Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/18 23:37:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR053611.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_SRR053611 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR053611.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 18 23:37:42 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR053611.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,200,574
Mapped reads	6,784,407 / 82.73%
Unmapped reads	1,416,167 / 17.27%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	280 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	1,228,919 / 14.99%
Duplication rate	13.66%
Clipped reads	629,713 / 7.68%

2.2. ACGT Content

Number/percentage of A's	94,269,585 / 29.47%
Number/percentage of C's	61,924,979 / 19.36%
Number/percentage of T's	95,922,702 / 29.99%
Number/percentage of G's	67,763,331 / 21.18%
Number/percentage of N's	7,292 / 0%
GC Percentage	40.54%

2.3. Coverage

Mean	0.1034

Standard Deviation	0.7154

2.4. Mapping Quality

Mean Mapping Quality	45.87

2.5. Mismatches and indels

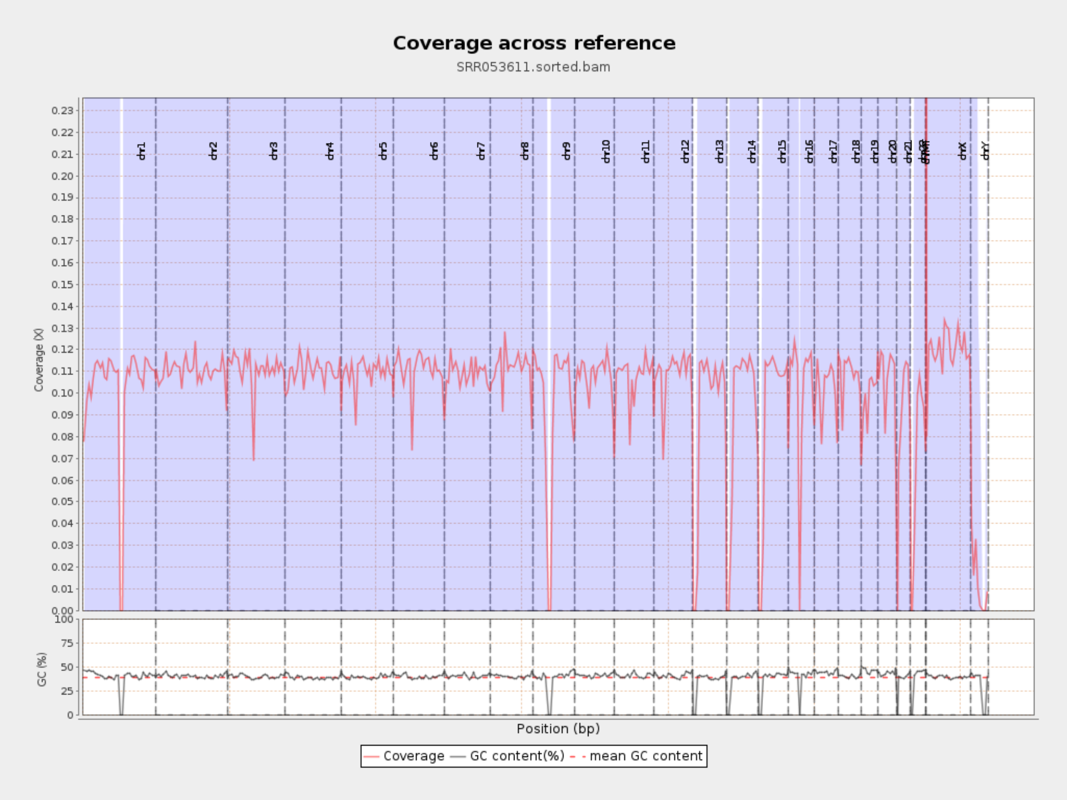
General error rate	0.55%
Mismatches	1,741,109
Insertions	13,123
Mapped reads with at least one insertion	0.19%
Deletions	43,998
Mapped reads with at least one deletion	0.65%
Homopolymer indels	47.2%

2.6. Chromosome stats

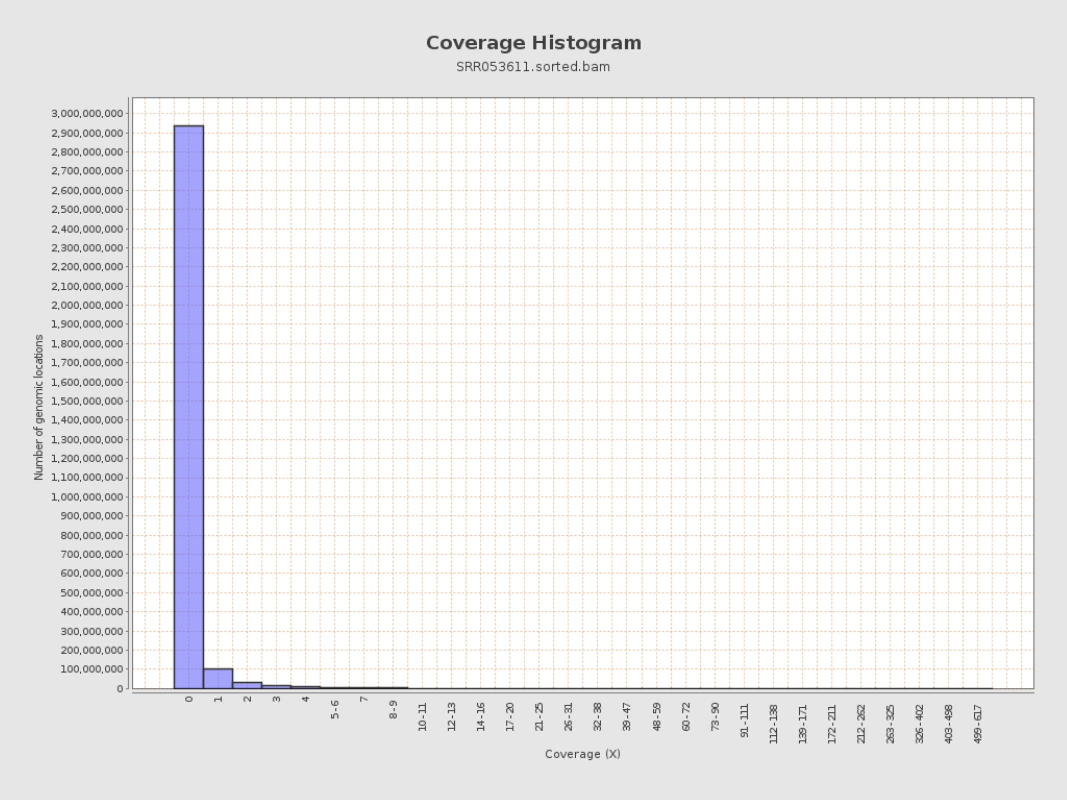
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	25436877	0.1021	0.7738
chr2	243199373	26840269	0.1104	0.8392
chr3	198022430	21956849	0.1109	0.6807
chr4	191154276	21107593	0.1104	0.7145
chr5	180915260	19786100	0.1094	0.6689
chr6	171115067	18996653	0.111	0.7542
chr7	159138663	17314724	0.1088	0.7672

chr8	146364022	16297637	0.1114	0.7528
chr9	141213431	13273189	0.094	0.6769
chr10	135534747	14774909	0.109	0.7168
chr11	135006516	14480390	0.1073	0.7456
chr12	133851895	14695694	0.1098	0.6799
chr13	115169878	10435976	0.0906	0.611
chr14	107349540	9883004	0.0921	0.7308
chr15	102531392	9224818	0.09	0.6061
chr16	90354753	8925641	0.0988	0.6625
chr17	81195210	8318269	0.1024	0.6361
chr18	78077248	8503481	0.1089	0.7702
chr19	59128983	5810701	0.0983	0.754
chr20	63025520	6810874	0.1081	0.693
chr21	48129895	4194751	0.0872	0.6967
chr22	51304566	3494181	0.0681	0.5174
chrMT	16571	38581	2.3282	4.2201
chrX	155270560	18604124	0.1198	0.7421
chrY	59373566	748203	0.0126	0.2498

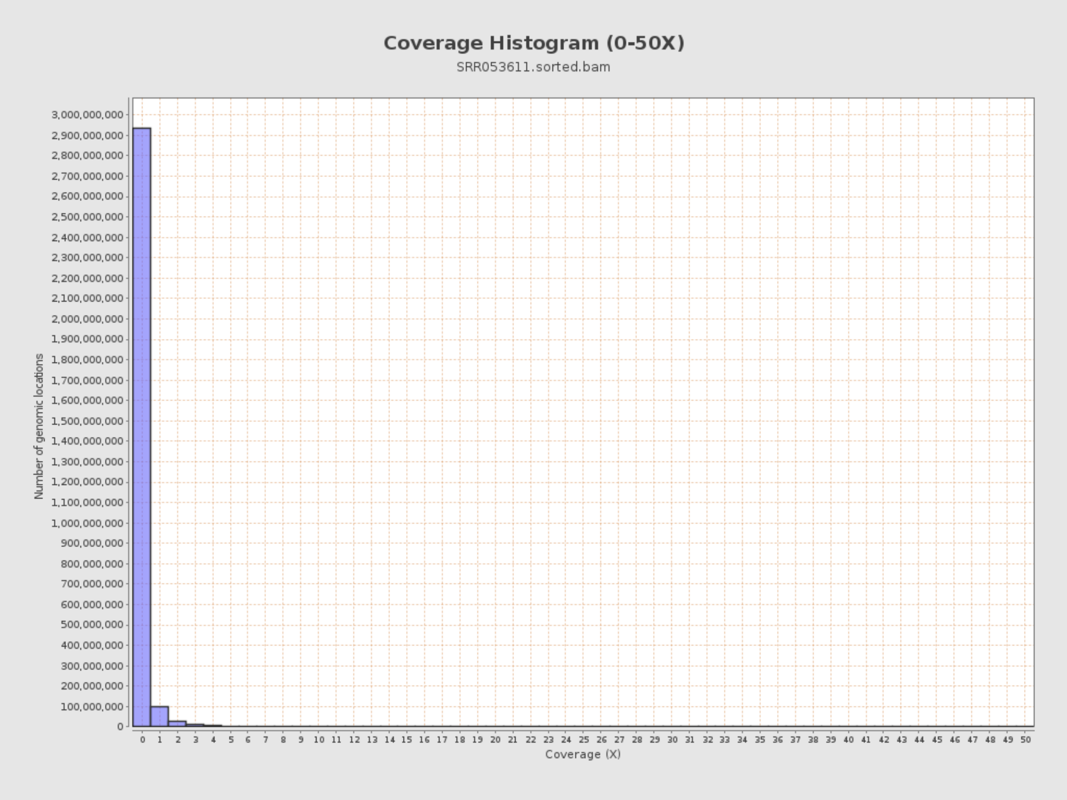
3. Results : Coverage across reference



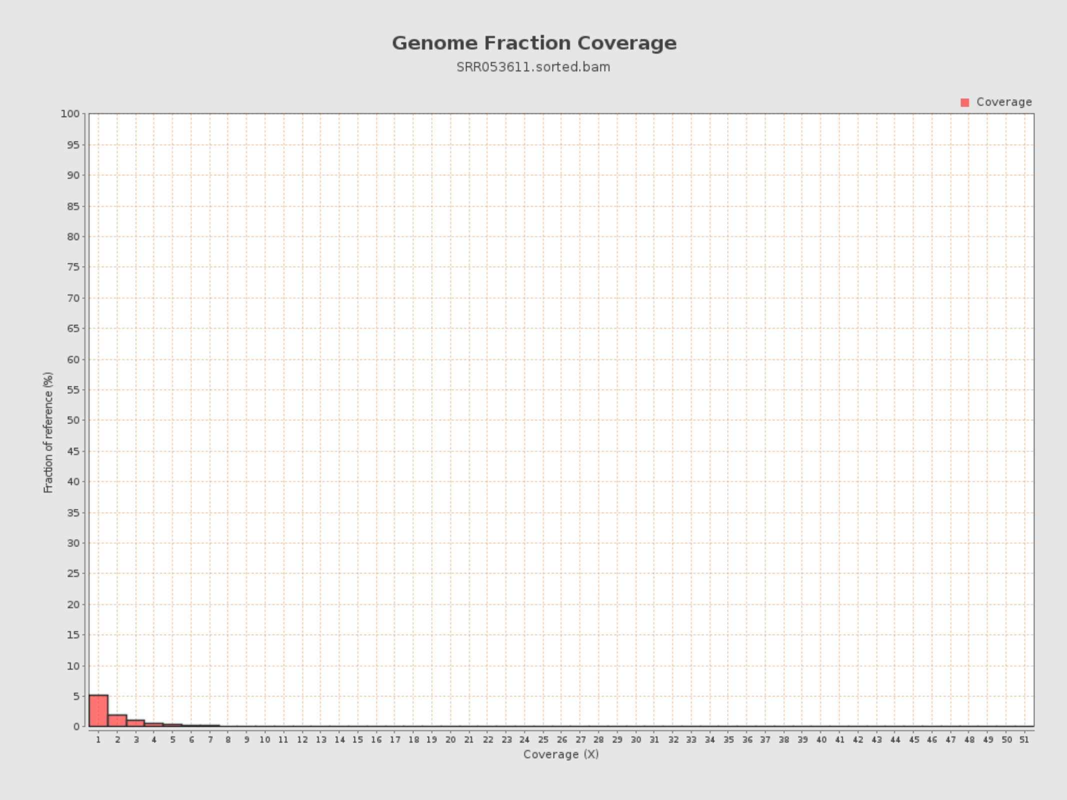
4. Results : Coverage Histogram



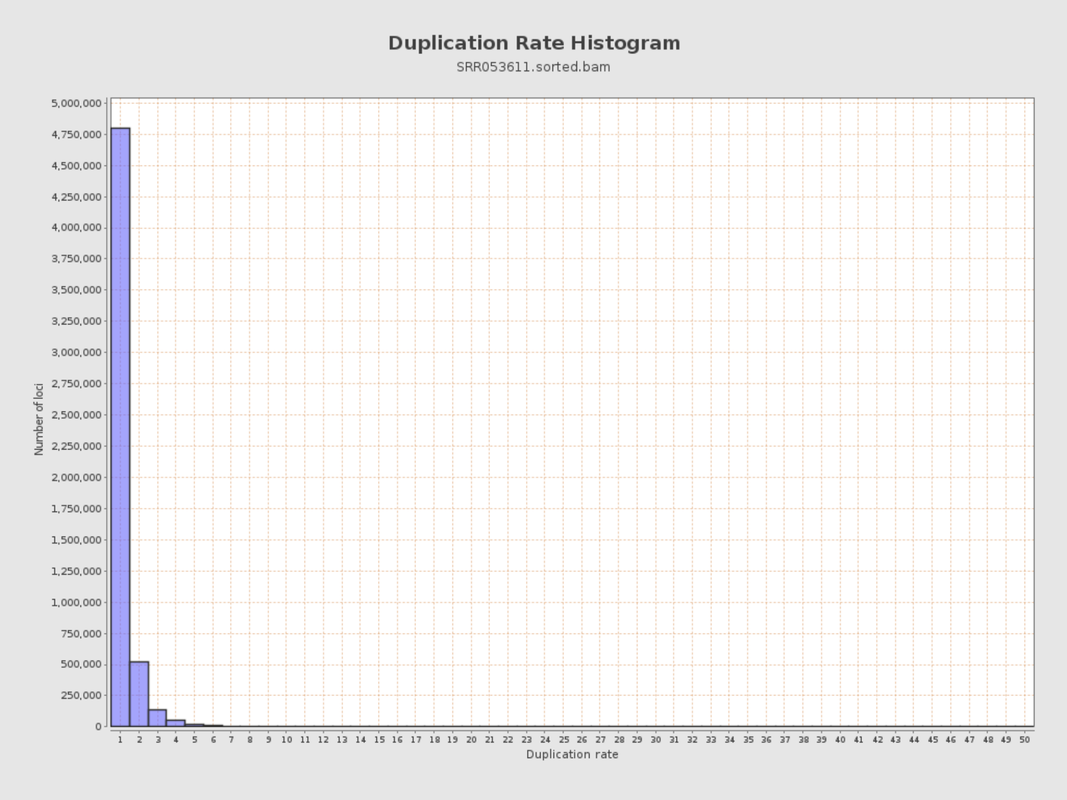
5. Results : Coverage Histogram (0-50X)



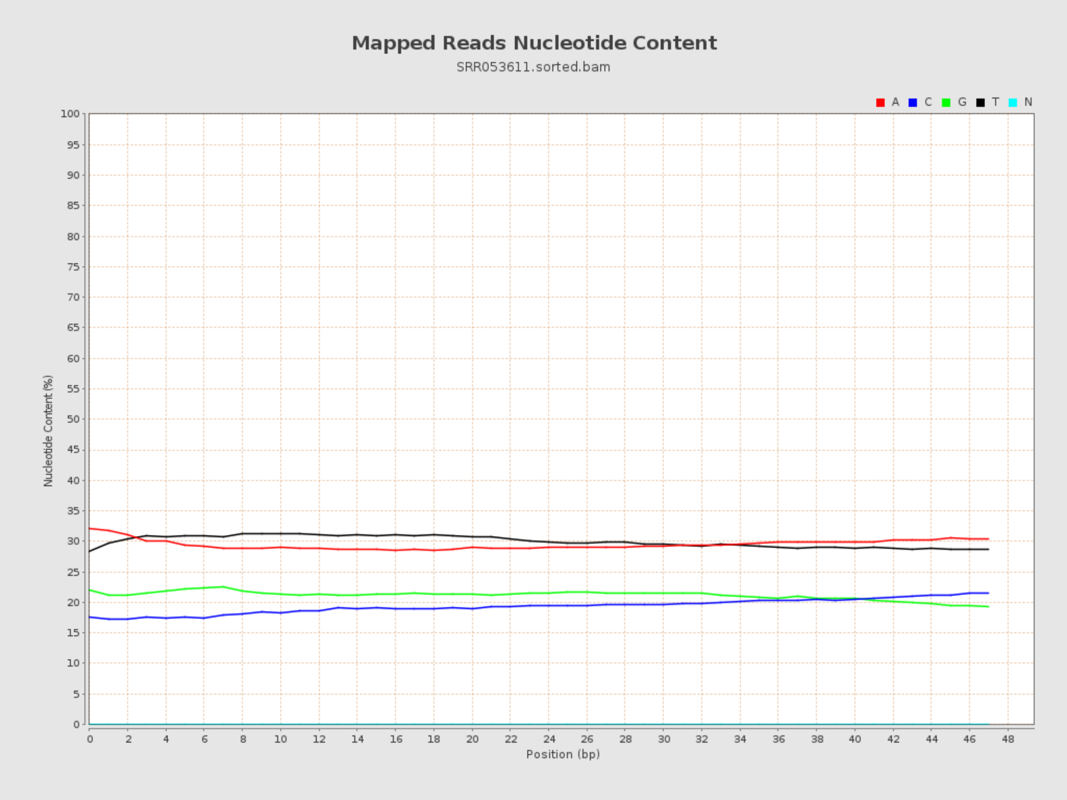
6. Results : Genome Fraction Coverage



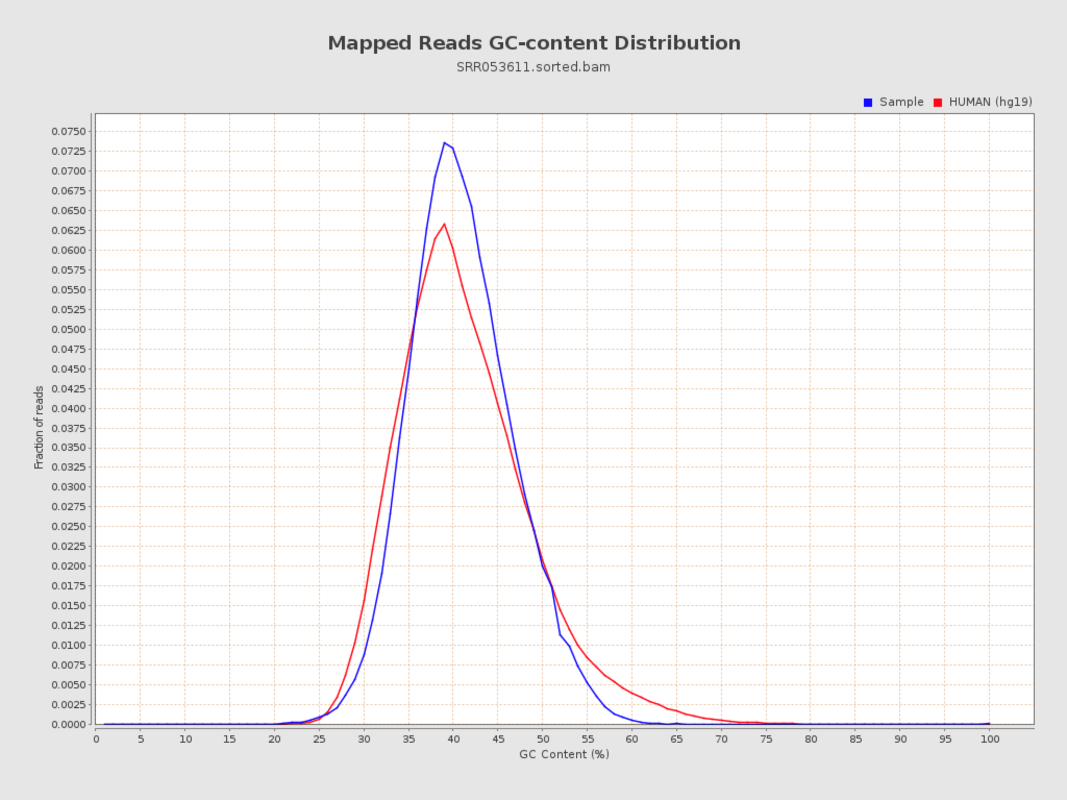
7. Results : Duplication Rate Histogram



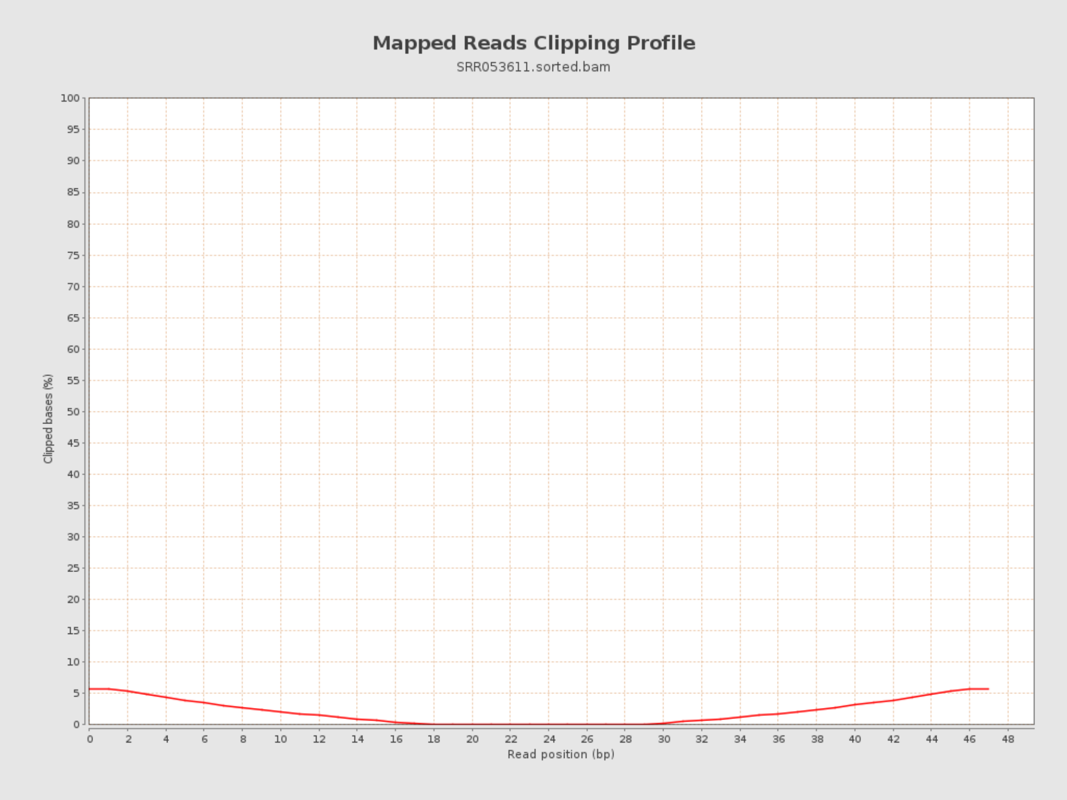
8. Results : Mapped Reads Nucleotide Content



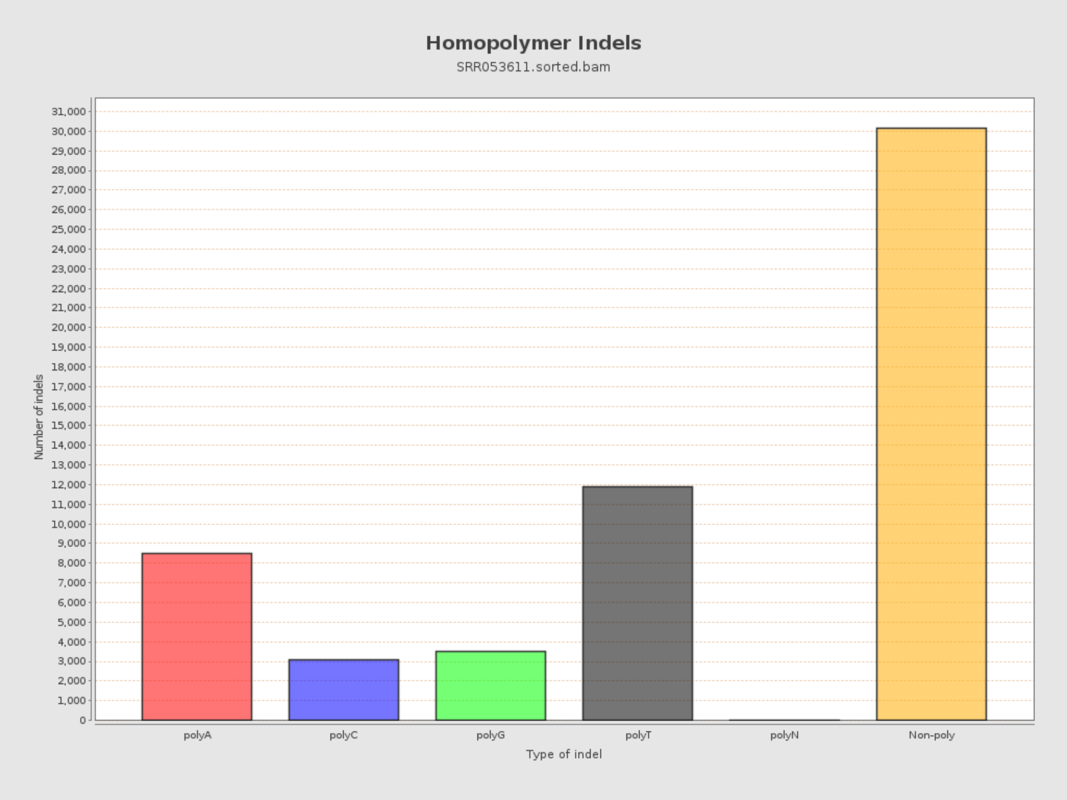
9. Results : Mapped Reads GC-content Distribution



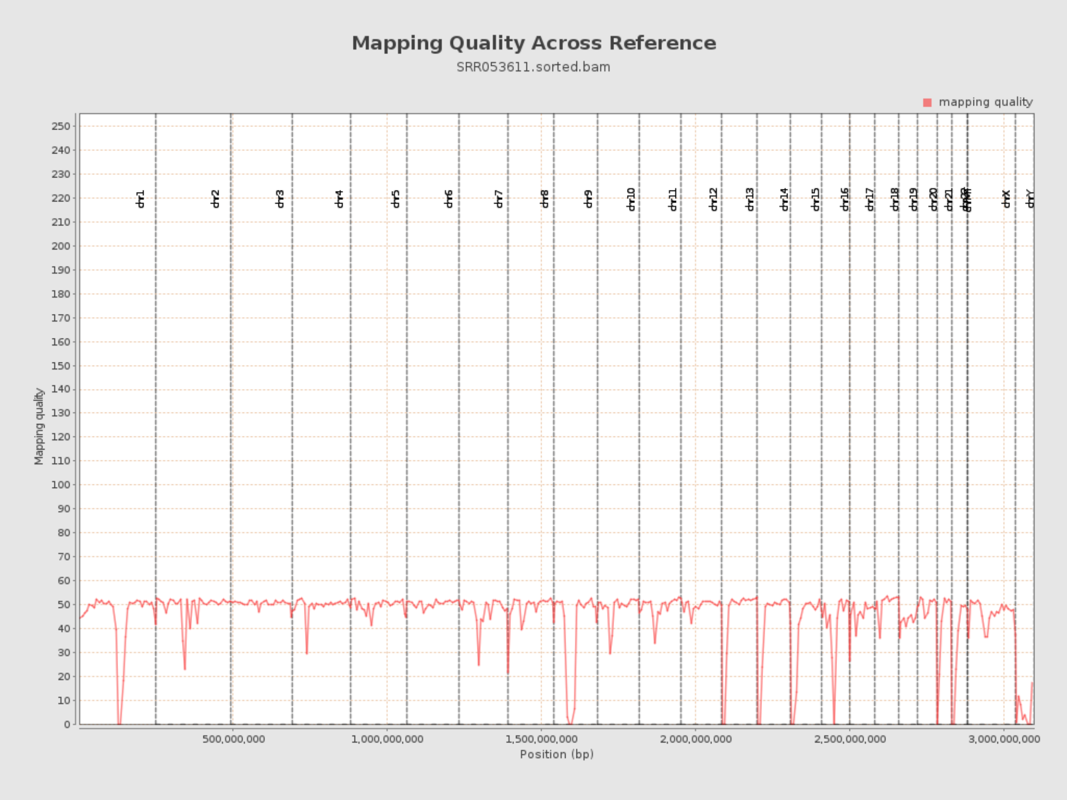
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram