Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 21:15:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524289.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_SRR10524289 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524289.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 21:15:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524289.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	568,787
Mapped reads	519,418 / 91.32%
Unmapped reads	49,369 / 8.68%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,880 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	11,545 / 2.03%
Duplication rate	1.69%
Clipped reads	519,797 / 91.39%

2.2. ACGT Content

Number/percentage of A's	7,881,785 / 26.01%
Number/percentage of C's	5,560,995 / 18.35%
Number/percentage of T's	9,825,799 / 32.43%
Number/percentage of G's	7,027,912 / 23.2%
Number/percentage of N's	663 / 0%
GC Percentage	41.55%

2.3. Coverage

Mean	0.0098

Standard Deviation	0.1262

2.4. Mapping Quality

Mean Mapping Quality	45.76

2.5. Mismatches and indels

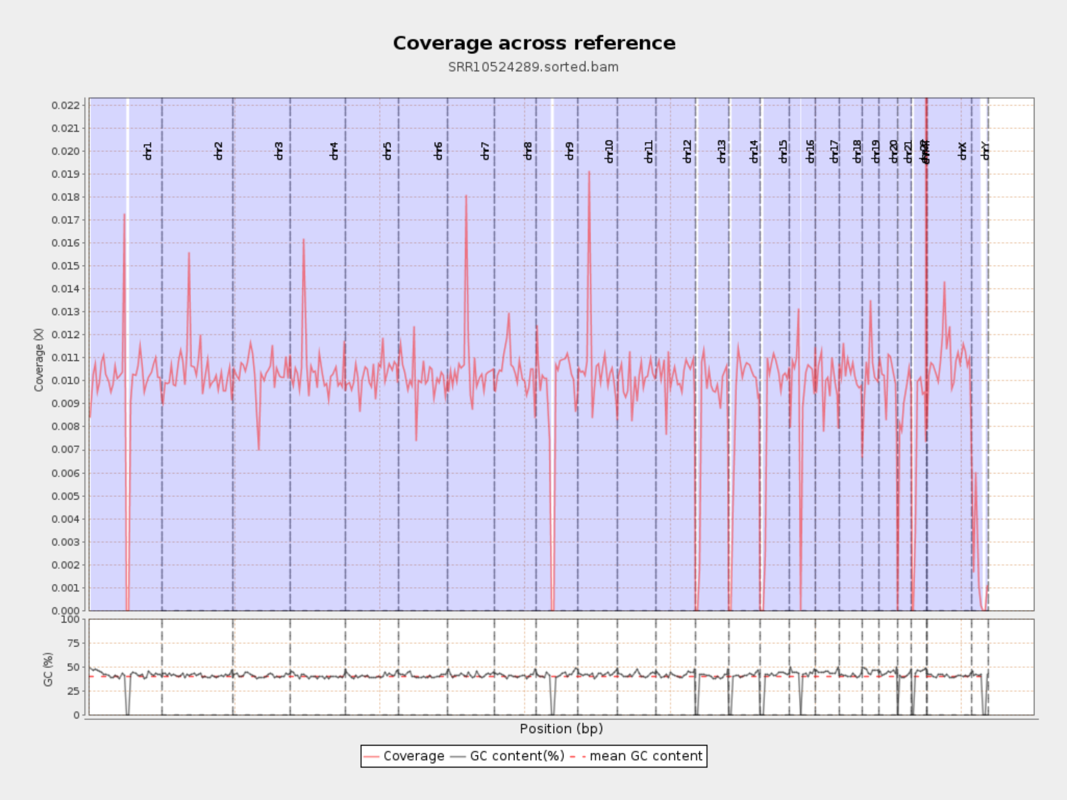
General error rate	0.52%
Mismatches	153,802
Insertions	2,390
Mapped reads with at least one insertion	0.46%
Deletions	6,344
Mapped reads with at least one deletion	1.21%
Homopolymer indels	43.67%

2.6. Chromosome stats

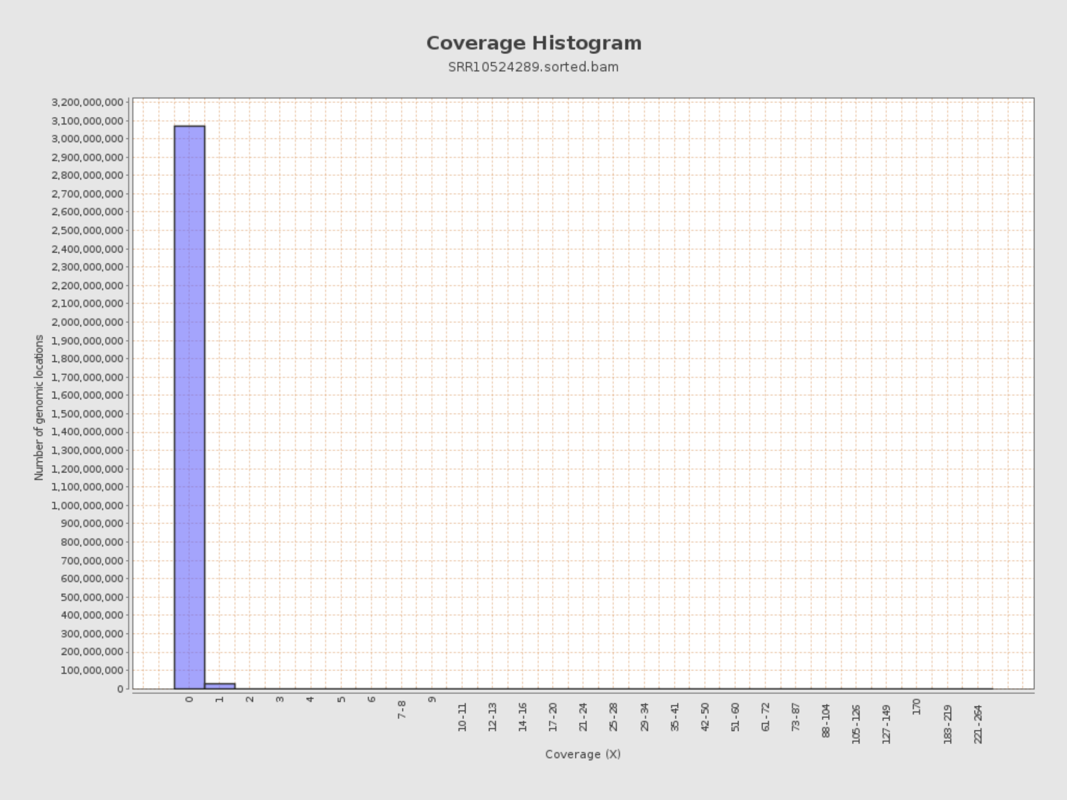
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2440436	0.0098	0.1902
chr2	243199373	2534753	0.0104	0.1537
chr3	198022430	2040182	0.0103	0.105
chr4	191154276	1995256	0.0104	0.11
chr5	180915260	1855084	0.0103	0.1046
chr6	171115067	1738716	0.0102	0.1093
chr7	159138663	1690783	0.0106	0.1604

chr8	146364022	1525367	0.0104	0.1393
chr9	141213431	1285069	0.0091	0.1124
chr10	135534747	1452995	0.0107	0.1277
chr11	135006516	1351321	0.01	0.1118
chr12	133851895	1373323	0.0103	0.1051
chr13	115169878	967498	0.0084	0.0954
chr14	107349540	929806	0.0087	0.0982
chr15	102531392	861499	0.0084	0.0959
chr16	90354753	864584	0.0096	0.1054
chr17	81195210	796501	0.0098	0.1042
chr18	78077248	812105	0.0104	0.1575
chr19	59128983	616684	0.0104	0.1528
chr20	63025520	637268	0.0101	0.1047
chr21	48129895	399804	0.0083	0.0978
chr22	51304566	343296	0.0067	0.0846
chrMT	16571	2643	0.1595	0.3989
chrX	155270560	1692161	0.0109	0.1115
chrY	59373566	100216	0.0017	0.0625

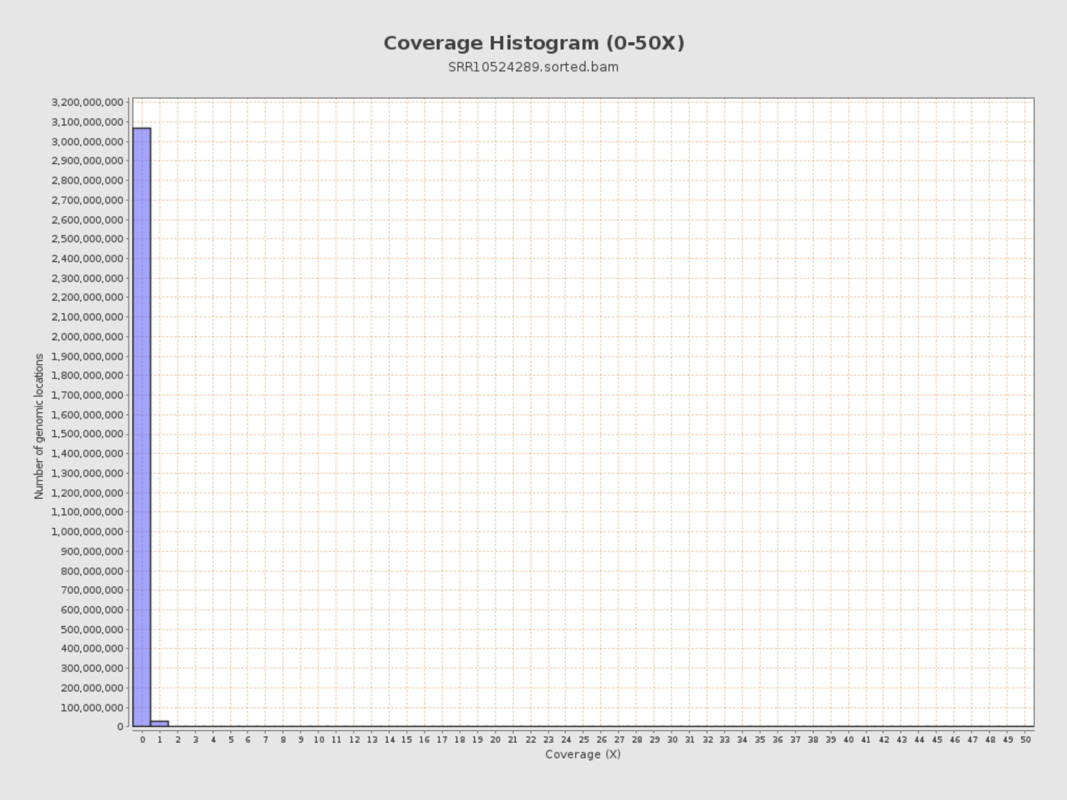
3. Results : Coverage across reference



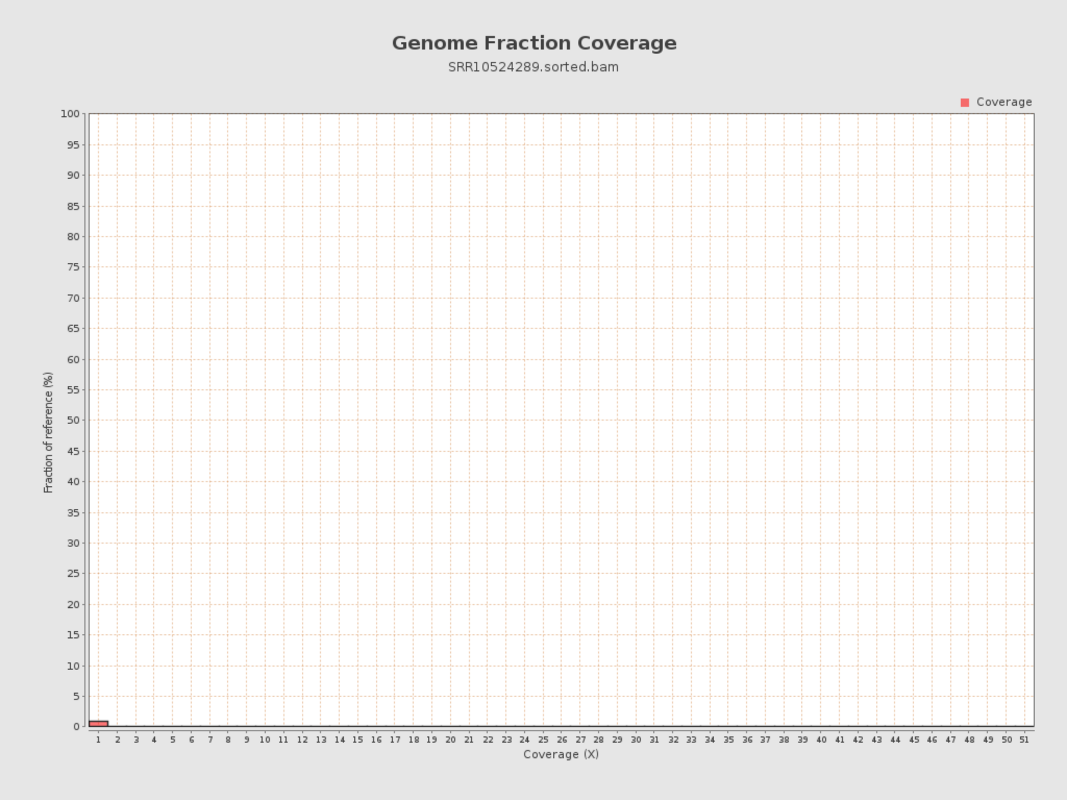
4. Results : Coverage Histogram



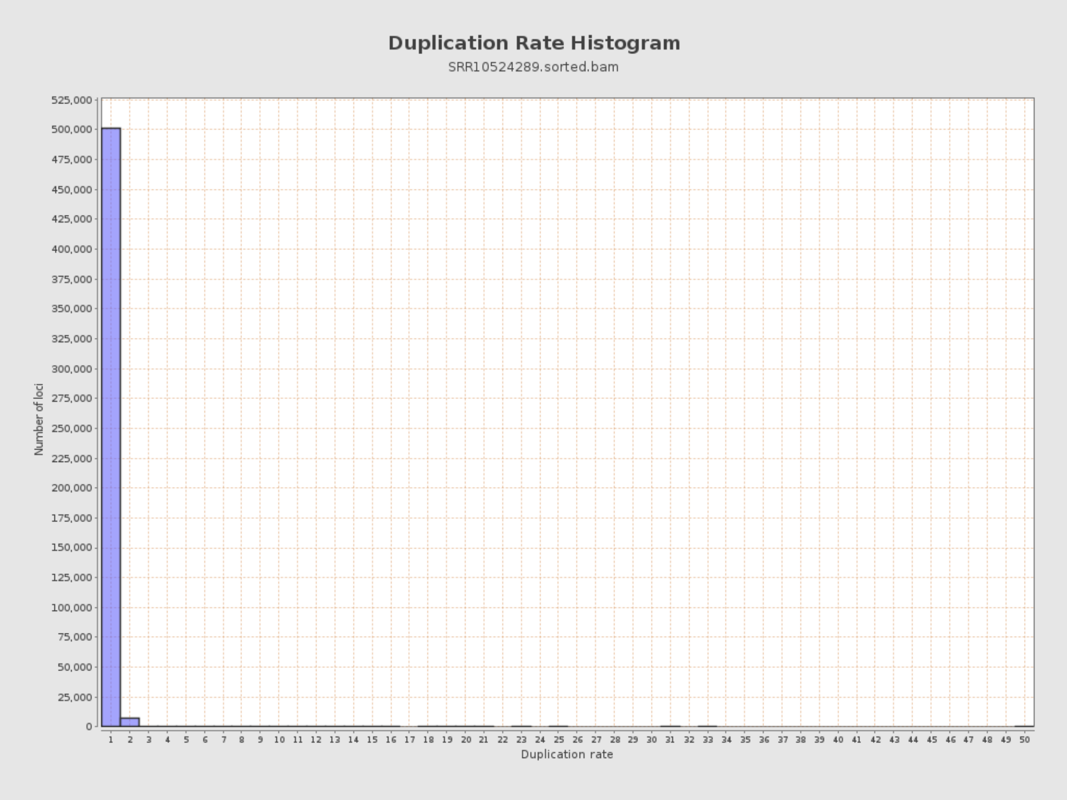
5. Results : Coverage Histogram (0-50X)



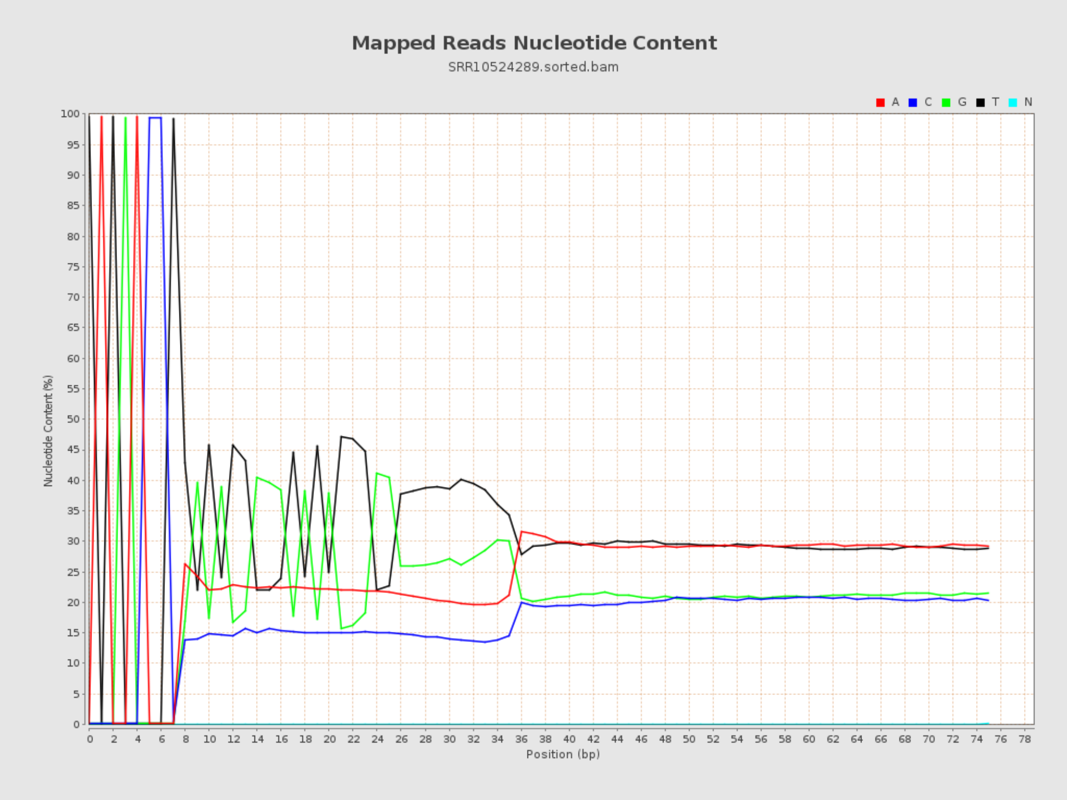
6. Results : Genome Fraction Coverage



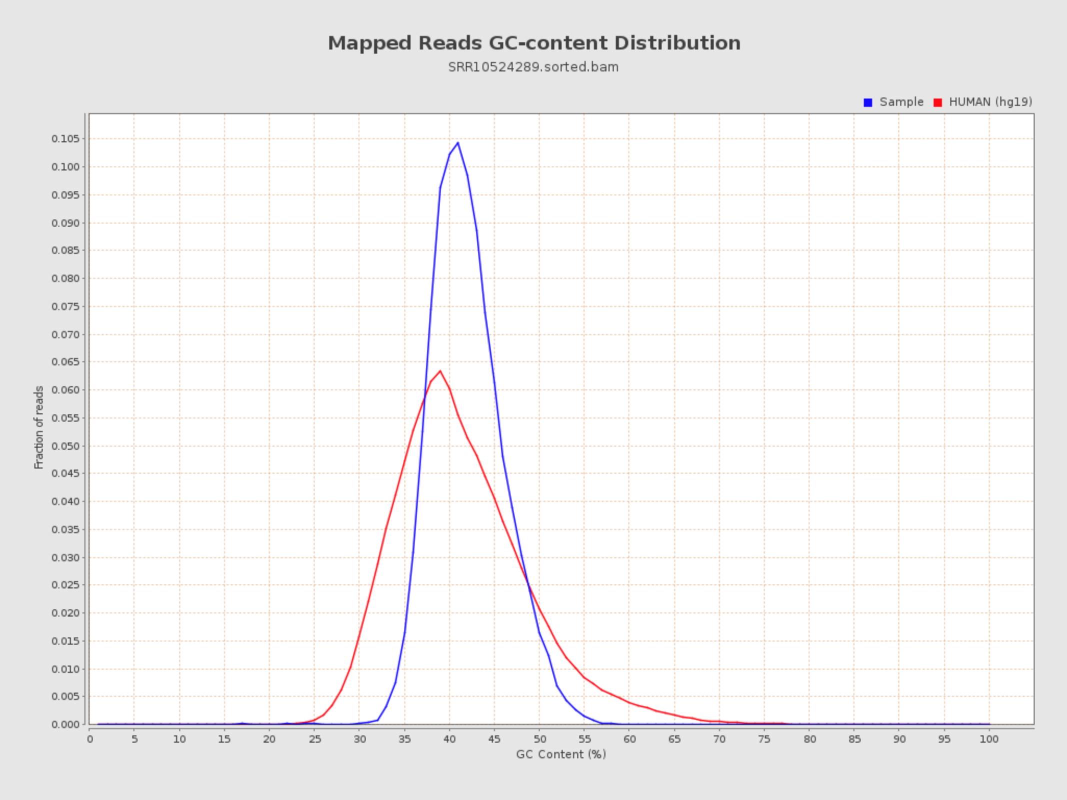
7. Results : Duplication Rate Histogram



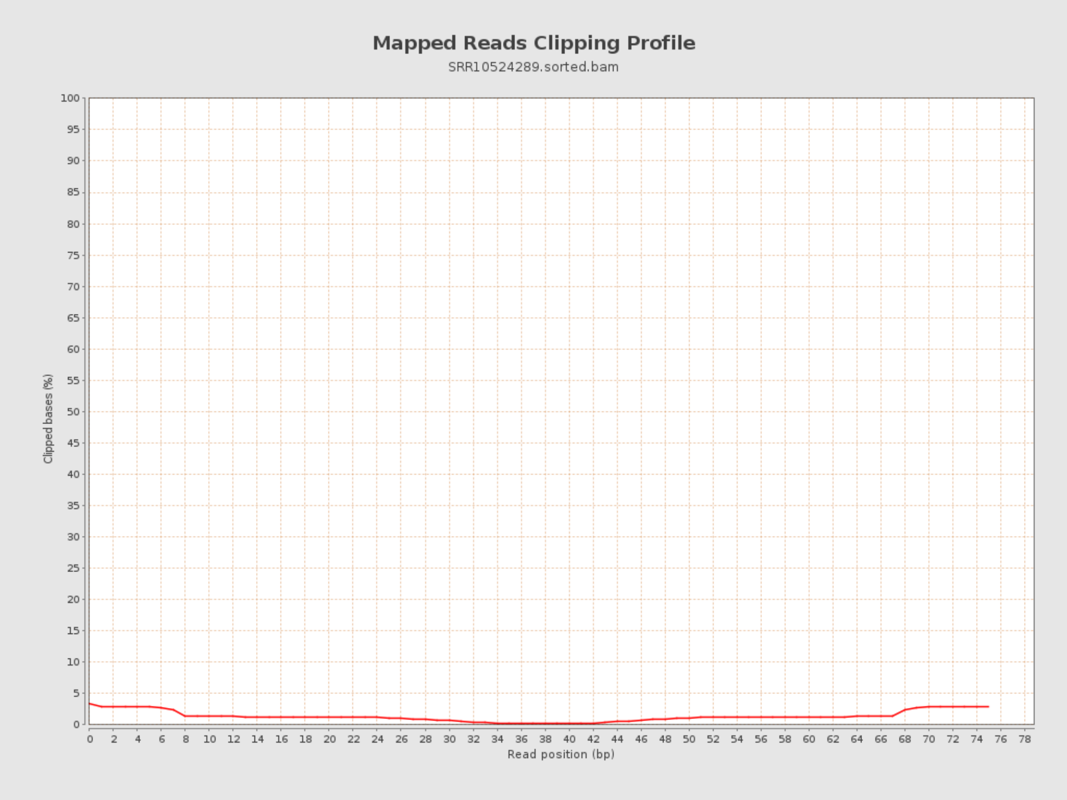
8. Results : Mapped Reads Nucleotide Content



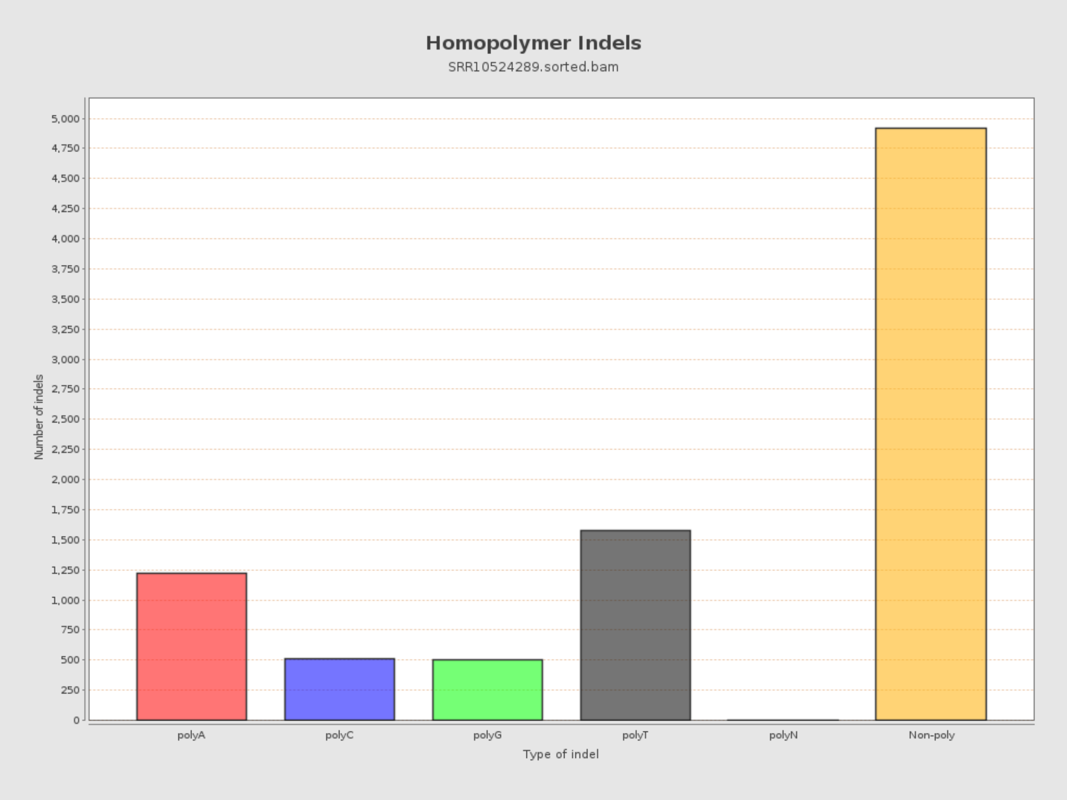
9. Results : Mapped Reads GC-content Distribution



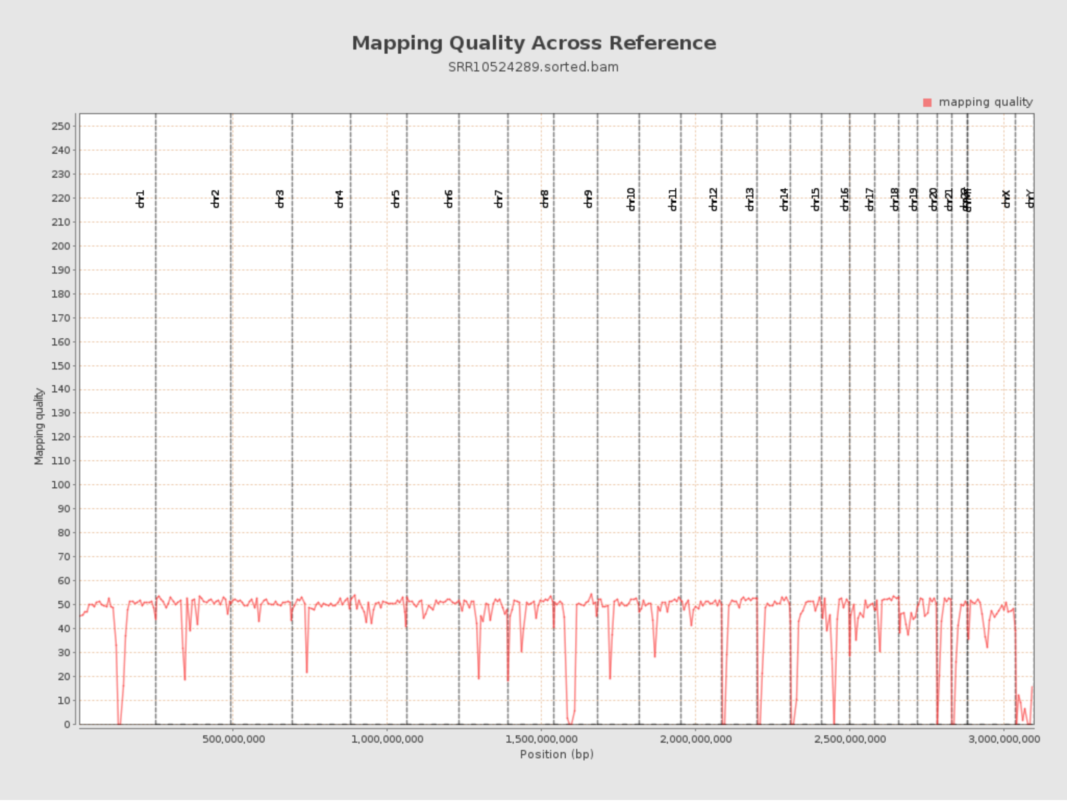
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram