Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 00:06:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237282.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_SRR6237282 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237282.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 00:06:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237282.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,056,714
Mapped reads	236,770 / 7.75%
Unmapped reads	2,819,944 / 92.25%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,427 / 0.08%
Read min/max/mean length	30 / 76 / 76.03
Duplicated reads (estimated)	32,362 / 1.06%
Duplication rate	7.09%
Clipped reads	183,543 / 6%

2.2. ACGT Content

Number/percentage of A's	3,498,555 / 28.67%
Number/percentage of C's	2,120,434 / 17.38%
Number/percentage of T's	3,977,776 / 32.6%
Number/percentage of G's	2,606,747 / 21.36%
Number/percentage of N's	114 / 0%
GC Percentage	38.74%

2.3. Coverage

Mean	0.0039

Standard Deviation	0.1623

2.4. Mapping Quality

Mean Mapping Quality	29.98

2.5. Mismatches and indels

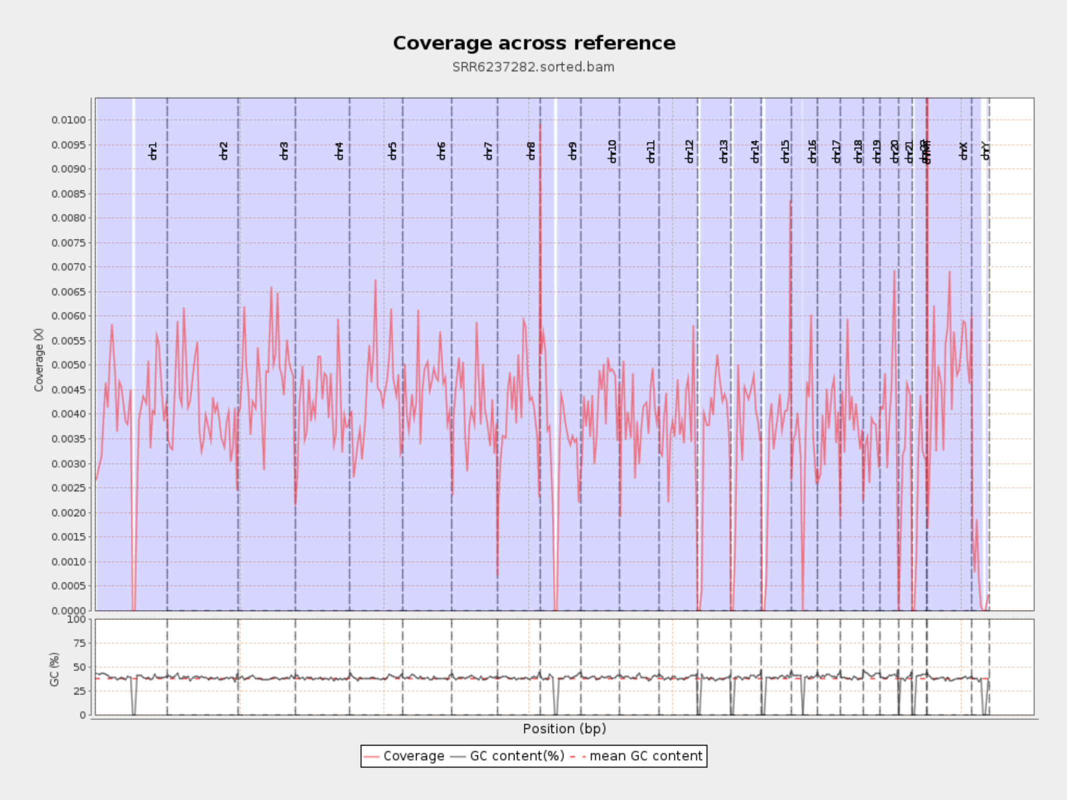
General error rate	1.97%
Mismatches	231,999
Insertions	4,490
Mapped reads with at least one insertion	1.83%
Deletions	5,763
Mapped reads with at least one deletion	2.35%
Homopolymer indels	38.5%

2.6. Chromosome stats

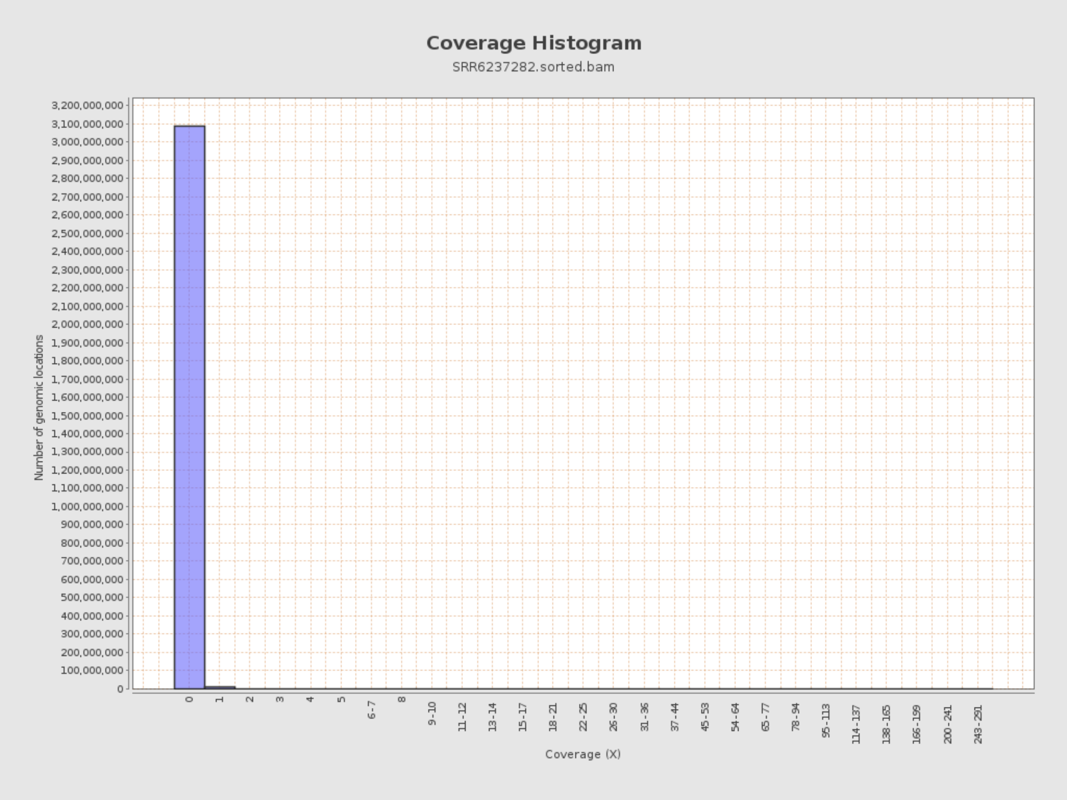
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	978281	0.0039	0.1651
chr2	243199373	993392	0.0041	0.1932
chr3	198022430	952579	0.0048	0.1452
chr4	191154276	794940	0.0042	0.1419
chr5	180915260	795303	0.0044	0.1921
chr6	171115067	769733	0.0045	0.1257
chr7	159138663	655772	0.0041	0.2065

chr8	146364022	608194	0.0042	0.112
chr9	141213431	481291	0.0034	0.1097
chr10	135534747	571676	0.0042	0.1201
chr11	135006516	533477	0.004	0.1434
chr12	133851895	507973	0.0038	0.1651
chr13	115169878	406441	0.0035	0.1041
chr14	107349540	367831	0.0034	0.1231
chr15	102531392	336135	0.0033	0.1948
chr16	90354753	310466	0.0034	0.0803
chr17	81195210	295723	0.0036	0.1382
chr18	78077248	317733	0.0041	0.1684
chr19	59128983	200016	0.0034	0.0949
chr20	63025520	267201	0.0042	0.2623
chr21	48129895	145141	0.003	0.1251
chr22	51304566	120343	0.0023	0.164
chrMT	16571	11814	0.7129	0.9934
chrX	155270560	755960	0.0049	0.2708
chrY	59373566	36666	0.0006	0.0364

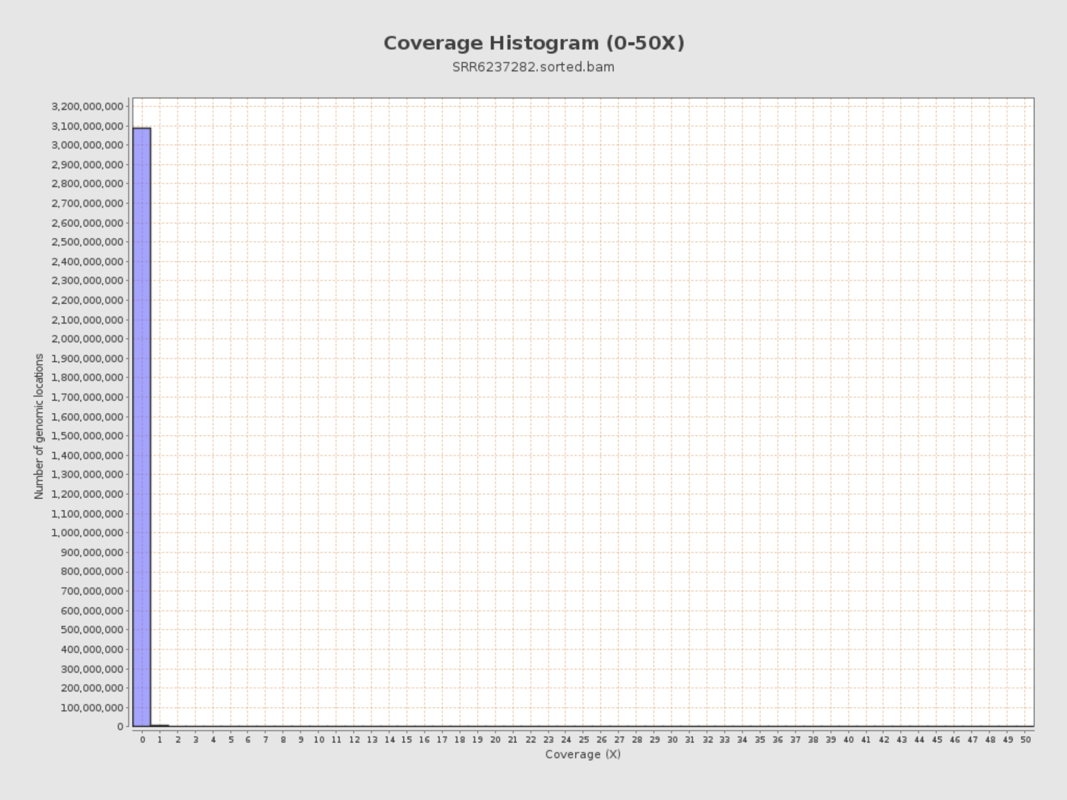
3. Results : Coverage across reference



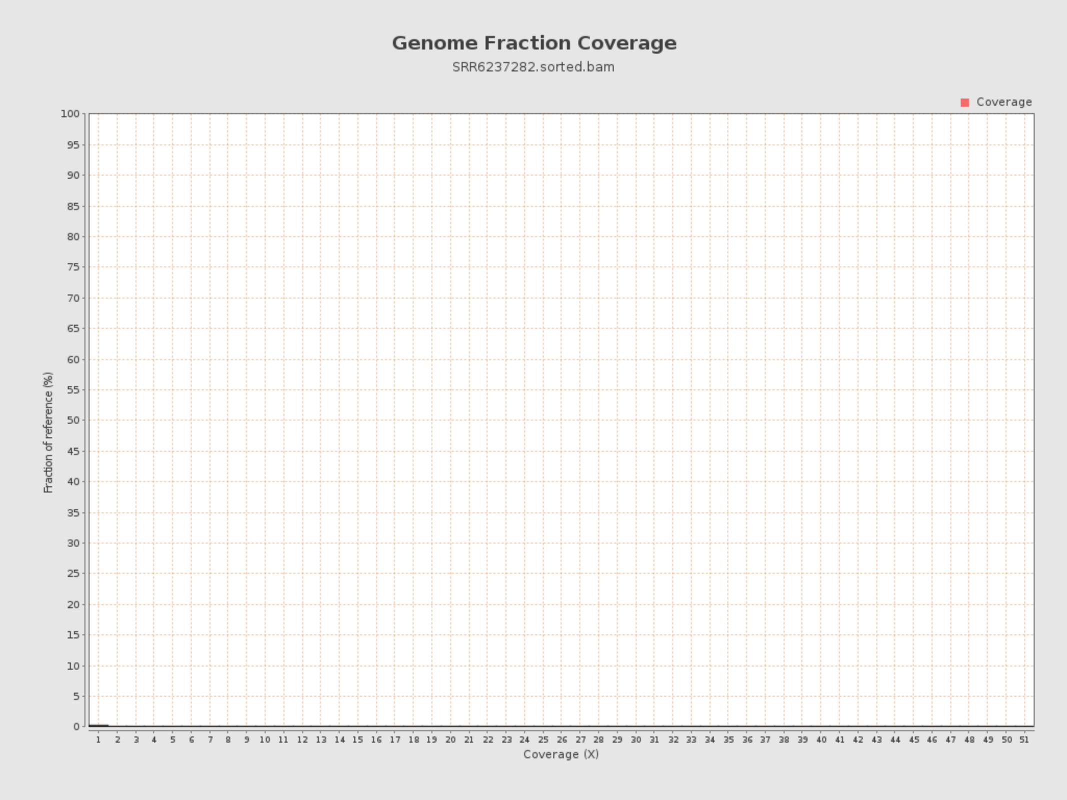
4. Results : Coverage Histogram



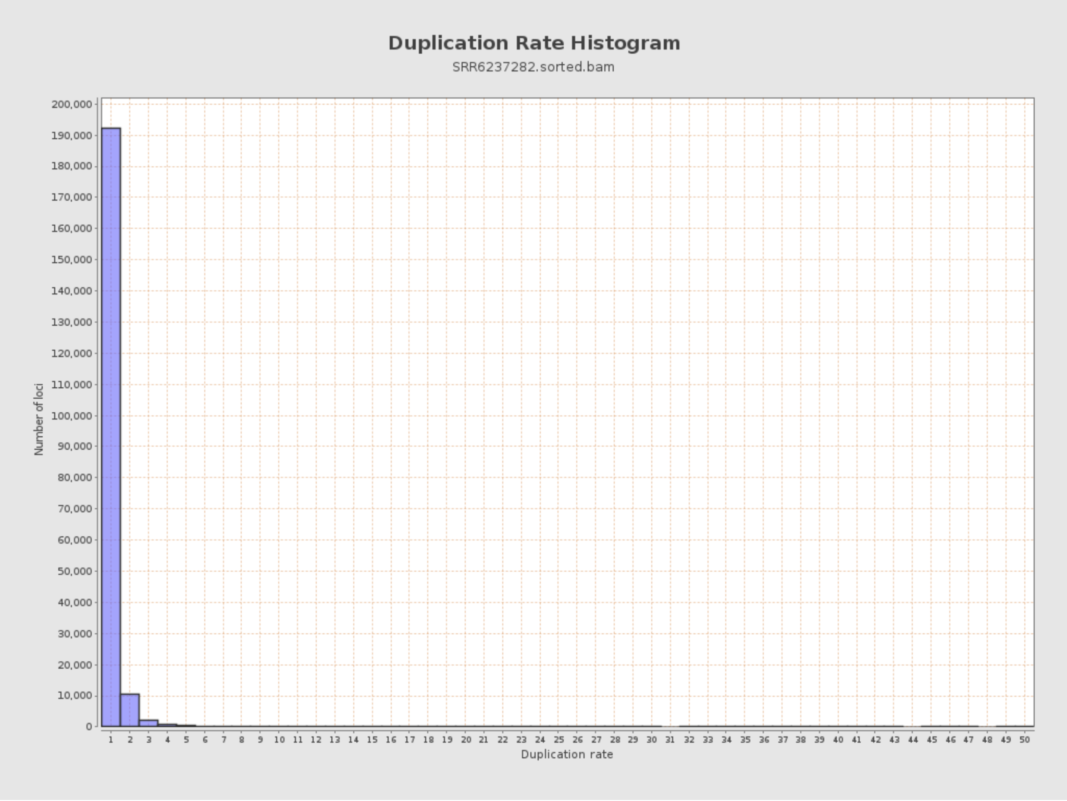
5. Results : Coverage Histogram (0-50X)



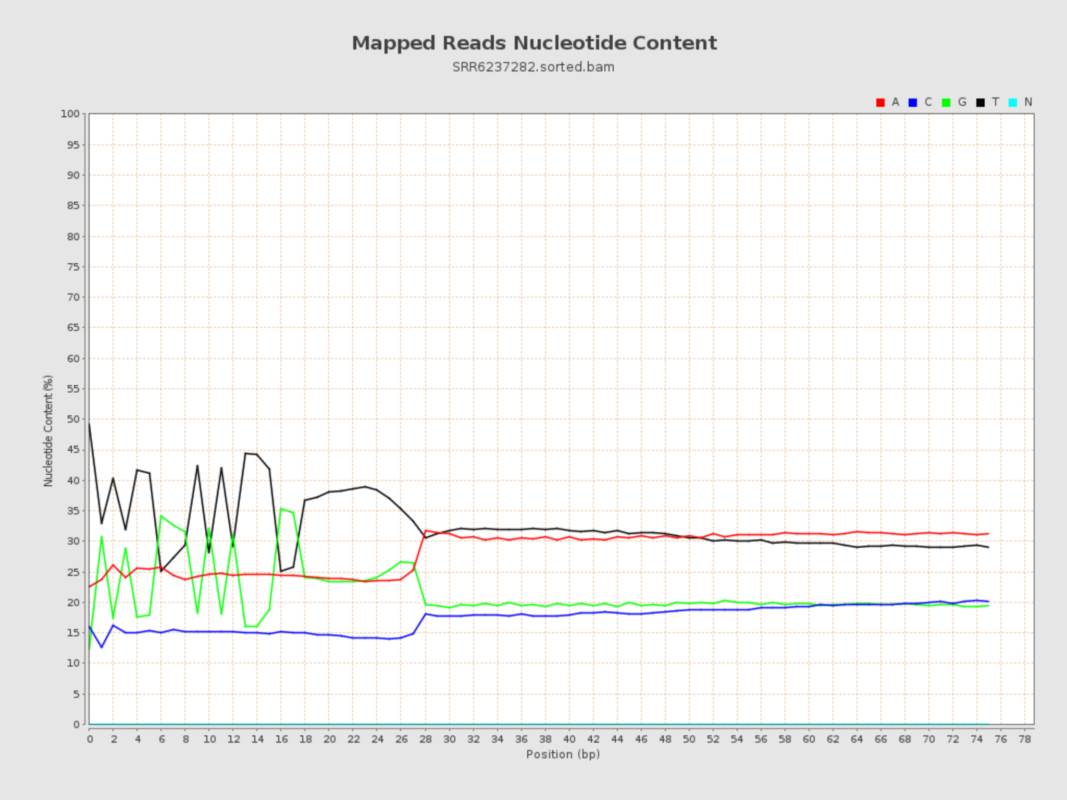
6. Results : Genome Fraction Coverage



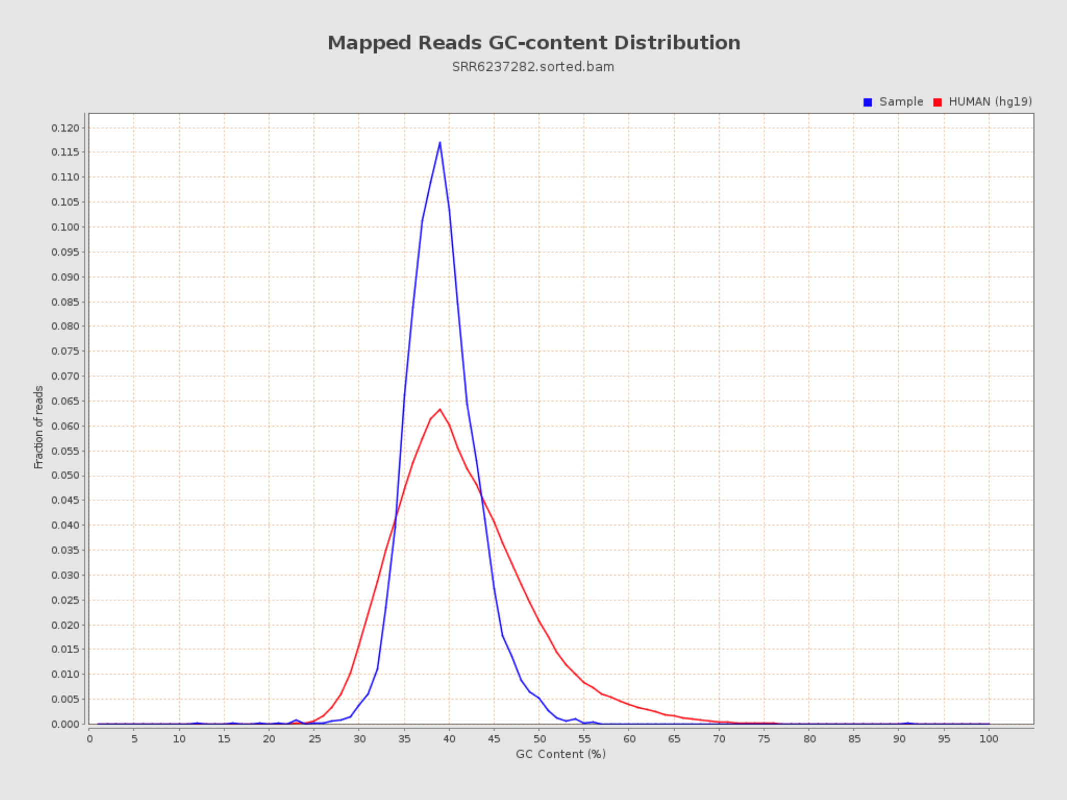
7. Results : Duplication Rate Histogram



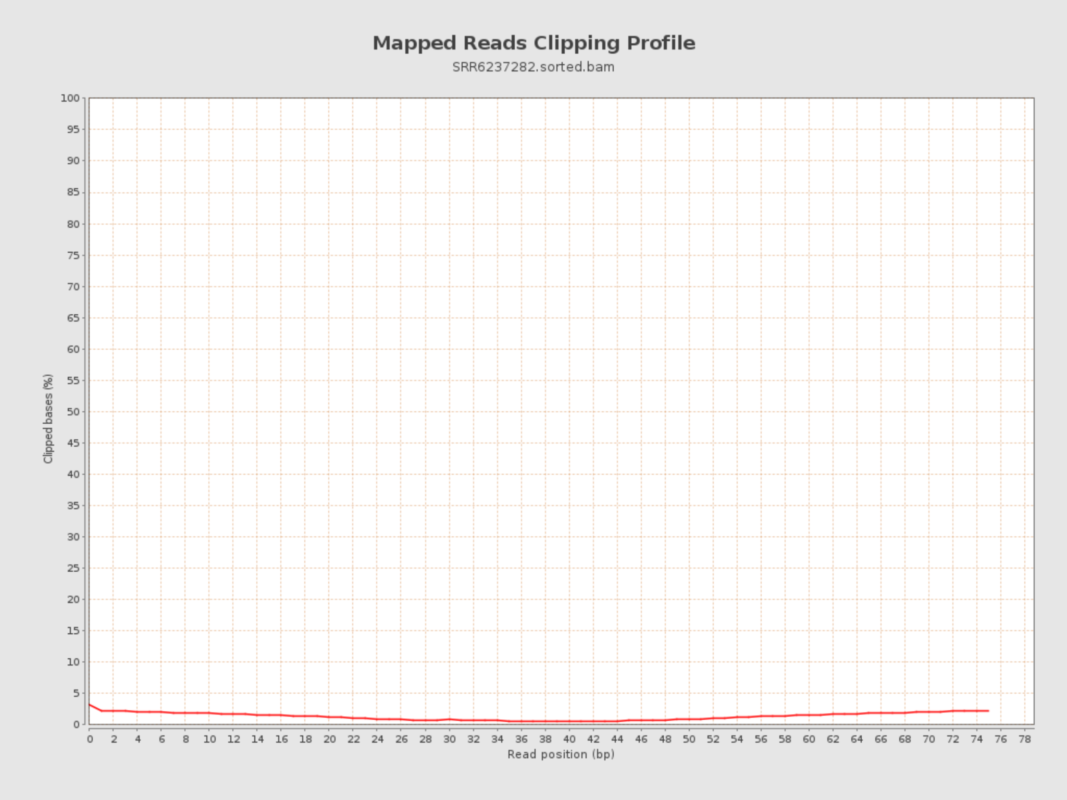
8. Results : Mapped Reads Nucleotide Content



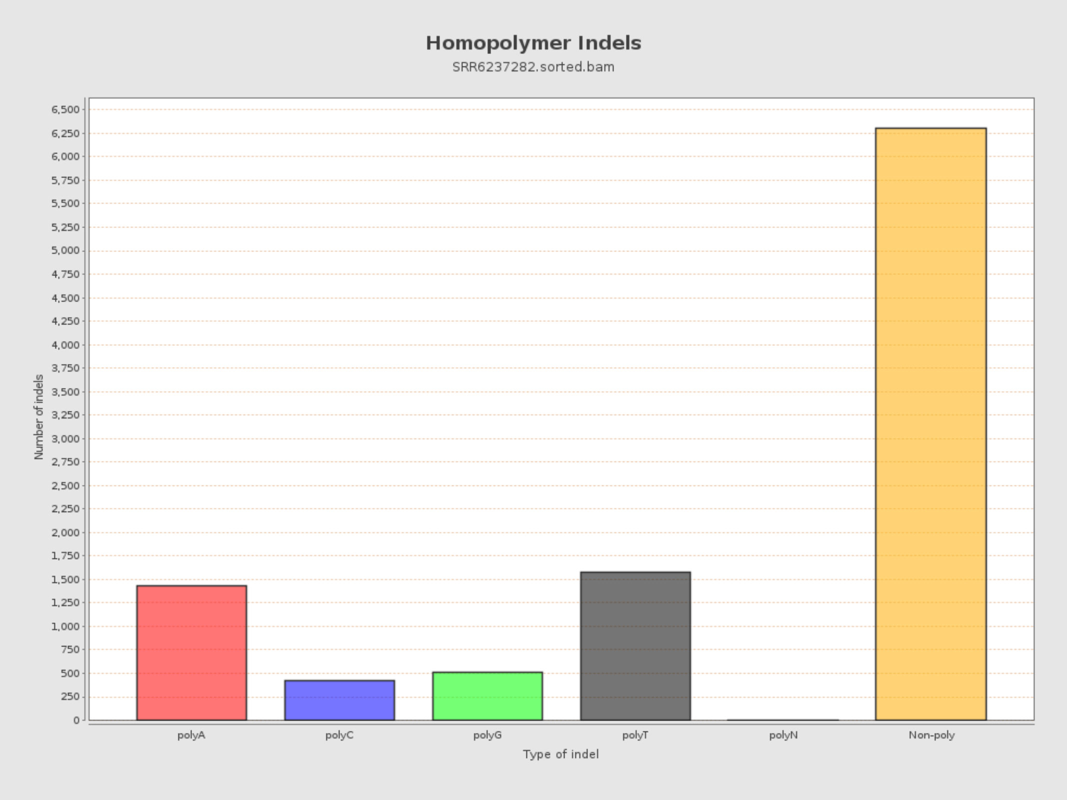
9. Results : Mapped Reads GC-content Distribution



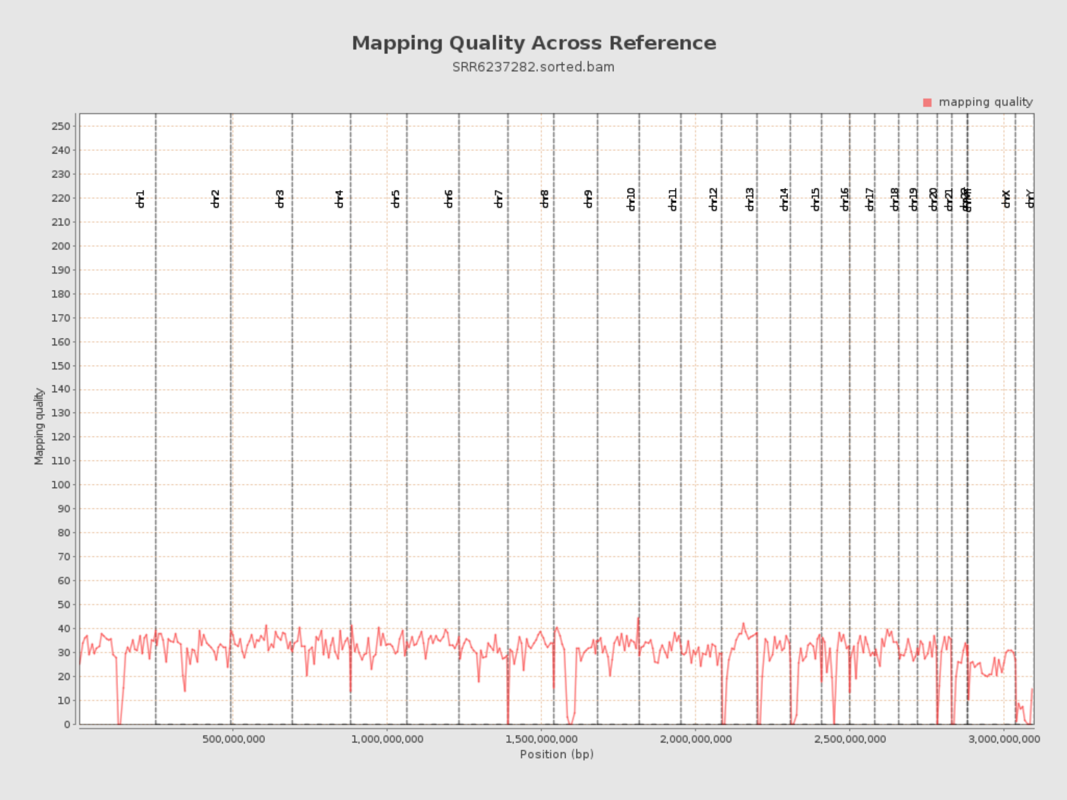
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram