

Supplementary Table 3. Statistics of sequencing data

	Primary		Xenograft	Primary		Xenograft	Primary		Xenograft
	CCA-1N	CCA-1T	CCA-1T	CCA-2N	CCA-2T	CCA-2T	CCA-3N	CCA-3T	CCA-3T
No. of mapped reads	1,211,025	1,132,600	1,139,017	1,188,445	1,055,317	1,169,268	1,143,642	1,270,779	998,669
Percent reads on target	98.47	98.66	98.51	98.20	98.48	97.76	98.58	98.47	98.72
Total aligned base reads	16,713,485	16,713,485	14,847,336	15,669,639	16,210,358	14,847,336	16,713,485	16,713,485	14,847,336
Total base reads on target	16,612,548	16,612,548	14,810,437	15,611,083	16,152,353	14,810,437	16,612,548	16,612,548	14,810,437
Bases in target regions	136,918	136,918	136,918	136,918	136,918	136,918	136,918	136,918	136,918
Percent base reads on target	94.95	95.11	95.24	94.68	94.97	94.17	95.17	94.99	95.56
Average base coverage depth	1,017	953.3	945.7	995.4	884.9	967.7	960.5	1067	834.4
Uniformity of base coverage (%)	96.94	97.04	94.47	97.25	97.28	96.34	97.03	96.72	96.02
Target base coverage at $\times 1$ (%)	99.95	100.00	99.92	99.95	99.95	99.95	99.95	99.95	100.00
Target base coverage at $\times 20$ (%)	99.36	99.58	99.19	99.61	99.60	99.34	99.60	99.61	99.27
Target base coverage at $\times 100$ (%)	98.39	98.65	97.60	98.49	98.51	98.07	98.62	98.66	97.76
Target bases with no strand bias (%)	98.11	97.88	95.78	98.20	98.00	97.71	97.79	97.83	98.02

N, normal; T, tumor.