Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 06:14:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237799.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_SRR6237799 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237799.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 06:14:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237799.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,849,357
Mapped reads	3,656,323 / 94.99%
Unmapped reads	193,034 / 5.01%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	38,371 / 1%
Read min/max/mean length	30 / 76 / 76.35
Duplicated reads (estimated)	317,638 / 8.25%
Duplication rate	6.83%
Clipped reads	959,298 / 24.92%

2.2. ACGT Content

Number/percentage of A's	80,033,770 / 30.41%
Number/percentage of C's	51,451,083 / 19.55%
Number/percentage of T's	78,817,927 / 29.95%
Number/percentage of G's	52,400,082 / 19.91%
Number/percentage of N's	456,077 / 0.17%
GC Percentage	39.46%

2.3. Coverage

Mean	0.0851

Standard Deviation	1.0304

2.4. Mapping Quality

Mean Mapping Quality	48.42

2.5. Mismatches and indels

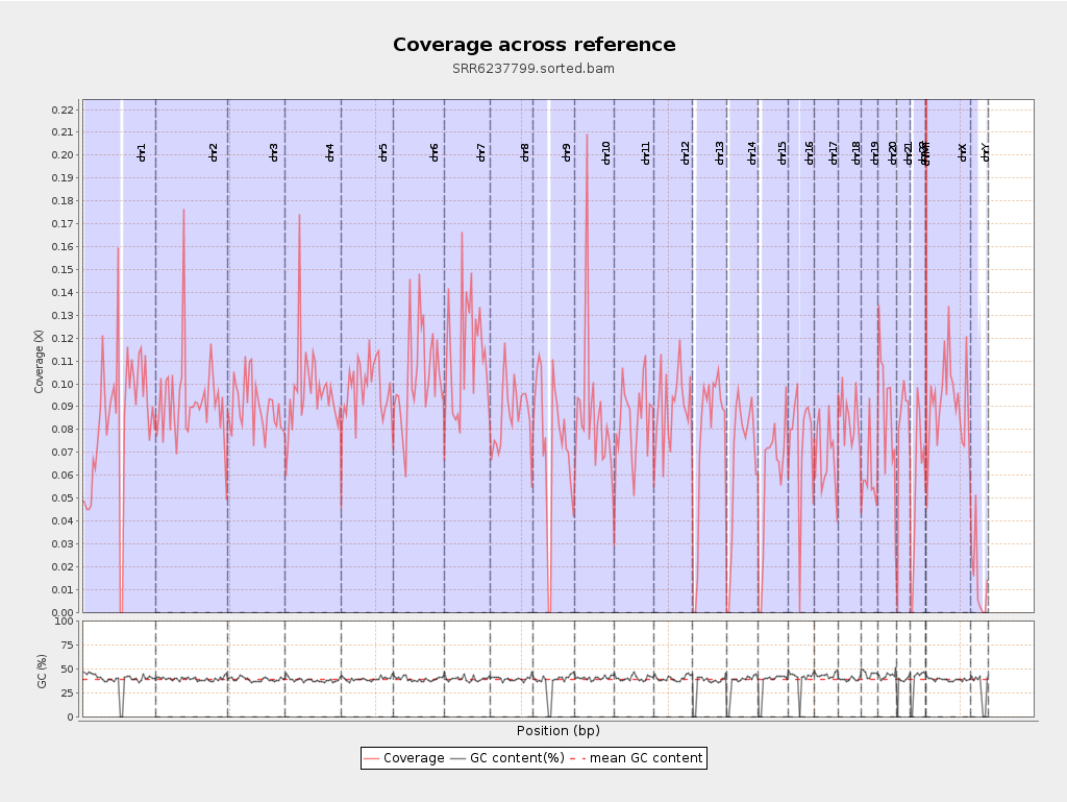
General error rate	0.88%
Mismatches	2,270,085
Insertions	20,814
Mapped reads with at least one insertion	0.57%
Deletions	71,961
Mapped reads with at least one deletion	1.94%
Homopolymer indels	46.69%

2.6. Chromosome stats

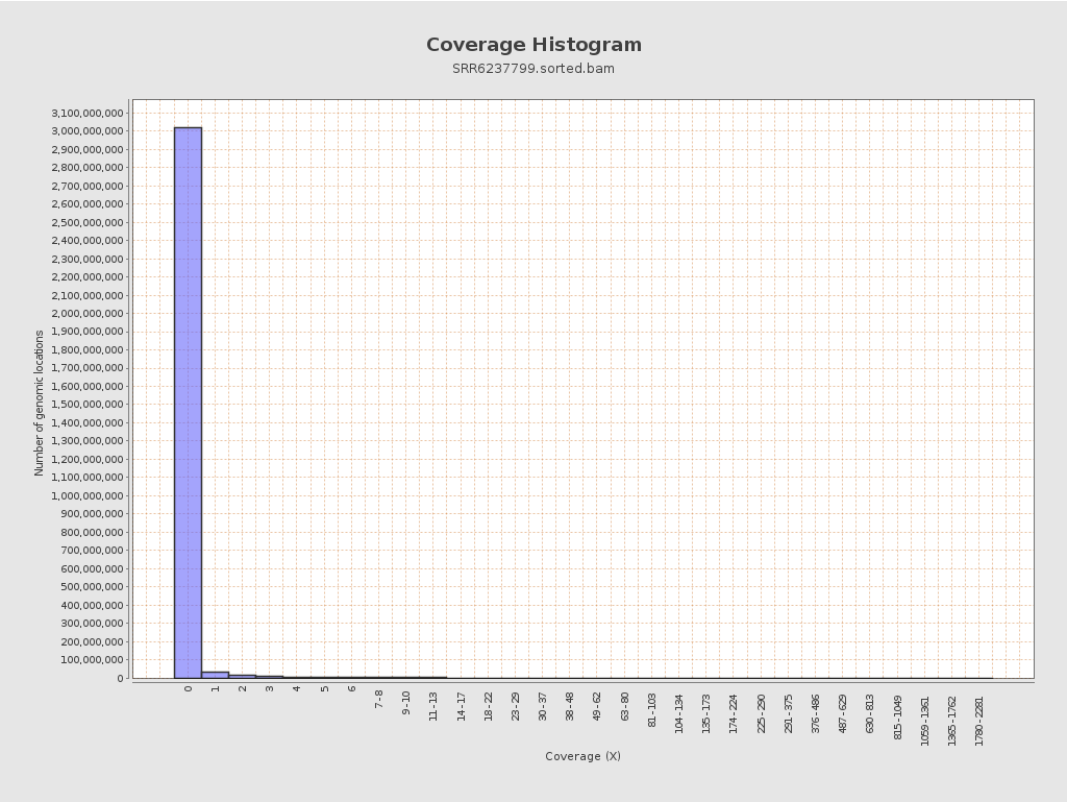
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	20825974	0.0836	1.836
chr2	243199373	22543972	0.0927	1.0388
chr3	198022430	17789887	0.0898	0.8081
chr4	191154276	18572502	0.0972	0.8781
chr5	180915260	17632261	0.0975	0.832
chr6	171115067	17820025	0.1041	0.888
chr7	159138663	17878068	0.1123	1.2808

chr8	146364022	12610926	0.0862	1.1248
chr9	141213431	10561479	0.0748	0.9033
chr10	135534747	11715844	0.0864	1.1805
chr11	135006516	11385959	0.0843	0.8684
chr12	133851895	12006829	0.0897	0.8003
chr13	115169878	8768042	0.0761	0.7187
chr14	107349540	7352799	0.0685	0.716
chr15	102531392	6076255	0.0593	0.6378
chr16	90354753	6584953	0.0729	0.7469
chr17	81195210	5553687	0.0684	0.7915
chr18	78077248	6672828	0.0855	1.395
chr19	59128983	3539647	0.0599	1.2087
chr20	63025520	5583947	0.0886	0.8155
chr21	48129895	3845947	0.0799	0.7975
chr22	51304566	2840967	0.0554	0.6162
chrMT	16571	204071	12.3149	9.9127
chrX	155270560	14097571	0.0908	0.8208
chrY	59373566	826354	0.0139	0.4446

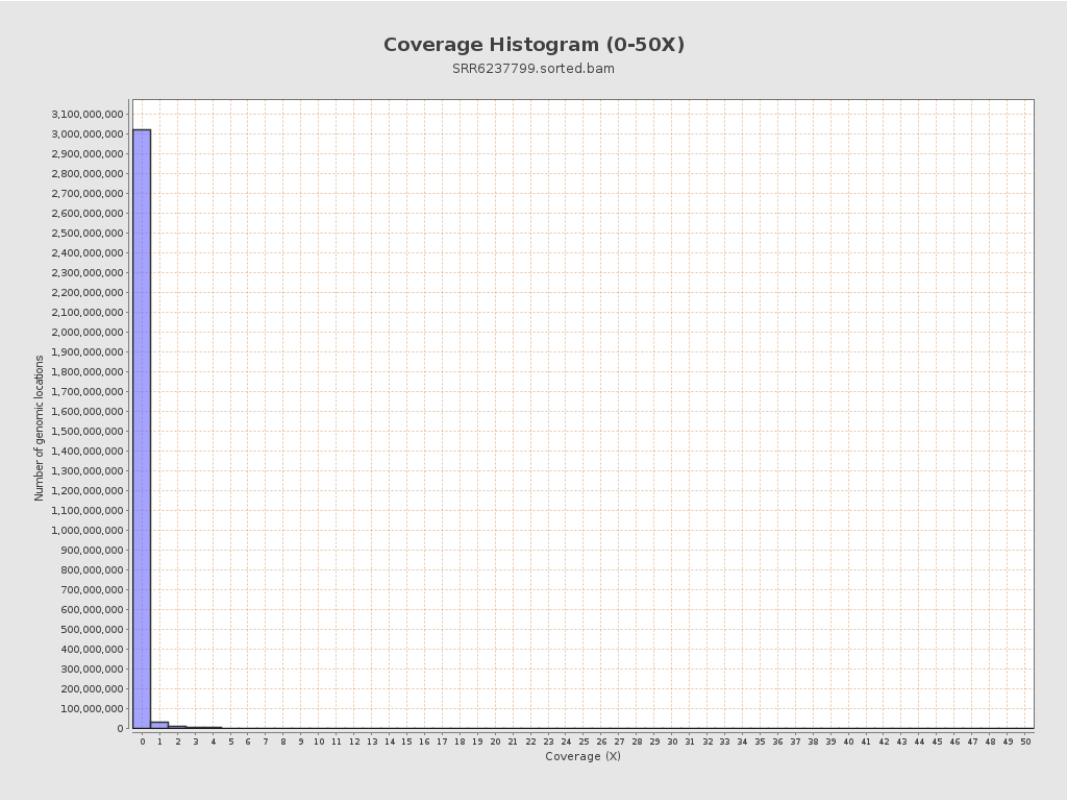
3. Results : Coverage across reference



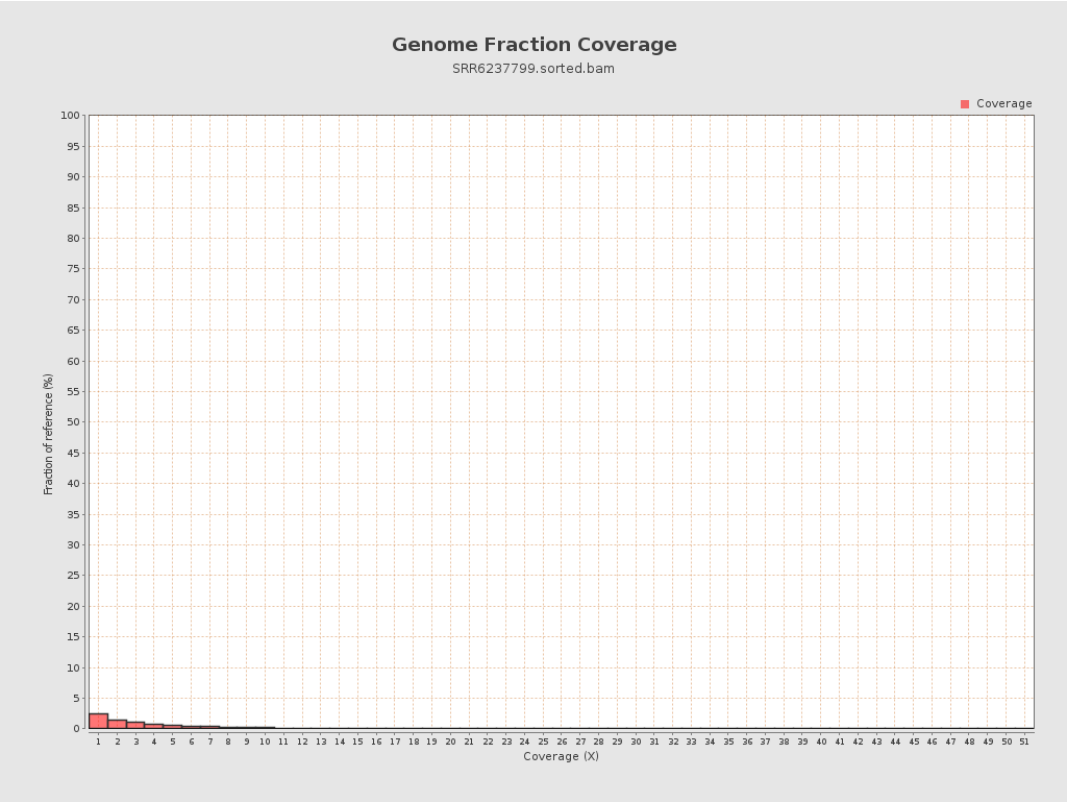
4. Results : Coverage Histogram



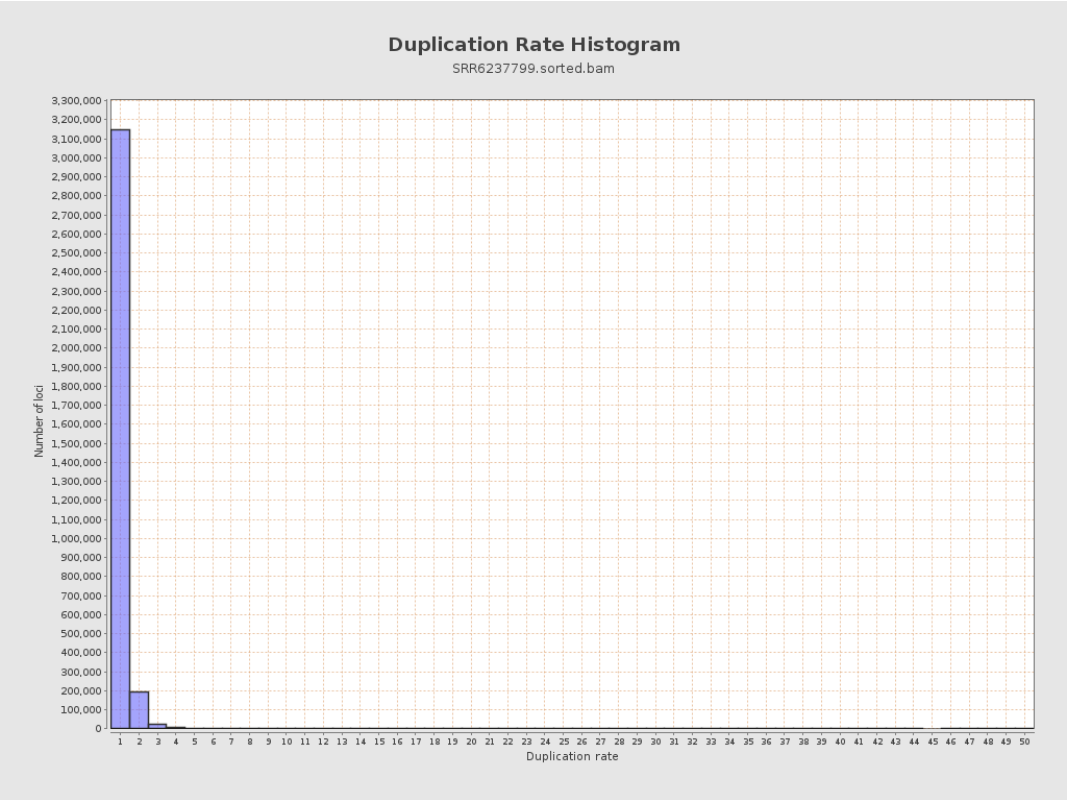
5. Results : Coverage Histogram (0-50X)



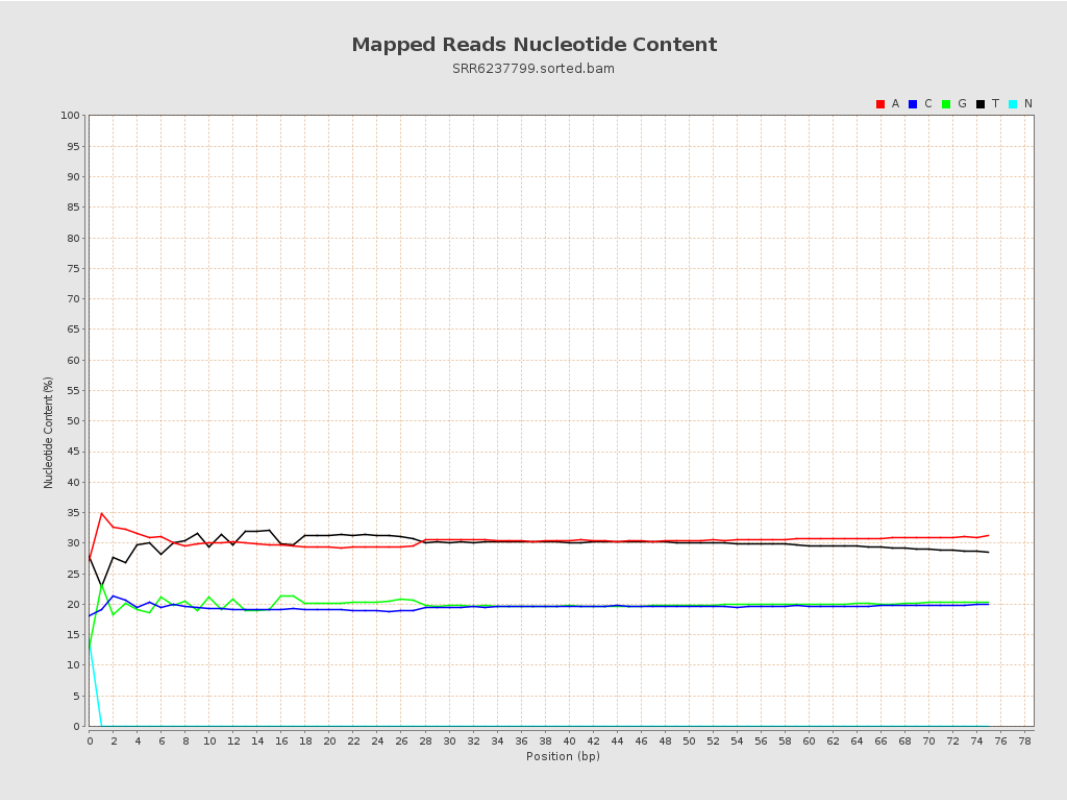
6. Results : Genome Fraction Coverage



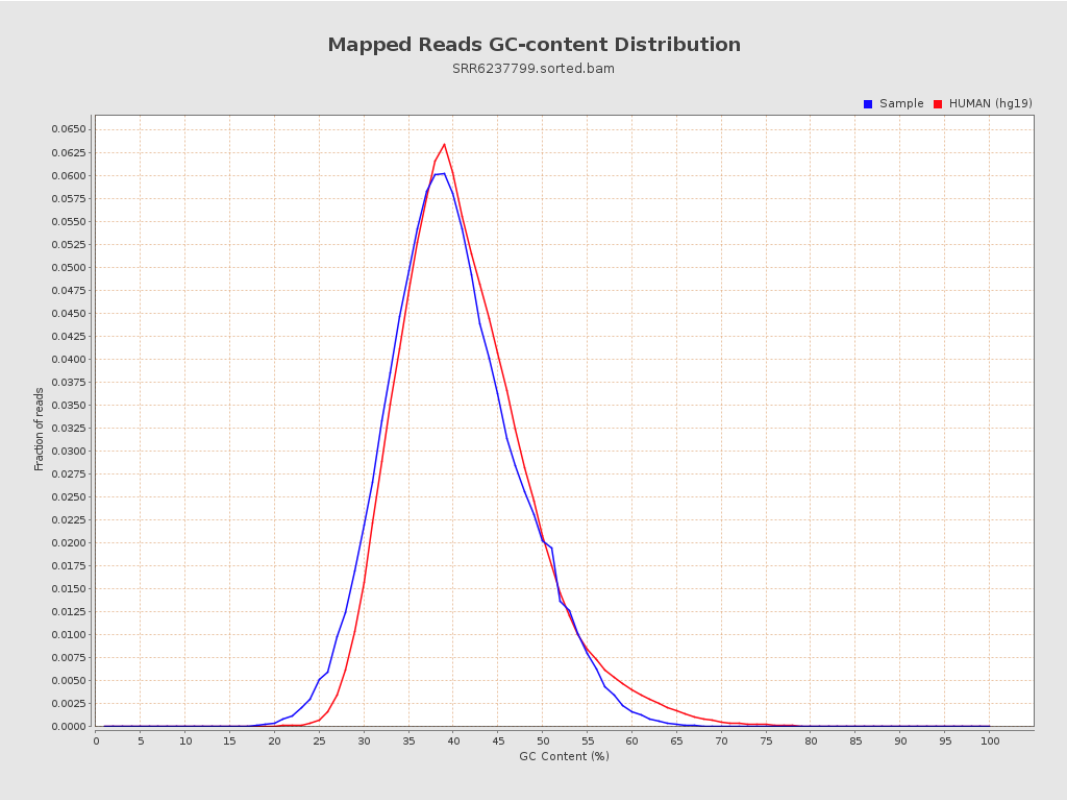
7. Results : Duplication Rate Histogram



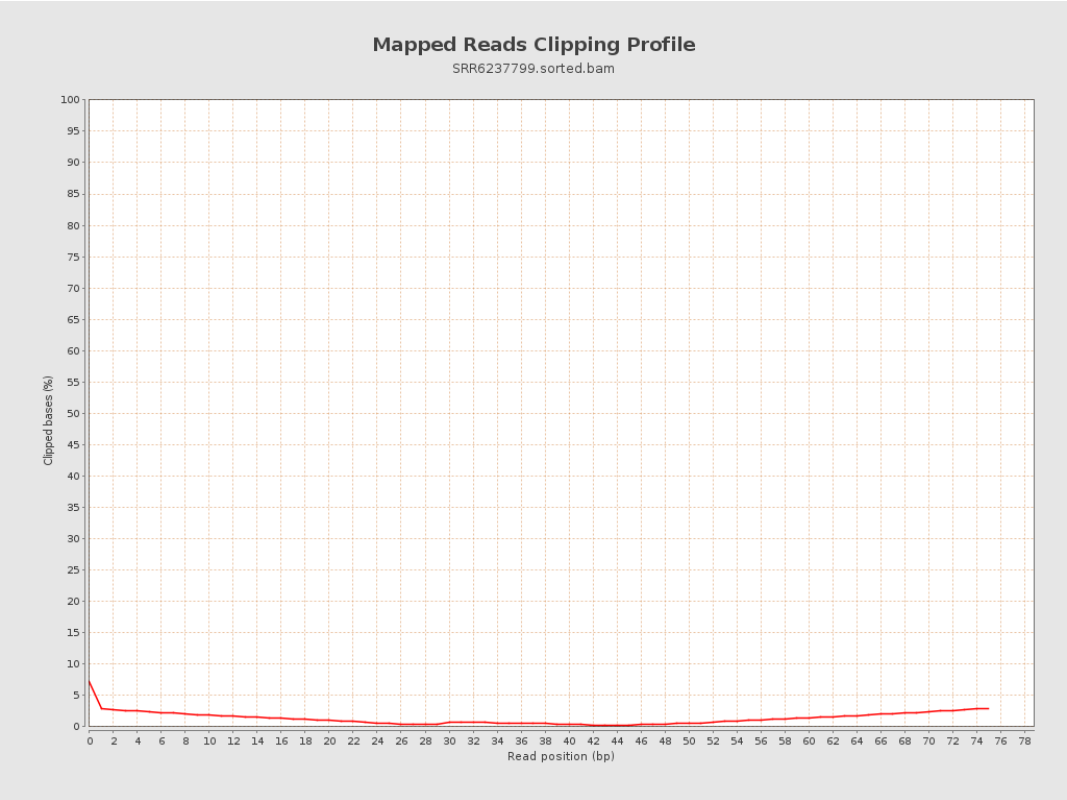
8. Results : Mapped Reads Nucleotide Content



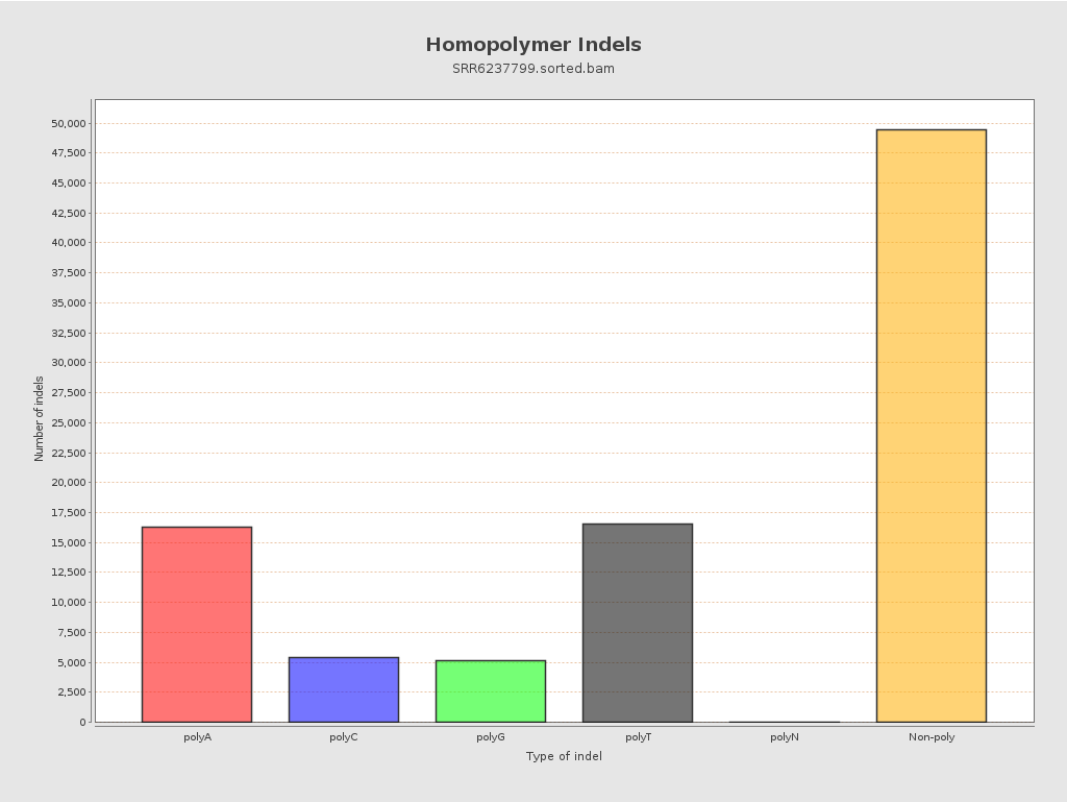
9. Results : Mapped Reads GC-content Distribution



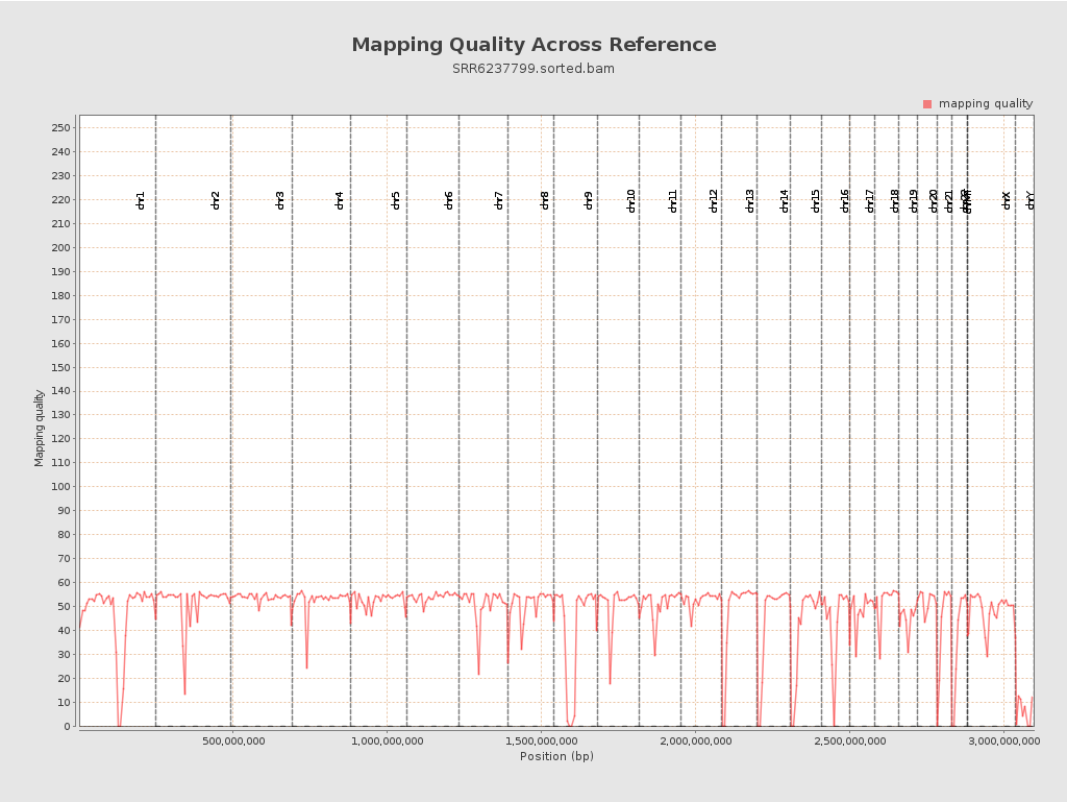
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram