

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 08:06:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008713.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_SRR6008713 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008713.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 08:06:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008713.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,884,594
Mapped reads	1,222,539 / 64.87%
Unmapped reads	662,055 / 35.13%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,474 / 0.24%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	38,288 / 2.03%
Duplication rate	2.61%
Clipped reads	715,006 / 37.94%

2.2. ACGT Content

Number/percentage of A's	21,557,140 / 28.12%
Number/percentage of C's	12,873,971 / 16.79%
Number/percentage of T's	23,524,076 / 30.69%
Number/percentage of G's	18,699,125 / 24.39%
Number/percentage of N's	1,893 / 0%
GC Percentage	41.19%

2.3. Coverage

Mean	0.0248

Standard Deviation	0.2112
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2.4. Mapping Quality

Mean Mapping Quality	45.68
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2.5. Mismatches and indels

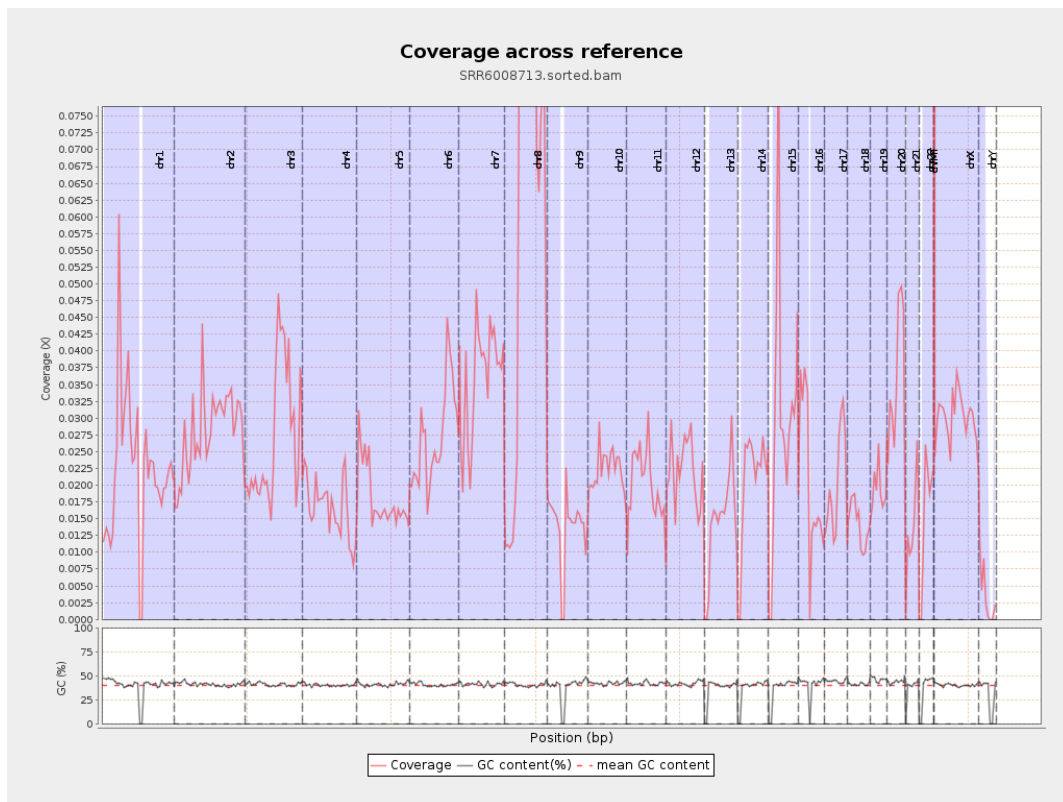
General error rate	1.07%
Mismatches	808,541
Insertions	6,078
Mapped reads with at least one insertion	0.49%
Deletions	25,892
Mapped reads with at least one deletion	2.09%
Homopolymer indels	47.71%

2.6. Chromosome stats

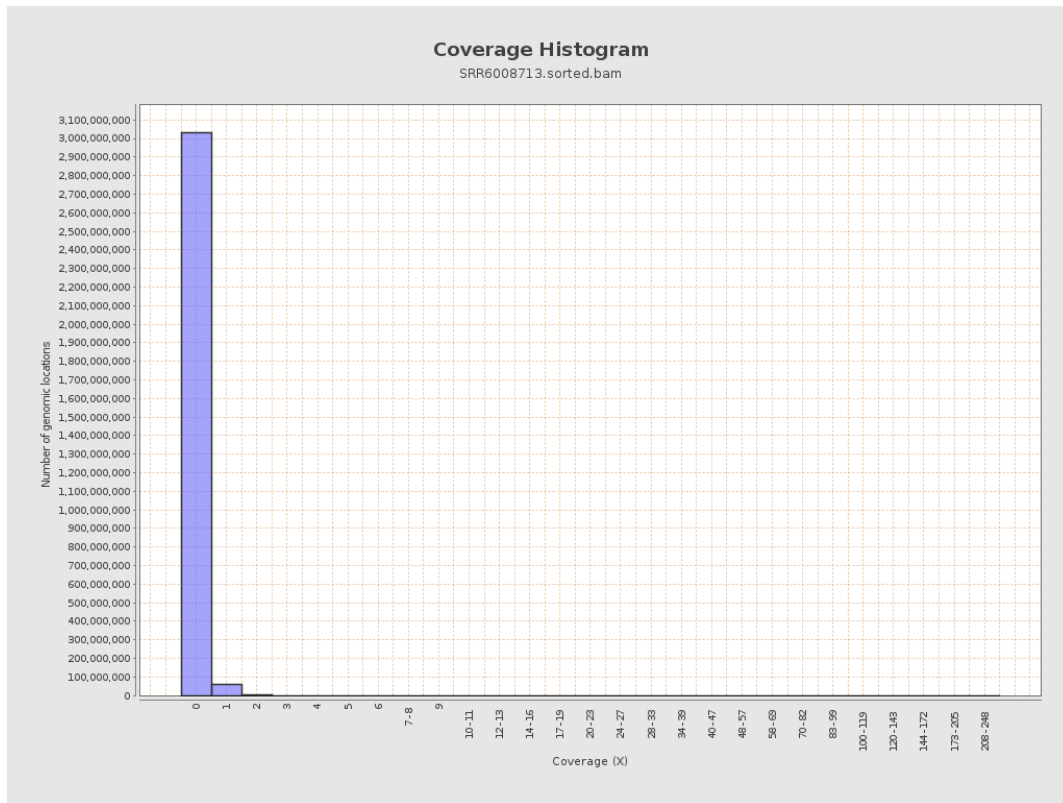
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5521904	0.0222	0.2489
chr2	243199373	6840822	0.0281	0.2647
chr3	198022430	5375991	0.0271	0.1855
chr4	191154276	3195551	0.0167	0.1477
chr5	180915260	3302959	0.0183	0.1507
chr6	171115067	4635543	0.0271	0.1943
chr7	159138663	5746305	0.0361	0.3224

chr8	146364022	9939062	0.0679	0.3415
chr9	141213431	1946631	0.0138	0.1649
chr10	135534747	3014996	0.0222	0.1838
chr11	135006516	2769587	0.0205	0.1869
chr12	133851895	2992515	0.0224	0.1679
chr13	115169878	1687277	0.0147	0.1349
chr14	107349540	2202635	0.0205	0.162
chr15	102531392	3064806	0.0299	0.1984
chr16	90354753	1824081	0.0202	0.1639
chr17	81195210	1643108	0.0202	0.1703
chr18	78077248	1095842	0.014	0.2659
chr19	59128983	1164269	0.0197	0.1813
chr20	63025520	2271374	0.036	0.2143
chr21	48129895	667918	0.0139	0.1349
chr22	51304566	820515	0.016	0.14
chrMT	16571	62188	3.7528	3.3644
chrX	155270560	4706230	0.0303	0.2016
chrY	59373566	204744	0.0034	0.0782

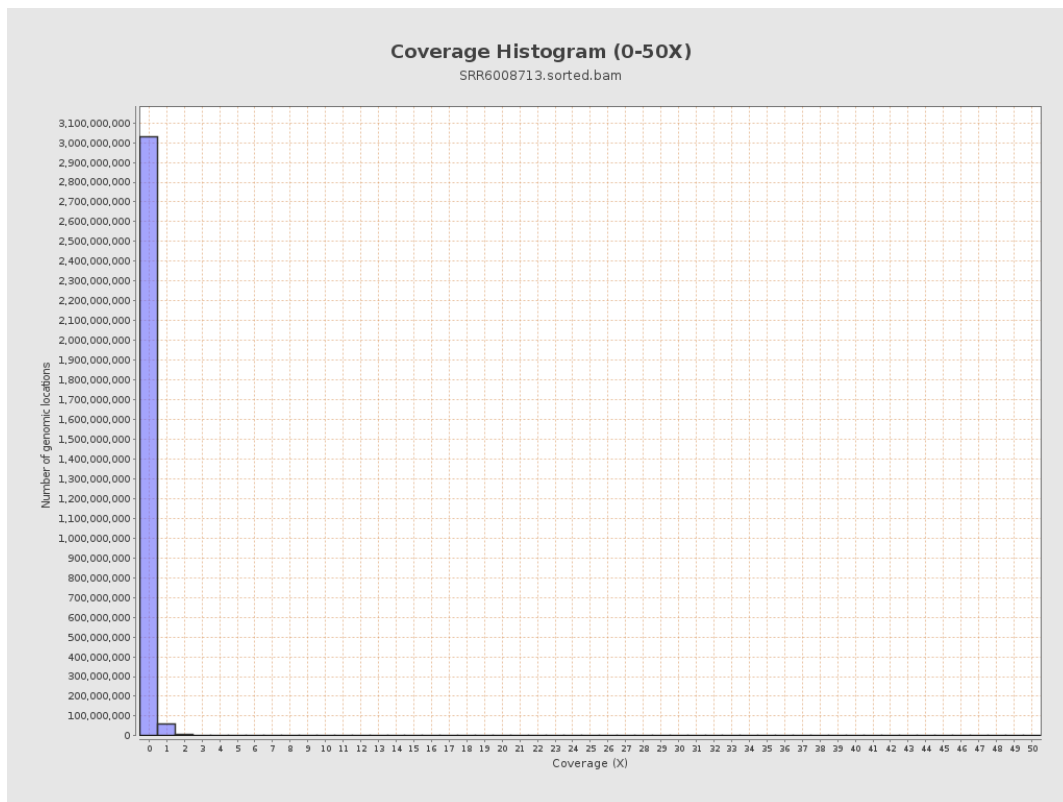
3. Results : Coverage across reference



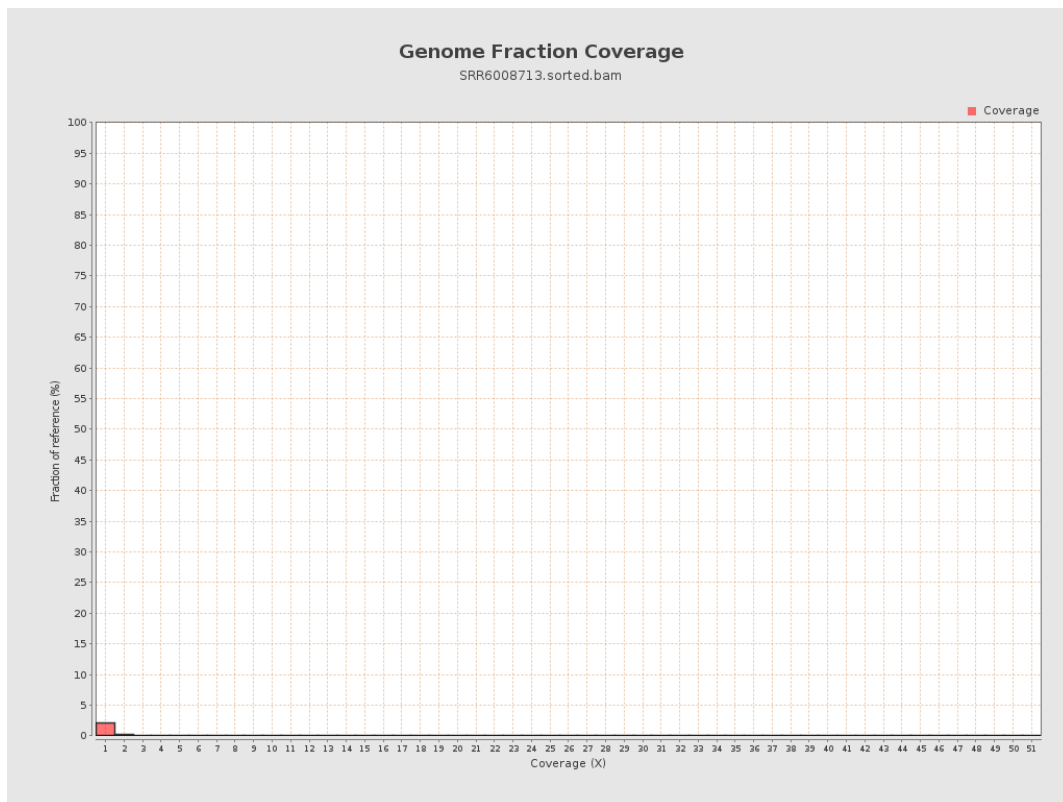
4. Results : Coverage Histogram



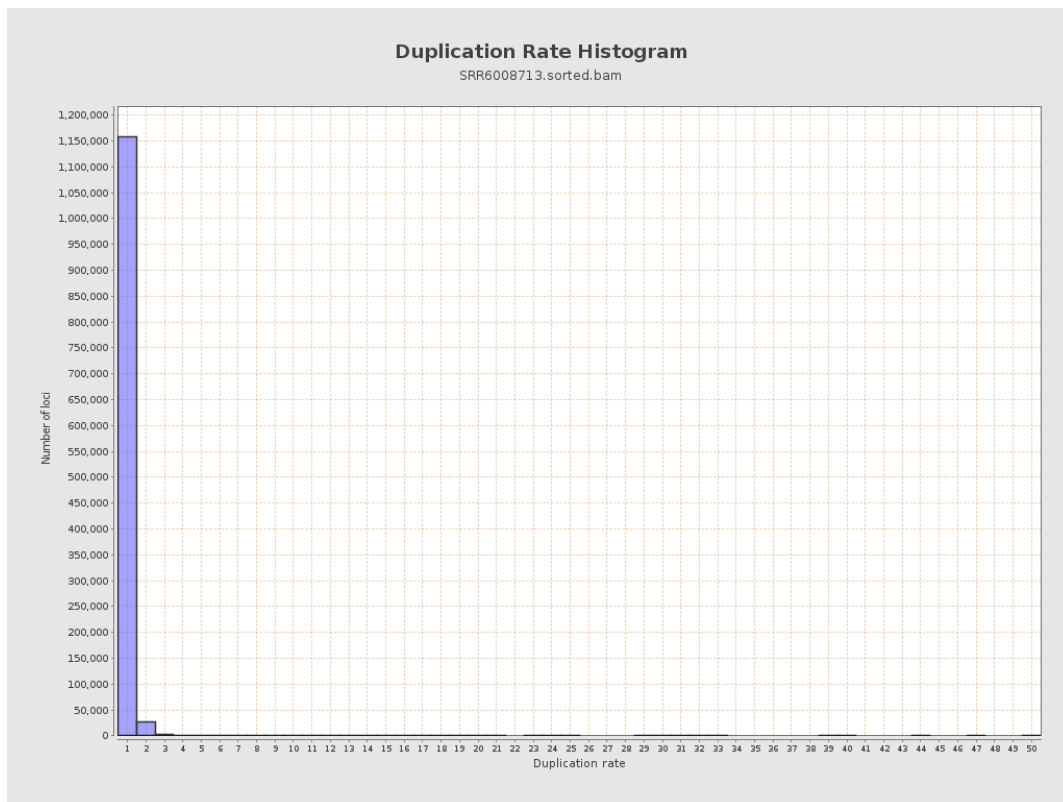
5. Results : Coverage Histogram (0-50X)



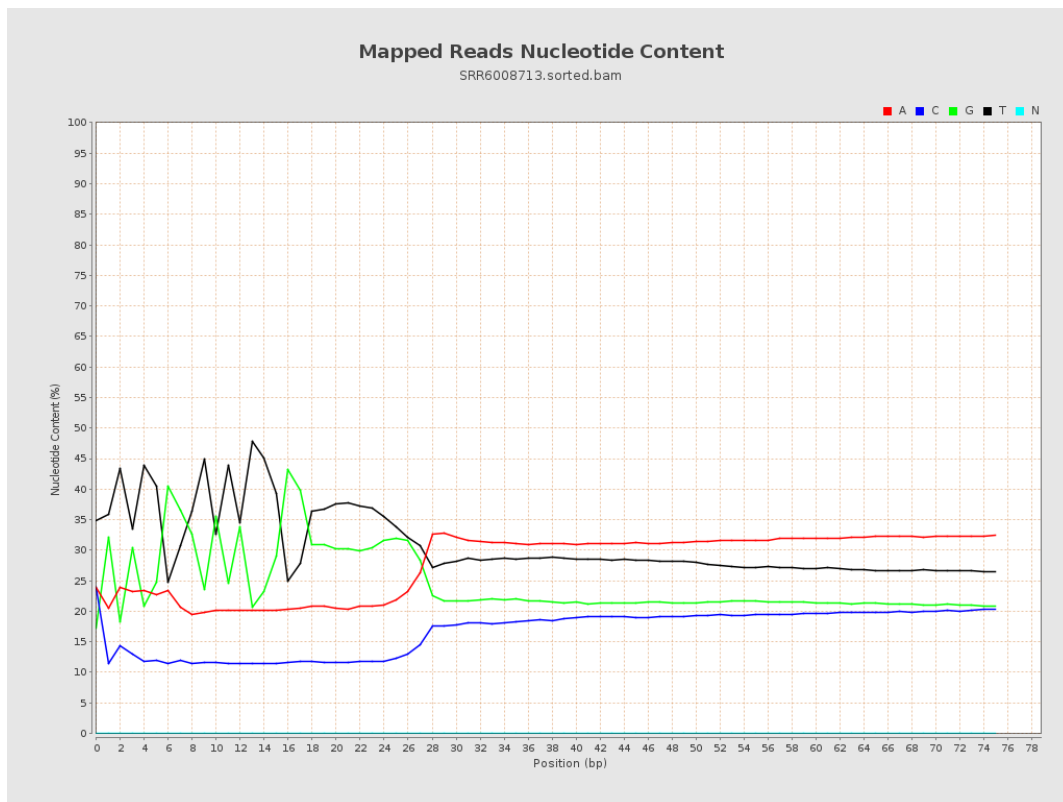
6. Results : Genome Fraction Coverage



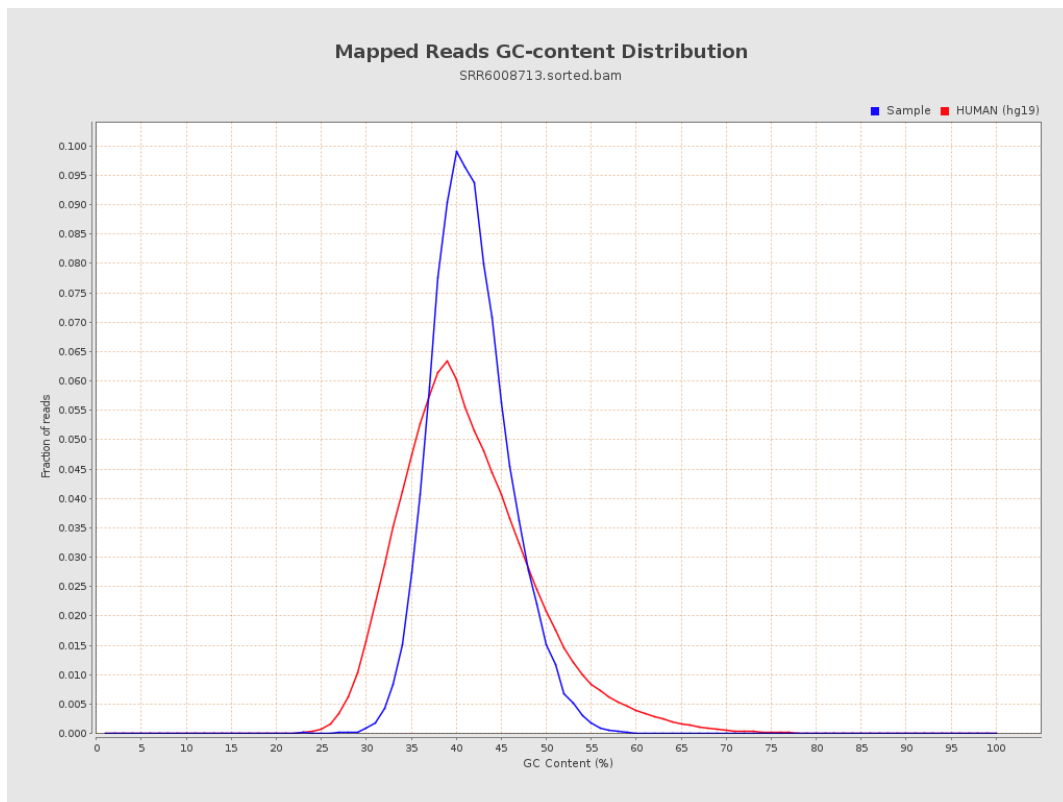
7. Results : Duplication Rate Histogram



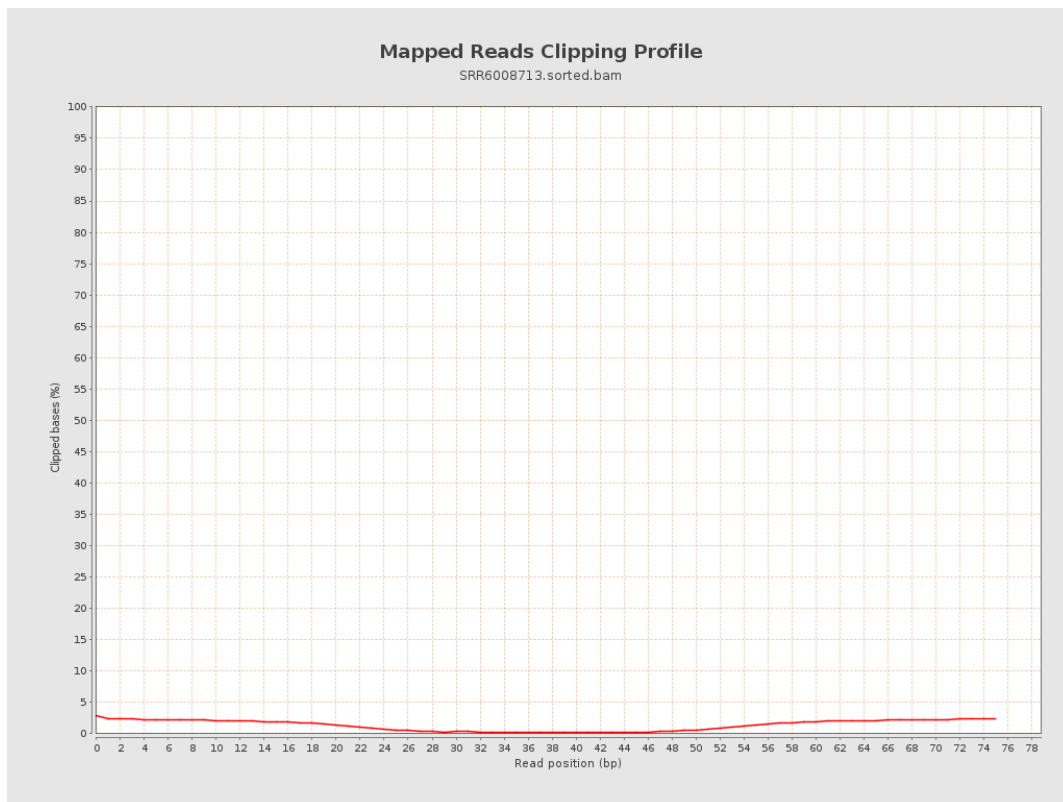
8. Results : Mapped Reads Nucleotide Content



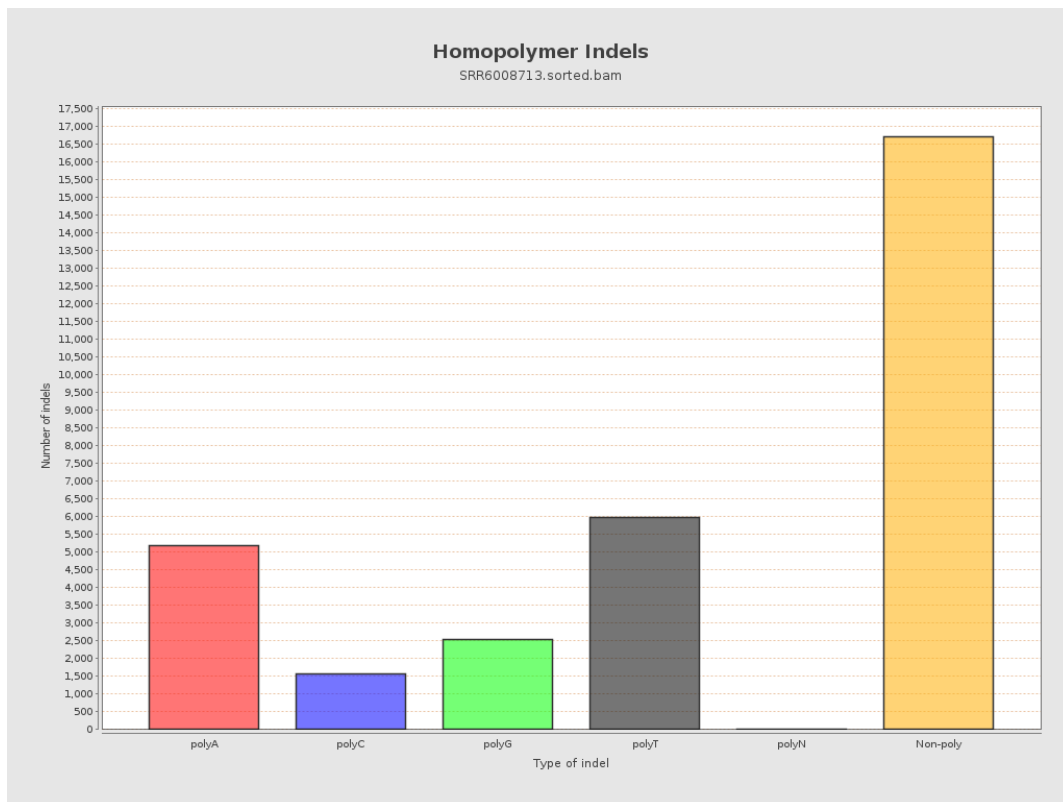
9. Results : Mapped Reads GC-content Distribution



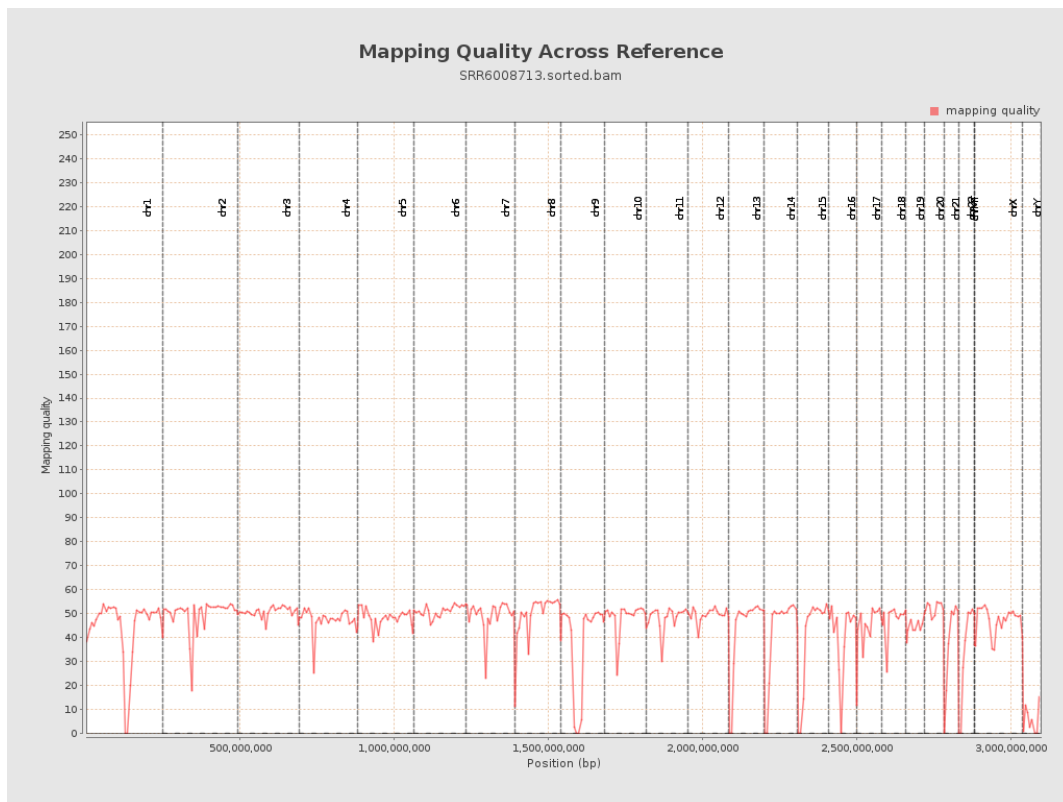
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

