

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 17:54:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013248.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_SRR6013248 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013248.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 17:54:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013248.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,257,792
Mapped reads	1,032,145 / 82.06%
Unmapped reads	225,647 / 17.94%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,755 / 1.17%
Read min/max/mean length	30 / 76 / 76.41
Duplicated reads (estimated)	129,661 / 10.31%
Duplication rate	10.02%
Clipped reads	602,881 / 47.93%

2.2. ACGT Content

Number/percentage of A's	18,620,387 / 28.42%
Number/percentage of C's	11,251,693 / 17.18%
Number/percentage of T's	21,751,535 / 33.2%
Number/percentage of G's	13,873,667 / 21.18%
Number/percentage of N's	13,580 / 0.02%
GC Percentage	38.35%

2.3. Coverage

Mean	0.0212

Standard Deviation	0.3072
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2.4. Mapping Quality

Mean Mapping Quality	39.67
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2.5. Mismatches and indels

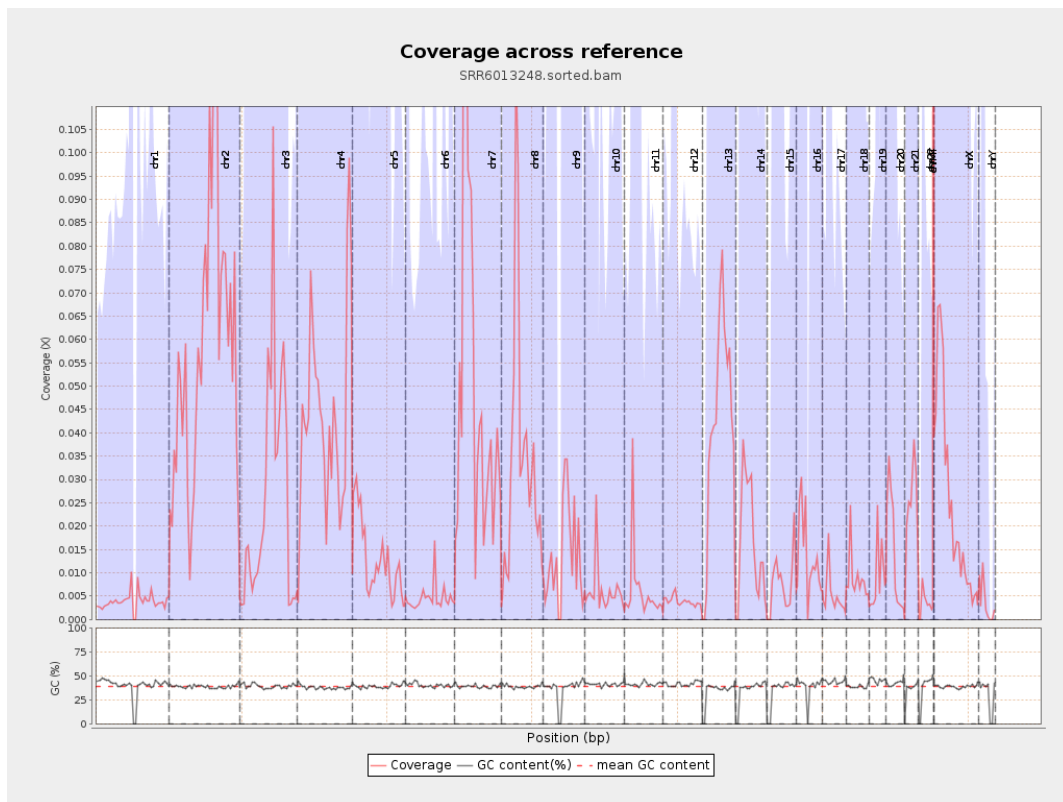
General error rate	1.05%
Mismatches	678,847
Insertions	5,138
Mapped reads with at least one insertion	0.49%
Deletions	40,592
Mapped reads with at least one deletion	3.85%
Homopolymer indels	42.04%

2.6. Chromosome stats

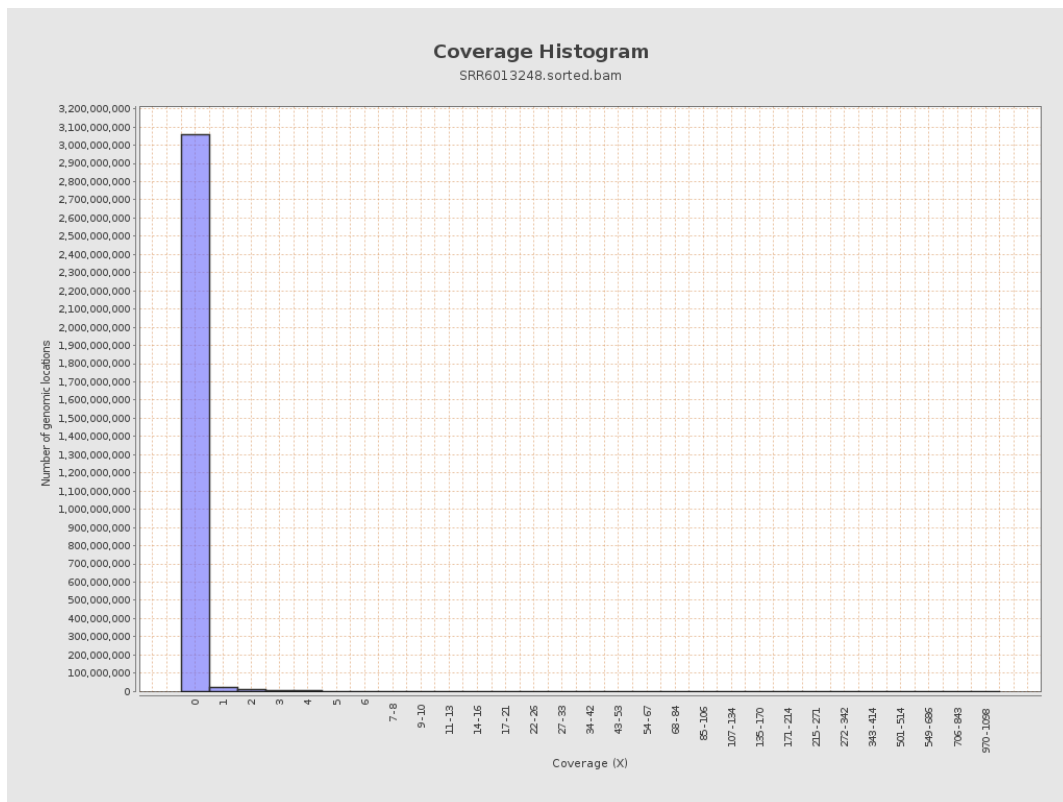
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	968580	0.0039	0.1511
chr2	243199373	14208563	0.0584	0.442
chr3	198022430	5043639	0.0255	0.2462
chr4	191154276	8468944	0.0443	0.3469
chr5	180915260	2301339	0.0127	0.1684
chr6	171115067	788669	0.0046	0.1086
chr7	159138663	8000424	0.0503	0.5937

chr8	146364022	4990657	0.0341	0.685
chr9	141213431	1944547	0.0138	0.2429
chr10	135534747	820012	0.0061	0.2074
chr11	135006516	835350	0.0062	0.1281
chr12	133851895	522651	0.0039	0.1006
chr13	115169878	4882314	0.0424	0.3224
chr14	107349540	1811090	0.0169	0.2208
chr15	102531392	807775	0.0079	0.1329
chr16	90354753	1250760	0.0138	0.1838
chr17	81195210	408568	0.005	0.1175
chr18	78077248	704427	0.009	0.3788
chr19	59128983	534288	0.009	0.1725
chr20	63025520	937968	0.0149	0.213
chr21	48129895	1139950	0.0237	0.2538
chr22	51304566	179178	0.0035	0.0832
chrMT	16571	14007	0.8453	1.4931
chrX	155270560	3815617	0.0246	0.2486
chrY	59373566	202607	0.0034	0.1372

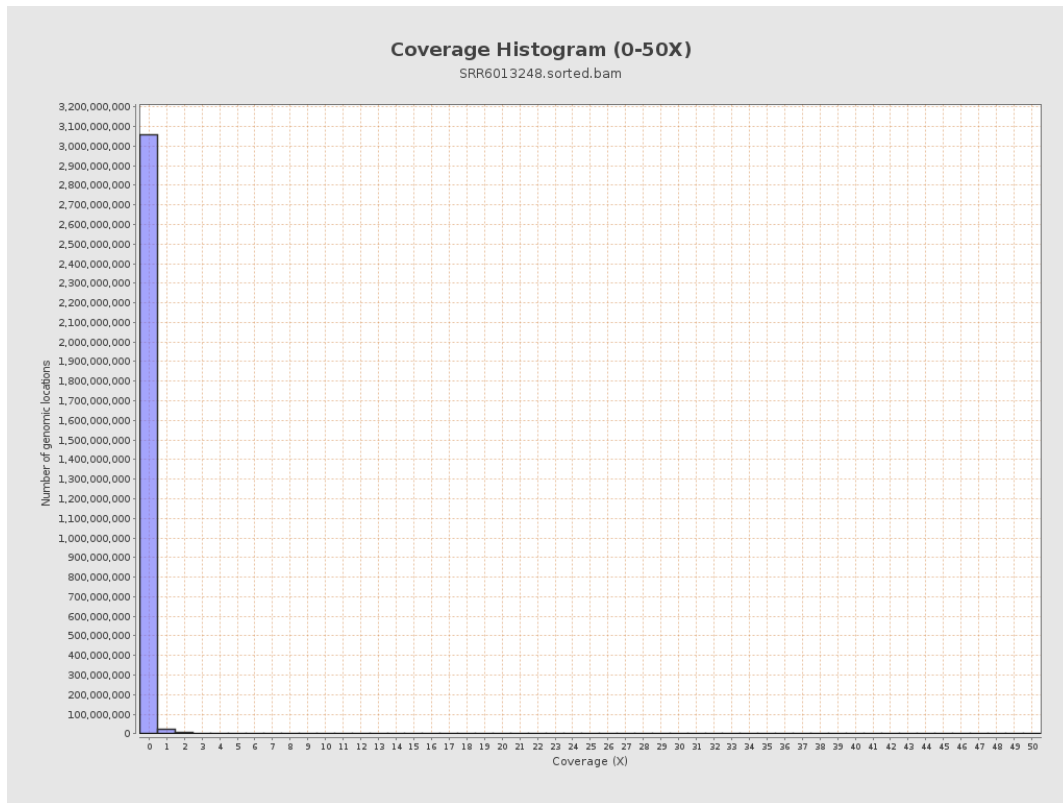
3. Results : Coverage across reference



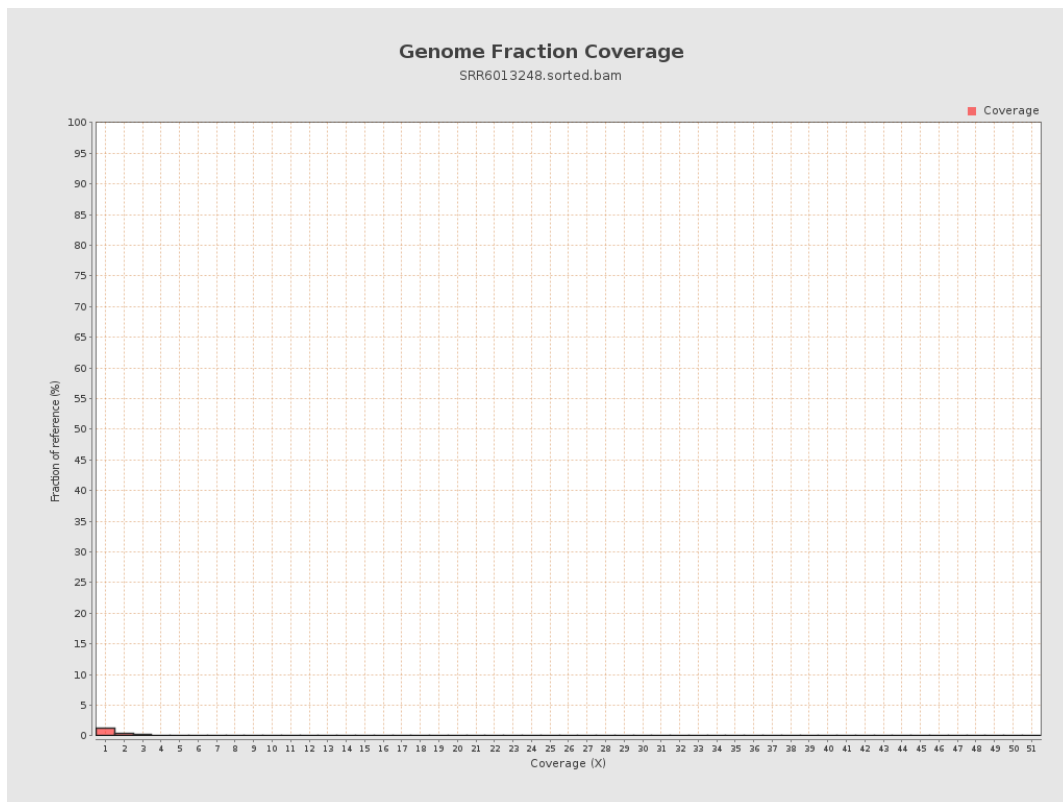
4. Results : Coverage Histogram



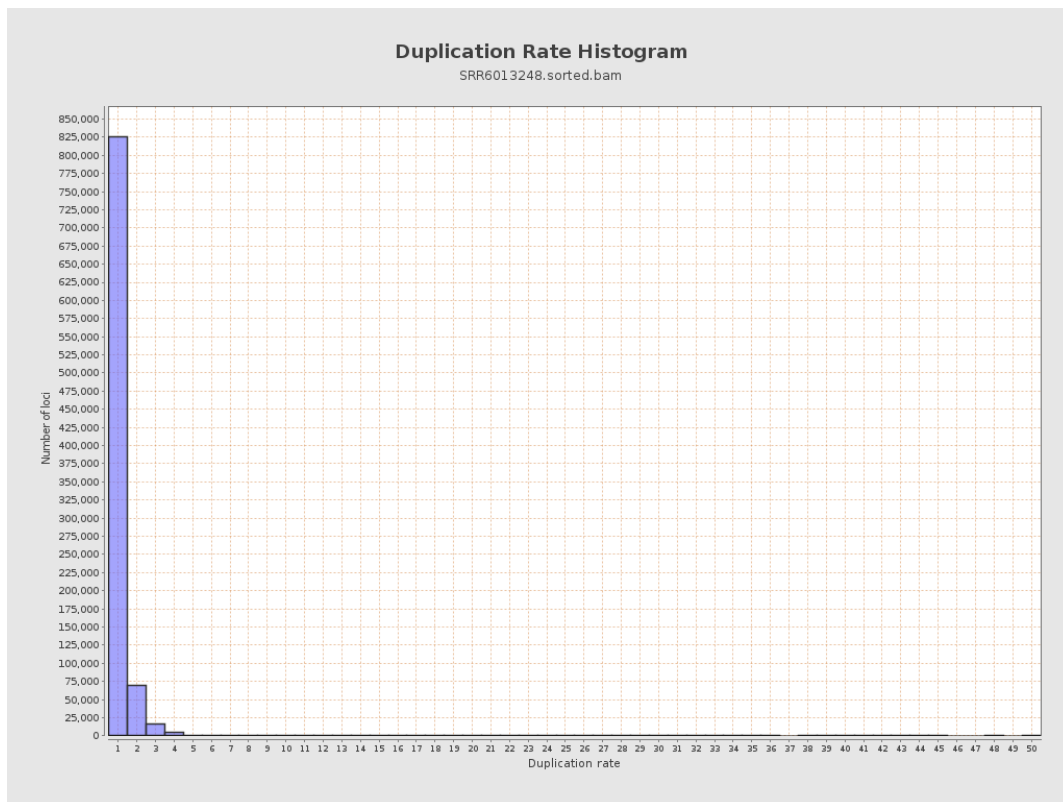
5. Results : Coverage Histogram (0-50X)



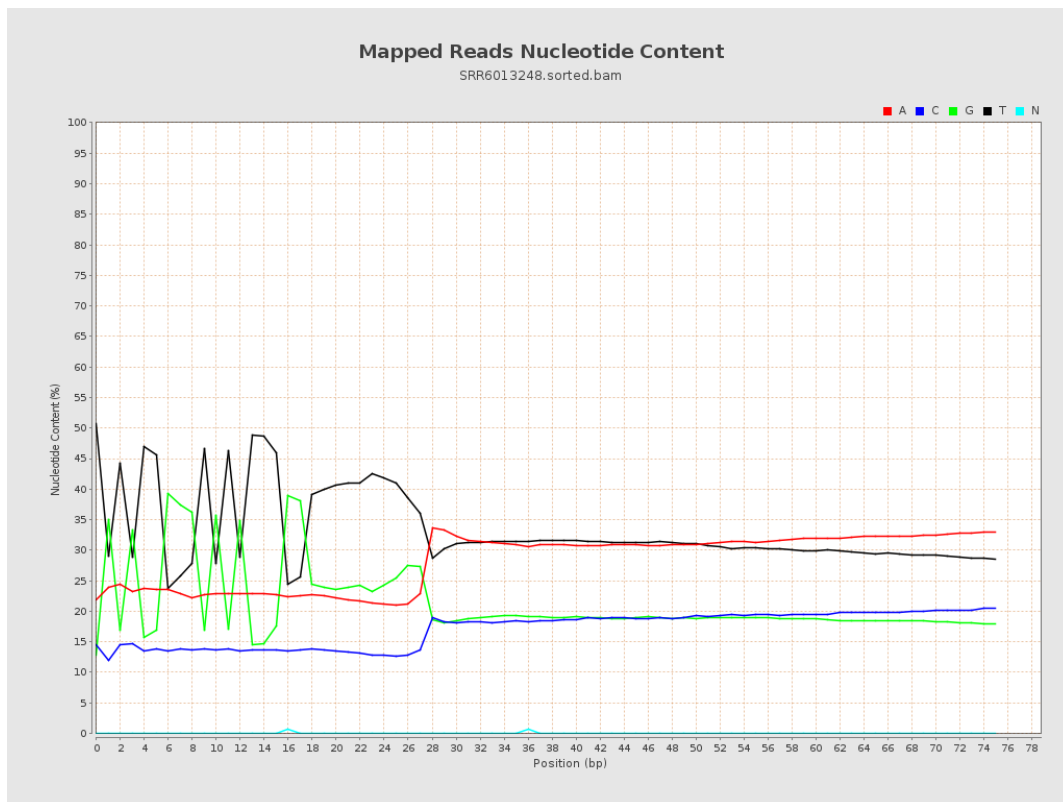
6. Results : Genome Fraction Coverage



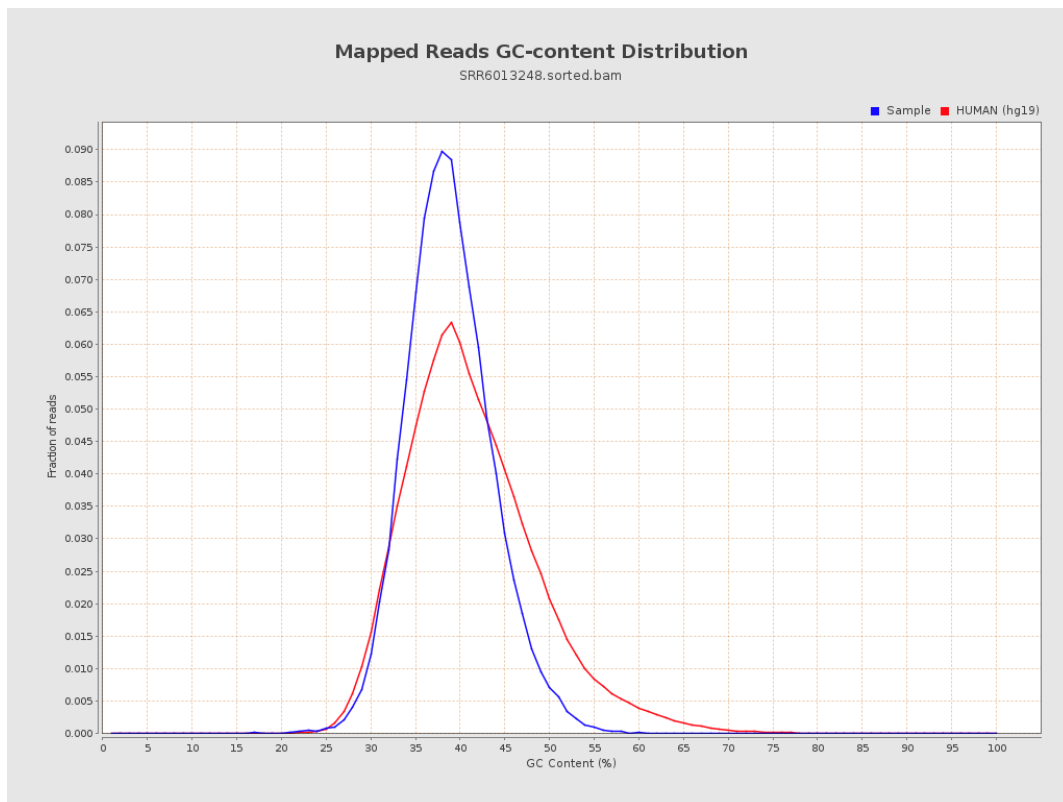
7. Results : Duplication Rate Histogram



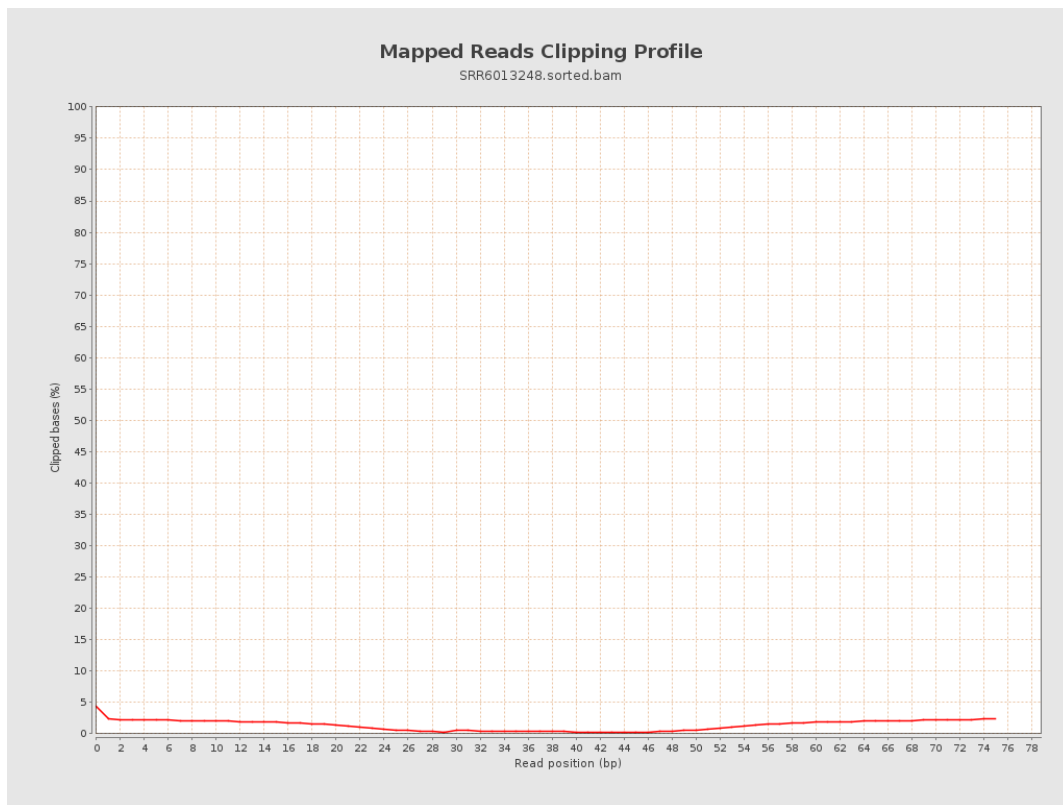
8. Results : Mapped Reads Nucleotide Content



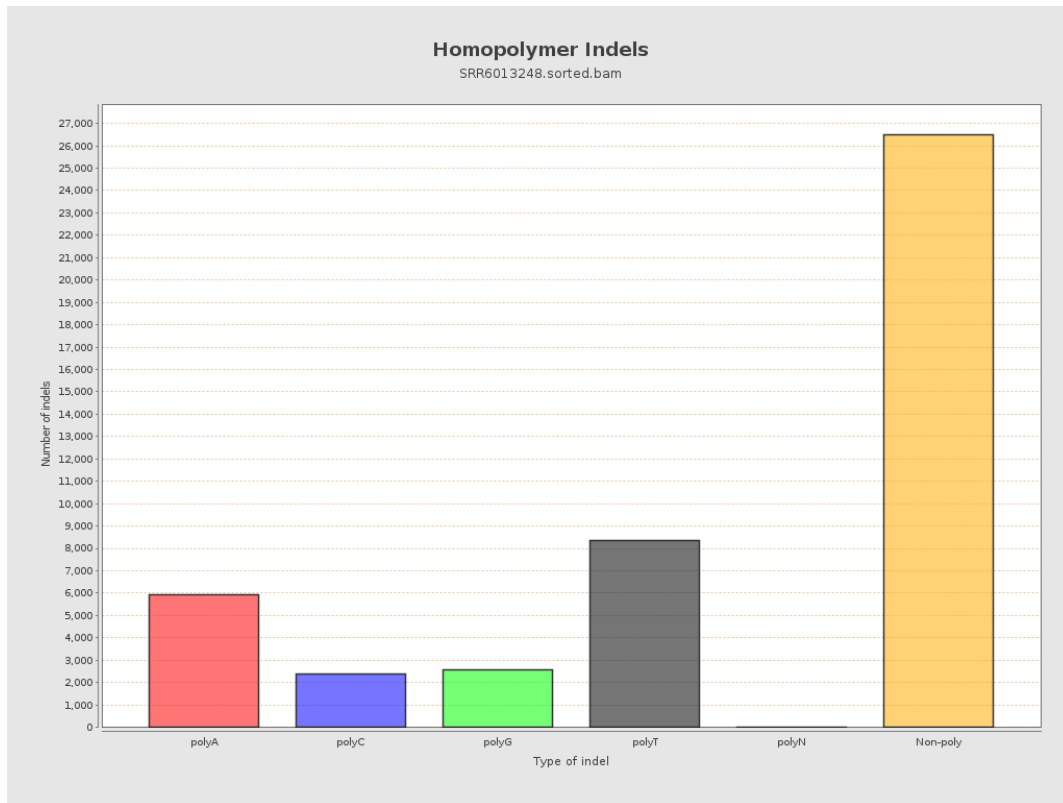
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

