

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 10:06:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238034.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_SRR6238034 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238034.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 10:06:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238034.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,011,511
Mapped reads	1,826,894 / 90.82%
Unmapped reads	184,617 / 9.18%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,681 / 0.63%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	69,239 / 3.44%
Duplication rate	2.84%
Clipped reads	766,775 / 38.12%

2.2. ACGT Content

Number/percentage of A's	33,013,899 / 27.03%
Number/percentage of C's	23,220,480 / 19.01%
Number/percentage of T's	37,965,651 / 31.09%
Number/percentage of G's	27,911,826 / 22.86%
Number/percentage of N's	7,120 / 0.01%
GC Percentage	41.87%

2.3. Coverage

Mean	0.0395

Standard Deviation	0.3801
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2.4. Mapping Quality

Mean Mapping Quality	45.9
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2.5. Mismatches and indels

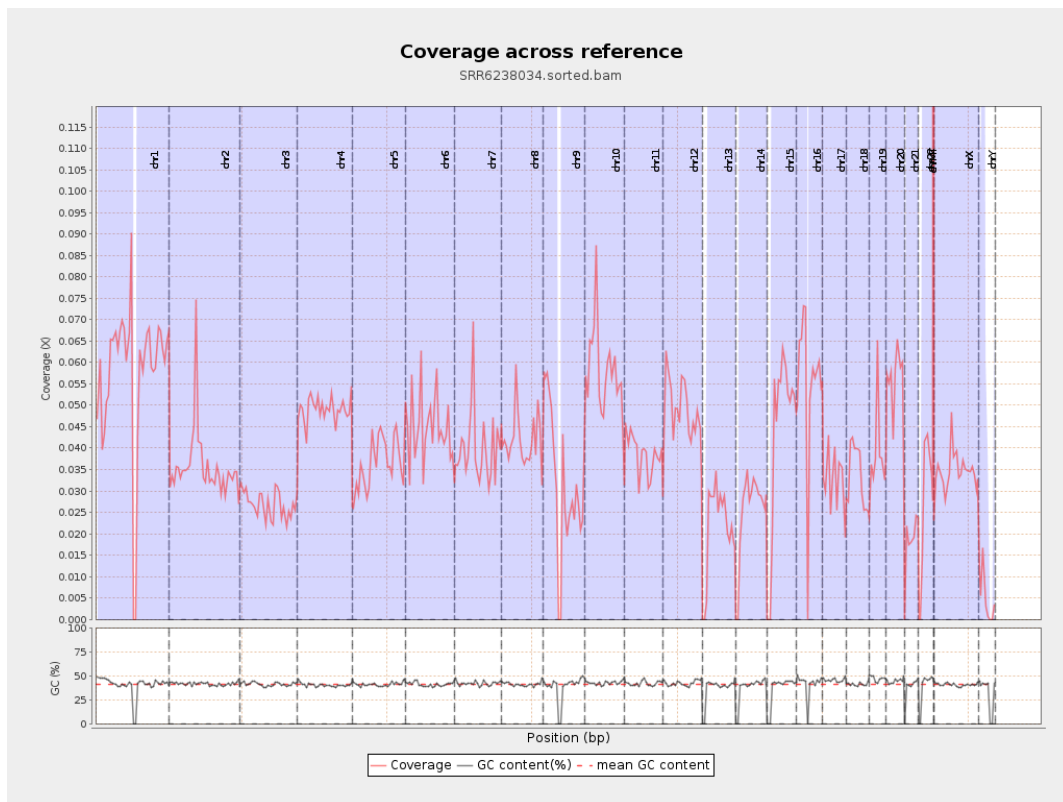
General error rate	0.74%
Mismatches	885,109
Insertions	8,409
Mapped reads with at least one insertion	0.46%
Deletions	29,832
Mapped reads with at least one deletion	1.62%
Homopolymer indels	46.36%

2.6. Chromosome stats

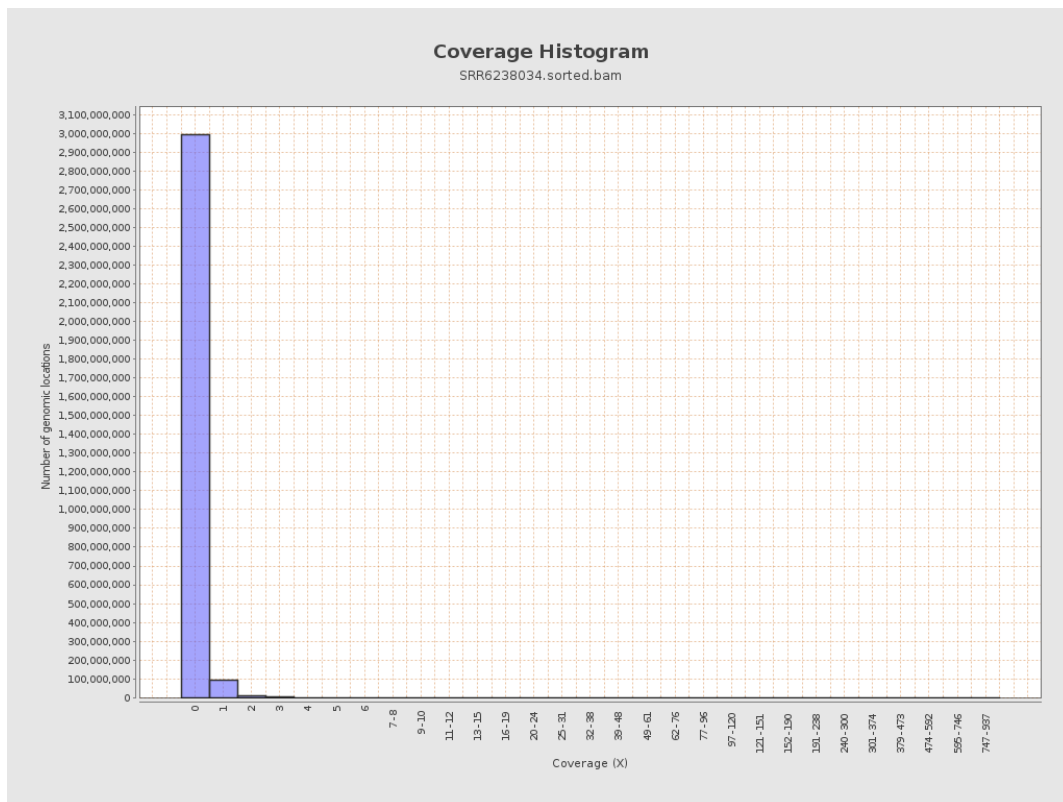
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	14333842	0.0575	0.8123
chr2	243199373	8706818	0.0358	0.3935
chr3	198022430	5314319	0.0268	0.189
chr4	191154276	9376939	0.0491	0.267
chr5	180915260	6600940	0.0365	0.2175
chr6	171115067	7646492	0.0447	0.3029
chr7	159138663	6335097	0.0398	0.485

chr8	146364022	6143363	0.042	0.3649
chr9	141213431	4384657	0.031	0.3274
chr10	135534747	7886668	0.0582	0.4366
chr11	135006516	5193478	0.0385	0.2658
chr12	133851895	6540946	0.0489	0.2568
chr13	115169878	2464216	0.0214	0.1643
chr14	107349540	2699138	0.0251	0.2152
chr15	102531392	4522480	0.0441	0.2395
chr16	90354753	5026759	0.0556	0.2985
chr17	81195210	2599232	0.032	0.2167
chr18	78077248	2634056	0.0337	0.5636
chr19	59128983	2313304	0.0391	0.5049
chr20	63025520	3526186	0.0559	0.2735
chr21	48129895	898781	0.0187	0.1936
chr22	51304566	1386275	0.027	0.1871
chrMT	16571	15296	0.9231	1.0757
chrX	155270560	5339040	0.0344	0.2328
chrY	59373566	284015	0.0048	0.134

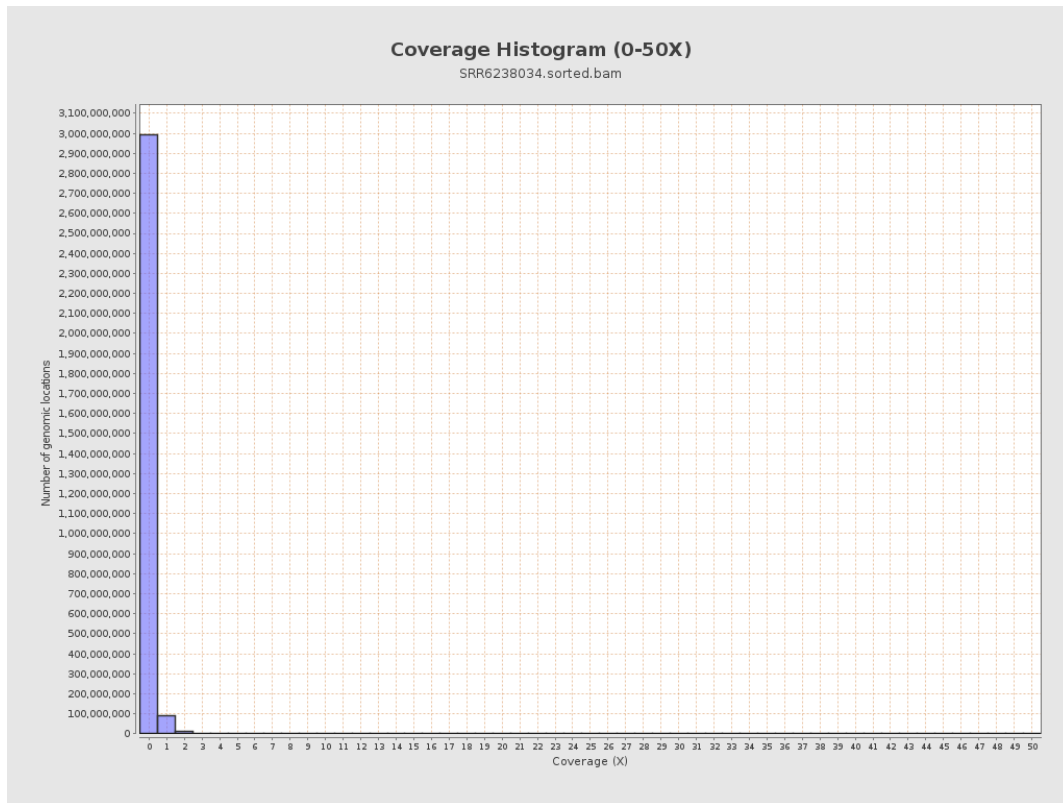
3. Results : Coverage across reference



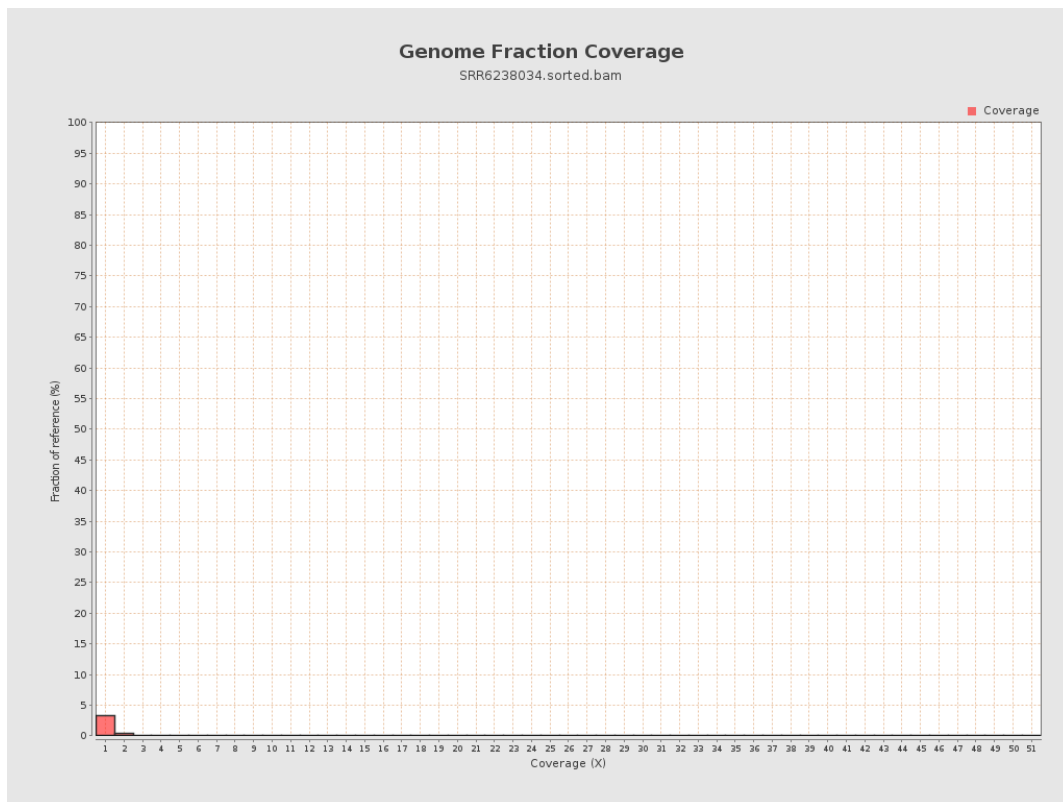
4. Results : Coverage Histogram



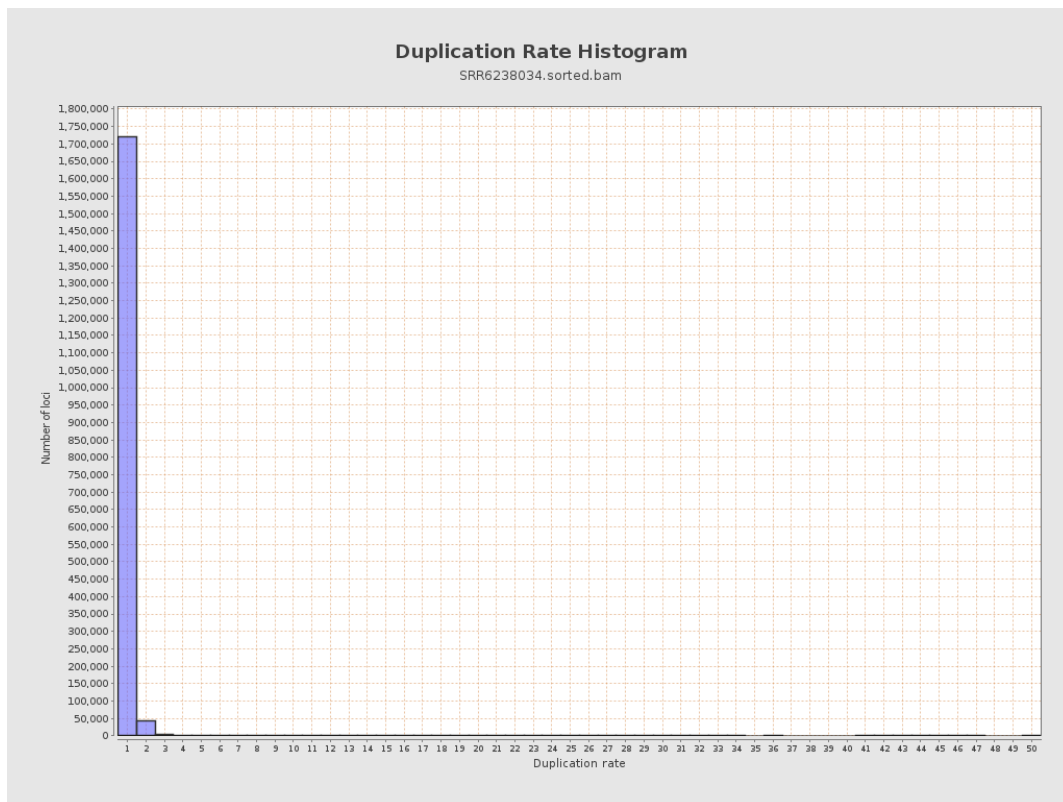
5. Results : Coverage Histogram (0-50X)



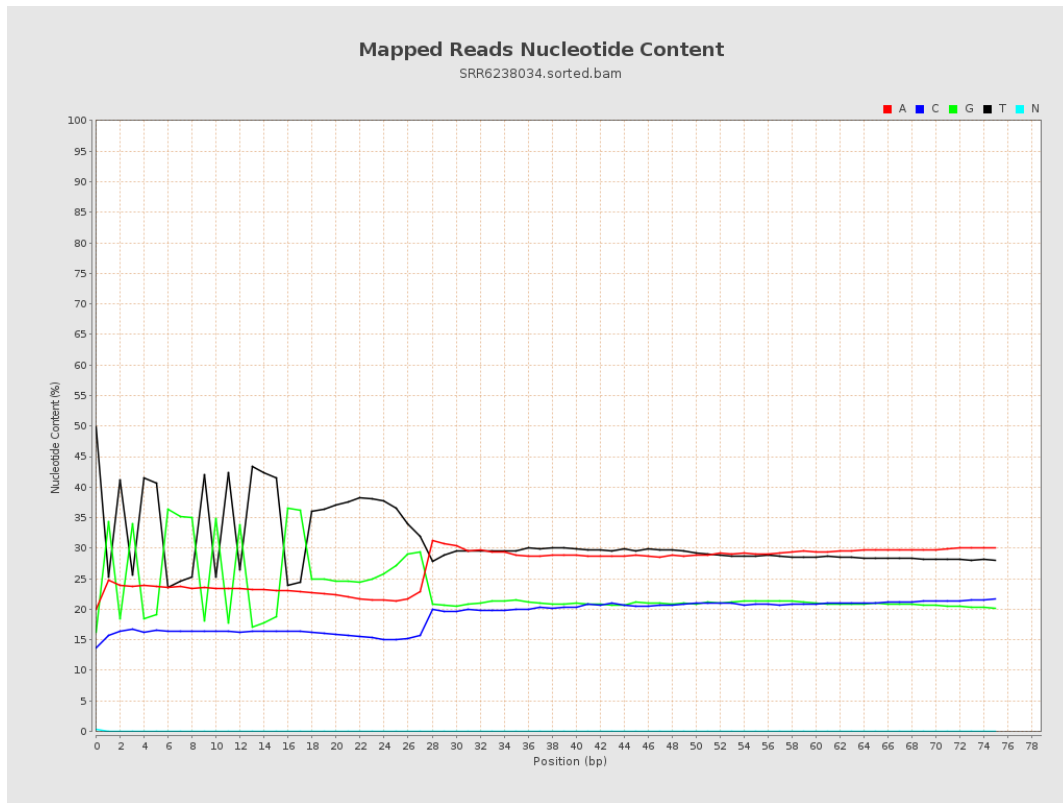
6. Results : Genome Fraction Coverage



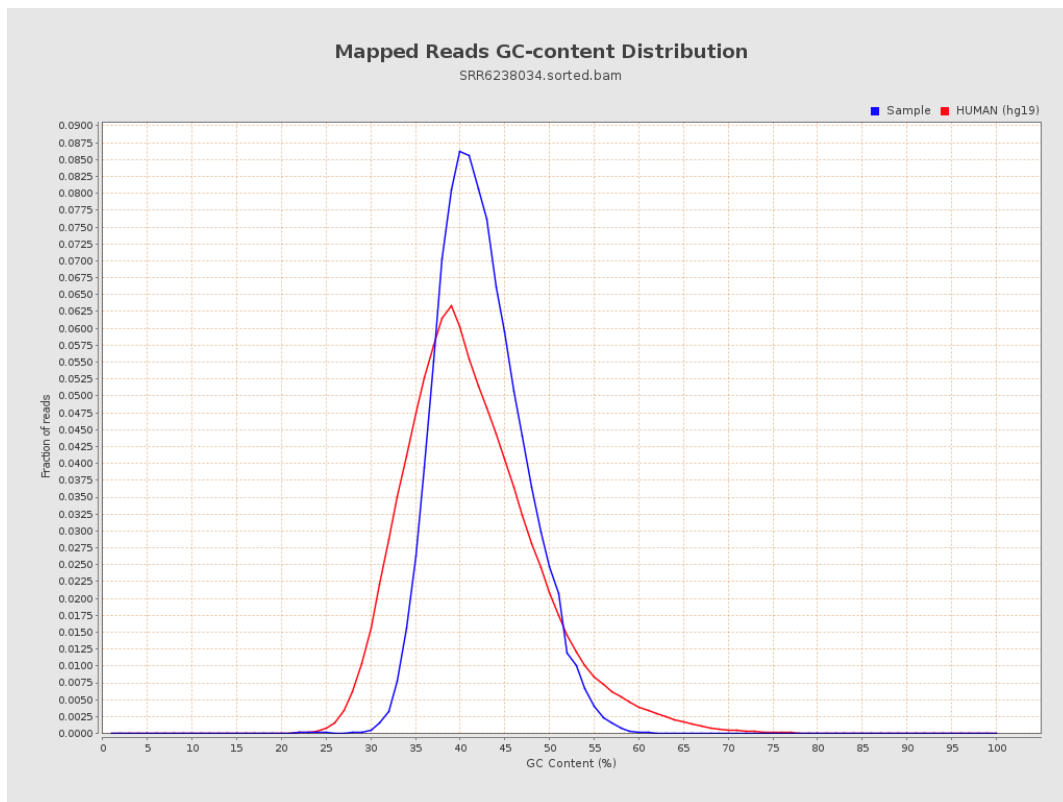
7. Results : Duplication Rate Histogram



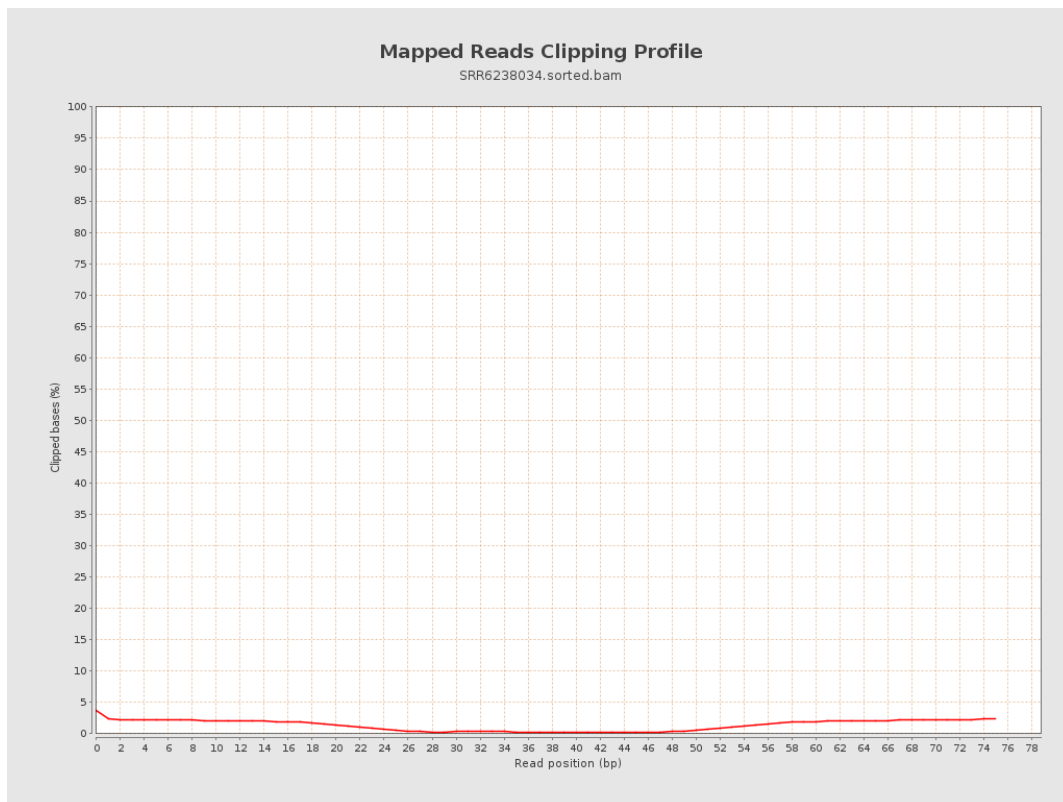
8. Results : Mapped Reads Nucleotide Content



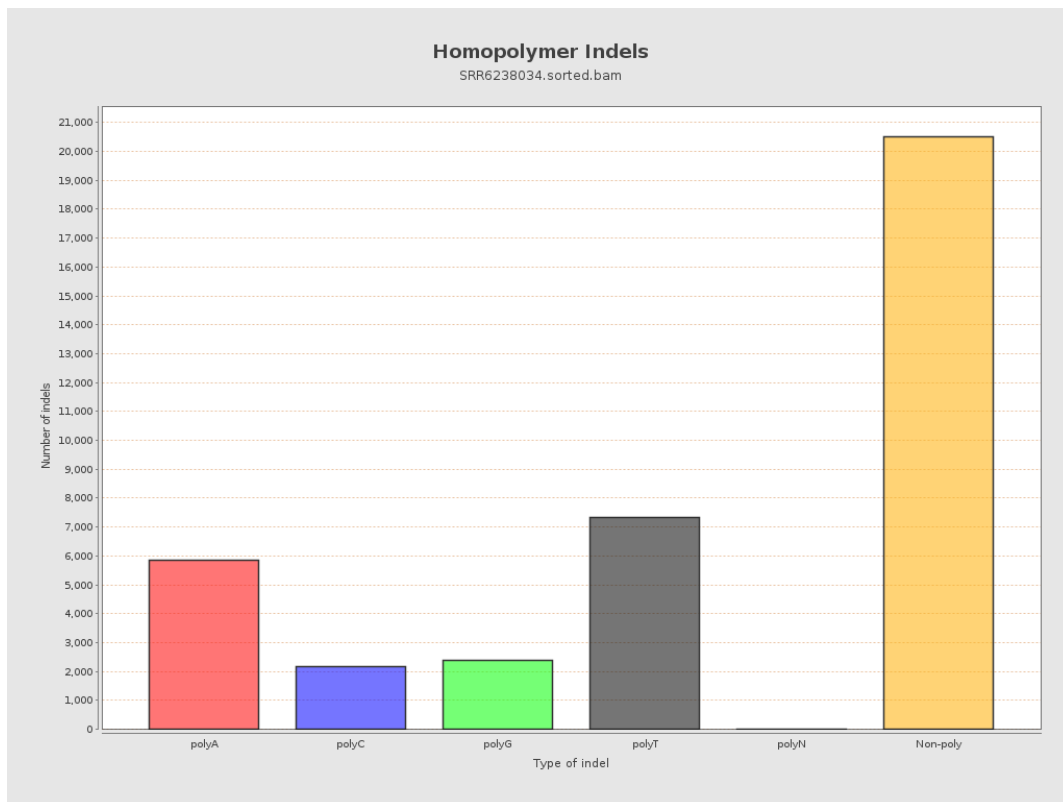
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

