

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 16:29:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068941.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_SRR6068941 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068941.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 16:29:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068941.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,132,196
Mapped reads	1,721,326 / 80.73%
Unmapped reads	410,870 / 19.27%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,566 / 0.64%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	87,152 / 4.09%
Duplication rate	3.99%
Clipped reads	724,367 / 33.97%

2.2. ACGT Content

Number/percentage of A's	31,924,500 / 27.6%
Number/percentage of C's	20,749,382 / 17.94%
Number/percentage of T's	37,593,535 / 32.5%
Number/percentage of G's	25,128,429 / 21.72%
Number/percentage of N's	287,591 / 0.25%
GC Percentage	39.66%

2.3. Coverage

Mean	0.0374

Standard Deviation	0.379
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2.4. Mapping Quality

Mean Mapping Quality	47.01
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2.5. Mismatches and indels

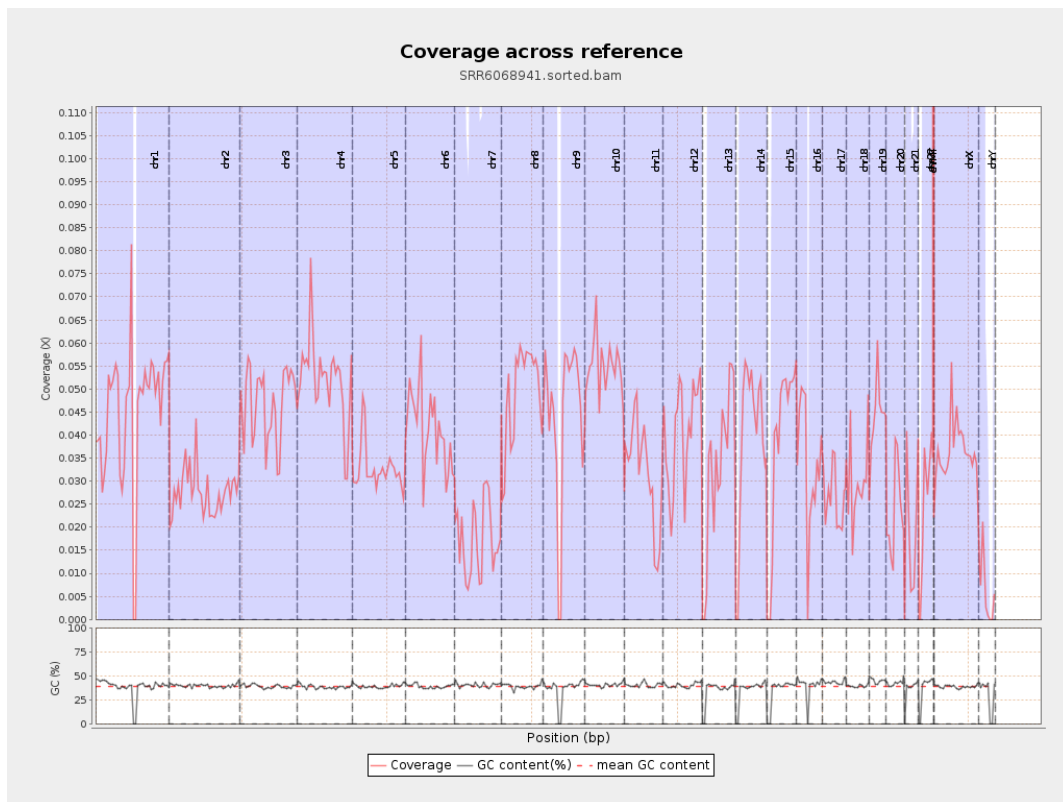
General error rate	1.08%
Mismatches	1,228,093
Insertions	11,118
Mapped reads with at least one insertion	0.64%
Deletions	31,057
Mapped reads with at least one deletion	1.78%
Homopolymer indels	48.26%

2.6. Chromosome stats

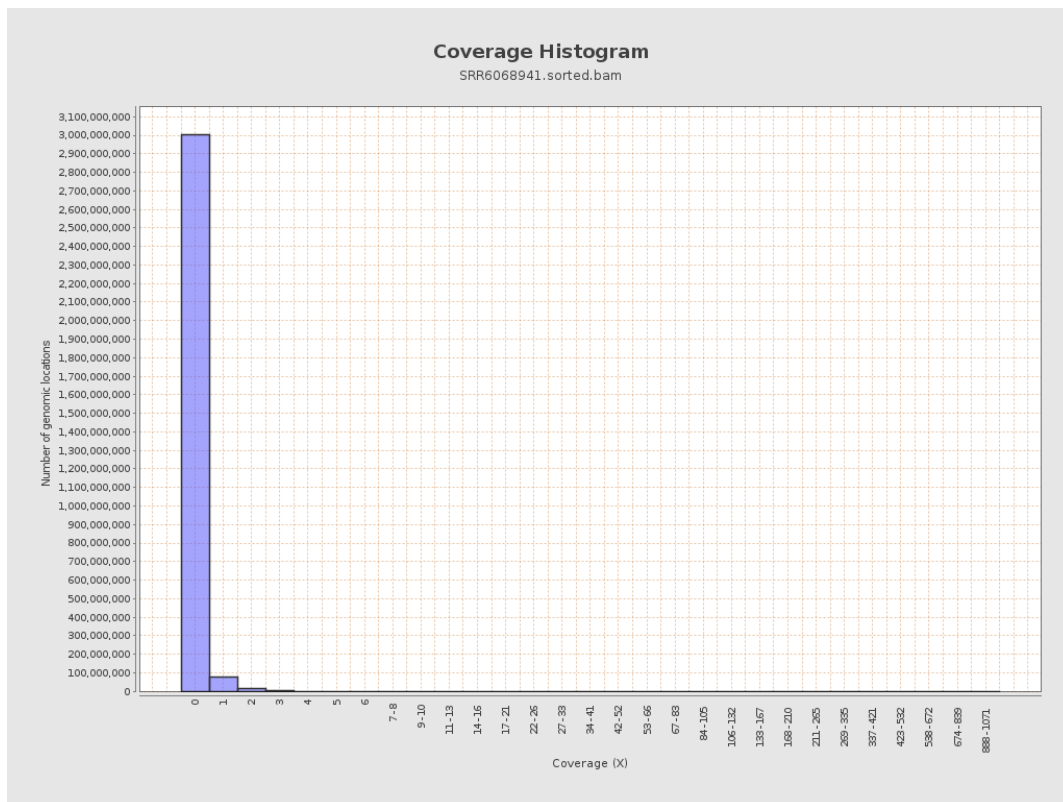
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	11165146	0.0448	0.7632
chr2	243199373	6734030	0.0277	0.2987
chr3	198022430	9265019	0.0468	0.257
chr4	191154276	9955535	0.0521	0.3094
chr5	180915260	5926907	0.0328	0.2176
chr6	171115067	7079020	0.0414	0.2965
chr7	159138663	2725913	0.0171	0.21

chr8	146364022	7243233	0.0495	0.699
chr9	141213431	6283956	0.0445	0.3511
chr10	135534747	7476737	0.0552	0.3581
chr11	135006516	4352126	0.0322	0.2698
chr12	133851895	5442582	0.0407	0.2451
chr13	115169878	3810696	0.0331	0.2169
chr14	107349540	4296577	0.04	0.2541
chr15	102531392	3930548	0.0383	0.2321
chr16	90354753	3080241	0.0341	0.2395
chr17	81195210	2175517	0.0268	0.206
chr18	78077248	2293435	0.0294	0.6499
chr19	59128983	2662021	0.045	0.4337
chr20	63025520	1449190	0.023	0.1979
chr21	48129895	946976	0.0197	0.2072
chr22	51304566	1248093	0.0243	0.182
chrMT	16571	184742	11.1485	7.152
chrX	155270560	5658576	0.0364	0.2485
chrY	59373566	348746	0.0059	0.1818

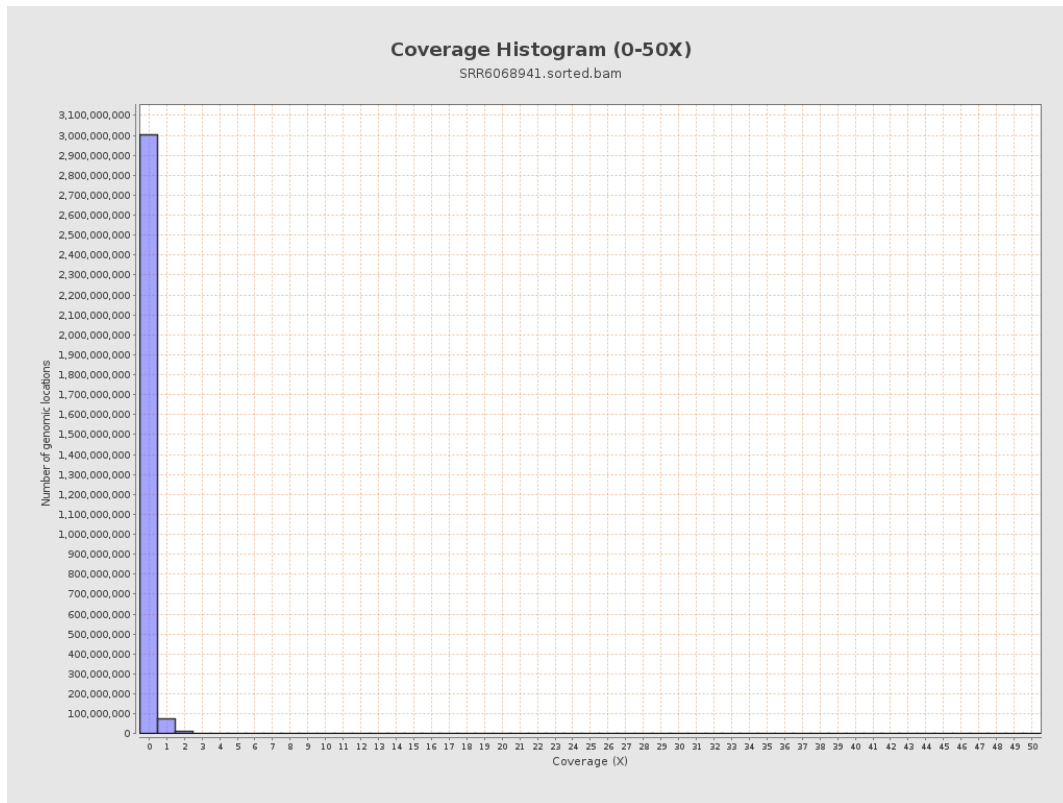
3. Results : Coverage across reference



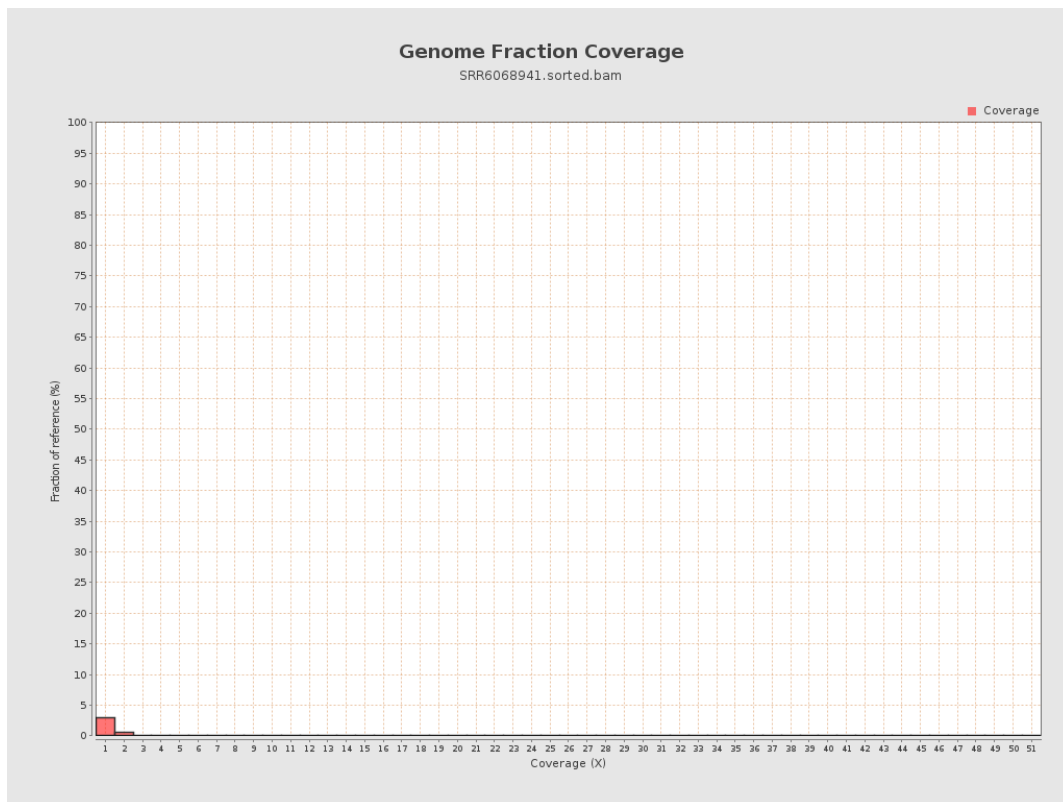
4. Results : Coverage Histogram



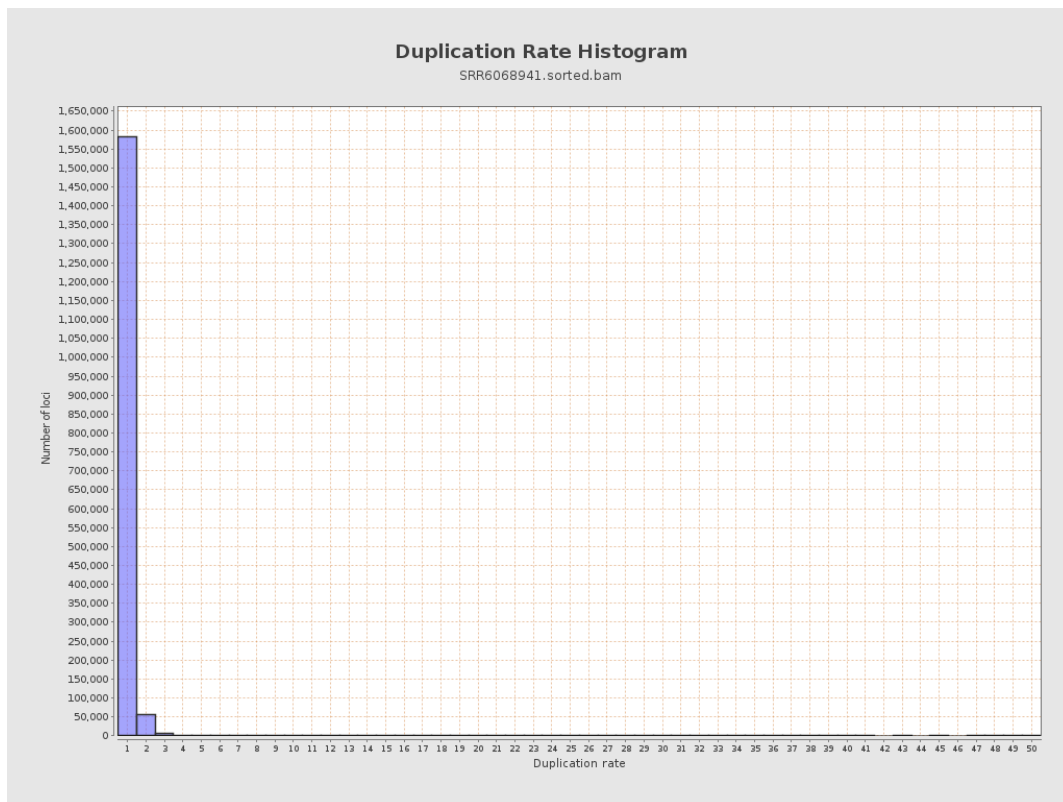
5. Results : Coverage Histogram (0-50X)



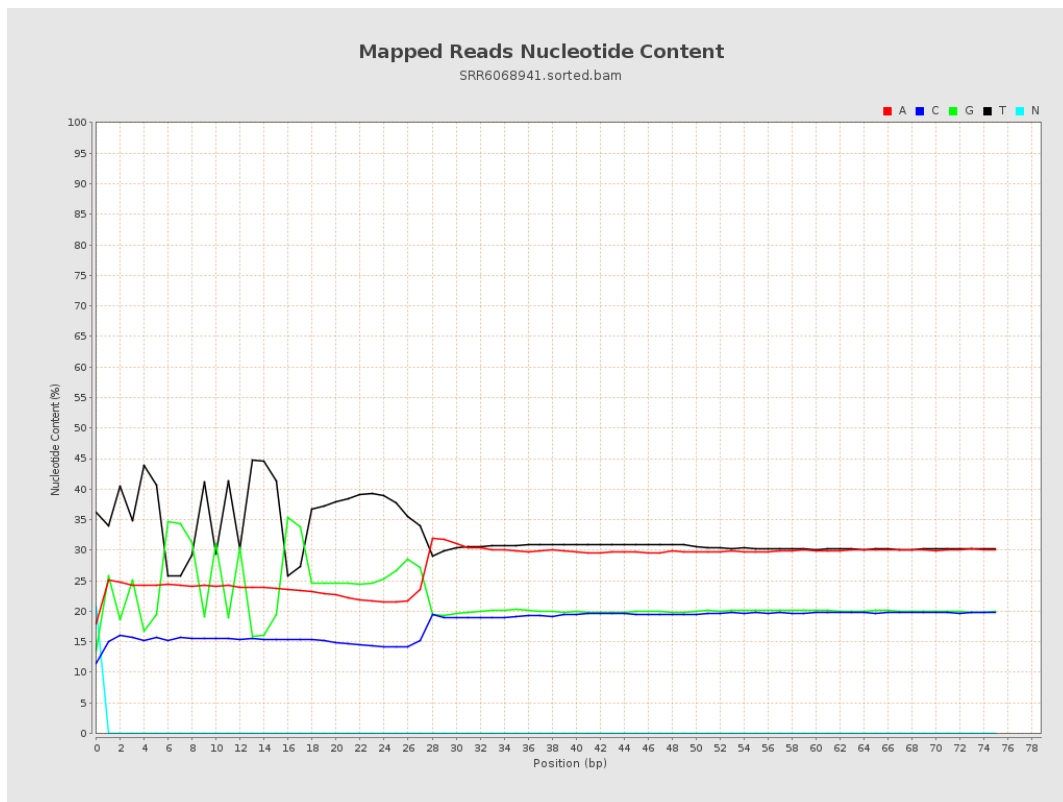
6. Results : Genome Fraction Coverage



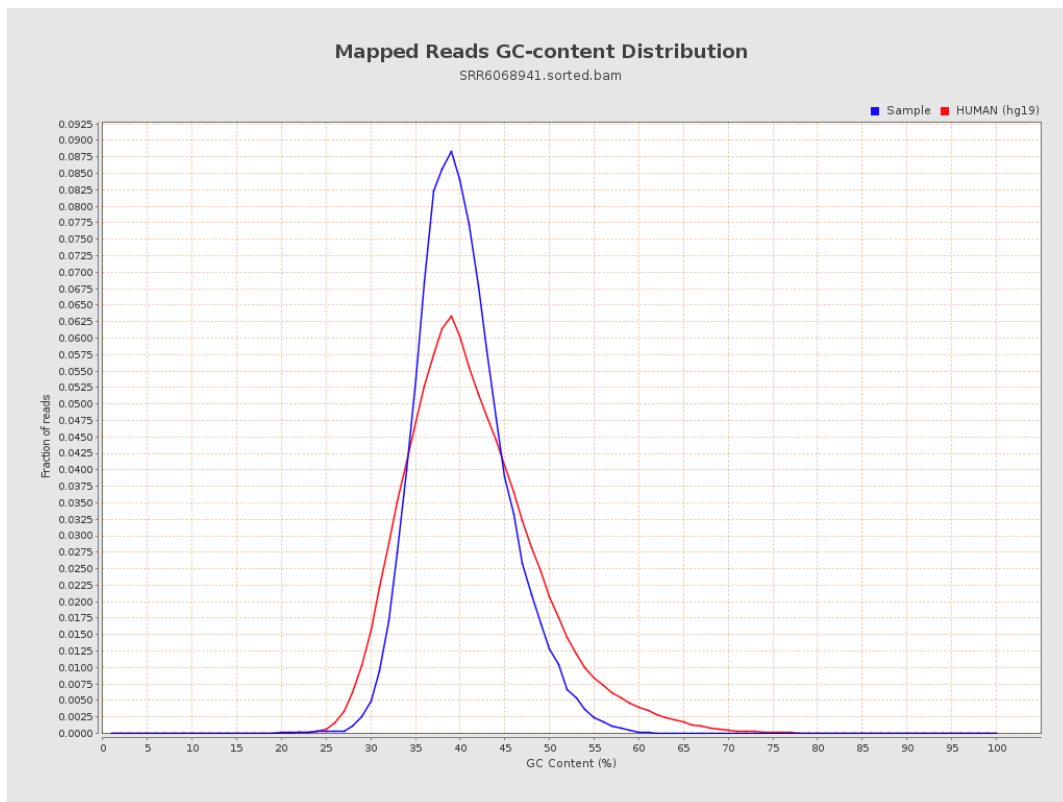
7. Results : Duplication Rate Histogram



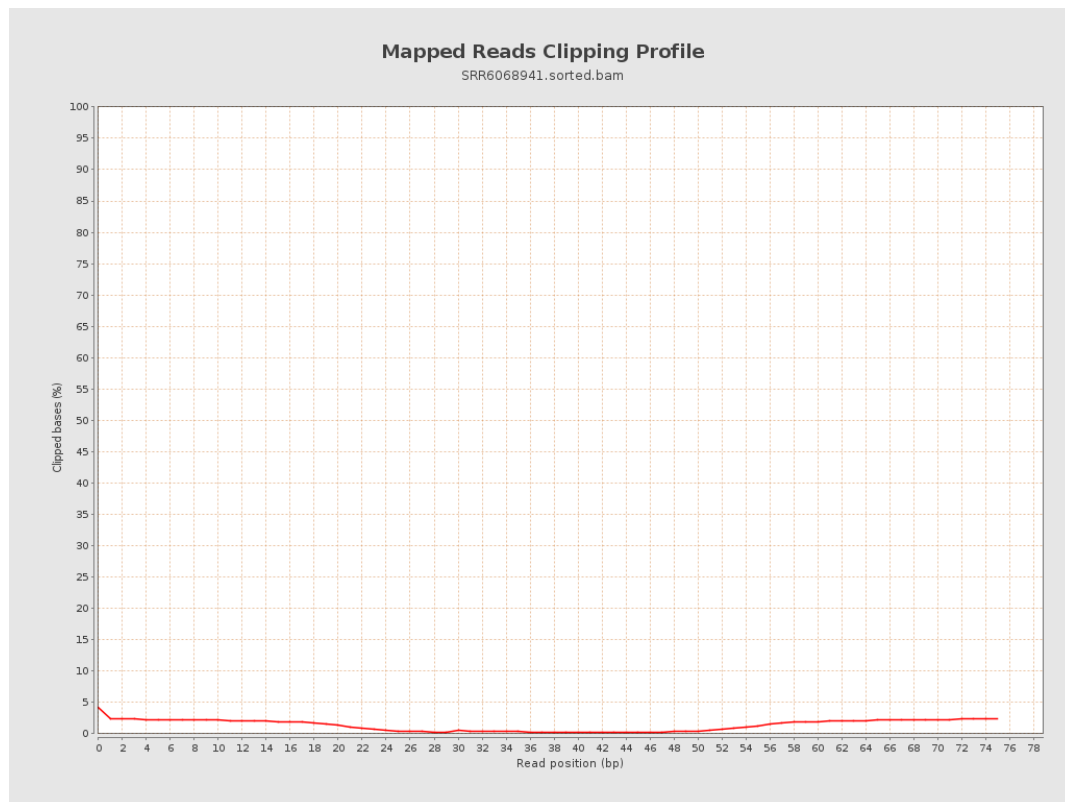
8. Results : Mapped Reads Nucleotide Content



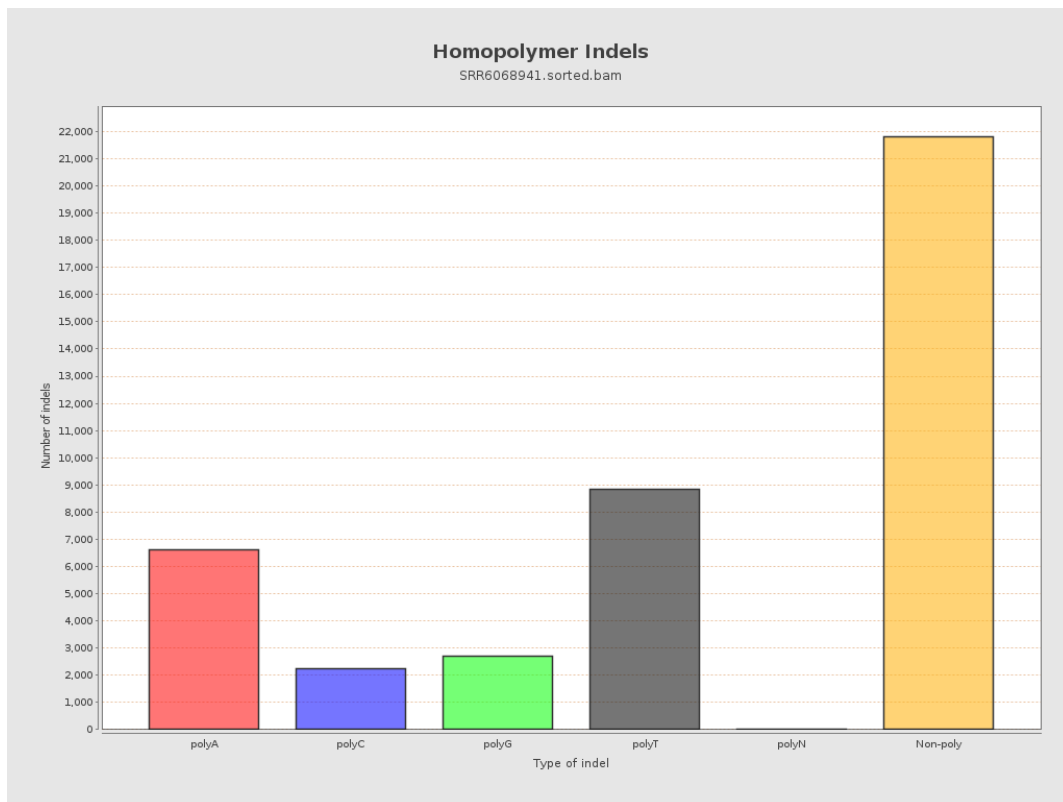
9. Results : Mapped Reads GC-content Distribution



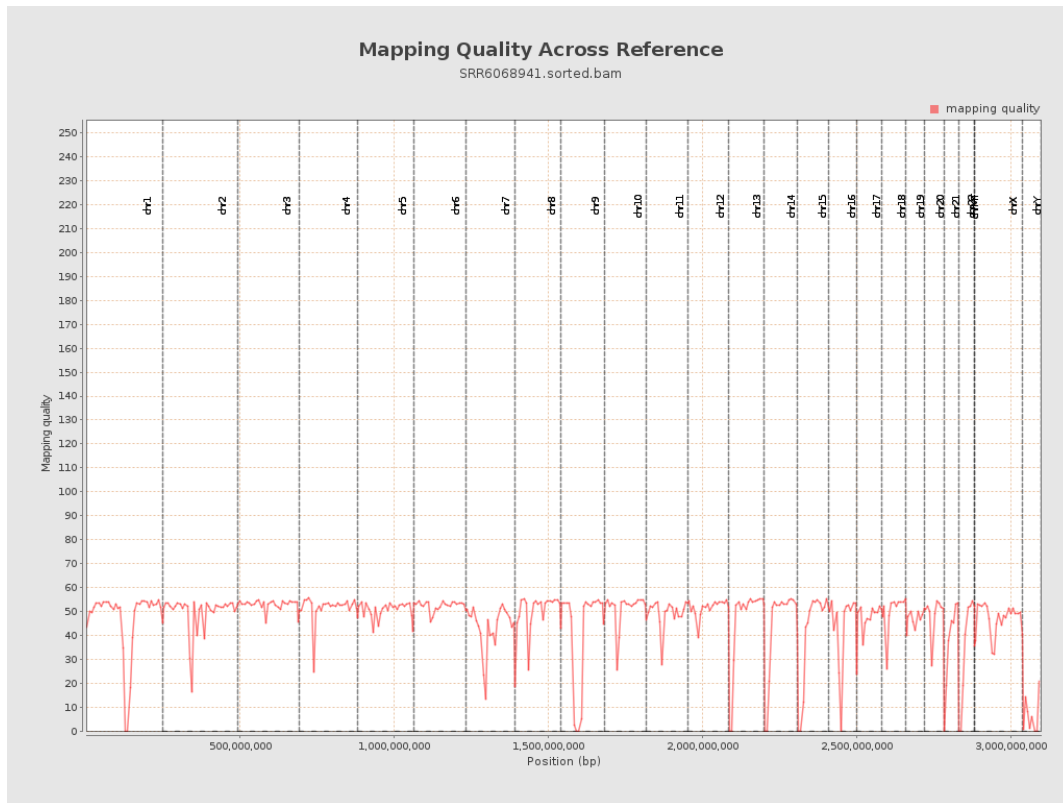
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

