

Table S1. Groups with ≥15 homologous sequences, which were identified by data analysis of the NGS pool using the two-step clustering and alignment method. Each group consists of a different number of clusters (containing identical sequences) and singletons (unique sequences also called orphans). All grouped sequences are listed.

group (size ≥15 seq.)	non-redundant NGS pool (1. clustering)		no. seq.	aptameric sequence (5' → 3') ATACCAGCTTATTCAATT ---- intern region ---- ACAATCGTAATCAGTTAG	length of intern region (nt)	aptamer from Sanger pool identified	new aptamer
	cluster or singleton	name					
group 1	* cluster	C1	54	AGCAACATGAGGGGGATAGAGGGGTGGGTTCTCTCGGCT	40	PA#2/8	PA-C4 PA-C7
	cluster	C4	41	AGCAACATGAGGGGGATGAGGGGGTGGGTTCTCTCGGCT	40		
	cluster	C7	25	AGCAACATGAGGGGGATAGAGGGGTGGGTTCTCTCGGCT	41		
	cluster	C23	11	AGCAACATNAGGGGGATNAGGGGTGGGTTCTCTCGGCT	41		
	cluster	C31	8	AGCAACATNAGGGGGATNAGGGGTGGGTTCTCTCGGCT	42		
	cluster	C34	8	AGCAACATNAGGGGGATGAGGGGTGGGTTCTCTCGGCT	40		
	cluster	C41	7	AGCAACATGAGGGGGATAGAGGGGTGGGTTCTCTCGGCT	43		
	cluster	C54	6	AGCAACATNAGGGGGATAGAGGGGTGGGTTCTCTCGGCT	41		
	cluster	C55	6	AGCAACATGAGGGGGATGAGGGGTGGGTTCTCTCGGCT	41		
	cluster	C64	5	AGCAACATNAGGGGGATGAGGGGTGGGTTCTCTCGGCT	41		
	cluster	C67	5	AGCAACATNAGGGGGATNAGGGGTGGGTTCTCTCGGCT	40		
	cluster	C104	4	AGCAACATGAGGGGGATAGAGGGGTGGGTTCTCTCGGTT	40		
	cluster	C139	3	AGCAACATGAGGGGGATAGAGGGGTGGGTTCTCTCGACT	40		
	cluster	C152	2	AGCAACATGAGGGGGATGAGGGGTGGGTTCTCTCGGCT	42		
	cluster	C154	2	AGCAACATGAGGGGGATAGAGGGGTGGGTTCTCTCGGCT	42		
	cluster	C189	2	AGCAACATGAGGGGGATAGAGGGGTGGGTTCTCTCGTCT	40		
	cluster	C207	2	AGCAACATGAGGGGGATGAAGGGGTGGGTTCTCTCGGCT	40		
	cluster	C240	2	AGCAACATGAGGGGGATGAGGGGTGGGTTCTCTCGACT	40		
	cluster	C269	2	AGCAACATGAGGGGGATAGAGGGGTGGGTTCTCTCGGCT	39		
	cluster	C272	2	AGCAACATGAGGGGGATGAGGGGTGGGTTCTCTCGGCT	39		
	singleton	S292	1	AGCAACATNAGGGGGGATNAGGGGGGTGGGTTCTCTCGGCT	45		
	singleton	S298	1	AGCAACATGAGGGGGGATAGAGGGGGGTGGGTTCTCTCGTCT	44		
	singleton	S301	1	AGCAACATGAGGGGGGATAGAGGGGGGTGGGTTCTCTCGGCT	44		
	singleton	S302	1	AGCTAACGATGACGGGGGATGAGGGGGTGGGTTCTCTCGGCTA	44		
	singleton	S309	1	AGCAACATGAGGGGGATAGAGGGGGGTGGGTTCTCTCGGCT	43		
	singleton	S310	1	AGCAACATGAGGGGGGATAGAGGGGGGTGGGTTCTCTCGGCC	43		
	singleton	S313	1	TAGCAACATNAGGGGGGATNAGGGGGGTGGGTTCTCTCGGCT	43		
	singleton	S314	1	AGCAACATGAGGGGGGATAGAGGGGGGTGGGTTCTCTCGGCT	43		
	singleton	S316	1	AGCAACATNAGGGGGGATNAGGGGGGTGGGTTCTCTCGGCT	42		
	singleton	S321	1	AGCAACAATGAGGGGGGATGAGGGGGGTGGGTTCTCTCGGCT	42		
	singleton	S326	1	AGCAACATNAGGGGGGATNAGGGGGGTGGGTTCTCTCGTCT	42		
	singleton	S330	1	AGCAACATAGAGGGGGATAGAGGGGTGGGTTCTCTCGGACT	42		
	singleton	S334	1	AGCAACATGAGGGGGGATGAGGGGGGTGGGTTCTCTTGCT	42		
	singleton	S336	1	AGCAACATNAGGGGGGATAGAGGGGGGTGGGTTCTCTCGGCT	42		
	singleton	S339	1	AGCAACATGAGGGGGGATAGAGGGGGGTGGGTTCTCTCGGCT	42		
	singleton	S346	1	AGCAACATGAGGGGGATAGAGGGGGGTGGGTTCTCTCGGCT	42		
	singleton	S355	1	AGCAACATNAGGGGGGATGAGGGGGGTGGGTTCTCTCGGCC	41		
	singleton	S359	1	CGCAACATGAGGGGGGATAGAGGGGGGTGGGTTCTCTCGGCT	41		
	singleton	S360	1	AGCAACATGAGGGGGGATAGGGGGGGTGGGTTCTCTCGGCT	41		
	singleton	S367	1	AGCAACATGAGGGGGGATAAGGGGGGTGGGTTCTCTCGGCT	41		
	singleton	S368	1	AGCAACATNAGGGGGGATNAGGGGGGTGGGTTCTCTCGTCT	41		
	singleton	S389	1	AGCAACATGAGGGGGATGAGGGGGGTGGGTTCTCTCGGCT	41		
	singleton	S397	1	AGCAACATGAGGGGGATAGAGGGGGGTGGGTTCTCTCGGCT	41		
	singleton	S405	1	AGCAACATNAGGGGGGATNAGGGGGGTGGGTTCTCTCGACT	41		
	singleton	S406	1	AGCAACATGAGGGGGGATAGAGGGGGGTGGGTTCTCTCGGTT	41		
	singleton	S412	1	AGCAACATGAGGGGGGATAGAGGGGGGTGGGTTCTCTTGCT	41		
	singleton	S421	1	AGCAACATNAGGGGGGATAAGGGGGGTGGGTTCTCTCGGCT	41		
	singleton	S423	1	AGCAACATGAGGGGGGATGAGGGGGGTGGGTTCTCTCGGCT	41		
	singleton	S437	1	AGCAACATGAGGGGGATAGAGGGGGGTGGGTTCTCTCGGCT	41		
	singleton	S442	1	AGCAACATGAGGGGGATAGAGGGGGGTGGGTTCTCTCGACT	41		
	singleton	S451	1	AGCAACATGAGGGGGATAGAGGGGGGTGGGTTCTCTCGGCT	41		
	singleton	S455	1	AGCAACATGAGGGGGGATAGAGGGGGGTGGGTTCTCTCGACT	41		
	singleton	S464	1	GGCAACATGAGGGGGATAGAGGGGGGTGGGTTACTCTCAGCT	41		
	singleton	S489	1	AGCAACATNAGGGGGATGAGGGGGGTGGGTTCTCTCGGCT	40		
	singleton	S557	1	AGCAACATGAGGGGGATGAGGGGGGTGGGTTCTCTGGCT	40		
	singleton	S763	1	AGCAACATNAGGGGGGATAAGGGGGGTGGGTTCTCTCGGCT	40		
	singleton	S1010	1	AGCAACATNAGGGGGGATAAGGGGGGTGGGTTCTCTCAGCT	40		
	singleton	S1034	1	AGCAACATGAGGGGGATGAGGGGGGTGGGTTCTCTTGCT	40		
	singleton	S1047	1	AGCAACATGAGGGGGATGAGGGGGGTGGGTTCTCTCGGCC	40		
	singleton	S1060	1	AGCAACATGAGGGGGATGAGGGGGGTGGGTTCTCTCGGTT	40		
	singleton	S1064	1	AGCAACATGAGGGGGATTGAGGGGGGTGGGTTCTCTCGGCT	40		
	singleton	S1268	1	AGCAACATNAGGGGGATGAGGGGGGNGGGTTTCTCGGCT	39		
	singleton	S1270	1	AGCAACATGAGGGGGATAGAGGGGGGTGGGTTCTCTCGGCT	39		
	singleton	S1312	1	AGCAACATGAGGGGGATGAGGGGGGTGGGTTCTCTCGGCT	39		
	singleton	S1328	1	AGCAACATGAGGGGGATGAGGGGGGTGGGTTCTCTCGTCT	39		
	singleton	S1329	1	AGCAACATNAGGGGNTAAGGGGGNGGGTTCTCTCGGCT	39		
	singleton	S1352	1	AGCAACATNAGGGGGATGAGGGGGGTGGGTTCTCTCGACT	39		
	singleton	S1386	1	AGCAACATGAGGGGGATAGAGGGGGTGGTCTCTCGGCT	38		
	singleton	S1387	1	AGCAACATNAGGGGGATGAGGGGGTGGTCTCTCGGCT	38		
	singleton	S1416	1	AGCAACATGAGGGGGATAGAGGGGGTGGTCTCTCGGCT	37		
group 2	* cluster	C10	20	GCGCACCACGGGAGTTGGCCACATTTGGAGTTGTTTTGTC	40	PA#14/89	PA-C10
	cluster	C21	12	GCGCACCACGGGAGTCGGCCACATTTGGAGTTGTTTTGTC	40		
	cluster	C51	7	GCGCACCACGGGAGTTGGCCACATTTGGAGTTGTTTTGTC	39		
	cluster	C52	7	GCGCACCACGGGAGTCGGCCACATTTGGAGTTGTTTTGTC	39		
	cluster	C60	6	GGGCACCACGGGAGTCGGCCACATTTGGAGTTGTTTTGTC	40		
	cluster	C77	5	GGGCACCACGGGAGTCGGCCACATTTGGAGTTGTTTTGTC	39		
	cluster	C86	4	GTGCACCACGGGAGTTGGCCACATTTGGAGTTGTTTTGTC	40		
	cluster	C99	4	GGGCACCACGGGAGTTGGCCACATTTGGAGTTGTTTTGTC	40		
	cluster	C142	3	GTGCACCACGGGAGTCGGCCACATTTGGAGTTGTTTTGTC	40		
	cluster	C156	2	GCGCACCACGGGAGTCGGCCACATTTGGAGTTGTTTTGTC	41		
	cluster	C187	2	GGGCACCACGGGAGTCGGCCACATTTGGAGTTGTTTTGTC	40		
	cluster	C280	2	GCGCACCACGGGAGTCGGCCACATTTGGAGTTGTTTTGTC	39		
	singleton	S333	1	GCGCACCACGGGAGTCGGCCACATTTGGAGTTGTTTTGTC	42		
	singleton	S401	1	GCGCACCACGGGAGTTGGCCACATTTGGAGTTGTTTTGTC	41		
	singleton	S428	1	GCGCACCACGGGAGTCGGCCACATTTGGAGTTGTTTTGTC	41		
	singleton	S449	1	GCGCACCACGGGAGTCGGCCACATTTGGAGTTGTTTTGTC	41		
	singleton	S481	1	GCGCACCACGGGAGTTGGCCACATTTGGAGTTGTTTTGTC	40		
	singleton	S581	1	GCGCACCACGGGAGTTGGCCACATTTGGAGTTGTTTTGTC	40		
	singleton	S894	1	GGGGCACCACGGGAGTCGGCCACATTTGGAGTTGTTTTGTC	40		
	singleton	S916	1	GGGCACCACAGGAGTCGGCCACATTTGGAGTTGTTTTGTC	40		
	singleton	S1125	1	ACGCACCACGGGAGTTGGCCACATTTGGAGTTGTTTTGTC	40		
	singleton	S1281	1	GCGCACCACGGGAGTTGGCCACATTTGGAGTTGTTTTGTC	39		
	singleton	S1314	1	GTGCACCACGGGAGTTGGCCACATTTGGAGTTGTTTTGTC	39		

group (size ≥15 seq.)	non-redundant NGS pool (1. clustering)			aptameric sequence (5' → 3')	length of intern region (nt)	aptamer from Sanger pool identified	new aptamer
	cluster or singleton	name	no. seq.				
				ATACCAGCTTATTC AATT ---- intern region ---- ACAATCGTAATCAGTTAG			
group 3							
	* cluster	C3	48	GCAGTACTGATGAGTGTAGCCGTATGATTATCGTTTGTGG	40	PA#4/22	
	cluster	C12	17	GCAGTACTGATGAGTGTAGCCGTATGATTANCGTTTGTGG	40		
	cluster	C229	2	GCAGTACTGATGAGTGTAGCCGTATGATTATCGTTTGTGC	40		
	cluster	C238	2	GTAGTACTGATGAGTGTAGCCGTATGATTATCGTTTGTGG	40		
	singleton	S327	1	GCGAGTACTGATGAGTGTAGCCGTATGATTACTCGTTTGTGG	42		
	singleton	S383	1	GCAGTACTGATGAGTGTAGCCGTATGATTATCGTTTGTCCG	41		
	singleton	S462	1	GCAGTACTGATGAGTGTAGCCGTATGATTATCGTTTGTGG	41		
	singleton	S522	1	GCAGTACTGATGAATGTAGCCGTATGATTATCGTTTGTGG	40		
	singleton	S624	1	GGAGTACTGATGAGTGTAGCCGTATGATTATCGTTTGTGG	40		
	singleton	S743	1	GCAGTACTGATGAGTGTAGCCGTATGATTANCGTTTGTGC	40		
	singleton	S1303	1	GCAGTACTGATGAGTGTAGCCGTATGATTANCGTTTNTG	39		
group 4							
	* cluster	C0	56	CCCCAACGAGTCGATATGTAGCCACACTCTGATTCTGCTCC	40	PA#4/34	
	cluster	C57	6	ACCCAACGAGTCGATATGTAGCCACACTCTGATTCTGCTCC	40		
	singleton	S297	1	CCCCAACGAGTCGATAATGTAGCCACACGCTCTGATTCTGCTCA	44		
	singleton	S651	1	CCCTAACGAGTCGATATGTAGCCACACTCTGATTCTGCTCC	40		
	singleton	S782	1	CCCCAATGAGTCGATATGTAGCCACACTCTGATTCTGCTCC	40		
	singleton	S815	1	CCCCAACGAGTCGATATGTAGCTCACACTCTGATTCTGCTCC	40		
	singleton	S967	1	CCCCAACGAGTCGATATGTAGCCACACTCTGATTCTGTAC	40		
	singleton	S1004	1	GCACAACGAGTCGATATGTAGCCACACTCTGATTCTGCTCC	40		
	singleton	S1172	1	CCCCAACGAGTCGATATGTAGCCACACTCTGATTCTGCCCC	40		
	singleton	S1304	1	CCCAACGAGTCGATATGTAGCCACACTCTGATTCTGCTCC	39		
group 5							
	* cluster	C2	52	GGAGACGACAAACTATTACGTACTACGGCATGCACCTTGGT	40	PA#2/11	
	singleton	S578	1	GGAGACGACAAACTATTACGTACTACGGTATGCACCTTGGT	40		
	singleton	S738	1	GGAGACGACAAACTATTACGTACTACGGCATGCACCTTGGT	40		
	singleton	S742	1	GCAGACGACAAACTATTACGTACTACGGCATGCACCTTGGT	40		
	singleton	S927	1	GGAGACGACAAACTATTACGTACTACGGCATACACTTGGT	40		
	singleton	S1185	1	GTAGACGACAAACTATTACGTACTACGGCATGCACCTTGGT	40		
group 6							
	* cluster	C8	22	AGGCCAGATGAGGGGTGCCATGCGGGGTGGCTGCTCCA	40		PA-C8
	cluster	C61	6	AGGCCAGATGAGGGGTGCCATGCGGGGTGGCTGCTCCA	40		
	cluster	C108	4	AGGCCAGATGAGGGGTGCCATGCGGGTGGCTGCTCCA	38		
	cluster	C151	3	AGGCCAGATGAGGGGTGCCATGCGGGGTGGCTGCTCCA	39		
	cluster	C282	2	AGGCCAGATNAGGGGTGCCATGCGGGTGGCTGCTCC	37		
	cluster	C284	2	AGGCCAGATGAGGGGTGCCATGCGGGTGGCTGCTCCA	37		
	singleton	S311	1	AGGCCAGATGAGGGGTGCCATGCGGGGTGGGTGCTCCA	43		
	singleton	S534	1	AGGCCAGATGAGGGGTGCCATGCGGGGTGGCTGCTCCA	40		
	singleton	S1372	1	AGGCCAGATGAGGGGTGCCATGCGGGGTGGCTGCTCCA	39		
	singleton	S1395	1	AGGCCAGATNAGGGGTGCCATGCGGGTGGCTGCTCCA	38		
	singleton	S1408	1	AGGCCAGATGAGGGGTGCCATGCGGGTGGCTGCTCCA	37		
group 7							
	* cluster	C5	33	CCACAACCGAACTCGTAAGACGTATGTAGCCGCCAACTGT	40	PA#14/82	
	cluster	C201	2	CGACAACCGAACTCGTAAGACGTATGTAGCCGCCAACTGT	40		
	singleton	S294	1	CCACAACCGAACTCGTAAGACGTATGTAGCCGCCACTTTGATTCC	45		
	singleton	S408	1	CCACAACCGAACTCGTAAGACGTATGTAGCCGCCAACTGT	41		
	singleton	S667	1	CCACAACCGAACTCATAAGACGTATGTAGCCGCCAACTGT	40		
	singleton	S1063	1	CCACAACCGAACTCGTAAGACGTATGTAGCCGCCAACTGT	40		
group 8							
	* cluster	C6	28	CGACAAGTGGGCATTACGATTCTAGCCCTGATTATGTTCC	40	PA#2/3	
	cluster	C68	5	CGACAAGTGGGCATTACGATTCTAGCCCTGATTANGTTCC	40		
	singleton	S343	1	CGACAAGTGGGCATTACGATTCTAGCCCTGATTATGTTCC	42		
	singleton	S347	1	CGACAAGTGGGCATTACGATTCTAGCCCTGATTATGTTCC	41		
	singleton	S363	1	CGACAAGTGGGCATTACGATTCTAGCCCTGATTATGTTCC	41		
	singleton	S375	1	CGACAAGTGGGCATTACGAATCTAGCCCTGATTATGTTCC	41		
	singleton	S611	1	CGACAAGTGGGCATTATGATTCTAGCCCTGATTATGTTCC	40		
	singleton	S1006	1	CGACAAGTGTGCATTACGATTCTAGCCCTGATTATGTTCC	40		
group 9							
	* cluster	C9	22	ACCGAGGAGATAACGTTGTAGCCGTCCATCATCTGATTCCG	40	PA-C9	
	singleton	S446	1	ACCGAGGAGATAACGTTGTAGCCGTCCATCAGTCTGATTCCG	41		
	singleton	S751	1	ACCGAGGAGATAACGTTGTAGCTGTCCATCATCTGATTCCG	40		
group 10							
	* cluster	C14	15	ACCGATCACTAGCCGACTAATTGGTTTCCGATCGCAGTCC	40	PA#2/6	
	cluster	C147	3	ACCGATCACTAGCCGACTAATTGGTTTCCGATCGCAGTCC	39		
	cluster	C260	2	ACCGATCACTAGCCGACTAATTGGTTTCCGATTGCACTCC	40		
	singleton	S576	1	ACCGATCACTAGCCGACTAATTGGTTTCCGATCGCAGTCT	40		
	singleton	S1289	1	ACCGATCACTAGCCGACTAATTGGTTTCCGATCGCACTCC	39		
group 11							
	* cluster	C11	19	CGATGGAGCTGATGATTGTTGCCGATCTGACTGTTGTTCC	40	PA-C11	
	cluster	C266	2	CGATGGAGCTGATGATTGTTGCCGATCTGACTGTTGTTCC	39		
	singleton	S342	1	CGATGGAGCTGATGATTGTTGCCGAGTCTGACTGTTGTTCC	42		
group 12							
	* cluster	C13	17	CCCCTAACGTTACTGGATGTAGTCCGACTAACTTATGCGT	40	PA-C13	
	singleton	S574	1	CCCCTAACGTTACTGGATGTAGTCCGACTAACTTATGCGT	40		
	singleton	S779	1	ACCCTAACGTTACTGGATGTAGTCCGACTAACTTATGCGT	40		

group (size ≥15 seq.)	non-redundant NGS pool (1. clustering)			aptameric sequence (5' → 3')	length of intern region (nt)	aptamer from Sanger pool identified	new aptamer
	cluster or singleton	name	no. seq.				
group 13				ATACCAGCTTATTCAATT ---- Intern region ---- ACAATCGTAATCAGTTAG			
	* cluster	C42	7	GCAGATTACGCCTTGTAGCCCGCACTGATCTCGATGTTTGG	41		PA-C42
	cluster	C158	2	GCAGATTACGCCTTGTAGCCCGCACTGATCTCGANGTTTGG	41		
	singleton	S320	1	GCAGATTACGCCTTGTAGCCCGCACTGATCTCGATGTTTGG	42		
	singleton	S370	1	GCAGATTACGTCCTTGTAGCCCGCACTGATCTCGATGTTTGC	41		
	singleton	S379	1	GCAGATTACGTCCTTGTAGCCCGCACTGATCTCGATGTTTGG	41		
	singleton	S385	1	ACAGATTACGCCTTGTAGCCCGCACTGATCTCGATGTTTGG	41		
	singleton	S394	1	GCAGATTACGCCTTGTAGCCCGCACTGATCTCGANGTTTGC	41		
	singleton	S413	1	GCAGATTACGCCTTGTAGCCCGCACTGATCTCGATGTTTGC	41		
	singleton	S431	1	GCAGATTACGCCTTGTAGCCCGCACTGATCTCGATGTCTGG	41		
group 14							
	* cluster	C16	13	CCCACGAGTGTAGCCGATTCTTCTGTACTCTTGTCCTCGT	40		PA-C16
	singleton	S291	1	GCAGTACTGATGAGTGTAGCCGATTCTTCTGTACTCTTGTCCTCGT	46		
	singleton	S467	1	CCCACGAGTGTAGCCGATTCTTCTGTACTCTTGTCCTCGT	41		
group 15							
	* cluster	C15	14	ACGTGTTGTAGCCGACCCCTGTTGATTGTTTTCCTGTACC	40		PA-C15
	singleton	S1409	1	ACGTGTAGCCGACCCCTGTTGATTGTTTTCCTGTACC	37		
no. groups 15		no. clstr 60	no. clstr seq. 677				
		no. singleton 113	no. singleton 113				
			sum seq. 790				

* = representative clusters of the groups
cluster = clustered identical sequences after the 1. clustering
singleton = orphans after the 1. clustering