Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 06:02:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524488.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_SRR10524488 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524488.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 06:02:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524488.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	879,536
Mapped reads	816,355 / 92.82%
Unmapped reads	63,181 / 7.18%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,946 / 0.22%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	23,899 / 2.72%
Duplication rate	2.28%
Clipped reads	817,315 / 92.93%

2.2. ACGT Content

Number/percentage of A's	11,408,482 / 23.96%
Number/percentage of C's	8,479,930 / 17.81%
Number/percentage of T's	15,574,595 / 32.71%
Number/percentage of G's	12,152,611 / 25.52%
Number/percentage of N's	838 / 0%
GC Percentage	43.33%

2.3. Coverage

Mean	0.0154

Standard Deviation	0.1637

2.4. Mapping Quality

Mean Mapping Quality	45.39

2.5. Mismatches and indels

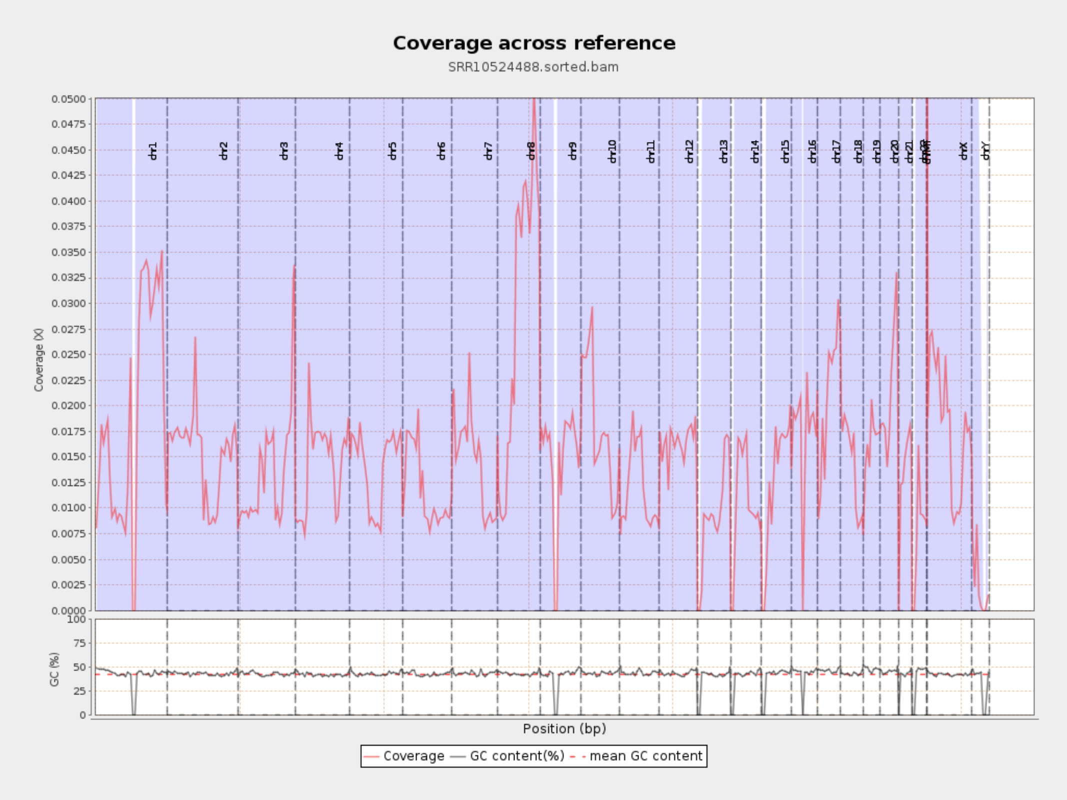
General error rate	0.47%
Mismatches	219,177
Insertions	2,513
Mapped reads with at least one insertion	0.31%
Deletions	8,625
Mapped reads with at least one deletion	1.05%
Homopolymer indels	46.12%

2.6. Chromosome stats

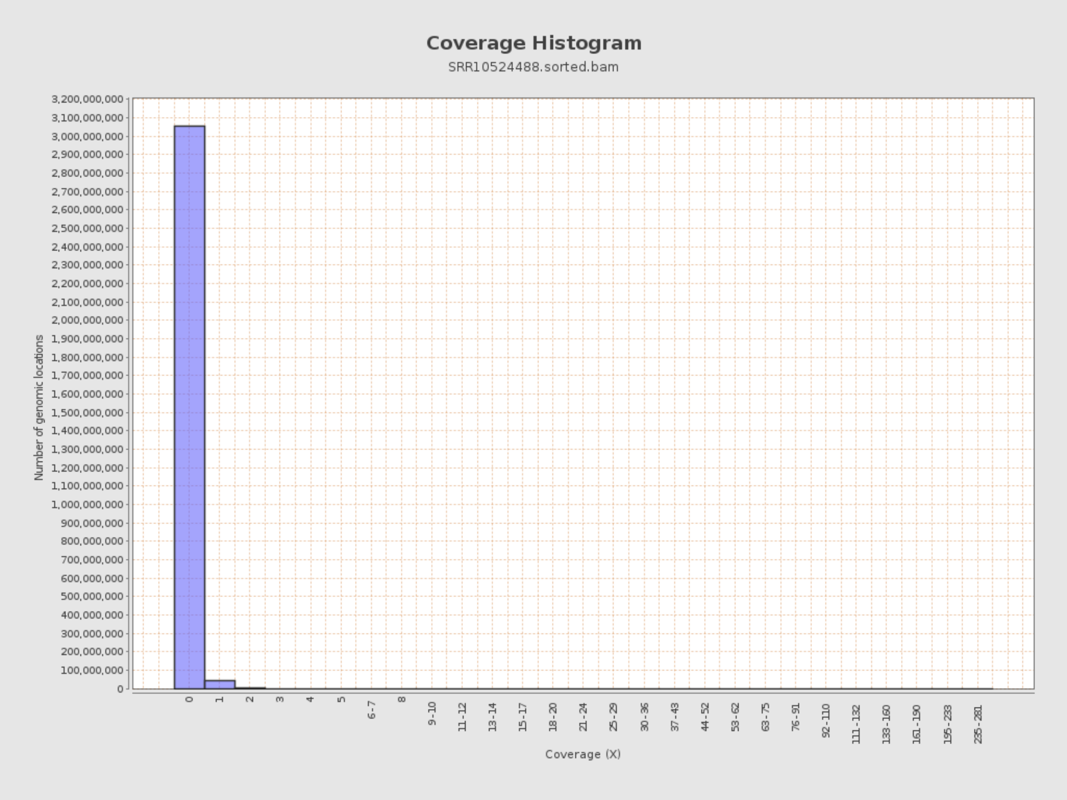
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4692690	0.0188	0.2559
chr2	243199373	3742000	0.0154	0.1794
chr3	198022430	2658756	0.0134	0.1238
chr4	191154276	2741303	0.0143	0.1376
chr5	180915260	2560072	0.0142	0.1268
chr6	171115067	2018495	0.0118	0.1285
chr7	159138663	2334034	0.0147	0.1954

chr8	146364022	4328861	0.0296	0.1958
chr9	141213431	2074044	0.0147	0.1554
chr10	135534747	2484272	0.0183	0.1764
chr11	135006516	1628814	0.0121	0.1549
chr12	133851895	2196675	0.0164	0.1364
chr13	115169878	1072282	0.0093	0.1046
chr14	107349540	1126818	0.0105	0.1102
chr15	102531392	1265837	0.0123	0.1207
chr16	90354753	1526064	0.0169	0.1441
chr17	81195210	1679791	0.0207	0.1572
chr18	78077248	1124545	0.0144	0.2311
chr19	59128983	965150	0.0163	0.1992
chr20	63025520	1368151	0.0217	0.1588
chr21	48129895	655946	0.0136	0.1294
chr22	51304566	397916	0.0078	0.0938
chrMT	16571	2223	0.1342	0.3664
chrX	155270560	2840526	0.0183	0.1532
chrY	59373566	146133	0.0025	0.0748

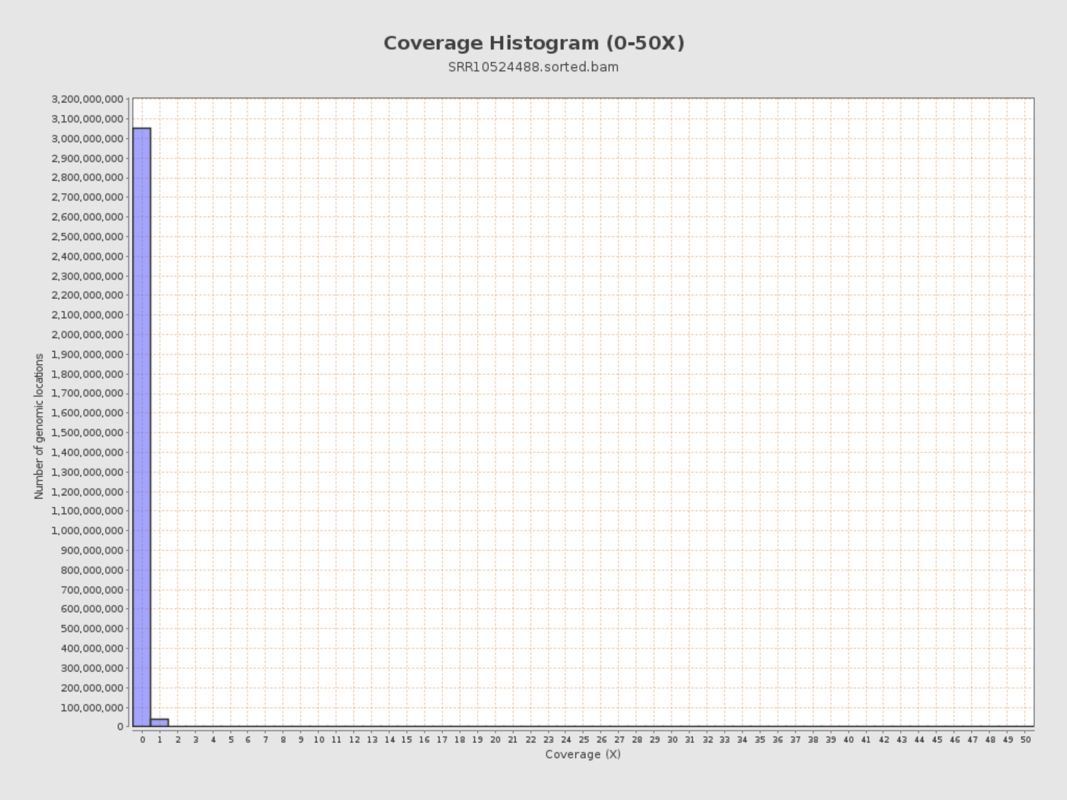
3. Results : Coverage across reference



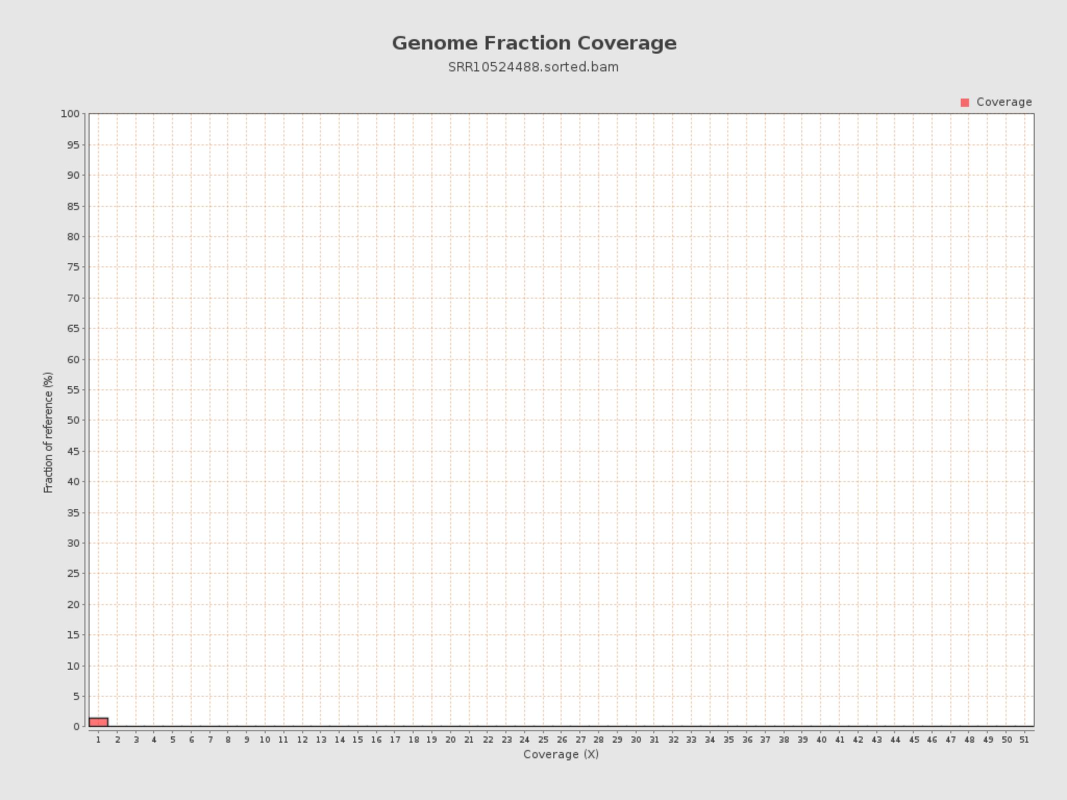
4. Results : Coverage Histogram



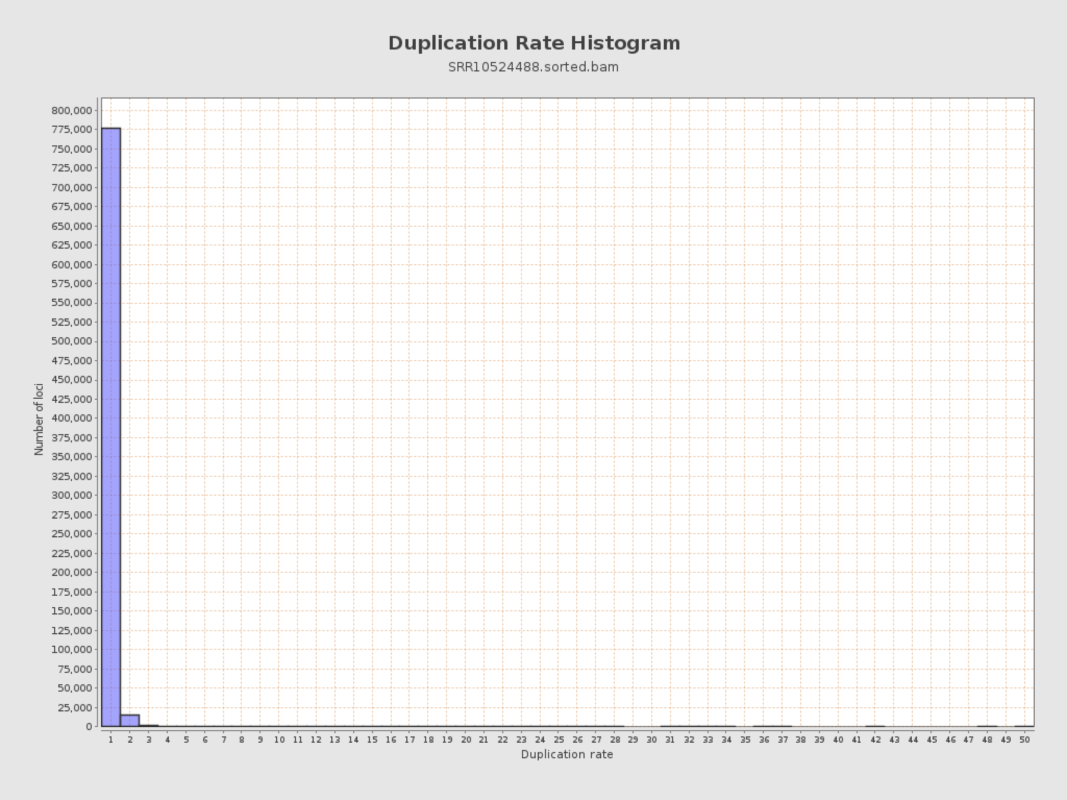
5. Results : Coverage Histogram (0-50X)



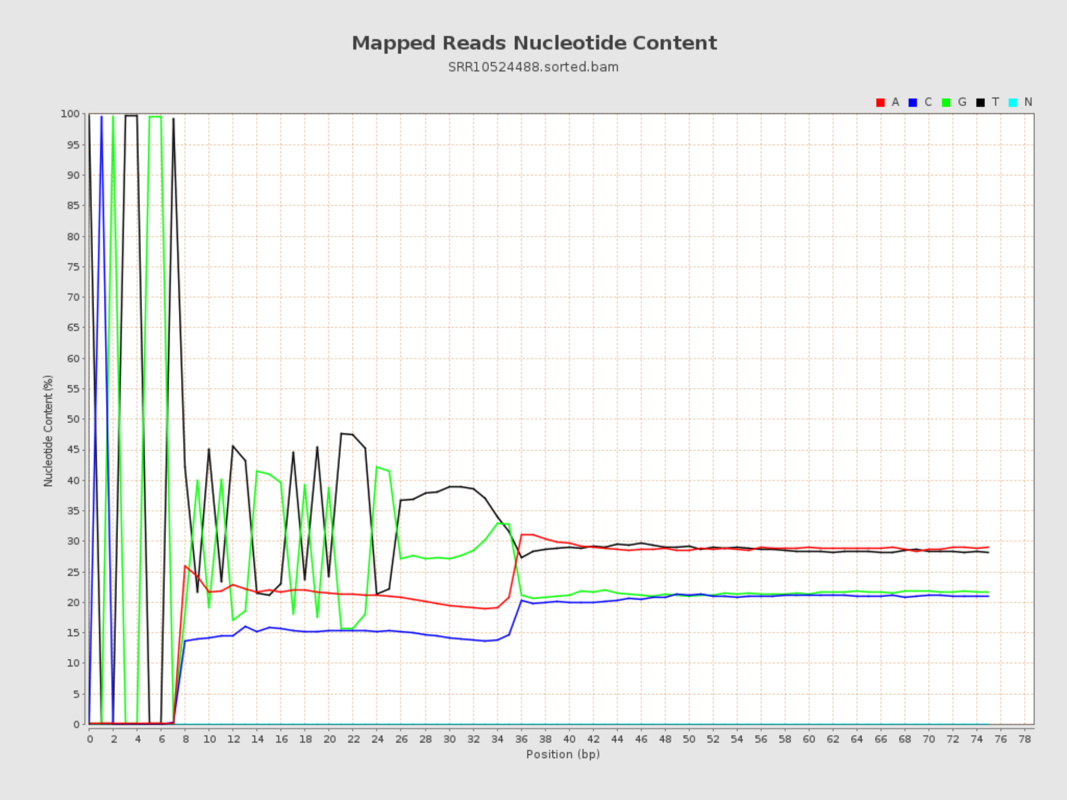
6. Results : Genome Fraction Coverage



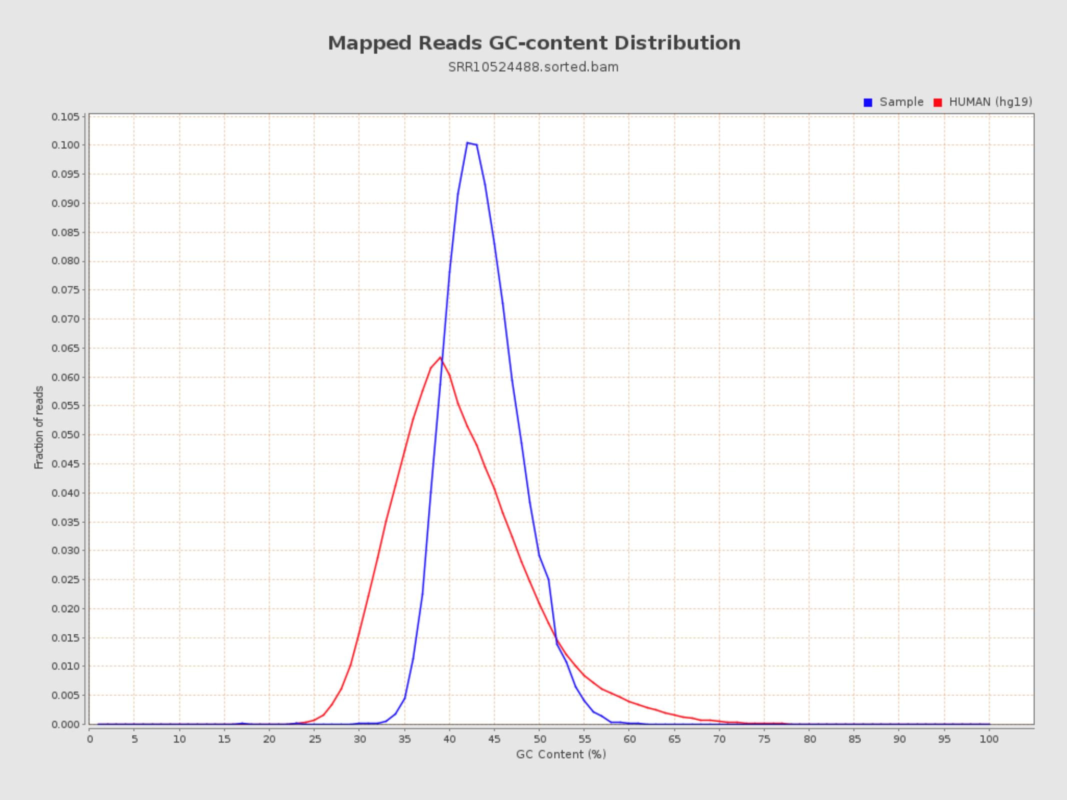
7. Results : Duplication Rate Histogram



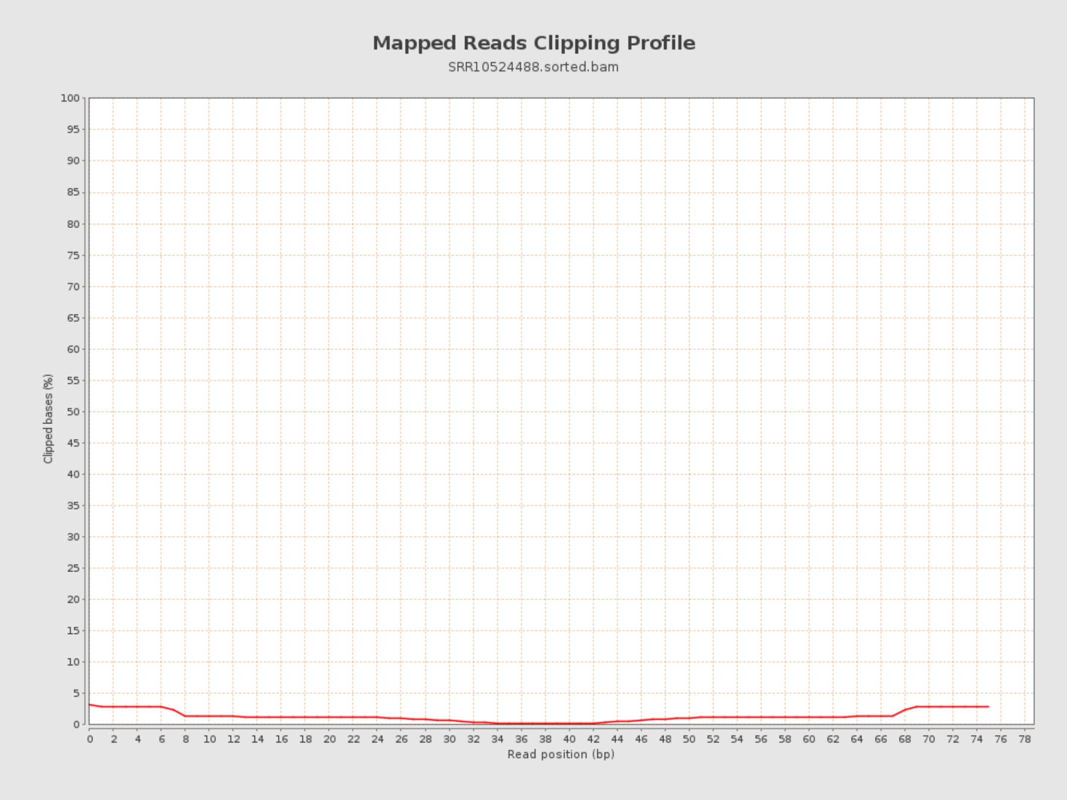
8. Results : Mapped Reads Nucleotide Content



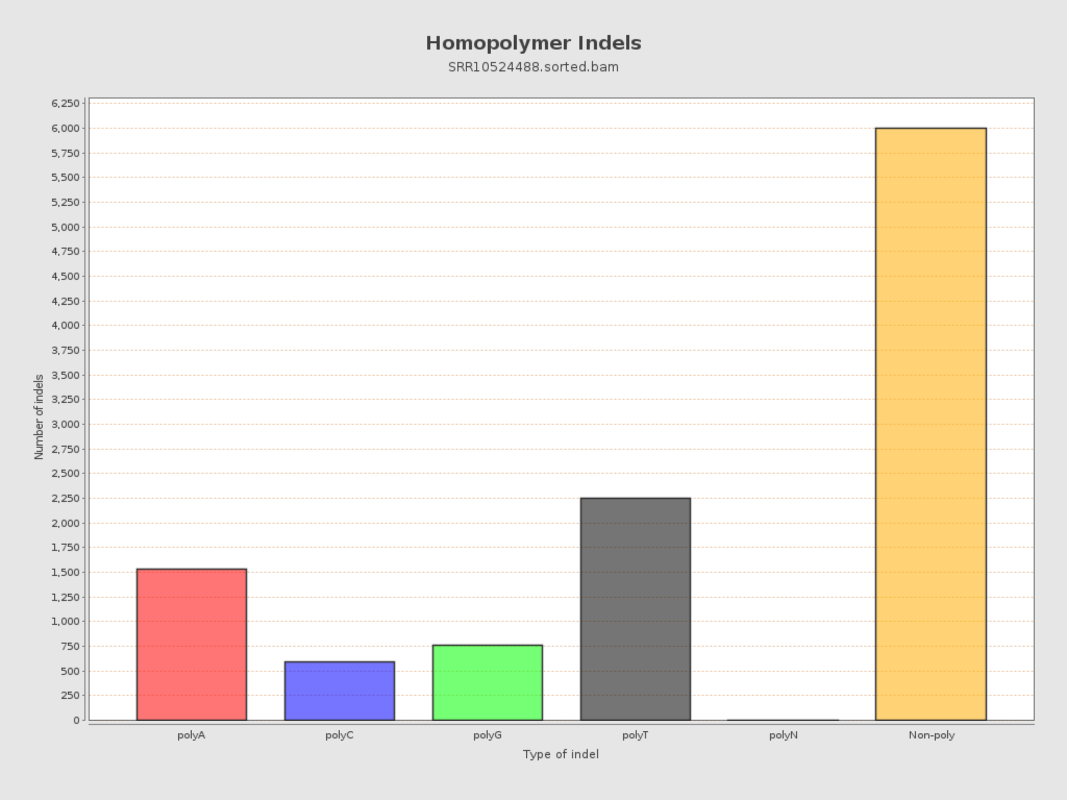
9. Results : Mapped Reads GC-content Distribution



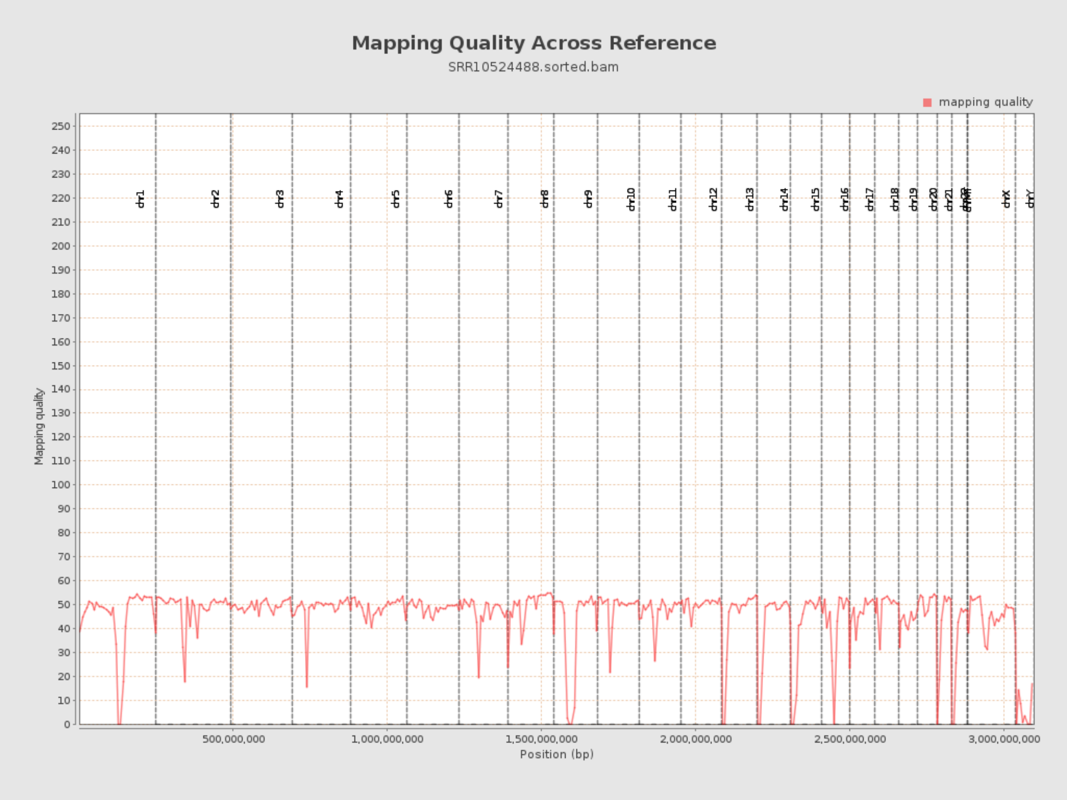
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram