Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 13:02:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084777.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_SRR3084777 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084777.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 13:02:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084777.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,237,030
Mapped reads	1,134,575 / 91.72%
Unmapped reads	102,455 / 8.28%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,762 / 0.71%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	32,048 / 2.59%
Duplication rate	2.14%
Clipped reads	377,091 / 30.48%

2.2. ACGT Content

Number/percentage of A's	22,692,398 / 28.82%
Number/percentage of C's	14,687,392 / 18.66%
Number/percentage of T's	24,922,671 / 31.66%
Number/percentage of G's	16,400,409 / 20.83%
Number/percentage of N's	23,908 / 0.03%
GC Percentage	39.49%

2.3. Coverage

Mean	0.0254

Standard Deviation	0.2476

2.4. Mapping Quality

Mean Mapping Quality	47.92

2.5. Mismatches and indels

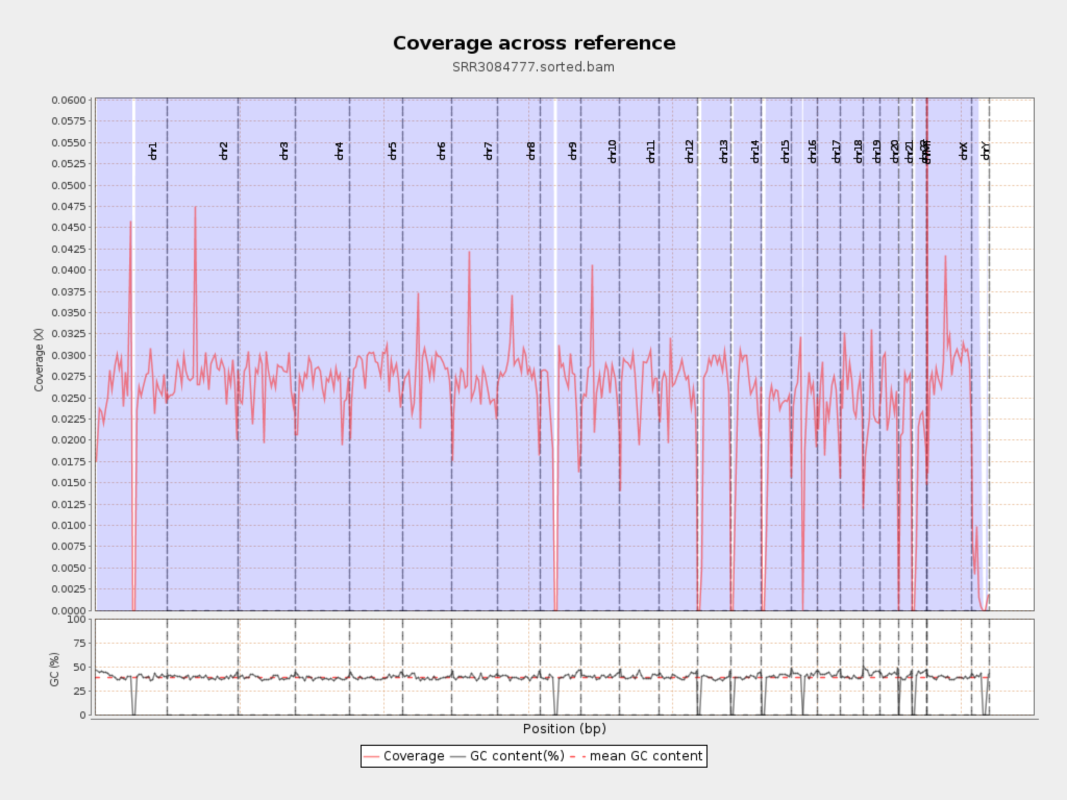
General error rate	0.88%
Mismatches	681,262
Insertions	6,280
Mapped reads with at least one insertion	0.55%
Deletions	21,027
Mapped reads with at least one deletion	1.83%
Homopolymer indels	47.23%

2.6. Chromosome stats

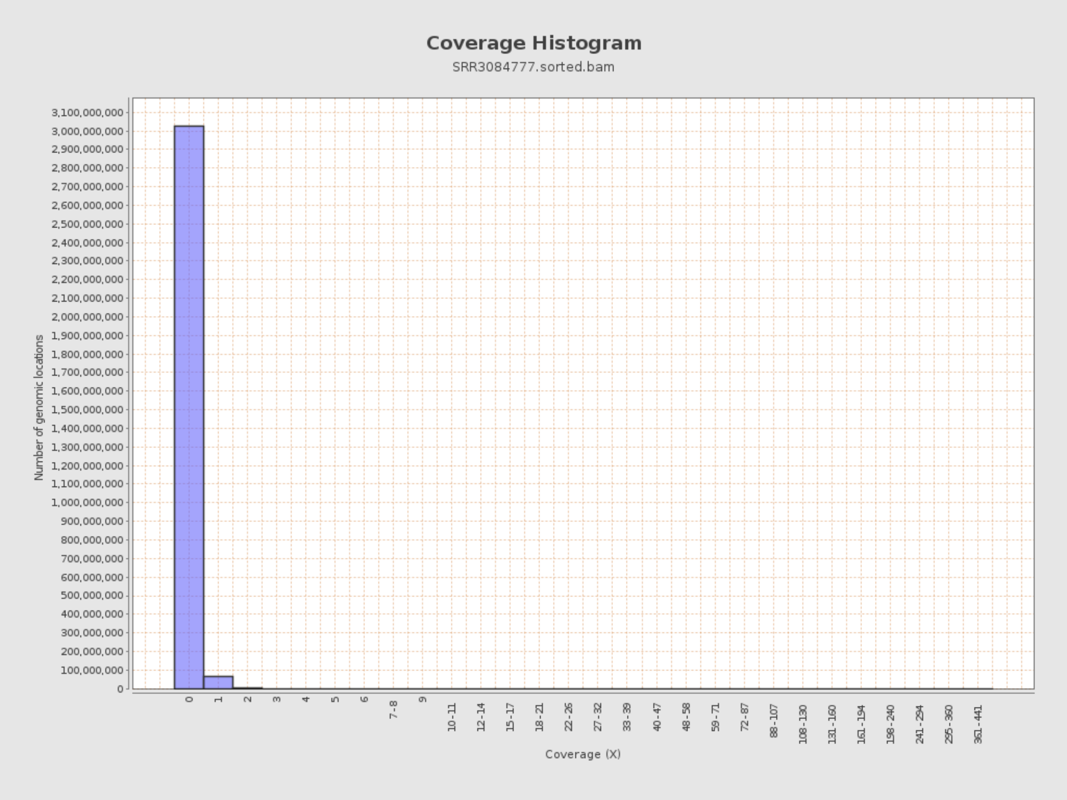
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6224766	0.025	0.4155
chr2	243199373	6834568	0.0281	0.2718
chr3	198022430	5389312	0.0272	0.1751
chr4	191154276	5050267	0.0264	0.178
chr5	180915260	5163947	0.0285	0.1798
chr6	171115067	4821749	0.0282	0.2075
chr7	159138663	4225709	0.0266	0.2954

chr8	146364022	4173889	0.0285	0.3299
chr9	141213431	3320022	0.0235	0.2276
chr10	135534747	3663669	0.027	0.2424
chr11	135006516	3678880	0.0272	0.2242
chr12	133851895	3532152	0.0264	0.1746
chr13	115169878	2750852	0.0239	0.164
chr14	107349540	2411621	0.0225	0.17
chr15	102531392	2065838	0.0201	0.1533
chr16	90354753	2036498	0.0225	0.1786
chr17	81195210	1942050	0.0239	0.1905
chr18	78077248	2050943	0.0263	0.4675
chr19	59128983	1334846	0.0226	0.2974
chr20	63025520	1569983	0.0249	0.1738
chr21	48129895	1055199	0.0219	0.1633
chr22	51304566	763514	0.0149	0.1285
chrMT	16571	1611	0.0972	0.3287
chrX	155270560	4518560	0.0291	0.2005
chrY	59373566	180649	0.003	0.0832

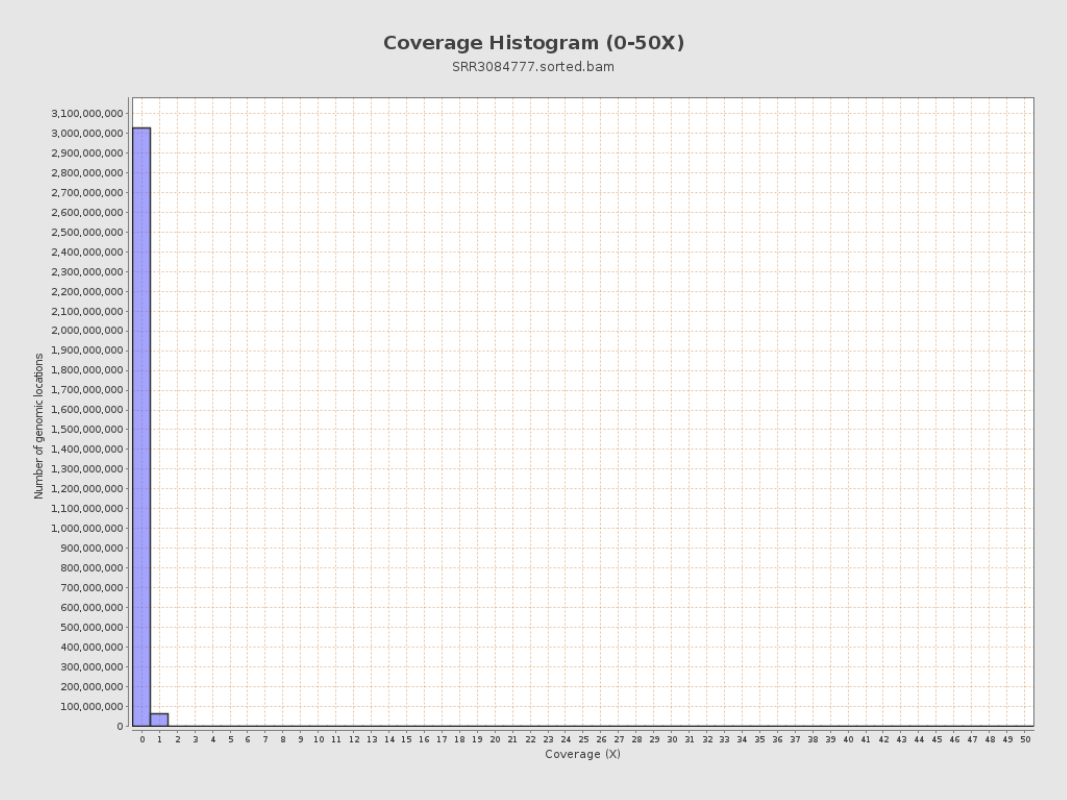
3. Results : Coverage across reference



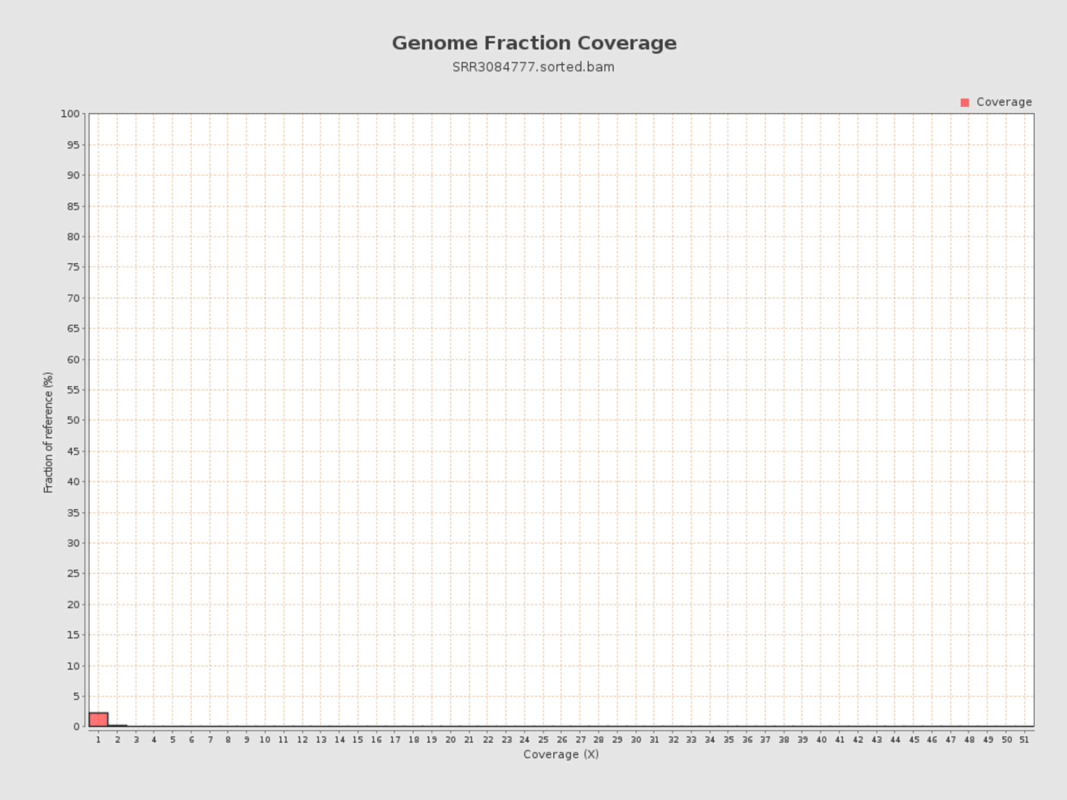
4. Results : Coverage Histogram



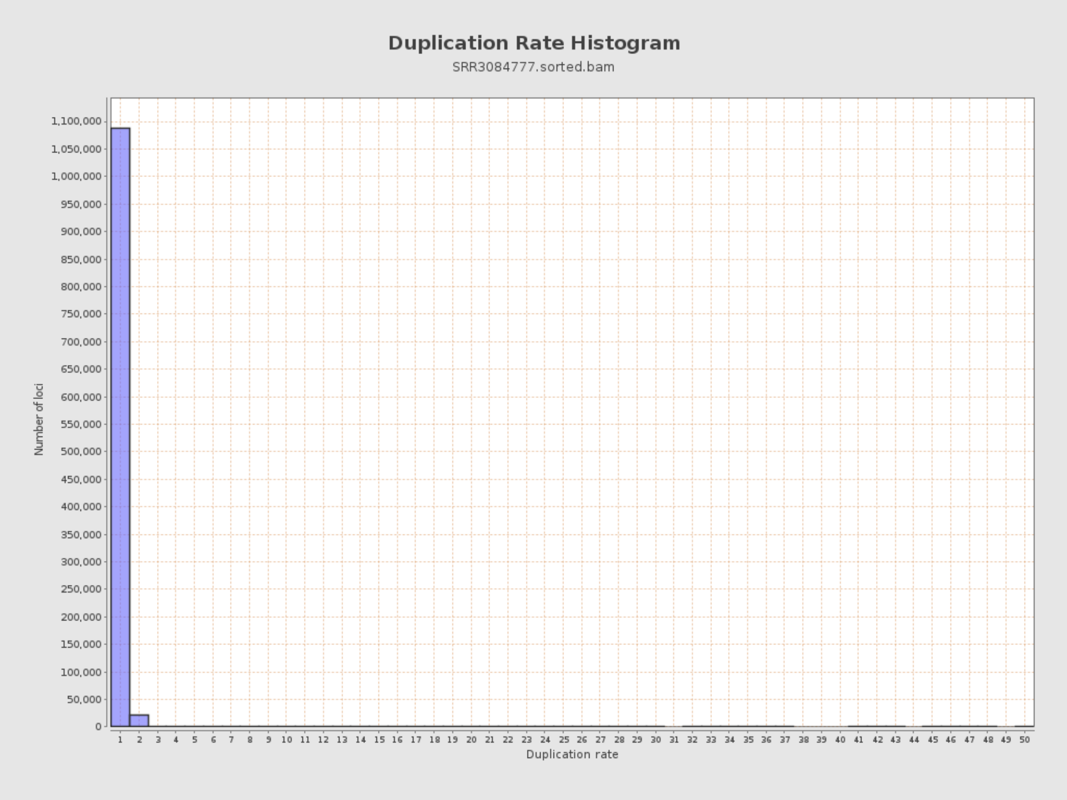
5. Results : Coverage Histogram (0-50X)



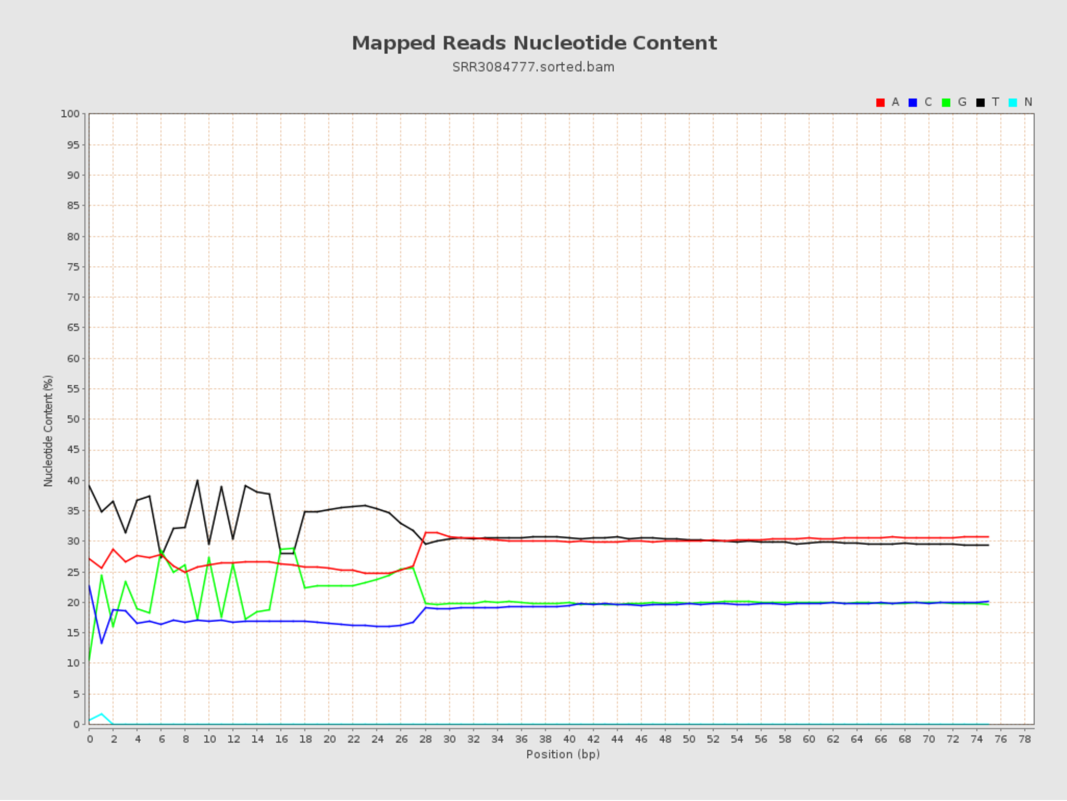
6. Results : Genome Fraction Coverage



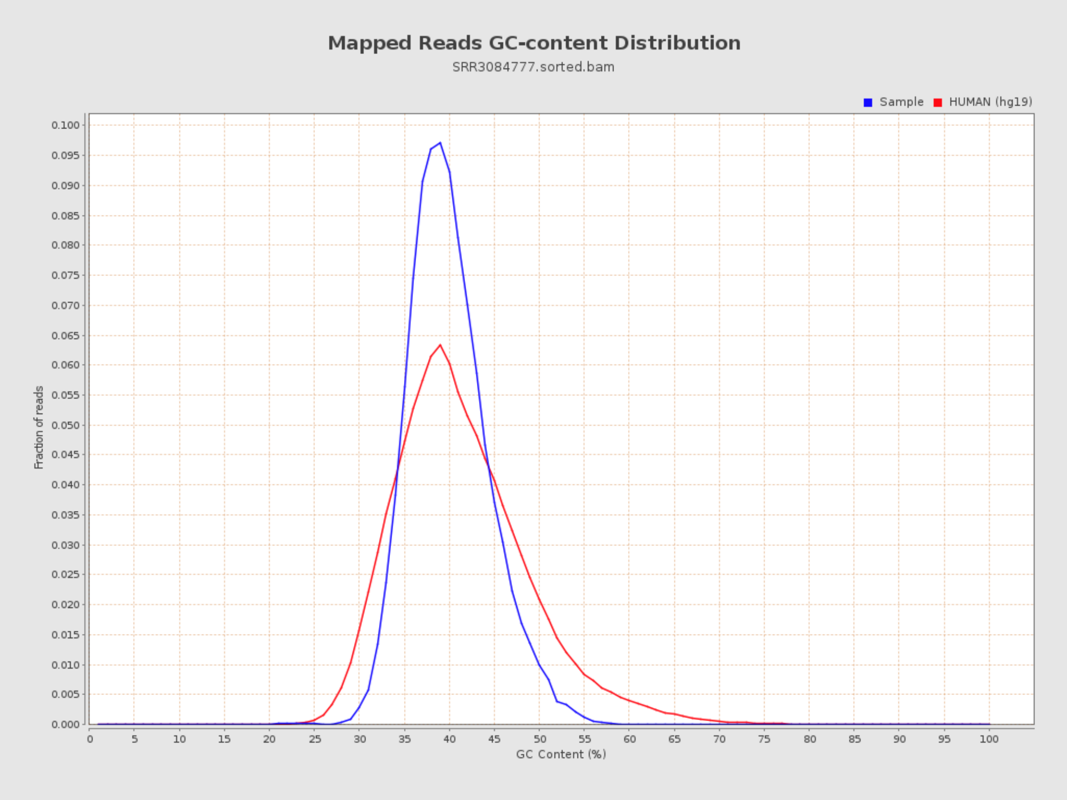
7. Results : Duplication Rate Histogram



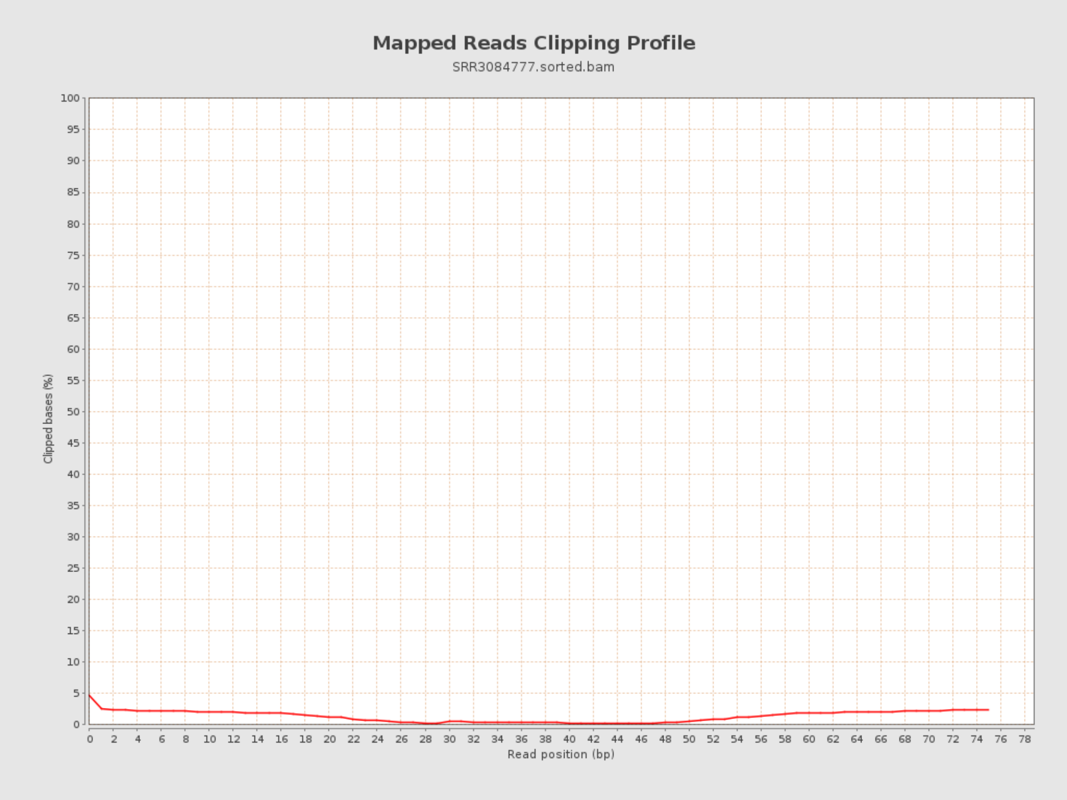
8. Results : Mapped Reads Nucleotide Content



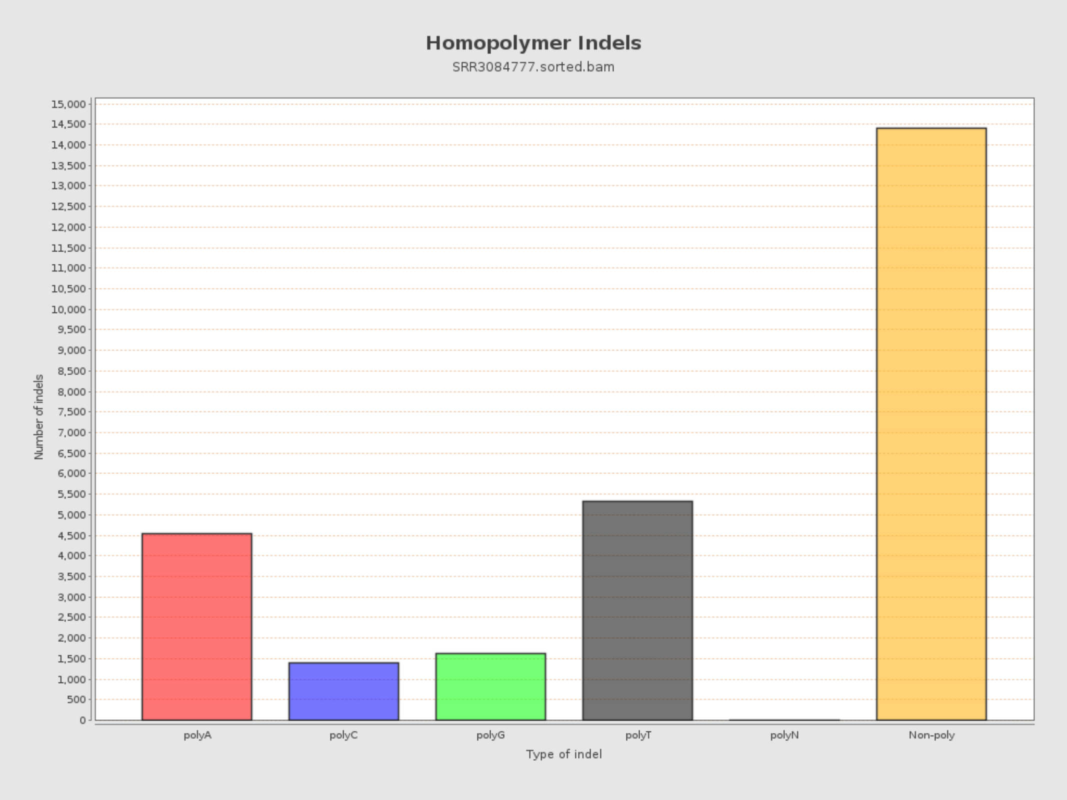
9. Results : Mapped Reads GC-content Distribution



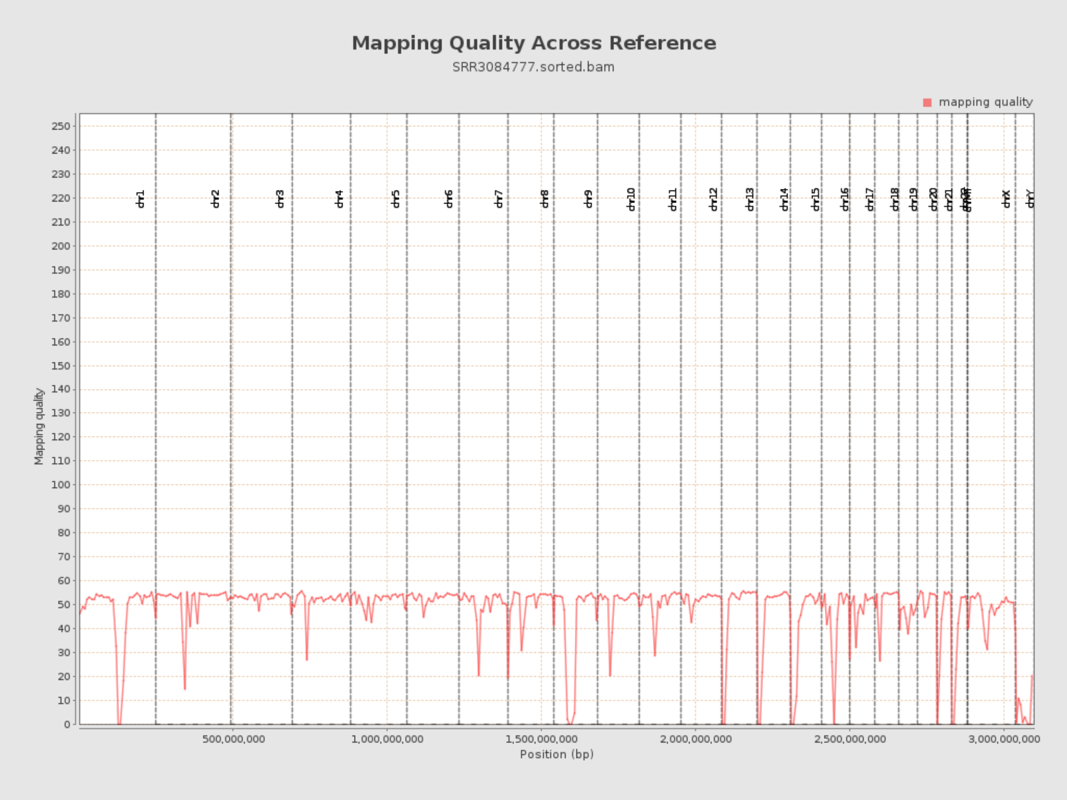
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram