VIB Nucleomics Core*- SEQUEL CCS report

8plex_CCS_1_0.8

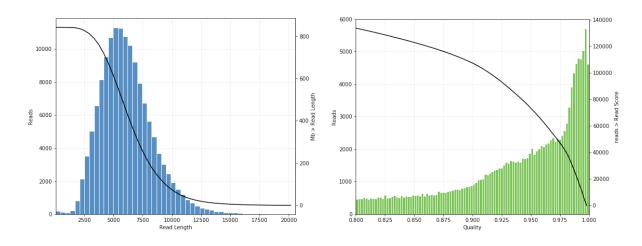
 $sample: Ecoli_8plex_demo$

 $dataset: /data/NC_projects/PB_Coli_8-plex/Ecoli_8plex_demo.barcoded.subreads.bam$

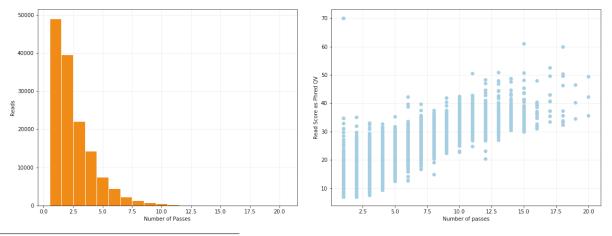
min_passes: 1; min_predicted_accuracy: 0.8

	value
CCS reads	142'740.00
Number of CCS bases	872'194'516.00
CCS Read Length (mean)	6'110.00
CCS Read Score (mean)	0.94
Number of Passes (mean)	3.00

CCS Read Length - CCS Read Score



Number of Passes - Number of Passes vs. Read Score



 $^{^*\}mathrm{VIB}$ - Nucleomics Core, nucleomics@vib.be



Run Options

pbccs.task_options.min_passes 1 pbccs.task_options.min_predicted_accuracy 0.8 pbccs.task_options.by_strand FALSE pbccs.task_options.max_drop_fraction 0.34 pbccs.task_options.max_length 21000 pbccs.task_options.min_length 10 pbccs.task_options.min_read_score 0.65 pbccs.task_options.min_snr 3.75 pbccs.task_options.min_zscore -3.4 pbccs.task_options.polish TRUE pbccs.task_options.report file ccs report.txt		
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pbccs.task options.report file ccs report.txt	TRU	pbccs.task_options.polish
r	ccs_report.t	pbccs.task_options.report_file
pbccs.task_options.rich_qvs FALSE	FALS	pbccs.task_options.rich_qvs
$pbcoretools. task_options. other_filters$		$pbcoretools.task_options.other_filters$

ZMW filtering

	count	fraction
Success – CCS generated	142740.00	28.85%
Failed – Below SNR threshold	0.00	0.00%
Failed – No usable subreads	575.00	0.12%
Failed – Insert size too long	8.00	0.00%
Failed – Insert size too small	0.00	0.00%
Failed – Not enough full passes	343318.00	69.38%
Failed – Too many unusable subreads	254.00	0.05%
Failed – CCS did not converge	1518.00	0.31%
Failed – CCS below minimum predicted accuracy	6394.00	1.29%
Failed – Unknown error during processing	0.00	0.00%

Subread filtering

count	fraction
623048.00	52.23%
0.00	0.00%
8164.00	0.68%
0.00	0.00%
4821.00	0.40%
60253.00	5.05%
0.00	0.00%
473845.00	39.72%
22824.00	1.91%
	623048.00 0.00 8164.00 0.00 4821.00 60253.00 0.00 473845.00

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