

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 07:44:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549137.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_SRR1549137 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549137.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 07:44:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549137.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,655,253
Mapped reads	9,404,802 / 88.26%
Unmapped reads	1,250,451 / 11.74%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	408,622 / 3.83%
Duplication rate	3.38%
Clipped reads	460,138 / 4.32%

2.2. ACGT Content

Number/percentage of A's	106,726,028 / 28.58%
Number/percentage of C's	79,162,700 / 21.2%
Number/percentage of T's	107,734,532 / 28.85%
Number/percentage of G's	79,751,364 / 21.35%
Number/percentage of N's	81,083 / 0.02%
GC Percentage	42.55%

2.3. Coverage

Mean	0.1206
Standard Deviation	0.6775

2.4. Mapping Quality

Mean Mapping Quality	43.21
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2.5. Mismatches and indels

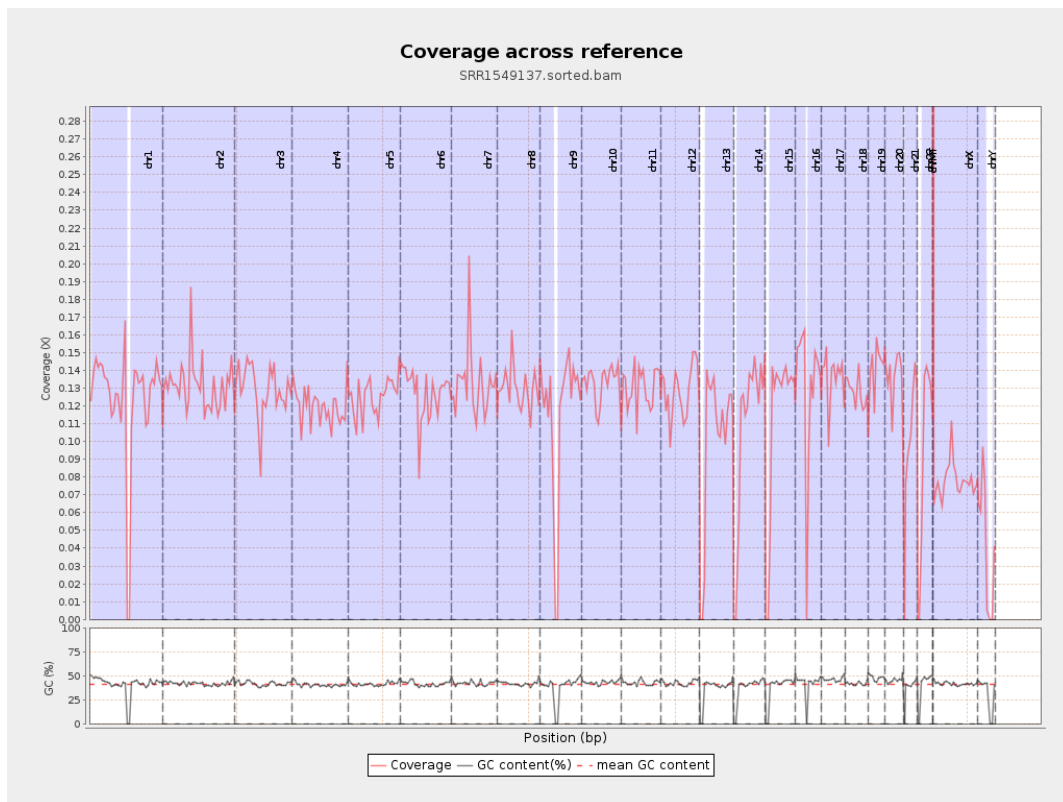
General error rate	0.32%
Mismatches	1,199,505
Insertions	9,565
Mapped reads with at least one insertion	0.1%
Deletions	29,086
Mapped reads with at least one deletion	0.31%
Homopolymer indels	46.86%

2.6. Chromosome stats

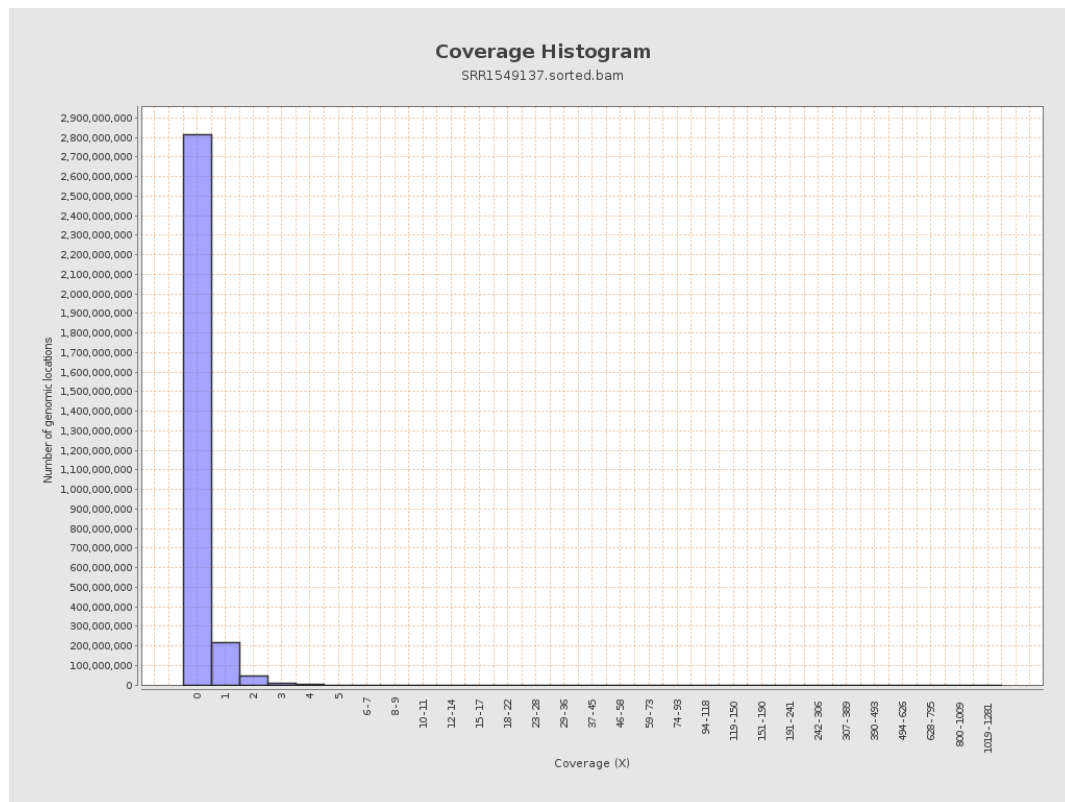
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	30821688	0.1237	1.0614
chr2	243199373	32016213	0.1316	0.7078
chr3	198022430	25517221	0.1289	0.4557
chr4	191154276	22897244	0.1198	0.4484
chr5	180915260	22760417	0.1258	0.4618
chr6	171115067	21778812	0.1273	0.5117
chr7	159138663	21150624	0.1329	1.1057
chr8	146364022	18938940	0.1294	0.6454

chr9	141213431	16204986	0.1148	0.6945
chr10	135534747	18009071	0.1329	0.5856
chr11	135006516	17510449	0.1297	0.6592
chr12	133851895	17275558	0.1291	0.4754
chr13	115169878	11591951	0.1007	0.3998
chr14	107349540	11676113	0.1088	0.5688
chr15	102531392	11314275	0.1103	0.4204
chr16	90354753	11596456	0.1283	0.5168
chr17	81195210	11111575	0.1369	0.5227
chr18	78077248	9988563	0.1279	1.3751
chr19	59128983	8371912	0.1416	0.9656
chr20	63025520	8577439	0.1361	0.4973
chr21	48129895	4849135	0.1008	0.4933
chr22	51304566	4791123	0.0934	0.4217
chrMT	16571	103348	6.2367	8.6694
chrX	155270560	12115422	0.078	0.4507
chrY	59373566	2523808	0.0425	0.3005

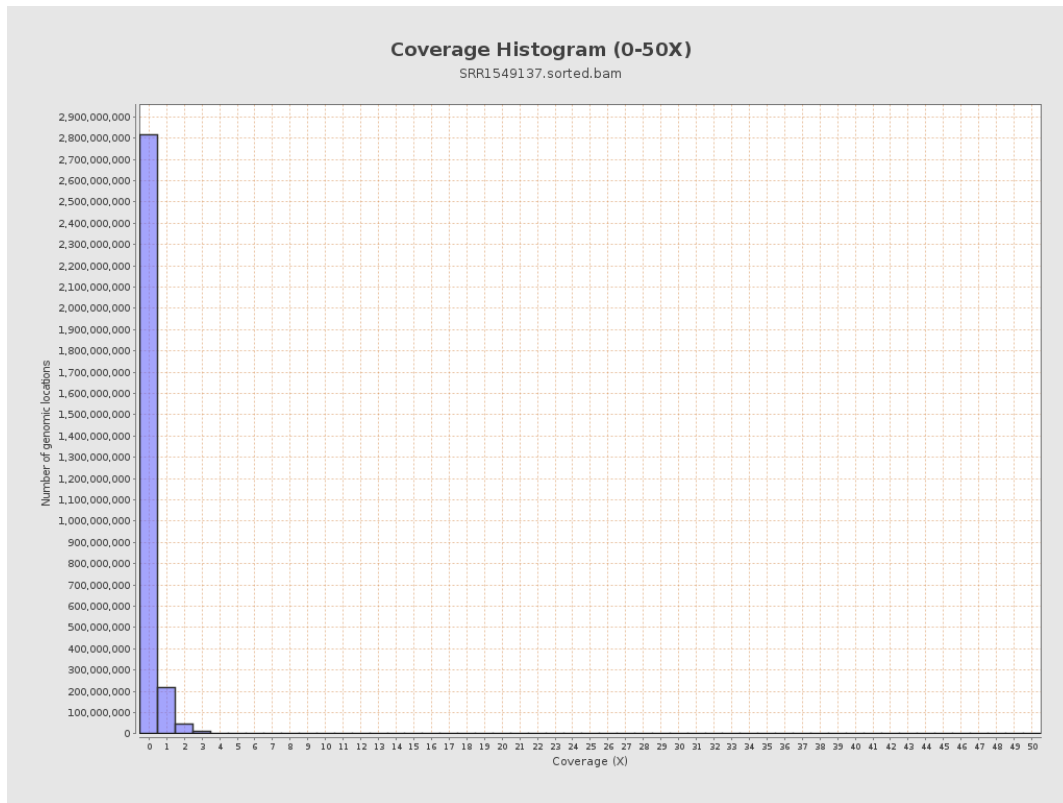
3. Results : Coverage across reference



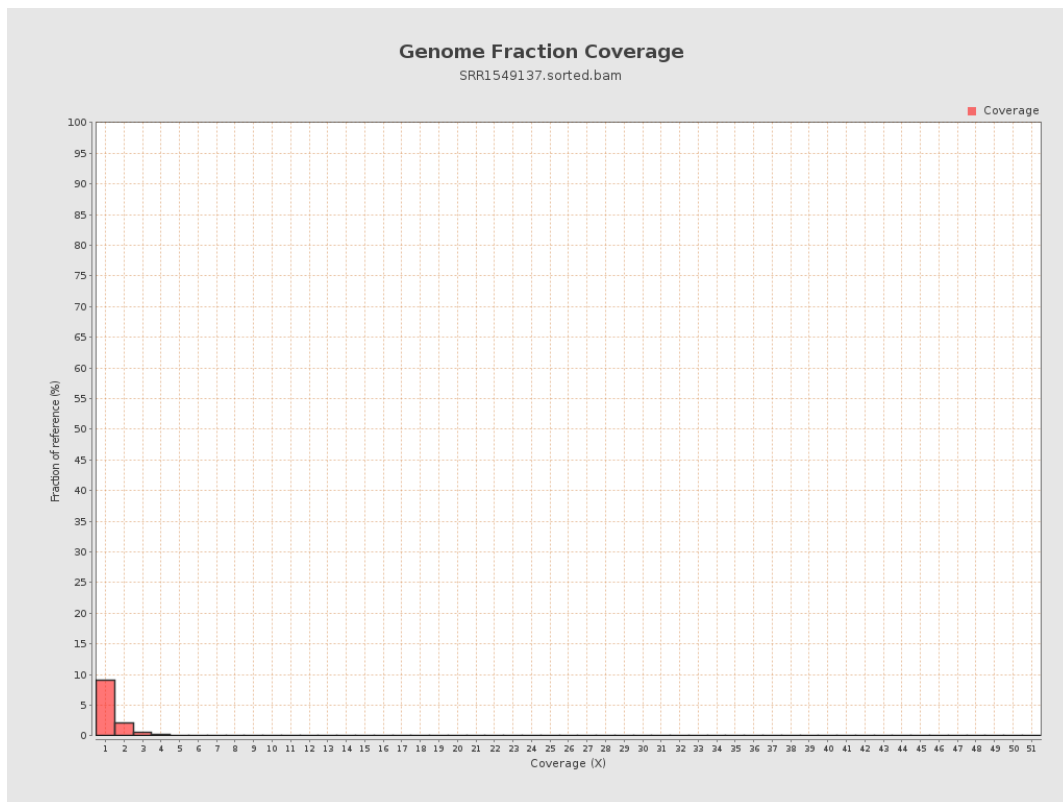
4. Results : Coverage Histogram



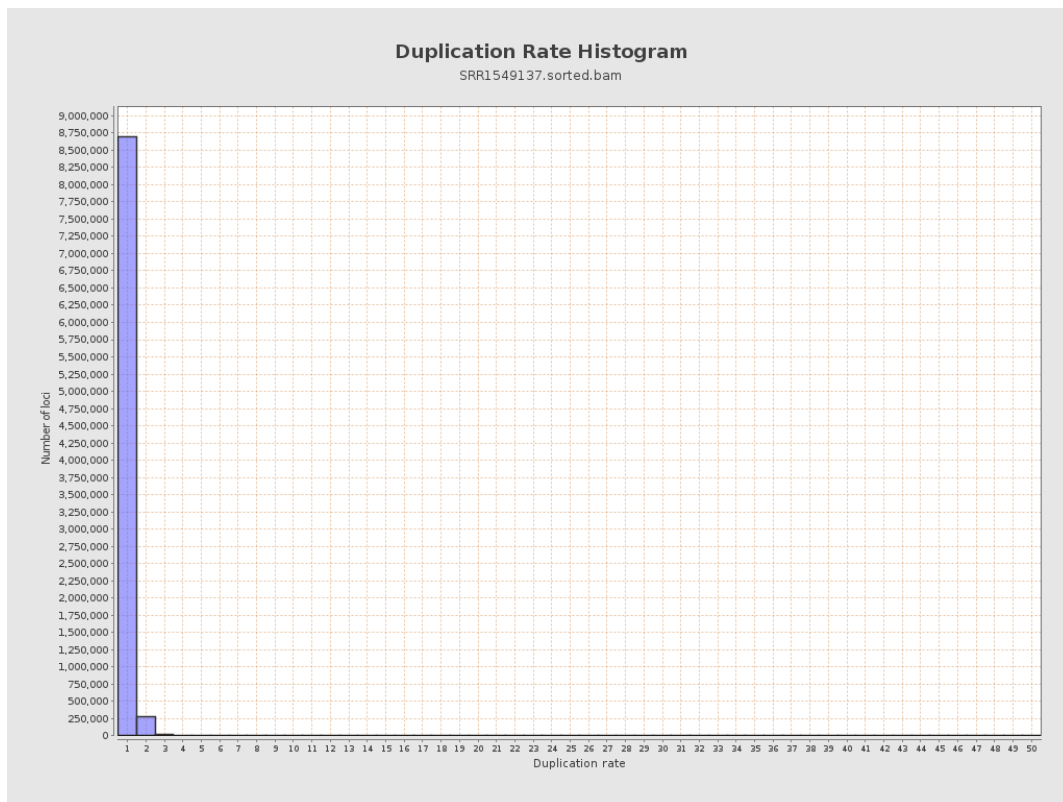
5. Results : Coverage Histogram (0-50X)



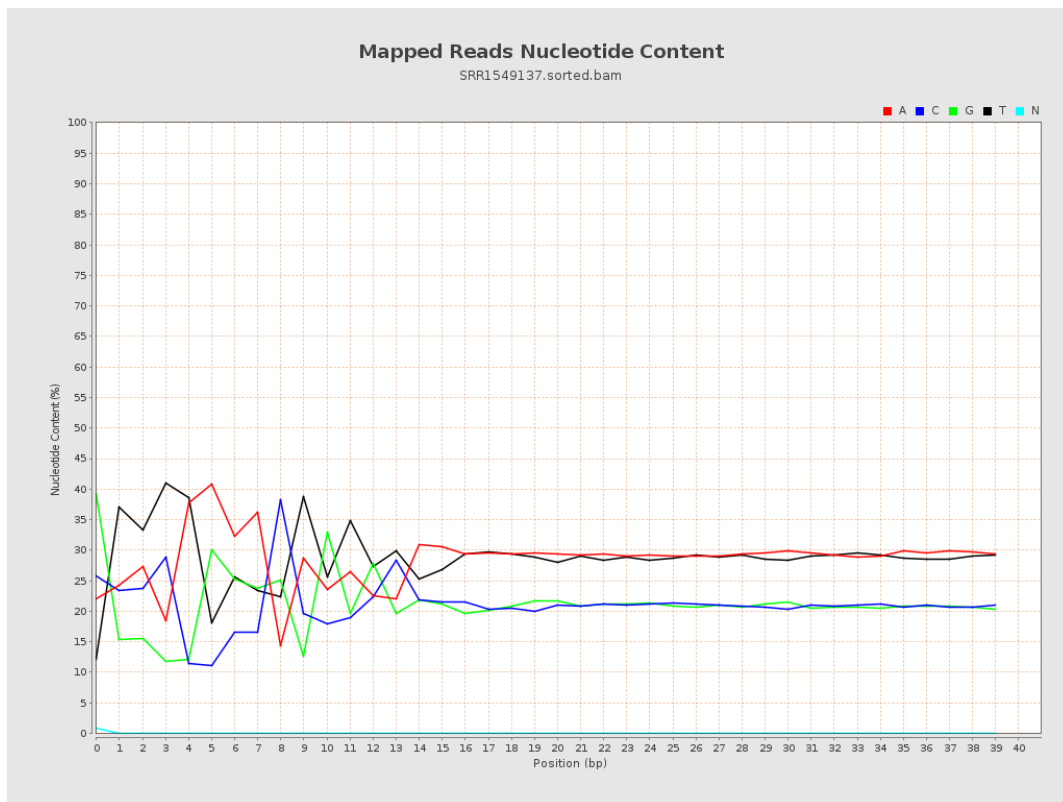
6. Results : Genome Fraction Coverage



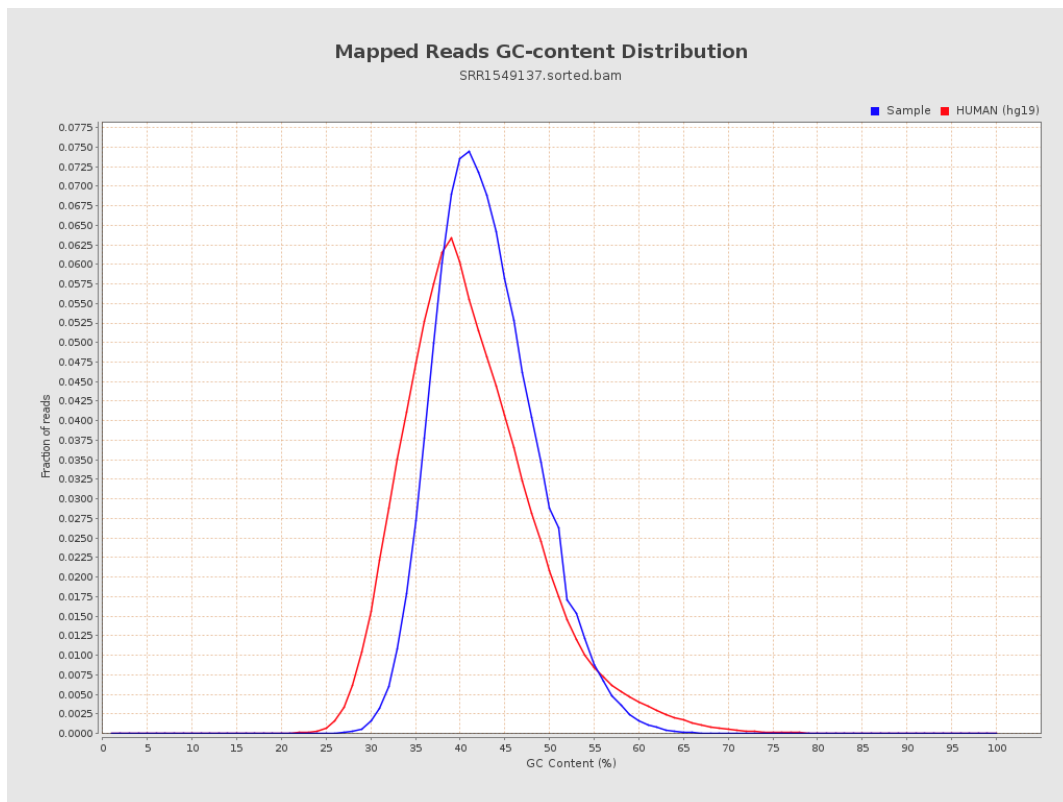
7. Results : Duplication Rate Histogram



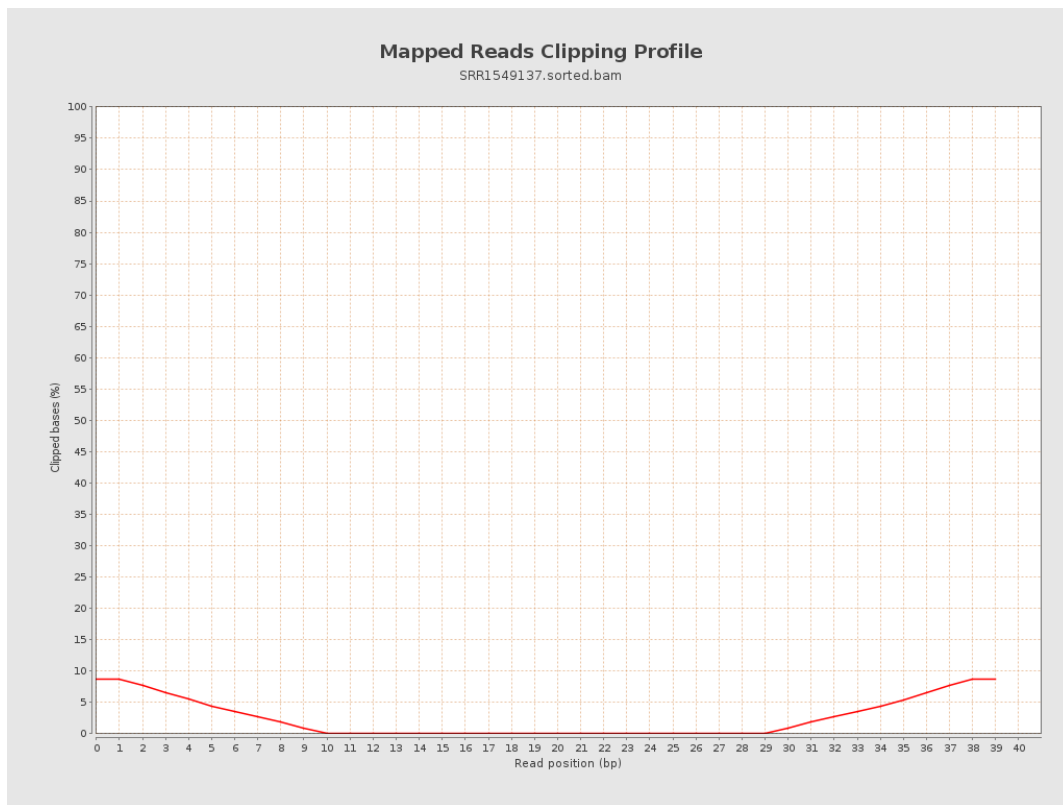
8. Results : Mapped Reads Nucleotide Content



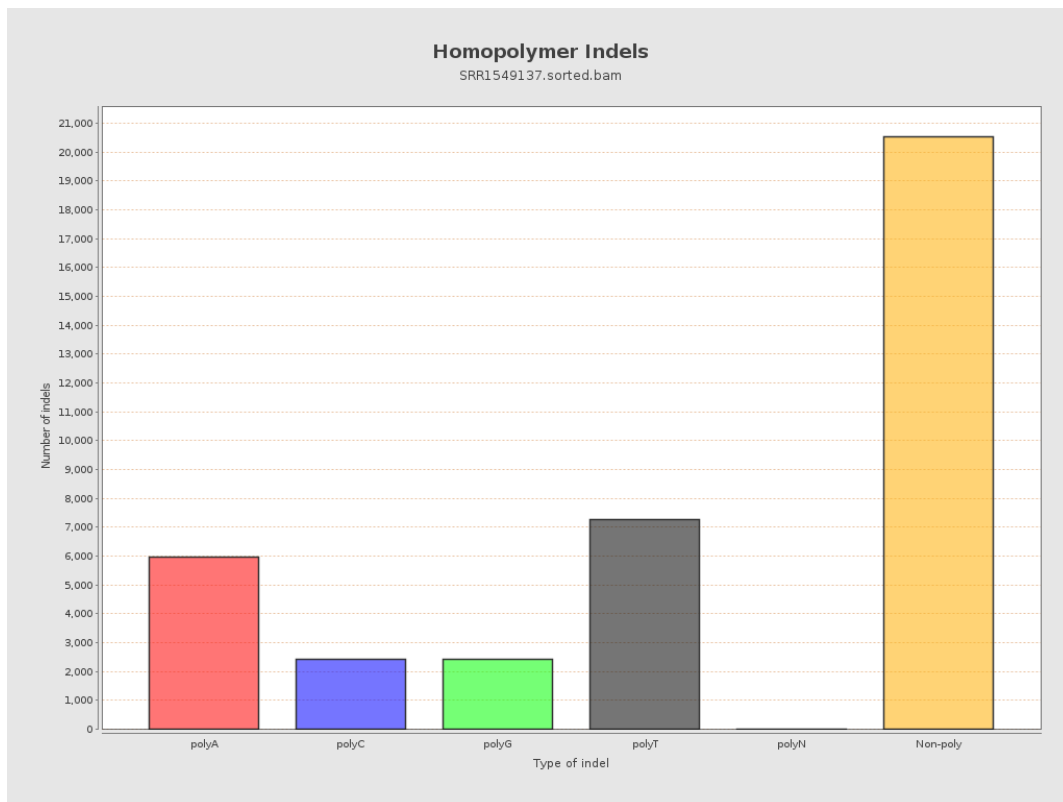
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

