Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 08:18:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR054616.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_SRR054616 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR054616.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 08:18:19 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR054616.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,484,340
Mapped reads	14,552,704 / 78.73%
Unmapped reads	3,931,636 / 21.27%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,078 / 0.01%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	2,821,278 / 15.26%
Duplication rate	13.84%
Clipped reads	1,566,042 / 8.47%

2.2. ACGT Content

Number/percentage of A's	201,987,533 / 29.54%
Number/percentage of C's	134,503,202 / 19.67%
Number/percentage of T's	202,093,646 / 29.55%
Number/percentage of G's	145,182,008 / 21.23%
Number/percentage of N's	73,693 / 0.01%
GC Percentage	40.9%

2.3. Coverage

Mean	0.2209

Standard Deviation	1.2837

2.4. Mapping Quality

Mean Mapping Quality	45.03

2.5. Mismatches and indels

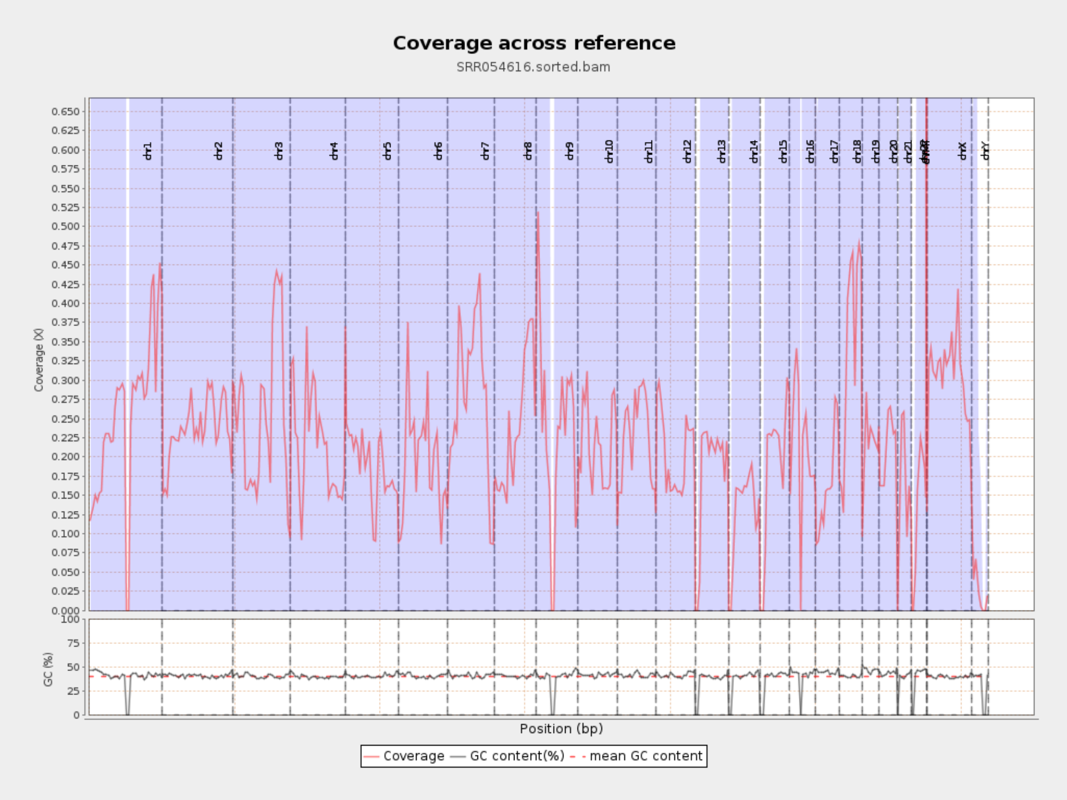
General error rate	0.48%
Mismatches	3,201,967
Insertions	32,686
Mapped reads with at least one insertion	0.22%
Deletions	100,549
Mapped reads with at least one deletion	0.69%
Homopolymer indels	45.35%

2.6. Chromosome stats

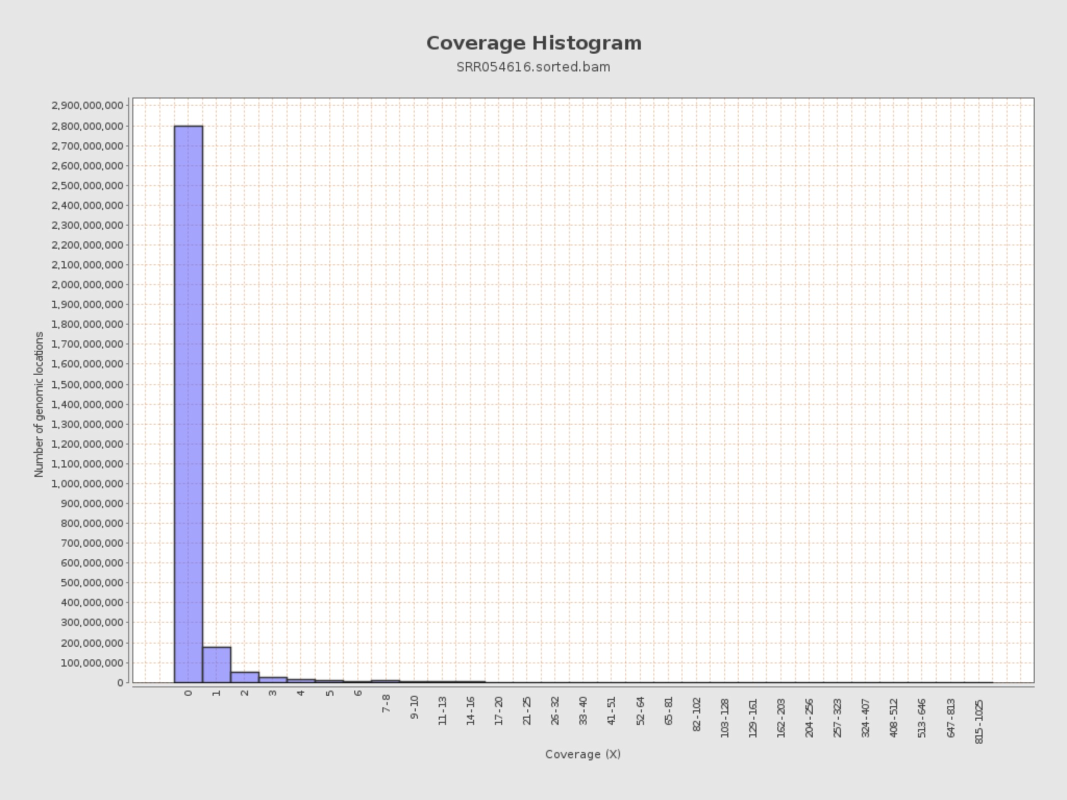
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	62653487	0.2514	1.5847
chr2	243199373	57533719	0.2366	1.3887
chr3	198022430	50637644	0.2557	1.2931
chr4	191154276	41068106	0.2148	1.1868
chr5	180915260	33933028	0.1876	1.0223
chr6	171115067	33072696	0.1933	1.2001
chr7	159138663	45061638	0.2832	1.5543

chr8	146364022	35551079	0.2429	1.3348
chr9	141213431	33629199	0.2381	1.3019
chr10	135534747	29735373	0.2194	1.297
chr11	135006516	30838541	0.2284	1.2662
chr12	133851895	27332171	0.2042	1.111
chr13	115169878	20653512	0.1793	1.0505
chr14	107349540	13796113	0.1285	0.9971
chr15	102531392	19082518	0.1861	1.0349
chr16	90354753	19349957	0.2142	1.2465
chr17	81195210	13328631	0.1642	0.959
chr18	78077248	26821888	0.3435	1.7429
chr19	59128983	13070812	0.2211	1.4214
chr20	63025520	13158989	0.2088	1.1546
chr21	48129895	7589550	0.1577	1.1323
chr22	51304566	6649757	0.1296	0.8202
chrMT	16571	33388	2.0148	5.715
chrX	155270560	47761628	0.3076	1.5207
chrY	59373566	1648334	0.0278	0.4683

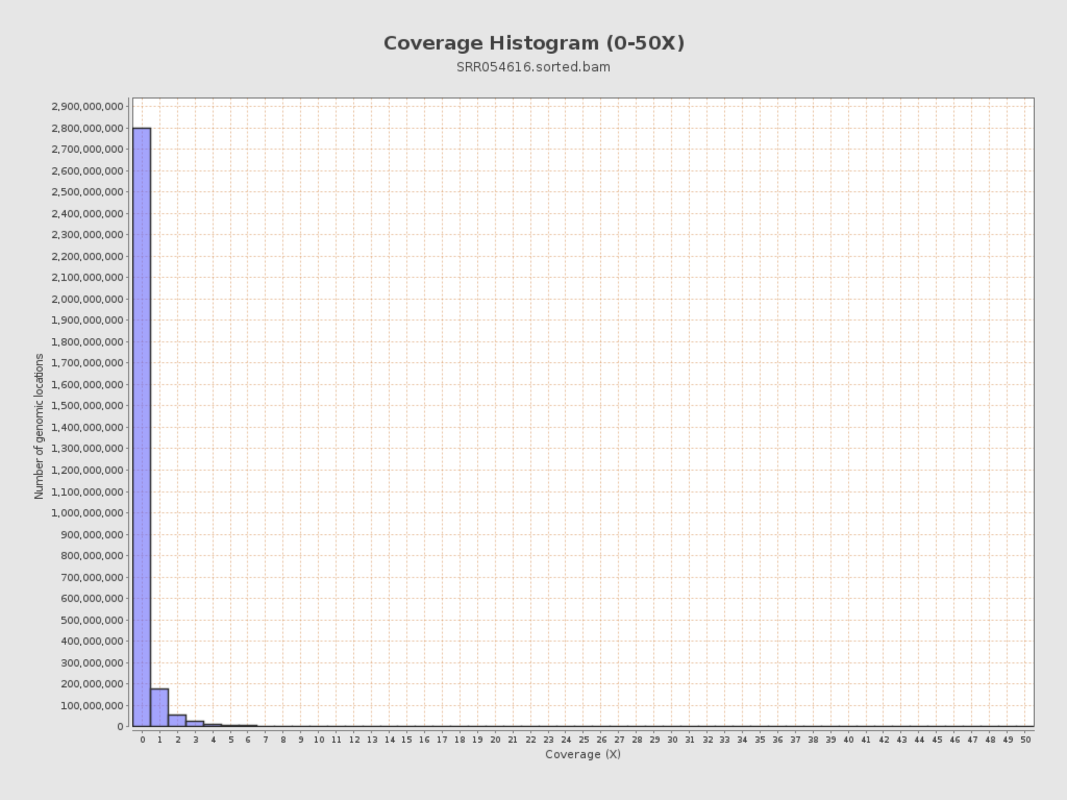
3. Results : Coverage across reference



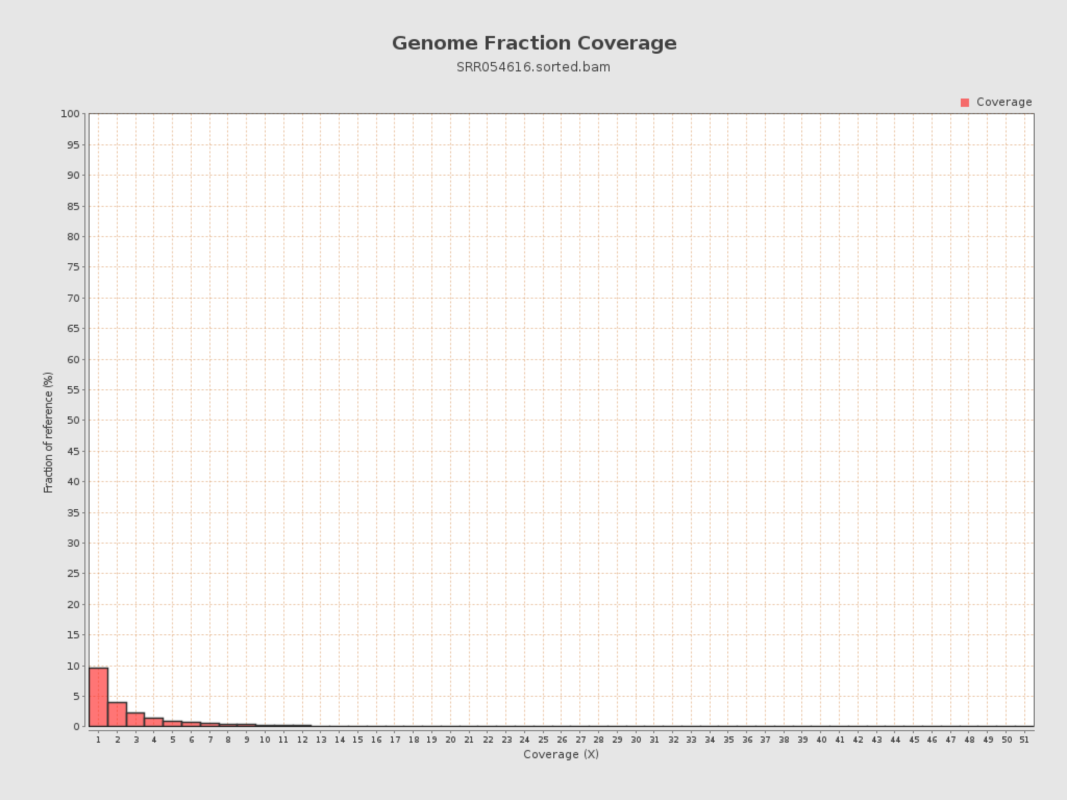
4. Results : Coverage Histogram



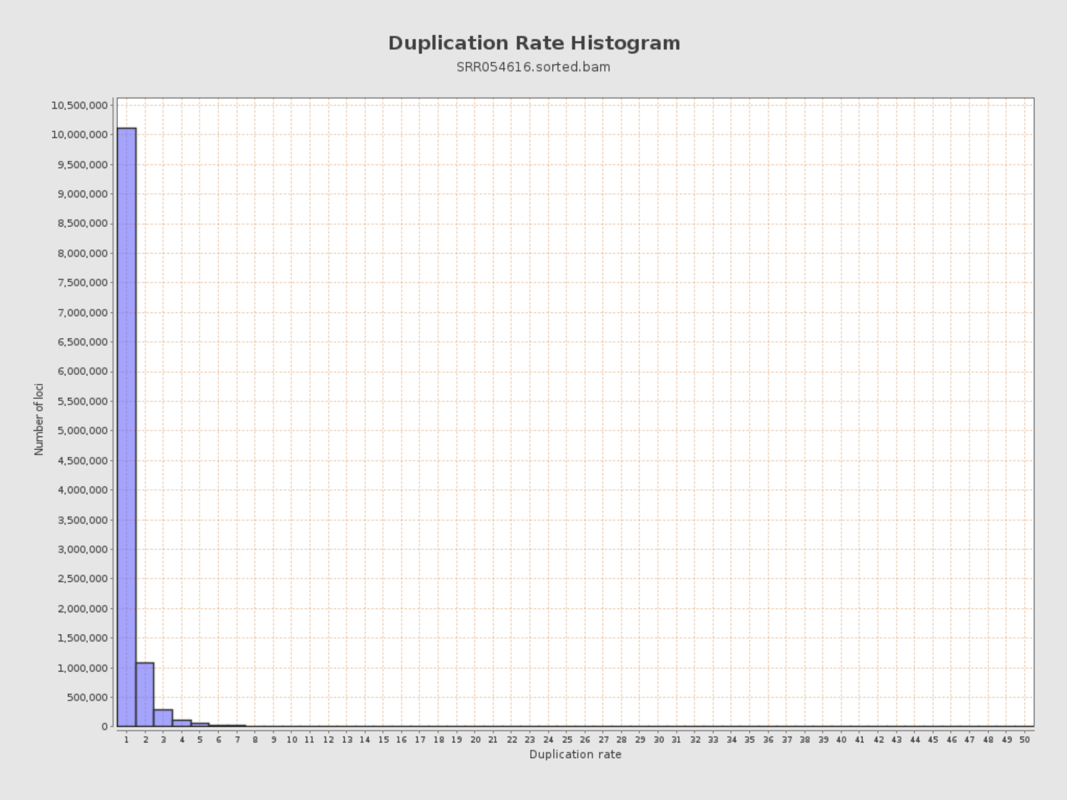
5. Results : Coverage Histogram (0-50X)



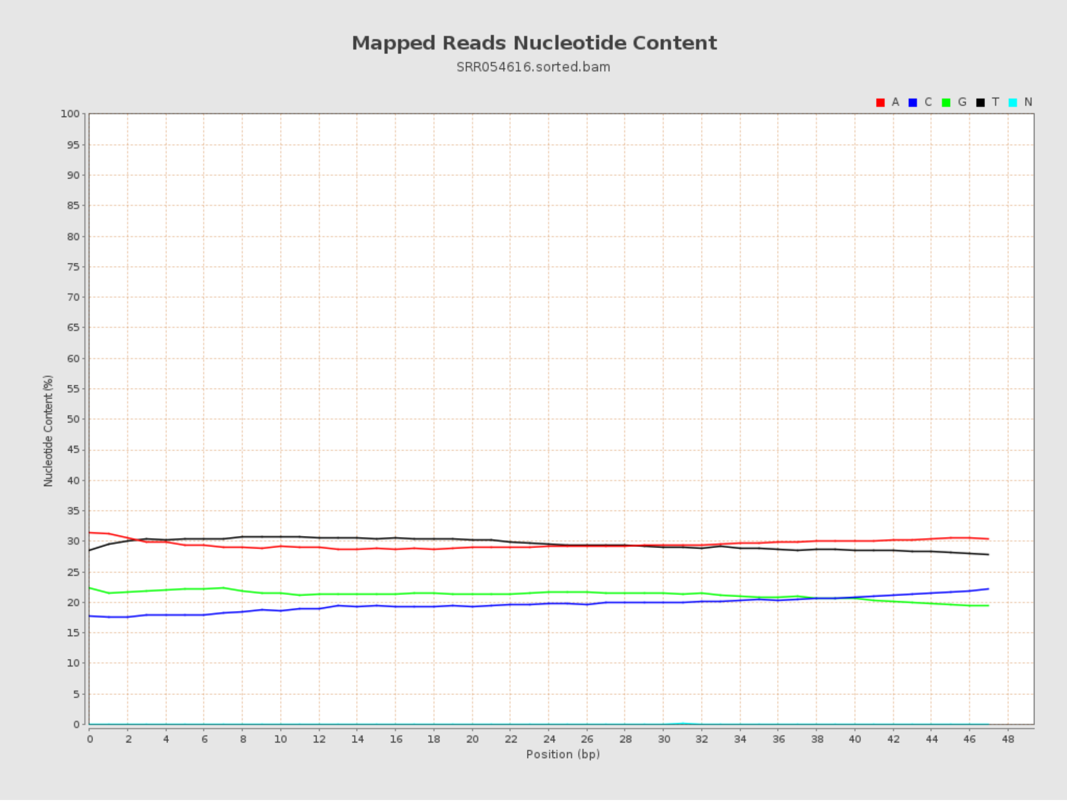
6. Results : Genome Fraction Coverage



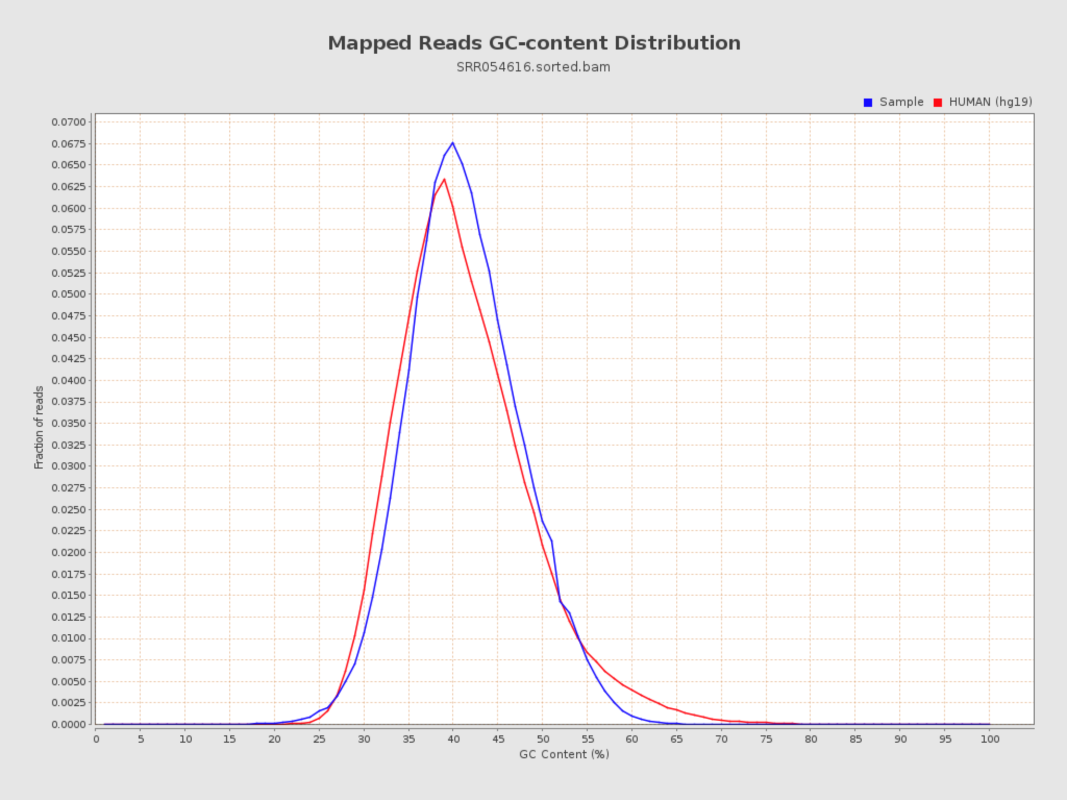
7. Results : Duplication Rate Histogram



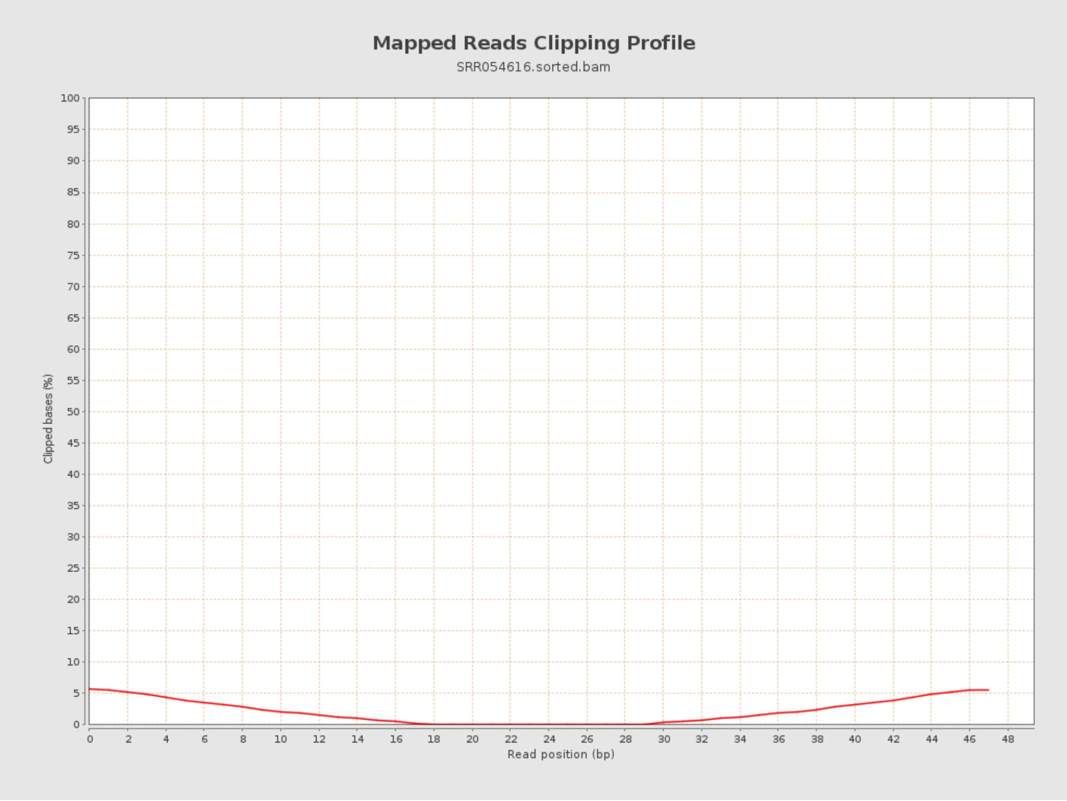
8. Results : Mapped Reads Nucleotide Content



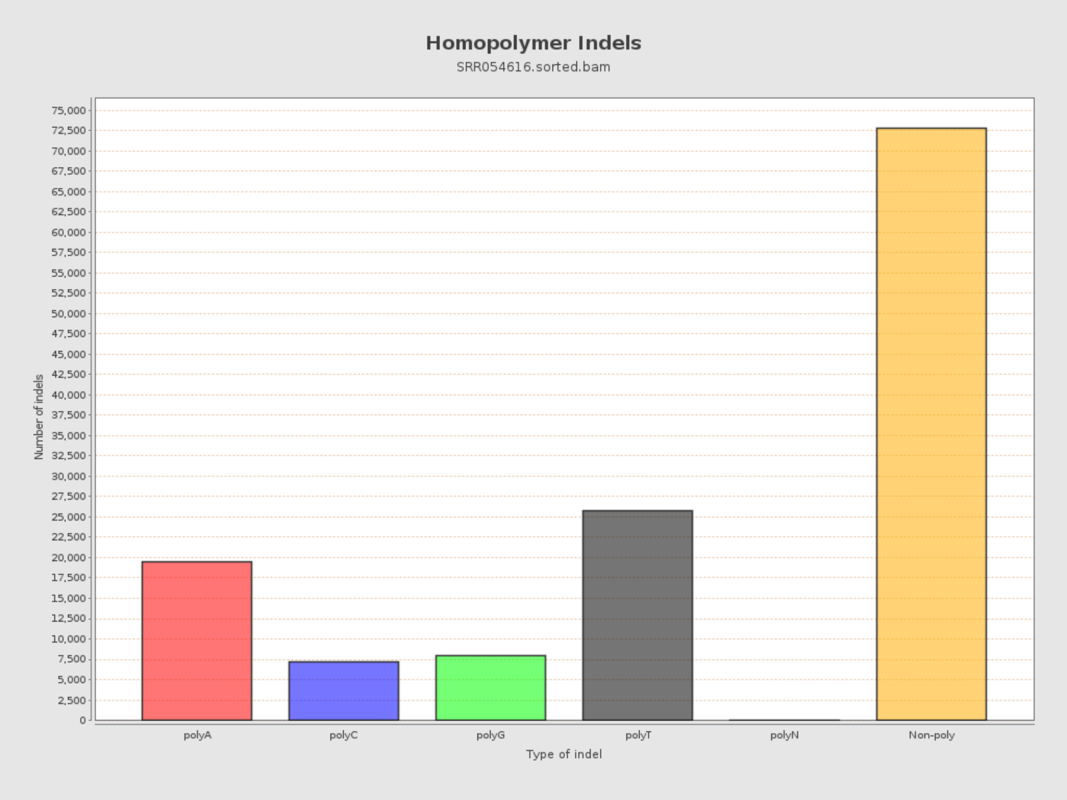
9. Results : Mapped Reads GC-content Distribution



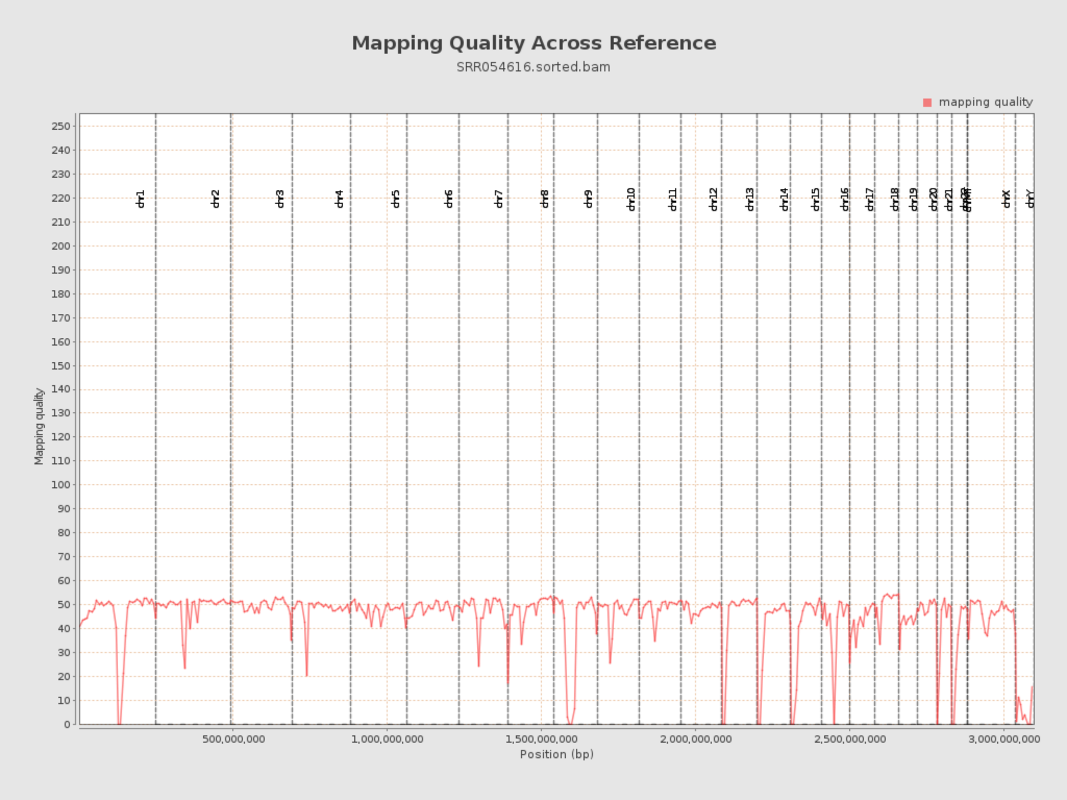
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram