Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 04:01:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237578.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_SRR6237578 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237578.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 04:01:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237578.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,275,351
Mapped reads	1,048,754 / 82.23%
Unmapped reads	226,597 / 17.77%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,385 / 0.42%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	40,878 / 3.21%
Duplication rate	2.87%
Clipped reads	610,691 / 47.88%

2.2. ACGT Content

Number/percentage of A's	17,376,746 / 26.11%
Number/percentage of C's	12,225,618 / 18.37%
Number/percentage of T's	20,156,725 / 30.29%
Number/percentage of G's	16,755,273 / 25.18%
Number/percentage of N's	39,136 / 0.06%
GC Percentage	43.55%

2.3. Coverage

Mean	0.0215

Standard Deviation	0.2139

2.4. Mapping Quality

Mean Mapping Quality	40.78

2.5. Mismatches and indels

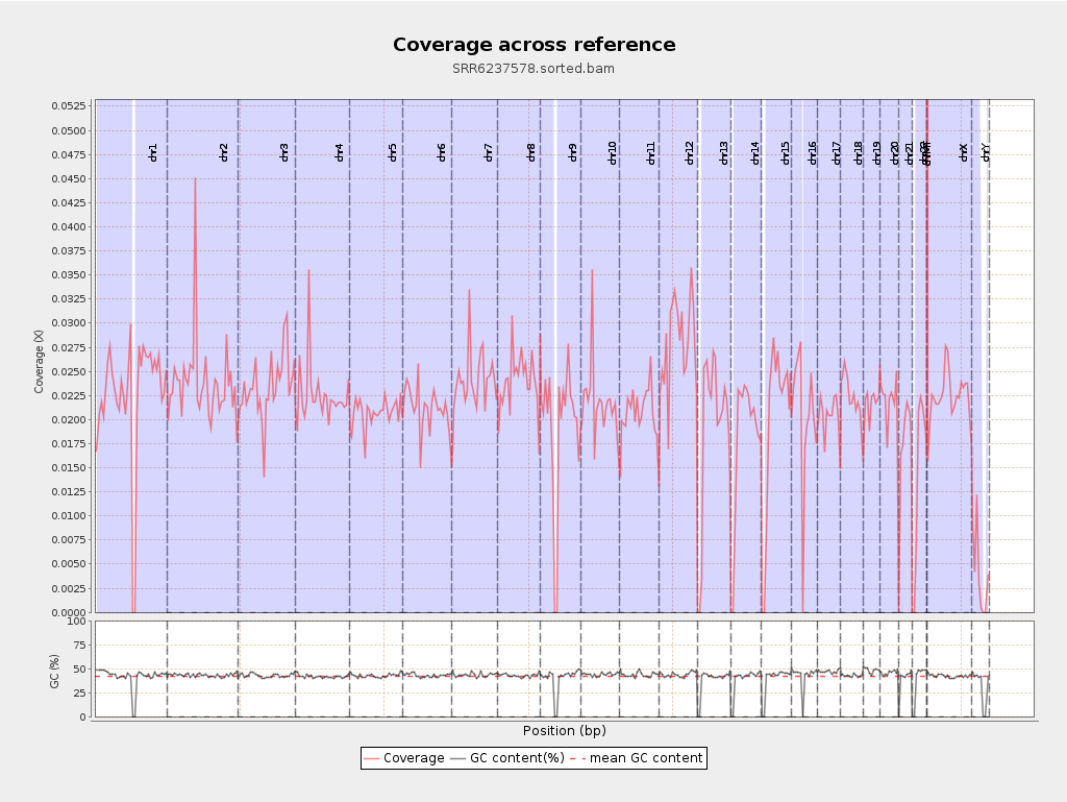
General error rate	0.95%
Mismatches	622,557
Insertions	6,164
Mapped reads with at least one insertion	0.58%
Deletions	22,363
Mapped reads with at least one deletion	2.1%
Homopolymer indels	46.83%

2.6. Chromosome stats

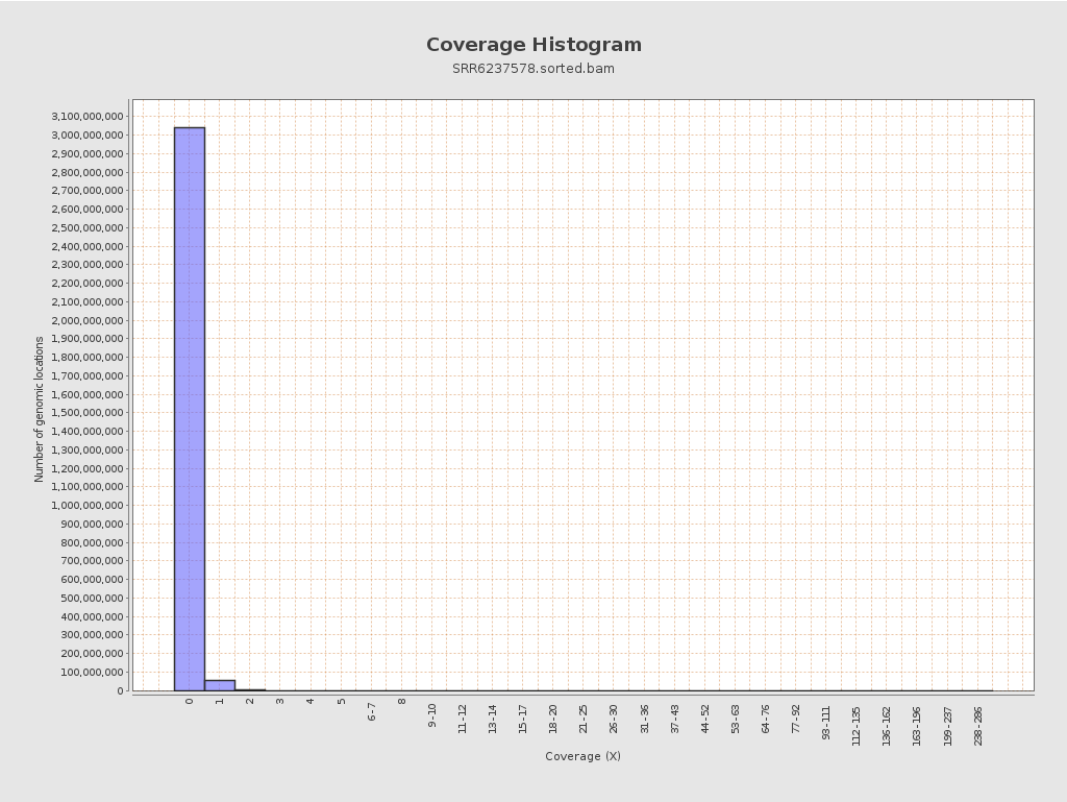
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5624493	0.0226	0.2532
chr2	243199373	5791600	0.0238	0.2897
chr3	198022430	4614751	0.0233	0.1799
chr4	191154276	4293701	0.0225	0.1854
chr5	180915260	3757678	0.0208	0.1645
chr6	171115067	3611490	0.0211	0.1813
chr7	159138663	3826187	0.024	0.2893

chr8	146364022	3494604	0.0239	0.2124
chr9	141213431	2696910	0.0191	0.2209
chr10	135534747	2932802	0.0216	0.2176
chr11	135006516	2830360	0.021	0.2187
chr12	133851895	3743318	0.028	0.2028
chr13	115169878	2183849	0.019	0.1622
chr14	107349540	1909132	0.0178	0.1681
chr15	102531392	2037590	0.0199	0.1696
chr16	90354753	1830548	0.0203	0.1836
chr17	81195210	1657676	0.0204	0.1755
chr18	78077248	1752842	0.0225	0.3338
chr19	59128983	1282546	0.0217	0.2098
chr20	63025520	1375380	0.0218	0.1784
chr21	48129895	831973	0.0173	0.1729
chr22	51304566	734429	0.0143	0.1403
chrMT	16571	53970	3.2569	2.5987
chrX	155270560	3490343	0.0225	0.1843
chrY	59373566	232450	0.0039	0.1003

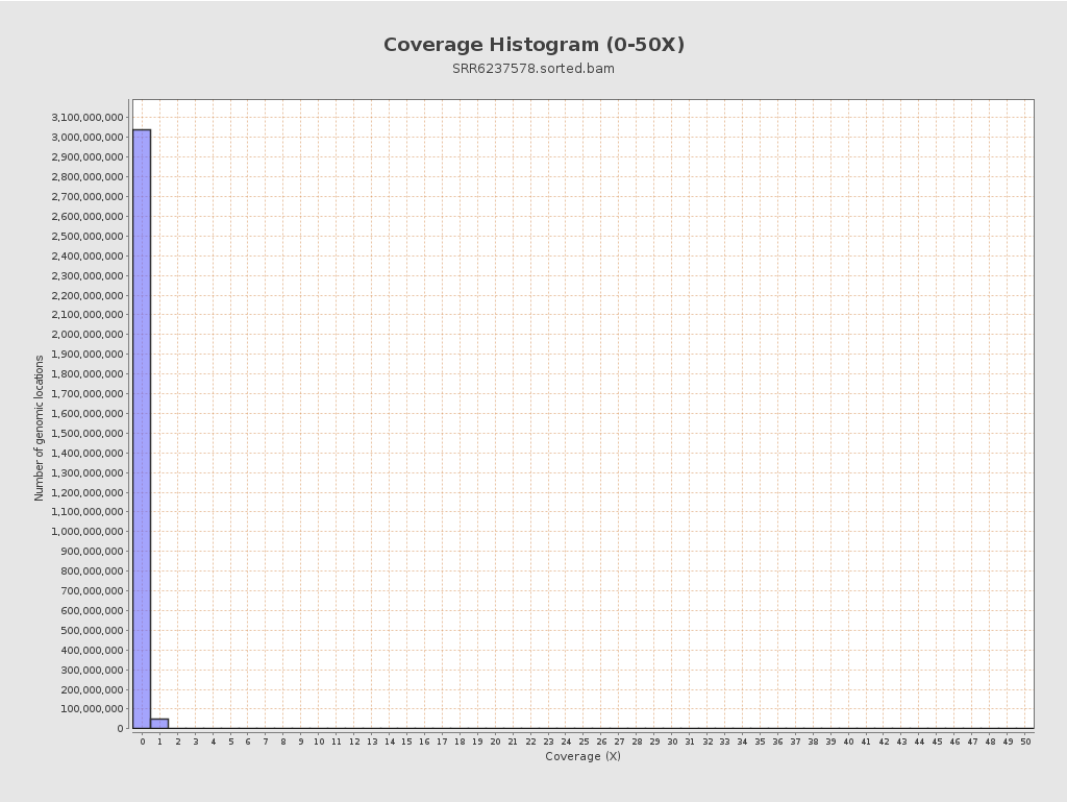
3. Results : Coverage across reference



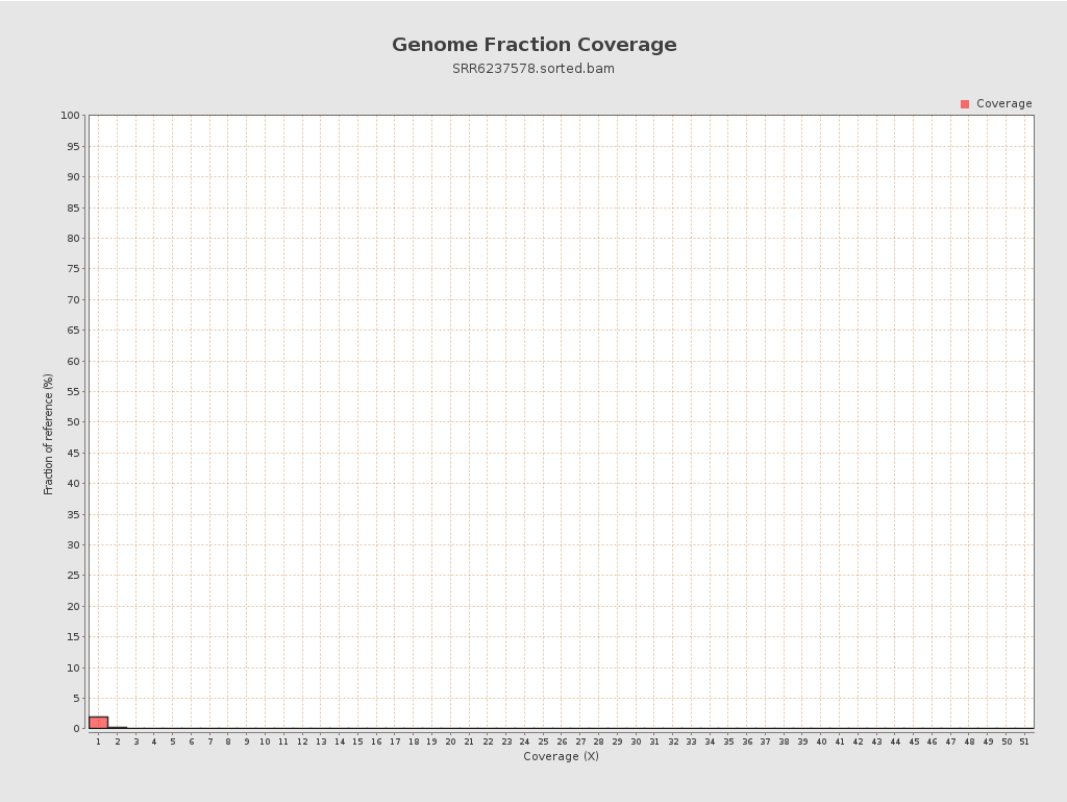
4. Results : Coverage Histogram



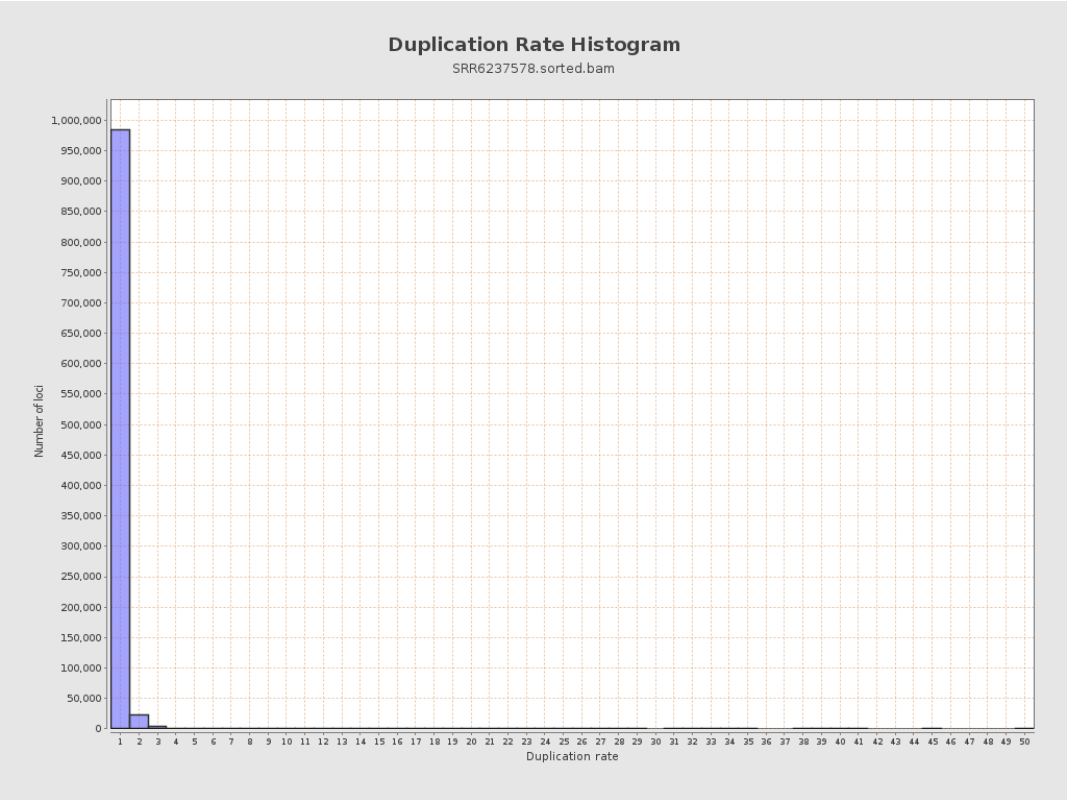
5. Results : Coverage Histogram (0-50X)



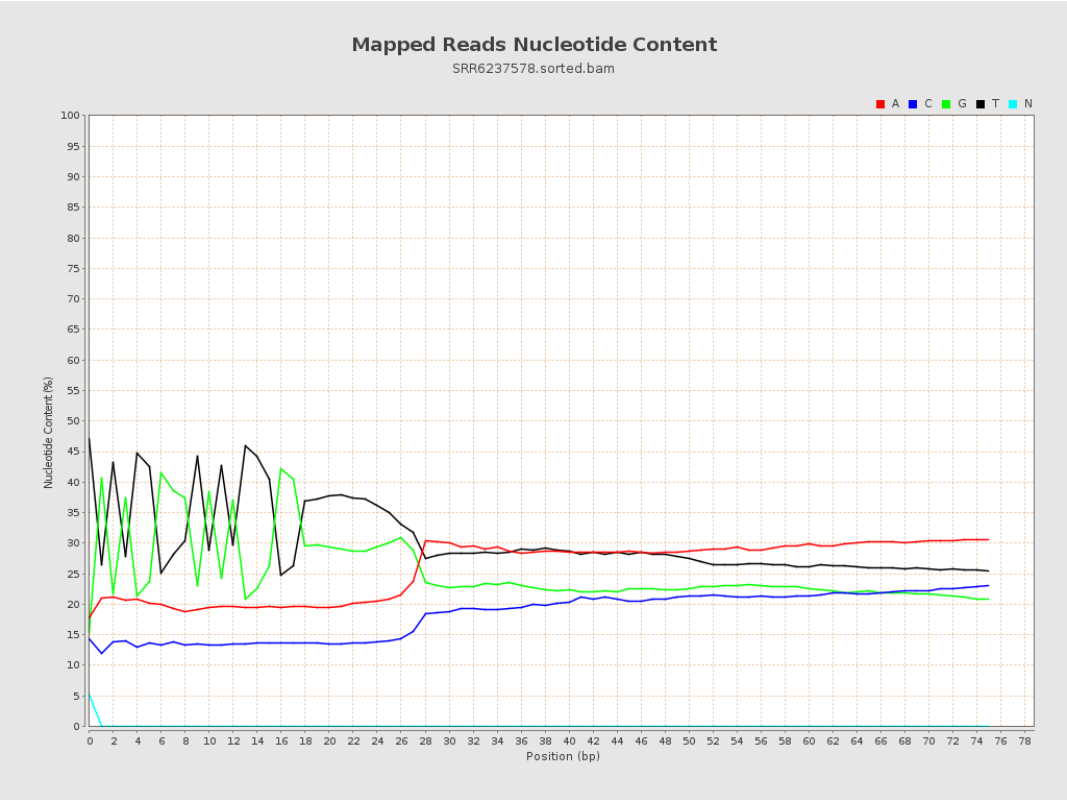
6. Results : Genome Fraction Coverage



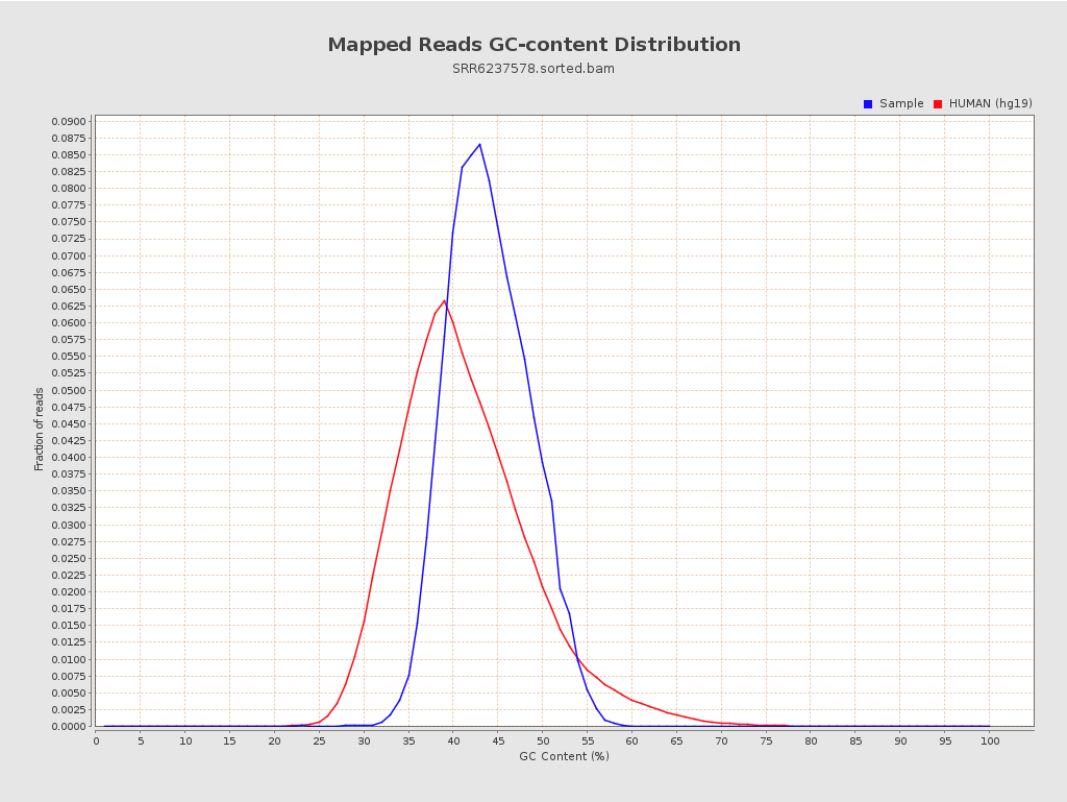
7. Results : Duplication Rate Histogram



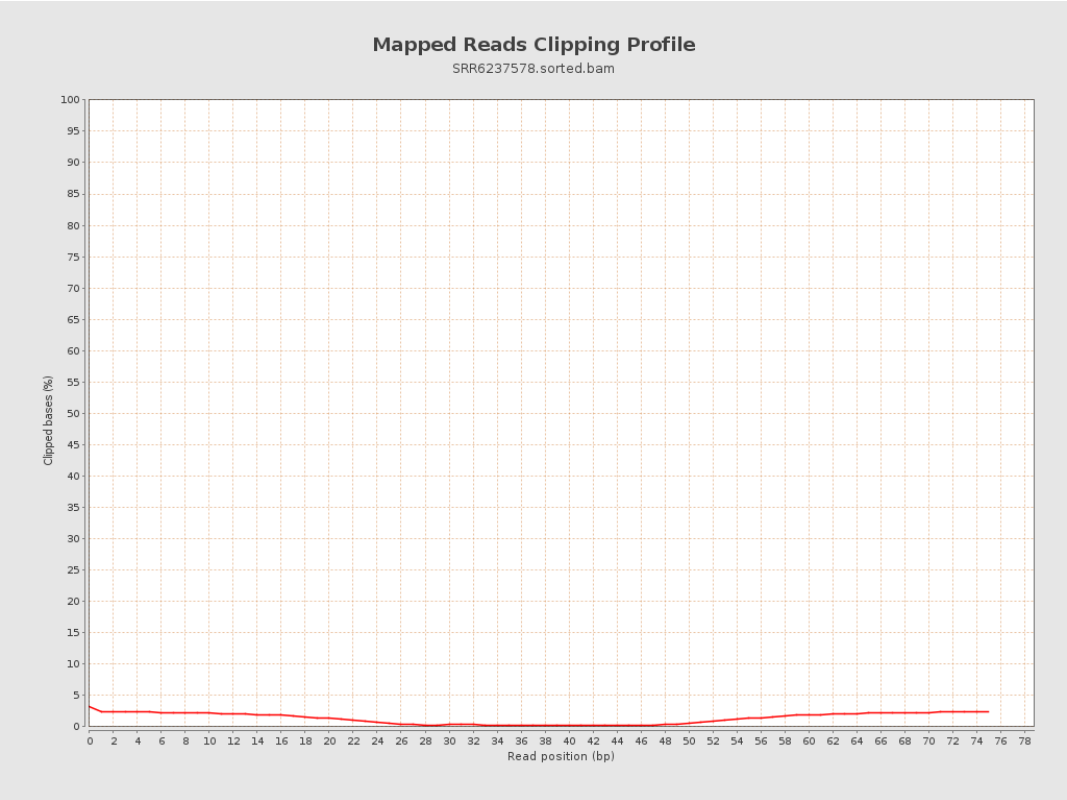
8. Results : Mapped Reads Nucleotide Content



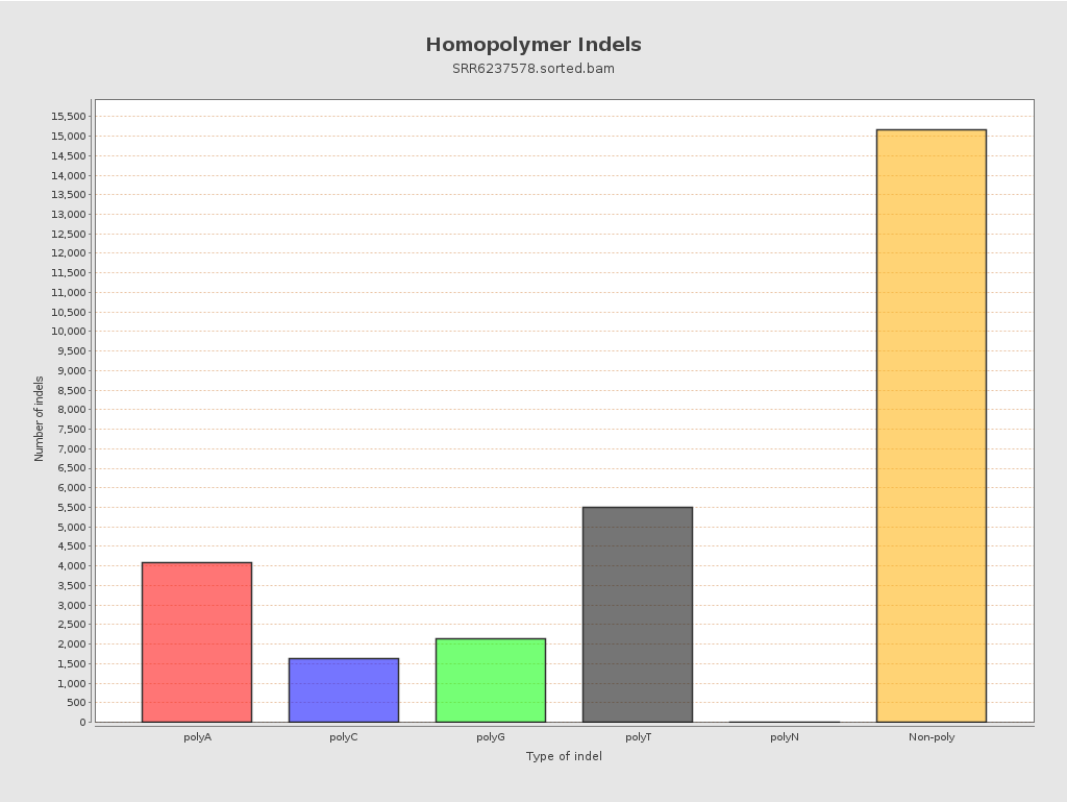
9. Results : Mapped Reads GC-content Distribution



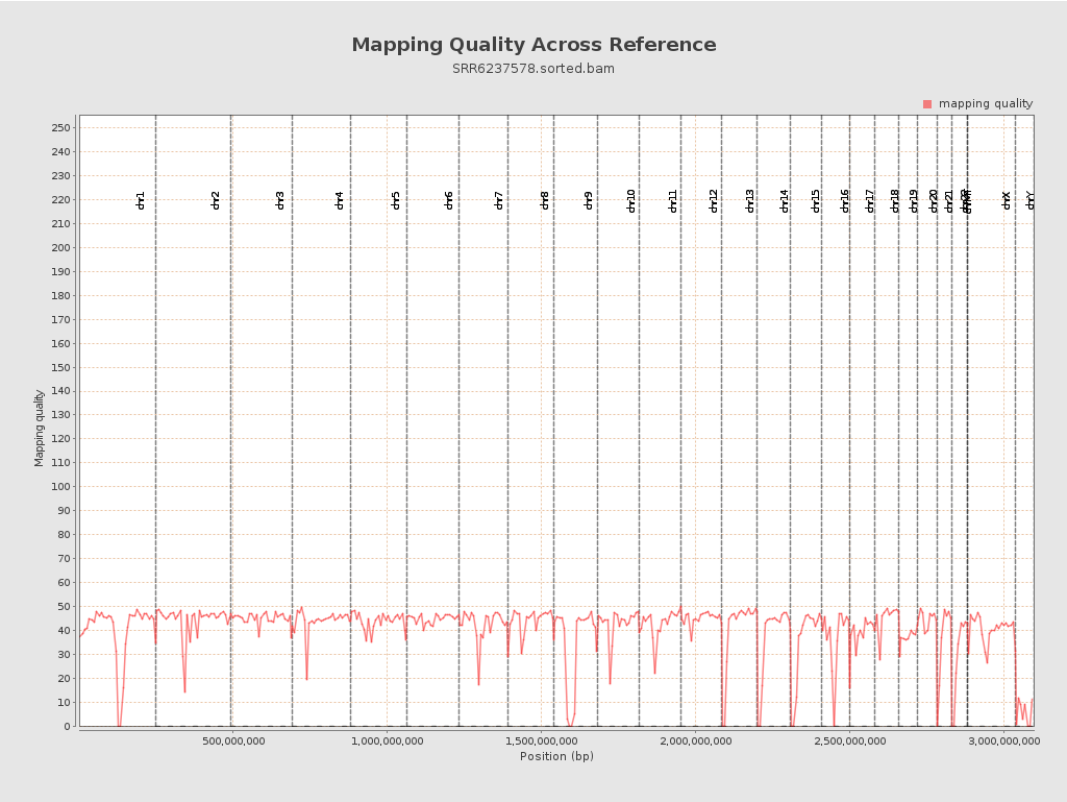
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram