Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 22:31:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238615.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_SRR6238615 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238615.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 22:31:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238615.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,407,718
Mapped reads	2,785,494 / 81.74%
Unmapped reads	622,224 / 18.26%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,467 / 0.66%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	637,395 / 18.7%
Duplication rate	17.39%
Clipped reads	1,625,365 / 47.7%

2.2. ACGT Content

Number/percentage of A's	43,074,908 / 24.6%
Number/percentage of C's	32,193,925 / 18.39%
Number/percentage of T's	57,088,739 / 32.61%
Number/percentage of G's	42,719,596 / 24.4%
Number/percentage of N's	9,082 / 0.01%
GC Percentage	42.79%

2.3. Coverage

Mean	0.0566

Standard Deviation	0.7363

2.4. Mapping Quality

Mean Mapping Quality	44.29

2.5. Mismatches and indels

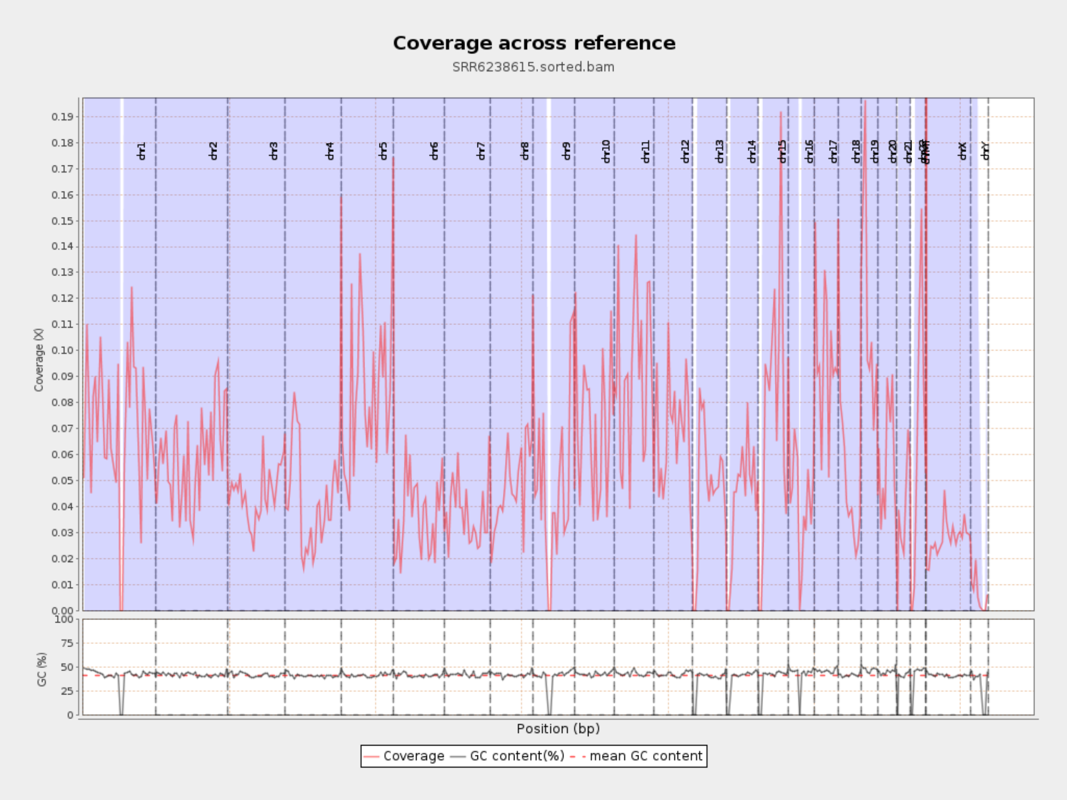
General error rate	0.55%
Mismatches	937,678
Insertions	11,792
Mapped reads with at least one insertion	0.42%
Deletions	45,305
Mapped reads with at least one deletion	1.61%
Homopolymer indels	43.52%

2.6. Chromosome stats

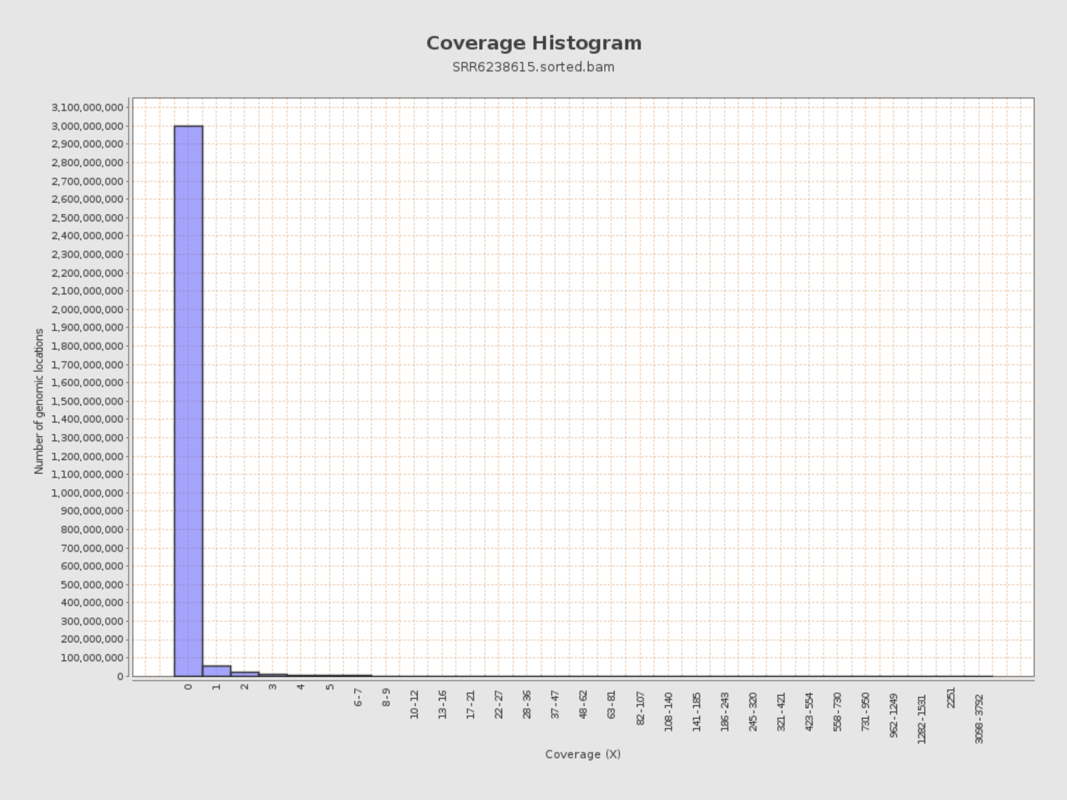
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17279493	0.0693	1.1273
chr2	243199373	14260820	0.0586	1.6898
chr3	198022430	8876695	0.0448	0.3618
chr4	191154276	8153932	0.0427	0.3487
chr5	180915260	15317984	0.0847	0.4969
chr6	171115067	6271871	0.0367	0.6174
chr7	159138663	5910812	0.0371	0.4379

chr8	146364022	6957248	0.0475	0.6099
chr9	141213431	6715491	0.0476	0.4143
chr10	135534747	9626095	0.071	0.544
chr11	135006516	12270808	0.0909	0.5354
chr12	133851895	9304307	0.0695	0.4488
chr13	115169878	5493685	0.0477	0.4781
chr14	107349540	4692633	0.0437	0.3578
chr15	102531392	7700189	0.0751	0.551
chr16	90354753	3871657	0.0428	0.3829
chr17	81195210	7923078	0.0976	0.538
chr18	78077248	3867088	0.0495	1.1386
chr19	59128983	6771896	0.1145	0.7794
chr20	63025520	3677375	0.0583	0.4246
chr21	48129895	1878051	0.039	0.3543
chr22	51304566	3508782	0.0684	0.4487
chrMT	16571	140562	8.4824	5.9822
chrX	155270560	4331761	0.0279	0.2912
chrY	59373566	362852	0.0061	0.2518

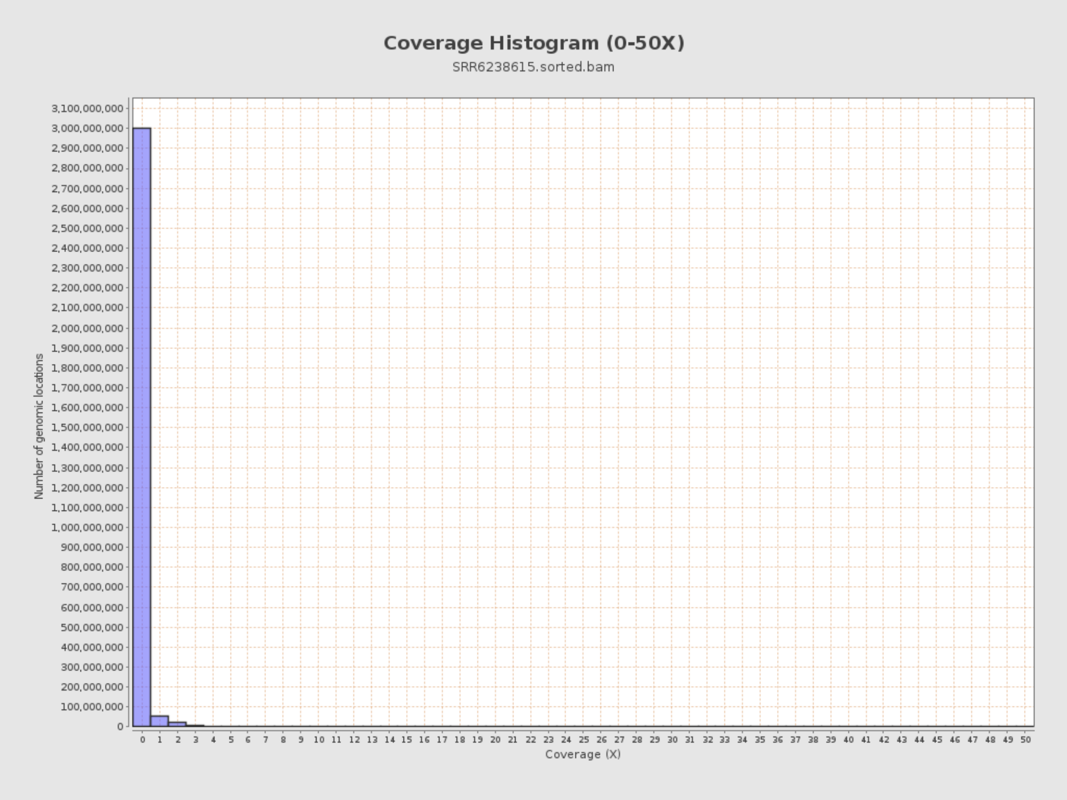
3. Results : Coverage across reference



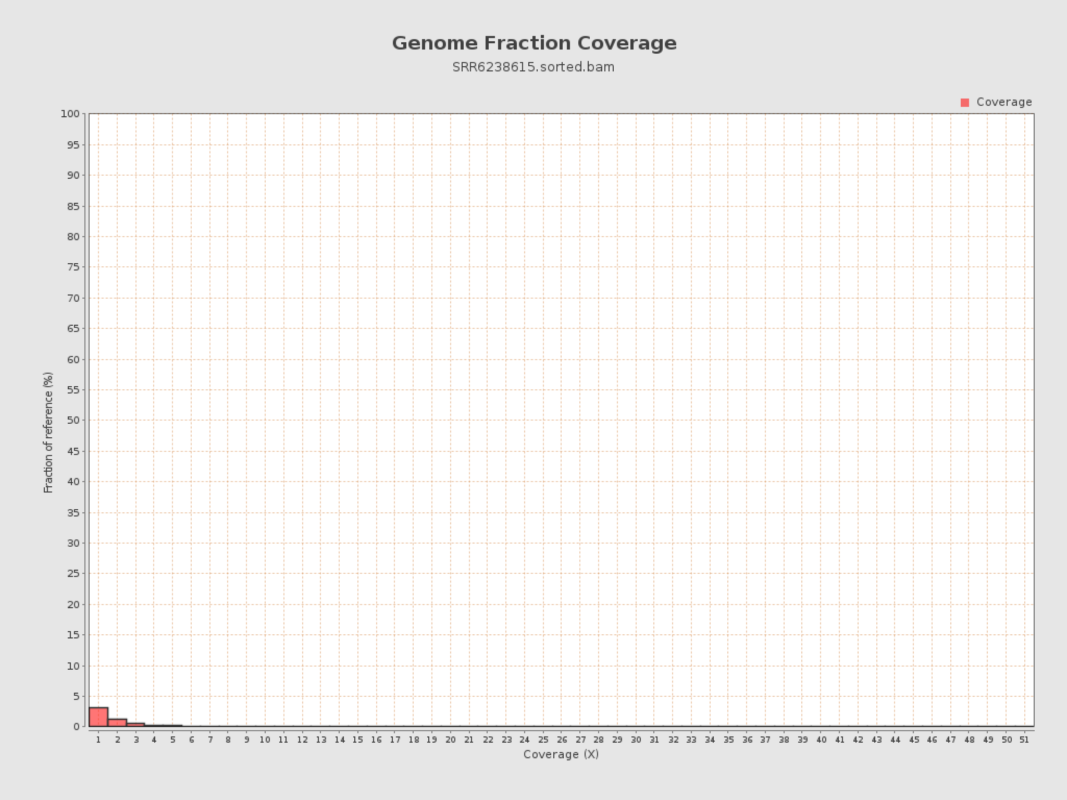
4. Results : Coverage Histogram



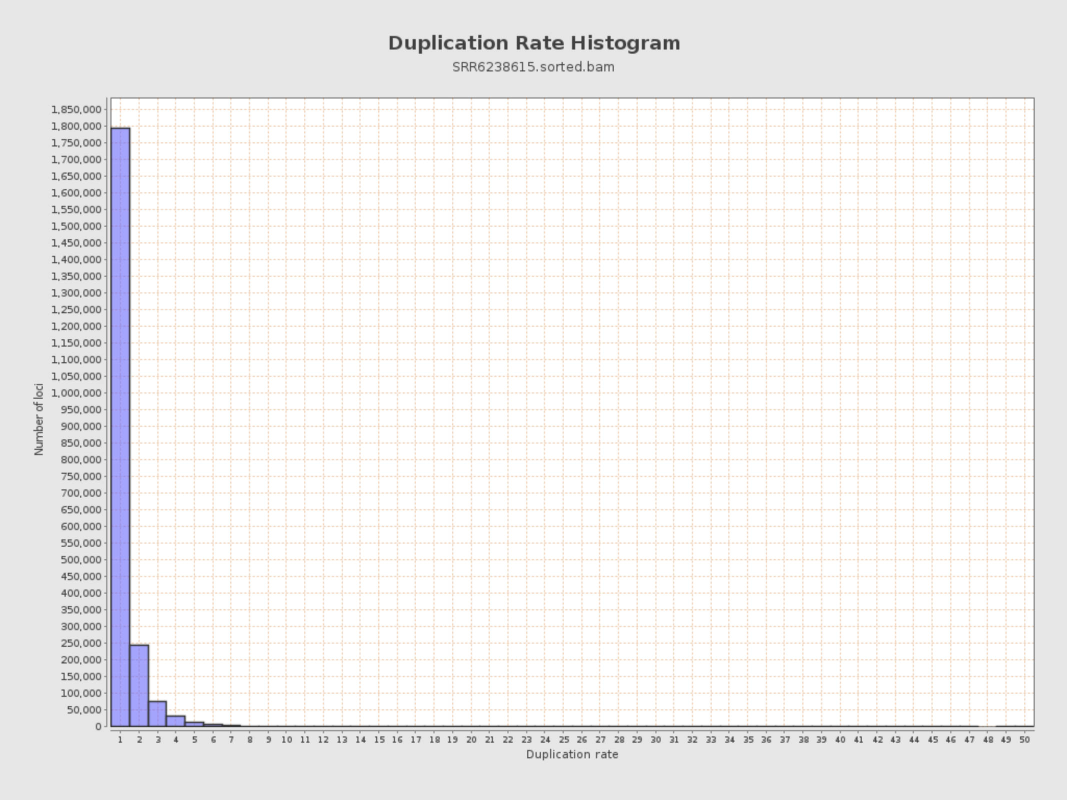
5. Results : Coverage Histogram (0-50X)



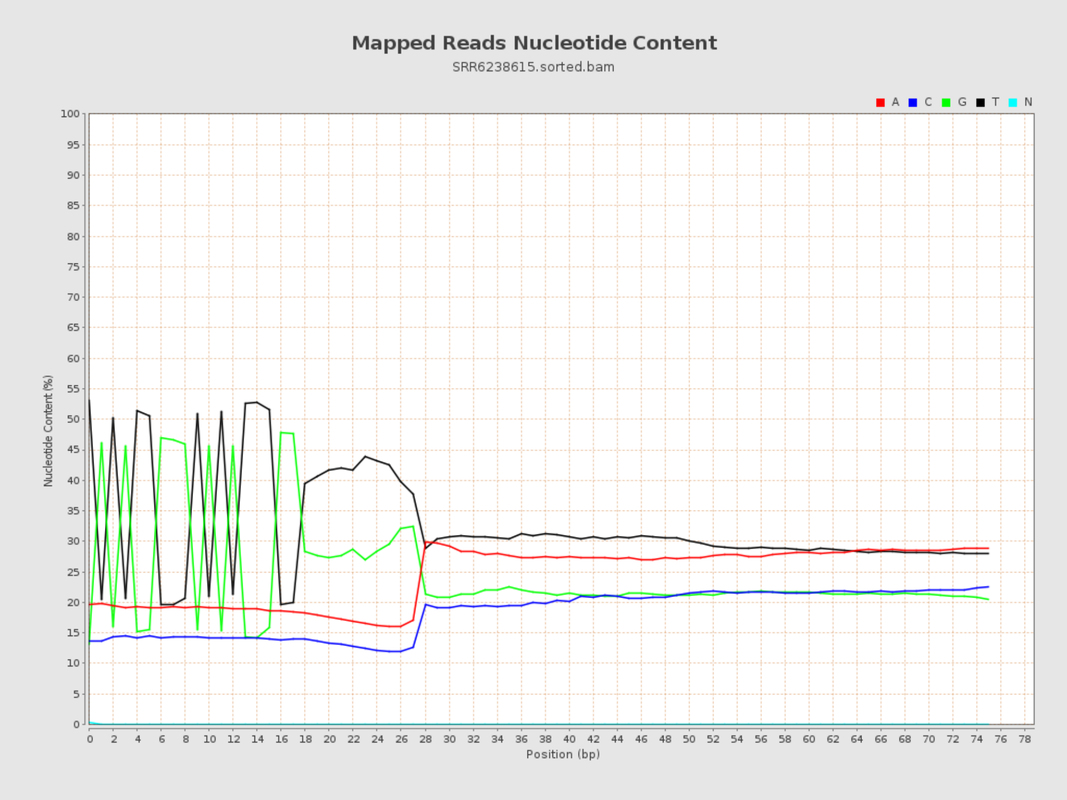
6. Results : Genome Fraction Coverage



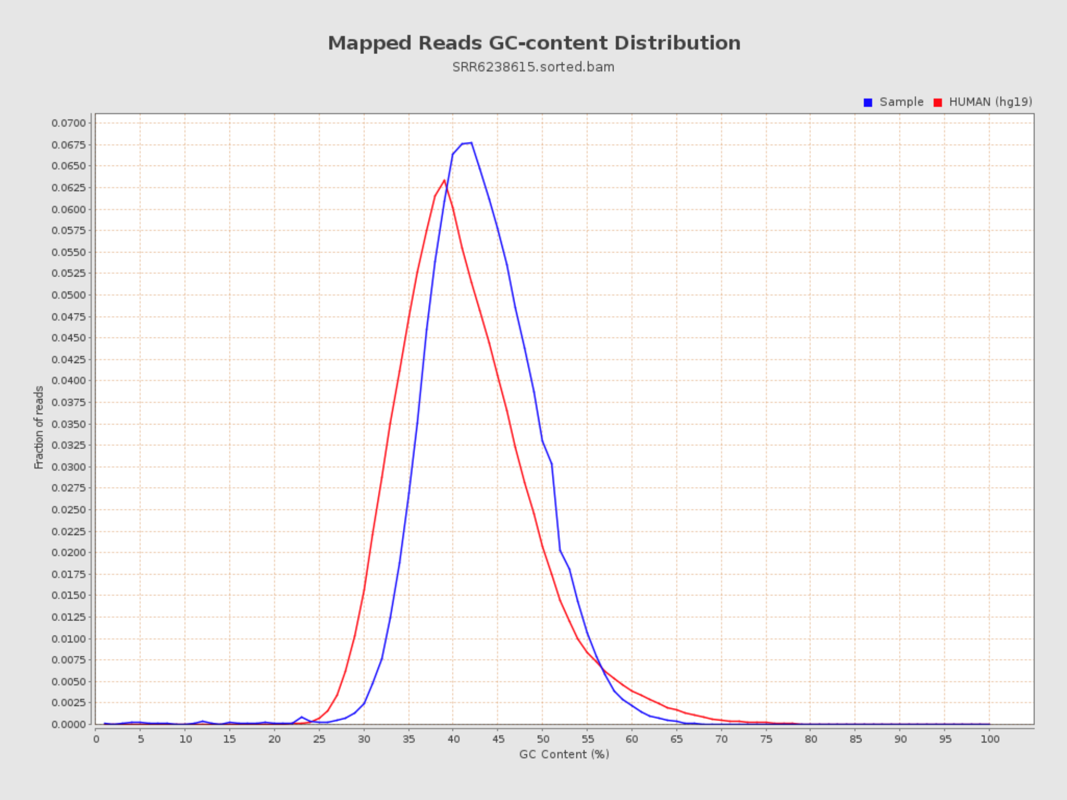
7. Results : Duplication Rate Histogram



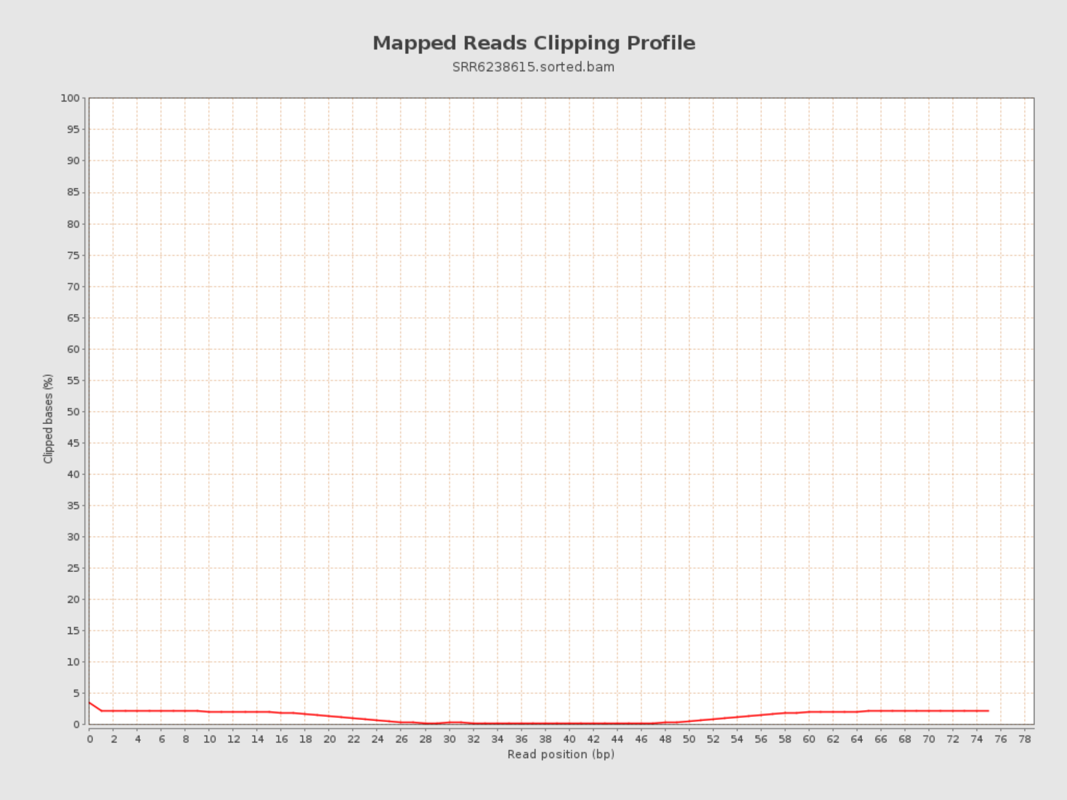
8. Results : Mapped Reads Nucleotide Content



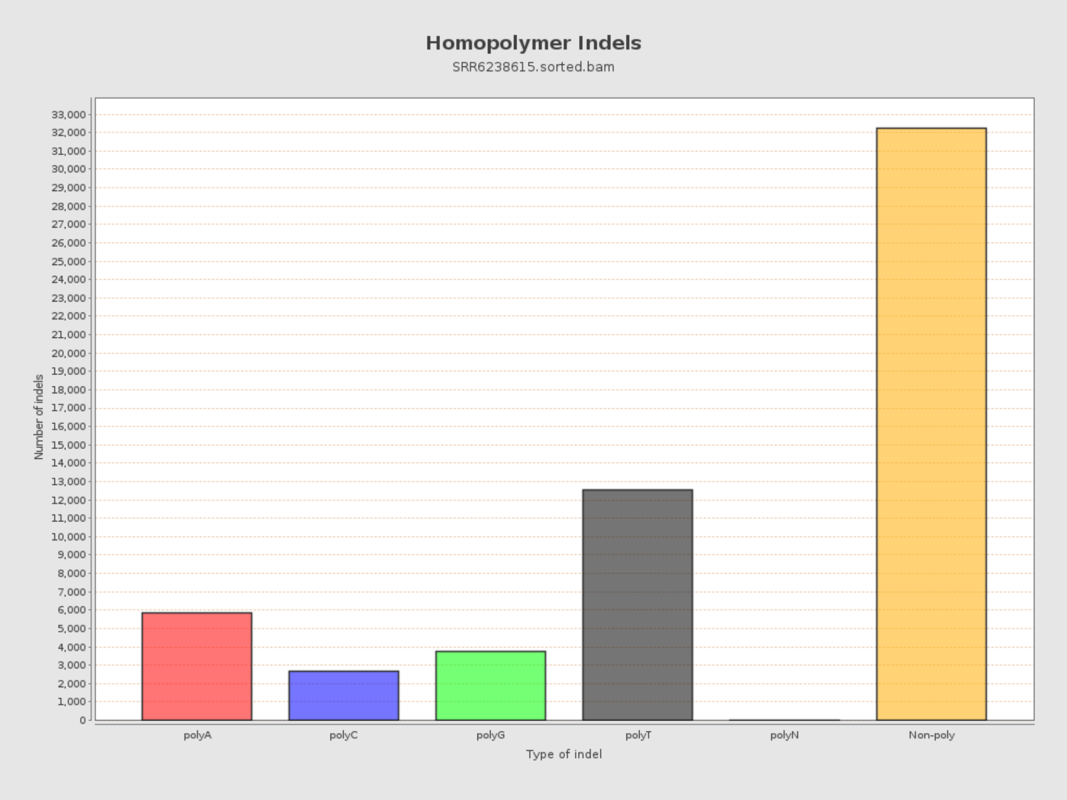
9. Results : Mapped Reads GC-content Distribution



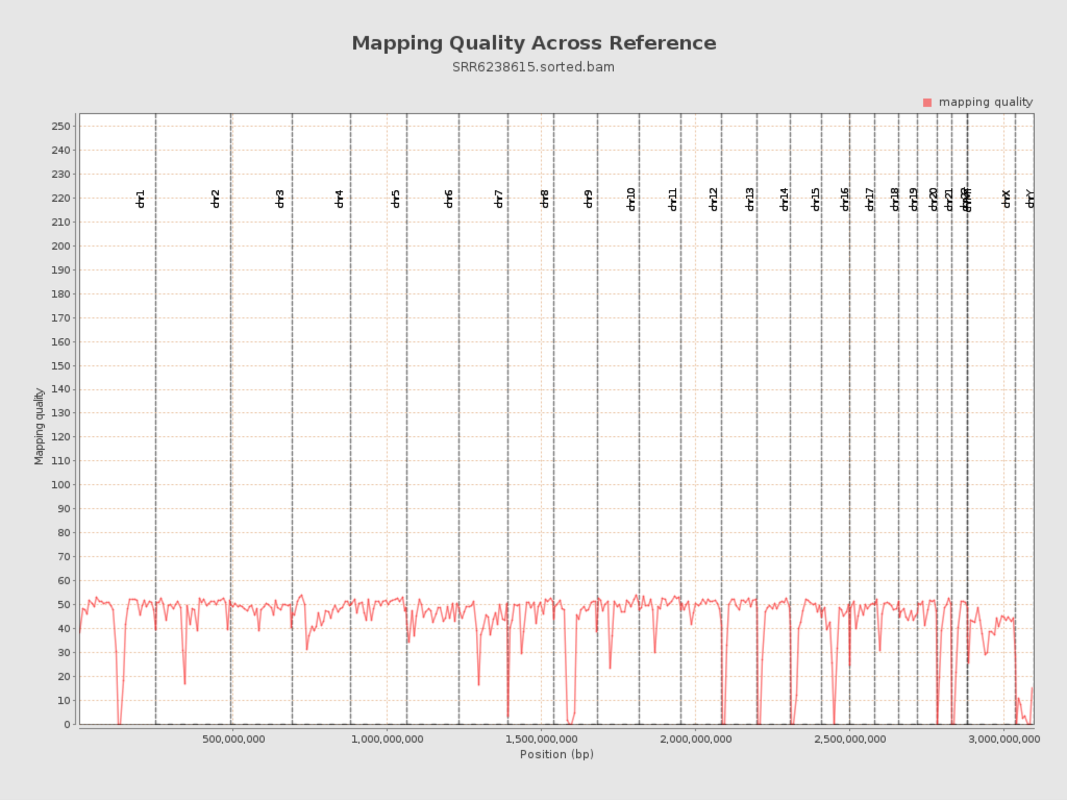
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram