Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 17:32:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524711.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_SRR10524711 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524711.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 17:32:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524711.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,666,737
Mapped reads	3,341,484 / 91.13%
Unmapped reads	325,253 / 8.87%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,222 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	209,712 / 5.72%
Duplication rate	4.57%
Clipped reads	3,346,450 / 91.27%

2.2. ACGT Content

Number/percentage of A's	49,738,362 / 25.72%
Number/percentage of C's	36,634,884 / 18.95%
Number/percentage of T's	61,969,893 / 32.05%
Number/percentage of G's	45,016,943 / 23.28%
Number/percentage of N's	3,879 / 0%
GC Percentage	42.23%

2.3. Coverage

Mean	0.0625

Standard Deviation	0.601

2.4. Mapping Quality

Mean Mapping Quality	45.04

2.5. Mismatches and indels

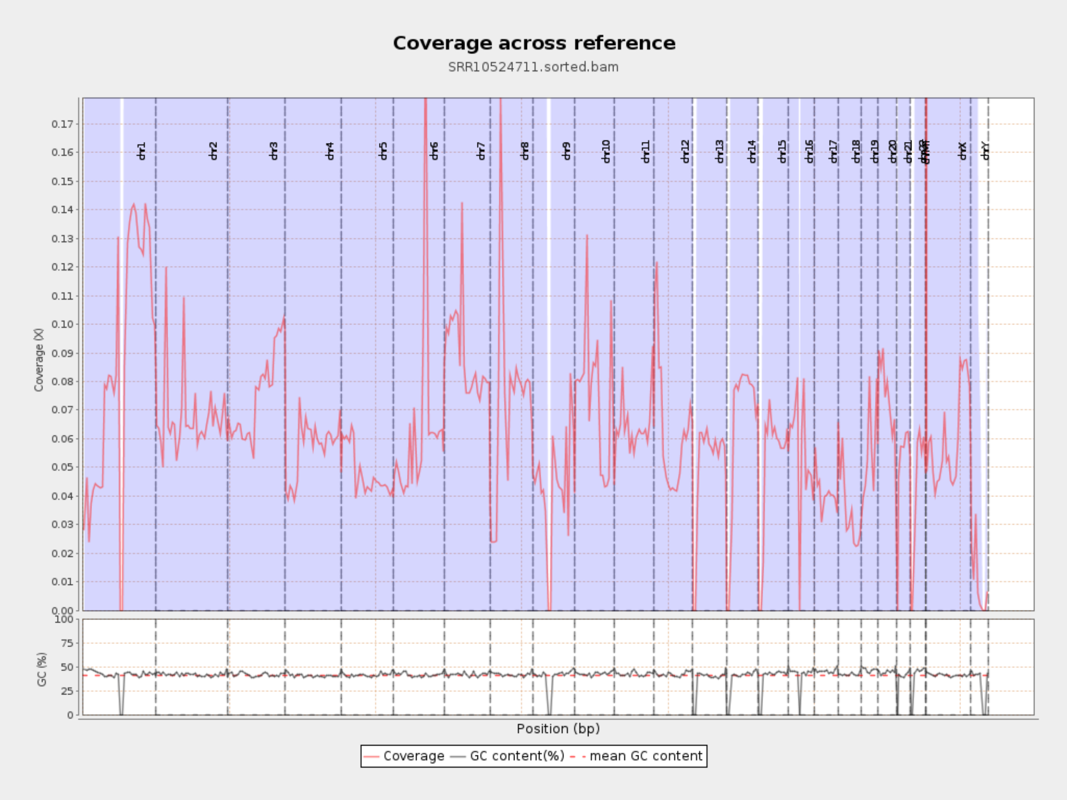
General error rate	0.53%
Mismatches	998,400
Insertions	13,043
Mapped reads with at least one insertion	0.39%
Deletions	40,785
Mapped reads with at least one deletion	1.21%
Homopolymer indels	43.75%

2.6. Chromosome stats

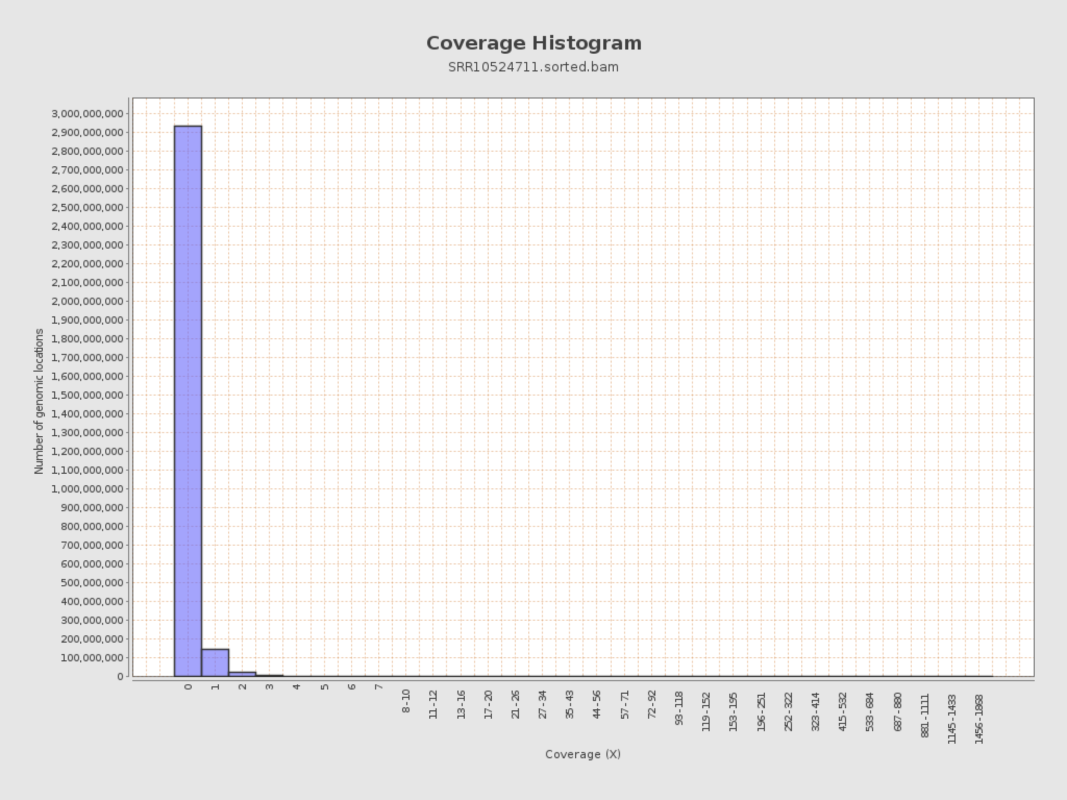
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	21225433	0.0852	1.2219
chr2	243199373	16446662	0.0676	0.8494
chr3	198022430	14828781	0.0749	0.3259
chr4	191154276	10936797	0.0572	0.3144
chr5	180915260	8699186	0.0481	0.2598
chr6	171115067	10846042	0.0634	0.3657
chr7	159138663	14208385	0.0893	1.0469

chr8	146364022	11097805	0.0758	0.5993
chr9	141213431	6109324	0.0433	0.3963
chr10	135534747	10203444	0.0753	0.5686
chr11	135006516	8707625	0.0645	0.4279
chr12	133851895	8486211	0.0634	0.3056
chr13	115169878	5860362	0.0509	0.2752
chr14	107349540	7009076	0.0653	0.3098
chr15	102531392	5094966	0.0497	0.2705
chr16	90354753	4920042	0.0545	0.3277
chr17	81195210	3360286	0.0414	0.2562
chr18	78077248	2765875	0.0354	0.8207
chr19	59128983	3277727	0.0554	0.7513
chr20	63025520	4736033	0.0751	0.3255
chr21	48129895	2479923	0.0515	0.3005
chr22	51304566	2105544	0.041	0.2325
chrMT	16571	135612	8.1837	5.4404
chrX	155270560	9317755	0.06	0.3357
chrY	59373566	570322	0.0096	0.263

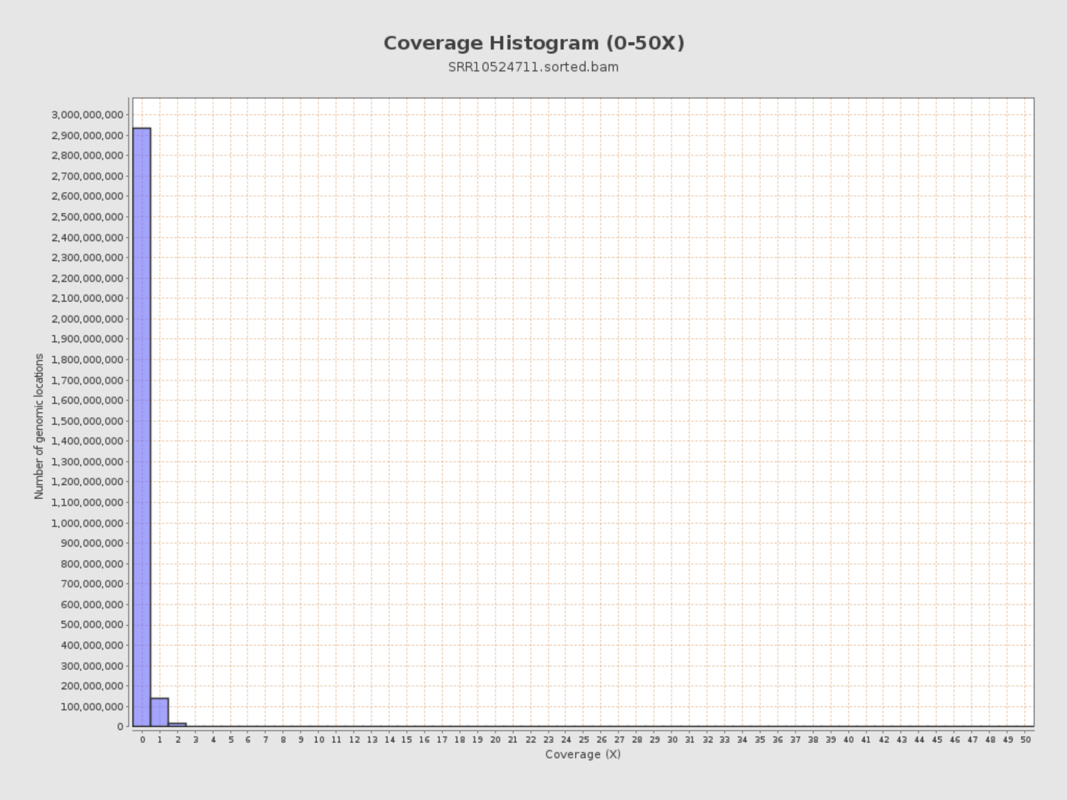
3. Results : Coverage across reference



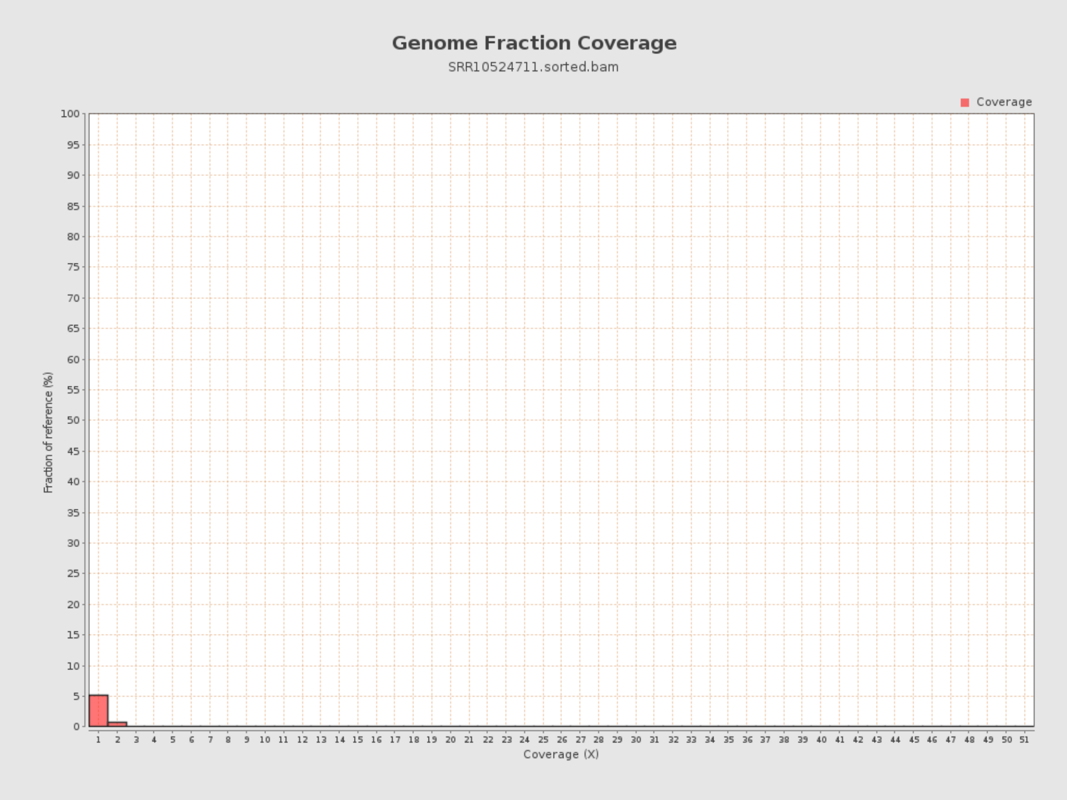
4. Results : Coverage Histogram



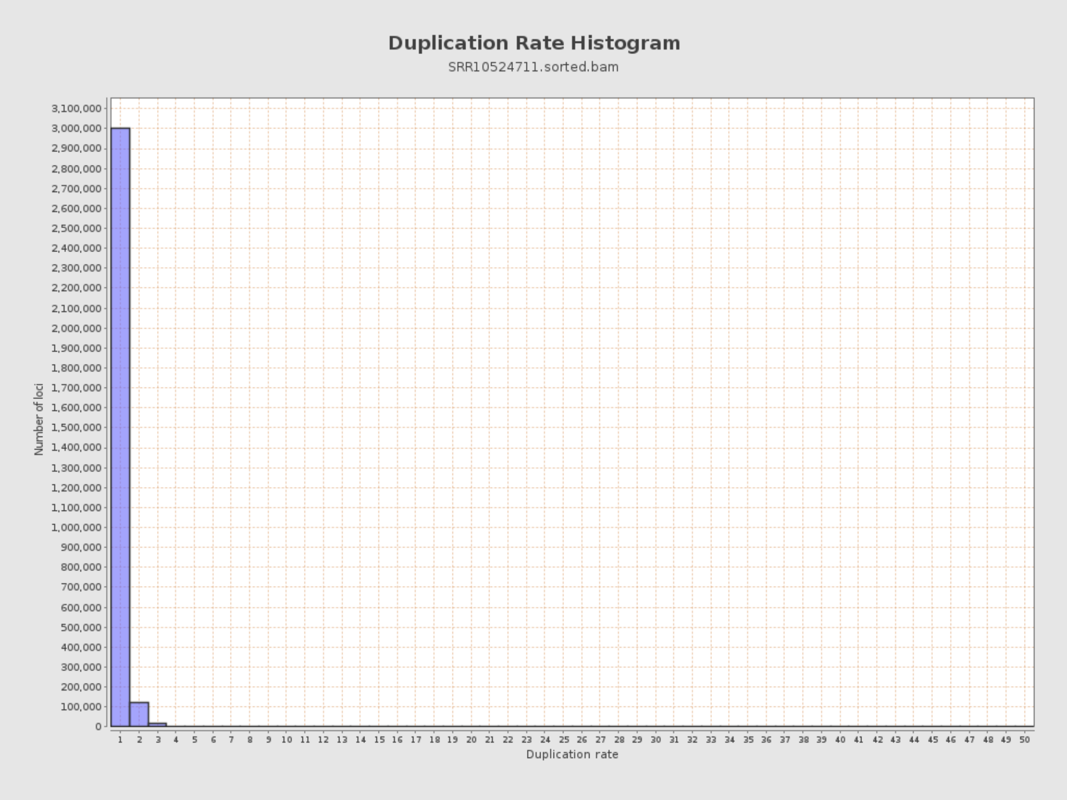
5. Results : Coverage Histogram (0-50X)



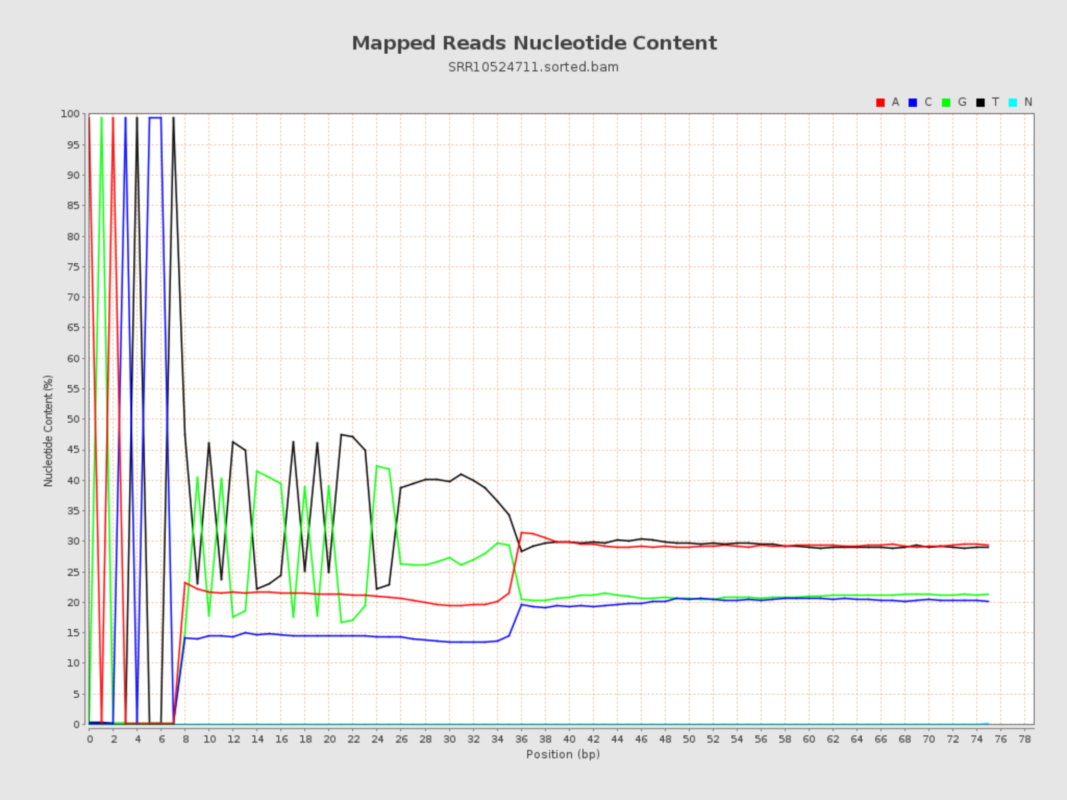
6. Results : Genome Fraction Coverage



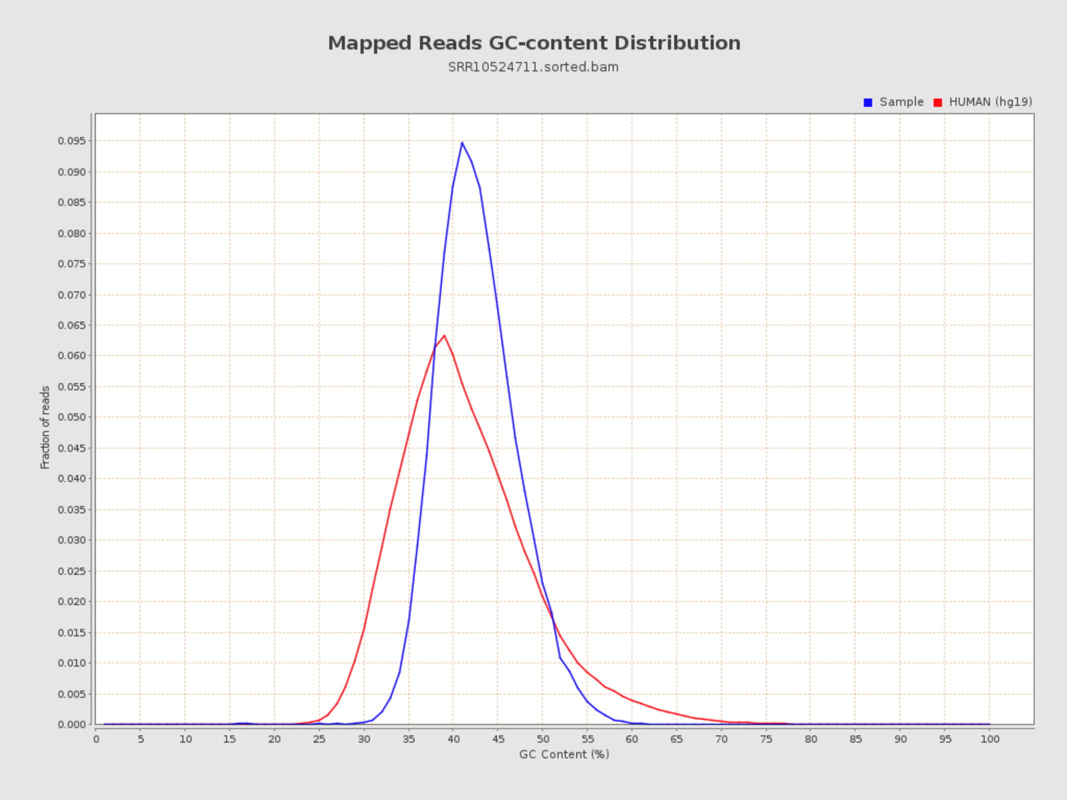
7. Results : Duplication Rate Histogram



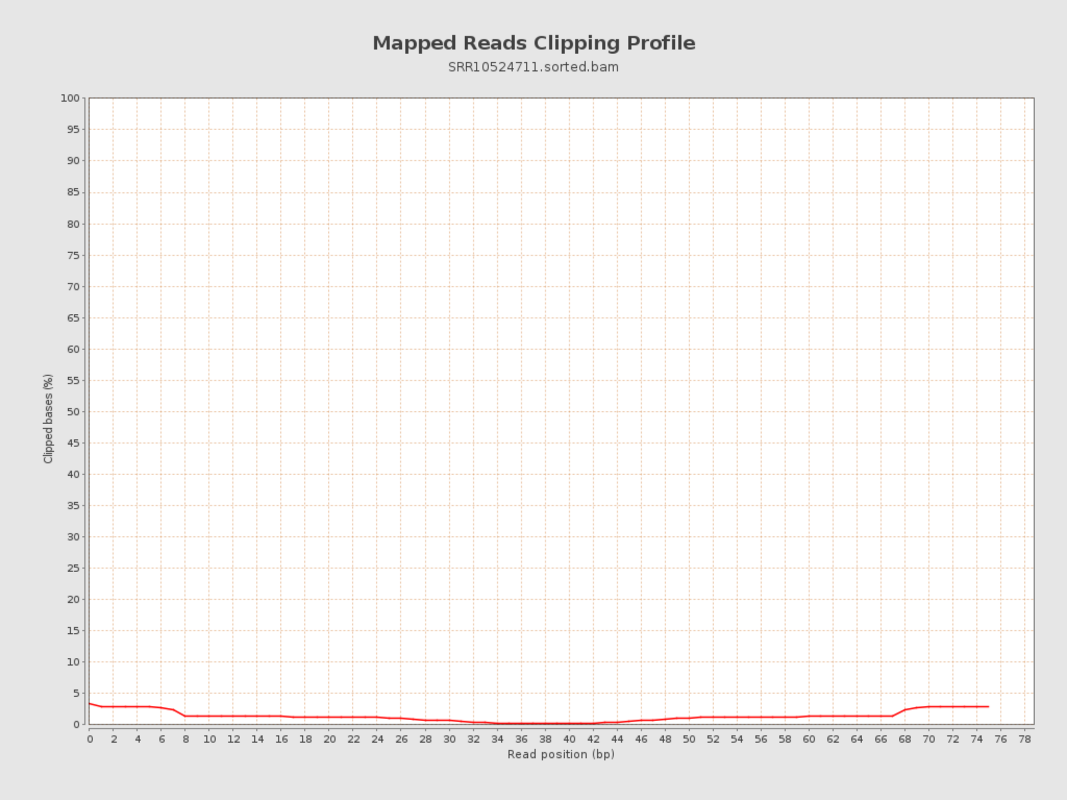
8. Results : Mapped Reads Nucleotide Content



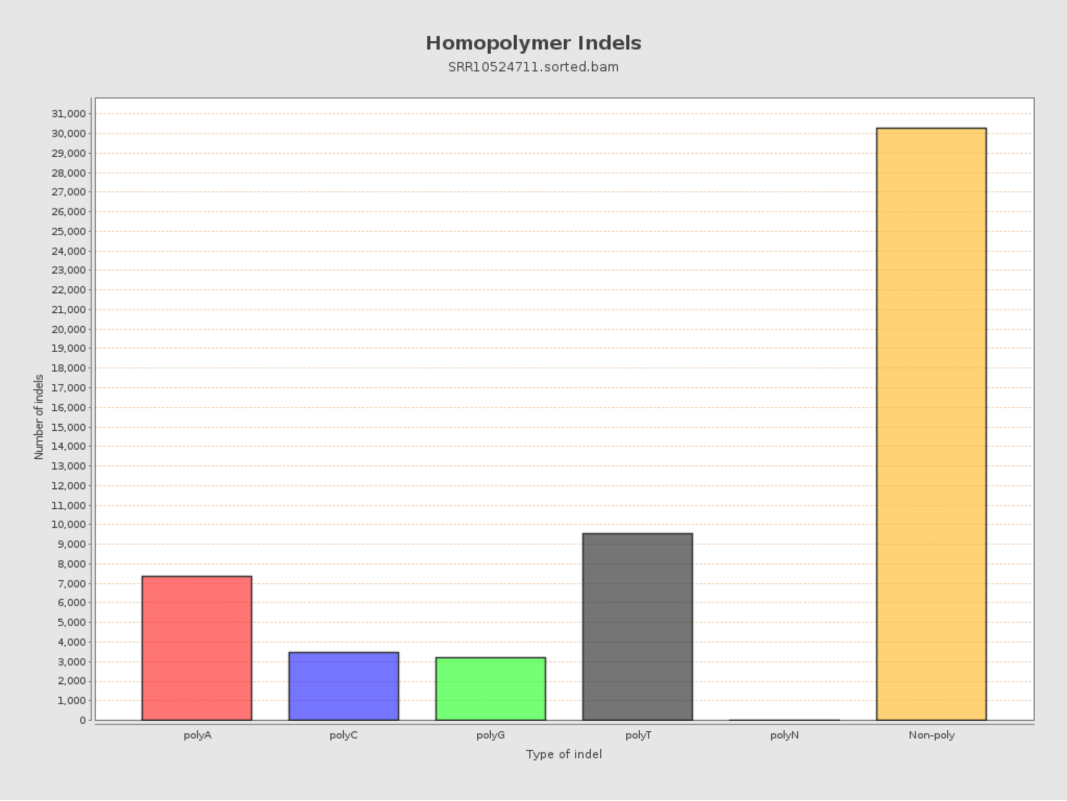
9. Results : Mapped Reads GC-content Distribution



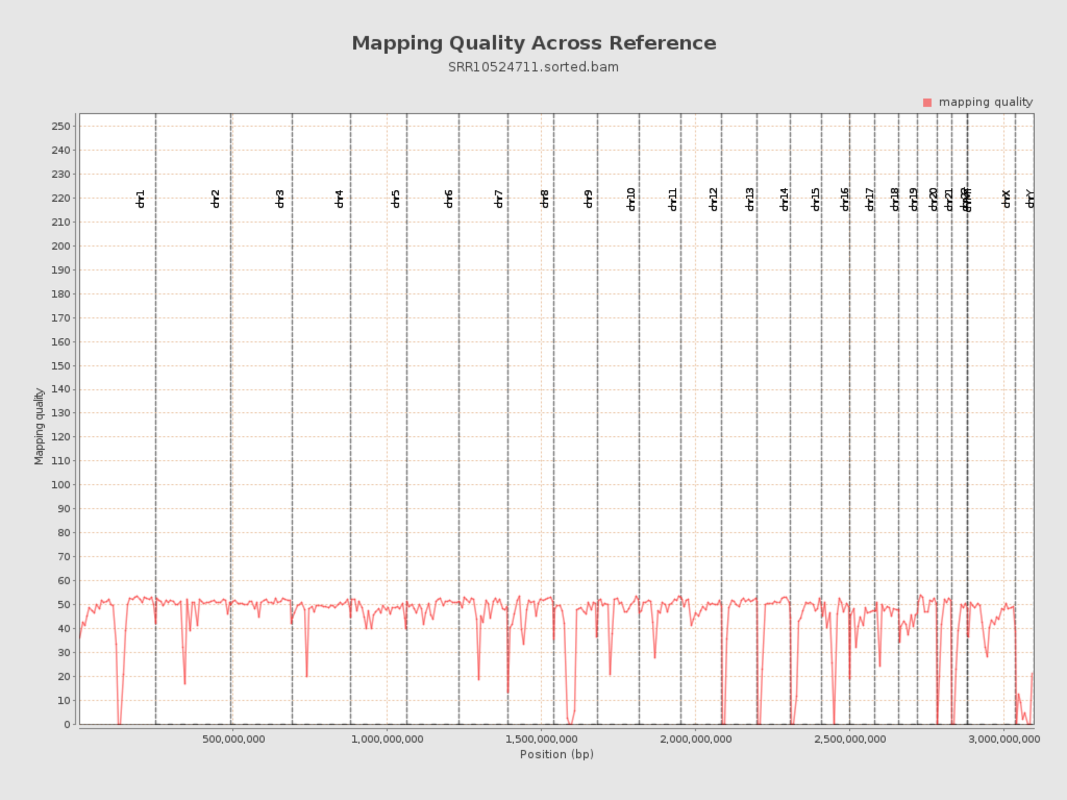
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram