

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 05:02:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548983.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_SRR1548983 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548983.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 05:02:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1548983.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,937,993
Mapped reads	3,076,419 / 44.34%
Unmapped reads	3,861,574 / 55.66%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	66,169 / 0.95%
Duplication rate	1.52%
Clipped reads	205,262 / 2.96%

2.2. ACGT Content

Number/percentage of A's	36,813,161 / 30.2%
Number/percentage of C's	23,746,811 / 19.48%
Number/percentage of T's	37,233,599 / 30.55%
Number/percentage of G's	24,080,480 / 19.76%
Number/percentage of N's	6,722 / 0.01%
GC Percentage	39.24%

2.3. Coverage

Mean	0.0394
Standard Deviation	0.2968

2.4. Mapping Quality

Mean Mapping Quality	43.99
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2.5. Mismatches and indels

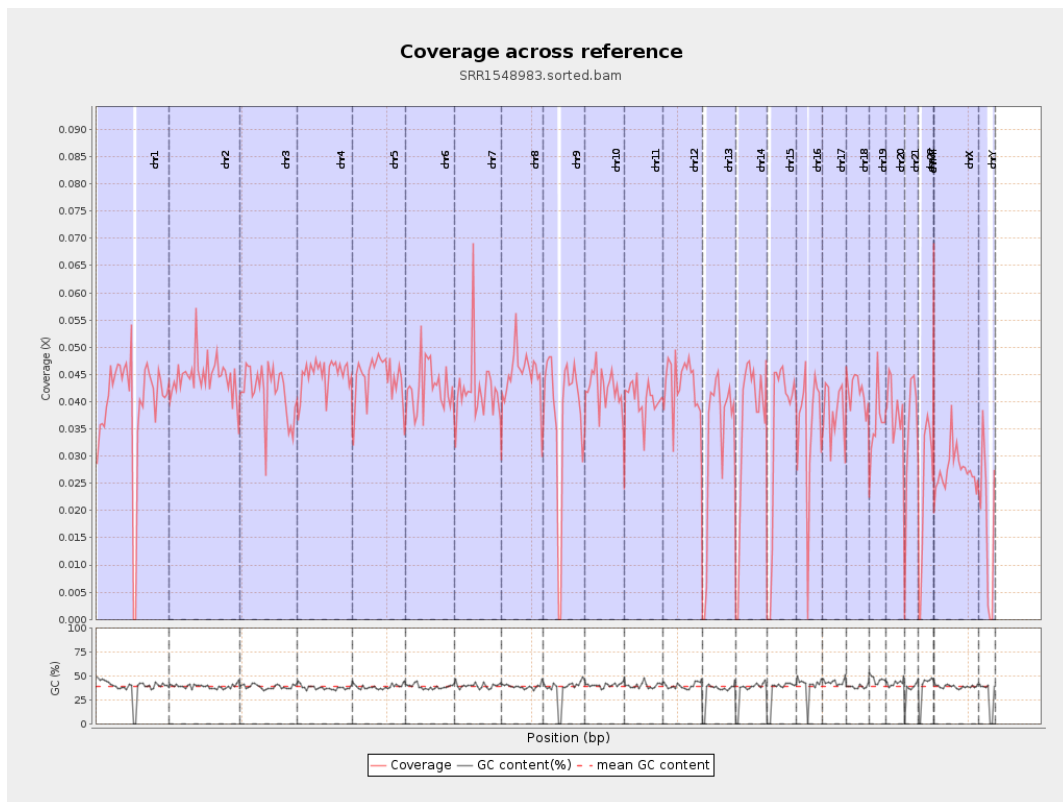
General error rate	0.28%
Mismatches	339,188
Insertions	4,013
Mapped reads with at least one insertion	0.13%
Deletions	11,992
Mapped reads with at least one deletion	0.39%
Homopolymer indels	46.63%

2.6. Chromosome stats

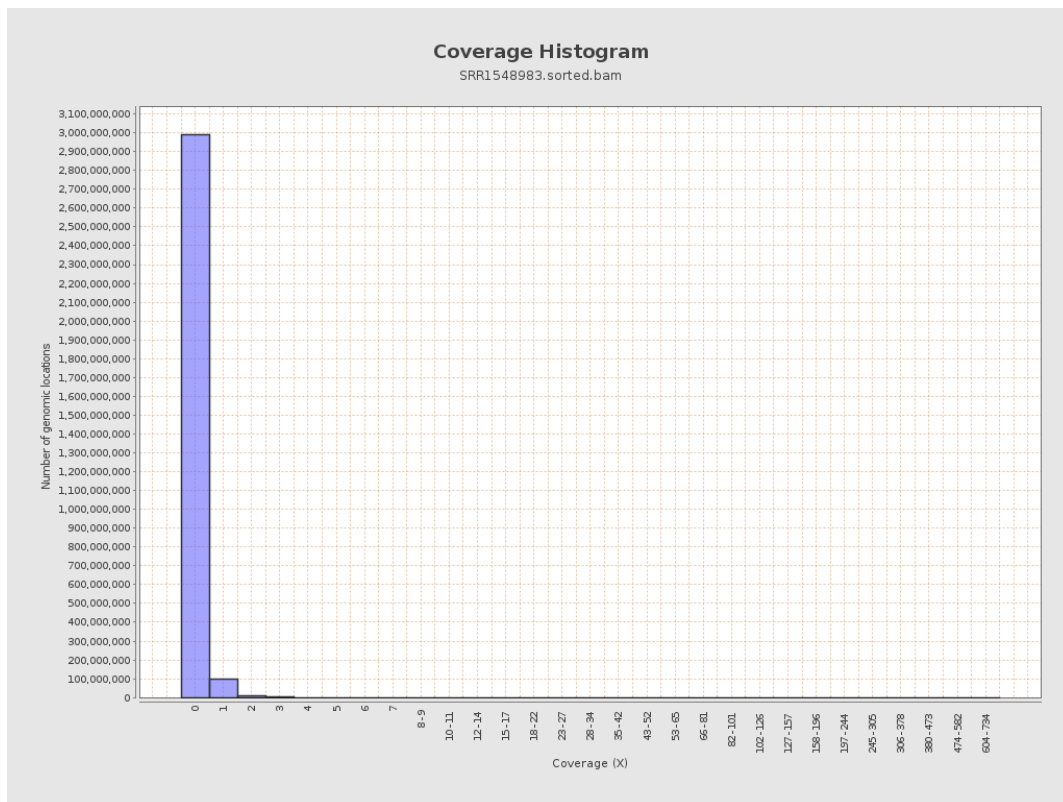
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	9869230	0.0396	0.4902
chr2	243199373	10839082	0.0446	0.2812
chr3	198022430	8271096	0.0418	0.2252
chr4	191154276	8629294	0.0451	0.2373
chr5	180915260	8023811	0.0444	0.2329
chr6	171115067	7274147	0.0425	0.2533
chr7	159138663	6735033	0.0423	0.4222
chr8	146364022	6579146	0.045	0.4364

chr9	141213431	5346007	0.0379	0.2554
chr10	135534747	5768232	0.0426	0.2587
chr11	135006516	5440563	0.0403	0.2733
chr12	133851895	5756341	0.043	0.2319
chr13	115169878	3787998	0.0329	0.1986
chr14	107349540	3820607	0.0356	0.2295
chr15	102531392	3573850	0.0349	0.2042
chr16	90354753	3204782	0.0355	0.212
chr17	81195210	3048459	0.0375	0.2214
chr18	78077248	3269885	0.0419	0.3944
chr19	59128983	2145882	0.0363	0.4068
chr20	63025520	2410485	0.0382	0.2185
chr21	48129895	1637043	0.034	0.2194
chr22	51304566	1220680	0.0238	0.1843
chrMT	16571	1146	0.0692	0.2678
chrX	155270560	4244101	0.0273	0.2049
chrY	59373566	999031	0.0168	0.1847

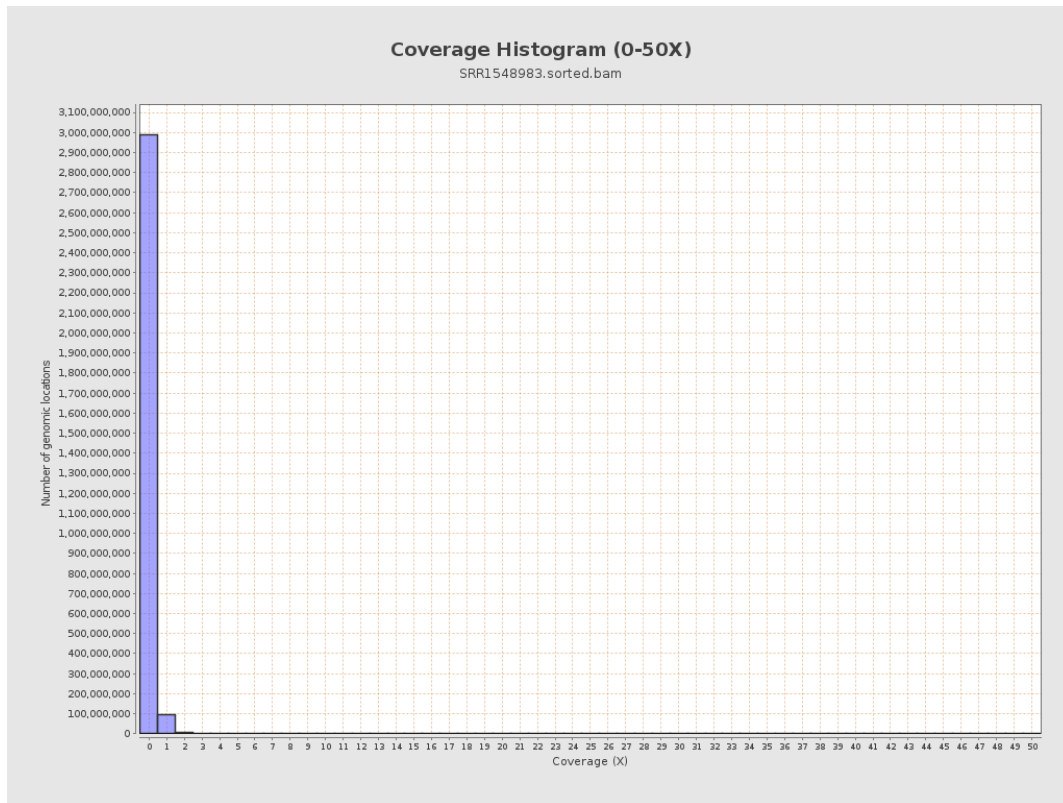
3. Results : Coverage across reference



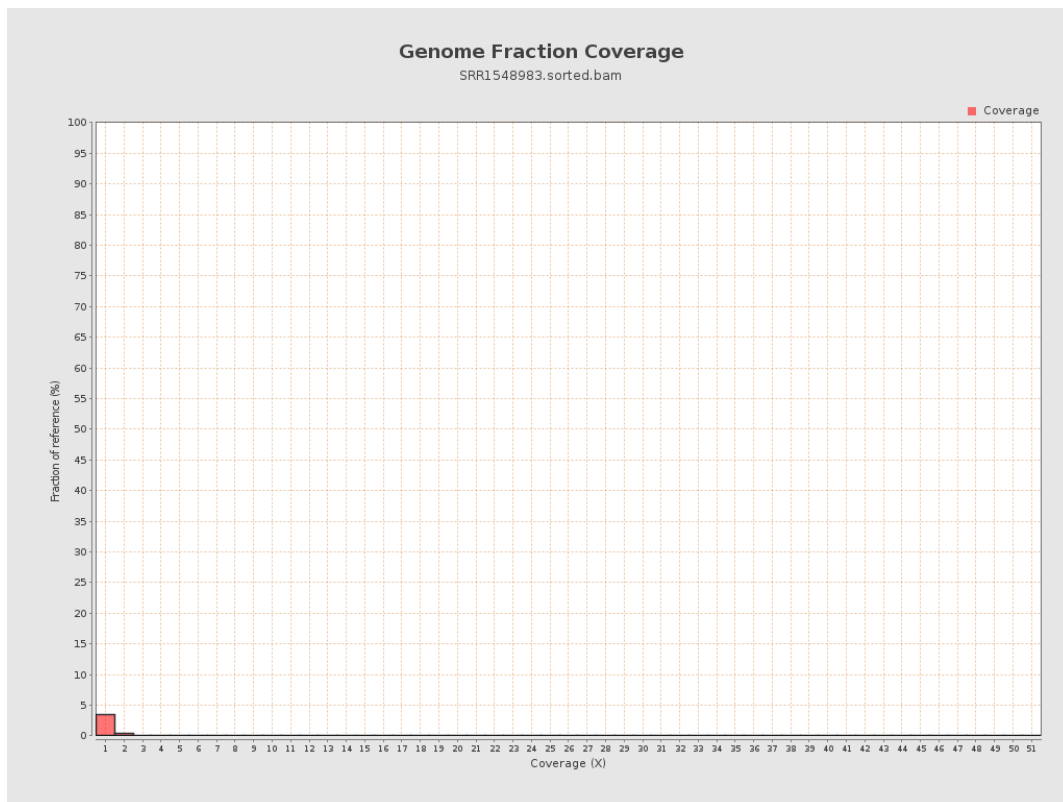
4. Results : Coverage Histogram



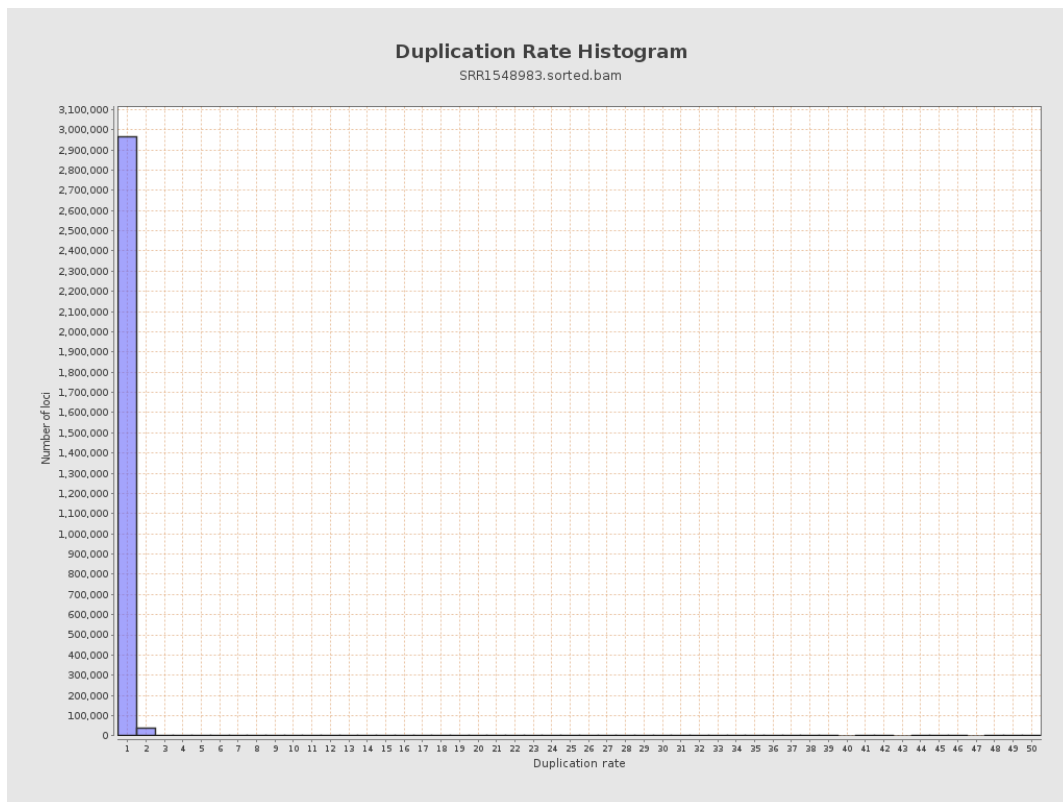
5. Results : Coverage Histogram (0-50X)



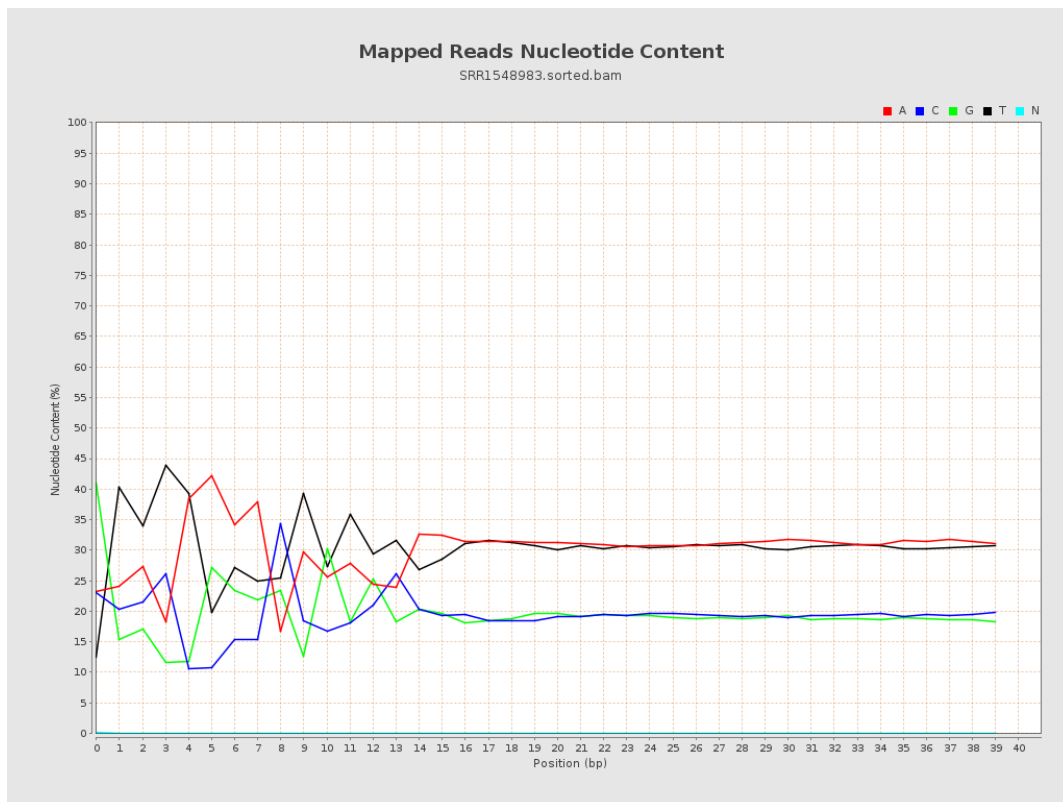
6. Results : Genome Fraction Coverage



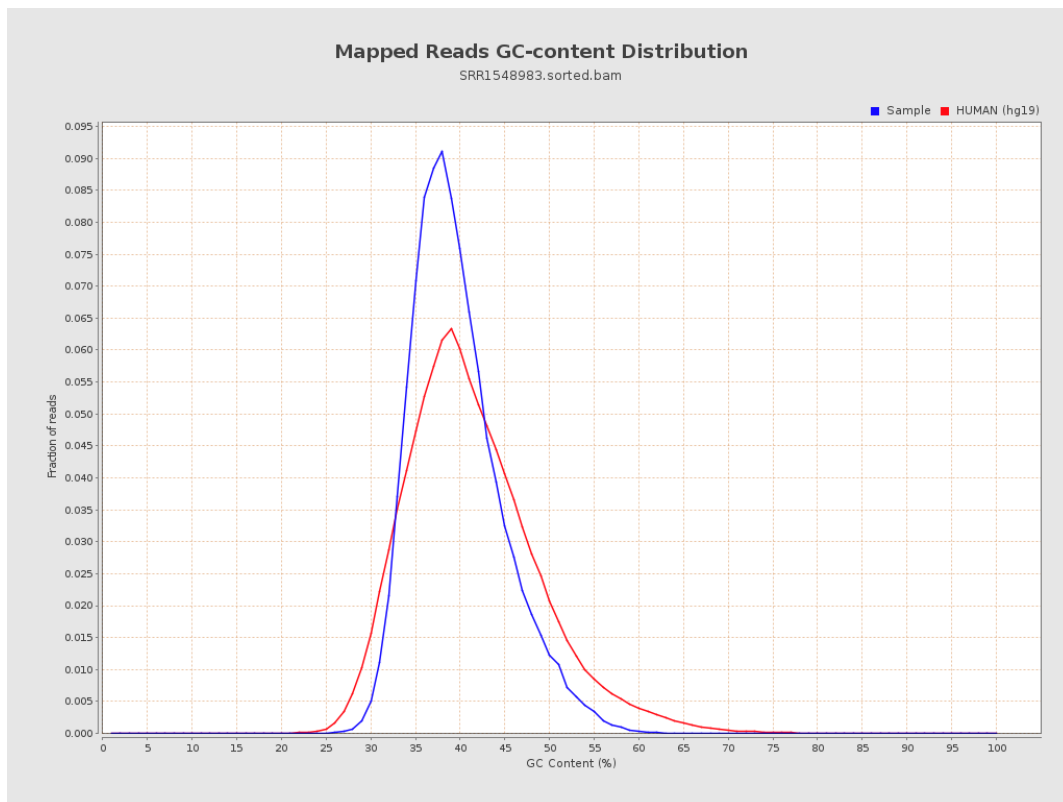
7. Results : Duplication Rate Histogram



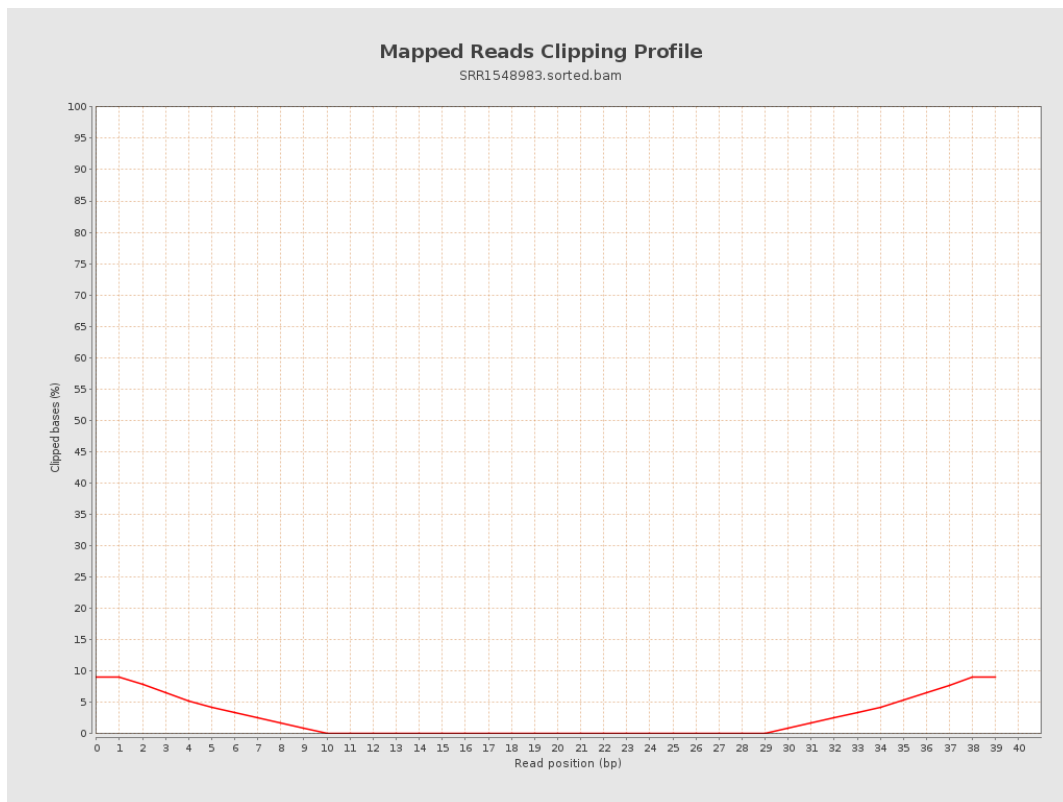
8. Results : Mapped Reads Nucleotide Content



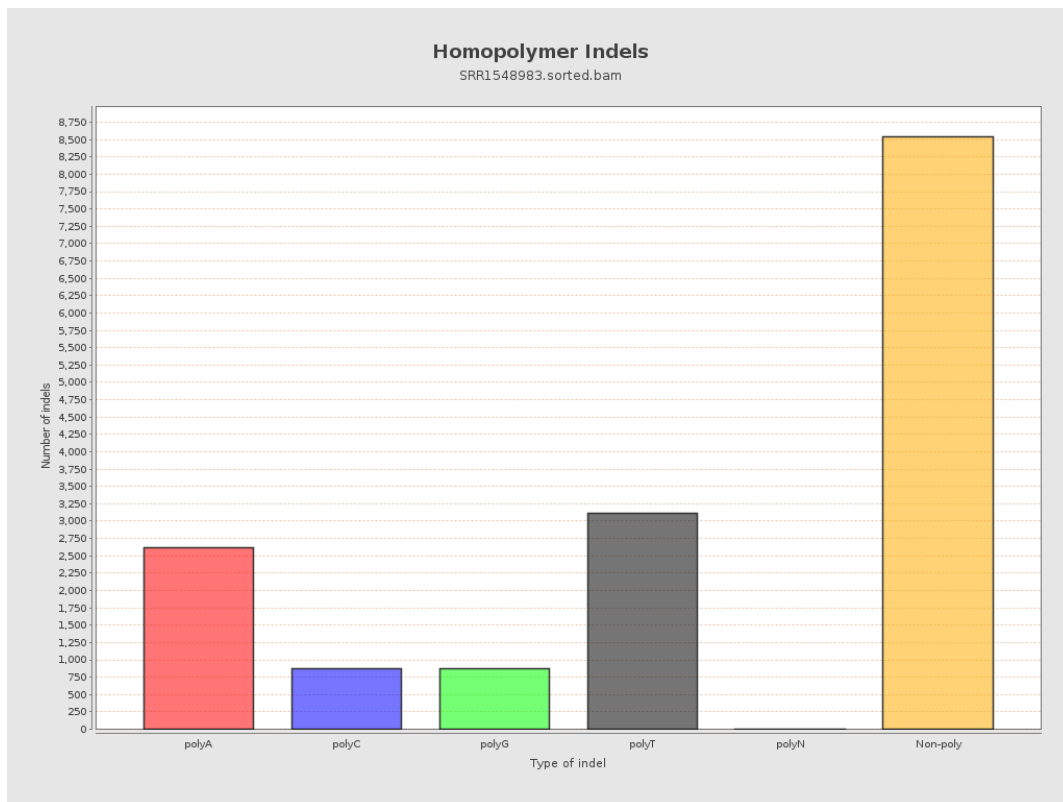
9. Results : Mapped Reads GC-content Distribution



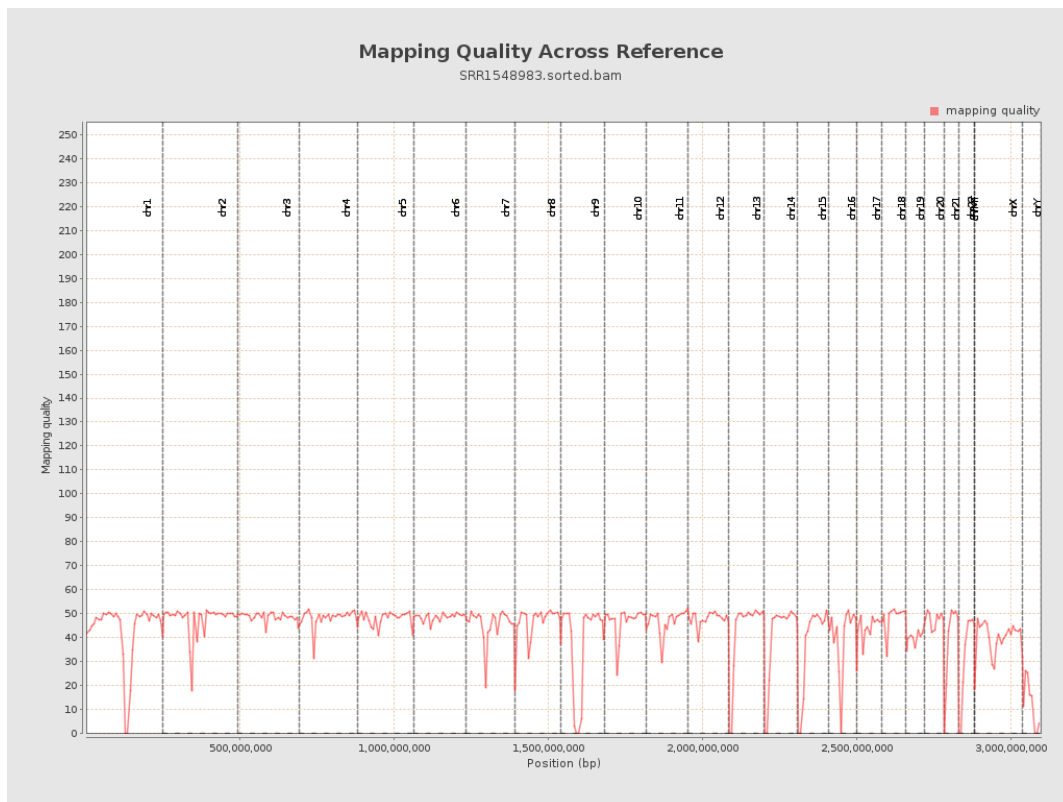
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

