

Supplemental Table 1. Mate Pair sequencing data statistics.

Sample Name	Illumina Machine	Number of Lanes	Total Fragments	Fragments not mapped (%)	Replication (%)	Bridged Coverage (X)	Base Coverage (X)	Average MP Fragment (bp)
PA21	HiSeq+	0.5	90,447,078	7.7	10.6	39	5	2243
PA29	HiSeq+	0.5	92,893,065	8.2	11.8	31	5	1768
PA30	HiSeq+	0.5	100,071,528	10.0	9.9	34	6	1781
PA32	HiSeq+	0.5	68,402,027	10.5	10.0	27	4	2197
PA33	HiSeq+	0.5	105,973,848	5.5	5.5	30	7	1363
PA34	HiSeq+	0.5	87,340,065	15.1	15.8	31	4	2217
PA37	HiSeq+	0.5	78,585,214	10.0	12.9	33	4	2353
PA40	HiSeq+	0.5	52,841,401	7.9	7.3	22	3	2117
PA41	HiSeq+	0.5	61,168,973	18.2	7.7	21	3	1991
PA42	HiSeq+	0.5	95,373,534	8.9	9.6	35	5	2004
PA44	HiSeq+	0.5	86,695,601	13.9	12.3	33	5	2169
PA54	HiSeq+	0.5	86,264,189	12.2	13.5	32	4	2116
PA56	HiSeq+	0.5	90,537,963	6.5	8.1	36	5	2015
PA62	HiSeq+	0.5	96,787,007	18.5	20.0	31	4	2233
PA63	HiSeq+	0.5	87,997,120	12.3	23.4	28	4	2019
<i>average</i>			85,425,241	11	12	31	5	2,039

Supplemental Figure 1. G12/G13 KRAS Mutations in PDAC Tumors

A Summary of KRAS mutations detected in each tumor by Sanger sequencing.

	G12 Codon			G13 Codon				
PAX18	G	G	T	G	G	C	G12	G13
PA29	G	G	T	G	A	C	G12	G13D
PA33	G	T	T	G	G	C	G12V	G13
PA37	G	T	T	G	G	C	G12V	G13
PA41	G	T	T	G	G	C	G12V	G13
PA44	G	T	T	G	G	C	G12V	G13
PA56	G	T	T	G	G	C	G12V	G13
PAX04	G	T	T	G	G	C	G12V	G13
PAX14	G	T	T	G	G	C	G12V	G13
PAX15	G	T	T	G	G	C	G12V	G13
PAX22	G	T	T	G	G	C	G12V	G13
PAX27	G	T	T	G	G	C	G12V	G13

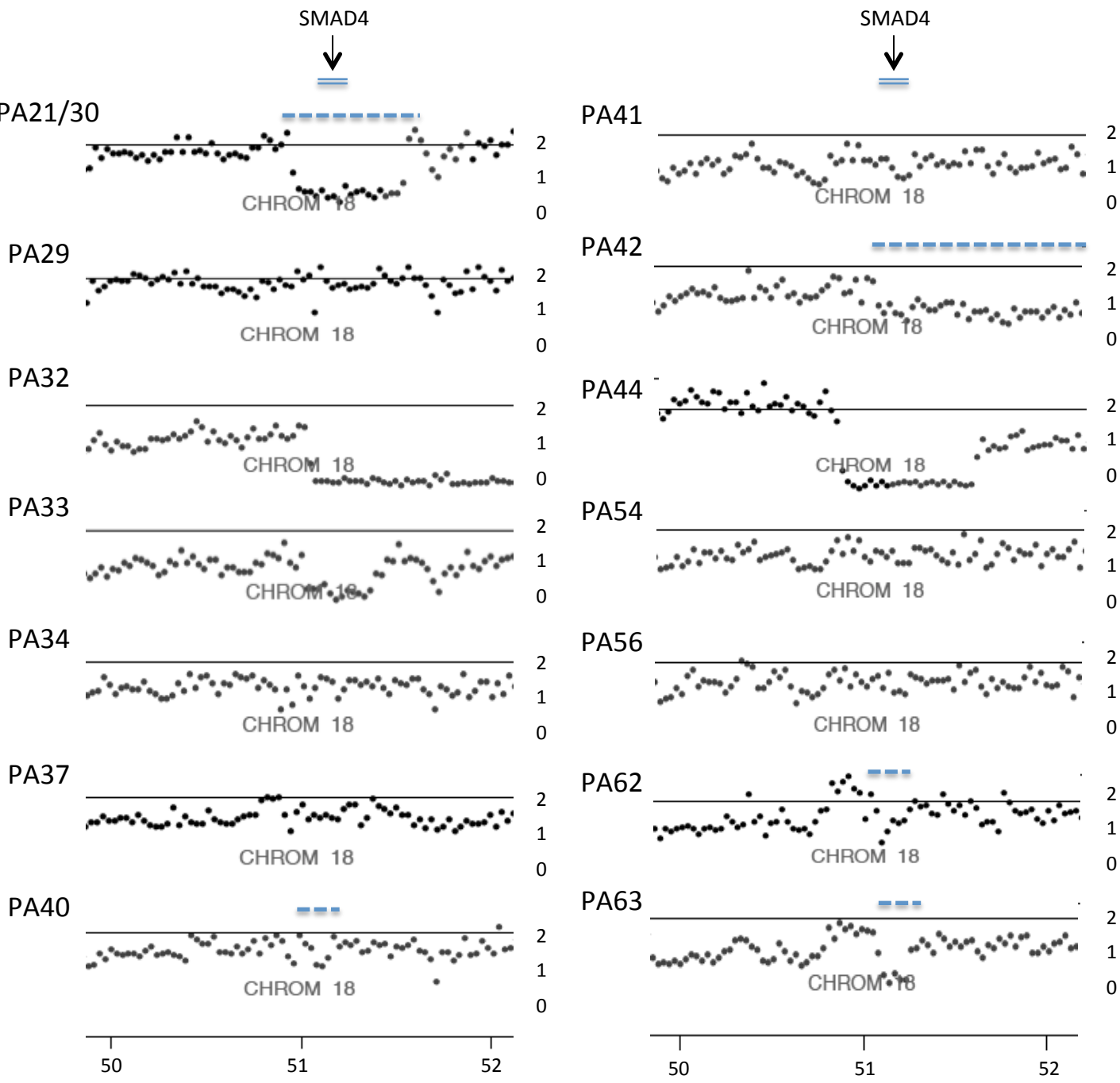
	G12 Codon			G13 Codon				
PA62	T	G	T	G	G	C	G12C	G13
PAX05	T	G	T	G	G	C	G12C	G13
PA32	C	G	T	G	G	C	G12R	G13
PAX12	C	G	T	G	G	C	G12R	G13
PAX46	C	G	T	G	G	C	G12R	G13
PA34	G	A	T	G	G	C	G12D	G13
PA40	G	A	T	G	G	C	G12D	G13
PA42	G	A	T	G	G	C	G12D	G13
PA54	G	A	T	G	G	C	G12D	G13
PA63	G	A	T	G	G	C	G12D	G13
PA21/30	G	A	T	G	G	C	G12D	G13
PAX51	G	A	T	G	G	C	G12D	G13

B

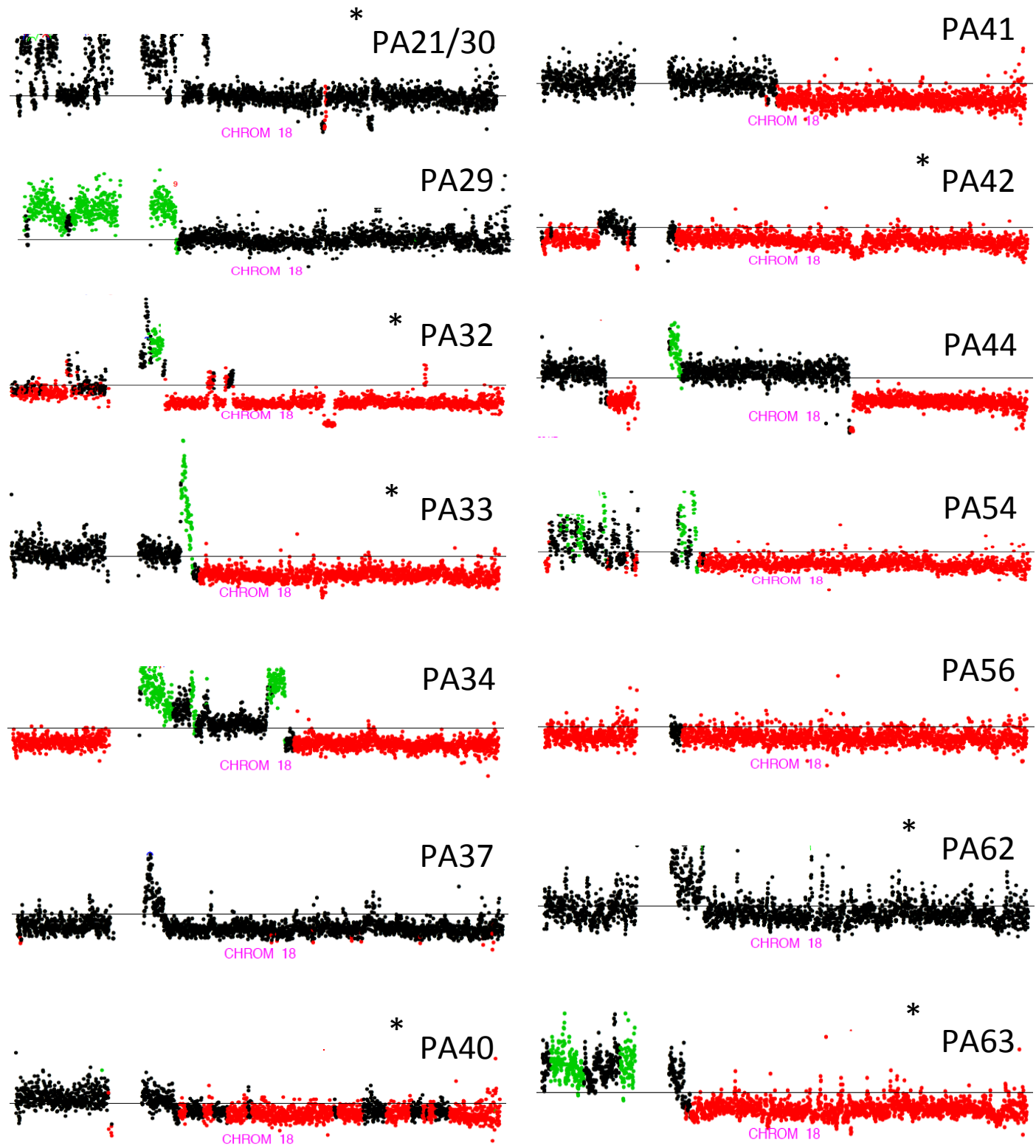
* = Both Strands Mut'd



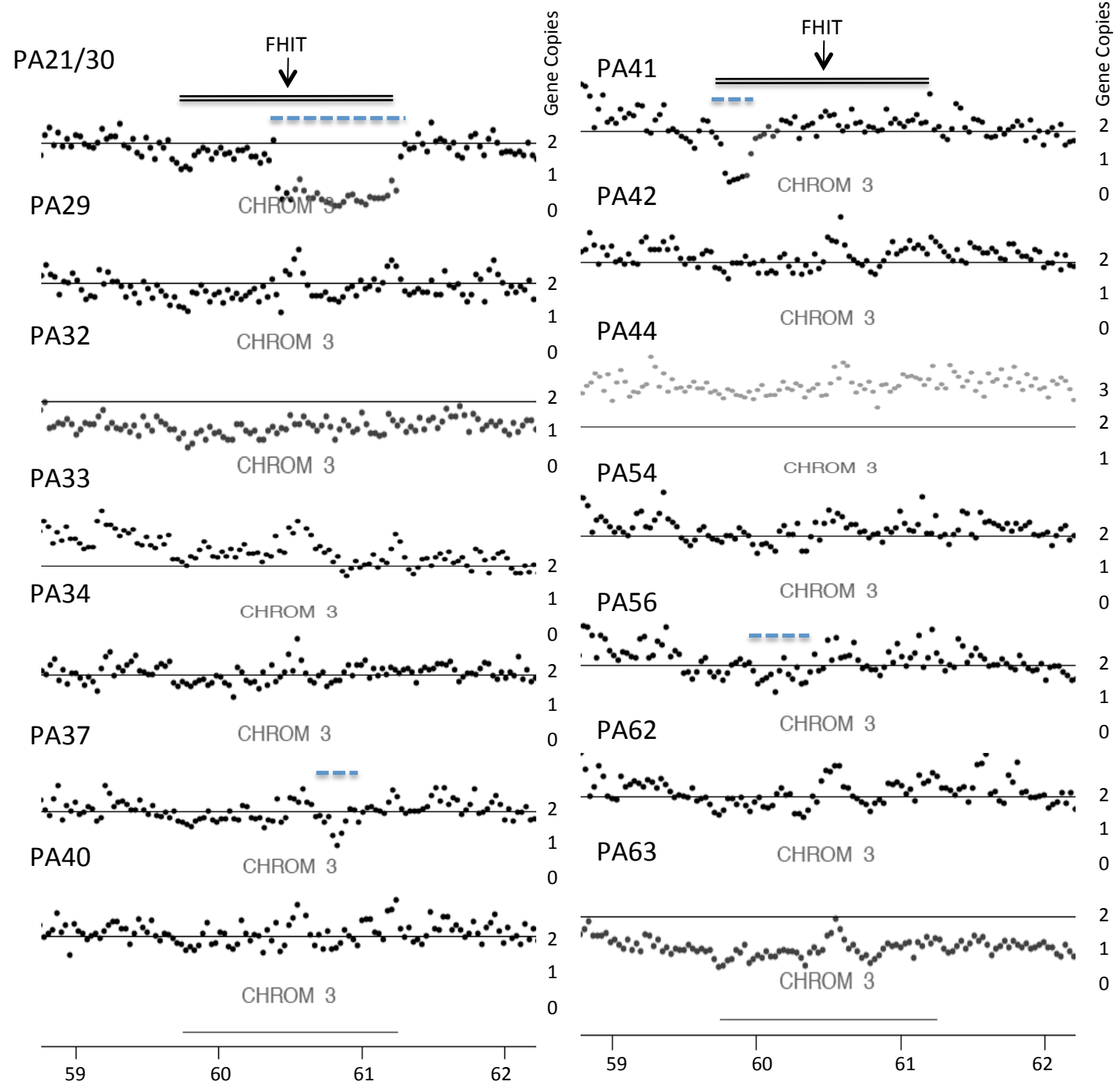
Supplemental Figure 2A. CNV at the SMAD4 Locus



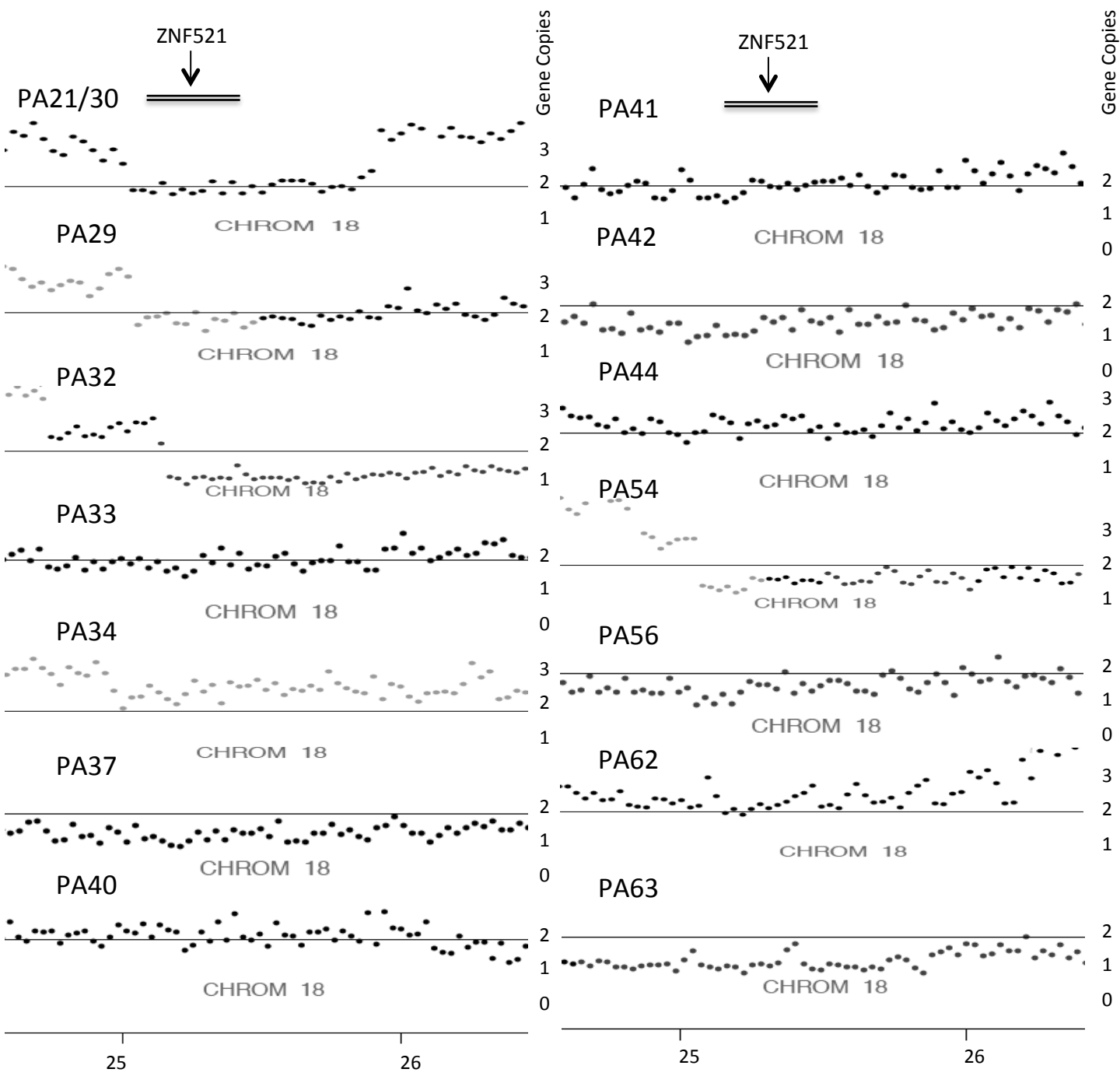
Supplemental Figure 2B. CNV of Chromosome 18



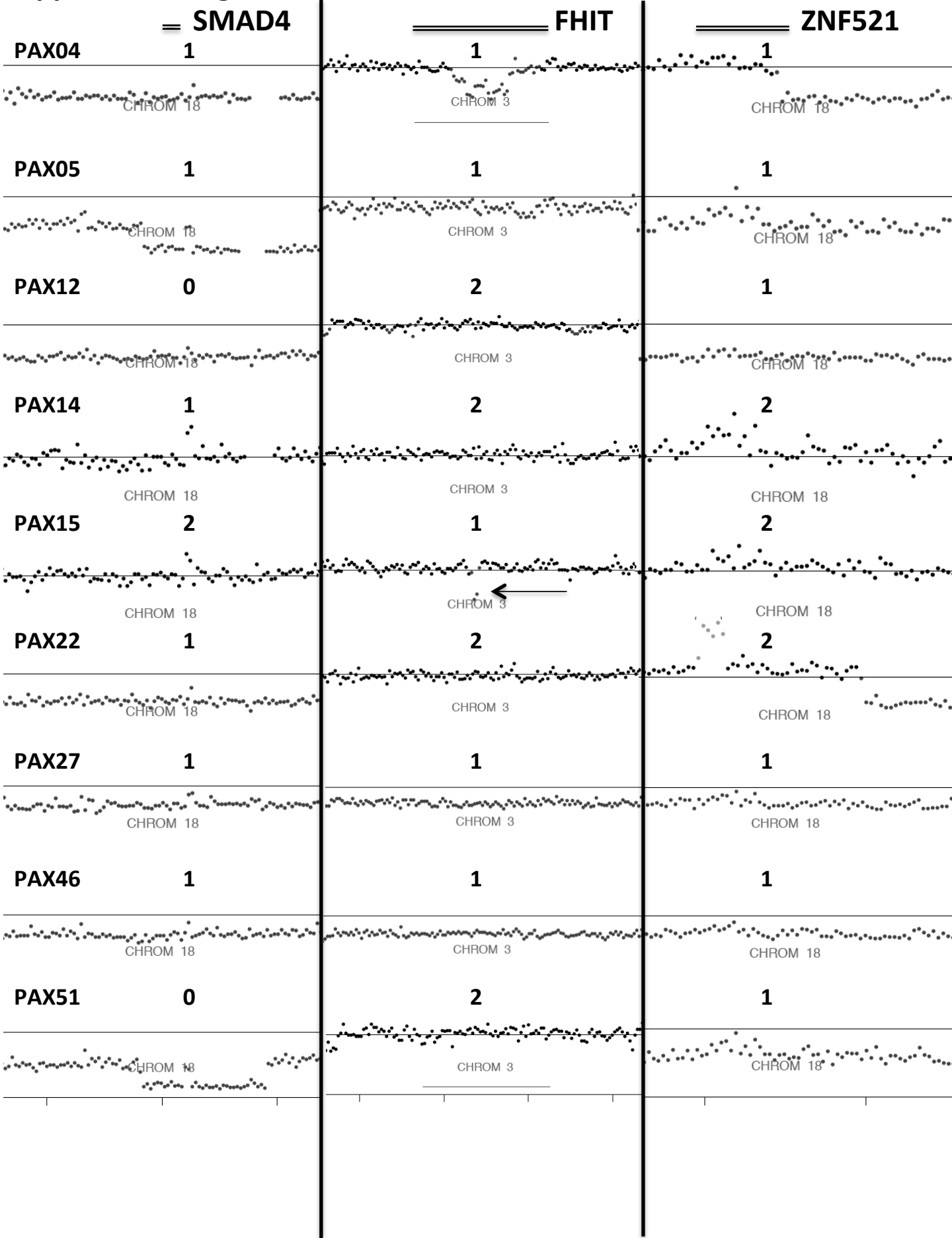
Supplemental Figure 2C. CNV at the FHIT locus.



Supplemental Figure 2D. CNV at the ZNF521 locus.



Supplemental Figure 2E. PAX Tissues



Supplemental Figure 4. TGFbeta activated genes.

