Table S4. Sequencing statistics for eight mutants for pre-multiplexed target enrichment

Line	5-24	7-3B	D14-03	D14-13	D14-15	D14-27	D14-39	D14-48
Total read bases	6,175,695,800	6,265,268,000	6,595,272,300	5,778,349,800	6,110,537,900	6,494,204,700	6,769,304,200	5,921,027,700
Fold target	181.42	184.05	193.75	169.75	179.51	190.78	198.86	173.94
Total reads aligned	61,381,532	62,315,604	65,531,678	57,459,155	60,708,668	64,602,576	67,242,840	58,925,509
% aligned	99.39	99.46	99.36	99.44	99.35	99.48	99.33	99.52
Total bases aligned	6,096,723,407	6,193,535,506	6,506,873,176	5,708,159,354	6,027,282,394	6,423,477,398	6,676,148,738	5,858,349,385
On bait bases	3,264,345,883	3,338,414,084	3,404,027,532	3,054,289,596	3,192,231,463	3,481,575,513	3,494,483,661	3,179,299,216
Near bait bases	1,654,123,768	1,626,706,071	1,767,551,356	1,506,133,829	1,656,127,727	1,667,584,908	1,838,909,132	1,452,697,759
% on/near bait	80.67	80.17	79.48	79.89	80.44	80.16	79.89	79.07
Mean target coverage	63.21	64.71	65.81	59.32	61.56	67.57	67.54	61.92
% target read > 1x	88.52	87.64	86.98	87.89	85.85	87.15	88.17	89.82
% target read > 10x	63.31	61.82	61.68	64.36	61.01	61.17	61.40	63.82
% target read > 20x	58.91	57.85	57.76	59.68	57.12	57.43	57.54	59.20
% target read > 30x	56.25	55.51	55.40	56.73	54.74	55.21	55.25	56.43
% target read > 50x	52.04	51.79	51.71	51.81	50.89	51.77	51.76	52.04