Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 13:42:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084786.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_SRR3084786 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084786.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 13:42:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084786.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,095,256
Mapped reads	983,186 / 89.77%
Unmapped reads	112,070 / 10.23%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,991 / 1.37%
Read min/max/mean length	30 / 76 / 76.48
Duplicated reads (estimated)	32,814 / 3%
Duplication rate	2.06%
Clipped reads	459,441 / 41.95%

2.2. ACGT Content

Number/percentage of A's	18,724,781 / 28.62%
Number/percentage of C's	12,154,787 / 18.58%
Number/percentage of T's	19,872,669 / 30.37%
Number/percentage of G's	14,655,875 / 22.4%
Number/percentage of N's	20,705 / 0.03%
GC Percentage	40.98%

2.3. Coverage

Mean	0.0211

Standard Deviation	0.3081

2.4. Mapping Quality

Mean Mapping Quality	43.83

2.5. Mismatches and indels

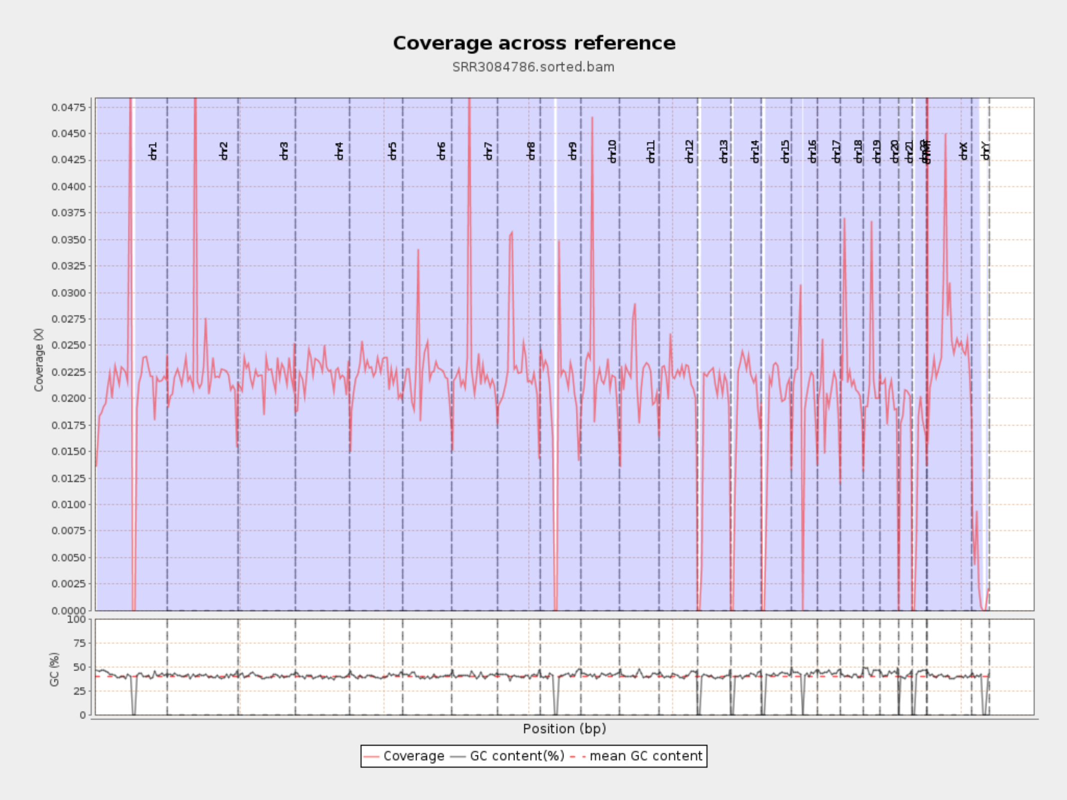
General error rate	0.87%
Mismatches	558,366
Insertions	5,782
Mapped reads with at least one insertion	0.58%
Deletions	14,064
Mapped reads with at least one deletion	1.41%
Homopolymer indels	44.08%

2.6. Chromosome stats

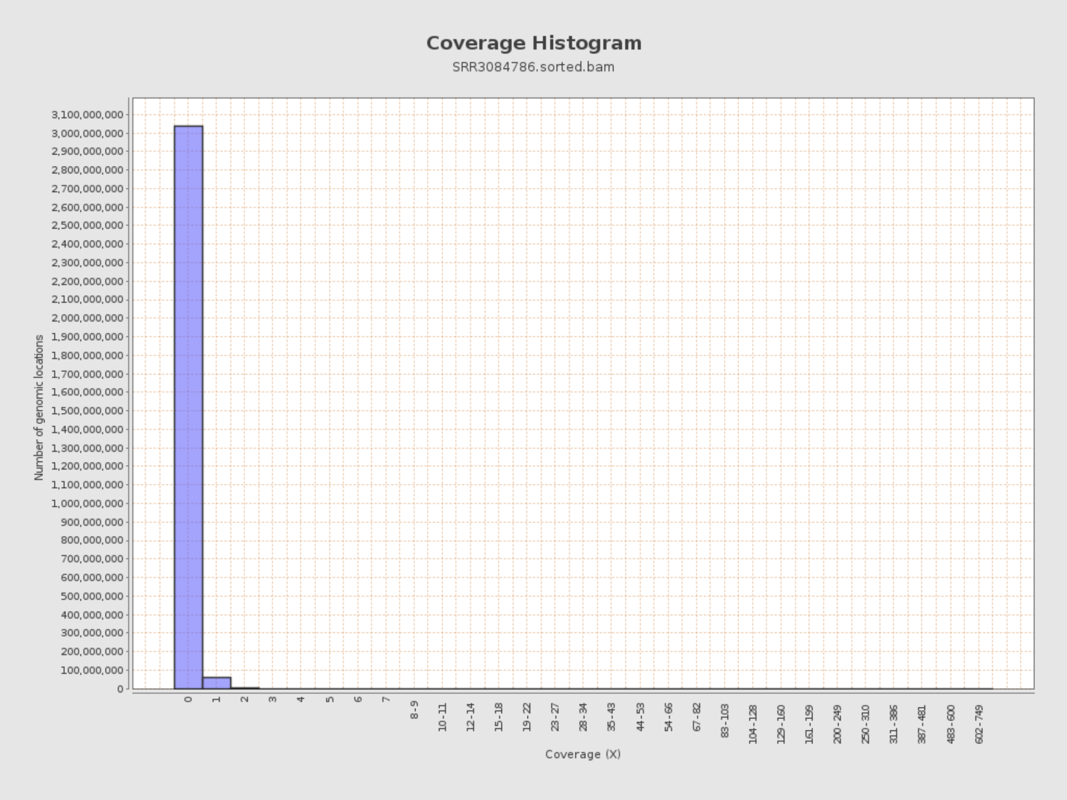
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5212665	0.0209	0.6428
chr2	243199373	5597411	0.023	0.3316
chr3	198022430	4393696	0.0222	0.157
chr4	191154276	4270685	0.0223	0.1595
chr5	180915260	4040402	0.0223	0.1579
chr6	171115067	3844365	0.0225	0.2002
chr7	159138663	3693458	0.0232	0.4199

chr8	146364022	3367252	0.023	0.4053
chr9	141213431	2782475	0.0197	0.2819
chr10	135534747	3106009	0.0229	0.2751
chr11	135006516	2986975	0.0221	0.2489
chr12	133851895	2943533	0.022	0.1613
chr13	115169878	2069847	0.018	0.1382
chr14	107349540	1990606	0.0185	0.1574
chr15	102531392	1800382	0.0176	0.1429
chr16	90354753	1767346	0.0196	0.1768
chr17	81195210	1630815	0.0201	0.1719
chr18	78077248	1777791	0.0228	0.5166
chr19	59128983	1310161	0.0222	0.4944
chr20	63025520	1246946	0.0198	0.1526
chr21	48129895	834720	0.0173	0.1493
chr22	51304566	643841	0.0125	0.1151
chrMT	16571	7956	0.4801	0.7252
chrX	155270560	3949350	0.0254	0.2035
chrY	59373566	183617	0.0031	0.0817

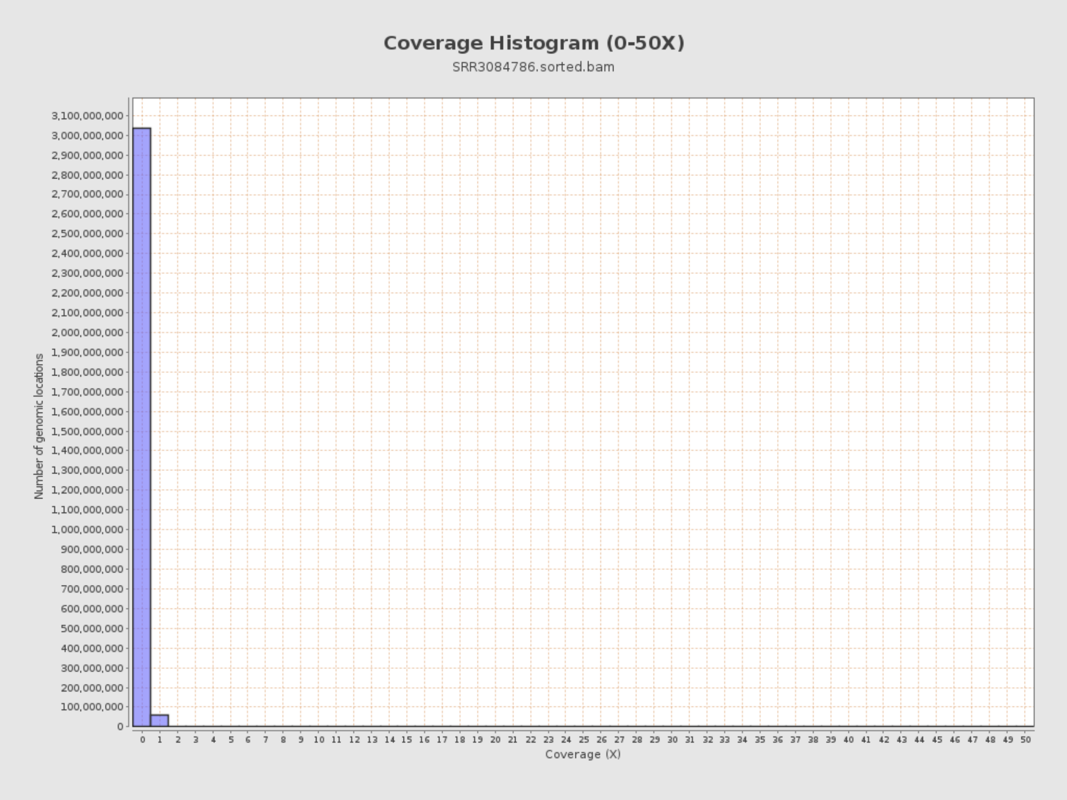
3. Results : Coverage across reference



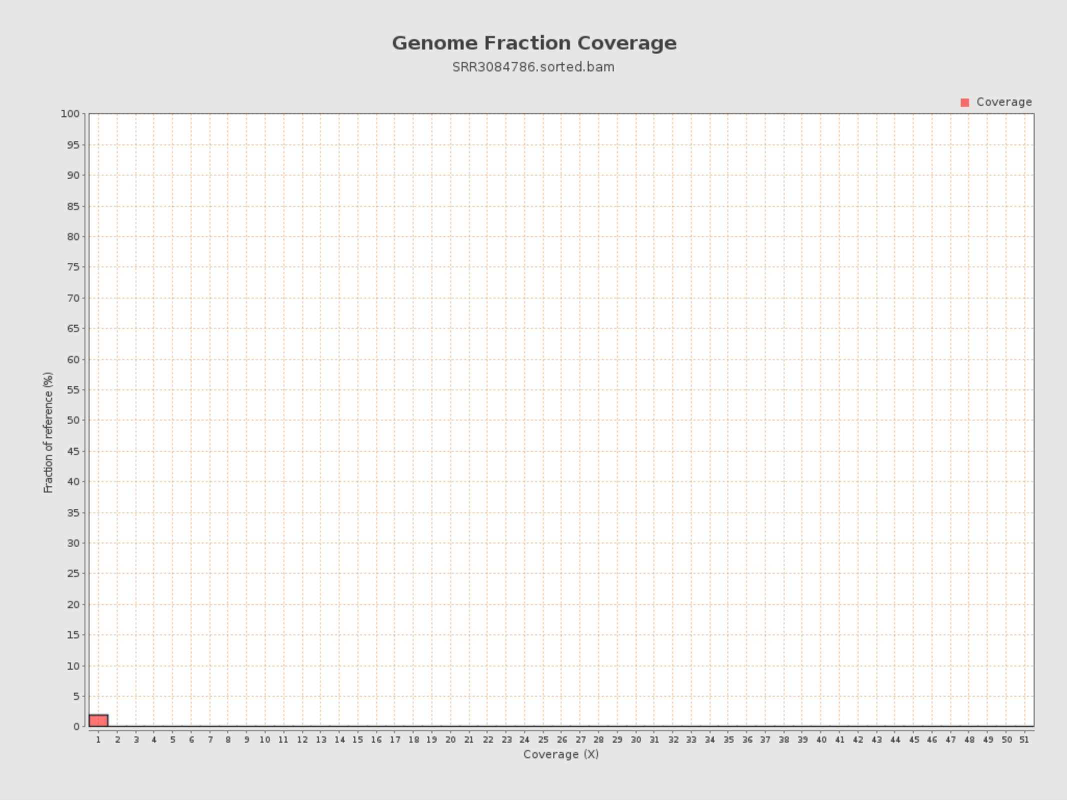
4. Results : Coverage Histogram



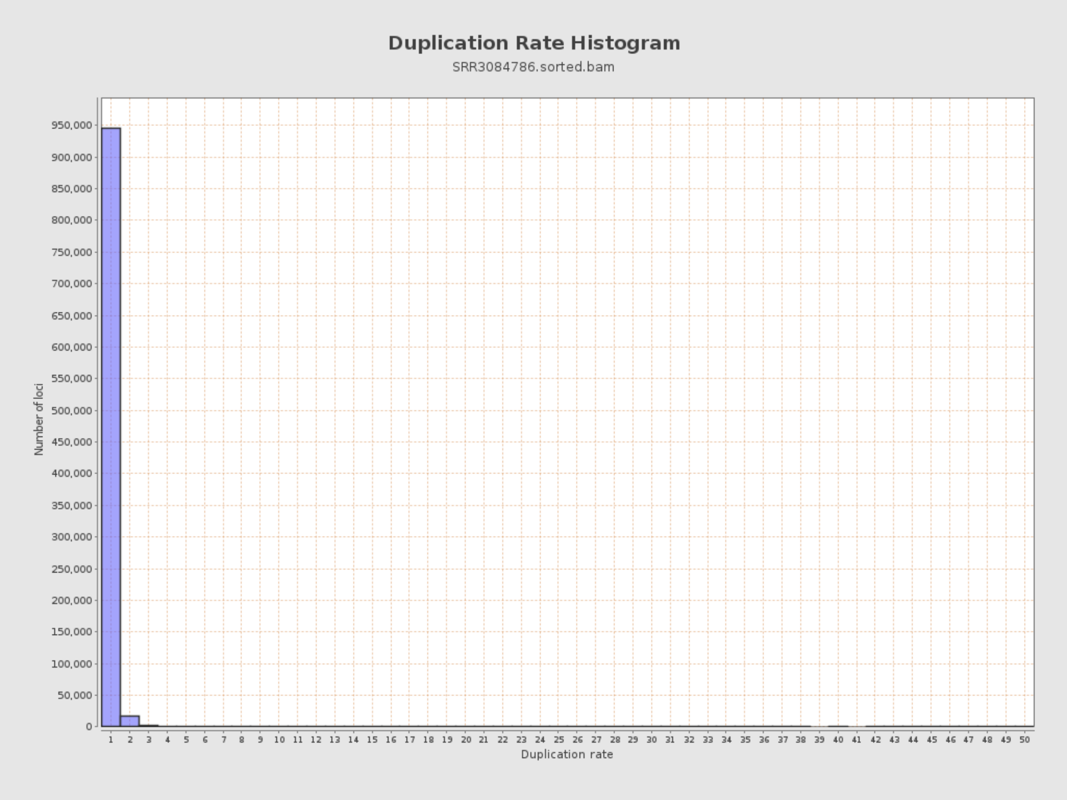
5. Results : Coverage Histogram (0-50X)



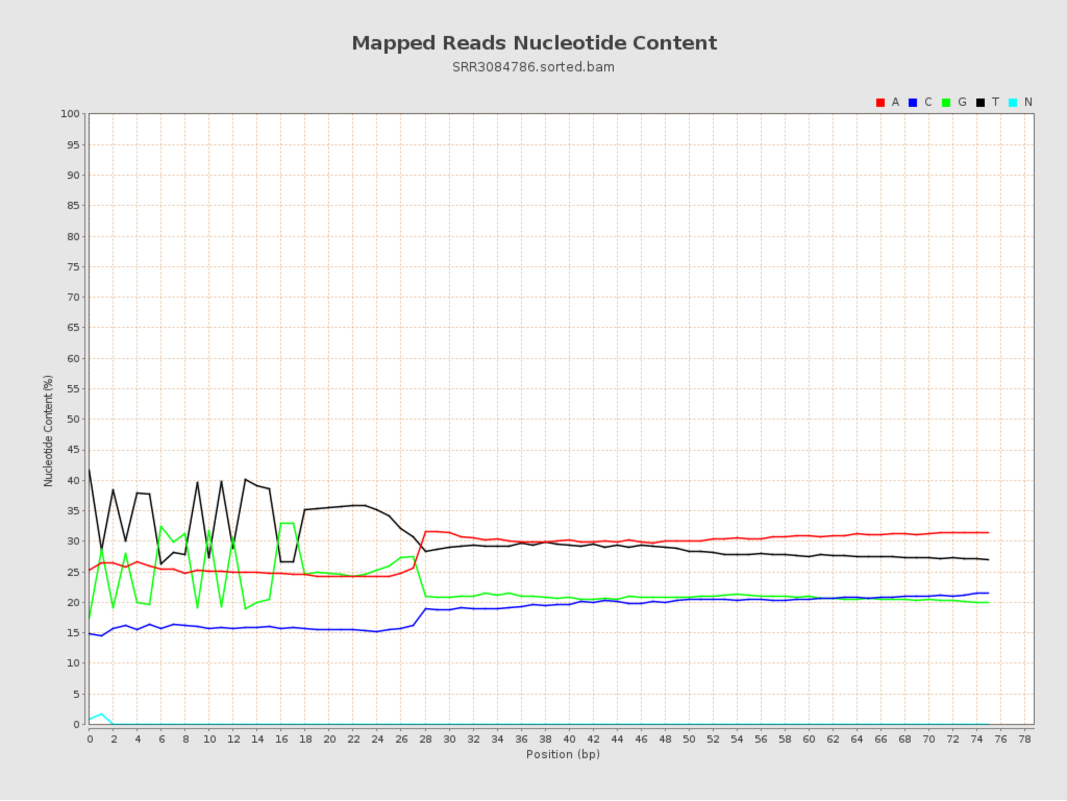
6. Results : Genome Fraction Coverage



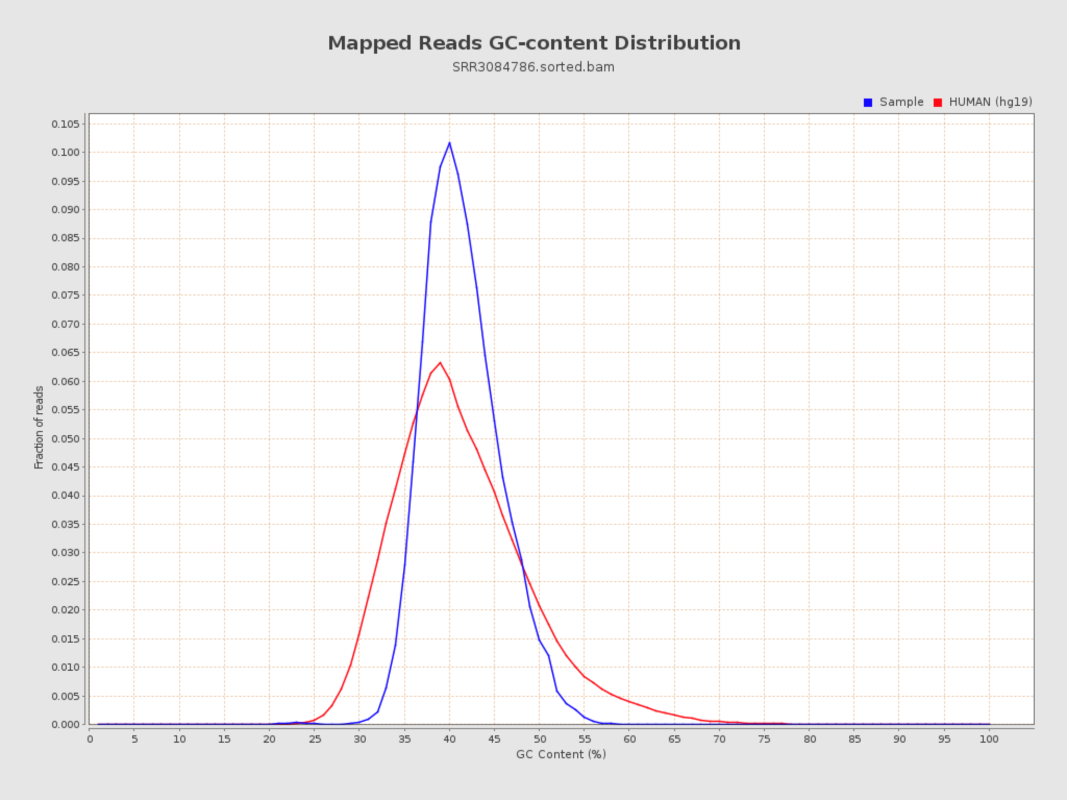
7. Results : Duplication Rate Histogram



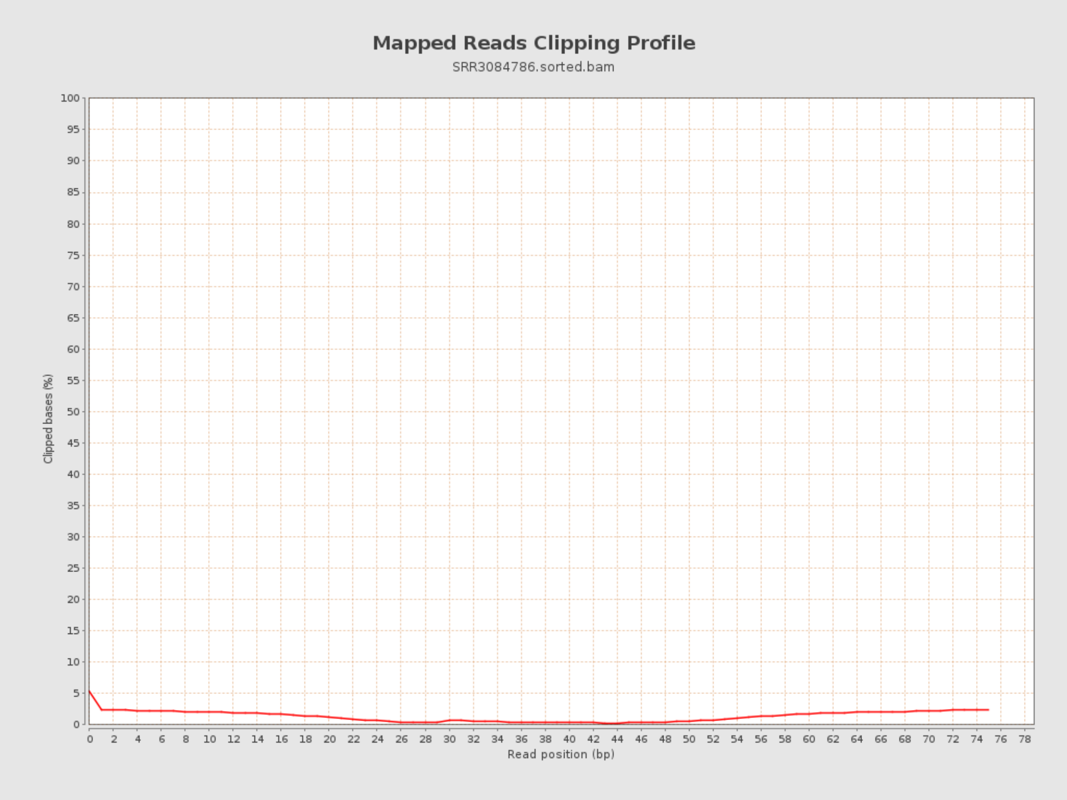
8. Results : Mapped Reads Nucleotide Content



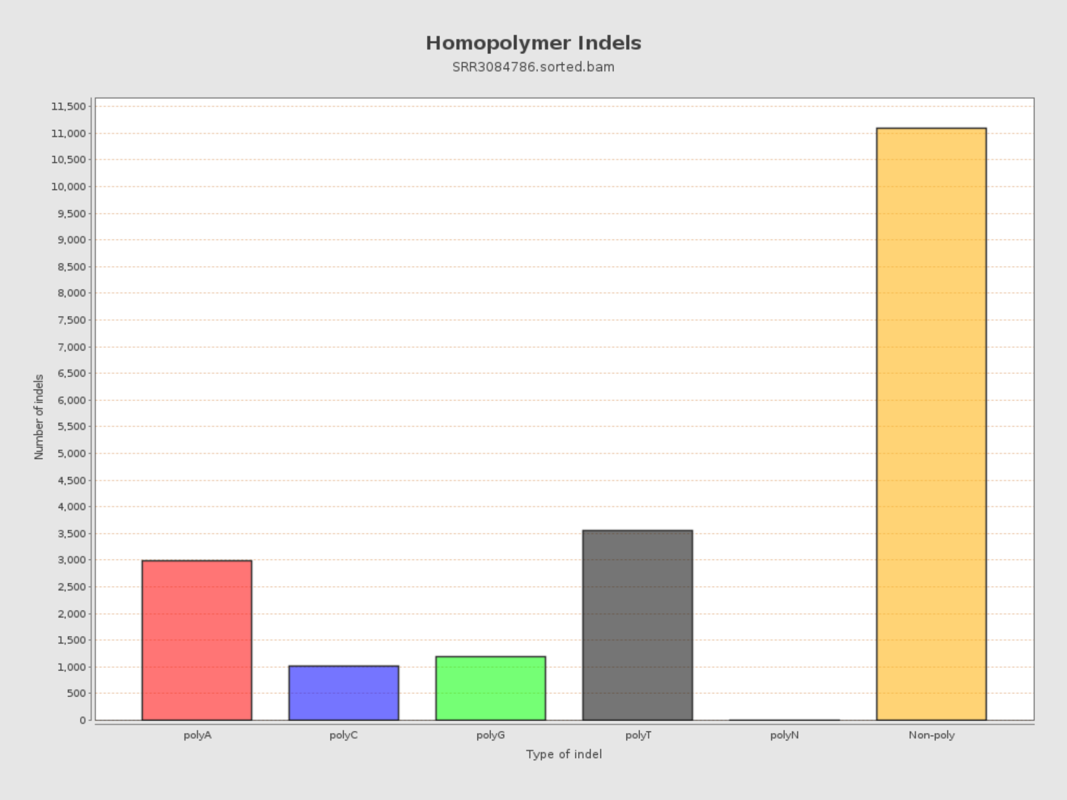
9. Results : Mapped Reads GC-content Distribution



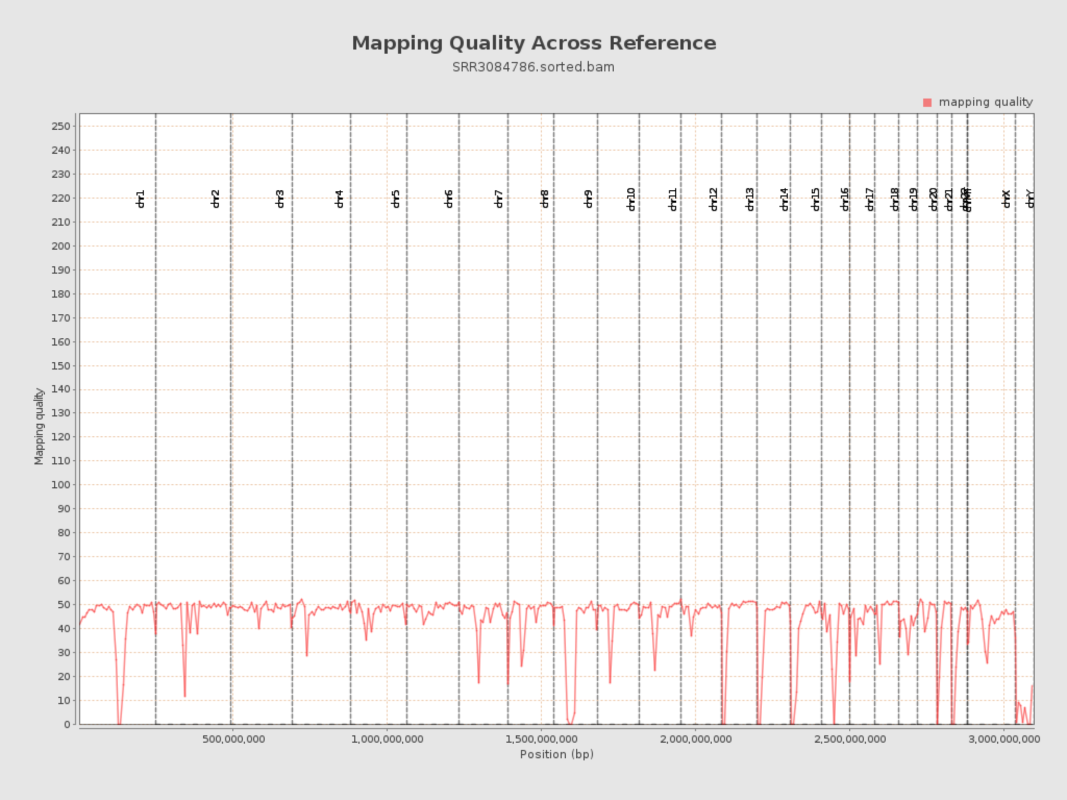
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram