Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 15:36:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525065.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_SRR10525065 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525065.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 15:36:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525065.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,158,297
Mapped reads	1,044,355 / 90.16%
Unmapped reads	113,942 / 9.84%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,178 / 0.27%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	54,358 / 4.69%
Duplication rate	4.32%
Clipped reads	1,046,391 / 90.34%

2.2. ACGT Content

Number/percentage of A's	15,212,737 / 25.04%
Number/percentage of C's	10,634,370 / 17.5%
Number/percentage of T's	19,286,076 / 31.74%
Number/percentage of G's	15,618,819 / 25.71%
Number/percentage of N's	6,877 / 0.01%
GC Percentage	43.21%

2.3. Coverage

Mean	0.0196

Standard Deviation	0.2071

2.4. Mapping Quality

Mean Mapping Quality	46.2

2.5. Mismatches and indels

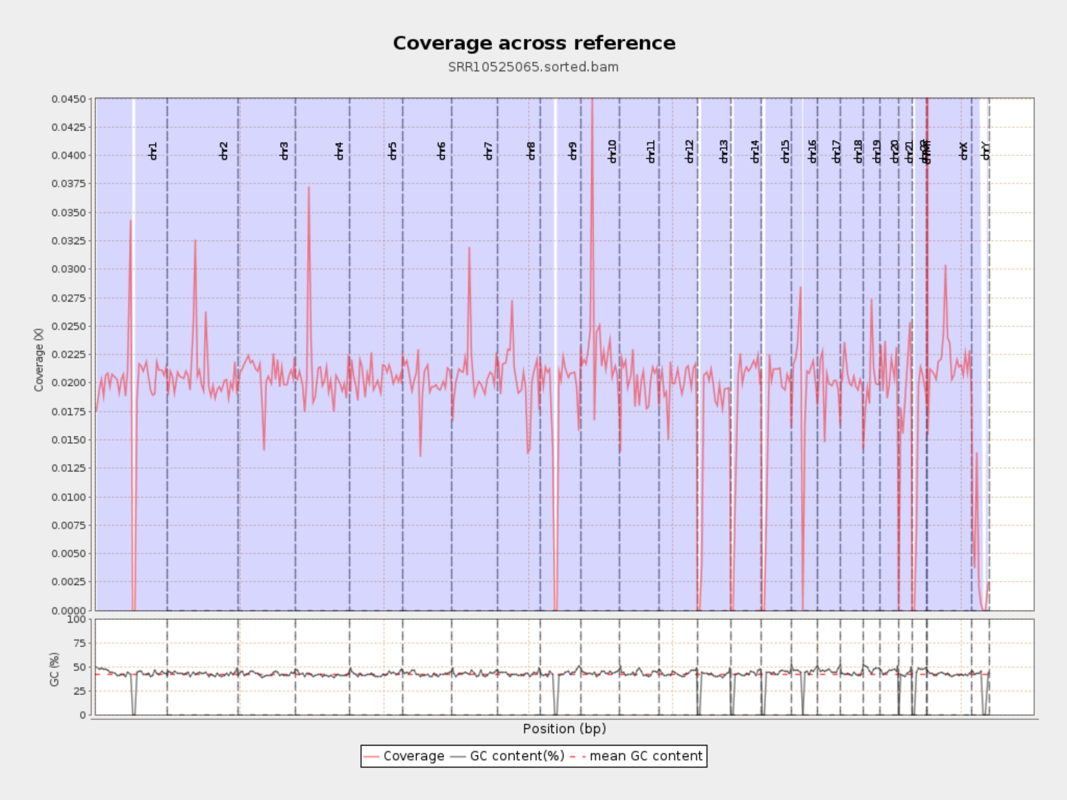
General error rate	0.5%
Mismatches	294,879
Insertions	3,747
Mapped reads with at least one insertion	0.36%
Deletions	11,930
Mapped reads with at least one deletion	1.13%
Homopolymer indels	45.12%

2.6. Chromosome stats

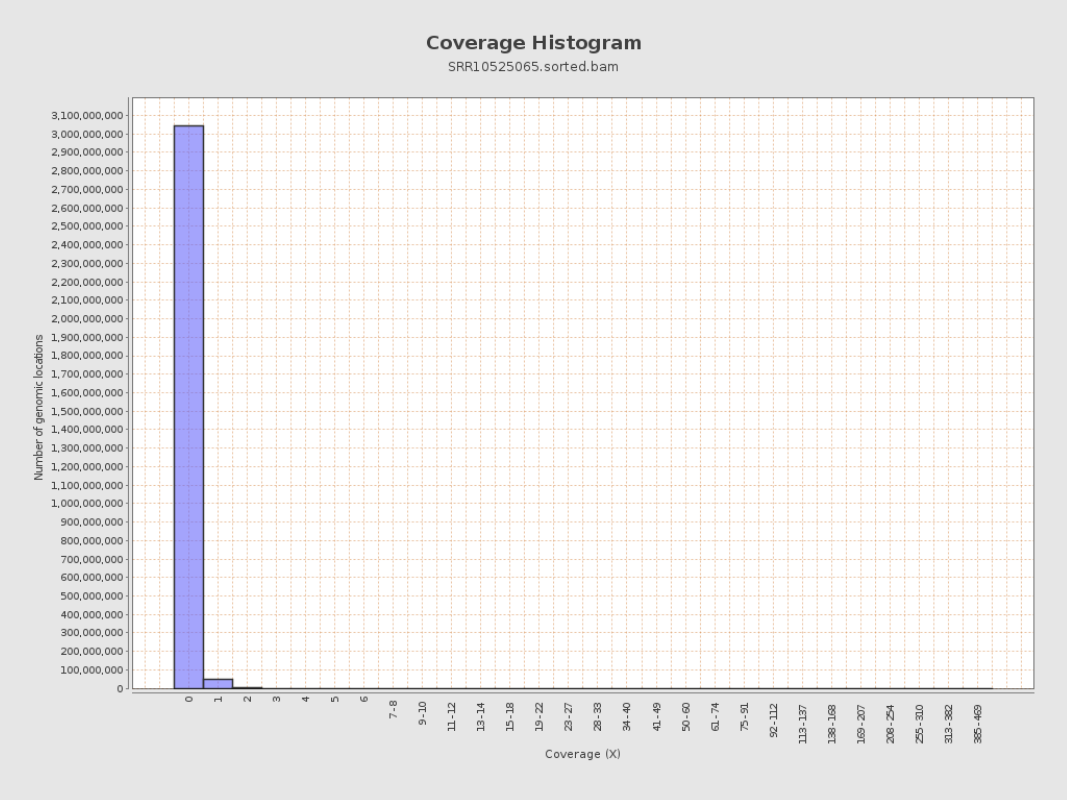
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4849649	0.0195	0.3677
chr2	243199373	5044858	0.0207	0.2401
chr3	198022430	4095957	0.0207	0.1581
chr4	191154276	3976805	0.0208	0.1723
chr5	180915260	3720888	0.0206	0.1567
chr6	171115067	3453853	0.0202	0.1629
chr7	159138663	3327251	0.0209	0.2347

chr8	146364022	2986797	0.0204	0.216
chr9	141213431	2540384	0.018	0.1709
chr10	135534747	3153260	0.0233	0.2351
chr11	135006516	2730432	0.0202	0.1782
chr12	133851895	2683782	0.0201	0.1578
chr13	115169878	1885015	0.0164	0.1391
chr14	107349540	1900003	0.0177	0.1479
chr15	102531392	1729039	0.0169	0.1412
chr16	90354753	1763045	0.0195	0.1625
chr17	81195210	1606444	0.0198	0.1589
chr18	78077248	1597657	0.0205	0.2678
chr19	59128983	1199084	0.0203	0.2703
chr20	63025520	1322878	0.021	0.161
chr21	48129895	858597	0.0178	0.1629
chr22	51304566	715857	0.014	0.1294
chrMT	16571	15692	0.947	1.196
chrX	155270560	3407329	0.0219	0.1756
chrY	59373566	213344	0.0036	0.1303

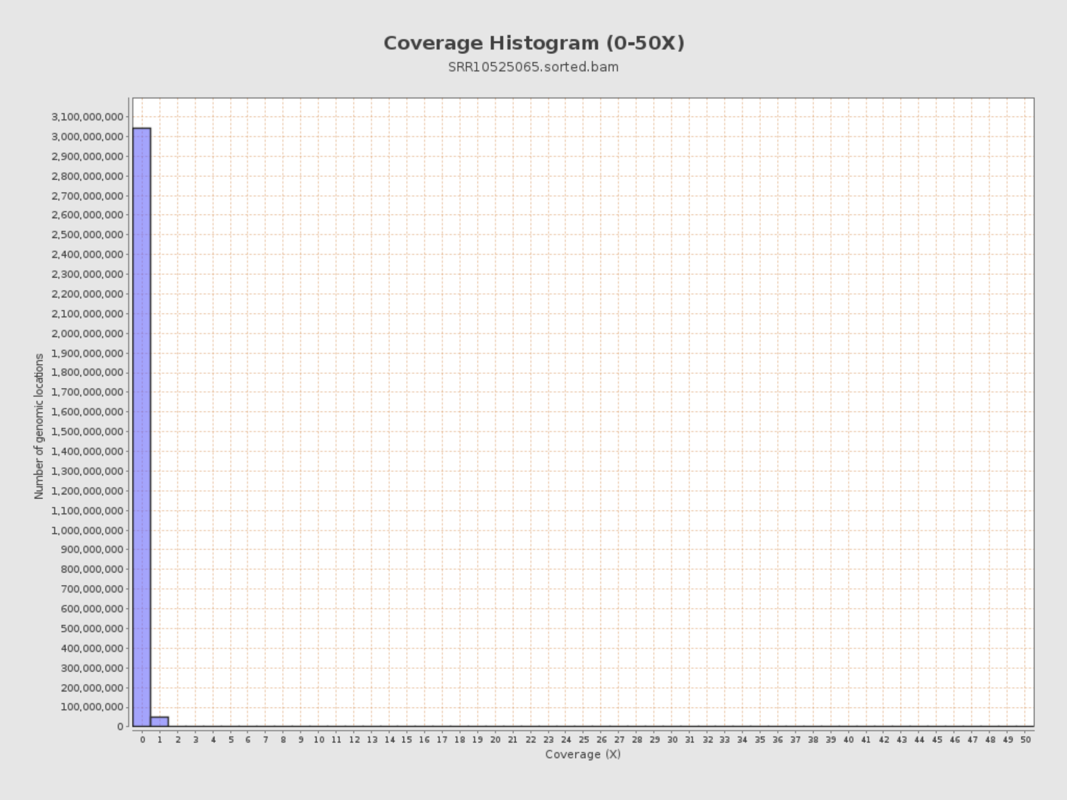
3. Results : Coverage across reference



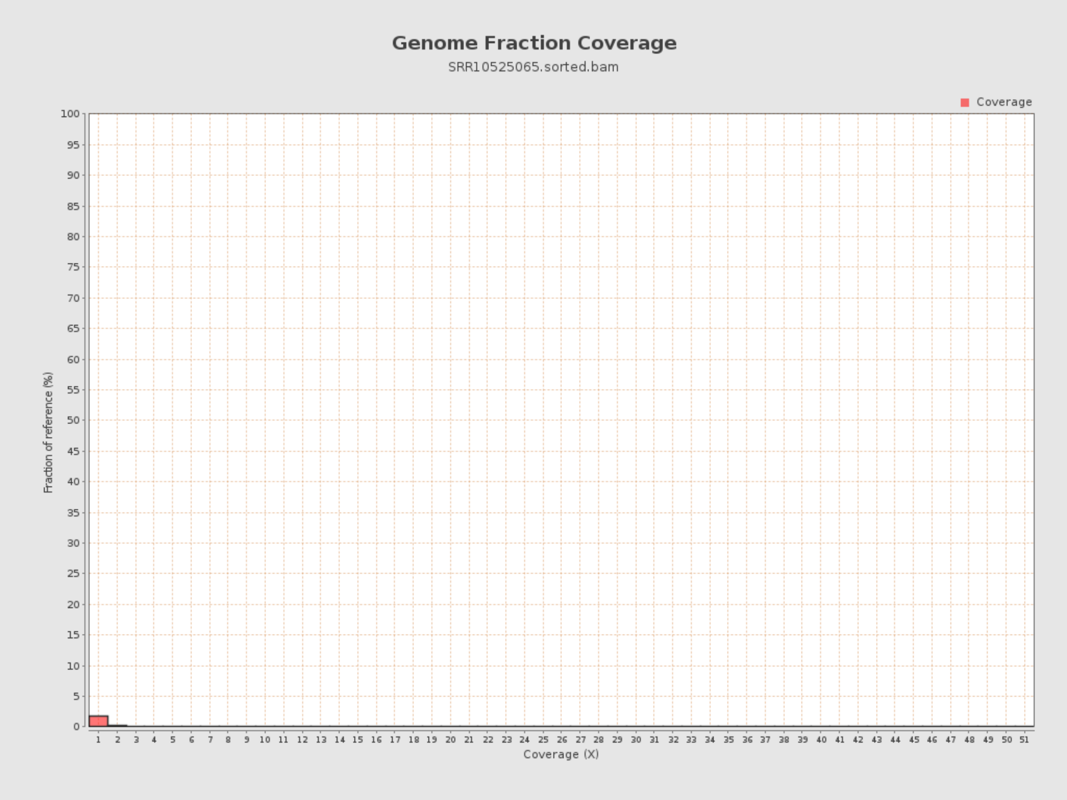
4. Results : Coverage Histogram



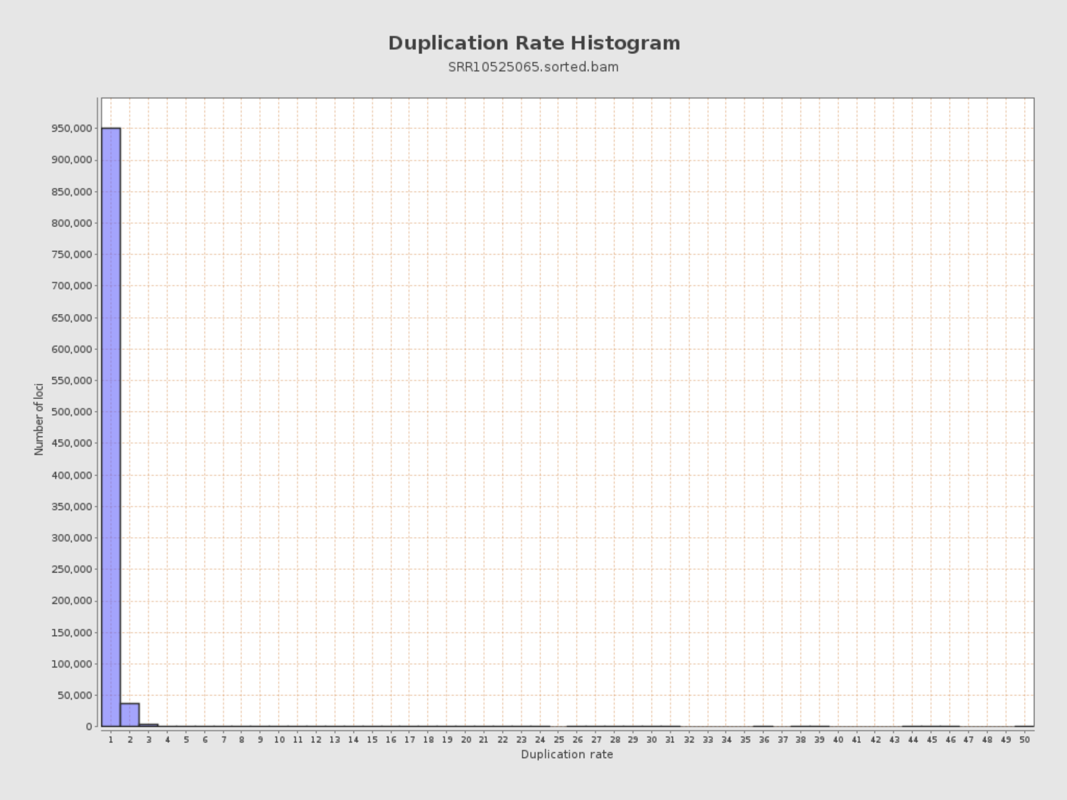
5. Results : Coverage Histogram (0-50X)



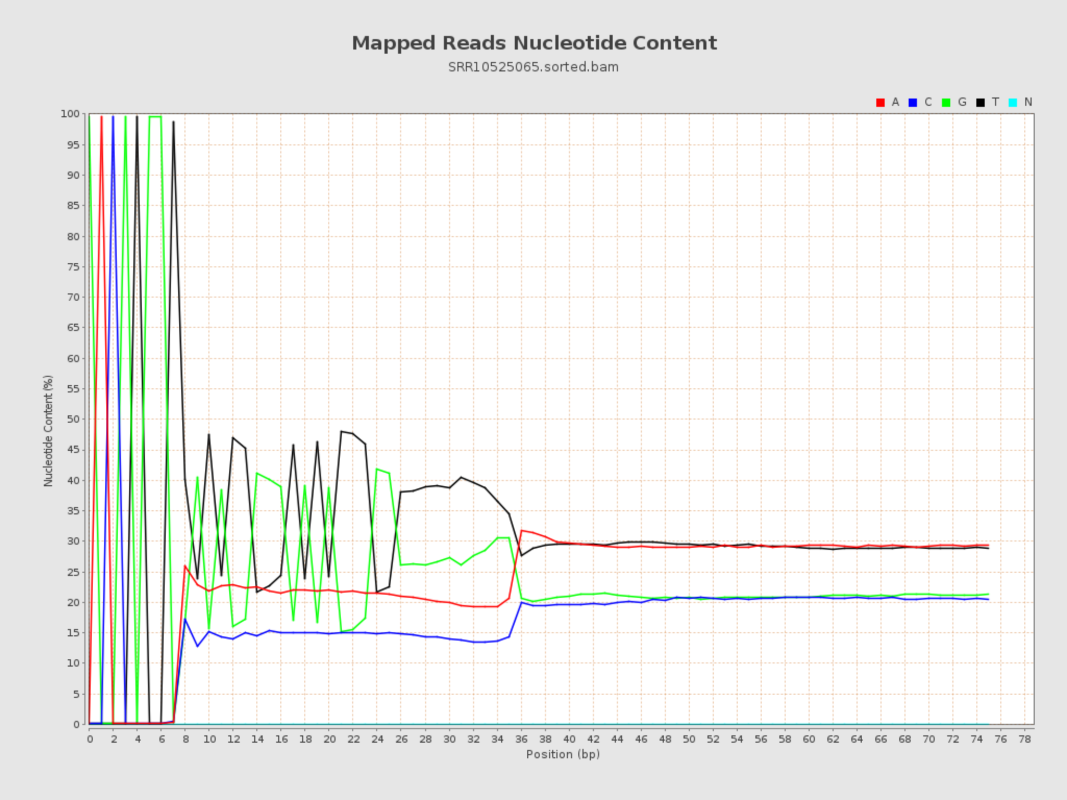
6. Results : Genome Fraction Coverage



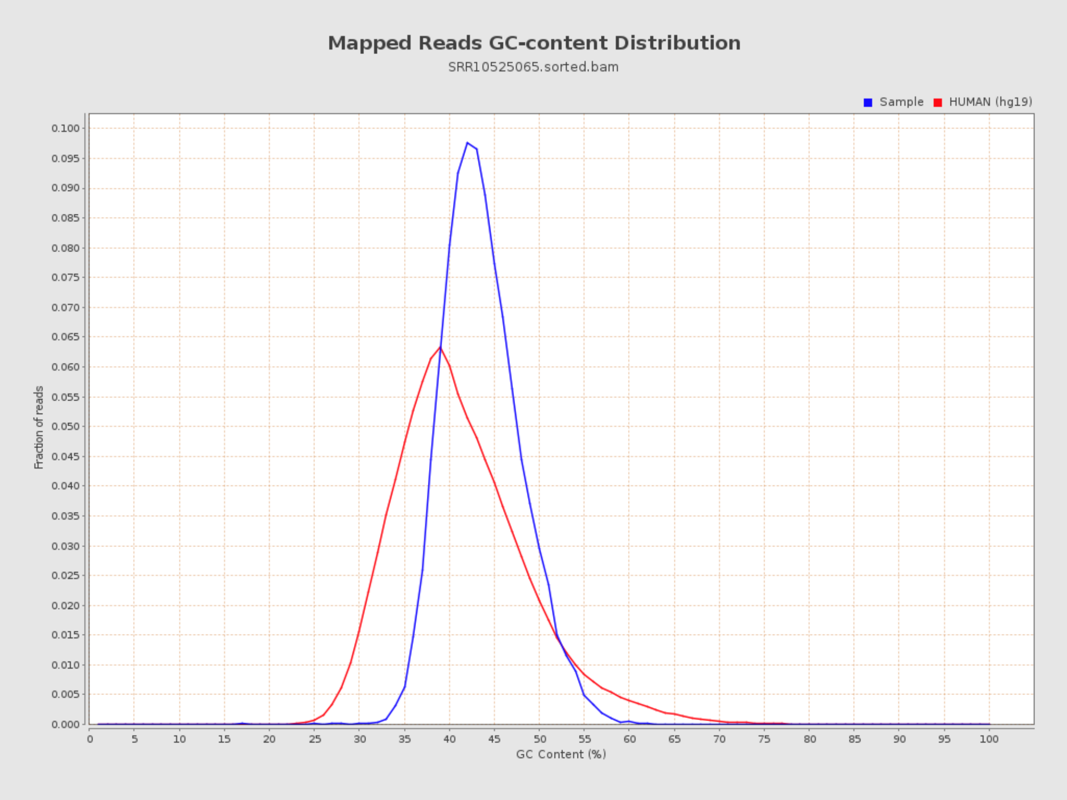
7. Results : Duplication Rate Histogram



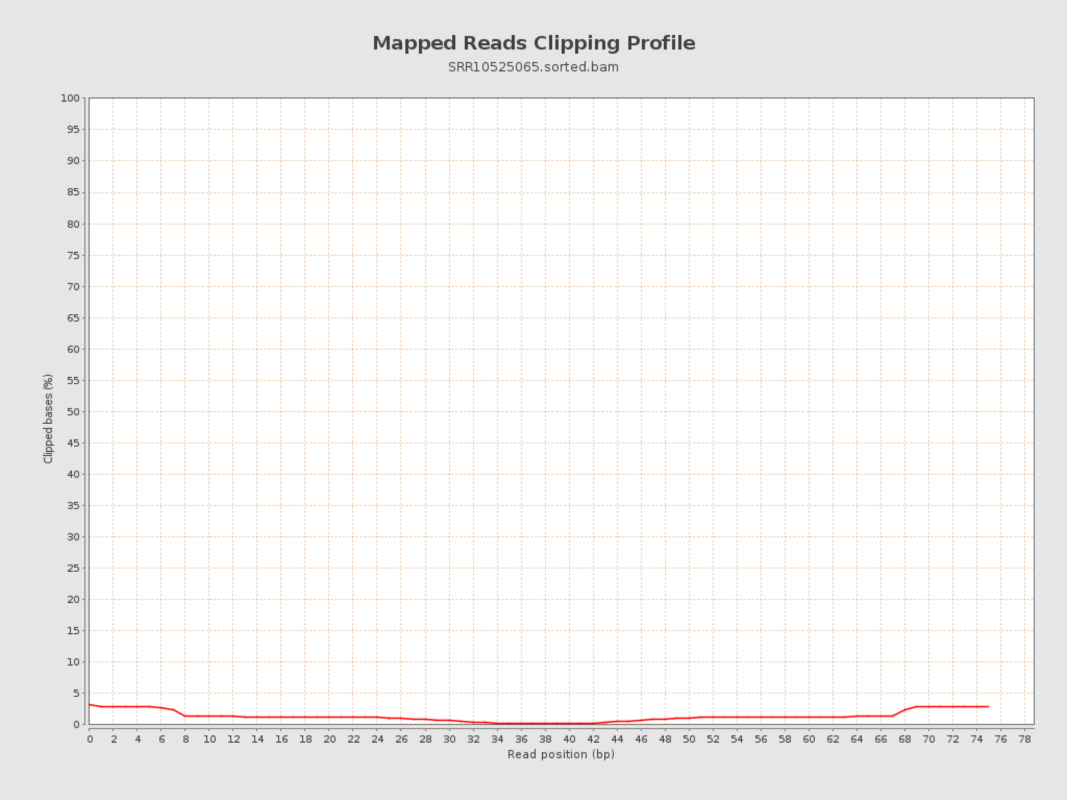
8. Results : Mapped Reads Nucleotide Content



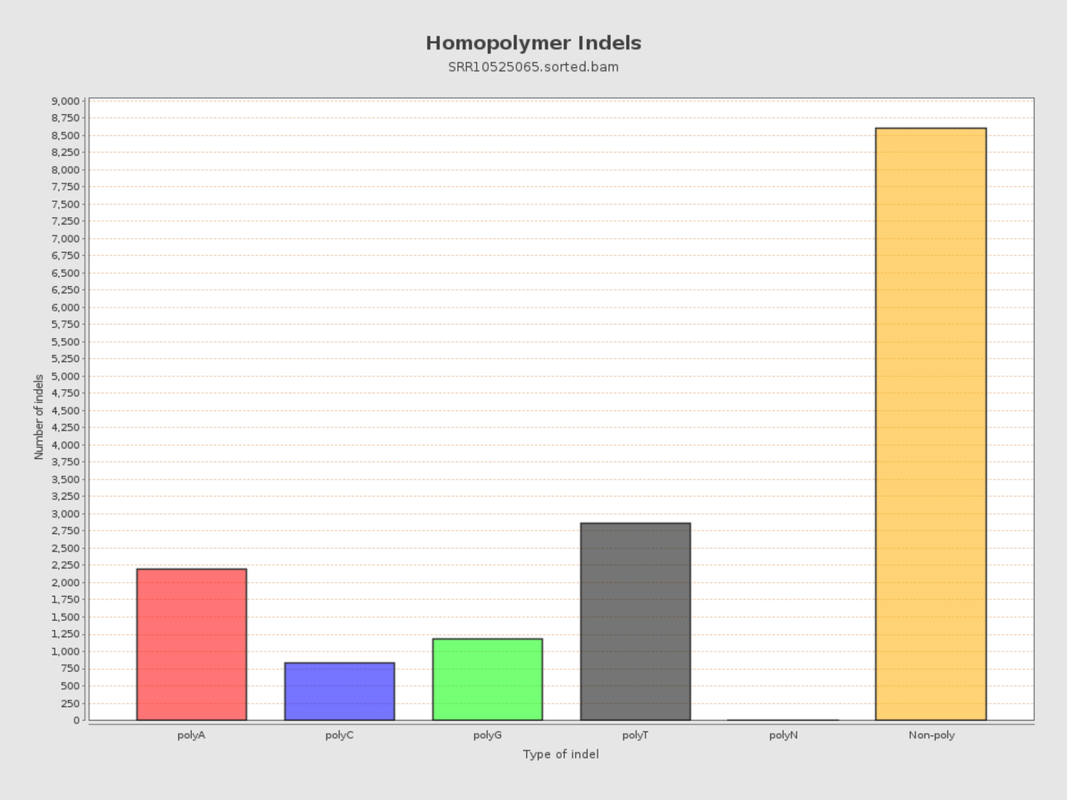
9. Results : Mapped Reads GC-content Distribution



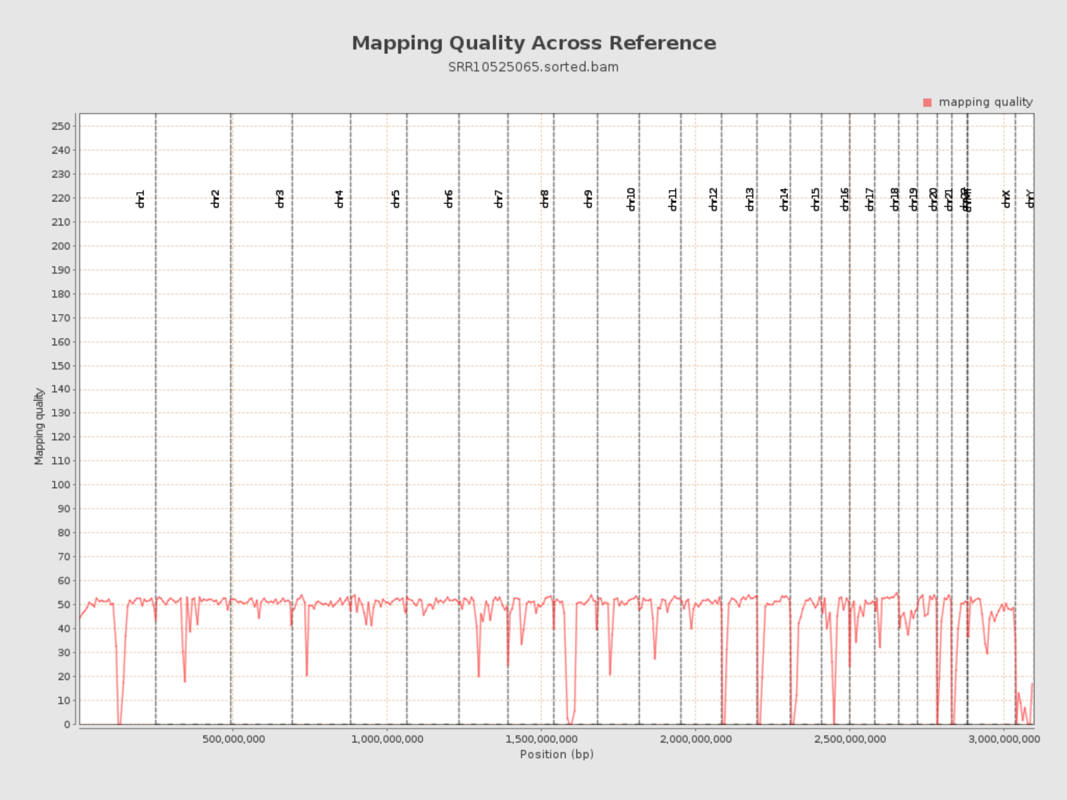
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram