

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 11:23:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008783.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_SRR6008783 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008783.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 11:23:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008783.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,312,099
Mapped reads	1,148,500 / 87.53%
Unmapped reads	163,599 / 12.47%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,841 / 0.98%
Read min/max/mean length	30 / 76 / 76.34
Duplicated reads (estimated)	127,921 / 9.75%
Duplication rate	8.46%
Clipped reads	561,868 / 42.82%

2.2. ACGT Content

Number/percentage of A's	20,352,560 / 26.99%
Number/percentage of C's	14,599,496 / 19.36%
Number/percentage of T's	23,184,956 / 30.74%
Number/percentage of G's	17,173,354 / 22.77%
Number/percentage of N's	109,217 / 0.14%
GC Percentage	42.13%

2.3. Coverage

Mean	0.0244

Standard Deviation	0.3298
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2.4. Mapping Quality

Mean Mapping Quality	43.84
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2.5. Mismatches and indels

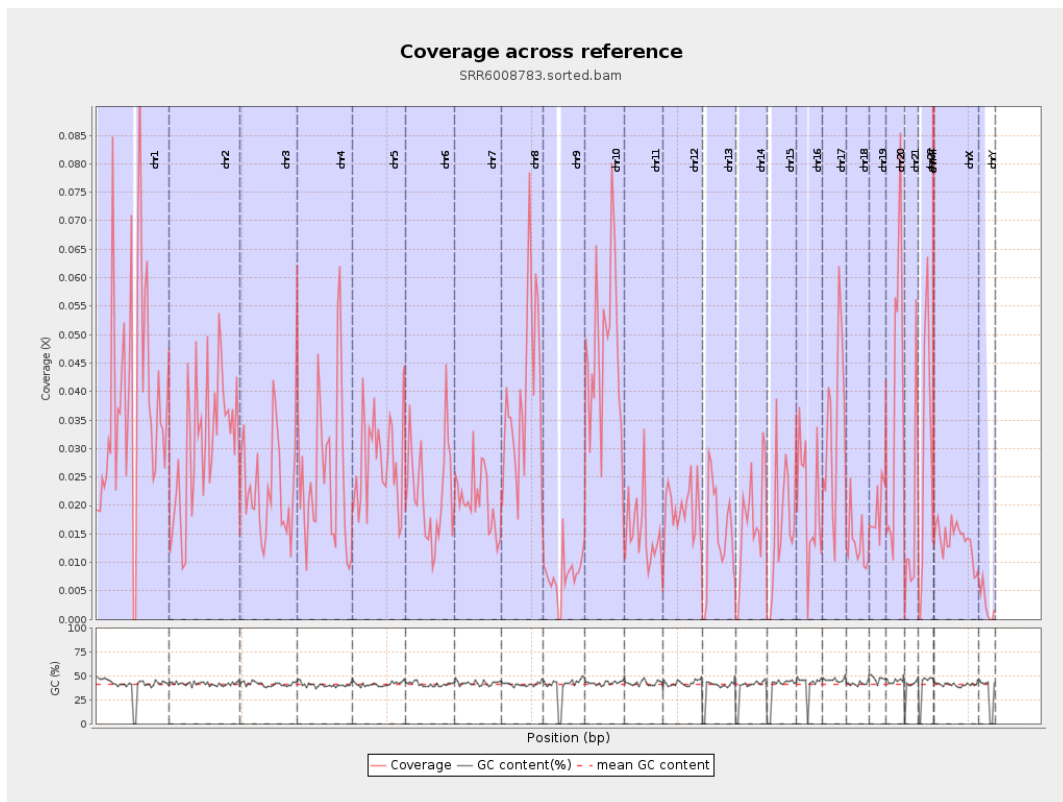
General error rate	0.89%
Mismatches	661,296
Insertions	5,626
Mapped reads with at least one insertion	0.48%
Deletions	22,192
Mapped reads with at least one deletion	1.91%
Homopolymer indels	44.3%

2.6. Chromosome stats

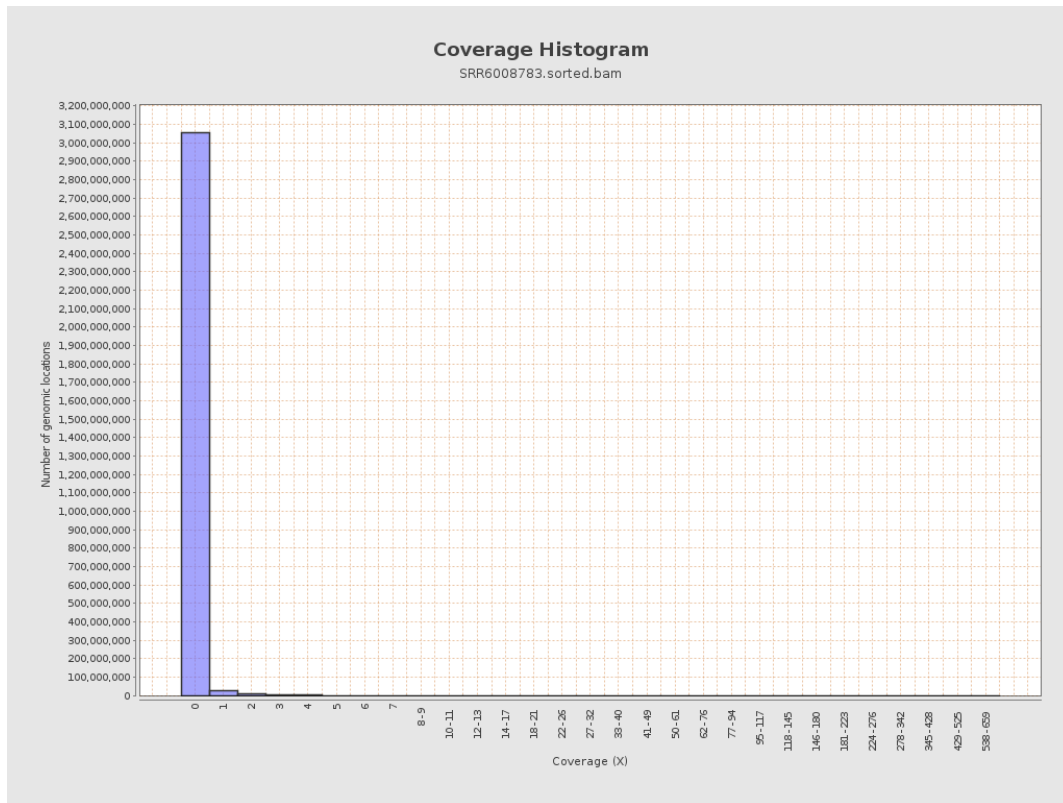
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	9426681	0.0378	0.5645
chr2	243199373	7508321	0.0309	0.4351
chr3	198022430	4553281	0.023	0.2414
chr4	191154276	4765863	0.0249	0.2519
chr5	180915260	5094473	0.0282	0.2673
chr6	171115067	3829490	0.0224	0.257
chr7	159138663	3327282	0.0209	0.3015

chr8	146364022	5713235	0.039	0.46
chr9	141213431	1074041	0.0076	0.1946
chr10	135534747	6368089	0.047	0.4386
chr11	135006516	2032472	0.0151	0.2097
chr12	133851895	2563804	0.0192	0.2184
chr13	115169878	1685411	0.0146	0.1938
chr14	107349540	1829700	0.017	0.2123
chr15	102531392	1635988	0.016	0.1989
chr16	90354753	1848609	0.0205	0.2712
chr17	81195210	2741338	0.0338	0.3126
chr18	78077248	1043507	0.0134	0.3949
chr19	59128983	1175040	0.0199	0.4112
chr20	63025520	2372160	0.0376	0.3226
chr21	48129895	822164	0.0171	0.2089
chr22	51304566	1491748	0.0291	0.2772
chrMT	16571	240473	14.5117	10.5402
chrX	155270560	2158287	0.0139	0.1869
chrY	59373566	157707	0.0027	0.097

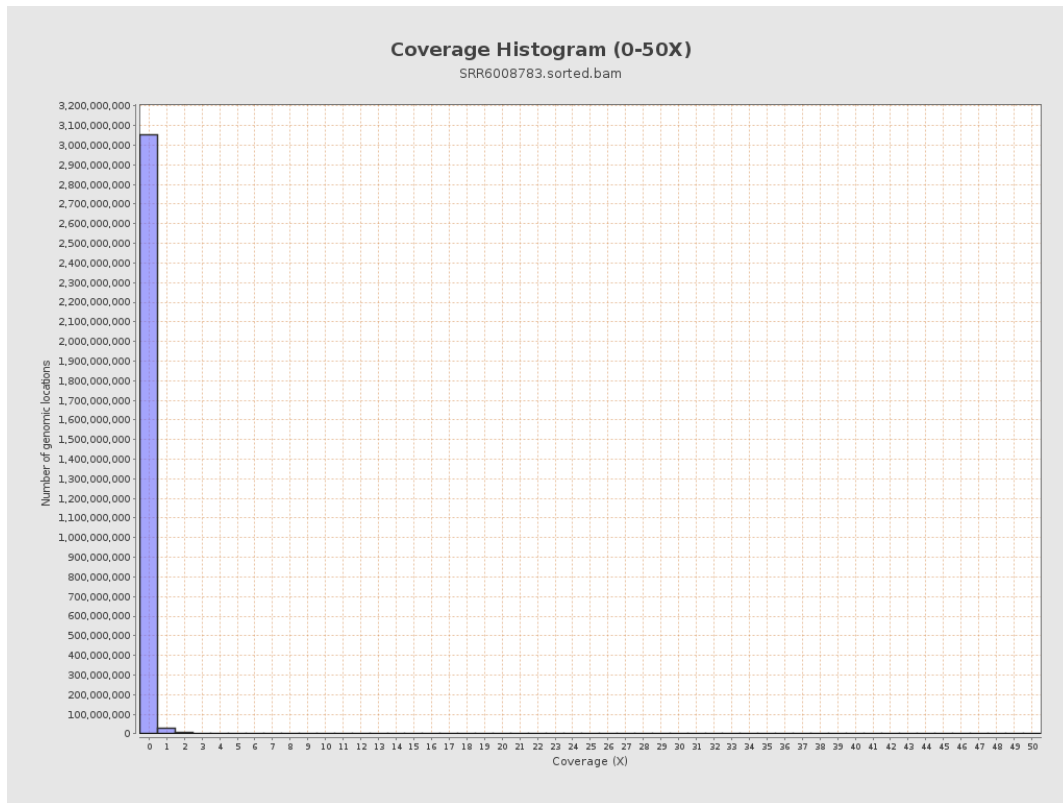
3. Results : Coverage across reference



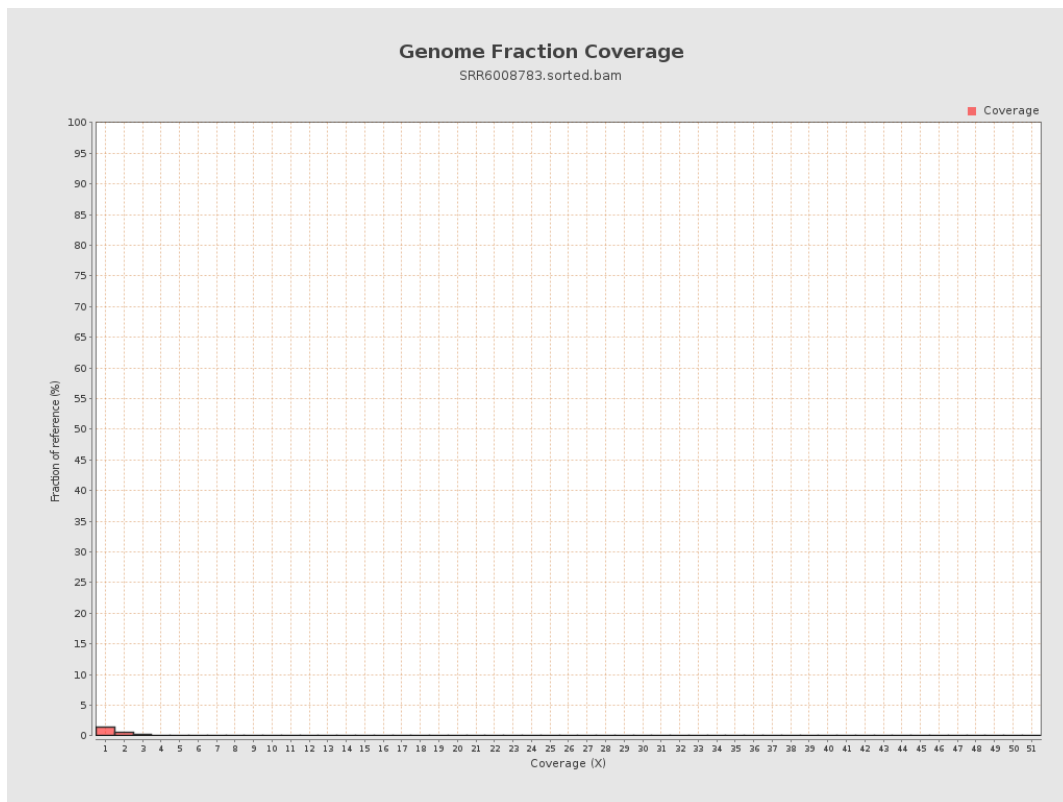
4. Results : Coverage Histogram



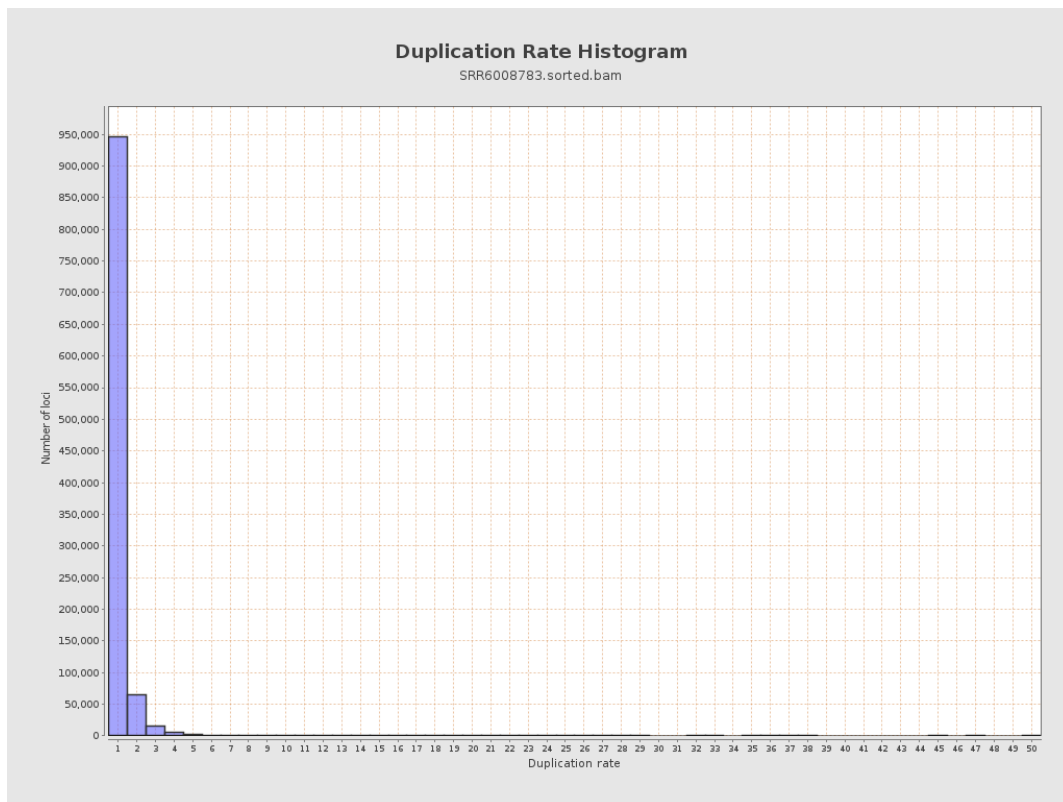
5. Results : Coverage Histogram (0-50X)



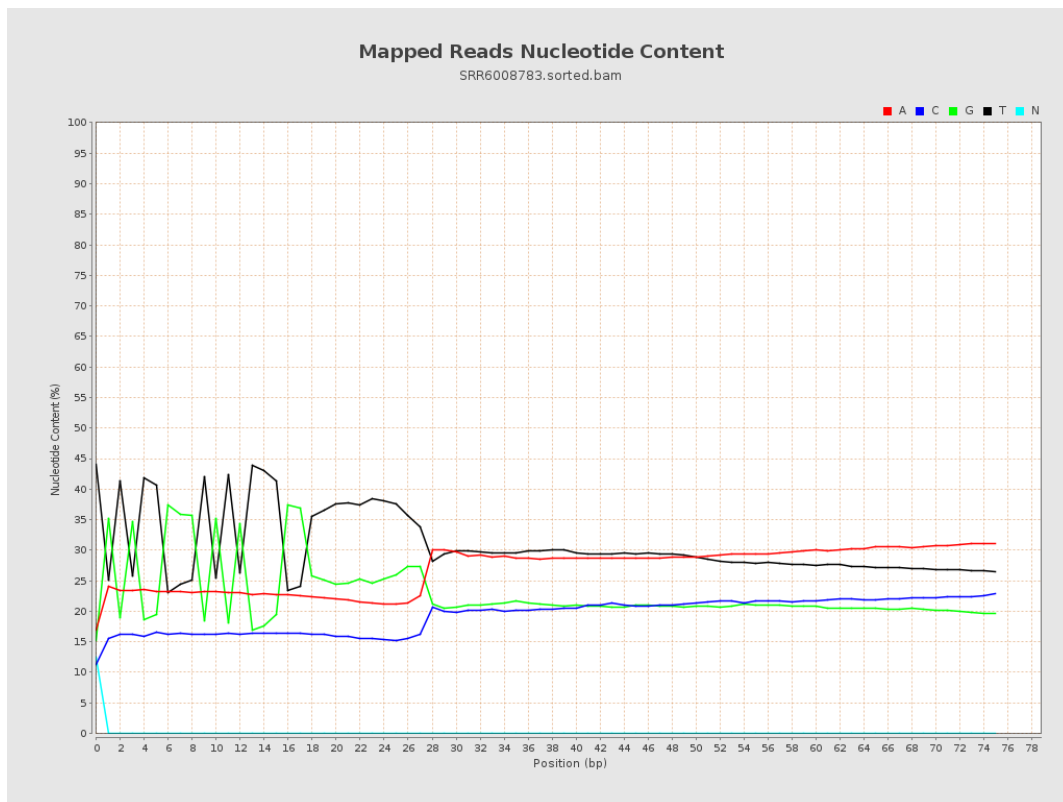
6. Results : Genome Fraction Coverage



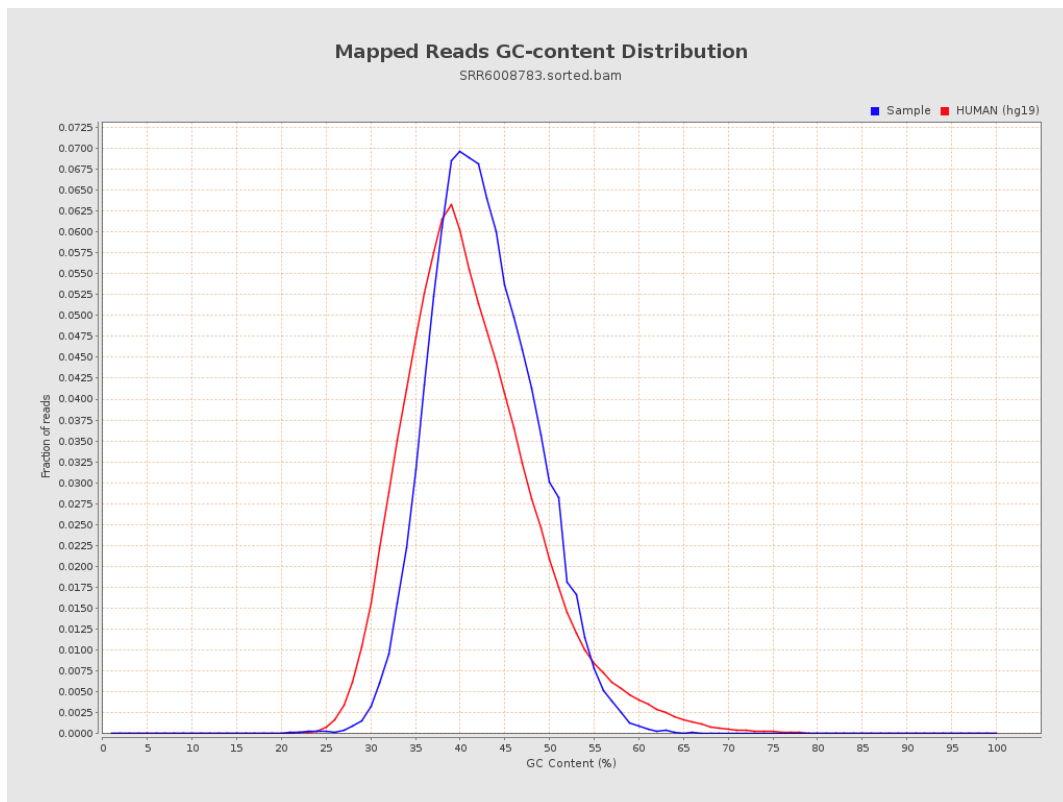
7. Results : Duplication Rate Histogram



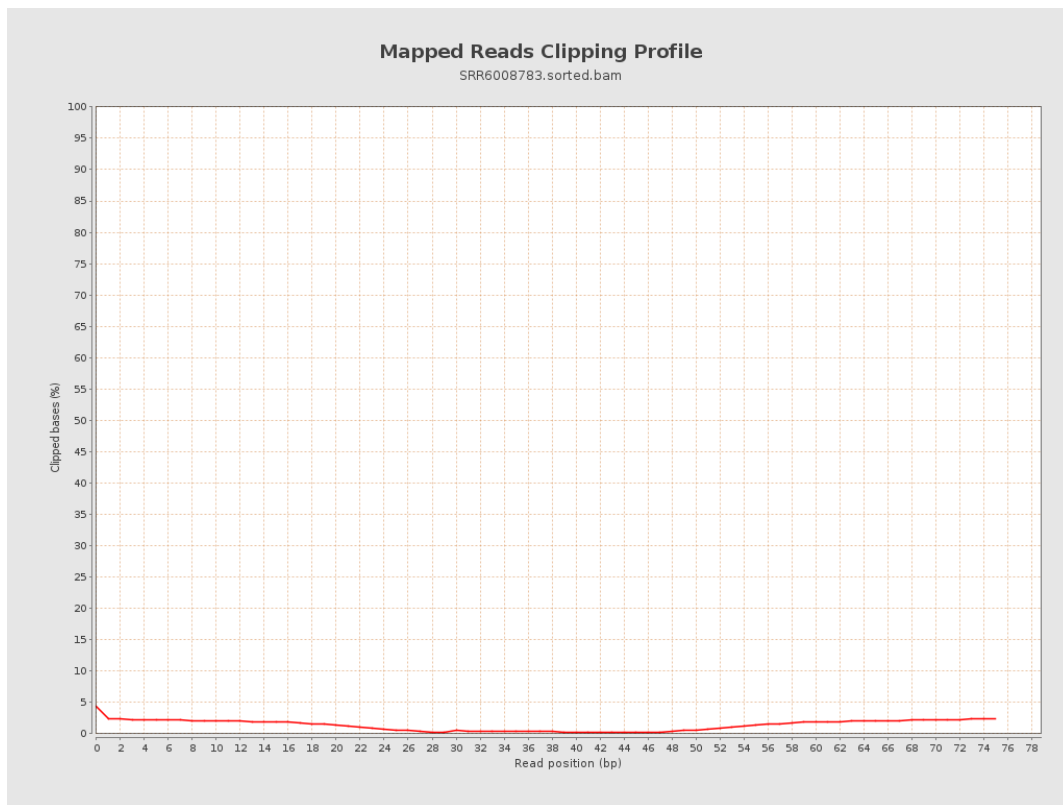
8. Results : Mapped Reads Nucleotide Content



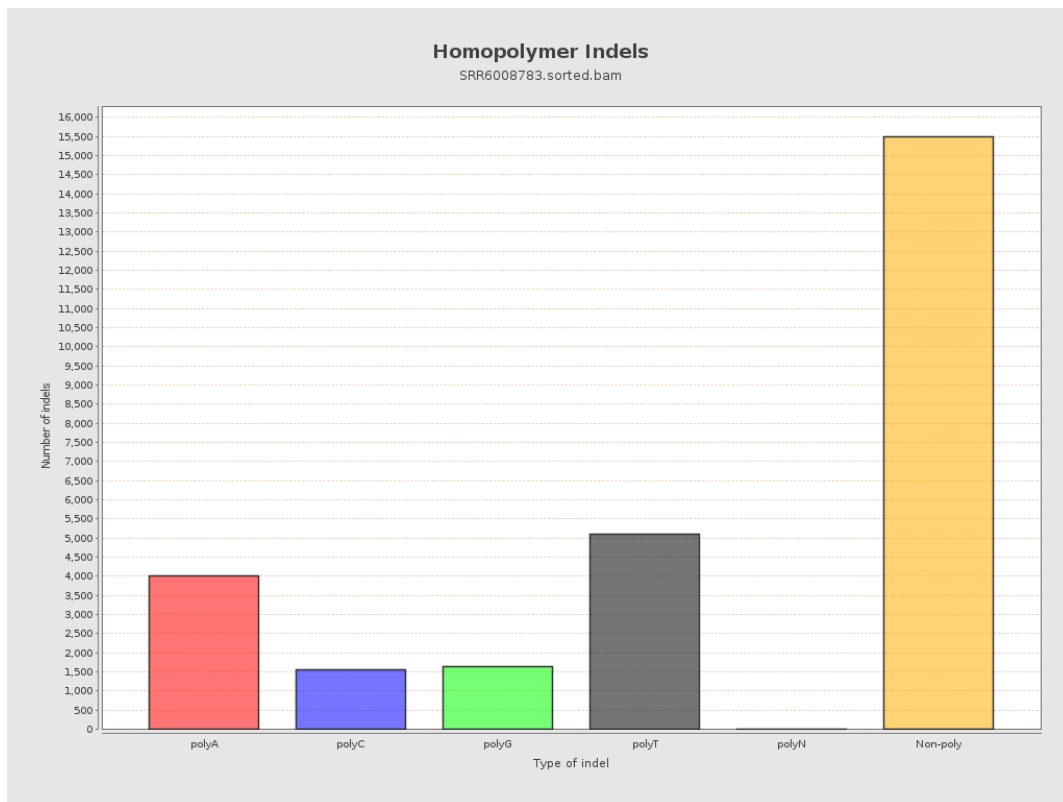
9. Results : Mapped Reads GC-content Distribution



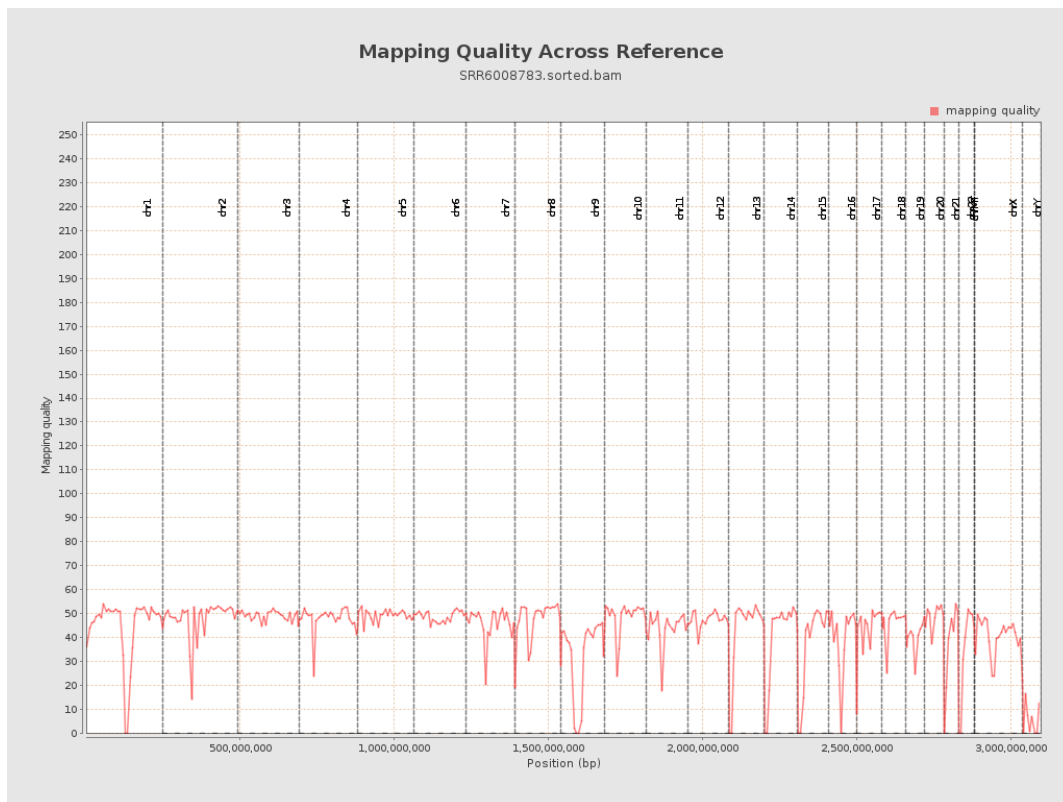
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

