Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 01:43:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238665.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_SRR6238665 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238665.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 01:43:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238665.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,797,305
Mapped reads	8,209,583 / 93.32%
Unmapped reads	587,722 / 6.68%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	68,506 / 0.78%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	856,208 / 9.73%
Duplication rate	8.26%
Clipped reads	4,846,642 / 55.09%

2.2. ACGT Content

Number/percentage of A's	127,761,161 / 24.8%
Number/percentage of C's	93,843,052 / 18.22%
Number/percentage of T's	165,588,504 / 32.14%
Number/percentage of G's	127,957,576 / 24.84%
Number/percentage of N's	26,529 / 0.01%
GC Percentage	43.05%

2.3. Coverage

Mean	0.1665

Standard Deviation	1.5703

2.4. Mapping Quality

Mean Mapping Quality	42.02

2.5. Mismatches and indels

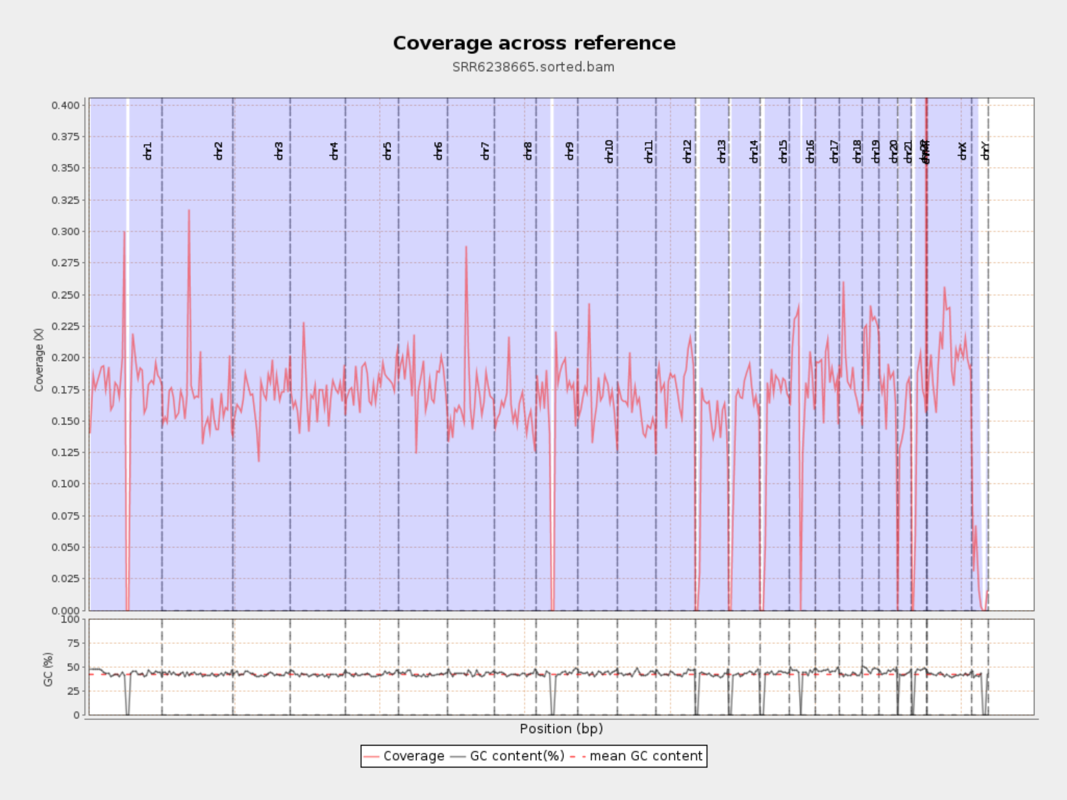
General error rate	0.56%
Mismatches	2,807,990
Insertions	39,276
Mapped reads with at least one insertion	0.47%
Deletions	118,697
Mapped reads with at least one deletion	1.43%
Homopolymer indels	43.05%

2.6. Chromosome stats

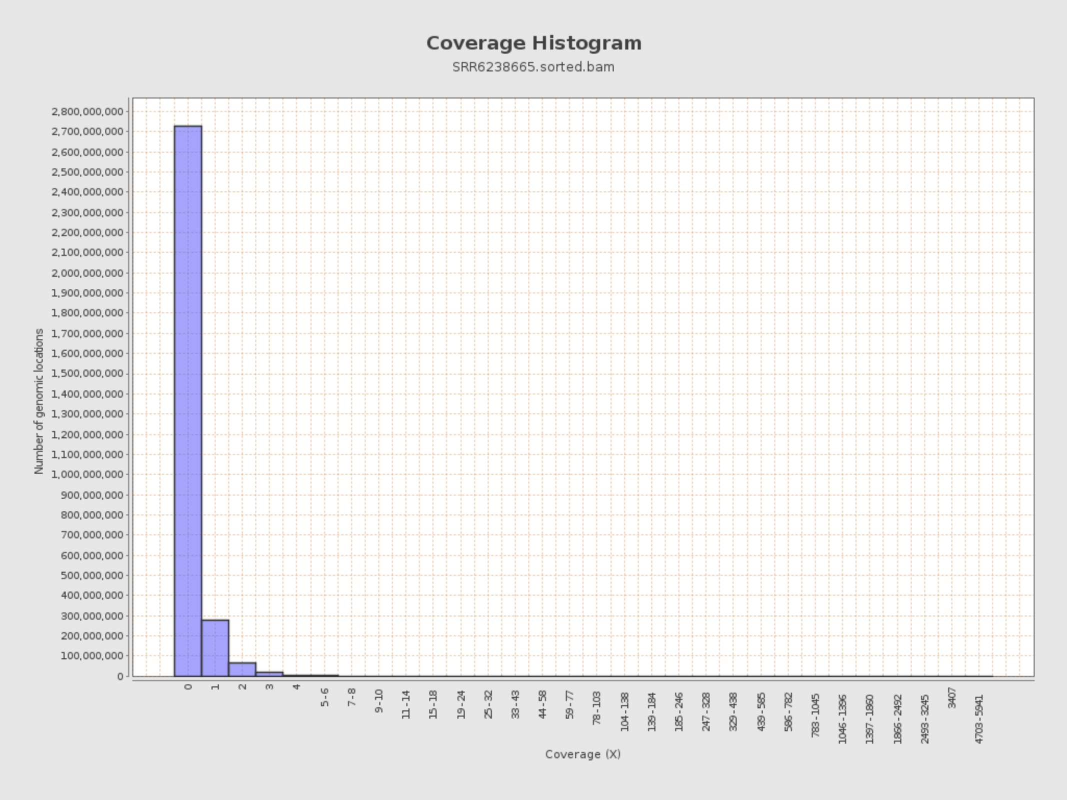
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	43214966	0.1734	2.6602
chr2	243199373	40469551	0.1664	2.8666
chr3	198022430	33563947	0.1695	0.5851
chr4	191154276	32425527	0.1696	0.68
chr5	180915260	32495510	0.1796	0.6293
chr6	171115067	31208498	0.1824	1.1136
chr7	159138663	27009863	0.1697	2.0438

chr8	146364022	23117205	0.1579	1.2831
chr9	141213431	22411315	0.1587	1.5062
chr10	135534747	22965006	0.1694	1.2964
chr11	135006516	21544201	0.1596	1.2731
chr12	133851895	24283833	0.1814	0.6805
chr13	115169878	14940629	0.1297	0.6986
chr14	107349540	15584251	0.1452	0.7796
chr15	102531392	14705617	0.1434	0.7489
chr16	90354753	15849276	0.1754	0.8715
chr17	81195210	15169346	0.1868	0.7203
chr18	78077248	14600235	0.187	3.6579
chr19	59128983	12880132	0.2178	1.6788
chr20	63025520	10952160	0.1738	0.6728
chr21	48129895	6739221	0.14	0.7036
chr22	51304566	6448925	0.1257	0.4911
chrMT	16571	37577	2.2676	2.7096
chrX	155270560	31328988	0.2018	0.8449
chrY	59373566	1441220	0.0243	0.5449

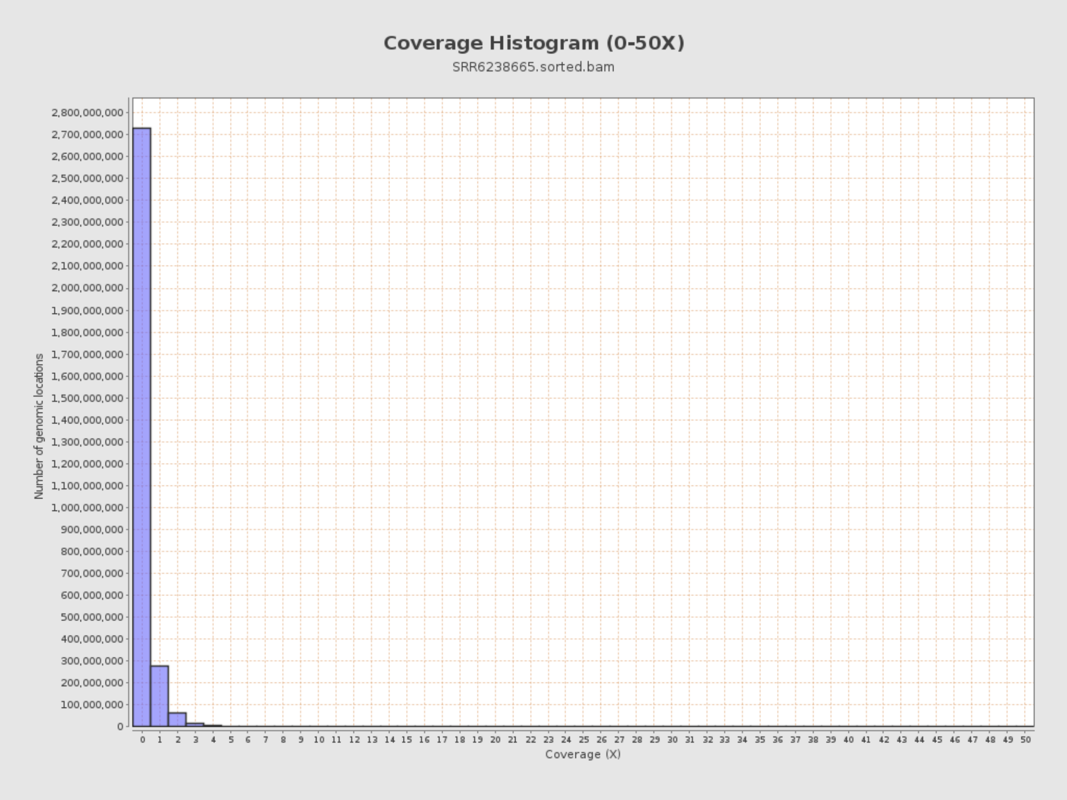
3. Results : Coverage across reference



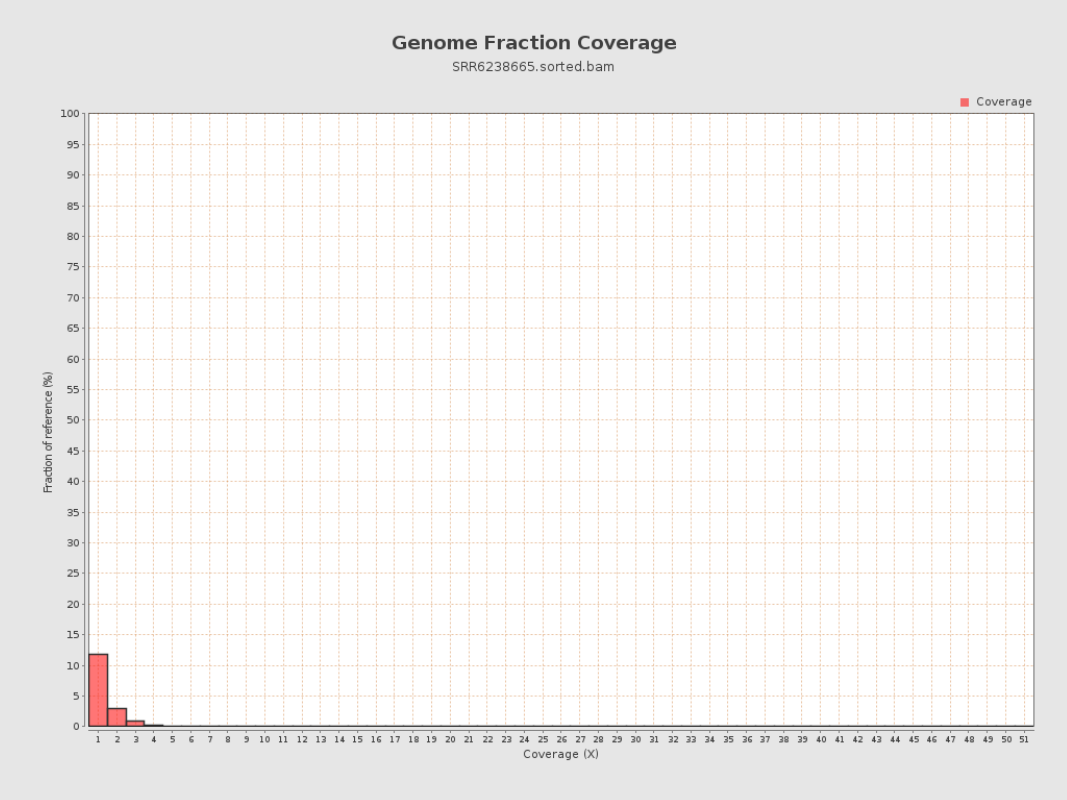
4. Results : Coverage Histogram



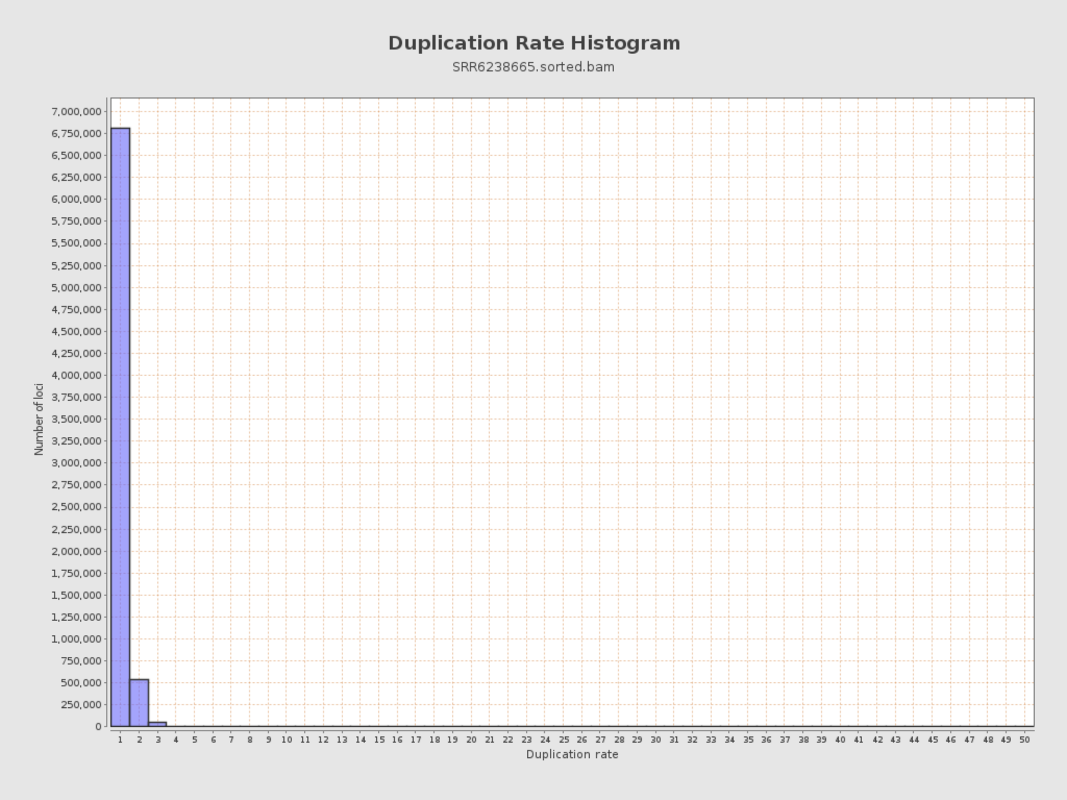
5. Results : Coverage Histogram (0-50X)



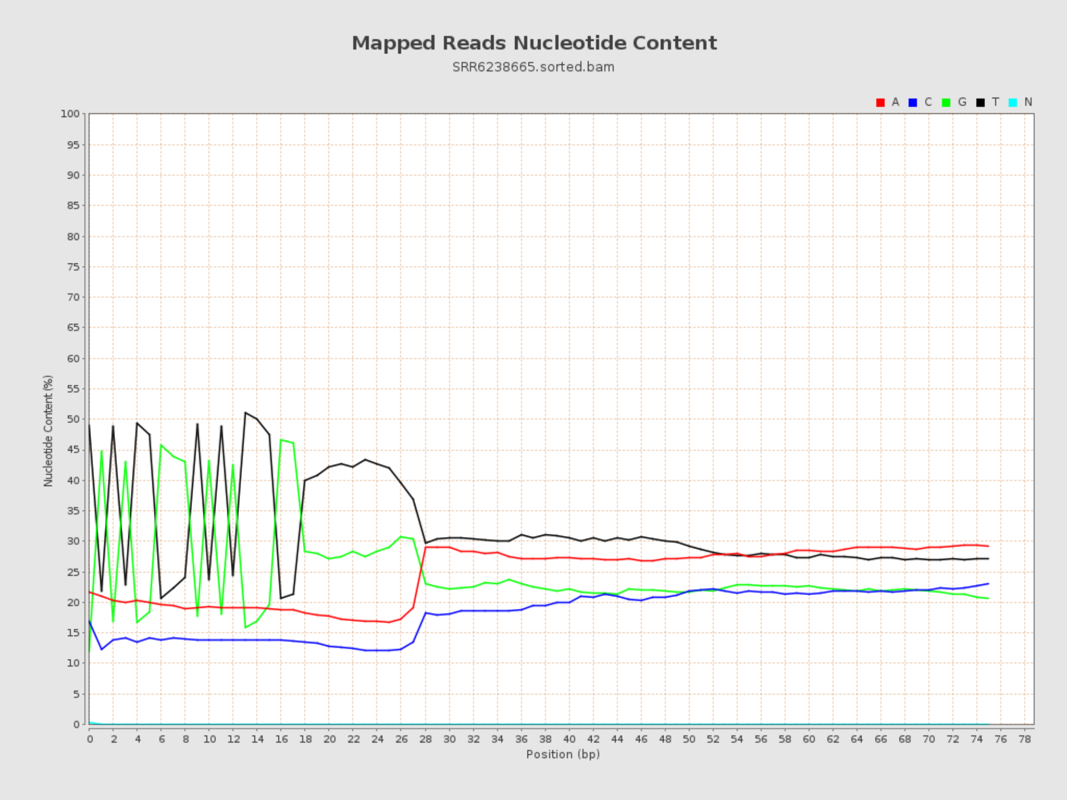
6. Results : Genome Fraction Coverage



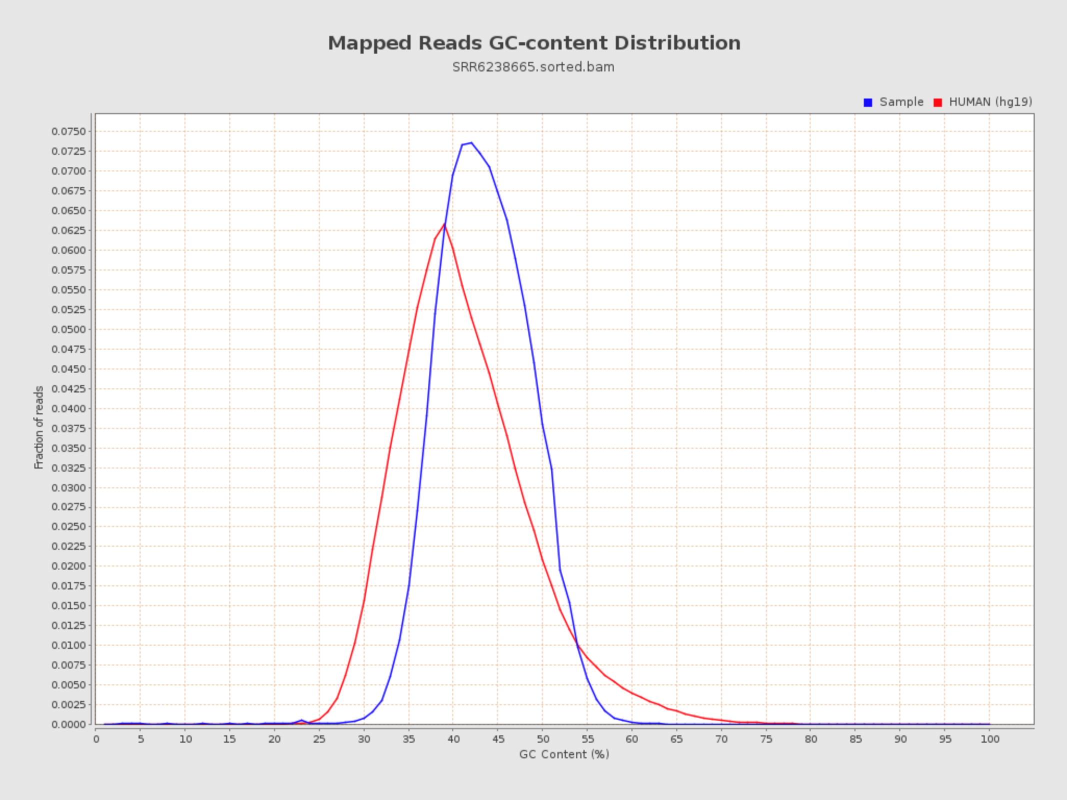
7. Results : Duplication Rate Histogram



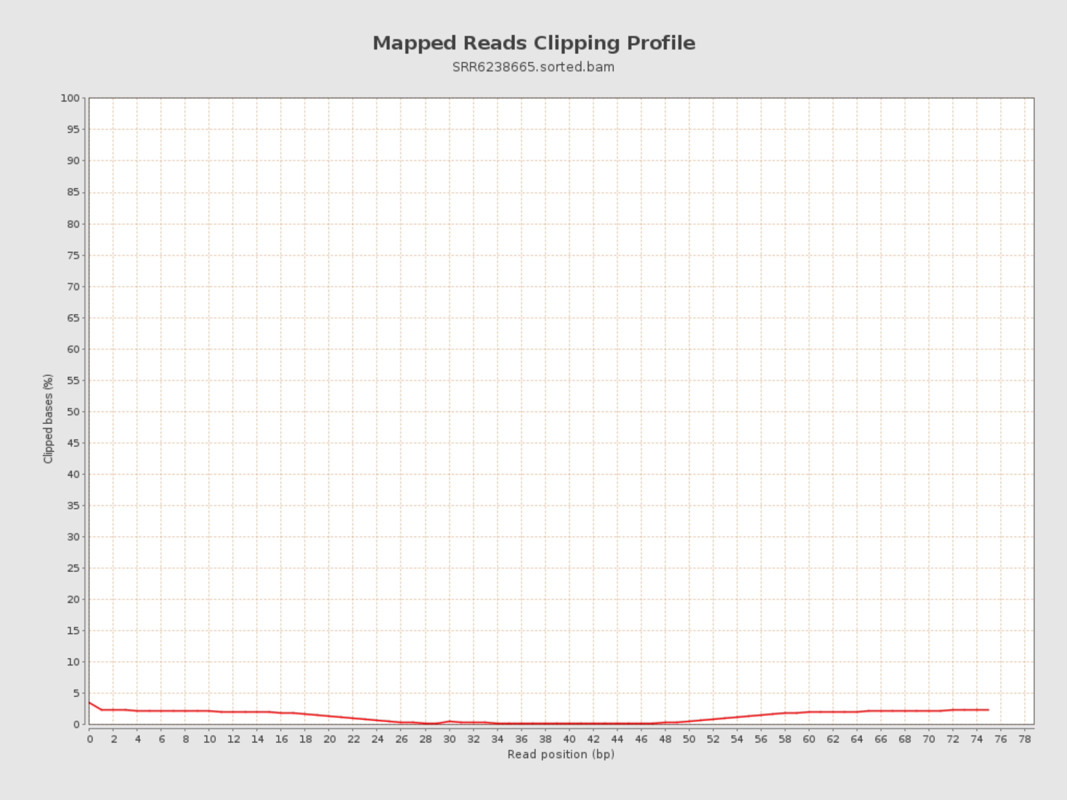
8. Results : Mapped Reads Nucleotide Content



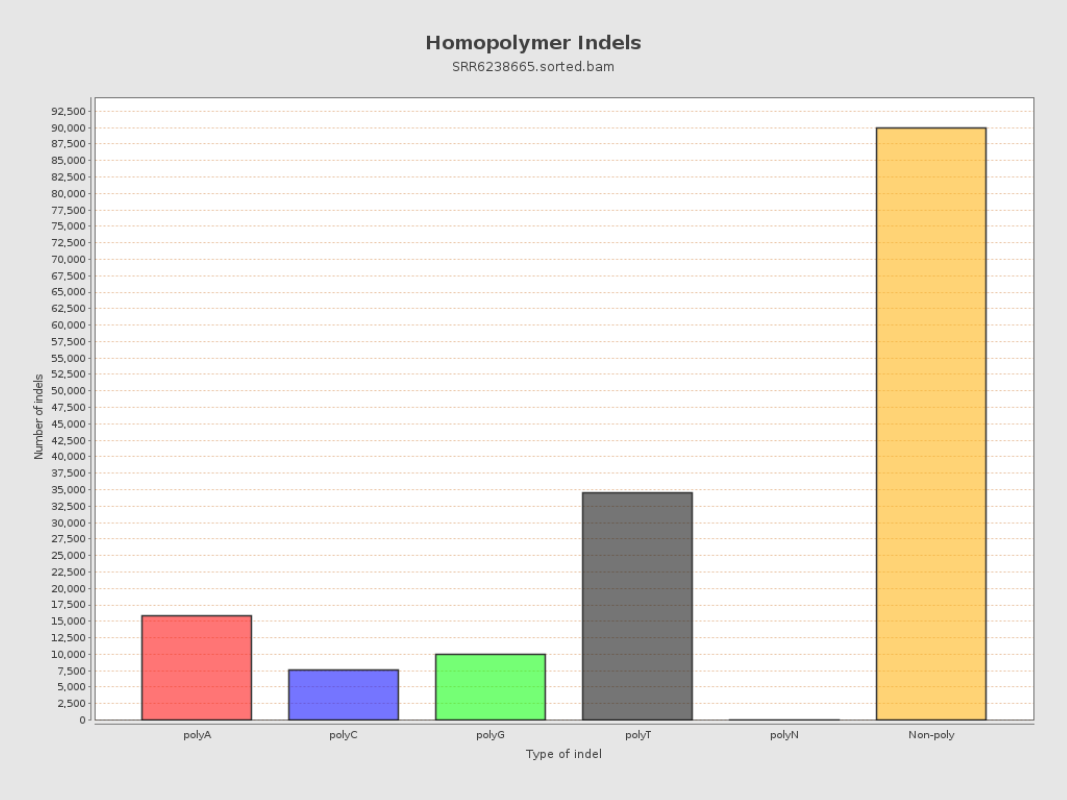
9. Results : Mapped Reads GC-content Distribution



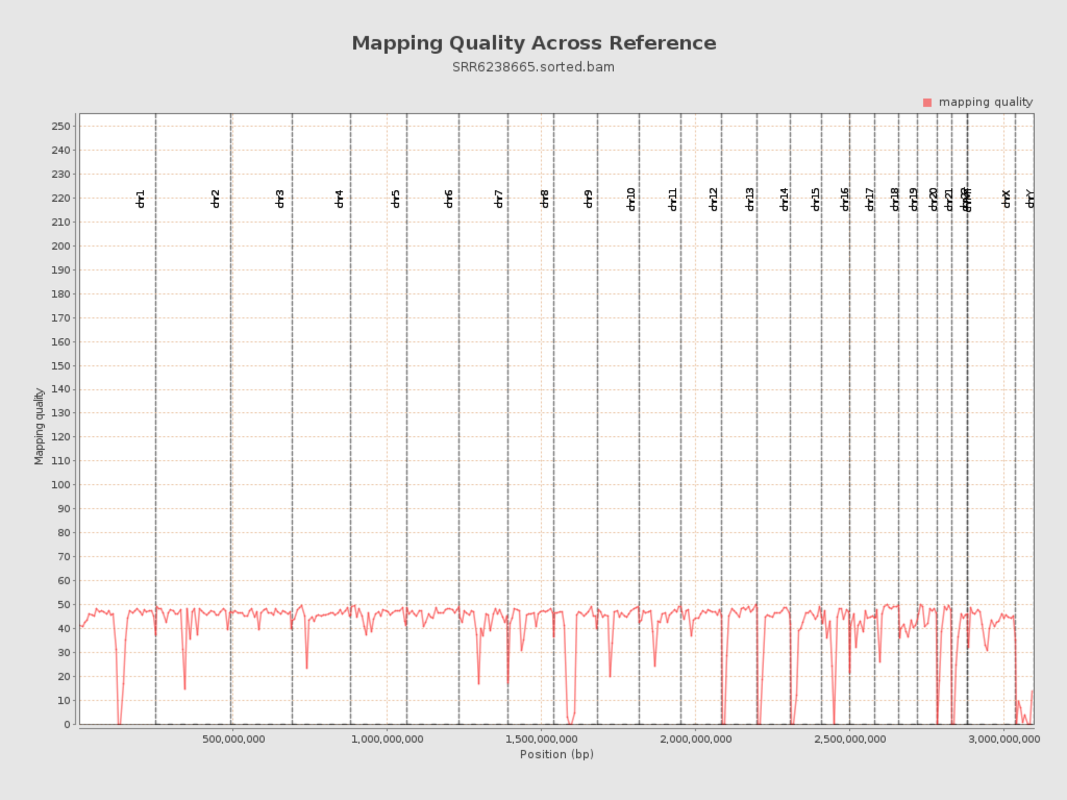
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram