Table S1.
Enzymes' efficiency at sampling CpG islands.
The table divides the CpG islands based on the type of genomic elements with which they are overlapping. The "sampled" columns show how many CpG islands in a given group contain at least one enzyme recognition motif i.e. theoretically, how many members of the group of CpG islands will a specific endonuclease be able to cleave. The columns labeled "[%]" which immediately follow the "sampled" columns, show the percentage of all CpG islands belonging to a specific sub group that have at least one enzyme recognition site, or showing the theoretical capacity or efficiency for an enzyme to cleave the sequences of the particular sub-category of CpG islands. Analogously, the "failed" columns show how many CpG islands do not contain the enzyme recognition motif, which is shown in relative terms in the column labeled [%] immediately following the "failed" column.
The ability of enzymes to cleave particular subgroups of CpG island in the "sampled" colums, i.e. the sampling efficiency for an enzyme, is shown with respect to AciI and HHaI enzymes (used in a single buffer, and thus the numbers in "sampled" columns indicate whether a CpG island contained either AciI or HHaI motif), McrBC, and, collectively, for all three enzymes.

Table S2.
A compilation of observations about ages of lineages within families of repetitive elements.
A) MaLR
B) Alu
C) SVA
D) L1PA

Table S3.
A summary of an enrichment analysis where a set of probes significantly differentiating tumors and non-tumor adjacent experiments was chosen using Wilcoxon non-parametric t.test and Benjamini-Hochenberg FDR correction to arrive at 15,587 probes. Probe categories defined by their proximity to a specific category of repetitive element were then checked for their enrichment in significant probes. The expected number is calculated based on the total number of probes in the array 339,314, and the total number of probes in a given category. The enrichment is then confirmed using hyper geometric test. Table sorted based on p-values, from most significant to least significant.

Table S4.
A compilation of annotation about the tissue samples analyzed in this manuscript. In addition to the self explanatory column names such as "id", "sex", "age" containing the appropriate information, "tob" indicates whether the patient admitted to heavy tobacco usage in their lifetime. "tob_quit" indicates whether at the time of the medical interview with the patient they indicated having quit smoking. Similarly, "etoh" and "etoh_quit" indicate whether the patient used alcohol, and became abstinent. The remainder of the table describes the pathology of the tumor samples, i.e. their diagnosis, location, hpv status, grade and stage.

Table S1.
Enzymes’ efficiency at sampling CpG islands.

CpG island near:	AciI & HhaI				McrBC[40-3000]				AciI & HhaI plus McrBC			
	sampled	**[%]**	**failed**	**[%]**	**sampled**	**[%]**	**failed**	**[%]**	**sampled**	**[%]**	**failed**	**[%]**
Gene	22065	99.84%	36	0.16%	22100	100.00%	1	0.00%	22101	100.00%	0	0.00%
LINE	34297	99.44%	193	0.56%	34485	99.99%	5	0.01%	34487	99.99%	3	0.01%
SINE	178849	99.45%	993	0.55%	179818	99.99%	24	0.01%	179840	100.00%	2	0.00%
LTR	22588	99.53%	106	0.47%	22692	99.99%	2	0.01%	22693	100.00%	1	0.00%
Satellite	993	99.50%	5	0.50%	998	100.00%	0	0.00%	998	100.00%	0	0.00%
DNA	8411	99.60%	34	0.40%	8441	99.95%	4	0.05%	8443	99.98%	2	0.02%
Other repetitive element	3988	99.97%	1	0.03%	3989	100.00%	0	0.00%	3989	100.00%	0	0.00%
tandem repeat	674	88.68%	86	11.32%	750	98.68%	10	1.32%	756	99.47%	4	0.53%
Unique, unclassified genomic sequence	65947	99.38%	409	0.62%	66338	99.97%	18	0.03%	66350	99.99%	6	0.01%
Total CpG Islands	**337812**	**99.42%**	**1863**	**0.58%**	**339611**	**99.98%**	**64**	**0.02%**	**339657**	**99.99%**	**18**	**0.01%**

Table S2A.
A compilation of observations about ages of lineages within families of repetitive elements.

Element Family	Element subfamily	Estimated age of appearance in the genome (MYA)	references
MaLR	**MLT1d**	100	Figure 4 in Smit, 1993
MaLR	**MLT1c**	85	Figure 4 in Smit, 1993
MaLR	**MLT1b**	80	Figure 4 in Smit, 1993
MaLR	**MLT1a**	77	Figure 4 in Smit, 1993
MaLR	**MSTb**	75	Figure 4 in Smit, 1993
MaLR	**MSTa**	60	Figure 4 in Smit, 1993
MaLR	**THE1c**	55	Figure 4 in Smit, 1993
MaLR	**THE1b**	50	Figure 4 in Smit, 1993
MaLR	**THE1a**	45	Figure 4 in Smit, 1993

Table S2B.
A compilation of observations about ages of lineages within families of repetitive elements.

Element Family	Element subfamily	Estimated age of appearance in the genome (MYA)	references
Alu	**FLA**	112	Table 3 in Kapitonov and Jurka, 1996
Alu	**Jo**	44, 81	Table 3 in Kapitonov and Jurka, 1996, Table S1 in Pace and Feschotte, 2007
Alu	**Jb**	42, 81	Table 3 in Kapitonov and Jurka, 1996, Table S1 in Pace and Feschotte, 2007
Alu	**S**	48	Table 3 in Kapitonov and Jurka, 1996
Alu	**Sx**	28, 37, 44, 55	Table 3 in Kapitonov and Jurka, 1996, Figure 2 in Batzer and Deininger, 2002, Table S1 in Pace and Feschotte, 2007, Table 2 in Xing et al. 2004
Alu	**Sg**	23, 31, 34, 40	Table 3 in Kapitonov and Jurka, 1996, Figure 2 in Batzer and Deininger, 2002, Table S1 in Pace and Feschotte, 2007, Table 2 in Xing et al. 2004
Alu	**Sq**	25, 39, 44	Table 3 in Kapitonov and Jurka, 1996, Table S1 in Pace and Feschotte, 2007, Table 2 in Xing et al. 2004
Alu	**Sp**	28, 37	Table 3 in Kapitonov and Jurka, 1996, Table 2 in Xing et al. 2004
Alu	**Sc**	22, 30, 35	Table 3 in Kapitonov and Jurka, 1996, Table S1 in Pace and Feschotte, 2007, Table 2 in Xing et al. 2004
Alu	**Sb**	19	Table 3 in Kapitonov and Jurka, 1996
Alu	**Y**	16, 35	Figure 2 in Batzer and Deininger, 2002, Table S1 in Pace and Feschotte, 2007
Alu	**Yd**	15	Table 2 in Xing et al. 2004
Alu	**Ye5**	12	Table 2 in Xing et al. 2004
Alu	**Yb8**	11	Figure 2 in Batzer and Deininger, 2002
Alu	**Ya5**	2, 11	Figure 2 in Batzer and Deininger, 2002, Table 2 in Xing et al. 2004
Alu	**Yc1**	2, 5	Figure 2 in Batzer and Deininger, 2002, Table 2 in Xing et al. 2004
Alu	**Ya5a2**	5	Figure 2 in Batzer and Deininger, 2002
Alu	**Yg6**	3	Table 2 in Xing et al. 2004
Alu	**Yb9**	2, 5	Figure 2 in Batzer and Deininger, 2002, Table 2 in Xing et al. 2004
Alu	**Ya8**	1	Table 2 in Xing et al. 2004

Table S2C.
A compilation of observations about ages of lineages within families of repetitive elements.

Element Family	Element subfamily	Estimated age of appearance in the genome (MYA)	references
SVA	**A**	10 - 17	Table 2 in Wang et al. 2005
SVA	**B**	11 - 12	Table 2 in Wang et al. 2005
SVA	**C**	10 - 11	Table 2 in Wang et al. 2005
SVA	**D**	9.4 - 9.5	Table 2 in Wang et al. 2005
SVA	**E**	2.4 - 4.5	Table 2 in Wang et al. 2005
SVA	**F**	2.7 - 3.6	Table 2 in Wang et al. 2005

Table S2D.
A compilation of observations about ages of lineages within families of repetitive elements.

Element Family	Element subfamily	Estimated age of appearance in the genome (MYA)	references
L1PA	**L1PA1**	3.1	Table 1 in Khan et al. 2006
L1PA	**L1PA2**	7.6	Table 1 in Khan et al. 2006
L1PA	**L1PA3**	12.5	Table 1 in Khan et al. 2006
L1PA	**L1PA4**	18.0	Table 1 in Khan et al. 2006
L1PA	**L1PA5**	20.4	Table 1 in Khan et al. 2006
L1PA	**L1PA6**	26.8	Table 1 in Khan et al. 2006
L1PA	**L1PA7**	31.4	Table 1 in Khan et al. 2006
L1PA	**L1PA8**	40.9	Table 1 in Khan et al. 2006
L1PA	**L1PA8A**	41.7	Table 1 in Khan et al. 2006
L1PA	**L1PA10**	46.4	Table 1 in Khan et al. 2006
L1PA	**L1PA11**	53.3	Table 1 in Khan et al. 2006
L1PA	**L1PA13B**	59.8	Table 1 in Khan et al. 2006
L1PA	**L1PA12**	59.7	Table 1 in Khan et al. 2006
L1PA	**L1PA13A**	59.9	Table 1 in Khan et al. 2006
L1PA	**L1PA14**	60.6	Table 1 in Khan et al. 2006
L1PA	**L1PA15**	70.5	Table 1 in Khan et al. 2006
L1PA	**L1PA16**	79.7	Table 1 in Khan et al. 2006
L1PA	**L1PA17**	101.1	Table 1 in Khan et al. 2006
L1PB	**L1PB1**	46.7	Table 1 in Khan et al. 2006
L1PB	**L1PB2**	58.2	Table 1 in Khan et al. 2006
L1PB	**L1PB3**	73.5	Table 1 in Khan et al. 2006
L1PB	**L1PB4**	96.0	Table 1 in Khan et al. 2006
L1MA	**L1MA1**	61.6	Table 1 in Khan et al. 2006
L1MA	**L1MA2**	65.8	Table 1 in Khan et al. 2006
L1MA	**L1MA3**	68.1	Table 1 in Khan et al. 2006
L1MA	**L1MA4**	102.3	Table 1 in Khan et al. 2006
L1MA	**L1MA5**	98.6	Table 1 in Khan et al. 2006

Table S3.
A summary of an enrichment analysis

category	# of probes significantly differentiating non-tumor adjacents and tumors (no pairs)	expected at random	enrichment	total number of probes in category	hyperGeometric p-val	# of genomic repeats	# of probed repeats
L1P	800	18.9	42	8,000	3.18E-151	1,589	8,681
L1	2913	452.8	6	52,747	8.70E-139	895,230	64,191
LINE	3699	829.7	4	76,107	2.08E-101	1,354,049	92,711
L1PA3	223	0.8	295	1,150	9.25E-96	10,281	1,146
AluY	3211	680.7	5	71,931	7.80E-48	135,761	72,224
SINE	7232	3,919.1	2	183,877	2.42E-39	1,744,457	245,936
L1PA2	121	0.3	382	888	1.06E-36	4,666	874
L1PA4	96	0.2	572	593	9.76E-36	11,462	602
L1M	1891	227.7	8	40,860	7.82E-34	11,466	50,879
Alu	6390	3,073.2	2	163,190	2.17E-28	1,160,276	205,535
LTR	1539	151.1	10	33,309	6.57E-27	641,720	40,016
L1HS	56	0.1	961	353	2.11E-21	1,696	357
L1PA5	47	0.1	812	418	1.73E-12	10,904	428
ERV1	619	24.2	26	13,292	7.68E-12	175,007	16,078
L1MC	449	12.6	36	9,506	9.72E-10	16,426	11,128
MaLR	663	29.0	23	14,865	1.60E-09	327,397	16,710
ERVL	287	4.9	59	5,763	9.40E-09	128,284	6,401
L1P1	21	0.0	2,247	151	2.34E-08	2,860	149
L1MA1	41	0.1	691	491	2.29E-07	3,940	525
L1PA7	31	0.0	1,019	333	4.86E-07	12,334	343
L1MCc	27	0.0	1,234	275	7.76E-07	6,889	340
L1ME3	170	1.7	103	3,304	1.16E-06	7,572	3,897
MLT1A	100	0.5	193	1,756	2.60E-06	8,650	1,929
U3	19	0.0	1,984	171	3.46E-06	228	103
L1MC3	55	0.1	411	826	4.84E-06	12,792	963

category	# of probes significantly differentiating non-tumor adjacents and tumors (no pairs)	expected at random	enrichment	total number of probes in category	hyperGeometric p-val	# of genomic repeats	# of probed repeats
L1MA9	47	0.1	506	671	5.48E-06	14,394	745
L2	1048	80.3	13	26,009	1.03E-05	403,973	27,360
LTR7	42	0.1	568	597	1.38E-05	2,349	610
L1PA16	39	0.1	625	543	1.62E-05	13,098	589
L1MD	160	1.5	104	3,250	2.34E-05	10,847	3,749
L1ME1	98	0.5	186	1,821	3.01E-05	26,938	2,131
L1ME3B	91	0.4	202	1,677	4.05E-05	27,528	1,993
L1MC1	49	0.1	437	777	5.63E-05	11,868	864
THE1D	34	0.0	704	482	6.96E-05	12,381	512
L1MA2	25	0.0	1,054	322	1.06E-04	6,911	347
L1M4	108	0.7	159	2,131	1.37E-04	19,504	2,520
L1PA15	28	0.0	884	384	1.43E-04	8,233	429
L1PB	70	0.3	268	1,264	1.43E-04	1,520	1,379
AluSc	504	18.0	28	12,148	1.88E-04	48,789	11,969
ERVK	53	0.1	372	911	2.35E-04	10,461	1,019
L1P4	23	0.0	1,116	304	2.67E-04	5,156	328
L1M4c	29	0.0	806	421	3.00E-04	7,787	504
L1MB1	21	0.0	1,257	270	3.05E-04	5,670	299
LTR2	46	0.1	440	771	3.11E-04	847	861
L1PA8	27	0.0	881	385	3.38E-04	7,715	405
MIR	1517	176.1	9	39,390	3.63E-04	584,181	40,401
L3	170	1.9	92	3,702	4.11E-04	47,228	3,473
L1MA6	17	0.0	1,593	213	6.72E-04	4,693	238
L1MA4A	21	0.0	1,170	290	7.97E-04	5,823	334
Tigger3b	26	0.0	875	388	8.30E-04	4,998	434
HERVH	25	0.0	917	370	8.89E-04	5,774	461
LTR33A	15	0.0	1,844	184	9.61E-04	3,521	174

category	# of probes significantly differentiating non-tumor adjacents and tumors (no pairs)	expected at random	enrichment	total number of probes in category	hyperGeometric p-val	# of genomic repeats	# of probed repeats
MLT1A1	23	0.0	1,019	333	9.71E-04	6,611	371
L1M2	29	0.0	749	453	9.82E-04	9,352	524
MER57A	20	0.0	1,229	276	9.95E-04	2,633	323
L1M4b	27	0.0	816	416	1.11E-03	7,423	504
L1MA4	42	0.1	463	733	1.15E-03	8,983	824
L1MA10	21	0.0	1,131	300	1.23E-03	5,419	313
Tigger1	45	0.1	422	805	1.35E-03	11,928	951
LTR33	38	0.1	517	656	1.49E-03	9,302	668
L1MCb	11	0.0	2,759	123	1.51E-03	2,863	147
MER94	17	0.0	1,475	230	1.61E-03	4,680	232
L1PA13	25	0.0	872	389	1.80E-03	10,722	410
MLT1E2	15	0.0	1,731	196	1.85E-03	3,960	213
L1PB1	30	0.0	683	497	2.09E-03	11,421	532
MER39	20	0.0	1,124	302	2.96E-03	3,125	339
AcHobo	56	0.2	311	1,092	3.05E-03	18,762	1,106
MLT1J	64	0.2	265	1,280	3.12E-03	15,375	1,332
L1ME3A	56	0.2	309	1,097	3.35E-03	16,330	1,269
L1MD1	27	0.0	752	451	3.53E-03	6,126	523
MER4D	16	0.0	1,482	229	3.67E-03	1,275	259
MER103	22	0.0	967	351	4.04E-03	6,812	348
MSTD	23	0.0	910	373	4.23E-03	7,421	412
LTR12_	11	0.0	2,406	141	4.67E-03	664	136
THE1C	20	0.0	1,064	319	5.52E-03	9,731	330
MLT1A0	51	0.2	335	1,014	6.23E-03	20,156	1,102
L1PA10	17	0.0	1,290	263	6.59E-03	6,962	271
MLT1J2	21	0.0	984	345	6.60E-03	7,867	331
L1MD2	44	0.1	395	858	7.07E-03	12,388	990

category	# of probes significantly differentiating non-tumor adjacents and tumors (no pairs)	expected at random	enrichment	total number of probes in category	hyperGeometric p-val	# of genomic repeats	# of probed repeats
L1MA8	29	0.0	650	522	7.63E-03	9,992	576
MER57A-int	9	0.0	2,900	117	9.06E-03	1,965	146
Mariner	47	0.1	361	941	9.07E-03	16,055	984
MER4A	19	0.0	1,084	313	9.07E-03	1,084	366
MIR3	213	3.2	66	5,136	1.05E-02	70,044	4,603
LTR9	18	0.0	1,139	298	1.10E-02	1,919	314
MLT2B1	12	0.0	1,917	177	1.11E-02	4,186	191
L1PA6	13	0.0	1,722	197	1.13E-02	5,617	201
L1MEe	37	0.1	471	720	1.13E-02	12,492	890
THE1B	33	0.1	539	630	1.17E-02	22,106	659
MLT2A2	8	0.0	3,263	104	1.20E-02	3,754	106
HERV16	11	0.0	2,108	161	1.28E-02	4,493	183
L1MEc	56	0.2	288	1,179	1.35E-02	21,328	1,421
L1MA3	25	0.0	741	458	1.41E-02	8,131	490
LTR16B	12	0.0	1,834	185	1.55E-02	3,456	183
PiggyBac	9	0.0	2,630	129	1.71E-02	2,068	138
DNA	948	69.9	14	25,027	1.84E-02	386,466	28,225
CR1	135	1.3	106	3,198	2.00E-02	54,846	3,185
MER50	19	0.0	998	340	2.05E-02	2,576	390
MER2_type	206	3.1	67	5,048	2.05E-02	81,748	5,863
MLT1E	30	0.1	577	588	2.06E-02	3,378	660
MER2	287	6.1	47	7,202	2.25E-02	8,174	8,171
L1P3	11	0.0	1,928	176	2.41E-02	4,518	184
MIRm	108	0.8	134	2,528	2.45E-02	32,156	2,288
L1M1	25	0.0	704	482	2.49E-02	10,118	540
LTR1	165	1.9	85	4,006	2.54E-02	1,396	4,070

category	# of probes significantly differentiating non-tumor adjacents and tumors (no pairs)	expected at random	enrichment	total number of probes in category	hyperGeometric p-val	# of genomic repeats	# of probed repeats
MER6	84	0.5	177	1,922	2.55E-02	926	2,123
MER8	41	0.1	393	864	2.77E-02	1,884	891
ERVL-E	21	0.0	855	397	2.84E-02	9,525	453
L1PB4	17	0.0	1,095	310	2.99E-02	6,330	328
MER39B	7	0.0	3,294	103	3.07E-02	1,166	113
LTR67	17	0.0	1,091	311	3.07E-02	6,289	306
FAM	31	0.1	537	632	3.08E-02	4,424	525
MLT1I	26	0.0	655	518	3.27E-02	11,191	533
MER4A1	13	0.0	1,495	227	3.34E-02	2,150	267
L1PA14	9	0.0	2,356	144	3.35E-02	3,561	160
MLT2B3	8	0.0	2,693	126	3.63E-02	2,966	126
MLT1F	33	0.1	490	692	3.84E-02	4,498	769
L1MC5	67	0.3	220	1,544	4.42E-02	20,412	1,780
AluYg	19	0.0	915	371	4.47E-02	111	363
L1MA5	20	0.0	857	396	4.67E-02	4,086	435
MIRb	736	42.4	17	19,543	4.77E-02	278,083	19,026
MADE2	9	0.0	2,203	154	4.91E-02	2,609	139
LTR49	9	0.0	2,203	154	4.91E-02	1,406	182

Table S4.

A compilation of annotation about the tissue samples analyzed in this manuscript.

id	age	sex	ethnicity	tob	tob_quit	etoh	etoh_quit	hpv	diagnosis	primary_location	differentiation	t	n
dk-11	64	M	n/a	yes	yes	yes	no	neg	scc	oral cavity:mandible	poor	t2	n0
dk-12	59	M	n/a	yes	yes	yes	no	neg	scc	oral cavity:tongue	moderate	t4	n2b
dk-14	71	M	caucasian	yes	no	yes	no	neg	scc	larynx:cord	well	t1a	n0
dk-15	49	M	caucasian	yes	no	yes	no	pos	scc	oral pharynx:bot	moderate	t2	n0
dk-16	49	F	african american	n/a	n/a	n/a	n/a	neg	scc	oral pharynx:bot	moderate	n/a	n/a
dk-17	66	M	caucasian	yes	yes	yes	yes	neg	scc	oral pharynx:tonsil	moderate	t3	n1
dk-19	76	M	caucasian	yes	yes	n/a	n/a	neg	scc	larynx:cord	moderate	t2	n0
dk-21	86	F	caucasian	yes	yes	n/a	n/a	neg	scc	oral cavity:mandible	poor	t4	n2b
dk-22	65	F	caucasian	yes	no	n/a	n/a	neg	scc	larynx:sub	moderate	t4	n1
dk-23	79	M	n/a	yes	no	yes	no	neg	scc	oral cavity:mandible	moderate	t3	n0
dk-26	80	M	caucasian	yes	no	n/a	n/a	neg	scc	oral cavity:tongue	moderate	t2	n1
dk-27	66	M	caucsian	yes	no	yes	no	neg	scc	hypopharynx:ps	moderate	t3	n1
dk-3	76	F	african american	yes	yes	yes	yes	neg	scc	oral cavity:fom	moderate	t2	n2a
dk-32	85	M	n/a	n/a	n/a	n/a	n/a	n/a	scc	larynx:supra	moderate	n/a	n/a
dk-33	41	M	caucasian	yes	yes	yes	yes	n/a	scc	larynx:cord	moderate	t1	n0
dk-34	64	F	caucasian	yes	no	n/a	n/a	n/a	scc	oral cavity:mandible	moderate	t2	n2
dk-4	51	F	n/a	yes	no	n/a	n/a	neg	scc	oral pharynx:s.palate	moderate	t3	n2c
dk-48	92	M	caucasian	yes	yes	n/a	n/a	n/a	scc	oral cavity:lip	moderate	t2	n1
dk-50	75	M	caucasian	yes	yes	yes	no	n/a	carcinoma	oral cavity:buccal mucosa	poor	t2	n0
dk-52	69	M	caucasian	yes	no	yes	no	n/a	scc	oral pharynx:ps	moderate	t2	n0
dk-54	52	M	african american	yes	no	yes	no	n/a	scc	larynx:glottis	moderate	t3	n0
dk-58	51	M	n/a	yes	no	yes	no	n/a	scc	oral pharynx:tonsil, bot	poor	t4	n1

id	age	sex	ethnicity	tob	tob_quit	etoh	etoh_quit	hpv	diagnosis	primary_location	differentiation	t	n
dk-6	78	F	african american	n/a	n/a	n/a	n/a	neg	scc	oral cavity:gingiva	well	t4	n2c
dk-62	65	M	indian (india)	yes	yes	n/a	n/a	n/a	scc	oral cavity:mandible	moderate	t4	n2b
dk-66	56	M	n/a	n/a	n/a	n/a	n/a	n/a	scc	oral cavity:tongue	mod. to poor	t3	n1
dk-69	62	M	hispanic	yes	no	yes	no	n/a	scc	oral cavity:mandible	moderate	t4	n0
dk-7	58	M	n/a	yes	no	yes	no	pos	scc	oral cavity:tongue	in-situ	n/a	n1
dk-9	51	M	caucasian	yes	yes	yes	no	pos	scc	oral pharynx:bot	moderate	t3	n0
dk-a	57	M	caucasian	yes	no	yes	no	neg	scc	oral cavity:fom	moderate	t3	n2c
dk-h	77	M	n/a	yes	no	yes	no	neg	scc	oral cavity:tongue	poor	t2	n0
dk-n	68	M	n/a	yes	no	yes	no	neg	scc	larynx:supra	poor	t2	n2c
dk-o	73	M	african american	yes	yes	n/a	n/a	n/a	scc	oral pharynx:bot, palate, tonsil	poor	t3	n0
dk-t	80	M	n/a	yes	no	n/a	n/a	neg	scc	larynx:cord	moderate	t1	n0
dk-x	57	M	caucasian	yes	no	yes	yes	neg	scc	larynx:cord	poor	t4	n0
no-12	38	F	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
no-15	32	M	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
no-18	43	F	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
no-19	29	M	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
no-22	31	M	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
no-23	34	M	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
no-24	37	M	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
no-6	62	M	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
no-7	42	F	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
no-9	33	M	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a