

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 23:48:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525220.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_SRR10525220 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525220.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 23:48:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525220.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,319,503
Mapped reads	1,183,641 / 89.7%
Unmapped reads	135,862 / 10.3%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,271 / 0.25%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	37,530 / 2.84%
Duplication rate	2.25%
Clipped reads	1,183,877 / 89.72%

2.2. ACGT Content

Number/percentage of A's	17,295,353 / 25.34%
Number/percentage of C's	12,524,085 / 18.35%
Number/percentage of T's	22,058,508 / 32.32%
Number/percentage of G's	16,378,985 / 24%
Number/percentage of N's	1,511 / 0%
GC Percentage	42.34%

2.3. Coverage

Mean	0.0221

Standard Deviation	0.2341
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2.4. Mapping Quality

Mean Mapping Quality	44.55
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2.5. Mismatches and indels

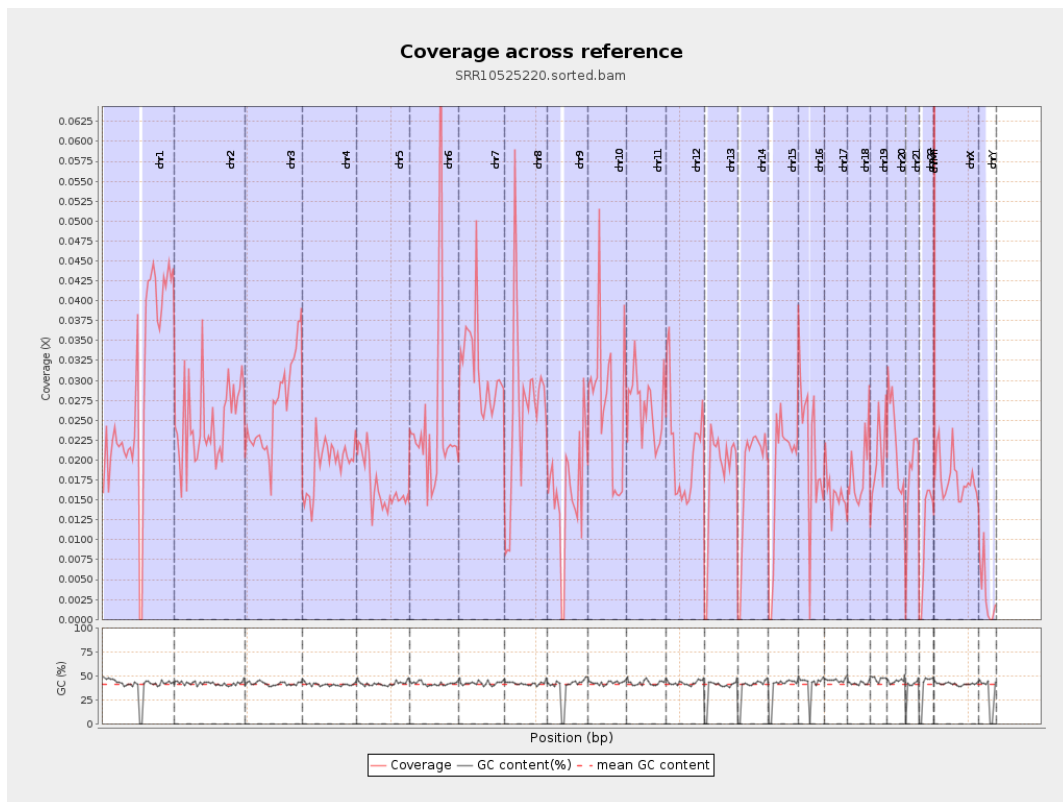
General error rate	0.53%
Mismatches	355,109
Insertions	4,726
Mapped reads with at least one insertion	0.4%
Deletions	13,453
Mapped reads with at least one deletion	1.13%
Homopolymer indels	42.11%

2.6. Chromosome stats

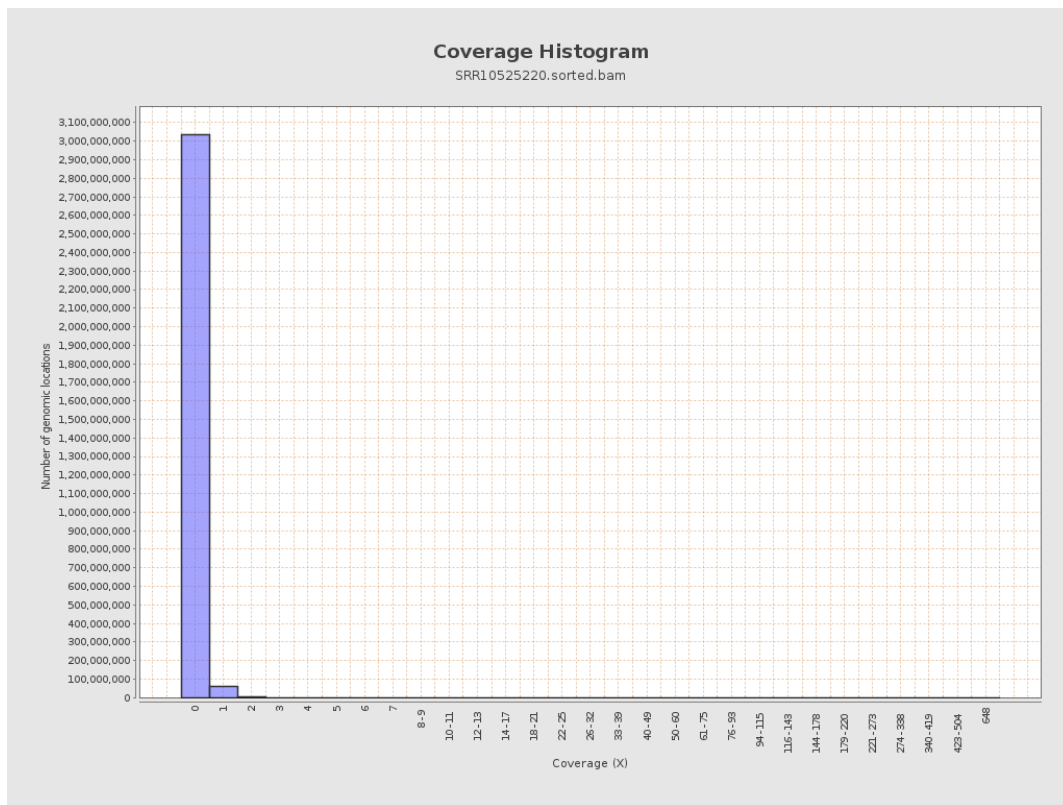
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	7203245	0.0289	0.4035
chr2	243199373	6011920	0.0247	0.3228
chr3	198022430	5245351	0.0265	0.1767
chr4	191154276	3742722	0.0196	0.1561
chr5	180915260	3023366	0.0167	0.138
chr6	171115067	4232195	0.0247	0.1859
chr7	159138663	4996901	0.0314	0.398

chr8	146364022	3876724	0.0265	0.2159
chr9	141213431	2229679	0.0158	0.1723
chr10	135534747	3675181	0.0271	0.2664
chr11	135006516	3603595	0.0267	0.1965
chr12	133851895	2843957	0.0212	0.1569
chr13	115169878	2100310	0.0182	0.1463
chr14	107349540	1951587	0.0182	0.1485
chr15	102531392	1880833	0.0183	0.1471
chr16	90354753	1956908	0.0217	0.1712
chr17	81195210	1279977	0.0158	0.1377
chr18	78077248	1433583	0.0184	0.2679
chr19	59128983	1214284	0.0205	0.279
chr20	63025520	1398151	0.0222	0.1614
chr21	48129895	868495	0.018	0.151
chr22	51304566	553326	0.0108	0.1108
chrMT	16571	5552	0.335	0.634
chrX	155270560	2760424	0.0178	0.1547
chrY	59373566	191580	0.0032	0.0996

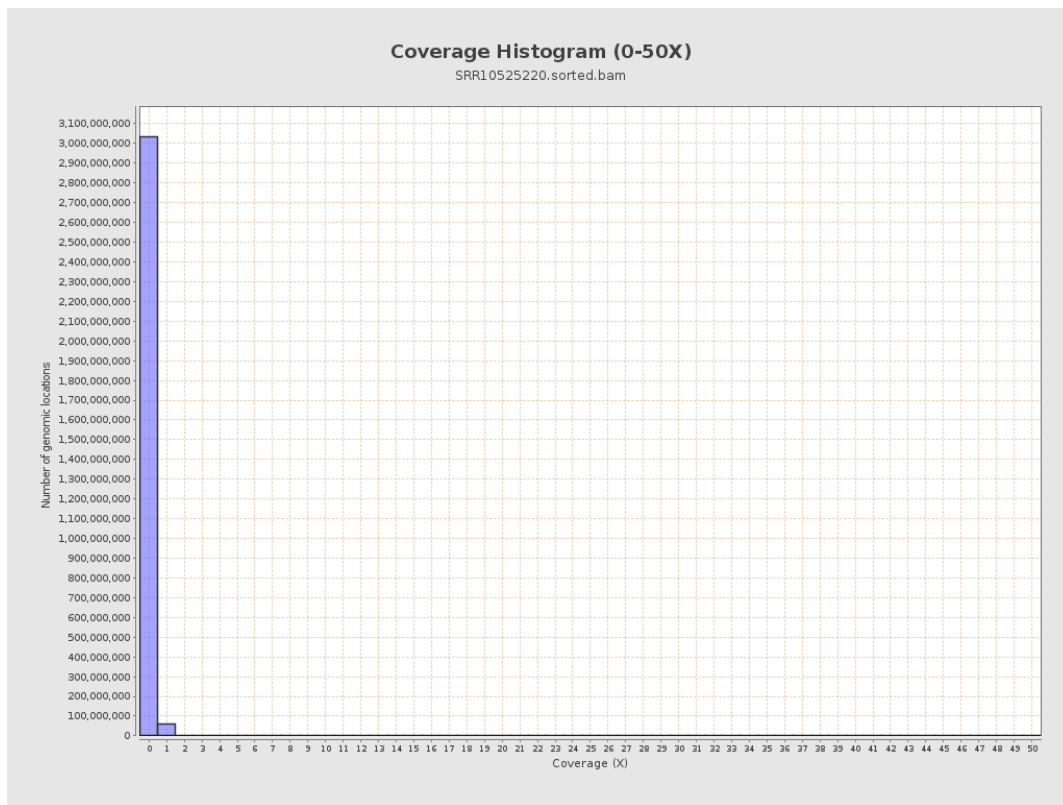
3. Results : Coverage across reference



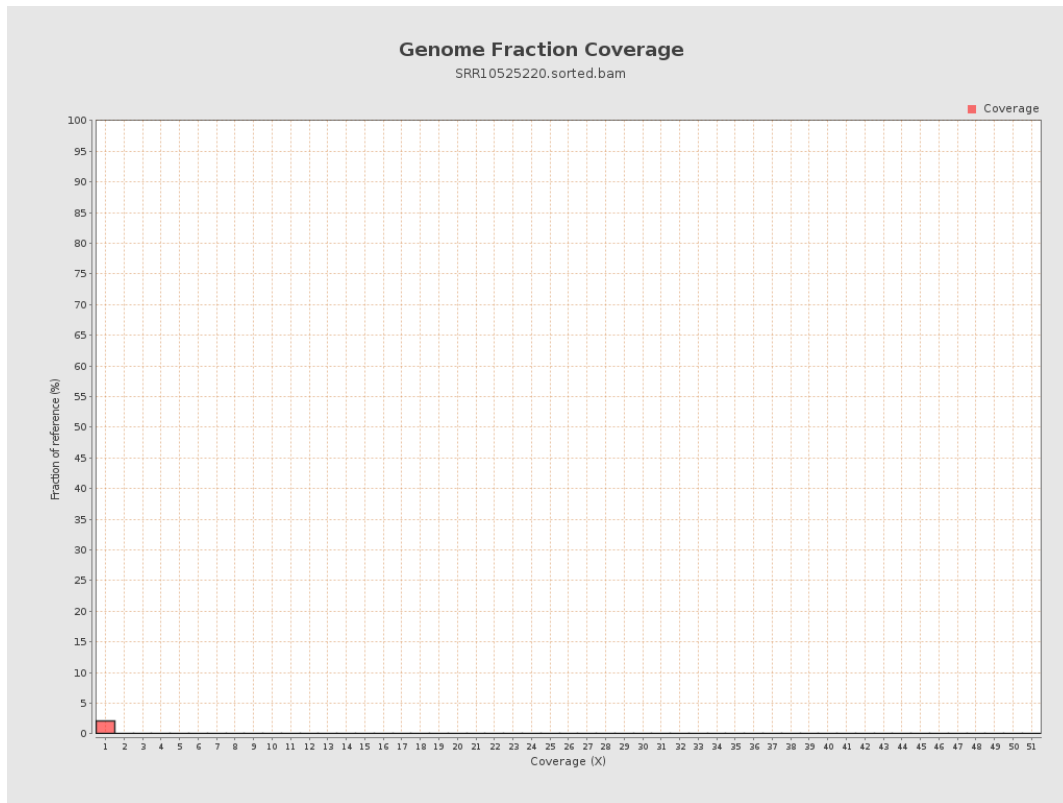
4. Results : Coverage Histogram



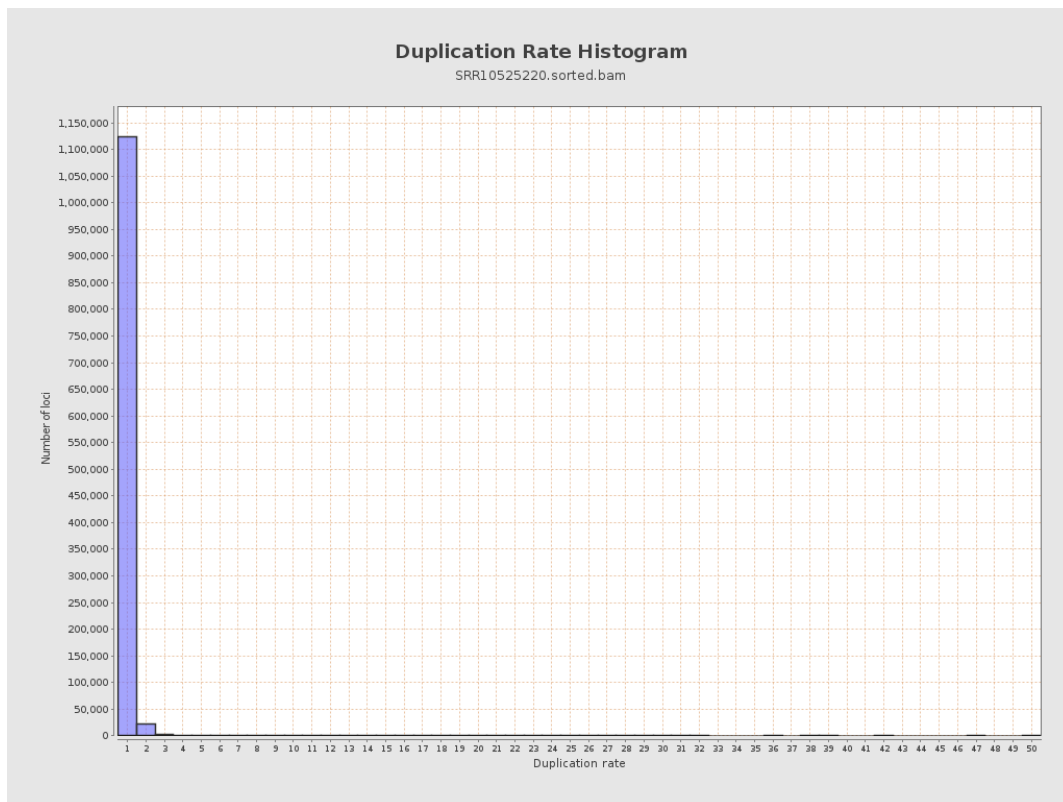
5. Results : Coverage Histogram (0-50X)



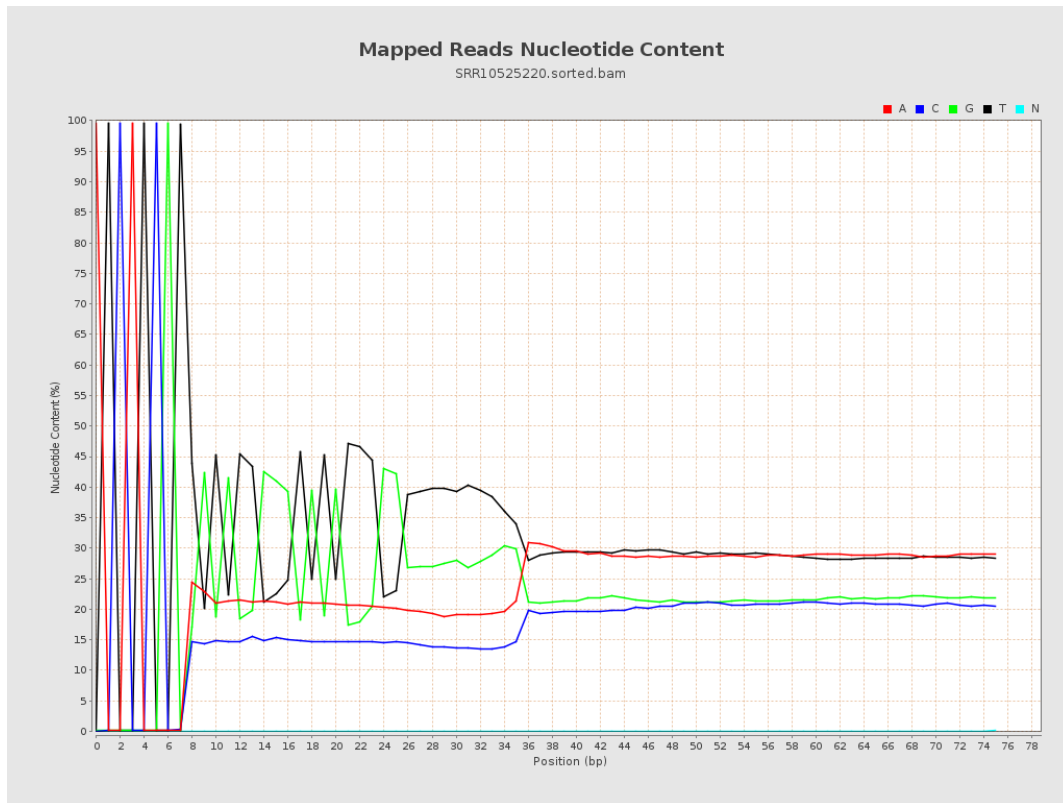
6. Results : Genome Fraction Coverage



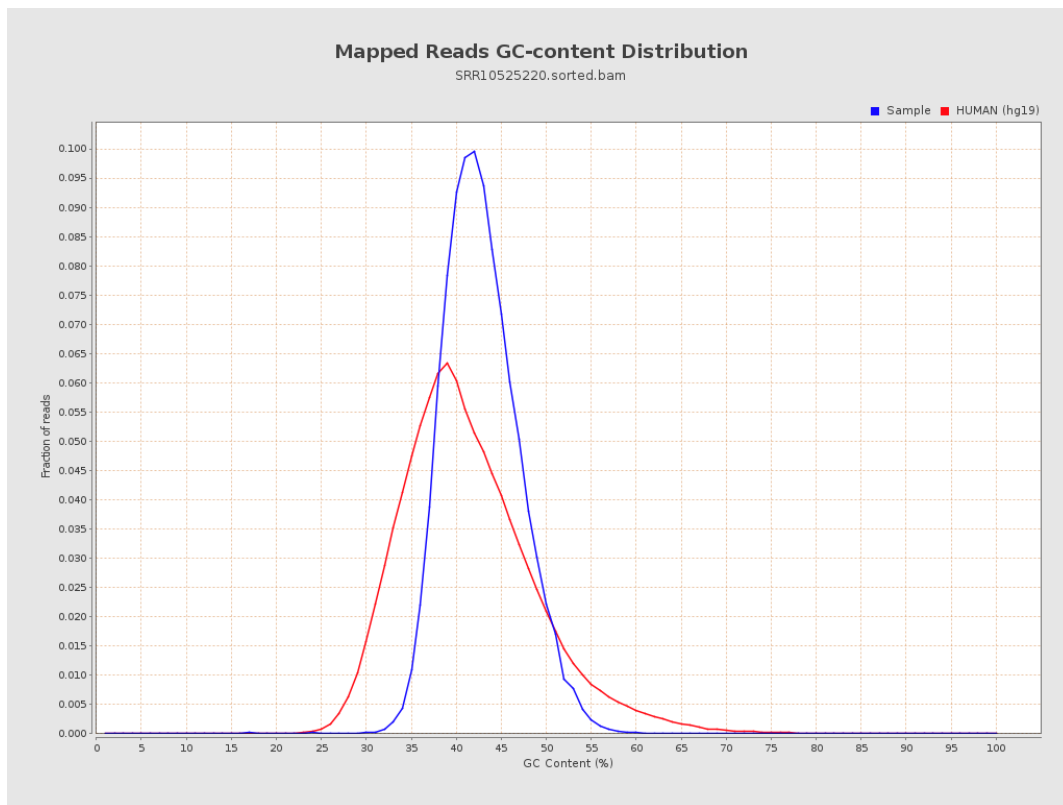
7. Results : Duplication Rate Histogram



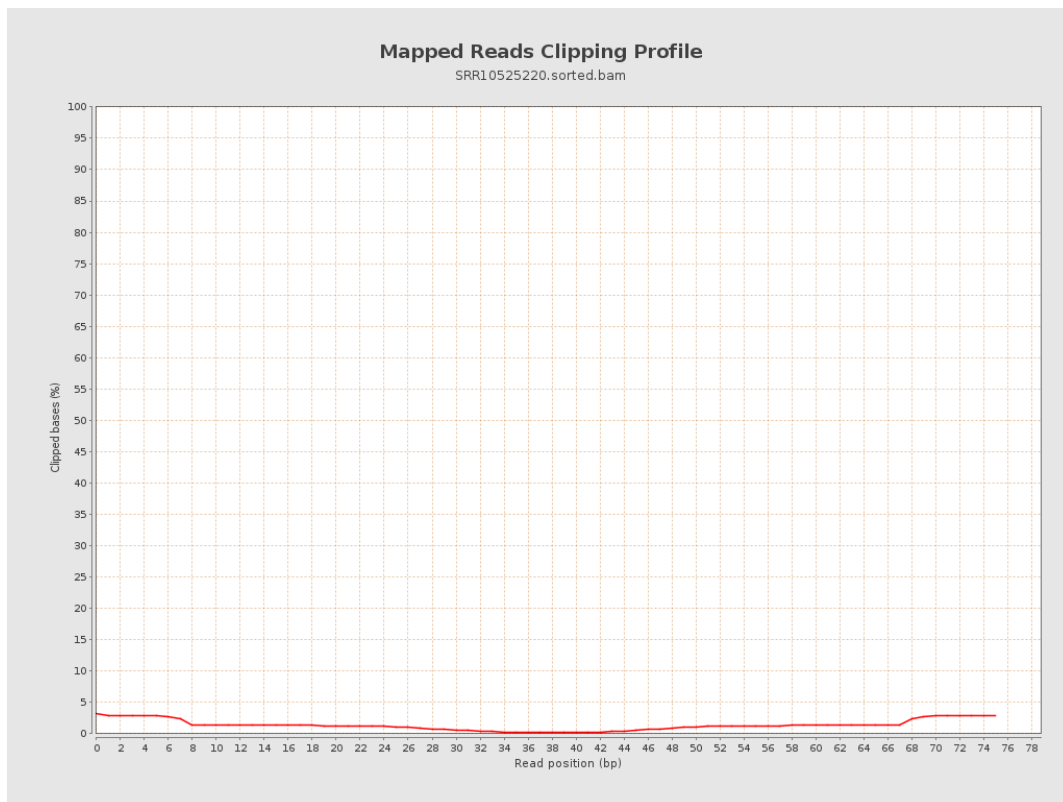
8. Results : Mapped Reads Nucleotide Content



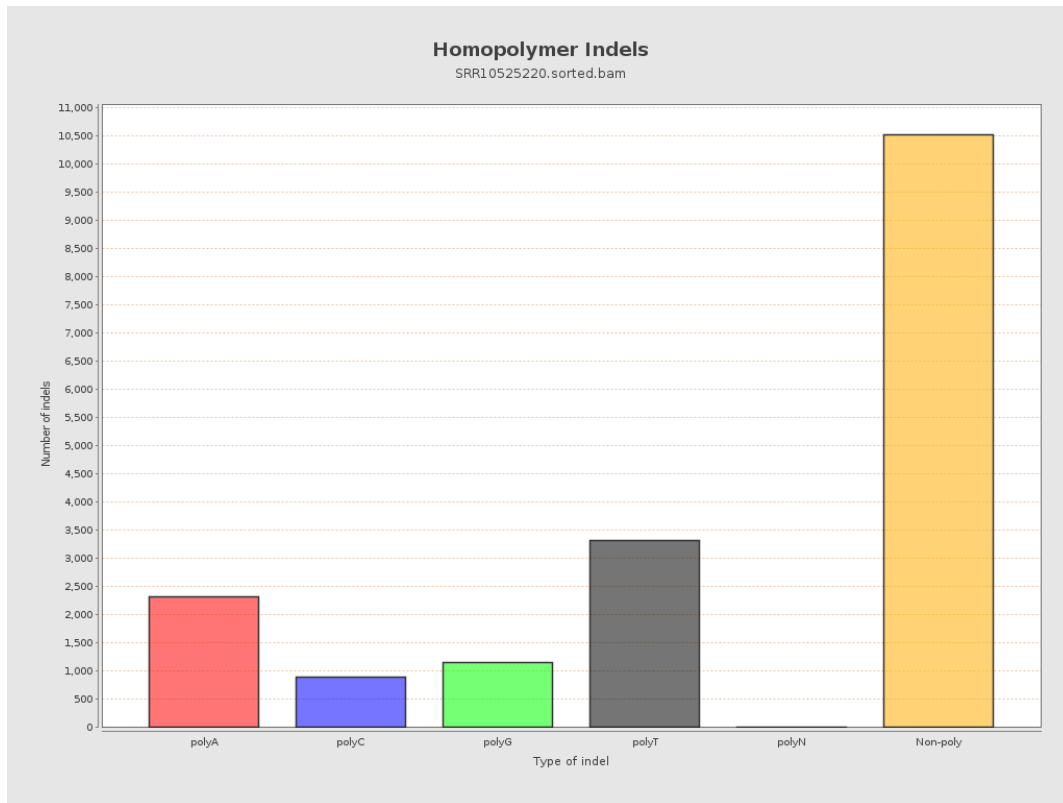
9. Results : Mapped Reads GC-content Distribution



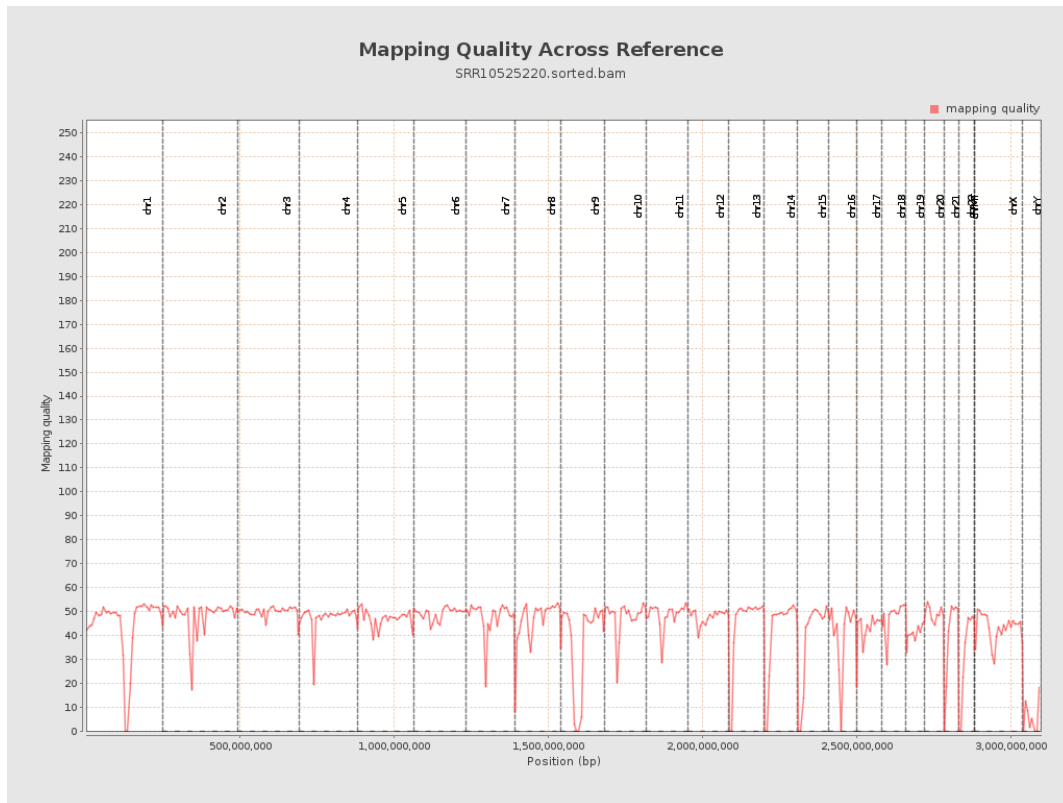
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

