

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 14:25:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238282.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_SRR6238282 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238282.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 14:25:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238282.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,120,761
Mapped reads	1,808,903 / 85.29%
Unmapped reads	311,858 / 14.71%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,249 / 1.1%
Read min/max/mean length	30 / 76 / 76.38
Duplicated reads (estimated)	81,671 / 3.85%
Duplication rate	3.51%
Clipped reads	903,877 / 42.62%

2.2. ACGT Content

Number/percentage of A's	33,078,532 / 27.85%
Number/percentage of C's	22,991,468 / 19.35%
Number/percentage of T's	36,308,844 / 30.56%
Number/percentage of G's	26,387,582 / 22.21%
Number/percentage of N's	26,353 / 0.02%
GC Percentage	41.57%

2.3. Coverage

Mean	0.0384

Standard Deviation	0.3374
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2.4. Mapping Quality

Mean Mapping Quality	44.17
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2.5. Mismatches and indels

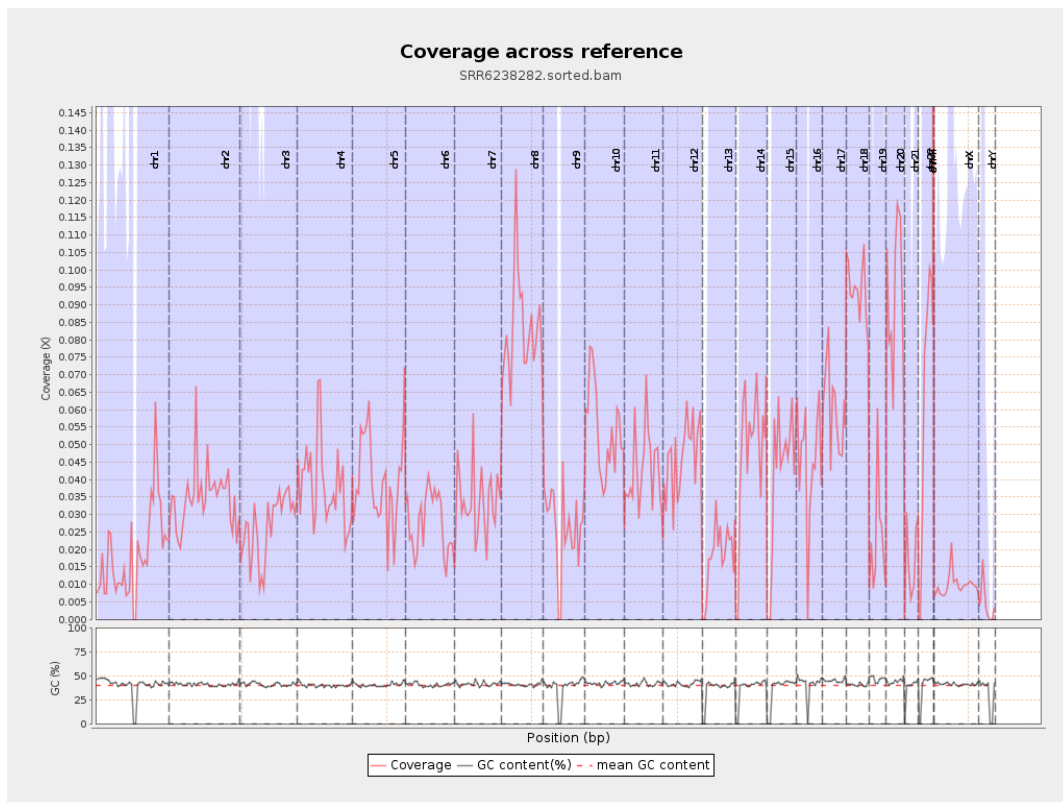
General error rate	0.88%
Mismatches	1,031,660
Insertions	9,162
Mapped reads with at least one insertion	0.5%
Deletions	37,034
Mapped reads with at least one deletion	2.02%
Homopolymer indels	45.11%

2.6. Chromosome stats

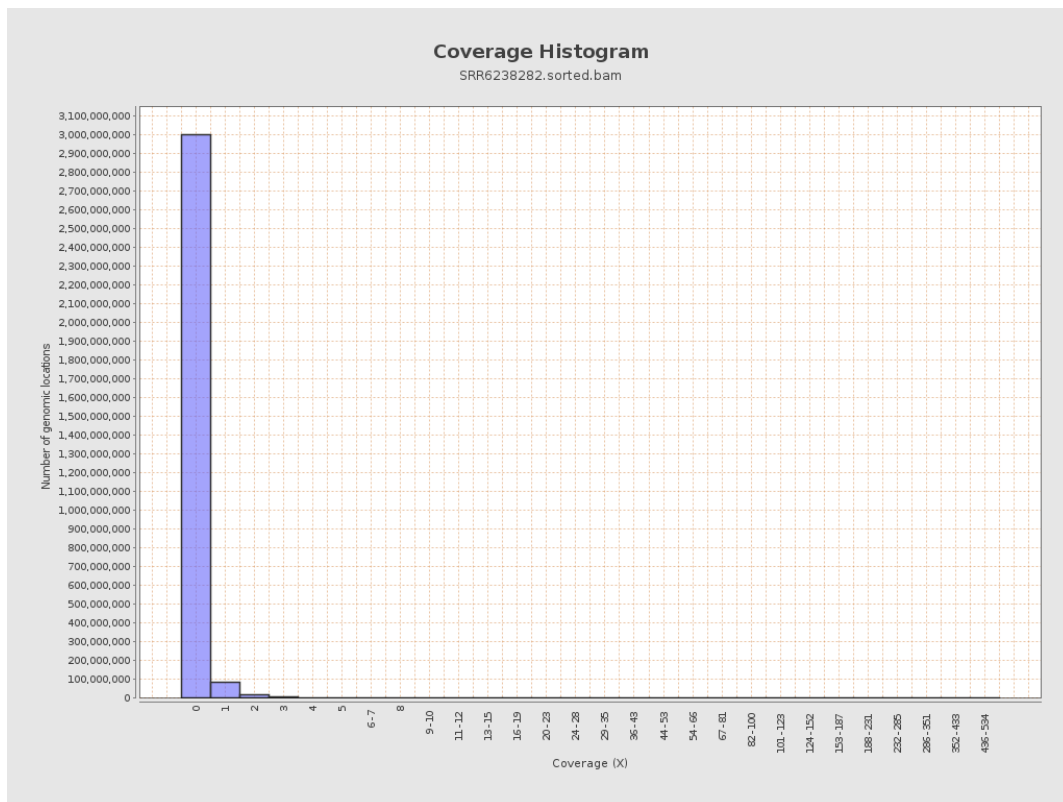
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	4672389	0.0187	0.3681
chr2	243199373	8423284	0.0346	0.4549
chr3	198022430	5236533	0.0264	0.1893
chr4	191154276	7346230	0.0384	0.2378
chr5	180915260	7140576	0.0395	0.2375
chr6	171115067	4724886	0.0276	0.2442
chr7	159138663	5403780	0.034	0.4658

chr8	146364022	12239723	0.0836	0.5603
chr9	141213431	3641362	0.0258	0.3333
chr10	135534747	7368570	0.0544	0.346
chr11	135006516	5790212	0.0429	0.3009
chr12	133851895	6186132	0.0462	0.2561
chr13	115169878	2071127	0.018	0.1561
chr14	107349540	5028937	0.0468	0.2731
chr15	102531392	4264200	0.0416	0.2397
chr16	90354753	4042845	0.0447	0.2729
chr17	81195210	4872577	0.06	0.3598
chr18	78077248	7370884	0.0944	0.6614
chr19	59128983	1390919	0.0235	0.3579
chr20	63025520	5820530	0.0924	0.3638
chr21	48129895	816700	0.017	0.1751
chr22	51304566	3207175	0.0625	0.2965
chrMT	16571	11364	0.6858	0.963
chrX	155270560	1531974	0.0099	0.1672
chrY	59373566	251441	0.0042	0.126

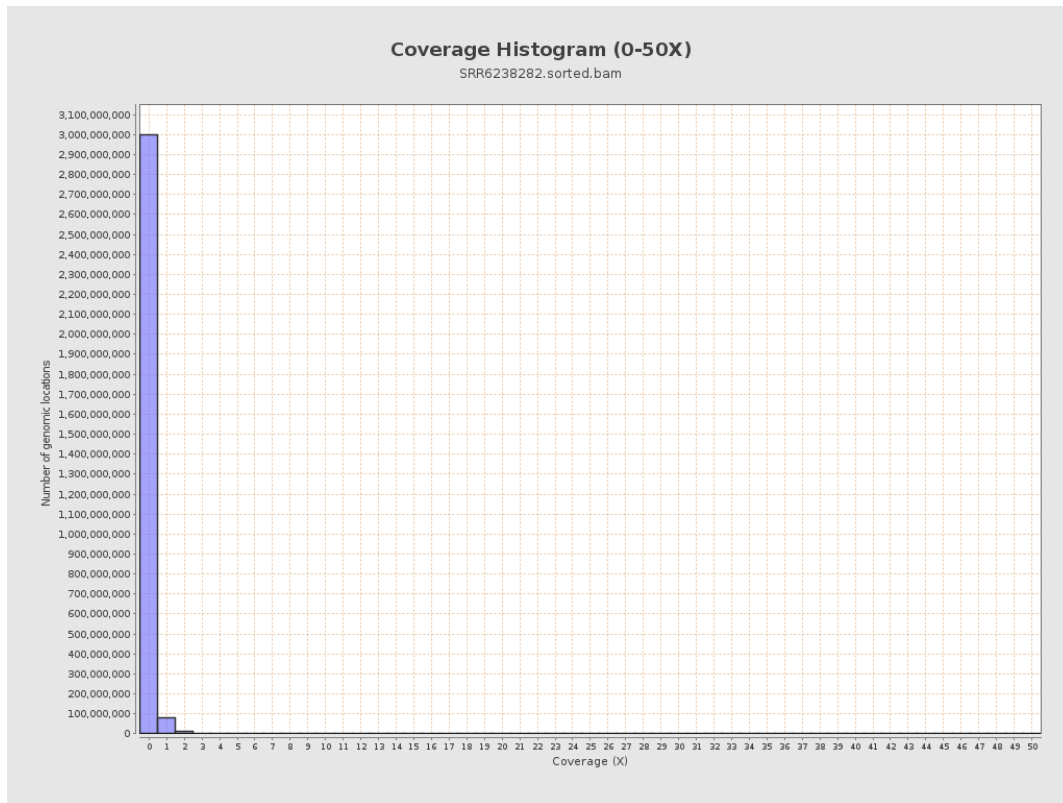
3. Results : Coverage across reference



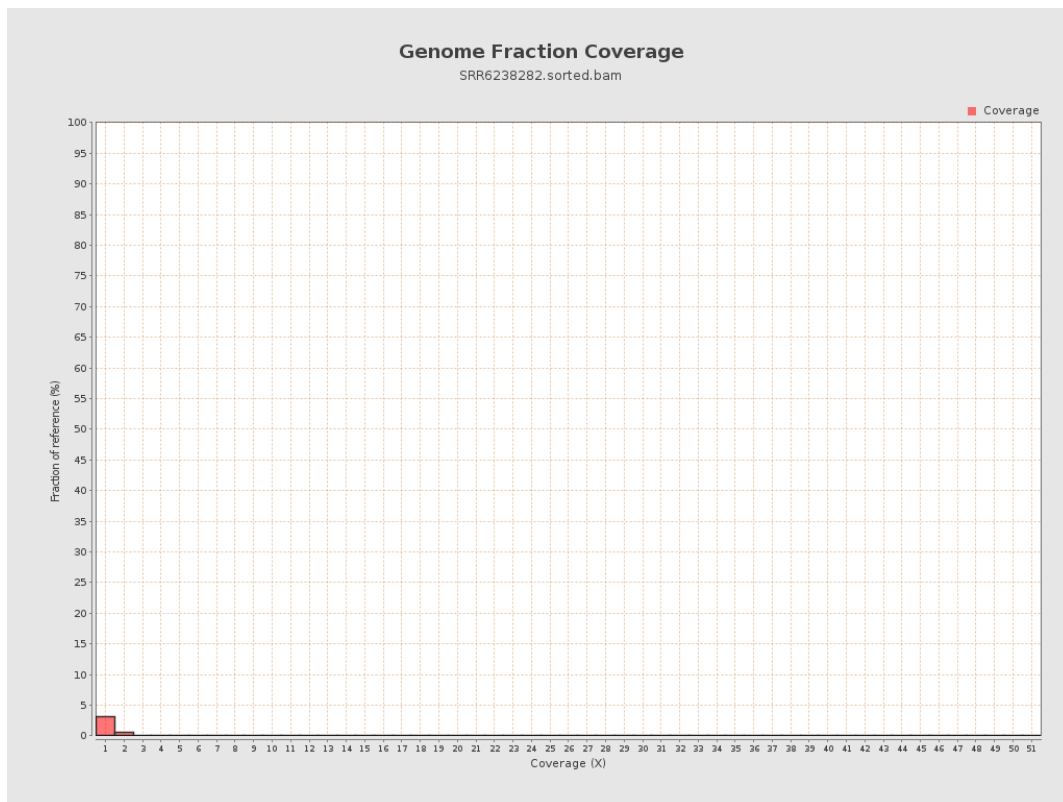
4. Results : Coverage Histogram



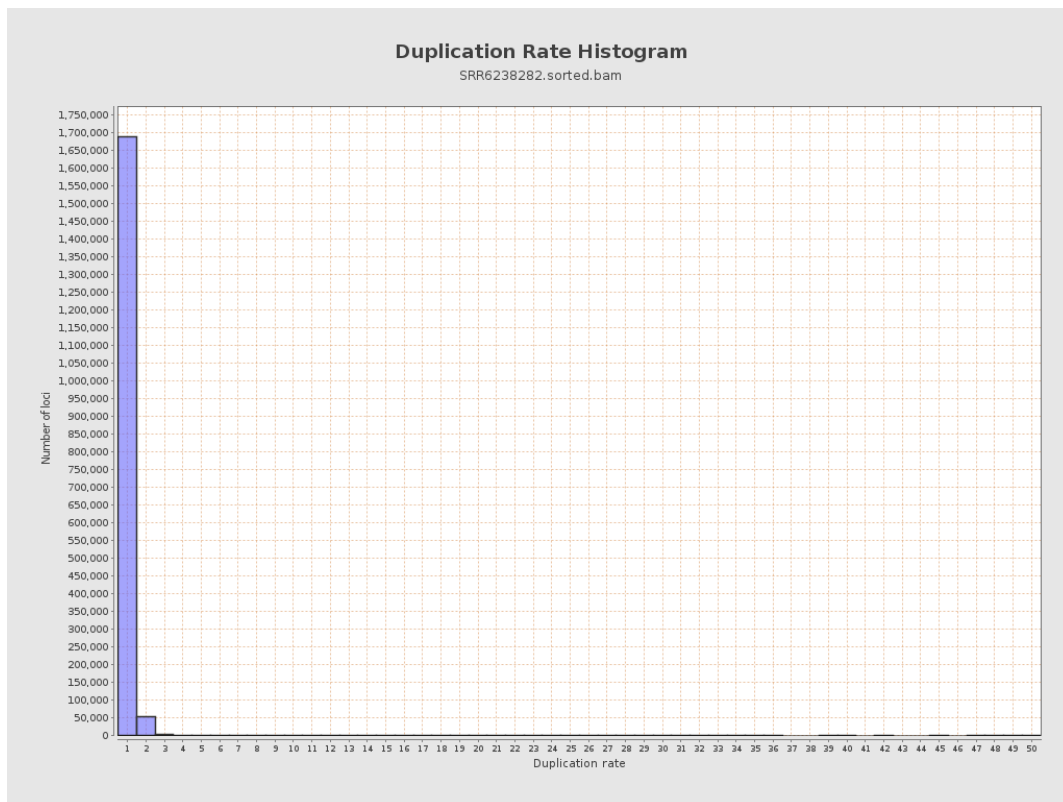
5. Results : Coverage Histogram (0-50X)



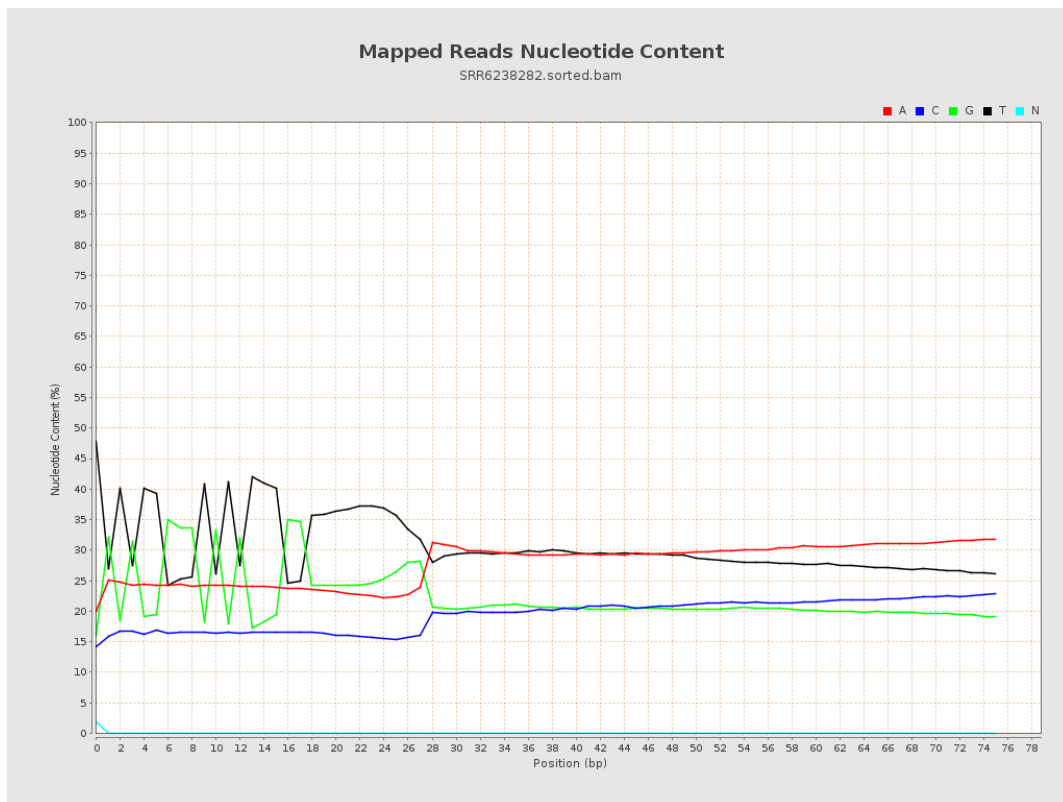
6. Results : Genome Fraction Coverage



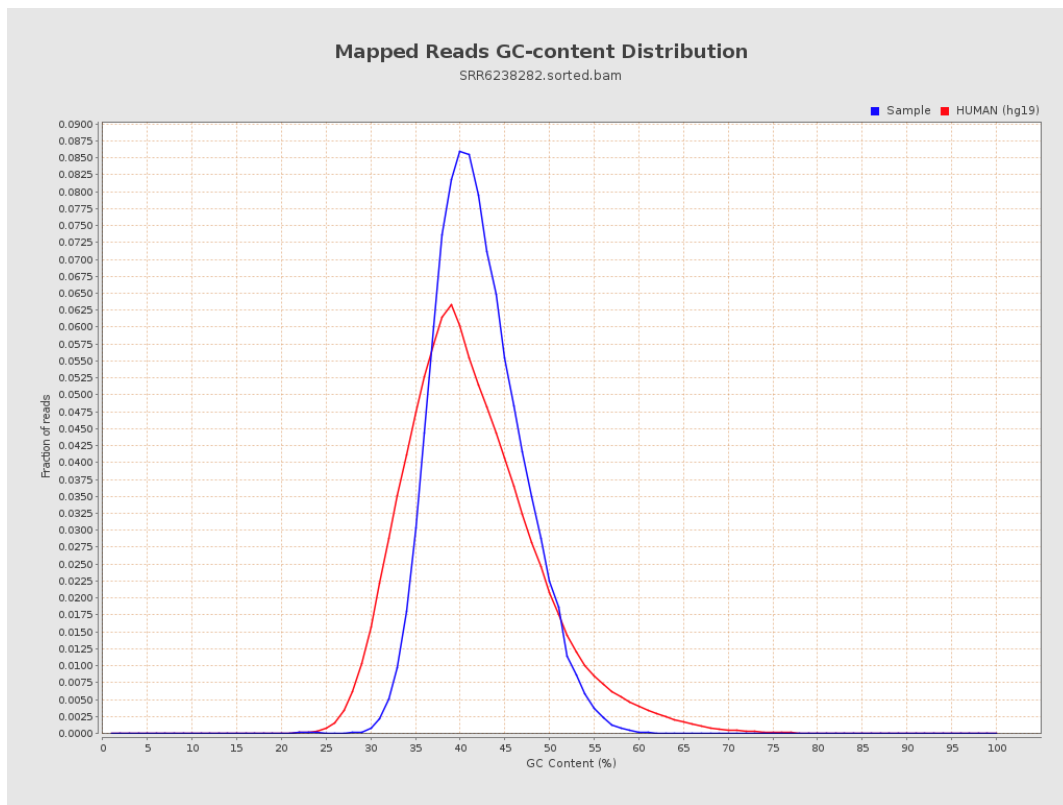
7. Results : Duplication Rate Histogram



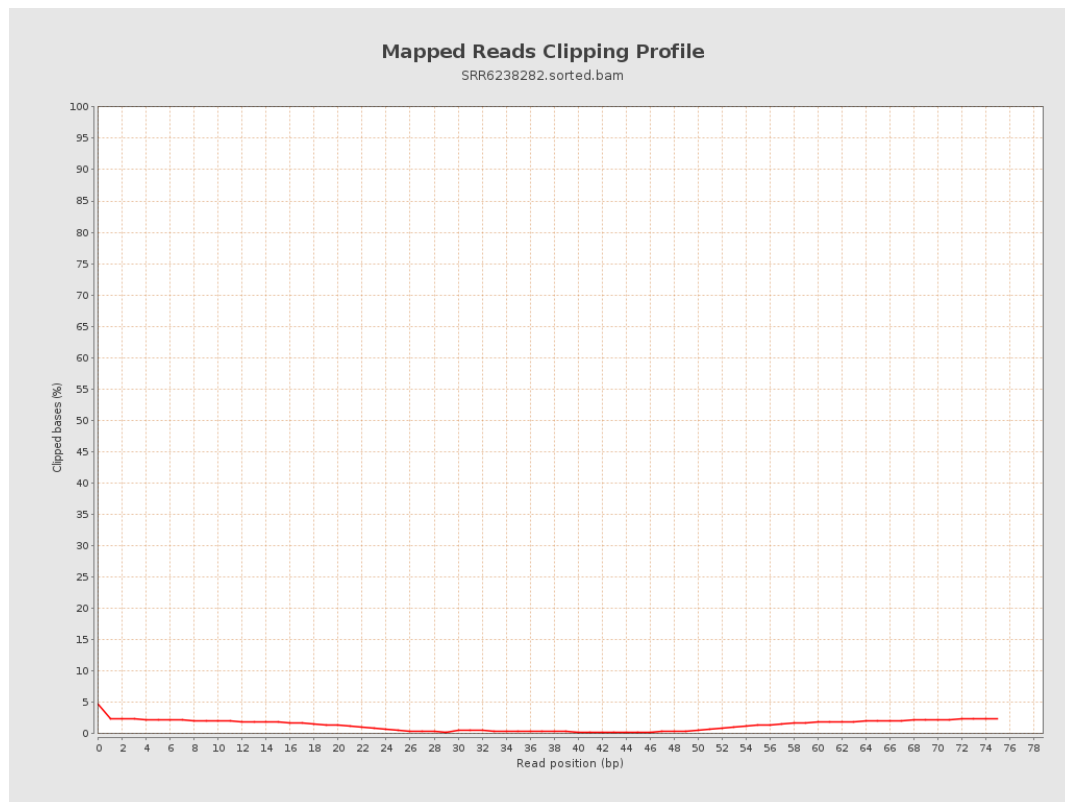
8. Results : Mapped Reads Nucleotide Content



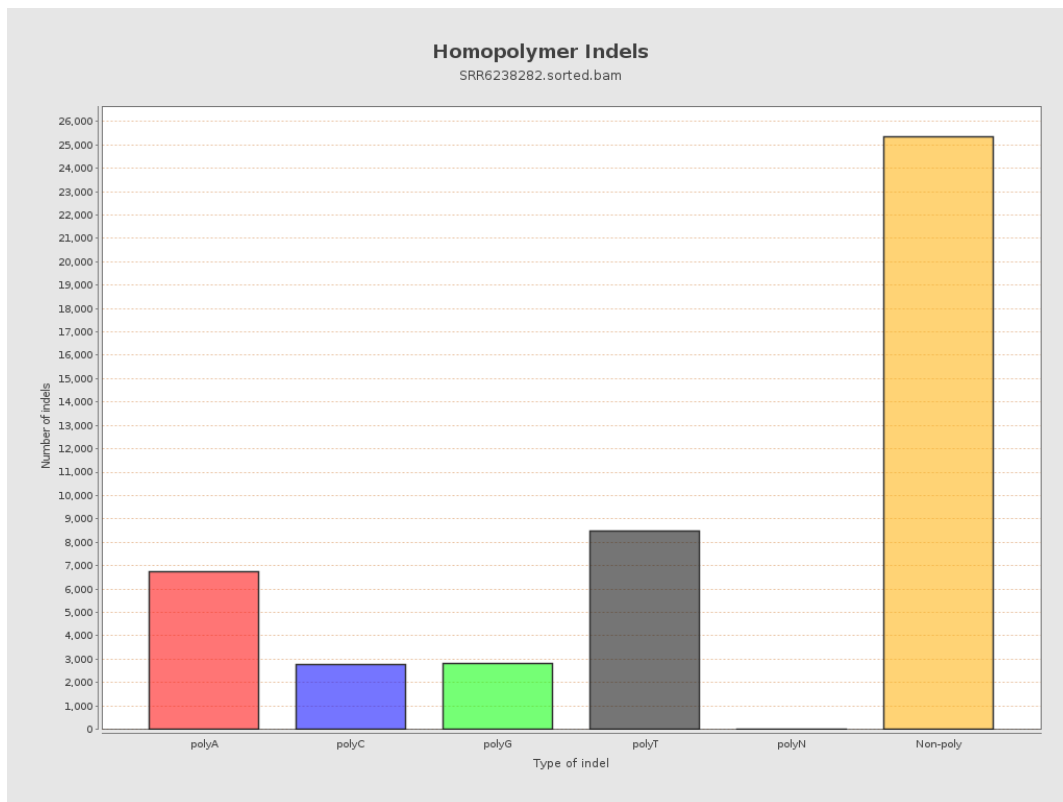
9. Results : Mapped Reads GC-content Distribution



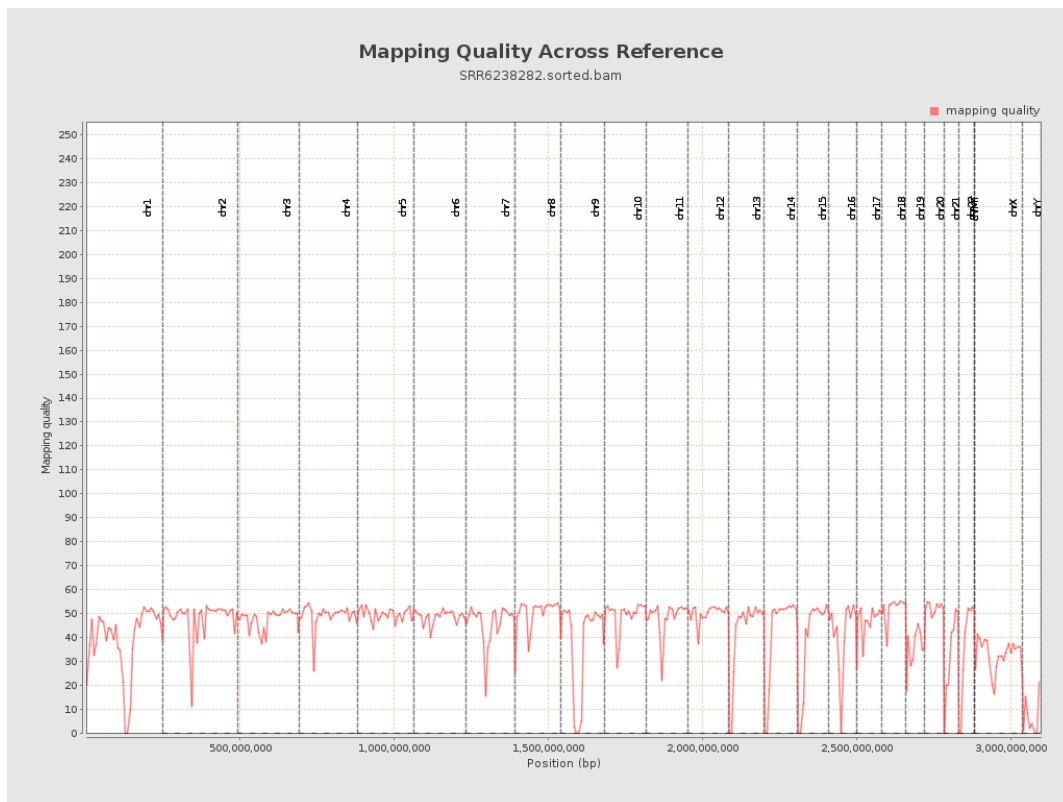
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

