Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 11:39:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524583.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_SRR10524583 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524583.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 11:39:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524583.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	996,569
Mapped reads	907,302 / 91.04%
Unmapped reads	89,267 / 8.96%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,906 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	24,466 / 2.46%
Duplication rate	2.01%
Clipped reads	908,980 / 91.21%

2.2. ACGT Content

Number/percentage of A's	13,234,000 / 25.02%
Number/percentage of C's	9,491,526 / 17.94%
Number/percentage of T's	17,343,041 / 32.79%
Number/percentage of G's	12,827,120 / 24.25%
Number/percentage of N's	781 / 0%
GC Percentage	42.19%

2.3. Coverage

Mean	0.0171

Standard Deviation	0.181

2.4. Mapping Quality

Mean Mapping Quality	45.09

2.5. Mismatches and indels

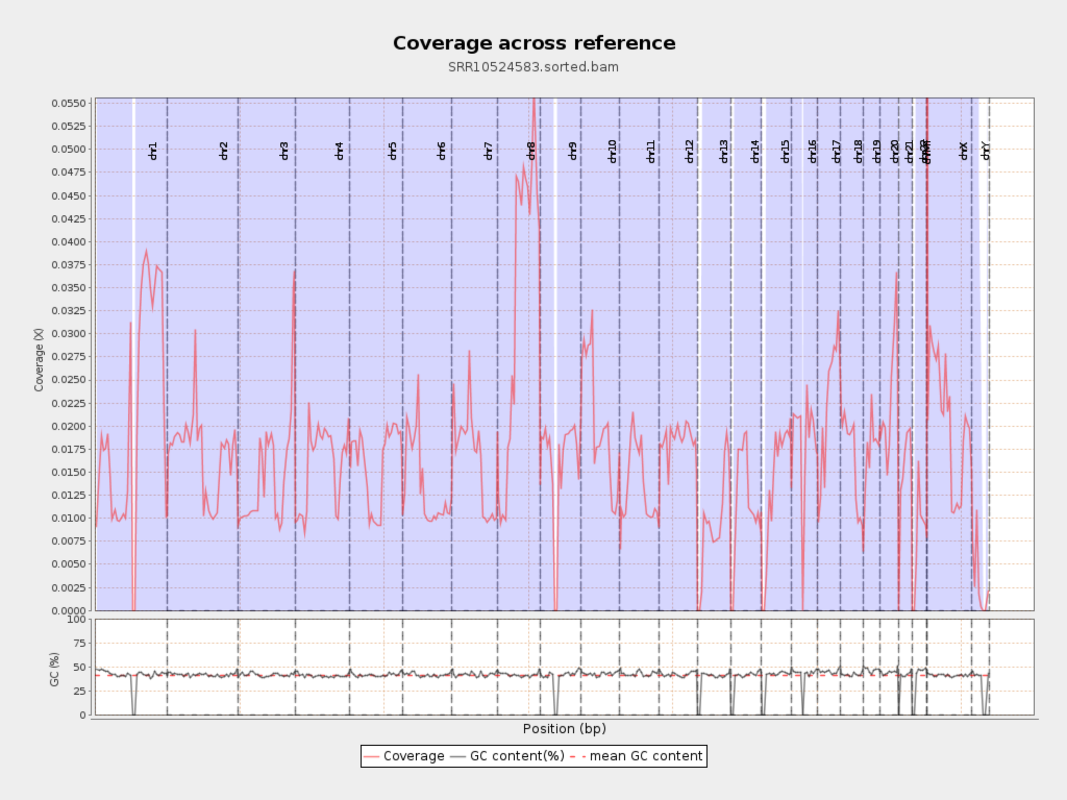
General error rate	0.54%
Mismatches	278,009
Insertions	3,306
Mapped reads with at least one insertion	0.36%
Deletions	11,583
Mapped reads with at least one deletion	1.27%
Homopolymer indels	43.97%

2.6. Chromosome stats

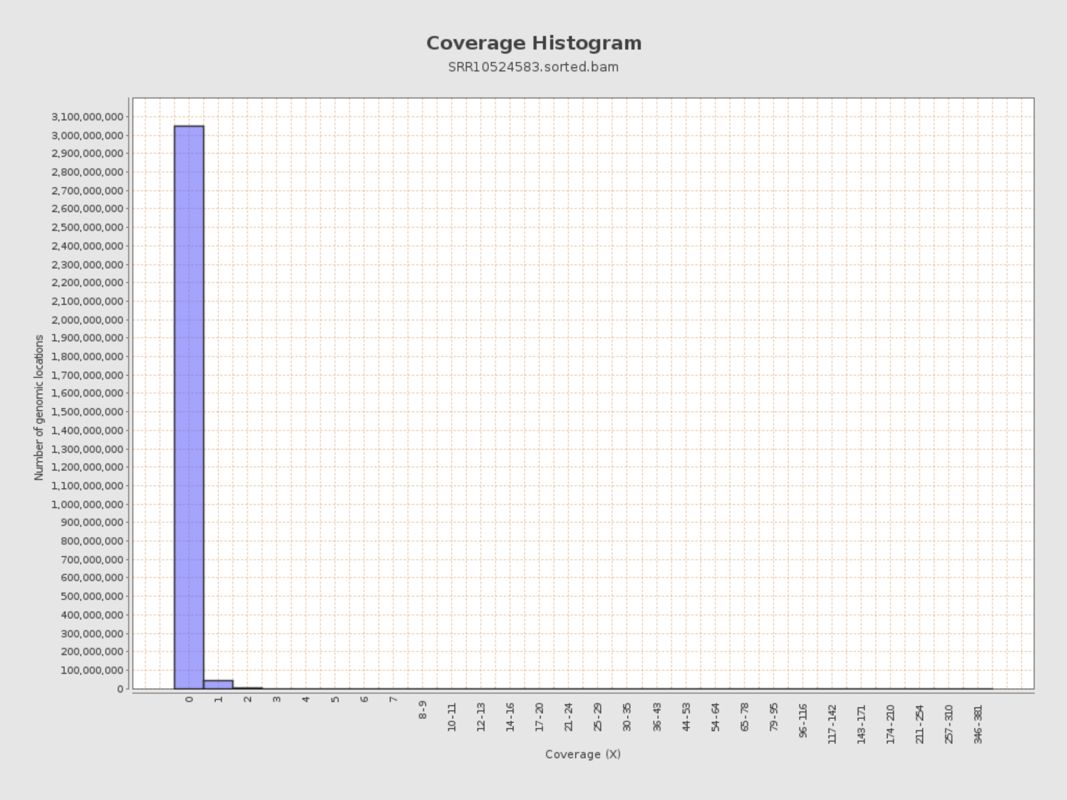
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5213688	0.0209	0.3161
chr2	243199373	4140371	0.017	0.199
chr3	198022430	2891257	0.0146	0.1286
chr4	191154276	3017808	0.0158	0.1437
chr5	180915260	2900158	0.016	0.1345
chr6	171115067	2322054	0.0136	0.1451
chr7	159138663	2646894	0.0166	0.2137

chr8	146364022	4916515	0.0336	0.2158
chr9	141213431	2246430	0.0159	0.1564
chr10	135534747	2789032	0.0206	0.1883
chr11	135006516	1844615	0.0137	0.1602
chr12	133851895	2489938	0.0186	0.1444
chr13	115169878	1082635	0.0094	0.1028
chr14	107349540	1248992	0.0116	0.1158
chr15	102531392	1394482	0.0136	0.1266
chr16	90354753	1632837	0.0181	0.1489
chr17	81195210	1802612	0.0222	0.1647
chr18	78077248	1291531	0.0165	0.2569
chr19	59128983	1030982	0.0174	0.2147
chr20	63025520	1476161	0.0234	0.163
chr21	48129895	725259	0.0151	0.1362
chr22	51304566	413917	0.0081	0.0948
chrMT	16571	12737	0.7686	0.9355
chrX	155270560	3208582	0.0207	0.1621
chrY	59373566	176213	0.003	0.1015

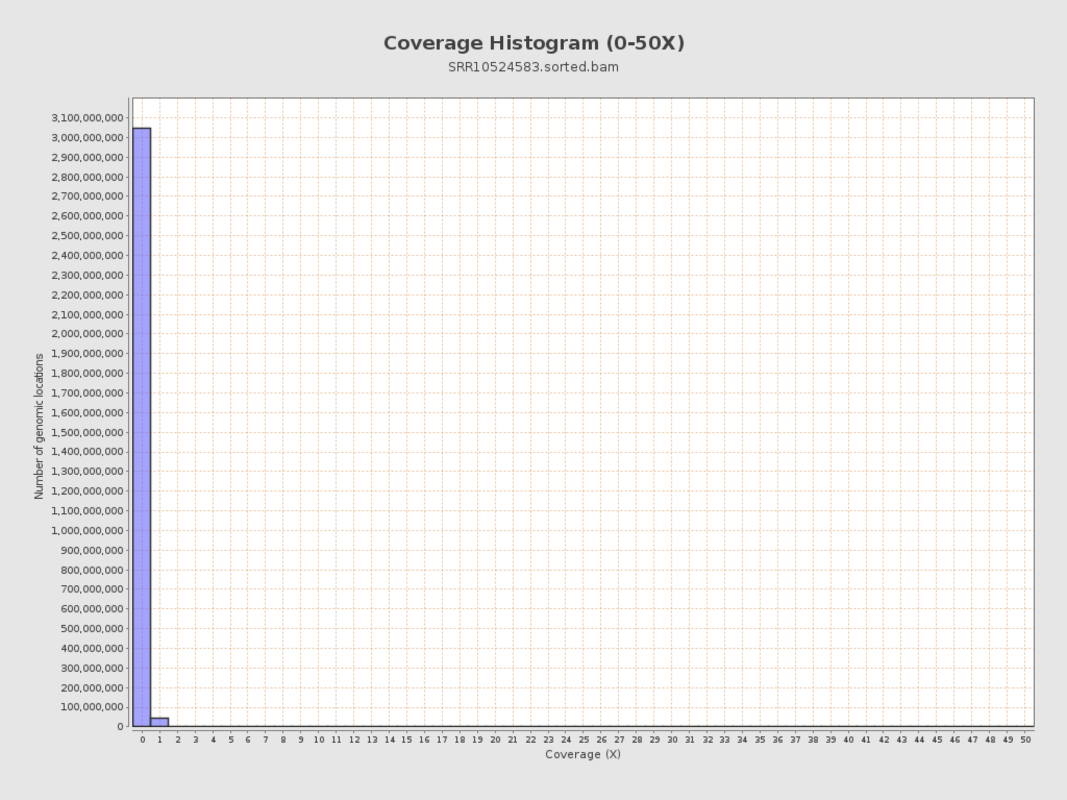
3. Results : Coverage across reference



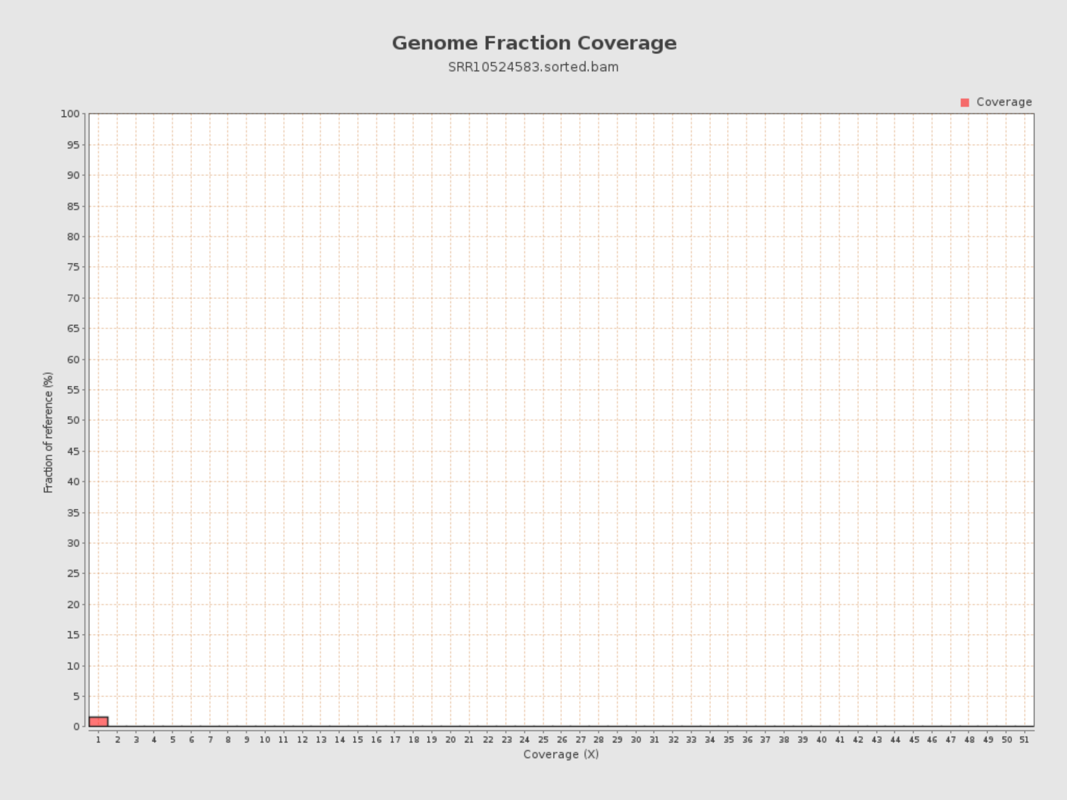
4. Results : Coverage Histogram



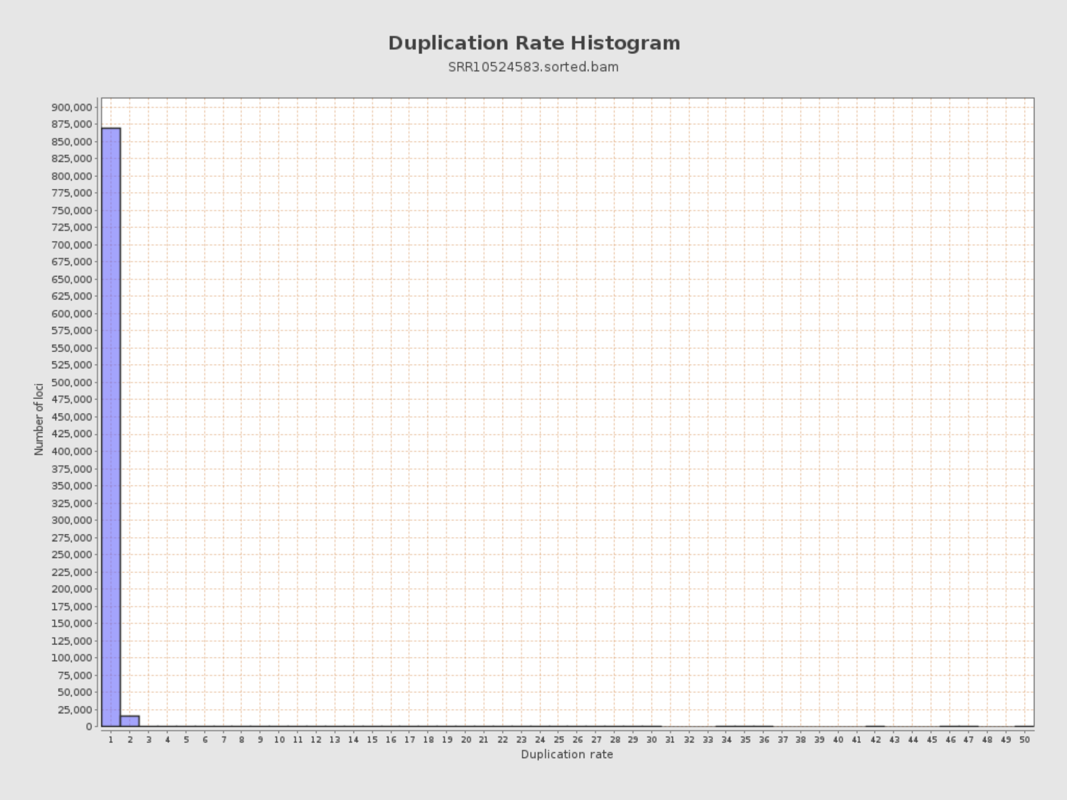
5. Results : Coverage Histogram (0-50X)



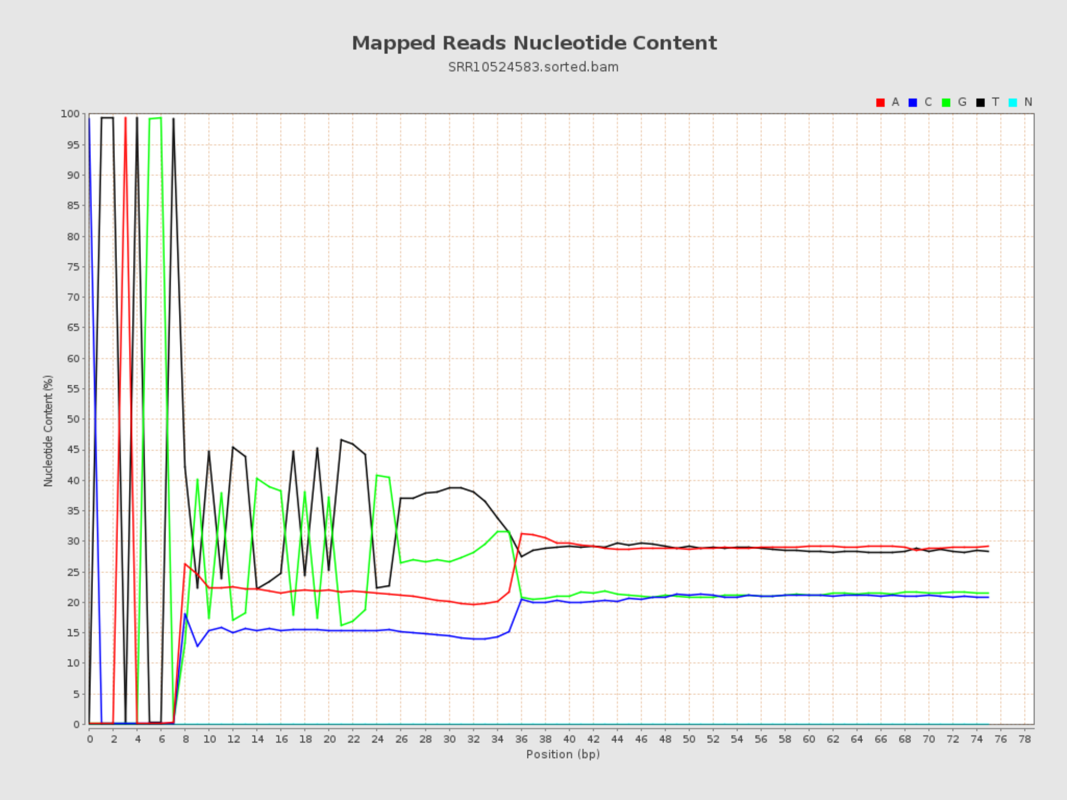
6. Results : Genome Fraction Coverage



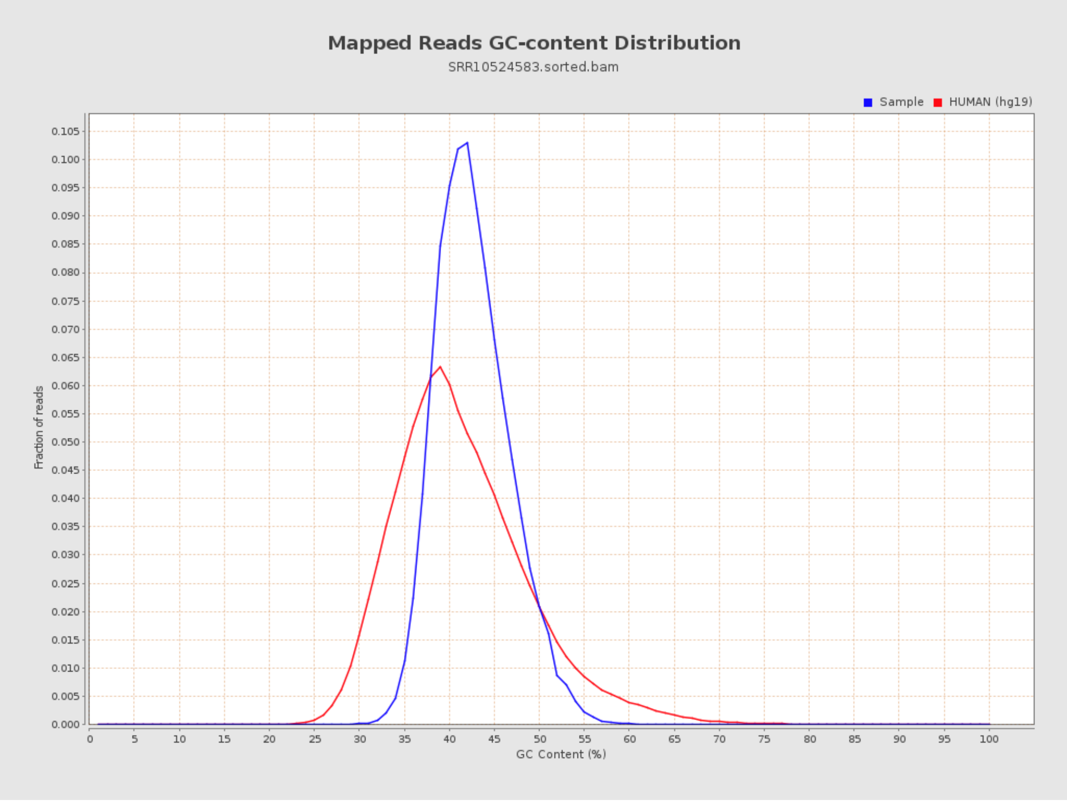
7. Results : Duplication Rate Histogram



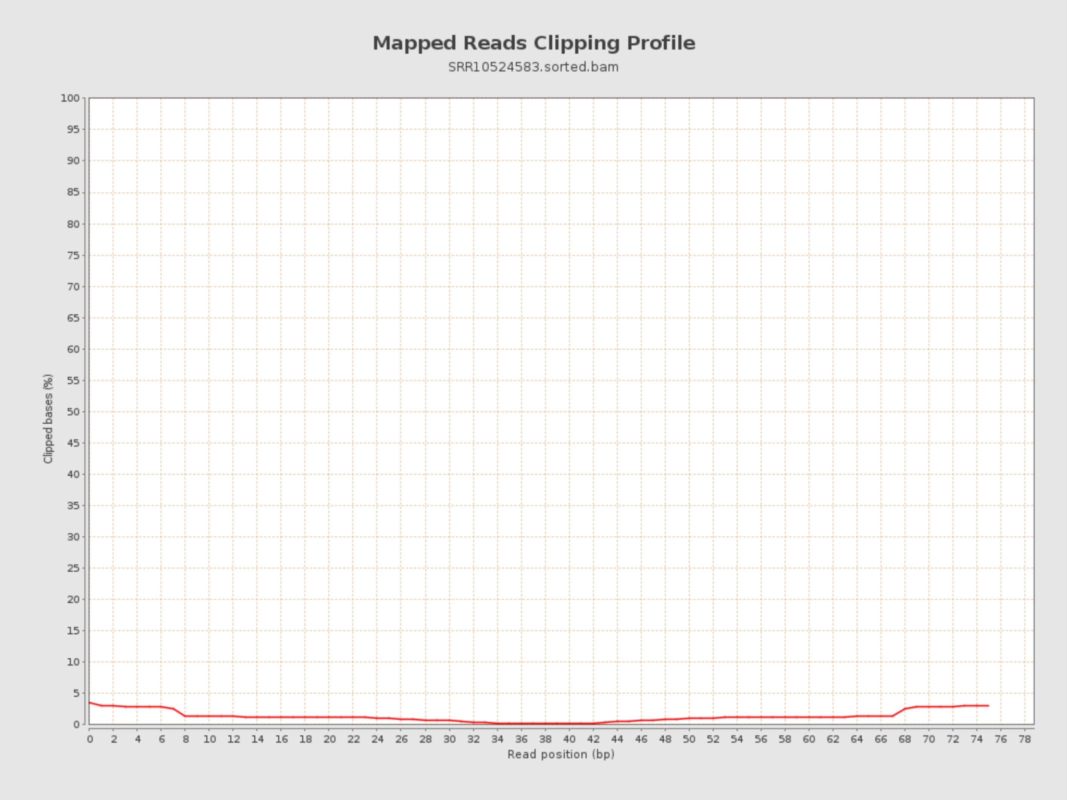
8. Results : Mapped Reads Nucleotide Content



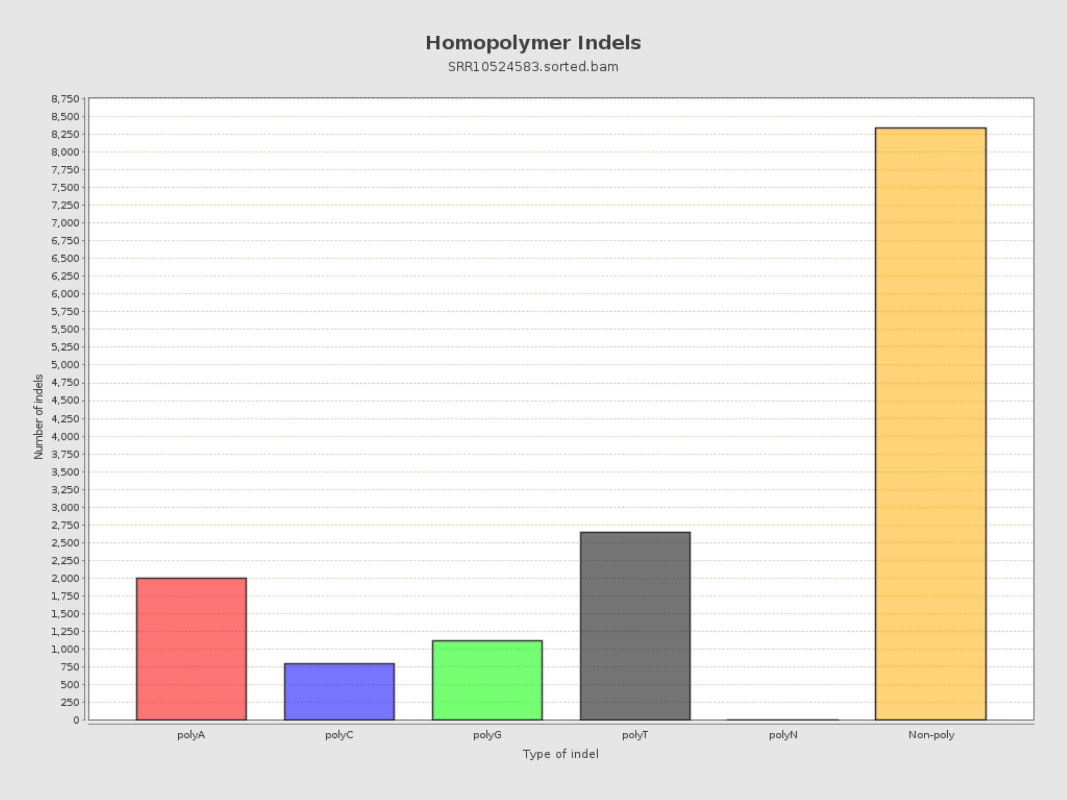
9. Results : Mapped Reads GC-content Distribution



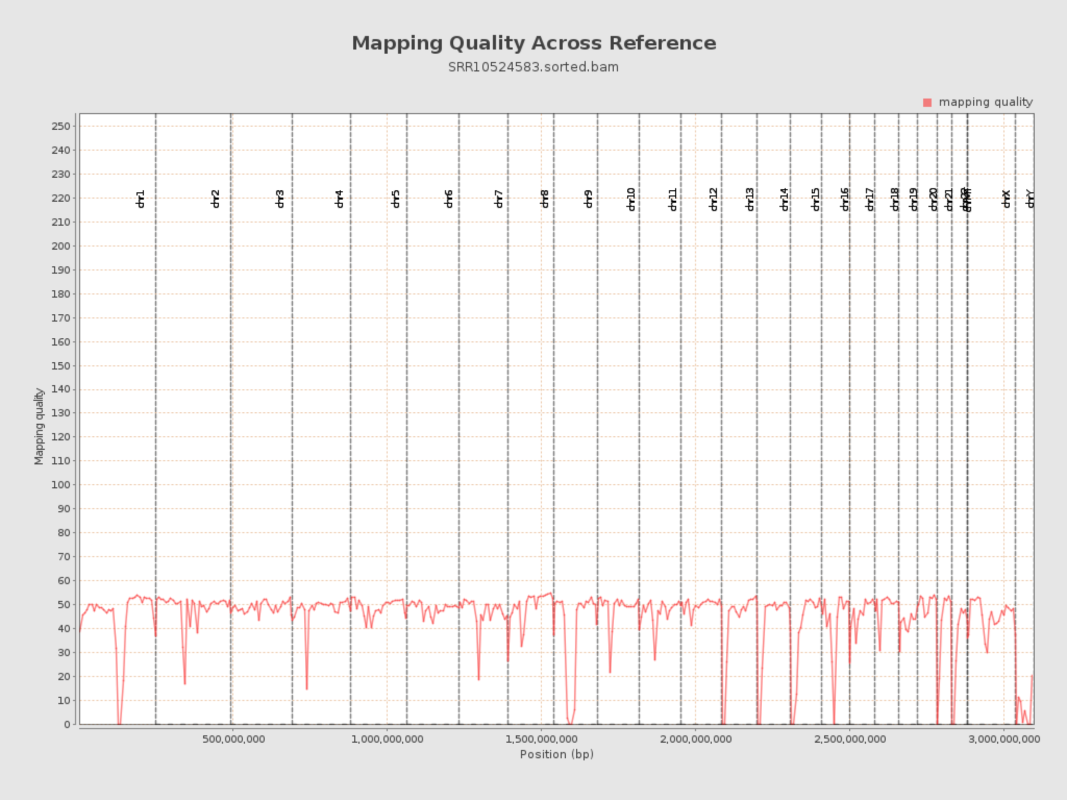
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram