Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 03:49:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237574.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_SRR6237574 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237574.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 03:49:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237574.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,239,385
Mapped reads	1,890,504 / 84.42%
Unmapped reads	348,881 / 15.58%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,447 / 0.65%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	101,084 / 4.51%
Duplication rate	4.3%
Clipped reads	1,157,606 / 51.69%

2.2. ACGT Content

Number/percentage of A's	32,545,174 / 27.55%
Number/percentage of C's	20,385,750 / 17.26%
Number/percentage of T's	38,215,479 / 32.35%
Number/percentage of G's	26,776,690 / 22.67%
Number/percentage of N's	213,085 / 0.18%
GC Percentage	39.92%

2.3. Coverage

Mean	0.0382

Standard Deviation	0.3504

2.4. Mapping Quality

Mean Mapping Quality	45.3

2.5. Mismatches and indels

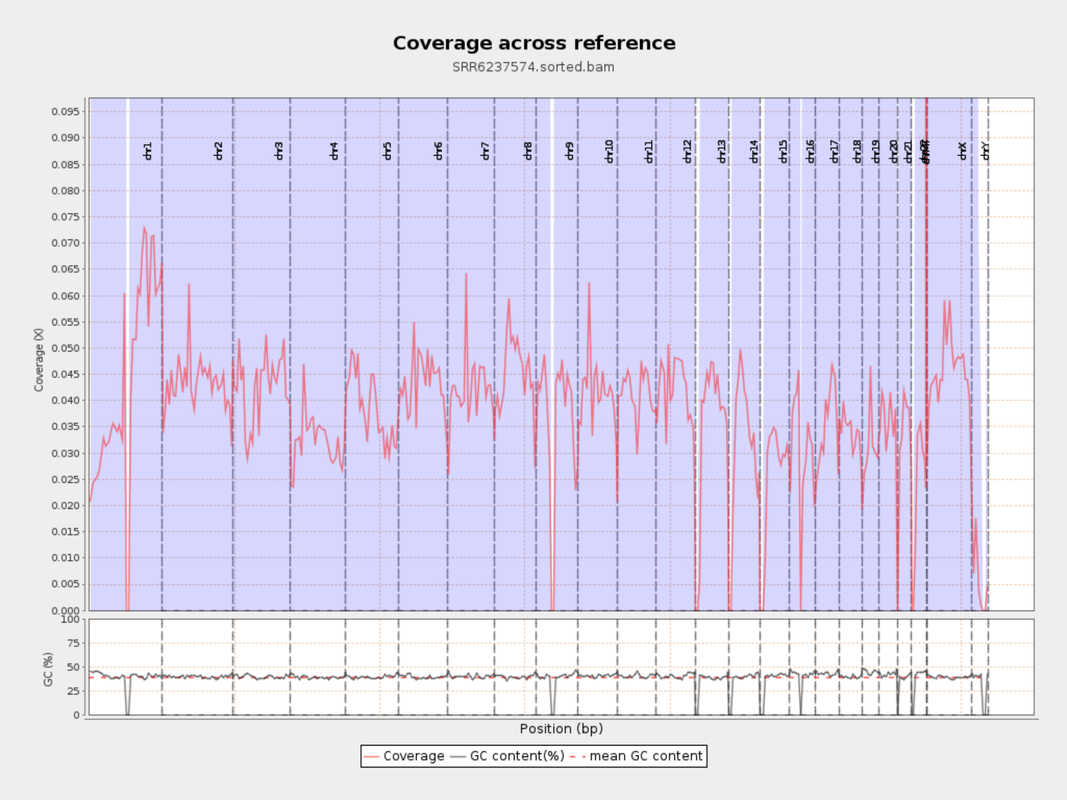
General error rate	0.93%
Mismatches	1,080,797
Insertions	10,075
Mapped reads with at least one insertion	0.53%
Deletions	42,086
Mapped reads with at least one deletion	2.2%
Homopolymer indels	46.45%

2.6. Chromosome stats

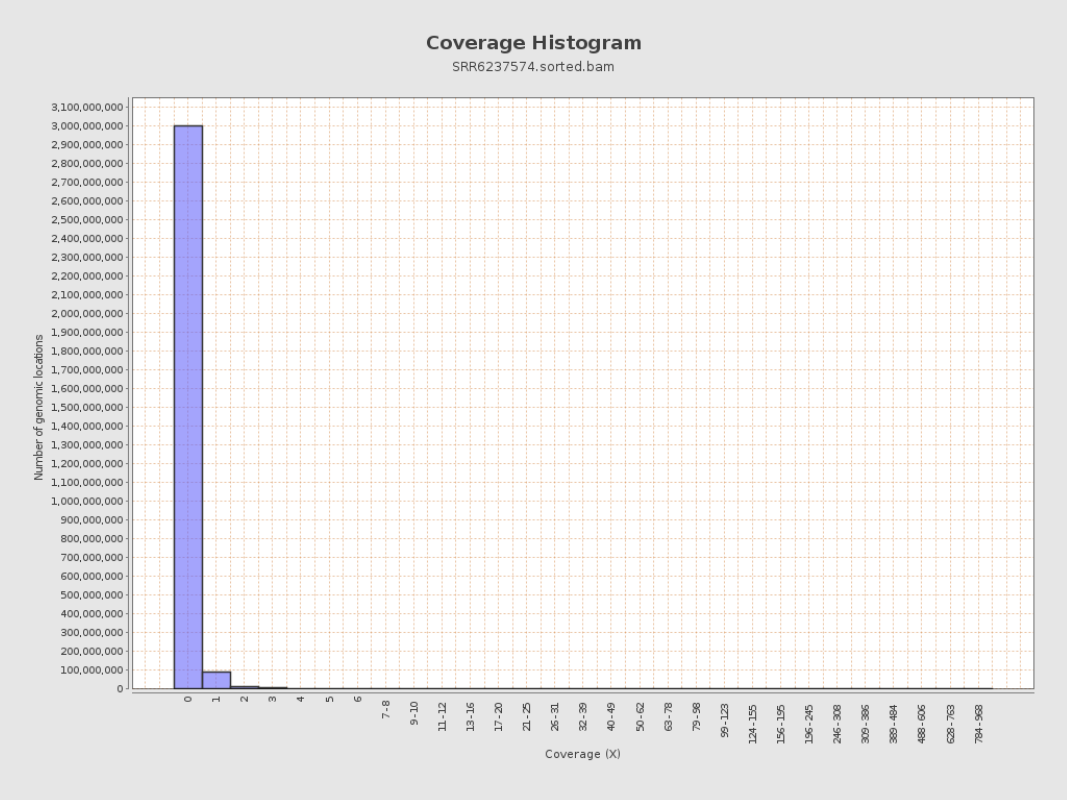
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10748165	0.0431	0.5939
chr2	243199373	10531576	0.0433	0.4173
chr3	198022430	8478758	0.0428	0.2407
chr4	191154276	6165554	0.0323	0.2255
chr5	180915260	6980753	0.0386	0.2271
chr6	171115067	7417520	0.0433	0.2752
chr7	159138663	6765171	0.0425	0.434

chr8	146364022	6643580	0.0454	0.612
chr9	141213431	5116691	0.0362	0.3106
chr10	135534747	5691651	0.042	0.3223
chr11	135006516	5543454	0.0411	0.292
chr12	133851895	5643321	0.0422	0.2448
chr13	115169878	3967964	0.0345	0.2159
chr14	107349540	3325114	0.031	0.2219
chr15	102531392	2585807	0.0252	0.187
chr16	90354753	2737859	0.0303	0.2216
chr17	81195210	2872232	0.0354	0.2323
chr18	78077248	2667509	0.0342	0.5115
chr19	59128983	1843253	0.0312	0.4261
chr20	63025520	2261915	0.0359	0.2257
chr21	48129895	1549706	0.0322	0.2221
chr22	51304566	1134739	0.0221	0.1689
chrMT	16571	110327	6.6578	4.5585
chrX	155270560	7082141	0.0456	0.2658
chrY	59373566	340033	0.0057	0.1269

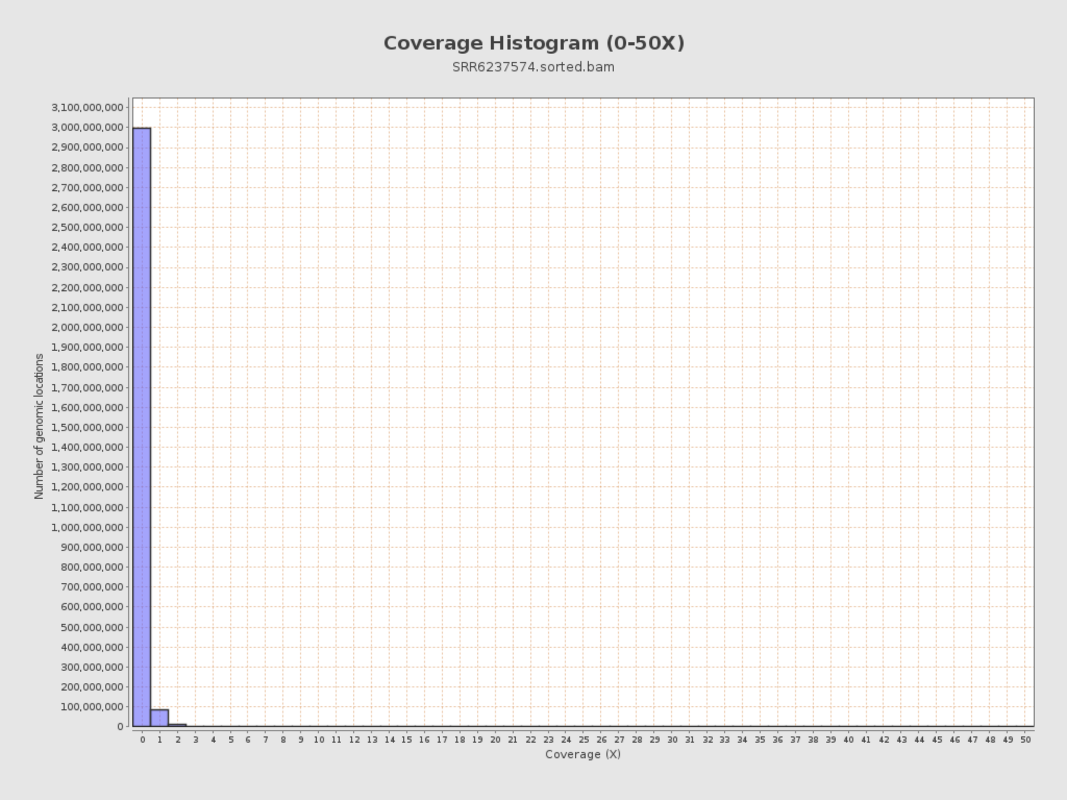
3. Results : Coverage across reference



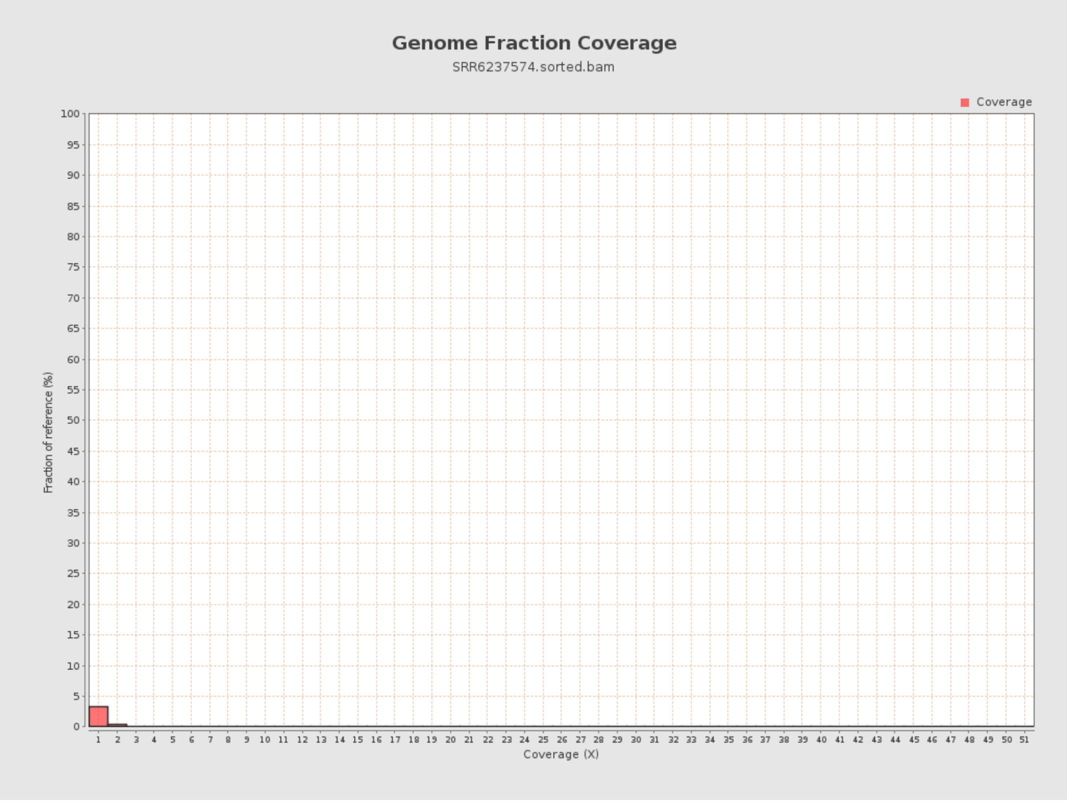
4. Results : Coverage Histogram



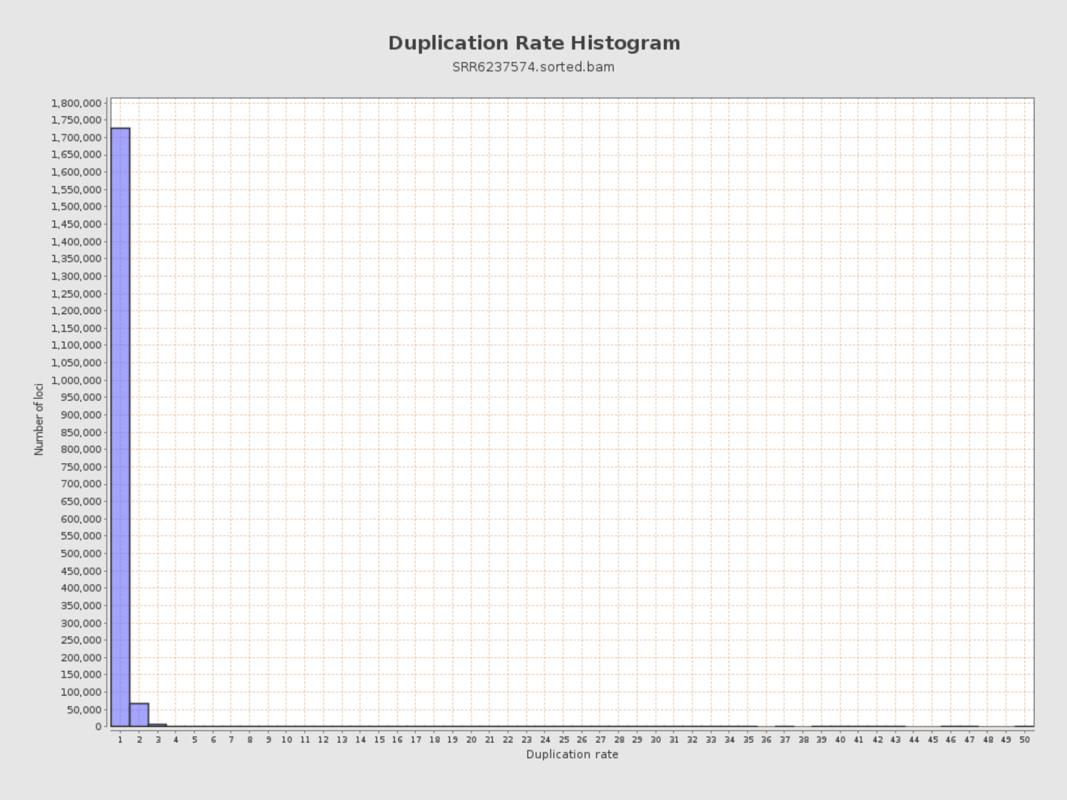
5. Results : Coverage Histogram (0-50X)



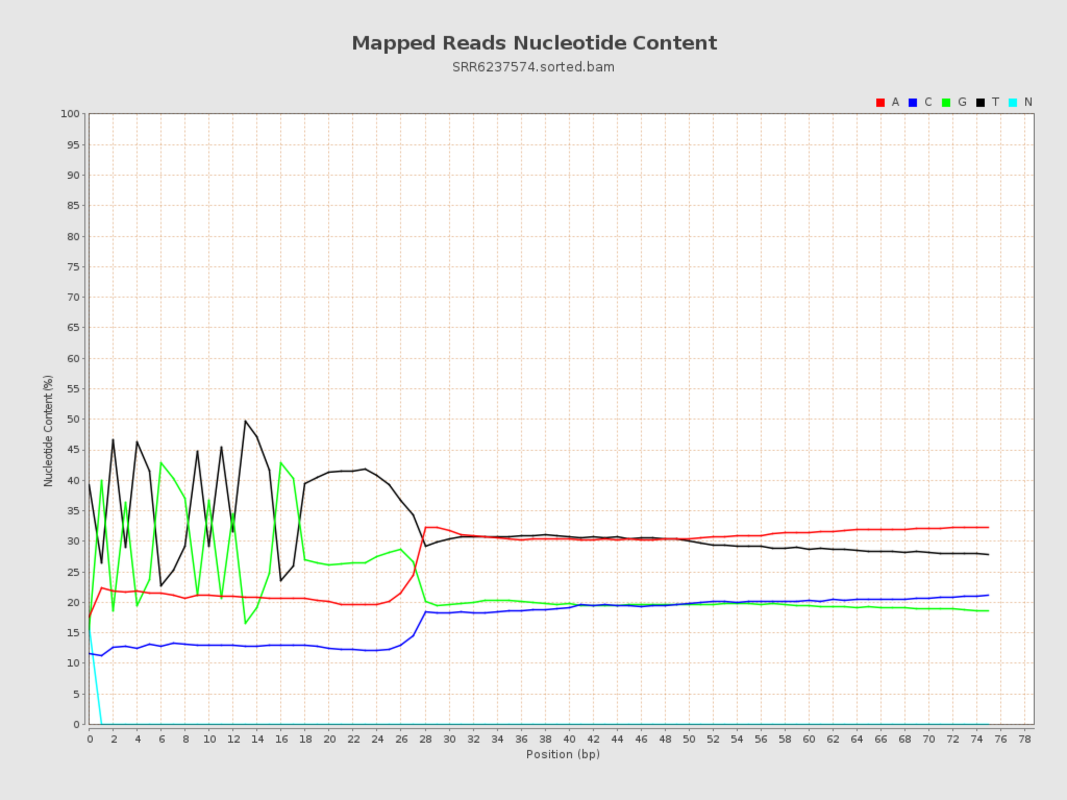
6. Results : Genome Fraction Coverage



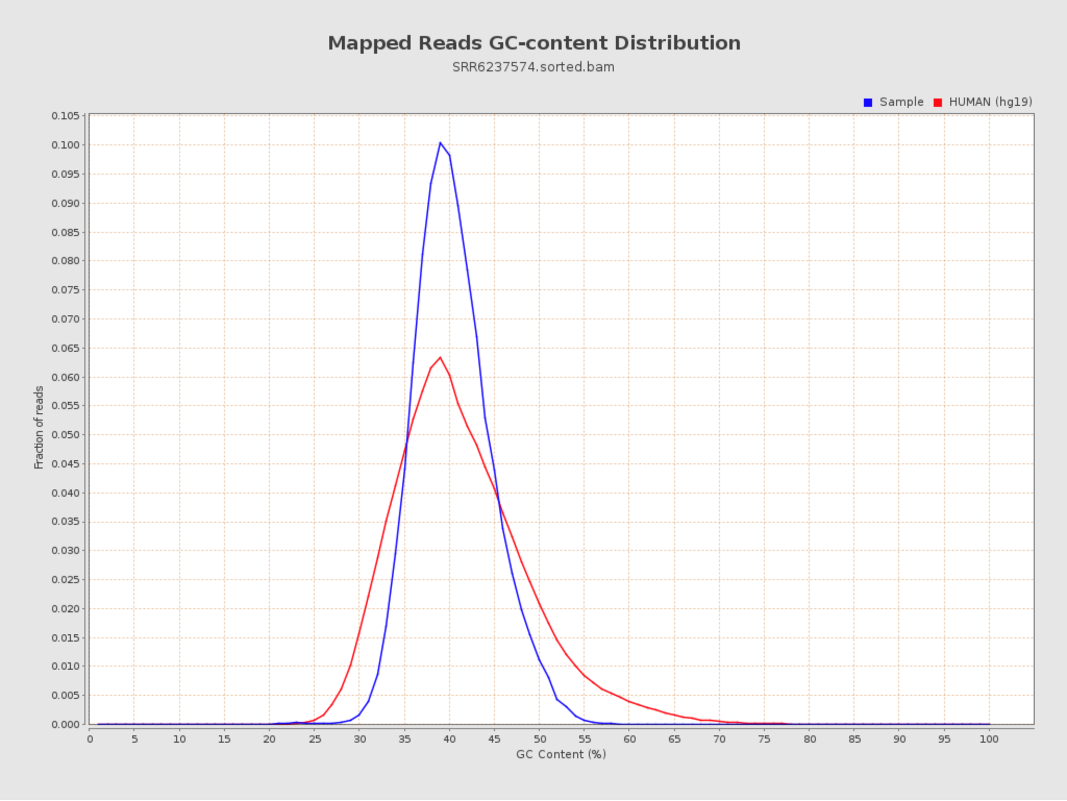
7. Results : Duplication Rate Histogram



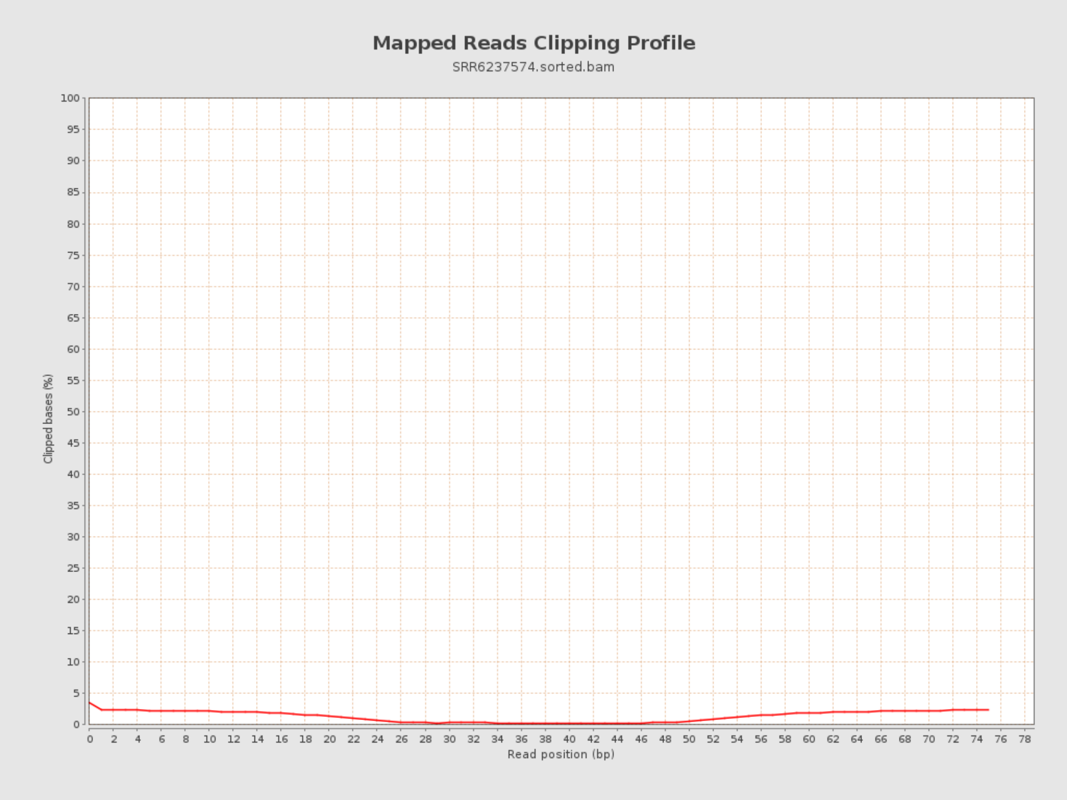
8. Results : Mapped Reads Nucleotide Content



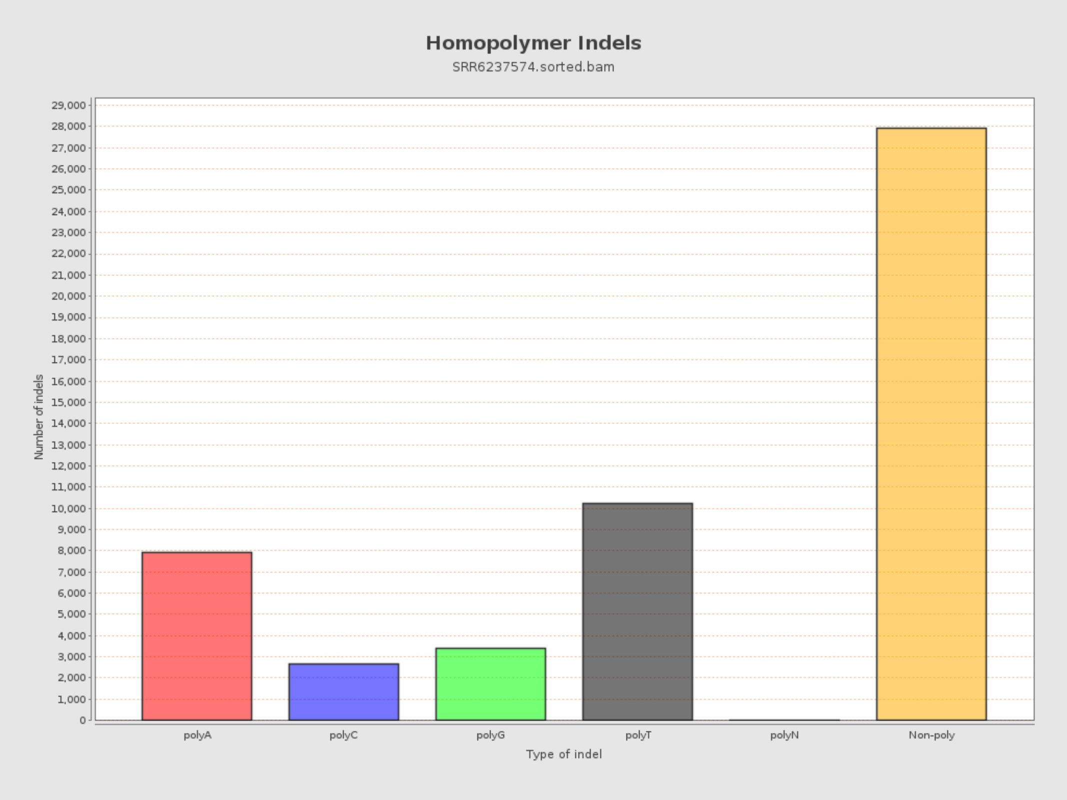
9. Results : Mapped Reads GC-content Distribution



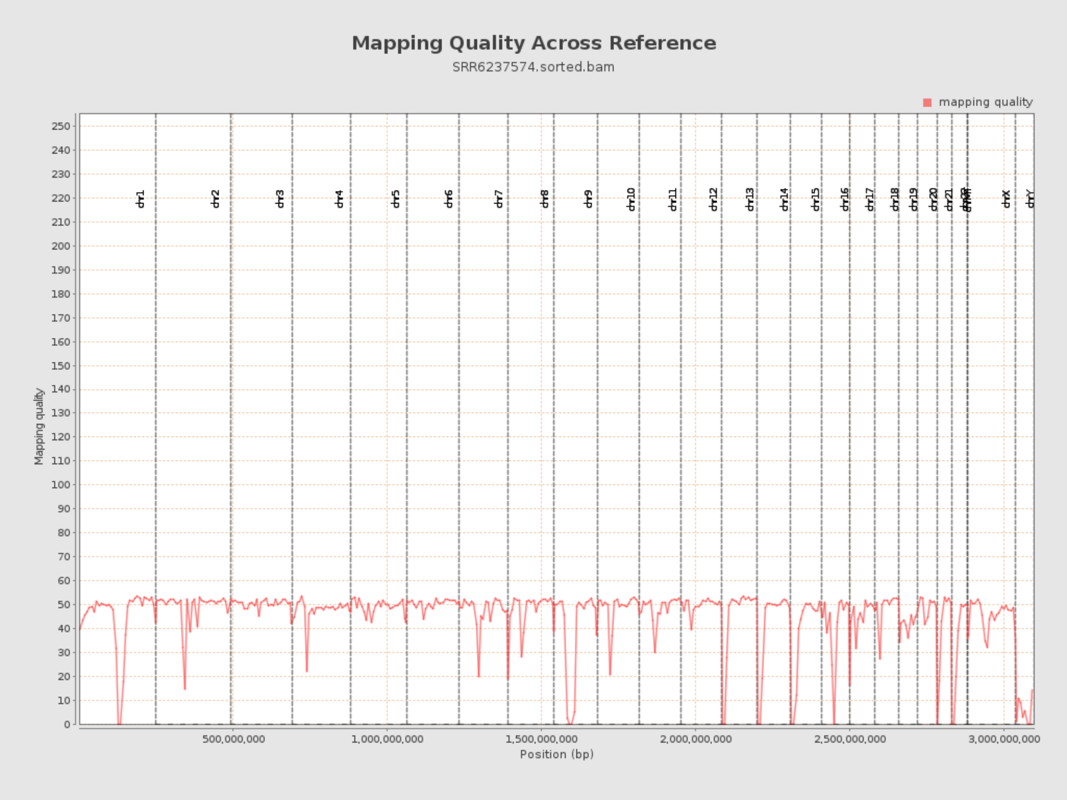
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram