Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 12:29:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524997.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_SRR10524997 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524997.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 12:29:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524997.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,491,479
Mapped reads	3,138,030 / 89.88%
Unmapped reads	353,449 / 10.12%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,428 / 0.27%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	147,713 / 4.23%
Duplication rate	3.28%
Clipped reads	3,136,052 / 89.82%

2.2. ACGT Content

Number/percentage of A's	46,463,168 / 25.92%
Number/percentage of C's	31,637,530 / 17.65%
Number/percentage of T's	56,408,669 / 31.46%
Number/percentage of G's	44,770,460 / 24.97%
Number/percentage of N's	1,705 / 0%
GC Percentage	42.62%

2.3. Coverage

Mean	0.0579

Standard Deviation	0.4894

2.4. Mapping Quality

Mean Mapping Quality	43.73

2.5. Mismatches and indels

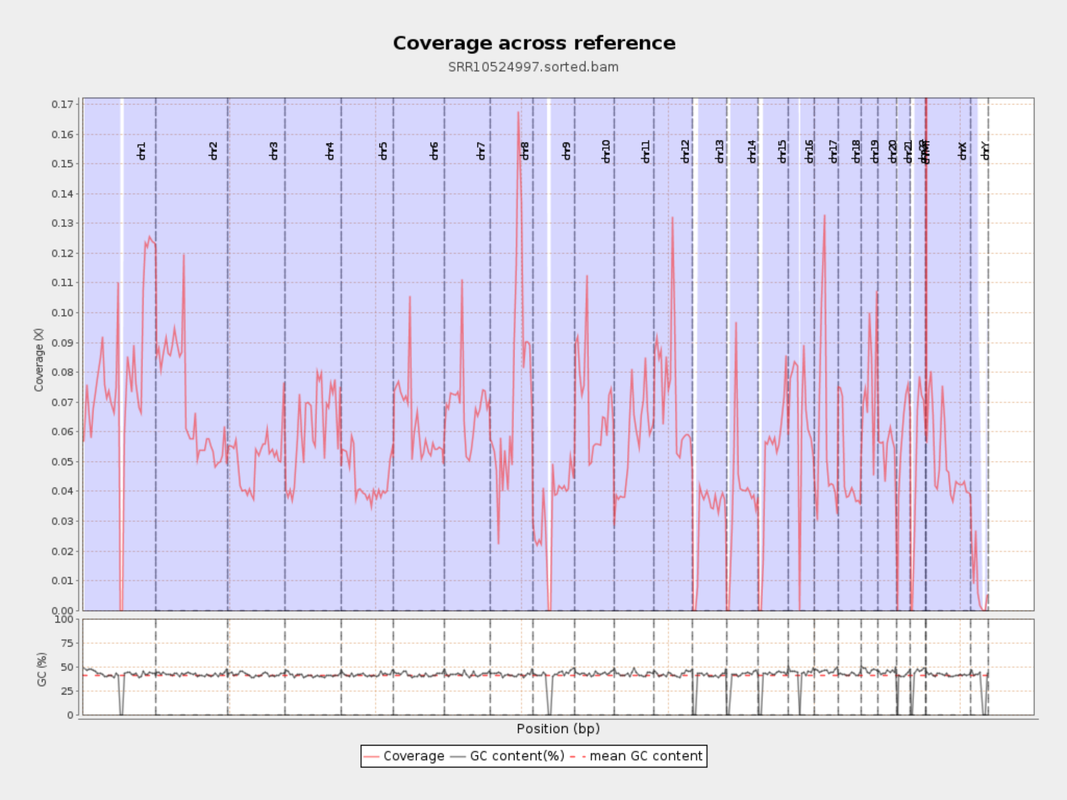
General error rate	0.52%
Mismatches	895,295
Insertions	14,397
Mapped reads with at least one insertion	0.46%
Deletions	35,099
Mapped reads with at least one deletion	1.11%
Homopolymer indels	42.67%

2.6. Chromosome stats

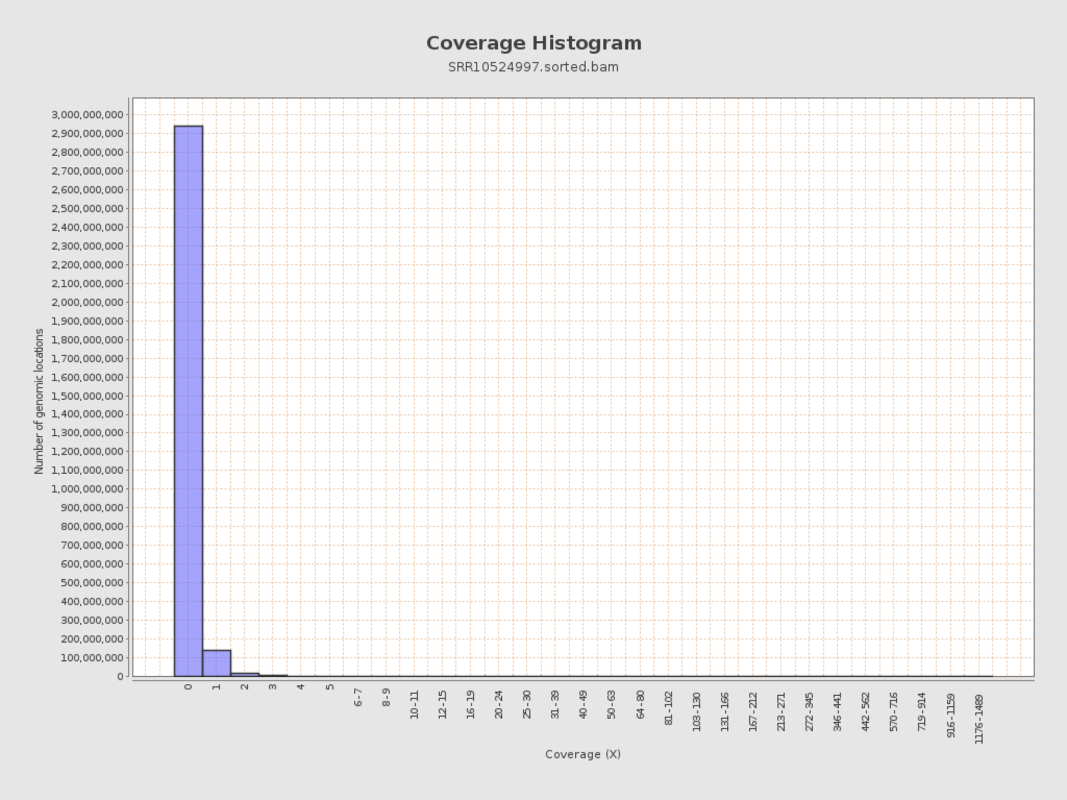
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	19698730	0.079	1.039
chr2	243199373	16899341	0.0695	0.5604
chr3	198022430	10093989	0.051	0.2652
chr4	191154276	11790572	0.0617	0.3185
chr5	180915260	8000916	0.0442	0.2499
chr6	171115067	10762593	0.0629	0.4793
chr7	159138663	10895497	0.0685	0.6748

chr8	146364022	10865856	0.0742	0.4405
chr9	141213431	4655016	0.033	0.3528
chr10	135534747	9343075	0.0689	0.4713
chr11	135006516	7679569	0.0569	0.4109
chr12	133851895	9968398	0.0745	0.3187
chr13	115169878	3607414	0.0313	0.2102
chr14	107349540	4192076	0.0391	0.2355
chr15	102531392	5073552	0.0495	0.3021
chr16	90354753	5849411	0.0647	0.3176
chr17	81195210	4738322	0.0584	0.4273
chr18	78077248	3686294	0.0472	0.6025
chr19	59128983	4554894	0.077	0.6108
chr20	63025520	3432572	0.0545	0.2735
chr21	48129895	2694904	0.056	0.2893
chr22	51304566	2529572	0.0493	0.2519
chrMT	16571	41702	2.5166	2.1505
chrX	155270560	7787722	0.0502	0.3351
chrY	59373566	498168	0.0084	0.1818

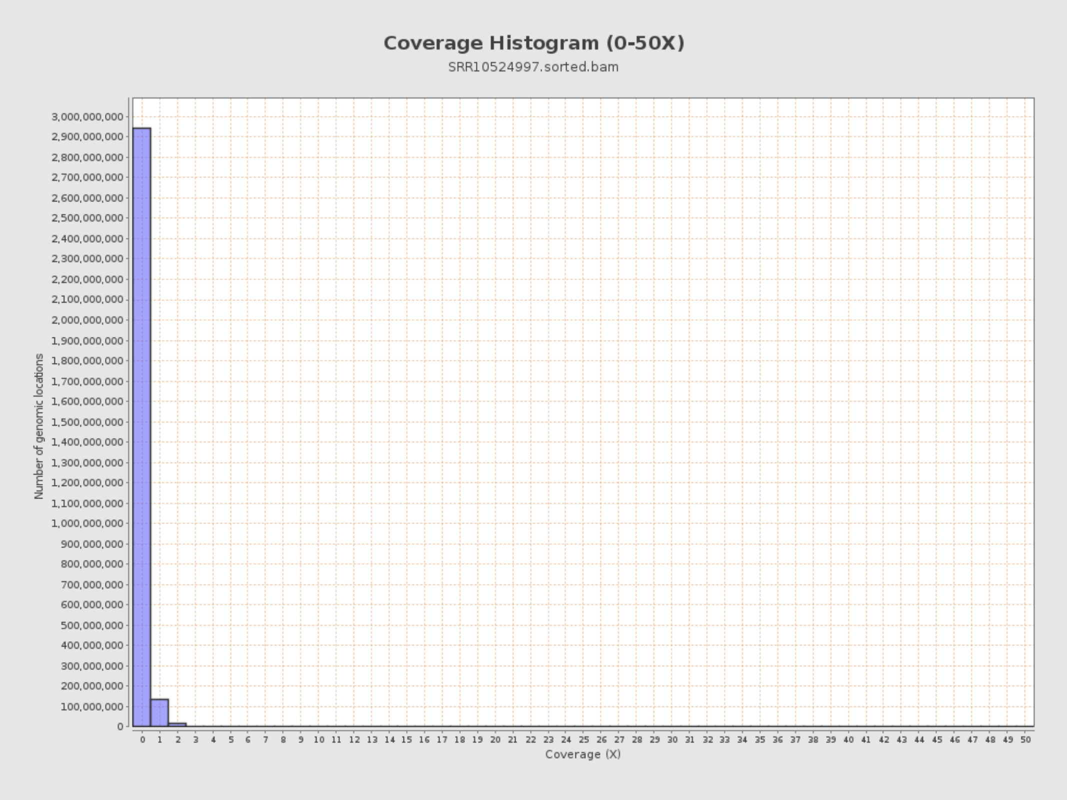
3. Results : Coverage across reference



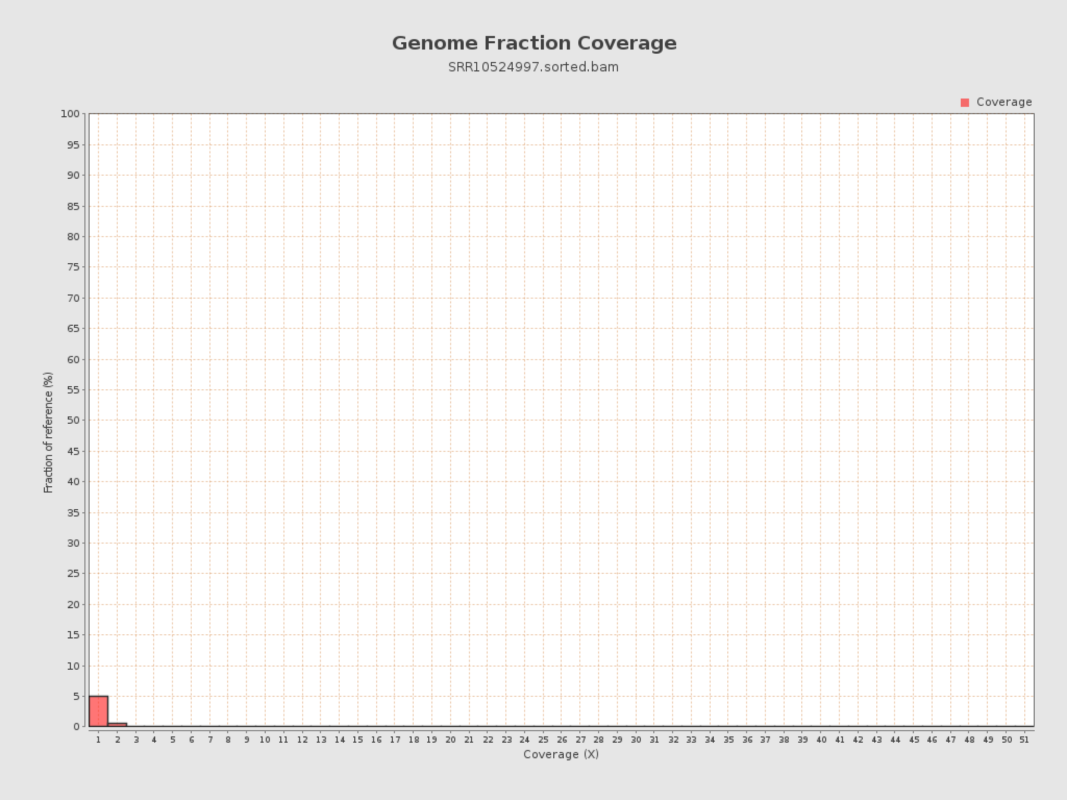
4. Results : Coverage Histogram



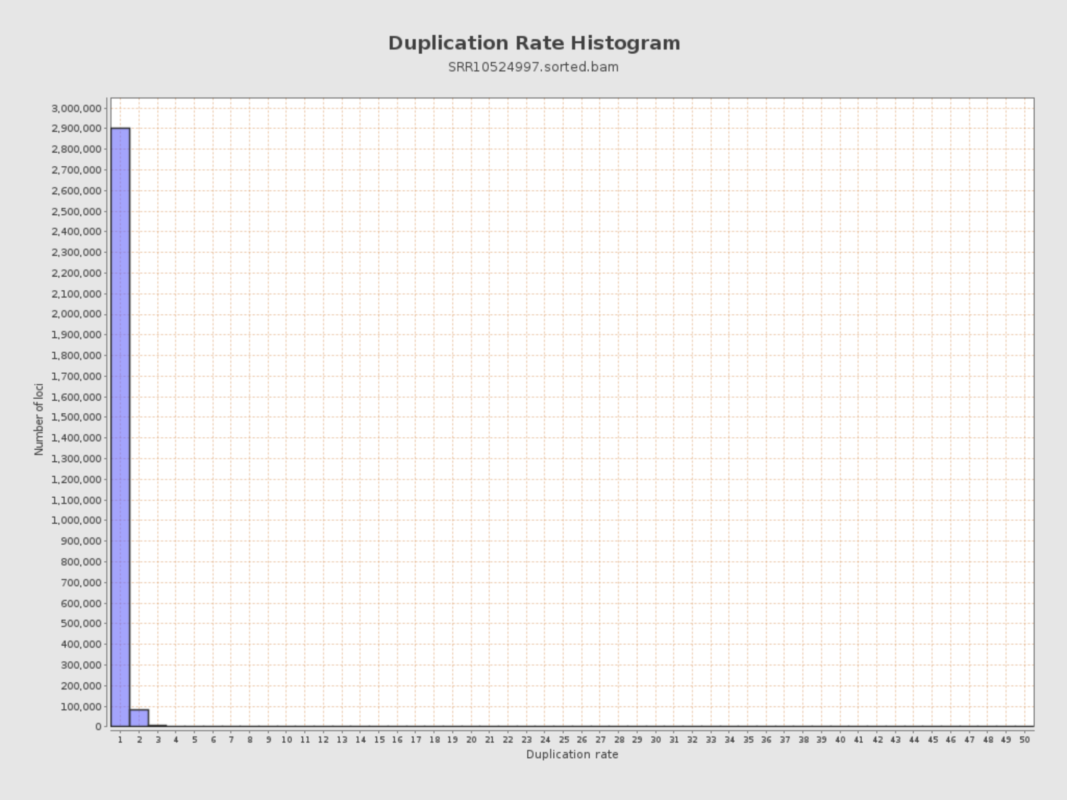
5. Results : Coverage Histogram (0-50X)



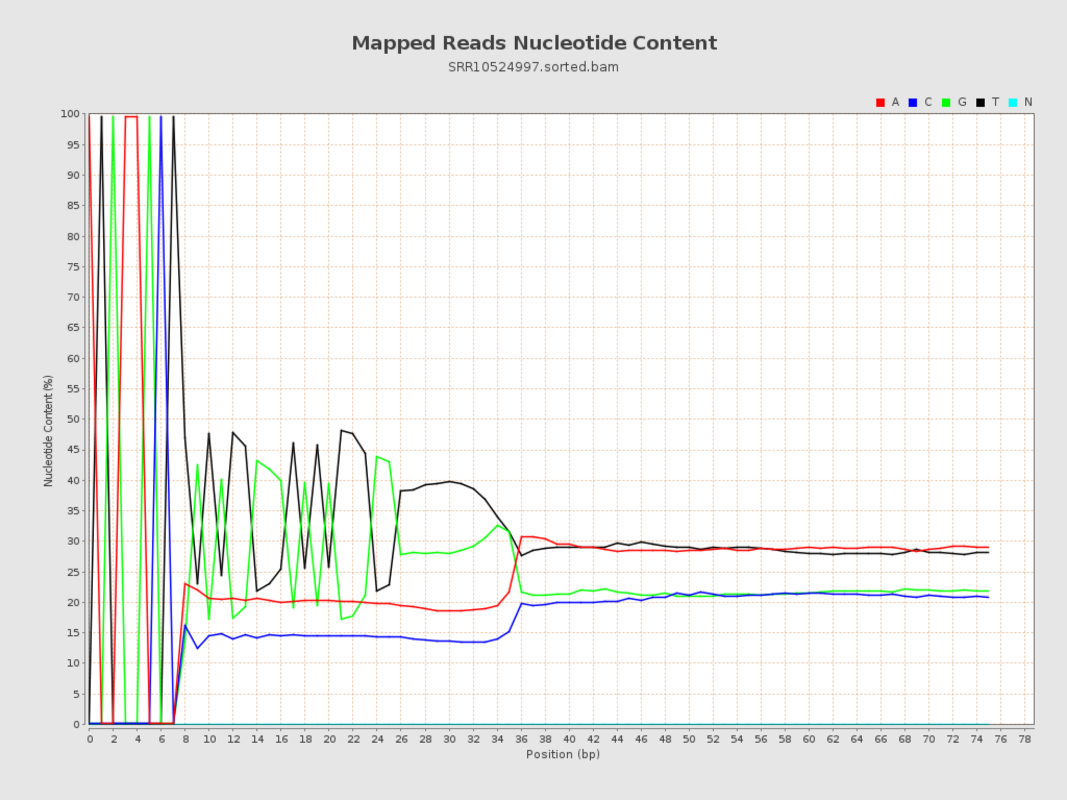
6. Results : Genome Fraction Coverage



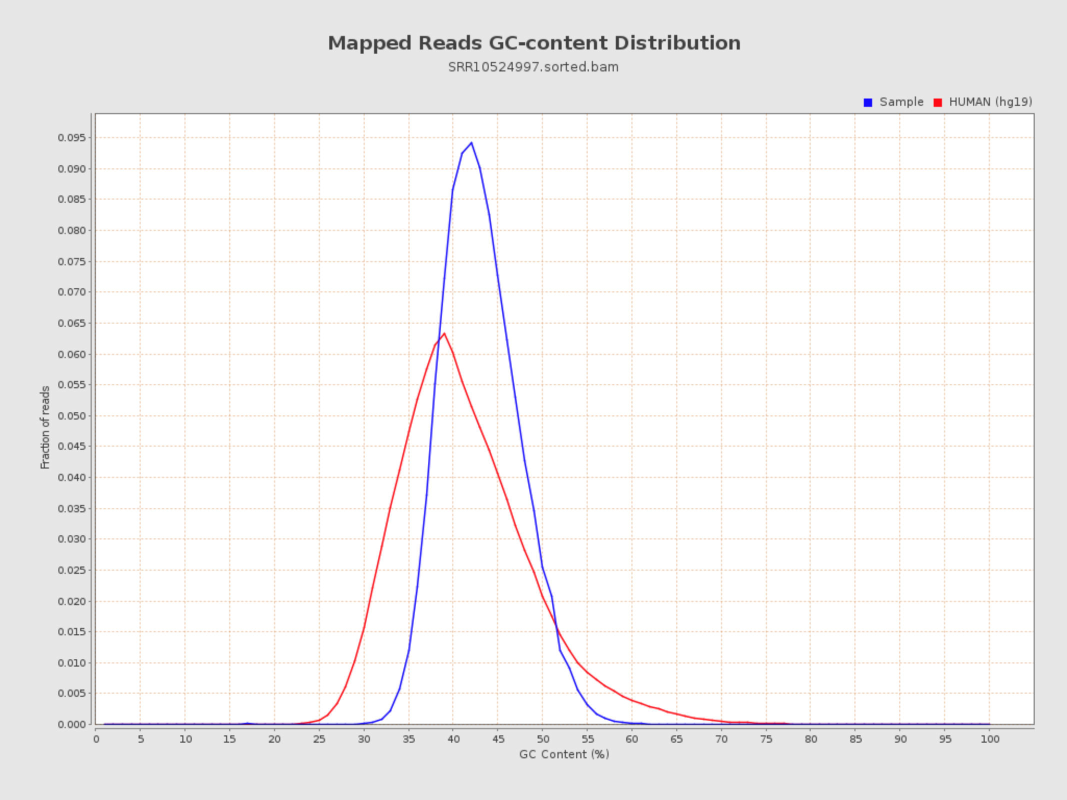
7. Results : Duplication Rate Histogram



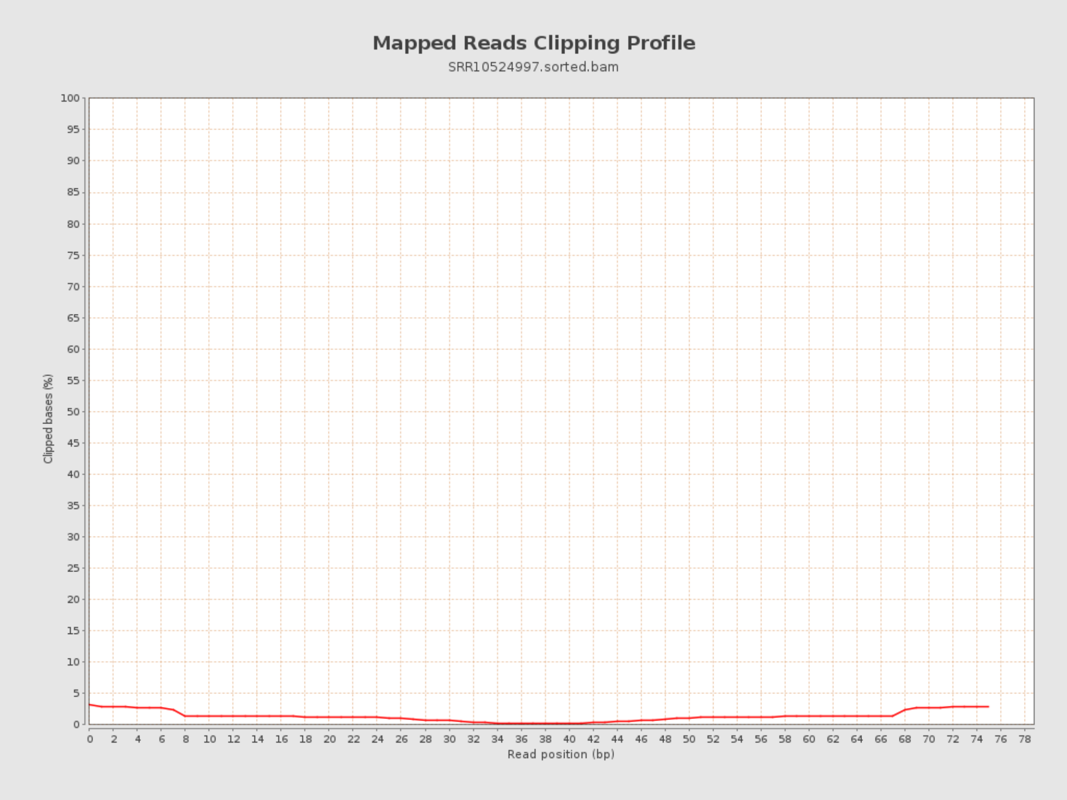
8. Results : Mapped Reads Nucleotide Content



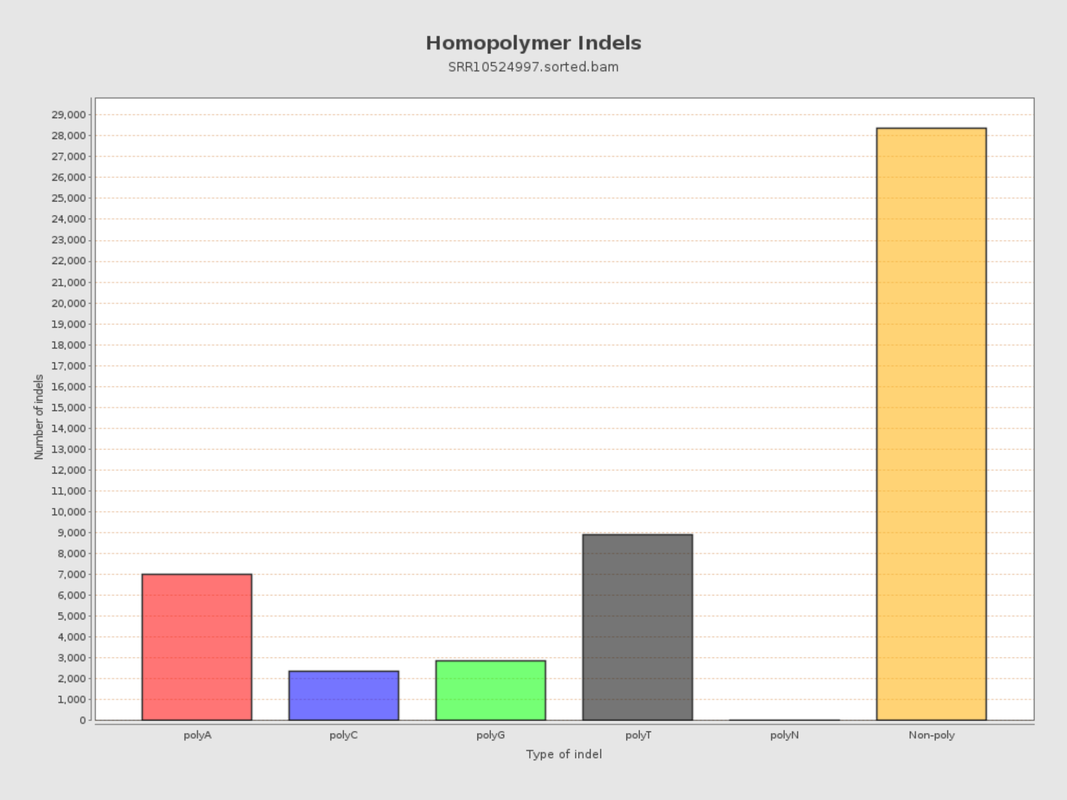
9. Results : Mapped Reads GC-content Distribution



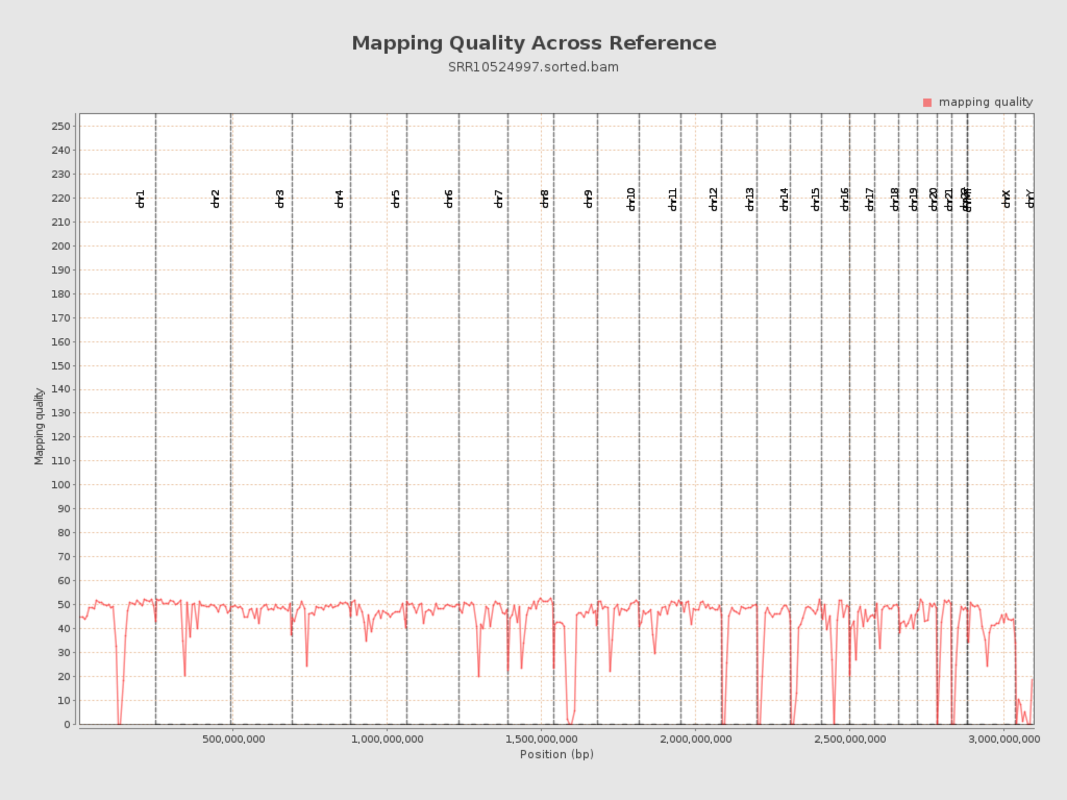
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram