

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 13:27:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548943.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_SRR1548943 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548943.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 13:27:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1548943.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,913,772
Mapped reads	6,920,943 / 87.45%
Unmapped reads	992,829 / 12.55%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	255,654 / 3.23%
Duplication rate	2.5%
Clipped reads	590,842 / 7.47%

2.2. ACGT Content

Number/percentage of A's	79,080,623 / 28.91%
Number/percentage of C's	57,601,943 / 21.06%
Number/percentage of T's	79,467,498 / 29.05%
Number/percentage of G's	57,411,599 / 20.99%
Number/percentage of N's	2,399 / 0%
GC Percentage	42.04%

2.3. Coverage

Mean	0.0884
Standard Deviation	0.9254

2.4. Mapping Quality

Mean Mapping Quality	38.61
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2.5. Mismatches and indels

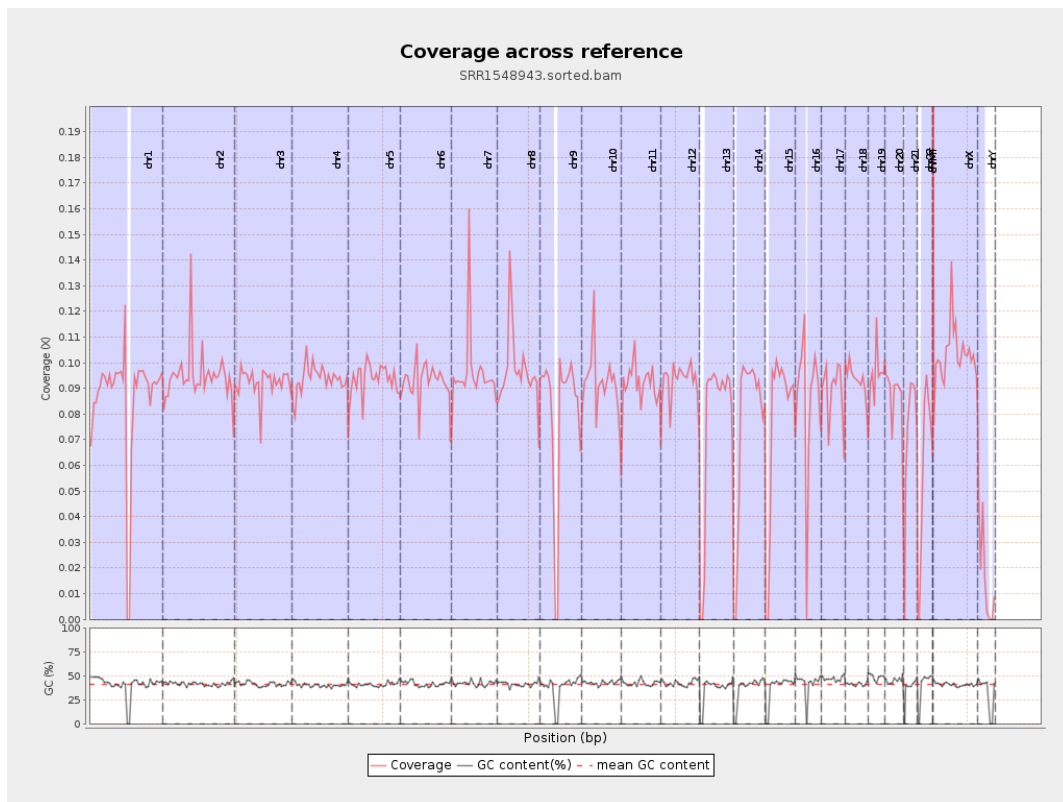
General error rate	0.32%
Mismatches	854,763
Insertions	9,777
Mapped reads with at least one insertion	0.14%
Deletions	21,780
Mapped reads with at least one deletion	0.31%
Homopolymer indels	39.49%

2.6. Chromosome stats

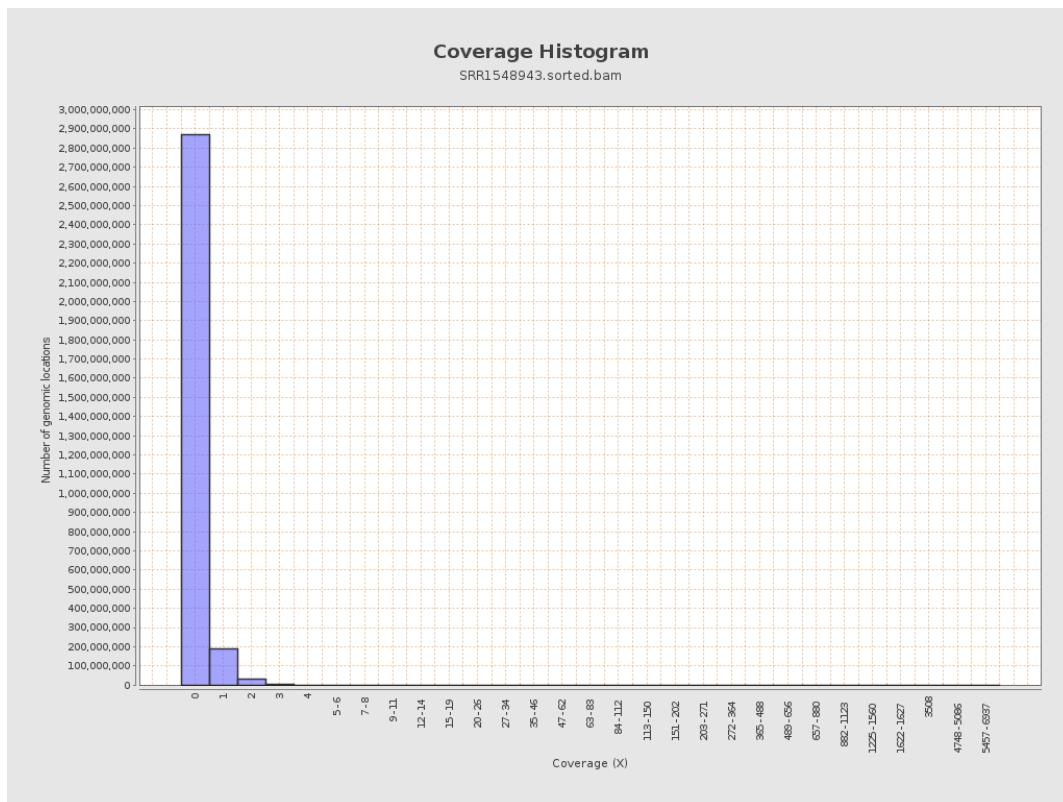
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	21494492	0.0862	0.9639
chr2	243199373	23040550	0.0947	0.6134
chr3	198022430	18315725	0.0925	0.3545
chr4	191154276	17950909	0.0939	0.3826
chr5	180915260	16894167	0.0934	0.366
chr6	171115067	15893632	0.0929	0.3989
chr7	159138663	15258229	0.0959	0.8757
chr8	146364022	14220145	0.0972	3.3668

chr9	141213431	11407060	0.0808	0.6174
chr10	135534747	12542423	0.0925	0.5268
chr11	135006516	12404842	0.0919	0.605
chr12	133851895	12473820	0.0932	0.3761
chr13	115169878	8761280	0.0761	0.3181
chr14	107349540	8330050	0.0776	0.4248
chr15	102531392	7802243	0.0761	0.3238
chr16	90354753	7586659	0.084	0.398
chr17	81195210	7281036	0.0897	0.3808
chr18	78077248	7327025	0.0938	1.1224
chr19	59128983	5638918	0.0954	0.9666
chr20	63025520	5498427	0.0872	0.3715
chr21	48129895	3481985	0.0723	0.3807
chr22	51304566	3019966	0.0589	0.3305
chrMT	16571	11052	0.6669	1.0372
chrX	155270560	15986758	0.103	0.4845
chrY	59373566	971007	0.0164	0.2258

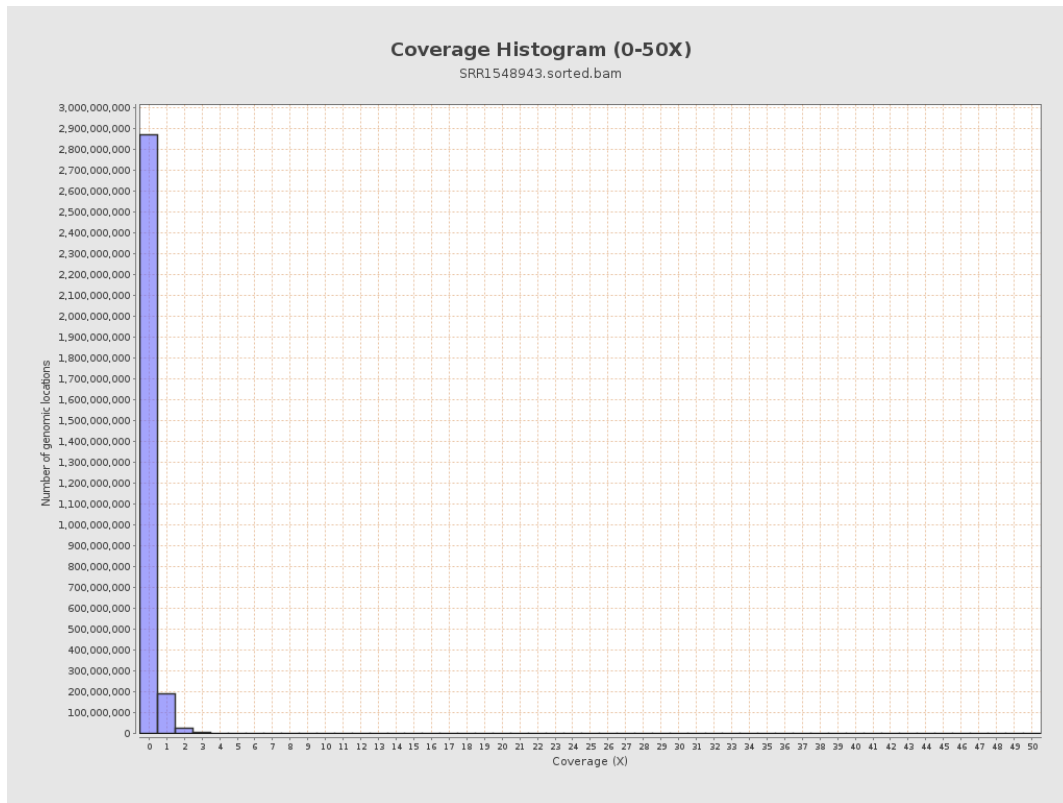
3. Results : Coverage across reference



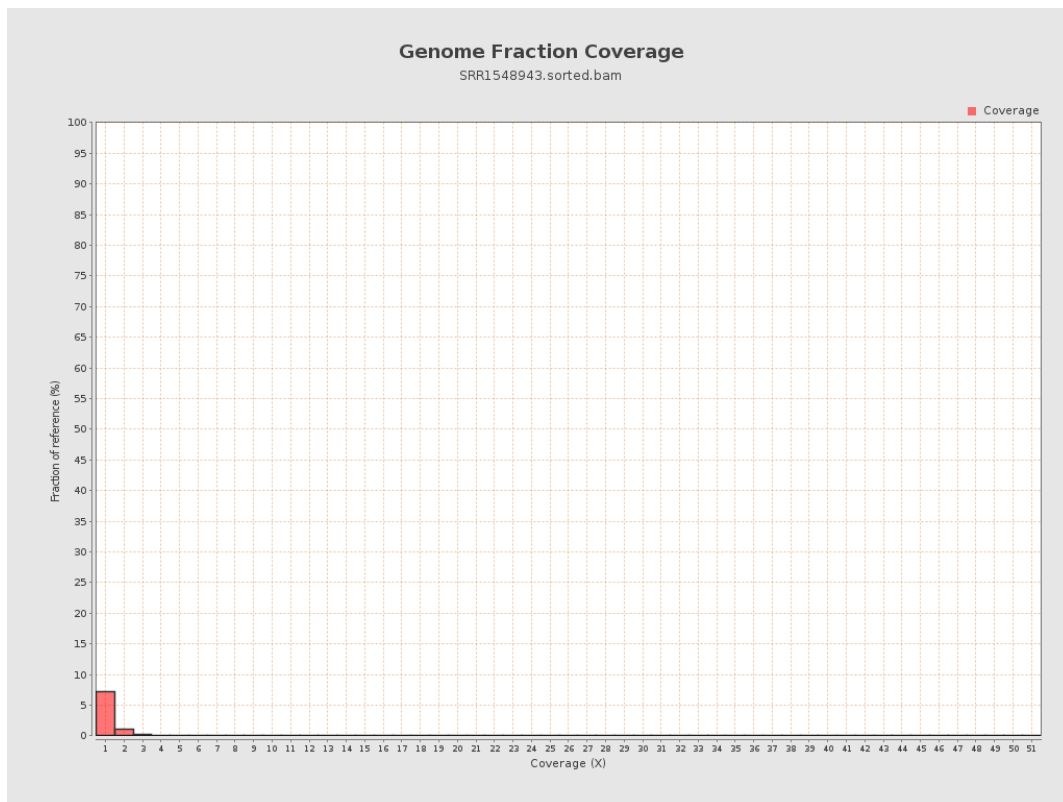
4. Results : Coverage Histogram



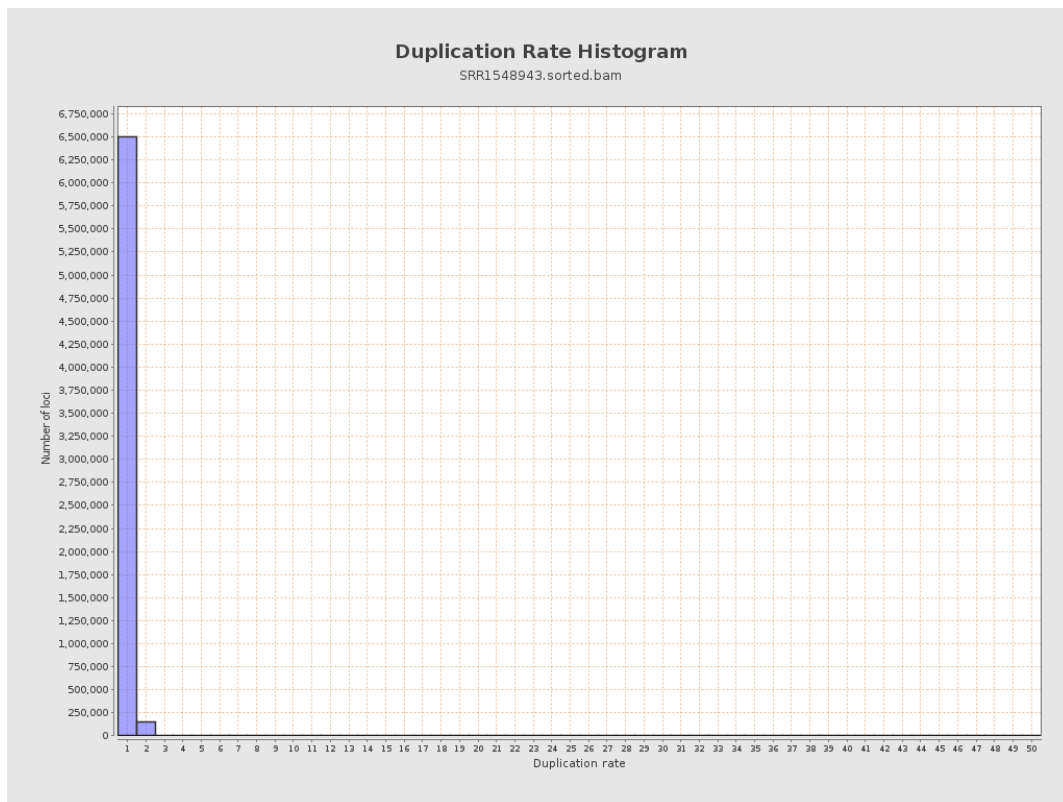
5. Results : Coverage Histogram (0-50X)



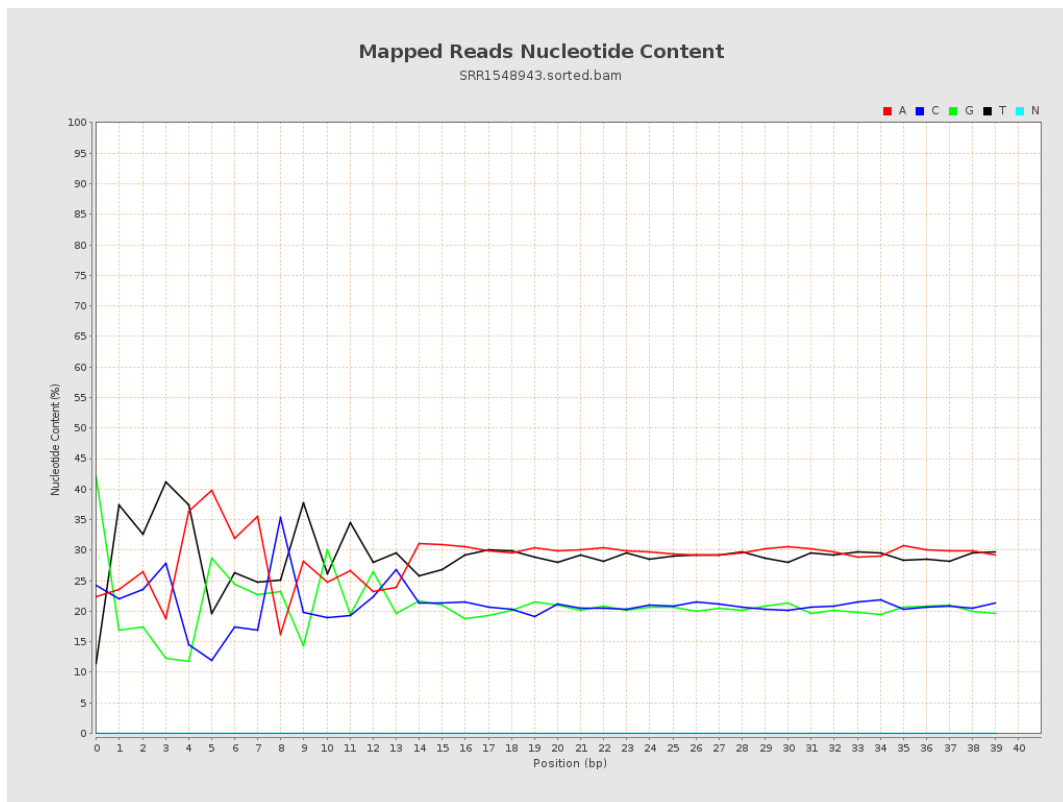
6. Results : Genome Fraction Coverage



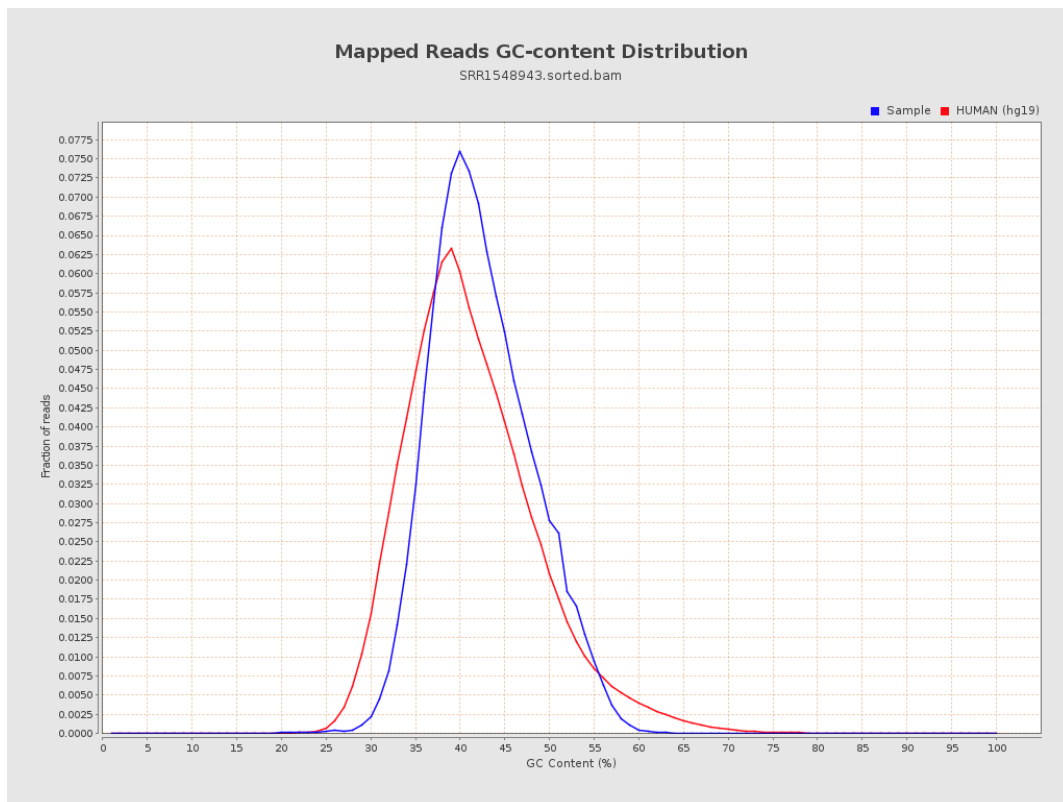
7. Results : Duplication Rate Histogram



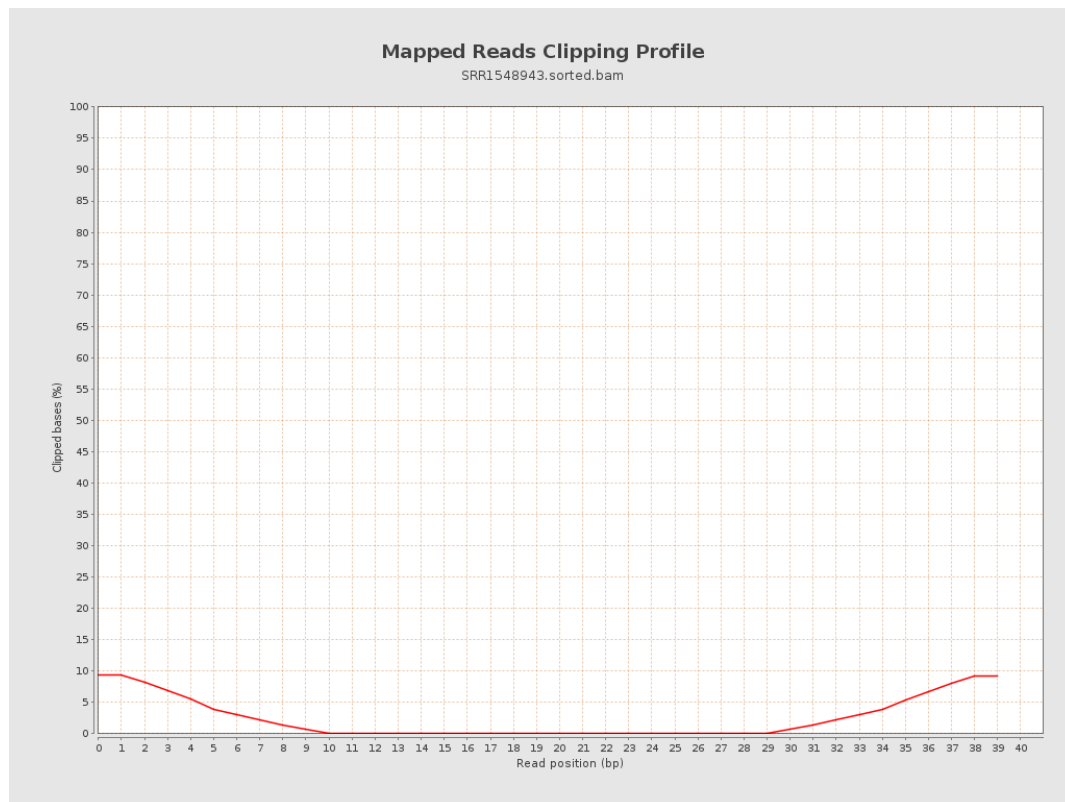
8. Results : Mapped Reads Nucleotide Content



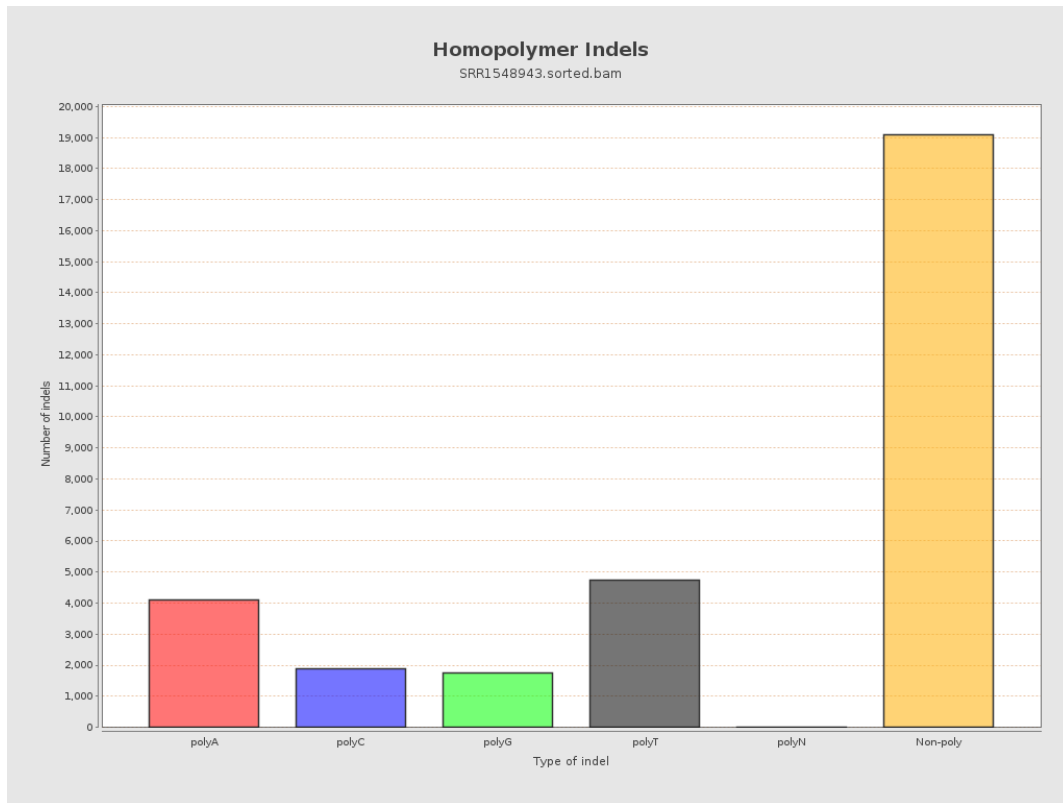
9. Results : Mapped Reads GC-content Distribution



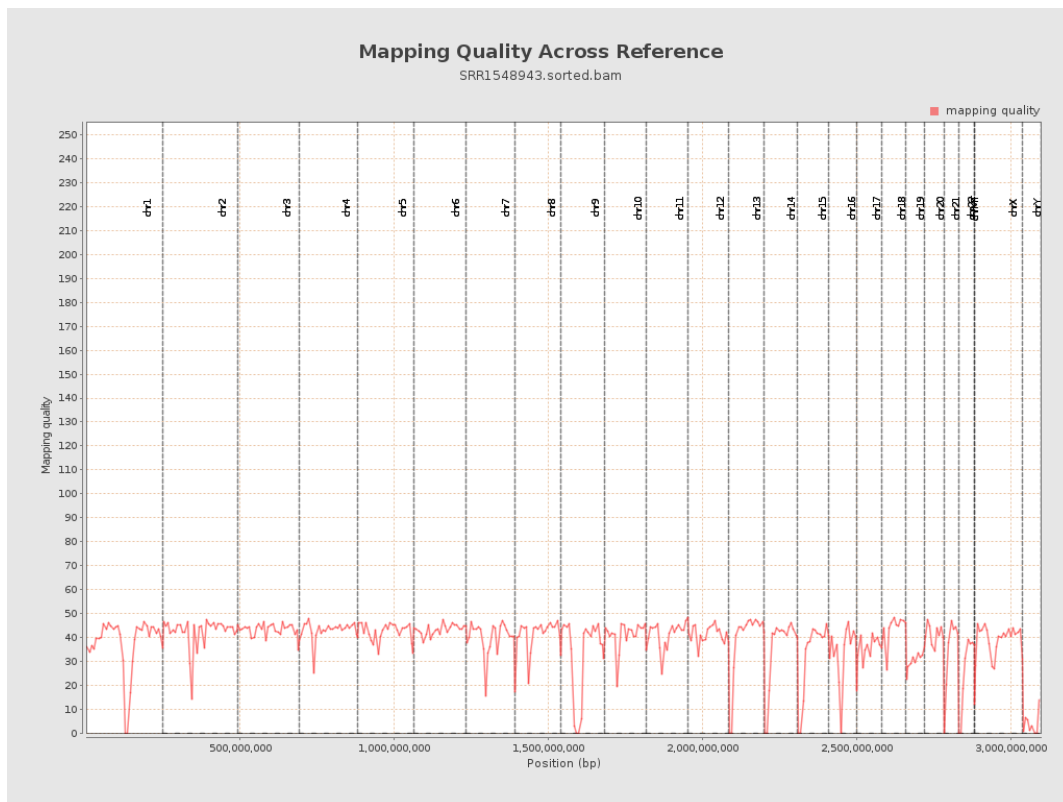
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

