Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 16:24:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9867860.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_SRR9867860 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9867860.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 16:24:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9867860.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,133,981
Mapped reads	1,967,522 / 92.2%
Unmapped reads	166,459 / 7.8%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,588 / 0.4%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	97,555 / 4.57%
Duplication rate	3.66%
Clipped reads	1,970,322 / 92.33%

2.2. ACGT Content

Number/percentage of A's	29,228,244 / 25.16%
Number/percentage of C's	21,704,944 / 18.68%
Number/percentage of T's	37,257,430 / 32.07%
Number/percentage of G's	27,985,634 / 24.09%
Number/percentage of N's	15,150 / 0.01%
GC Percentage	42.77%

2.3. Coverage

Mean	0.0375

Standard Deviation	0.3522

2.4. Mapping Quality

Mean Mapping Quality	45.91

2.5. Mismatches and indels

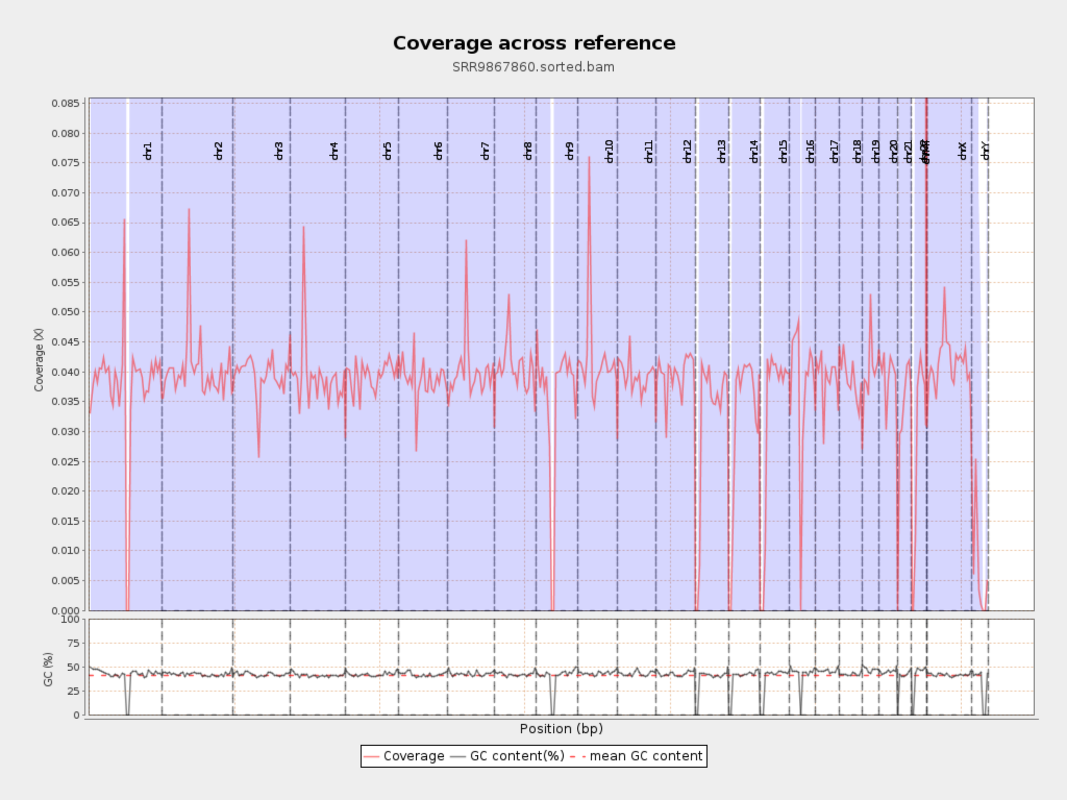
General error rate	0.51%
Mismatches	576,844
Insertions	9,665
Mapped reads with at least one insertion	0.49%
Deletions	21,677
Mapped reads with at least one deletion	1.09%
Homopolymer indels	41.62%

2.6. Chromosome stats

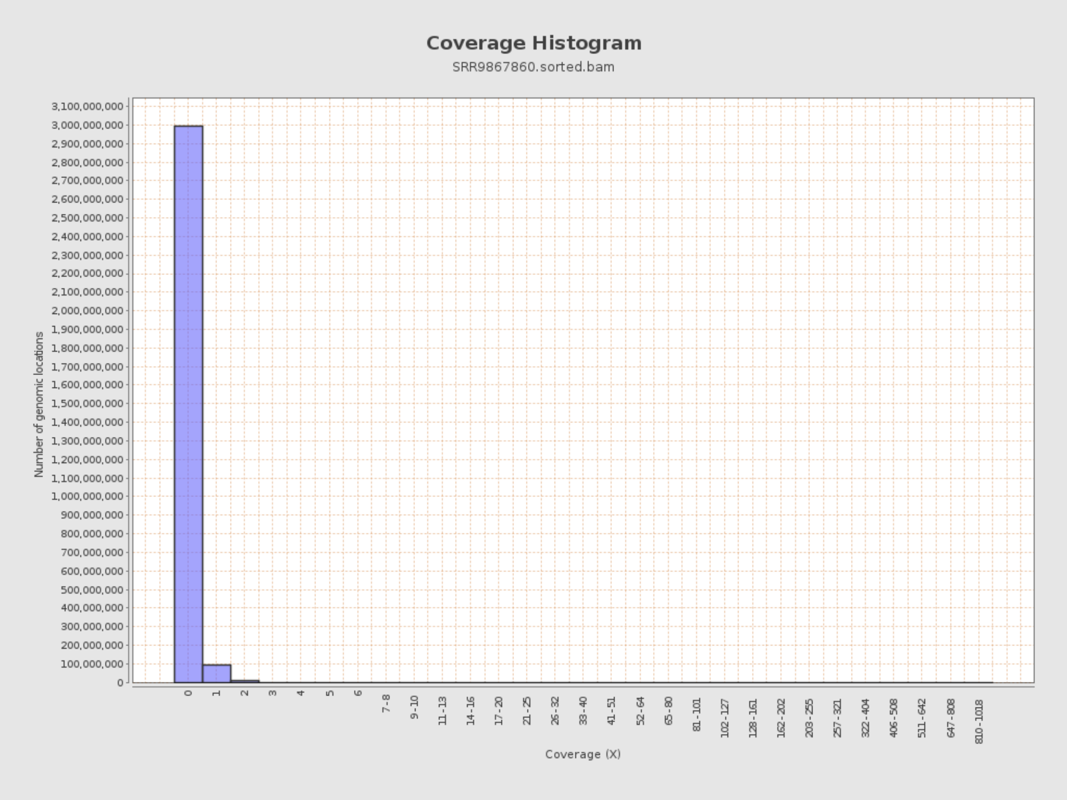
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9289693	0.0373	0.6537
chr2	243199373	9844163	0.0405	0.5035
chr3	198022430	7791331	0.0393	0.2195
chr4	191154276	7453090	0.039	0.2572
chr5	180915260	7113492	0.0393	0.2215
chr6	171115067	6647652	0.0388	0.2548
chr7	159138663	6401958	0.0402	0.4109

chr8	146364022	5954852	0.0407	0.3798
chr9	141213431	4884841	0.0346	0.2841
chr10	135534747	5693631	0.042	0.3654
chr11	135006516	5289968	0.0392	0.3043
chr12	133851895	5284975	0.0395	0.2231
chr13	115169878	3634247	0.0316	0.1984
chr14	107349540	3386690	0.0315	0.2049
chr15	102531392	3329805	0.0325	0.2013
chr16	90354753	3405147	0.0377	0.2355
chr17	81195210	3141360	0.0387	0.2388
chr18	78077248	3039832	0.0389	0.4992
chr19	59128983	2398509	0.0406	0.4743
chr20	63025520	2466417	0.0391	0.225
chr21	48129895	1557110	0.0324	0.2387
chr22	51304566	1373830	0.0268	0.1814
chrMT	16571	16239	0.98	1.1355
chrX	155270560	6430212	0.0414	0.2506
chrY	59373566	396878	0.0067	0.257

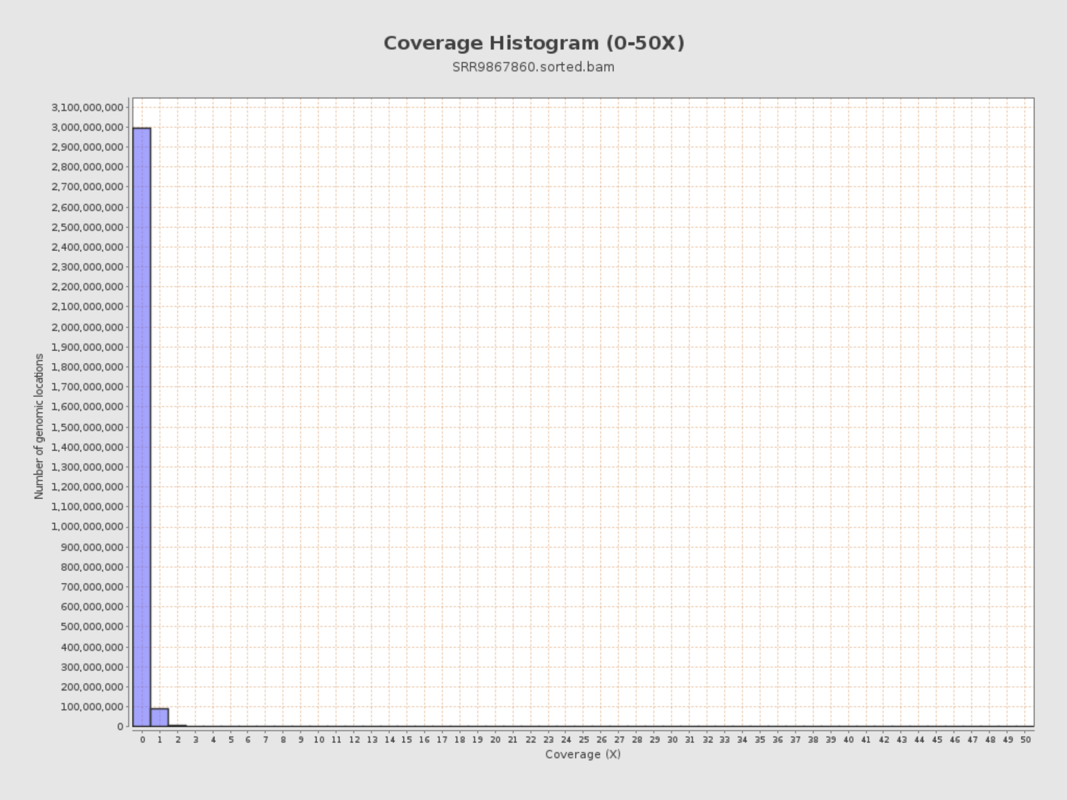
3. Results : Coverage across reference



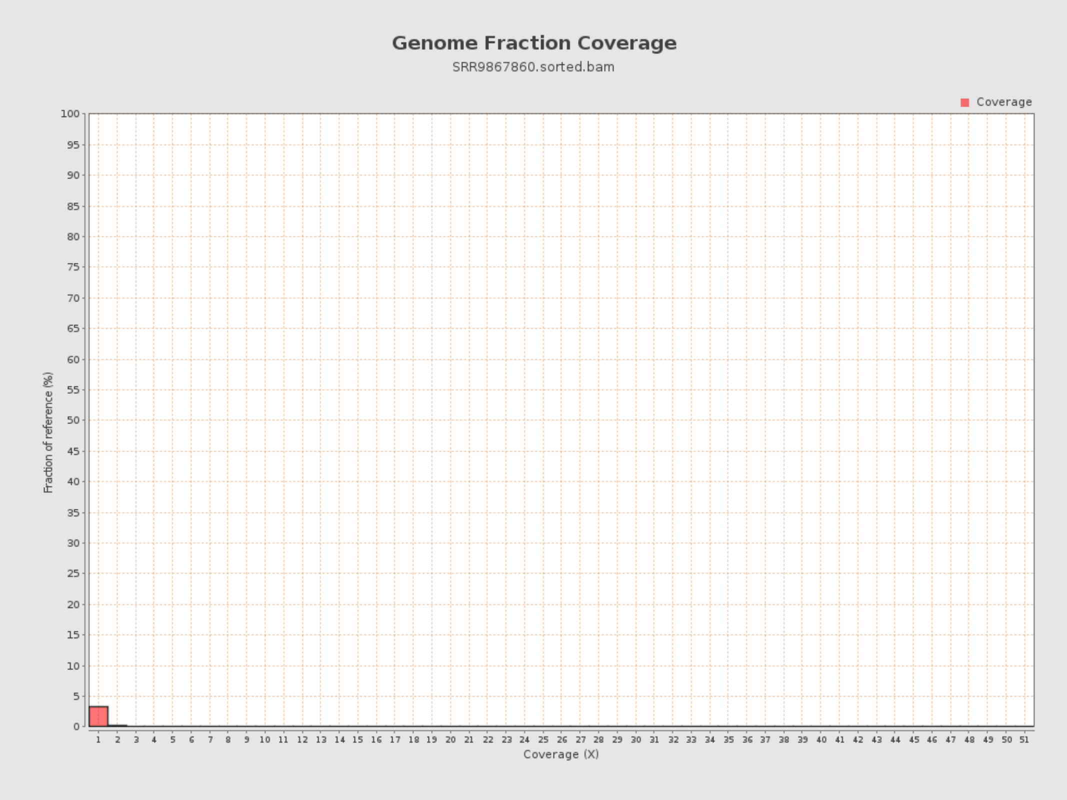
4. Results : Coverage Histogram



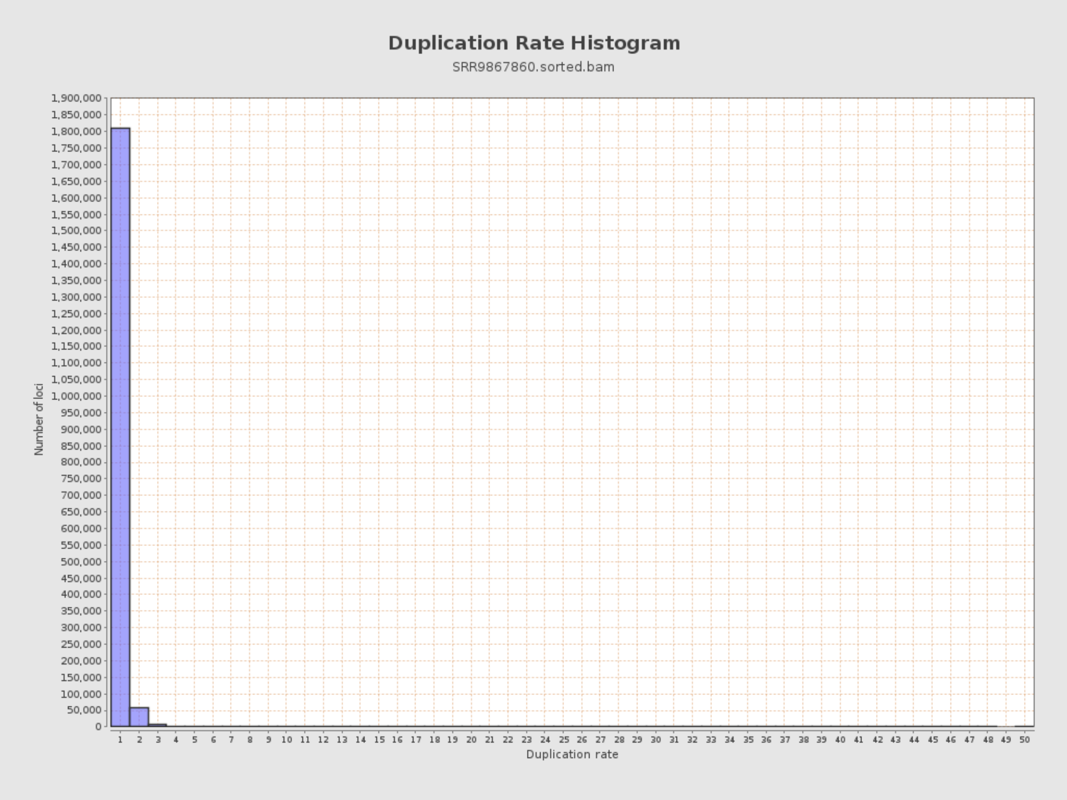
5. Results : Coverage Histogram (0-50X)



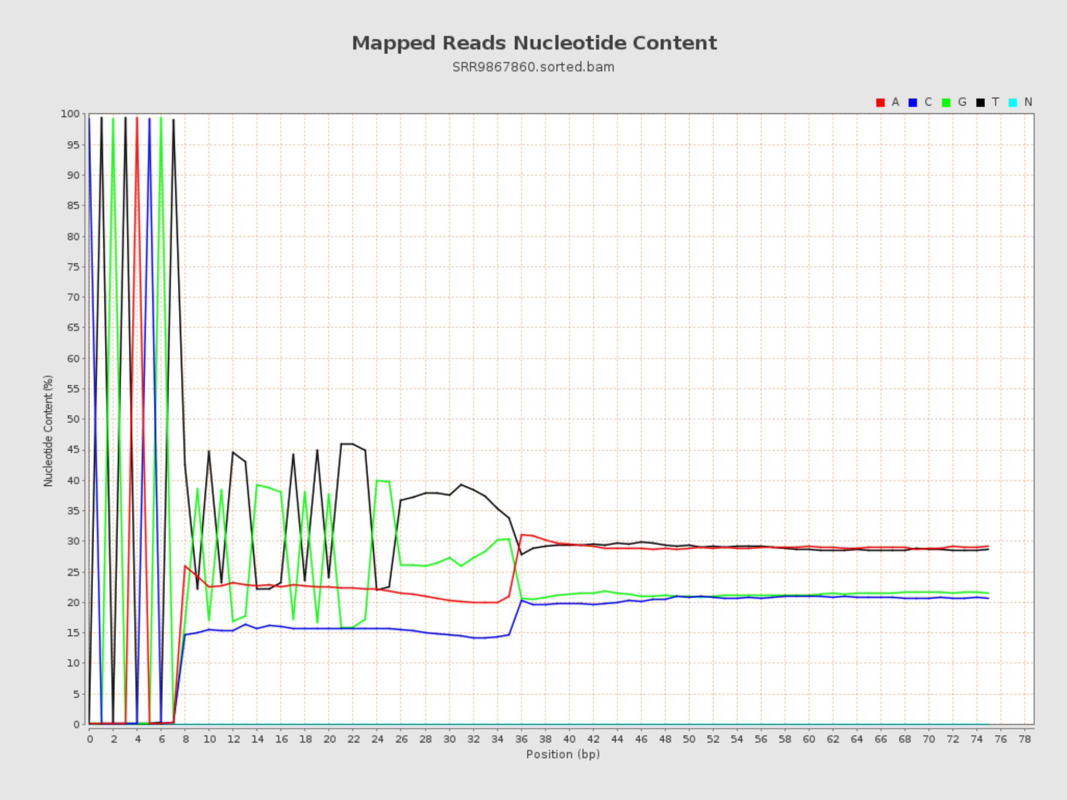
6. Results : Genome Fraction Coverage



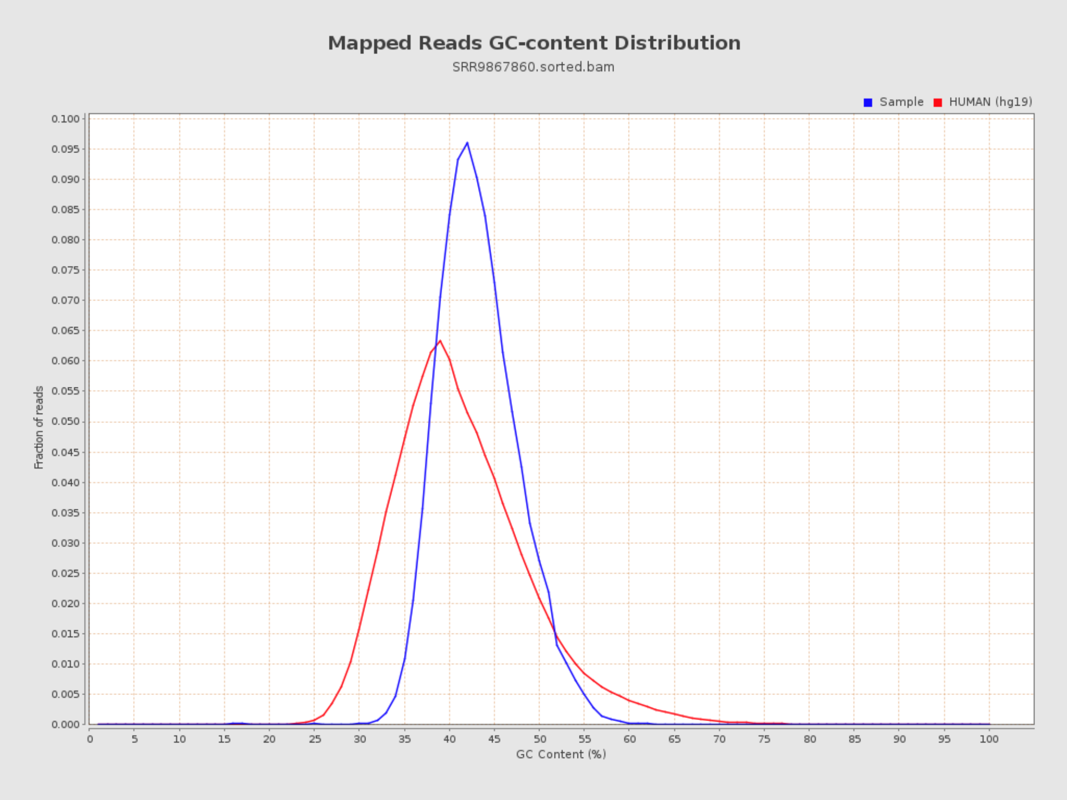
7. Results : Duplication Rate Histogram



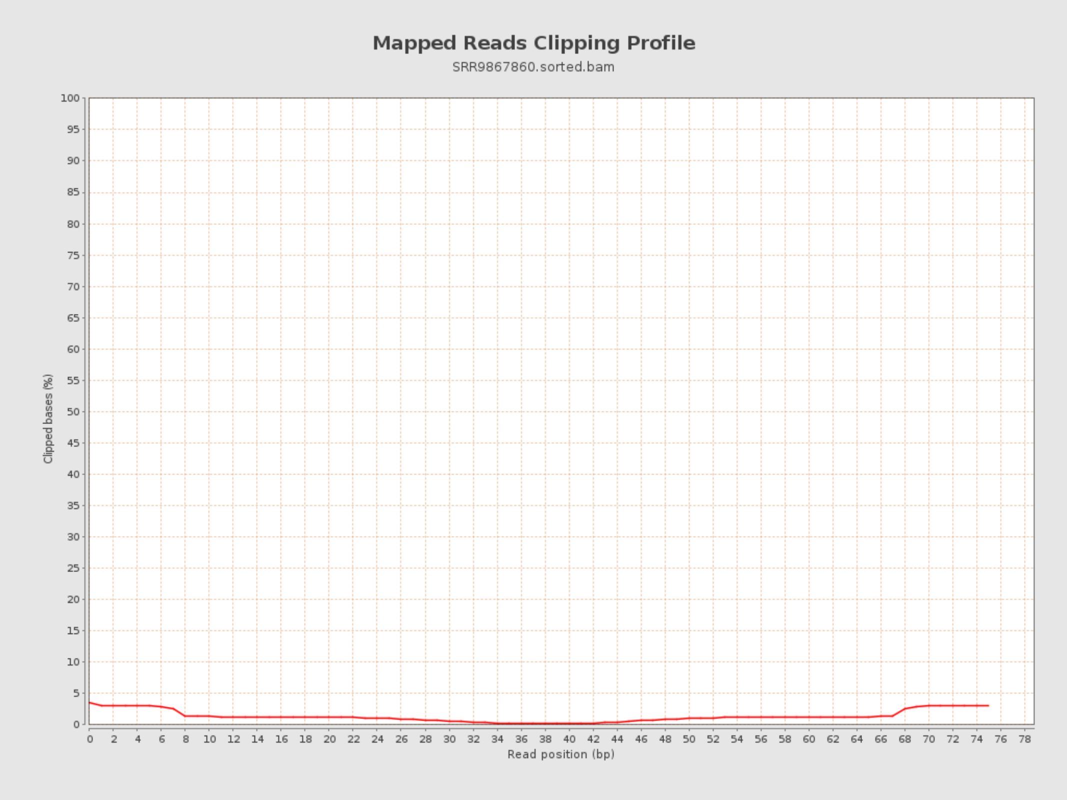
8. Results : Mapped Reads Nucleotide Content



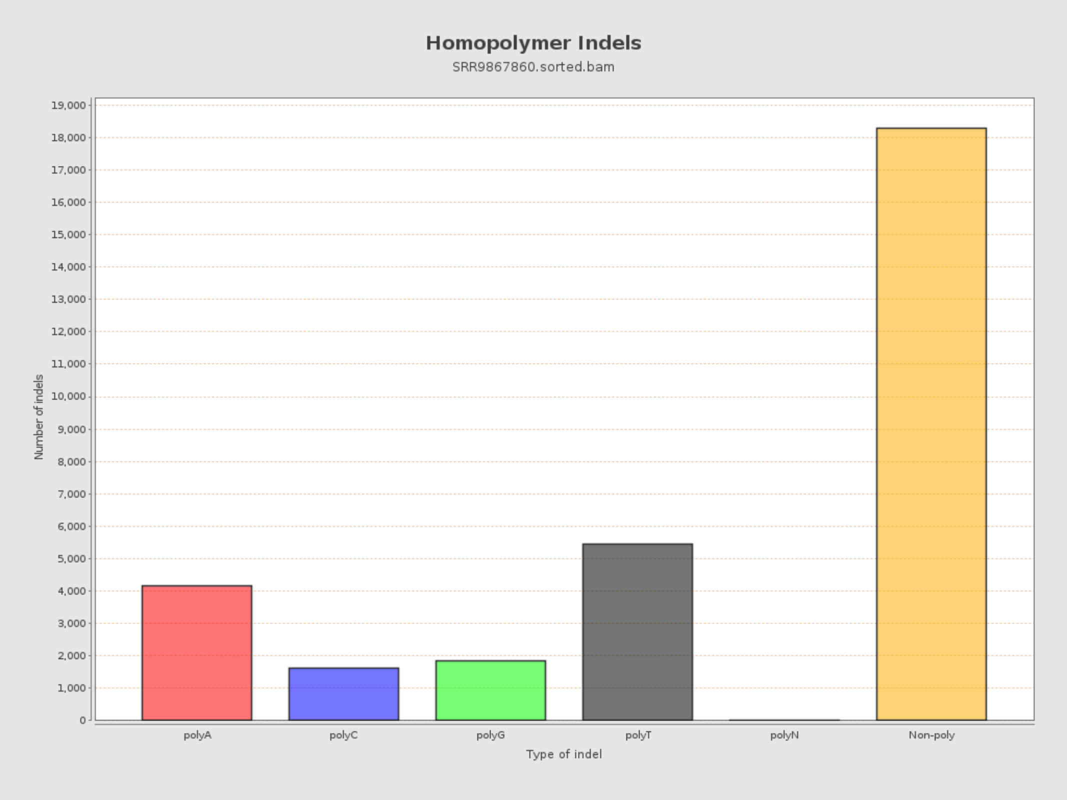
9. Results : Mapped Reads GC-content Distribution



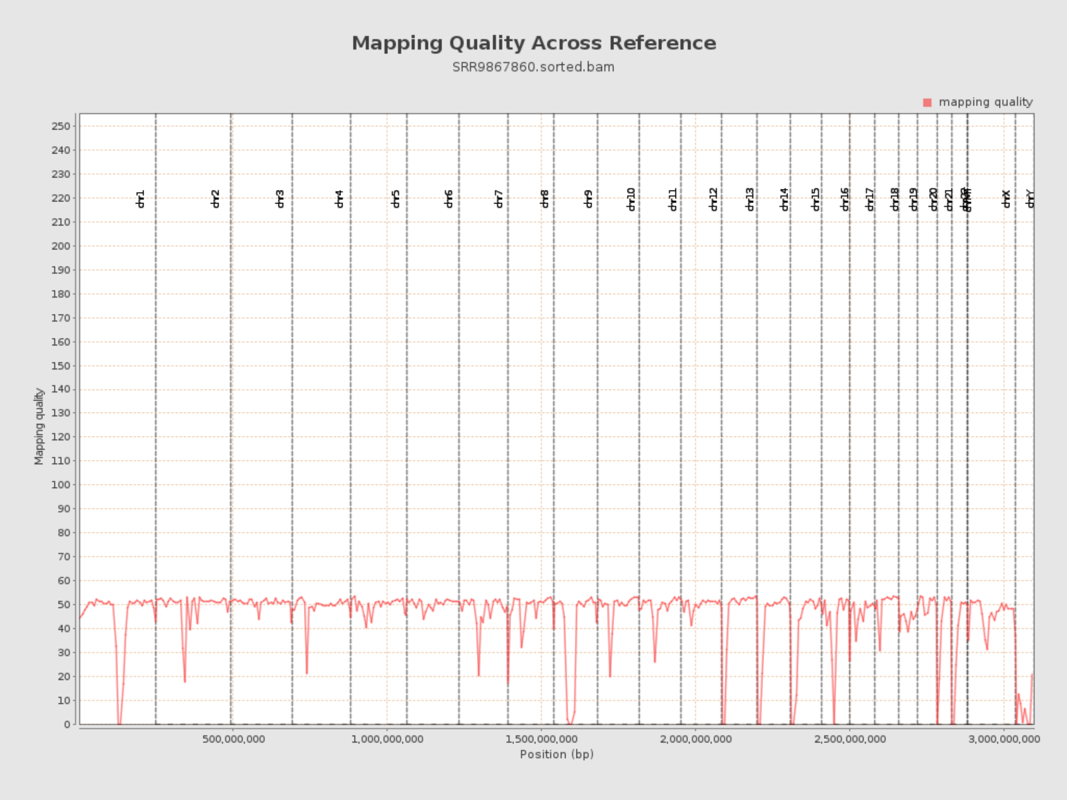
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram