Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 12:33:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524600.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_SRR10524600 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524600.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 12:33:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524600.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	412,693
Mapped reads	378,893 / 91.81%
Unmapped reads	33,800 / 8.19%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,322 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	5,061 / 1.23%
Duplication rate	0.99%
Clipped reads	378,924 / 91.82%

2.2. ACGT Content

Number/percentage of A's	5,739,272 / 26.15%
Number/percentage of C's	4,272,612 / 19.47%
Number/percentage of T's	6,800,698 / 30.99%
Number/percentage of G's	5,131,519 / 23.38%
Number/percentage of N's	648 / 0%
GC Percentage	42.85%

2.3. Coverage

Mean	0.0071

Standard Deviation	0.0971

2.4. Mapping Quality

Mean Mapping Quality	45.66

2.5. Mismatches and indels

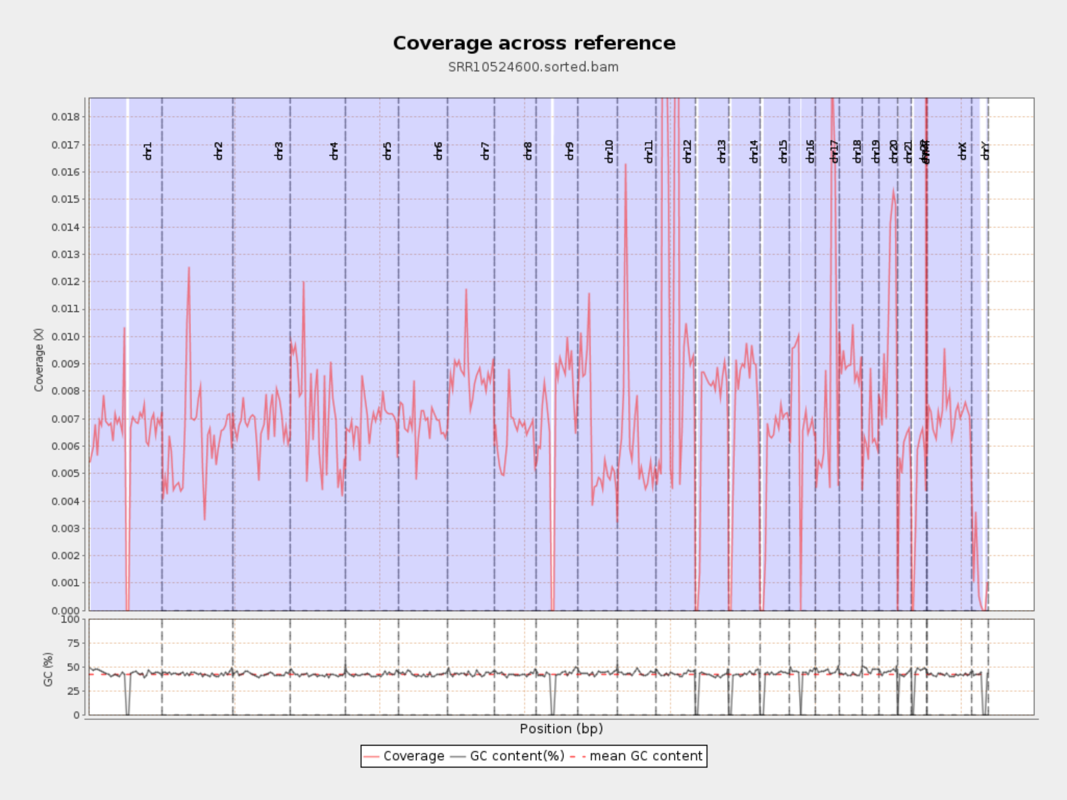
General error rate	0.48%
Mismatches	102,658
Insertions	1,840
Mapped reads with at least one insertion	0.48%
Deletions	3,523
Mapped reads with at least one deletion	0.92%
Homopolymer indels	42.92%

2.6. Chromosome stats

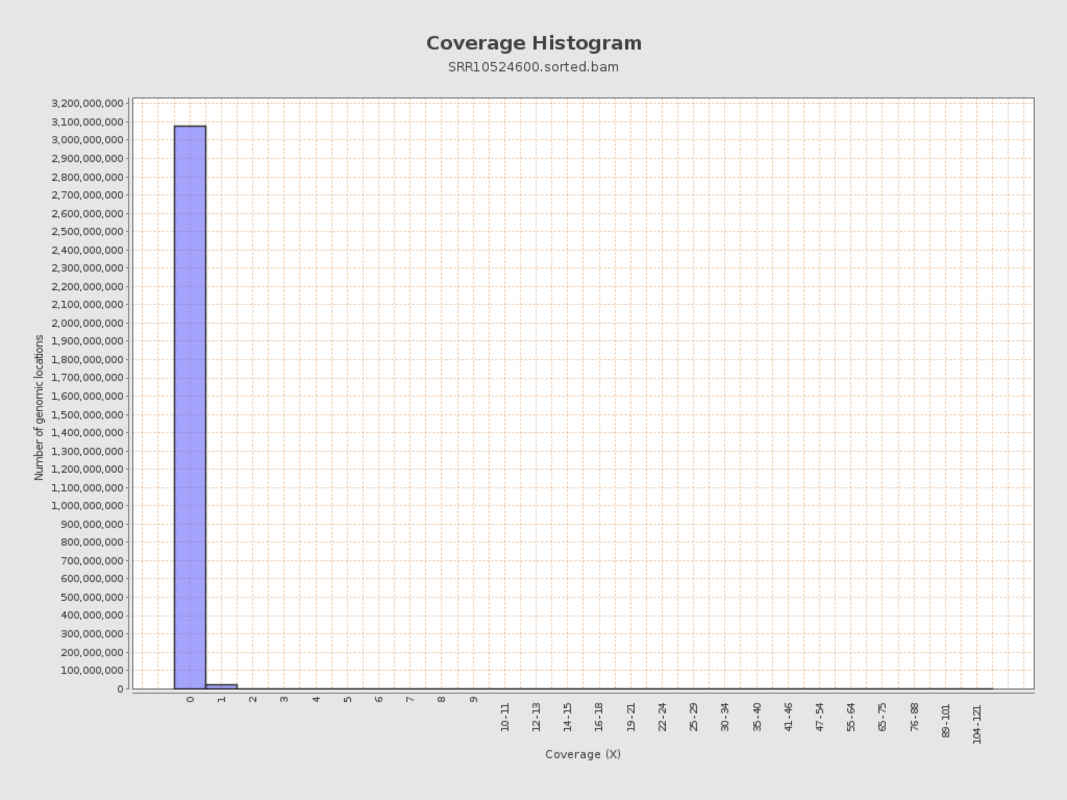
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1603815	0.0064	0.1242
chr2	243199373	1519544	0.0062	0.0963
chr3	198022430	1356221	0.0068	0.0846
chr4	191154276	1390195	0.0073	0.0905
chr5	180915260	1259653	0.007	0.0856
chr6	171115067	1173981	0.0069	0.087
chr7	159138663	1375182	0.0086	0.1159

chr8	146364022	944730	0.0065	0.0944
chr9	141213431	1009901	0.0072	0.0999
chr10	135534747	859544	0.0063	0.0942
chr11	135006516	879288	0.0065	0.0884
chr12	133851895	1675509	0.0125	0.1177
chr13	115169878	809496	0.007	0.0859
chr14	107349540	790092	0.0074	0.0894
chr15	102531392	565059	0.0055	0.0759
chr16	90354753	646827	0.0072	0.0875
chr17	81195210	664633	0.0082	0.0935
chr18	78077248	705239	0.009	0.1394
chr19	59128983	377826	0.0064	0.11
chr20	63025520	676449	0.0107	0.1072
chr21	48129895	254508	0.0053	0.0766
chr22	51304566	221036	0.0043	0.067
chrMT	16571	12688	0.7657	0.9556
chrX	155270560	1115139	0.0072	0.09
chrY	59373566	63789	0.0011	0.0391

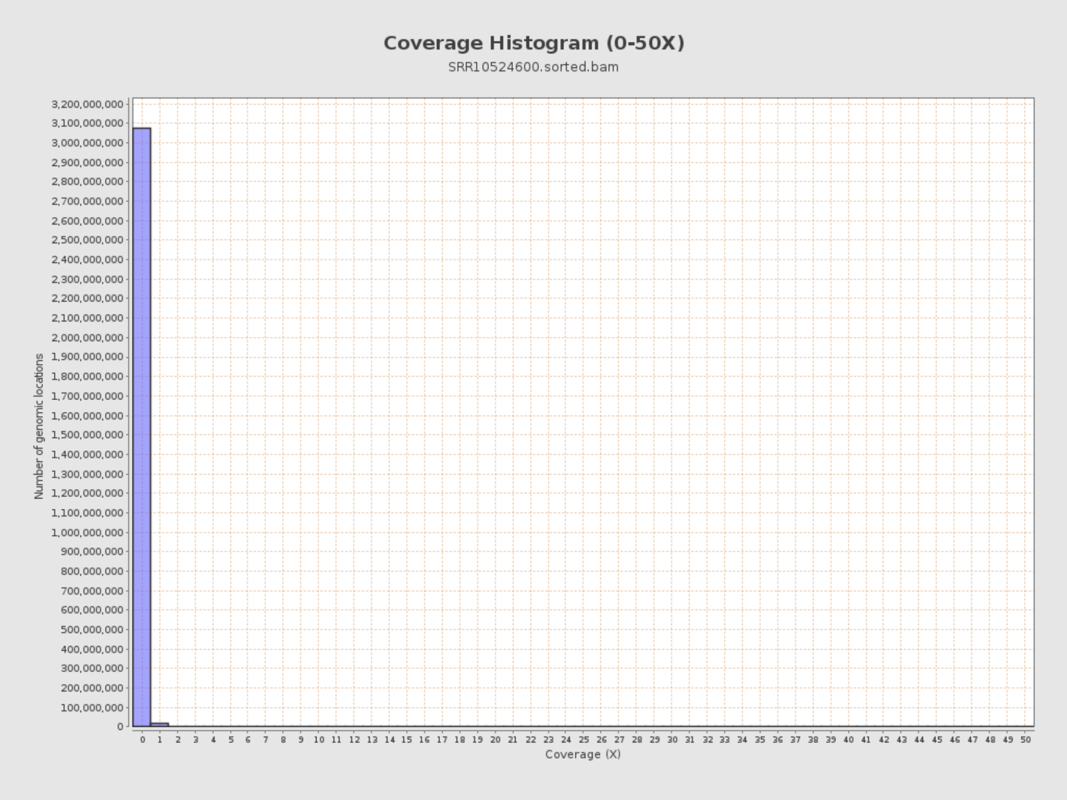
3. Results : Coverage across reference



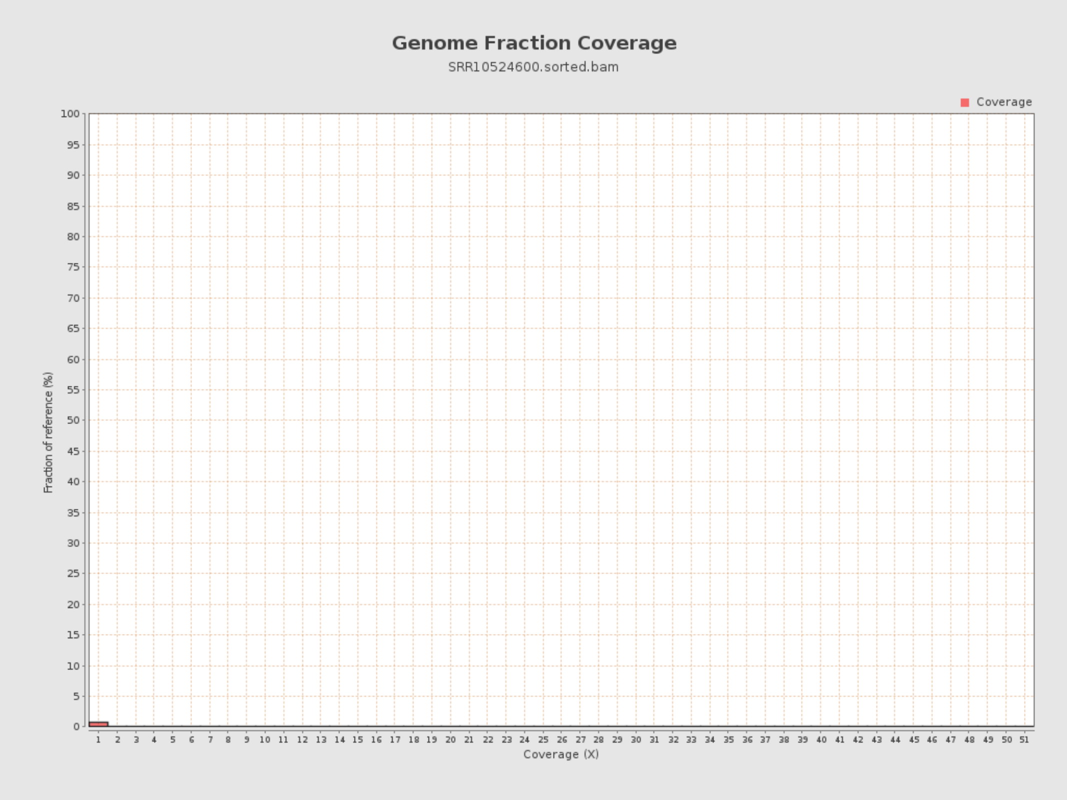
4. Results : Coverage Histogram



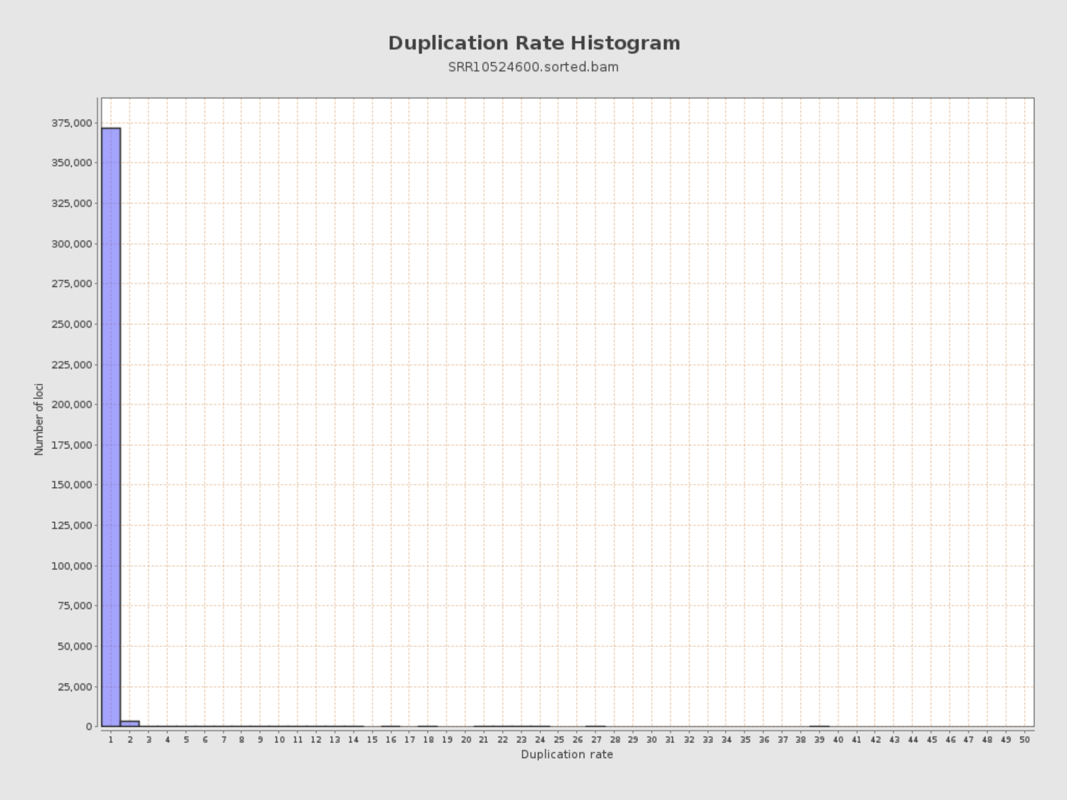
5. Results : Coverage Histogram (0-50X)



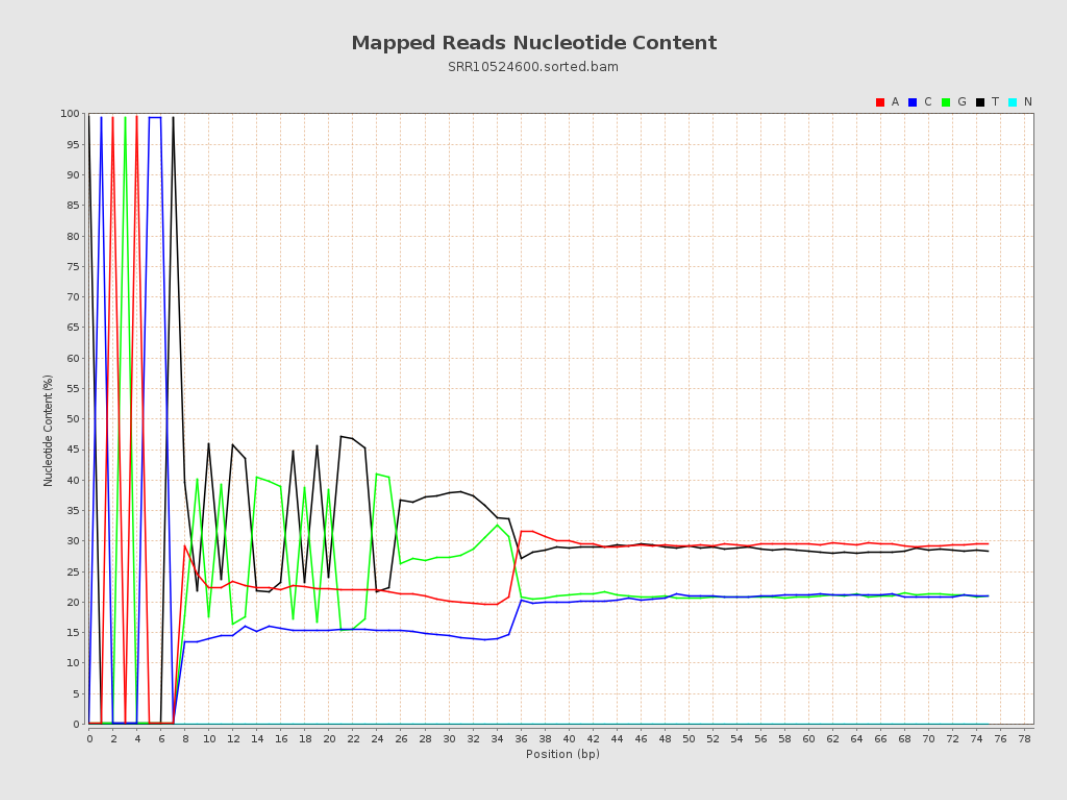
6. Results : Genome Fraction Coverage



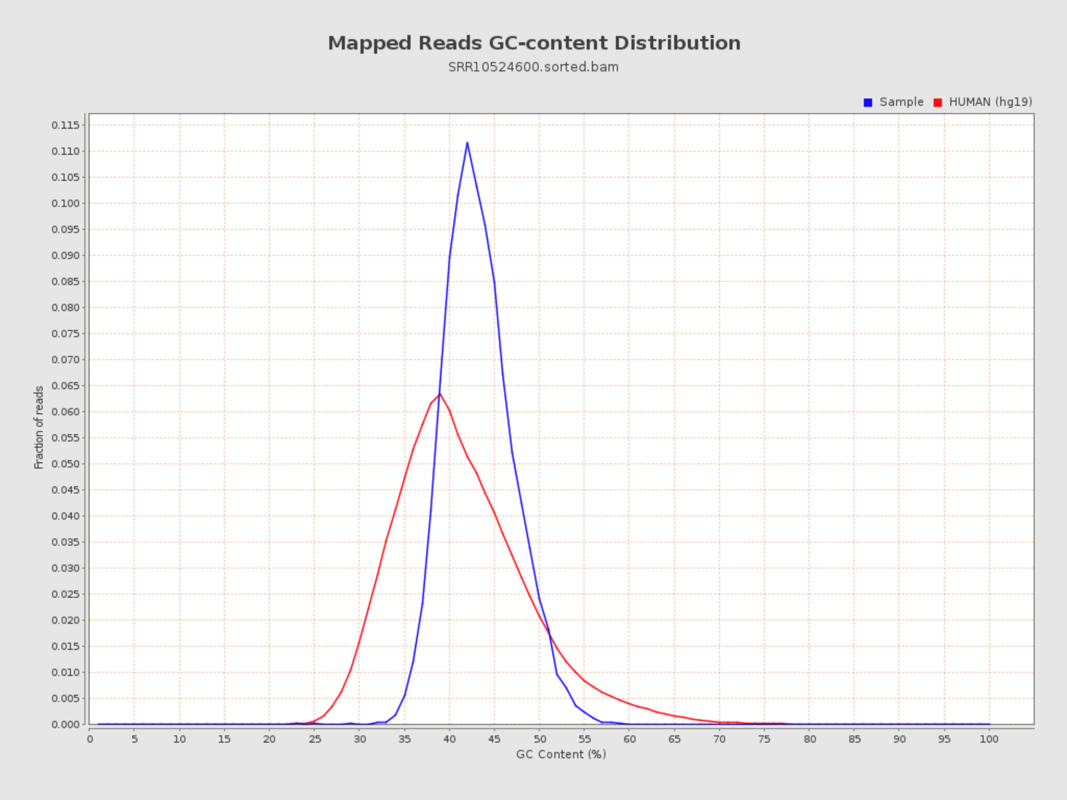
7. Results : Duplication Rate Histogram



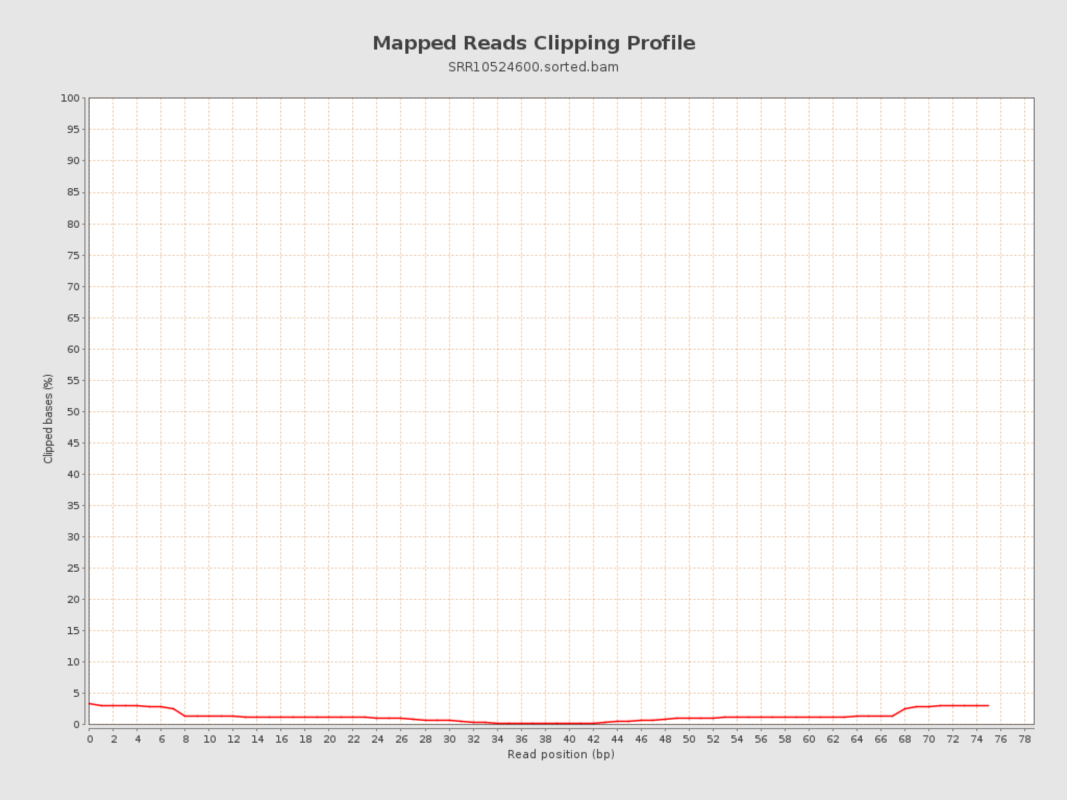
8. Results : Mapped Reads Nucleotide Content



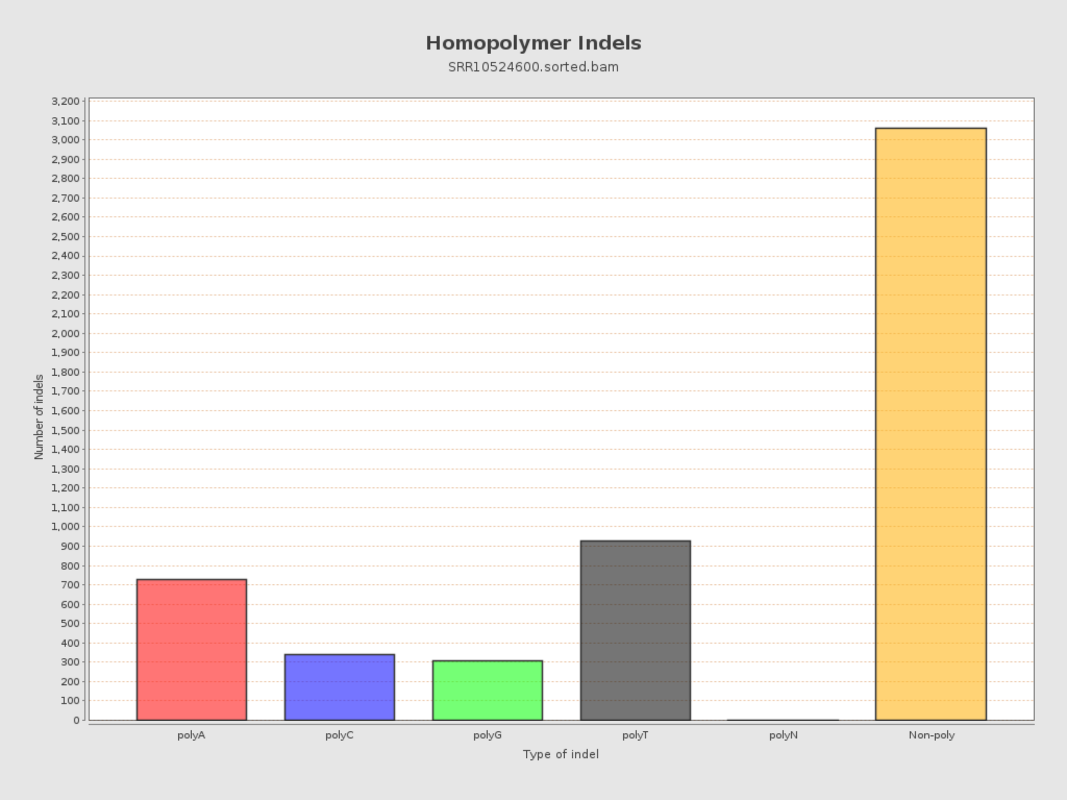
9. Results : Mapped Reads GC-content Distribution



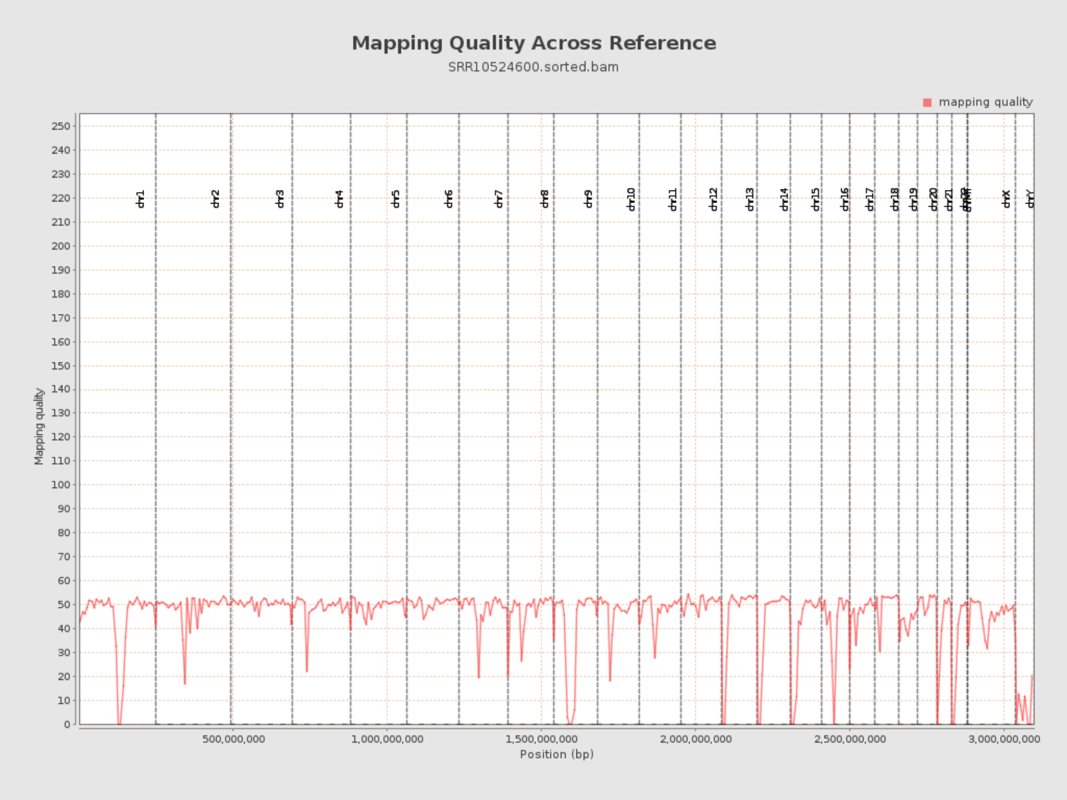
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram