Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 18:00:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524727.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_SRR10524727 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524727.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 18:00:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524727.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,558,702
Mapped reads	1,417,856 / 90.96%
Unmapped reads	140,846 / 9.04%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,152 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	56,136 / 3.6%
Duplication rate	3.02%
Clipped reads	1,418,889 / 91.03%

2.2. ACGT Content

Number/percentage of A's	18,729,592 / 23.23%
Number/percentage of C's	14,007,749 / 17.37%
Number/percentage of T's	27,039,451 / 33.54%
Number/percentage of G's	20,839,871 / 25.85%
Number/percentage of N's	10,509 / 0.01%
GC Percentage	43.22%

2.3. Coverage

Mean	0.0261

Standard Deviation	0.2379

2.4. Mapping Quality

Mean Mapping Quality	44.54

2.5. Mismatches and indels

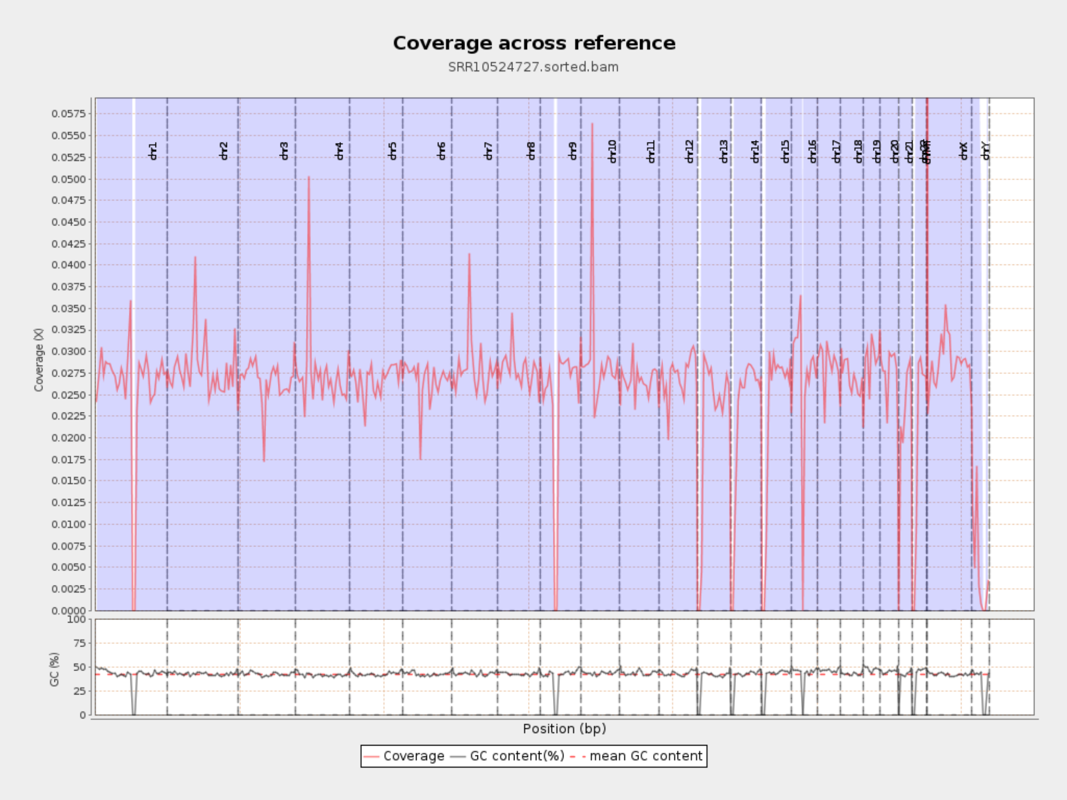
General error rate	0.53%
Mismatches	413,688
Insertions	5,815
Mapped reads with at least one insertion	0.41%
Deletions	16,373
Mapped reads with at least one deletion	1.15%
Homopolymer indels	43.1%

2.6. Chromosome stats

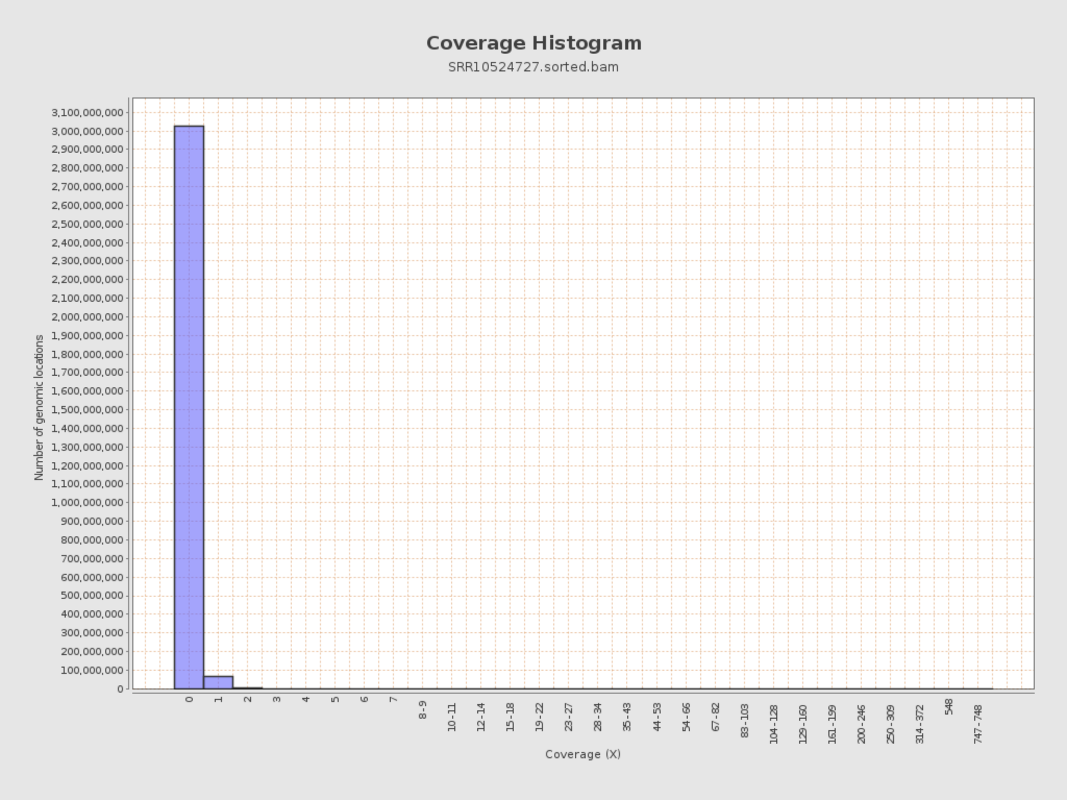
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6418807	0.0258	0.3294
chr2	243199373	6827516	0.0281	0.3672
chr3	198022430	5250938	0.0265	0.1808
chr4	191154276	5261111	0.0275	0.2082
chr5	180915260	4856096	0.0268	0.1796
chr6	171115067	4554715	0.0266	0.1941
chr7	159138663	4468670	0.0281	0.286

chr8	146364022	4086641	0.0279	0.221
chr9	141213431	3435514	0.0243	0.2053
chr10	135534747	3938580	0.0291	0.2849
chr11	135006516	3614595	0.0268	0.2131
chr12	133851895	3627509	0.0271	0.1824
chr13	115169878	2499359	0.0217	0.1624
chr14	107349540	2392754	0.0223	0.1701
chr15	102531392	2318723	0.0226	0.1658
chr16	90354753	2405498	0.0266	0.1965
chr17	81195210	2307707	0.0284	0.1929
chr18	78077248	2102587	0.0269	0.3191
chr19	59128983	1716148	0.029	0.2773
chr20	63025520	1736817	0.0276	0.1881
chr21	48129895	1058286	0.022	0.1847
chr22	51304566	994277	0.0194	0.1544
chrMT	16571	25018	1.5097	1.594
chrX	155270560	4470880	0.0288	0.2029
chrY	59373566	284905	0.0048	0.1354

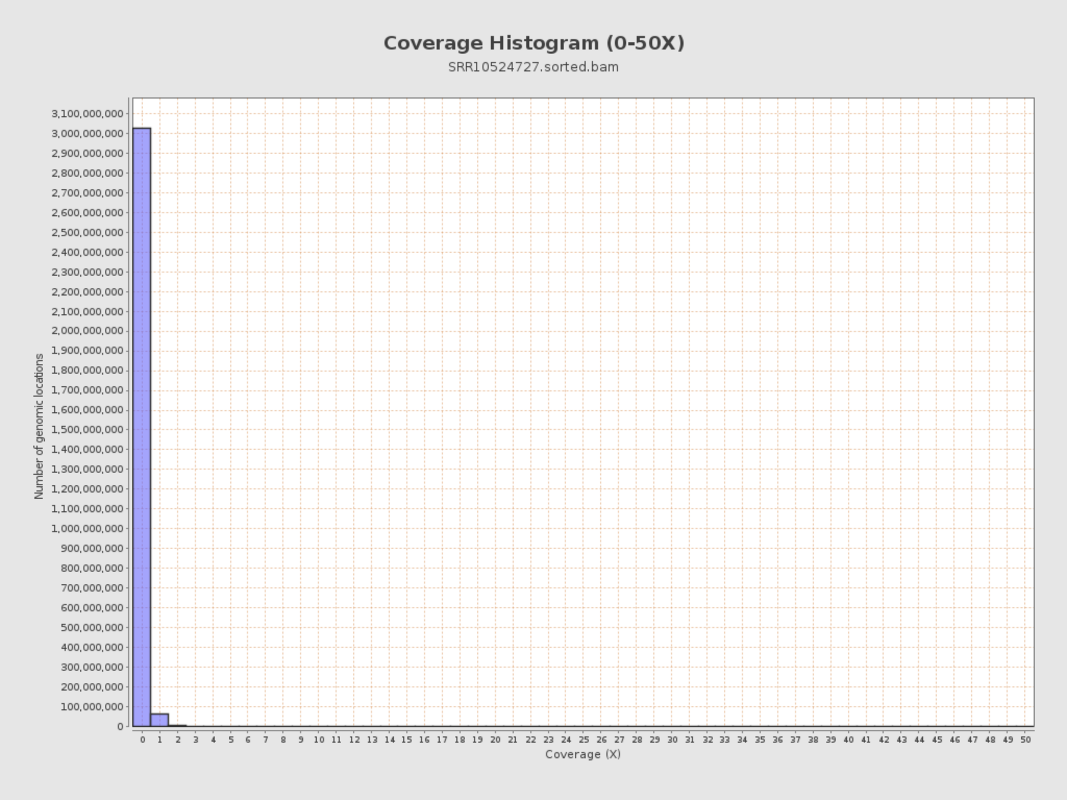
3. Results : Coverage across reference



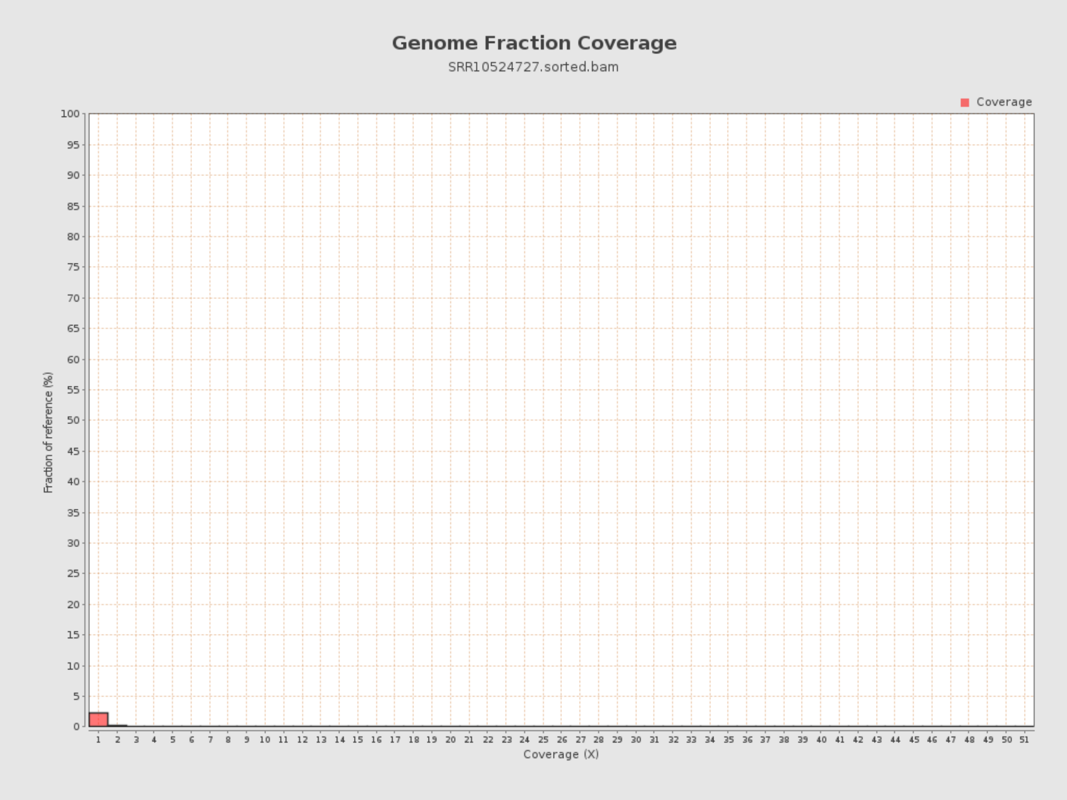
4. Results : Coverage Histogram



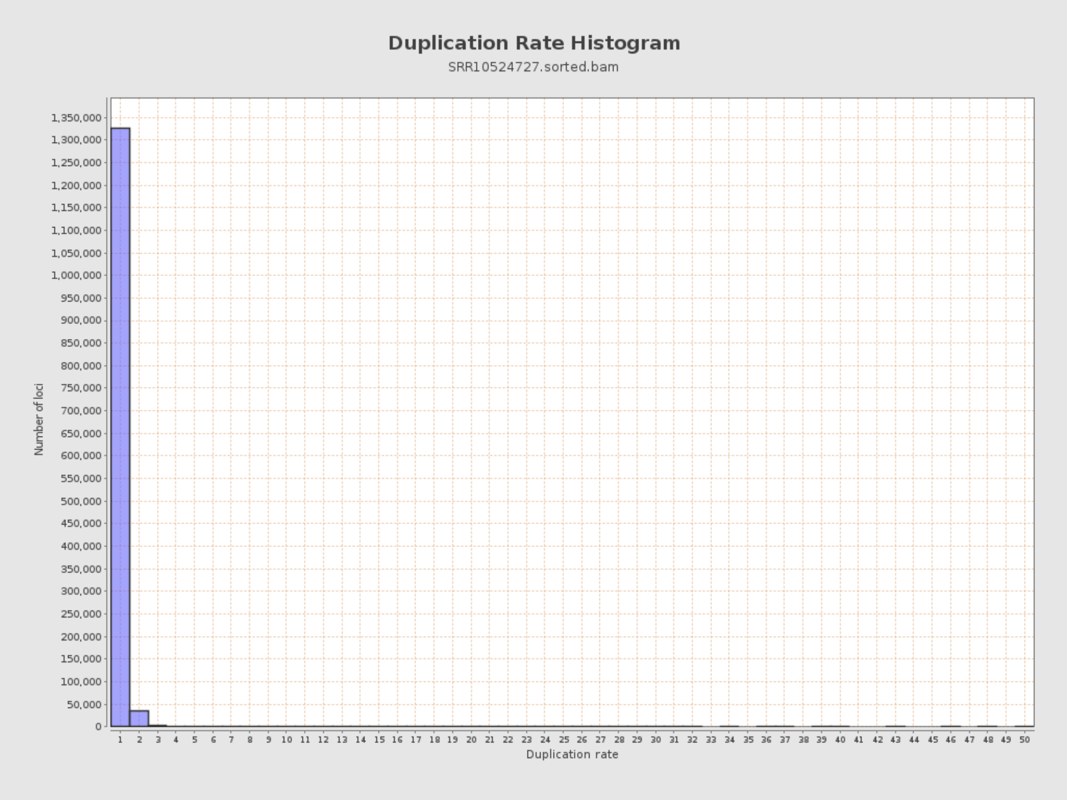
5. Results : Coverage Histogram (0-50X)



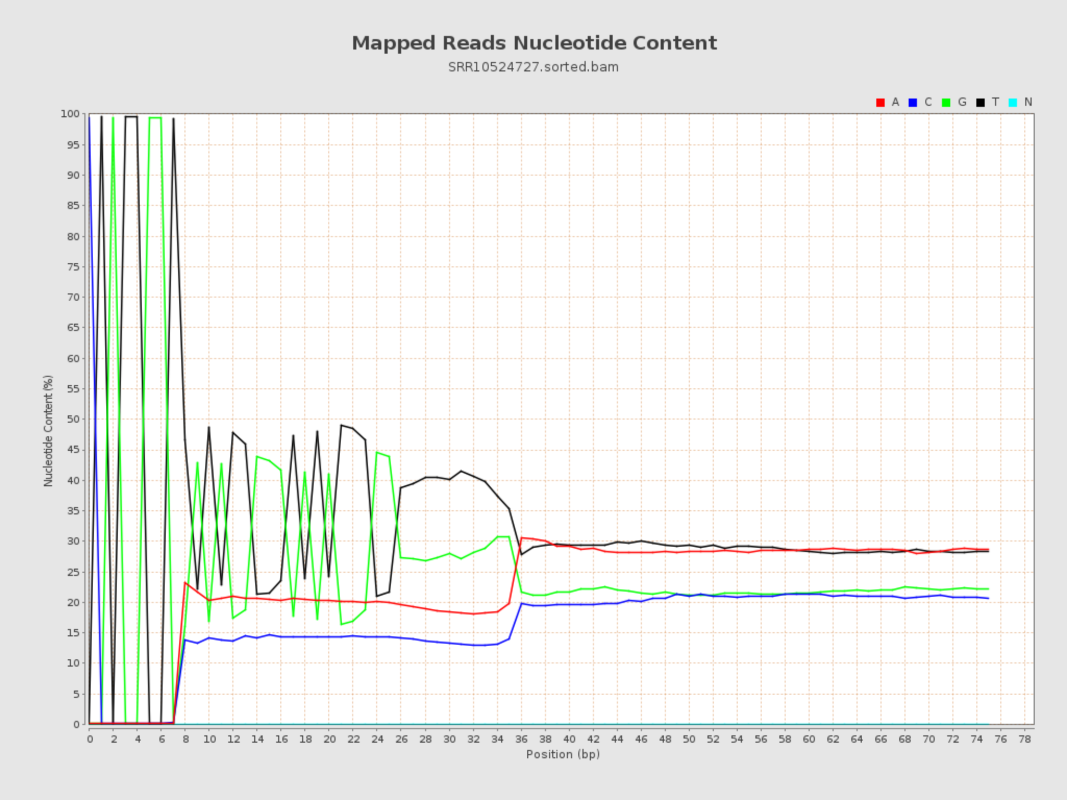
6. Results : Genome Fraction Coverage



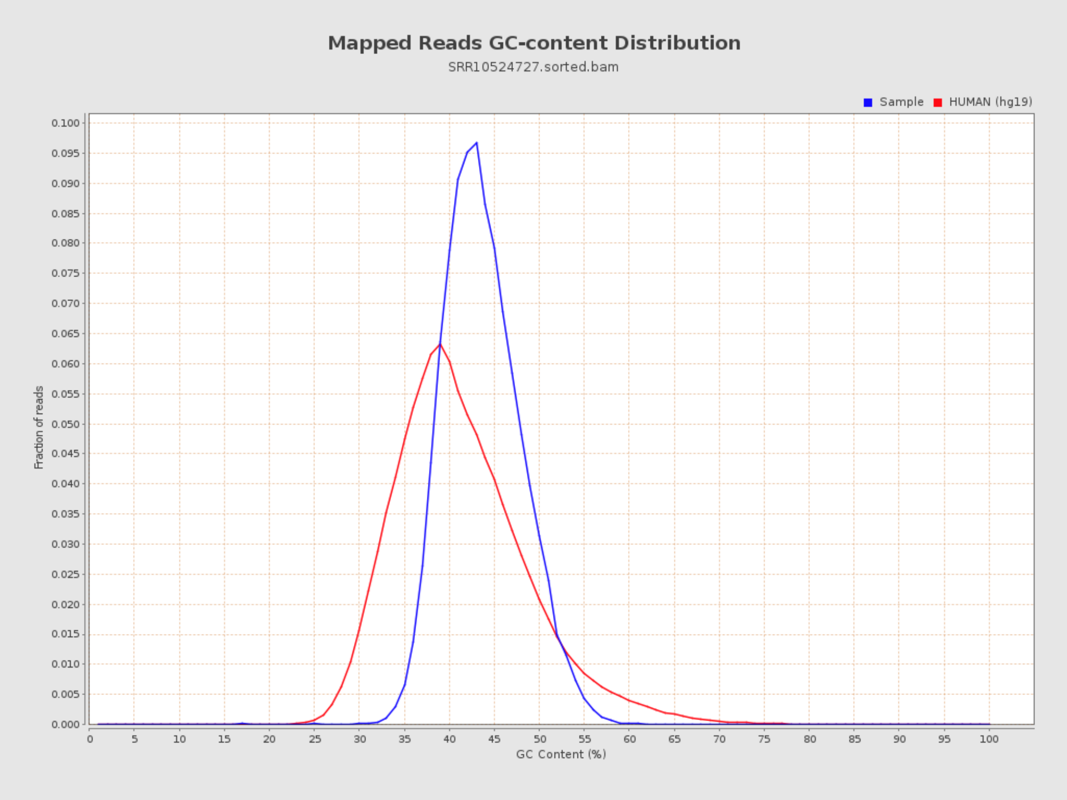
7. Results : Duplication Rate Histogram



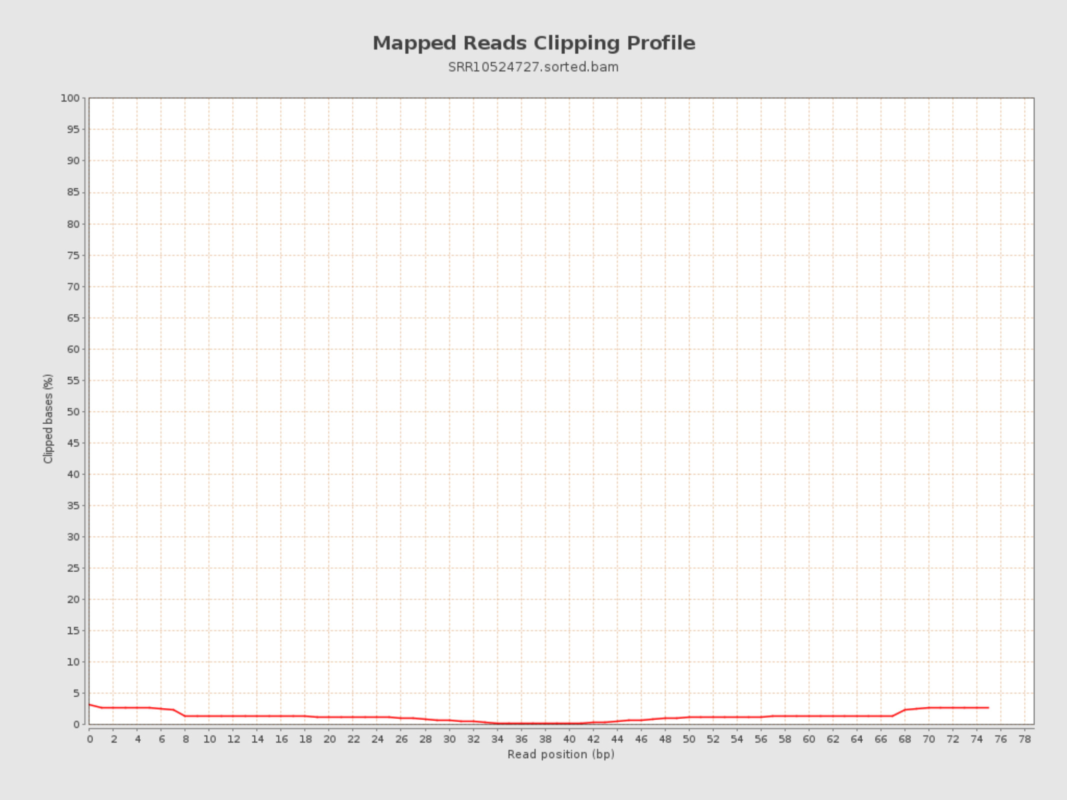
8. Results : Mapped Reads Nucleotide Content



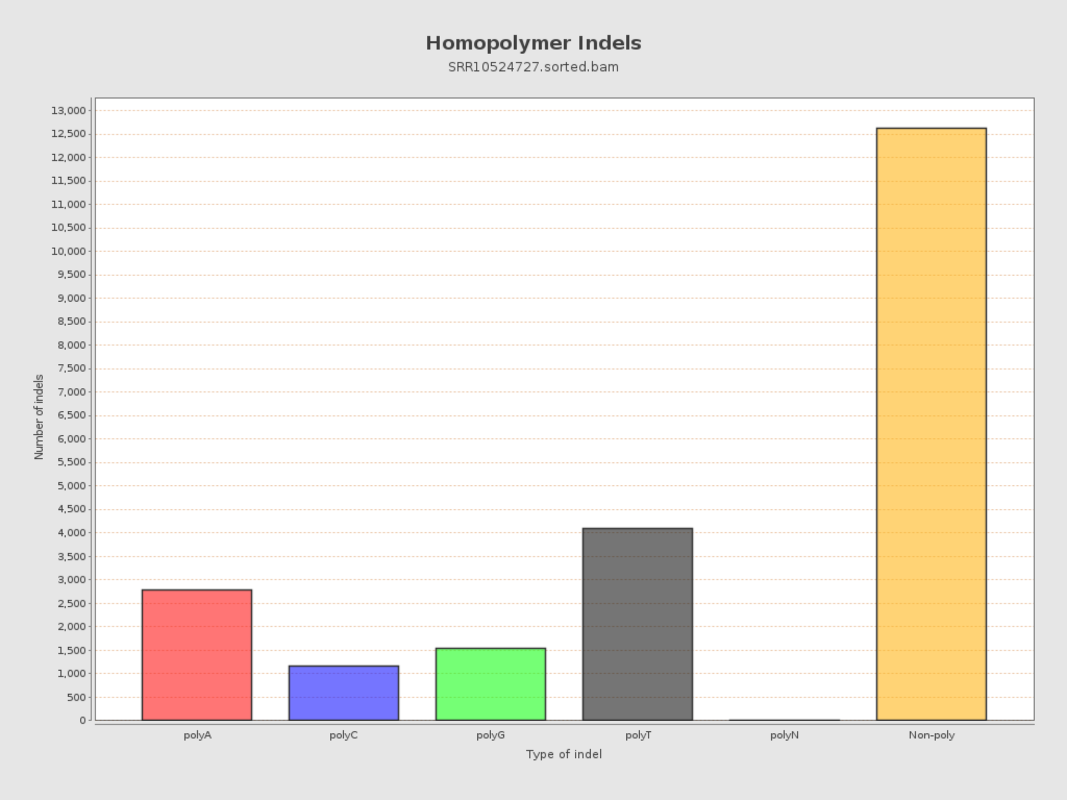
9. Results : Mapped Reads GC-content Distribution



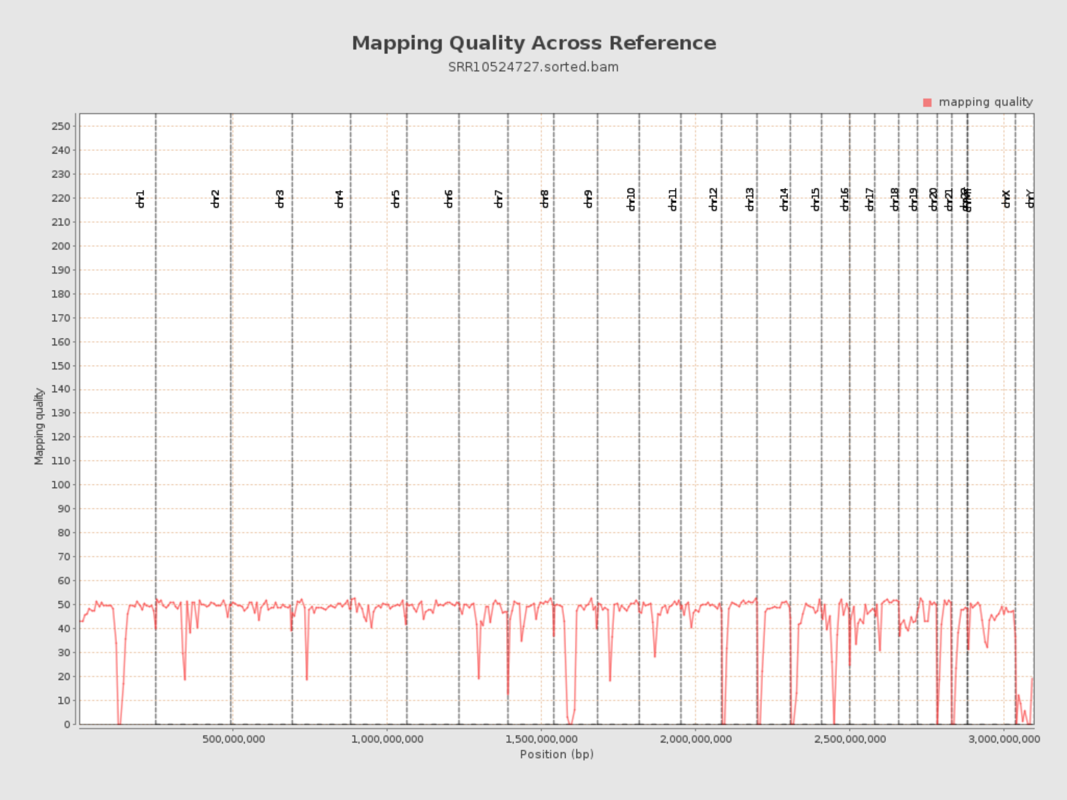
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram