

**Table S1: Summary of sequence analysis of adenoid cystic carcinoma**

Sample ID	HN 308 PT2		HN 312 PT		HN 313 PT		HN 317 PT		HN 318 PT	
	Tumor	Normal	Tumor	Normal	Tumor	Normal	Tumor	Normal	Tumor	Normal
Bases in Target Region	50,195,330	50,195,330	50,353,573	50,353,573	50,353,573	50,353,573	50,195,330	50,195,330	50,195,330	50,195,330
Bases Sequenced (after quality filtering)	255,207,459,600	147,979,118,200	299,619,544,200	137,377,597,000	297,862,710,600	142,078,116,600	260,531,900,400	139,486,322,000	307,484,478,600	131,654,942,200
Bases Mapped to Genome (filtered)	224,133,316,300	129,361,281,500	262,766,299,200	121,316,184,400	260,287,573,700	123,880,097,500	228,580,990,800	123,070,351,400	262,515,038,400	115,366,772,500
Percent Bases Mapped to Genome	88%	87%	88%	88%	87%	87%	88%	88%	85%	88%
Bases Mapped to ROI	3,183,412,045	2,140,281,005	4,166,259,723	2,046,259,144	4,125,897,974	2,085,503,384	3,612,979,990	2,023,441,301	4,235,619,077	1,954,022,886
Percent Bases Mapped to ROI	1%	2%	2%	2%	2%	2%	2%	2%	2%	2%
Targeted bases with at least 10 reads (%)	98%	98%	98%	98%	98%	98%	98%	98%	98%	98%
Average Raw Coverage	63.42	42.64	82.74	40.64	81.94	41.42	71.98	40.31	84.38	38.93
Average High Quality Coverage	54.06	39.44	72.69	38.42	68.92	38.84	62.40	37.39	72.59	36.35

Sample ID	HN 320 PT		HN 323 PT		HN 324 PT		HN 325 PT		HN 332 PT	
	Tumor	Normal	Tumor	Normal	Tumor	Normal	Tumor	Normal	Tumor	Normal
Bases in Target Region	50,195,330	50,195,330	50,405,174	50,405,174	50,353,573	50,353,573	50,195,330	50,195,330	50,195,330	50,195,330
Bases Sequenced (after quality filtering)	268,588,041,000	133,045,592,400	294,100,000,000	128,483,000,000	286,531,794,800	121,924,771,200	261,424,817,800	131,149,585,800	229,142,382,200	126,778,866,800
Bases Mapped to Genome (filtered)	236,860,129,700	116,481,835,200	256,958,000,000	112,668,000,000	251,113,623,800	107,373,056,700	230,912,740,000	115,452,395,800	198,612,201,200	110,123,256,200
Percent Bases Mapped to Genome	88%	88%	87%	88%	88%	88%	88%	88%	87%	87%
Bases Mapped to ROI	3,869,161,305	1,927,161,203	4,041,676,926	1,855,359,506	4,143,282,002	1,757,048,303	3,720,190,338	1,913,469,258	3,204,123,737	1,864,106,672
Percent Bases Mapped to ROI	2%	2%	2%	2%	2%	2%	2%	2%	2%	2%
Targeted bases with at least 10 reads (%)	98%	98%	98%	98%	98%	98%	98%	98%	98%	98%
Average Raw Coverage	77.08	38.39	80.27	36.85	82.28	34.89	74.11	38.12	63.83	37.14
Average High Quality Coverage	65.83	35.95	70.65	35.02	69.77	33.33	64.50	36.06	58.16	35.16

Sample ID	HN 333 PT		HN 334 PT		HN 335 PT		HN 336 PT		HN 337	
	Tumor	Normal	Tumor	Normal	Tumor	Normal	Tumor	Normal	Tumor	Normal
Bases in Target Region	50,195,330	50,195,330	50,195,330	50,195,330	50,195,330	50,195,330	50,353,573	50,353,573	50,353,573	50,353,573
Bases Sequenced (after quality filtering)	208,561,221,400	111,030,223,000	218,054,165,000	108,146,443,800	261,144,154,800	138,234,132,400	138,000,000,000	121,000,000,000	136,531,000,000	130,121,000,000
Bases Mapped to Genome (filtered)	180,062,028,300	97,254,078,700	190,291,926,000	94,967,253,500	227,927,398,400	120,552,077,900	128,000,000,000	111,000,000,000	125,870,000,000	119,978,000,000
Percent Bases Mapped to Genome	86%	88%	87%	88%	87%	87%	92%	92%	92%	92%
Bases Mapped to ROI	2,941,123,561	1,632,226,576	3,017,713,020	1,585,209,252	3,513,989,874	2,030,631,799	2,080,000,000	1,810,000,000	1,936,900,824	1,976,431,990
Percent Bases Mapped to ROI	2%	2%	2%	2%	2%	2%	2%	2%	2%	2%
Targeted bases with at least 10 reads (%)	98%	98%	98%	98%	98%	98%	99%	99%	99%	99%
Average Raw Coverage	58.59	32.52	60.12	31.58	70.01	40.45	41.30	36.01	38.47	39.25
Average High Quality Coverage	54.19	30.22	55.25	29.51	63.26	38.48	35.83	34.77	33.68	37.78

Sample ID	HN 338 PT		HN 340 PT		HN 341 PT		HN 343 PT		HN 344 PT	
	Tumor	Normal	Tumor	Normal	Tumor	Normal	Tumor	Normal	Tumor	Normal
Bases in Target Region	50,195,330	50,195,330	50,353,573	50,353,573	50,195,330	50,195,330	50,353,573	50,353,573	50,195,330	50,195,330
Bases Sequenced (after quality filtering)	251,352,688,600	103,200,384,200	130,734,115,400	181,144,265,600	228,722,862,200	111,066,821,000	130,984,465,400	152,099,689,400	248,066,220,400	141,263,655,800
Bases Mapped to Genome (filtered)	219,408,566,700	90,014,169,400	120,318,876,800	168,182,710,000	201,397,258,300	97,222,274,300	120,628,021,600	140,107,405,700	218,182,635,100	123,498,184,800
Percent Bases Mapped to Genome	87%	87%	92%	93%	88%	88%	92%	92%	88%	87%
Bases Mapped to ROI	3,521,538,624	1,527,040,088	1,936,966,126	2,724,335,135	3,216,227,443	1,642,611,093	1,897,462,973	2,294,814,943	3,519,478,290	2,055,760,913
Percent Bases Mapped to ROI	2%	2%	2%	2%	2%	2%	2%	2%	2%	2%
Targeted bases with at least 10 reads (%)	98%	98%	99%	99%	98%	98%	99%	99%	98%	98%
Average Raw Coverage	70.16	30.42	38.47	54.10	64.07	32.72	37.68	45.57	70.12	40.96
Average High Quality Coverage	63.54	28.56	33.85	51.30	58.39	30.69	33.17	43.42	64.61	38.72

Sample ID	HN 345 PT		HN 347 PT		HN 348 PT		HN 349 PT		HN 350 PT	
	Tumor	Normal	Tumor	Normal	Tumor	Normal	Tumor	Normal	Tumor	Normal
Bases in Target Region	50,195,330	50,195,330	50,353,573	50,353,573	50,195,330	50,195,330	50,195,330	50,195,330	50,195,330	50,195,330
Bases Sequenced (after quality filtering)	247,192,000,000	106,117,000,000	125,927,029,200	149,404,025,600	245,542,186,600	116,750,028,800	259,260,680,600	124,222,681,800	258,790,231,200	118,781,849,800
Bases Mapped to Genome (filtered)	216,592,000,000	92,914,950,800	116,462,448,700	137,586,363,100	214,837,685,600	101,250,554,200	226,681,194,100	107,778,592,300	227,371,680,600	103,770,090,900
Percent Bases Mapped to Genome	88%	88%	92%	92%	87%	87%	87%	87%	88%	87%
Bases Mapped to ROI	3,421,306,540	1,547,921,258	1,856,983,174	2,237,610,109	3,445,092,075	1,704,236,621	3,566,139,700	1,844,396,943	3,738,783,885	1,713,682,489
Percent Bases Mapped to ROI	2%	2%	2%	2%	2%	2%	2%	2%	2%	2%
Targeted bases with at least 10 reads (%)	98%	98%	99%	99%	98%	98%	98%	98%	98%	98%
Average Raw Coverage	68.16	30.84	36.88	44.44	68.63	33.95	71.05	36.74	74.48	34.14
Average High Quality Coverage	58.09	28.87	32.88	42.31	60.96	31.67	63.46	34.27	66.77	31.34

Abbreviation: ROI, region of interest