Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 20:35:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525160.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_SRR10525160 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525160.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 20:35:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525160.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	810,492
Mapped reads	630,703 / 77.82%
Unmapped reads	179,789 / 22.18%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,519 / 0.31%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	10,980 / 1.35%
Duplication rate	1.27%
Clipped reads	630,773 / 77.83%

2.2. ACGT Content

Number/percentage of A's	10,213,403 / 26.35%
Number/percentage of C's	7,015,931 / 18.1%
Number/percentage of T's	11,807,363 / 30.47%
Number/percentage of G's	9,716,185 / 25.07%
Number/percentage of N's	937 / 0%
GC Percentage	43.18%

2.3. Coverage

Mean	0.0125

Standard Deviation	0.1467

2.4. Mapping Quality

Mean Mapping Quality	45.9

2.5. Mismatches and indels

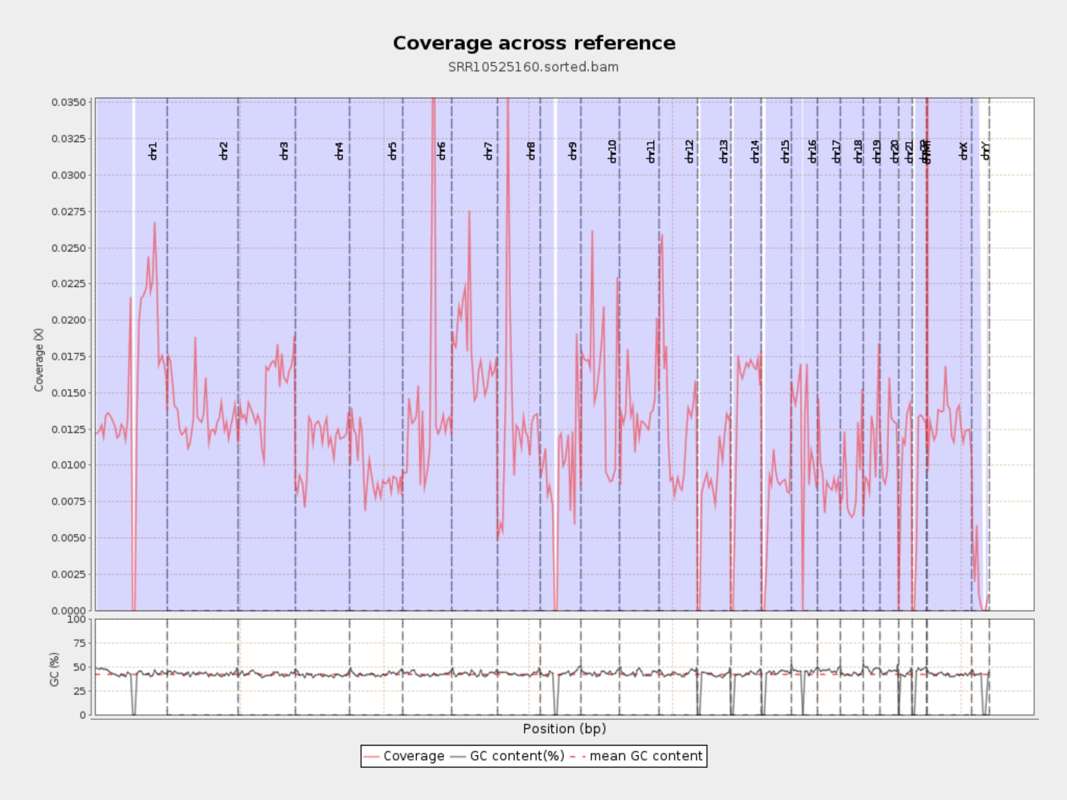
General error rate	0.49%
Mismatches	184,313
Insertions	2,818
Mapped reads with at least one insertion	0.44%
Deletions	7,558
Mapped reads with at least one deletion	1.19%
Homopolymer indels	43.79%

2.6. Chromosome stats

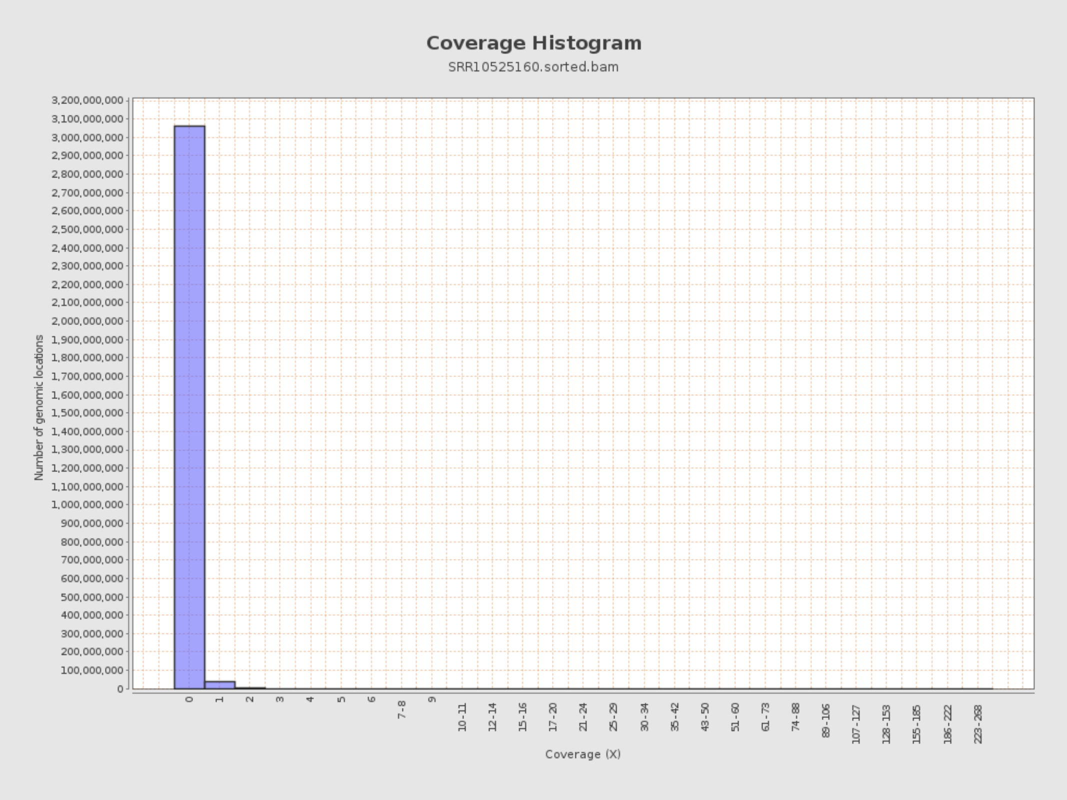
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3868781	0.0155	0.2373
chr2	243199373	3271617	0.0135	0.1599
chr3	198022430	2969004	0.015	0.1271
chr4	191154276	2182884	0.0114	0.1128
chr5	180915260	1746535	0.0097	0.1014
chr6	171115067	2453606	0.0143	0.1301
chr7	159138663	2878397	0.0181	0.2323

chr8	146364022	1919444	0.0131	0.132
chr9	141213431	1326435	0.0094	0.1141
chr10	135534747	2130343	0.0157	0.1546
chr11	135006516	1854715	0.0137	0.136
chr12	133851895	1784913	0.0133	0.1203
chr13	115169878	1033110	0.009	0.0979
chr14	107349540	1493549	0.0139	0.1238
chr15	102531392	751433	0.0073	0.0881
chr16	90354753	1087318	0.012	0.1193
chr17	81195210	745931	0.0092	0.1013
chr18	78077248	698656	0.0089	0.1907
chr19	59128983	661174	0.0112	0.1772
chr20	63025520	731428	0.0116	0.1123
chr21	48129895	517029	0.0107	0.1082
chr22	51304566	465518	0.0091	0.0981
chrMT	16571	80982	4.887	3.201
chrX	155270560	2005707	0.0129	0.1209
chrY	59373566	107384	0.0018	0.0619

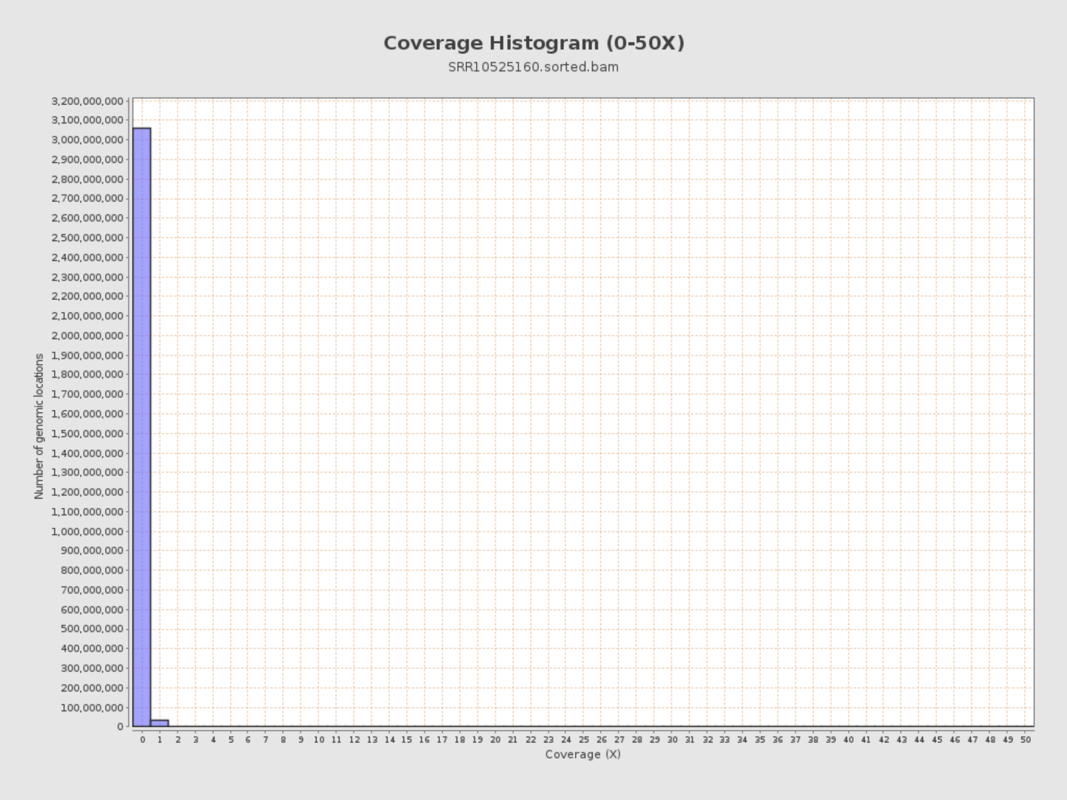
3. Results : Coverage across reference



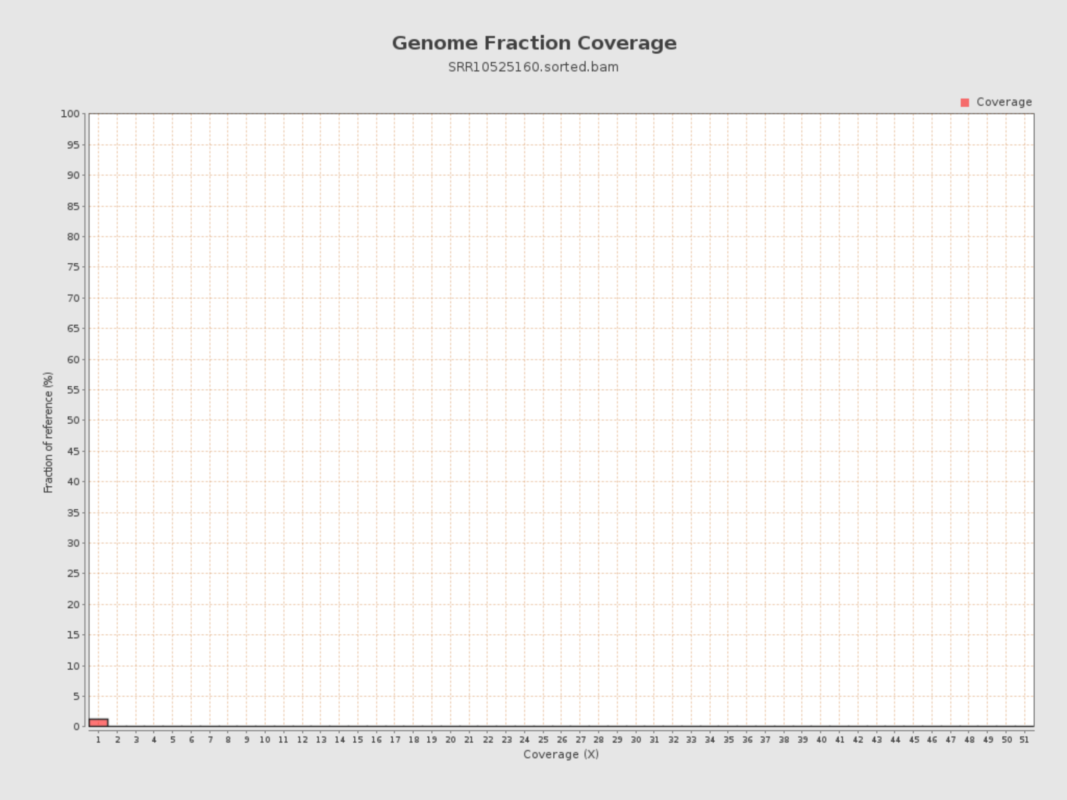
4. Results : Coverage Histogram



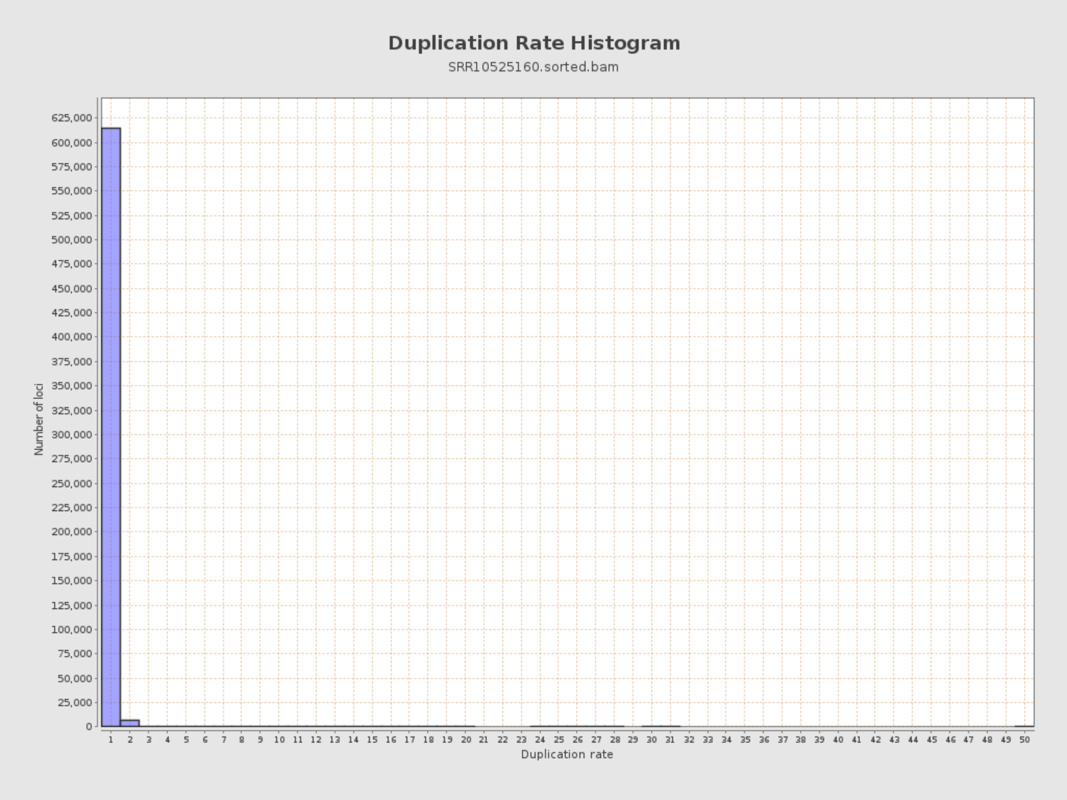
5. Results : Coverage Histogram (0-50X)



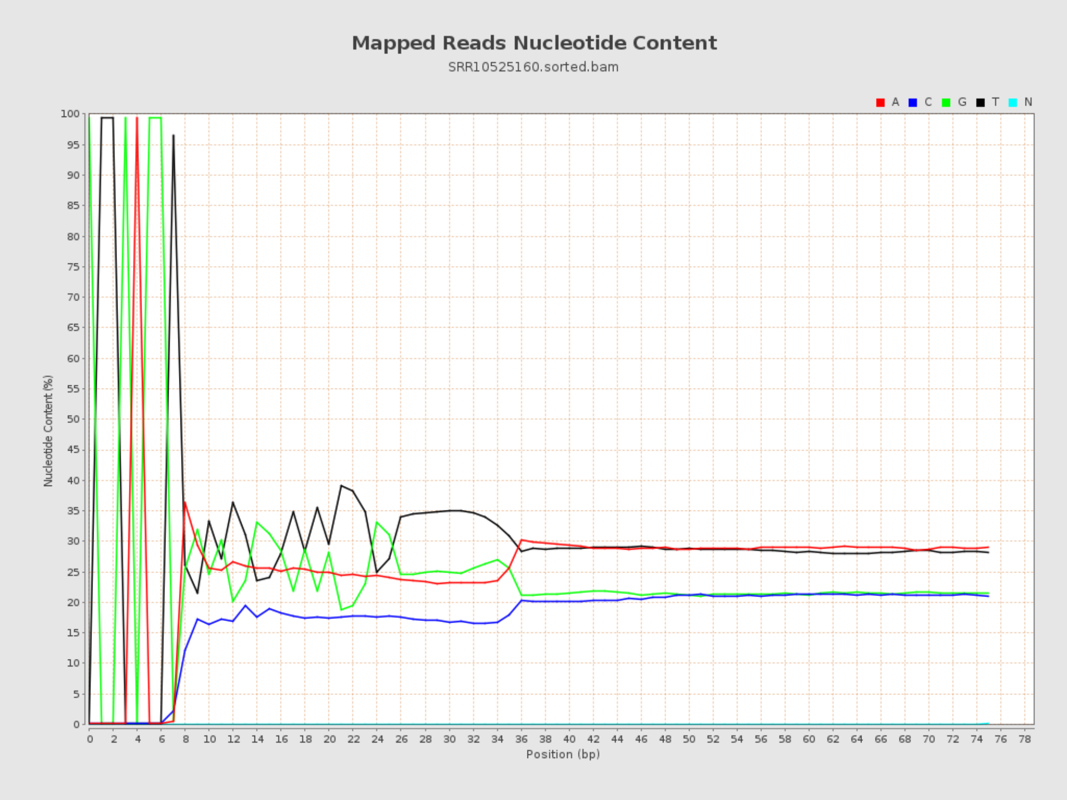
6. Results : Genome Fraction Coverage



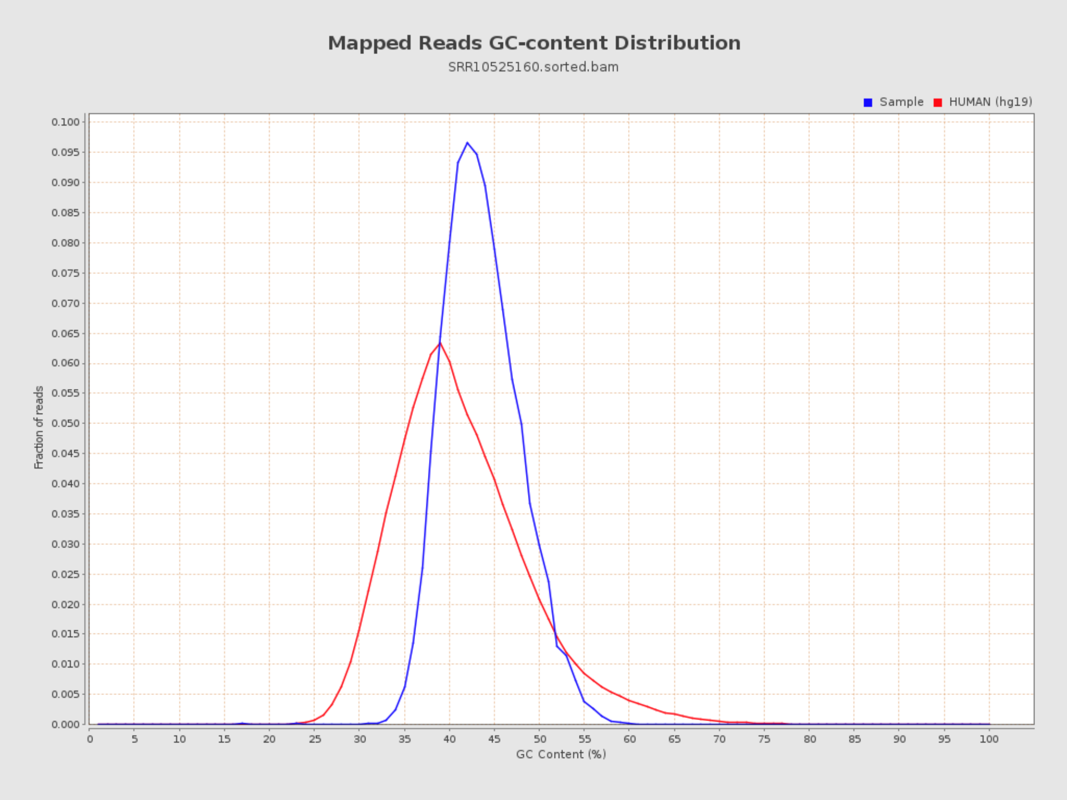
7. Results : Duplication Rate Histogram



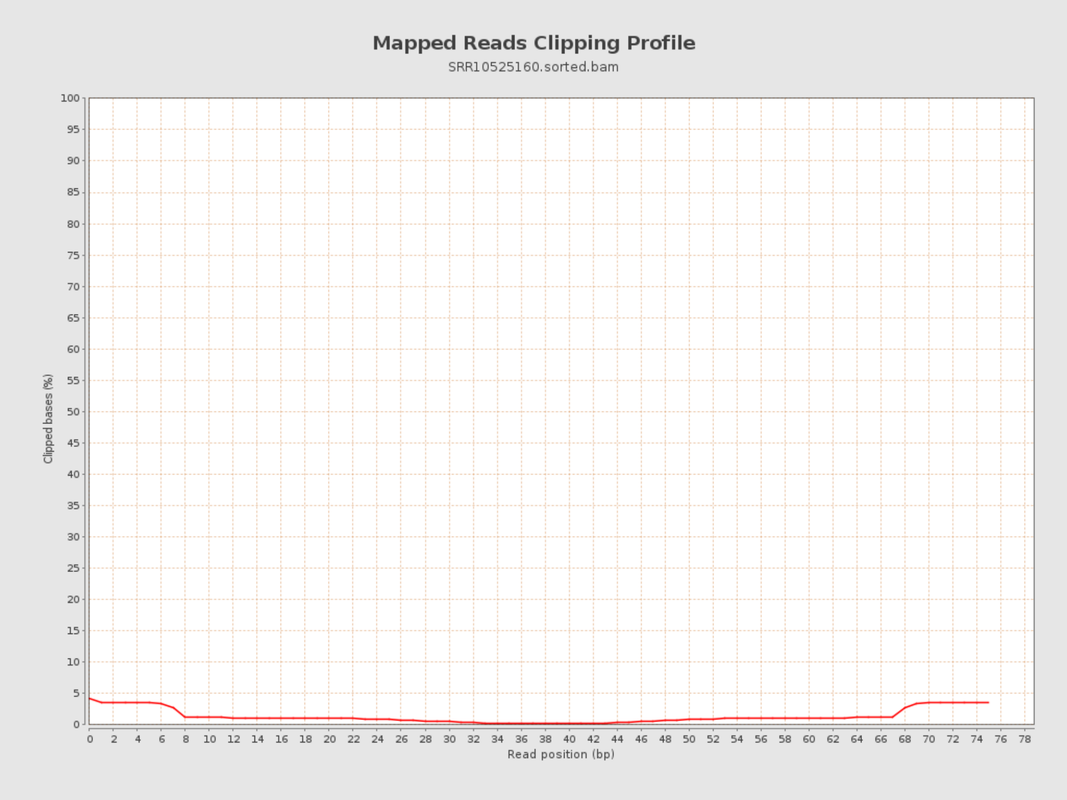
8. Results : Mapped Reads Nucleotide Content



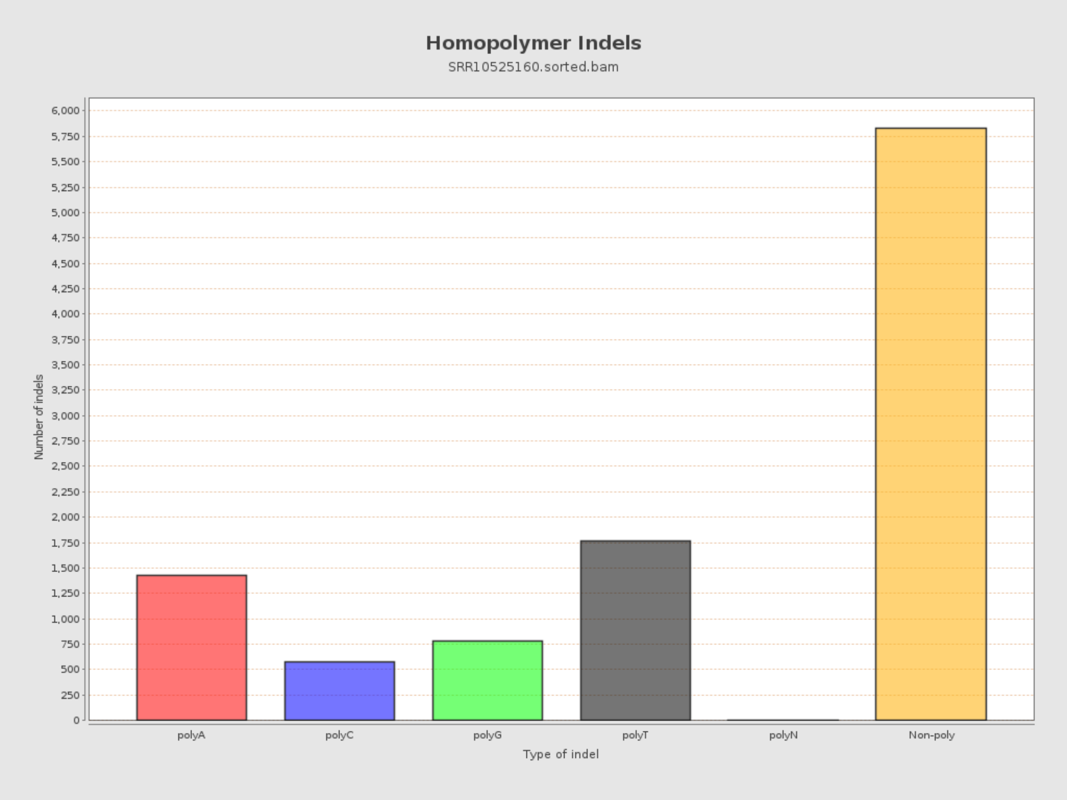
9. Results : Mapped Reads GC-content Distribution



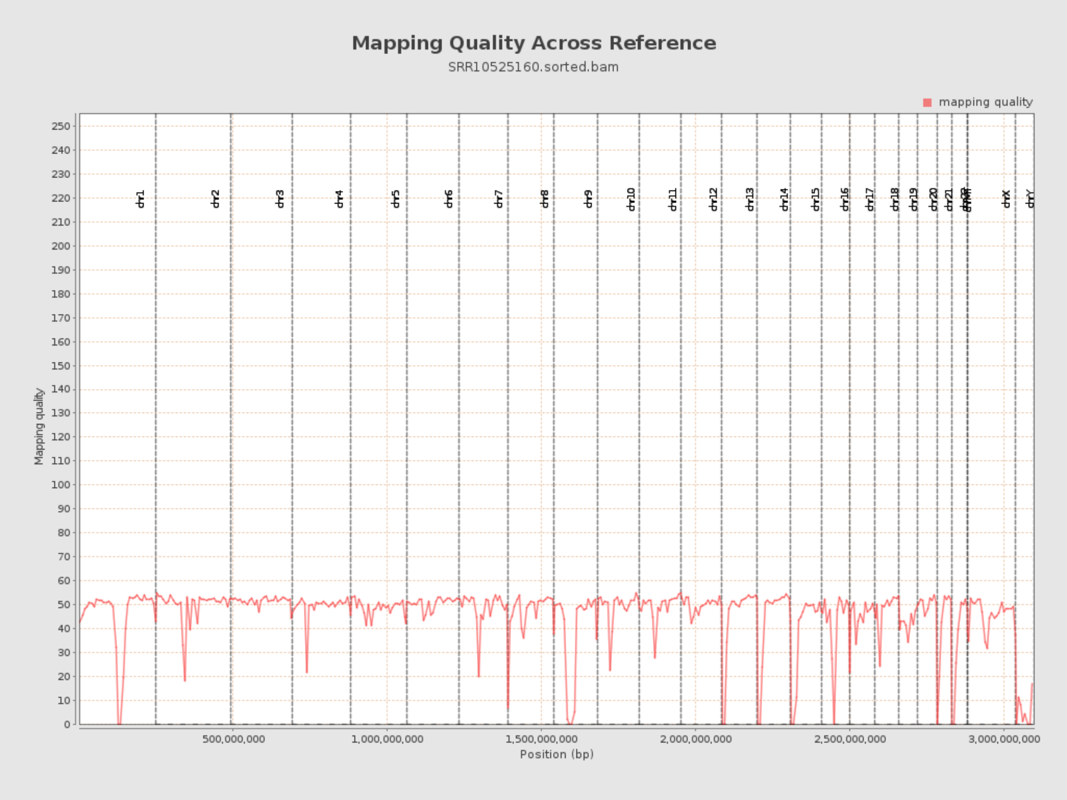
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram