

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 02:21:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6063558.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_SRR6063558 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6063558.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 02:21:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6063558.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,663,310
Mapped reads	3,146,888 / 85.9%
Unmapped reads	516,422 / 14.1%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	30,718 / 0.84%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	251,661 / 6.87%
Duplication rate	6.31%
Clipped reads	1,782,253 / 48.65%

2.2. ACGT Content

Number/percentage of A's	54,238,133 / 26.91%
Number/percentage of C's	36,608,576 / 18.16%
Number/percentage of T's	64,418,008 / 31.96%
Number/percentage of G's	46,274,037 / 22.96%
Number/percentage of N's	4,953 / 0%
GC Percentage	41.12%

2.3. Coverage

Mean	0.0651

Standard Deviation	0.6251
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2.4. Mapping Quality

Mean Mapping Quality	45.16
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2.5. Mismatches and indels

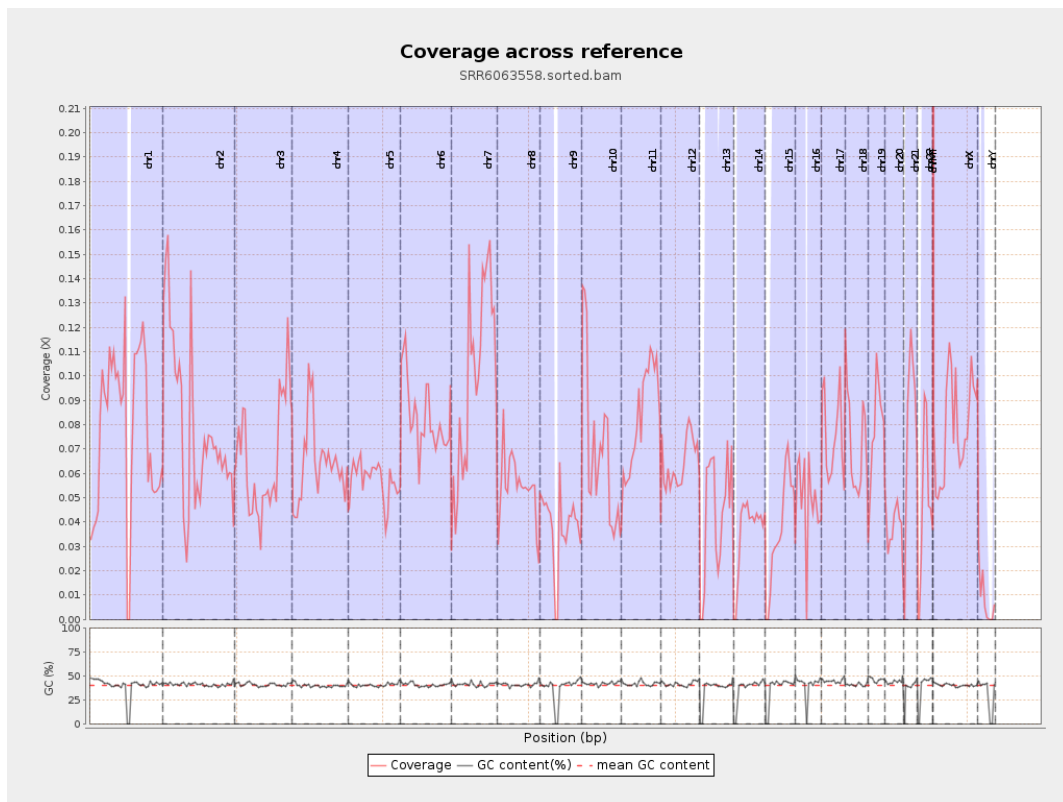
General error rate	0.86%
Mismatches	1,707,391
Insertions	14,835
Mapped reads with at least one insertion	0.47%
Deletions	55,943
Mapped reads with at least one deletion	1.76%
Homopolymer indels	45.87%

2.6. Chromosome stats

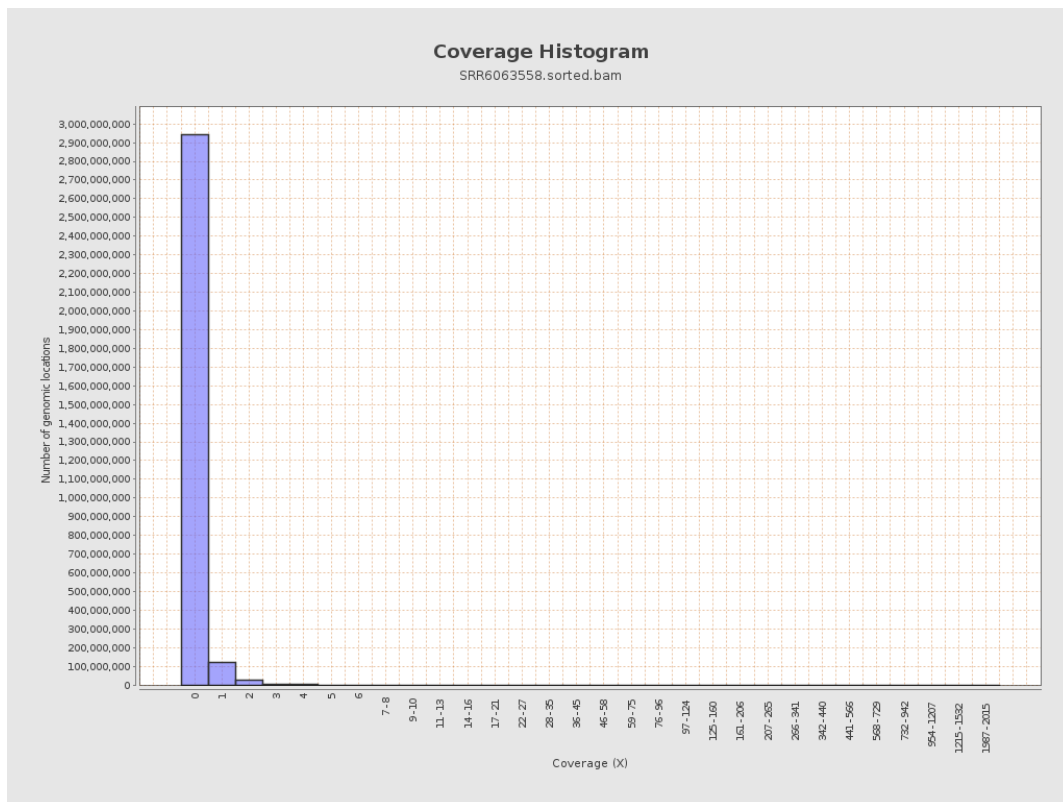
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	19391755	0.0778	1.1661
chr2	243199373	19334591	0.0795	0.9776
chr3	198022430	13045203	0.0659	0.3249
chr4	191154276	12311305	0.0644	0.3498
chr5	180915260	10321787	0.0571	0.3039
chr6	171115067	14263021	0.0834	0.4474
chr7	159138663	15760606	0.099	1.0071

chr8	146364022	7941768	0.0543	0.745
chr9	141213431	5355022	0.0379	0.4674
chr10	135534747	9327779	0.0688	0.4296
chr11	135006516	11188507	0.0829	0.5452
chr12	133851895	8662258	0.0647	0.344
chr13	115169878	4956643	0.043	0.2763
chr14	107349540	3902182	0.0364	0.3143
chr15	102531392	3758801	0.0367	0.2647
chr16	90354753	4347234	0.0481	0.3118
chr17	81195210	6205208	0.0764	0.4034
chr18	78077248	5614613	0.0719	0.8075
chr19	59128983	4660731	0.0788	0.8393
chr20	63025520	2392984	0.038	0.2726
chr21	48129895	3768500	0.0783	0.374
chr22	51304566	2392536	0.0466	0.2682
chrMT	16571	52371	3.1604	2.7169
chrX	155270560	12201553	0.0786	0.4354
chrY	59373566	476325	0.008	0.1613

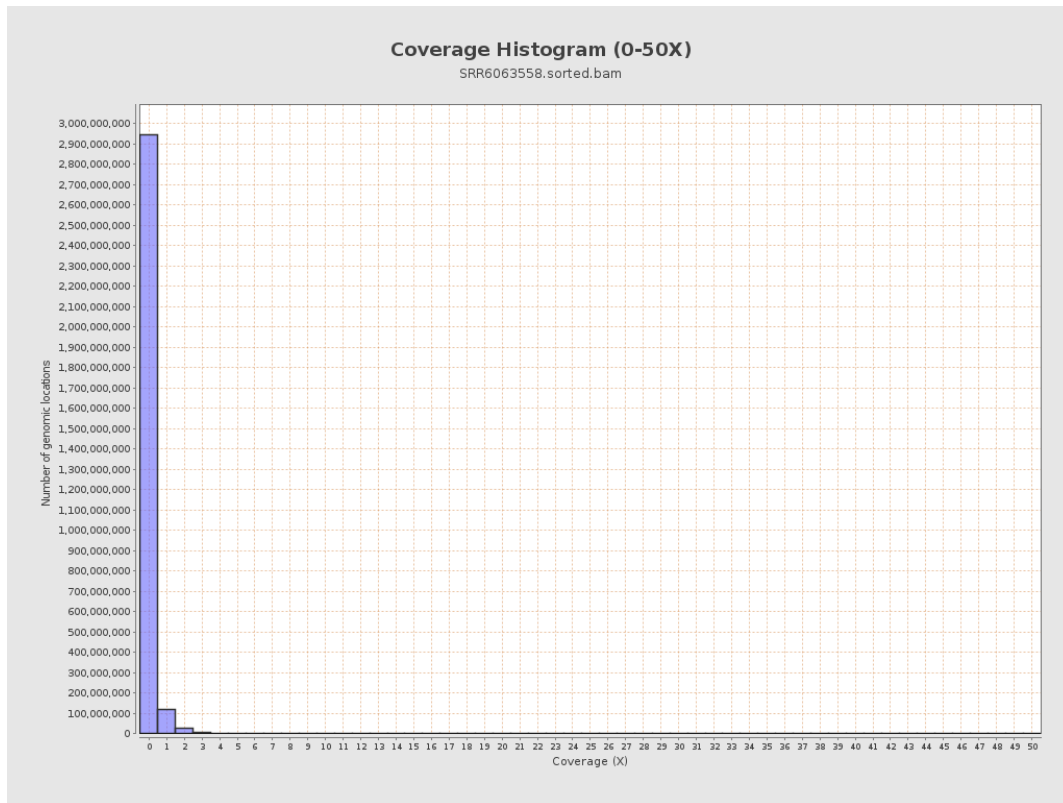
3. Results : Coverage across reference



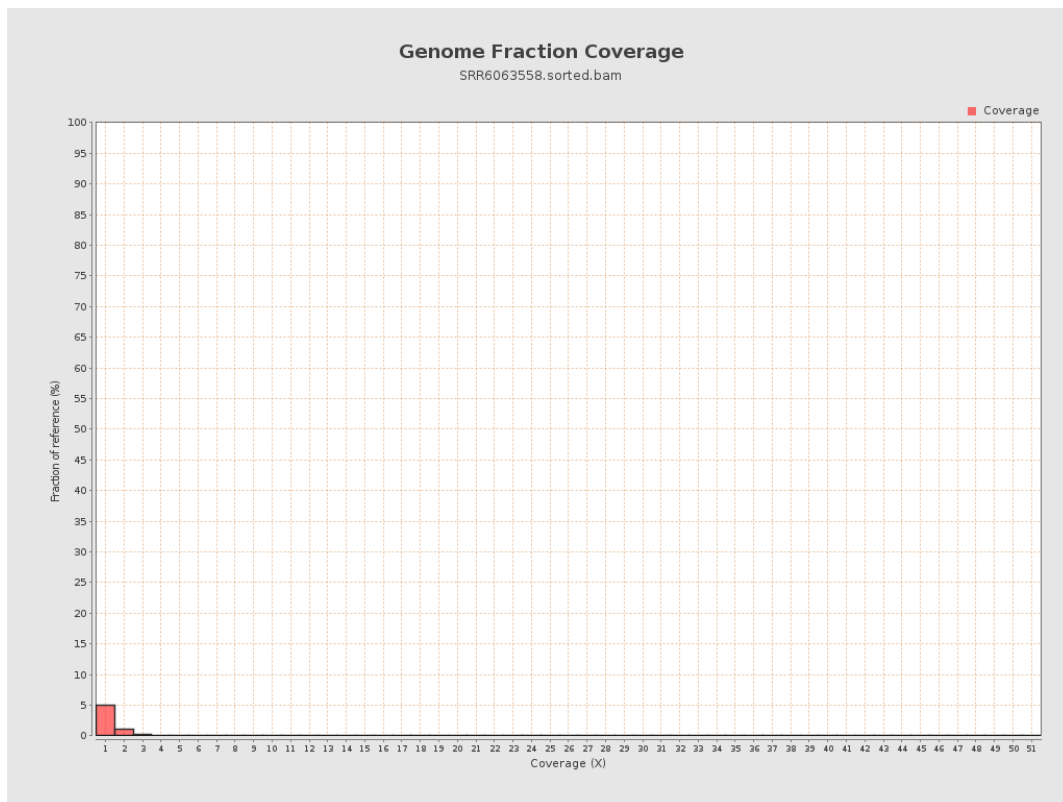
4. Results : Coverage Histogram



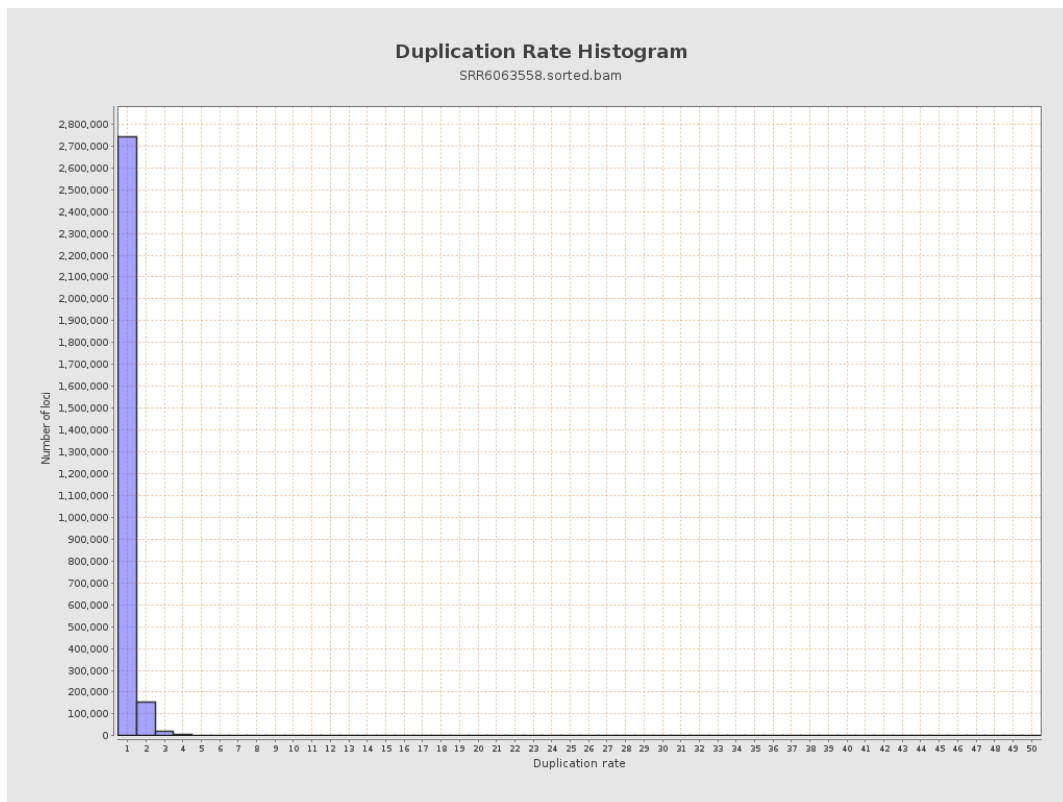
5. Results : Coverage Histogram (0-50X)



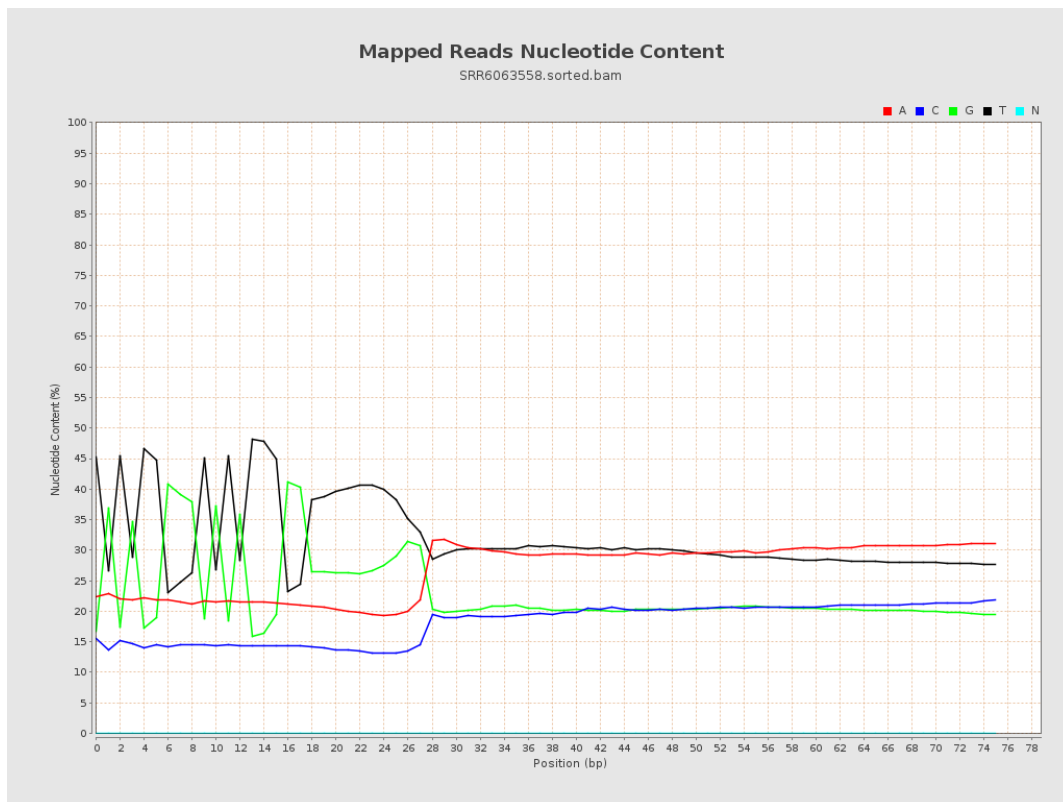
6. Results : Genome Fraction Coverage



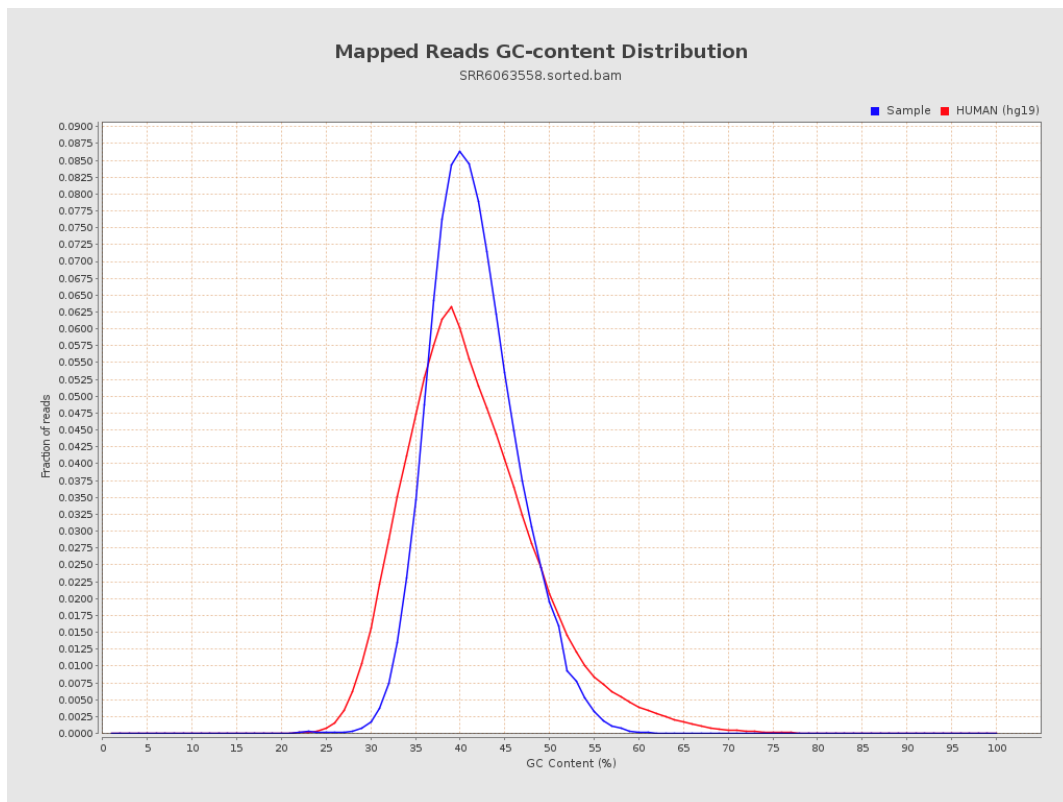
7. Results : Duplication Rate Histogram



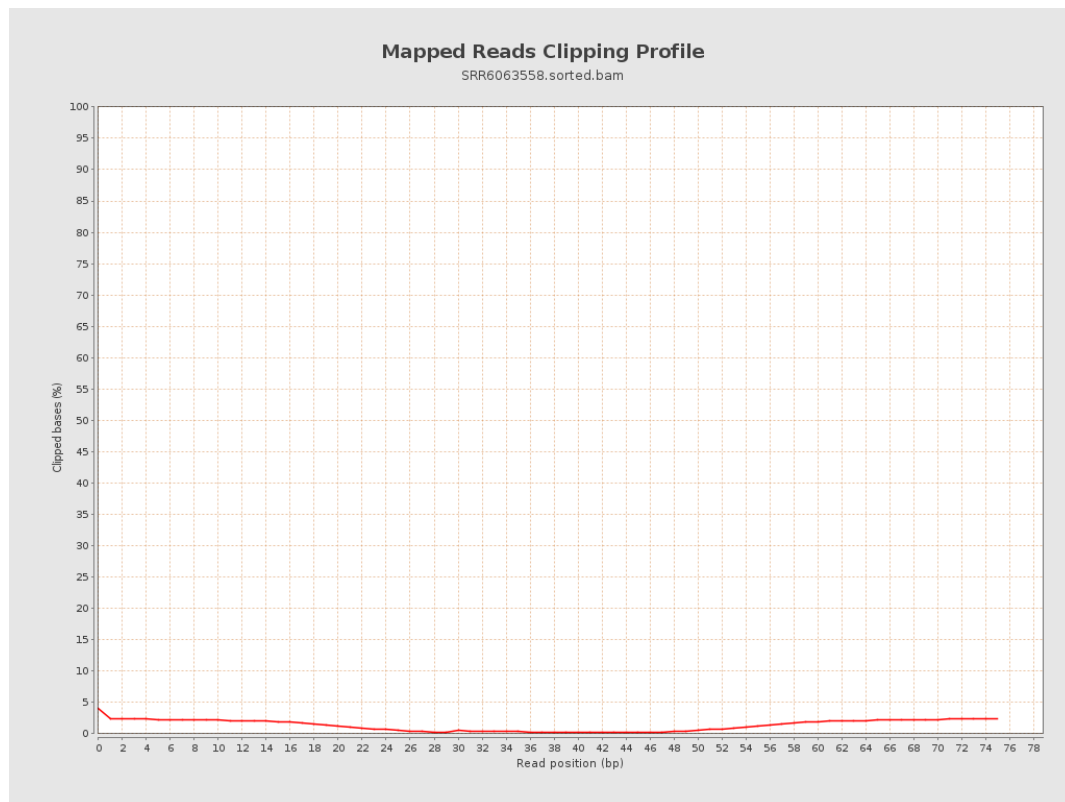
8. Results : Mapped Reads Nucleotide Content



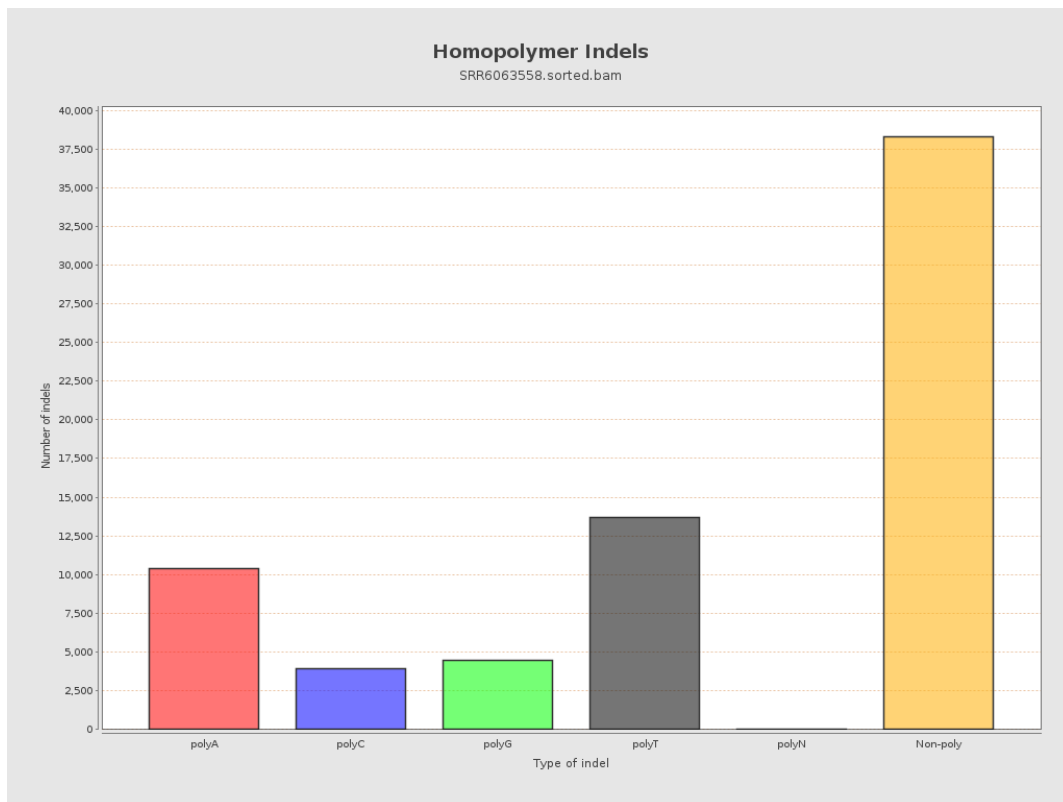
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

