

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 19:35:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525137.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_SRR10525137 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525137.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 19:35:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525137.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,953,574
Mapped reads	1,787,264 / 91.49%
Unmapped reads	166,310 / 8.51%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,521 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	66,922 / 3.43%
Duplication rate	2.77%
Clipped reads	1,789,459 / 91.6%

2.2. ACGT Content

Number/percentage of A's	26,655,978 / 25.63%
Number/percentage of C's	19,834,372 / 19.07%
Number/percentage of T's	32,790,256 / 31.53%
Number/percentage of G's	24,713,897 / 23.76%
Number/percentage of N's	3,139 / 0%
GC Percentage	42.84%

2.3. Coverage

Mean	0.0336

Standard Deviation	0.3052
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2.4. Mapping Quality

Mean Mapping Quality	45.95
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2.5. Mismatches and indels

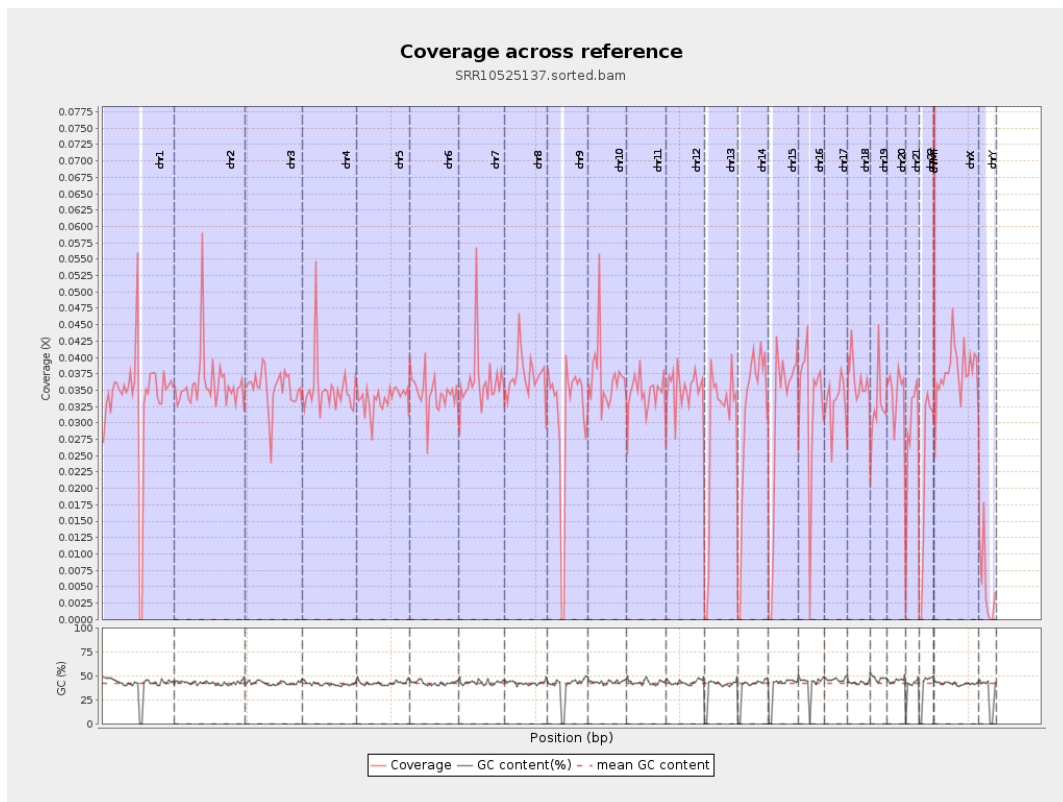
General error rate	0.49%
Mismatches	495,799
Insertions	7,056
Mapped reads with at least one insertion	0.39%
Deletions	16,717
Mapped reads with at least one deletion	0.93%
Homopolymer indels	42.68%

2.6. Chromosome stats

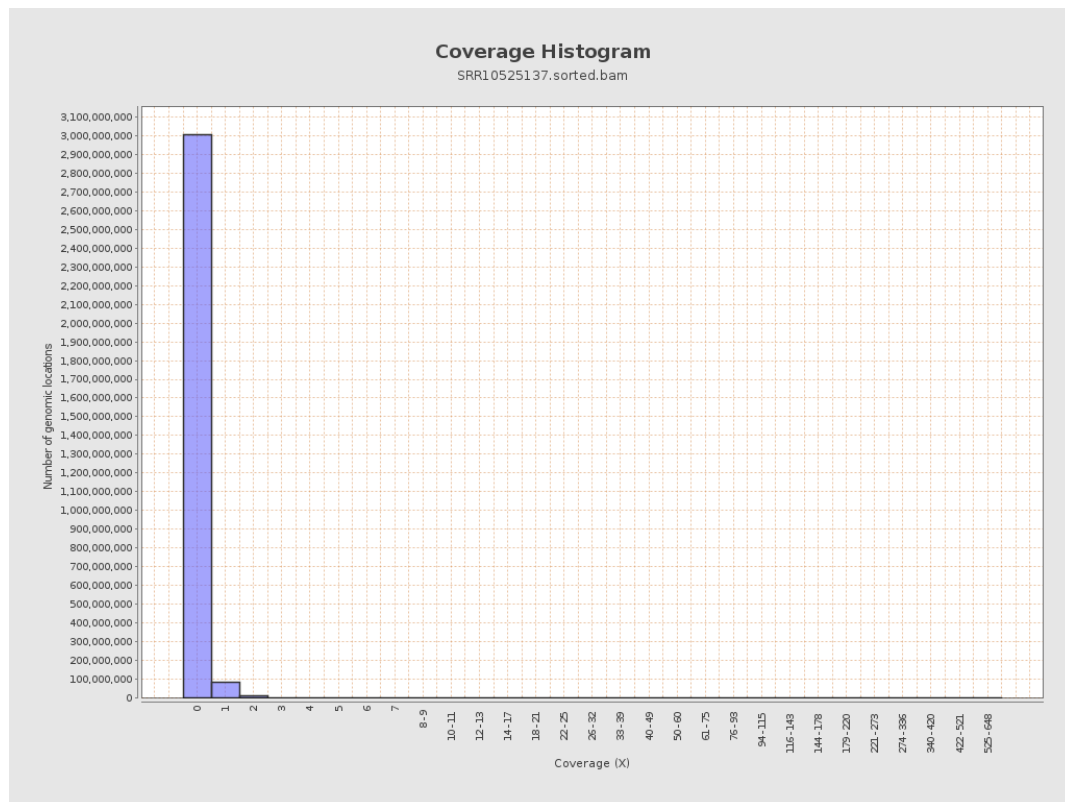
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	8329964	0.0334	0.5486
chr2	243199373	8749912	0.036	0.3176
chr3	198022430	6978149	0.0352	0.2068
chr4	191154276	6715796	0.0351	0.2336
chr5	180915260	6096681	0.0337	0.2051
chr6	171115067	5908036	0.0345	0.225
chr7	159138663	5802259	0.0365	0.3758

chr8	146364022	5435041	0.0371	0.3672
chr9	141213431	4371183	0.031	0.2923
chr10	135534747	5006987	0.0369	0.2813
chr11	135006516	4684204	0.0347	0.282
chr12	133851895	4729550	0.0353	0.2152
chr13	115169878	3327218	0.0289	0.1879
chr14	107349540	3352248	0.0312	0.2119
chr15	102531392	3151752	0.0307	0.1946
chr16	90354753	2957023	0.0327	0.2158
chr17	81195210	2688541	0.0331	0.2158
chr18	78077248	2859444	0.0366	0.5611
chr19	59128983	1941882	0.0328	0.4009
chr20	63025520	2165605	0.0344	0.2124
chr21	48129895	1381298	0.0287	0.2106
chr22	51304566	1171619	0.0228	0.1662
chrMT	16571	26121	1.5763	1.6416
chrX	155270560	5889426	0.0379	0.2445
chrY	59373566	305294	0.0051	0.1334

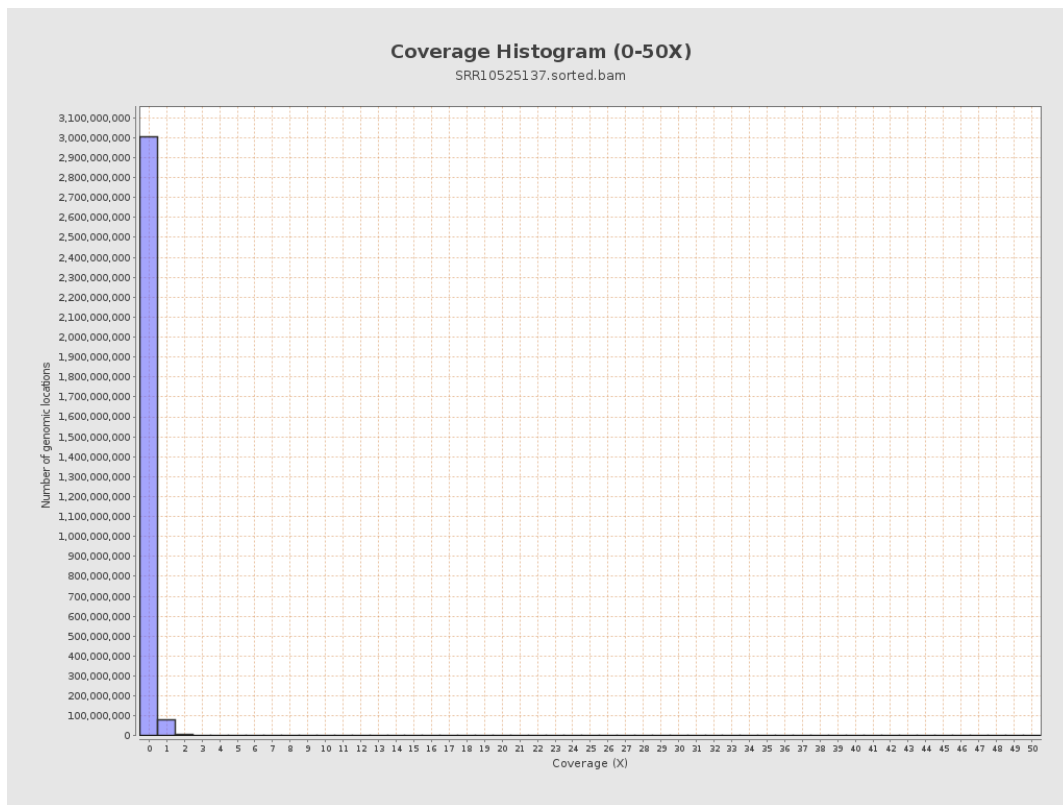
3. Results : Coverage across reference



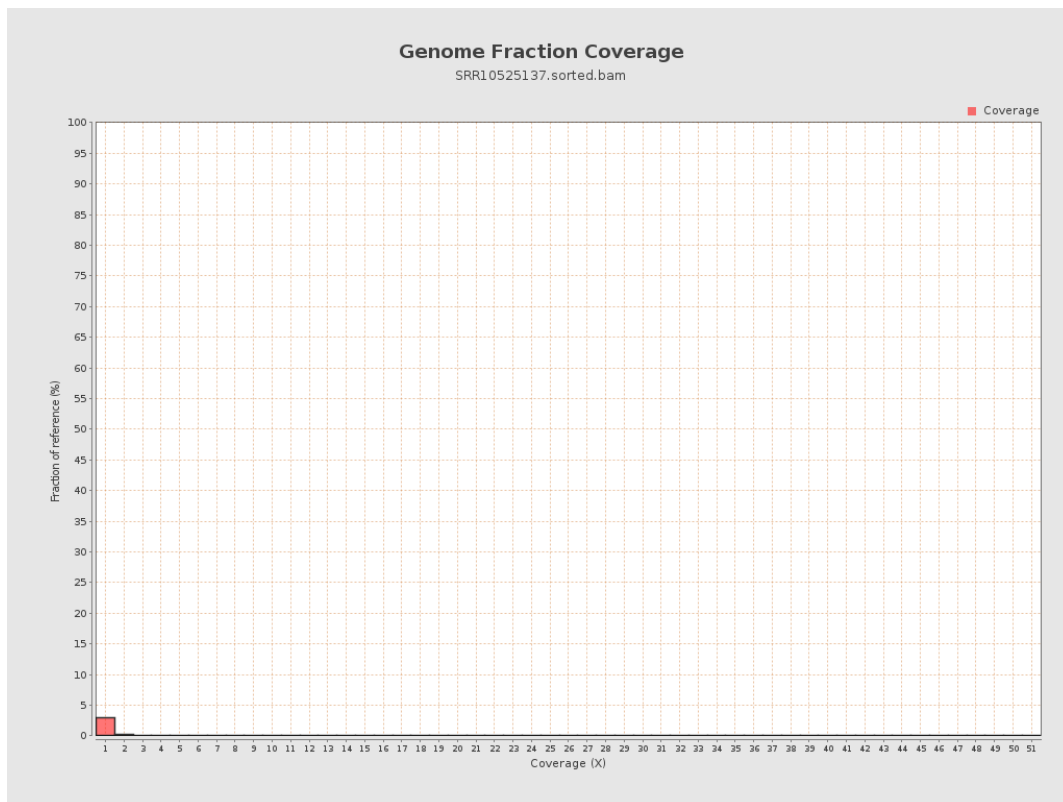
4. Results : Coverage Histogram



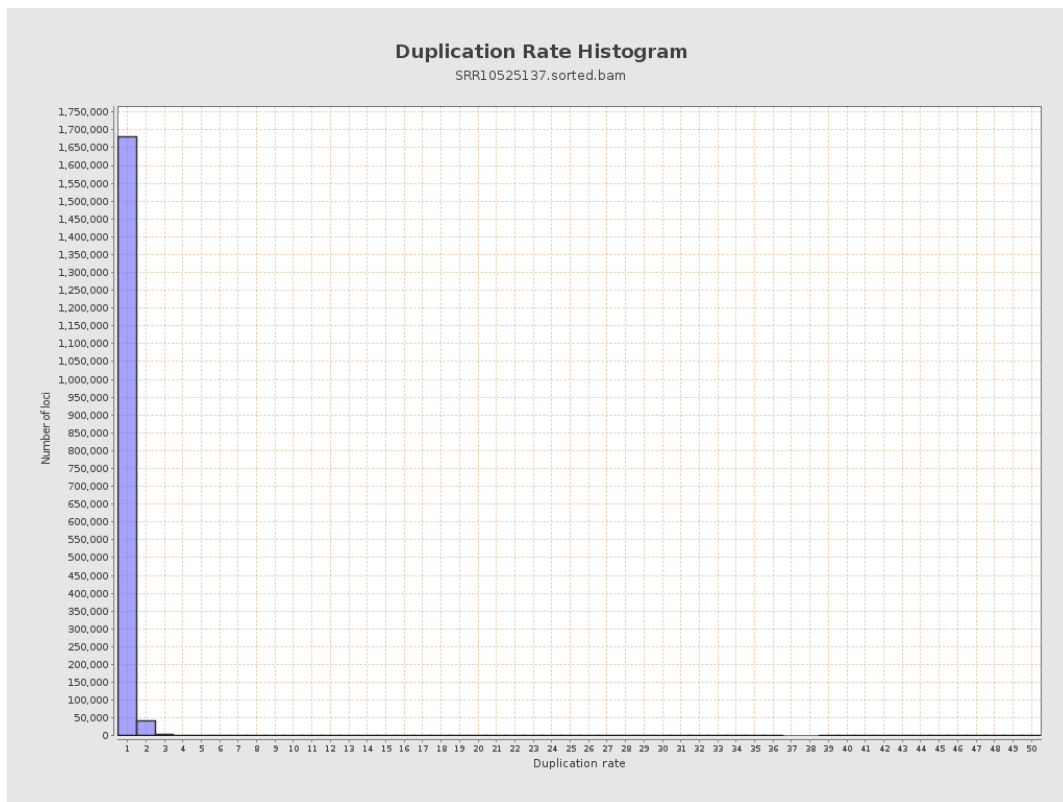
5. Results : Coverage Histogram (0-50X)



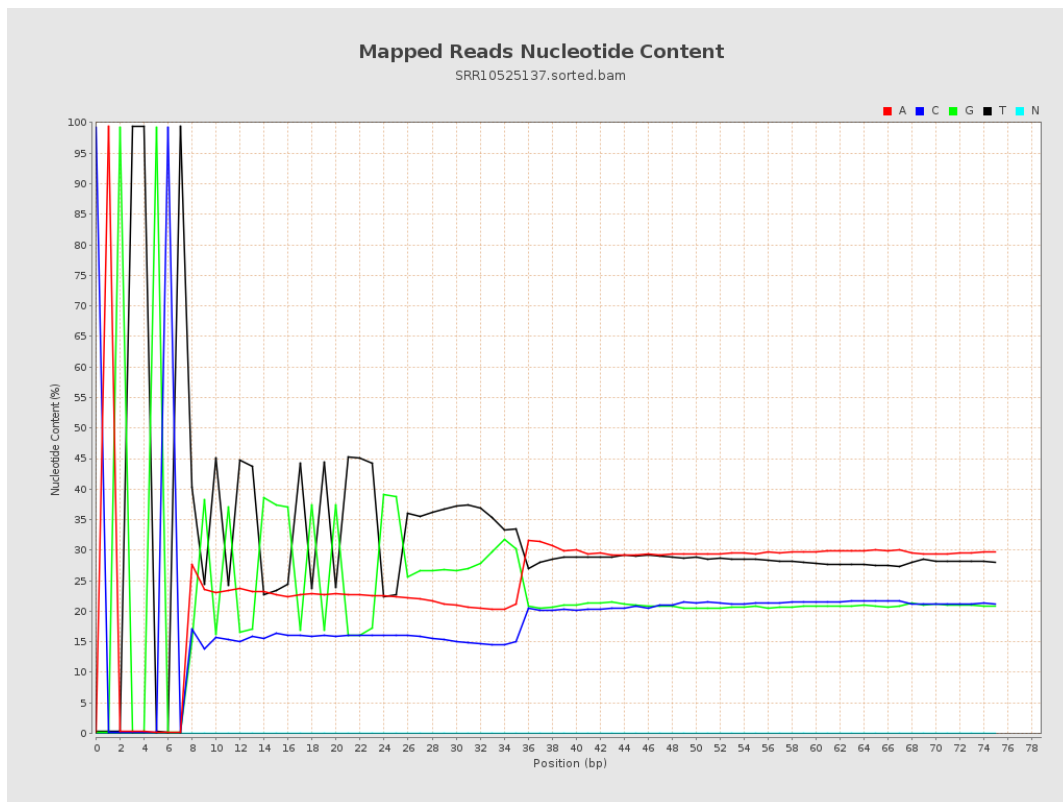
6. Results : Genome Fraction Coverage



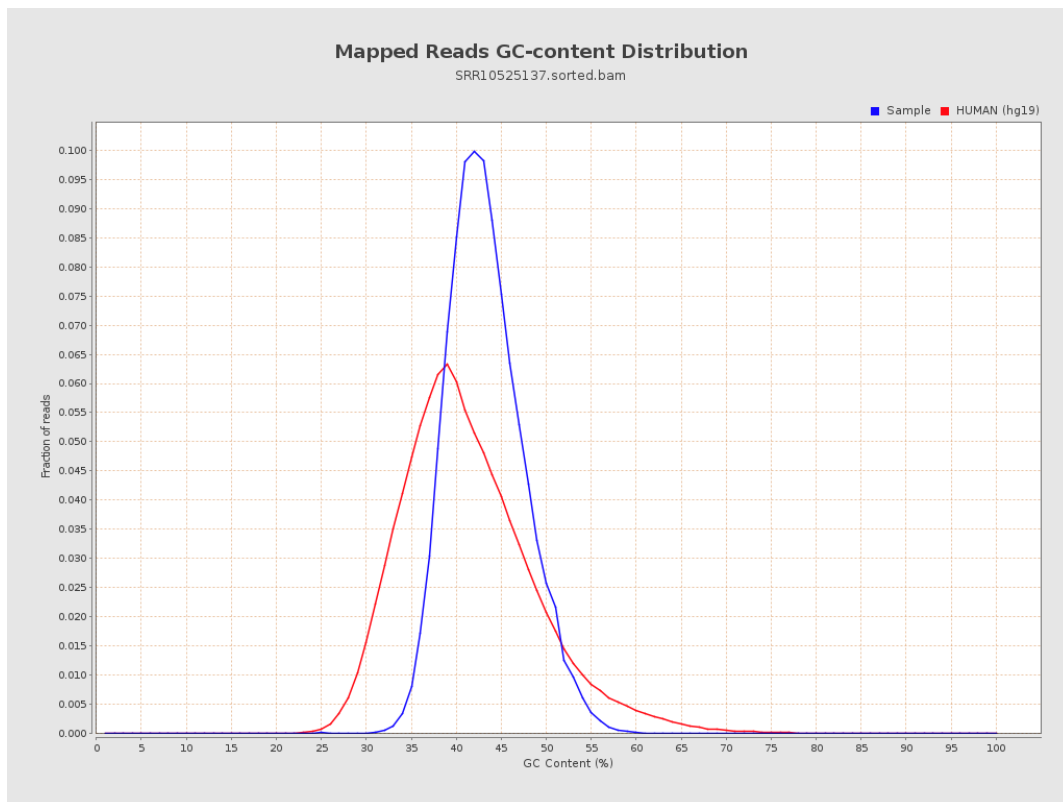
7. Results : Duplication Rate Histogram



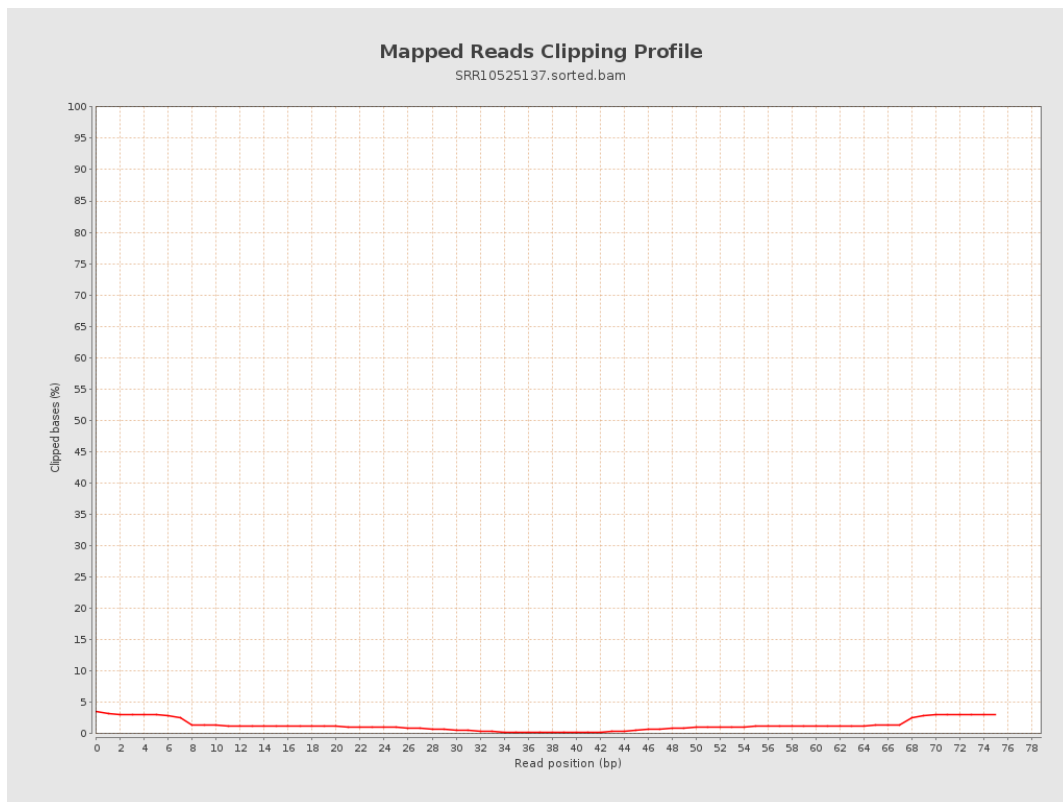
8. Results : Mapped Reads Nucleotide Content



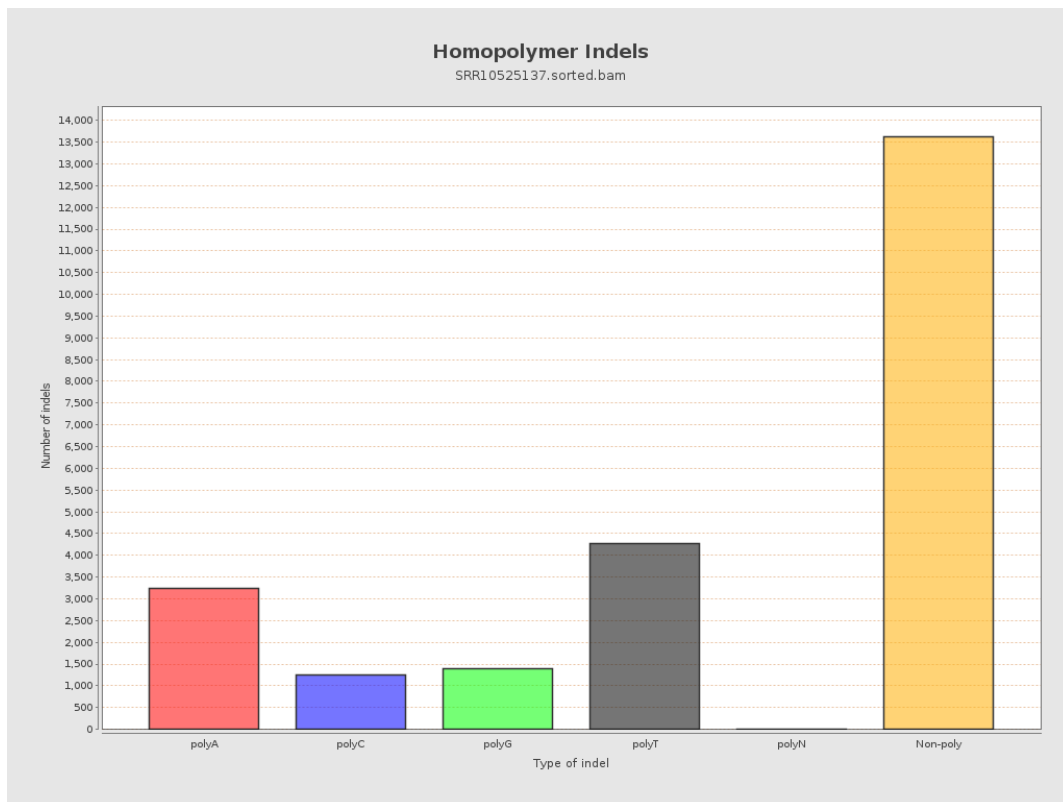
9. Results : Mapped Reads GC-content Distribution



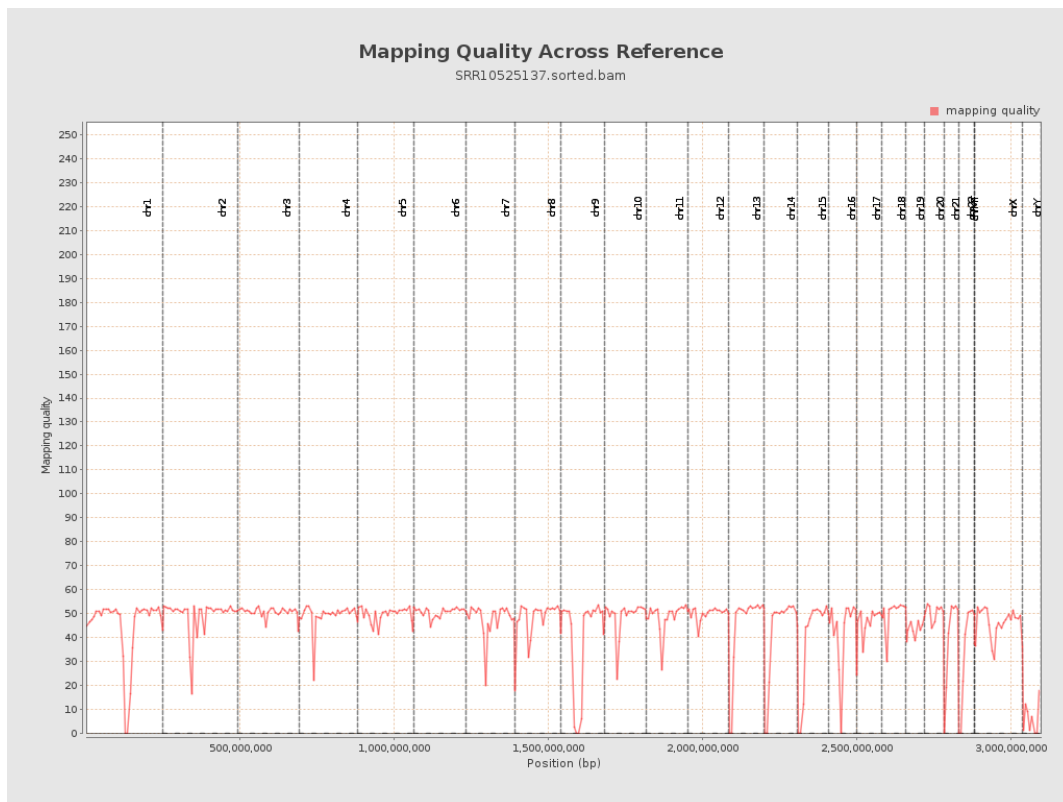
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

