

a

Sample	Run Time (hr)	Sequence Yield (GB)	Total Reads	Cluster Density (K/mm ²)	Nucleotides with Q score >30 (%)	Reads Passing Filter (%)	Raw Error rate (%)	Aligned Reads (%)	Aligned Reads with mapQ >20 (%)
CMH_184	26	137	1,539,534,606	1044	90	89	0.65	95.0	91.0
CMH_185	26	117	1,252,265,788	849	93	93	0.50	97.1	93.3
CMH_531	26	103	1,015,355,810	746	90.2	92.4	n.d.	97.8	94.1
CMH_569	26	101	995,793,286	1120	80.2	60.3	1.61	84.1	79.9
UDT_173	26	139	1,600,532,150	1085	89	87	0.55	94.7	90.6
	18	106	966,794,602	760	92.4	94	0.50	99.3	96.9
NA12878	18	143	1,330,334,428	1137	85	85	0.77	98.5	96.4
UDT_103	18	130	1,215,158,762	970	90	90.7	0.56	99.2	97.0

b

Metric	Sequence Yield (GB)	Cluster Density (K/mm ²)	% > Q30	Passing Filter (%)	Error rate (%)
Correlation with cluster density	0.64		-0.72	-0.59	0.69
Mean of 18 Runs (n=3)	126.7	976.7	89.1	89.9	0.8
Mean of 26 Runs (n=5)	119.4	968.8	88.5	84.3	0.8