

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 23:42:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083611.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_SRR3083611 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083611.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 23:42:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3083611.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,996,048
Mapped reads	1,797,621 / 90.06%
Unmapped reads	198,427 / 9.94%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,479 / 0.88%
Read min/max/mean length	30 / 76 / 76.31
Duplicated reads (estimated)	87,999 / 4.41%
Duplication rate	4.21%
Clipped reads	845,243 / 42.35%

2.2. ACGT Content

Number/percentage of A's	31,661,435 / 26.66%
Number/percentage of C's	22,464,022 / 18.92%
Number/percentage of T's	37,030,565 / 31.18%
Number/percentage of G's	27,583,086 / 23.23%
Number/percentage of N's	5,976 / 0.01%
GC Percentage	42.15%

2.3. Coverage

Mean	0.0384

Standard Deviation	0.2967
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2.4. Mapping Quality

Mean Mapping Quality	45.28
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2.5. Mismatches and indels

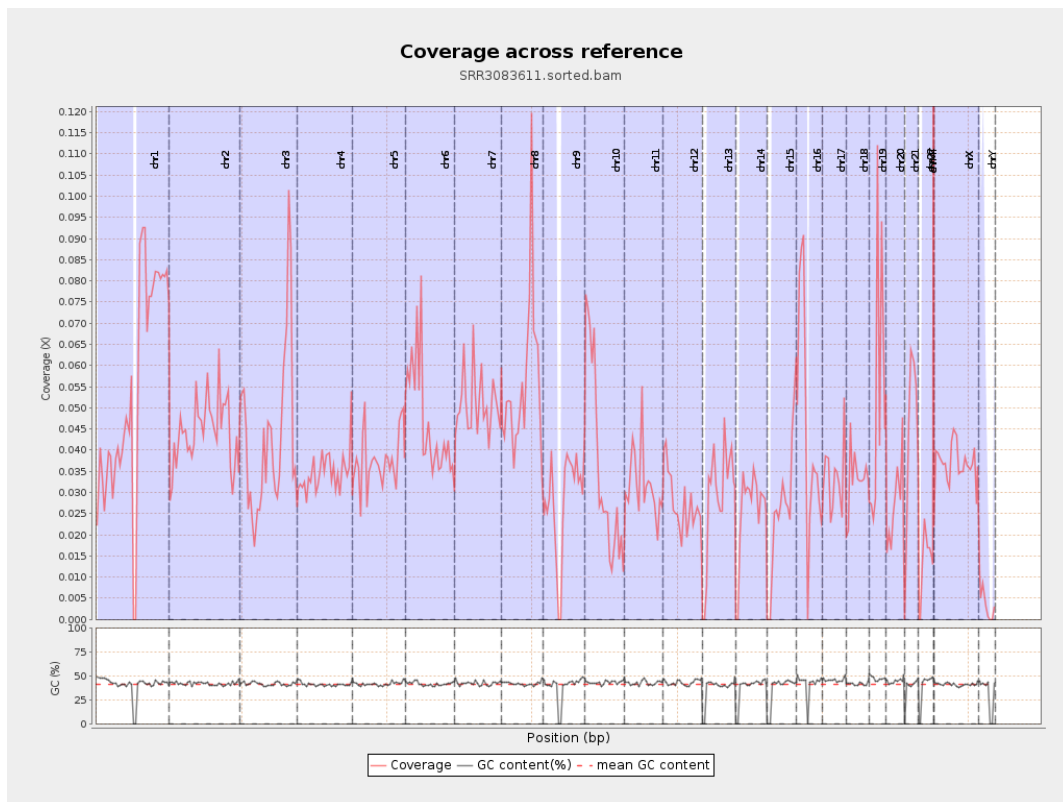
General error rate	0.7%
Mismatches	815,932
Insertions	8,573
Mapped reads with at least one insertion	0.47%
Deletions	26,646
Mapped reads with at least one deletion	1.47%
Homopolymer indels	47.57%

2.6. Chromosome stats

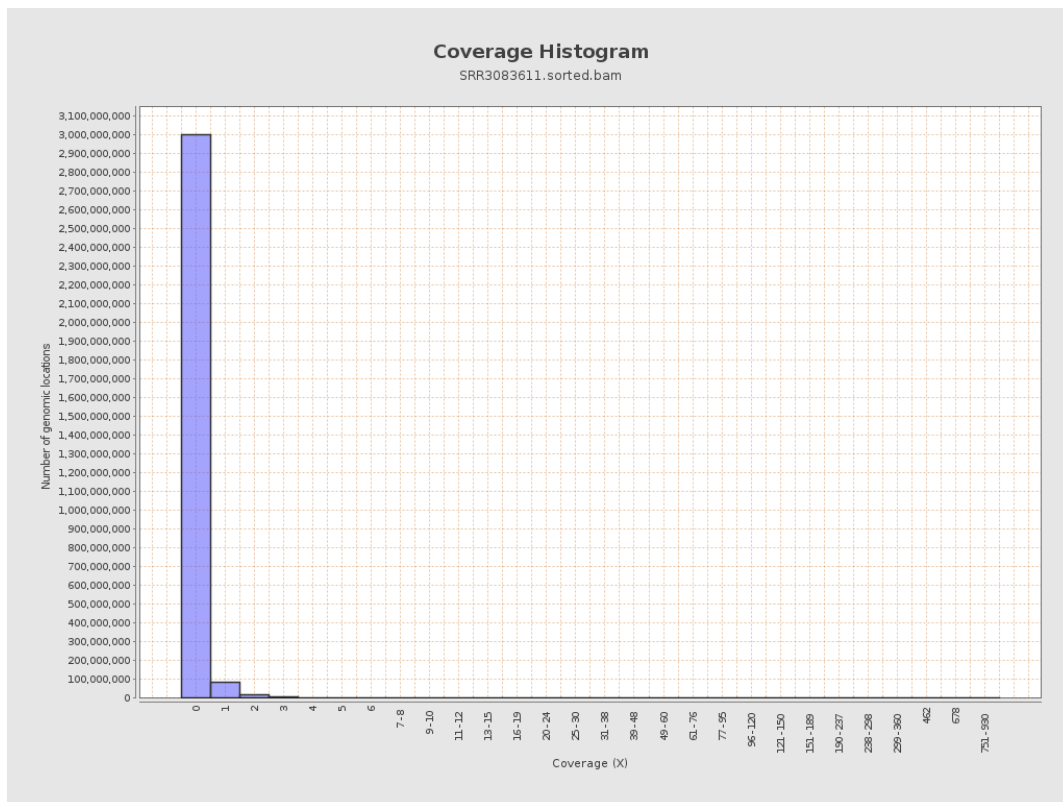
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	13440201	0.0539	0.4162
chr2	243199373	10735422	0.0441	0.4617
chr3	198022430	8424427	0.0425	0.2459
chr4	191154276	6652990	0.0348	0.2216
chr5	180915260	6805893	0.0376	0.2284
chr6	171115067	8024689	0.0469	0.3106
chr7	159138663	8149969	0.0512	0.4646

chr8	146364022	8151717	0.0557	0.2999
chr9	141213431	3952522	0.028	0.2248
chr10	135534747	4902143	0.0362	0.2486
chr11	135006516	4277454	0.0317	0.2271
chr12	133851895	3644055	0.0272	0.1957
chr13	115169878	3299234	0.0286	0.2018
chr14	107349540	2754344	0.0257	0.1907
chr15	102531392	2675378	0.0261	0.2066
chr16	90354753	4084151	0.0452	0.2592
chr17	81195210	2749683	0.0339	0.2238
chr18	78077248	2602679	0.0333	0.3411
chr19	59128983	3067632	0.0519	0.3541
chr20	63025520	1720054	0.0273	0.2014
chr21	48129895	2095464	0.0435	0.2511
chr22	51304566	689658	0.0134	0.1346
chrMT	16571	4038	0.2437	0.6103
chrX	155270560	5669566	0.0365	0.2308
chrY	59373566	215571	0.0036	0.0726

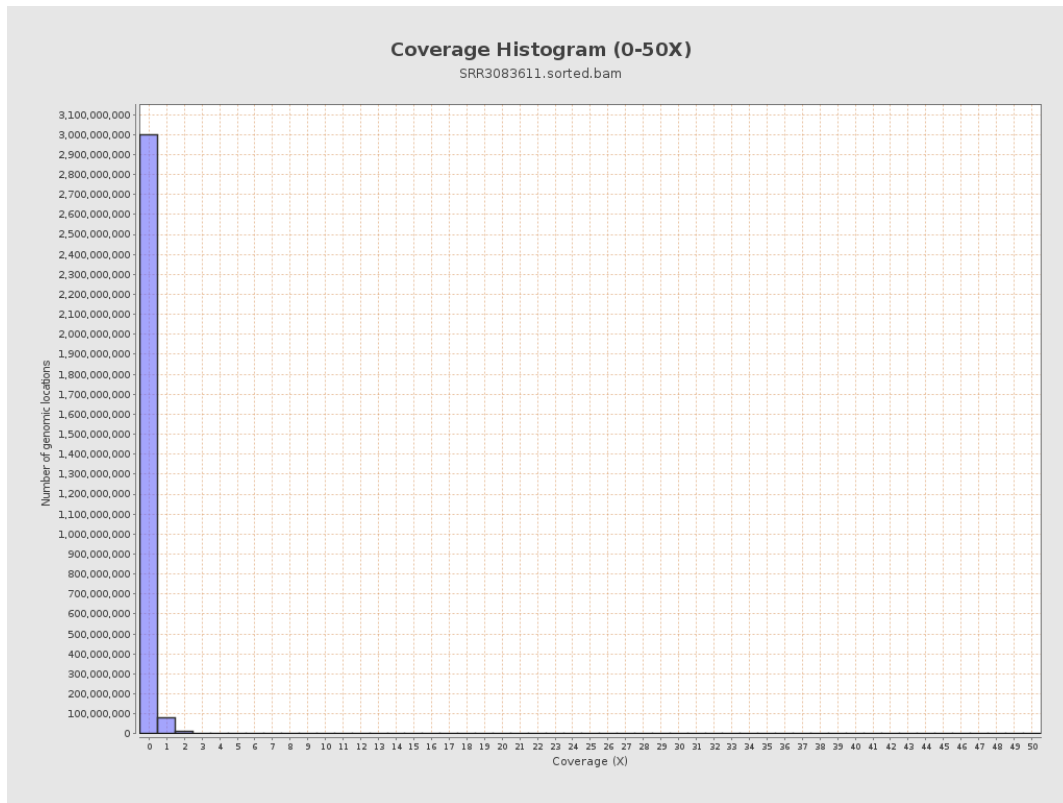
3. Results : Coverage across reference



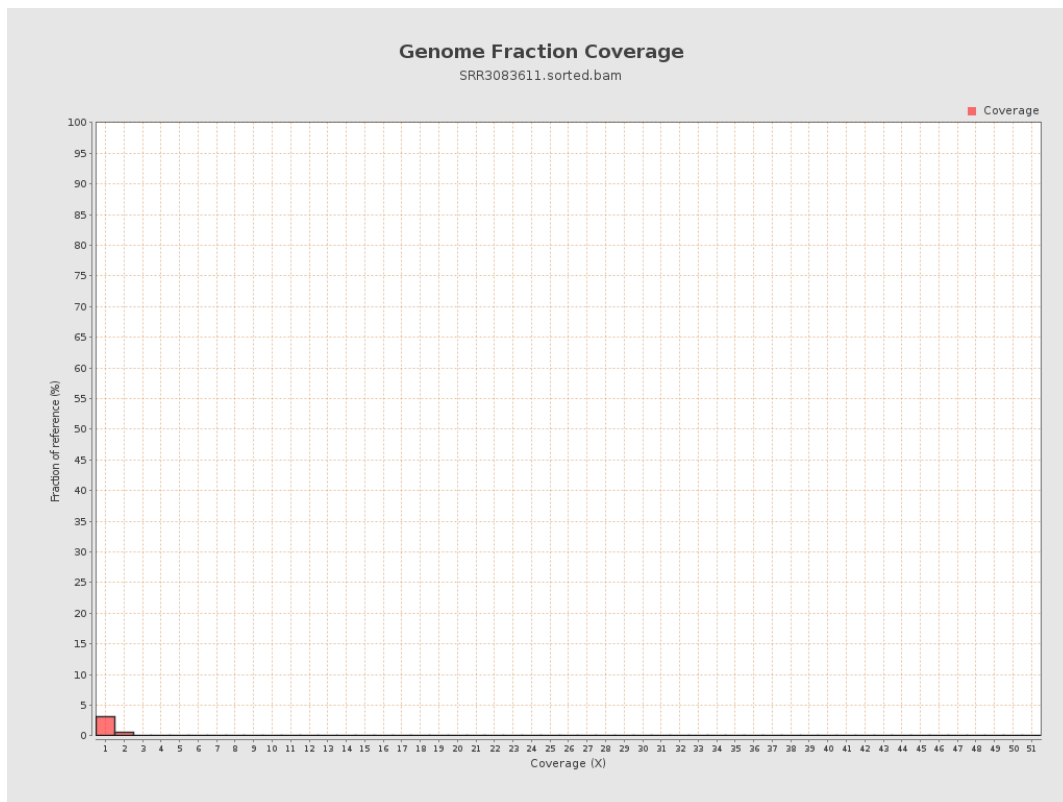
4. Results : Coverage Histogram



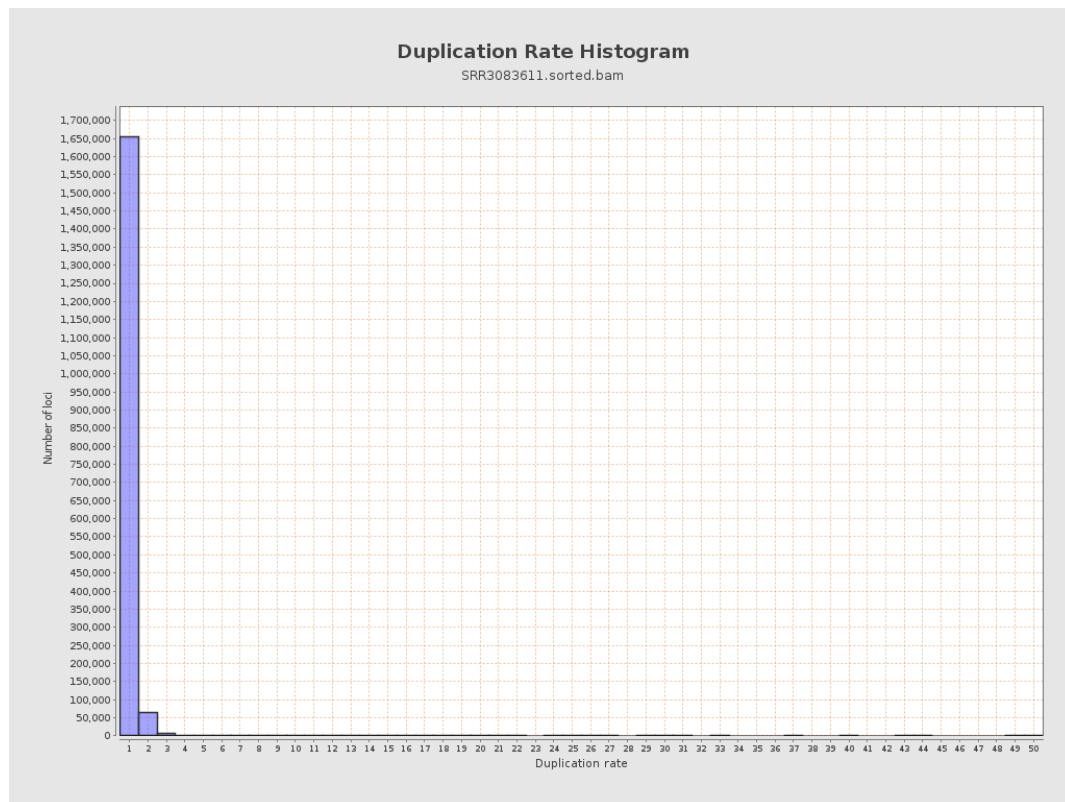
5. Results : Coverage Histogram (0-50X)



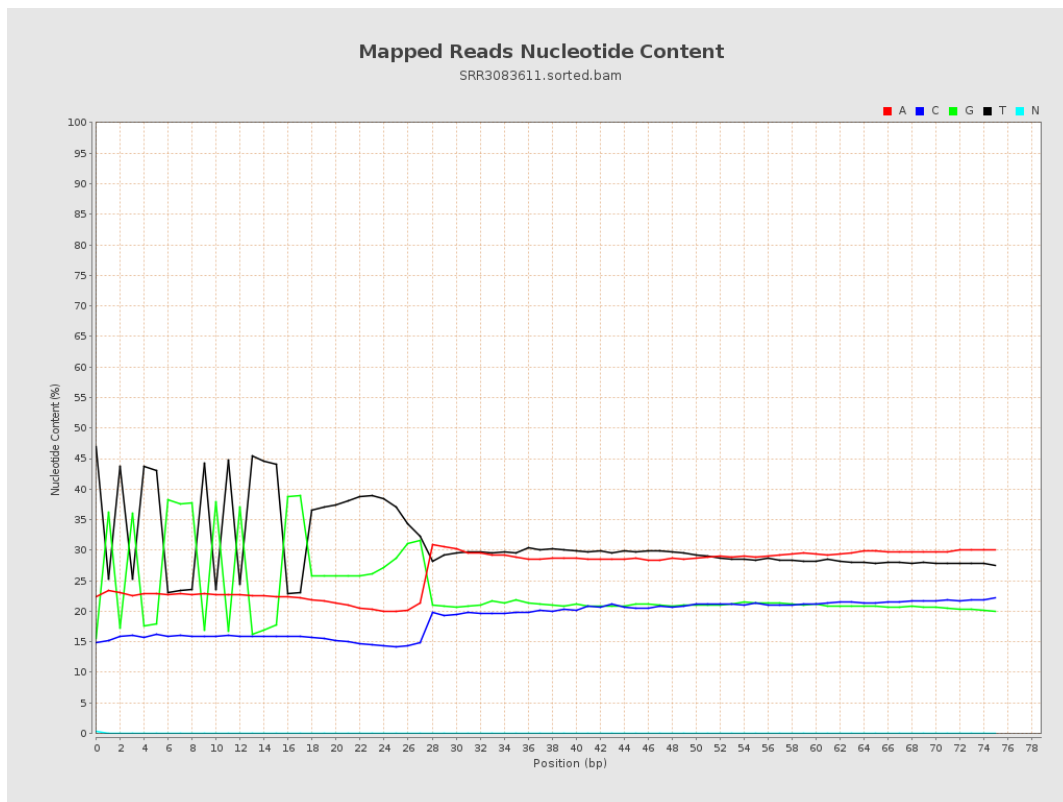
6. Results : Genome Fraction Coverage



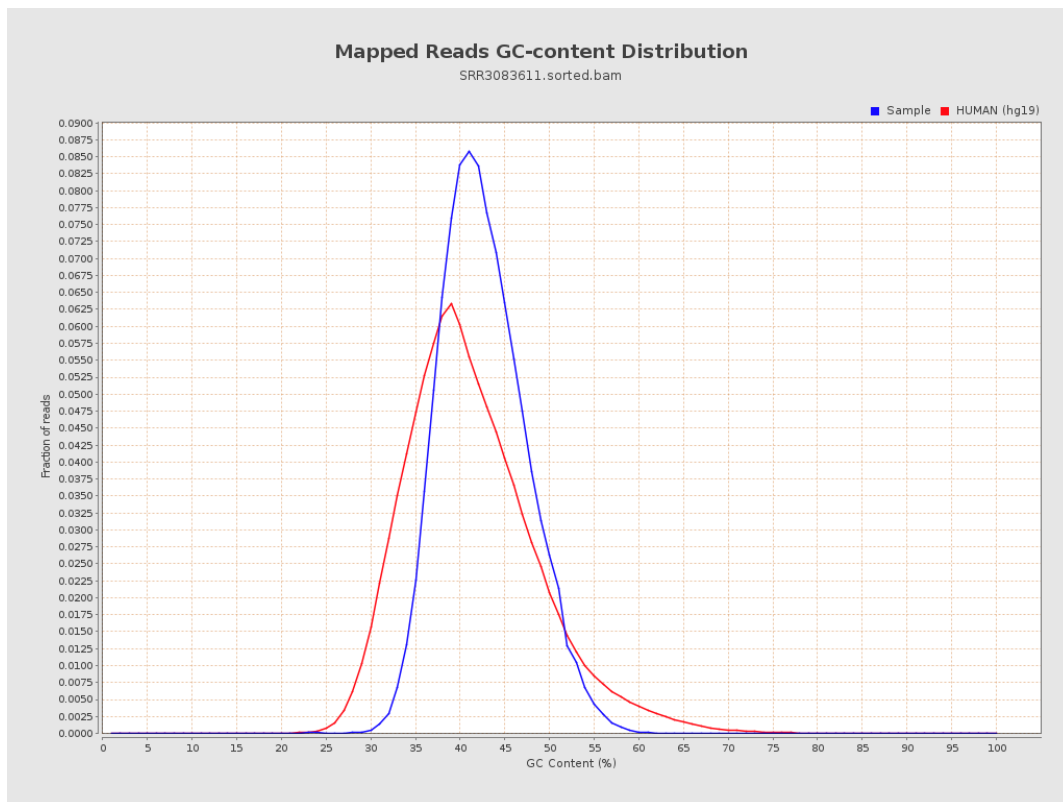
7. Results : Duplication Rate Histogram



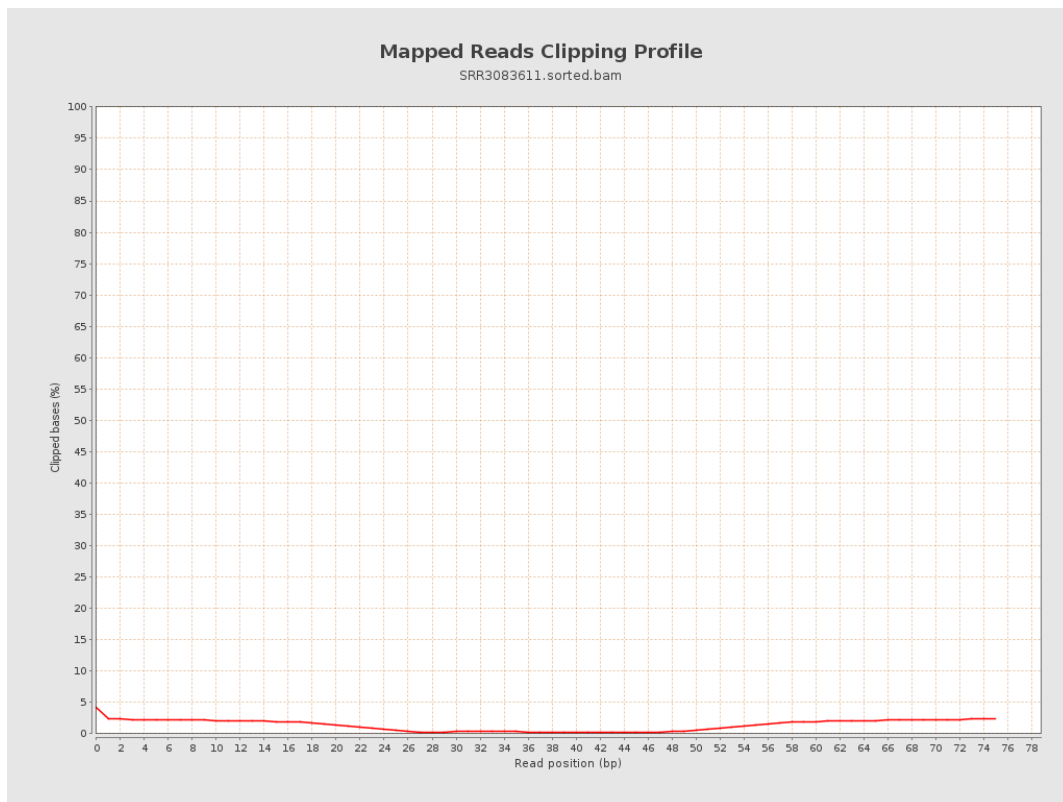
8. Results : Mapped Reads Nucleotide Content



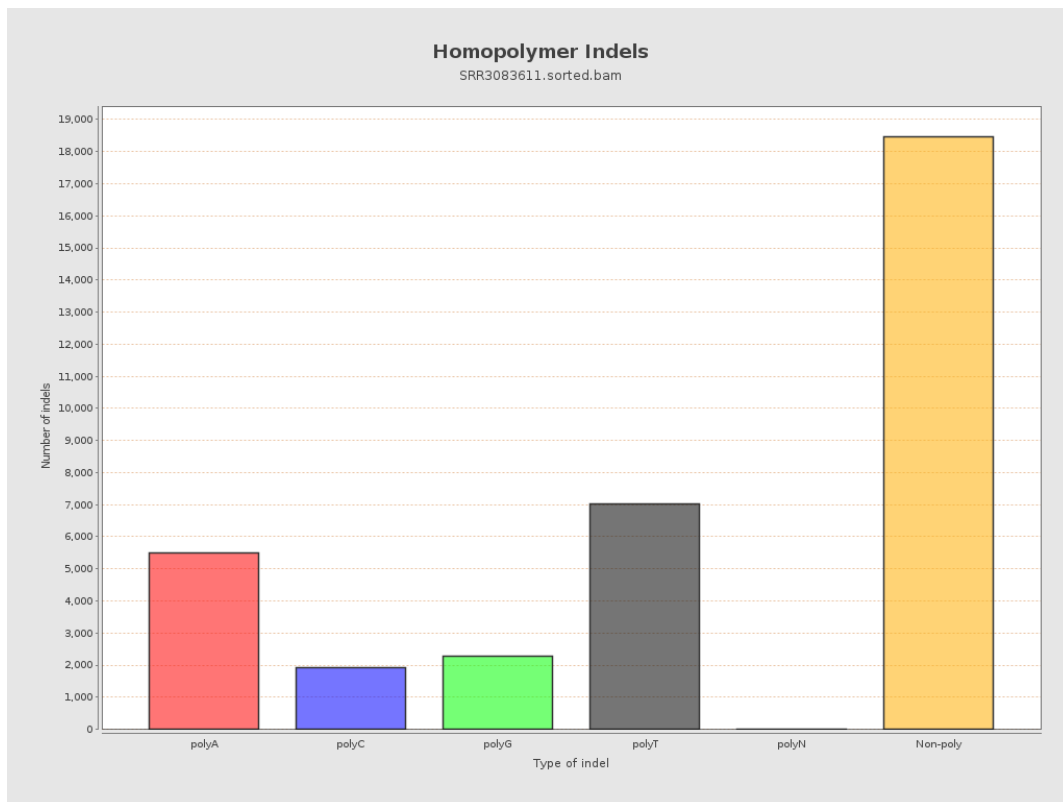
9. Results : Mapped Reads GC-content Distribution



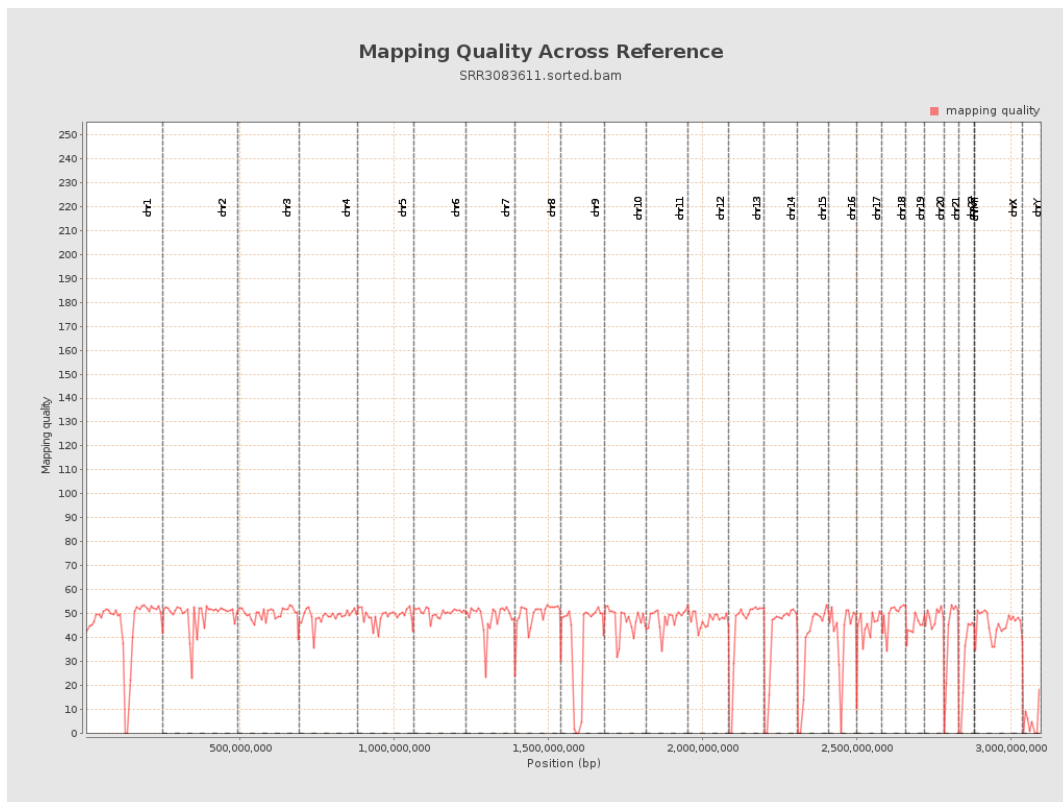
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

