

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 21:27:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549084.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_SRR1549084 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549084.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 21:27:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549084.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,653,152
Mapped reads	8,387,707 / 86.89%
Unmapped reads	1,265,445 / 13.11%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	293,421 / 3.04%
Duplication rate	1.98%
Clipped reads	530,358 / 5.49%

2.2. ACGT Content

Number/percentage of A's	100,501,764 / 30.23%
Number/percentage of C's	65,772,811 / 19.78%
Number/percentage of T's	101,838,152 / 30.63%
Number/percentage of G's	64,254,476 / 19.33%
Number/percentage of N's	83,062 / 0.02%
GC Percentage	39.11%

2.3. Coverage

Mean	0.1074
Standard Deviation	0.9235

2.4. Mapping Quality

Mean Mapping Quality	43.66
----------------------	-------

2.5. Mismatches and indels

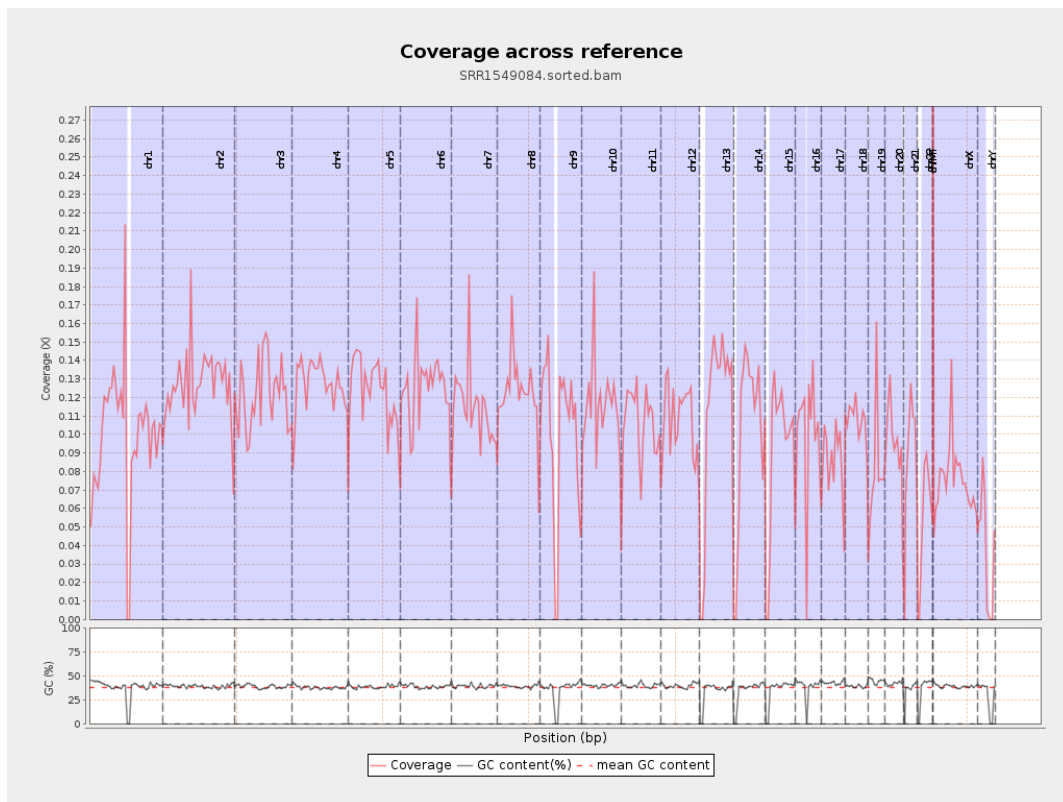
General error rate	0.43%
Mismatches	1,403,538
Insertions	9,226
Mapped reads with at least one insertion	0.11%
Deletions	26,040
Mapped reads with at least one deletion	0.31%
Homopolymer indels	45.05%

2.6. Chromosome stats

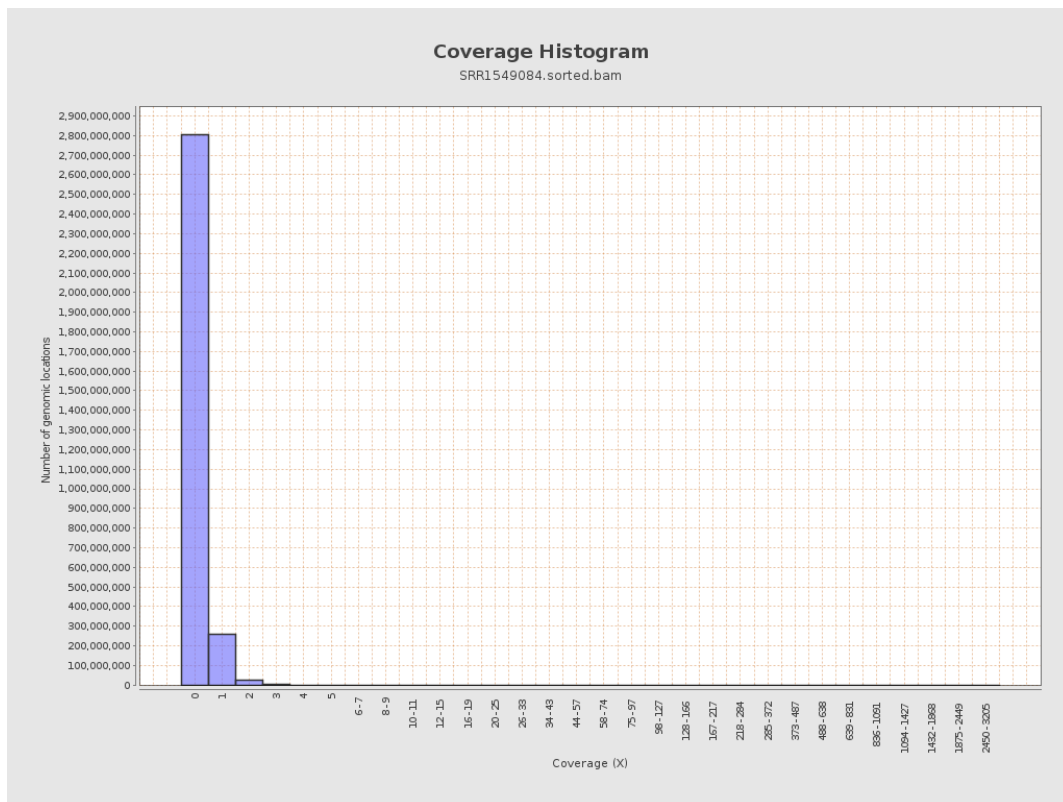
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	24766348	0.0994	2.2864
chr2	243199373	30969804	0.1273	0.7687
chr3	198022430	24092724	0.1217	0.4138
chr4	191154276	24288603	0.1271	0.3922
chr5	180915260	22269082	0.1231	0.4126
chr6	171115067	21599114	0.1262	0.6197
chr7	159138663	18136038	0.114	0.9273
chr8	146364022	17964027	0.1227	0.6482

chr9	141213431	14336226	0.1015	0.7376
chr10	135534747	15753967	0.1162	0.8831
chr11	135006516	14334793	0.1062	0.7603
chr12	133851895	14430880	0.1078	0.4243
chr13	115169878	12938836	0.1123	0.3574
chr14	107349540	11115314	0.1035	0.51
chr15	102531392	9268978	0.0904	0.3289
chr16	90354753	8796402	0.0974	0.5649
chr17	81195210	7032293	0.0866	0.4246
chr18	78077248	8461801	0.1084	1.4772
chr19	59128983	4805447	0.0813	1.8908
chr20	63025520	6155237	0.0977	0.3749
chr21	48129895	4191376	0.0871	0.4264
chr22	51304566	2803061	0.0546	0.3484
chrMT	16571	8392	0.5064	0.8894
chrX	155270560	11659855	0.0751	0.5168
chrY	59373566	2303839	0.0388	0.2979

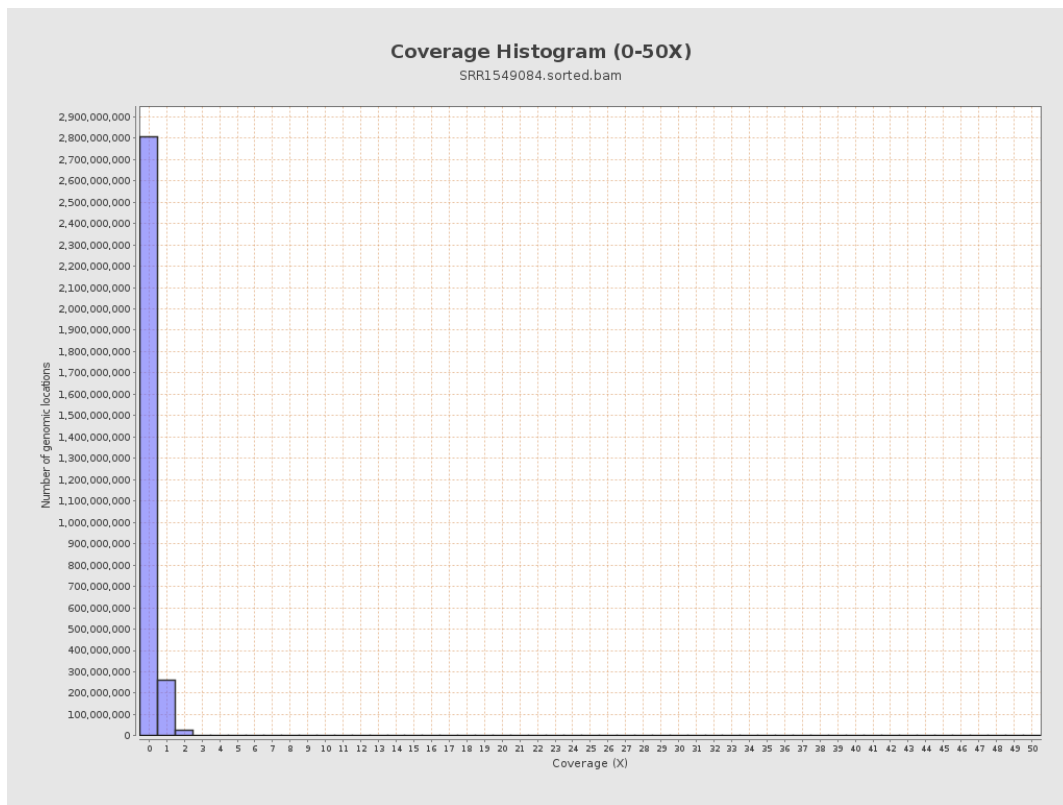
3. Results : Coverage across reference



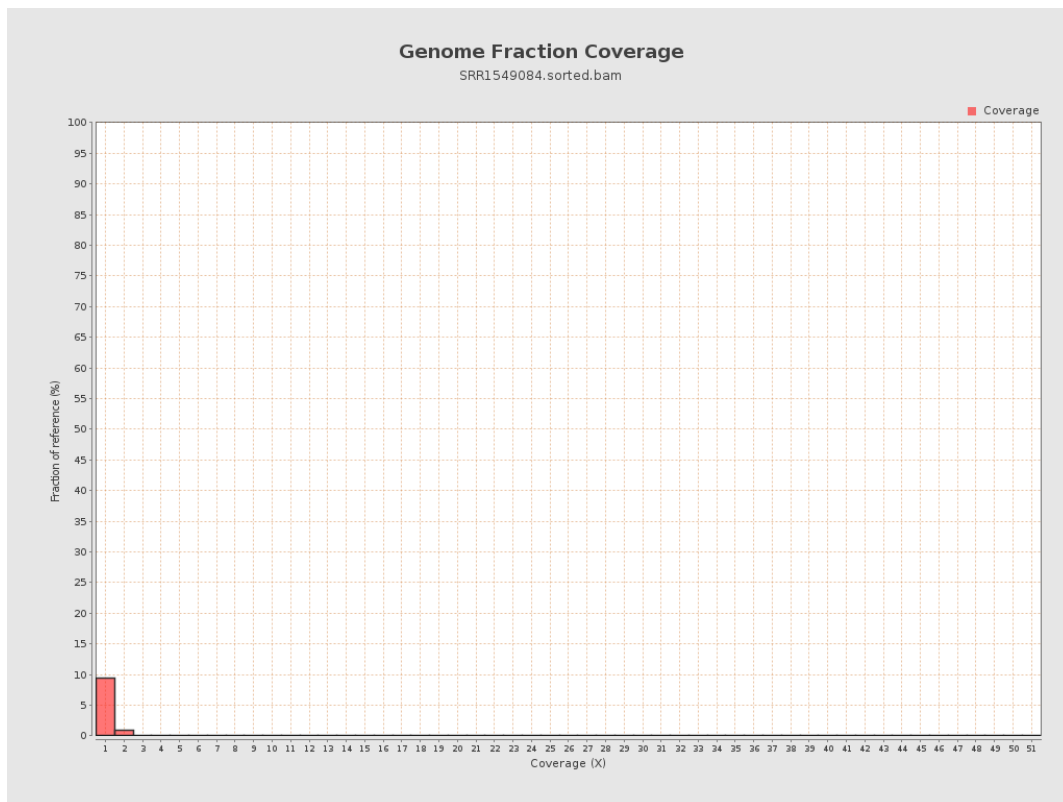
4. Results : Coverage Histogram



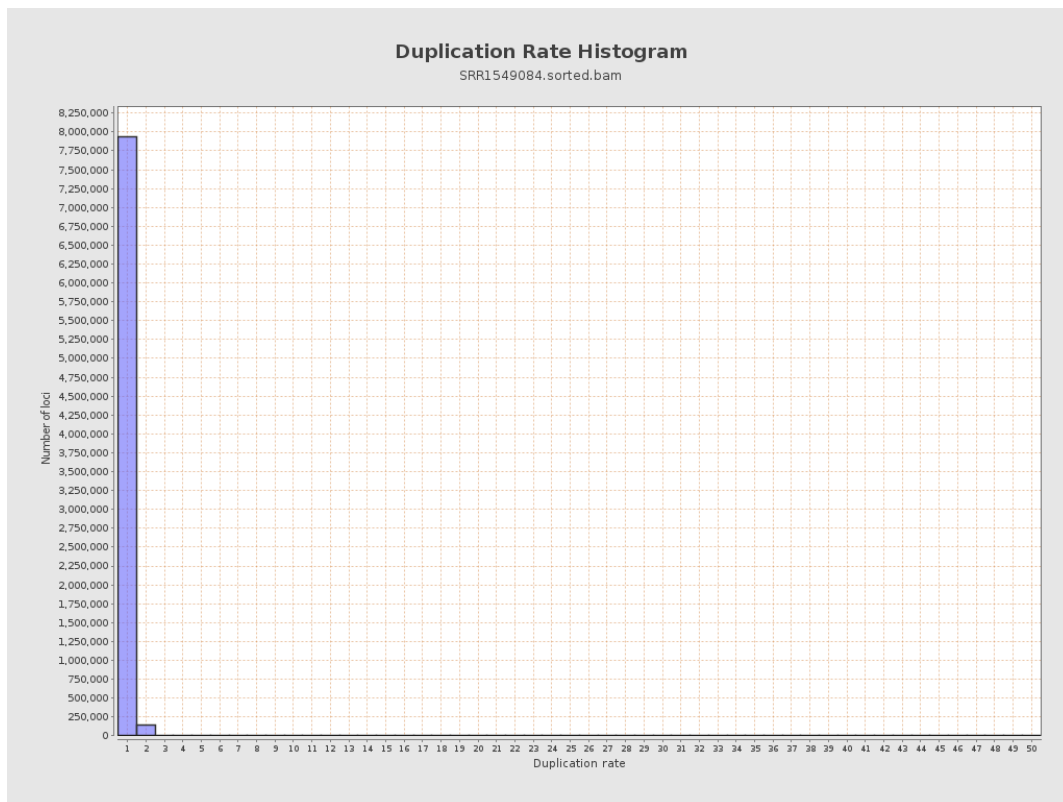
5. Results : Coverage Histogram (0-50X)



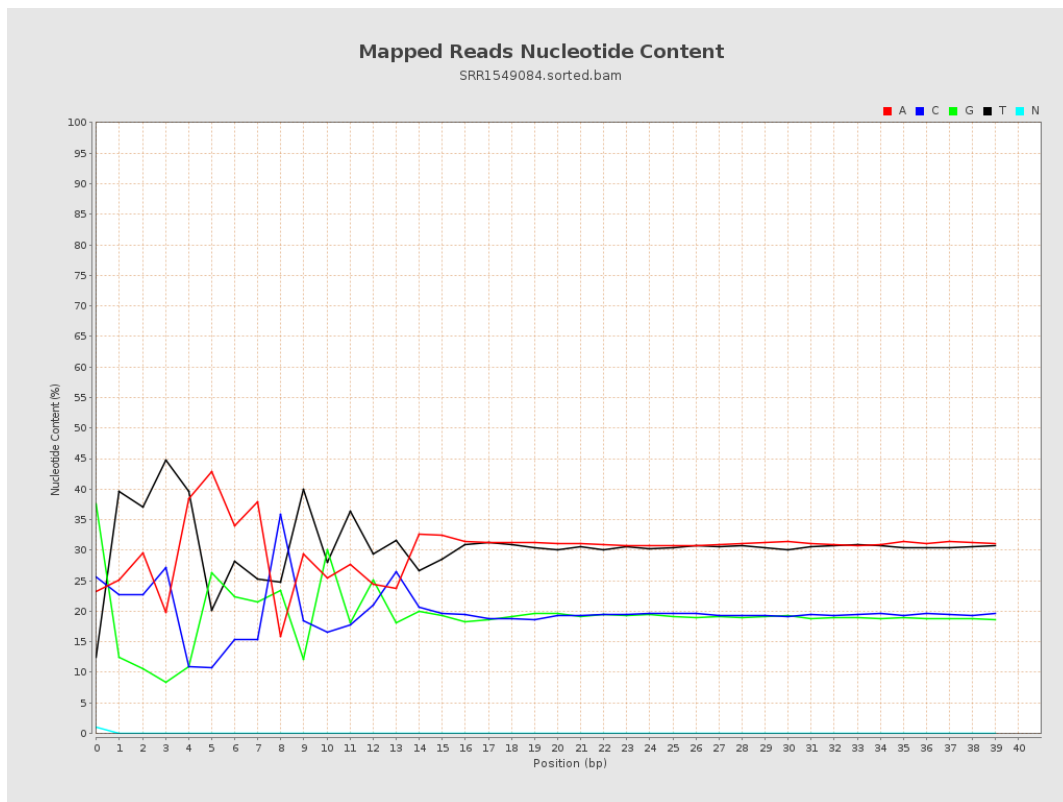
6. Results : Genome Fraction Coverage



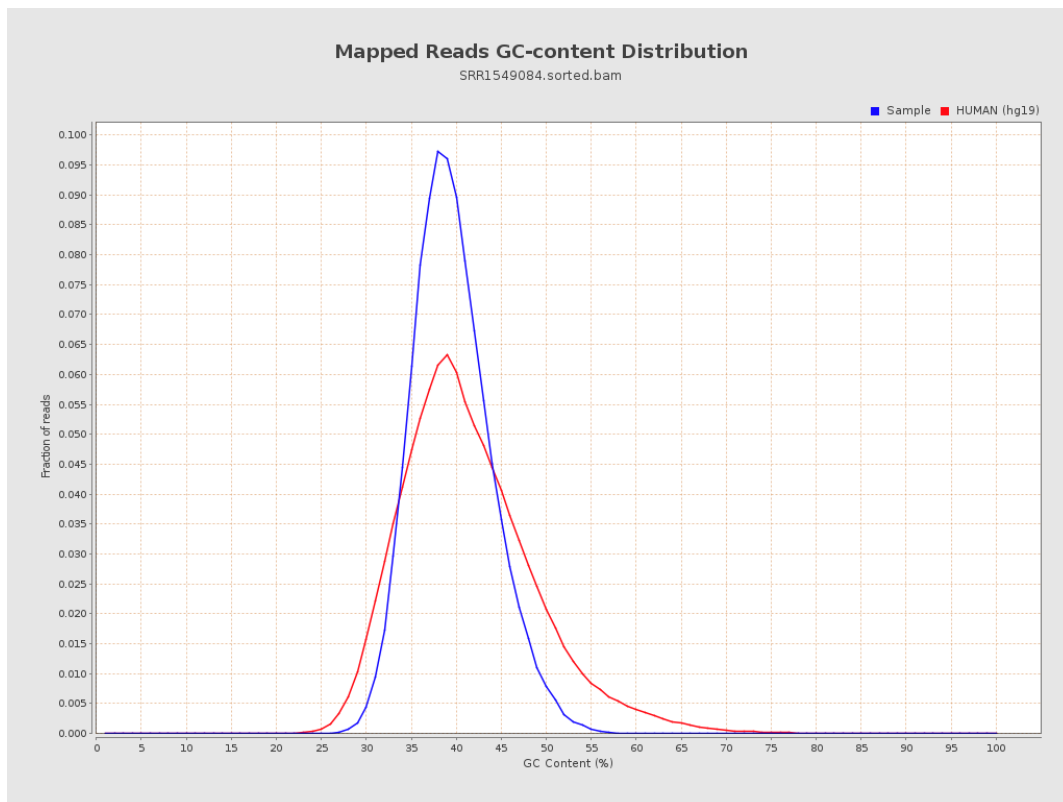
7. Results : Duplication Rate Histogram



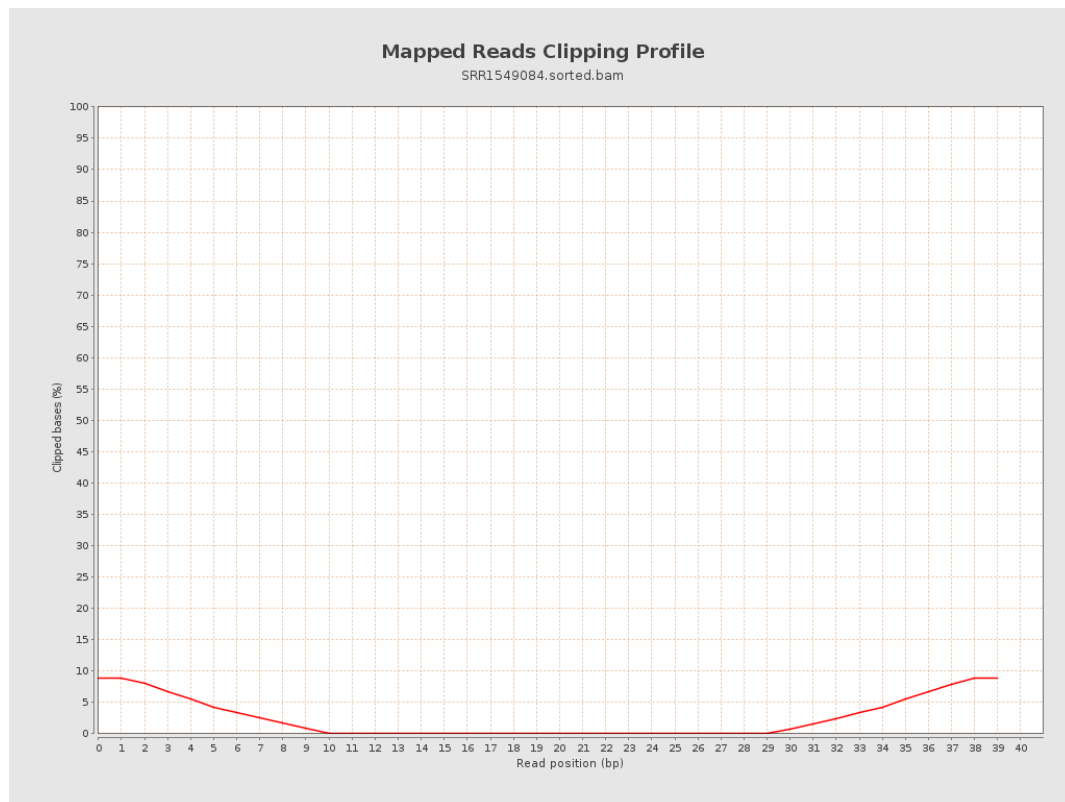
8. Results : Mapped Reads Nucleotide Content



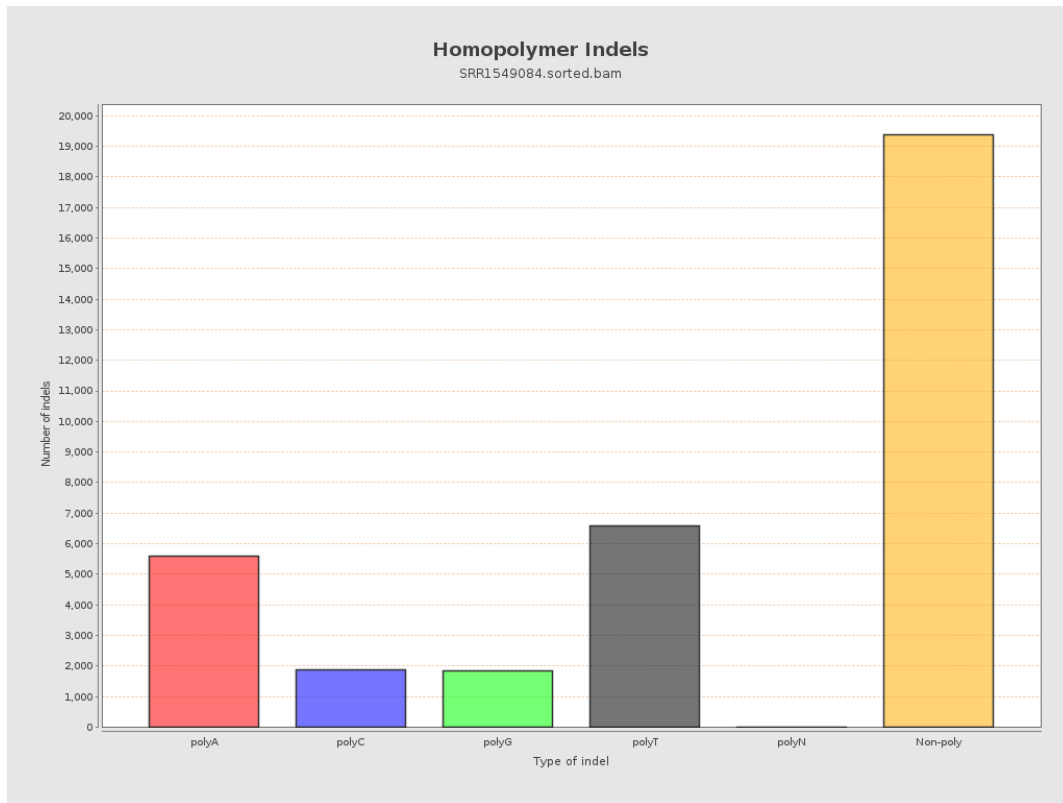
9. Results : Mapped Reads GC-content Distribution



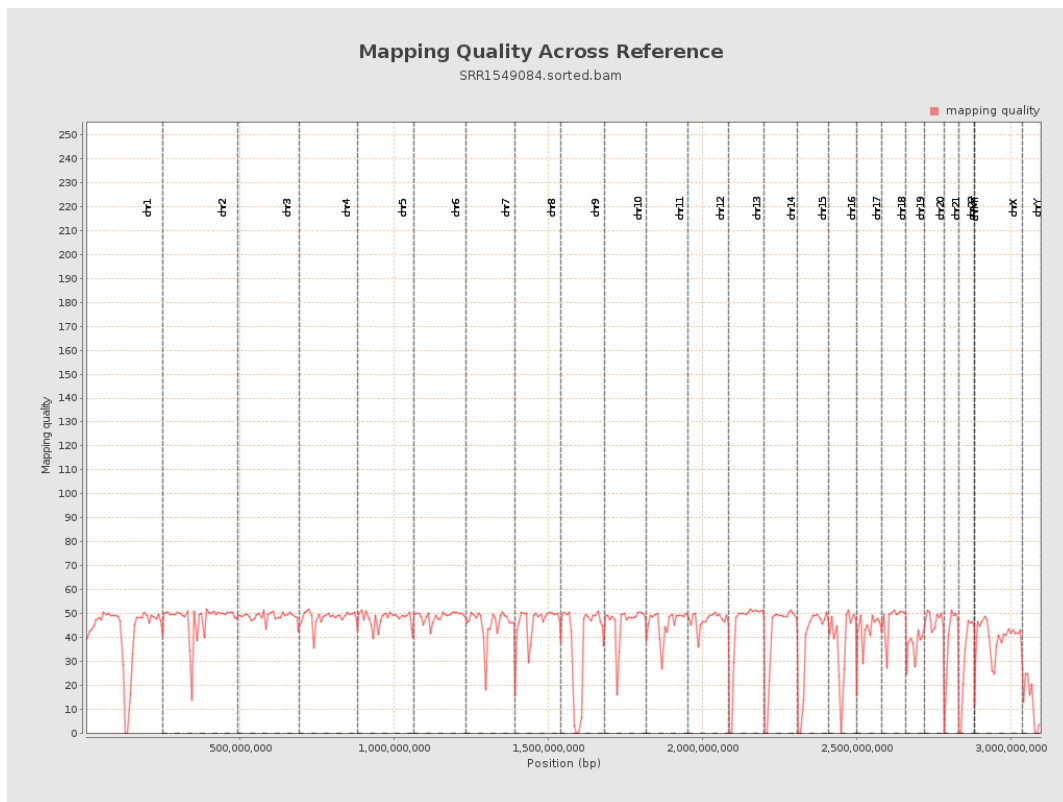
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

