

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 19:08:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013275.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_SRR6013275 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013275.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 19:08:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013275.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,768,976
Mapped reads	2,391,631 / 86.37%
Unmapped reads	377,345 / 13.63%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,565 / 0.67%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	68,240 / 2.46%
Duplication rate	1.95%
Clipped reads	1,270,968 / 45.9%

2.2. ACGT Content

Number/percentage of A's	42,490,929 / 27.53%
Number/percentage of C's	30,260,281 / 19.61%
Number/percentage of T's	45,939,012 / 29.77%
Number/percentage of G's	35,596,328 / 23.07%
Number/percentage of N's	33,290 / 0.02%
GC Percentage	42.68%

2.3. Coverage

Mean	0.0499

Standard Deviation	0.4112
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2.4. Mapping Quality

Mean Mapping Quality	43.15
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2.5. Mismatches and indels

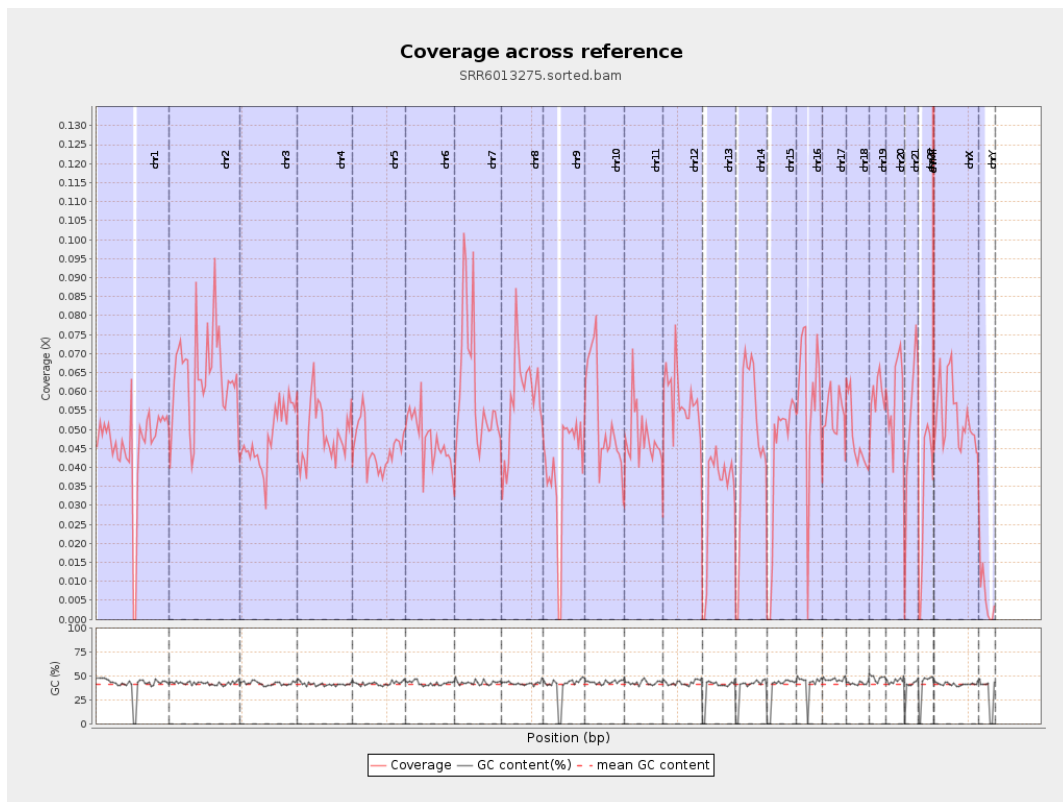
General error rate	0.82%
Mismatches	1,242,461
Insertions	11,064
Mapped reads with at least one insertion	0.46%
Deletions	35,244
Mapped reads with at least one deletion	1.46%
Homopolymer indels	44.22%

2.6. Chromosome stats

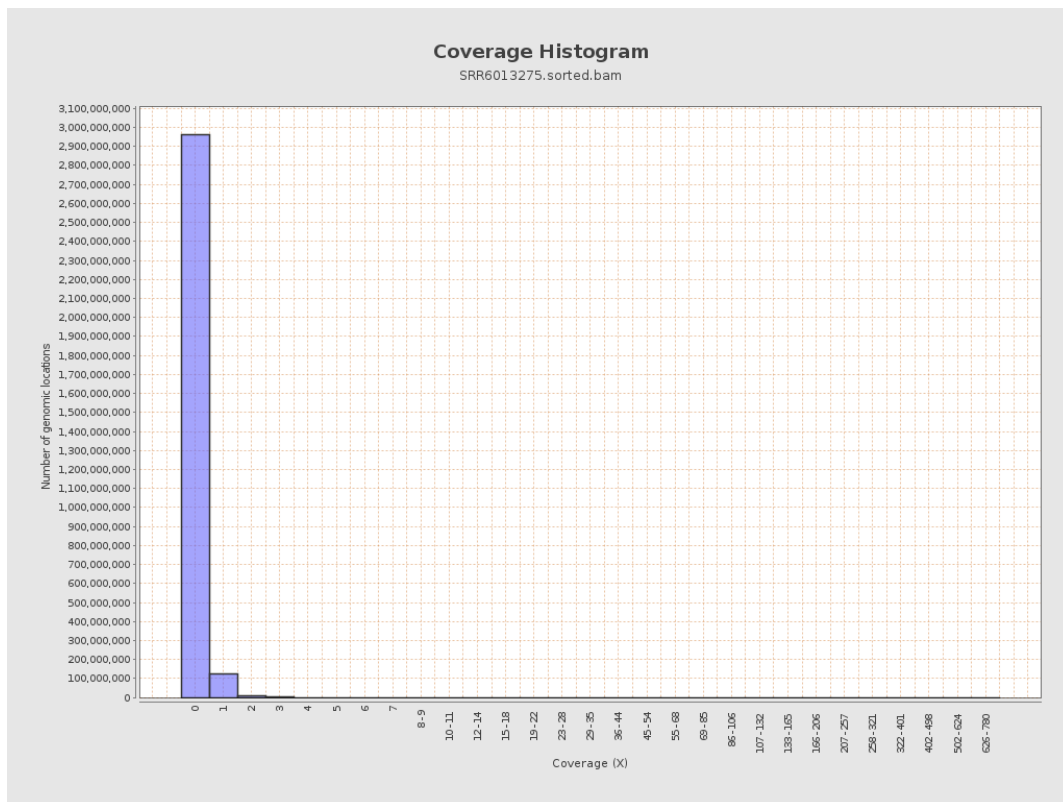
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	11356568	0.0456	0.6053
chr2	243199373	15526327	0.0638	0.5371
chr3	198022430	9534496	0.0481	0.2387
chr4	191154276	9292772	0.0486	0.2509
chr5	180915260	8164849	0.0451	0.2365
chr6	171115067	8069532	0.0472	0.2967
chr7	159138663	9639374	0.0606	0.7845

chr8	146364022	8480112	0.0579	0.3736
chr9	141213431	5606504	0.0397	0.3373
chr10	135534747	7228830	0.0533	0.4172
chr11	135006516	6464370	0.0479	0.3143
chr12	133851895	7762972	0.058	0.2676
chr13	115169878	3789771	0.0329	0.207
chr14	107349540	5163124	0.0481	0.2758
chr15	102531392	4347275	0.0424	0.2306
chr16	90354753	5273120	0.0584	0.2979
chr17	81195210	4360797	0.0537	0.2802
chr18	78077248	3721713	0.0477	0.625
chr19	59128983	3487450	0.059	0.502
chr20	63025520	3658736	0.0581	0.2693
chr21	48129895	2527629	0.0525	0.2722
chr22	51304566	1689953	0.0329	0.1982
chrMT	16571	576741	34.8042	25.1174
chrX	155270560	8294956	0.0534	0.2832
chrY	59373566	363019	0.0061	0.118

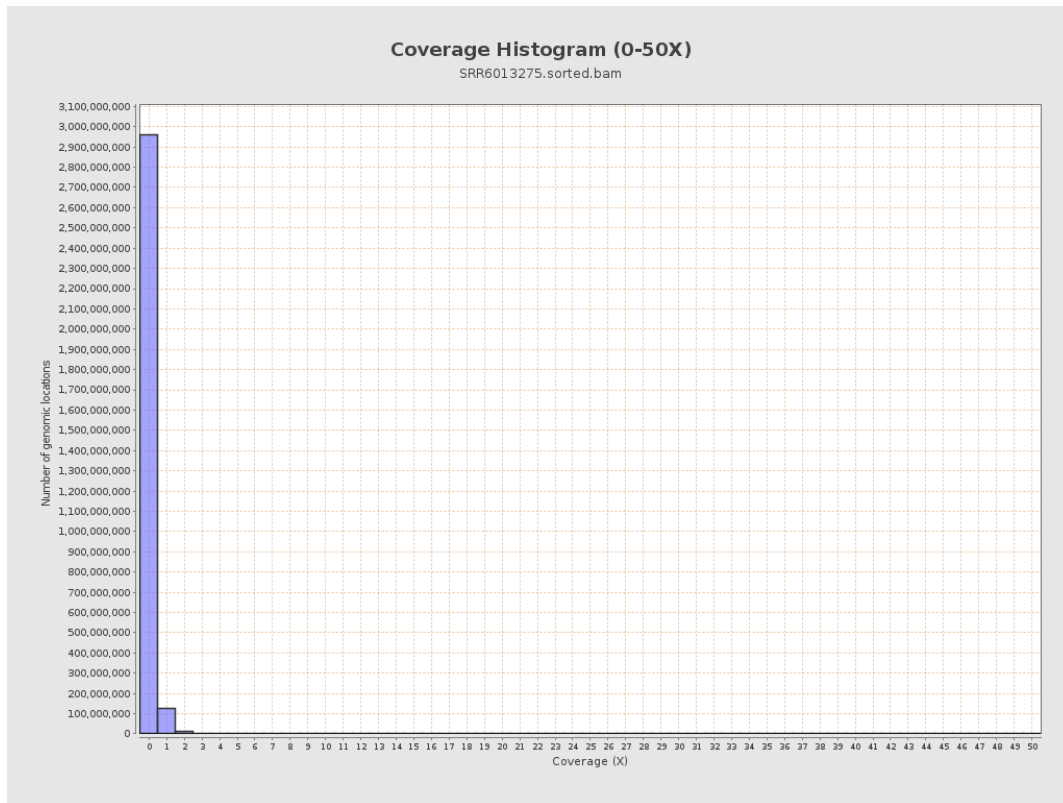
3. Results : Coverage across reference



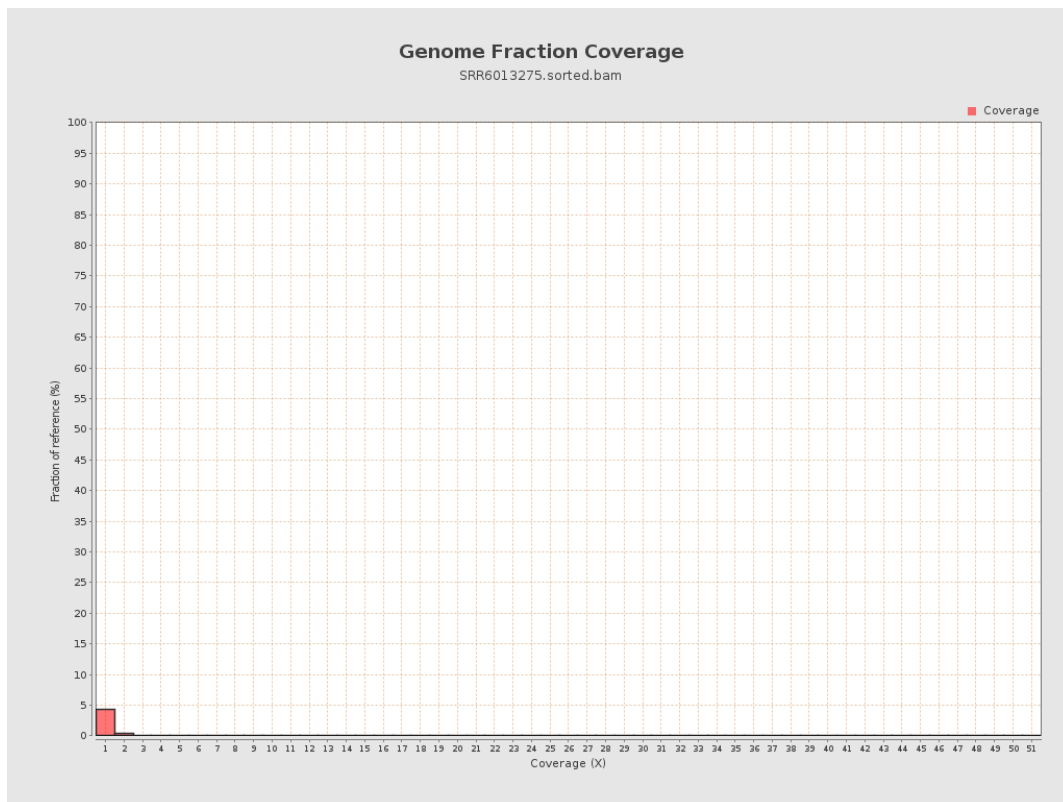
4. Results : Coverage Histogram



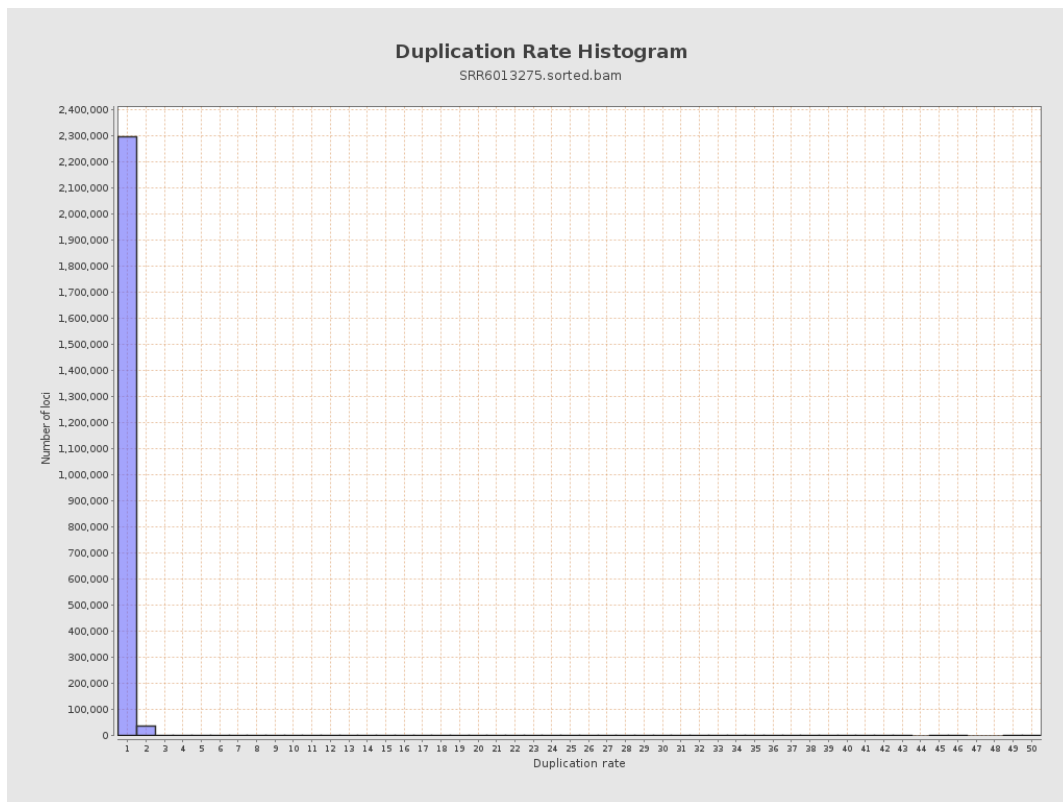
5. Results : Coverage Histogram (0-50X)



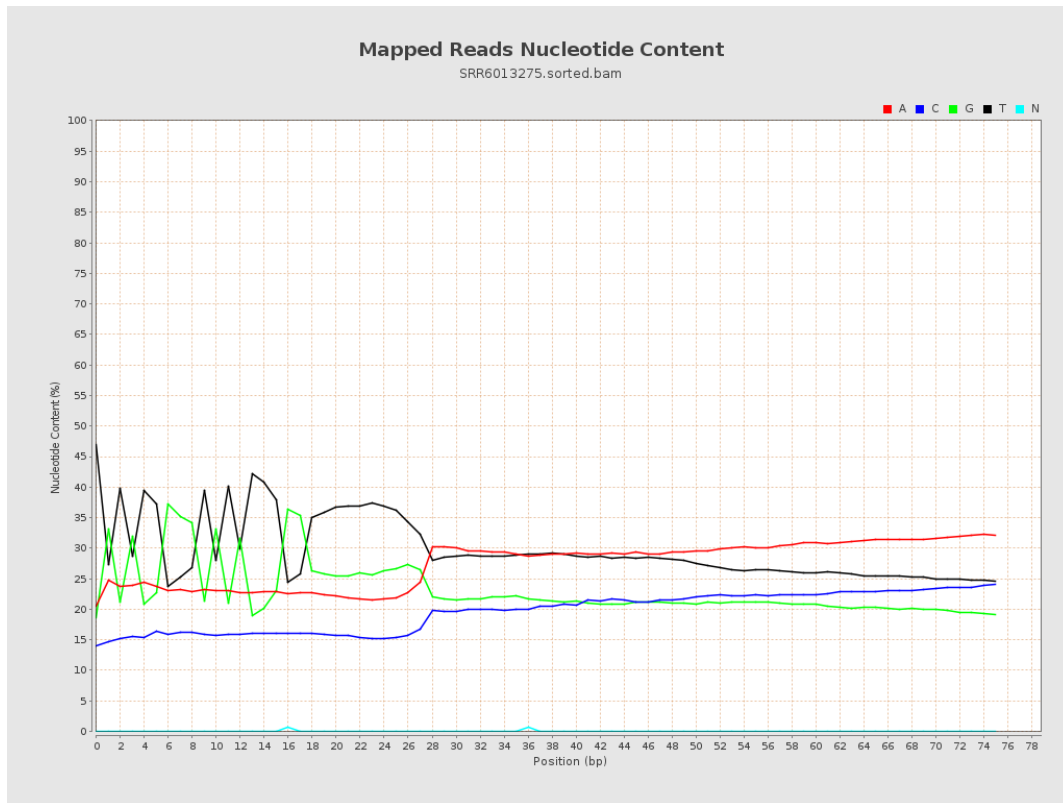
6. Results : Genome Fraction Coverage



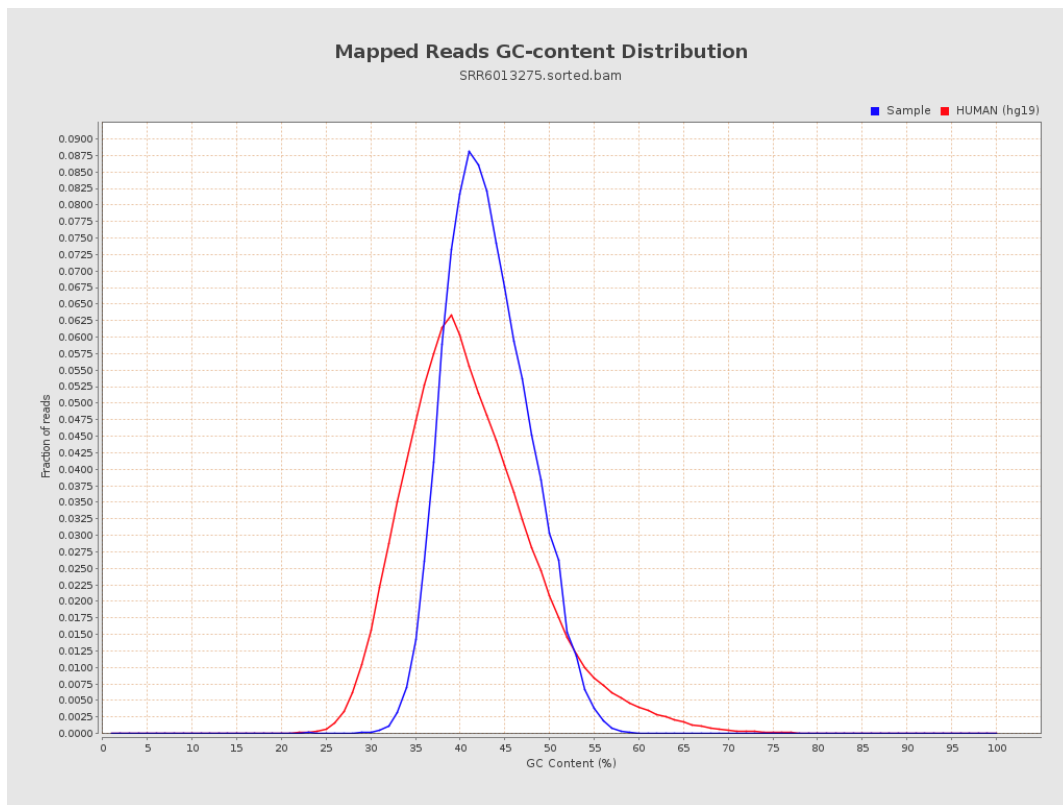
7. Results : Duplication Rate Histogram



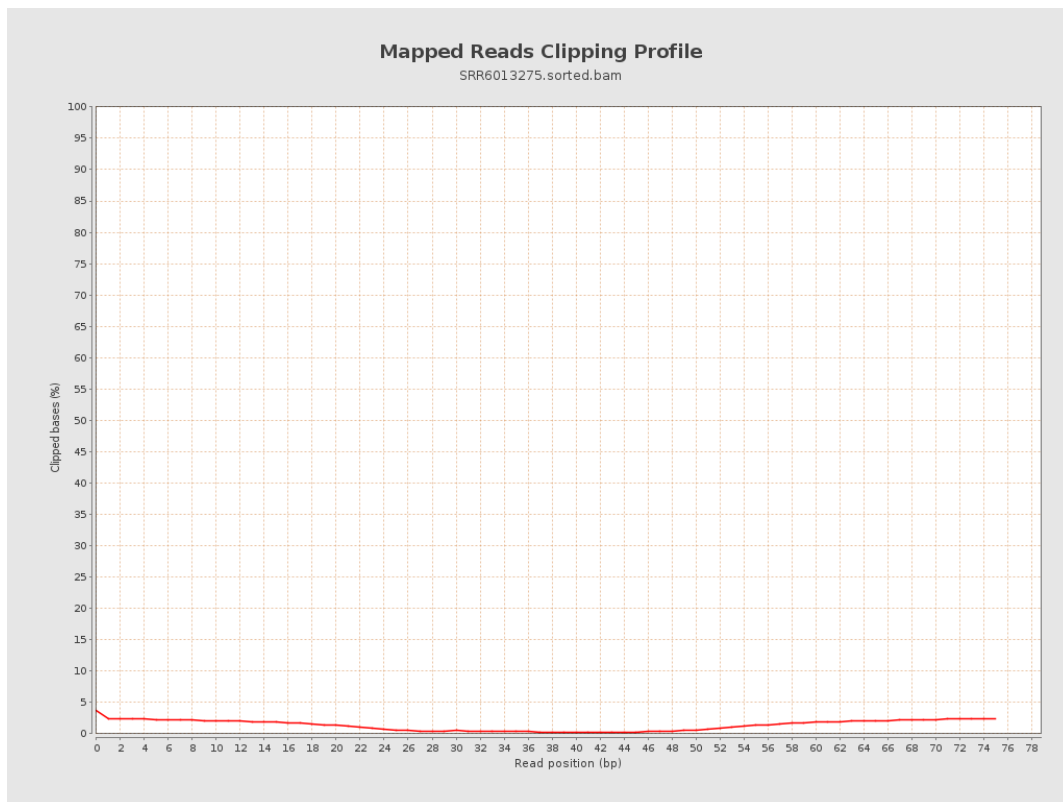
8. Results : Mapped Reads Nucleotide Content



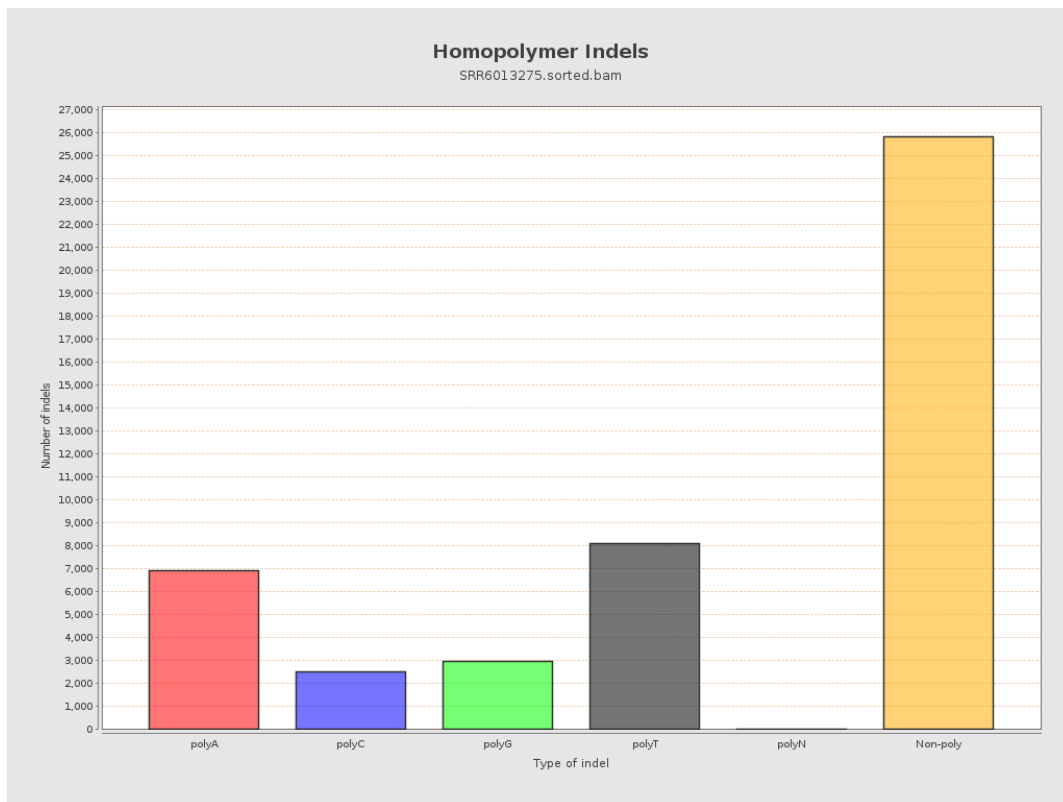
9. Results : Mapped Reads GC-content Distribution



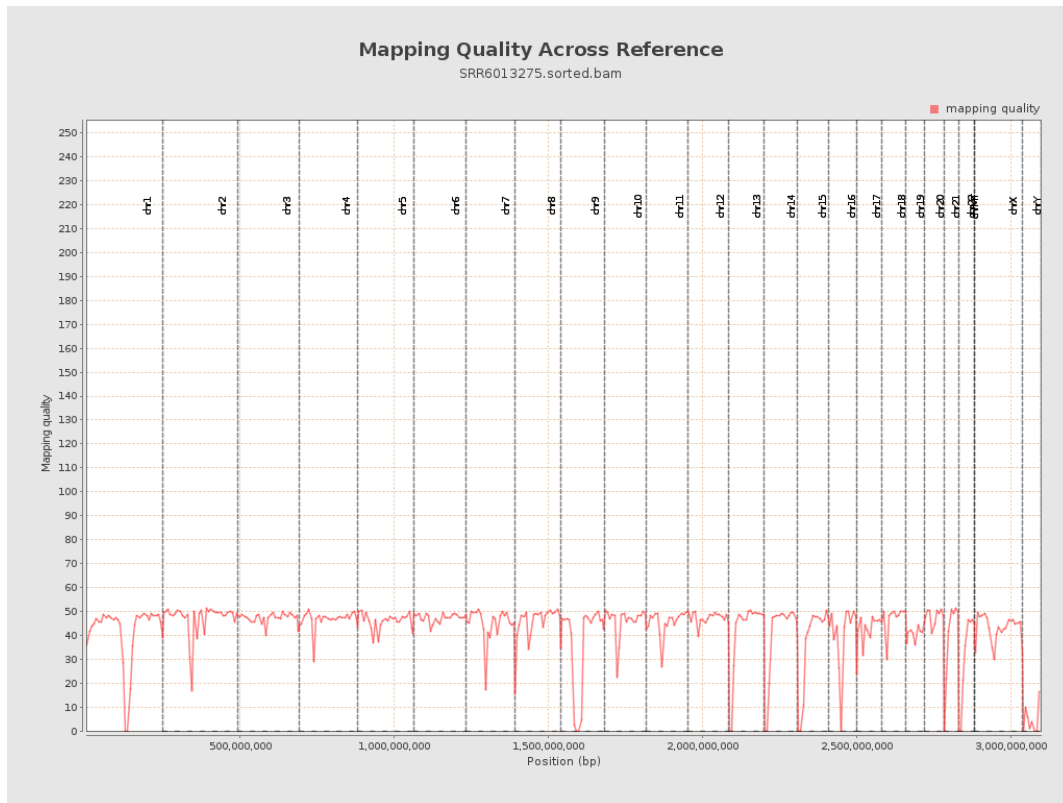
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

