Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 08:43:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237846.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_SRR6237846 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237846.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 08:43:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237846.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,132,819
Mapped reads	2,700,745 / 65.35%
Unmapped reads	1,432,074 / 34.65%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,270 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	278,395 / 6.74%
Duplication rate	7.88%
Clipped reads	1,903,901 / 46.07%

2.2. ACGT Content

Number/percentage of A's	43,870,426 / 27.34%
Number/percentage of C's	30,632,130 / 19.09%
Number/percentage of T's	49,709,183 / 30.98%
Number/percentage of G's	36,129,599 / 22.51%
Number/percentage of N's	138,746 / 0.09%
GC Percentage	41.6%

2.3. Coverage

Mean	0.0519

Standard Deviation	0.456

2.4. Mapping Quality

Mean Mapping Quality	44.67

2.5. Mismatches and indels

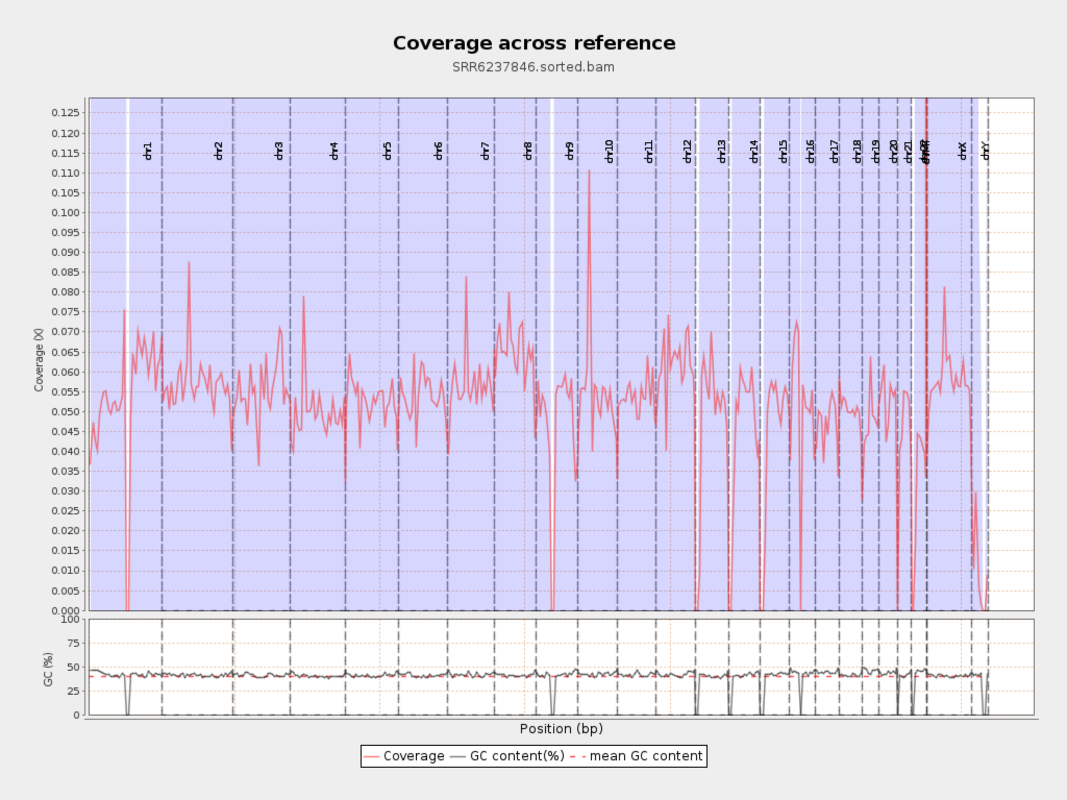
General error rate	0.99%
Mismatches	1,564,666
Insertions	12,471
Mapped reads with at least one insertion	0.46%
Deletions	59,032
Mapped reads with at least one deletion	2.15%
Homopolymer indels	46.04%

2.6. Chromosome stats

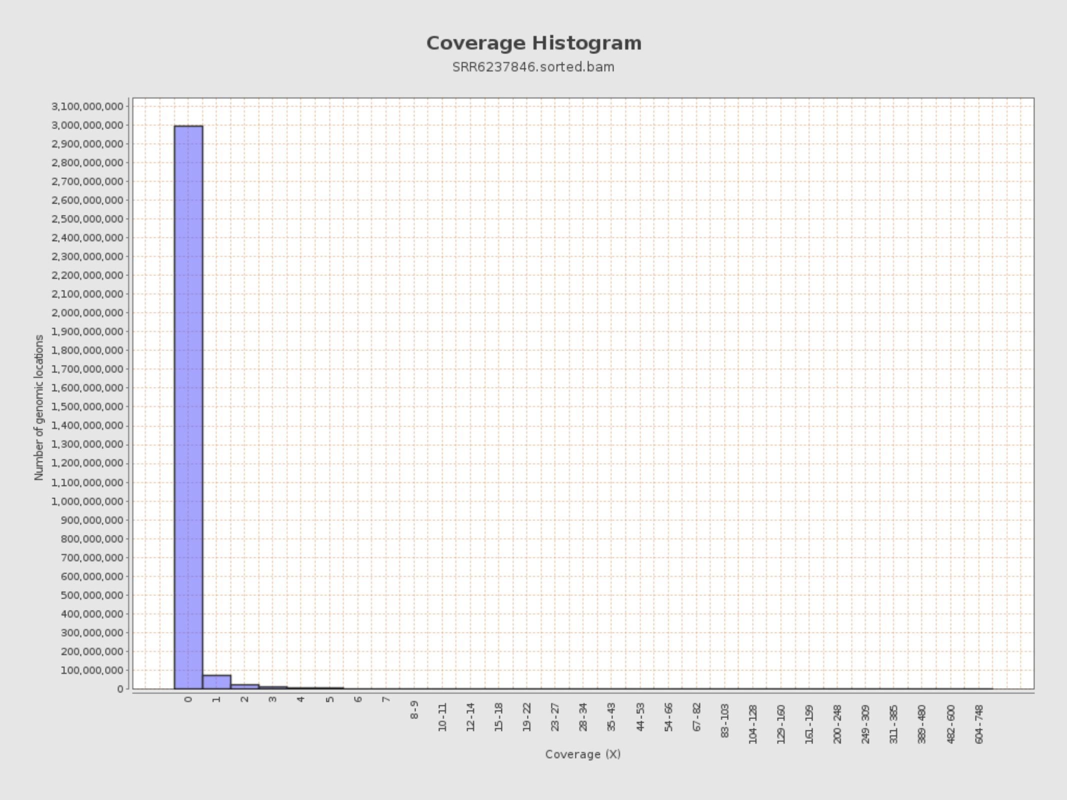
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13229777	0.0531	0.6807
chr2	243199373	13863804	0.057	0.5233
chr3	198022430	10946887	0.0553	0.3682
chr4	191154276	9511440	0.0498	0.3647
chr5	180915260	9553027	0.0528	0.3447
chr6	171115067	9251372	0.0541	0.3866
chr7	159138663	9029855	0.0567	0.617

chr8	146364022	9471393	0.0647	0.532
chr9	141213431	6475785	0.0459	0.3988
chr10	135534747	7538130	0.0556	0.5604
chr11	135006516	7206105	0.0534	0.4409
chr12	133851895	8264725	0.0617	0.3863
chr13	115169878	5332230	0.0463	0.3323
chr14	107349540	4739710	0.0442	0.3305
chr15	102531392	4437527	0.0433	0.3164
chr16	90354753	4643732	0.0514	0.405
chr17	81195210	3771966	0.0465	0.3503
chr18	78077248	3960270	0.0507	0.605
chr19	59128983	2800581	0.0474	0.4988
chr20	63025520	3298591	0.0523	0.3588
chr21	48129895	2088565	0.0434	0.3425
chr22	51304566	1492886	0.0291	0.265
chrMT	16571	159460	9.6228	7.0161
chrX	155270560	8972261	0.0578	0.3906
chrY	59373566	533475	0.009	0.2099

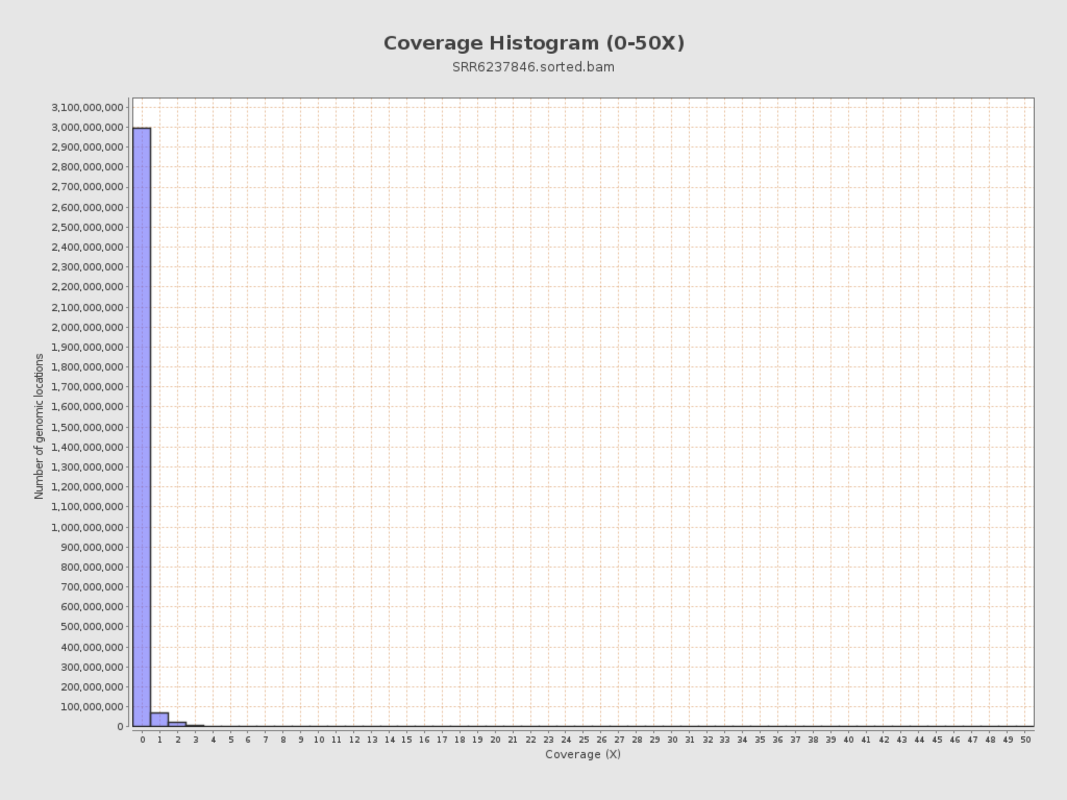
3. Results : Coverage across reference



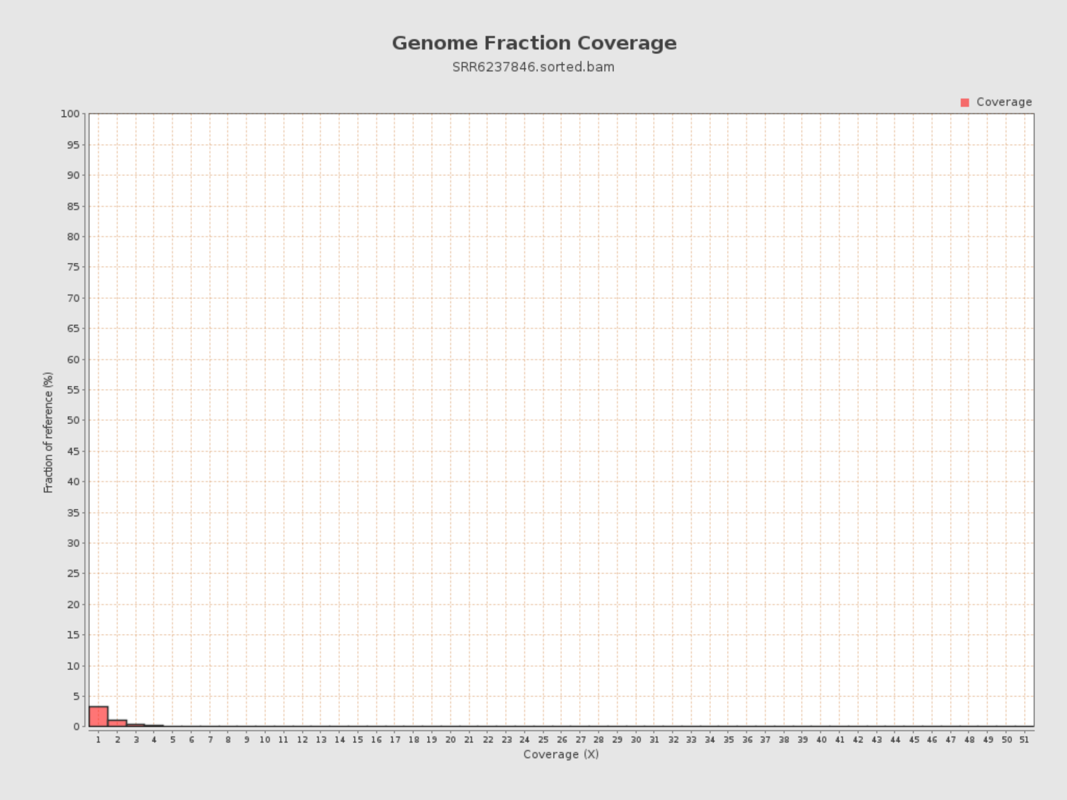
4. Results : Coverage Histogram



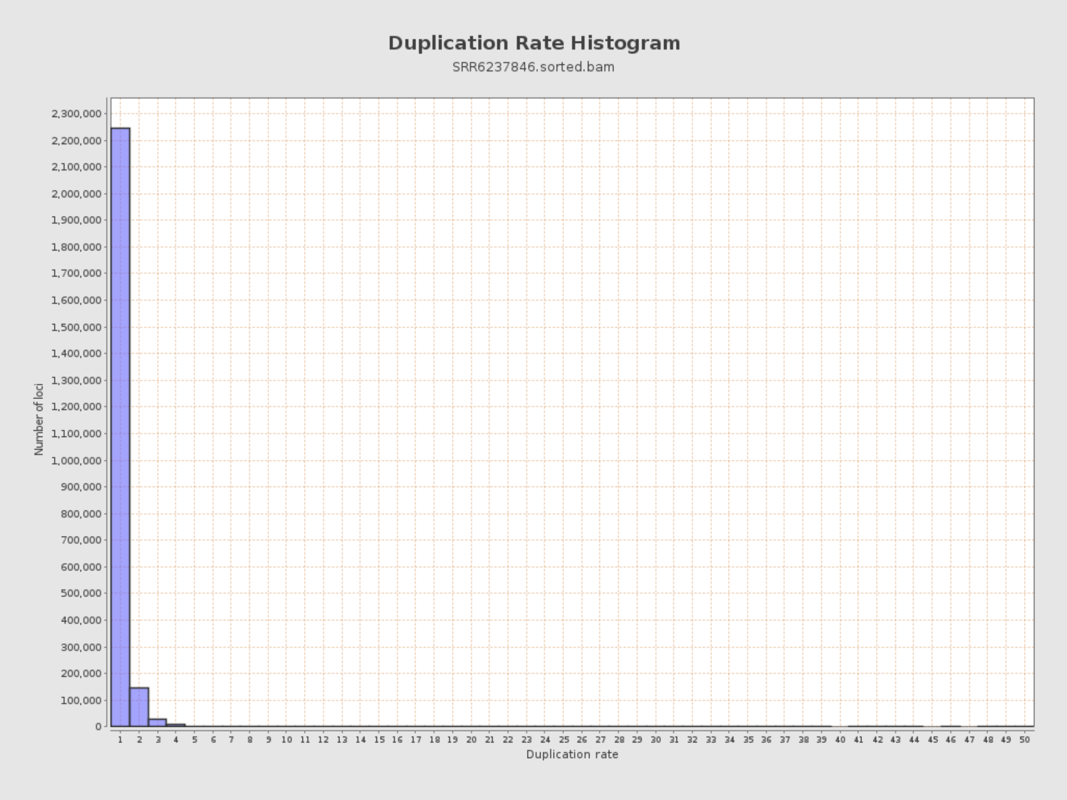
5. Results : Coverage Histogram (0-50X)



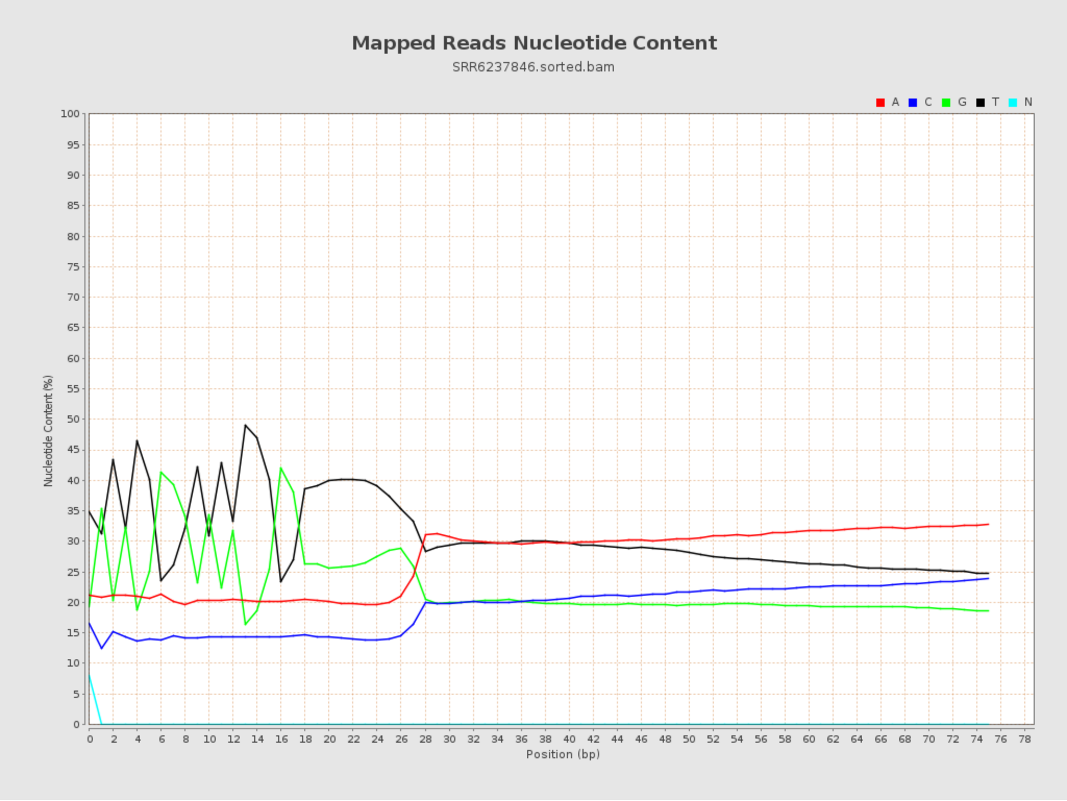
6. Results : Genome Fraction Coverage



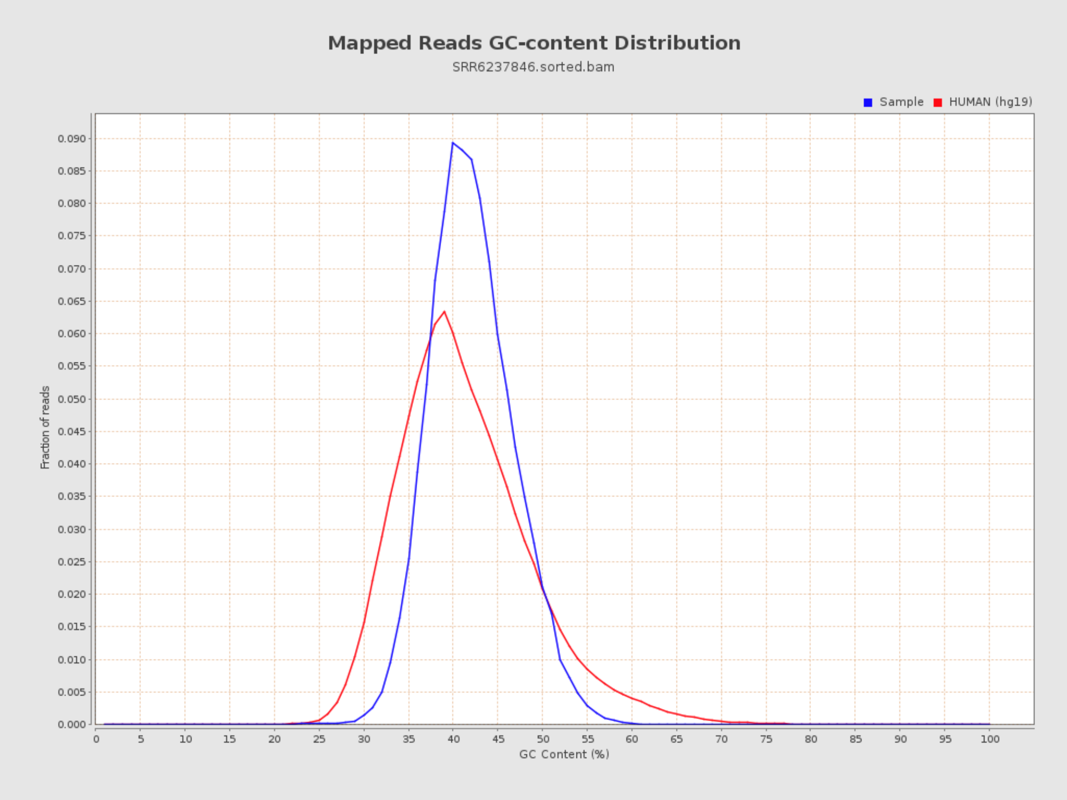
7. Results : Duplication Rate Histogram



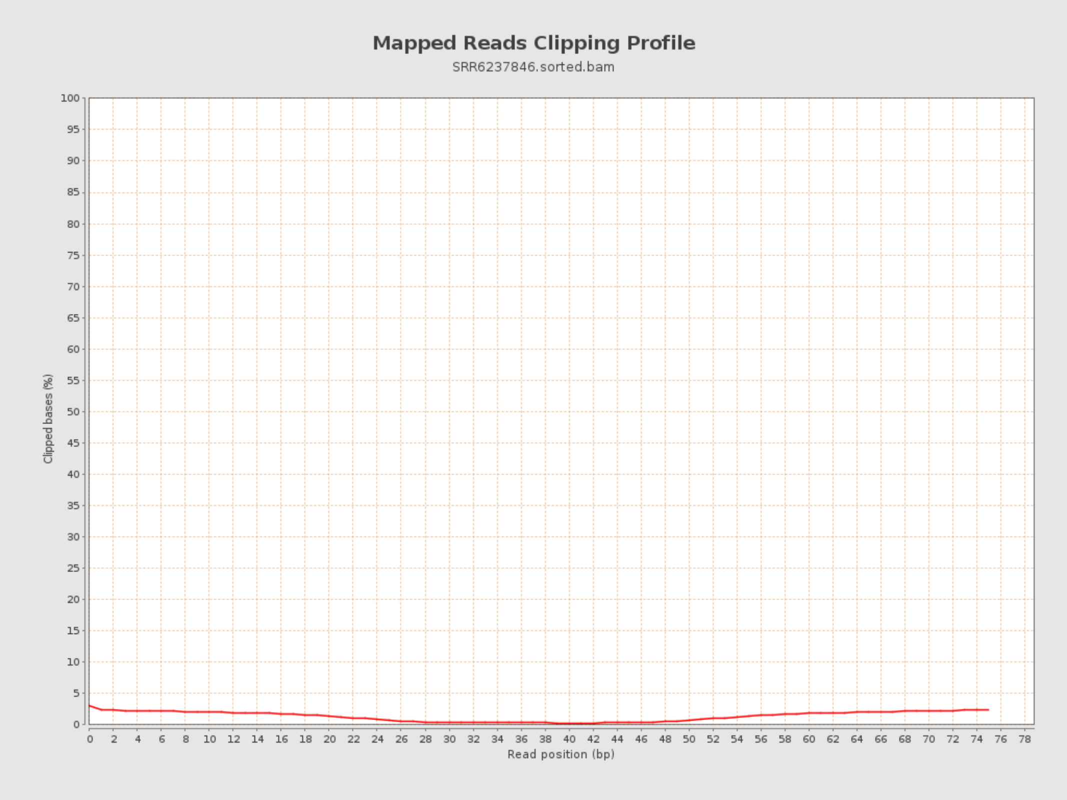
8. Results : Mapped Reads Nucleotide Content



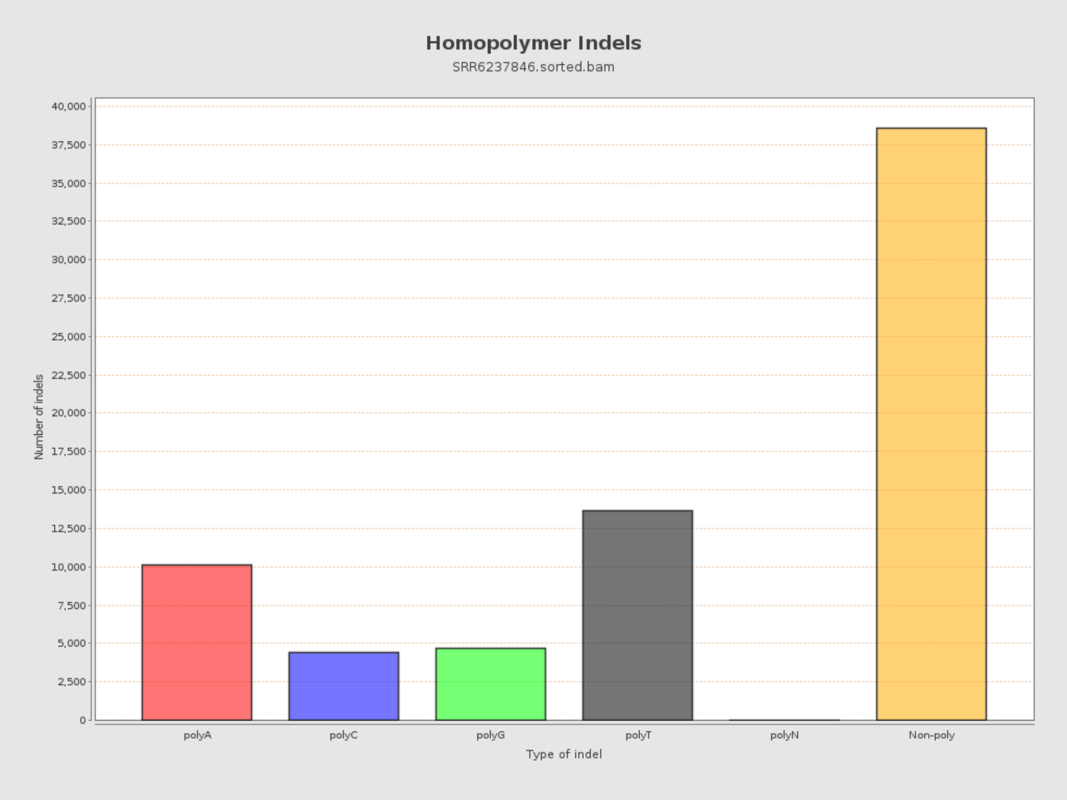
9. Results : Mapped Reads GC-content Distribution



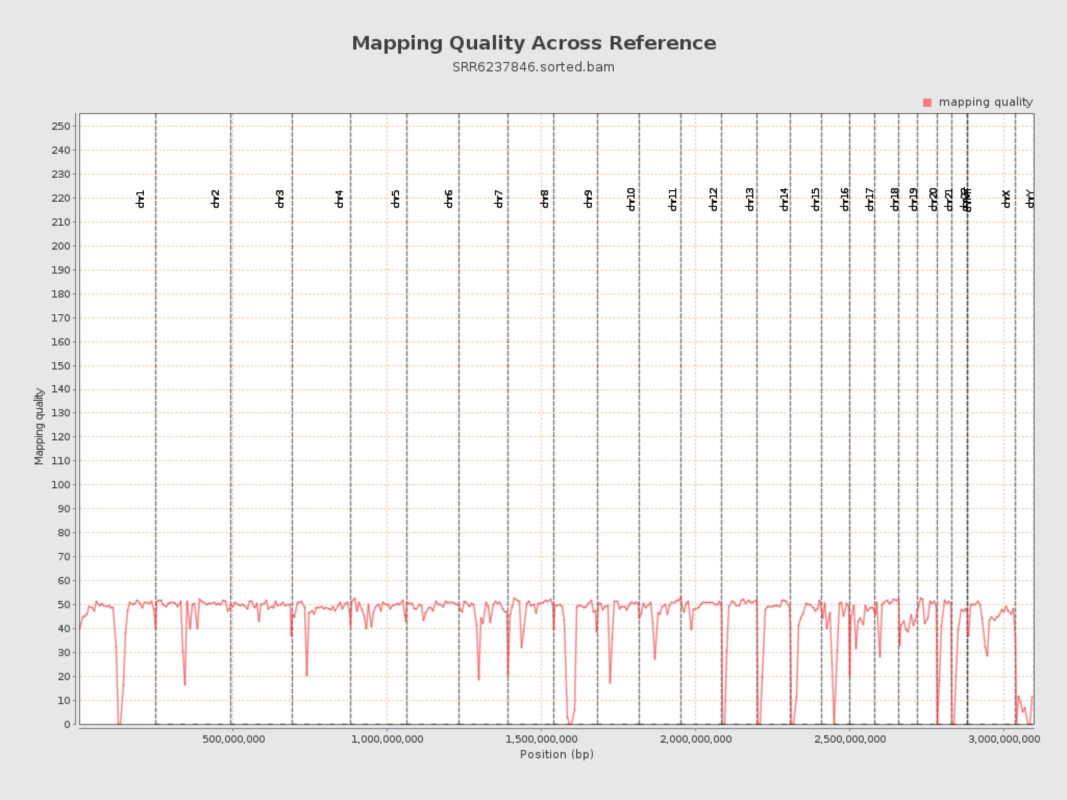
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram