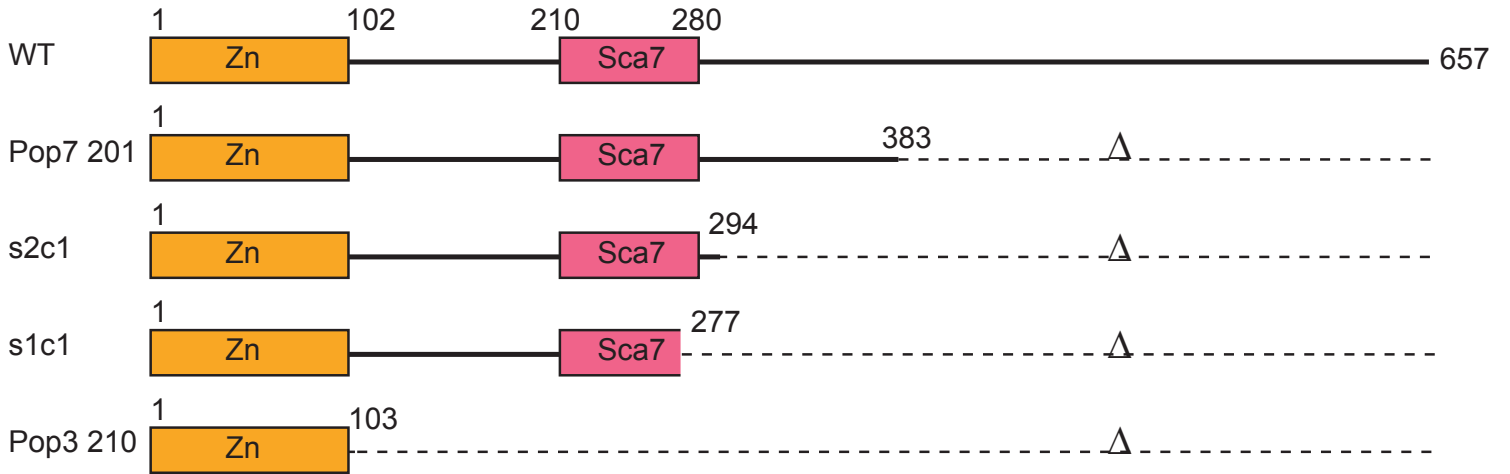


Figure S6



WT	1	MRSGDAEIKG KPKV EEYSLSQSGSPSND SWKSLMSSAKD TPLQYDHMNRSLKKYFNPAQL EDPLDKP QYRVCEKCGKPLALTA VDHLENHCAGAS GS SSDPRDES	113
Pop3 210	1	MRSGDAEIKG KPKV EEYSLSQSGSPSND SWKSLMSSAKD TPLQYDHMNRSLKKYFNPAQL EDPLDKP QYRVCEKCGKPLALTA VDHLENHCAGAS GS SSDPRDES	113
Pop7 201	1	MRSGDAEIKG KPKV EEYSLSQSGSPSND SWKSLMSSAKD TPLQYDHMNRSLKKYFNPAQL EDPLDKP QYRVCEKCGKPLALTA VDHLENHCAGAS GS SSDPRDES	113
s1c1	1	MRSGDAEIKG KPKV EEYSLSQSGSPSND SWKSLMSSAKD TPLQYDHMNRSLKKYFNPAQL EDPLDKP QYRVCEKCGKPLALTA VDHLENHCAGAS GS SSDPRDES	113
s2c1	1	MRSGDAEIKG KPKV EEYSLSQSGSPSND SWKSLMSSAKD TPLQYDHMNRSLKKYFNPAQL EDPLDKP QYRVCEKCGKPLALTA VDHLENHCAGAS GS SSDPRDES	113
114	TRET IRNGVESTGRNNDDDDNSNDNNDDDDDDDDDDNDDNEDDDDDDDDDDDNSNGANYKKNDSSFNPLKRSTSMESANTPNMDTKRSKTGTPQTFSSS KKQKVKQRNPTEKHL	226	
114	TRET IRNGVESTGRNNDDDDNSNDNNDDDDDDDDDDNDDNEDDDDDDDDDDDNSNGANYKKNDSSFNPLKRSTSMESANTPNMDTKRSKTGTPQTFSSS KKQKVKQRNPTEKHL	226	
114	TRET IRNGVESTGRNNDDDDNSNDNNDDDDDDDDDDNDDNEDDDDDDDDDDDNSNGANYKKNDSSFNPLKRSTSMESANTPNMDTKRSKTGTPQTFSSS KKQKVKQRNPTEKHL	226	
114	TRET IRNGVESTGRNNDDDDNSNDNNDDDDDDDDDDNDDNEDDDDDDDDDDDNSNGANYKKNDSSFNPLKRSTSMESANTPNMDTKRSKTGTPQTFSSS KKQKVKQRNPTEKHL	226	
114	TRET IRNGVESTGRNNDDDDNSNDNNDDDDDDDDDDNDDNEDDDDDDDDDDDNSNGANYKKNDSSFNPLKRSTSMESANTPNMDTKRSKTGTPQTFSSS KKQKVKQRNPTEKHL	226	
227	DFNKQCGVELPEGGYCARSLTCKSHSMGAKRAVSGRSKPYDVLADYHREHQT GAAAEKRAKQQLQKLQKQ QKEQKKHTQQQKQGRSKQRNVNGGKSAKNGGKSTVH	339	
227	DFNKQCGVELPEGGYCARSLTCKSHSMGAKRAVSGRSKPYDVLADYHREHQT GAAAEKRAKQQLQKLQKQ QKEQKKHTQQQKQGRSKQRNVNGGKSAKNGGKSTVH	339	
227	DFNKQCGVELPEGGYCARSLTCKSHSMGAKRAVSGRSKPYDVLADYHREHQT GAAAEKRAKQQLQKLQKQ QKEQKKHTQQQKQGRSKQRNVNGGKSAKNGGKSTVH	339	
227	DFNKQCGVELPEGGYCARSLTCKSHSMGAKRAVSGRSKPYDVLADYHREHQT GAAAEKRAKQQLQKLQKQ QKEQKKHTQQQKQGRSKQRNVNGGKSAKNGGKSTVH	339	
227	DFNKQCGVELPEGGYCARSLTCKSHSMGAKRAVSGRSKPYDVLADYHREHQT GAAAEKRAKQQLQKLQKQ QKEQKKHTQQQKQGRSKQRNVNGGKSAKNGGKSTVH	339	
340	NGNNINE GHVNLTPPEETTQVLNGVSRSPFLPLESTVLSVRYRRTKYFRMREMFASSFSVKPGYTPGYGA HSRVGCLDLDRITDYKFRVRTPOP INHLTNQNLNPKQ QR	452	
340	NGNNINE GHVNLTPPEETTQVLNGVSRSPFLPLESTVLSVRYRRTKYFRMREMFASSFSVKPGYTPGYGA HSRVGCLDLDRITDYKFRVRTPOP INHLTNQNLNPKQ QR	452	
340	NGNNINE GHVNLTPPEETTQVLNGVSRSPFLPLESTVLSVRYRRTKYFRMREMFASSFSVKPGYTPGYGA HSRVGCLDLDRITDYKFRVRTPOP INHLTNQNLNPKQ QR	452	
340	NGNNINE GHVNLTPPEETTQVLNGVSRSPFLPLESTVLSVRYRRTKYFRMREMFASSFSVKPGYTPGYGA HSRVGCLDLDRITDYKFRVRTPOP INHLTNQNLNPKQ QR	452	
340	NGNNINE GHVNLTPPEETTQVLNGVSRSPFLPLESTVLSVRYRRTKYFRMREMFASSFSVKPGYTPGYGA HSRVGCLDLDRITDYKFRVRTPOP INHLTNQNLNPKQ QR	452	
453	LQQQRALQAQLL SQQQQQQQQQQHHSPQAQAQASTQQPTQGMVFNHFGGATNSSFANVSSKQ QQQQQQQHKSDTGLTPLE QSQQQLRQQQLQQQKFEAAASYLAN	565	
453	LQQQRALQAQLL SQQQQQQQQQQHHSPQAQAQASTQQPTQGMVFNHFGGATNSSFANVSSKQ QQQQQQQHKSDTGLTPLE QSQQQLRQQQLQQQKFEAAASYLAN	565	
453	LQQQRALQAQLL SQQQQQQQQQQHHSPQAQAQASTQQPTQGMVFNHFGGATNSSFANVSSKQ QQQQQQQHKSDTGLTPLE QSQQQLRQQQLQQQKFEAAASYLAN	565	
453	LQQQRALQAQLL SQQQQQQQQQQHHSPQAQAQASTQQPTQGMVFNHFGGATNSSFANVSSKQ QQQQQQQHKSDTGLTPLE QSQQQLRQQQLQQQKFEAAASYLAN	565	
453	LQQQRALQAQLL SQQQQQQQQQQHHSPQAQAQASTQQPTQGMVFNHFGGATNSSFANVSSKQ QQQQQQQHKSDTGLTPLE QSQQQLRQQQLQQQKFEAAASYLAN	565	
566	ATKLMQESNQD SHL SGTHNNNS SKNGNNL MTMKAS SSPNTSVNS QSPPSVNSVNSGQGVSTG INVSGNNGR EVG GNSVNPYNGR IN	658	
566	ATKLMQESNQD SHL SGTHNNNS SKNGNNL MTMKAS SSPNTSVNS QSPPSVNSVNSGQGVSTG INVSGNNGR EVG GNSVNPYNGR IN	658	
566	ATKLMQESNQD SHL SGTHNNNS SKNGNNL MTMKAS SSPNTSVNS QSPPSVNSVNSGQGVSTG INVSGNNGR EVG GNSVNPYNGR IN	658	
566	ATKLMQESNQD SHL SGTHNNNS SKNGNNL MTMKAS SSPNTSVNS QSPPSVNSVNSGQGVSTG INVSGNNGR EVG GNSVNPYNGR IN	658	
566	ATKLMQESNQD SHL SGTHNNNS SKNGNNL MTMKAS SSPNTSVNS QSPPSVNSVNSGQGVSTG INVSGNNGR EVG GNSVNPYNGR IN	658	

Figure S6. *SGF73* mutations identified in four independent sulfate-limited evolutions. TOP: Diagrammatic representation of the Sgf73 protein. Boxes show protein domains. Residue numbering for the domains is shown above the protein. The extents of recovered truncations are shown by dashed lines with the last included amino acid indicated by the residue number. BOTTOM: ClustalW multiple alignment of Sgf73 sequences from a wildtype strain and four evolved strains carrying truncation mutations in *SGF73*.