Supporting Online Material for

Impaired expression of NER gene network in sporadic solid tumors

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Supplementary Methods

Analysis of SAGE libraries

To illustrate the mathematical definitions used for the analysis presented in the text, consider two hypothetical SAGE libraries (with a set of ten SAGE tags), as presented in **Figure S1**. If a tag is randomly selected, the probability distribution describes the probability $p(i,\alpha)$ that the observed tag will be of a particular type i. The quantity H_α indicates how diverse a distribution is, giving an estimate of diversity observed in the distribution of tags. In this case, the distribution **(B)** is more heterogeneous compared to distribution **(A)**, since in **(B)** the tags are equally dispersed, while in **(A)** the tags are more concentrated in two types. The distribution **(B)** shows the highest possible diversity value, with $H_\alpha = 1.0$. Therefore, an increase in heterogeneity of some SAGE library implies higher H_α, indicating higher diversity. Having **(A)** as reference for normal condition, the relative increase of diversity in **(B)** is expressed by the term $h_\alpha = 0.595$. Since both distributions have the activity (*e.g.* $N^c_\alpha = N^r_\alpha = 30.0$), the normalized number of SAGE tags is $n_\alpha = 0.50$. In addition, we present another example in **Figure S2** where the normalization condition gives the same h_α regardless the different numbers of SAGE tags in the libraries.

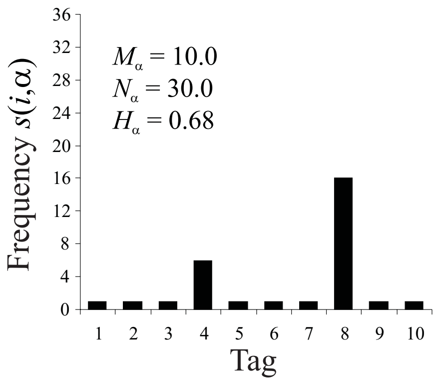
Figure S1

(A)

Tag	Frequency $s(i,\alpha)$	$p(i,\alpha)$	$p(i,\alpha).\ln p(i,\alpha)$
1. CAGATCCAAA	1	0.03	-0.11
2. CAGATCCCCA	1	0.03	-0.11
3. CAGATCGGAT	1	0.03	-0.11
4. CAGATCTATT	6	0.20	-0.32
5. CAGATCTTTG	1	0.03	-0.11
6. CAGATCTTTT	1	0.03	-0.11
7. CAGATGAATA	1	0.03	-0.11
8. CAGATGAATG	16	0.53	-0.34
9. CAGATGAGAA	1	0.03	-0.11
10. CAGATGCAAA	1	0.03	-0.11
Σ	30	1.00	-1.56

(B)

Tag	Frequency $s(i,\alpha)$	$p(i,\alpha)$	$p(i,\alpha).\ln p(i,\alpha)$
1. CAGATCCAAA	3	0.10	-0.23
2. CAGATCCCCA	3	0.10	-0.23
3. CAGATCGGAT	3	0.10	-0.23
4. CAGATCTATT	3	0.10	-0.23
5. CAGATCTTTG	3	0.10	-0.23
6. CAGATCTTTT	3	0.10	-0.23
7. CAGATGAATA	3	0.10	-0.23
8. CAGATGAATG	3	0.10	-0.23
9. CAGATGAGAA	3	0.10	-0.23
10. CAGATGCAAA	3	0.10	-0.23
Σ	30	1.00	-2.30



$\boldsymbol{h_\alpha = 0.595}$

$\boldsymbol{n_\alpha = 0.500}$

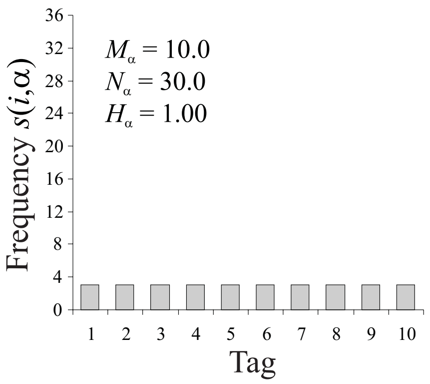


Figure S1. Illustrative distributions of SAGE tags for two hypothetical libraries. Each table presents thirty SAGE tags ($N_\alpha = 30.0$) with ten possible different SAGE tags ($M_\alpha = 10.0$). For a given SAGE library α, $s(i,\alpha)$ is the number of tags of type i; $p(i,\alpha)$ is the normalized probability function (*e.g.* the probability that among all tags we randomly choose one that is of type i). Below each table the histogram of $s(i,\alpha)$ is presented and the resulting h_α and n_α are obtained by eq.(3) and eq.(4), respectively. **(A)** When SAGE tags distribution are concentrated between two possibilities. **(B)** When SAGE tags are equally distributed among all possibilities.

Figure S2

(A)

Tag	Frequency $s(i,\alpha)$	$p(i,\alpha)$	$p(i,\alpha).\ln p(i,\alpha)$
1. CAGATCCAAA	2	0.03	-0.11
2. CAGATCCCCA	2	0.03	-0.11
3. CAGATCGGAT	2	0.03	-0.11
4. CAGATCTATT	12	0.20	-0.32
5. CAGATCTTTG	2	0.03	-0.11
6. CAGATCTTTT	2	0.03	-0.11
7. CAGATGAATA	2	0.03	-0.11
8. CAGATGAATG	32	0.53	-0.34
9. CAGATGAGAA	2	0.03	-0.11
10. CAGATGCAAA	2	0.03	-0.11
Σ	60	1.00	-1.56

(B)

Tag	Frequency $s(i,\alpha)$	$p(i,\alpha)$	$p(i,\alpha).\ln p(i,\alpha)$
1. CAGATCCAAA	1	0.10	-0.23
2. CAGATCCCCA	1	0.10	-0.23
3. CAGATCGGAT	1	0.10	-0.23
4. CAGATCTATT	1	0.10	-0.23
5. CAGATCTTTG	1	0.10	-0.23
6. CAGATCTTTT	1	0.10	-0.23
7. CAGATGAATA	1	0.10	-0.23
8. CAGATGAATG	1	0.10	-0.23
9. CAGATGAGAA	1	0.10	-0.23
10. CAGATGCAAA	1	0.10	-0.23
Σ	10	1.00	-2.30

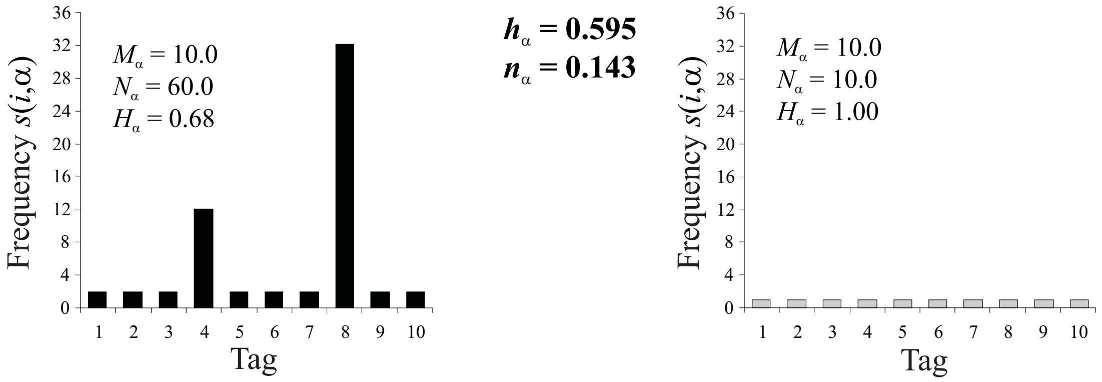


Figure S2. Illustrative distributions of SAGE libraries for different number of SAGE tags. Data table presenting different number of tags, but with the same ten possible SAGE tags (M_α = 10.0) as illustrated in **Figure S1**. **(A)** When SAGE tags distribution are concentrated between two possibilities. **(B)** When SAGE tags are equally distributed among all possibilities.

Figure S3

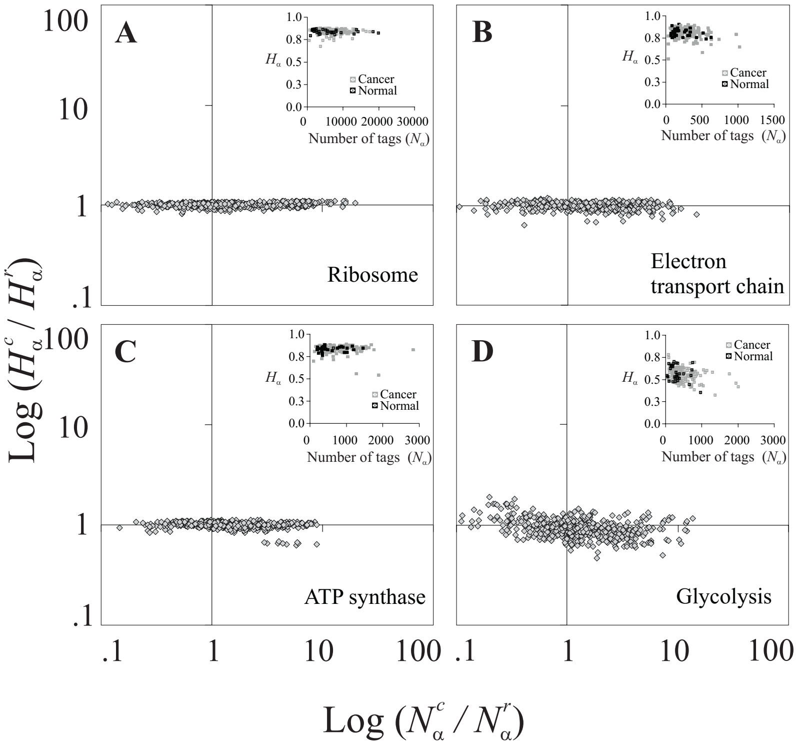


Figure S3. Diversity of gene expression pathways involved in core cell functions. Log-log scatter plots showing the ratio of cancer and normal tissue diversity (H^c_α / H^r_α) as a function of the corresponding number of SAGE tags (ratio N^c_α / N^r_α). The plots for absolute values of H_α as a function of N_α are shown in the inserts. The groups of genes that form each pathway are presented in **Tables S5** to **S8** and were defined accordingly to Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways (1): (A) Ribosome pathway, as described in *Ribosome - Homo sapiens (human)*; (B) Electron transport chain (ETC) pathway, derived from *Oxidative phosphorylation - Homo sapiens (human)*; (C) ATP synthase pathway, derived from *Oxidative phosphorylation - Homo sapiens (human);* (D) Glycolysis pathway, derived from *Glycolysis / Gluconeogenesis - Homo sapiens (human)*.

Figure S4

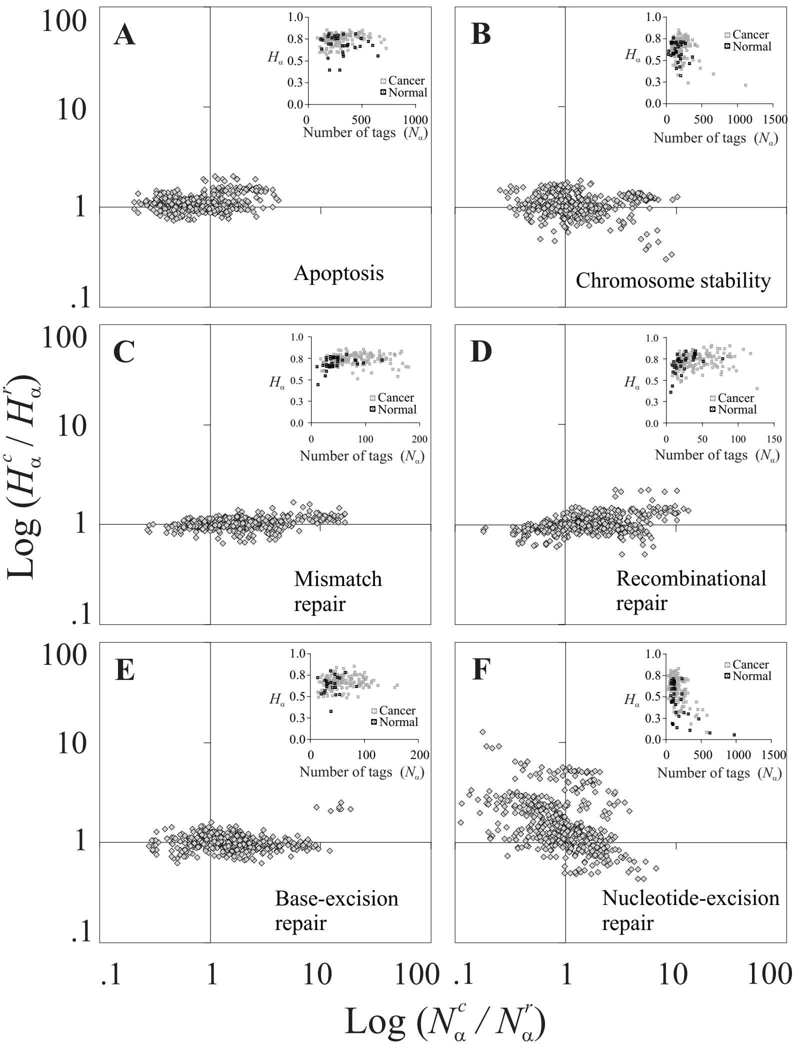


Figure S4. Diversity of gene expression pathways involved in genomic stability. Log-log scatter plots showing the ratio of cancer and normal tissue diversity (H_α^c / H_α^r) as a function of the corresponding number of SAGE tags (ratio N_α^c / N_α^r). The plots for absolute values of diversity H_α as a function of number N_α of SAGE tags are shown in the inserts. The groups of genes that form each pathway are presented in **Tables S9** to **S14** and were defined accordingly to several references: **(A)** Apoptosis pathway, as described in *Apoptosis - Homo sapiens (human)* KEGG pathway (1); **(B)** Chromosome stability pathway, derived from compilation of genes that may trigger chromosome instability when mutated, accordingly to Wang et al. (2); **(C)** Mismatch repair (MMR) pathway, compilation of genes constructed accordingly to Wood et al. (3) and Jiricny (4); **(D)** Recombinational repair (RER) pathway, **(E)** Base-excision repair (BER) pathway, and **(F)** Nucleotide-excision repair (NER) pathway, compilations of genes accordingly to Wood et al. (3).

Figure S5

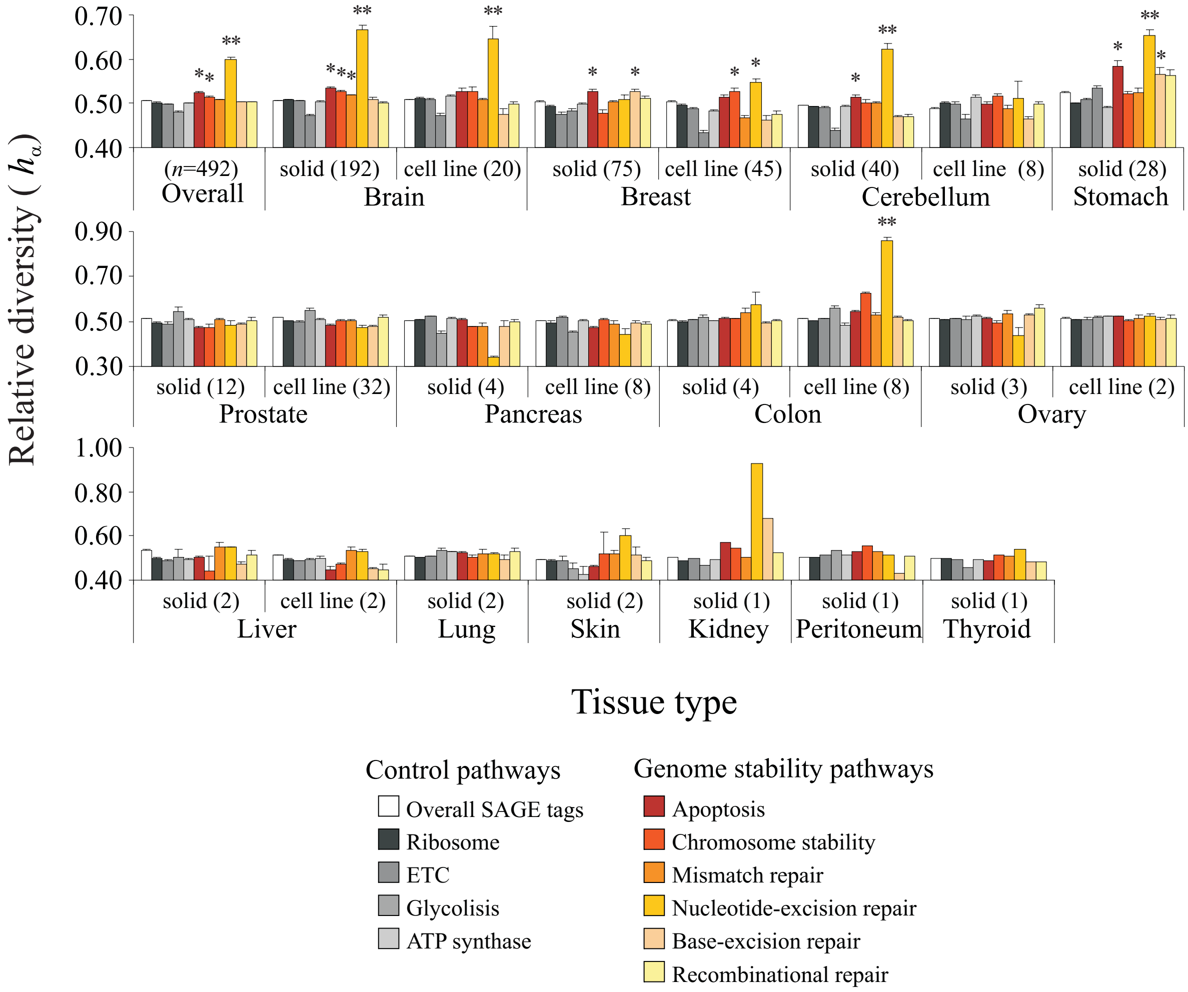


Figure S5. Stochastic contrasts among gene expression pathways according to diversity of SAGE tags. Statistical analyses are carried out by Kruskal-Wallis one-way analysis of variance followed by Mann-Whitney test for comparisons. *Different from controls with $P<0.02$; **Different from others with $P<0.001$.

Figure S6

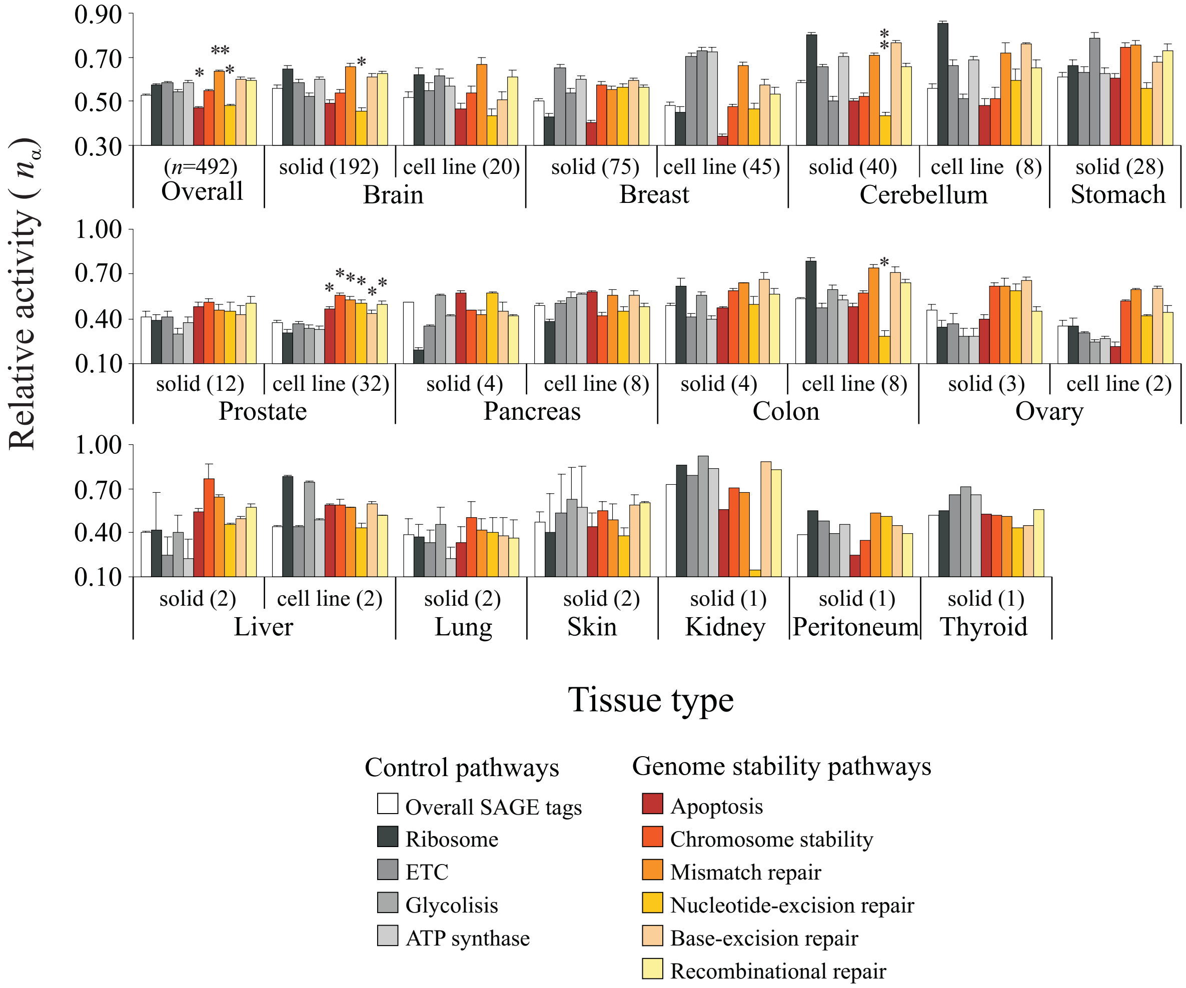


Figure S6. Stochastic contrasts among gene expression pathways according to number of SAGE tags. Statistical analyses are carried out by Kruskal-Wallis one-way analysis of variance followed by Mann-Whitney test for comparisons.*Different from controls with $P<0.04$; **different from others with $P<0.04$.

Figure S7

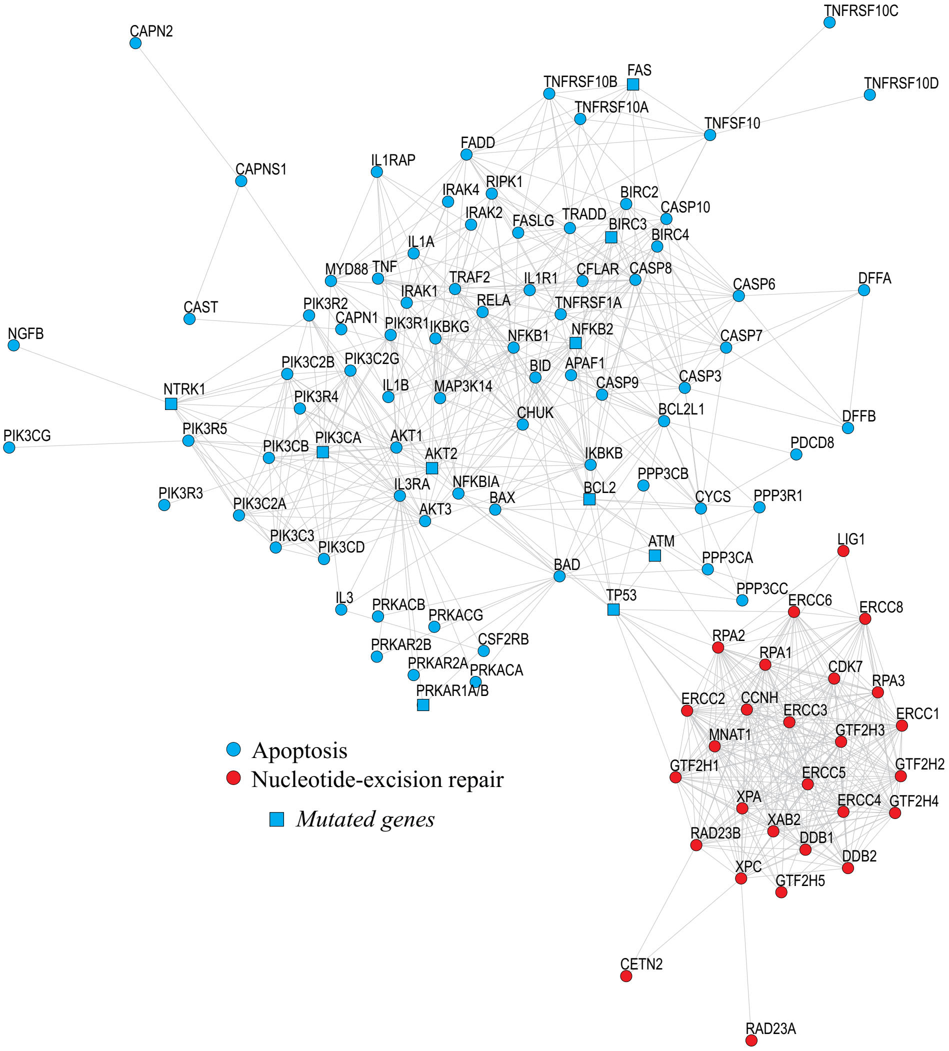


Figure S7. Graph of interactions among genes involved only in apoptosis and NER pathways. The graph is generated using database STRING (*5*). Different pathways are represented by different colors. Square nodes represent genes whose somatic mutations have been causally implicated in oncogenesis (6).

Figure S8

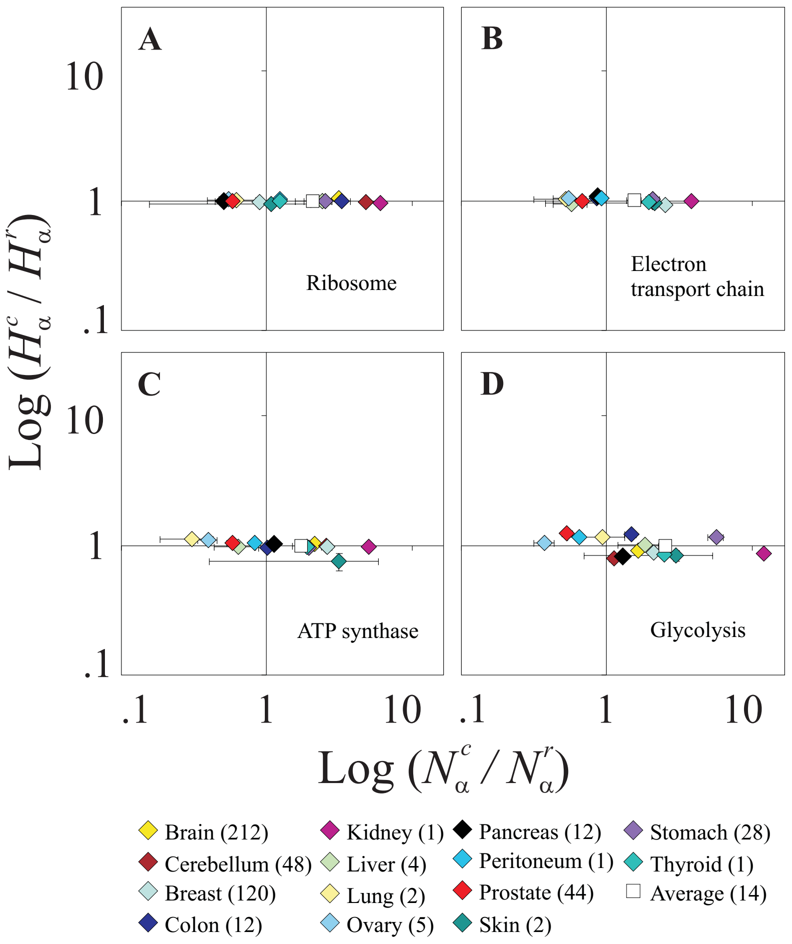


Figure S8. Average diversity of gene expression pathways involved in core cell functions. Log-log scatter plots showing average diversity of the ratio H^c_α / H^r_α by tissue type as a function of the corresponding number of SAGE tags (ratio N^c_α / N^r_α). The groups of genes that form each pathway are presented in **Tables S5** to **S8** and were defined as in **Figure S3**. The number of matched pairs of each tissue type is showed in the legend. Error bars: SEM of pairwise ratio H^c_α / H^r_α of each specific tissue type.

Figure S9

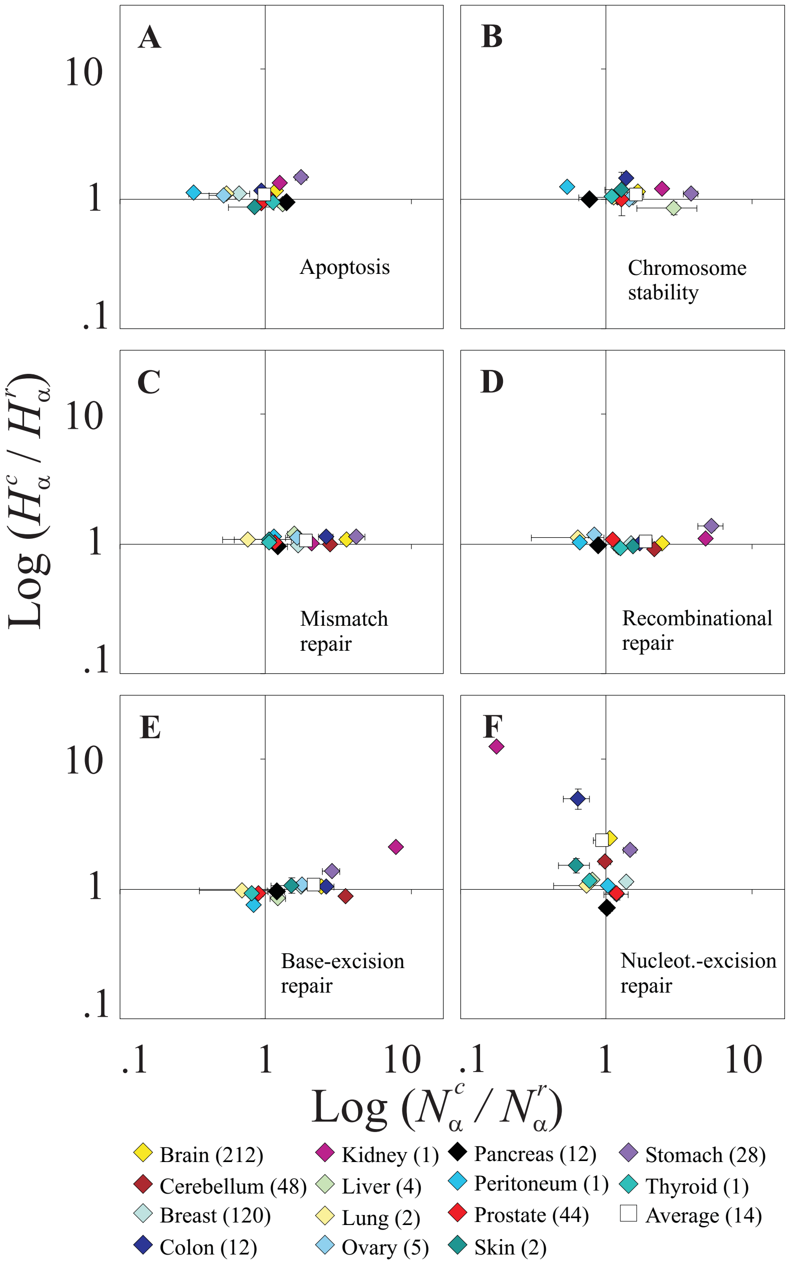


Figure S9. Average diversity of gene expression pathways involved in genomic stability. Log-log scatter plots showing average diversity of the ratio H^c_α / H^r_α by tissue type as a function of the corresponding number of SAGE tags (ratio N^c_α / N^r_α). The groups of genes that form each pathway are presented in **Tables S9** to **S14** and were defined as in **Figure S4**. The number of matched pairs of each tissue type is showed in the legend. Error bars: SEM of pairwise ratio H^c_α / H^r_α of each specific tissue type.

Figure S10

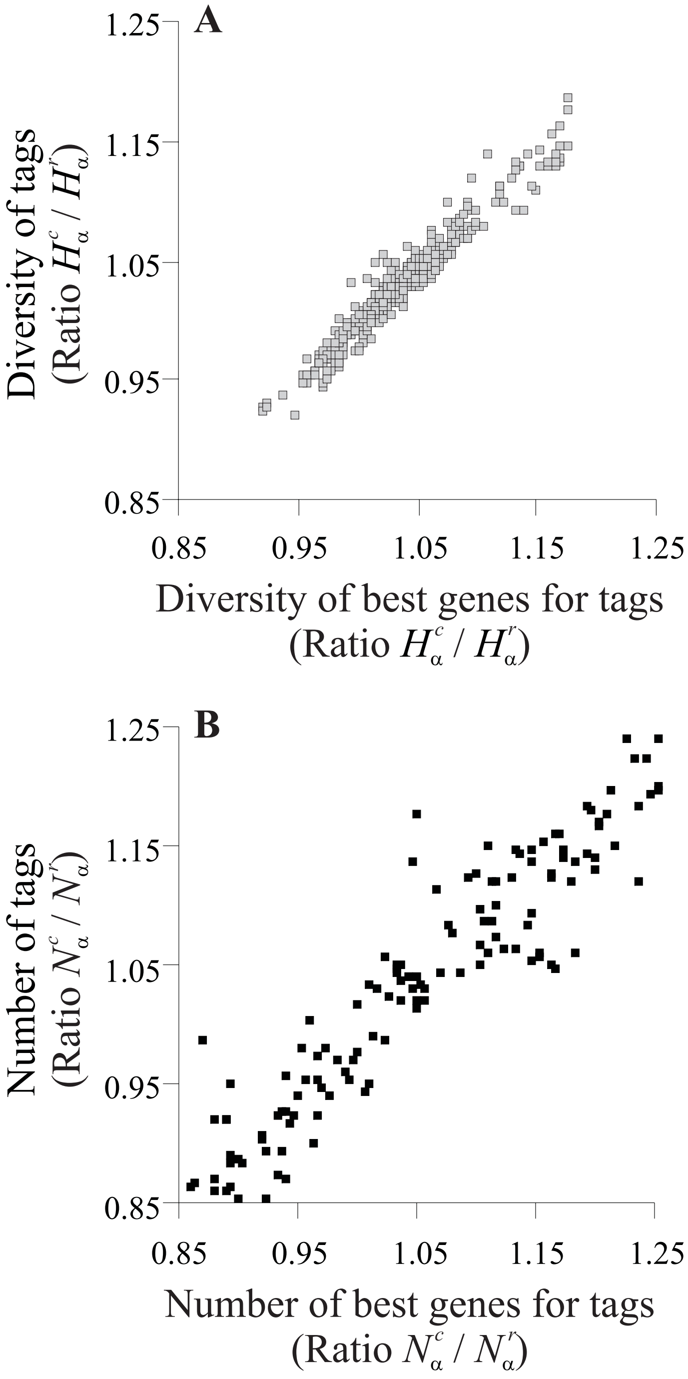


Figure S10. Correlation between SAGE tag and SAGE tag-to-gene databases. **(A)** Diversity of tags as a function of best genes for tags (ratio H^c_α / H^r_α). **(B)** Number of tags as a function of best genes for tags (ratio N^c_α / N^r_α).

Supplementary tables

Table S1. Diversity of normal tissue SAGE libraries.

Library Title [a]	**Tissue**	**Preparation**	H_α [b]	M_α [c]	N_α [d]	
SAGE_Brain_normal_cerebellum_B_1	cerebellum	bulk	0.909	24357	50385	🟥
SAGE_Brain_normal_cerebellum_B_BB542	cerebellum	bulk	0.906	19163	40500	🟥
SAGE_Breast_normal_myoepithelium_AP_myoep.1	breast	ABP	0.905	26342	57222	🟥
SAGE_Peritoneum_normal_B_13	peritoneum	bulk	0.896	22799	53527	🟥
SAGE_Skin_normal_B_NS	skin	bulk	0.892	15246	36615	🟪
SAGE_Breast_normal_epithelium_AP_1	breast	ABP	0.880	18276	48729	🟪
SAGE_Pancreas_normal_CS_HX	pancreas	STC	0.877	12392	31985	🟪
SAGE_Pancreas_normal_CS_H126	pancreas	STC	0.877	12360	32223	🟪
SAGE_Brain_normal_peds_cortex_B_H1571	brain	bulk	0.874	24161	77554	🟦
SAGE_Breast_normal_epithelium_AP_Br_N	breast	ABP	0.866	19190	50512	🟦
SAGE_Prostate_normal_MD_PR317	prostate	MCD	0.865	18732	59277	🟦
SAGE_Brain_normal_leptomeninges_B_AL2	brain	bulk	0.864	26220	72473	🟦
SAGE_Thyroid_normal_B_001	thyroid	bulk	0.863	35845	115938	🟦
SAGE_Ovary_normal_CS_HOSE_4	ovary	STC	0.861	15994	47728	🟦
SAGE_Brain_normal_cortex_B_BB542	brain	bulk	0.861	31683	94233	🟦
SAGE_Breast_normal_organoid_B	breast	bulk	0.860	19602	58181	🟦
SAGE_Prostate_normal_B_2	prostate	bulk	0.855	20456	64058	🟦
SAGE_Lung_normal_B_1	lung	bulk	0.852	24764	88708	🟦
SAGE_Stomach_normal_B_antrum	stomach	bulk	0.848	9349	26653	🟦
SAGE_Colon_normal_B_NC1	colon	bulk	0.847	17703	49610	🟦
SAGE_Brain_normal_thalamus_B_1	brain	bulk	0.847	10115	24015	🟦
SAGE_Colon_normal_B_NC2	colon	bulk	0.846	16270	48479	🟦
SAGE_Kidney_normal_B_1	kidney	bulk	0.844	16295	40993	🟦
SAGE_Breast_normal_stroma_AP_1	breast	ABP	0.825	23409	79152	🟦
SAGE_Stomach_normal_MD_14S	stomach	MCD	0.819	18718	73353	🟦
SAGE_Prostate_normal_epithelium_CS_senescent	prostate	STC	0.800	16963	71717	🟦
SAGE_Liver_normal_B_1	liver	bulk	0.792	15496	66308	🟦
SAGE_Prostate_normal_epithelium_CS_confluent	prostate	STC	0.786	15164	71897	🟦
SAGE_Stomach_normal_MD_13S	gastr. tract	MCD	0.785	15700	45908	🟦
SAGE_Stomach_normal_epithelium_B_body1	stomach	bulk	0.783	8907	24761	🟦

[a] Normal SAGE libraries retrieved based on the search criteria: tag length (short 10bp); tissue preparation [bulk, short term culture (STC), antibody purified (ABP) or microscope dissected (MCD)]; and tissue histology (normal). The list contains only normal libraries that have at least one cancer equivalent tissue library, matching the search criteria. One normal library (SAGE_Brain_normal_cortex_B_pool6) was not included because is derived from pooled samples.

[b] Diversity (color code indicates de H_α level); [c] Number of unique tags; [d] Number of tags.

Color code	🟦	🟦	🟦	🟦	🟪	🟪	🟪	🟪	🟥	🟥
H_α	<0.860	<0.865	<0.870	<0.875	<0.880	<0.885	<0.890	<0.895	<0.900	≥0.900

Table S2. Diversity of brain cancer SAGE libraries.

Library Title [a]	**Tissue**	**Preparation**	H_α [b]	M_α [c]	N_α [d]	
SAGE_Brain_astrocytoma_grade_III_B_H1020	brain	bulk	0.926	30738	51573	🟥
SAGE_Brain_ependymoblastoma_B_819	brain	bulk	0.914	14845	33975	🟥
SAGE_Brain_ependymoma_B_1150	brain	bulk	0.910	23324	62373	🟥
SAGE_Brain_glioblastoma_CS_TA2	brain	STC	0.910	21568	46678	🟥
SAGE_Brain_ependymoma_B_239	brain	bulk	0.908	20459	46653	🟥
SAGE_Brain_oligodendroglioma_B_H988	brain	bulk	0.905	13982	27864	🟥
SAGE_Brain_glioblastoma_B_pooled	brain	bulk	0.902	24020	56428	🟥
SAGE_Brain_glioblastoma_B_H1371	brain	bulk	0.901	22909	49338	🟥
SAGE_Brain_ependymoma_B_R353	brain	bulk	0.900	27211	73822	🟥
SAGE_Brain_ependymoma_B_H580	brain	bulk	0.900	25883	68614	🟥
SAGE_Brain_ependymoma_B_R455	brain	bulk	0.898	19611	51825	🟥
SAGE_Brain_ependymoma_B_R510	brain	bulk	0.897	30595	84073	🟥
SAGE_Brain_ependymoma_B_1394	brain	bulk	0.896	22956	56314	🟥
SAGE_Brain_astrocytoma_grade_I_B_H1043	brain	bulk	0.894	30880	75922	🟪
SAGE_Brain_oligodendroglioma_B_1001	brain	bulk	0.891	14369	32442	🟪
SAGE_Brain_astrocytoma_grade_II_B_H516	brain	bulk	0.891	42250	108116	🟪
SAGE_Brain_glioblastoma_B_H1110	brain	bulk	0.891	25812	68986	🟪
SAGE_Brain_glioblastoma_B_R20	brain	bulk	0.887	35474	101053	🟪
SAGE_Brain_ependymoma_B_R1023	brain	bulk	0.884	40027	122690	🟪
SAGE_Brain_ependymoma_B_R512	brain	bulk	0.883	27374	75379	🟪
SAGE_Brain_astrocytoma_grade_II_B_H530	brain	bulk	0.881	34715	102439	🟪
SAGE_Brain_astrocytoma_grade_III_B_H272	brain	bulk	0.880	34171	96059	🟪
SAGE_Brain_astrocytoma_grade_II_B_H563	brain	bulk	0.880	30054	88568	🟪
SAGE_Brain_astrocytoma_grade_III_B_H970	brain	bulk	0.880	35207	106982	🟪
SAGE_Brain_astrocytoma_grade_III_B_828	brain	bulk	0.879	32109	99939	🟪
SAGE_Brain_glioblastoma_B_R336	brain	bulk	0.878	34762	102322	🟪
SAGE_Brain_astrocytoma_grade_III_B_R140	brain	bulk	0.878	36465	118733	🟪
SAGE_Brain_astrocytoma_grade_III_B_H1055	brain	bulk	0.878	37250	109886	🟪
SAGE_Brain_astrocytoma_grade_III_B_R927	brain	bulk	0.877	33747	107344	🟪
SAGE_Brain_astrocytoma_grade_II_B_H359	brain	bulk	0.877	35555	105764	🟪
SAGE_Brain_ependymoma_B_R628	brain	bulk	0.875	39836	120431	🟪
SAGE_Brain_glioblastoma_B_H1353	brain	bulk	0.875	37773	124805	🟦
SAGE_Brain_glioblastoma_B_H1425C	brain	bulk	0.874	28204	88990	🟦
SAGE_Brain_meningioma_grade_II_B_SF3622	brain	bulk	0.872	16264	44857	🟦
SAGE_Brain_ependymoma_B_R582	brain	bulk	0.871	17282	52189	🟦
SAGE_Brain_astrocytoma_grade_II_B_H501	brain	bulk	0.871	38047	128309	🟦
SAGE_Brain_glioblastoma_B_H833	brain	bulk	0.870	34143	100600	🟦
SAGE_Brain_meningioma_grade_III_B_SF2366	brain	bulk	0.867	20161	59786	🟦
SAGE_Brain_astrocytoma_grade_II_B_H388	brain	bulk	0.864	34081	106285	🟦
SAGE_Brain_meningioma_grade_II_B_SF2176	brain	bulk	0.864	16920	48711	🟦
SAGE_Brain_astrocytoma_grade_III_B_407	brain	bulk	0.863	32819	108312	🟦
SAGE_Brain_glioblastoma_B_R70	brain	bulk	0.863	32108	99099	🟦
SAGE_Brain_astrocytoma_grade_II_B_H518	brain	bulk	0.863	36310	116022	🟦
SAGE_Brain_astrocytoma_grade_III_B_439	brain	bulk	0.861	34620	107824	🟦
SAGE_Brain_astrocytoma_grade_III_B_343	brain	bulk	0.858	29620	100158	🟦
SAGE_Brain_astrocytoma_grade_III_B_584	brain	bulk	0.858	30772	103008	🟦
SAGE_Brain_astrocytoma_grade_II_B_H127	brain	bulk	0.844	31165	114489	🟦
SAGE_Brain_glioblastoma_B_GBM1062	brain	bulk	0.820	15504	59762	🟦

Table S2 (*Continued*).

Library Title [a]	**Tissue**	**Preparation**	H_α [b]	M_α [c]	N_α [d]	
SAGE_Brain_medulloblastoma_B_H1322	cerebellum	bulk	0.928	28969	59498	🟥
SAGE_Brain_medulloblastoma_B_98-05-P608	cerebellum	bulk	0.921	22675	48451	🟥
SAGE_Brain_medulloblastoma_B_C609	cerebellum	bulk	0.914	32456	74612	🟥
SAGE_Brain_medulloblastoma_B_1273	cerebellum	bulk	0.905	17236	38614	🟥
SAGE_Brain_medulloblastoma_B_H484	cerebellum	bulk	0.904	25712	57469	🟥
SAGE_Brain_medulloblastoma_B_98-09-P558	cerebellum	bulk	0.903	33598	85984	🟥
SAGE_Brain_medulloblastoma_B_96-04-P019	cerebellum	bulk	0.903	22017	52645	🟥
SAGE_Brain_medulloblastoma_B_98-13-P301	cerebellum	bulk	0.897	17313	45342	🟥
SAGE_Brain_medulloblastoma_B_98-04-P117	cerebellum	bulk	0.893	14766	32570	🟪
SAGE_Brain_medulloblastoma_B_98-05-P040	cerebellum	bulk	0.889	34995	89258	🟪
SAGE_Brain_medulloblastoma_B_H972	cerebellum	bulk	0.886	30675	85376	🟪
SAGE_Brain_medulloblastoma_B_98-04-P494	cerebellum	bulk	0.884	16247	43068	🟪
SAGE_Brain_medulloblastoma_B_H306	cerebellum	bulk	0.883	24714	60454	🟪
SAGE_Brain_medulloblastoma_B_DL7	cerebellum	bulk	0.883	25370	68392	🟪
SAGE_Brain_medulloblastoma_B_97-05-P312	cerebellum	bulk	0.881	28029	74295	🟪
SAGE_Brain_medulloblastoma_B_H275	cerebellum	bulk	0.877	26151	72318	🟪
SAGE_Brain_medulloblastoma_B_H876	cerebellum	bulk	0.876	25648	67404	🟪
SAGE_Brain_medulloblastoma_B_97-05-P015	cerebellum	bulk	0.868	24631	69971	🟦
SAGE_Brain_medulloblastoma_B_DL5	cerebellum	bulk	0.868	28721	83671	🟦
SAGE_Brain_medulloblastoma_B_H1413	cerebellum	bulk	0.842	22833	61853	🟦

[a] Brain cancer SAGE libraries retrieved based on the search criteria: tag length (short 10bp); tissue preparation [bulk, short term culture (STC), antibody purified (ABP) or microscope dissected (MCD)]; and tissue histology (cancer). The list contains only cancer libraries that have at least one normal equivalent tissue library, matching the search criteria. Cerebellum tissue libraries are retrieved by specific access in CGAP search tools and, therefore, are listed separately from brain tissue.

[b] Diversity (color code indicates de H_α level); [c] Number of unique tags; [d] Number of tags.

Color code	🟦	🟦	🟦	🟦	🟪	🟪	🟪	🟪	🟥	🟥
H_α	<0.860	<0.865	<0.870	<0.875	<0.880	<0.885	<0.890	<0.895	<0.900	≥0.900

Table S3. Diversity of epithelial cancer SAGE libraries.

Library Title [a]	**Tissue**	**Preparation**	H_α [b]	M_α [c]	N_α [d]	
SAGE_Liver_cholangiocarcinoma_B_K1	liver	bulk	0.940	40476	60319	🟥
SAGE_Skin_melanoma_B_DB3	skin	bulk	0.928	6267	11399	🟥
SAGE_Ovary_adenocarcinoma_B_OVT-8	ovary	bulk	0.925	16312	31987	🟥
SAGE_Peritoneum_mesothelioma_B_12	peritoneum	bulk	0.906	14103	32529	🟥
SAGE_Ovary_adenocarcinoma_B_OVT-6	ovary	bulk	0.905	18440	41443	🟥
SAGE_Stomach_adenocarcinoma_MD_G329	stomach	MCD	0.898	19208	46802	🟥
SAGE_Pancreas_adenocarcinoma_B_91-16113	pancreas	bulk	0.895	15793	33582	🟥
SAGE_Prostate_carcinoma_B_LN-1	prostate	bulk	0.895	10601	22599	🟥
SAGE_Lung_adenocarcinoma_MD_L9	lung	MCD	0.895	15131	35916	🟥
SAGE_Liver_cholangiocarcinoma_B_K2D	liver	bulk	0.894	20722	46853	🟪
SAGE_Breast_carcinoma_epithelium_AP_DCIS6	breast	ABP	0.894	30256	72857	🟪
SAGE_Stomach_adenocarcinoma_MD_HG7	stomach	MCD	0.891	34469	93714	🟪
SAGE_Breast_carcinoma_epithelium_AP_DCIS-3	breast	ABP	0.891	31142	57402	🟪
SAGE_Breast_carcinoma_B_IDC-4	breast	bulk	0.891	21531	64095	🟪
SAGE_Breast_carcinoma_B_DCIS-5	breast	bulk	0.889	15935	43098	🟪
SAGE_Stomach_carcinoma_B_xenograft_X101	stomach	bulk	0.888	25022	69749	🟪
SAGE_Stomach_carcinoma_B_xenograph_X43	stomach	bulk	0.886	19923	51620	🟪
SAGE_Stomach_adenocarcinoma_MD_HS29	stomach	MCD	0.886	22385	58831	🟪
SAGE_Pancreas_adenocarcinoma_B_96-6252	pancreas	bulk	0.885	14339	33213	🟪
SAGE_Colon_adenocarcinoma_B_Tu98	colon	bulk	0.884	18794	41371	🟪
SAGE_Skin_melanoma_B_DB2	skin	bulk	0.884	15667	41338	🟪
SAGE_Breast_carcinoma_metastasis_B_2	breast	bulk	0.883	18625	49794	🟪
SAGE_Ovary_adenocarcinoma_B_OVT-7	ovary	bulk	0.878	19479	53514	🟪
SAGE_Breast_carcinoma_epithelium_AP_DCIS7	breast	ABP	0.878	31311	89184	🟪
SAGE_Breast_carcinoma_B_95-259	breast	bulk	0.877	14924	39364	🟪
SAGE_Lung_adenocarcinoma_MD_L10	lung	MCD	0.876	29062	86887	🟪
SAGE_Stomach_adenocarcinoma_B_G234	stomach	bulk	0.872	21447	64925	🟦
SAGE_Breast_carcinoma_B_IDC-5	breast	bulk	0.871	20457	60451	🟦
SAGE_Breast_metastatic_carcinoma_B_95-348	breast	bulk	0.871	20057	60343	🟦
SAGE_Breast_carcinoma_B_IDC-3	breast	bulk	0.871	22732	68891	🟦
SAGE_Kidney_carcinoma_B_D2	kidney	bulk	0.867	32412	100281	🟦
SAGE_Breast_carcinoma_B_95-347	breast	bulk	0.866	22561	67070	🟦
SAGE_Breast_carcinoma_MD_DCIS	breast	MCD	0.865	14237	40783	🟦
SAGE_Skin_melanoma_B_DB1	skin	bulk	0.864	11905	26032	🟦
SAGE_Breast_metastatic_carcinoma_B_95-260	breast	bulk	0.864	15708	45087	🟦
SAGE_Breast_carcinoma_B_DCIS-4	breast	bulk	0.863	20224	60605	🟦
SAGE_Thyroid_follicular_carcinoma_B_TT004	thyroid	bulk	0.861	36863	124664	🟦
SAGE_Breast_carcinoma_epithelium_AP_DCIS-2	breast	ABP	0.860	20611	66168	🟦
SAGE_Prostate_carcinoma_B_pool2	prostate	bulk	0.859	22306	66034	🟦
SAGE_Prostate_adenocarcinoma_MD_PR317	prostate	MCD	0.857	18877	64951	🟦
SAGE_Stomach_carcinoma_B_G189	stomach	bulk	0.857	17672	63075	🟦
SAGE_Colon_adenocarcinoma_B_Tu102	colon	bulk	0.854	22713	55700	🟦

[a] Epithelial cancer SAGE libraries retrieved based on the search criteria: tag length (short 10bp); tissue preparation [bulk, short term culture (STC), antibody purified (ABP) or microscope dissected (MCD)]; and tissue histology (cancer). The list contains only epithelial cancer libraries that have at least one normal equivalent tissue library, matching the search criteria.

[b] Diversity (color code indicates de H_α level); [c] Number of unique tags; [d] Number of tags.

Color code	🟦	🟦	🟦	🟦	🟪	🟪	🟪	🟪	🟥	🟥
H_α	<0.860	<0.865	<0.870	<0.875	<0.880	<0.885	<0.890	<0.895	<0.900	≥0.900

Table S4. Diversity of cancer cell lines SAGE libraries.

Library Title [a]	**Tissue**	**Preparation**	H_α [b]	M_α [c]	N_α [d]	
Brain cancer cell lines						
SAGE_Brain_glioblastoma_CL_H392	brain	cell line	0.886	19417	55990	🟪
SAGE_Brain_glioblastoma_hypoxia_CL_H247	brain	cell line	0.884	24770	71765	🟪
SAGE_Brain_glioblastoma_control_CL_H247	brain	cell line	0.881	19237	60428	🟪
SAGE_Brain_medulloblastoma_CL_4-HCR	cerebellum	cell line	0.879	26573	66599	🟪
SAGE_Brain_medulloblastoma_CL_mhh-1	cerebellum	cell line	0.879	18542	47858	🟪
SAGE_Brain_glioblastoma_CL_H54+LacZ	brain	cell line	0.878	20539	66908	🟪
SAGE_Brain_glioblastoma_CL_H54+EGFRvIII	brain	cell line	0.877	19079	56982	🟪
SAGE_Brain_medulloblastoma_CL_D283	cerebellum	cell line	0.872	25279	66316	🟦
SAGE_Brain_medulloblastoma_CL_H341	cerebellum	cell line	0.839	15220	43920	🟦
Epithelial cancer cell lines						
SAGE_Ovary_carcinoma_CL_A2780	ovary	cell line	0.928	10675	21369	🟥
SAGE_Prostate_carcinoma_CL_PC3_AS2	prostate	cell line	0.925	20661	40768	🟥
SAGE_Prostate_carcinoma_CL_PC3_Mock	prostate	cell line	0.915	15961	38819	🟥
SAGE_Breast_carcinoma_CL_MDA435H48	breast	cell line	0.908	18060	40323	🟥
SAGE_Breast_carcinoma_CL_MDA435C	breast	cell line	0.906	20080	47270	🟥
SAGE_Breast_carcinoma_CL_MDA435H24	breast	cell line	0.906	20234	46631	🟥
SAGE_Ovary_carcinoma_CL_ES2-1	ovary	cell line	0.898	13583	31159	🟥
SAGE_Pancreas_adenocarcinoma_CL_CAPAN1	pancreas	cell line	0.897	14815	37674	🟥
SAGE_Prostate_carcinoma_CL_LNCaP-C	prostate	cell line	0.894	15561	40029	🟪
SAGE_Colon_adenocarcinoma_CL_HCT116	colon	cell line	0.893	24585	55641	🟪
SAGE_Pancreas_adenocarcinoma_CL_Panc1	pancreas	cell line	0.891	10293	24749	🟪
SAGE_Colon_adenocarcinoma_CL_RKO	colon	cell line	0.889	23086	51294	🟪
SAGE_Prostate_carcinoma_CL_A+	prostate	cell line	0.888	12281	30298	🟪
SAGE_Prostate_adenocarcinoma_CL_LNCaP	prostate	cell line	0.888	9155	22344	🟪
SAGE_Colon_adenocarcinoma_CL_Caco2	colon	cell line	0.885	23111	60682	🟪
SAGE_Prostate_carcinoma_CL_LNCaP-T	prostate	cell line	0.884	15922	43542	🟪
SAGE_Breast_carcinoma_CL_ZR75_1_tamoxifen	breast	cell line	0.883	5017	40052	🟪
SAGE_Breast_carcinoma_CL_ZR75_1_untreated	breast	cell line	0.882	3983	32303	🟪
SAGE_Pancreas_carcinoma_CL_PL45	pancreas	cell line	0.876	11121	29557	🟪
SAGE_Colon_adenocarcinoma_CL_SW837	colon	cell line	0.870	20756	61148	🟦
SAGE_Breast_carcinoma_CL_ZR75_1_estrogen	breast	cell line	0.859	4282	38797	🟦
SAGE_Breast_carcinoma_CL_MCF7estradiol_3h	breast	cell line	0.856	17821	60162	🟦
SAGE_Breast_carcinoma_CL_MCF7estradiol_10H	breast	cell line	0.853	17213	60725	🟦
SAGE_Prostate_carcinoma_CL_LNCaP	prostate	cell line	0.849	18404	60250	🟦
SAGE_Pancreas_carcinoma_CL_ASPC	pancreas	cell line	0.847	10622	31224	🟦
SAGE_Liver_cholangiocarcinoma_CL_K4	liver	cell line	0.837	16652	52973	🟦
SAGE_Liver_cholangiocarcinoma_CL_K3	liver	cell line	0.836	16356	54842	🟦
SAGE_ Prostate_carcinoma_CL_LNCaP_no-DHT	prostate	cell line	0.835	16768	62160	🟦
SAGE_Breast_carcinoma_CL_MCF7control_0h	breast	cell line	0.834	15401	59877	🟦

[a] Epithelial and brain cell lines SAGE libraries retrieved based on the search criteria: tag length (short 10bp); tissue preparation (cell lines); and tissue histology (cancer). The list contains only cell lines libraries that have at least one normal equivalent tissue library, matching the search criteria.

[b] Diversity (color code indicates de H_α level); [c] Number of unique tags; [d] Number of tags.

Color code	🟦	🟦	🟦	🟦	🟪	🟪	🟪	🟪	🟥	🟥
H_α	<0.860	<0.865	<0.870	<0.875	<0.880	<0.885	<0.890	<0.895	<0.900	≥0.900

Table S5. Ribosome.

Gene Name [a]	Symbol	UniGene
Ribosomal protein S27-like	RPS27L	Hs.108957
Ribosomal protein L41	RPL41	Hs.112553
Ribosomal protein L3	RPL3	Hs.119598
Ribosomal protein L36a	RPL36A	Hs.12332
Ribosomal protein S28	RPS28	Hs.153177
Ribosomal protein S29	RPS29	Hs.156367
Ribosomal protein L8	RPL8	Hs.178551
Ribosomal protein L5	RPL5	Hs.180946
Ribosomal protein L35	RPL35	Hs.182825
Ribosomal protein L4	RPL4	Hs.186350
Ribosomal protein S10	RPS10	Hs.188882
Ribosomal protein S21	RPS21	Hs.190968
Ribosomal protein L41	RPL41	Hs.242947
Ribosomal protein L32	RPL32	Hs.265174
Chromosome 15 open reading frame 15	C15orf15	Hs.274772
Ribosomal protein S4, Y-linked 1	RPS4Y1	Hs.282376
Ribosomal protein L41	RPL41	Hs.282998
Ribosomal protein L17	RPL17	Hs.293653
Ribosomal protein L39	RPL39	Hs.300141
Ribosomal protein L10-like	RPL10L	Hs.308332
Ribosomal protein S27a	RPS27A	Hs.311640
Ribosomal protein S28	RPS28	Hs.322473
Ribosomal protein L18a	RPL18A	Hs.337766
Ribosomal protein S2	RPS2	Hs.356366
Ribosomal protein L28	RPL28	Hs.356371
Ribosomal protein, large, P1	RPLP1	Hs.356502
Ribosomal protein S3A	RPS3A	Hs.356572
Ribosomal protein S24	RPS24	Hs.356794
Ribosomal protein L41	RPL41	Hs.356799
Ribosomal protein S15a	RPS15A	Hs.370504
Ribosomal protein L17	RPL17	Hs.374588
Ribosomal protein S5	RPS5	Hs.378103
Ribosomal protein L38	RPL38	Hs.380953
Ribosomal protein L19	RPL19	Hs.381061
Ribosomal protein S2	RPS2	Hs.381079
Ribosomal protein L21	RPL21	Hs.381123
Ribosomal protein S14	RPS14	Hs.381126
Ribosomal protein L15	RPL15	Hs.381219
Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously expressed (fox derived); ribosomal protein S30	FAU	Hs.387208
Ribosomal protein L11	RPL11	Hs.388664
Ribosomal protein S16	RPS16	Hs.397609
Ribosomal protein L30	RPL30	Hs.400295
Ribosomal protein L23	RPL23	Hs.406300
Ribosomal protein S10	RPS10	Hs.406620
Ribosomal protein S15	RPS15	Hs.406683
Ribosomal protein L36	RPL36	Hs.408018
Ribosomal protein S6	RPS6	Hs.408073
Ribosomal protein L13	RPL13	Hs.410817

Table S5. (*Continued*)

Gene Name [a]	Symbol	UniGene
Ribosomal protein L9	RPL9	Hs.412370
Ribosomal protein L23a	RPL23A	Hs.419463
Ribosomal protein L7	RPL7	Hs.421257
Ribosomal protein L29	RPL29	Hs.425125
Ribosomal protein L36a	RPL36A	Hs.432485
Ribosomal protein S17	RPS17	Hs.433427
Ribosomal protein S11	RPS11	Hs.433529
Ribosomal protein L37a	RPL37A	Hs.433701
Ribosomal protein L34	RPL34	Hs.438227
Ribosomal protein S19	RPS19	Hs.438429
Ribosomal protein L14	RPL14	Hs.446522
Ribosomal protein S13	RPS13	Hs.446588
Ribosomal protein S4, X-linked	RPS4X	Hs.446628
Ribosomal protein S26	RPS26	Hs.447562
Ribosomal protein, large, P0	RPLP0	Hs.448226
Ribosomal protein SA	RPSA	Hs.449909
Ribosomal protein L19	RPL19	Hs.458593
Ribosomal protein S9	RPS9	Hs.467284
Ribosomal protein L31	RPL31	Hs.469473
Ribosomal protein L24	RPL24	Hs.477028
Ribosomal protein L26	RPL26	Hs.482144
Ribosomal protein L17	RPL17	Hs.485090
Ribosomal protein L29	RPL29	Hs.486304
Ribosomal protein L9	RPL9	Hs.495851
Ribosomal protein S2	RPS2	Hs.498569
Ribosomal protein L7a	RPL7A	Hs.499839
Ribosomal protein S2	RPS2	Hs.506997
Ribosomal protein L23	RPL23	Hs.512542
Ribosomal protein S8	RPS8	Hs.512675
Ribosomal protein S25	RPS25	Hs.512676
Ribosomal protein L9	RPL9	Hs.513083
Ribosomal protein L21	RPL21	Hs.514118
Ribosomal protein L27	RPL27	Hs.514196
Ribosomal protein L22	RPL22	Hs.515329
Ribosomal protein L18	RPL18	Hs.515517
Ribosomal protein L27a	RPL27A	Hs.523463
Ribosomal protein S23	RPS23	Hs.527193
Ribosomal protein L6	RPL6	Hs.528668
Ribosomal protein L35a	RPL35A	Hs.529631
Ubiquitin A-52 residue ribosomal protein fusion product 1	UBA52	Hs.5308
Ribosomal protein L5	RPL5	Hs.532359
Ribosomal protein S7	RPS7	Hs.534346
Ribosomal protein L10	RPL10	Hs.534404
Ribosomal protein L10a	RPL10A	Hs.546269
Ribosomal protein L6	RPL6	Hs.546283
Ribosomal protein, large, P0	RPLP0	Hs.546285
Ribosomal protein S3	RPS3	Hs.546286
Ribosomal protein S7	RPS7	Hs.546287
Ribosomal protein S9	RPS9	Hs.546288
Ribosomal protein S12	RPS12	Hs.546289
Ribosomal protein S27 (metallopanstimulin 1)	RPS27	Hs.546291

Table S5. (*Continued*)

Gene Name [a]	Symbol	UniGene
Ribosomal protein S27a	RPS27A	Hs.546292
Ribosomal protein L13a	RPL13A	Hs.546356
Ribosomal protein L26-like 1	RPL26L1	Hs.546390
Ribosomal protein L24	RPL24	Hs.547172
Ribosomal protein L39	RPL39	Hs.558387
Ribosomal protein L37	RPL37	Hs.558601
Ribosomal protein SA	RPSA	Hs.560655
Ribosomal protein S26	RPS26	Hs.567235
Ribosomal protein L14	RPL14	Hs.567699
Ribosomal protein L26	RPL26	Hs.569777
Ribosomal protein L7	RPL7	Hs.571841
Ribosomal protein L12	RPL12	Hs.579823
Ribosomal protein S2	RPS2	Hs.584910
Ribosomal protein S17	RPS17	Hs.591117
Ribosomal protein L4	RPL4	Hs.591306
Ribosomal protein L15	RPL15	Hs.592455
Ribosomal protein L9	RPL9	Hs.610444
Ribosomal protein S18	RPS18	Hs.627414
Ribosomal protein S27 (metallopanstimulin 1)	RPS27	Hs.631658
Ribosomal protein L41	RPL41	Hs.632703
Ribosomal protein S26	RPS26	Hs.632726
Ribosomal protein L24	RPL24	Hs.637250
Ribosomal protein S3	RPS3	Hs.642582
Ribosomal protein S14	RPS14	Hs.643170
Ribosomal protein S2	RPS2	Hs.643542
Ribosomal protein L26	RPL26	Hs.643630
Ribosomal protein L37	RPL37	Hs.80545
Ribosomal protein S20	RPS20	Hs.8102

[a] Gene set from Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway, Ribosome - Homo sapiens (human) (1). The gene list was also checked in HUGO Database (7) and NCBI Entrez (8) to link the approved gene name with respective UniGene cluster.

Table S6. Electron transport chain (ETC).

Gene Name[a]	Symbol	UniGene
COX10 homolog, cytochrome c oxidase assembly protein, heme A: farnesyltransferase (yeast)	COX10	Hs.462278
COX11 homolog, cytochrome c oxidase assembly protein (yeast)	COX11	Hs.591171
COX15 homolog, cytochrome c oxidase assembly protein (yeast)	COX15	Hs.591916
COX17 cytochrome c oxidase assembly homolog (S. cerevisiae)	COX17	Hs.534383
Cytochrome c oxidase subunit IV isoform 1	COX4I1	Hs.433419
Cytochrome c oxidase subunit IV isoform 2 (lung)	COX4I2	Hs.277101
Cytochrome c oxidase subunit Va	COX5A	Hs.401903
Cytochrome c oxidase subunit Vb	COX5B	Hs.1342
Cytochrome c oxidase subunit VIa polypeptide 1	COX6A1	Hs.497118
Cytochrome c oxidase subunit VIa polypeptide 2	COX6A2	Hs.250760
Cytochrome c oxidase subunit Vib polypeptide 1 (ubiquitous)	COX6B1	Hs.431668
Cytochrome c oxidase subunit VIb polypeptide 2 (testis)	COX6B2	Hs.550544
Cytochrome c oxidase subunit VIc	COX6C	Hs.351875
Cytochrome c oxidase subunit VIIa polypeptide 1 (muscle)	COX7A1	Hs.421621
Cytochrome c oxidase subunit VIIa polypeptide 2 (liver)	COX7A2	Hs.70312
Cytochrome c oxidase subunit VIIa polypeptide 2 like	COX7A2L	Hs.339639
Cytochrome c oxidase subunit VIIb	COX7B	Hs.522699
Cytochrome c oxidase subunit VIIb2	COX7B2	Hs.479656
Cytochrome c oxidase subunit VIIc	COX7C	Hs.430075
Cytochrome c oxidase subunit 8A (ubiquitous)	COX8A	Hs.433901
Cytochrome c-1	CYC1	Hs.289271
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1, 7.5kDa	NDUFA1	Hs.534168
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 10, 42kDa	NDUFA10	Hs.277677
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 11, 14.7kDa	NDUFA11	Hs.406062
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 12	NDUFA12	Hs.506374
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 13	NDUFA13	Hs.534453
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2, 8kDa	NDUFA2	Hs.534333
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 3, 9kDa	NDUFA3	Hs.198269
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4, 9kDa	NDUFA4	Hs.50098
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4-like 2	NDUFA4L2	Hs.221447
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5, 13kDa	NDUFA5	Hs.643550
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6, 14kDa	NDUFA6	Hs.274416
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7, 14.5kDa	NDUFA7	Hs.333427
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 8, 19kDa	NDUFA8	Hs.495039
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9, 39kDa	NDUFA9	Hs.75227
NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1, 8kDa	NDUFAB1	Hs.189716
NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 1, 7kDa	NDUFB1	Hs.183435
NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10, 22kDa	NDUFB10	Hs.513266
NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 11, 17.3kDa	NDUFB11	Hs.521969
NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2, 8kDa	NDUFB2	Hs.324250
NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 3, 12kDa	NDUFB3	Hs.109760
NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 4, 15kDa	NDUFB4	Hs.304613
NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 4, 15kDa	NDUFB4	Hs.594079
NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5, 16kDa	NDUFB5	Hs.518424
NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6, 17kDa	NDUFB6	Hs.493668
NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7, 18kDa	NDUFB7	Hs.532853
NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8, 19kDa	NDUFB8	Hs.523215
NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9, 22kDa	NDUFB9	Hs.15977
NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 1, 6kDa	NDUFC1	Hs.84549

Table S6. (*Continued*).

Gene Name [a]	Symbol	UniGene
NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2, 14.5kDa	NDUFC2	Hs.407860
NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa (NADH-coenzyme Q reductase)	NDUFS1	Hs.471207
NADH dehydrogenase (ubiquinone) Fe-S protein 2, 49kDa (NADH-coenzyme Q reductase)	NDUFS2	Hs.173611
NADH dehydrogenase (ubiquinone) Fe-S protein 3, 30kDa (NADH-coenzyme Q reductase)	NDUFS3	Hs.502528
NADH dehydrogenase (ubiquinone) Fe-S protein 4, 18kDa (NADH-coenzyme Q reductase)	NDUFS4	Hs.528222
NADH dehydrogenase (ubiquinone) Fe-S protein 5, 15kDa (NADH-coenzyme Q reductase)	NDUFS5	Hs.632385
NADH dehydrogenase (ubiquinone) Fe-S protein 6, 13kDa (NADH-coenzyme Q reductase)	NDUFS6	Hs.408257
NADH dehydrogenase (ubiquinone) Fe-S protein 7, 20kDa (NADH-coenzyme Q reductase)	NDUFS7	Hs.211914
NADH dehydrogenase (ubiquinone) Fe-S protein 8, 23kDa (NADH-coenzyme Q reductase)	NDUFS8	Hs.90443
NADH dehydrogenase (ubiquinone) flavoprotein 1, 51kDa	NDUFV1	Hs.7744
NADH dehydrogenase (ubiquinone) flavoprotein 2, 24kDa	NDUFV2	Hs.464572
NADH dehydrogenase (ubiquinone) flavoprotein 3, 10kDa	NDUFV3	Hs.473937
Pyrophosphatase (inorganic) 1	PPA1	Hs.437403
Pyrophosphatase (inorganic) 2	PPA2	Hs.480452
Succinate dehydrogenase complex, subunit A, flavoprotein (Fp)	SDHA	Hs.440475
Succinate dehydrogenase complex, subunit B, iron sulfur (Ip)	SDHB	Hs.465924
Succinate dehydrogenase complex, subunit C, integral membrane protein, 15kDa	SDHC	Hs.444472
Succinate dehydrogenase complex, subunit D, integral membrane protein	SDHD	Hs.356270
Ubiquinol-cytochrome c reductase complex (7.2 kD)	UCRC	Hs.284292
Ubiquinol-cytochrome c reductase, 6.4kDa subunit	UQCR	Hs.8372
Ubiquinol-cytochrome c reductase binding protein	UQCRB	Hs.131255
Ubiquinol-cytochrome c reductase core protein I	UQCRC1	Hs.119251
Ubiquinol-cytochrome c reductase core protein II	UQCRC2	Hs.592048
Ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1	UQCRFS1	Hs.170107
Ubiquinol-cytochrome c reductase hinge protein	UQCRH	Hs.481571
Ubiquinol-cytochrome c reductase, complex III subunit VII, 9.5kDa	UQCRQ	Hs.146602

[a] Selected genes from Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway, Oxidative phosphorylation - Homo sapiens (human) (1). The gene list was checked in HUGO Database (7) and NCBI Entrez (8) to link the approved gene name with respective UniGene cluster.

Table S7. ATP synthase.

Gene Name [a]	Symbol	UniGene
ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit 1, cardiac muscle	ATP5A1	Hs.298280
ATP synthase, H+ transporting, mitochondrial F1 complex, beta polypeptide	ATP5B	Hs.406510
ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	ATP5C1	Hs.271135
ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit	ATP5D	Hs.418668
ATP synthase, H+ transporting, mitochondrial F1 complex, epsilon subunit	ATP5E	Hs.177530
ATP synthase, H+ transporting, mitochondrial F0 complex, subunit B1	ATP5F1	Hs.514870
ATP synthase, H+ transporting, mitochondrial F0 complex, subunit C1 (subunit 9)	ATP5G1	Hs.80986
ATP synthase, H+ transporting, mitochondrial F0 complex, subunit C2 (subunit 9)	ATP5G2	Hs.524464
ATP synthase, H+ transporting, mitochondrial F0 complex, subunit C3 (subunit 9)	ATP5G3	Hs.429
ATP synthase, H+ transporting, mitochondrial F0 complex, subunit d	ATP5H	Hs.514465
ATP synthase, H+ transporting, mitochondrial F0 complex, subunit E	ATP5I	Hs.85539
ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F6	ATP5J	Hs.246310
ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F2	ATP5J2	Hs.521056
ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F2	ATP5J2	Hs.567610
ATP synthase, H+ transporting, mitochondrial F0 complex, subunit G	ATP5L	Hs.486360
ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein)	ATP5O	Hs.409140

[a] Selected genes from Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway, Oxidative phosphorylation - Homo sapiens (human) (1). The gene list was checked in HUGO Database (7) and NCBI Entrez (8) to link the approved gene name with respective UniGene cluster.

Table S8. Glycolysis.

Gene Name [a]	Symbol	UniGene
Hexokinase 1	HK1	Hs.370365
Glucose phosphate isomerase	GPI	Hs.466471
Phosphofructokinase, liver	PFKL	Hs.255093
Phosphofructokinase, muscle	PFKM	Hs.75160
Phosphofructokinase, platelet	PFKP	Hs.26010
Aldolase A, fructose-bisphosphate	ALDOA	Hs.513490
Aldolase B, fructose-bisphosphate	ALDOB	Hs.530274
Aldolase C, fructose-bisphosphate	ALDOC	Hs.155247
Triosephosphate isomerase 1	TPI1	Hs.524219
Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	Hs.479728
Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	Hs.544577
Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	Hs.592355
Phosphoglycerate kinase 1	PGK1	Hs.78771
Phosphoglycerate kinase 2	PGK2	Hs.367727
Phosphoglycerate mutase 1 (brain)	PGAM1	Hs.447492
Phosphoglycerate mutase 1 (brain)	PGAM1	Hs.592599
Phosphoglycerate mutase 2 (muscle)	PGAM2	Hs.632642
Enolase 1, (alpha)	ENO1	Hs.517145
Enolase 2 (gamma, neuronal)	ENO2	Hs.511915
Enolase 3 (beta, muscle)	ENO3	Hs.224171
Pyruvate kinase, liver and RBC	PKLR	Hs.95990
Pyruvate kinase, muscle	PKM2	Hs.534770

[a] Selected genes from Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway, Glycolysis / Gluconeogenesis - Homo sapiens (human) (1). The gene list was checked in HUGO Database (7) and NCBI Entrez (8) to link the approved gene name with respective UniGene cluster.

Table S9. Apoptosis.

Gene Name [a]	Symbol	UniGene
V-akt murine thymoma viral oncogene homolog 1	AKT1	Hs.525622
V-akt murine thymoma viral oncogene homolog 2	AKT2	Hs.631535
V-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma)	AKT3	Hs.498292
Apoptotic peptidase activating factor	APAF1	Hs.552567
Ataxia telangiectasia mutated (includes complementation groups A, C and D)	ATM	Hs.435561
BCL2-antagonist of cell death	BAD	Hs.370254
BCL2-associated X protein	BAX	Hs.631546
B-cell CLL/lymphoma 2	BCL2	Hs.150749
BCL2-like 1	BCL2L1	Hs.516966
BH3 interacting domain death agonist	BID	Hs.591054
Baculoviral IAP repeat-containing 2	BIRC2	Hs.643515
Baculoviral IAP repeat-containing 3	BIRC3	Hs.127799
Baculoviral IAP repeat-containing 4	BIRC4	Hs.356076
Calpain 1, (mu/I) large subunit	CAPN1	Hs.502842
Calpain 1, (mu/I) large subunit	CAPN1	Hs.521800
Calpain 10	CAPN10	Hs.112218
Calpain 11	CAPN11	Hs.225953
Calpain 2, (m/II) large subunit	CAPN2	Hs.350899
Calpain 3, (p94)	CAPN3	Hs.143261
Calpain 5	CAPN5	Hs.248153
Calpain 6	CAPN6	Hs.496593
Calpain 7	CAPN7	Hs.631920
Calpain 9	CAPN9	Hs.498021
Calpain, small subunit 1	CAPNS1	Hs.515371
Caspase 10, apoptosis-related cysteine peptidase	CASP10	Hs.5353
Caspase 3, apoptosis-related cysteine peptidase	CASP3	Hs.141125
Caspase 6, apoptosis-related cysteine peptidase	CASP6	Hs.389452
Caspase 7, apoptosis-related cysteine peptidase	CASP7	Hs.9216
Caspase 8, apoptosis-related cysteine peptidase	CASP8	Hs.591630
Caspase 9, apoptosis-related cysteine peptidase	CASP9	Hs.329502
Calpastatin	CAST	Hs.440961
CASP8 and FADD-like apoptosis regulator	CFLAR	Hs.390736
Conserved helix-loop-helix ubiquitous kinase	CHUK	Hs.198998
Colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage)	CSF2RB	Hs.592192
Cytochrome c, somatic	CYCS	Hs.437060
Cytochrome c, somatic	CYCS	Hs.617193
DNA fragmentation factor, 45kDa, alpha polypeptide	DFFA	Hs.484782
DNA fragmentation factor, 40kDa, beta polypeptide (caspase-activated DNase)	DFFB	Hs.133089
Endonuclease G	ENDOG	Hs.591905
Fas (TNFRSF6)-associated via death domain	FADD	Hs.86131
Fas (TNF receptor superfamily, member 6)	FAS	Hs.244139
Fas ligand (TNF superfamily, member 6)	FASLG	Hs.2007
Inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase beta	IKBKB	Hs.413513

Table S9. (*Continued*)

Gene Name [a]	Symbol	UniGene
Inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase gamma	IKBKG	Hs.43505
Interleukin 1, alpha	IL1A	Hs.1722
Interleukin 1, beta	IL1B	Hs.126256
Interleukin 1 receptor, type I	IL1R1	Hs.557403
Interleukin 1 receptor accessory protein	IL1RAP	Hs.478673
Interleukin 3 (colony-stimulating factor, multiple)	IL3	Hs.694
Interleukin 3 receptor, alpha (low affinity)	IL3RA	Hs.632790
Interleukin-1 receptor-associated kinase 1	IRAK1	Hs.522819
Interleukin-1 receptor-associated kinase 2	IRAK2	Hs.449207
Interleukin-1 receptor-associated kinase 4	IRAK4	Hs.138499
Mitogen-activated protein kinase kinase kinase 14	MAP3K14	Hs.404183
Myeloid differentiation primary response gene (88)	MYD88	Hs.82116
Nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105)	NFKB1	Hs.431926
Nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p49/p100)	NFKB2	Hs.73090
Nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha	NFKBIA	Hs.81328
Nerve growth factor, beta polypeptide	NGFB	Hs.2561
Neurotrophic tyrosine kinase, receptor, type 1	NTRK1	Hs.406293
Programmed cell death 8 (apoptosis-inducing factor)	PDCD8	Hs.424932
Phosphoinositide-3-kinase, class 2, alpha polypeptide	PIK3C2A	Hs.175343
Phosphoinositide-3-kinase, class 2, beta polypeptide	PIK3C2B	Hs.497487
Phosphoinositide-3-kinase, class 2, gamma polypeptide	PIK3C2G	Hs.22500
Phosphoinositide-3-kinase, class 3	PIK3C3	Hs.464971
Phosphoinositide-3-kinase, catalytic, alpha polypeptide	PIK3CA	Hs.642725
Phosphoinositide-3-kinase, catalytic, beta polypeptide	PIK3CB	Hs.239818
Phosphoinositide-3-kinase, catalytic, delta polypeptide	PIK3CD	Hs.518451
Phosphoinositide-3-kinase, catalytic, gamma polypeptide	PIK3CG	Hs.32942
Phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha)	PIK3R1	Hs.132225
Phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha)	PIK3R1	Hs.604502
Phosphoinositide-3-kinase, regulatory subunit 2 (p85 beta)	PIK3R2	Hs.371344
Phosphoinositide-3-kinase, regulatory subunit 3 (p55, gamma)	PIK3R3	Hs.534951
Phosphoinositide-3-kinase, regulatory subunit 4, p150	PIK3R4	Hs.149032
Phosphoinositide-3-kinase, regulatory subunit 5, p101	PIK3R5	Hs.278901
Protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha)	PPP3CA	Hs.435512
Protein phosphatase 3 (formerly 2B), catalytic subunit, beta isoform (calcineurin A beta)	PPP3CB	Hs.500067
Protein phosphatase 3 (formerly 2B), catalytic subunit, gamma isoform (calcineurin A gamma)	PPP3CC	Hs.149413
Protein phosphatase 3 (formerly 2B), regulatory subunit B, 19kDa, alpha isoform (calcineurin B, type I)	PPP3R1	Hs.280604
Protein kinase, cAMP-dependent, catalytic, alpha	PRKACA	Hs.631630
Protein kinase, cAMP-dependent, catalytic, beta	PRKACB	Hs.487325
Protein kinase, cAMP-dependent, catalytic, gamma	PRKACG	Hs.158029
Protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1)	PRKAR1A	Hs.280342
Protein kinase, cAMP-dependent, regulatory, type I, beta	PRKAR1B	Hs.520851
Protein kinase, cAMP-dependent, regulatory, type II, alpha	PRKAR2A	Hs.631923
Protein kinase, cAMP-dependent, regulatory, type II, beta	PRKAR2B	Hs.433068

Table S9. (*Continued*)

Gene Name [a]	Symbol	UniGene
V-rel reticuloendotheliosis viral oncogene homolog A, nuclear factor of kappa light polypeptide gene enhancer in B-cells 3, p65 (avian)	RELA	Hs.502875
Receptor (TNFRSF)-interacting serine-threonine kinase 1	RIPK1	Hs.519842
Tumor necrosis factor (TNF superfamily, member 2)	TNF	Hs.241570
Tumor necrosis factor receptor superfamily, member 10a	TNFRSF10A	Hs.591834
Tumor necrosis factor receptor superfamily, member 10b	TNFRSF10B	Hs.521456
Tumor necrosis factor receptor superfamily, member 10c, decoy without an intracellular domain	TNFRSF10C	Hs.145269
Tumor necrosis factor receptor superfamily, member 10d, decoy with truncated death domain	TNFRSF10D	Hs.213467
Tumor necrosis factor receptor superfamily, member 1A	TNFRSF1A	Hs.279594
Tumor necrosis factor (ligand) superfamily, member 10	TNFSF10	Hs.478275
Tumor protein p53 (Li-Fraumeni syndrome)	TP53	Hs.408312
TNFRSF1A-associated via death domain	TRADD	Hs.460996
TNF receptor-associated factor 2	TRAF2	Hs.522506

[a] Gene set from Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway, Apoptosis - Homo sapiens (human) (1). The gene list was also checked in HUGO Database (7) and NCBI Entrez (8) to link the approved gene name with respective UniGene cluster.

Table S10. Chromosome stability.

Gene Name [a]	Symbol	UniGene
Ankyrin repeat domain 26	ANKRD26	Hs.361041
Adenomatosis polyposis coli 2	APC2	Hs.446376
AT rich interactive domain 4B (RBP1- like)	ARID4B	Hs.575782
Ataxia telangiectasia and Rad3 related	ATR	Hs.271791
BRCA1 associated protein	BRAP	Hs.577448
BR serine/threonine kinase 1	BRSK1	Hs.182081
Calcium/calmodulin-dependent protein kinase IG	CAMK1G	Hs.199068
Calcium/calmodulin-dependent protein kinase (CaM kinase) II beta	CAMK2B	Hs.351887
CDC6 cell division cycle 6 homolog (S. cerevisiae)	CDC6	Hs.405958
Centromere protein E, 312kDa	CENPE	Hs.75573
Centromere protein H	CENPH	Hs.631967
CHK1 checkpoint homolog (S. pombe)	CHEK1	Hs.24529
CHK2 checkpoint homolog (S. pombe)	CHEK2	Hs.291363
Cylicin, basic protein of sperm head cytoskeleton 2	CYLC2	Hs.3232
Death-associated protein kinase 3	DAPK3	Hs.631844
Doublecortin and CaM kinase-like 1	DCAMKL1	Hs.507755
Doublecortin and CaM kinase-like 2	DCAMKL2	Hs.591683
DMC1 dosage suppressor of mck1 homolog, meiosis-specific homologous recombination (yeast)	DMC1	Hs.339396
Excision repair cross-complementing rodent repair deficiency, complementation group 5 (xeroderma pigmentosum, complementation group G (Cockayne syndrome))	ERCC5	Hs.258429
Extra spindle poles like 1 (S. cerevisiae)	ESPL1	Hs.153479
Flap structure-specific endonuclease 1	FEN1	Hs.409065
GRIP and coiled-coil domain containing 2	GCC2	Hs.436505
Hormonally upregulated Neu-associated kinase	HUNK	Hs.109437
KIAA1166	KIAA1166	Hs.28249
Kinetochore associated 1	KNTC1	Hs.300559
LATS, large tumor suppressor, homolog 1 (Drosophila)	LATS1	Hs.549084
MAD1 mitotic arrest deficient-like 1 (yeast)	MAD1L1	Hs.209128
Maternal embryonic leucine zipper kinase	MELK	Hs.184339
M-phase phosphoprotein 1	MPHOSPH1	Hs.240
MRE11 meiotic recombination 11 homolog A (S. cerevisiae)	MRE11A	Hs.192649
Nibrin	NBN	Hs.492208
Neurofilament, heavy polypeptide 200kDa	NEFH	Hs.198760
NUAK family, SNF1-like kinase, 1	NUAK1	Hs.524692
Origin recognition complex, subunit 1-like (yeast)	ORC1L	Hs.17908
P21(CDKN1A)-activated kinase 7	PAK7	Hs.32539
Proliferating cell nuclear antigen	PCNA	Hs.147433
Phosphoinositide-3-kinase, class 2, alpha polypeptide	PIK3C2A	Hs.175343
Phosphoinositide-3-kinase, class 2, beta polypeptide	PIK3C2B	Hs.497487
Phosphoinositide-3-kinase, class 3	PIK3C3	Hs.464971
Phosphoinositide-3-kinase, catalytic, beta polypeptide	PIK3CB	Hs.239818
Phosphoinositide-3-kinase, catalytic, delta polypeptide	PIK3CD	Hs.518451
Phosphoinositide-3-kinase, catalytic, gamma polypeptide	PIK3CG	Hs.32942
Polymerase (DNA directed), delta 1, catalytic subunit 125kDa	POLD1	Hs.279413
Polymerase (DNA directed), epsilon	POLE	Hs.524871
Protein kinase, DNA-activated, catalytic polypeptide	PRKDC	Hs.491682
RAD1 homolog (S. pombe)	RAD1	Hs.531879
RAD17 homolog (S. pombe)	RAD17	Hs.16184
RAD50 homolog (S. cerevisiae)	RAD50	Hs.128904

Table S10. (*Continued*).

Gene Name[a]	Symbol	UniGene
RAD51 homolog (RecA homolog, E. coli) (S. cerevisiae)	RAD51	Hs.631709
RAD51 homolog C (S. cerevisiae)	RAD51C	Hs.412587
RAD51-like 3 (S. cerevisiae)	RAD51L3	Hs.631757
RAD52 homolog (S. cerevisiae)	RAD52	Hs.642610
RAD54 homolog B (S. cerevisiae)	RAD54B	Hs.30561
RAD54-like (S. cerevisiae)	RAD54L	Hs.523220
Replication factor C (activator 1) 1, 145kDa	RFC1	Hs.507475
Replication factor C (activator 1) 3, 38kDa	RFC3	Hs.115474
Replication factor C (activator 1) 4, 37kDa	RFC4	Hs.591322
Replication factor C (activator 1) 5, 36.5kDa	RFC5	Hs.506989
Replication protein A1, 70kDa	RPA1	Hs.461925
Sirtuin (silent mating type information regulation 2 homolog) 1 (S. cerevisiae)	SIRT1	Hs.369779
Sirtuin (silent mating type information regulation 2 homolog) 2 (S. cerevisiae)	SIRT2	Hs.466693
Sirtuin (silent mating type information regulation 2 homolog) 3 (S. cerevisiae)	SIRT3	Hs.19306
Sirtuin (silent mating type information regulation 2 homolog) 4 (S. cerevisiae)	SIRT4	Hs.50861
Sirtuin (silent mating type information regulation 2 homolog) 5 (S. cerevisiae)	SIRT5	Hs.567431
Sirtuin (silent mating type information regulation 2 homolog) 6 (S. cerevisiae)	SIRT6	Hs.423756
Sirtuin (silent mating type information regulation 2 homolog) 7 (S. cerevisiae)	SIRT7	Hs.514636
Smu-1 suppressor of mec-8 and unc-52 homolog (C. elegans) (SMU1)	SMU-1	Hs.642743
SNF related kinase	SNRK	Hs.476052
Topoisomerase (DNA) II binding protein 1	TOPBP1	Hs.53454
Translocated promoter region (to activated MET oncogene)	TPR	Hs.279640
Xeroderma pigmentosum, complementation group C	XPC	Hs.475538
X-ray repair complementing defective repair in Chinese hamster cells 1	XRCC1	Hs.98493
X-ray repair complementing defective repair in Chinese hamster cells 3	XRCC3	Hs.592325
Zinc finger CCCH-type containing 13	ZC3H13	Hs.136102
ZW10, kinetochore associated, homolog (Drosophila)	ZW10	Hs.503886
Zwilch, kinetochore associated, homolog (Drosophila)	ZWILCH	Hs.21331
ZW10 interactor	ZWINT	Hs.591363

[a] List of genes that may trigger chromosome instability when mutated (2). The gene list was checked in HUGO Database (7) and NCBI Entrez (8) to link the approved gene name with respective UniGene cluster.

Table S11. Mismatch repair (MMR).

Gene Name [a]	Symbol	UniGene
Replication protein A3, 14kDa	RPA3	Hs.487540
Replication protein A2, 32kDa	RPA2	Hs.79411
Replication protein A1, 70kDa	RPA1	Hs.461925
Replication factor C (activator 1) 5, 36.5kDa	RFC5	Hs.506989
Replication factor C (activator 1) 4, 37kDa	RFC4	Hs.591322
Replication factor C (activator 1) 3, 38kDa	RFC3	Hs.115474
Replication factor C (activator 1) 1, 145kDa	RFC1	Hs.507475
Polymerase (DNA-directed), delta 4	POLD4	Hs.523829
Polymerase (DNA-directed), delta 3, accessory subunit	POLD3	Hs.82502
Polymerase (DNA directed), delta 2, regulatory subunit 50kDa	POLD2	Hs.306791
Polymerase (DNA directed), delta 1, catalytic subunit 125kDa	POLD1	Hs.279413
Postmeiotic segregation increased 2-like 3	PMS2L3	Hs.225784
PMS2 postmeiotic segregation increased 2 (S. cerevisiae)	PMS2	Hs.632637
PMS1 postmeiotic segregation increased 1 (S. cerevisiae)	PMS1	Hs.111749
Proliferating cell nuclear antigen	PCNA	Hs.147433
MutS homolog 6 (E. coli)	MSH6	Hs.445052
MutS homolog 5 (E. coli)	MSH5	Hs.371225
MutS homolog 4 (E. coli)	MSH4	Hs.216639
MutS homolog 3 (E. coli)	MSH3	Hs.280987
MutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)	MSH2	Hs.597656
MutL homolog 3 (E. coli)	MLH3	Hs.436650
MutL homolog 1, colon cancer, nonpolyposis type 2 (E. coli)	MLH1	Hs.195364
Postmeiotic segregation increased 2-like 4	PMS2L4	Hs.632011
Ligase I, DNA, ATP-dependent	LIG1	Hs.1770
High-mobility group box 1	HMGB1	Hs.633298
High-mobility group box 1	HMGB1	Hs.593339
High-mobility group box 1	HMGB1	Hs.434102
Exonuclease 1	EXO1	Hs.498248

[a] The list was constructed accordingly to Wood et al. (3) and Jiricny (4). The gene list was checked in HUGO Database (7) and NCBI Entrez (8) to link the approved gene name with respective UniGene cluster.

Table S12. Nucleotide-excision repair (NER).

Gene Name [a]	Symbol	UniGene
Cyclin H	CCNH	Hs.292524
Cyclin-dependent kinase 7 (MO15 homolog, Xenopus laevis, cdk-activating kinase)	CDK7	Hs.184298
Centrin, EF-hand protein, 2	CETN2	Hs.82794
Damage-specific DNA binding protein 1, 127kDa	DDB1	Hs.290758
Damage-specific DNA binding protein 2, 48kDa	DDB2	Hs.643521
General transcription factor IIH, polypeptide 2, 44kDa	GTF2H2	Hs.202179
Excision repair cross-complementing rodent repair deficiency, complementation group 1 (includes overlapping antisense sequence)	ERCC1	Hs.435981
Excision repair cross-complementing rodent repair deficiency, complementation group 2 (xeroderma pigmentosum D)	ERCC2	Hs.487294
Excision repair cross-complementing rodent repair deficiency, complementation group 3 (xeroderma pigmentosum group B complementing)	ERCC3	Hs.469872
Excision repair cross-complementing rodent repair deficiency, complementation group 4	ERCC4	Hs.567265
Excision repair cross-complementing rodent repair deficiency, complementation group 5 (xeroderma pigmentosum, complementation group G (Cockayne syndrome))	ERCC5	Hs.258429
Excision repair cross-complementing rodent repair deficiency, complementation group 8	ERCC8	Hs.435237
General transcription factor IIH, polypeptide 1, 62kDa	GTF2H1	Hs.577202
General transcription factor IIH, polypeptide 3, 34kDa	GTF2H3	Hs.355348
General transcription factor IIH, polypeptide 4, 52kDa	GTF2H4	Hs.485070
General transcription factor IIH, polypeptide 5	GTF2H5	Hs.356224
Ligase I, DNA, ATP-dependent	LIG1	Hs.1770
MMS19-like (MET18 homolog, S. cerevisiae)	MMS19L	Hs.500721
Menage a trois homolog 1, cyclin H assembly factor (Xenopus laevis)	MNAT1	Hs.509523
Excision repair cross-complementing rodent repair deficiency, complementation group 6	ERCC6	Hs.133444
RAD23 homolog A (S. cerevisiae)	RAD23A	Hs.643267
RAD23 homolog B (S. cerevisiae)	RAD23B	Hs.521640
Replication protein A1, 70kDa	RPA1	Hs.461925
Replication protein A2, 32kDa	RPA2	Hs.79411
Replication protein A3, 14kDa	RPA3	Hs.487540
XPA binding protein 2	XAB2	Hs.9822
Xeroderma pigmentosum, complementation group A	XPA	Hs.591907
Xeroderma pigmentosum, complementation group C	XPC	Hs.475538

[a] NER genes accordingly to Wood et al. (3). The gene list was checked in HUGO Database (7) and NCBI Entrez (8) to link the approved gene name with respective UniGene cluster.

Table S13. Base-excision repair (BER).

Gene Name [a]	Symbol	UniGene
APEX nuclease (multifunctional DNA repair enzyme) 1	APEX1	Hs.73722
APEX nuclease (apurinic/apyrimidinic endonuclease) 2	APEX2	Hs.555936
Ligase III, DNA, ATP-dependent	LIG3	Hs.100299
Methyl-CpG binding domain protein 4	MBD4	Hs.35947
N-methylpurine-DNA glycosylase	MPG	Hs.459596
MutY homolog (E. coli)	MUTYH	Hs.271353
Nei endonuclease VIII-like 1 (E. coli)	NEIL1	Hs.512732
Nei like 2 (E. coli)	NEIL2	Hs.293818
Nth endonuclease III-like 1 (E. coli)	NTHL1	Hs.66196
8-oxoguanine DNA glycosylase	OGG1	Hs.380271
Poly (ADP-ribose) polymerase family, member 1	PARP1	Hs.177766
Poly (ADP-ribose) polymerase family, member 2	PARP2	Hs.409412
Polynucleotide kinase 3'-phosphatase	PNKP	Hs.78016
Single-strand-selective monofunctional uracil-DNA glycosylase 1	SMUG1	Hs.632721
Thymine-DNA glycosylase	TDG	Hs.584809
Uracil-DNA glycosylase	UNG	Hs.191334
X-ray repair complementing defective repair in Chinese hamster cells 1	XRCC1	Hs.98493

[a] BER genes accordingly to Wood et al. (3). The gene list was checked in HUGO Database (7) and NCBI Entrez (8) to link the approved gene name with respective UniGene cluster.

Table S14. Recombinational repair (RER).

Gene Name[a]	Symbol	UniGene
RAD51 homolog (RecA homolog, E. coli) (S. cerevisiae)	RAD51	Hs.631709
RAD51-like 1 (S. cerevisiae)	RAD51L1	Hs.172587
RAD51 homolog C (S. cerevisiae)	RAD51C	Hs.412587
RAD51-like 3 (S. cerevisiae)	RAD51L3	Hs.631757
DMC1 dosage suppressor of mck1 homolog, meiosis-specific homologous recombination (yeast)	DMC1	Hs.339396
X-ray repair complementing defective repair in Chinese hamster cells 3	XRCC3	Hs.592325
RAD52 homolog (S. cerevisiae)	RAD52	Hs.642610
RAD54-like (S. cerevisiae)	RAD54L	Hs.523220
RAD54 homolog B (S. cerevisiae)	RAD54B	Hs.30561
Breast cancer 1, early onset	BRCA1	Hs.194143
Breast cancer 2, early onset	BRCA2	Hs.34012
Split hand/foot malformation (ectrodactyly) type 1	SHFM1	Hs.489201
RAD50 homolog (S. cerevisiae)	RAD50	Hs.128904
MRE11 meiotic recombination 11 homolog A (S. cerevisiae)	MRE11A	Hs.192649
Nibrin	NBN	Hs.492208
MUS81 endonuclease homolog (S. cerevisiae)	MUS81	Hs.288798
Essential meiotic endonuclease 1 homolog 1 (S. pombe)	EME1	Hs.514330
X-ray repair complementing defective repair in Chinese hamster cells 6 (Ku autoantigen, 70kDa)	XRCC6	Hs.292493
X-ray repair complementing defective repair in Chinese hamster cells 5 (double-strand-break rejoining; Ku autoantigen, 80kDa)	XRCC5	Hs.388739
Protein kinase, DNA-activated, catalytic polypeptide	PRKDC	Hs.491682
Ligase IV, DNA, ATP-dependent	LIG4	Hs.166091
X-ray repair complementing defective repair in Chinese hamster cells 4	XRCC4	Hs.567359
DNA cross-link repair 1C (PSO2 homolog, S. cerevisiae)	DCLRE1C	Hs.612774
Nonhomologous end-joining factor 1	NHEJ1	Hs.225988
X-ray repair complementing defective repair in Chinese hamster cells 2	XRCC2	-

[a] Recombinational repair genes accordingly to Wood et al. (3). The gene list was checked in HUGO Database (7) and NCBI Entrez (8) to link the approved gene name with respective UniGene cluster.

Table S15. Diversity of SAGE libraries and conserved pathways.

Tissue[a]	Histology[b]	SAGE Library[b]	Preparation[b]	SAGE tag[c]			SAGE tag-to-gene[d]			Ribosome[e,f]			ETC[e,f]			ATP synthase[e,f]			Glycolysis[e,f]		
				$H\alpha$	$M\alpha$	$N\alpha$	$H\alpha$	$M\alpha$	$N\alpha$	$H\alpha$	$M\alpha$	$N\alpha$	$H\alpha$	$M\alpha$	$N\alpha$	$H\alpha$	$M\alpha$	$N\alpha$	$H\alpha$	$M\alpha$	$N\alpha$
Brain	Cancer	SAGE_Brain_astrocytoma_grade_I_B_H1043	bulk	0,894	30880	75922	0,885	13453	66645	0,866	127	3766	0,876	75	544	0,903	16	177	0,700	22	230
		SAGE_Brain_astrocytoma_grade_II_B_H127	bulk	0,844	31165	114489	0,841	13425	104130	0,817	127	9502	0,809	75	1379	0,789	16	553	0,578	22	684
		SAGE_Brain_astrocytoma_grade_II_B_H359	bulk	0,877	35555	105764	0,872	14602	94991	0,847	127	9128	0,855	75	1245	0,802	16	386	0,548	22	592
		SAGE_Brain_astrocytoma_grade_II_B_H388	bulk	0,864	34081	106285	0,857	14136	94747	0,854	127	5915	0,876	75	1165	0,846	16	356	0,591	22	827
		SAGE_Brain_astrocytoma_grade_II_B_H501	bulk	0,871	38047	128309	0,868	15065	116431	0,875	127	4706	0,881	75	1682	0,862	16	581	0,600	22	1136
		SAGE_Brain_astrocytoma_grade_II_B_H516	bulk	0,891	42250	108116	0,884	15948	93538	0,872	127	5734	0,867	75	917	0,855	16	315	0,664	22	471
		SAGE_Brain_astrocytoma_grade_II_B_H518	bulk	0,863	36310	116022	0,858	14711	103026	0,816	127	6340	0,847	75	1218	0,797	16	501	0,576	22	1090
		SAGE_Brain_astrocytoma_grade_II_B_H530	bulk	0,881	34715	102439	0,876	14304	90879	0,836	127	6770	0,843	75	1032	0,787	16	288	0,603	22	449
		SAGE_Brain_astrocytoma_grade_II_B_H563	bulk	0,880	30054	88568	0,871	13252	79479	0,851	127	5214	0,855	75	909	0,840	16	356	0,576	22	757
		SAGE_Brain_astrocytoma_grade_III_B_343	bulk	0,858	29620	100158	0,852	13086	91522	0,822	127	12732	0,813	75	1412	0,793	16	588	0,541	22	958
		SAGE_Brain_astrocytoma_grade_III_B_407	bulk	0,863	32819	108312	0,858	14158	99266	0,841	127	16352	0,835	75	1226	0,838	16	271	0,530	22	661
		SAGE_Brain_astrocytoma_grade_III_B_439	bulk	0,861	34620	107824	0,853	14068	97274	0,868	127	13341	0,855	75	1458	0,830	16	439	0,601	22	599
		SAGE_Brain_astrocytoma_grade_III_B_584	bulk	0,858	30772	103008	0,854	13453	93489	0,867	127	12766	0,860	75	1275	0,824	16	418	0,590	22	722
		SAGE_Brain_astrocytoma_grade_III_B_828	bulk	0,879	32109	99939	0,874	13965	90631	0,872	127	8221	0,877	75	1152	0,877	16	356	0,622	22	636
		SAGE_Brain_astrocytoma_grade_III_B_H1020	bulk	0,926	30738	51573	0,903	12491	40436	0,864	127	1918	0,855	75	210	0,862	16	61	0,746	22	81
		SAGE_Brain_astrocytoma_grade_III_B_H1055	bulk	0,878	37250	109886	0,872	14891	98235	0,870	127	10603	0,877	75	1061	0,864	16	330	0,624	22	494
		SAGE_Brain_astrocytoma_grade_III_B_H272	bulk	0,880	34171	96059	0,873	14313	85675	0,858	127	6608	0,852	75	1155	0,823	16	383	0,568	22	692
		SAGE_Brain_astrocytoma_grade_III_B_H970	bulk	0,880	35207	106982	0,875	14281	96595	0,864	127	5796	0,849	75	1614	0,866	16	445	0,606	22	1043
		SAGE_Brain_astrocytoma_grade_III_B_R140	bulk	0,878	36465	118733	0,876	14791	108165	0,857	127	9503	0,823	75	1747	0,826	16	453	0,442	22	716
		SAGE_Brain_astrocytoma_grade_III_B_R927	bulk	0,877	33747	107344	0,873	14082	97949	0,831	127	13224	0,862	75	1529	0,776	16	573	0,534	22	604
		SAGE_Brain_ependymoblastoma_B_819	bulk	0,914	14845	33975	0,903	8670	30962	0,874	127	3001	0,855	75	326	0,883	16	126	0,490	22	465
		SAGE_Brain_ependymoma_B_1150	bulk	0,910	23324	62373	0,904	11754	57238	0,859	127	5021	0,874	75	558	0,849	16	228	0,515	22	331
		SAGE_Brain_ependymoma_B_1394	bulk	0,896	22956	56314	0,885	11446	51381	0,861	127	4629	0,841	75	580	0,866	16	157	0,491	22	421
		SAGE_Brain_ependymoma_B_239	bulk	0,908	20459	46653	0,898	10838	41835	0,861	127	3038	0,842	75	560	0,872	16	152	0,601	22	191
		SAGE_Brain_ependymoma_B_H580	bulk	0,900	25883	68614	0,890	12506	62408	0,862	127	6882	0,874	75	937	0,847	16	274	0,597	22	389
		SAGE_Brain_ependymoma_B_R1023	bulk	0,884	40027	122690	0,879	15439	109956	0,855	127	9749	0,858	75	1471	0,892	16	394	0,692	22	795
		SAGE_Brain_ependymoma_B_R353	bulk	0,900	27211	73822	0,894	12972	66928	0,851	127	5010	0,856	75	549	0,800	16	233	0,470	22	791
		SAGE_Brain_ependymoma_B_R455	bulk	0,898	19611	51825	0,887	10233	47665	0,877	127	3609	0,851	75	987	0,849	16	334	0,605	22	301
		SAGE_Brain_ependymoma_B_R510	bulk	0,897	30595	84073	0,892	13690	75150	0,869	127	4404	0,867	75	851	0,817	16	303	0,628	22	492
		SAGE_Brain_ependymoma_B_R512	bulk	0,883	27374	75379	0,874	12781	67584	0,866	127	4834	0,872	75	836	0,822	16	319	0,531	22	826
		SAGE_Brain_ependymoma_B_R582	bulk	0,871	17282	52189	0,863	9848	48700	0,861	127	7778	0,872	75	646	0,853	16	195	0,537	22	464
		SAGE_Brain_ependymoma_B_R628	bulk	0,875	39836	120431	0,868	15386	107654	0,874	127	6261	0,889	75	991	0,899	16	306	0,681	22	673
		SAGE_Brain_glioblastoma_B_GBM1062	bulk	0,820	15504	59762	0,812	8718	55174	0,760	127	12550	0,821	75	635	0,582	16	503	0,511	22	477
		SAGE_Brain_glioblastoma_B_H1110	bulk	0,891	25812	68986	0,885	12376	62283	0,858	127	4071	0,857	75	576	0,842	16	239	0,562	22	735
		SAGE_Brain_glioblastoma_B_H1353	bulk	0,875	37773	124805	0,871	15013	113146	0,849	127	5784	0,840	75	1528	0,829	16	590	0,458	22	1943
		SAGE_Brain_glioblastoma_B_H1371	bulk	0,901	22909	49338	0,879	10914	41889	0,860	127	4263	0,879	75	401	0,738	16	170	0,546	22	250
		SAGE_Brain_glioblastoma_B_H1425C	bulk	0,874	28204	88990	0,866	12786	82000	0,837	127	7393	0,845	75	974	0,763	16	467	0,382	22	790
		SAGE_Brain_glioblastoma_B_H833	bulk	0,870	34143	100600	0,859	13995	89877	0,849	127	5890	0,845	75	988	0,826	16	302	0,417	22	2005
		SAGE_Brain_glioblastoma_B_pooled	bulk	0,902	24020	56428	0,890	11398	49245	0,847	127	3242	0,851	75	503	0,825	16	146	0,635	22	413
		SAGE_Brain_glioblastoma_B_R20	bulk	0,887	35474	101053	0,876	14295	91008	0,850	127	5332	0,854	75	1275	0,852	16	455	0,569	22	874
		SAGE_Brain_glioblastoma_B_R336	bulk	0,878	34762	102322	0,871	14187	90281	0,825	127	5609	0,860	75	895	0,816	16	369	0,322	22	1365
		SAGE_Brain_glioblastoma_B_R70	bulk	0,863	32108	99099	0,856	13532	89969	0,837	127	7163	0,855	75	1018	0,826	16	340	0,520	22	561
		SAGE_Brain_meningioma_grade_II_B_SF2176	bulk	0,864	16920	48711	0,853	9042	44148	0,821	127	5135	0,826	75	1418	0,842	16	387	0,586	22	500
		SAGE_Brain_meningioma_grade_II_B_SF3622	bulk	0,872	16264	44857	0,860	8722	40784	0,815	127	5055	0,796	75	875	0,852	16	171	0,476	22	533
		SAGE_Brain_meningioma_grade_III_B_SF2366	bulk	0,867	20161	59786	0,857	10451	54622	0,822	127	9896	0,837	75	734	0,834	16	188	0,587	22	218
		SAGE_Brain_oligodendroglioma_B_1001	bulk	0,891	14369	32442	0,878	8289	28438	0,877	127	3627	0,852	75	357	0,856	16	119	0,675	22	116
		SAGE_Brain_oligodendroglioma_B_H988	bulk	0,905	13982	27864	0,891	8054	24683	0,866	127	2248	0,827	75	240	0,767	16	62	0,658	22	100
		SAGE_Brain_glioblastoma_CS_TA2	STC	0,910	21568	46678	0,891	10313	40586	0,860	127	2739	0,822	75	519	0,848	16	143	0,544	22	206
		SAGE_Brain_glioblastoma_CL_H392	cell line	0,886	19417	55990	0,877	9822	50812	0,831	127	3885	0,851	75	493	0,875	16	157	0,515	22	729
		SAGE_Brain_glioblastoma_CL_H54+EGFRvIII	cell line	0,877	19079	56982	0,872	10278	52624	0,868	127	4830	0,867	75	666	0,889	16	204	0,551	22	610
		SAGE_Brain_glioblastoma_CL_H54+LacZ	cell line	0,878	20539	66908	0,877	10730	62267	0,868	127	6159	0,868	75	820	0,875	16	268	0,556	22	757
		SAGE_Brain_glioblastoma_control_CL_H247	cell line	0,881	19237	60428	0,879	10332	56036	0,870	127	5501	0,848	75	950	0,860	16	346	0,589	22	784
		SAGE_Brain_glioblastoma_hypoxia_CL_H247	cell line	0,884	24770	71765	0,879	11715	65384	0,872	127	5450	0,872	75	815	0,859	16	306	0,581	22	1290
	Normal	SAGE_Brain_normal_cortex_B_BB542	bulk	0,861	31683	94233	0,854	13350	81781	0,861	127	4246	0,862	75	853	0,839	16	279	0,691	22	739
		SAGE_Brain_normal_leptomeninges_B_AL2	bulk	0,864	26220	72473	0,853	12171	64666	0,817	127	5493	0,844	75	640	0,829	16	158	0,560	22	495
		SAGE_Brain_normal_peds_cortex_B_H1571	bulk	0,874	24161	77554	0,870	11948	70082	0,811	127	3575	0,796	75	1016	0,816	16	337	0,607	22	723
		SAGE_Brain_normal_thalamus_B_1	bulk	0,847	10115	24015	0,829	6525	21182	0,794	127	826	0,824	75	196	0,780	16	70	0,646	22	189

Table S15. (*Continued*)

Tissue[a]	Histology[b]	SAGE Library[b]	Preparation[b]	SAGE tag[c]			SAGE tag-to-gene[d]			Ribosome[e,f]			ETC[e,f]			ATP synthase[e,f]			Glycolysis[e,f]		
				$H\alpha$	$M\alpha$	$N\alpha$	$H\alpha$	$M\alpha$	$N\alpha$	$H\alpha$	$M\alpha$	$N\alpha$	$H\alpha$	$M\alpha$	$N\alpha$	$H\alpha$	$M\alpha$	$N\alpha$	$H\alpha$	$M\alpha$	$N\alpha$
Cerebellum	Cancer	SAGE_Brain_medulloblastoma_B_1273	bulk	0,905	17236	38614	0,893	9480	34366	0,847	127	3309	0,838	75	429	0,870	16	142	0,635	22	209
		SAGE_Brain_medulloblastoma_B_96-04-P019	bulk	0,903	22017	52645	0,893	10818	46181	0,827	127	5013	0,814	75	535	0,740	16	281	0,622	22	342
		SAGE_Brain_medulloblastoma_B_97-05-P015	bulk	0,868	24631	69971	0,857	11682	62376	0,840	127	13089	0,816	75	627	0,775	16	293	0,470	22	362
		SAGE_Brain_medulloblastoma_B_97-05-P312	bulk	0,881	28029	74295	0,869	12587	65679	0,863	127	10412	0,826	75	952	0,863	16	304	0,640	22	354
		SAGE_Brain_medulloblastoma_B_98-04-P117	bulk	0,893	14766	32570	0,877	8254	28353	0,854	127	6358	0,812	75	376	0,825	16	131	0,483	22	117
		SAGE_Brain_medulloblastoma_B_98-04-P494	bulk	0,884	16247	43068	0,870	8824	39238	0,796	127	6578	0,809	75	678	0,764	16	350	0,427	22	361
		SAGE_Brain_medulloblastoma_B_98-05-P040	bulk	0,889	34995	89258	0,876	13979	77507	0,830	127	10945	0,828	75	1005	0,731	16	487	0,555	22	348
		SAGE_Brain_medulloblastoma_B_98-05-P608	bulk	0,921	22675	48451	0,907	10898	42024	0,851	127	3166	0,853	75	391	0,843	16	155	0,662	22	154
		SAGE_Brain_medulloblastoma_B_98-09-P558	bulk	0,903	33598	85984	0,895	13722	74991	0,854	127	6783	0,849	75	1091	0,812	16	442	0,540	22	361
		SAGE_Brain_medulloblastoma_B_98-13-P301	bulk	0,897	17313	45342	0,887	9639	40948	0,824	127	5428	0,839	75	551	0,829	16	275	0,520	22	165
		SAGE_Brain_medulloblastoma_B_C609	bulk	0,914	32456	74612	0,905	13517	63799	0,857	127	4613	0,845	75	830	0,788	16	346	0,579	22	467
		SAGE_Brain_medulloblastoma_B_DL5	bulk	0,868	28721	83671	0,857	12481	74376	0,840	127	10221	0,844	75	1330	0,870	16	380	0,550	22	852
		SAGE_Brain_medulloblastoma_B_DL7	bulk	0,883	25370	68392	0,874	11994	61145	0,851	127	6734	0,827	75	1175	0,792	16	463	0,624	22	585
		SAGE_Brain_medulloblastoma_B_H1322	bulk	0,928	28969	59498	0,907	12155	50920	0,813	127	4566	0,812	75	590	0,787	16	195	0,624	22	176
		SAGE_Brain_medulloblastoma_B_H1413	bulk	0,842	22833	61853	0,823	10701	53596	0,810	127	9612	0,821	75	510	0,680	16	380	0,445	22	404
		SAGE_Brain_medulloblastoma_B_H275	bulk	0,877	26151	72318	0,865	11938	64203	0,824	127	11000	0,817	75	857	0,773	16	401	0,559	22	404
		SAGE_Brain_medulloblastoma_B_H306	bulk	0,883	24714	60454	0,865	11363	53564	0,833	127	11380	0,815	75	794	0,835	16	290	0,496	22	203
		SAGE_Brain_medulloblastoma_B_H484	bulk	0,904	25712	57469	0,887	11509	49865	0,836	127	7074	0,835	75	683	0,786	16	353	0,479	22	316
		SAGE_Brain_medulloblastoma_B_H876	bulk	0,876	25648	67404	0,864	11737	59243	0,840	127	11815	0,826	75	698	0,791	16	395	0,452	22	313
		SAGE_Brain_medulloblastoma_B_H972	bulk	0,886	30675	85376	0,878	13091	74770	0,811	127	9478	0,806	75	819	0,761	16	397	0,422	22	506
		SAGE_Brain_medulloblastoma_CL_4-HCR	cell line	0,879	26573	66599	0,869	11920	58373	0,871	127	9538	0,852	75	928	0,879	16	318	0,628	22	364
		SAGE_Brain_medulloblastoma_CL_D283	cell line	0,872	25279	66316	0,862	11551	58600	0,869	127	9697	0,866	75	823	0,868	16	322	0,633	22	339
		SAGE_Brain_medulloblastoma_CL_H341	cell line	0,839	15220	43920	0,821	8188	39605	0,861	127	13133	0,875	75	428	0,860	16	203	0,635	22	230
		SAGE_Brain_medulloblastoma_CL_mhh-1	cell line	0,879	18542	47858	0,865	9495	42848	0,863	127	8735	0,834	75	808	0,848	16	270	0,483	22	402
	Normal	SAGE_Brain_normal_cerebellum_B_1	bulk	0,909	24357	50385	0,896	11634	42625	0,868	127	1879	0,881	75	397	0,851	16	125	0,681	22	330
		SAGE_Brain_normal_cerebellum_B_BB542	bulk	0,906	19163	40500	0,893	10026	34765	0,854	127	1570	0,836	75	332	0,780	16	121	0,687	22	293
Breast	Cancer	SAGE_Breast_carcinoma_B_95-259	bulk	0,877	14924	39364	0,858	8418	35804	0,759	127	6189	0,714	75	638	0,770	16	226	0,548	22	186
		SAGE_Breast_carcinoma_B_95-347	bulk	0,866	22561	67070	0,856	11559	61410	0,782	127	9269	0,745	75	1028	0,824	16	225	0,558	22	265
		SAGE_Breast_carcinoma_B_DCIS-4	bulk	0,863	20224	60605	0,854	10892	55348	0,821	127	4435	0,833	75	680	0,755	16	309	0,556	22	340
		SAGE_Breast_carcinoma_B_DCIS-5	bulk	0,889	15935	43098	0,881	9387	39685	0,830	127	4408	0,750	75	633	0,813	16	168	0,562	22	268
		SAGE_Breast_carcinoma_B_IDC-3	bulk	0,871	22732	68891	0,862	11728	63359	0,819	127	9192	0,841	75	615	0,860	16	251	0,518	22	336
		SAGE_Breast_carcinoma_B_IDC-4	bulk	0,891	21531	64095	0,885	11191	59283	0,821	127	6812	0,825	75	864	0,841	16	290	0,478	22	614
		SAGE_Breast_carcinoma_B_IDC-5	bulk	0,871	20457	60451	0,863	10945	55322	0,835	127	7085	0,781	75	716	0,802	16	296	0,594	22	242
		SAGE_Breast_carcinoma_metastasis_B_2	bulk	0,883	18625	49794	0,872	10067	45074	0,777	127	5332	0,793	75	411	0,704	16	259	0,633	22	296
		SAGE_Breast_metastatic_carcinoma_B_95-260	bulk	0,864	15708	45087	0,845	8721	41292	0,741	127	7325	0,794	75	547	0,718	16	285	0,463	22	239
		SAGE_Breast_metastatic_carcinoma_B_95-348	bulk	0,871	20057	60343	0,862	10370	54989	0,786	127	6730	0,540	75	1877	0,812	16	270	0,535	22	327
		SAGE_Breast_carcinoma_MD_DCIS	MD	0,865	14237	40783	0,853	8139	37162	0,771	127	7326	0,796	75	462	0,753	16	176	0,532	22	93
		SAGE_Breast_carcinoma_epithelium_AP_DCIS-2	AP	0,860	20611	66168	0,852	10498	60800	0,825	127	5361	0,556	75	1270	0,740	16	279	0,623	22	181
		SAGE_Breast_carcinoma_epithelium_AP_DCIS-3	AP	0,891	31142	57402	0,866	12707	46125	0,868	127	1796	0,857	75	163	0,682	16	33	0,778	22	76
		SAGE_Breast_carcinoma_epithelium_AP_DCIS6	AP	0,894	30256	72857	0,879	12779	63350	0,842	127	3332	0,857	75	306	0,818	16	113	0,556	22	247
		SAGE_Breast_carcinoma_epithelium_AP_DCIS7	AP	0,878	31311	89184	0,865	13083	79329	0,864	127	4392	0,803	75	832	0,749	16	298	0,414	22	680
		SAGE_Breast_carcinoma_CL_MCF7control_0h	cell line	0,834	15401	59877	0,830	8701	56035	0,815	127	11026	0,805	75	1405	0,648	16	1020	0,426	22	713
		SAGE_Breast_carcinoma_CL_MCF7estradiol_10H	cell line	0,853	17213	60725	0,850	9350	56730	0,829	127	10700	0,811	75	1264	0,733	16	732	0,506	22	552
		SAGE_Breast_carcinoma_CL_MCF7estradiol_3h	cell line	0,856	17821	60162	0,851	9692	55880	0,830	127	9952	0,832	75	1154	0,733	16	627	0,463	22	471
		SAGE_Breast_carcinoma_CL_MDA435C	cell line	0,906	20080	47270	0,861	15629	110405	0,807	127	3110	0,770	75	445	0,766	16	194	0,443	22	986
		SAGE_Breast_carcinoma_CL_MDA435H24	cell line	0,906	20234	46631	0,894	9821	41176	0,794	127	2852	0,795	75	405	0,826	16	188	0,428	22	1031
		SAGE_Breast_carcinoma_CL_MDA435H48	cell line	0,908	18060	40323	0,899	9274	35857	0,819	127	2609	0,806	75	380	0,771	16	153	0,415	22	716
		SAGE_Breast_carcinoma_CL_ZR75_1_estrogen	cell line	0,859	4282	38797	0,854	3331	37379	0,809	127	8234	0,782	75	1286	0,674	16	624	0,476	22	432
		SAGE_Breast_carcinoma_CL_ZR75_1_tamoxifen	cell line	0,883	5017	40052	0,876	3871	38614	0,827	127	6995	0,798	75	1016	0,709	16	411	0,446	22	482
		SAGE_Breast_carcinoma_CL_ZR75_1_untreated	cell line	0,882	3983	32303	0,875	3209	31346	0,838	127	6395	0,796	75	946	0,690	16	387	0,450	22	402
	Normal	SAGE_Breast_normal_epithelium_AP_1	AP	0,880	18276	48729	0,869	9389	44032	0,844	127	5616	0,852	75	398	0,777	16	144	0,676	22	207
		SAGE_Breast_normal_epithelium_AP_Br_N	AP	0,866	19190	50512	0,850	9273	44222	0,841	127	8026	0,854	75	324	0,830	16	175	0,620	22	125
		SAGE_Breast_normal_myoepithelium_AP_myoepithelial1	AP	0,905	26342	57222	0,878	11088	48131	0,855	127	5099	0,841	75	212	0,778	16	70	0,535	22	302
		SAGE_Breast_normal_stroma_AP_1	AP	0,825	23409	79152	0,803	10831	72318	0,809	127	13069	0,833	75	428	0,751	16	232	0,661	22	177
		SAGE_Breast_normal_organoid_B	bulk	0,860	19602	58181	0,846	9606	53201	0,802	127	7607	0,804	75	317	0,762	16	115	0,486	22	325
Colon	Cancer	SAGE_Colon_adenocarcinoma_B_Tu102	bulk	0,854	22713	55700	0,838	10576	47732	0,838	127	3636	0,864	75	334	0,862	16	99	0,552	22	327
		SAGE_Colon_adenocarcinoma_B_Tu98	bulk	0,884	18794	41371	0,869	9608	35515	0,860	127	2434	0,854	75	266	0,855	16	82	0,530	22	238
		SAGE_Colon_adenocarcinoma_CL_Caco2	cell line	0,885	23111	60682	0,879	11195	54400	0,857	127	5357	0,878	75	444	0,830	16	161	0,640	22	350
		SAGE_Colon_adenocarcinoma_CL_HCT116	cell line	0,893	24585	55641	0,882	11621	48693	0,855	127	6207	0,885	75	384	0,829	16	123	0,687	22	256
		SAGE_Colon_adenocarcinoma_CL_RKO	cell line	0,889	23086	51294	0,874	10790	44050	0,852	127	7060	0,855	75	228	0,721	16	120	0,629	22	272
		SAGE_Colon_adenocarcinoma_CL_SW837	cell line	0,870	20756	61148	0,864	10501	55375	0,851	127	8793	0,870	75	544	0,826	16	244	0,579	22	521
	Normal	SAGE_Colon_normal_B_NC1	bulk	0,847	17703	49610	0,834	8988	43818	0,850	127	1309	0,830	75	380	0,838	16	121	0,471	22	204
		SAGE_Colon_normal_B_NC2	bulk	0,846	16270	48479	0,834	8559	43141	0,849	127	2468	0,823	75	487	0,862	16	160	0,527	22	243
Kidney	Cancer	SAGE_Kidney_carcinoma_B_D2	bulk	0,867	32412	100281	0,847	12682	91434	0,829	127	11637	0,857	75	1410	0,811	16	624	0,563	22	1752
	Normal	SAGE_Kidney_normal_B_1	bulk	0,844	16295	40993	0,829	8712	34671	0,862	127	1913	0,861	75	367	0,826	16	124	0,646	22	144

Table S15. (*Continued*)

Tissue[a]	Histology[b]	SAGE Library[b]	Preparation[b]	SAGE tag[c]			SAGE tag-to-gene[d]			Ribosome[e,f]			ETC[e,f]			ATP synthase[e,f]			Glycolysis[e,f]		
				$H\alpha$	$M\alpha$	$N\alpha$	$H\alpha$	$M\alpha$	$N\alpha$	$H\alpha$	$M\alpha$	$N\alpha$	$H\alpha$	$M\alpha$	$N\alpha$	$H\alpha$	$M\alpha$	$N\alpha$	$H\alpha$	$M\alpha$	$N\alpha$
Liver	Cancer	SAGE_Liver_cholangiocarcinoma_B_K1	bulk	0,940	40476	60319	0,910	14330	42726	0,854	127	625	0,807	75	118	0,769	16	34	0,601	22	102
		SAGE_Liver_cholangiocarcinoma_B_K2D	bulk	0,894	20722	46853	0,880	10307	41521	0,819	127	6778	0,833	75	474	0,742	16	177	0,460	22	277
		SAGE_Liver_cholangiocarcinoma_CL_K3	cell line	0,836	16356	54842	0,824	8882	50894	0,827	127	12513	0,815	75	648	0,811	16	303	0,496	22	737
		SAGE_Liver_cholangiocarcinoma_CL_K4	cell line	0,837	16652	52973	0,821	8648	48419	0,814	127	11574	0,804	75	619	0,751	16	316	0,506	22	779
	Normal	SAGE_Liver_normal_B_1	bulk	0,792	15496	66308	0,776	8701	61928	0,840	127	3272	0,855	75	805	0,780	16	325	0,514	22	257
Lung	Cancer	SAGE_Lung_adenocarcinoma_MD_L10	MD	0,876	29062	86887	0,867	13208	80012	0,841	127	7991	0,878	75	653	0,852	16	180	0,614	22	416
		SAGE_Lung_adenocarcinoma_MD_L9	MD	0,895	15131	35916	0,881	8933	33205	0,830	127	3704	0,874	75	283	0,846	16	78	0,661	22	169
	Normal	SAGE_Lung_normal_B_1	bulk	0,852	24764	88708	0,847	12086	82620	0,824	127	9438	0,854	75	899	0,753	16	421	0,551	22	313
Ovary	Cancer	SAGE_Ovary_adenocarcinoma_B_OVT-6	bulk	0,905	18440	41443	0,893	9945	36749	0,862	127	2920	0,864	75	266	0,855	16	102	0,503	22	311
		SAGE_Ovary_adenocarcinoma_B_OVT-7	bulk	0,878	19479	53514	0,866	10285	48468	0,856	127	4883	0,857	75	606	0,874	16	192	0,588	22	387
		SAGE_Ovary_adenocarcinoma_B_OVT-8	bulk	0,925	16312	31987	0,912	9210	27910	0,861	127	2530	0,866	75	241	0,836	16	85	0,601	22	152
		SAGE_Ovary_carcinoma_CL_A2780	cell line	0,928	10675	21369	0,917	6718	19236	0,867	127	2708	0,870	75	269	0,851	16	122	0,593	22	202
		SAGE_Ovary_carcinoma_CL_ES2-1	cell line	0,898	13583	31159	0,887	7738	28155	0,857	127	4360	0,815	75	258	0,839	16	105	0,575	22	247
	Normal	SAGE_Ovary_normal_CS_HOSE_4	STC	0,861	15994	47728	0,849	8499	43479	0,832	127	6384	0,813	75	599	0,776	16	305	0,542	22	692
Pancreas	Cancer	SAGE_Pancreas_adenocarcinoma_B_91-16113	bulk	0,895	15793	33582	0,878	8768	29772	0,857	127	1487	0,862	75	155	0,802	16	66	0,563	22	184
		SAGE_Pancreas_adenocarcinoma_B_96-6252	bulk	0,885	14339	33213	0,871	8573	30189	0,841	127	1809	0,858	75	195	0,849	16	70	0,512	22	200
		SAGE_Pancreas_adenocarcinoma_CL_CAPAN1	cell line	0,897	14815	37674	0,888	8929	34728	0,854	127	5542	0,871	75	398	0,828	16	131	0,564	22	170
		SAGE_Pancreas_adenocarcinoma_CL_Panc1	cell line	0,891	10293	24749	0,877	6504	22560	0,674	127	3653	0,838	75	296	0,764	16	120	0,576	22	100
		SAGE_Pancreas_carcinoma_CL_ASPC	cell line	0,847	10622	31224	0,837	6626	28740	0,853	127	4052	0,857	75	296	0,787	16	121	0,546	22	208
		SAGE_Pancreas_carcinoma_CL_PL45	cell line	0,876	11121	29557	0,865	6869	27210	0,857	127	4052	0,848	75	359	0,823	16	116	0,504	22	299
	Normal	SAGE_Pancreas_normal_CS_H126	STC	0,877	12360	32223	0,863	7265	28925	0,827	127	6821	0,784	75	324	0,821	16	97	0,656	22	152
		SAGE_Pancreas_normal_CS_HX	STC	0,877	12392	31985	0,864	7351	28811	0,827	127	6802	0,790	75	329	0,753	16	89	0,658	22	150
Peritoneum	Cancer	SAGE_Peritoneum_mesothelioma_B_12	bulk	0,906	14103	32529	0,894	8282	29621	0,861	127	2334	0,875	75	258	0,844	16	98	0,599	22	214
	Normal	SAGE_Peritoneum_normal_B_13	bulk	0,896	22799	53527	0,879	10824	46937	0,840	127	1902	0,836	75	280	0,804	16	118	0,517	22	331
Prostate	Cancer	SAGE_Prostate_carcinoma_B_LN-1	bulk	0,895	10601	22599	0,861	6100	20615	0,739	127	4328	0,725	75	315	0,723	16	137	0,619	22	94
		SAGE_Prostate_carcinoma_B_pool2	bulk	0,859	22306	66034	0,846	10923	59110	0,860	127	13632	0,865	75	1102	0,865	16	320	0,566	22	267
		SAGE_Prostate_adenocarcinoma_MD_PR317	MD	0,857	18877	64951	0,853	10352	61176	0,854	127	10985	0,853	75	925	0,856	16	317	0,534	22	299
		SAGE_Prostate_adenocarcinoma_CL_LNCaP	cell line	0,888	9155	22344	0,880	5829	20292	0,825	127	4024	0,837	75	337	0,744	16	132	0,569	22	206
		SAGE_Prostate_carcinoma_CL_A+	cell line	0,888	12281	30298	0,878	7159	27027	0,823	127	5409	0,830	75	395	0,764	16	164	0,551	22	188
		SAGE_Prostate_carcinoma_CL_LNCaP	cell line	0,849	18404	60250	0,838	9865	55391	0,859	127	13769	0,870	75	1090	0,876	16	368	0,566	22	302
		SAGE_Prostate_carcinoma_CL_LNCaP_no-DHT	cell line	0,835	16768	62160	0,825	9081	57219	0,854	127	15525	0,843	75	1252	0,865	16	383	0,637	22	323
		SAGE_Prostate_carcinoma_CL_LNCaP-C	cell line	0,894	15561	40029	0,886	9010	36721	0,871	127	5259	0,868	75	578	0,846	16	196	0,575	22	214
		SAGE_Prostate_carcinoma_CL_LNCaP-T	cell line	0,884	15922	43542	0,878	9155	40045	0,875	127	5843	0,863	75	605	0,850	16	220	0,566	22	273
		SAGE_Prostate_carcinoma_CL_PC3_AS2	cell line	0,925	20661	40768	0,912	10356	35425	0,847	127	2275	0,824	75	316	0,849	16	103	0,665	22	191
		SAGE_Prostate_carcinoma_CL_PC3_Mock	cell line	0,915	15961	38819	0,906	8922	35577	0,836	127	3094	0,823	75	493	0,808	16	153	0,523	22	338
	Normal	SAGE_Prostate_normal_epithelium_CS_confluent	STC	0,786	15164	71897	0,778	8489	66766	0,823	127	19885	0,826	75	1199	0,756	16	624	0,440	22	652
		SAGE_Prostate_normal_epithelium_CS_senescent	STC	0,800	16963	71717	0,788	9010	66633	0,836	127	18367	0,845	75	1009	0,736	16	555	0,352	22	961
		SAGE_Prostate_normal_MD_PR317	MD	0,865	18732	59277	0,856	10242	55625	0,857	127	7969	0,844	75	751	0,816	16	258	0,561	22	379
		SAGE_Prostate_normal_B_2	bulk	0,855	20456	64058	0,843	10563	58427	0,860	127	13690	0,865	75	1154	0,862	16	337	0,580	22	285
Skin	Cancer	SAGE_Skin_melanoma_B_DB1	bulk	0,864	11905	26032	0,839	6115	21341	0,739	127	508	0,699	75	87	0,511	16	30	0,509	22	60
		SAGE_Skin_melanoma_B_DB2	bulk	0,884	15667	41338	0,858	8012	38189	0,783	127	6595	0,812	75	894	0,688	16	432	0,624	22	459
		SAGE_Skin_melanoma_B_DB3	bulk	0,928	6267	11399	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	Normal	SAGE_Skin_normal_B_NS	bulk	0,892	15246	36615	0,878	8386	31892	0,806	127	3282	0,788	75	228	0,799	16	74	0,679	22	86
Stomach	Cancer	SAGE_Stomach_adenocarcinoma_B_G234	bulk	0,872	21447	64925	0,864	11095	60662	0,863	127	5653	0,854	75	873	0,826	16	241	0,571	22	415
		SAGE_Stomach_carcinoma_B_G189	bulk	0,857	17672	63075	0,854	9937	59313	0,841	127	10001	0,851	75	762	0,854	16	232	0,478	22	409
		SAGE_Stomach_carcinoma_B_xenograft_X101	bulk	0,888	25022	69749	0,879	11485	60158	0,865	127	5987	0,848	75	937	0,829	16	268	0,585	22	425
		SAGE_Stomach_carcinoma_B_xenograph_X43	bulk	0,886	19923	51620	0,875	9990	45238	0,852	127	4803	0,823	75	644	0,794	16	206	0,603	22	289
		SAGE_Stomach_adenocarcinoma_MD_G329	MD	0,898	19208	46802	0,883	10167	42208	0,823	127	4483	0,816	75	449	0,758	16	159	0,564	22	257
		SAGE_Stomach_adenocarcinoma_MD_HG7	MD	0,891	34469	93714	0,879	14083	81077	0,853	127	7540	0,836	75	808	0,823	16	332	0,632	22	473
		SAGE_Stomach_adenocarcinoma_MD_HS29	MD	0,886	22385	58831	0,870	11319	53416	0,844	127	5229	0,847	75	524	0,811	16	174	0,641	22	310
	Normal	SAGE_Stomach_normal_MD_13S	MD	0,785	15700	45908	0,753	8420	40109	0,868	127	2419	0,838	75	365	0,838	16	121	0,530	22	56
		SAGE_Stomach_normal_MD_14S	MD	0,819	18718	73353	0,811	10176	67718	0,833	127	7237	0,796	75	941	0,834	16	269	0,477	22	267
		SAGE_Stomach_normal_B_antrum	bulk	0,848	9349	26653	0,836	6247	24850	0,829	127	2748	0,762	75	341	0,813	16	102	0,479	22	87
		SAGE_Stomach_normal_epithelium_B_body1	bulk	0,783	8907	24761	0,757	5700	22385	0,861	127	1435	0,855	75	201	0,886	16	84	0,544	22	35
Thyroid	Cancer	SAGE_Thyroid_follicular_carcinoma_B_TT004	bulk	0,861	36863	124664	0,857	14498	111981	0,838	127	17459	0,825	75	2828	0,788	16	974	0,435	22	932
	Normal	SAGE_Thyroid_normal_B_001	bulk	0,863	35845	115938	0,859	14312	104045	0,838	127	14160	0,842	75	1448	0,805	16	512	0,512	22	372

[a] The skin library "SAGE_Skin_melanoma_B_DB3" is not integrated with SAGE Absolute Level Lister (SALL) tool and, therefore, could not be retrieved for tag-to-gene analysis. Cerebellum tissue libraries are retrieved by specific access in CGAP search tools and, therefore, are analyzed separately from brain tissue.

[b] List of SAGE libraries selected based on the search criteria: tag length (short 10bp); tissue preparation [bulk, short term culture (STC), antibody purified (ABP) or microscope dissected (MCD)]; and tissue histology (cancer or normal). The list contains only libraries that had at least one mached pair cancer/normal (*e.g.* one cancer and one equivalent normal tissue library).

[c] SAGE tag collections are retrieved using SAGE Library Finder tool at SAGE Genie website (http://cgap.nci.nih.gov/SAGE), which returns the list of libraries presented here. The diversity $H\alpha$ of each library are obtained for the entire set of tags of a given library.

[d] SAGE tag-to-gene collections are retrieved using SAGE Absolute Level Lister (SALL) tool. This tool links SAGE unique tags to genes via UniGene cluster ids (*e.g.* it links Tag, Frequency, UniGene Cluster and Gene Symbol). Therefore, here diversity $H\alpha$ of each SAGE library are obtained for tag-to-UniGene libraries, as decribed in material and methods.

[e] $H\alpha$ = diversity of tags; $M\alpha$ = number of unique tags; $N\alpha$ = number of tags (for details, material and methods).

[f] We consider each expression pathways as a specific group of genes (*e.g.* group of UniGene ids), which are presented in Tables S1 to S10. Therefore, the diversity $H\alpha$ of each SAGE library was obtained for groups of UniGene clusters, as described in material and methods. Electron transport chain (ETC).

Table S16. Diversity of genome stability pathways.

Tissue[a]	Histology[b]	SAGE Library[b]	Preparation[b]	Apoptosis[c,d]			Chromosome stability[c,d]			MMR[c,d]			NER[d,e]			BER[d,e]			RER[c,d]		
				$H\alpha$	$M\alpha$	$N\alpha$	$H\alpha$	$M\alpha$	$N\alpha$	$H\alpha$	$M\alpha$	$N\alpha$	$H\alpha$	$M\alpha$	$N\alpha$	$H\alpha$	$M\alpha$	$N\alpha$	$H\alpha$	$M\alpha$	$N\alpha$
Brain	Cancer	SAGE_Brain_astrocytoma_grade_I_B_H1043	bulk	0,798	99	382	0,538	77	363	0,729	28	80	0,531	28	223	0,835	17	27	0,782	24	64
		SAGE_Brain_astrocytoma_grade_II_B_H127	bulk	0,764	99	580	0,705	77	244	0,709	28	117	0,541	28	265	0,722	17	63	0,652	24	94
		SAGE_Brain_astrocytoma_grade_II_B_H359	bulk	0,812	99	451	0,757	77	266	0,794	28	126	0,541	28	306	0,785	17	86	0,702	24	101
		SAGE_Brain_astrocytoma_grade_II_B_H388	bulk	0,641	99	725	0,721	77	272	0,707	28	101	0,281	28	580	0,763	17	73	0,708	24	76
		SAGE_Brain_astrocytoma_grade_II_B_H501	bulk	0,779	99	663	0,691	77	326	0,793	28	109	0,677	28	265	0,902	17	88	0,701	24	90
		SAGE_Brain_astrocytoma_grade_II_B_H516	bulk	0,813	99	500	0,663	77	436	0,793	28	105	0,540	28	241	0,825	17	71	0,853	24	81
		SAGE_Brain_astrocytoma_grade_II_B_H518	bulk	0,711	99	679	0,721	77	278	0,777	28	125	0,352	28	452	0,777	17	95	0,657	24	113
		SAGE_Brain_astrocytoma_grade_II_B_H530	bulk	0,770	99	460	0,665	77	319	0,831	28	125	0,563	28	220	0,766	17	90	0,665	24	81
		SAGE_Brain_astrocytoma_grade_II_B_H563	bulk	0,784	99	397	0,615	77	286	0,717	28	105	0,719	28	167	0,723	17	52	0,686	24	66
		SAGE_Brain_astrocytoma_grade_III_B_343	bulk	0,781	99	436	0,722	77	226	0,763	28	88	0,437	28	281	0,650	17	71	0,630	24	125
		SAGE_Brain_astrocytoma_grade_III_B_407	bulk	0,828	99	400	0,664	77	271	0,771	28	91	0,346	28	522	0,775	17	85	0,642	24	89
		SAGE_Brain_astrocytoma_grade_III_B_439	bulk	0,810	99	390	0,725	77	266	0,732	28	134	0,582	28	266	0,868	17	74	0,614	24	79
		SAGE_Brain_astrocytoma_grade_III_B_584	bulk	0,757	99	485	0,757	77	253	0,719	28	132	0,574	28	259	0,813	17	60	0,626	24	73
		SAGE_Brain_astrocytoma_grade_III_B_828	bulk	0,778	99	468	0,742	77	213	0,735	28	146	0,675	28	236	0,742	17	51	0,654	24	78
		SAGE_Brain_astrocytoma_grade_III_B_H1020	bulk	0,806	99	218	0,537	77	253	0,842	28	54	0,587	28	126	0,644	17	17	0,711	24	43
		SAGE_Brain_astrocytoma_grade_III_B_H1055	bulk	0,815	99	469	0,731	77	308	0,690	28	146	0,709	28	281	0,867	17	81	0,651	24	91
		SAGE_Brain_astrocytoma_grade_III_B_H272	bulk	0,825	99	471	0,790	77	251	0,851	28	96	0,634	28	187	0,797	17	40	0,748	24	86
		SAGE_Brain_astrocytoma_grade_III_B_H970	bulk	0,800	99	519	0,743	77	284	0,779	28	114	0,565	28	257	0,813	17	80	0,682	24	90
		SAGE_Brain_astrocytoma_grade_III_B_R140	bulk	0,848	99	504	0,778	77	303	0,687	28	168	0,712	28	197	0,810	17	117	0,725	24	104
		SAGE_Brain_astrocytoma_grade_III_B_R927	bulk	0,827	99	474	0,763	77	293	0,807	28	164	0,723	28	203	0,653	17	93	0,605	24	156
		SAGE_Brain_ependymoblastoma_B_819	bulk	0,751	99	157	0,685	77	83	0,703	28	23	0,669	28	121	0,719	17	17	0,592	24	32
		SAGE_Brain_ependymoma_B_1150	bulk	0,771	99	290	0,757	77	196	0,708	28	102	0,773	28	167	0,849	17	56	0,775	24	67
		SAGE_Brain_ependymoma_B_1394	bulk	0,815	99	218	0,729	77	132	0,695	28	85	0,711	28	131	0,717	17	27	0,760	24	45
		SAGE_Brain_ependymoma_B_239	bulk	0,790	99	161	0,709	77	117	0,674	28	57	0,804	28	65	0,858	17	36	0,654	24	35
		SAGE_Brain_ependymoma_B_H580	bulk	0,816	99	259	0,655	77	173	0,736	28	92	0,736	28	154	0,821	17	35	0,747	24	62
		SAGE_Brain_ependymoma_B_R1023	bulk	0,762	99	507	0,673	77	400	0,764	28	128	0,696	28	312	0,886	17	62	0,632	24	102
		SAGE_Brain_ependymoma_B_R353	bulk	0,820	99	310	0,676	77	228	0,806	28	78	0,776	28	144	0,746	17	46	0,678	24	43
		SAGE_Brain_ependymoma_B_R455	bulk	0,770	99	228	0,660	77	102	0,775	28	47	0,710	28	110	0,792	17	36	0,649	24	43
		SAGE_Brain_ependymoma_B_R510	bulk	0,802	99	362	0,666	77	335	0,774	28	103	0,714	28	188	0,881	17	52	0,730	24	71
		SAGE_Brain_ependymoma_B_R512	bulk	0,785	99	316	0,697	77	221	0,824	28	66	0,713	28	154	0,809	17	38	0,686	24	57
		SAGE_Brain_ependymoma_B_R582	bulk	0,777	99	233	0,668	77	116	0,687	28	44	0,596	28	111	0,806	17	30	0,734	24	45
		SAGE_Brain_ependymoma_B_R628	bulk	0,776	99	554	0,686	77	402	0,795	28	133	0,705	28	241	0,870	17	71	0,741	24	97
		SAGE_Brain_glioblastoma_B_GBM1062	bulk	0,703	99	212	0,490	77	131	0,707	28	43	0,595	28	53	0,716	17	23	0,642	24	36
		SAGE_Brain_glioblastoma_B_H1110	bulk	0,756	99	317	0,659	77	244	0,822	28	98	0,513	28	270	0,750	17	41	0,677	24	55
		SAGE_Brain_glioblastoma_B_H1353	bulk	0,807	99	573	0,748	77	306	0,829	28	166	0,688	28	238	0,858	17	107	0,689	24	117
		SAGE_Brain_glioblastoma_B_H1371	bulk	0,821	99	193	0,652	77	93	0,720	28	38	0,643	28	74	0,758	17	30	0,730	24	30
		SAGE_Brain_glioblastoma_B_H1425C	bulk	0,786	99	383	0,737	77	241	0,761	28	109	0,710	28	173	0,740	17	47	0,699	24	102
		SAGE_Brain_glioblastoma_B_H833	bulk	0,793	99	441	0,722	77	229	0,800	28	110	0,704	28	182	0,793	17	56	0,671	24	73
		SAGE_Brain_glioblastoma_B_pooled	bulk	0,714	99	267	0,604	77	201	0,736	28	51	0,478	28	216	0,777	17	17	0,675	24	35
		SAGE_Brain_glioblastoma_B_R20	bulk	0,761	99	570	0,735	77	364	0,803	28	145	0,688	28	216	0,779	17	66	0,727	24	97
		SAGE_Brain_glioblastoma_B_R336	bulk	0,750	99	522	0,774	77	233	0,729	28	126	0,437	28	433	0,766	17	89	0,781	24	100
		SAGE_Brain_glioblastoma_B_R70	bulk	0,768	99	470	0,768	77	288	0,782	28	154	0,587	28	278	0,782	17	58	0,601	24	98
		SAGE_Brain_meningioma_grade_II_B_SF2176	bulk	0,704	99	161	0,329	77	160	0,696	28	44	0,599	28	90	0,732	17	22	0,506	24	31
		SAGE_Brain_meningioma_grade_II_B_SF3622	bulk	0,736	99	191	0,397	77	209	0,789	28	50	0,720	28	63	0,674	17	14	0,501	24	24
		SAGE_Brain_meningioma_grade_III_B_SF2366	bulk	0,769	99	244	0,468	77	250	0,778	28	63	0,686	28	89	0,804	17	39	0,528	24	70
		SAGE_Brain_oligodendroglioma_B_1001	bulk	0,593	99	195	0,577	77	96	0,695	28	37	0,371	28	113	0,750	17	20	0,724	24	29
		SAGE_Brain_oligodendroglioma_B_H988	bulk	0,638	99	124	0,544	77	119	0,604	28	23	0,322	28	113	0,718	17	17	0,680	24	24
		SAGE_Brain_glioblastoma_CS_TA2	STC	0,763	99	196	0,741	77	103	0,783	28	50	0,782	28	94	0,604	17	17	0,641	24	36
		SAGE_Brain_glioblastoma_CL_H392	cell line	0,692	99	293	0,580	77	209	0,728	28	63	0,483	28	191	0,705	17	28	0,600	24	58
		SAGE_Brain_glioblastoma_CL_H54+EGFRvIII	cell line	0,726	99	321	0,643	77	184	0,722	28	68	0,474	28	188	0,540	17	15	0,633	24	43
		SAGE_Brain_glioblastoma_CL_H54+LacZ	cell line	0,739	99	365	0,685	77	262	0,742	28	122	0,557	28	159	0,524	17	27	0,746	24	53
		SAGE_Brain_glioblastoma_control_CL_H247	cell line	0,775	99	251	0,718	77	202	0,746	28	105	0,638	28	145	0,807	17	45	0,635	24	75
		SAGE_Brain_glioblastoma_hypoxia_CL_H247	cell line	0,811	99	330	0,699	77	246	0,673	28	94	0,540	28	163	0,853	17	37	0,711	24	75
	Normal	SAGE_Brain_normal_cortex_B_BB542	bulk	0,721	99	557	0,692	77	268	0,721	28	82	0,242	28	464	0,804	17	40	0,660	24	45
		SAGE_Brain_normal_leptomeninges_B_AL2	bulk	0,794	99	275	0,464	77	323	0,726	28	57	0,644	28	115	0,767	17	37	0,602	24	54
		SAGE_Brain_normal_peds_cortex_B_H1571	bulk	0,674	99	599	0,711	77	200	0,706	28	48	0,299	28	315	0,839	17	40	0,696	24	54
		SAGE_Brain_normal_thalamus_B_1	bulk	0,528	99	181	0,558	77	63	0,649	28	10	0,137	28	153	0,592	17	9	0,727	24	13

Table S16. (*Continued*)

Tissue[a]	Histology[b]	SAGE Library[b]	Preparation[b]	Apoptosis[c,d]			Chromosome stability[c,d]			MMR[c,d]			NER[d,e]			BER[d,e]			RER[c,d]		
				$H\alpha$	$M\alpha$	$N\alpha$	$H\alpha$	$M\alpha$	$N\alpha$	$H\alpha$	$M\alpha$	$N\alpha$	$H\alpha$	$M\alpha$	$N\alpha$	$H\alpha$	$M\alpha$	$N\alpha$	$H\alpha$	$M\alpha$	$N\alpha$
Cerebellum	Cancer	SAGE_Brain_medulloblastoma_B_1273	bulk	0,788	99	165	0,599	77	183	0,755	28	69	0,660	28	68	0,781	17	22	0,559	24	40
		SAGE_Brain_medulloblastoma_B_96-04-P019	bulk	0,747	99	225	0,725	77	133	0,763	28	57	0,592	28	80	0,698	17	45	0,706	24	53
		SAGE_Brain_medulloblastoma_B_97-05-P015	bulk	0,757	99	239	0,746	77	150	0,788	28	64	0,783	28	80	0,689	17	54	0,718	24	55
		SAGE_Brain_medulloblastoma_B_97-05-P312	bulk	0,828	99	256	0,659	77	226	0,806	28	98	0,706	28	103	0,800	17	58	0,659	24	58
		SAGE_Brain_medulloblastoma_B_98-04-P117	bulk	0,735	99	115	0,563	77	89	0,713	28	48	0,620	28	38	0,636	17	38	0,656	24	31
		SAGE_Brain_medulloblastoma_B_98-04-P494	bulk	0,719	99	162	0,763	77	94	0,697	28	80	0,659	28	76	0,643	17	49	0,507	24	58
		SAGE_Brain_medulloblastoma_B_98-05-P040	bulk	0,799	99	383	0,701	77	215	0,763	28	112	0,741	28	142	0,659	17	78	0,657	24	92
		SAGE_Brain_medulloblastoma_B_98-05-P608	bulk	0,768	99	227	0,759	77	144	0,759	28	83	0,754	28	70	0,661	17	33	0,659	24	45
		SAGE_Brain_medulloblastoma_B_98-09-P558	bulk	0,790	99	354	0,813	77	180	0,737	28	138	0,804	28	142	0,713	17	76	0,680	24	113
		SAGE_Brain_medulloblastoma_B_98-13-P301	bulk	0,771	99	169	0,691	77	121	0,730	28	63	0,650	28	65	0,719	17	33	0,710	24	50
		SAGE_Brain_medulloblastoma_B_C609	bulk	0,776	99	345	0,805	77	193	0,811	28	109	0,780	28	113	0,805	17	88	0,714	24	99
		SAGE_Brain_medulloblastoma_B_DL5	bulk	0,780	99	293	0,504	77	374	0,814	28	90	0,798	28	117	0,684	17	67	0,486	24	67
		SAGE_Brain_medulloblastoma_B_DL7	bulk	0,791	99	233	0,747	77	177	0,772	28	89	0,731	28	99	0,626	17	87	0,657	24	64
		SAGE_Brain_medulloblastoma_B_H1322	bulk	0,773	99	223	0,749	77	181	0,727	28	98	0,722	28	134	0,695	17	20	0,737	24	75
		SAGE_Brain_medulloblastoma_B_H1413	bulk	0,655	99	225	0,525	77	196	0,752	28	55	0,334	28	214	0,555	17	50	0,603	24	58
		SAGE_Brain_medulloblastoma_B_H275	bulk	0,704	99	257	0,847	77	170	0,812	28	81	0,638	28	115	0,666	17	69	0,668	24	98
		SAGE_Brain_medulloblastoma_B_H306	bulk	0,795	99	184	0,522	77	245	0,709	28	57	0,702	28	85	0,687	17	52	0,715	24	45
		SAGE_Brain_medulloblastoma_B_H484	bulk	0,790	99	202	0,749	77	181	0,740	28	131	0,761	28	102	0,742	17	69	0,616	24	108
		SAGE_Brain_medulloblastoma_B_H876	bulk	0,784	99	239	0,724	77	173	0,805	28	64	0,775	28	63	0,647	17	64	0,645	24	93
		SAGE_Brain_medulloblastoma_B_H972	bulk	0,762	99	313	0,808	77	185	0,709	28	128	0,681	28	105	0,562	17	76	0,604	24	109
		SAGE_Brain_medulloblastoma_CL_4-HCR	cell line	0,715	99	288	0,713	77	279	0,649	28	174	0,387	28	253	0,685	17	57	0,756	24	82
		SAGE_Brain_medulloblastoma_CL_D283	cell line	0,669	99	296	0,797	77	274	0,794	28	153	0,269	28	419	0,671	17	52	0,758	24	92
		SAGE_Brain_medulloblastoma_CL_H341	cell line	0,743	99	123	0,717	77	94	0,752	28	43	0,501	28	126	0,645	17	48	0,706	24	33
		SAGE_Brain_medulloblastoma_CL_mhh-1	cell line	0,744	99	185	0,726	77	107	0,702	28	63	0,656	28	92	0,679	17	40	0,655	24	66
	Normal	SAGE_Brain_normal_cerebellum_B_1	bulk	0,752	99	250	0,677	77	204	0,754	28	40	0,531	28	112	0,801	17	15	0,711	24	41
		SAGE_Brain_normal_cerebellum_B_BB542	bulk	0,689	99	211	0,699	77	122	0,756	28	27	0,318	28	137	0,740	17	16	0,738	24	27
Breast	Cancer	SAGE_Breast_carcinoma_B_95-259	bulk	0,628	99	170	0,585	77	146	0,734	28	27	0,585	28	62	0,828	17	26	0,644	24	50
		SAGE_Breast_carcinoma_B_95-347	bulk	0,760	99	268	0,517	77	289	0,743	28	66	0,536	28	169	0,780	17	47	0,616	24	46
		SAGE_Breast_carcinoma_B_DCIS-4	bulk	0,754	99	290	0,541	77	176	0,751	28	54	0,575	28	110	0,795	17	39	0,669	24	58
		SAGE_Breast_carcinoma_B_DCIS-5	bulk	0,736	99	230	0,544	77	134	0,685	28	35	0,457	28	97	0,765	17	24	0,699	24	43
		SAGE_Breast_carcinoma_B_IDC-3	bulk	0,750	99	343	0,627	77	200	0,787	28	81	0,612	28	134	0,771	17	58	0,755	24	81
		SAGE_Breast_carcinoma_B_IDC-4	bulk	0,774	99	291	0,656	77	210	0,751	28	92	0,699	28	104	0,748	17	40	0,622	24	90
		SAGE_Breast_carcinoma_B_IDC-5	bulk	0,772	99	268	0,573	77	169	0,762	28	49	0,535	28	136	0,769	17	63	0,706	24	76
		SAGE_Breast_carcinoma_metastasis_B_2	bulk	0,682	99	254	0,611	77	210	0,692	28	77	0,682	28	83	0,802	17	43	0,633	24	40
		SAGE_Breast_metastatic_carcinoma_B_95-260	bulk	0,655	99	209	0,649	77	123	0,661	28	49	0,557	28	64	0,652	17	30	0,671	24	50
		SAGE_Breast_metastatic_carcinoma_B_95-348	bulk	0,715	99	279	0,650	77	207	0,773	28	79	0,655	28	116	0,766	17	47	0,634	24	54
		SAGE_Breast_carcinoma_MD_DCIS	MD	0,754	99	145	0,612	77	90	0,719	28	55	0,624	28	65	0,690	17	17	0,570	24	23
		SAGE_Breast_carcinoma_epithelium_AP_DCIS-2	AP	0,781	99	308	0,463	77	226	0,756	28	46	0,332	28	191	0,755	17	45	0,581	24	36
		SAGE_Breast_carcinoma_epithelium_AP_DCIS-3	AP	0,816	99	212	0,211	77	1112	0,752	28	58	0,319	28	167	0,699	17	26	0,837	24	48
		SAGE_Breast_carcinoma_epithelium_AP_DCIS6	AP	0,818	99	327	0,340	77	659	0,787	28	75	0,387	28	232	0,755	17	31	0,732	24	58
		SAGE_Breast_carcinoma_epithelium_AP_DCIS7	AP	0,745	99	705	0,493	77	461	0,811	28	82	0,287	28	437	0,808	17	55	0,768	24	39
		SAGE_Breast_carcinoma_CL_MCF7control_0h	cell line	0,749	99	212	0,715	77	106	0,618	28	150	0,591	28	137	0,400	17	126	0,659	24	48
		SAGE_Breast_carcinoma_CL_MCF7estradiol_10H	cell line	0,780	99	239	0,800	77	160	0,537	28	159	0,613	28	171	0,610	17	97	0,639	24	105
		SAGE_Breast_carcinoma_CL_MCF7estradiol_3h	cell line	0,774	99	235	0,757	77	111	0,611	28	161	0,587	28	186	0,598	17	77	0,651	24	68
		SAGE_Breast_carcinoma_CL_MDA435C	cell line	0,742	99	232	0,742	77	169	0,780	28	82	0,687	28	84	0,679	17	25	0,496	24	88
		SAGE_Breast_carcinoma_CL_MDA435H24	cell line	0,765	99	249	0,731	77	189	0,784	28	71	0,657	28	87	0,806	17	28	0,627	24	92
		SAGE_Breast_carcinoma_CL_MDA435H48	cell line	0,734	99	226	0,716	77	137	0,709	28	42	0,667	28	68	0,813	17	24	0,597	24	67
		SAGE_Breast_carcinoma_CL_ZR75_1_estrogen	cell line	0,594	99	152	0,441	77	136	0,575	28	76	0,479	28	29	0,514	17	16	0,550	24	15
		SAGE_Breast_carcinoma_CL_ZR75_1_tamoxifen	cell line	0,608	99	204	0,491	77	192	0,676	28	98	0,465	28	62	0,496	17	21	0,492	24	15
		SAGE_Breast_carcinoma_CL_ZR75_1_untreated	cell line	0,617	99	132	0,456	77	133	0,509	28	85	0,586	28	39	0,480	17	20	0,550	24	14
	Normal	SAGE_Breast_normal_epithelium_AP_1	AP	0,670	99	316	0,514	77	197	0,752	28	46	0,410	28	134	0,632	17	25	0,795	24	30
		SAGE_Breast_normal_epithelium_AP_Br_N	AP	0,670	99	361	0,473	77	160	0,688	28	38	0,444	28	104	0,663	17	20	0,685	24	25
		SAGE_Breast_normal_myoepithelium_AP_myoepithelial1	AP	0,804	99	325	0,563	77	209	0,663	28	47	0,447	28	82	0,793	17	24	0,592	24	50
		SAGE_Breast_normal_stroma_AP_1	AP	0,652	99	434	0,707	77	137	0,789	28	65	0,652	28	97	0,789	17	39	0,650	24	46
		SAGE_Breast_normal_organoid_B	bulk	0,554	99	646	0,633	77	121	0,765	28	41	0,513	28	66	0,553	17	21	0,522	24	47
Colon	Cancer	SAGE_Colon_adenocarcinoma_B_Tu102	bulk	0,642	99	302	0,436	77	232	0,844	28	50	0,084	28	577	0,677	17	24	0,756	24	50
		SAGE_Colon_adenocarcinoma_B_Tu98	bulk	0,596	99	279	0,432	77	221	0,706	28	50	0,178	28	352	0,689	17	21	0,707	24	34
		SAGE_Colon_adenocarcinoma_CL_Caco2	cell line	0,665	99	316	0,693	77	239	0,744	28	128	0,359	28	337	0,809	17	39	0,709	24	76
		SAGE_Colon_adenocarcinoma_CL_HCT116	cell line	0,727	99	269	0,689	77	232	0,678	28	75	0,681	28	155	0,795	17	30	0,662	24	59
		SAGE_Colon_adenocarcinoma_CL_RKO	cell line	0,740	99	217	0,626	77	196	0,735	28	54	0,691	28	120	0,730	17	17	0,795	24	41
		SAGE_Colon_adenocarcinoma_CL_SW837	cell line	0,692	99	410	0,752	77	190	0,791	28	83	0,652	28	135	0,670	17	33	0,752	24	59
	Normal	SAGE_Colon_normal_B_NC1	bulk	0,599	99	319	0,426	77	183	0,730	28	28	0,107	28	341	0,673	17	8	0,716	24	37
		SAGE_Colon_normal_B_NC2	bulk	0,572	99	323	0,405	77	139	0,597	28	28	0,075	28	624	0,727	17	15	0,721	24	27
Kidney	Cancer	SAGE_Kidney_carcinoma_B_D2	bulk	0,740	99	409	0,693	77	248	0,783	28	73	0,663	28	171	0,905	17	63	0,671	24	96
	Normal	SAGE_Kidney_normal_B_1	bulk	0,552	99	325	0,573	77	102	0,769	28	35	0,052	28	970	0,428	17	8	0,603	24	20

Table S16. (*Continued*)

Tissue[a]	**Histology**[b]	**SAGE Library**[b]	**Preparation**[b]	**Apoptosis**[c,d]			**Chromosome stability**[c,d]			**MMR**[c,d]			**NER**[d,e]			**BER**[d,e]			**RER**[c,d]		
				$H\alpha$	$M\alpha$	$N\alpha$	$H\alpha$	$M\alpha$	$N\alpha$	$H\alpha$	$M\alpha$	$N\alpha$	$H\alpha$	$M\alpha$	$N\alpha$	$H\alpha$	$M\alpha$	$N\alpha$	$H\alpha$	$M\alpha$	$N\alpha$
Liver	Cancer	SAGE_Liver_cholangiocarcinoma_B_K1	bulk	0,798	99	194	0,409	77	475	0,861	28	64	0,729	28	61	0,647	17	28	0,795	24	46
		SAGE_Liver_cholangiocarcinoma_B_K2D	bulk	0,788	99	238	0,710	77	136	0,740	28	55	0,712	28	67	0,707	17	25	0,659	24	57
		SAGE_Liver_cholangiocarcinoma_CL_K3	cell line	0,671	99	246	0,637	77	118	0,786	28	45	0,693	28	66	0,627	17	43	0,620	24	41
		SAGE_Liver_cholangiocarcinoma_CL_K4	cell line	0,598	99	267	0,598	77	88	0,711	28	43	0,650	28	53	0,601	17	36	0,509	24	41
	Normal	SAGE_Liver_normal_B_1	bulk	0,778	99	181	0,692	77	70	0,649	28	33	0,591	28	77	0,752	17	27	0,690	24	38
Lung	Cancer	SAGE_Lung_adenocarcinoma_MD_L10	MD	0,848	99	384	0,653	77	269	0,802	28	95	0,785	28	106	0,751	17	52	0,784	24	82
		SAGE_Lung_adenocarcinoma_MD_L9	MD	0,804	99	146	0,687	77	109	0,691	28	49	0,740	28	45	0,662	17	18	0,680	24	26
	Normal	SAGE_Lung_normal_B_1	bulk	0,754	99	490	0,657	77	168	0,690	28	96	0,710	28	103	0,717	17	51	0,649	24	85
Ovary	Cancer	SAGE_Ovary_adenocarcinoma_B_OVT-6	bulk	0,695	99	256	0,668	77	117	0,671	28	47	0,388	28	123	0,739	17	24	0,620	24	37
		SAGE_Ovary_adenocarcinoma_B_OVT-7	bulk	0,705	99	288	0,728	77	150	0,775	28	91	0,574	28	120	0,691	17	32	0,697	24	45
		SAGE_Ovary_adenocarcinoma_B_OVT-8	bulk	0,765	99	198	0,681	77	117	0,796	28	41	0,588	28	73	0,723	17	25	0,745	24	31
		SAGE_Ovary_carcinoma_CL_A2780	cell line	0,764	99	84	0,722	77	86	0,721	28	52	0,681	28	51	0,694	17	23	0,601	24	43
		SAGE_Ovary_carcinoma_CL_ES2-1	cell line	0,757	99	119	0,726	77	81	0,654	28	48	0,746	28	53	0,636	17	20	0,535	24	30
	Normal	SAGE_Ovary_normal_CS_HOSE_4	STC	0,688	99	367	0,707	77	77	0,647	28	34	0,654	28	71	0,639	17	14	0,541	24	45
Pancreas	Cancer	SAGE_Pancreas_adenocarcinoma_B_91-16113	bulk	0,751	99	177	0,540	77	115	0,599	28	19	0,300	28	154	0,550	17	8	0,637	24	24
		SAGE_Pancreas_adenocarcinoma_B_96-6252	bulk	0,789	99	151	0,552	77	110	0,700	28	21	0,319	28	167	0,780	17	15	0,667	24	21
		SAGE_Pancreas_adenocarcinoma_CL_CAPAN1	cell line	0,721	99	170	0,617	77	134	0,704	28	68	0,559	28	115	0,837	17	18	0,684	24	38
		SAGE_Pancreas_adenocarcinoma_CL_Panc1	cell line	0,572	99	168	0,608	77	115	0,697	28	27	0,669	28	58	0,695	17	14	0,622	24	29
		SAGE_Pancreas_carcinoma_CL_ASPC	cell line	0,641	99	170	0,643	77	73	0,544	28	26	0,292	28	141	0,596	17	23	0,574	24	21
		SAGE_Pancreas_carcinoma_CL_PL45	cell line	0,717	99	179	0,611	77	75	0,779	28	29	0,430	28	93	0,660	17	14	0,660	24	30
	Normal	SAGE_Pancreas_normal_CS_H126	STC	0,735	99	131	0,599	77	138	0,741	28	35	0,599	28	113	0,715	17	10	0,723	24	32
		SAGE_Pancreas_normal_CS_HX	STC	0,748	99	114	0,592	77	131	0,665	28	21	0,591	28	127	0,716	17	18	0,605	24	30
Peritoneum	Cancer	SAGE_Peritoneum_mesothelioma_B_12	bulk	0,749	99	155	0,679	77	95	0,760	28	32	0,507	28	103	0,562	17	14	0,538	24	25
	Normal	SAGE_Peritoneum_normal_B_13	bulk	0,663	99	481	0,549	77	175	0,671	28	28	0,476	28	100	0,748	17	17	0,521	24	38
Prostate	Cancer	SAGE_Prostate_carcinoma_B_LN-1	bulk	0,606	99	123	0,444	77	90	0,604	28	23	0,746	28	24	0,687	17	7	0,671	24	16
		SAGE_Prostate_carcinoma_B_pool2	bulk	0,745	99	273	0,593	77	152	0,724	28	60	0,482	28	252	0,798	17	46	0,730	24	51
		SAGE_Prostate_adenocarcinoma_MD_PR317	MD	0,733	99	282	0,682	77	85	0,788	28	54	0,546	28	125	0,668	17	38	0,531	24	61
		SAGE_Prostate_adenocarcinoma_CL_LNCaP	cell line	0,657	99	106	0,637	77	85	0,666	28	49	0,567	28	85	0,642	17	13	0,751	24	22
		SAGE_Prostate_carcinoma_CL_A+	cell line	0,718	99	186	0,655	77	76	0,677	28	26	0,597	28	43	0,686	17	22	0,724	24	19
		SAGE_Prostate_carcinoma_CL_LNCaP	cell line	0,774	99	231	0,641	77	152	0,692	28	57	0,501	28	243	0,584	17	38	0,680	24	51
		SAGE_Prostate_carcinoma_CL_LNCaP_no-DHT	cell line	0,668	99	271	0,566	77	178	0,781	28	72	0,647	28	164	0,736	17	47	0,640	24	43
		SAGE_Prostate_carcinoma_CL_LNCaP-C	cell line	0,717	99	266	0,690	77	139	0,642	28	49	0,506	28	141	0,738	17	18	0,673	24	40
		SAGE_Prostate_carcinoma_CL_LNCaP-T	cell line	0,723	99	267	0,655	77	124	0,744	28	61	0,435	28	172	0,835	17	25	0,642	24	41
		SAGE_Prostate_carcinoma_CL_PC3_AS2	cell line	0,851	99	171	0,600	77	176	0,684	28	55	0,638	28	87	0,674	17	22	0,771	24	42
		SAGE_Prostate_carcinoma_CL_PC3_Mock	cell line	0,748	99	181	0,695	77	130	0,681	28	107	0,587	28	152	0,668	17	34	0,584	24	49
	Normal	SAGE_Prostate_normal_epithelium_CS_confluent	STC	0,762	99	219	0,579	77	93	0,652	28	39	0,692	28	77	0,733	17	37	0,800	24	30
		SAGE_Prostate_normal_epithelium_CS_senescent	STC	0,807	99	189	0,574	77	86	0,661	28	39	0,672	28	115	0,720	17	21	0,567	24	27
		SAGE_Prostate_normal_MD_PR317	MD	0,784	99	246	0,704	77	89	0,742	28	49	0,682	28	116	0,768	17	39	0,530	24	49
		SAGE_Prostate_normal_B_2	bulk	0,756	99	273	0,685	77	150	0,679	28	85	0,467	28	215	0,813	17	39	0,663	24	47
Skin	Cancer	SAGE_Skin_melanoma_B_DB1	bulk	0,596	99	104	0,239	77	306	0,743	28	17	0,583	28	34	0,602	17	12	0,627	24	35
		SAGE_Skin_melanoma_B_DB2	bulk	0,604	99	212	0,515	77	194	0,673	28	42	0,746	28	55	0,792	17	21	0,560	24	38
		SAGE_Skin_melanoma_B_DB3	bulk	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	Normal	SAGE_Skin_normal_B_NS	bulk	0,691	99	187	0,322	77	197	0,654	28	28	0,435	28	72	0,652	17	11	0,618	24	24
Stomach	Cancer	SAGE_Stomach_adenocarcinoma_B_G234	bulk	0,801	99	320	0,708	77	163	0,579	28	111	0,364	28	223	0,799	17	17	0,702	24	59
		SAGE_Stomach_carcinoma_B_G189	bulk	0,749	99	254	0,775	77	101	0,607	28	96	0,581	28	114	0,628	17	37	0,701	24	61
		SAGE_Stomach_carcinoma_B_xenograft_X101	bulk	0,641	99	446	0,698	77	160	0,702	28	96	0,433	28	246	0,790	17	34	0,737	24	37
		SAGE_Stomach_carcinoma_B_xenograph_X43	bulk	0,620	99	367	0,732	77	138	0,658	28	83	0,321	28	215	0,762	17	19	0,735	24	59
		SAGE_Stomach_adenocarcinoma_MD_G329	MD	0,718	99	265	0,642	77	120	0,653	28	44	0,407	28	139	0,678	17	17	0,684	24	49
		SAGE_Stomach_adenocarcinoma_MD_HG7	MD	0,744	99	505	0,715	77	278	0,647	28	179	0,569	28	244	0,784	17	61	0,825	24	61
		SAGE_Stomach_adenocarcinoma_MD_HS29	MD	0,746	99	343	0,717	77	158	0,736	28	68	0,454	28	144	0,776	17	29	0,701	24	74
	Normal	SAGE_Stomach_normal_MD_13S	MD	0,392	99	291	0,708	77	66	0,665	28	33	0,270	28	180	0,673	17	12	0,757	24	19
		SAGE_Stomach_normal_MD_14S	MD	0,670	99	342	0,758	77	99	0,761	28	49	0,313	28	255	0,733	17	26	0,651	24	55
		SAGE_Stomach_normal_B_antrum	bulk	0,636	99	122	0,606	77	30	0,543	28	25	0,185	28	89	0,576	17	12	0,613	24	20
		SAGE_Stomach_normal_epithelium_B_body1	bulk	0,391	99	196	0,567	77	27	0,442	28	12	0,175	28	99	0,357	17	6	0,327	24	4
Thyroid	Cancer	SAGE_Thyroid_follicular_carcinoma_B_TT004	bulk	0,766	99	497	0,744	77	260	0,753	28	138	0,827	28	175	0,697	17	63	0,634	24	161
	Normal	SAGE_Thyroid_normal_B_001	bulk	0,807	99	440	0,708	77	238	0,727	28	130	0,710	28	228	0,749	17	78	0,678	24	128

[a] The skin library "SAGE_Skin_melanoma_B_DB3" is not integrated with SAGE Absolute Level Lister (SALL) tool and, therefore, could not be retrieved for tag-to-gene analysis. Cerebellum tissue libraries are retrieved by specific access in CGAP search tools and, therefore, are analyzed separately from brain tissue.

[b] List of SAGE libraries selected based on the search criteria: tag length (short 10bp); tissue preparation [bulk, short term culture (STC), antibody purified (ABP) or microscope dissected (MCD)]; and tissue histology (cancer or normal). The list contains only libraries that had at least one mached pair cancer/normal (*e.g.* one cancer and one equivalent normal tissue library).

[c] $H\alpha$ = diversity of tags; $M\alpha$ = number of unique tags; $N\alpha$ = number of tags (for details, material and methods).

[d] We consider each expression pathways as a specific group of genes (*e.g.* group of UniGene ids), which are presented in Tables S1 to S10. Therefore, the diversity $H\alpha$ of each SAGE library was obtained for groups of UniGene clusters, as described in material and methods. Mismatch repair (MMR); nucleotide-excision repair (NER); base-excision repair (BER); recombinational repair (RER).

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