Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 09:47:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080821.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_SRR3080821 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080821.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 09:47:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080821.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,970,769
Mapped reads	2,769,694 / 93.23%
Unmapped reads	201,075 / 6.77%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,748 / 0.63%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	158,328 / 5.33%
Duplication rate	4.76%
Clipped reads	897,663 / 30.22%

2.2. ACGT Content

Number/percentage of A's	55,959,979 / 29%
Number/percentage of C's	36,366,497 / 18.85%
Number/percentage of T's	60,478,034 / 31.35%
Number/percentage of G's	40,111,026 / 20.79%
Number/percentage of N's	27,153 / 0.01%
GC Percentage	39.64%

2.3. Coverage

Mean	0.0623

Standard Deviation	0.492

2.4. Mapping Quality

Mean Mapping Quality	47.13

2.5. Mismatches and indels

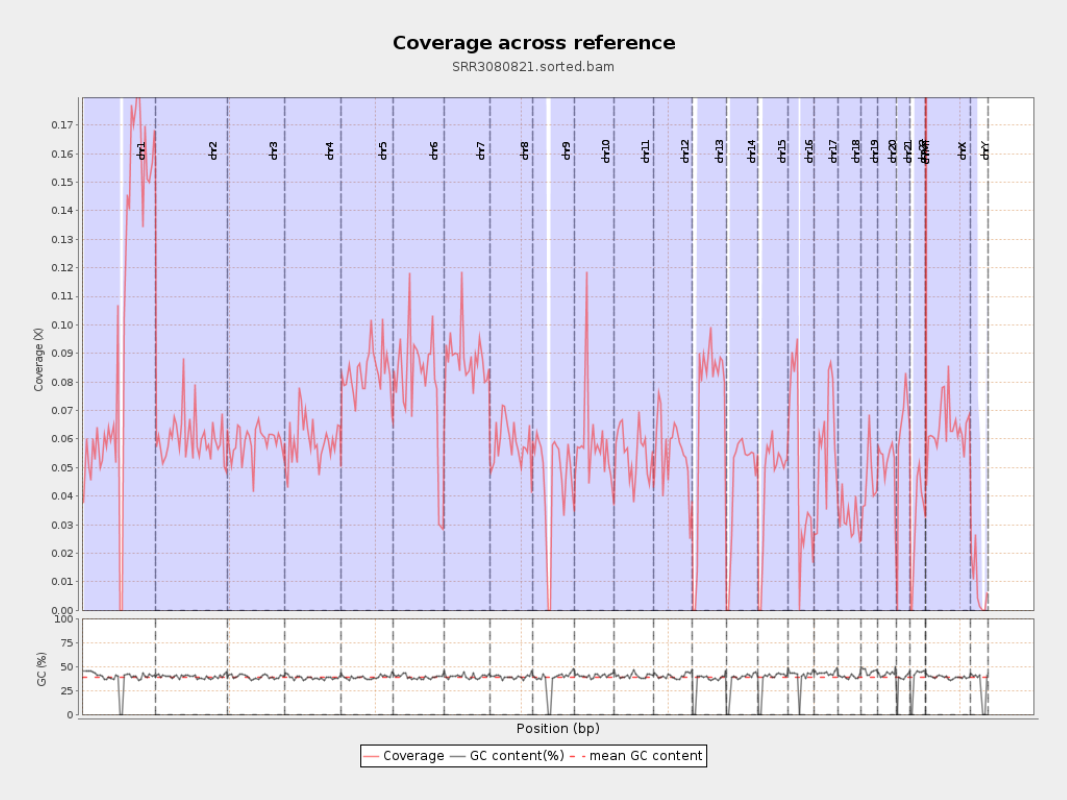
General error rate	0.83%
Mismatches	1,572,511
Insertions	14,651
Mapped reads with at least one insertion	0.52%
Deletions	41,432
Mapped reads with at least one deletion	1.48%
Homopolymer indels	47.64%

2.6. Chromosome stats

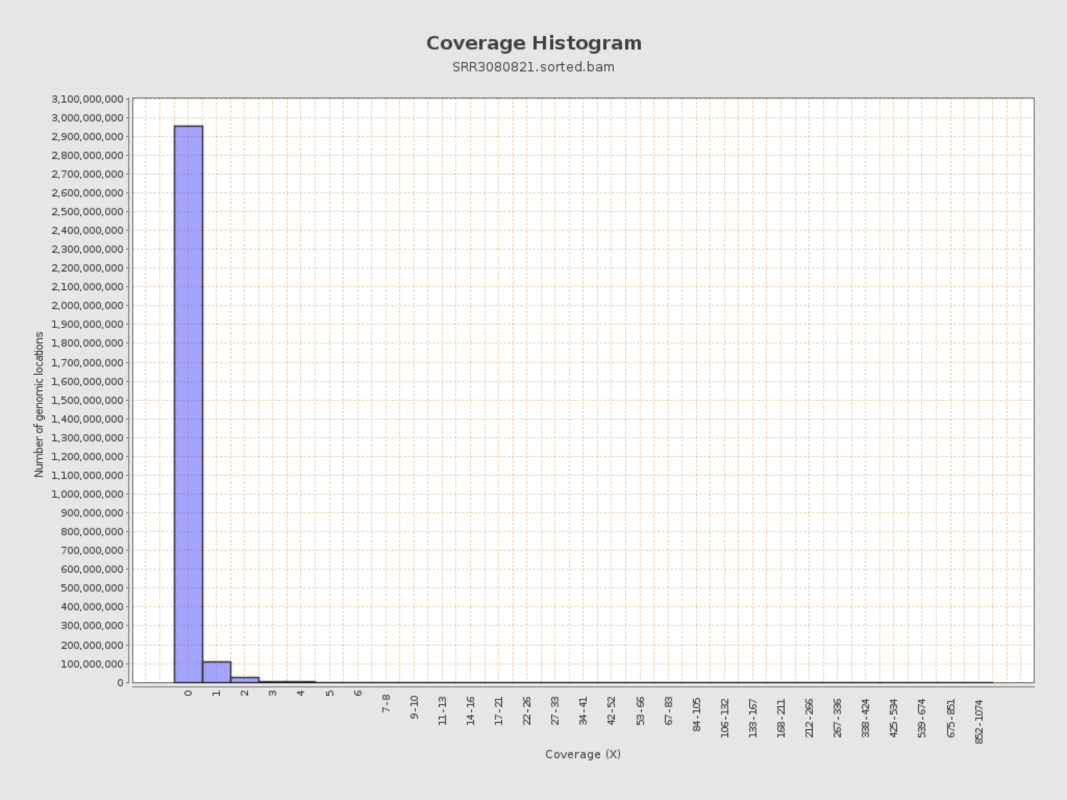
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	24527784	0.0984	0.944
chr2	243199373	14681921	0.0604	0.4418
chr3	198022430	11693792	0.0591	0.3242
chr4	191154276	11411227	0.0597	0.3333
chr5	180915260	15029201	0.0831	0.368
chr6	171115067	13716493	0.0802	0.4552
chr7	159138663	13986646	0.0879	0.7277

chr8	146364022	8561666	0.0585	0.7326
chr9	141213431	6495422	0.046	0.3331
chr10	135534747	7884223	0.0582	0.5765
chr11	135006516	7418154	0.0549	0.3296
chr12	133851895	7455773	0.0557	0.3024
chr13	115169878	8250544	0.0716	0.343
chr14	107349540	4956425	0.0462	0.2834
chr15	102531392	4468704	0.0436	0.2647
chr16	90354753	4243095	0.047	0.3154
chr17	81195210	4687102	0.0577	0.3219
chr18	78077248	2517743	0.0322	0.5364
chr19	59128983	2676469	0.0453	0.6207
chr20	63025520	3320703	0.0527	0.2984
chr21	48129895	3003240	0.0624	0.3459
chr22	51304566	1584166	0.0309	0.2209
chrMT	16571	67460	4.071	2.8636
chrX	155270560	9898580	0.0638	0.3377
chrY	59373566	479769	0.0081	0.2007

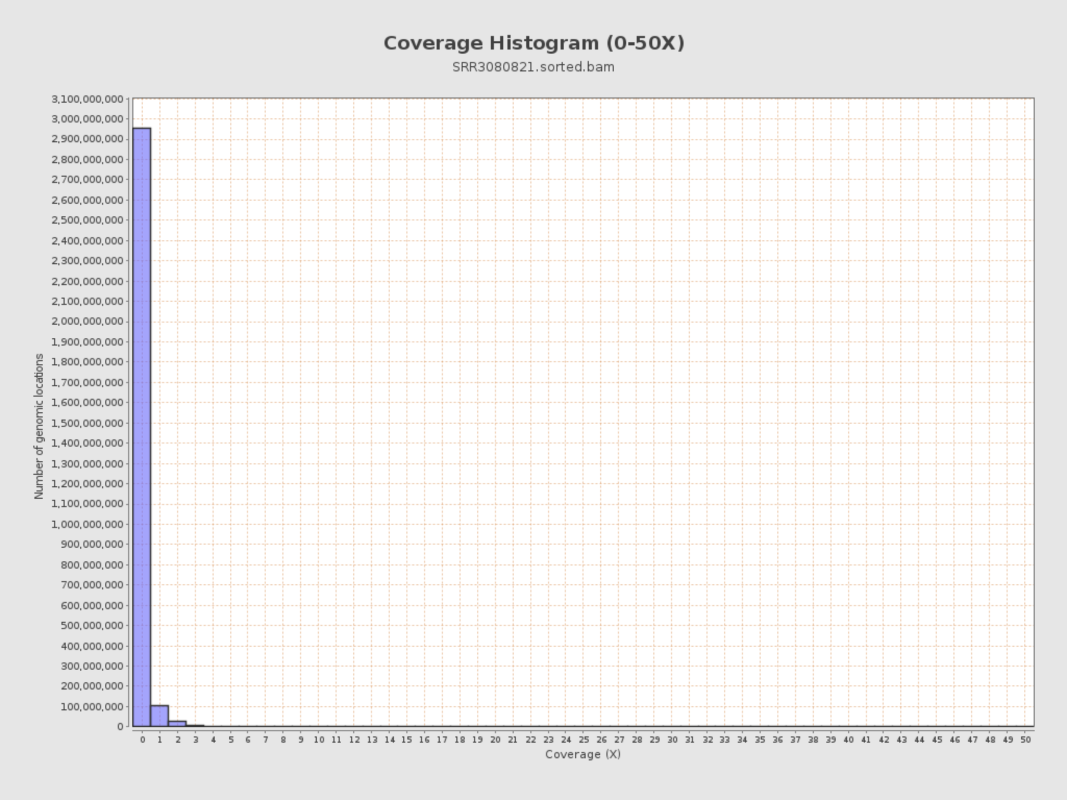
3. Results : Coverage across reference



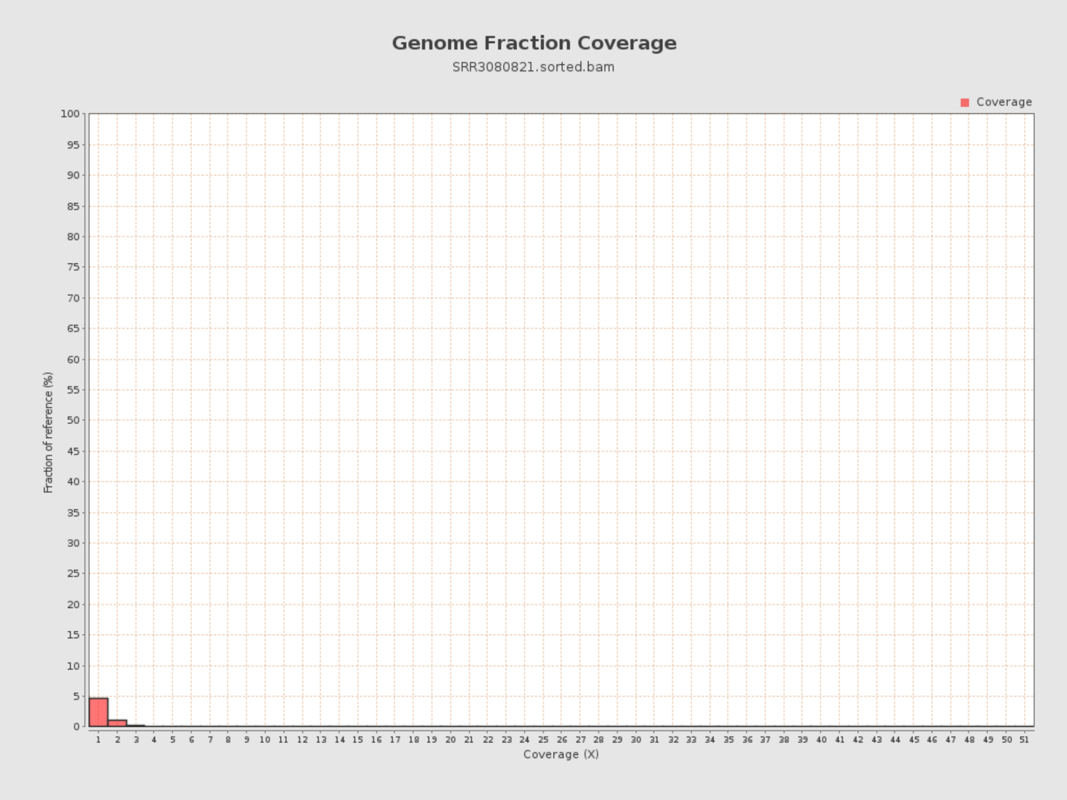
4. Results : Coverage Histogram



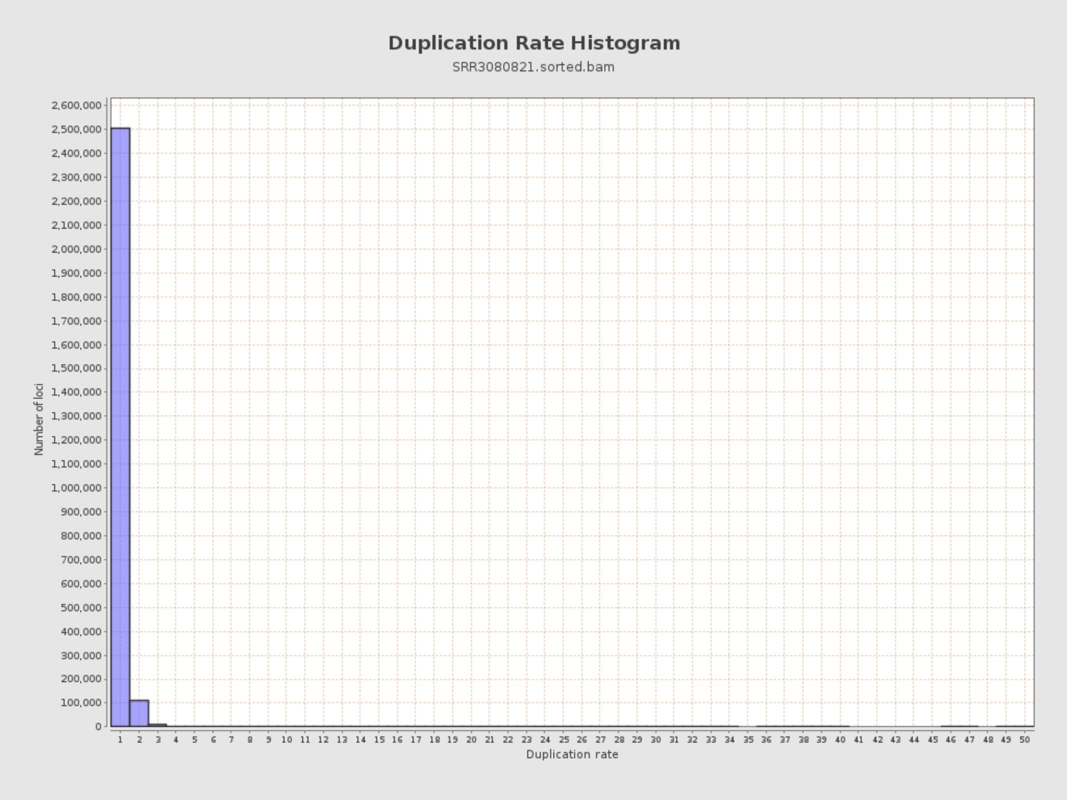
5. Results : Coverage Histogram (0-50X)



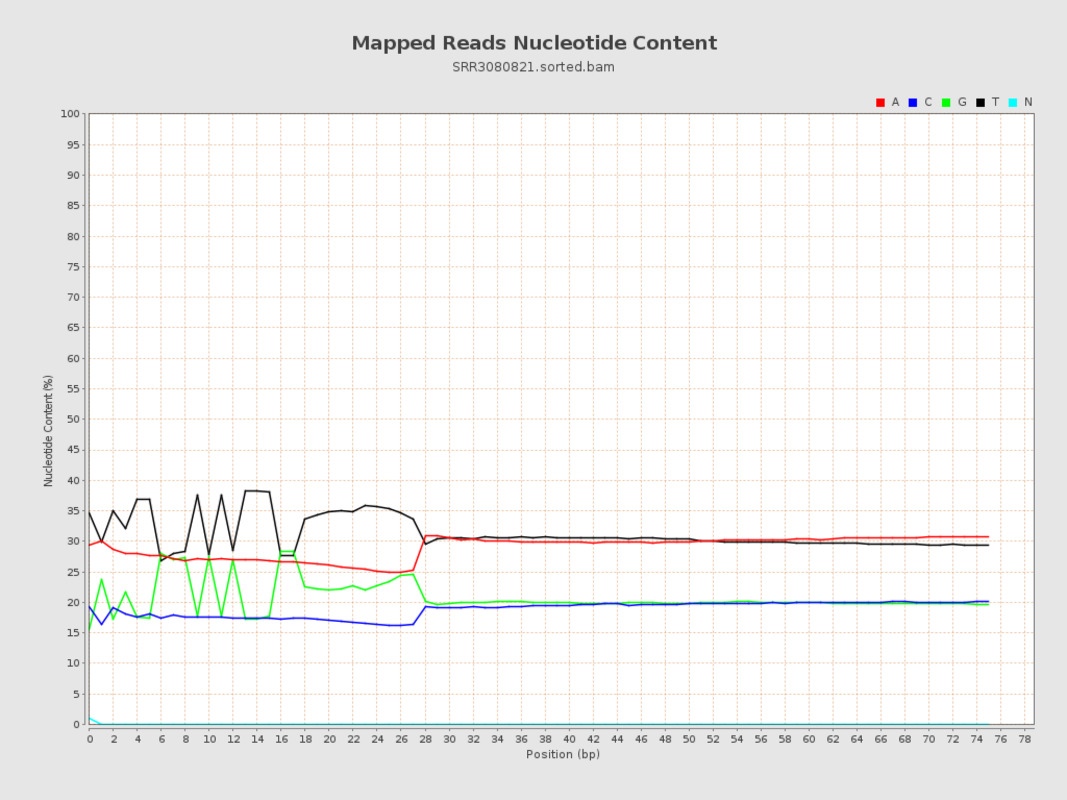
6. Results : Genome Fraction Coverage



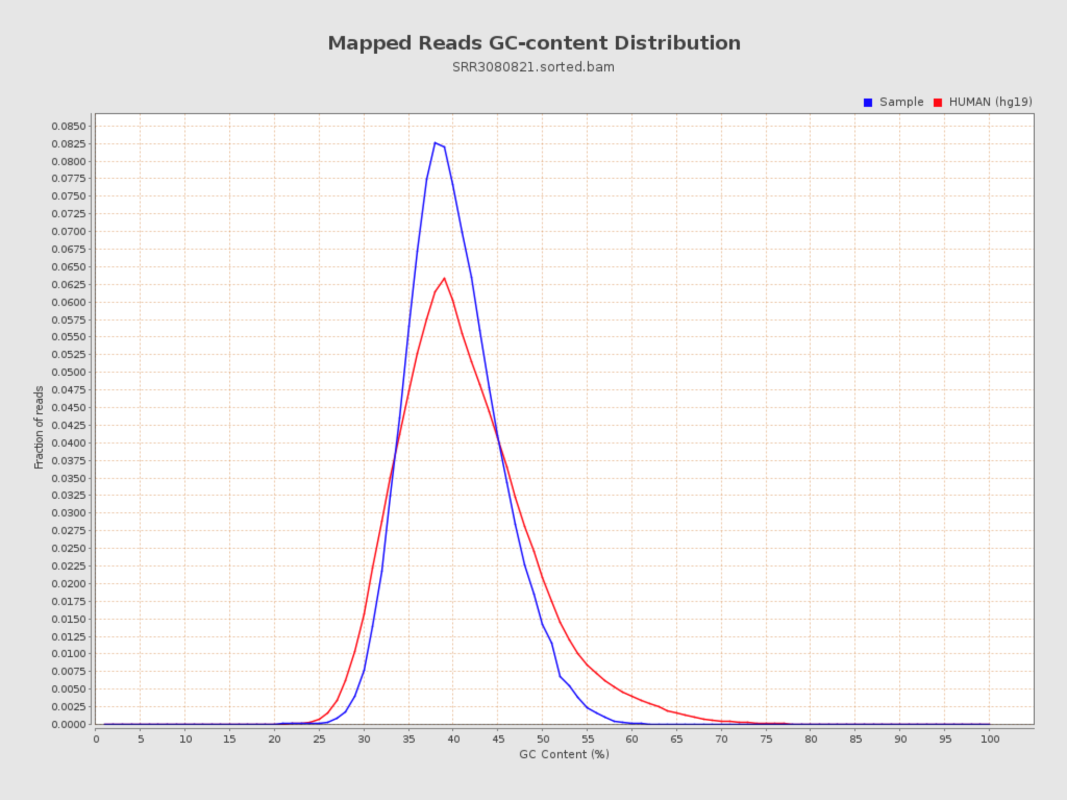
7. Results : Duplication Rate Histogram



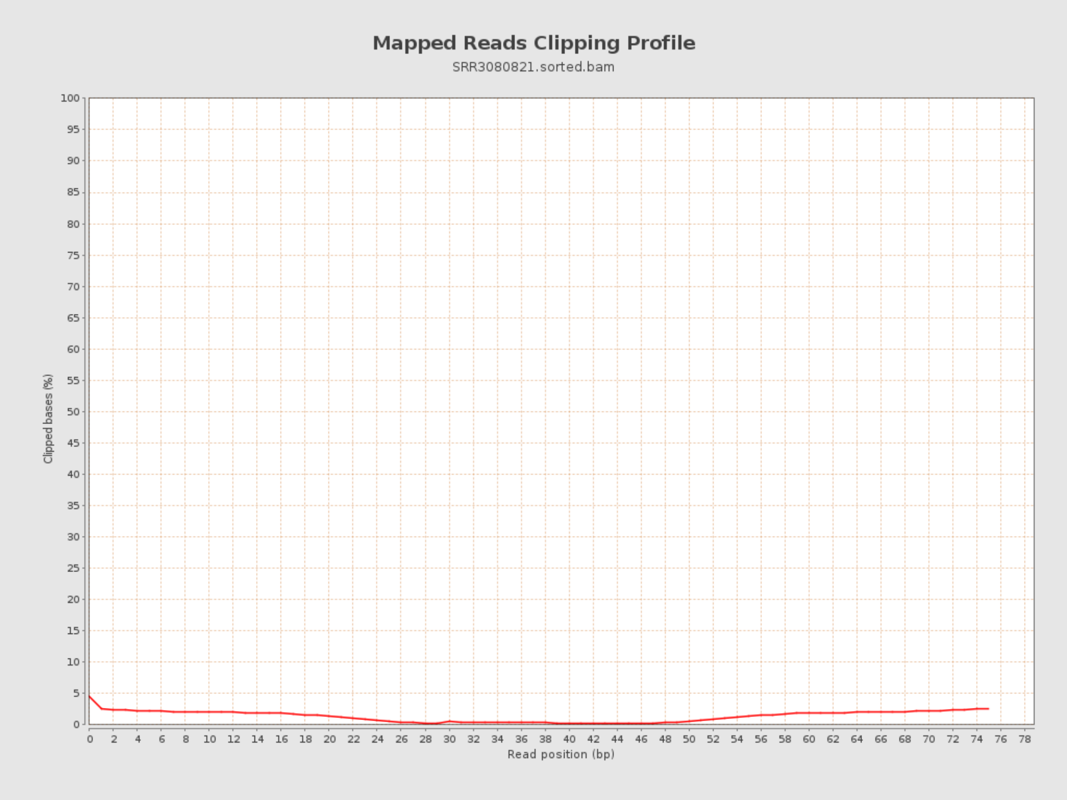
8. Results : Mapped Reads Nucleotide Content



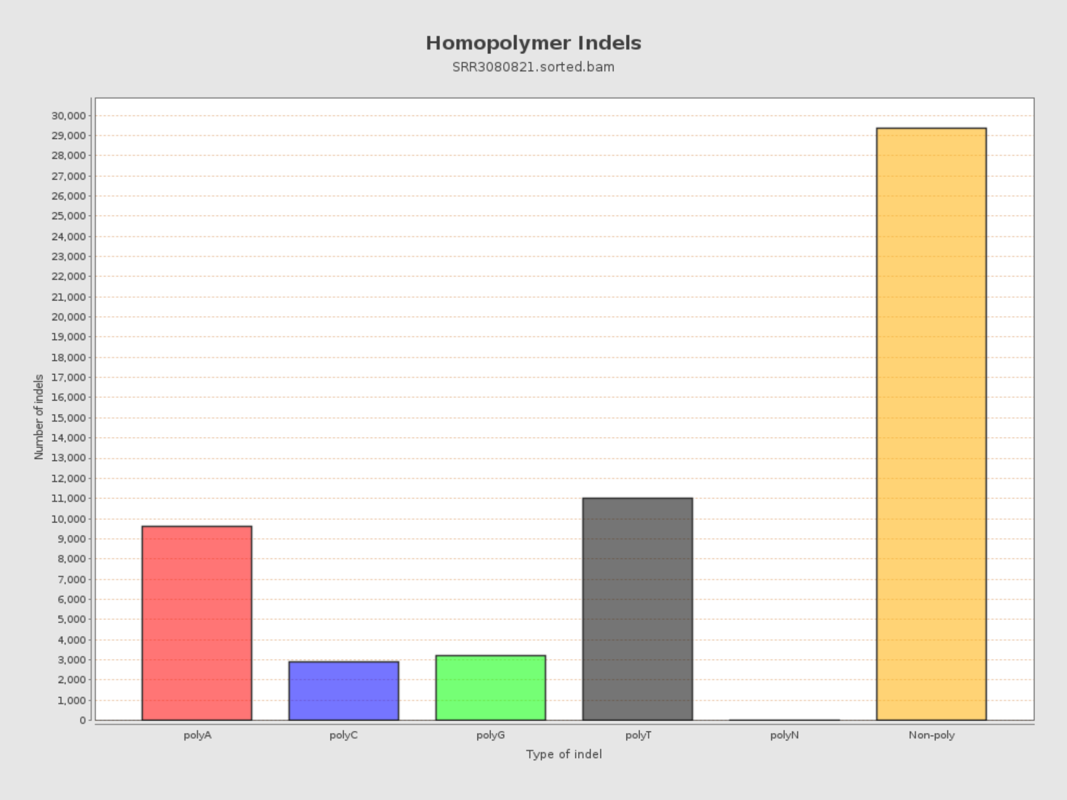
9. Results : Mapped Reads GC-content Distribution



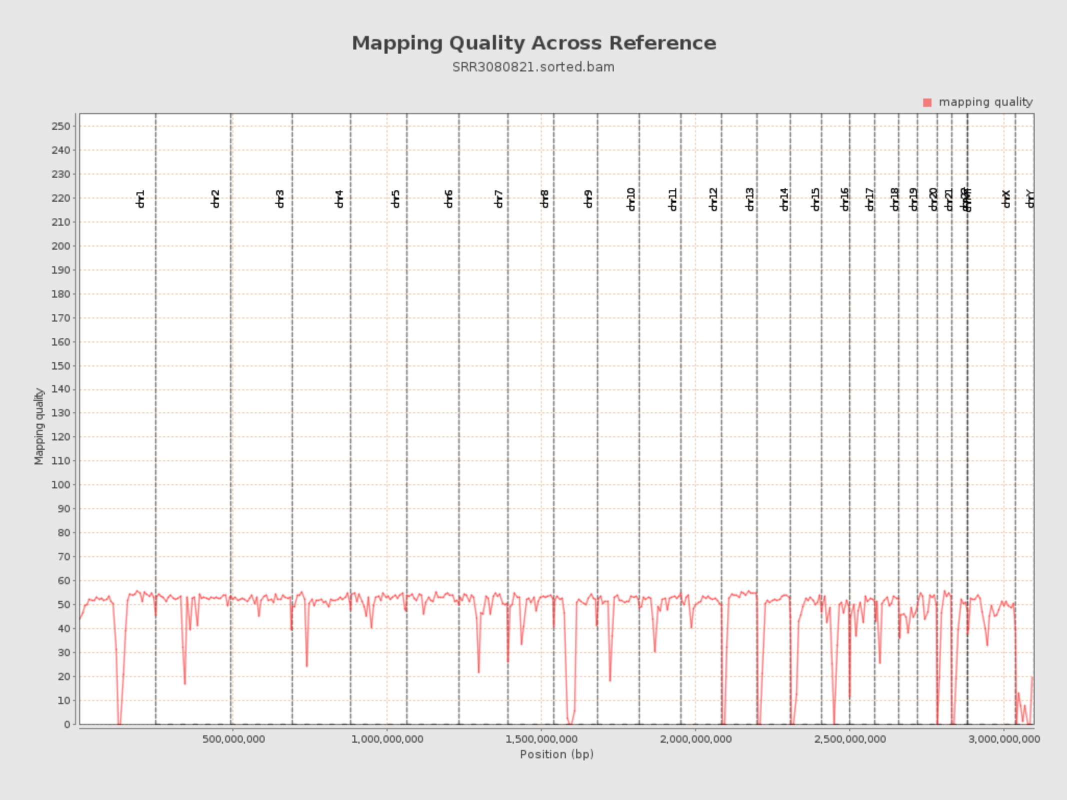
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram