

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 21:42:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238601.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_SRR6238601 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238601.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 21:42:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238601.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,147,366
Mapped reads	2,745,609 / 87.24%
Unmapped reads	401,757 / 12.76%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,444 / 0.71%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	908,977 / 28.88%
Duplication rate	20.51%
Clipped reads	1,826,897 / 58.05%

2.2. ACGT Content

Number/percentage of A's	40,914,052 / 24.46%
Number/percentage of C's	29,544,010 / 17.66%
Number/percentage of T's	56,171,748 / 33.58%
Number/percentage of G's	40,630,956 / 24.29%
Number/percentage of N's	7,656 / 0%
GC Percentage	41.95%

2.3. Coverage

Mean	0.0541

Standard Deviation	0.966
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2.4. Mapping Quality

Mean Mapping Quality	39.88
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2.5. Mismatches and indels

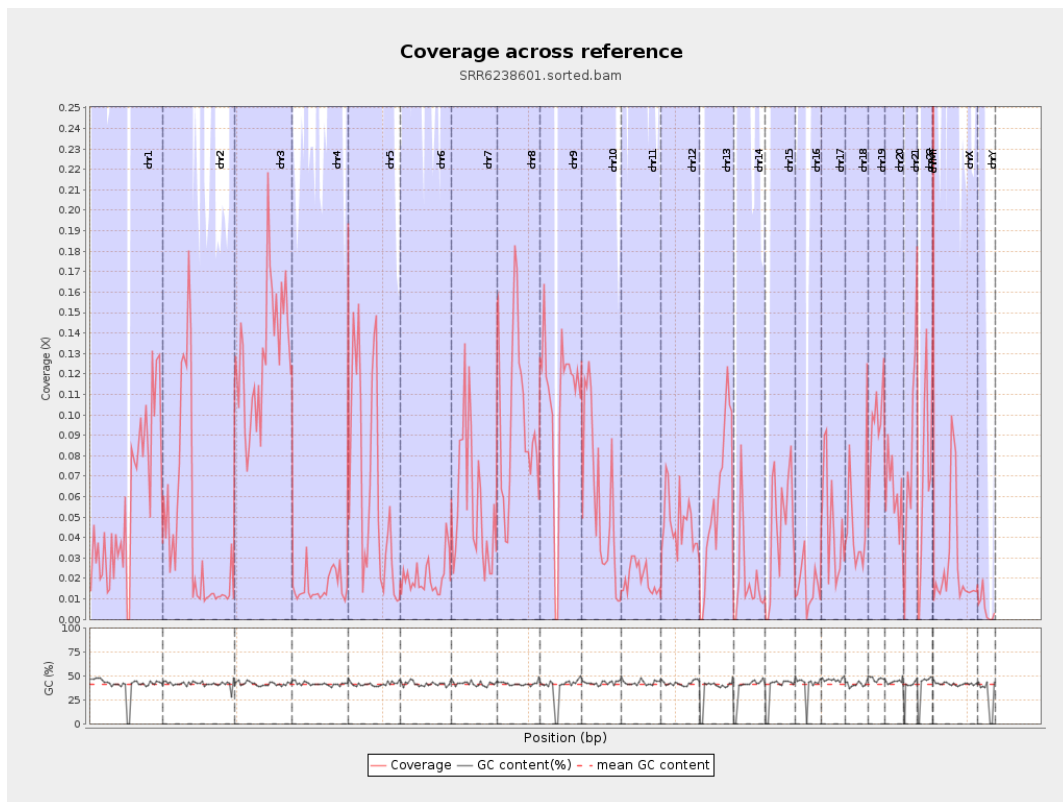
General error rate	0.67%
Mismatches	1,104,950
Insertions	11,680
Mapped reads with at least one insertion	0.42%
Deletions	52,299
Mapped reads with at least one deletion	1.89%
Homopolymer indels	40.61%

2.6. Chromosome stats

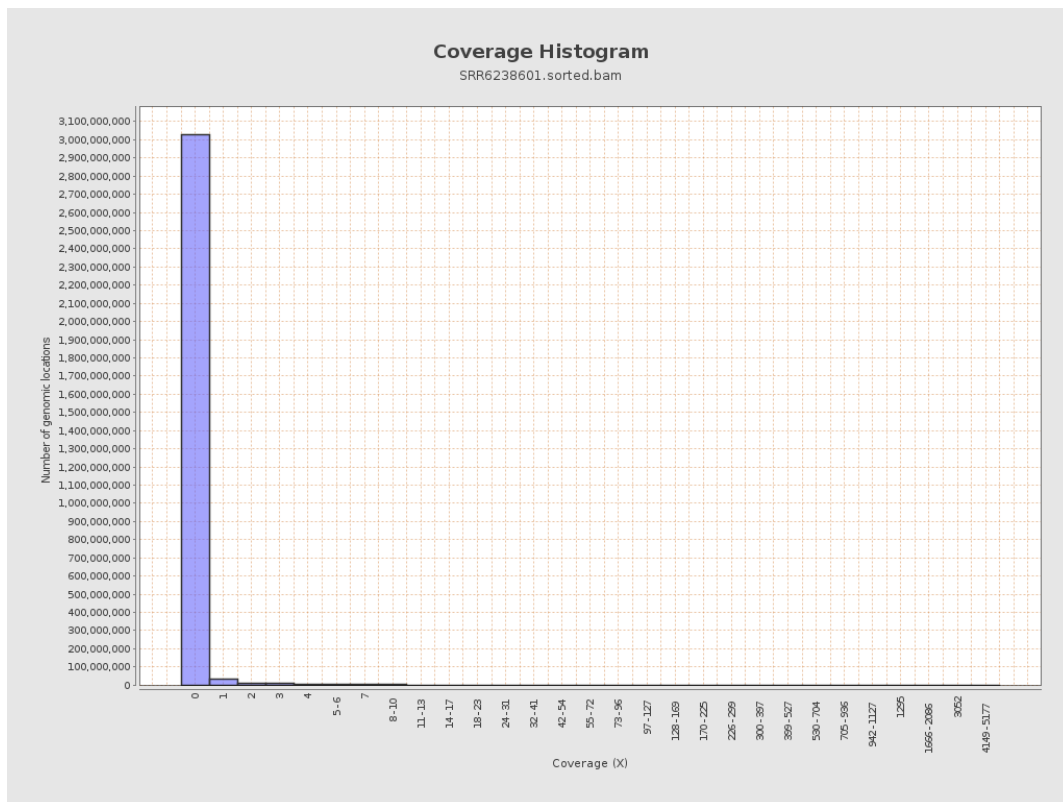
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	13841648	0.0555	1.033
chr2	243199373	10316269	0.0424	2.3068
chr3	198022430	25721949	0.1299	0.8074
chr4	191154276	3074085	0.0161	0.2611
chr5	180915260	11757946	0.065	0.56
chr6	171115067	3543842	0.0207	0.7399
chr7	159138663	8994155	0.0565	1.081

chr8	146364022	13964587	0.0954	0.7745
chr9	141213431	15089214	0.1069	0.8923
chr10	135534747	7888859	0.0582	0.5928
chr11	135006516	2687418	0.0199	0.3817
chr12	133851895	6323683	0.0472	0.5042
chr13	115169878	6765188	0.0587	0.6725
chr14	107349540	2123624	0.0198	0.3678
chr15	102531392	4631216	0.0452	0.5965
chr16	90354753	1411004	0.0156	0.4074
chr17	81195210	3796829	0.0468	0.4949
chr18	78077248	3679715	0.0471	1.8687
chr19	59128983	5654665	0.0956	0.8386
chr20	63025520	3950335	0.0627	0.5858
chr21	48129895	4026977	0.0837	0.6632
chr22	51304566	3495768	0.0681	0.5892
chrMT	16571	29877	1.803	4.3256
chrX	155270560	4249477	0.0274	0.4018
chrY	59373566	338094	0.0057	0.3461

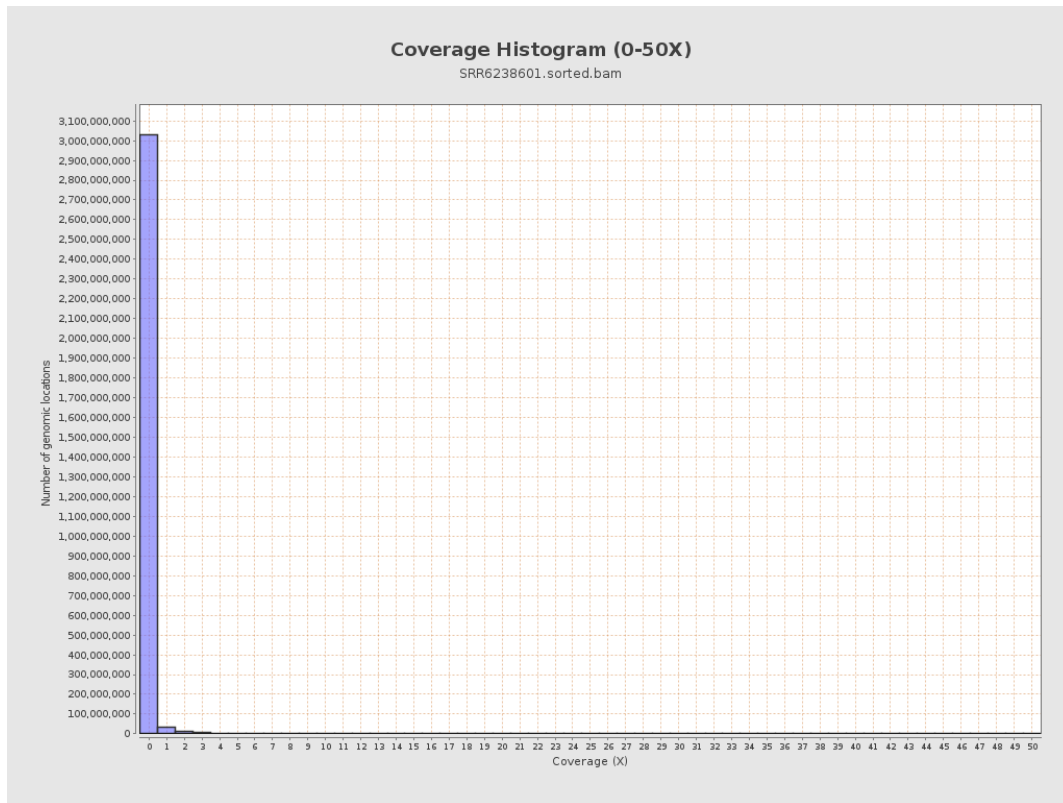
3. Results : Coverage across reference



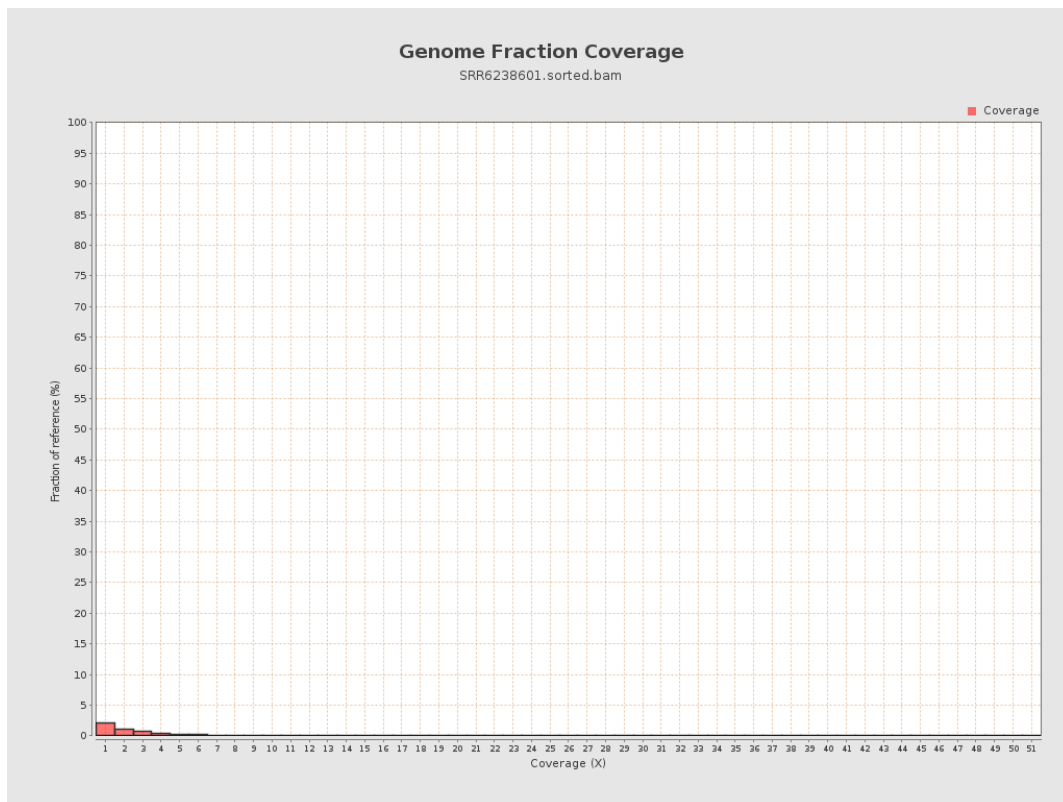
4. Results : Coverage Histogram



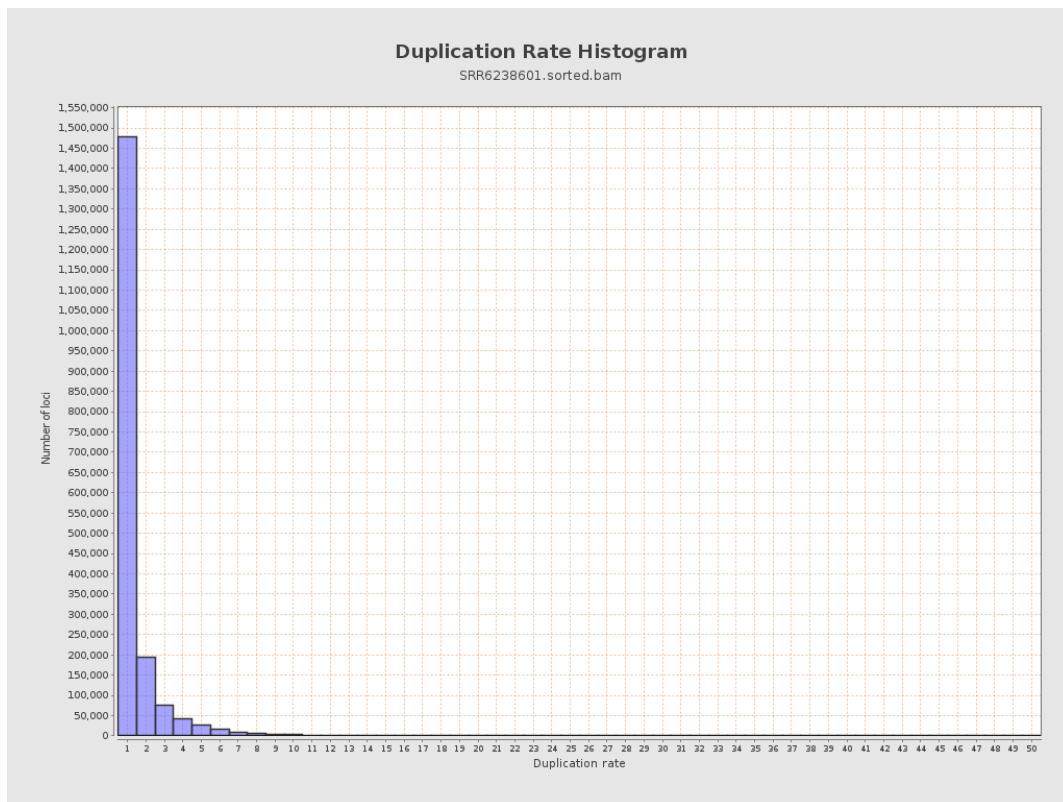
5. Results : Coverage Histogram (0-50X)



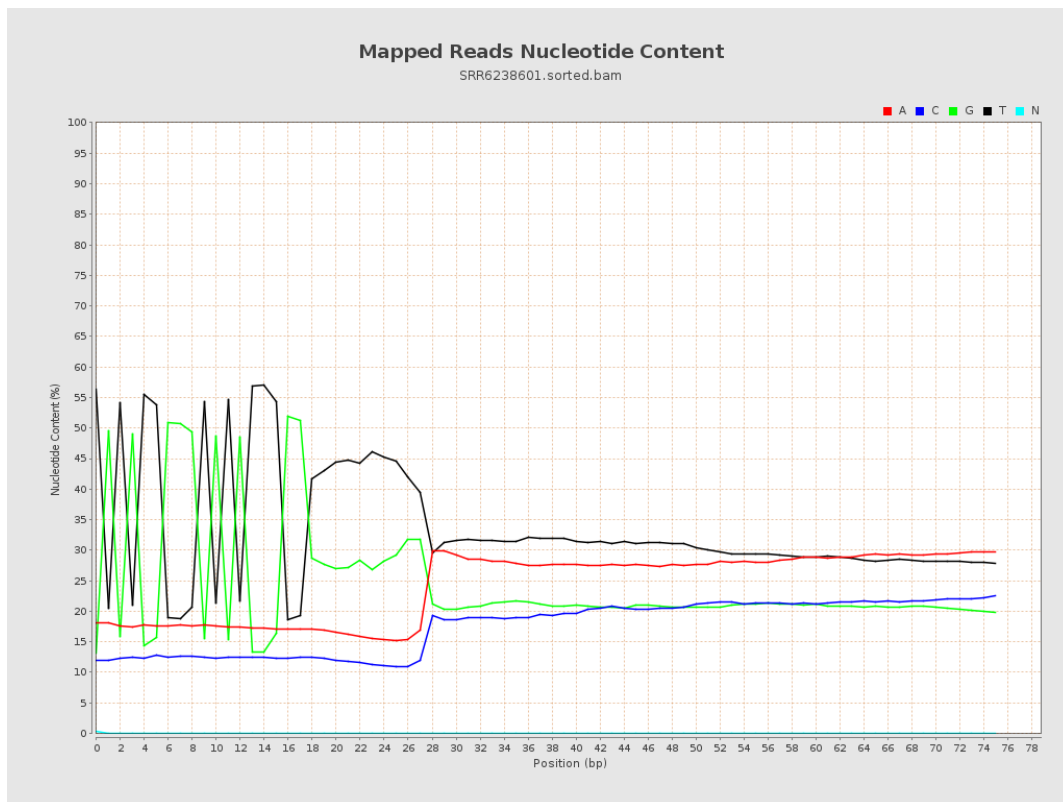
6. Results : Genome Fraction Coverage



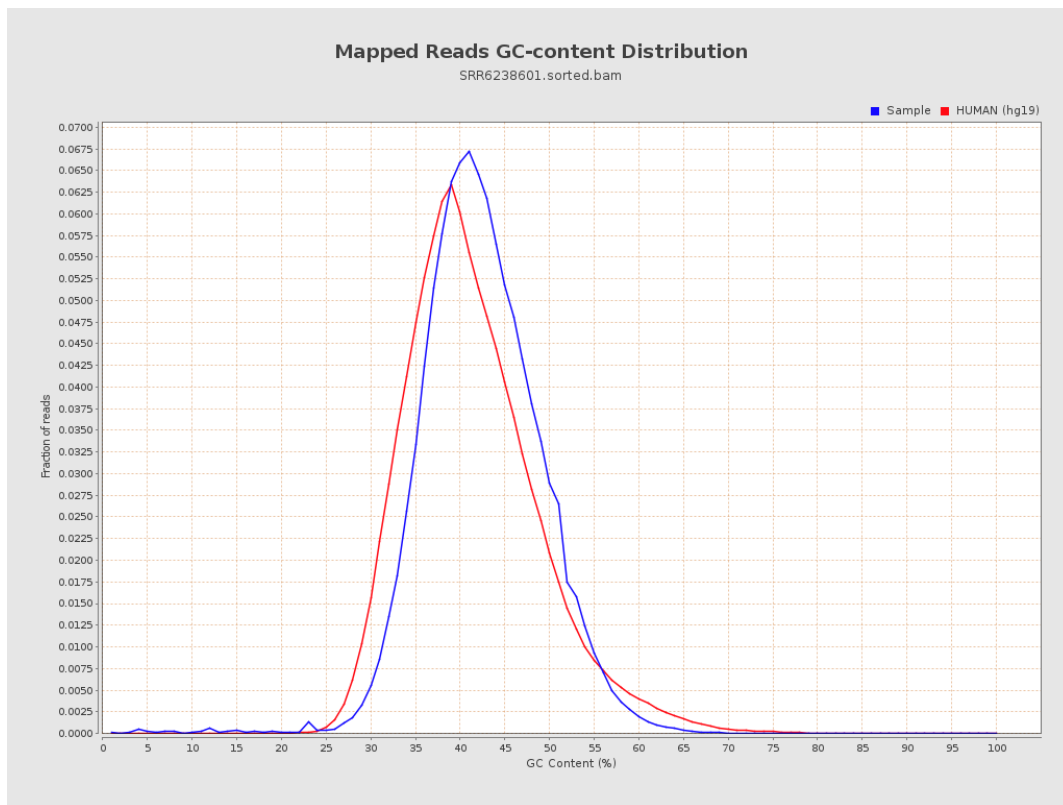
7. Results : Duplication Rate Histogram



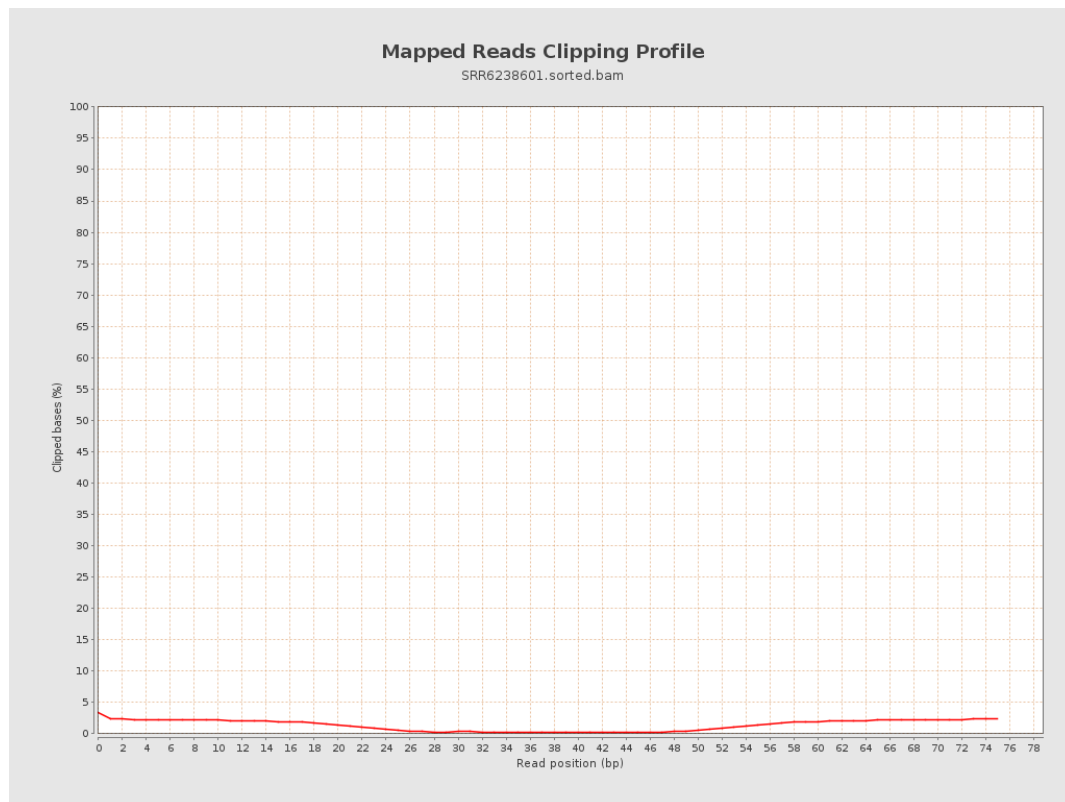
8. Results : Mapped Reads Nucleotide Content



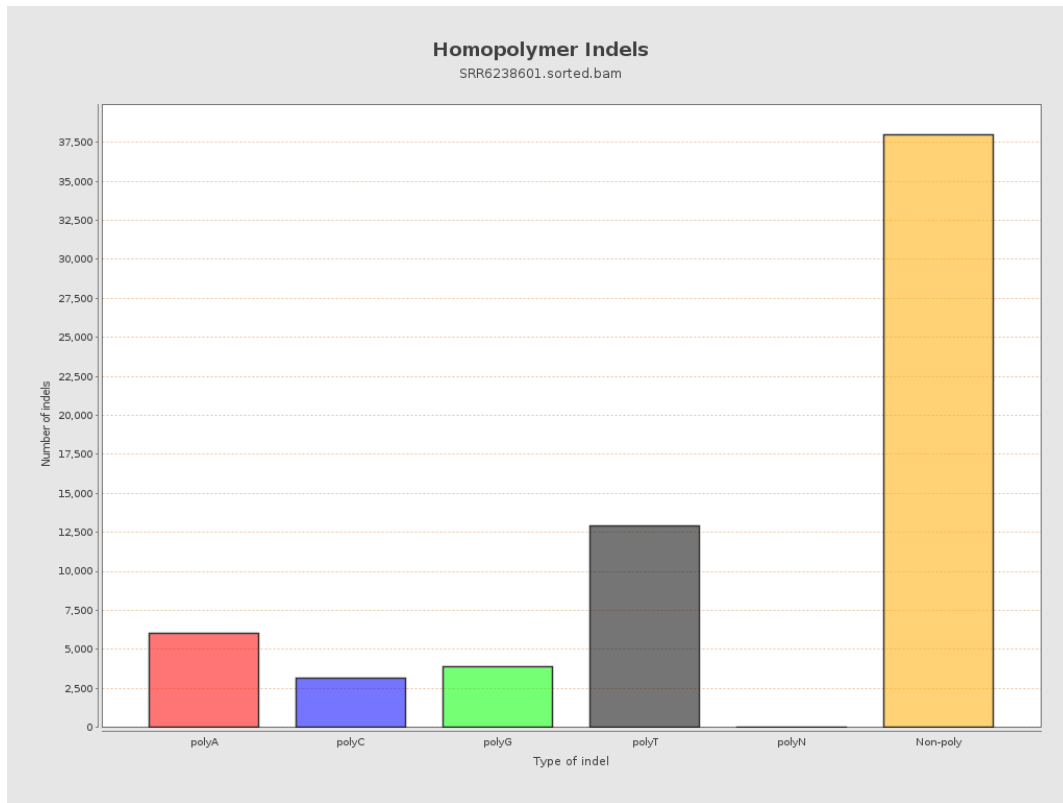
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

