

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 02:12:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525271.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_SRR10525271 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525271.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 02:12:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525271.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	835,367
Mapped reads	764,766 / 91.55%
Unmapped reads	70,601 / 8.45%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,646 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	18,186 / 2.18%
Duplication rate	1.71%
Clipped reads	765,873 / 91.68%

2.2. ACGT Content

Number/percentage of A's	11,196,597 / 25.12%
Number/percentage of C's	7,756,676 / 17.4%
Number/percentage of T's	14,178,802 / 31.81%
Number/percentage of G's	11,434,610 / 25.66%
Number/percentage of N's	884 / 0%
GC Percentage	43.06%

2.3. Coverage

Mean	0.0144

Standard Deviation	0.1673
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2.4. Mapping Quality

Mean Mapping Quality	45.19
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2.5. Mismatches and indels

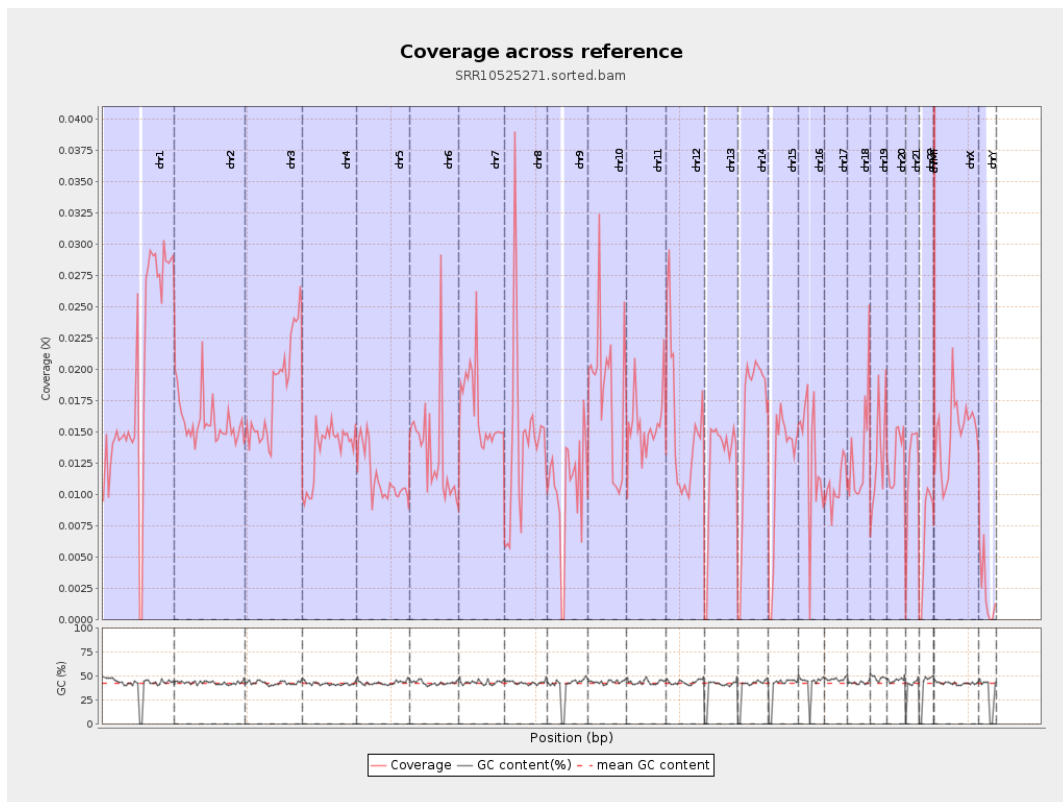
General error rate	0.52%
Mismatches	226,072
Insertions	3,148
Mapped reads with at least one insertion	0.41%
Deletions	9,307
Mapped reads with at least one deletion	1.21%
Homopolymer indels	42.89%

2.6. Chromosome stats

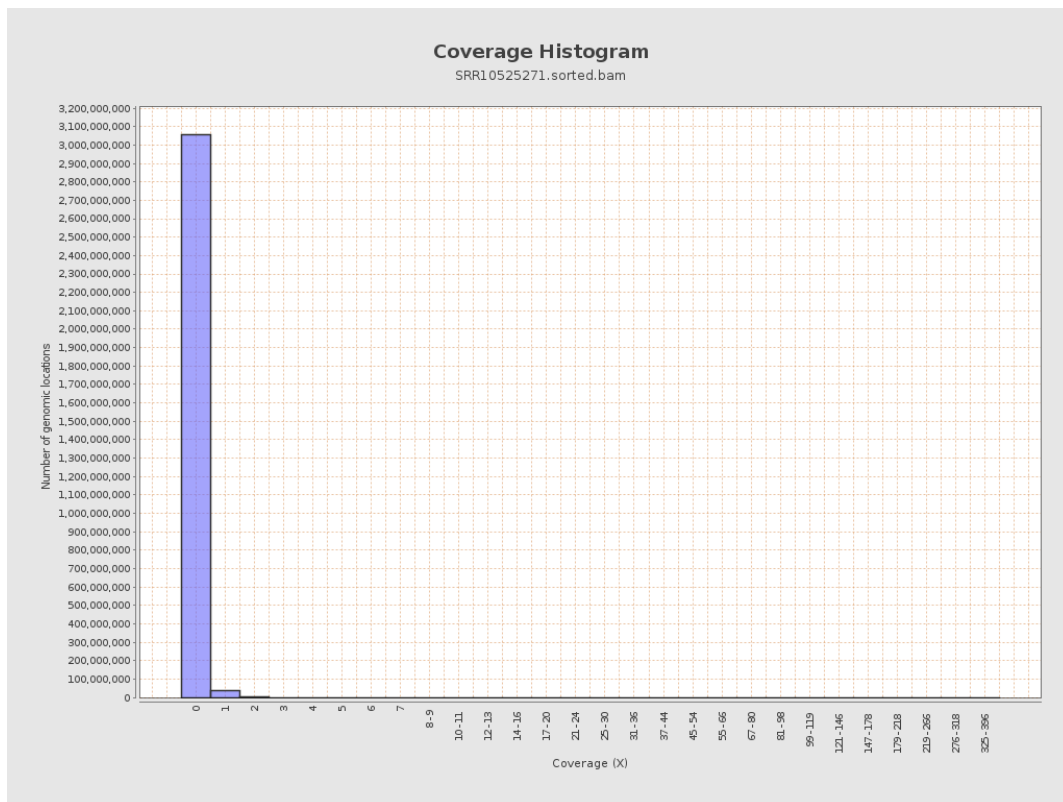
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	4832014	0.0194	0.2887
chr2	243199373	3838287	0.0158	0.2108
chr3	198022430	3610922	0.0182	0.1411
chr4	191154276	2596053	0.0136	0.1239
chr5	180915260	2057463	0.0114	0.1115
chr6	171115067	2285129	0.0134	0.13
chr7	159138663	2664413	0.0167	0.229

chr8	146364022	2122033	0.0145	0.1618
chr9	141213431	1477549	0.0105	0.1263
chr10	135534747	2449567	0.0181	0.1848
chr11	135006516	2108244	0.0156	0.1478
chr12	133851895	2058167	0.0154	0.1301
chr13	115169878	1429129	0.0124	0.1167
chr14	107349540	1724436	0.0161	0.1333
chr15	102531392	1236397	0.0121	0.1152
chr16	90354753	1169339	0.0129	0.1267
chr17	81195210	868790	0.0107	0.1106
chr18	78077248	1007990	0.0129	0.2117
chr19	59128983	784621	0.0133	0.2113
chr20	63025520	812770	0.0129	0.1193
chr21	48129895	592144	0.0123	0.119
chr22	51304566	350671	0.0068	0.0862
chrMT	16571	44964	2.7134	2.029
chrX	155270560	2333285	0.015	0.1353
chrY	59373566	127995	0.0022	0.0689

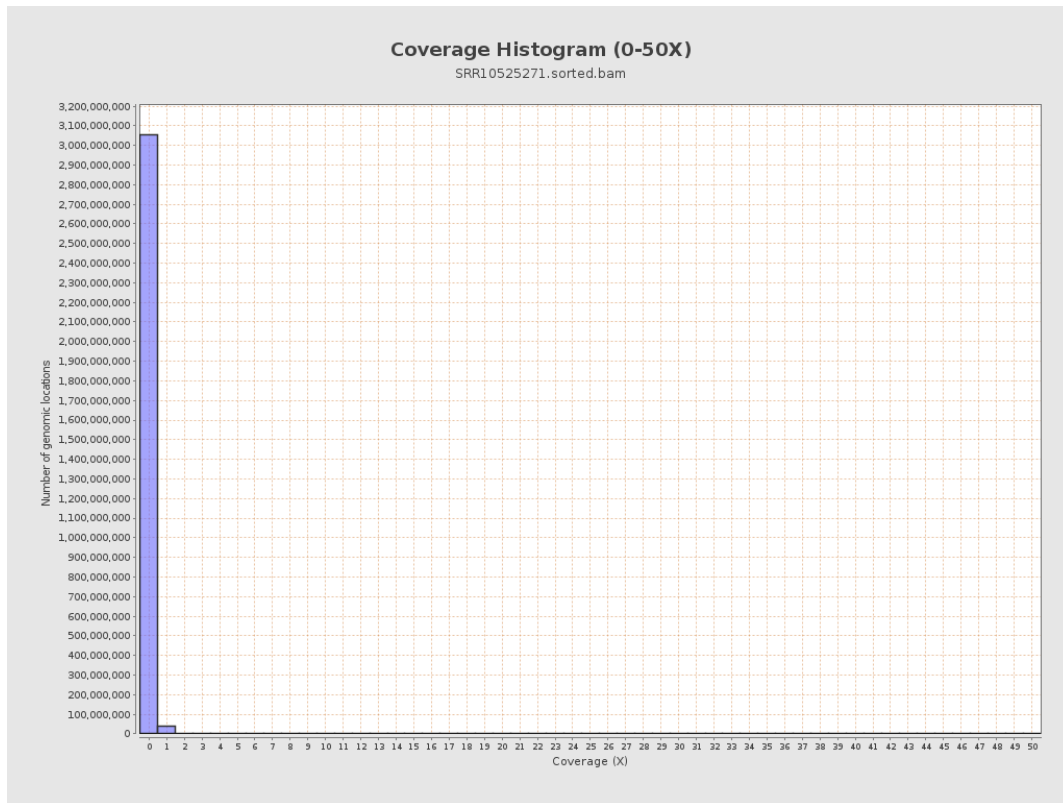
3. Results : Coverage across reference



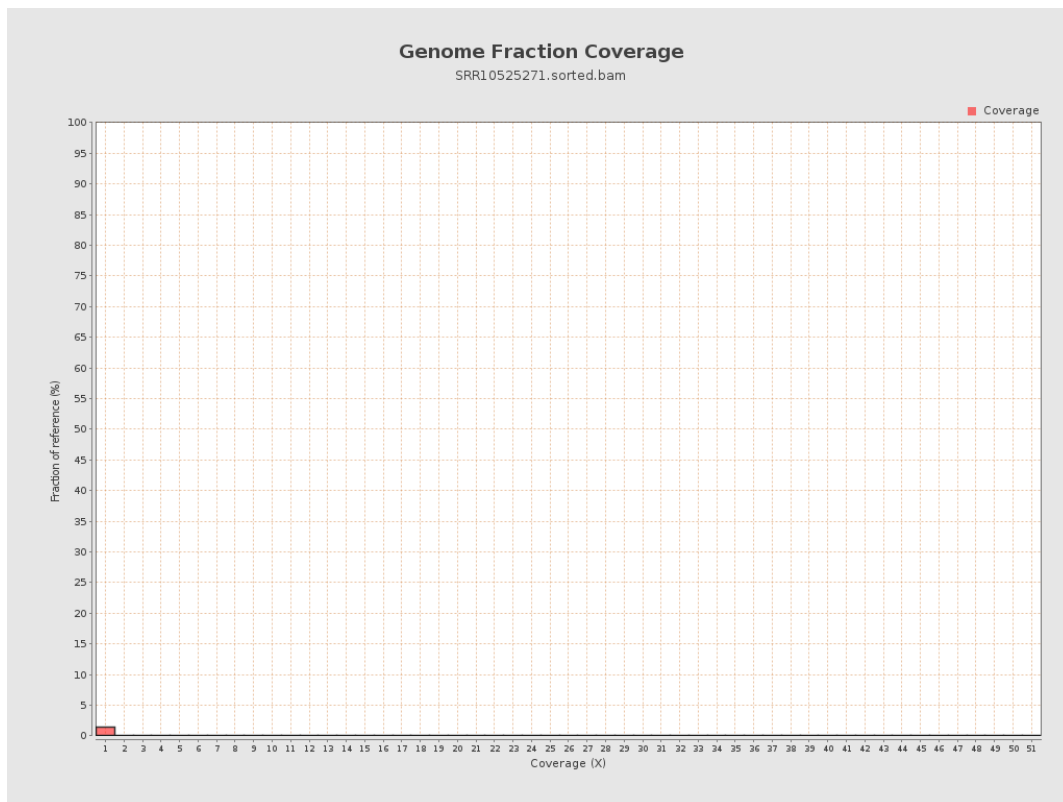
4. Results : Coverage Histogram



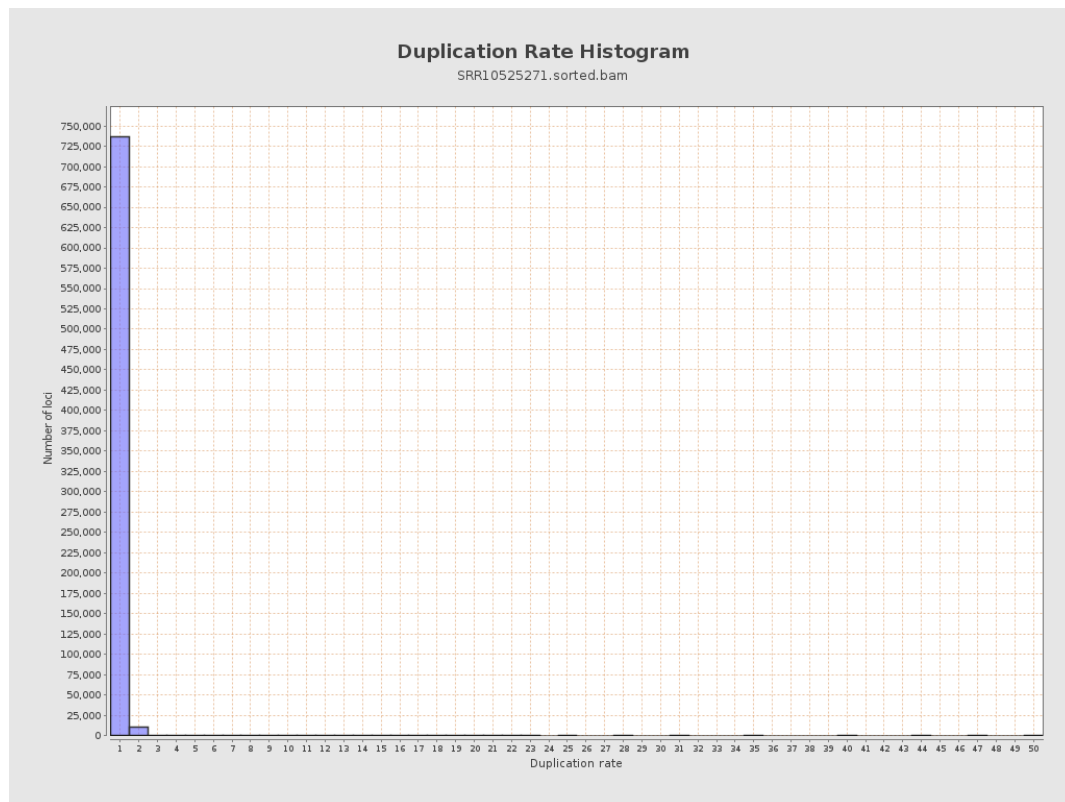
5. Results : Coverage Histogram (0-50X)



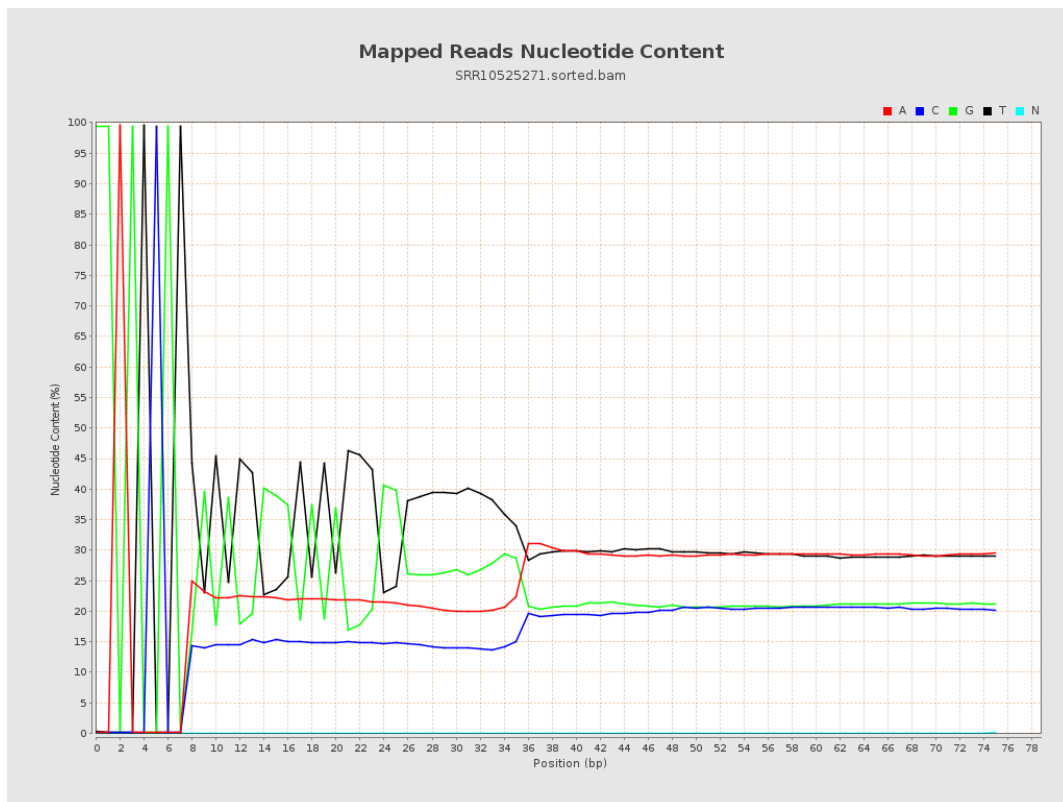
6. Results : Genome Fraction Coverage



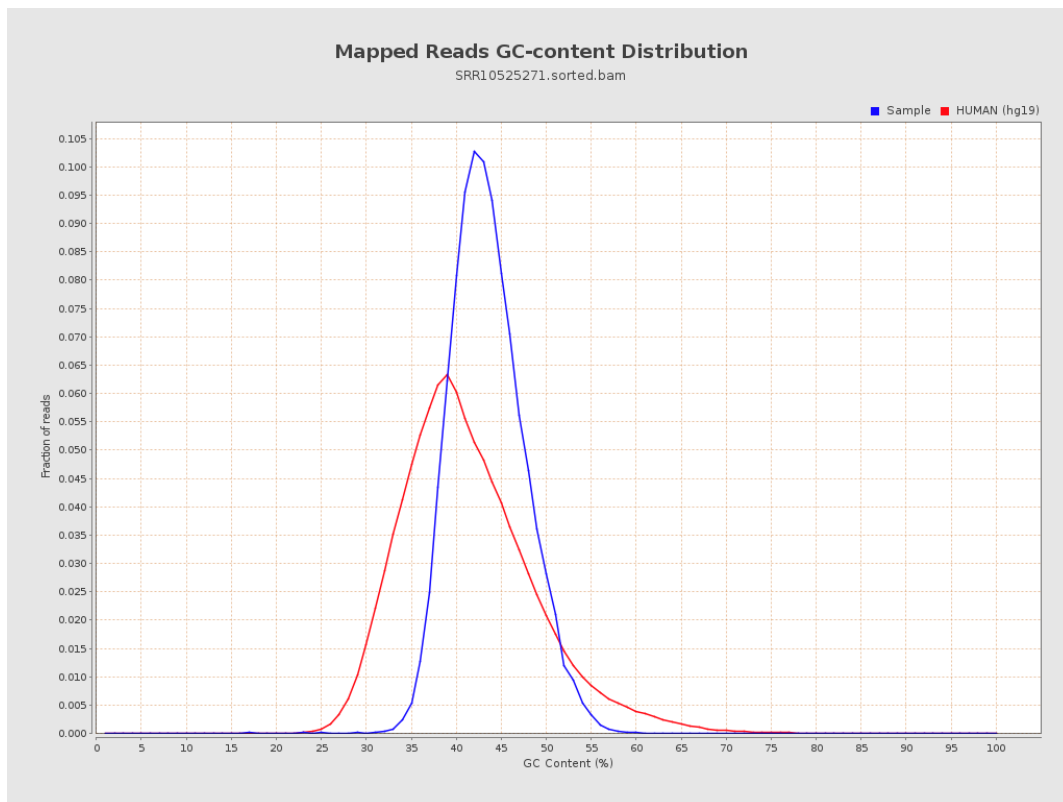
7. Results : Duplication Rate Histogram



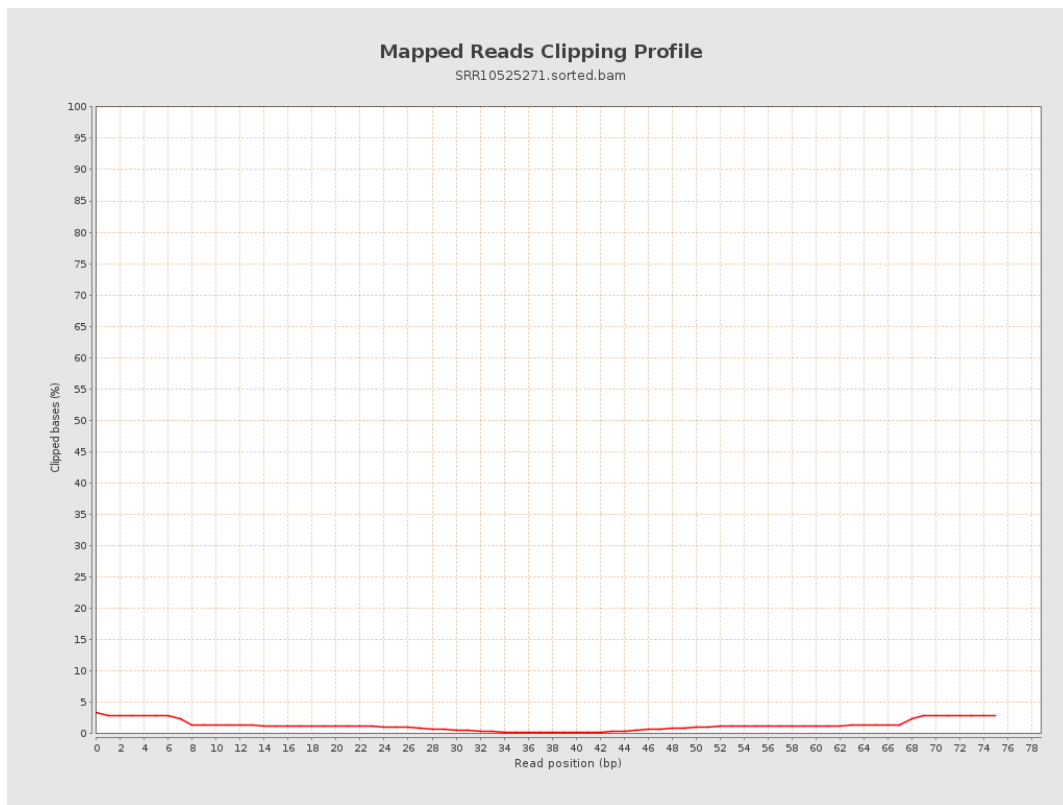
8. Results : Mapped Reads Nucleotide Content



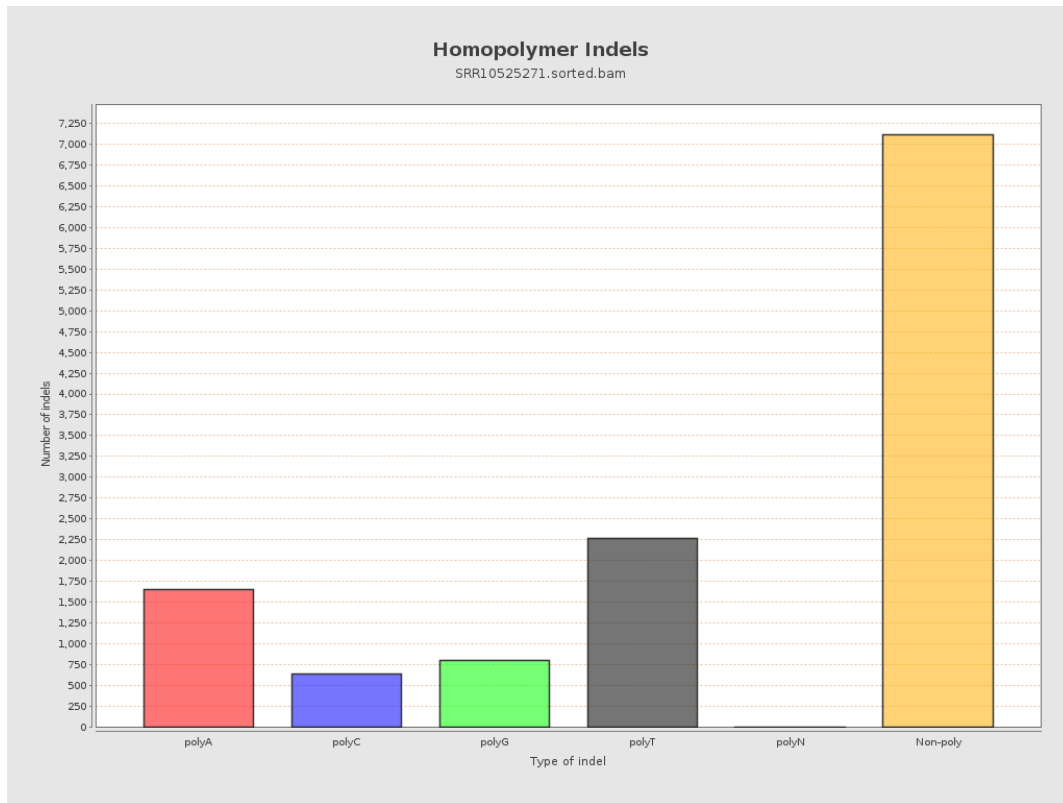
9. Results : Mapped Reads GC-content Distribution



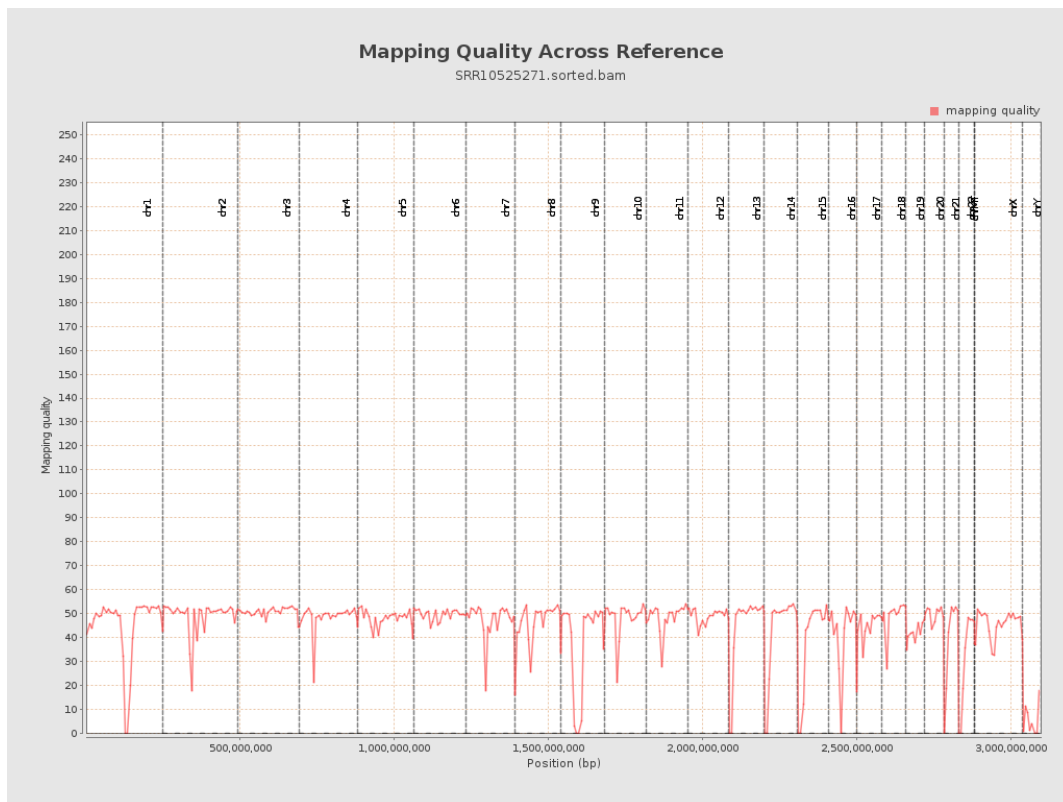
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

