Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 20:37:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524787.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_SRR10524787 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524787.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 20:37:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524787.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,152,321
Mapped reads	1,038,376 / 90.11%
Unmapped reads	113,945 / 9.89%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,967 / 0.34%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	36,868 / 3.2%
Duplication rate	2.75%
Clipped reads	1,040,347 / 90.28%

2.2. ACGT Content

Number/percentage of A's	14,366,672 / 24.57%
Number/percentage of C's	10,593,115 / 18.11%
Number/percentage of T's	19,262,355 / 32.94%
Number/percentage of G's	14,251,774 / 24.37%
Number/percentage of N's	6,363 / 0.01%
GC Percentage	42.48%

2.3. Coverage

Mean	0.0189

Standard Deviation	0.1887

2.4. Mapping Quality

Mean Mapping Quality	44.23

2.5. Mismatches and indels

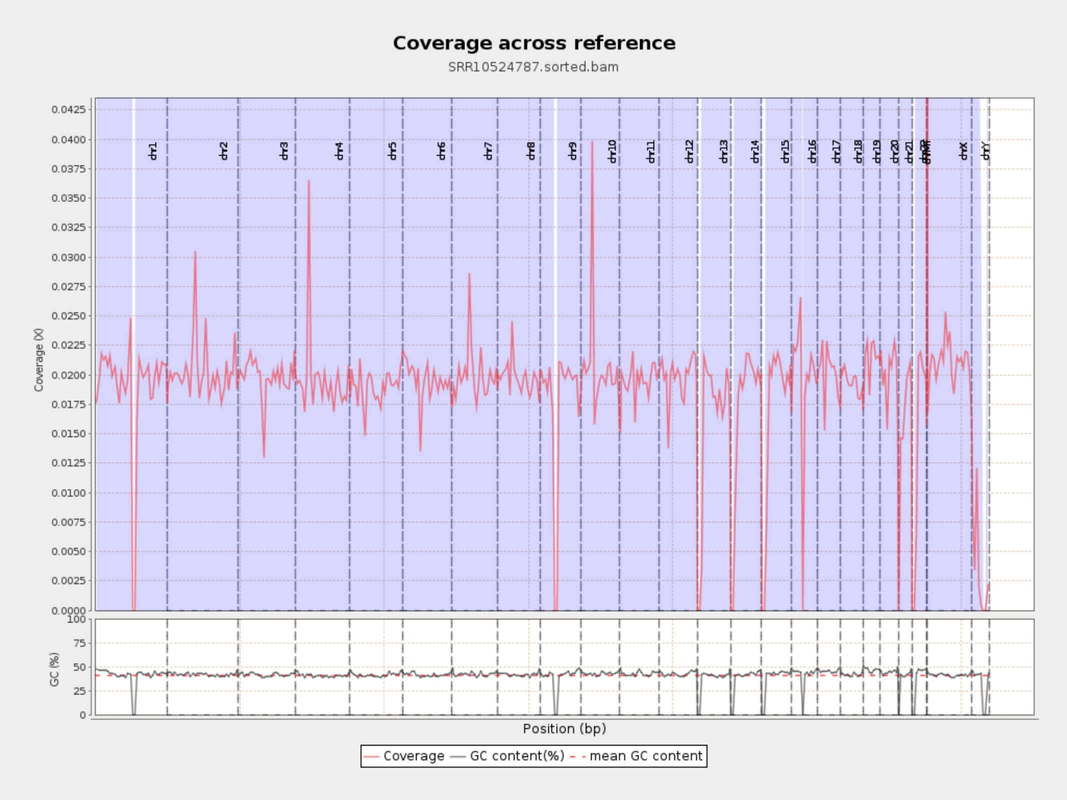
General error rate	0.53%
Mismatches	299,429
Insertions	4,279
Mapped reads with at least one insertion	0.41%
Deletions	11,246
Mapped reads with at least one deletion	1.08%
Homopolymer indels	42.67%

2.6. Chromosome stats

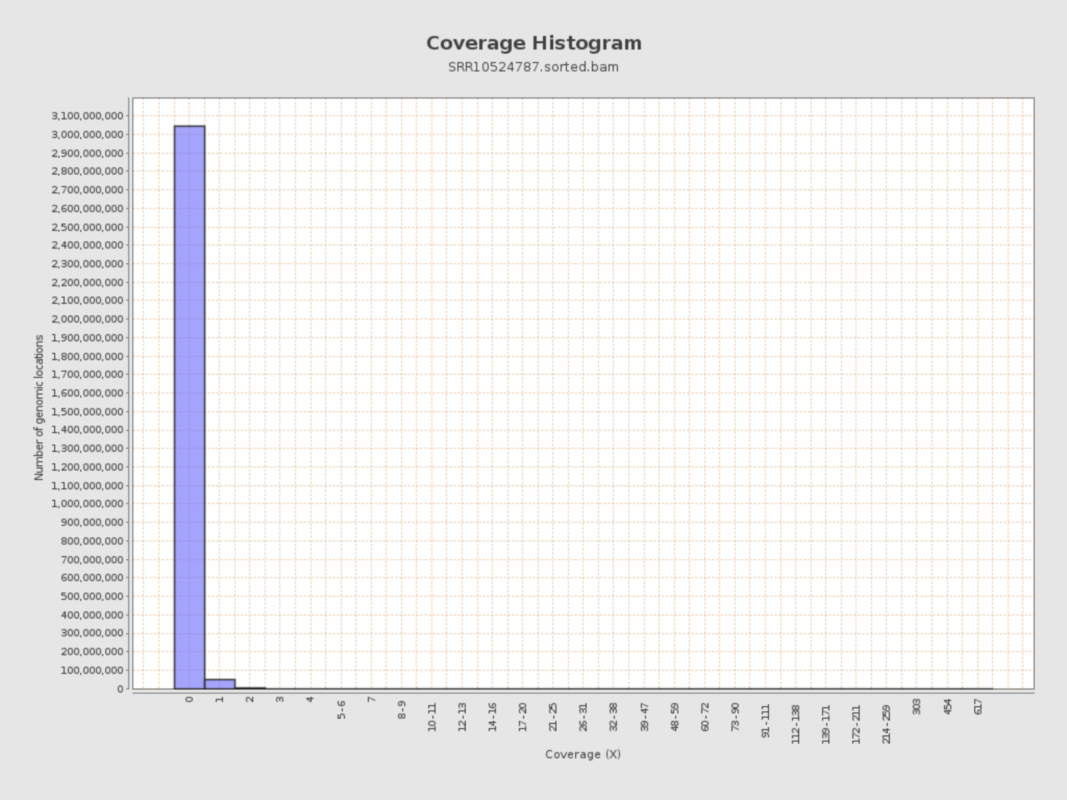
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4689714	0.0188	0.2318
chr2	243199373	4940619	0.0203	0.3035
chr3	198022430	3914615	0.0198	0.1531
chr4	191154276	3763290	0.0197	0.167
chr5	180915260	3447138	0.0191	0.1487
chr6	171115067	3333777	0.0195	0.1653
chr7	159138663	3188041	0.02	0.2087

chr8	146364022	2896616	0.0198	0.177
chr9	141213431	2465431	0.0175	0.1662
chr10	135534747	2816177	0.0208	0.2241
chr11	135006516	2641519	0.0196	0.1699
chr12	133851895	2661124	0.0199	0.1542
chr13	115169878	1822636	0.0158	0.1368
chr14	107349540	1793922	0.0167	0.1424
chr15	102531392	1692666	0.0165	0.1422
chr16	90354753	1742517	0.0193	0.1635
chr17	81195210	1637990	0.0202	0.1602
chr18	78077248	1514585	0.0194	0.2382
chr19	59128983	1267394	0.0214	0.2085
chr20	63025520	1268094	0.0201	0.161
chr21	48129895	771646	0.016	0.1456
chr22	51304566	732376	0.0143	0.1304
chrMT	16571	15788	0.9527	1.0711
chrX	155270560	3278374	0.0211	0.1671
chrY	59373566	202366	0.0034	0.1025

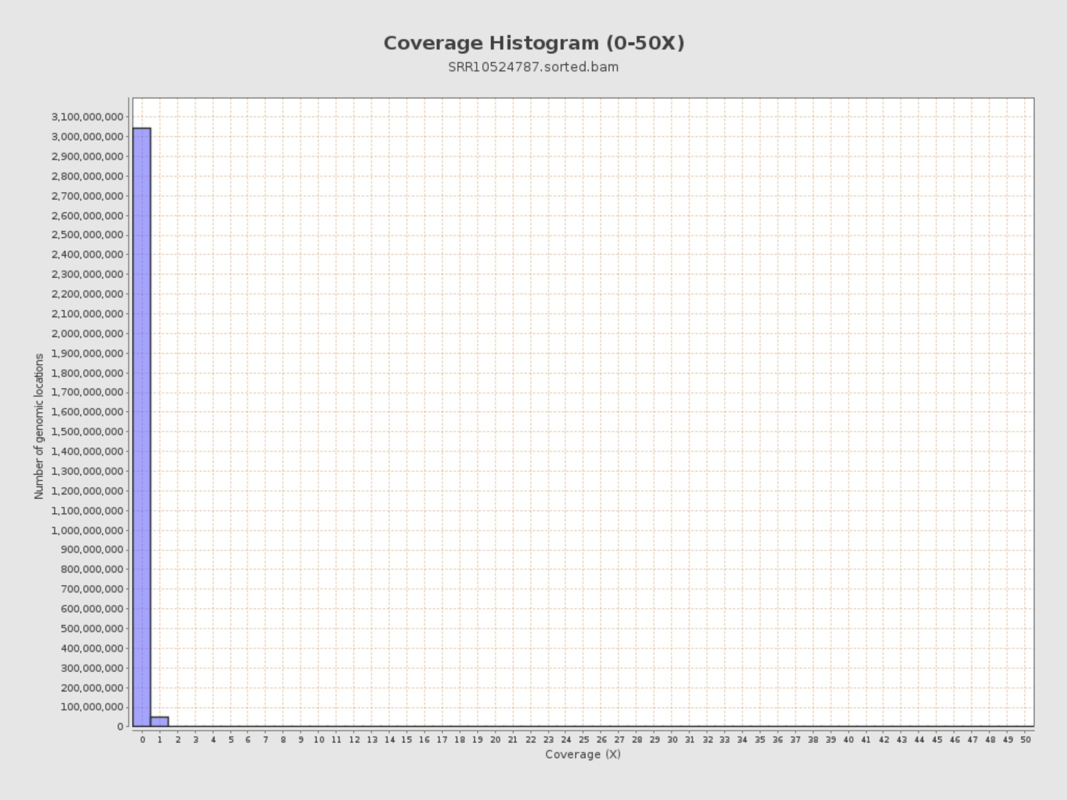
3. Results : Coverage across reference



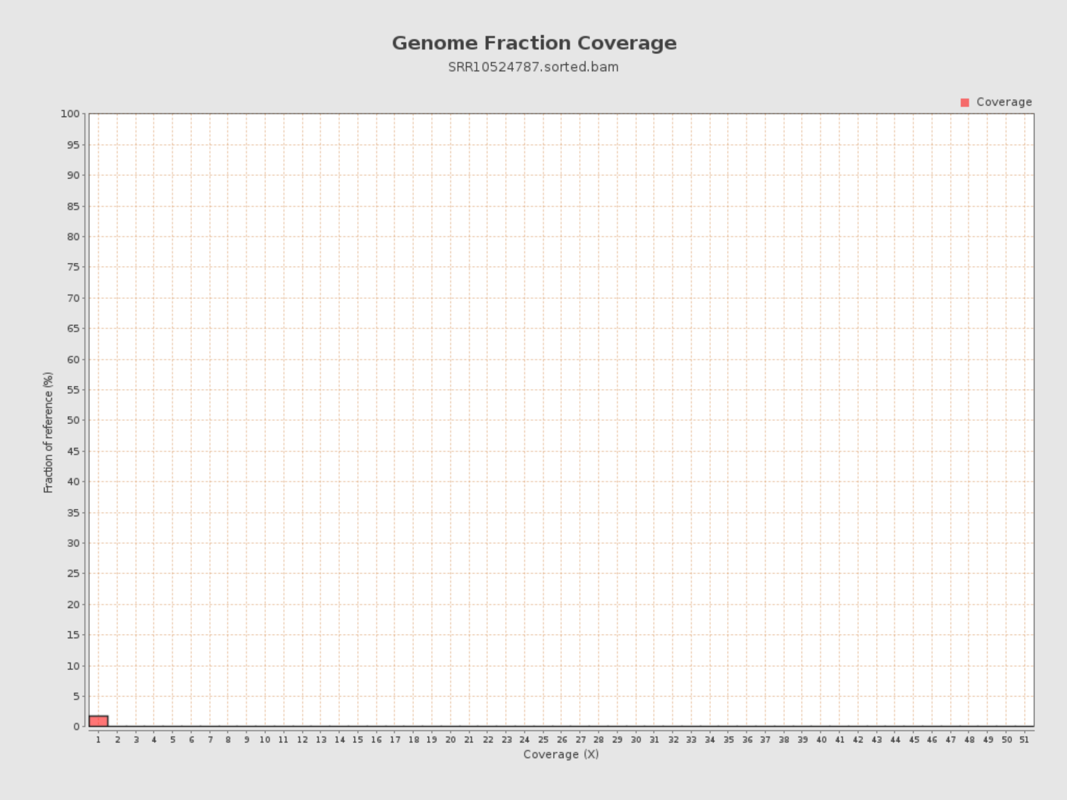
4. Results : Coverage Histogram



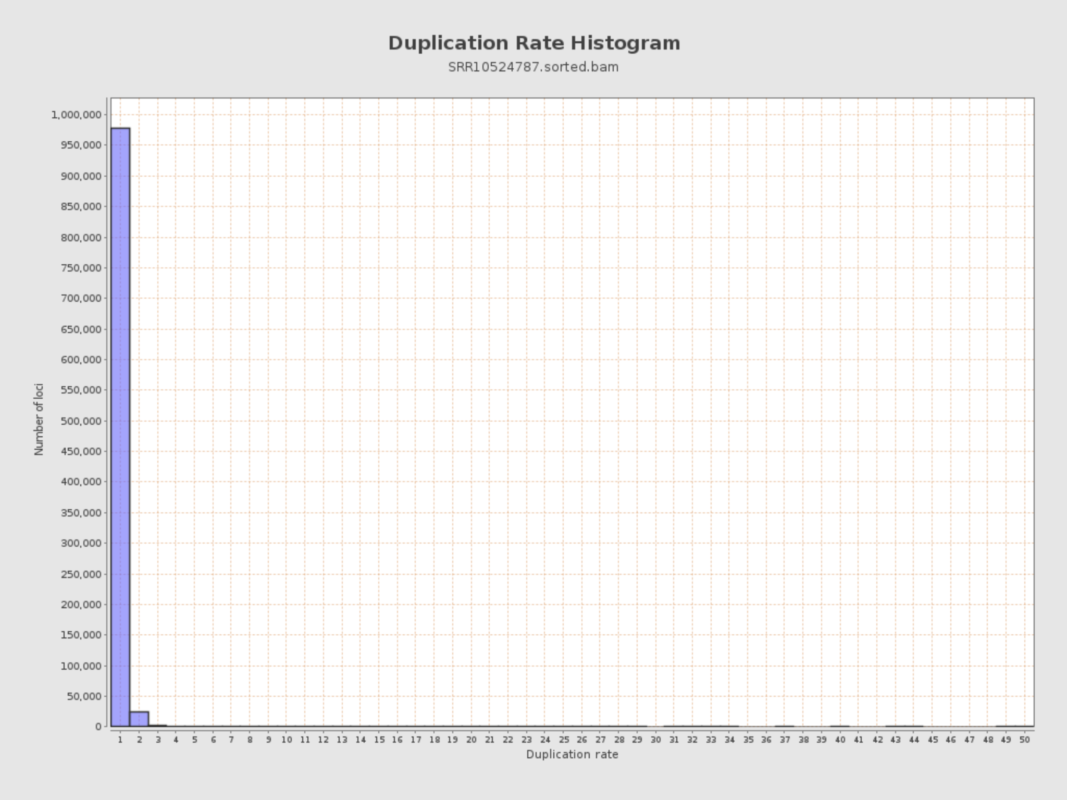
5. Results : Coverage Histogram (0-50X)



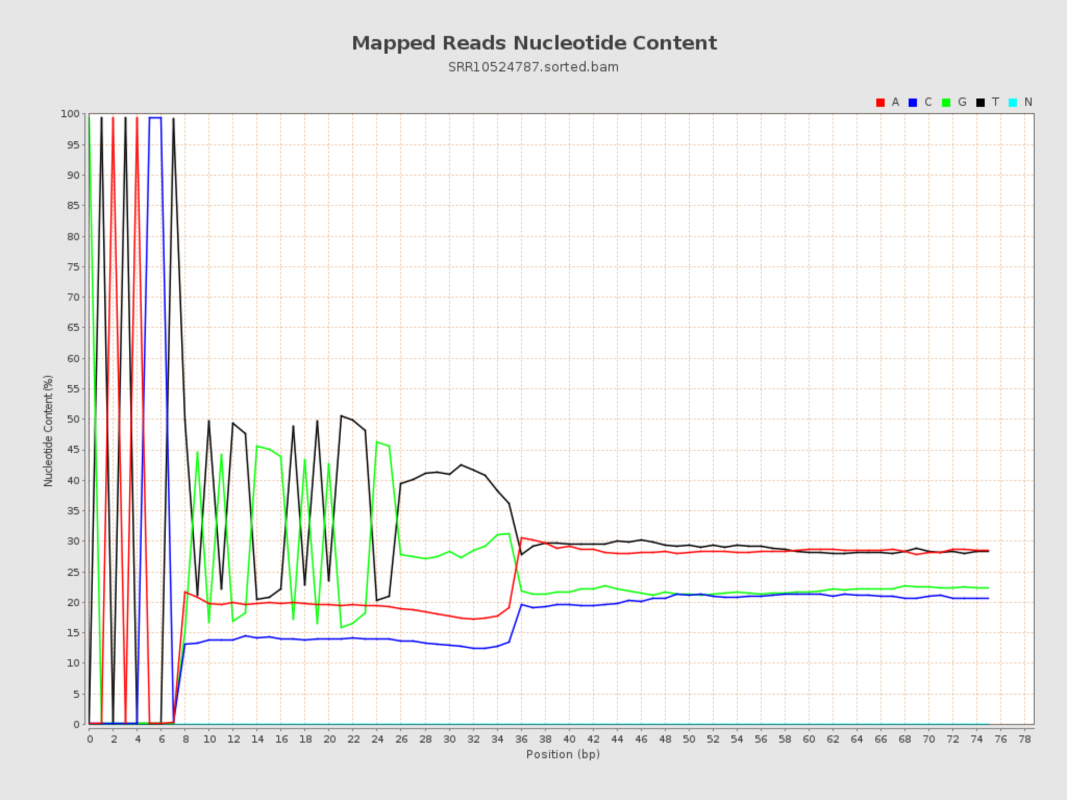
6. Results : Genome Fraction Coverage



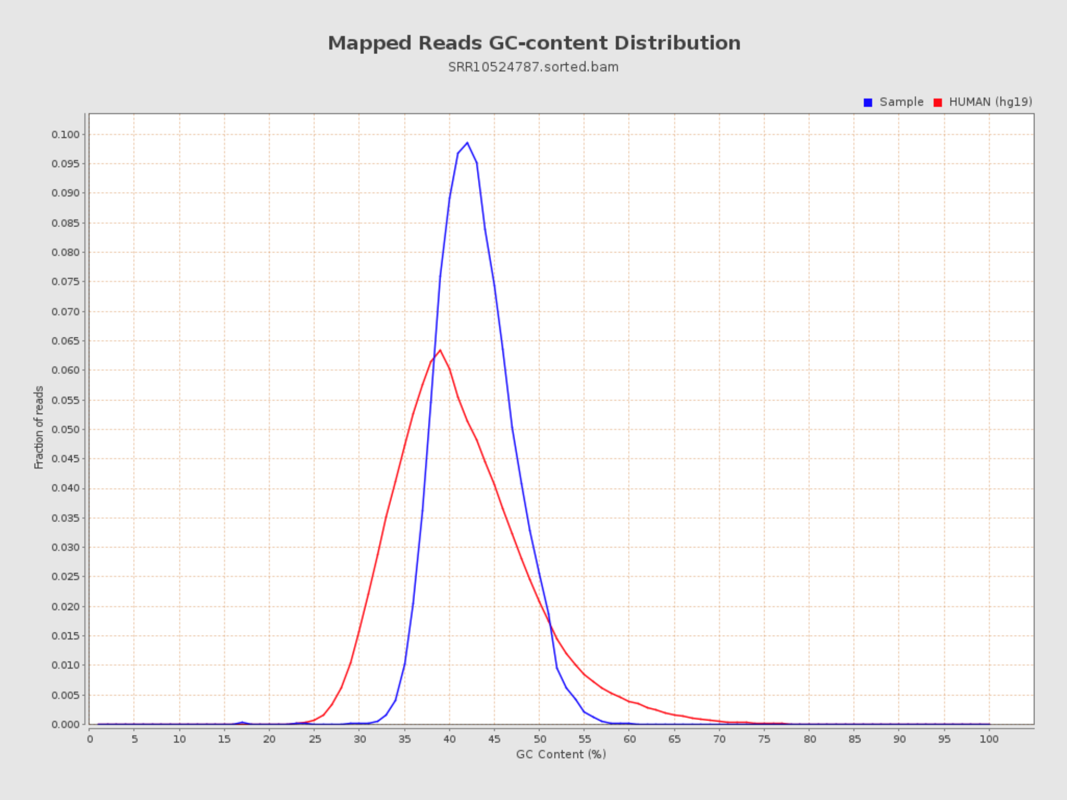
7. Results : Duplication Rate Histogram



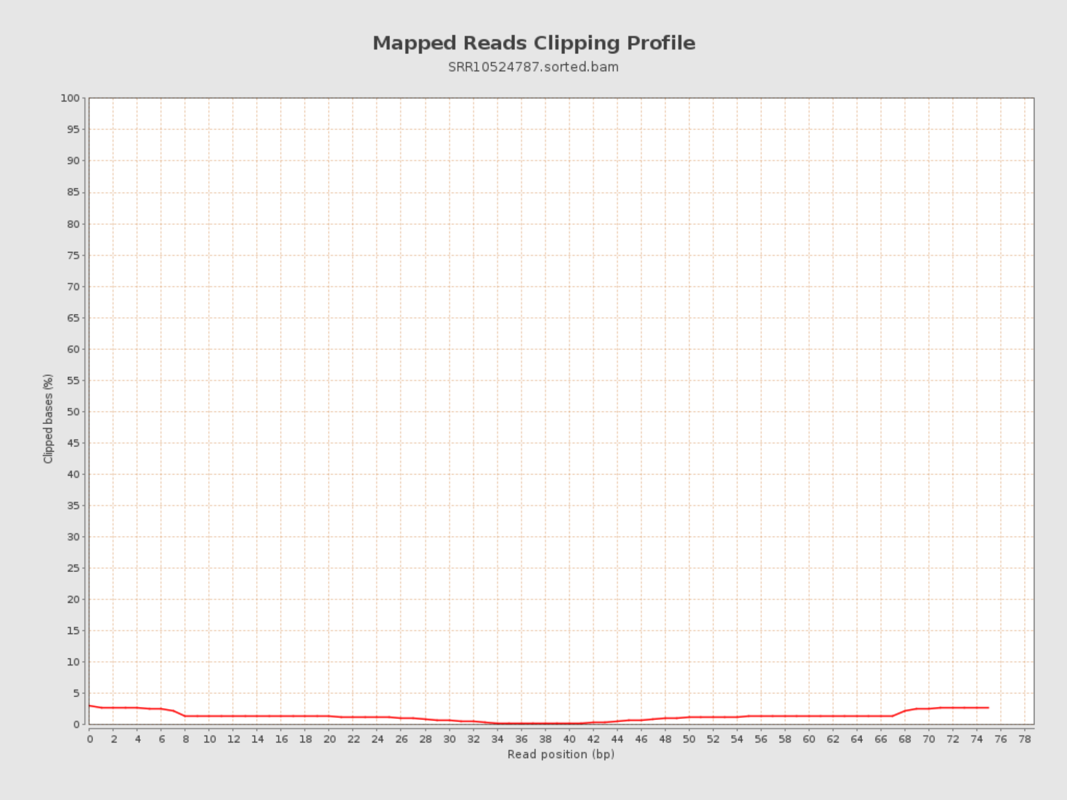
8. Results : Mapped Reads Nucleotide Content



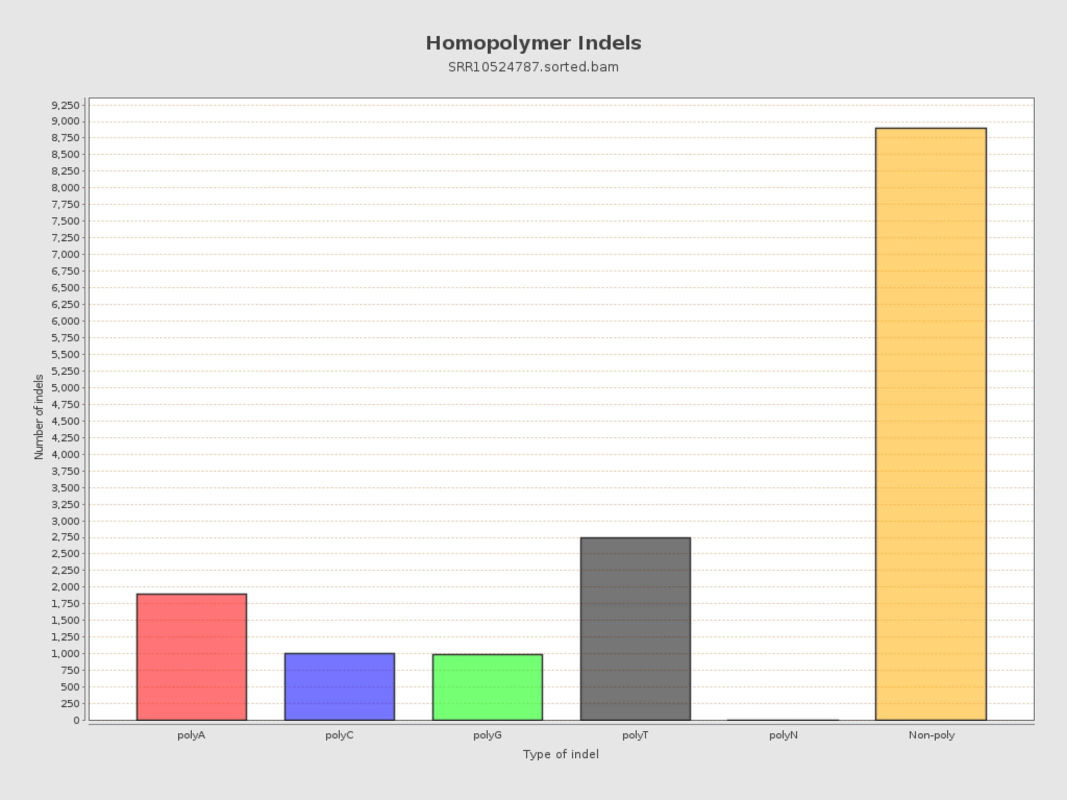
9. Results : Mapped Reads GC-content Distribution



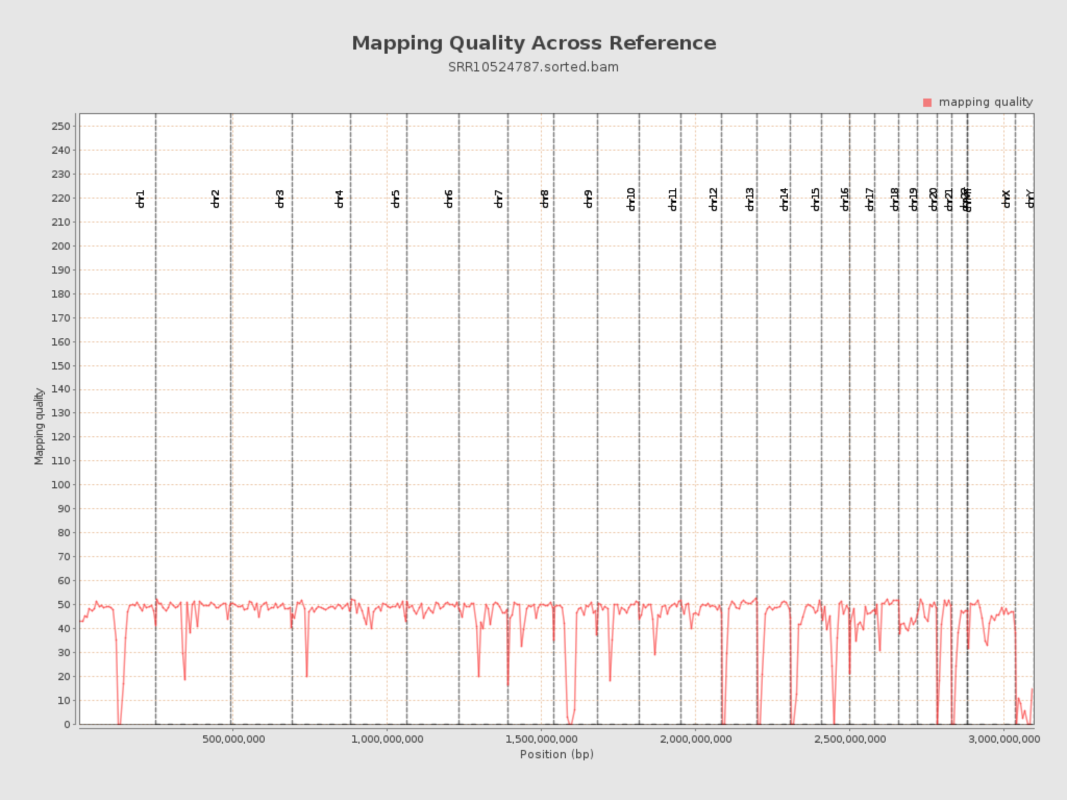
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram