Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 09:11:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237855.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_SRR6237855 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237855.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 09:11:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237855.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,153,249
Mapped reads	2,050,454 / 95.23%
Unmapped reads	102,795 / 4.77%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,765 / 0.55%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	63,676 / 2.96%
Duplication rate	1.82%
Clipped reads	276,937 / 12.86%

2.2. ACGT Content

Number/percentage of A's	46,342,021 / 30.53%
Number/percentage of C's	30,227,592 / 19.91%
Number/percentage of T's	45,180,416 / 29.77%
Number/percentage of G's	29,772,112 / 19.61%
Number/percentage of N's	263,020 / 0.17%
GC Percentage	39.53%

2.3. Coverage

Mean	0.0491

Standard Deviation	0.5659

2.4. Mapping Quality

Mean Mapping Quality	47.07

2.5. Mismatches and indels

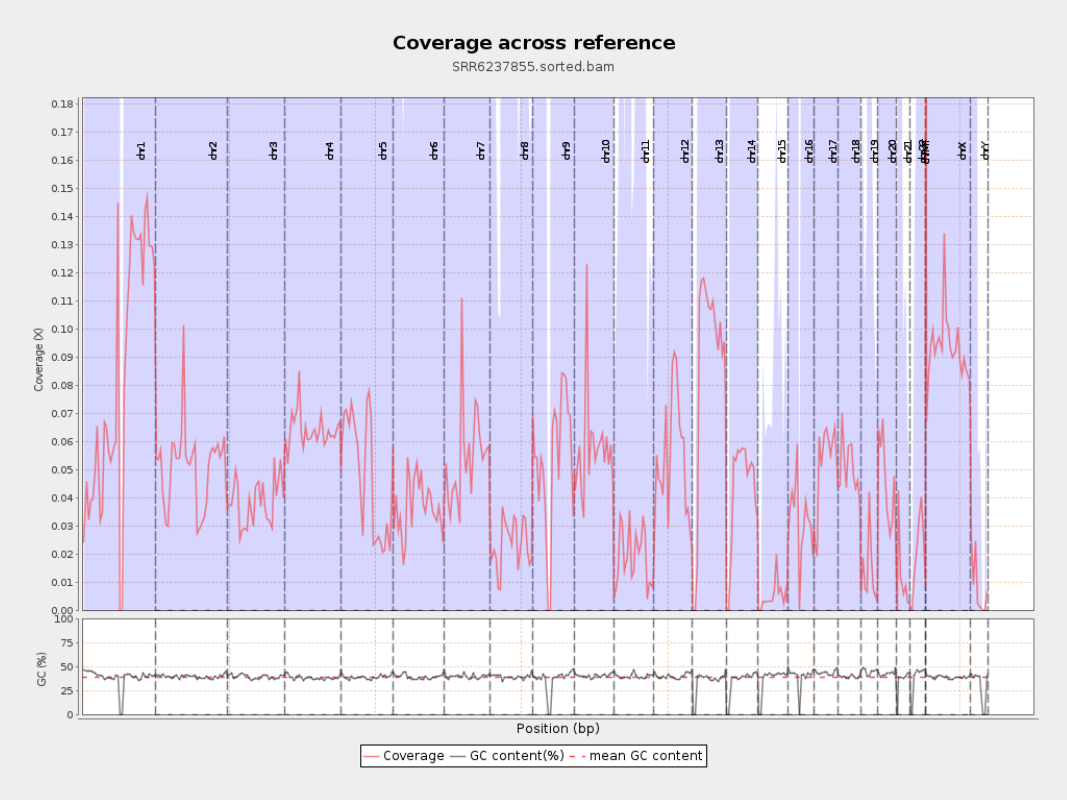
General error rate	0.89%
Mismatches	1,324,112
Insertions	11,986
Mapped reads with at least one insertion	0.58%
Deletions	43,229
Mapped reads with at least one deletion	2.08%
Homopolymer indels	46.66%

2.6. Chromosome stats

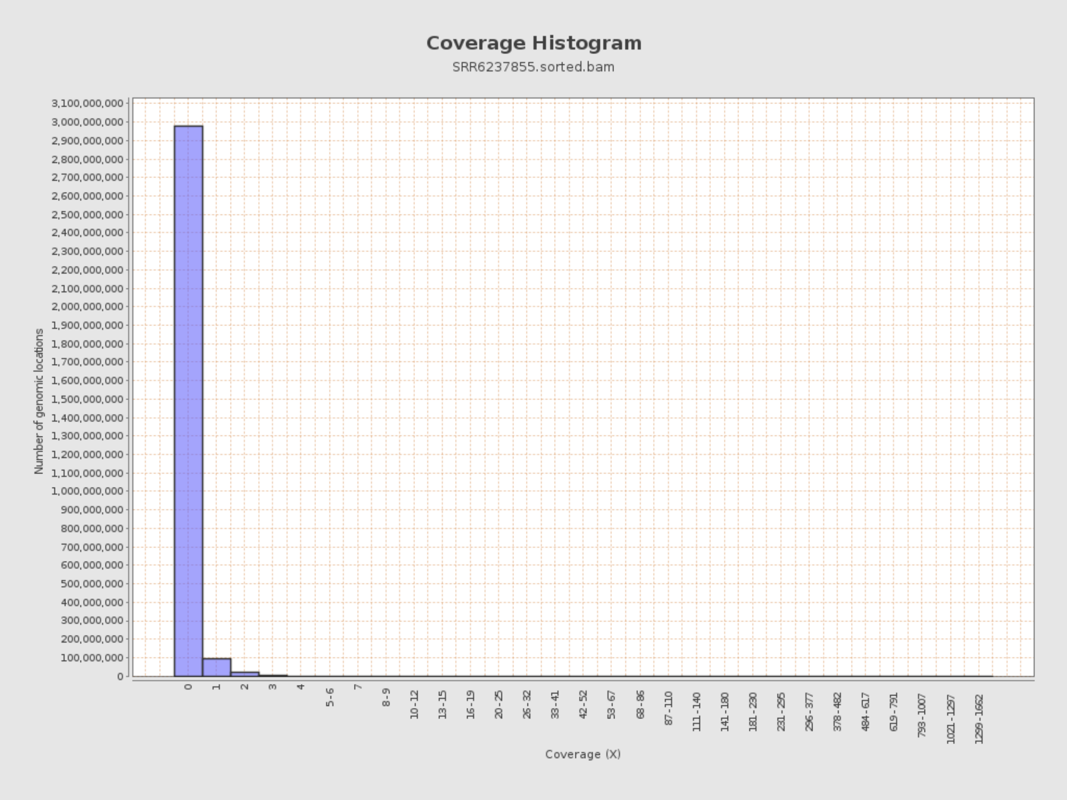
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	20490453	0.0822	1.3387
chr2	243199373	12396708	0.051	0.4797
chr3	198022430	7674351	0.0388	0.2575
chr4	191154276	12227630	0.064	0.3541
chr5	180915260	8809356	0.0487	0.2767
chr6	171115067	6314002	0.0369	0.2627
chr7	159138663	8638281	0.0543	0.7767

chr8	146364022	3443270	0.0235	0.4296
chr9	141213431	7565980	0.0536	0.4891
chr10	135534747	7774577	0.0574	0.6277
chr11	135006516	2607940	0.0193	0.2634
chr12	133851895	7238128	0.0541	0.2952
chr13	115169878	10077678	0.0875	0.3648
chr14	107349540	4668020	0.0435	0.29
chr15	102531392	529629	0.0052	0.085
chr16	90354753	2815781	0.0312	0.3033
chr17	81195210	4267098	0.0526	0.3919
chr18	78077248	3954450	0.0506	0.8987
chr19	59128983	855415	0.0145	0.8495
chr20	63025520	2921273	0.0464	0.2883
chr21	48129895	568674	0.0118	0.2271
chr22	51304566	1075295	0.021	0.1738
chrMT	16571	24417	1.4735	1.4309
chrX	155270560	14448860	0.0931	0.4303
chrY	59373566	477247	0.008	0.2389

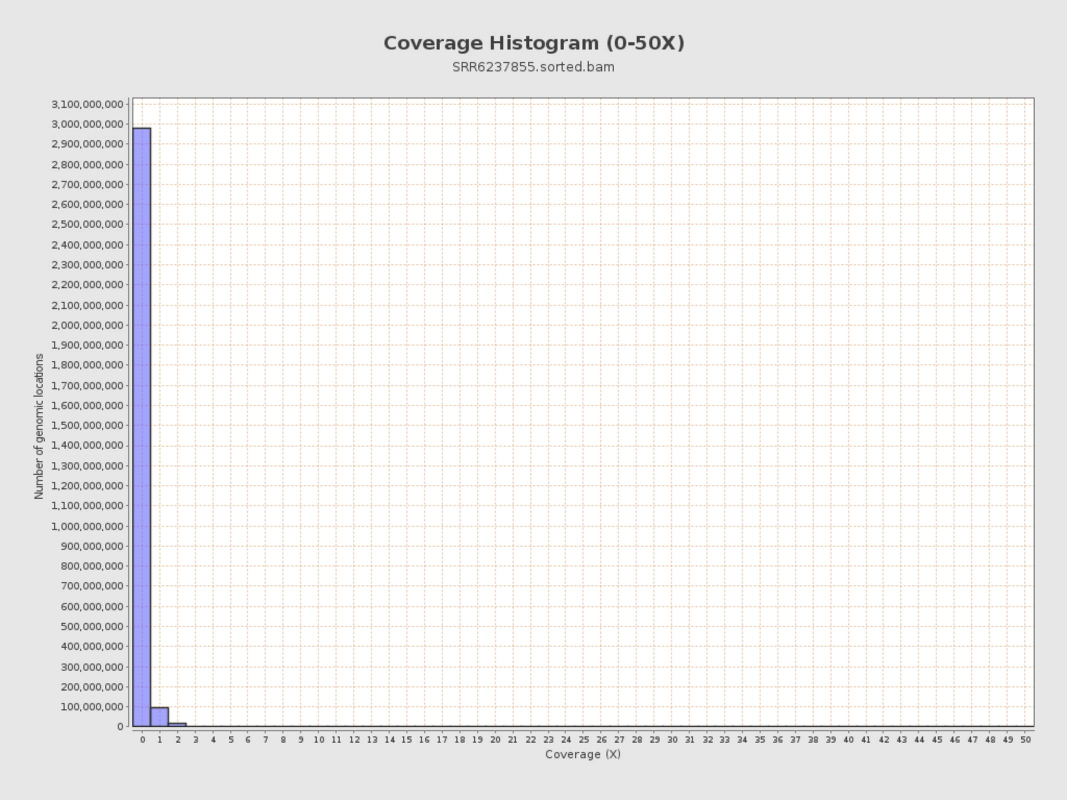
3. Results : Coverage across reference



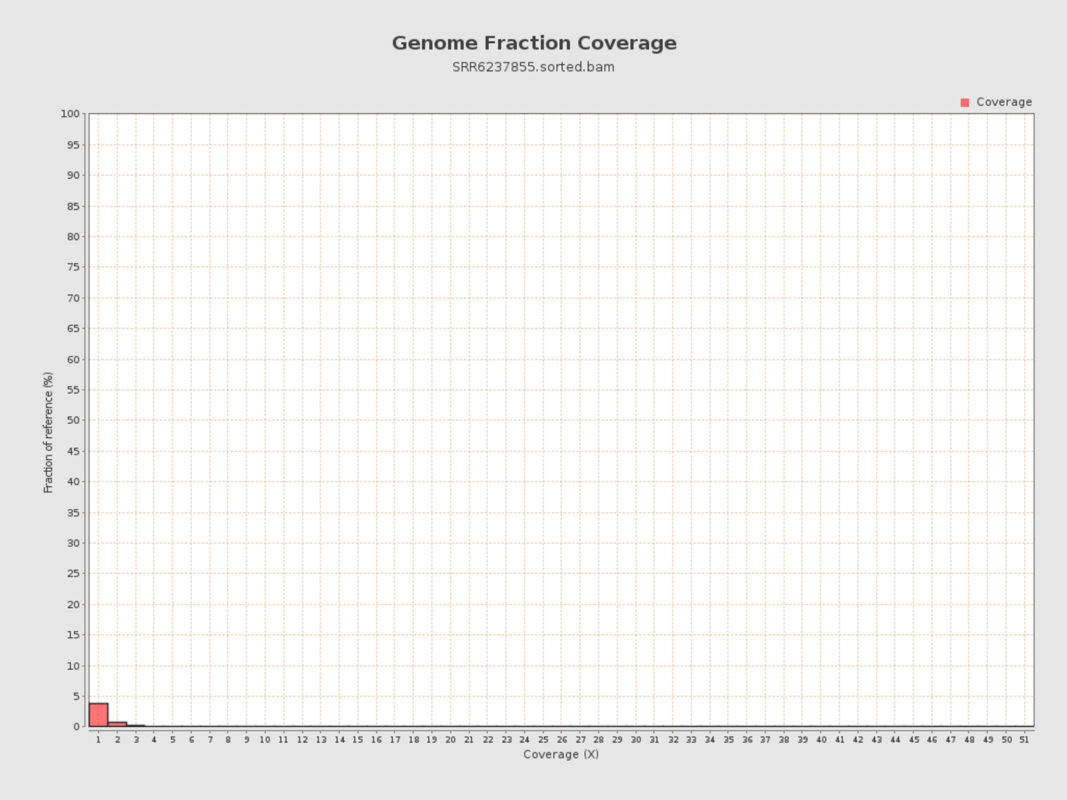
4. Results : Coverage Histogram



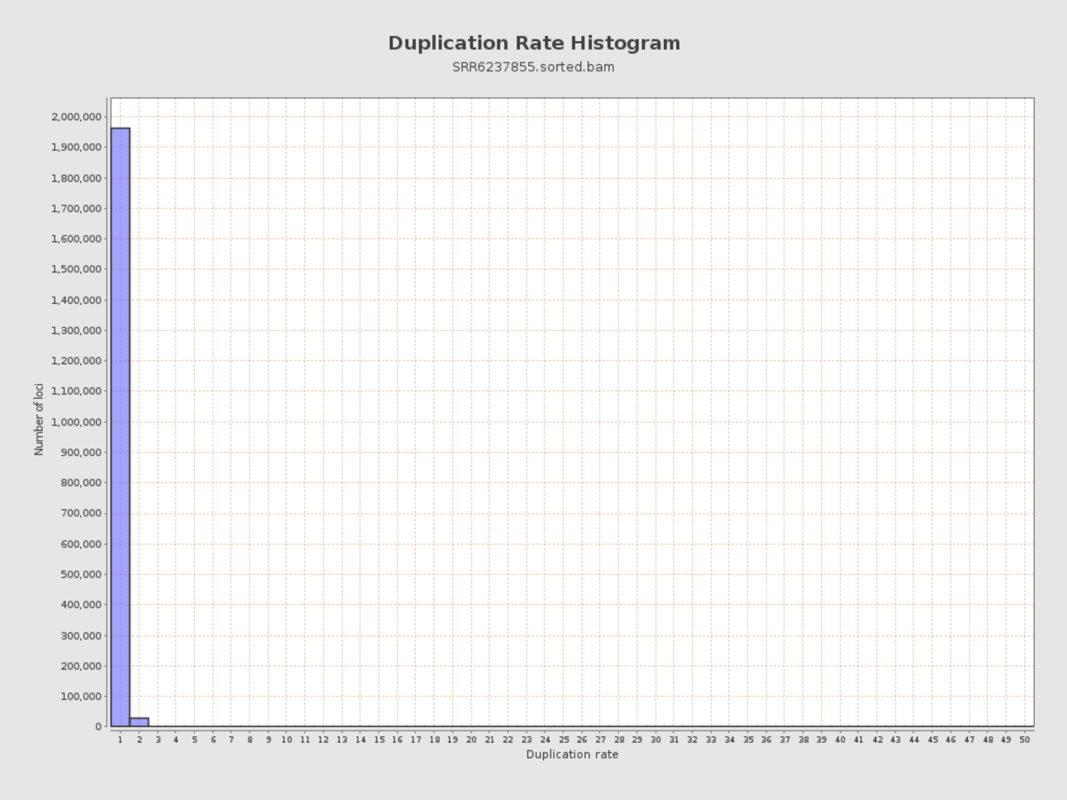
5. Results : Coverage Histogram (0-50X)



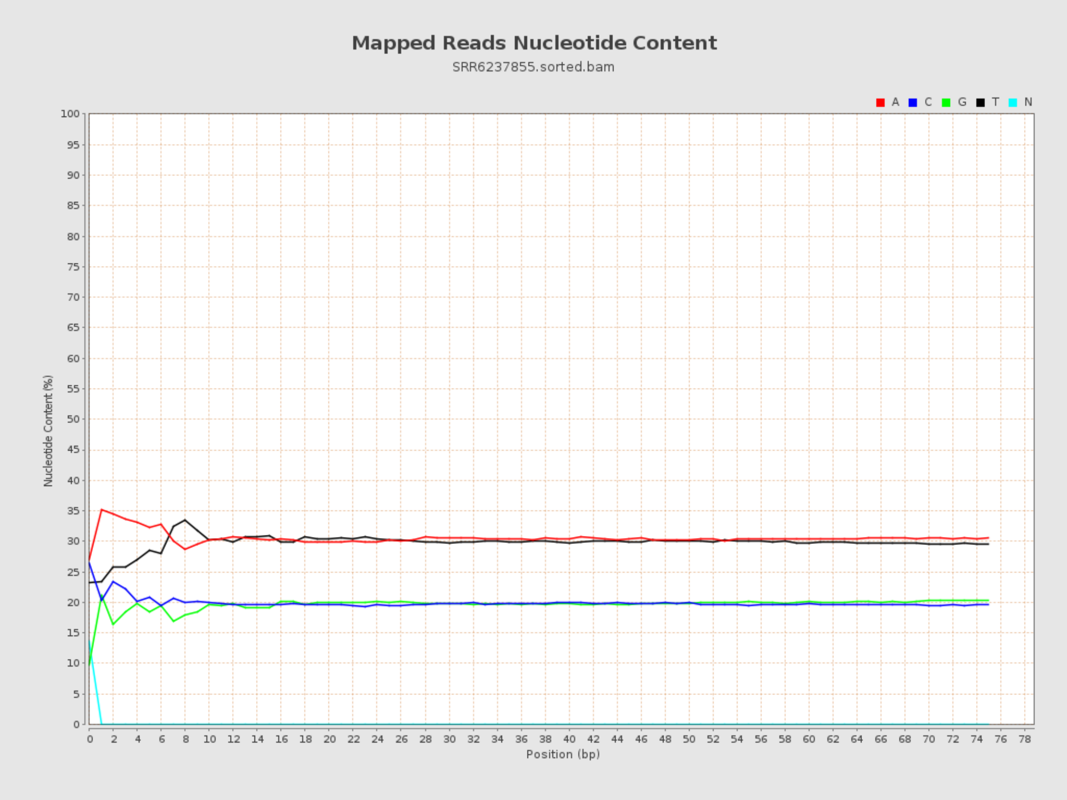
6. Results : Genome Fraction Coverage



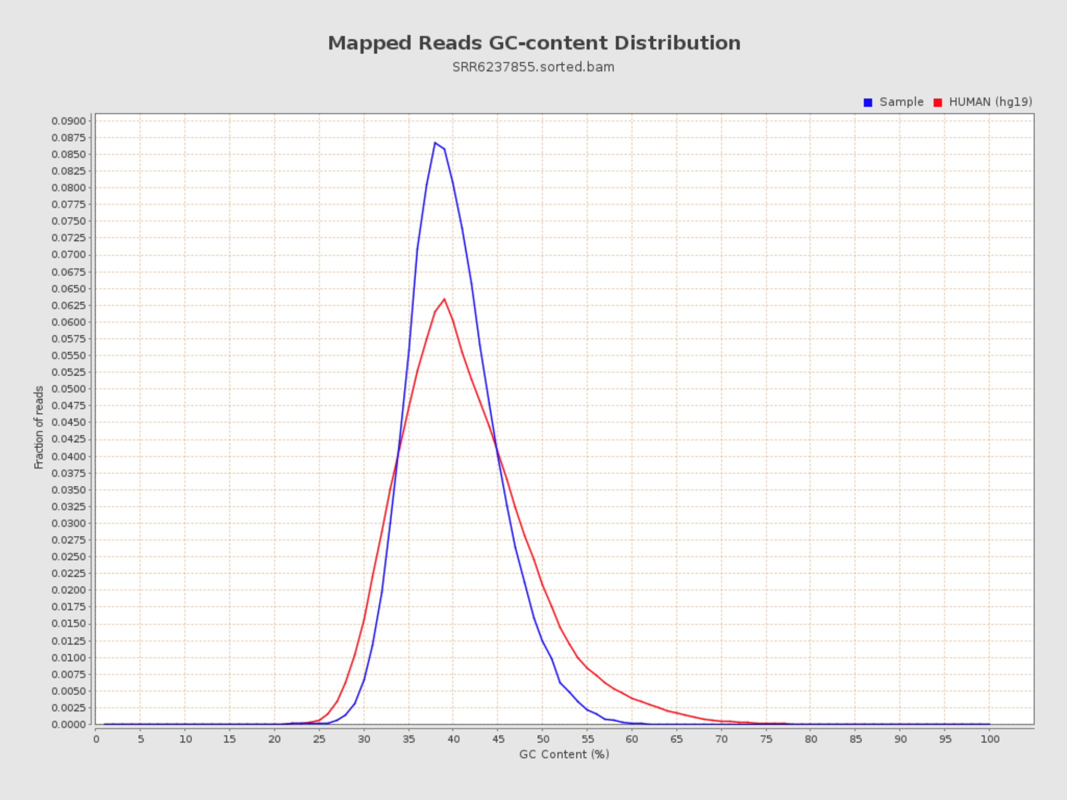
7. Results : Duplication Rate Histogram



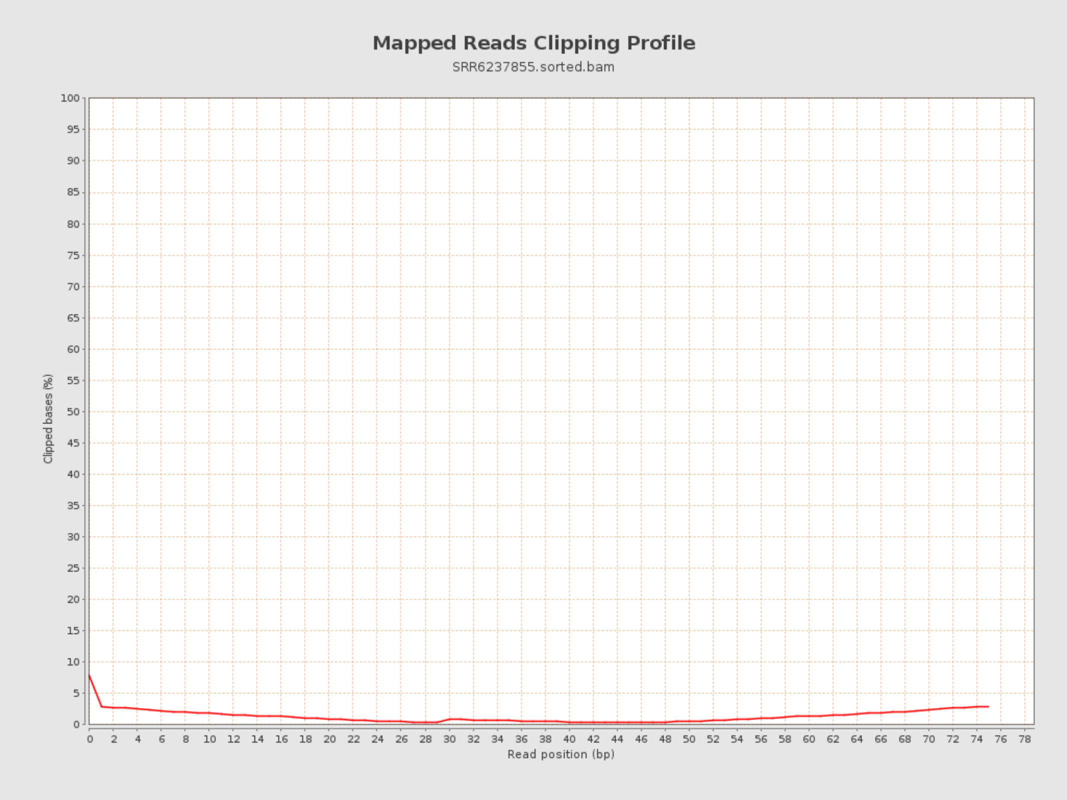
8. Results : Mapped Reads Nucleotide Content



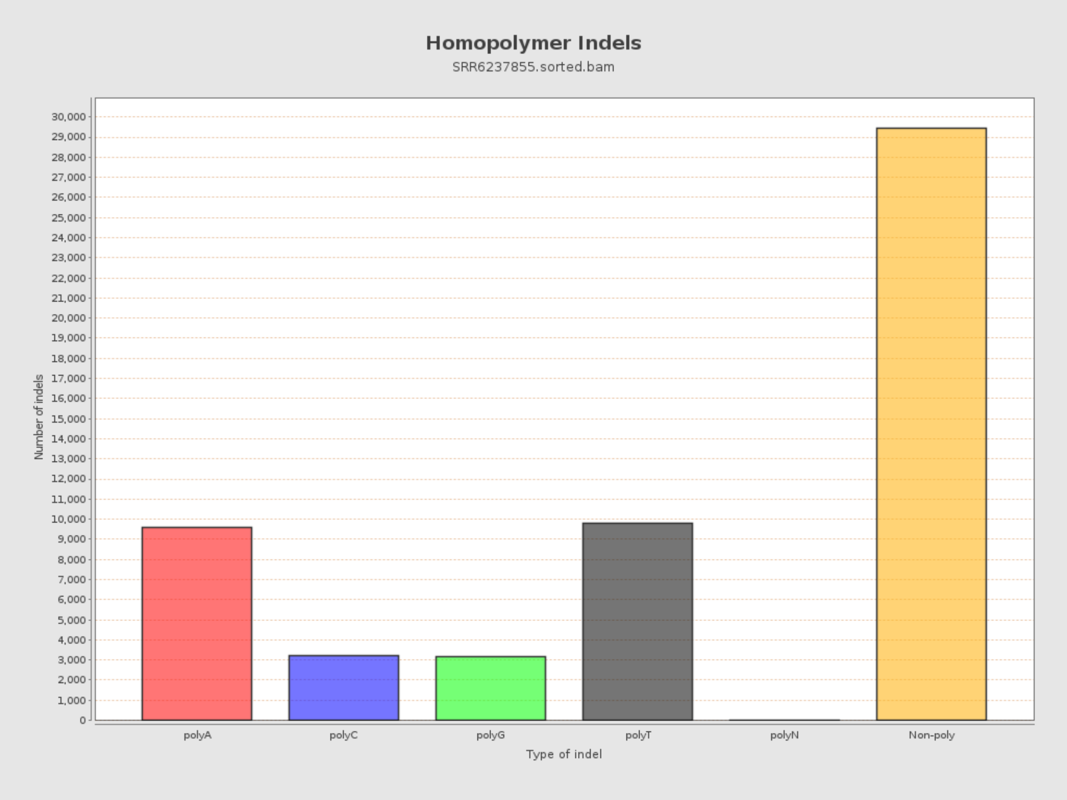
9. Results : Mapped Reads GC-content Distribution



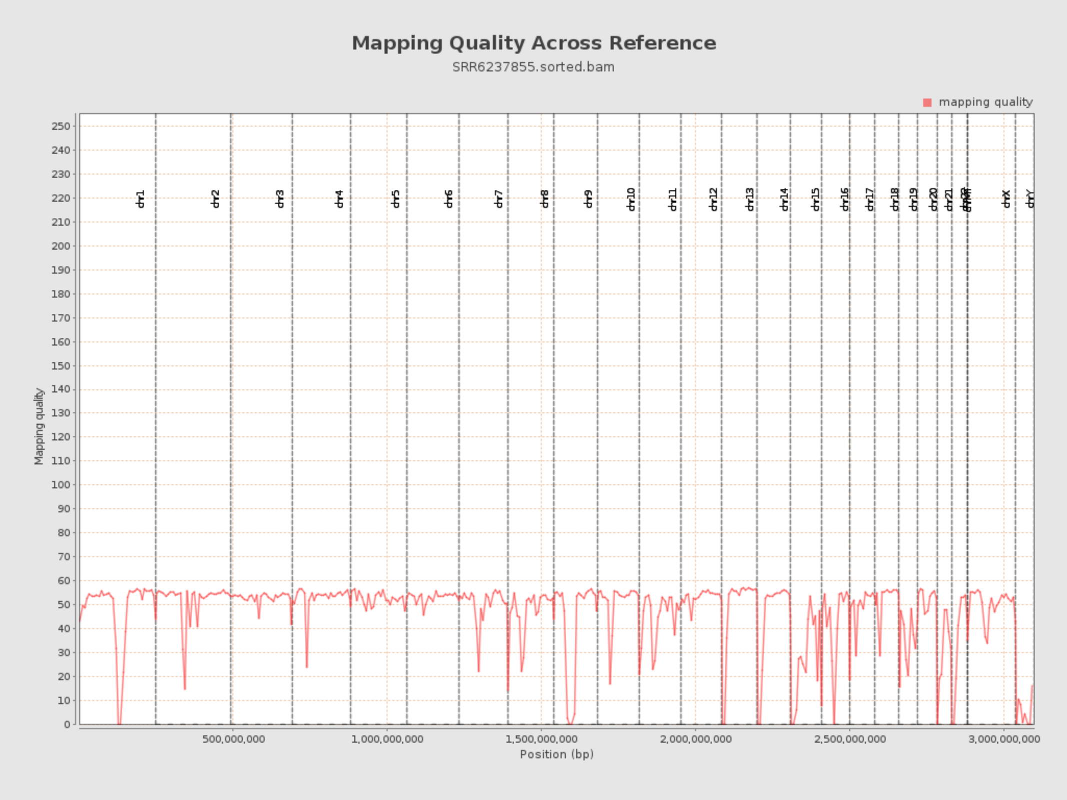
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram