

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 12:31:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008811.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_SRR6008811 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008811.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 12:31:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008811.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	973,145
Mapped reads	627,235 / 64.45%
Unmapped reads	345,910 / 35.55%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,116 / 0.53%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	11,949 / 1.23%
Duplication rate	1.16%
Clipped reads	258,933 / 26.61%

2.2. ACGT Content

Number/percentage of A's	12,082,788 / 28.68%
Number/percentage of C's	7,797,588 / 18.51%
Number/percentage of T's	12,521,010 / 29.72%
Number/percentage of G's	9,668,422 / 22.95%
Number/percentage of N's	55,089 / 0.13%
GC Percentage	41.46%

2.3. Coverage

Mean	0.0136

Standard Deviation	0.188
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2.4. Mapping Quality

Mean Mapping Quality	43.76
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2.5. Mismatches and indels

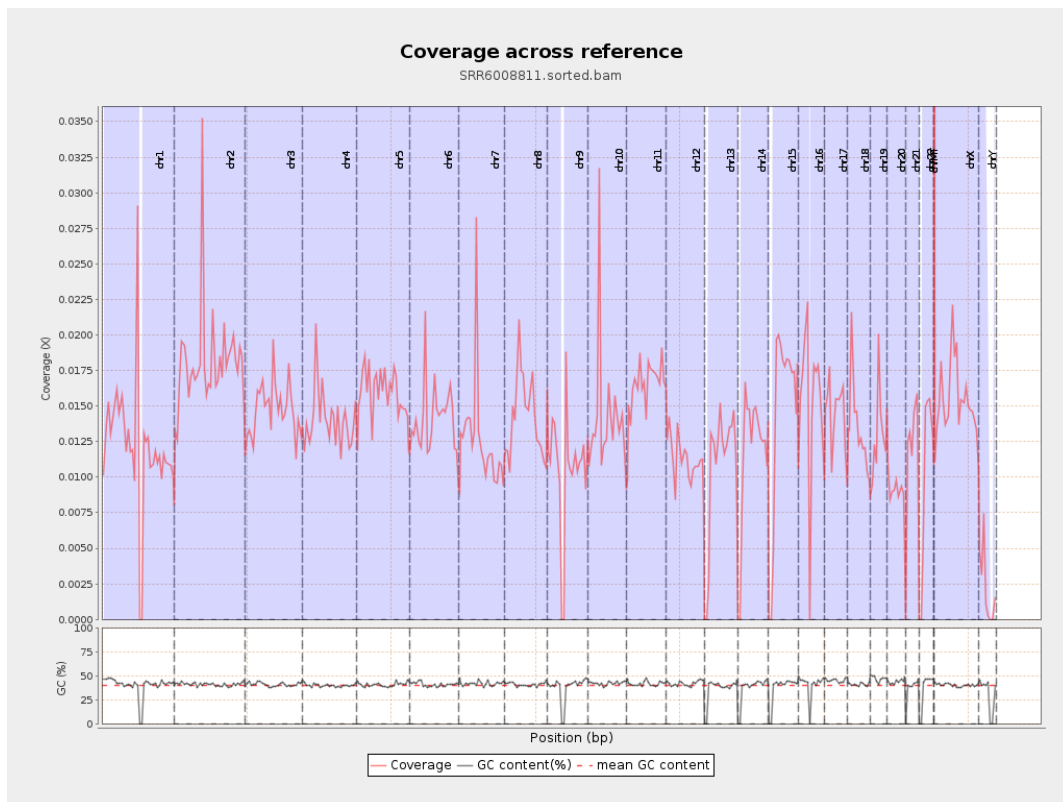
General error rate	0.93%
Mismatches	385,820
Insertions	3,602
Mapped reads with at least one insertion	0.57%
Deletions	11,408
Mapped reads with at least one deletion	1.8%
Homopolymer indels	45.72%

2.6. Chromosome stats

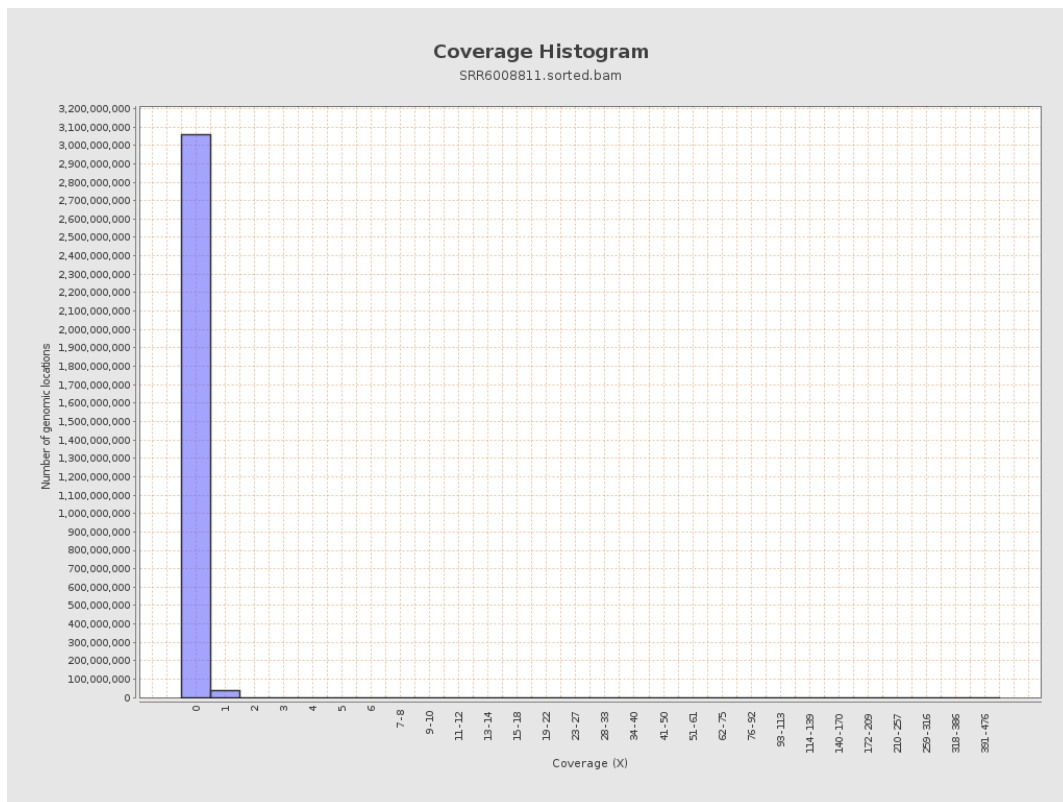
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	3017324	0.0121	0.3813
chr2	243199373	4408897	0.0181	0.1976
chr3	198022430	2916396	0.0147	0.1262
chr4	191154276	2689539	0.0141	0.1275
chr5	180915260	2904329	0.0161	0.1304
chr6	171115067	2405739	0.0141	0.1327
chr7	159138663	2000491	0.0126	0.2321

chr8	146364022	2105964	0.0144	0.1882
chr9	141213431	1491831	0.0106	0.1545
chr10	135534747	1920453	0.0142	0.1811
chr11	135006516	2233210	0.0165	0.1702
chr12	133851895	1511933	0.0113	0.1111
chr13	115169878	1229207	0.0107	0.1054
chr14	107349540	1244520	0.0116	0.1195
chr15	102531392	1488948	0.0145	0.126
chr16	90354753	1368293	0.0151	0.1406
chr17	81195210	1172189	0.0144	0.1337
chr18	78077248	1053071	0.0135	0.3108
chr19	59128983	770004	0.013	0.2554
chr20	63025520	567588	0.009	0.1023
chr21	48129895	571337	0.0119	0.1179
chr22	51304566	523588	0.0102	0.1036
chrMT	16571	4348	0.2624	0.5353
chrX	155270560	2416743	0.0156	0.1363
chrY	59373566	129486	0.0022	0.0701

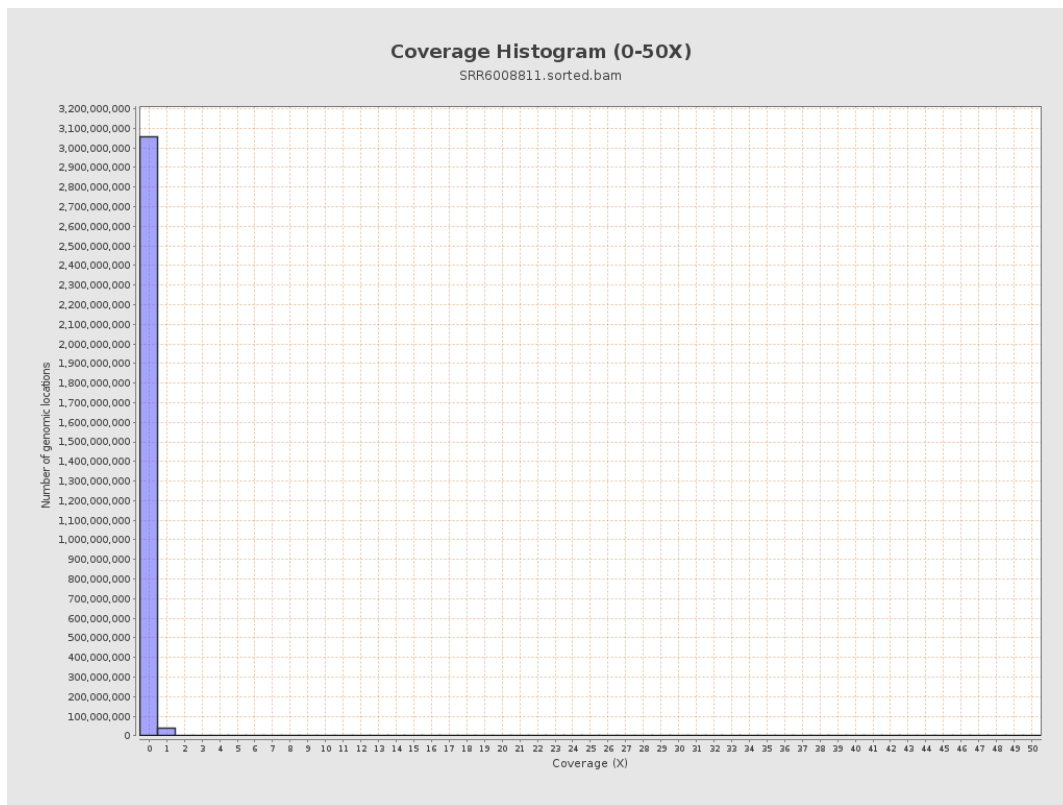
3. Results : Coverage across reference



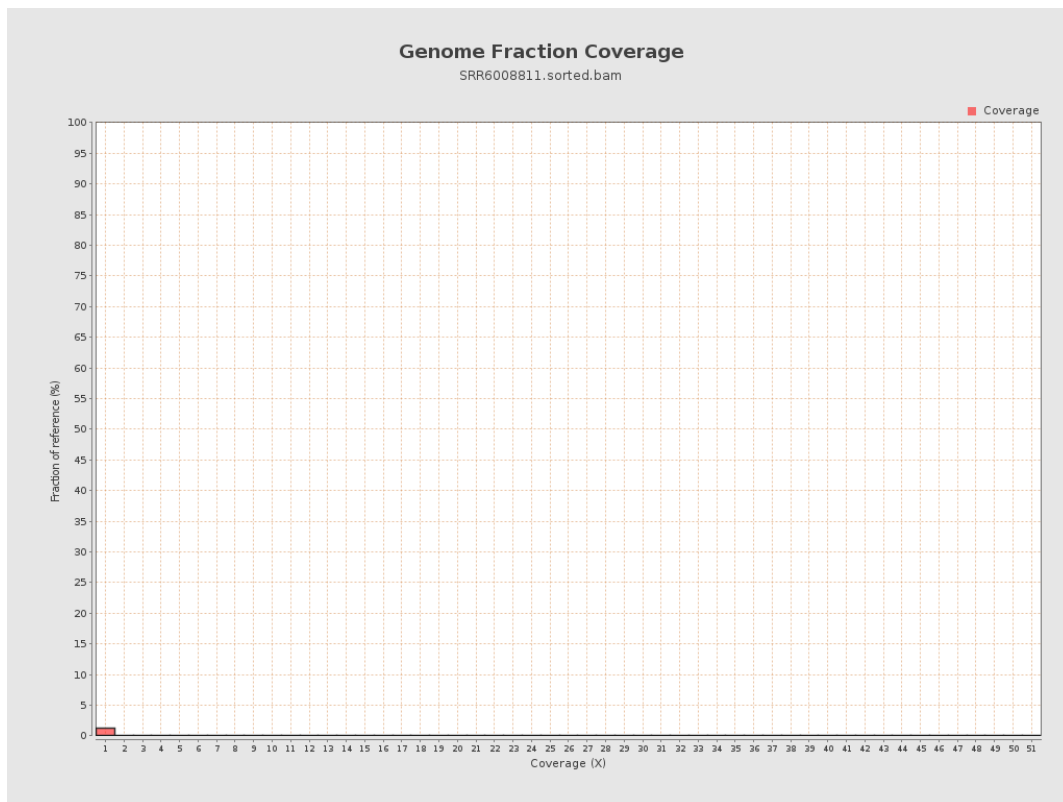
4. Results : Coverage Histogram



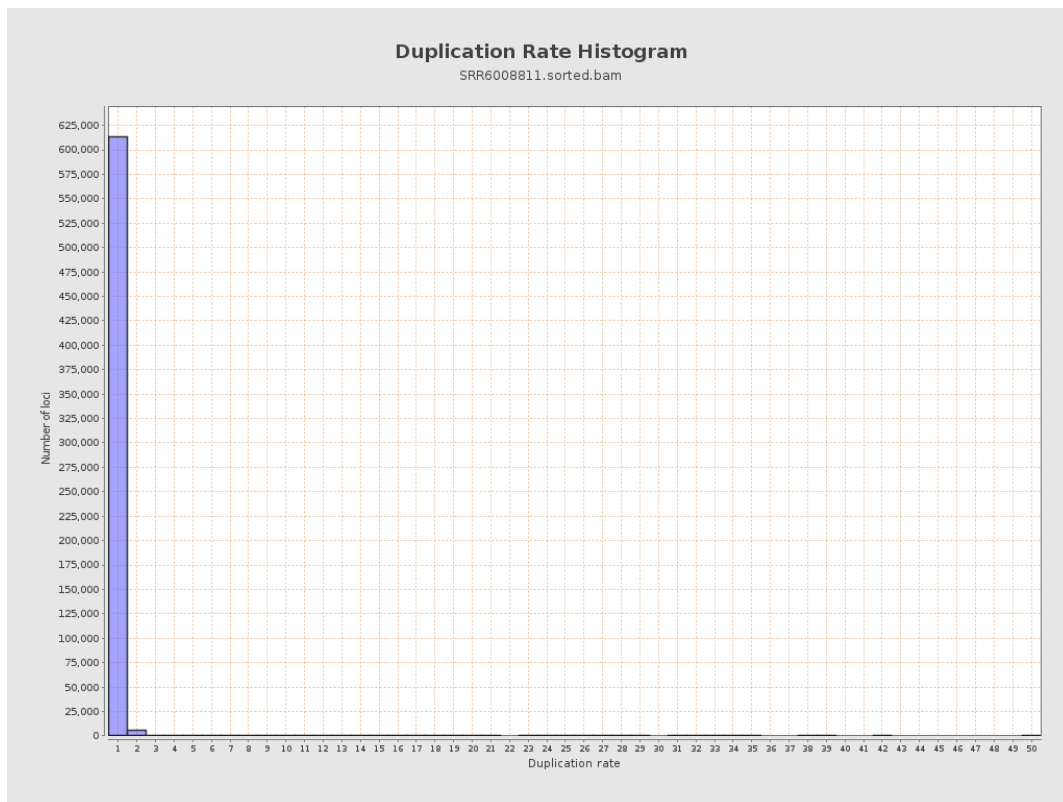
5. Results : Coverage Histogram (0-50X)



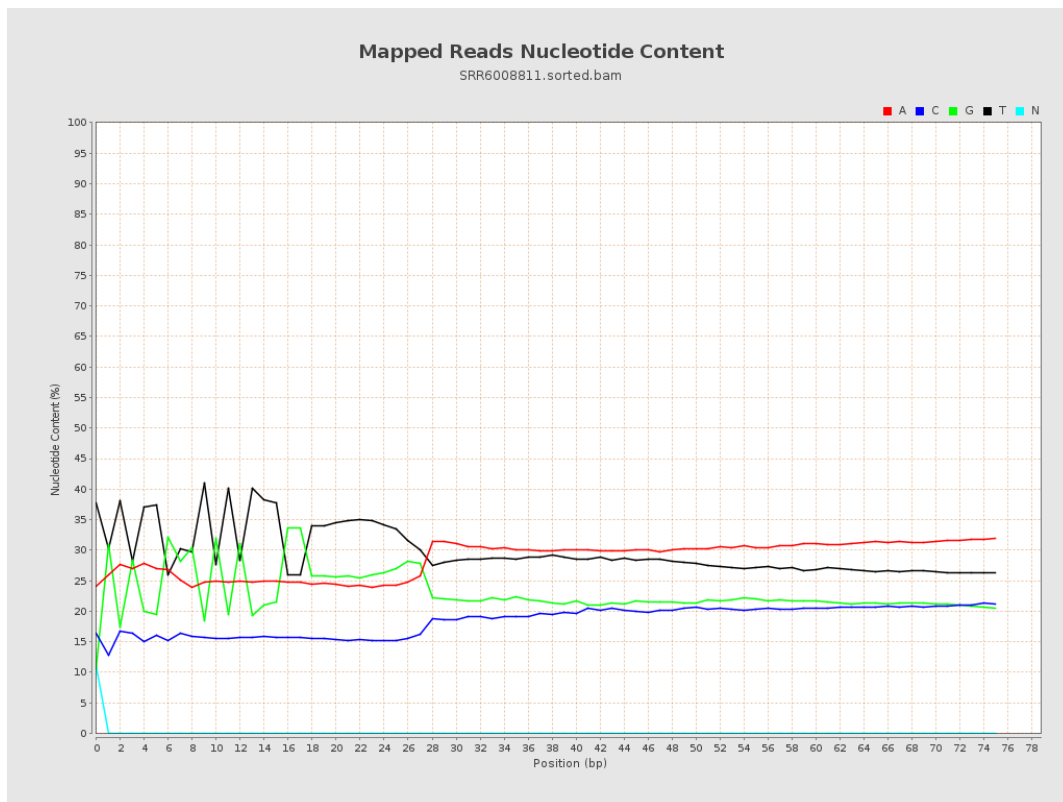
6. Results : Genome Fraction Coverage



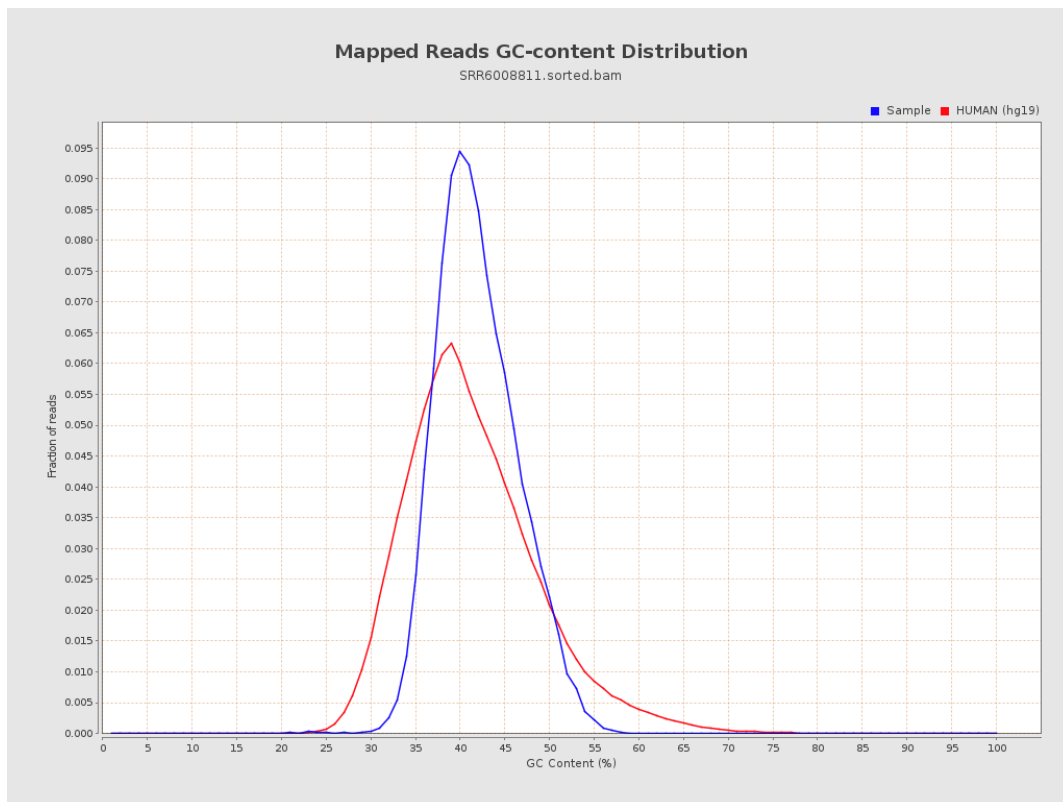
7. Results : Duplication Rate Histogram



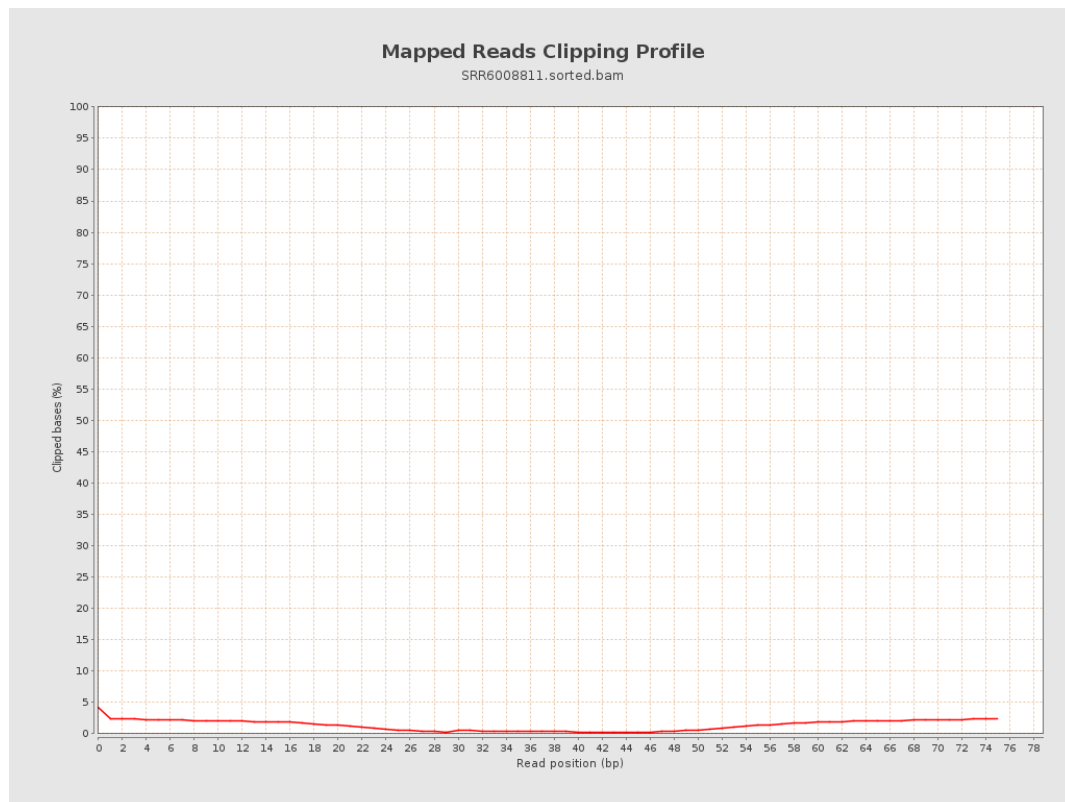
8. Results : Mapped Reads Nucleotide Content



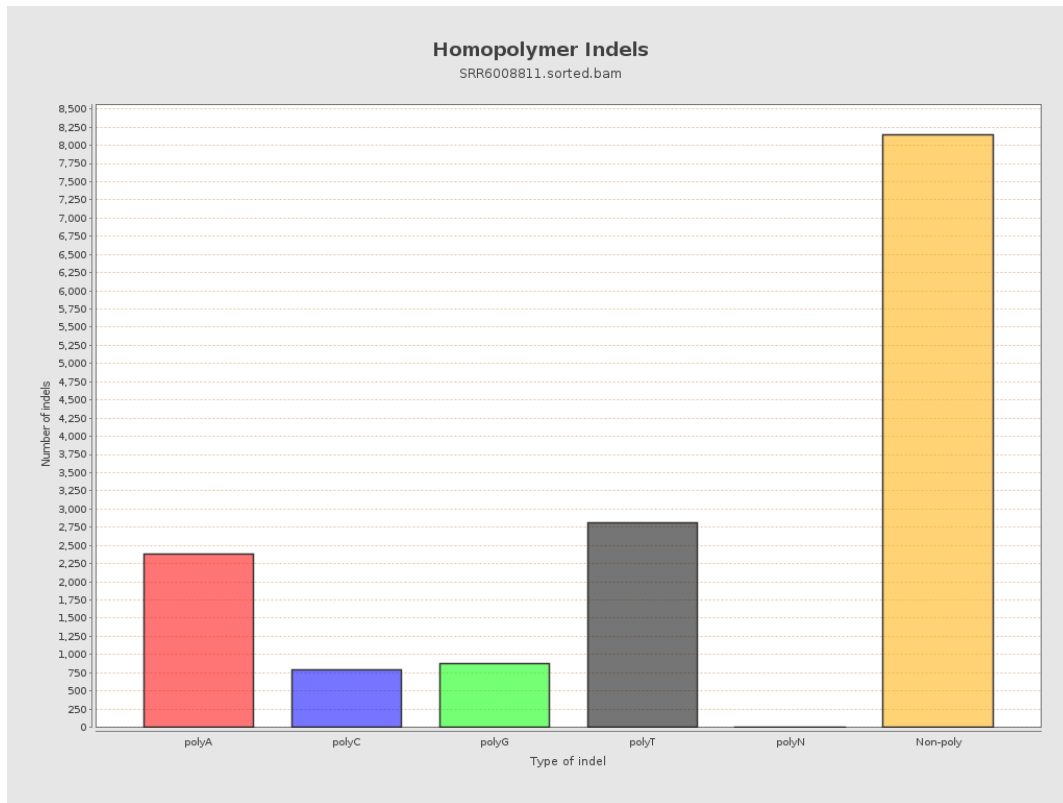
9. Results : Mapped Reads GC-content Distribution



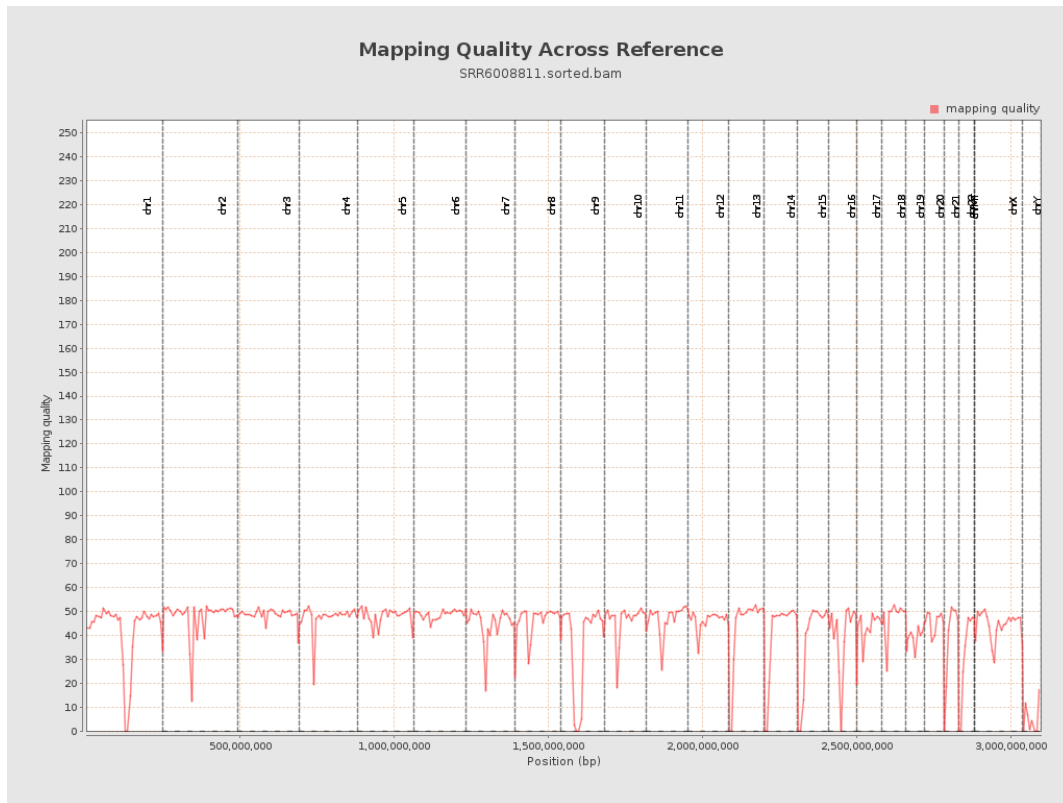
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

