

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/18 19:43:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR536749.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_SRR536749 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR536749.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Mar 18 19:43:45 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR536749.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	24,042,579
Mapped reads	23,167,722 / 96.36%
Unmapped reads	874,857 / 3.64%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	473 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	232,694 / 0.97%
Duplication rate	0.99%
Clipped reads	381,105 / 1.59%

2.2. ACGT Content

Number/percentage of A's	361,186,989 / 31.27%
Number/percentage of C's	215,041,733 / 18.62%
Number/percentage of T's	359,591,669 / 31.13%
Number/percentage of G's	218,823,253 / 18.94%
Number/percentage of N's	482,976 / 0.04%
GC Percentage	37.56%

2.3. Coverage

Mean	0.3732

Standard Deviation	0.7073
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2.4. Mapping Quality

Mean Mapping Quality	47.45
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2.5. Mismatches and indels

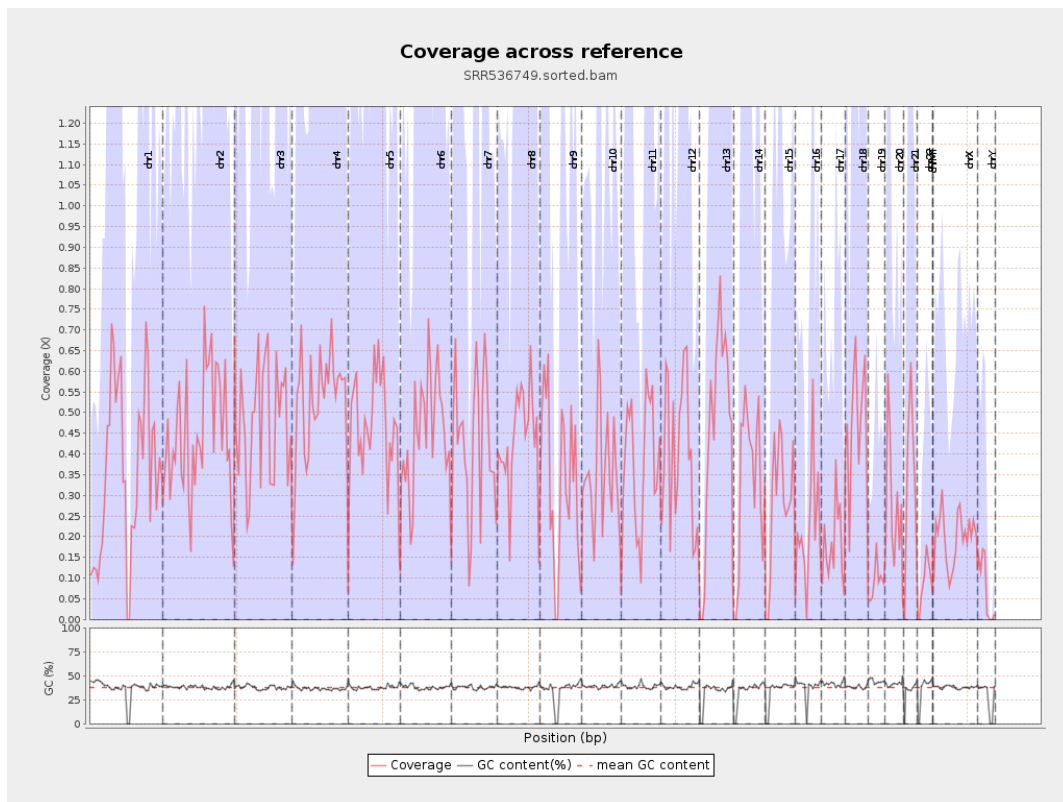
General error rate	0.36%
Mismatches	4,014,460
Insertions	78,156
Mapped reads with at least one insertion	0.34%
Deletions	59,308
Mapped reads with at least one deletion	0.26%
Homopolymer indels	49.07%

2.6. Chromosome stats

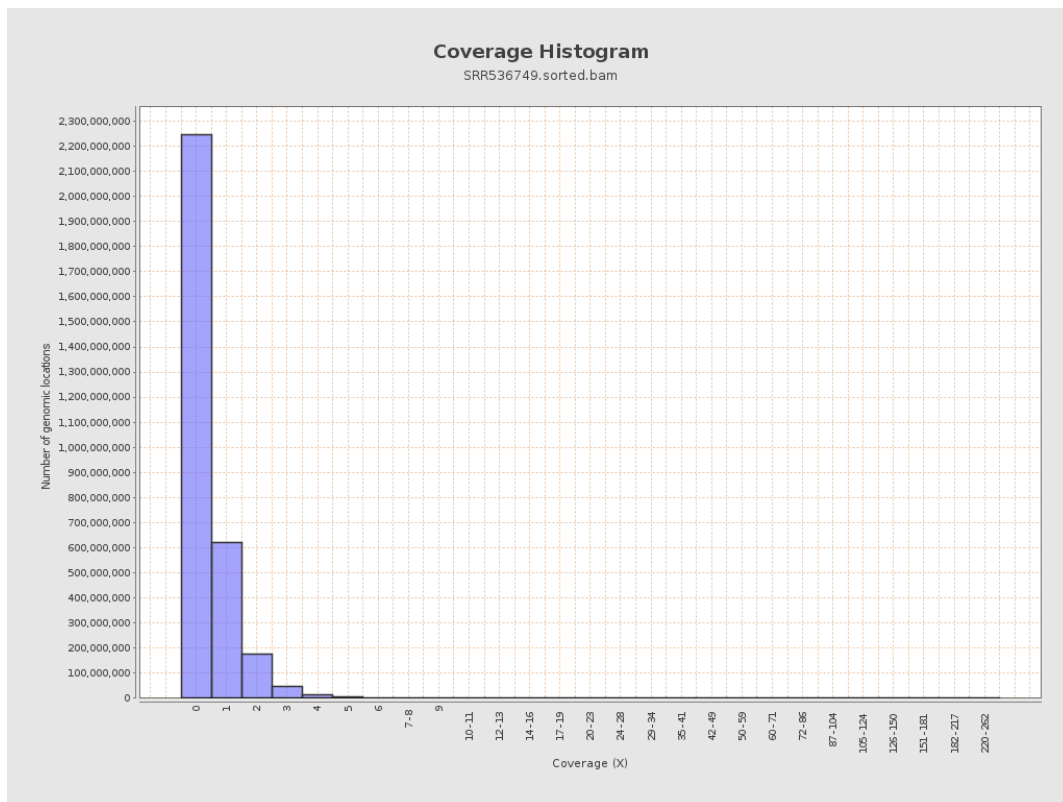
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	88714172	0.3559	0.7017
chr2	243199373	108662408	0.4468	0.7596
chr3	198022430	95388908	0.4817	0.7834
chr4	191154276	100623973	0.5264	0.82
chr5	180915260	83584711	0.462	0.7636
chr6	171115067	78160041	0.4568	0.7695
chr7	159138663	66744212	0.4194	0.7458

chr8	146364022	64029458	0.4375	0.759
chr9	141213431	47776927	0.3383	0.6791
chr10	135534747	48257355	0.3561	0.6683
chr11	135006516	51587098	0.3821	0.7108
chr12	133851895	52451275	0.3919	0.719
chr13	115169878	53529469	0.4648	0.7929
chr14	107349540	35953578	0.3349	0.673
chr15	102531392	28955790	0.2824	0.6147
chr16	90354753	19699127	0.218	0.5361
chr17	81195210	14973417	0.1844	0.4985
chr18	78077248	37297799	0.4777	0.7805
chr19	59128983	5570179	0.0942	0.3383
chr20	63025520	17773869	0.282	0.6174
chr21	48129895	15661609	0.3254	0.6921
chr22	51304566	4674953	0.0911	0.3364
chrMT	16571	3381	0.204	0.445
chrX	155270560	30673096	0.1975	0.4728
chrY	59373566	4477486	0.0754	0.3101

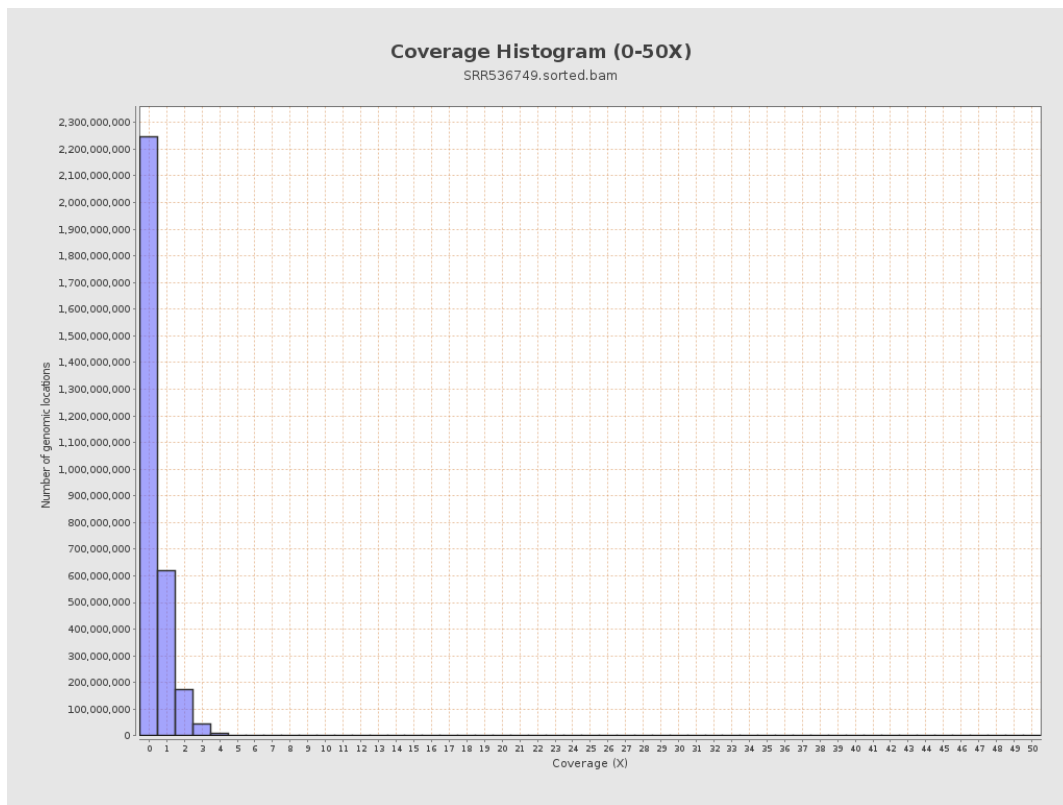
3. Results : Coverage across reference



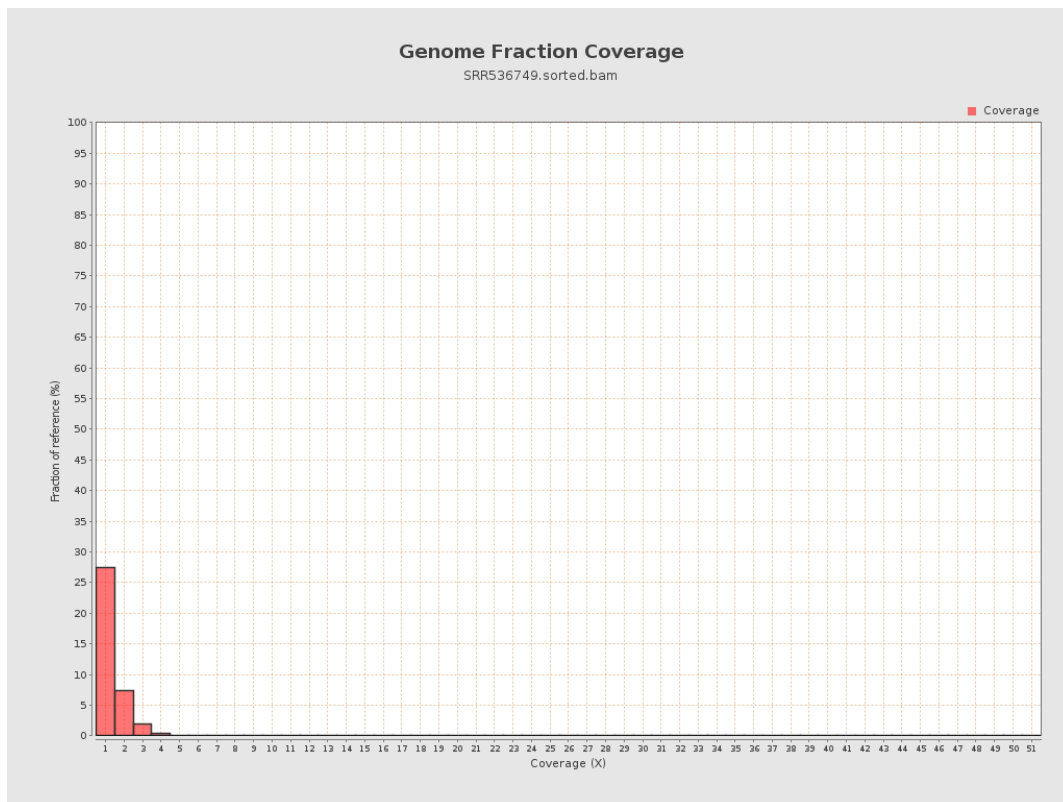
4. Results : Coverage Histogram



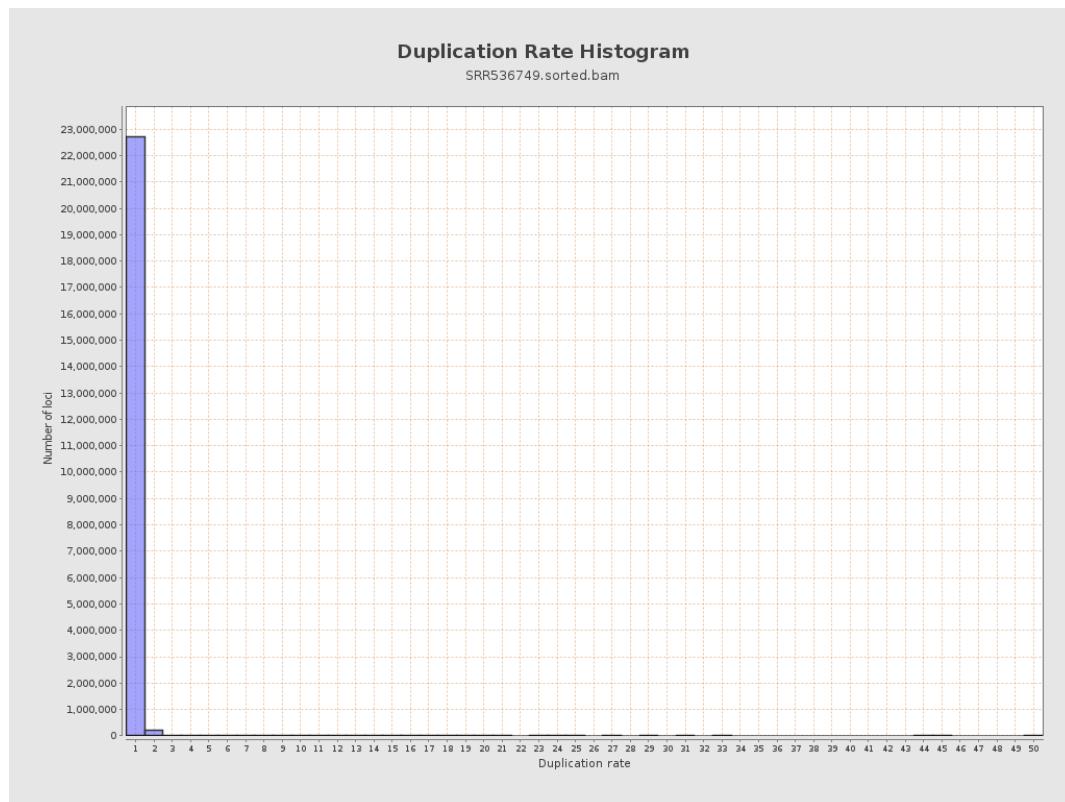
5. Results : Coverage Histogram (0-50X)



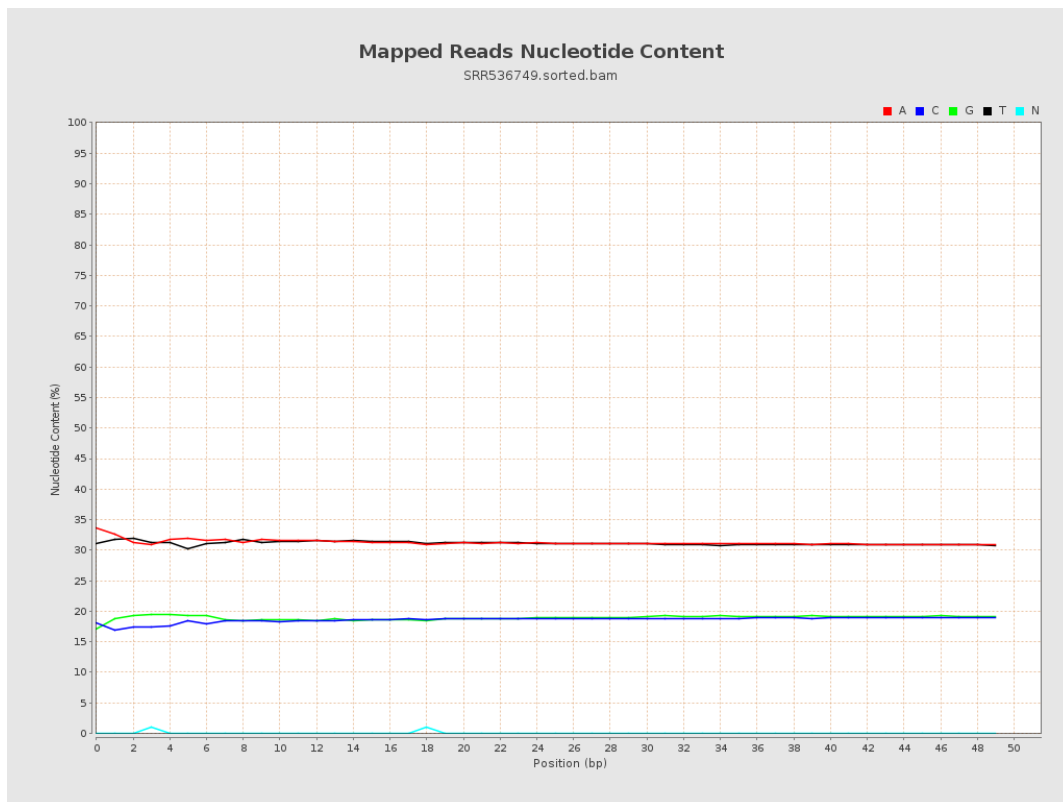
6. Results : Genome Fraction Coverage



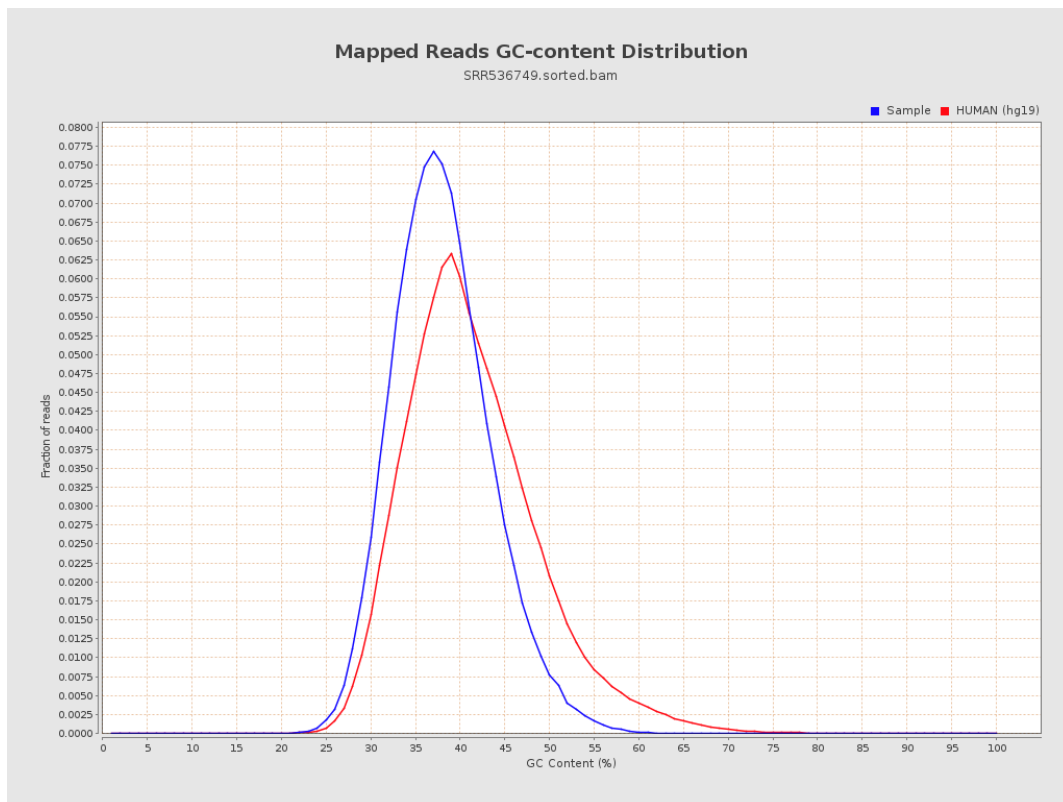
7. Results : Duplication Rate Histogram



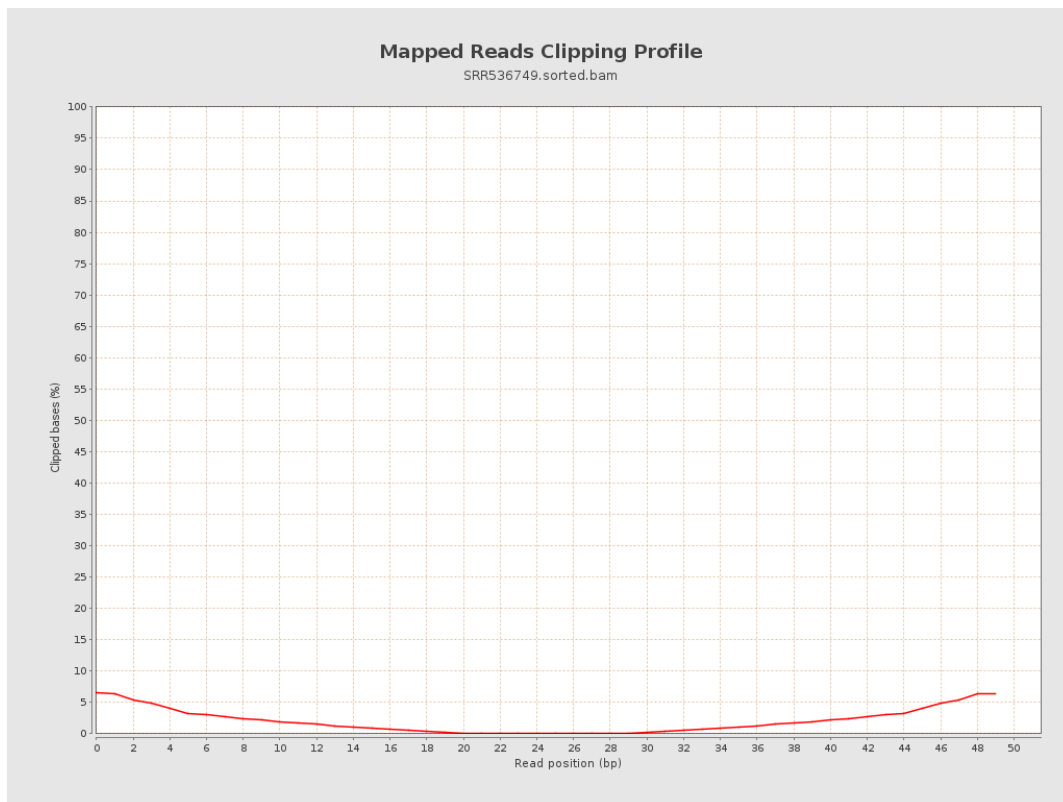
8. Results : Mapped Reads Nucleotide Content



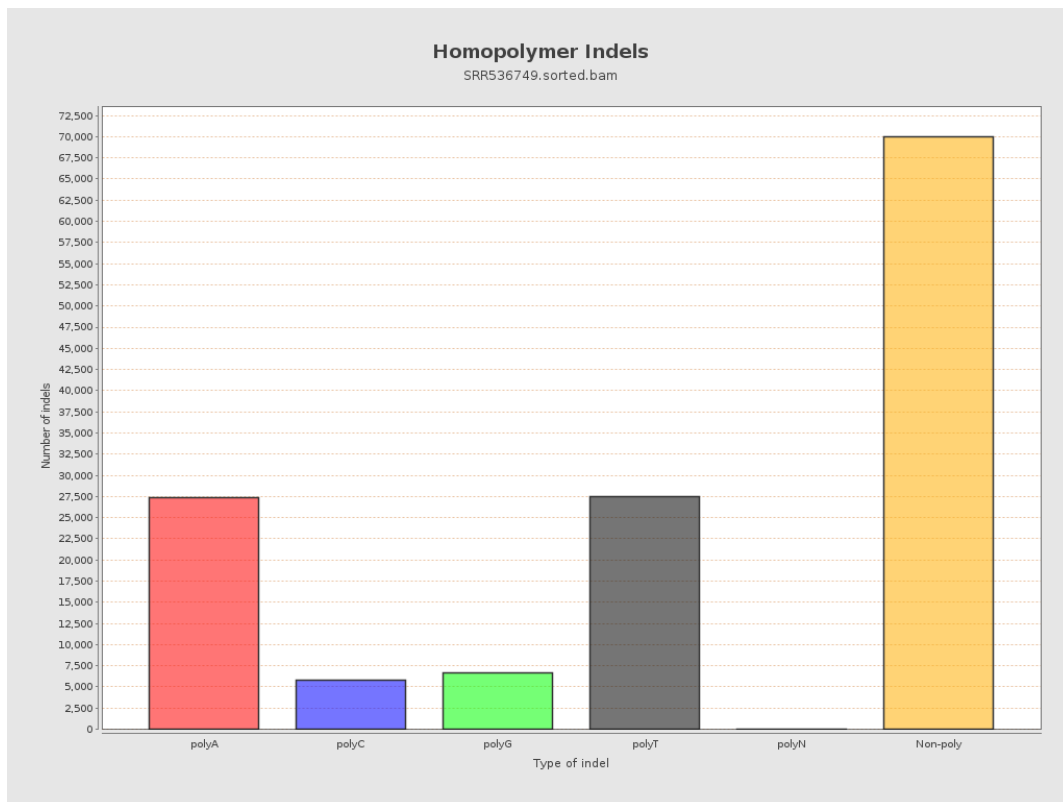
9. Results : Mapped Reads GC-content Distribution



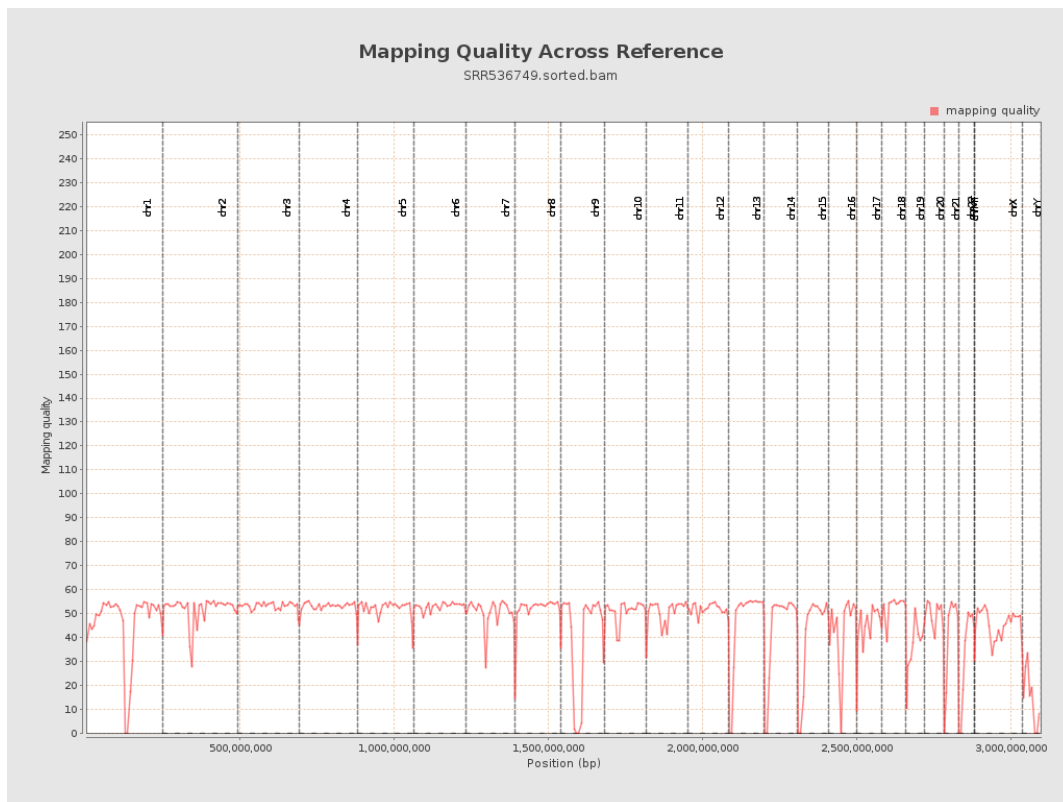
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

