Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/18 23:12:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR053606.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_SRR053606 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR053606.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 18 23:12:51 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR053606.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,969,157
Mapped reads	2,927,375 / 58.91%
Unmapped reads	2,041,782 / 41.09%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	69 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	375,244 / 7.55%
Duplication rate	10.32%
Clipped reads	317,602 / 6.39%

2.2. ACGT Content

Number/percentage of A's	40,941,187 / 29.76%
Number/percentage of C's	26,558,572 / 19.31%
Number/percentage of T's	40,865,393 / 29.71%
Number/percentage of G's	28,850,733 / 20.97%
Number/percentage of N's	352,222 / 0.26%
GC Percentage	40.28%

2.3. Coverage

Mean	0.0444

Standard Deviation	0.4278

2.4. Mapping Quality

Mean Mapping Quality	44.87

2.5. Mismatches and indels

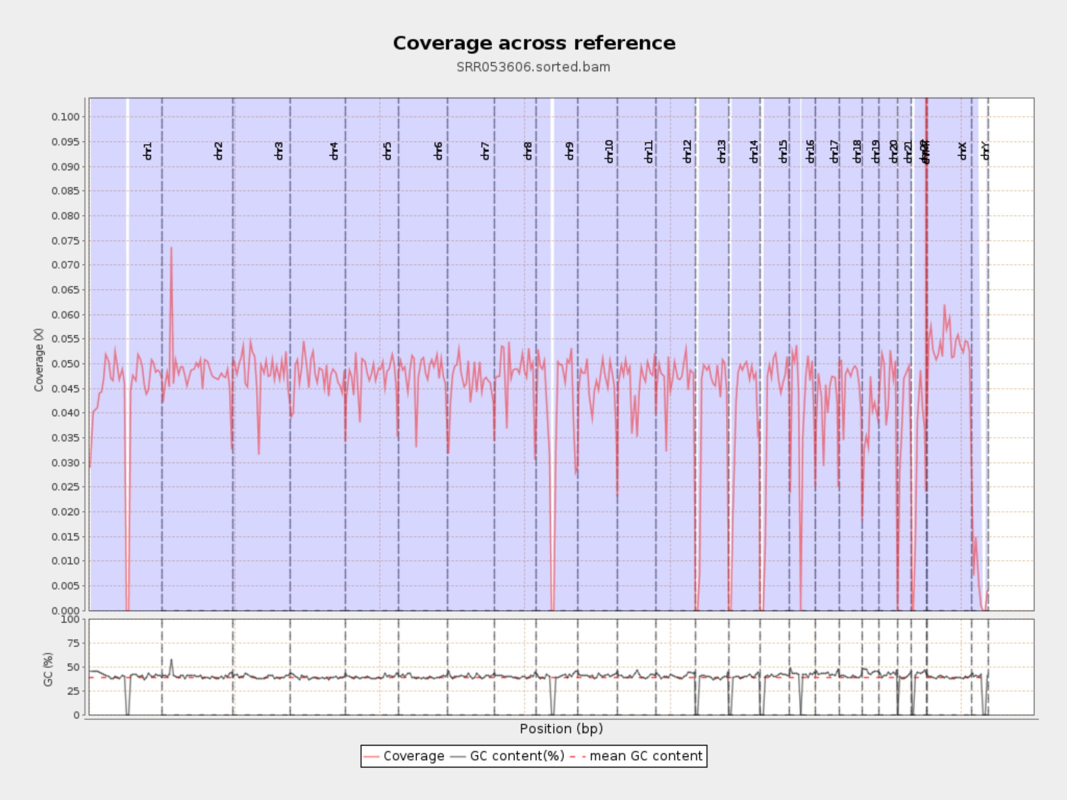
General error rate	1.04%
Mismatches	1,425,990
Insertions	6,635
Mapped reads with at least one insertion	0.23%
Deletions	18,138
Mapped reads with at least one deletion	0.62%
Homopolymer indels	45.44%

2.6. Chromosome stats

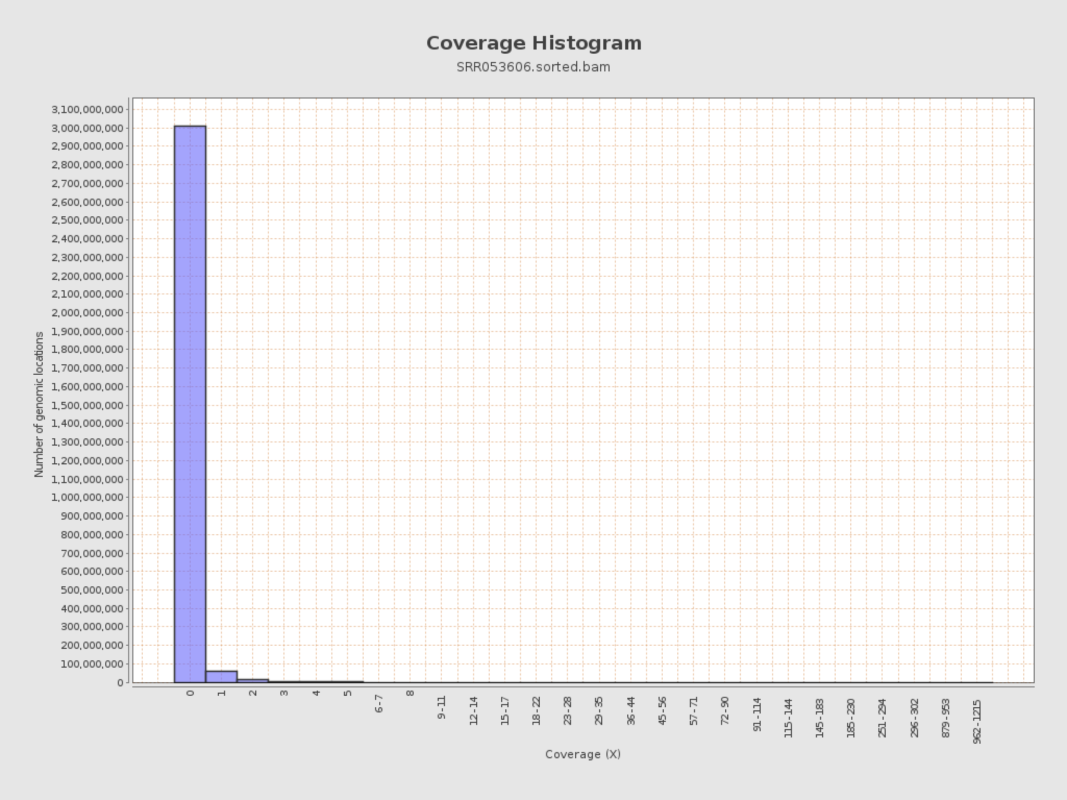
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10896397	0.0437	0.3763
chr2	243199373	11759622	0.0484	0.9035
chr3	198022430	9601219	0.0485	0.3613
chr4	191154276	9089089	0.0475	0.3713
chr5	180915260	8589588	0.0475	0.3543
chr6	171115067	8232812	0.0481	0.3846
chr7	159138663	7408041	0.0466	0.3956

chr8	146364022	7046868	0.0481	0.3684
chr9	141213431	5679700	0.0402	0.3375
chr10	135534747	6289615	0.0464	0.3666
chr11	135006516	6224375	0.0461	0.3704
chr12	133851895	6268062	0.0468	0.3512
chr13	115169878	4534596	0.0394	0.3229
chr14	107349540	4186311	0.039	0.3426
chr15	102531392	3972405	0.0387	0.3176
chr16	90354753	3757878	0.0416	0.3445
chr17	81195210	3393634	0.0418	0.3246
chr18	78077248	3648532	0.0467	0.3826
chr19	59128983	2235143	0.0378	0.3476
chr20	63025520	2892384	0.0459	0.3557
chr21	48129895	1768203	0.0367	0.3377
chr22	51304566	1433126	0.0279	0.2659
chrMT	16571	26761	1.6149	2.7819
chrX	155270560	8316198	0.0536	0.4182
chrY	59373566	343675	0.0058	0.1268

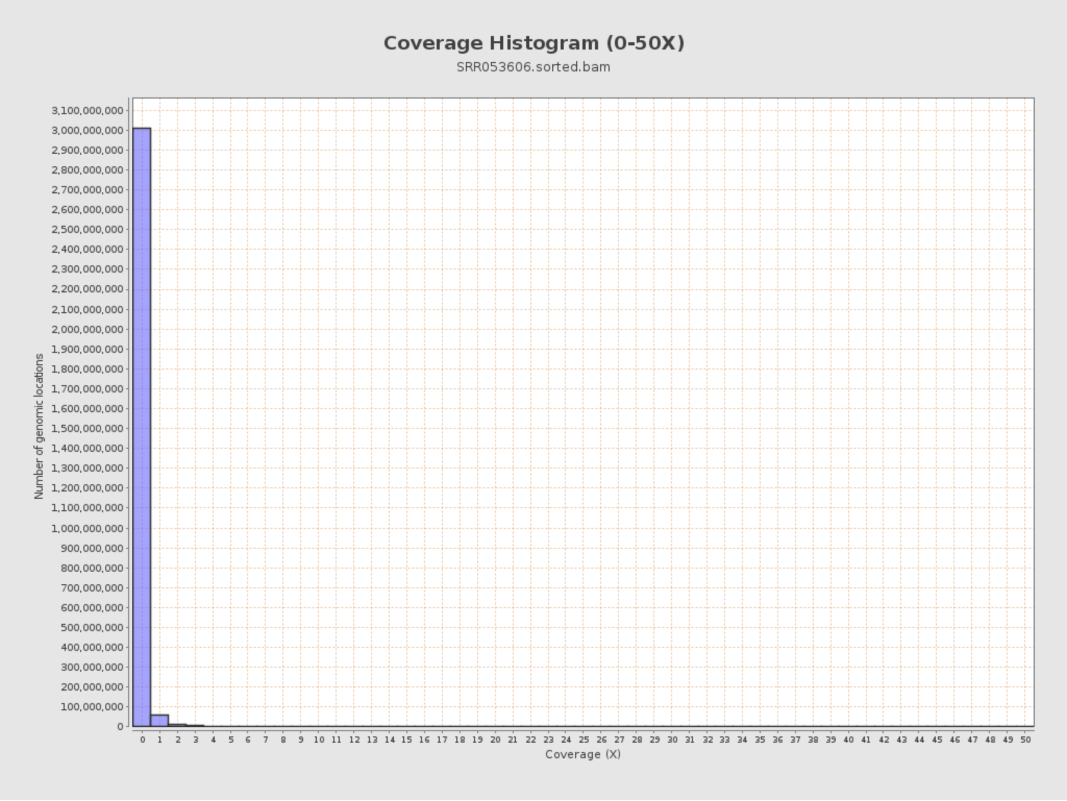
3. Results : Coverage across reference



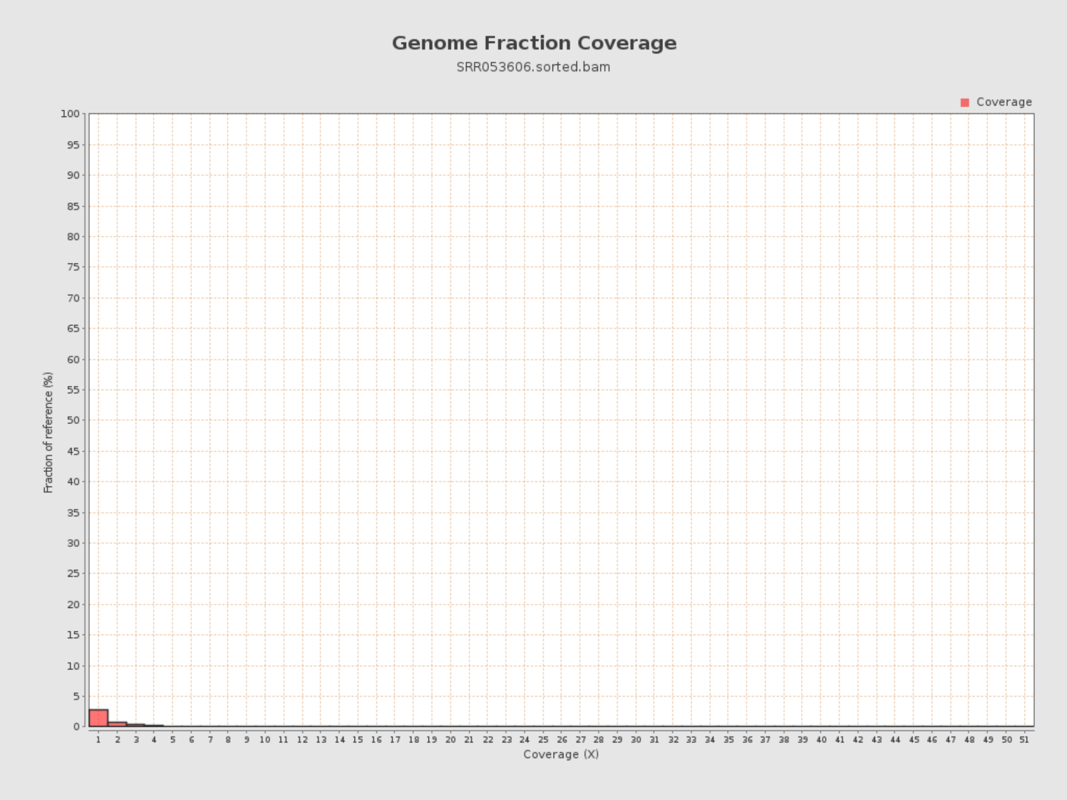
4. Results : Coverage Histogram



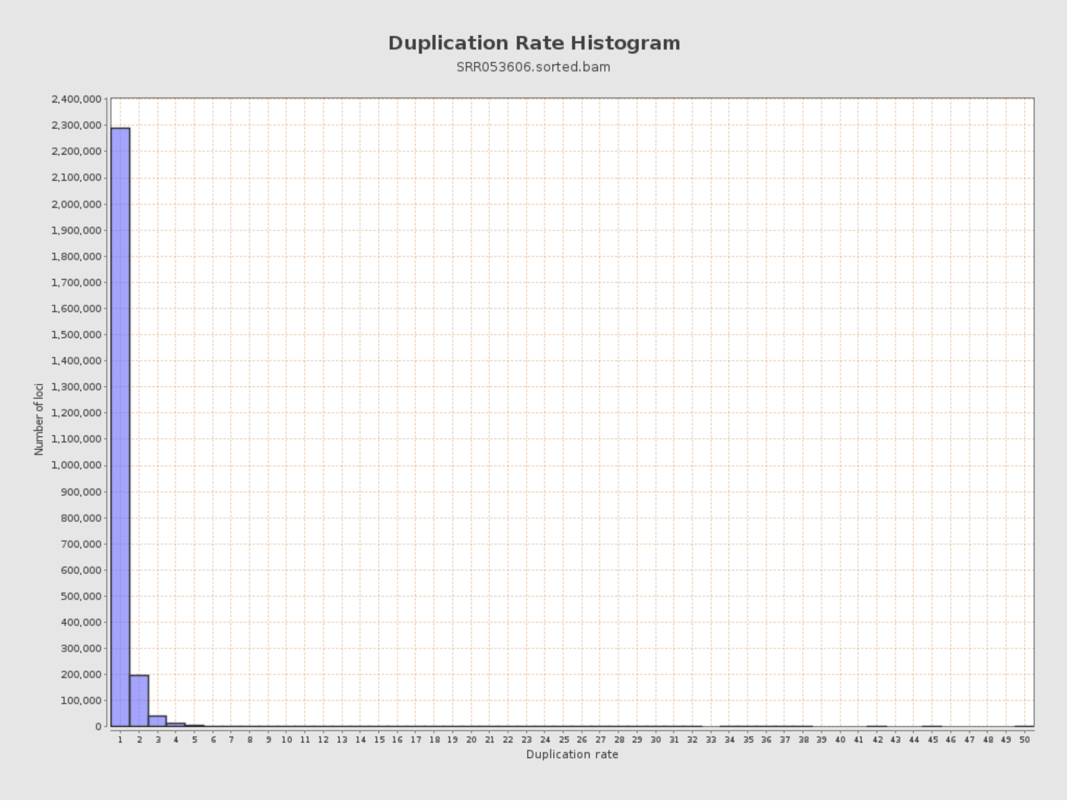
5. Results : Coverage Histogram (0-50X)



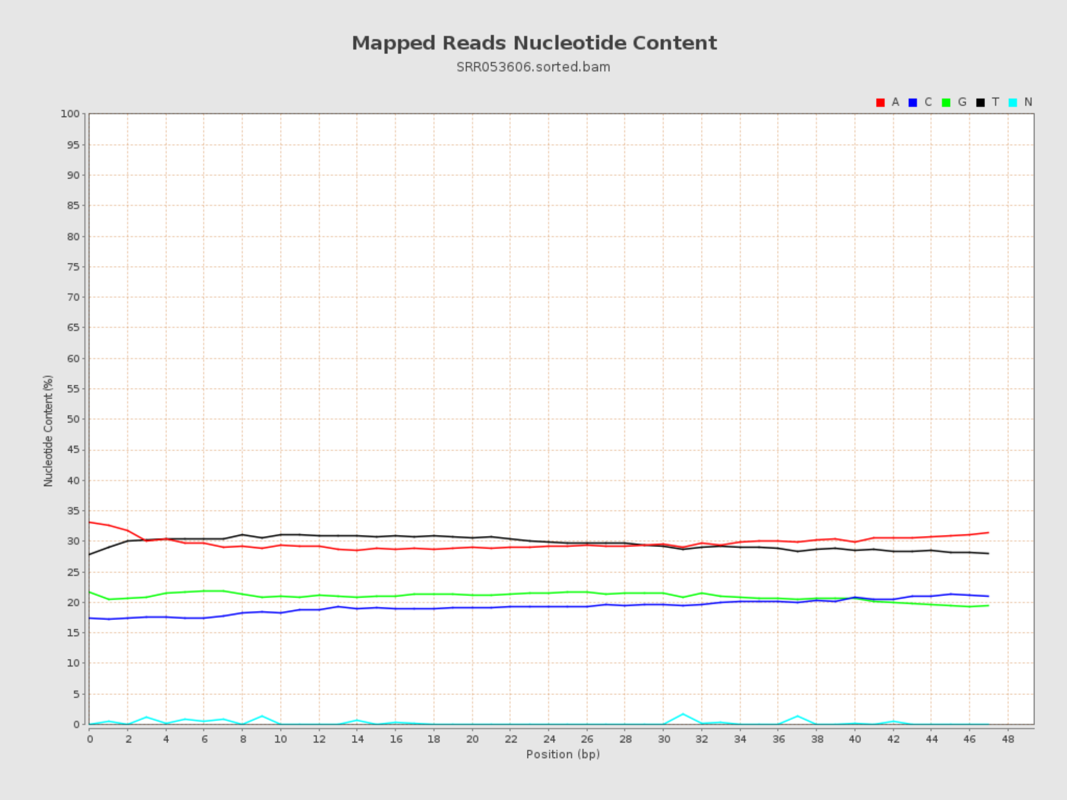
6. Results : Genome Fraction Coverage



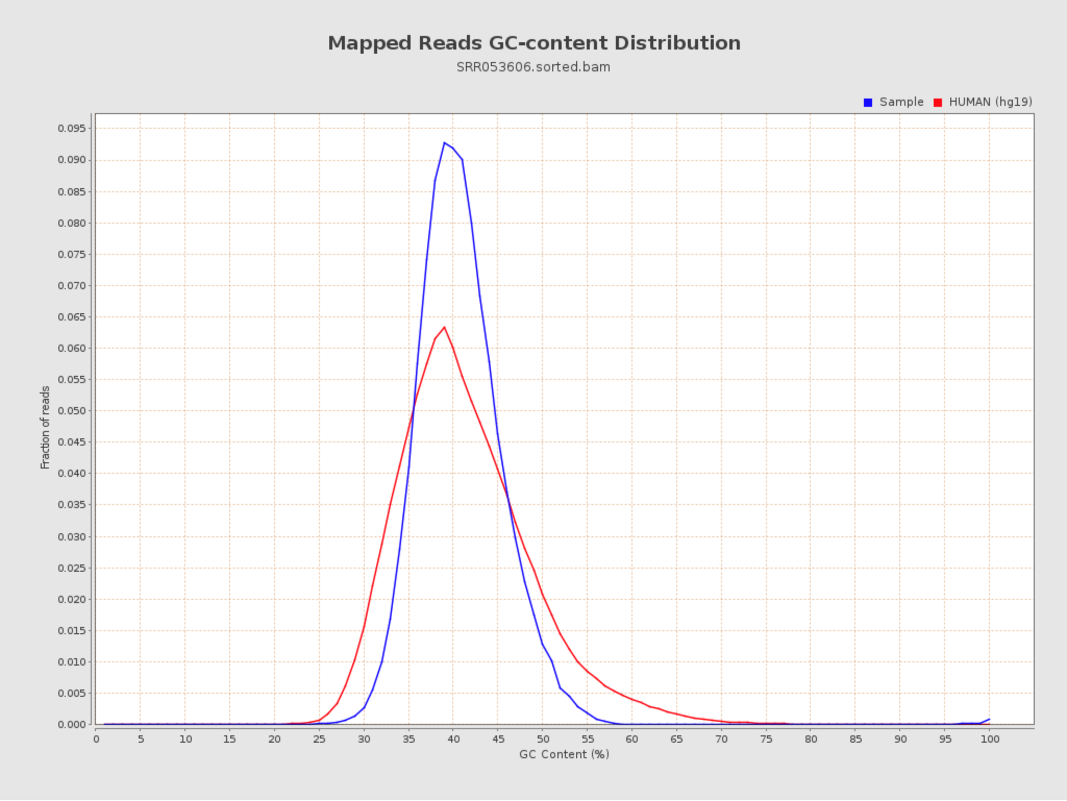
7. Results : Duplication Rate Histogram



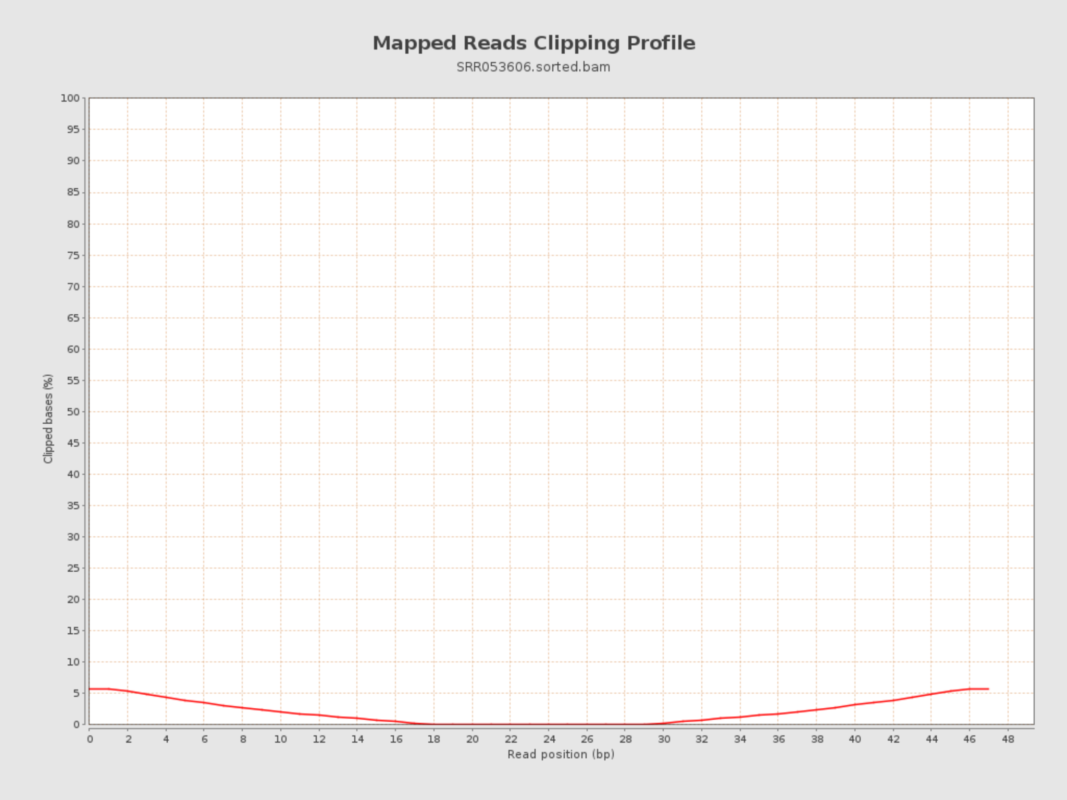
8. Results : Mapped Reads Nucleotide Content



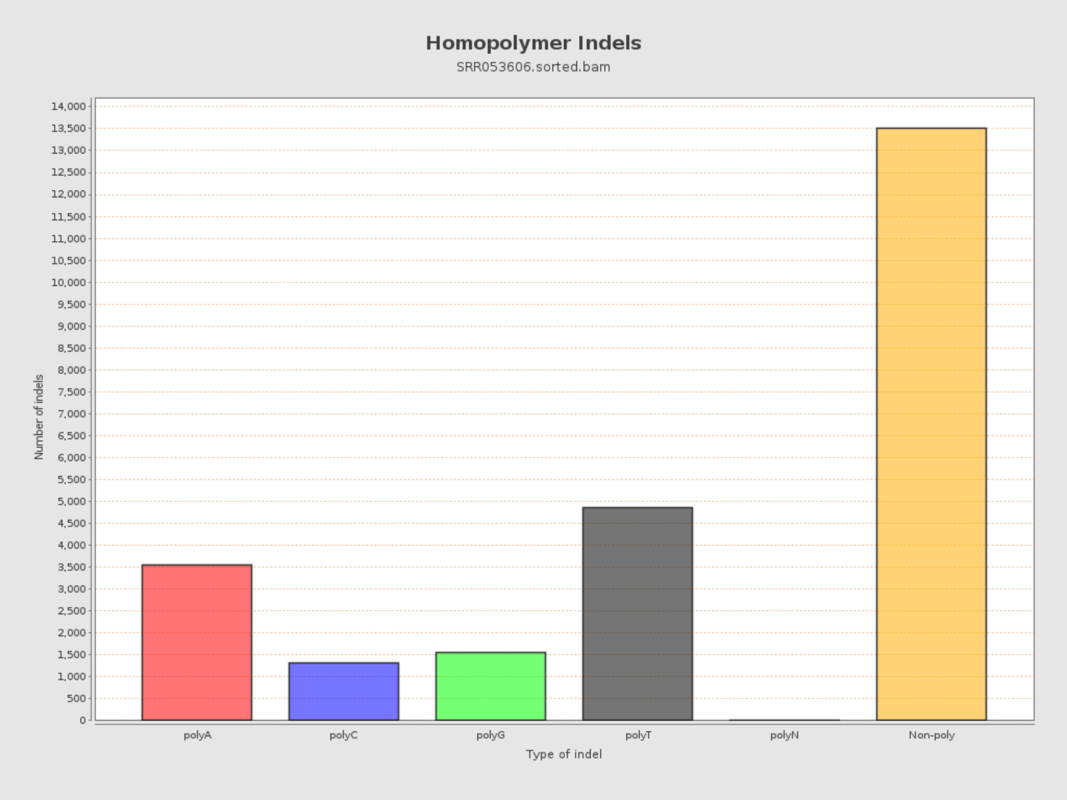
9. Results : Mapped Reads GC-content Distribution



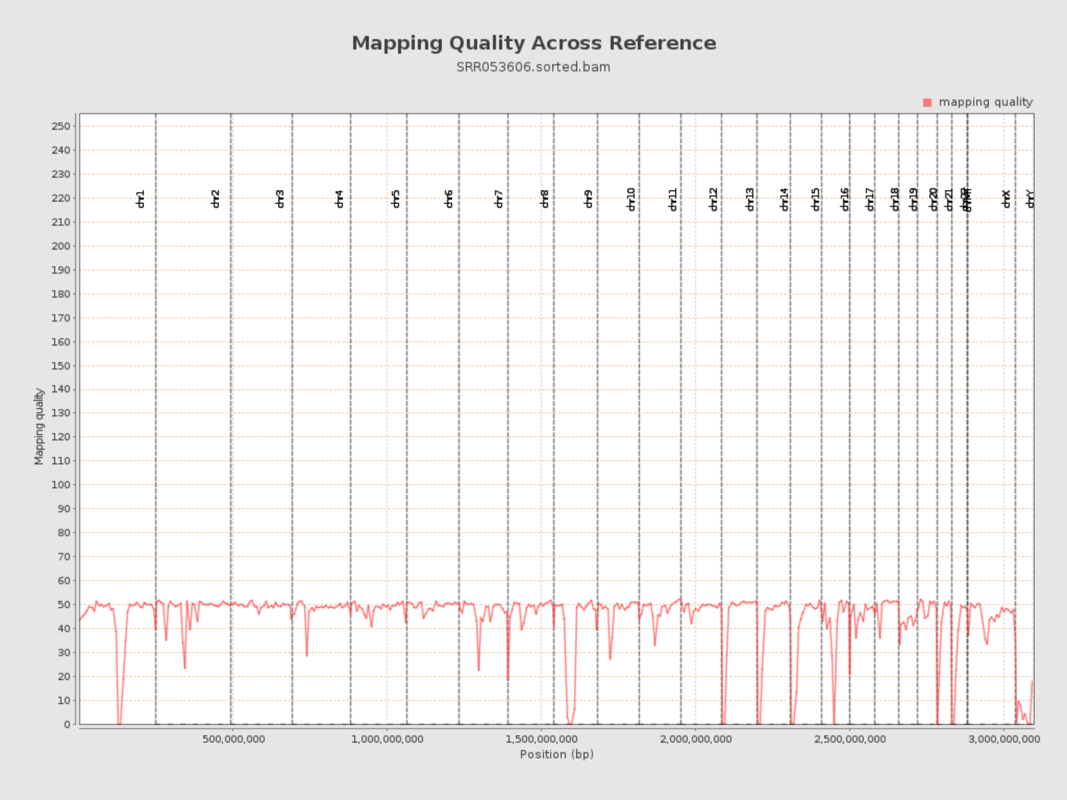
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram