

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 04:33:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548927.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_SRR1548927 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548927.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 04:33:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1548927.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,089,646
Mapped reads	7,996,127 / 87.97%
Unmapped reads	1,093,519 / 12.03%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	293,050 / 3.22%
Duplication rate	2.63%
Clipped reads	529,070 / 5.82%

2.2. ACGT Content

Number/percentage of A's	92,861,475 / 29.31%
Number/percentage of C's	65,105,995 / 20.55%
Number/percentage of T's	93,544,809 / 29.53%
Number/percentage of G's	65,315,337 / 20.62%
Number/percentage of N's	2,710 / 0%
GC Percentage	41.16%

2.3. Coverage

Mean	0.1024
Standard Deviation	0.8996

2.4. Mapping Quality

Mean Mapping Quality	41.61
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2.5. Mismatches and indels

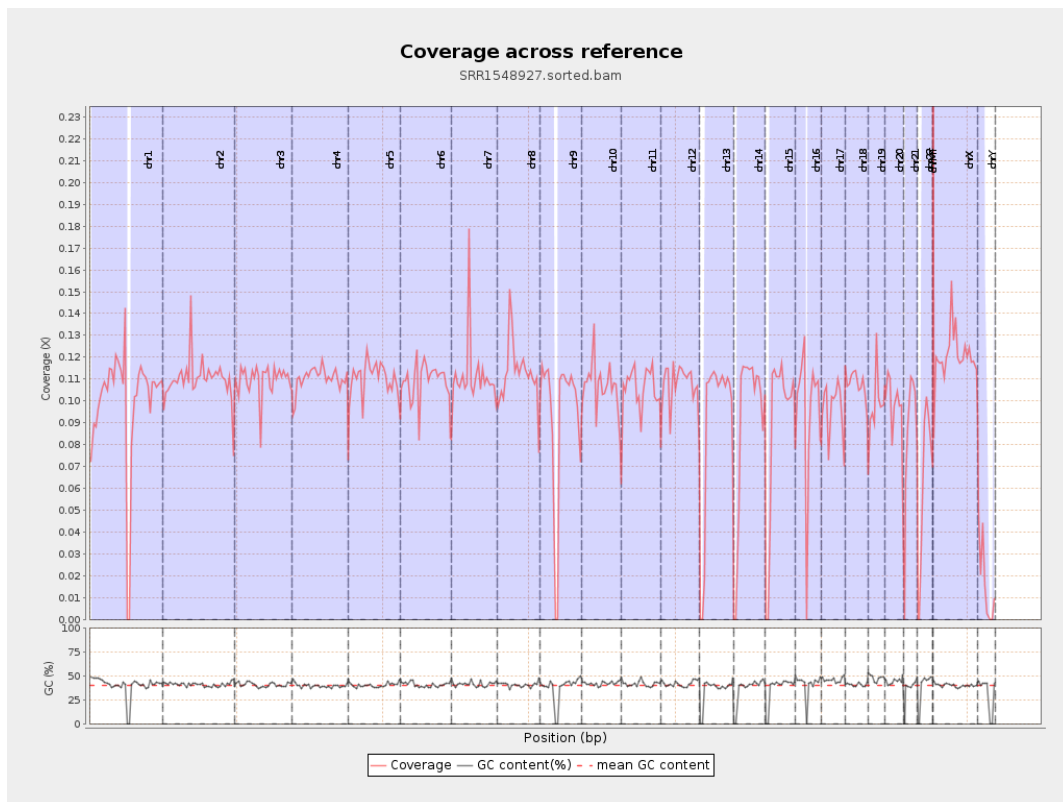
General error rate	0.28%
Mismatches	861,049
Insertions	9,228
Mapped reads with at least one insertion	0.12%
Deletions	24,590
Mapped reads with at least one deletion	0.31%
Homopolymer indels	42.16%

2.6. Chromosome stats

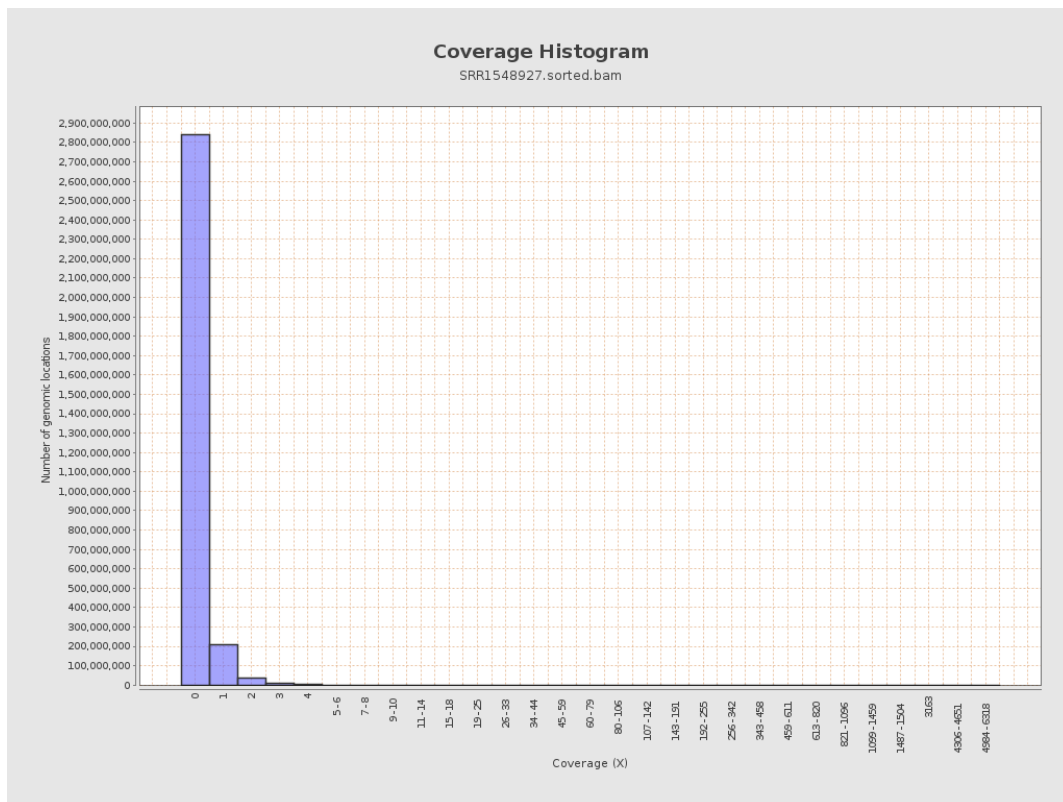
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	24839215	0.0997	1.0791
chr2	243199373	26776053	0.1101	0.6027
chr3	198022430	21715240	0.1097	0.3934
chr4	191154276	21115836	0.1105	0.4095
chr5	180915260	19881833	0.1099	0.403
chr6	171115067	18675838	0.1091	0.4512
chr7	159138663	17671350	0.111	0.9603
chr8	146364022	16516977	0.1128	3.0841

chr9	141213431	13234506	0.0937	0.5963
chr10	135534747	14491786	0.1069	0.5416
chr11	135006516	14281504	0.1058	0.6357
chr12	133851895	14462697	0.108	0.4076
chr13	115169878	10400051	0.0903	0.353
chr14	107349540	9816906	0.0914	0.4333
chr15	102531392	9043889	0.0882	0.3537
chr16	90354753	8518271	0.0943	0.4122
chr17	81195210	7915474	0.0975	0.4065
chr18	78077248	8433809	0.108	1.0935
chr19	59128983	5860525	0.0991	0.9831
chr20	63025520	6201408	0.0984	0.3906
chr21	48129895	4073066	0.0846	0.4052
chr22	51304566	3247006	0.0633	0.3315
chrMT	16571	9648	0.5822	1.0311
chrX	155270560	18715788	0.1205	0.513
chrY	59373566	964272	0.0162	0.2099

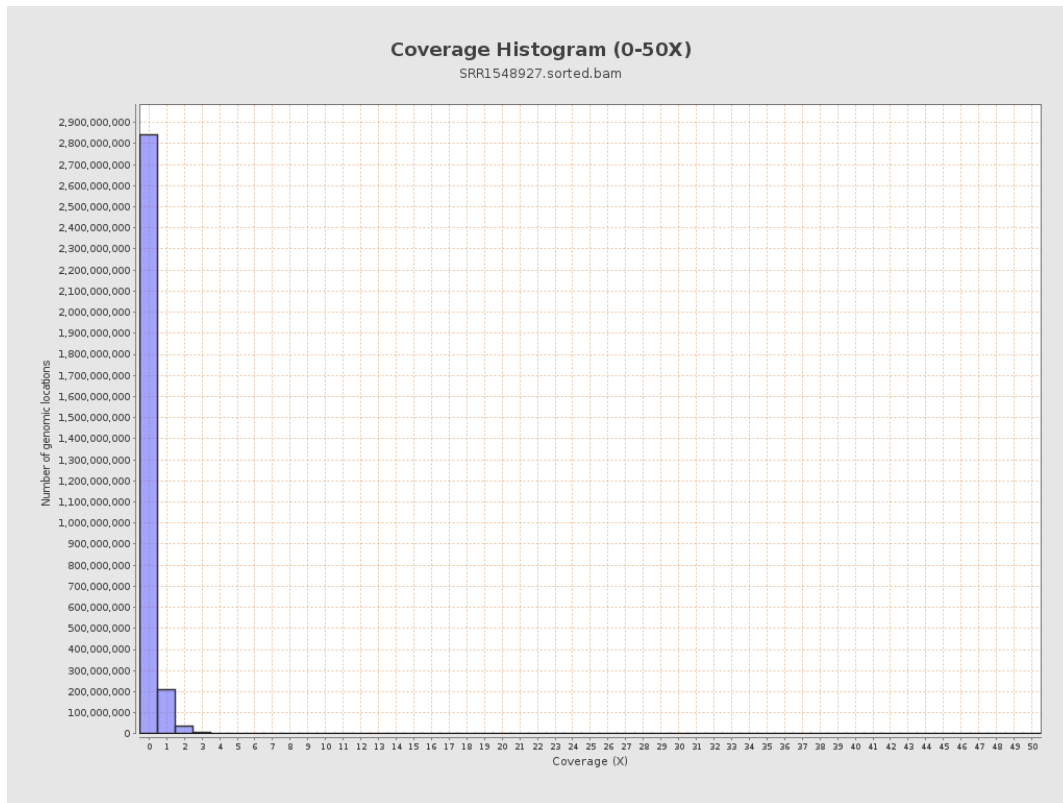
3. Results : Coverage across reference



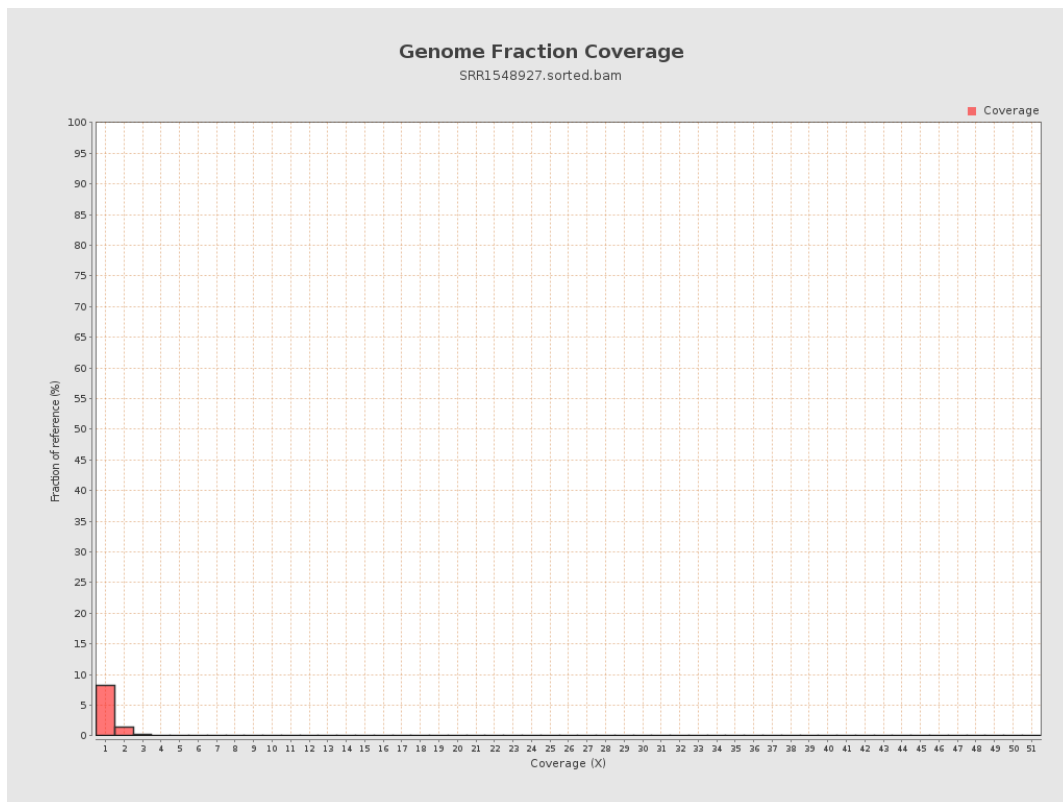
4. Results : Coverage Histogram



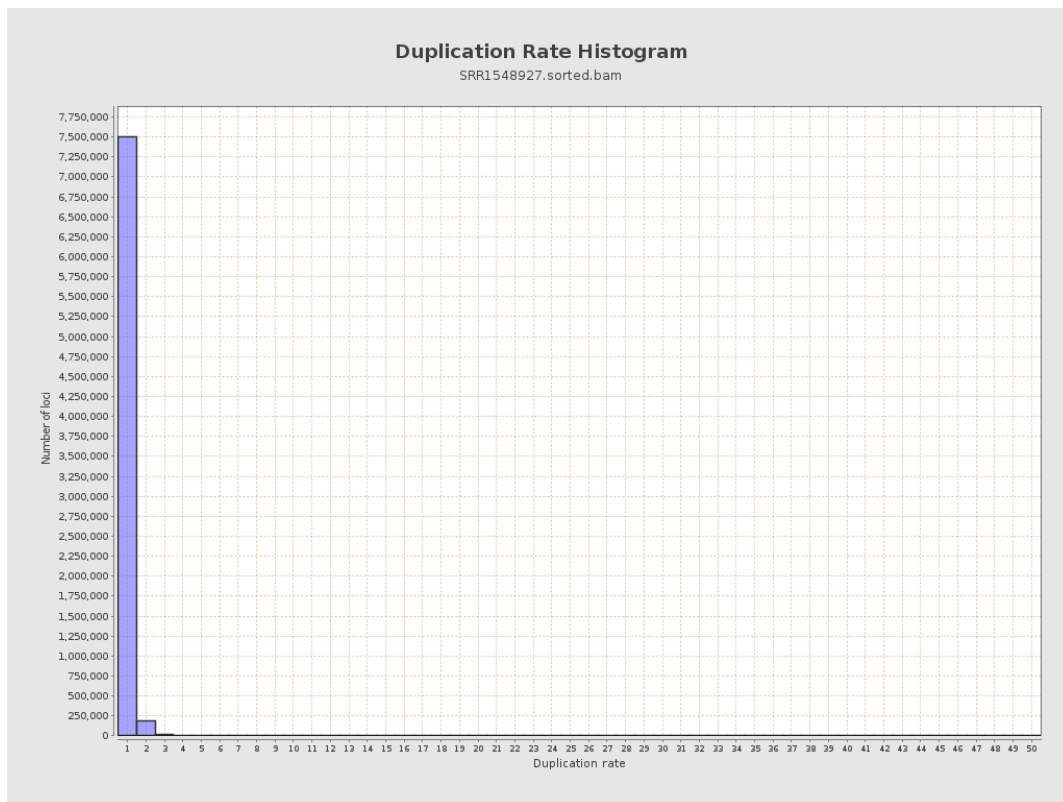
5. Results : Coverage Histogram (0-50X)



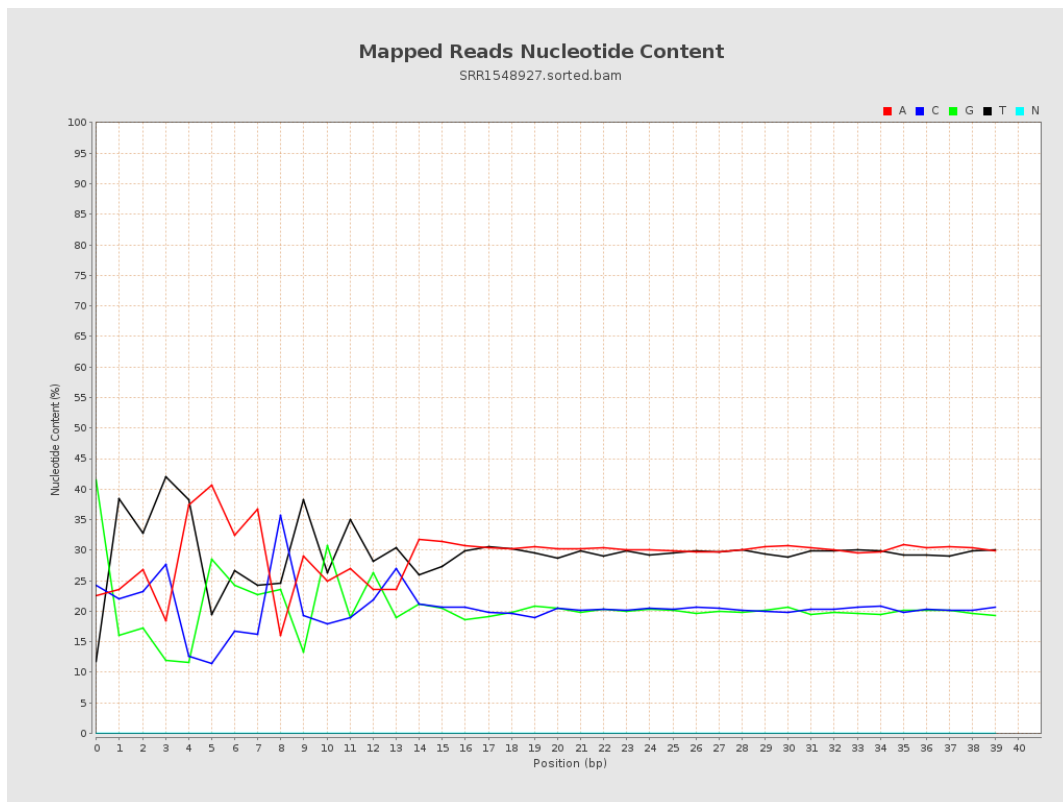
6. Results : Genome Fraction Coverage



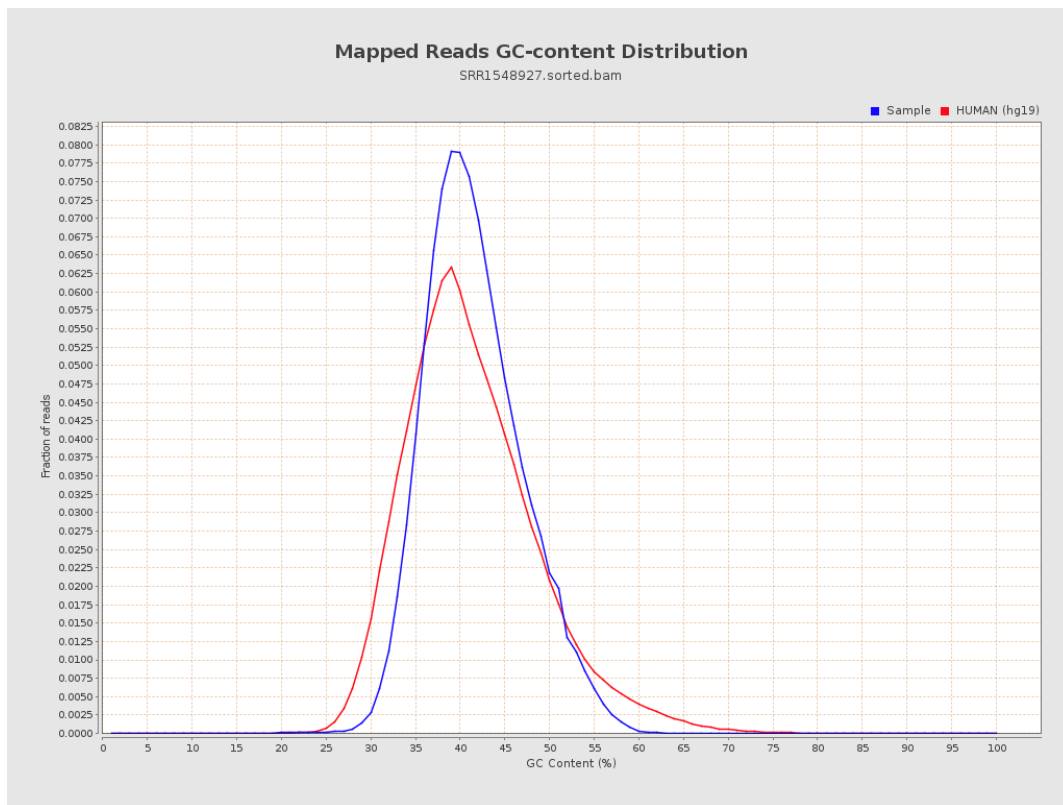
7. Results : Duplication Rate Histogram



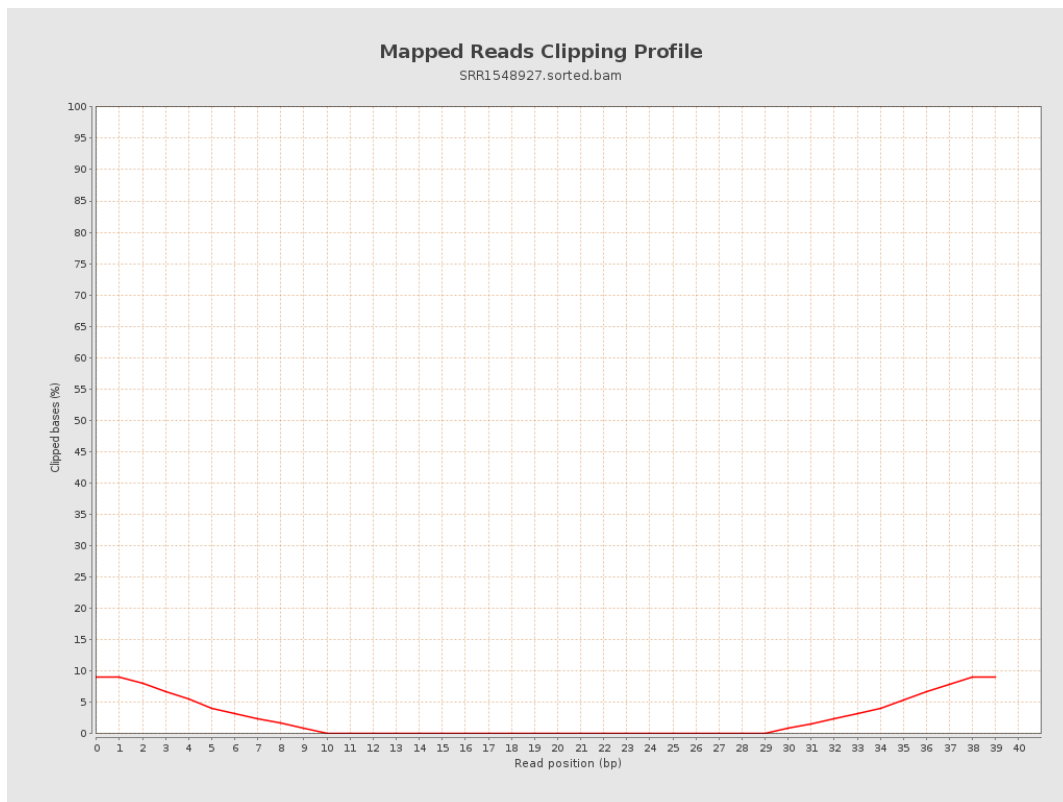
8. Results : Mapped Reads Nucleotide Content



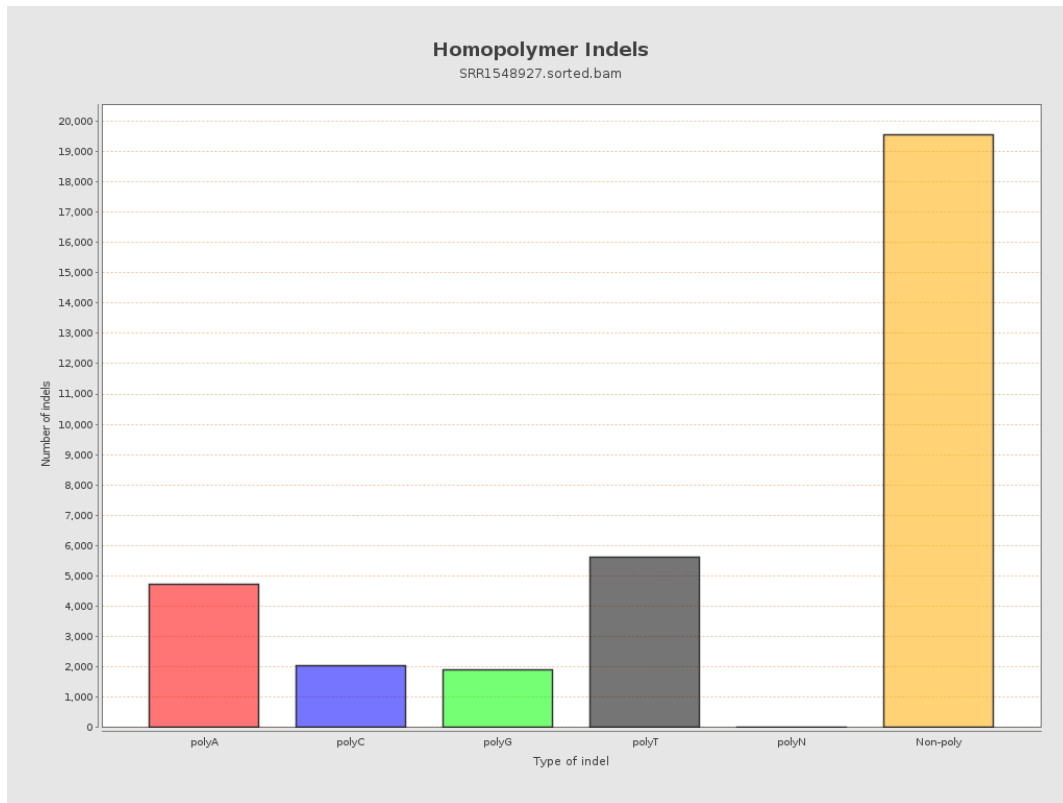
9. Results : Mapped Reads GC-content Distribution



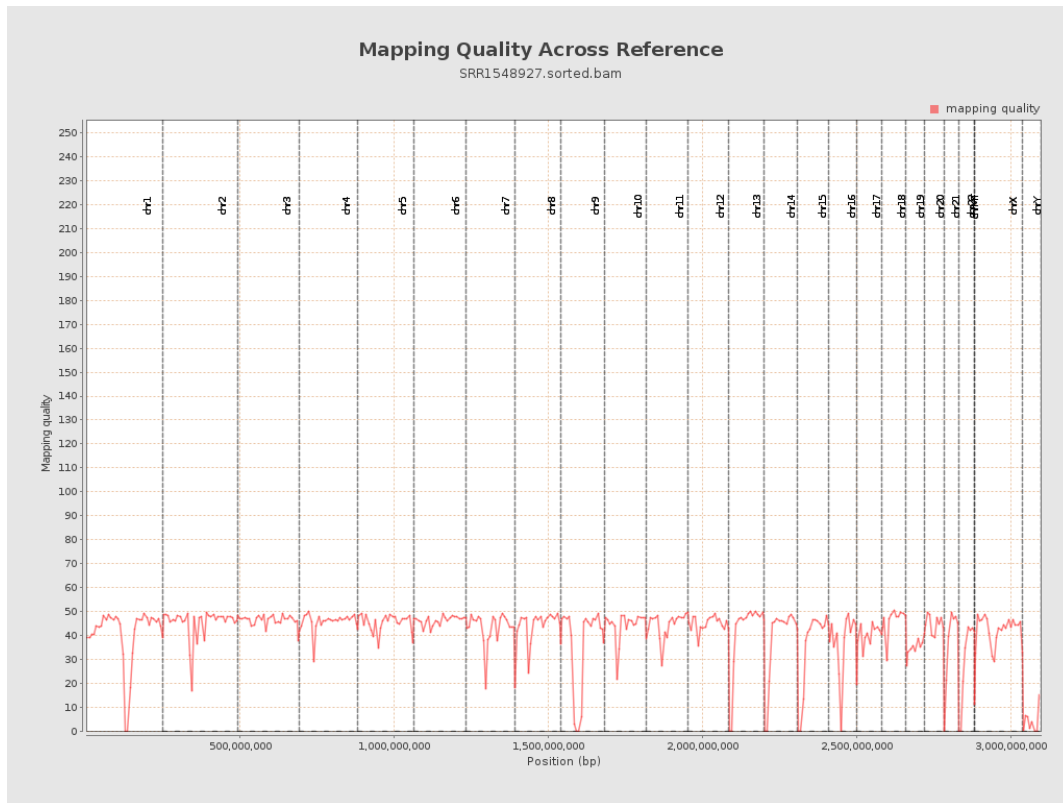
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

