Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 02:07:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525269.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_SRR10525269 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525269.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 02:07:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525269.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,462,840
Mapped reads	1,336,582 / 91.37%
Unmapped reads	126,258 / 8.63%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,311 / 0.29%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	44,296 / 3.03%
Duplication rate	2.45%
Clipped reads	1,337,251 / 91.41%

2.2. ACGT Content

Number/percentage of A's	19,821,887 / 25.66%
Number/percentage of C's	13,308,440 / 17.23%
Number/percentage of T's	24,772,906 / 32.07%
Number/percentage of G's	19,352,163 / 25.05%
Number/percentage of N's	1,511 / 0%
GC Percentage	42.28%

2.3. Coverage

Mean	0.025

Standard Deviation	0.2481

2.4. Mapping Quality

Mean Mapping Quality	44.91

2.5. Mismatches and indels

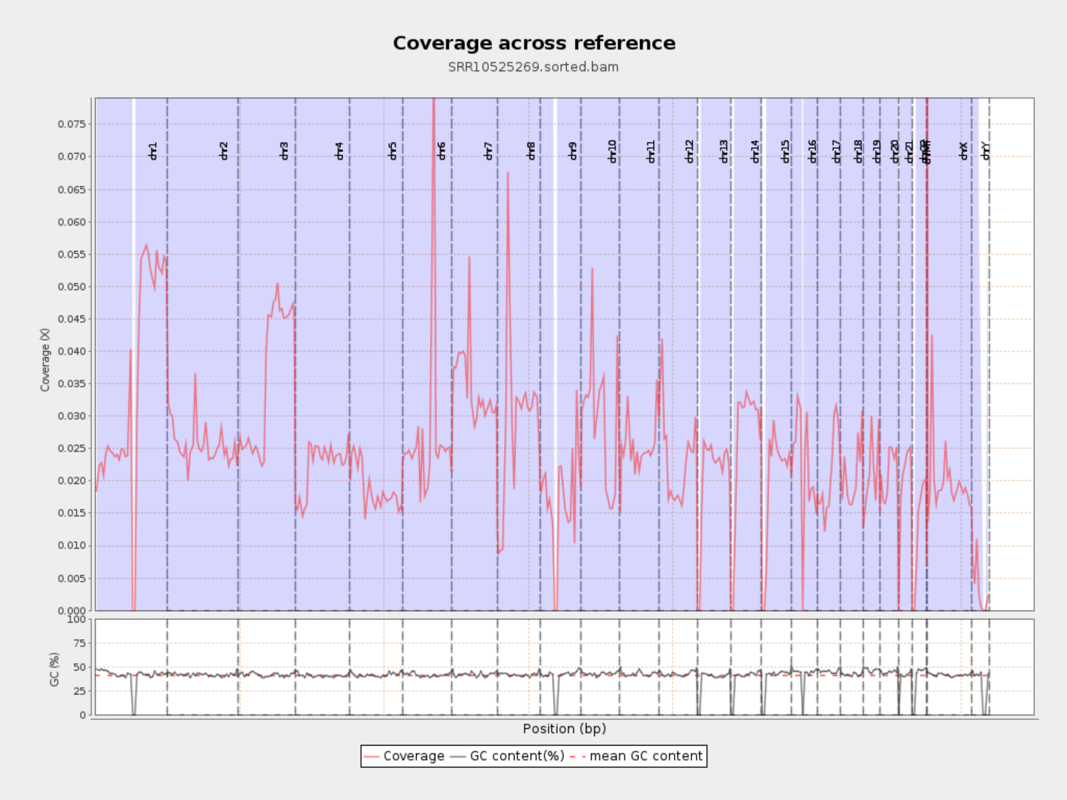
General error rate	0.51%
Mismatches	380,867
Insertions	5,380
Mapped reads with at least one insertion	0.4%
Deletions	14,656
Mapped reads with at least one deletion	1.09%
Homopolymer indels	44.16%

2.6. Chromosome stats

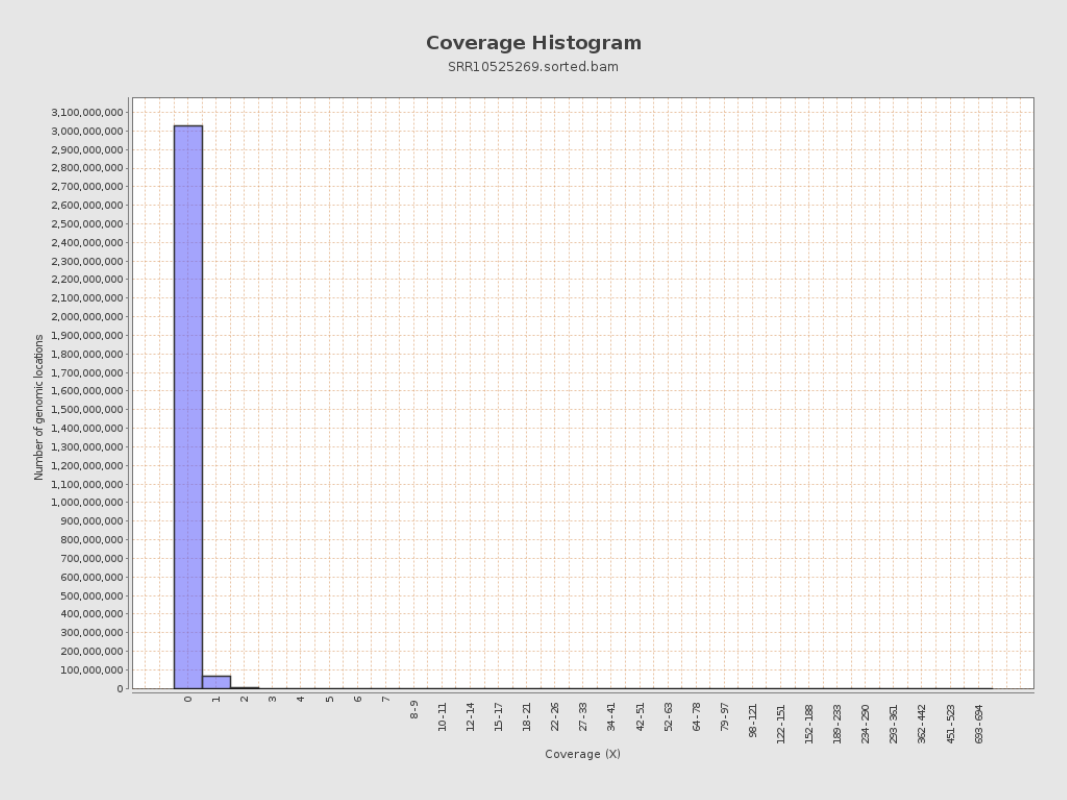
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8660361	0.0347	0.4184
chr2	243199373	6229746	0.0256	0.3295
chr3	198022430	7089318	0.0358	0.204
chr4	191154276	4270535	0.0223	0.1677
chr5	180915260	3408898	0.0188	0.1479
chr6	171115067	4786748	0.028	0.1961
chr7	159138663	5521644	0.0347	0.4259

chr8	146364022	4362440	0.0298	0.2587
chr9	141213431	2403915	0.017	0.175
chr10	135534747	3993631	0.0295	0.2618
chr11	135006516	3410885	0.0253	0.2037
chr12	133851895	3138702	0.0234	0.1659
chr13	115169878	2385252	0.0207	0.1556
chr14	107349540	2803696	0.0261	0.1774
chr15	102531392	2029908	0.0198	0.1557
chr16	90354753	1972307	0.0218	0.1716
chr17	81195210	1710748	0.0211	0.161
chr18	78077248	1597775	0.0205	0.3161
chr19	59128983	1260970	0.0213	0.2934
chr20	63025520	1338455	0.0212	0.1586
chr21	48129895	961872	0.02	0.16
chr22	51304566	626554	0.0122	0.1184
chrMT	16571	6194	0.3738	0.6981
chrX	155270560	3110649	0.02	0.1641
chrY	59373566	198530	0.0033	0.1027

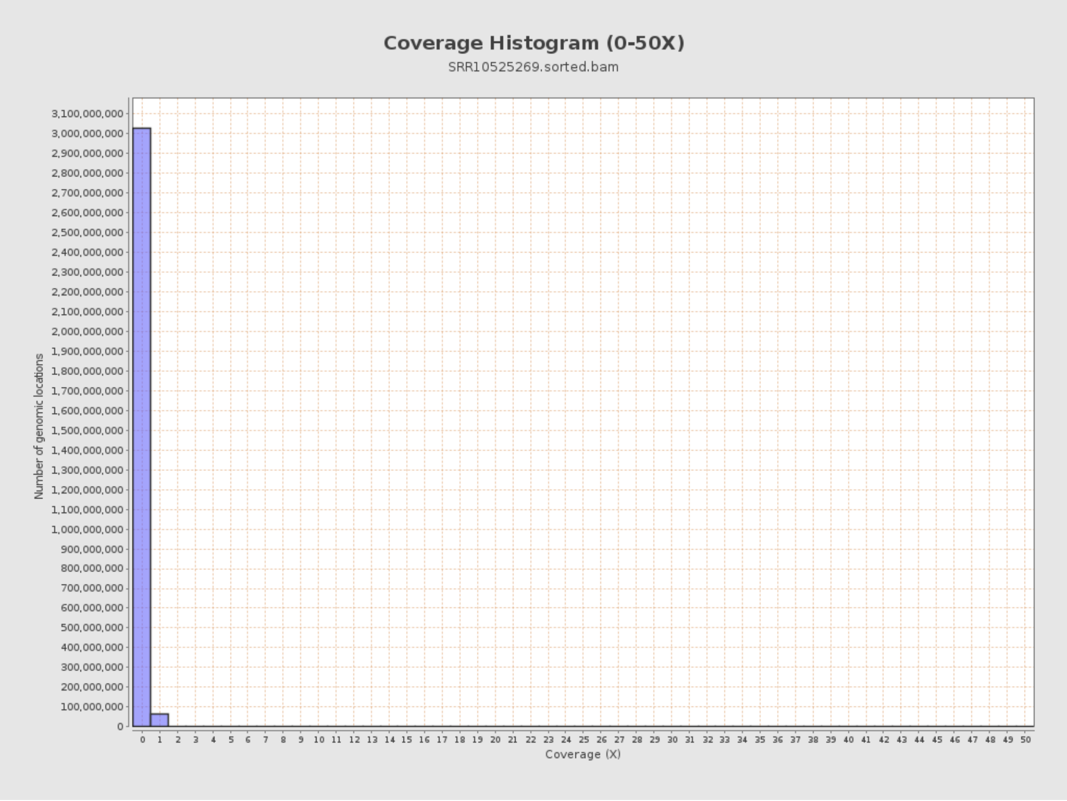
3. Results : Coverage across reference



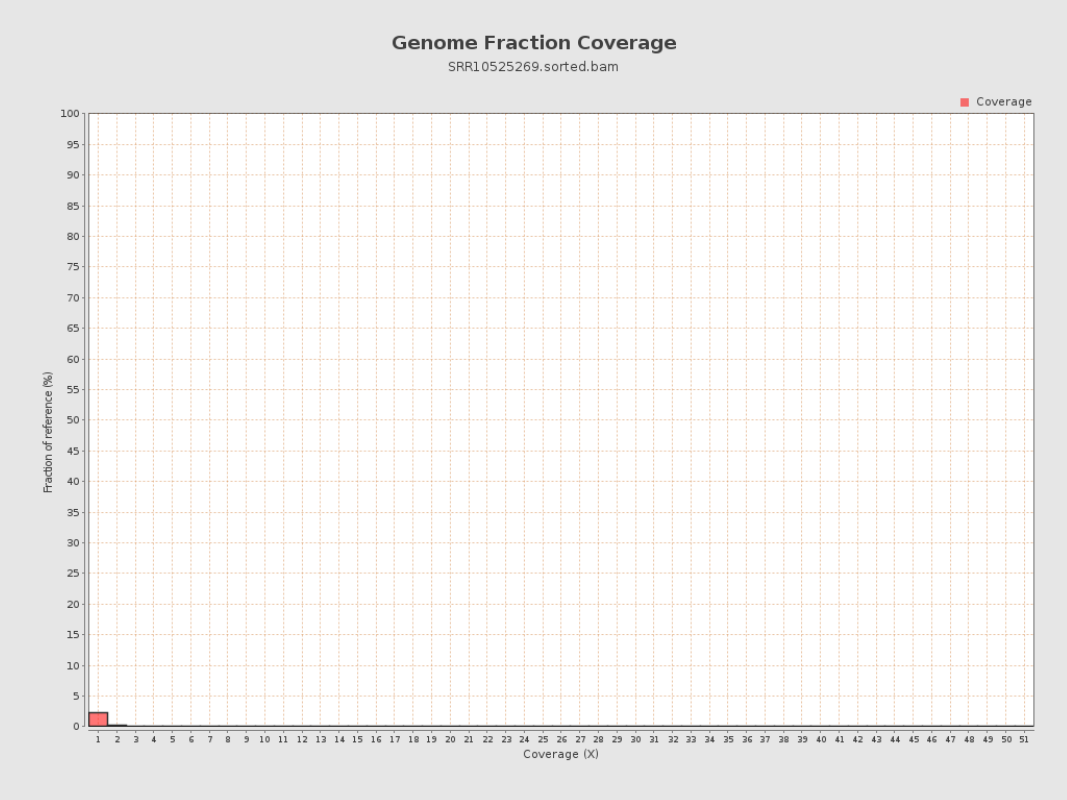
4. Results : Coverage Histogram



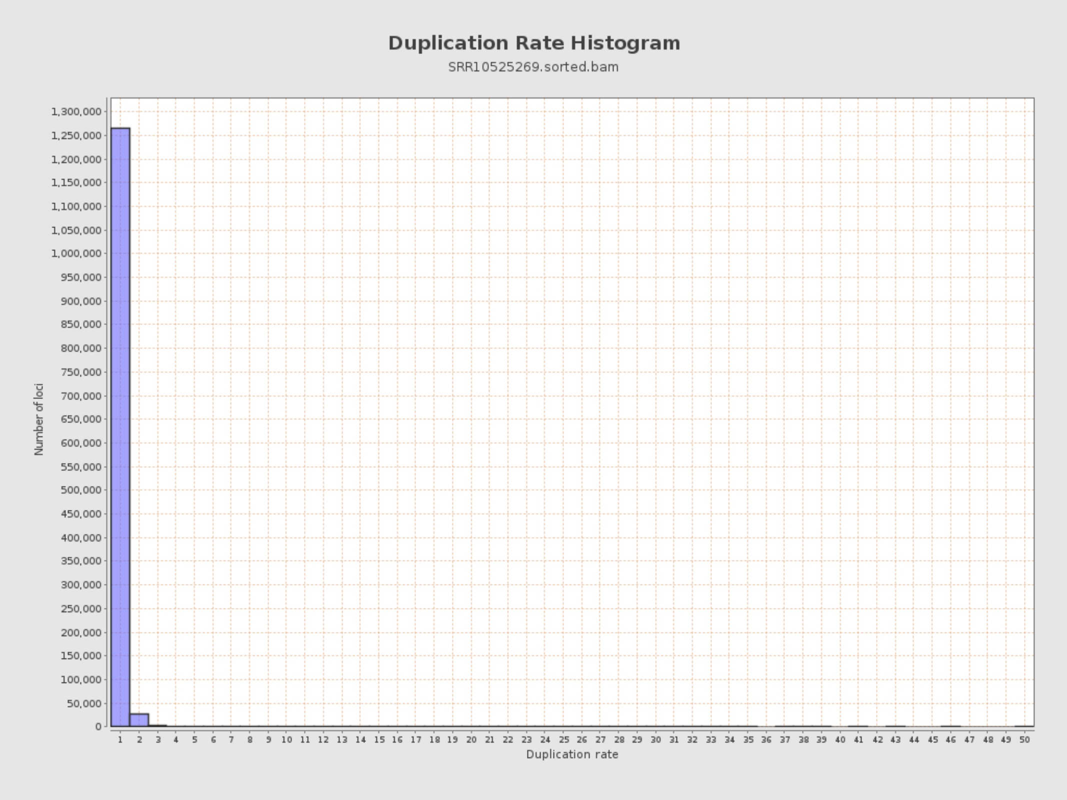
5. Results : Coverage Histogram (0-50X)



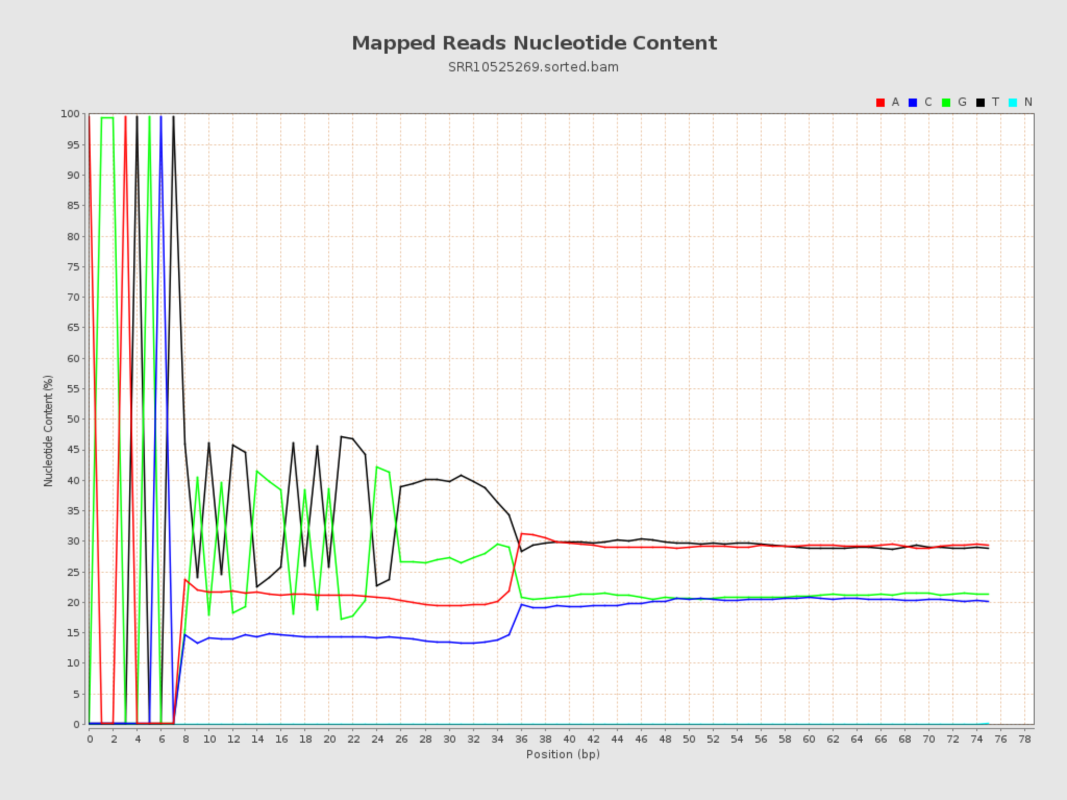
6. Results : Genome Fraction Coverage



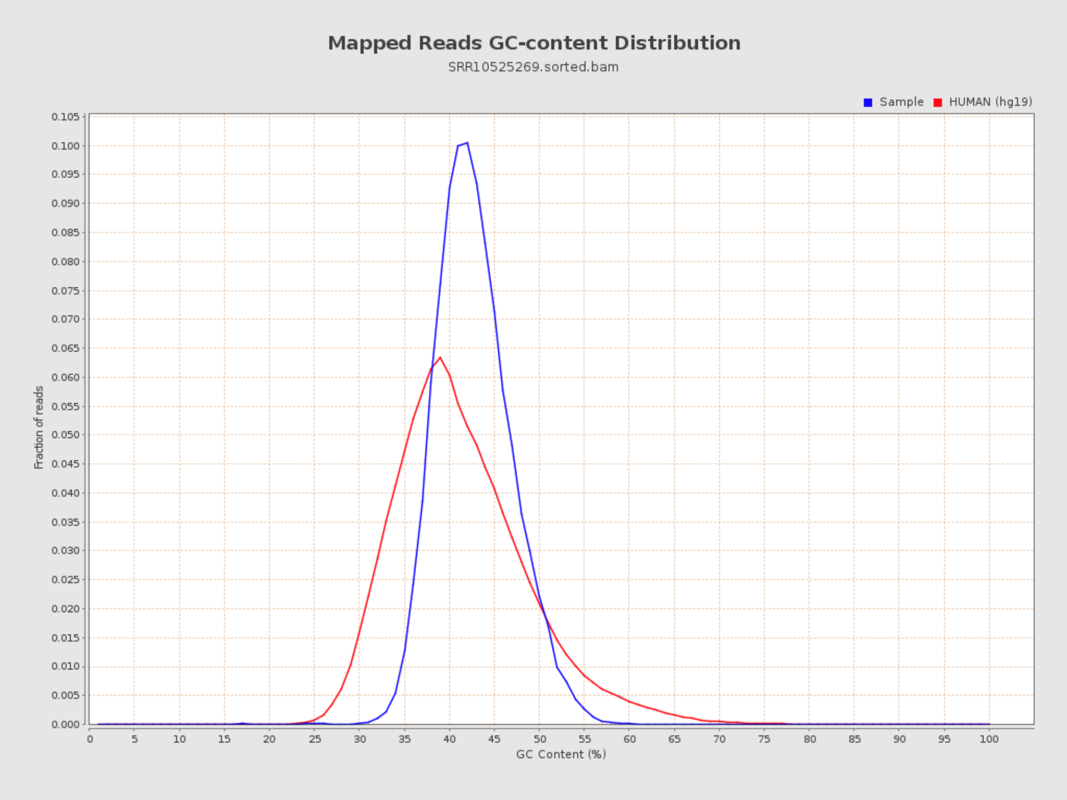
7. Results : Duplication Rate Histogram



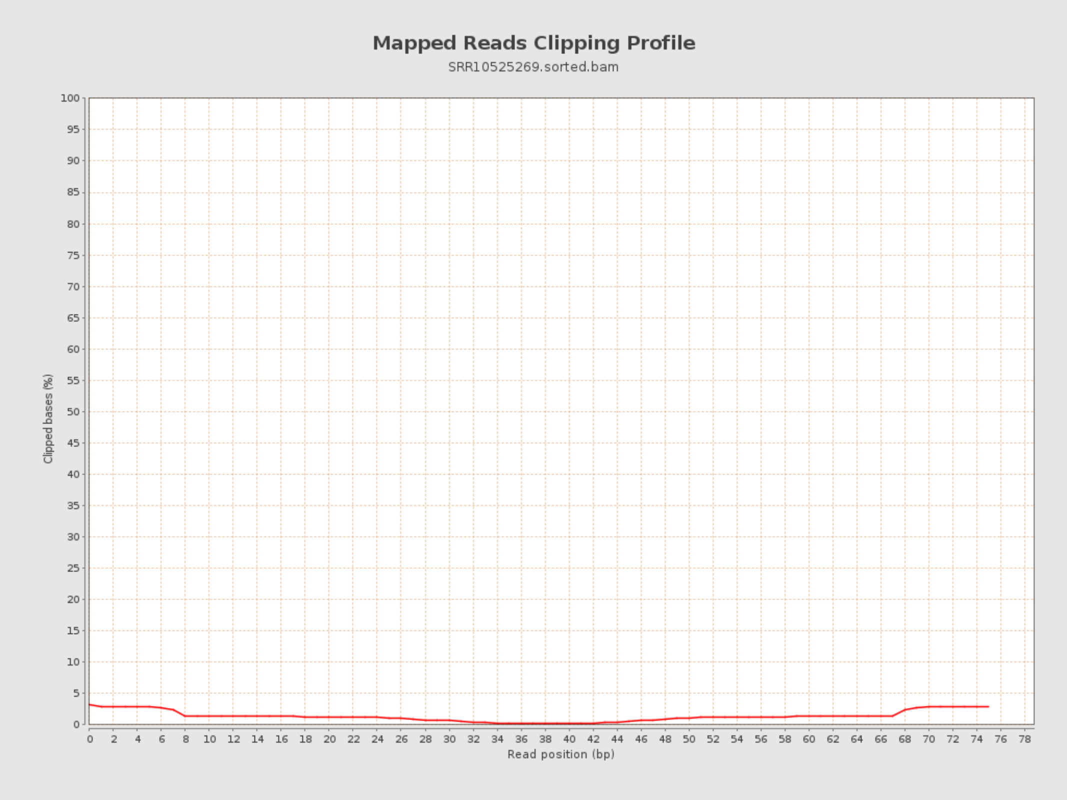
8. Results : Mapped Reads Nucleotide Content



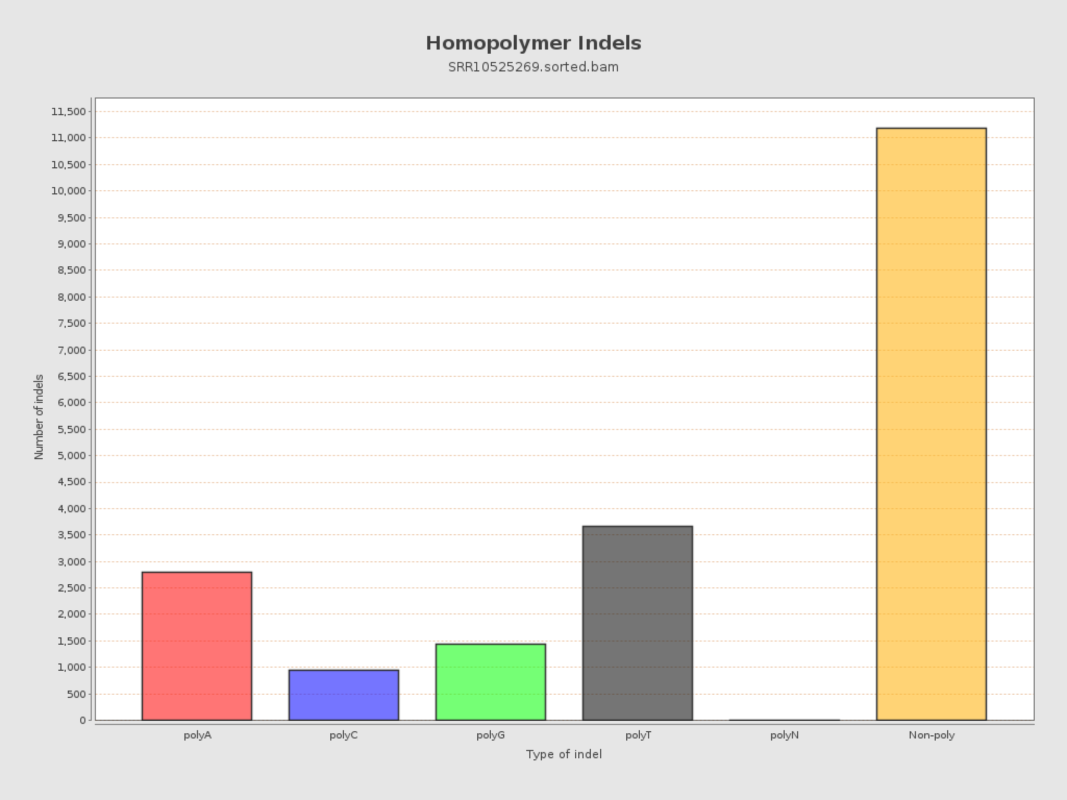
9. Results : Mapped Reads GC-content Distribution



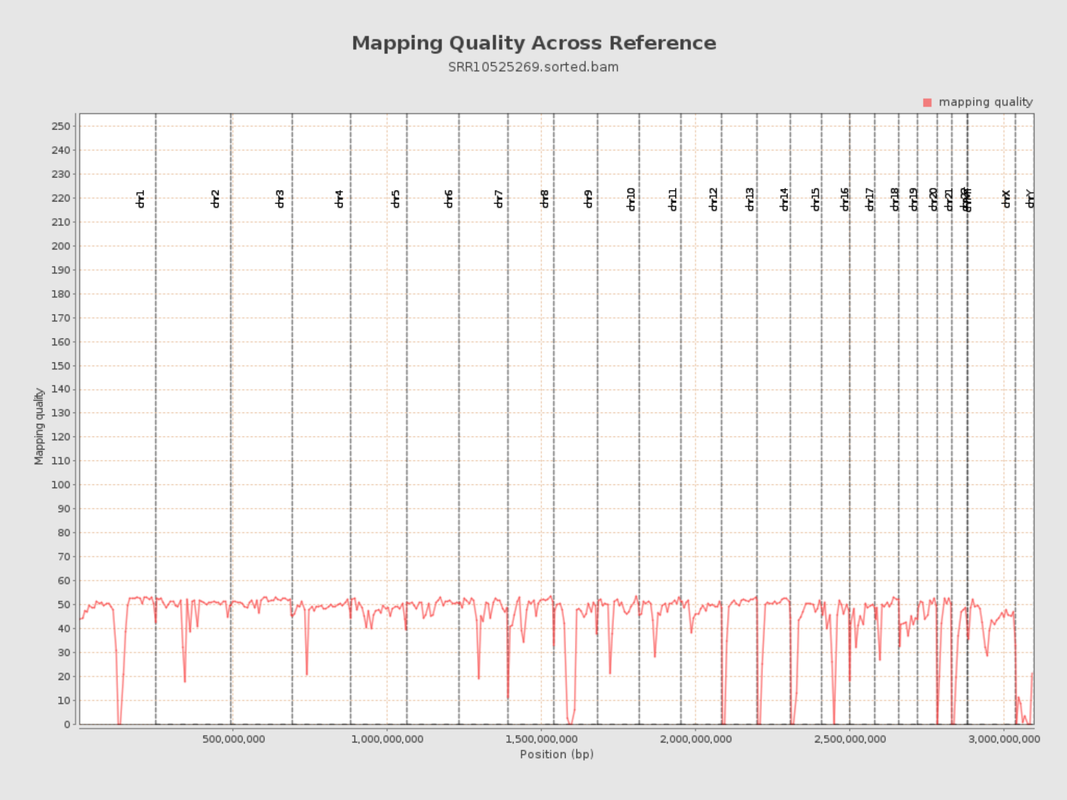
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram