Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 10:20:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081924.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_SRR3081924 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081924.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 10:20:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081924.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,813,471
Mapped reads	2,566,207 / 91.21%
Unmapped reads	247,264 / 8.79%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,237 / 0.65%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	131,011 / 4.66%
Duplication rate	3.63%
Clipped reads	1,096,945 / 38.99%

2.2. ACGT Content

Number/percentage of A's	47,518,587 / 27.61%
Number/percentage of C's	32,159,749 / 18.68%
Number/percentage of T's	53,709,638 / 31.21%
Number/percentage of G's	38,706,720 / 22.49%
Number/percentage of N's	21,341 / 0.01%
GC Percentage	41.17%

2.3. Coverage

Mean	0.0556

Standard Deviation	0.5846

2.4. Mapping Quality

Mean Mapping Quality	44.35

2.5. Mismatches and indels

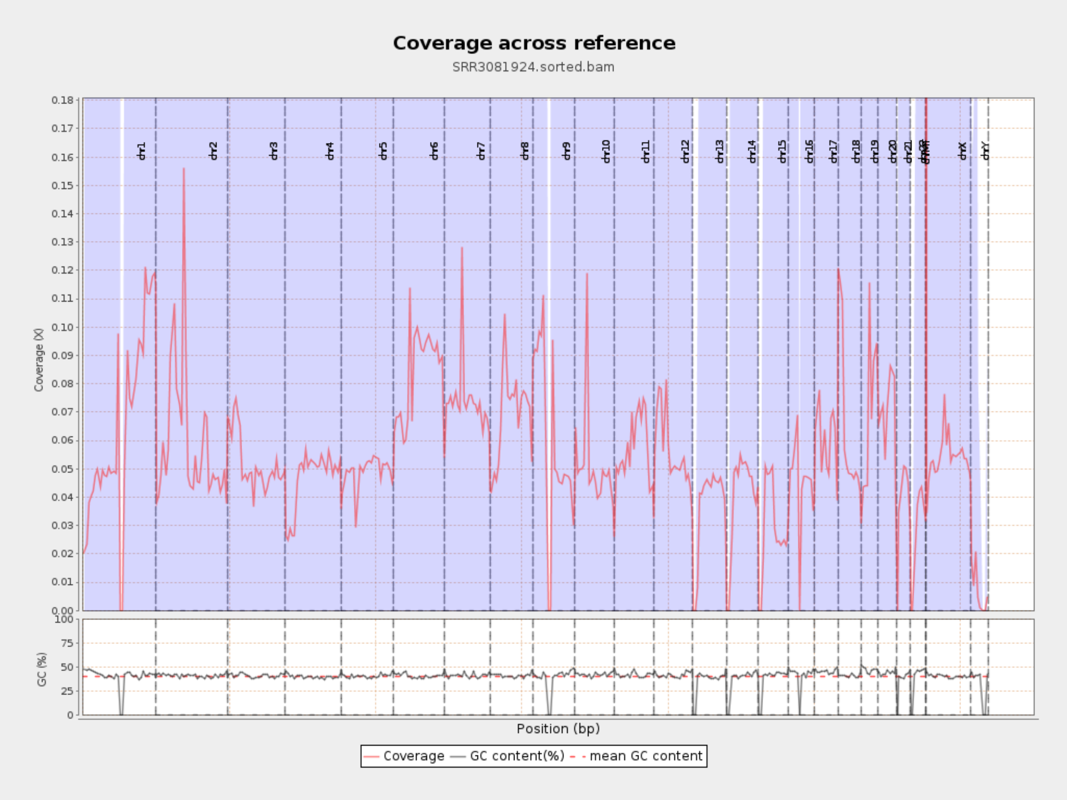
General error rate	0.82%
Mismatches	1,392,356
Insertions	12,691
Mapped reads with at least one insertion	0.49%
Deletions	40,798
Mapped reads with at least one deletion	1.57%
Homopolymer indels	46.7%

2.6. Chromosome stats

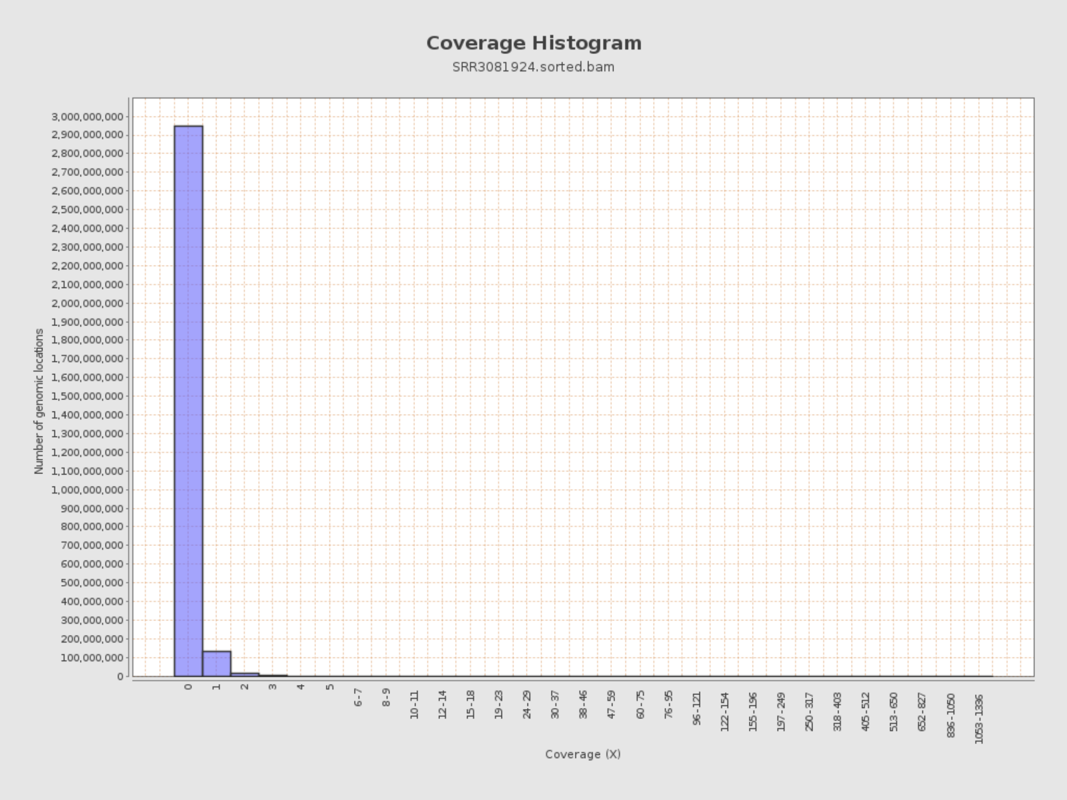
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16079909	0.0645	1.1264
chr2	243199373	14716564	0.0605	0.8508
chr3	198022430	10330781	0.0522	0.2601
chr4	191154276	8931691	0.0467	0.2673
chr5	180915260	8799502	0.0486	0.2542
chr6	171115067	14416133	0.0842	0.4504
chr7	159138663	11773651	0.074	0.8643

chr8	146364022	10158011	0.0694	0.6751
chr9	141213431	8344681	0.0591	0.608
chr10	135534747	6979965	0.0515	0.5683
chr11	135006516	7751905	0.0574	0.417
chr12	133851895	7598286	0.0568	0.2871
chr13	115169878	4220187	0.0366	0.2156
chr14	107349540	4347193	0.0405	0.2823
chr15	102531392	2897509	0.0283	0.198
chr16	90354753	3974291	0.044	0.3
chr17	81195210	5005233	0.0616	0.3249
chr18	78077248	5060474	0.0648	0.9314
chr19	59128983	4101124	0.0694	0.8427
chr20	63025520	4533091	0.0719	0.3161
chr21	48129895	1872091	0.0389	0.2679
chr22	51304566	1417919	0.0276	0.1844
chrMT	16571	53770	3.2448	2.5949
chrX	155270560	8426717	0.0543	0.339
chrY	59373566	396923	0.0067	0.1648

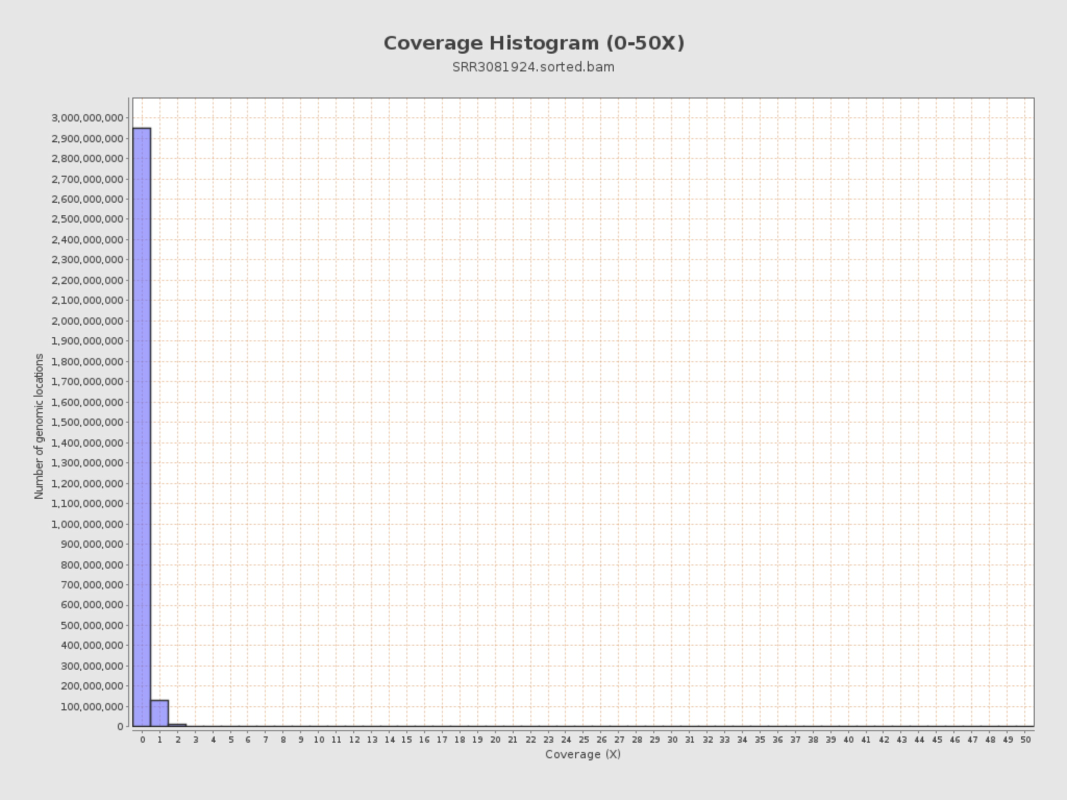
3. Results : Coverage across reference



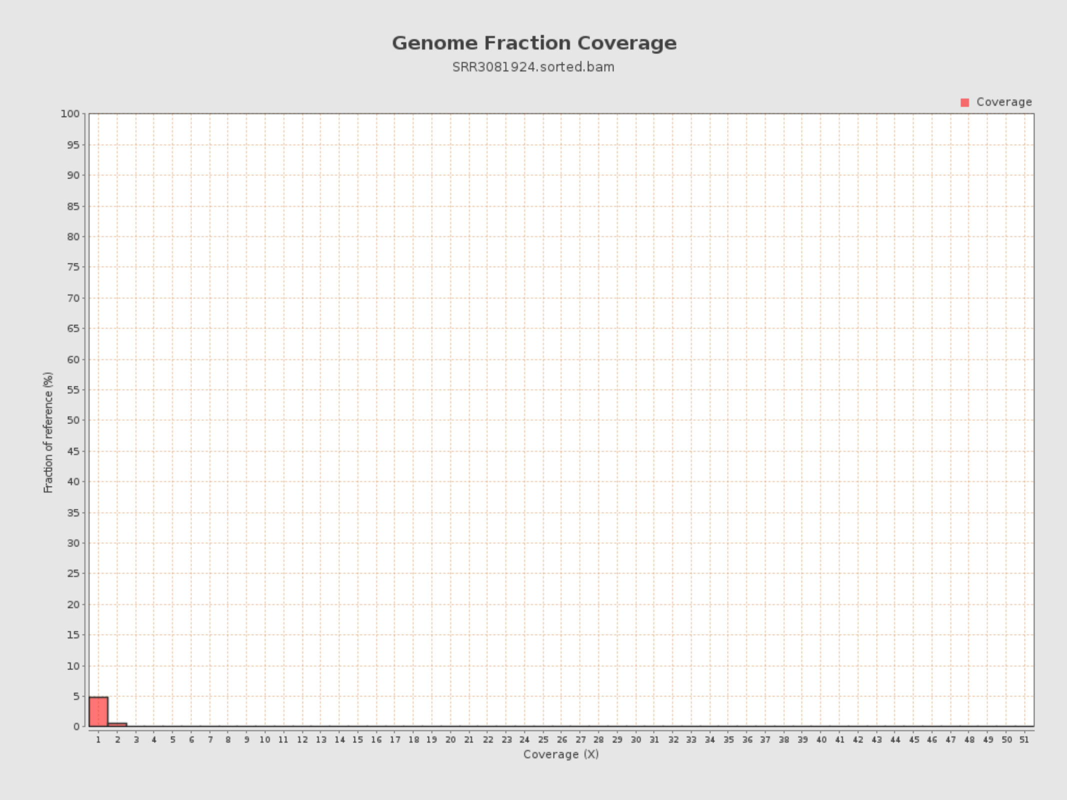
4. Results : Coverage Histogram



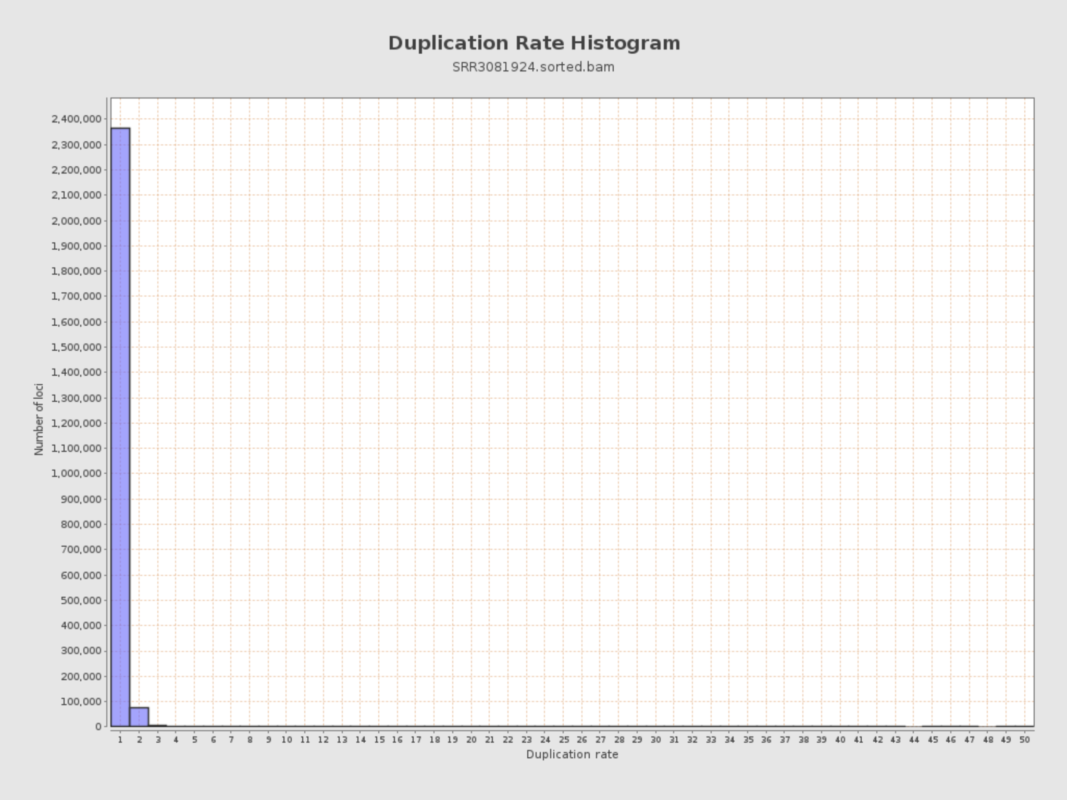
5. Results : Coverage Histogram (0-50X)



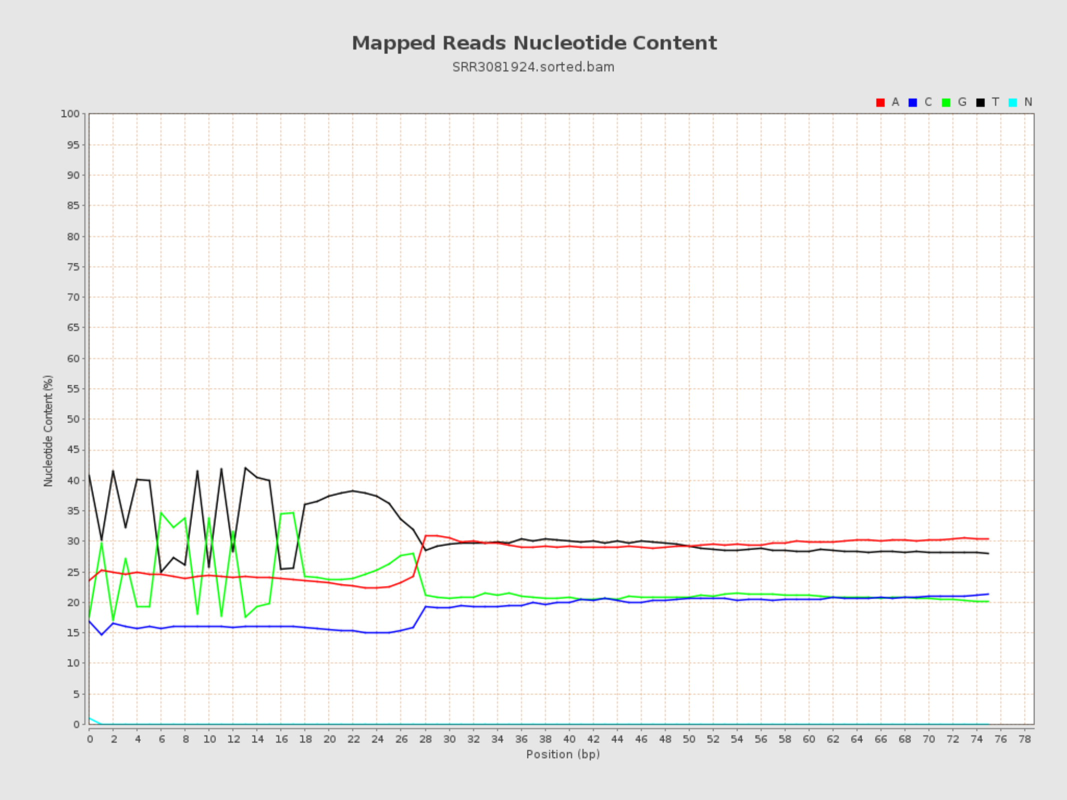
6. Results : Genome Fraction Coverage



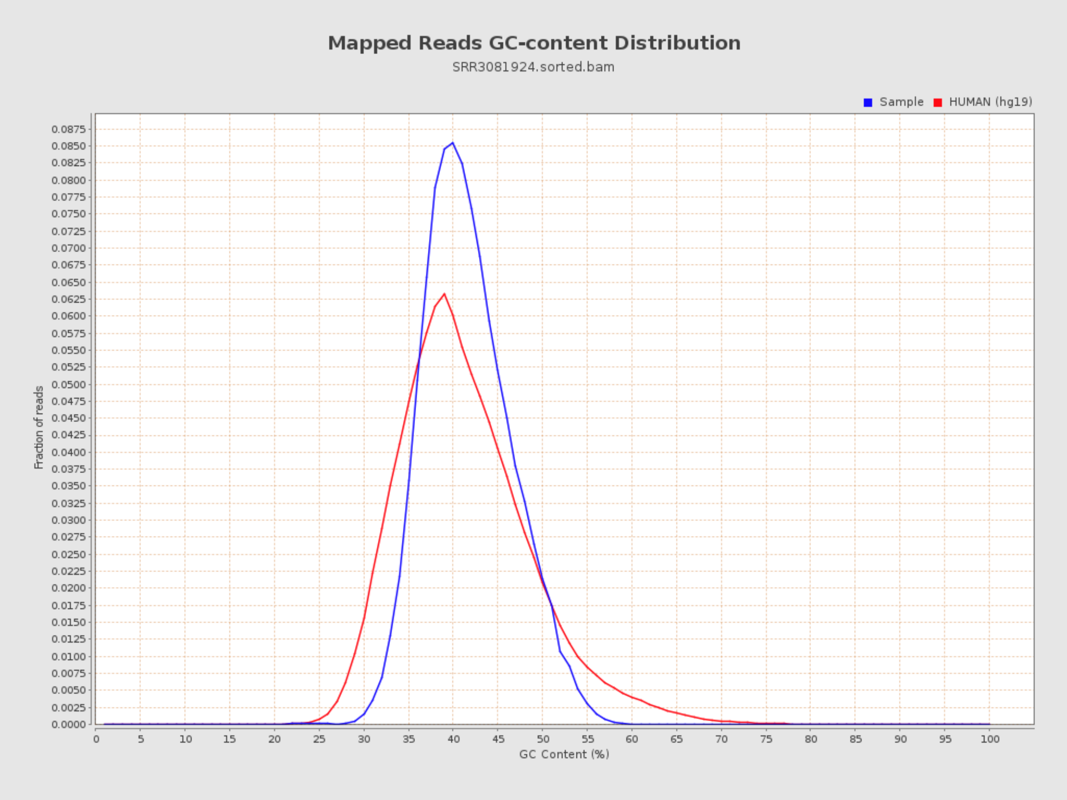
7. Results : Duplication Rate Histogram



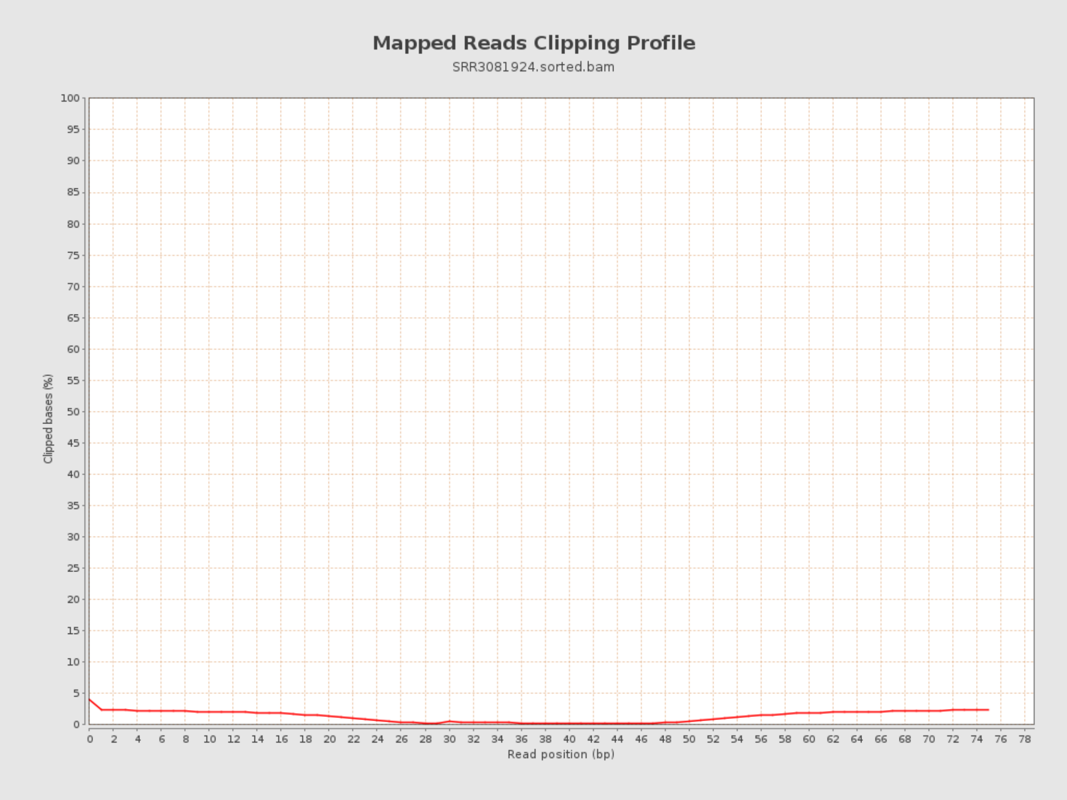
8. Results : Mapped Reads Nucleotide Content



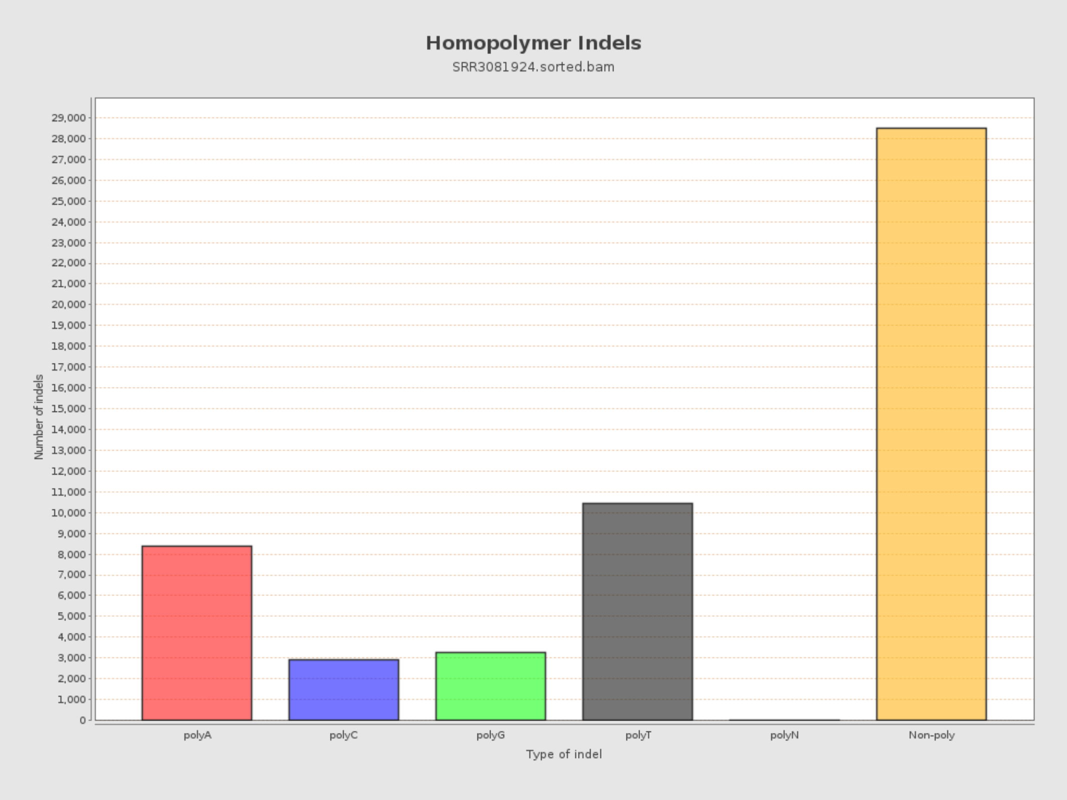
9. Results : Mapped Reads GC-content Distribution



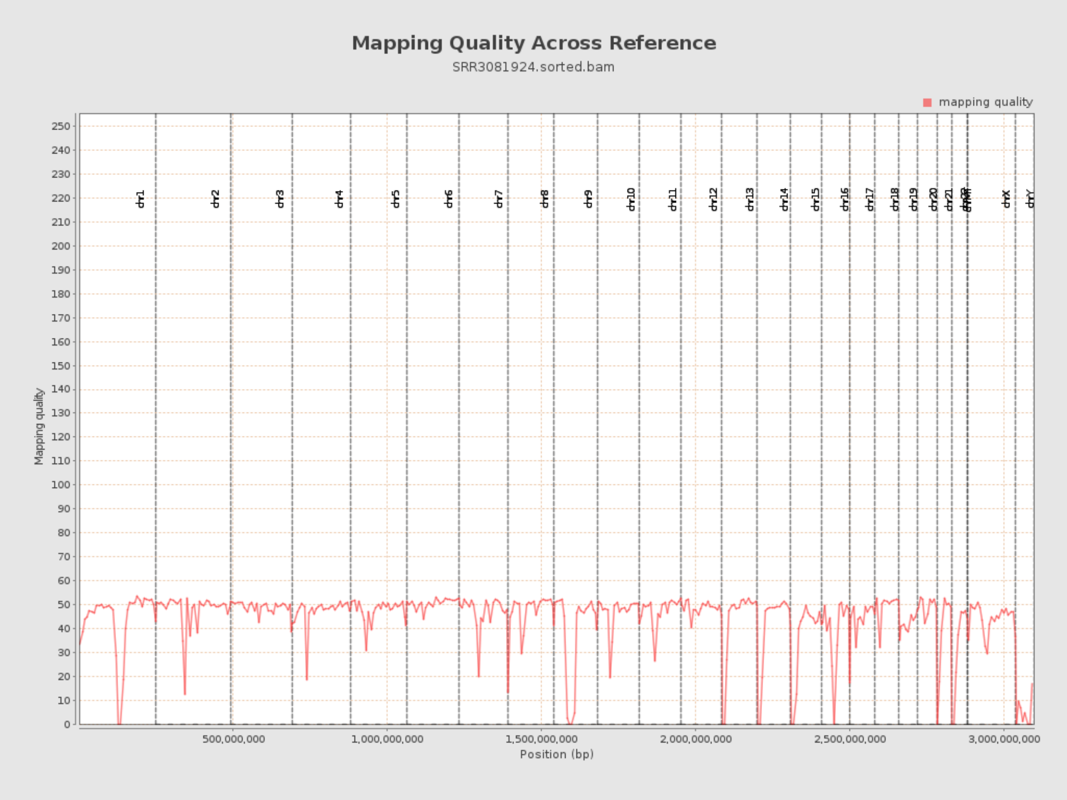
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram