Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 15:29:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084812.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_SRR3084812 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084812.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 15:29:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084812.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,330,291
Mapped reads	2,106,410 / 90.39%
Unmapped reads	223,881 / 9.61%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,694 / 0.89%
Read min/max/mean length	30 / 76 / 76.31
Duplicated reads (estimated)	99,279 / 4.26%
Duplication rate	4.07%
Clipped reads	939,980 / 40.34%

2.2. ACGT Content

Number/percentage of A's	38,040,353 / 27.08%
Number/percentage of C's	26,342,899 / 18.76%
Number/percentage of T's	44,023,207 / 31.34%
Number/percentage of G's	32,028,501 / 22.8%
Number/percentage of N's	20,184 / 0.01%
GC Percentage	41.56%

2.3. Coverage

Mean	0.0454

Standard Deviation	0.3099

2.4. Mapping Quality

Mean Mapping Quality	45.15

2.5. Mismatches and indels

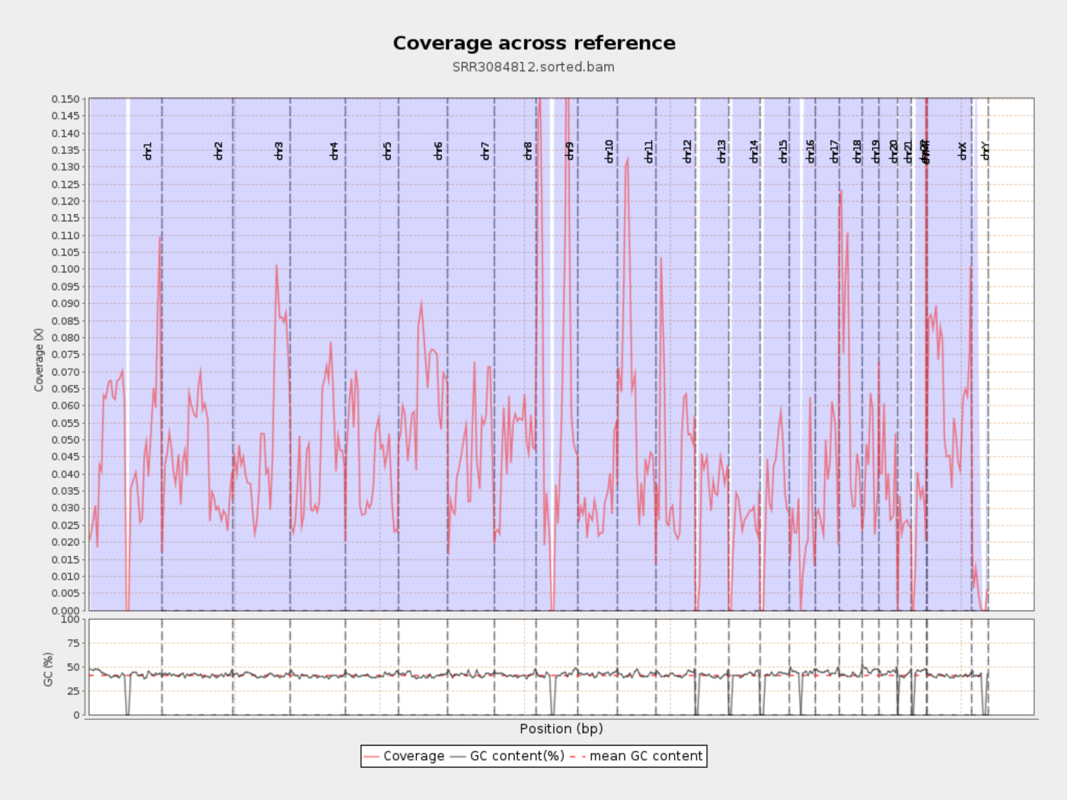
General error rate	0.79%
Mismatches	1,087,699
Insertions	10,922
Mapped reads with at least one insertion	0.52%
Deletions	32,146
Mapped reads with at least one deletion	1.51%
Homopolymer indels	47.57%

2.6. Chromosome stats

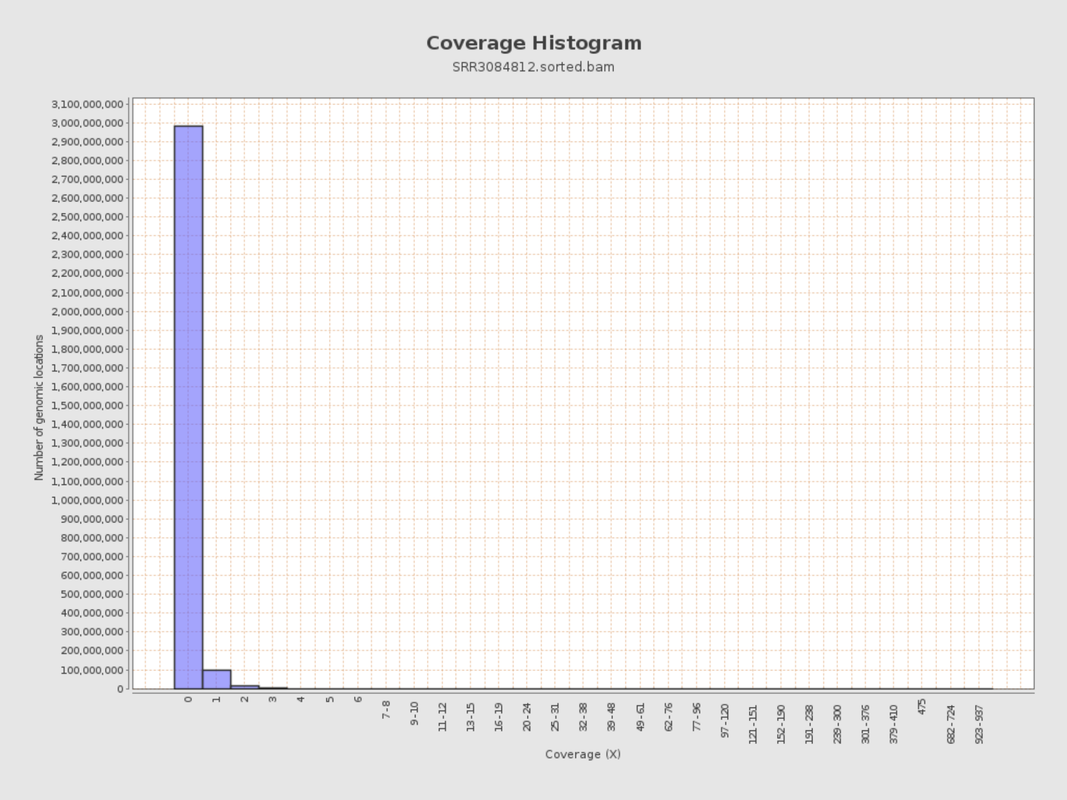
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11995773	0.0481	0.3582
chr2	243199373	10559433	0.0434	0.4819
chr3	198022430	10282887	0.0519	0.2671
chr4	191154276	8502584	0.0445	0.2511
chr5	180915260	7841496	0.0433	0.2445
chr6	171115067	11056513	0.0646	0.3193
chr7	159138663	7330842	0.0461	0.3146

chr8	146364022	7006802	0.0479	0.298
chr9	141213431	9615316	0.0681	0.3608
chr10	135534747	4204385	0.031	0.2165
chr11	135006516	8363104	0.0619	0.4195
chr12	133851895	5919228	0.0442	0.2494
chr13	115169878	3778085	0.0328	0.2126
chr14	107349540	2549374	0.0237	0.1879
chr15	102531392	3485989	0.034	0.2309
chr16	90354753	2134876	0.0236	0.1916
chr17	81195210	3091294	0.0381	0.2671
chr18	78077248	5153252	0.066	0.4581
chr19	59128983	2558583	0.0433	0.2951
chr20	63025520	2468931	0.0392	0.2364
chr21	48129895	1147759	0.0238	0.1903
chr22	51304566	1215436	0.0237	0.178
chrMT	16571	22859	1.3795	1.4578
chrX	155270560	9920830	0.0639	0.3185
chrY	59373566	302757	0.0051	0.0934

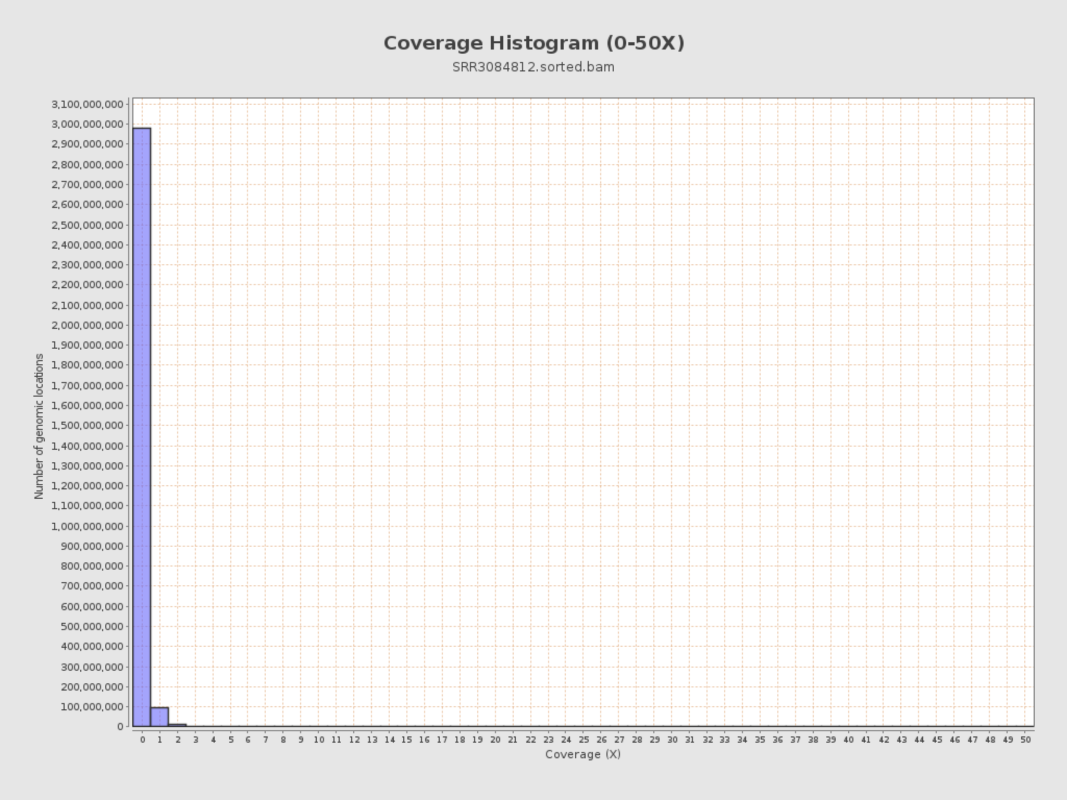
3. Results : Coverage across reference



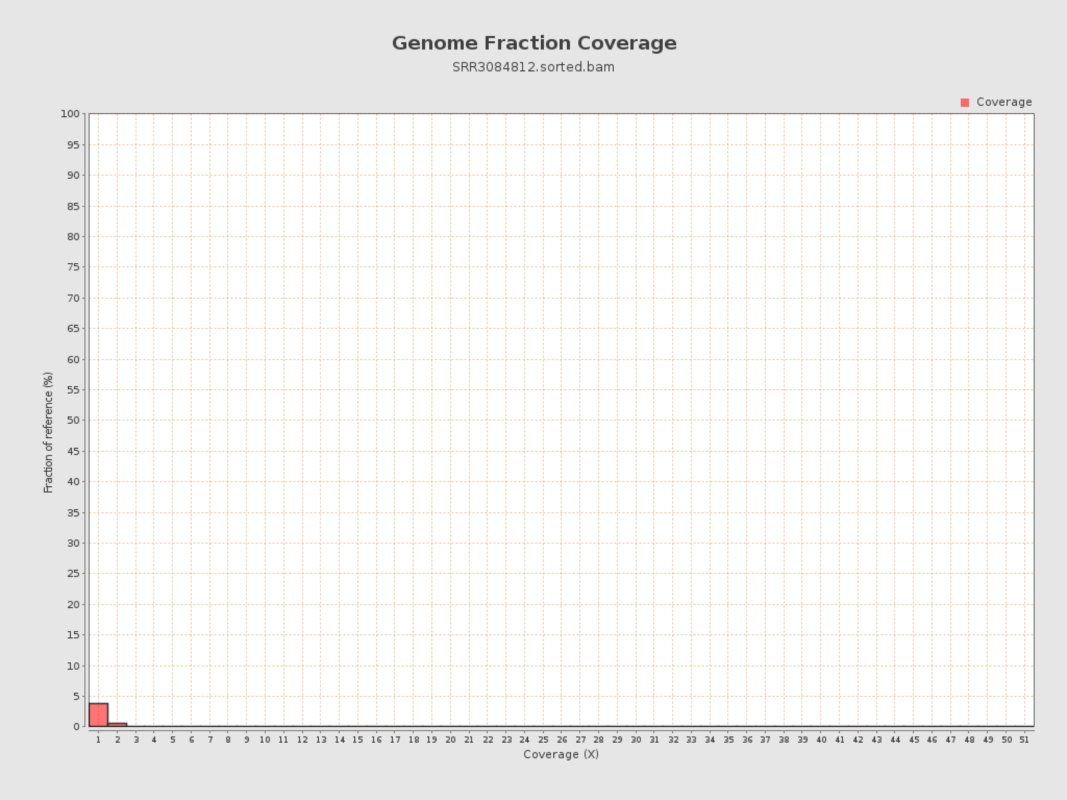
4. Results : Coverage Histogram



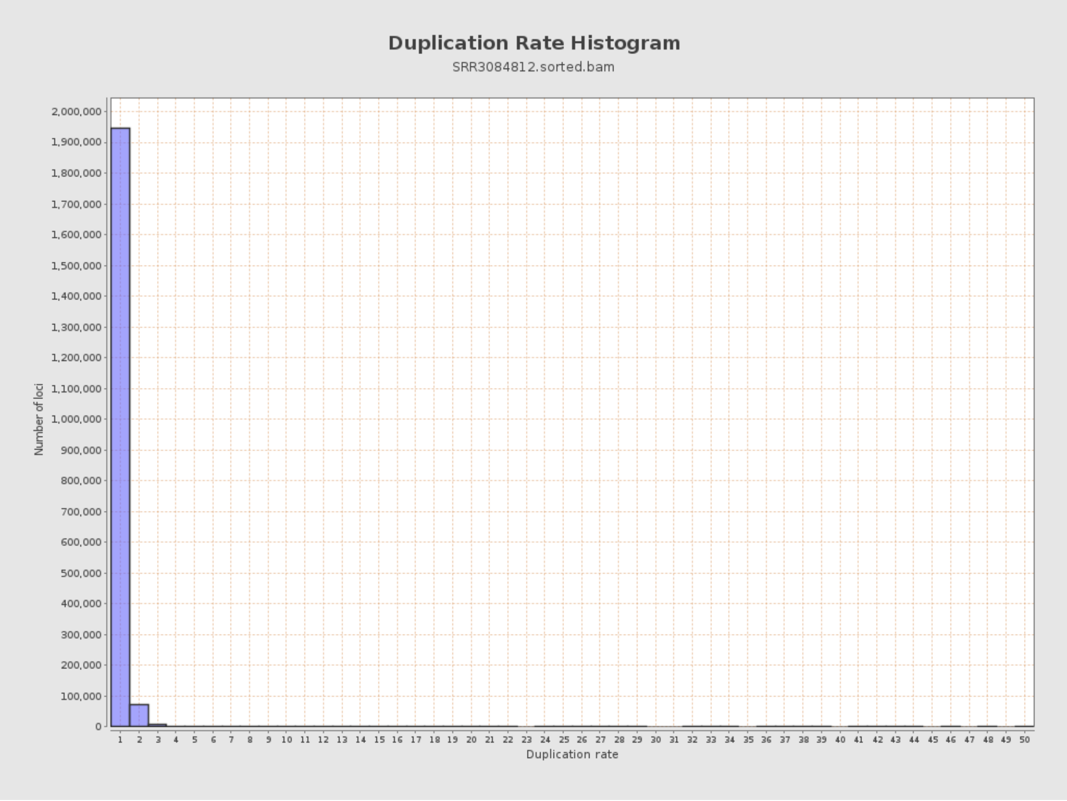
5. Results : Coverage Histogram (0-50X)



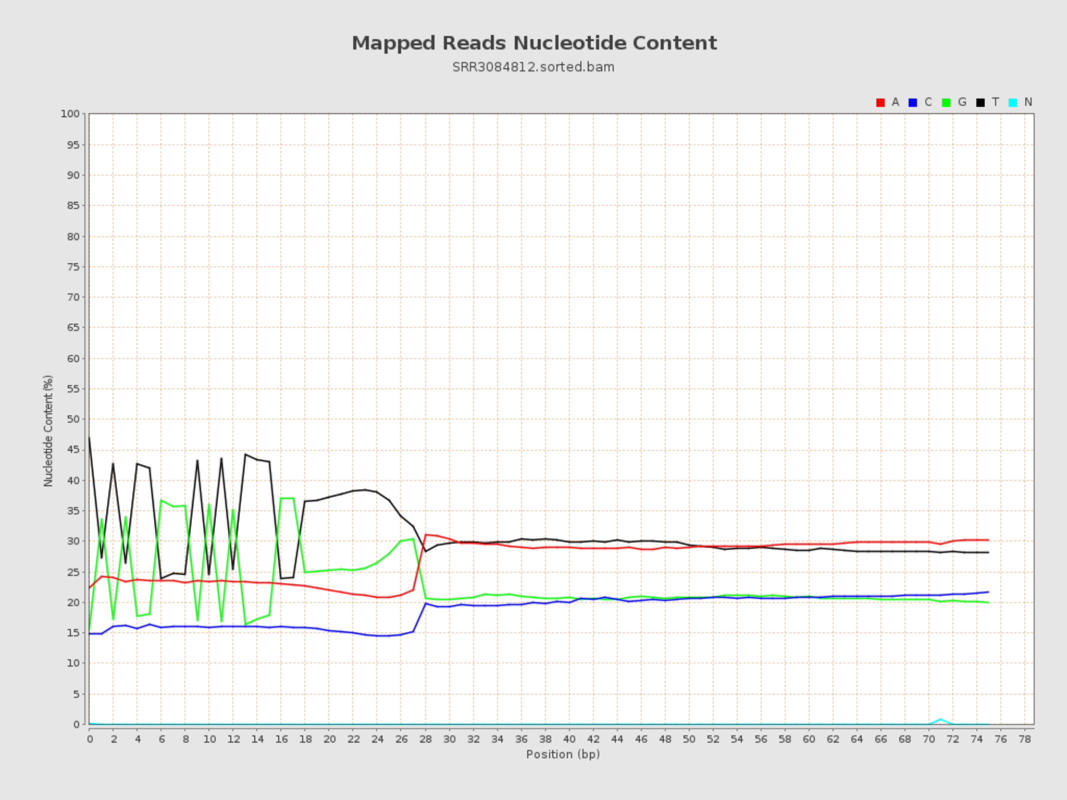
6. Results : Genome Fraction Coverage



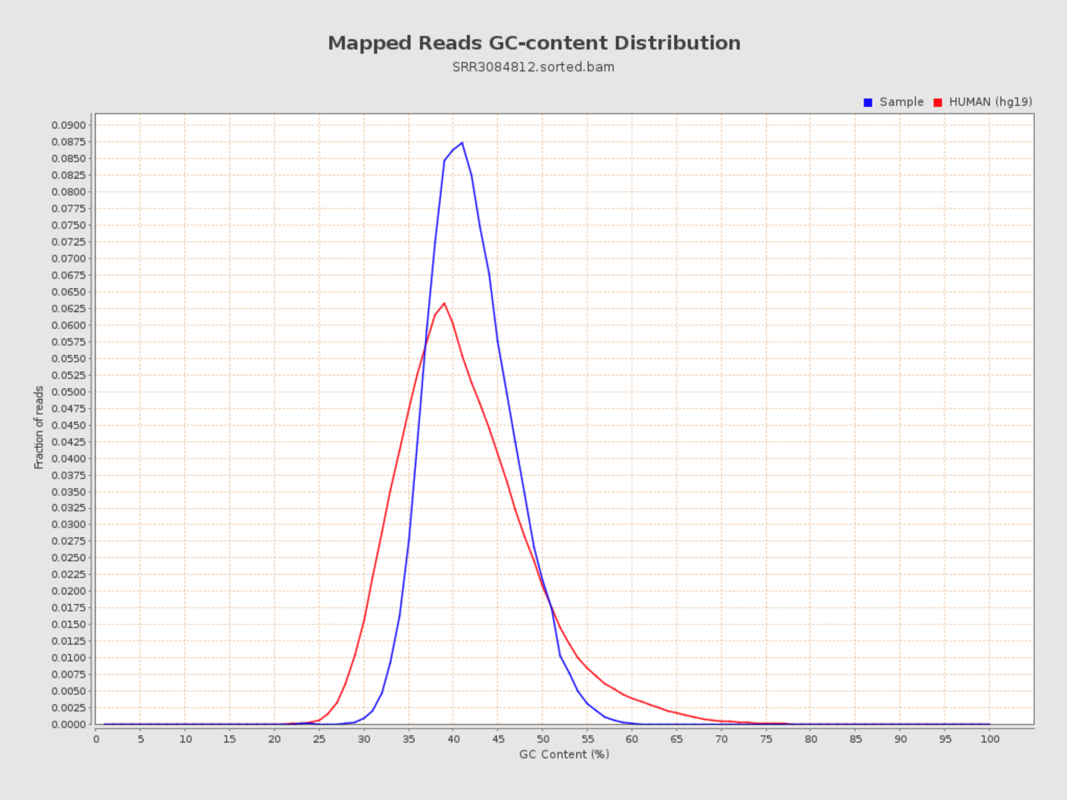
7. Results : Duplication Rate Histogram



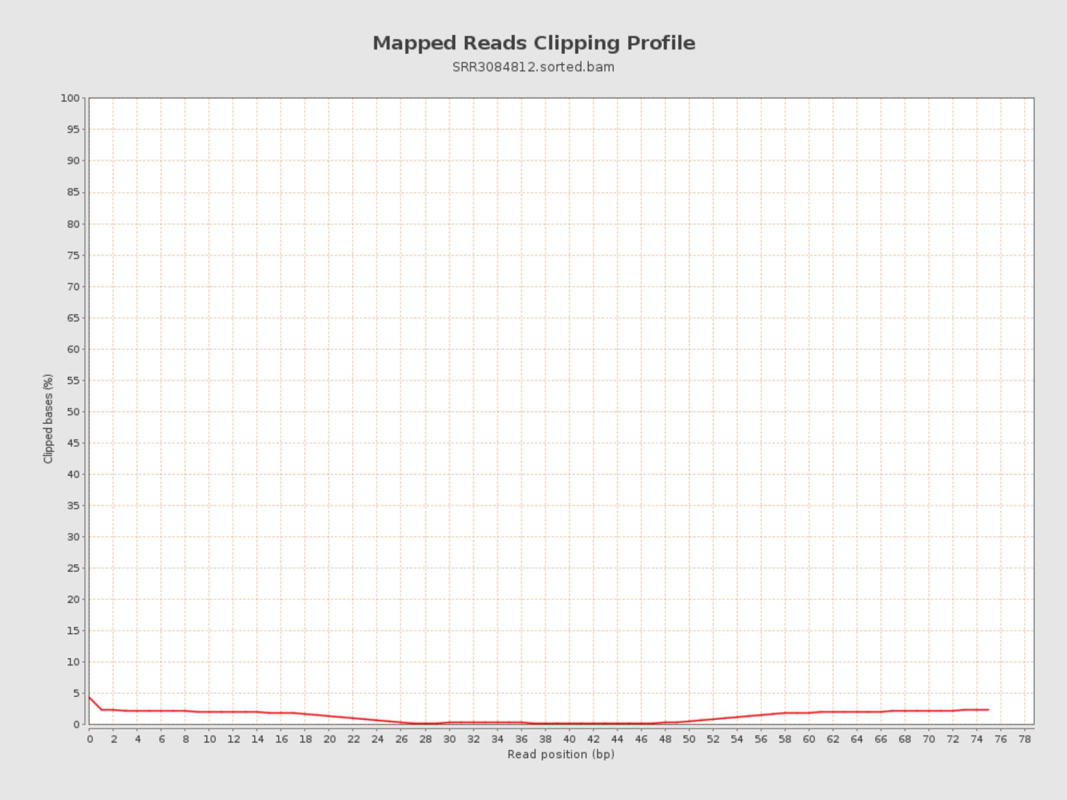
8. Results : Mapped Reads Nucleotide Content



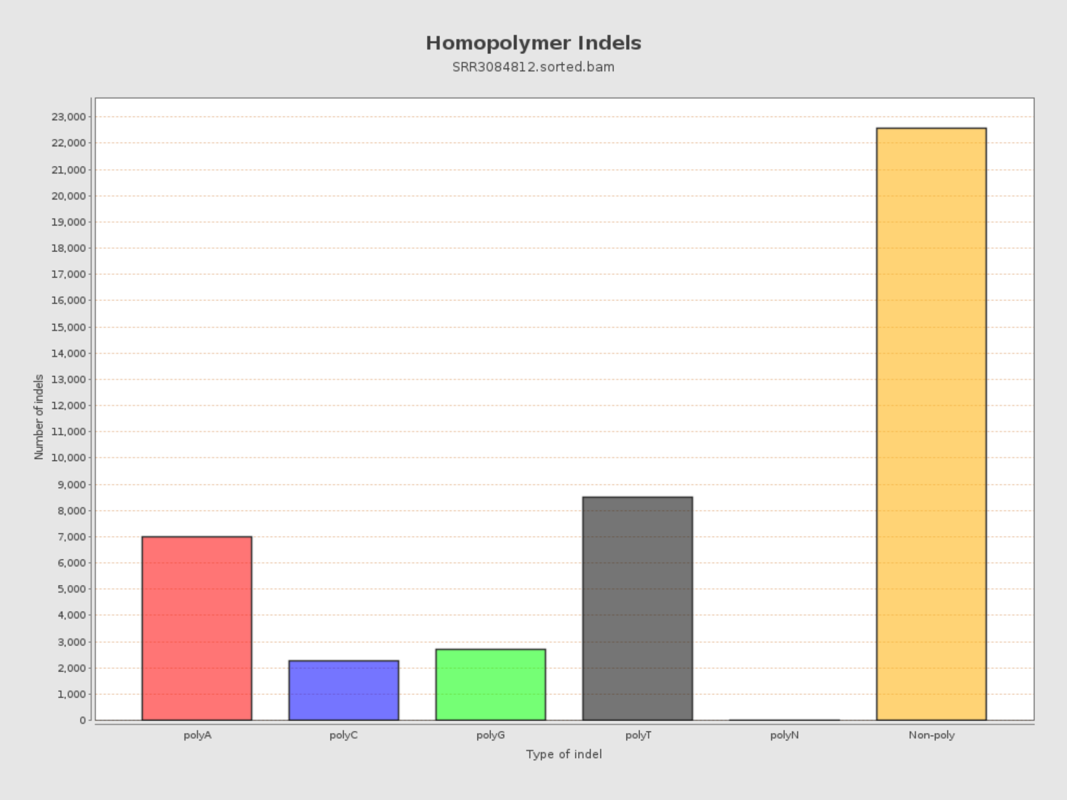
9. Results : Mapped Reads GC-content Distribution



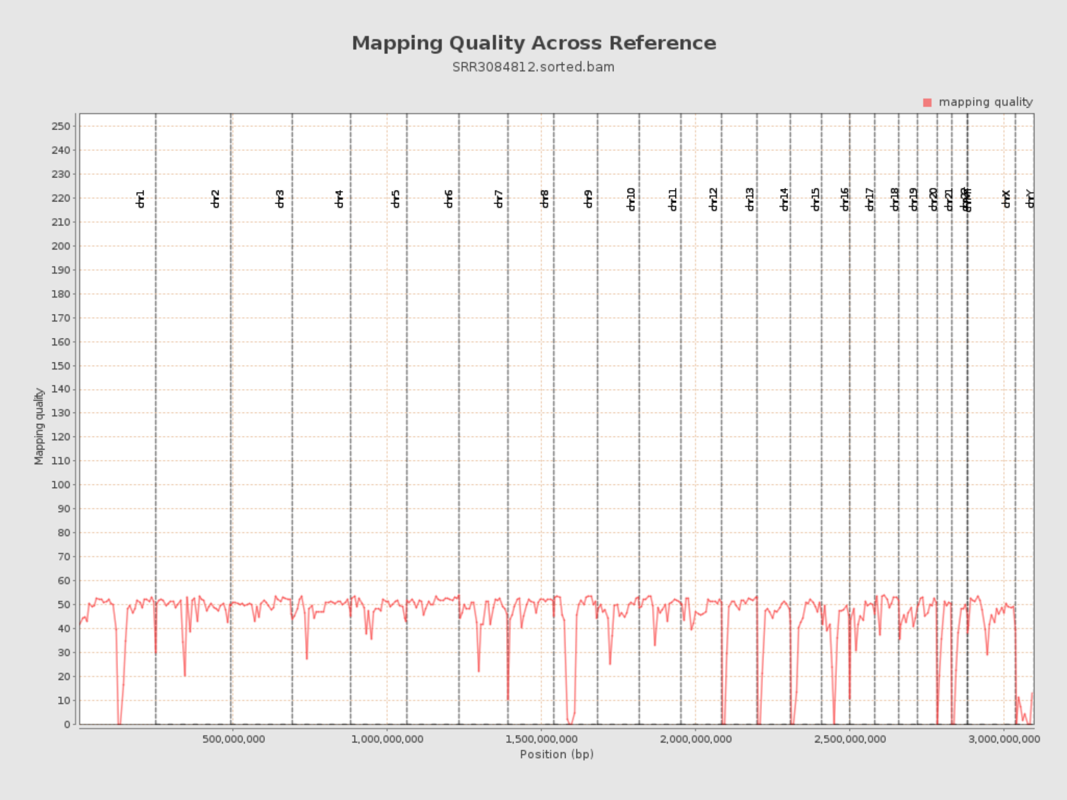
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram