Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 11:59:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524985.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_SRR10524985 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524985.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 11:59:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524985.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,165,951
Mapped reads	1,077,259 / 92.39%
Unmapped reads	88,692 / 7.61%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,433 / 0.21%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	37,513 / 3.22%
Duplication rate	2.63%
Clipped reads	1,077,766 / 92.44%

2.2. ACGT Content

Number/percentage of A's	15,784,517 / 25.21%
Number/percentage of C's	11,420,586 / 18.24%
Number/percentage of T's	20,266,667 / 32.37%
Number/percentage of G's	15,130,820 / 24.17%
Number/percentage of N's	773 / 0%
GC Percentage	42.41%

2.3. Coverage

Mean	0.0202

Standard Deviation	0.2092

2.4. Mapping Quality

Mean Mapping Quality	45.61

2.5. Mismatches and indels

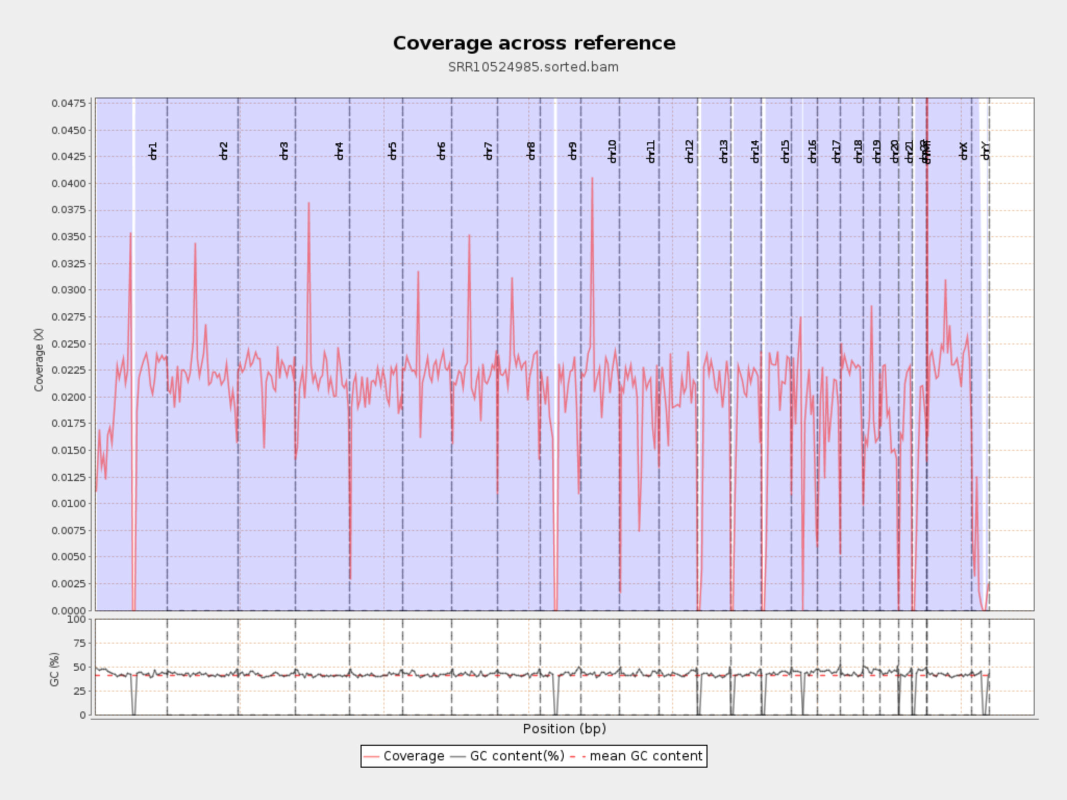
General error rate	0.5%
Mismatches	304,476
Insertions	4,077
Mapped reads with at least one insertion	0.38%
Deletions	11,232
Mapped reads with at least one deletion	1.04%
Homopolymer indels	43.12%

2.6. Chromosome stats

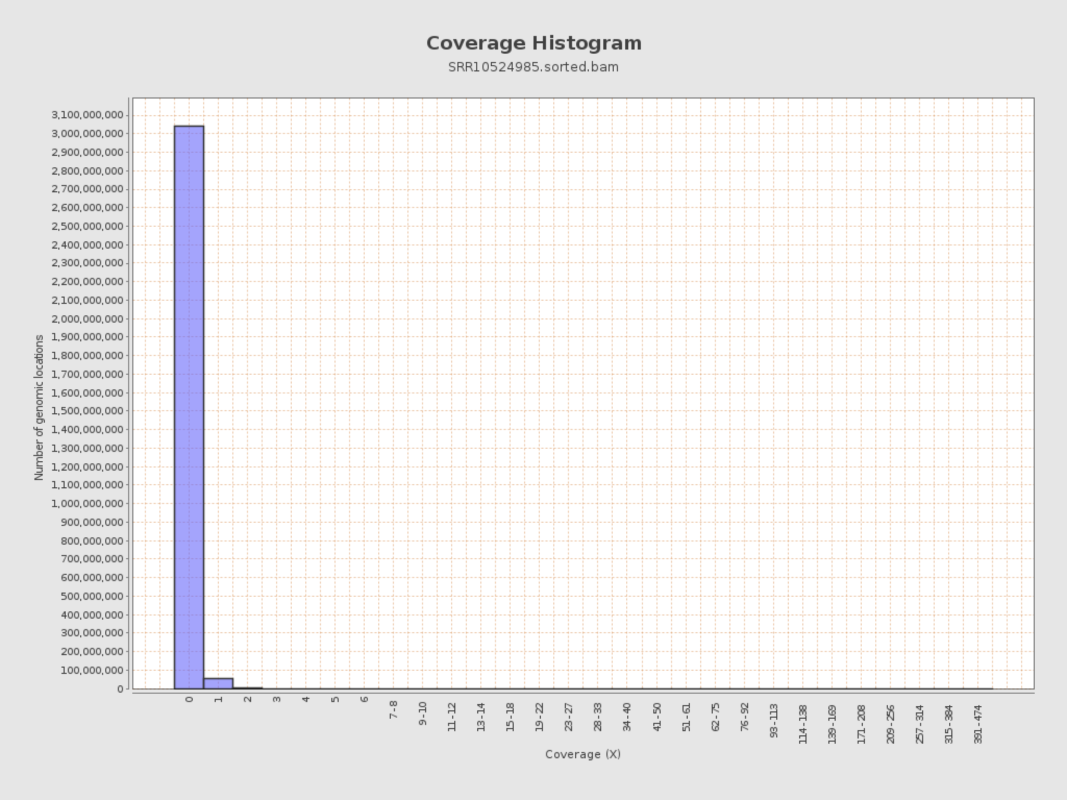
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4853042	0.0195	0.3688
chr2	243199373	5389660	0.0222	0.2306
chr3	198022430	4432551	0.0224	0.1613
chr4	191154276	4184475	0.0219	0.1801
chr5	180915260	3763825	0.0208	0.1563
chr6	171115067	3888472	0.0227	0.1931
chr7	159138663	3545047	0.0223	0.2477

chr8	146364022	3339944	0.0228	0.2225
chr9	141213431	2545903	0.018	0.1811
chr10	135534747	3151528	0.0233	0.2185
chr11	135006516	2596063	0.0192	0.1874
chr12	133851895	2723896	0.0204	0.1547
chr13	115169878	2099672	0.0182	0.1462
chr14	107349540	1918331	0.0179	0.1489
chr15	102531392	1865084	0.0182	0.1507
chr16	90354753	1586721	0.0176	0.1522
chr17	81195210	1450494	0.0179	0.1569
chr18	78077248	1759749	0.0225	0.2855
chr19	59128983	1065235	0.018	0.2557
chr20	63025520	1099321	0.0174	0.1452
chr21	48129895	843036	0.0175	0.1538
chr22	51304566	658638	0.0128	0.1213
chrMT	16571	1325	0.08	0.292
chrX	155270560	3667941	0.0236	0.179
chrY	59373566	192436	0.0032	0.1055

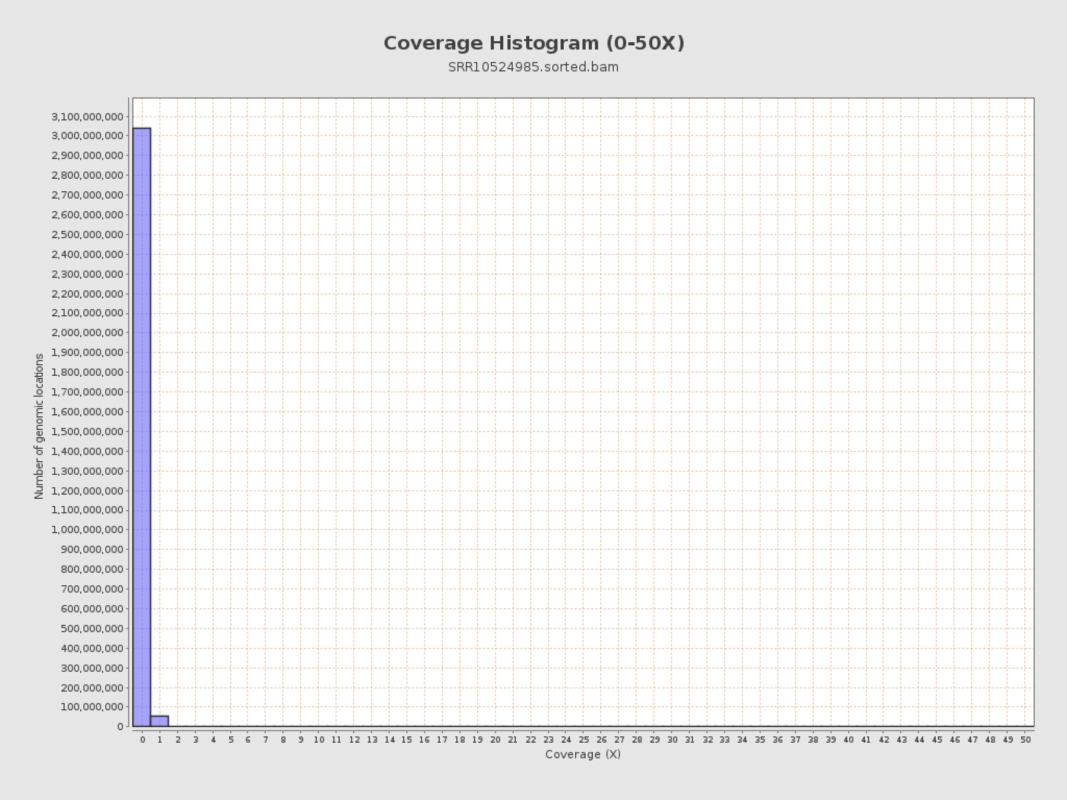
3. Results : Coverage across reference



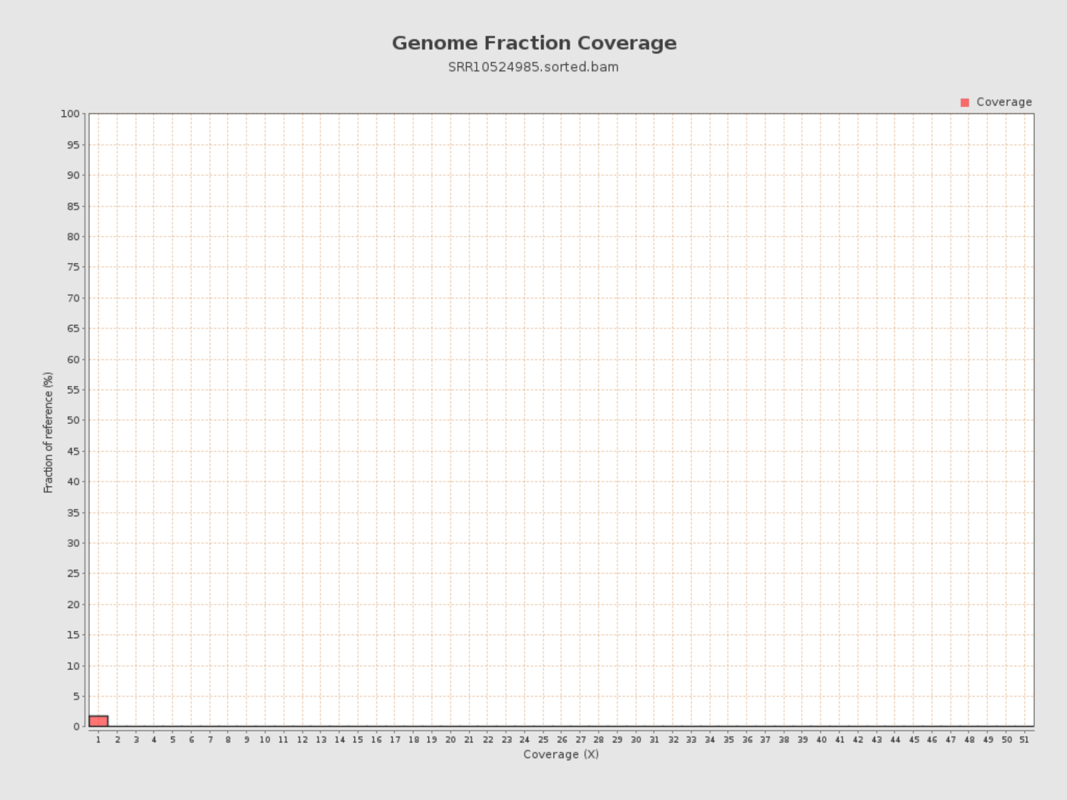
4. Results : Coverage Histogram



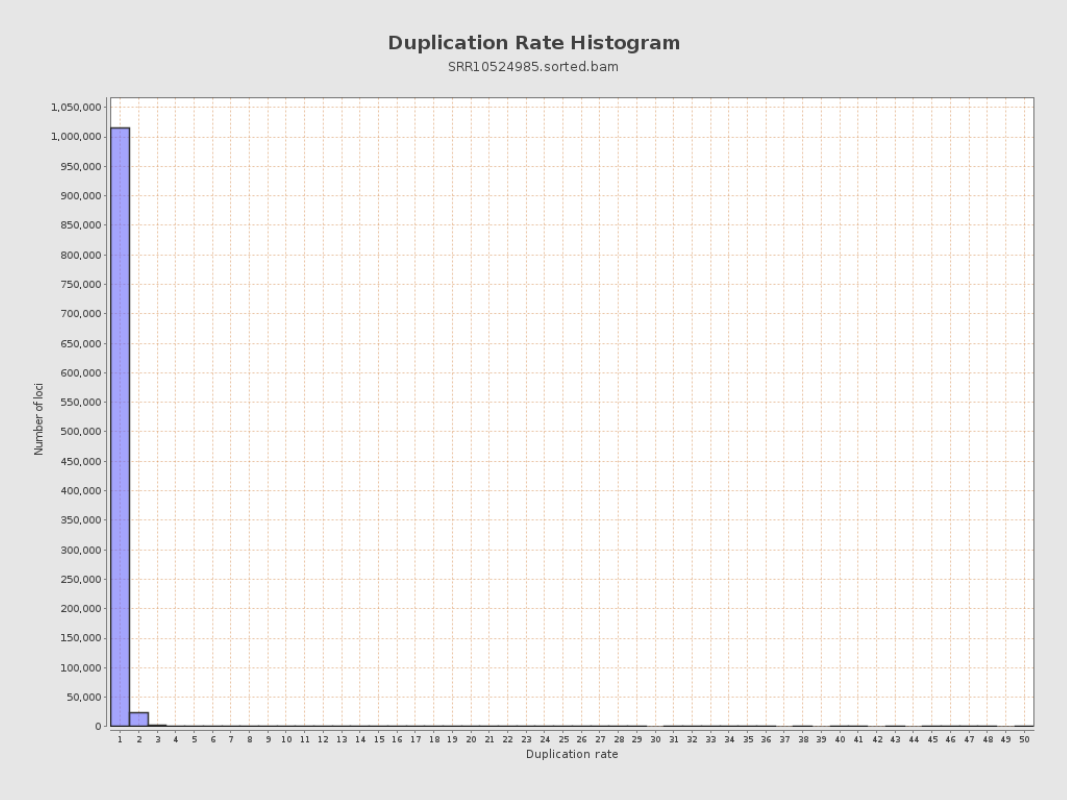
5. Results : Coverage Histogram (0-50X)



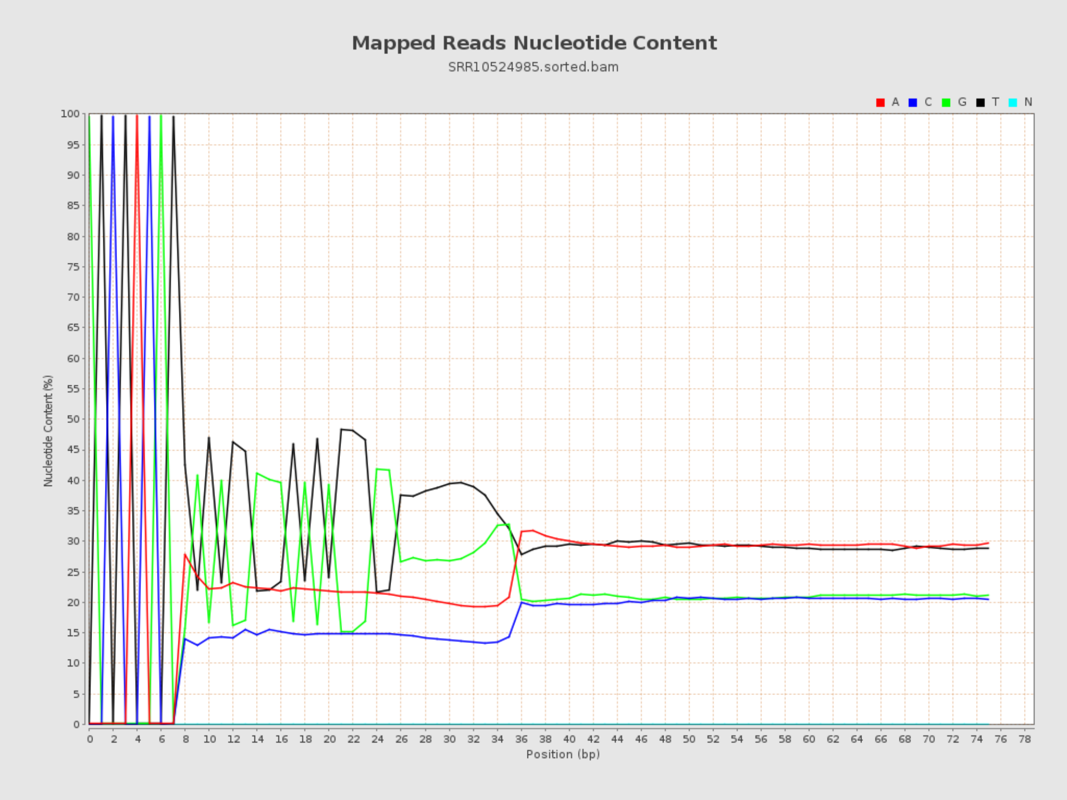
6. Results : Genome Fraction Coverage



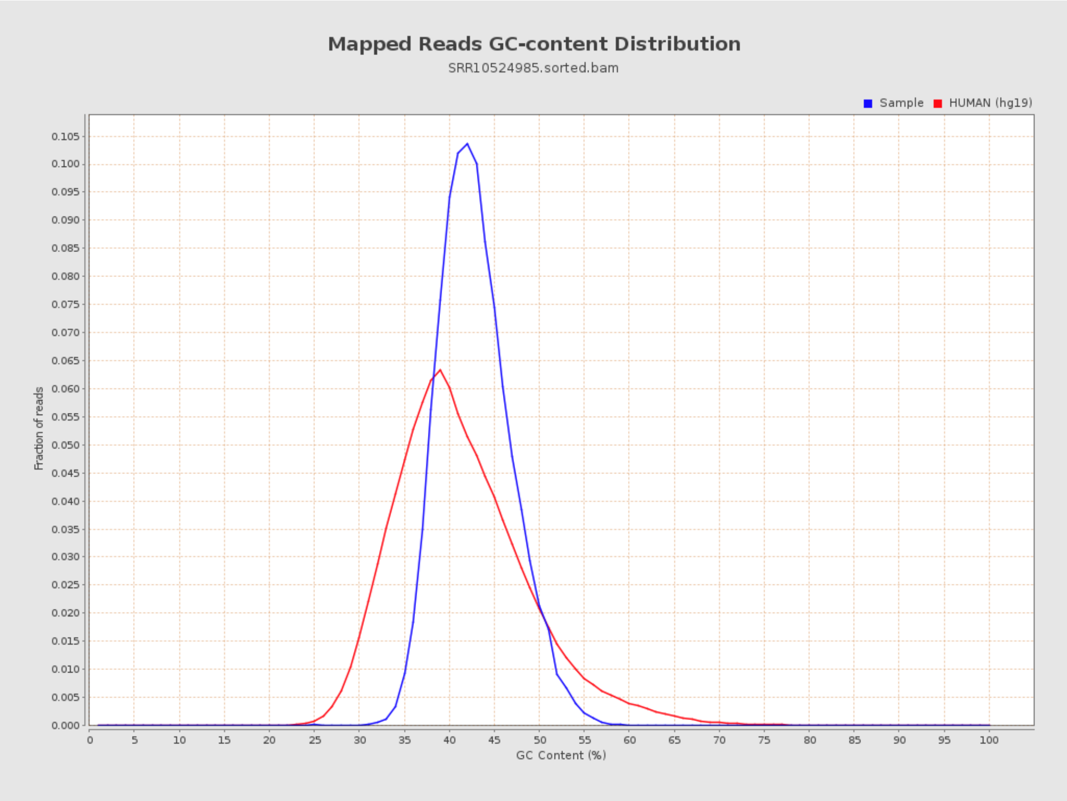
7. Results : Duplication Rate Histogram



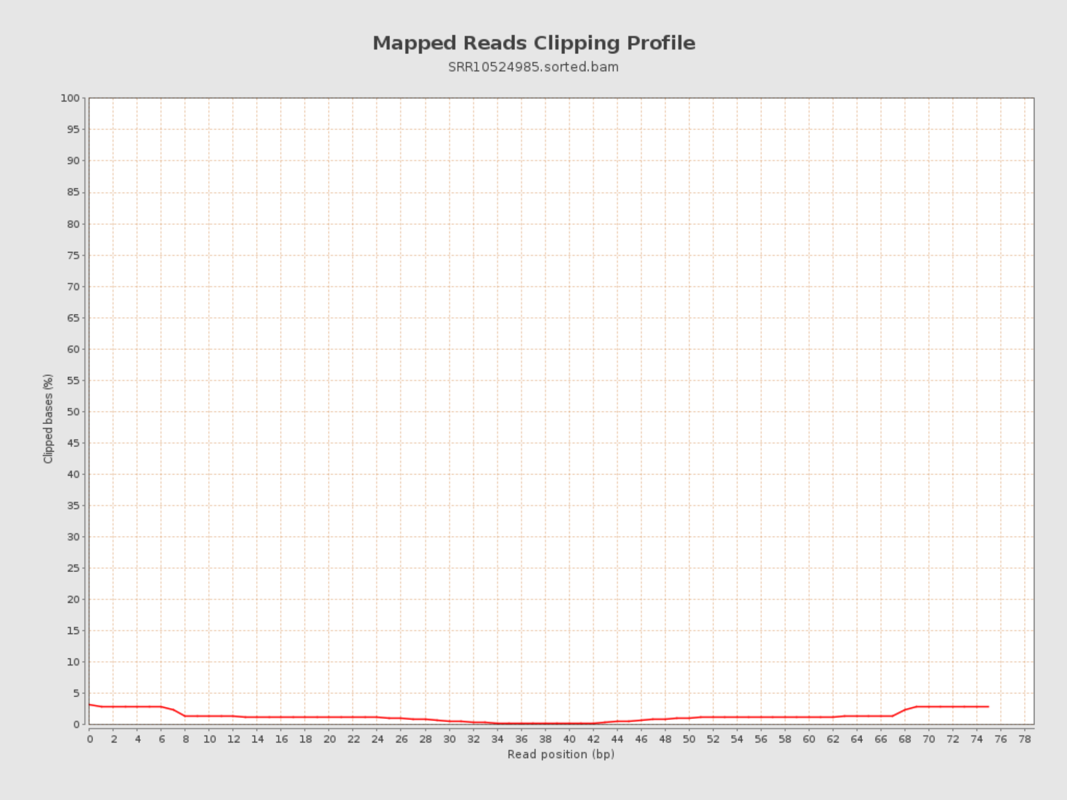
8. Results : Mapped Reads Nucleotide Content



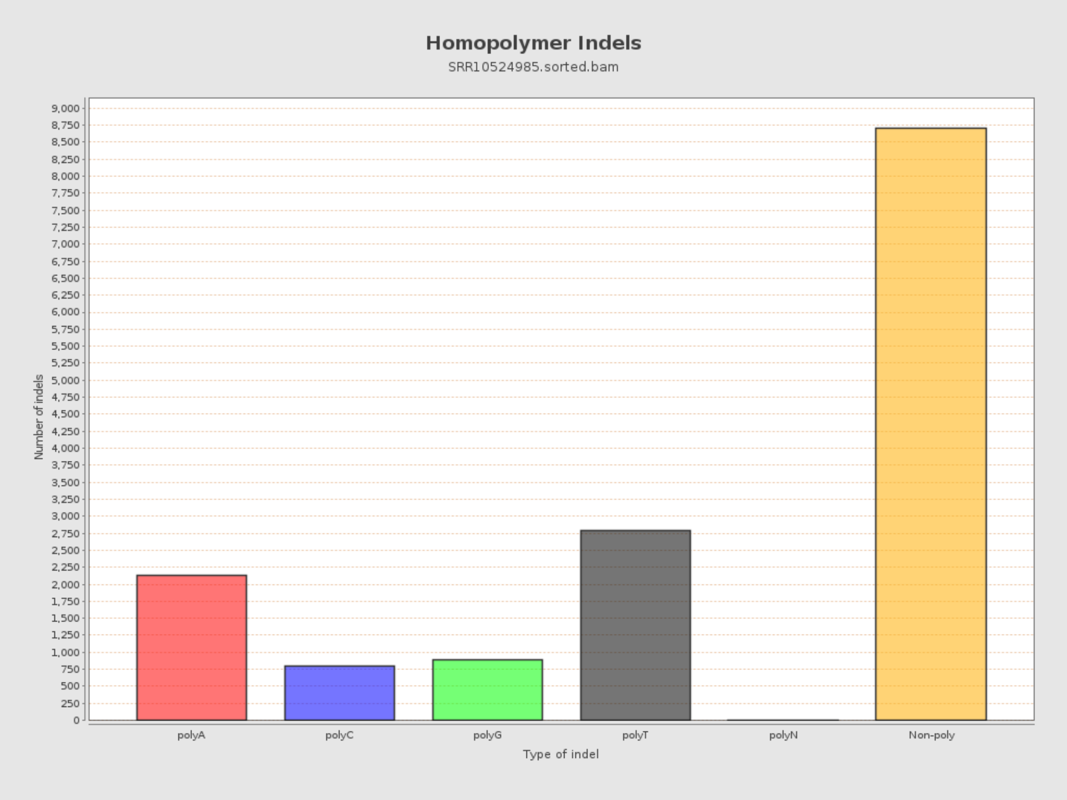
9. Results : Mapped Reads GC-content Distribution



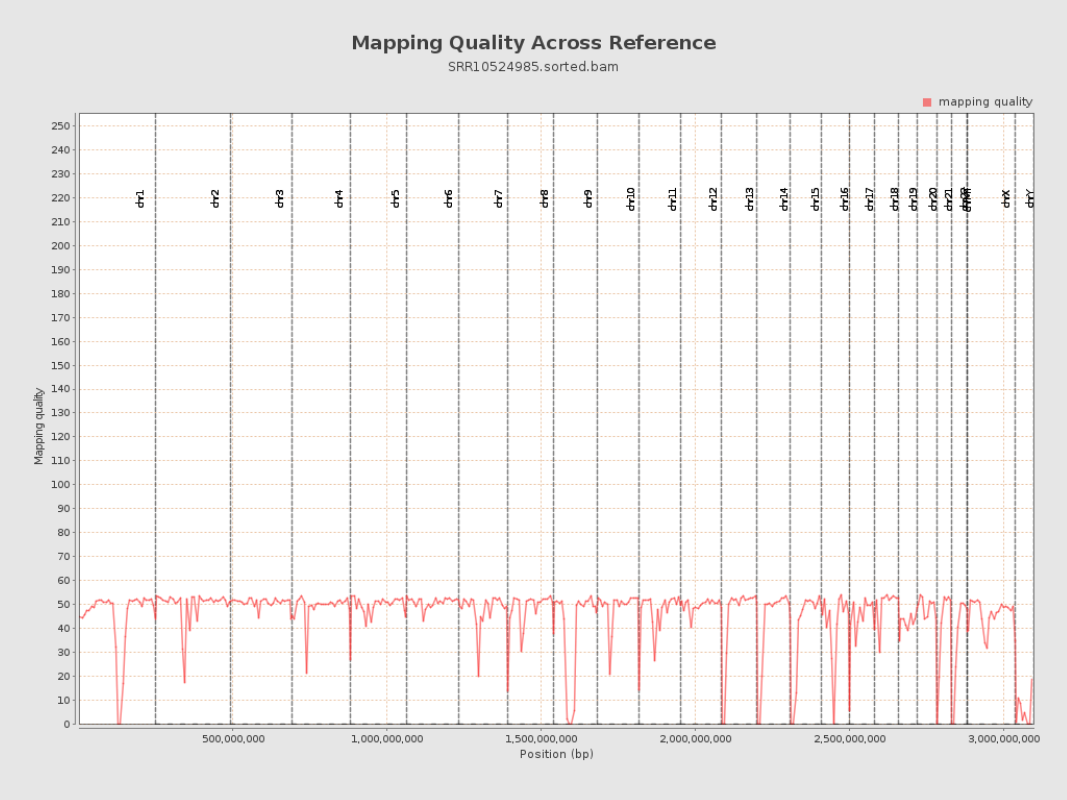
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram