

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 18:08:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082773.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_SRR3082773 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082773.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 18:08:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082773.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,780,500
Mapped reads	4,263,547 / 89.19%
Unmapped reads	516,953 / 10.81%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	32,192 / 0.67%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	233,555 / 4.89%
Duplication rate	4.45%
Clipped reads	1,549,900 / 32.42%

2.2. ACGT Content

Number/percentage of A's	84,107,662 / 28.63%
Number/percentage of C's	54,021,732 / 18.39%
Number/percentage of T's	94,897,174 / 32.3%
Number/percentage of G's	60,721,724 / 20.67%
Number/percentage of N's	16,657 / 0.01%
GC Percentage	39.06%

2.3. Coverage

Mean	0.0949

Standard Deviation	0.6306
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2.4. Mapping Quality

Mean Mapping Quality	47.53
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2.5. Mismatches and indels

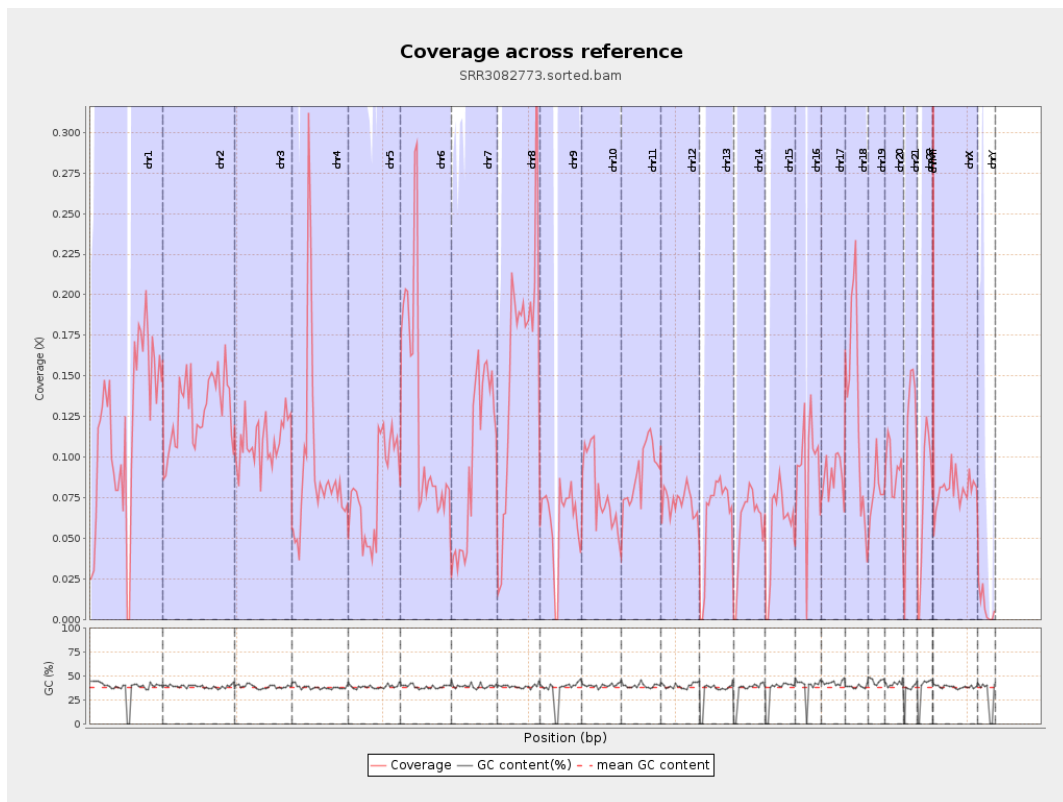
General error rate	0.87%
Mismatches	2,503,486
Insertions	22,826
Mapped reads with at least one insertion	0.53%
Deletions	64,634
Mapped reads with at least one deletion	1.5%
Homopolymer indels	48.11%

2.6. Chromosome stats

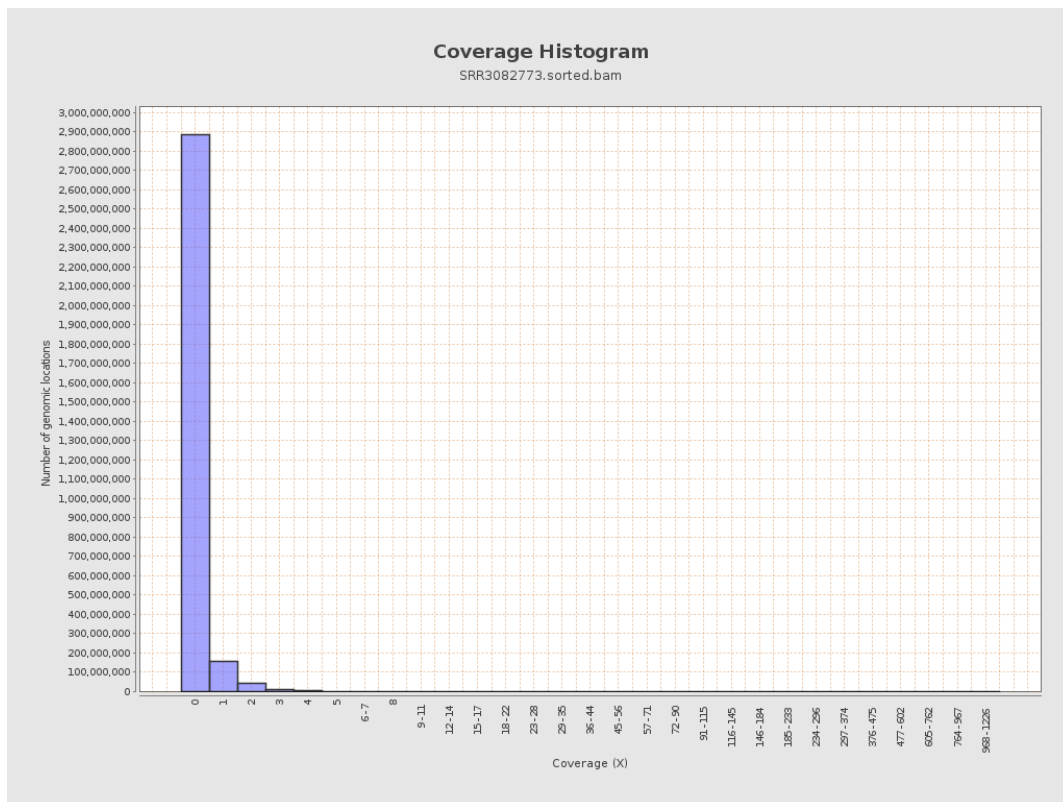
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	29399261	0.118	1.1551
chr2	243199373	31334542	0.1288	0.7593
chr3	198022430	21687555	0.1095	0.4334
chr4	191154276	17928789	0.0938	0.4201
chr5	180915260	14462695	0.0799	0.3695
chr6	171115067	21261444	0.1243	0.6835
chr7	159138663	15527315	0.0976	0.6045

chr8	146364022	23371085	0.1597	0.9231
chr9	141213431	8676190	0.0614	0.5618
chr10	135534747	10597160	0.0782	0.4977
chr11	135006516	12170713	0.0901	0.5035
chr12	133851895	9602756	0.0717	0.3578
chr13	115169878	7340771	0.0637	0.3276
chr14	107349540	6302981	0.0587	0.3489
chr15	102531392	5777121	0.0563	0.3037
chr16	90354753	8344748	0.0924	0.4385
chr17	81195210	7236089	0.0891	0.44
chr18	78077248	10322737	0.1322	1.1892
chr19	59128983	4682826	0.0792	0.7604
chr20	63025520	5845428	0.0927	0.4158
chr21	48129895	5251614	0.1091	0.4419
chr22	51304566	3874283	0.0755	0.3541
chrMT	16571	14586	0.8802	1.2131
chrX	155270560	12383372	0.0798	0.4153
chrY	59373566	480369	0.0081	0.1579

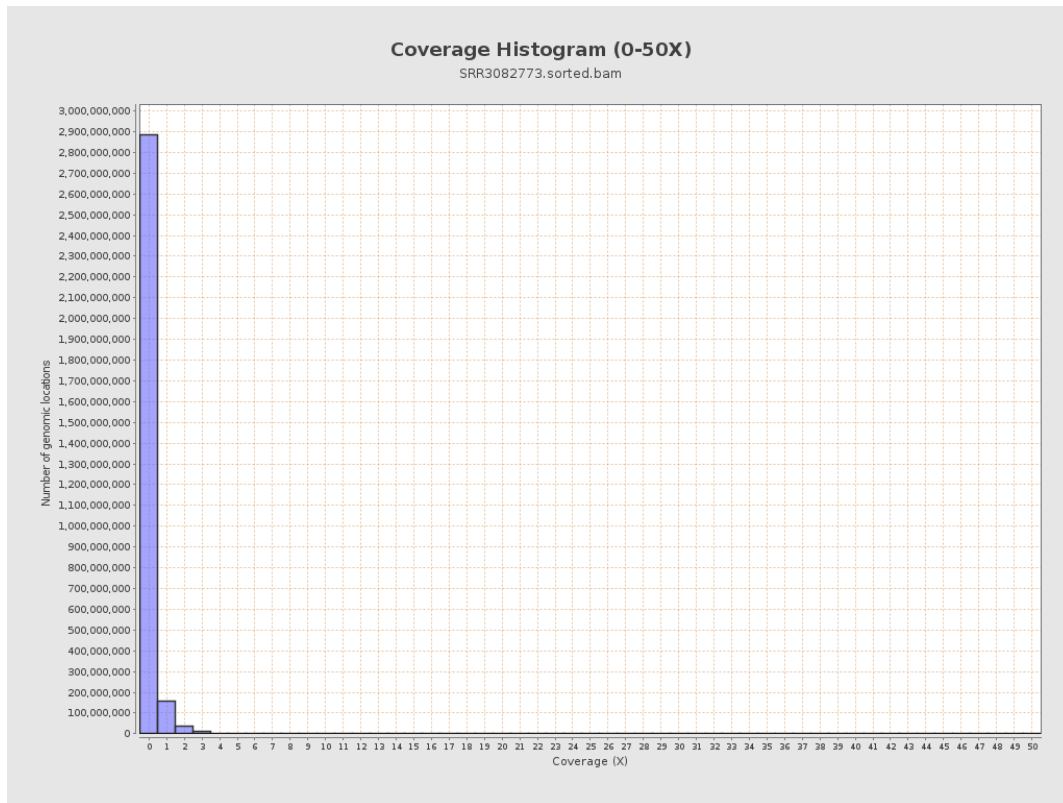
3. Results : Coverage across reference



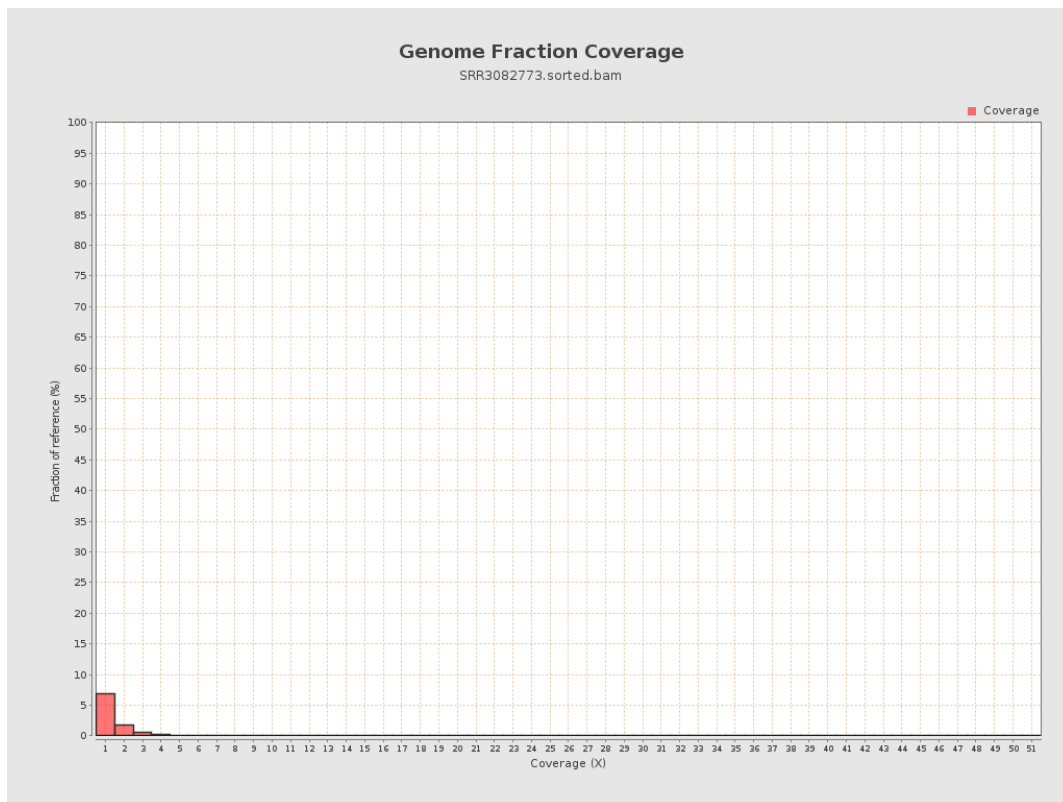
4. Results : Coverage Histogram



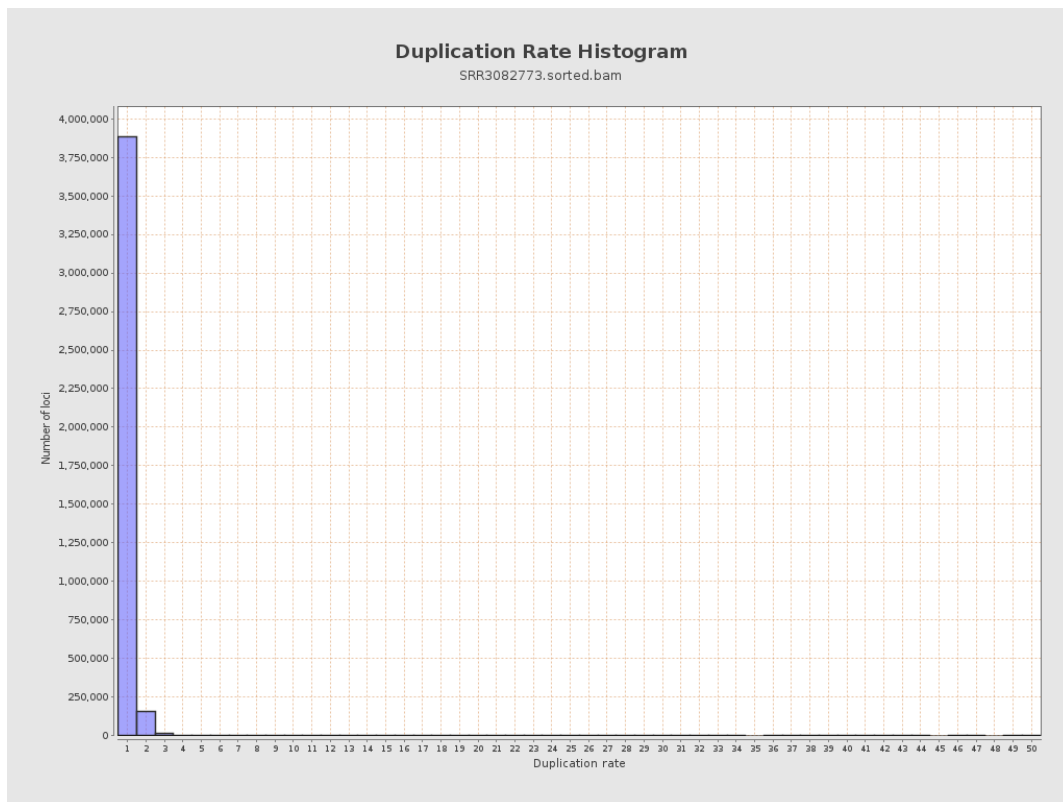
5. Results : Coverage Histogram (0-50X)



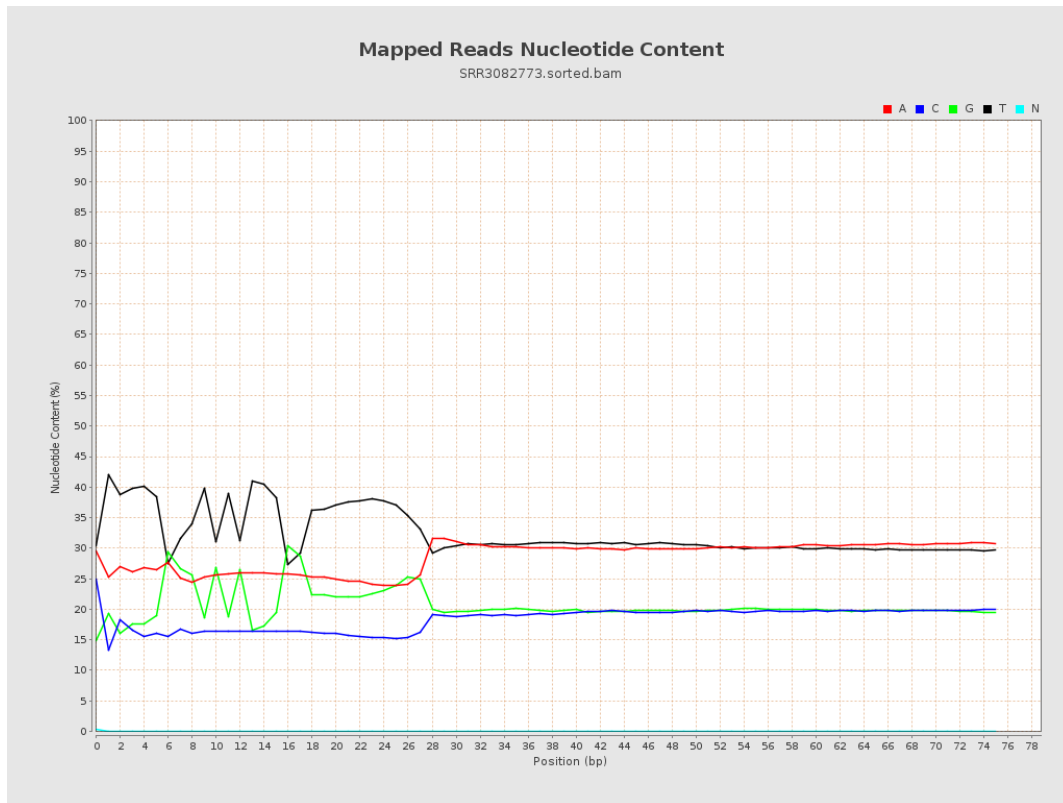
6. Results : Genome Fraction Coverage



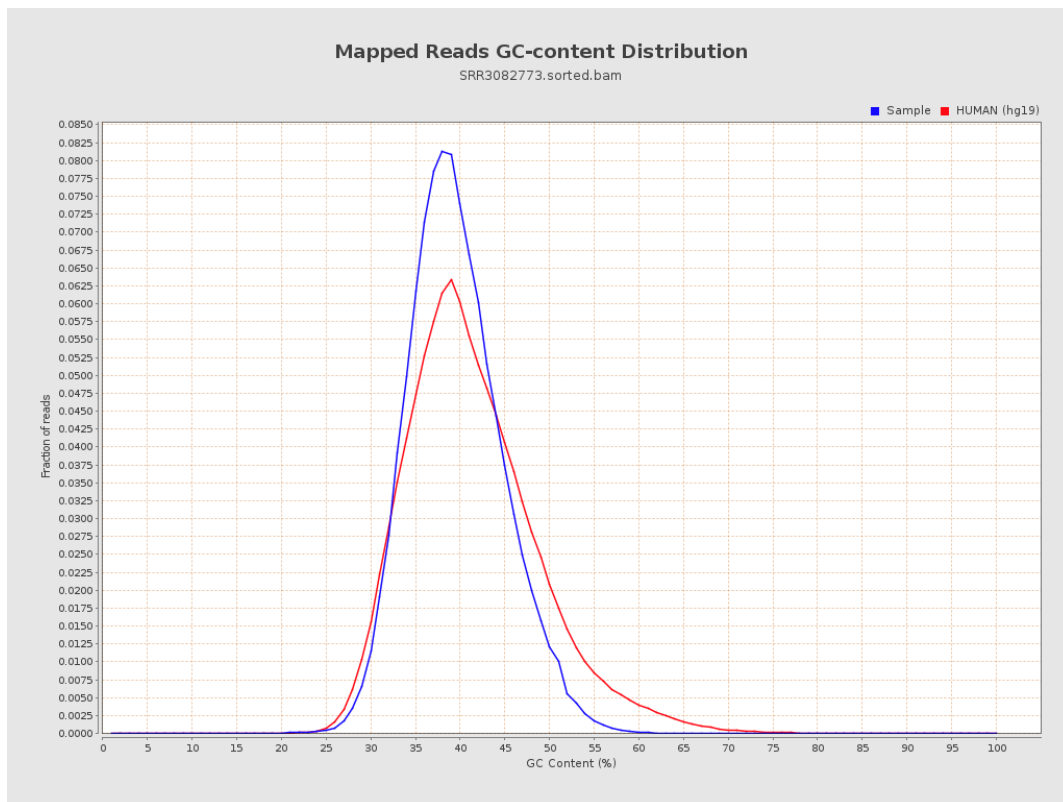
7. Results : Duplication Rate Histogram



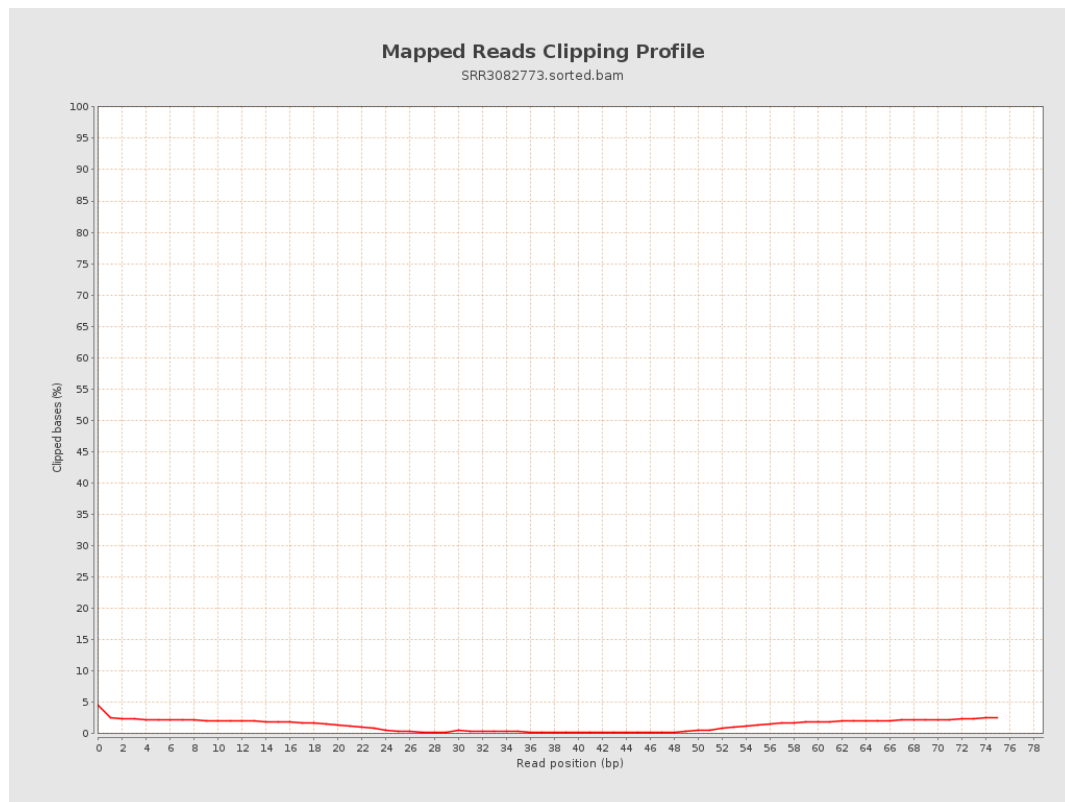
8. Results : Mapped Reads Nucleotide Content



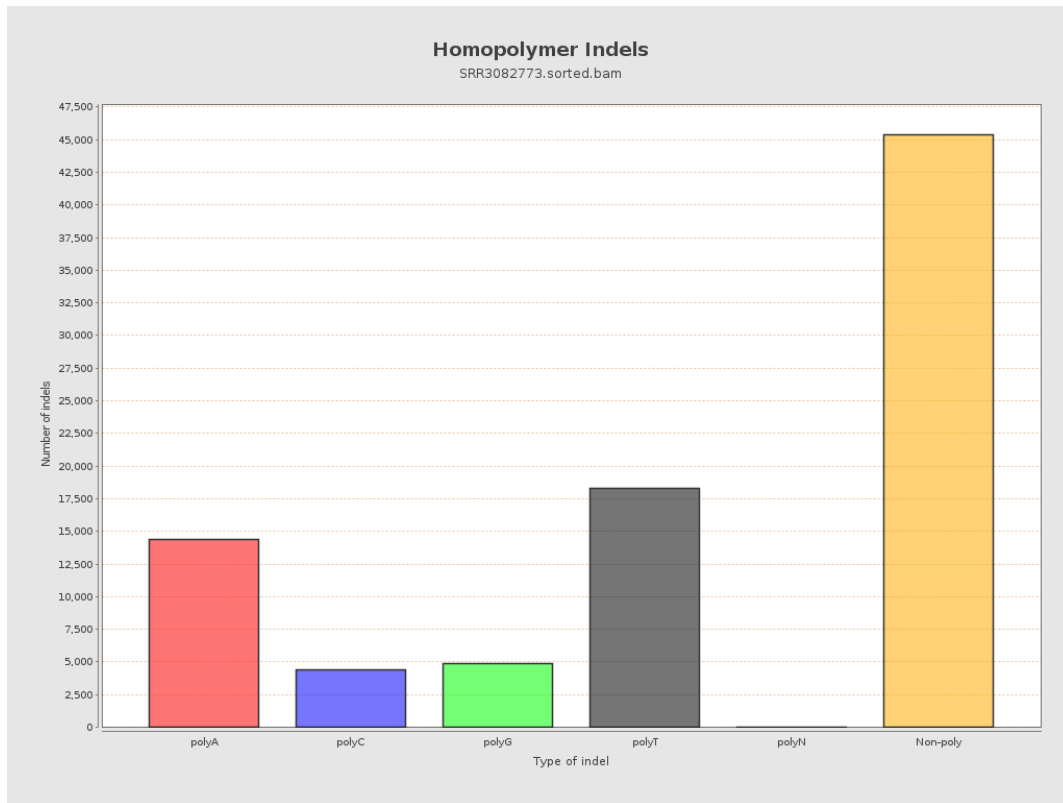
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

