

**Supplementary Table 3: Depth of whole exome sequencing coverage**

Sample	No. of bases targeted	No. of bases covered by at least one read	% of targeted bases covered by at least one read	Average depth of coverage (x) for aligned reads	No. of targeted bases with sufficient coverage ( $\geq 5$ ) and quality (MPG/MPV $\geq 10$ ) for variant calling	% of targeted bases with sufficient coverage ( $\geq 5$ ) and quality (MPG/MPV $\geq 10$ ) for variant calling	Exome Capture Kit	Sequencing Platform
<i>Tumor samples</i>								
187T	61,884,224	58,852,061	95.1%	85	55,249,666	89.3%	Illumina TruSeqV2	Illumina HiSeq2000
188T	61,884,224	58,957,051	95.3%	78	55,373,733	89.5%	Illumina TruSeqV2	Illumina HiSeq2000
189T	61,884,224	58,991,292	95.3%	81	55,313,205	89.4%	Illumina TruSeqV2	Illumina HiSeq2000
190T	61,884,224	59,012,230	95.4%	84	55,511,946	89.7%	Illumina TruSeqV2	Illumina HiSeq2000
191T	61,884,224	59,117,696	95.5%	81	55,482,142	89.7%	Illumina TruSeqV2	Illumina HiSeq2000
192T	61,884,224	59,086,195	95.5%	73	55,239,833	89.3%	Illumina TruSeqV2	Illumina HiSeq2000
193T	61,884,224	59,104,064	95.5%	81	55,457,401	89.6%	Illumina TruSeqV2	Illumina HiSeq2000
194T	61,884,224	59,222,650	95.7%	80	55,518,118	89.7%	Illumina TruSeqV2	Illumina HiSeq2000
195T	61,884,224	59,320,144	95.9%	75	55,729,981	90.1%	Illumina TruSeqV2	Illumina HiSeq2000
196T	61,884,224	59,268,289	95.8%	86	55,629,702	89.9%	Illumina TruSeqV2	Illumina HiSeq2000
198T	61,884,224	59,759,772	96.6%	120	56,923,612	92.0%	Illumina TruSeqV2	Illumina HiSeq2000
199T	61,884,224	59,665,374	96.4%	110	56,809,635	91.8%	Illumina TruSeqV2	Illumina HiSeq2000
200T	61,884,224	59,512,754	96.2%	55	54,711,324	88.4%	Illumina TruSeqV2	Illumina HiSeq2000
201T	61,884,224	59,843,081	96.7%	104	56,778,806	91.8%	Illumina TruSeqV2	Illumina HiSeq2000
<i>Matched normal samples</i>								
187N	61,884,224	58,821,743	95.1%	78	54,930,377	88.8%	Illumina TruSeqV2	Illumina HiSeq2000
188N	61,884,224	59,042,485	95.4%	79	55,298,287	89.4%	Illumina TruSeqV2	Illumina HiSeq2000
189N	61,884,224	59,032,800	95.4%	81	55,335,801	89.4%	Illumina TruSeqV2	Illumina HiSeq2000
190N	61,884,224	58,991,708	95.3%	82	55,363,168	89.5%	Illumina TruSeqV2	Illumina HiSeq2000
191N	61,884,224	59,161,939	95.6%	83	55,530,299	89.7%	Illumina TruSeqV2	Illumina HiSeq2000
192N	61,884,224	59,060,948	95.4%	72	55,060,055	89.0%	Illumina TruSeqV2	Illumina HiSeq2000
193N	61,884,224	59,124,046	95.5%	77	55,358,066	89.5%	Illumina TruSeqV2	Illumina HiSeq2000
194N	61,884,224	59,192,409	95.7%	74	55,354,416	89.4%	Illumina TruSeqV2	Illumina HiSeq2000
195N	61,884,224	59,229,462	95.7%	78	55,465,540	89.6%	Illumina TruSeqV2	Illumina HiSeq2000
196N	61,884,224	59,393,624	96.0%	85	55,899,495	90.3%	Illumina TruSeqV2	Illumina HiSeq2000
198N	61,884,224	59,501,316	96.1%	48	53,991,049	87.2%	Illumina TruSeqV2	Illumina HiSeq2000
199N	61,884,224	59,462,258	96.1%	38	52,521,615	84.9%	Illumina TruSeqV2	Illumina HiSeq2000
200N	61,884,224	59,336,895	95.9%	44	53,206,065	86.0%	Illumina TruSeqV2	Illumina HiSeq2000
201N	61,884,224	59,629,892	96.4%	40	53,216,015	86.0%	Illumina TruSeqV2	Illumina HiSeq2000
<b>Weighted average of all samples</b>			95.7%	77	55,223,548	89.2%		