

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 03:46:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237573.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_SRR6237573 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237573.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 03:46:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237573.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,133,192
Mapped reads	1,549,827 / 72.65%
Unmapped reads	583,365 / 27.35%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,221 / 0.34%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	204,393 / 9.58%
Duplication rate	10.92%
Clipped reads	1,040,538 / 48.78%

2.2. ACGT Content

Number/percentage of A's	24,768,185 / 26.33%
Number/percentage of C's	16,064,528 / 17.08%
Number/percentage of T's	31,129,458 / 33.1%
Number/percentage of G's	21,931,699 / 23.32%
Number/percentage of N's	157,358 / 0.17%
GC Percentage	40.4%

2.3. Coverage

Mean	0.0304

Standard Deviation	0.2997
--------------------	--------

2.4. Mapping Quality

Mean Mapping Quality	45.6
----------------------	------

2.5. Mismatches and indels

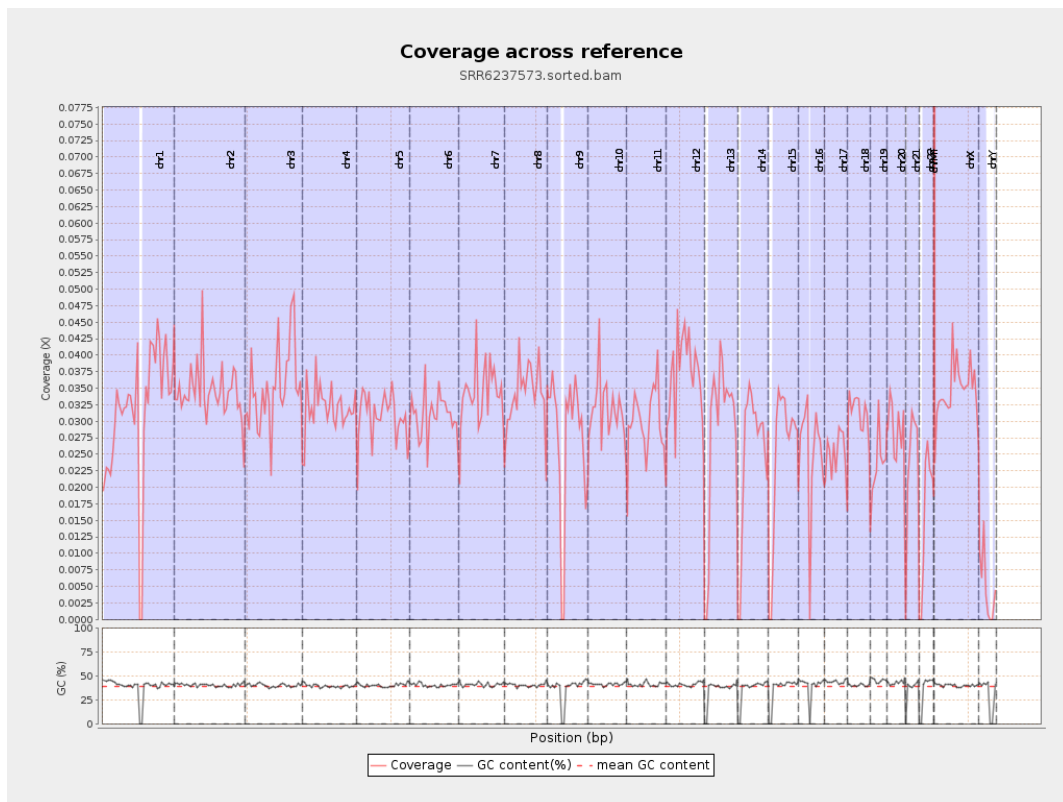
General error rate	1.08%
Mismatches	1,001,416
Insertions	7,920
Mapped reads with at least one insertion	0.51%
Deletions	37,632
Mapped reads with at least one deletion	2.4%
Homopolymer indels	49.05%

2.6. Chromosome stats

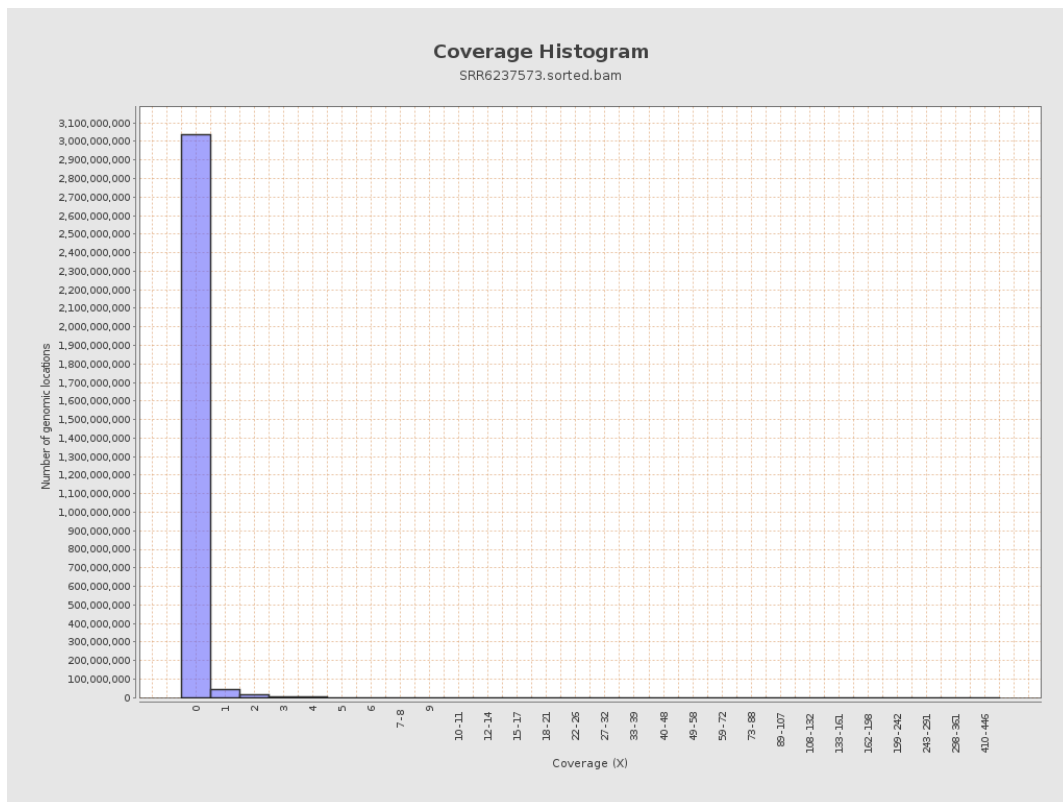
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	7853979	0.0315	0.3646
chr2	243199373	8378507	0.0345	0.3511
chr3	198022430	6936137	0.035	0.2765
chr4	191154276	6093922	0.0319	0.2649
chr5	180915260	5603178	0.031	0.2544
chr6	171115067	5293244	0.0309	0.2761
chr7	159138663	5452824	0.0343	0.3895

chr8	146364022	4990163	0.0341	0.3757
chr9	141213431	3881968	0.0275	0.2884
chr10	135534747	4294041	0.0317	0.2985
chr11	135006516	4065665	0.0301	0.2972
chr12	133851895	4970913	0.0371	0.2867
chr13	115169878	3256152	0.0283	0.2506
chr14	107349540	2688189	0.025	0.2363
chr15	102531392	2569879	0.0251	0.2307
chr16	90354753	2255561	0.025	0.2407
chr17	81195210	2025568	0.0249	0.24
chr18	78077248	2460522	0.0315	0.4224
chr19	59128983	1406862	0.0238	0.2831
chr20	63025520	1794432	0.0285	0.2522
chr21	48129895	1166035	0.0242	0.233
chr22	51304566	842001	0.0164	0.1801
chrMT	16571	123001	7.4227	5.4946
chrX	155270560	5420304	0.0349	0.2809
chrY	59373566	287539	0.0048	0.1106

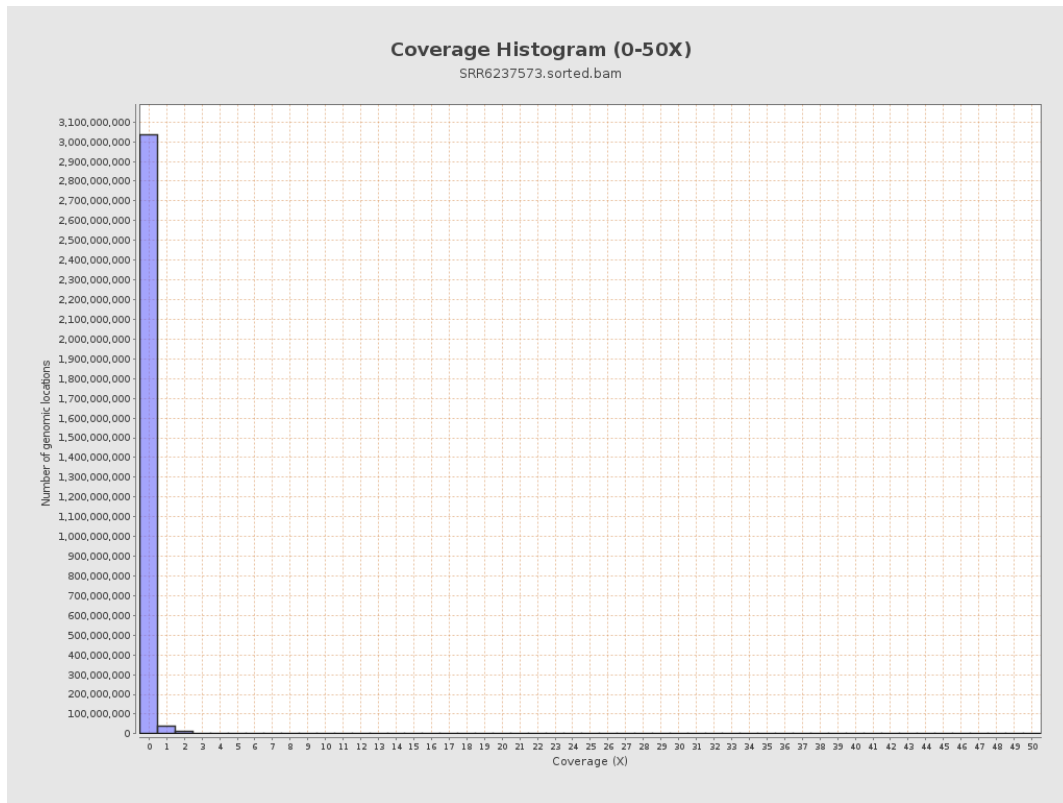
3. Results : Coverage across reference



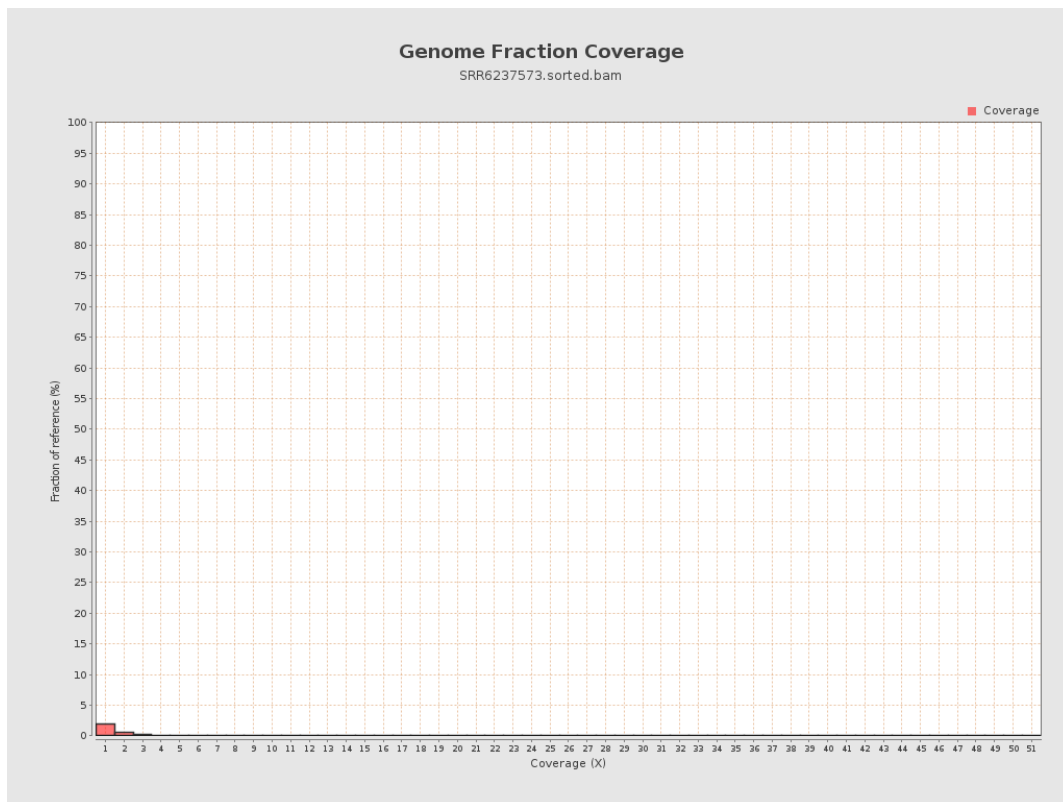
4. Results : Coverage Histogram



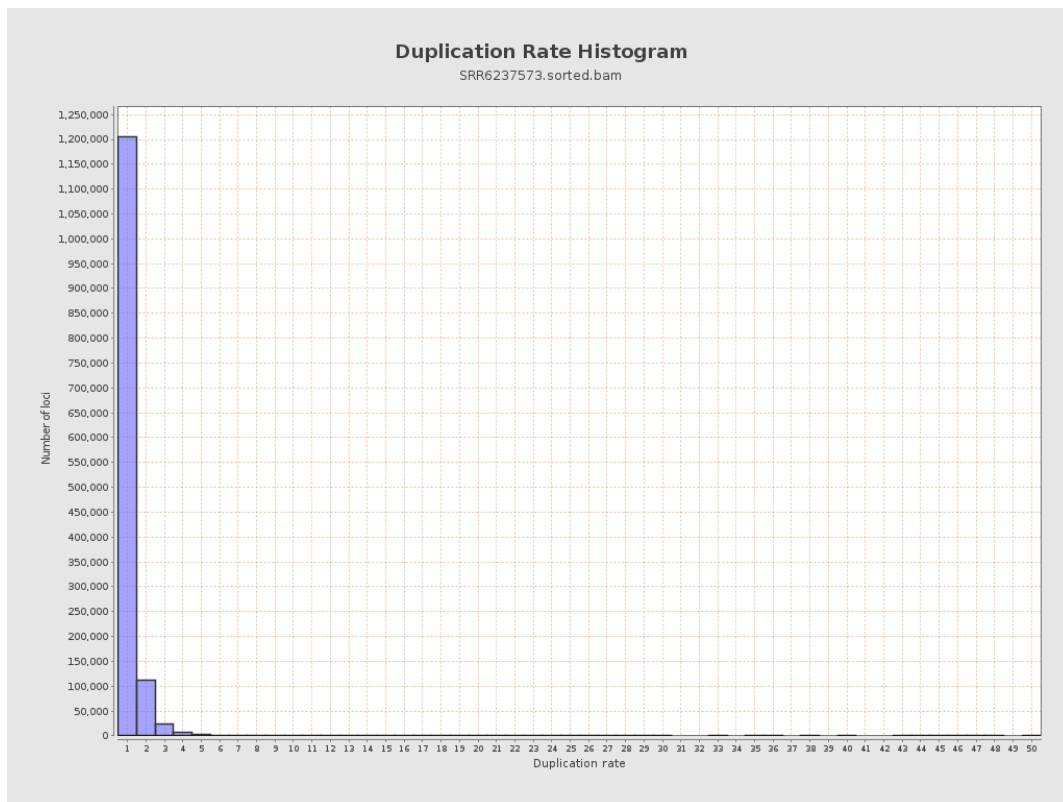
5. Results : Coverage Histogram (0-50X)



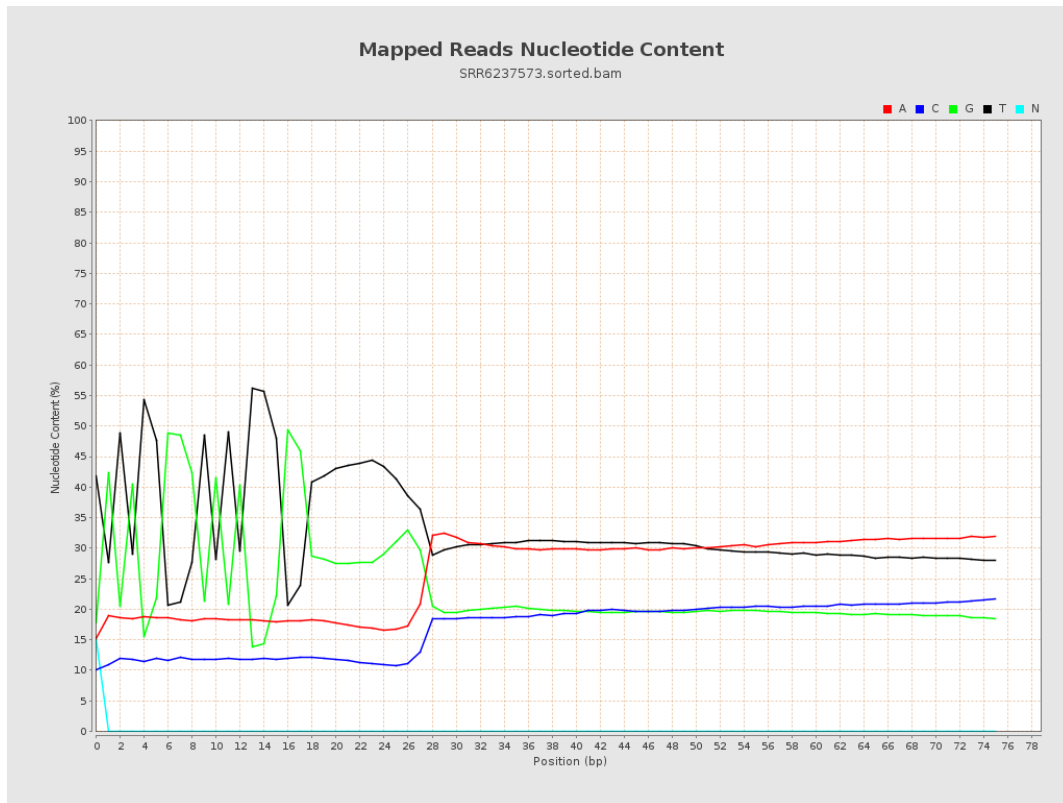
6. Results : Genome Fraction Coverage



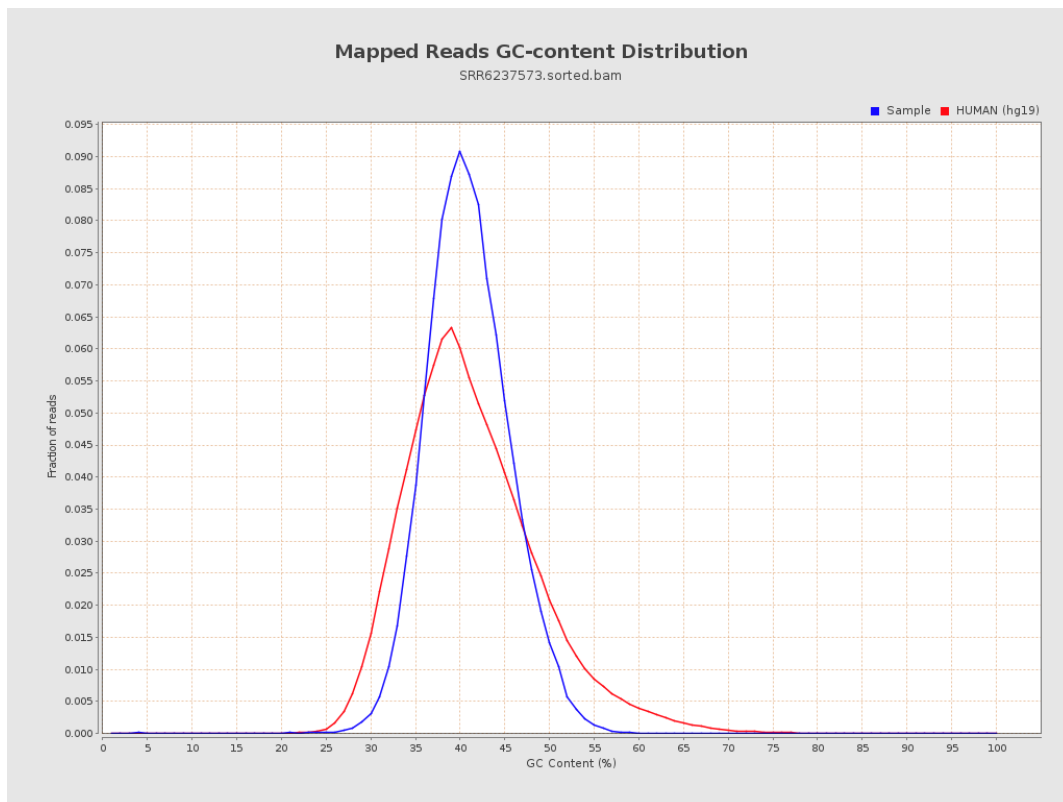
7. Results : Duplication Rate Histogram



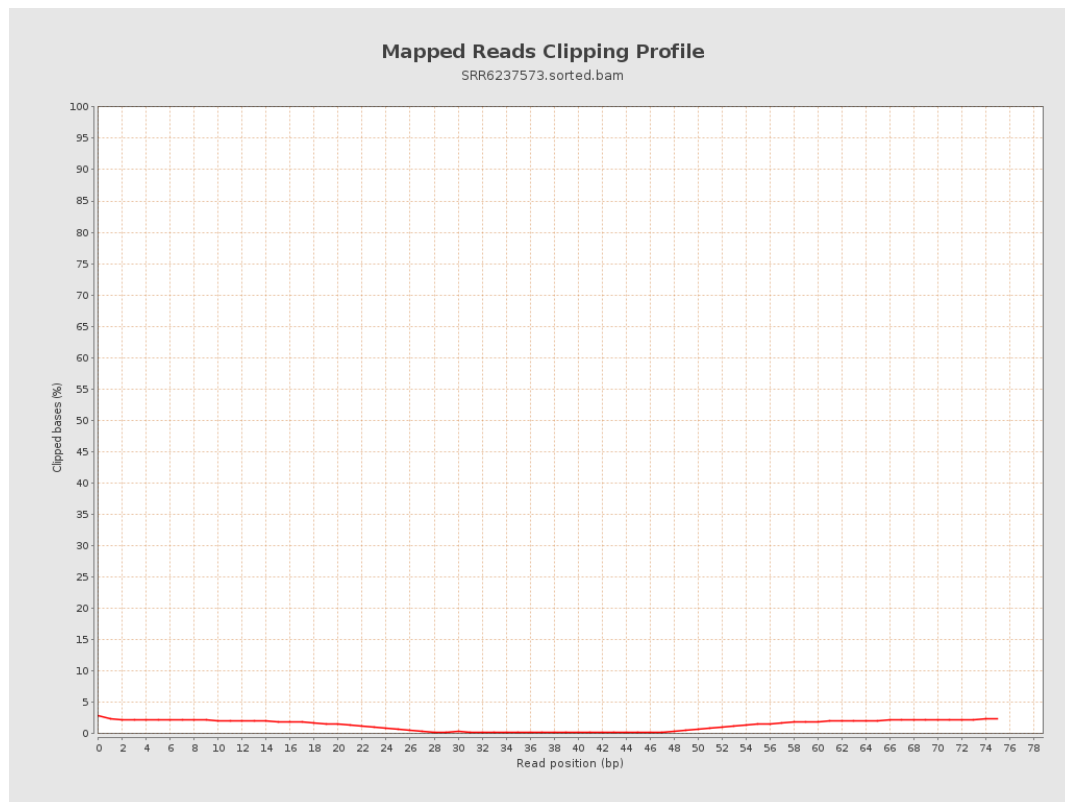
8. Results : Mapped Reads Nucleotide Content



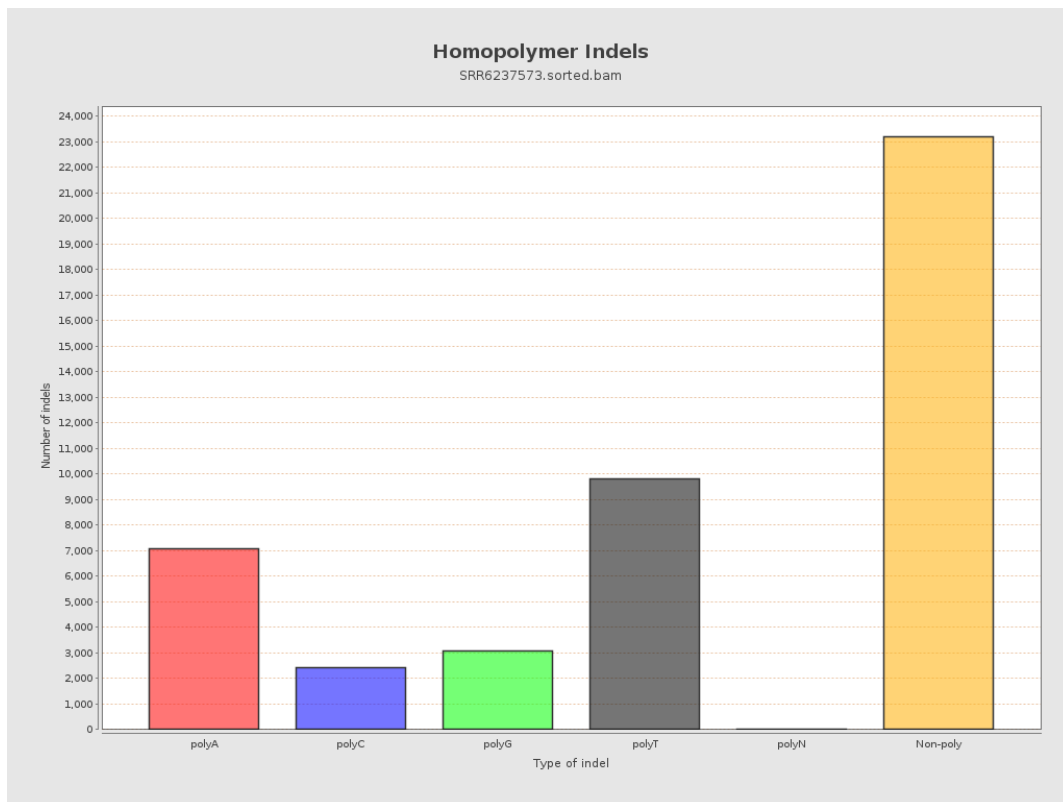
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

