

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 14:28:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238283.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_SRR6238283 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238283.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 14:28:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238283.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,648,121
Mapped reads	1,265,351 / 76.78%
Unmapped reads	382,770 / 23.22%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,817 / 0.84%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	146,526 / 8.89%
Duplication rate	9.04%
Clipped reads	684,538 / 41.53%

2.2. ACGT Content

Number/percentage of A's	22,606,558 / 27.66%
Number/percentage of C's	15,777,020 / 19.3%
Number/percentage of T's	25,109,190 / 30.72%
Number/percentage of G's	18,218,802 / 22.29%
Number/percentage of N's	21,906 / 0.03%
GC Percentage	41.59%

2.3. Coverage

Mean	0.0264

Standard Deviation	0.299
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2.4. Mapping Quality

Mean Mapping Quality	45.2
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2.5. Mismatches and indels

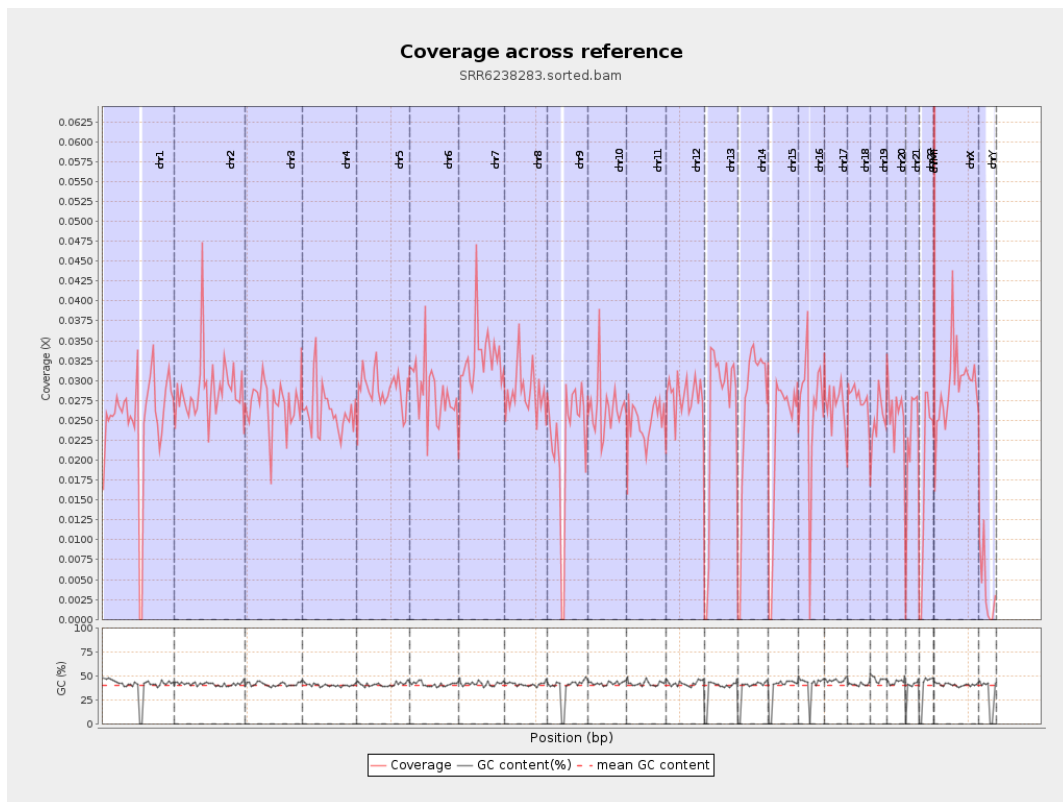
General error rate	1.03%
Mismatches	832,573
Insertions	6,636
Mapped reads with at least one insertion	0.52%
Deletions	31,424
Mapped reads with at least one deletion	2.45%
Homopolymer indels	46.84%

2.6. Chromosome stats

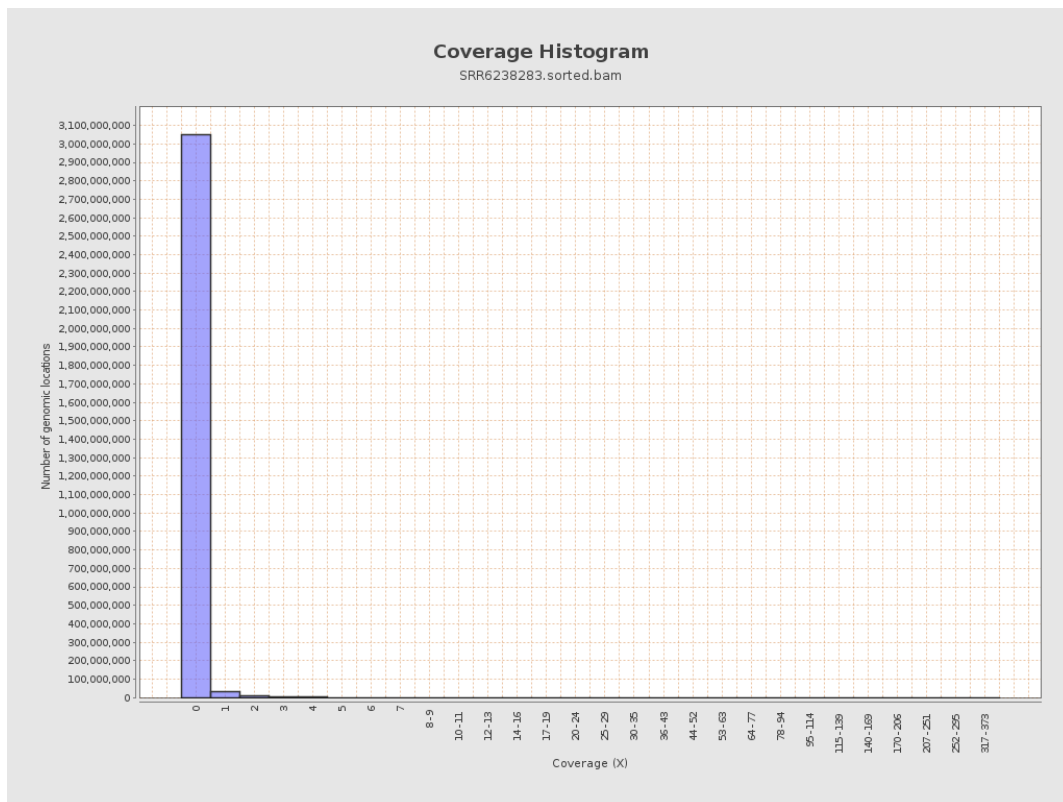
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	6210275	0.0249	0.3759
chr2	243199373	7005984	0.0288	0.3524
chr3	198022430	5336313	0.0269	0.2553
chr4	191154276	5001920	0.0262	0.2648
chr5	180915260	5259739	0.0291	0.2653
chr6	171115067	4856267	0.0284	0.2929
chr7	159138663	5220679	0.0328	0.3976

chr8	146364022	4189948	0.0286	0.3475
chr9	141213431	3144324	0.0223	0.2642
chr10	135534747	3595435	0.0265	0.29
chr11	135006516	3361074	0.0249	0.274
chr12	133851895	3763340	0.0281	0.2616
chr13	115169878	2972403	0.0258	0.2553
chr14	107349540	2842445	0.0265	0.2885
chr15	102531392	2325974	0.0227	0.2698
chr16	90354753	2379895	0.0263	0.2555
chr17	81195210	2173476	0.0268	0.2621
chr18	78077248	2169049	0.0278	0.3845
chr19	59128983	1500189	0.0254	0.3085
chr20	63025520	1623132	0.0258	0.2523
chr21	48129895	1087282	0.0226	0.2394
chr22	51304566	965195	0.0188	0.208
chrMT	16571	9330	0.563	1.2602
chrX	155270560	4561907	0.0294	0.2763
chrY	59373566	229292	0.0039	0.1148

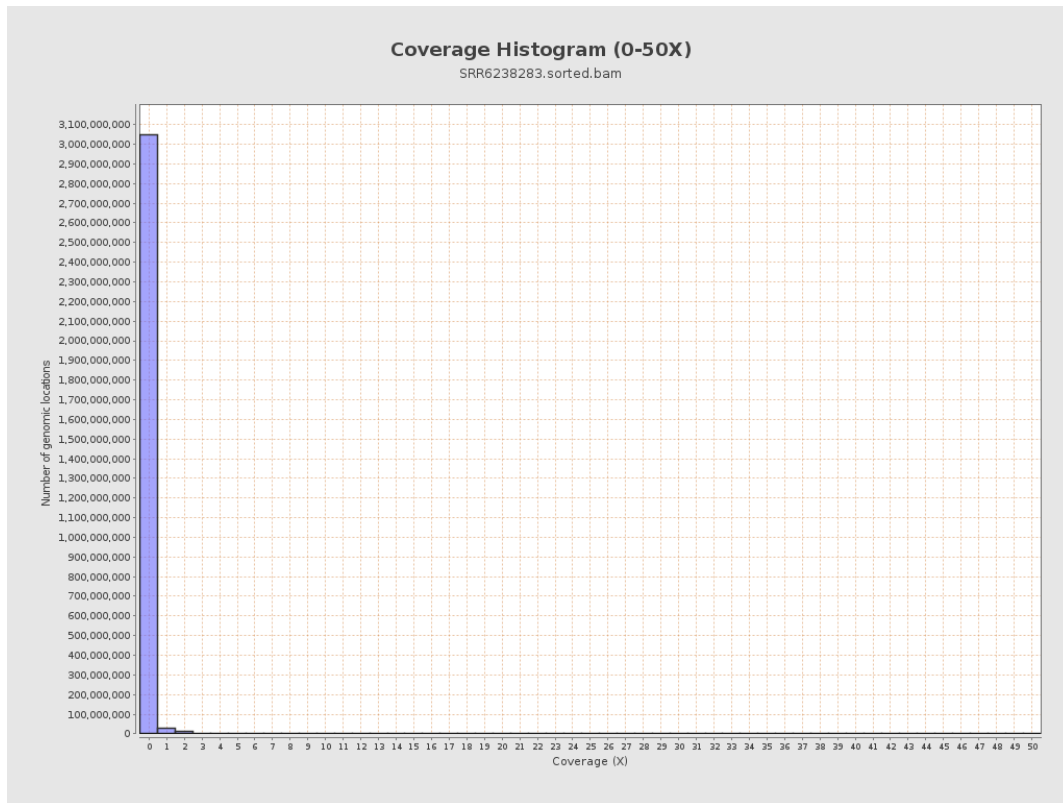
3. Results : Coverage across reference



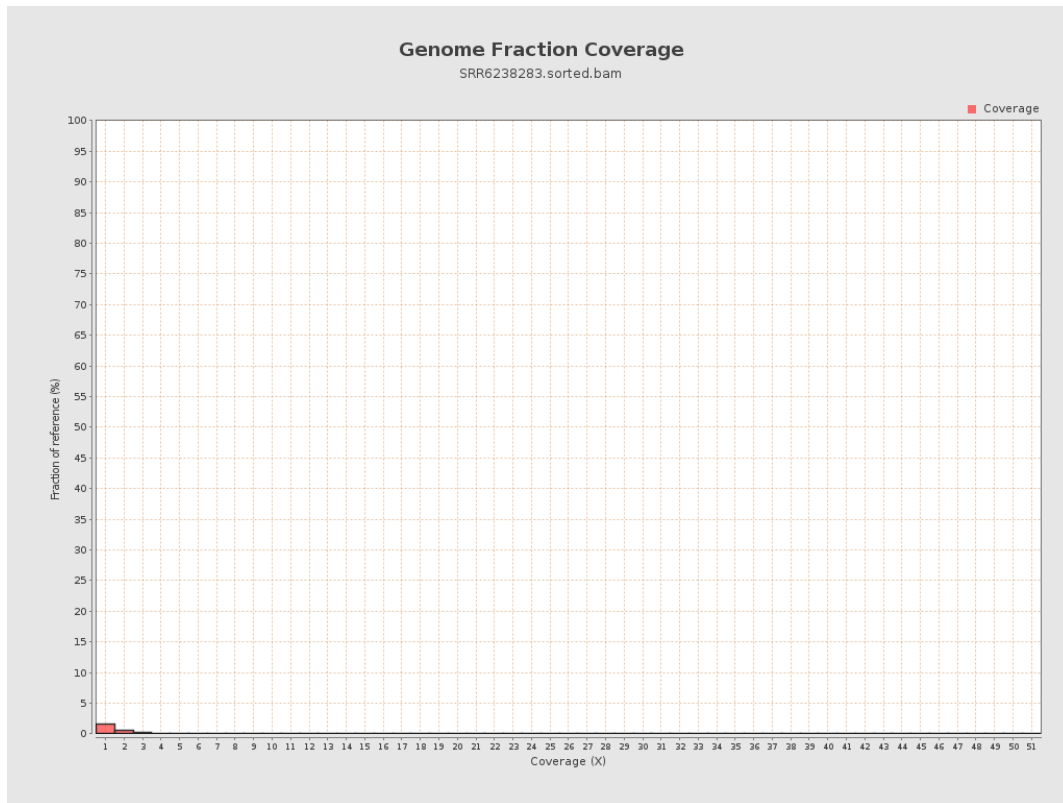
4. Results : Coverage Histogram



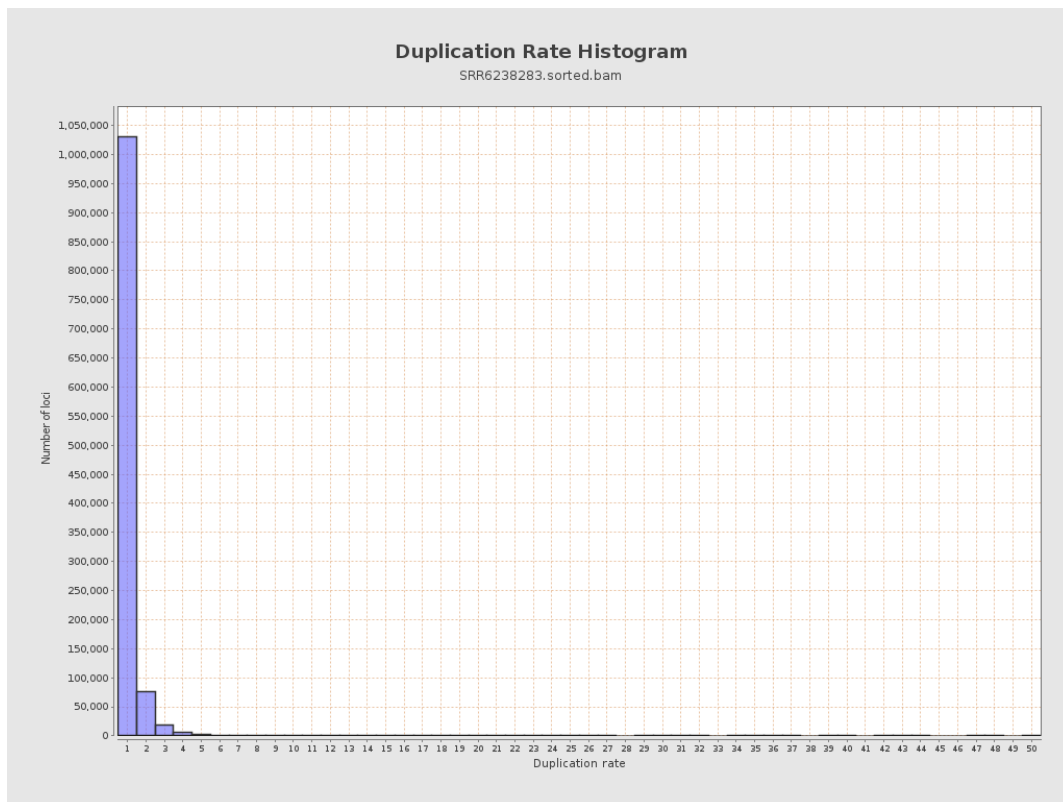
5. Results : Coverage Histogram (0-50X)



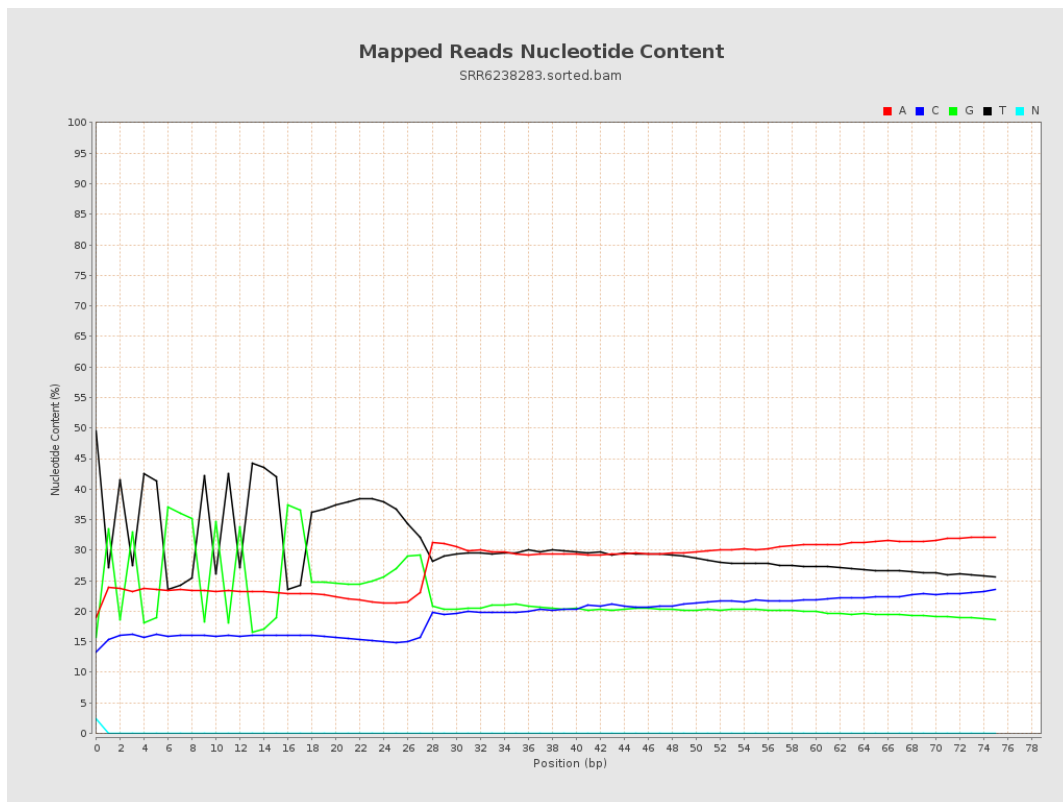
6. Results : Genome Fraction Coverage



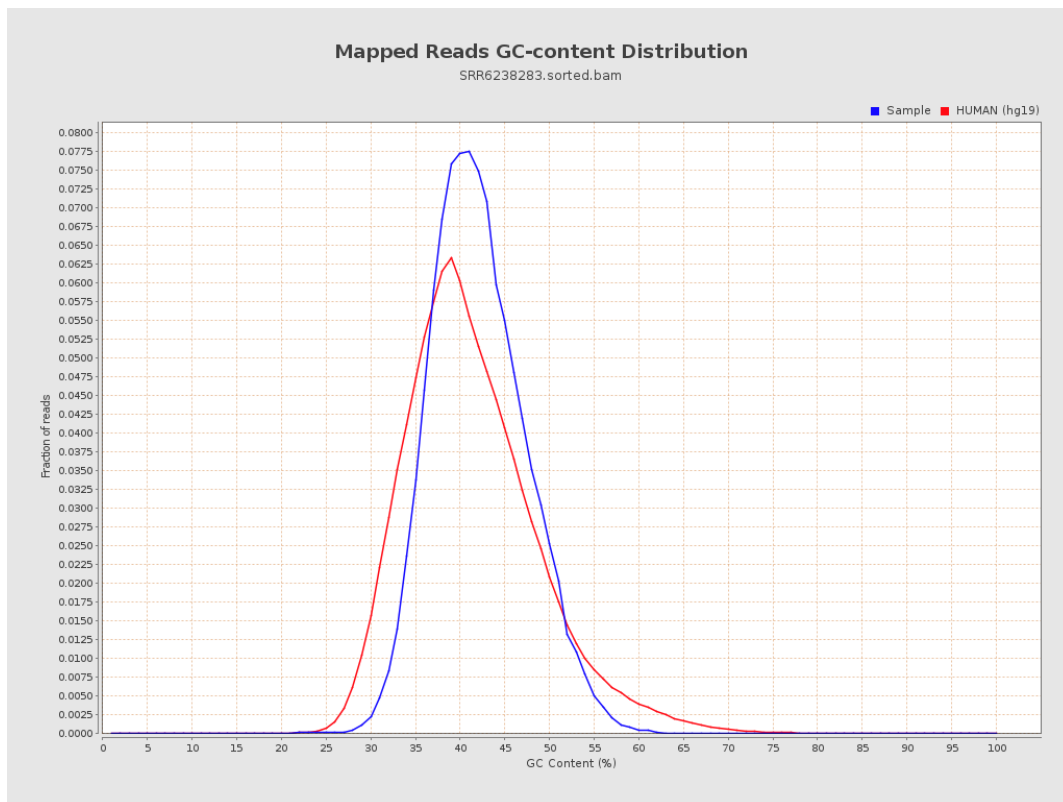
7. Results : Duplication Rate Histogram



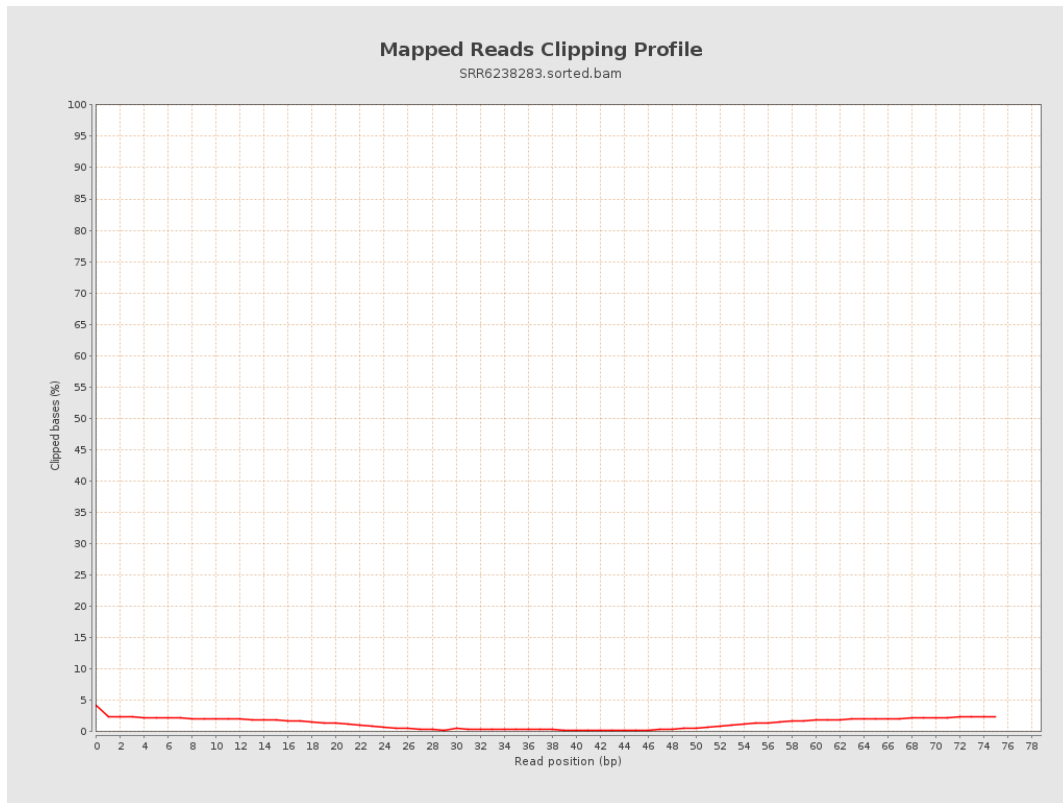
8. Results : Mapped Reads Nucleotide Content



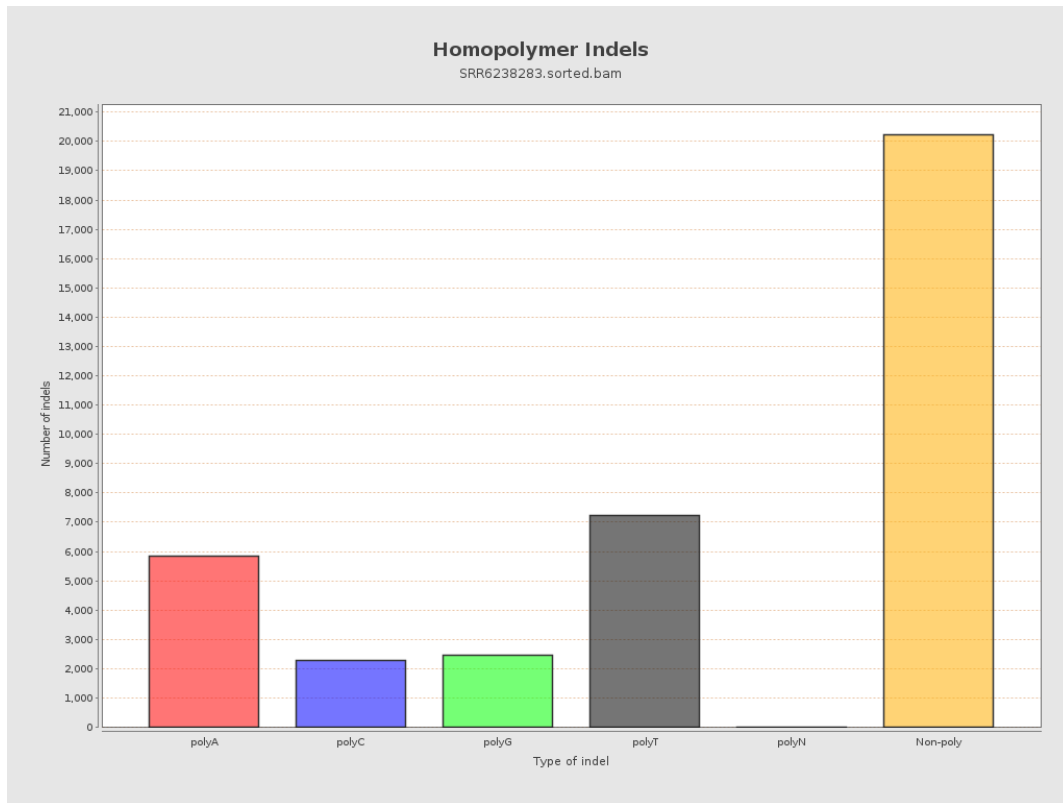
9. Results : Mapped Reads GC-content Distribution



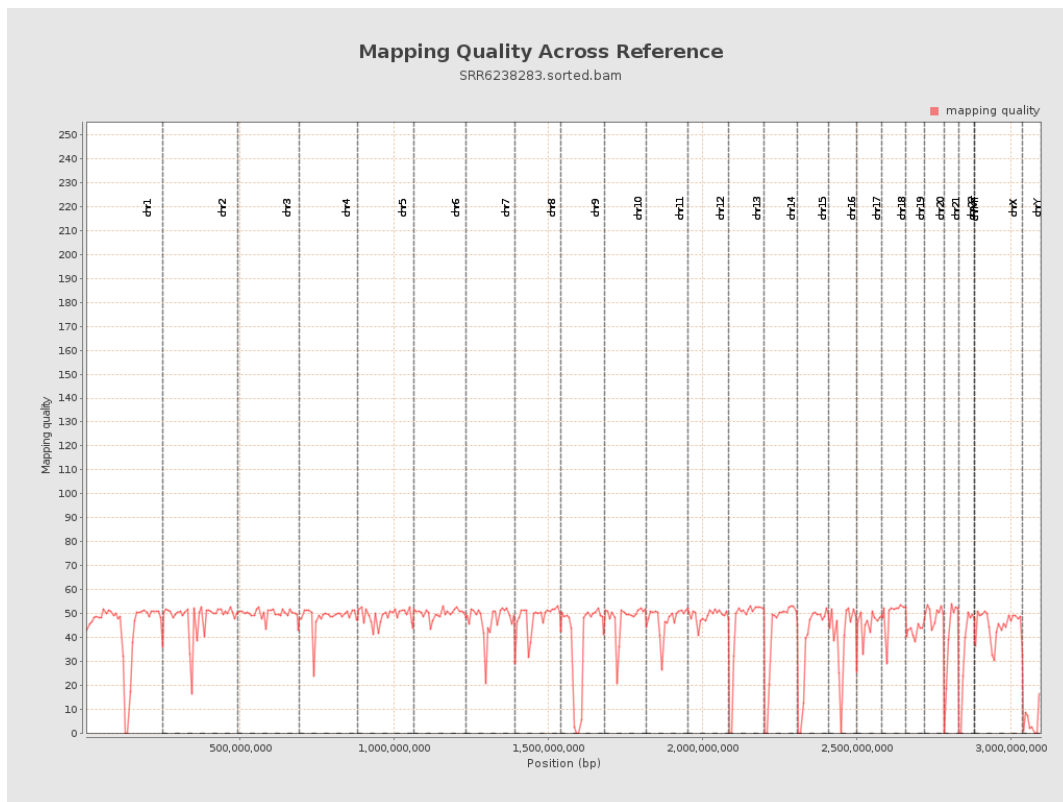
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

