Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 13:28:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084783.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_SRR3084783 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084783.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 13:28:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084783.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,085,550
Mapped reads	1,888,846 / 90.57%
Unmapped reads	196,704 / 9.43%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,516 / 0.94%
Read min/max/mean length	30 / 76 / 76.33
Duplicated reads (estimated)	103,802 / 4.98%
Duplication rate	4.47%
Clipped reads	793,697 / 38.06%

2.2. ACGT Content

Number/percentage of A's	35,859,265 / 28.12%
Number/percentage of C's	23,691,315 / 18.58%
Number/percentage of T's	40,240,763 / 31.55%
Number/percentage of G's	27,694,552 / 21.72%
Number/percentage of N's	42,856 / 0.03%
GC Percentage	40.29%

2.3. Coverage

Mean	0.0412

Standard Deviation	0.3534

2.4. Mapping Quality

Mean Mapping Quality	47.21

2.5. Mismatches and indels

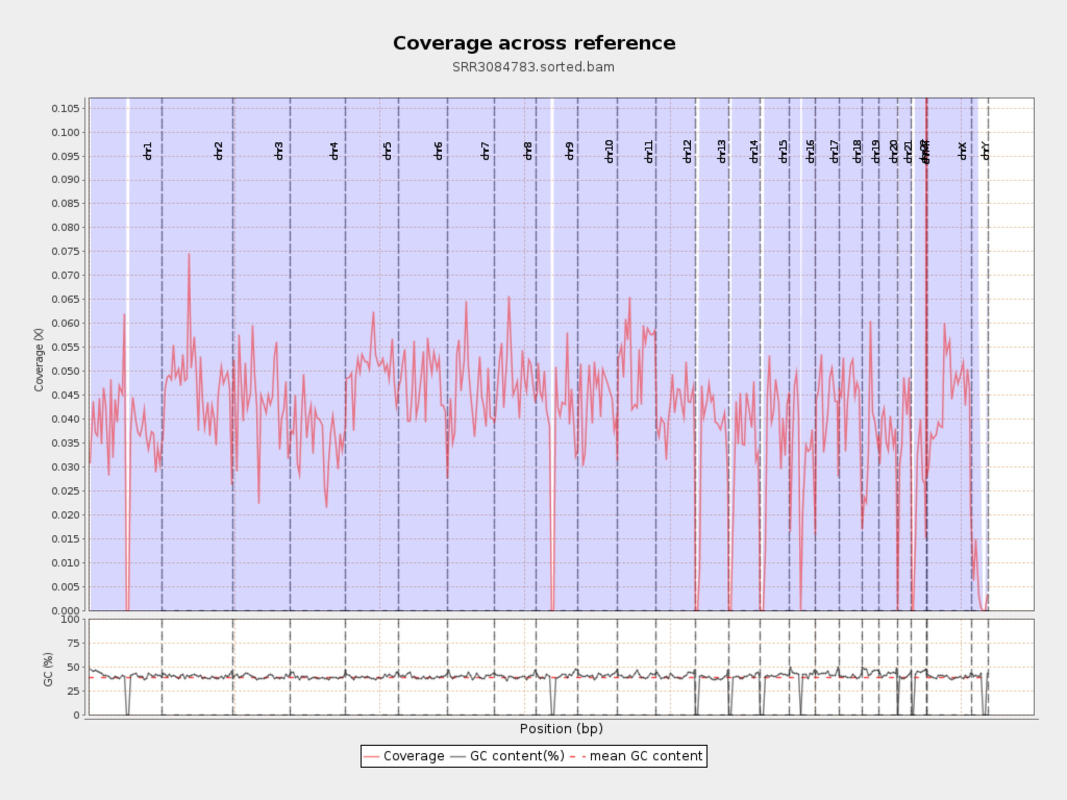
General error rate	0.86%
Mismatches	1,084,723
Insertions	10,032
Mapped reads with at least one insertion	0.53%
Deletions	29,527
Mapped reads with at least one deletion	1.55%
Homopolymer indels	47.48%

2.6. Chromosome stats

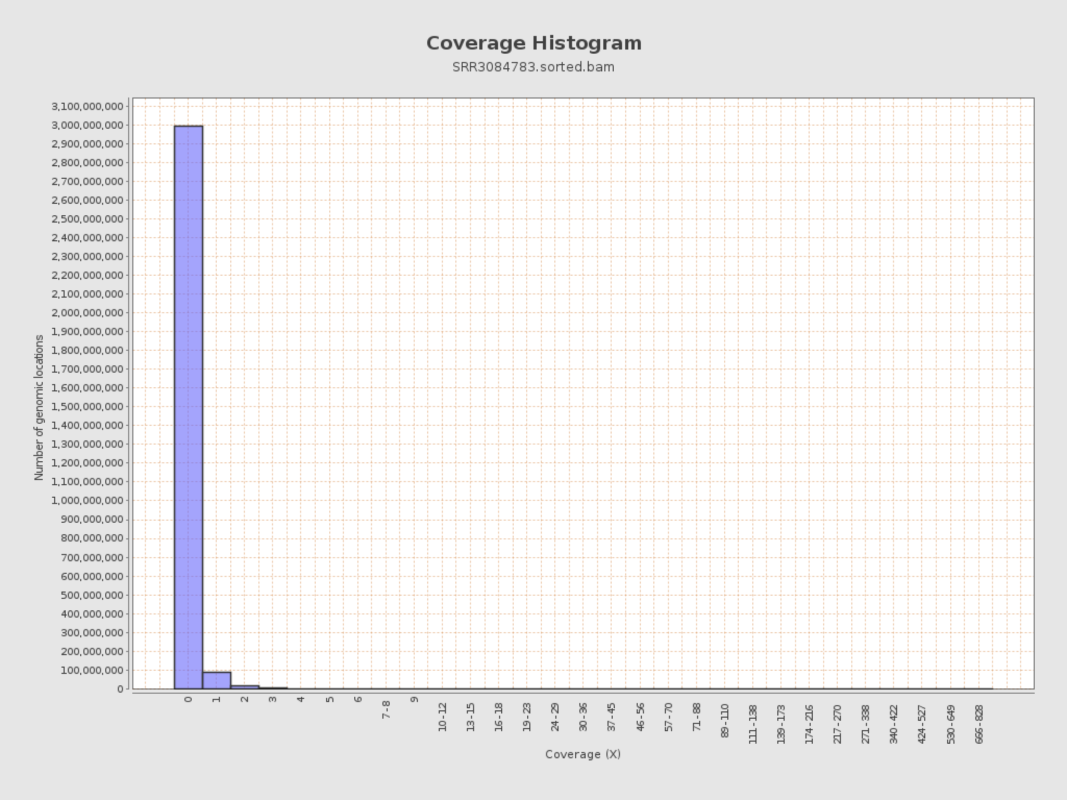
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9165410	0.0368	0.5531
chr2	243199373	11455043	0.0471	0.4297
chr3	198022430	8752989	0.0442	0.25
chr4	191154276	6950039	0.0364	0.2417
chr5	180915260	9168659	0.0507	0.2697
chr6	171115067	8122090	0.0475	0.3091
chr7	159138663	7246576	0.0455	0.3748

chr8	146364022	7200357	0.0492	0.5749
chr9	141213431	5557249	0.0394	0.3349
chr10	135534747	5998790	0.0443	0.3187
chr11	135006516	7185773	0.0532	0.3686
chr12	133851895	5663018	0.0423	0.25
chr13	115169878	3971618	0.0345	0.2229
chr14	107349540	3492404	0.0325	0.2298
chr15	102531392	3450543	0.0337	0.2212
chr16	90354753	2842816	0.0315	0.2296
chr17	81195210	3517002	0.0433	0.3043
chr18	78077248	3513583	0.045	0.5754
chr19	59128983	2102043	0.0356	0.4215
chr20	63025520	2294071	0.0364	0.2362
chr21	48129895	1710605	0.0355	0.2358
chr22	51304566	1113580	0.0217	0.1729
chrMT	16571	4630	0.2794	0.6237
chrX	155270560	6822199	0.0439	0.2747
chrY	59373566	275336	0.0046	0.1127

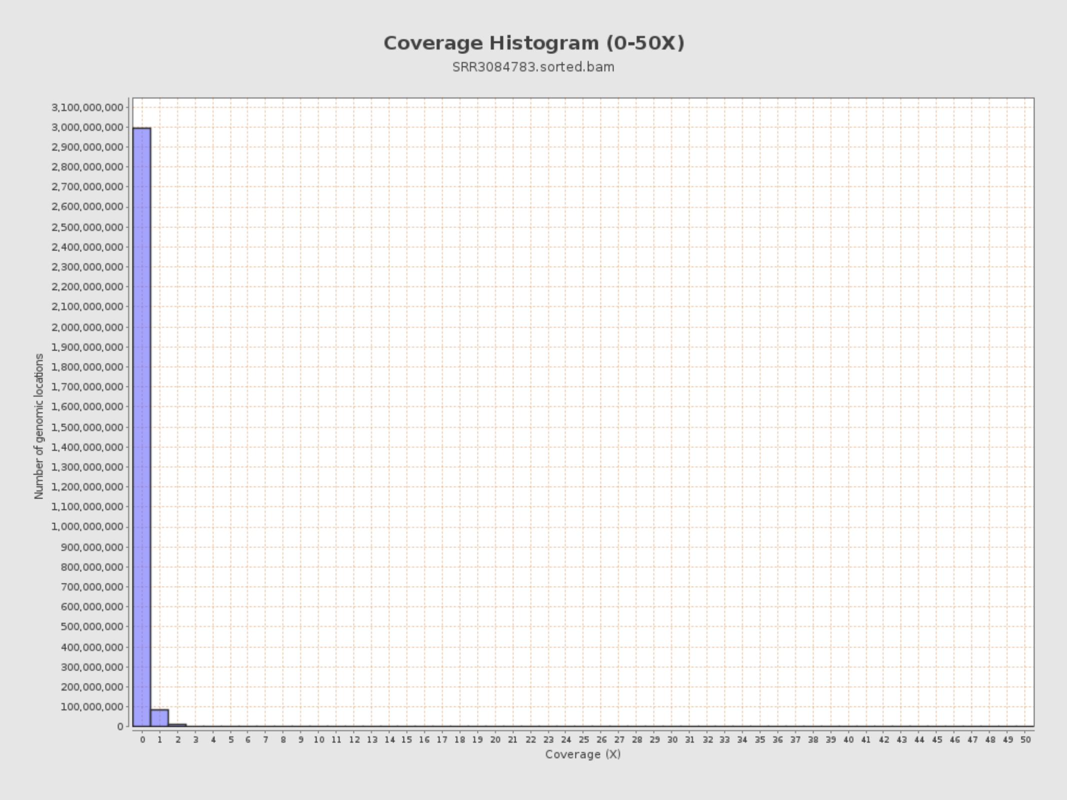
3. Results : Coverage across reference



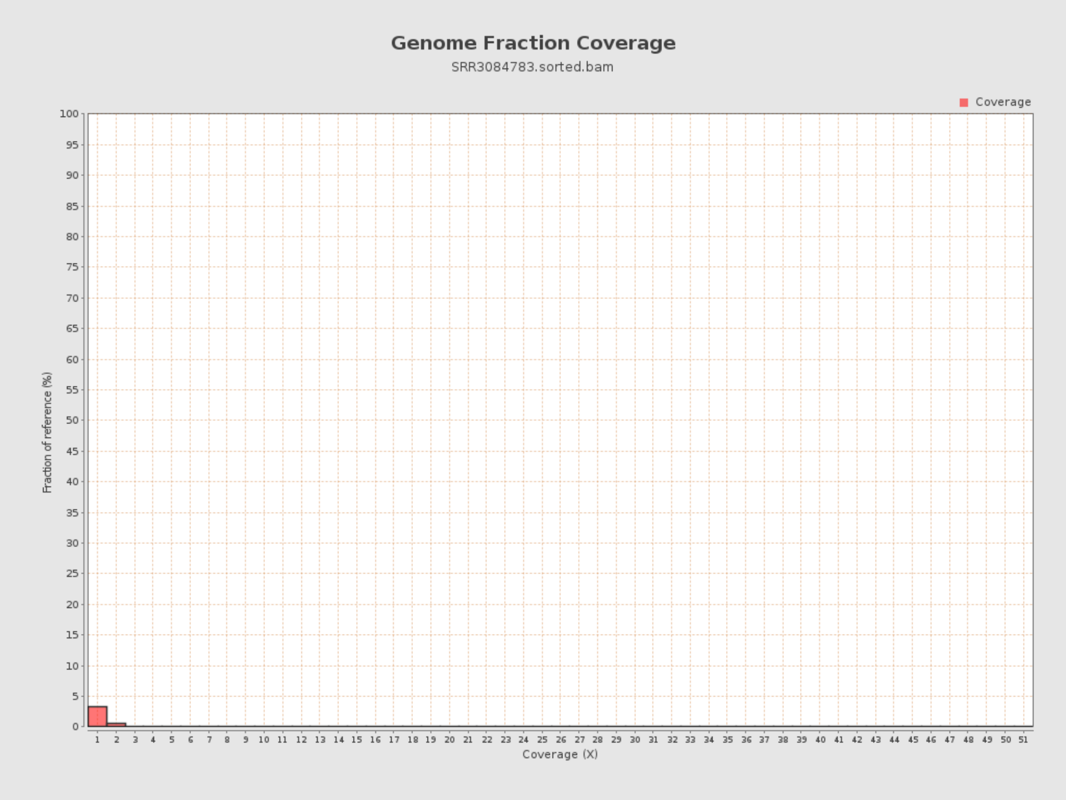
4. Results : Coverage Histogram



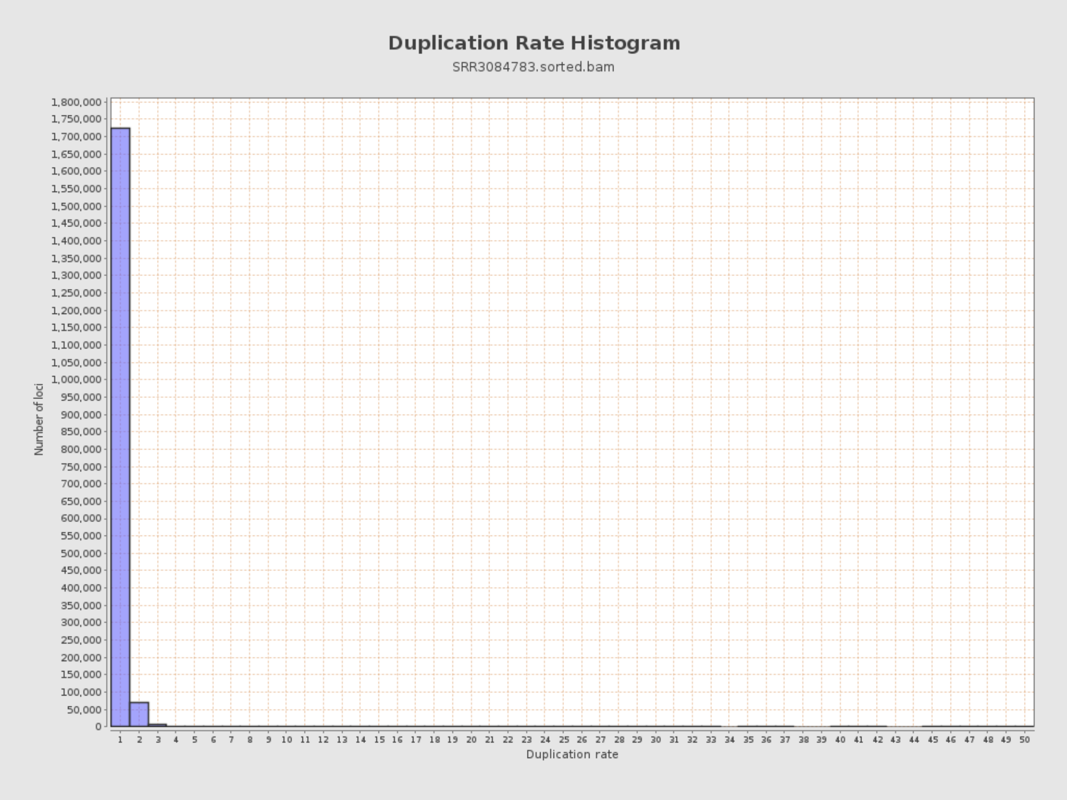
5. Results : Coverage Histogram (0-50X)



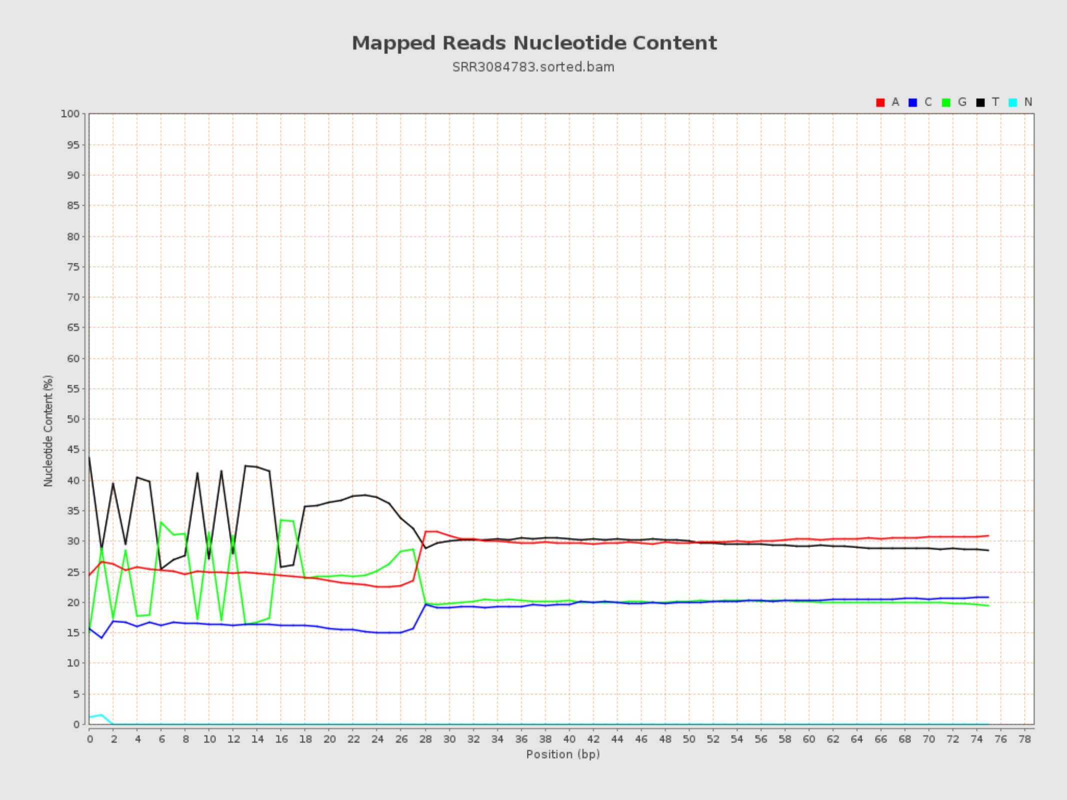
6. Results : Genome Fraction Coverage



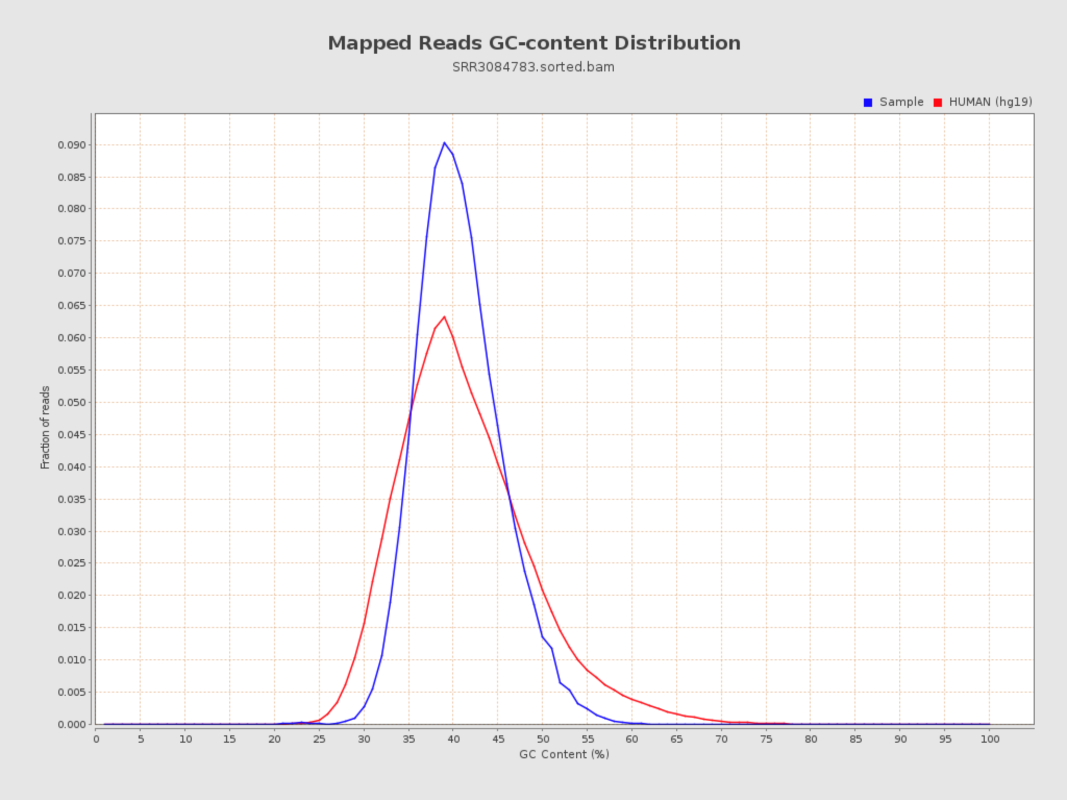
7. Results : Duplication Rate Histogram



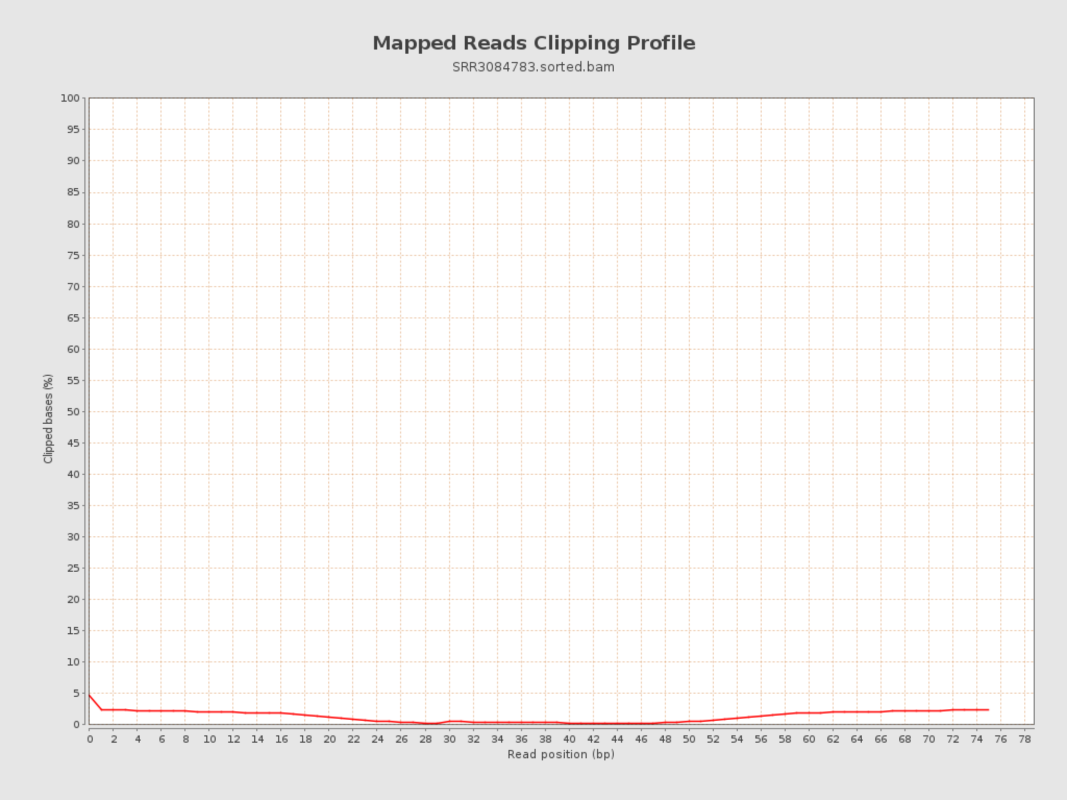
8. Results : Mapped Reads Nucleotide Content



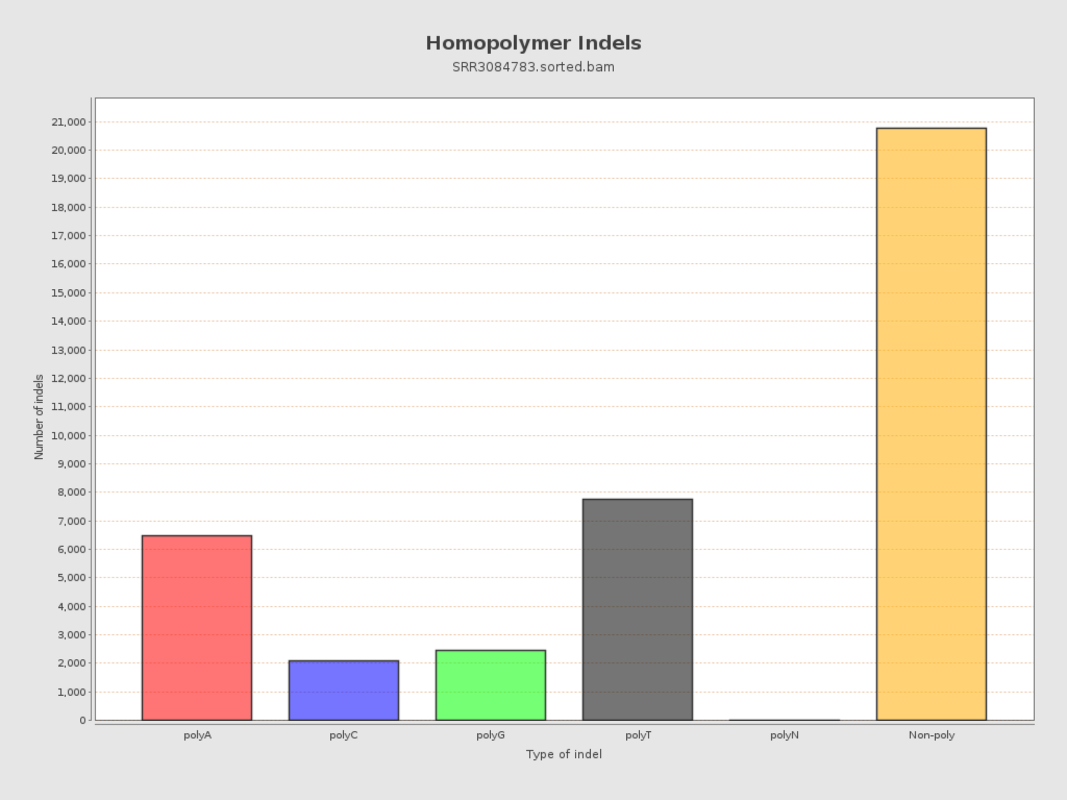
9. Results : Mapped Reads GC-content Distribution



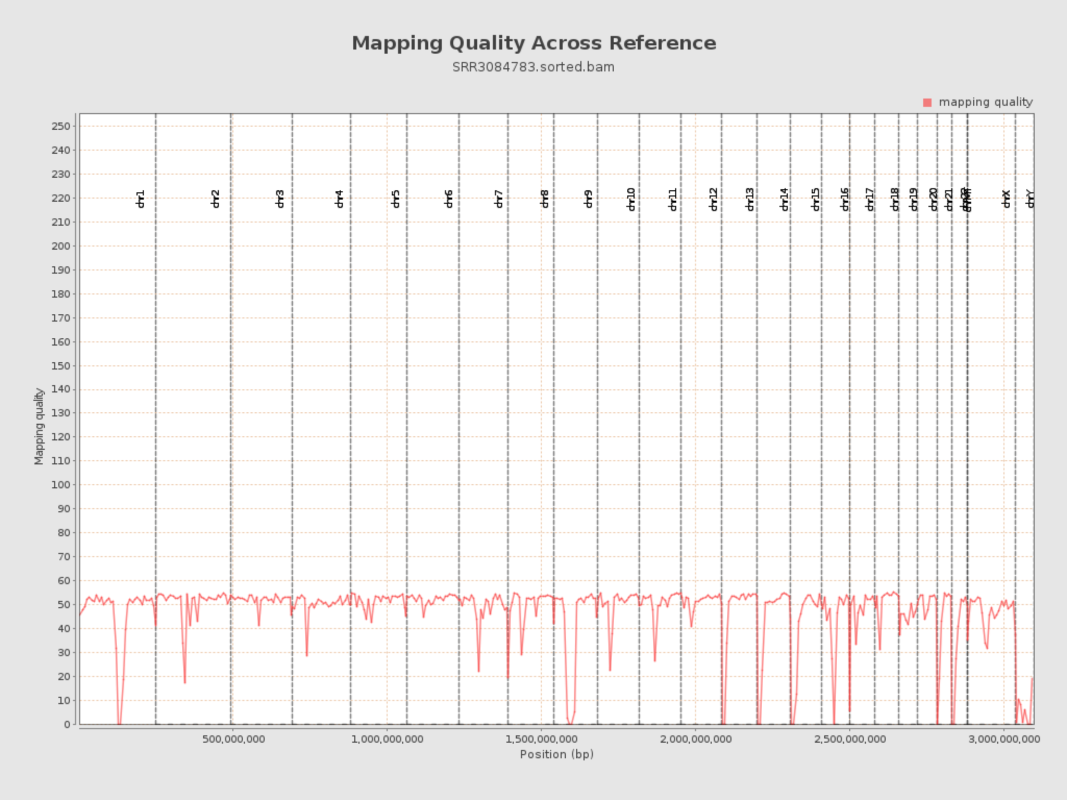
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram