

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 12:25:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10251077.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_SRR10251077 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10251077.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 12:25:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10251077.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,319,258
Mapped reads	3,214,667 / 96.85%
Unmapped reads	104,591 / 3.15%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	29,489 / 0.89%
Read min/max/mean length	30 / 80 / 80.32
Duplicated reads (estimated)	609,578 / 18.36%
Duplication rate	16.51%
Clipped reads	464,747 / 14%

2.2. ACGT Content

Number/percentage of A's	73,372,707 / 29.44%
Number/percentage of C's	49,617,885 / 19.91%
Number/percentage of T's	73,991,668 / 29.68%
Number/percentage of G's	52,255,617 / 20.96%
Number/percentage of N's	19,496 / 0.01%
GC Percentage	40.87%

2.3. Coverage

Mean	0.0806

Standard Deviation	0.9361
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2.4. Mapping Quality

Mean Mapping Quality	48.03
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2.5. Mismatches and indels

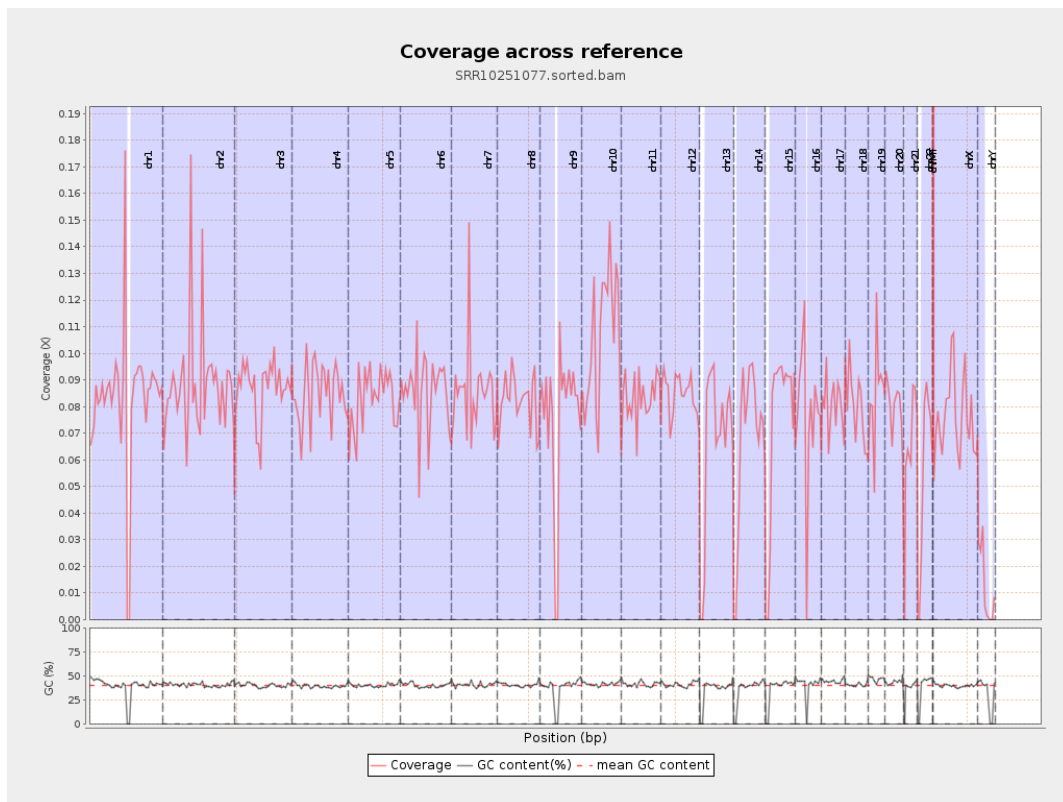
General error rate	0.62%
Mismatches	1,468,783
Insertions	31,804
Mapped reads with at least one insertion	0.97%
Deletions	87,471
Mapped reads with at least one deletion	2.67%
Homopolymer indels	45.15%

2.6. Chromosome stats

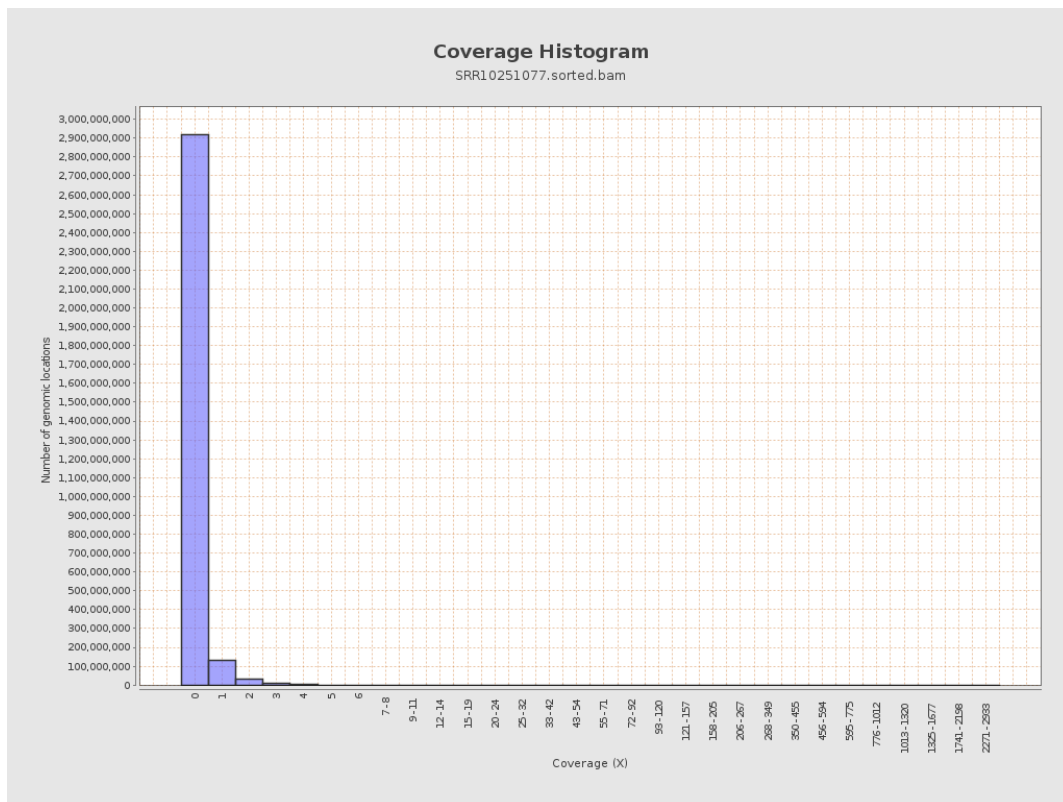
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	20721361	0.0831	2.0251
chr2	243199373	21588372	0.0888	1.1762
chr3	198022430	17126942	0.0865	0.3883
chr4	191154276	16238599	0.085	0.4557
chr5	180915260	14999904	0.0829	0.4012
chr6	171115067	14626800	0.0855	0.5204
chr7	159138663	13553402	0.0852	1.3239

chr8	146364022	11985294	0.0819	0.6144
chr9	141213431	10774610	0.0763	0.9701
chr10	135534747	14381874	0.1061	0.9243
chr11	135006516	11245285	0.0833	0.5809
chr12	133851895	11404952	0.0852	0.4037
chr13	115169878	7650549	0.0664	0.3373
chr14	107349540	7341075	0.0684	0.5461
chr15	102531392	7400817	0.0722	0.3518
chr16	90354753	6864303	0.076	0.6995
chr17	81195210	6579857	0.081	0.5063
chr18	78077248	6293612	0.0806	1.2022
chr19	59128983	4999473	0.0846	1.9537
chr20	63025520	5056764	0.0802	0.4165
chr21	48129895	3125844	0.0649	0.3727
chr22	51304566	2833557	0.0552	0.3393
chrMT	16571	77713	4.6897	3.5768
chrX	155270560	11806866	0.076	0.456
chrY	59373566	735379	0.0124	0.8286

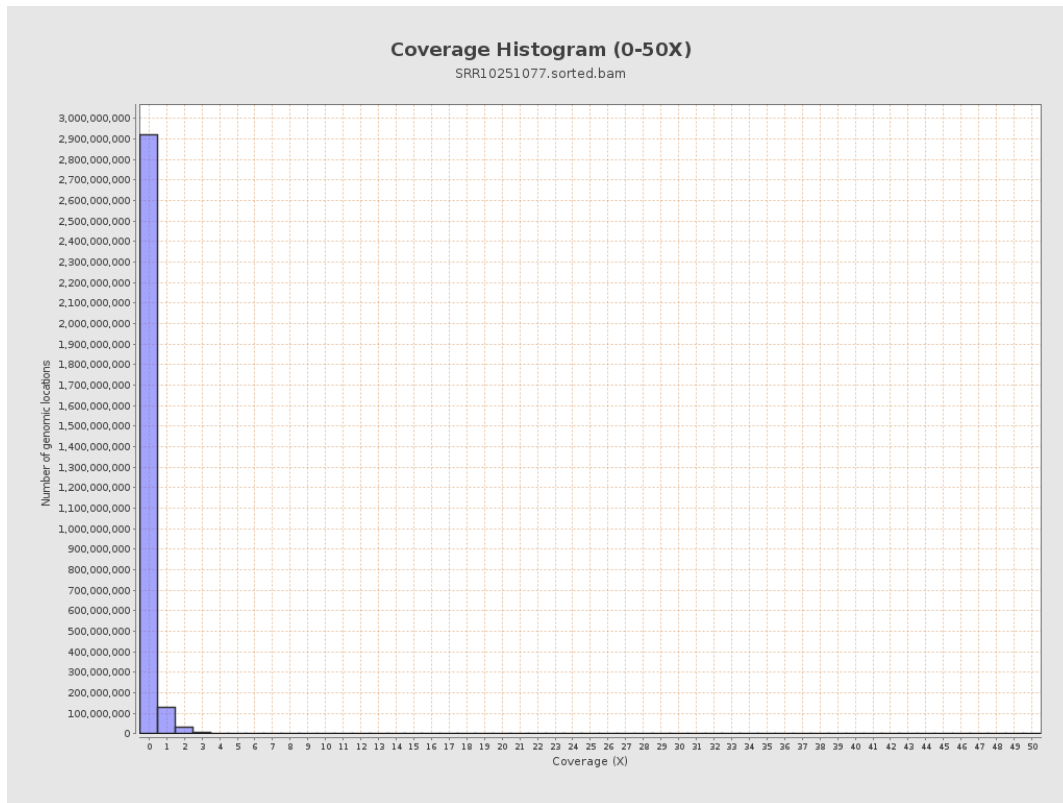
3. Results : Coverage across reference



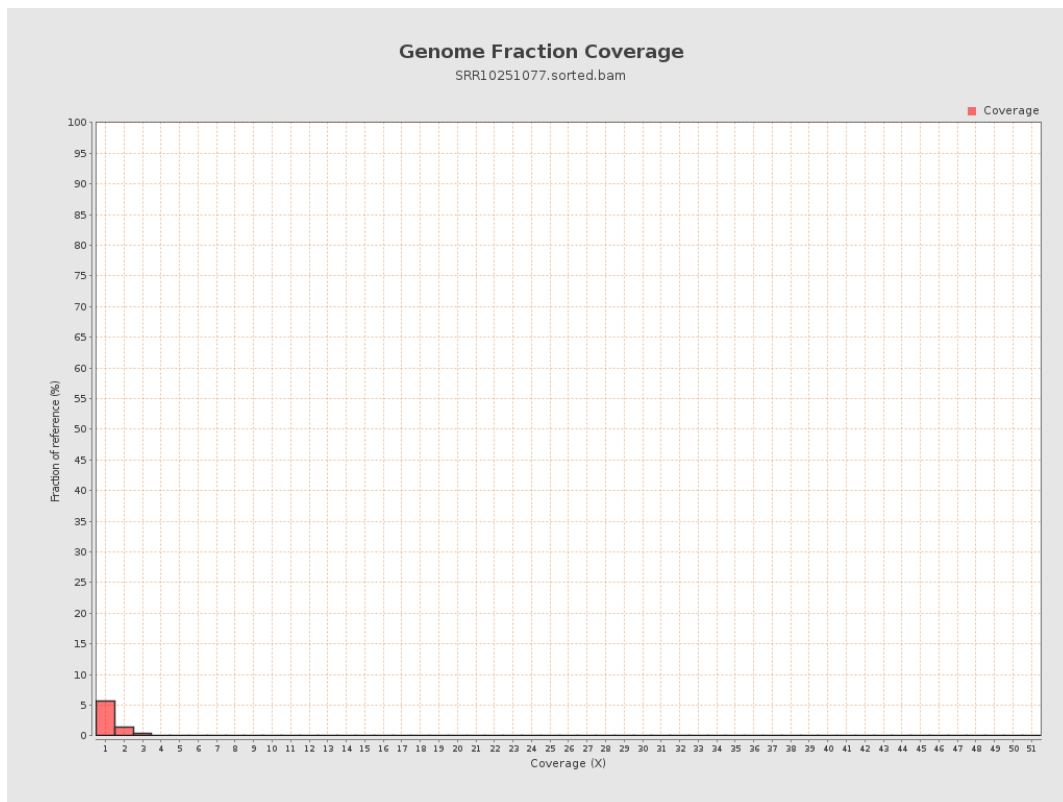
4. Results : Coverage Histogram



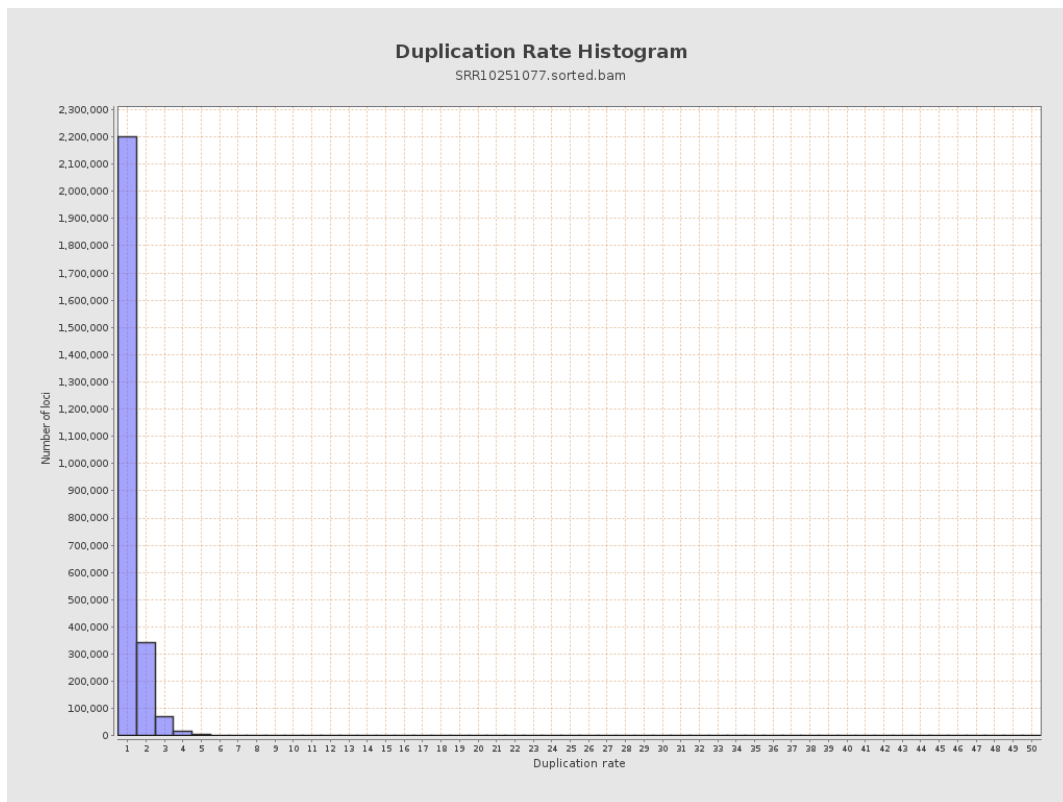
5. Results : Coverage Histogram (0-50X)



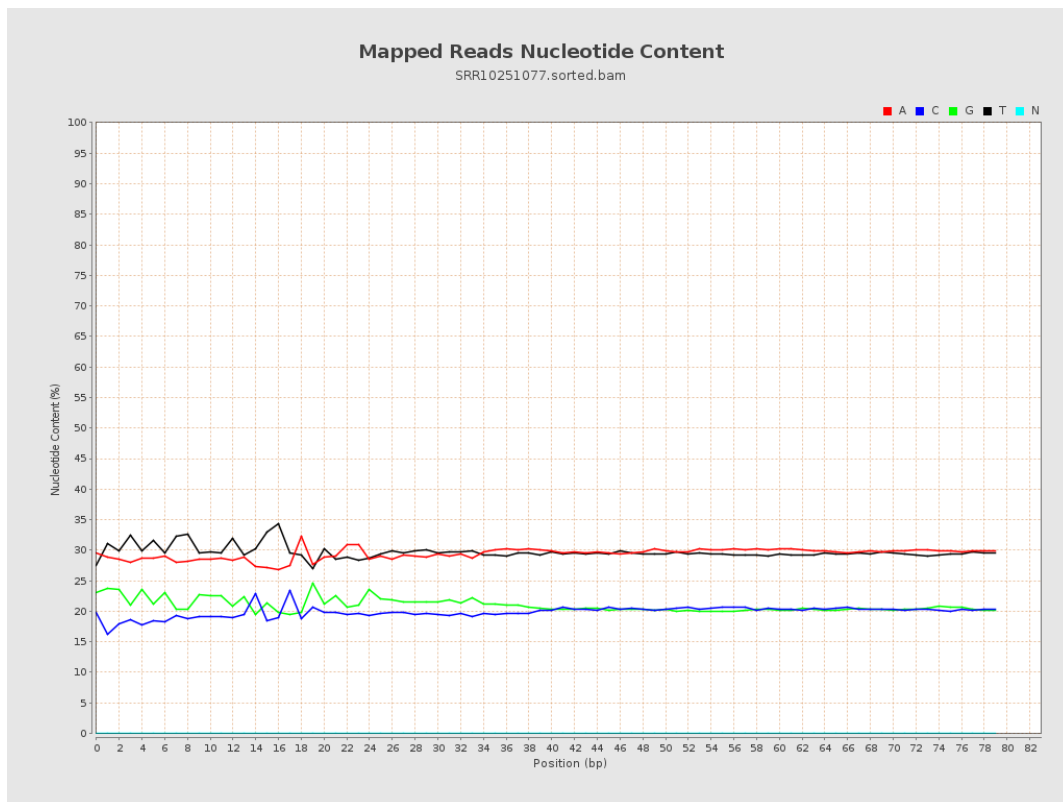
6. Results : Genome Fraction Coverage



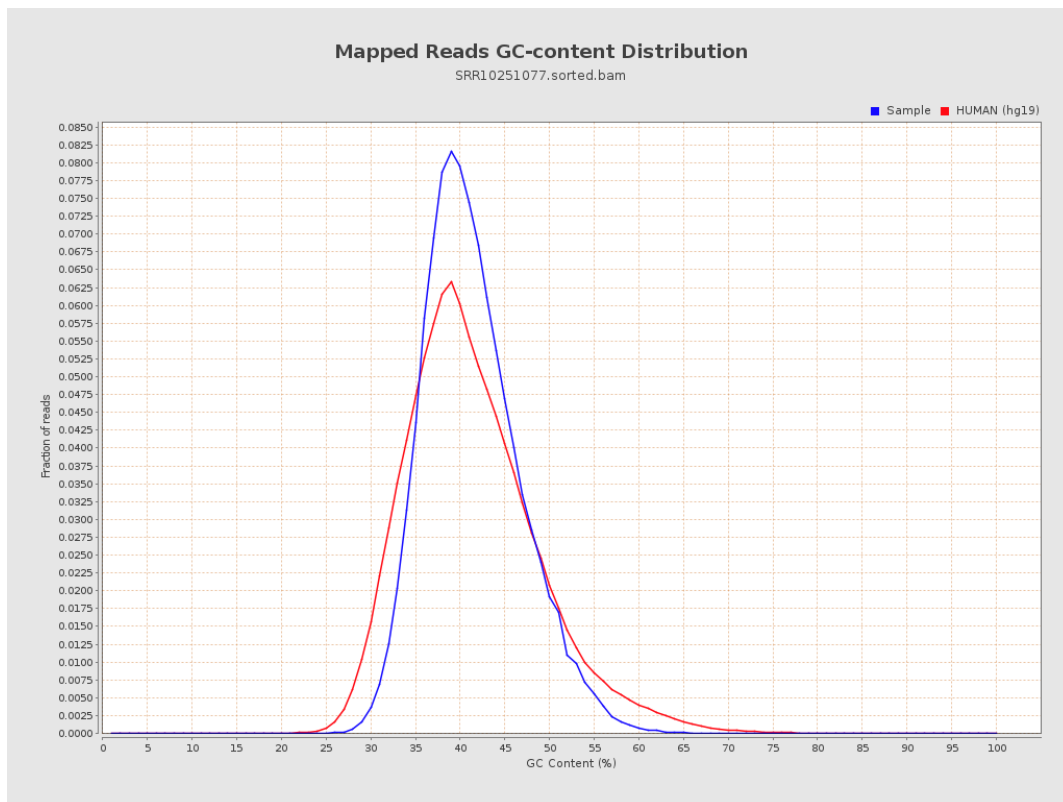
7. Results : Duplication Rate Histogram



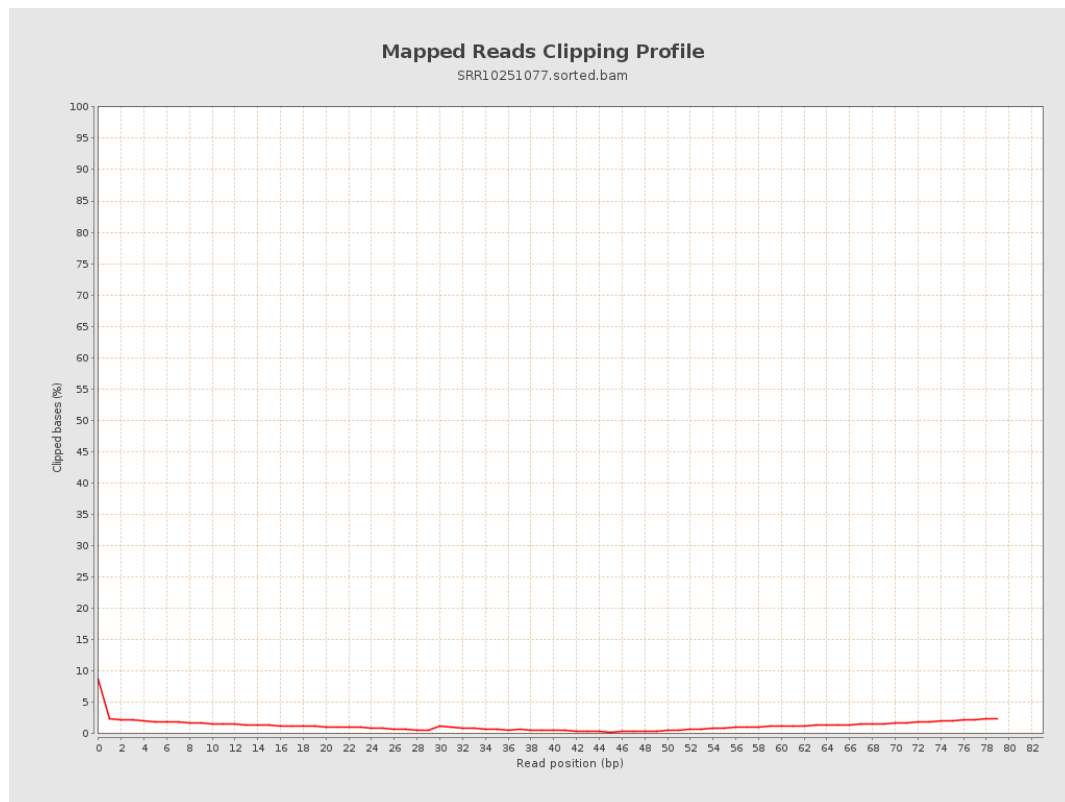
8. Results : Mapped Reads Nucleotide Content



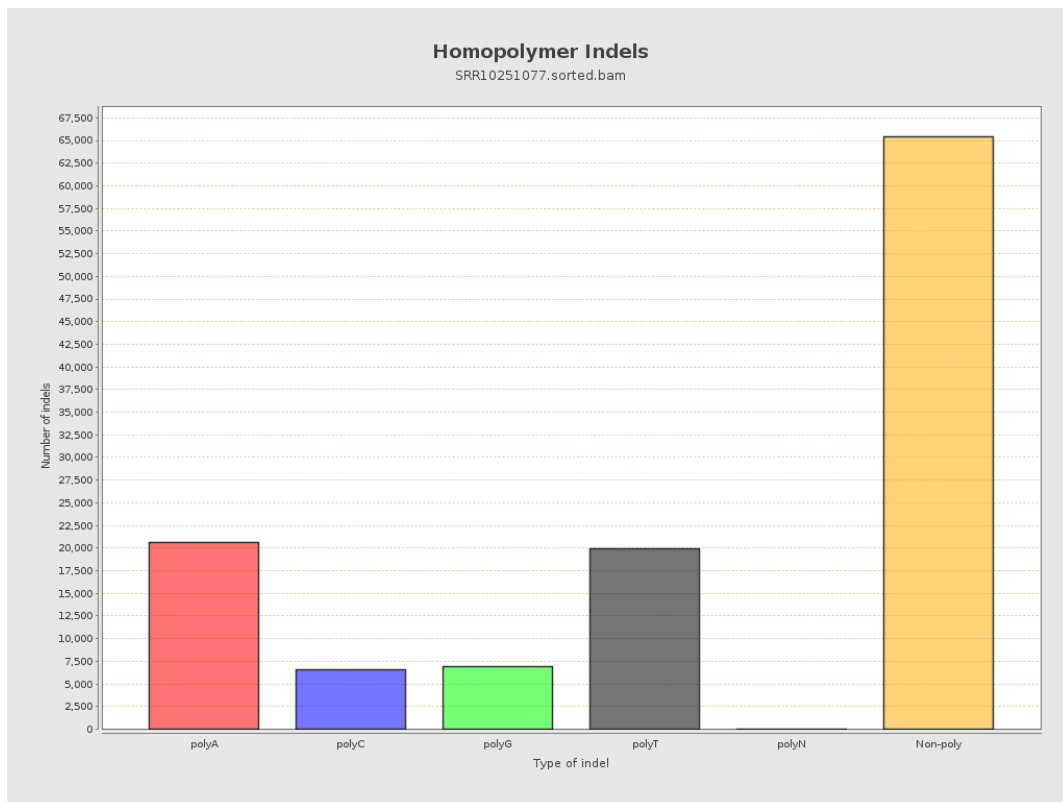
9. Results : Mapped Reads GC-content Distribution



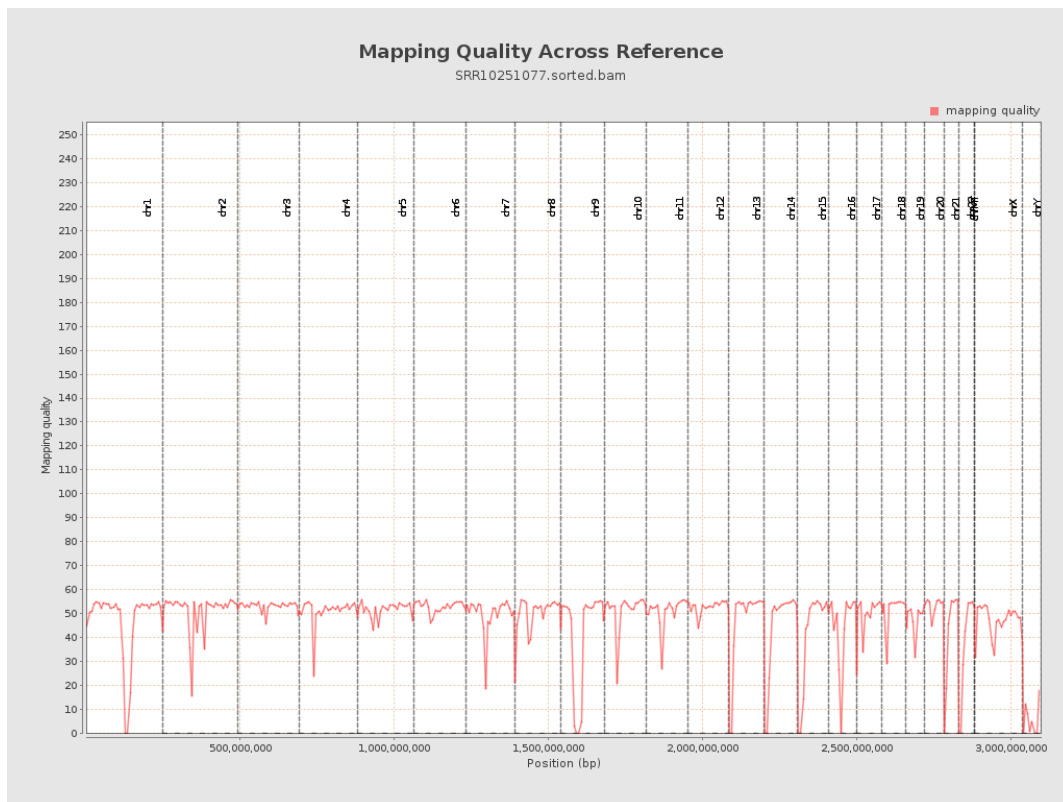
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

