

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 10:12:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238036.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_SRR6238036 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238036.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 10:12:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238036.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,468,827
Mapped reads	1,289,396 / 87.78%
Unmapped reads	179,431 / 12.22%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,758 / 0.73%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	135,820 / 9.25%
Duplication rate	8.62%
Clipped reads	626,755 / 42.67%

2.2. ACGT Content

Number/percentage of A's	22,952,806 / 27.21%
Number/percentage of C's	15,301,435 / 18.14%
Number/percentage of T's	26,931,193 / 31.93%
Number/percentage of G's	19,007,515 / 22.54%
Number/percentage of N's	151,717 / 0.18%
GC Percentage	40.68%

2.3. Coverage

Mean	0.0273

Standard Deviation	0.2731
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2.4. Mapping Quality

Mean Mapping Quality	44.22
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2.5. Mismatches and indels

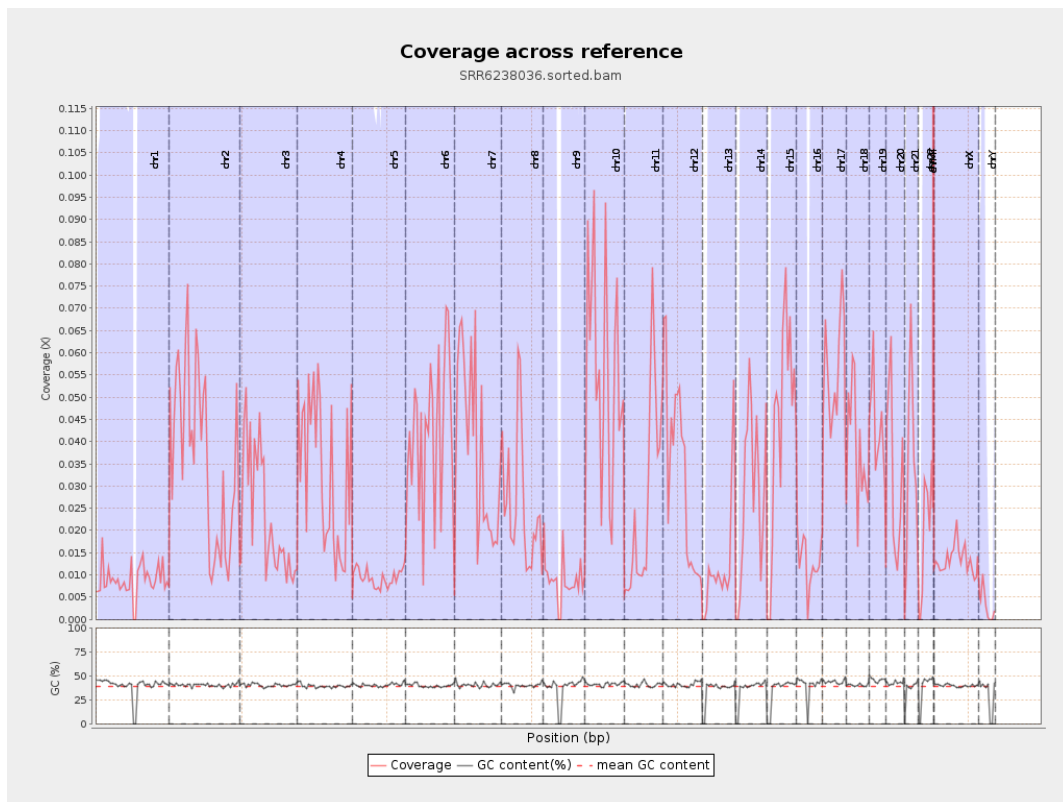
General error rate	0.86%
Mismatches	714,170
Insertions	7,216
Mapped reads with at least one insertion	0.55%
Deletions	25,320
Mapped reads with at least one deletion	1.94%
Homopolymer indels	48.2%

2.6. Chromosome stats

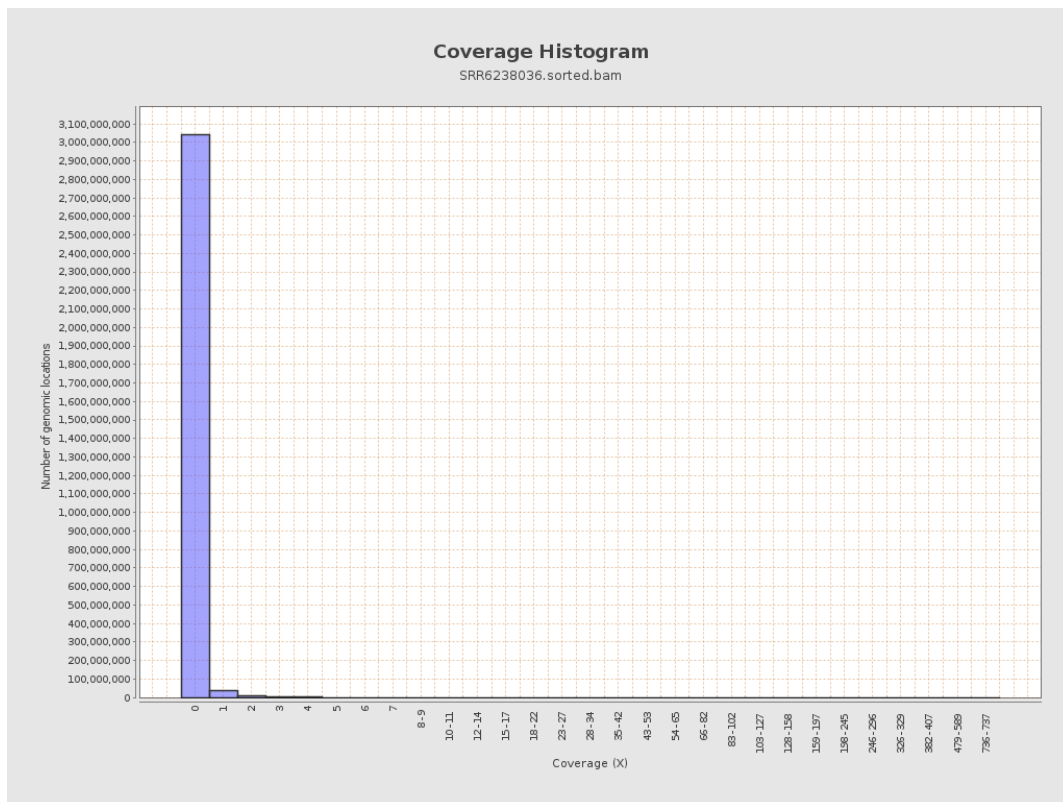
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	2206655	0.0089	0.2146
chr2	243199373	8861162	0.0364	0.4239
chr3	198022430	4521990	0.0228	0.2116
chr4	191154276	6334101	0.0331	0.2592
chr5	180915260	1684891	0.0093	0.1325
chr6	171115067	7067835	0.0413	0.3375
chr7	159138663	6094950	0.0383	0.3724

chr8	146364022	3835479	0.0262	0.3425
chr9	141213431	1187993	0.0084	0.1656
chr10	135534747	7608441	0.0561	0.3462
chr11	135006516	3628690	0.0269	0.2329
chr12	133851895	4286058	0.032	0.2522
chr13	115169878	1468597	0.0128	0.16
chr14	107349540	2987587	0.0278	0.2378
chr15	102531392	4503249	0.0439	0.2941
chr16	90354753	1152019	0.0127	0.1563
chr17	81195210	4490909	0.0553	0.3276
chr18	78077248	3029999	0.0388	0.3089
chr19	59128983	2506044	0.0424	0.3016
chr20	63025520	2100563	0.0333	0.2587
chr21	48129895	1583310	0.0329	0.259
chr22	51304566	996582	0.0194	0.1893
chrMT	16571	8537	0.5152	0.823
chrX	155270560	2062524	0.0133	0.1627
chrY	59373566	178263	0.003	0.0912

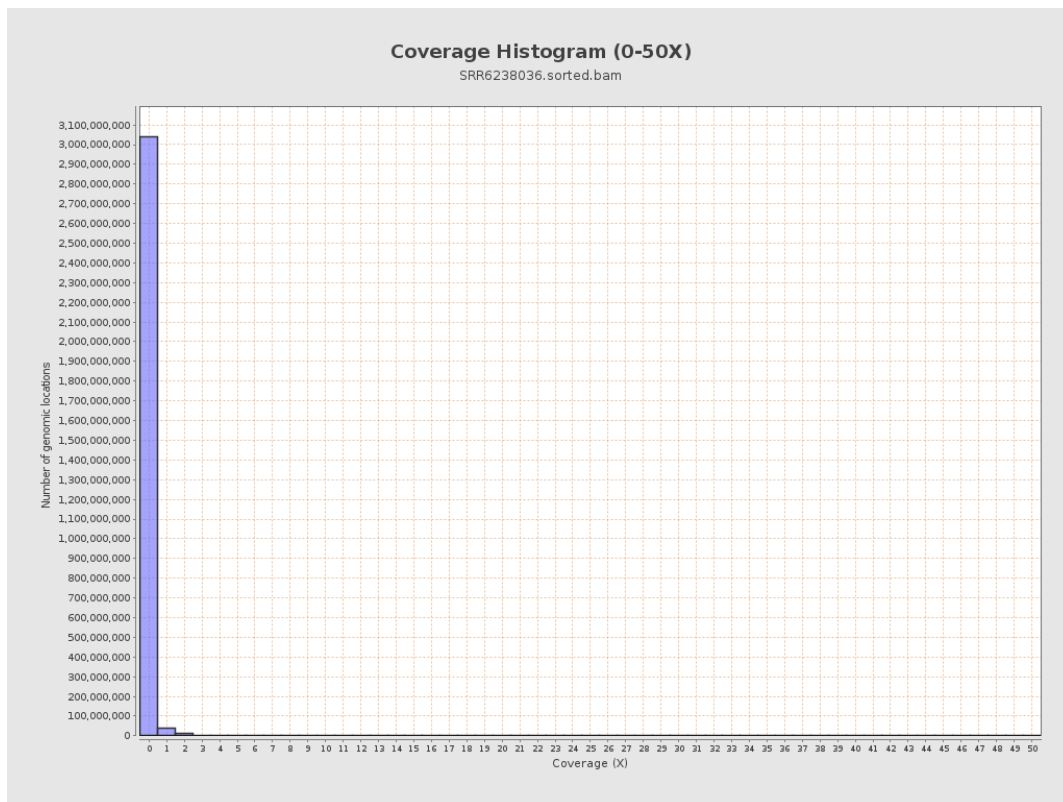
3. Results : Coverage across reference



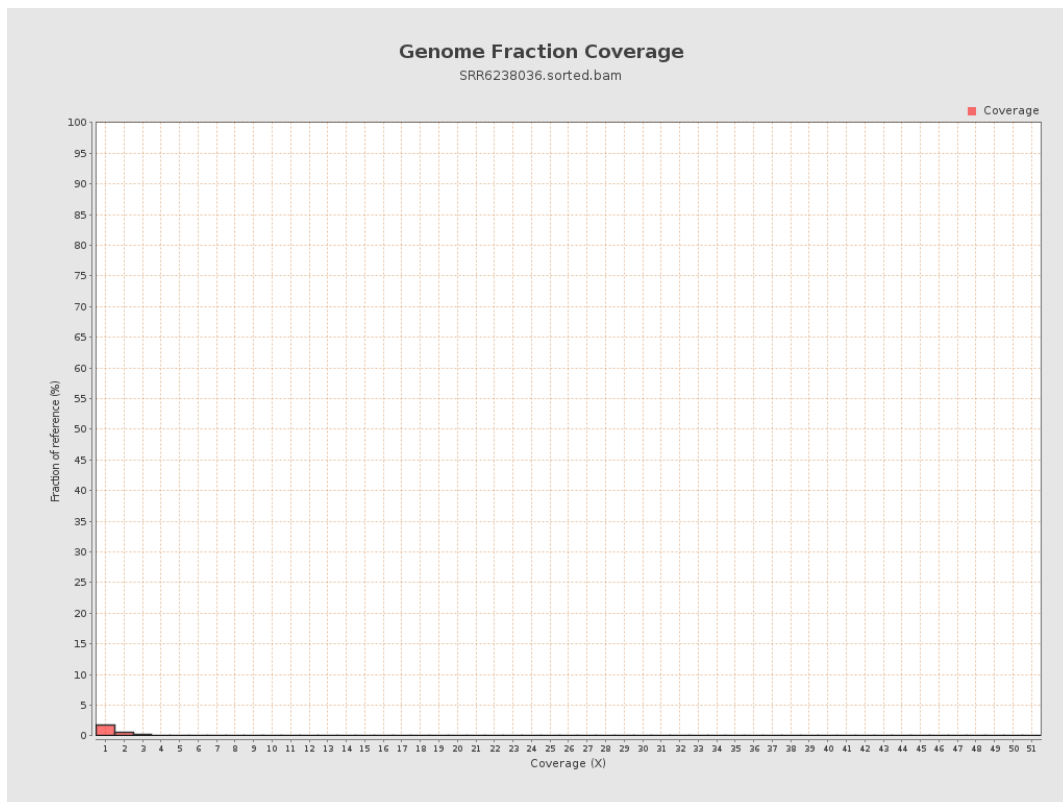
4. Results : Coverage Histogram



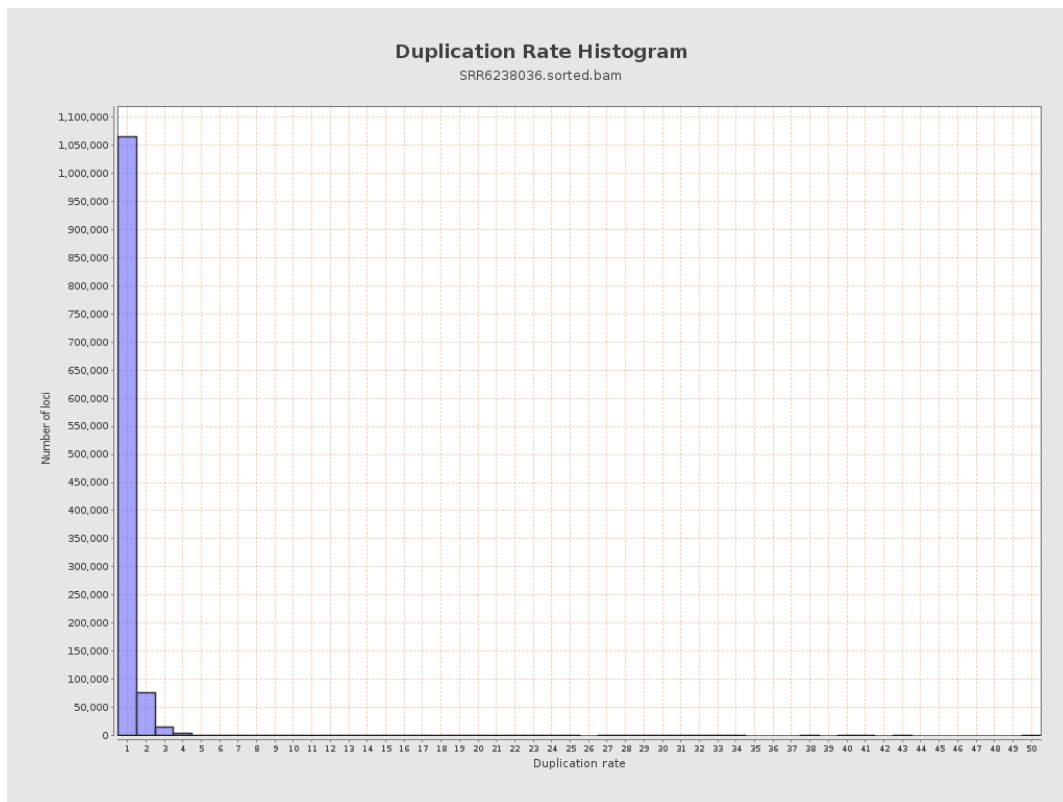
5. Results : Coverage Histogram (0-50X)



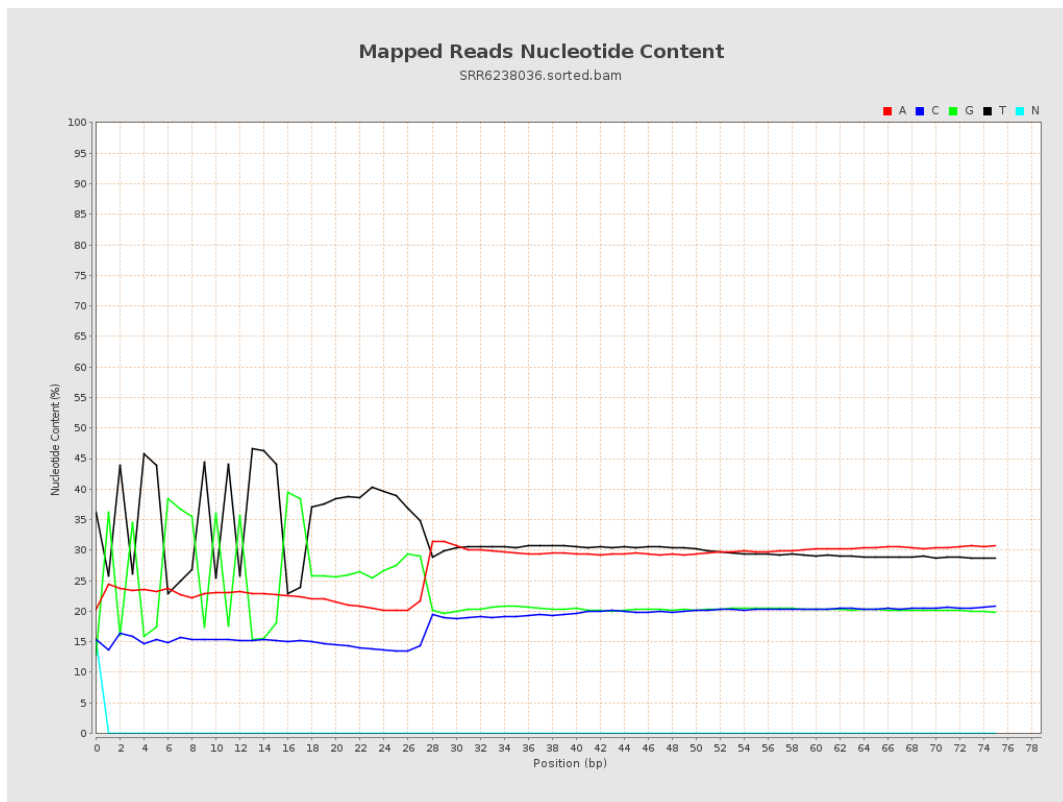
6. Results : Genome Fraction Coverage



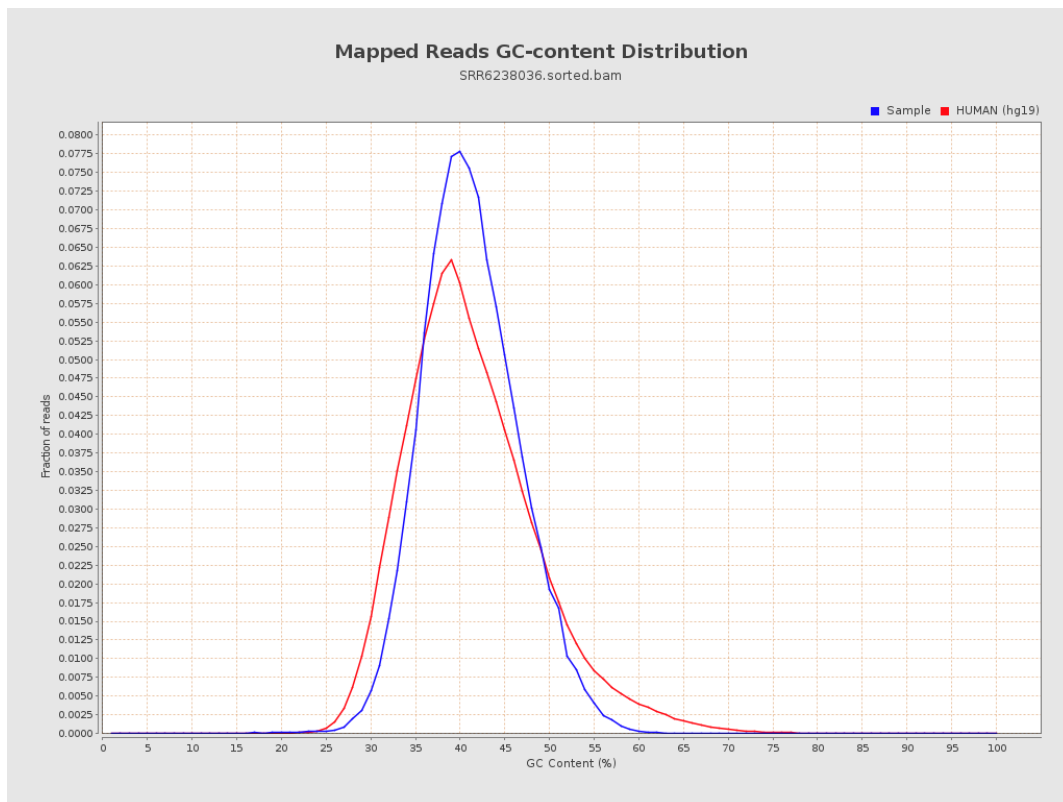
7. Results : Duplication Rate Histogram



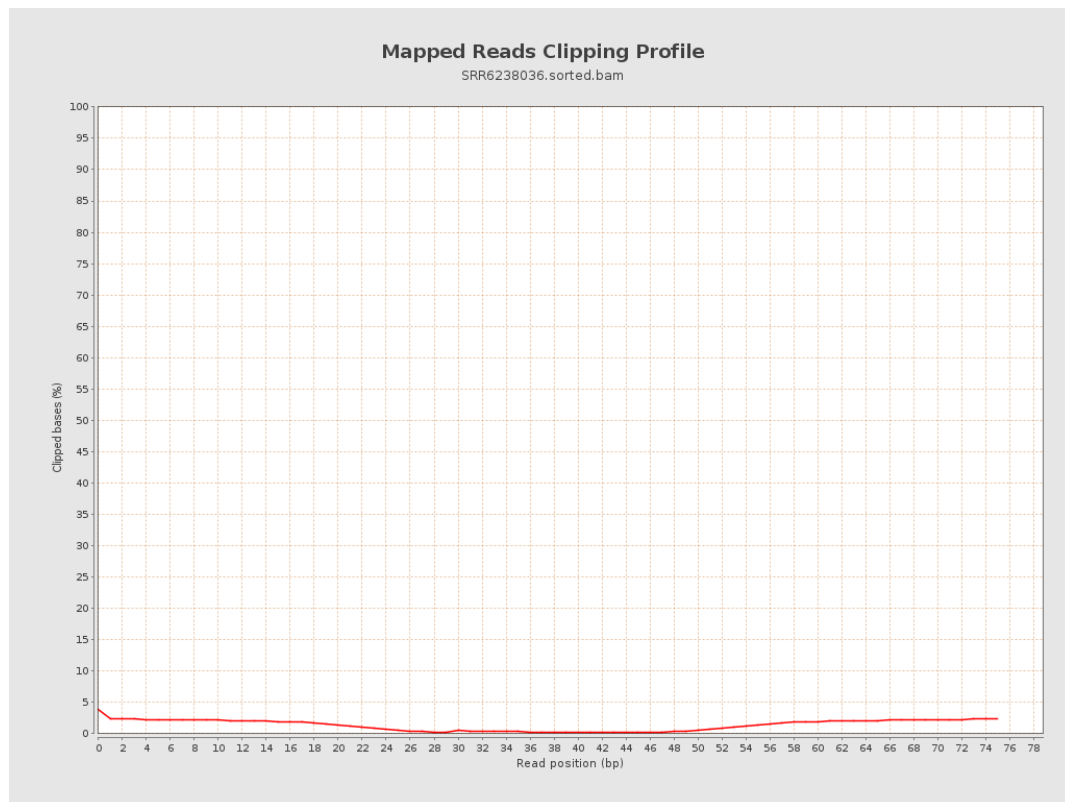
8. Results : Mapped Reads Nucleotide Content



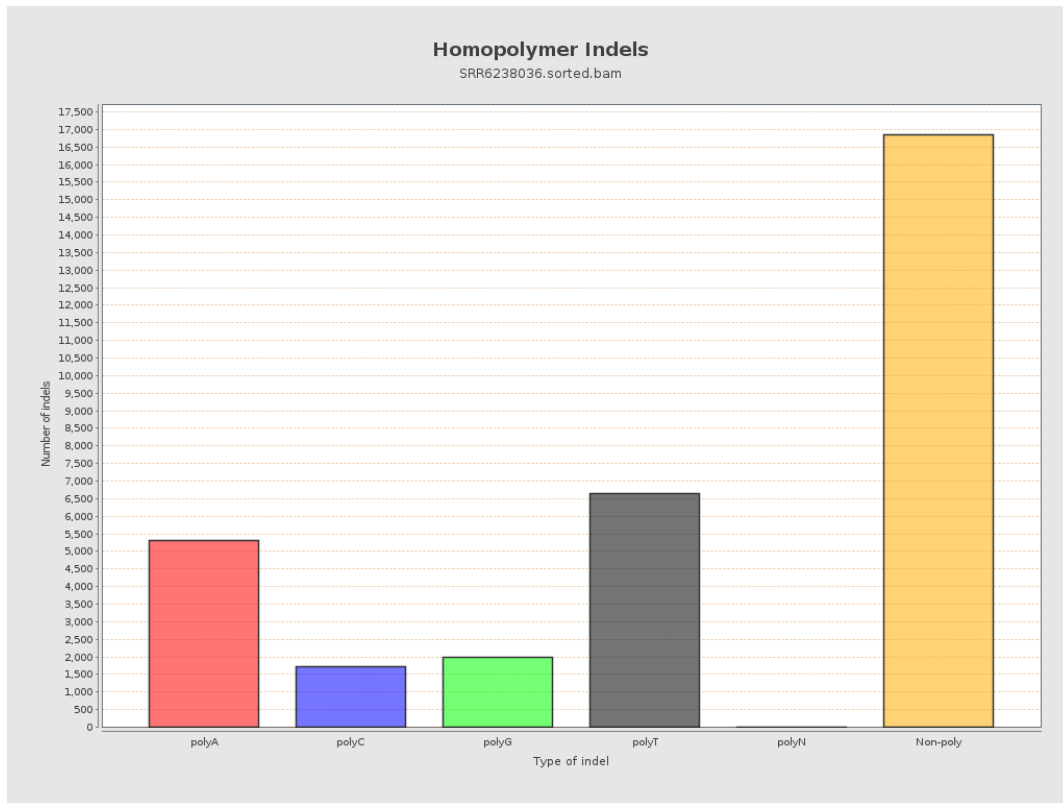
9. Results : Mapped Reads GC-content Distribution



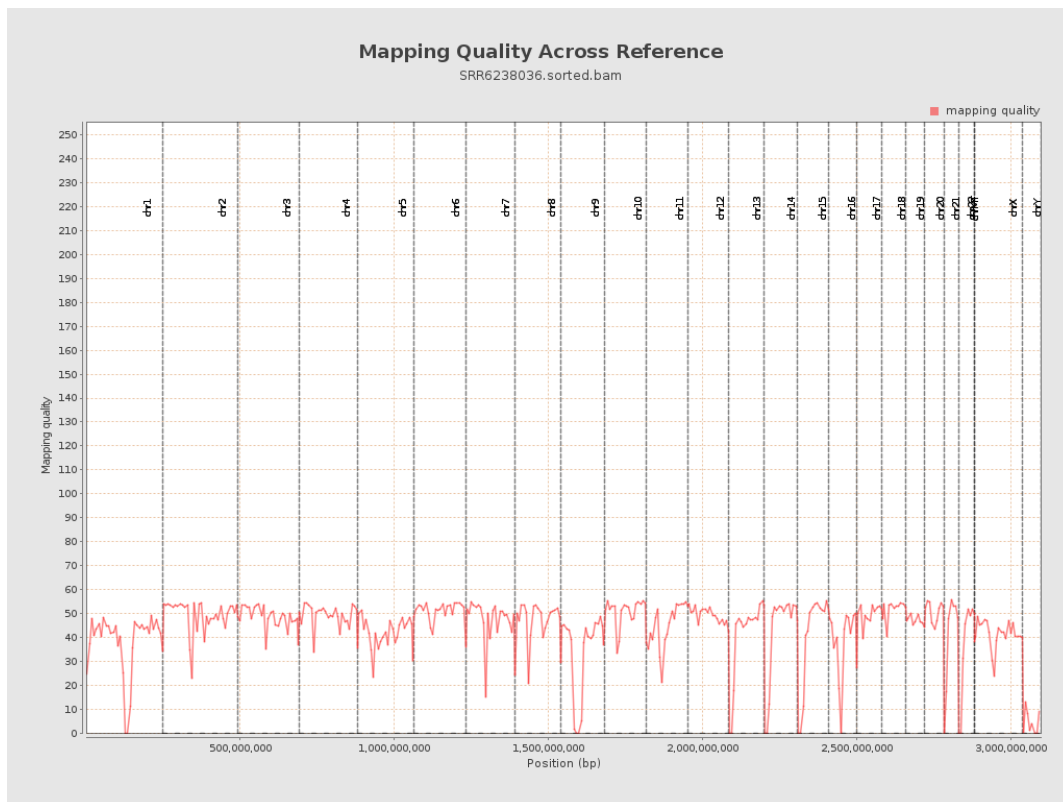
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

