Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 23:29:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237270.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_SRR6237270 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237270.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 23:29:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237270.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	933,991
Mapped reads	809,855 / 86.71%
Unmapped reads	124,136 / 13.29%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,583 / 0.49%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	22,709 / 2.43%
Duplication rate	2.11%
Clipped reads	356,101 / 38.13%

2.2. ACGT Content

Number/percentage of A's	15,794,824 / 29.19%
Number/percentage of C's	9,786,744 / 18.09%
Number/percentage of T's	17,240,118 / 31.86%
Number/percentage of G's	11,292,612 / 20.87%
Number/percentage of N's	874 / 0%
GC Percentage	38.95%

2.3. Coverage

Mean	0.0175

Standard Deviation	0.2051

2.4. Mapping Quality

Mean Mapping Quality	46.46

2.5. Mismatches and indels

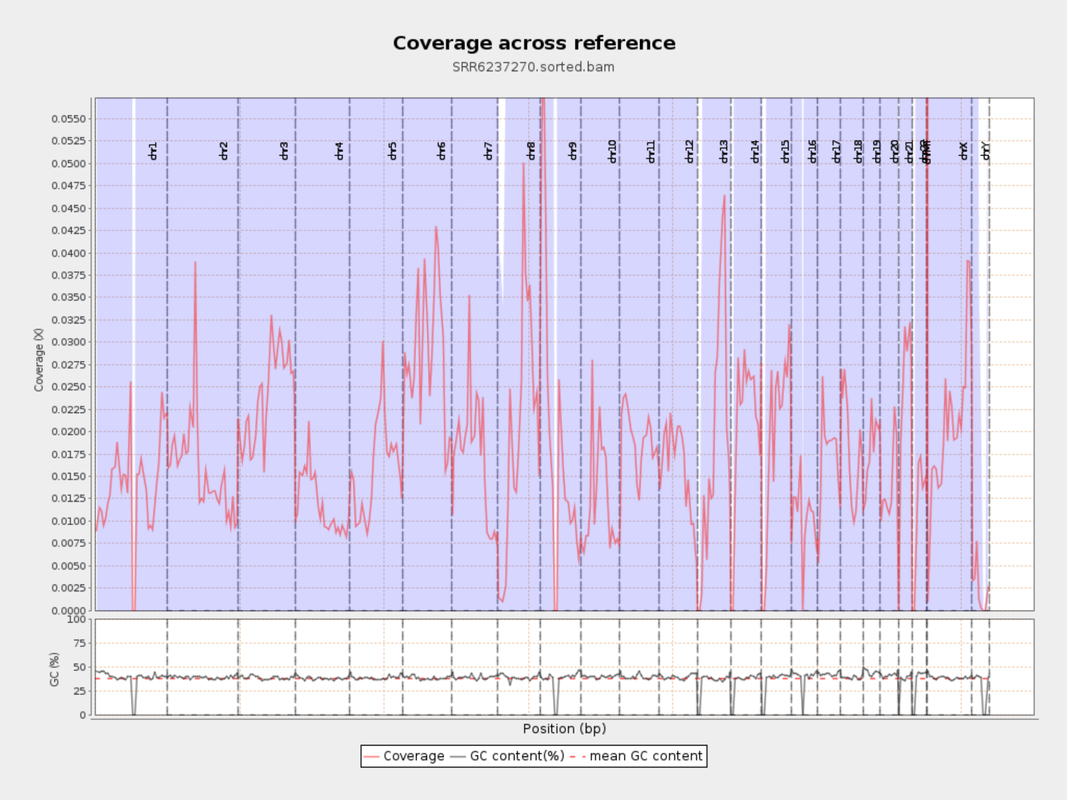
General error rate	0.85%
Mismatches	450,848
Insertions	4,296
Mapped reads with at least one insertion	0.53%
Deletions	17,106
Mapped reads with at least one deletion	2.09%
Homopolymer indels	45.06%

2.6. Chromosome stats

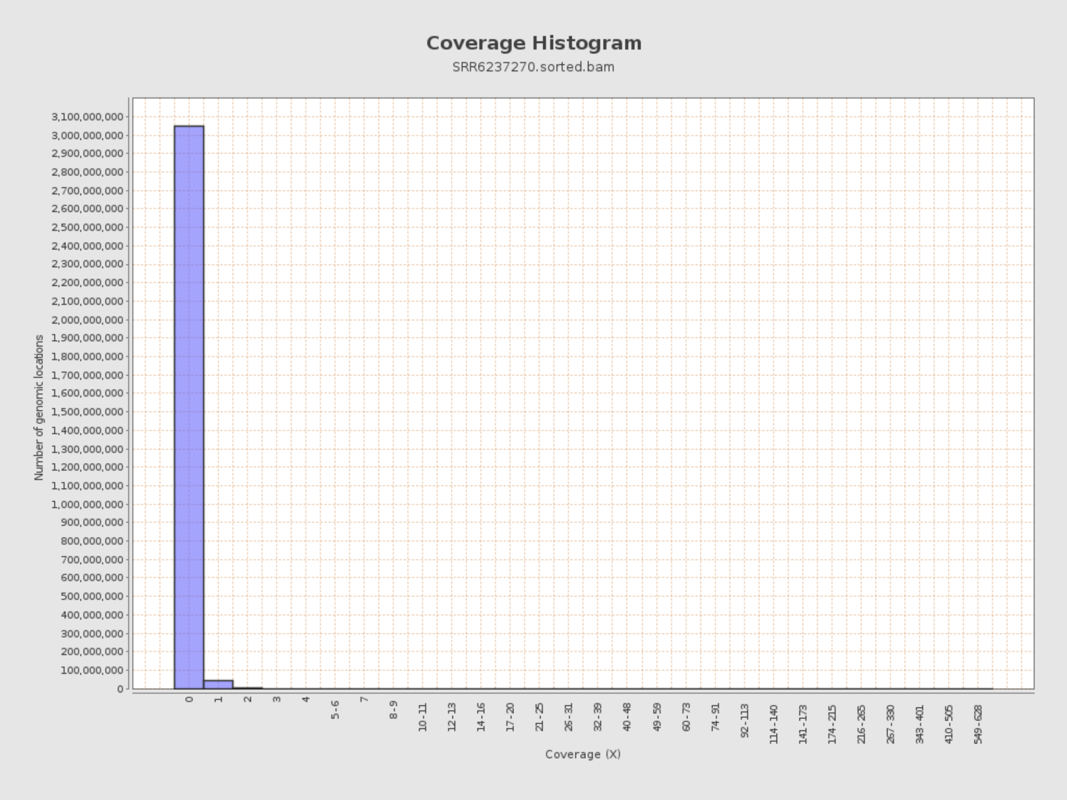
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3445175	0.0138	0.2789
chr2	243199373	3824259	0.0157	0.1976
chr3	198022430	4788829	0.0242	0.1651
chr4	191154276	2252345	0.0118	0.1222
chr5	180915260	2891548	0.016	0.1357
chr6	171115067	4891080	0.0286	0.2037
chr7	159138663	2767136	0.0174	0.2364

chr8	146364022	2948667	0.0201	0.4256
chr9	141213431	2761311	0.0196	0.2056
chr10	135534747	1679176	0.0124	0.1771
chr11	135006516	2581582	0.0191	0.1774
chr12	133851895	2146476	0.016	0.1375
chr13	115169878	2193066	0.019	0.1469
chr14	107349540	2202362	0.0205	0.1576
chr15	102531392	2002312	0.0195	0.1484
chr16	90354753	927370	0.0103	0.1235
chr17	81195210	1387141	0.0171	0.1679
chr18	78077248	1390499	0.0178	0.3387
chr19	59128983	1062139	0.018	0.2109
chr20	63025520	871588	0.0138	0.1261
chr21	48129895	1191831	0.0248	0.1749
chr22	51304566	567757	0.0111	0.1108
chrMT	16571	32644	1.9699	1.8277
chrX	155270560	3200369	0.0206	0.1606
chrY	59373566	138352	0.0023	0.0718

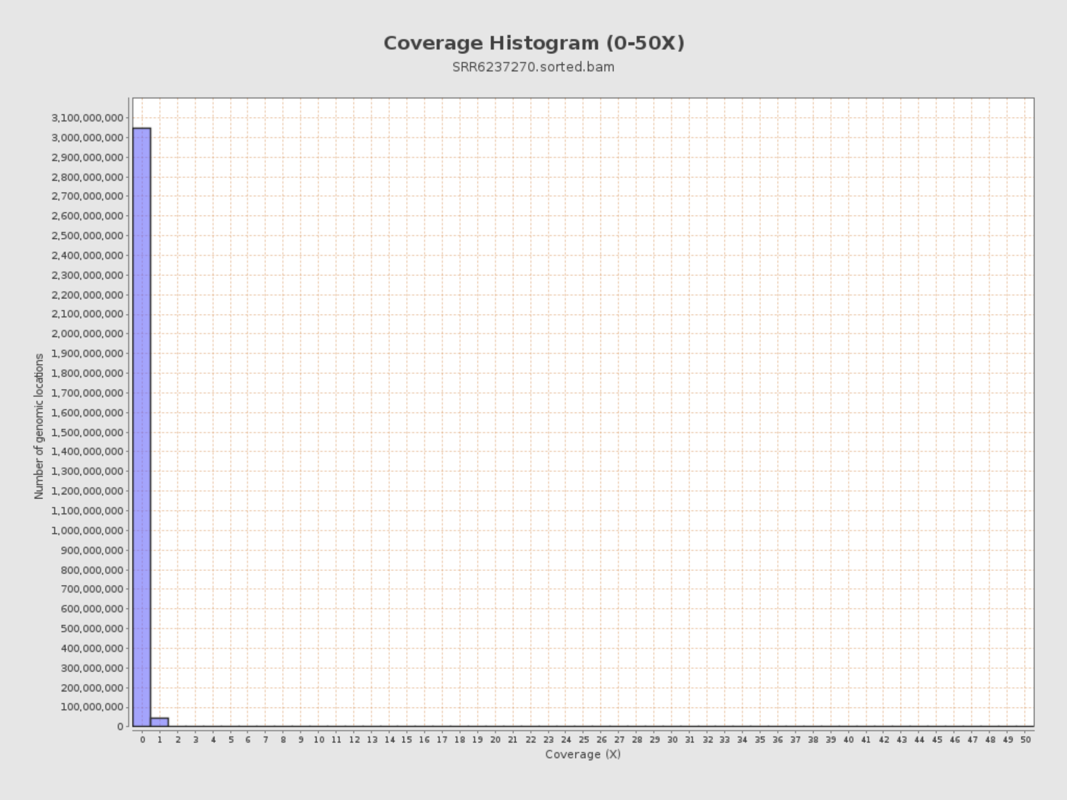
3. Results : Coverage across reference



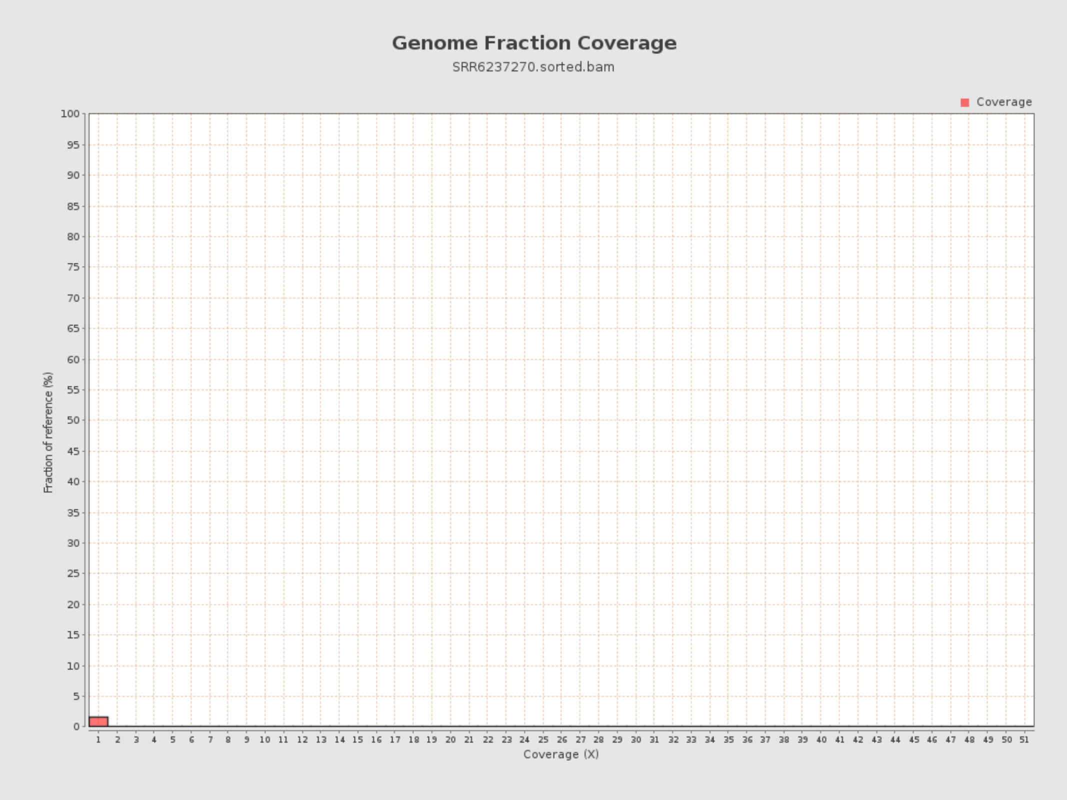
4. Results : Coverage Histogram



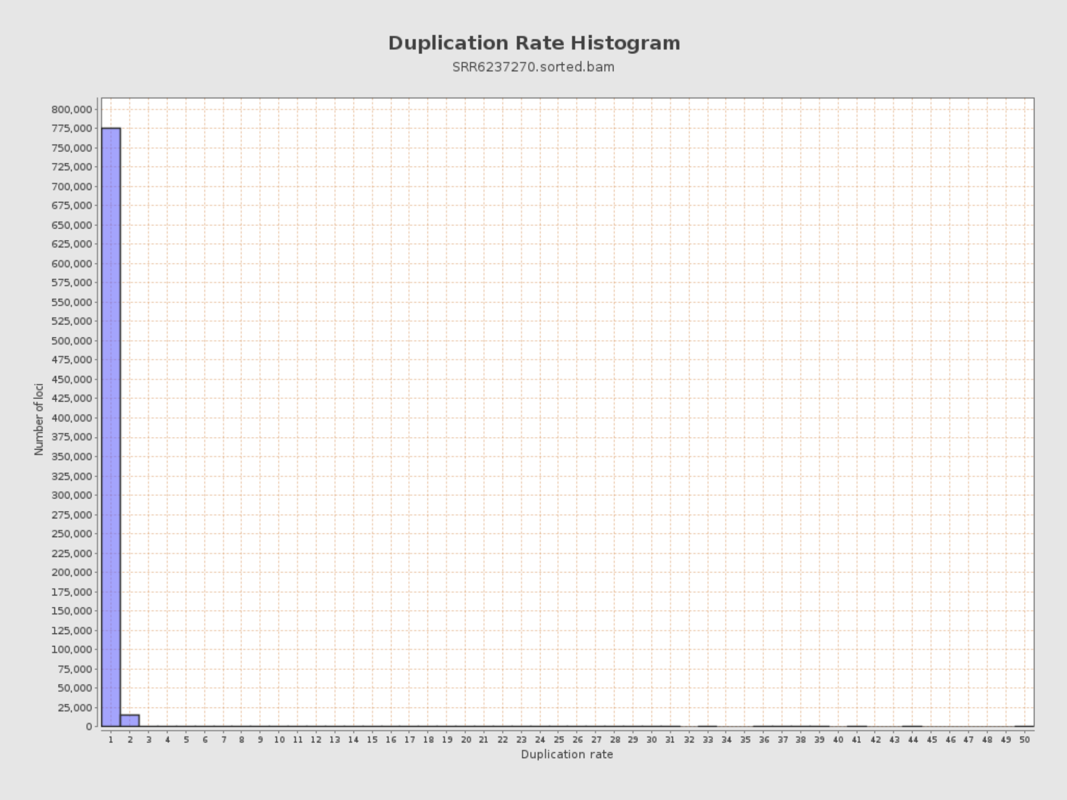
5. Results : Coverage Histogram (0-50X)



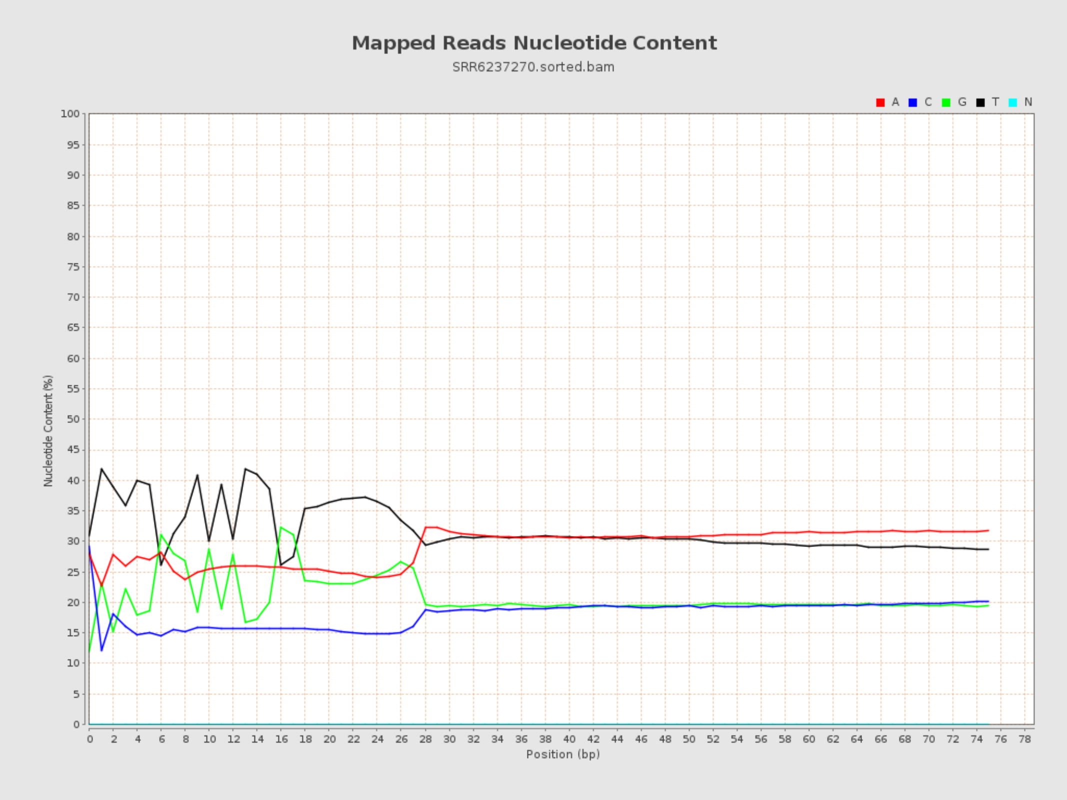
6. Results : Genome Fraction Coverage



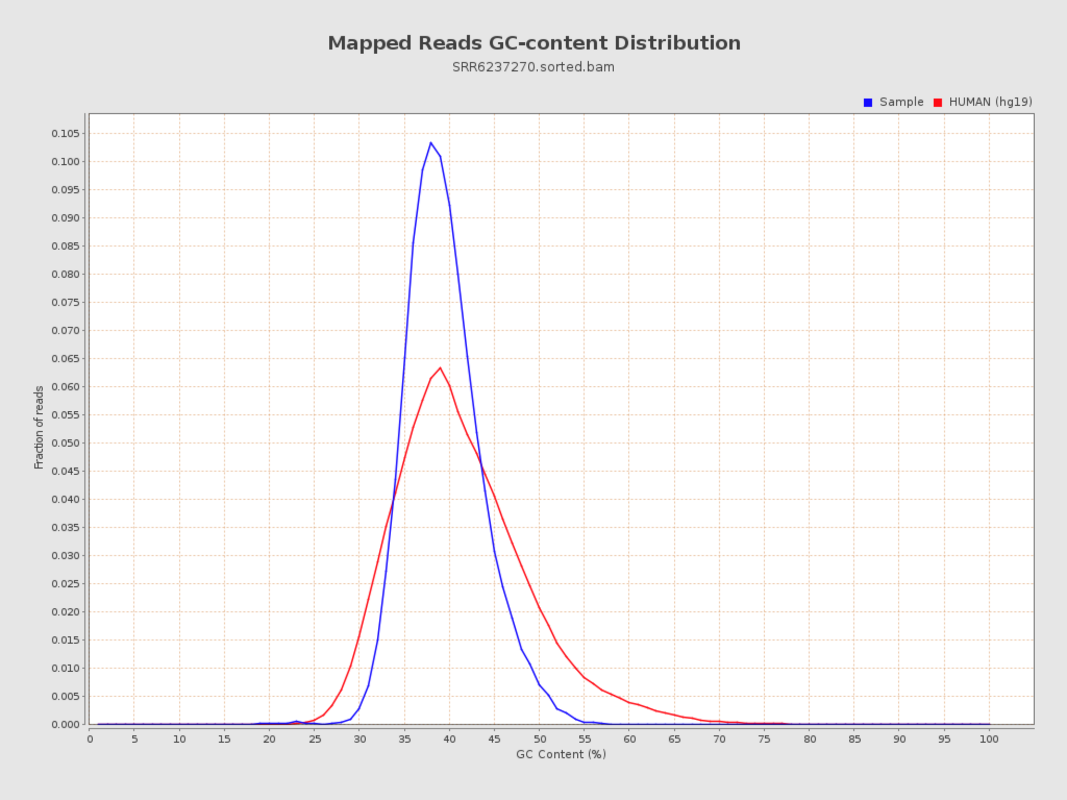
7. Results : Duplication Rate Histogram



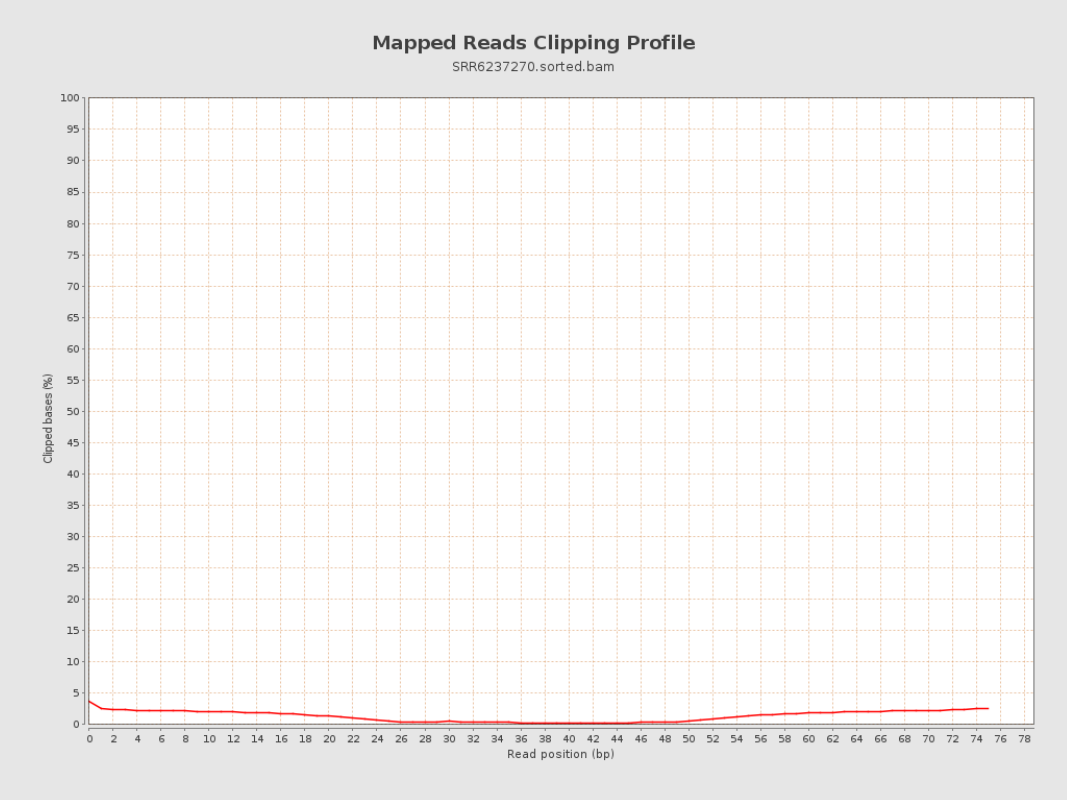
8. Results : Mapped Reads Nucleotide Content



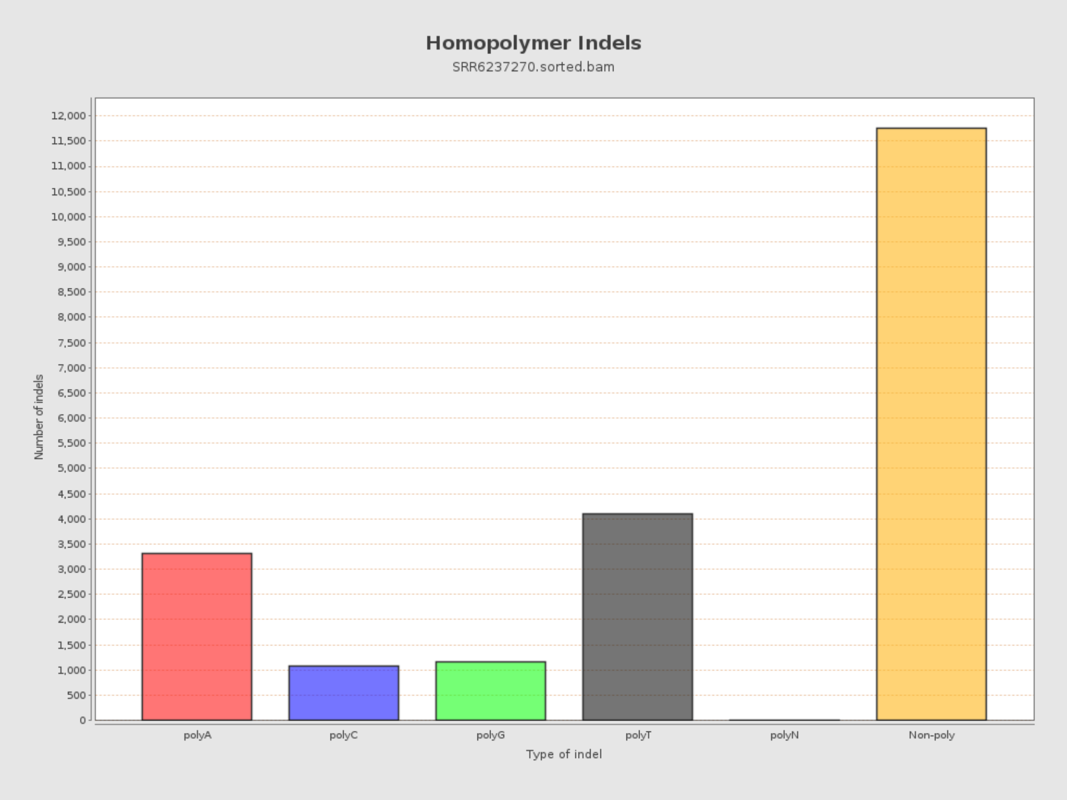
9. Results : Mapped Reads GC-content Distribution



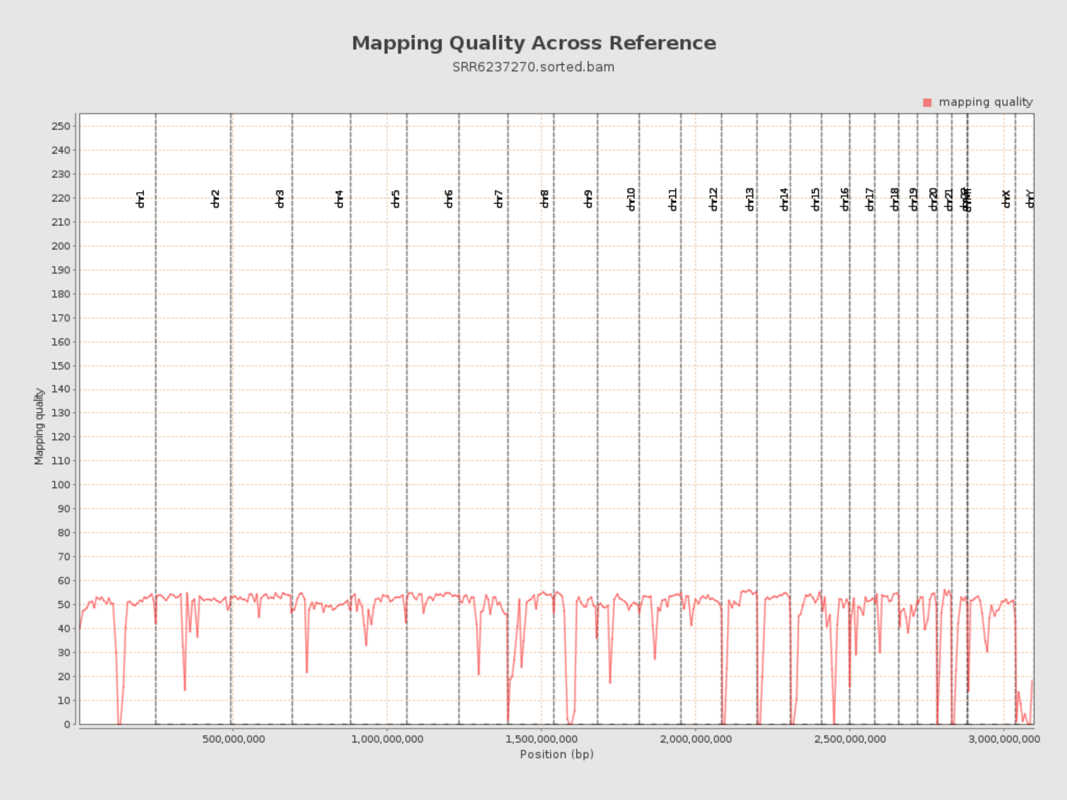
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram