Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 05:42:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237790.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_SRR6237790 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237790.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 05:42:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237790.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	779,233
Mapped reads	510,764 / 65.55%
Unmapped reads	268,469 / 34.45%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,799 / 0.49%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	15,621 / 2%
Duplication rate	2.54%
Clipped reads	318,063 / 40.82%

2.2. ACGT Content

Number/percentage of A's	8,888,064 / 28.21%
Number/percentage of C's	5,570,177 / 17.68%
Number/percentage of T's	9,837,718 / 31.22%
Number/percentage of G's	7,187,552 / 22.81%
Number/percentage of N's	27,447 / 0.09%
GC Percentage	40.49%

2.3. Coverage

Mean	0.0102

Standard Deviation	0.1327

2.4. Mapping Quality

Mean Mapping Quality	45.77

2.5. Mismatches and indels

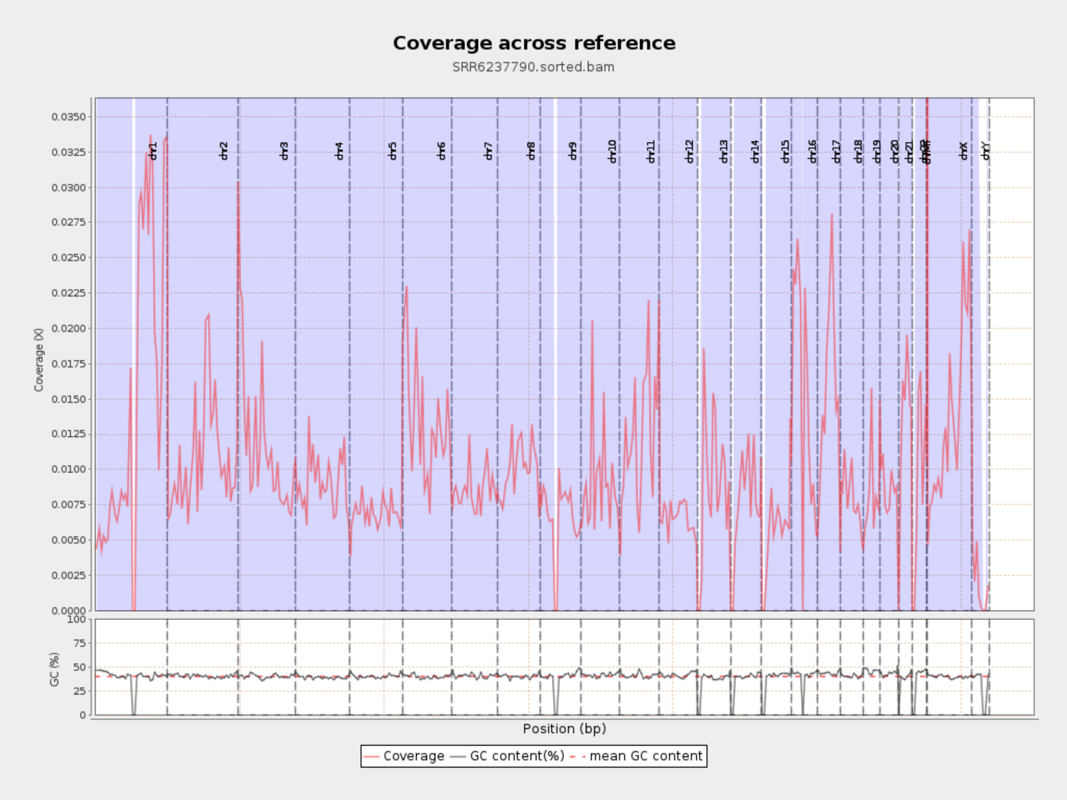
General error rate	0.87%
Mismatches	269,146
Insertions	2,199
Mapped reads with at least one insertion	0.43%
Deletions	8,544
Mapped reads with at least one deletion	1.65%
Homopolymer indels	47.1%

2.6. Chromosome stats

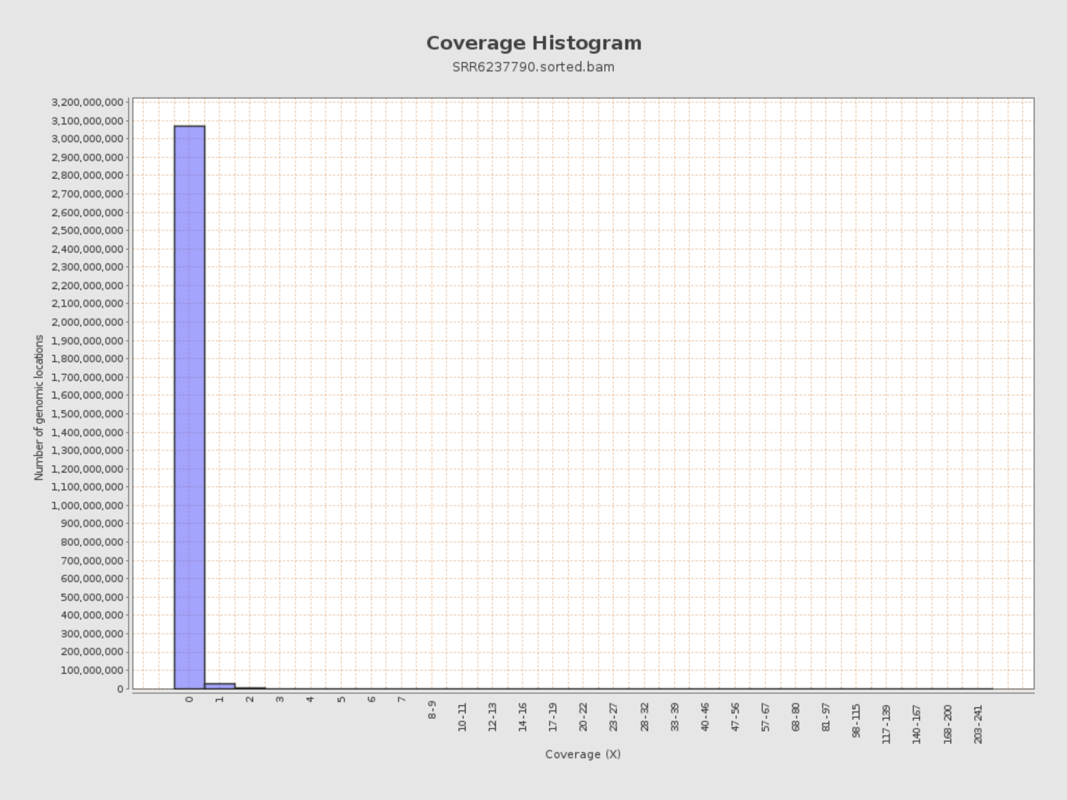
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3710072	0.0149	0.1832
chr2	243199373	2612832	0.0107	0.1287
chr3	198022430	2303660	0.0116	0.1193
chr4	191154276	1747869	0.0091	0.1067
chr5	180915260	1261606	0.007	0.0917
chr6	171115067	2341431	0.0137	0.1301
chr7	159138663	1363073	0.0086	0.1163

chr8	146364022	1469149	0.01	0.1519
chr9	141213431	927286	0.0066	0.0987
chr10	135534747	1213104	0.009	0.1535
chr11	135006516	1639207	0.0121	0.144
chr12	133851895	886154	0.0066	0.0891
chr13	115169878	998100	0.0087	0.1047
chr14	107349540	818260	0.0076	0.0986
chr15	102531392	555170	0.0054	0.0807
chr16	90354753	1365993	0.0151	0.2177
chr17	81195210	1251488	0.0154	0.1768
chr18	78077248	633968	0.0081	0.1828
chr19	59128983	495875	0.0084	0.1371
chr20	63025520	532181	0.0084	0.1038
chr21	48129895	656399	0.0136	0.1303
chr22	51304566	480837	0.0094	0.1108
chrMT	16571	12864	0.7763	1.2714
chrX	155270560	2146735	0.0138	0.1371
chrY	59373566	100991	0.0017	0.0494

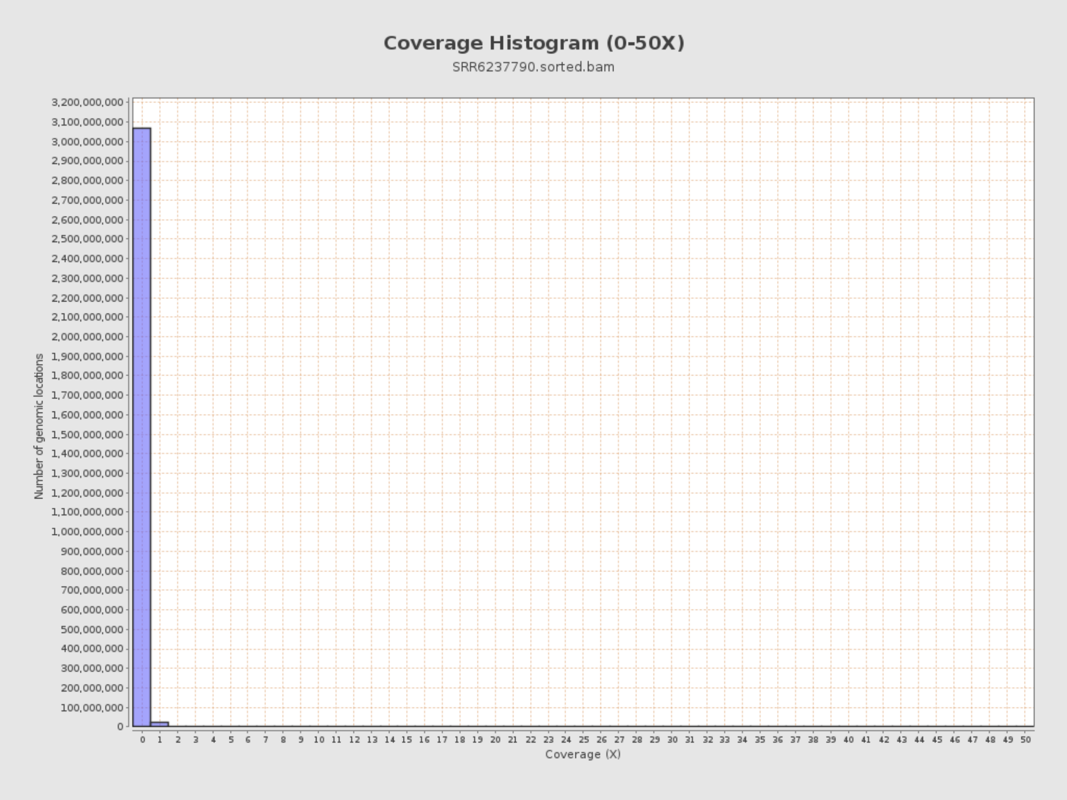
3. Results : Coverage across reference



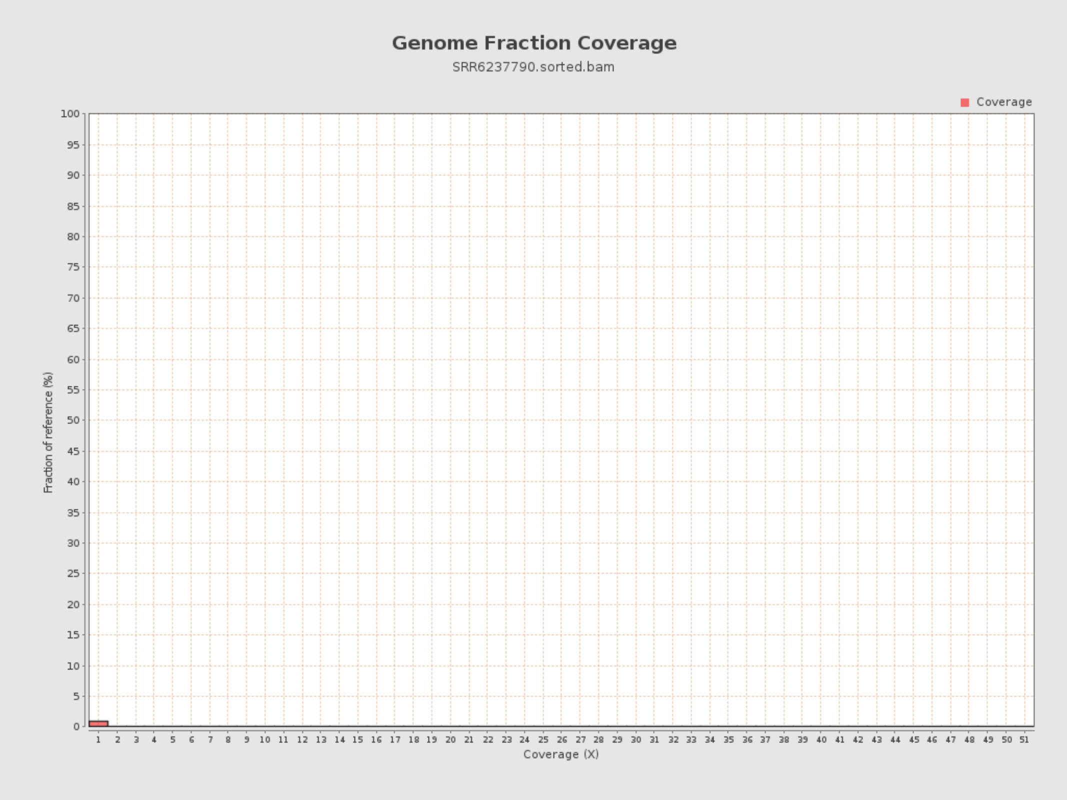
4. Results : Coverage Histogram



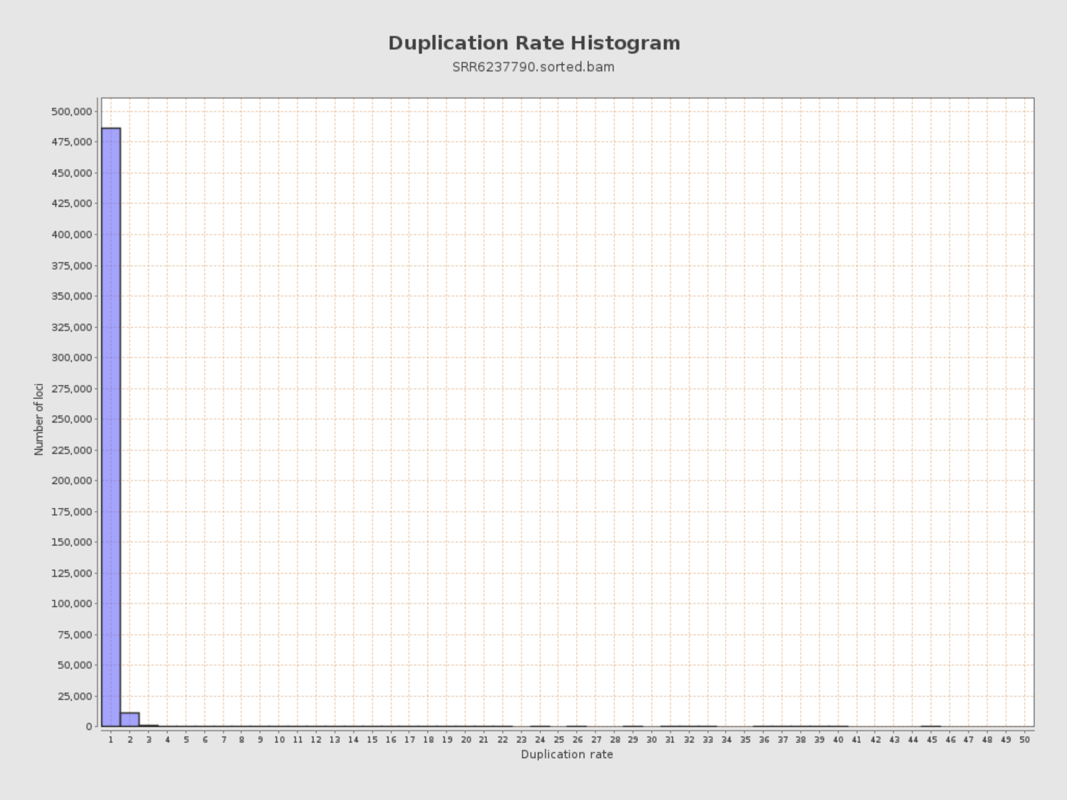
5. Results : Coverage Histogram (0-50X)



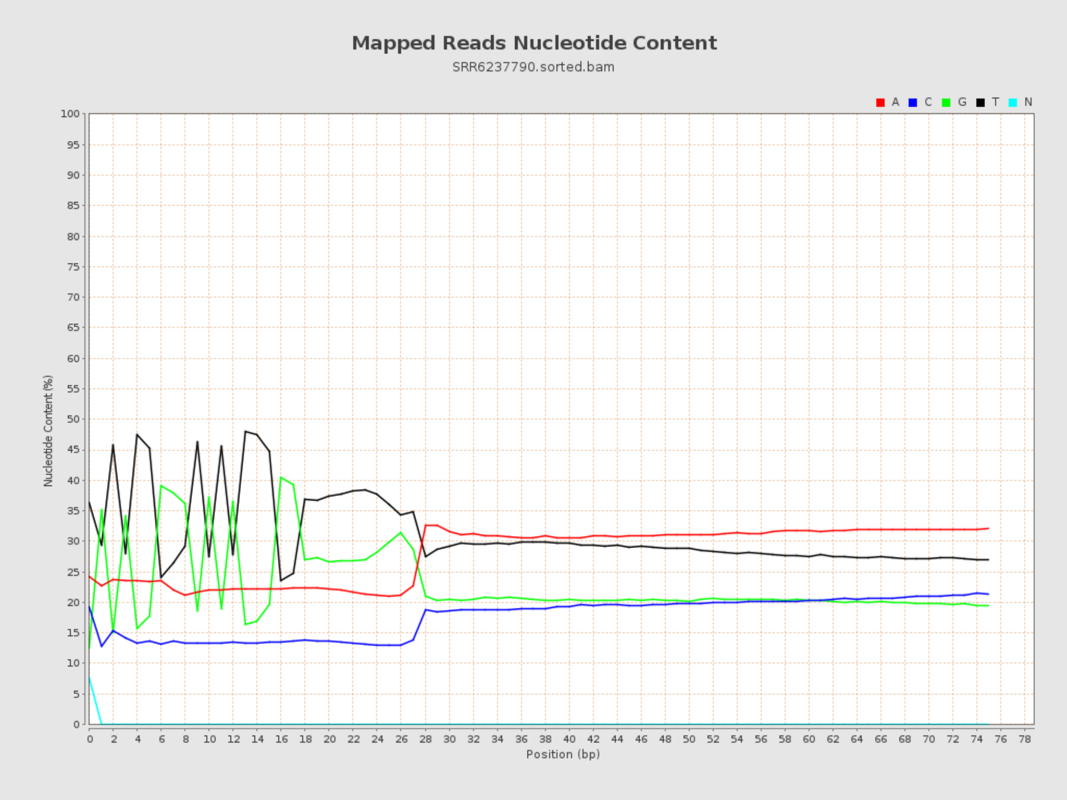
6. Results : Genome Fraction Coverage



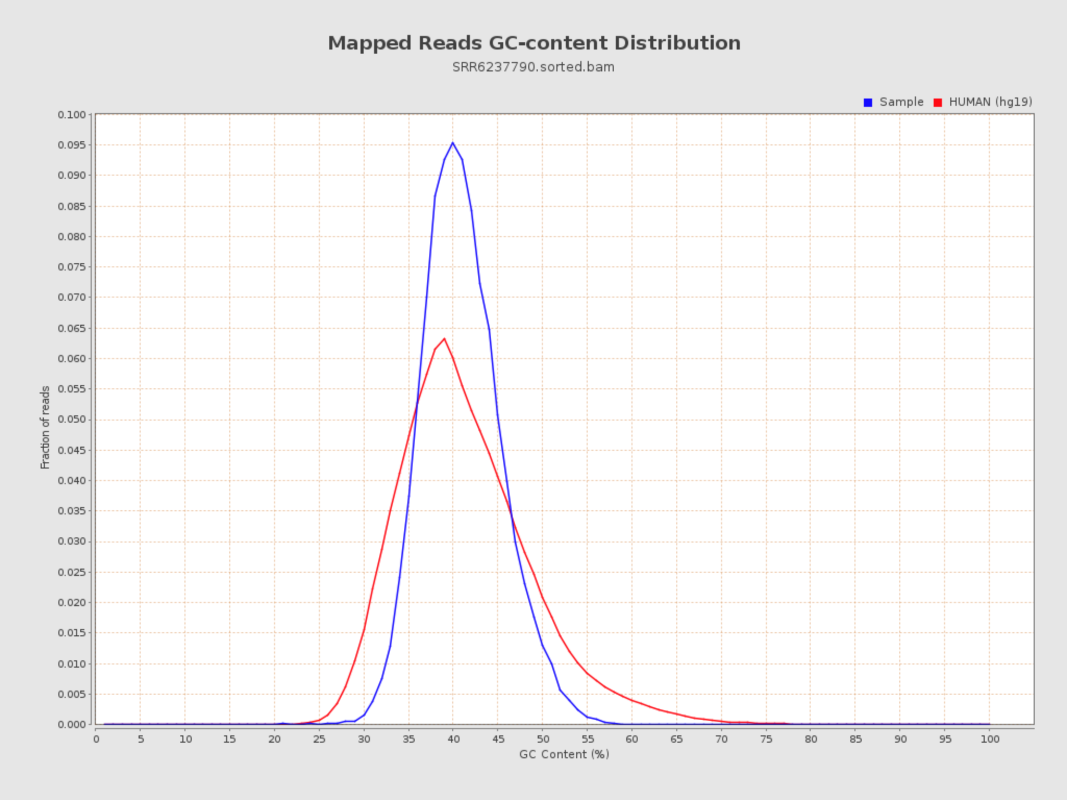
7. Results : Duplication Rate Histogram



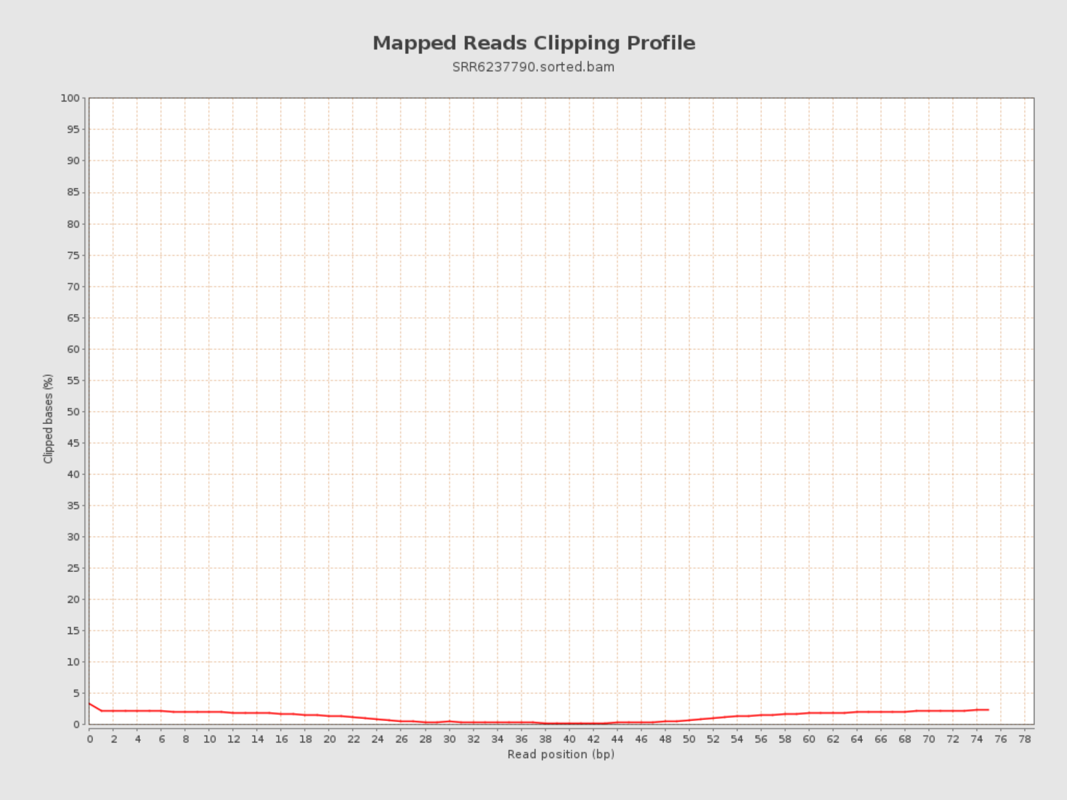
8. Results : Mapped Reads Nucleotide Content



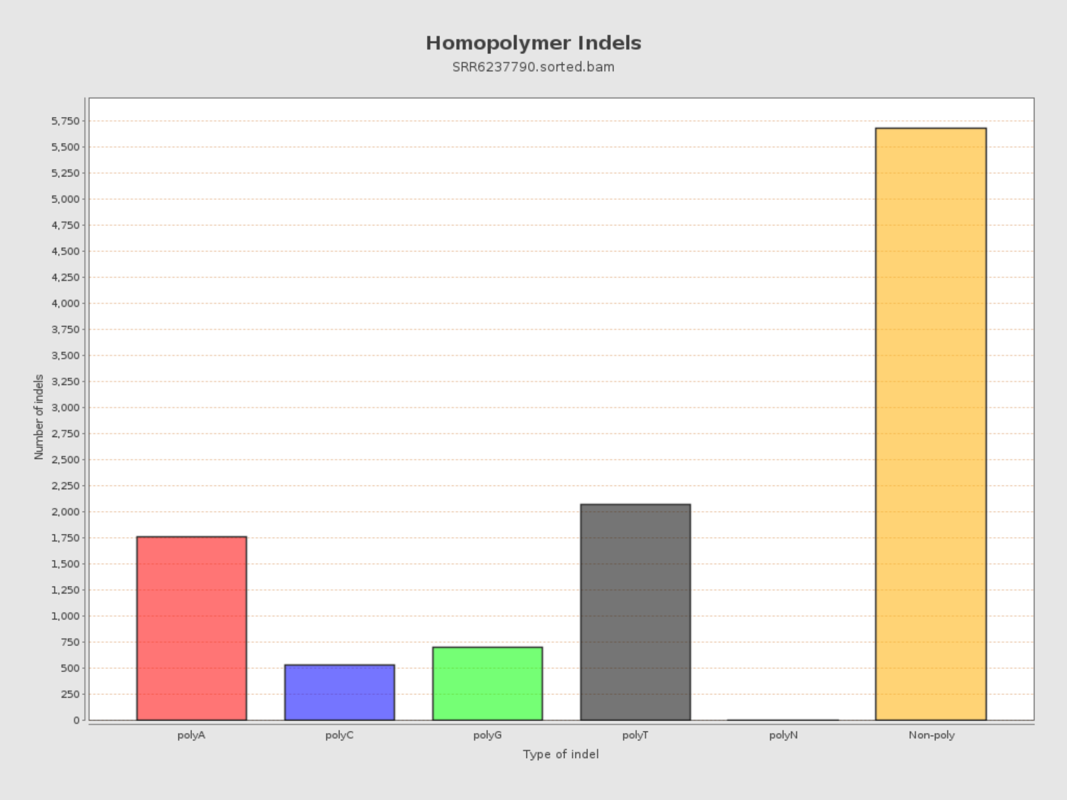
9. Results : Mapped Reads GC-content Distribution



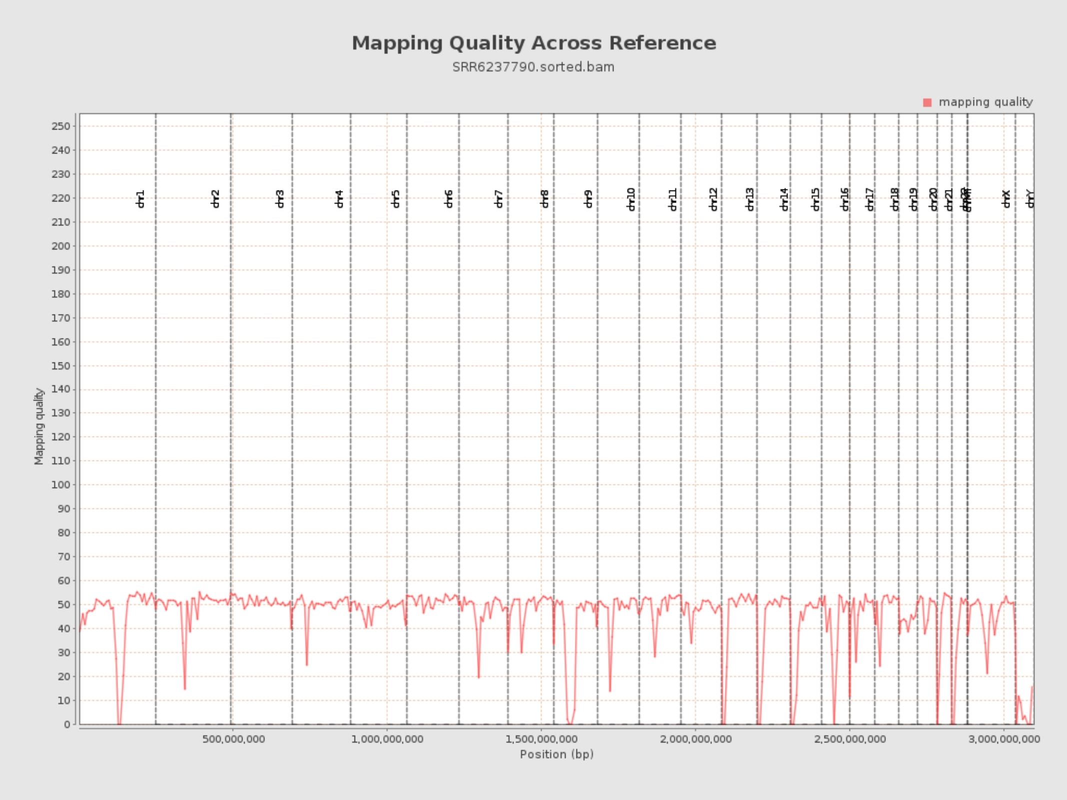
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram