Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 04:16:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237583.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_SRR6237583 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237583.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 04:16:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237583.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,726,138
Mapped reads	1,400,278 / 81.12%
Unmapped reads	325,860 / 18.88%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,279 / 0.48%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	81,020 / 4.69%
Duplication rate	3.94%
Clipped reads	865,253 / 50.13%

2.2. ACGT Content

Number/percentage of A's	22,490,170 / 25.54%
Number/percentage of C's	16,684,902 / 18.95%
Number/percentage of T's	26,647,992 / 30.26%
Number/percentage of G's	22,212,458 / 25.23%
Number/percentage of N's	15,646 / 0.02%
GC Percentage	44.18%

2.3. Coverage

Mean	0.0285

Standard Deviation	0.2963

2.4. Mapping Quality

Mean Mapping Quality	39.45

2.5. Mismatches and indels

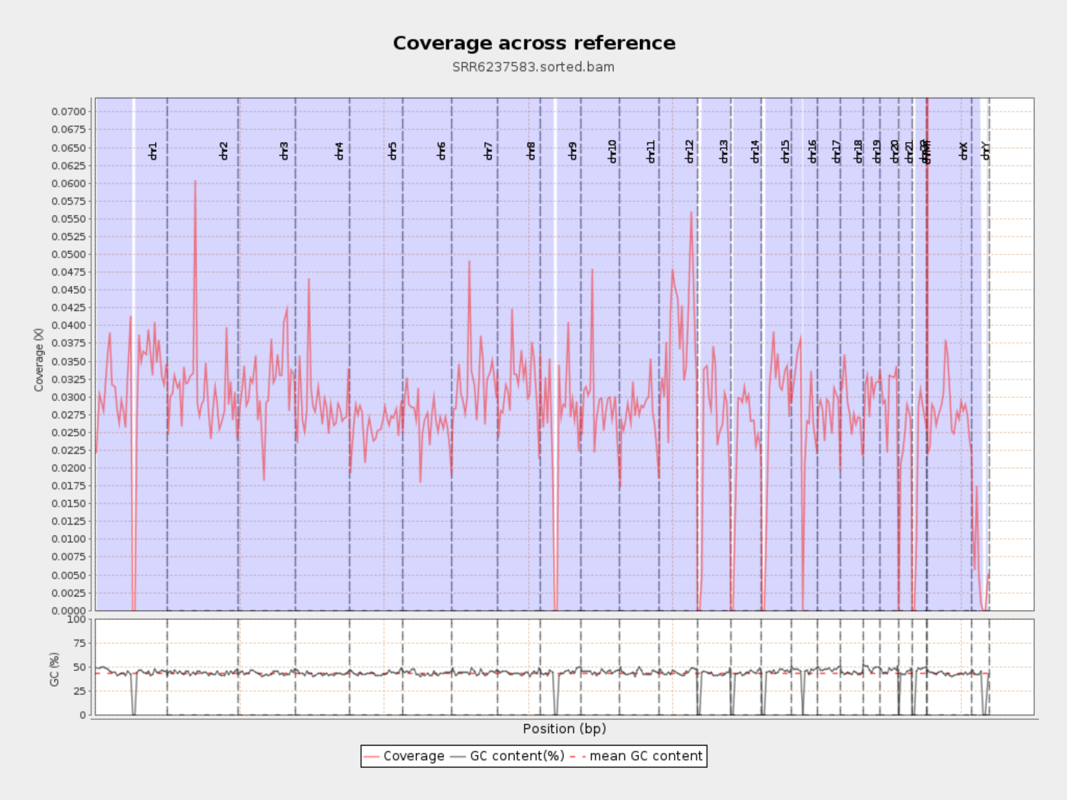
General error rate	0.96%
Mismatches	830,952
Insertions	8,305
Mapped reads with at least one insertion	0.59%
Deletions	32,233
Mapped reads with at least one deletion	2.27%
Homopolymer indels	46.1%

2.6. Chromosome stats

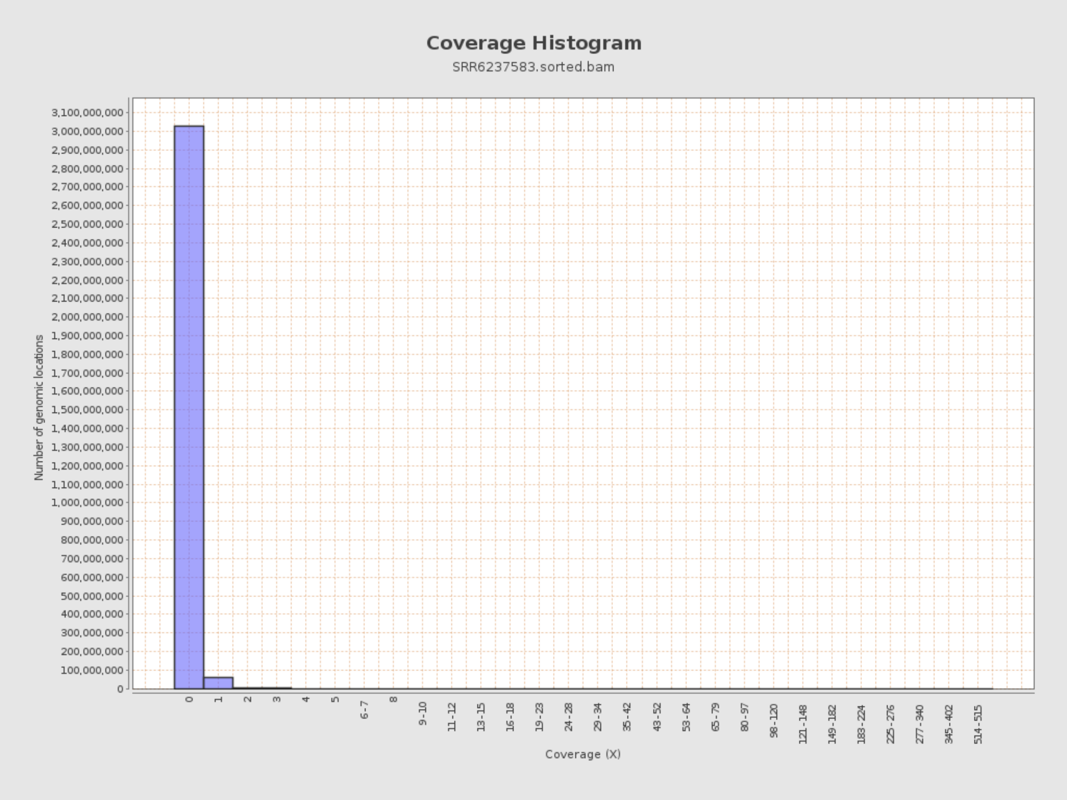
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7687617	0.0308	0.3672
chr2	243199373	7510704	0.0309	0.4225
chr3	198022430	6267876	0.0317	0.2342
chr4	191154276	5533959	0.029	0.239
chr5	180915260	4737973	0.0262	0.2072
chr6	171115067	4564802	0.0267	0.233
chr7	159138663	5100409	0.0321	0.4219

chr8	146364022	4622445	0.0316	0.2841
chr9	141213431	3652769	0.0259	0.323
chr10	135534747	3926634	0.029	0.2867
chr11	135006516	3764677	0.0279	0.3254
chr12	133851895	5175001	0.0387	0.2723
chr13	115169878	2814489	0.0244	0.2077
chr14	107349540	2473408	0.023	0.239
chr15	102531392	2753438	0.0269	0.2248
chr16	90354753	2444009	0.027	0.2449
chr17	81195210	2276060	0.028	0.2381
chr18	78077248	2209404	0.0283	0.4432
chr19	59128983	1828802	0.0309	0.3168
chr20	63025520	1903746	0.0302	0.2372
chr21	48129895	1078686	0.0224	0.2149
chr22	51304566	1008390	0.0197	0.1874
chrMT	16571	78163	4.7169	3.9028
chrX	155270560	4365528	0.0281	0.2367
chrY	59373566	325633	0.0055	0.1377

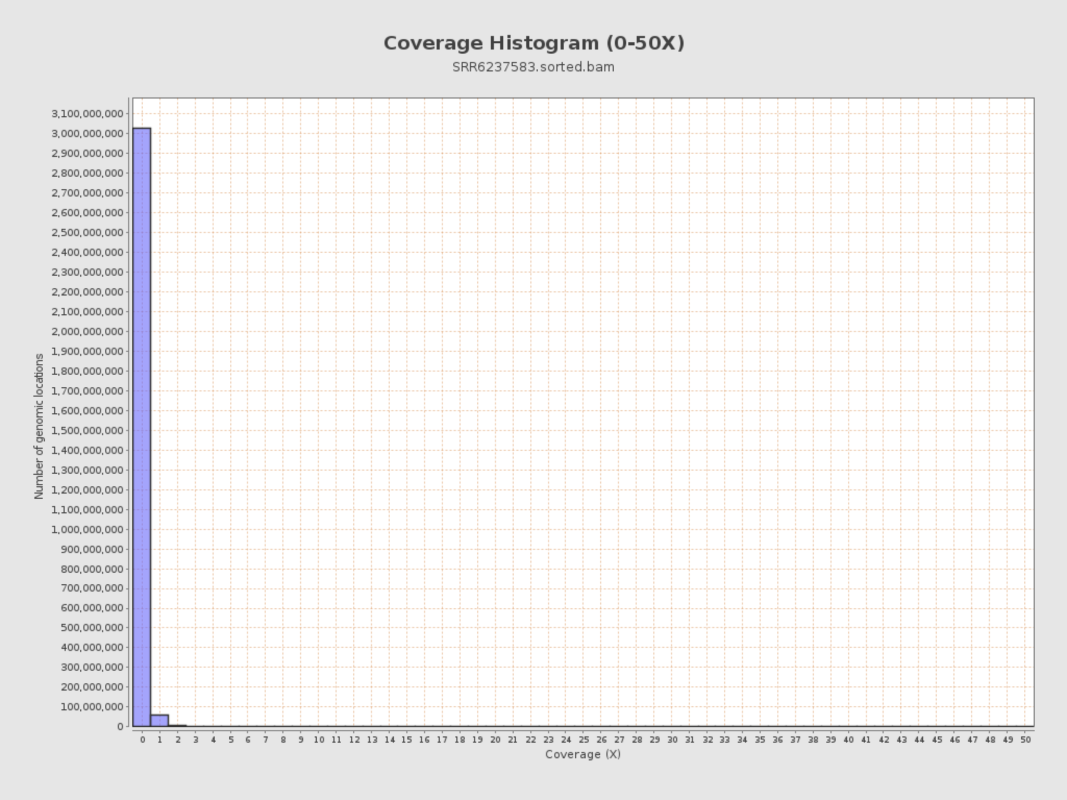
3. Results : Coverage across reference



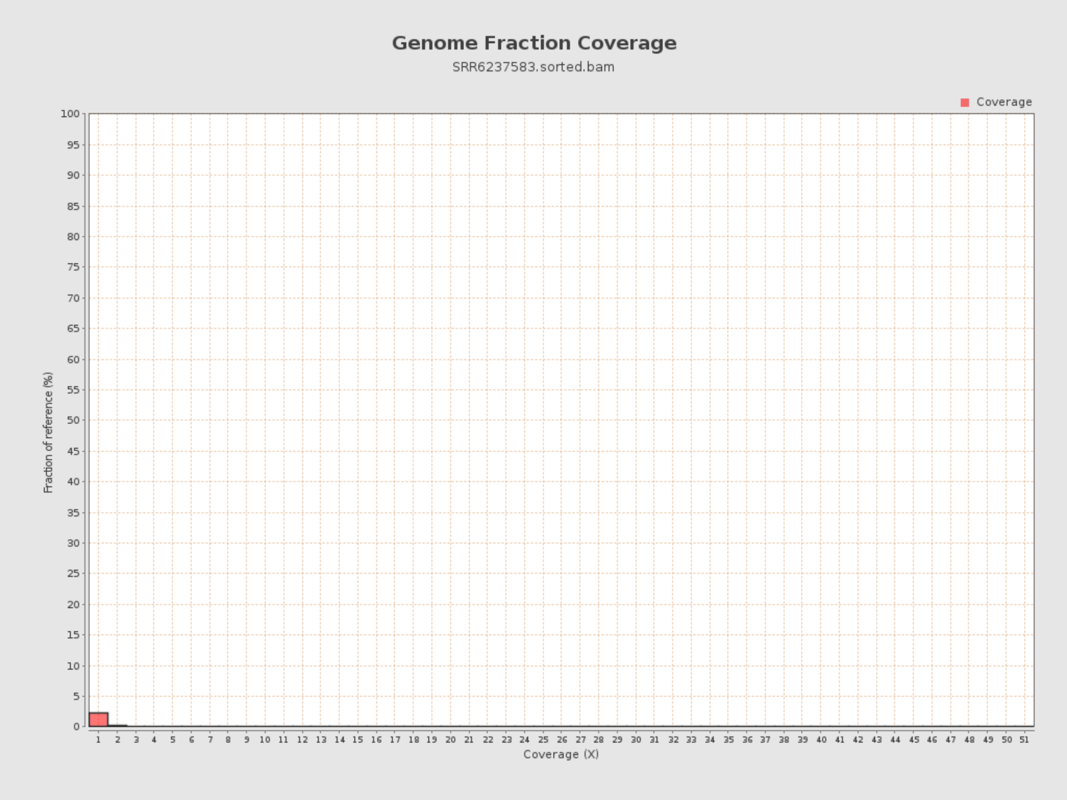
4. Results : Coverage Histogram



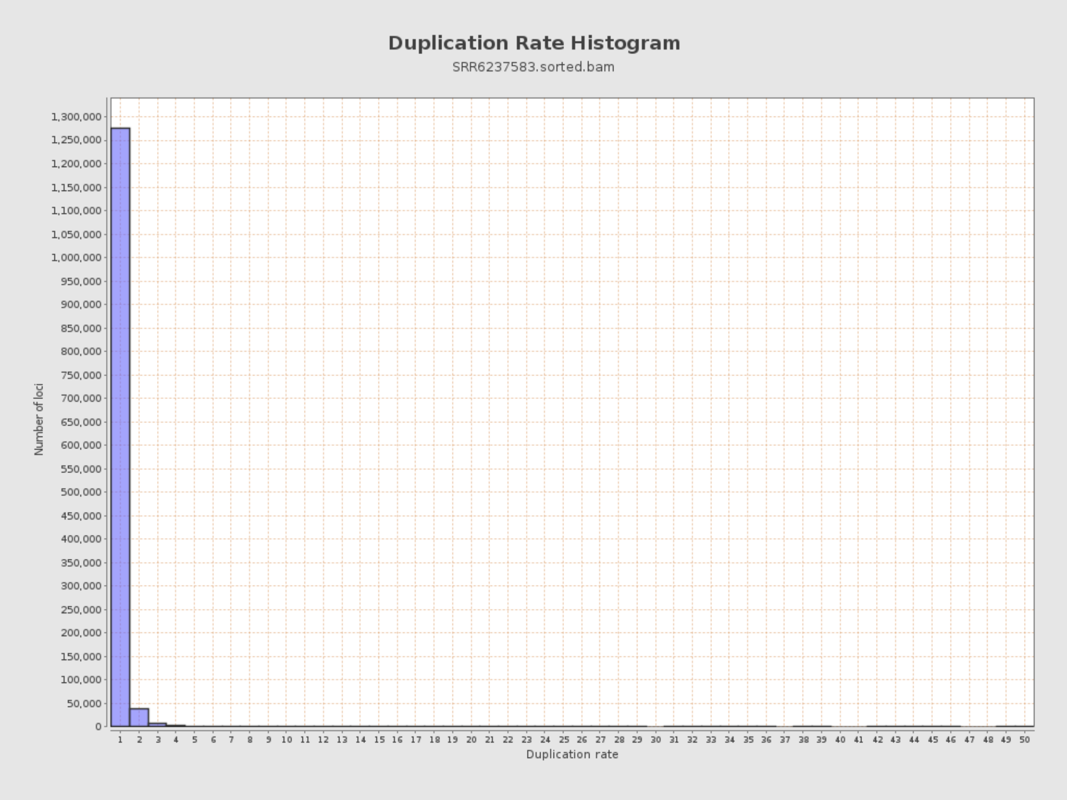
5. Results : Coverage Histogram (0-50X)



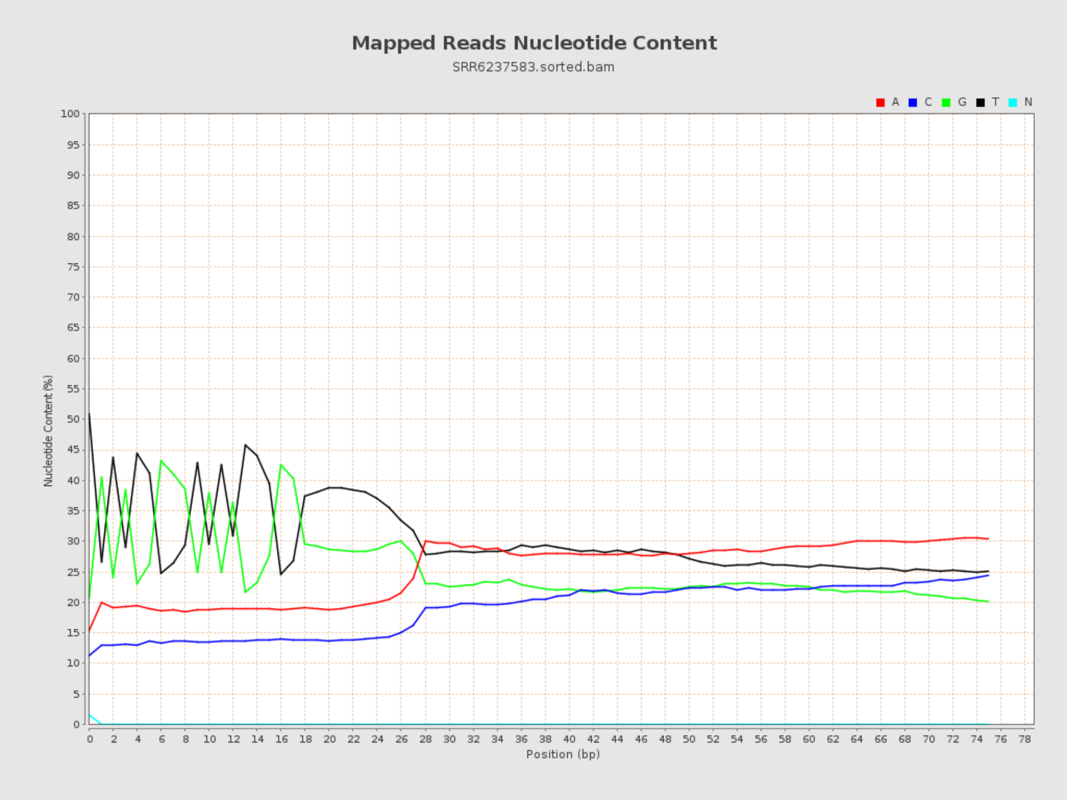
6. Results : Genome Fraction Coverage



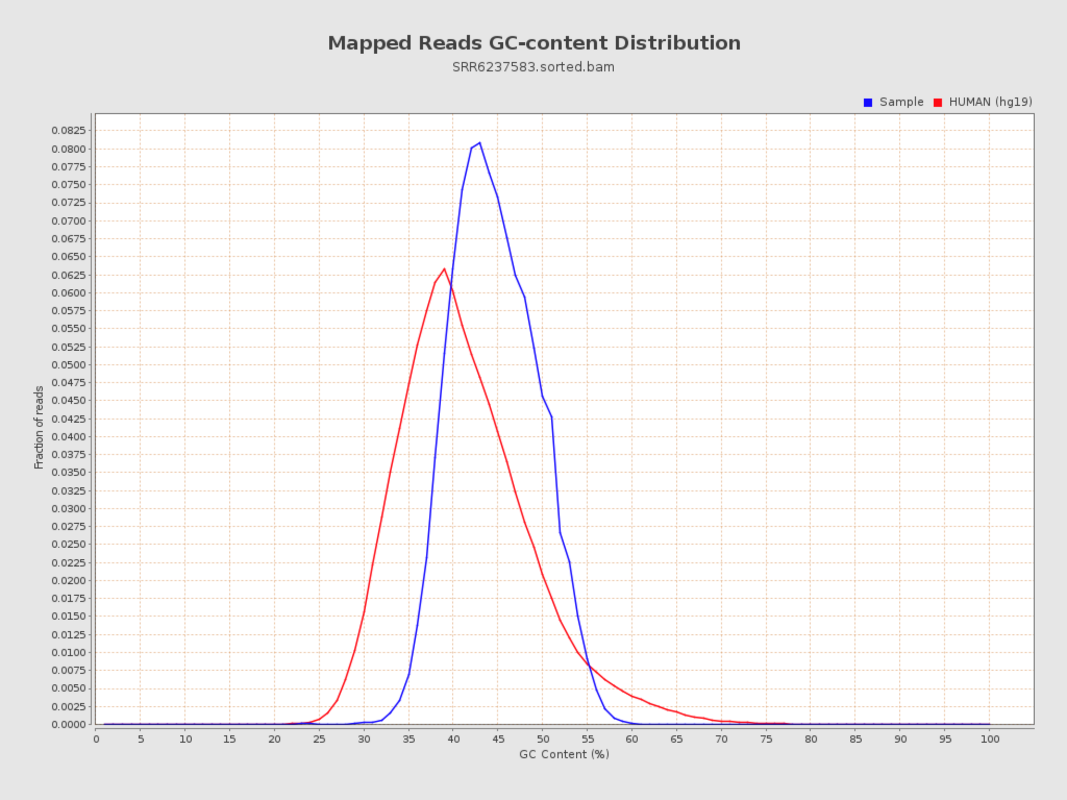
7. Results : Duplication Rate Histogram



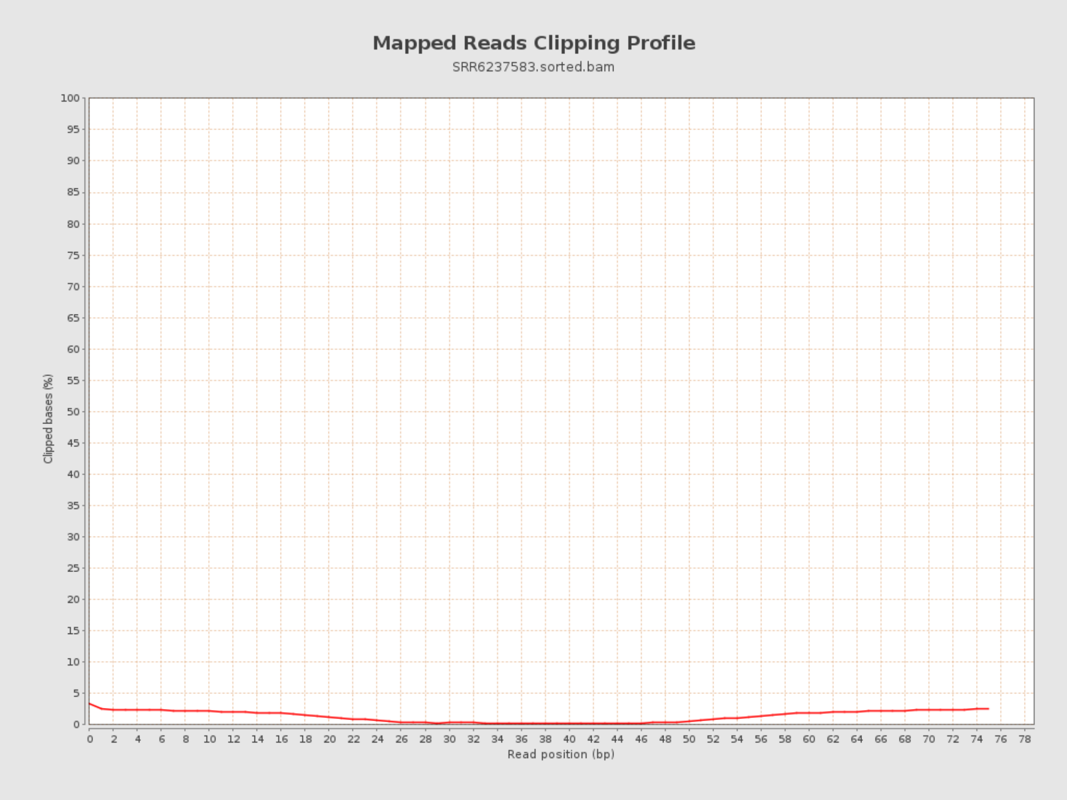
8. Results : Mapped Reads Nucleotide Content



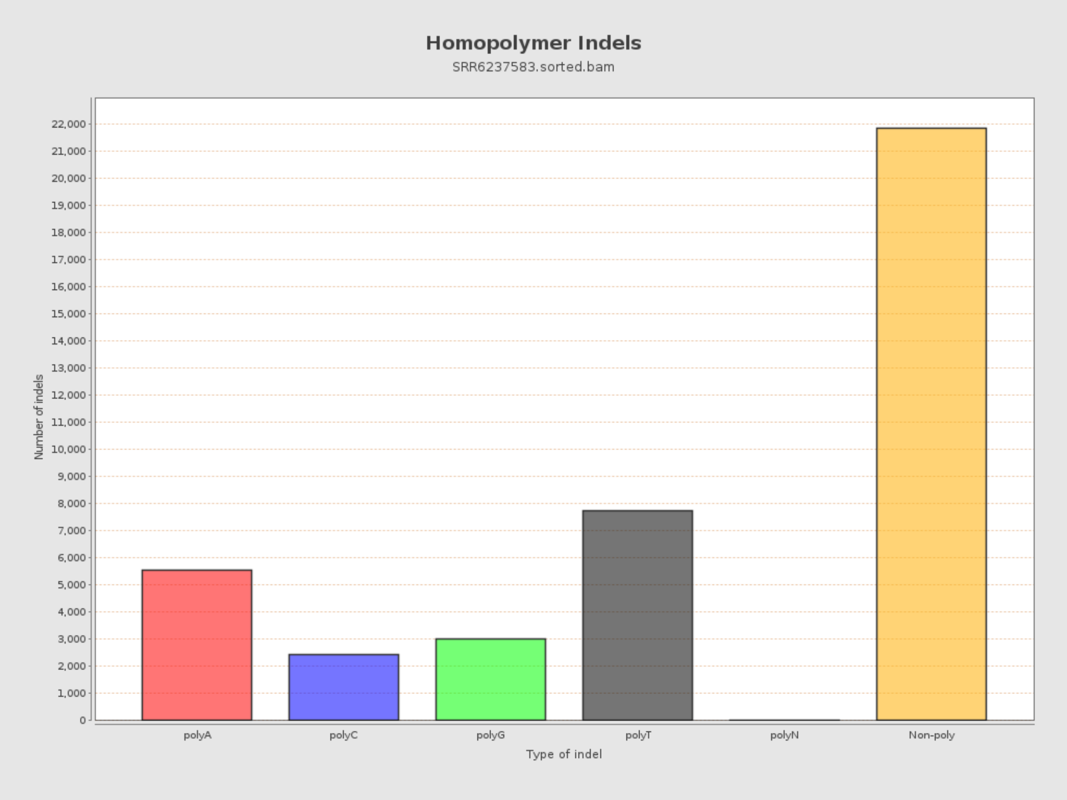
9. Results : Mapped Reads GC-content Distribution



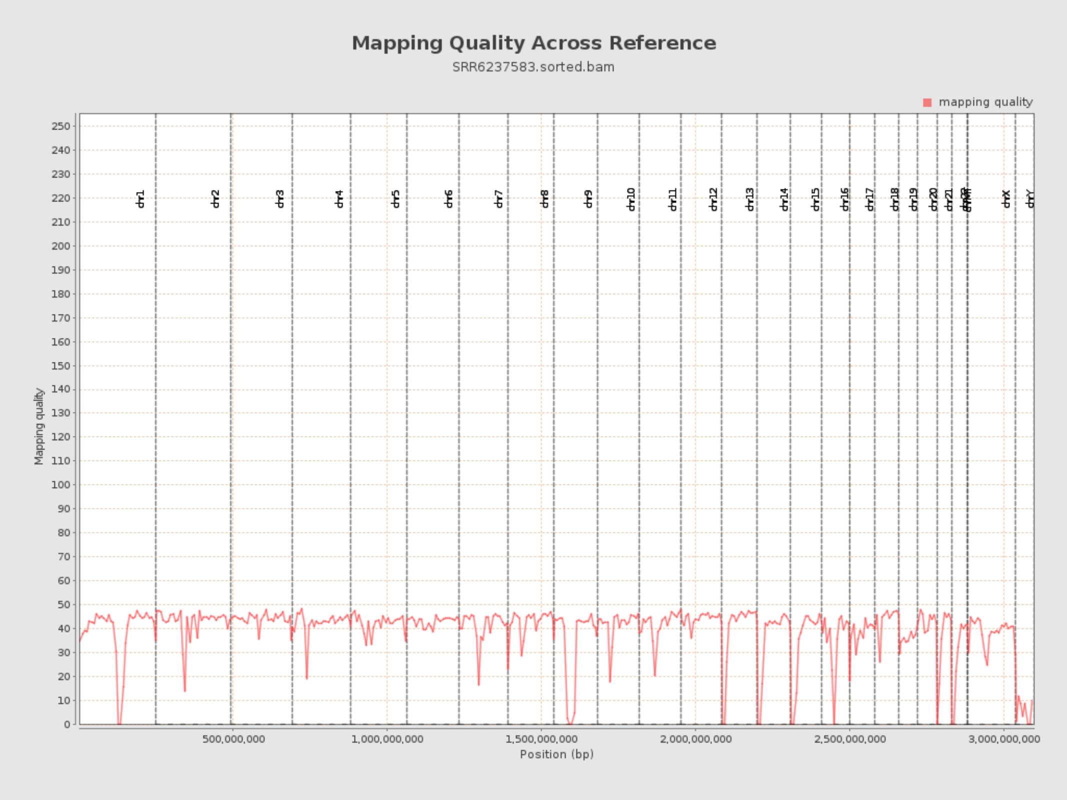
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram