

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 07:18:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068057.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_SRR6068057 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068057.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 07:18:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068057.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,324,369
Mapped reads	5,904,795 / 93.37%
Unmapped reads	419,574 / 6.63%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	60,667 / 0.96%
Read min/max/mean length	30 / 76 / 76.33
Duplicated reads (estimated)	1,915,320 / 30.28%
Duplication rate	18.14%
Clipped reads	3,107,939 / 49.14%

2.2. ACGT Content

Number/percentage of A's	96,358,409 / 25.18%
Number/percentage of C's	72,767,887 / 19.02%
Number/percentage of T's	120,270,367 / 31.43%
Number/percentage of G's	93,245,060 / 24.37%
Number/percentage of N's	44,003 / 0.01%
GC Percentage	43.38%

2.3. Coverage

Mean	0.1237

Standard Deviation	1.2934
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2.4. Mapping Quality

Mean Mapping Quality	43.02
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2.5. Mismatches and indels

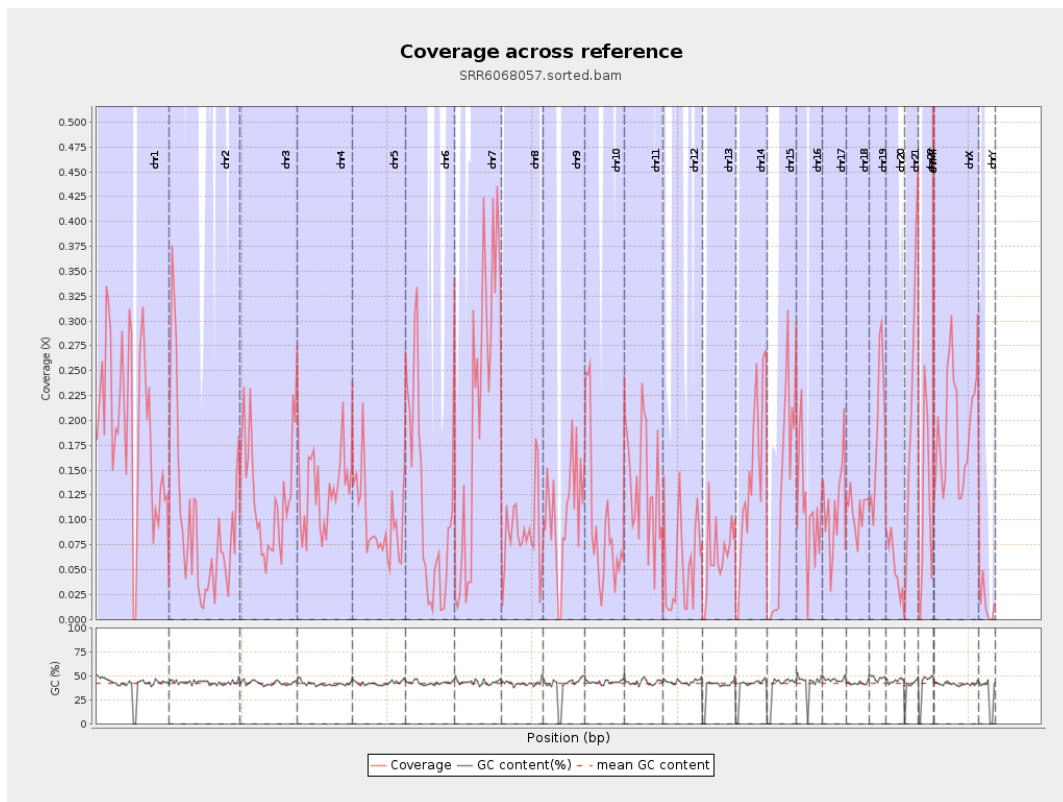
General error rate	0.52%
Mismatches	1,940,294
Insertions	24,691
Mapped reads with at least one insertion	0.41%
Deletions	77,249
Mapped reads with at least one deletion	1.3%
Homopolymer indels	44.51%

2.6. Chromosome stats

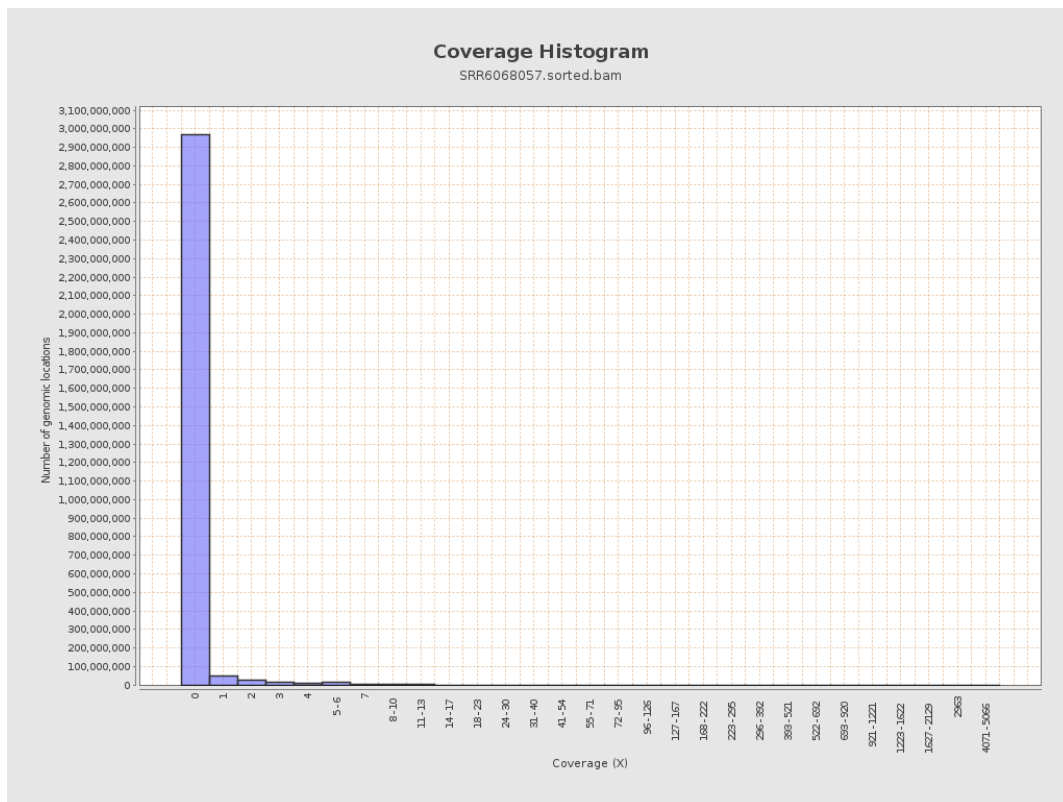
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	47810834	0.1918	1.8516
chr2	243199373	24397667	0.1003	2.3455
chr3	198022430	24512675	0.1238	0.8213
chr4	191154276	24579782	0.1286	0.8773
chr5	180915260	18012466	0.0996	0.7285
chr6	171115067	20096886	0.1174	1.0291
chr7	159138663	33680228	0.2116	2.2197

chr8	146364022	12698736	0.0868	1.376
chr9	141213431	14917371	0.1056	0.8776
chr10	135534747	12971843	0.0957	0.8027
chr11	135006516	18323381	0.1357	1.0827
chr12	133851895	7623442	0.057	0.5774
chr13	115169878	7369354	0.064	0.6502
chr14	107349540	15043418	0.1401	0.9146
chr15	102531392	11823425	0.1153	0.8269
chr16	90354753	9918924	0.1098	0.8101
chr17	81195210	9105447	0.1121	0.8364
chr18	78077248	8590176	0.11	1.527
chr19	59128983	10935833	0.1849	1.3928
chr20	63025520	3394584	0.0539	0.5903
chr21	48129895	10815891	0.2247	1.18
chr22	51304566	5363645	0.1045	0.7601
chrMT	16571	204857	12.3624	11.3497
chrX	155270560	29784255	0.1918	1.1534
chrY	59373566	846338	0.0143	0.4232

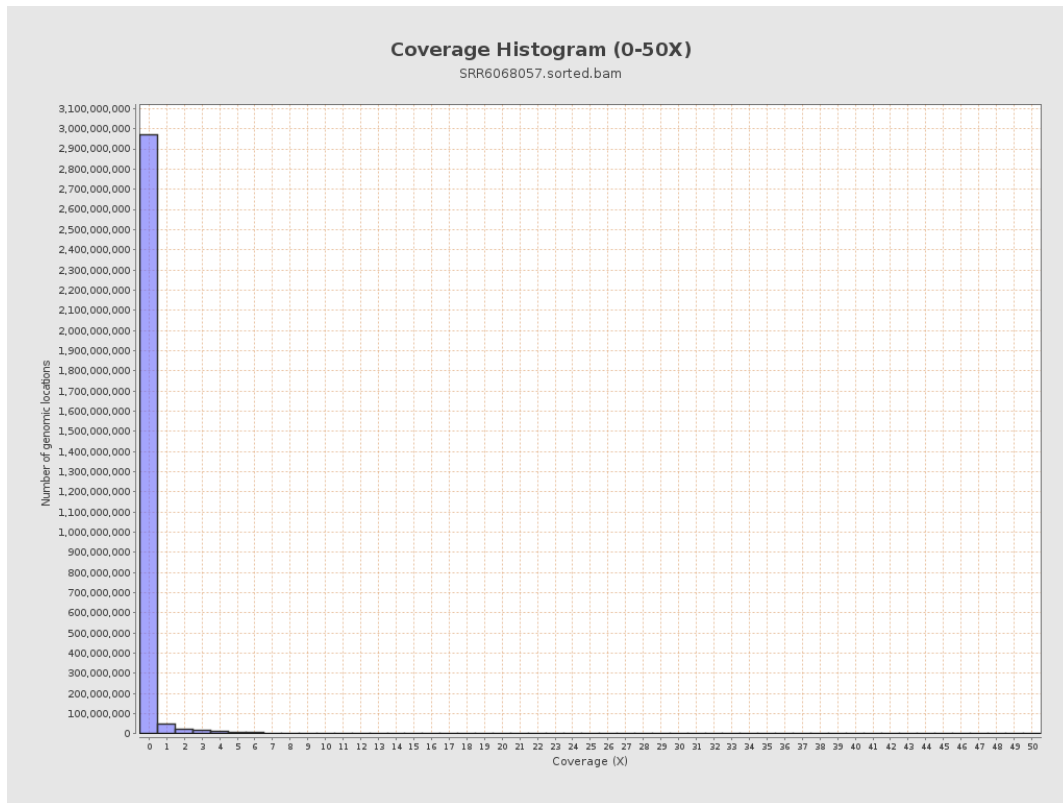
3. Results : Coverage across reference



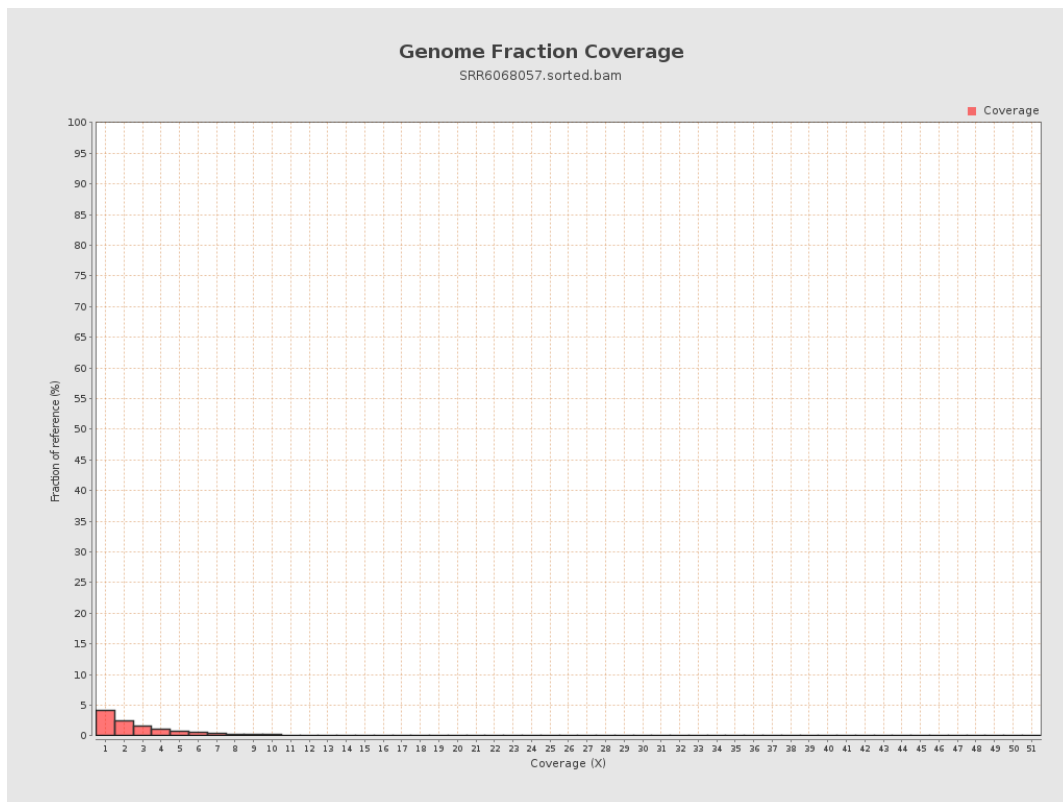
4. Results : Coverage Histogram



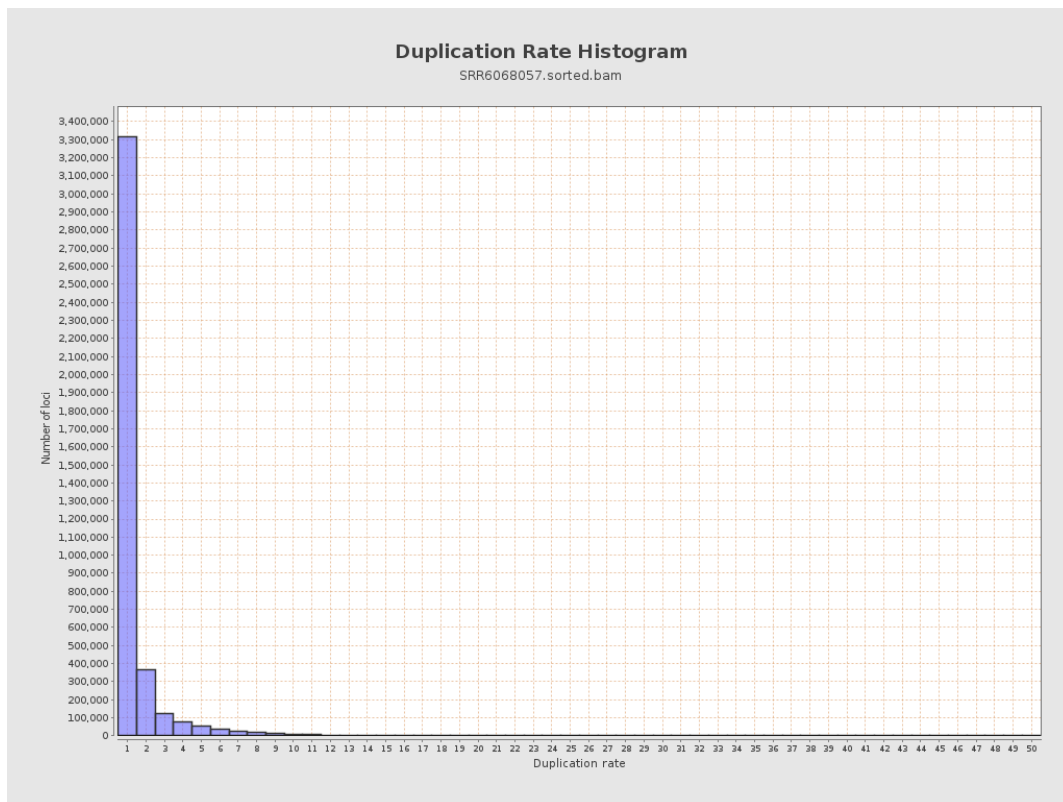
5. Results : Coverage Histogram (0-50X)



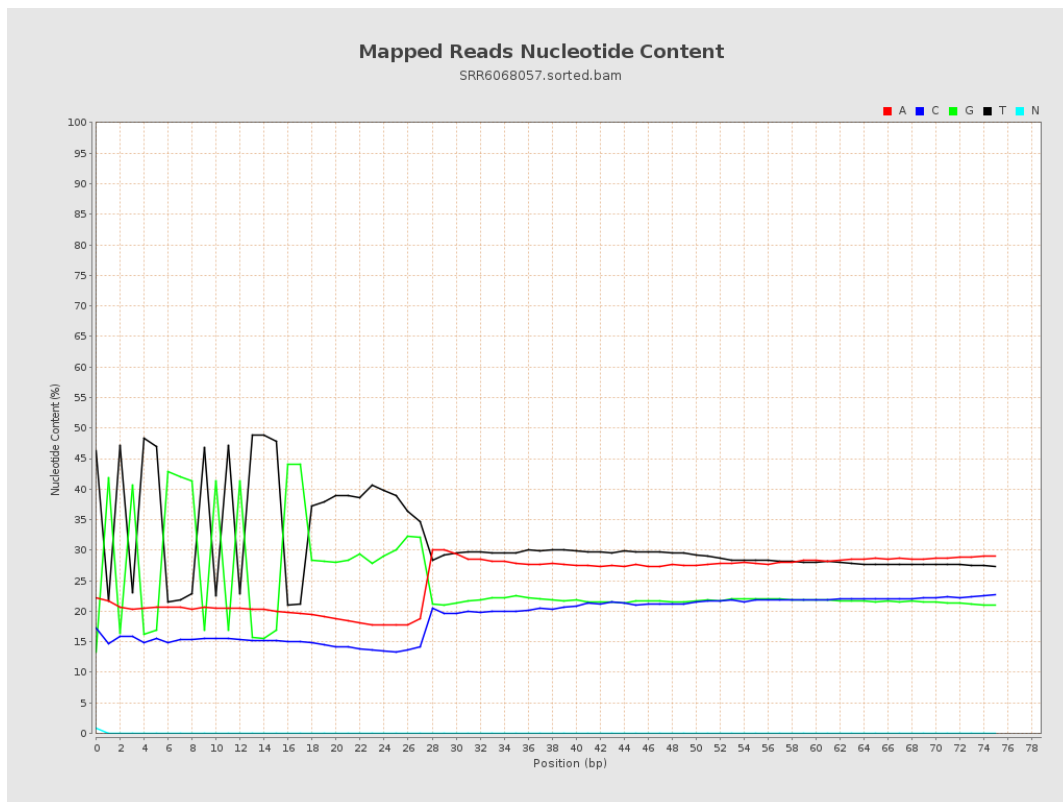
6. Results : Genome Fraction Coverage



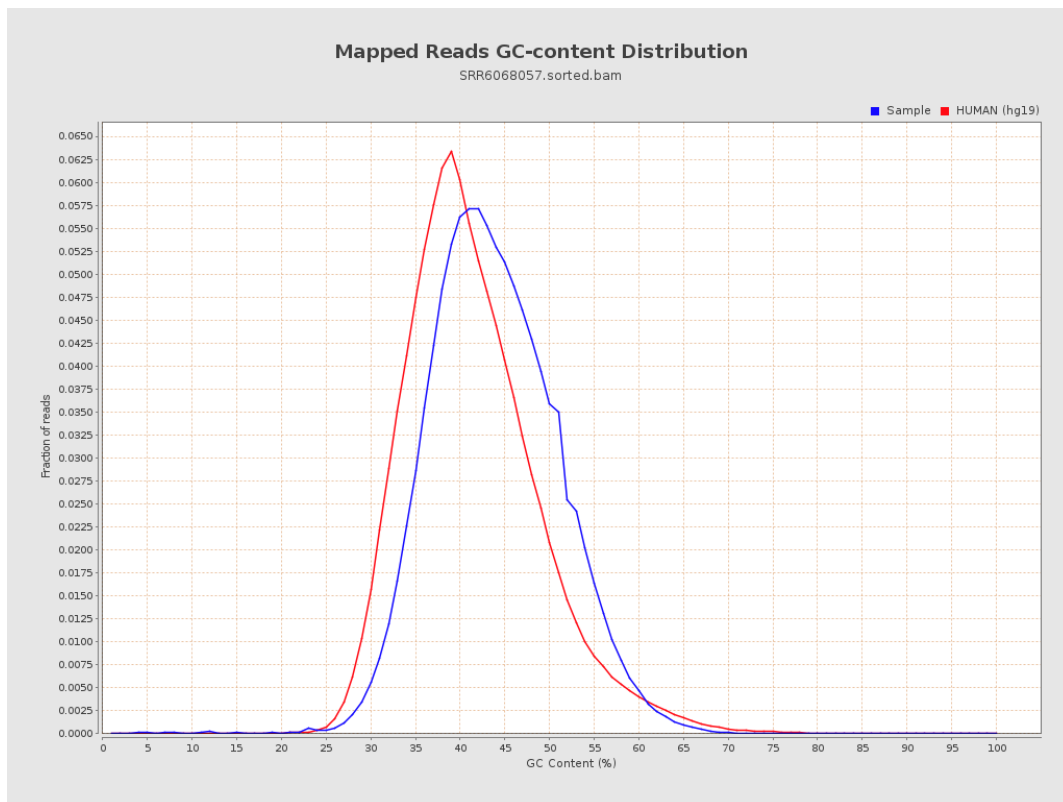
7. Results : Duplication Rate Histogram



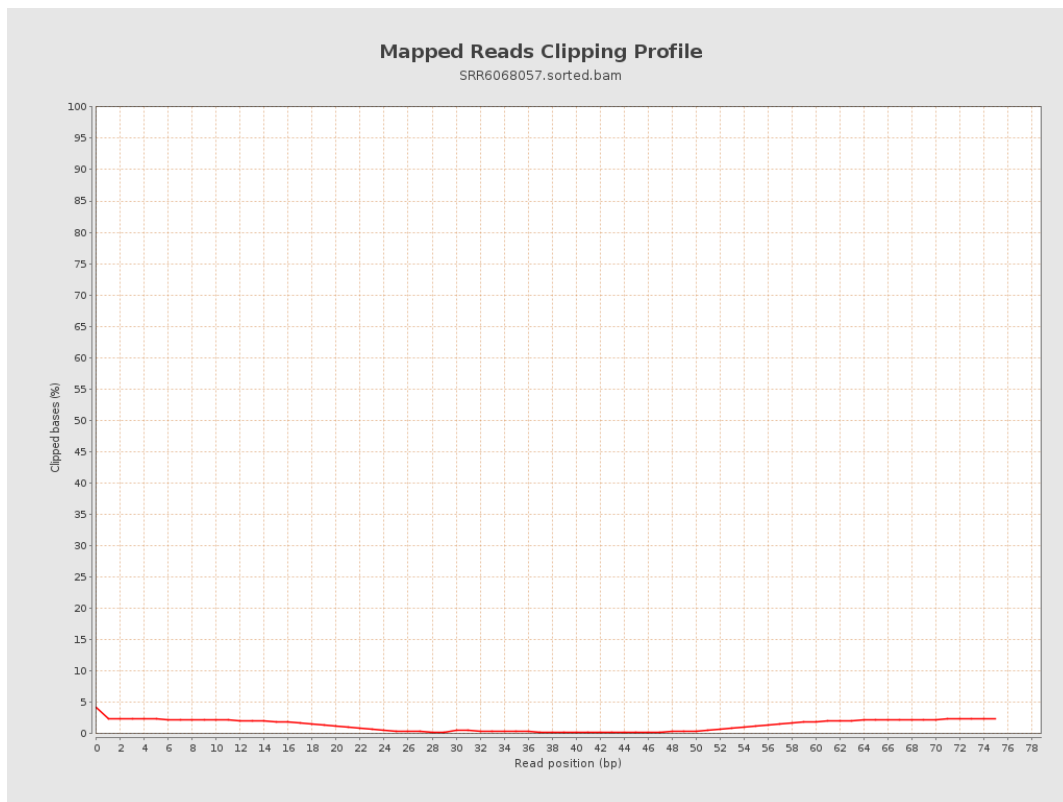
8. Results : Mapped Reads Nucleotide Content



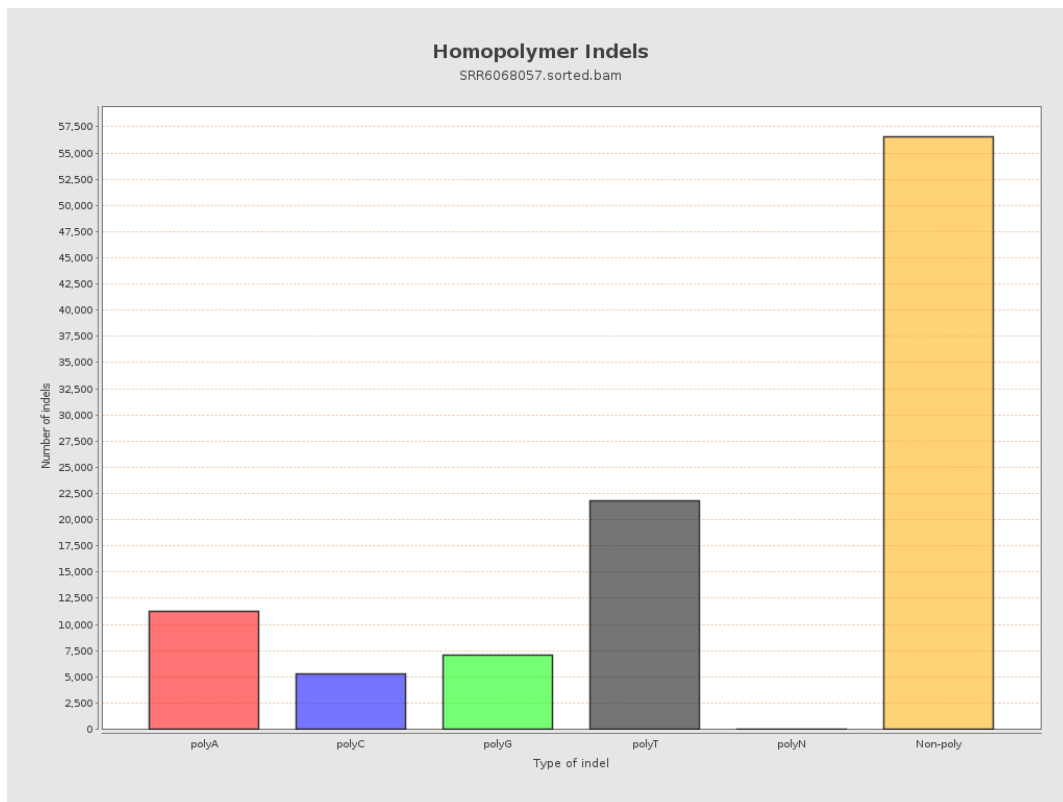
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

