

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 09:06:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008734.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_SRR6008734 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008734.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 09:06:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008734.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,351,857
Mapped reads	1,137,830 / 84.17%
Unmapped reads	214,027 / 15.83%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,409 / 0.7%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	58,102 / 4.3%
Duplication rate	4.21%
Clipped reads	671,339 / 49.66%

2.2. ACGT Content

Number/percentage of A's	18,559,300 / 25.82%
Number/percentage of C's	13,179,436 / 18.34%
Number/percentage of T's	22,853,039 / 31.8%
Number/percentage of G's	17,244,601 / 23.99%
Number/percentage of N's	38,157 / 0.05%
GC Percentage	42.33%

2.3. Coverage

Mean	0.0232

Standard Deviation	0.2268
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2.4. Mapping Quality

Mean Mapping Quality	44.64
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2.5. Mismatches and indels

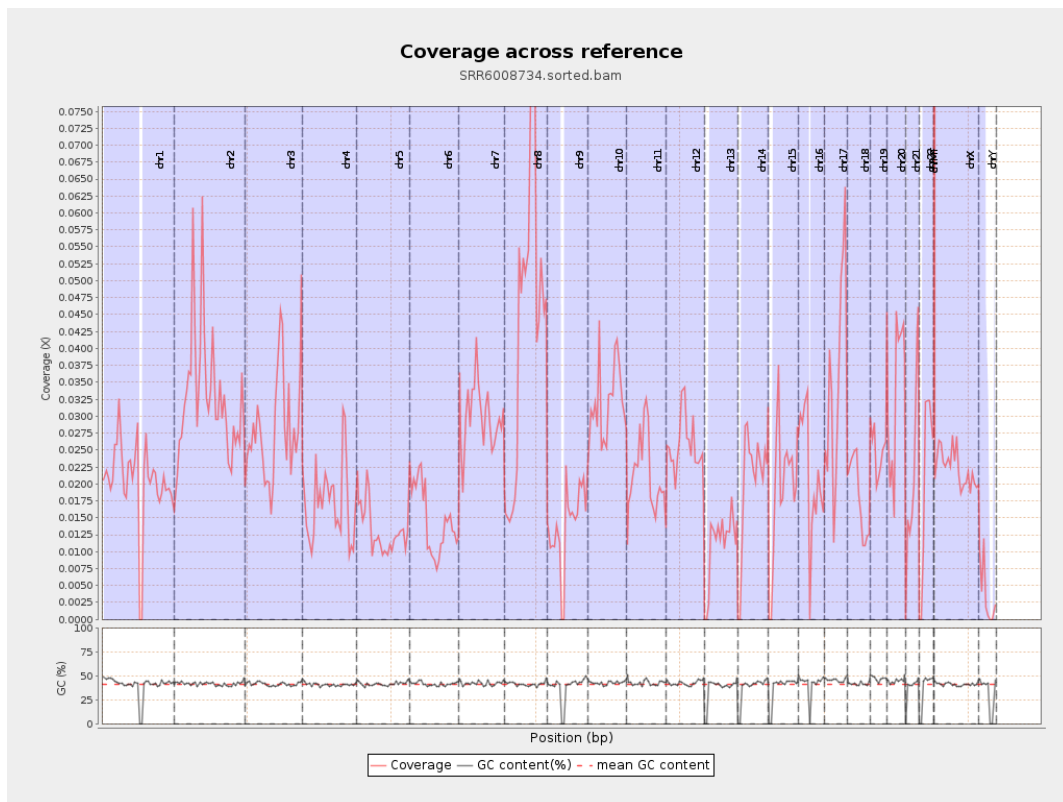
General error rate	0.91%
Mismatches	640,579
Insertions	5,504
Mapped reads with at least one insertion	0.48%
Deletions	25,896
Mapped reads with at least one deletion	2.25%
Homopolymer indels	44.85%

2.6. Chromosome stats

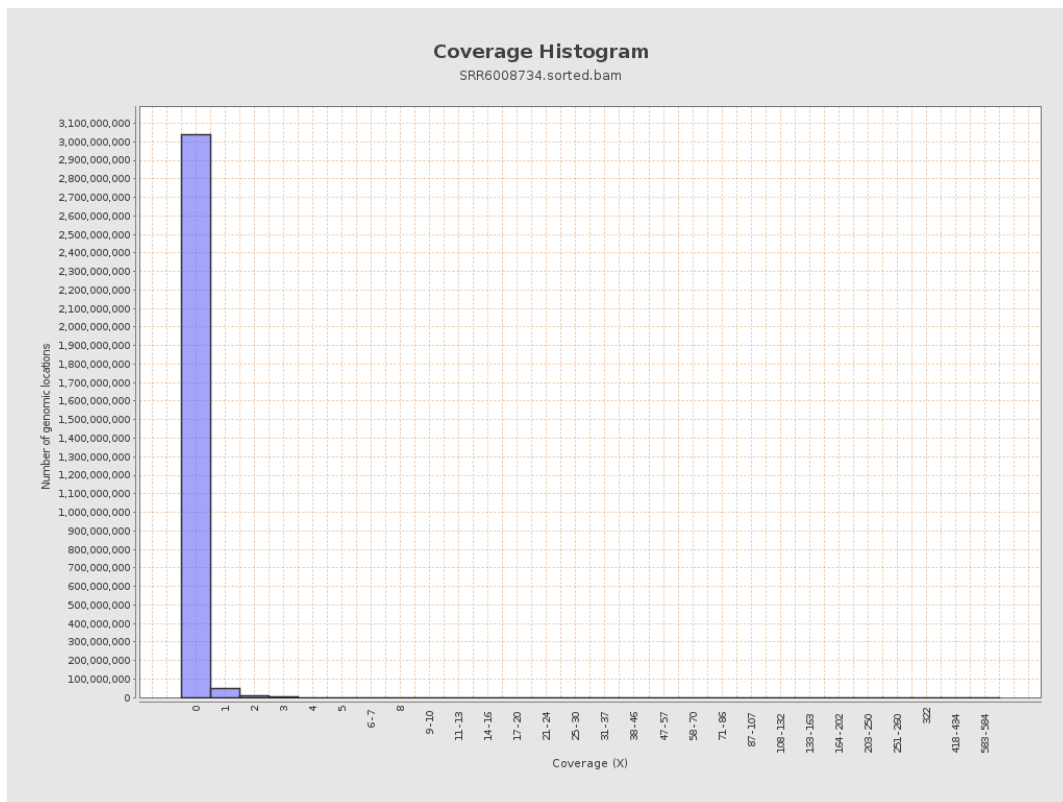
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5065979	0.0203	0.2648
chr2	243199373	8011882	0.0329	0.3774
chr3	198022430	5542633	0.028	0.1931
chr4	191154276	3308754	0.0173	0.1617
chr5	180915260	2370989	0.0131	0.1335
chr6	171115067	2514862	0.0147	0.1581
chr7	159138663	4801639	0.0302	0.2812

chr8	146364022	6496117	0.0444	0.2846
chr9	141213431	1963081	0.0139	0.1949
chr10	135534747	4362873	0.0322	0.2378
chr11	135006516	2925681	0.0217	0.2363
chr12	133851895	3422790	0.0256	0.1876
chr13	115169878	1279353	0.0111	0.1211
chr14	107349540	2174541	0.0203	0.1668
chr15	102531392	1954814	0.0191	0.1651
chr16	90354753	1917441	0.0212	0.1823
chr17	81195210	2857680	0.0352	0.2489
chr18	78077248	1409747	0.0181	0.2556
chr19	59128983	1496410	0.0253	0.2263
chr20	63025520	2072039	0.0329	0.2134
chr21	48129895	1040359	0.0216	0.1781
chr22	51304566	1093592	0.0213	0.169
chrMT	16571	144222	8.7033	6.0104
chrX	155270560	3479302	0.0224	0.1832
chrY	59373566	211520	0.0036	0.1121

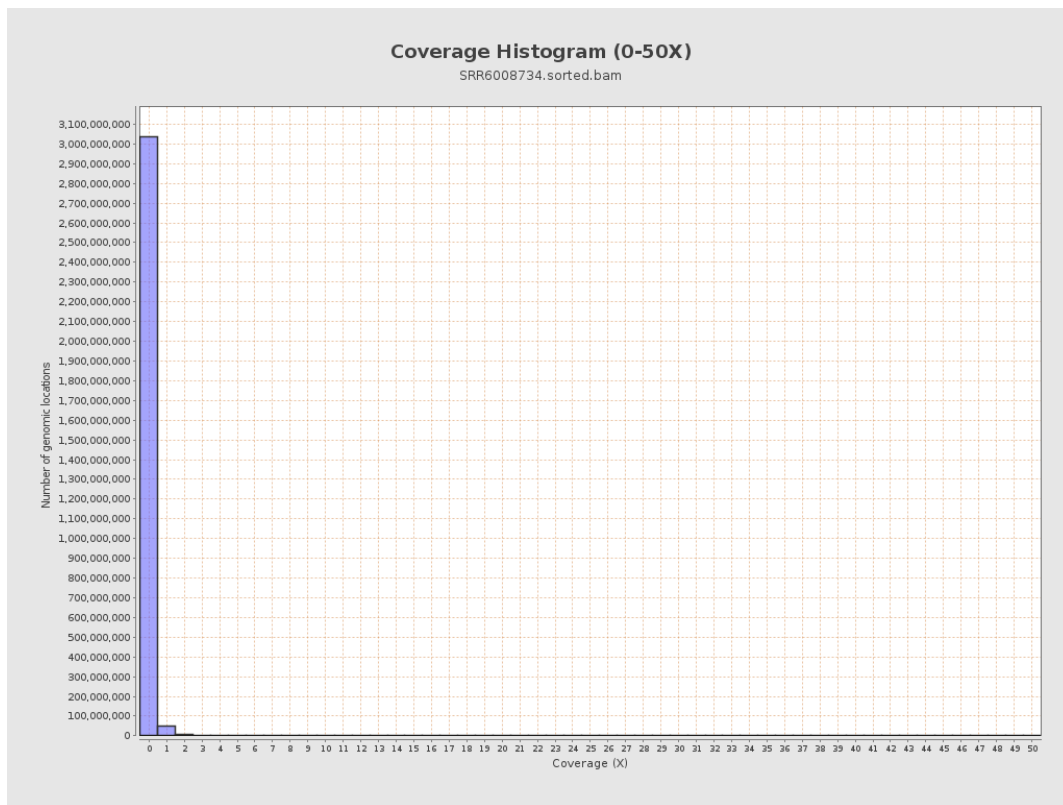
3. Results : Coverage across reference



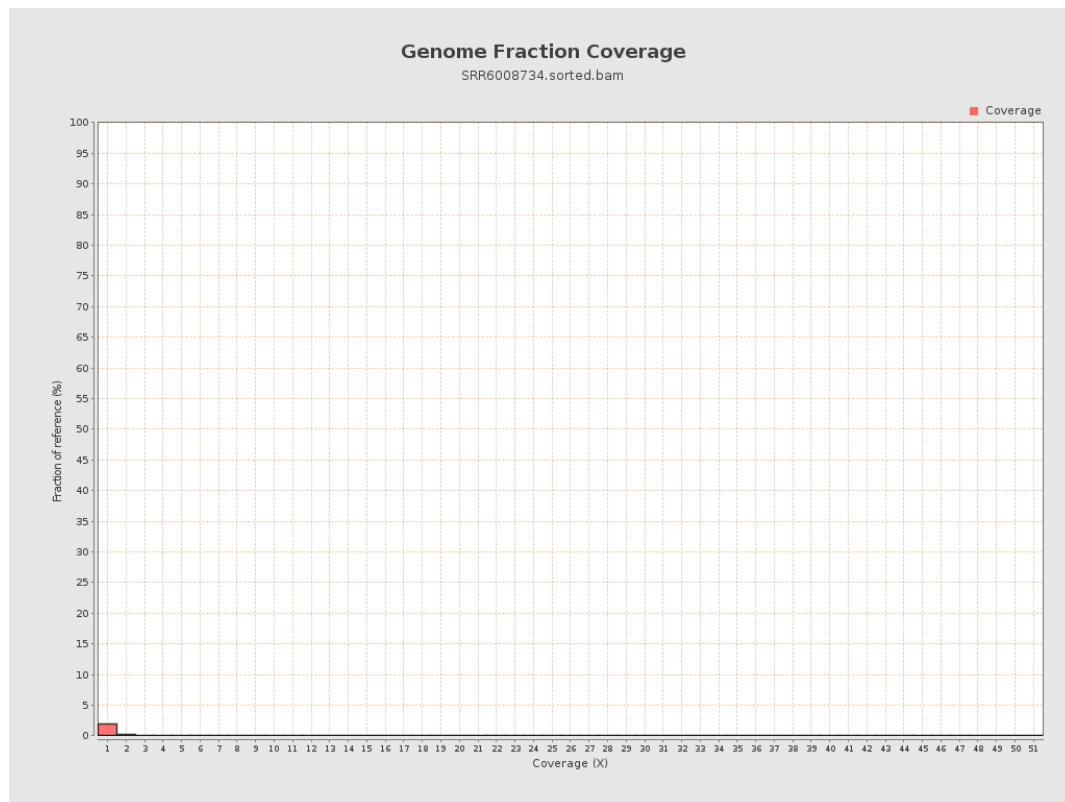
4. Results : Coverage Histogram



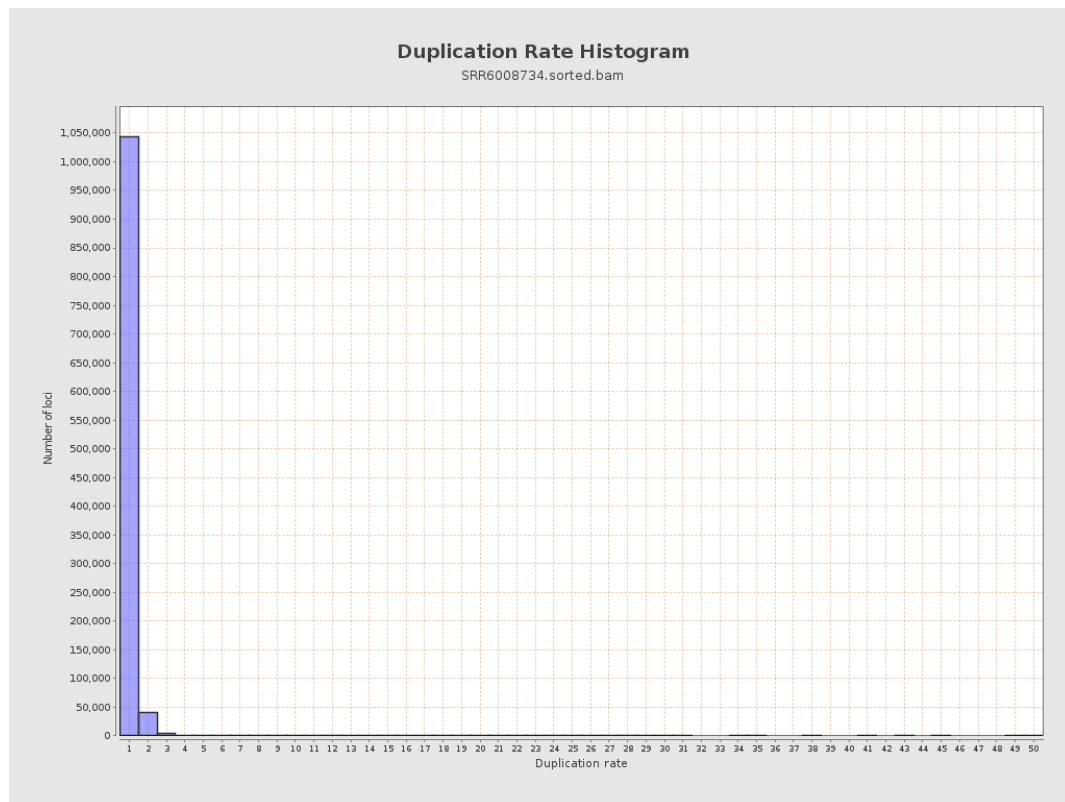
5. Results : Coverage Histogram (0-50X)



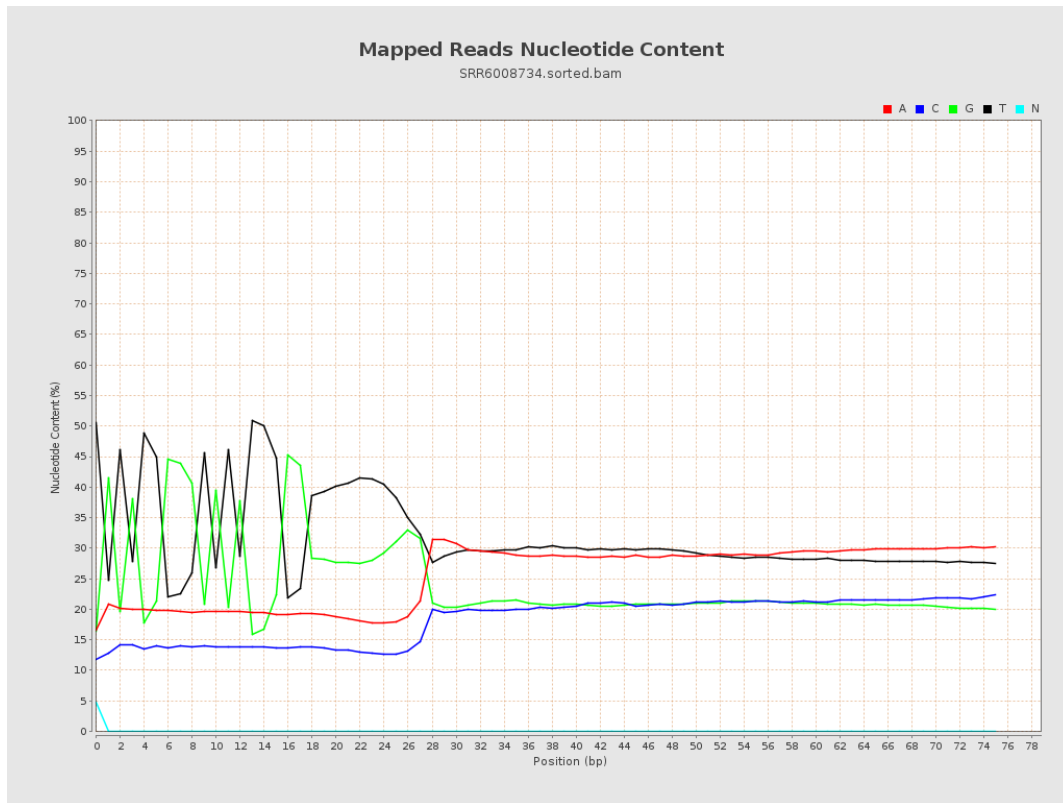
6. Results : Genome Fraction Coverage



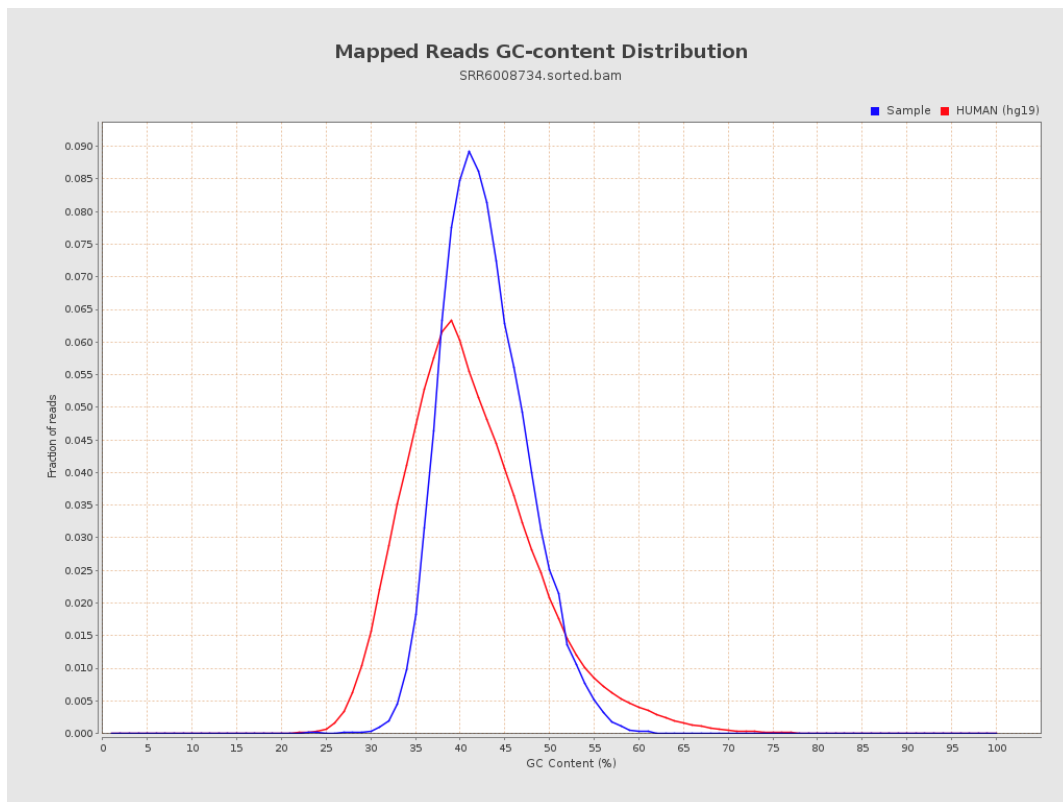
7. Results : Duplication Rate Histogram



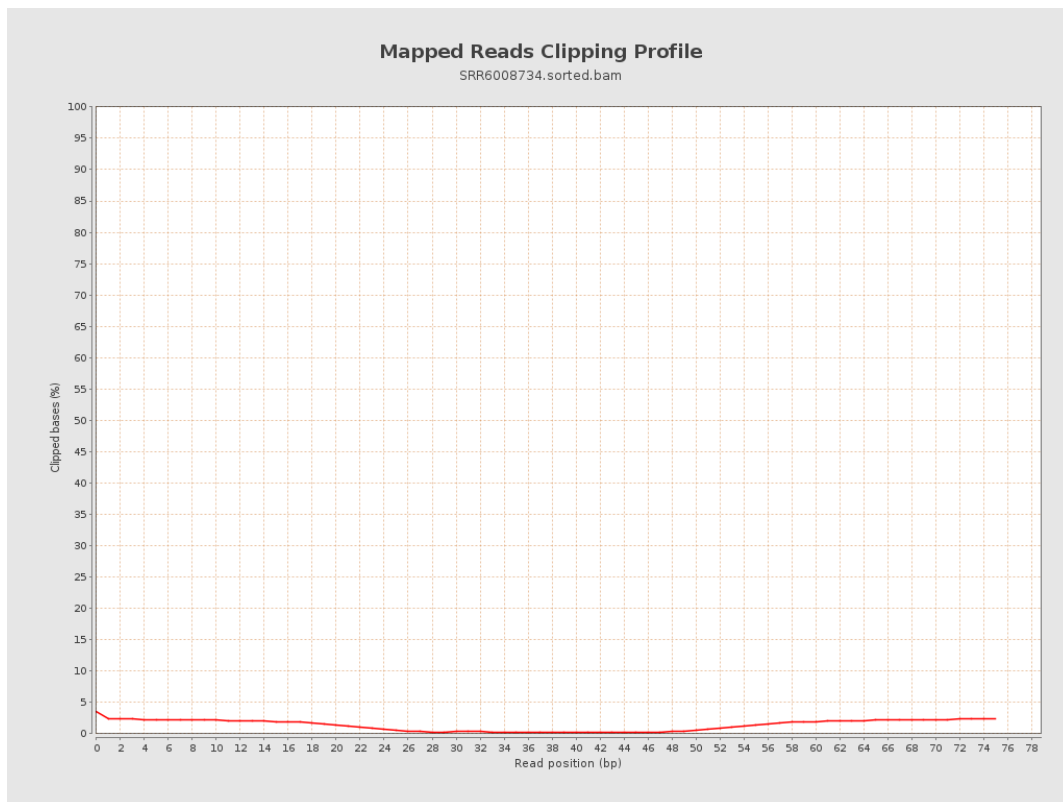
8. Results : Mapped Reads Nucleotide Content



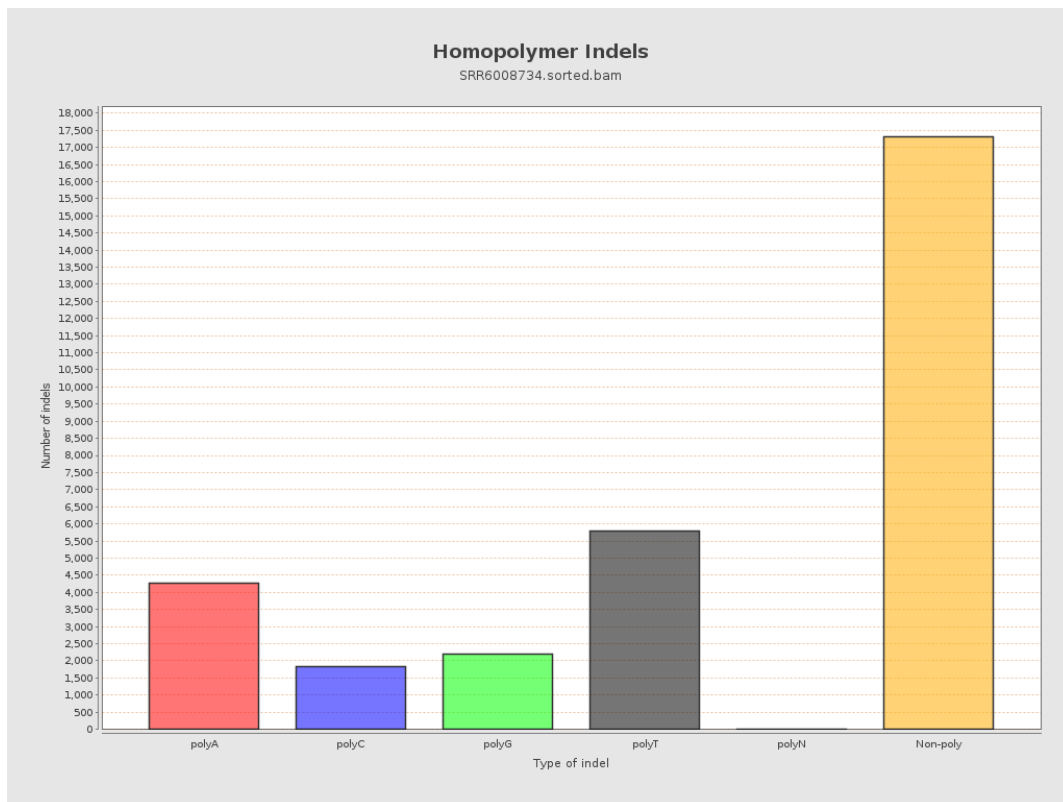
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

