

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 04:28:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548980.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_SRR1548980 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548980.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 04:28:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1548980.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,819,273
Mapped reads	3,016,940 / 44.24%
Unmapped reads	3,802,333 / 55.76%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	64,957 / 0.95%
Duplication rate	1.46%
Clipped reads	205,748 / 3.02%

2.2. ACGT Content

Number/percentage of A's	35,074,804 / 29.35%
Number/percentage of C's	24,324,746 / 20.36%
Number/percentage of T's	35,433,984 / 29.65%
Number/percentage of G's	24,650,794 / 20.63%
Number/percentage of N's	6,506 / 0.01%
GC Percentage	40.99%

2.3. Coverage

Mean	0.0386
Standard Deviation	0.2963

2.4. Mapping Quality

Mean Mapping Quality	43.17
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2.5. Mismatches and indels

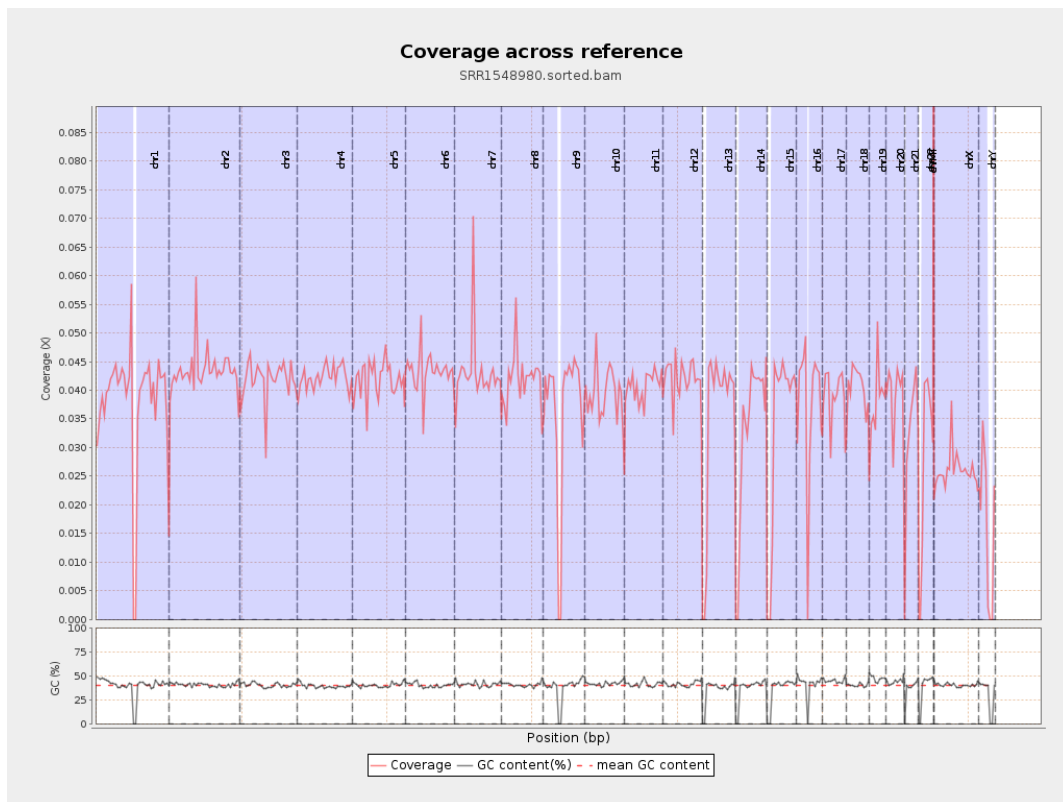
General error rate	0.28%
Mismatches	333,320
Insertions	3,792
Mapped reads with at least one insertion	0.13%
Deletions	11,213
Mapped reads with at least one deletion	0.37%
Homopolymer indels	45.74%

2.6. Chromosome stats

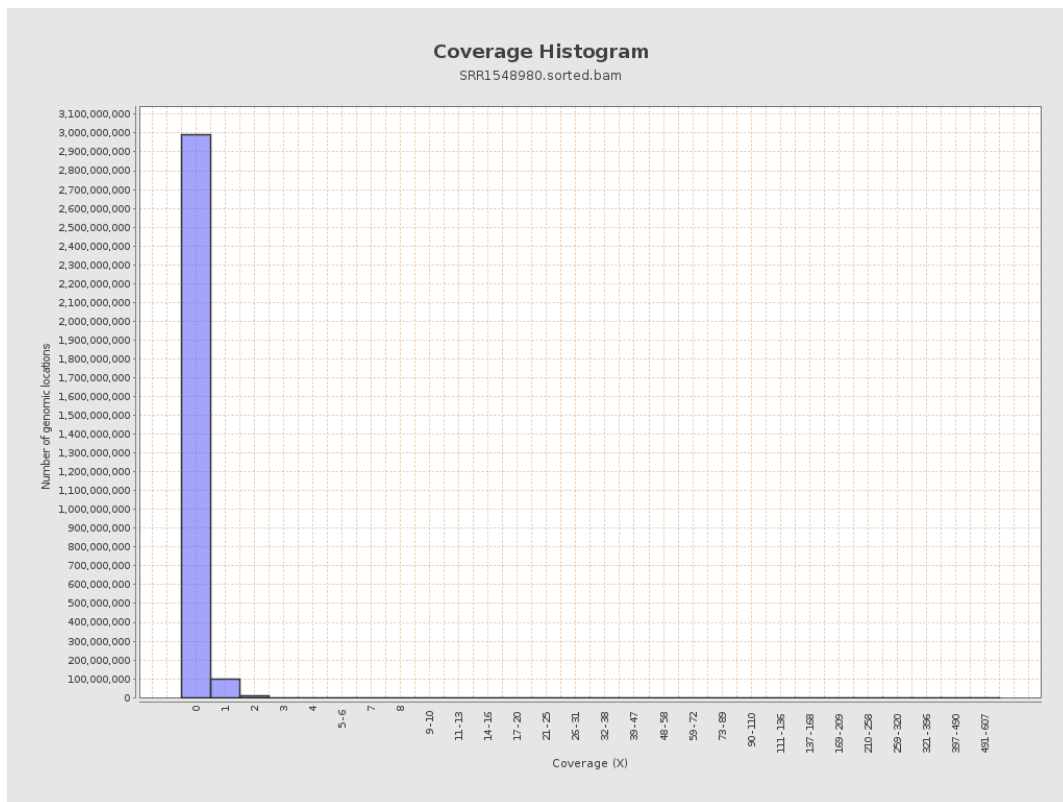
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	9530463	0.0382	0.4892
chr2	243199373	10580713	0.0435	0.2892
chr3	198022430	8299538	0.0419	0.2236
chr4	191154276	8073430	0.0422	0.2285
chr5	180915260	7560679	0.0418	0.2265
chr6	171115067	7409964	0.0433	0.2578
chr7	159138663	6891041	0.0433	0.4452
chr8	146364022	6131644	0.0419	0.387

chr9	141213431	5146193	0.0364	0.2631
chr10	135534747	5344289	0.0394	0.2525
chr11	135006516	5480082	0.0406	0.2705
chr12	133851895	5622241	0.042	0.2294
chr13	115169878	4054894	0.0352	0.2043
chr14	107349540	3517622	0.0328	0.2164
chr15	102531392	3502193	0.0342	0.2016
chr16	90354753	3402106	0.0377	0.2223
chr17	81195210	3143475	0.0387	0.2279
chr18	78077248	3172463	0.0406	0.4222
chr19	59128983	2269382	0.0384	0.4251
chr20	63025520	2456103	0.039	0.2208
chr21	48129895	1558804	0.0324	0.2134
chr22	51304566	1384375	0.027	0.1891
chrMT	16571	2334	0.1408	0.4521
chrX	155270560	4038521	0.026	0.2025
chrY	59373566	932439	0.0157	0.1683

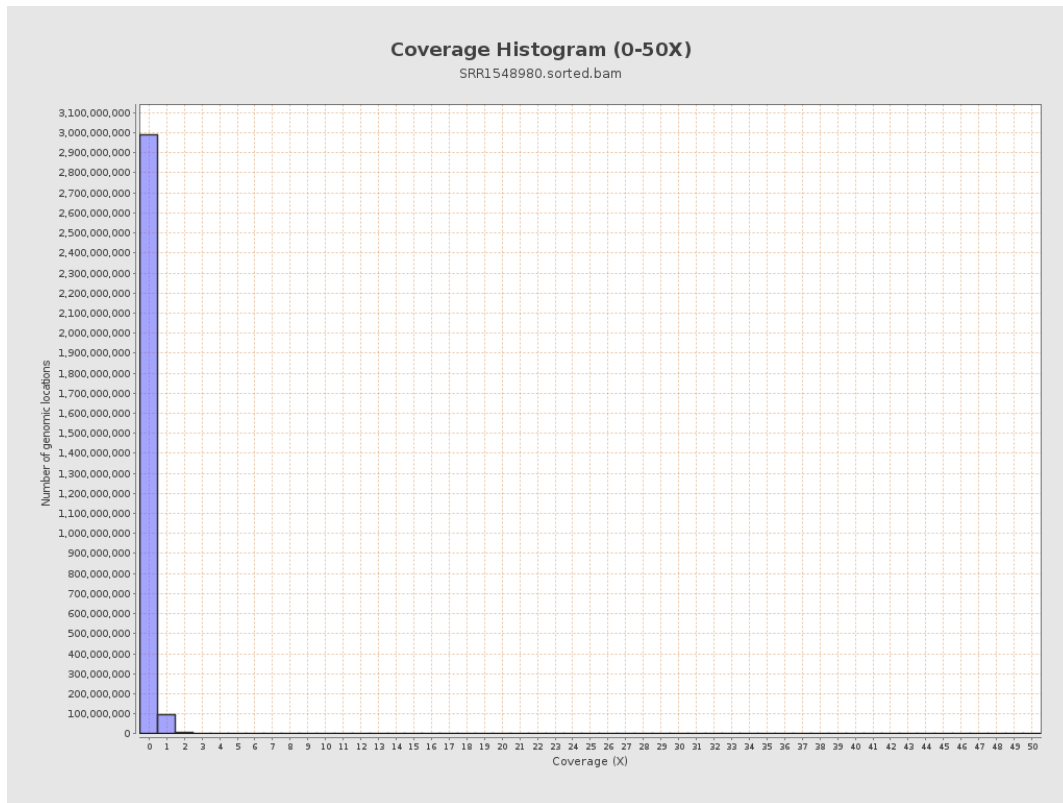
3. Results : Coverage across reference



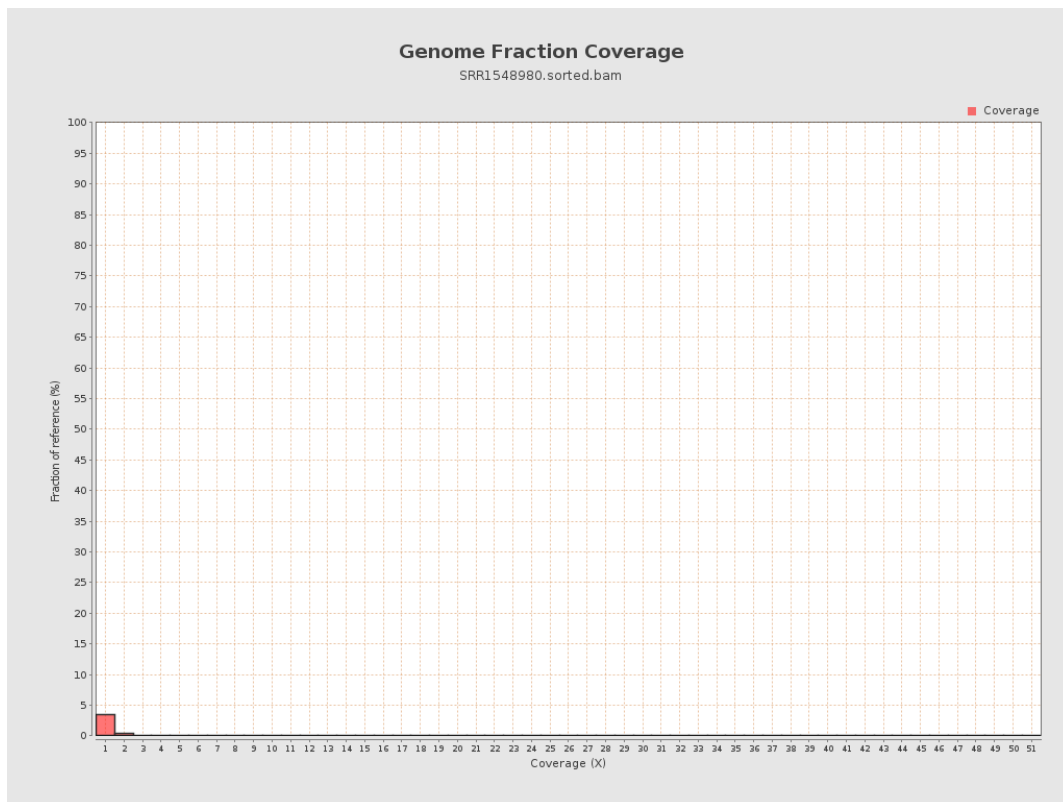
4. Results : Coverage Histogram



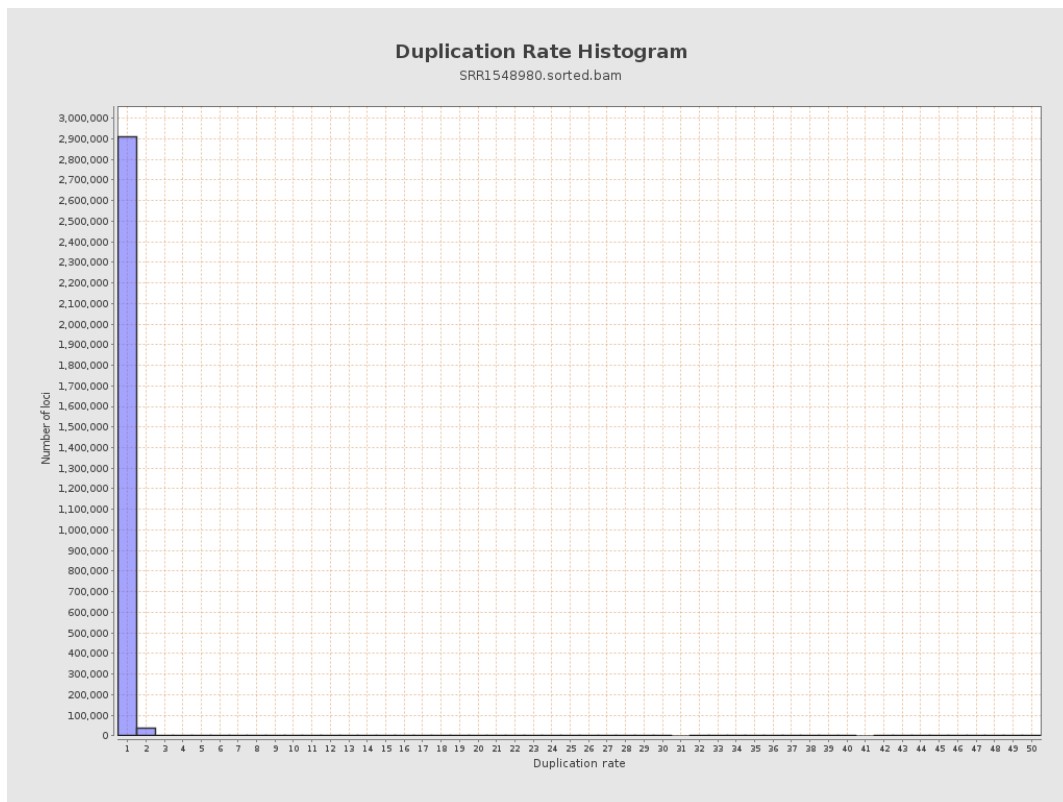
5. Results : Coverage Histogram (0-50X)



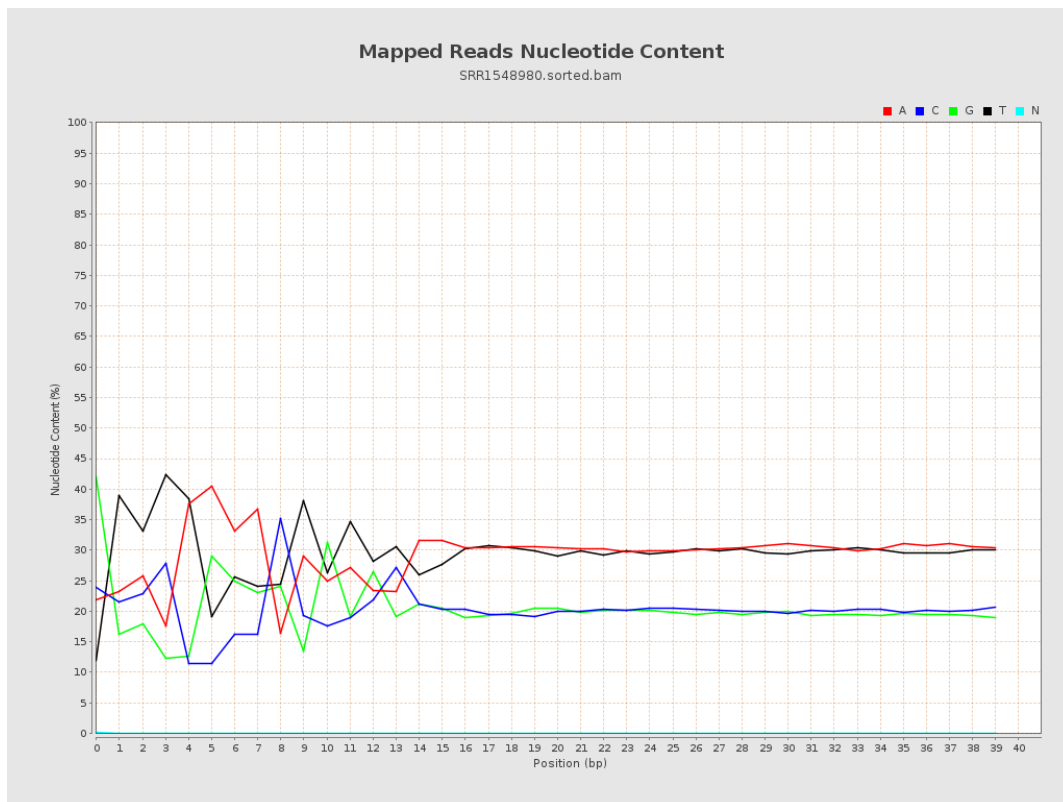
6. Results : Genome Fraction Coverage



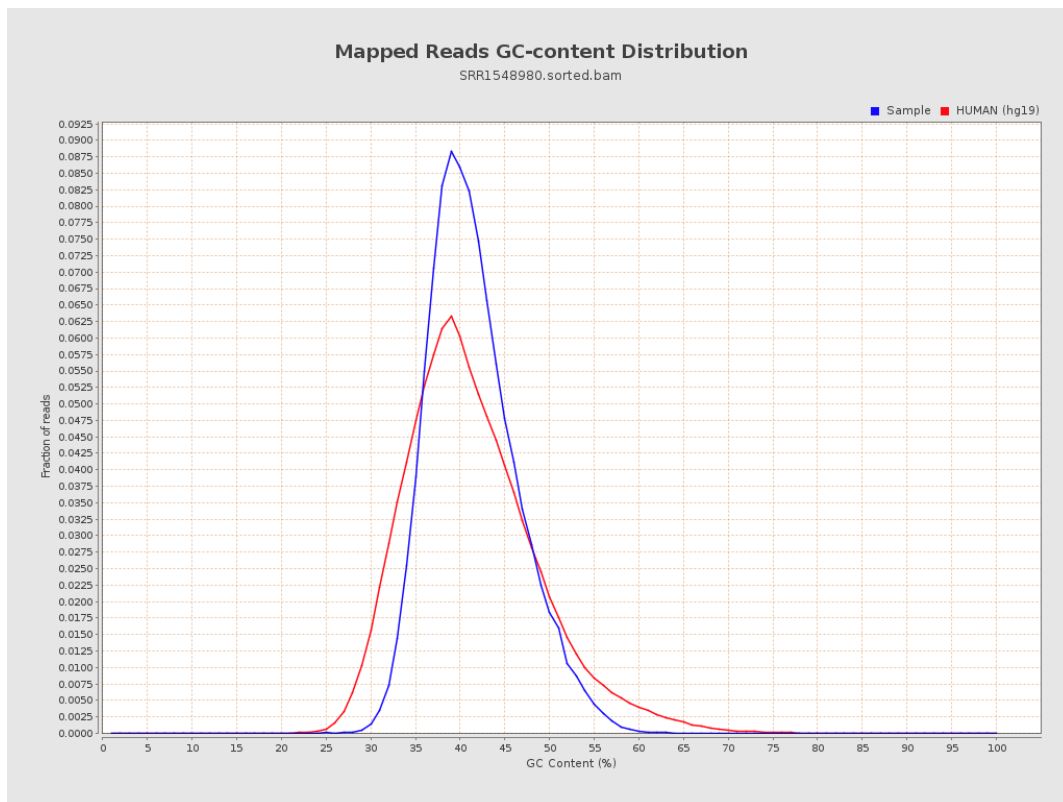
7. Results : Duplication Rate Histogram



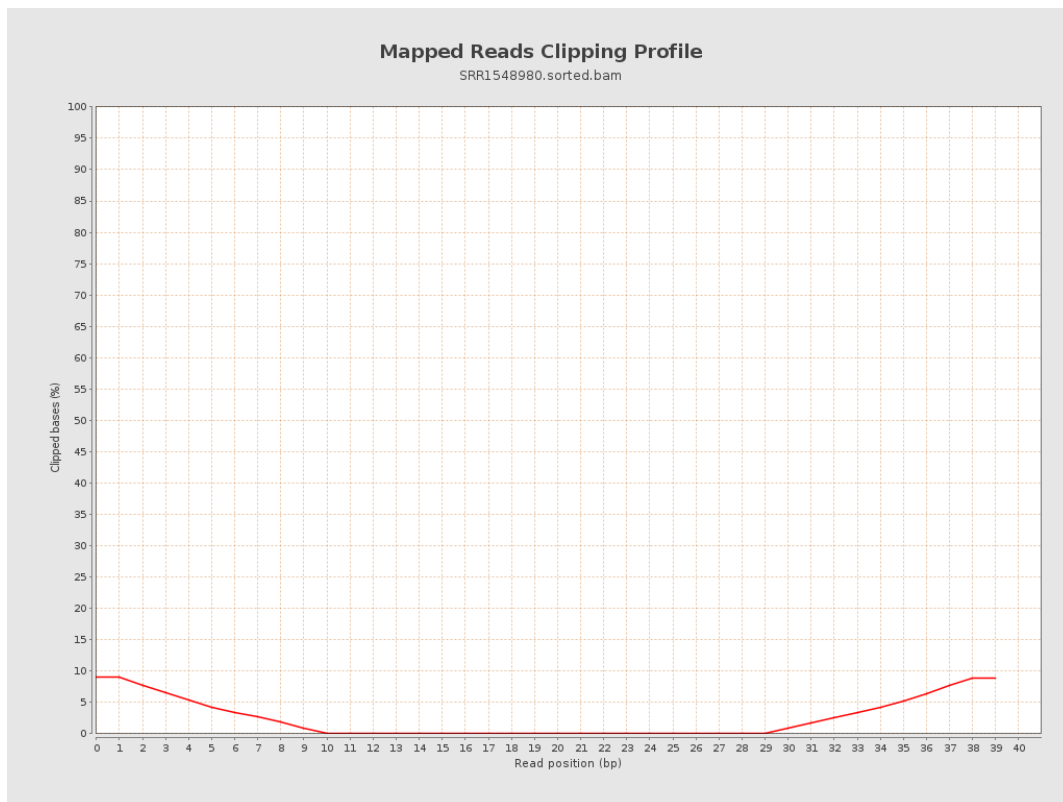
8. Results : Mapped Reads Nucleotide Content



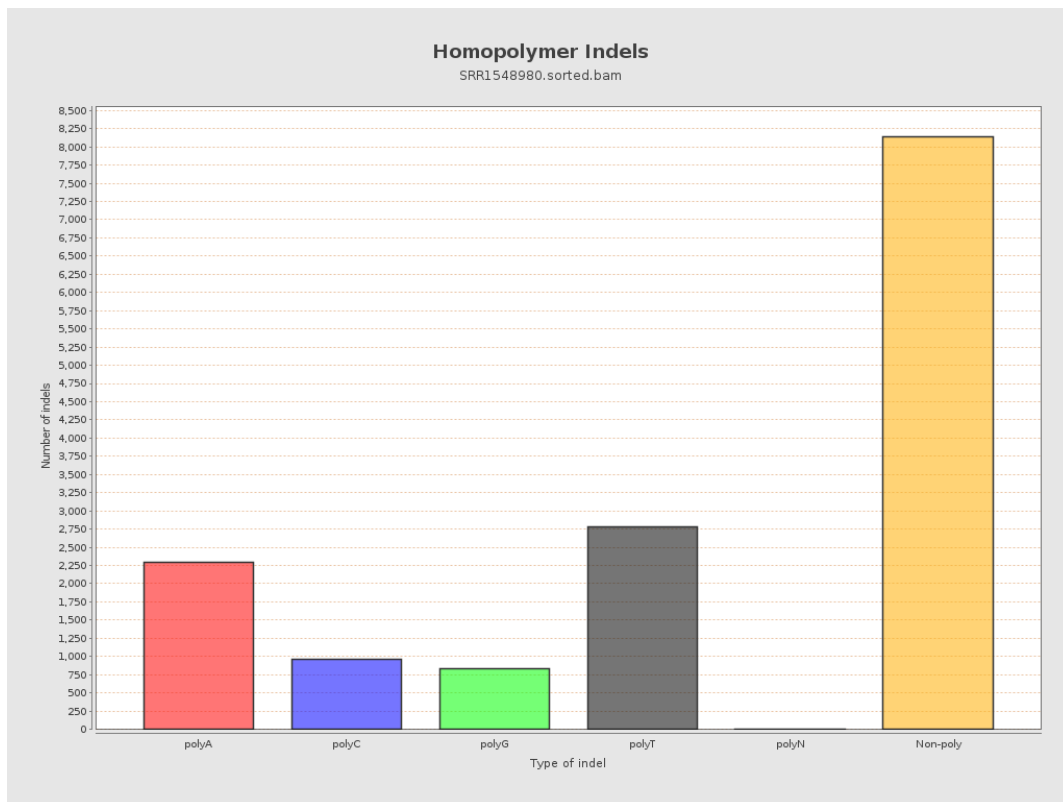
9. Results : Mapped Reads GC-content Distribution



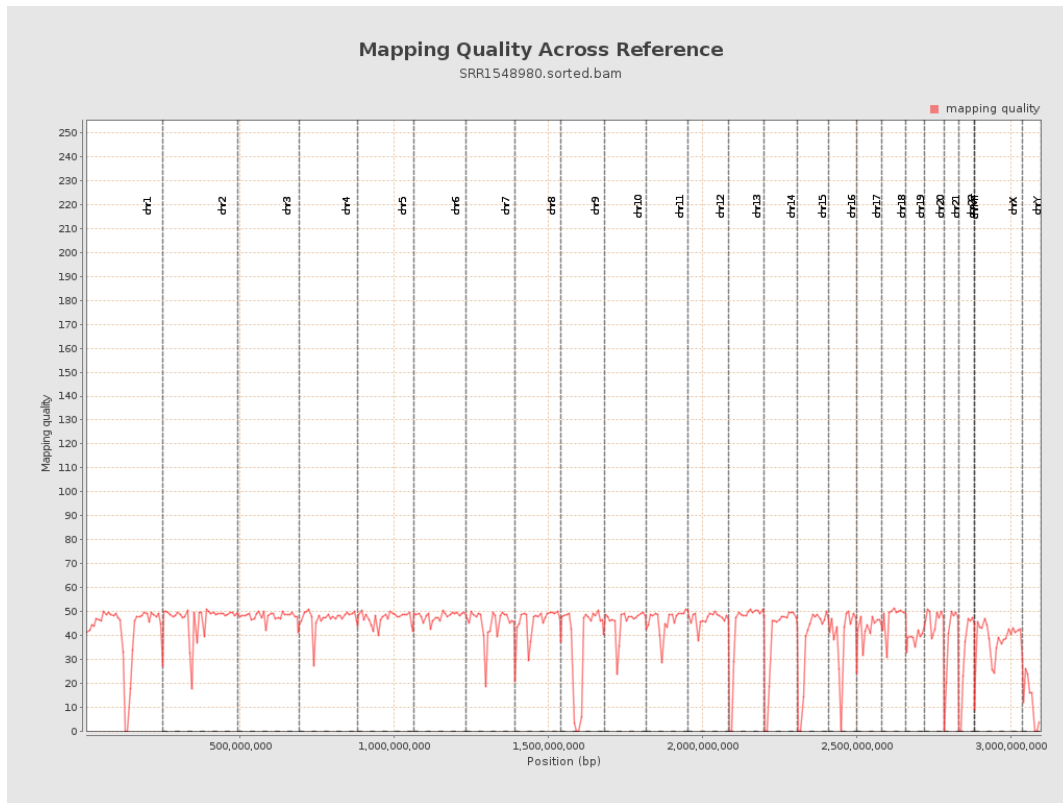
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

