Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 21:38:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238600.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_SRR6238600 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238600.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 21:38:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238600.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,251,607
Mapped reads	4,847,516 / 92.31%
Unmapped reads	404,091 / 7.69%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,315 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	568,566 / 10.83%
Duplication rate	9.7%
Clipped reads	2,761,438 / 52.58%

2.2. ACGT Content

Number/percentage of A's	76,338,899 / 24.89%
Number/percentage of C's	55,450,674 / 18.08%
Number/percentage of T's	100,747,041 / 32.85%
Number/percentage of G's	74,175,958 / 24.18%
Number/percentage of N's	16,384 / 0.01%
GC Percentage	42.26%

2.3. Coverage

Mean	0.0991

Standard Deviation	0.947

2.4. Mapping Quality

Mean Mapping Quality	43.88

2.5. Mismatches and indels

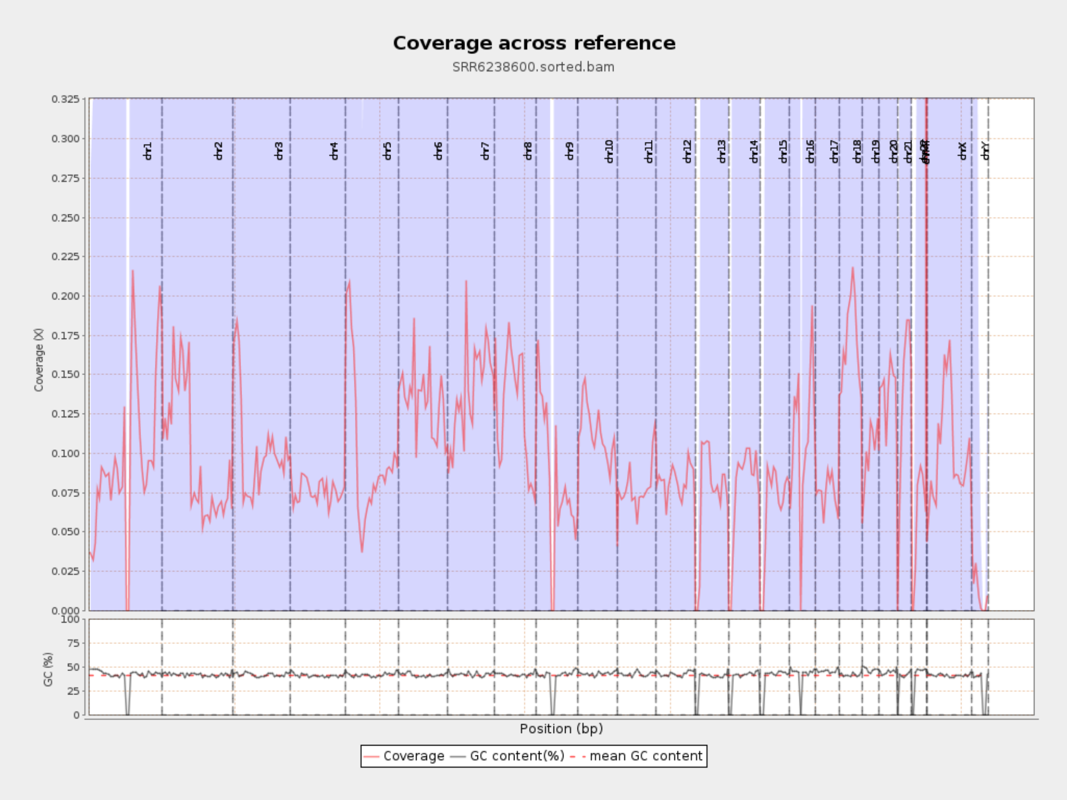
General error rate	0.57%
Mismatches	1,706,706
Insertions	20,267
Mapped reads with at least one insertion	0.41%
Deletions	83,680
Mapped reads with at least one deletion	1.71%
Homopolymer indels	42.71%

2.6. Chromosome stats

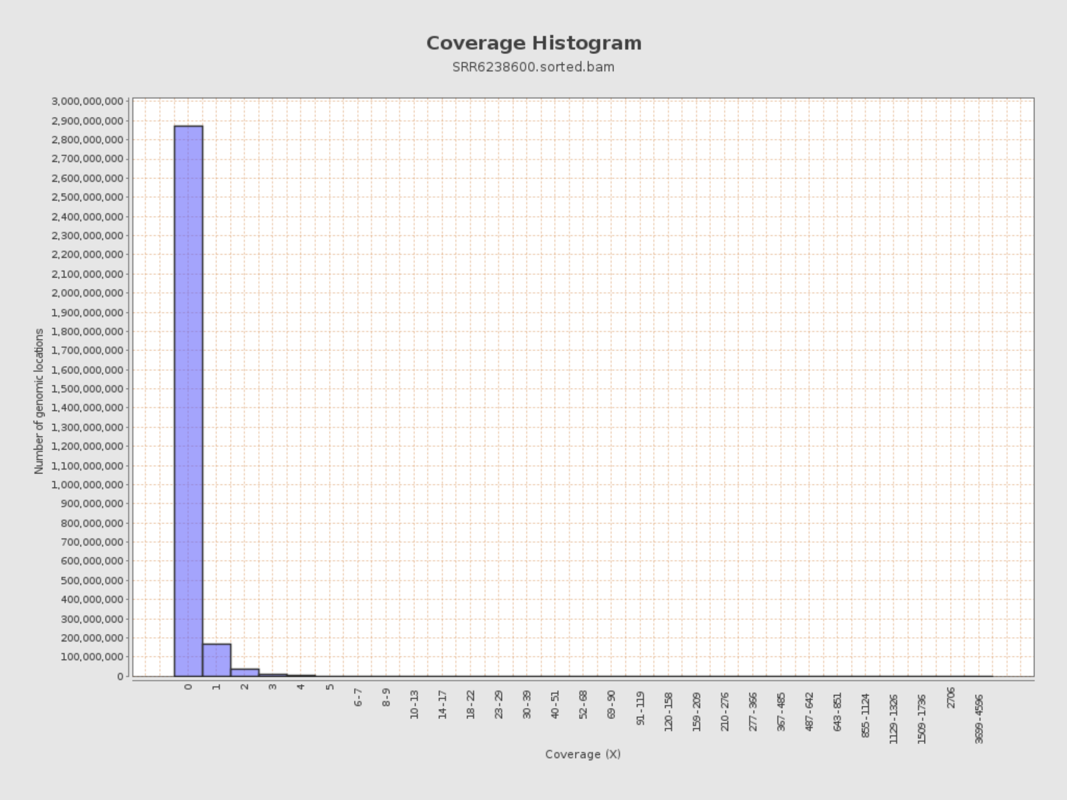
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	24063917	0.0965	1.0641
chr2	243199373	24069267	0.099	2.1136
chr3	198022430	20429835	0.1032	0.4368
chr4	191154276	14435766	0.0755	0.3825
chr5	180915260	17849182	0.0987	0.4307
chr6	171115067	22948305	0.1341	0.9026
chr7	159138663	22439479	0.141	1.4581

chr8	146364022	18548264	0.1267	0.9074
chr9	141213431	11631280	0.0824	0.8154
chr10	135534747	15332020	0.1131	0.5961
chr11	135006516	10560945	0.0782	0.5253
chr12	133851895	10992042	0.0821	0.4404
chr13	115169878	8410635	0.073	0.5029
chr14	107349540	8236681	0.0767	0.5009
chr15	102531392	6754571	0.0659	0.4898
chr16	90354753	10163329	0.1125	0.5886
chr17	81195210	6020523	0.0741	0.38
chr18	78077248	13435668	0.1721	1.8098
chr19	59128983	5991163	0.1013	0.7899
chr20	63025520	8852841	0.1405	0.5472
chr21	48129895	6327176	0.1315	0.5529
chr22	51304566	2891711	0.0564	0.3072
chrMT	16571	47347	2.8572	2.9488
chrX	155270560	15762611	0.1015	0.5229
chrY	59373566	678576	0.0114	0.2947

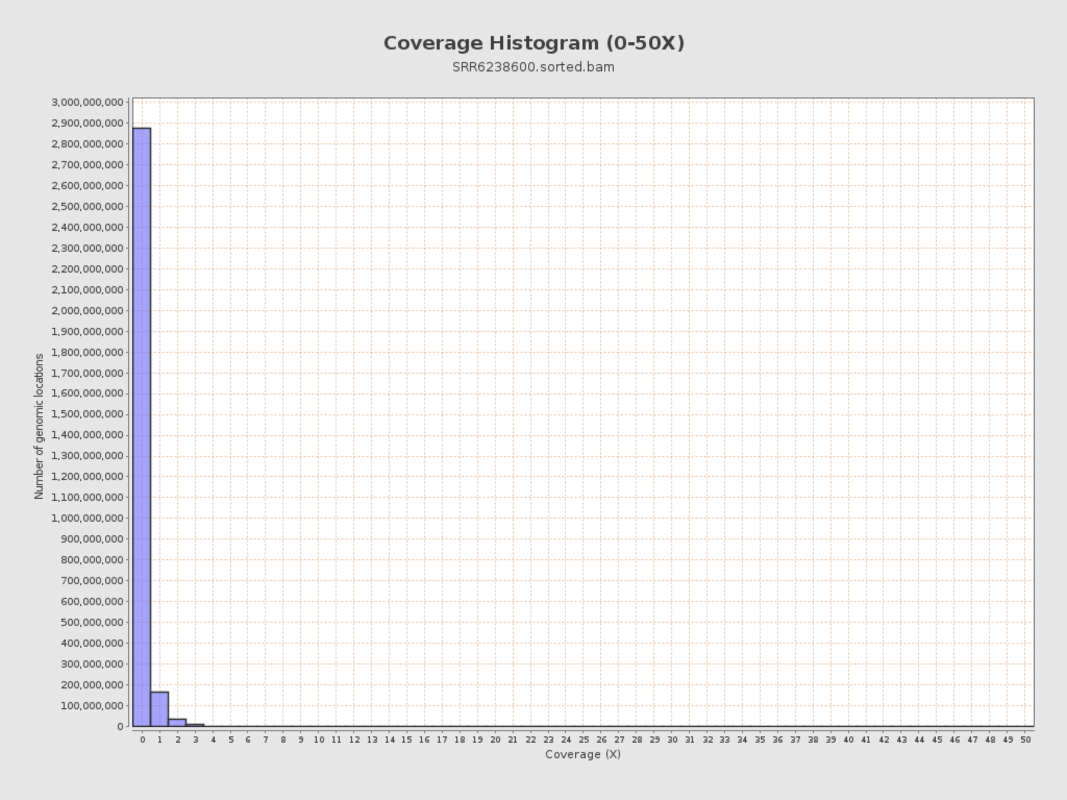
3. Results : Coverage across reference



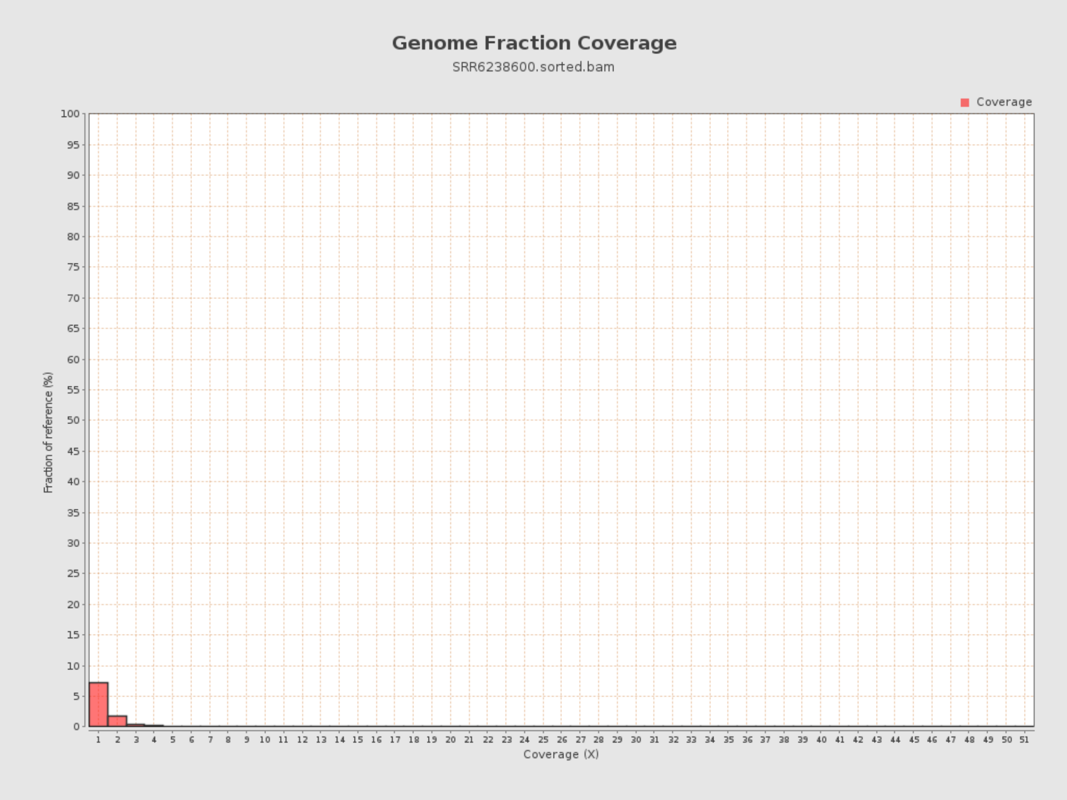
4. Results : Coverage Histogram



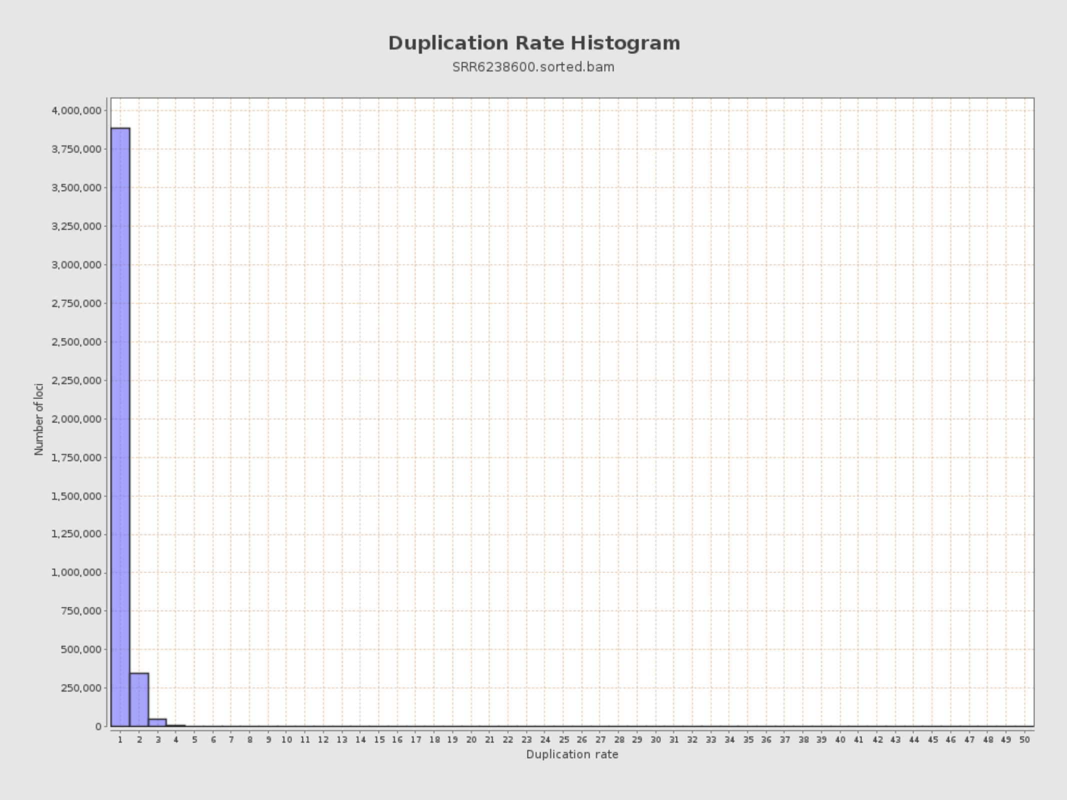
5. Results : Coverage Histogram (0-50X)



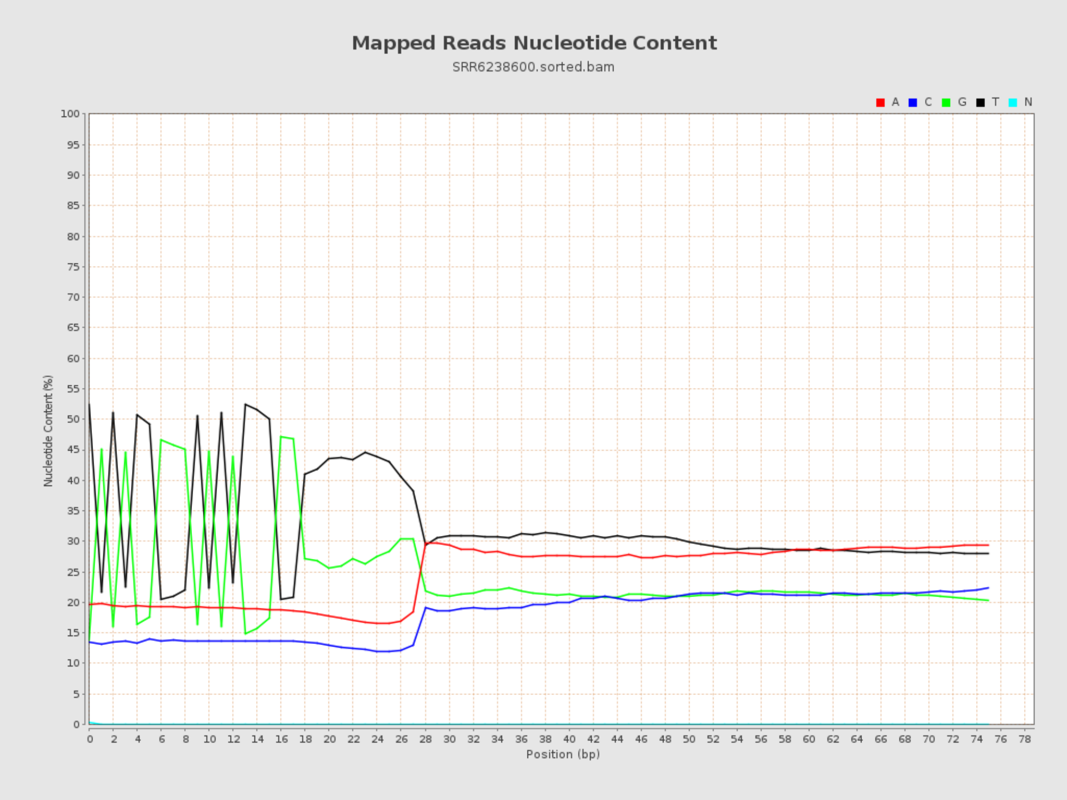
6. Results : Genome Fraction Coverage



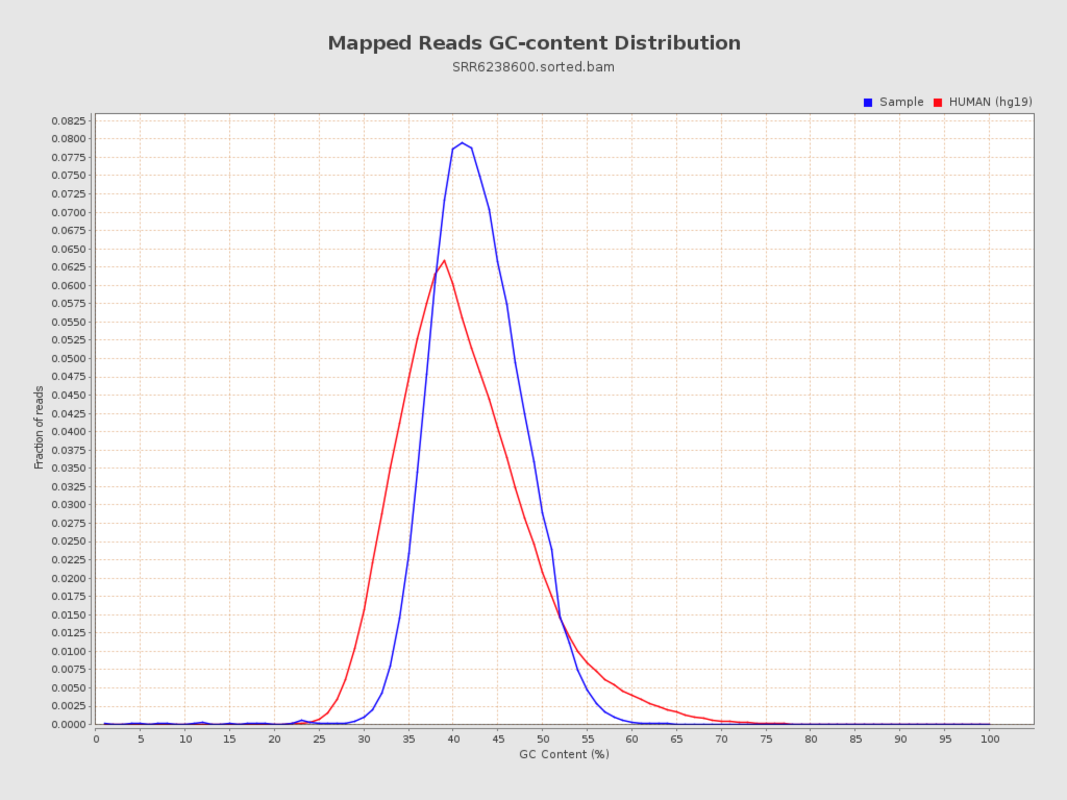
7. Results : Duplication Rate Histogram



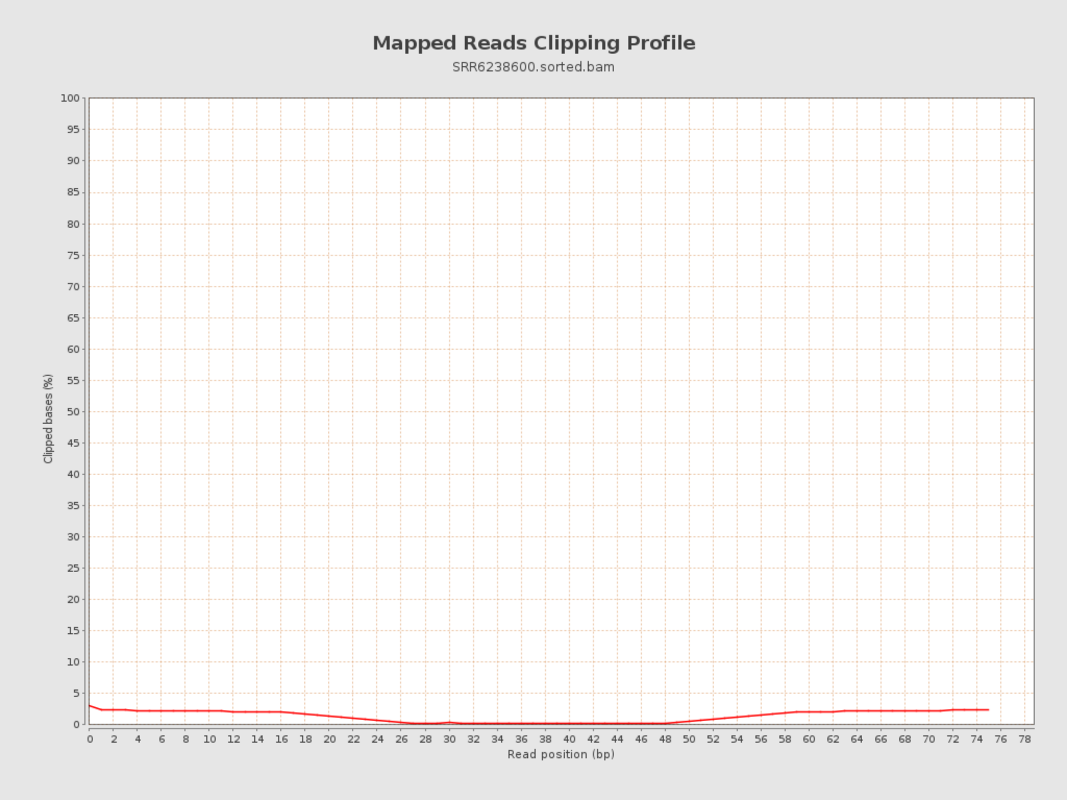
8. Results : Mapped Reads Nucleotide Content



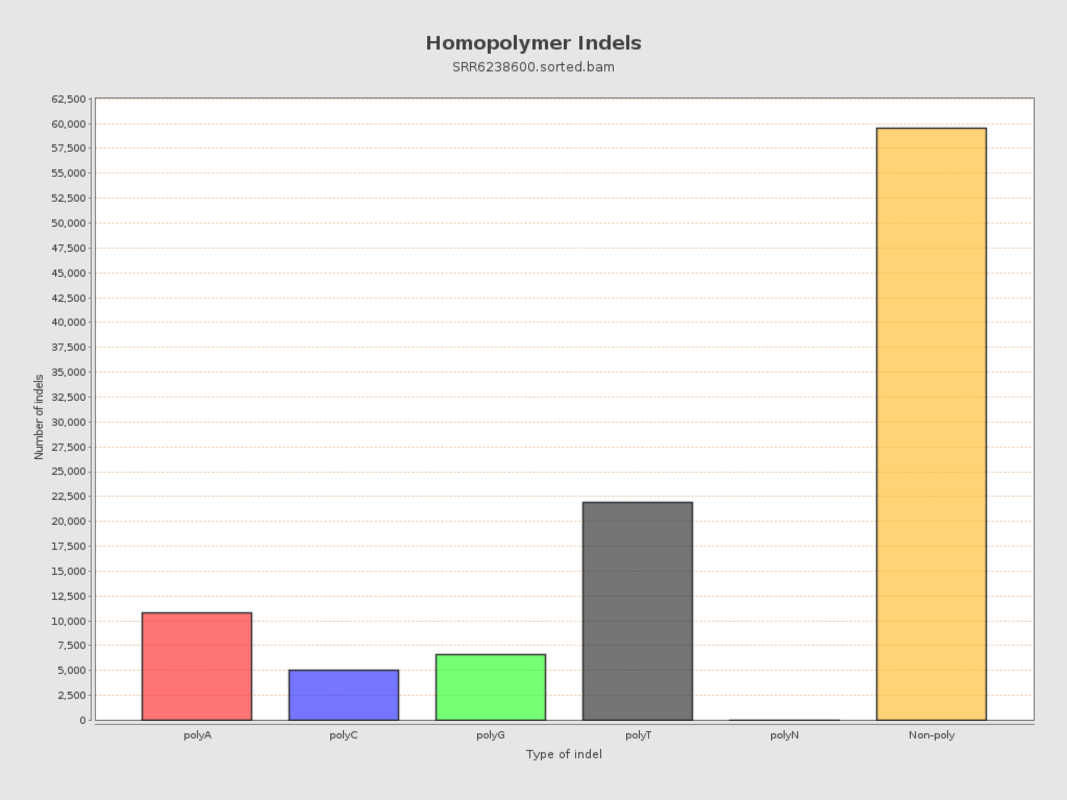
9. Results : Mapped Reads GC-content Distribution



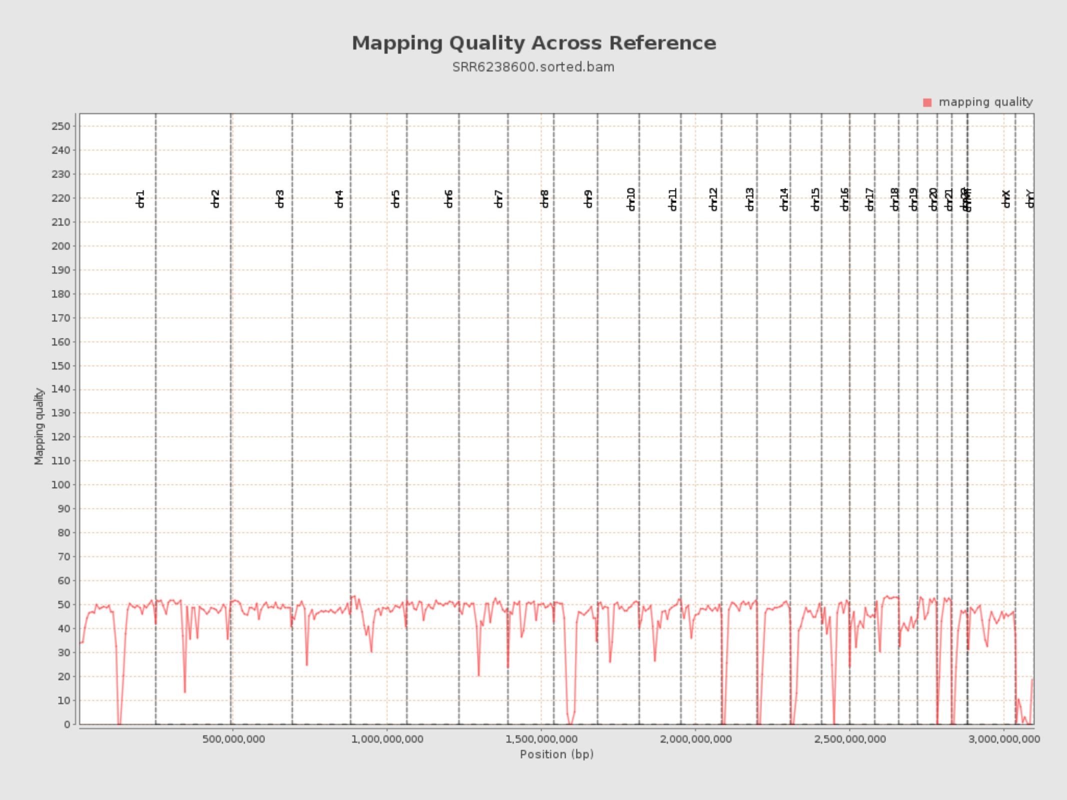
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram