

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 20:22:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6230377.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_SRR6230377 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6230377.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 20:22:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6230377.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,899,487
Mapped reads	4,141,080 / 84.52%
Unmapped reads	758,407 / 15.48%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	43,948 / 0.9%
Read min/max/mean length	30 / 76 / 76.31
Duplicated reads (estimated)	409,809 / 8.36%
Duplication rate	7.04%
Clipped reads	1,494,947 / 30.51%

2.2. ACGT Content

Number/percentage of A's	86,694,960 / 30.06%
Number/percentage of C's	56,886,950 / 19.72%
Number/percentage of T's	85,823,773 / 29.76%
Number/percentage of G's	58,866,546 / 20.41%
Number/percentage of N's	161,133 / 0.06%
GC Percentage	40.13%

2.3. Coverage

Mean	0.0932

Standard Deviation	1.3181
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2.4. Mapping Quality

Mean Mapping Quality	42.77
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2.5. Mismatches and indels

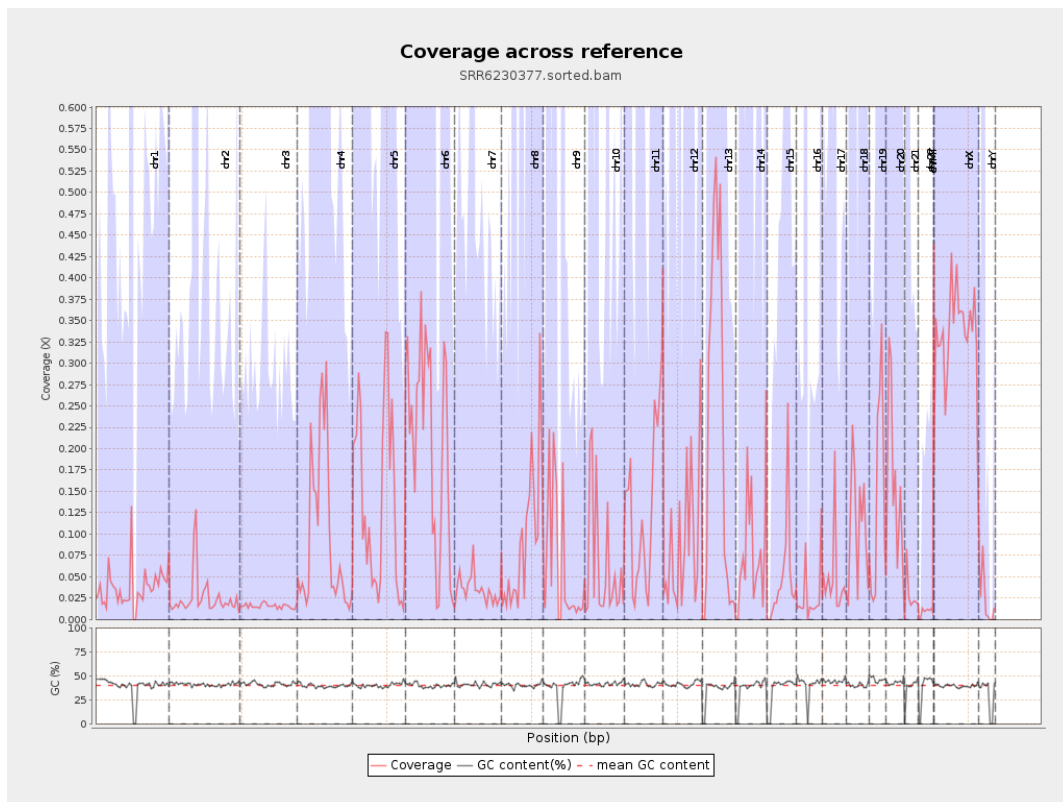
General error rate	0.93%
Mismatches	2,612,629
Insertions	30,291
Mapped reads with at least one insertion	0.72%
Deletions	80,277
Mapped reads with at least one deletion	1.91%
Homopolymer indels	45.18%

2.6. Chromosome stats

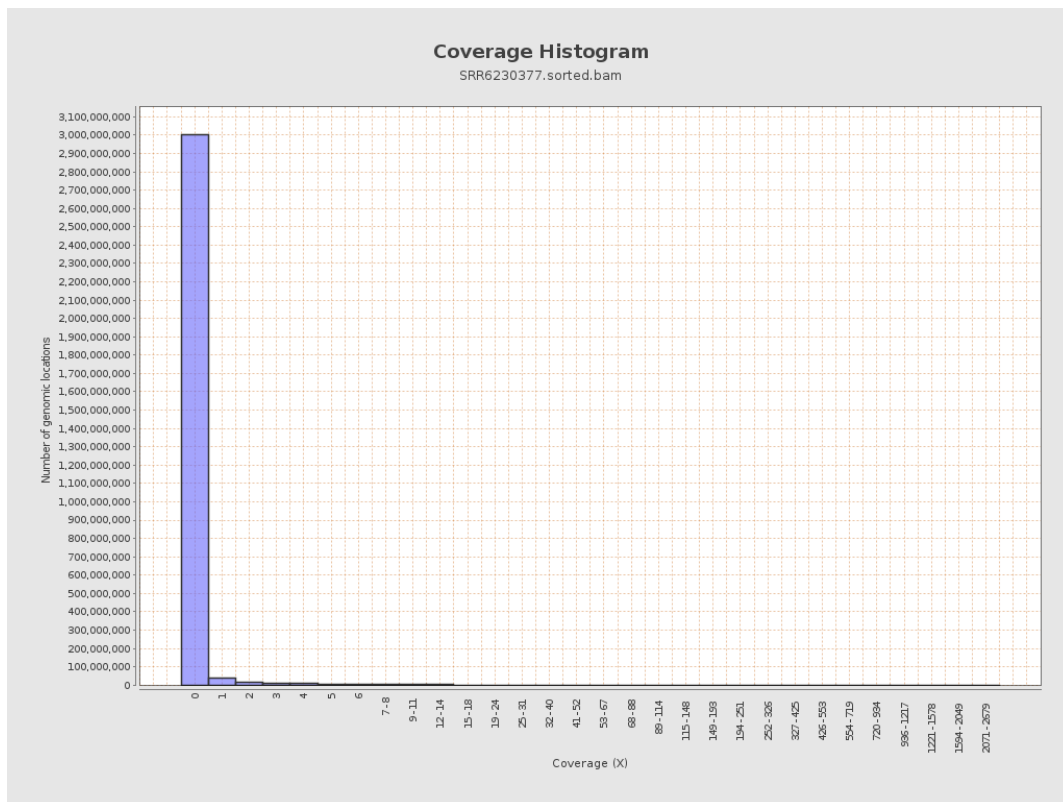
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	9167793	0.0368	2.0678
chr2	243199373	6336975	0.0261	1.4972
chr3	198022430	3075727	0.0155	0.2875
chr4	191154276	18054255	0.0944	1.3551
chr5	180915260	24412427	0.1349	0.9181
chr6	171115067	34644791	0.2025	1.8567
chr7	159138663	5627535	0.0354	0.6438

chr8	146364022	13543946	0.0925	0.8791
chr9	141213431	8359440	0.0592	1.0765
chr10	135534747	8496907	0.0627	1.9406
chr11	135006516	17554309	0.13	0.9821
chr12	133851895	12406793	0.0927	0.7581
chr13	115169878	24826041	0.2156	1.1614
chr14	107349540	7958977	0.0741	0.8329
chr15	102531392	4933701	0.0481	0.5368
chr16	90354753	2659988	0.0294	0.7787
chr17	81195210	4022077	0.0495	0.6496
chr18	78077248	8672529	0.1111	2.4434
chr19	59128983	8138785	0.1376	1.5487
chr20	63025520	10341652	0.1641	1.1157
chr21	48129895	1374640	0.0286	1.07
chr22	51304566	477695	0.0093	0.1958
chrMT	16571	7299	0.4405	1.147
chrX	155270560	52164578	0.336	1.5688
chrY	59373566	1315842	0.0222	1.3248

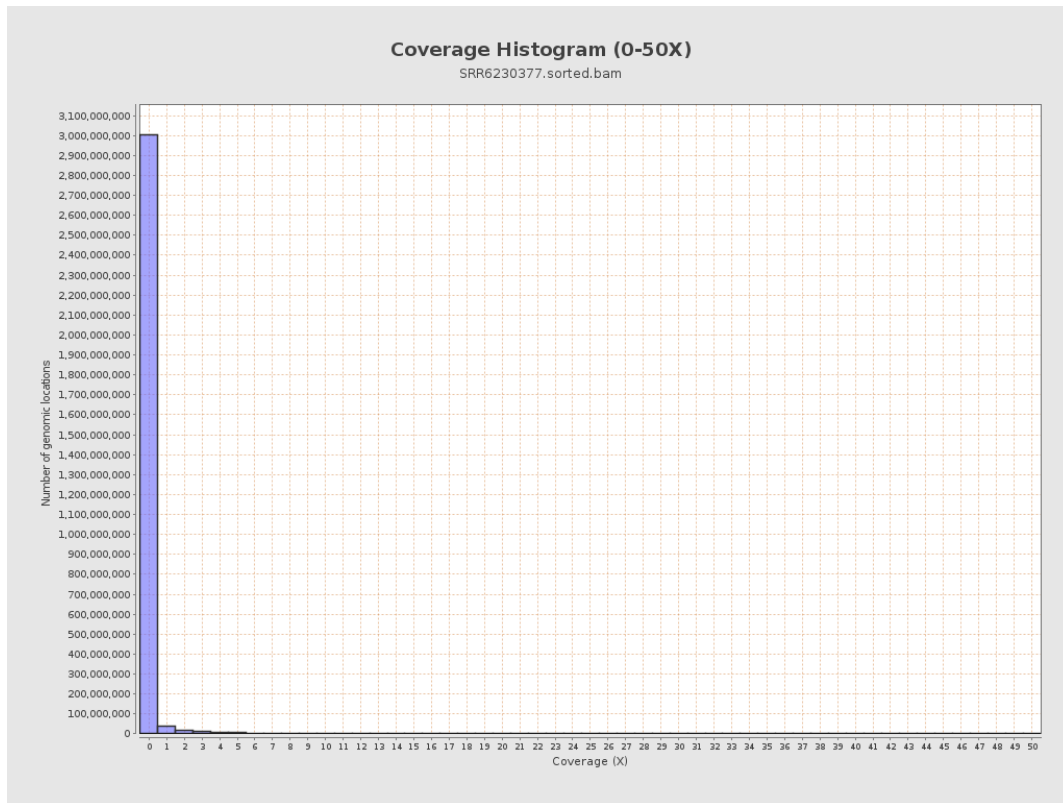
3. Results : Coverage across reference



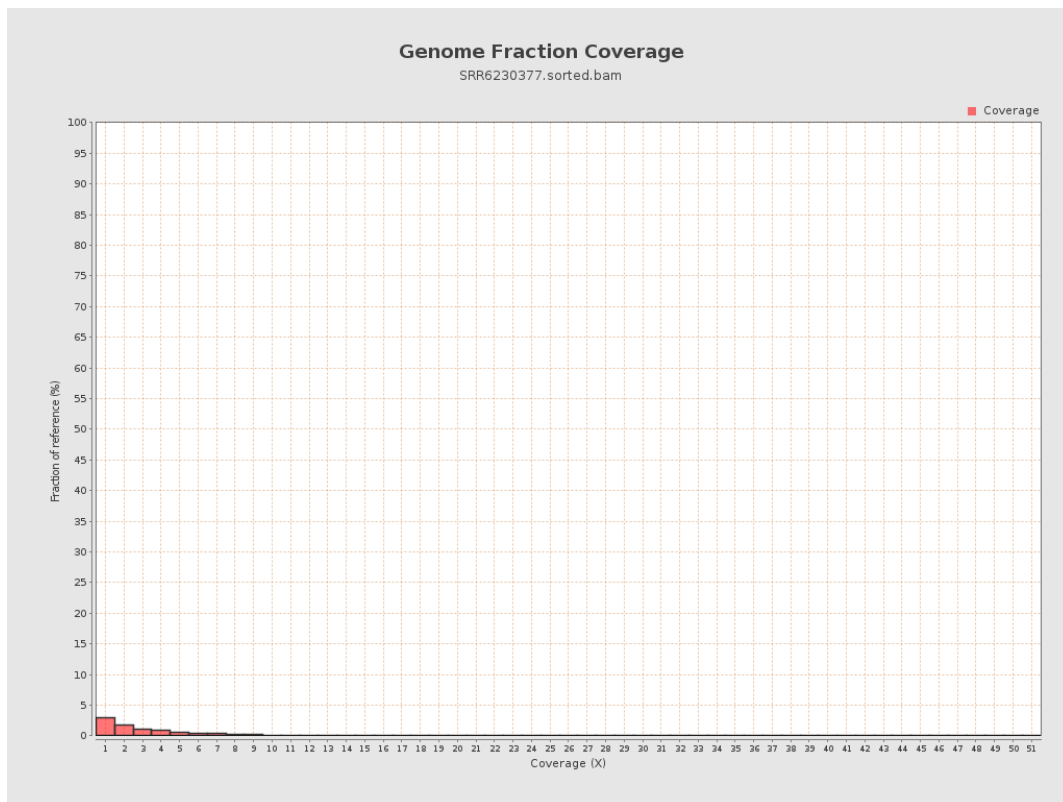
4. Results : Coverage Histogram



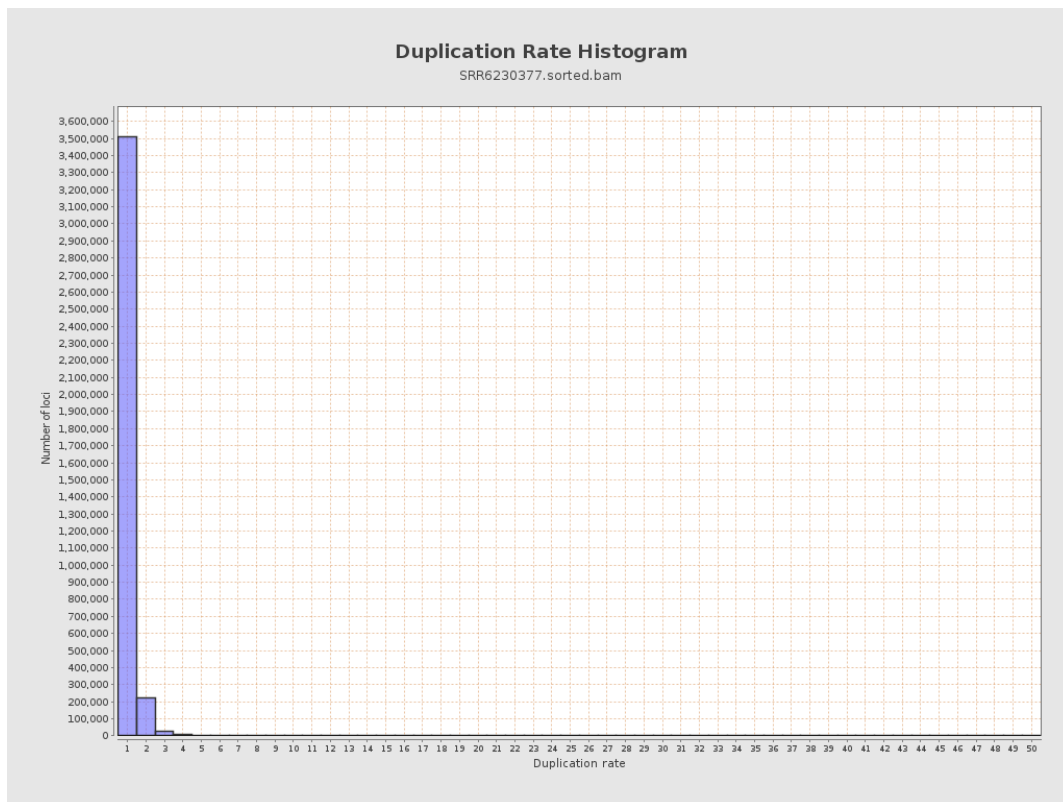
5. Results : Coverage Histogram (0-50X)



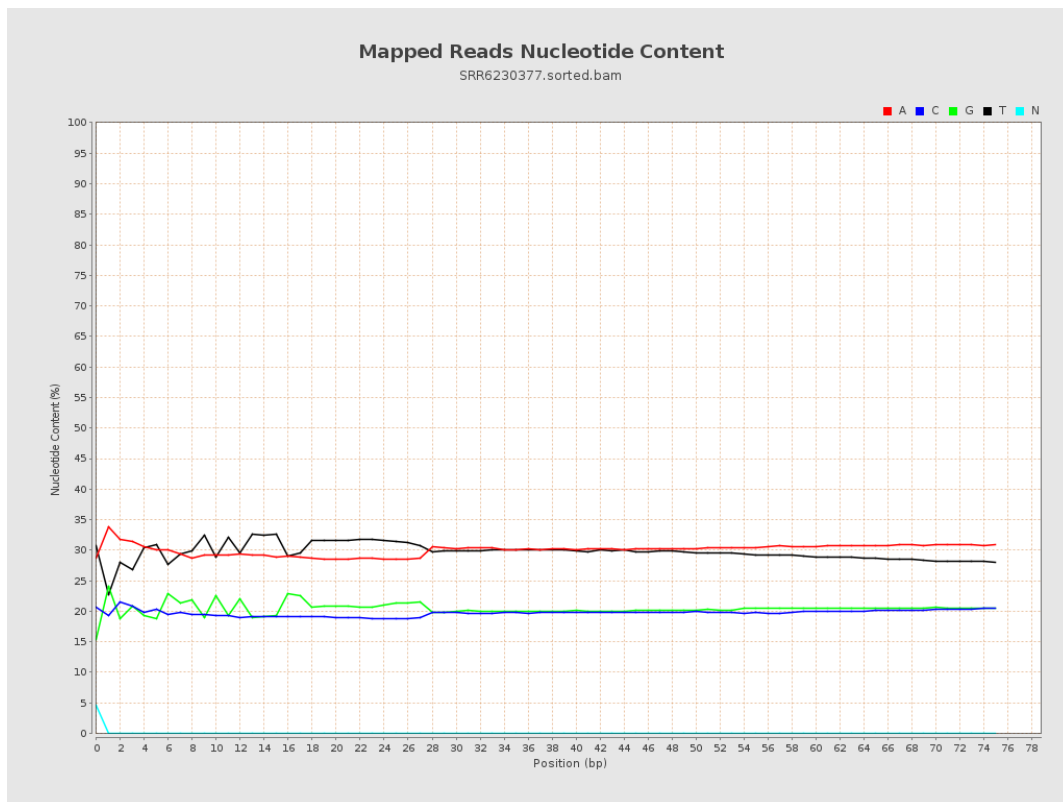
6. Results : Genome Fraction Coverage



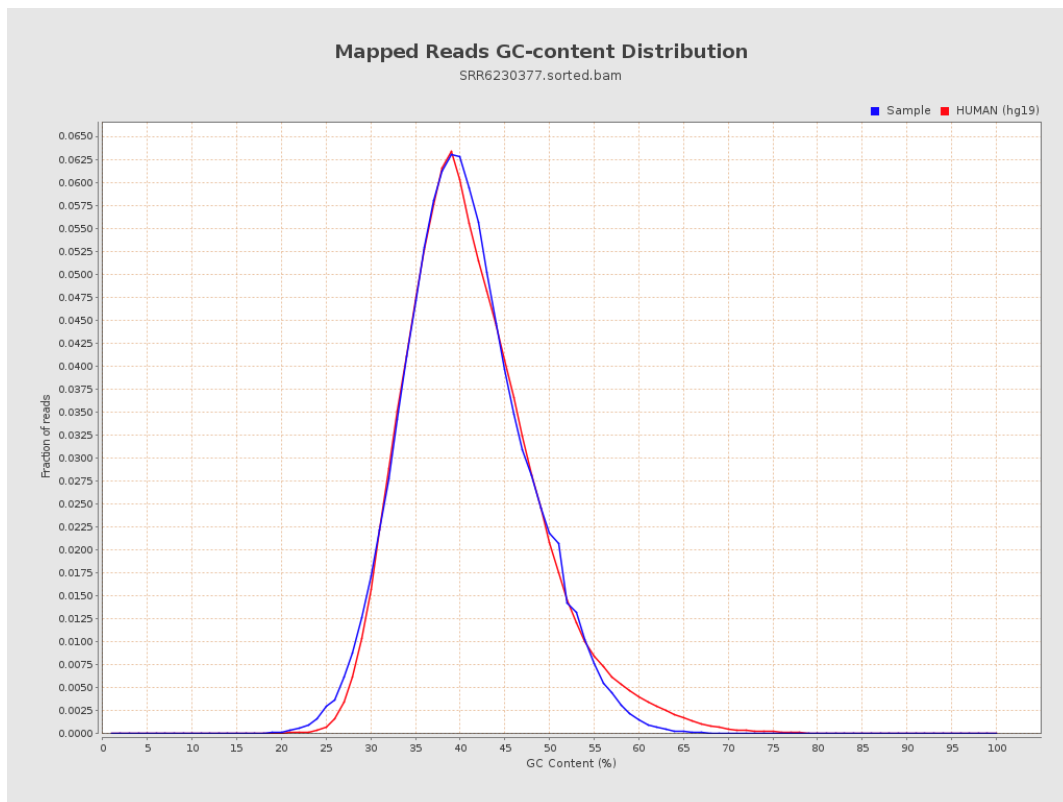
7. Results : Duplication Rate Histogram



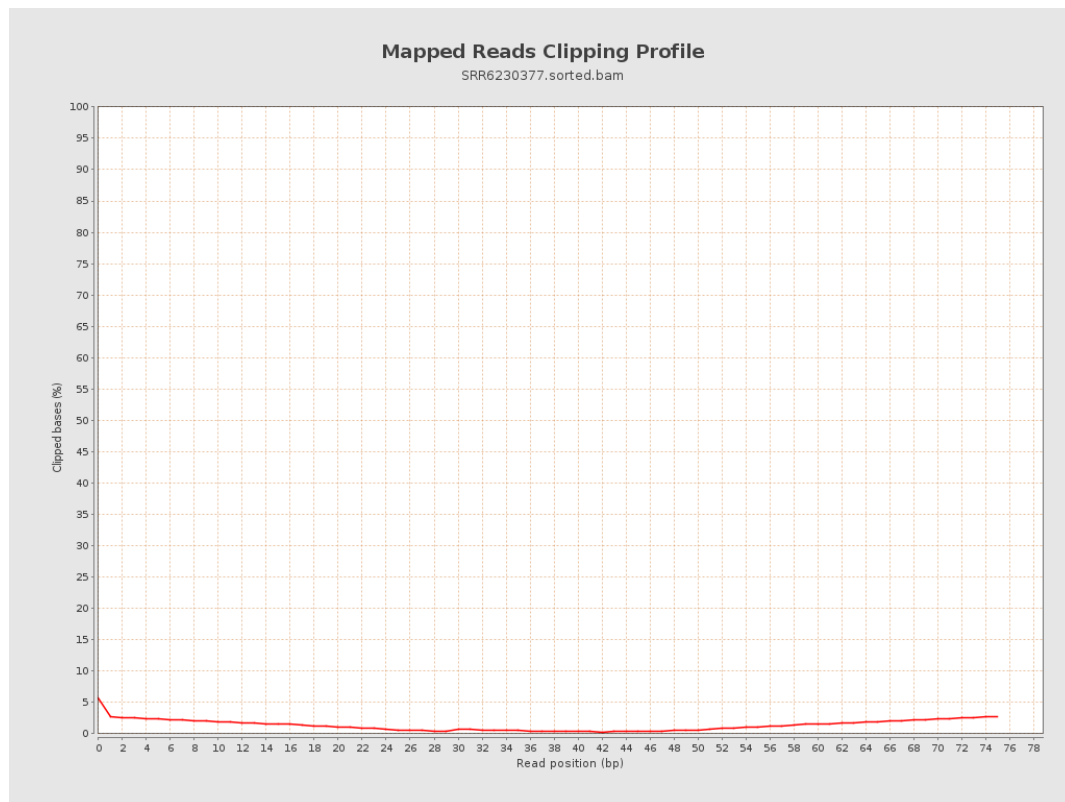
8. Results : Mapped Reads Nucleotide Content



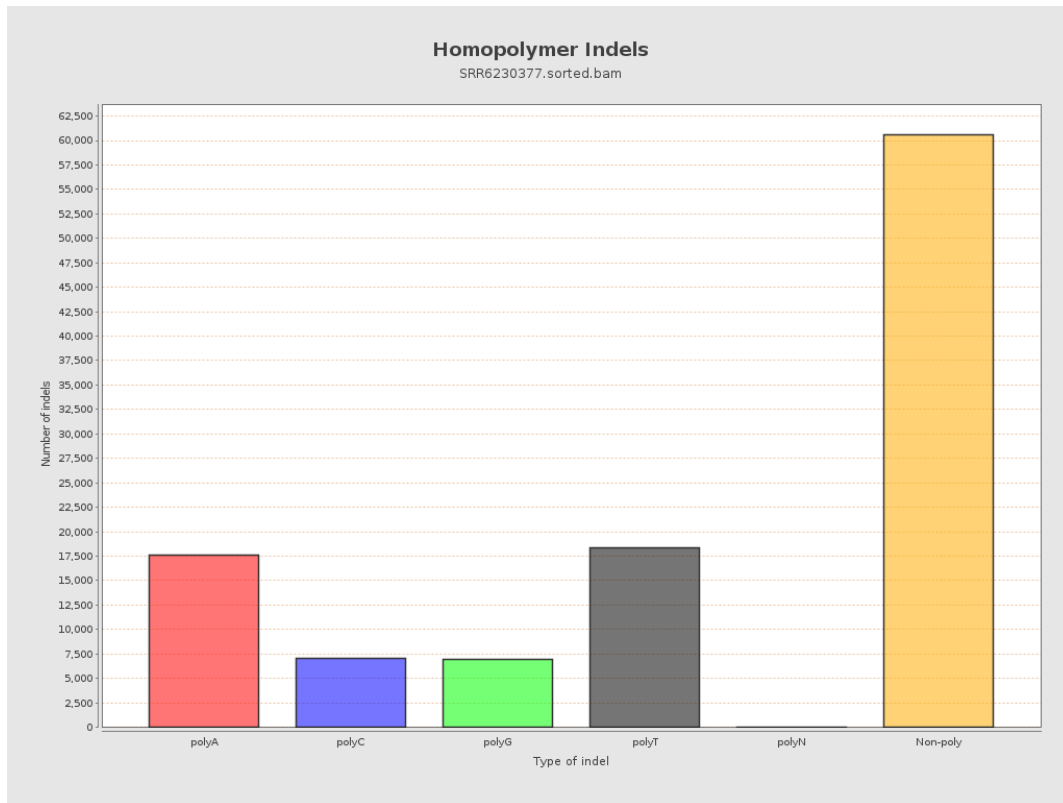
9. Results : Mapped Reads GC-content Distribution



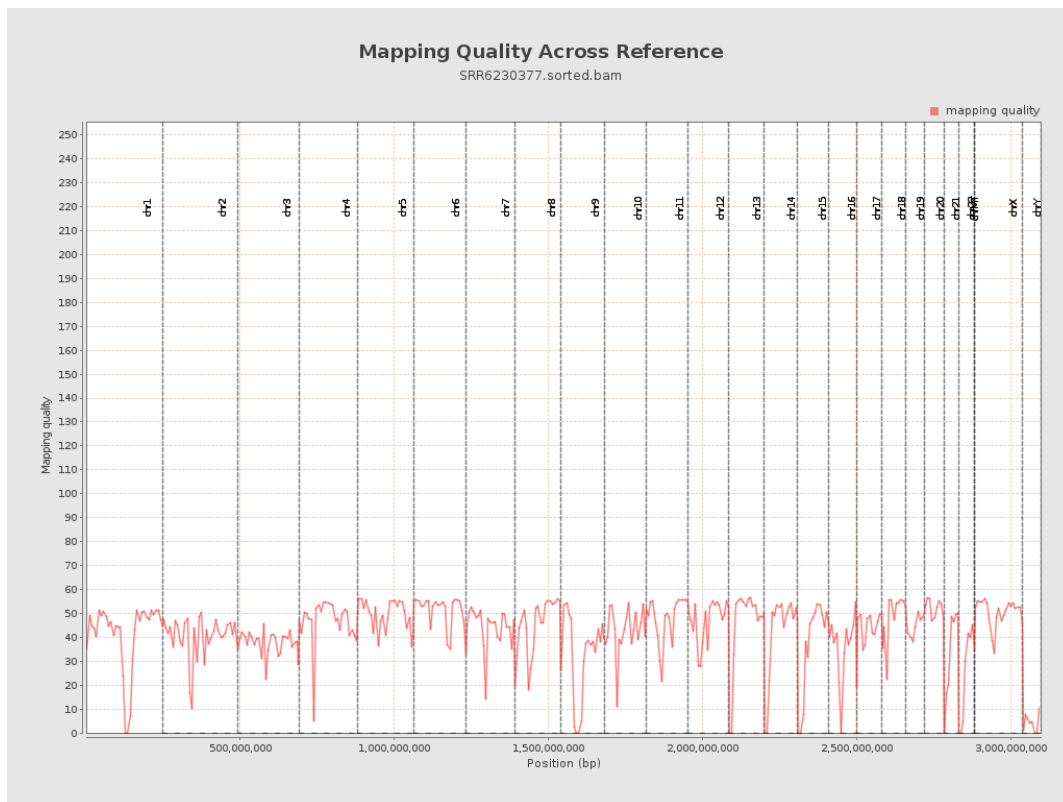
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

