

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 14:03:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525030.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_SRR10525030 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525030.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 14:03:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525030.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	778,537
Mapped reads	677,246 / 86.99%
Unmapped reads	101,291 / 13.01%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,461 / 0.7%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	14,273 / 1.83%
Duplication rate	1.21%
Clipped reads	681,011 / 87.47%

2.2. ACGT Content

Number/percentage of A's	9,141,557 / 23.66%
Number/percentage of C's	7,113,963 / 18.42%
Number/percentage of T's	12,431,164 / 32.18%
Number/percentage of G's	9,943,970 / 25.74%
Number/percentage of N's	351 / 0%
GC Percentage	44.16%

2.3. Coverage

Mean	0.0125

Standard Deviation	0.1638
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2.4. Mapping Quality

Mean Mapping Quality	41.15
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2.5. Mismatches and indels

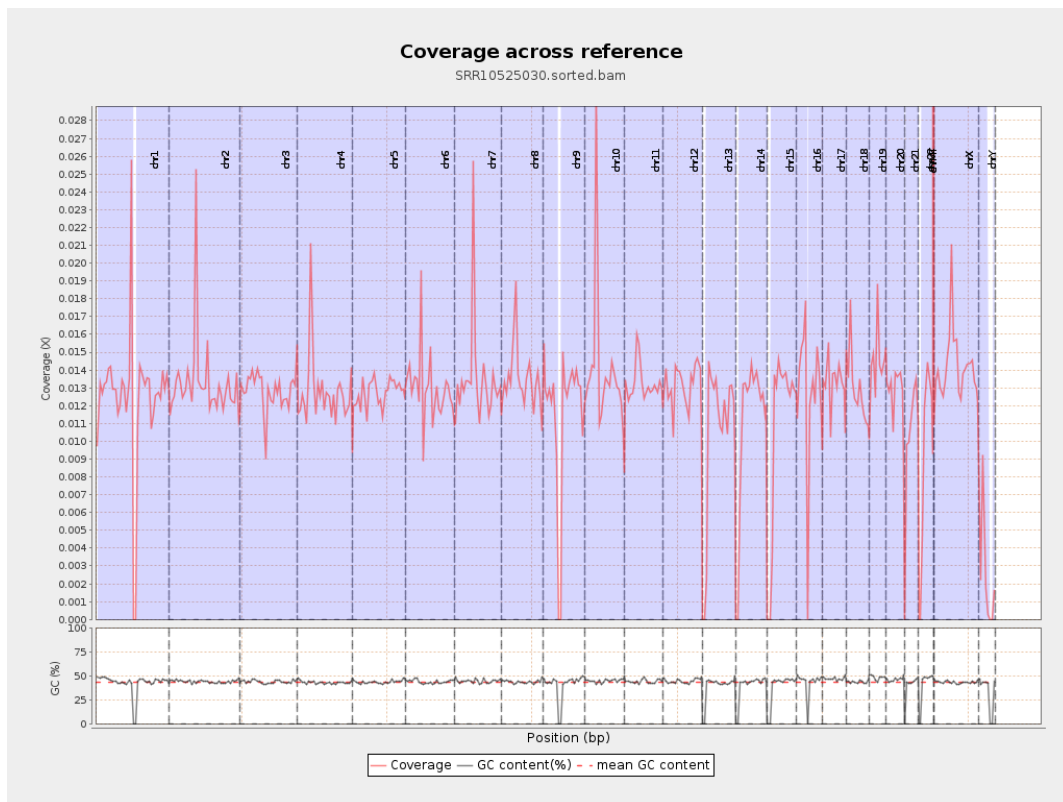
General error rate	0.5%
Mismatches	189,458
Insertions	2,739
Mapped reads with at least one insertion	0.4%
Deletions	6,477
Mapped reads with at least one deletion	0.95%
Homopolymer indels	42.48%

2.6. Chromosome stats

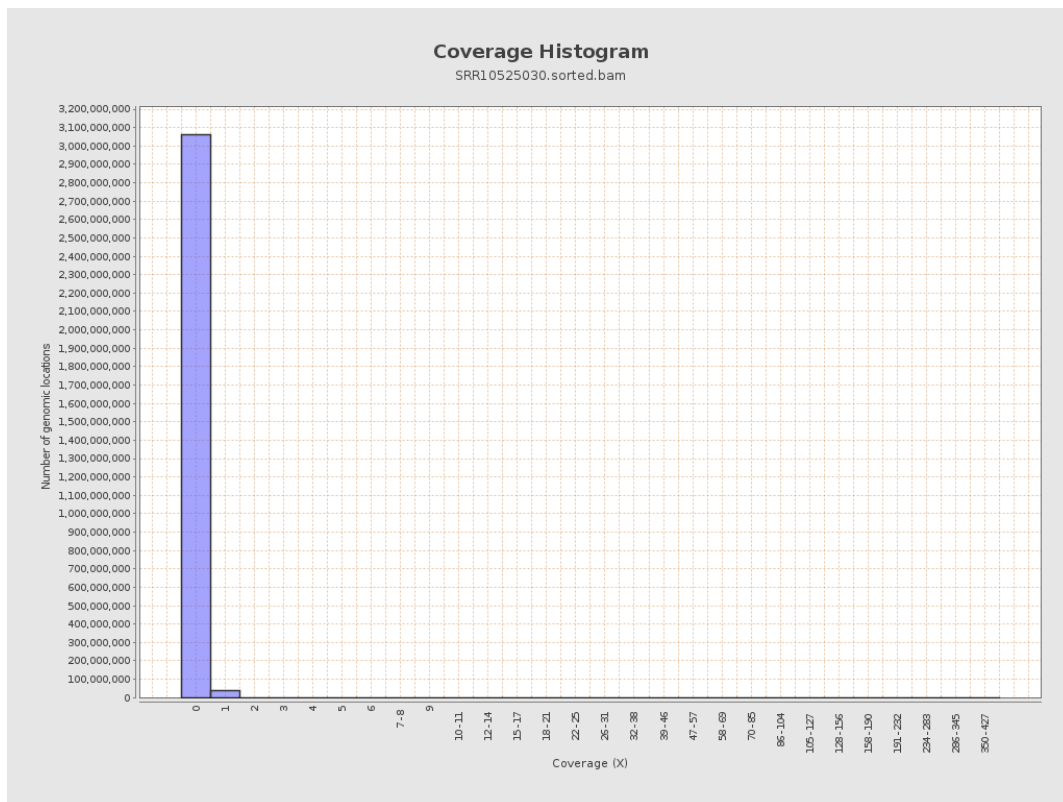
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	3092950	0.0124	0.3087
chr2	243199373	3227688	0.0133	0.1686
chr3	198022430	2535320	0.0128	0.1183
chr4	191154276	2434137	0.0127	0.1257
chr5	180915260	2303433	0.0127	0.1179
chr6	171115067	2215028	0.0129	0.1398
chr7	159138663	2147507	0.0135	0.1991

chr8	146364022	1971093	0.0135	0.1565
chr9	141213431	1609627	0.0114	0.1393
chr10	135534747	1887538	0.0139	0.1741
chr11	135006516	1774167	0.0131	0.1539
chr12	133851895	1754990	0.0131	0.1195
chr13	115169878	1191683	0.0103	0.1044
chr14	107349540	1176695	0.011	0.1124
chr15	102531392	1105478	0.0108	0.1163
chr16	90354753	1152454	0.0128	0.1263
chr17	81195210	1071380	0.0132	0.13
chr18	78077248	1016749	0.013	0.23
chr19	59128983	860273	0.0145	0.2135
chr20	63025520	807594	0.0128	0.1183
chr21	48129895	498183	0.0104	0.1114
chr22	51304566	459950	0.009	0.0969
chrMT	16571	5418	0.327	0.6588
chrX	155270560	2196020	0.0141	0.1361
chrY	59373566	146426	0.0025	0.0843

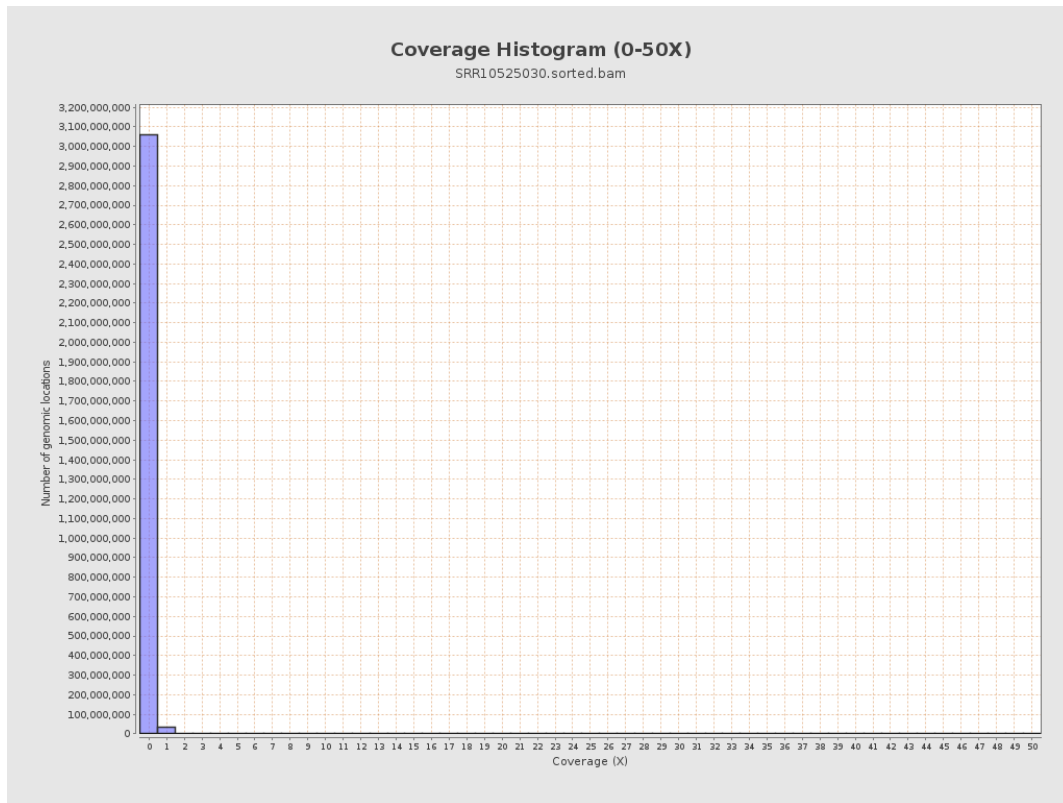
3. Results : Coverage across reference



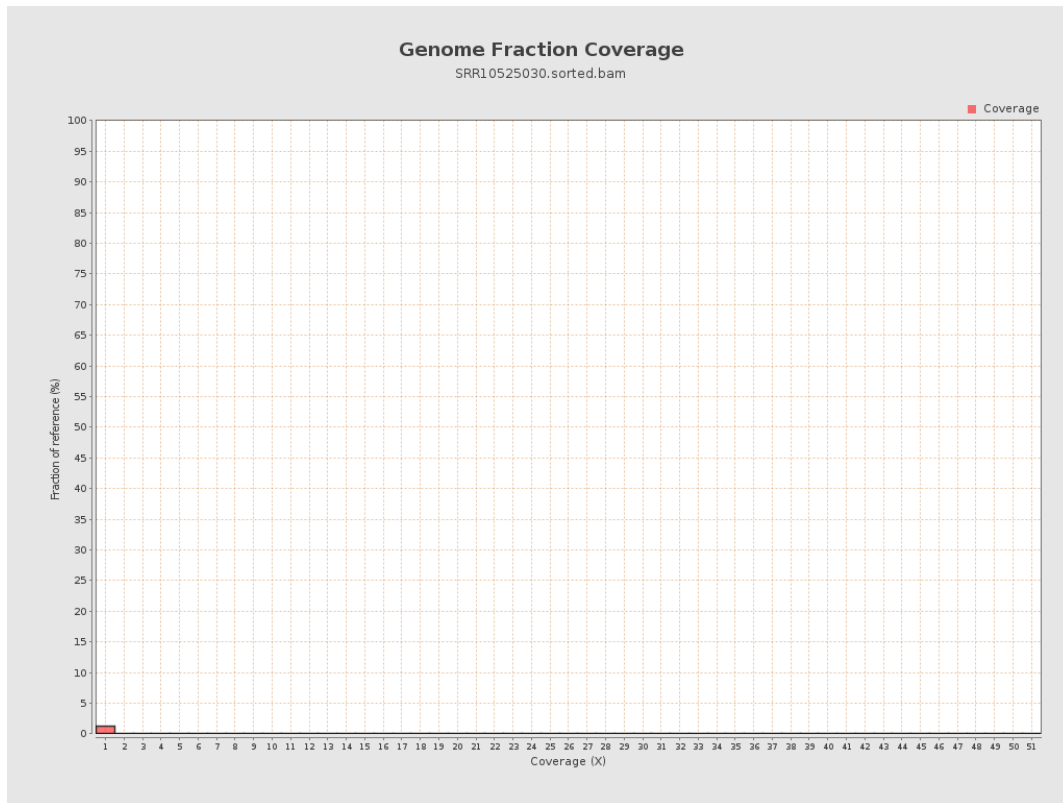
4. Results : Coverage Histogram



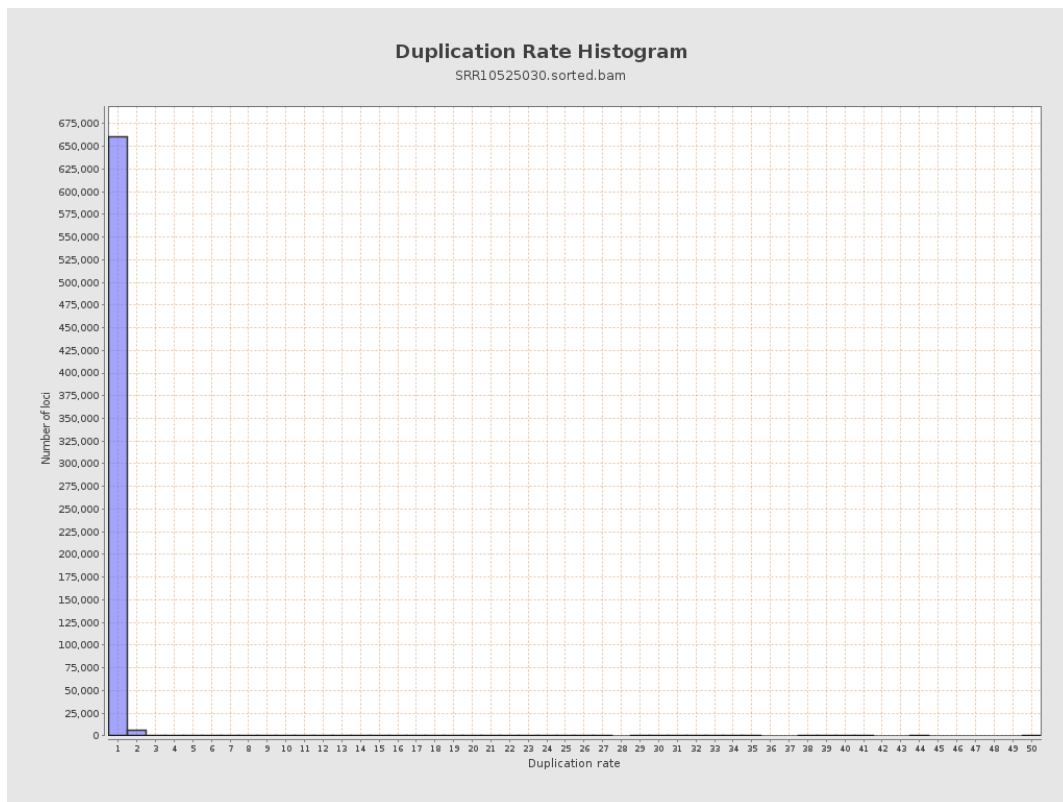
5. Results : Coverage Histogram (0-50X)



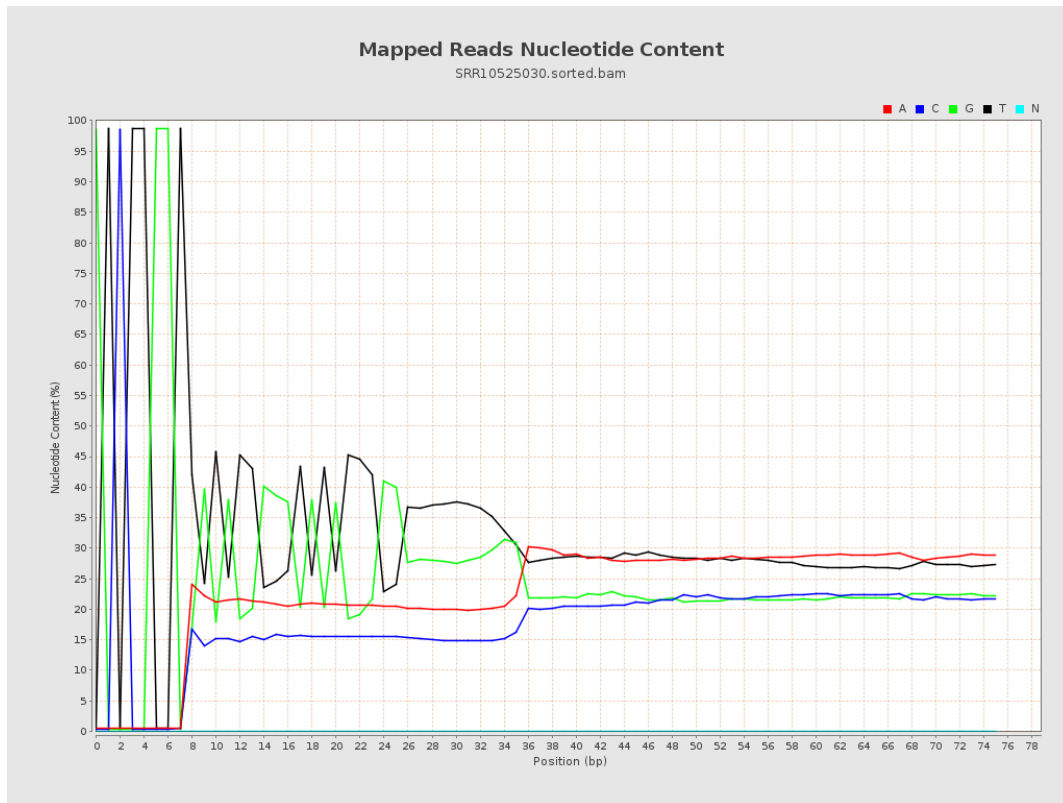
6. Results : Genome Fraction Coverage



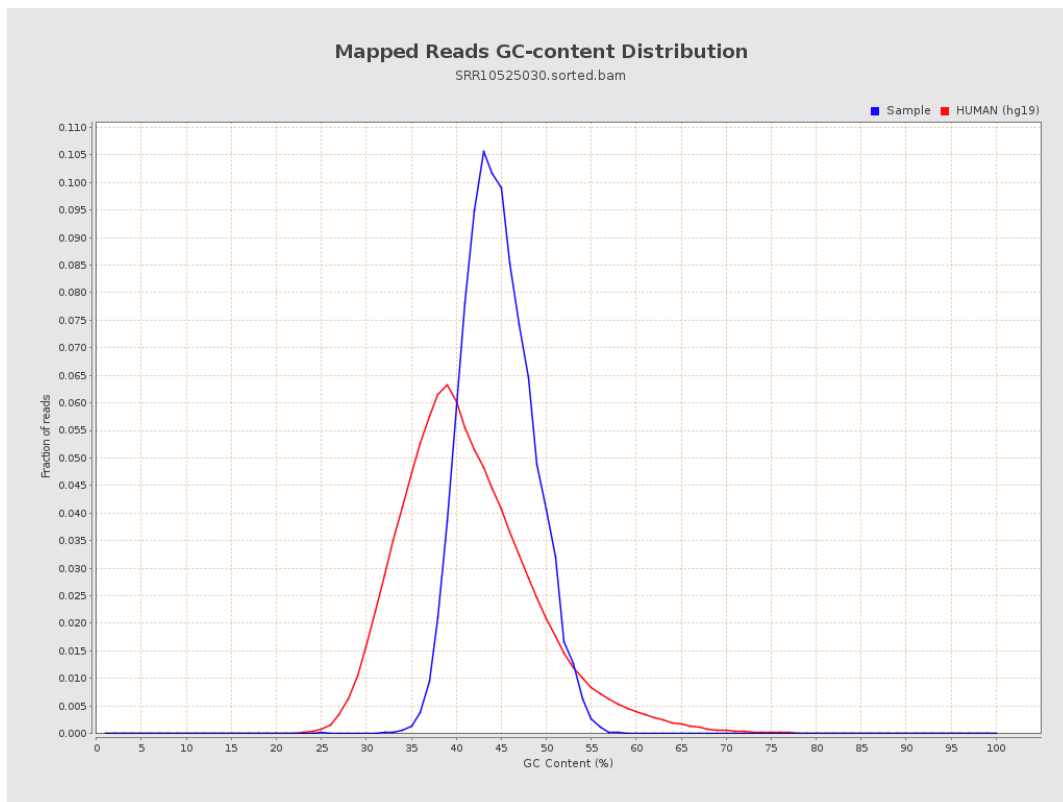
7. Results : Duplication Rate Histogram



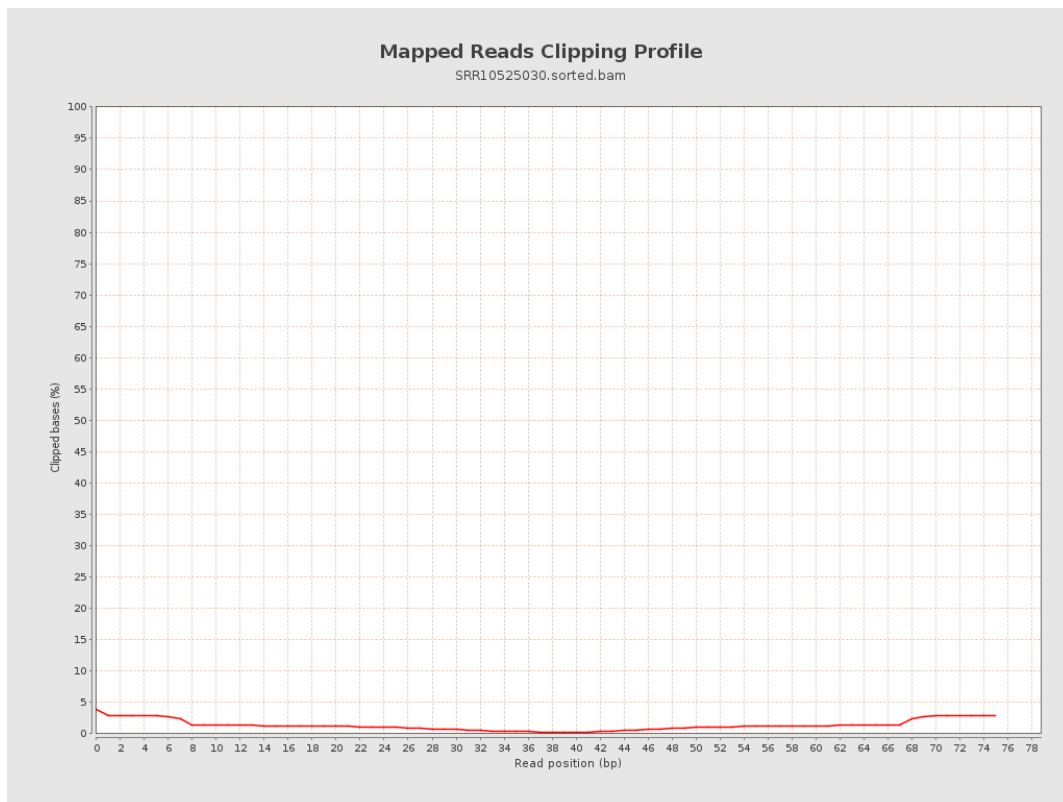
8. Results : Mapped Reads Nucleotide Content



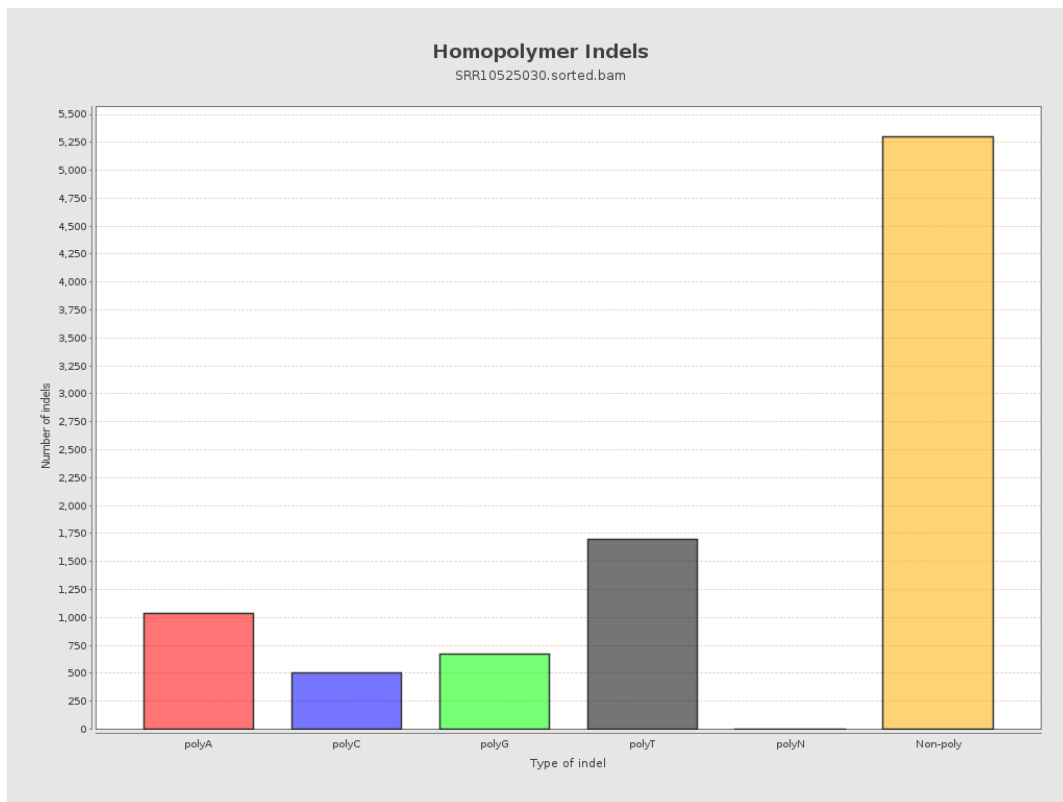
9. Results : Mapped Reads GC-content Distribution



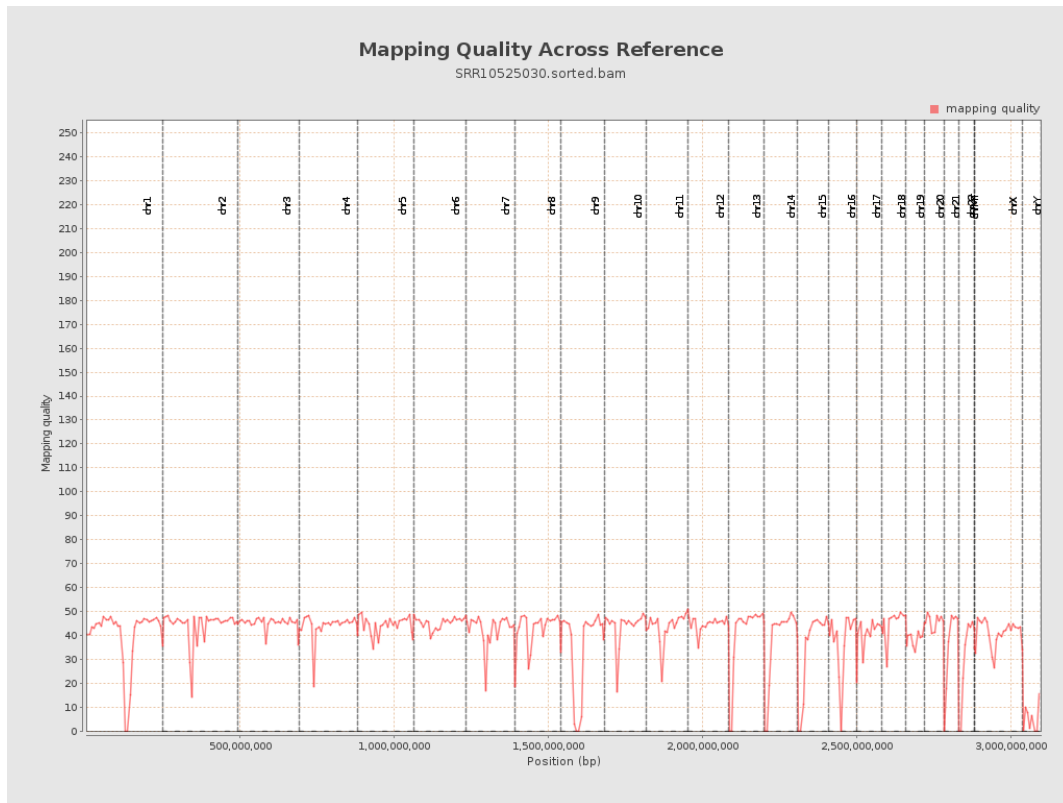
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

