Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/01 09:01:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472829.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_SRR3472829 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472829.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 01 09:01:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472829.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,076,015
Mapped reads	2,590,740 / 84.22%
Unmapped reads	485,275 / 15.78%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	25,292 / 0.82%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	80,394 / 2.61%
Duplication rate	2.21%
Clipped reads	1,343,459 / 43.68%

2.2. ACGT Content

Number/percentage of A's	45,210,630 / 26.9%
Number/percentage of C's	33,601,476 / 19.99%
Number/percentage of T's	49,842,453 / 29.65%
Number/percentage of G's	39,437,920 / 23.46%
Number/percentage of N's	3,889 / 0%
GC Percentage	43.45%

2.3. Coverage

Mean	0.0543

Standard Deviation	0.3913

2.4. Mapping Quality

Mean Mapping Quality	43.91

2.5. Mismatches and indels

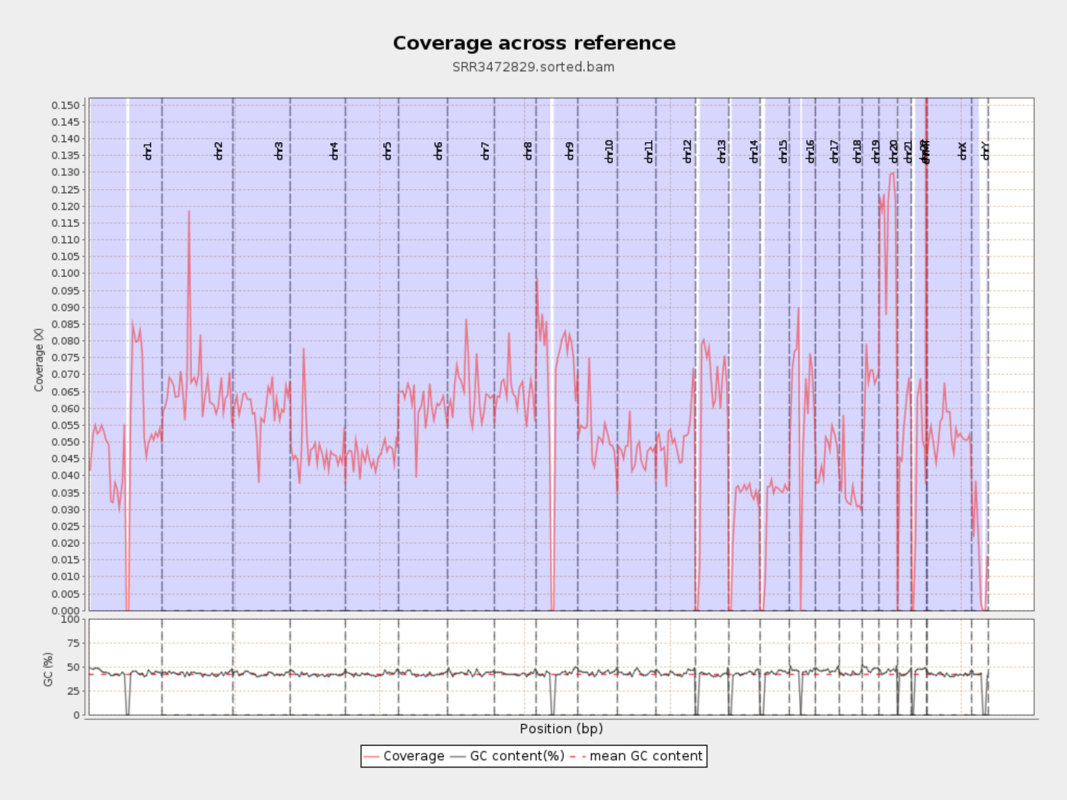
General error rate	0.87%
Mismatches	1,429,063
Insertions	13,506
Mapped reads with at least one insertion	0.52%
Deletions	37,507
Mapped reads with at least one deletion	1.43%
Homopolymer indels	44.67%

2.6. Chromosome stats

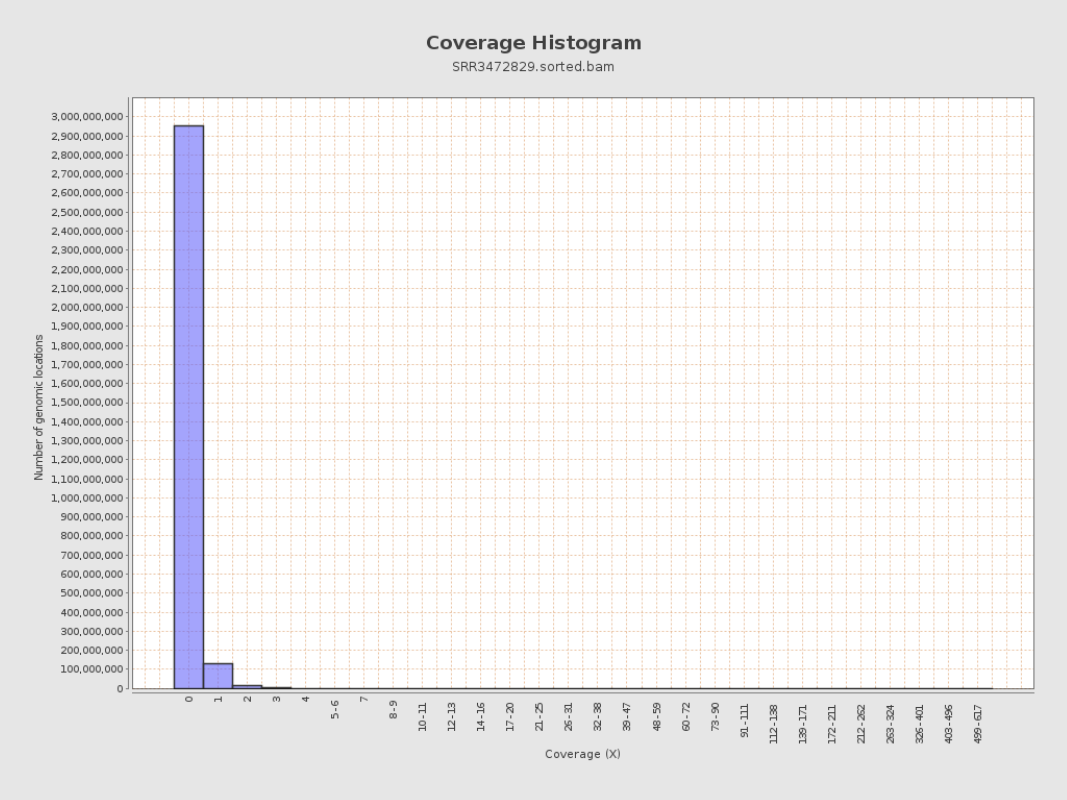
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12431256	0.0499	0.488
chr2	243199373	16173999	0.0665	0.5974
chr3	198022430	11900098	0.0601	0.2735
chr4	191154276	9059460	0.0474	0.2834
chr5	180915260	8352212	0.0462	0.2422
chr6	171115067	10453199	0.0611	0.3068
chr7	159138663	10363267	0.0651	0.5068

chr8	146364022	9441372	0.0645	0.3821
chr9	141213431	9702704	0.0687	0.4683
chr10	135534747	6996354	0.0516	0.3623
chr11	135006516	6326235	0.0469	0.3871
chr12	133851895	6830035	0.051	0.2638
chr13	115169878	6793369	0.059	0.282
chr14	107349540	3219505	0.03	0.248
chr15	102531392	2993472	0.0292	0.2186
chr16	90354753	5658970	0.0626	0.3224
chr17	81195210	3754101	0.0462	0.2697
chr18	78077248	2785734	0.0357	0.7913
chr19	59128983	3992124	0.0675	0.4154
chr20	63025520	7407619	0.1175	0.4143
chr21	48129895	2436384	0.0506	0.3061
chr22	51304566	2005059	0.0391	0.2387
chrMT	16571	19870	1.1991	1.1842
chrX	155270560	8176038	0.0527	0.3003
chrY	59373566	891761	0.015	0.2032

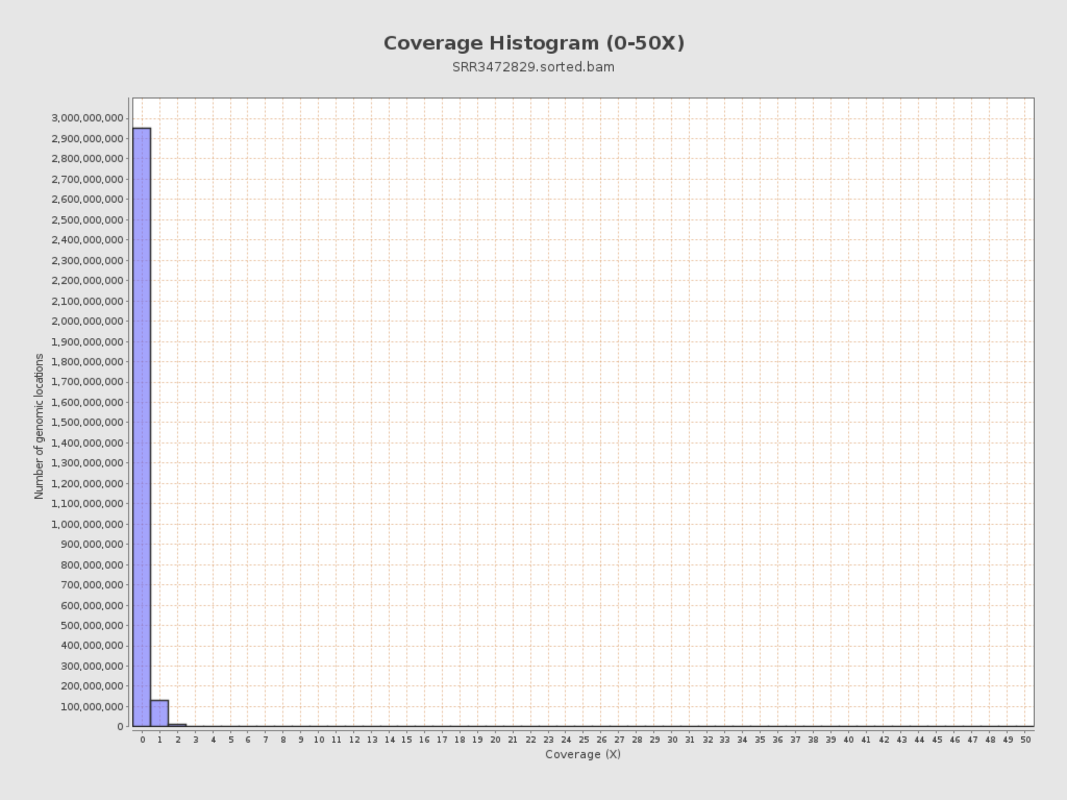
3. Results : Coverage across reference



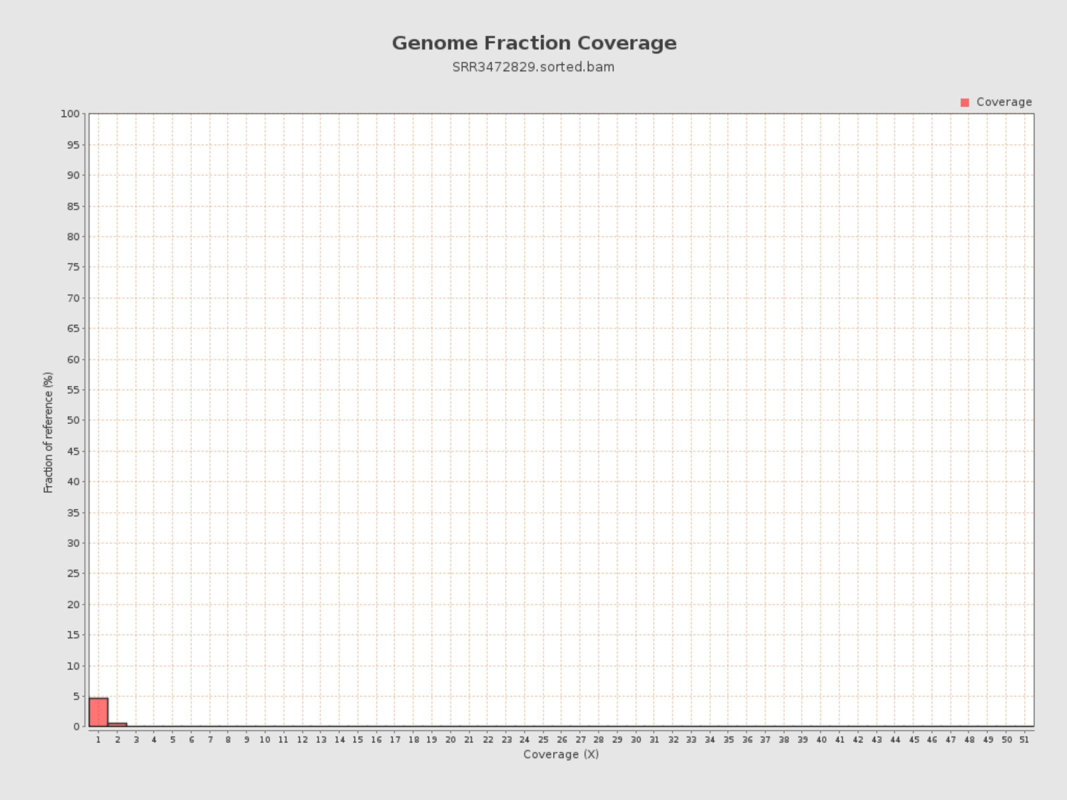
4. Results : Coverage Histogram



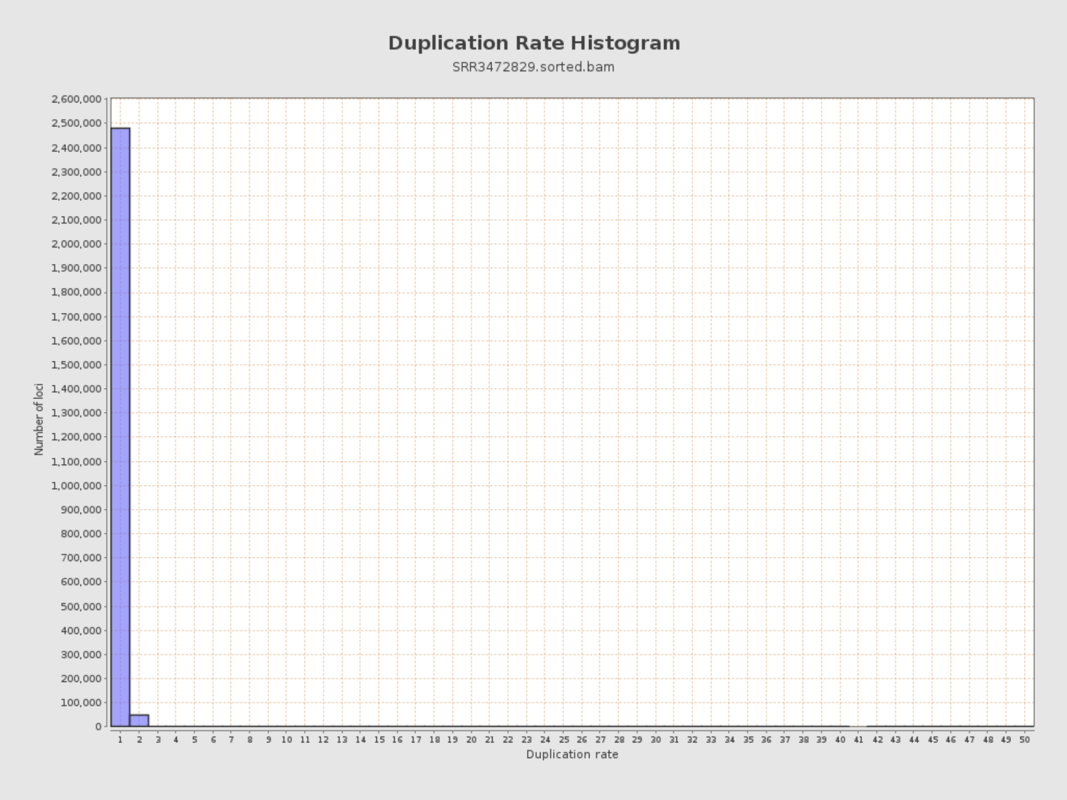
5. Results : Coverage Histogram (0-50X)



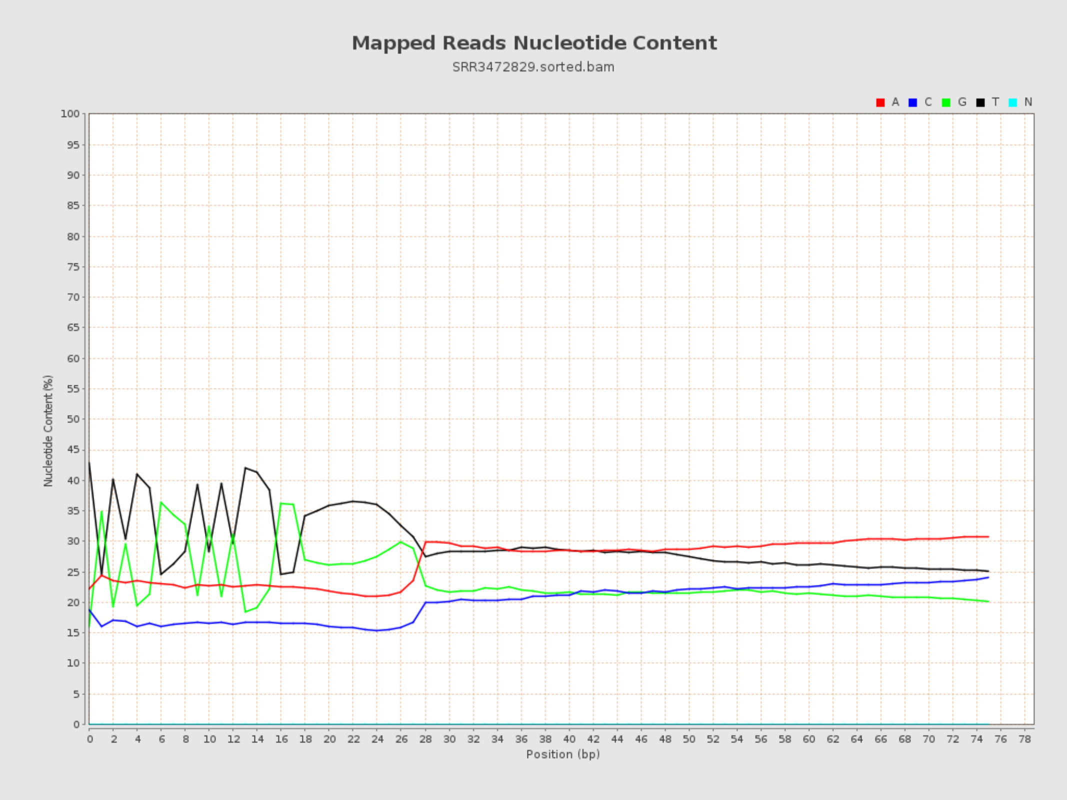
6. Results : Genome Fraction Coverage



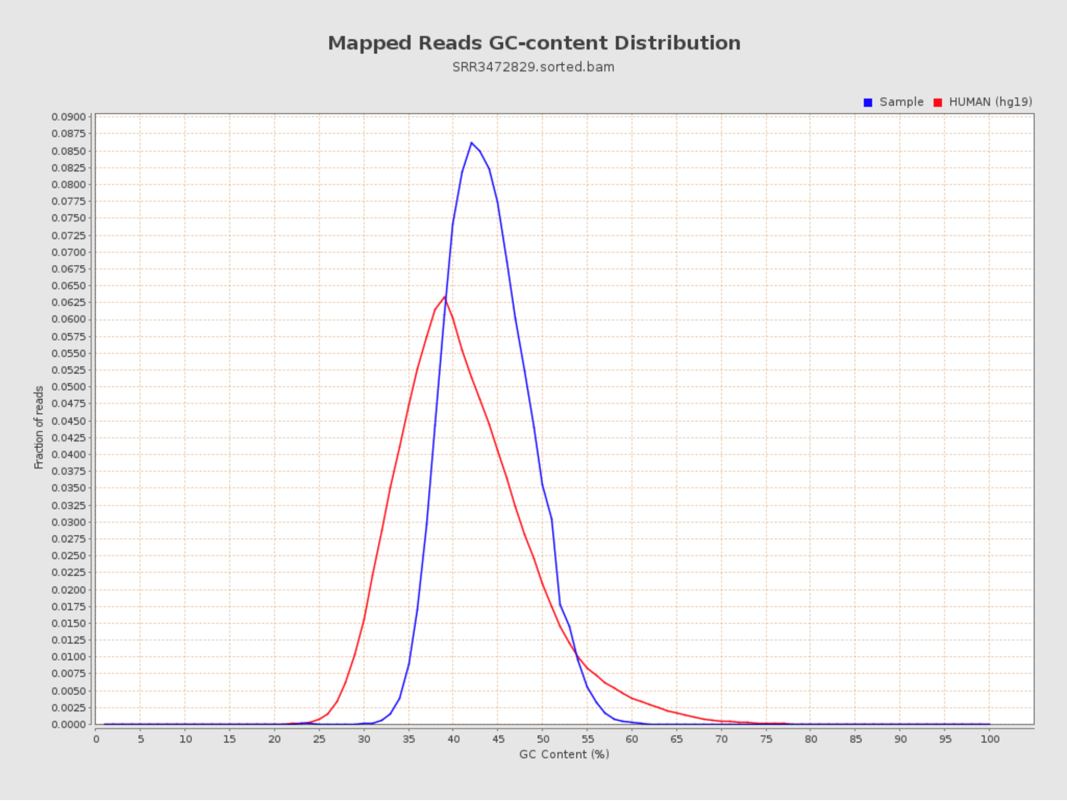
7. Results : Duplication Rate Histogram



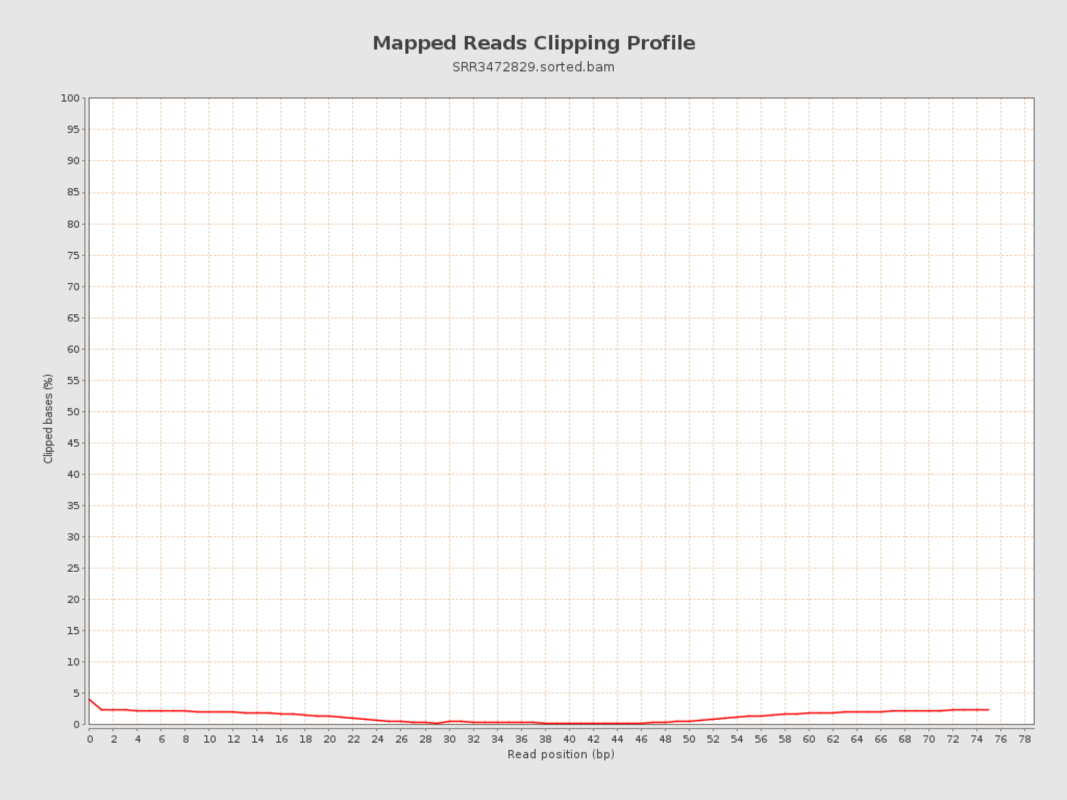
8. Results : Mapped Reads Nucleotide Content



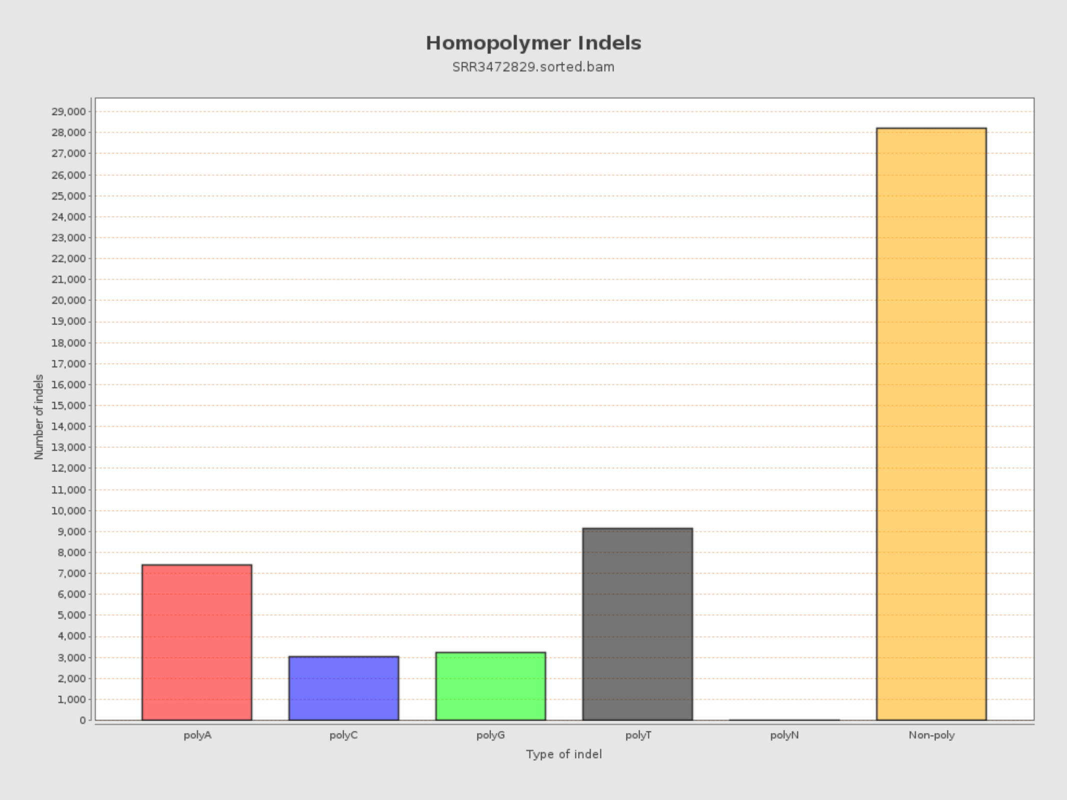
9. Results : Mapped Reads GC-content Distribution



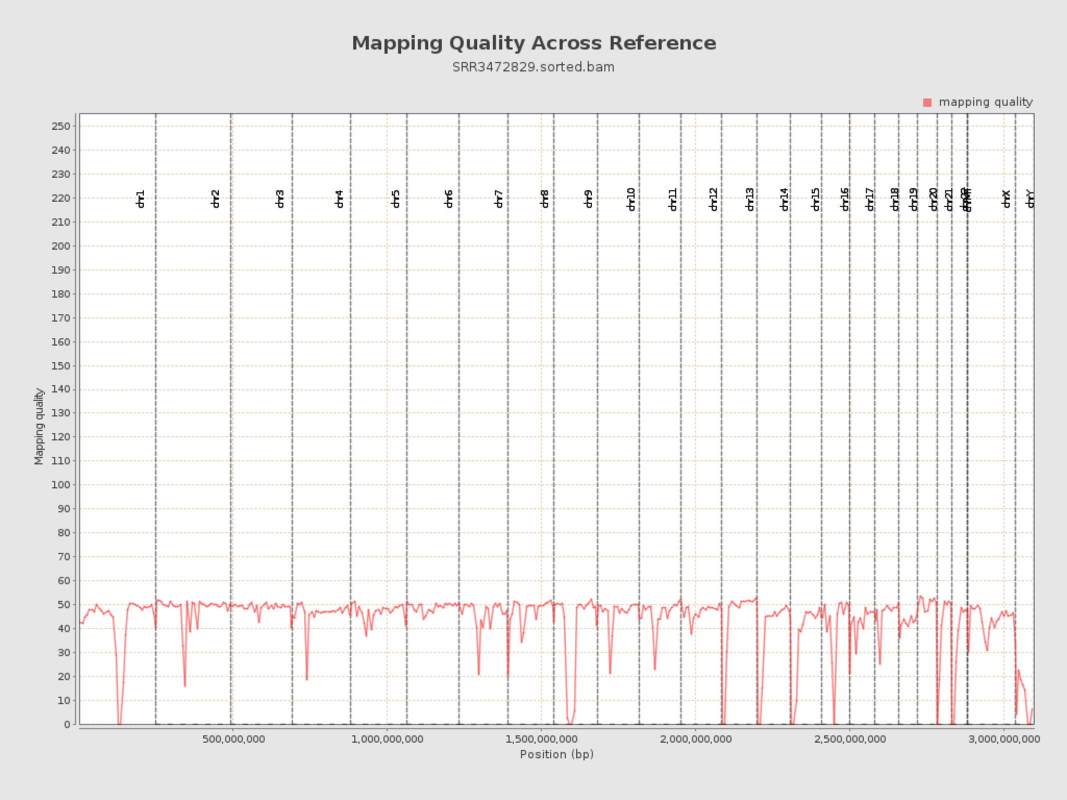
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram