Before additio			Dycle 1	Cycle 2	Cycle 3	7																															
Sar		Assigned (Lane1)	NumPolonies Assigned (Lane2)			NumPolonis Assigned (Merge)	Number of Reads	Valid Barcodes Valid	UMis Setur	ncing Q30 Base stion Barcode	os in Q30 Base Probe Ra	es in Q30 Bases ad in UMI	Reads Mapped to Probe Set	Reads Mapped Confidently to Probe Set	Fraction Reads in Squares Under Tissue	Reads Mappi enes Detected Confidently I Filtered Prob	Mumber of othe Genes	Reads Half- Mapped to Pro Set	Reads Split- be Mapped to Prob Set	Estimated UMIs to from Genomic DNA	Estimated UMIs from Genomic DNA per Unspliced Probe	Number of Me Squares Under Th Tissue 2 µm µm	ean Reads Under saue per Square 2 1	Fraction of Squares Under U Squares Under U	Mean Genes Under Tissue per Square 2 µm	Mean UMIs Under Total Tissue per Square Detec 2 µm Tissu	enes Num ed Under Unde 2 µm µm	ber of Bins Mean R or Tissue & Under I per Bin	leads Fract Tissue Bins 5 pm Tissu	ion of Mean Under Under Under se 5 µm per Bi	Genes Mean UMIs Tissue Under Tissue ; n 5 µm Sin 5 µm	Total Genes or Detected Under Tissue 8 µm	Number of Bins Under Tissue 16 µm	Mean Reads Fractio Under Tissue Sins Us per Sin 16 pm Tissue		Mean UMIs per Under Tissue per Bin 16 µm	Total Genes Detected Under Tissue 16 µm
544	_4M_HCC	427,894,5	25 438,807,589			866,702,3		90.90%	93.98%	65.95%	97.67% 98.	18% 98.54	99.661	99.37%	97.41%	16,033	99.02% 15	,059 0.2	7% 0.02	% 0.01	1	8,029,804	108.21	71.37%	27.4	32.15	16,033	504,773	1717.01	71.88%	326.38 512	15 16,0	35 127,35	6805.51	2.54% 99	1.27 2037.0	J1 16,039
575	_control	473,455,0	005 485,993,598			959,448,6	603 959,448,603	89.52%	93.99%	70.26%	98.17% 98.	56% 98.75	99.661	99.29%	99.03%	15,797	98.95% 15	,059 0.5	5% 0.03	% 0.01	1	8,767,098	109.44	78.12%	23.9	28.44	15,797	552,945	1735.16	78.74%	279.83 451	13 15,7	139,72	6866.50	9.59% 84	6.10 1788.3	J4 15,800

After additional sequence	ng	Cycle	1	1	Cycle 2		-	Cycle 3	\neg																																				
Sample ID	Numi	nPolonies 1 ssigned	NumPolonies Assigned	NumPole Assign	onies Nu	imPolonies Assigned	NumPolonie Assigned	NumPolor Assigne	nies Nur d A	mPolonies assigned	lumber of	Valid Barcodes Valid	UMis So	quencing C	330 Bases in larcode	Q30 Bases Probe Reso	in Q30 Bases in UMI	Reads Mapp to Probe Set	Reads Mapped Confidently to	Fraction Reads in Squares Under Tissue	Rea nes Detected Con	ds Mapped fidently to the Gen	ber of	leads Half- dapped to Probe	Reads Split- Mapped to Probe	Estimated UMIs from Genomic	Estimated UMIs for Genomic DNA per	Number of Squares Under	Mean Reads Unde Tissue per Square	fraction of 2 Squares Und	Mean Genes or Under Tissue per	Mean UMIs Under Tissue per Squan	Total Genes Detected Under	Number of I Under Tissu	Sins Mean Reads to 5 Under Tissu	Fraction o so Sins Und	f Mean Gen r Under Tiss	Mean UMIs ue Under Tisso	Total Genes ue per Detected Under	Number of Under Tiss	Bins Mean Reads ue 16 Under Tissu	Fraction of 6 Sins Under	Mean Genes Under Tissue p	Mean UMIs r Under Tissue	Total Genes Detected Under
544_4M_HCC	(1)	427894525	(Lane2) 43880758	(Lane 9 358,5	585,640	(Lane2) 373,230,052	(Lane1) 386,093,0	(Lane2 104 383,47	1,636 2	Merge) ,378,082,446	2,378,082,446	90.57%	99.96%	85.82%	96.75	% 97.62	97.719	99.30	Probe Set 99.01	97.41%	16,115	red Probe Set 98.66%	19,059	0.27%	0.029	0.00	Unapliced Probe	1 8,000,80	pm 2963	71.	37% 30.7	2 µm 6 36.3	71ssue 2 µm 34 16;	115 504	773 471	11.19 7	m per Bin 8 y	2.44 S	78.95 16	,117 1	27,353 18673	n Tissue 16 µm .16 72.54	Bin 16 µm 1079.	per Bin 16 µm i4 2302.7	16,121
\$75_control		473455005	48599359	8 372,5	990,535	384,362,801	376,699,1	367,56	0,741 2	,461,061,815	2,461,061,815	89.32%	92.97%	87.30%	97.85	% 98.42	58,475	22.43	99.10	99.03%	15,852	98.76%	19,059	0.35%	0.039	0.01		1 8,767,05	8 280.	72 78.	12% 25.8	30.5	94 15,1	852 552	,945 445	0.83 7	1.74% 25	8.50 4	191.14 15	,854 1	39,729 17613	.11 79.59	897.	1945.6	15,855