Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 16:17:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084827.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_SRR3084827 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084827.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 16:17:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084827.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,962,926
Mapped reads	1,807,921 / 92.1%
Unmapped reads	155,005 / 7.9%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,370 / 0.94%
Read min/max/mean length	30 / 76 / 76.33
Duplicated reads (estimated)	84,056 / 4.28%
Duplication rate	3.67%
Clipped reads	707,918 / 36.06%

2.2. ACGT Content

Number/percentage of A's	34,768,849 / 28.32%
Number/percentage of C's	22,231,983 / 18.11%
Number/percentage of T's	39,580,049 / 32.24%
Number/percentage of G's	26,163,782 / 21.31%
Number/percentage of N's	17,635 / 0.01%
GC Percentage	39.42%

2.3. Coverage

Mean	0.0397

Standard Deviation	0.3641

2.4. Mapping Quality

Mean Mapping Quality	46.08

2.5. Mismatches and indels

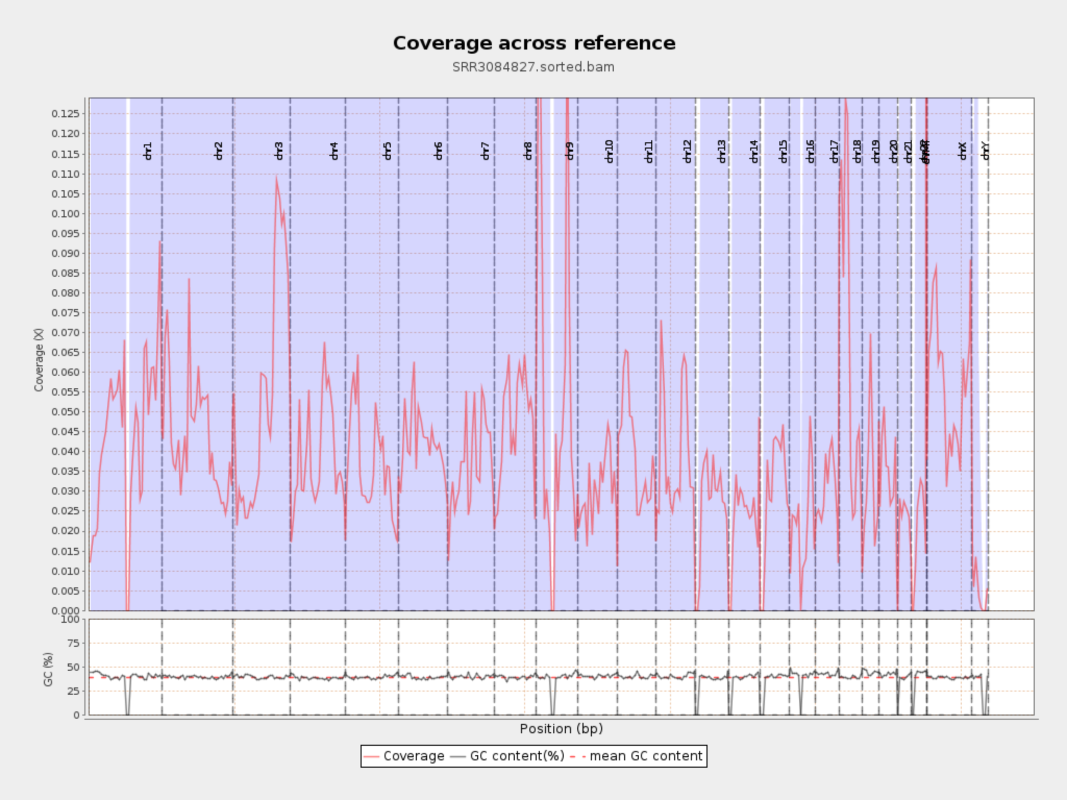
General error rate	0.83%
Mismatches	1,003,692
Insertions	10,376
Mapped reads with at least one insertion	0.57%
Deletions	29,686
Mapped reads with at least one deletion	1.63%
Homopolymer indels	48.96%

2.6. Chromosome stats

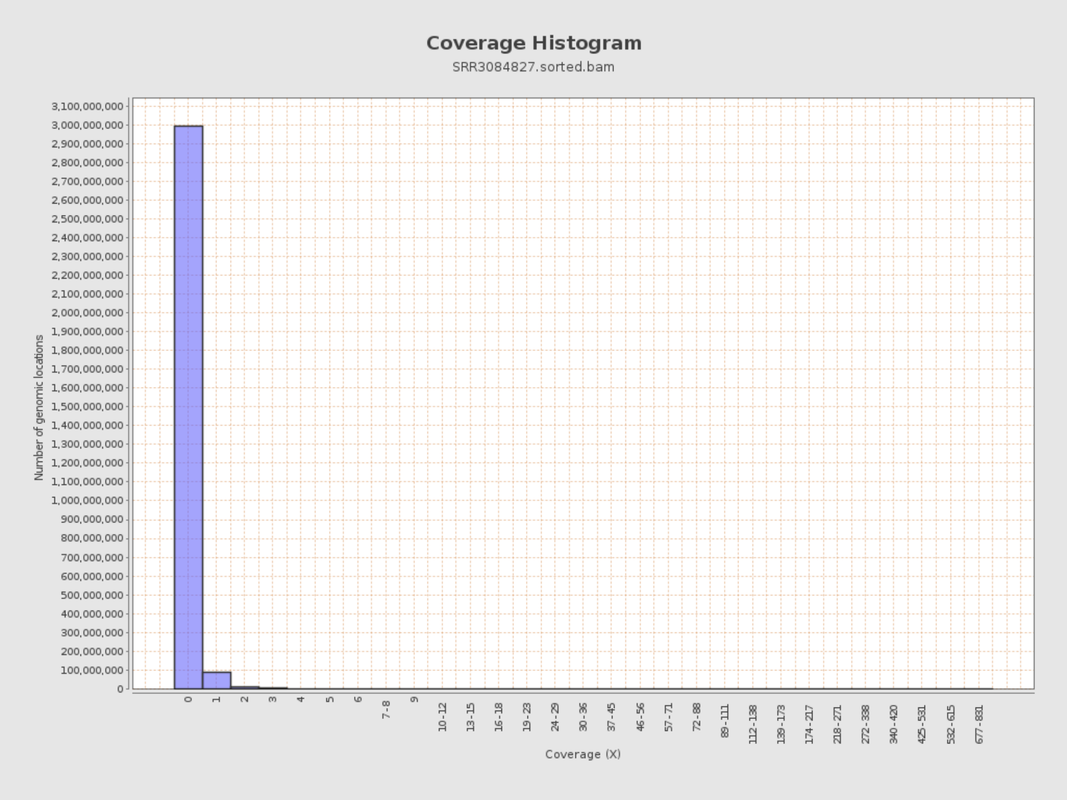
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11130512	0.0447	0.5856
chr2	243199373	10724297	0.0441	0.495
chr3	198022430	10728830	0.0542	0.2703
chr4	191154276	7439895	0.0389	0.2303
chr5	180915260	6703479	0.0371	0.2292
chr6	171115067	7251509	0.0424	0.2573
chr7	159138663	5960590	0.0375	0.3551

chr8	146364022	6859209	0.0469	0.6055
chr9	141213431	7696729	0.0545	0.4159
chr10	135534747	4120440	0.0304	0.2512
chr11	135006516	5352985	0.0396	0.3246
chr12	133851895	5233604	0.0391	0.2346
chr13	115169878	3003092	0.0261	0.1853
chr14	107349540	2403808	0.0224	0.1906
chr15	102531392	3083721	0.0301	0.2083
chr16	90354753	1988490	0.022	0.1943
chr17	81195210	2439213	0.03	0.2154
chr18	78077248	5313693	0.0681	0.7296
chr19	59128983	1997713	0.0338	0.3895
chr20	63025520	2251635	0.0357	0.2284
chr21	48129895	1053432	0.0219	0.1837
chr22	51304566	979849	0.0191	0.1553
chrMT	16571	13335	0.8047	1.055
chrX	155270560	8798264	0.0567	0.3007
chrY	59373566	282614	0.0048	0.1333

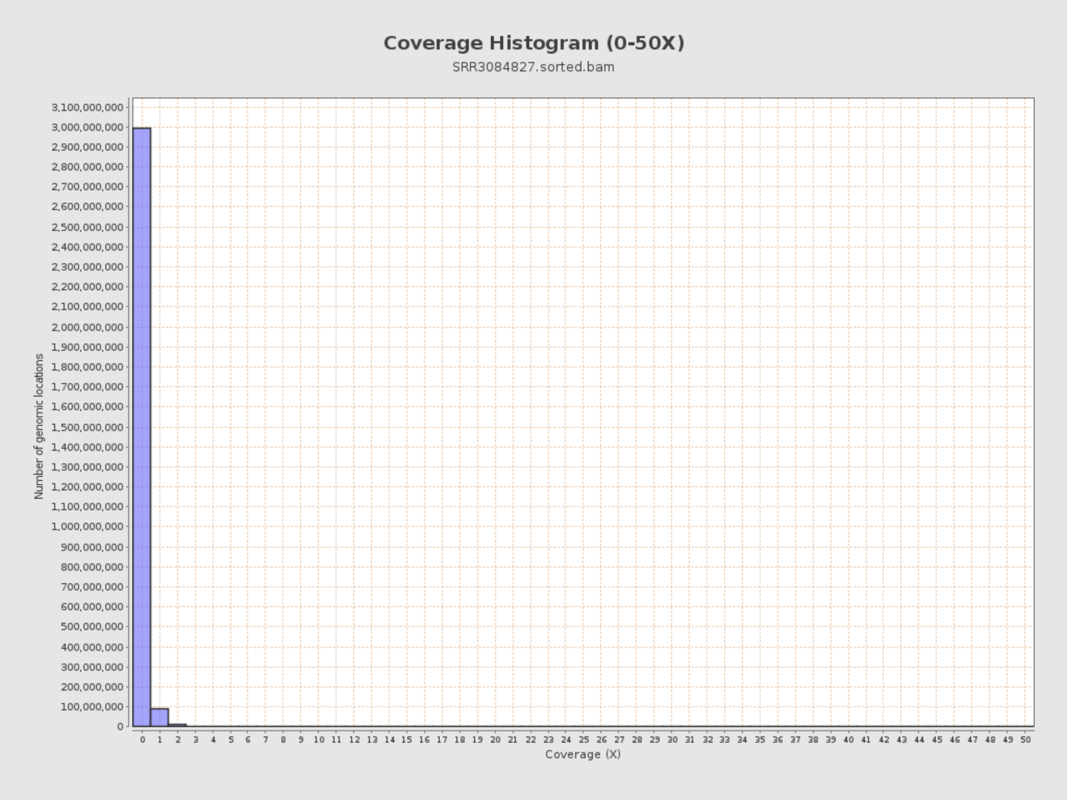
3. Results : Coverage across reference



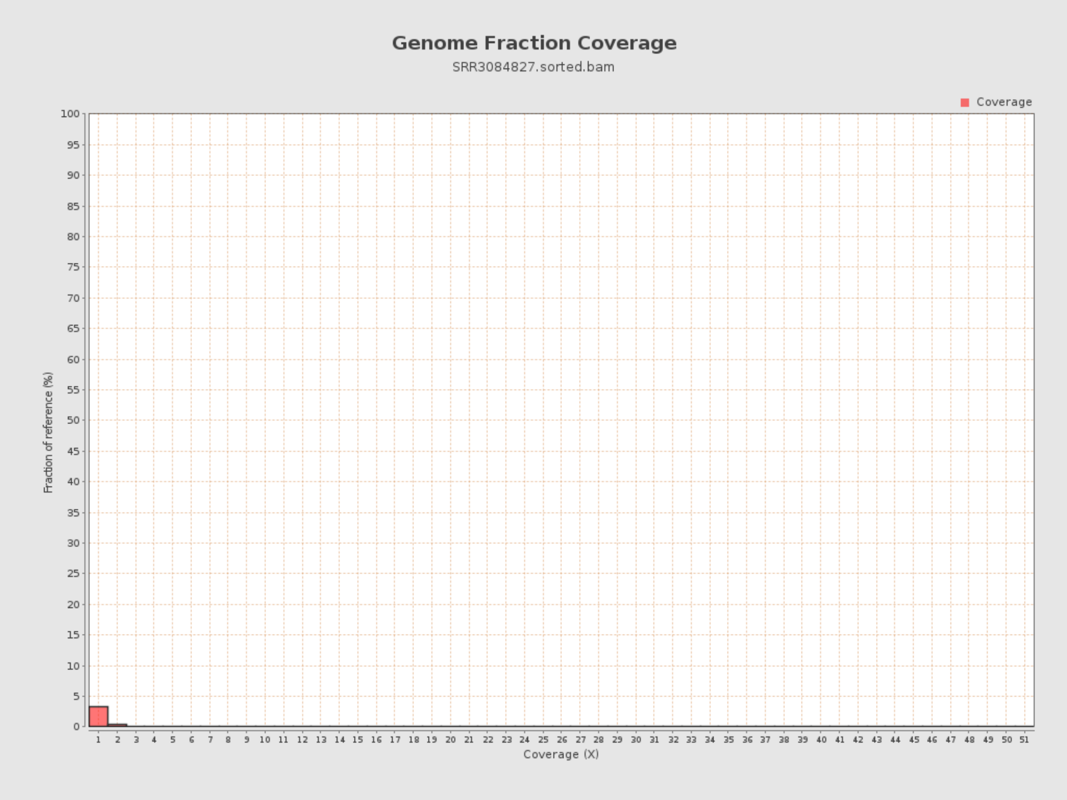
4. Results : Coverage Histogram



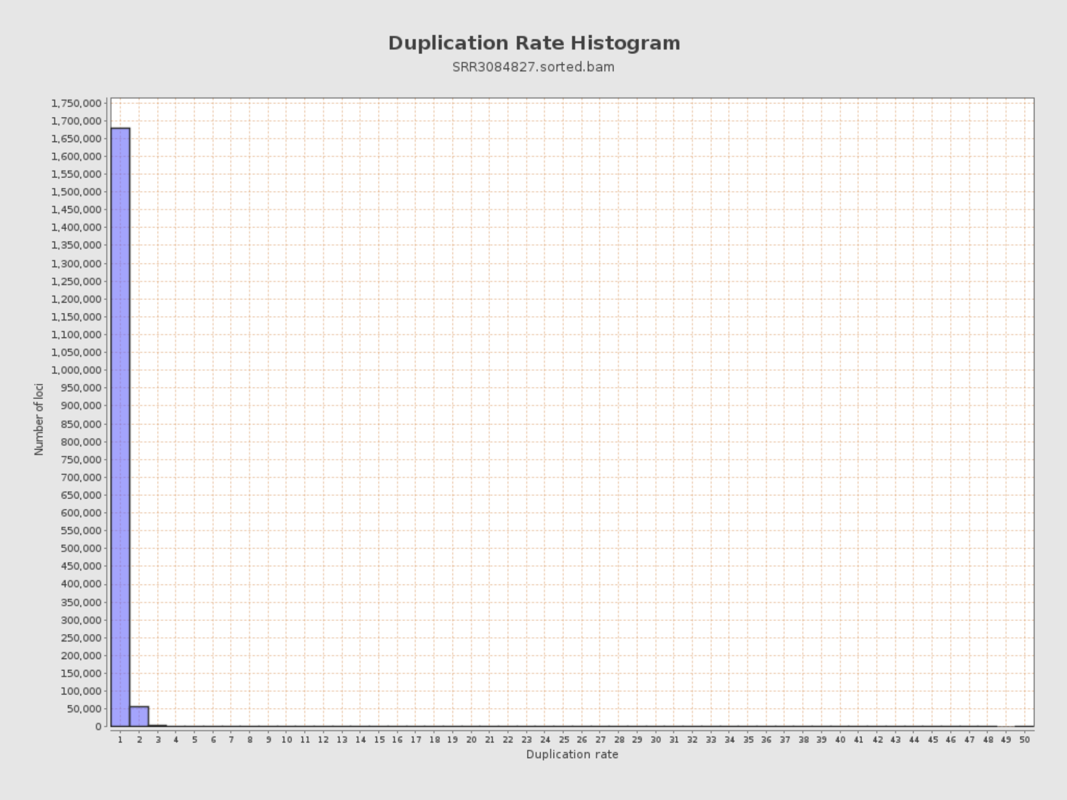
5. Results : Coverage Histogram (0-50X)



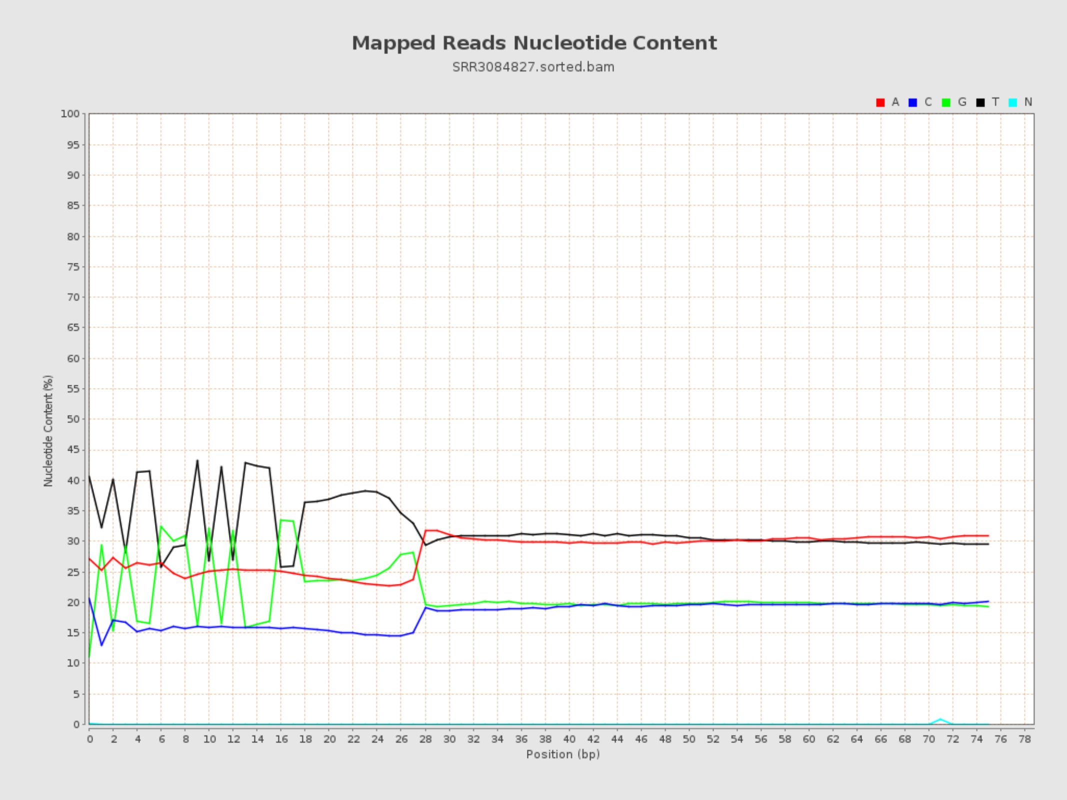
6. Results : Genome Fraction Coverage



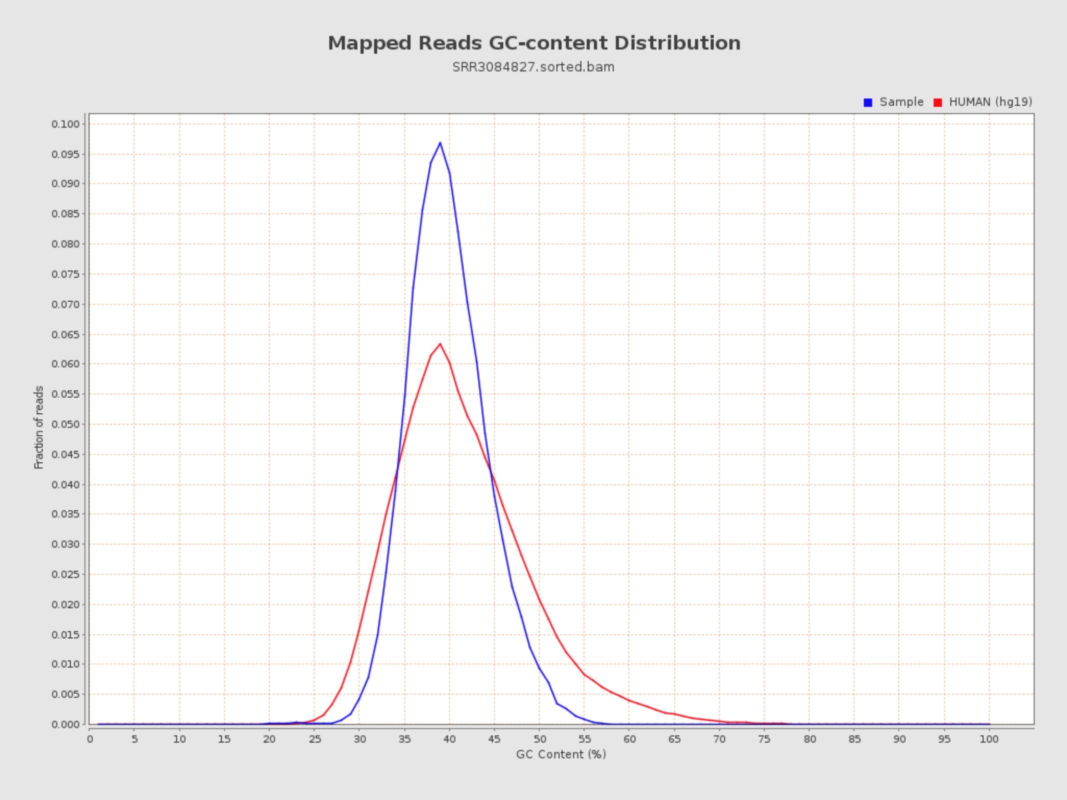
7. Results : Duplication Rate Histogram



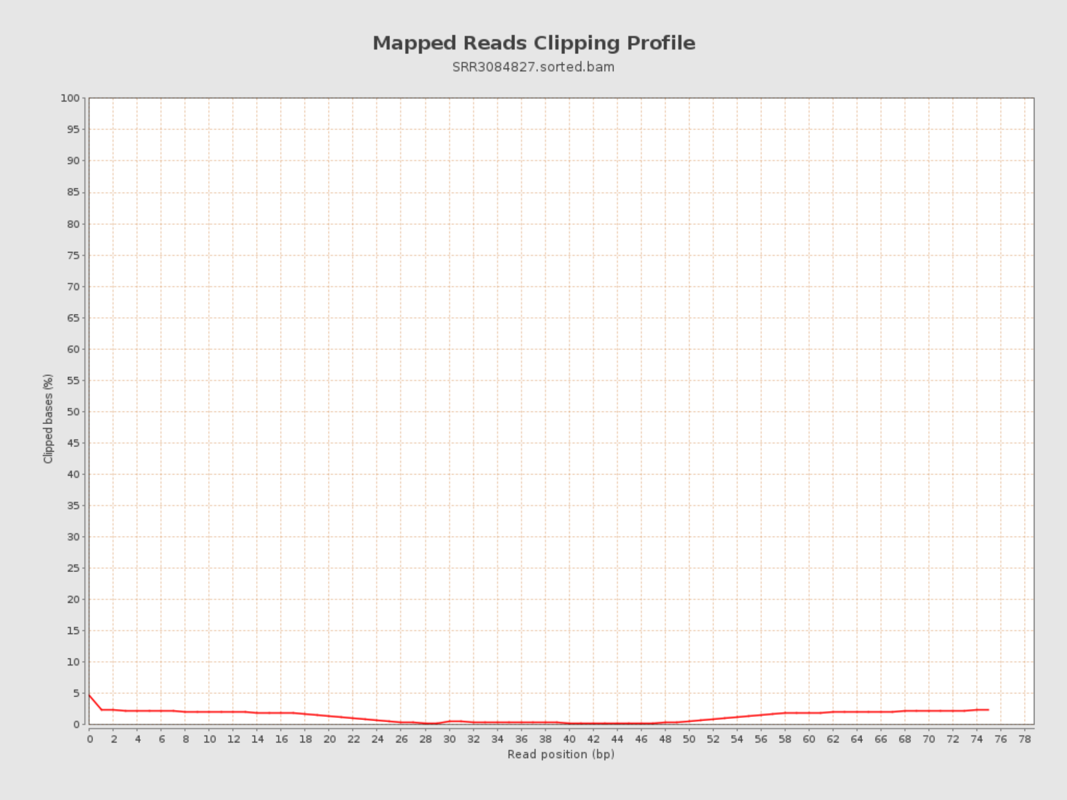
8. Results : Mapped Reads Nucleotide Content



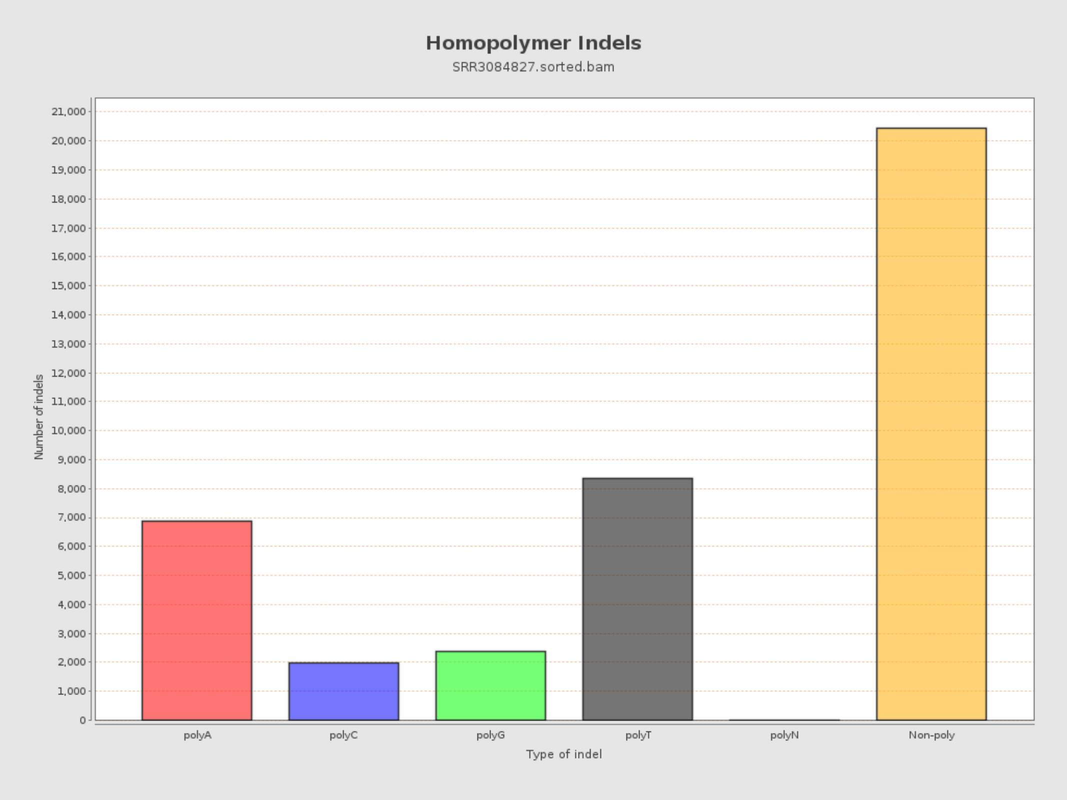
9. Results : Mapped Reads GC-content Distribution



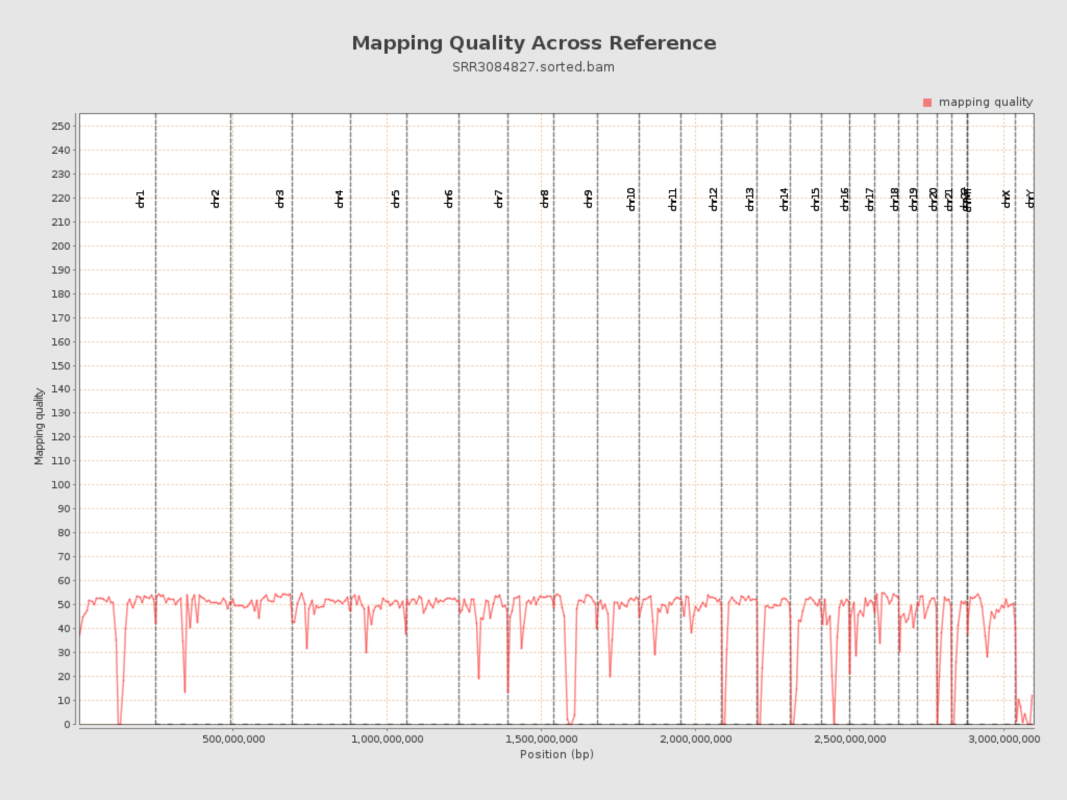
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram