Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 01:27:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237305.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_SRR6237305 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237305.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 01:27:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237305.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,073,811
Mapped reads	2,749,970 / 89.46%
Unmapped reads	323,841 / 10.54%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	31,223 / 1.02%
Read min/max/mean length	30 / 76 / 76.35
Duplicated reads (estimated)	1,006,735 / 32.75%
Duplication rate	20.22%
Clipped reads	1,675,987 / 54.52%

2.2. ACGT Content

Number/percentage of A's	43,547,679 / 25.28%
Number/percentage of C's	31,143,141 / 18.08%
Number/percentage of T's	55,908,330 / 32.46%
Number/percentage of G's	41,619,264 / 24.16%
Number/percentage of N's	18,632 / 0.01%
GC Percentage	42.25%

2.3. Coverage

Mean	0.0557

Standard Deviation	0.8128

2.4. Mapping Quality

Mean Mapping Quality	40.94

2.5. Mismatches and indels

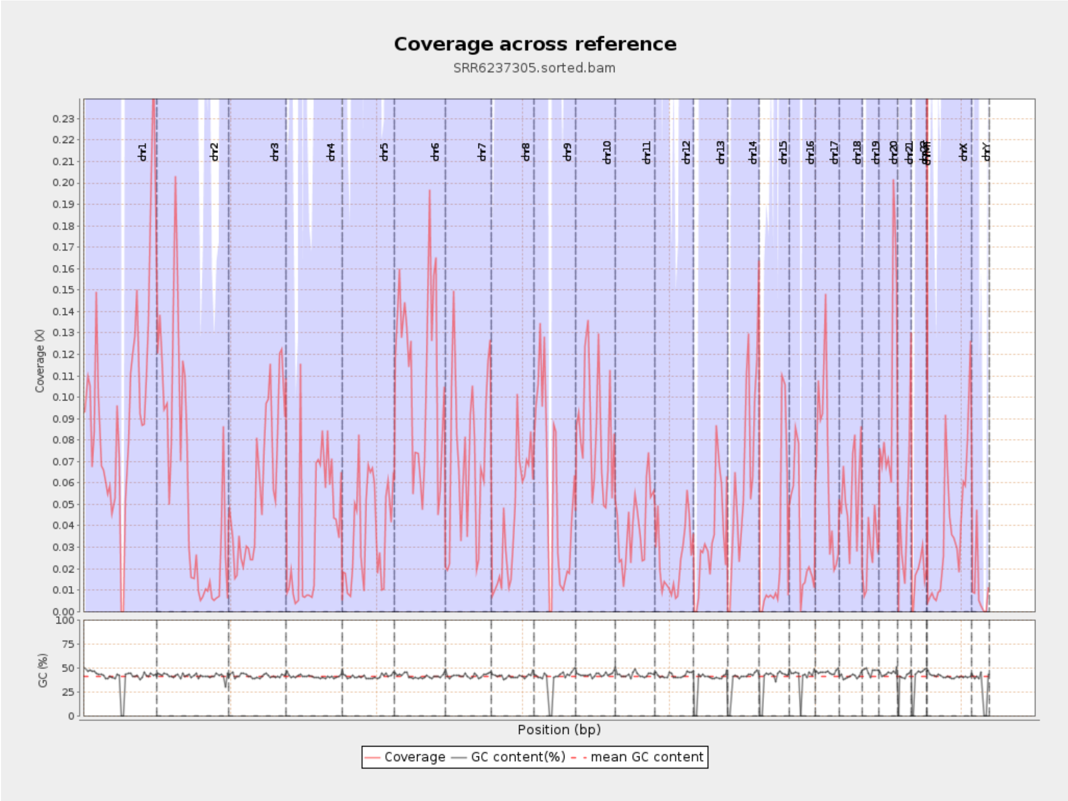
General error rate	0.59%
Mismatches	984,622
Insertions	13,436
Mapped reads with at least one insertion	0.48%
Deletions	43,140
Mapped reads with at least one deletion	1.55%
Homopolymer indels	42.05%

2.6. Chromosome stats

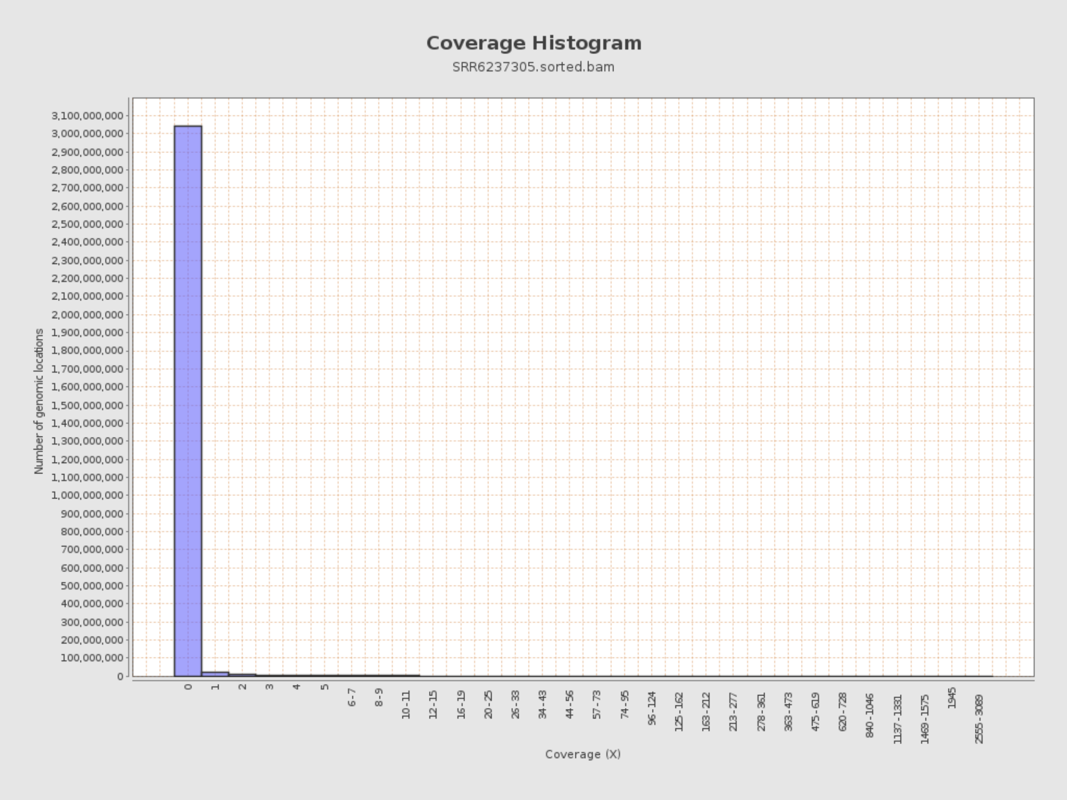
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	23988080	0.0962	0.902
chr2	243199373	14500684	0.0596	1.5865
chr3	198022430	11389857	0.0575	0.5931
chr4	191154276	7459482	0.039	0.6566
chr5	180915260	6998010	0.0387	0.4782
chr6	171115067	18611787	0.1088	1.0012
chr7	159138663	11256505	0.0707	0.724

chr8	146364022	6340329	0.0433	0.6477
chr9	141213431	8018160	0.0568	0.6714
chr10	135534747	11236782	0.0829	0.9817
chr11	135006516	5367264	0.0398	0.5176
chr12	133851895	3192713	0.0239	0.4004
chr13	115169878	3839109	0.0333	0.4887
chr14	107349540	6602368	0.0615	0.6378
chr15	102531392	2709447	0.0264	0.4225
chr16	90354753	3137008	0.0347	0.5075
chr17	81195210	5404099	0.0666	0.6478
chr18	78077248	4305960	0.0551	1.5364
chr19	59128983	1609629	0.0272	0.5637
chr20	63025520	6518700	0.1034	0.8253
chr21	48129895	2223022	0.0462	0.5944
chr22	51304566	865720	0.0169	0.2992
chrMT	16571	11583	0.699	1.9447
chrX	155270560	6100024	0.0393	0.4947
chrY	59373566	627491	0.0106	0.4896

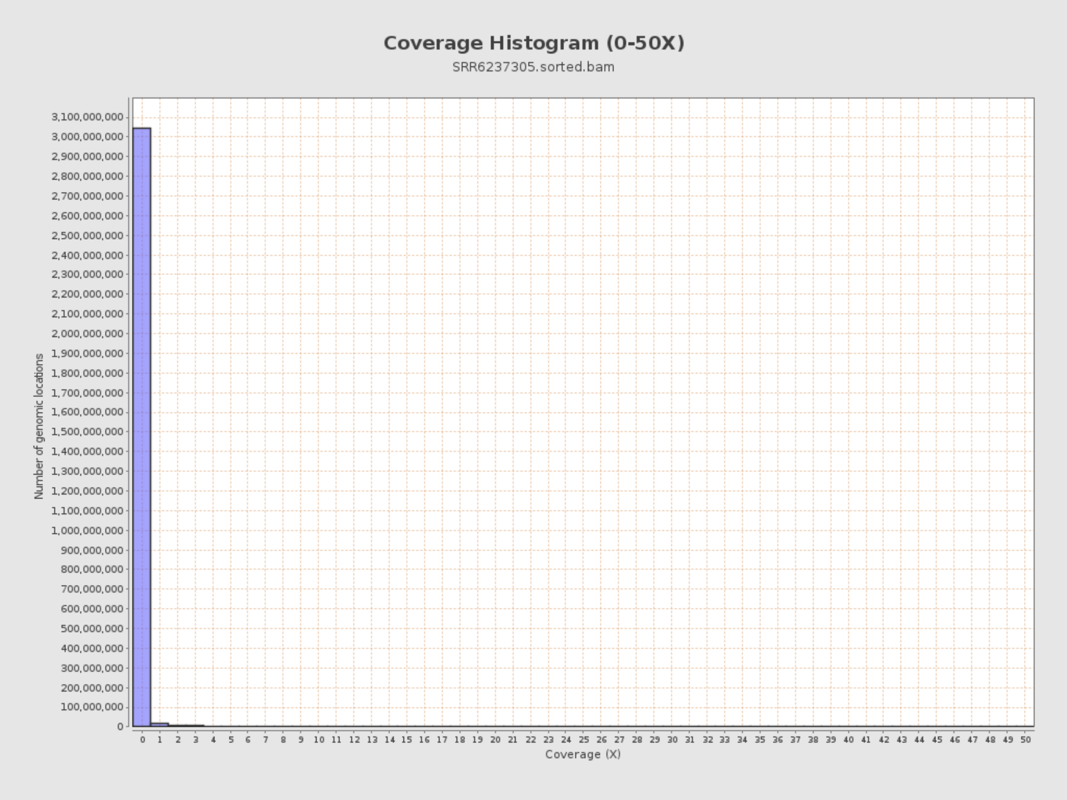
3. Results : Coverage across reference



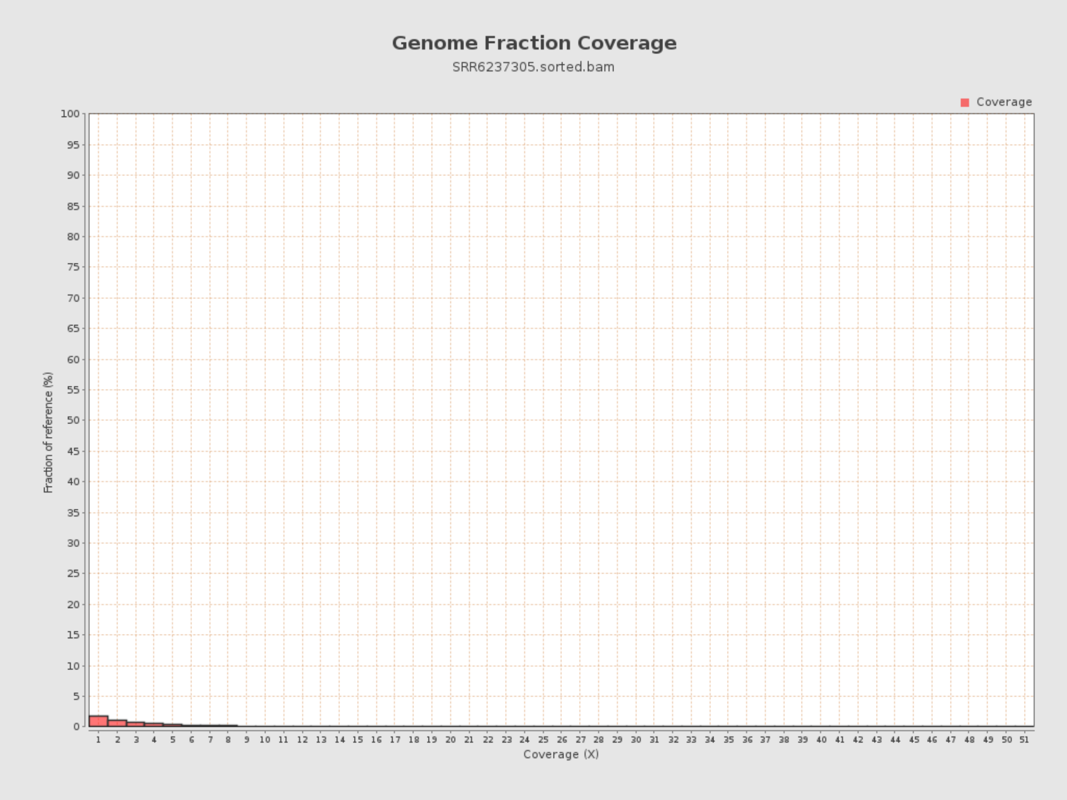
4. Results : Coverage Histogram



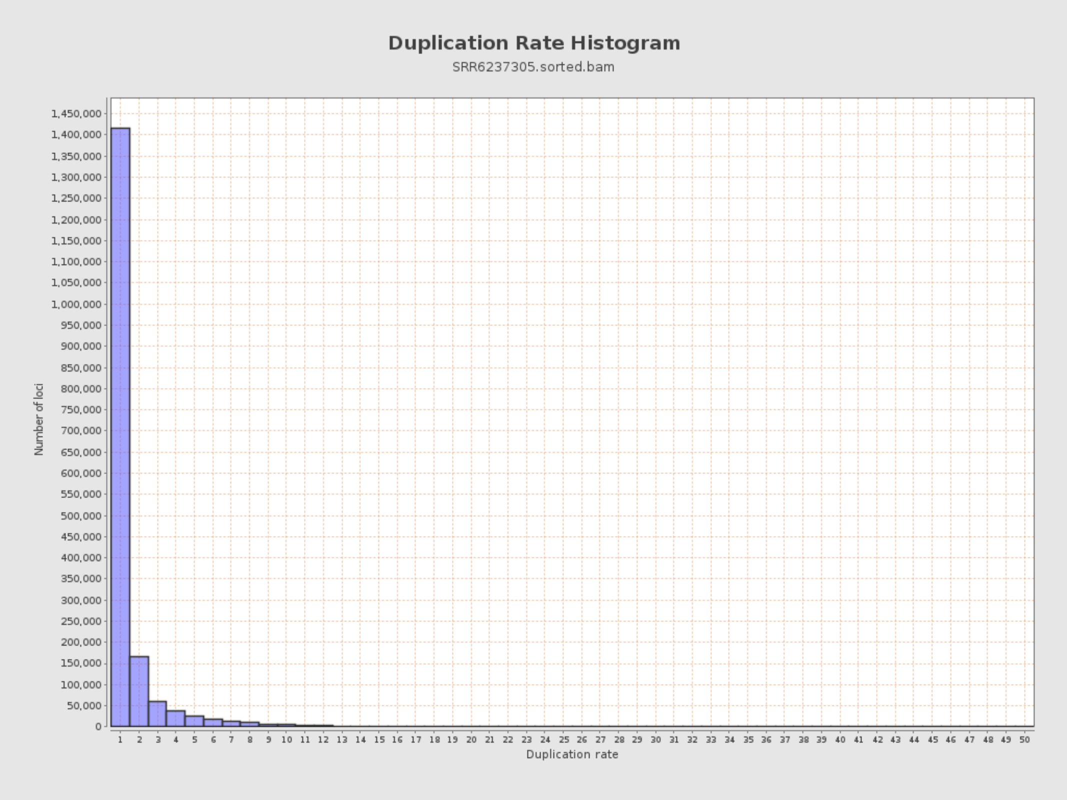
5. Results : Coverage Histogram (0-50X)



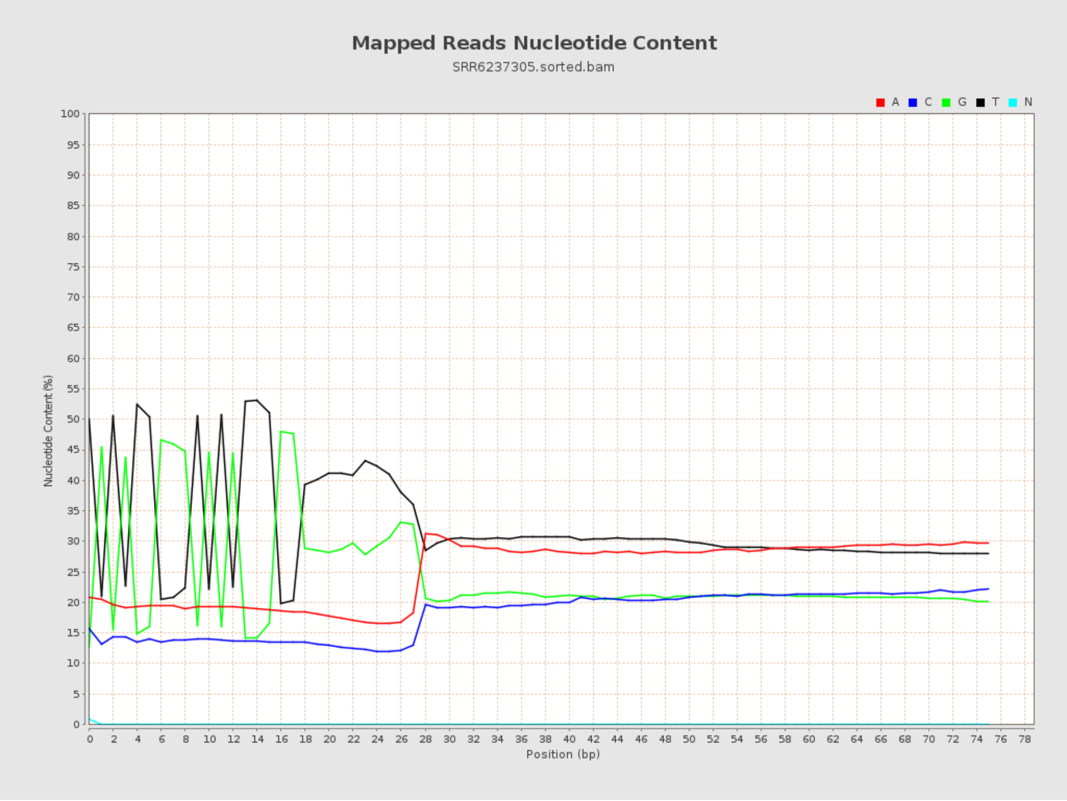
6. Results : Genome Fraction Coverage



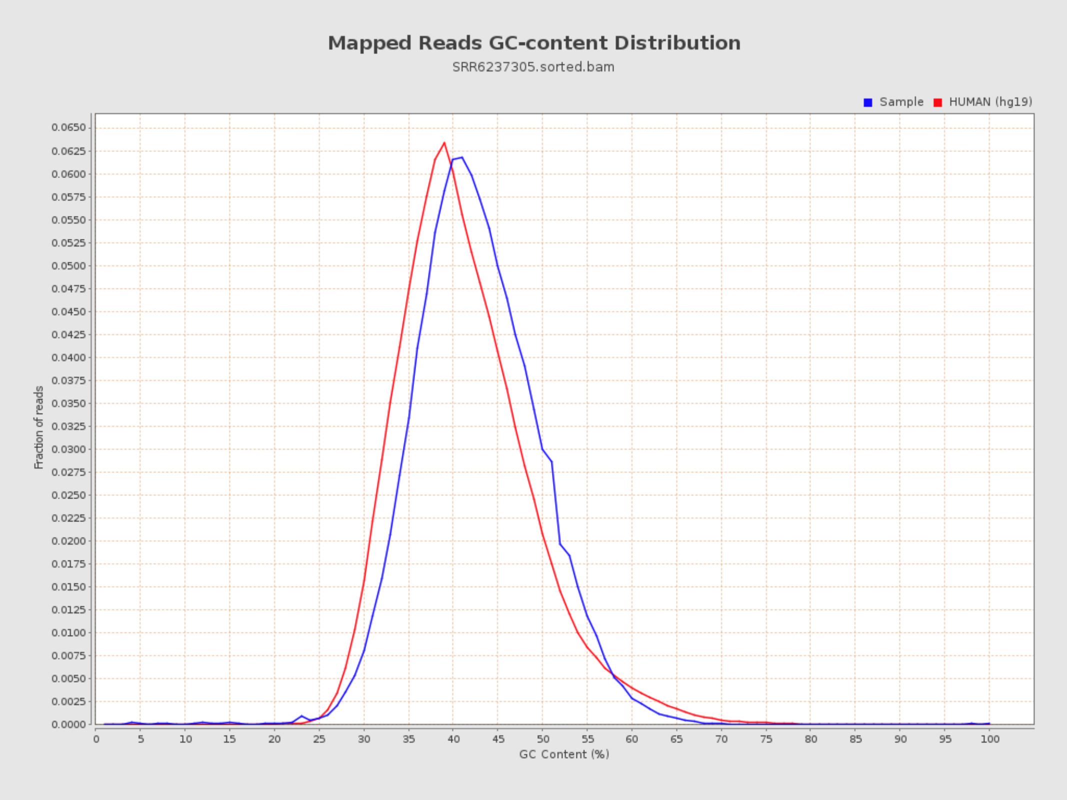
7. Results : Duplication Rate Histogram



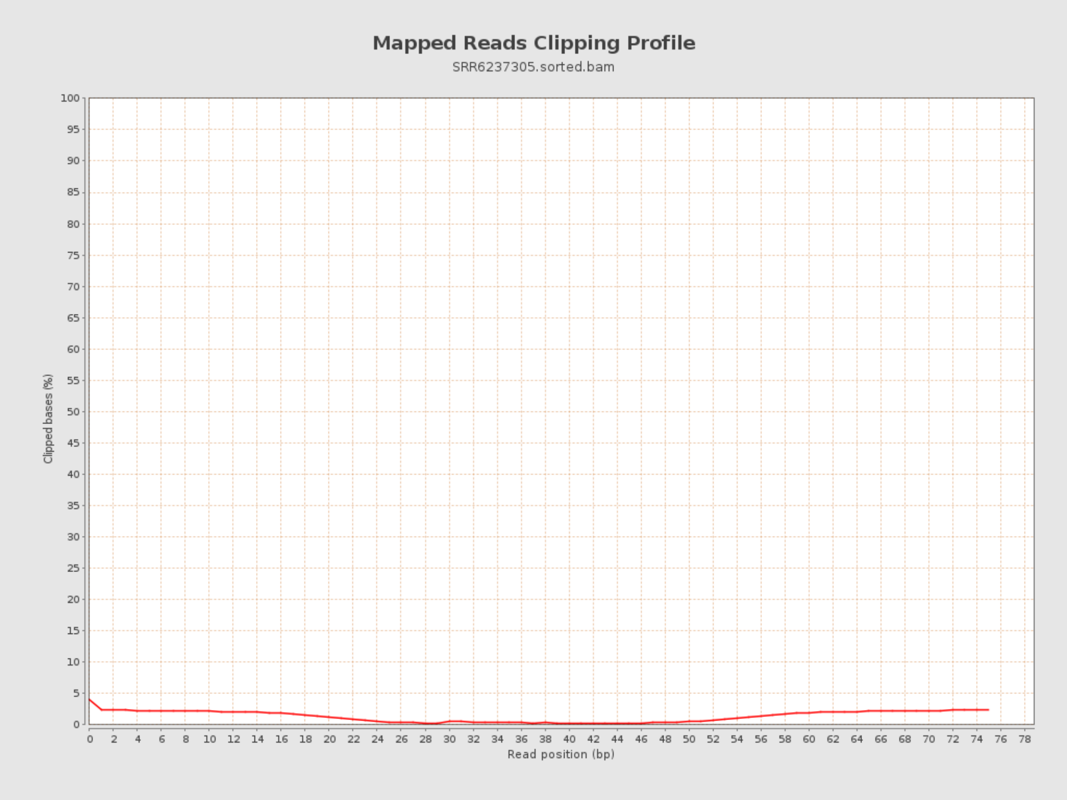
8. Results : Mapped Reads Nucleotide Content



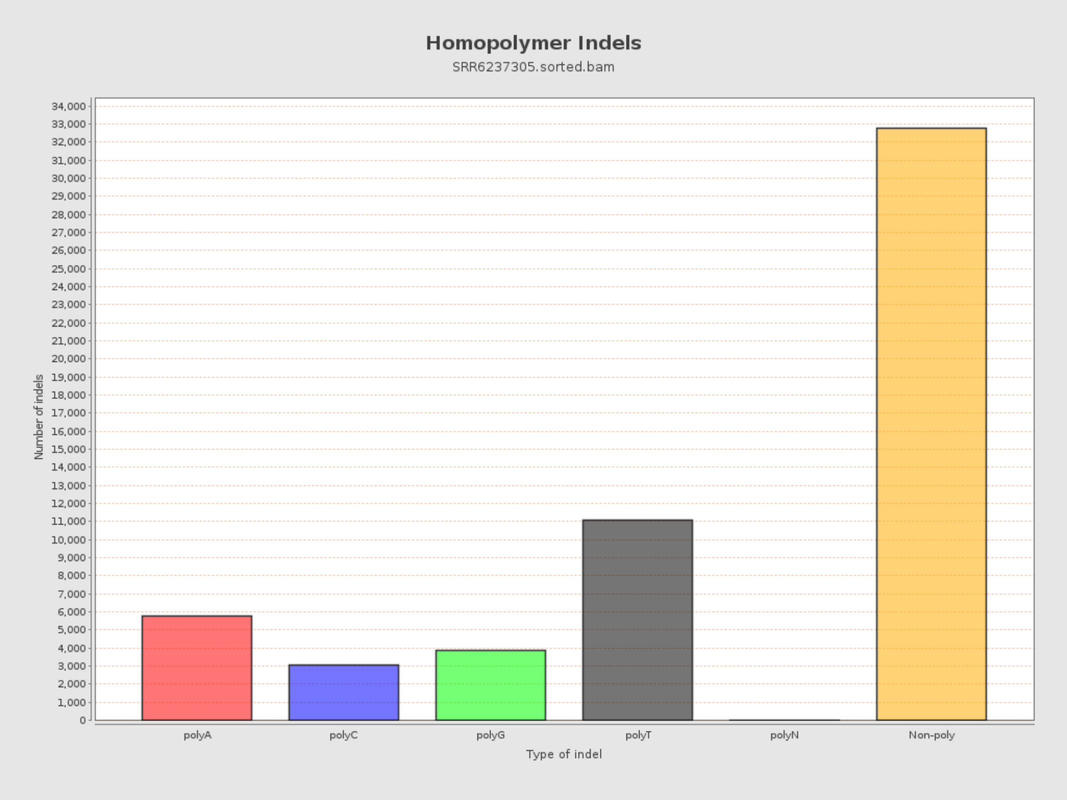
9. Results : Mapped Reads GC-content Distribution



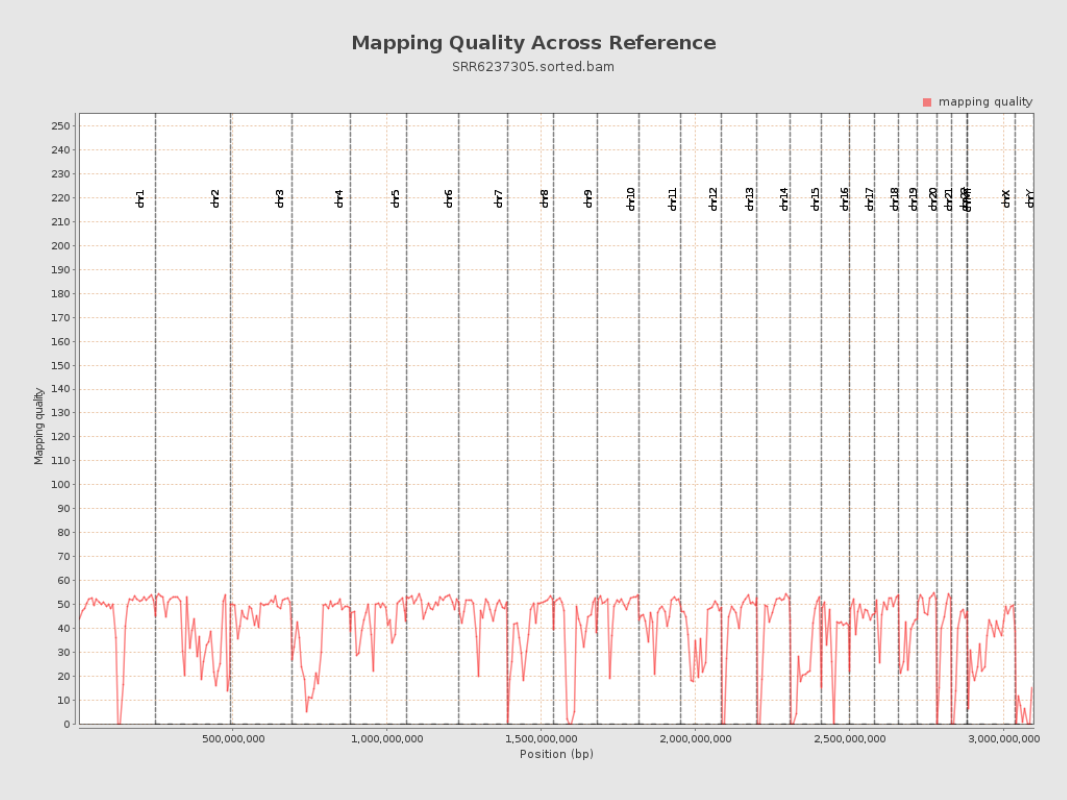
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram