Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 02:54:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237330.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_SRR6237330 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237330.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 02:54:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237330.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,429,242
Mapped reads	3,033,869 / 88.47%
Unmapped reads	395,373 / 11.53%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	32,748 / 0.95%
Read min/max/mean length	30 / 76 / 76.33
Duplicated reads (estimated)	764,848 / 22.3%
Duplication rate	19.12%
Clipped reads	1,993,525 / 58.13%

2.2. ACGT Content

Number/percentage of A's	48,147,351 / 25.94%
Number/percentage of C's	31,465,983 / 16.95%
Number/percentage of T's	62,816,037 / 33.85%
Number/percentage of G's	43,145,329 / 23.25%
Number/percentage of N's	19,408 / 0.01%
GC Percentage	40.2%

2.3. Coverage

Mean	0.06

Standard Deviation	0.8311

2.4. Mapping Quality

Mean Mapping Quality	43.78

2.5. Mismatches and indels

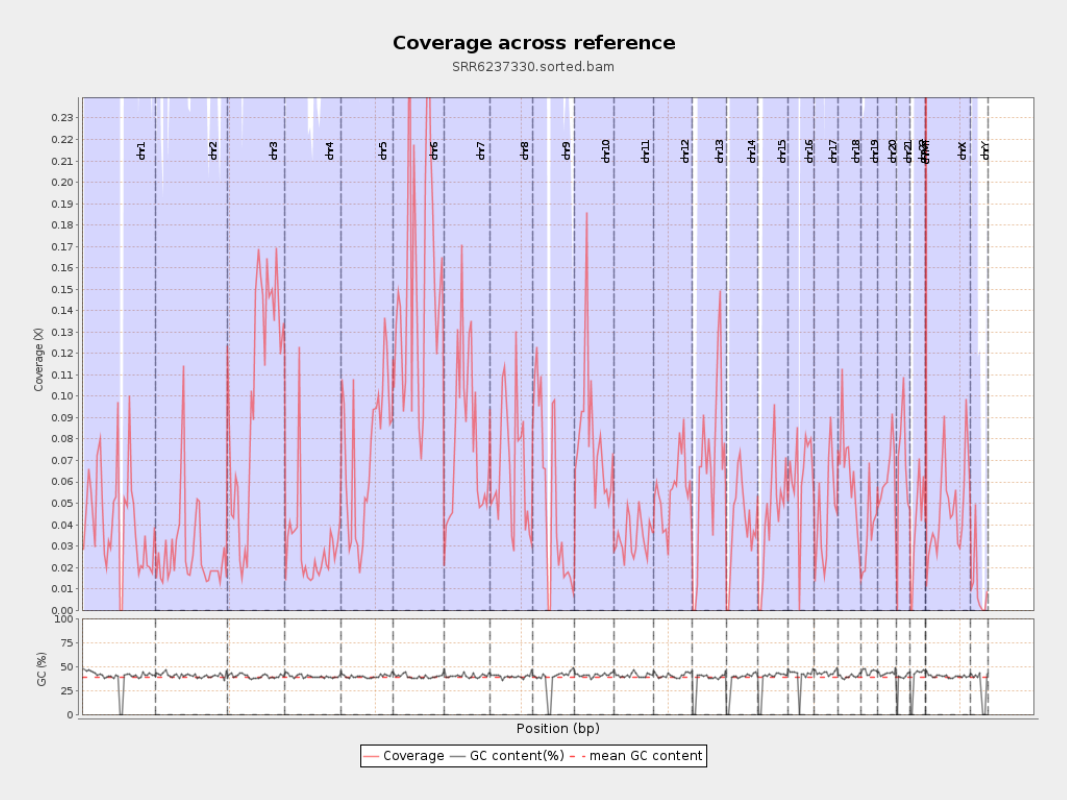
General error rate	0.65%
Mismatches	1,179,557
Insertions	14,100
Mapped reads with at least one insertion	0.46%
Deletions	58,128
Mapped reads with at least one deletion	1.89%
Homopolymer indels	42.21%

2.6. Chromosome stats

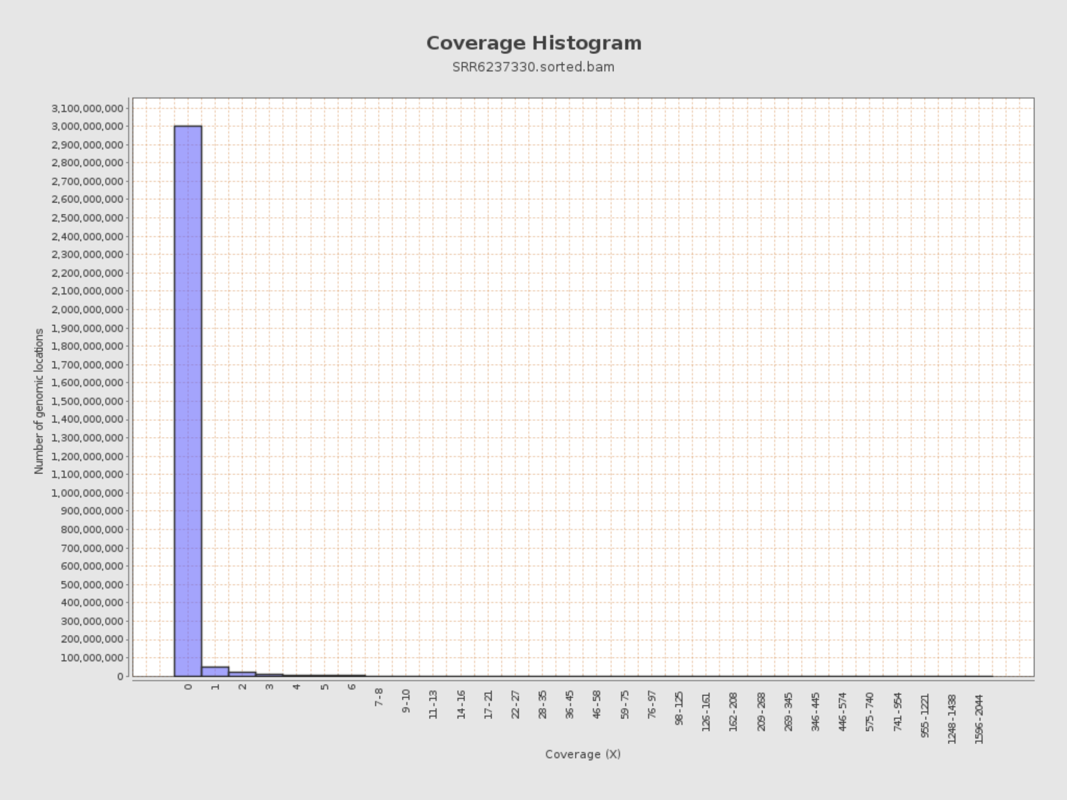
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10246400	0.0411	1.007
chr2	243199373	6872346	0.0283	1.2354
chr3	198022430	20297713	0.1025	0.5526
chr4	191154276	5700990	0.0298	0.5341
chr5	180915260	13470963	0.0745	0.4766
chr6	171115067	26248250	0.1534	1.2978
chr7	159138663	12586258	0.0791	1.1383

chr8	146364022	9643440	0.0659	1.1947
chr9	141213431	7266662	0.0515	0.6283
chr10	135534747	10710196	0.079	0.9737
chr11	135006516	4594773	0.034	0.4344
chr12	133851895	7518253	0.0562	0.4343
chr13	115169878	7739666	0.0672	0.4861
chr14	107349540	4361900	0.0406	0.3775
chr15	102531392	4618074	0.045	0.385
chr16	90354753	5638925	0.0624	0.4889
chr17	81195210	3701784	0.0456	0.4373
chr18	78077248	5026252	0.0644	1.6656
chr19	59128983	2156119	0.0365	0.7073
chr20	63025520	4026216	0.0639	0.4611
chr21	48129895	3178948	0.066	0.5503
chr22	51304566	2075546	0.0405	0.3379
chrMT	16571	23769	1.4344	2.3931
chrX	155270560	7328332	0.0472	0.4287
chrY	59373566	664734	0.0112	0.4739

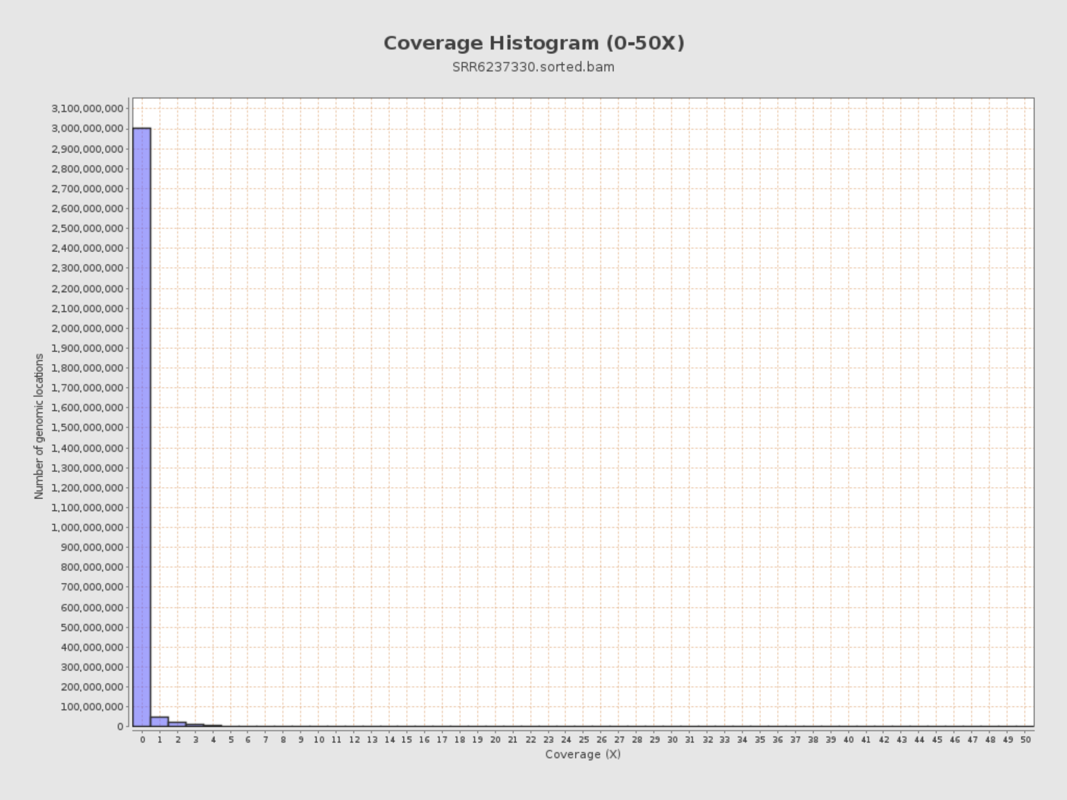
3. Results : Coverage across reference



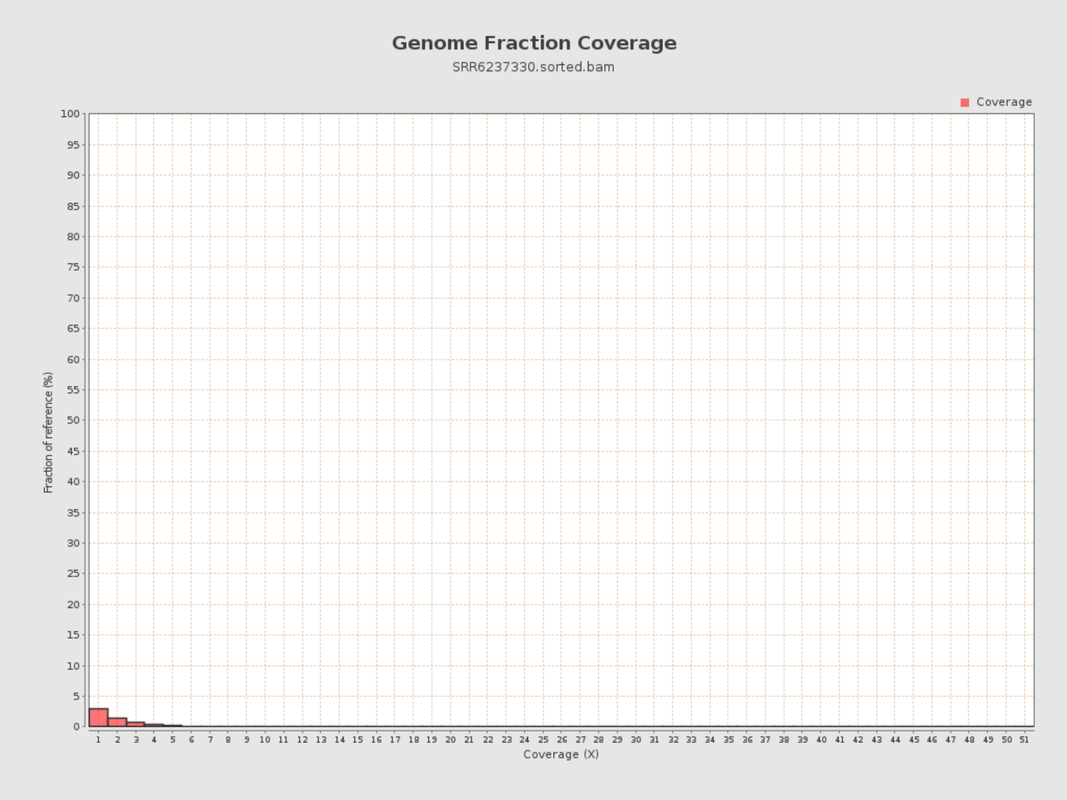
4. Results : Coverage Histogram



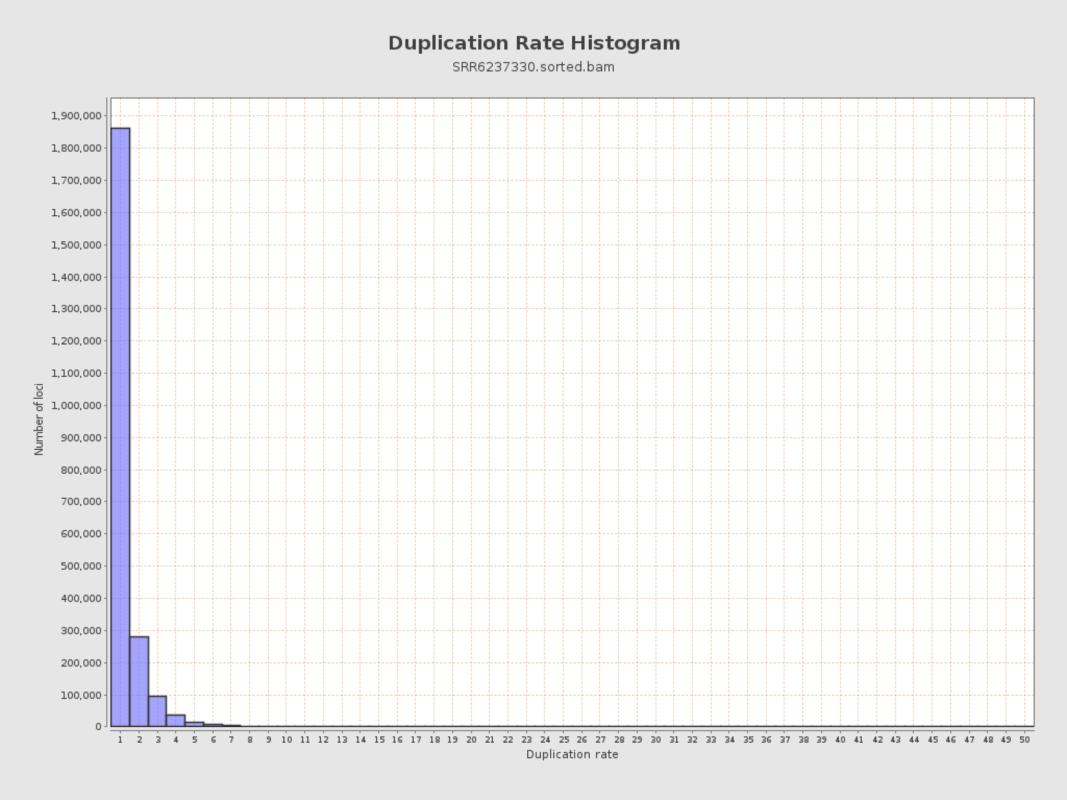
5. Results : Coverage Histogram (0-50X)



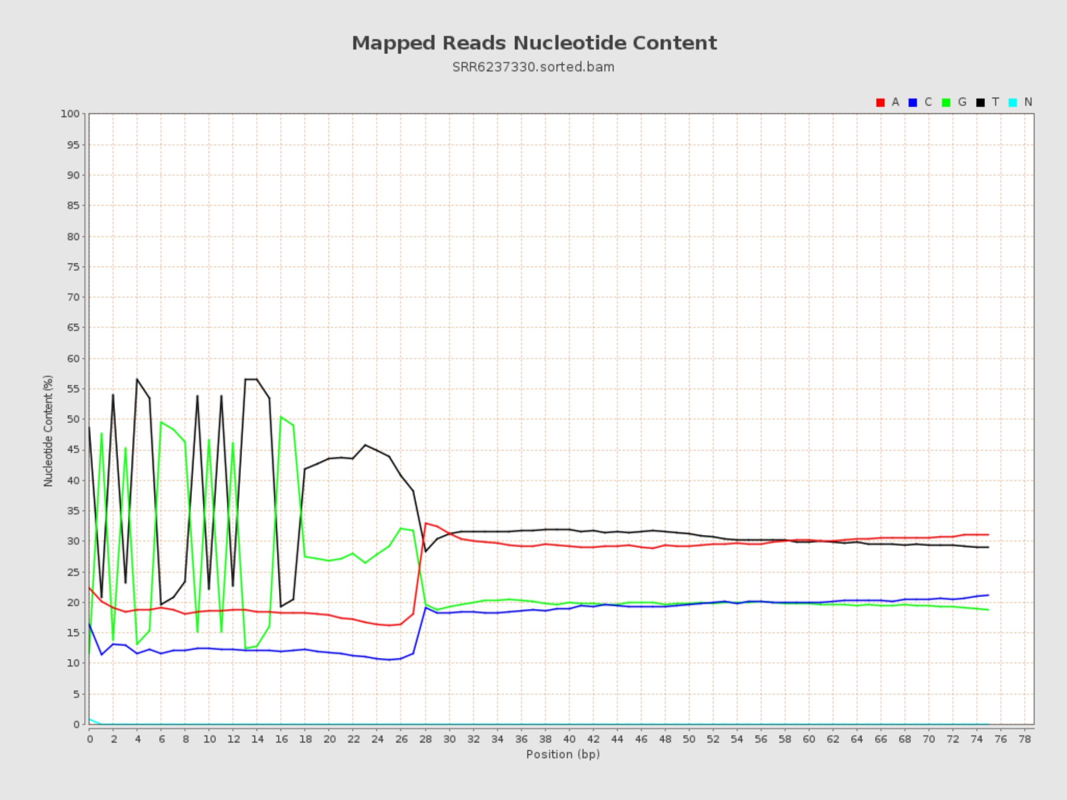
6. Results : Genome Fraction Coverage



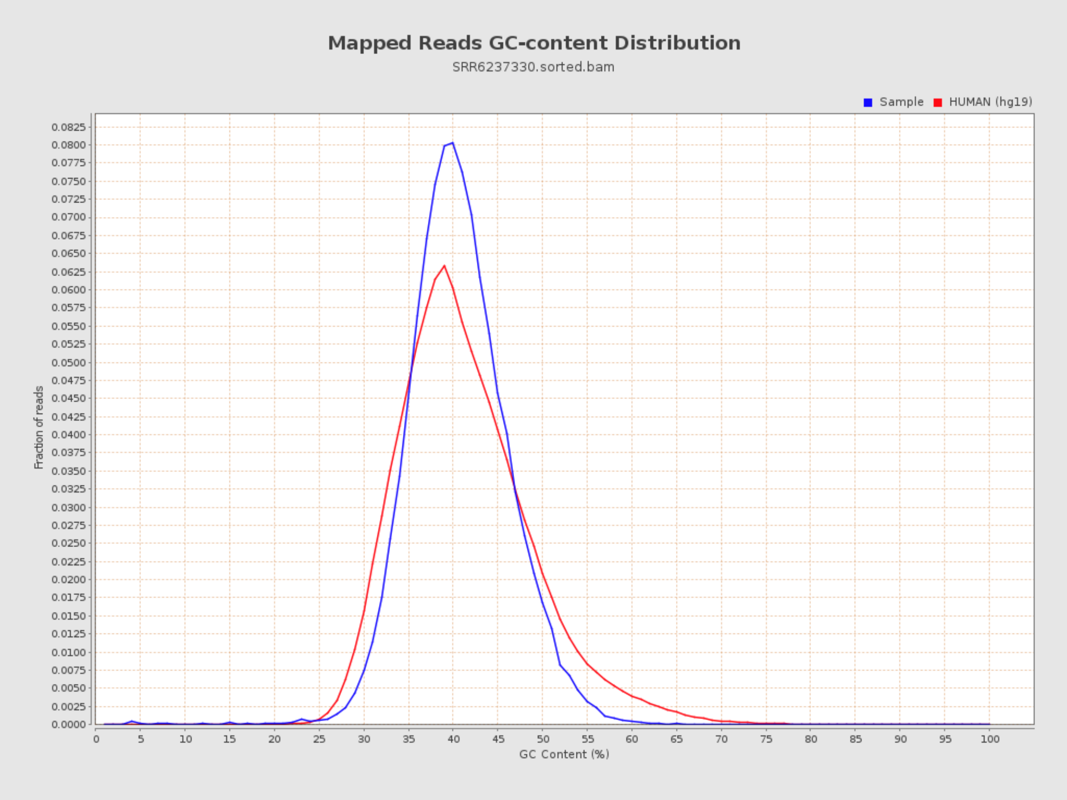
7. Results : Duplication Rate Histogram



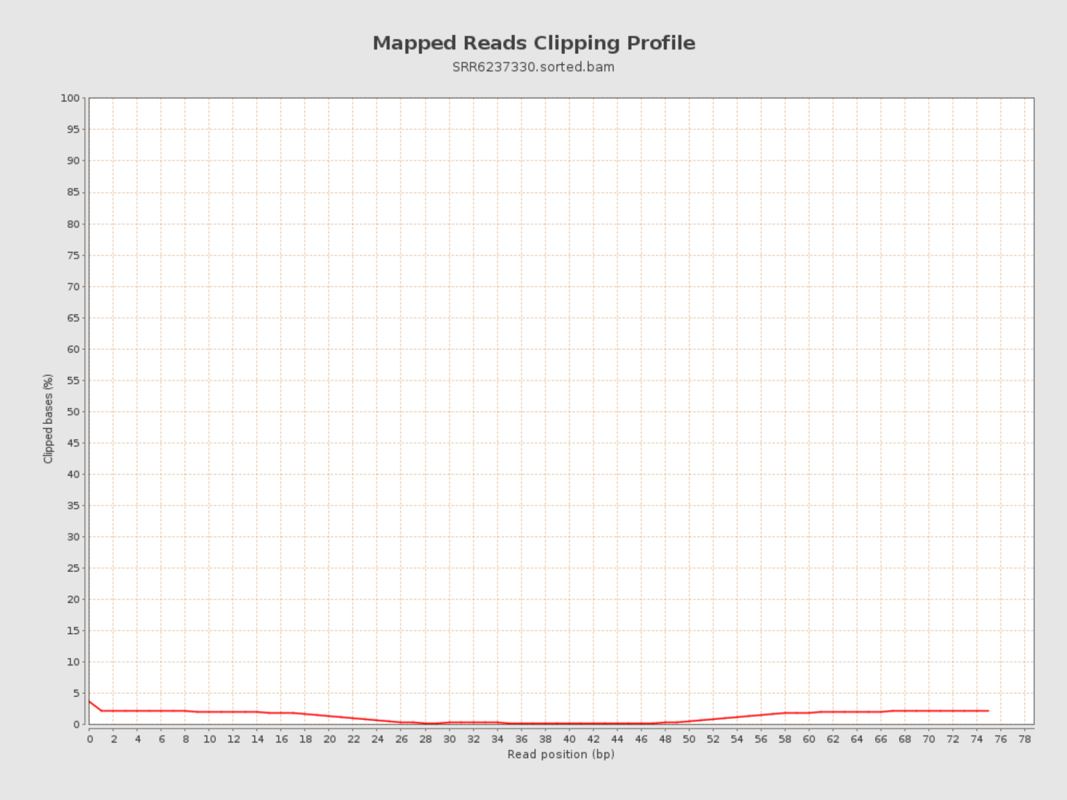
8. Results : Mapped Reads Nucleotide Content



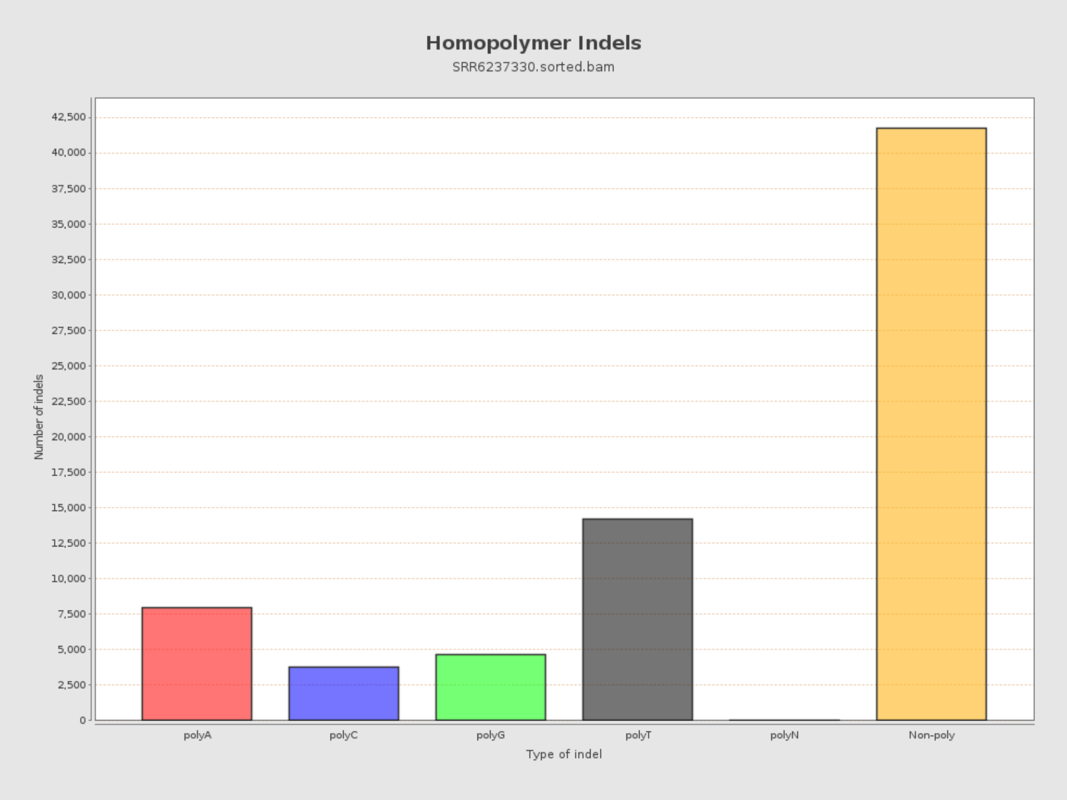
9. Results : Mapped Reads GC-content Distribution



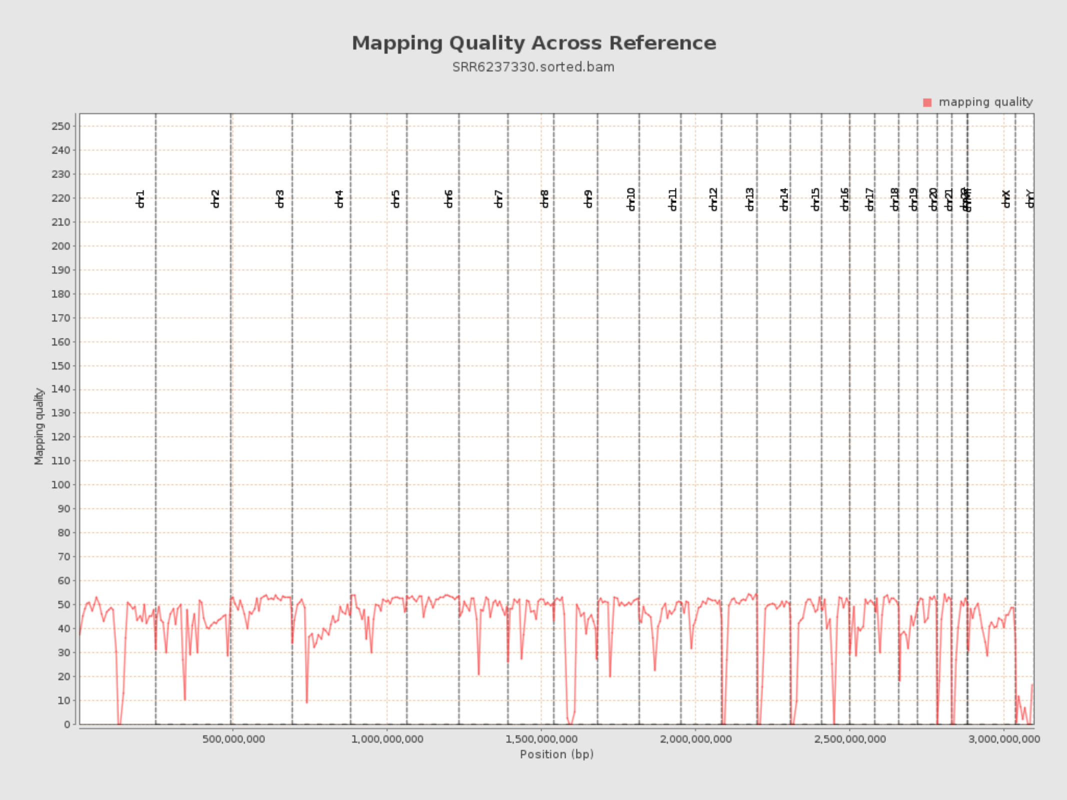
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram