Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 21:36:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524297.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_SRR10524297 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524297.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 21:36:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524297.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,113,956
Mapped reads	1,926,623 / 91.14%
Unmapped reads	187,333 / 8.86%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,194 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	66,513 / 3.15%
Duplication rate	2.33%
Clipped reads	1,932,596 / 91.42%

2.2. ACGT Content

Number/percentage of A's	26,491,451 / 23.68%
Number/percentage of C's	22,912,373 / 20.48%
Number/percentage of T's	35,886,841 / 32.08%
Number/percentage of G's	26,545,578 / 23.73%
Number/percentage of N's	15,792 / 0.01%
GC Percentage	44.22%

2.3. Coverage

Mean	0.0361

Standard Deviation	0.3438

2.4. Mapping Quality

Mean Mapping Quality	43.72

2.5. Mismatches and indels

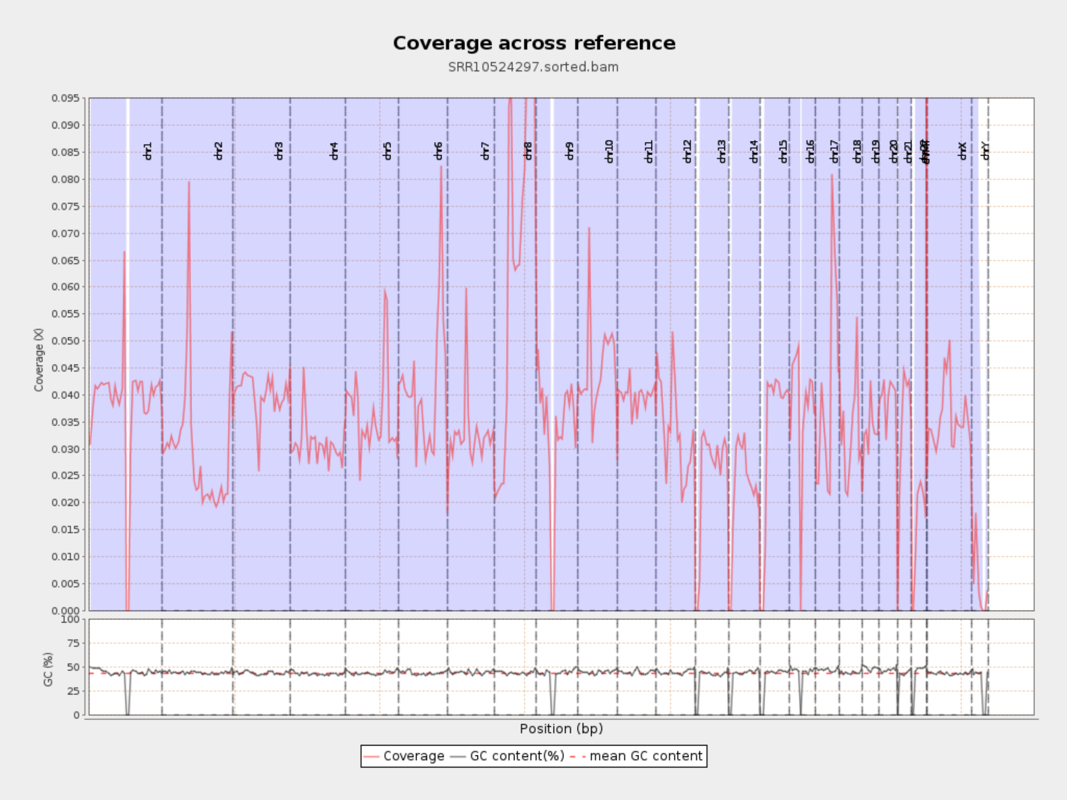
General error rate	0.53%
Mismatches	576,342
Insertions	6,497
Mapped reads with at least one insertion	0.34%
Deletions	19,219
Mapped reads with at least one deletion	0.99%
Homopolymer indels	43.72%

2.6. Chromosome stats

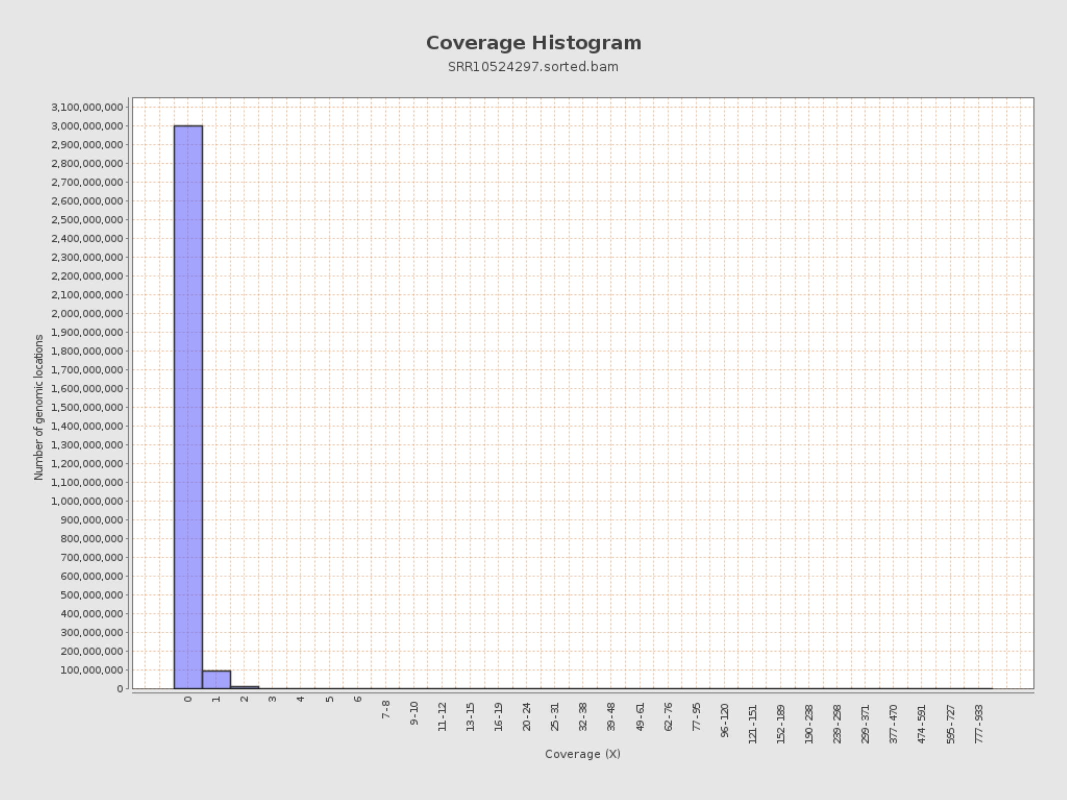
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9556858	0.0383	0.681
chr2	243199373	7212685	0.0297	0.4396
chr3	198022430	7941710	0.0401	0.2219
chr4	191154276	5871278	0.0307	0.2107
chr5	180915260	6660889	0.0368	0.2109
chr6	171115067	7056096	0.0412	0.2461
chr7	159138663	5234632	0.0329	0.4454

chr8	146364022	11079258	0.0757	0.4036
chr9	141213431	4634105	0.0328	0.2641
chr10	135534747	6092282	0.0449	0.3439
chr11	135006516	5356418	0.0397	0.2854
chr12	133851895	4468913	0.0334	0.2033
chr13	115169878	2855572	0.0248	0.1716
chr14	107349540	2414639	0.0225	0.1827
chr15	102531392	3392428	0.0331	0.205
chr16	90354753	3437070	0.038	0.2287
chr17	81195210	3291654	0.0405	0.2461
chr18	78077248	2633642	0.0337	0.4858
chr19	59128983	1983609	0.0335	0.4716
chr20	63025520	2473693	0.0392	0.2187
chr21	48129895	1616445	0.0336	0.2169
chr22	51304566	785790	0.0153	0.1351
chrMT	16571	3931	0.2372	0.498
chrX	155270560	5521343	0.0356	0.2367
chrY	59373566	307117	0.0052	0.1368

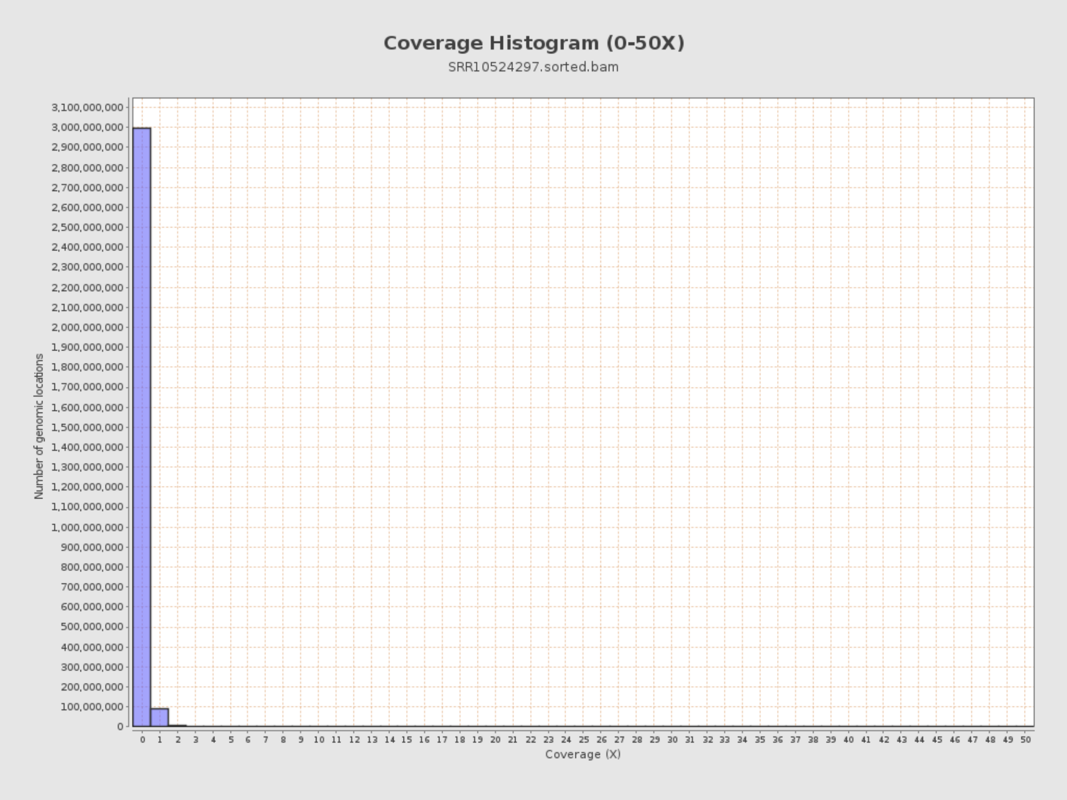
3. Results : Coverage across reference



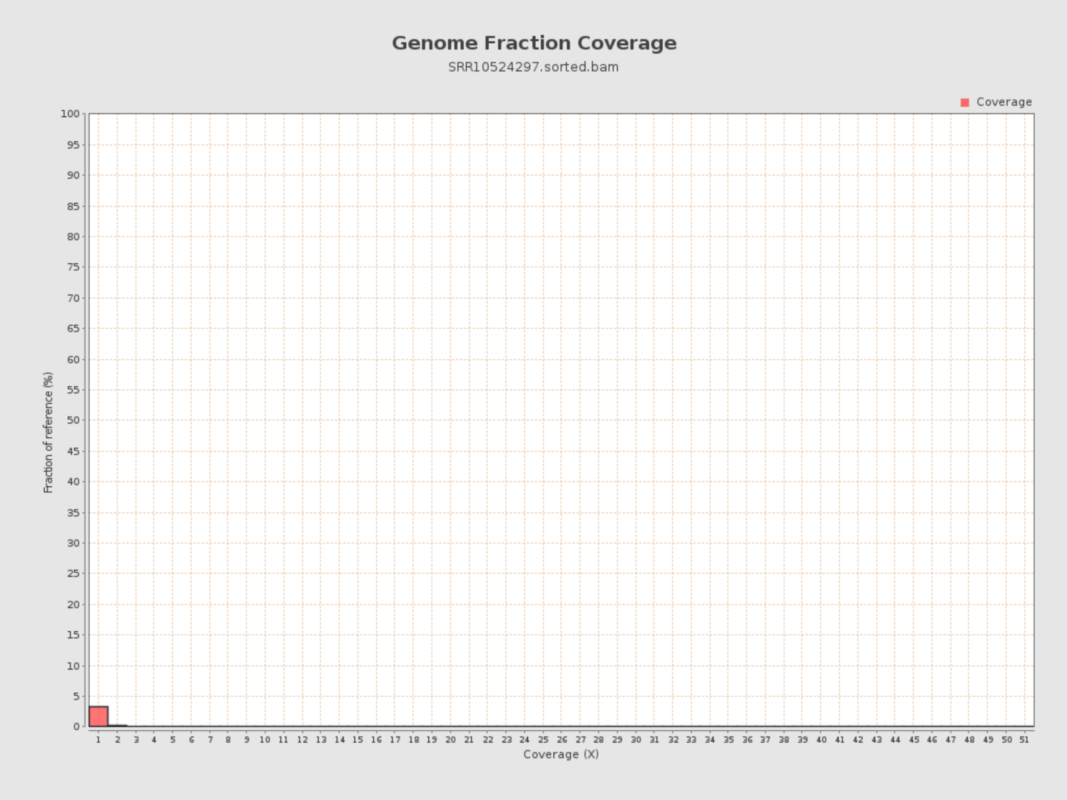
4. Results : Coverage Histogram



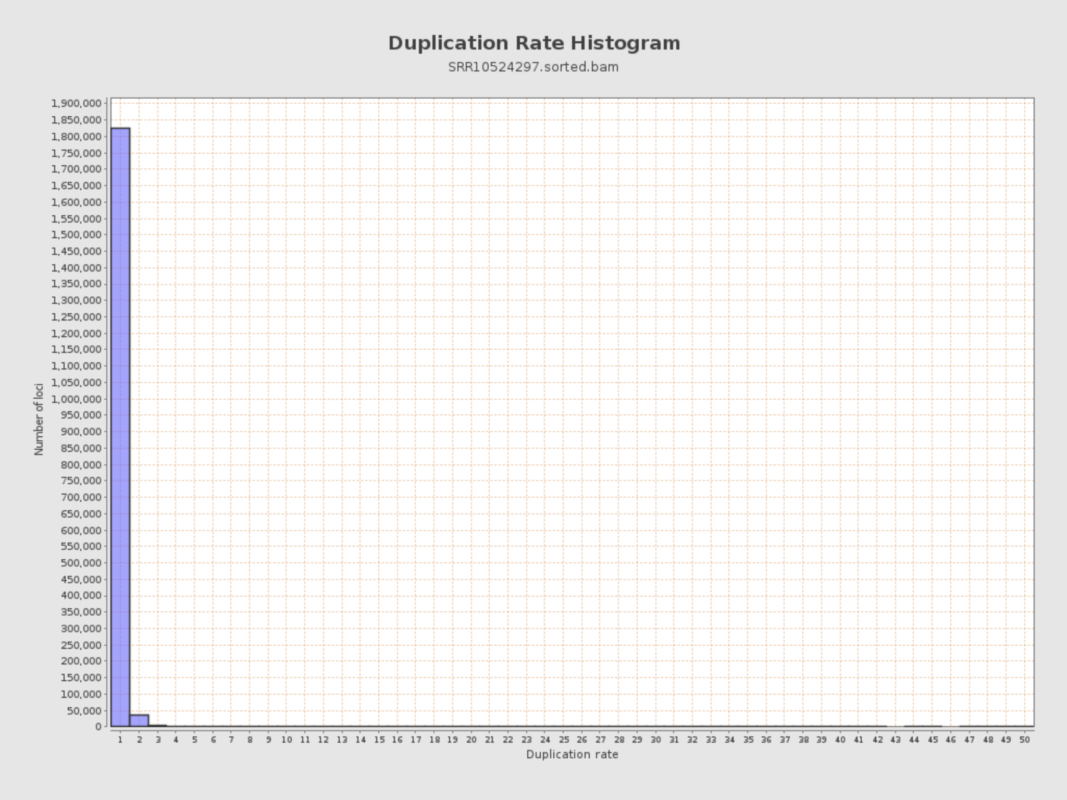
5. Results : Coverage Histogram (0-50X)



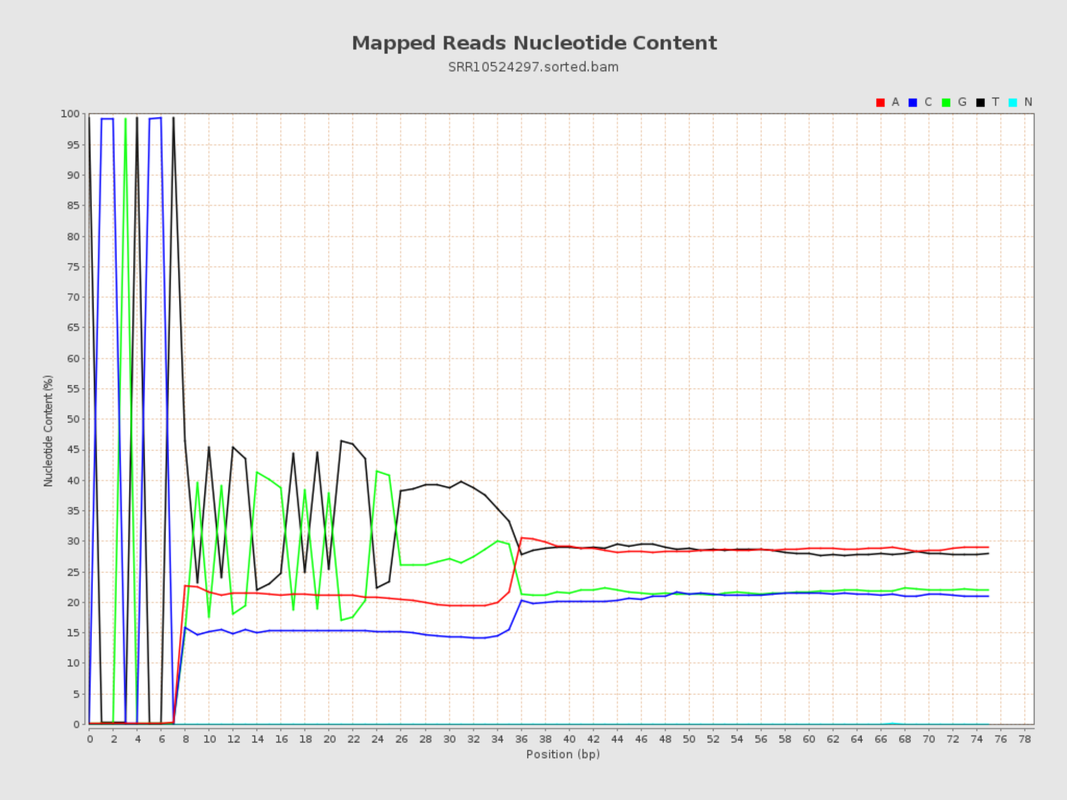
6. Results : Genome Fraction Coverage



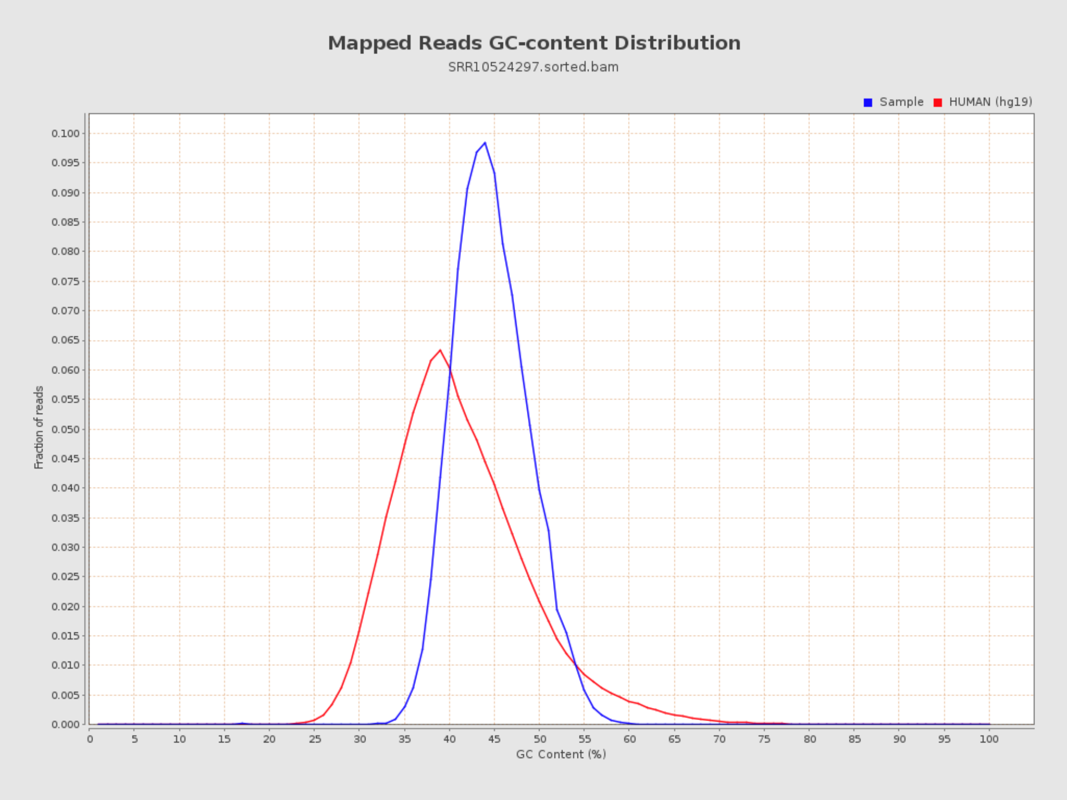
7. Results : Duplication Rate Histogram



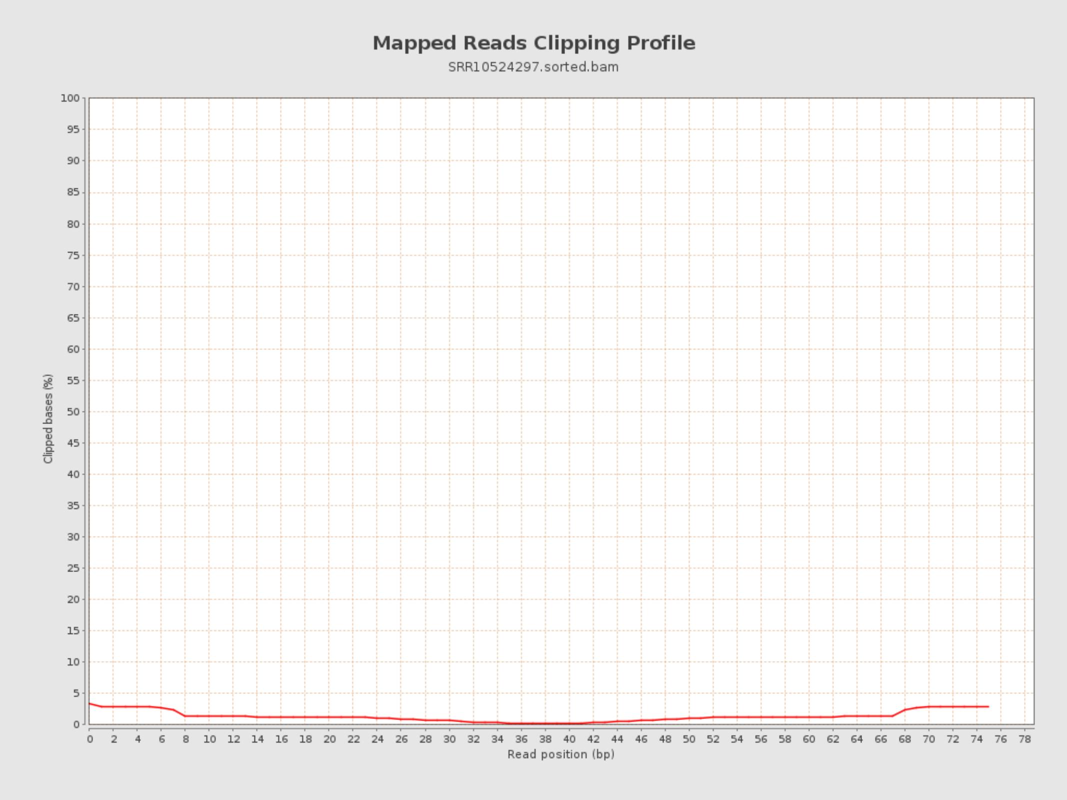
8. Results : Mapped Reads Nucleotide Content



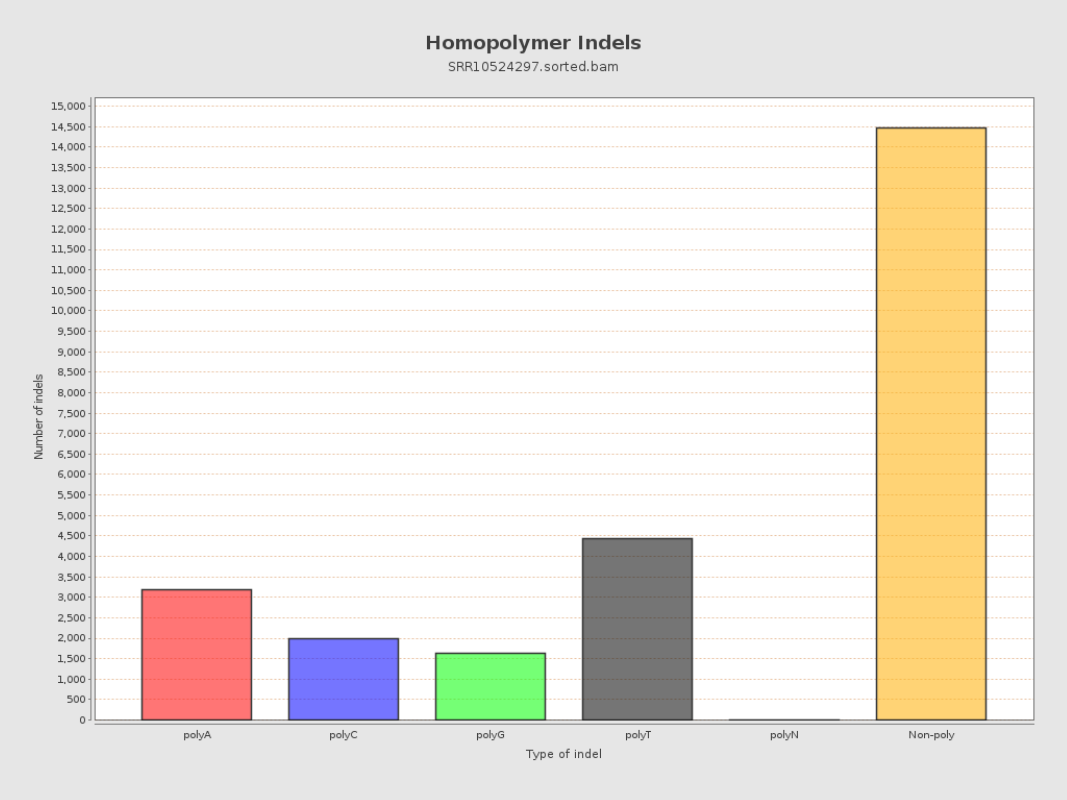
9. Results : Mapped Reads GC-content Distribution



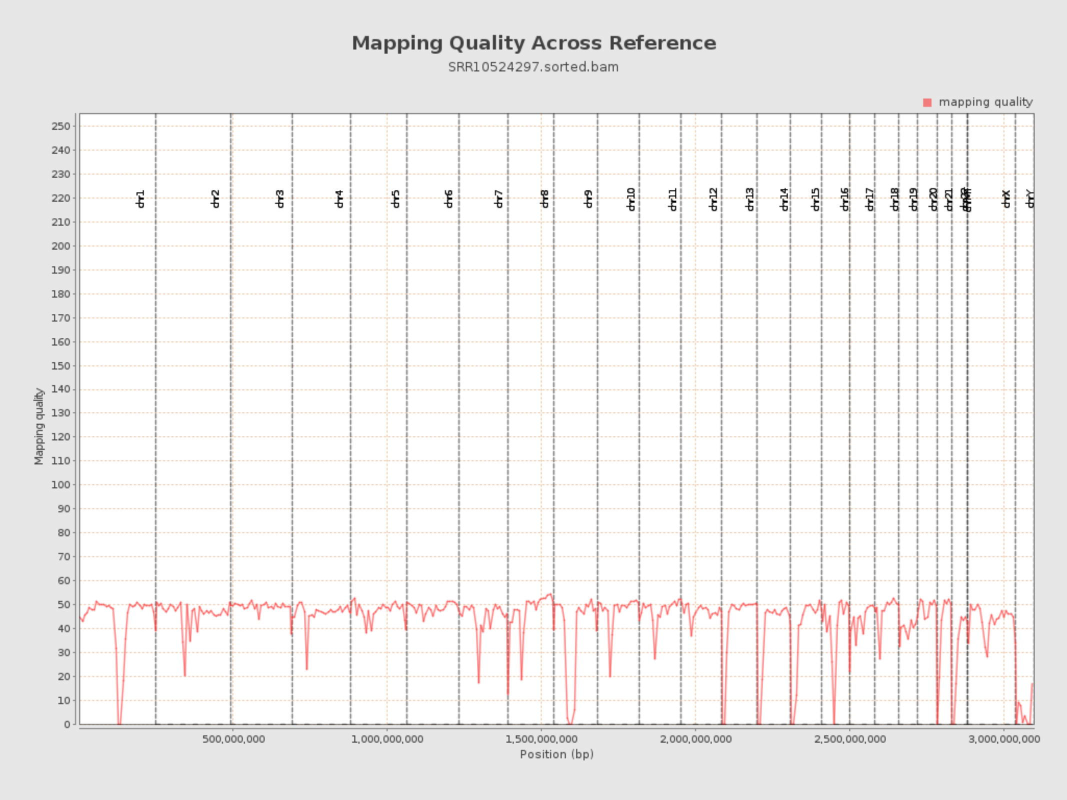
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram