Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 04:51:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237597.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_SRR6237597 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237597.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 04:51:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237597.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	815,515
Mapped reads	583,314 / 71.53%
Unmapped reads	232,201 / 28.47%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,750 / 0.34%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	50,793 / 6.23%
Duplication rate	7.68%
Clipped reads	392,599 / 48.14%

2.2. ACGT Content

Number/percentage of A's	9,185,778 / 25.95%
Number/percentage of C's	5,794,531 / 16.37%
Number/percentage of T's	11,962,480 / 33.8%
Number/percentage of G's	8,388,857 / 23.7%
Number/percentage of N's	61,109 / 0.17%
GC Percentage	40.07%

2.3. Coverage

Mean	0.0114

Standard Deviation	0.1445

2.4. Mapping Quality

Mean Mapping Quality	46.04

2.5. Mismatches and indels

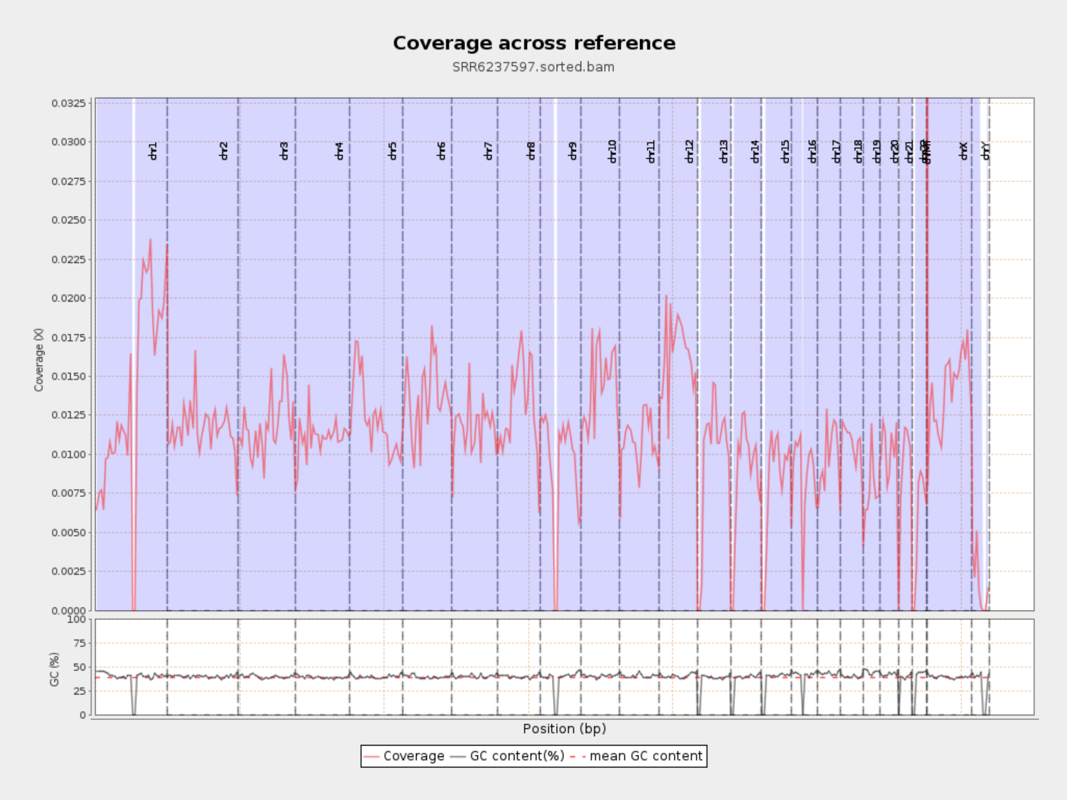
General error rate	1.02%
Mismatches	356,953
Insertions	2,866
Mapped reads with at least one insertion	0.49%
Deletions	13,207
Mapped reads with at least one deletion	2.24%
Homopolymer indels	48.58%

2.6. Chromosome stats

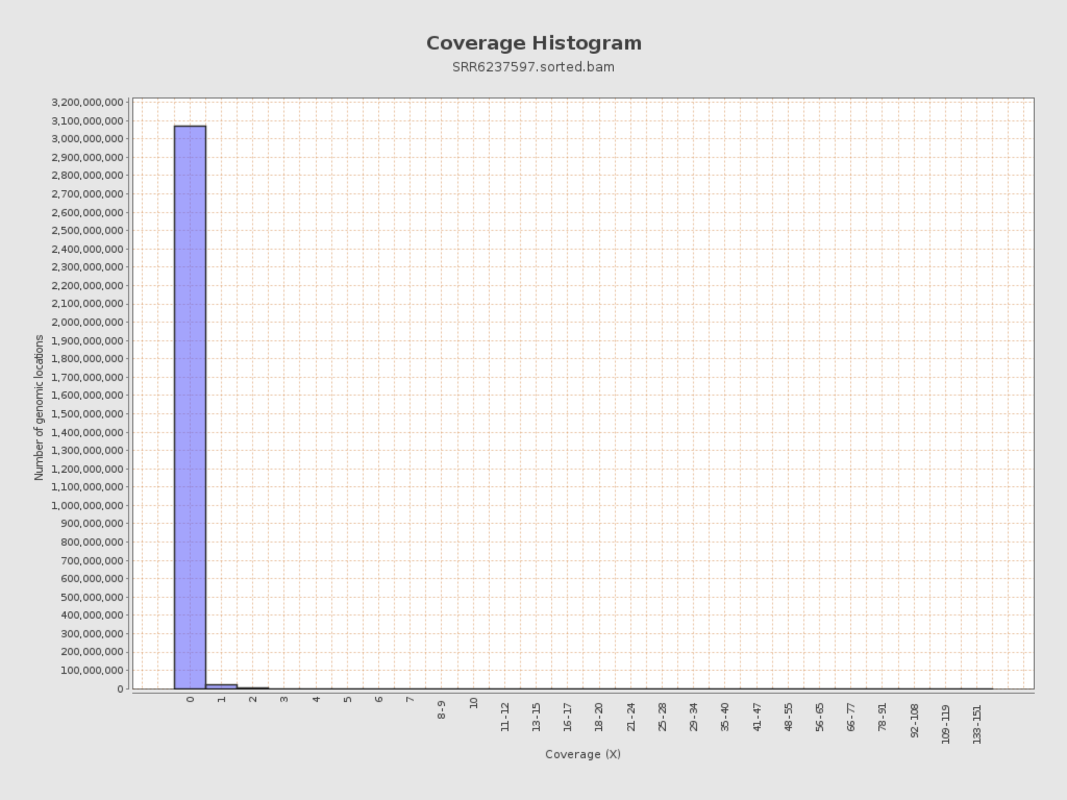
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3441569	0.0138	0.1836
chr2	243199373	2849386	0.0117	0.1567
chr3	198022430	2347338	0.0119	0.1366
chr4	191154276	2112608	0.0111	0.1318
chr5	180915260	2227745	0.0123	0.1367
chr6	171115067	2334483	0.0136	0.1497
chr7	159138663	1869221	0.0117	0.1607

chr8	146364022	1918896	0.0131	0.1587
chr9	141213431	1321772	0.0094	0.1321
chr10	135534747	1926877	0.0142	0.1622
chr11	135006516	1463173	0.0108	0.14
chr12	133851895	2191830	0.0164	0.1588
chr13	115169878	1116107	0.0097	0.1262
chr14	107349540	911259	0.0085	0.1144
chr15	102531392	829190	0.0081	0.1117
chr16	90354753	757538	0.0084	0.1143
chr17	81195210	794165	0.0098	0.1215
chr18	78077248	839491	0.0108	0.1718
chr19	59128983	460880	0.0078	0.1293
chr20	63025520	637140	0.0101	0.1264
chr21	48129895	434415	0.009	0.1204
chr22	51304566	288587	0.0056	0.0928
chrMT	16571	31917	1.9261	2.0997
chrX	155270560	2207289	0.0142	0.151
chrY	59373566	100559	0.0017	0.051

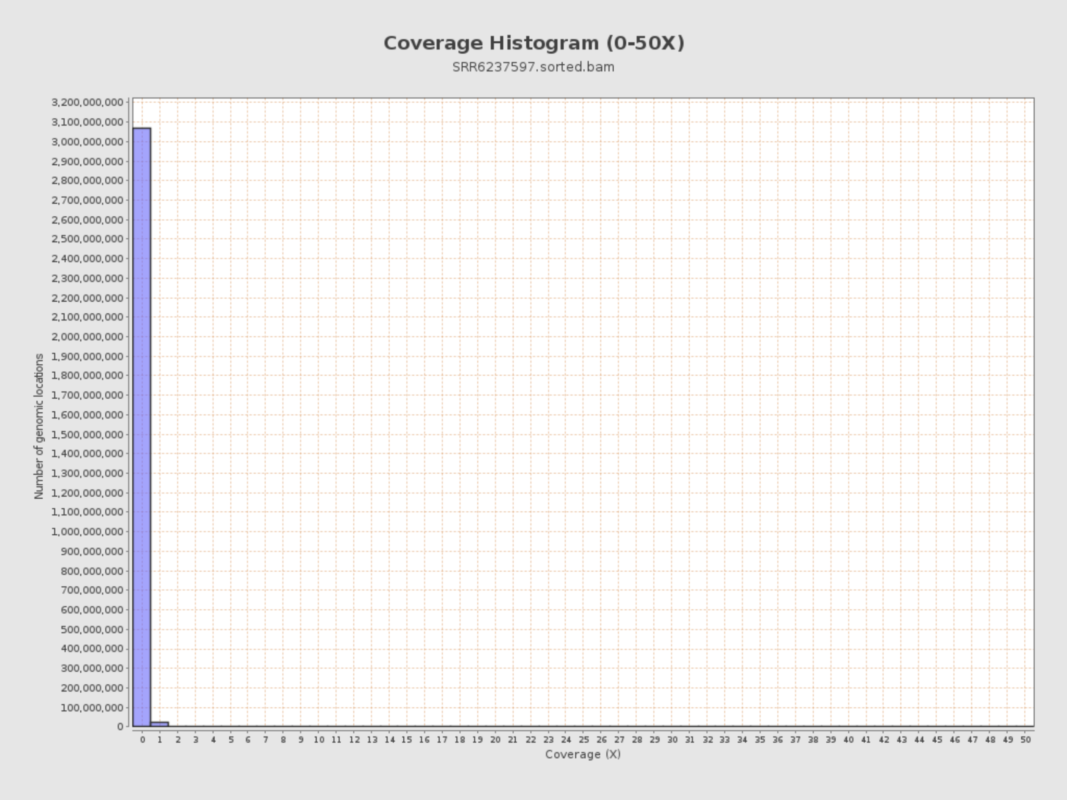
3. Results : Coverage across reference



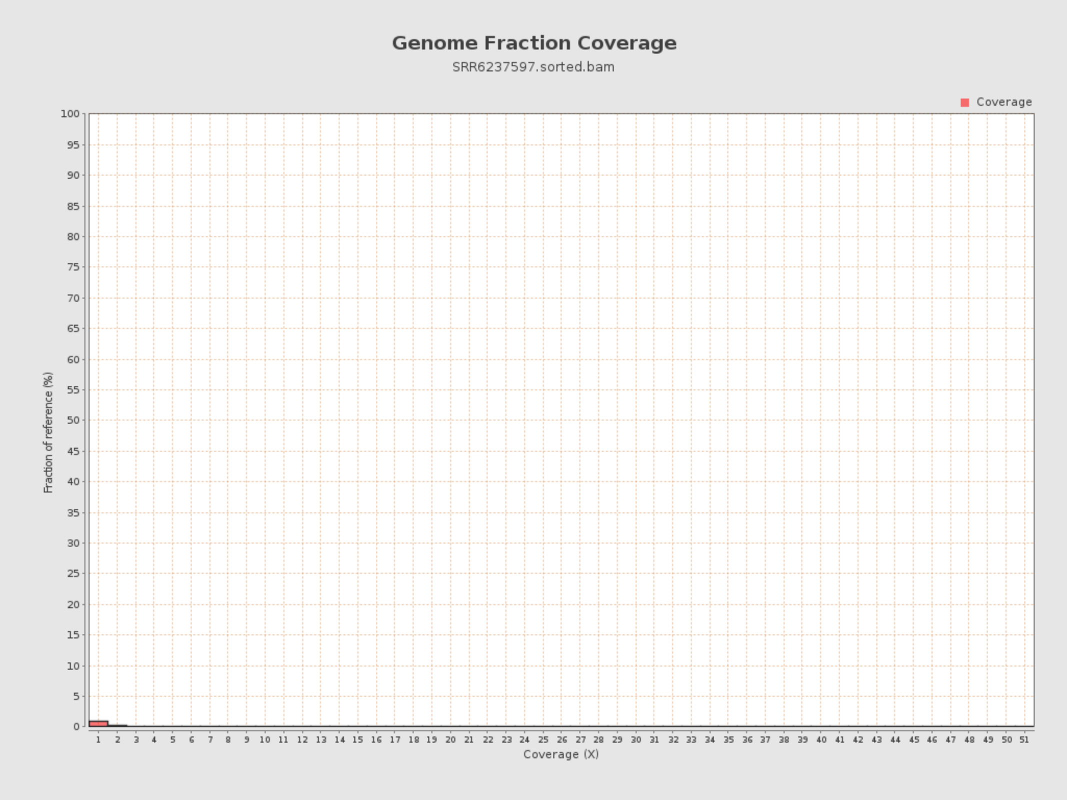
4. Results : Coverage Histogram



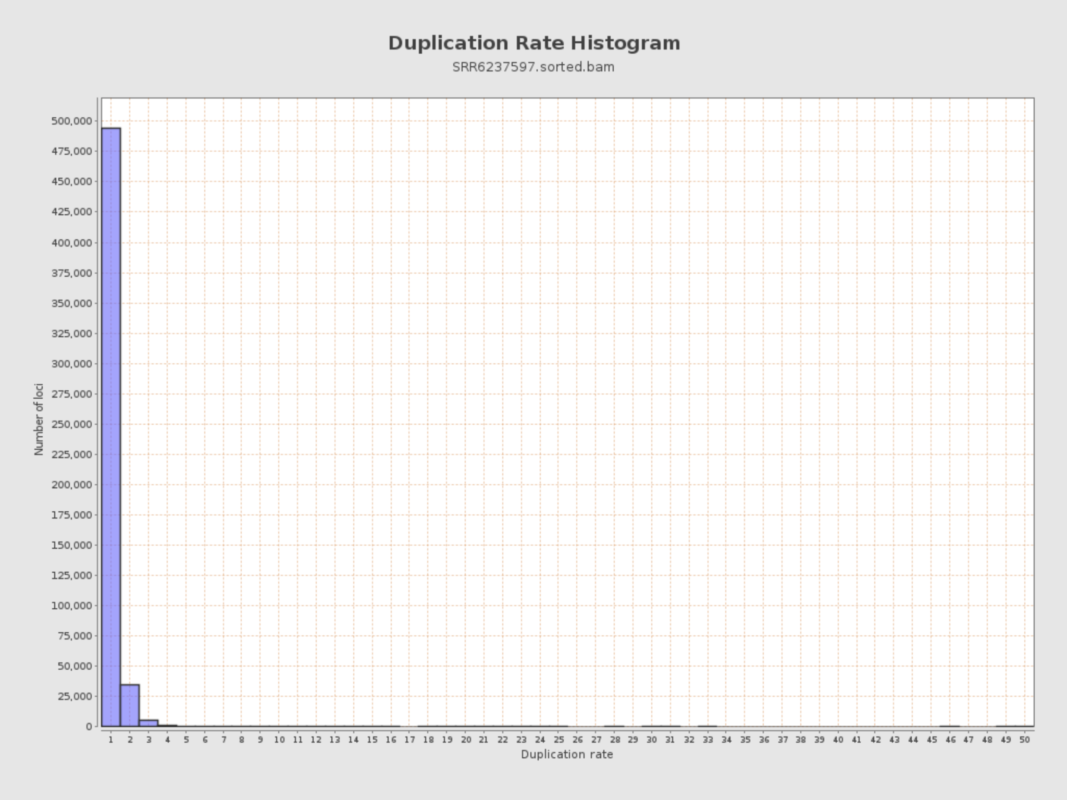
5. Results : Coverage Histogram (0-50X)



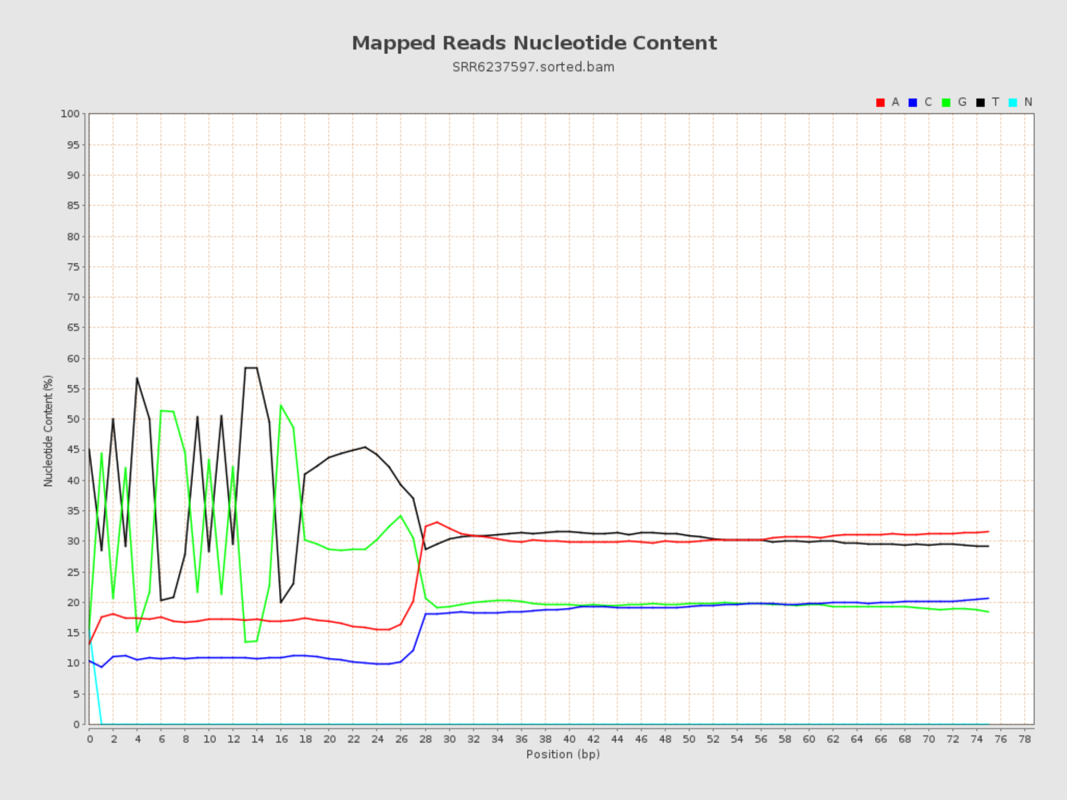
6. Results : Genome Fraction Coverage



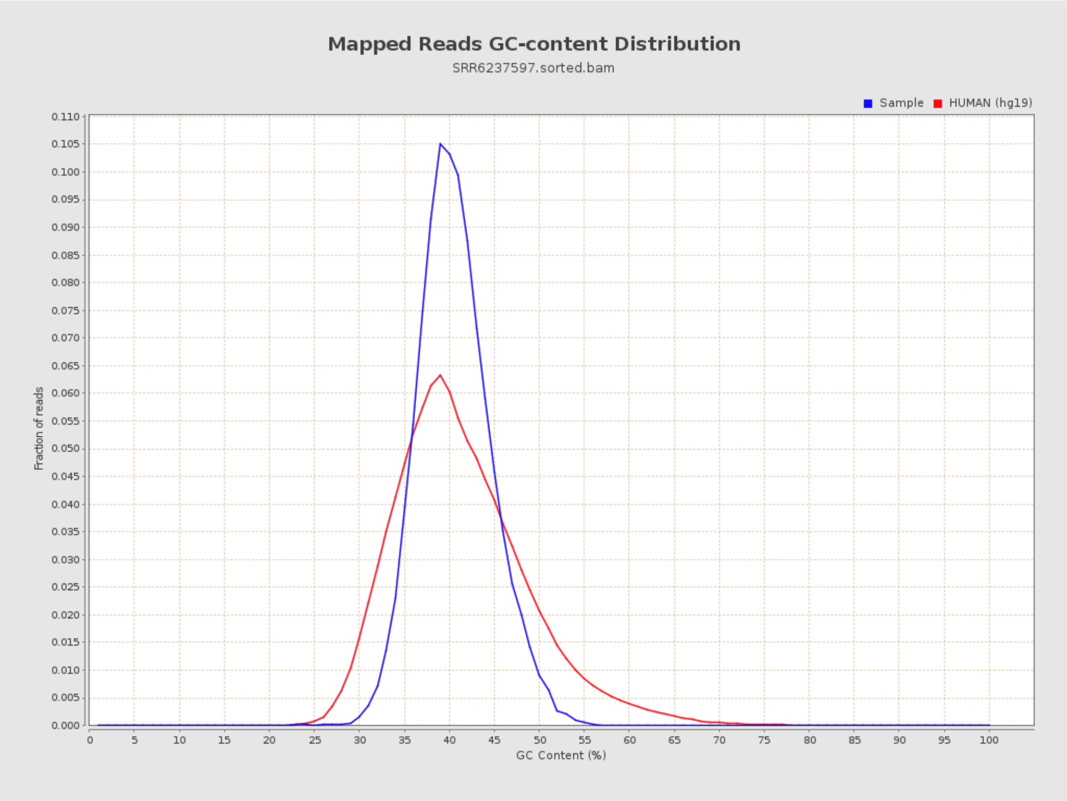
7. Results : Duplication Rate Histogram



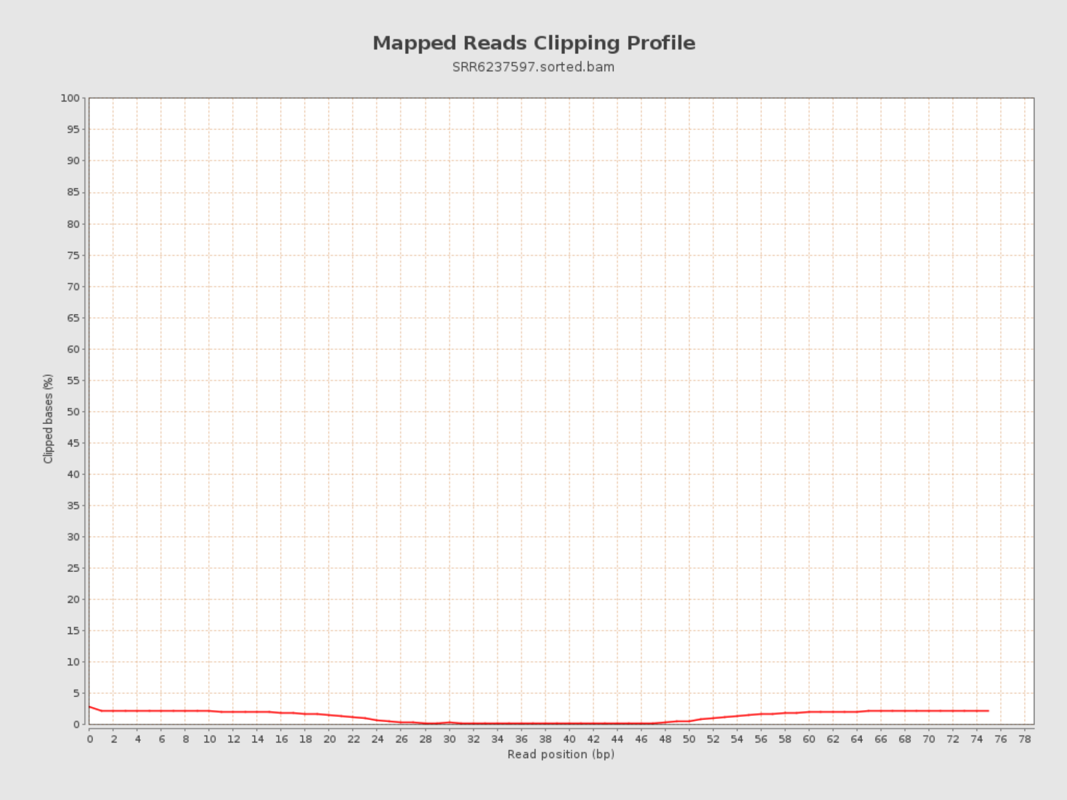
8. Results : Mapped Reads Nucleotide Content



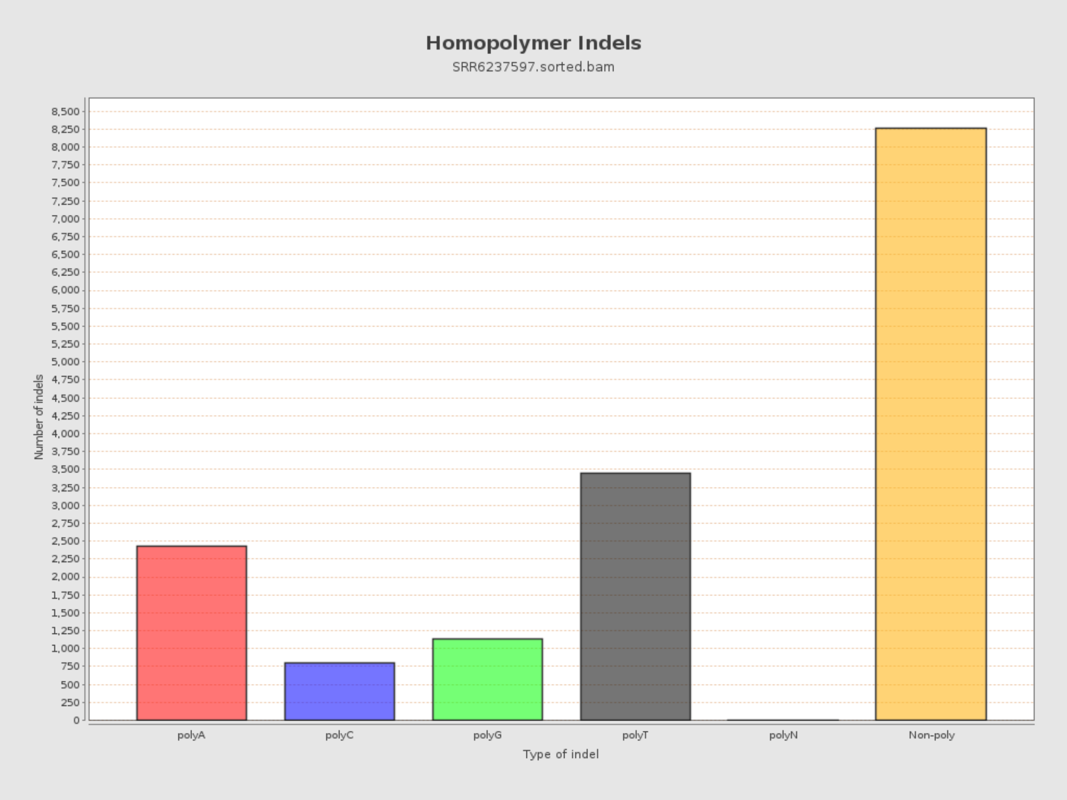
9. Results : Mapped Reads GC-content Distribution



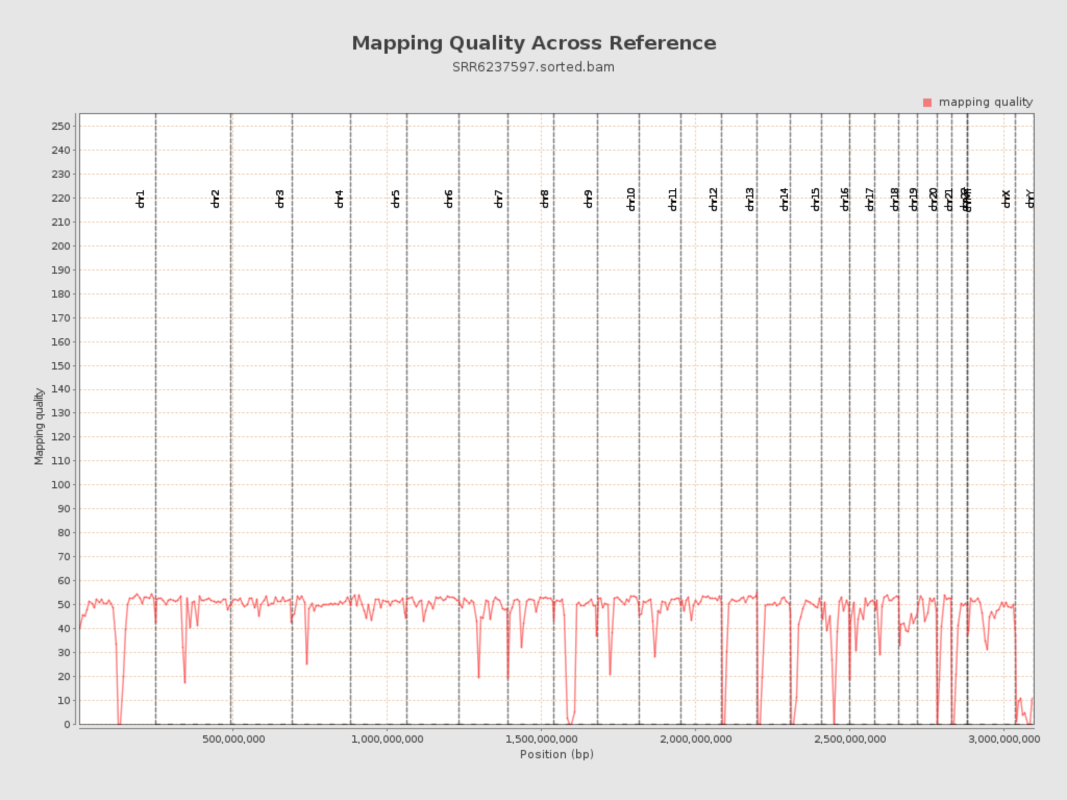
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram