

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 10:53:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548938.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_SRR1548938 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548938.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 10:53:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1548938.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,452,628
Mapped reads	7,357,570 / 87.04%
Unmapped reads	1,095,058 / 12.96%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	254,615 / 3.01%
Duplication rate	2.45%
Clipped reads	563,719 / 6.67%

2.2. ACGT Content

Number/percentage of A's	85,922,308 / 29.51%
Number/percentage of C's	59,596,173 / 20.47%
Number/percentage of T's	86,194,092 / 29.6%
Number/percentage of G's	59,475,190 / 20.42%
Number/percentage of N's	2,697 / 0%
GC Percentage	40.89%

2.3. Coverage

Mean	0.0941
Standard Deviation	1.1069

2.4. Mapping Quality

Mean Mapping Quality	41.94
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2.5. Mismatches and indels

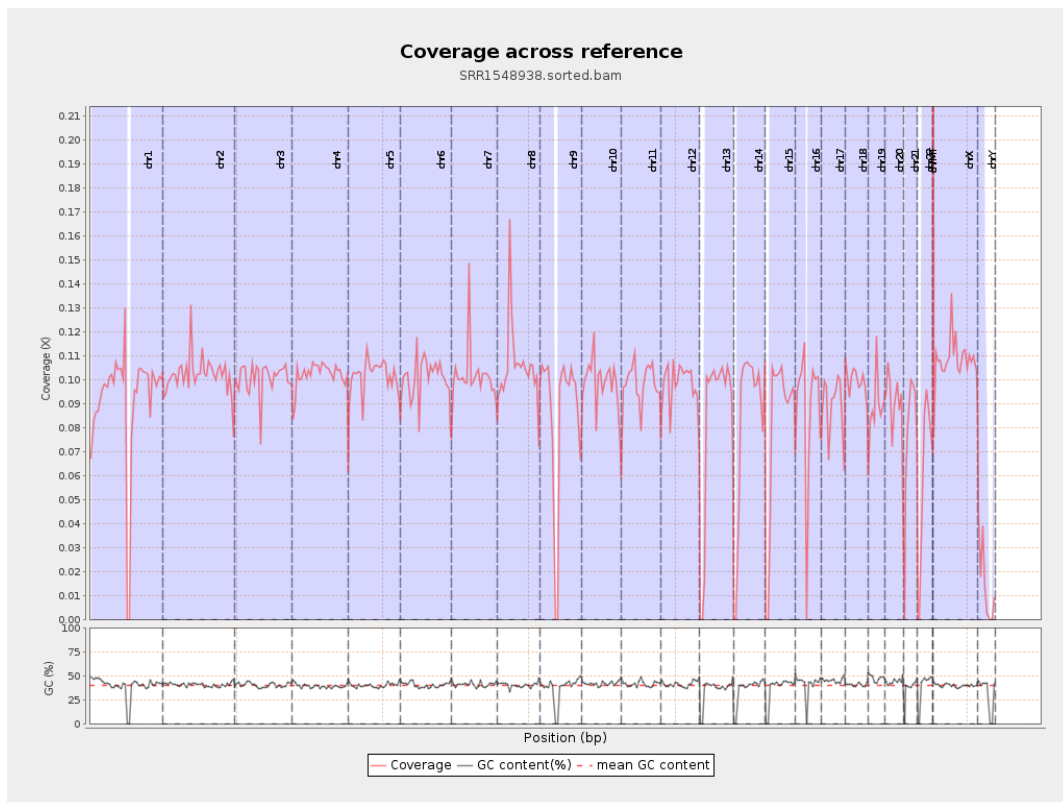
General error rate	0.28%
Mismatches	809,799
Insertions	9,631
Mapped reads with at least one insertion	0.13%
Deletions	24,110
Mapped reads with at least one deletion	0.33%
Homopolymer indels	41.01%

2.6. Chromosome stats

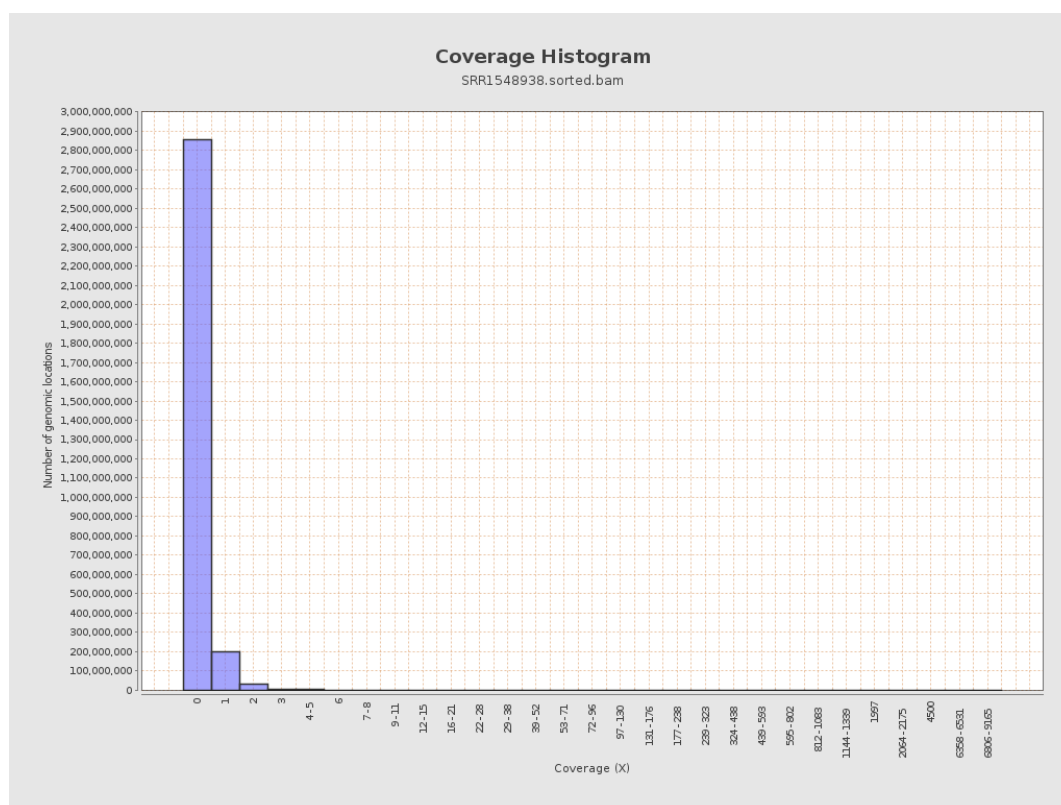
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	22793893	0.0914	1.0224
chr2	243199373	24794993	0.102	0.5402
chr3	198022430	19925050	0.1006	0.3724
chr4	191154276	19518918	0.1021	0.3867
chr5	180915260	18289762	0.1011	0.3808
chr6	171115067	17262623	0.1009	0.4193
chr7	159138663	16109952	0.1012	0.7786
chr8	146364022	15460401	0.1056	4.4371

chr9	141213431	12159851	0.0861	0.5073
chr10	135534747	13415570	0.099	0.4935
chr11	135006516	13243116	0.0981	0.5817
chr12	133851895	13188297	0.0985	0.383
chr13	115169878	9642188	0.0837	0.3346
chr14	107349540	8944547	0.0833	0.4092
chr15	102531392	8217421	0.0801	0.3309
chr16	90354753	7754477	0.0858	0.3772
chr17	81195210	7298884	0.0899	0.3785
chr18	78077248	7761875	0.0994	0.9047
chr19	59128983	5293558	0.0895	0.8957
chr20	63025520	5720597	0.0908	0.3667
chr21	48129895	3695202	0.0768	0.3653
chr22	51304566	3084177	0.0601	0.3361
chrMT	16571	13876	0.8374	1.2154
chrX	155270560	16777590	0.1081	0.4719
chrY	59373566	855662	0.0144	0.193

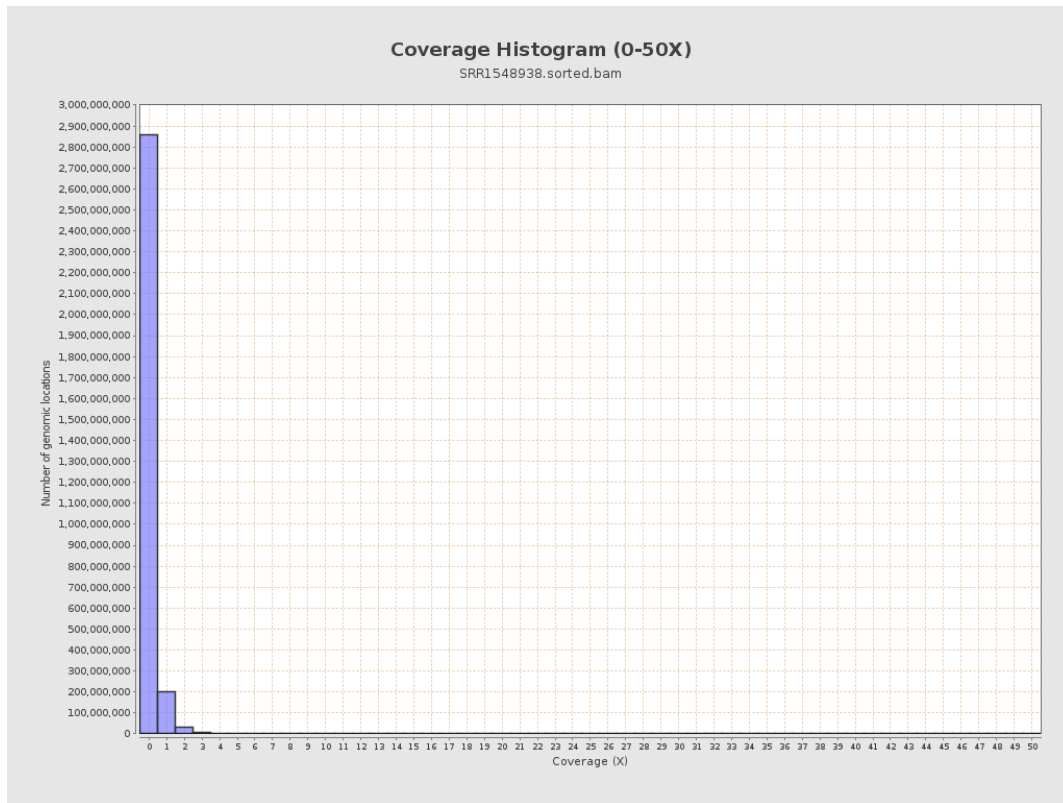
3. Results : Coverage across reference



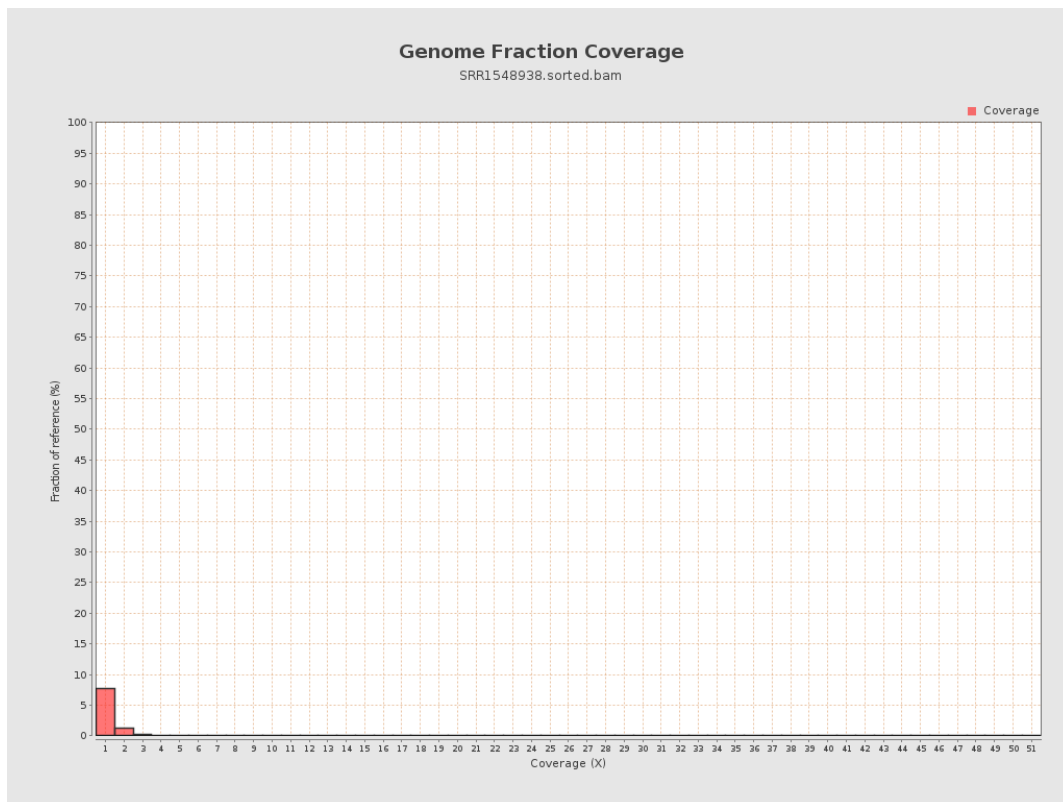
4. Results : Coverage Histogram



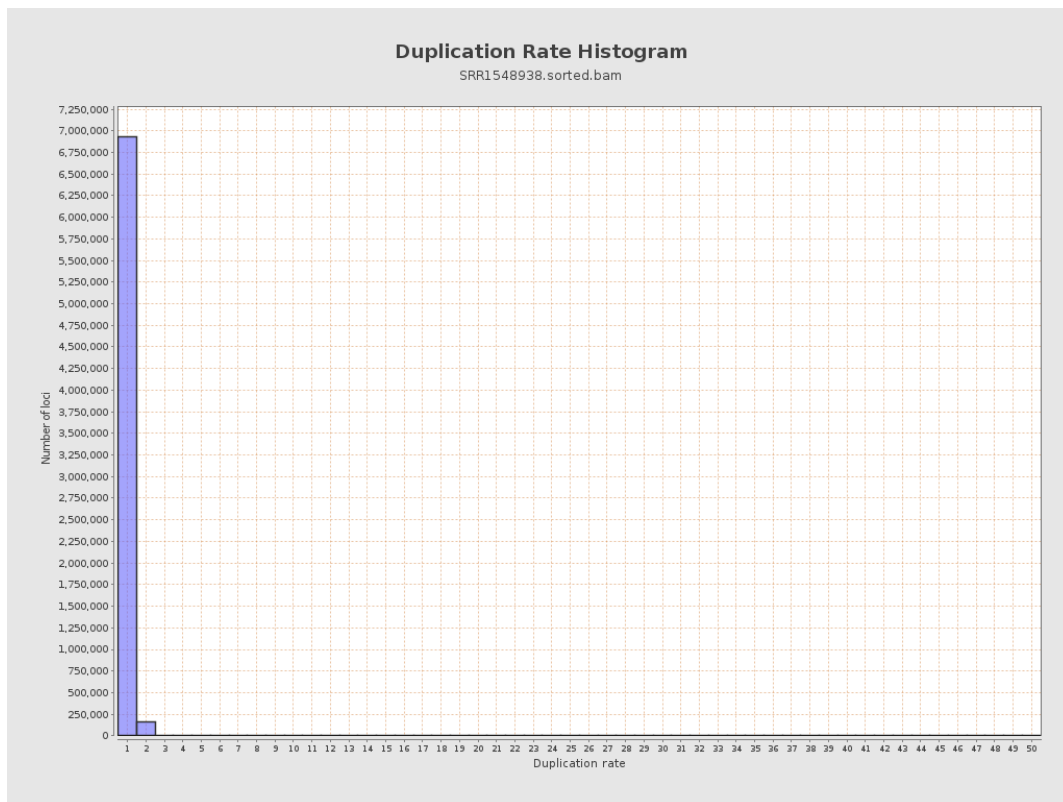
5. Results : Coverage Histogram (0-50X)



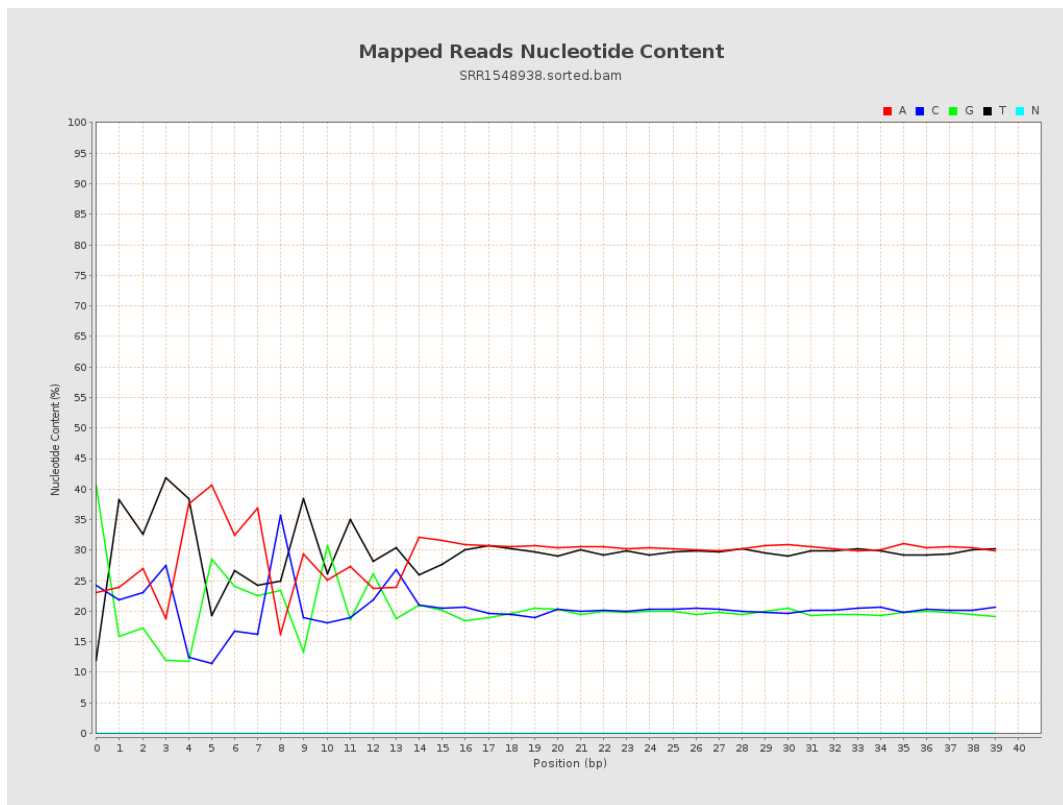
6. Results : Genome Fraction Coverage



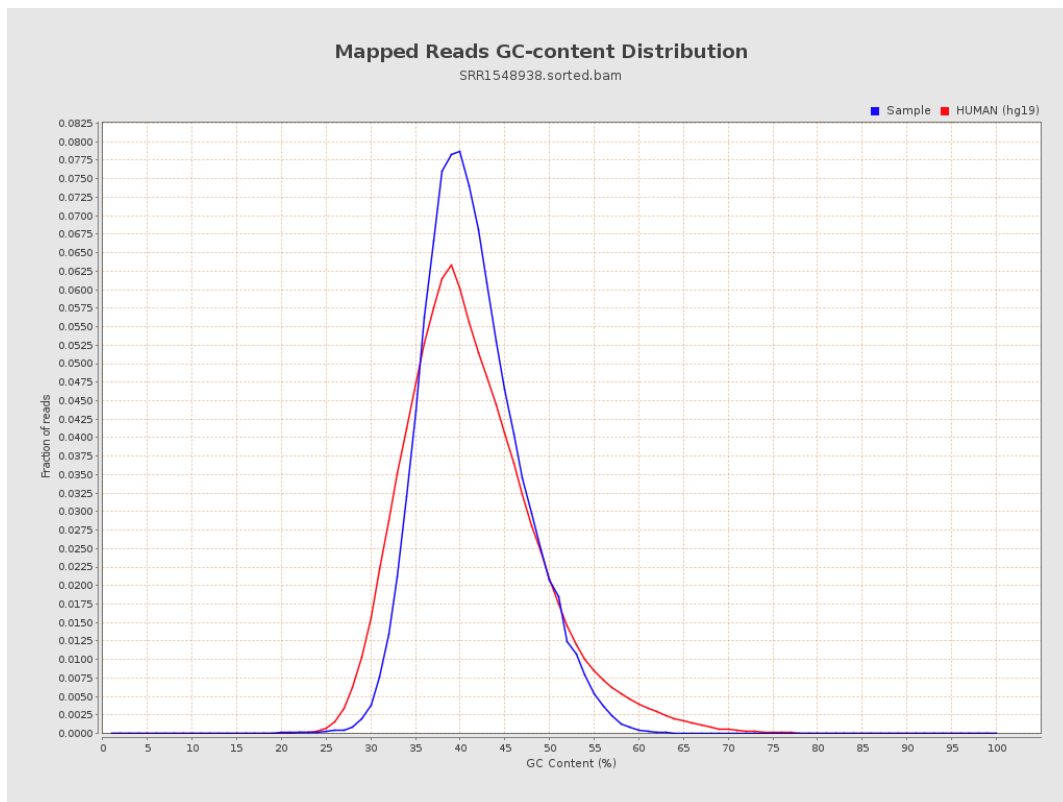
7. Results : Duplication Rate Histogram



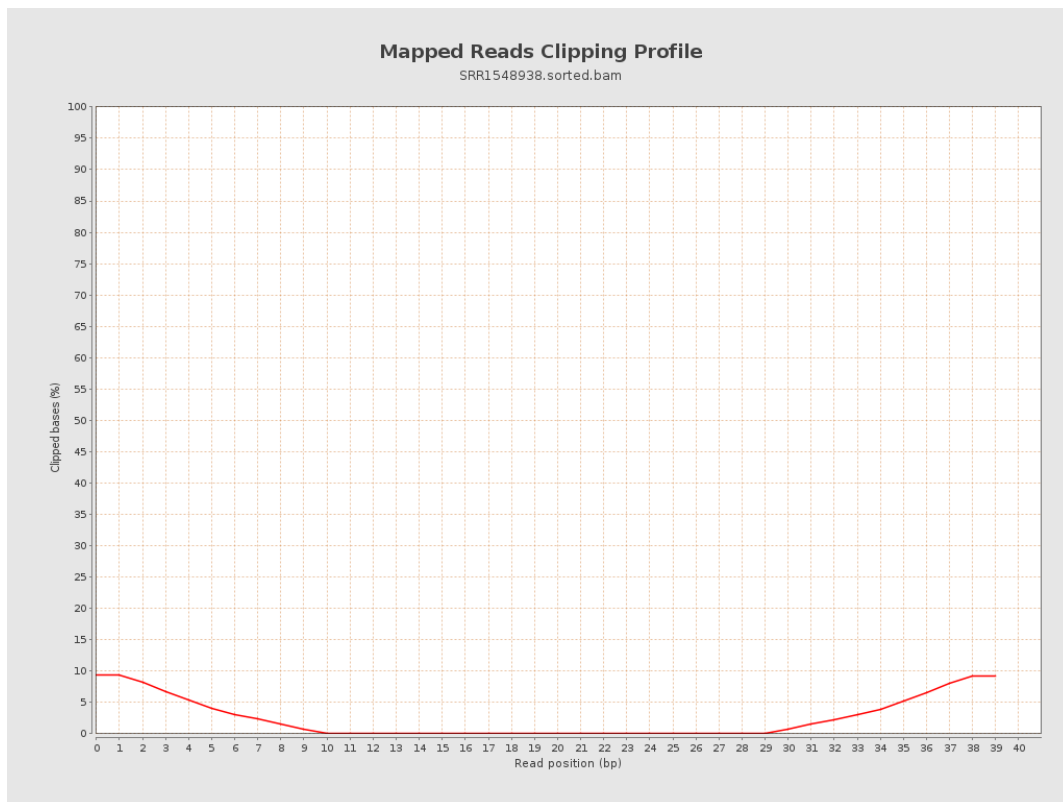
8. Results : Mapped Reads Nucleotide Content



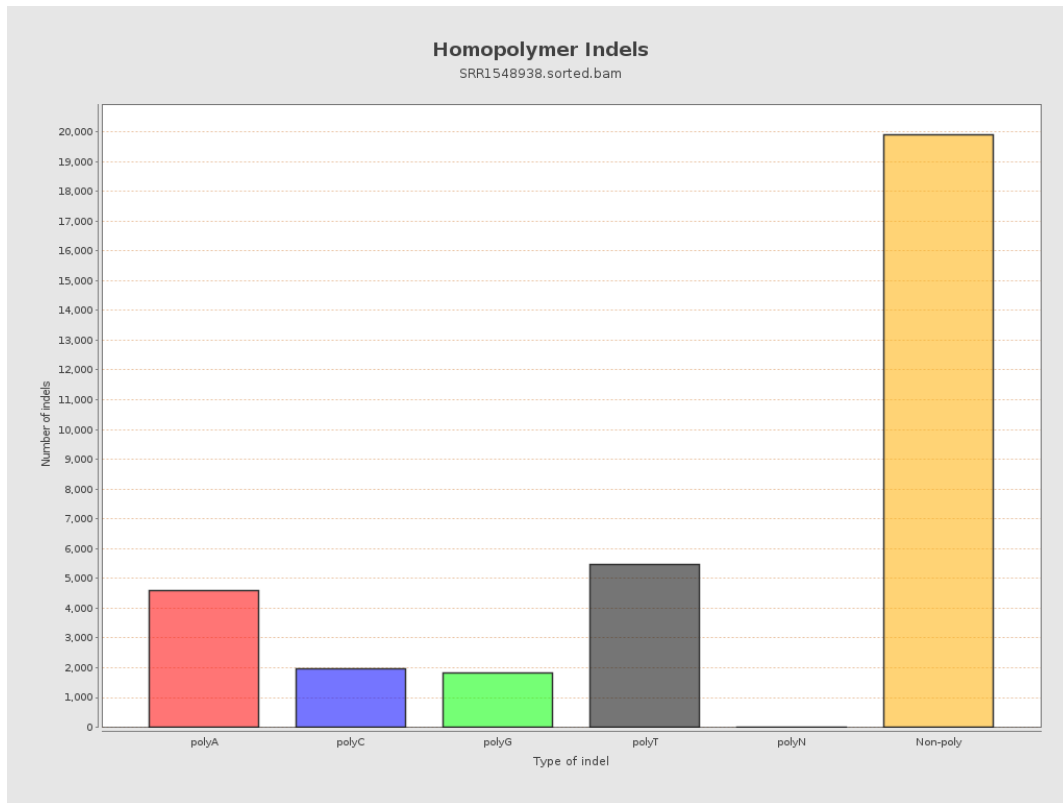
9. Results : Mapped Reads GC-content Distribution



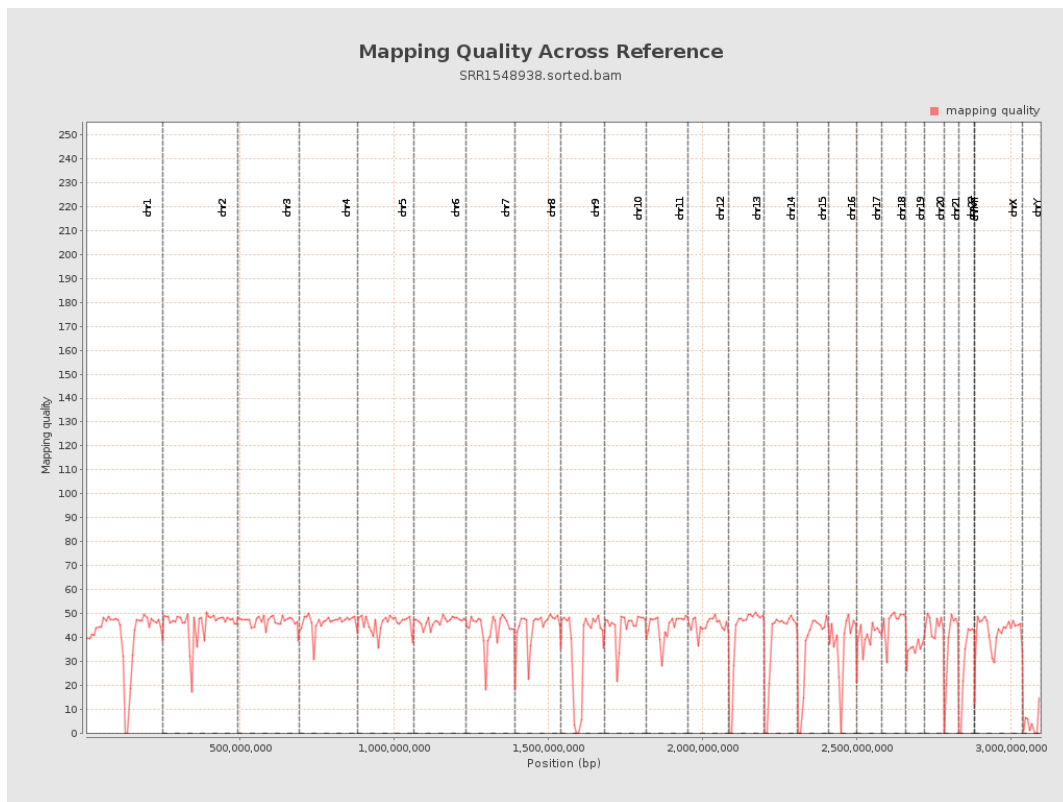
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

