Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 00:33:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524362.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_SRR10524362 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524362.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 00:33:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524362.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	708,494
Mapped reads	651,469 / 91.95%
Unmapped reads	57,025 / 8.05%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,098 / 0.44%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	18,761 / 2.65%
Duplication rate	2.16%
Clipped reads	652,643 / 92.12%

2.2. ACGT Content

Number/percentage of A's	9,879,750 / 25.66%
Number/percentage of C's	7,483,687 / 19.44%
Number/percentage of T's	11,491,023 / 29.84%
Number/percentage of G's	9,645,621 / 25.05%
Number/percentage of N's	5,362 / 0.01%
GC Percentage	44.49%

2.3. Coverage

Mean	0.0124

Standard Deviation	0.153

2.4. Mapping Quality

Mean Mapping Quality	45.31

2.5. Mismatches and indels

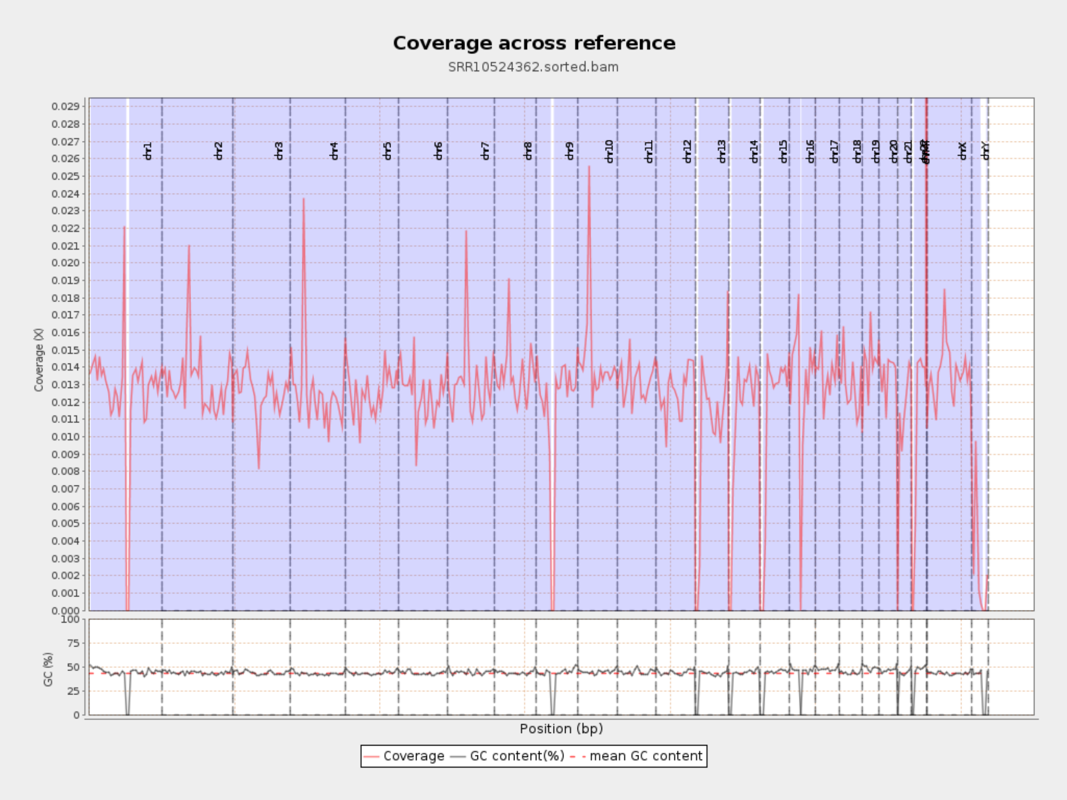
General error rate	0.53%
Mismatches	196,490
Insertions	3,053
Mapped reads with at least one insertion	0.47%
Deletions	6,612
Mapped reads with at least one deletion	1.01%
Homopolymer indels	40.79%

2.6. Chromosome stats

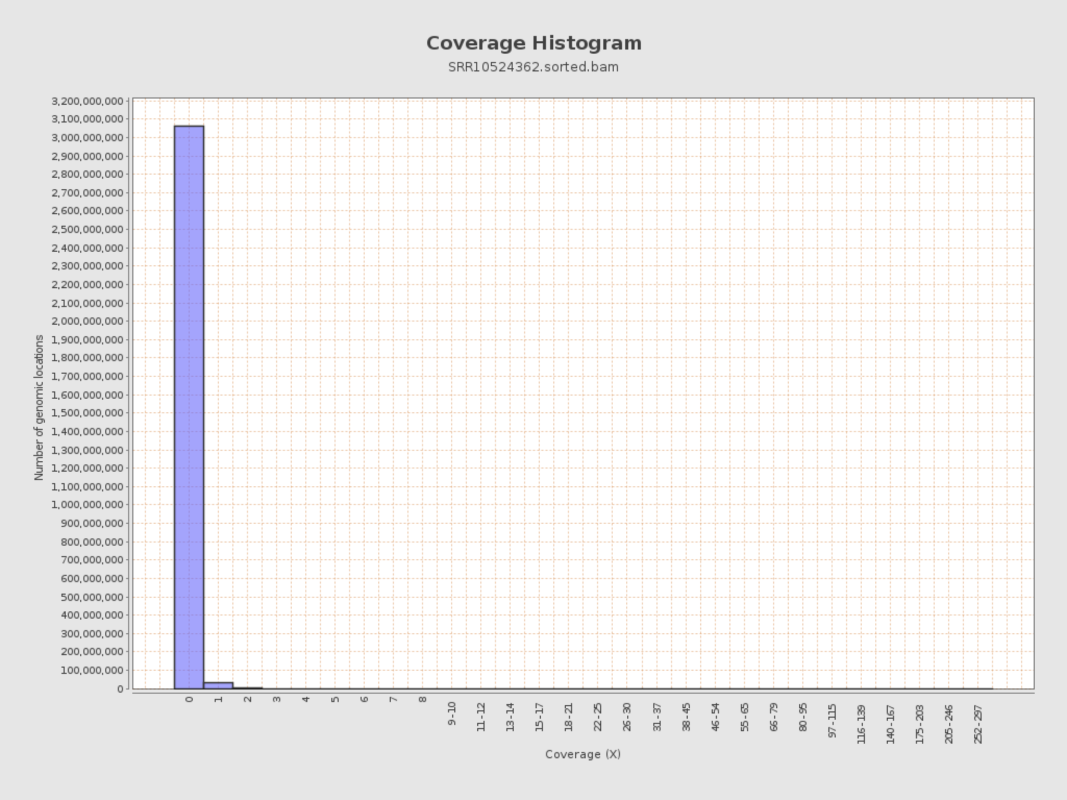
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3113740	0.0125	0.2617
chr2	243199373	3217816	0.0132	0.1763
chr3	198022430	2490860	0.0126	0.118
chr4	191154276	2399808	0.0126	0.1297
chr5	180915260	2271645	0.0126	0.1179
chr6	171115067	2150149	0.0126	0.1219
chr7	159138663	2092792	0.0132	0.1785

chr8	146364022	1986501	0.0136	0.1519
chr9	141213431	1598340	0.0113	0.1358
chr10	135534747	1954818	0.0144	0.1597
chr11	135006516	1781915	0.0132	0.1405
chr12	133851895	1703212	0.0127	0.1209
chr13	115169878	1166044	0.0101	0.1055
chr14	107349540	1172181	0.0109	0.1137
chr15	102531392	1123192	0.011	0.11
chr16	90354753	1171764	0.013	0.1261
chr17	81195210	1110856	0.0137	0.1308
chr18	78077248	1011016	0.0129	0.216
chr19	59128983	843927	0.0143	0.1801
chr20	63025520	853598	0.0135	0.125
chr21	48129895	521204	0.0108	0.1215
chr22	51304566	503409	0.0098	0.1048
chrMT	16571	10228	0.6172	0.8452
chrX	155270560	2122518	0.0137	0.1294
chrY	59373566	144580	0.0024	0.087

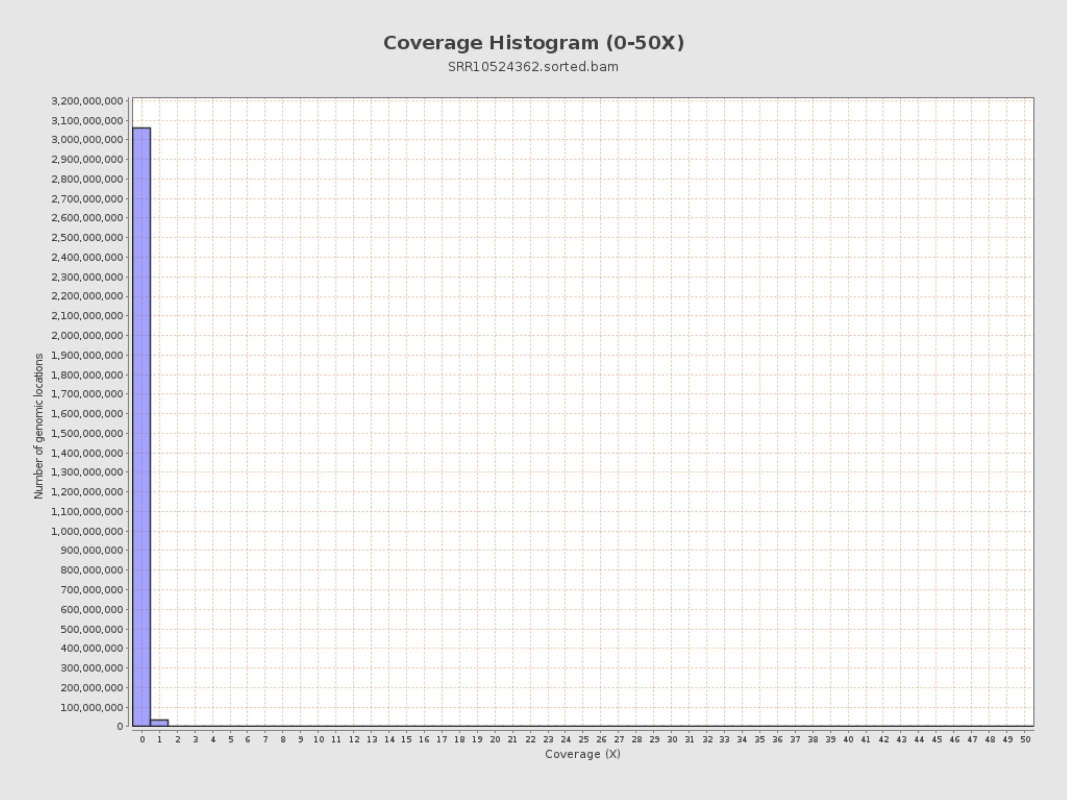
3. Results : Coverage across reference



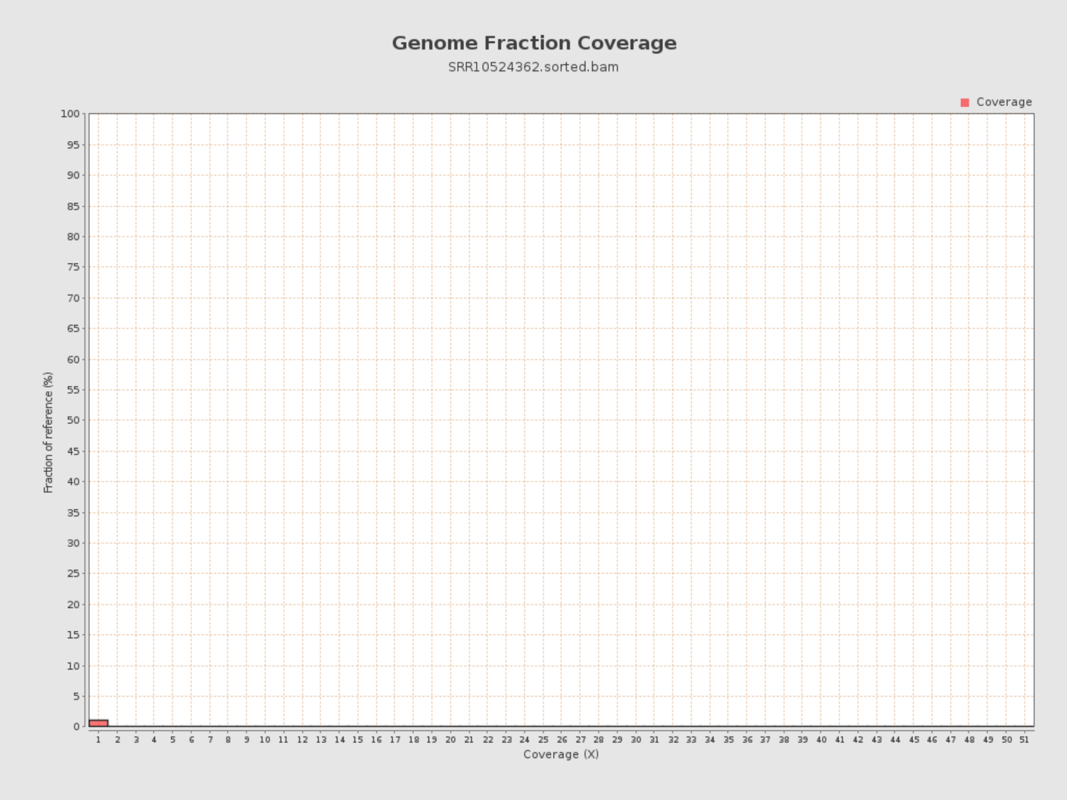
4. Results : Coverage Histogram



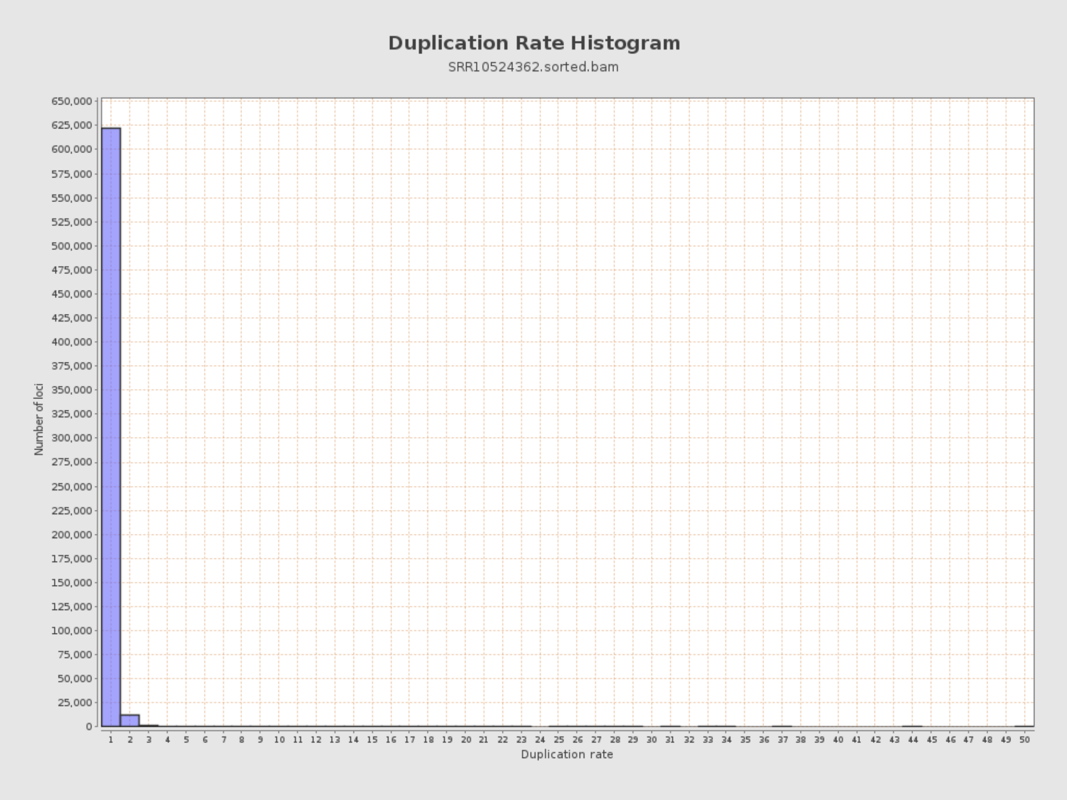
5. Results : Coverage Histogram (0-50X)



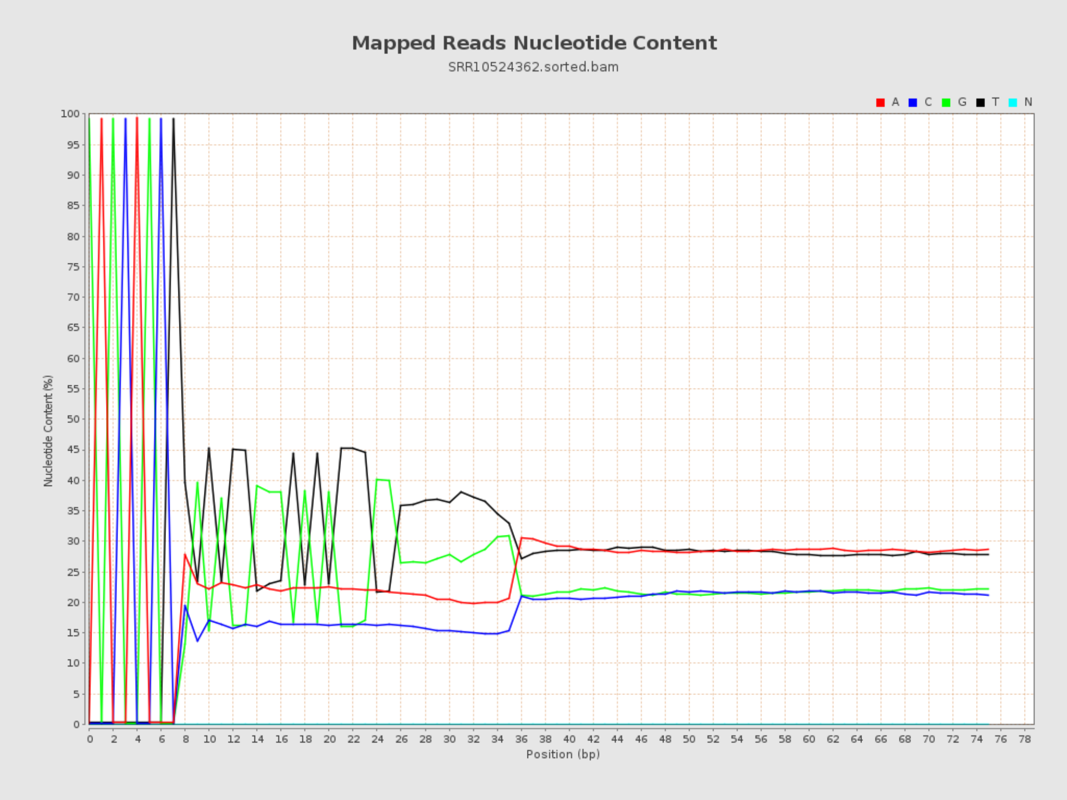
6. Results : Genome Fraction Coverage



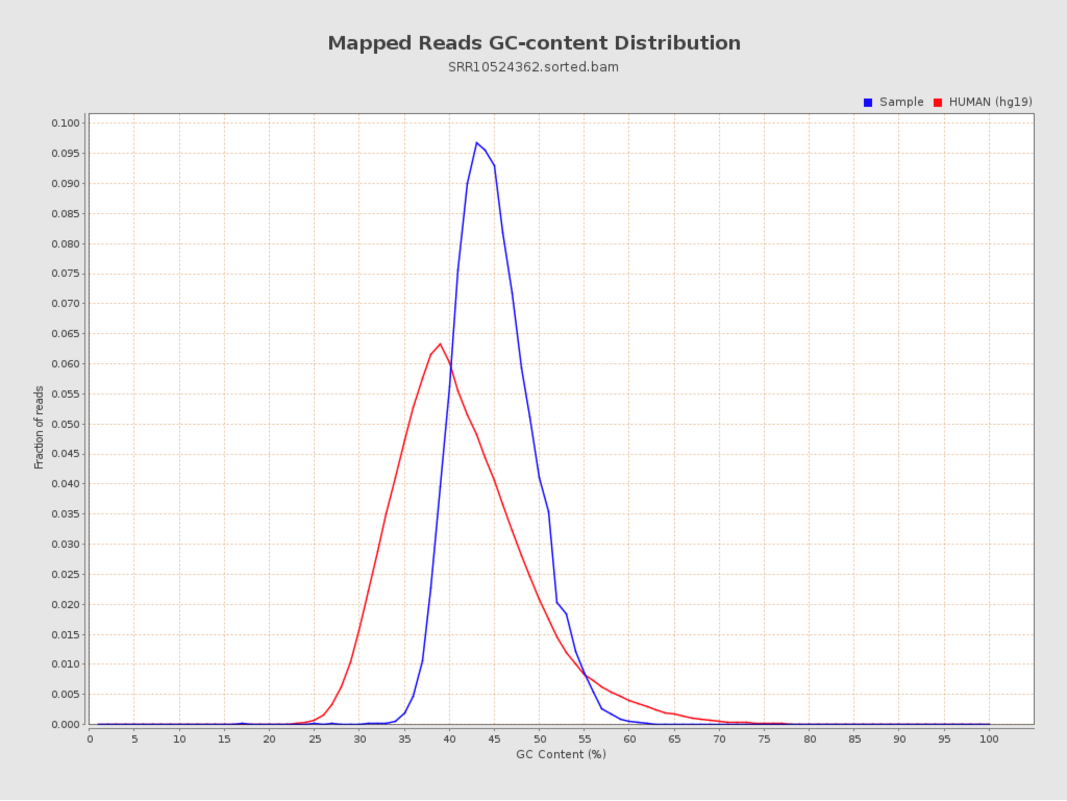
7. Results : Duplication Rate Histogram



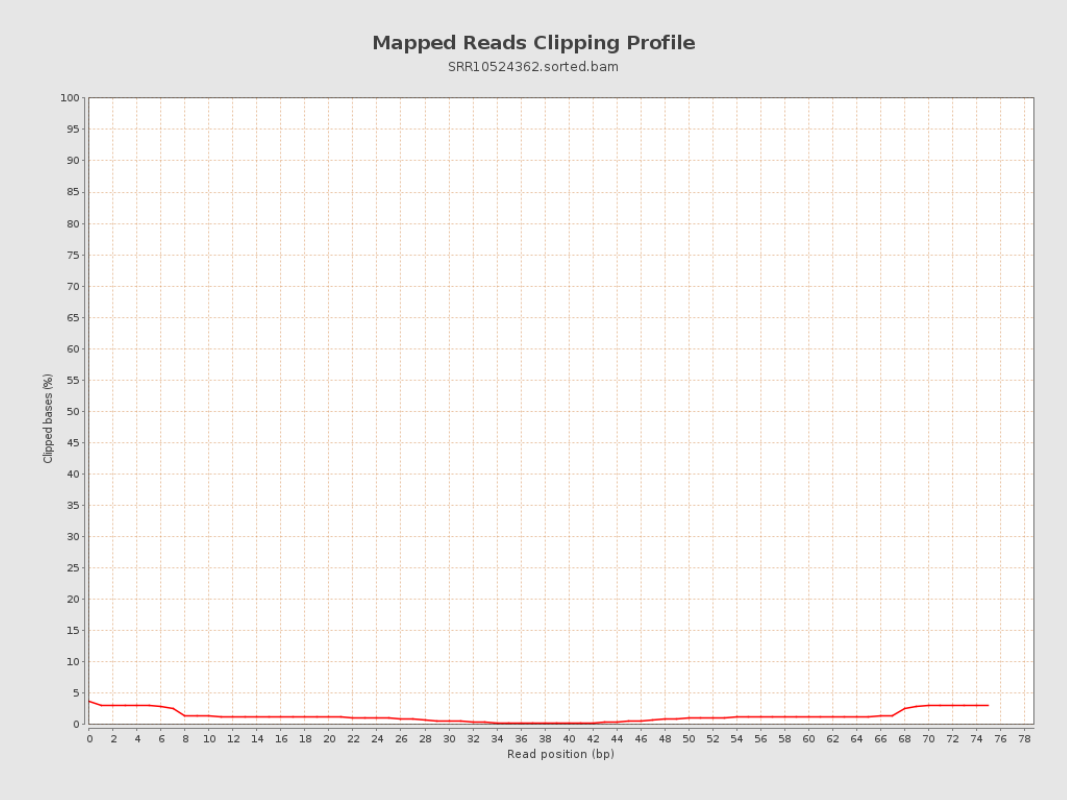
8. Results : Mapped Reads Nucleotide Content



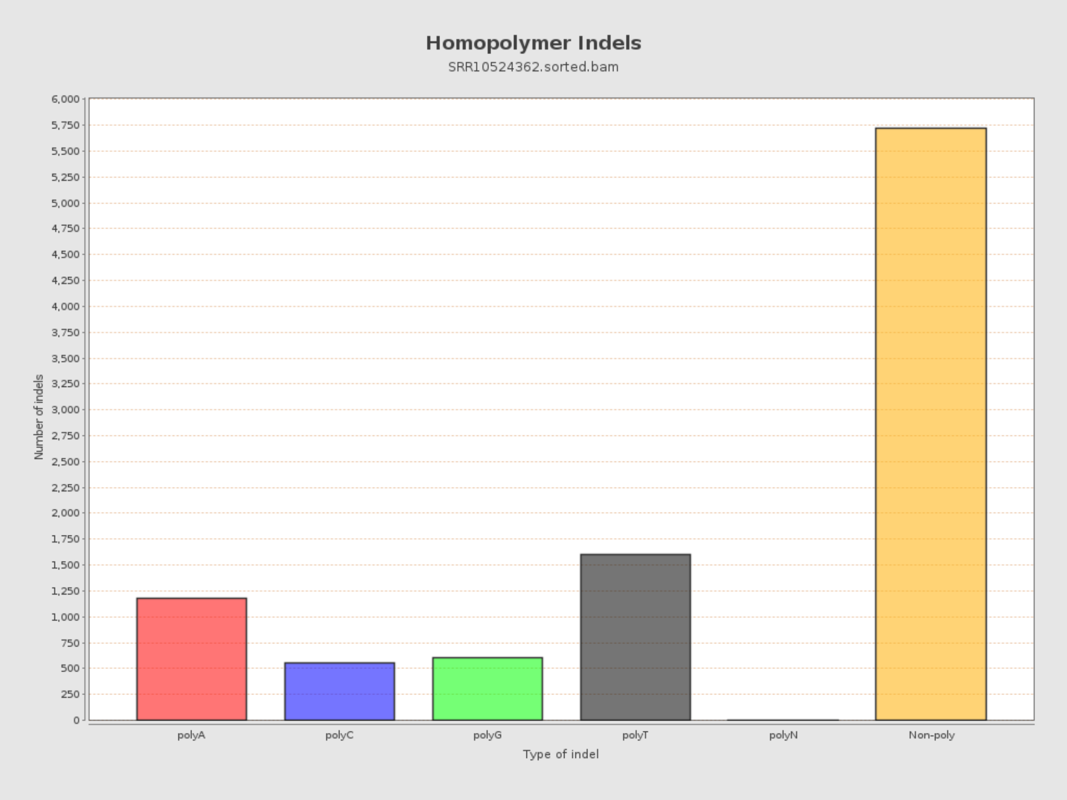
9. Results : Mapped Reads GC-content Distribution



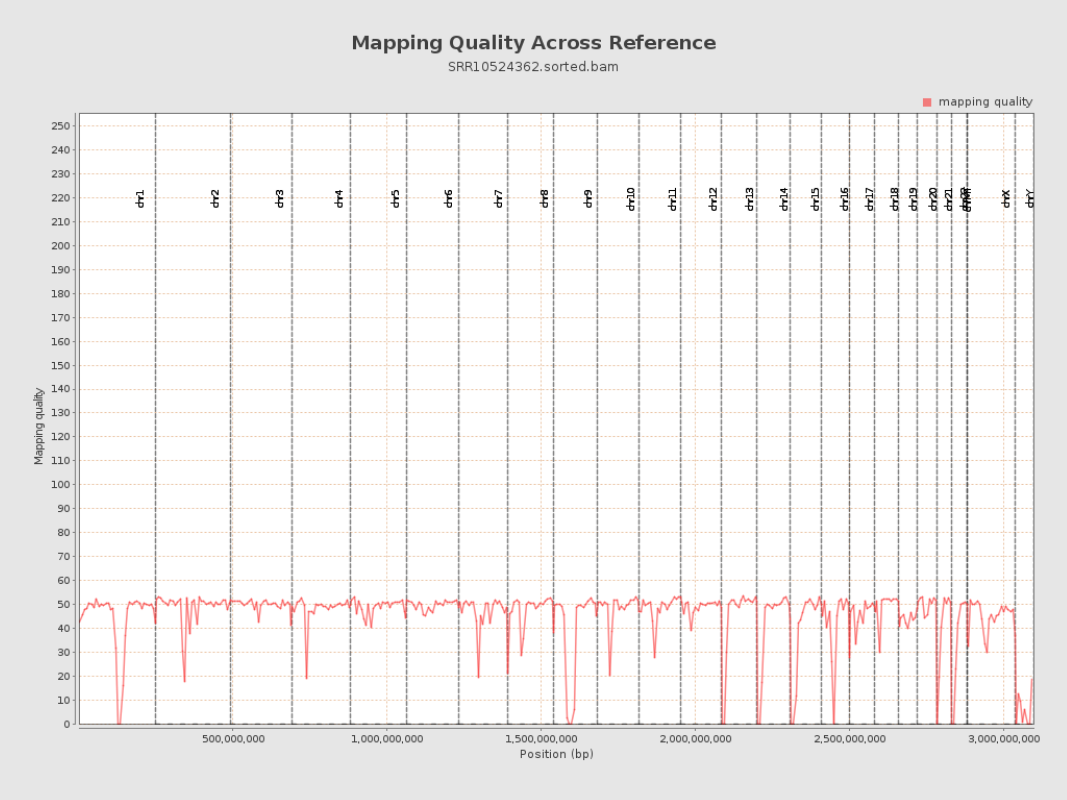
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram