Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 17:26:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238487.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_SRR6238487 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238487.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 17:26:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238487.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,974,823
Mapped reads	2,551,710 / 85.78%
Unmapped reads	423,113 / 14.22%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,784 / 0.7%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	752,509 / 25.3%
Duplication rate	21.12%
Clipped reads	1,714,331 / 57.63%

2.2. ACGT Content

Number/percentage of A's	37,760,782 / 24.4%
Number/percentage of C's	26,723,170 / 17.26%
Number/percentage of T's	52,262,841 / 33.77%
Number/percentage of G's	38,026,013 / 24.57%
Number/percentage of N's	10,244 / 0.01%
GC Percentage	41.83%

2.3. Coverage

Mean	0.05

Standard Deviation	0.6722

2.4. Mapping Quality

Mean Mapping Quality	42.68

2.5. Mismatches and indels

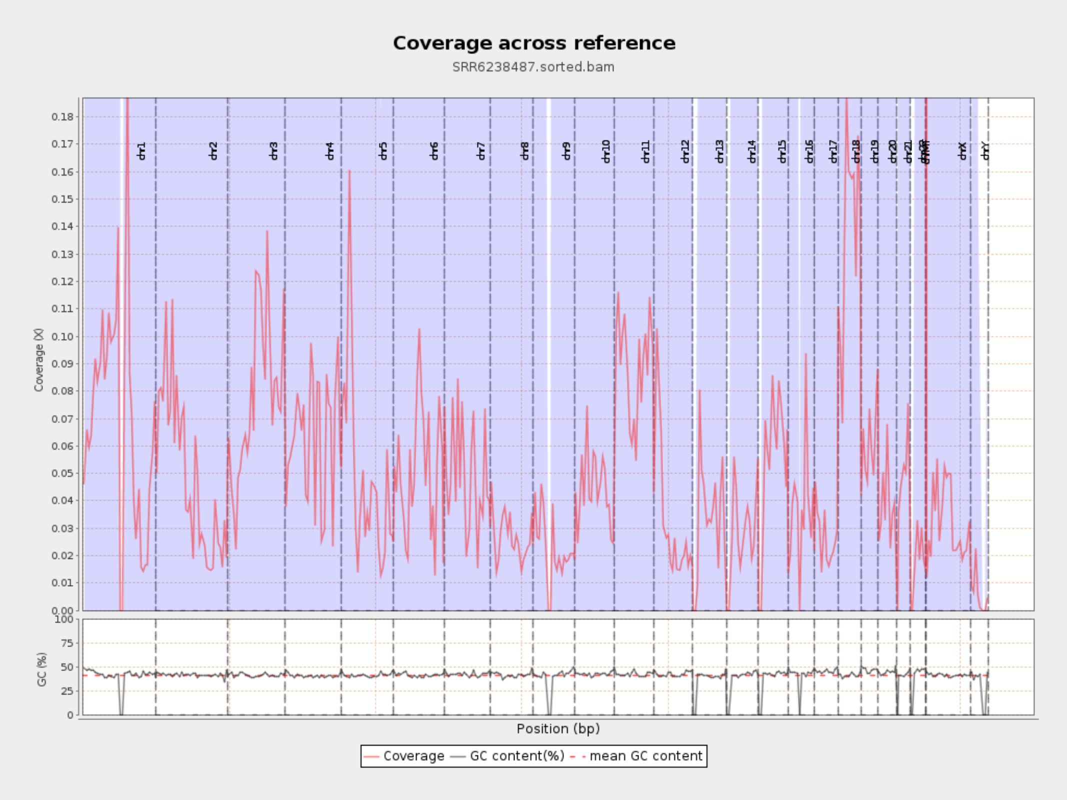
General error rate	0.62%
Mismatches	942,313
Insertions	9,391
Mapped reads with at least one insertion	0.36%
Deletions	49,405
Mapped reads with at least one deletion	1.92%
Homopolymer indels	42.18%

2.6. Chromosome stats

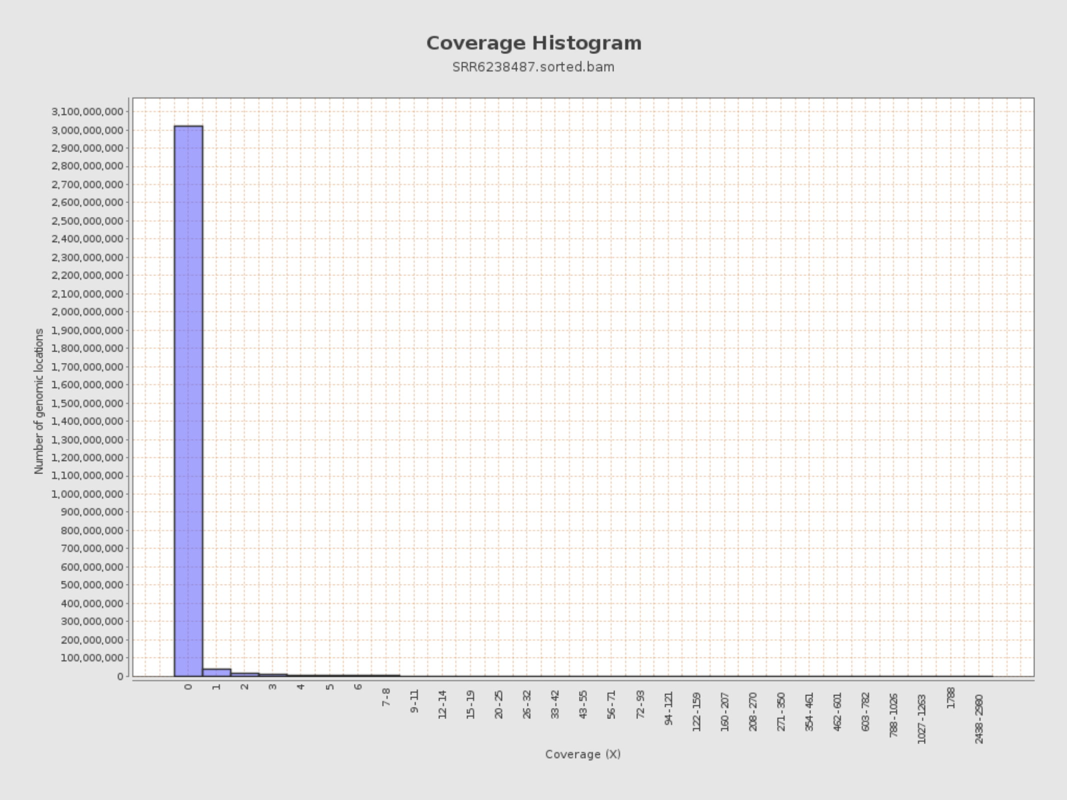
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17259250	0.0692	1.0907
chr2	243199373	11822768	0.0486	1.3579
chr3	198022430	15403175	0.0778	0.5303
chr4	191154276	12093620	0.0633	0.4681
chr5	180915260	8635408	0.0477	0.4093
chr6	171115067	8803775	0.0514	0.6199
chr7	159138663	7906290	0.0497	0.5613

chr8	146364022	3884005	0.0265	0.6042
chr9	141213431	3213051	0.0228	0.3346
chr10	135534747	6026777	0.0445	0.4763
chr11	135006516	11928845	0.0884	0.5901
chr12	133851895	4549628	0.034	0.3504
chr13	115169878	3945179	0.0343	0.4248
chr14	107349540	2957378	0.0275	0.3165
chr15	102531392	5522801	0.0539	0.5122
chr16	90354753	3312632	0.0367	0.3747
chr17	81195210	2161384	0.0266	0.3205
chr18	78077248	10878342	0.1393	1.1037
chr19	59128983	3620002	0.0612	0.7115
chr20	63025520	2397171	0.038	0.3651
chr21	48129895	2180728	0.0453	0.3993
chr22	51304566	908930	0.0177	0.2466
chrMT	16571	30489	1.8399	2.5357
chrX	155270560	5062549	0.0326	0.3413
chrY	59373566	362299	0.0061	0.2257

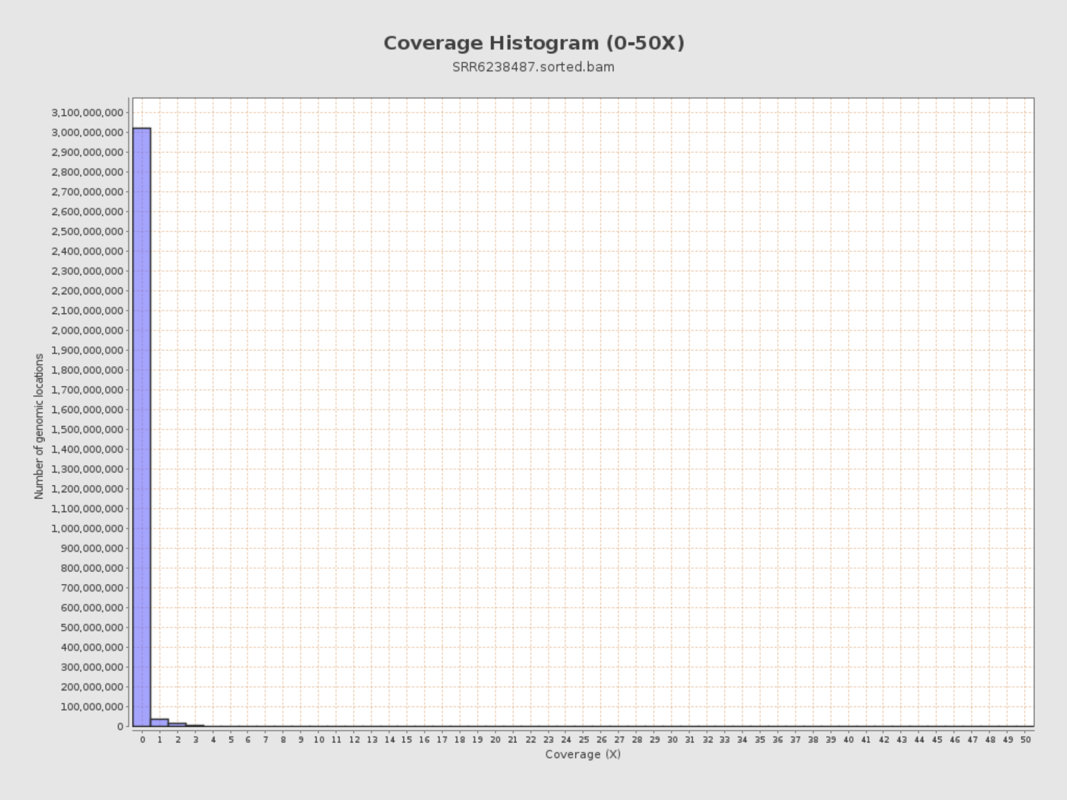
3. Results : Coverage across reference



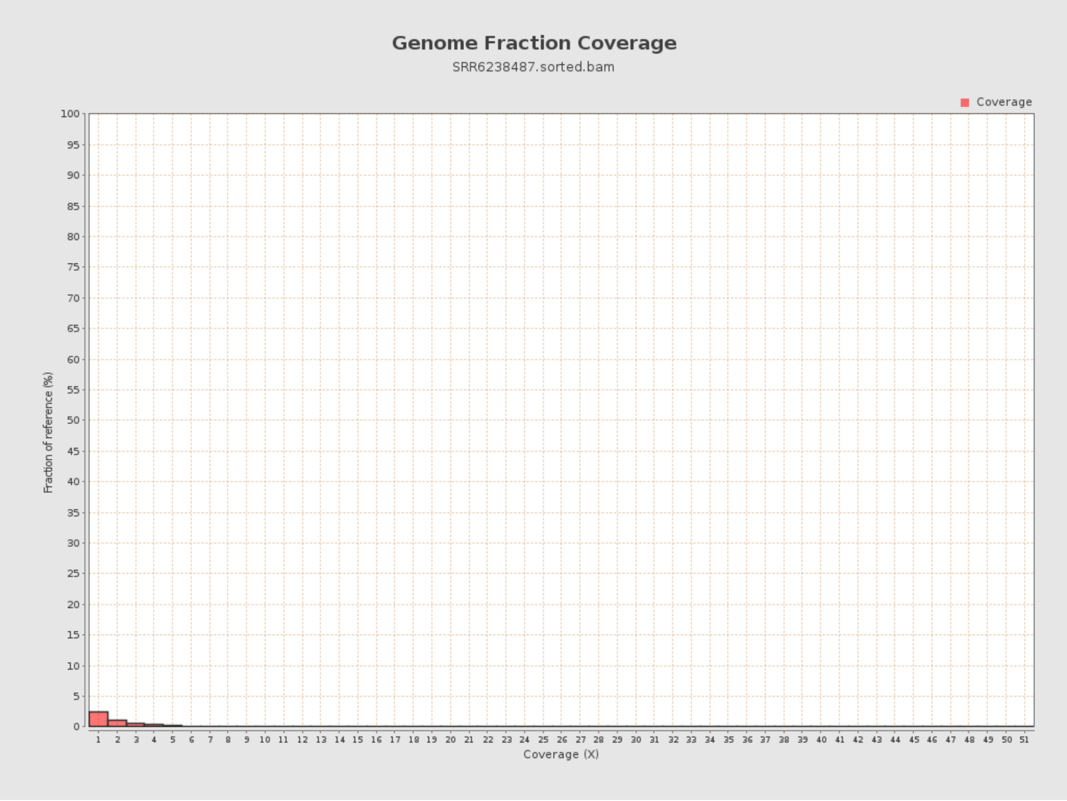
4. Results : Coverage Histogram



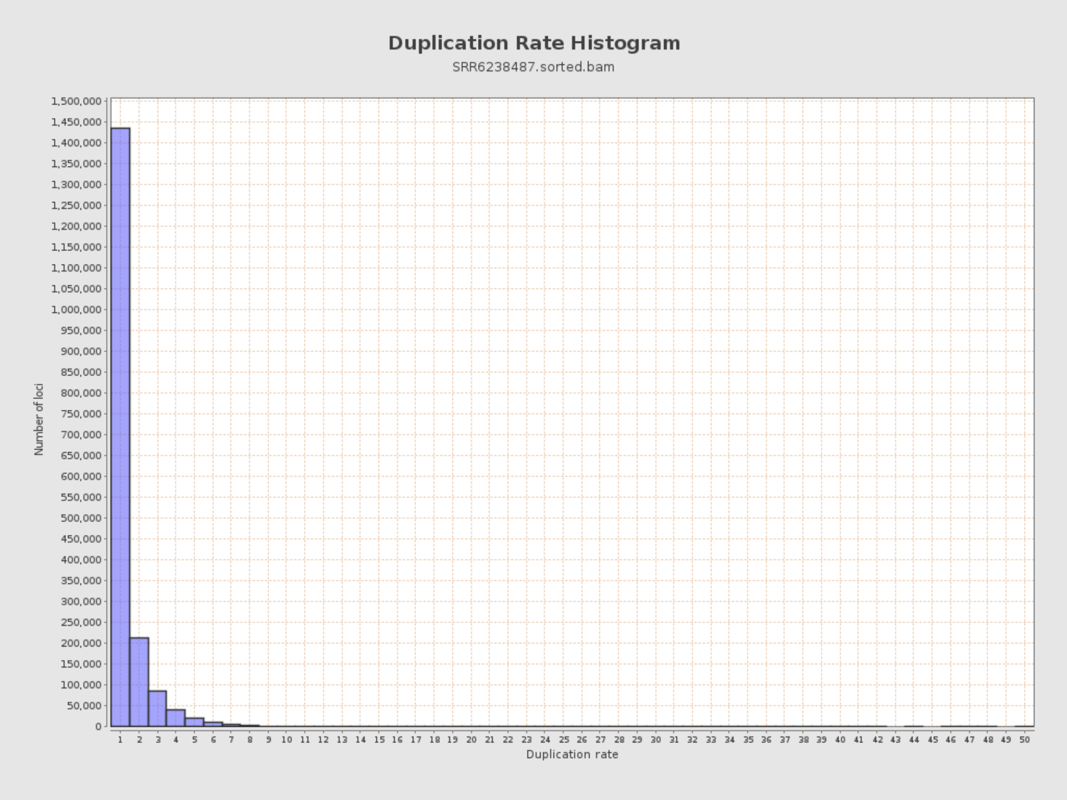
5. Results : Coverage Histogram (0-50X)



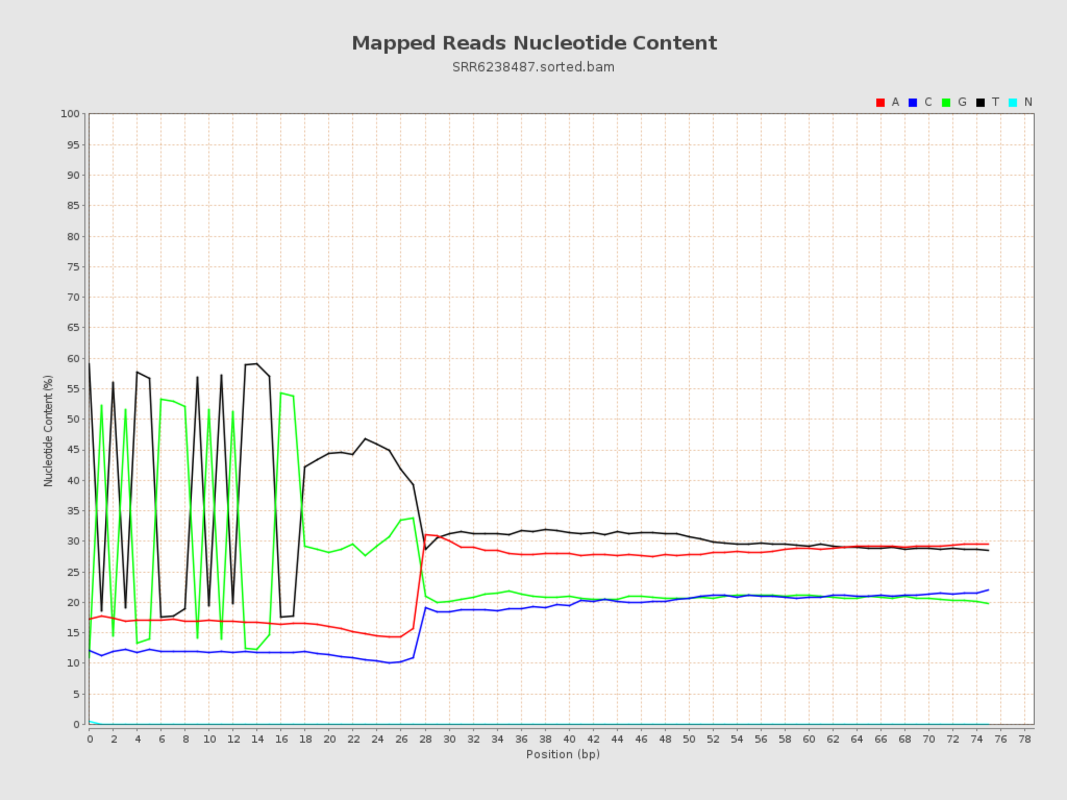
6. Results : Genome Fraction Coverage



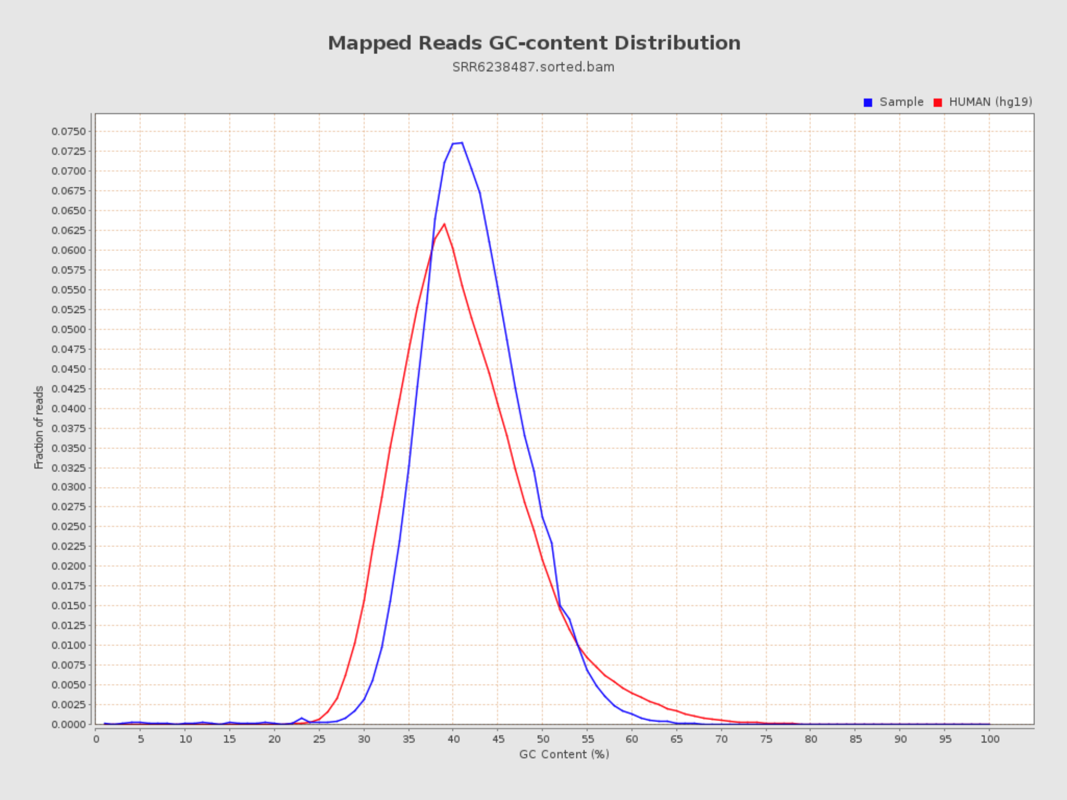
7. Results : Duplication Rate Histogram



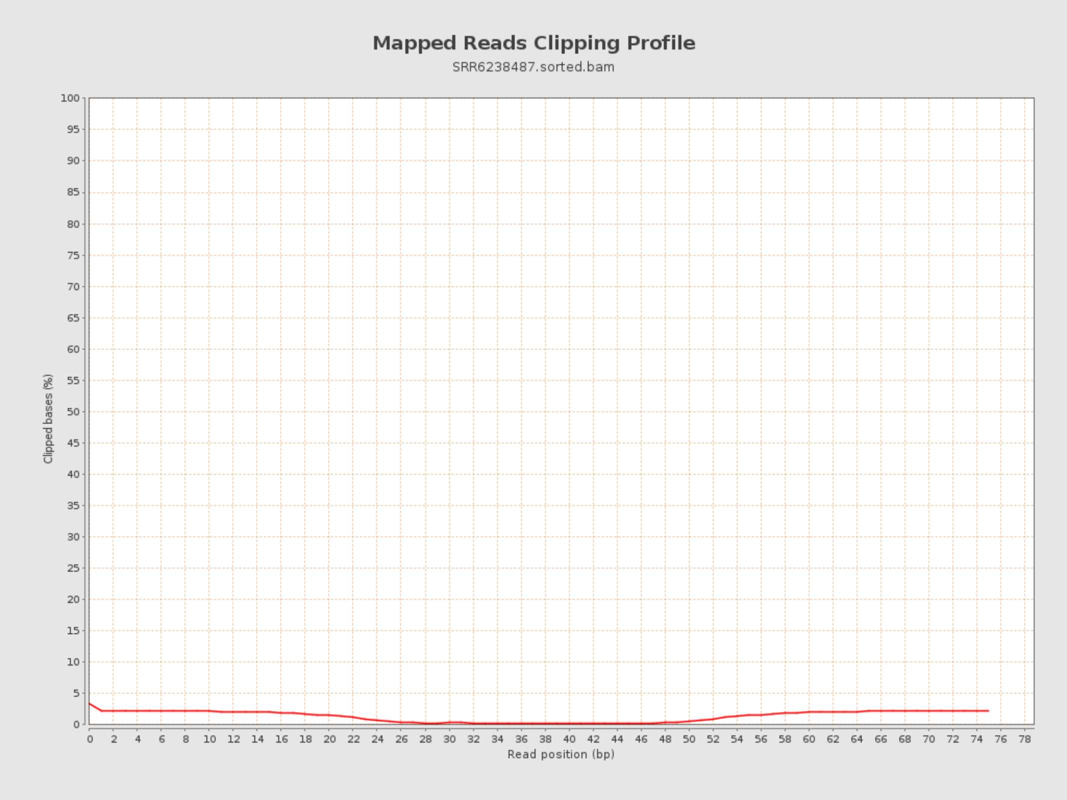
8. Results : Mapped Reads Nucleotide Content



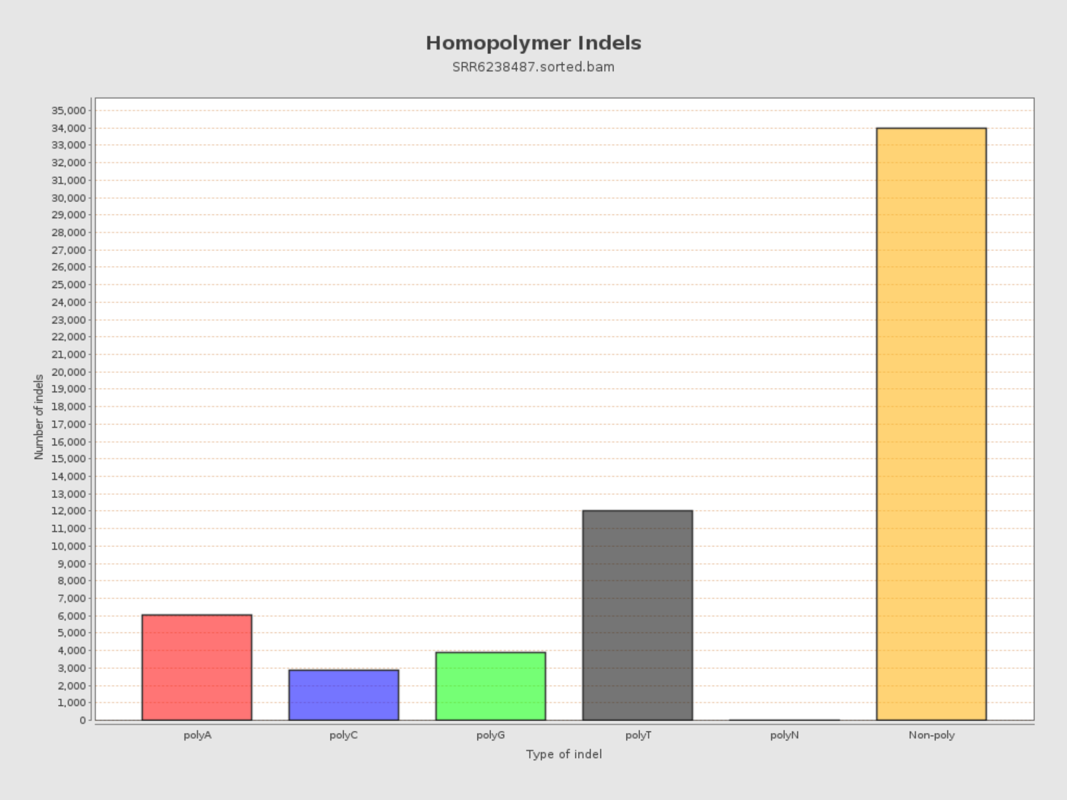
9. Results : Mapped Reads GC-content Distribution



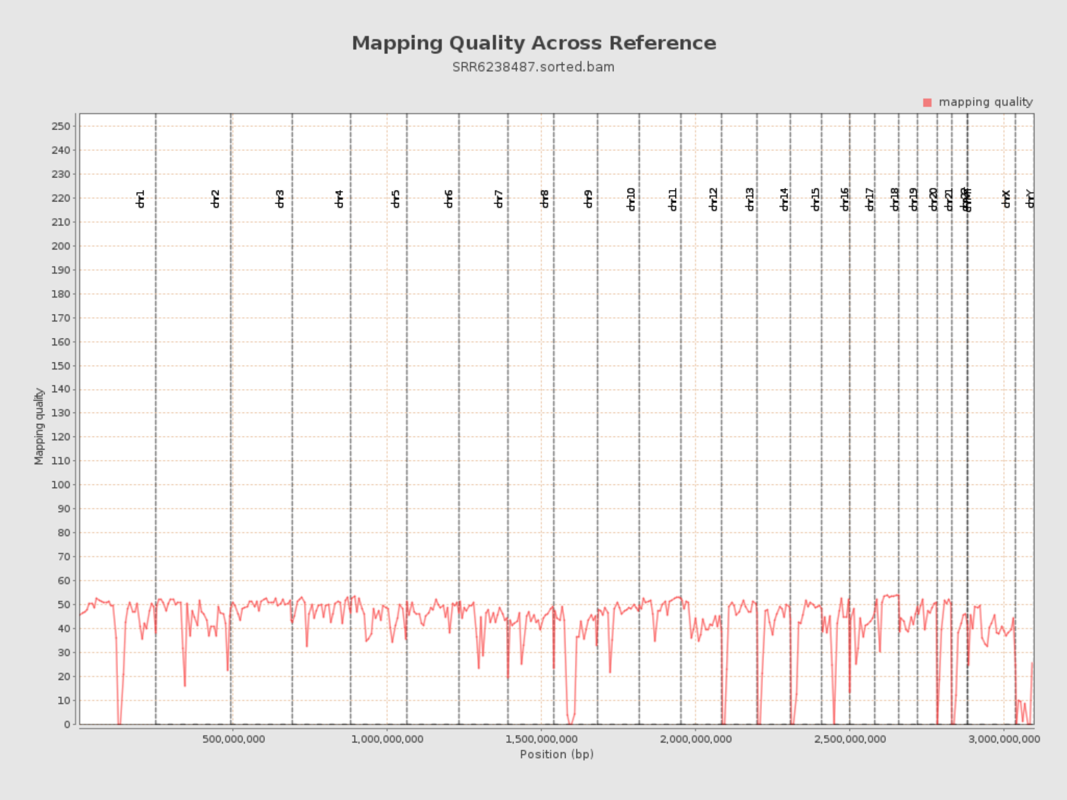
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram