Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 01:26:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525260.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_SRR10525260 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525260.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 01:26:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525260.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	968,341
Mapped reads	885,809 / 91.48%
Unmapped reads	82,532 / 8.52%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,311 / 0.34%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	22,890 / 2.36%
Duplication rate	1.84%
Clipped reads	886,152 / 91.51%

2.2. ACGT Content

Number/percentage of A's	13,247,226 / 25.86%
Number/percentage of C's	9,653,502 / 18.85%
Number/percentage of T's	16,442,168 / 32.1%
Number/percentage of G's	11,876,578 / 23.19%
Number/percentage of N's	1,098 / 0%
GC Percentage	42.03%

2.3. Coverage

Mean	0.0166

Standard Deviation	0.189

2.4. Mapping Quality

Mean Mapping Quality	44.91

2.5. Mismatches and indels

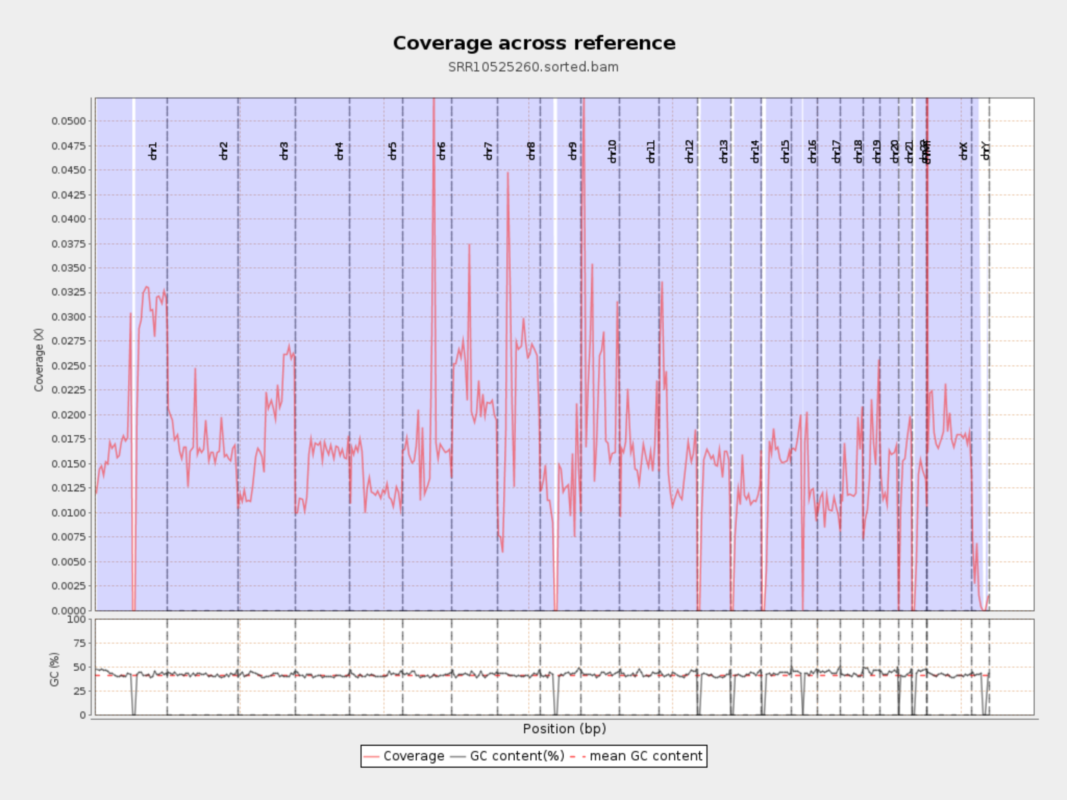
General error rate	0.52%
Mismatches	257,553
Insertions	4,280
Mapped reads with at least one insertion	0.48%
Deletions	10,705
Mapped reads with at least one deletion	1.2%
Homopolymer indels	42.87%

2.6. Chromosome stats

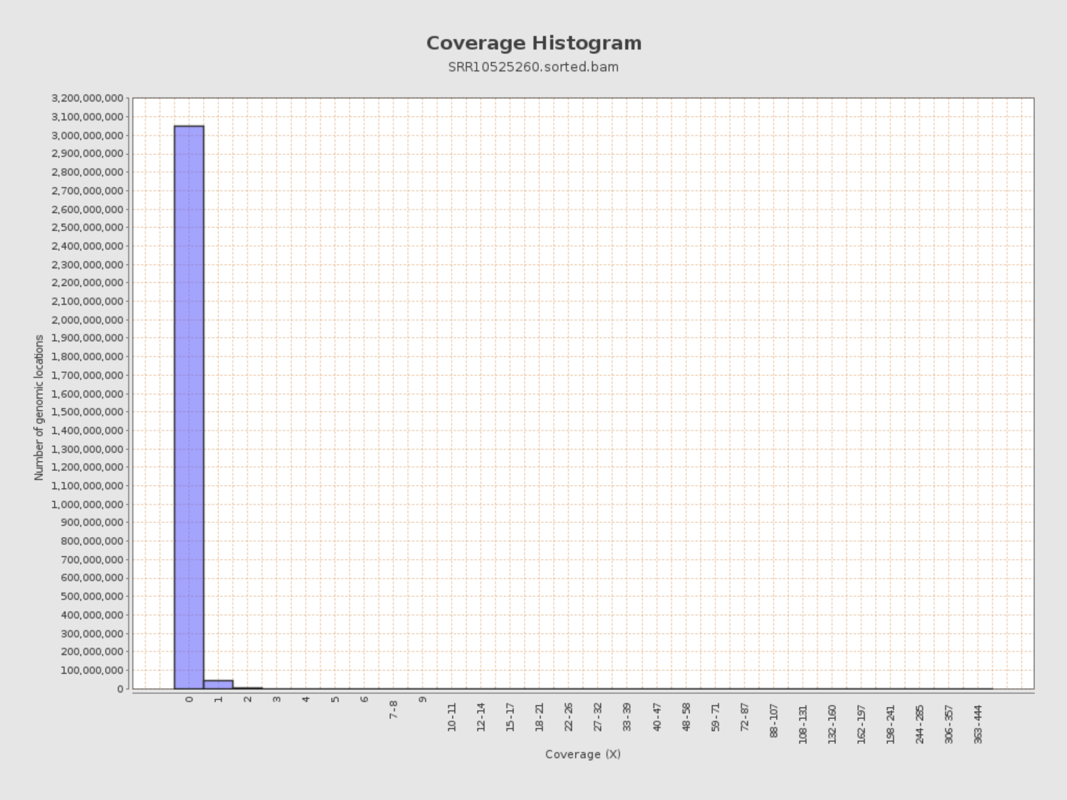
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5421216	0.0218	0.3267
chr2	243199373	4107271	0.0169	0.2225
chr3	198022430	3641605	0.0184	0.1436
chr4	191154276	2892222	0.0151	0.1312
chr5	180915260	2364838	0.0131	0.1204
chr6	171115067	3103150	0.0181	0.1507
chr7	159138663	3677104	0.0231	0.3161

chr8	146364022	3405917	0.0233	0.2021
chr9	141213431	1626402	0.0115	0.1357
chr10	135534747	3328234	0.0246	0.2172
chr11	135006516	2207029	0.0163	0.1536
chr12	133851895	2249472	0.0168	0.1372
chr13	115169878	1545868	0.0134	0.1213
chr14	107349540	1099358	0.0102	0.1074
chr15	102531392	1334786	0.013	0.1209
chr16	90354753	1269889	0.0141	0.1361
chr17	81195210	854720	0.0105	0.1098
chr18	78077248	1100947	0.0141	0.2418
chr19	59128983	925525	0.0157	0.2492
chr20	63025520	880315	0.014	0.1248
chr21	48129895	696989	0.0145	0.1274
chr22	51304566	501620	0.0098	0.1036
chrMT	16571	5282	0.3187	0.6317
chrX	155270560	2858413	0.0184	0.1499
chrY	59373566	139291	0.0023	0.0687

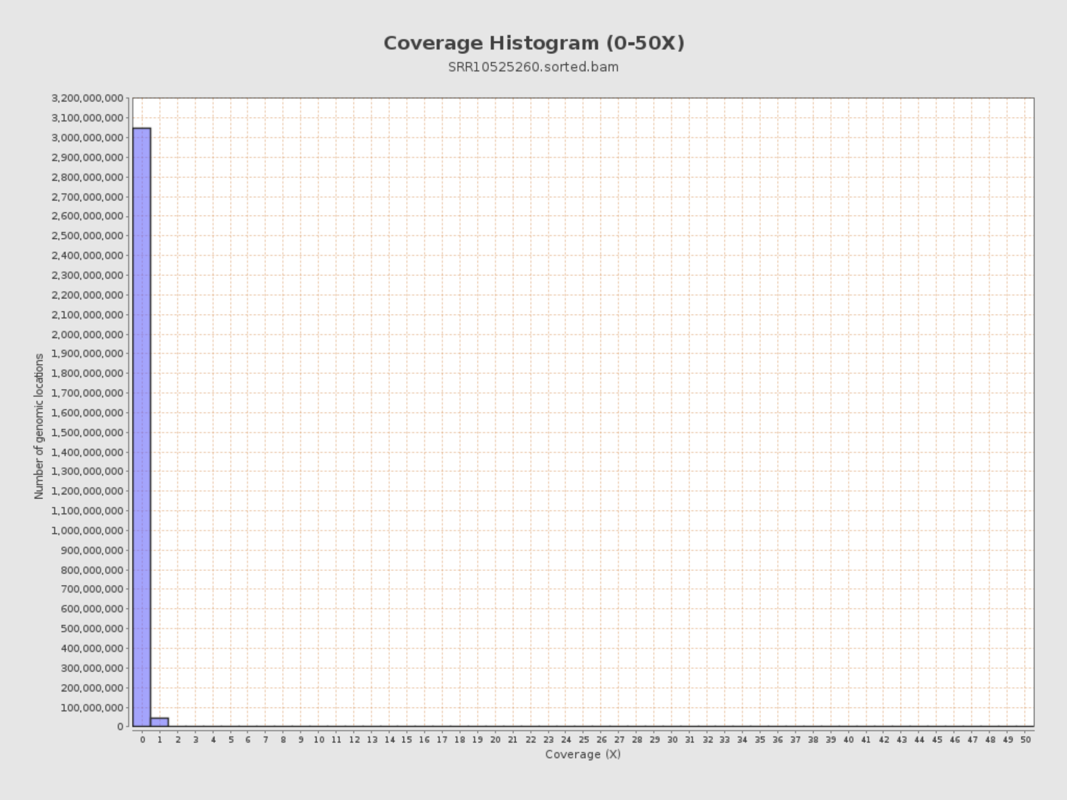
3. Results : Coverage across reference



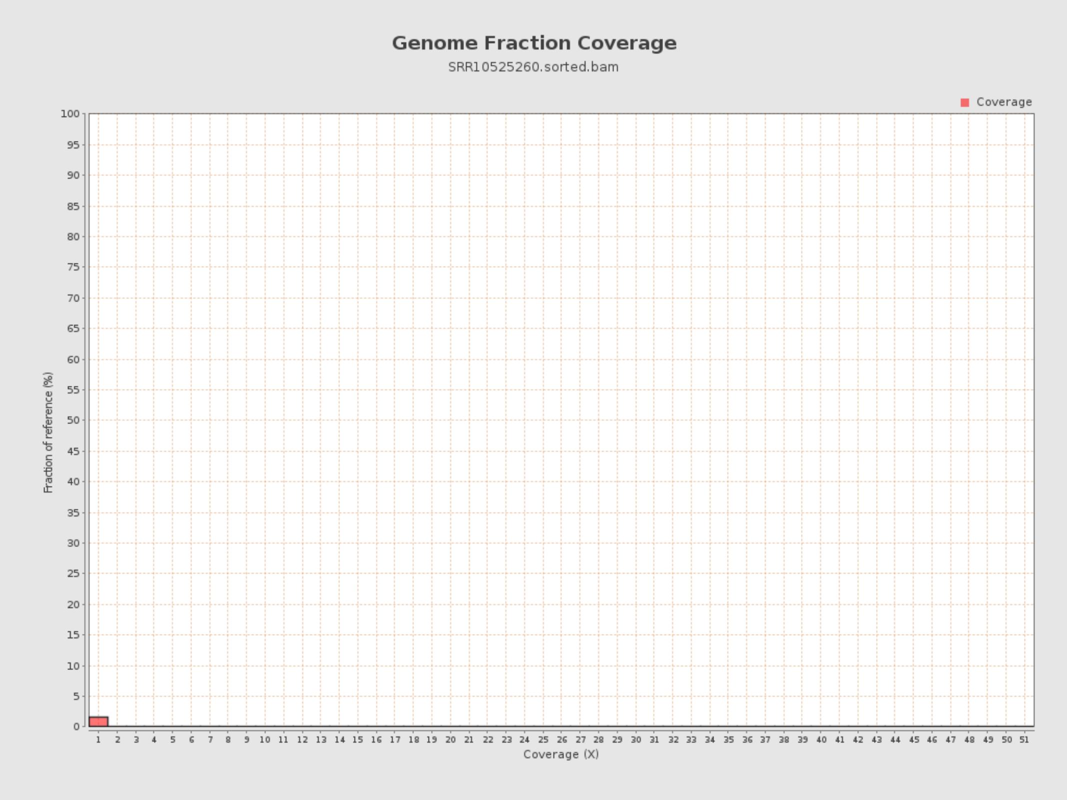
4. Results : Coverage Histogram



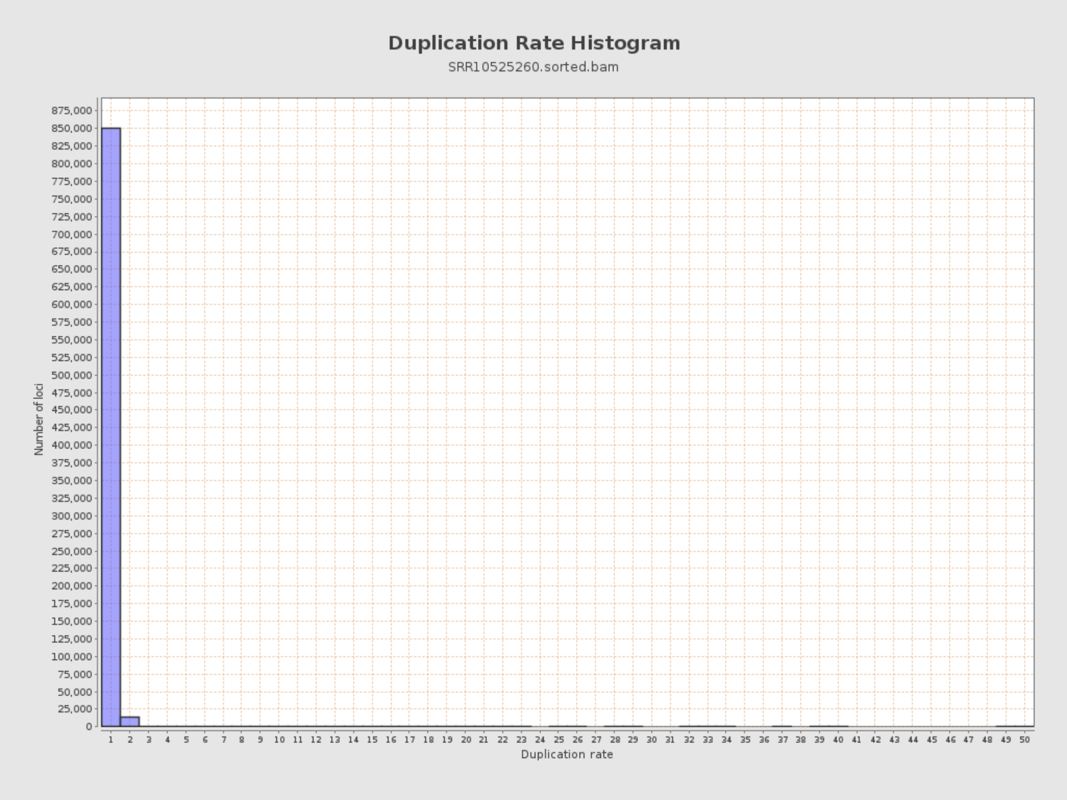
5. Results : Coverage Histogram (0-50X)



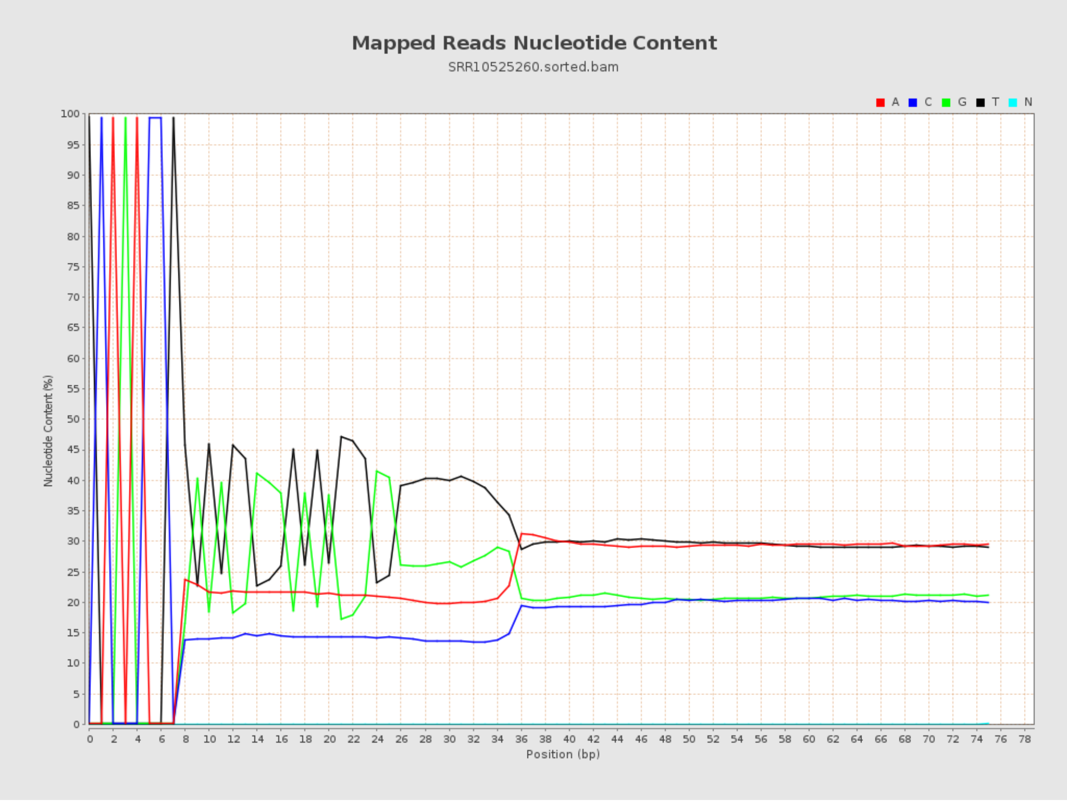
6. Results : Genome Fraction Coverage



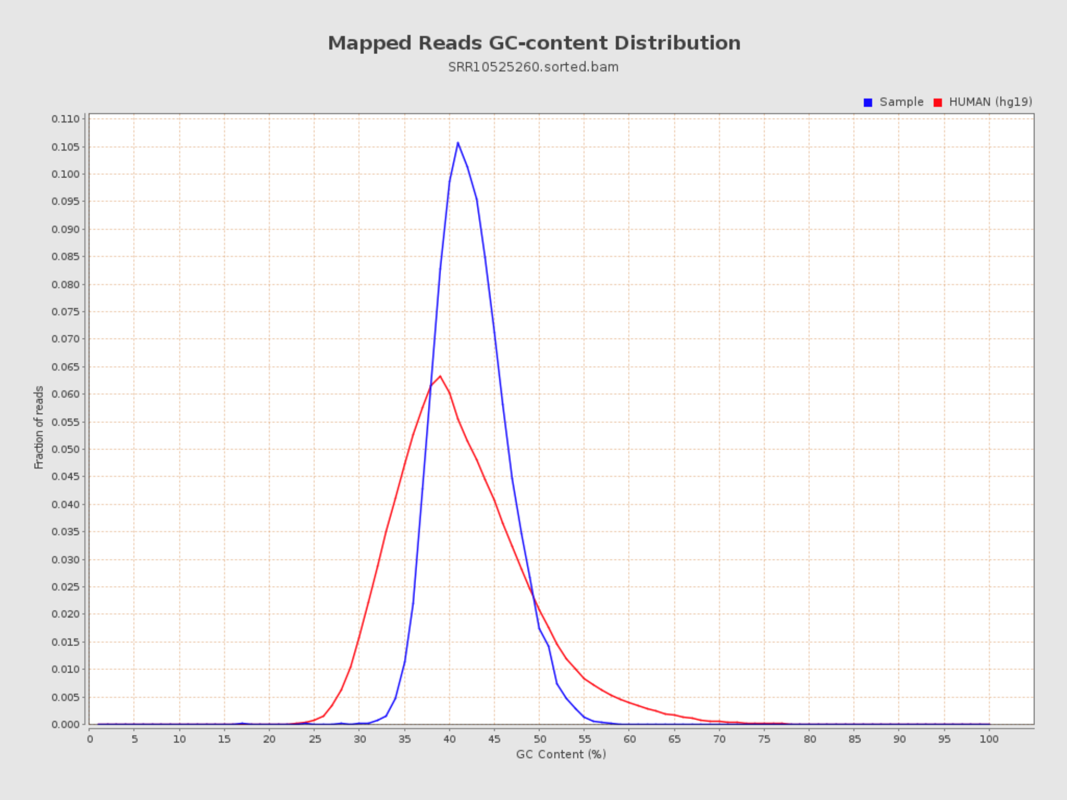
7. Results : Duplication Rate Histogram



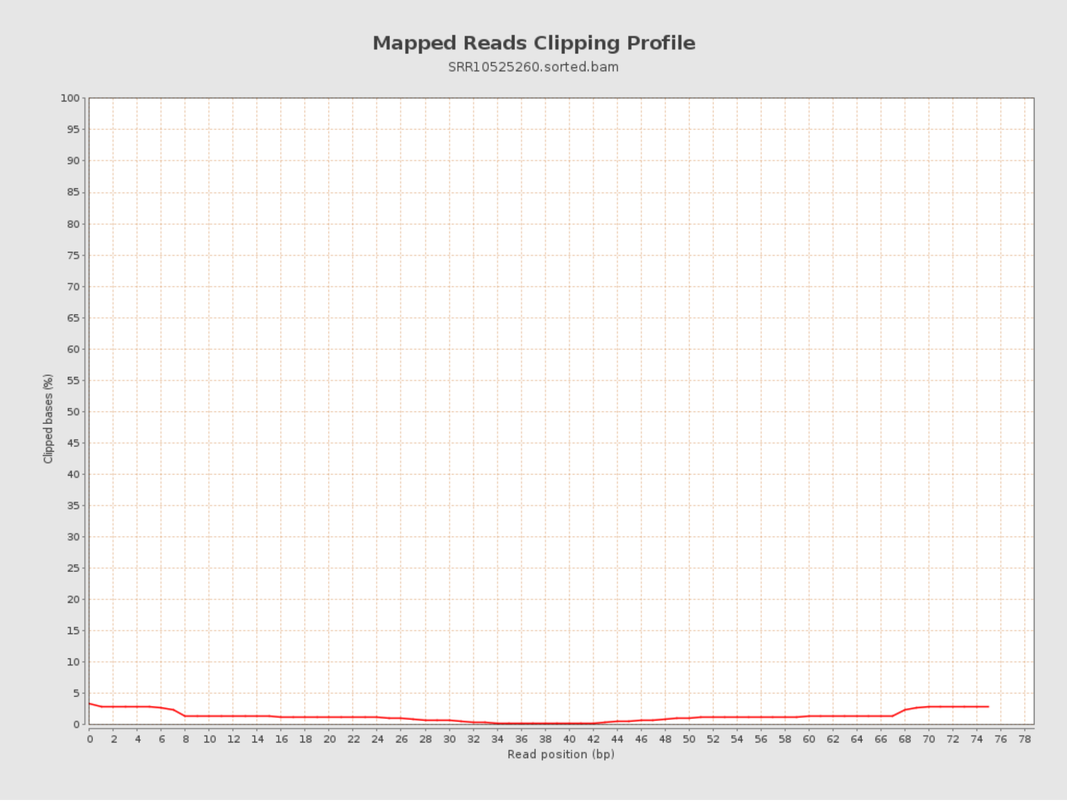
8. Results : Mapped Reads Nucleotide Content



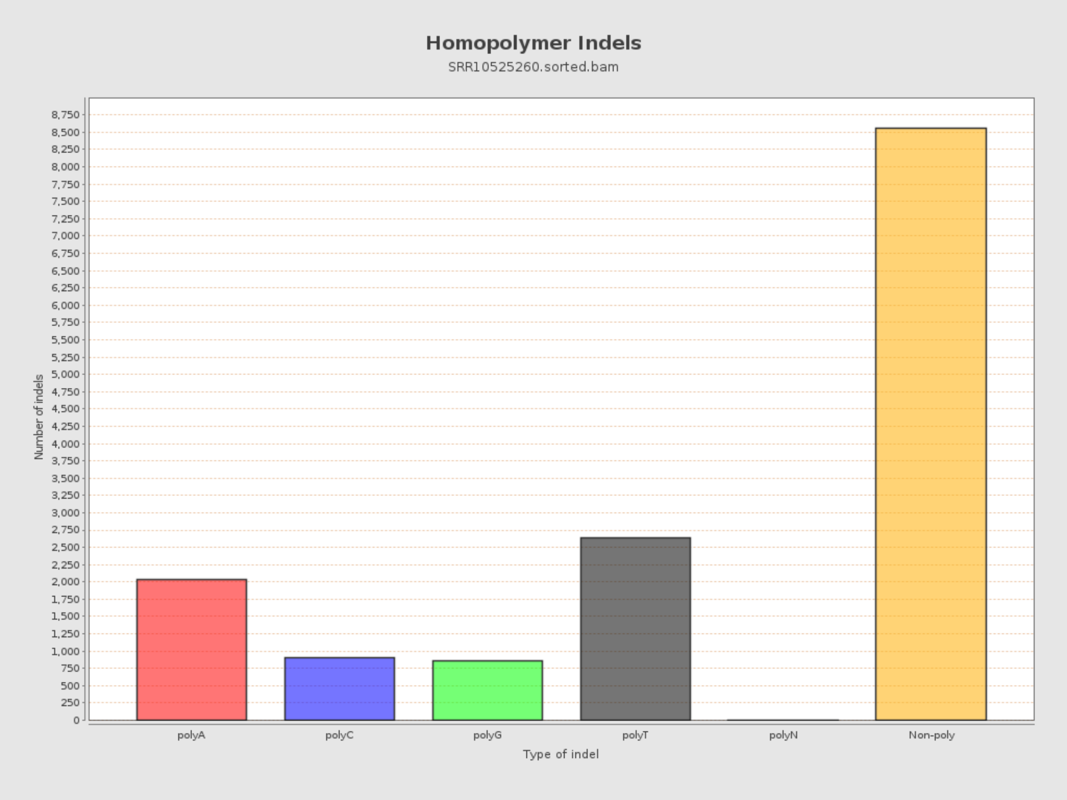
9. Results : Mapped Reads GC-content Distribution



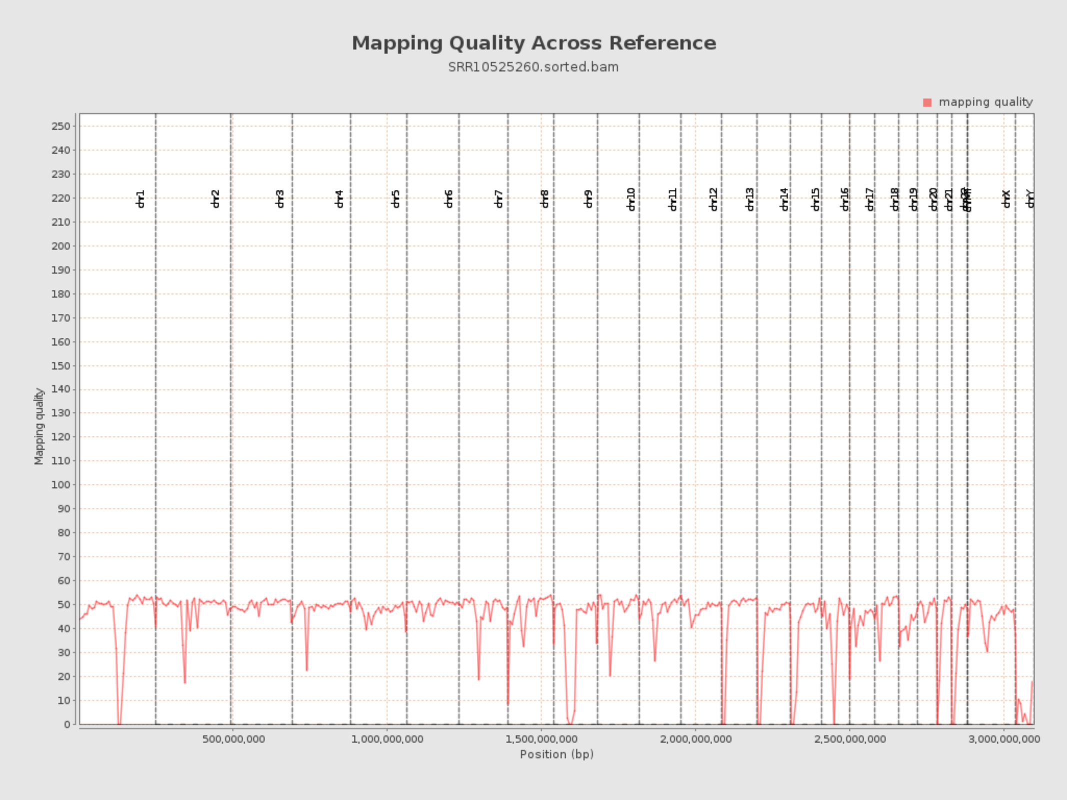
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram