Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 17:30:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082742.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_SRR3082742 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082742.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 17:30:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082742.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,383,224
Mapped reads	2,927,443 / 86.53%
Unmapped reads	455,781 / 13.47%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,099 / 0.51%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	158,870 / 4.7%
Duplication rate	4.42%
Clipped reads	1,243,841 / 36.76%

2.2. ACGT Content

Number/percentage of A's	54,925,673 / 27.93%
Number/percentage of C's	35,383,985 / 17.99%
Number/percentage of T's	64,129,935 / 32.61%
Number/percentage of G's	42,208,288 / 21.46%
Number/percentage of N's	10,774 / 0.01%
GC Percentage	39.46%

2.3. Coverage

Mean	0.0636

Standard Deviation	0.4916

2.4. Mapping Quality

Mean Mapping Quality	46.91

2.5. Mismatches and indels

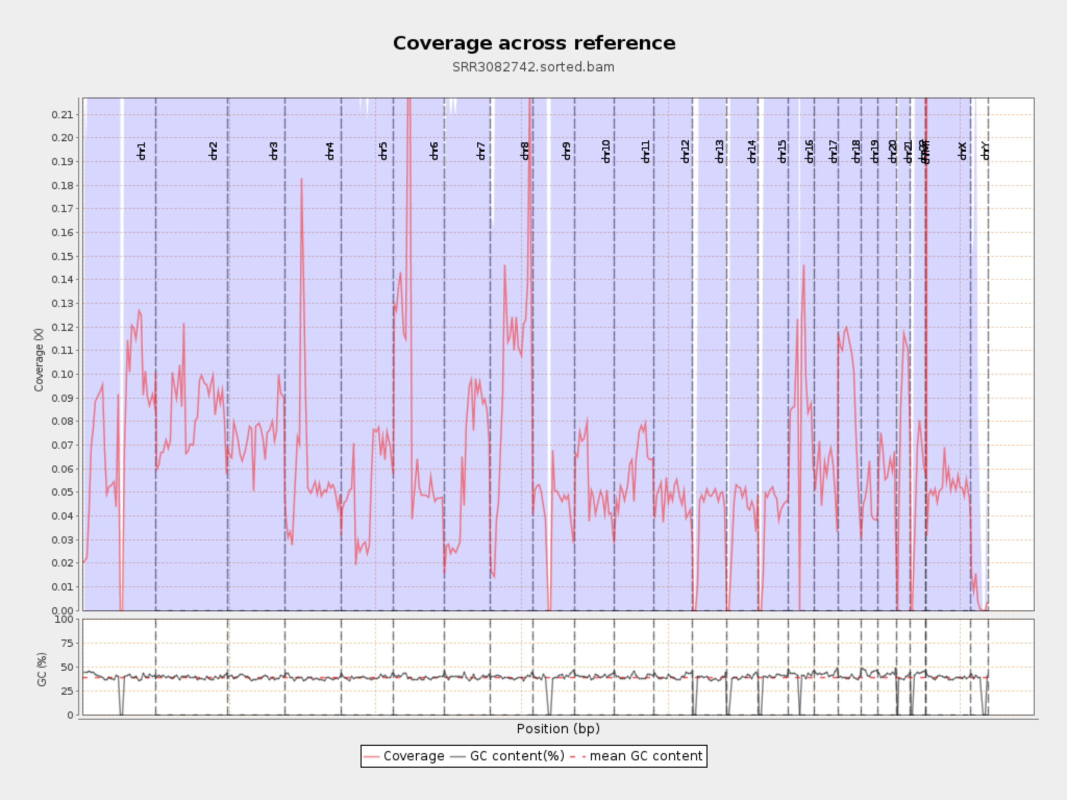
General error rate	0.87%
Mismatches	1,678,840
Insertions	15,431
Mapped reads with at least one insertion	0.52%
Deletions	43,054
Mapped reads with at least one deletion	1.46%
Homopolymer indels	48.59%

2.6. Chromosome stats

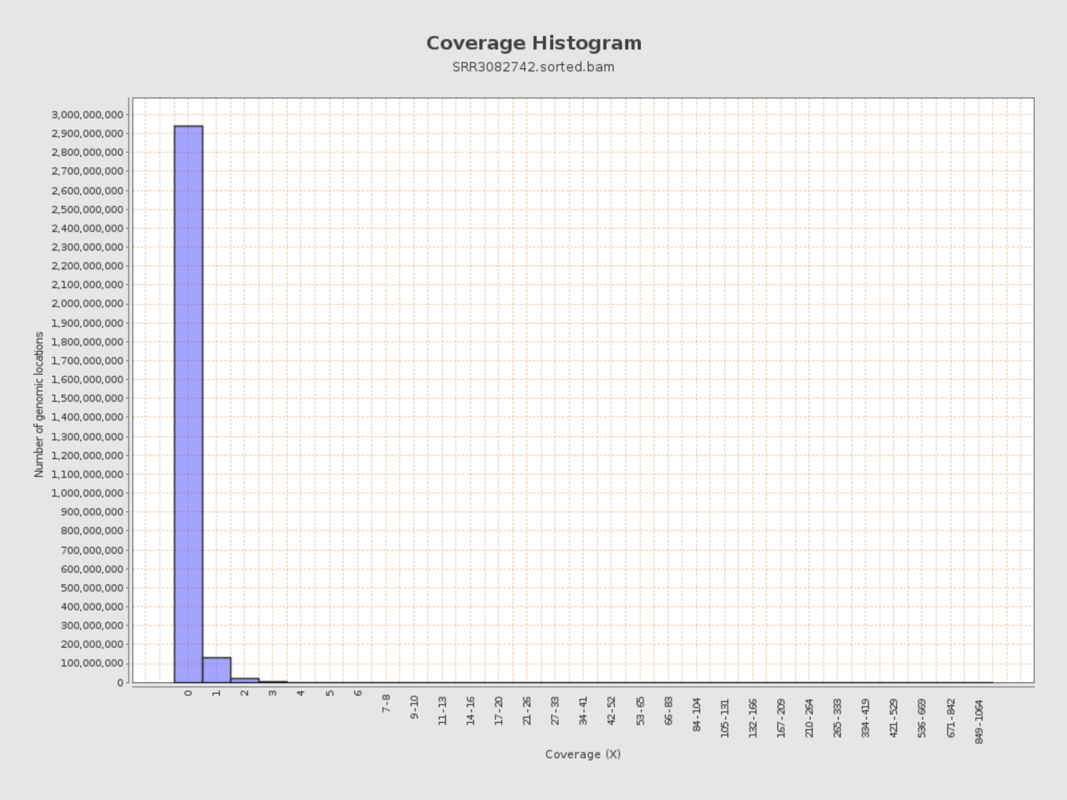
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	19124714	0.0767	0.9412
chr2	243199373	20424071	0.084	0.6531
chr3	198022430	14718462	0.0743	0.3253
chr4	191154276	11486200	0.0601	0.3013
chr5	180915260	9345148	0.0517	0.272
chr6	171115067	14620736	0.0854	0.5173
chr7	159138663	9842406	0.0618	0.4433

chr8	146364022	14925790	0.102	0.6041
chr9	141213431	6011435	0.0426	0.4499
chr10	135534747	7272284	0.0537	0.3764
chr11	135006516	8088611	0.0599	0.3635
chr12	133851895	6292500	0.047	0.2709
chr13	115169878	4631814	0.0402	0.238
chr14	107349540	4217465	0.0393	0.2688
chr15	102531392	3877637	0.0378	0.2316
chr16	90354753	7839815	0.0868	0.397
chr17	81195210	4734000	0.0583	0.3374
chr18	78077248	7671986	0.0983	0.8865
chr19	59128983	2710929	0.0458	0.6586
chr20	63025520	3903744	0.0619	0.3093
chr21	48129895	3950175	0.0821	0.3489
chr22	51304566	2517783	0.0491	0.2621
chrMT	16571	156626	9.4518	5.9251
chrX	155270560	8033898	0.0517	0.3218
chrY	59373566	334055	0.0056	0.1163

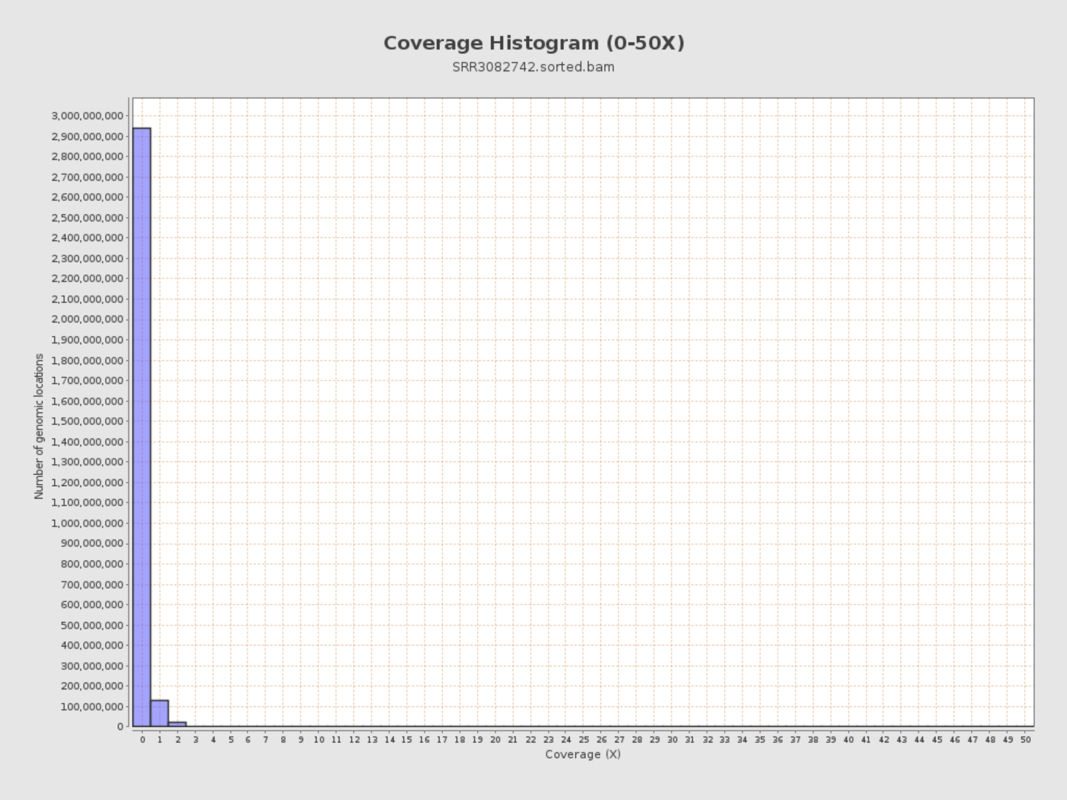
3. Results : Coverage across reference



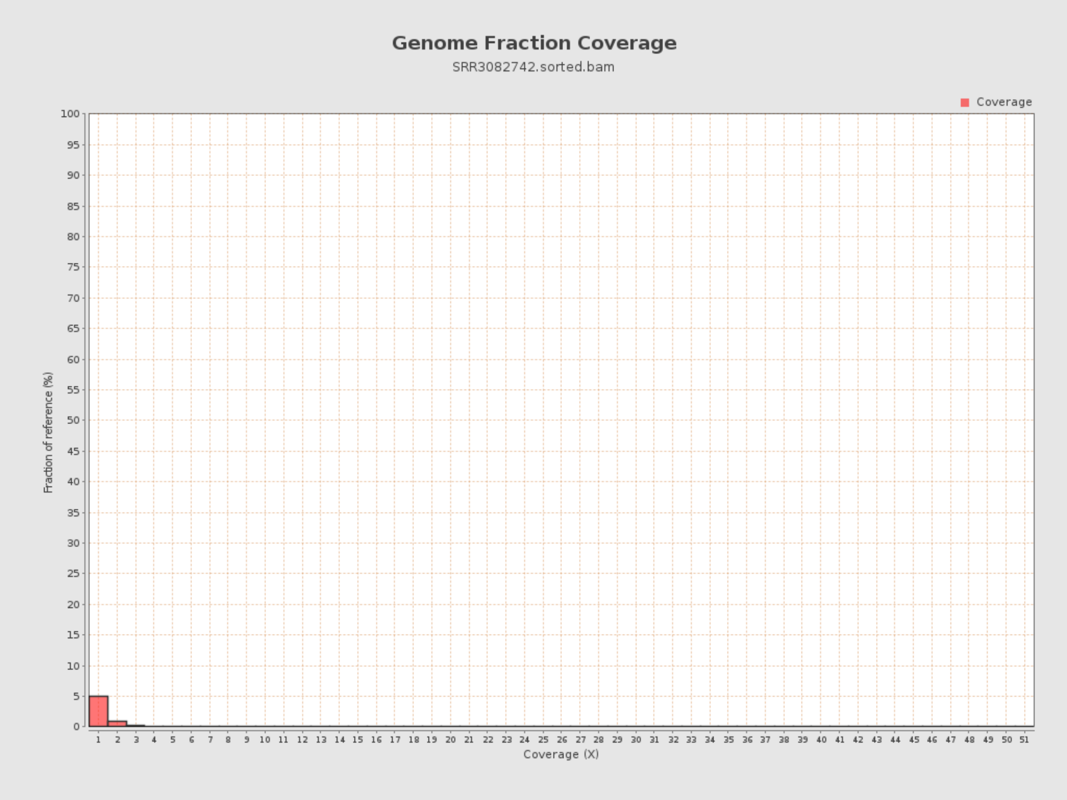
4. Results : Coverage Histogram



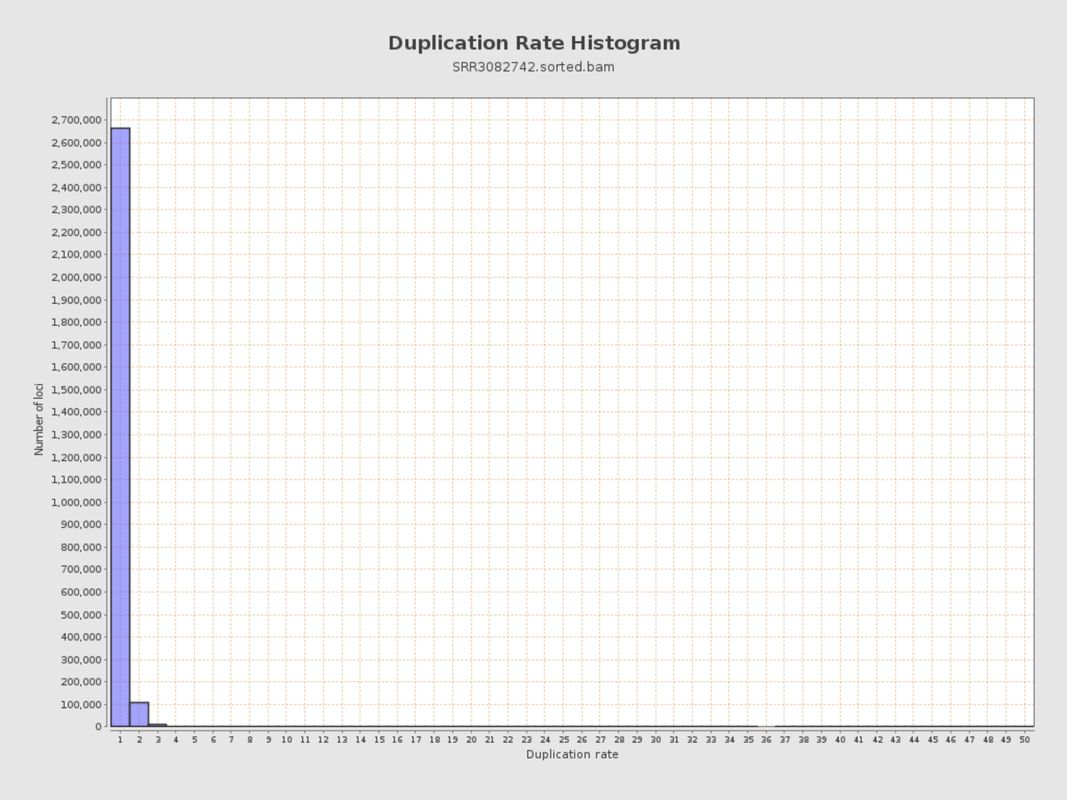
5. Results : Coverage Histogram (0-50X)



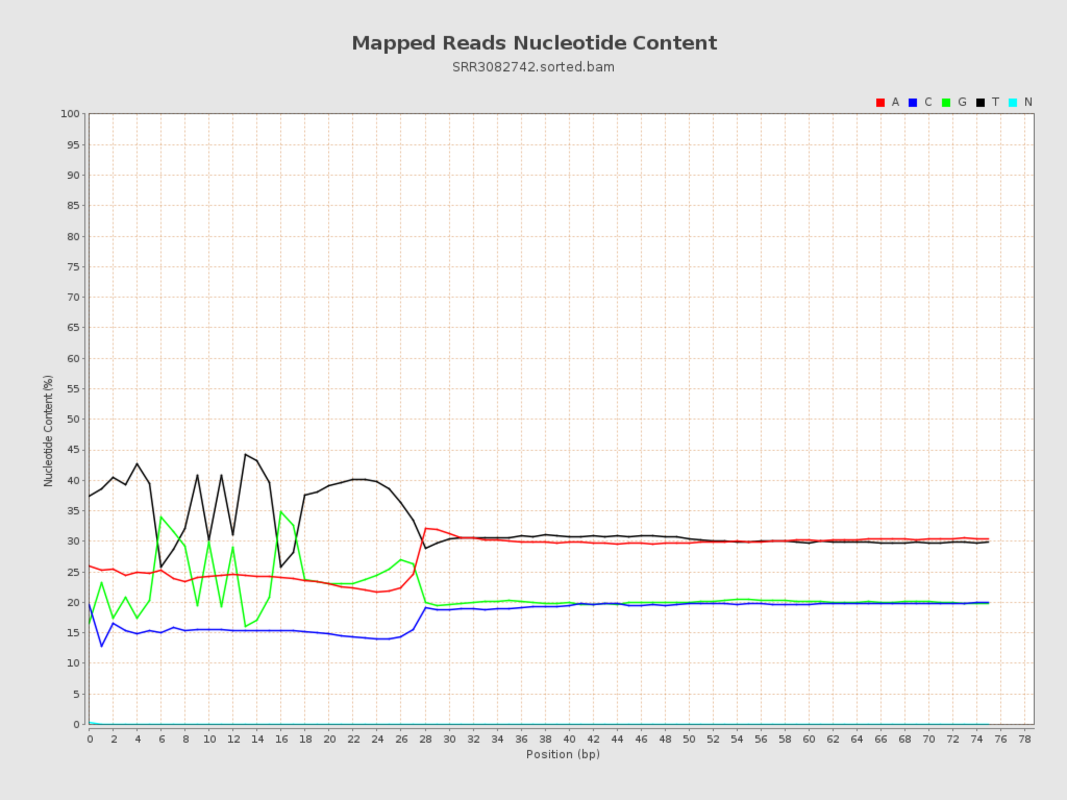
6. Results : Genome Fraction Coverage



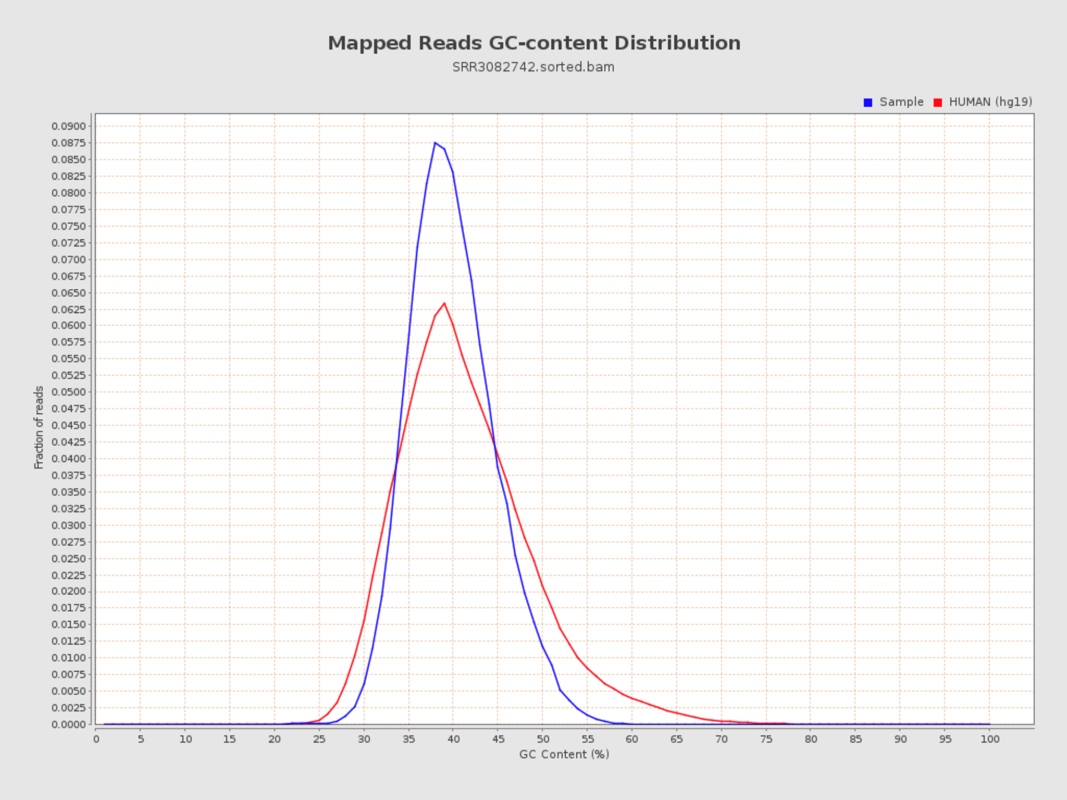
7. Results : Duplication Rate Histogram



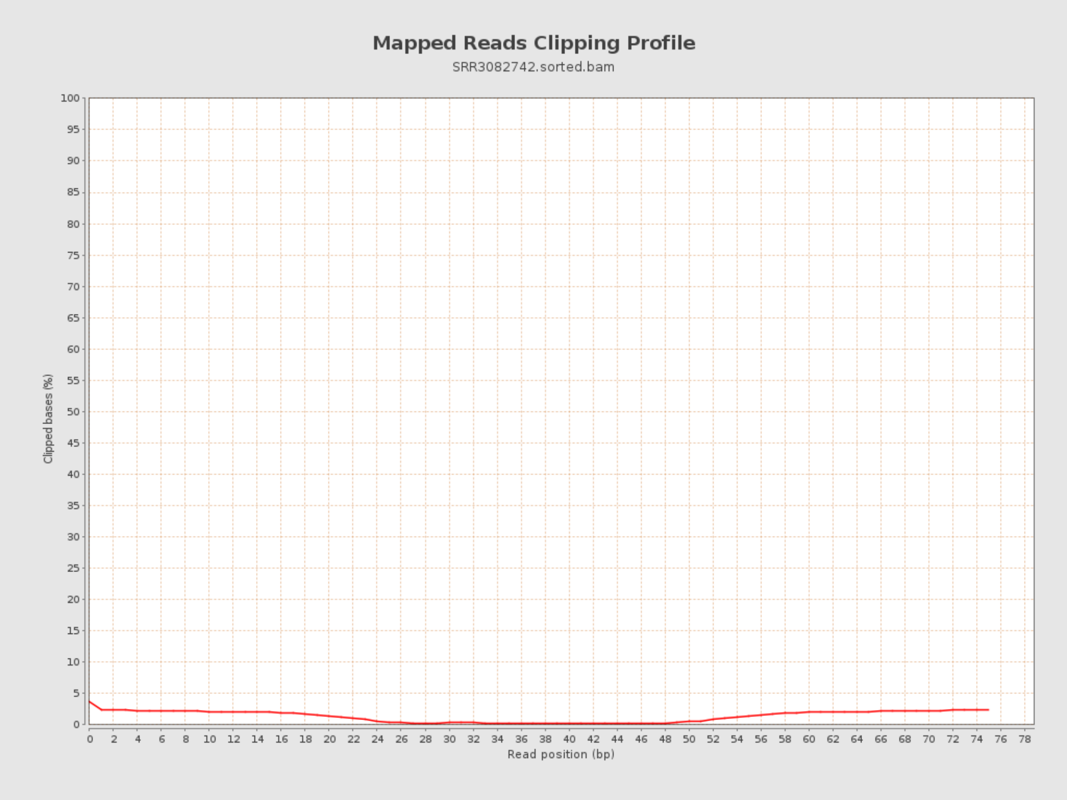
8. Results : Mapped Reads Nucleotide Content



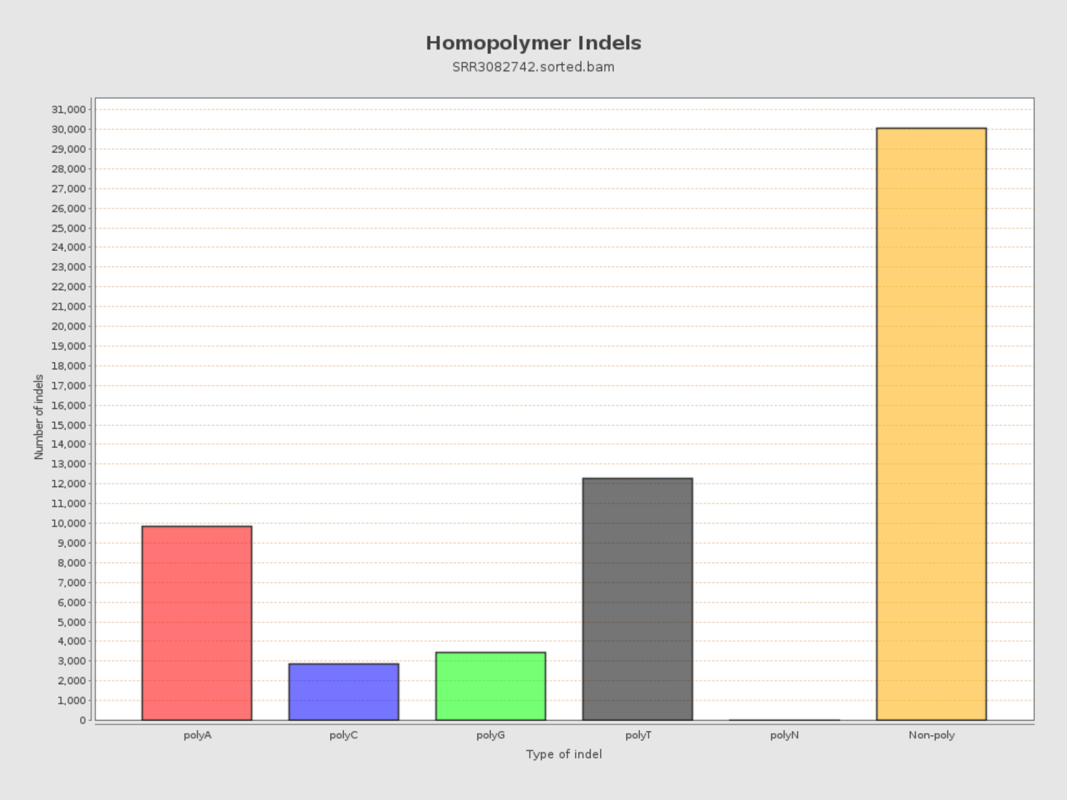
9. Results : Mapped Reads GC-content Distribution



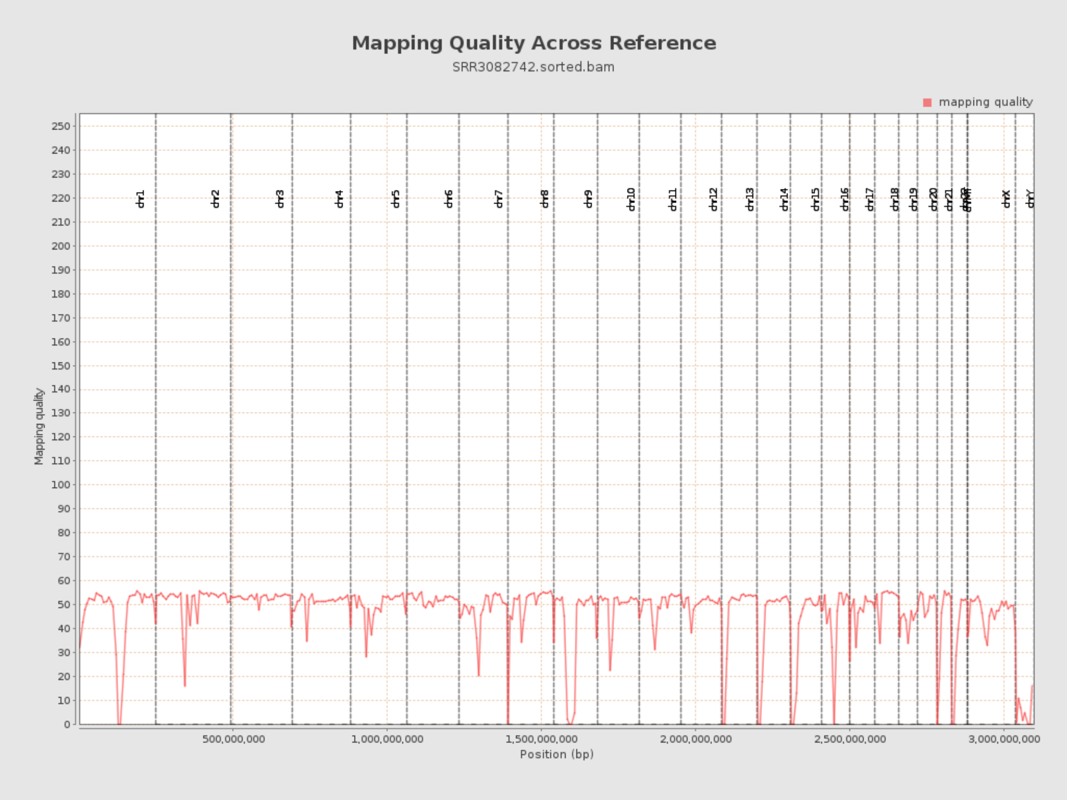
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram