

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 02:25:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240013.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_SRR6240013 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240013.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 02:25:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240013.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,214,487
Mapped reads	976,101 / 80.37%
Unmapped reads	238,386 / 19.63%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,126 / 0.34%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	33,932 / 2.79%
Duplication rate	2.7%
Clipped reads	591,667 / 48.72%

2.2. ACGT Content

Number/percentage of A's	16,778,050 / 27.34%
Number/percentage of C's	10,707,763 / 17.45%
Number/percentage of T's	19,147,084 / 31.2%
Number/percentage of G's	14,695,635 / 23.95%
Number/percentage of N's	38,776 / 0.06%
GC Percentage	41.4%

2.3. Coverage

Mean	0.0198

Standard Deviation	0.2189
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2.4. Mapping Quality

Mean Mapping Quality	42.72
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2.5. Mismatches and indels

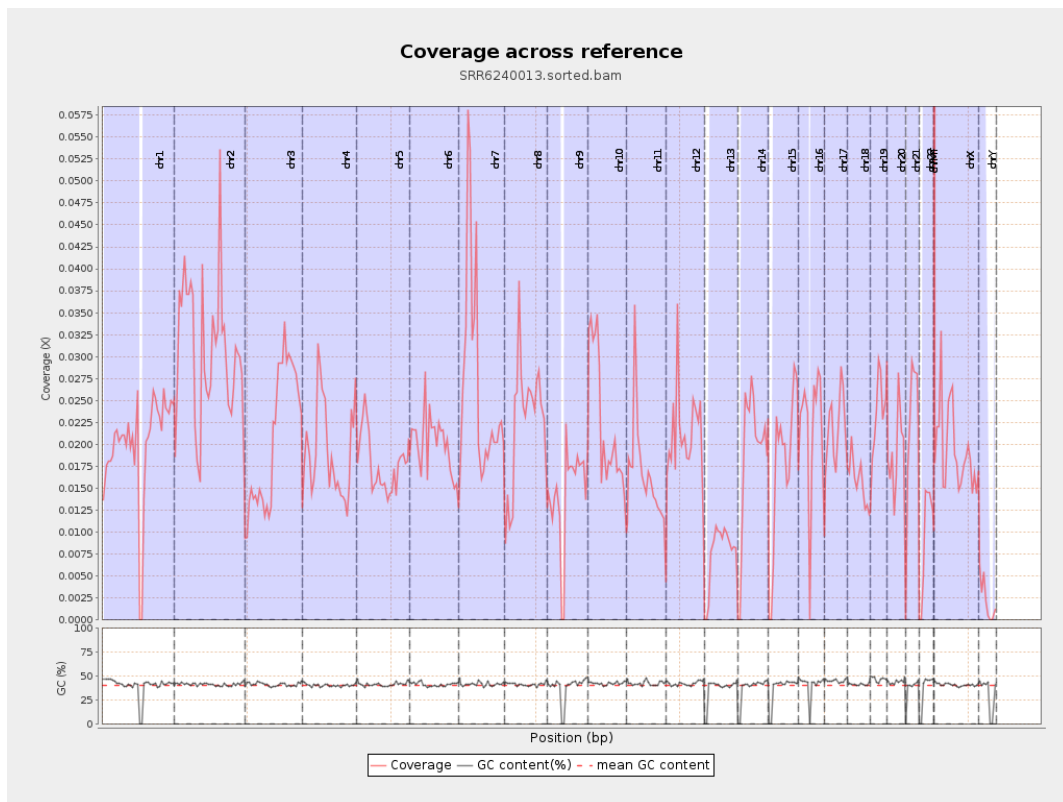
General error rate	1.05%
Mismatches	638,891
Insertions	4,473
Mapped reads with at least one insertion	0.46%
Deletions	20,308
Mapped reads with at least one deletion	2.06%
Homopolymer indels	49.61%

2.6. Chromosome stats

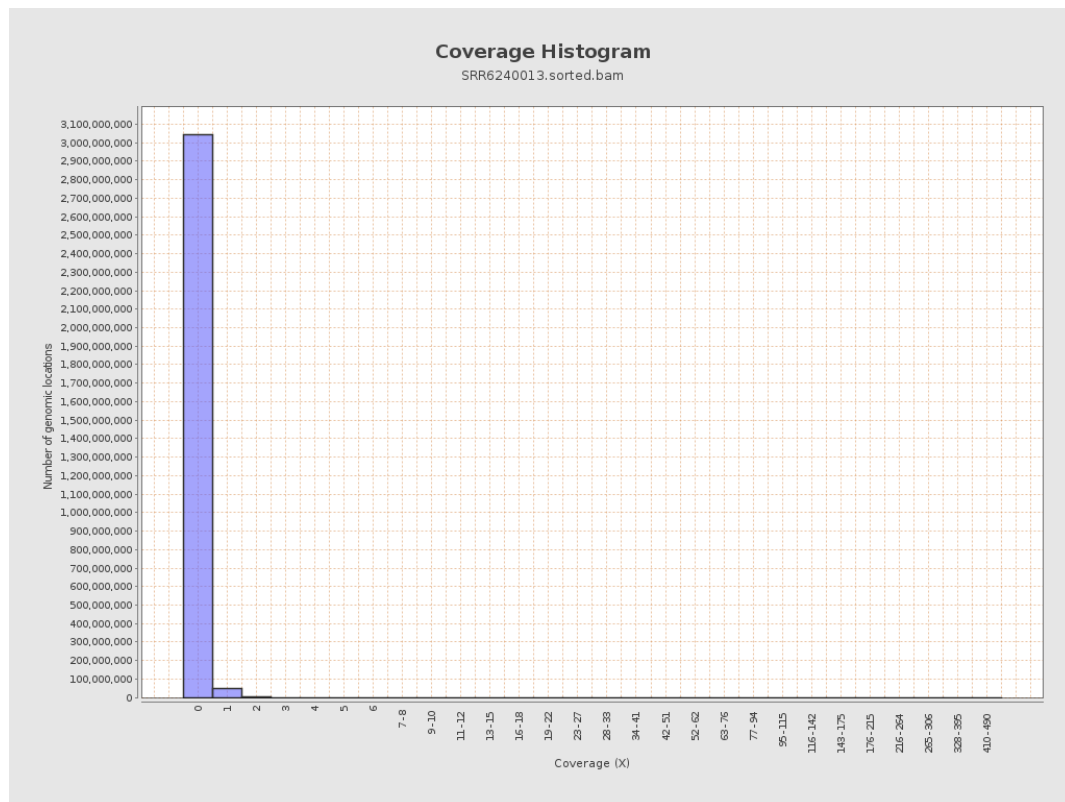
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	4978166	0.02	0.3112
chr2	243199373	7444474	0.0306	0.2638
chr3	198022430	4086467	0.0206	0.1587
chr4	191154276	3631733	0.019	0.1616
chr5	180915260	3216190	0.0178	0.1482
chr6	171115067	3407486	0.0199	0.1828
chr7	159138663	4237407	0.0266	0.4565

chr8	146364022	3329304	0.0227	0.2506
chr9	141213431	2018332	0.0143	0.1895
chr10	135534747	3020777	0.0223	0.1873
chr11	135006516	2234475	0.0166	0.1678
chr12	133851895	2826765	0.0211	0.1608
chr13	115169878	877135	0.0076	0.0965
chr14	107349540	2035284	0.019	0.1585
chr15	102531392	1814012	0.0177	0.1743
chr16	90354753	1929745	0.0214	0.1641
chr17	81195210	1775498	0.0219	0.176
chr18	78077248	1229979	0.0158	0.2489
chr19	59128983	1404530	0.0238	0.2367
chr20	63025520	1173611	0.0186	0.1534
chr21	48129895	1080309	0.0224	0.1715
chr22	51304566	492450	0.0096	0.1056
chrMT	16571	14340	0.8654	1.2689
chrX	155270560	3017326	0.0194	0.1671
chrY	59373566	127603	0.0021	0.0542

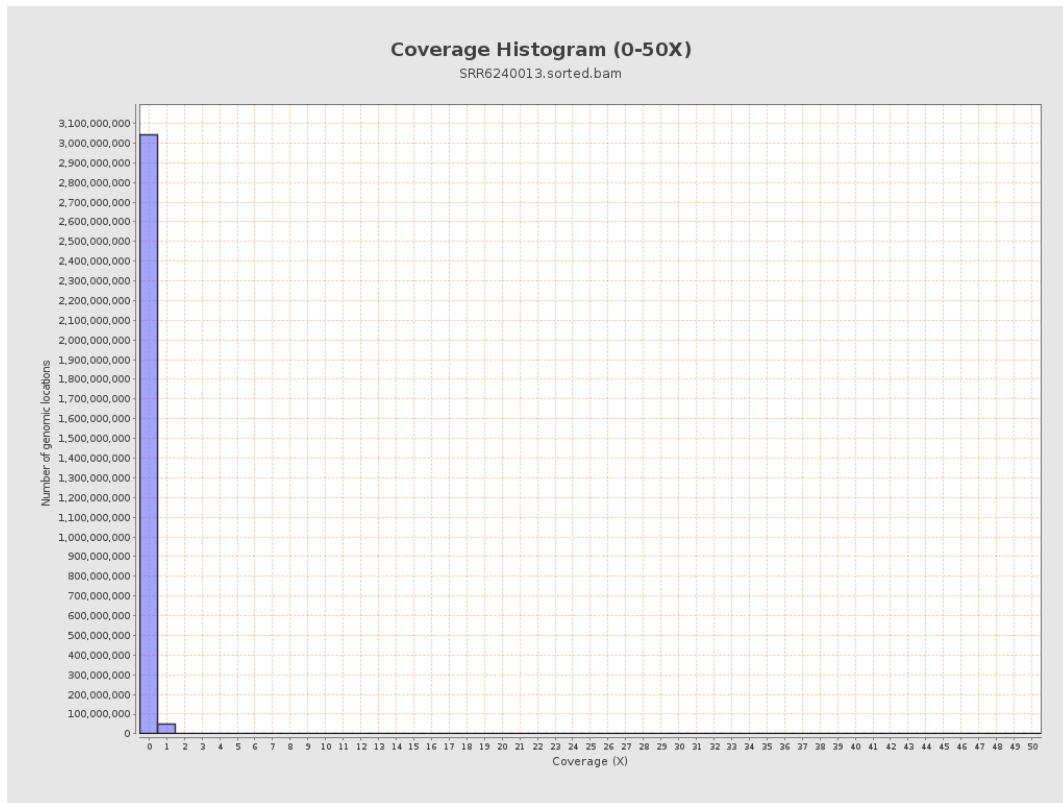
3. Results : Coverage across reference



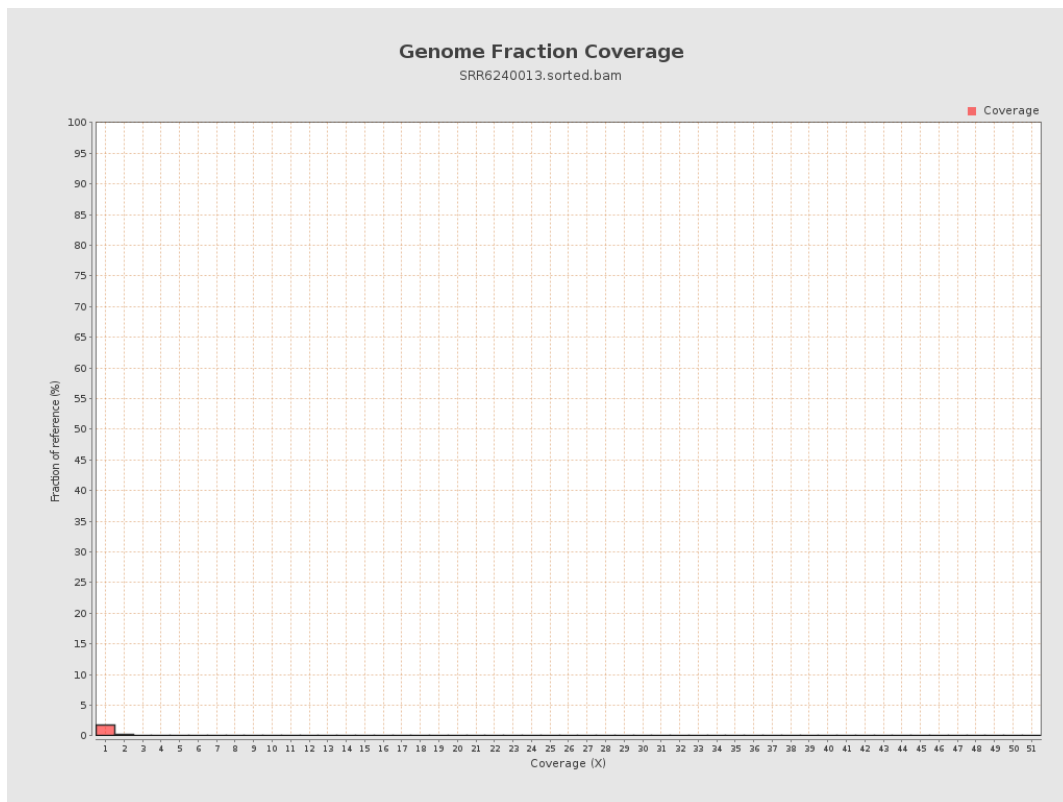
4. Results : Coverage Histogram



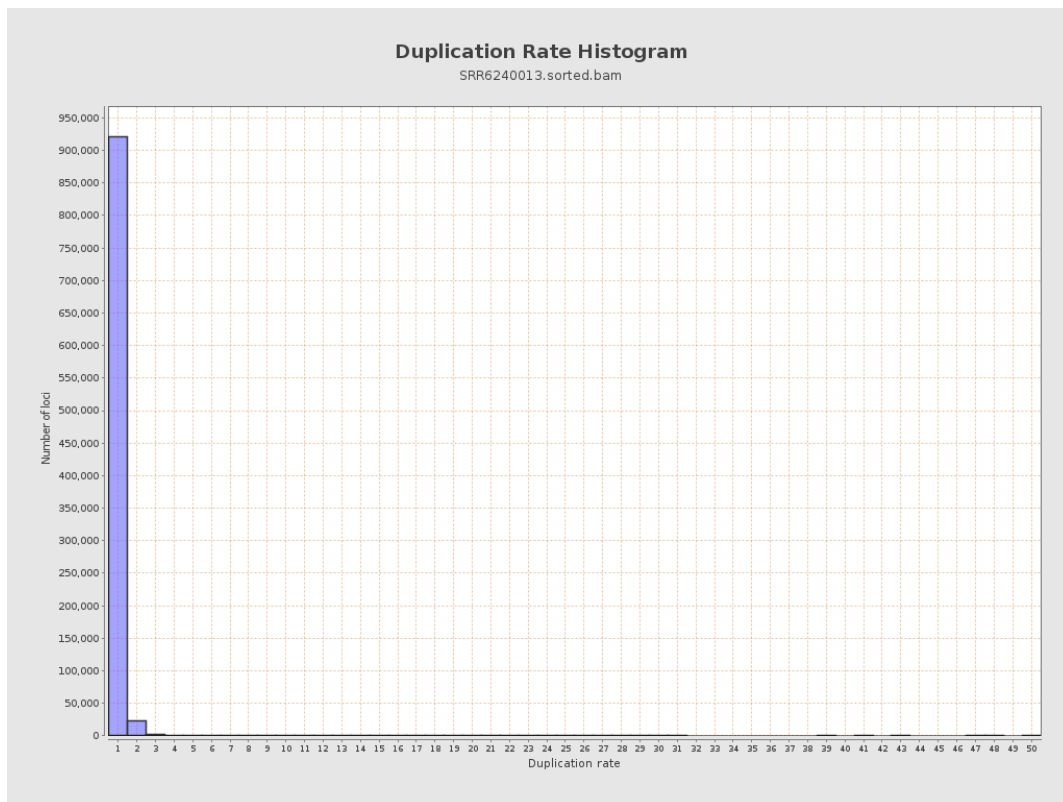
5. Results : Coverage Histogram (0-50X)



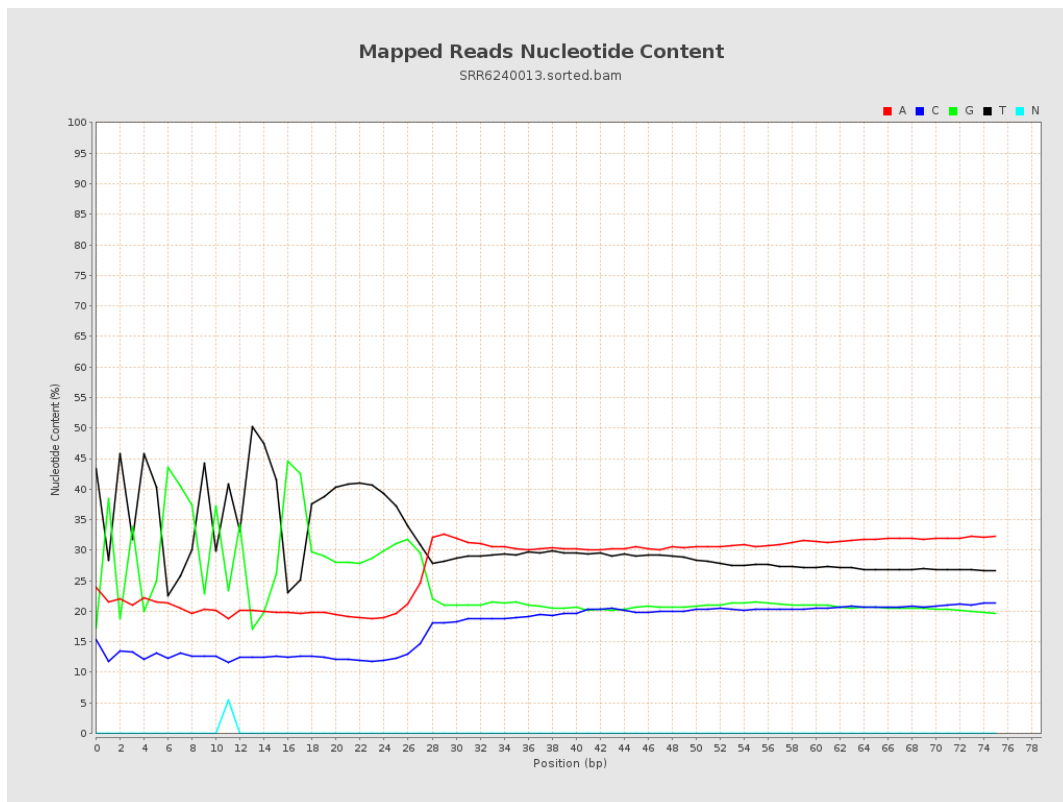
6. Results : Genome Fraction Coverage



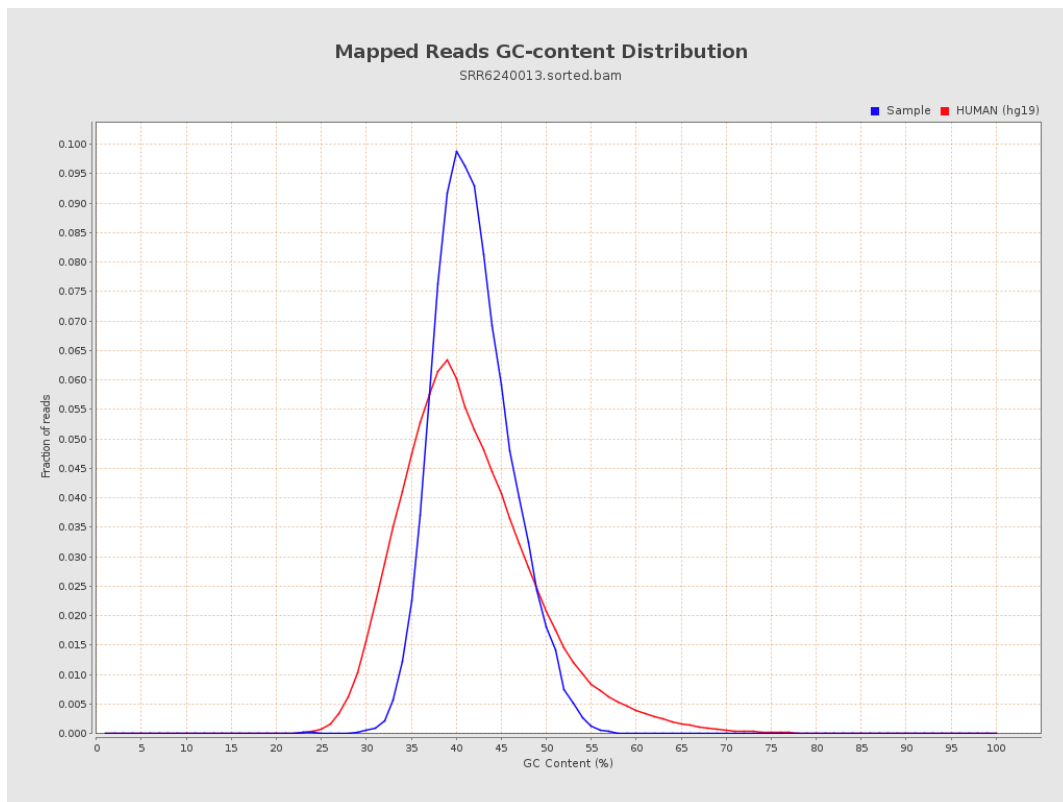
7. Results : Duplication Rate Histogram



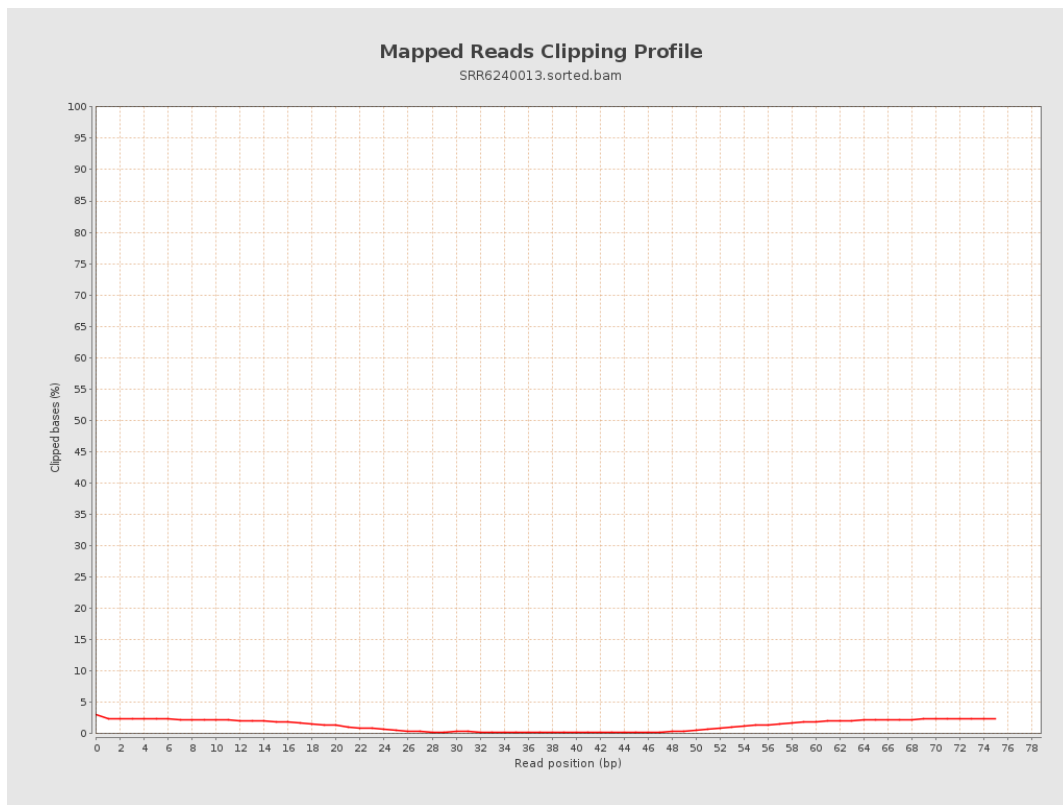
8. Results : Mapped Reads Nucleotide Content



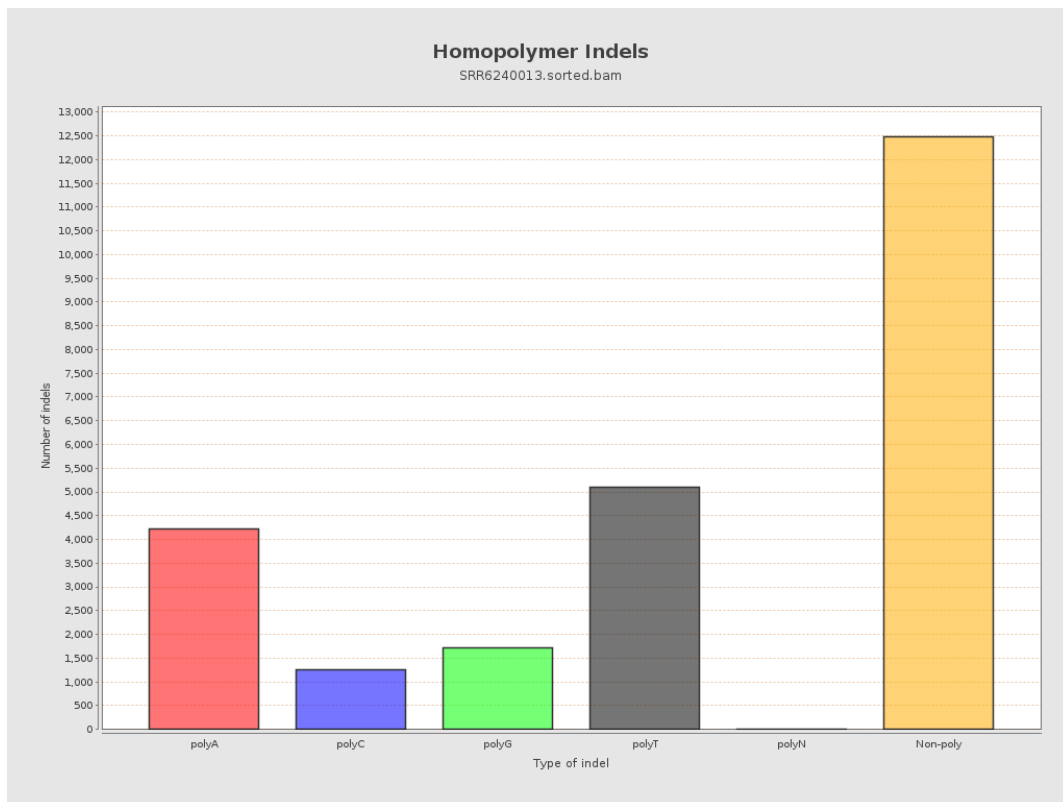
9. Results : Mapped Reads GC-content Distribution



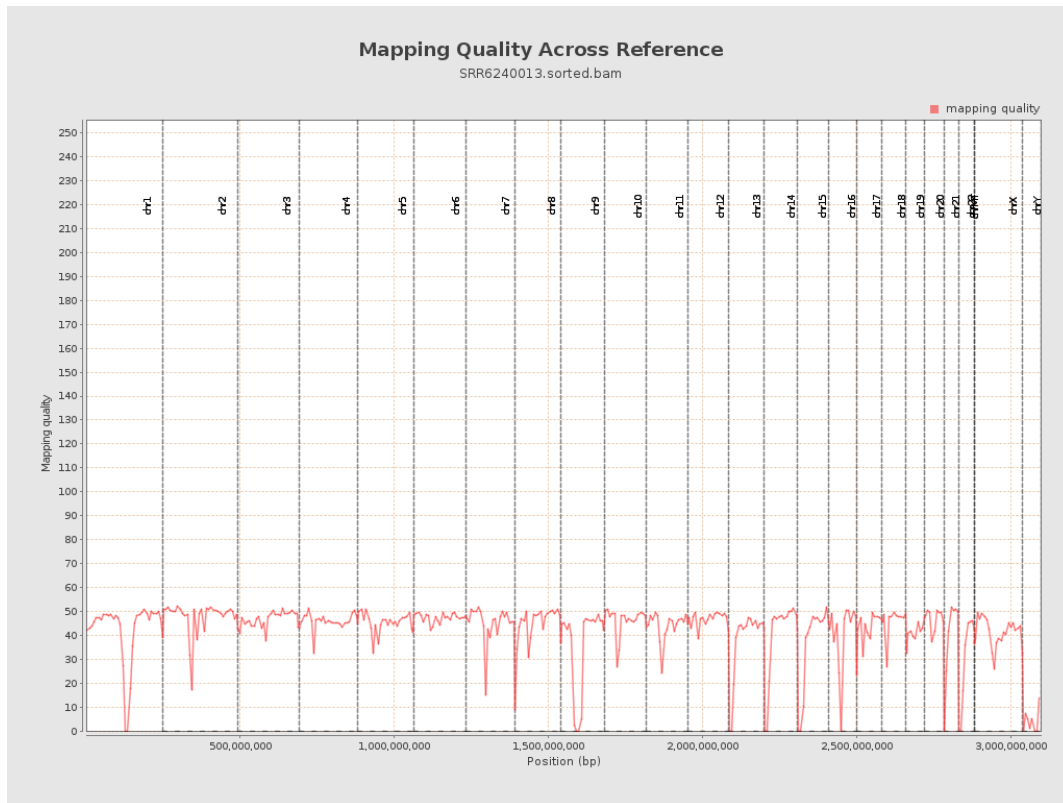
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

