Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/18 23:32:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR053610.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_SRR053610 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR053610.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 18 23:32:02 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR053610.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,458,168
Mapped reads	5,681,563 / 76.18%
Unmapped reads	1,776,605 / 23.82%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	185 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	1,098,230 / 14.73%
Duplication rate	15.46%
Clipped reads	455,626 / 6.11%

2.2. ACGT Content

Number/percentage of A's	78,386,966 / 29.18%
Number/percentage of C's	51,641,452 / 19.22%
Number/percentage of T's	81,410,237 / 30.3%
Number/percentage of G's	57,075,287 / 21.25%
Number/percentage of N's	122,900 / 0.05%
GC Percentage	40.47%

2.3. Coverage

Mean	0.0868

Standard Deviation	0.7387

2.4. Mapping Quality

Mean Mapping Quality	45.95

2.5. Mismatches and indels

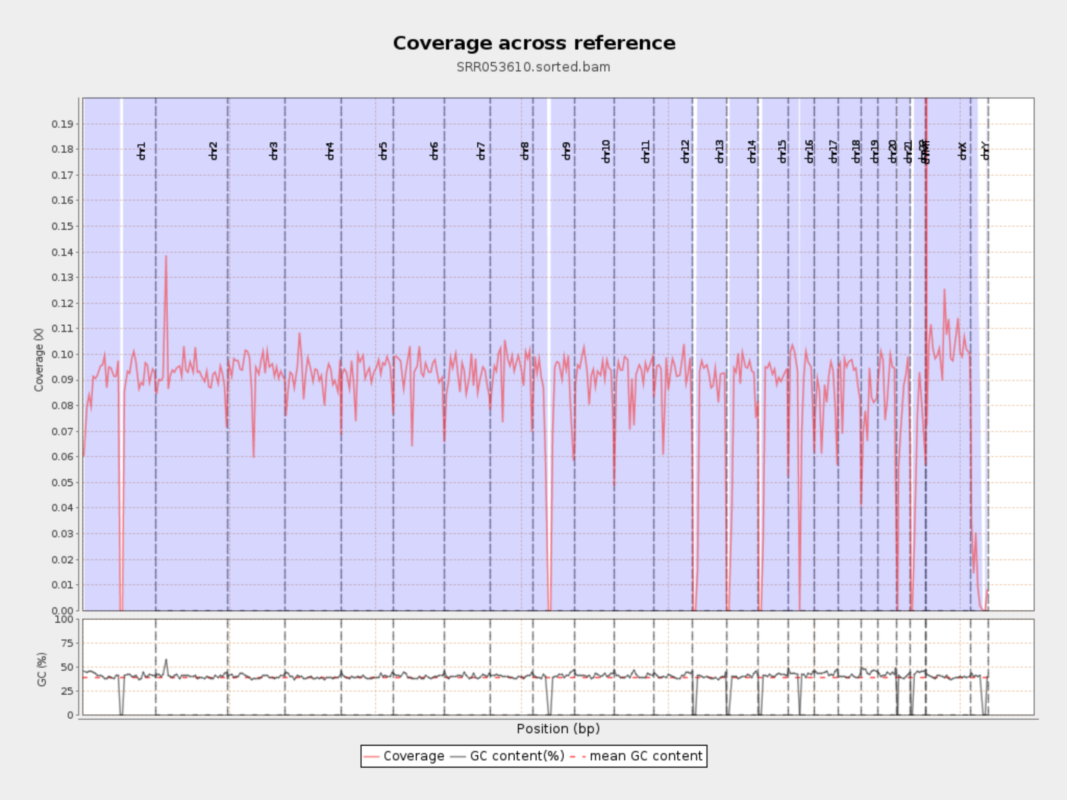
General error rate	0.65%
Mismatches	1,735,267
Insertions	12,306
Mapped reads with at least one insertion	0.22%
Deletions	36,337
Mapped reads with at least one deletion	0.64%
Homopolymer indels	48.22%

2.6. Chromosome stats

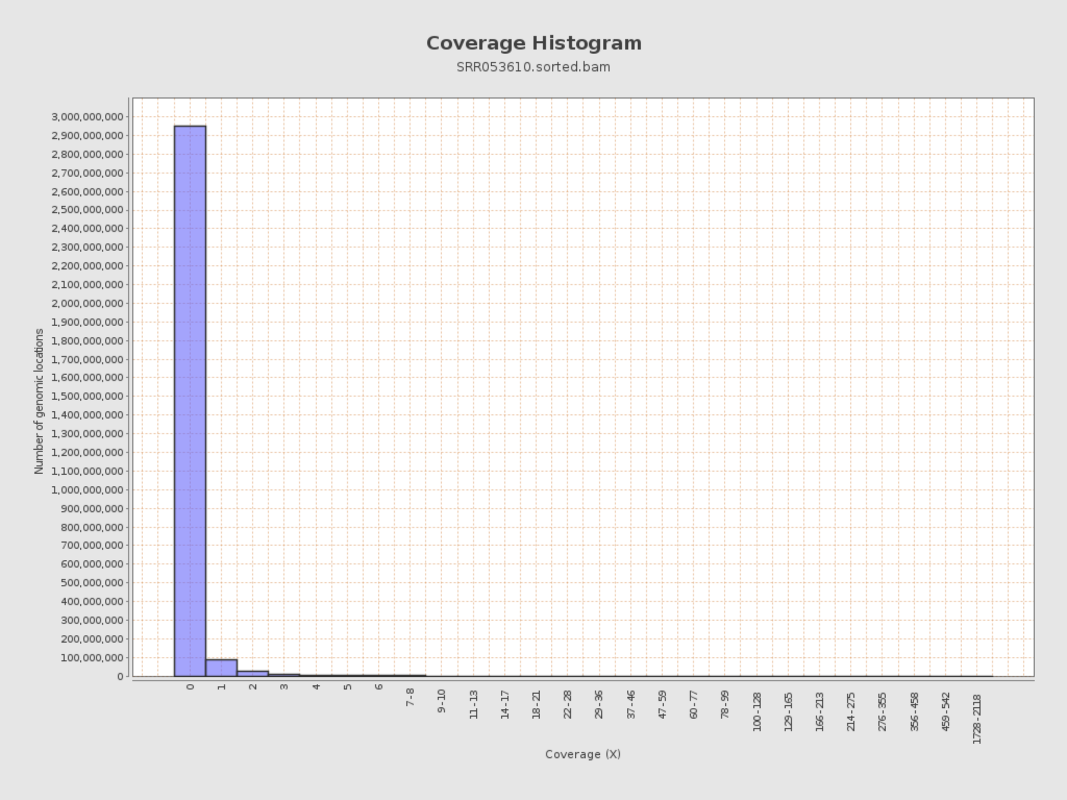
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	21240198	0.0852	0.6572
chr2	243199373	22742051	0.0935	1.6703
chr3	198022430	18581951	0.0938	0.5686
chr4	191154276	17520406	0.0917	0.5897
chr5	180915260	16781167	0.0928	0.563
chr6	171115067	16007047	0.0935	0.6335
chr7	159138663	14470315	0.0909	0.7223

chr8	146364022	13813835	0.0944	0.6171
chr9	141213431	11036108	0.0782	0.5453
chr10	135534747	12564619	0.0927	0.6398
chr11	135006516	12276745	0.0909	0.6238
chr12	133851895	12273423	0.0917	0.5621
chr13	115169878	8757516	0.076	0.5104
chr14	107349540	8347036	0.0778	0.5659
chr15	102531392	7674387	0.0748	0.4945
chr16	90354753	7455193	0.0825	0.5532
chr17	81195210	6772075	0.0834	0.5297
chr18	78077248	7165423	0.0918	0.6862
chr19	59128983	4605853	0.0779	0.6256
chr20	63025520	5672814	0.09	0.5729
chr21	48129895	3469341	0.0721	0.5649
chr22	51304566	2796237	0.0545	0.4047
chrMT	16571	33303	2.0097	3.5066
chrX	155270560	15959662	0.1028	0.6592
chrY	59373566	673212	0.0113	0.2312

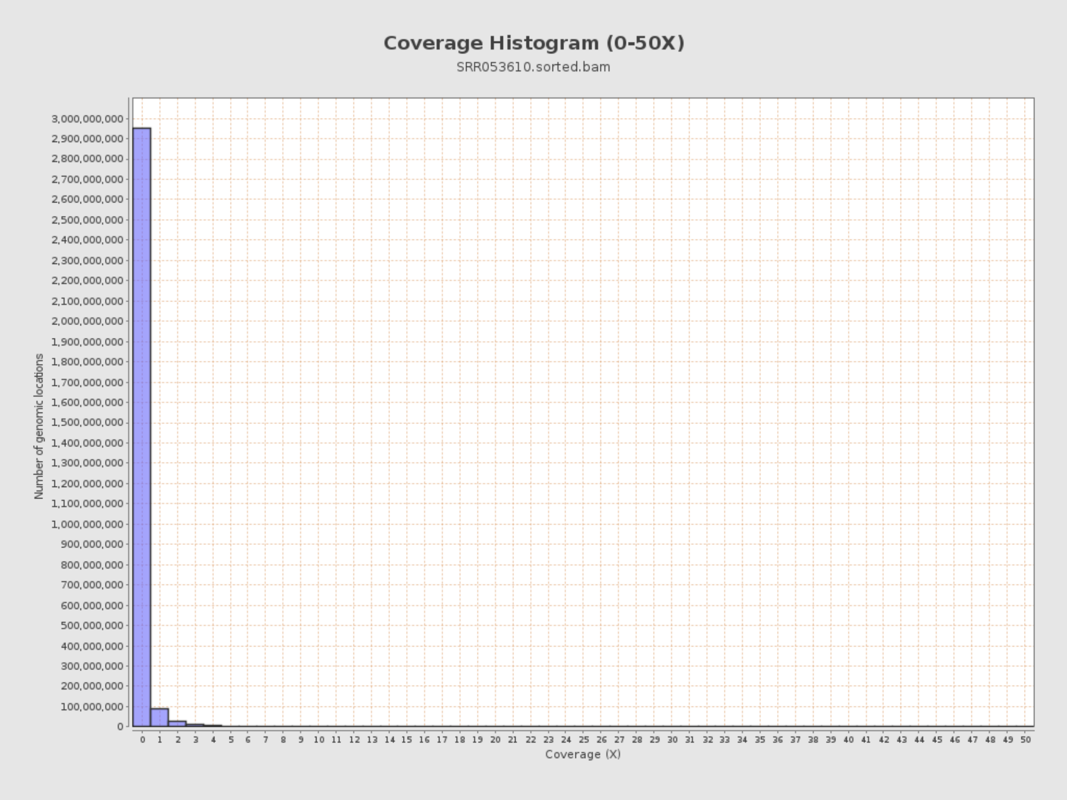
3. Results : Coverage across reference



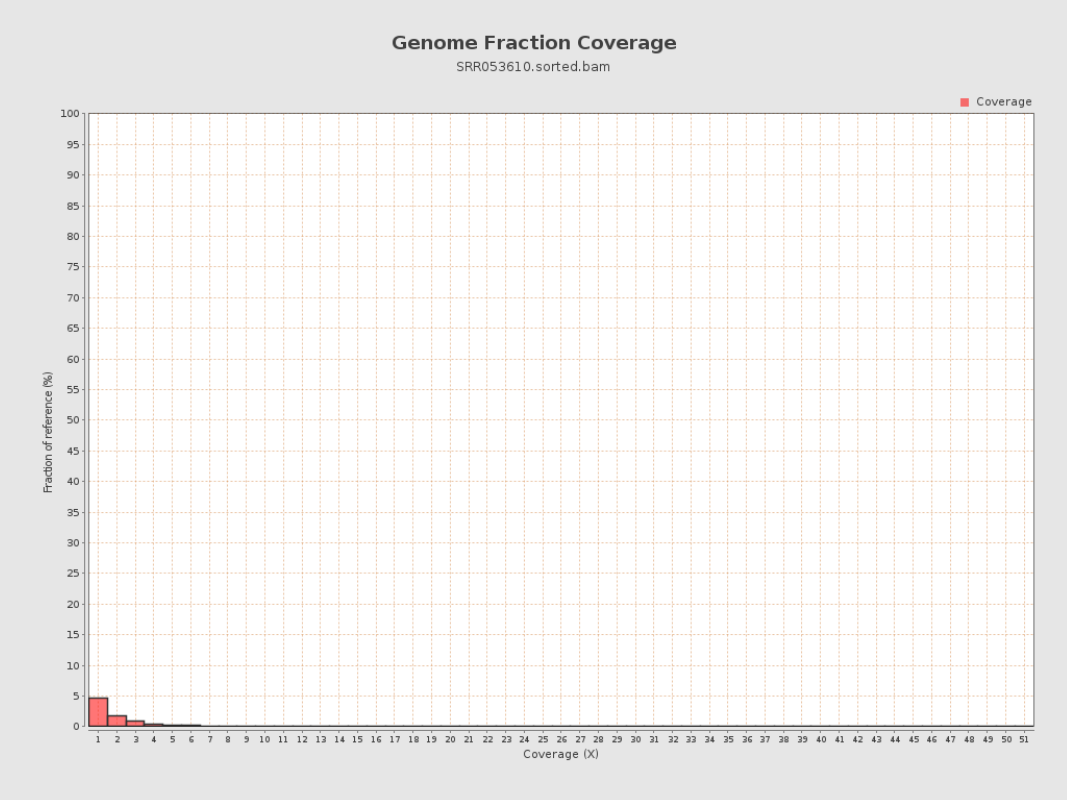
4. Results : Coverage Histogram



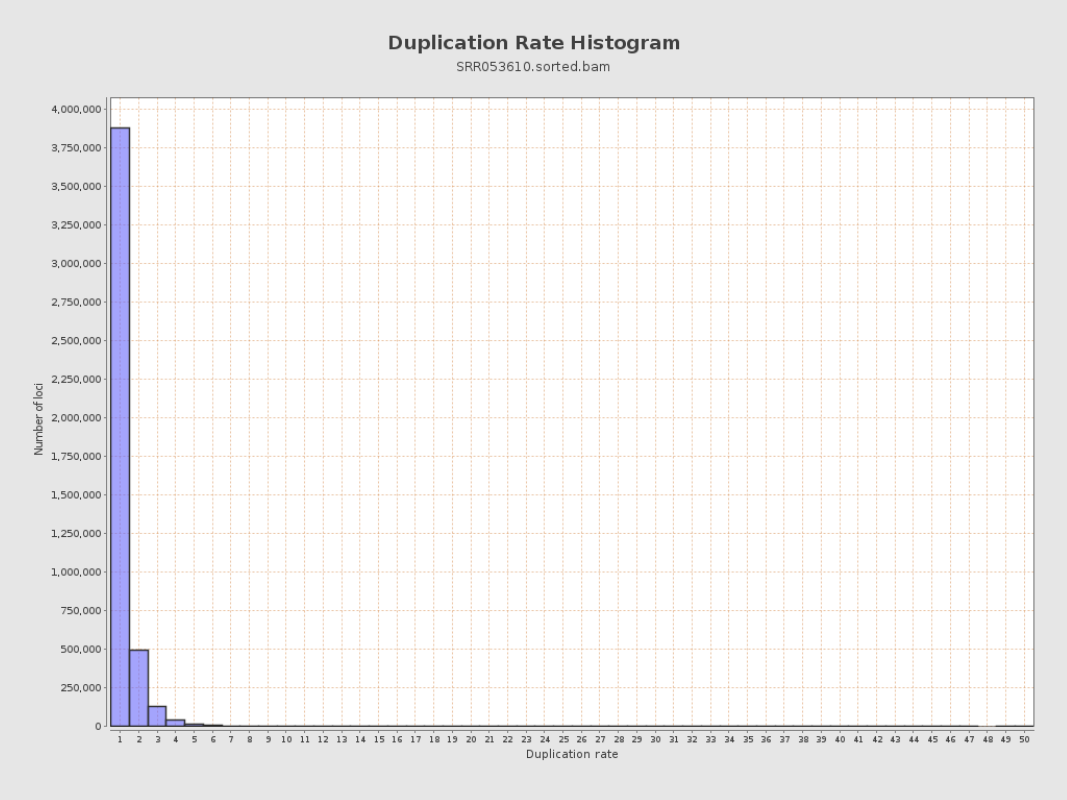
5. Results : Coverage Histogram (0-50X)



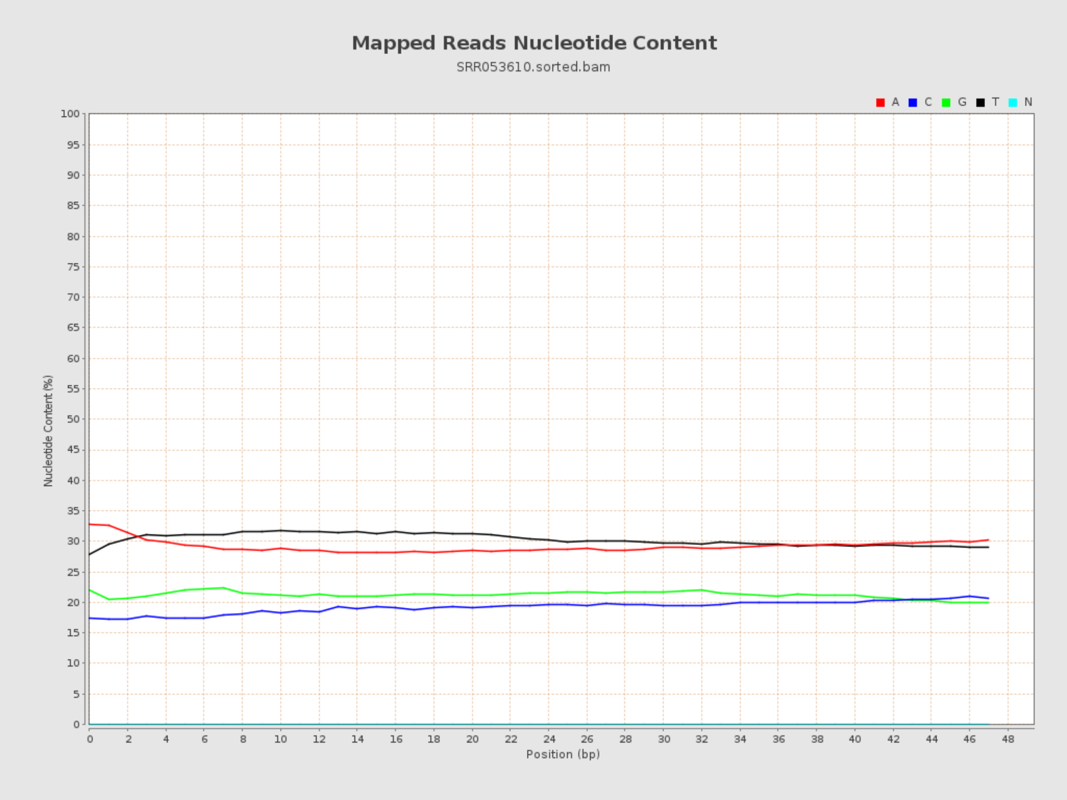
6. Results : Genome Fraction Coverage



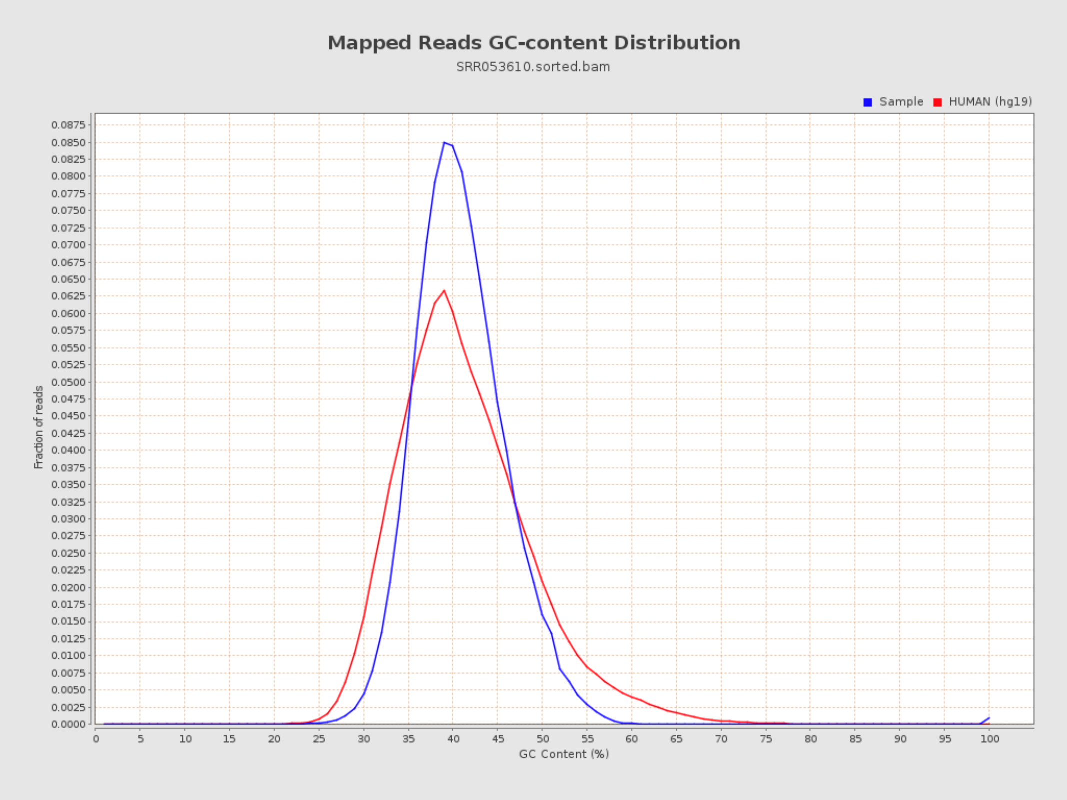
7. Results : Duplication Rate Histogram



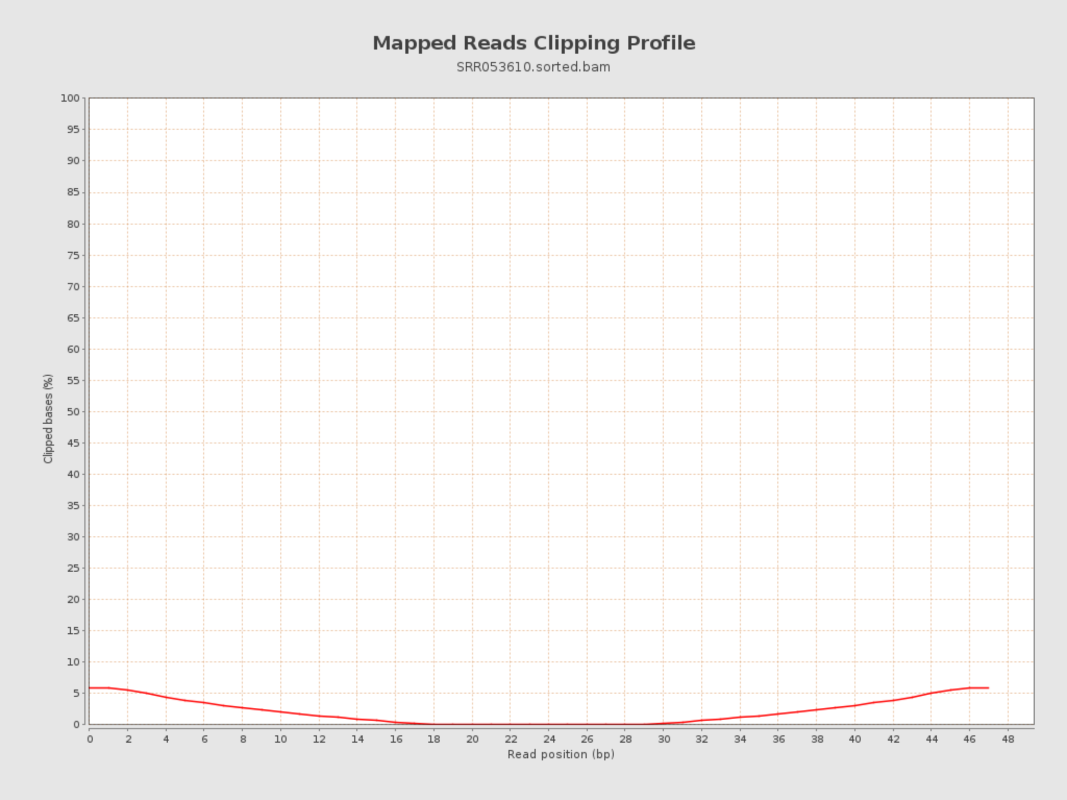
8. Results : Mapped Reads Nucleotide Content



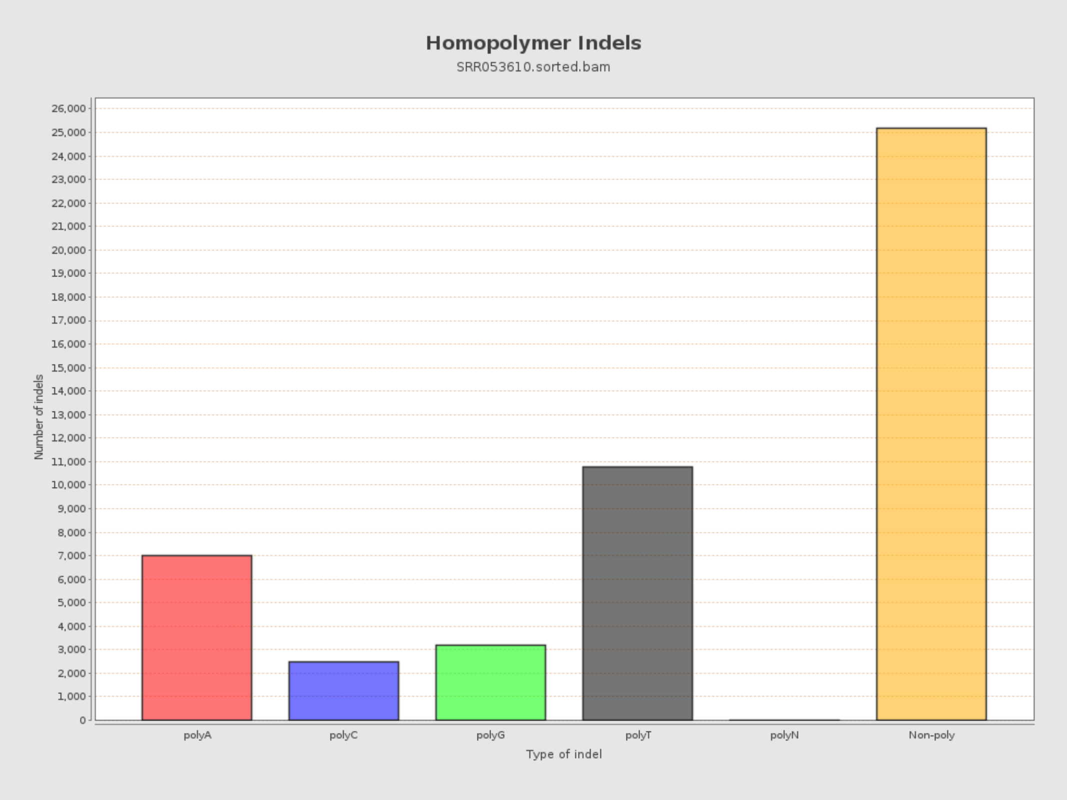
9. Results : Mapped Reads GC-content Distribution



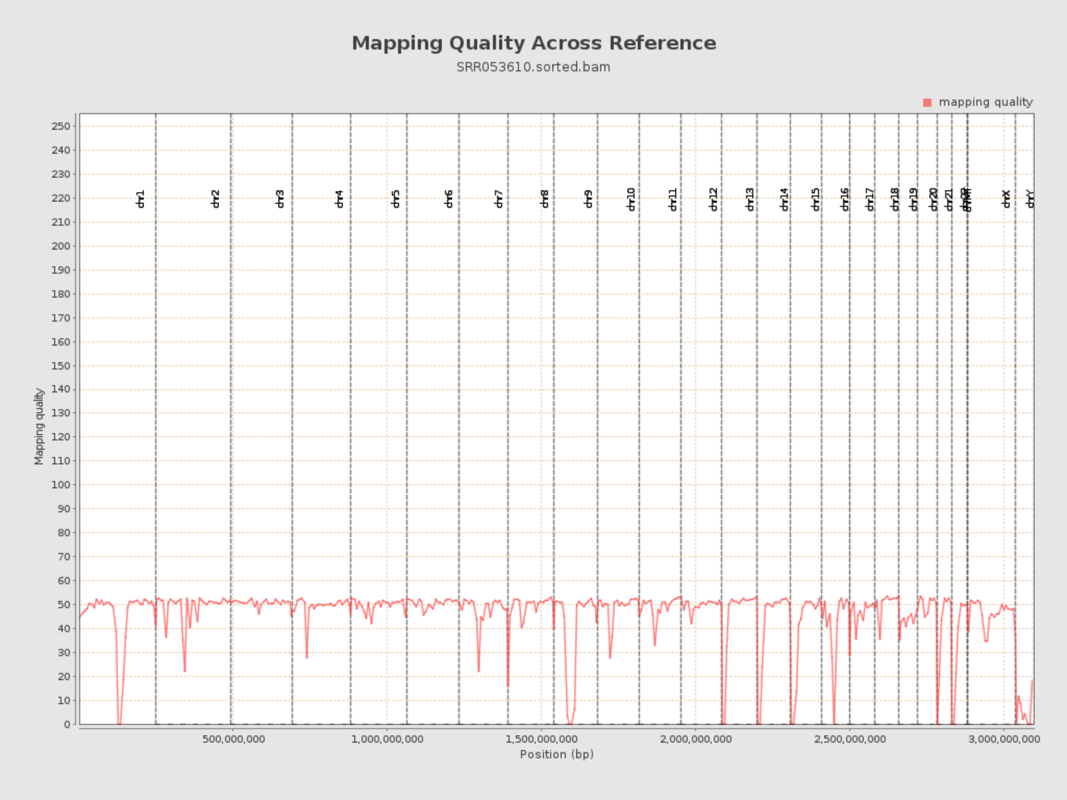
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram