Supplementary Table 1: Codon Adaptation Index (CAI) calculation of genes of most highly expressed cellular proteins, HIV-1 viral genes, and genes related to DNA damage response signaling.

Most Highly Expressed Cellular Proteins

Gene Name	Gene ID	CDS Length	CAI
GAPDH	2597	1008	**0.81**
RPL37A	6168	279	0.78
CFL1	1072	501	0.85
PPIA	5478	498	0.78
LGALS1	3956	408	0.87
PKM	5315	1818	0.78
EEF1A1	1915	1389	0.75
ENO1	2023	1305	0.78
VIM	7431	1401	0.79
ACTB	60	1128	0.88
TPI1	7167	750	0.75
PRDX1	5052	600	0.73
ANXA2	302	1074	0.79
PFN1	5216	423	0.71
TAGLN2	8407	663	0.78
TUBA1C	84790	1560	0.80
HIST1H2BK	85236	381	0.82
DHRS2	10202	903	0.76
MIF	4282	348	0.81
HNRNPA1	3178	1119	0.73
ALDOA	226	1095	0.81
HSPA8	3312	1941	0.75
HSP90AB1	3326	2175	0.78
HSPB1	3315	618	0.77
Average (CAI)			**0.79**
StdDev (CAI)			0.04

HIV-1 Viral Genes (pNL4-3), M19921.2

Gene Name	Gene ID	CDS Length	CAI
Gag		1503	0.59
Pol		3012	0.56
Vif		579	0.59
Vpr		291	0.61
Vpu		246	0.45
Env		7695	0.61
Tat		261	0.68
Rev		351	0.68
Average (CAI)			**0.60**
StdDev (CAI)			0.07

DNA Damage Response Signaling Related Genes

Gene Name	Gene ID	CDS Length	CAI
ATM	472	9171	**0.64**
ATR	545	7935	**0.65**
PRKDC	5591	12387	0.70
BRCA1	672	5592	0.67
BRCA2	675	10257	0.63
MDM2	4193	1494	0.65
MDM4	4194	1473	0.69
CHEK1	1111	1431	0.69
CHEK2	11200	1632	0.70
MRE11	4361	2127	0.66
NBN	4683	2265	0.63
RAD50	10111	3939	0.64
Average (CAI)			**0.66**
StdDev (CAI)			0.03

CAI calculation was done using the web application at http://genomes.urv.es/CAIcal/. The sequences of 80 human ribosome protein genes as the reference gene set were retrieved from Ribosome Protein Gene Database (RPG, http://ribosome.med.miyazaki-u.ac.jp/).

Supplementary Table 2: Codon Adaptation Index (CAI) calculation of genes affiliated with various DNA damage repair mechanisms including HDR, NHEJ, and MMR.

Homology Directed Repair (HDR)

Gene Name	Gene ID	CDS Length	CAI
ATM	472	9171	0.64
ATR	545	7935	0.65
ATRX	546	7476	0.67
BARD1	580	2334	0.67
BLM	641	4254	0.66
BRCA1	672	5592	0.67
BRCA2	675	10257	0.63
BRIP1	83990	3750	0.64
EME1	146956	1752	0.72
FANCF	2188	1125	0.71
FANCM	57697	6147	0.64
GEN1	348654	2727	0.65
MRE11	4361	2127	0.66
MUS81	80198	1659	0.76
NBN	4683	2265	0.63
PALB2	79728	3561	0.65
PARPBP	55010	1971	0.65
POLQ	10721	7773	0.64
RAD50	10111	3939	0.64
RAD51	5888	1023	0.69
RAD52	5893	1257	0.73
RBBP8	5932	2694	0.65
RPA1	6117	1851	0.72
SLX4	84464	5505	0.74
WRN	7486	4299	0.67
XRCC2	7516	843	0.63
XRCC3	7517	1041	0.78
Average (CAI)			**0.67**
StdDev (CAI)			0.04

Nonhomologous End-Joining (NHEJ)

Gene Name	Gene ID	CDS Length	CAI
APLF	200558	1536	0.66
ATM	472	9171	0.64
ATR	545	7935	0.65
DCLRE1C	64421	2079	0.69
LIG4	3981	2736	0.64
NHEJ1	79840	900	0.70
PAXX	286257	672	0.68
POLL	27343	1728	0.78
PRKDC	5591	12387	0.70
WRN	7486	4299	0.67
XRCC4	7518	1011	0.67
XRCC5	7520	2199	0.69
XRCC6	2547	1830	0.76
Average (CAI)			**0.69**
StdDev (CAI)			0.04

Mismatch Mediated Repair (MMR)

Gene Name	Gene ID	CDS Length	CAI
EXO1	9156	2541	0.65
HMGB1	3146	648	0.75
LIG1	3978	2760	0.79
MLH1	4292	2271	0.72
MLH3	27030	4362	0.67
MSH2	4436	2805	0.65
MSH3	4437	3414	0.64
MSH6	2956	4083	0.68
PCNA	5111	786	0.67
PMS1	5378	2799	0.62
PMS2	5395	2589	0.69
POLD1	5424	3402	0.80
RFC1	5981	3444	0.67
RPA1	6117	1851	0.72
Average (CAI)			**0.69**
StdDev (CAI)			0.05

Supplementary Table 3: Codon Adaptation Index (CAI) calculation of genes affiliated with various DNA damage repair mechanisms including NER and BER.

Nucleotide Excision Repair (NER)

Gene Name	Gene ID	CDS Length	CAI
CETN2	1069	519	0.74
CUL4A	8451	2280	0.72
DDB1	1642	3423	0.77
DDB2	1643	1284	0.76
ERCC1	2067	972	0.76
ERCC2	2068	2283	0.82
ERCC4	2072	2751	0.67
ERCC5	2073	3561	0.67
ERCC6	2074	4482	0.71
ERCC8	1161	1191	0.65
LIG1	3978	2760	0.79
LIG3	3980	3030	0.76
POLD1	5424	3402	0.80
POLE	5426	6861	0.80
RAD23B	5887	1230	0.65
RPA1	6117	1851	0.72
XPA	7507	822	0.62
XPC	7508	2823	0.75
XRCC1	7515	1902	0.76
Average (CAI)			**0.73**
StdDev (CAI)			0.06

Base Excision Repair (BER)

Gene Name	Gene ID	CDS Length	CAI
APEX1	328	957	0.71
APEX2	27301	1557	0.77
APTX	54840	1071	0.73
DNA2	1763	3183	0.63
FEN1	2237	1143	0.82
LIG1	3978	2760	0.79
LIG3	3980	3030	0.76
MBD4	8930	1743	0.67
MUTYH	4595	1650	0.76
NEIL1	79661	1431	0.77
NEIL2	252969	999	0.75
NEIL3	55247	1818	0.67
NTHL1	4913	939	0.77
NUDT1	4521	540	0.82
OGG1	4968	1038	0.76
PARP1	142	3045	0.75
PARP2	10038	1752	0.70
PNKP	11284	1566	0.76
POLB	5423	1113	0.67
POLG	5428	3720	0.78
SMUG1	23583	813	0.78
TDG	6996	1233	0.65
TDP1	55775	1827	0.72
UNG	7374	942	0.70
XRCC1	7515	1902	0.76
Average (CAI)			**0.74**
StdDev (CAI)			0.05

Supplementary Table 4: Codon TTA (Leu) usage frequency of human genome, genes of most highly expressed cellular proteins, HIV-1 viral genes, and genes related to DNA damage response signaling.

Human Genome*	%TTA (Leu)
	8%

Most Highly Expressed Cellular Proteins

Gene Name	Gene ID	%TTA (Leu)
GAPDH	2597	**5%**
RPL37A	6168	0%
CFL1	1072	0%
PPIA	5478	0%
LGALS1	3956	0%
PKM	5315	2%
EEF1A1	1915	0%
ENO1	2023	0%
VIM	7431	0%
ACTB	60	0%
TPI1	7167	0%
PRDX1	5052	8%
ANXA2	302	3%
PFN1	5216	0%
TAGLN2	8407	5%
TUBA1C	84790	5%
HIST1H2BK	85236	0%
DHRS2	10202	0%
MIF	4282	0%
HNRNPA1	3178	13%
ALDOA	226	0%
HSPA8	3312	2%
HSP90AB1	3326	2%
HSPB1	3315	6%
Average		**2%**
StdDev		3%

HIV-1 Viral Genes (pNL4-3), M19921.2

Gene Name	Gene ID	%TTA (Leu)
Gag		37%
Pol		42%
Vif		27%
Vpr		22%
Vpu		50%
Env		25%
Tat		33%
Rev		0%
Average		**30%**
StdDev		15%

DNA Damage Response Signaling Related Genes

Gene Name	Gene ID	%TTA (Leu)
ATM	472	**23%**
ATR	545	**21%**
PRKDC	5591	13%
BRCA1	672	22%
BRCA2	675	30%
MDM2	4193	14%
MDM4	4194	24%
CHEK1	1111	12%
CHEK2	11200	16%
MRE11	4361	24%
NBN	4683	21%
RAD50	10111	17%
Average		**20%**
StdDev		5%

* Based on Codon Usage Database (www.kazusa.or.jp/codon) - Homo sapiens [gbpri]: 93487 CDS's (40662582 codons).

The codon usage analysis was done using the web application (Sequence Manipulation Suite) at http://www.bioinformatics.org/sms2/codon_usage.html.

Supplementary Table 5: Codon TTA (Leu) usage frequency of genes affiliated with various DNA damage repair mechanisms including HDR, NHEJ, and MMR.

Homology Directed Repair (HDR)

Gene Name	Gene ID	%TTA (Leu)
ATM	472	23%
ATR	545	21%
ATRX	546	28%
BARD1	580	14%
BLM	641	20%
BRCA1	672	22%
BRCA2	675	30%
BRIP1	83990	22%
EME1	146956	10%
FANCF	2188	6%
FANCM	57697	30%
GEN1	348654	26%
MRE11	4361	24%
MUS81	80198	3%
NBN	4683	21%
PALB2	79728	20%
PARPBP	55010	17%
POLQ	10721	21%
RAD50	10111	17%
RAD51	5888	3%
RAD52	5893	15%
RBBP8	5932	22%
RPA1	6117	9%
SLX4	84464	3%
WRN	7486	24%
XRCC2	7516	18%
XRCC3	7517	4%
Average		**18%**
StdDev		8%

Nonhomologous End-Joining (NHEJ)

Gene Name	Gene ID	%TTA (Leu)
APLF	200558	23%
ATM	472	23%
ATR	545	21%
DCLRE1C	64421	27%
LIG4	3981	22%
NHEJ1	79840	5%
PAXX	286257	4%
POLL	27343	2%
PRKDC	5591	13%
WRN	7486	24%
XRCC4	7518	10%
XRCC5	7520	18%
XRCC6	2547	4%
Average		**15%**
StdDev		9%

Mismatch Mediated Repair (MMR)

Gene Name	Gene ID	%TTA (Leu)
EXO1	9156	15%
HMGB1	3146	0%
LIG1	3978	0%
MLH1	4292	12%
MLH3	27030	23%
MSH2	4436	20%
MSH3	4437	17%
MSH6	2956	14%
PCNA	5111	7%
PMS1	5378	34%
PMS2	5395	16%
POLD1	5424	0%
RFC1	5981	15%
RPA1	6117	9%
Average		**13%**
StdDev		10%

Supplementary Table 6: Codon TTA (Leu) usage frequency of genes affiliated with various DNA damage repair mechanisms including NER and BER.

Nucleotide Excision Repair (NER)

Gene Name	Gene ID	%TTA (Leu)
CETN2	1069	8%
CUL4A	8451	15%
DDB1	1642	6%
DDB2	1643	5%
ERCC1	2067	5%
ERCC2	2068	0%
ERCC4	2072	14%
ERCC5	2073	14%
ERCC6	2074	7%
ERCC8	1161	23%
LIG1	3978	0%
LIG3	3980	2%
POLD1	5424	0%
POLE	5426	2%
RAD23B	5887	30%
RPA1	6117	9%
XPA	7507	27%
XPC	7508	3%
XRCC1	7515	2%
Average		**9%**
StdDev		9%

Base Excision Repair (BER)

Gene Name	Gene ID	%TTA (Leu)
APEX1	328	8%
APEX2	27301	2%
APTX	54840	3%
DNA2	1763	16%
FEN1	2237	0%
LIG1	3978	0%
LIG3	3980	2%
MBD4	8930	10%
MUTYH	4595	2%
NEIL1	79661	0%
NEIL2	252969	9%
NEIL3	55247	14%
NTHL1	4913	0%
NUDT1	4521	0%
OGG1	4968	0%
PARP1	142	7%
PARP2	10038	13%
PNKP	11284	0%
POLB	5423	24%
POLG	5428	4%
SMUG1	23583	0%
TDG	6996	12%
TDP1	55775	11%
UNG	7374	4%
XRCC1	7515	2%
Average		**6%**
StdDev		6%