Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 03:35:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237569.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_SRR6237569 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237569.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 03:35:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237569.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,997,286
Mapped reads	1,563,092 / 78.26%
Unmapped reads	434,194 / 21.74%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,882 / 0.64%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	121,977 / 6.11%
Duplication rate	6.51%
Clipped reads	922,156 / 46.17%

2.2. ACGT Content

Number/percentage of A's	26,814,513 / 27.27%
Number/percentage of C's	17,048,125 / 17.34%
Number/percentage of T's	32,003,367 / 32.55%
Number/percentage of G's	22,285,788 / 22.66%
Number/percentage of N's	180,642 / 0.18%
GC Percentage	40%

2.3. Coverage

Mean	0.0318

Standard Deviation	0.3157

2.4. Mapping Quality

Mean Mapping Quality	46.27

2.5. Mismatches and indels

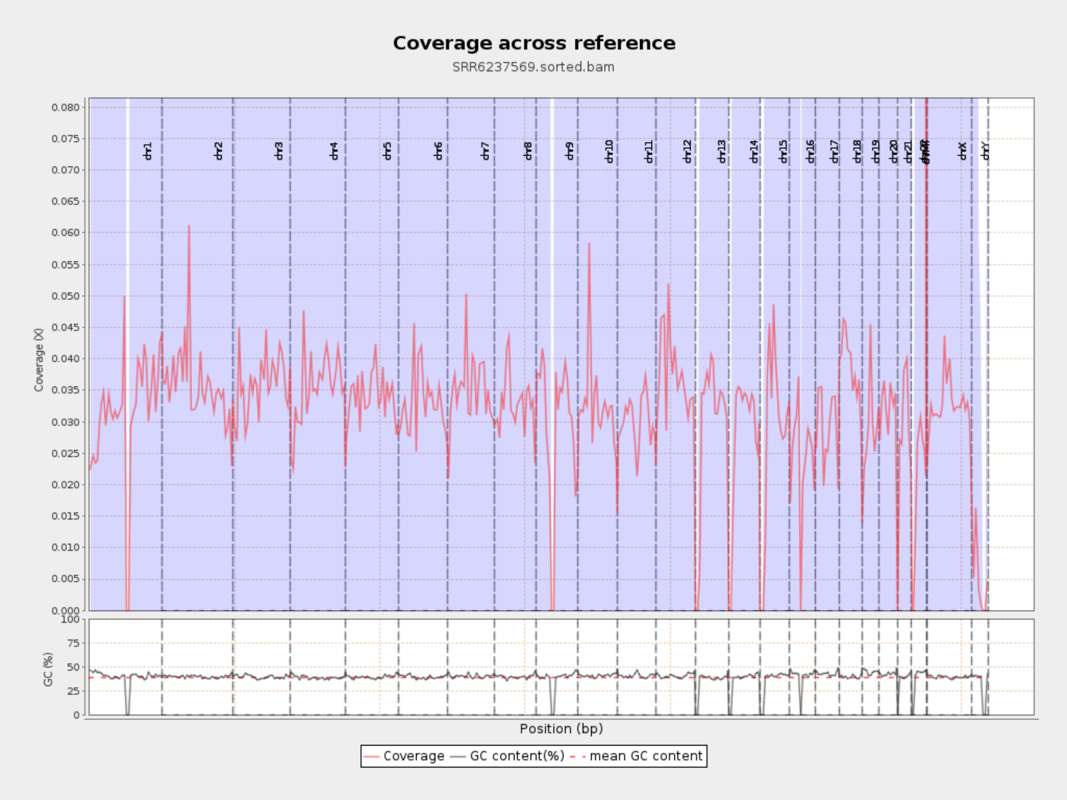
General error rate	0.95%
Mismatches	914,500
Insertions	8,213
Mapped reads with at least one insertion	0.52%
Deletions	33,888
Mapped reads with at least one deletion	2.14%
Homopolymer indels	48.15%

2.6. Chromosome stats

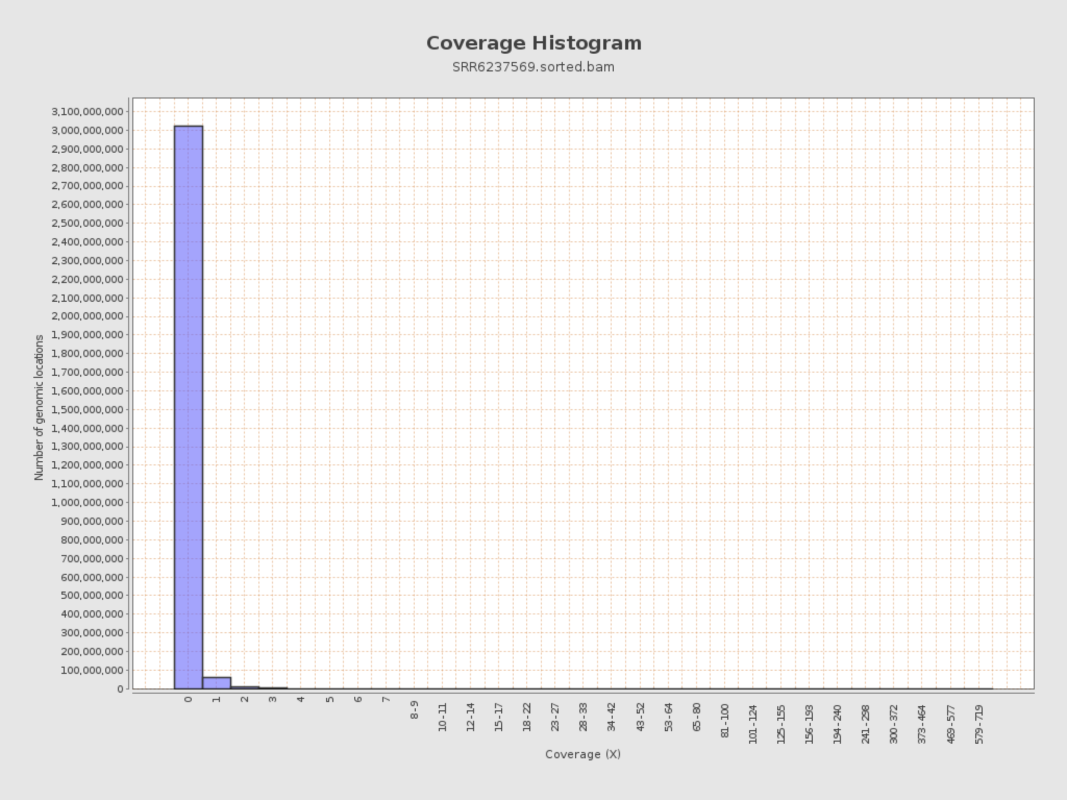
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7814146	0.0314	0.5009
chr2	243199373	8743106	0.036	0.3695
chr3	198022430	7105828	0.0359	0.2386
chr4	191154276	6767930	0.0354	0.2476
chr5	180915260	6154087	0.034	0.2304
chr6	171115067	5647311	0.033	0.2616
chr7	159138663	5619568	0.0353	0.3584

chr8	146364022	4788515	0.0327	0.4788
chr9	141213431	4143944	0.0293	0.3004
chr10	135534747	4448474	0.0328	0.323
chr11	135006516	4039696	0.0299	0.2777
chr12	133851895	4980847	0.0372	0.245
chr13	115169878	3320983	0.0288	0.213
chr14	107349540	2923827	0.0272	0.223
chr15	102531392	2890209	0.0282	0.2097
chr16	90354753	2179866	0.0241	0.2103
chr17	81195210	2324827	0.0286	0.2329
chr18	78077248	3046033	0.039	0.5215
chr19	59128983	1722508	0.0291	0.3384
chr20	63025520	2011791	0.0319	0.2285
chr21	48129895	1338331	0.0278	0.2212
chr22	51304566	979315	0.0191	0.1677
chrMT	16571	53836	3.2488	2.9068
chrX	155270560	5055660	0.0326	0.2445
chrY	59373566	286230	0.0048	0.1276

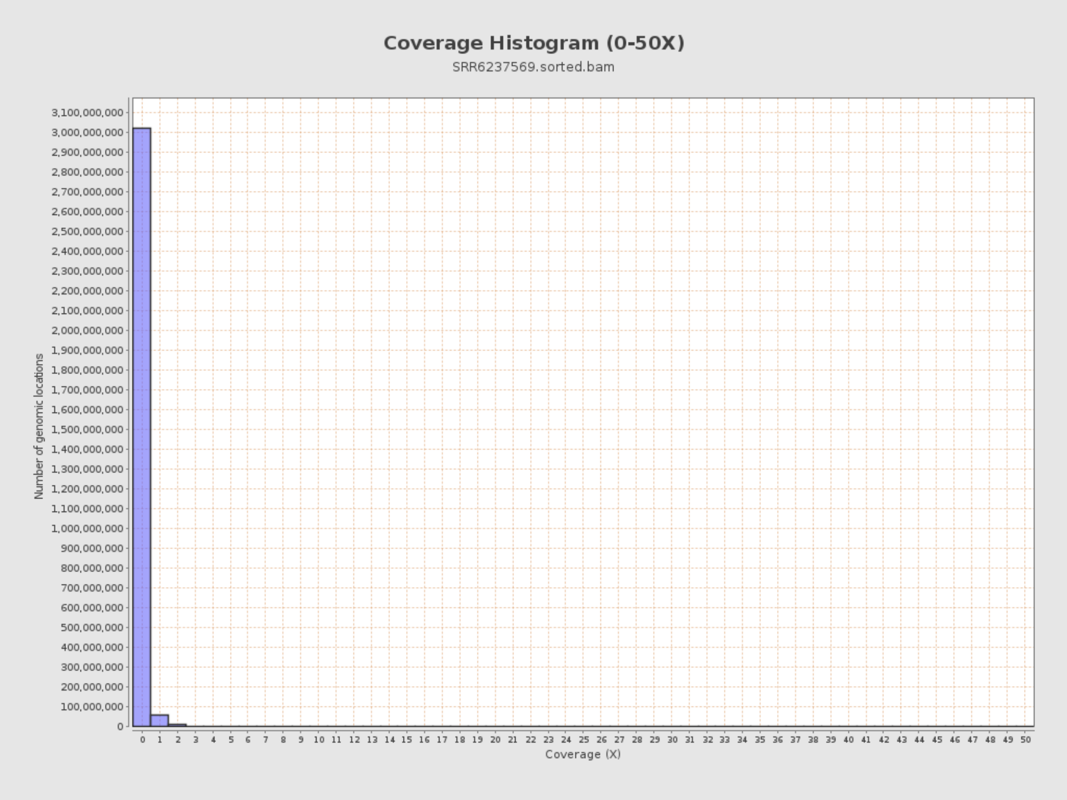
3. Results : Coverage across reference



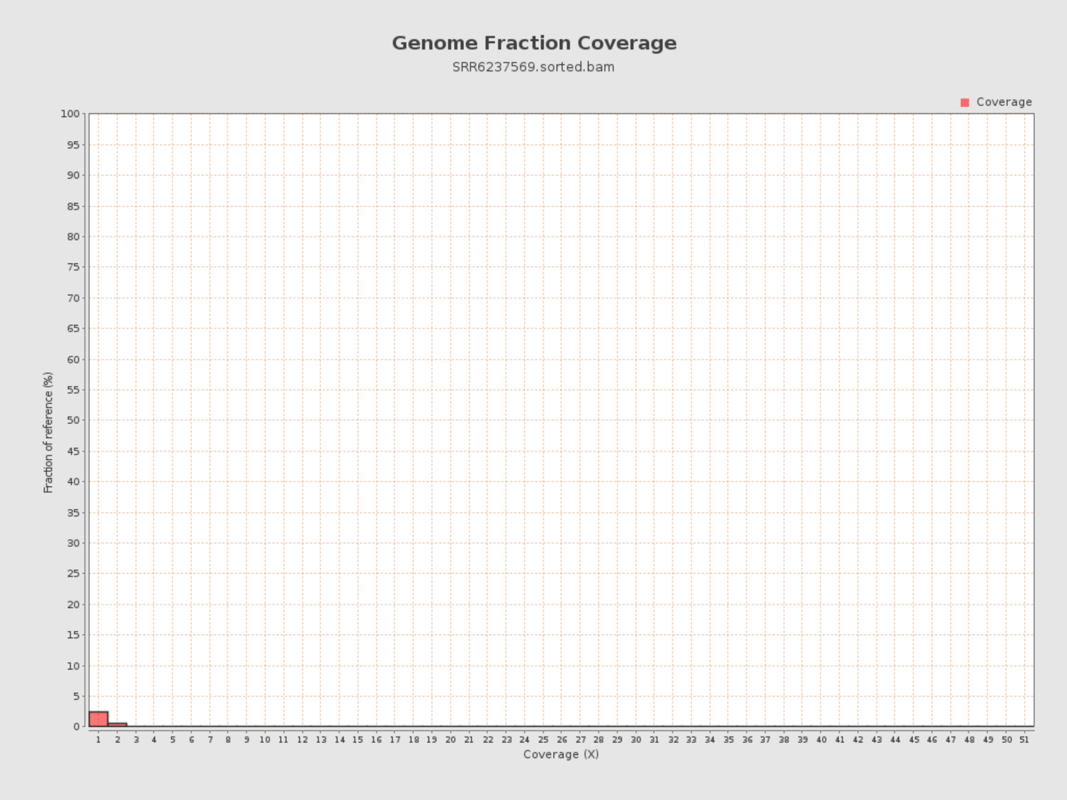
4. Results : Coverage Histogram



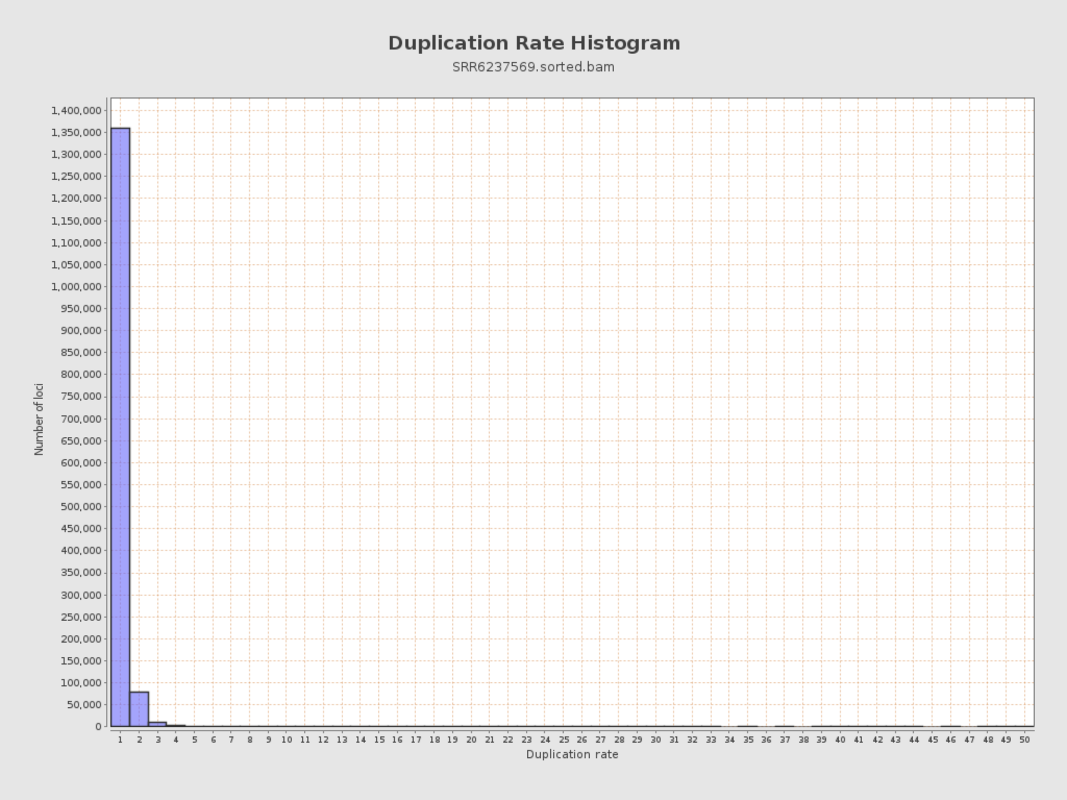
5. Results : Coverage Histogram (0-50X)



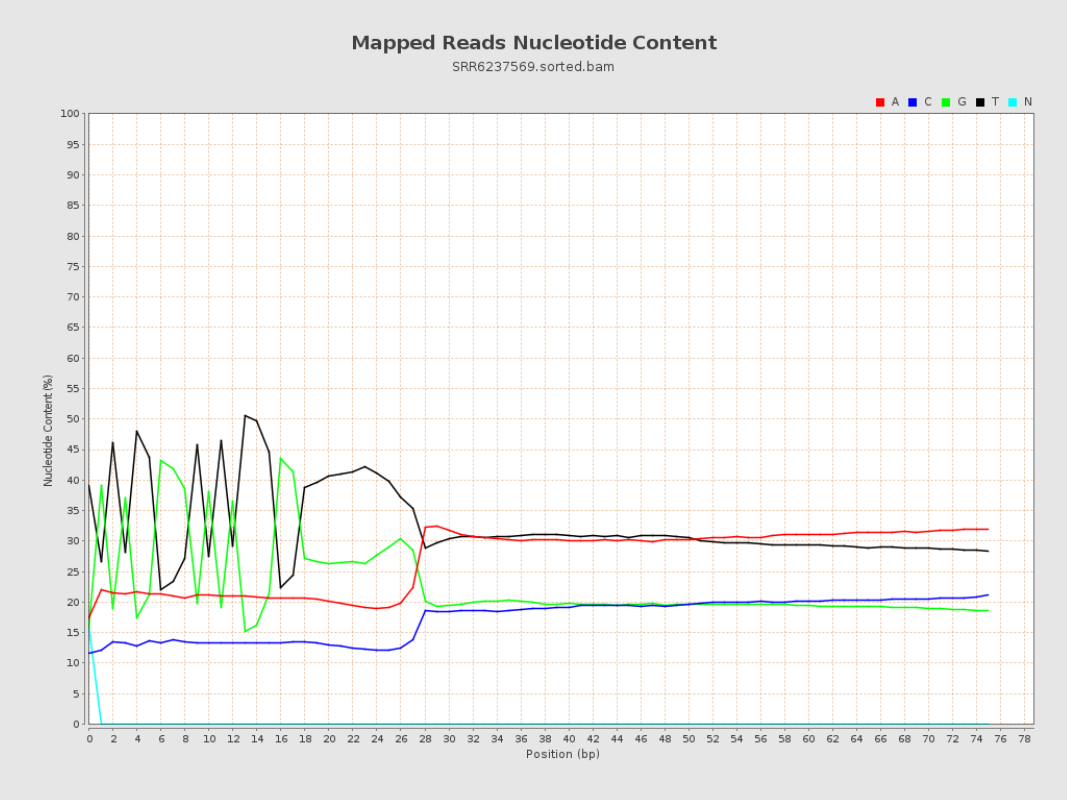
6. Results : Genome Fraction Coverage



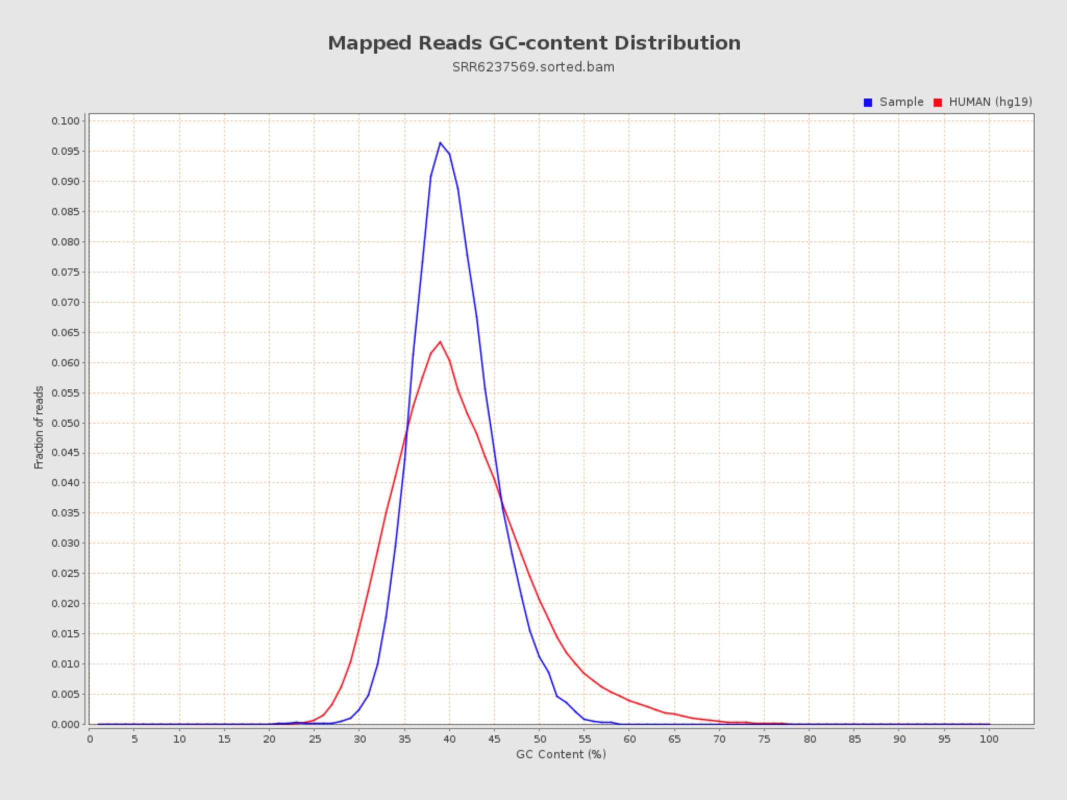
7. Results : Duplication Rate Histogram



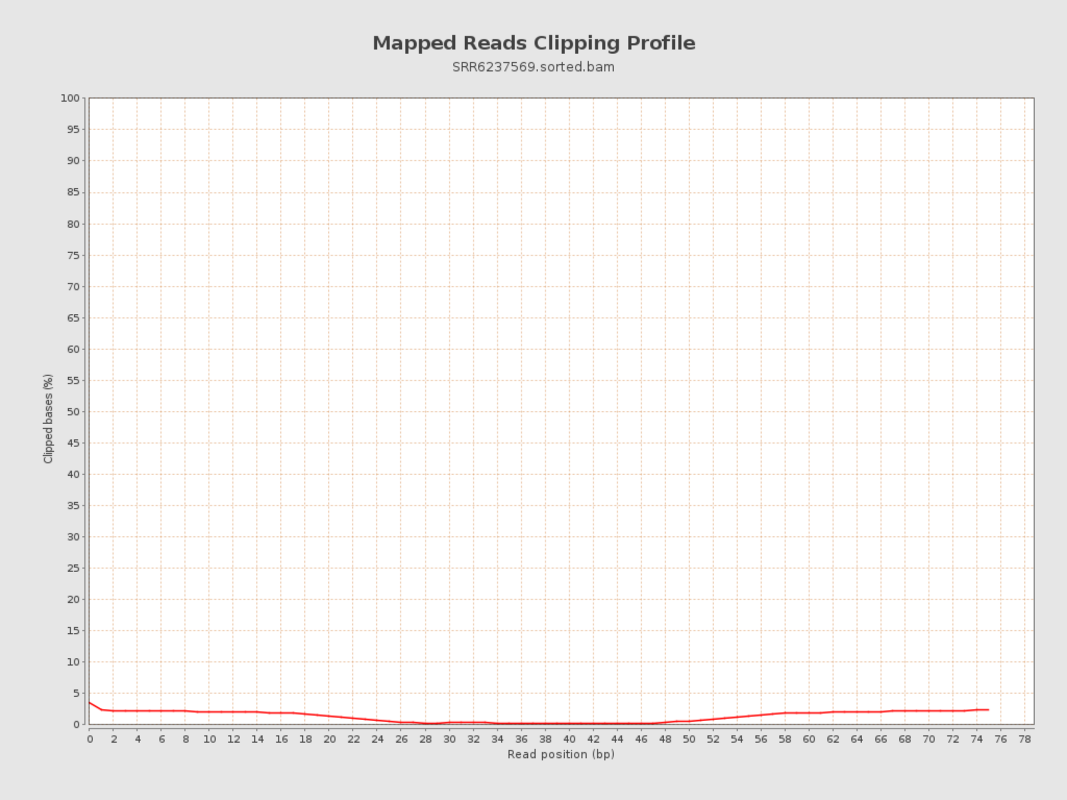
8. Results : Mapped Reads Nucleotide Content



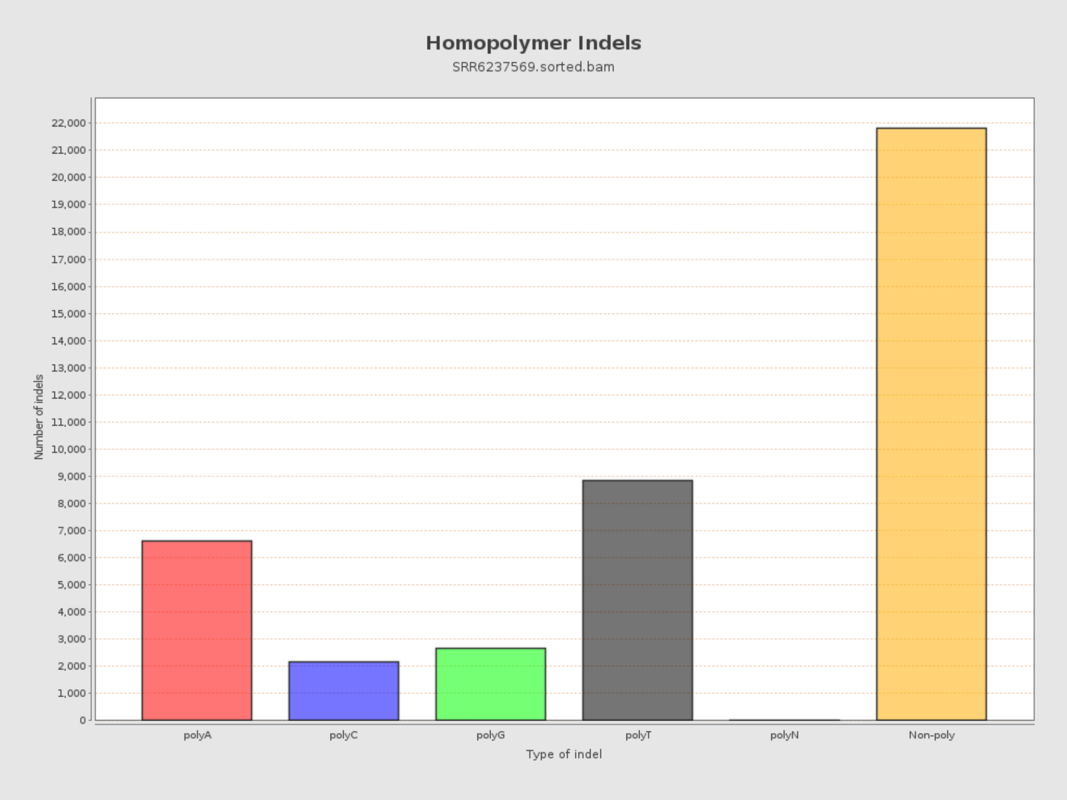
9. Results : Mapped Reads GC-content Distribution



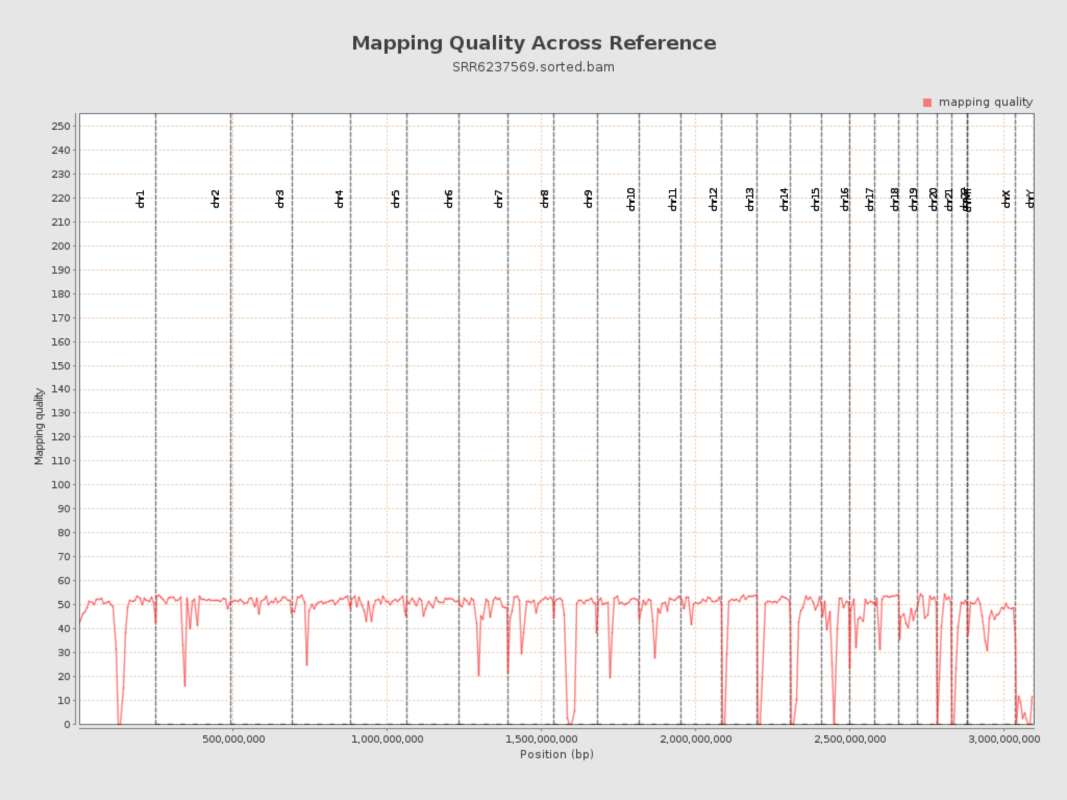
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram