Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 23:24:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525211.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_SRR10525211 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525211.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 23:24:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525211.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,044,667
Mapped reads	981,525 / 93.96%
Unmapped reads	63,142 / 6.04%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,588 / 0.34%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	24,324 / 2.33%
Duplication rate	1.76%
Clipped reads	981,697 / 93.97%

2.2. ACGT Content

Number/percentage of A's	15,833,684 / 26.62%
Number/percentage of C's	12,630,095 / 21.23%
Number/percentage of T's	17,474,750 / 29.37%
Number/percentage of G's	13,549,550 / 22.78%
Number/percentage of N's	1,611 / 0%
GC Percentage	44.01%

2.3. Coverage

Mean	0.0192

Standard Deviation	0.2068

2.4. Mapping Quality

Mean Mapping Quality	45.68

2.5. Mismatches and indels

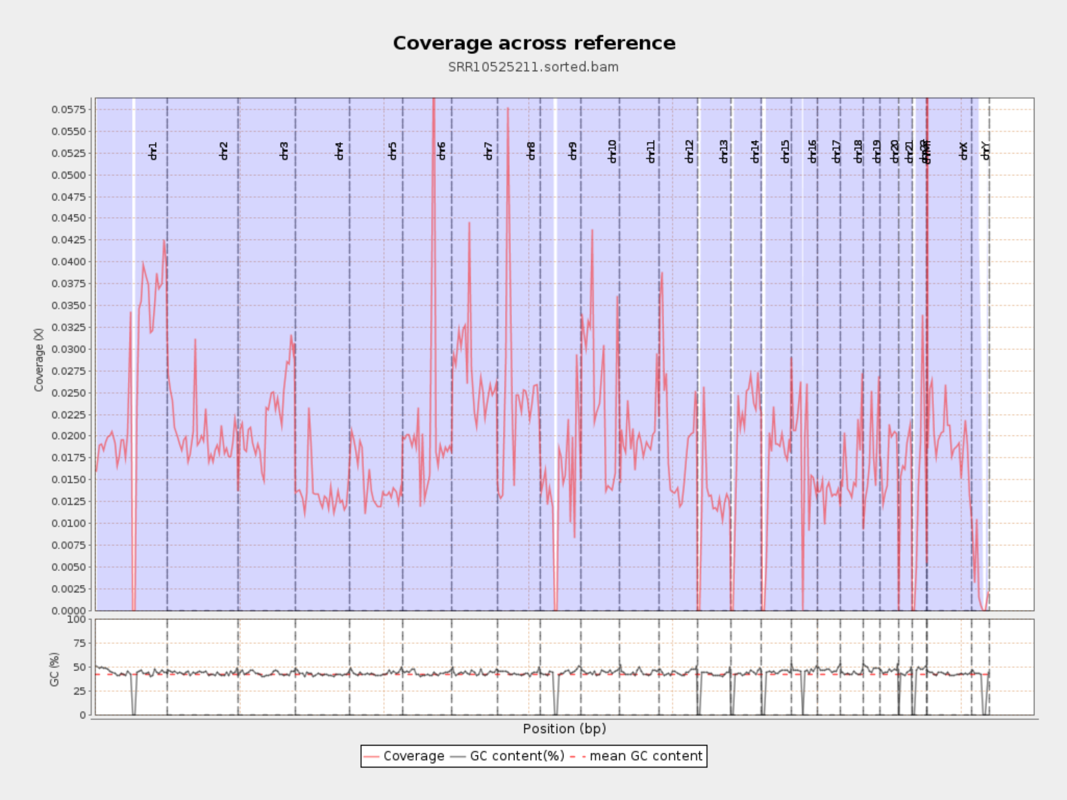
General error rate	0.5%
Mismatches	285,908
Insertions	4,421
Mapped reads with at least one insertion	0.45%
Deletions	11,926
Mapped reads with at least one deletion	1.21%
Homopolymer indels	42.36%

2.6. Chromosome stats

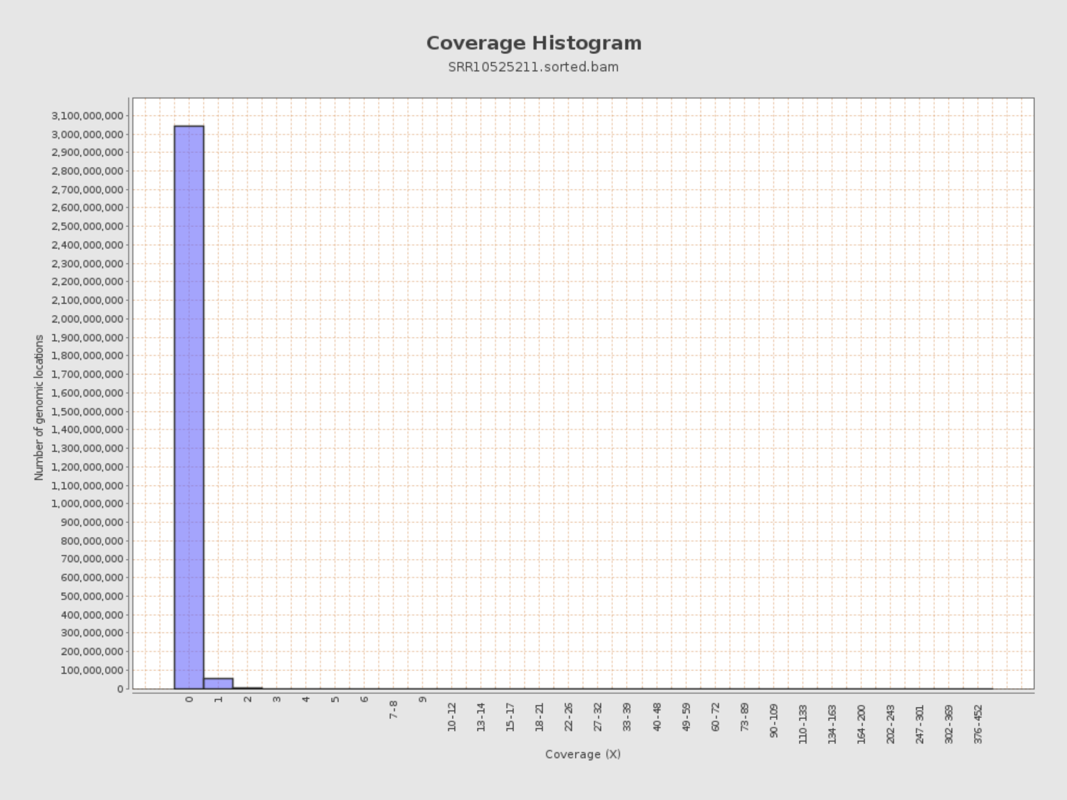
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6401385	0.0257	0.3705
chr2	243199373	4884798	0.0201	0.2348
chr3	198022430	4400960	0.0222	0.1577
chr4	191154276	2587825	0.0135	0.1305
chr5	180915260	2655657	0.0147	0.1272
chr6	171115067	3660813	0.0214	0.1654
chr7	159138663	4385708	0.0276	0.3461

chr8	146364022	3623487	0.0248	0.204
chr9	141213431	2055174	0.0146	0.1571
chr10	135534747	3482753	0.0257	0.2283
chr11	135006516	2692574	0.0199	0.1683
chr12	133851895	2682276	0.02	0.15
chr13	115169878	1370668	0.0119	0.115
chr14	107349540	2141809	0.02	0.1507
chr15	102531392	1599971	0.0156	0.1305
chr16	90354753	1610752	0.0178	0.1513
chr17	81195210	1085174	0.0134	0.1255
chr18	78077248	1303523	0.0167	0.2764
chr19	59128983	1051814	0.0178	0.2626
chr20	63025520	1092649	0.0173	0.1399
chr21	48129895	774551	0.0161	0.1406
chr22	51304566	688237	0.0134	0.1214
chrMT	16571	10860	0.6554	0.8852
chrX	155270560	3081196	0.0198	0.1551
chrY	59373566	183976	0.0031	0.104

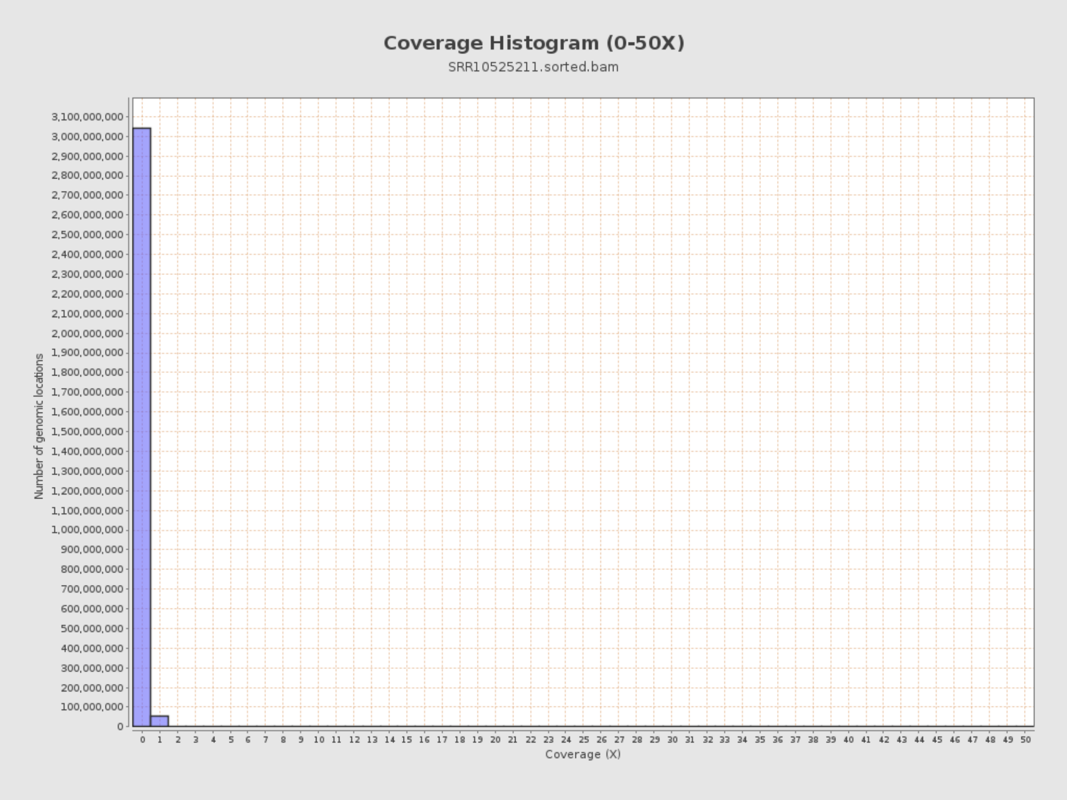
3. Results : Coverage across reference



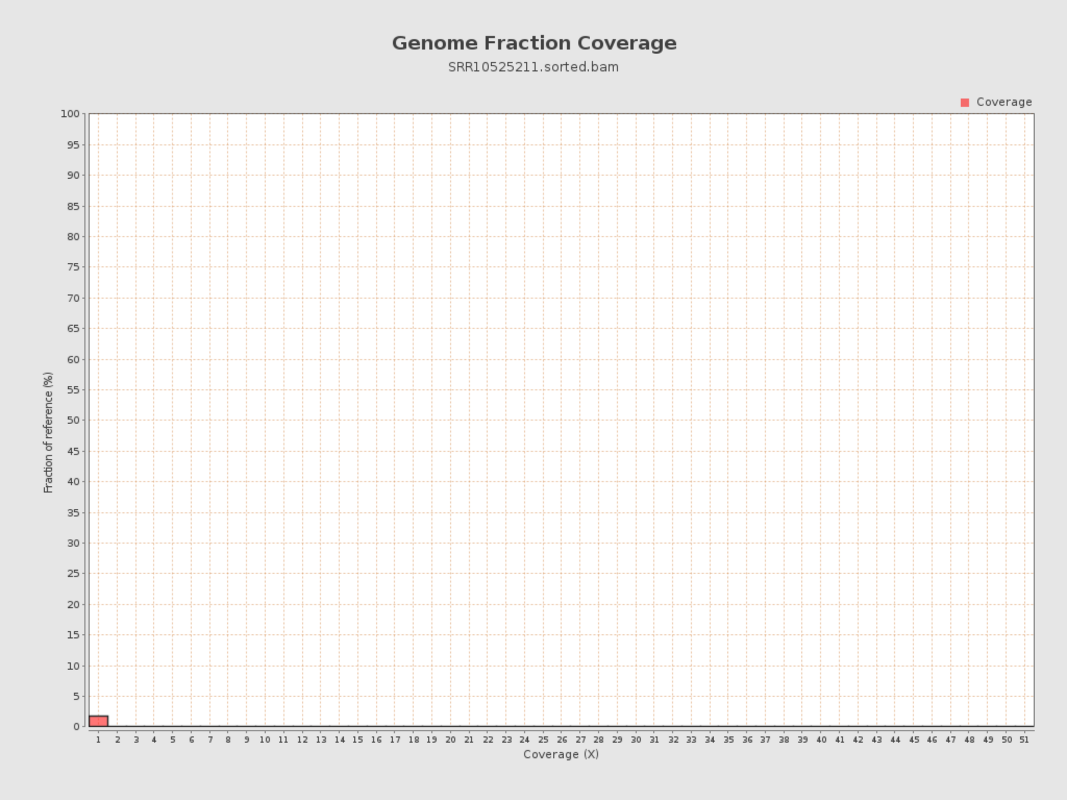
4. Results : Coverage Histogram



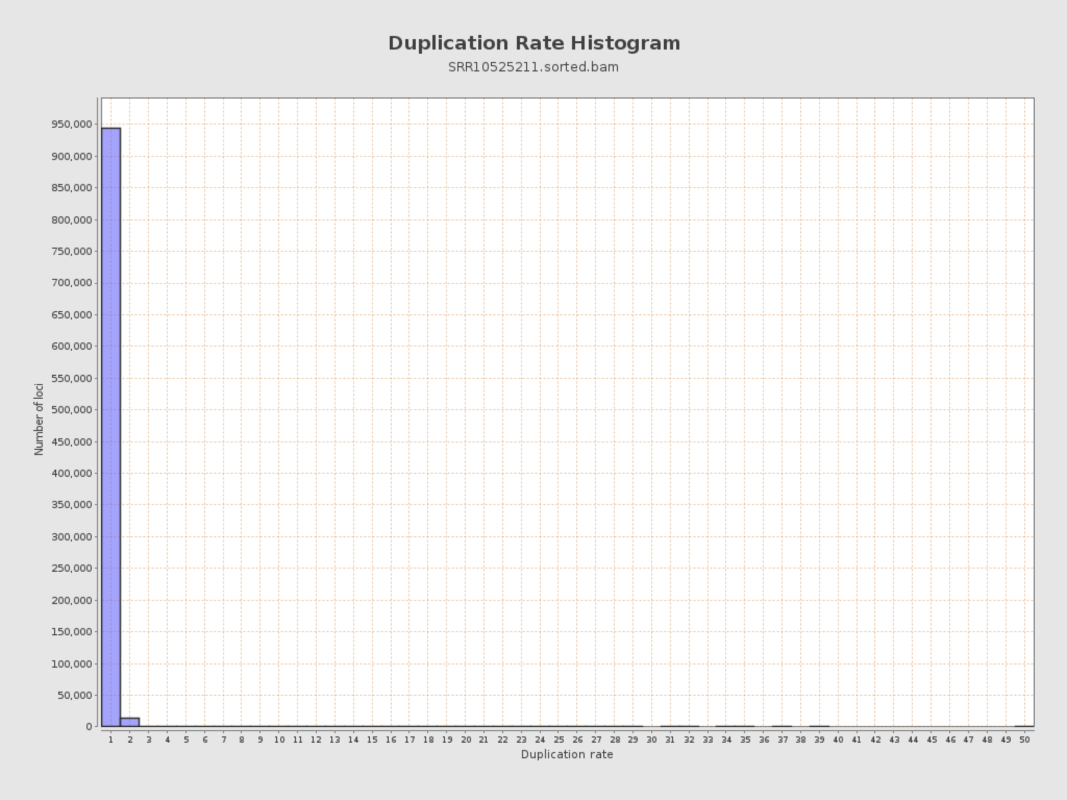
5. Results : Coverage Histogram (0-50X)



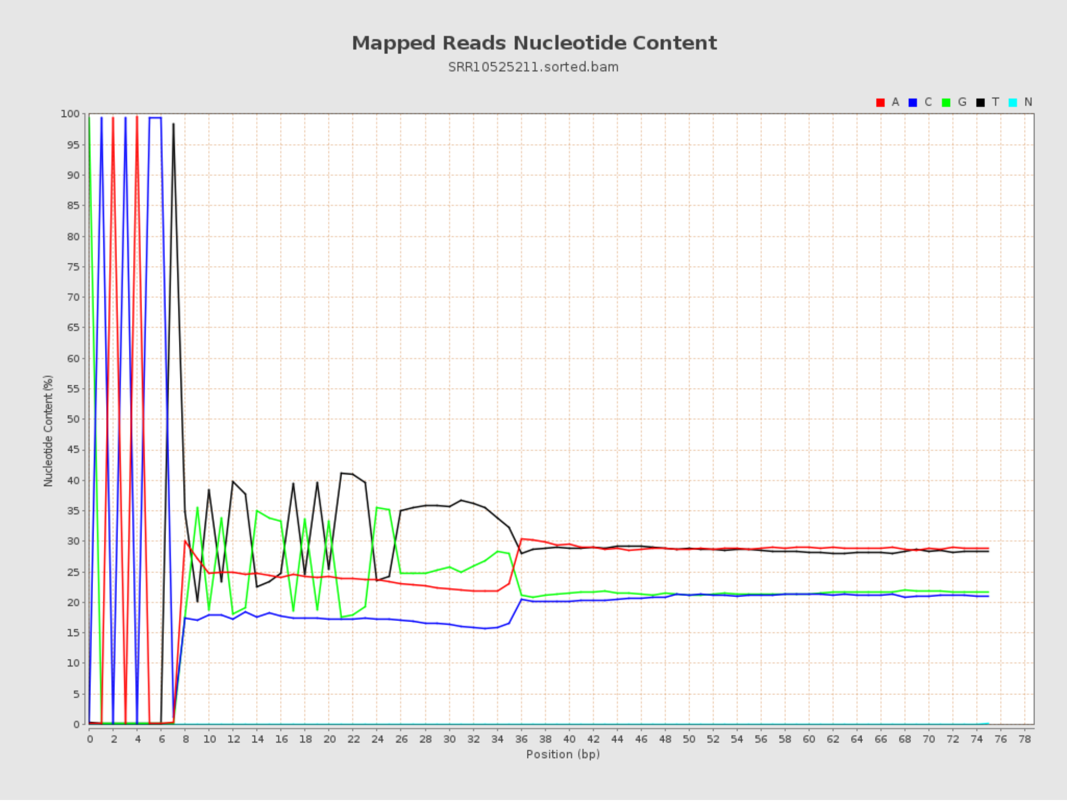
6. Results : Genome Fraction Coverage



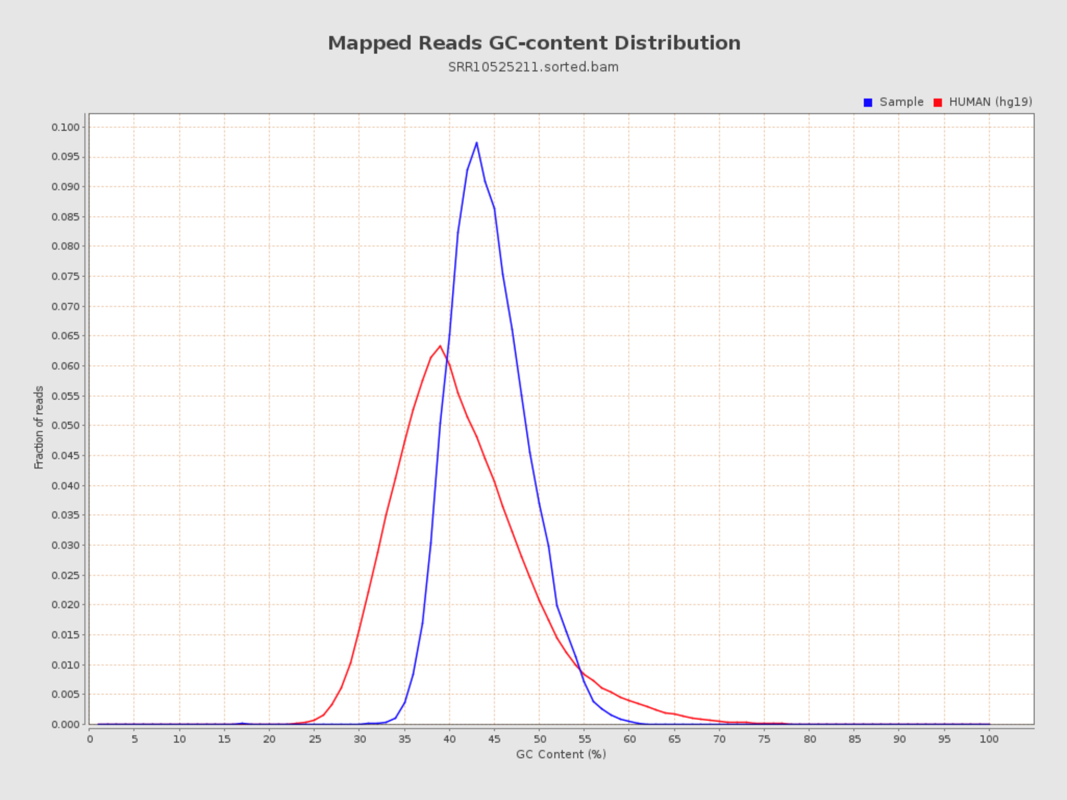
7. Results : Duplication Rate Histogram



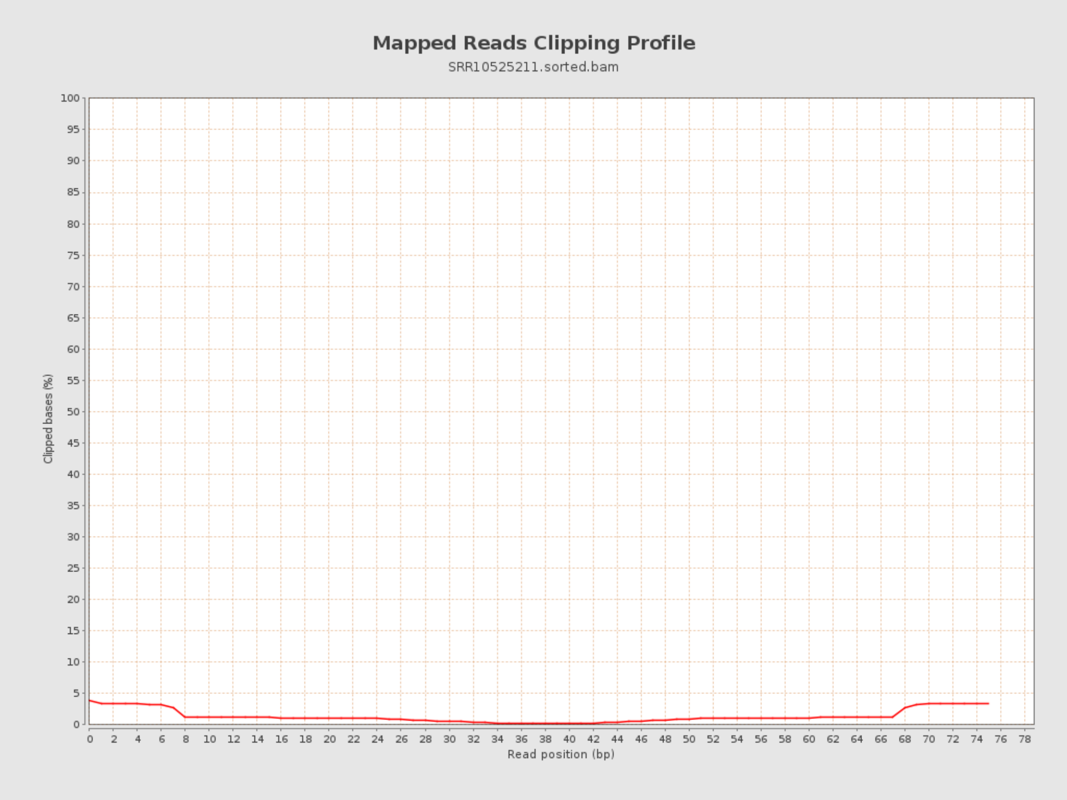
8. Results : Mapped Reads Nucleotide Content



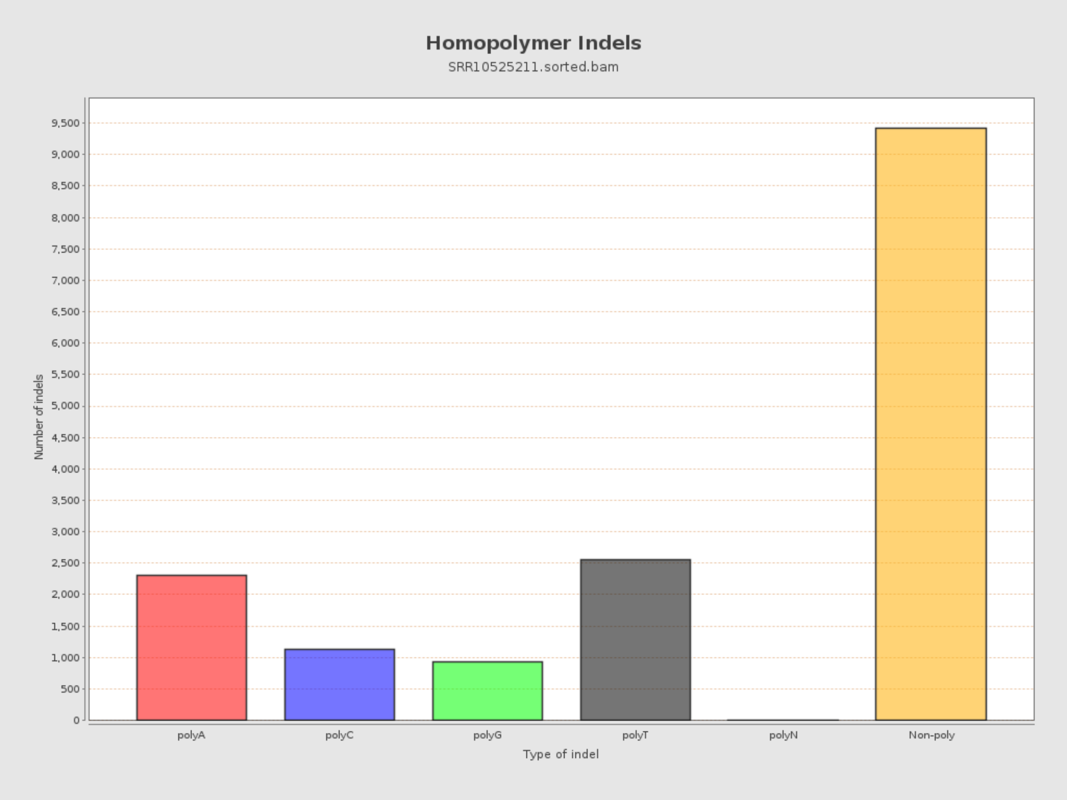
9. Results : Mapped Reads GC-content Distribution



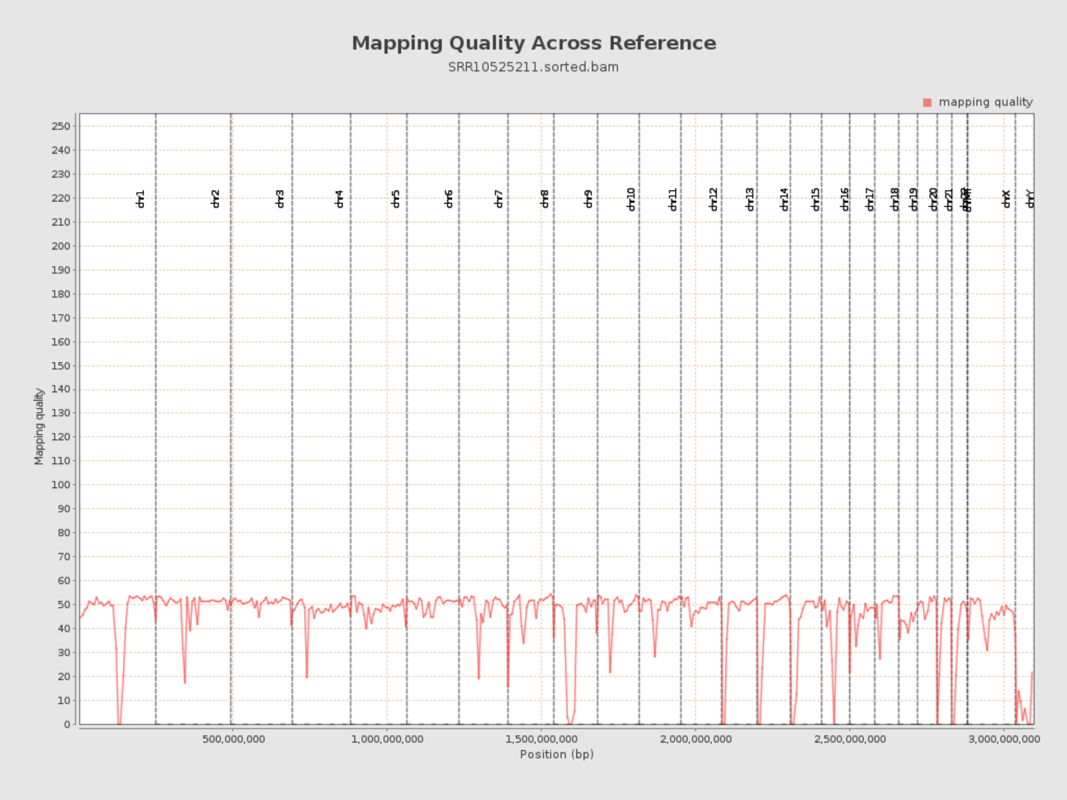
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram