

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 05:53:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083773.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_SRR3083773 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083773.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 05:53:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3083773.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,074,692
Mapped reads	1,211,729 / 58.41%
Unmapped reads	862,963 / 41.59%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,511 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	35,144 / 1.69%
Duplication rate	2.45%
Clipped reads	641,934 / 30.94%

2.2. ACGT Content

Number/percentage of A's	21,741,747 / 28.21%
Number/percentage of C's	14,459,585 / 18.76%
Number/percentage of T's	23,711,772 / 30.77%
Number/percentage of G's	17,155,626 / 22.26%
Number/percentage of N's	875 / 0%
GC Percentage	41.02%

2.3. Coverage

Mean	0.0249

Standard Deviation	0.2034
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2.4. Mapping Quality

Mean Mapping Quality	45.86
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2.5. Mismatches and indels

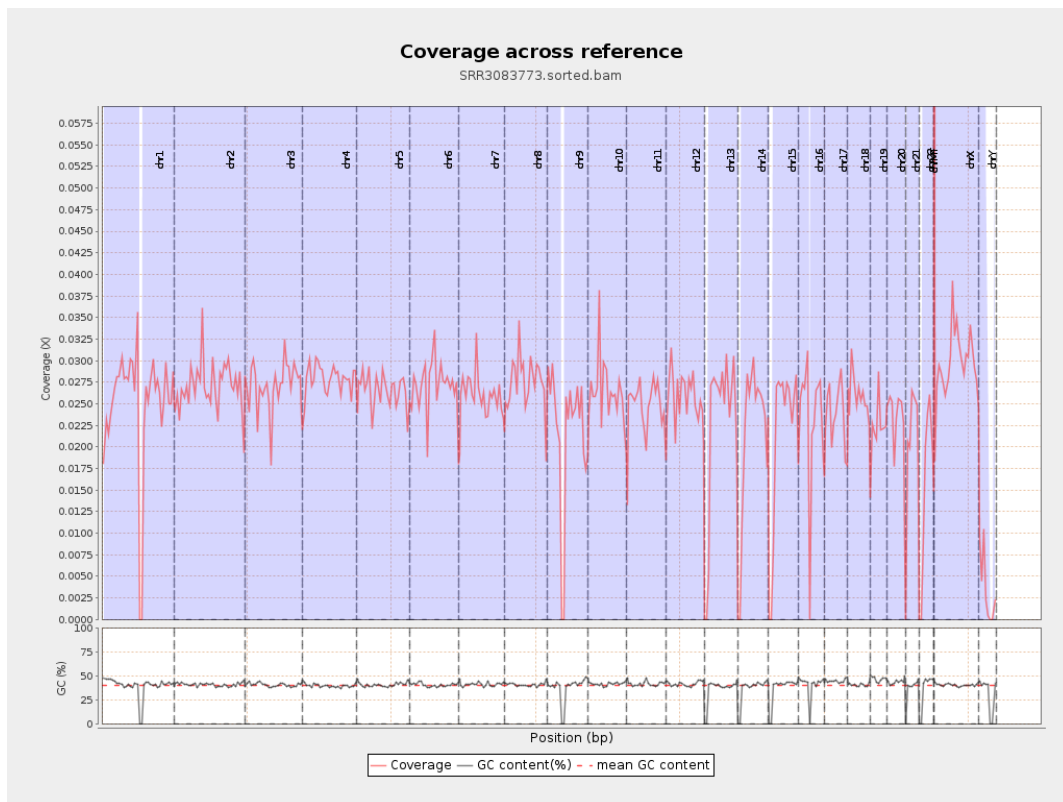
General error rate	0.84%
Mismatches	640,556
Insertions	5,697
Mapped reads with at least one insertion	0.47%
Deletions	16,623
Mapped reads with at least one deletion	1.36%
Homopolymer indels	46.81%

2.6. Chromosome stats

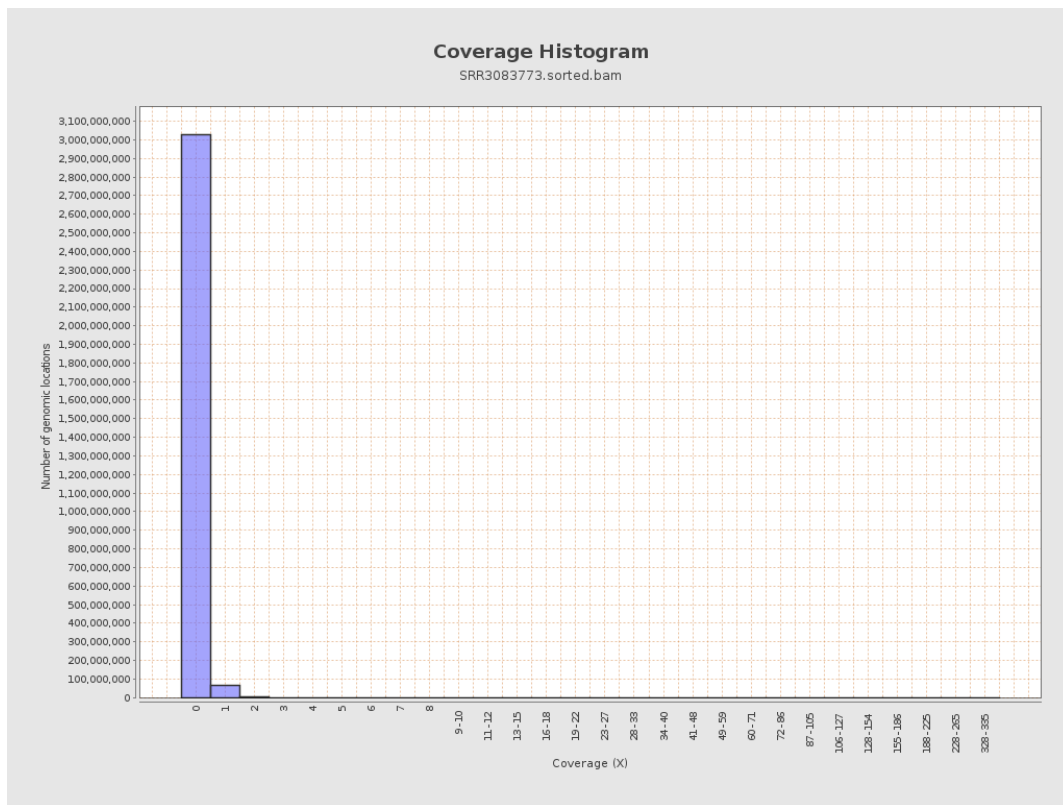
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	6232640	0.025	0.2774
chr2	243199373	6584945	0.0271	0.247
chr3	198022430	5371510	0.0271	0.1769
chr4	191154276	5310279	0.0278	0.1836
chr5	180915260	4802162	0.0265	0.1746
chr6	171115067	4637787	0.0271	0.1902
chr7	159138663	4134729	0.026	0.2178

chr8	146364022	4032662	0.0276	0.2177
chr9	141213431	3079341	0.0218	0.1894
chr10	135534747	3561404	0.0263	0.2196
chr11	135006516	3362507	0.0249	0.1849
chr12	133851895	3470377	0.0259	0.1734
chr13	115169878	2587361	0.0225	0.1608
chr14	107349540	2288712	0.0213	0.1612
chr15	102531392	2182478	0.0213	0.1581
chr16	90354753	2062971	0.0228	0.1717
chr17	81195210	1931022	0.0238	0.1736
chr18	78077248	2024313	0.0259	0.3203
chr19	59128983	1333319	0.0225	0.2355
chr20	63025520	1454581	0.0231	0.1669
chr21	48129895	998673	0.0207	0.1605
chr22	51304566	793424	0.0155	0.133
chrMT	16571	6757	0.4078	0.6921
chrX	155270560	4648108	0.0299	0.1952
chrY	59373566	204124	0.0034	0.0814

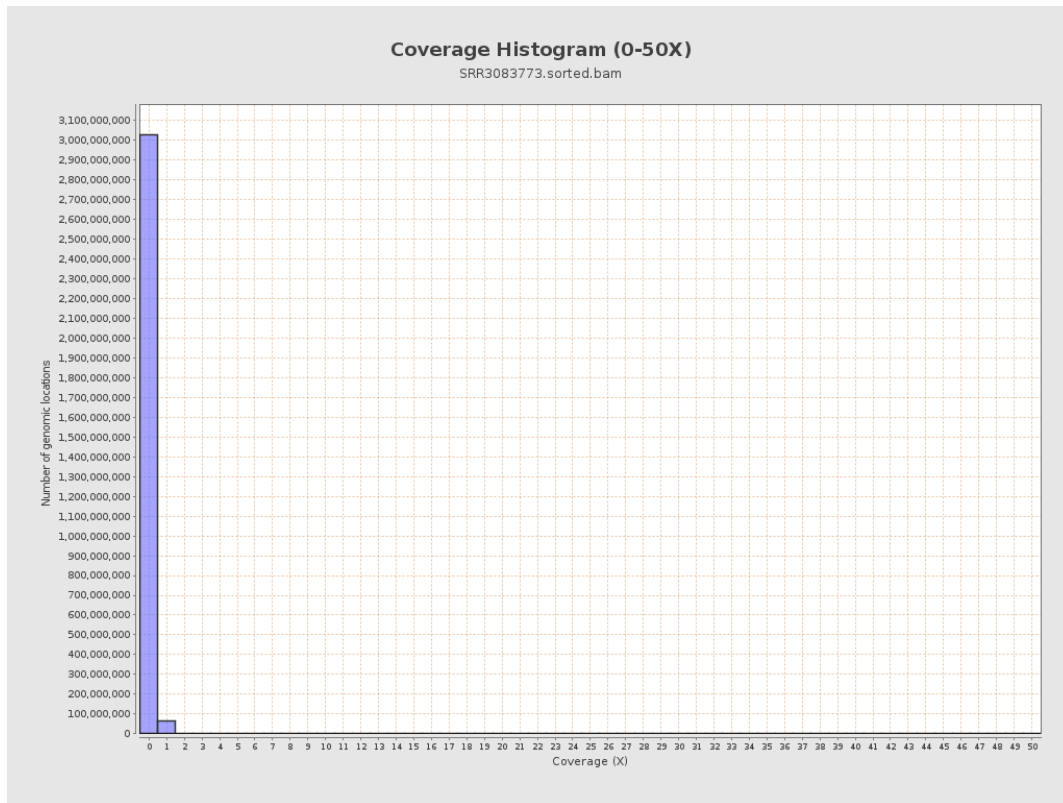
3. Results : Coverage across reference



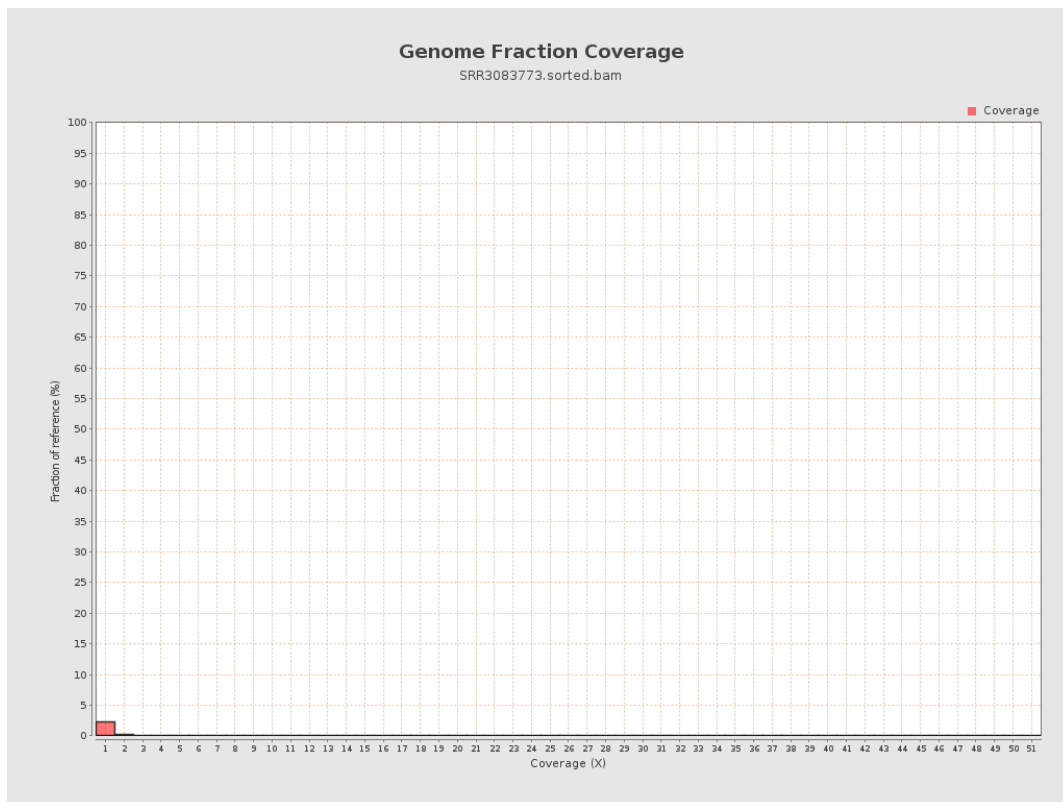
4. Results : Coverage Histogram



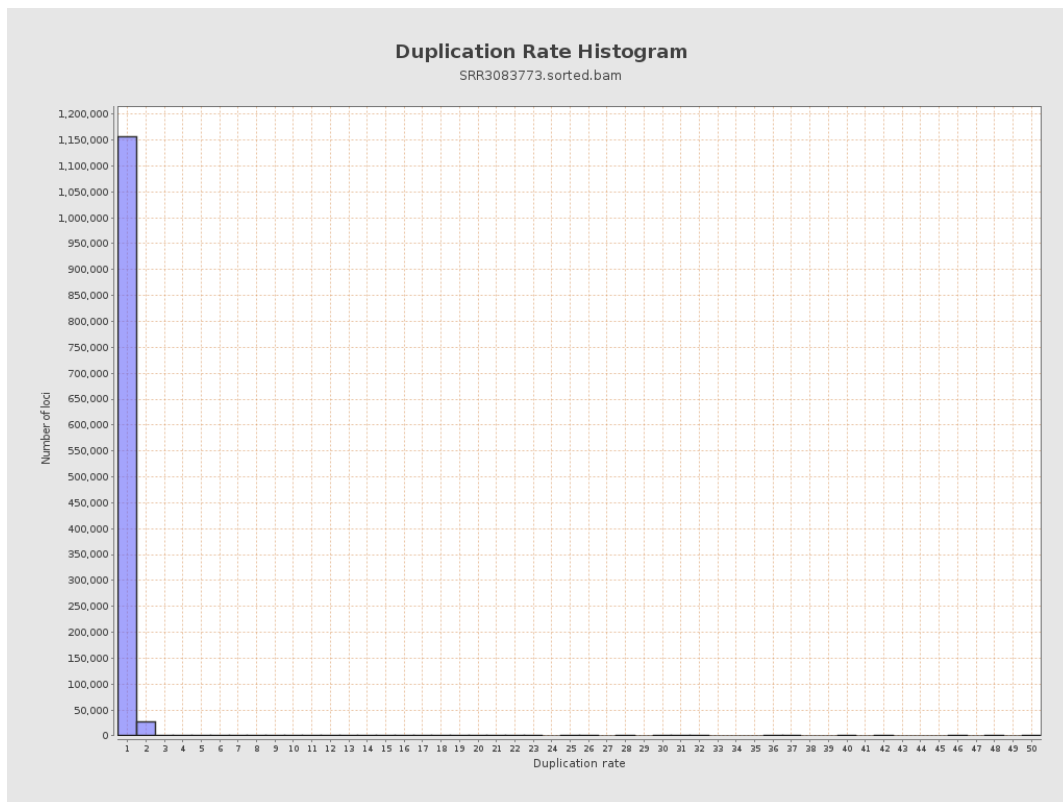
5. Results : Coverage Histogram (0-50X)



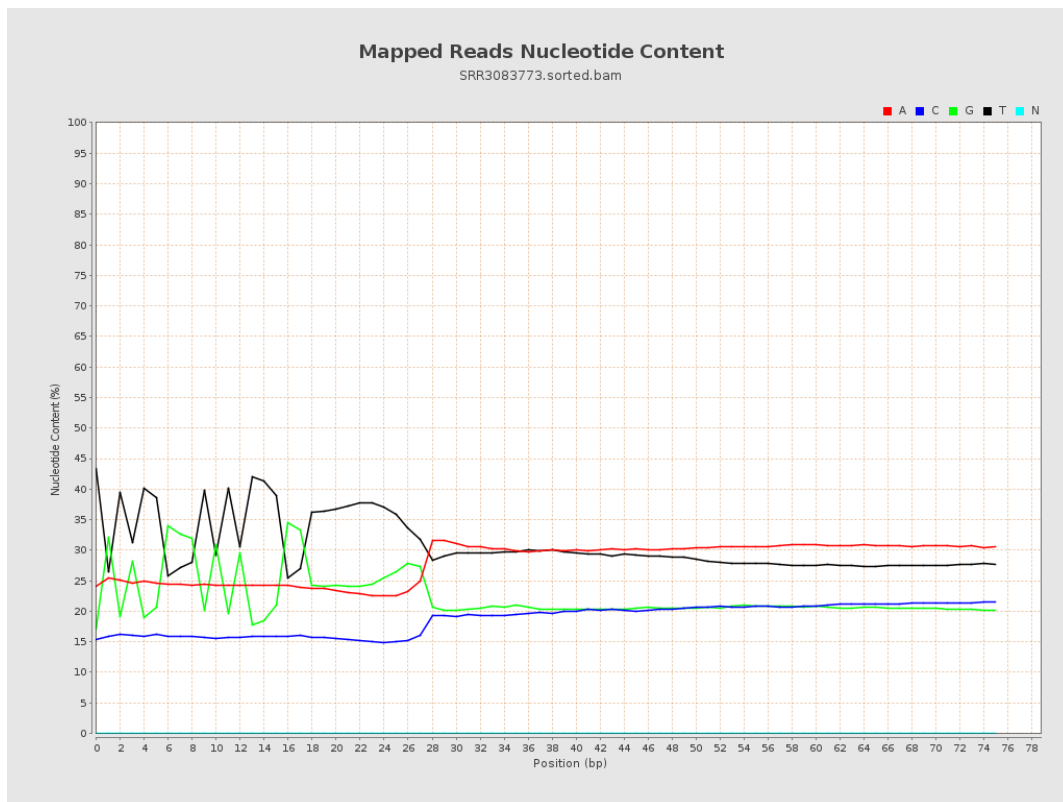
6. Results : Genome Fraction Coverage



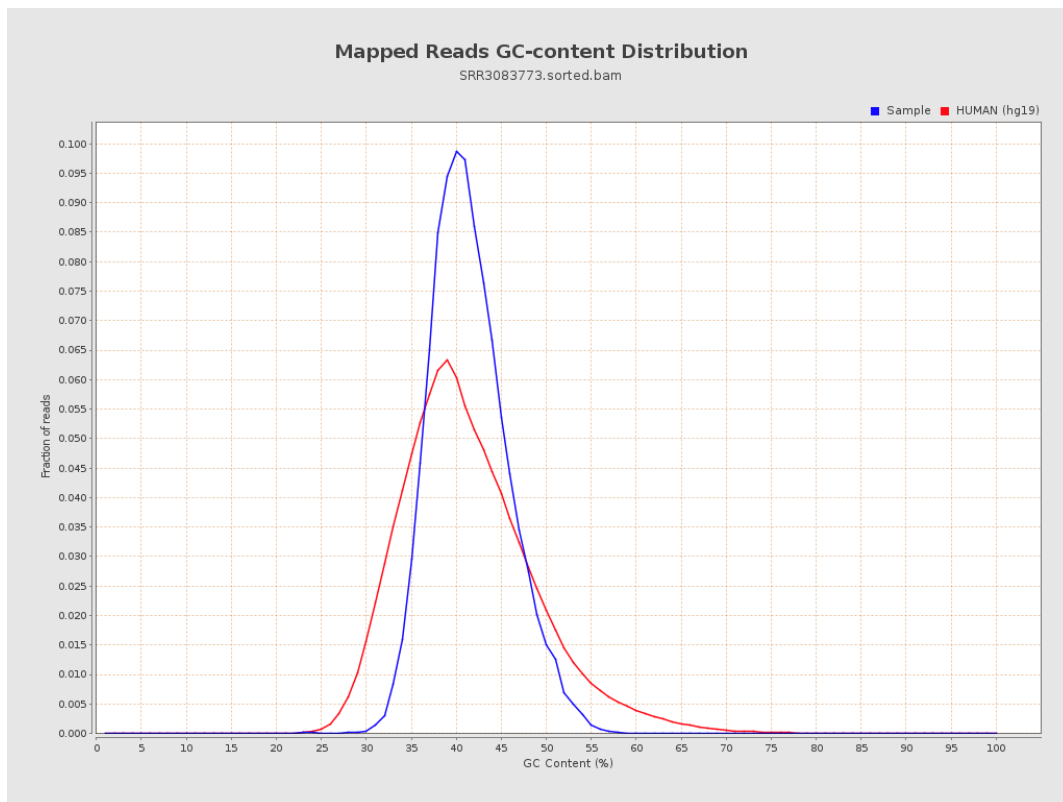
7. Results : Duplication Rate Histogram



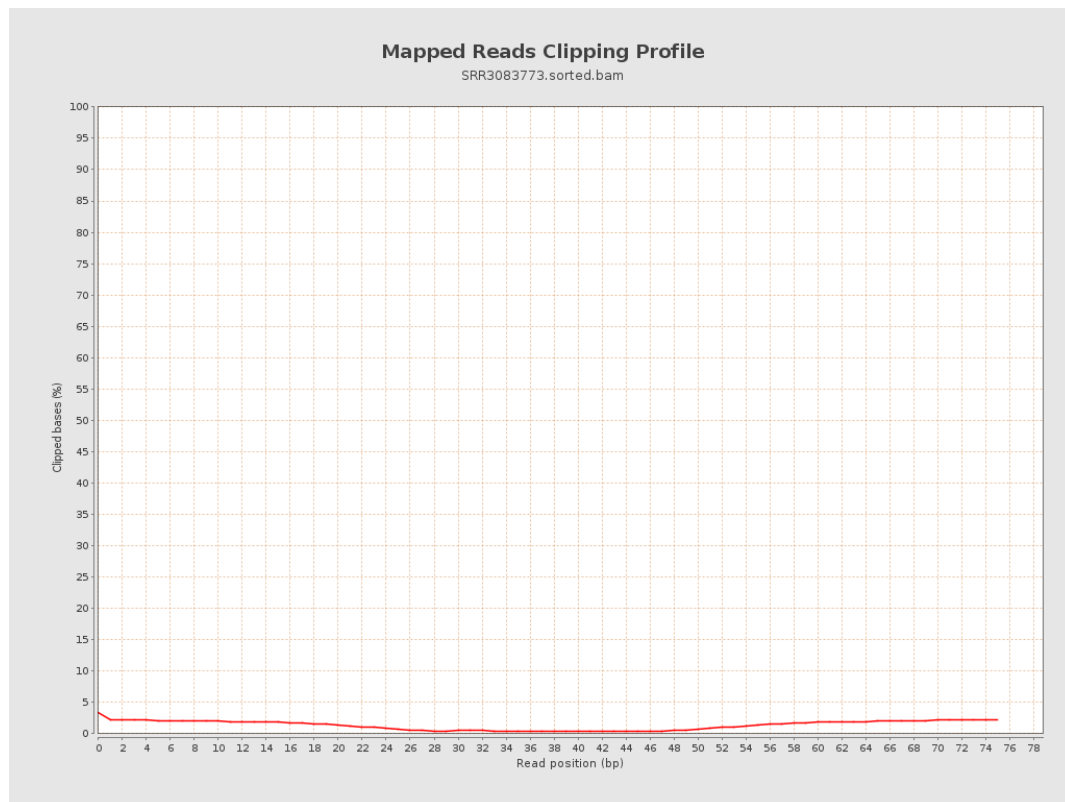
8. Results : Mapped Reads Nucleotide Content



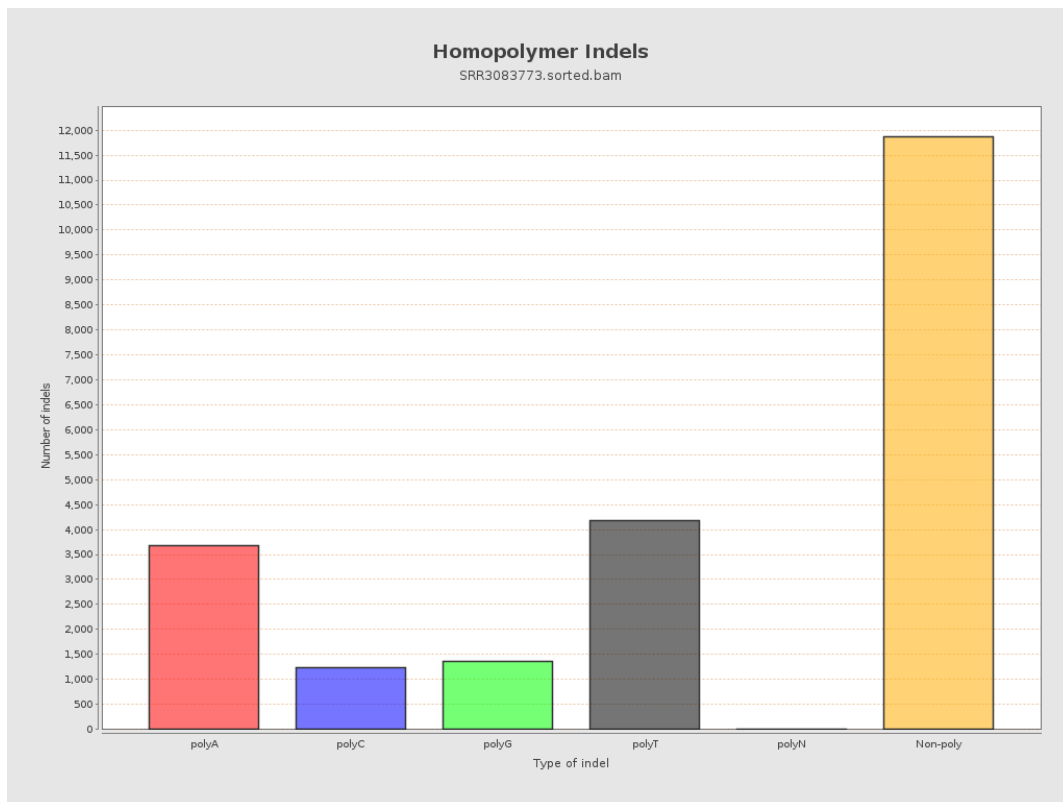
9. Results : Mapped Reads GC-content Distribution



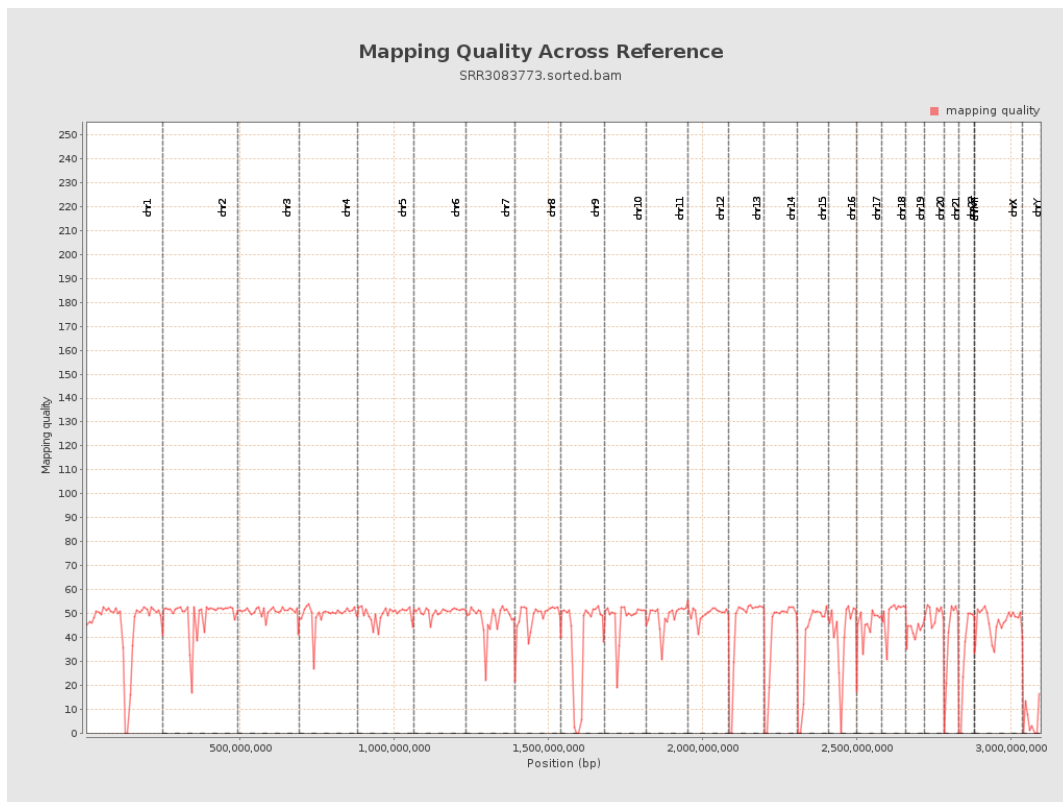
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

