Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 07:14:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3212677.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_SRR3212677 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3212677.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 07:14:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3212677.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,978,966
Mapped reads	2,798,630 / 93.95%
Unmapped reads	180,336 / 6.05%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,544 / 0.45%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	158,498 / 5.32%
Duplication rate	4.75%
Clipped reads	1,082,903 / 36.35%

2.2. ACGT Content

Number/percentage of A's	54,647,873 / 28.61%
Number/percentage of C's	36,283,763 / 18.99%
Number/percentage of T's	59,731,492 / 31.27%
Number/percentage of G's	40,375,976 / 21.13%
Number/percentage of N's	2,155 / 0%
GC Percentage	40.13%

2.3. Coverage

Mean	0.0617

Standard Deviation	0.4237

2.4. Mapping Quality

Mean Mapping Quality	48.1

2.5. Mismatches and indels

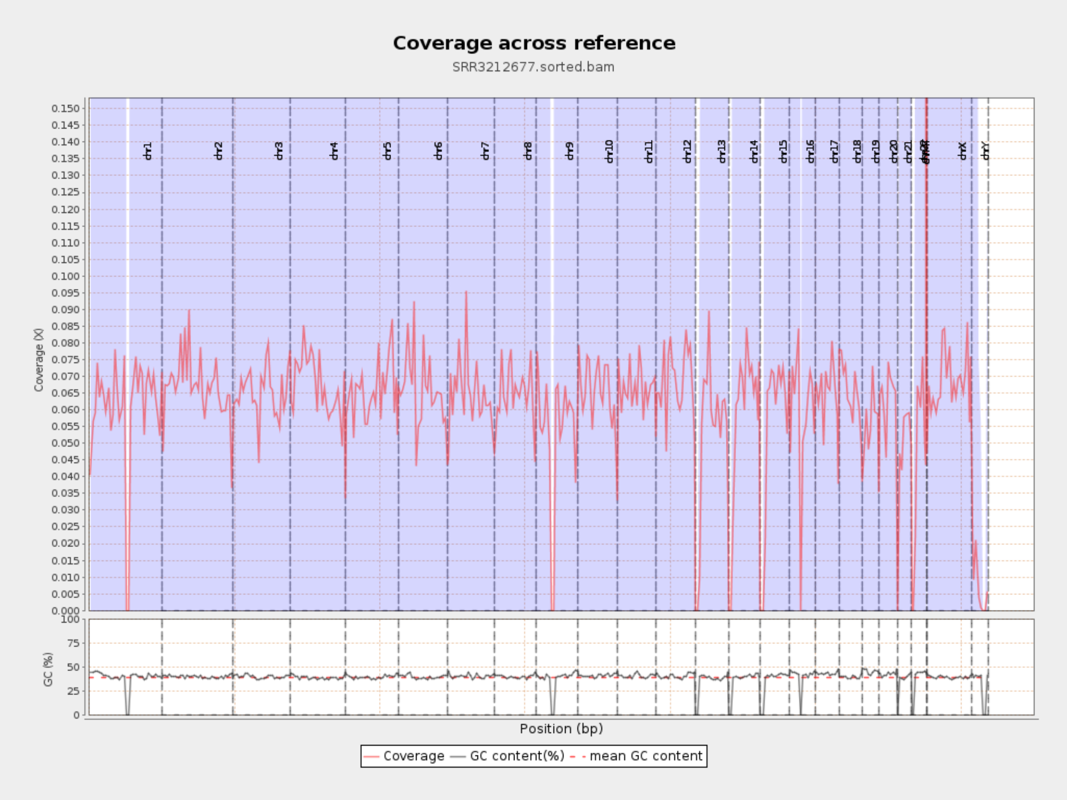
General error rate	0.79%
Mismatches	1,490,758
Insertions	12,953
Mapped reads with at least one insertion	0.46%
Deletions	36,118
Mapped reads with at least one deletion	1.28%
Homopolymer indels	48.3%

2.6. Chromosome stats

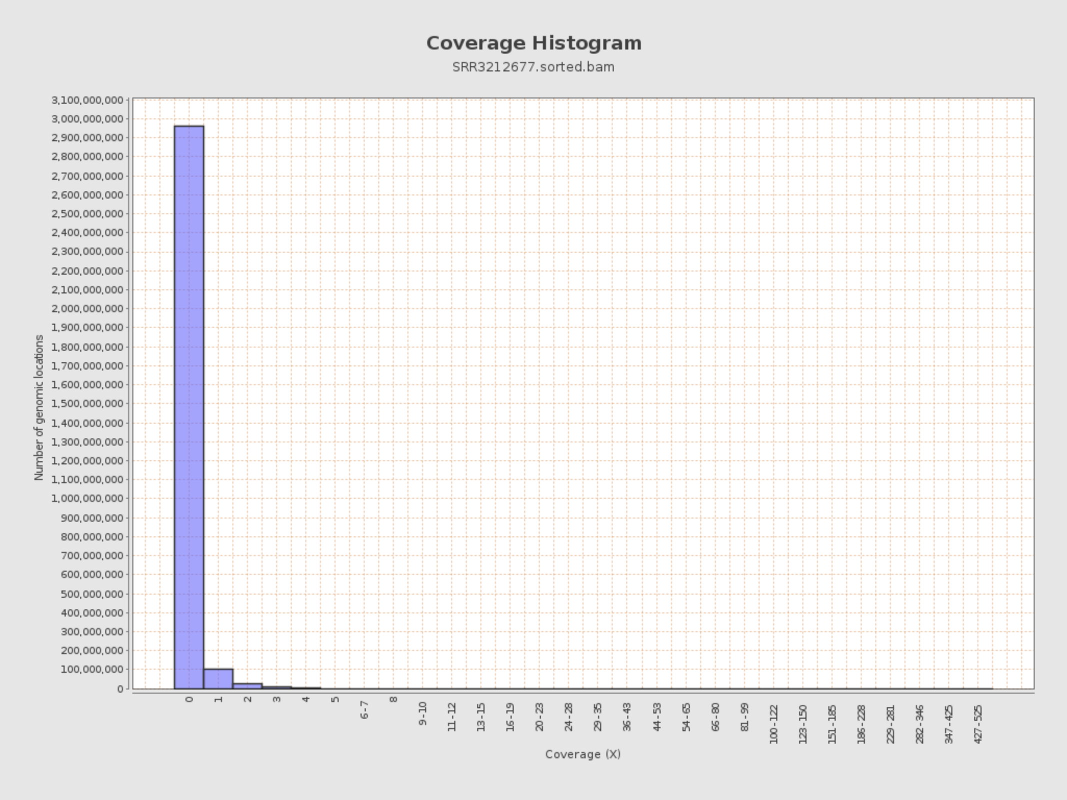
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14965893	0.06	0.5445
chr2	243199373	16392417	0.0674	0.4686
chr3	198022430	12877650	0.065	0.3394
chr4	191154276	12880054	0.0674	0.3613
chr5	180915260	11891484	0.0657	0.3428
chr6	171115067	11305028	0.0661	0.4581
chr7	159138663	10416251	0.0655	0.5571

chr8	146364022	9477578	0.0648	0.4866
chr9	141213431	7406478	0.0524	0.4067
chr10	135534747	8955685	0.0661	0.4028
chr11	135006516	8965145	0.0664	0.4517
chr12	133851895	9265292	0.0692	0.3543
chr13	115169878	5957107	0.0517	0.3024
chr14	107349540	6078202	0.0566	0.336
chr15	102531392	5546019	0.0541	0.3149
chr16	90354753	5358399	0.0593	0.3461
chr17	81195210	5236142	0.0645	0.372
chr18	78077248	5166607	0.0662	0.7223
chr19	59128983	3298742	0.0558	0.4322
chr20	63025520	3952252	0.0627	0.3434
chr21	48129895	2292138	0.0476	0.3155
chr22	51304566	2225716	0.0434	0.2732
chrMT	16571	200984	12.1287	9.0594
chrX	155270560	10563413	0.068	0.3733
chrY	59373566	430557	0.0073	0.1561

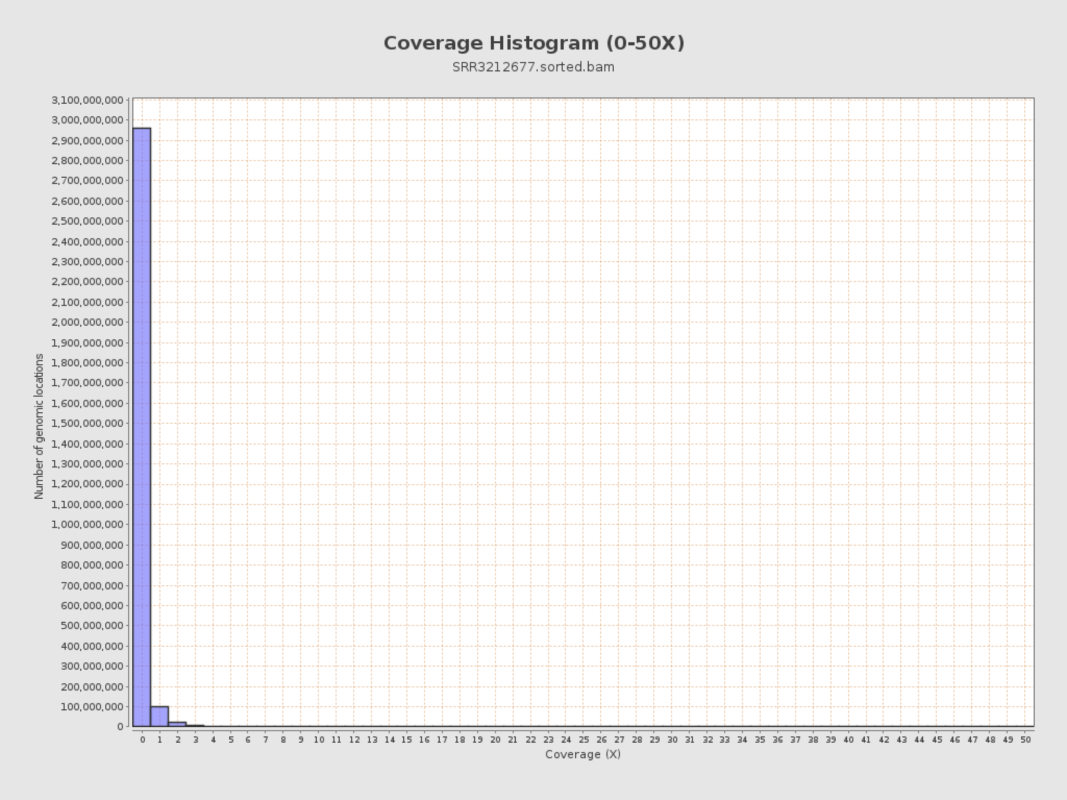
3. Results : Coverage across reference



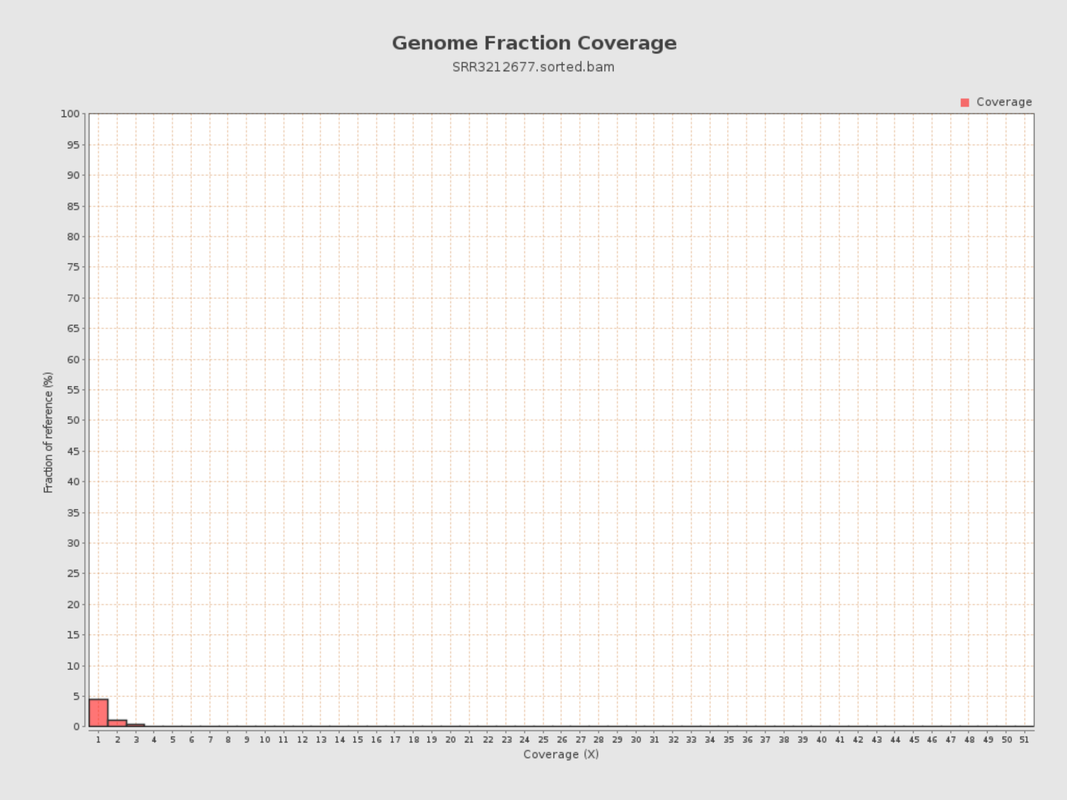
4. Results : Coverage Histogram



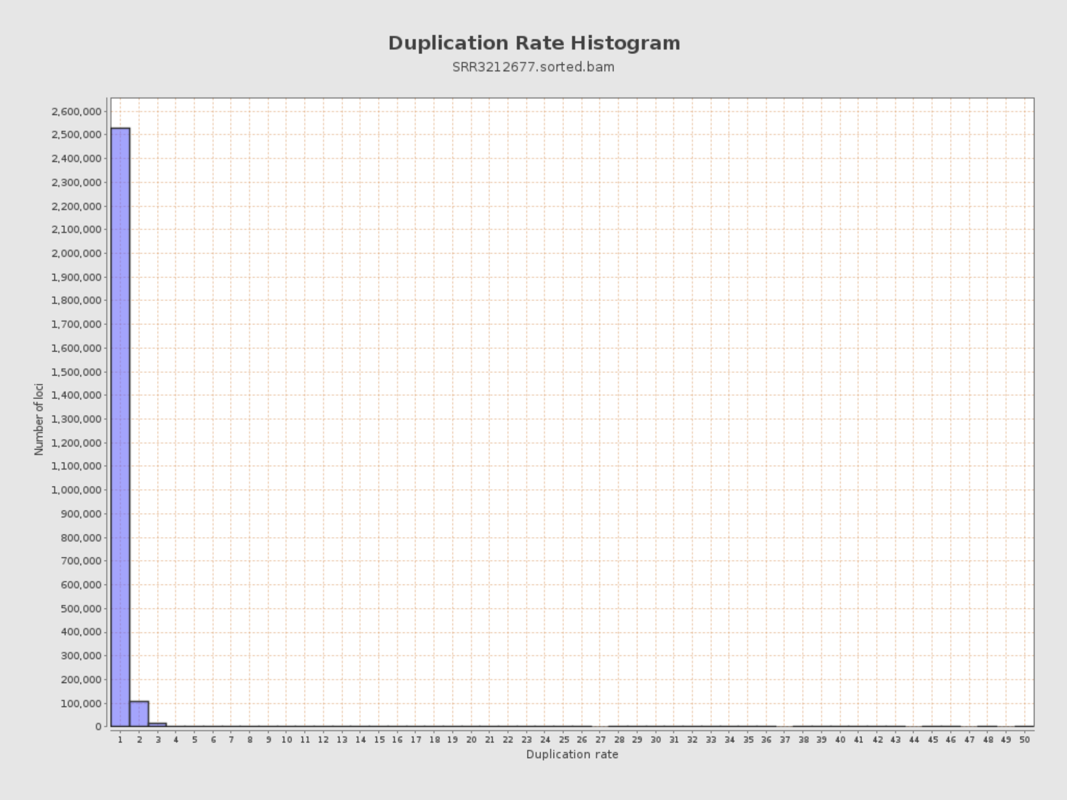
5. Results : Coverage Histogram (0-50X)



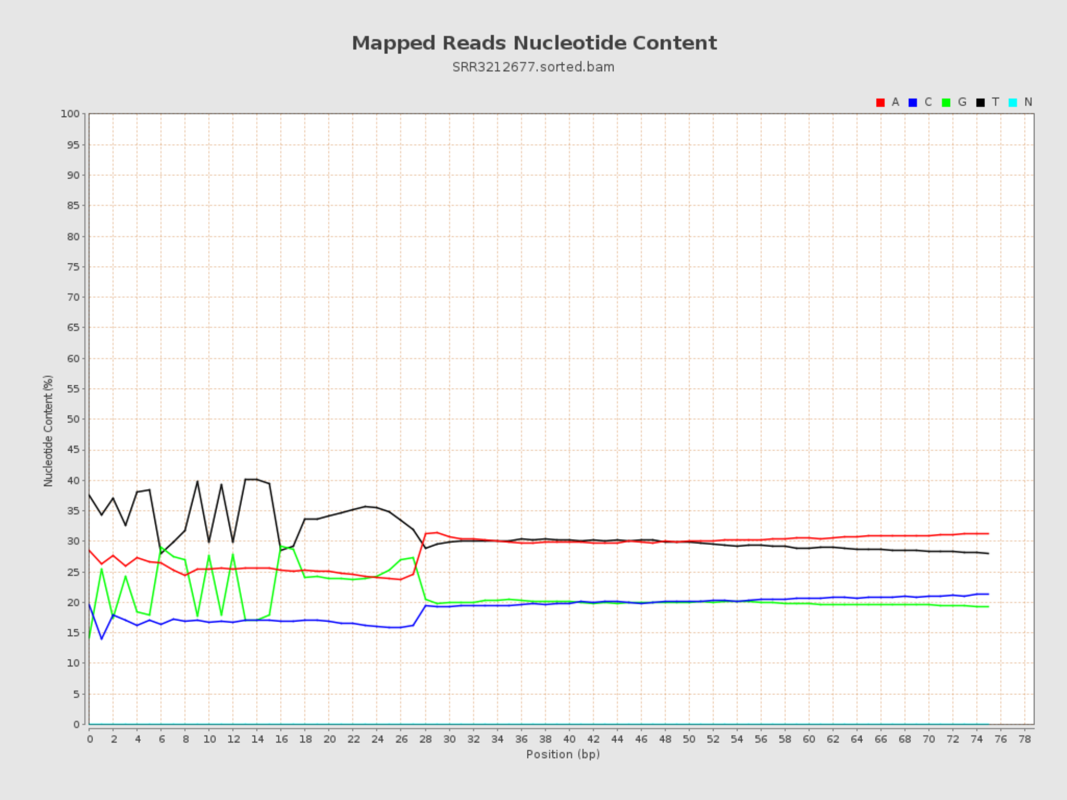
6. Results : Genome Fraction Coverage



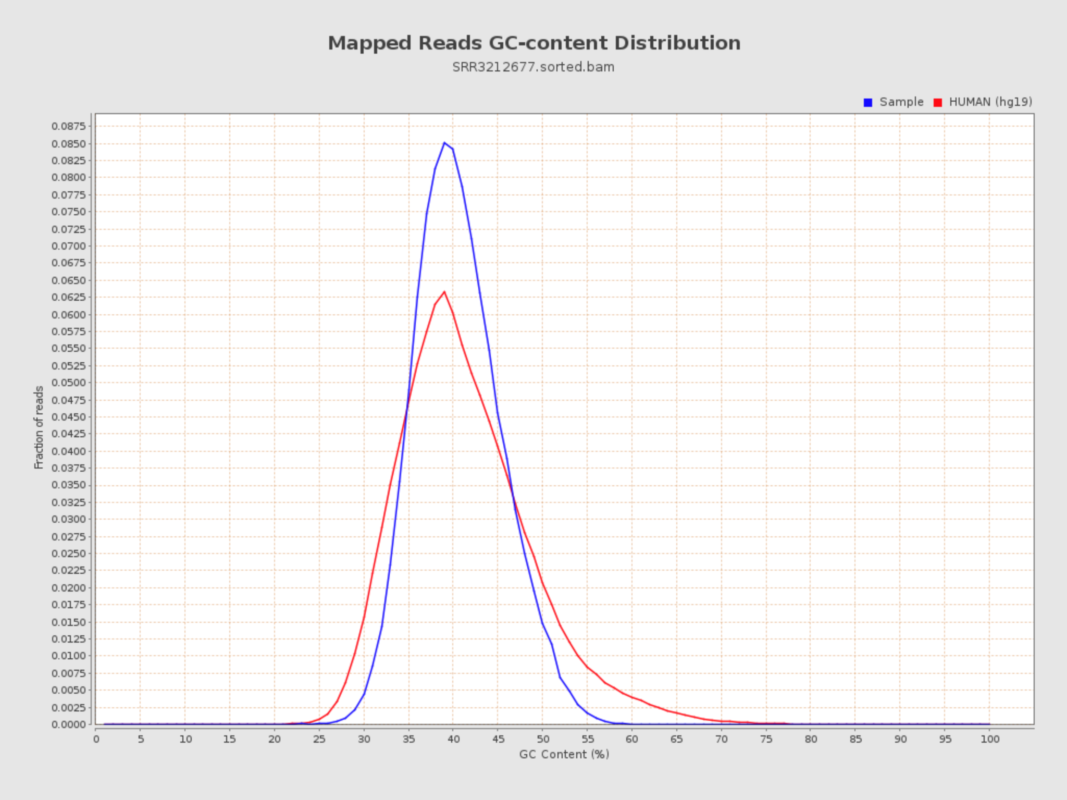
7. Results : Duplication Rate Histogram



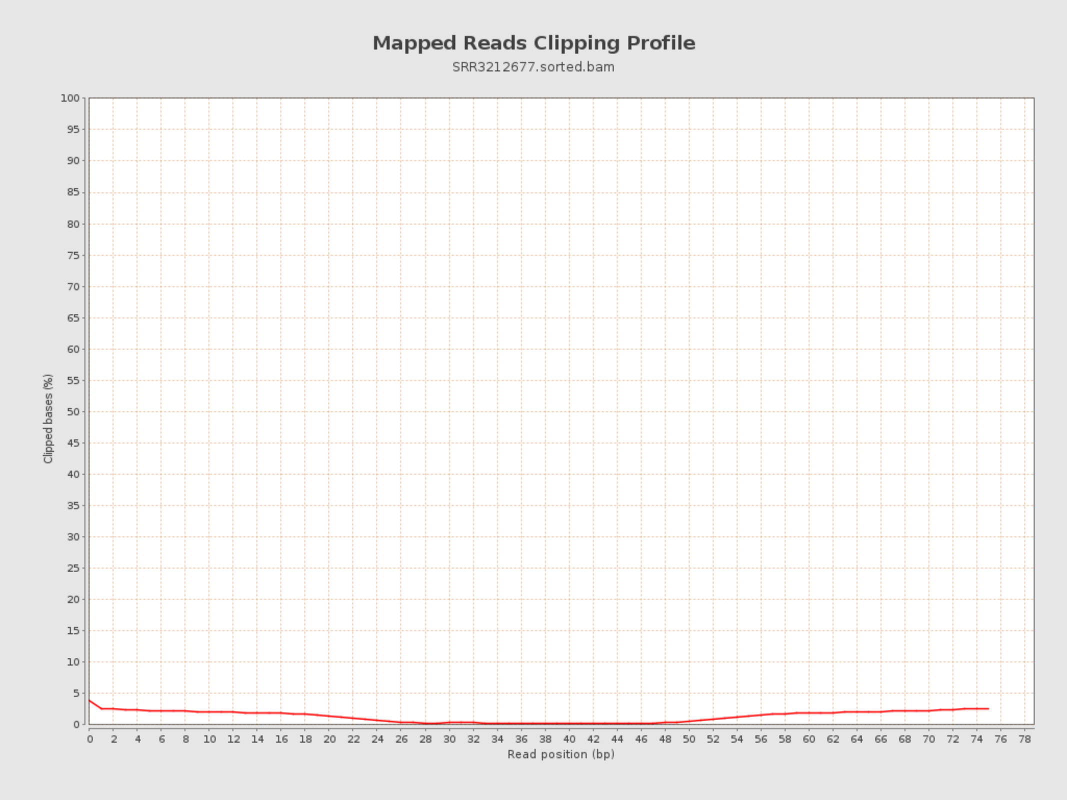
8. Results : Mapped Reads Nucleotide Content



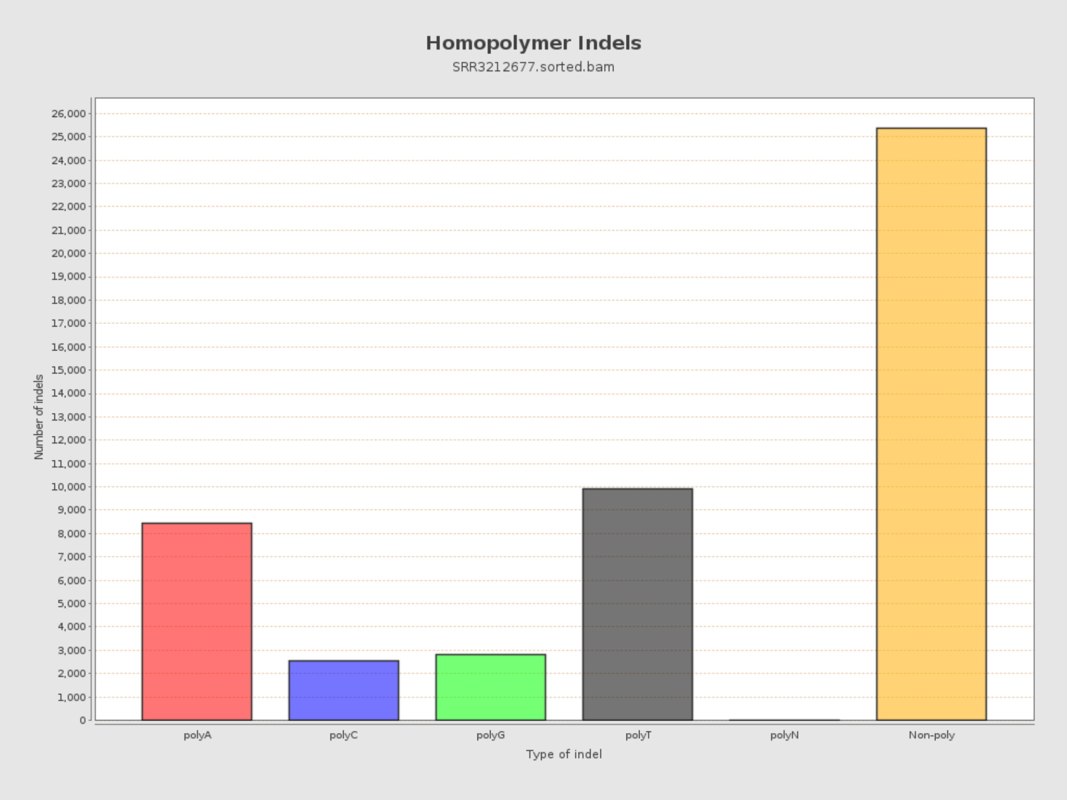
9. Results : Mapped Reads GC-content Distribution



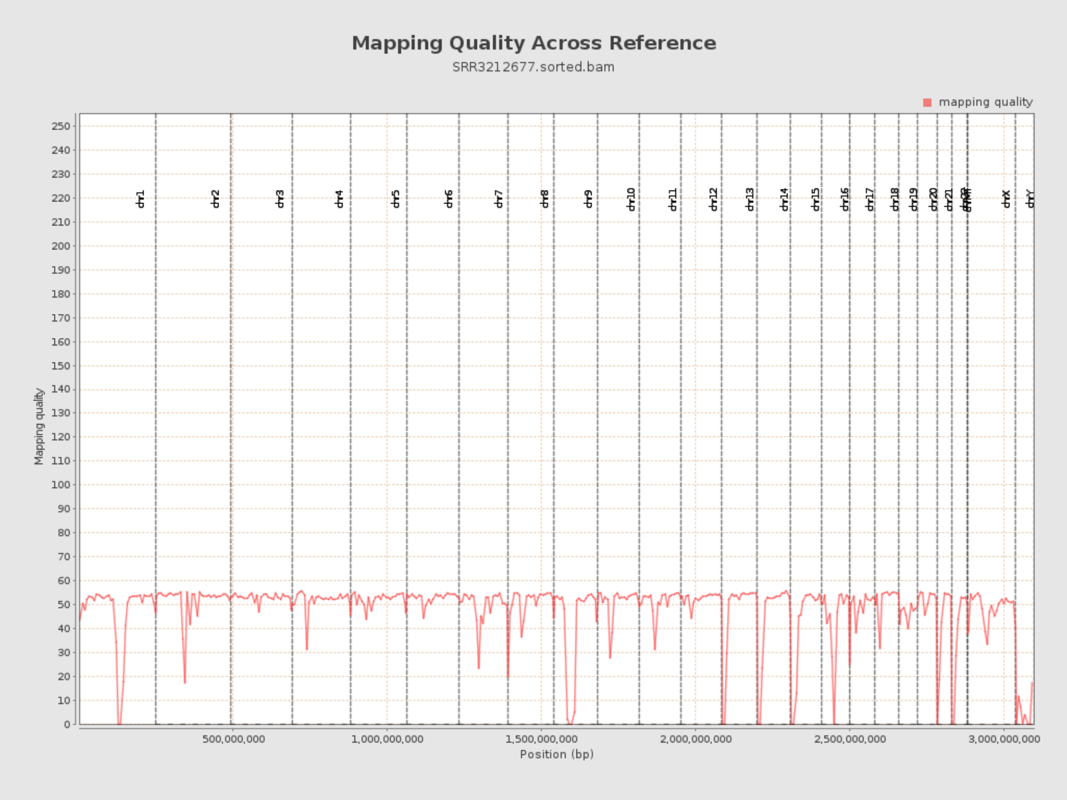
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram