Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 08:24:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237840.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_SRR6237840 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237840.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 08:24:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237840.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,218,677
Mapped reads	756,195 / 62.05%
Unmapped reads	462,482 / 37.95%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,241 / 0.51%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	56,573 / 4.64%
Duplication rate	6.53%
Clipped reads	425,002 / 34.87%

2.2. ACGT Content

Number/percentage of A's	12,874,660 / 26.89%
Number/percentage of C's	8,639,748 / 18.04%
Number/percentage of T's	15,400,627 / 32.16%
Number/percentage of G's	10,937,869 / 22.84%
Number/percentage of N's	34,794 / 0.07%
GC Percentage	40.88%

2.3. Coverage

Mean	0.0155

Standard Deviation	0.188

2.4. Mapping Quality

Mean Mapping Quality	46.71

2.5. Mismatches and indels

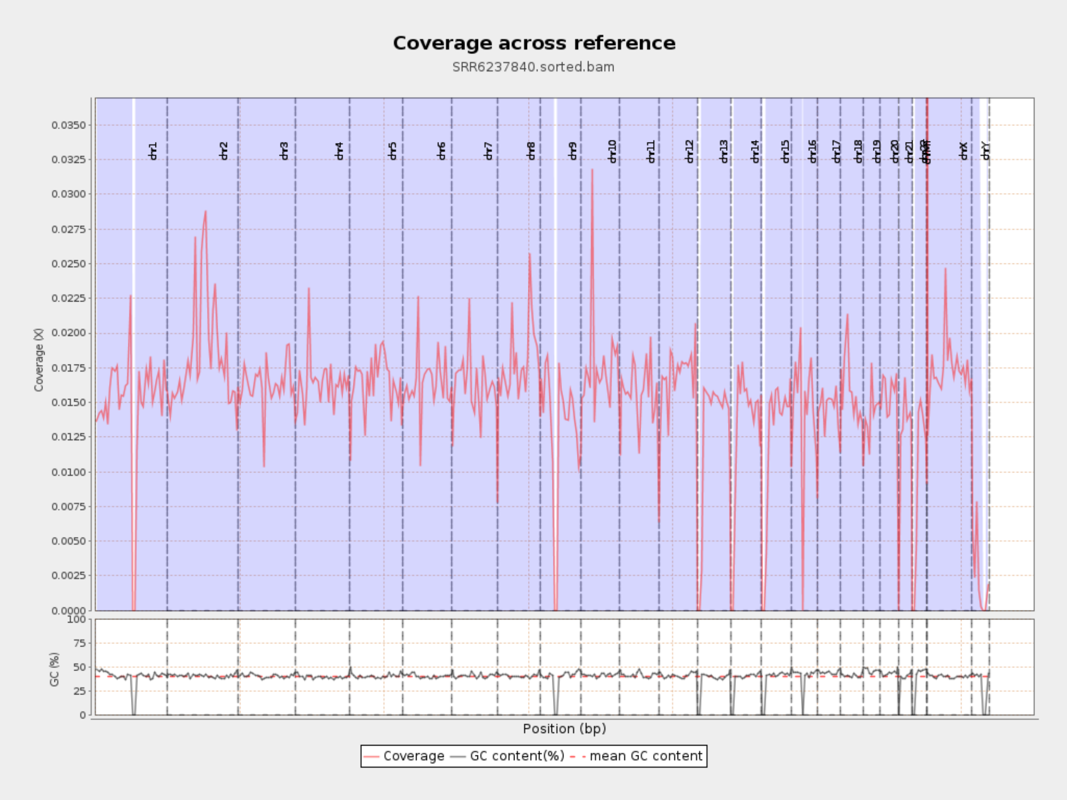
General error rate	0.78%
Mismatches	366,258
Insertions	3,846
Mapped reads with at least one insertion	0.5%
Deletions	11,695
Mapped reads with at least one deletion	1.53%
Homopolymer indels	47.9%

2.6. Chromosome stats

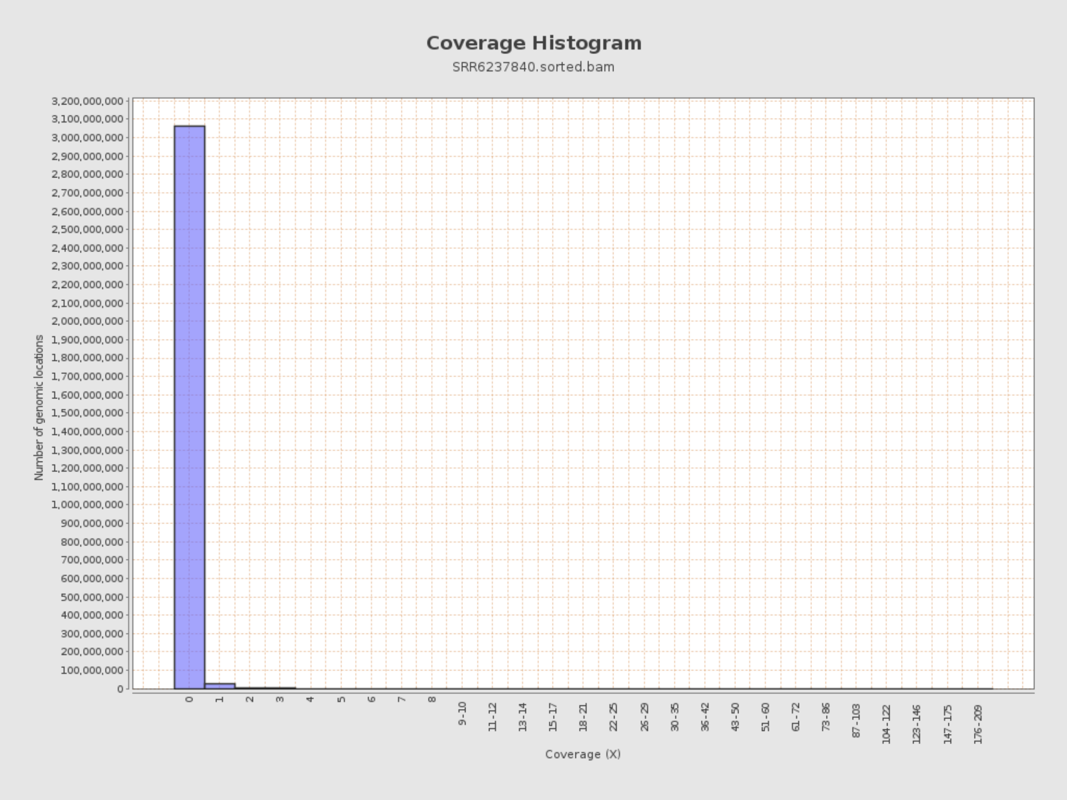
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3718866	0.0149	0.2412
chr2	243199373	4488572	0.0185	0.2114
chr3	198022430	3226393	0.0163	0.168
chr4	191154276	3128703	0.0164	0.1772
chr5	180915260	3017296	0.0167	0.1706
chr6	171115067	2809974	0.0164	0.1836
chr7	159138663	2593283	0.0163	0.1937

chr8	146364022	2643137	0.0181	0.2138
chr9	141213431	1870175	0.0132	0.1747
chr10	135534747	2379248	0.0176	0.2184
chr11	135006516	2132175	0.0158	0.177
chr12	133851895	2263716	0.0169	0.1752
chr13	115169878	1465534	0.0127	0.147
chr14	107349540	1378927	0.0128	0.1525
chr15	102531392	1232558	0.012	0.1428
chr16	90354753	1287232	0.0142	0.1662
chr17	81195210	1184880	0.0146	0.165
chr18	78077248	1234192	0.0158	0.2688
chr19	59128983	835213	0.0141	0.1906
chr20	63025520	973749	0.0155	0.1654
chr21	48129895	612479	0.0127	0.1586
chr22	51304566	487566	0.0095	0.1249
chrMT	16571	97226	5.8672	4.7826
chrX	155270560	2708451	0.0174	0.1802
chrY	59373566	137141	0.0023	0.0777

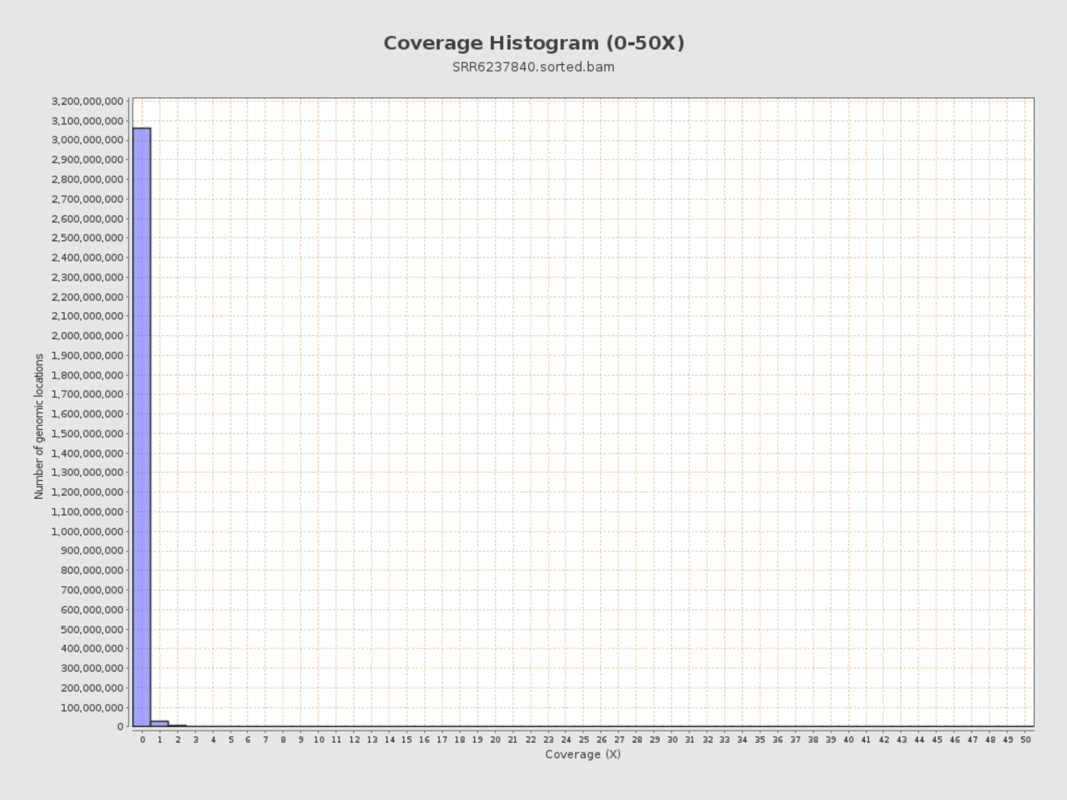
3. Results : Coverage across reference



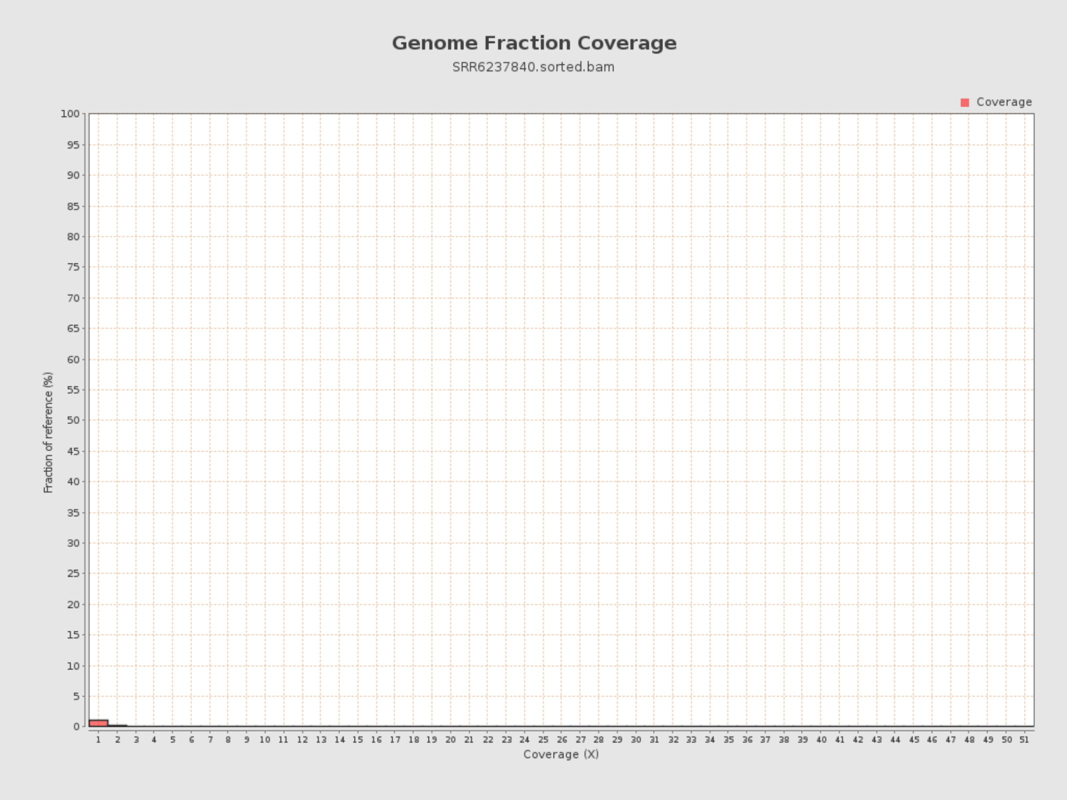
4. Results : Coverage Histogram



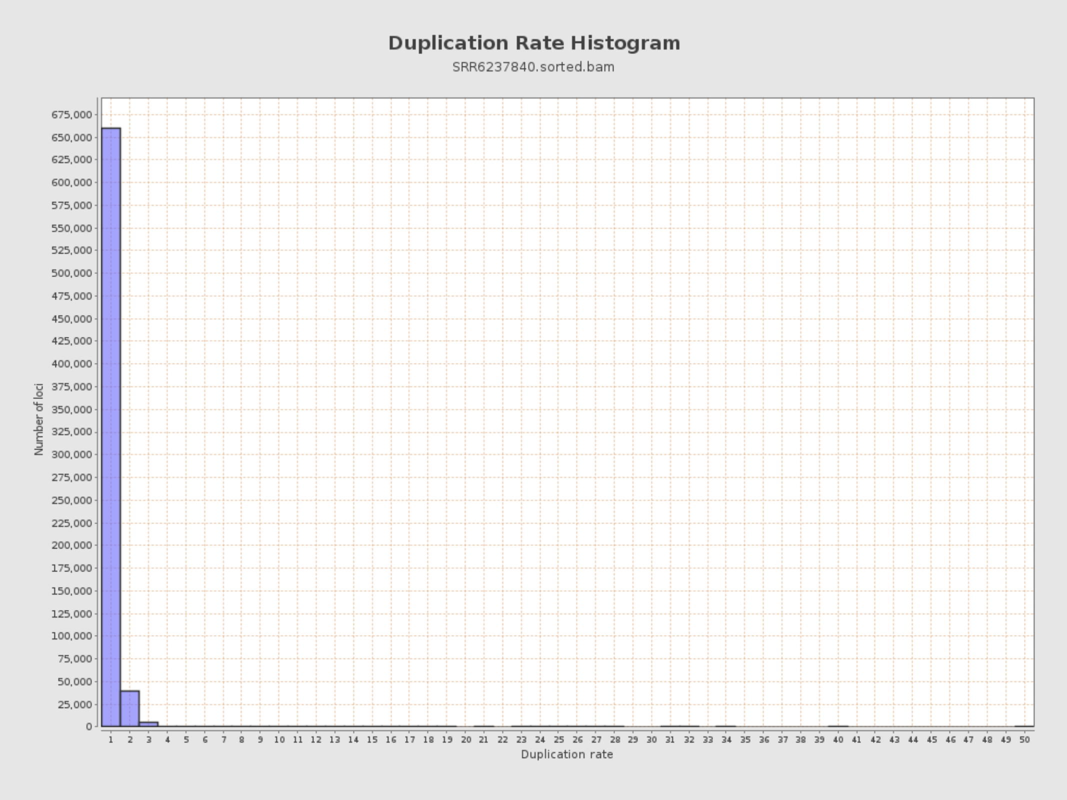
5. Results : Coverage Histogram (0-50X)



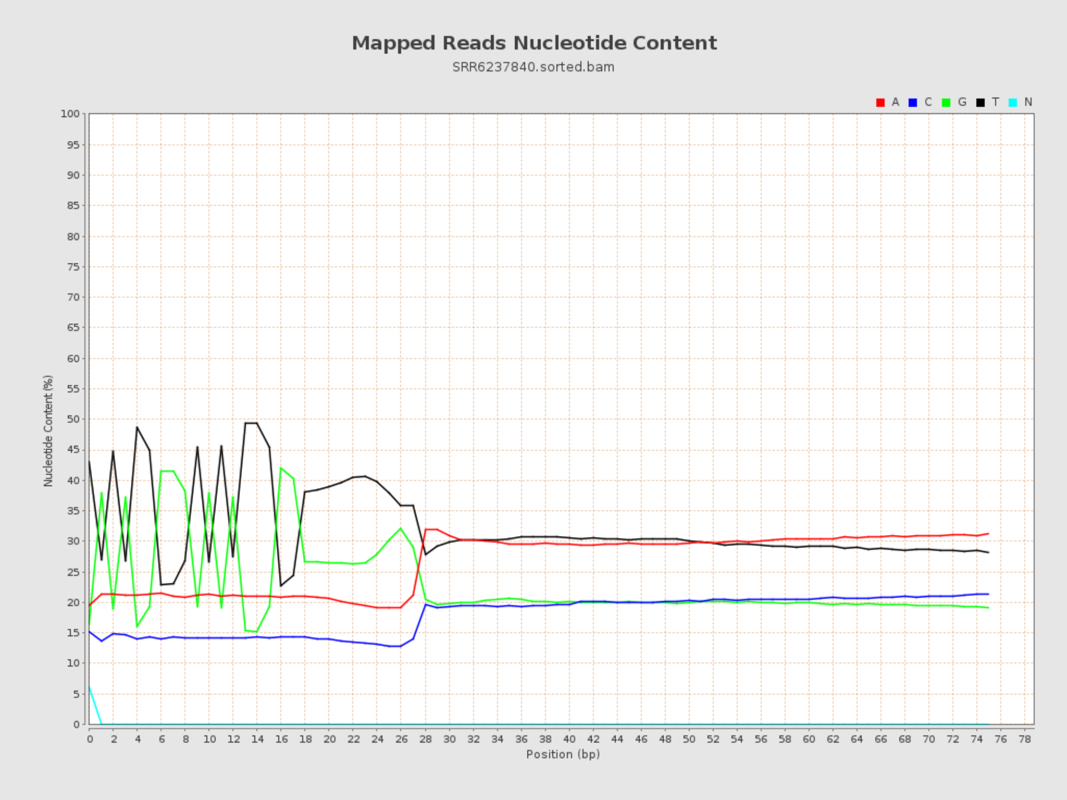
6. Results : Genome Fraction Coverage



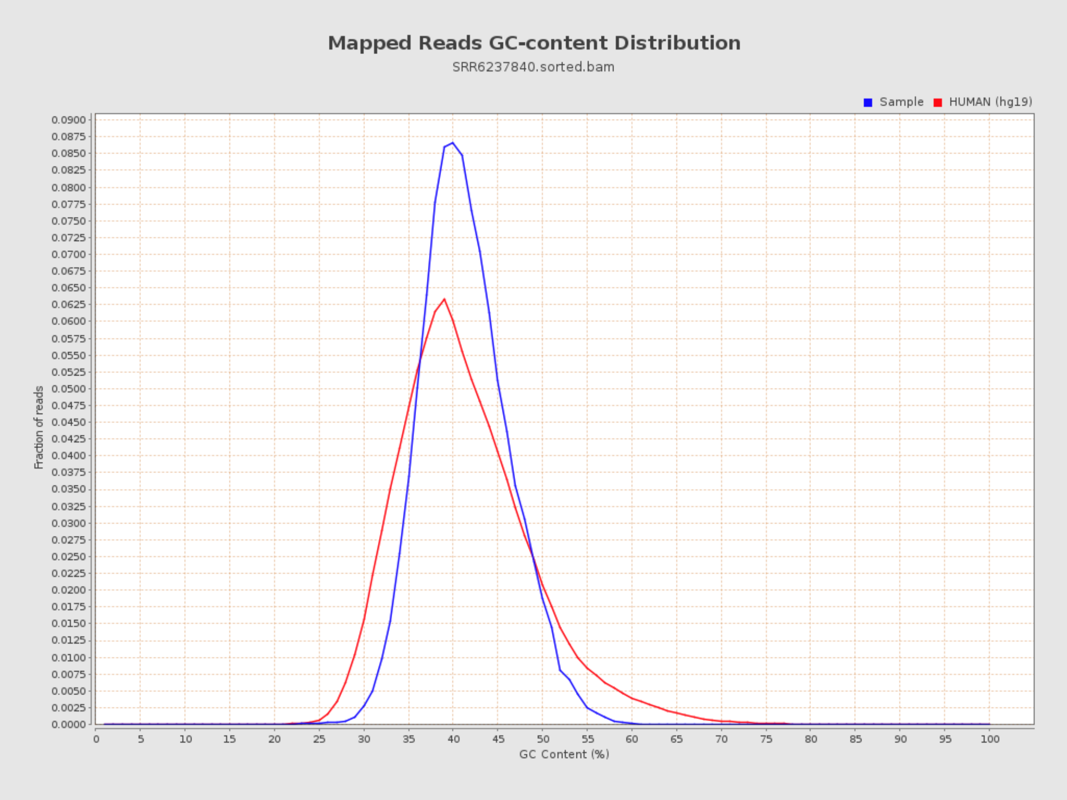
7. Results : Duplication Rate Histogram



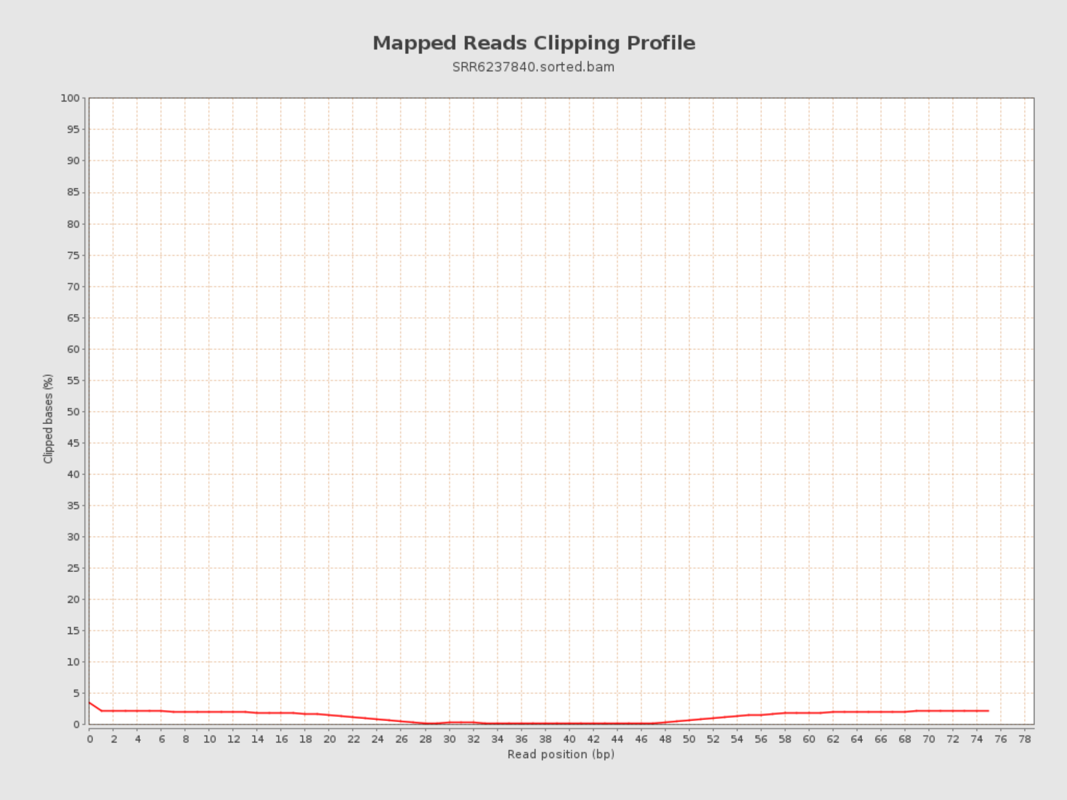
8. Results : Mapped Reads Nucleotide Content



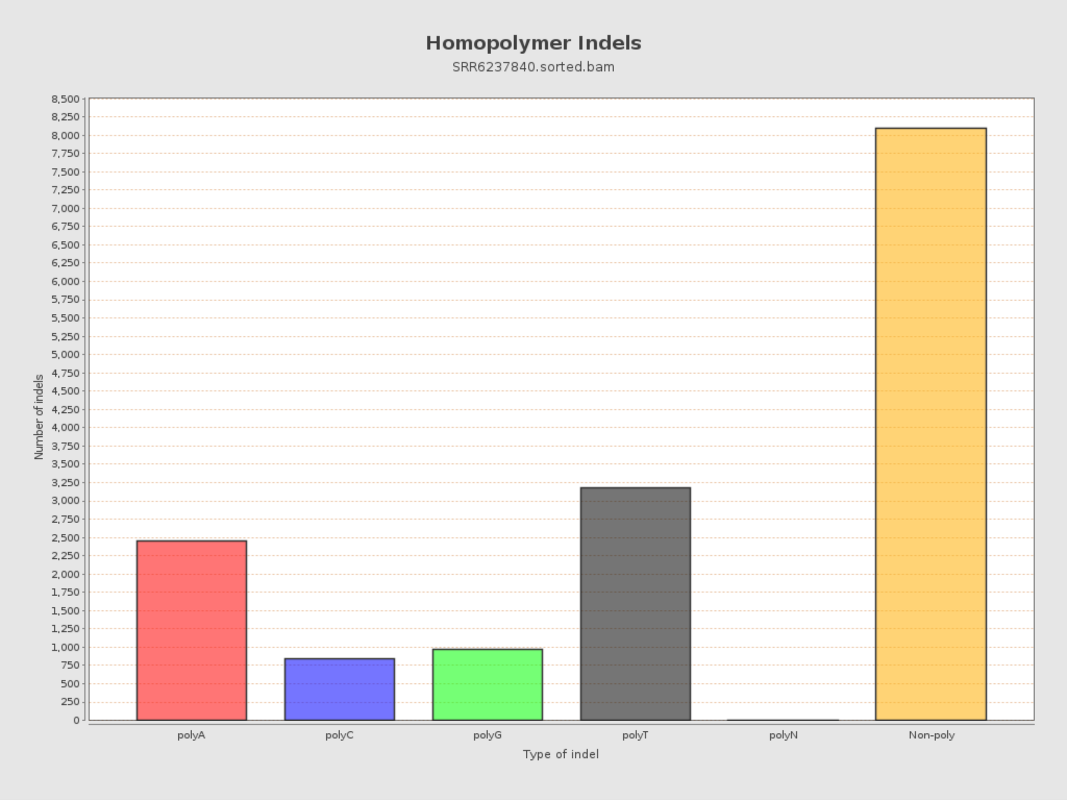
9. Results : Mapped Reads GC-content Distribution



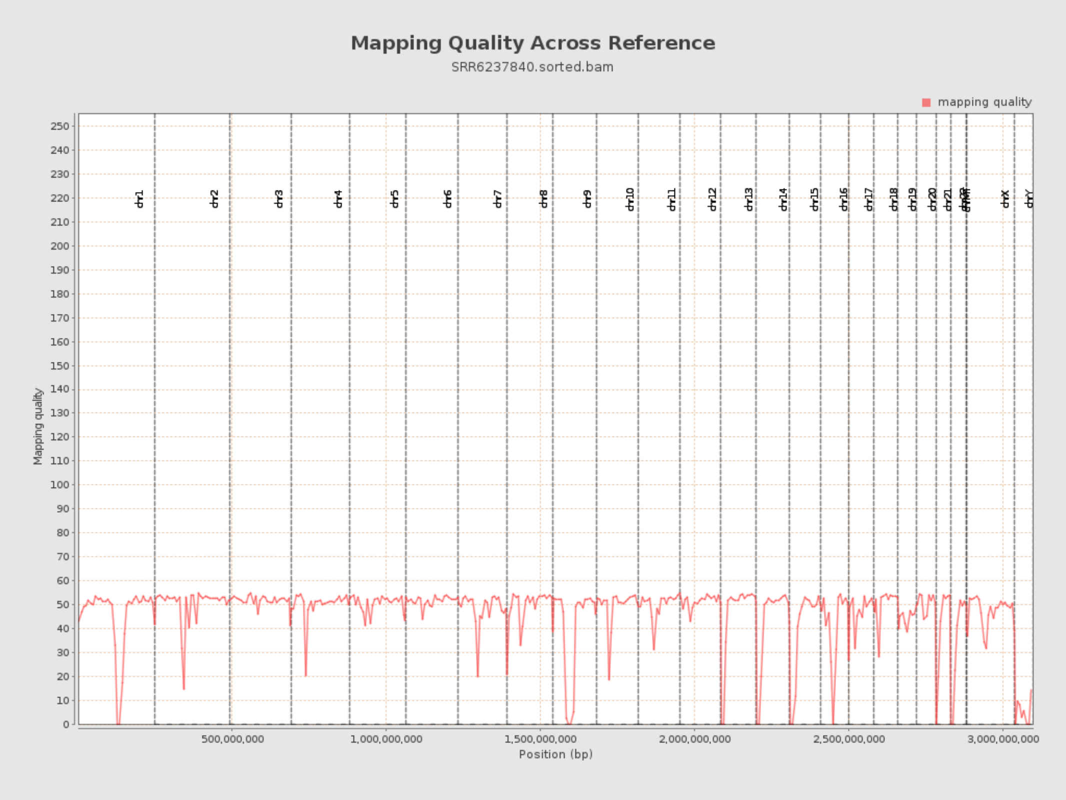
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram