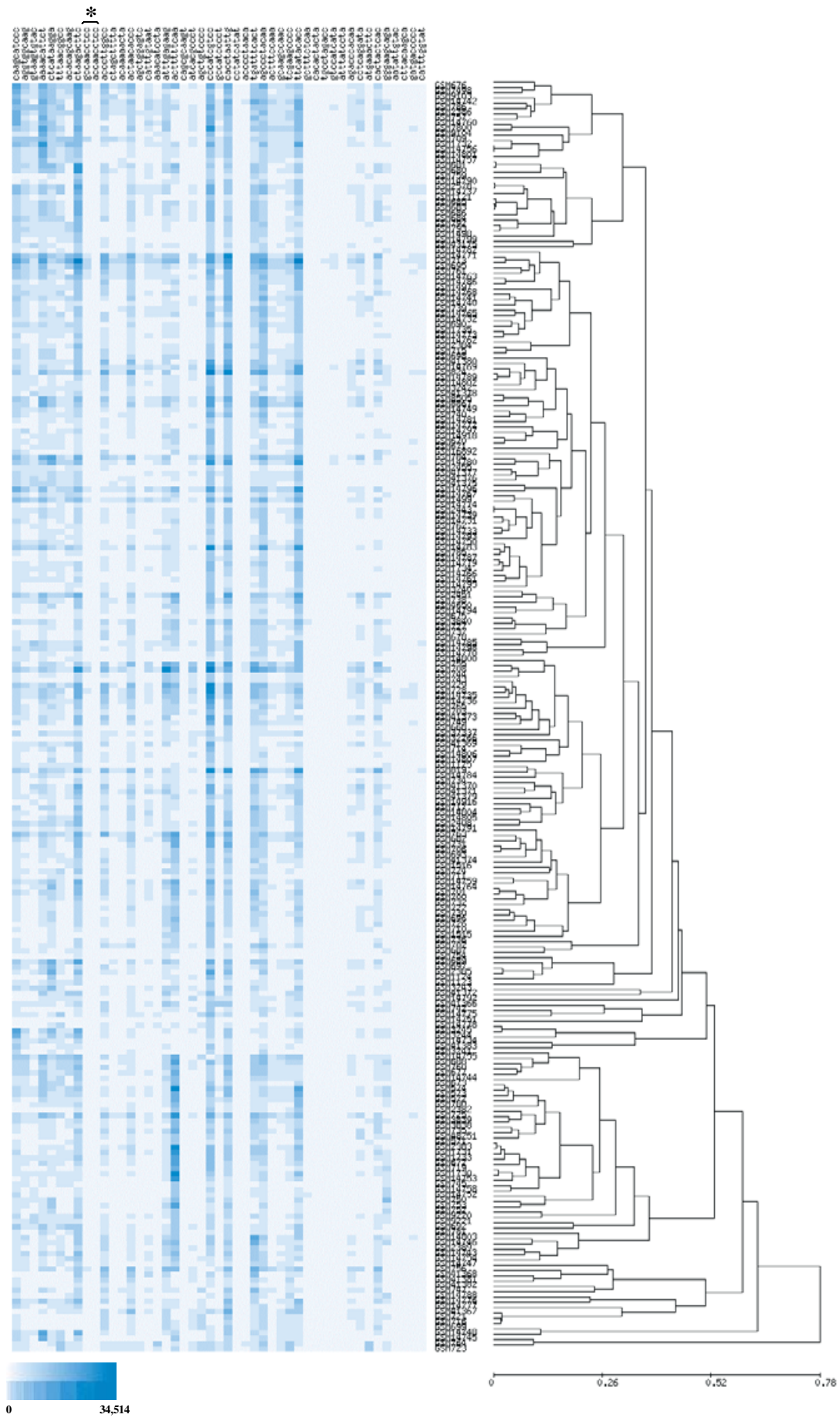
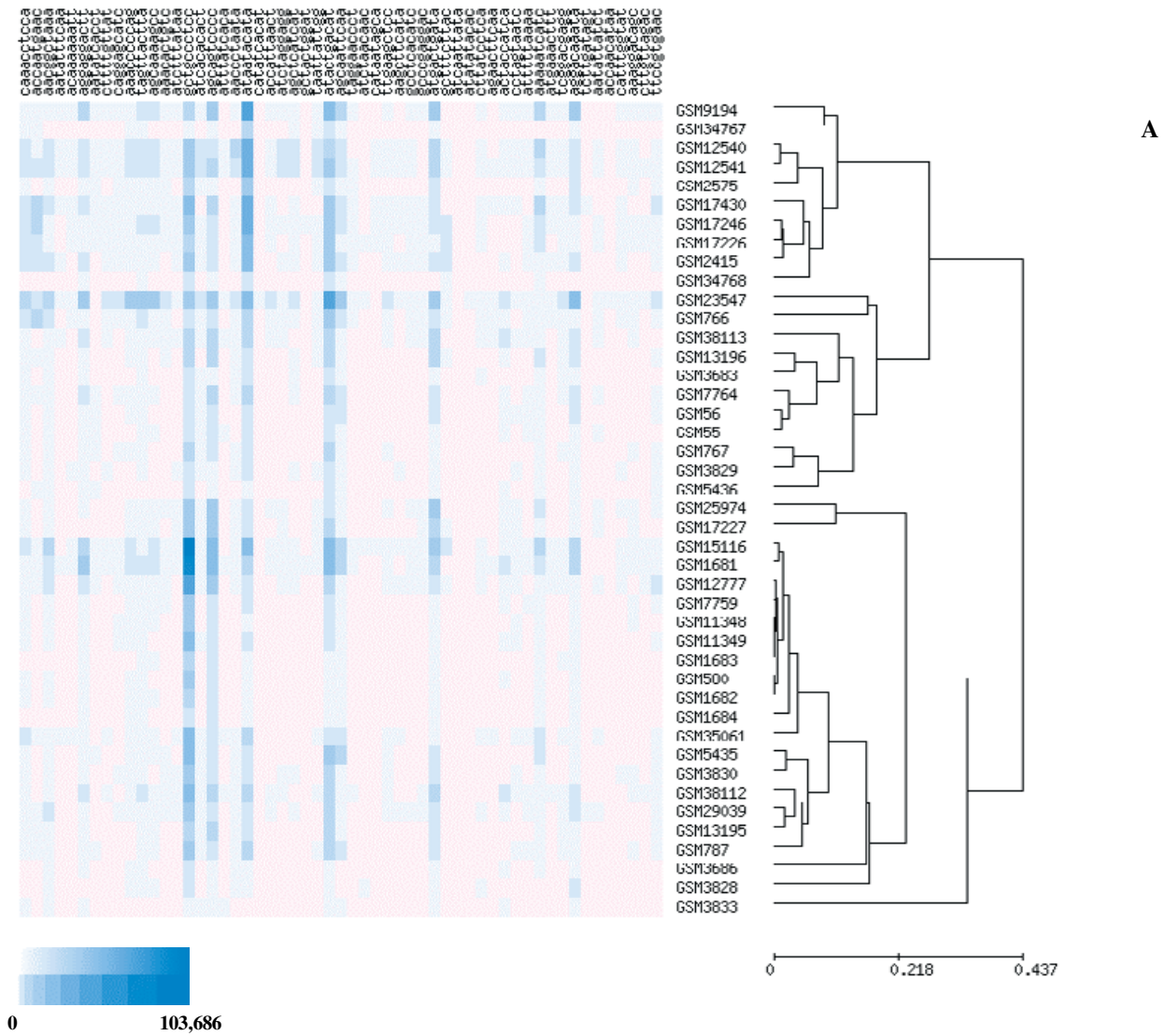


Supplemental Fig. 1. Distribution and relative positions of SAGE *NlaIII* anchoring enzyme restriction sites in human, mouse, rat, bovine and swine mitochondrial genomes. Circular mitochondrial DNA is plotted in linear form. Oblique strokes indicate overlaps in the coding sequences; the vertical arrow (↓) with an asterisk (*) indicates the starting position; scale bars correspond to 1 kb. Shaded areas represent tRNAs (black) and control region (D-loop; grey). Left-headed arrows (←) indicate areas encoded by the light strand (L strand). Filled triangles under the bars (▲) indicate *NlaIII* restriction sites.

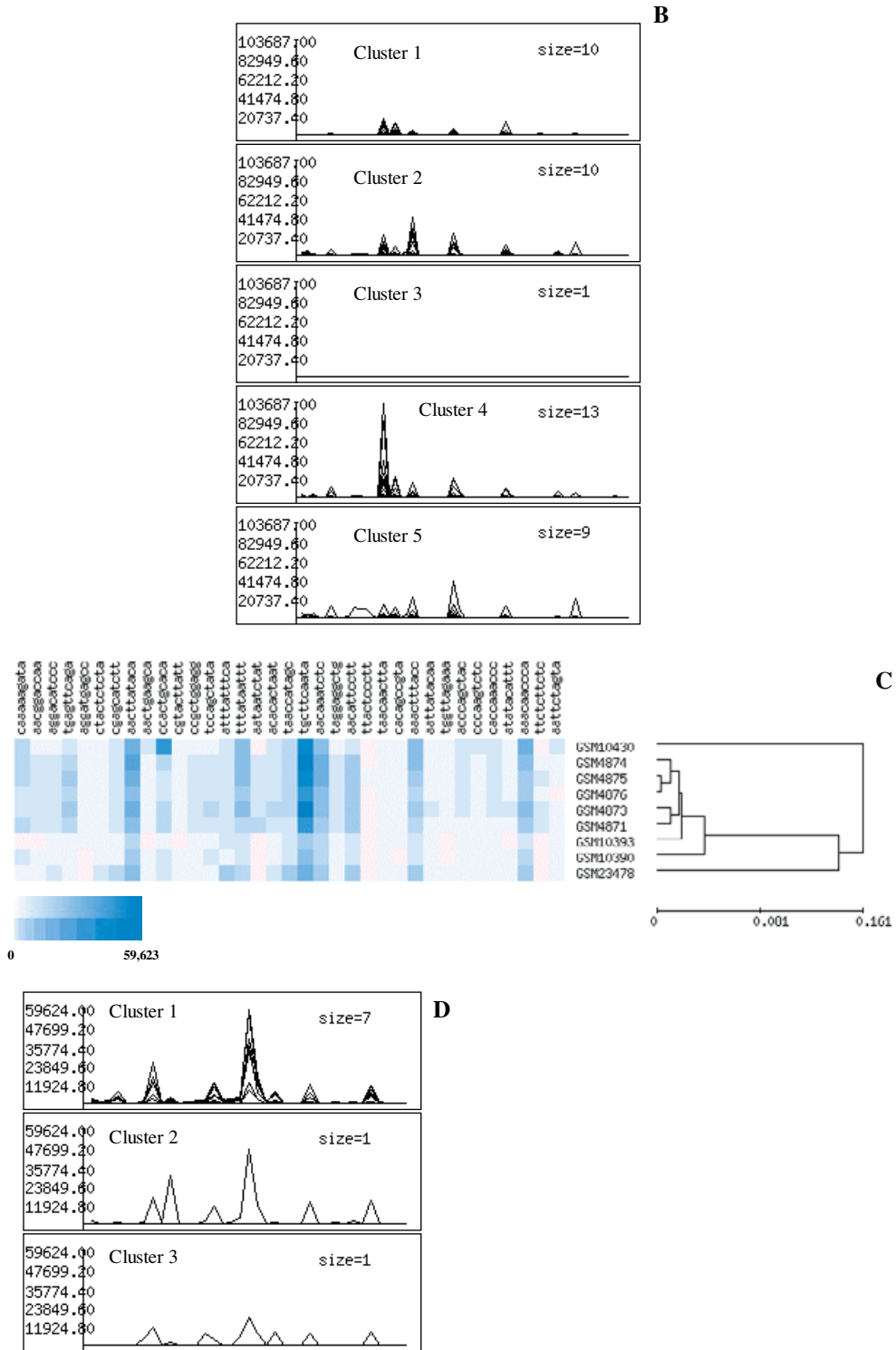


Supplemental Fig. 2 For legend see opposite page.

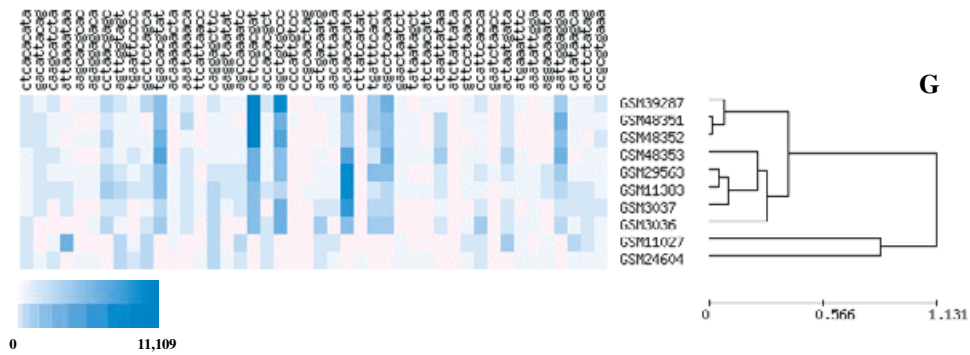
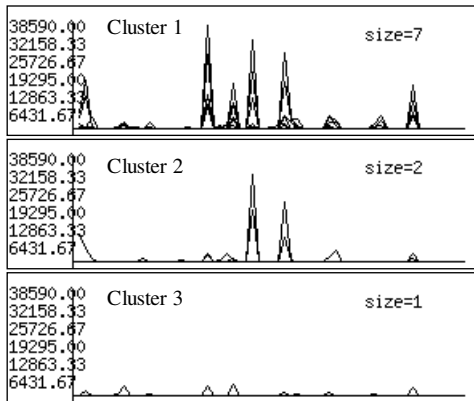
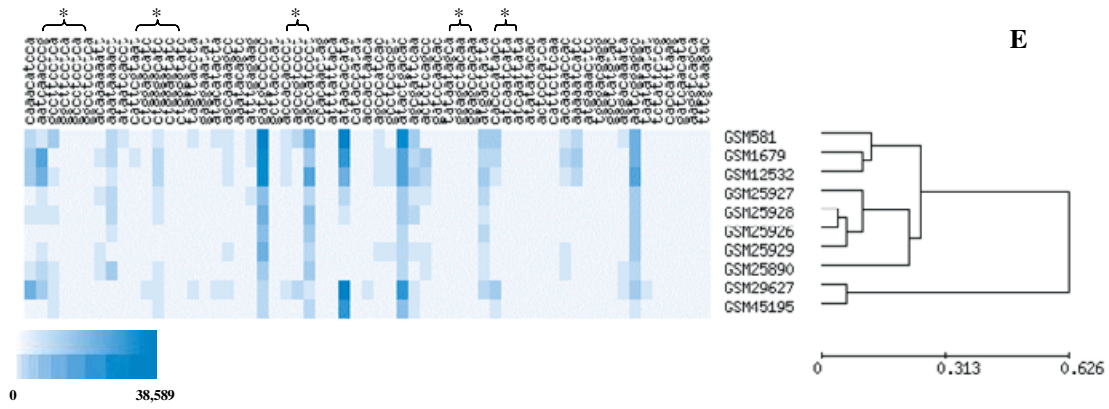


Supplemental Fig. 3. (Cont.)

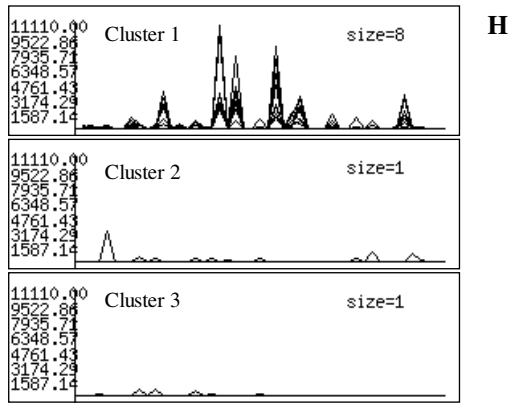
Supplemental Fig. 2. Hierarchical cluster tree for human *NlaIII*-derived SAGE dataset (239 libraries). Average linkage (average distance, UPGMA (unweighted pair group method with arithmetic mean)) clustering method based on linear correlation-based distance (Pearson, centered) have been used. Harmonic color code (20 colors) is based on the normalized tpm values. Asterisk (*) denotes variant SAGE tags.



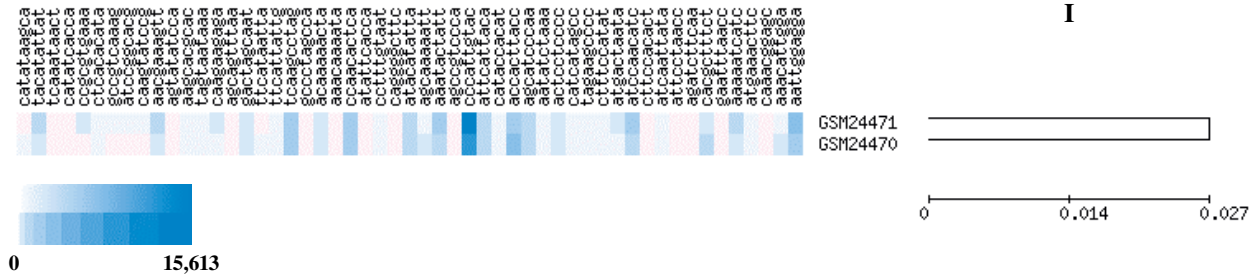
Supplemental Fig. 3. (Cont.)



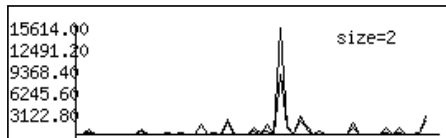
Supplemental Fig. 3. (Cont.)



H



I



J

Supplemental Fig. 3. Hierarchical cluster trees and gene expression patterns recognized by K-mean clustering analysis, as identified for: *Mus musculus*, *NlaIII*, *Sau3A I* (A, B and C, D, respectively); *Rattus norvegicus*, *NlaIII* (E, F); *Bos taurus*, *NlaIII* (G, H); and *Sus scrofa*, *NlaIII* (I, J). Harmonic colour code (10 colours) is based on the normalized tpm values for each individual dataset. Asterisks (*) denote variant SAGE tags. Note the significant diversity among possible transcription profiles with either relatively high expression characteristic for a few individual transcripts (e.g. B, Cluster 4 and D, Cluster 1), or with more proportional expression profiles (e.g. D, Cluster 3).

Supplemental Table 1. *Particulars of SAGE libraries used in the study*

N	SAGE library	Sample	Selection ^a	Tag ^b	Notes ^c
<i>Homo sapiens, GPL4 (NalIII)</i>					
1	GSM1	Foreskin fibroblasts	×		9742 tags
2	GSM2	HCMV-infected foreskin fibroblasts	—		
3	GSM571	Retinal pigment epithelium (RPE)	+	53 655	
4	GSM572	Peripheral retina	+	59 580	
5	GSM573	Peripheral retina	+	104 848	
6	GSM574	Central retina (macula)	+	102 053	
7	GSM668	Kidney, embryonic cell line 293, uninduced cells	+	43 457	
8	GSM669	Kidney, induced embryonic cell line 293, expressing β -catenin	—		
9	GSM670	Breast tumour	+	40 164	
10	GSM671	Metastasis from breast tumour	+	45 611	
11	GSM672	Breast, invasive ductal carcinoma	+	67 319	
12	GSM673	Metastasis from breast tumour	+	60 910	
13	GSM674	Cell line induced with synthetic androgen (R1881)	—		
14	GSM675	Ovary	+	22 259	
15	GSM676	Brain, normal, greater than 95% white matter	+	94 652	
16	GSM677	Breast, normal luminal mammary epithelium	+	37 565	
17	GSM678	Pancreas	+	37 894	
18	GSM680	Prostate carcinoma cell line	+	41 450	
19	GSM681	Prostate carcinoma cell line	+	43 934	
20	GSM682	Colon, colorectal carcinoma cell line	+	61 494	
21	GSM683	Prostate carcinoma cell line	+	62 493	
22	GSM684	Prostate carcinoma cell line	+	64 983	
23	GSM685	Normal prostate tissue	+	66 384	
24	GSM686	Prostate tumour tissue	+	68 540	
25	GSM687	Breast, ductal carcinoma <i>in situ</i>	+	41 274	
26	GSM688	Breast, ductal carcinoma <i>in situ</i>	+	28 896	
27	GSM689	Primary tumour, well-differentiated oligodendroglioma	+	28 112	
28	GSM690	Brain, medulloblastoma grade IV	×	38 931	
29	GSM691	Mammary gland, epithelium, ductal, normal	×		7139 tags
30	GSM692	Mammary gland, epithelium, ductal, normal	+	12 123	
31	GSM693	Medulloblastoma tumour	+	19 504	
32	GSM694	Mammary gland, ductal, carcinoma	×		5608 tags
33	GSM695	Brain, normal, greater than 95% white matter	+	58 770	
34	GSM696	Brain, Duke glioblastoma multiforme primary tumour	+	69 779	
35	GSM697	Brain, anaplastic astrocytoma, primary tumour	+	52 432	
36	GSM698	Primary tumour, pilocytic astrocytoma	+	76 972	
37	GSM699	Brain, astrocytoma	+	28 150	
38	GSM700	Brain, glioblastoma multiforme	+	71 840	
39	GSM701	Brain, glioblastoma multiforme	+	60 477	
40	GSM702	Brain, <i>c-myc</i> positive medulloblastoma cell line H341	+	44 572	
41	GSM703	Brain, Duke glioblastoma multiforme cell line	+	57 549	
42	GSM704	Brain, glioblastoma multiforme cell line, stably transfected with epidermal growth factor receptor vIII mutant	—		
43	GSM705	Brain, glioblastoma multiforme cell line, stably transfected with the β -galactosidase gene	—		
44	GSM706	Microvascular endothelial cells (HMVEC)	+	52 447	
45	GSM707	Microvascular endothelial cells (HMVEC) treated with VEGF	—		
46	GSM708	Normal kidney tissue	+	41 652	
47	GSM709	Leukocyte	+	48 447	
48	GSM710	Brain, <i>c-myc</i> negative medulloblastoma cell line mhh-1	+	48 370	
49	GSM711	Skin, post-crisis survival fibroblast cell-line	+	22 317	
50	GSM712	Skin, large T antigen transformed human fibroblasts clones, precrisis	×		8783 tags
51	GSM713	Brain, normal thalamus	+	48 502	
52	GSM714	Ovarian clear cell carcinoma cell line ES-2, poorly differentiated	+	31 484	
53	GSM715	Brain, primary tumour, well-differentiated, fibrillary astrocytoma	+	17 558	
54	GSM716	Pancreas, epithelium, ductal, normal, cell line	+	32 511	
55	GSM717	Colon, cell line derived from colorectal carcinoma	+	60 310	
56	GSM718	Mammary gland, epithelium, normal	×		1423 tags

Supplemental Table 1. (Cont.)

<i>N</i>	SAGE library	Sample	Selection ^a	Tag ^b	Notes ^c
57	GSM719	Ovary, normal surface epithelium	+	48 421	
58	GSM721	Pancreas, normal duct epithelial cells	+	32 224	
59	GSM722	Ovarian surface epithelium cell line	+	48 415	
60	GSM723	Prostate, advanced tumour	+	23 009	
61	GSM724	Prostate, adenocarcinoma, cell line	+	22 601	
62	GSM725	Mammary gland, adenocarcinoma	+	18 994	
63	GSM726	Ovary cystadenoma	+	56 950	
64	GSM727	Abdominal peritoneum, primary mesothelioma (pure epithelial)	+	35 076	
65	GSM728	Normal colonic epithelium	+	50 162	
66	GSM729	Normal colonic epithelium	+	49 554	
67	GSM730	Brain, normal human astrocyte cells	+	52 140	
68	GSM731	Ovarian carcinoma	+	17 441	
69	GSM732	Ovary, carcinoma cell line	+	38 895	
70	GSM733	Ovary, carcinoma cell line	×		2871 tags
71	GSM734	Ovary, pooled cancer cell lines	+	10 884	
72	GSM735	Primary ovarian tumour, serous adenocarcinoma	+	42 296	
73	GSM736	Primary ovarian tumour, serous adenocarcinoma	+	54 934	
74	GSM737	Primary ovarian tumour, serous adenocarcinoma	+	33 551	
75	GSM738	Peritoneum, sheet (>90% mesothelial cells)	+	53 976	
76	GSM739	Normal prostate tissue	+	59 441	
77	GSM740	Prostate, adenocarcinoma	+	65 252	
78	GSM741	Breast, cancer cell line	×		9372 tags
79	GSM742	Pancreas, cancer cell line	+	24 890	
80	GSM743	Pancreas tumour	+	33 924	
81	GSM744	Pancreas tumour	+	35 716	
82	GSM745	Brain, primary tumour parietal lobe	+	59 414	
83	GSM746	Prostate, carcinoma	×		9232 tags
84	GSM747	Colon, cancer cell line	+	51 959	
85	GSM748	Mammary gland, adenocarcinoma, malignant effusion	×		8094 tags
86	GSM749	Adenocarcinoma, colon, cell line	+	60 850	
87	GSM750	Breast carcinoma, pleural effusion	+	61 349	
88	GSM751	Breast carcinoma, pleural effusion	×		5890 tags
89	GSM752	Breast carcinoma, pleural effusion	+	60 623	
90	GSM753	Breast carcinoma, pleural effusion	+	59 949	
91	GSM754	Prostate, cell line	+	11 363	
92	GSM755	Adenocarcinoma, colon	+	57 653	
93	GSM756	Adenocarcinoma, colon	+	49 017	
94	GSM757	Stomach, human primary gastric cancer gastroesophageal junction adenocarcinoma	+	65 855	
95	GSM758	Stomach, human primary gastric cancer tissue propagated through nude mice (xenograft)	—		
96	GSM759	Breast, cancer cell line	+	18 472	
97	GSM760	Mammary gland, epithelium, ductal, normal	+	49 208	
98	GSM761	Normal cerebellum	+	51 137	
99	GSM762	Normal lung tissue	+	88 901	
100	GSM763	Brain, normal	+	63 085	
101	GSM764	Prostate, normal	+	13 293	
102	GSM765	Brain, glioblastoma multiforme primary tumour	+	61 795	
103	GSM780	Breast, normal breast tissue (gestational hyperplasia)	+	63 206	
104	GSM781	Breast, normal mammary myoepithelial cells	+	58 432	
105	GSM784	Normal gastric epithelial tissues	+	25 252	
106	GSM785	Normal liver tissue	+	66 601	
107	GSM786	Frontal cortex	+	77 570	
108	GSM792	Brain, ependymoblastoma, primary tumour	+	34 486	
109	GSM793	Brain, ependymoma, recurrent tumour	+	56 831	
110	GSM819	Normal human muscle (old)	+	53 853	
111	GSM824	Normal human muscle (young)	+	53 875	
112	GSM1121	Cultured human epidermal keratinocytes	+	12 799	
113	GSM1122	Cultured human epidermal keratinocytes, stimulated with TNF- α	—		
114	GSM1123	Epidermis	+	15 150	
115	GSM1124	Epidermis	+	11 556	

Supplemental Table 1. (Cont.)

N	SAGE library	Sample	Selection ^a	Tag ^b	Notes ^c
116	GSM1125	Affected epidermis of kidney transplant recipient suffering from actinic keratosis (AK)	+	10 074	
117	GSM1128	Breast cancer cell line	×		1 tag (–)
118	GSM1129	Breast cancer cell line; estrogen-treated	–		
119	GSM1130	Breast cancer cell line; tamoxifen-treated	–		
120	GSM1497	Brain, ependymoma	+	46 837	
121	GSM1498	Brain, glioblastoma multiforme (glioma)	+	62 629	
122	GSM1499	Normal heart tissue	+	84 153	
123	GSM1514	PC3 cells, JNK2AS treatment	–		*
124	GSM1515	PC3 cells	+	38 819	*
125	GSM1516	Hemangioma tumour	+	76 075	
126	GSM1652	Normal corneal endothelium	×		9536 tags
127	GSM1653	Fuchs' corneal endothelium	×		9874 tags
128	GSM1730	Breast, ductal carcinoma <i>in situ</i>	+	60 894	
129	GSM1731	Breast, ductal carcinoma <i>in situ</i>	+	43 689	
130	GSM1732	Brain, astrocytoma tumour	+	81 208	
131	GSM1733	Mammary gland, invasive ductal carcinoma with some <i>in situ</i> component	+	69 957	
132	GSM1734	Pooled organs and tissues include: B-lymphocyte (plasmacytoma, myeloma), mammary gland (adenocarcinoma), liver (hepatoblastoma), cervix (adenocarcinoma), testis (embryonal carcinoma), brain (glioblastoma), melanoma, liposarcoma, macrophage (histiocytic lymphoma, histiocyte), and T-lymphoblast (lymphoblastic leukemia) // Universal reference	+	51 711	
133	GSM1735	Brain, ependymoma	+	74 373	
134	GSM2382	Mammary gland, ductal, invasive carcinoma	+	64 908	
135	GSM2383	Mammary gland, ductal, invasive carcinoma	+	61 235	
136	GSM2384	Brain, ependymoma	+	52 871	
137	GSM2385	Primary gastric cancer tissue	+	63 882	
138	GSM2386	Normal spinal cord	+	55 199	
139	GSM2389	Mammary gland, ductal carcinoma	+	58 779	
140	GSM2408	Brain, ependymoma	+	52 579	
141	GSM2443	Brain, astrocytoma	+	80 165	
142	GSM2451	Brain, astrocytoma	+	38 603	
143	GSM2455	Uterine cervix normal	+	30 344	
144	GSM2578	Brain, astrocytoma	+	69 447	
145	GSM3240	Nodular skin lesion of an AIDS-KS patient	+	45 907	
146	GSM3241	Nodular skin lesion of an AIDS-KS patient	+	47 311	
147	GSM3242	Normal skin	+	37 247	
148	GSM3243	AIDS-KS lesion	+	45 973	
149	GSM3244	AIDS-KS lesion	+	45 766	
150	GSM3245	CD4+ T-cells	+	51 116	
151	GSM3838	Normal pancreatic exocrine cells	+	17 768	
152	GSM3839	Pancreatic islets	+	18 765	
153	GSM3840	Pancreatic islets	+	12 252	
154	GSM4650	Normal thyroid tissue	+	10 982	
155	GSM7498	Type 2 Gaucher patient cerebral cortex gray matter	+	31 360	
156	GSM7800	Primary gastric cancer tissue, poorly differentiated (scirrhous type)	+	34 571	
157	GSM8505	Primary gastric cancer tissue	+	31 974	
158	GSM8867	Primary gastric cancer tissue	+	43 633	
159	GSM9103	Primary gastric cancer tissue, poorly differentiated (diffuse-adherent type)	+	11 545	
160	GSM9104	Lymph node metastasis from gastric cancer	+	15 312	
161	GSM9220	Undifferentiated HES3 40P human embryonic stem cells	+	67 632	
162	GSM9221	Undifferentiated HES4 40P human embryonic stem cells	+	76 983	
163	GSM14731	Medulloblastoma, cerebellum	+	52 200	
164	GSM14732	Medulloblastoma, cerebellum	+	48 287	
165	GSM14733	Medulloblastoma, cerebellum	+	42 903	
166	GSM14734	Medulloblastoma, cerebellum	+	69 574	
167	GSM14735	Pancreas, epithelium, ductal, carcinoma, cell line	+	31 184	
168	GSM14736	Pancreas, epithelium, ductal, carcinoma, cell line	+	29 495	

Supplemental Table 1. (Cont.)

N	SAGE library	Sample	Selection ^a	Tag ^b	Notes ^c
169	GSM14737	Brain astrocytoma	+	105 659	
170	GSM14739	Brain astrocytoma	+	88 464	
171	GSM14740	Brain ependymoma	+	122 655	
172	GSM14741	Brain ependymoma	+	120 382	
173	GSM14742	Brain cortex, oligodendroglioma	+	32 272	
174	GSM14743	Mammary gland, epithelium, ductal, carcinoma	+	72 816	
175	GSM14744	Leucocytes from breast carcinoma	+	66 136	
176	GSM14745	Breast carcinoma myoepithelium	+	81 376	
177	GSM14746	Breast carcinoma epithelium	+	89 156	
178	GSM14747	Breast carcinoma myoepithelium	+	37 392	
179	GSM14748	Mammary gland, endothelium, ductal, carcinoma	+	65 236	
180	GSM14749	Normal first trimester placenta	+	89 080	
181	GSM14750	Normal term placenta	+	117 562	
182	GSM14751	Skin, melanoma	+	26 030	
183	GSM14752	Normal prostate epithelium	+	70 944	
184	GSM14753	Breast carcinoma metastasis to lung	+	49 538	
185	GSM14754	Mammary gland, normal endothelium	+	33 089	
186	GSM14755	Normal leucocytes	+	31 970	
187	GSM14756	Mammary gland	+	58 039	
188	GSM14757	Normal breast stroma	+	78 921	
189	GSM14758	Normal prostate epithelium, senescent cells	+	70 949	
190	GSM14759	Brain, medulloblastoma, cell line	+	66 000	
191	GSM14760	Stomach, poorly differentiated carcinoma	+	51 456	
192	GSM14761	Brain, medulloblastoma	+	84 891	
193	GSM14762	Brain ependymoma	+	68 552	
194	GSM14763	Brain anaplastic astrocytoma	+	106 942	
195	GSM14764	Brain, medulloblastoma, cell line	+	66 210	
196	GSM14765	Brain, astrocytoma	+	102 362	
197	GSM14766	Brain, astrocytoma, anaplastic	+	107 172	
198	GSM14767	Brain, glioblastoma	+	100 496	
199	GSM14768	Brain, glioblastoma	+	102 261	
200	GSM14769	Brain, glioblastoma	+	99 061	
201	GSM14770	Normal pancreas	+	21 715	
202	GSM14771	Placenta	+	101 557	
203	GSM14772	Brain, medulloblastoma	+	60 405	
204	GSM14773	Brain, anaplastic astrocytoma	+	118 642	
205	GSM14774	Brain, medulloblastoma with neuroblastic differentiation	+	85 699	
206	GSM14775	Skin, primary malignant melanoma	+	41 332	
207	GSM14776	Brain, ependymoma	+	75 215	
208	GSM14777	Thyroid	+	115 752	
209	GSM14778	Skin, desmoplastic melanoma metastasis	+	11 392	
210	GSM14779	Brain, medulloblastoma	+	72 077	
211	GSM14780	Normal gastric epithelial tissue from the antrum	+	26 619	
212	GSM14781	Brain desmoplastic medulloblastoma	+	83 506	
213	GSM14782	Brain desmoplastic medulloblastoma	+	68 158	
214	GSM14783	Brain anaplastic medulloblastoma	+	71 698	
215	GSM14784	Bone marrow	+	36 358	
216	GSM14785	Lymph node	+	99 084	
217	GSM14786	Brain, ependymoma	+	83 857	
218	GSM14787	Brain, anaplastic medulloblastoma	+	57 376	
219	GSM14788	Brain, medulloblastoma	+	74 158	
220	GSM14789	Normal bone marrow	+	86 377	
221	GSM14790	Brain, medulloblastoma	+	45 296	
222	GSM14791	Brain, medulloblastoma	+	32 406	
223	GSM14792	Brain, large cell medulloblastoma, metastasis	+	59 458	
224	GSM14793	Brain, medulloblastoma, metastasis	+	88 976	
225	GSM14794	Brain, medulloblastoma	+	74 167	
226	GSM14795	Brain, large cell medulloblastoma	+	67 134	
227	GSM14796	Brain, substantia nigra	+	42 326	
228	GSM14797	Breast, carcinoma, ductal, invasive	+	21 909	
229	GSM14798	Normal liver	+	78 257	
230	GSM14799	Fetal brain	+	308 295	
231	GSM14800	Primary ductal <i>in situ</i> breast carcinoma	+	50 866	

Supplemental Table 1. (Cont.)

N	SAGE library	Sample	Selection ^a	Tag ^b	Notes ^c
232	GSM14801	Normal breast tissue	+	59 185	
233	GSM14802	Normal bone marrow	+	81 576	
234	GSM14803	Lymph nodes, invasive breast tumour	+	18 741	
235	GSM14804	Lung cell line	+	28 928	
236	GSM14805	Lung cell line	+	42 168	
237	GSM14806	Lung, well differentiated adenocarcinoma with lymphoplasmatic infiltration	+	35 889	
238	GSM14807	Lung, poor differentiated adenocarcinoma with lymphoplasmatic infiltration	+	86 827	
239	GSM14916	Neonatal BJ foreskin primary fibroblasts	+	57 431	
240	GSM14917	Neonatal BJ foreskin primary fibroblasts immortalized by telomerase overexpression	–		
241	GSM14918	AT dermal fibroblasts	+	64 180	
242	GSM14919	AT dermal fibroblasts immortalized by telomerase overexpression	–		
243	GSM16892	Glomerular endothelial cell	+	68 978	
244	GSM23393	Cultured THP-1 cells, differentiating	×		3222 tags
245	GSM23394	Cultured THP-1 cells, proliferating	×		3519 tags
246	GSM32266	Microvascular endothelial cells exposed to sustained high shear stress	+	30 615	
247	GSM37211	Normal adrenal cortex	×		1 tag (–)
248	GSM37212	Primary pigmented nodular adrenocortical disease	×		1 tag (–)
249	GSM37337	Primary human bronchial epithelial cells	+	28 577	
250	GSM37339	Primary human bronchial epithelial cells stimulated with IL1 β and TNF α	–		
251	GSM37341	Primary human bronchial epithelial cells stimulated with heat-inactivated <i>P. aeruginosa</i>	–		
252	GSM41366	Cartilage chondrosarcoma grade 2	+	74 769	
253	GSM41367	Cartilage chondrosarcoma grade 2	+	93 446	
254	GSM41368	Cartilage chondrosarcoma grade 2	+	77 452	
255	GSM41369	Cartilage dedifferentiated chondrosarcoma metastasis	+	85 790	
256	GSM41370	Cartilage dedifferentiated chondrosarcoma metastasis	+	107 940	
257	GSM41371	Cartilage dedifferentiated chondrosarcoma metastasis	+	109 491	
258	GSM41372	Cartilage dedifferentiated chondrosarcoma metastasis	+	37 723	
259	GSM41373	Cartilage dedifferentiated chondrosarcoma metastasis	+	87 490	
260	GSM41374	Estrogen responsive cells purified from normal mammary epithelium	+	34 544	
261	GSM41375	ER negative breast cancer cell line	+	47 016	
262	GSM41376	ER negative breast cancer cell line	+	46 438	
263	GSM41377	ER negative breast cancer cell line	+	40 159	
264	GSM41378	Embryonic stem cell H9	+	150 657	
265	GSM41379	Eye lens	+	85 769	
266	GSM41380	Lung tumour, focal fibrosis and chronic inflammation	+	98 527	
267	GSM41381	Pelvis myxoid chondrosarcoma grade 2	+	83 241	
268	GSM41382	Cartilage chondrosarcoma grade 3	+	67 809	
269	GSM41383	Cartilage chondrosarcoma grade 1	+	33 043	
270	GSM43175	Bone marrow CD34+ stem/progenitor cells	+	99 488	
271	GSM48251	Cultured Schwann cells	+	42 870	
		Subtotal		13 762 568	
		<i>Homo sapiens, GPL6 (Sau3A I)</i>			
272	GSM10419	Kidney glomerulus	+	44 280	
273	GSM10423	Kidney proximal convoluted tubule	+	45 050	
274	GSM10424	Kidney proximal straight tubule	+	46 642	
275	GSM10425	Kidney medullary thick ascending limb	+	49 071	
276	GSM10426	Kidney cortical thick ascending limb	+	48 964	
277	GSM10427	Kidney distal convoluted tubule	+	59 134	
278	GSM10428	Kidney cortical collecting duct	+	53 758	
279	GSM10429	Kidney outer medullary collecting duct	+	67 433	
280	GSM32698	U937 cell line	+	24 692	
281	GSM32699	U937 differentiated cells	+	18 469	
282	GSM32700	Purified blood reticulocytes	×		1 tag (–)
		Subtotal		457 493	
		Total		14 130 061	

Supplemental Table 1. (Cont.)

N	SAGE library	Sample	Selection ^a	Tag ^b	Notes ^c
<i>Mus musculus, GPL11 (NlaIII)</i>					
283	GSM55	E115 intact developing B6C3H forelimb	+	68 336	
284	GSM56	E115 intact developing B6C3H hindlimbs	+	68 372	
285	GSM580	R1 embryonic stem (ES) cells	+	137 832	*
286	GSM766	Medulloblastoma	+	43 131	
287	GSM767	Granular cell precursor cells	+	61 433	
288	GSM787	Primary granule cell precursor cells	+	87 657	
289	GSM788	Primary granule cell precursor cells with sonic hedgehog	–		
290	GSM1681	Heart	+	84 192	*
291	GSM1682	P19 embryonic carcinoma (EC) cells	+	64 952	*
292	GSM1683	P19 embryonic carcinoma (EC) cells, differentiation Day 3 + 05	+	50 983	*
293	GSM1684	P19 embryonic carcinoma (EC) cells, differentiation Day 3 + 30	+	53 022	*
294	GSM2415	Cerebellum	+	19 332	
295	GSM2575	Cartilage cell line (ATDC5 cells)	+	21 755	
296	GSM2576	BMP4-induced ATDC5 cells	–		
297	GSM3677	CD4+ Th1 clone (R22) from a primed A1 × RAG-1 –/– TCR transgenic mouse specific for H-Y + H2Ek	–		
298	GSM3678	CD4+ Th2 clone (R24) from a primed A1 × RAG-1 –/– TCR transgenic mouse specific for H-Y + H2Ek	–		
299	GSM3679	CD4+ Treg/Tr1-like clone from a naive A1 × RAG-1 –/– TCR transgenic mouse specific for H-Y + H2Ek	–		
300	GSM3680	Draining lymph nodes, skin grafted anti-HY TCR transgenic female A1 × RAG-1 –/– mice	–		
301	GSM3681	CD4+ Treg/Tr1-like clone from a naive A1 × RAG-1 –/– TCR transgenic mouse specific for H-Y + H2Ek	–		
302	GSM3682	CD4+ Treg/Tr1-like H-Y + H2Ek specific line grown from the accepted male skin grafts of female A1(M) TCR transgenic mice	–		
303	GSM3683	CD4+ CD25-negative spleen cells	+	23 343	
304	GSM3684	CD4+ CD25+ spleen cells (CD3 X-linked)	–		
305	GSM3685	CD4+ CD25- spleen cells (CD3 X-linked)	–		
306	GSM3686	CD4+ CD25+ spleen cells	+	20 041	
307	GSM3687	Draining lymph nodes were pooled from normal CBA/Ca mice grafted with B10BR (multiple minor antigen mismatched) skin	×		5 411 tags
308	GSM3824	CD4+ Treg/Tr1-like H-Y + H2Ek specific line grown from the accepted male skin grafts of female A1(M) TCR transgenic mice in the presence of anti-CTLA4	–		
309	GSM3825	CD4+ Treg/Tr1-like clone from naive A1 × RAG-1 –/– TCR transgenic mouse specific for H-Y + H2Ek	–		
310	GSM3826	CD4+ Th2 clone (R24) from a primed A1 × RAG-1 –/– TCR transgenic mouse specific for H-Y + H2Ek	–		
311	GSM3827	CD4+ Th1 clone (R22) from a primed A1 × RAG-1 –/– TCR transgenic mouse specific for H-Y + H2Ek	–		
312	GSM3828	Mouse thymoma cell line	+	19 605	
313	GSM3829	Embryonic stem cell line ESF 116	+	15 094	
314	GSM3830	Dendritic cells derived from ESF 116 stem cell line	+	30 696	
315	GSM3831	Dendritic cells derived from ESF 116 stem cell line treated with LPS	–		
316	GSM3832	Murine bone marrow derived dendritic cells (LPS treated)	–		
317	GSM3833	Mouse bone marrow derived dendritic cells	+	21 785	
318	GSM3834	Mouse bone marrow derived dendritic cells (IL-10 treated)	–		
319	GSM3835	Mouse bone marrow derived dendritic cells (IL-10 plus LPS treated)	–		
320	GSM3836	Mouse bone marrow derived dendritic cells (Vitamin D3 treated)	–		
321	GSM3837	Mouse splenic B cells	×		9 624 tags
322	GSM5050	Cerebellum	×		464 tags
323	GSM5051	Cerebellum of postnatal day 10 Lurcher (Lc +/–) mouse	×		813 tags
324	GSM5435	Adult mouse testis	+	81 474	
325	GSM5436	Fetal testis somatic cells	+	61 935	

Supplemental Table 1. (Cont.)

N	SAGE library	Sample	Selection ^a	Tag ^b	Notes ^c
326	GSM7759	Primary mouse embryonic fibroblasts	+	64 882	*
327	GSM7764	Cardiac fibroblasts isolated from adult mouse heart	+	109 958	
328	GSM9194	Whole kidney	+	11 300	
329	GSM9195	Whole kidney, treated with AngII	—		
330	GSM11348	EG-1 cells	+	47 544	*
331	GSM11349	D3 embryonic stem (ES) cells	+	37 652	*
332	GSM12513	Cerebellum	×		7513 tags
333	GSM12540	Hippocampus: short attack latency (SAL) mice	+	31 122	
334	GSM12541	Hippocampus: long attack latency (LAL) mice	+	30 822	
335	GSM12757	ApoE3-Leiden (E3L) transgenic mice	—		
336	GSM12777	Liver	+	18 741	
337	GSM13195	6-week mouse total cornea	+	62 204	
338	GSM13196	Postnatal day 9 mouse total cornea	+	64 271	
339	GSM15116	Old mouse heart	+	25 664	*
340	GSM16635	Cerebellum	×		8507 tags
341	GSM17226	Cerebellum	+	18 360	
342	GSM17227	Retroperitoneal adipose tissue	+	45 938	
343	GSM17246	Cerebellum	+	17 934	
344	GSM17430	Cerebellum	+	16 319	
345	GSM23547	Heart	+	18 460	
346	GSM23548	Heart, treated with AngII	—		
347	GSM24251	Kidney (9- to 11-week)	×		1 tag (—)
348	GSM24255	Kidney (9- to 11-week), exposed to uranyl nitrate	—		
349	GSM24256	Kidney (25- to 28-week)	×		1 tag (—)
350	GSM24257	Kidney (25- to 28-week), exposed to uranyl nitrate	—		
351	GSM25974	Retroperitoneal adipose tissue of gonadectomized C57BL6 male mice	+	45 450	
352	GSM25975	Retroperitoneal adipose tissue of gonadectomized C57BL6 male mice injected with dihydrotestosterone	—		
353	GSM25976	Retroperitoneal adipose tissue of gonadectomized C57BL6 male mice injected with dihydrotestosterone	—		
354	GSM29039	Liver sinusoidal endothelial cells	+	32 830	
355	GSM29040	Liver sinusoidal endothelial cells, injured liver by carbon tetrachloride administration	—		
356	GSM30721	Granulosa cells isolated from immature mice (18–22days) treated 48 h earlier with 5IU PMSG	—		
357	GSM30722	Granulosa cells isolated from immature mice (18–22days) treated with 5IU PMSG followed 48 h later with 5IU hCG	—		
358	GSM34767	Total testis	+	24 714	
359	GSM34768	Total testis	+	51 592	
360	GSM35061	Normal sciatic nerve	+	10 521	
361	GSM35062	C22 sciatic nerve (CMT1A transgenic model)	—		
362	GSM38112	Skeletal muscle (m. gastrocnemius)	+	58 900	
363	GSM38113	Skeletal muscle (m. gastrocnemius) of adrenalectomized mice	+	149 087	
364	GSM38207	Skeletal muscle (m. gastrocnemius) of adrenalectomized mice, 3 h after an IP injection with cortisol	—		
365	GSM38208	Skeletal muscle (m. gastrocnemius) of adrenalectomized mice, 24 h after an IP injection with cortisol	—		
		Subtotal		2 029 235	
		Mus musculus, GPL275 (Sla3A I)			
366	GSM4871	Whole brain (8- to 12-week-old), C57BL/6 mouse	+	26 029	
367	GSM4873	Lateral striatum (8- to 12-week-old), C57BL/6 mouse	+	22 367	
368	GSM4874	Medial striatum (8- to 12-week-old) C57BL/6 mouse	+	23 615	
369	GSM4875	Nucleus accumbens (8- to 12-week-old), C57BL/6 mouse	+	24 547	
370	GSM4876	Somatosensory cortex (8- to 12-week-old), C57BL/6 mouse	+	21 938	
371	GSM10390	Cortical collecting duct, kidney	+	39 035	
372	GSM10391	Cortical collecting duct, kidney, treated with aldosterone	—		
373	GSM10392	Cortical collecting duct, kidney, treated with vasopressin	—		
374	GSM10393	Whole embryo (65 dpc)	+	26 803	
375	GSM10394	Whole embryo (65 dpc), Otx —/—	—		
376	GSM10430	Kidneys (8–10 weeks old)	+	14 394	

Supplemental Table 1. (Cont.)

N	SAGE library	Sample	Selection ^a	Tag ^b	Notes ^c
377	GSM23474	Kidney, outer medullary collecting duct, 3 days potassium-depleted diet	—		
378	GSM23478	Kidney, outer medullary collecting duct	+	19 684	
		Subtotal		218 412	
		Total		2 247 647	
<i>Rattus norvegicus, GPL23 (NlaIII)</i>					
379	GSM581	Extraocular muscle	+	54 653	
380	GSM1679	Hippocampus (Wistar)	+	76 666	
381	GSM3893	Extraocular muscle in dark-reared	—		
382	GSM12532	Hippocampus (Sprague Dawley)	+	10 464	
383	GSM12533	Hippocampus (Sprague Dawley), status epilepticus	—		
384	GSM12542	Hippocampus: adrenalectomized Wistar rat (ADX)	—		
385	GSM12543	Hippocampus: ADX + low CORT Wistar rat	—		
386	GSM12544	Hippocampus: (ADX + low CORT) + acute high CORT Wistar rat	—		
387	GSM25890	Subcutaneous Swarm rat chondrosarcoma	+	89 778	
388	GSM25926	Femoral head cartilage, Sprague-Dawley	+	120 032	
389	GSM25927	Chondrosarcoma tibia tumour	+	101 578	
390	GSM25928	Subcutaneous Swarm rat chondrosarcoma tibia tumour	+	106 125	
391	GSM25929	Swarm rat chondrosarcoma lung tumour	+	108 719	
392	GSM29626	Striatum (Sprague-Dawley), METH treatment	—		
393	GSM45195	Normal lung	+	28 061	
394	GSM29627	Striatum (Sprague-Dawley)	+	22 086	
		Total		718 162	
<i>Bos taurus, GPL223 (NlaIII)</i>					
395	GSM3036	Renal glomerular endothelial cells	+	36 837	
396	GSM3037	Aortic endothelial cells	+	26 408	
397	GSM11027	Madin-Darby bovine kidney (MDBK) cells	+	20 138	
398	GSM11028	BVDV2-infected MDBK cells	—		
399	GSM11383	Immature B cells isolated from ileal Peyer's patch	+	97 007	
400	GSM24604	Circulating γ/δ T cells	+	51 138	
401	GSM29563	Circulating CD4 T lymphocytes	+	97 053	
402	GSM39287	Circulating CD8 lymphocytes	+	104 711	
403	GSM48351	Granulosa cells from dominant follicles	+	52 622	
404	GSM48352	Granulosa cells from subordinate follicles	+	49 505	
405	GSM48353	Granulosa cells from cohort follicles	+	50 582	
		Total		586 001	
<i>Sus scrofa, GPL1270 (NlaIII)</i>					
406	GSM24470	Day 11 pre-implantation embryos	+	42 272	
407	GSM24471	Day 12 pre-implantation embryos	+	42 344	
		Total		84 616	
		Total		17 766 487	

Indexes (GSM#) represent GEO database accession numbers for SAGE libraries.

^a (+), selected for analysis; (—), genetically modified species or cell cultures; (×), SAGE libraries with a total number of reliable tags $\leq 10\,000$ or with complete dataset unavailable.

^b Number of tags subjected for analysis (with (A)₁₀ tags excluded).

^c Number of tags for SAGE libraries with a total number of reliable tags $\leq 10\,000$ is shown; (1 tag (—)), tags detected once in a library are not available via GEO database; Asterisks (*) indicate SAGE libraries constructed by author and co-workers and subjected to 'clean-up' procedure (Anisimov & Sharov, 2004).

Supplemental Table 2. Individual SAGE tags matching mammal mitochondrial genomes

N	Tag	Gene ^a	SNPs ^b	Average tpm ^c	% to Total ^d	% to Mt ^e
<i>Homo sapiens NlaIII</i>						
1	CAAGCATCCC	<i>mt-Rnr1</i>		2024	0.20 %	4.30 %
2	AGGTGGCAAG	<i>mt-Rnr1</i>		819	0.08 %	1.74 %
3	GTAAGTGAC	<i>mt-Rnr1</i>		484	0.05 %	1.03 %
4	AAAACATTCT	<i>mt-Rnr2</i>		2349	0.23 %	4.99 %
5	CTCATAAGGA	<i>mt-Rnr2</i>		1407	0.14 %	2.99 %
6	TTTAACGGCC	<i>mt-Rnr2</i>		786	0.08 %	1.67 %
7	ACACAGCAAG	<i>mt-Rnr2</i>		736	0.07 %	1.56 %
8	CTAAGACTTC	<i>mt-Rnr2</i>		4140	0.41 %	8.80 %
9	GCCAACCTCC	<i>mt-Nd1</i>	Variant	154	0.02 %	0.33 %
	ACCAACCTCC	<i>mt-Nd1</i>		<1	<0.01 %	<0.01 %
10	ACCCTTGCC	<i>mt-Nd1</i>		1420	0.14 %	3.02 %
11	CTAGCTTTTA	<i>mt-Nd2</i>		203	0.02 %	0.43 %
12	ACAAAACTA	<i>mt-Nd2</i>		251	0.03 %	0.53 %
13	ACTAACACCC	<i>mt-Nd2</i>		1495	0.15 %	3.18 %
14	AGCTGGAGTC	<i>mt-Co1</i>		93	0.01 %	0.20 %
15	CATTTGTAAT	<i>mt-Co1</i>		420	0.04 %	0.89 %
16	AAACATCCTA	<i>mt-Co1</i>		174	0.02 %	0.37 %
17	ATTTGAGAAG	<i>mt-Co1</i>		1510	0.15 %	3.21 %
18	ACTTTTTCAA	<i>tRNA</i>		2996	0.30 %	6.37 %
19	CAGCGCAAGT	<i>mt-Co2</i>		4	<0.01 %	<0.01 %
20	ATCACGCCCT	<i>mt-Co2</i>		373	0.04 %	0.79 %
21	AGCTGTCCCC	<i>mt-Co2</i>		149	0.01 %	0.32 %
22	CCCATCGTCC	<i>mt-Co2</i>		5733	0.57 %	12.19 %
23	GCCATCCCCT	<i>mt-Atp8</i>		269	0.03 %	0.57 %
24	CACCTAATTG	<i>mt-Atp6</i>		4162	0.42 %	8.85 %
25	CCTATCATAT	<i>mt-Co3</i>		6	<0.01 %	0.01 %
26	ACCCCTAACA	<i>mt-Co3</i>		57	<0.01 %	0.12 %
27	TGATTTCACT	<i>mt-Co3</i>		2413	0.24 %	5.13 %
28	AGCCCTACAA	<i>mt-Nd3</i>		2884	0.29 %	6.13 %
29	ACTTTCCAAA	<i>mt-Nd4</i>		356	0.04 %	0.76 %
30	GCAAGCCAAC	<i>mt-Nd4</i>		435	0.04 %	0.92 %
31	TCGAAGCCCC	<i>mt-Nd4</i>		850	0.08 %	1.81 %
32	TTCATACACC	<i>mt-Nd4</i>		3948	0.39 %	8.39 %
33	GCTTTCTCAA	<i>tRNA</i>		43	<0.01 %	0.09 %
34	CACACTACTA	<i>mt-Nd5</i>		11	<0.01 %	0.02 %
35	TGCCTAGACC	<i>mt-Nd5</i>		37	<0.01 %	0.08 %
36	GTCCATCATA	<i>mt-Nd5</i>		72	<0.01 %	0.15 %
37	ATTTATCCTA	<i>mt-Nd5</i>		11	<0.00 %	0.02 %
38	AGACCCACAA	<i>mt-Nd5</i>		296	0.03 %	0.63 %
39	CCTCAGGATA	<i>mt-Nd6</i>		629	0.06 %	1.34 %
40	ATGAAACTTC	<i>mt-Cytb</i>		117	<0.01 %	0.25 %
41	CACTACTCAC	<i>mt-Cytb</i>		988	0.10 %	2.10 %
42	GGGAAGCAGA	<i>D-Loop</i>		374	0.04 %	0.79 %
43	AATATGTAC	<i>D-Loop</i>		22	<0.01 %	0.05 %
44	CTTACAAGCA	<i>D-Loop</i>		49	<0.01 %	0.10 %
45	GATGACCCCC	<i>D-Loop</i>		121	0.01 %	0.26 %
46	CATTTGGTAT	<i>D-Loop</i>		100	0.01 %	0.21 %
	<i>Total</i>			47 034	4.70 %	100.00 %
<i>Homo sapiens Sau3A I</i>						
1	ACAGGTCTAT	<i>tRNA</i>		344	0.03 %	0.43 %
2	AAAAGGGACA	<i>mt-Rnr1</i>		1747	0.17 %	2.17 %
3	ACCCCTCCC	<i>mt-Rnr1</i>		2387	0.24 %	2.97 %
4	AACCTCACCA	<i>mt-Rnr1</i>		4748	0.47 %	5.91 %
5	AAAACACTGA	<i>mt-Rnr2</i>		2	<0.01 %	<0.01 %
6	CAATAACTTG	<i>mt-Rnr2</i>		705	0.07 %	0.88 %
7	AGGACATCCC	<i>mt-Rnr2</i>		4275	0.43 %	5.32 %
8	TGAGTTCAGA	<i>mt-Rnr2</i>		5587	0.56 %	6.95 %
9	AGGGTGAGCA	<i>mt-Nd1</i>		2218	0.22 %	2.76 %
10	GGCGCACTGC	<i>mt-Nd1</i>		7505	0.75 %	9.34 %
11	CGTCCTAATC	<i>mt-Co1</i>		3135	0.31 %	3.90 %
12	TGCTGCAGTG	<i>mt-Co1</i>		9161	0.92 %	11.40 %

Supplemental Table 2. (Cont.)

<i>N</i>	Tag	Gene ^a	SNPs ^b	Average tpm ^c	% to Total ^d	% to Mt ^e
13	ACGCCCTCAT	<i>mt-Co2</i>		2175	0.22 %	2.71 %
14	CCTCCCTTAC	<i>mt-Co2</i>		6439	0.64 %	8.01 %
15	ATTCTATTTTC	<i>mt-Atp6</i>		180	0.02 %	0.22 %
16	CCCACCTCCA	<i>mt-Atp6</i>		1994	0.20 %	2.48 %
17	TCTTATACTA	<i>mt-Atp6</i>		7245	0.72 %	9.02 %
18	TAGAAATTGC	<i>mt-Nd3</i>		5585	0.56 %	6.95 %
19	AAATATCACT	<i>mt-Nd4</i>		8122	0.81 %	10.11 %
20	CTCCCGAATC	<i>mt-Nd6</i>	Variant	1650	0.16 %	2.05 %
	CTCCCGAATG	<i>mt-Nd6</i>		ND	0.00 %	0.00 %
21	CTCCAAATCA	<i>mt-Cytb</i>		279	0.03 %	0.35 %
22	ATTTCTCTAC	<i>mt-Cytb</i>		335	0.03 %	0.42 %
23	AAACAACCCC	<i>mt-Cytb</i>		1558	0.16 %	1.94 %
24	CGTCCCTAAC	<i>mt-Cytb</i>		2969	0.30 %	3.70 %
	<i>Total</i>			80 348	8.03 %	100.00 %
<i>Mus musculus NlaIII</i>						
1	CAAACCTCCA	<i>mt-Rnr1</i>		712	0.07 %	1.77 %
2	ACCAATGAAC	<i>tRNA</i>		389	0.04 %	0.97 %
3	AACGGCTAAA	<i>mt-Rnr2</i>		772	0.08 %	1.92 %
4	AATATTTCAA	<i>mt-Nd2</i>		30	<0.01 %	0.07 %
5	ACAAAAAATT	<i>mt-Nd2</i>		43	<0.01 %	0.11 %
6	AGGAGGACTT	<i>mt-Nd2</i>		1585	0.16 %	3.95 %
7	AATATCACCT	<i>tRNA</i>		70	<0.01 %	0.17 %
8	CTTTTGTTAT	<i>mt-Co1</i>		120	0.01 %	0.30 %
9	CAGGAGCATC	<i>mt-Co1</i>		168	0.02 %	0.42 %
10	AAACCCCCAG	<i>mt-Co1</i>		658	0.07 %	1.64 %
11	TAGTTACTTA	<i>mt-Co1</i>		706	0.07 %	1.76 %
12	AGCAAAAGCC	<i>mt-Co1</i>		615	0.06 %	1.53 %
13	AAACACTGTC	<i>mt-Co1</i>		211	0.02 %	0.52 %
14	ATCTTTATAA	<i>mt-Co1</i>		117	0.01 %	0.29 %
15	GCTGCCCTCC	<i>mt-Co1</i>		11 248	1.12 %	28.02 %
16	ATCACACACT	<i>mt-Co2</i>		268	0.03 %	0.67 %
17	AGCAGTCCCC	<i>mt-Co2</i>		4191	0.42 %	10.44 %
18	ATTTATCACA	<i>mt-Atp8</i>		50	0.01 %	0.13 %
19	AACCCTAATA	<i>mt-Atp6</i>		486	0.05 %	1.21 %
20	ATAATACATA	<i>mt-Atp6</i>		6612	0.66 %	16.47 %
21	CATATCAGAT	<i>mt-Co3</i>		5	<0.01 %	0.01 %
22	ACCATTAACT	<i>mt-Co3</i>		89	<0.01 %	0.22 %
23	ATCTAGGAGG	<i>mt-Co3</i>		116	0.01 %	0.29 %
24	AGCTCATCAT	<i>mt-Co3</i>		168	0.02 %	0.42 %
25	GCTACTGGAT	<i>mt-Co3</i>		5	<0.01 %	0.01 %
26	TAATTATTGG	<i>mt-Co3</i>		157	0.02 %	0.39 %
27	ATACTGACAT	<i>mt-Co3</i>		6508	0.65 %	16.21 %
28	AGCAATTCAA	<i>mt-Nd3</i>		1437	0.14 %	3.58 %
29	TAGGAACCCT	<i>mt-Nd4</i>		41	<0.01 %	0.10 %
30	ATCTAACAAC	<i>mt-Nd4</i>		12	<0.01 %	0.03 %
31	CATAATAGCA	<i>mt-Nd4</i>		10	<0.01 %	0.02 %
32	TTGAAGCTCC	<i>mt-Nd4</i>		145	0.01 %	0.36 %
33	AAGCTTCATA	<i>mt-Nd4</i>		30	<0.01 %	0.08 %
34	GCCTCACATC	<i>mt-Nd4</i>		74	<0.01 %	0.19 %
35	GCCCCGAGGAC	<i>mt-Nd4</i>		45	<0.01 %	0.11 %
36	ATGACTGATA	<i>mt-Nd4</i>		2974	0.30 %	7.41 %
37	GCTTTCTTAC	<i>tRNA</i>		151	0.02 %	0.38 %
38	ATCAATTATA	<i>mt-Nd5</i>		1	<0.01 %	<0.01 %
39	ATATATACAC	<i>mt-Nd5</i>		6	<0.01 %	0.01 %
40	CTTATCCTCA	<i>mt-Nd5</i>		61	<0.01 %	0.15 %
41	AGAACTTCAA	<i>mt-Nd5</i>		25	<0.01 %	0.06 %
42	ACTACCATCA	<i>mt-Nd5</i>		267	0.03 %	0.67 %
43	CCTAGTAATC	<i>mt-Nd5</i>		114	0.01 %	0.29 %
44	ATTTTTAAAA	<i>mt-Nd5</i>		139	0.01 %	0.35 %
45	AAAAATCATC	<i>tRNA</i>		859	0.09 %	2.14 %
46	ATGAAACTTT	<i>mt-Cytb</i>		63	<0.01 %	0.16 %
47	TCGGACGAGG	<i>mt-Cytb</i>		137	0.01 %	0.34 %

Supplemental Table 2. (Cont.)

N	Tag	Gene ^a	SNPs ^b	Average tpm ^c	% to Total ^d	% to Mt ^e
48	AGGACAAATA	<i>mt-Cytb</i>		1932	0.19%	4.81%
49	TCTTGATAGT	<i>tRNA</i>		4	<0.01%	0.01%
50	AATATTATCT	<i>D-Loop</i>		45	<0.01%	0.11%
51	ACCAACATAA	<i>D-Loop</i>		3	<0.01%	0.01%
52	CATTTGGTAT	<i>D-Loop</i>		54	0.01%	0.14%
53	AAAGGACAGC	<i>D-Loop</i>		57	0.01%	0.14%
54	CTTGTTAGAC	<i>D-Loop</i>		32	<0.01%	0.08%
55	TTCCGTGAAC	<i>D-Loop</i>		229	0.02%	0.57%
	<i>Total</i>			40 142	4.01%	100.00%
<i>Mus musculus Sau3A I</i>						
1	CAAAAAGATA	<i>mt-Rnr2</i>		1619	0.16%	1.42%
2	AACGGACCAA	<i>mt-Rnr2</i>		698	0.07%	0.61%
3	AGGACATCCC	<i>mt-Rnr2</i>		937	0.09%	0.82%
4	TGAGTTCAGA	<i>mt-Rnr2</i>		3219	0.32%	2.82%
5	AGGATGAGCC	<i>mt-Nd1</i>		174	0.02%	0.15%
6	CTACTCTCTA	<i>mt-Nd1</i>		319	0.03%	0.28%
7	CGAGCATCTT	<i>mt-Nd1</i>		1662	0.17%	1.46%
8	AACTTATACA	<i>mt-Nd1</i>		13 672	1.37%	11.97%
9	AACTGAAGCA	<i>mt-Nd2</i>		395	0.04%	0.35%
10	CCACTGCACA	<i>mt-Nd2</i>		5402	0.54%	4.73%
11	CGTACTTATT	<i>mt-Co1</i>		155	0.02%	0.14%
12	CCGCTGGAGG	<i>mt-Co1</i>		660	0.07%	0.58%
13	TCCAGCTATA	<i>mt-Co1</i>		1149	0.11%	1.01%
14	ATTTATTTCA	<i>mt-Co1</i>		2082	0.21%	1.82%
15	TTTATAATTT	<i>mt-Co1</i>		7478	0.75%	6.55%
16	AATAATCTAT	<i>tRNA</i>		1165	0.12%	1.02%
17	ACACACTAAT	<i>mt-Co2</i>		1258	0.13%	1.10%
18	TAACCATAGC	<i>mt-Co2</i>		2968	0.30%	2.60%
19	TGCTTCAATA	<i>mt-Co2</i>		34 828	3.48%	30.50%
20	AACAAATCTC	<i>mt-Atp6</i>		9929	0.99%	8.70%
21	TAGGAGGCTG	<i>mt-Co3</i>		666	0.07%	0.58%
22	AACATTCCTT	<i>mt-Co3</i>		5311	0.53%	4.65%
23	TTACTCCCTT	<i>mt-Co3/tRNA</i>		9	<0.01%	<0.01%
24	TAACAACCTA	<i>mt-Nd4</i>		181	0.02%	0.16%
25	CACAGCCGTA	<i>mt-Nd4</i>		233	0.02%	0.20%
26	AAACTTTACC	<i>mt-Nd4</i>		6433	0.64%	5.63%
27	AATTATACAA	<i>mt-Nd5</i>		332	0.03%	0.29%
28	TGGTTAGAAA	<i>mt-Nd5</i>		174	0.02%	0.15%
29	ACCCAGCTAC	<i>mt-Nd6</i>		733	0.07%	0.64%
30	CCCAAGTCTC	<i>mt-Nd6</i>		323	0.03%	0.28%
31	CACCAAACCC	<i>mt-Nd6</i>		861	0.09%	0.75%
32	ATATACATTT	<i>mt-Cytb</i>		220	0.02%	0.19%
33	AAACAACCCA	<i>mt-Cytb</i>		8228	0.82%	7.21%
34	TTCTCTTCTC	<i>tRNA</i>		438	0.04%	0.38%
35	AATTCTAGTA	<i>D-Loop</i>		267	0.03%	0.23%
	<i>Total</i>			114 178	11.42%	100.00%
<i>Rattus norvegicus NlaIII</i>						
1	CAAACATCCA	<i>mt-Rnr1</i>		2755	0.28%	3.65%
2	AATCAACCCG	<i>mt-Rnr2</i>		4504	0.45%	5.96%
3	GCCTTCCTCA	<i>mt-Nd1</i>	Variant	949	0.09%	1.26%
	GGCTTCCTCA	<i>mt-Nd1</i>		5	<0.01%	<0.01%
	GCCCTCCTCA	<i>mt-Nd1</i>		4	<0.01%	<0.01%
	GGCCTCCTCA	<i>mt-Nd1</i>		ND	0.00%	0.00%
4	ACAAAAAATT	<i>mt-Nd2</i>		375	0.04%	0.50%
5	AAATAAAACT	<i>mt-Nd2</i>		1719	0.17%	2.28%
6	ATAATCACCT	<i>tRNA</i>		156	0.02%	0.21%
7	CATTCGTAAT	<i>mt-Co1</i>		127	0.01%	0.17%
8	CTGGAGCATC	<i>mt-Co1</i>	Variant	177	0.02%	0.23%
	CTGGGGCATC	<i>mt-Co1</i>		937	0.09%	1.24%
	CTGGAGTATC	<i>mt-Co1</i>		ND	0.00%	0.00%
	CTGGGGTATC	<i>mt-Co1</i>		ND	0.00%	0.00%
9	TAGTTACCTA	<i>mt-Co1</i>		212	0.02%	0.28%

Supplemental Table 2. (Cont.)

<i>N</i>	Tag	Gene ^a	SNPs ^b	Average tpm ^c	% to Total ^d	% to Mt ^e
10	GAGGAAATAT	<i>mt-Co1</i>		86	<0.01 %	0.11 %
11	ATACATACTA	<i>mt-Co1</i>		247	0.02 %	0.33 %
12	AGCAAAAGCC	<i>mt-Co1</i>		376	0.04 %	0.50 %
13	AAATACAGTC	<i>mt-Co1</i>		145	0.01 %	0.19 %
14	ATTTGAGAAG	<i>mt-Co1</i>		330	0.03 %	0.44 %
15	GATGCCCCCC	<i>mt-Co1</i>		15 808	1.58 %	20.92 %
16	GCTTACCCAT	<i>tRNA/mt-Co2</i>		ND	0.00 %	0.00 %
17	ACCACACCCT	<i>mt-Co2</i>		495	0.05 %	0.66 %
18	AGCCGTCCCT	<i>mt-Co2</i>	Variant	593	0.06 %	0.79 %
	AGCCATCCCT	<i>mt-Co2</i>		5964	0.60 %	7.89 %
19	CCACAACATAG	<i>tRNA/mt-Atp8</i>		1	<0.01 %	<0.01 %
20	ATTTATTACA	<i>mt-Atp8</i>		43	<0.01 %	0.06 %
21	ATAACACATA	<i>mt-Atp6</i>		11 203	1.12 %	14.83 %
22	CATACCATAT	<i>mt-Co3</i>		ND	0.00 %	0.00 %
23	ACCACTAACCA	<i>mt-Co3</i>		163	0.02 %	0.22 %
24	AGCCCATCAC	<i>mt-Co3</i>		335	0.03 %	0.44 %
25	GCCTCCCGT	<i>mt-Co3</i>		372	0.04 %	0.49 %
26	ATACTGACAC	<i>mt-Co3</i>		11 170	1.12 %	14.79 %
27	AGCGATTCAA	<i>mt-Nd3</i>		1855	0.19 %	2.45 %
28	ACTCTCAGCC	<i>mt-Nd4</i>		897	0.09 %	1.19 %
29	GATCCAACAC	<i>mt-Nd4</i>		ND	0.00 %	0.00 %
30	TATAATAGCA	<i>mt-Nd4</i>		42	<0.01 %	0.06 %
31	GGAGCTACAA	<i>mt-Nd4</i>	Variant	153	0.02 %	0.20 %
	GGAGCCACAA	<i>mt-Nd4</i>		ND	0.00 %	0.00 %
32	ATGACTATTA	<i>mt-Nd4</i>		2300	0.23 %	3.04 %
33	CACCCATACC	<i>tRNA</i>		1307	0.13 %	1.73 %
34	ATCAATCATA	<i>mt-Nd5</i>	Variant	ND	0.00 %	0.00 %
	ATCAATTATA	<i>mt-Nd5</i>		2	<0.01 %	<0.01 %
35	ATATATACAC	<i>mt-Nd5</i>		32	<0.01 %	0.04 %
36	ACTCCCATCA	<i>mt-Nd5</i>		103	0.01 %	0.14 %
37	CATTCTTCAA	<i>mt-Nd5</i>		52	<0.01 %	0.07 %
38	ACAAAACCAC	<i>mt-Nd5</i>		565	0.06 %	0.75 %
39	AAAAATCATC	<i>tRNA</i>		1201	0.12 %	1.59 %
40	ATGAAACTTC	<i>mt-Cytb</i>		68	0.01 %	0.09 %
41	TGGGACGAGG	<i>mt-Cytb</i>		84	0.01 %	0.11 %
42	GGCTATGTAC	<i>mt-Cytb</i>		14	<0.01 %	0.02 %
43	AGGACAAATA	<i>mt-Cytb</i>		294	0.03 %	0.39 %
44	AATCGGAGGC	<i>mt-Cytb</i>		7093	0.71 %	9.39 %
45	TAATATATAT	<i>D-Loop</i>		79	<0.01 %	0.10 %
46	TCTATTCTCG	<i>D-Loop</i>		ND	0.00 %	0.00 %
47	CACCATTAAG	<i>D-Loop</i>		71	<0.01 %	0.09 %
48	GATCAACATA	<i>D-Loop</i>		ND	0.00 %	0.00 %
49	AAGGTCAGCA	<i>D-Loop</i>		35	<0.01 %	0.05 %
50	TTTGTAAGAC	<i>D-Loop</i>		47	<0.01 %	0.06 %
	<i>Total</i>			75 548	7.55 %	100.00 %
<i>Bos Taurus NlaIII</i>						
1	CTCACACATA	<i>D-Loop</i>		160	0.02 %	0.85 %
2	GACATTACAG	<i>D-Loop</i>		66	<0.01 %	0.35 %
3	CAAGCATCTA	<i>mt-Rnr1</i>		111	0.01 %	0.59 %
4	ATTAAAATAA	<i>mt-Rnr1</i>		563	0.06 %	3.00 %
5	AAGCACGCAC	<i>mt-Rnr1</i>		44	<0.01 %	0.23 %
6	AGAGGAGACA	<i>mt-Rnr1</i>		40	<0.01 %	0.21 %
7	CCTAACGAGC	<i>mt-Rnr2</i>		507	0.05 %	2.70 %
8	AGTTGGTAGT	<i>mt-Rnr2</i>		423	0.04 %	2.25 %
9	TGAATTCCCC	<i>mt-Nd1</i>		71	<0.01 %	0.38 %
10	GCCTCTAGCA	<i>mt-Nd1</i>		332	0.03 %	1.77 %
11	TGACACGTAT	<i>mt-Nd1</i>		1292	0.13 %	6.89 %
12	ACAAAACTA	<i>mt-Nd2</i>		39	<0.01 %	0.21 %
13	AAATAAAACA	<i>mt-Nd2</i>		136	0.01 %	0.73 %
14	TTCATTAACC	<i>tRNA/mt-Co1</i>		14	<0.01 %	0.07 %
15	CAGGAGCTTC	<i>mt-Co1</i>		624	0.06 %	3.33 %
16	GAGGTAATAT	<i>mt-Co1</i>		74	<0.01 %	0.39 %

Supplemental Table 2. (Cont.)

N	Tag	Gene ^a	SNPs ^b	Average tpm ^c	% to Total ^d	% to Mt ^e
17	AGCCAAAATC	<i>mt-Co1</i>		211	0.02 %	1.12 %
18	CCTCGACGAT	<i>mt-Co1</i>		3021	0.30 %	16.10 %
19	ACCACACGCT	<i>mt-Co2</i>		128	0.01 %	0.68 %
20	AGCTGTGCC	<i>mt-Co2</i>		2588	0.26 %	13.79 %
21	CCCATTGTCC	<i>mt-Co2</i>		ND	0.00 %	0.00 %
22	CCGCAACTAG	<i>tRNA/mt-Atp8</i>		1	<0.01 %	<0.01 %
23	ACTGACAATG	<i>mt-Atp8</i>		289	0.03 %	1.54 %
24	AACATTAATA	<i>mt-Atp6</i>		67	<0.01 %	0.36 %
25	ACAACACATA	<i>mt-Atp6</i>		3904	0.39 %	20.80 %
26	CTTATCATAT	<i>mt-Co3</i>		3	<0.01 %	0.01 %
27	TGATTTCACT	<i>mt-Co3</i>		900	0.09 %	4.80 %
28	AGCCTCACAA	<i>mt-Nd3</i>		1097	0.11 %	5.85 %
29	GAACTAATCT	<i>mt-Nd4</i>		30	<0.01 %	0.16 %
30	TATAATAGCT	<i>mt-Nd4</i>		9	<0.01 %	0.05 %
31	ATCTAACATT	<i>mt-Nd4</i>		6	<0.01 %	0.03 %
32	CTAATTATAA	<i>mt-Nd4</i>		112	0.01 %	0.59 %
33	ATCTATTATA	<i>mt-Nd5</i>		ND	0.00 %	0.00 %
34	GTTCTAACA	<i>mt-Nd5</i>		38	<0.01 %	0.20 %
35	CCATTCACCA	<i>mt-Nd5</i>		362	0.04 %	1.93 %
36	GAATCTAACC	<i>tRNA</i>		1	<0.01 %	<0.01 %
37	ACTAATGATA	<i>tRNA</i>		300	0.03 %	1.60 %
38	ATGAAATTTT	<i>mt-Cytb</i>		35	<0.01 %	0.19 %
39	AAATATTGGA	<i>mt-Cytb</i>		19	<0.01 %	0.10 %
40	AGGACAAATA	<i>mt-Cytb</i>		91	<0.01 %	0.48 %
41	AATTGGAGGA	<i>mt-Cytb</i>		629	0.06 %	3.35 %
42	CATATAAGCA	<i>D-Loop</i>		207	0.02 %	1.10 %
43	ACCTCTATAG	<i>D-Loop</i>		133	0.01 %	0.71 %
44	CCGCGTGA	<i>D-Loop</i>		87	<0.01 %	0.46 %
	<i>Total</i>			18 764	1.88 %	100.00 %
		<i>Sus scrofa NlIII</i>				
1	CATATAAGCA	<i>D-Loop</i>		35	<0.01 %	0.11 %
2	TACATATTAT	<i>D-Loop</i>		615	0.06 %	1.93 %
3	TCAAATAACT	<i>D-Loop</i>		ND	0.00 %	0.00 %
4	CATATCACCA	<i>D-Loop</i>		ND	0.00 %	0.00 %
5	CCGCGTGA	<i>D-Loop</i>		83	<0.01 %	0.26 %
6	CTCACACATA	<i>D-Loop</i>		35	<0.01 %	0.11 %
7	GCCGTCAAAG	<i>D-Loop</i>		12	<0.01 %	0.04 %
8	ATCCGGCACG	<i>D-Loop</i>		24	<0.01 %	0.07 %
9	CAAGTATCCG	<i>mt-Rnr1</i>		47	<0.01 %	0.15 %
10	AACGAAAGTT	<i>mt-Rnr1</i>		733	0.07 %	2.30 %
11	AGTATATCCA	<i>mt-Rnr1</i>		ND	0.00 %	0.00 %
12	AAGCACGCAC	<i>mt-Rnr1</i>		24	<0.01 %	0.07 %
13	TAGTAATAAA	<i>mt-Rnr1</i>		24	<0.01 %	0.07 %
14	CAAGAAGAGA	<i>mt-Rnr1</i>		189	0.02 %	0.59 %
15	AGCAGTTTAA	<i>mt-Rnr2</i>		ND	0.00 %	0.00 %
16	GACTAGCAAT	<i>mt-Rnr2</i>		248	0.02 %	0.78 %
17	TTCATAATTA	<i>tRNA/mt-Nd1</i>		12	<0.01 %	0.04 %
18	TTCATTATTG	<i>mt-Nd1</i>		47	<0.01 %	0.15 %
19	TCAAGCCTAG	<i>mt-Nd1</i>		1548	0.15 %	4.86 %
20	GCCCTAGCCA	<i>mt-Nd2</i>		ND	0.00 %	0.00 %
21	ACAAAAACTA	<i>mt-Nd2</i>		225	0.02 %	0.70 %
22	AAACAAAATA	<i>mt-Nd2</i>		ND	0.00 %	0.00 %
23	CCAACACTCA	<i>mt-Nd2</i>		2116	0.21 %	6.64 %
24	ATATTCACCA	<i>tRNA</i>		ND	0.00 %	0.00 %
25	CCTTTGTAAT	<i>mt-Co1</i>		83	<0.01 %	0.26 %
26	CAGGGGCTTC	<i>mt-Co1</i>		ND	0.00 %	0.00 %
27	ATACATATTA	<i>mt-Co1</i>		898	0.09 %	2.82 %
28	AGCAAAAATT	<i>mt-Co1</i>		201	0.02 %	0.63 %
29	AAATACTATT	<i>mt-Co1</i>		1111	0.11 %	3.49 %
30	AGCCGTCCCA	<i>mt-Co2</i>		ND	0.00 %	0.00 %
31	CCCATTGTAC	<i>mt-Co2</i>		12 235	1.22 %	38.38 %
32	ATTCATTACA	<i>mt-Atp8</i>		1158	0.12 %	3.63 %

Supplemental Table 2. (Cont.)

<i>N</i>	Tag	Gene ^a	SNPs ^b	Average tpm ^c	% to Total ^d	% to Mt ^e
33	CATACCACAT	<i>mt-Co3</i>		24	<0.01 %	0.07 %
34	ACCACTTACC	<i>mt-Co3</i>		2422	0.24 %	7.60 %
35	AGCATCCCAA	<i>mt-Nd3</i>		1076	0.11 %	3.37 %
36	AATATCTAAA	<i>mt-Nd4</i>		47	<0.01 %	0.15 %
37	ACTCCTCCCC	<i>mt-Nd4</i>		378	0.04 %	1.19 %
38	CATCATAGCC	<i>mt-Nd4</i>		59	<0.01 %	0.19 %
39	TAGAAGCCCC	<i>mt-Nd4</i>		95	<0.01 %	0.30 %
40	CTTTCCATAT	<i>mt-Nd4</i>		95	<0.01 %	0.30 %
41	ATGACTAATA	<i>mt-Nd4</i>		130	0.01 %	0.41 %
42	ATCCAACATC	<i>mt-Nd4</i>		1513	0.15 %	4.75 %
43	CTTCCACACT	<i>tRNA</i>		ND	0.00 %	0.00 %
44	ATCAATTATA	<i>mt-Nd5</i>		24	<0.01 %	0.07 %
45	ATTCCTAACC	<i>mt-Nd5</i>		ND	0.00 %	0.00 %
46	AGATCTTCAA	<i>mt-Nd5</i>		ND	0.00 %	0.00 %
47	CACGCTTTCT	<i>mt-Nd5</i>		756	0.08 %	2.37 %
48	GAATTTAACC	<i>tRNA</i>		ND	0.00 %	0.00 %
49	AAAAATCATC	<i>tRNA</i>		768	0.08 %	2.41 %
50	ATGAAACTTC	<i>mt-Cytb</i>		59	<0.01 %	0.19 %
51	CAAACGGAGC	<i>mt-Cytb</i>		ND	0.00 %	0.00 %
52	AAACATTGGA	<i>mt-Cytb</i>		236	0.02 %	0.74 %
53	AATTGGAGGA	<i>mt-Cytb</i>		2494	0.25 %	7.82 %
	<i>Total</i>			31 878	3.19 %	100.00 %

SAGE tags are sorted based on their position in mitochondrial genome.

^a Ribosomal RNA mitochondrial genes and transfer RNAs sequences are shown. (/) SAGE tag is located in the boundary of two sequences.

^b SNPs single nucleotide polymorphisms and/or genetic variations within SAGE tags (located for *Homo sapiens* and *Rattus norvegicus* mitochondrial genomes only).

^c Average tag per million (tpm) values are calculated for complete datasets for individual anchoring enzymes/species. ND, not detected.

^d Expression of individual SAGE tags (% to the total number of analysed tags).

^e Expression of individual SAGE tags (% to the total number of tags matching mitochondrial genome). Boldface denotes SAGE tags accounting for over >2% of all tags matching the mitochondrial genome.

Supplemental Table 3. *Relative size of individual mammalian mitochondrial genome sequences*

Sequence	<i>Homo sapiens</i>	<i>Mus musculus</i>	<i>Rattus norvegicus</i>	<i>Bos taurus</i>	<i>Sus scrofa</i>
<i>tRNA</i> (1)	71	69	67	69	70
<i>mt-Rnr1</i>	954	955	958	955	960
<i>tRNA</i> (1)	69	69	68	67	68
<i>mt-Rnr2</i>	1558	1582	1571	1571	1571
<i>tRNA</i> (1)	77	75	75	77	77
<i>mt-Nd1</i>	957	957	957	957	957
<i>tRNA</i> (3)	206	206	207	208	208
<i>mt-Nd2</i>	1044	1038	1041	1044	1044
<i>tRNA</i> (5)	390	376	378	377	380
<i>mt-Co1</i>	1542	1545	1545	1547	1545
<i>tRNA</i> (2)	140	140	138	140	147
<i>mt-Co2</i>	684	684	684	684	688
<i>tRNA</i> (1)	96	69	68	71	68
<i>mt-Atp8</i>	1624	1625	1626	1622	1625
<i>mt-Atp6</i>					
<i>mt-Co3</i>					
<i>tRNA</i> (1)	69	68	67	72	69
<i>mt-Nd3</i>	345	348	348	358	346
<i>tRNA</i> (1)	66	71	71	58	70
<i>mt-Nd4l</i>	1667	1668	1668	1668	1668
<i>mt-Nd4</i>					
<i>tRNA</i> (3)	200	197	198	202	198
<i>mt-Nd5</i>	1812	2329	2326	2332	2332
<i>mt-Nd6</i>	525				
<i>tRNA</i> (1)	73	74	74	73	75
<i>mt-Cytb</i>	1140	1144	1143	1140	1140
<i>tRNA</i> (2)	137	134	137	138	132
<i>D-Loop</i>	1125	877	898	908	1175
Total	16571	16300	16313	16338	16613

Total sequence length is shown for tRNA-encoding sequences-separated mitochondrial genes and/or control region (D-Loop; number of individual tRNA sequences is given in parentheses). Summed sequence length is also shown for *mt-Atp8*, *-Atp6* and *-Co3* genes, *mt-Nd4l* and *-Nd4* (all organisms), *mt-Nd5* and *-Nd6* (all but *Homo sapiens*) owing to overlap in the coding sequences of the corresponding genes.

Supplemental Table 4. Individual SAGE tags matching mitochondrial genome; frequency in human mammary gland, pancreatic and prostatic samples

N	Tag	Gene ^a	SNPs ^b	Mammary gland ^c			Pancreas ^d			Prostate ^e		
				Normal	Cancer	Trend ^f	Normal	Cancer	Trend ^f	Normal	Cancer	Trend ^f
1	CAAGCATCCC	<i>mt-Rnr1</i>		0.20%	0.10%	↓ *	0.09%	0.08%		0.13%	0.20%	↑ *
2	AGGTGGCAAG	<i>mt-Rnr1</i>		0.10%	0.07%		0.03%	0.02%		0.05%	0.10%	↑ *
3	GTAAGTGAC	<i>mt-Rnr1</i>		0.06%	0.03%		0.02%	0.01%		0.04%	0.08%	
4	AAAACATTCT	<i>mt-Rnr2</i>		0.51%	0.24%	↓ ***	0.08%	0.12%	↑ **	0.08%	0.25%	↑ ***
5	CTCATAAGGA	<i>mt-Rnr2</i>		0.10%	0.12%		0.03%	0.05%	↑ *	0.08%	0.24%	↑ ***
6	TTTAACGGCC	<i>mt-Rnr2</i>		0.12%	0.10%		0.02%	0.02%		0.09%	0.15%	↑ **
7	ACACAGCAAG	<i>mt-Rnr2</i>		0.24%	0.03%	↓ ***	0.02%	0.02%		0.04%	0.02%	
8	CTAAGACTTC	<i>mt-Rnr2</i>		0.39%	0.31%		0.09%	0.30%	↑ ***	0.26%	0.86%	↑ ***
9	GCCAACCTCC	<i>mt-Nd1</i>	Variant	<0.01%	0.01%		<0.01%	0.02%		<0.01%	0.01%	
	ACCAACCTCC	<i>mt-Nd1</i>		0.00%	0.00%		<0.01%	0.00%		0.00%	<0.01%	
10	ACCCTGGCC	<i>mt-Nd1</i>		0.06%	0.08%		0.14%	0.17%	↑ *	0.03%	0.13%	↑ ***
11	CTAGCTTTTA	<i>mt-Nd2</i>		0.02%	0.01%		0.01%	<0.01%		0.01%	0.02%	
12	ACAAAACTA	<i>mt-Nd2</i>		0.03%	0.02%		0.02%	0.03%		0.03%	0.04%	
13	ACTAACACCC	<i>mt-Nd2</i>		0.06%	0.07%		0.11%	0.11%		0.09%	0.13%	
14	AGCTGGAGTC	<i>mt-Co1</i>		0.01%	<0.0%		<0.01%	<0.01%		0.03%	0.01%	
15	CATTTGTAAT	<i>mt-Co1</i>		0.02%	0.0%		0.01%	0.02%		0.02%	0.03%	
16	AAACATCCTA	<i>mt-Co1</i>		<0.01%	0.0%		<0.01%	<0.01%		0.07%	0.02%	
17	ATTTGAGAAG	<i>mt-Co1</i>		0.09%	0.12%	↑ *	0.11%	0.20%	↑ ***	0.06%	0.16%	↑ **
18	ACTTTTTCAA	<i>tRNA</i>		0.40%	0.93%	↑ ***	0.30%	0.18%		0.19%	0.24%	
19	CAGCGCAAGT	<i>mt-Co2</i>		0.00%	<0.01%		0.00%	0.00%		<0.01%	<0.01%	
20	ATCACGCCCT	<i>mt-Co2</i>		0.02%	0.02%		0.03%	0.05%		0.03%	0.04%	
21	AGCTGTCCCC	<i>mt-Co2</i>		<0.01%	<0.01%		0.07%	<0.01%	↓ ***	0.03%	0.02%	
22	CCCATCGTCC	<i>mt-Co2</i>		0.25%	0.37%	↑ *	0.28%	0.68%	↑ ***	0.30%	0.60%	↑ ***
23	GCCATCCCT	<i>mt-Atp8</i>		0.03%	0.02%		0.03%	0.01%		0.02%	0.03%	
24	CACCTAATTG	<i>mt-Atp6</i>		0.32%	0.32%		0.32%	0.24%		0.20%	0.30%	
25	CCTATCATAT	<i>mt-Co3</i>		<0.01%	<0.01%		<0.01%	<0.01%		<0.01%	<0.01%	
26	ACCCCTAACA	<i>mt-Co3</i>		<0.01%	<0.01%		<0.01%	<0.01%		0.01%	<0.01%	
27	TGATTTCACT	<i>mt-Co3</i>		0.18%	0.24%	↑ **	0.20%	0.19%	↓ **	0.20%	0.34%	↑ *
28	AGCCCTACAA	<i>mt-Nd3</i>		0.24%	0.22%		0.24%	0.16%		0.23%	0.30%	↑ *
29	ACTTTCCAAA	<i>mt-Nd4</i>		0.04%	0.03%		0.01%	0.02%		0.01%	0.02%	
30	GCAAGCCAAC	<i>mt-Nd4</i>		0.05%	0.04%		0.05%	0.01%		0.02%	0.03%	
31	TCGAAGCCCC	<i>mt-Nd4</i>		0.07%	0.06%		0.06%	0.06%		0.10%	0.09%	
32	TTCATACACC	<i>mt-Nd4</i>		0.26%	0.30%		0.32%	0.12%		0.18%	0.23%	
33	GCTTTCTCAA	<i>tRNA</i>		<0.01%	<0.01%		<0.01%	<0.01%		0.02%	<0.01%	↓ **
34	CACACTACTA	<i>mt-Nd5</i>		<0.01%	<0.01%		0.00%	0.00%		<0.01%	<0.01%	
35	TGCCATGACC	<i>mt-Nd5</i>		<0.01%	<0.01%		0.00%	<0.01%		<0.01%	<0.01%	
36	GTCCATCATA	<i>mt-Nd5</i>		<0.01%	<0.01%		<0.01%	<0.01%		<0.01%	<0.01%	
37	ATTTATCCTA	<i>mt-Nd5</i>		<0.01%	<0.01%		<0.01%	0.00%		<0.01%	<0.01%	
38	AGACCCACAA	<i>mt-Nd5</i>		0.02%	0.02%		0.02%	0.02%		<0.01%	0.02%	
39	CCTCAGGATA	<i>mt-Nd6</i>		0.02%	0.03%		0.03%	0.06%	↑ *	0.02%	0.05%	
40	ATGAAACTTC	<i>mt-Cytb</i>		<0.01%	<0.01%		0.01%	<0.01%		0.11%	0.05%	

Supplemental Table 4. (Cont.)

N	Tag	Gene ^a	SNPs ^b	Mammary gland ^c			Pancreas ^d			Prostate ^e		
				Normal	Cancer	Trend ^f	Normal	Cancer	Trend ^f	Normal	Cancer	Trend ^f
41	CACTACTCAC	<i>mt-Cytb</i>		0.03 %	0.06 %		0.14 %	0.06 %		0.04 %	0.12 %	↑ **
42	GGGAAGCAGA	<i>D-Loop</i>		0.03 %	0.09 %	↑ ***	0.04 %	0.04 %		0.07 %	0.04 %	
43	AATATTGTAC	<i>D-Loop</i>		<0.01 %	<0.01 %		<0.01 %	<0.01 %		<0.01 %	<0.01 %	
44	CTTACAAGCA	<i>D-Loop</i>		<0.01 %	<0.01 %		<0.01 %	0.01 %		<0.01 %	<0.01 %	
45	GATGACCCCC	<i>D-Loop</i>		0.01 %	0.01 %		<0.01 %	0.02 %		<0.01 %	<0.01 %	
46	CATTTGGTAT	<i>D-Loop</i>		0.01 %	<0.01 %		<0.01 %	<0.01 %		0.02 %	0.02 %	
	<i>Total</i>			4.05 %	4.65 %		2.99 %	3.15 %		2.95 %	5.08 %	

SAGE tags are sorted based on their position in human mitochondrial genome.

^a Ribosomal RNA, mitochondrial genes and transfer RNAs sequences are shown.

^b SNPs, single nucleotide polymorphisms and/or genetic variations within SAGE tags.

^c Mammary gland. Normal: GSM677, GSM692, GSM760, GSM781, GSM14754, GSM14756, GSM14757, GSM14801; Cancer: GSM670, GSM672, GSM687, GSM688, GSM725, GSM750, GSM752, GSM753, GSM1730, GSM1731, GSM1733, GSM2382, GSM2383, GSM2389, GSM14743, GSM14745, GSM14746, GSM14747, GSM14748, GSM14797, GSM14800.

^d Pancreas. Normal: GSM678, GSM716, GSM721, GSM3838, GSM3839, GSM3840, GSM14770; Cancer: GSM742, GSM743, GSM744, GSM14735, GSM14736.

^e Prostate. Normal: GSM685, GSM739, GSM754, GSM764, GSM14752, GSM14758; Cancer: GSM680, GSM681, GSM683, GSM684, GSM686, GSM723, GSM724, GSM740.

^f Trend to alteration is indicated by arrowheads (↑ or ↓). Asterisks (*, ** and ***), indicate statistical significance between averaged tag abundance in groups calculated according to Madden *et al.* (1997). * $P < 0.05$; ** $P < 0.01$; *** $P < 0.001$.

Expression of individual SAGE tags (group average) is shown as a percentage to the total number of analysed tags. Boldface denotes SAGE tags accounting for over 0.25 % of a total number of sequenced tags.