

## DNA binding by ZNF217

### SUPPLEMENTAL TABLES

Supplemental Table 1. Contribution of ZNF217-F67 amino acid residues to DNA binding. The table indicates the relative binding strength of each ZNF217-F67 mutant to the DNA consensus sequence TGCAGAAT, as assessed by EMSA (Figure 8). “++” indicates binding equivalent to wildtype ZNF217-F67, “+” indicates reduced binding and “-” indicates almost complete or total loss of detectable binding. Y506 was found not to fold correctly by NMR spectroscopy and has been omitted from the table.

<b>ZNF217-F67 mutated residue</b>	<b>Interaction</b>
C473	-
S474	++
Y475	+
G477	+
K478	-
F479	++
R481	-
S482	-
Y484	+
Y485	-
L486	++
N487	-
I488	-
H489	-
L490	++
R491	-
T492	+
T494	-
G495	-
E496	-
K497	-
P498	-
Y499	-
K500	++
E502	++
F503	++
C504	-
E505	+
A507	++
A509	-
Q510	-
K511	-
T512	-
S513	+
Y516	+
L518	+
E519	+
R520	-