

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 03:57:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549116.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_SRR1549116 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549116.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 03:57:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549116.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,202,628
Mapped reads	6,096,789 / 59.76%
Unmapped reads	4,105,839 / 40.24%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	162,970 / 1.6%
Duplication rate	1.81%
Clipped reads	327,681 / 3.21%

2.2. ACGT Content

Number/percentage of A's	72,404,133 / 29.93%
Number/percentage of C's	48,234,019 / 19.94%
Number/percentage of T's	72,753,930 / 30.07%
Number/percentage of G's	48,508,033 / 20.05%
Number/percentage of N's	10,013 / 0%
GC Percentage	39.99%

2.3. Coverage

Mean	0.0782
Standard Deviation	0.5055

2.4. Mapping Quality

Mean Mapping Quality	44.16
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2.5. Mismatches and indels

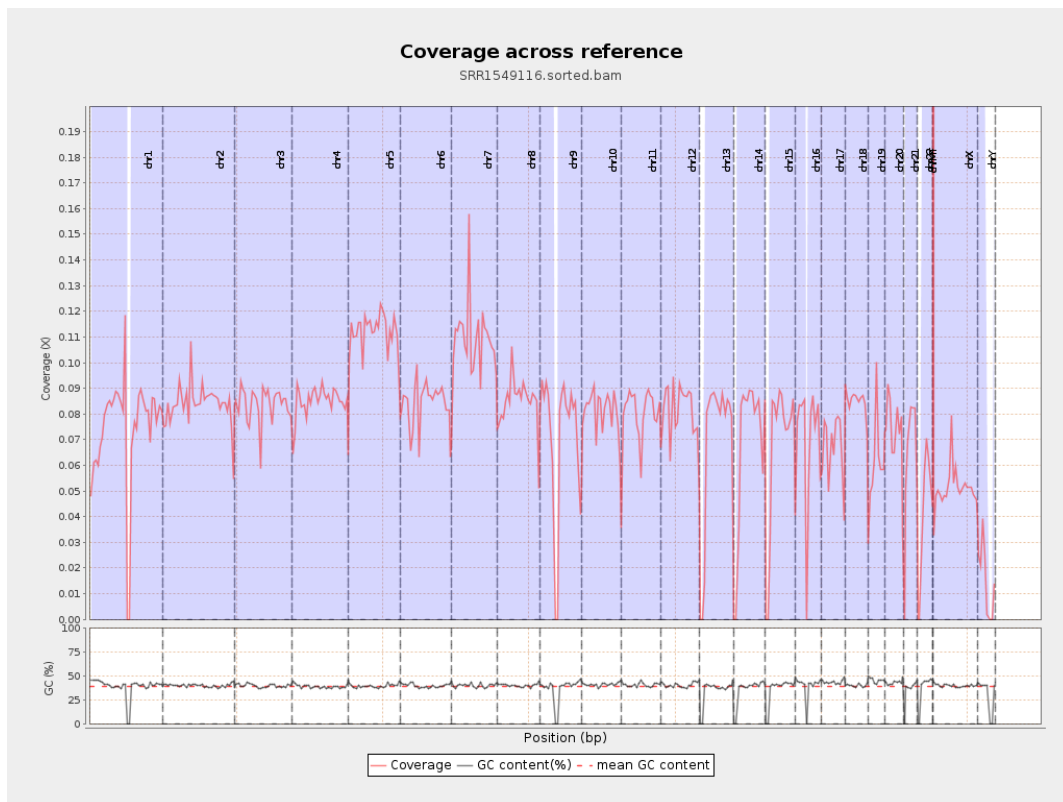
General error rate	0.31%
Mismatches	745,884
Insertions	6,389
Mapped reads with at least one insertion	0.1%
Deletions	18,791
Mapped reads with at least one deletion	0.31%
Homopolymer indels	46.48%

2.6. Chromosome stats

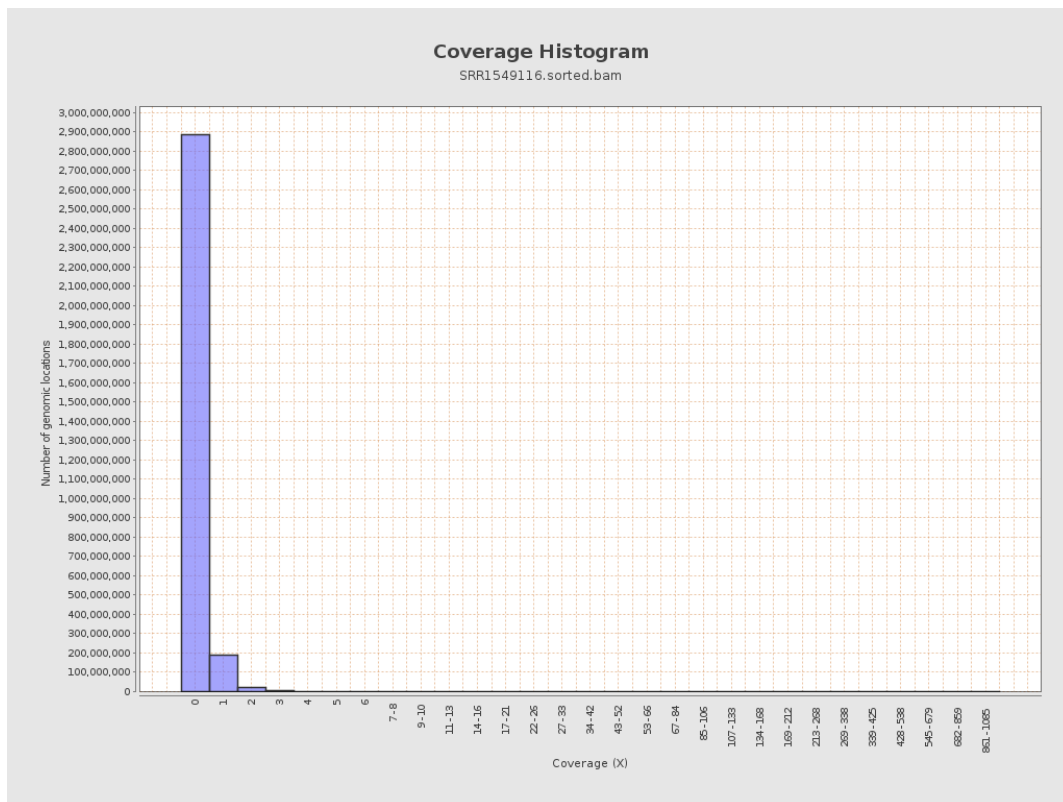
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	18501842	0.0742	0.8674
chr2	243199373	20485180	0.0842	0.4574
chr3	198022430	16581861	0.0837	0.3228
chr4	191154276	16291383	0.0852	0.3283
chr5	180915260	20108558	0.1111	0.3768
chr6	171115067	14473058	0.0846	0.3661
chr7	159138663	17272400	0.1085	0.893
chr8	146364022	12434477	0.085	0.6478

chr9	141213431	10040102	0.0711	0.4395
chr10	135534747	11022345	0.0813	0.4143
chr11	135006516	10850859	0.0804	0.4599
chr12	133851895	10909401	0.0815	0.3348
chr13	115169878	7985364	0.0693	0.2886
chr14	107349540	7322577	0.0682	0.3665
chr15	102531392	6793419	0.0663	0.2842
chr16	90354753	6153941	0.0681	0.3232
chr17	81195210	5502174	0.0678	0.3199
chr18	78077248	6649655	0.0852	0.8993
chr19	59128983	3682637	0.0623	0.7735
chr20	63025520	4720552	0.0749	0.3205
chr21	48129895	3089877	0.0642	0.3114
chr22	51304566	2159455	0.0421	0.2309
chrMT	16571	32951	1.9885	2.682
chrX	155270560	7956555	0.0512	0.3145
chrY	59373566	912931	0.0154	0.1582

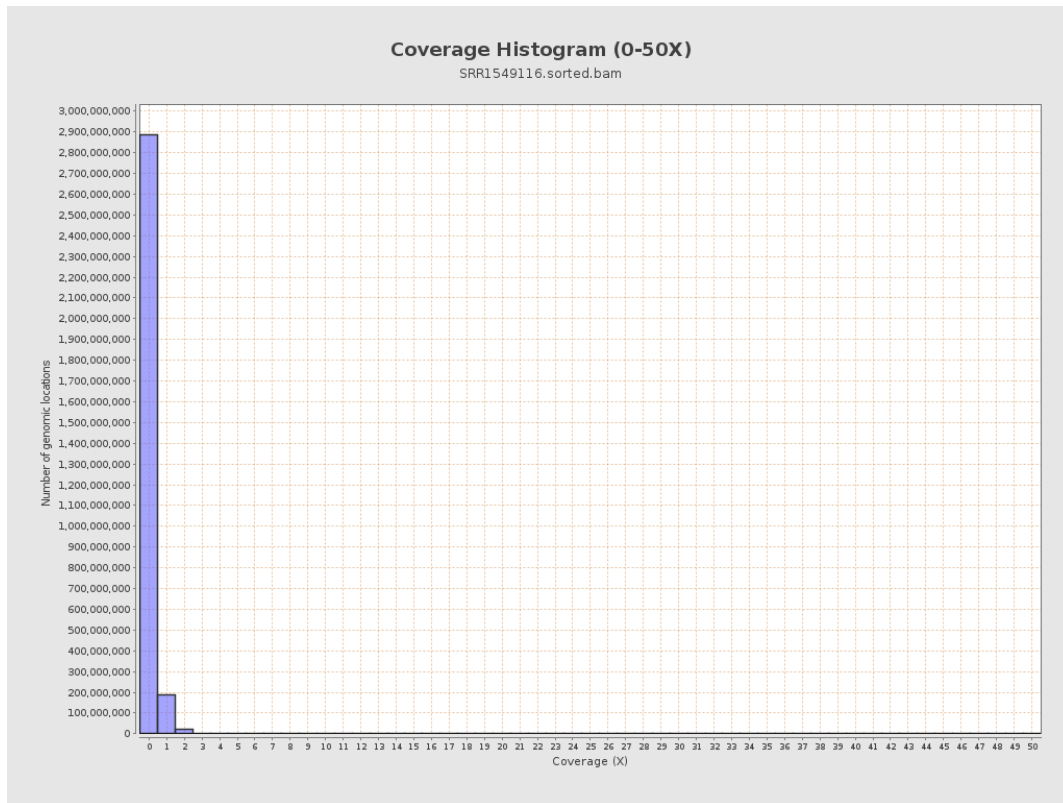
3. Results : Coverage across reference



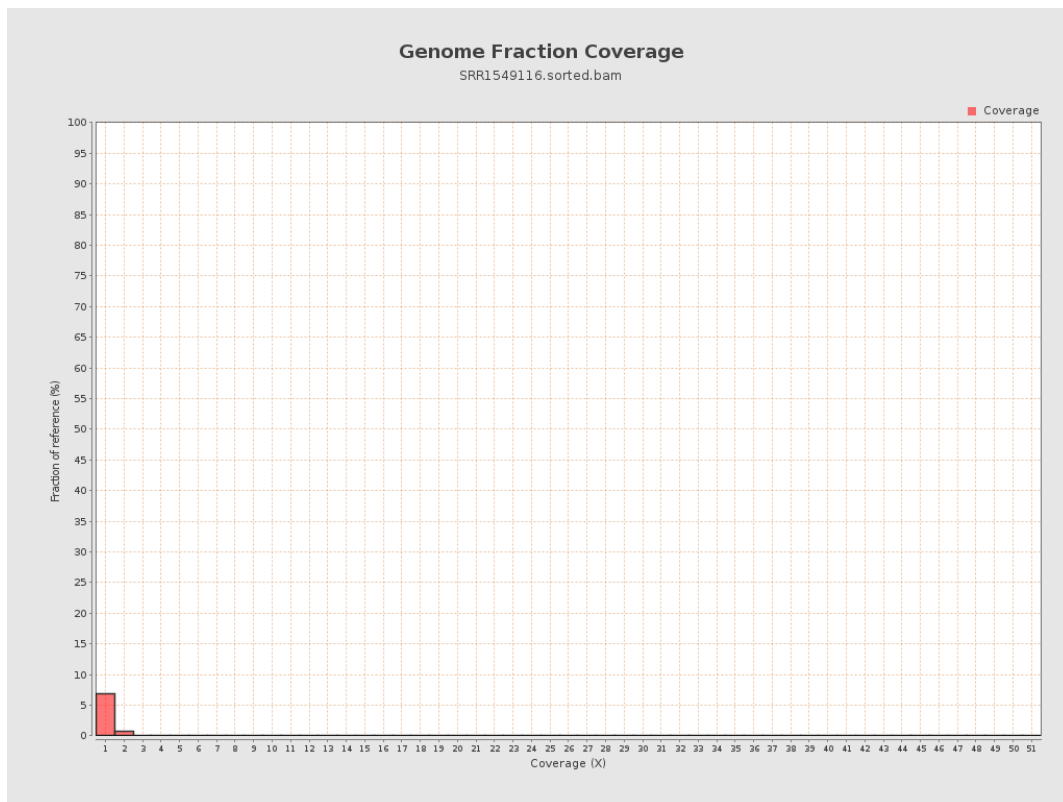
4. Results : Coverage Histogram



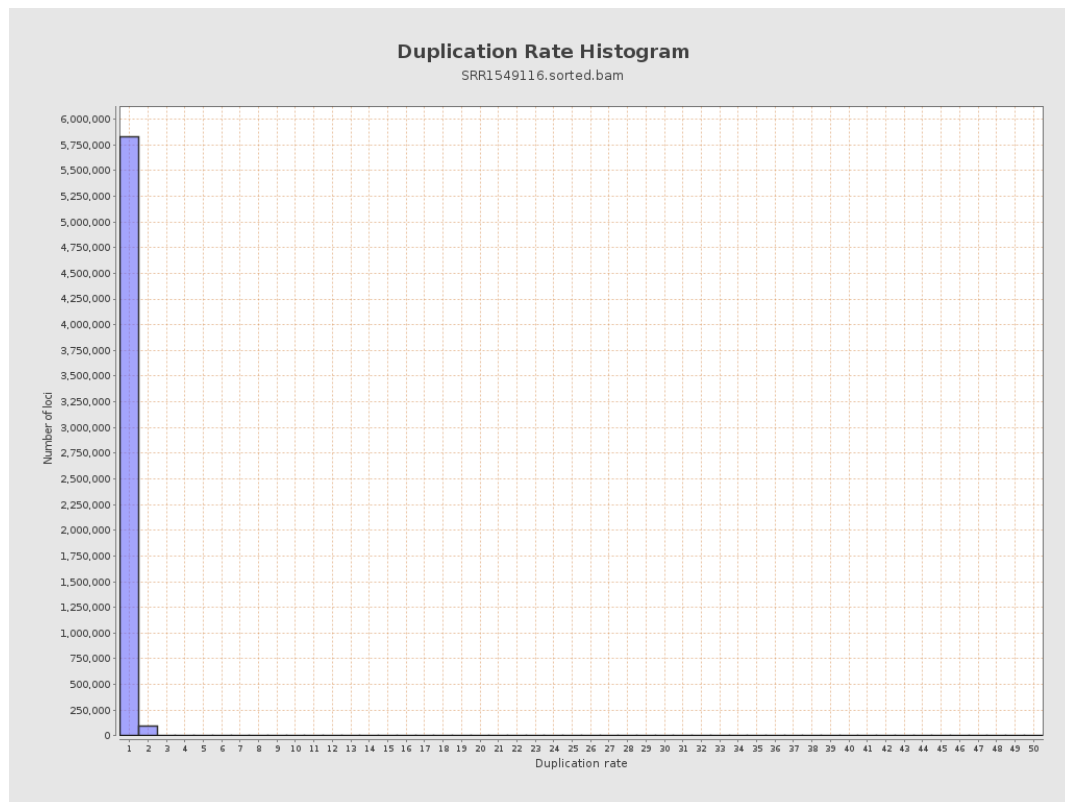
5. Results : Coverage Histogram (0-50X)



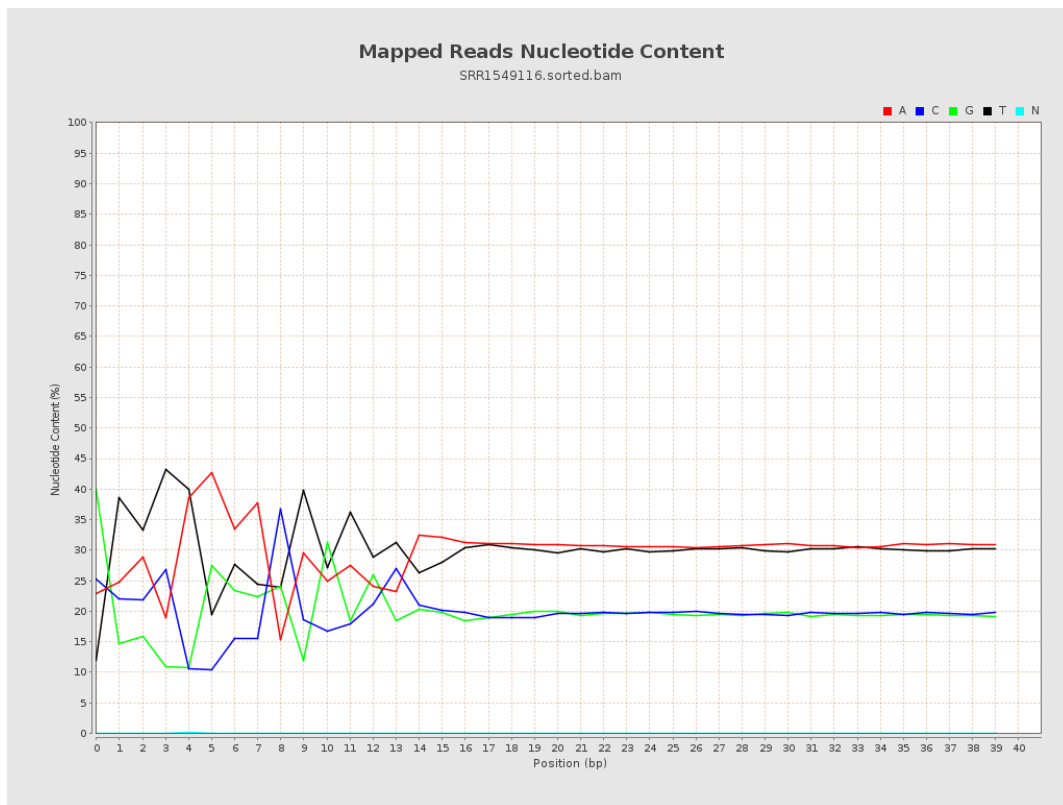
6. Results : Genome Fraction Coverage



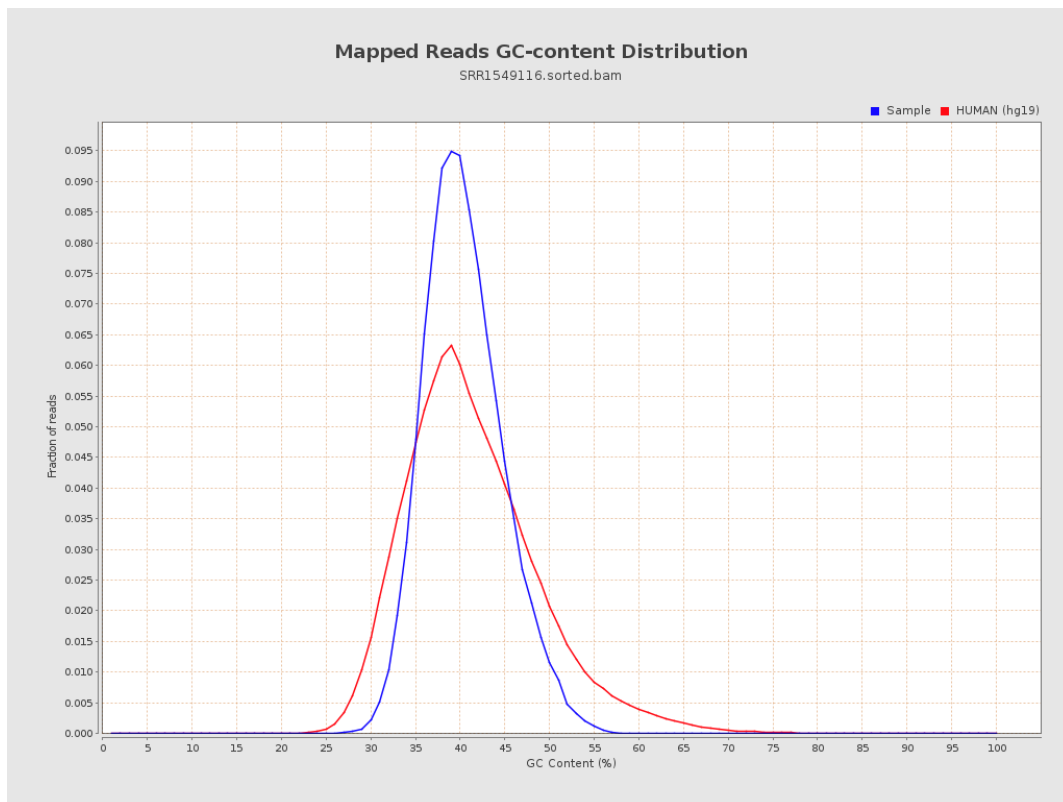
7. Results : Duplication Rate Histogram



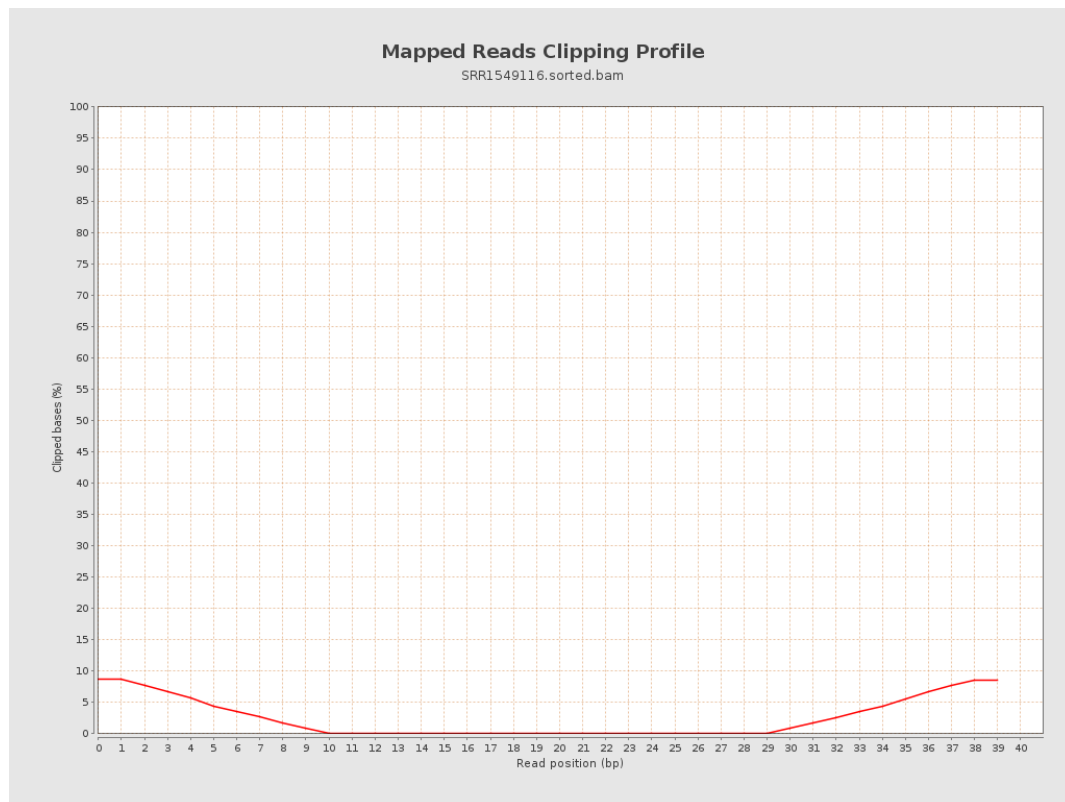
8. Results : Mapped Reads Nucleotide Content



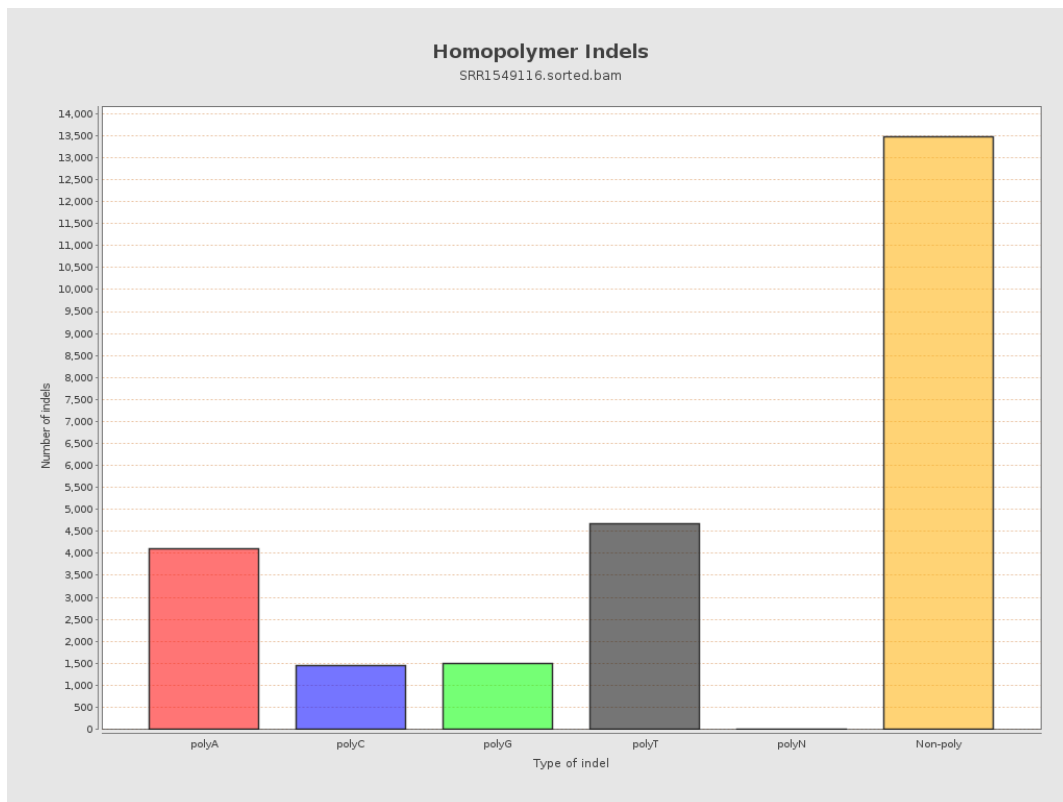
9. Results : Mapped Reads GC-content Distribution



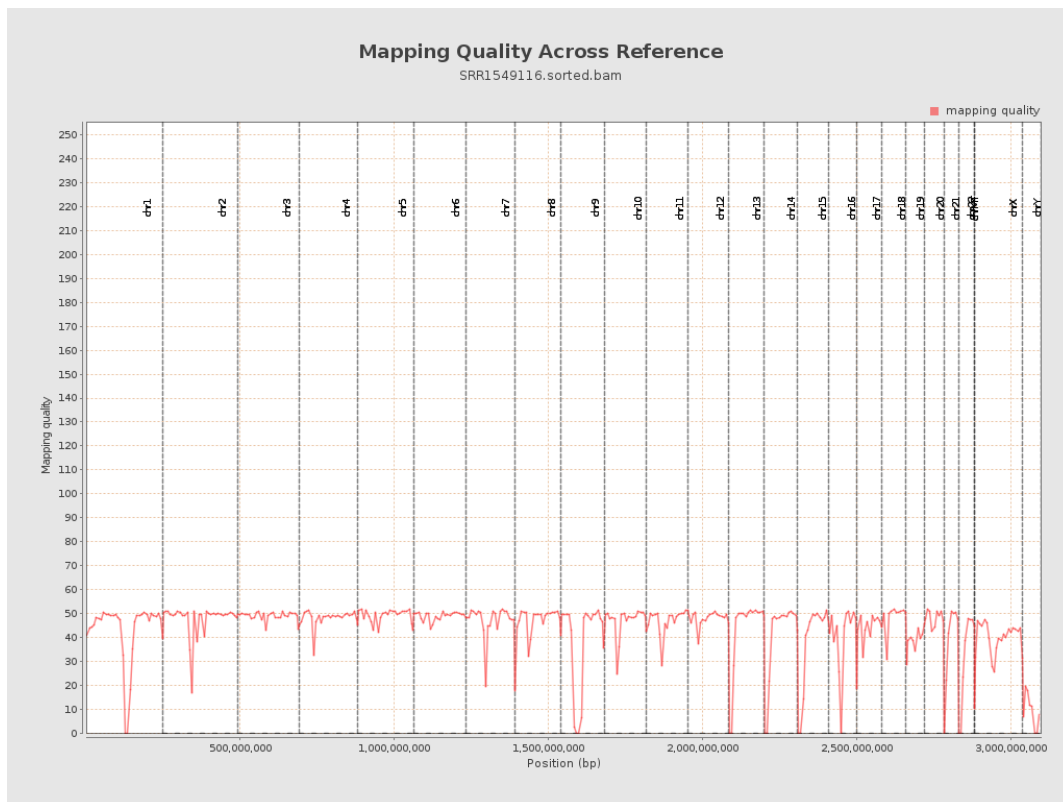
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

