

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 04:53:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237598.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_SRR6237598 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237598.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 04:53:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237598.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	862,629
Mapped reads	665,483 / 77.15%
Unmapped reads	197,146 / 22.85%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,817 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	58,613 / 6.79%
Duplication rate	7.74%
Clipped reads	408,687 / 47.38%

2.2. ACGT Content

Number/percentage of A's	11,022,561 / 26.69%
Number/percentage of C's	6,901,886 / 16.71%
Number/percentage of T's	13,846,985 / 33.53%
Number/percentage of G's	9,446,904 / 22.88%
Number/percentage of N's	77,984 / 0.19%
GC Percentage	39.59%

2.3. Coverage

Mean	0.0133

Standard Deviation	0.1614
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2.4. Mapping Quality

Mean Mapping Quality	46.6
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2.5. Mismatches and indels

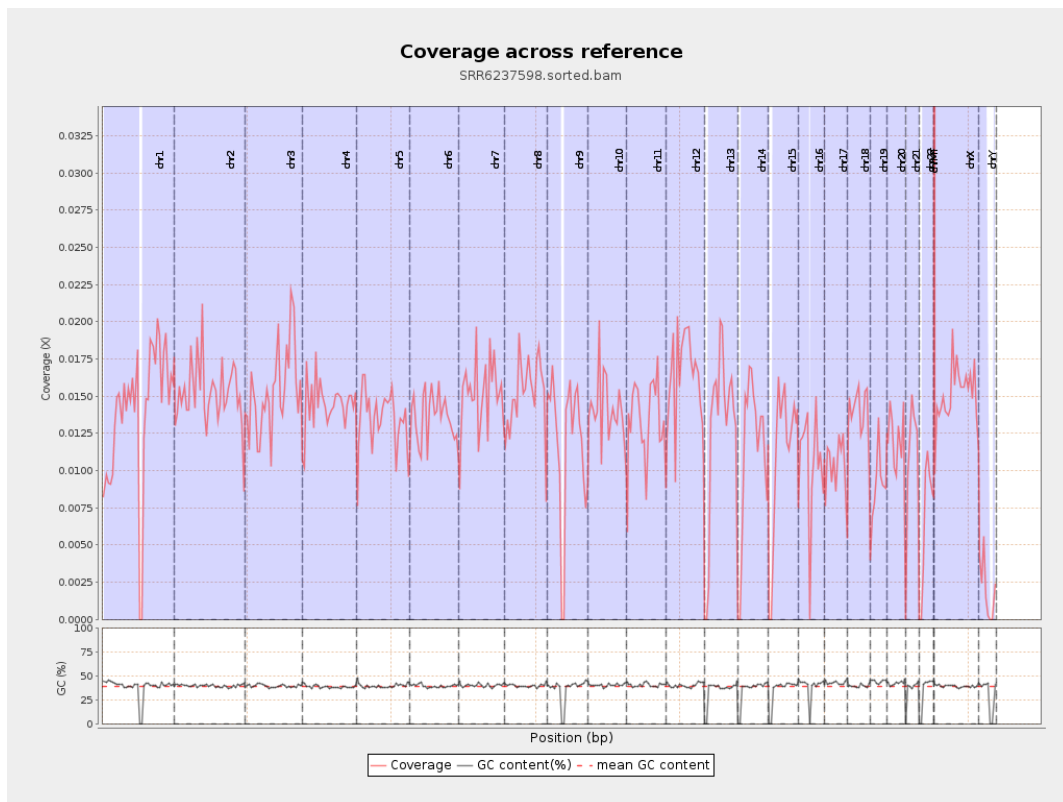
General error rate	1.06%
Mismatches	431,505
Insertions	3,437
Mapped reads with at least one insertion	0.51%
Deletions	17,380
Mapped reads with at least one deletion	2.57%
Homopolymer indels	49.94%

2.6. Chromosome stats

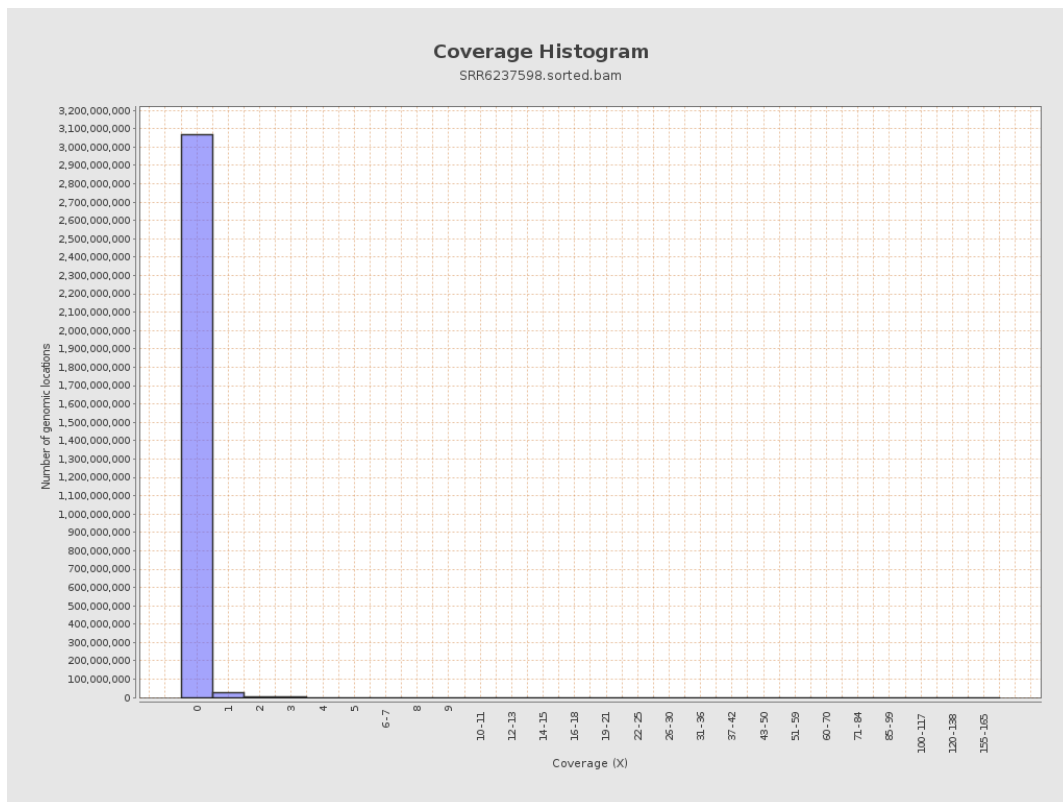
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	3470096	0.0139	0.1827
chr2	243199373	3702020	0.0152	0.1805
chr3	198022430	3022387	0.0153	0.1618
chr4	191154276	2756893	0.0144	0.1563
chr5	180915260	2463866	0.0136	0.1488
chr6	171115067	2314841	0.0135	0.1543
chr7	159138663	2405190	0.0151	0.1956

chr8	146364022	2217621	0.0152	0.1873
chr9	141213431	1688362	0.012	0.1549
chr10	135534747	1898027	0.014	0.1667
chr11	135006516	1827119	0.0135	0.158
chr12	133851895	2196145	0.0164	0.1663
chr13	115169878	1465755	0.0127	0.1466
chr14	107349540	1208703	0.0113	0.1388
chr15	102531392	1139636	0.0111	0.1363
chr16	90354753	934359	0.0103	0.1321
chr17	81195210	829584	0.0102	0.133
chr18	78077248	1099176	0.0141	0.2091
chr19	59128983	545602	0.0092	0.1388
chr20	63025520	756442	0.012	0.1407
chr21	48129895	529245	0.011	0.1391
chr22	51304566	349031	0.0068	0.1028
chrMT	16571	24905	1.5029	1.7006
chrX	155270560	2362428	0.0152	0.1601
chrY	59373566	116436	0.002	0.0565

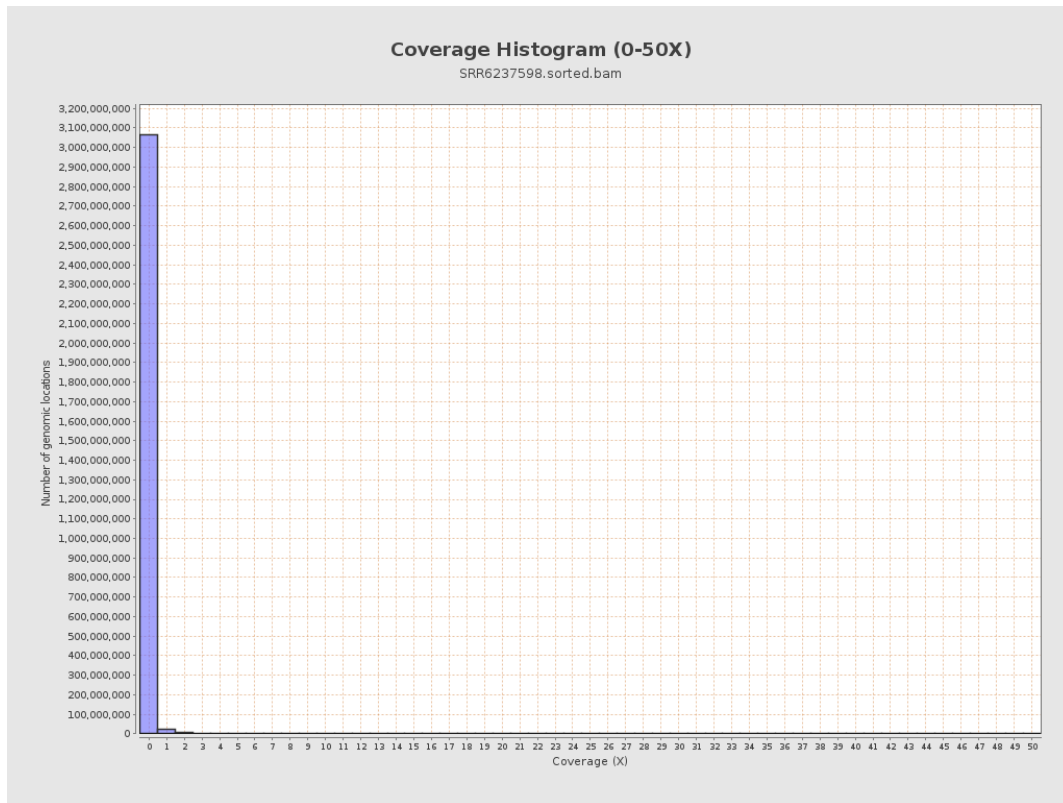
3. Results : Coverage across reference



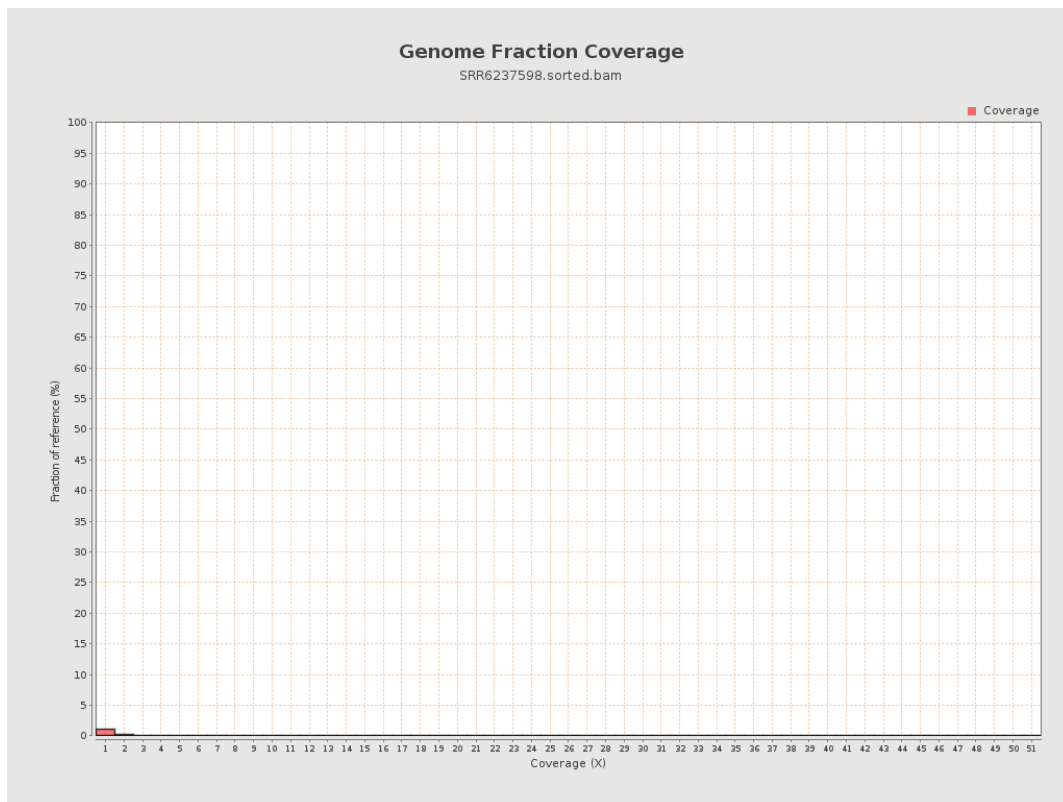
4. Results : Coverage Histogram



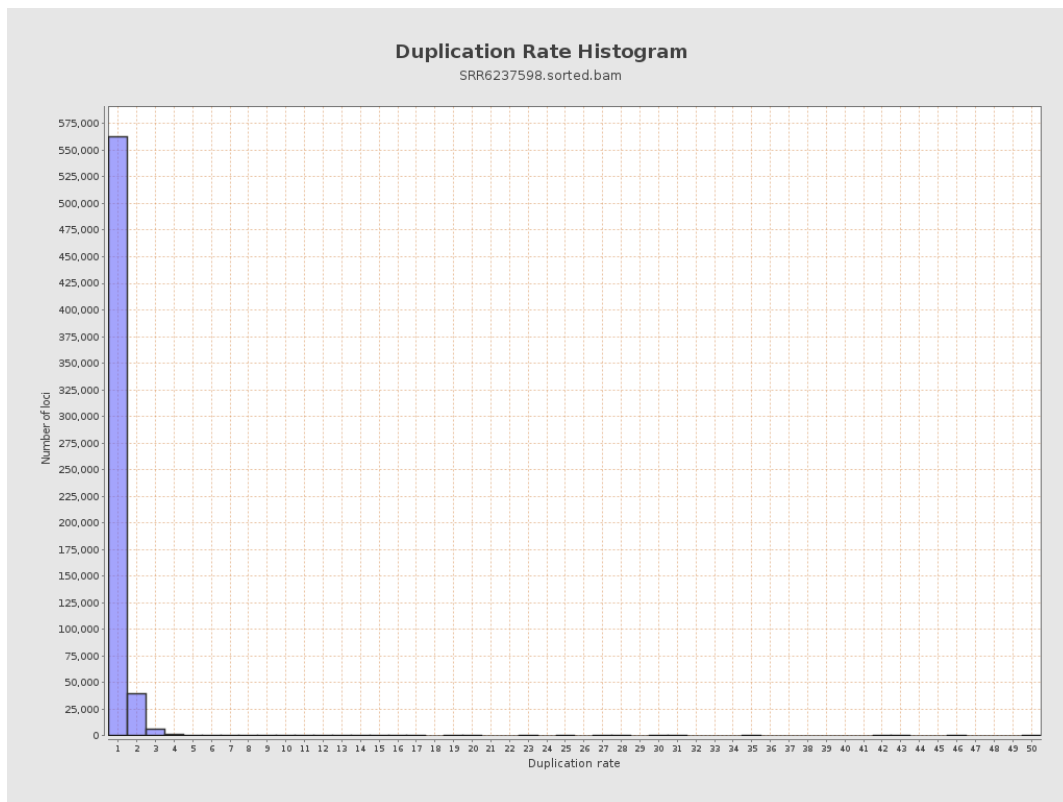
5. Results : Coverage Histogram (0-50X)



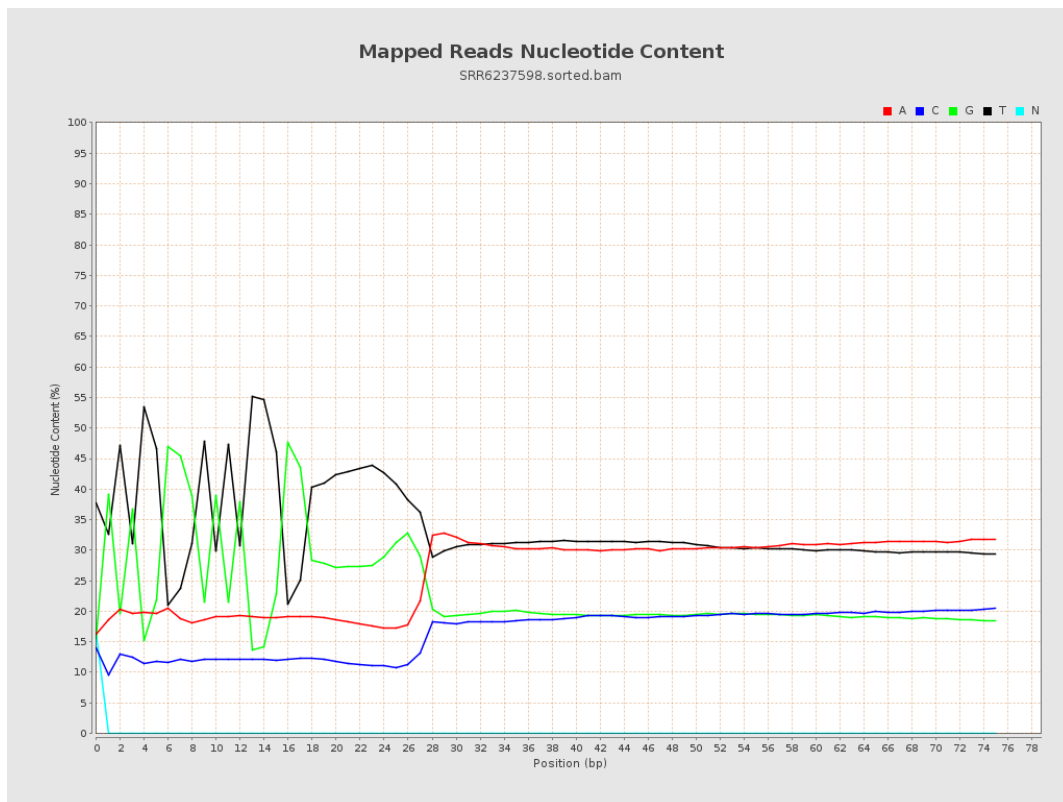
6. Results : Genome Fraction Coverage



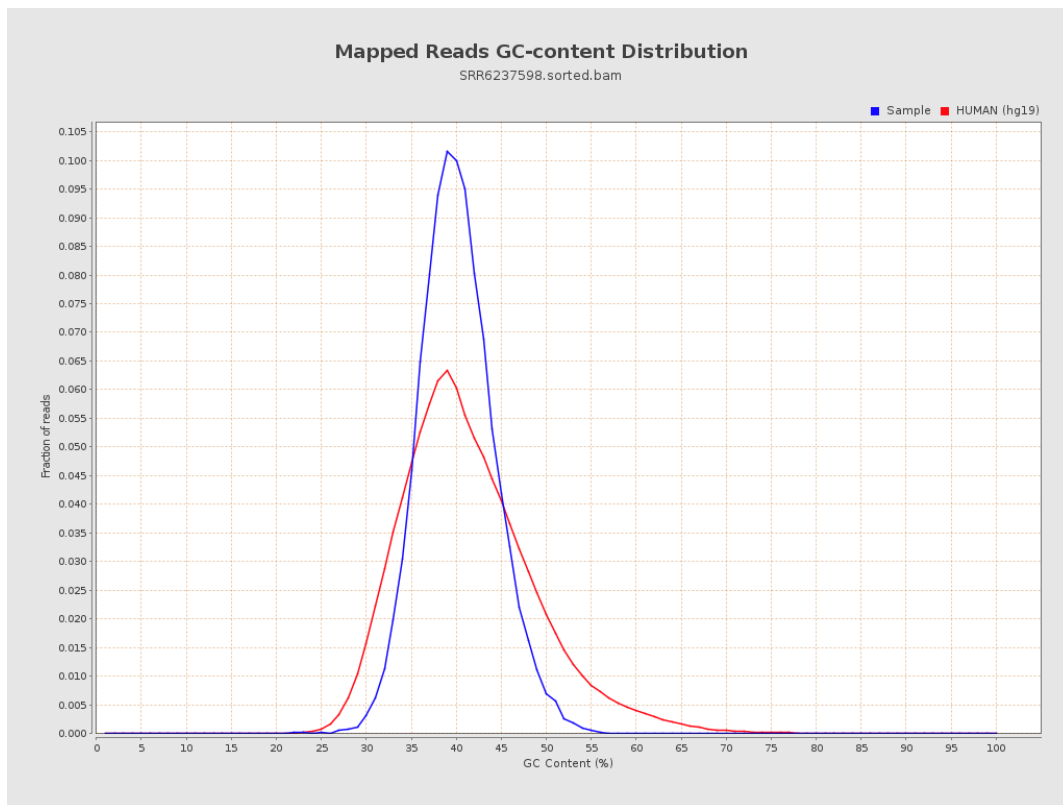
7. Results : Duplication Rate Histogram



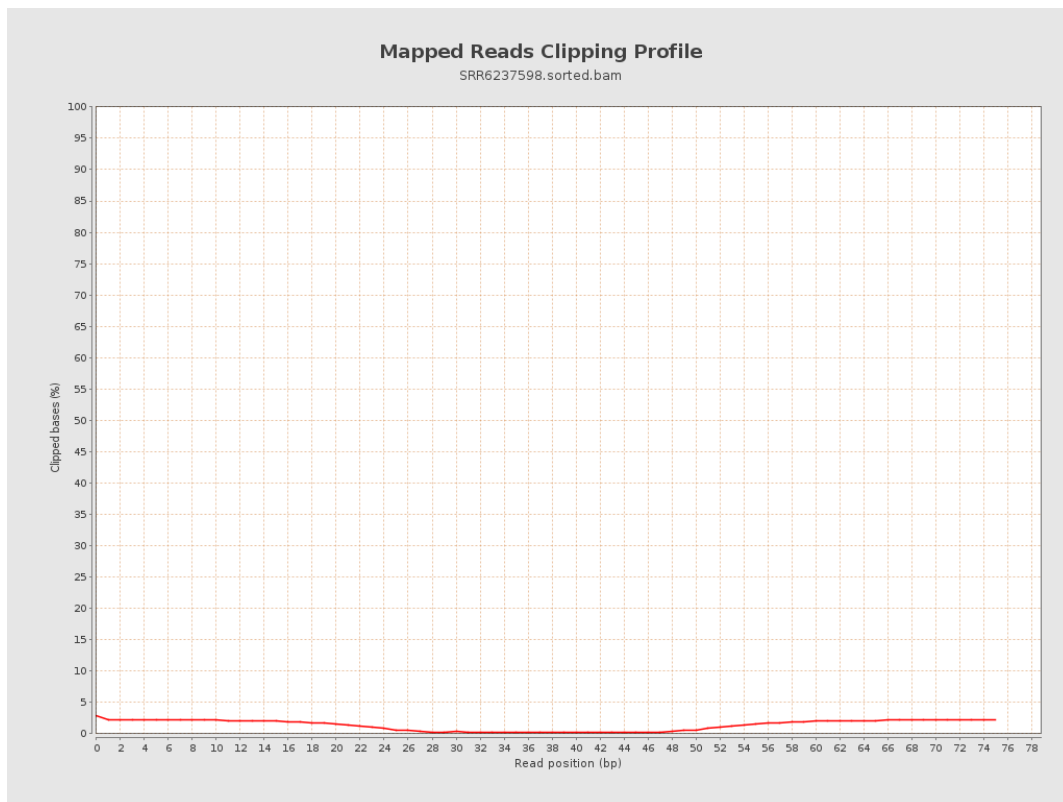
8. Results : Mapped Reads Nucleotide Content



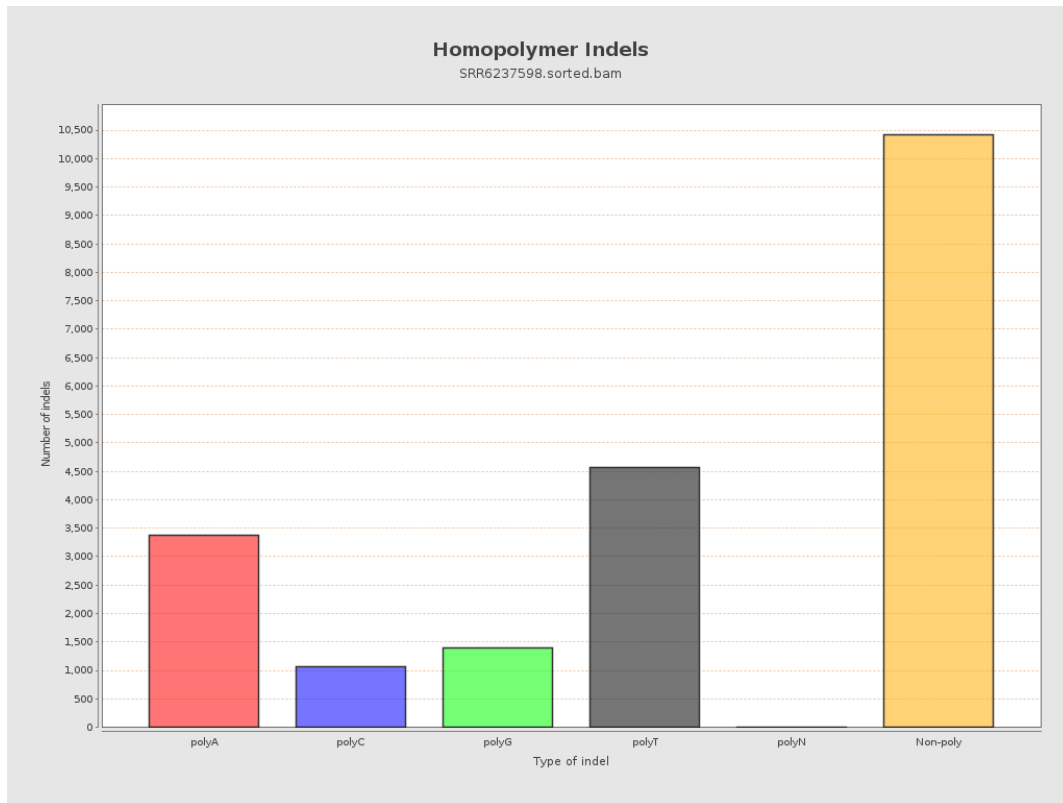
9. Results : Mapped Reads GC-content Distribution



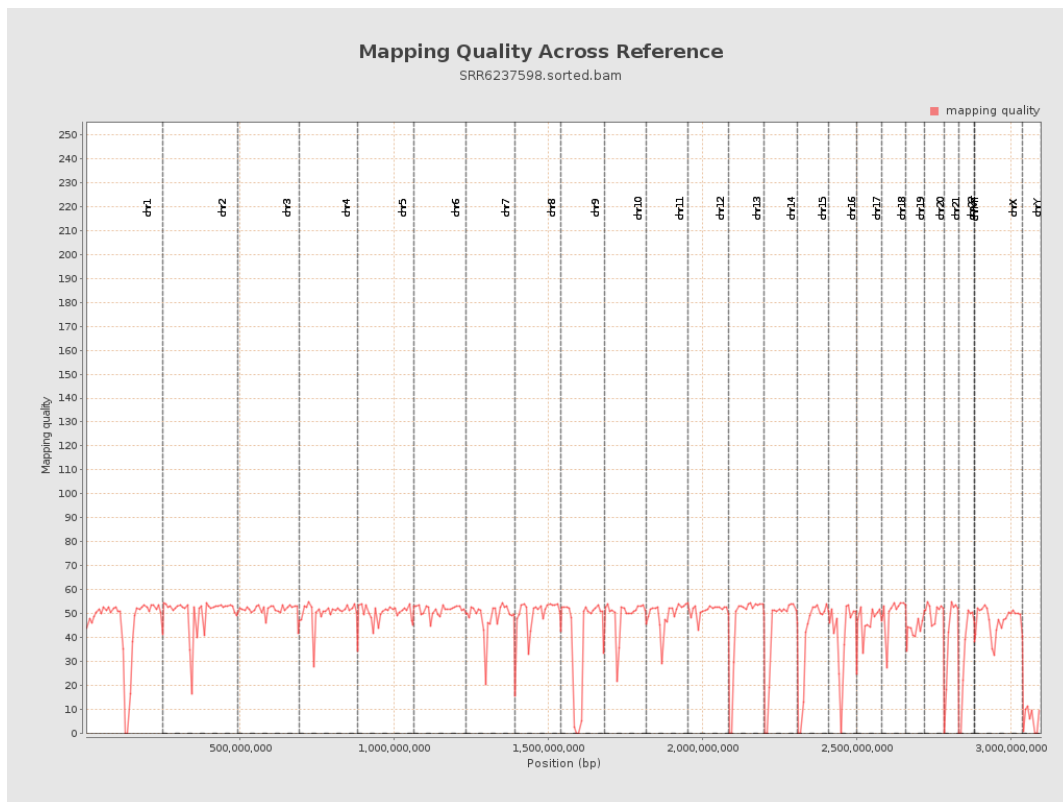
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

