

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 00:49:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083630.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_SRR3083630 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083630.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 00:49:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3083630.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,361,308
Mapped reads	1,944,482 / 82.35%
Unmapped reads	416,826 / 17.65%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,263 / 0.56%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	60,850 / 2.58%
Duplication rate	2.65%
Clipped reads	1,420,731 / 60.17%

2.2. ACGT Content

Number/percentage of A's	34,579,263 / 29.9%
Number/percentage of C's	22,733,028 / 19.66%
Number/percentage of T's	33,760,281 / 29.19%
Number/percentage of G's	24,551,512 / 21.23%
Number/percentage of N's	15,700 / 0.01%
GC Percentage	40.89%

2.3. Coverage

Mean	0.0374

Standard Deviation	0.2728
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2.4. Mapping Quality

Mean Mapping Quality	45.54
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2.5. Mismatches and indels

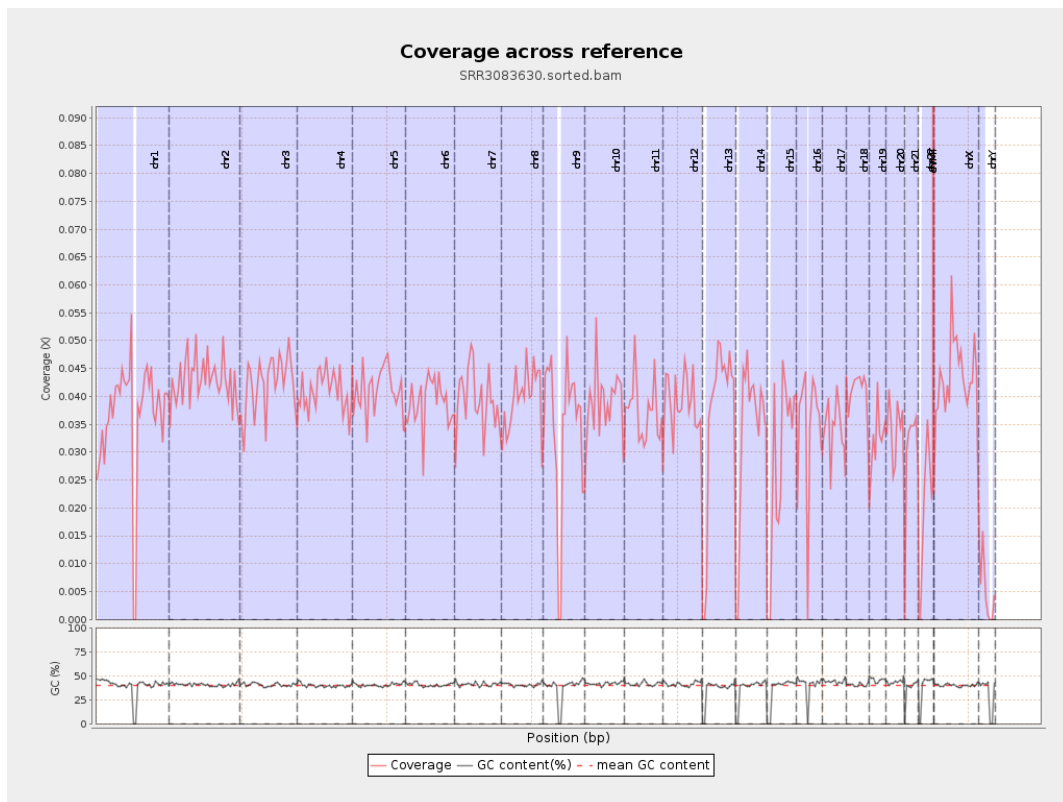
General error rate	0.84%
Mismatches	953,526
Insertions	8,077
Mapped reads with at least one insertion	0.41%
Deletions	22,375
Mapped reads with at least one deletion	1.14%
Homopolymer indels	45.24%

2.6. Chromosome stats

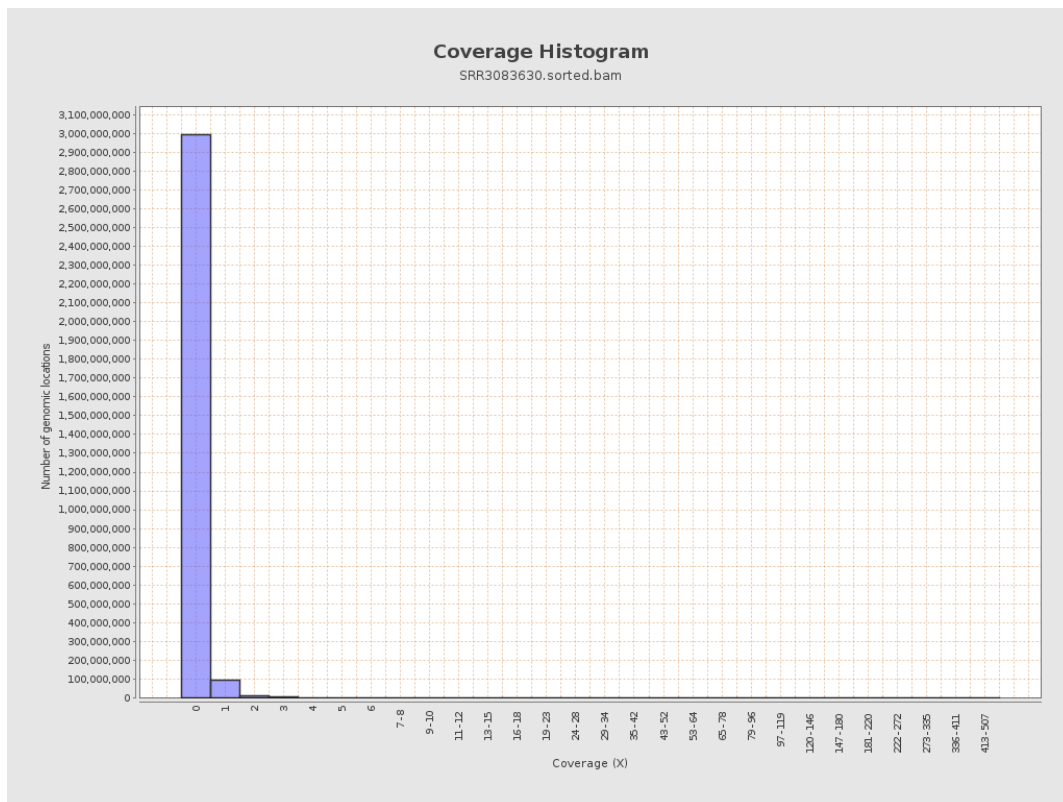
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	9128128	0.0366	0.466
chr2	243199373	10440344	0.0429	0.2688
chr3	198022430	8379304	0.0423	0.2264
chr4	191154276	7810325	0.0409	0.2287
chr5	180915260	7437606	0.0411	0.2238
chr6	171115067	6654474	0.0389	0.2257
chr7	159138663	6287447	0.0395	0.2969

chr8	146364022	5791634	0.0396	0.3486
chr9	141213431	4906230	0.0347	0.2485
chr10	135534747	5286416	0.039	0.2686
chr11	135006516	5047477	0.0374	0.2251
chr12	133851895	5184522	0.0387	0.2192
chr13	115169878	4171690	0.0362	0.2089
chr14	107349540	3623355	0.0338	0.211
chr15	102531392	2882927	0.0281	0.1853
chr16	90354753	3128758	0.0346	0.2171
chr17	81195210	2760384	0.034	0.211
chr18	78077248	3210473	0.0411	0.406
chr19	59128983	1916005	0.0324	0.3525
chr20	63025520	2138848	0.0339	0.2071
chr21	48129895	1442891	0.03	0.199
chr22	51304566	998070	0.0195	0.1528
chrMT	16571	41372	2.4967	1.9493
chrX	155270560	6710053	0.0432	0.2409
chrY	59373566	295728	0.005	0.1041

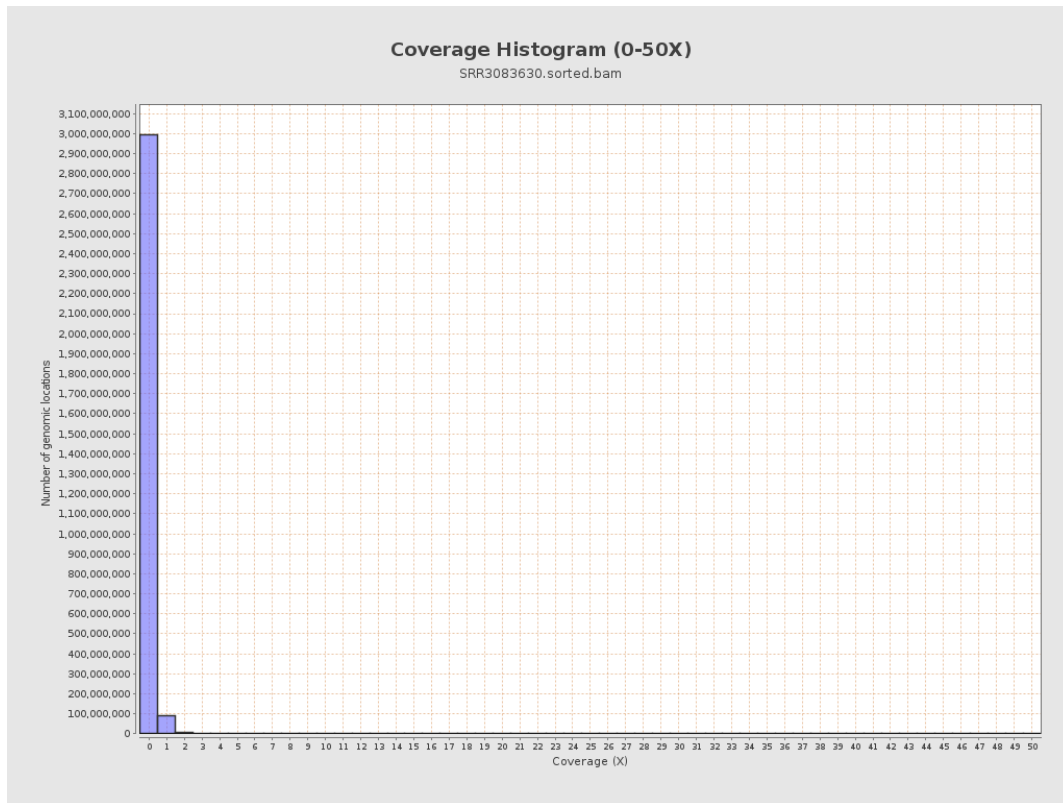
3. Results : Coverage across reference



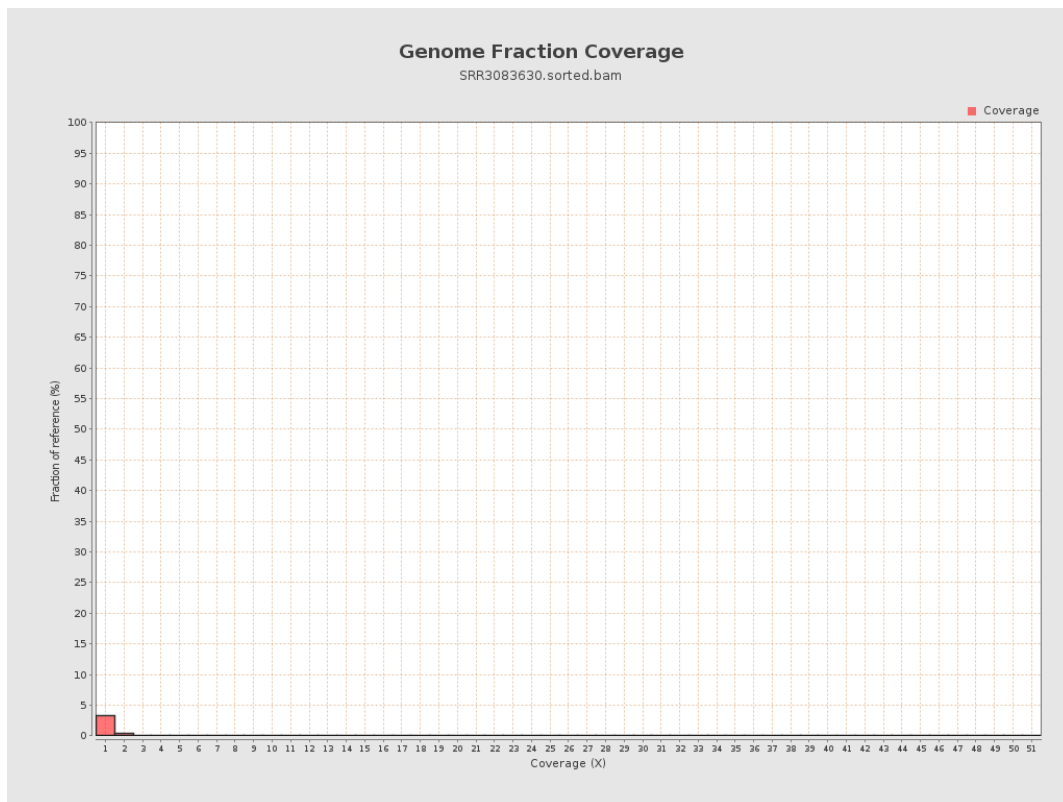
4. Results : Coverage Histogram



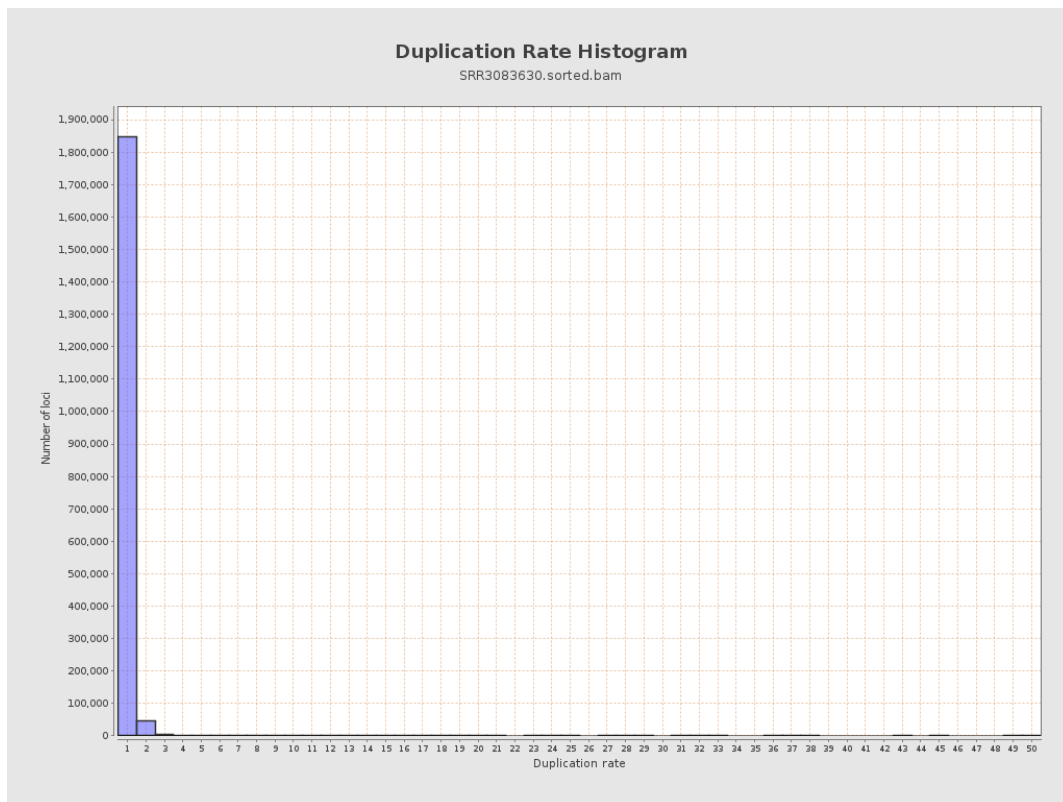
5. Results : Coverage Histogram (0-50X)



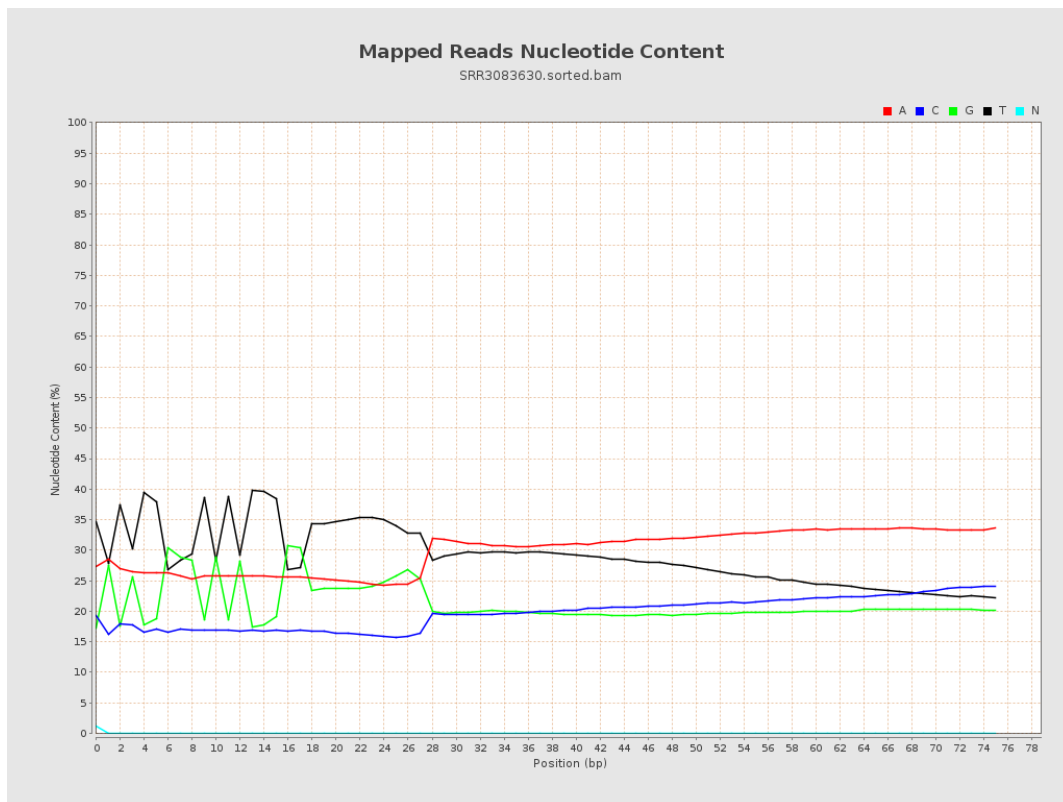
6. Results : Genome Fraction Coverage



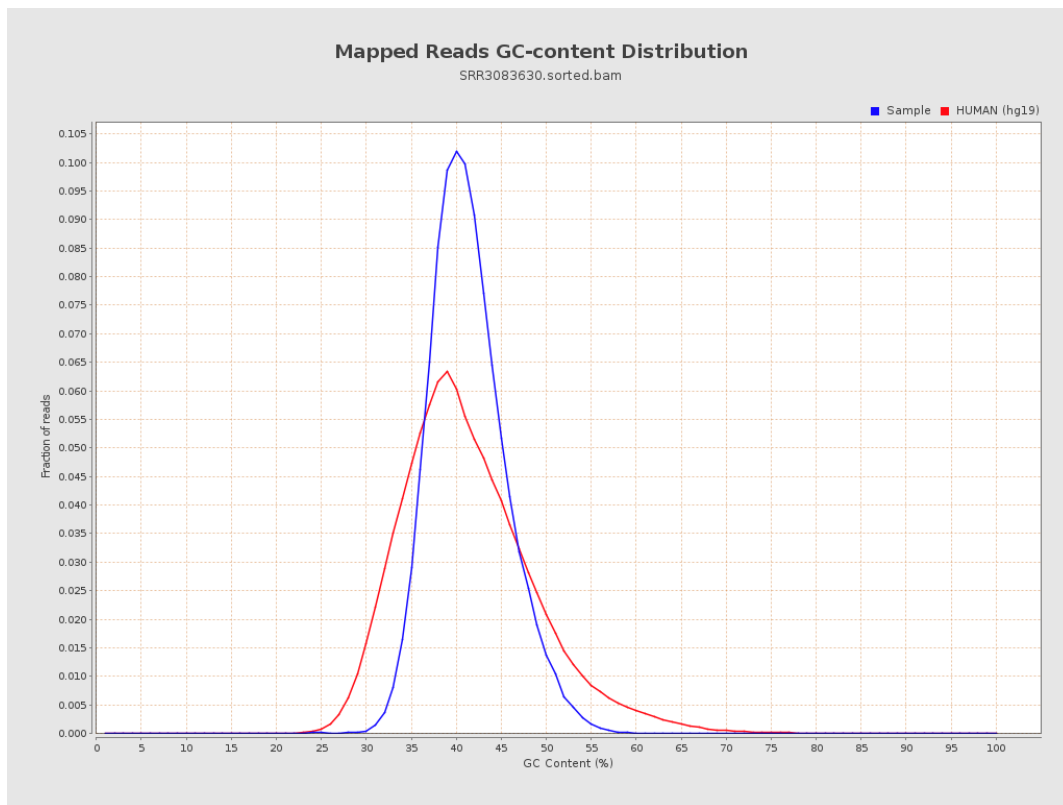
7. Results : Duplication Rate Histogram



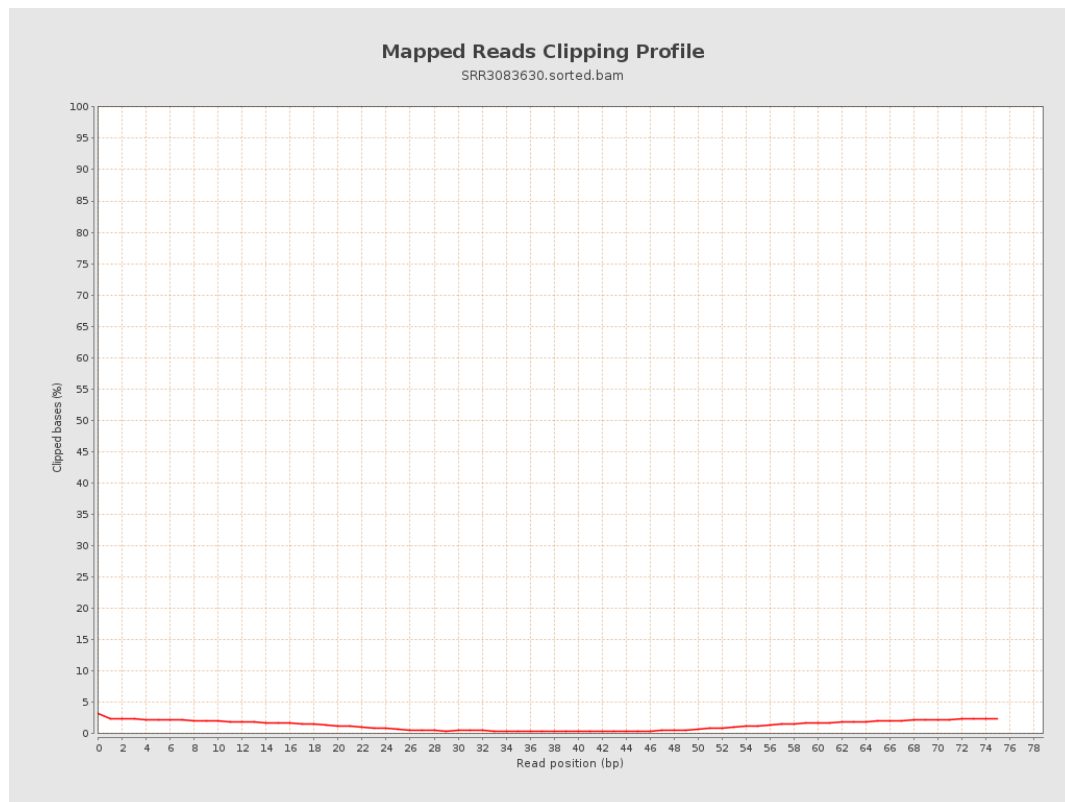
8. Results : Mapped Reads Nucleotide Content



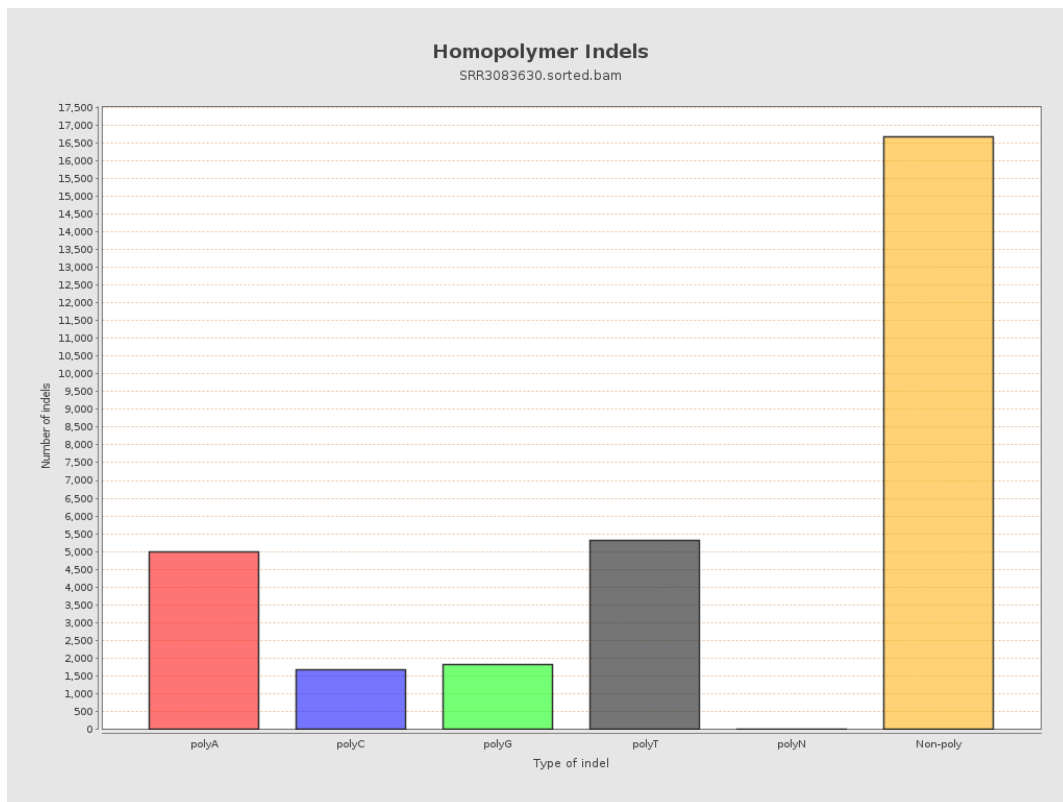
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

