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— GCB Sequencing and Genomic Technology Shared Resource

Order: 4956

Data distributed: 2018-08-27

Data availability expires on: 2018-09-24

Run Type: 51SR

Application Name: HiSeq Control Software

Application Version: HD 3.4.0.38

RTA Version: 2.7.7

Flow Cell: HiSeq 3000/4000 SR

Run Summary

Lane	PF* Yield (bp)	Number of PF* Clusters**	Q30%	Average Quality Score	Undetermined Reads(%)***
5	17,089,143,903	335,081,253	95.98	39.06	4.26

* PF: Passed Filter

** For single read sequencing (SR), number of reads = number of clusters; For paired end sequencing (PE), number of reads = 2x number of clusters

*** Percentage of reads with undetermined/unidentifiable barcodes

Plots

Barcode Results

Lane	Sample Name	PF* Yield (bp)	Number of PF* Clusters**	Q30%	Average Quality Score	Barcode
5	4956_S5	1,566,058,479	30,707,029	96.32	39.15	TTGTATCAGG+TTCTACATAC

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Lane	Sample Name	PF* Yield (bp)	Number of PF* Clusters**	Q30%	Average Quality Score	Barcode
5	4956_S4	2,368,839,330	46,447,830	96.24	39.12	AATTCTTGGA+GCCATATAAC
5	4956_S7	3,579,683,778	70,189,878	96.34	39.16	GATTCTGAAT+TTACCTGGAA
5	4956_S6	2,498,469,447	48,989,597	96.23	39.12	GAGAGGTTCG+TCTATCCTAA
5	4956_S1	1,769,186,073	34,689,923	96.32	39.15	GTAAC TTGGT+AGACTGCGAA
5	4956_S3	2,423,948,145	47,528,395	96.20	39.11	CATATGCGAT+CGGTTACGGC
5	4956_S2	2,154,857,508	42,252,108	96.28	39.13	TGTCTGGCCT+GGCGATCAGA

Please contact us at sequencing@duke.edu if you have any questions.