

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 00:49:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524874.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_SRR10524874 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524874.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 00:49:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524874.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,103,373
Mapped reads	1,919,824 / 91.27%
Unmapped reads	183,549 / 8.73%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,822 / 0.42%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	67,256 / 3.2%
Duplication rate	2.4%
Clipped reads	1,922,769 / 91.41%

2.2. ACGT Content

Number/percentage of A's	28,471,750 / 25.48%
Number/percentage of C's	22,059,673 / 19.74%
Number/percentage of T's	36,393,431 / 32.57%
Number/percentage of G's	24,793,752 / 22.19%
Number/percentage of N's	13,615 / 0.01%
GC Percentage	41.93%

2.3. Coverage

Mean	0.0361

Standard Deviation	0.3498
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2.4. Mapping Quality

Mean Mapping Quality	45.13
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2.5. Mismatches and indels

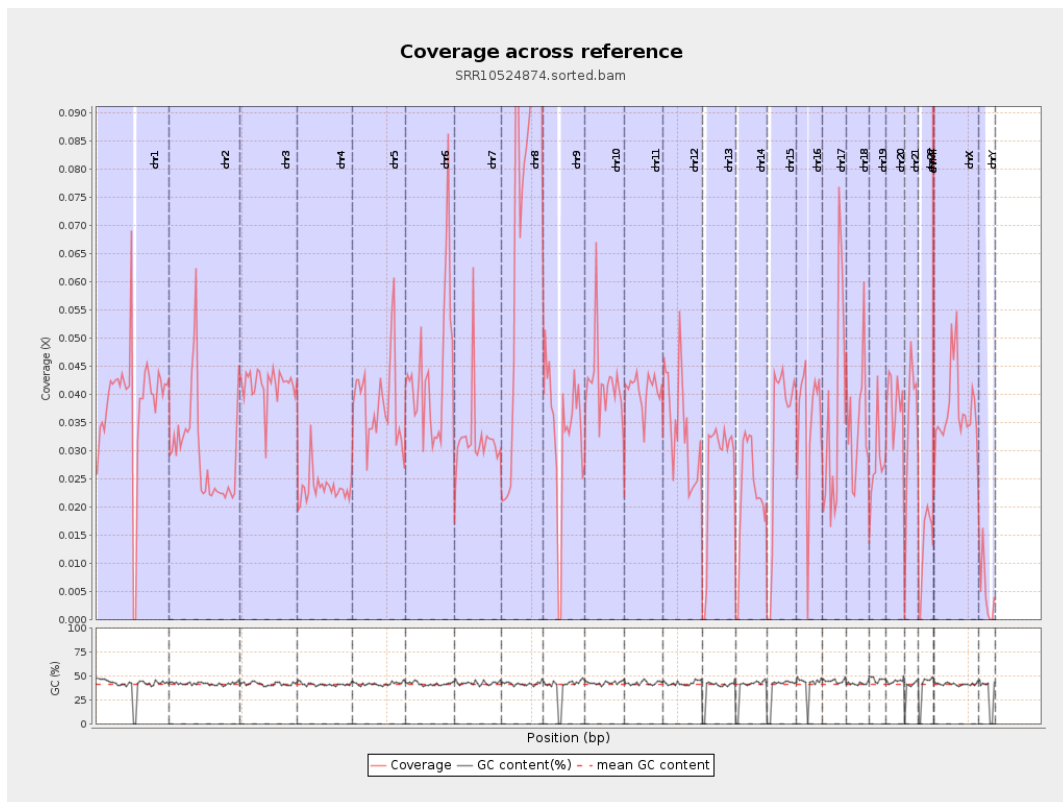
General error rate	0.51%
Mismatches	552,483
Insertions	7,323
Mapped reads with at least one insertion	0.38%
Deletions	21,884
Mapped reads with at least one deletion	1.13%
Homopolymer indels	44.26%

2.6. Chromosome stats

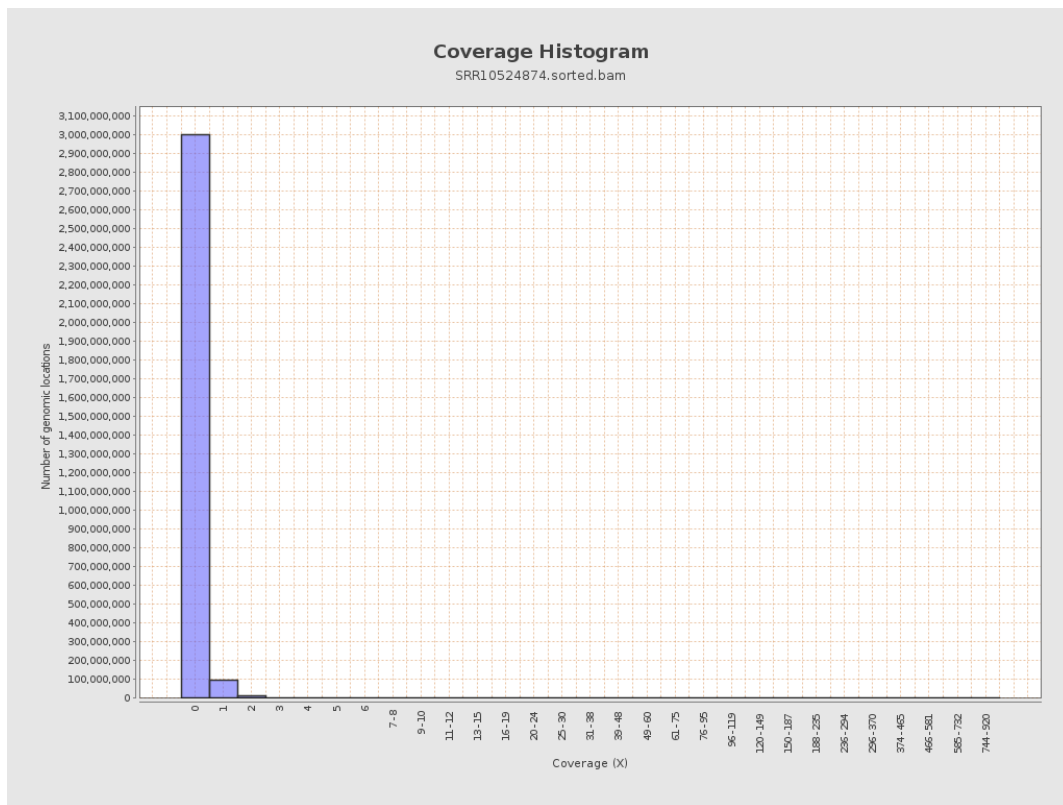
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	9532131	0.0382	0.7012
chr2	243199373	7186688	0.0296	0.357
chr3	198022430	8256686	0.0417	0.2205
chr4	191154276	4450613	0.0233	0.1869
chr5	180915260	6963097	0.0385	0.214
chr6	171115067	7392110	0.0432	0.2544
chr7	159138663	5160010	0.0324	0.4777

chr8	146364022	12350864	0.0844	0.473
chr9	141213431	4722853	0.0334	0.293
chr10	135534747	5693006	0.042	0.3178
chr11	135006516	5459691	0.0404	0.3116
chr12	133851895	4478943	0.0335	0.2052
chr13	115169878	3041407	0.0264	0.1781
chr14	107349540	2381801	0.0222	0.1773
chr15	102531392	3400929	0.0332	0.1981
chr16	90354753	3211895	0.0355	0.2261
chr17	81195210	2865972	0.0353	0.2364
chr18	78077248	2769362	0.0355	0.5685
chr19	59128983	1652255	0.0279	0.483
chr20	63025520	2405905	0.0382	0.2126
chr21	48129895	1643776	0.0342	0.2187
chr22	51304566	664779	0.013	0.1219
chrMT	16571	21701	1.3096	1.3961
chrX	155270560	5774601	0.0372	0.2457
chrY	59373566	285250	0.0048	0.1184

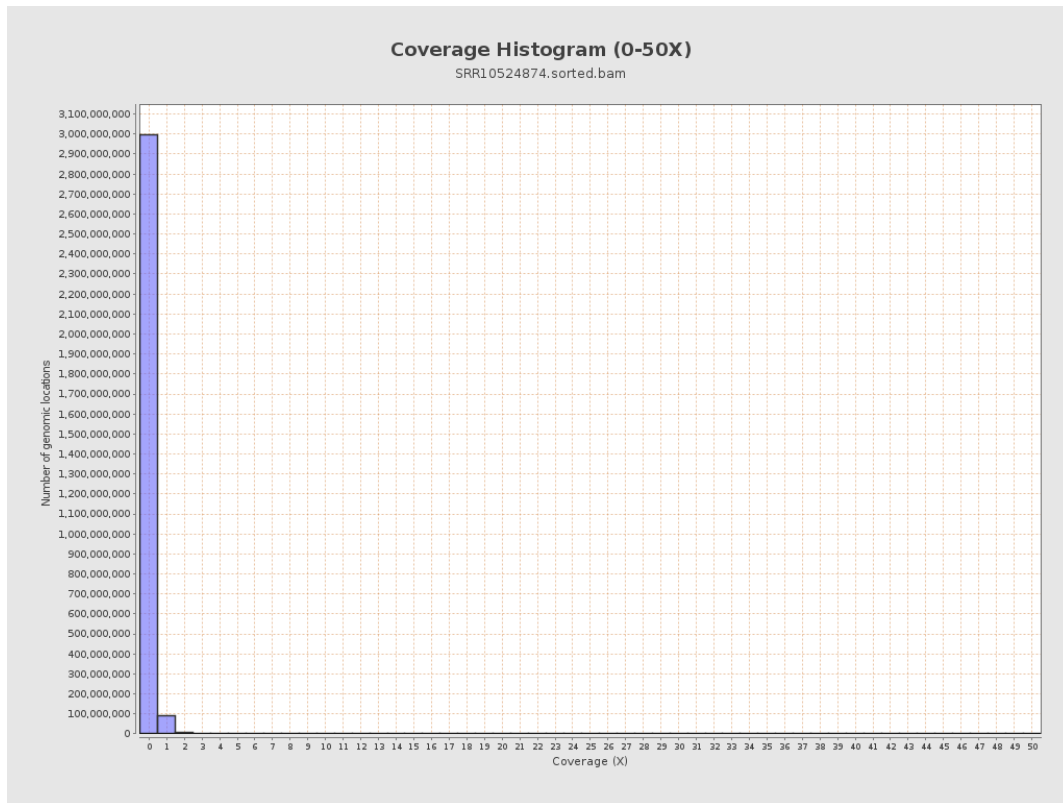
3. Results : Coverage across reference



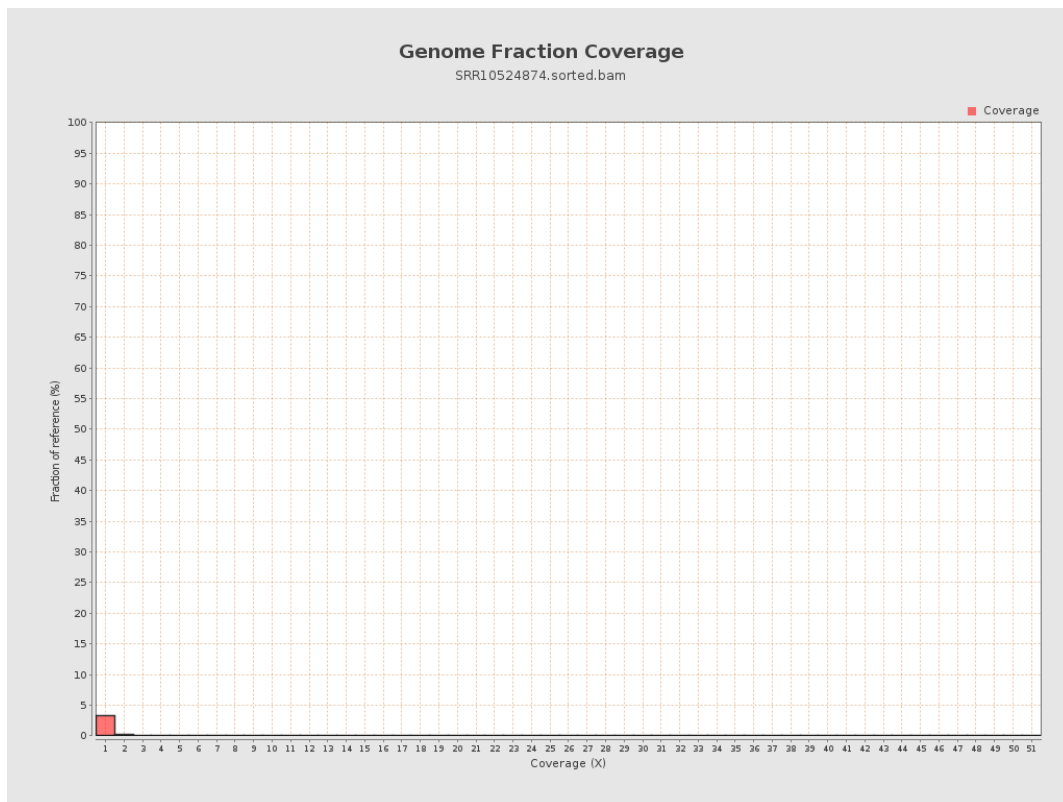
4. Results : Coverage Histogram



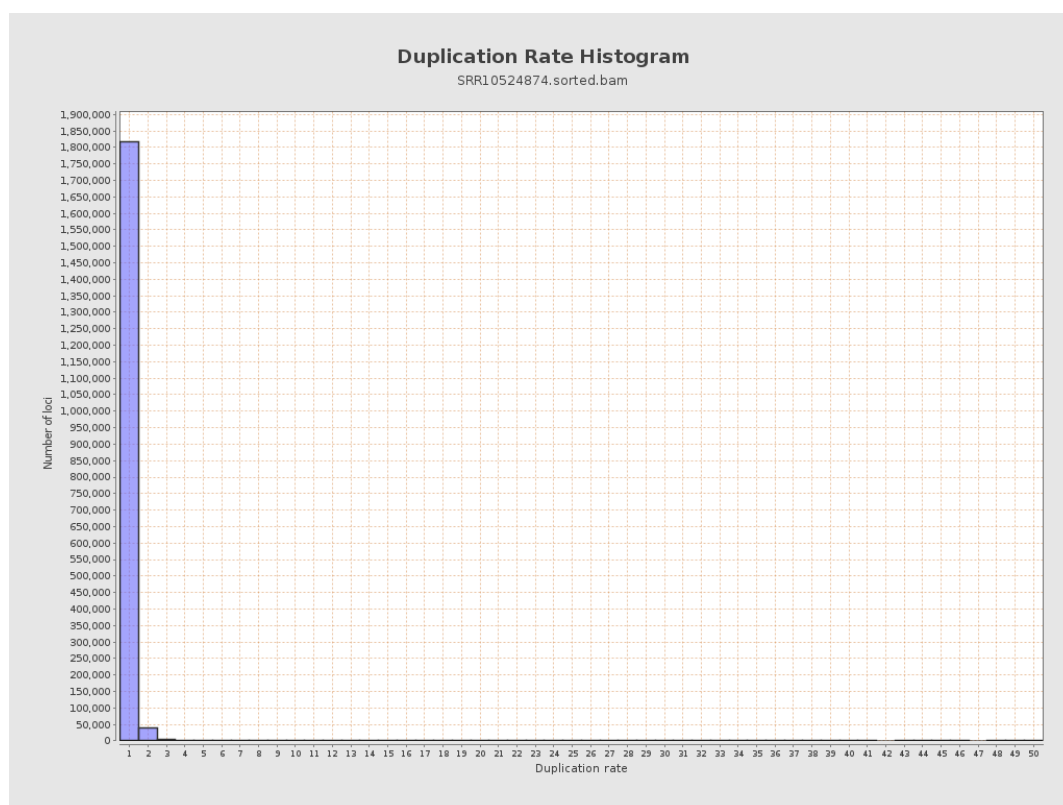
5. Results : Coverage Histogram (0-50X)



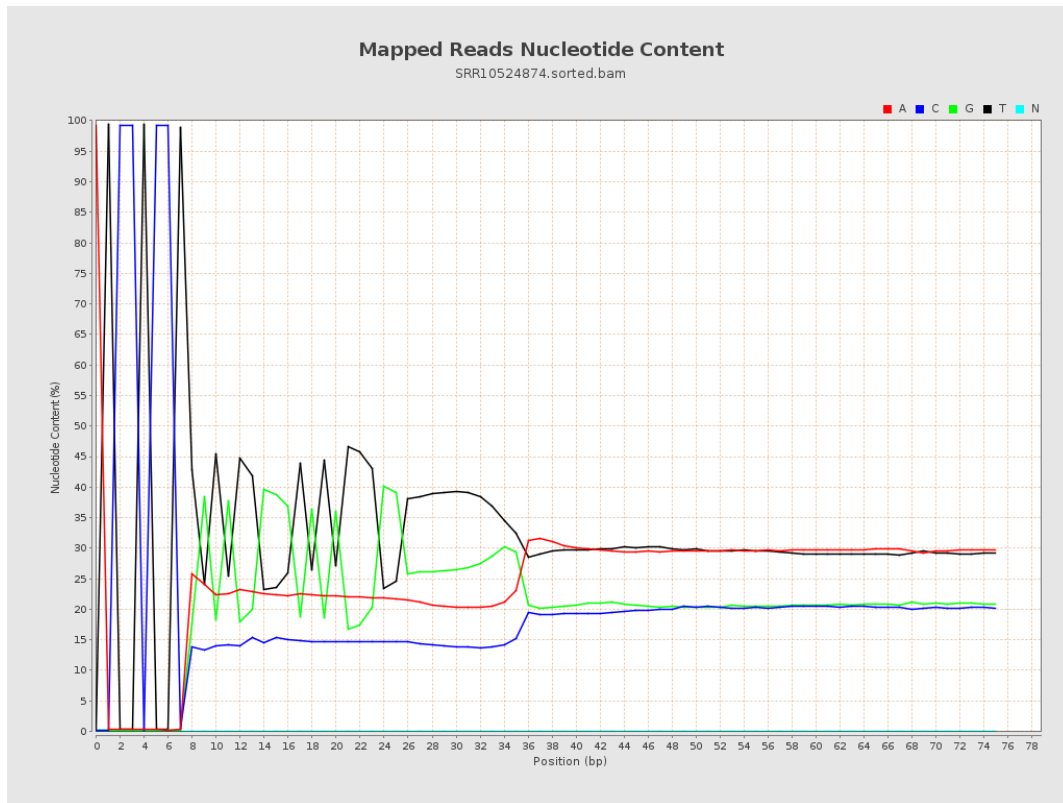
6. Results : Genome Fraction Coverage



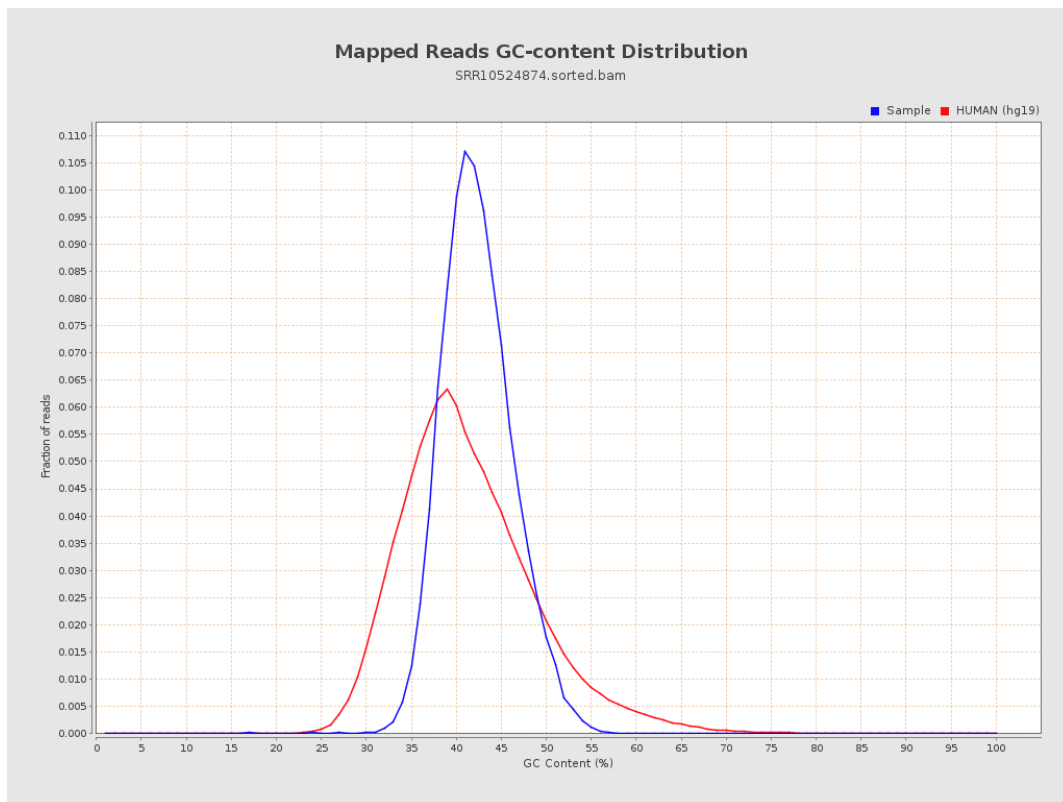
7. Results : Duplication Rate Histogram



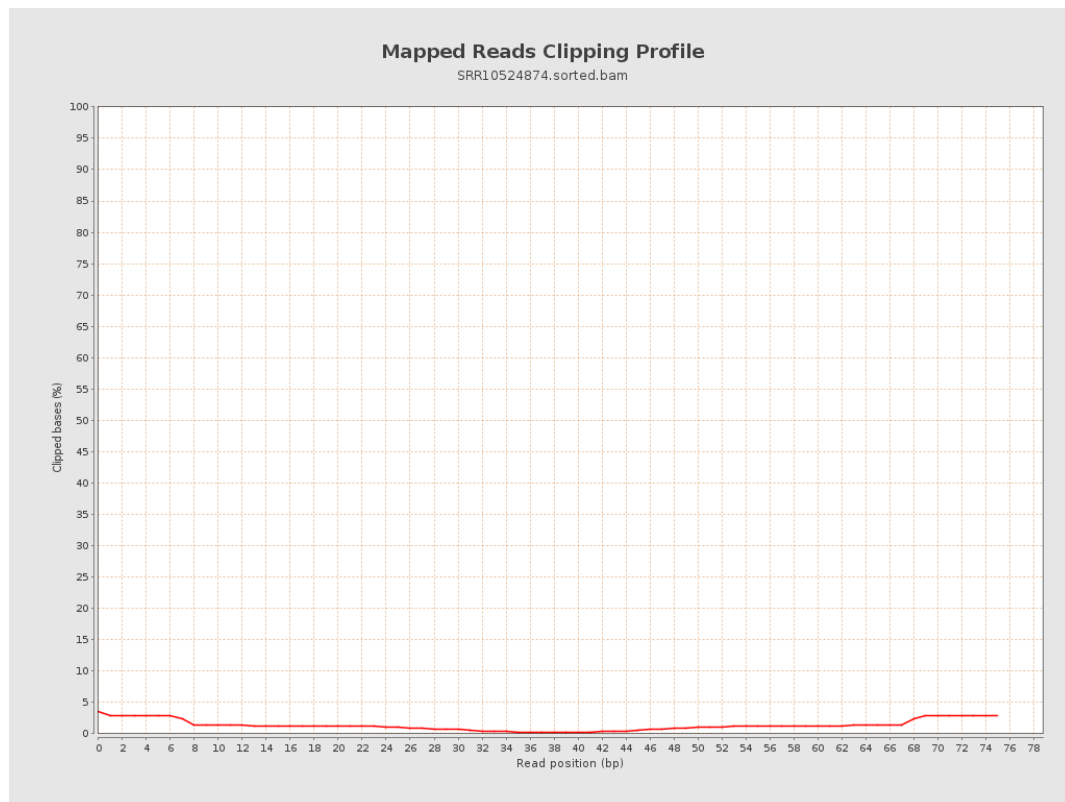
8. Results : Mapped Reads Nucleotide Content



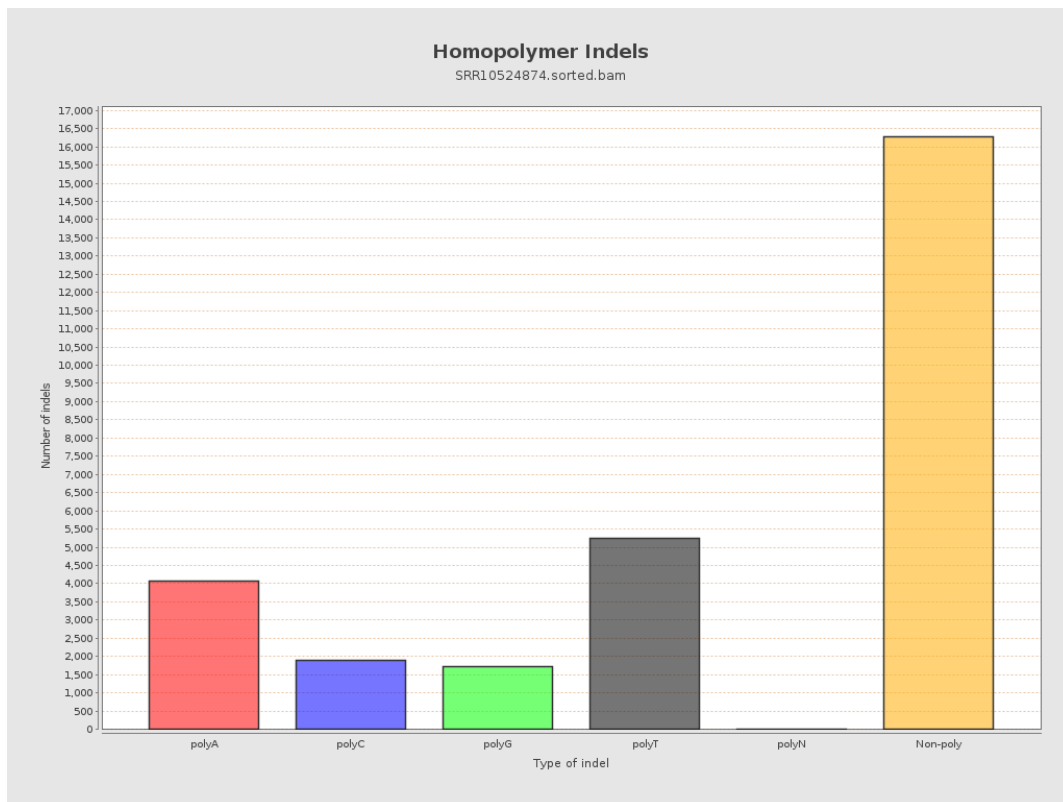
9. Results : Mapped Reads GC-content Distribution



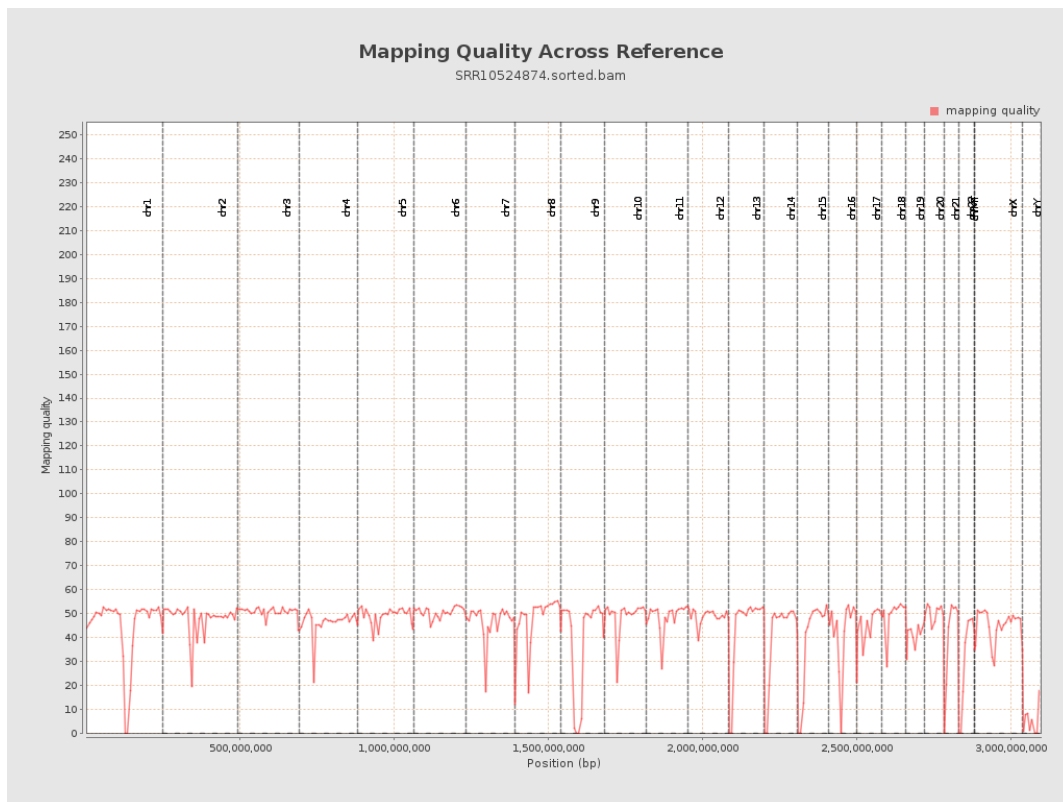
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

