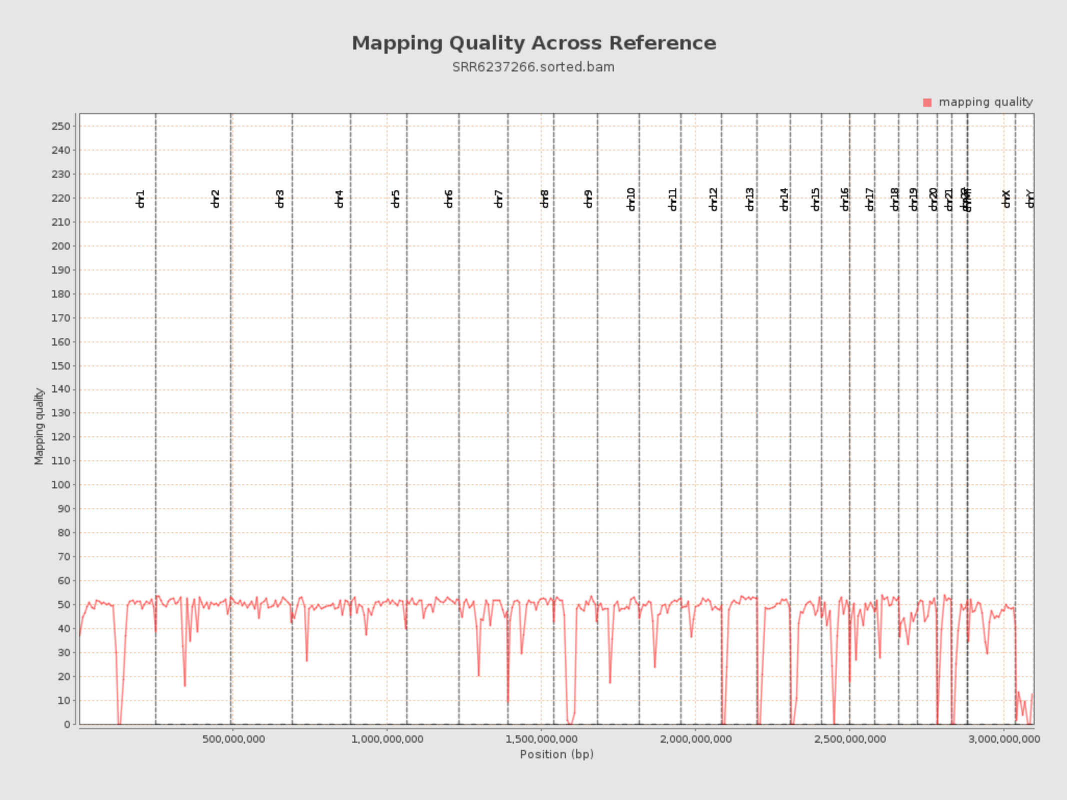
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram