Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 00:12:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR053620.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_SRR053620 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR053620.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 00:12:40 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR053620.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,737,323
Mapped reads	11,050,960 / 80.44%
Unmapped reads	2,686,363 / 19.56%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	320 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	2,759,538 / 20.09%
Duplication rate	17.49%
Clipped reads	807,758 / 5.88%

2.2. ACGT Content

Number/percentage of A's	154,998,811 / 29.63%
Number/percentage of C's	97,407,586 / 18.62%
Number/percentage of T's	160,324,145 / 30.65%
Number/percentage of G's	110,056,769 / 21.04%
Number/percentage of N's	310,326 / 0.06%
GC Percentage	39.66%

2.3. Coverage

Mean	0.169

Standard Deviation	1.1174

2.4. Mapping Quality

Mean Mapping Quality	46.15

2.5. Mismatches and indels

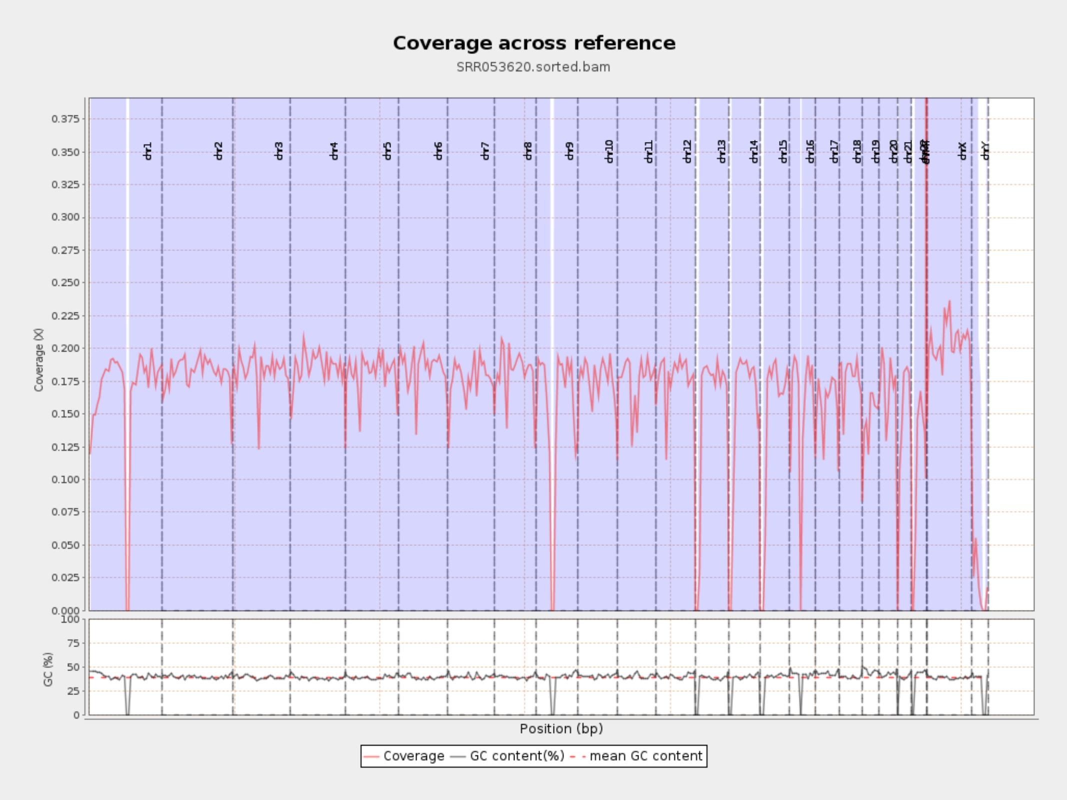
General error rate	0.58%
Mismatches	3,018,116
Insertions	23,344
Mapped reads with at least one insertion	0.21%
Deletions	70,274
Mapped reads with at least one deletion	0.63%
Homopolymer indels	48.61%

2.6. Chromosome stats

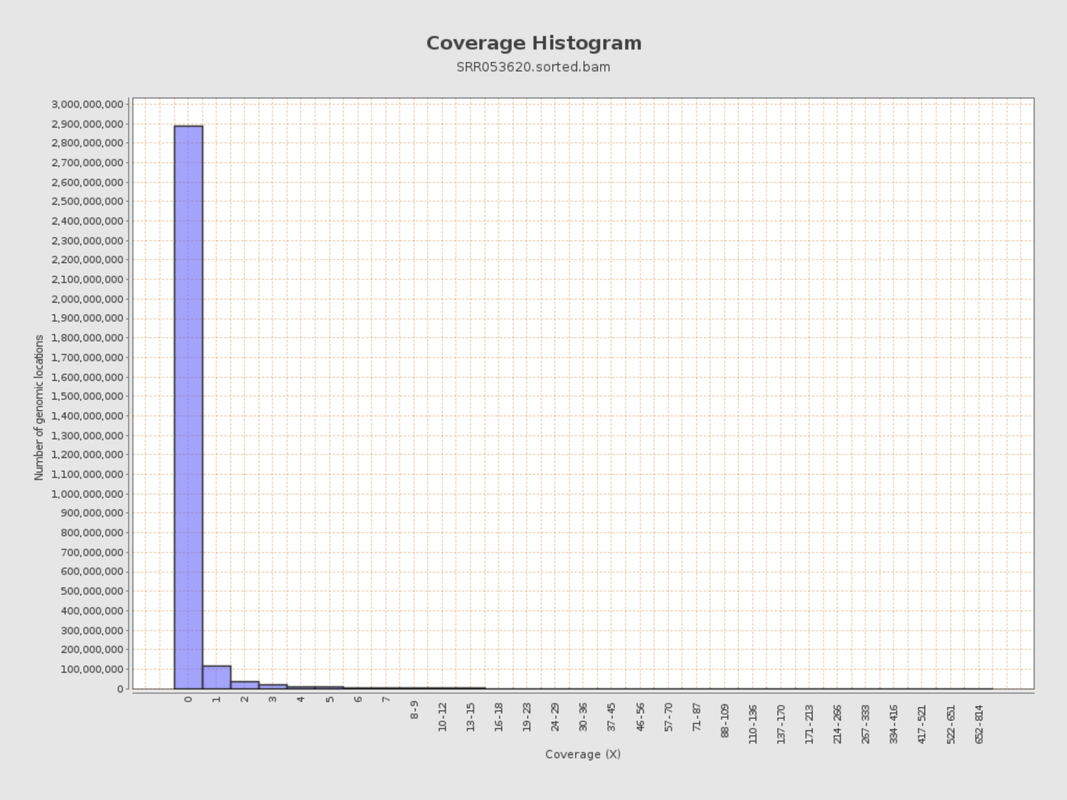
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	41425275	0.1662	1.1496
chr2	243199373	44326619	0.1823	1.3088
chr3	198022430	36302649	0.1833	1.0987
chr4	191154276	35527498	0.1859	1.1813
chr5	180915260	32897973	0.1818	1.0874
chr6	171115067	31770260	0.1857	1.1375
chr7	159138663	28293083	0.1778	1.1862

chr8	146364022	26652526	0.1821	1.1395
chr9	141213431	21514904	0.1524	1.0608
chr10	135534747	24129935	0.178	1.173
chr11	135006516	23631974	0.175	1.1462
chr12	133851895	23764543	0.1775	1.06
chr13	115169878	17219009	0.1495	0.9958
chr14	107349540	16082179	0.1498	1.1055
chr15	102531392	14645761	0.1428	0.9351
chr16	90354753	14079931	0.1558	1.0145
chr17	81195210	12752473	0.1571	0.963
chr18	78077248	13889317	0.1779	1.2443
chr19	59128983	8656469	0.1464	1.018
chr20	63025520	10638545	0.1688	1.0616
chr21	48129895	6795218	0.1412	1.0402
chr22	51304566	5254172	0.1024	0.7758
chrMT	16571	48859	2.9485	6.3801
chrX	155270560	31622209	0.2037	1.2309
chrY	59373566	1280391	0.0216	0.4714

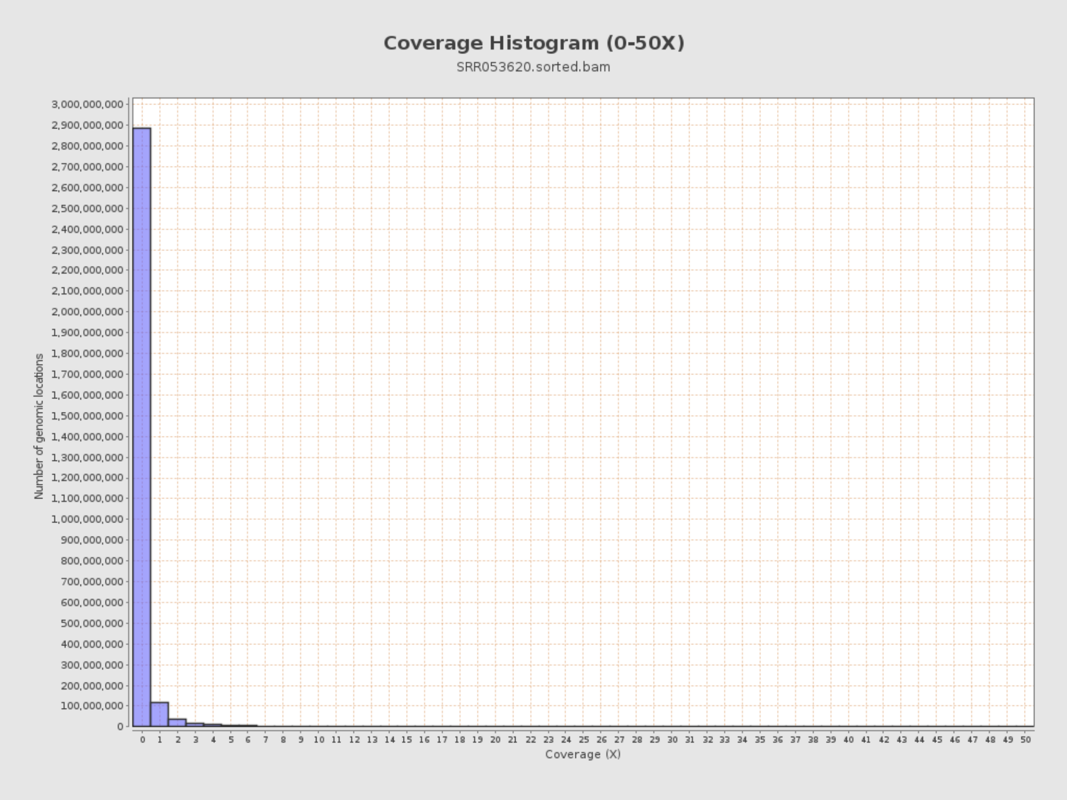
3. Results : Coverage across reference



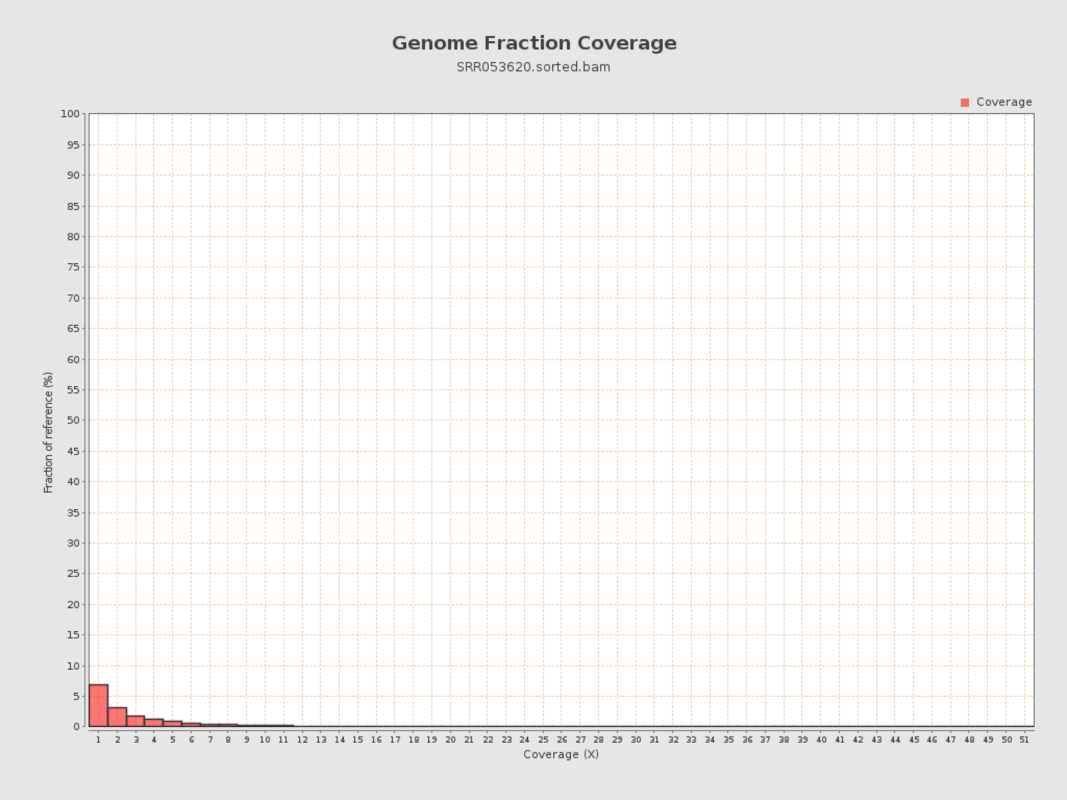
4. Results : Coverage Histogram



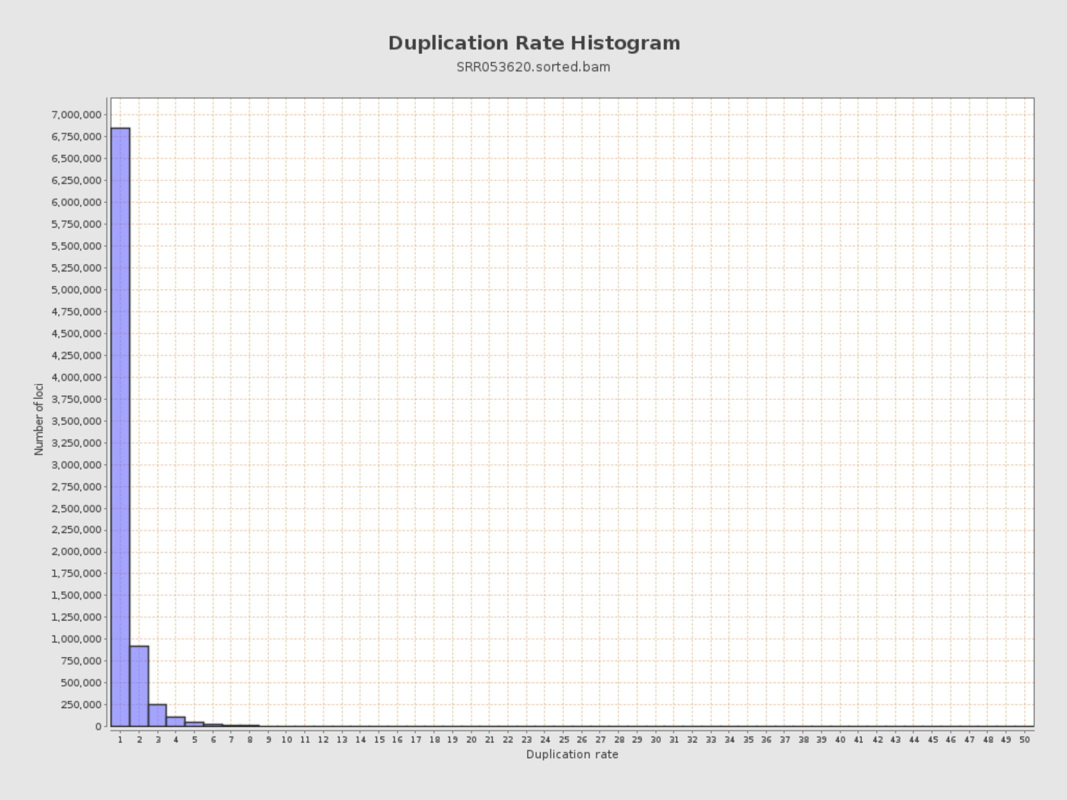
5. Results : Coverage Histogram (0-50X)



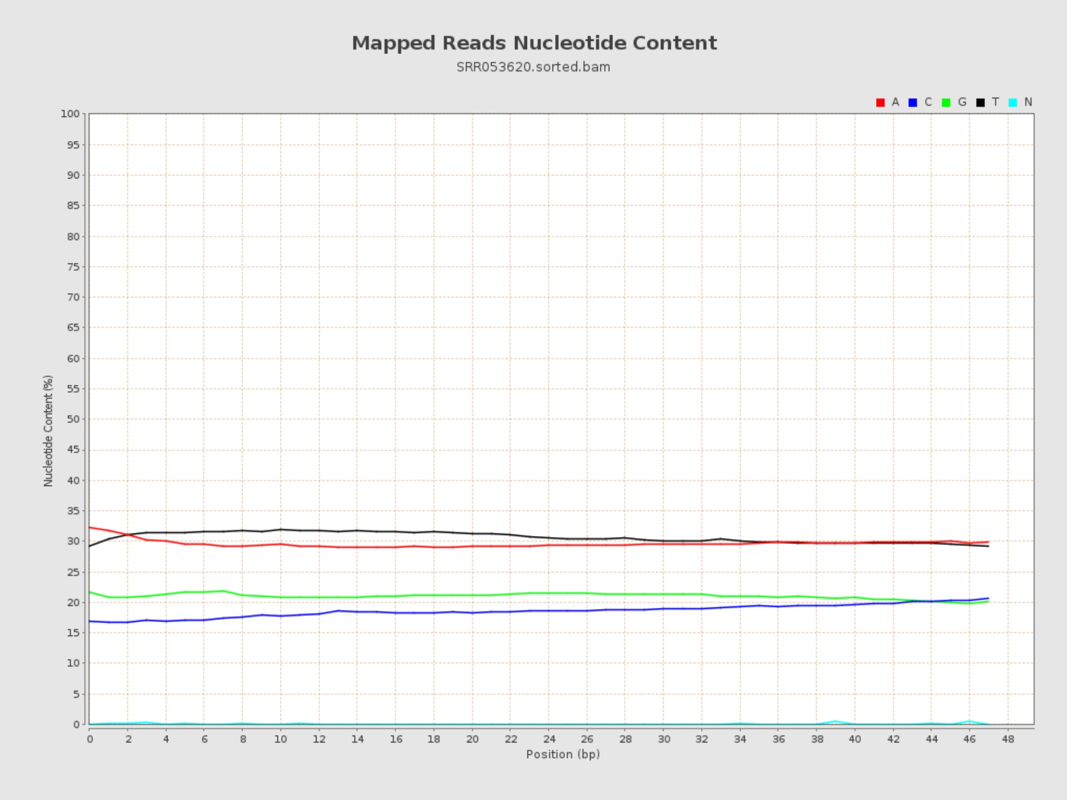
6. Results : Genome Fraction Coverage



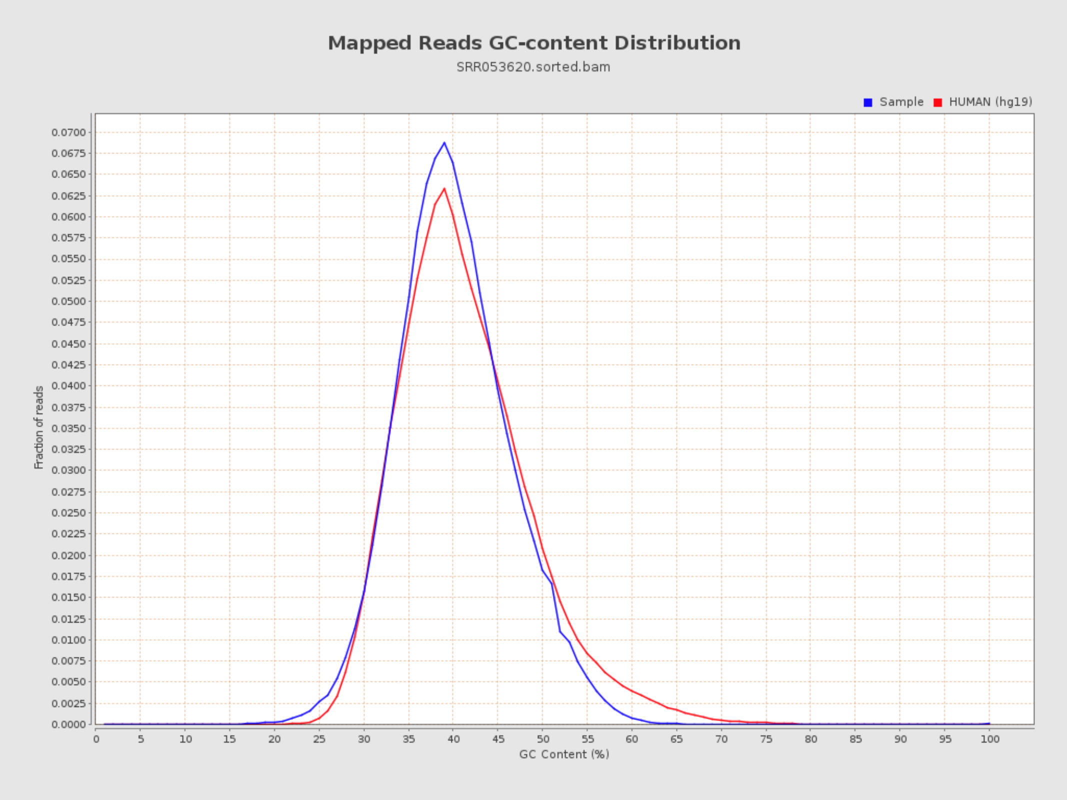
7. Results : Duplication Rate Histogram



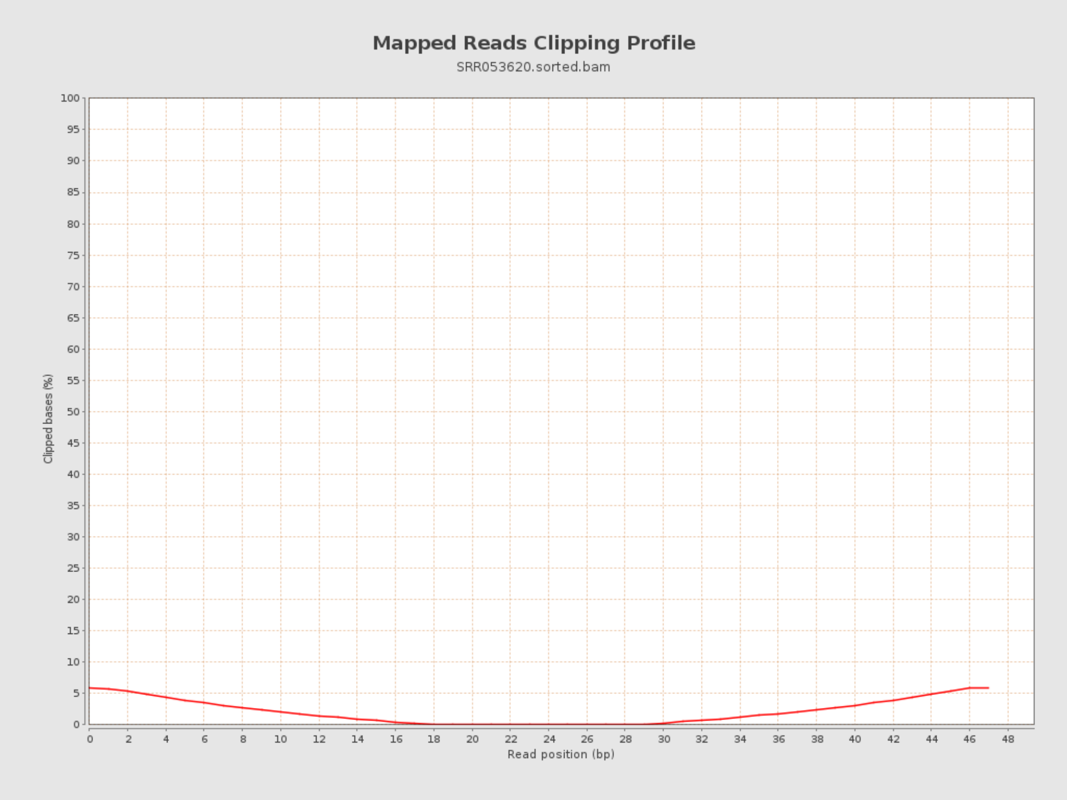
8. Results : Mapped Reads Nucleotide Content



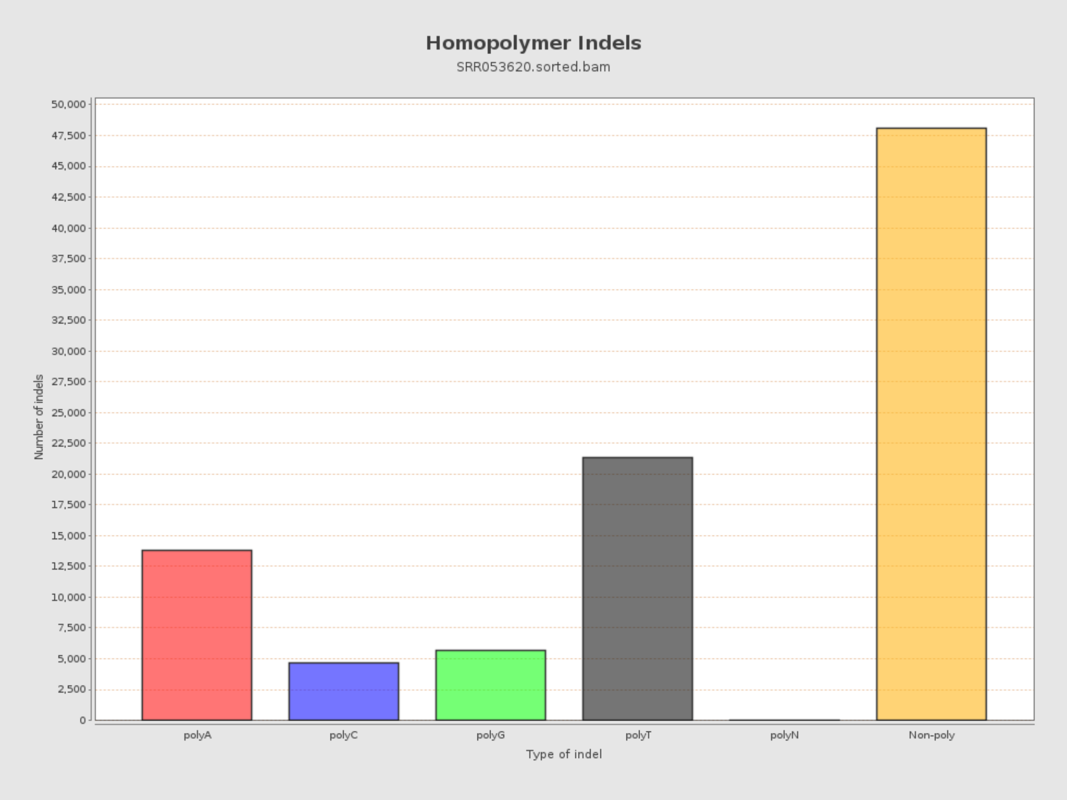
9. Results : Mapped Reads GC-content Distribution



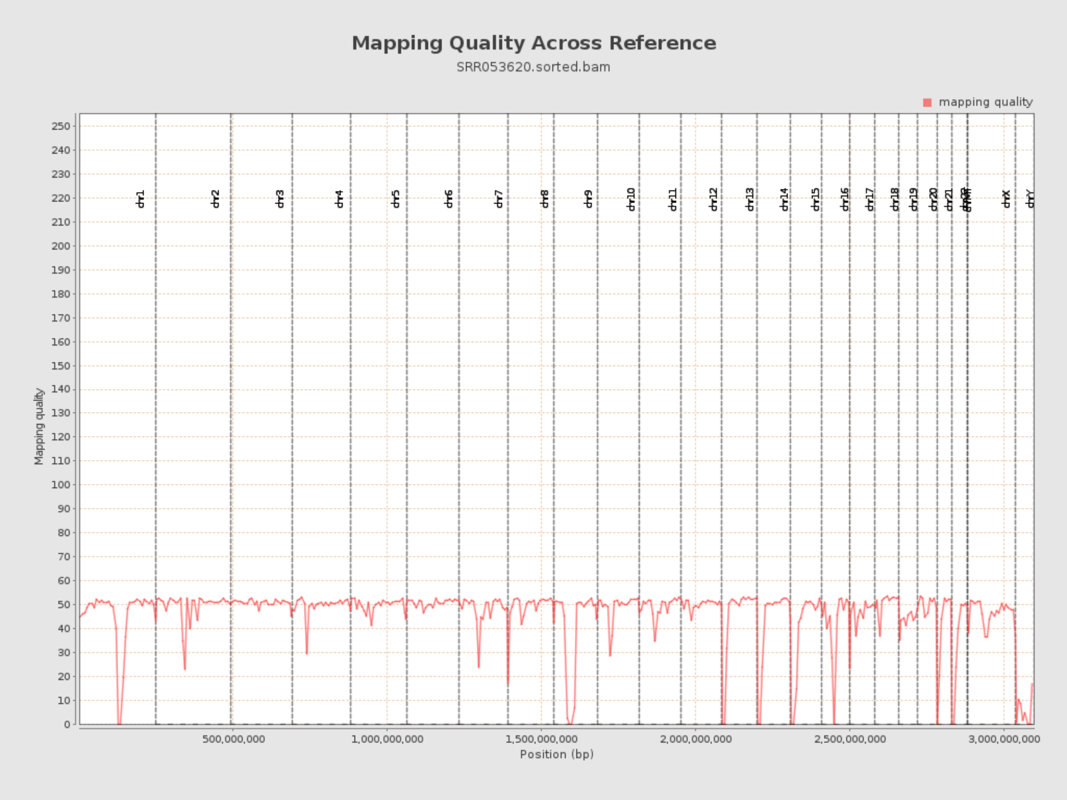
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram