Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 22:10:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524313.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_SRR10524313 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524313.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 22:10:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524313.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	679,842
Mapped reads	621,244 / 91.38%
Unmapped reads	58,598 / 8.62%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,737 / 0.4%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	10,871 / 1.6%
Duplication rate	1.18%
Clipped reads	622,039 / 91.5%

2.2. ACGT Content

Number/percentage of A's	8,555,644 / 23.66%
Number/percentage of C's	6,862,981 / 18.98%
Number/percentage of T's	11,534,820 / 31.9%
Number/percentage of G's	9,200,930 / 25.45%
Number/percentage of N's	4,431 / 0.01%
GC Percentage	44.43%

2.3. Coverage

Mean	0.0117

Standard Deviation	0.1397

2.4. Mapping Quality

Mean Mapping Quality	43.63

2.5. Mismatches and indels

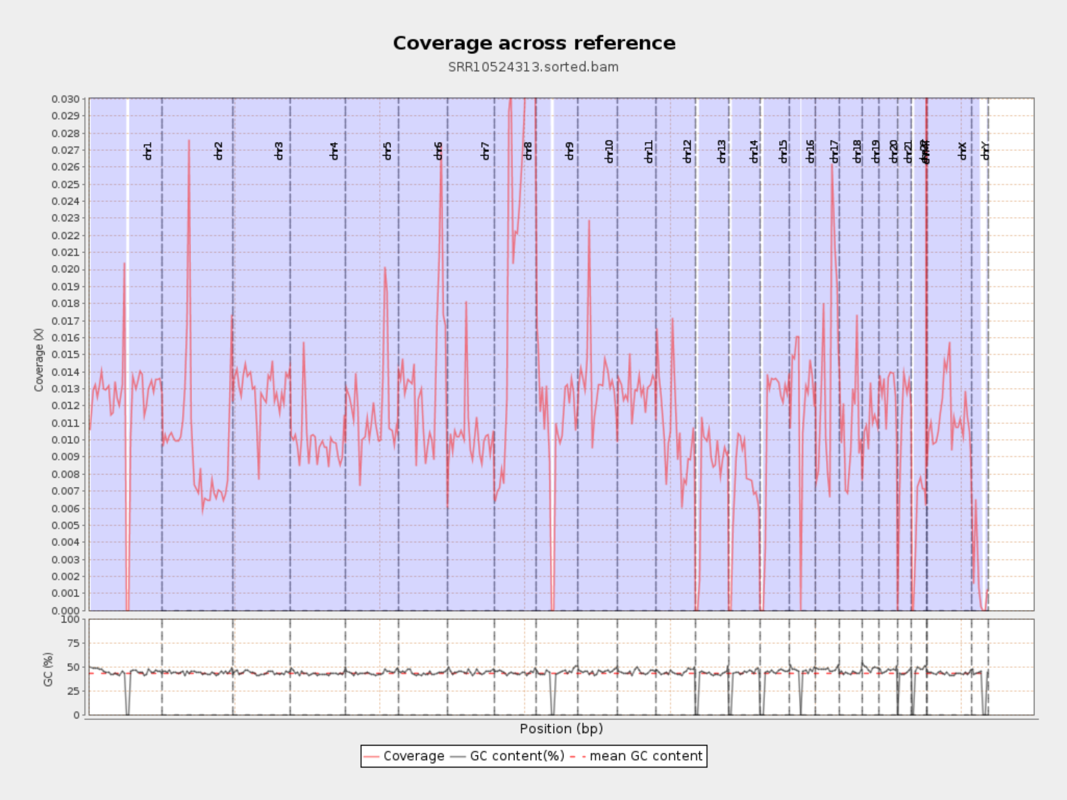
General error rate	0.52%
Mismatches	184,171
Insertions	2,373
Mapped reads with at least one insertion	0.38%
Deletions	5,955
Mapped reads with at least one deletion	0.95%
Homopolymer indels	42.17%

2.6. Chromosome stats

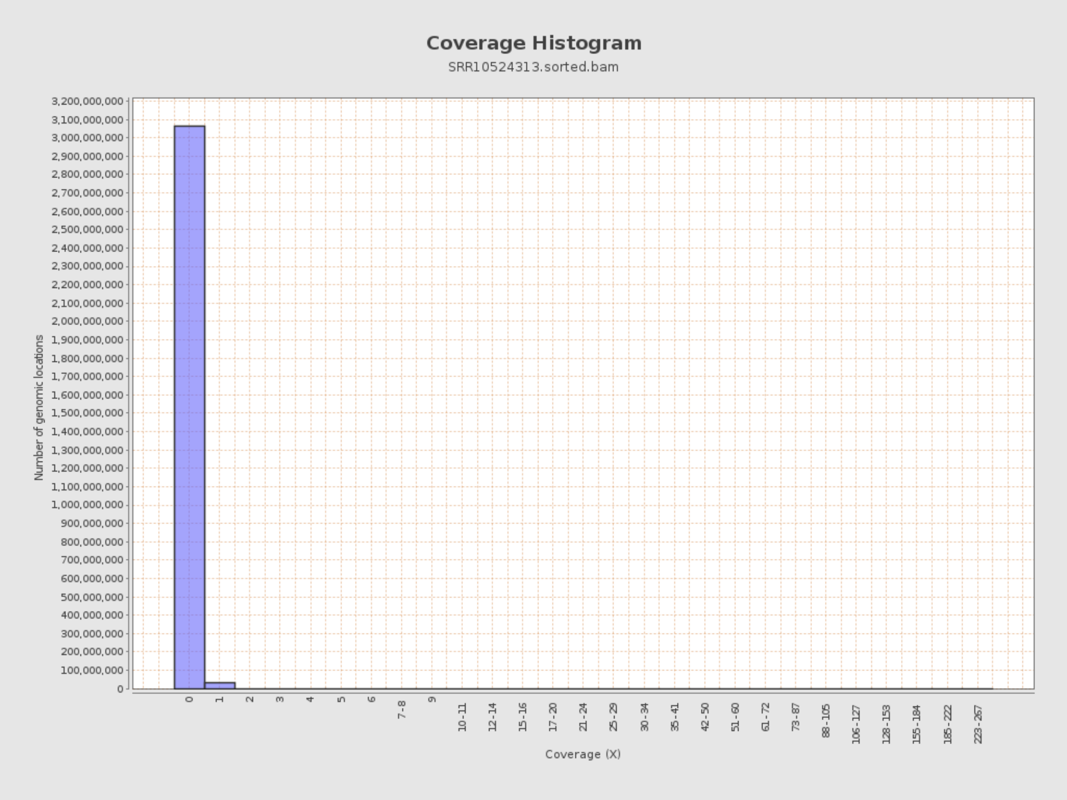
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3055672	0.0123	0.2327
chr2	243199373	2342964	0.0096	0.1535
chr3	198022430	2554661	0.0129	0.1172
chr4	191154276	1892732	0.0099	0.1071
chr5	180915260	2133307	0.0118	0.1123
chr6	171115067	2315731	0.0135	0.1253
chr7	159138663	1648459	0.0104	0.156

chr8	146364022	3755543	0.0257	0.1879
chr9	141213431	1497510	0.0106	0.119
chr10	135534747	1843957	0.0136	0.1421
chr11	135006516	1742716	0.0129	0.1314
chr12	133851895	1411770	0.0105	0.1068
chr13	115169878	910377	0.0079	0.0916
chr14	107349540	757856	0.0071	0.0887
chr15	102531392	1087369	0.0106	0.1073
chr16	90354753	1129560	0.0125	0.1197
chr17	81195210	1130192	0.0139	0.1277
chr18	78077248	849365	0.0109	0.1765
chr19	59128983	647615	0.011	0.1623
chr20	63025520	814243	0.0129	0.1181
chr21	48129895	511451	0.0106	0.1113
chr22	51304566	263634	0.0051	0.0742
chrMT	16571	1634	0.0986	0.3049
chrX	155270560	1763143	0.0114	0.1146
chrY	59373566	107005	0.0018	0.0615

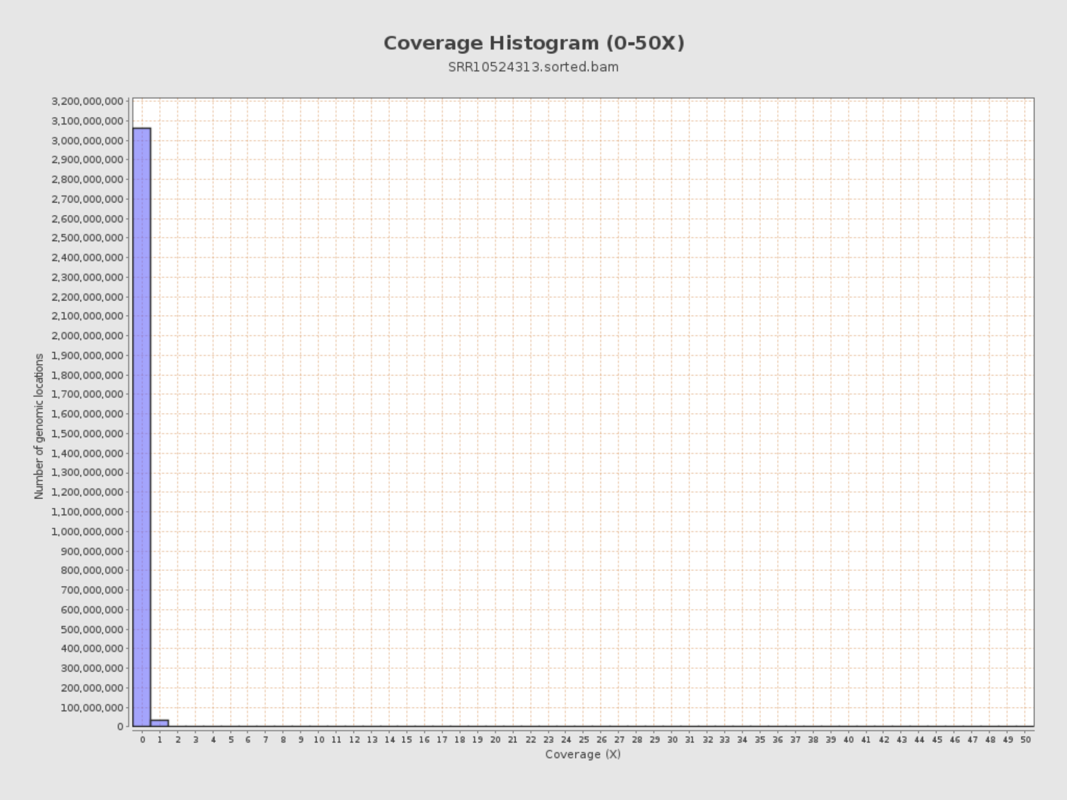
3. Results : Coverage across reference



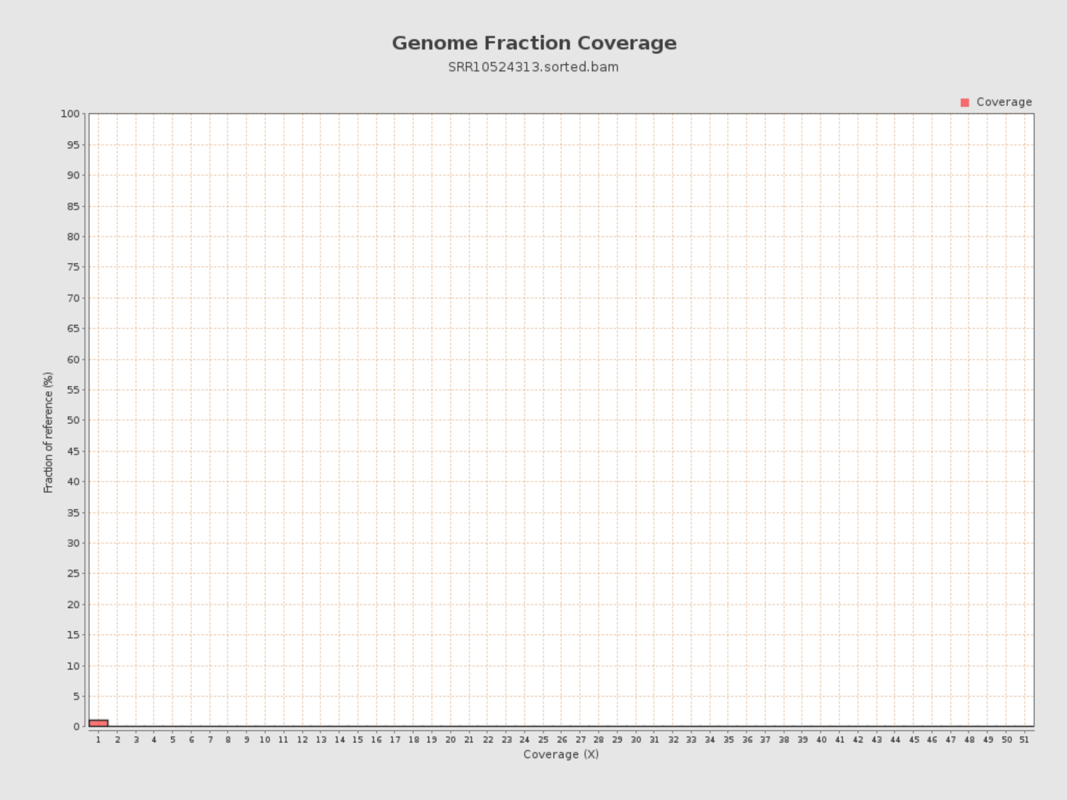
4. Results : Coverage Histogram



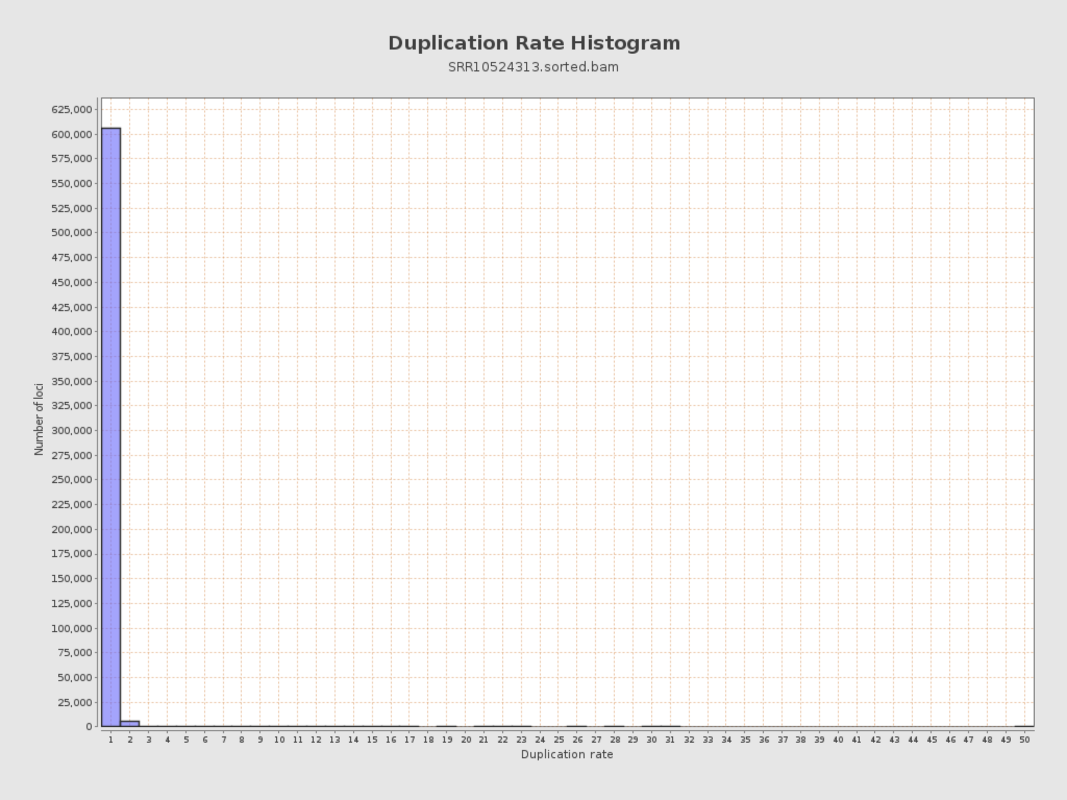
5. Results : Coverage Histogram (0-50X)



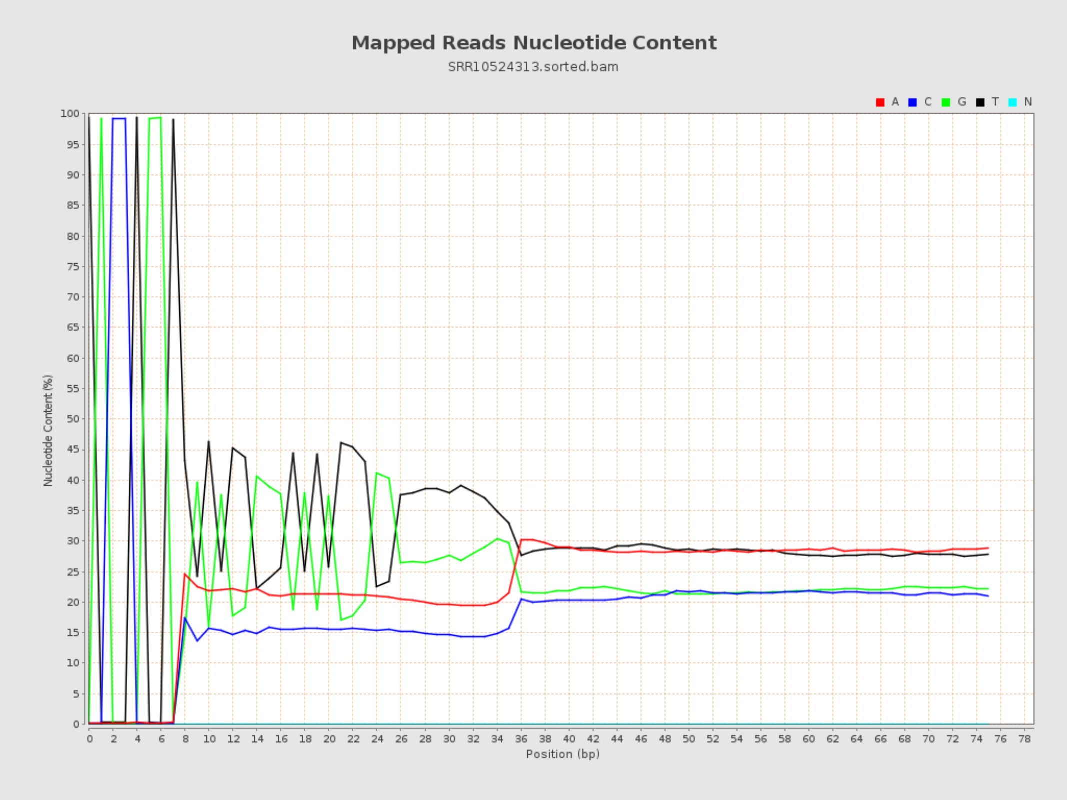
6. Results : Genome Fraction Coverage



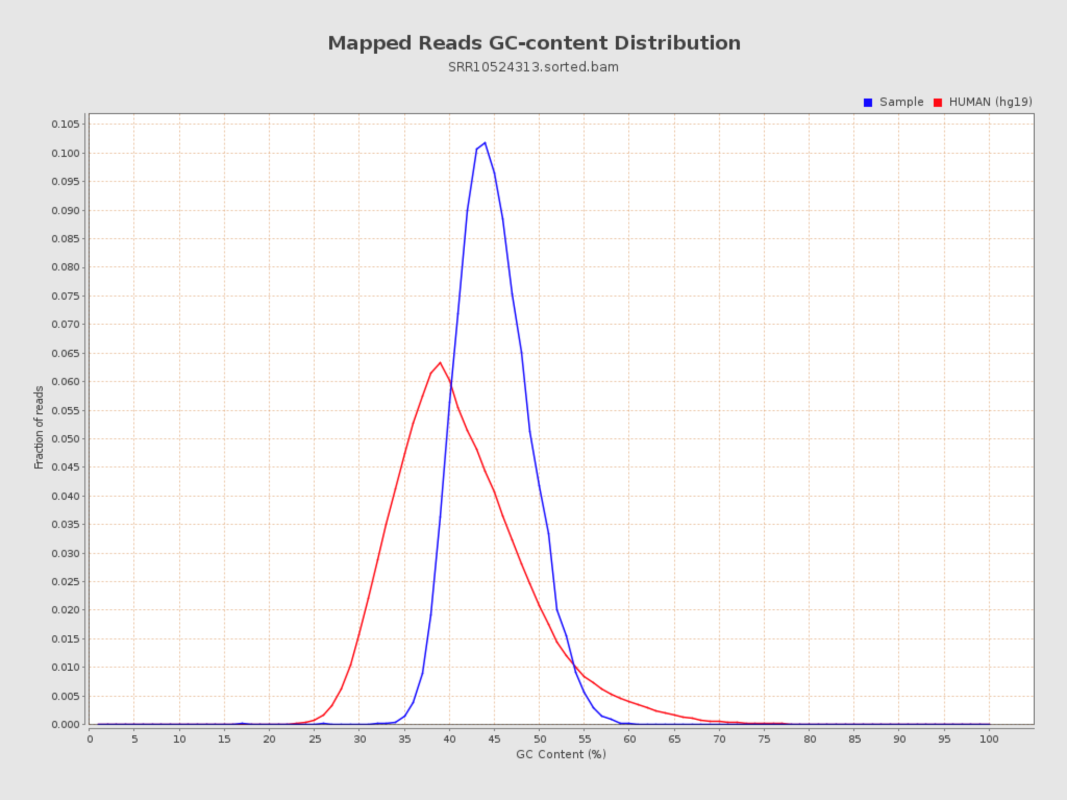
7. Results : Duplication Rate Histogram



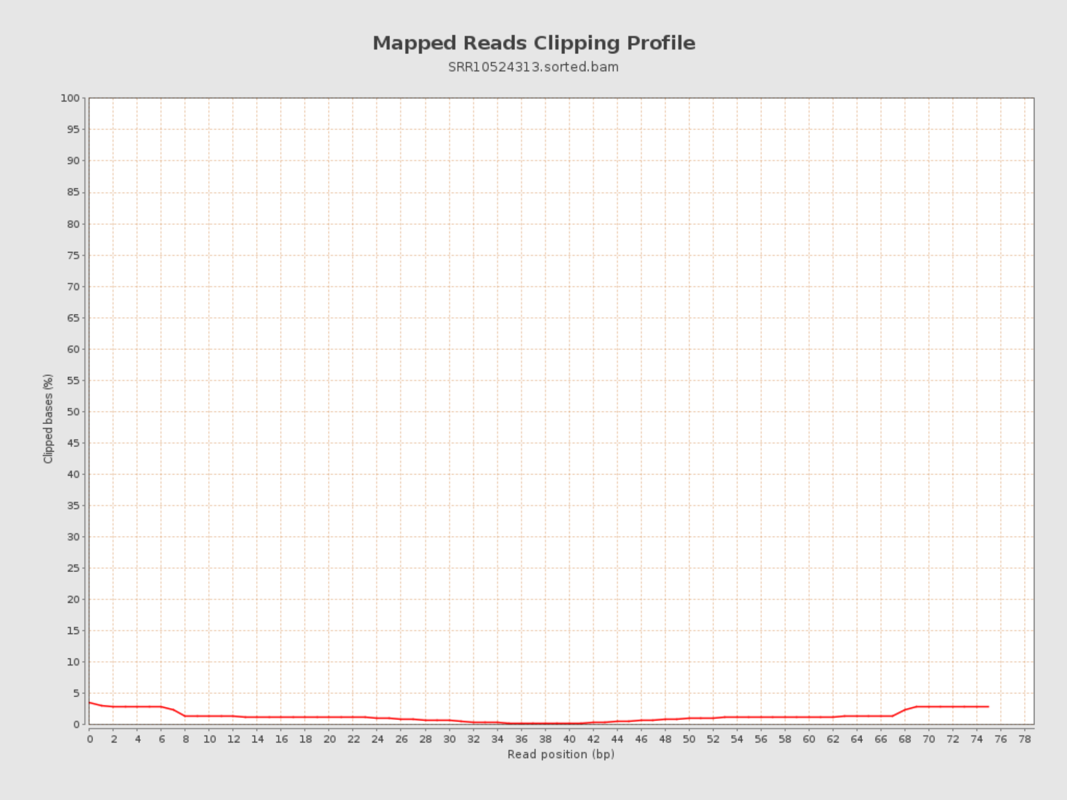
8. Results : Mapped Reads Nucleotide Content



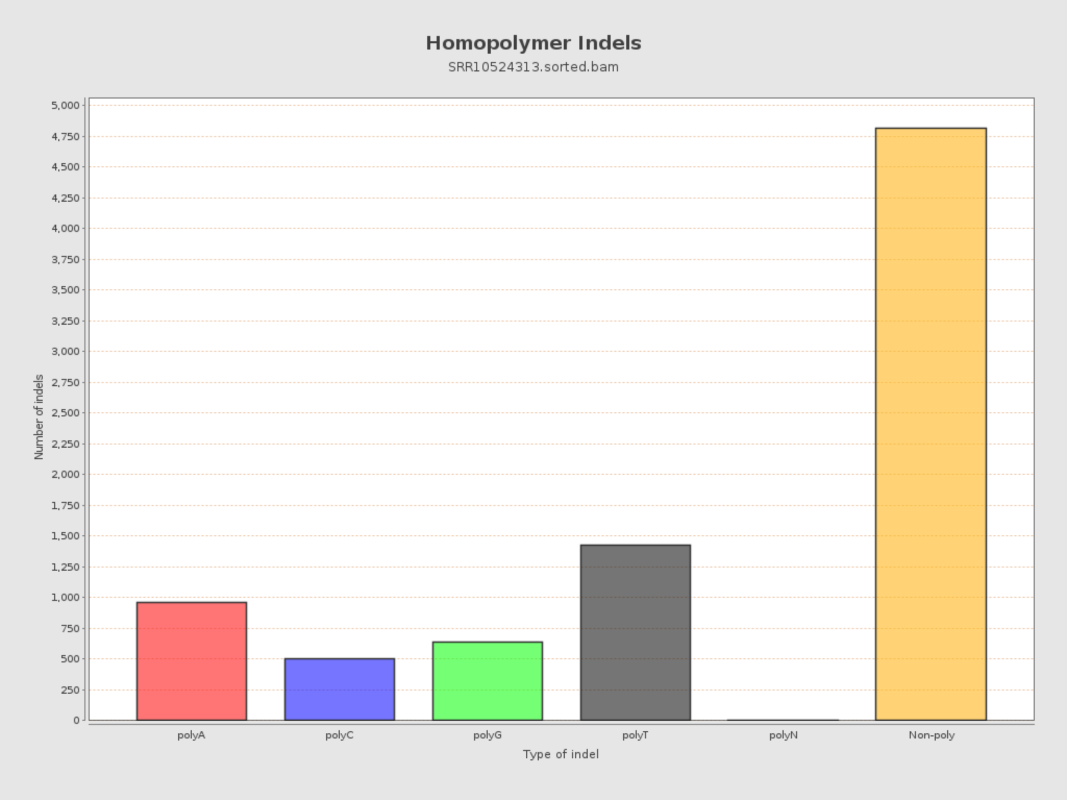
9. Results : Mapped Reads GC-content Distribution



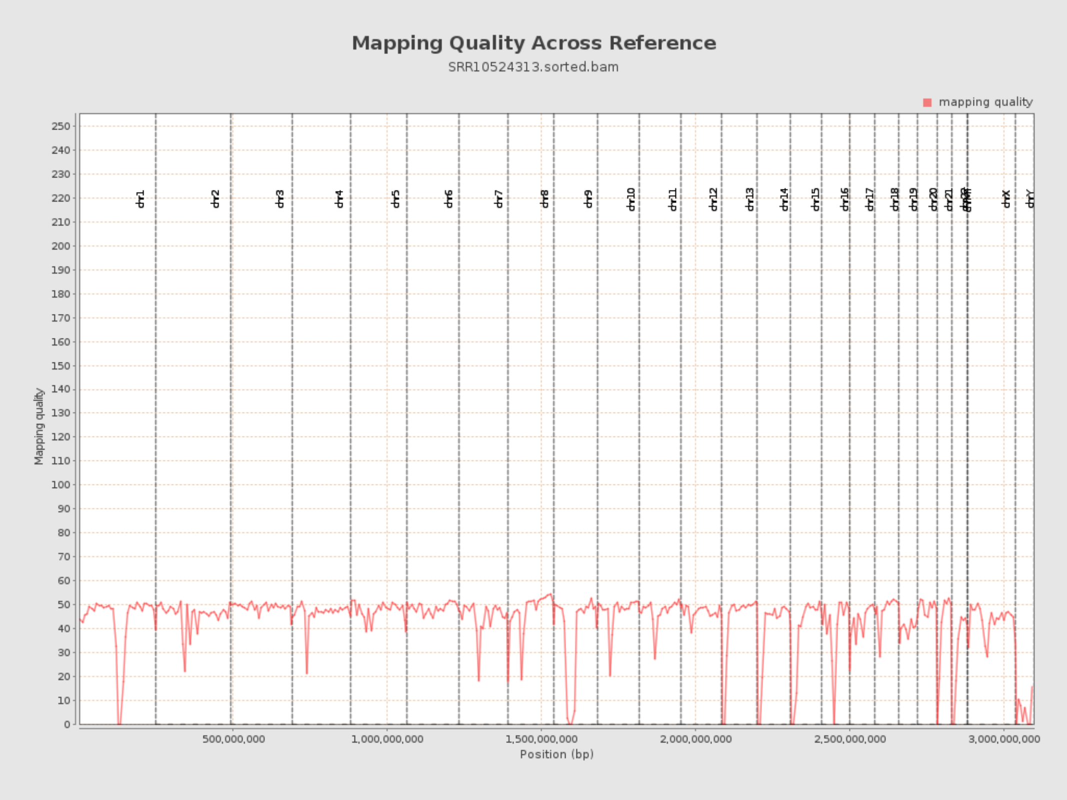
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram