Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 16:09:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084825.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_SRR3084825 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084825.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 16:09:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084825.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,667,889
Mapped reads	1,537,960 / 92.21%
Unmapped reads	129,929 / 7.79%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,930 / 0.72%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	56,446 / 3.38%
Duplication rate	3.27%
Clipped reads	618,368 / 37.07%

2.2. ACGT Content

Number/percentage of A's	28,797,332 / 27.74%
Number/percentage of C's	18,968,769 / 18.27%
Number/percentage of T's	33,165,453 / 31.95%
Number/percentage of G's	22,855,741 / 22.02%
Number/percentage of N's	15,257 / 0.01%
GC Percentage	40.29%

2.3. Coverage

Mean	0.0335

Standard Deviation	0.2353

2.4. Mapping Quality

Mean Mapping Quality	46.34

2.5. Mismatches and indels

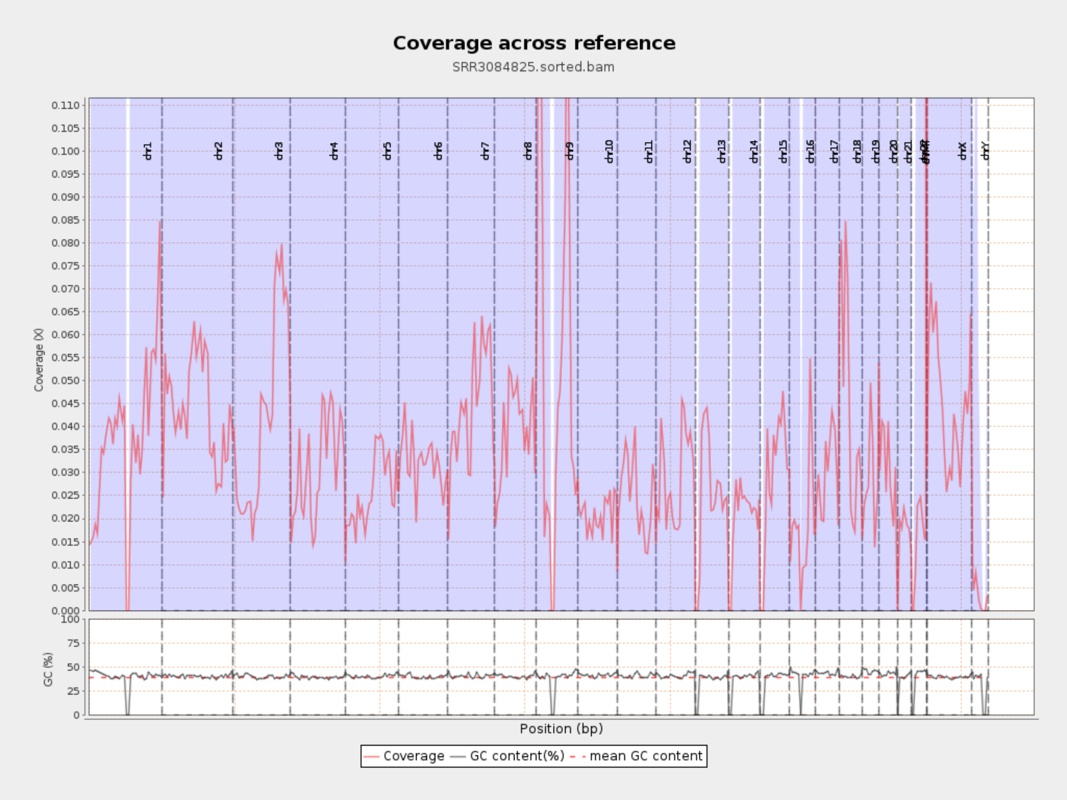
General error rate	0.77%
Mismatches	790,420
Insertions	8,158
Mapped reads with at least one insertion	0.53%
Deletions	24,408
Mapped reads with at least one deletion	1.57%
Homopolymer indels	49.28%

2.6. Chromosome stats

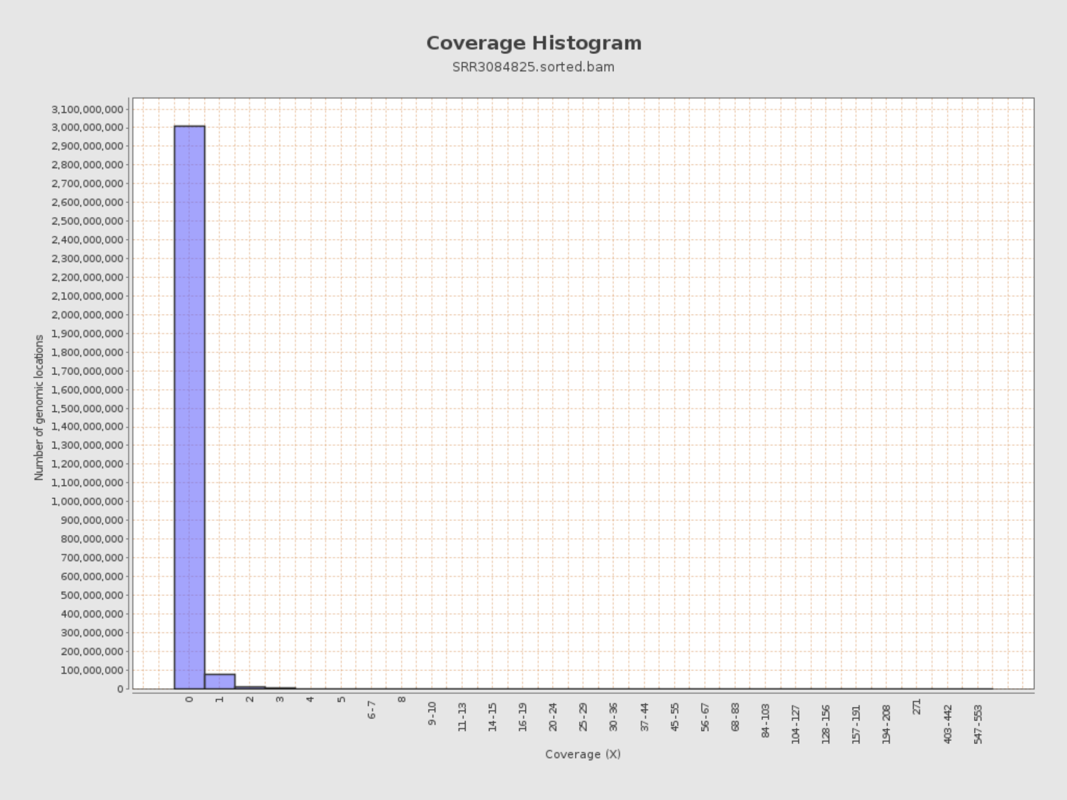
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9347022	0.0375	0.2684
chr2	243199373	10717902	0.0441	0.3401
chr3	198022430	8303538	0.0419	0.233
chr4	191154276	5969729	0.0312	0.2028
chr5	180915260	4730708	0.0261	0.1831
chr6	171115067	5498789	0.0321	0.2151
chr7	159138663	7196889	0.0452	0.3035

chr8	146364022	5715229	0.039	0.2488
chr9	141213431	8144491	0.0577	0.3007
chr10	135534747	2810273	0.0207	0.1674
chr11	135006516	3353453	0.0248	0.1931
chr12	133851895	3885071	0.029	0.1923
chr13	115169878	2851434	0.0248	0.1792
chr14	107349540	2148553	0.02	0.1614
chr15	102531392	3004464	0.0293	0.1996
chr16	90354753	1757032	0.0194	0.1609
chr17	81195210	2441870	0.0301	0.1984
chr18	78077248	3591681	0.046	0.3422
chr19	59128983	1720759	0.0291	0.2132
chr20	63025520	1949530	0.0309	0.2009
chr21	48129895	810226	0.0168	0.1503
chr22	51304566	729919	0.0142	0.1334
chrMT	16571	20714	1.25	1.4082
chrX	155270560	6950409	0.0448	0.2443
chrY	59373566	192582	0.0032	0.0731

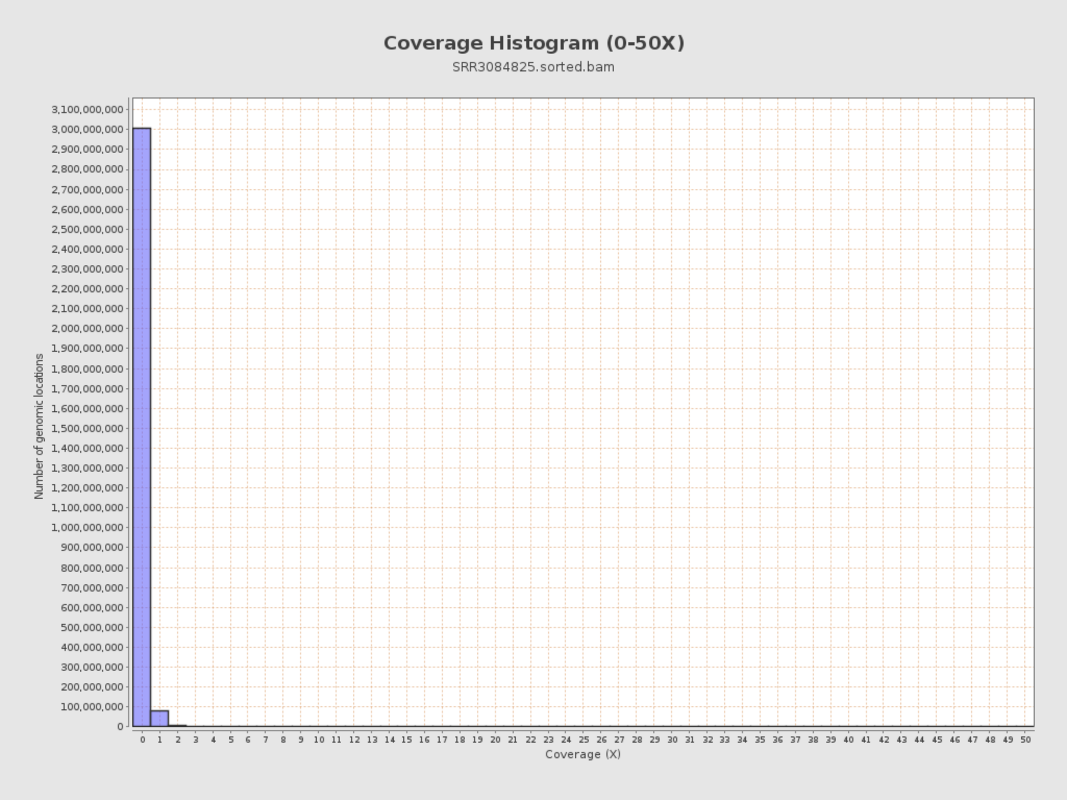
3. Results : Coverage across reference



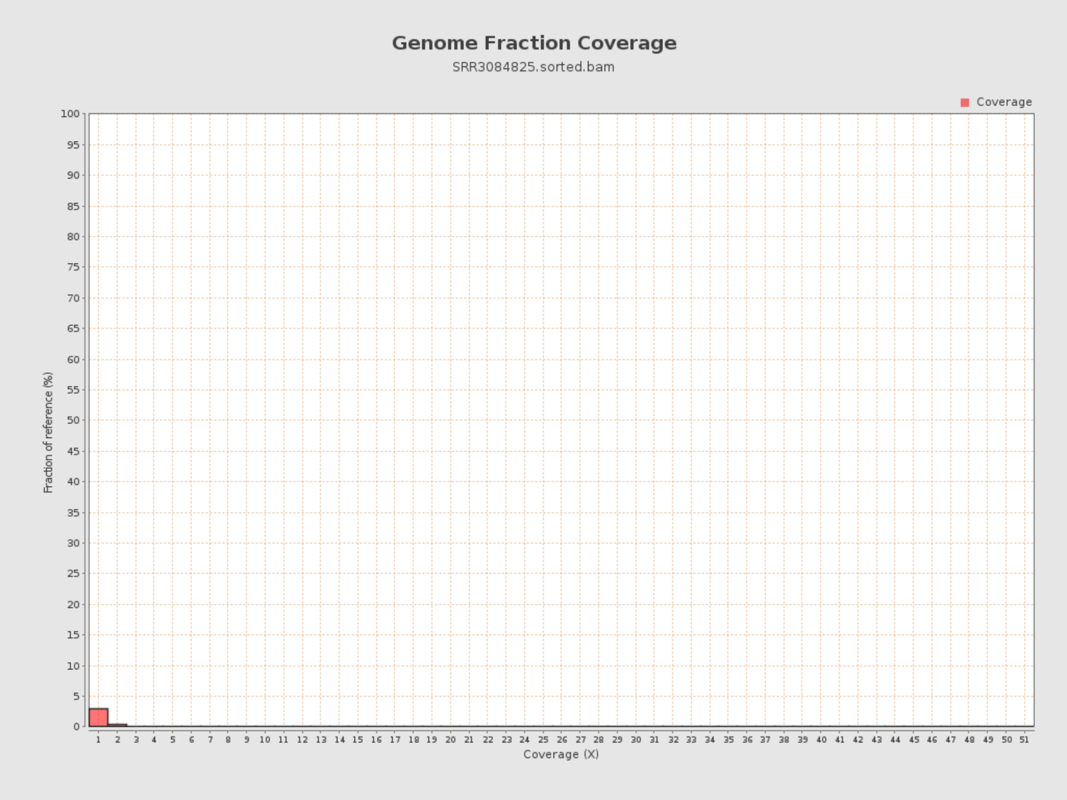
4. Results : Coverage Histogram



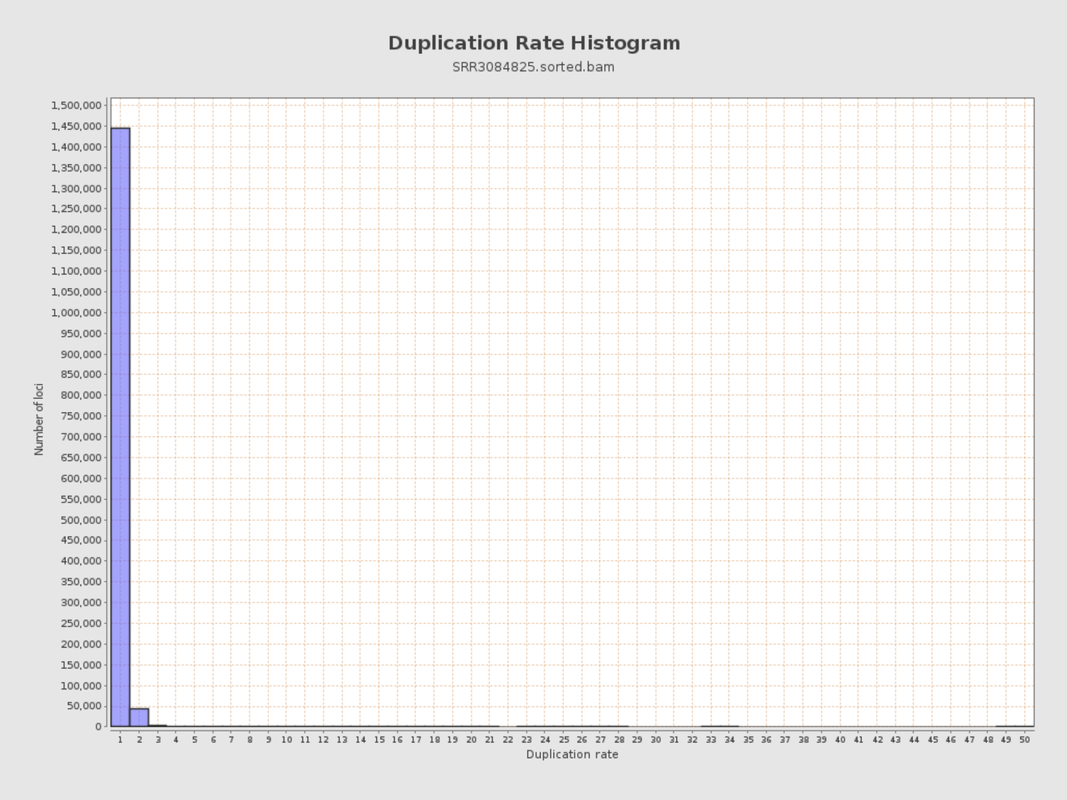
5. Results : Coverage Histogram (0-50X)



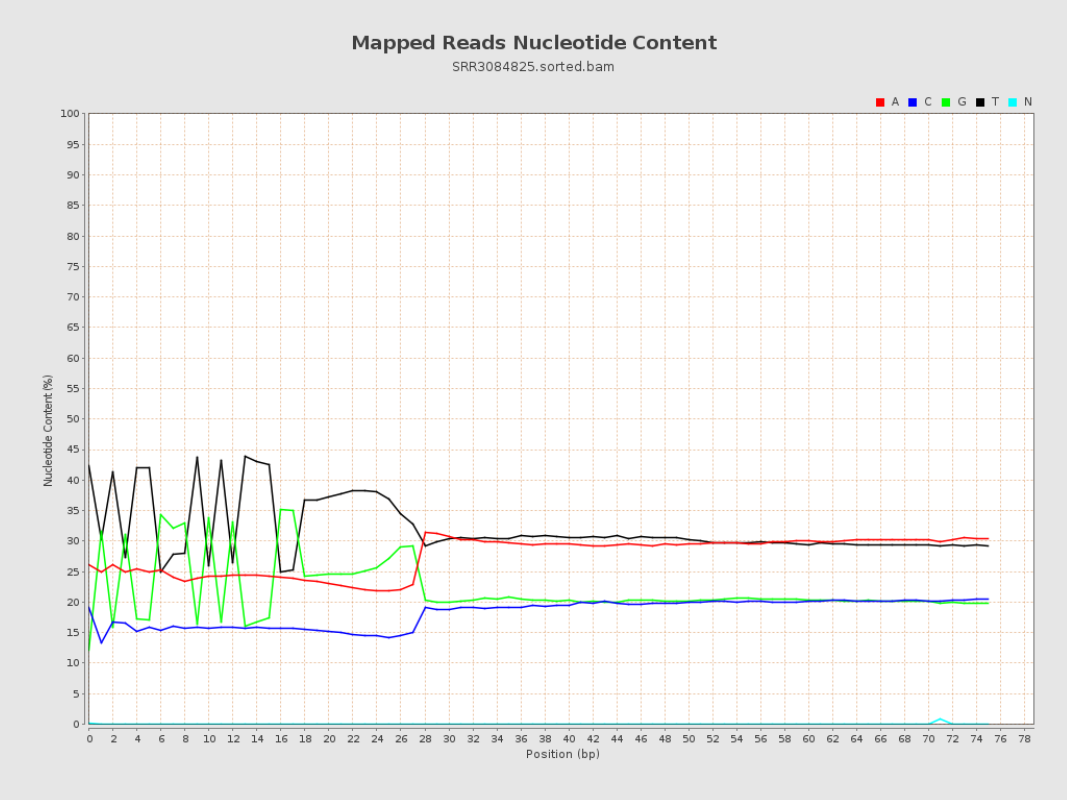
6. Results : Genome Fraction Coverage



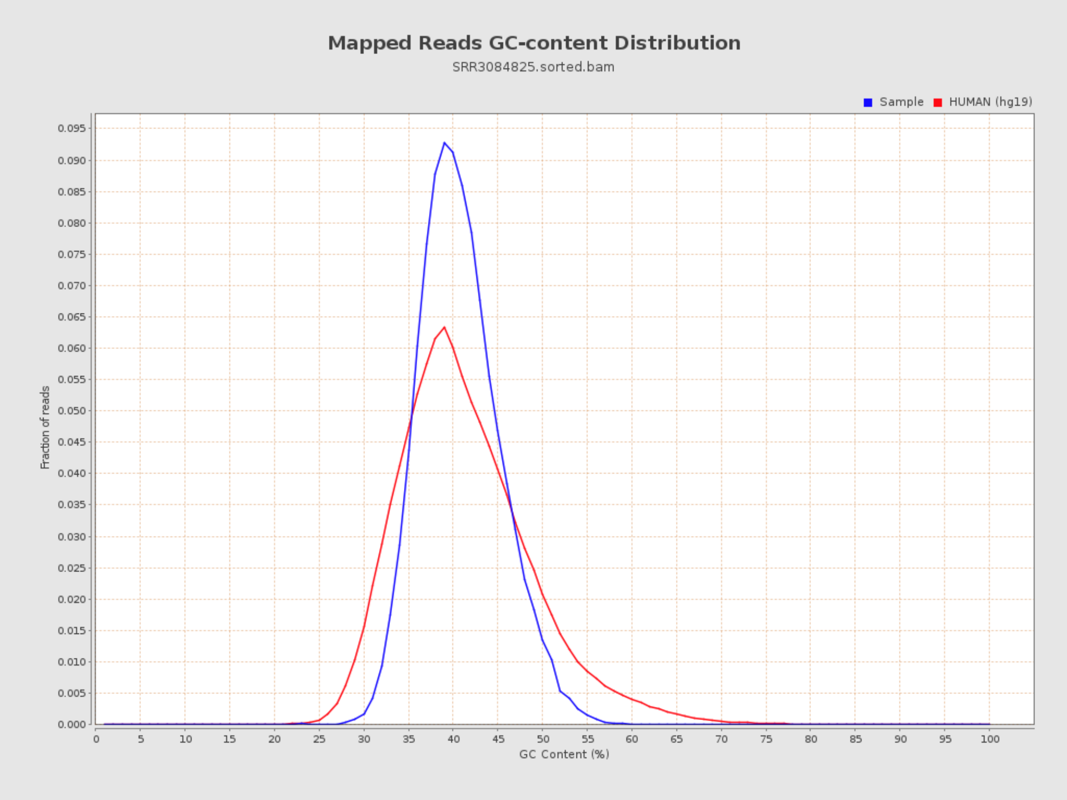
7. Results : Duplication Rate Histogram



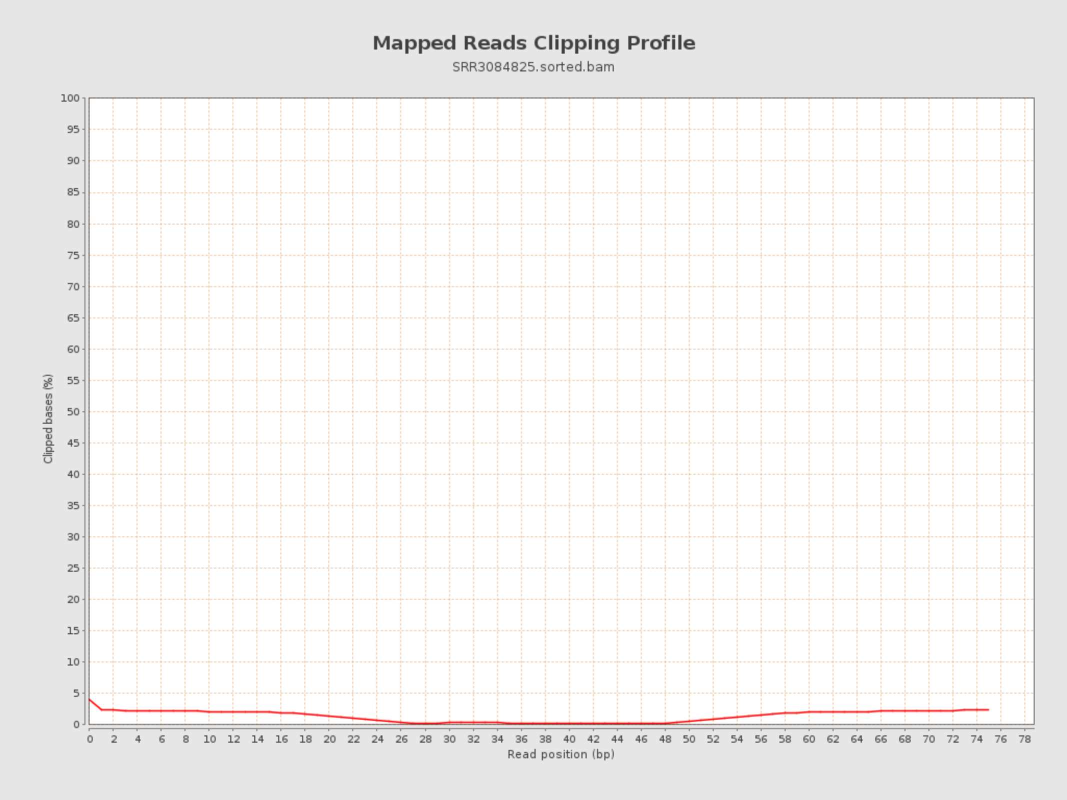
8. Results : Mapped Reads Nucleotide Content



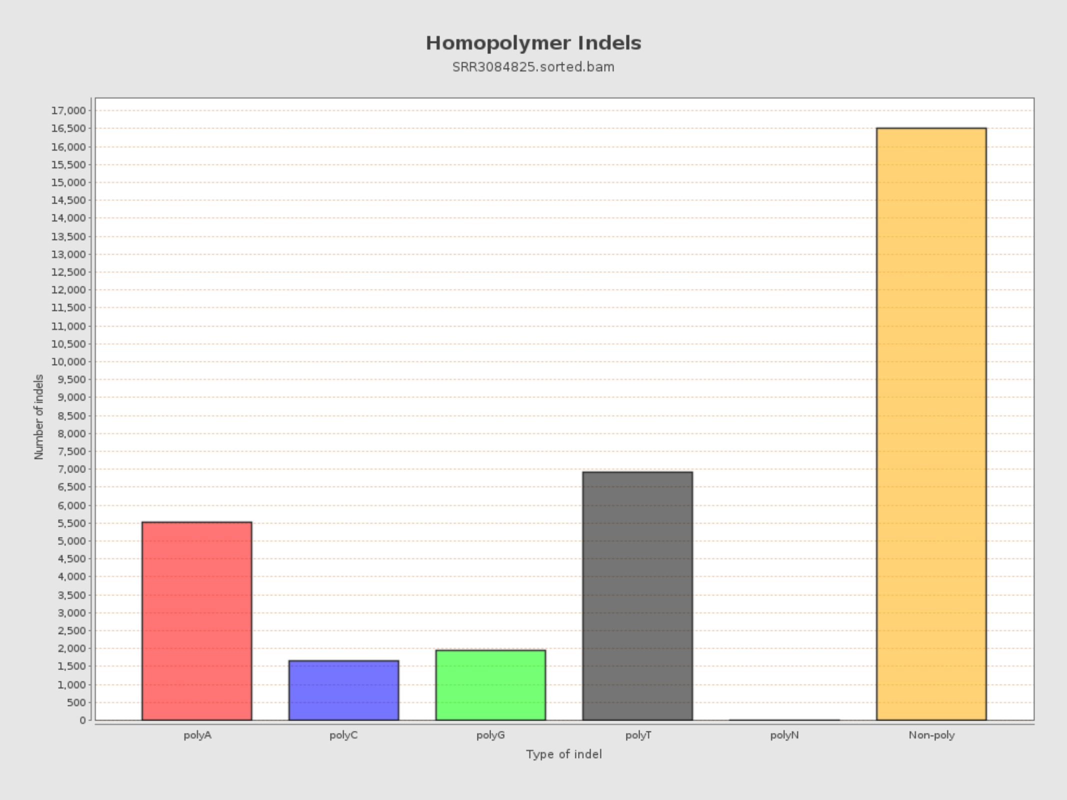
9. Results : Mapped Reads GC-content Distribution



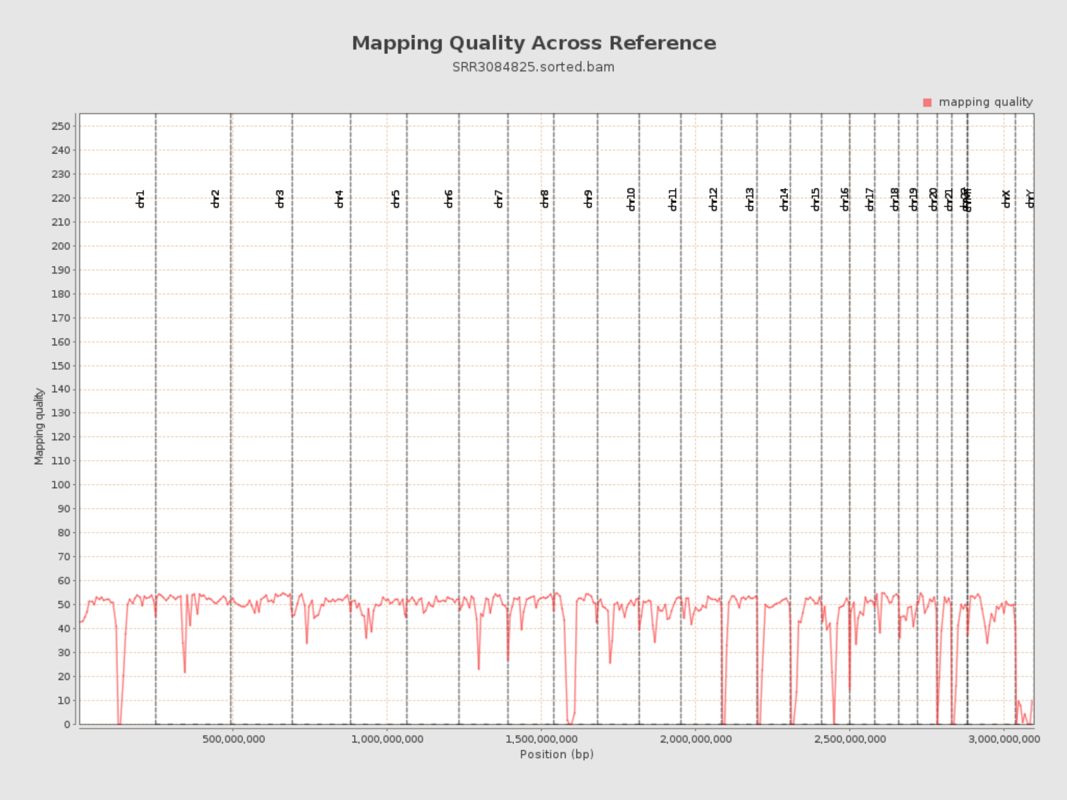
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram