Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 20:56:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524990.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_SRR10524990 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524990.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 20:56:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524990.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,294,594
Mapped reads	4,919,177 / 92.91%
Unmapped reads	375,417 / 7.09%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,801 / 0.2%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	422,341 / 7.98%
Duplication rate	6.29%
Clipped reads	4,924,652 / 93.01%

2.2. ACGT Content

Number/percentage of A's	71,234,878 / 24.88%
Number/percentage of C's	50,492,309 / 17.63%
Number/percentage of T's	89,582,147 / 31.29%
Number/percentage of G's	75,014,095 / 26.2%
Number/percentage of N's	3,337 / 0%
GC Percentage	43.83%

2.3. Coverage

Mean	0.0925

Standard Deviation	0.6829

2.4. Mapping Quality

Mean Mapping Quality	45.87

2.5. Mismatches and indels

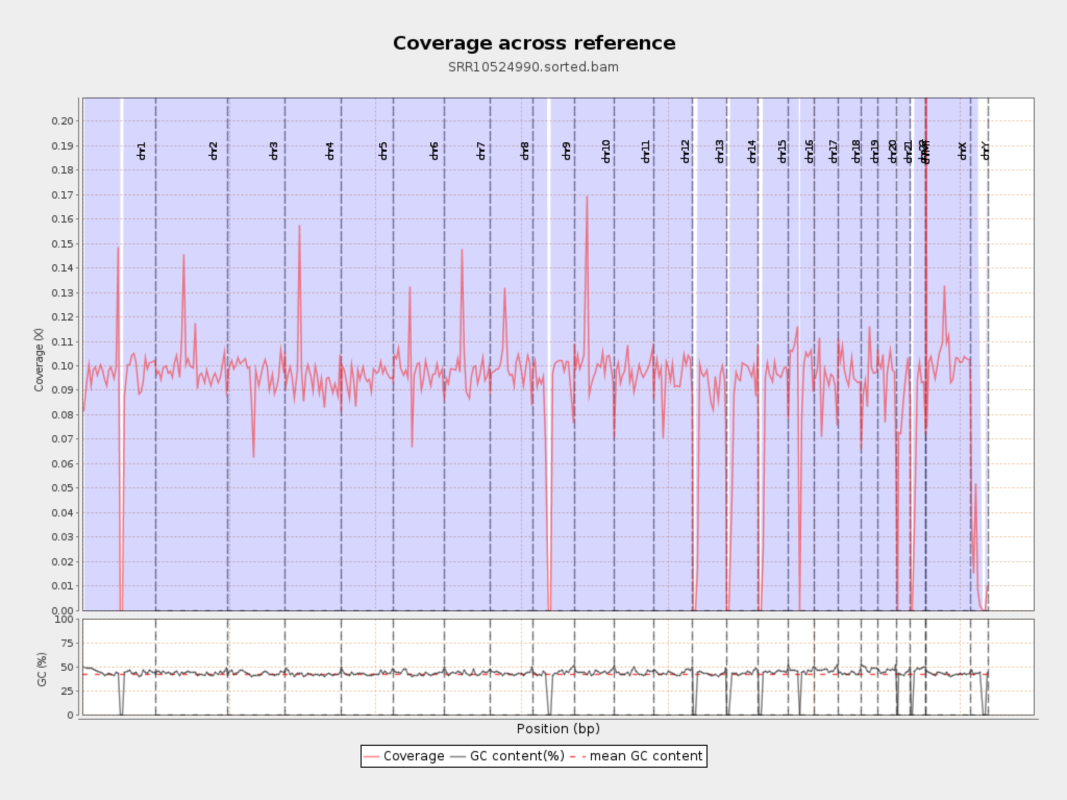
General error rate	0.49%
Mismatches	1,360,515
Insertions	15,350
Mapped reads with at least one insertion	0.31%
Deletions	53,191
Mapped reads with at least one deletion	1.07%
Homopolymer indels	44.94%

2.6. Chromosome stats

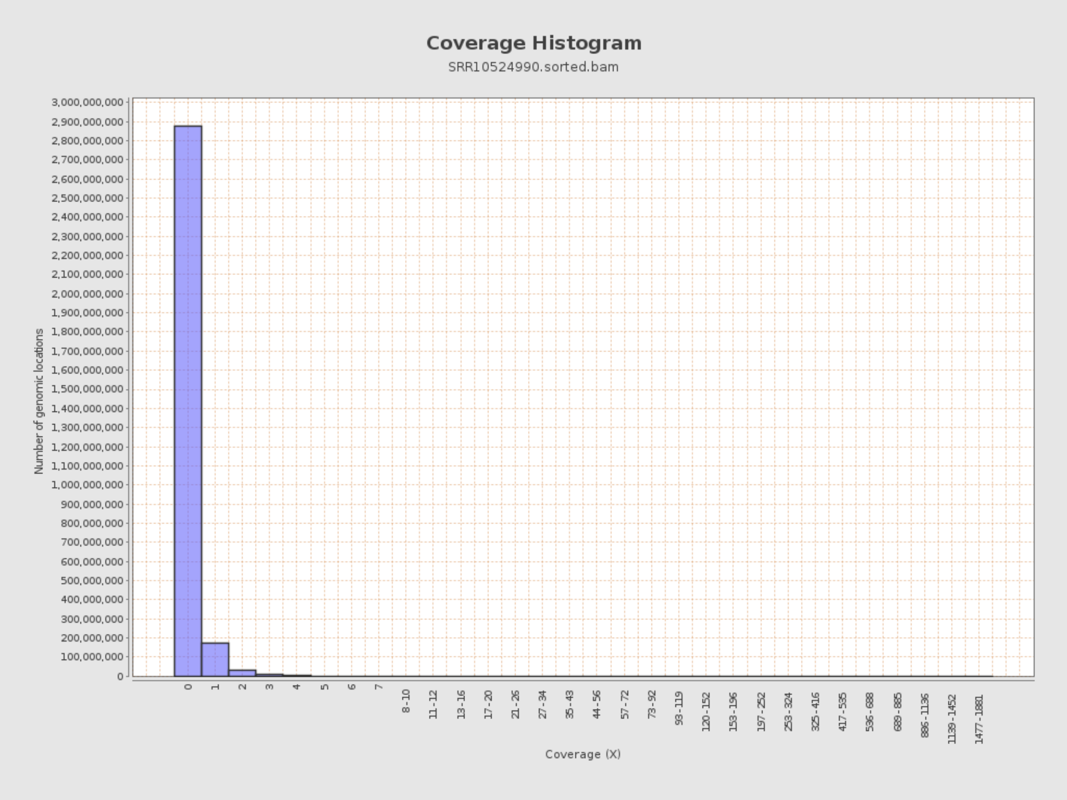
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	23117988	0.0927	1.3213
chr2	243199373	24326438	0.1	0.7817
chr3	198022430	19080780	0.0964	0.4017
chr4	191154276	18435885	0.0964	0.5155
chr5	180915260	17297969	0.0956	0.3978
chr6	171115067	16796824	0.0982	0.5945
chr7	159138663	15781512	0.0992	0.8818

chr8	146364022	14648617	0.1001	0.7239
chr9	141213431	11963999	0.0847	0.5728
chr10	135534747	13989903	0.1032	0.7452
chr11	135006516	13148120	0.0974	0.6679
chr12	133851895	12924618	0.0966	0.4094
chr13	115169878	8978138	0.078	0.3592
chr14	107349540	8652182	0.0806	0.3934
chr15	102531392	8017572	0.0782	0.4006
chr16	90354753	8322012	0.0921	0.4451
chr17	81195210	7606883	0.0937	0.4905
chr18	78077248	7667019	0.0982	1.0383
chr19	59128983	5646644	0.0955	0.8293
chr20	63025520	6073237	0.0964	0.4152
chr21	48129895	3774487	0.0784	0.4537
chr22	51304566	3350966	0.0653	0.3237
chrMT	16571	9352	0.5644	0.8735
chrX	155270560	15941428	0.1027	0.4944
chrY	59373566	865432	0.0146	0.3787

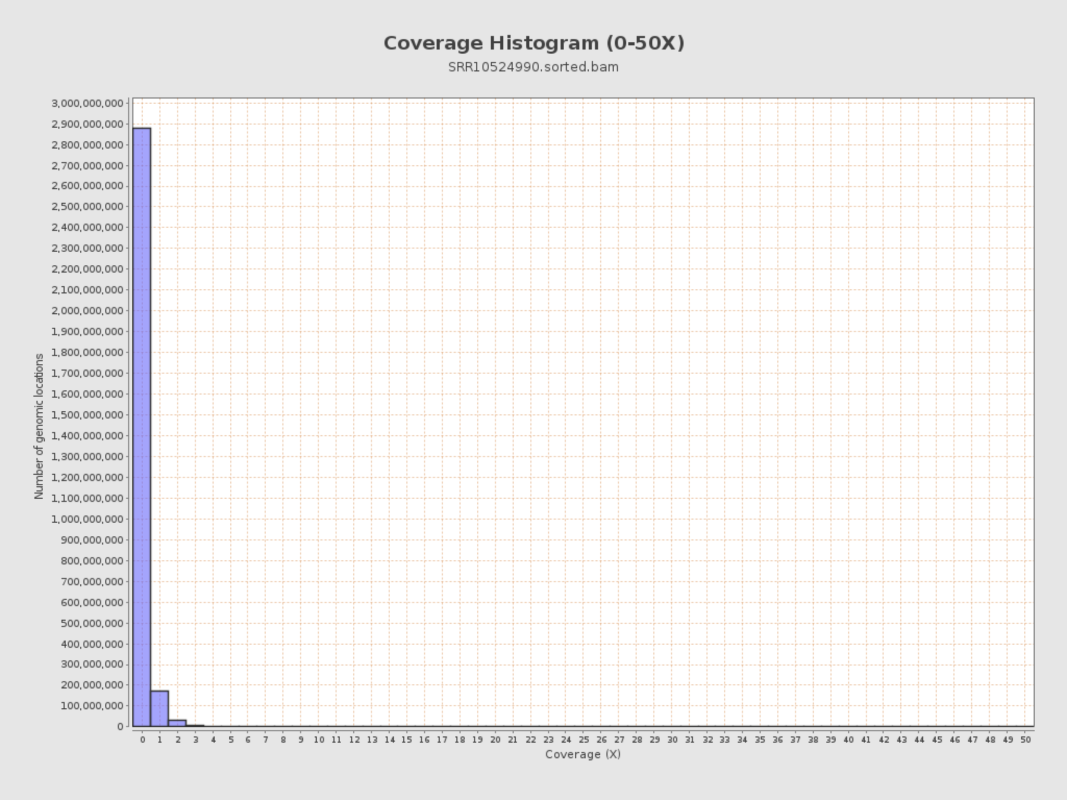
3. Results : Coverage across reference



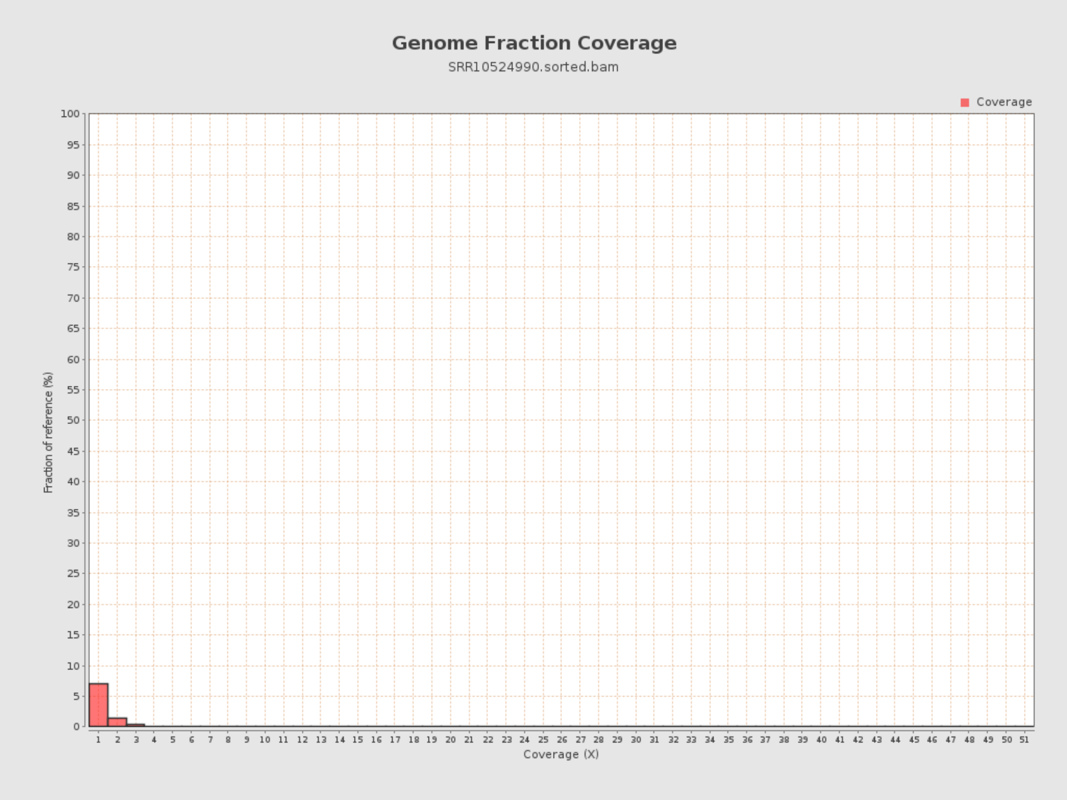
4. Results : Coverage Histogram



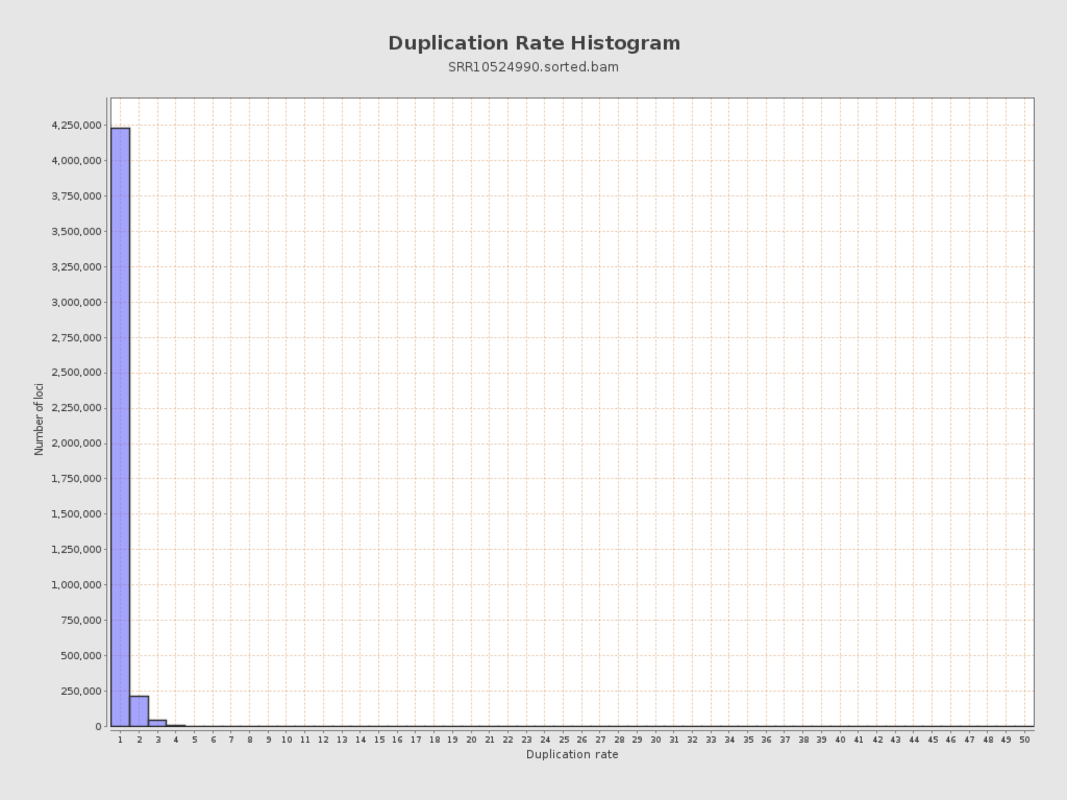
5. Results : Coverage Histogram (0-50X)



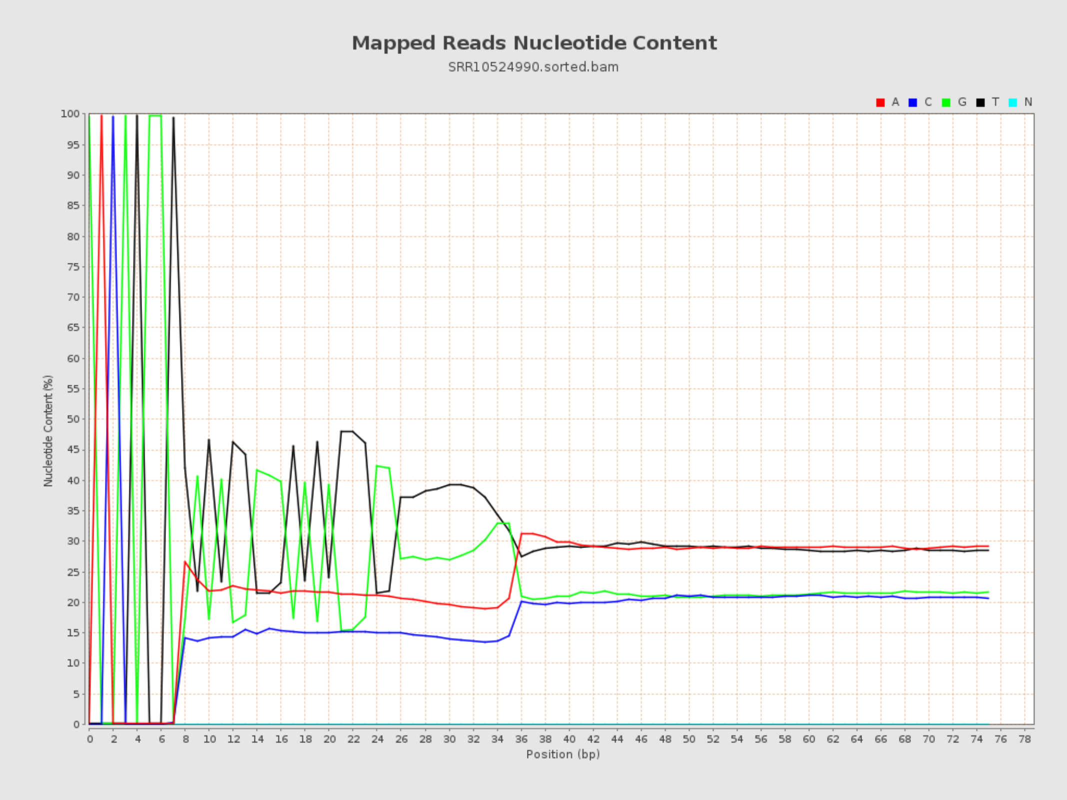
6. Results : Genome Fraction Coverage



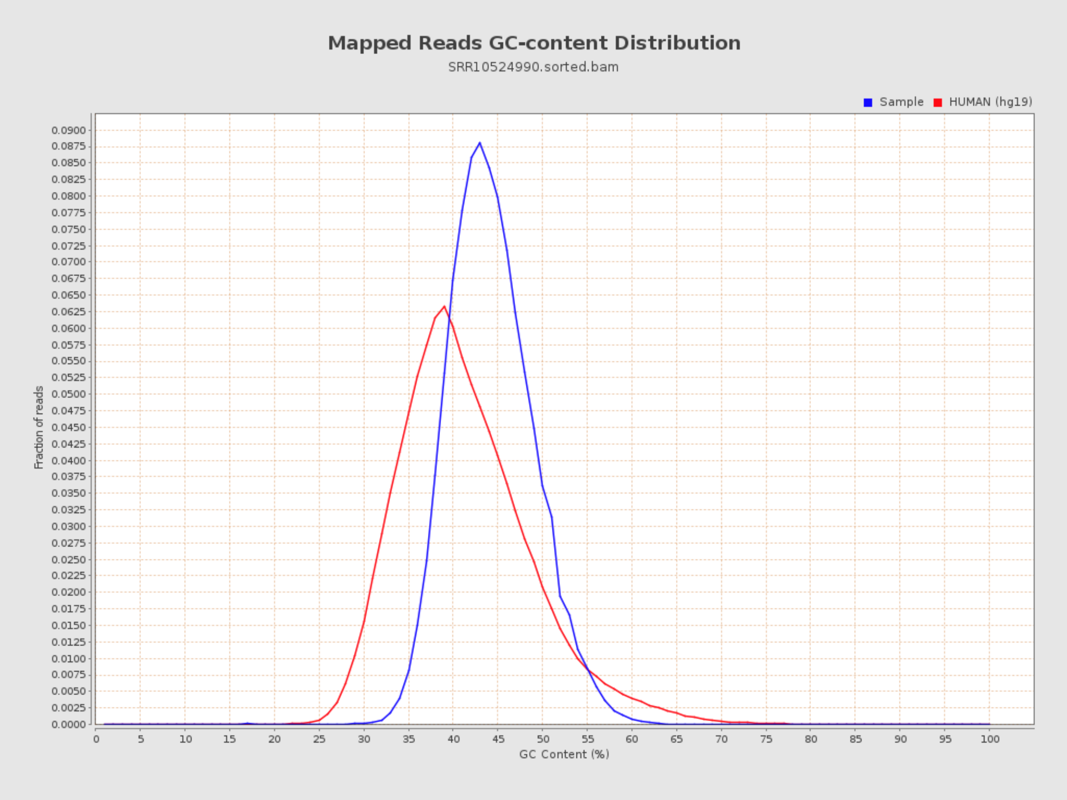
7. Results : Duplication Rate Histogram



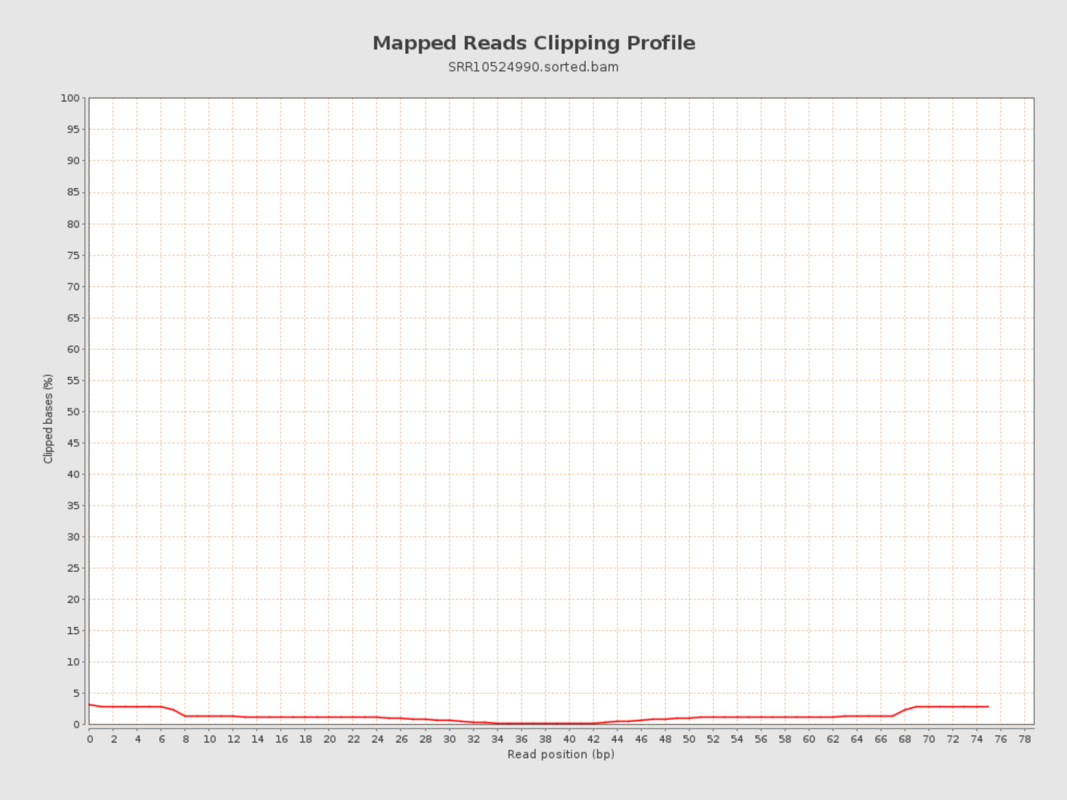
8. Results : Mapped Reads Nucleotide Content



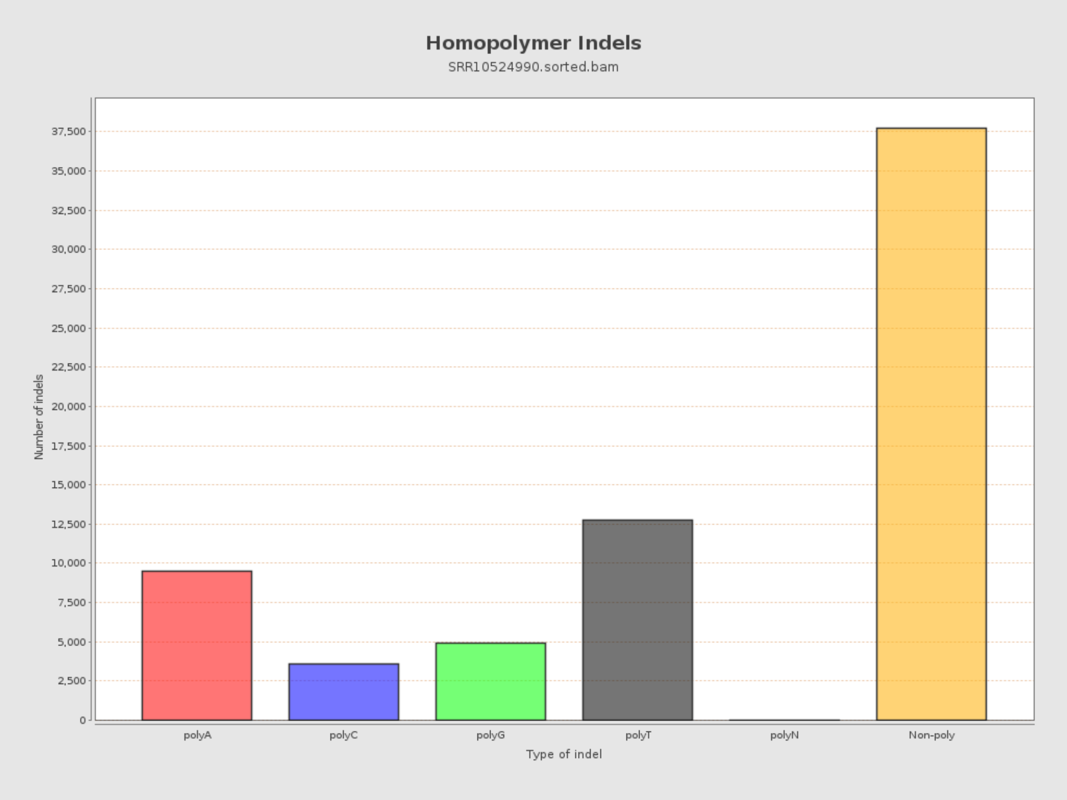
9. Results : Mapped Reads GC-content Distribution



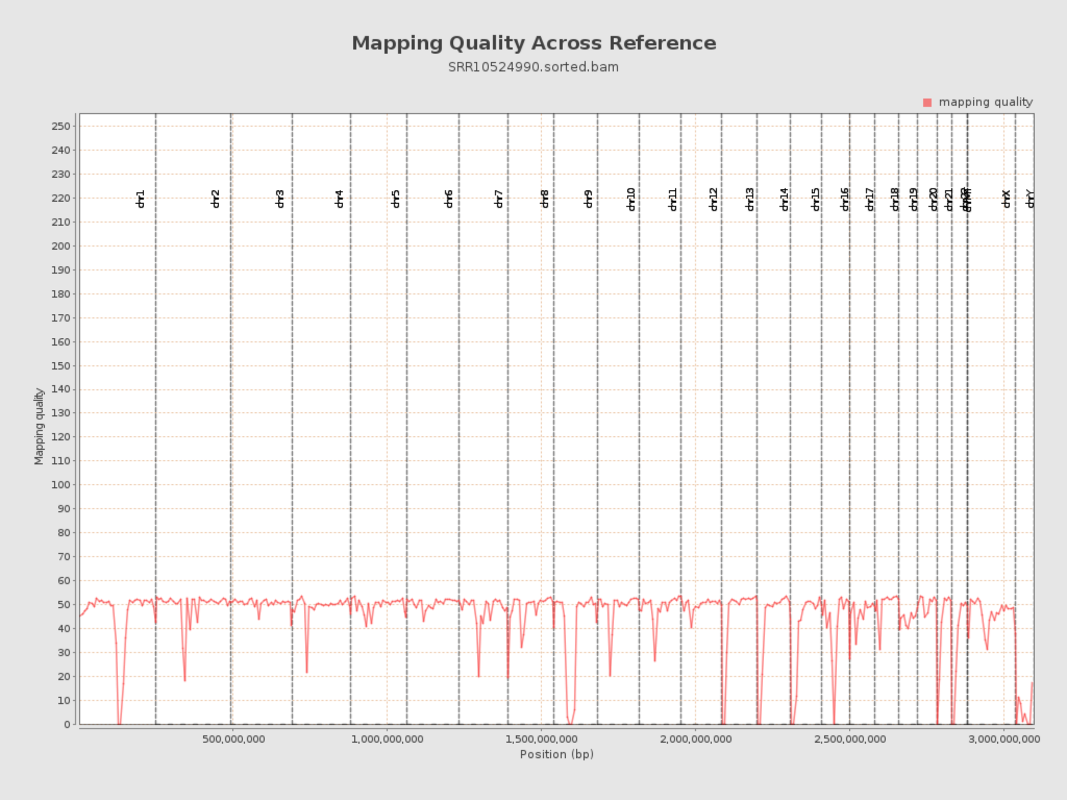
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram