Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 20:25:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524781.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_SRR10524781 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524781.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 20:25:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524781.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	907,371
Mapped reads	793,802 / 87.48%
Unmapped reads	113,569 / 12.52%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,551 / 0.28%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	18,818 / 2.07%
Duplication rate	1.77%
Clipped reads	794,479 / 87.56%

2.2. ACGT Content

Number/percentage of A's	11,148,419 / 24.79%
Number/percentage of C's	8,603,351 / 19.13%
Number/percentage of T's	14,266,601 / 31.72%
Number/percentage of G's	10,951,499 / 24.35%
Number/percentage of N's	5,868 / 0.01%
GC Percentage	43.48%

2.3. Coverage

Mean	0.0145

Standard Deviation	0.1539

2.4. Mapping Quality

Mean Mapping Quality	44.21

2.5. Mismatches and indels

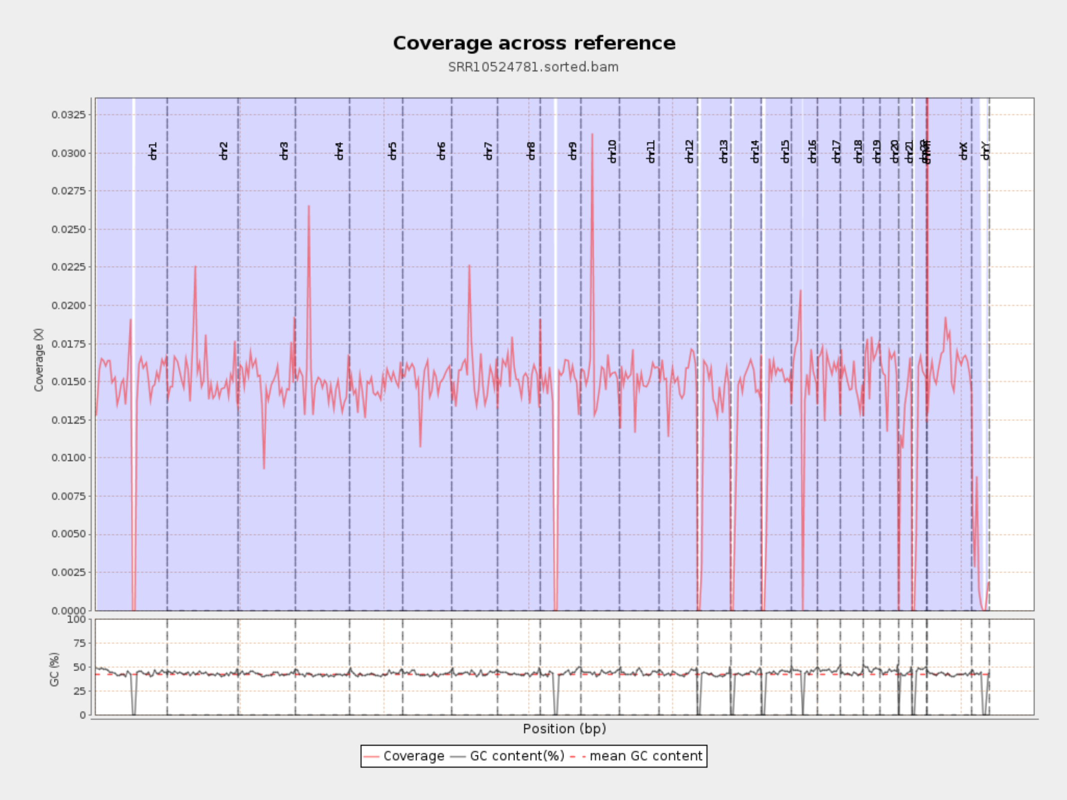
General error rate	0.54%
Mismatches	235,234
Insertions	3,042
Mapped reads with at least one insertion	0.38%
Deletions	9,175
Mapped reads with at least one deletion	1.15%
Homopolymer indels	42.65%

2.6. Chromosome stats

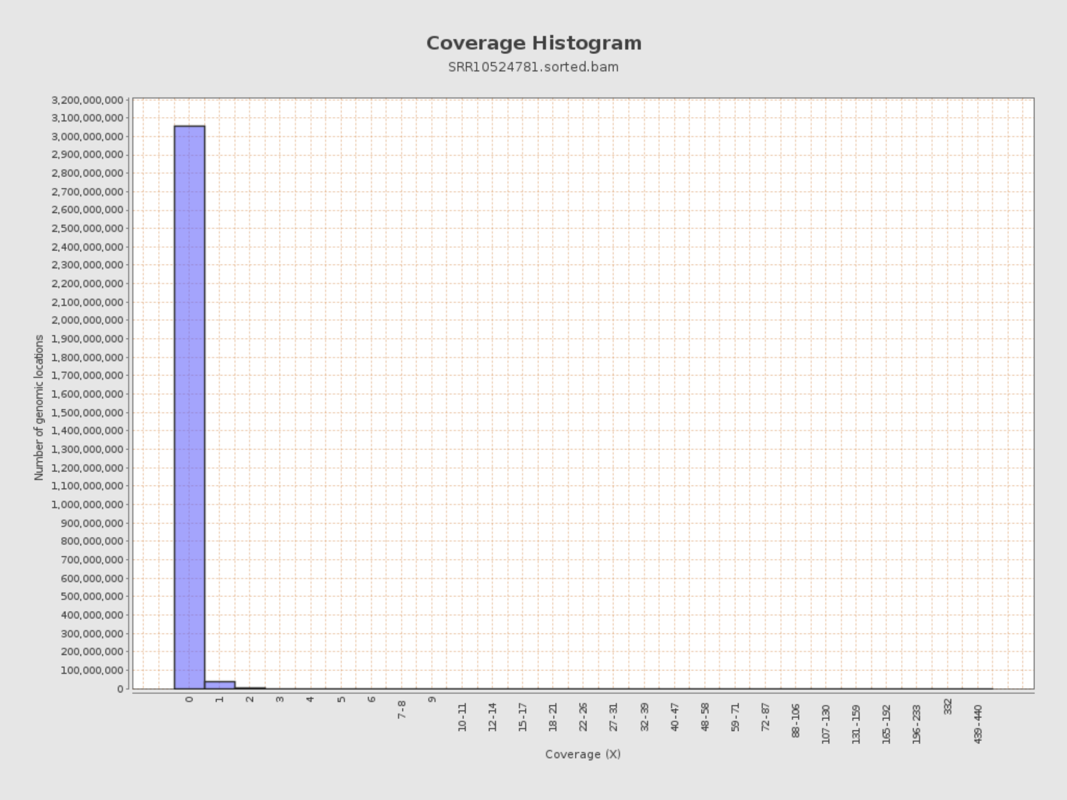
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3607538	0.0145	0.1926
chr2	243199373	3760895	0.0155	0.2258
chr3	198022430	2966333	0.015	0.1309
chr4	191154276	2888547	0.0151	0.1399
chr5	180915260	2665347	0.0147	0.1276
chr6	171115067	2587120	0.0151	0.1367
chr7	159138663	2475873	0.0156	0.1782

chr8	146364022	2252898	0.0154	0.1443
chr9	141213431	1916836	0.0136	0.136
chr10	135534747	2175508	0.0161	0.1764
chr11	135006516	2051210	0.0152	0.1422
chr12	133851895	2032550	0.0152	0.1299
chr13	115169878	1414132	0.0123	0.1163
chr14	107349540	1350066	0.0126	0.1189
chr15	102531392	1291202	0.0126	0.1176
chr16	90354753	1334031	0.0148	0.1383
chr17	81195210	1286259	0.0158	0.1368
chr18	78077248	1163944	0.0149	0.1941
chr19	59128983	979373	0.0166	0.1757
chr20	63025520	968115	0.0154	0.134
chr21	48129895	584780	0.0122	0.1221
chr22	51304566	557238	0.0109	0.1095
chrMT	16571	15418	0.9304	1.1649
chrX	155270560	2514342	0.0162	0.1404
chrY	59373566	150816	0.0025	0.0807

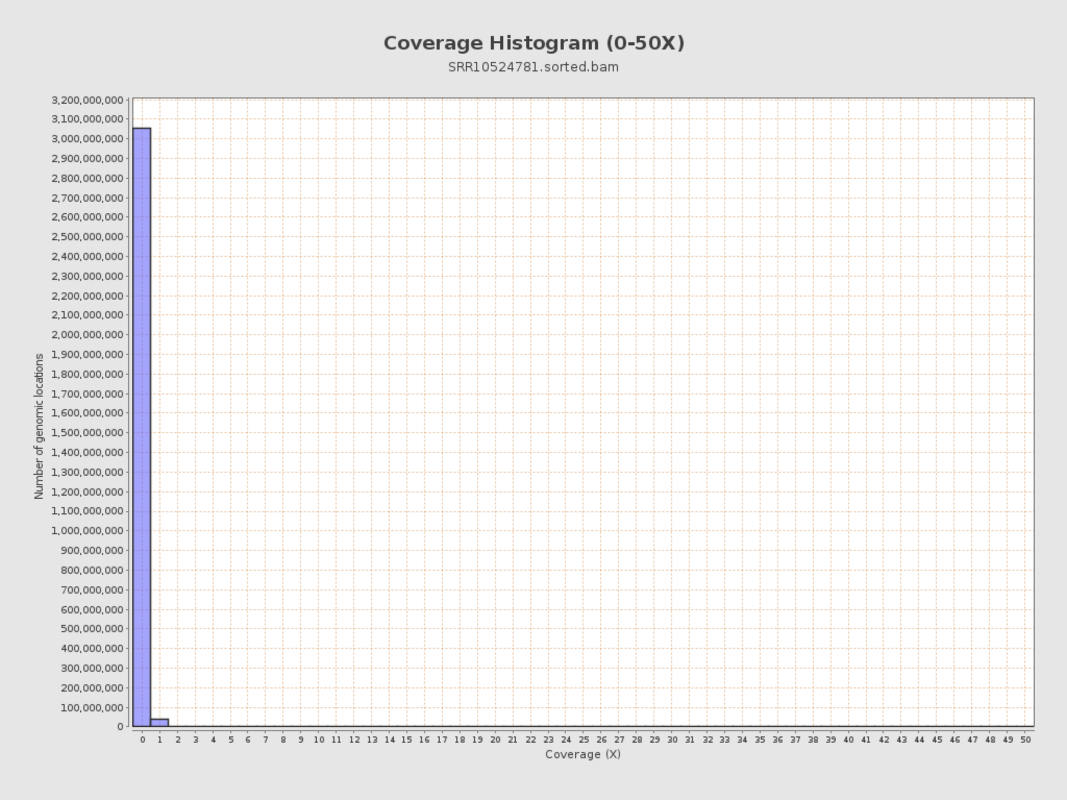
3. Results : Coverage across reference



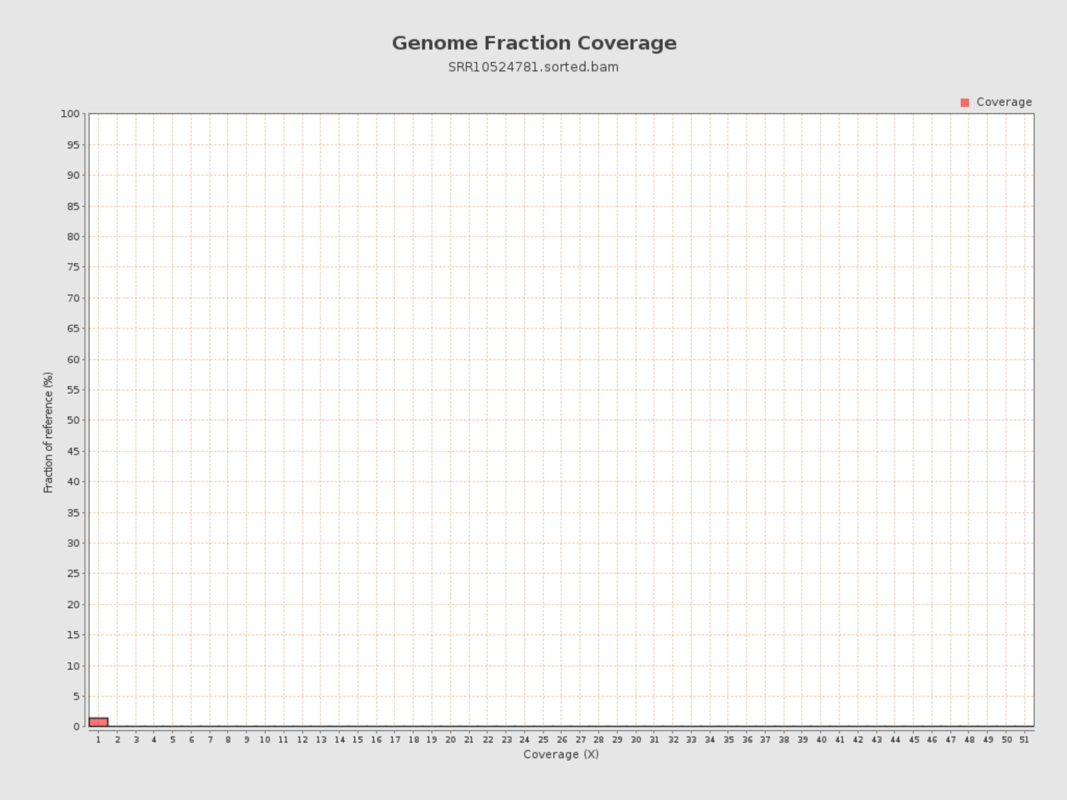
4. Results : Coverage Histogram



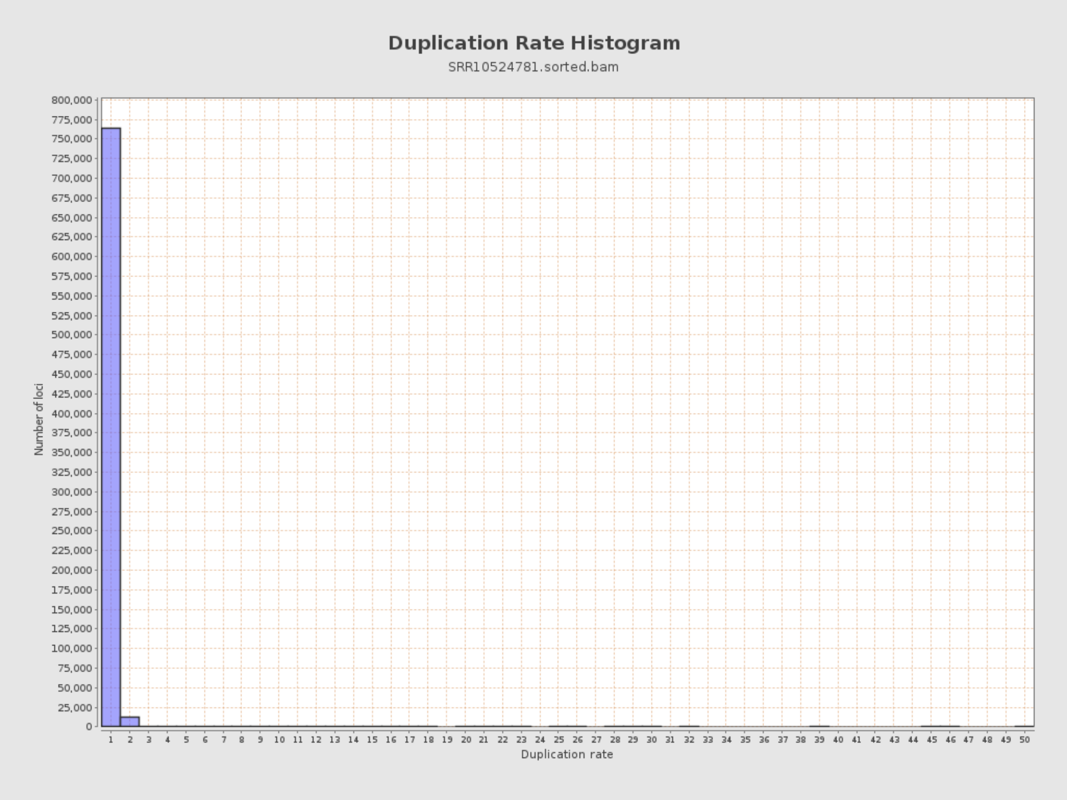
5. Results : Coverage Histogram (0-50X)



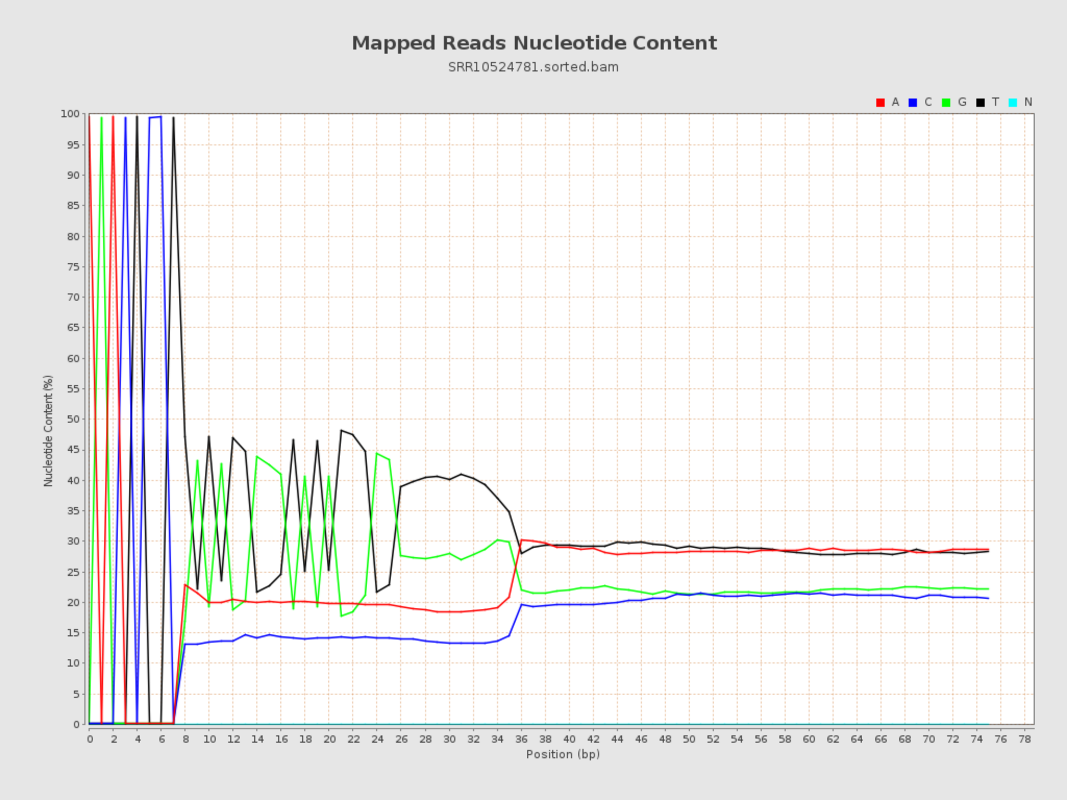
6. Results : Genome Fraction Coverage



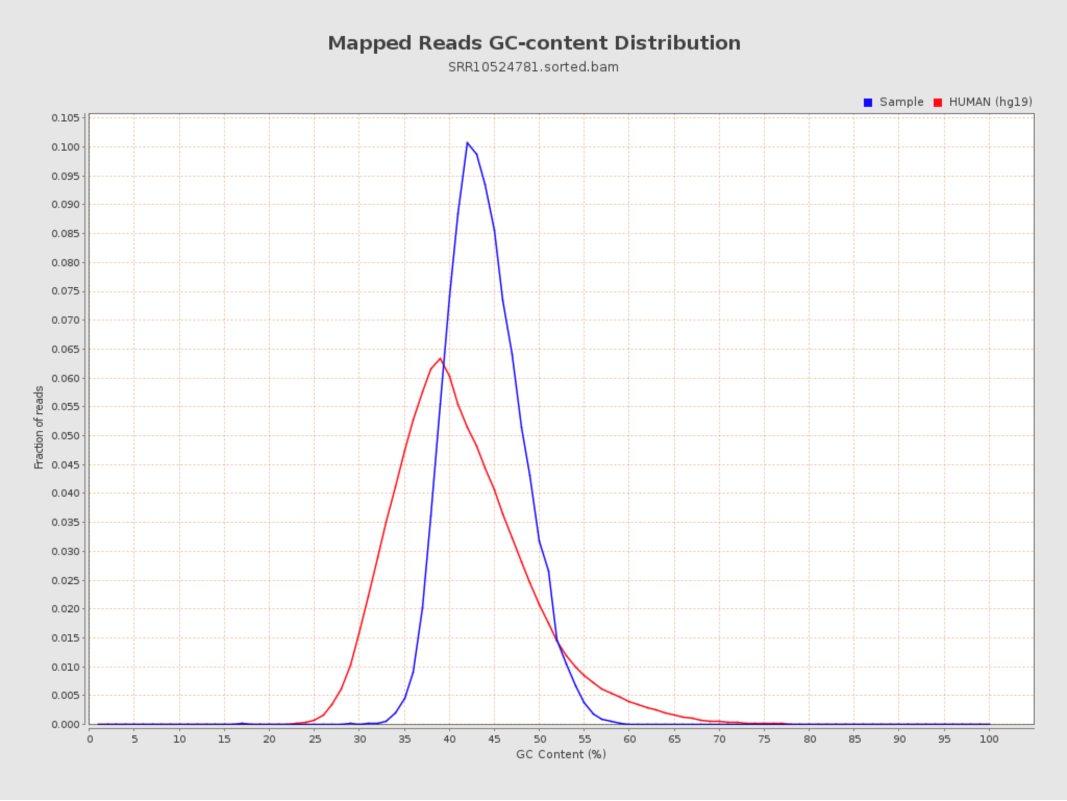
7. Results : Duplication Rate Histogram



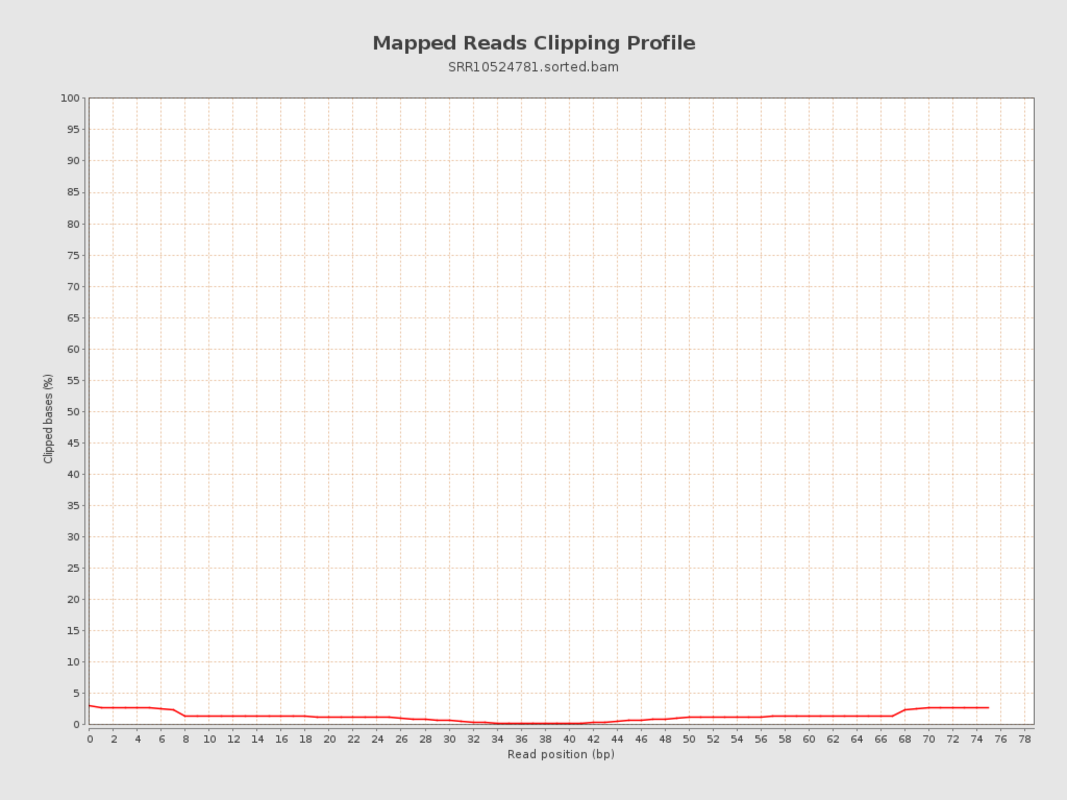
8. Results : Mapped Reads Nucleotide Content



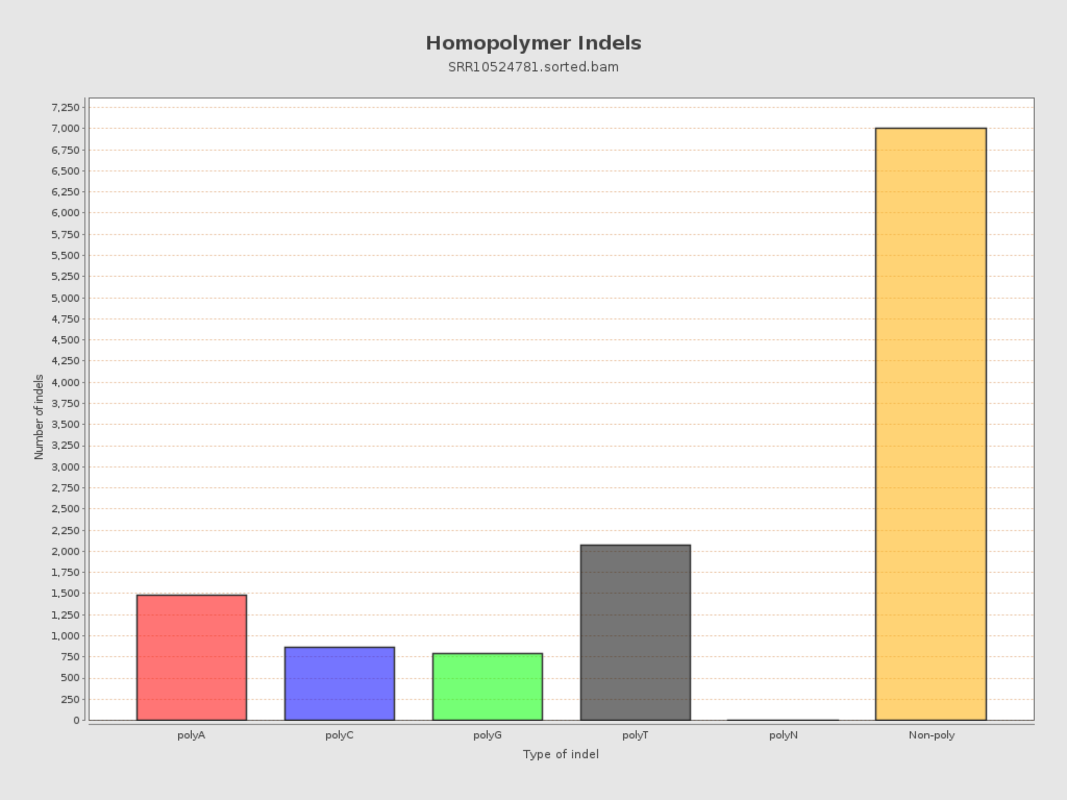
9. Results : Mapped Reads GC-content Distribution



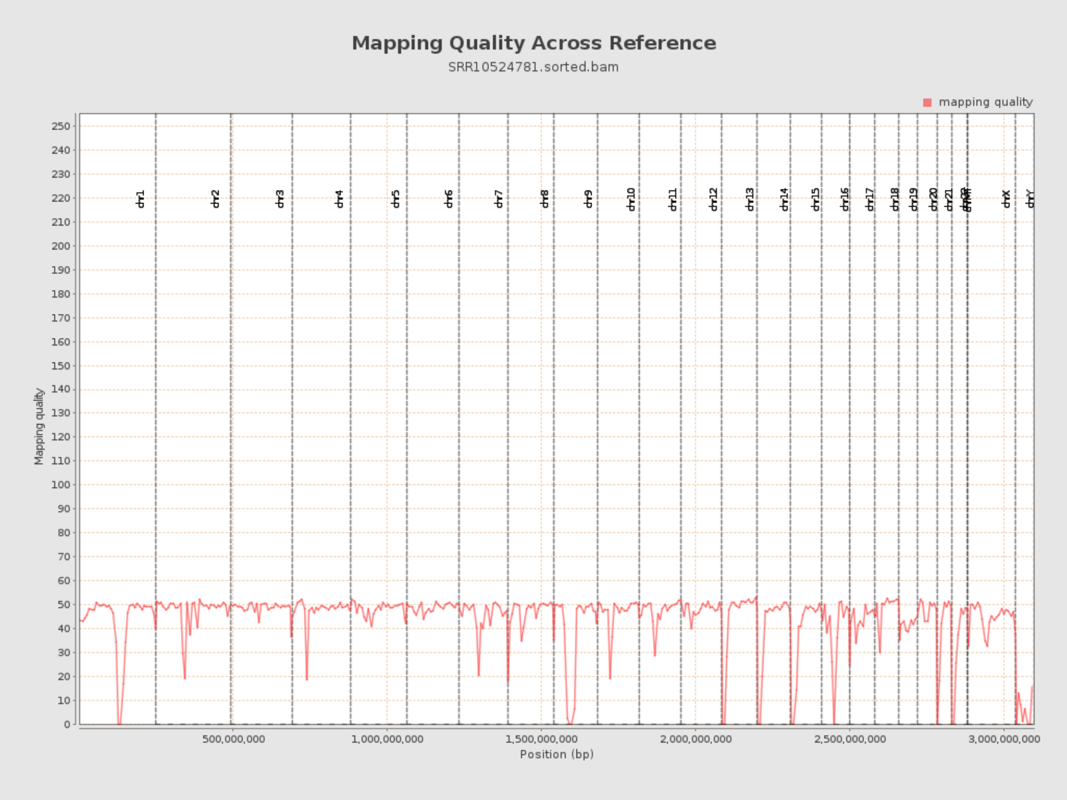
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram