

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 12:43:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238247.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_SRR6238247 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238247.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 12:43:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238247.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,003,235
Mapped reads	1,818,950 / 90.8%
Unmapped reads	184,285 / 9.2%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,544 / 0.98%
Read min/max/mean length	30 / 76 / 76.34
Duplicated reads (estimated)	64,114 / 3.2%
Duplication rate	2.8%
Clipped reads	965,457 / 48.19%

2.2. ACGT Content

Number/percentage of A's	33,568,856 / 28.31%
Number/percentage of C's	23,163,410 / 19.53%
Number/percentage of T's	35,935,574 / 30.31%
Number/percentage of G's	25,892,160 / 21.84%
Number/percentage of N's	19,562 / 0.02%
GC Percentage	41.37%

2.3. Coverage

Mean	0.0383

Standard Deviation	0.3205
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2.4. Mapping Quality

Mean Mapping Quality	44.31
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2.5. Mismatches and indels

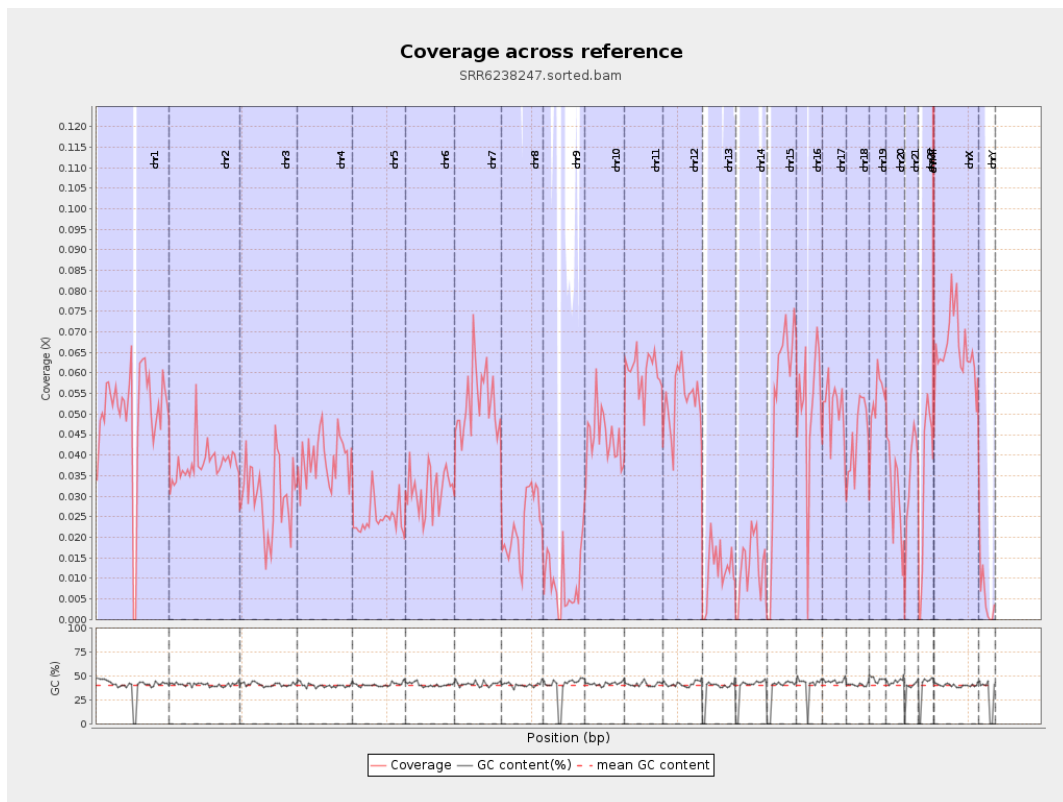
General error rate	0.86%
Mismatches	1,004,552
Insertions	9,436
Mapped reads with at least one insertion	0.51%
Deletions	34,655
Mapped reads with at least one deletion	1.88%
Homopolymer indels	45.59%

2.6. Chromosome stats

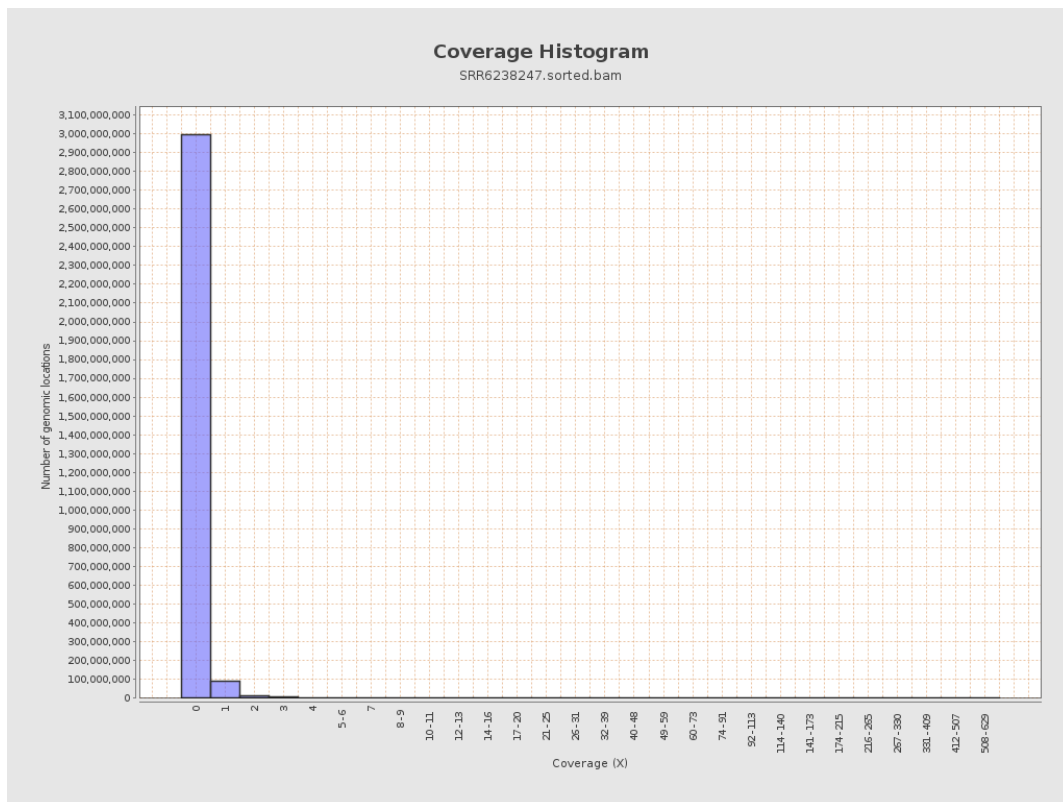
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	12457636	0.05	0.5718
chr2	243199373	9229696	0.038	0.3592
chr3	198022430	5934117	0.03	0.1962
chr4	191154276	7486681	0.0392	0.2289
chr5	180915260	4444579	0.0246	0.1784
chr6	171115067	5382354	0.0315	0.2316
chr7	159138663	8462872	0.0532	0.4825

chr8	146364022	3339838	0.0228	0.3478
chr9	141213431	1263314	0.0089	0.1702
chr10	135534747	5996033	0.0442	0.3218
chr11	135006516	8094656	0.06	0.3754
chr12	133851895	7187755	0.0537	0.2642
chr13	115169878	1342510	0.0117	0.1242
chr14	107349540	1386481	0.0129	0.1349
chr15	102531392	5382503	0.0525	0.2657
chr16	90354753	4685537	0.0519	0.2725
chr17	81195210	4138723	0.051	0.2906
chr18	78077248	3517500	0.0451	0.3749
chr19	59128983	3176514	0.0537	0.4399
chr20	63025520	1903105	0.0302	0.2005
chr21	48129895	1628828	0.0338	0.2152
chr22	51304566	1697544	0.0331	0.2063
chrMT	16571	8639	0.5213	0.8541
chrX	155270560	10166393	0.0655	0.3184
chrY	59373566	323047	0.0054	0.1264

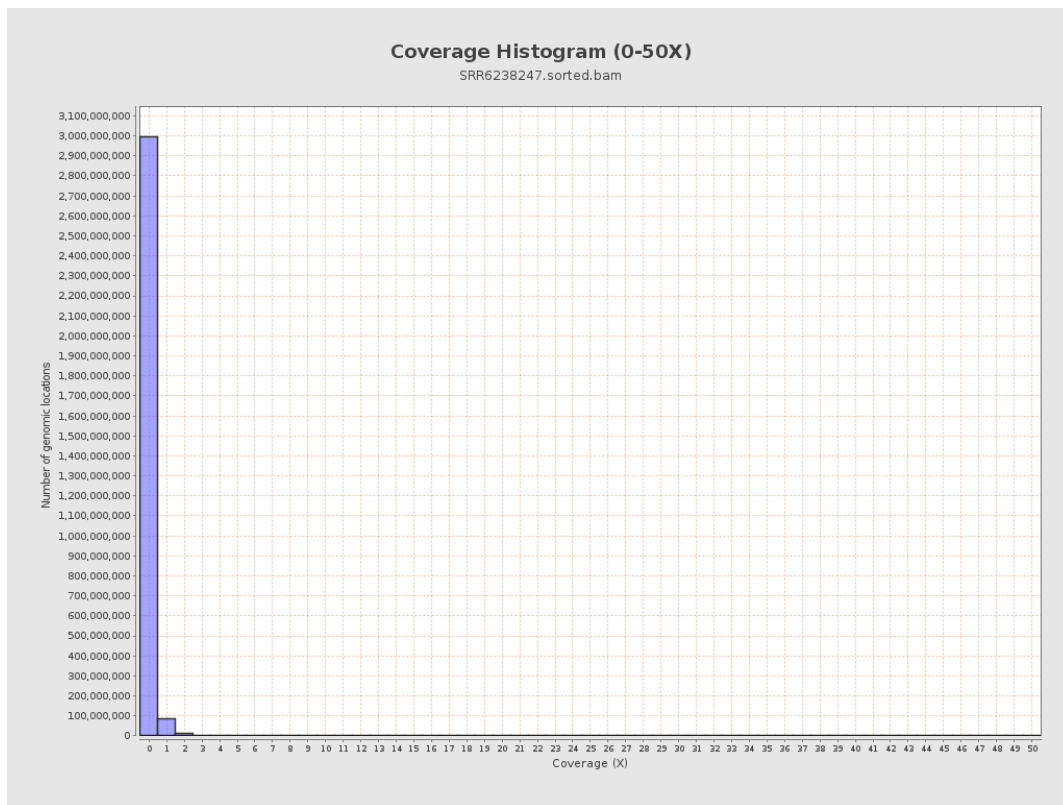
3. Results : Coverage across reference



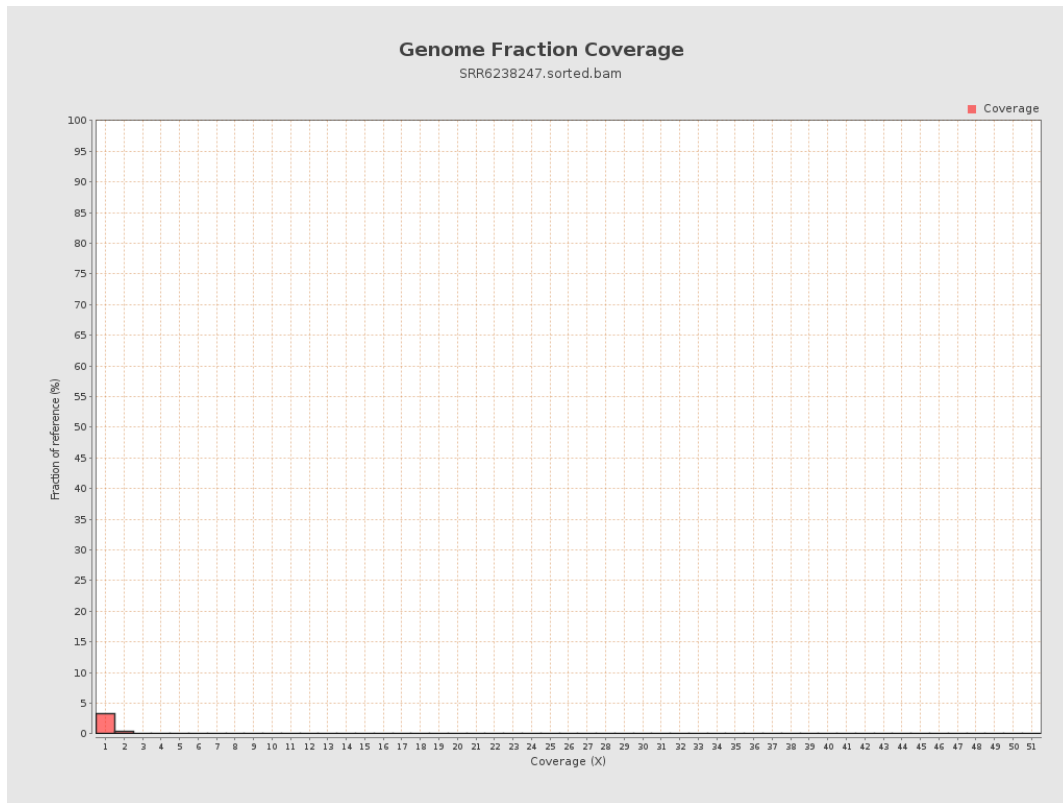
4. Results : Coverage Histogram



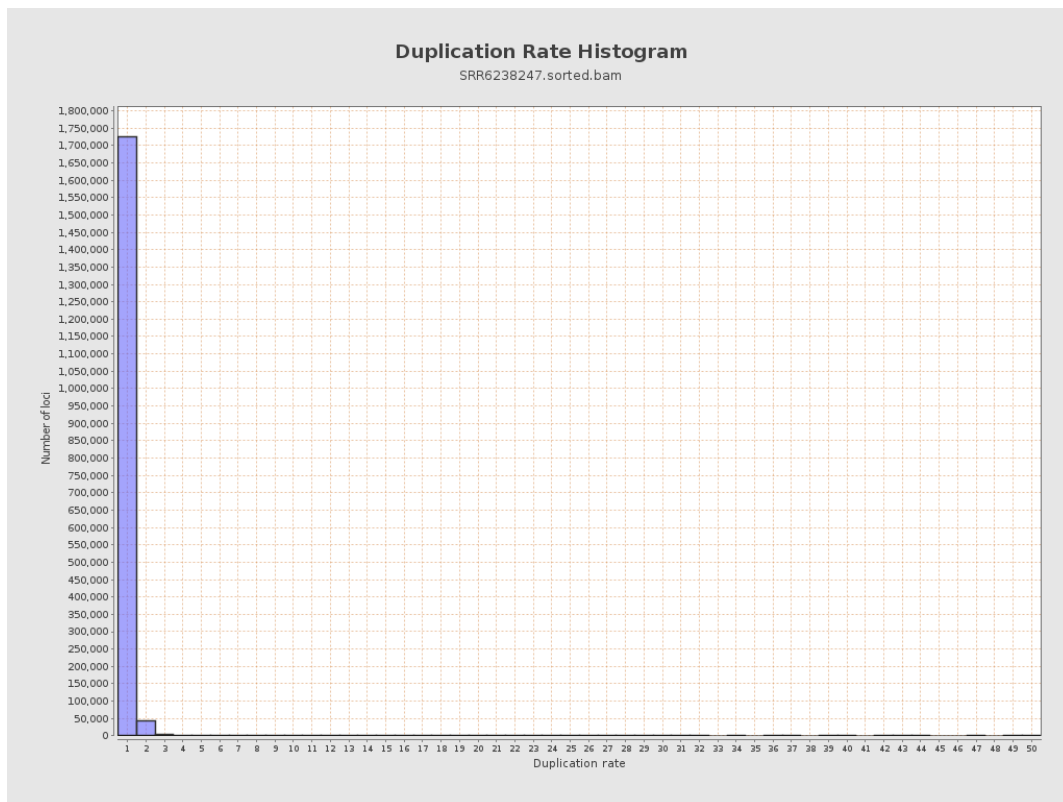
5. Results : Coverage Histogram (0-50X)



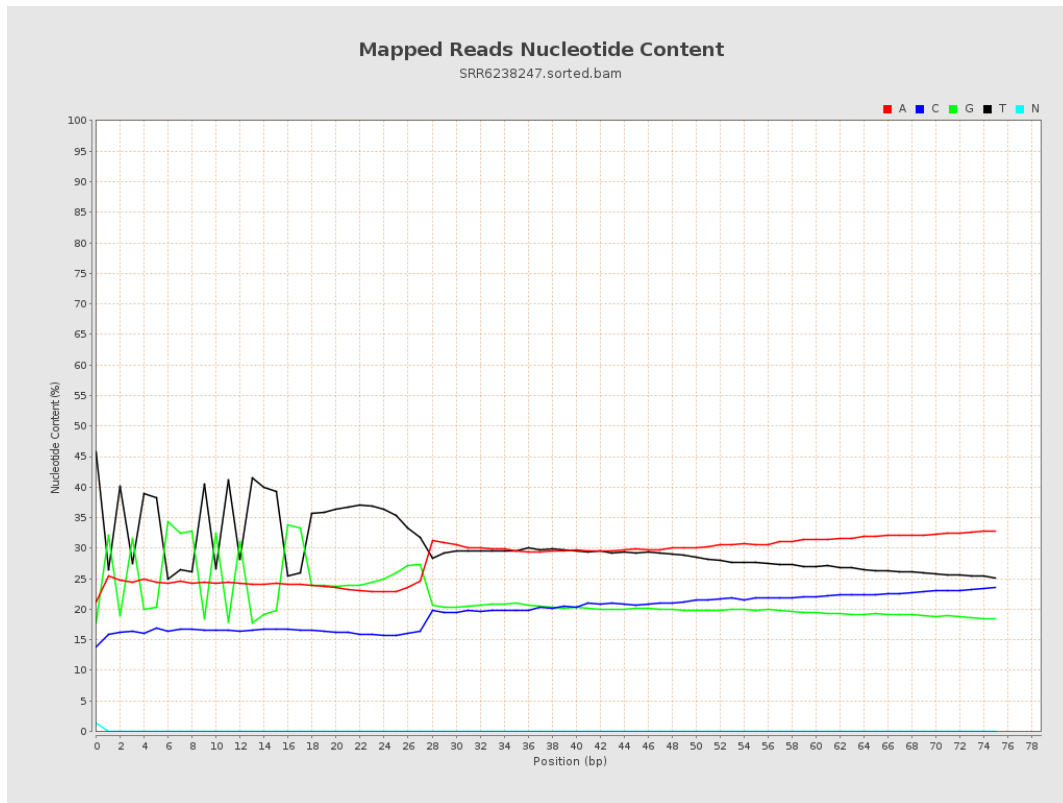
6. Results : Genome Fraction Coverage



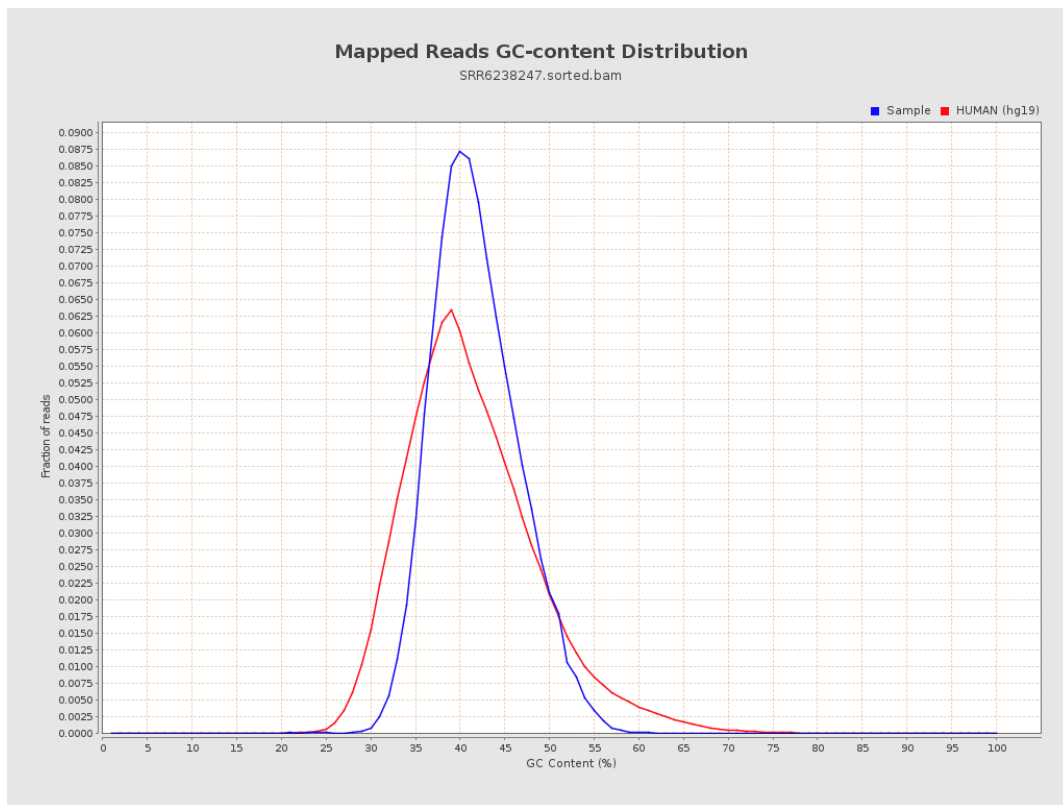
7. Results : Duplication Rate Histogram



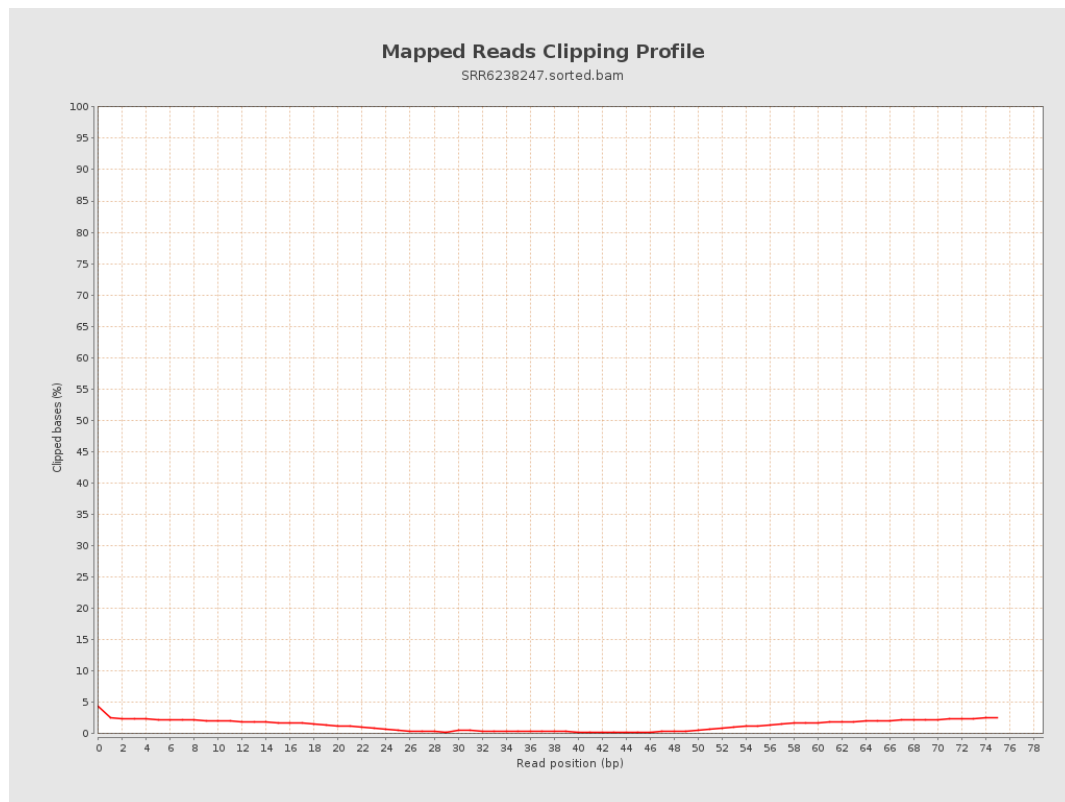
8. Results : Mapped Reads Nucleotide Content



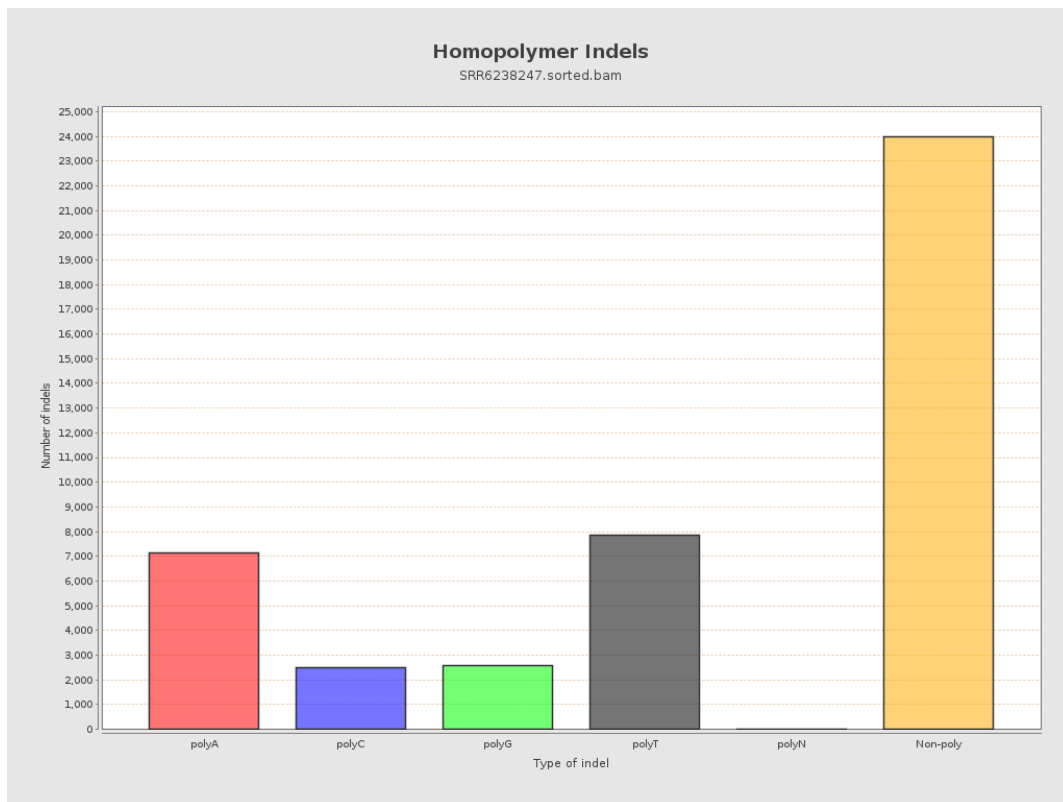
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

