

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 02:32:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085127.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_SRR3085127 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085127.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 02:32:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085127.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,124,314
Mapped reads	991,381 / 88.18%
Unmapped reads	132,933 / 11.82%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,609 / 0.68%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	28,921 / 2.57%
Duplication rate	2.16%
Clipped reads	440,383 / 39.17%

2.2. ACGT Content

Number/percentage of A's	18,719,610 / 28.21%
Number/percentage of C's	12,407,821 / 18.7%
Number/percentage of T's	20,407,642 / 30.76%
Number/percentage of G's	14,798,965 / 22.3%
Number/percentage of N's	14,345 / 0.02%
GC Percentage	41.01%

2.3. Coverage

Mean	0.0214

Standard Deviation	0.2329
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2.4. Mapping Quality

Mean Mapping Quality	44.7
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2.5. Mismatches and indels

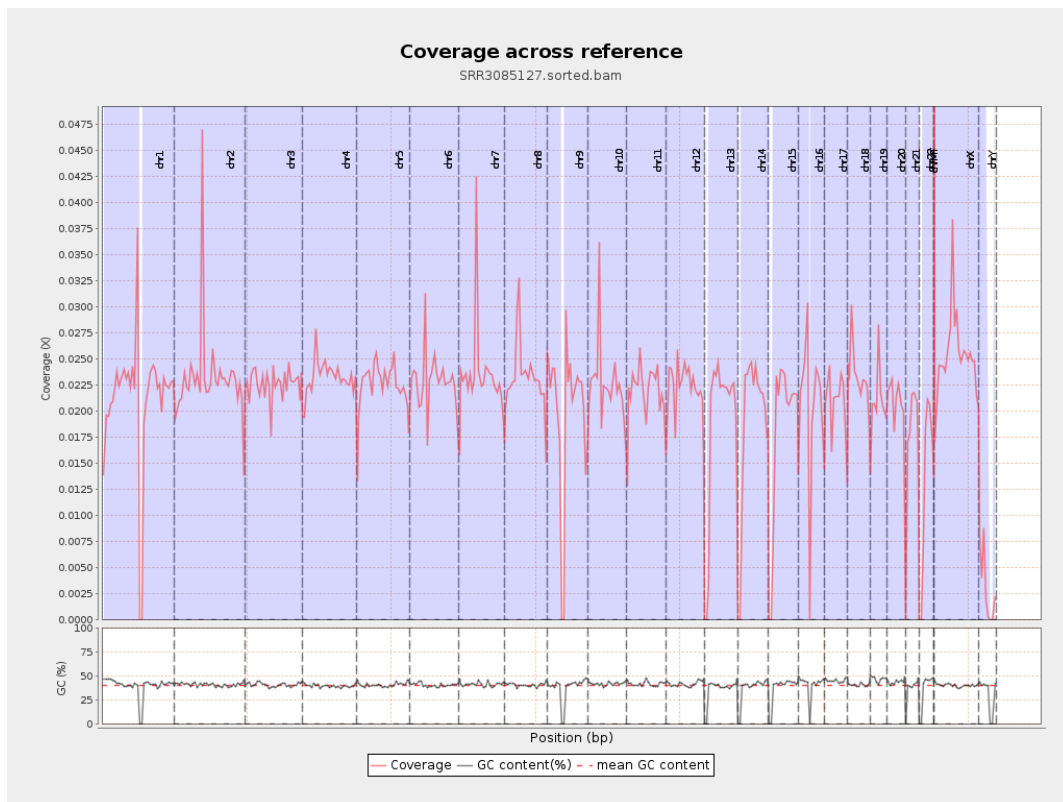
General error rate	0.91%
Mismatches	594,929
Insertions	5,743
Mapped reads with at least one insertion	0.57%
Deletions	15,490
Mapped reads with at least one deletion	1.55%
Homopolymer indels	46.56%

2.6. Chromosome stats

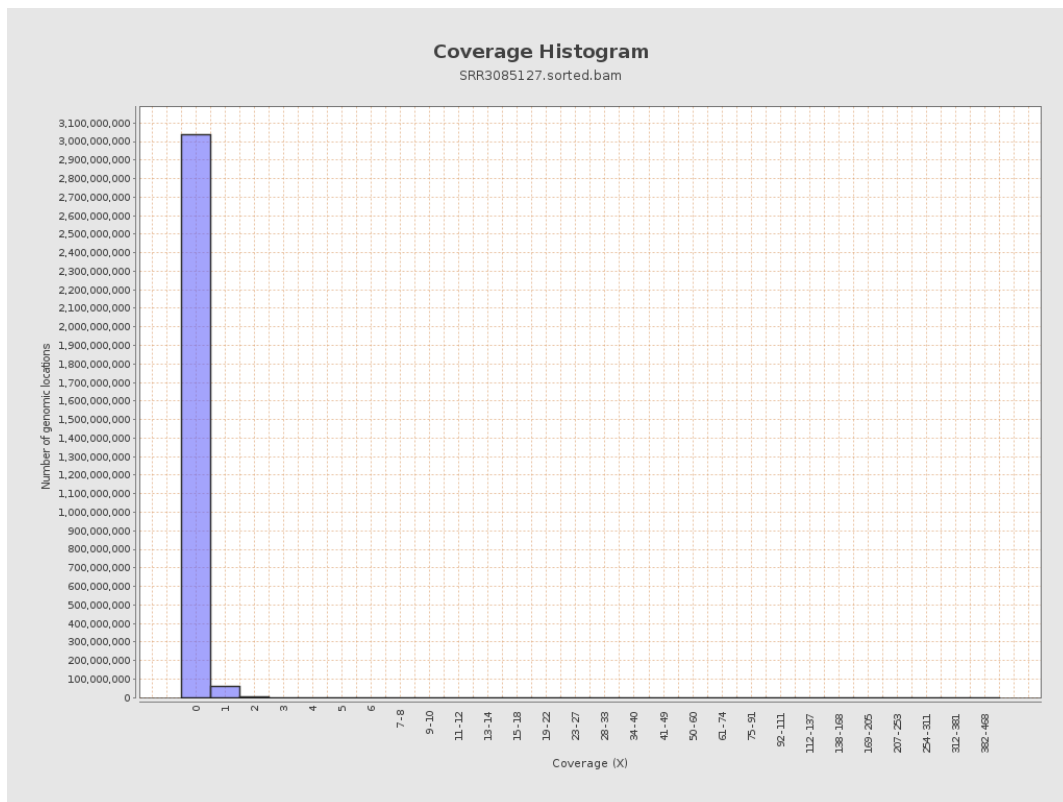
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5259664	0.0211	0.3689
chr2	243199373	5640143	0.0232	0.2869
chr3	198022430	4470299	0.0226	0.1587
chr4	191154276	4436347	0.0232	0.1654
chr5	180915260	4124660	0.0228	0.1602
chr6	171115067	3893788	0.0228	0.1819
chr7	159138663	3744633	0.0235	0.3221

chr8	146364022	3410194	0.0233	0.3306
chr9	141213431	2801501	0.0198	0.2341
chr10	135534747	3055914	0.0225	0.2091
chr11	135006516	2991356	0.0222	0.212
chr12	133851895	2992999	0.0224	0.1599
chr13	115169878	2140034	0.0186	0.1439
chr14	107349540	2013226	0.0188	0.1557
chr15	102531392	1848147	0.018	0.1433
chr16	90354753	1826739	0.0202	0.1656
chr17	81195210	1694050	0.0209	0.1664
chr18	78077248	1823464	0.0234	0.3889
chr19	59128983	1253745	0.0212	0.2922
chr20	63025520	1301941	0.0207	0.1558
chr21	48129895	843804	0.0175	0.1464
chr22	51304566	676369	0.0132	0.1208
chrMT	16571	2997	0.1809	0.4459
chrX	155270560	3952951	0.0255	0.1874
chrY	59373566	175113	0.0029	0.079

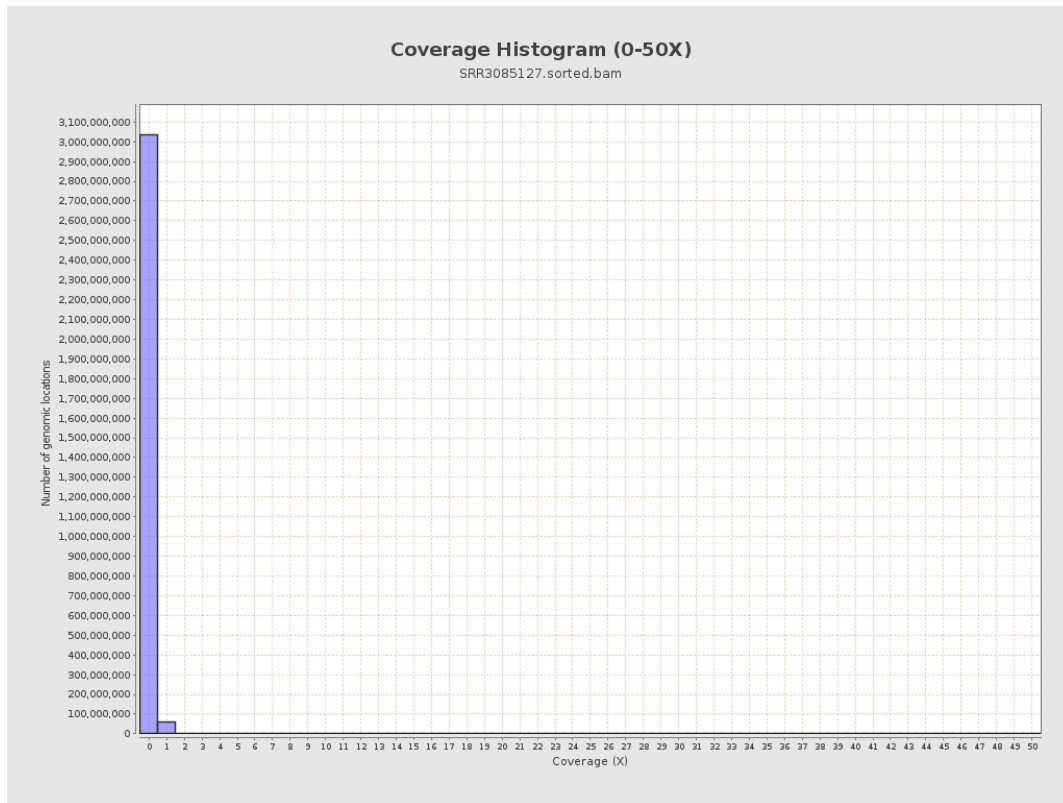
3. Results : Coverage across reference



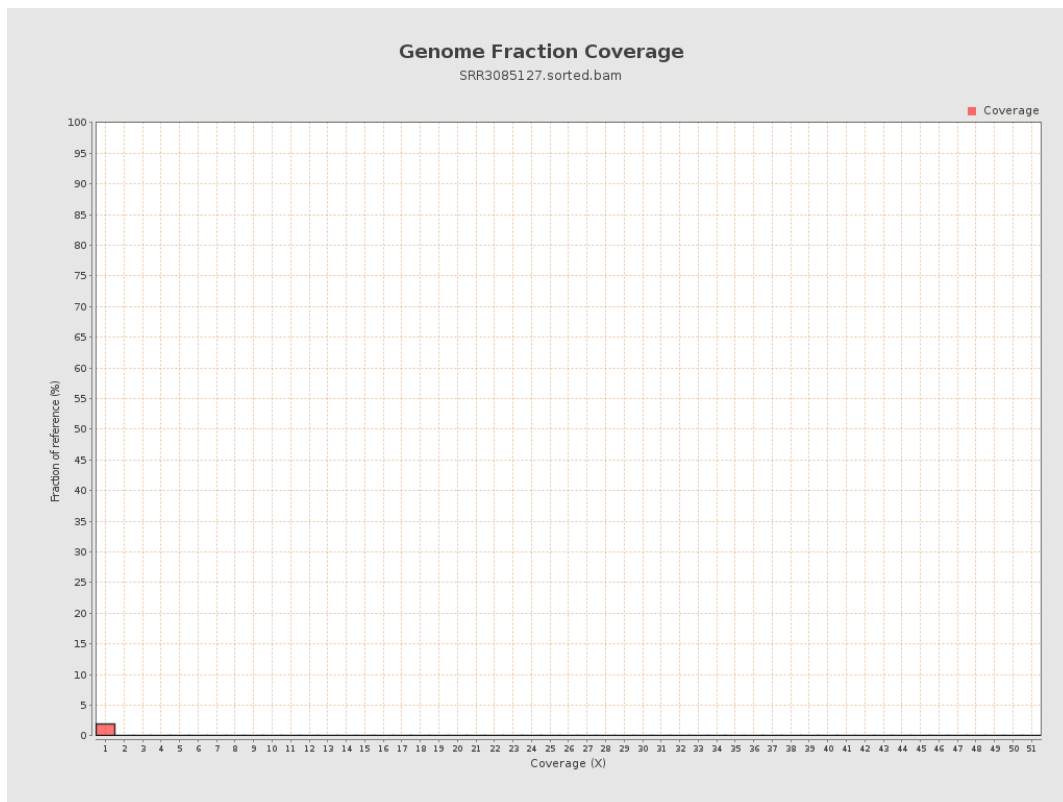
4. Results : Coverage Histogram



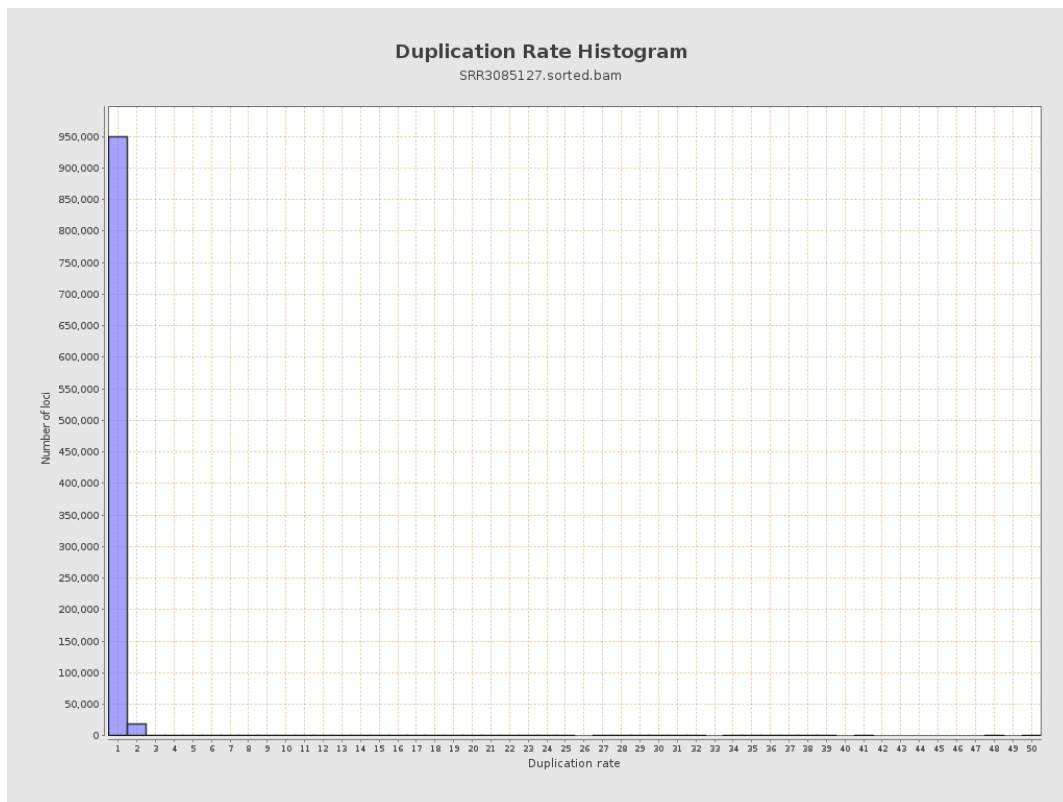
5. Results : Coverage Histogram (0-50X)



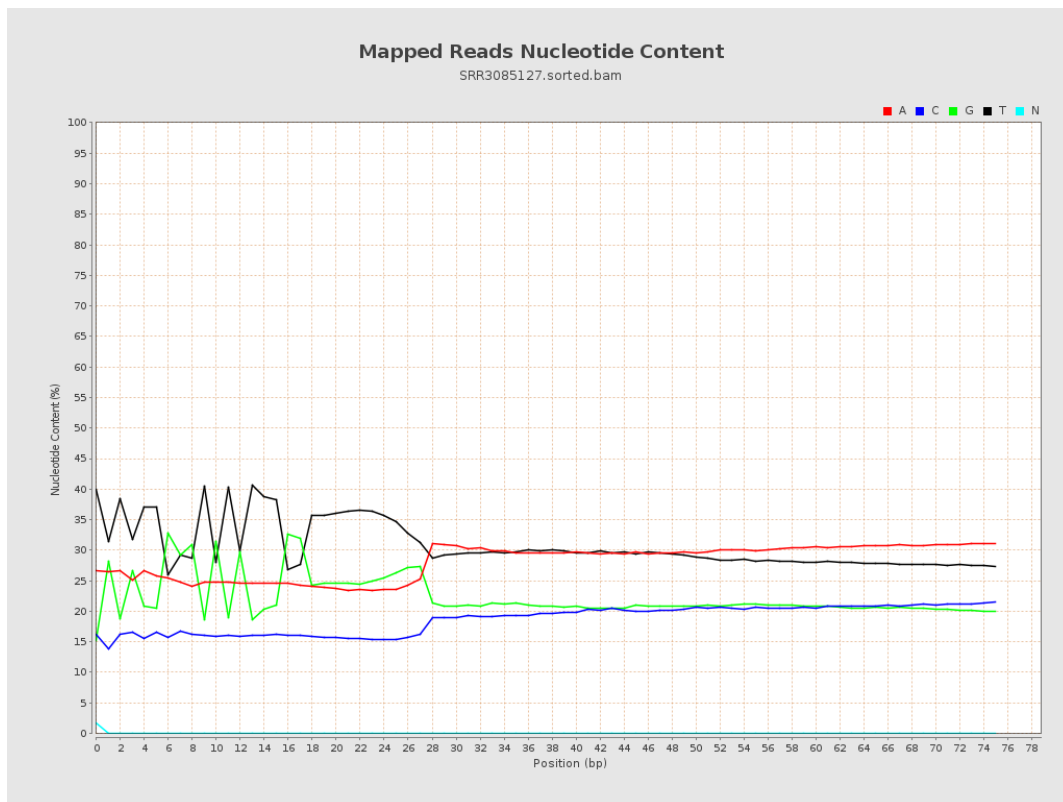
6. Results : Genome Fraction Coverage



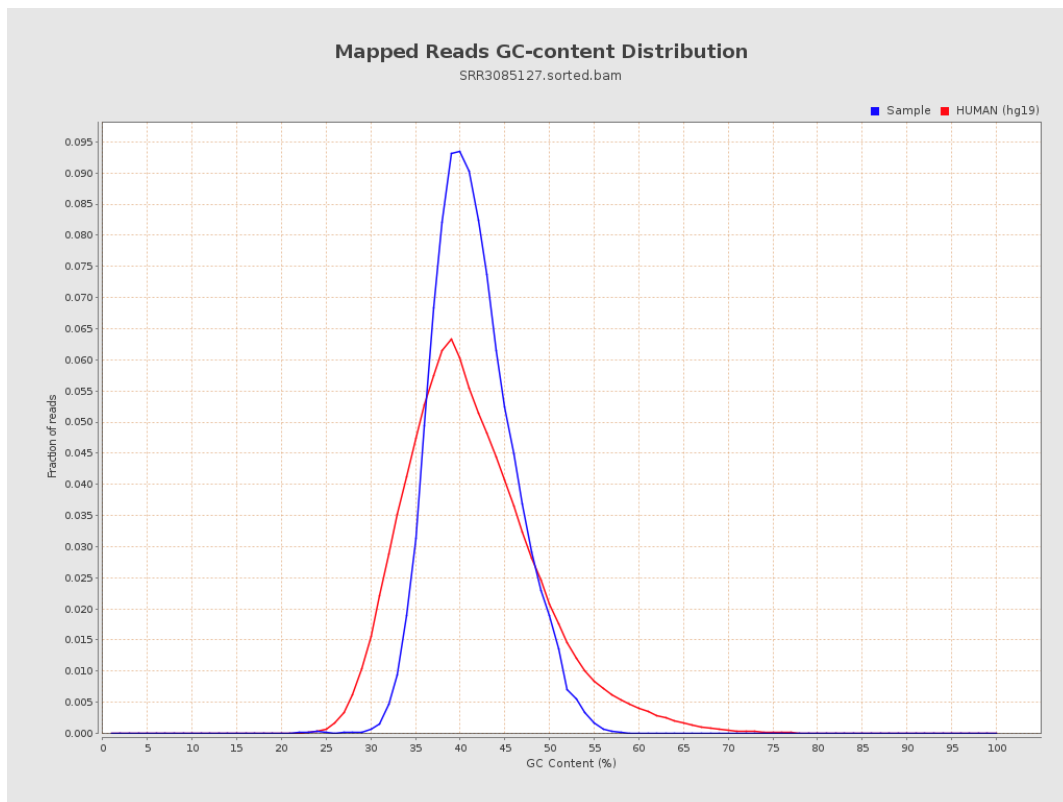
7. Results : Duplication Rate Histogram



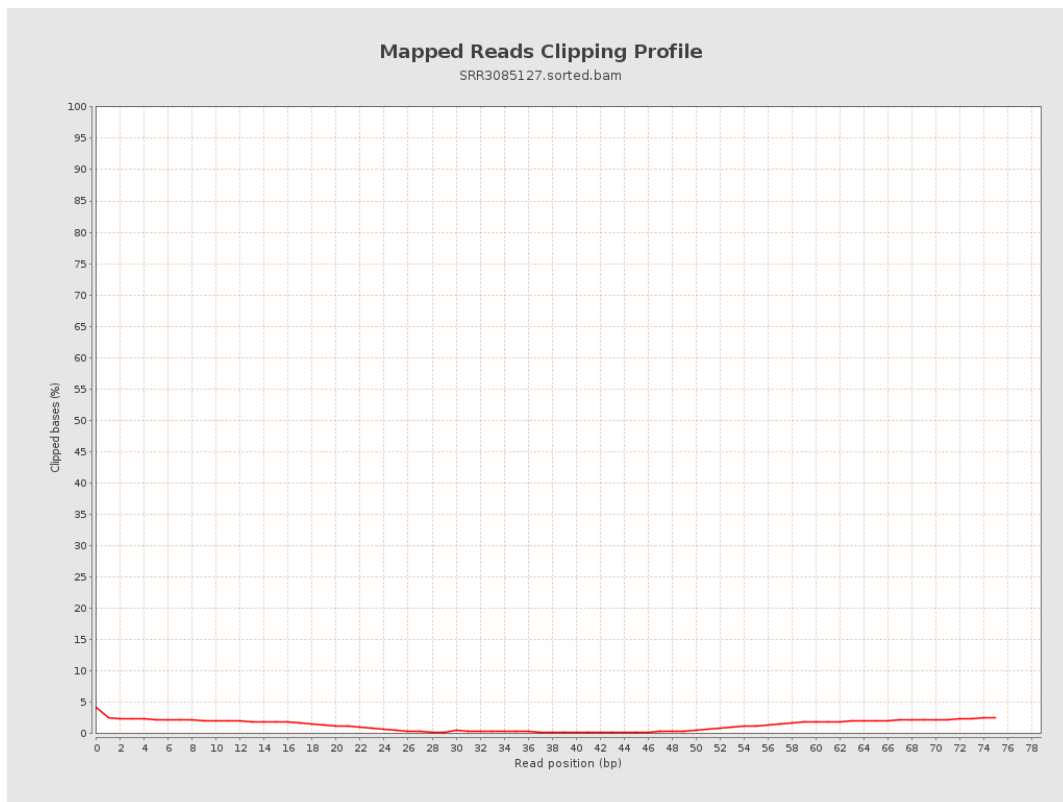
8. Results : Mapped Reads Nucleotide Content



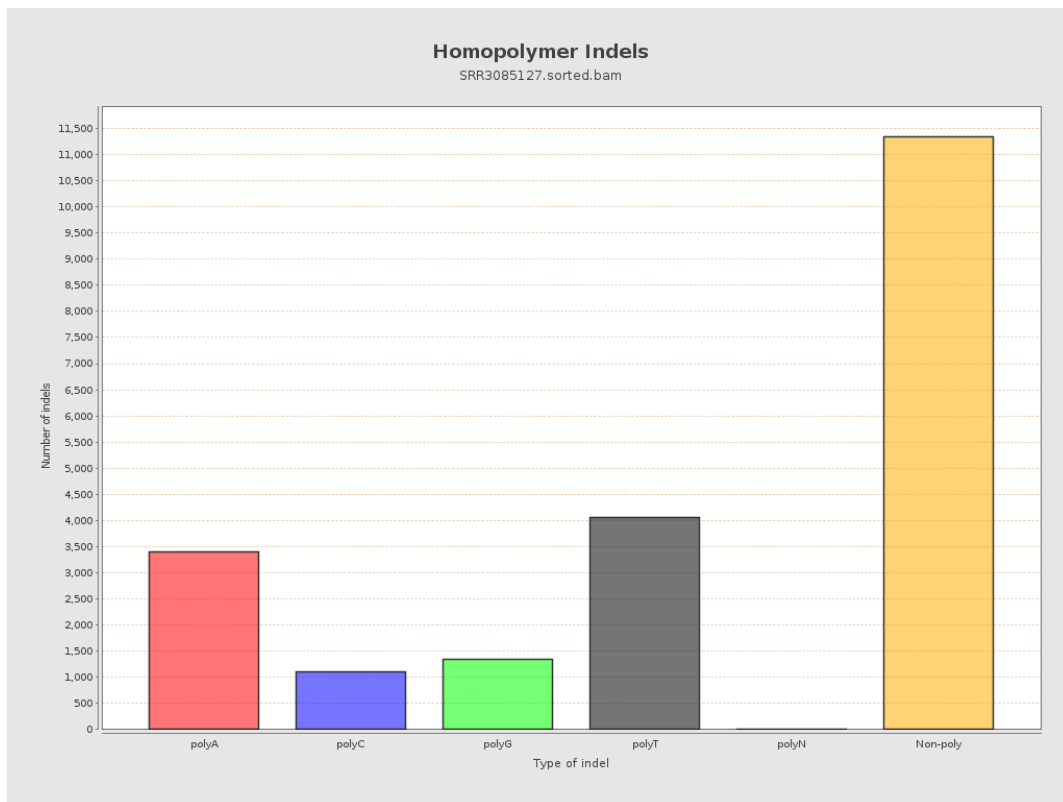
9. Results : Mapped Reads GC-content Distribution



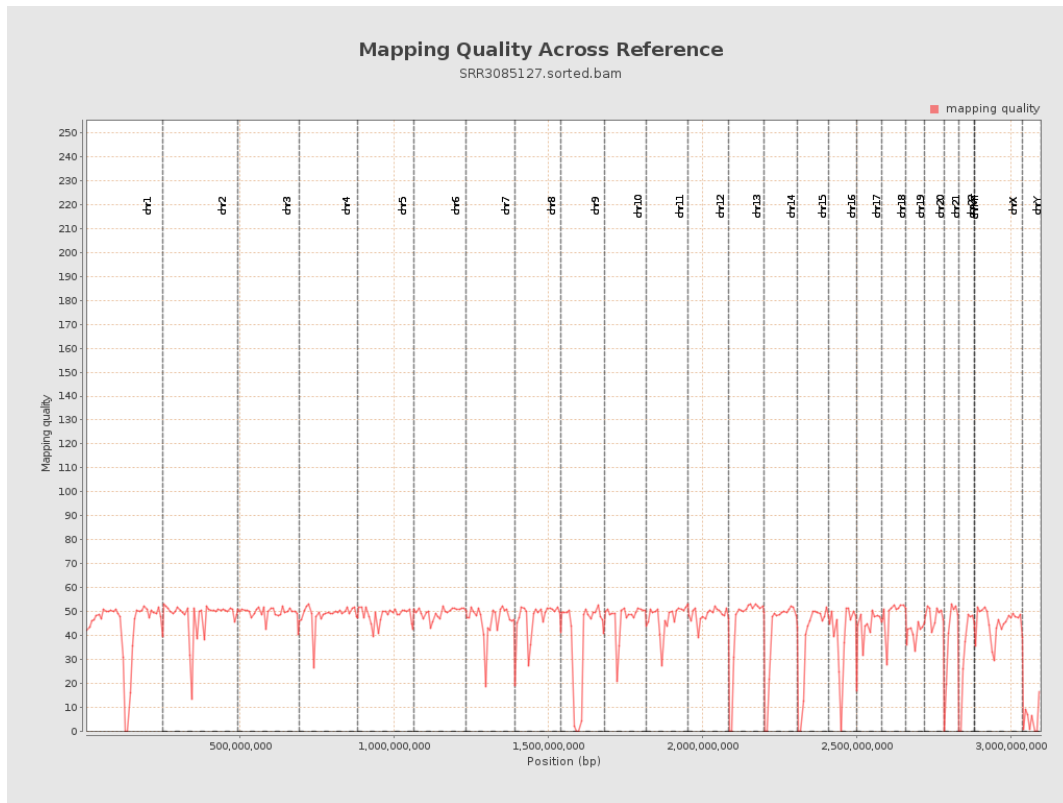
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

