Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 21:17:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238545.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_SRR6238545 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238545.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 21:17:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238545.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,673,576
Mapped reads	4,236,089 / 90.64%
Unmapped reads	437,487 / 9.36%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	37,609 / 0.8%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	950,997 / 20.35%
Duplication rate	16.98%
Clipped reads	2,595,938 / 55.55%

2.2. ACGT Content

Number/percentage of A's	66,261,422 / 25.17%
Number/percentage of C's	46,786,741 / 17.77%
Number/percentage of T's	87,380,651 / 33.19%
Number/percentage of G's	62,802,052 / 23.86%
Number/percentage of N's	18,173 / 0.01%
GC Percentage	41.63%

2.3. Coverage

Mean	0.0851

Standard Deviation	0.984

2.4. Mapping Quality

Mean Mapping Quality	42.81

2.5. Mismatches and indels

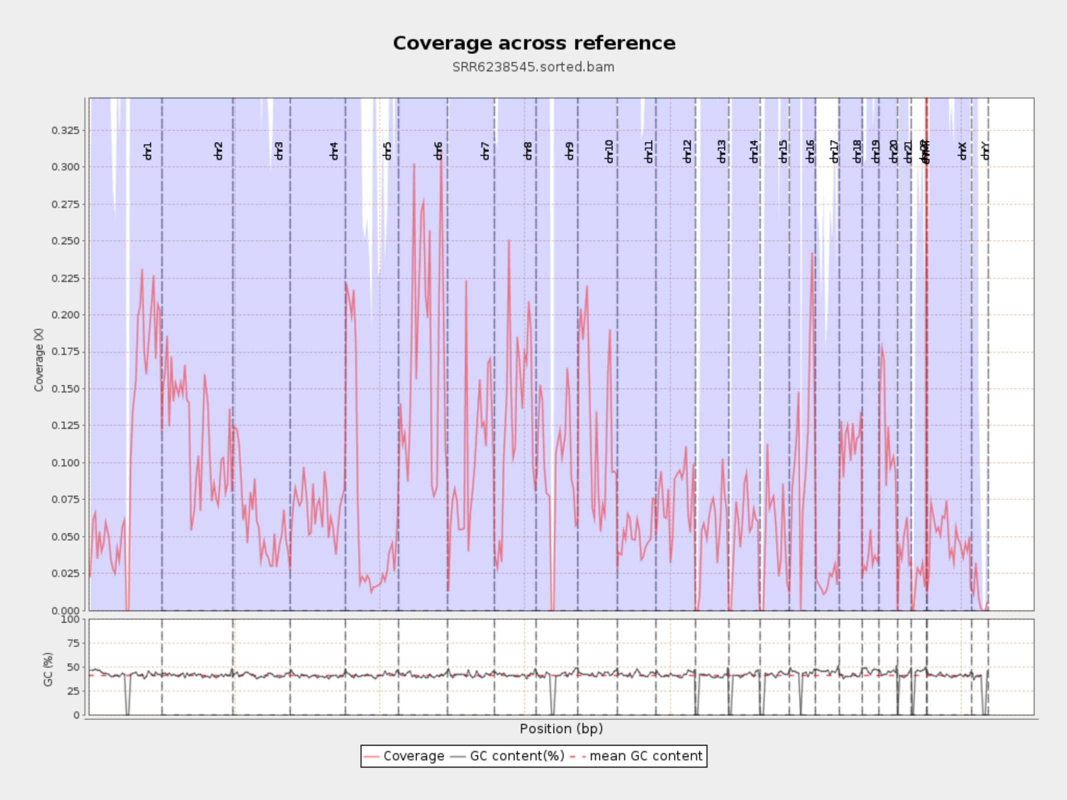
General error rate	0.62%
Mismatches	1,600,599
Insertions	16,649
Mapped reads with at least one insertion	0.39%
Deletions	90,071
Mapped reads with at least one deletion	2.1%
Homopolymer indels	41.09%

2.6. Chromosome stats

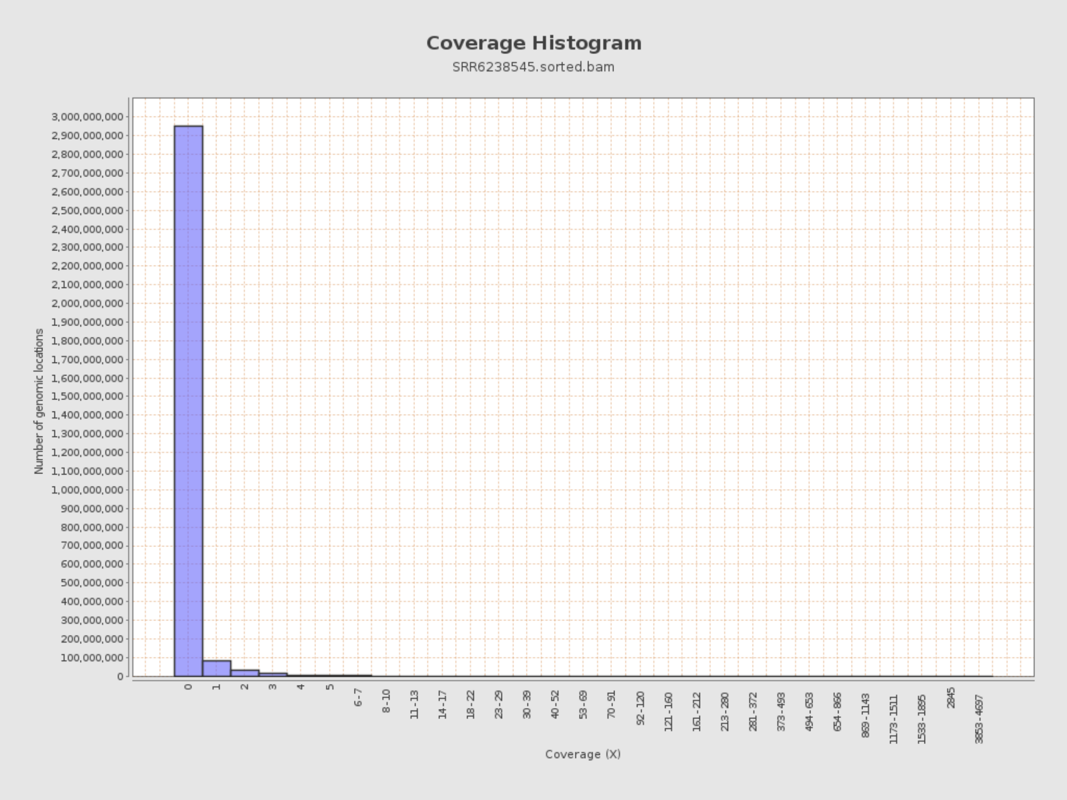
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	25503914	0.1023	0.7029
chr2	243199373	28828602	0.1185	2.1376
chr3	198022430	12178617	0.0615	0.4227
chr4	191154276	13154957	0.0688	0.4613
chr5	180915260	11952478	0.0661	0.4435
chr6	171115067	29896953	0.1747	1.4274
chr7	159138663	15862136	0.0997	1.7786

chr8	146364022	18696484	0.1277	0.9244
chr9	141213431	13892200	0.0984	0.7668
chr10	135534747	17504299	0.1291	0.927
chr11	135006516	6911686	0.0512	0.4364
chr12	133851895	10287289	0.0769	0.4939
chr13	115169878	6196205	0.0538	0.5109
chr14	107349540	5800008	0.054	0.4904
chr15	102531392	5048131	0.0492	0.5179
chr16	90354753	10427216	0.1154	0.6598
chr17	81195210	1641457	0.0202	0.2451
chr18	78077248	8942774	0.1145	1.6052
chr19	59128983	2097660	0.0355	0.5351
chr20	63025520	7578747	0.1202	0.5939
chr21	48129895	1879969	0.0391	0.3905
chr22	51304566	942857	0.0184	0.2162
chrMT	16571	175246	10.5755	6.9189
chrX	155270560	7490343	0.0482	0.4045
chrY	59373566	514943	0.0087	0.3241

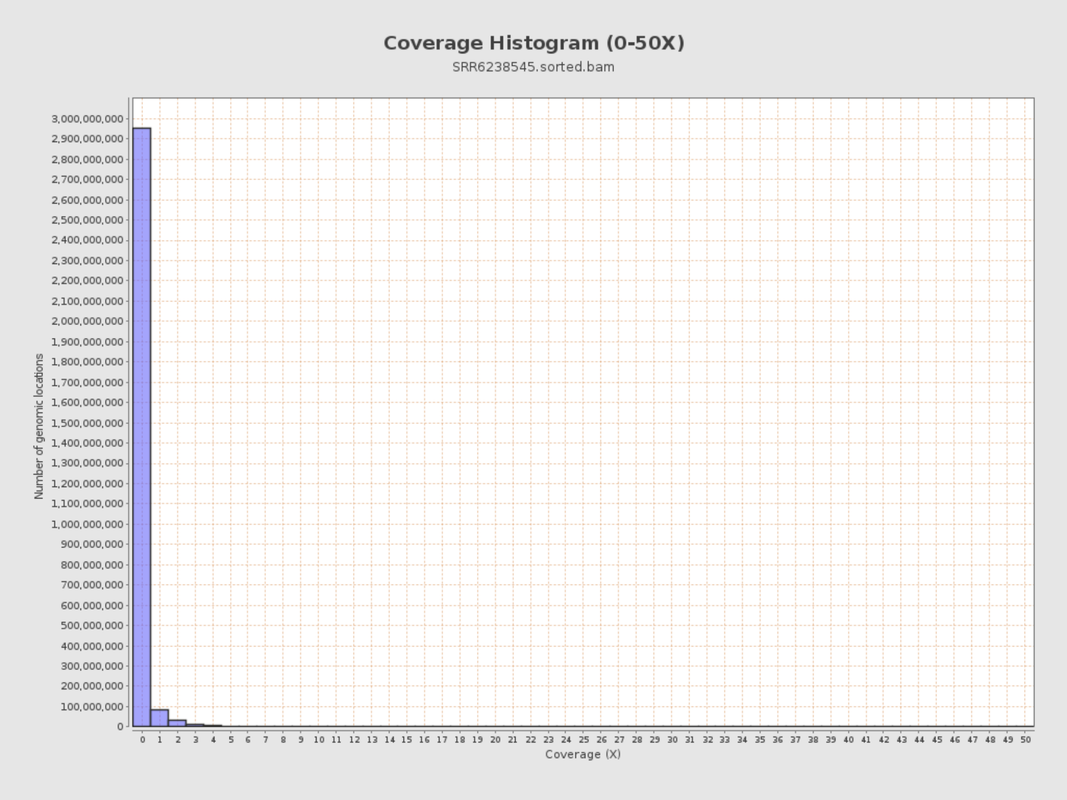
3. Results : Coverage across reference



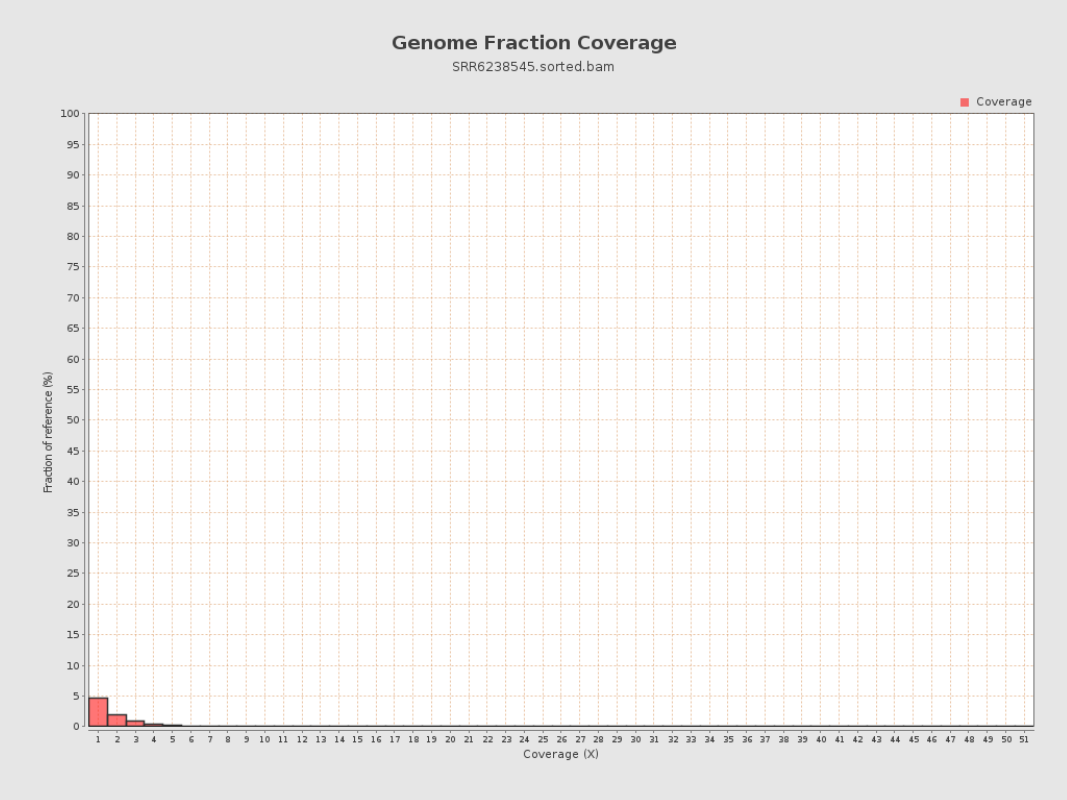
4. Results : Coverage Histogram



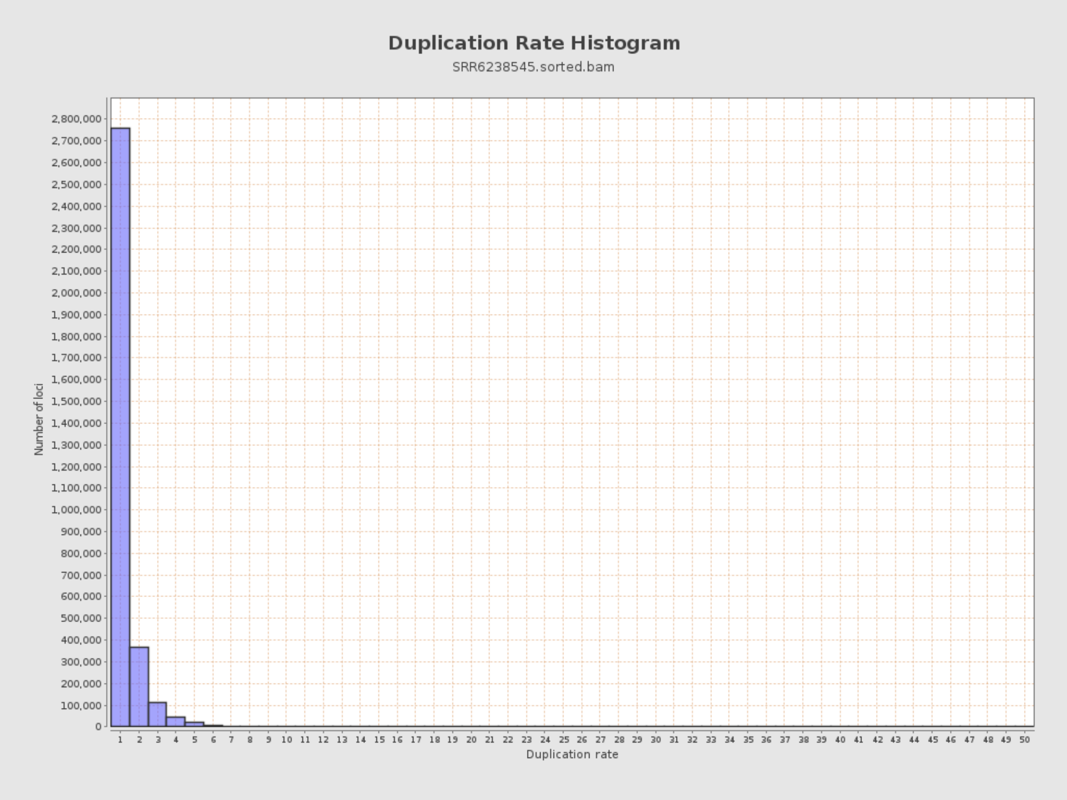
5. Results : Coverage Histogram (0-50X)



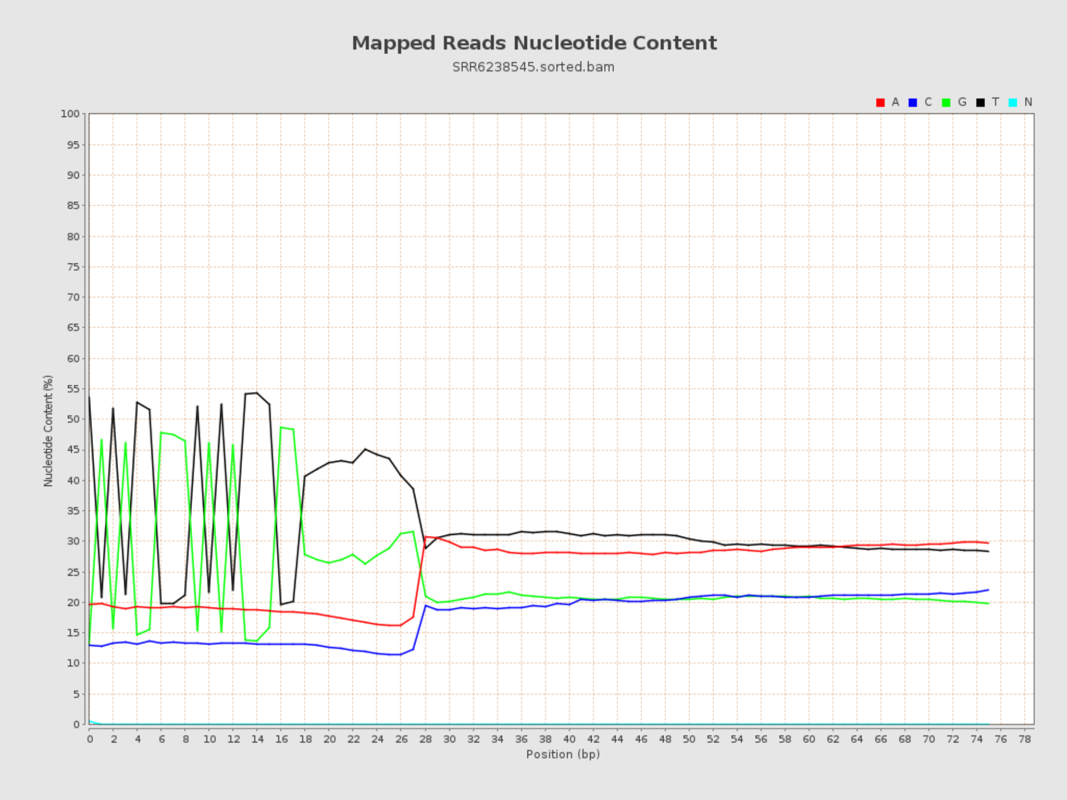
6. Results : Genome Fraction Coverage



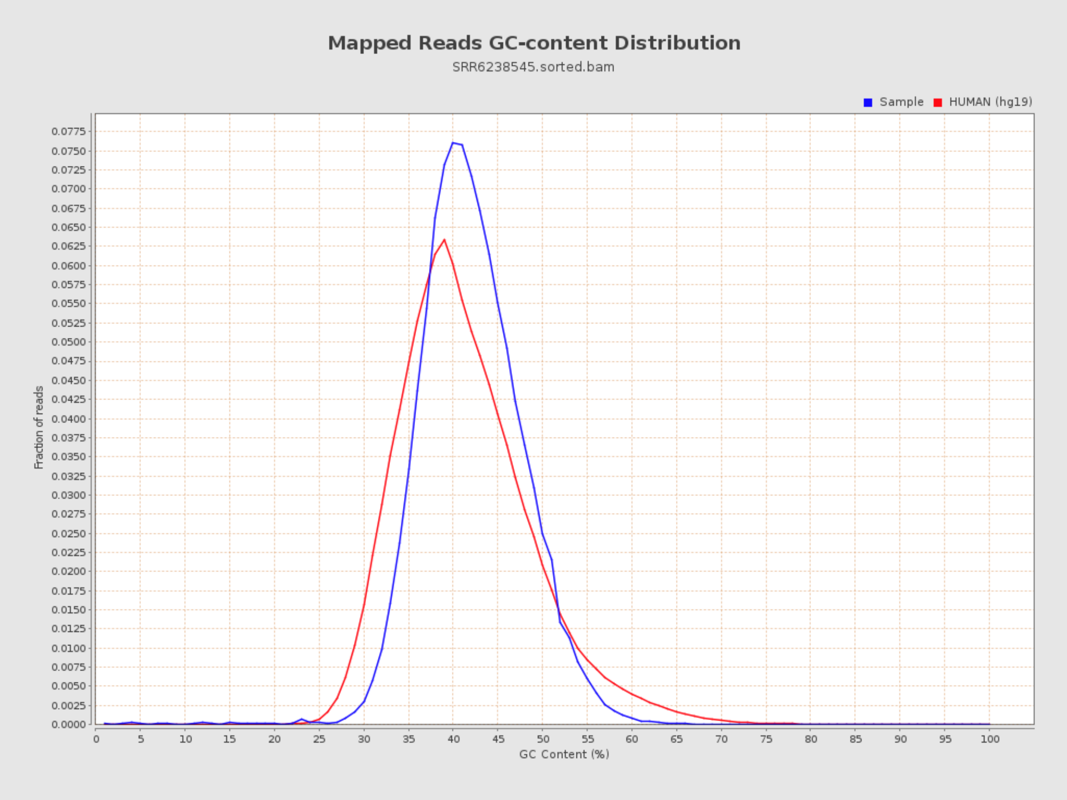
7. Results : Duplication Rate Histogram



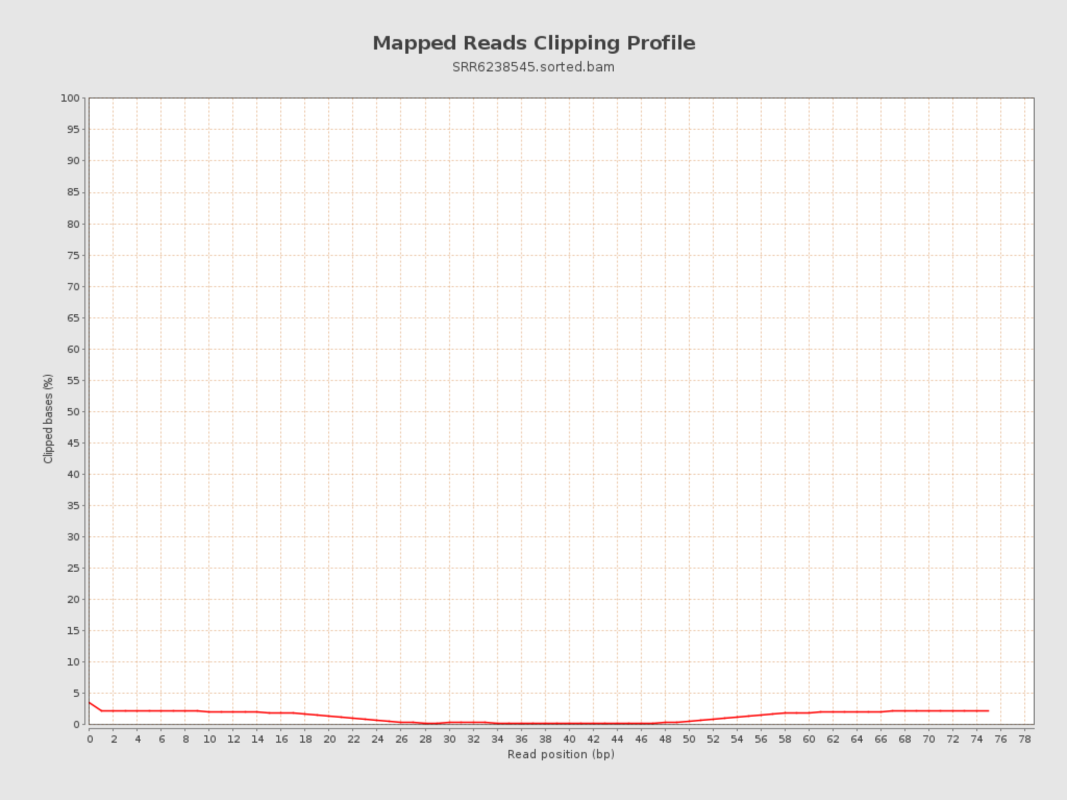
8. Results : Mapped Reads Nucleotide Content



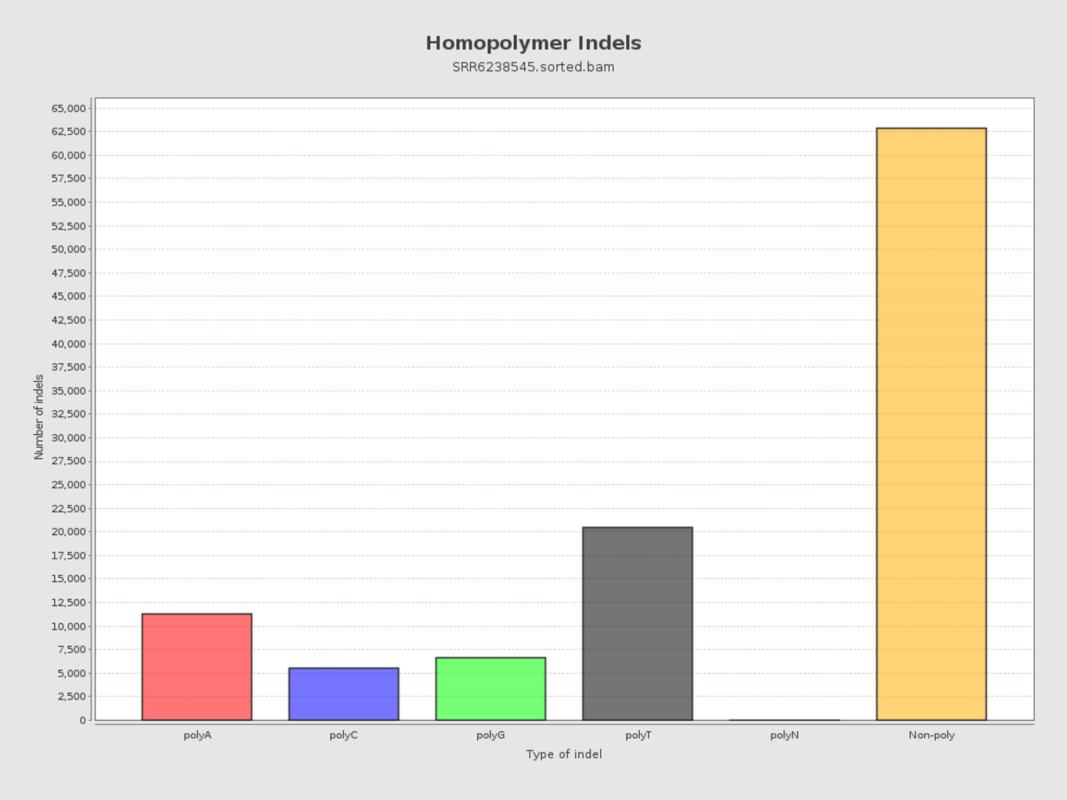
9. Results : Mapped Reads GC-content Distribution



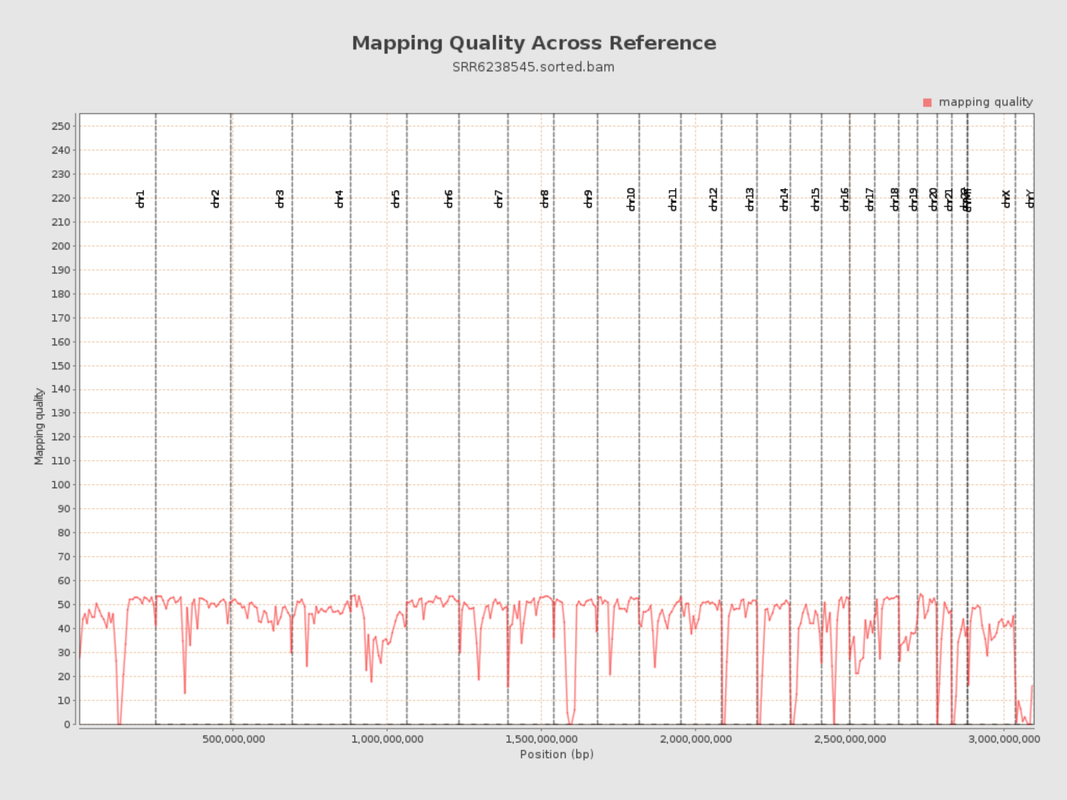
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram