Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 05:31:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237786.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_SRR6237786 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237786.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 05:31:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237786.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,688,920
Mapped reads	685,028 / 25.48%
Unmapped reads	2,003,892 / 74.52%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,836 / 0.11%
Read min/max/mean length	30 / 76 / 76.04
Duplicated reads (estimated)	20,770 / 0.77%
Duplication rate	2.61%
Clipped reads	478,159 / 17.78%

2.2. ACGT Content

Number/percentage of A's	11,122,090 / 27.79%
Number/percentage of C's	7,944,753 / 19.85%
Number/percentage of T's	11,728,366 / 29.31%
Number/percentage of G's	9,186,399 / 22.96%
Number/percentage of N's	33,831 / 0.08%
GC Percentage	42.81%

2.3. Coverage

Mean	0.0129

Standard Deviation	0.1398

2.4. Mapping Quality

Mean Mapping Quality	36.07

2.5. Mismatches and indels

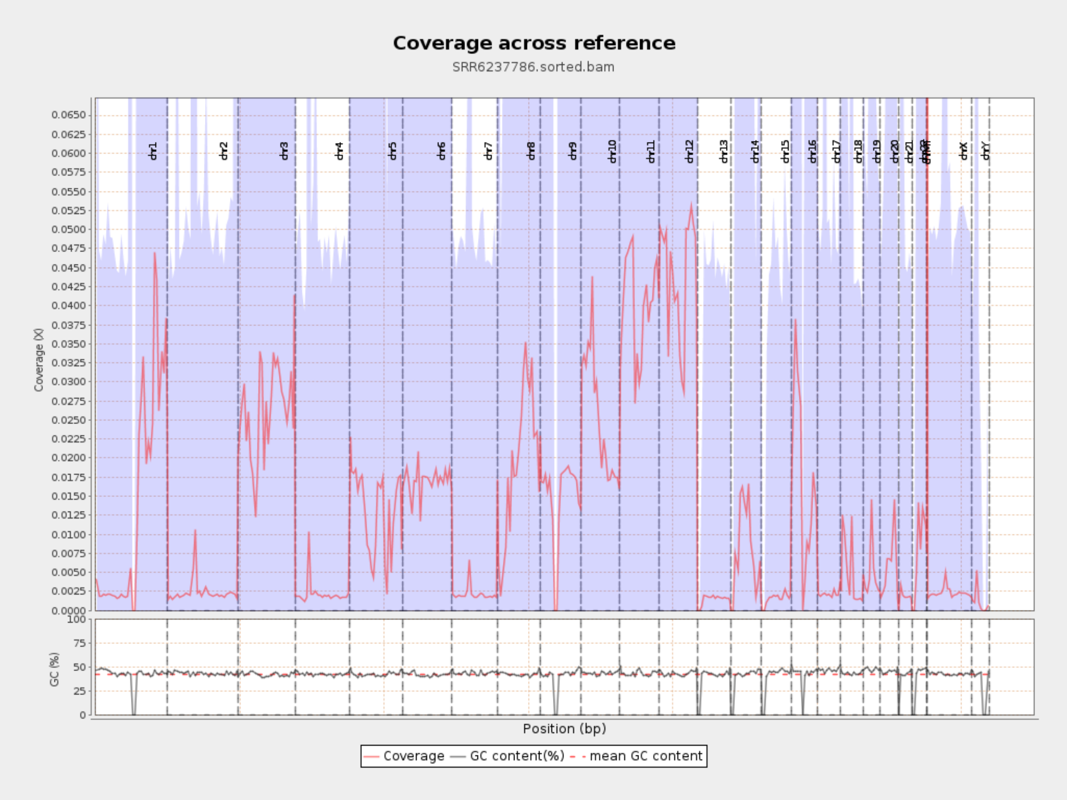
General error rate	0.78%
Mismatches	306,747
Insertions	2,805
Mapped reads with at least one insertion	0.41%
Deletions	10,348
Mapped reads with at least one deletion	1.5%
Homopolymer indels	44.99%

2.6. Chromosome stats

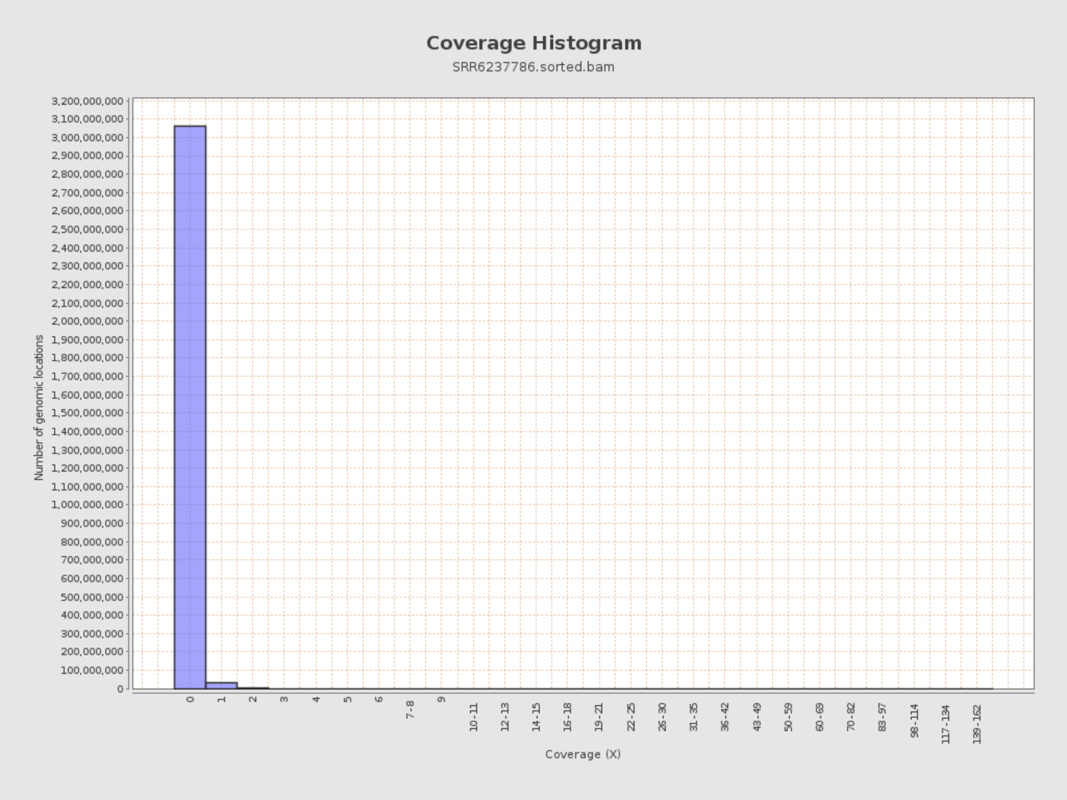
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3422752	0.0137	0.1377
chr2	243199373	597116	0.0025	0.0972
chr3	198022430	5198149	0.0263	0.1759
chr4	191154276	427352	0.0022	0.0671
chr5	180915260	2304765	0.0127	0.1215
chr6	171115067	2919958	0.0171	0.1477
chr7	159138663	347637	0.0022	0.071

chr8	146364022	2873023	0.0196	0.1584
chr9	141213431	2101236	0.0149	0.1398
chr10	135534747	3467314	0.0256	0.2332
chr11	135006516	5401595	0.04	0.2521
chr12	133851895	5889174	0.044	0.23
chr13	115169878	170040	0.0015	0.0403
chr14	107349540	889932	0.0083	0.0994
chr15	102531392	159336	0.0016	0.0416
chr16	90354753	1528320	0.0169	0.1443
chr17	81195210	178467	0.0022	0.0619
chr18	78077248	386080	0.0049	0.1178
chr19	59128983	296410	0.005	0.1083
chr20	63025520	375657	0.006	0.0846
chr21	48129895	91306	0.0019	0.0597
chr22	51304566	415088	0.0081	0.0965
chrMT	16571	154242	9.3079	6.0638
chrX	155270560	366566	0.0024	0.0661
chrY	59373566	71302	0.0012	0.0559

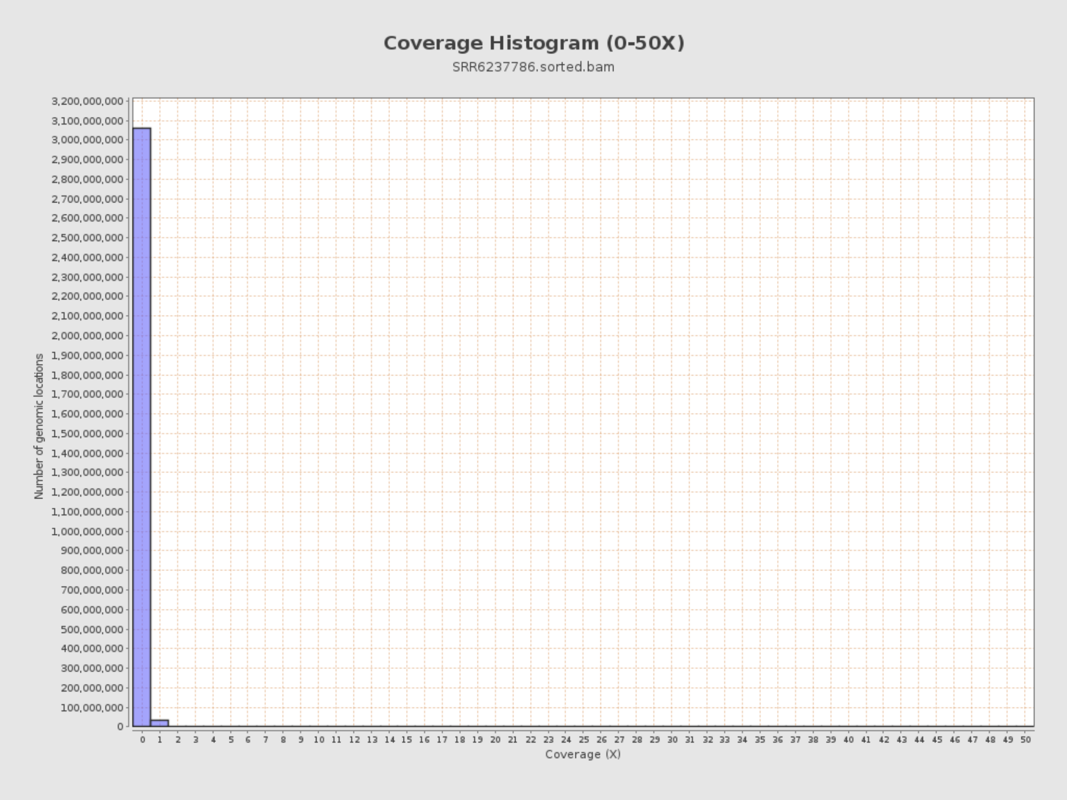
3. Results : Coverage across reference



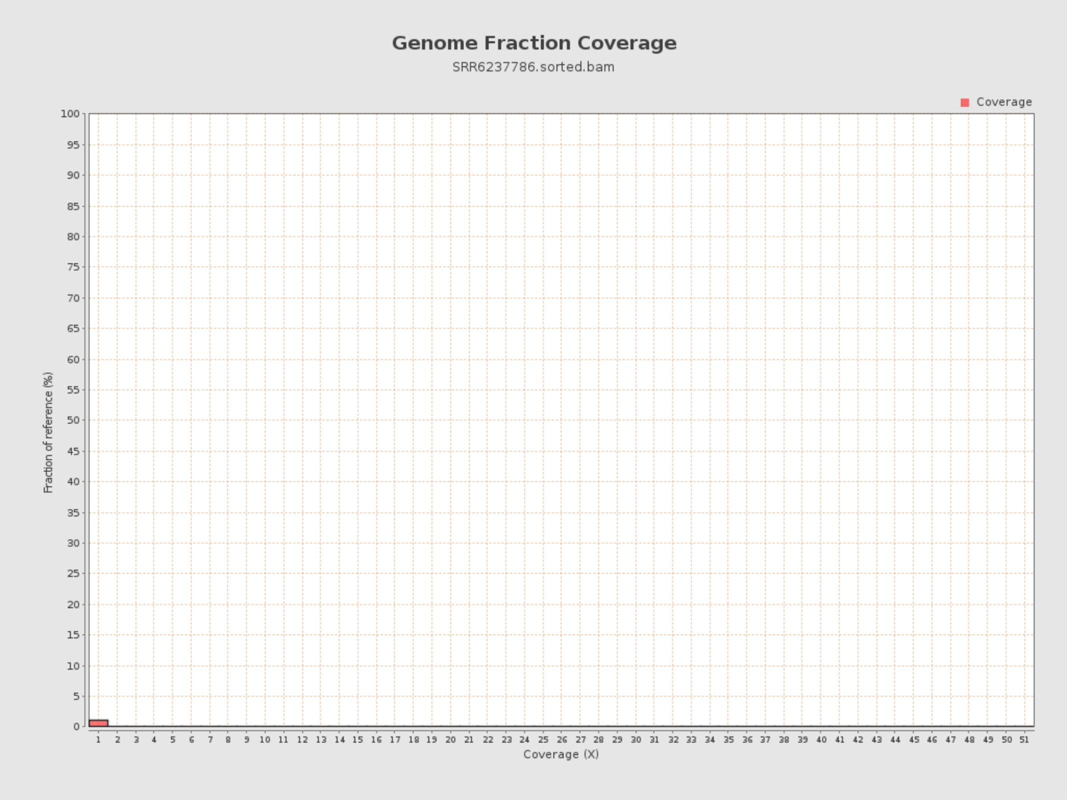
4. Results : Coverage Histogram



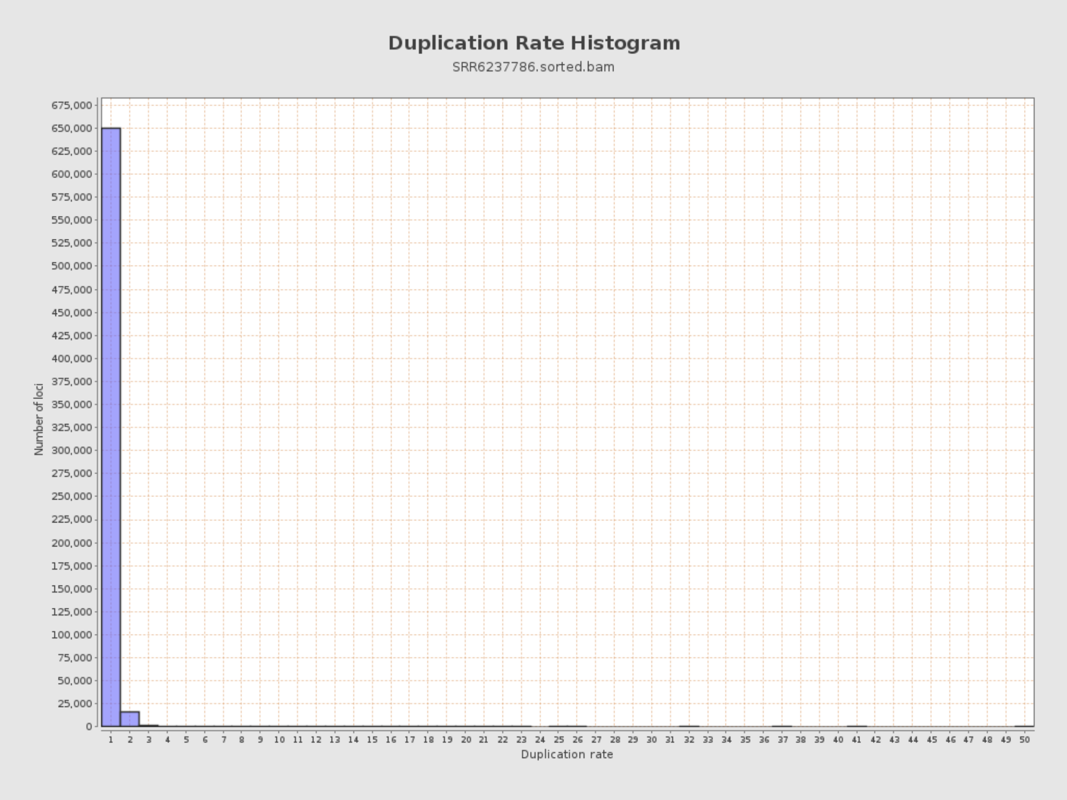
5. Results : Coverage Histogram (0-50X)



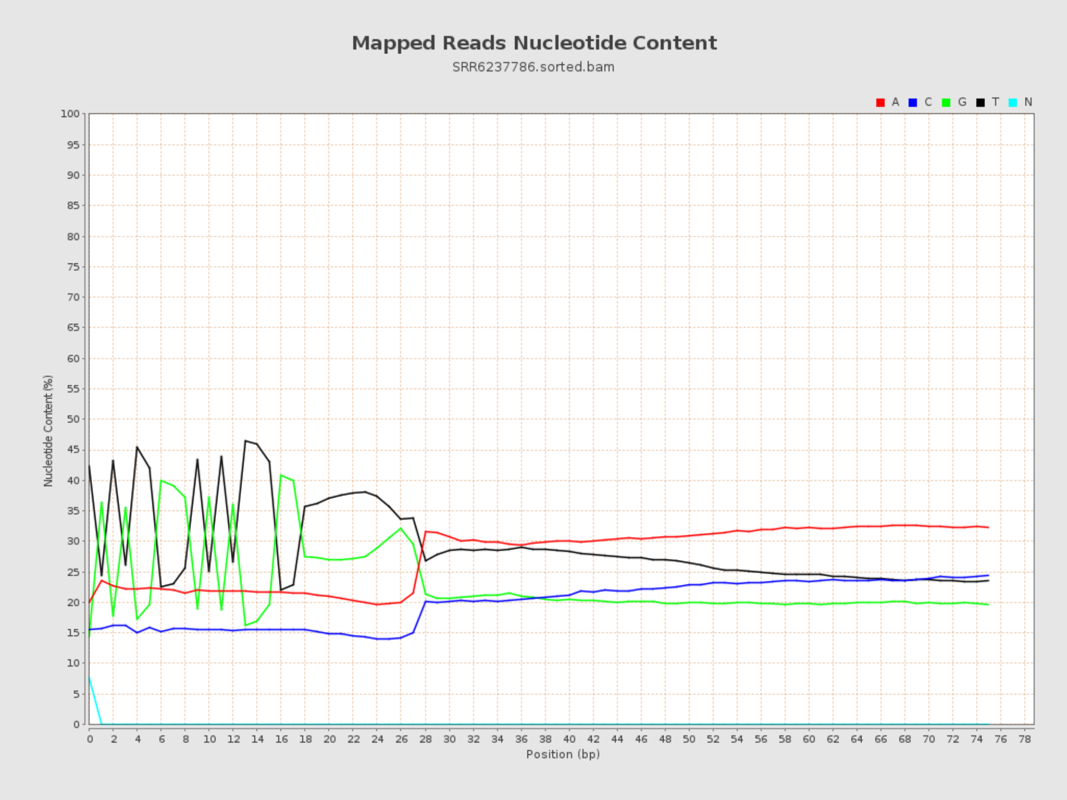
6. Results : Genome Fraction Coverage



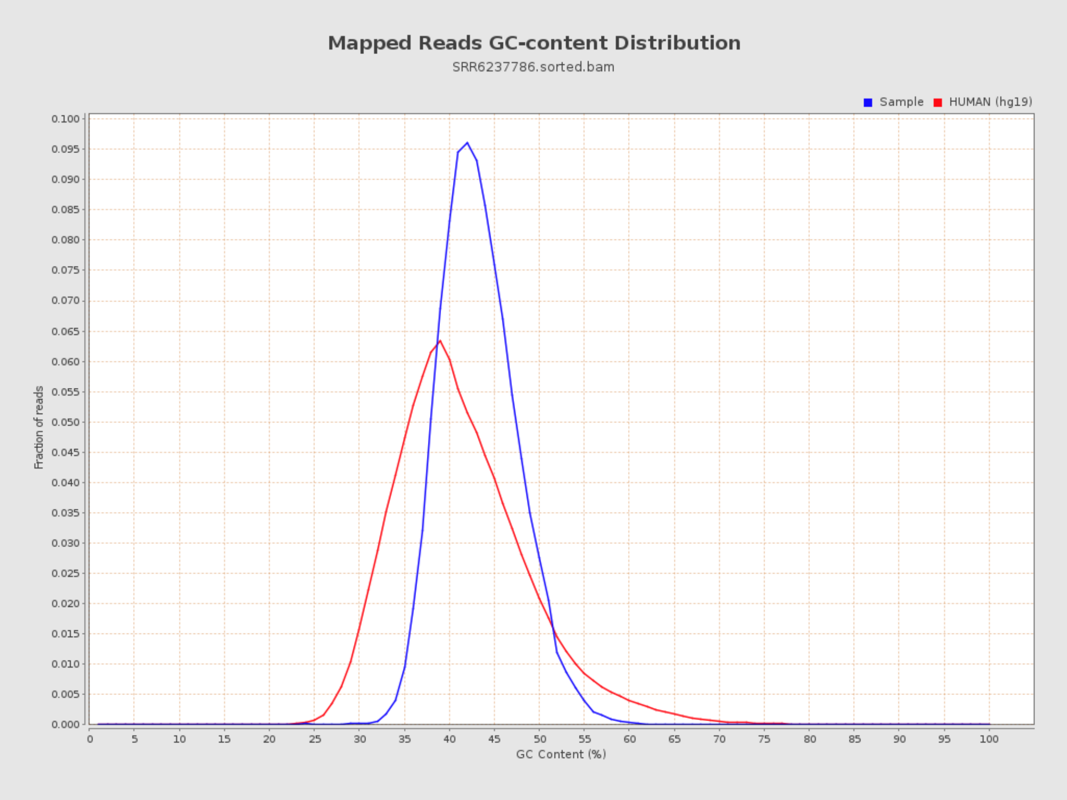
7. Results : Duplication Rate Histogram



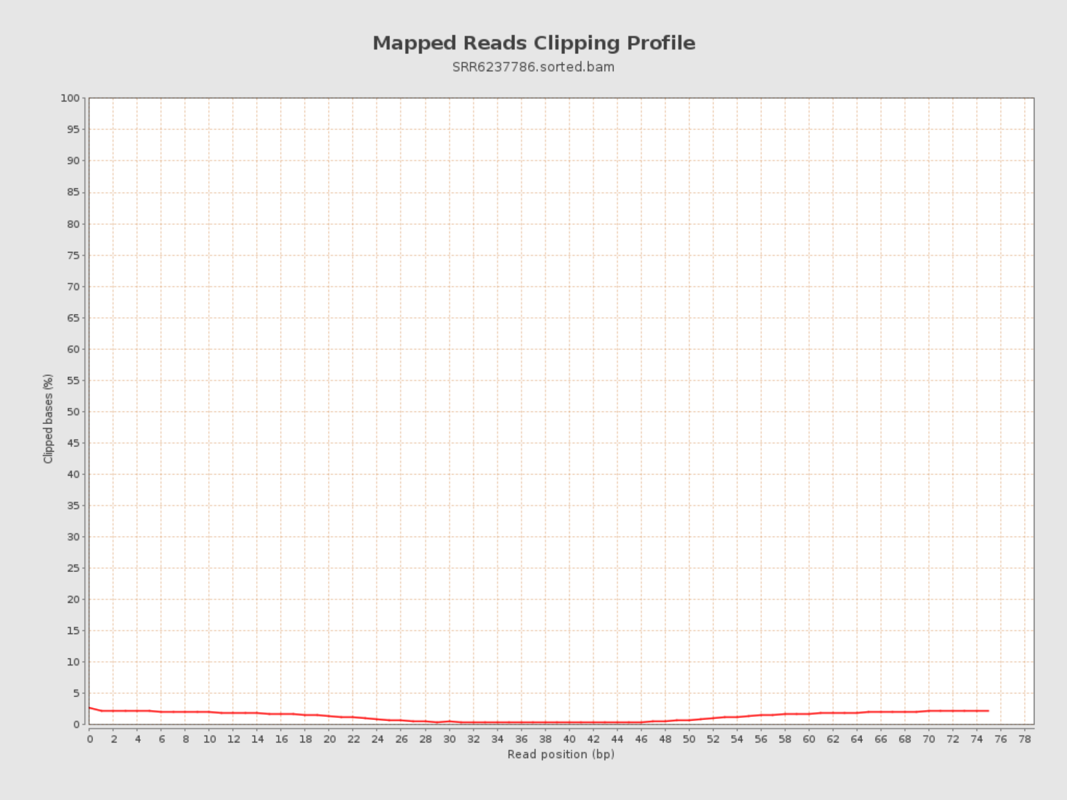
8. Results : Mapped Reads Nucleotide Content



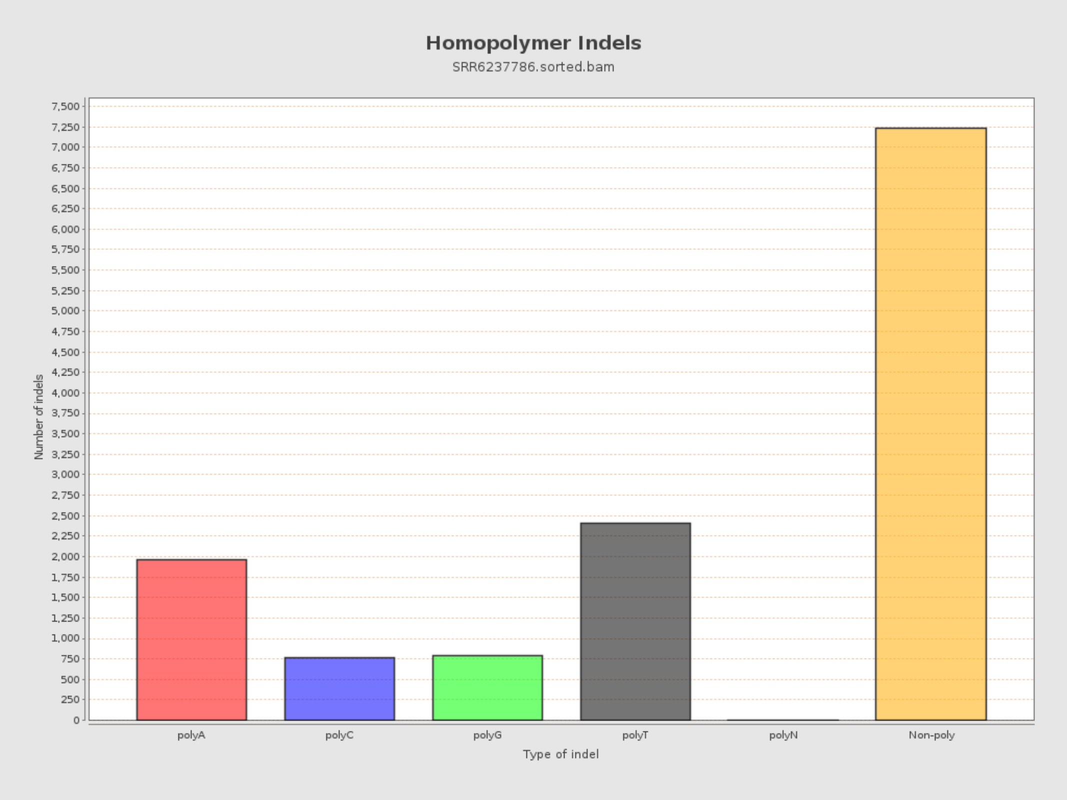
9. Results : Mapped Reads GC-content Distribution



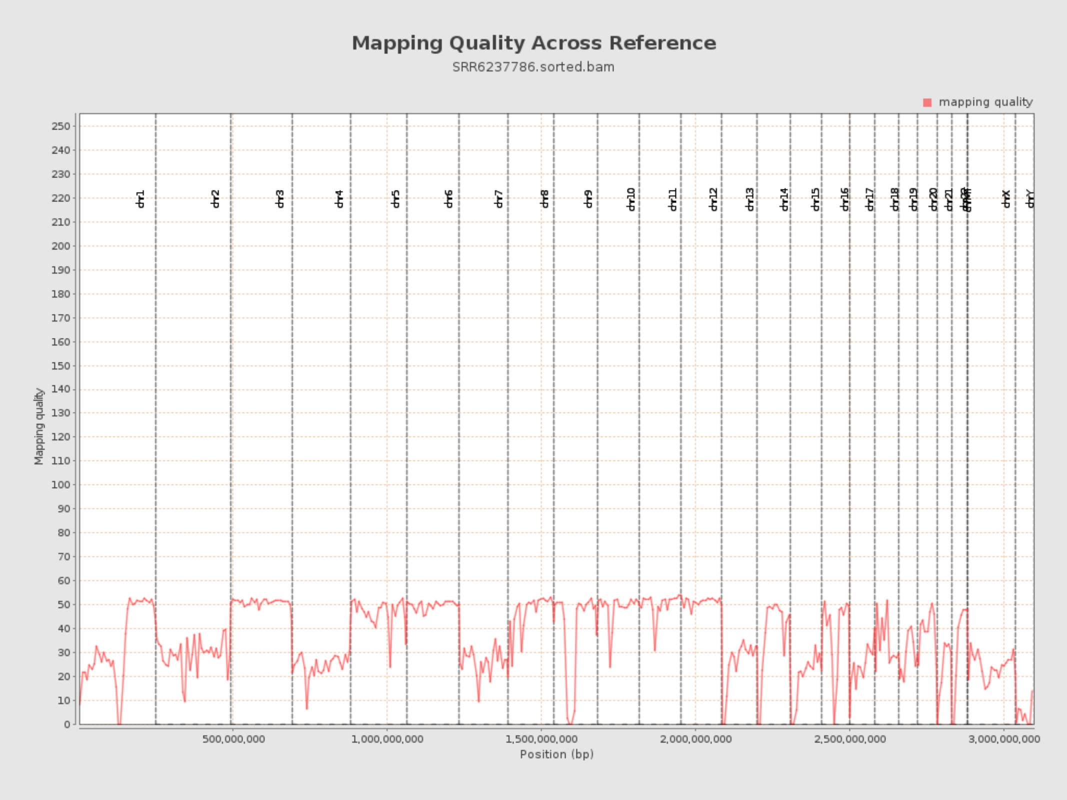
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram