

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 18:47:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013268.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_SRR6013268 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013268.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 18:47:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013268.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,051,592
Mapped reads	1,833,014 / 89.35%
Unmapped reads	218,578 / 10.65%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,809 / 0.43%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	74,242 / 3.62%
Duplication rate	3.03%
Clipped reads	791,626 / 38.59%

2.2. ACGT Content

Number/percentage of A's	34,322,262 / 27.95%
Number/percentage of C's	22,292,227 / 18.15%
Number/percentage of T's	39,225,546 / 31.94%
Number/percentage of G's	26,924,806 / 21.93%
Number/percentage of N's	27,033 / 0.02%
GC Percentage	40.08%

2.3. Coverage

Mean	0.0397

Standard Deviation	0.3981
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2.4. Mapping Quality

Mean Mapping Quality	45.49
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2.5. Mismatches and indels

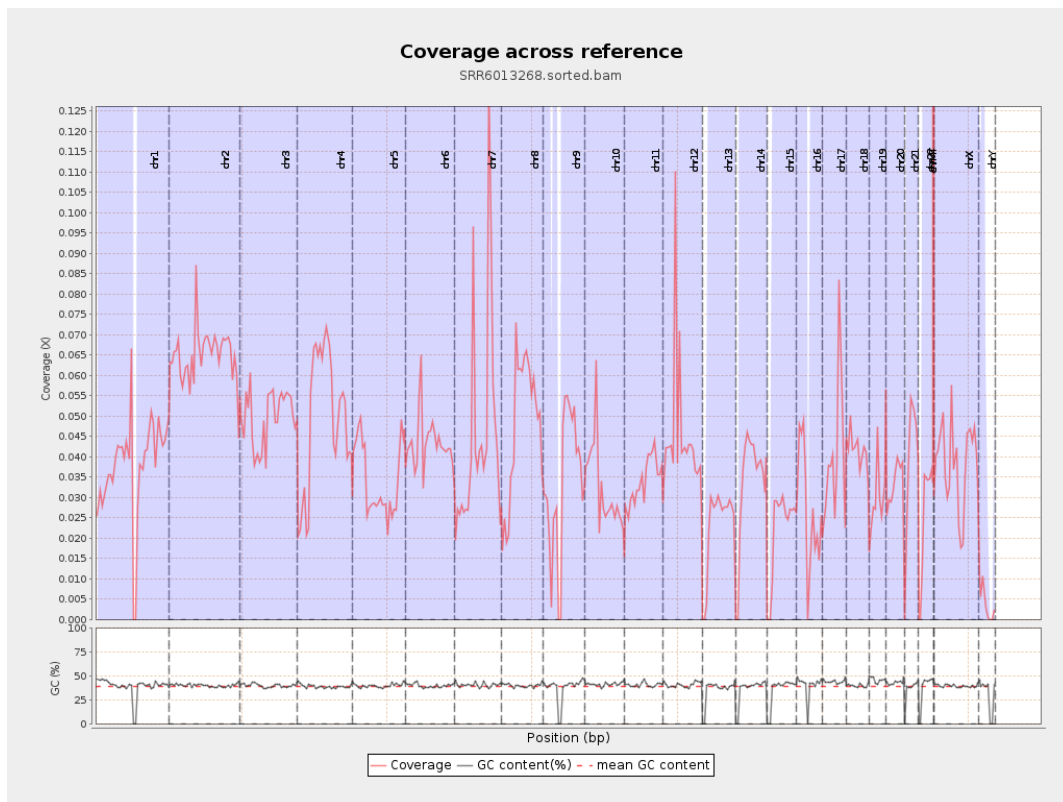
General error rate	0.82%
Mismatches	984,018
Insertions	9,274
Mapped reads with at least one insertion	0.5%
Deletions	30,880
Mapped reads with at least one deletion	1.67%
Homopolymer indels	45.72%

2.6. Chromosome stats

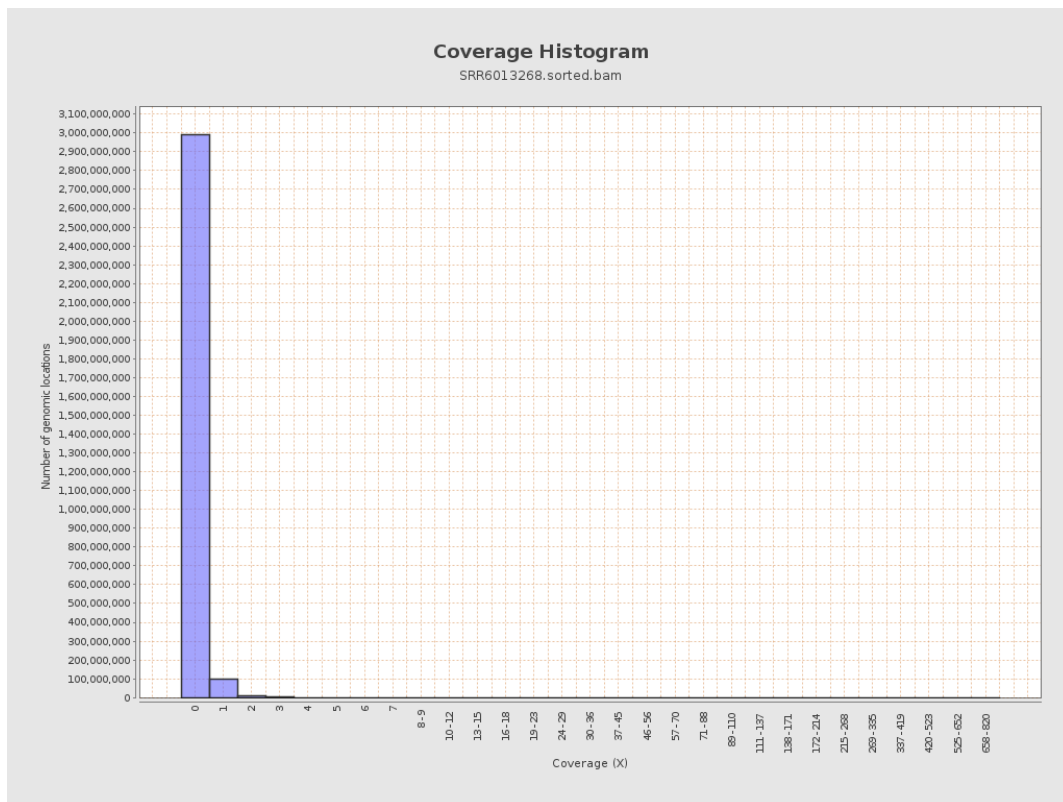
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	9432038	0.0378	0.6315
chr2	243199373	15842964	0.0651	0.501
chr3	198022430	9846617	0.0497	0.2471
chr4	191154276	9367621	0.049	0.2555
chr5	180915260	6197917	0.0343	0.2056
chr6	171115067	7414696	0.0433	0.2966
chr7	159138663	7352579	0.0462	0.8815

chr8	146364022	7002133	0.0478	0.4464
chr9	141213431	4699926	0.0333	0.328
chr10	135534747	4394514	0.0324	0.3995
chr11	135006516	4563739	0.0338	0.2475
chr12	133851895	6103809	0.0456	0.2443
chr13	115169878	2625563	0.0228	0.1683
chr14	107349540	3608498	0.0336	0.229
chr15	102531392	2283258	0.0223	0.1678
chr16	90354753	2432885	0.0269	0.2068
chr17	81195210	3170935	0.0391	0.2273
chr18	78077248	3261209	0.0418	0.5895
chr19	59128983	1816163	0.0307	0.4712
chr20	63025520	2084912	0.0331	0.206
chr21	48129895	1875000	0.039	0.2317
chr22	51304566	1265791	0.0247	0.173
chrMT	16571	71806	4.3332	3.3162
chrX	155270560	5904475	0.038	0.2363
chrY	59373566	225613	0.0038	0.0994

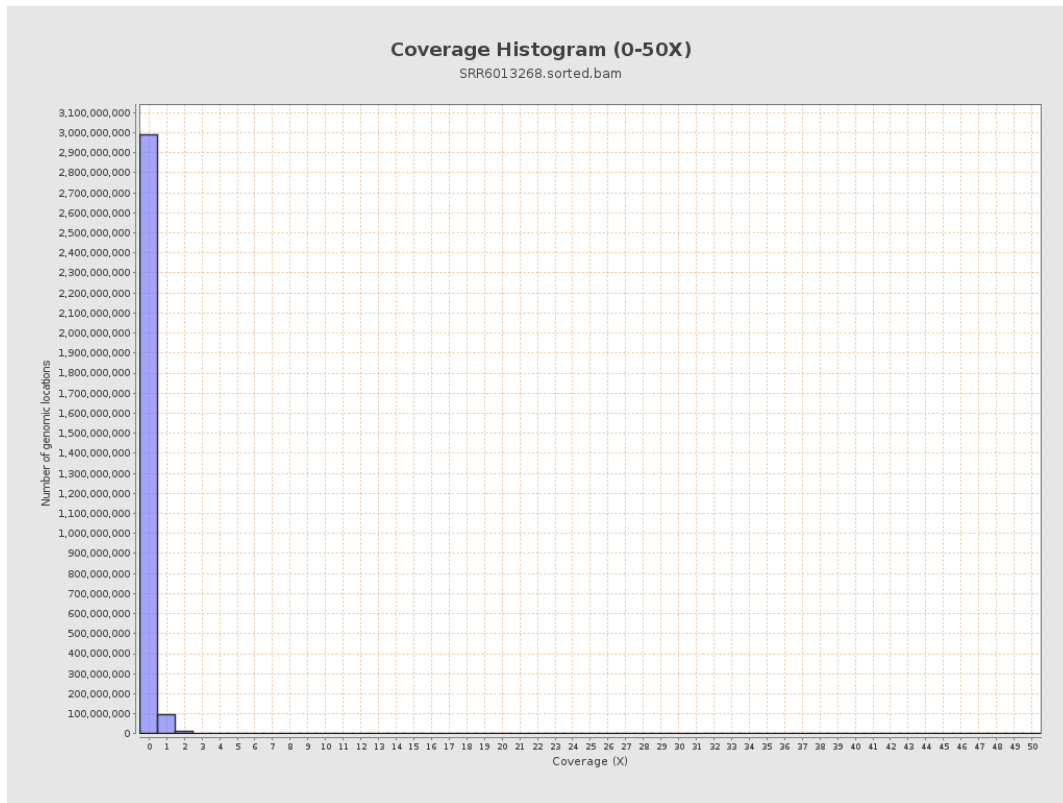
3. Results : Coverage across reference



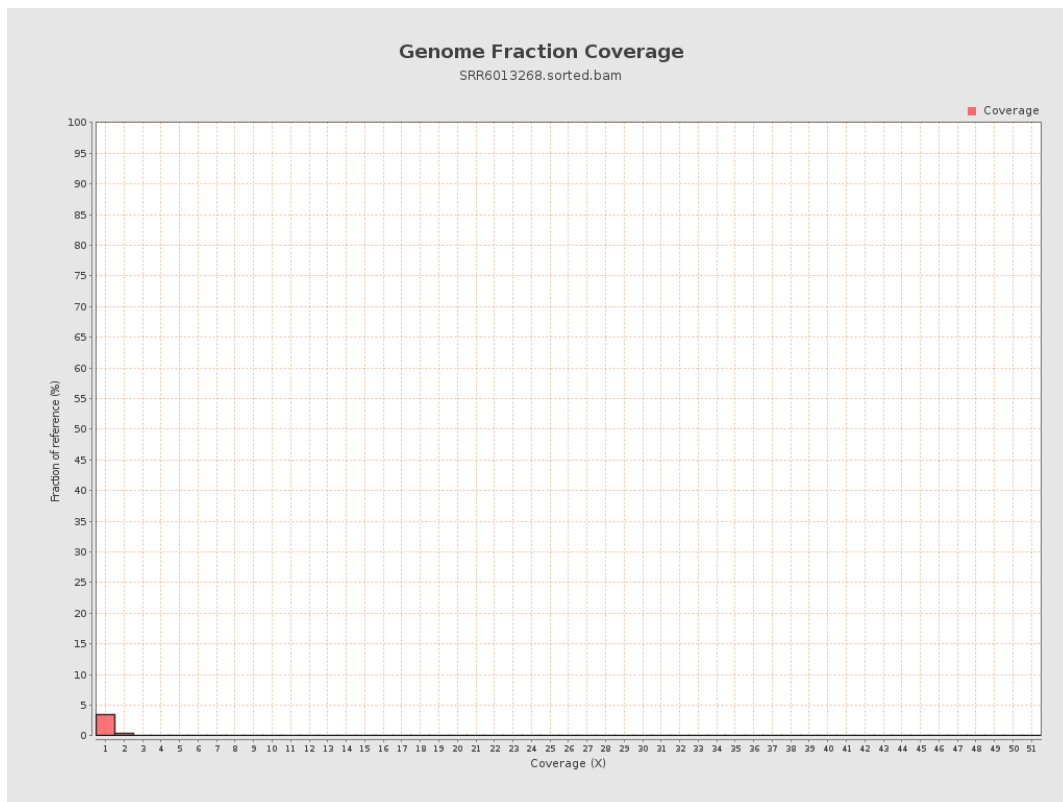
4. Results : Coverage Histogram



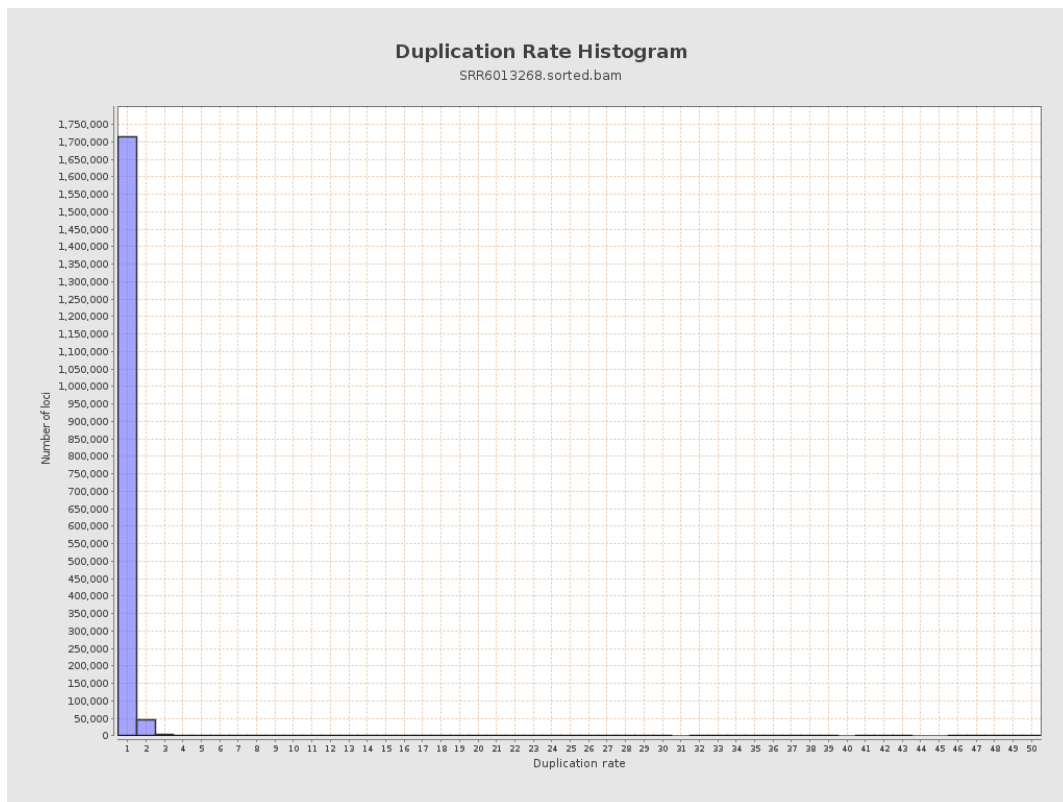
5. Results : Coverage Histogram (0-50X)



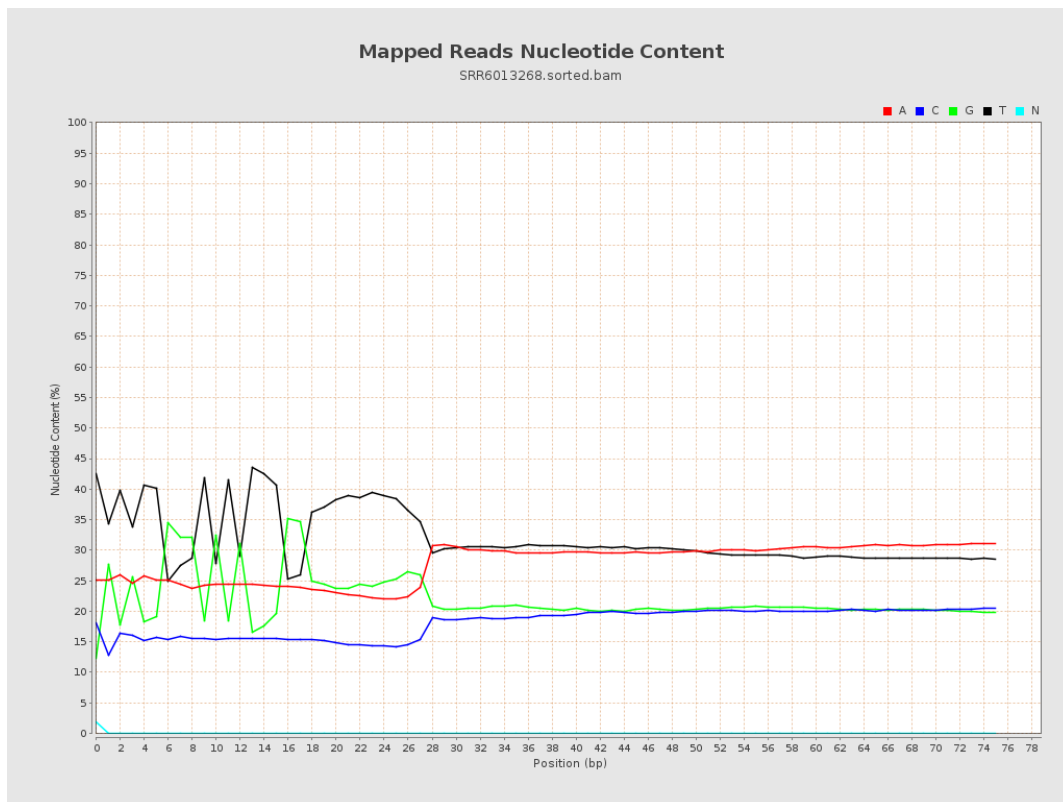
6. Results : Genome Fraction Coverage



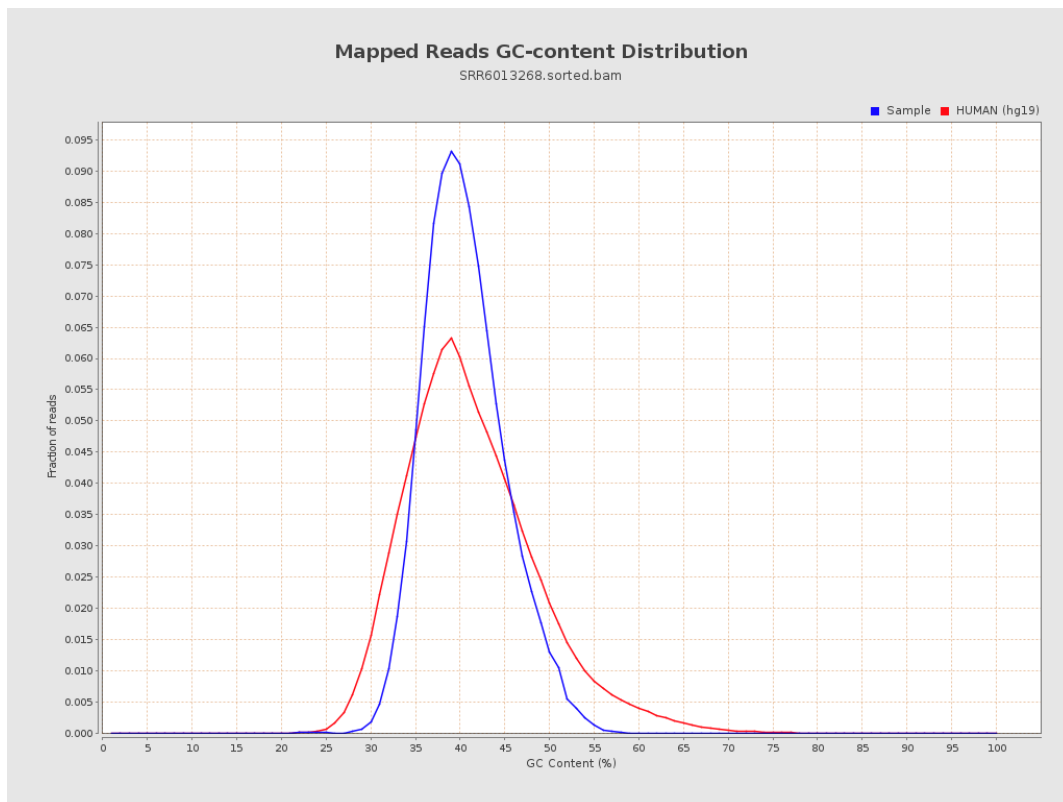
7. Results : Duplication Rate Histogram



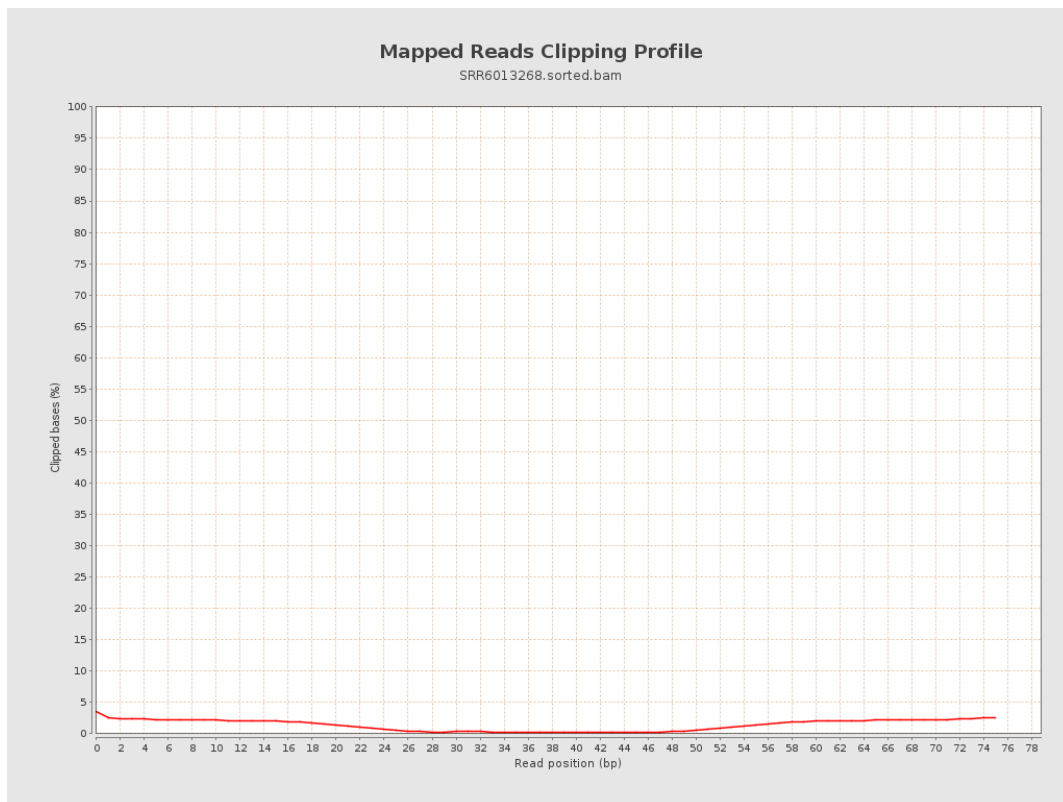
8. Results : Mapped Reads Nucleotide Content



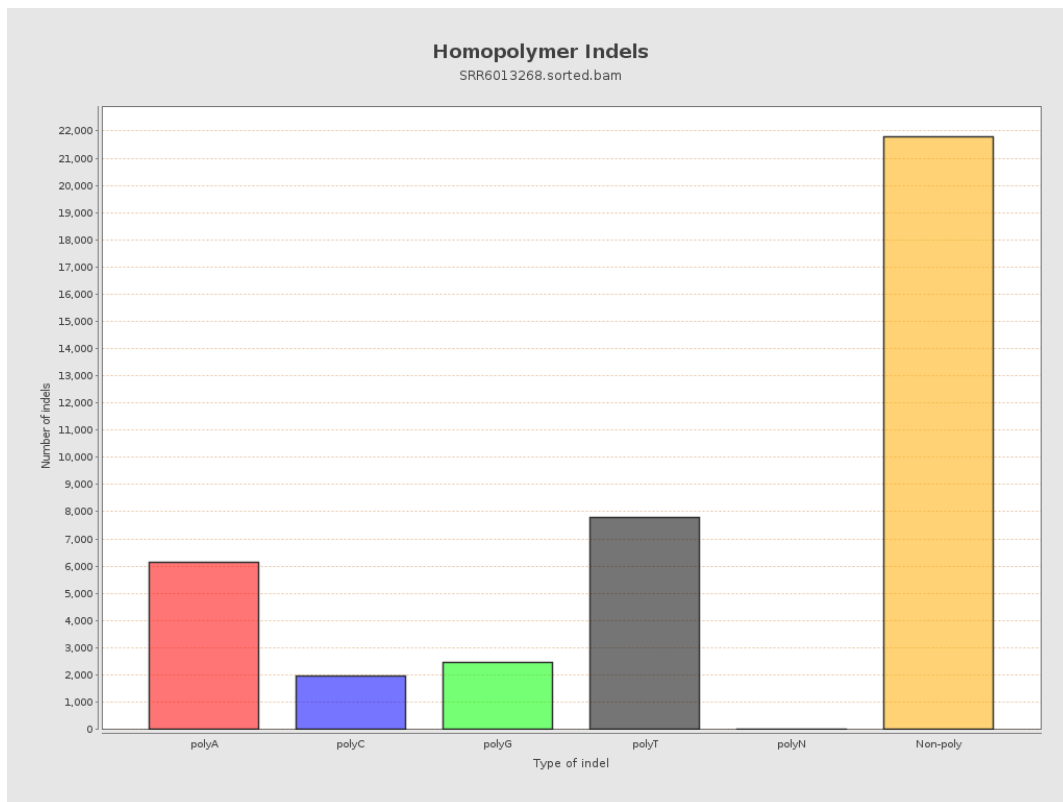
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

