Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 15:45:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525067.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_SRR10525067 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525067.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 15:45:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525067.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,992,851
Mapped reads	1,821,763 / 91.41%
Unmapped reads	171,088 / 8.59%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,194 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	68,658 / 3.45%
Duplication rate	2.82%
Clipped reads	1,827,991 / 91.73%

2.2. ACGT Content

Number/percentage of A's	26,520,021 / 25.23%
Number/percentage of C's	20,765,395 / 19.76%
Number/percentage of T's	32,406,945 / 30.83%
Number/percentage of G's	25,404,424 / 24.17%
Number/percentage of N's	3,360 / 0%
GC Percentage	43.93%

2.3. Coverage

Mean	0.034

Standard Deviation	0.3017

2.4. Mapping Quality

Mean Mapping Quality	45.62

2.5. Mismatches and indels

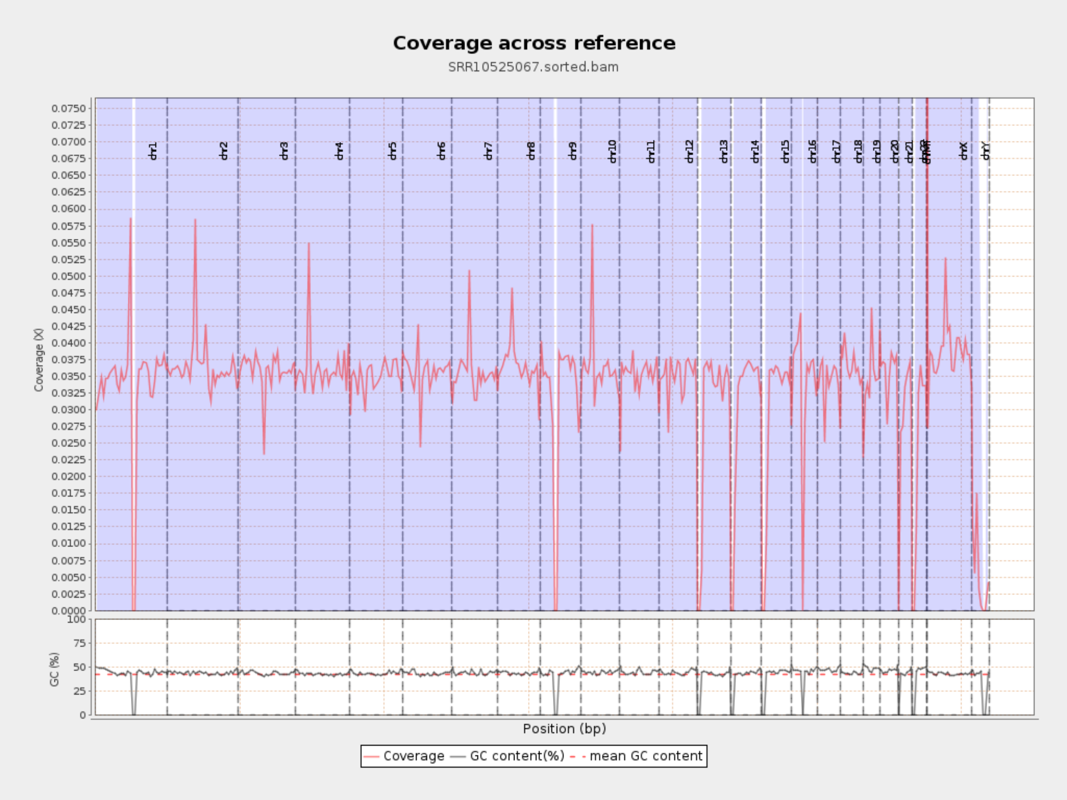
General error rate	0.48%
Mismatches	496,868
Insertions	5,743
Mapped reads with at least one insertion	0.31%
Deletions	16,353
Mapped reads with at least one deletion	0.89%
Homopolymer indels	43.66%

2.6. Chromosome stats

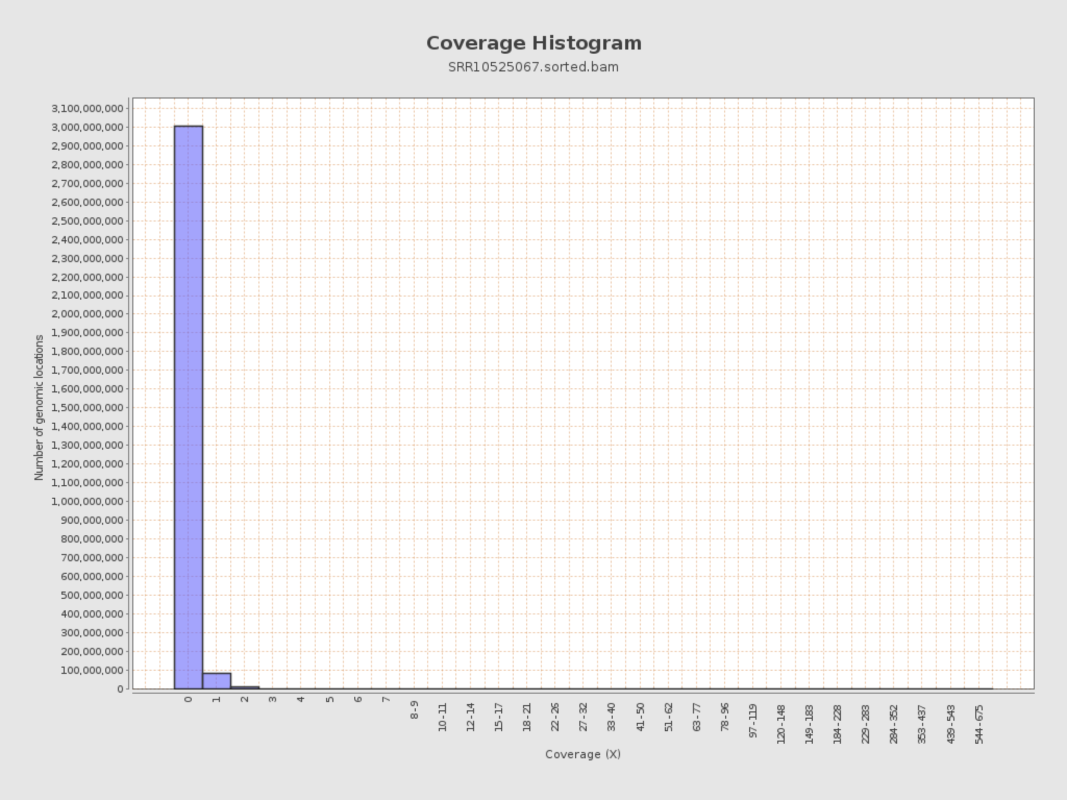
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8352564	0.0335	0.5707
chr2	243199373	8925858	0.0367	0.3132
chr3	198022430	7100747	0.0359	0.2091
chr4	191154276	6920379	0.0362	0.2334
chr5	180915260	6359791	0.0352	0.2079
chr6	171115067	6100294	0.0357	0.2282
chr7	159138663	5697234	0.0358	0.3297

chr8	146364022	5380273	0.0368	0.3526
chr9	141213431	4466111	0.0316	0.2869
chr10	135534747	4955576	0.0366	0.2831
chr11	135006516	4787299	0.0355	0.2742
chr12	133851895	4703328	0.0351	0.2138
chr13	115169878	3367597	0.0292	0.1874
chr14	107349540	3196351	0.0298	0.2069
chr15	102531392	2936755	0.0286	0.1867
chr16	90354753	3007570	0.0333	0.2172
chr17	81195210	2764825	0.0341	0.217
chr18	78077248	2865810	0.0367	0.4859
chr19	59128983	2074194	0.0351	0.4199
chr20	63025520	2227183	0.0353	0.2136
chr21	48129895	1392634	0.0289	0.2108
chr22	51304566	1207051	0.0235	0.1693
chrMT	16571	7170	0.4327	0.7433
chrX	155270560	6021978	0.0388	0.2521
chrY	59373566	308946	0.0052	0.1296

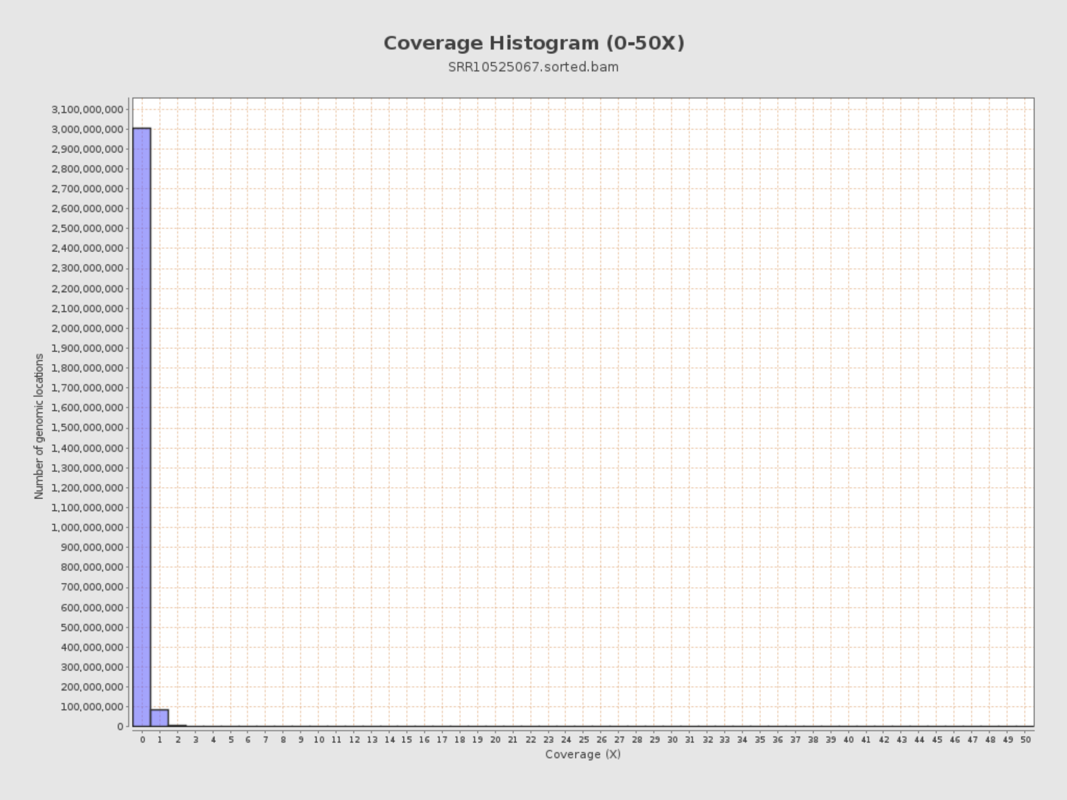
3. Results : Coverage across reference



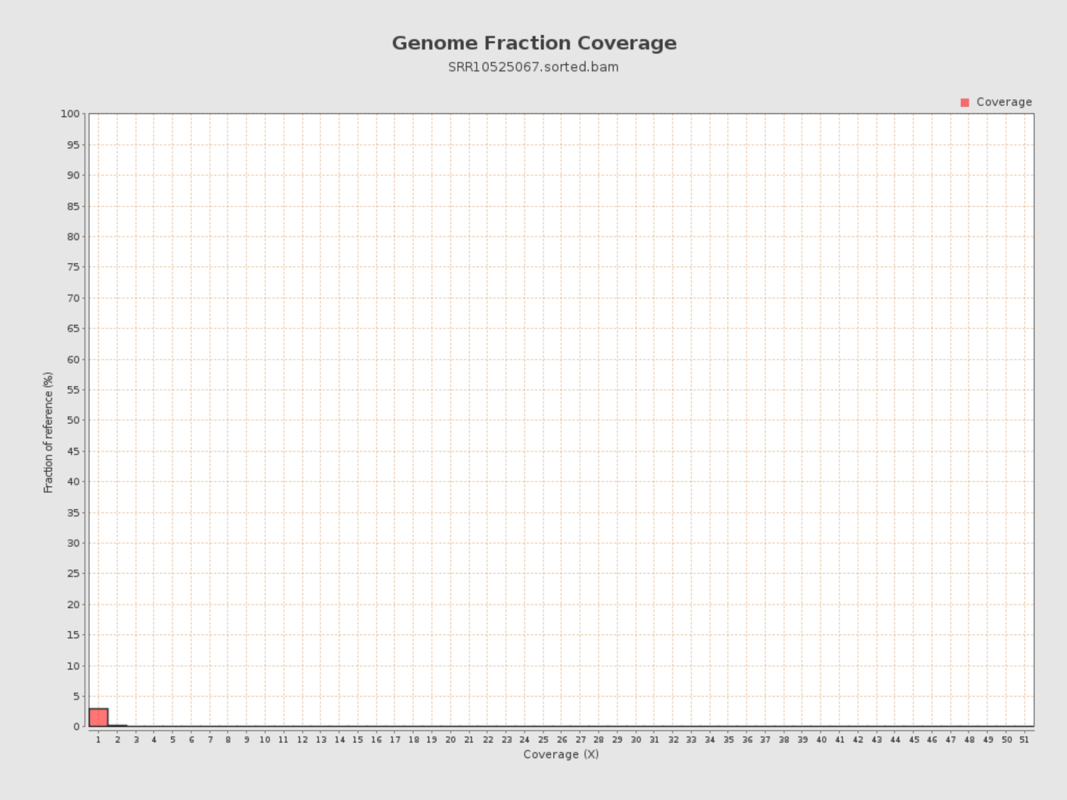
4. Results : Coverage Histogram



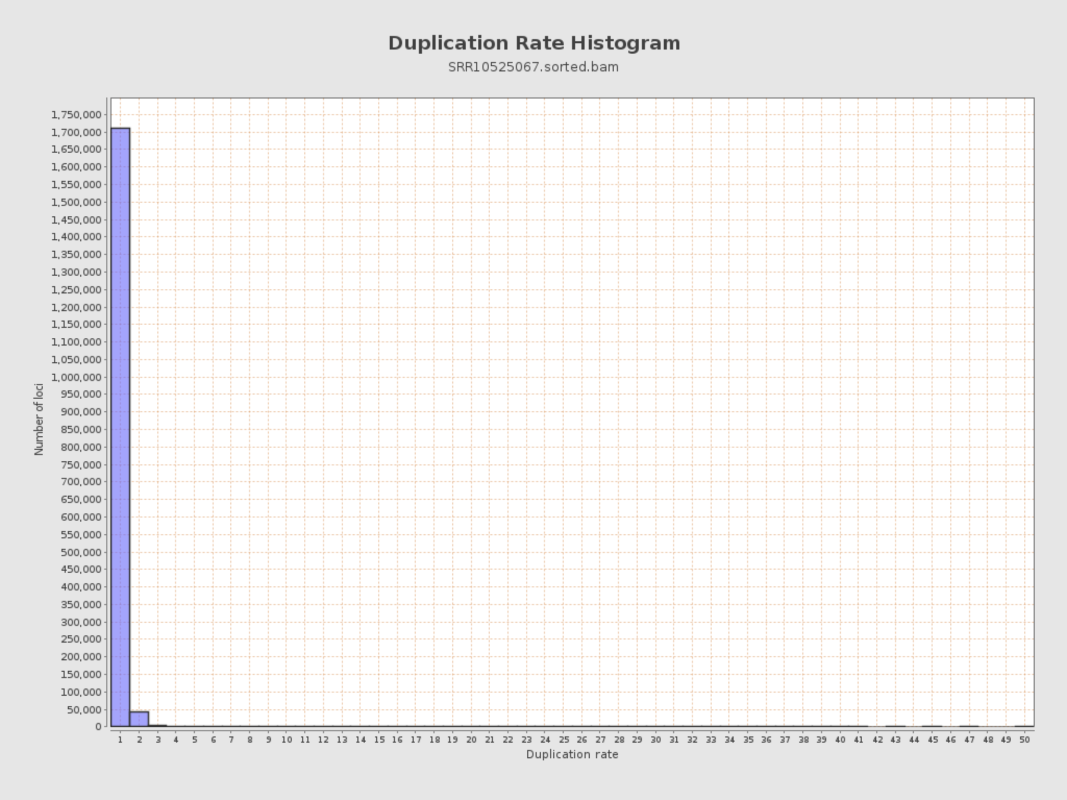
5. Results : Coverage Histogram (0-50X)



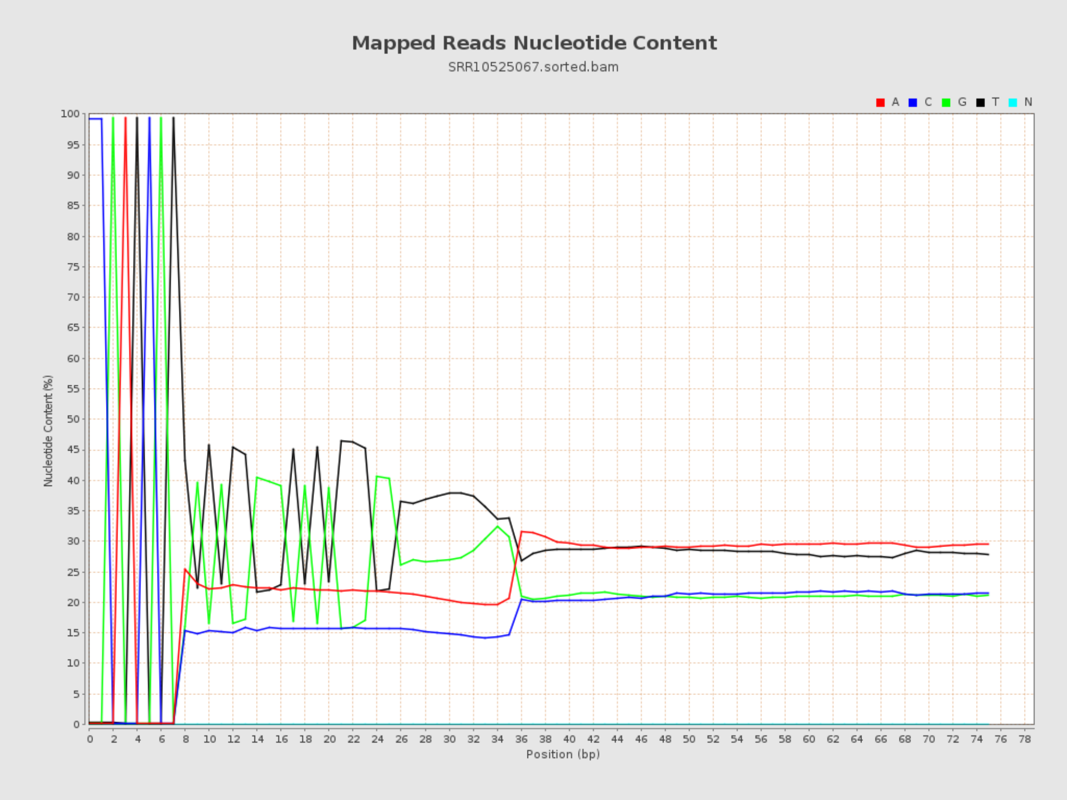
6. Results : Genome Fraction Coverage



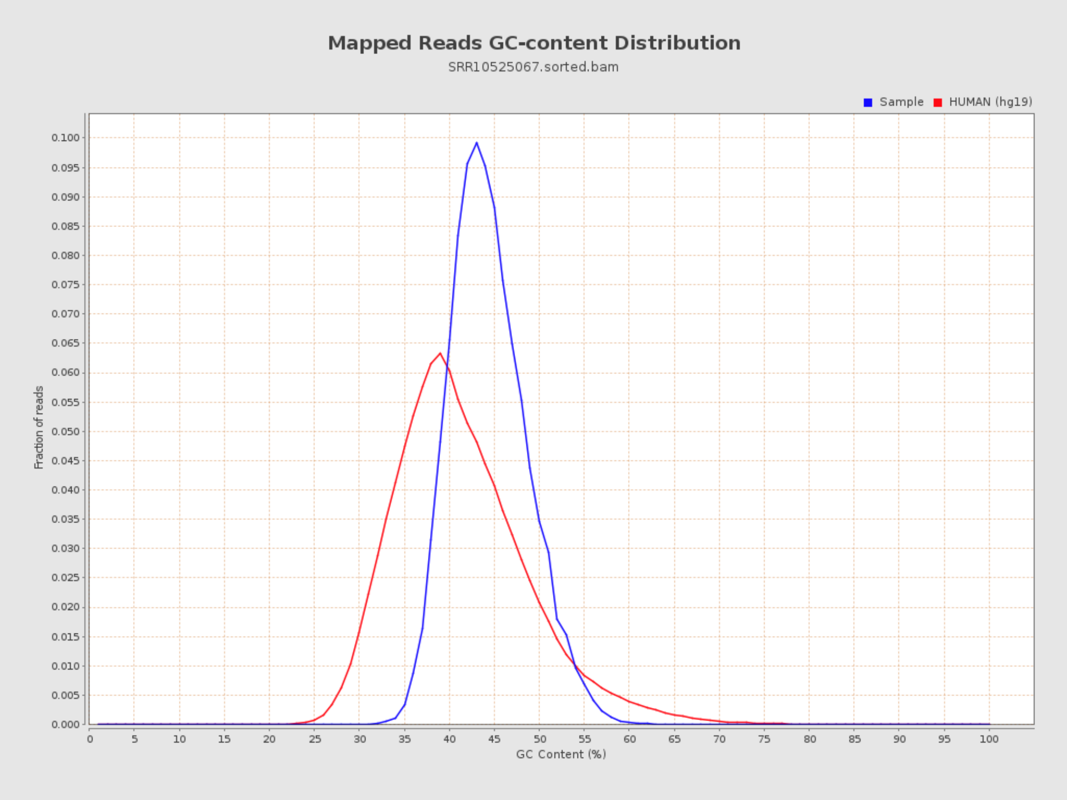
7. Results : Duplication Rate Histogram



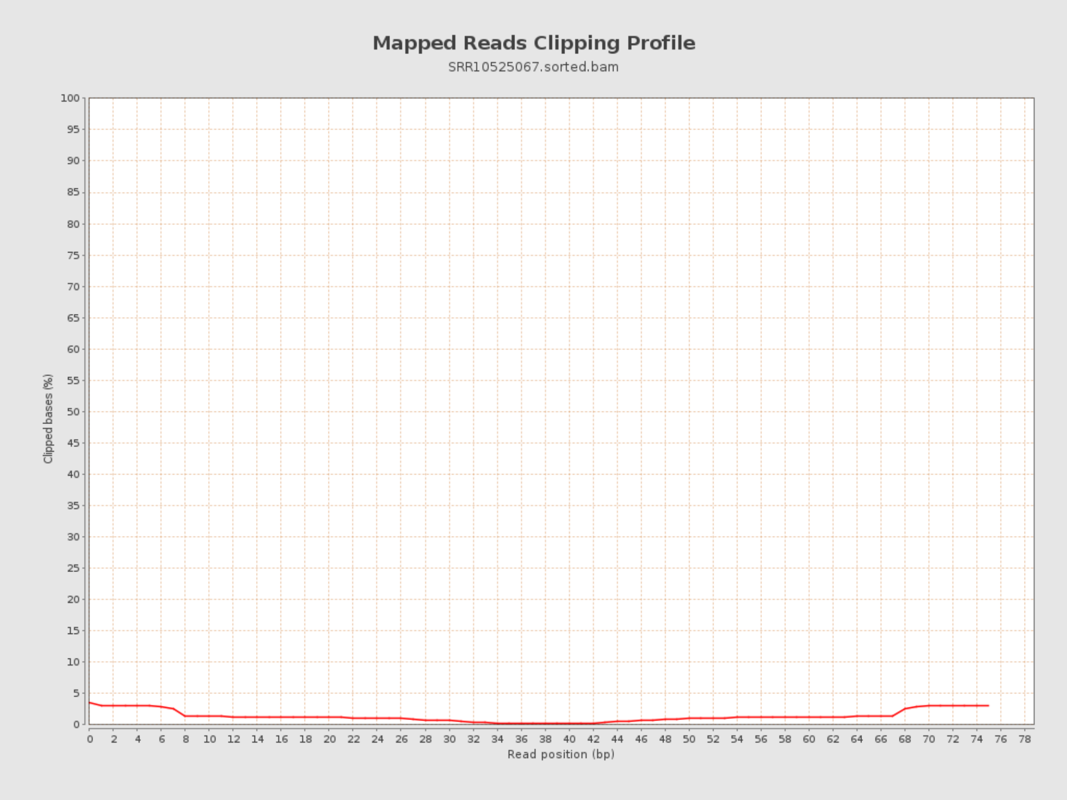
8. Results : Mapped Reads Nucleotide Content



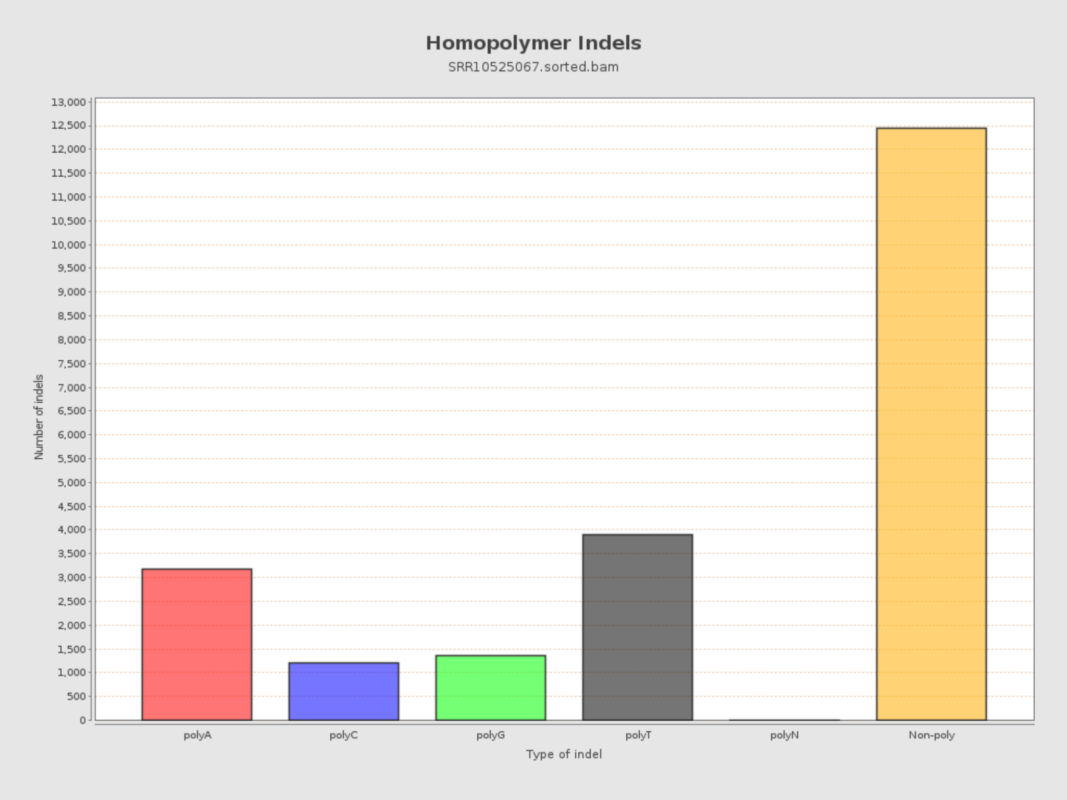
9. Results : Mapped Reads GC-content Distribution



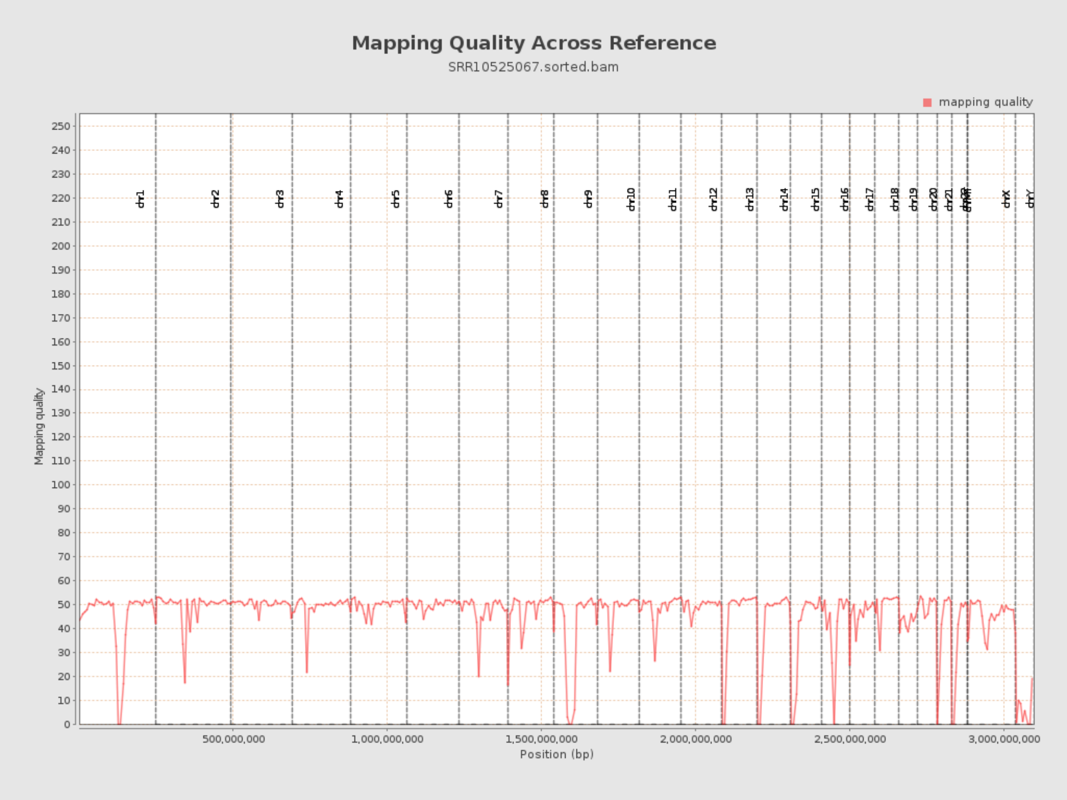
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram