

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 16:41:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068945.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_SRR6068945 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068945.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 16:41:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068945.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,391,884
Mapped reads	2,042,051 / 85.37%
Unmapped reads	349,833 / 14.63%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,526 / 0.52%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	80,615 / 3.37%
Duplication rate	2.89%
Clipped reads	937,187 / 39.18%

2.2. ACGT Content

Number/percentage of A's	37,322,010 / 27.58%
Number/percentage of C's	23,510,764 / 17.38%
Number/percentage of T's	44,869,811 / 33.16%
Number/percentage of G's	29,272,362 / 21.63%
Number/percentage of N's	334,041 / 0.25%
GC Percentage	39.01%

2.3. Coverage

Mean	0.0437

Standard Deviation	0.4288
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2.4. Mapping Quality

Mean Mapping Quality	46.91
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2.5. Mismatches and indels

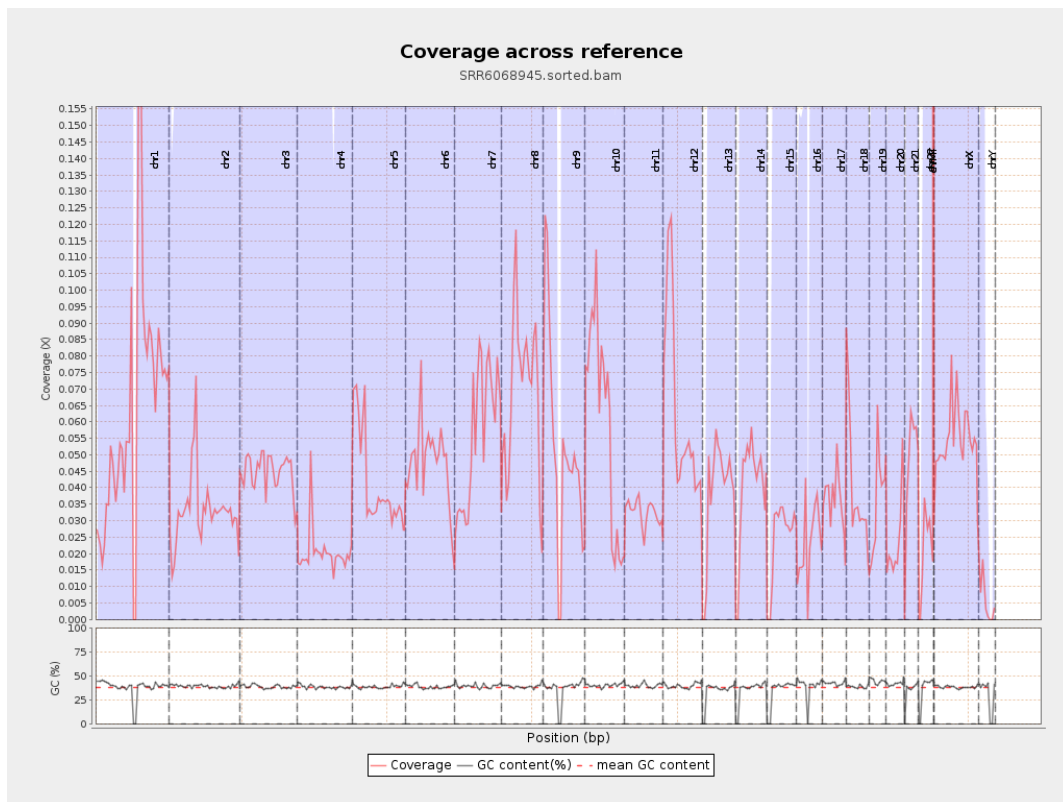
General error rate	1.07%
Mismatches	1,429,764
Insertions	12,263
Mapped reads with at least one insertion	0.6%
Deletions	35,390
Mapped reads with at least one deletion	1.72%
Homopolymer indels	48.36%

2.6. Chromosome stats

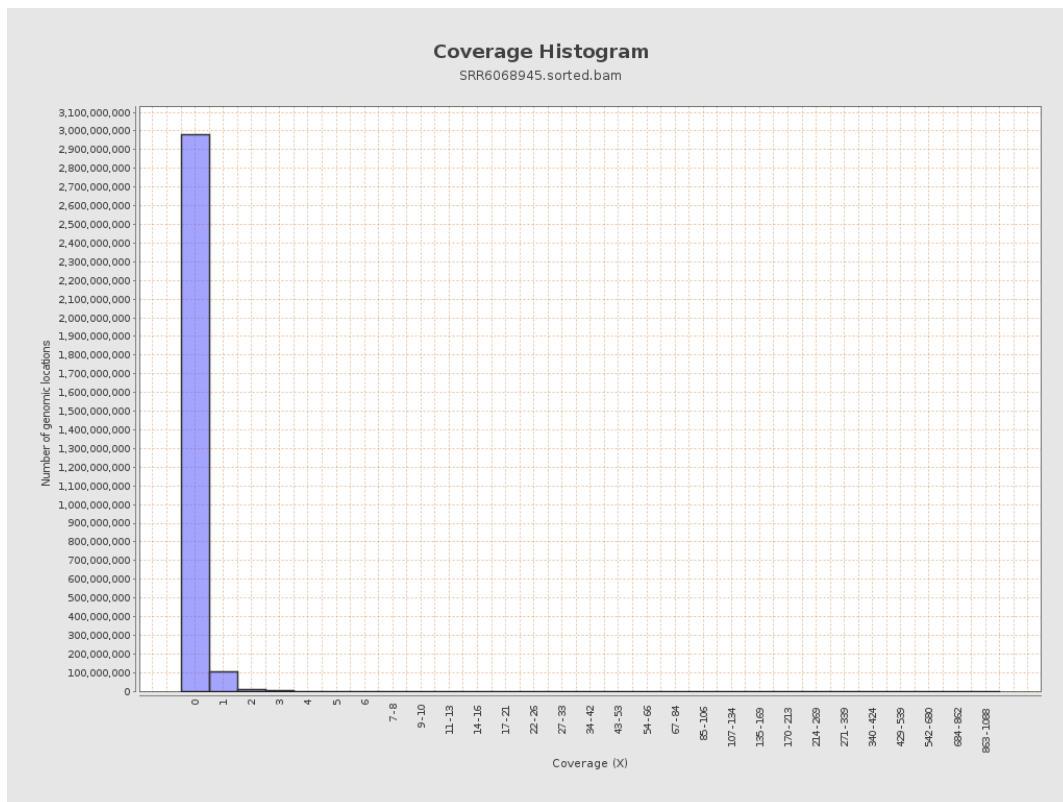
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	15621692	0.0627	0.8938
chr2	243199373	8115844	0.0334	0.3371
chr3	198022430	8883054	0.0449	0.2425
chr4	191154276	3853133	0.0202	0.2028
chr5	180915260	7477059	0.0413	0.2296
chr6	171115067	8145761	0.0476	0.3146
chr7	159138663	9020565	0.0567	0.4884

chr8	146364022	10106087	0.069	0.724
chr9	141213431	7415712	0.0525	0.345
chr10	135534747	8280349	0.0611	0.4773
chr11	135006516	4345719	0.0322	0.3143
chr12	133851895	8340686	0.0623	0.2828
chr13	115169878	4433206	0.0385	0.2193
chr14	107349540	4263924	0.0397	0.2388
chr15	102531392	2554439	0.0249	0.175
chr16	90354753	2135639	0.0236	0.2114
chr17	81195210	2934074	0.0361	0.2305
chr18	78077248	3087399	0.0395	0.6205
chr19	59128983	2136462	0.0361	0.5166
chr20	63025520	1548724	0.0246	0.1932
chr21	48129895	2294293	0.0477	0.2697
chr22	51304566	1046110	0.0204	0.1613
chrMT	16571	489994	29.5694	14.9821
chrX	155270560	8499999	0.0547	0.2972
chrY	59373566	337775	0.0057	0.1457

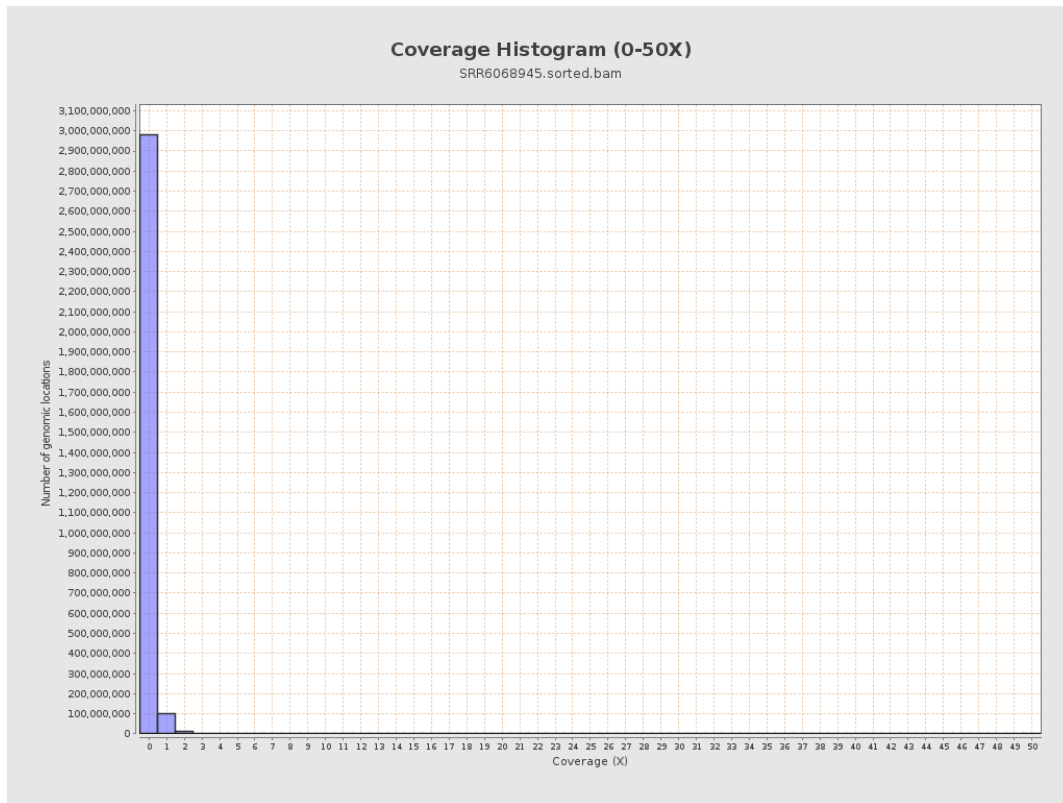
3. Results : Coverage across reference



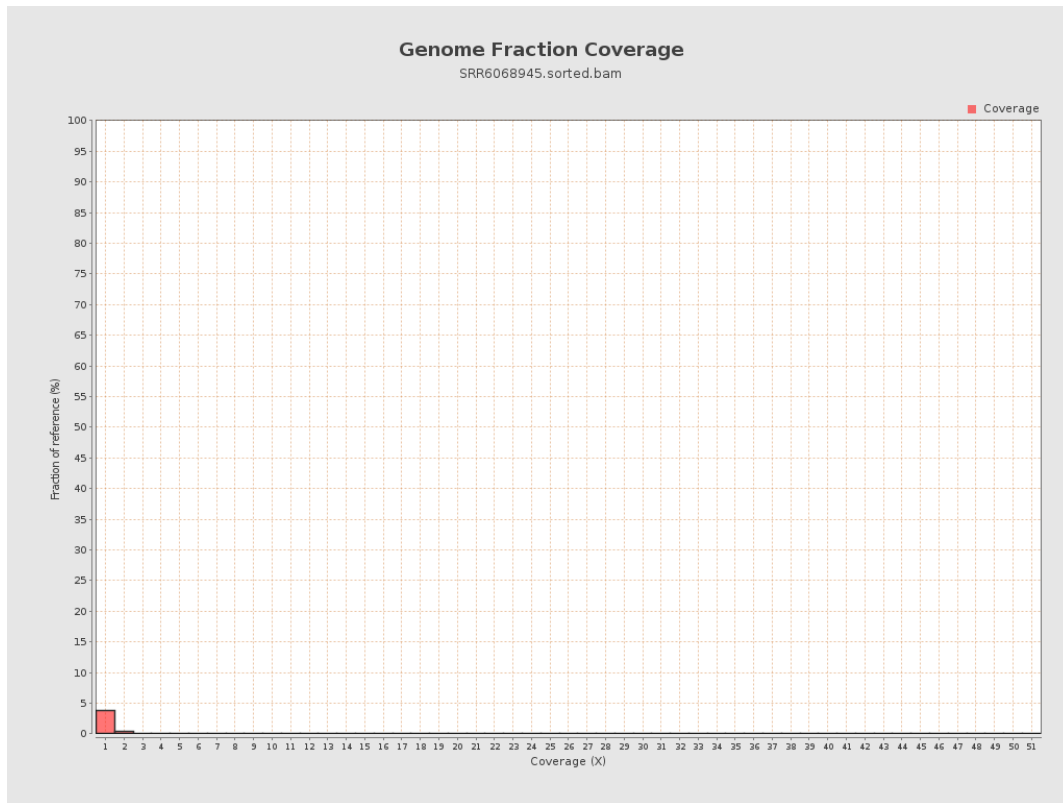
4. Results : Coverage Histogram



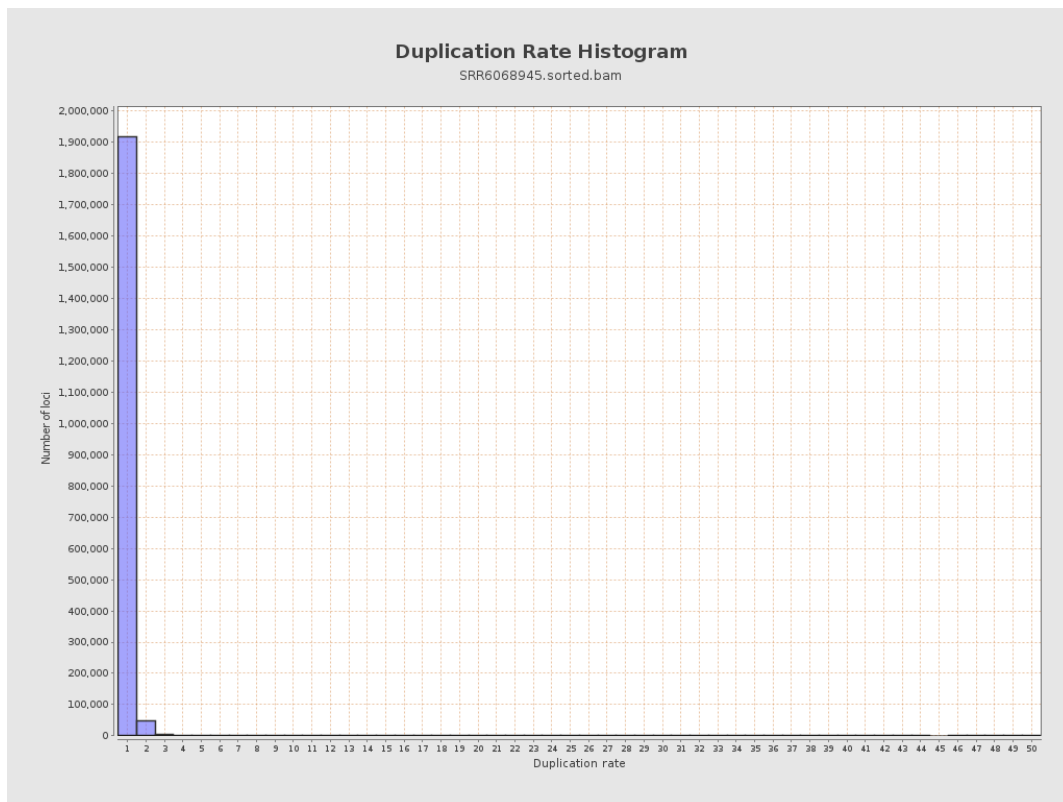
5. Results : Coverage Histogram (0-50X)



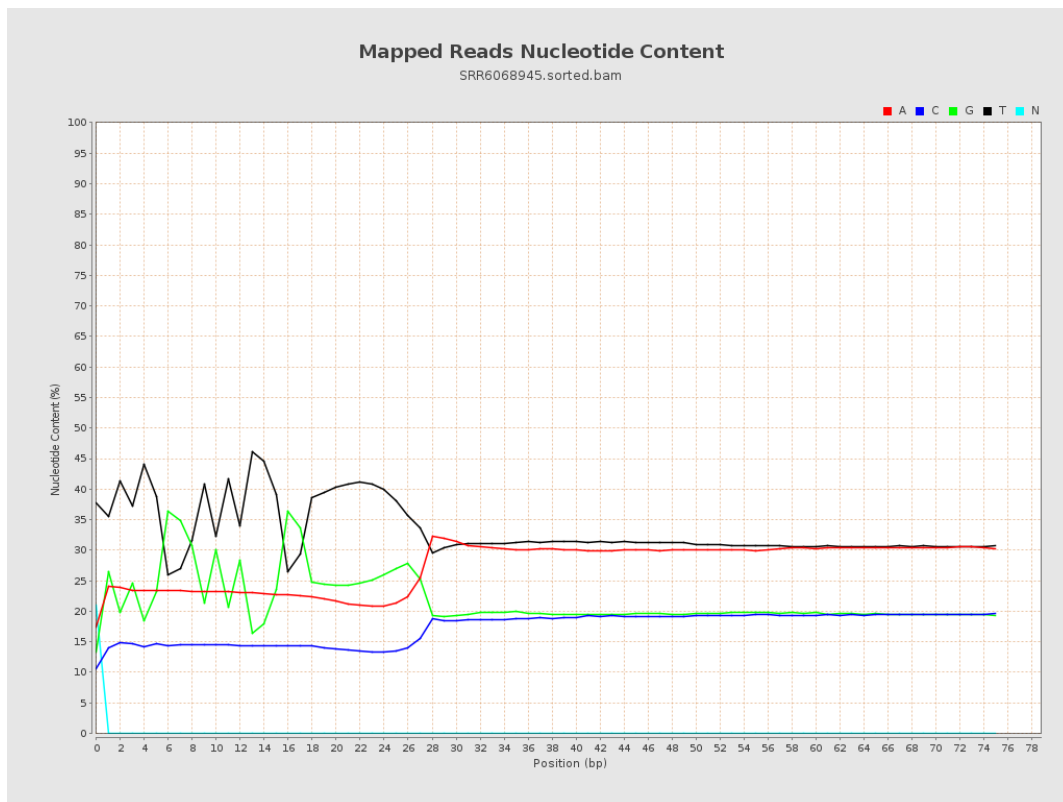
6. Results : Genome Fraction Coverage



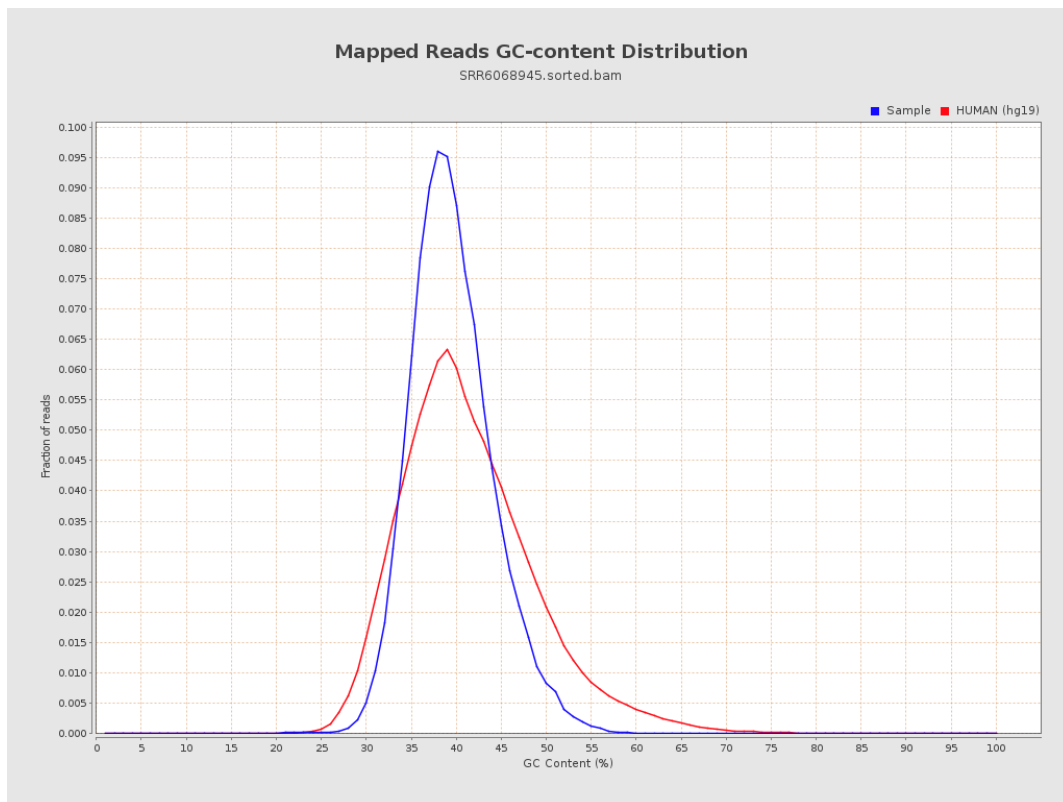
7. Results : Duplication Rate Histogram



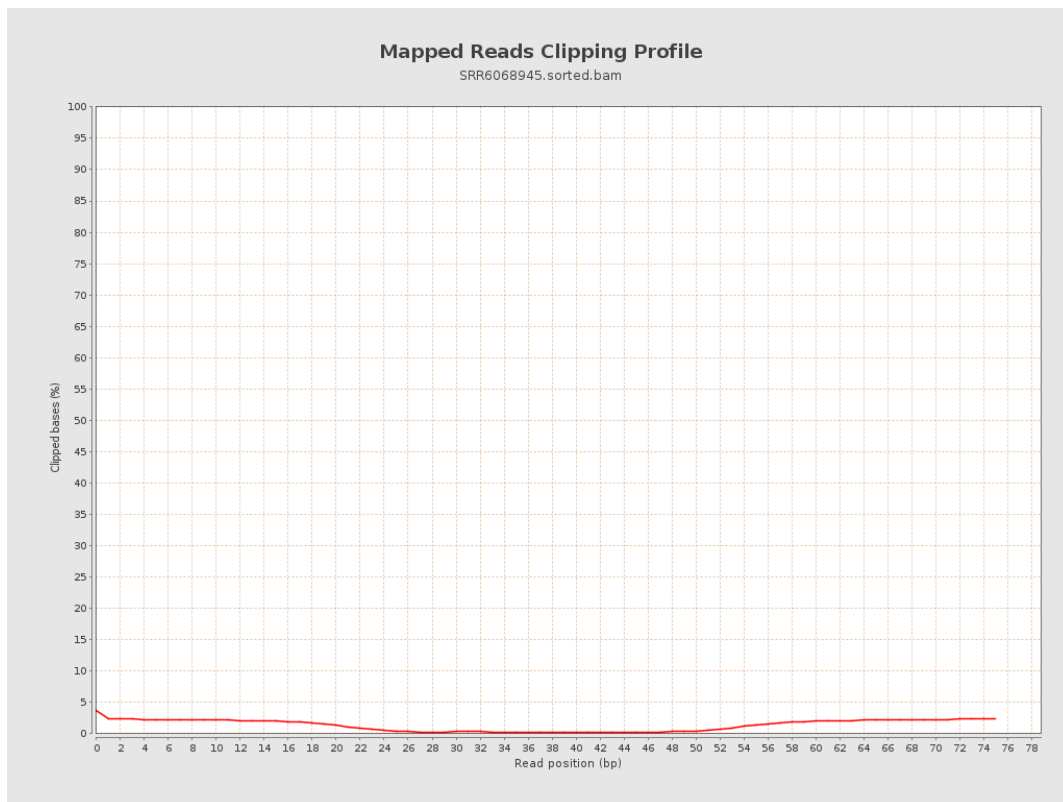
8. Results : Mapped Reads Nucleotide Content



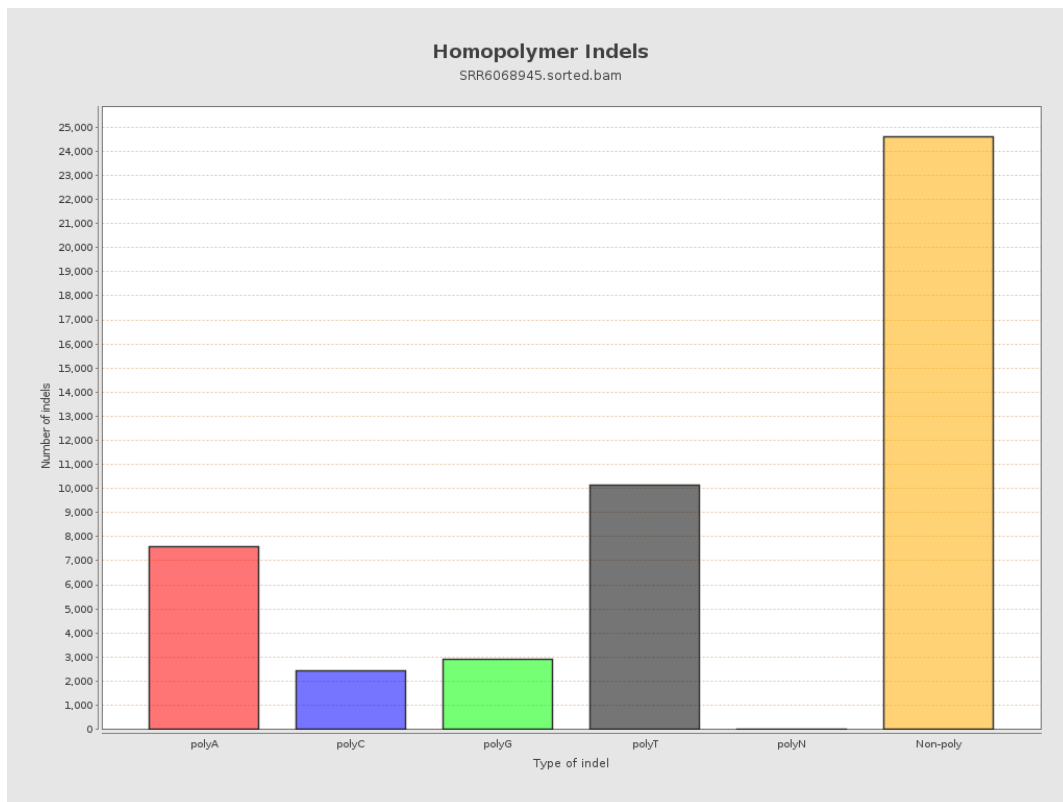
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

