Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 05:55:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237794.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_SRR6237794 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237794.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 05:55:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237794.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,909,964
Mapped reads	3,670,133 / 93.87%
Unmapped reads	239,831 / 6.13%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	25,495 / 0.65%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	151,214 / 3.87%
Duplication rate	2.74%
Clipped reads	631,166 / 16.14%

2.2. ACGT Content

Number/percentage of A's	79,899,482 / 29.77%
Number/percentage of C's	53,394,561 / 19.89%
Number/percentage of T's	80,104,890 / 29.84%
Number/percentage of G's	54,514,740 / 20.31%
Number/percentage of N's	507,057 / 0.19%
GC Percentage	40.2%

2.3. Coverage

Mean	0.0867

Standard Deviation	0.9411

2.4. Mapping Quality

Mean Mapping Quality	48.35

2.5. Mismatches and indels

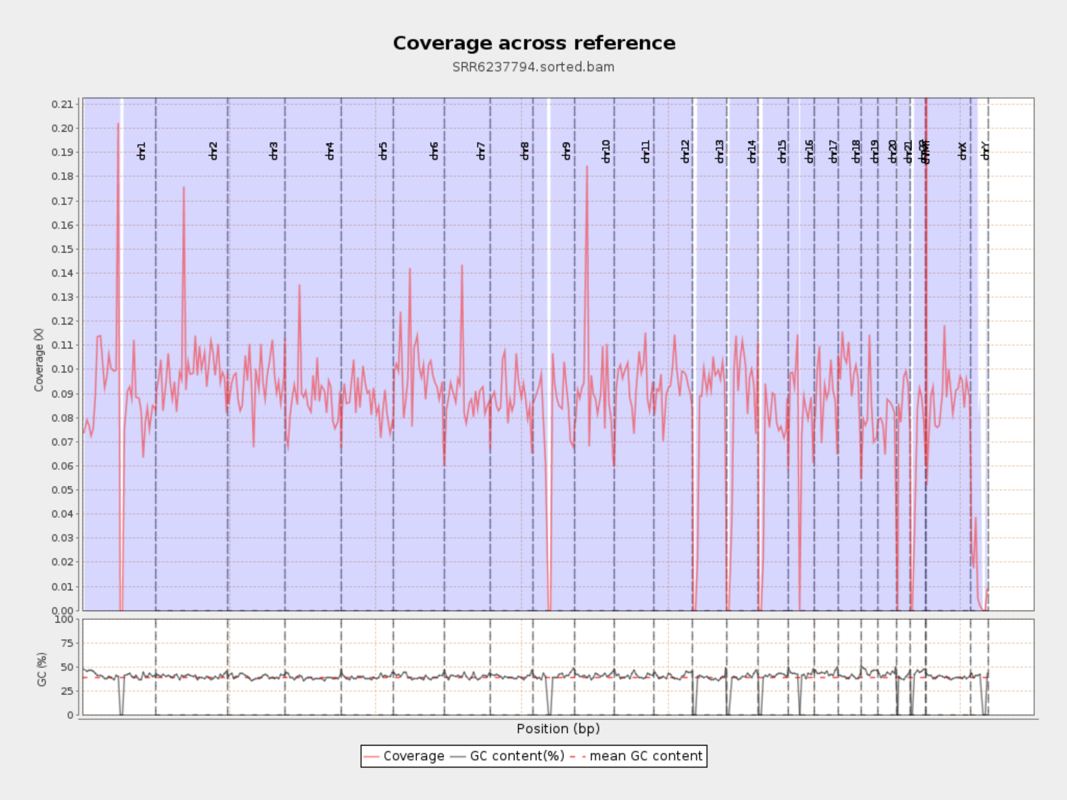
General error rate	0.83%
Mismatches	2,198,237
Insertions	20,532
Mapped reads with at least one insertion	0.55%
Deletions	57,597
Mapped reads with at least one deletion	1.55%
Homopolymer indels	47.99%

2.6. Chromosome stats

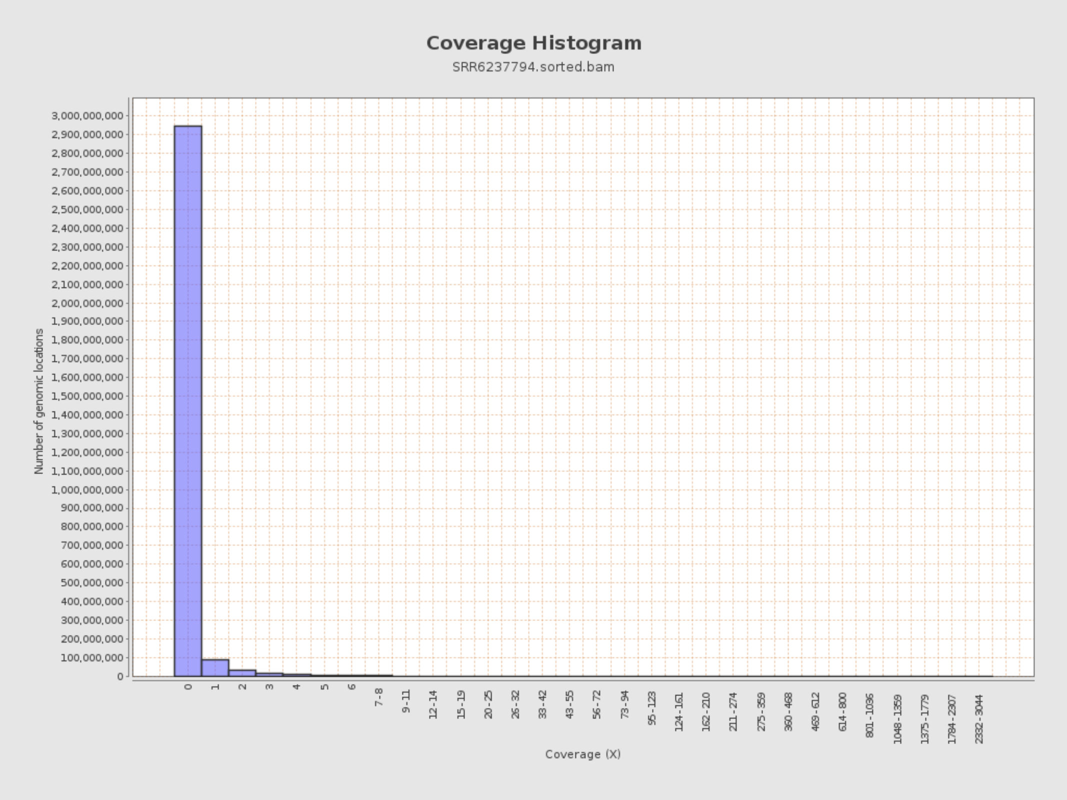
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	21681569	0.087	2.338
chr2	243199373	24551038	0.101	0.818
chr3	198022430	18796083	0.0949	0.5173
chr4	191154276	16973031	0.0888	0.5349
chr5	180915260	15764569	0.0871	0.4814
chr6	171115067	16935067	0.099	0.6962
chr7	159138663	14200746	0.0892	0.8809

chr8	146364022	12955707	0.0885	0.8437
chr9	141213431	10910384	0.0773	0.7311
chr10	135534747	12661936	0.0934	0.95
chr11	135006516	12750657	0.0944	0.6432
chr12	133851895	12525288	0.0936	0.505
chr13	115169878	9198636	0.0799	0.457
chr14	107349540	8692894	0.081	0.5078
chr15	102531392	6682304	0.0652	0.4068
chr16	90354753	7122953	0.0788	0.5851
chr17	81195210	7326762	0.0902	0.5868
chr18	78077248	7821239	0.1002	1.3767
chr19	59128983	4785228	0.0809	1.3581
chr20	63025520	4969331	0.0788	0.4817
chr21	48129895	3879855	0.0806	0.506
chr22	51304566	3010961	0.0587	0.3835
chrMT	16571	23026	1.3895	2.036
chrX	155270560	13616920	0.0877	0.5285
chrY	59373566	691379	0.0116	0.3002

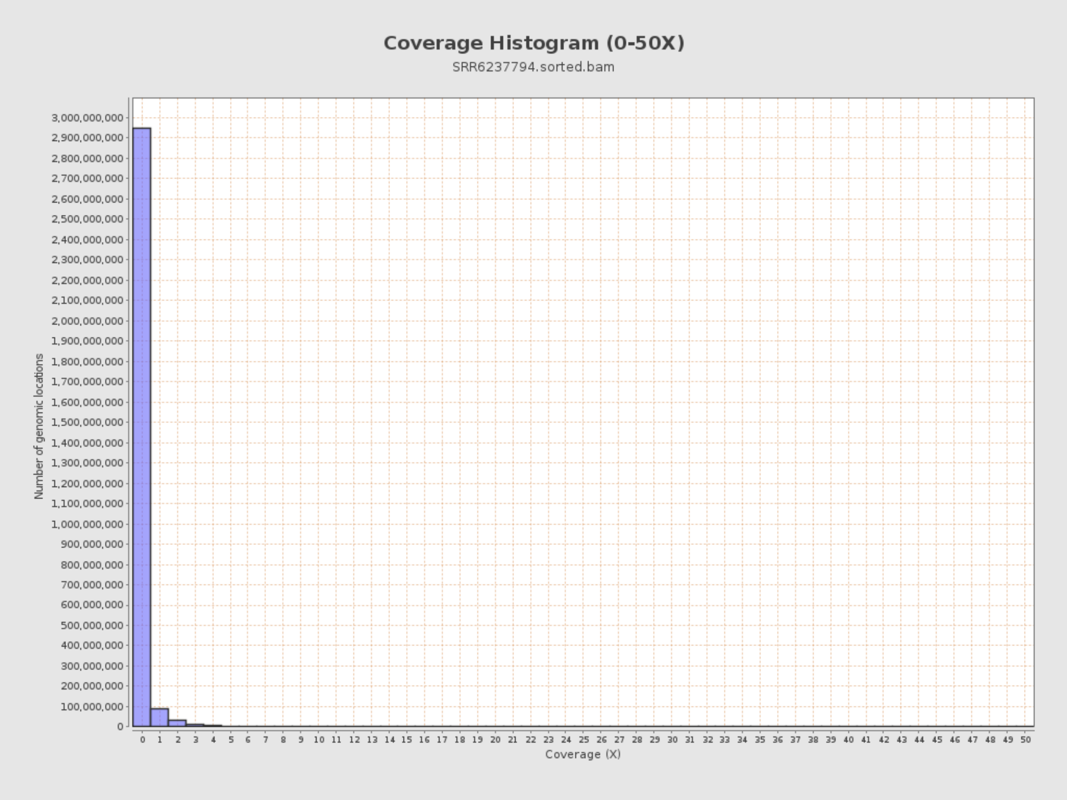
3. Results : Coverage across reference



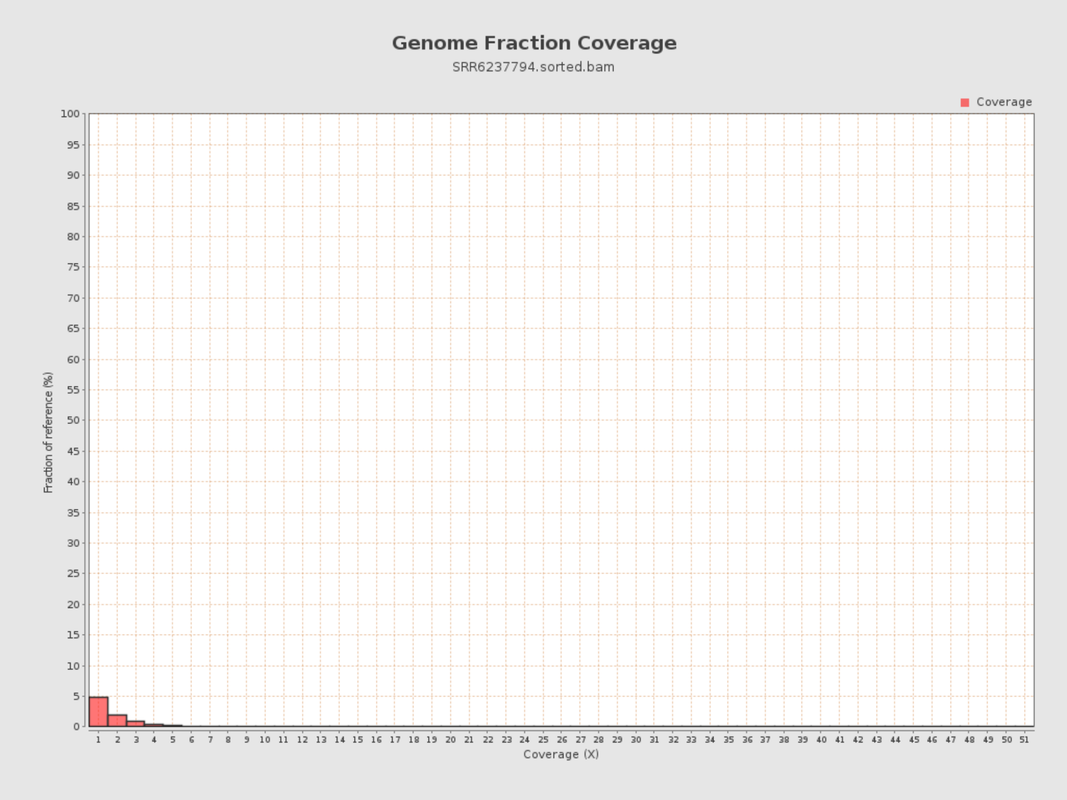
4. Results : Coverage Histogram



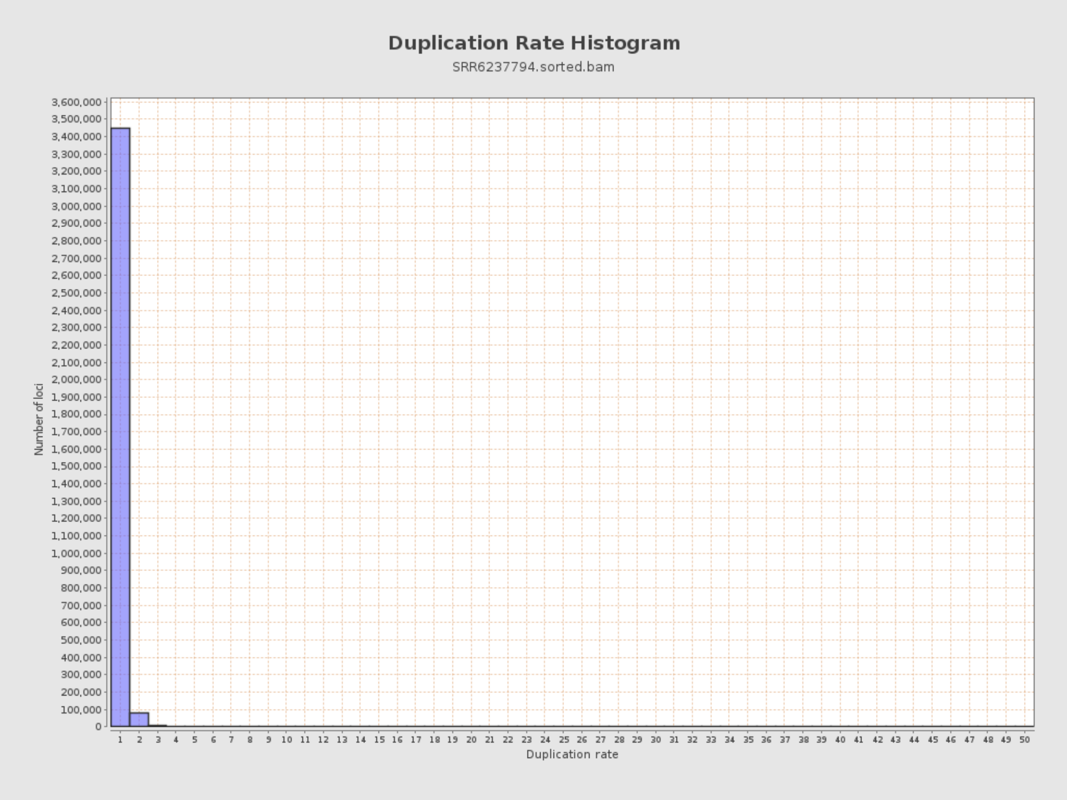
5. Results : Coverage Histogram (0-50X)



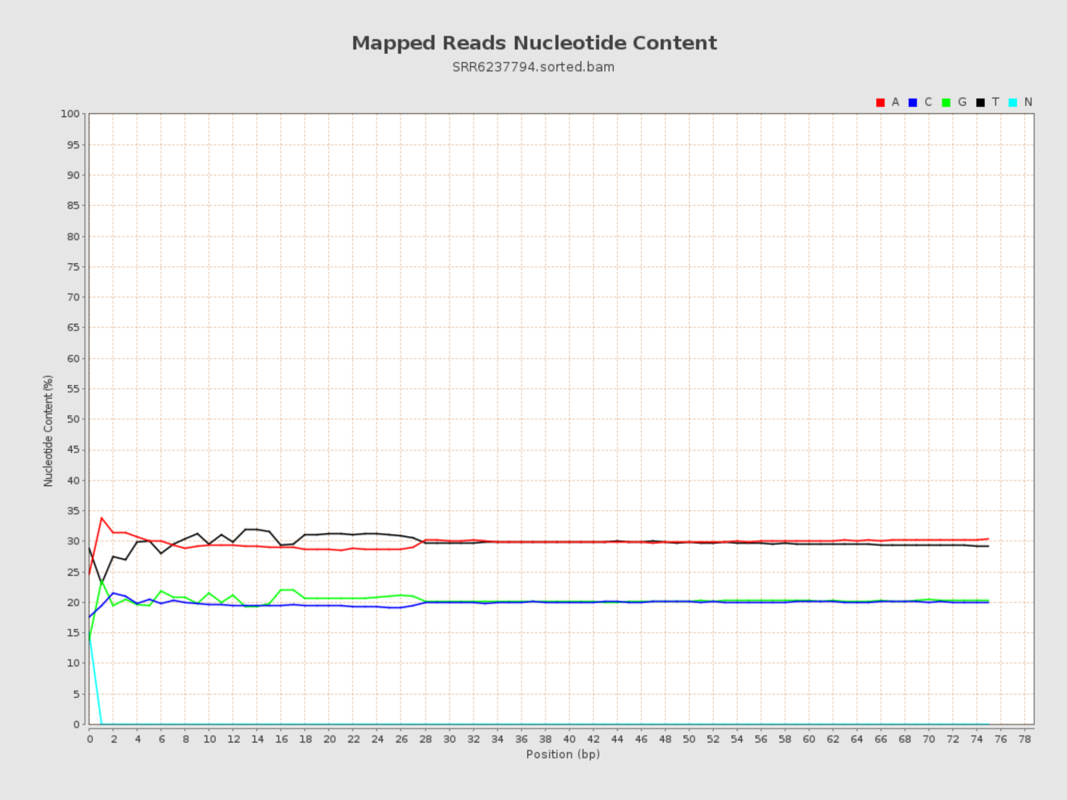
6. Results : Genome Fraction Coverage



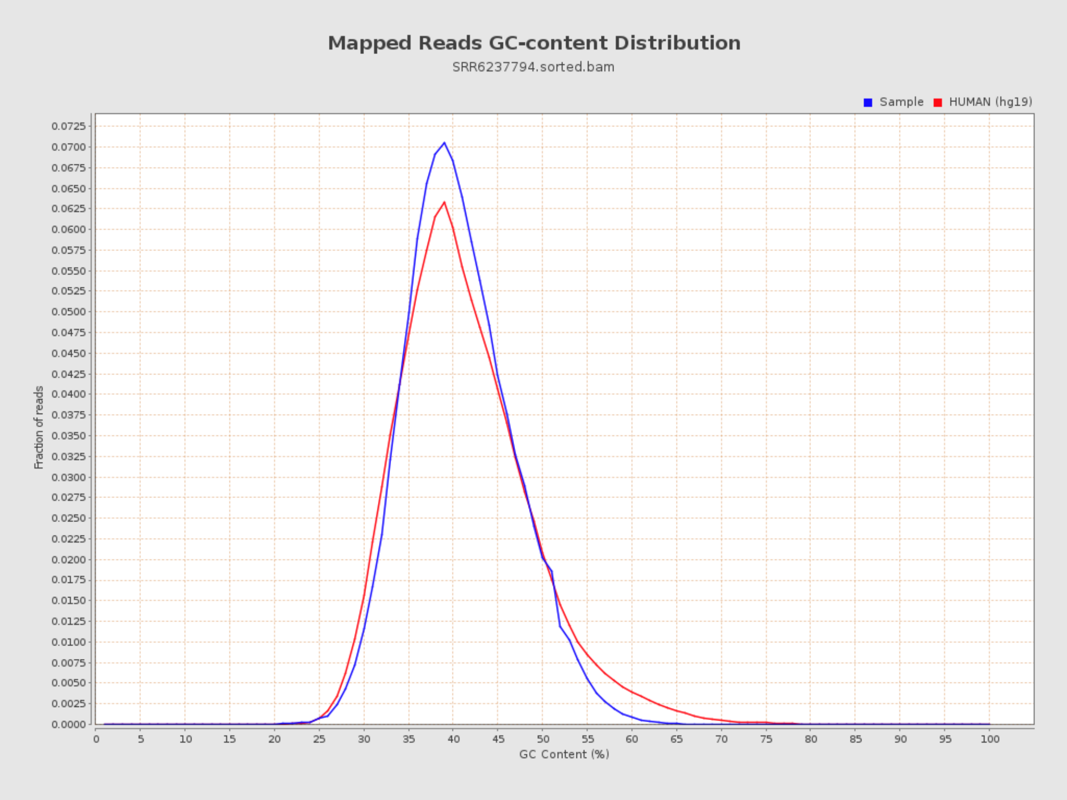
7. Results : Duplication Rate Histogram



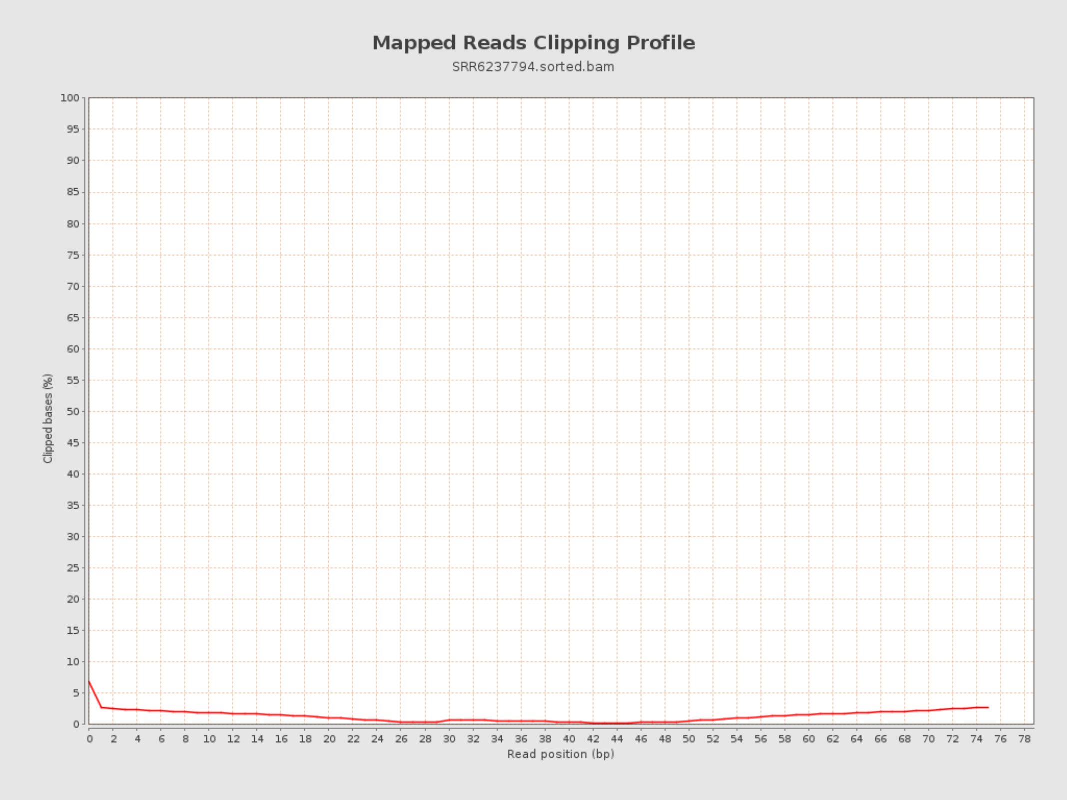
8. Results : Mapped Reads Nucleotide Content



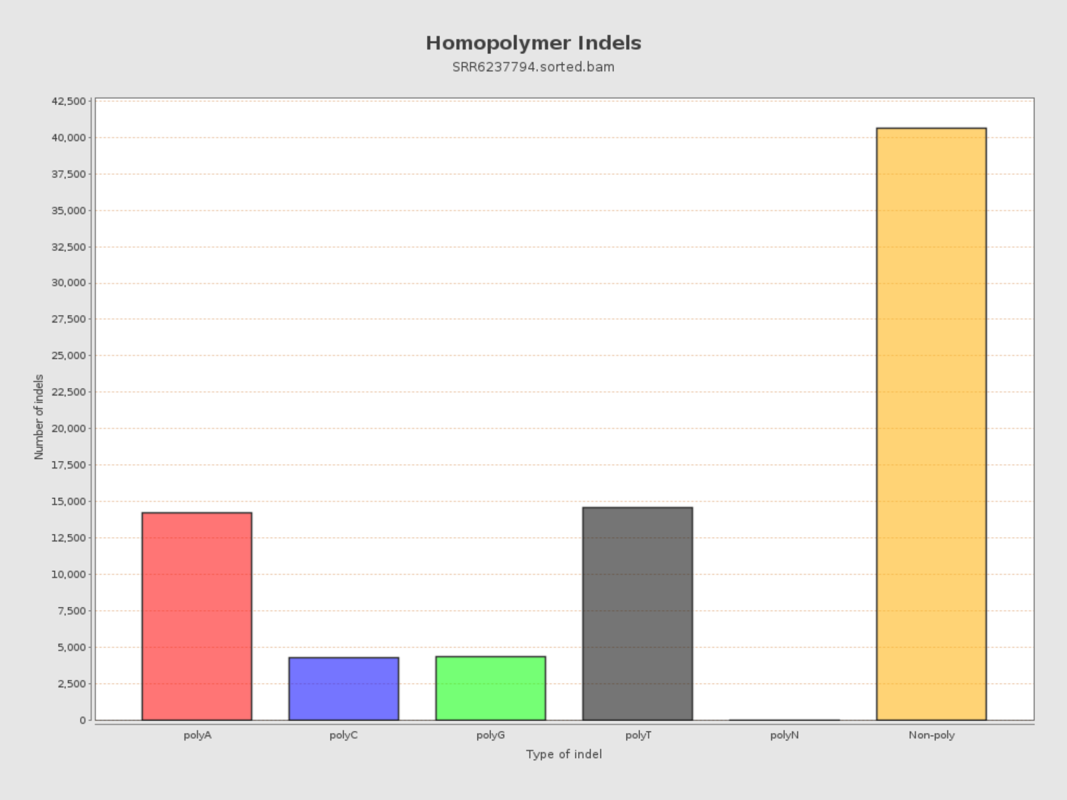
9. Results : Mapped Reads GC-content Distribution



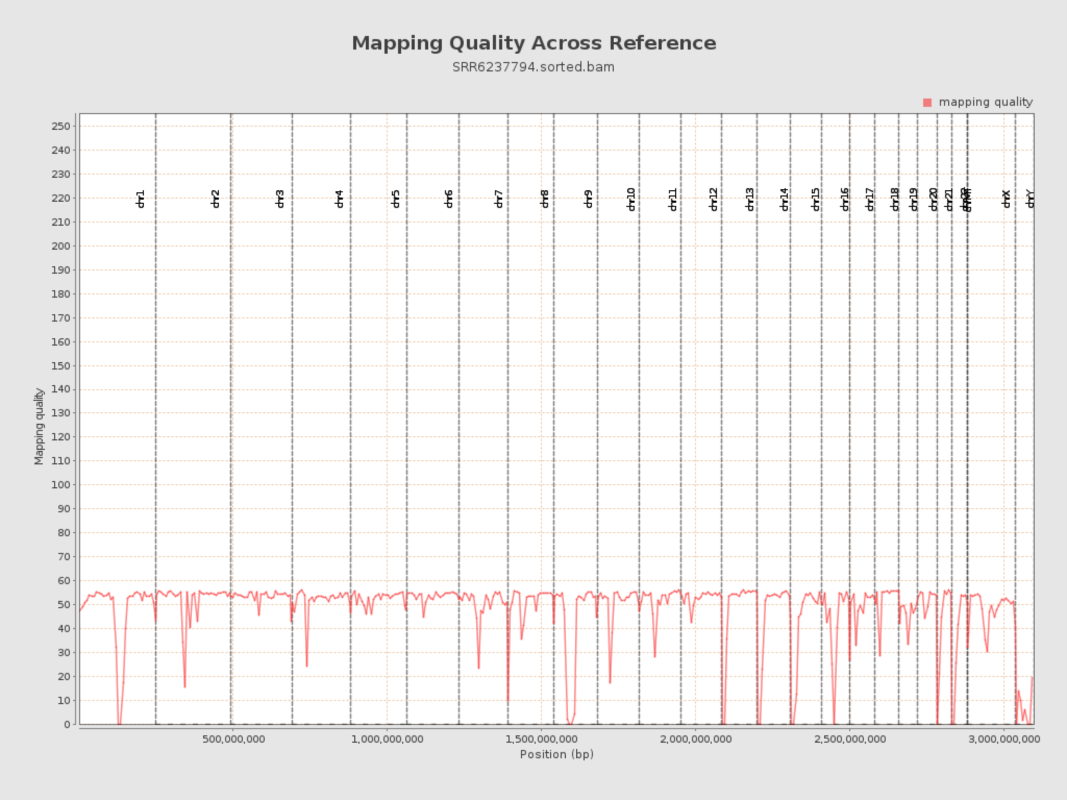
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram