

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 01:14:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238658.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_SRR6238658 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238658.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 01:14:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238658.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,121,660
Mapped reads	2,887,254 / 92.49%
Unmapped reads	234,406 / 7.51%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,239 / 0.68%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	1,137,043 / 36.42%
Duplication rate	21.77%
Clipped reads	1,709,066 / 54.75%

2.2. ACGT Content

Number/percentage of A's	45,374,282 / 25.01%
Number/percentage of C's	32,056,794 / 17.67%
Number/percentage of T's	61,047,612 / 33.65%
Number/percentage of G's	42,917,193 / 23.66%
Number/percentage of N's	4,416 / 0%
GC Percentage	41.33%

2.3. Coverage

Mean	0.0586

Standard Deviation	0.9447
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2.4. Mapping Quality

Mean Mapping Quality	43.31
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2.5. Mismatches and indels

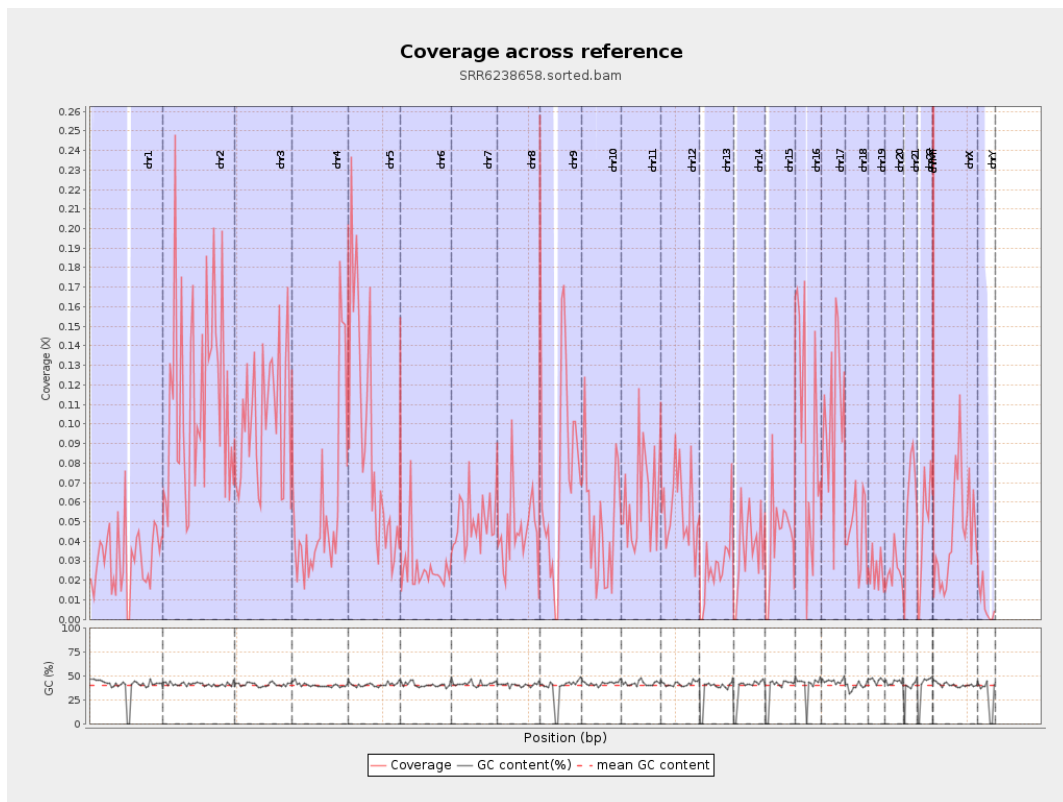
General error rate	0.51%
Mismatches	900,471
Insertions	12,496
Mapped reads with at least one insertion	0.43%
Deletions	41,758
Mapped reads with at least one deletion	1.44%
Homopolymer indels	43.72%

2.6. Chromosome stats

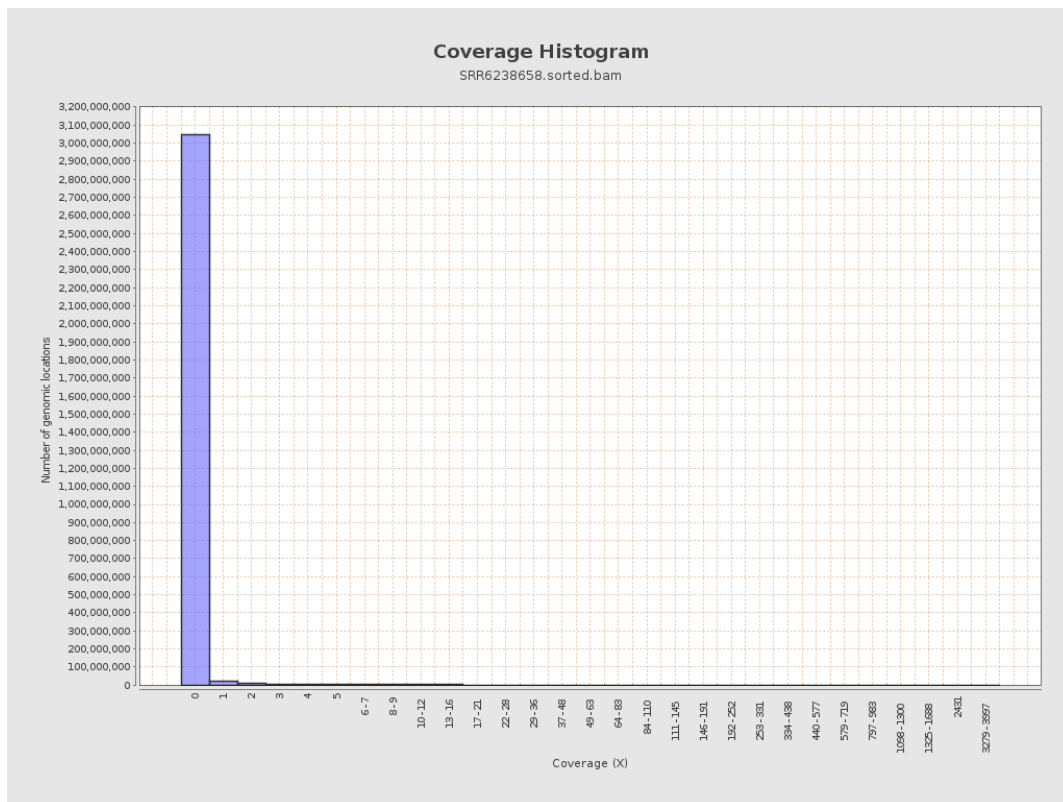
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	7637316	0.0306	0.7046
chr2	243199373	27630101	0.1136	1.9967
chr3	198022430	20221442	0.1021	0.9267
chr4	191154276	10646242	0.0557	0.6704
chr5	180915260	15873050	0.0877	0.8558
chr6	171115067	4357852	0.0255	0.7417
chr7	159138663	7879207	0.0495	0.7032

chr8	146364022	6553007	0.0448	0.6899
chr9	141213431	10168493	0.072	0.8141
chr10	135534747	6824840	0.0504	0.6875
chr11	135006516	8359789	0.0619	0.7296
chr12	133851895	7584815	0.0567	0.6932
chr13	115169878	3197992	0.0278	0.6288
chr14	107349540	3876517	0.0361	0.5857
chr15	102531392	4282577	0.0418	0.6909
chr16	90354753	8504882	0.0941	0.8907
chr17	81195210	8602613	0.1059	1.0047
chr18	78077248	3567813	0.0457	2.0181
chr19	59128983	1415670	0.0239	0.5796
chr20	63025520	1547675	0.0246	0.433
chr21	48129895	2940635	0.0611	0.6998
chr22	51304566	2413175	0.047	0.6177
chrMT	16571	43268	2.6111	4.6085
chrX	155270560	6875376	0.0443	0.6048
chrY	59373566	466324	0.0079	0.3478

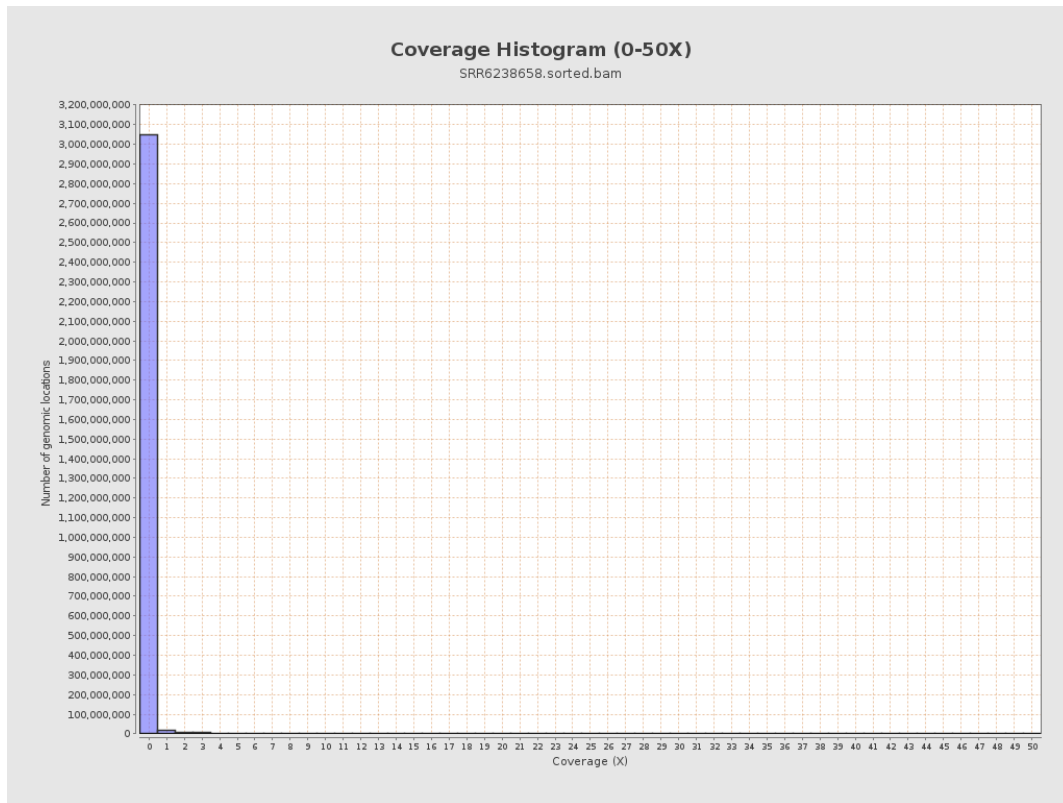
3. Results : Coverage across reference



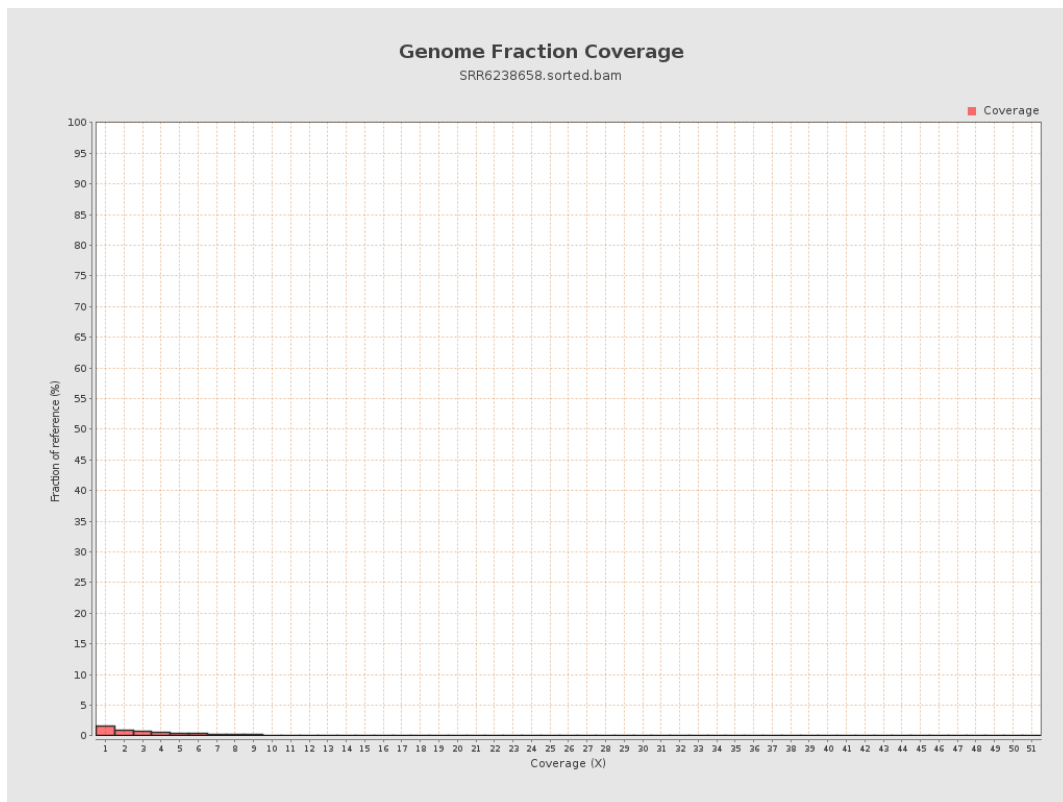
4. Results : Coverage Histogram



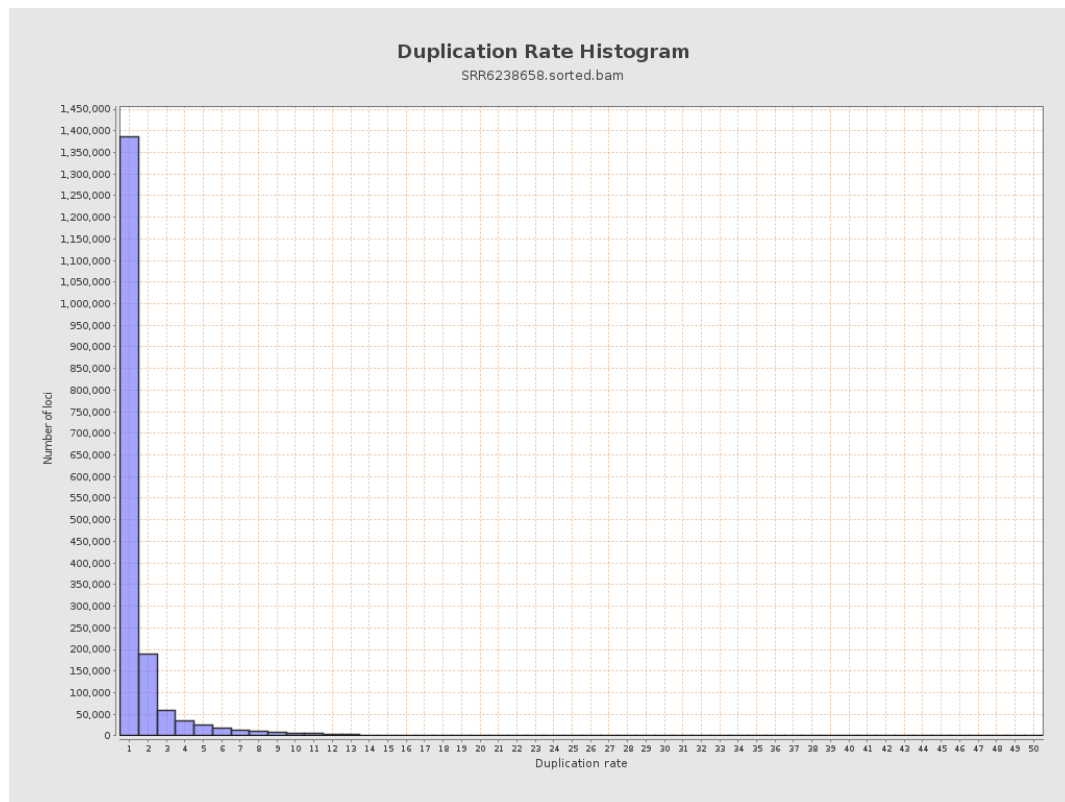
5. Results : Coverage Histogram (0-50X)



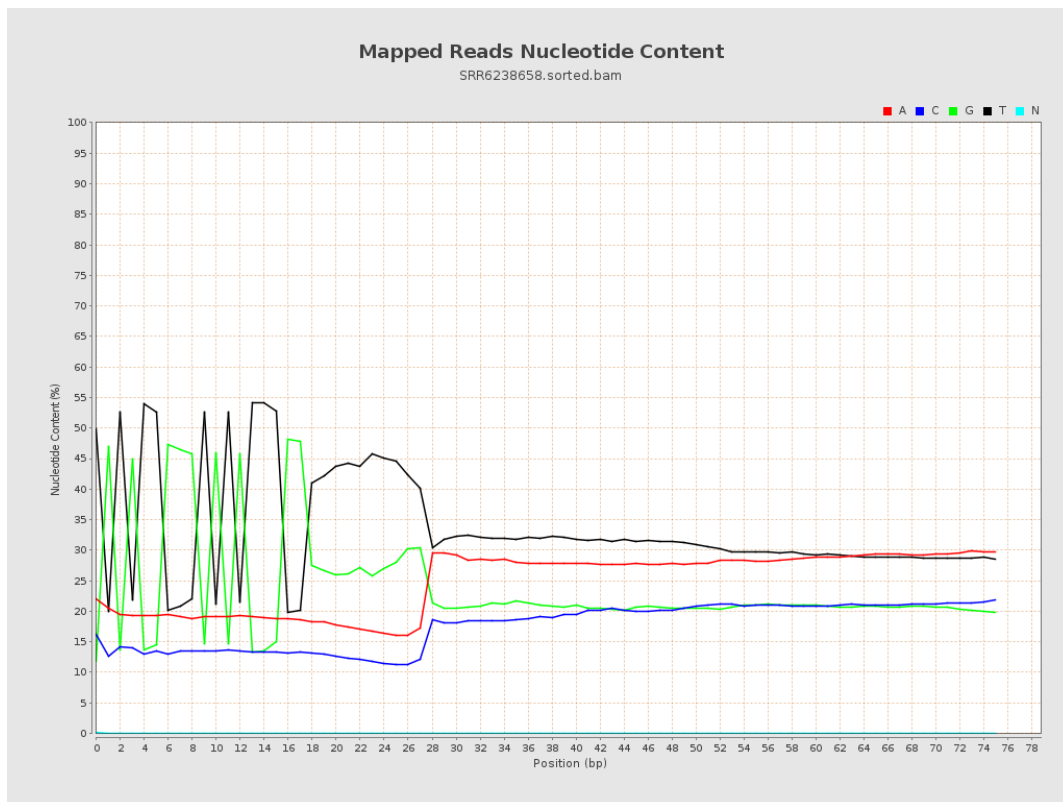
6. Results : Genome Fraction Coverage



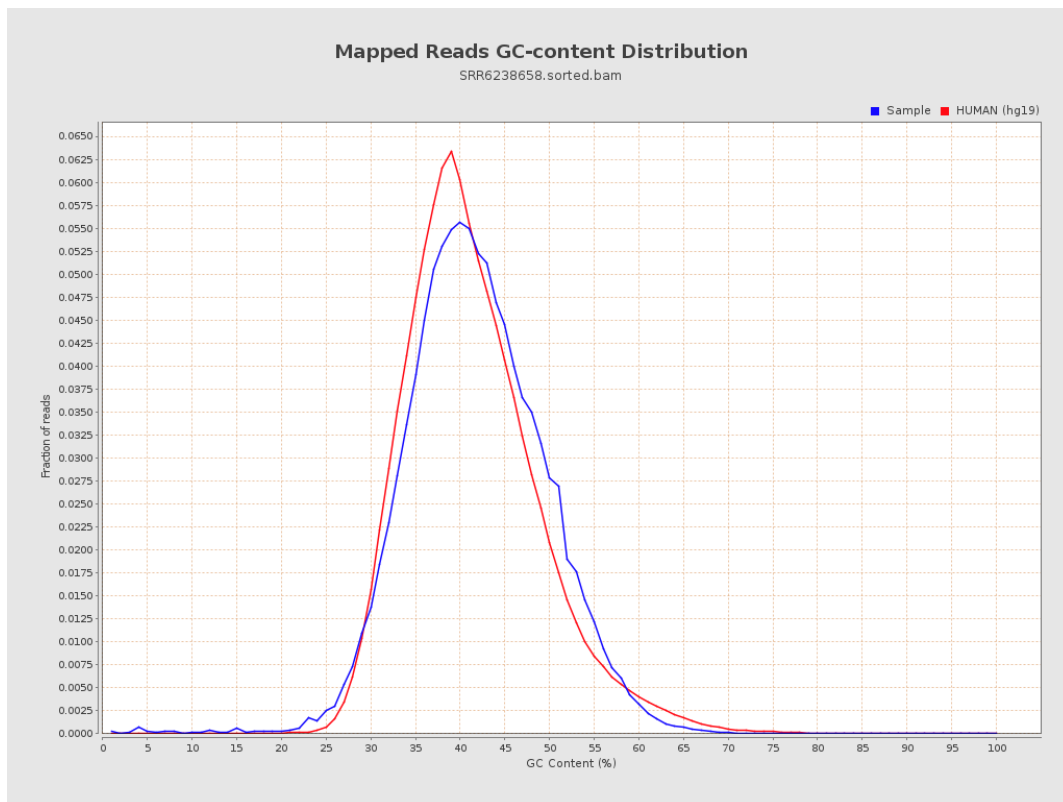
7. Results : Duplication Rate Histogram



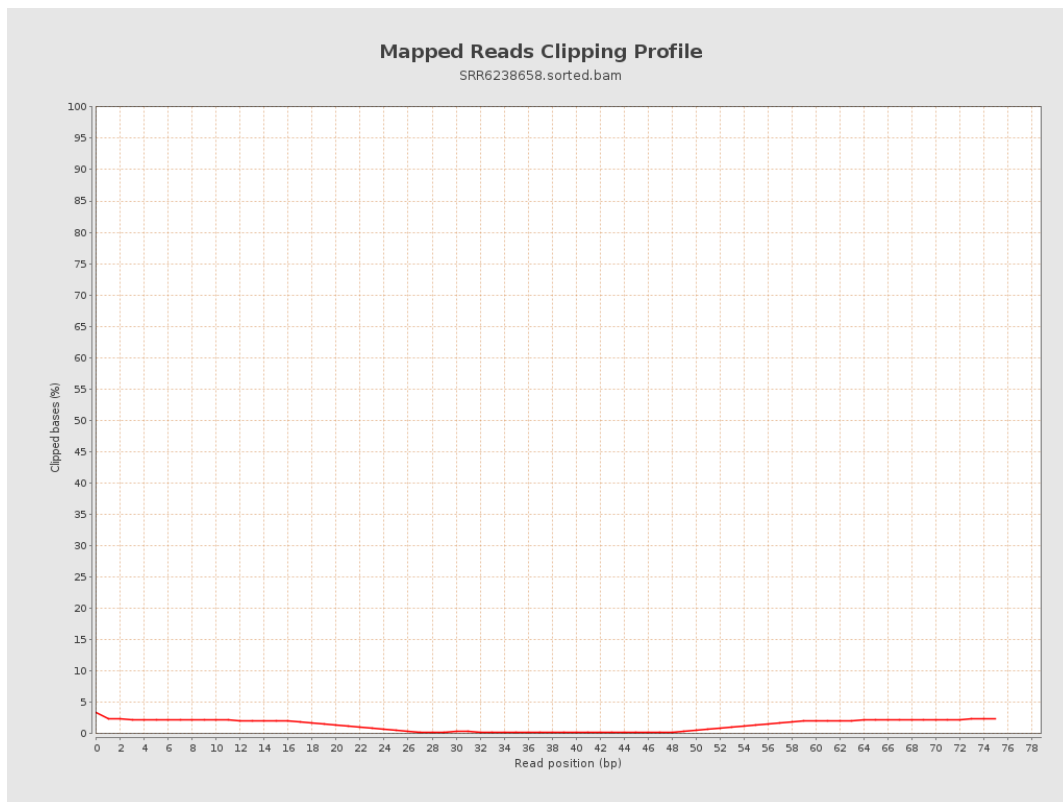
8. Results : Mapped Reads Nucleotide Content



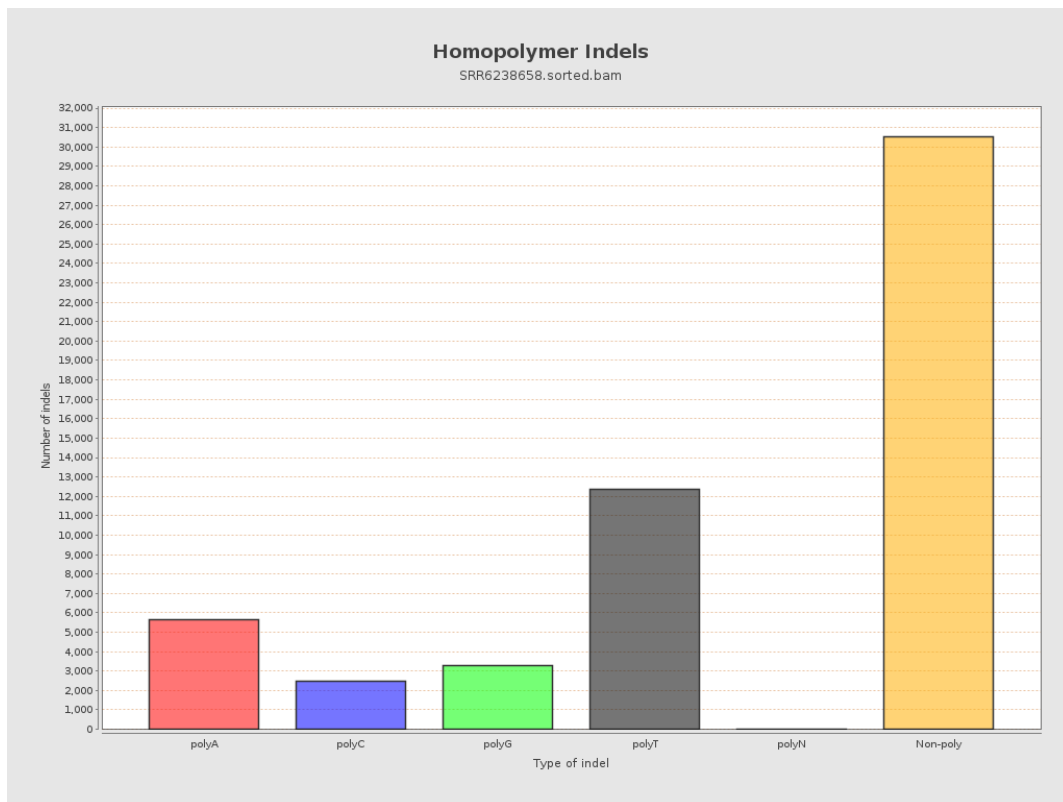
9. Results : Mapped Reads GC-content Distribution



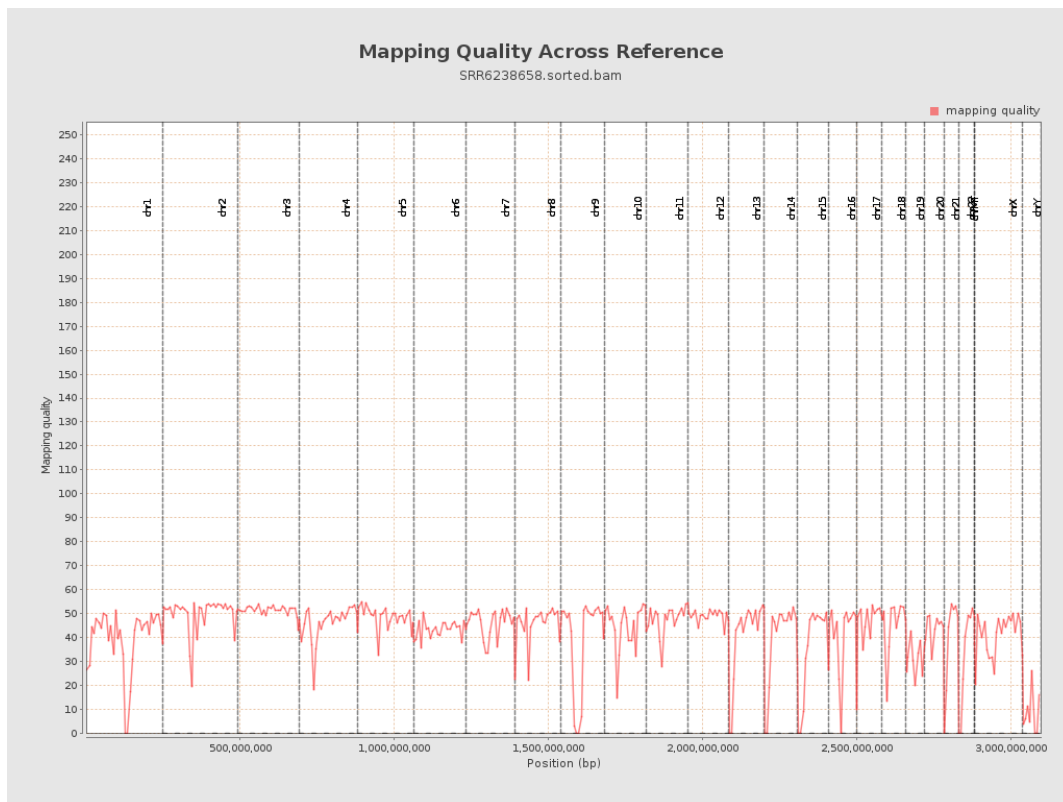
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

