Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 09:18:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237857.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_SRR6237857 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237857.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 09:18:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237857.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,083,478
Mapped reads	2,714,069 / 88.02%
Unmapped reads	369,409 / 11.98%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,935 / 0.65%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	125,240 / 4.06%
Duplication rate	3.15%
Clipped reads	574,378 / 18.63%

2.2. ACGT Content

Number/percentage of A's	59,733,144 / 30.19%
Number/percentage of C's	39,658,519 / 20.05%
Number/percentage of T's	58,406,985 / 29.52%
Number/percentage of G's	39,696,003 / 20.06%
Number/percentage of N's	343,135 / 0.17%
GC Percentage	40.11%

2.3. Coverage

Mean	0.0639

Standard Deviation	0.7337

2.4. Mapping Quality

Mean Mapping Quality	48.5

2.5. Mismatches and indels

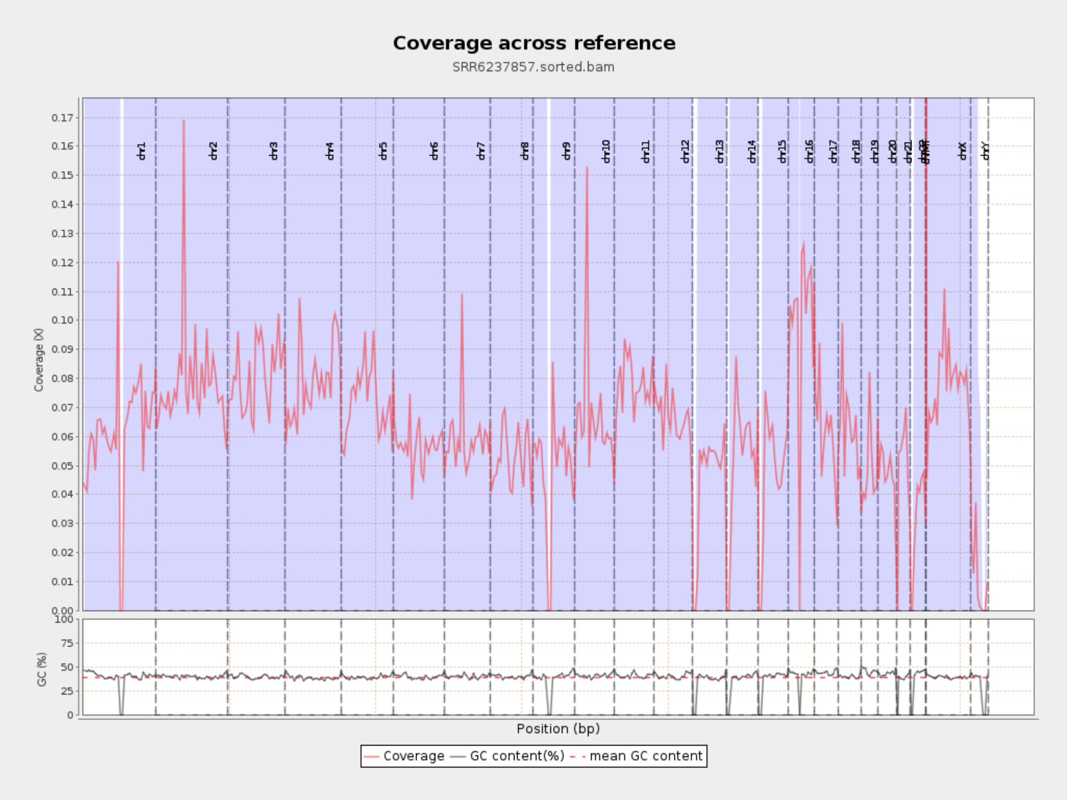
General error rate	0.89%
Mismatches	1,723,821
Insertions	15,553
Mapped reads with at least one insertion	0.57%
Deletions	49,006
Mapped reads with at least one deletion	1.78%
Homopolymer indels	46.94%

2.6. Chromosome stats

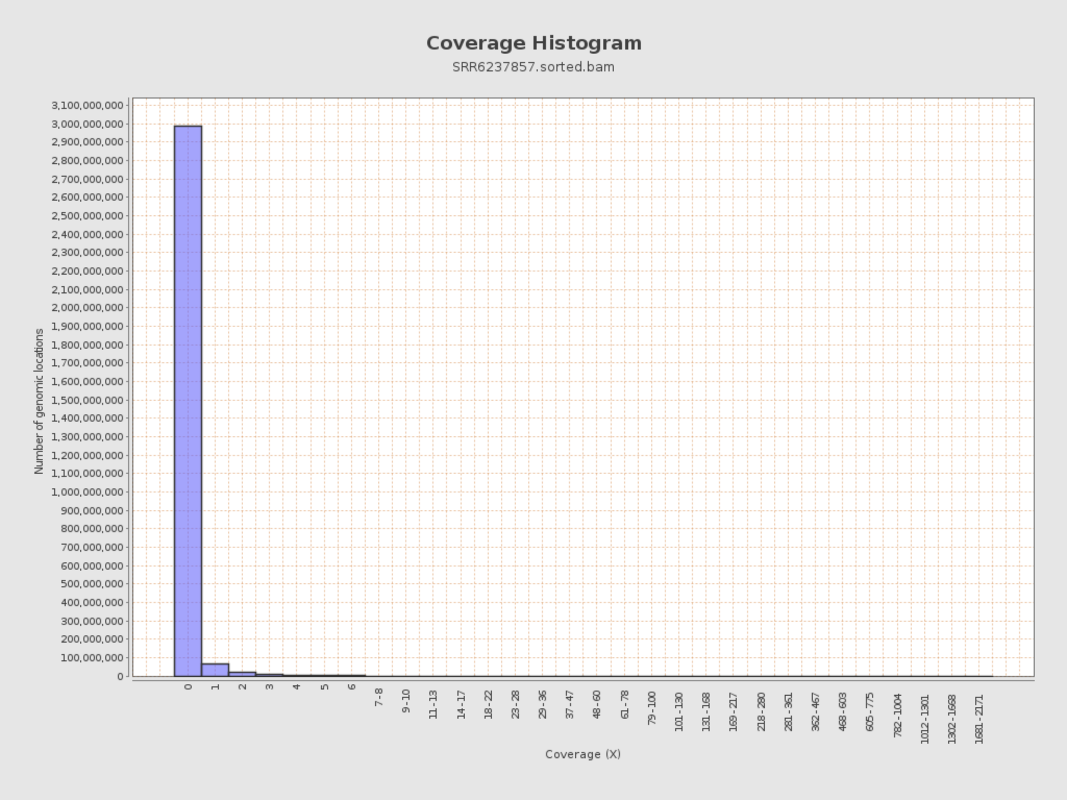
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15319366	0.0615	1.5751
chr2	243199373	19139095	0.0787	0.7579
chr3	198022430	16098104	0.0813	0.4843
chr4	191154276	15126770	0.0791	0.5113
chr5	180915260	13040321	0.0721	0.4469
chr6	171115067	9699050	0.0567	0.4276
chr7	159138663	9430305	0.0593	0.7597

chr8	146364022	7643101	0.0522	0.6291
chr9	141213431	6899990	0.0489	0.6489
chr10	135534747	9120822	0.0673	0.7977
chr11	135006516	10518325	0.0779	0.6848
chr12	133851895	8960482	0.0669	0.4353
chr13	115169878	5196232	0.0451	0.347
chr14	107349540	5618197	0.0523	0.4283
chr15	102531392	4717695	0.046	0.3535
chr16	90354753	8821466	0.0976	0.6081
chr17	81195210	5028120	0.0619	0.4839
chr18	78077248	4956692	0.0635	1.3193
chr19	59128983	2916184	0.0493	0.9758
chr20	63025520	3001357	0.0476	0.3932
chr21	48129895	2351060	0.0488	0.4157
chr22	51304566	1599836	0.0312	0.2845
chrMT	16571	77922	4.7023	3.6082
chrX	155270560	12022821	0.0774	0.5063
chrY	59373566	623770	0.0105	0.3178

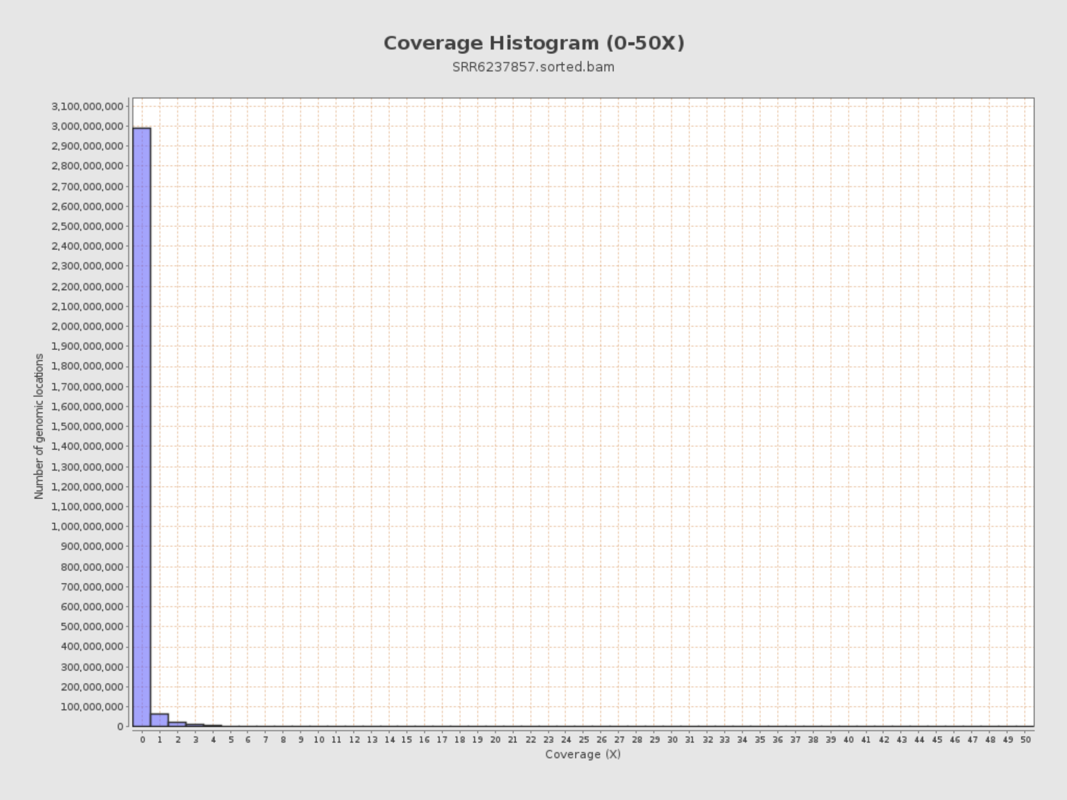
3. Results : Coverage across reference



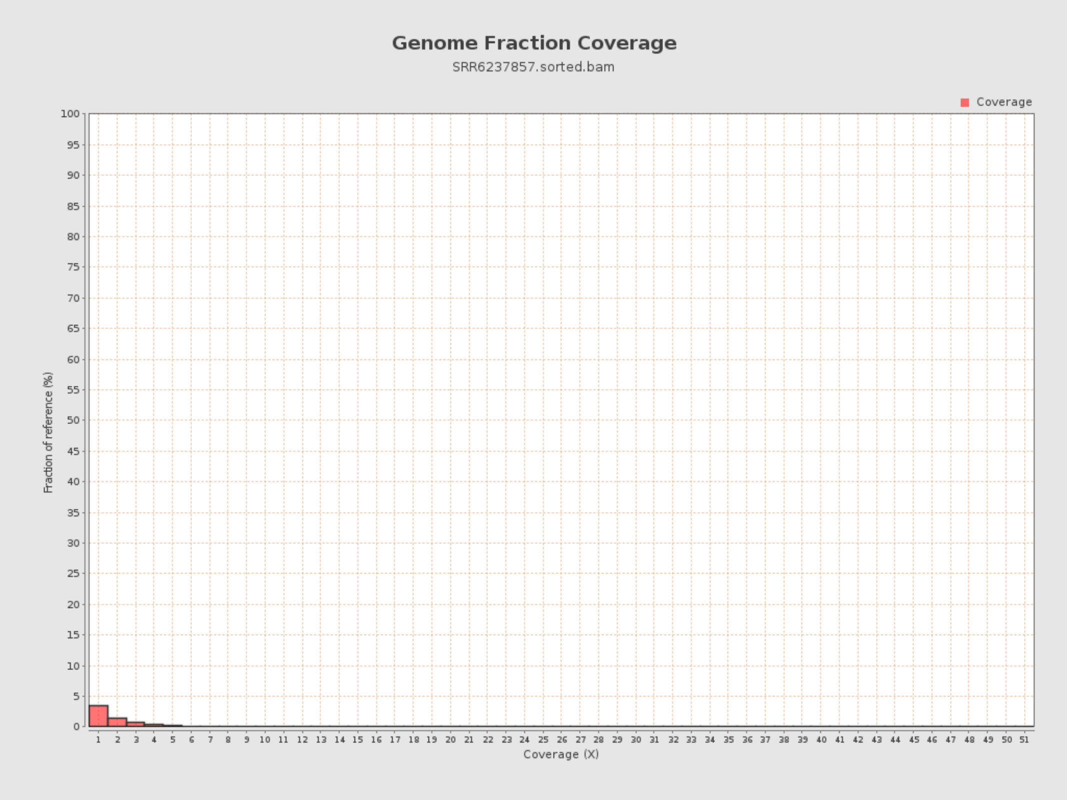
4. Results : Coverage Histogram



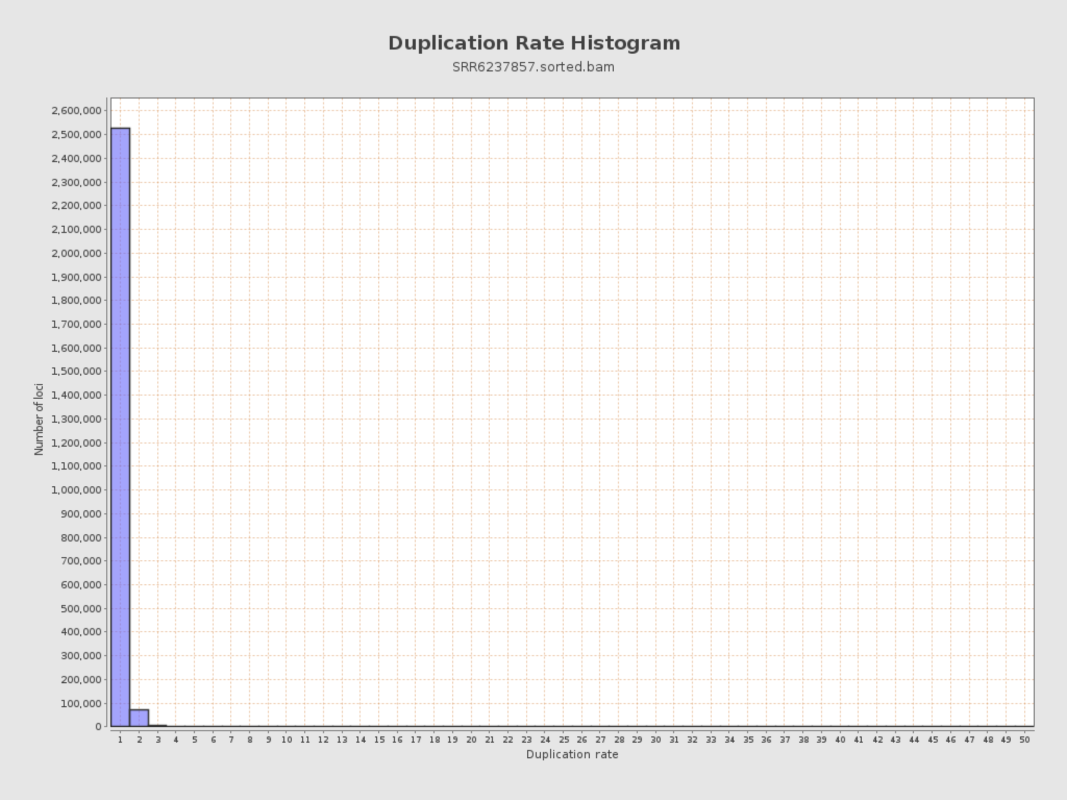
5. Results : Coverage Histogram (0-50X)



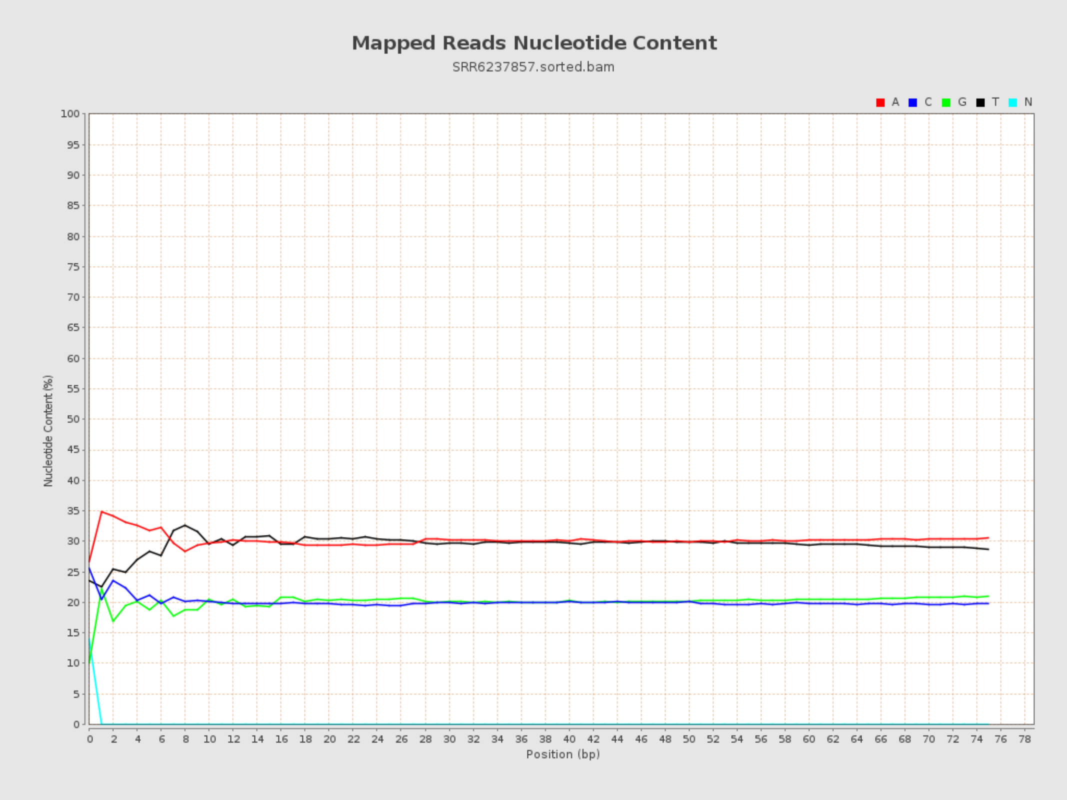
6. Results : Genome Fraction Coverage



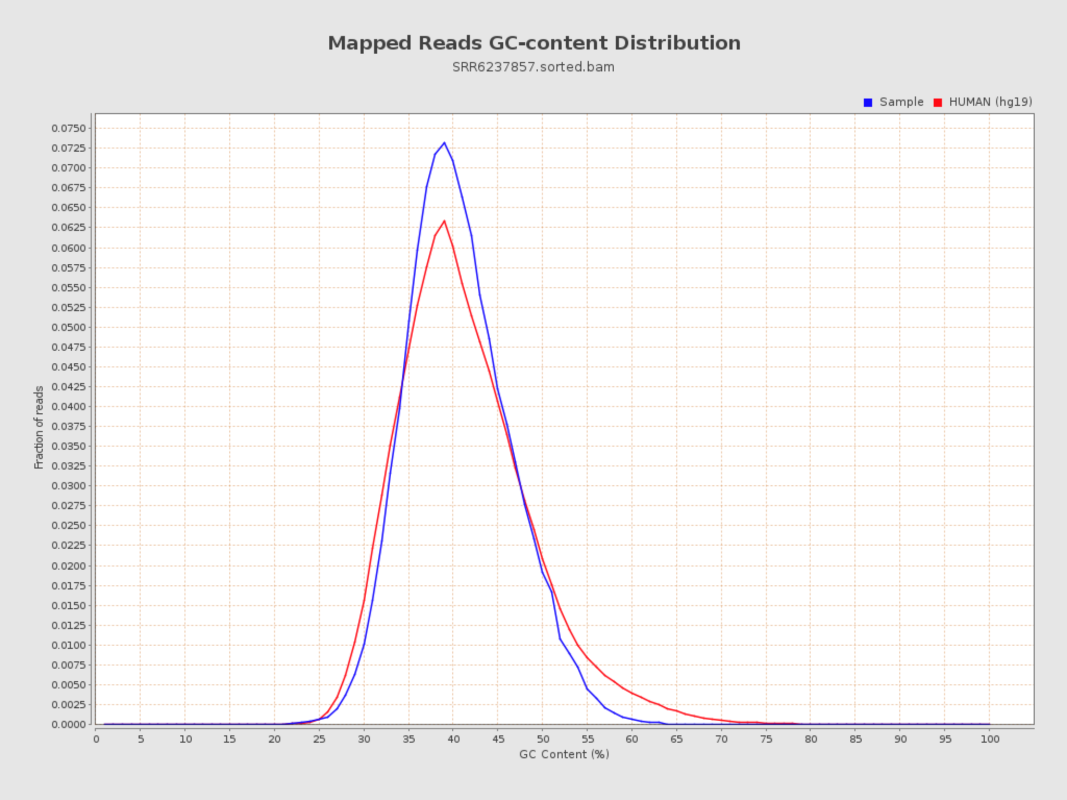
7. Results : Duplication Rate Histogram



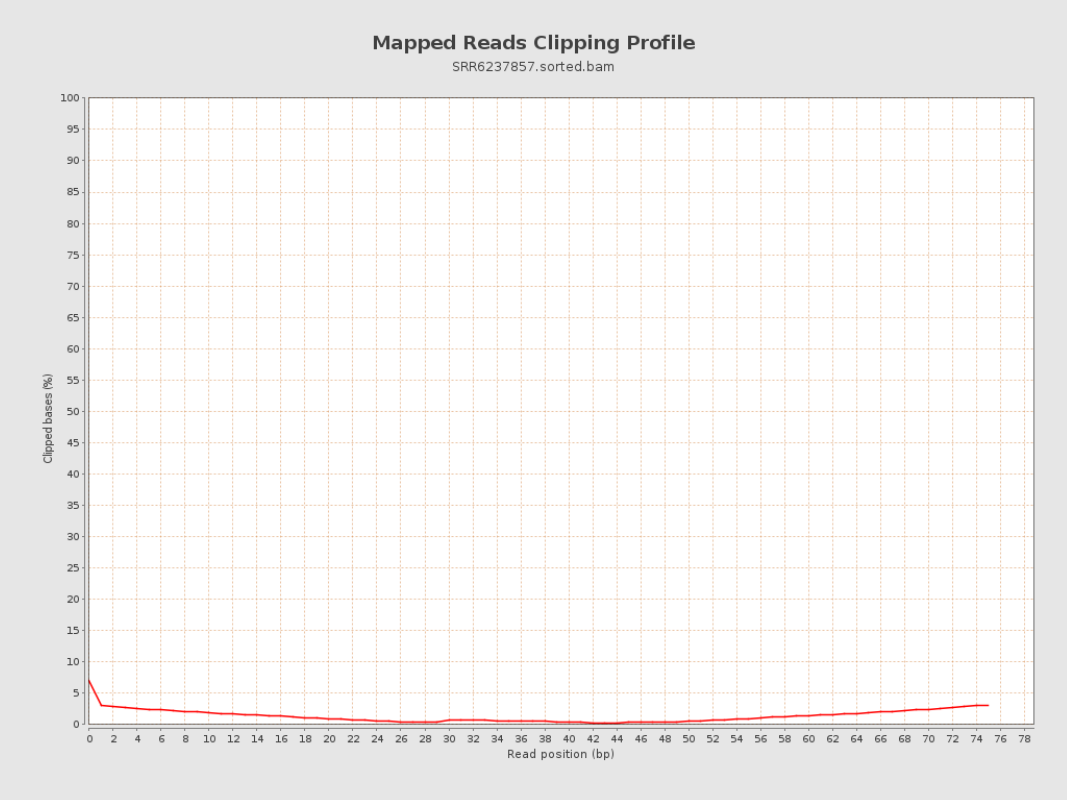
8. Results : Mapped Reads Nucleotide Content



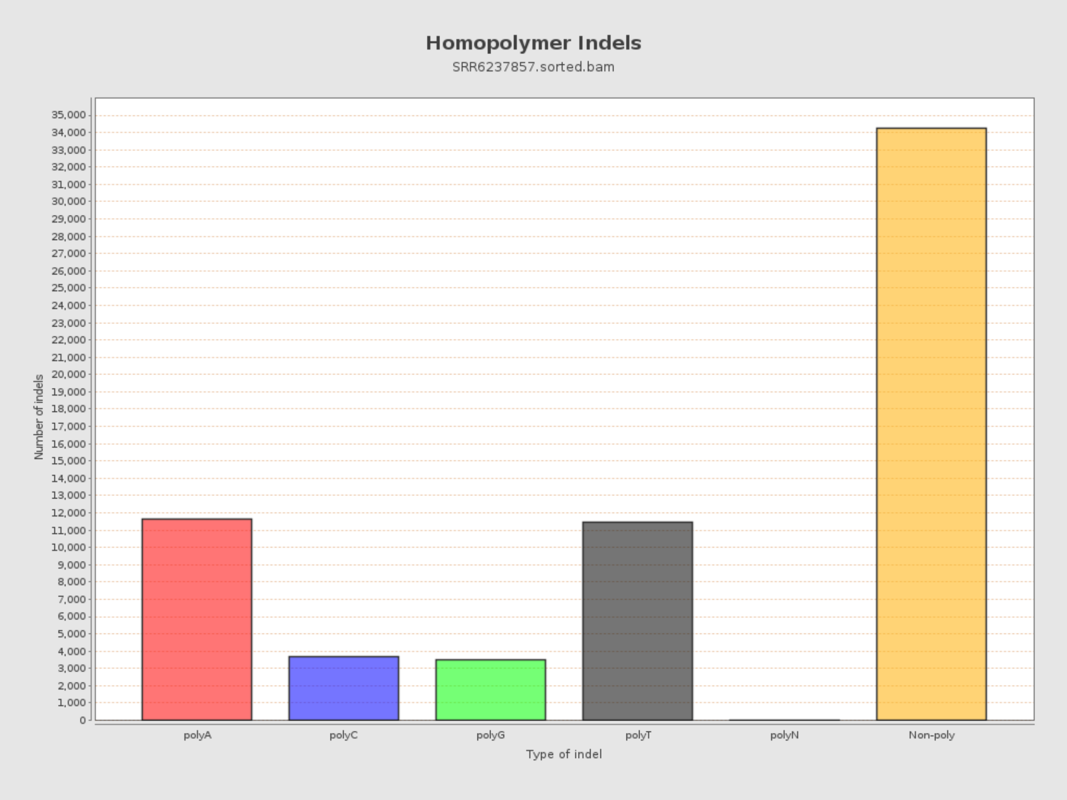
9. Results : Mapped Reads GC-content Distribution



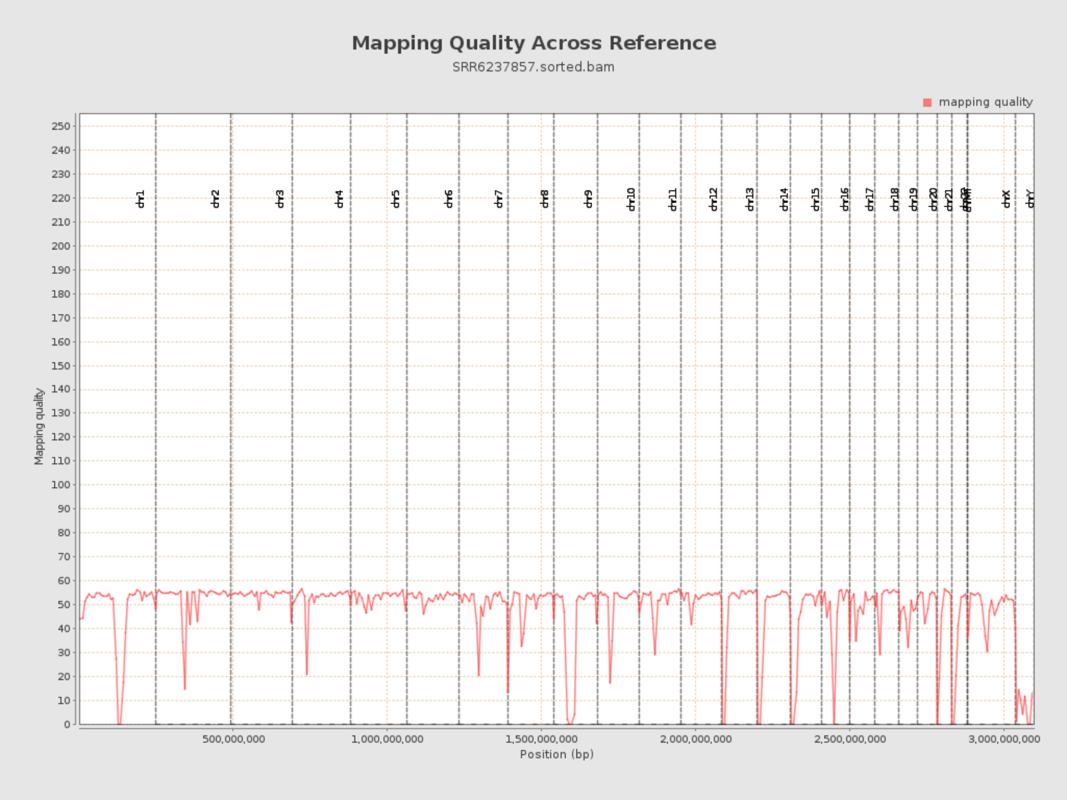
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram