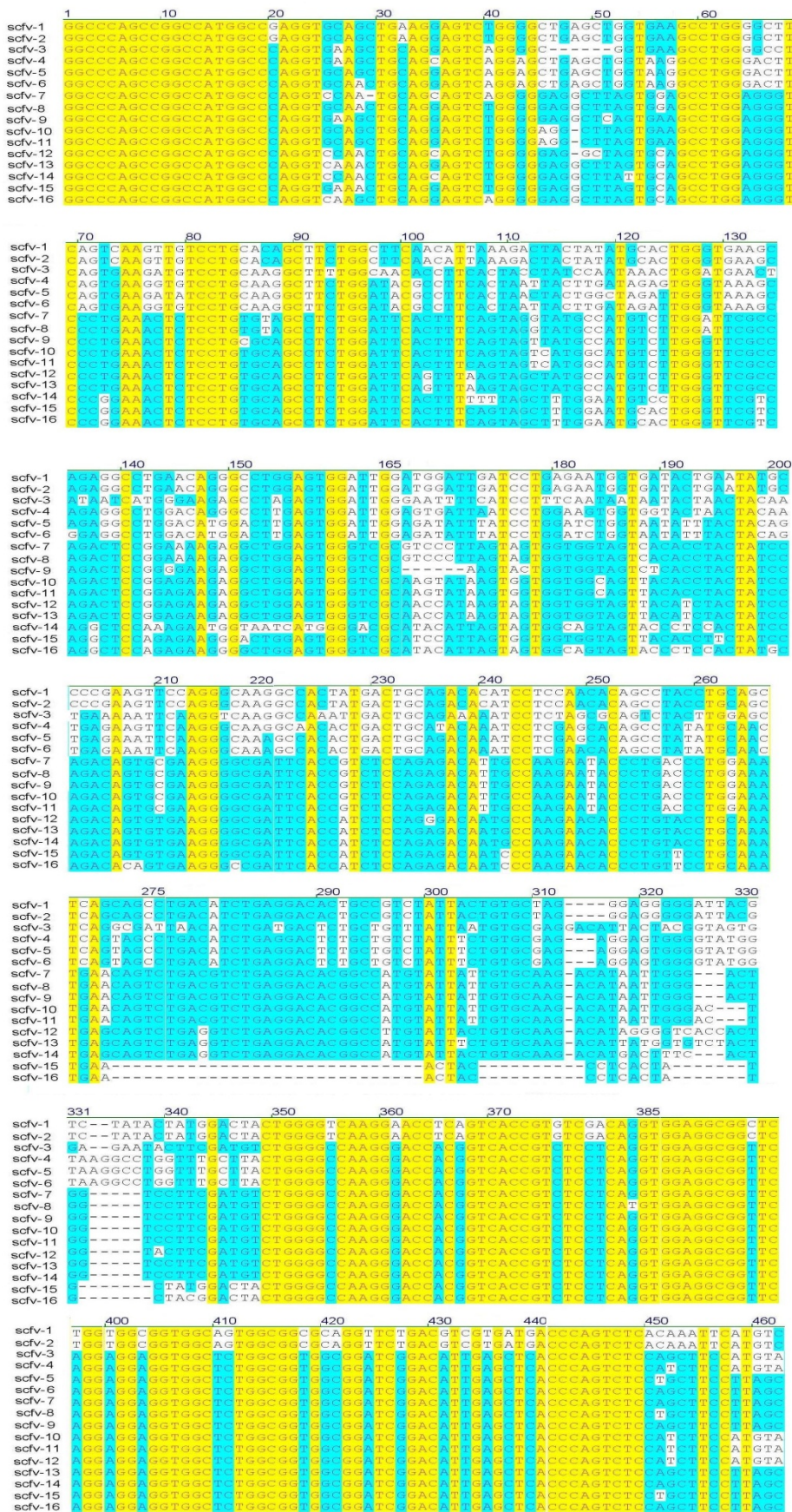


Supplementary Figure S1 Diversity of the constructed positive phage display library



	470	480	495	510	520
scfv-1	CACATCAGTAGGAGACAGGGTCAAGATCACCTGCAAGGCAG-----TCAGGATGT----GGG				
scfv-2	CACATCAGTAGGAGACAGGGTCAAGATCACCTGCAAGGCAG-----TCAGGATGT----GGG				
scfv-3	TGCATCTTAGGAGAGAGAGTCAATATCACCTTGCAAGGCGAG-----TCAGGACAT----TAA				
scfv-4	TGCATCTTAGGAGAGAGAGTCAATATCACCTTGCAAGGCGAG-----TCAGGACAT----TAA				
scfv-5	TGTATCTTGGGCGAGAGGGCCACATCTCATACAGGGCAGCAAAAGTGTCAGTACATCTGGCTA				
scfv-6	TGTATCTTGGGCGAGAGGGCCACATCTCATACAGGGCAGCAAAAGTGTCAGTACATCTGGCTA				
scfv-7	TGTATCTTGGGCGAGAGGGCCACATCTCATACAGGGCAGCAAAAGTGTCAGTACATCTGGCTA				
scfv-8	TGTATCTTGGGCGAGAGGGCCACATCTCATACAGGGCAGCAAAAGTGTCAGTACATCTGGCTA				
scfv-9	TGTATCTTGGGCGAGAGGGCCACATCTCATACAGGGCAGCAAAAGTGTCAGTACATCTGGCTA				
scfv-10	TGCATCTTAGGAGAGAGAGTCAATATCACCTTGCAAGGCGAG-----TCAGGACAT----TAA				
scfv-11	TGCATCTTAGGAGAGAGAGTCAATATCACCTTGCAAGGCGAG-----TCAGGACAT----TAA				
scfv-12	TGCATCTTAGGAGAGAGAGTCAATATCACCTTGCAAGGCGAG-----TCAGGACAT----TAA				
scfv-13	TGTATCTTGGGCGAGAGGGCCACATCTCATACAGGGCAGTGAAGCTTGTAGTGTATGGGAA				
scfv-14	TGTATCTTGGGCGAGAGGGCCACATCTCATACAGGGCAGTGAAGCTTGTAGTGTATGGGAA				
scfv-15	TGTATCTTGGGCGAGAGGGCCACATCTCATACAGGGCAGTGAAGCTTGTAGTGTATGGGAA				
scfv-16	TGTATCTTGGGCGAGAGGGCCACATCTCATACAGGGCAGTGAAGCTTGTAGTGTATGGGAA				

	530	540	550	560	570	580	590
scfv-1	TACTGCCTAGCTGGTTCAACAGAAACCAGGGCAATCTCTT--AAACTACTGATTCTGGG--A						
scfv-2	TACTGCCTAGCTGGTTCAACAGAAACCAGGGCAATCTCTT--AAACTACTGATTCTGGG--A						
scfv-3	TATTTTATTAAAGTACTTCAACAGAAACCAGGGCAATCTCTTA--AGAC--CTTGATTTCTGGG--A						
scfv-4	TATTTTATTAAAGTACTTCAACAGAAACCAGGGCAATCTCTTA--AGAC--CTTGATTTCTGGG--A						
scfv-5	TATTTATATGCACTGGAAACCAACAGAAACCAGGACAGCCACC--AAACTCTTATCTATCTGT--A						
scfv-6	TATTTATATGCACTGGAAACCAACAGAAACCAGGACAGCCACC--AAACTCTTATCTATCTGT--A						
scfv-7	TATTTATATGCACTGGAAACCAACAGAAACCAGGACAGCCACC--AAACTCTTATCTATCTGT--A						
scfv-8	TATTTATATGCACTGGAAACCAACAGAAACCAGGACAGCCACC--AAACTCTTATCTATCTGT--A						
scfv-9	TATTTATATGCACTGGAAACCAACAGAAACCAGGACAGCCACC--AAACTCTTATCTATCTGT--A						
scfv-10	TATTTTATTAAAGTACTTCAACAGAAACCAGGGCAATCTCTTA--AGAC--CTTGATTTCTGGG--A						
scfv-11	TATTTTATTAAAGTACTTCAACAGAAACCAGGGCAATCTCTTA--AGAC--CTTGATTTCTGGG--A						
scfv-12	TATTTTATTAAAGTACTTCAACAGAAACCAGGGCAATCTCTTA--AGAC--CTTGATTTCTGGG--A						
scfv-13	TATTTTATTAAAGTACTTCAACAGAAACCAGGGCAATCTCTTA--AGAC--CTTGATTTCTGGG--A						
scfv-14	TATTTATATGCACTGGAAACCAACAGAAACCAGGACAGCCACC--AAACTCTTATCTATCTGT--A						
scfv-15	TATTTATATGCACTGGAAACCAACAGAAACCAGGACAGCCACC--AAACTCTTATCTATCTGT--A						
scfv-16	TATTTATATGCACTGGAAACCAACAGAAACCAGGACAGCCACC--AAACTCTTATCTATCTGT--A						

	605	620	630	640	650	660
scfv-1	TCC--ACCGGGCACAATGGAGTCCCTGATCGCTTCAAG--G--CA--GTGGATCTTGGACAG					
scfv-2	TCC--ACCGGGCACAATGGAGTCCCTGATCGCTTCAAG--G--CA--GTGGATCTTGGACAG					
scfv-3	AA--AGATTTGTTGATGGGTCCCATCAAGGTC--TAG--TGG--CA--GTGGATCTTGGACAG					
scfv-4	AA--AGATTTGTTGATGGGTCCCATCAAGGTC--TAG--TGG--CA--GTGGATCTTGGACAG					
scfv-5	TCC--ACCGTAGAATCTGGGTCCCTGCCAGGTT--TAG--TGG--CA--GTGGTCTTGGACAG					
scfv-6	TCC--ACCGTAGAATCTGGGTCCCTGCCAGGTT--TAG--TGG--CA--GTGGTCTTGGACAG					
scfv-7	TCC--ACCGTAGAATCTGGGTCCCTGCCAGGTT--TAG--TGG--CA--GTGGTCTTGGACAG					
scfv-8	TCC--ACCGTAGAATCTGGGTCCCTGCCAGGTT--TAG--TGG--CA--GTGGTCTTGGACAG					
scfv-9	TCC--ACCGTAGAATCTGGGTCCCTGCCAGGTT--TAG--TGG--CA--GTGGTCTTGGACAG					
scfv-10	AA--AGATTTGTTGATGGGTCCCATCAAGGTC--TAG--TGG--CA--GTGGATCTTGGACAG					
scfv-11	AA--AGATTTGTTGATGGGTCCCATCAAGGTC--TAG--TGG--CA--GTGGATCTTGGACAG					
scfv-12	AA--AGATTTGTTGATGGGTCCCATCAAGGTC--TAG--TGG--CA--GTGGATCTTGGACAG					
scfv-13	TCC--ACCGTAGAATCTGGGTCCCTGCCAGGTT--TAG--TGG--CA--GTGGTCTTGGACAG					
scfv-14	TCC--ACCGTAGAATCTGGGTCCCTGCCAGGTT--TAG--TGG--CA--GTGGTCTTGGACAG					
scfv-15	TCC--ACCGTAGAATCTGGGTCCCTGCCAGGTT--TAG--TGG--CA--GTGGTCTTGGACAG					
scfv-16	TCC--ACCGTAGAATCTGGGTCCCTGCCAGGTT--TAG--TGG--CA--GTGGTCTTGGACAG					

	670	680	690	700	715
scfv-1	ATTTCACCT--CAAC--ATTAGCAATGTG--CAGTCTGA--AACT--TG--CAGATATTT--				
scfv-2	ATTTCACCT--CAAC--ATTAGCAATGTG--CAGTCTGA--AACT--TG--CAGATATTT--				
scfv-3	ATAATTCT--CAAC--TTTCAAGGCTG--GAGCTGA--CGATA--TG--GAATTTATTA--				
scfv-4	ATAATTCT--CAAC--TTTCAAGGCTG--GAGCTGA--CGATA--TG--GAATTTATTA--				
scfv-5	ACTTCACCT--CAAC--AT--CCATCCTGTGGAGGAGGA--GGATG--TG--CAACTATTA--				
scfv-6	ACTTCACCT--CAAC--AT--CCATCCTGTGGAGGAGGA--GGATG--TG--CAATGATTT--				
scfv-7	ACTTCACCT--CAAC--AT--CCATCCTGTGGAGGAGGA--GGATG--TG--CAACTATTA--				
scfv-8	ACTTCACCT--CAAC--AT--CCATCCTGTGGAGGAGGA--GGATG--TG--CAACTATTA--				
scfv-9	ACTTCACCT--CAAC--AT--CCATCCTGTGGAGGAGGA--GGATG--TG--CAACTATTA--				
scfv-10	ATAATTCT--CAAC--TTTCAAGGCTG--GAGCTGA--CGATA--TG--GAATTTATTA--				
scfv-11	ATAATTCT--CAAC--TTTCAAGGCTG--GAGCTGA--CGATA--TG--GAATTTATTA--				
scfv-12	ATAATTCT--CAAC--TTTCAAGGCTG--GAGCTGA--CGATA--TG--GAATTTATTA--				
scfv-13	ACTTCACCT--CAAC--AT--CCATCCTGTGGAGGCTGA--TGATG--TG--CAACTATTA--				
scfv-14	ACTTCACCT--CAAC--AT--CCATCCTGTGGAGGAGGA--GGATG--TG--CAACTATTA--				
scfv-15	ACTTCACCT--CAAC--AT--CCATCCTGTGGAGGAGGA--GGATG--TG--CAACTATTA--				
scfv-16	ACTTCACCT--CAAC--AT--CCATCCTGTGGAGGAGGA--GGATG--TG--CAACTATTA--				

	730	740	750	760	770	780	790
scfv-1	---CTGTCA--GCAATA--TAGCAGCTATCCGTACAG--TTCGGG--GGGG--ACCAAGCT--GGAA						
scfv-2	---CTGTCA--GCAATA--TAGCAGCTATCCGTACAG--TTCGGG--GGGG--ACCAAGCT--GGAA						
scfv-3	---TTGTCT--A--TAGTATGAGGATTTCCCTATG--TTCGGT--CTGGCACCAGCT--GGAA						
scfv-4	---TTGTCT--A--TAGTATGAGGATTTCCCTATG--TTCGGT--CTGGCACCAGCT--GGAG						
scfv-5	---CTGTCA--GCA--CATTA--GAGG--TTACAG--TTCGGG--GGGG--ACCAAGCT--GGAA						
scfv-6	---CTGTCA--GCA--CATTA--GAGG--TTACAG--TTCGGG--TCGGCAGCAAGCT--GGAA						
scfv-7	---CTGTCA--GCA--CATTA--GAGG--TTACAG--TTCGGG--GGGG--CAGCAAGCT--GGAA						
scfv-8	---CTGTCA--GCA--CATTA--GAGG--TTACAG--TTCGGG--GGGG--CAGCAAGCT--GGAG						
scfv-9	---CTGTCA--GCA--CATTA--GAGG--TTACAG--TTCGGG--GGGG--CAGCAAGCT--GGAA						
scfv-10	---TTGTCT--A--TAGTATGAGGATTTCCCTATG--TTCGGT--CTGGCACCAGCT--GGAA						
scfv-11	---TTGTCT--A--TAGTATGAGGATTTCCCTATG--TTCGGT--CTGGCACCAGCT--GGAA						
scfv-12	---TTGTCT--A--TAGTATGAGGATTTCCCTATG--TTCGGT--CTGGCACCAGCT--GGAA						
scfv-13	---CTGTCA--GCAAAATGATGAGGATCTCCGAGG--TTCGGC--TCGGGACAAAGTT--GGAA						
scfv-14	---CTGTCA--GCA--CATTA--GAGG--TTACAG--TTCGGG--GGGG--ACCAAGCT--GGAG						
scfv-15	AACCTGTCTAAGCAACATTAAG--GAGGCTTACACAGGTTTCGGGAAGGGCGGAAACCAACTG--GGAA						
scfv-16	---CTGTCA--GCA--CATTA--GAGG--TTACAG--TTCGGG--GGGG--ACCAAGCT--GGAG						

	809						
scfv-1	ATTAAAGGCG-----						
scfv-2	ATTAAAGGCGGGGGCGC-----						
scfv-3	ATTAAAGGCGGGGGCGC-----						
scfv-4	CTGAAAGGCGGGGGCGC-----						
scfv-5	ATTAAAGGCGGGGGCGC-----						
scfv-6	ATTAAAGGCGGGGGCGC-----						
scfv-7	ATTAAAGGCGGGGGCGC-----						
scfv-8	ATTAAAGGCGGGGGCGC-----						
scfv-9	CTGAAAGGCGGGGGCGC-----						
scfv-10	ATTAAAGGCGGGGGCGC-----						
scfv-11	ATTAAAGGCGGGGGCGC-----						
scfv-12	ATTAAAGGCGGGGGCGC-----						
scfv-13	ATTAAAGGCGGGGGCGC-----						
scfv-14	CTGAAAGGCGGGGGCGC-----						
scfv-15	ATTAAAGGCGGGGGCGC-----						
scfv-16	CTGAAAGGCGGGGGCGC-----						