Supplemental Table 2: Human 5' transducing SVAs

A. 5' transducing SVAs without source element: 62 transduction groups

Locus name	Position	TSD	length of 5'TD	Source locus
H1_50	chr1:33,108,165-33,110,530	GAAACCCTCCC	38bp	chr9:131,447,797-131,447,834
H1_108	chr1:91,068,764-91,070,156	AAATGAAAAGCA	1428bp	chrX:71,678,407-71,717,145
H1_147	chr1:143,156,103-143,158,108	AAGAAAAAGAGTACTTTG	293bp	chr20:61,755,720-61,756,011
H1_199	chr1:175,835,497-175,837,558	ACAAAAATT	301bp	chr8:81,246,552-81,246,842
H1_243	chr1:220,594,613-220,596,170	TGTTCTAAAATGGATT	26bp	chr17:41,010,350-41,010,375
H1_252	chr1:227,570,340-227,571,551	AAAGTATTAAAAAAA	172bp	chr22:22,188,846-22,189,017
H2_332	chr2:50,966,414-50,968,074	ATAAATAAAAACATTA	481bp	chr20:5,026,788-5,041,703
H2_402	chr2:152,841,731-152,843,536	CATTATATA	151bp	chr17:54,613,476-54,613,626
H2_423	chr2:175,797,762-175,799,423	TGTGTATG	47bp	chr7:23,406,390-23,406,436
H3_550	chr3:58,509,831-58,511,877	AACATTATC	447bp	chr6:56,878,393-56,879,234
H3_600	chr3:125,567,739-125,570,586	AGAAATACAATAAAATA	30bp	chr3:178,415,437-178,415,466
H3_606	chr3:130,155,185-130,157,734	AGAAAGA	33bp	chr4:40,177,717-40,177,749
H3_664	chr3:198,816,907-198,818,417	AAAAAAGATCTTC	26bp	chr5:134,825,929-134,825,954
H4_750	chr4:109,687,541-109,689,393	AAACAGCTGG	54bp	chr15:55,397,918-55,397,971
H5_815	chr5:18,344,828-18,346,608	TAAAAATAAAA	200bp	chr20:11,401,284-11,401,485
H5_848	chr5:55,369,855-55,371,191	AAGAGGCTA	130bp	chr20:3,147,827-3,147,964
H5_859	chr5:65,271,094-65,272,916	AAAGAACAATAC	33bp	chr9:87,291,456-87,291,487
H5_906	chr5:116,365,359-116,366,529	AAAACACTCTATT	172bp	chr7:100,308,816-100,309,139
H5_961	chr5:179,194,006-179,195,302	TAAGAAC	434bp	chr4:40,509,748-40,510,180
H6_1026	chr6:52,627,749-52,629,732	AAAGAAATACCTGAG	129bp	chr9:128,439,499-128,439,627
H6_1076	chr6:112,474,967-112,476,268	aGAAAATATCCCTATCTT	40bp	chr6:44,333,571-44,333,609
H7_1125	chr7:4,436,183-4,437,789	AAAGAAAACTG	24bp	chr6:30,863,694-30,863,716
H7_1139	chr7:22,858,156-22,860,275	TAAAAATAAAAAATTT	144bp	chr14:35,013,275-35,013,431
H7_1189	chr7:72,141,946-72,144,008	AAAAAGAAAAAGCAG	1-242	chr12:100,757,853-100,758,094
			244-283	chr4_random:208,290-208,329
H7_1226	chr7:127,810,015-127,811,750	AACAAAGAGTATT	25bp	chr1:199,581,697-199,581,720
H8_1307	chr8:55,200,220-55,201,572	AGAAAGCGCTAAAAGT	521bp	chr5:55,412,944-55,413,464
H8_1326	chr8:70,319,763-70,321,665	AAGAAtA	87bp	chr17:70,603,805-70,603,893
H9_1377	chr9:15,223,322-15,225,070	AAAACAGA	636bp	chr11:125,248,719-125,262,555
H9_1407	chr9:72,684,055-72,686,820	ATATATACCATTTTA	85bp	chr14:77,442,750-77,442,832
H9_1450	chr9:107,617,231-107,620,133	TAAAAATATTTTGTA	37bp	chr2:85,249,161-85,249,196
H9_1453	chr9:111,481,739-111,484,494	TAAATGTAAAACTAG	36bp	chr11:74,549,271-74,549,306
H9_1457	chr9:120,146,218-120,147,644	AAAGGTAGTAAGGATTA	31bp	chr19:4,578,220-4,578,250
H10_1490	chr10:9,354,522-9,355,945	GGCAGAATT	110bp	chr17:40,927,043-40,927,151
H10_1495	chr10:17,710,351-17,712,006	AAGATTTGTTATAAAGC	1-2125	chr20:19,682,979-19,685,096
			2126-2161	chr20:19,680,307-19,680,341
H10_1510	chr10:34,681,263-34,682,697	TCTTCAACA	32bp	chr2:32,368,923-32,368,953
H10_10	chr10:43,238,131-43,238,827	AAAAaTTTAATCTG	32bp	chr6:111,582,461-111,582,493
H10_1535	chr10:61,125,831-61,127,557	AAGATCAGAGGC	32bp	chr17:8,153,945-8,153,976
H10_1585	chr10:104,877,792-104,880,321	AAGTTTAGA	300bp	chr3:12,839,760-12,840,059
H10_1606	chr10:135,116,300-135,117,599	ACACAAAGAAATGAG	27bp	chr12:97,500,884-97,500,909
H11_A110	chr11:86,120,219-86,121,843	AAAAAGAATTAACACTA	25bp	chr16:8,143,117-8,143,141

H11_A113	chr11:89,232,811-89,234,434	AAAAATTTT	91bp	chr12:31,844,966-31,845,056
H12_A226	chr12:68,439,039-68,440,483	AAAGGAATGAACACACAGA	42bp	chr17:37,513,634-37,513,675
H13_A299	chr13:24,951,631-24,953,345	AAGAATCATACA	225bp	chr8:128,717,098-128,717,320
H13_A335	chr13:49,064,273-49,066,383	AAATGACTAGTC	1-201	chr21:29,307,409-29,307,609
			203-229	chr17:38,756,400-38,756,426
H13_A338	chr13:51,535,166-51,537,277	AAAAAAAAATGACCC	84bp	chr8:21,515,458-21,515,540
H14_A369	chr14:20,043,334-20,045,637	AAATTTTC	823bp	chr10:135,032,793-135,033,803
H14_A370	chr14:20,726,258-20,727,481	AAAAATGCACTTGTCACA	1-58	chr22:16,858,715-16,858,772
			59-290	chr22:22,056,356-22,058,467
H14_A405	chr14:56,869,527-56,870,945	AAAAAAGTTTCATC	510bp	chr6:42,228,585-42,229,093
H14_A428	chr14:72,719,756-72,722,099	AAAAATACAAAAATT	78bp	chr1:200,034,501-200,034,576
H15_A522	chr15:87,284,977-87,286,979	AAACCACACCACT	571bp	chr5:64,439,311-64,439,880
H16_A537	chr16:2,389,313-2,390,820	AAACAGAATA	38bp	chr11:43,908,421-43,908,458
H16_A580	chr16:46,649,945-46,651,082	AAAAATTCTACTCTA	530bp	chr16:70,281,923-70,315,283
H16_A588	chr16:52,288,736-52,290,819	TTGGTATTTTCC	400bp	chr1:27,228,194-27,228,590
H16_A591	chr16:55,791,322-55,793,404	AGAAATTTCACTGATA	323bp	chr17:45,831,131-45,831,453
H17_1710	chr17:22,562,587-22,564,480	AAATTCACATGGCA	1705bp	chr22:16,866,040-16,881,647
H18_1810	chr18:14,000,002-14,001,906	AGAAAAAAAATTCT	27bp	chr12:115,566,222-115,566,248
H18_1838	chr18:66,387,233-66,388,552	AGAGAAAAAGAAAATA	30bp	chr6:111,364,673-111,364,701
H19_38	chr19:20,503,705-20,506,000	AAAATCAACAACA	56bp	chr3:129,867,196-129,867,251
H21_1940	chr21:45,068,392-45,070,316	AAAAAGTGGTAAAGGGG	53bp	chr6:42,174,244-42,174,296
H22_1951	chr22:20,561,787-20,563,670	AAAAATTAGC	1187bp	chr18:11,880,989-11,898,316
H22_1987	chr22:41,470,434-41,471,807	GAAAATTAG	30bp	chr17:62,734,737-62,734,766
HX_2012	chrX:30,379,304-30,381,674	AAATAAAGT	1-945	chr16:66,585,466-66,603,434
			947-1120	chr17:3,316,557-3,316,730

B. 5' transducing SVAs with source element: 15 transduction groups

Locus name	Position	TSD	length of 5'TD	Source locus	Source Element
H2_393	chr2:135,623,922-135,626,159	ACAACATTTT	52bp	chr6:106,409,517-106,409,568	chr6:106,407,679-106,409,516
H2_413	chr2:170,187,021-170,188,485	AAAACTTCAGTTTTC	252bp	chr14:30,992,232-30,996,421	chr14:30,975,716-30,977,187
H3_623	chr3:144,287,158-144,289,178	AAAAATTATCCAGGA	98bp	chr6:76,209,216-76,209,313	chr6:76,207,424-76,209,215
H5_898	chr5:107,921,994-107,923,775	AAAACTTTATTGTC	39bp	chr1:222,610,417-222,610,455	chr1:222,608,735-222,610,416
H7_1117	chr7:850,174-853,069	AAAAAAAATCC	607bp	chr2:128,263,471-128,284,954	chr2:128,260,655-128,263,470
H8_1357	chr8:129,199,251-129,200,814	AGGAGTAAAG	147bp	chr10:69,120,430-69,120,576	chr10:69,120,622-69,122,520
H8_1360	chr8:134,838,293-134,840,486	AAAACAACACGCATTTA	110bp	chr17:39,670,185-39,670,287	chr17:39,670,289-39,672,495
H10_1571	chr10:95,719,811-95,721,374	AAAAATGGCAAAGT	22bp	chr20:36,440,113-36,440,134	chr20:36,440,246-36,442,002
H11_A8	chr11:5,911,795-5,913,047	AAAAAGTTCCGTTATC	250bp	chr19:52,203,731-52,204,198	chr19:52,204,180 - 52,205,744
H11_A60	chr11:60,338,548-60,340,458	ATCCCAAGTA	191bp	chr22:16,414,673-16,414,862	chr22:16,414,863-16,416,304
H14_A393	chr14:44,927,945-44,929,805	AAAGACAAAAGG	33bp	chr17:23,807,623-23,807,655	chr17:23,806,548-23,807,622
H19_132	chr19:45,845,099-45,847,858	TAAAAATACAAAAA	881bp	chr15:38,760,679-38,761,563	chr15:38,761,549-38,763,760
H19_153	chr19:50,842,212-50,844,334	AAAAATATTTTG	390bp	chr10:73,300,276-73,301,023	chr10:73,298,405-73,300,291
H19_76	chr19:58,380,982-58,383,779	AAAAAAAACAAAAACCC	50bp	chr10:43,238,004-43,238,053	chr10:43,238,007-43,238,853
H22_1972	chr22:35,010,984-35,012,242	AAAAGACAGTCAAACC	290bp	chr1:35,103,030-35,103,318	chr1:35,101,795-35,103,026

C. Transduction groups with 5' and 3' transductions: 4 transduction groups

5q13.1 TD group	Position	TSD	length of 5'TD/3'TD
SE H5_862	chr5:67,654,673-67,656,196	AGAAAAATCTACT	
H22_1982	chr22:40,014,486-40,016,867	AAACAAACA	26bp/626bp
H10_1601	chr10:123,951,509-123,953,742	AAAAGCTAAAGAAG	18bp/626bp
H11_A95	chr11:76,007,978-76,009,200	GAAATACCACTTCAT	5'trunc./626bp

6q24.3 TD group	Position	TSD	length of 5'TD/3'TD
SE H6_1095	chr6:148,540,962-148,542,603	AAATCCT	
H2_337	chr2:55,788,767-55,790,702	AACAATAACCTTCA	127bp/82bp
H5_884	chr5:80,274,796-80,275,515	AAAAAGTCCC	5'trunc./82bp

16p12.1 TD group	Position	TSD	length of 5'TD/3'TD
SE H16_A556	chr16:24,027,083-24,029,032	TAAAAGATTGGGGAC	
H4_712	chr4:53,943,893-53,946,593	AAAACAGTGACTTT	20bp/-
H7_1191	chr7:72,694,071-72,696,486	AAGAAATTC	20bp/116bp

22q13.31 TD group	Position	TSD	length of 5'TD/3'TD
SL	chr22:43,490,894-43,491,027		
H7_1123	chr7:2,346,240-2,348,354	ATTTCCAAAAAGG	88bp/85bp
H15_A479	chr15:45,211,168-45,213,833	AAAAATTTATATTCTG	-/85bp

D. Multimember transduction groups: 11

ZNF487 TD group	Position	TSD	length of 5'TD
SL (3'more)	chr3:161,871,969-161,872,000	MER94 AcHobo	32bp
SL2 (5'more)	chr10:43,252,580-43,252,716	ZNF 487 exon 1	137bp
H13_A311	chr13:34,011,892-34,013,880	AAGAAAGATTTGGTTT	27bp
H11_A16	chr11:17,027,686-17,029,817	AAGAAAAAGTTTATCCT	71bp
H13_A290	chr13:20,919,315-20,921,398	TAAACAACCA	92bp
H2_425	chr2:178,634,878-178,638,058	TAAAATCTTAATTTTA	136bp
H7_1194	chr7:76,782,330-76,784,571	AAAAAATGGT	170bp

5q31.2 TD group	Position	TSD	length of 5'TD
SL	chr5:138,903,956-138,903,986		
HX_2029	chrX:45,890,313-45,892,368	AAAAAGACAAATGACCC	31bp
H11_A81	chr11:71,890,184-71,892,345	AAAAGCTAATCCACCAC	16bp

6p21.2 TD group	Position	TSD	length of 5'TD	secondary transductions
SL	chr6:37,014,677-37,014,915			
H2_444	chr2:198,385,633-198,387,904	AAAGAATATACC	204bp	
H3_528	chr3:46,509,953-46,512,240	AGAGAAATCCTTCTT	360bp	2nd SL 1-151
				chr14:67,100,537-67,100,677
H3_545	chr3:51,866,497-51,868,749	AAAGAAGTTTAAGAAGACCTA	438bp	2nd SL 1-222
				chr17:17,757,536-17,816,41
H6_1049	chr6:74,426,240-74,428,436	AAAAATGG	239bp	
H12_A247	chr12:99,189,759-99,192,264	ACATGTAA	209bp	
H14_A408	chr14:62,701,052-62,703,319	AAATAGT	201bp	
H17_1694	chr17:17,755,676-17,757,544	AAAAGAATTTCCA	216bp	
HX_2039	chrX:50,854,967-50,856,900	AAAAAGTTAAATA	137bp	

10q26.11 TD group	Position	TSD	length of 5'TD
SE H10_1594	chr10:120,930,788-120,932,744	AAAAGAAAATCCTG	
H11_A19	chr11:18,097,944-18,100,174	AAAGAAAAATCTTTC	593bp
H9_1416	chr9:77,604,198-77,607,638	AAAAACAAAGGAAAAGGT	553bp

11q24.3 TD group	Position	TSD	length of 5'TD
SL	chr11:129,212,291-129,212,322		
H3_2	chr3:15,178,506 – 15,180,806	CAAATTGGCCTTTTG	30bp
H1_3	chr1:26,605,984-26,608,163	GTTAATATGTG	24bp
H19_142	chr19:62,685,545 – 62,687,083	AAAAATTC	24bp

12p11.21 TD group	Position	TSD	length of 5'TD	secondary transductions
SL	chr12:32,066,635-32,066,763	LTR9B		
H13_A331	chr13:48,849,403-48,851,876	AAACAAAAACAGT	110bp	
H6_1084	chr6:123,210,609-123,213,299	AAAAGAATACAAAATA	130bp	
H21_1924	chr21:17,585,678-17,587,446	AAGAATACTGAATA	135bp	2nd SL 1-91
				chr17:18,764,906-18,764,996

15q21.3 TD group	Position	TSD	length of 5'TD	secondary transductions
SL	chr15:56,654,055-56,654,126	MER96B		
H12_A218	chr12:64,813,903-64,816,159	GAAAATGGTATTAATA	21bp	
H2_445	chr2:198,612,216-198,614,560	AAGAATTTATCAATCA	128bp	2nd SL: 1-41
				chr7:139,804,950-139,804,990
H7_1178	chr7:63,759,958-63,762,223	AAGAATTTTATTTTA	24bp	
H16_A603	chr16:68,795,305-68,797,376	n/a	38bp	

16p13.3 TD group	Position	TSD	length of 5'TD
SL	chr16:3,354,093-3,354,136	MER51A	
H4_694	chr4:39,964,755-39,966,398	AGAGAATAAGTGCA	34bp
H14_A420	chr14:66,081,027-66,083,346	GAAAGGCTTGCATTC	33bp
H3_493	chr3:8,455,646-8,457,946	AAAAGATGAATGATG	35bp
H14_A409	chr14:63,058,346-63,060,243	AAAAATTAATTTGATGAG	46bp
H9_1394	chr9:34,126,761-34,128,807	AAAAATTAGCCAGGTGTGG	33bp
H11_A59	chr11:60,145,392-60,147,717	n/a	31bp
H2_285	chr2:15,701,574-15,703,814	AAAACAAGTCTGGGG	23bp

17p13.3 TD group	Position	TSD	length of 5'TD
SL	chr17:7,710,534-7,729,417	spliced RNA	
H10_1542	chr10:69,708,744-69,710,073	ATAAATTACCTAGTCTC	320bp
H6_1088	chr6:131,164,268-131,166,174	AACAATATTAAG	385bp
H8_1264	chr8:912,589-913,991	TTTTCT	313bp

RHOT1 TD group	Position	TSD	length of 5'TD
SE H17_1725	chr17:27,529,349-27,531,779	AAATAATAAATGC	
H13_A287	chr13:18,307,928-18,309,913	AAAAGATAAGTTC	491bp
H18_1811	chr18:14,212,333-14,215,655	AAAAGATAAGTTC	530bp
H21_1922	chr21:14,228,445-14,231,191	AAAAGATAAGTTC	530bp

GA repeat family	Position	TSD	length of 5'TD
SE H2_358	chr2:85,625,806-85,627,844	TTGGAAAGGCT	
H1_GA4	chr1:7,594,812-7,596,497	n/a	106bp
H1_86	chr1:50,558,519-50,560,276	AAGAAATGTCTATTC	116bp
H2_371	chr2:105,325,496-105,327,153	TAAAATACTGCTGCCG	27bp
H6_1070	chr6:108,230,451-108,231,991	AAGAGCATTGGCTC	85bp
H11_A15	chr11:16,884,333-16,886,428	AAGTTAAAATGAGGTA	75bp
H20_1915	chr20:51,903,526-51,905,201	AAGACAGAAACAAG	158bp

Transduction events involving spliced cellular RNAs are highlighted in yellow. TD - transduction; SL - source locus; SE - source element
Positions of all elements are given for hg17, May 2004