Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 20:31:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524784.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_SRR10524784 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524784.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 20:30:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524784.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,269,437
Mapped reads	1,162,961 / 91.61%
Unmapped reads	106,476 / 8.39%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,017 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	35,144 / 2.77%
Duplication rate	2.27%
Clipped reads	1,165,692 / 91.83%

2.2. ACGT Content

Number/percentage of A's	16,804,331 / 25.09%
Number/percentage of C's	12,496,191 / 18.65%
Number/percentage of T's	20,407,029 / 30.46%
Number/percentage of G's	17,270,874 / 25.78%
Number/percentage of N's	7,989 / 0.01%
GC Percentage	44.44%

2.3. Coverage

Mean	0.0216

Standard Deviation	0.2008

2.4. Mapping Quality

Mean Mapping Quality	44.82

2.5. Mismatches and indels

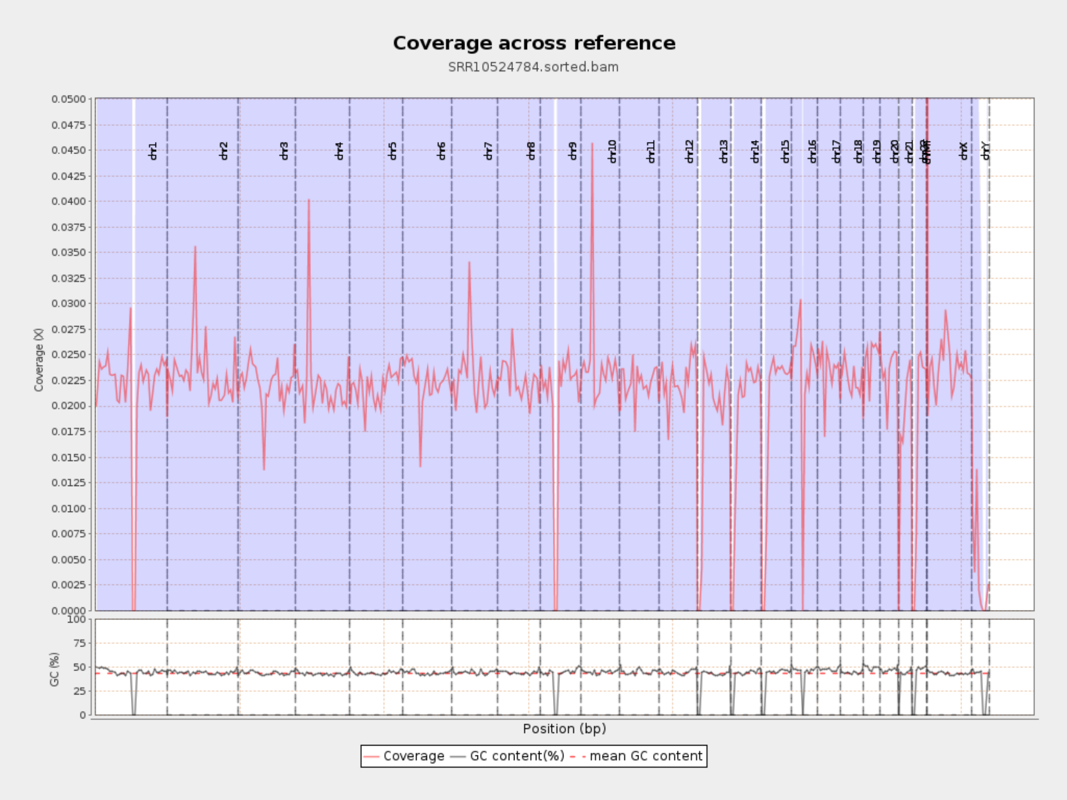
General error rate	0.51%
Mismatches	335,033
Insertions	4,292
Mapped reads with at least one insertion	0.37%
Deletions	13,100
Mapped reads with at least one deletion	1.12%
Homopolymer indels	42.27%

2.6. Chromosome stats

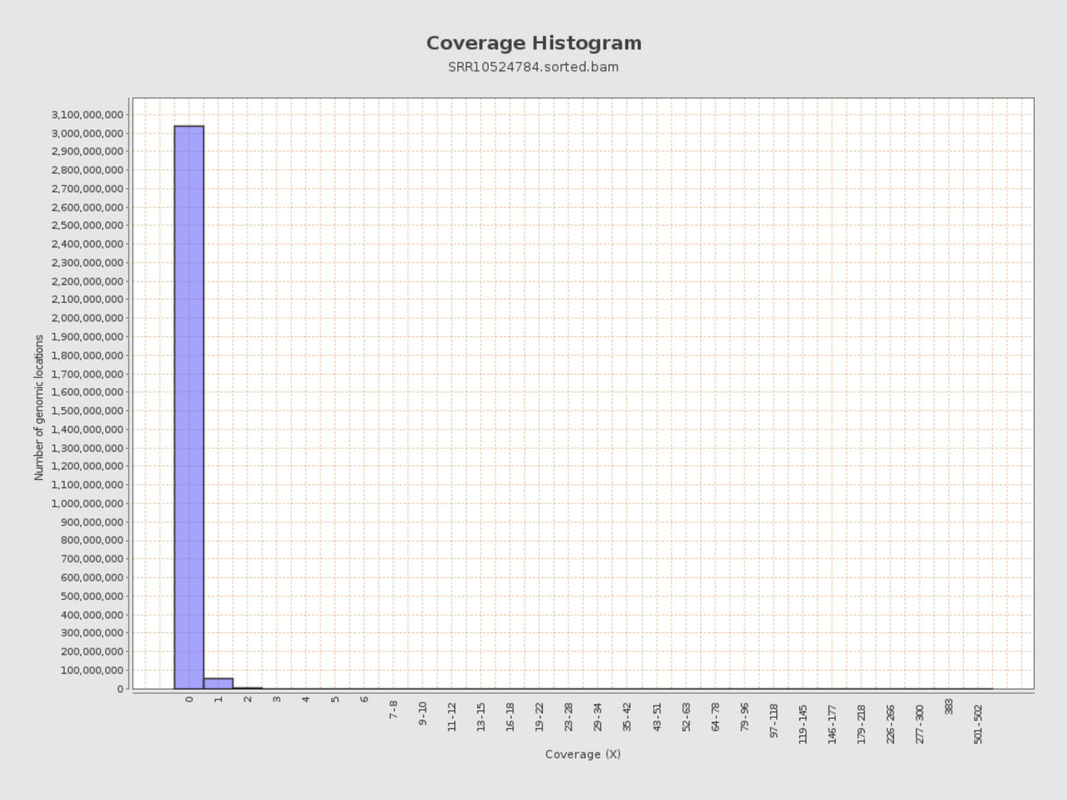
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5372418	0.0216	0.2661
chr2	243199373	5651856	0.0232	0.2883
chr3	198022430	4381568	0.0221	0.1616
chr4	191154276	4253768	0.0223	0.1793
chr5	180915260	3985785	0.022	0.1595
chr6	171115067	3826333	0.0224	0.1718
chr7	159138663	3659121	0.023	0.241

chr8	146364022	3301414	0.0226	0.1859
chr9	141213431	2865368	0.0203	0.183
chr10	135534747	3291858	0.0243	0.2437
chr11	135006516	3014405	0.0223	0.1857
chr12	133851895	3004269	0.0224	0.162
chr13	115169878	2084391	0.0181	0.1445
chr14	107349540	2012087	0.0187	0.1497
chr15	102531392	1950044	0.019	0.1489
chr16	90354753	2058943	0.0228	0.1753
chr17	81195210	1910887	0.0235	0.1733
chr18	78077248	1769902	0.0227	0.2748
chr19	59128983	1457764	0.0247	0.2223
chr20	63025520	1459830	0.0232	0.1692
chr21	48129895	881211	0.0183	0.1585
chr22	51304566	855160	0.0167	0.1397
chrMT	16571	28237	1.704	1.6514
chrX	155270560	3706879	0.0239	0.1752
chrY	59373566	224528	0.0038	0.1121

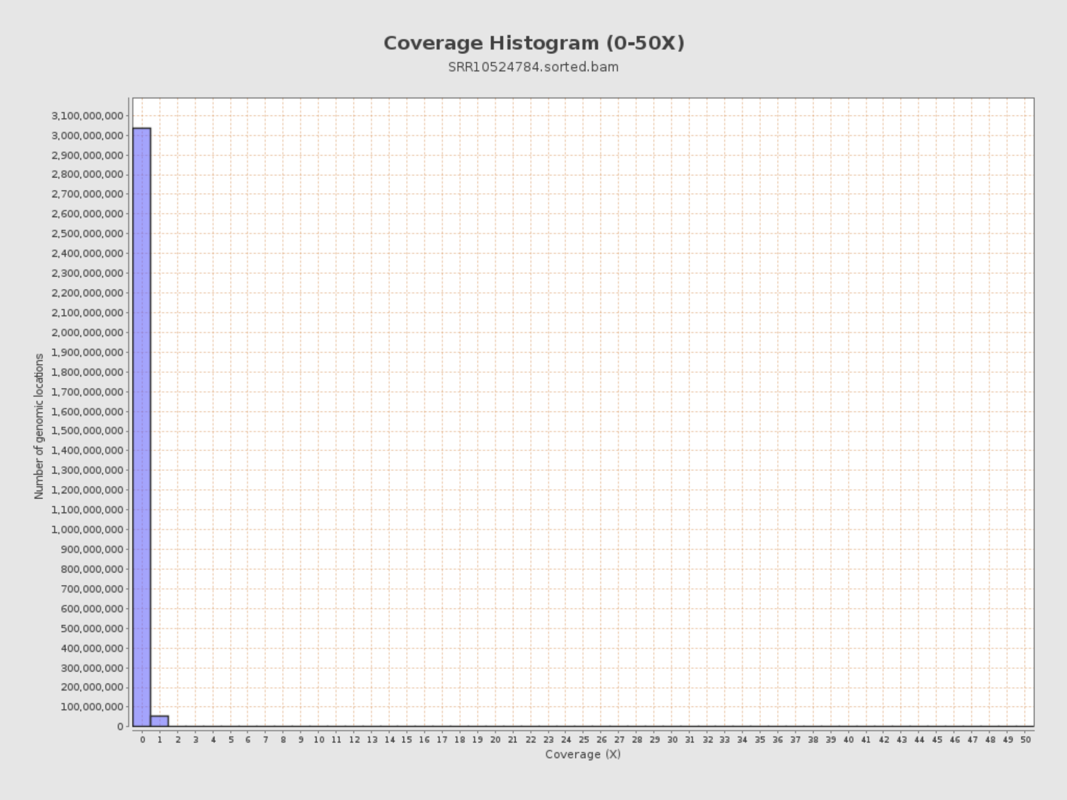
3. Results : Coverage across reference



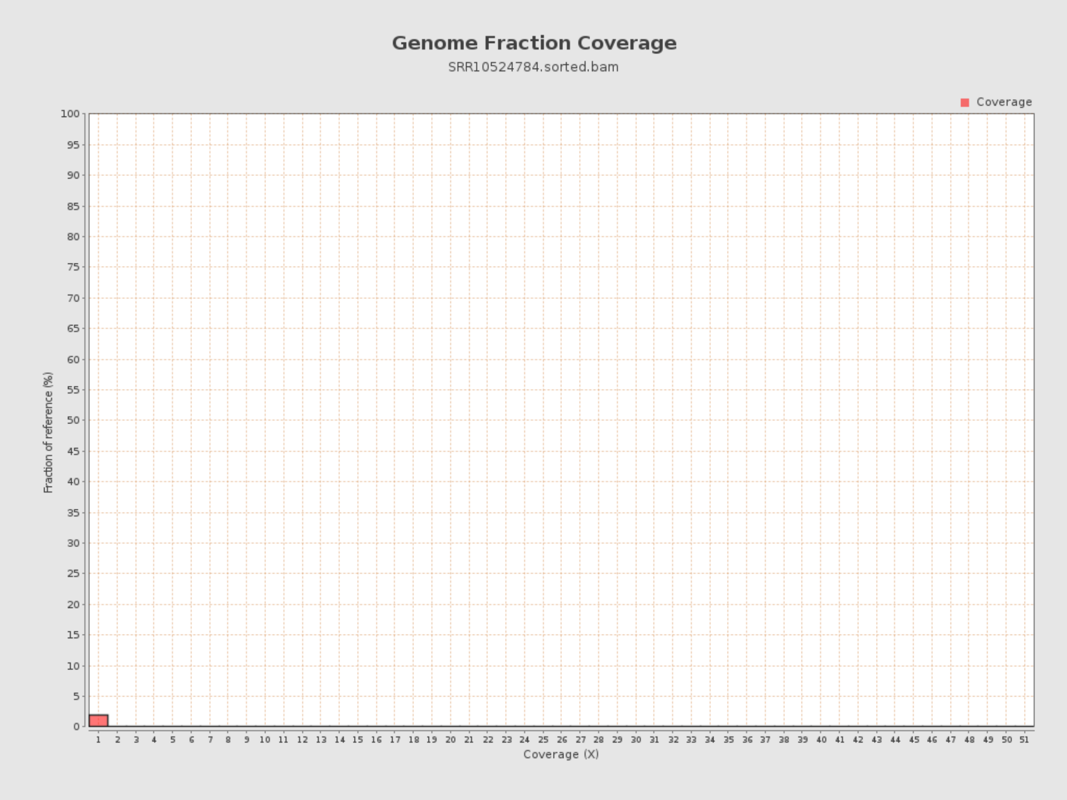
4. Results : Coverage Histogram



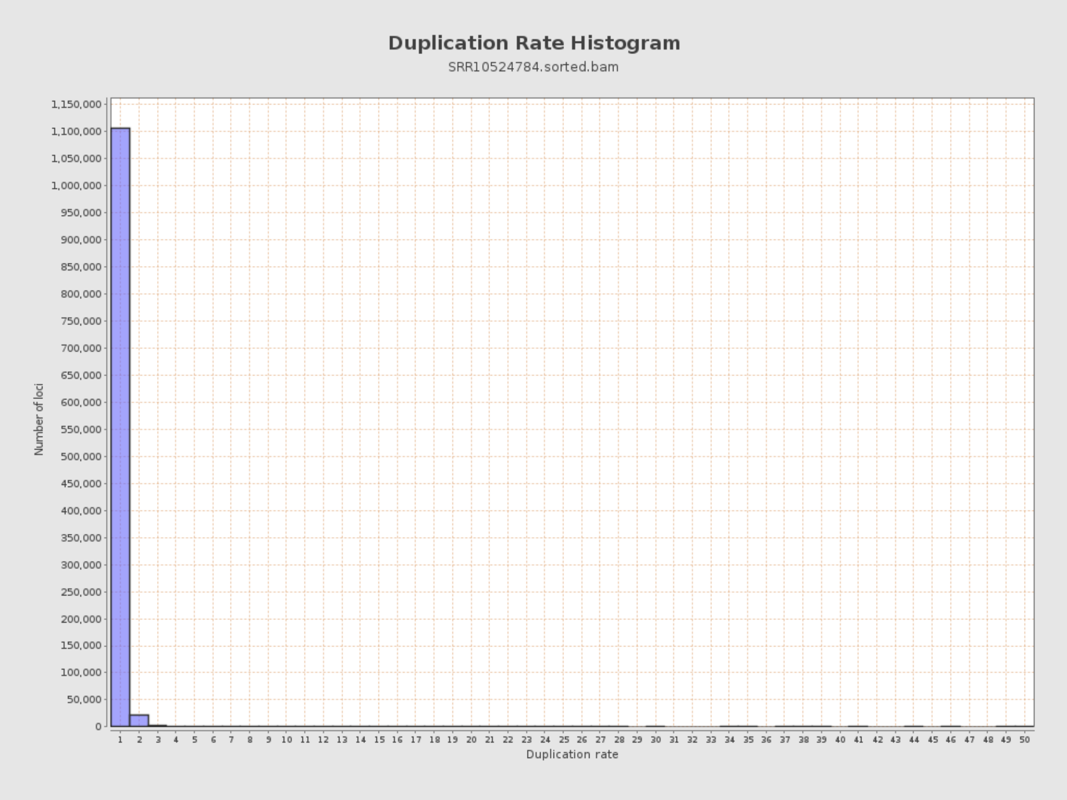
5. Results : Coverage Histogram (0-50X)



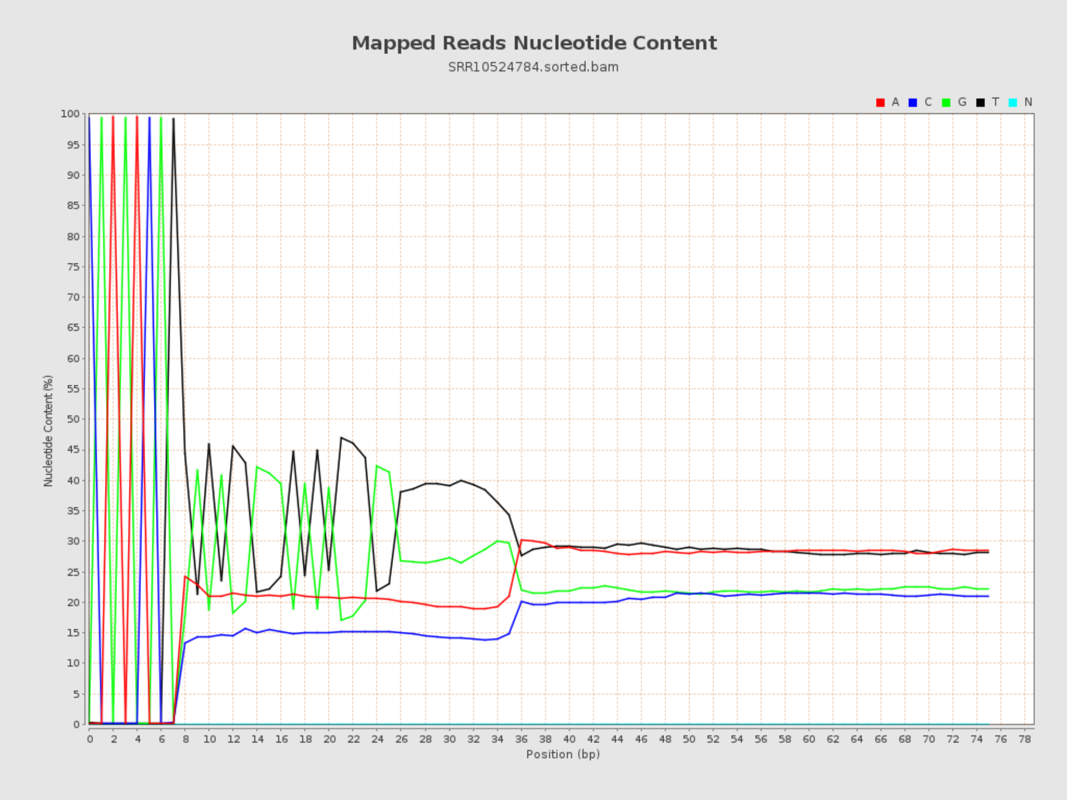
6. Results : Genome Fraction Coverage



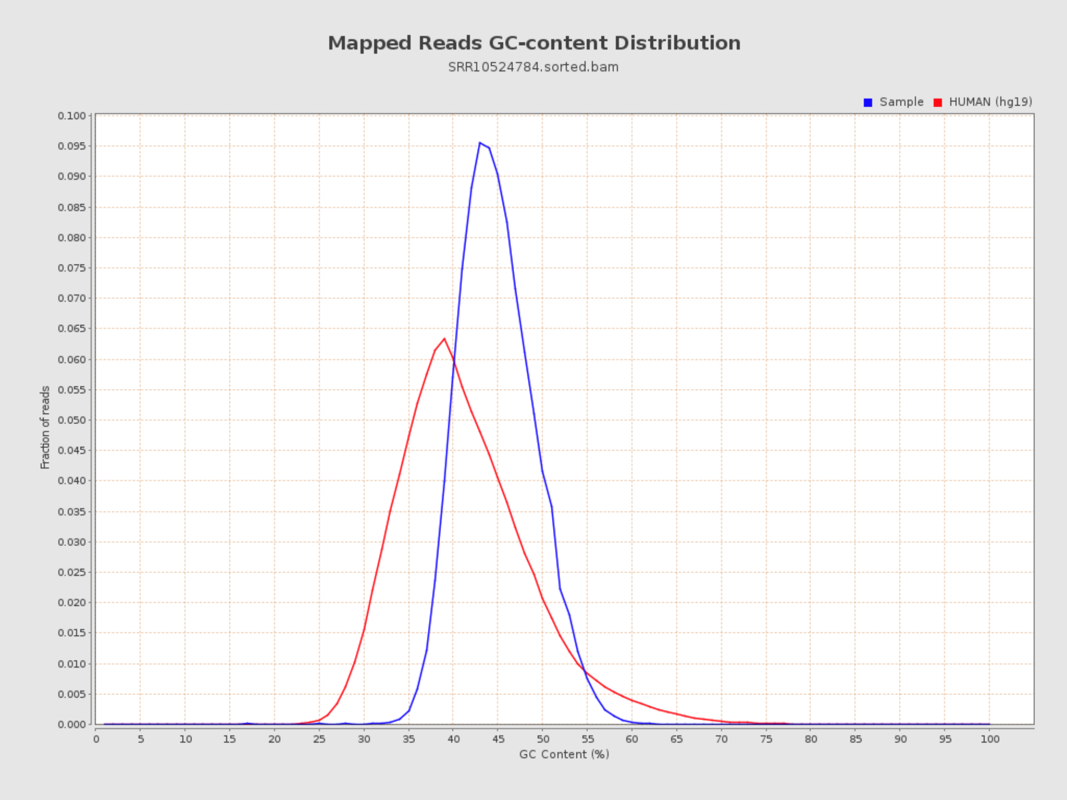
7. Results : Duplication Rate Histogram



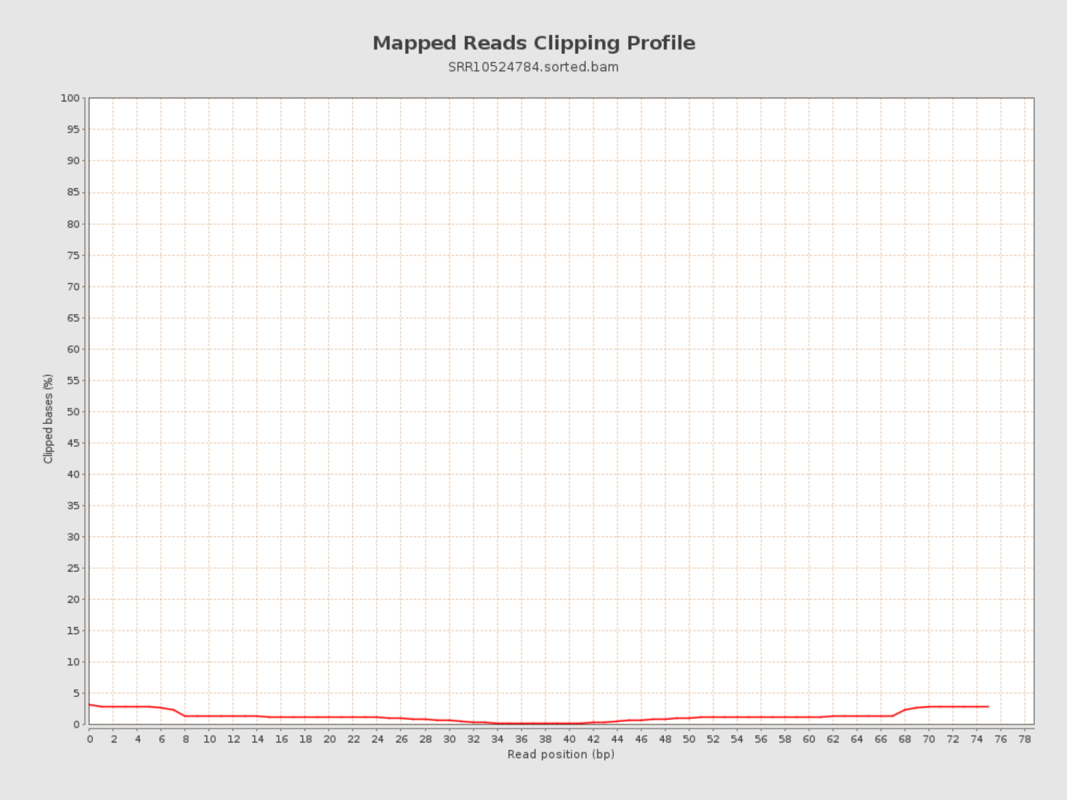
8. Results : Mapped Reads Nucleotide Content



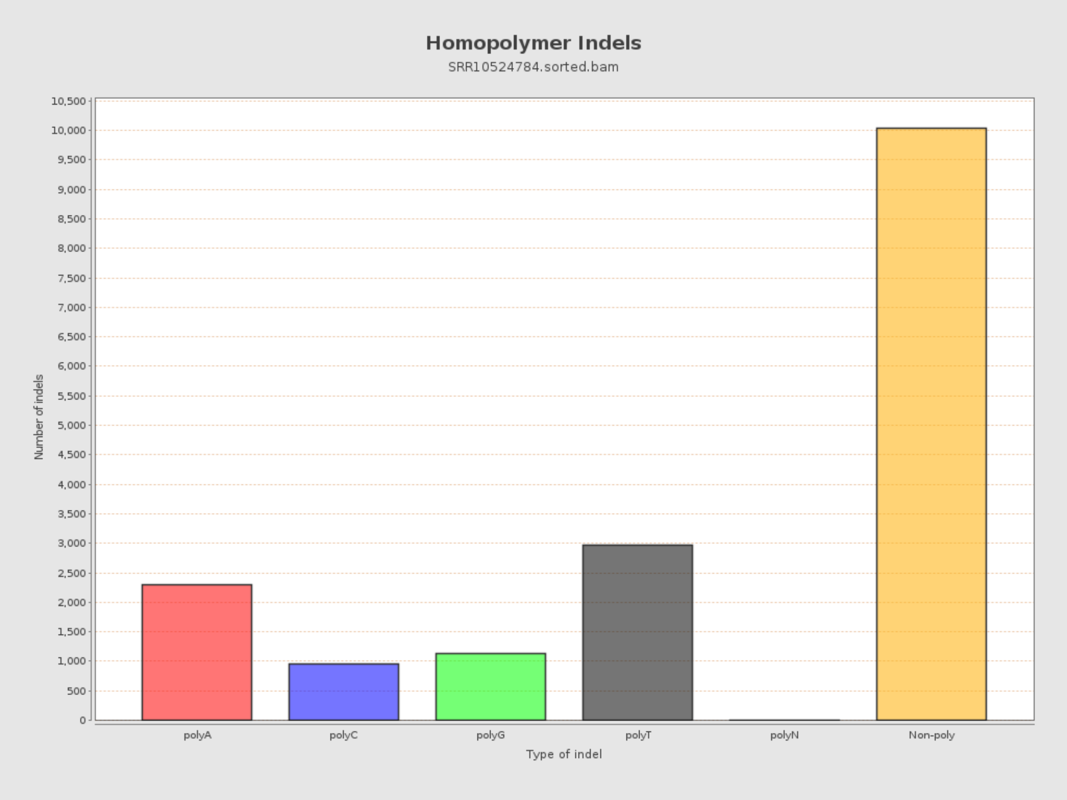
9. Results : Mapped Reads GC-content Distribution



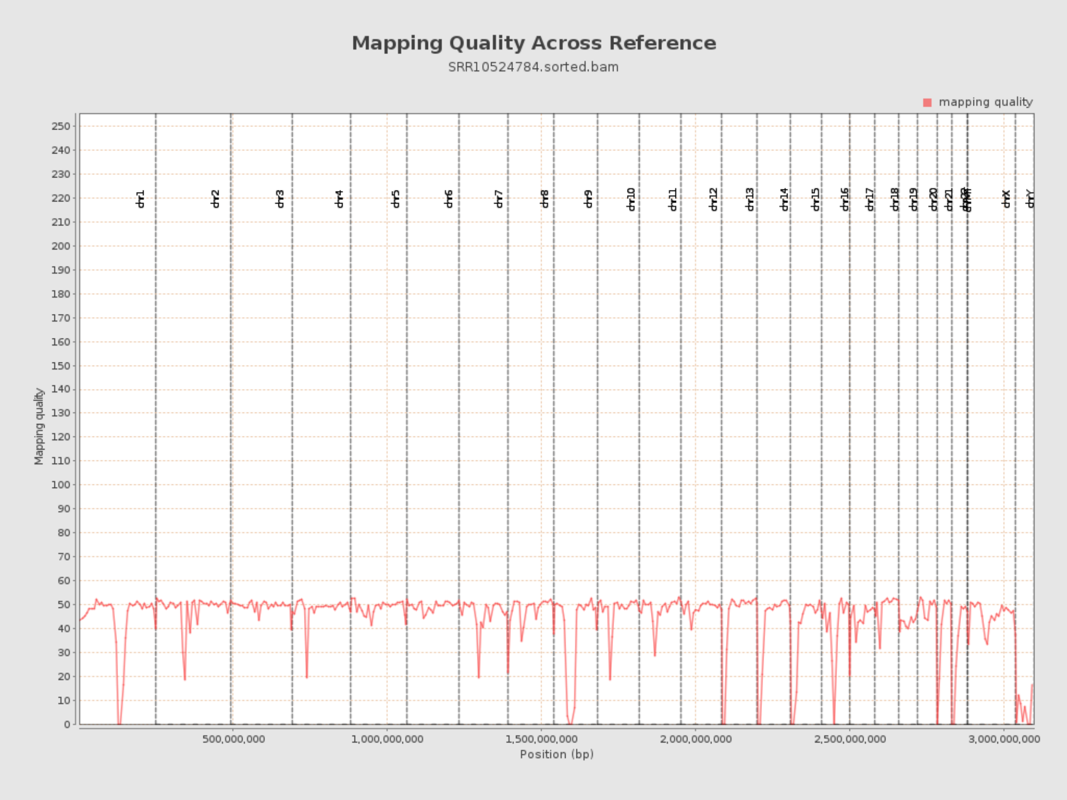
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram