Supplementary Material

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 Table S1
 List of genes detected in each tissue examined

	Testis	Brain	Adipose	Breast	Colon	Heart	Kidney	Liver	Lymphnode	Muscle
Testis	16708	13605	12866	13810	13442	12674	12671	11876	13869	11725
Brain		14222	12073	12652	12542	12070	11899	11251	12730	11217
Adipose			13159	12737	12489	11922	11535	11279	12746	11229
Breast				14272	12949	12363	12144	11580	13314	11553
Colon					13789	12106	11877	11418	13025	11343
Heart						12930	11613	11196	12371	11329
Kidney							13241	11289	12138	10893
Liver								12308	11626	10619
Lymphnode									14434	11481
Muscle										11891

 Table S2
 List of 9,732 ubiquitously-expressed genes and expression levels in 10 human tissues

Table S3 List of 646 EIGs

GO 0001735 structural constinuent of rhosome 2 2478-13 52 8 002016 Molecular Function GO 0001515 translation factor activity, nucleic acid binding 2 2878-14 13 60 091023 Molecular Function GO 0001617 translation factor activity, nucleic acid binding 0 002756 110 1085271 GO 00016787 hydrolass activity 9 0967-04 7 17 22 7907 GO 00016787 hydrolass activity, transsetmfication mechanism 0 0102756 118 16 74419 GO 00016787 hydrolass activity, transsetmfication mechanism 0 0102756 118 15 13783 GO 00016173 reliablishment of protein localization 9 441-11 15 4 13 1783 GO 0003164 reliablishment of localization in cell 1.564.07 64 10.31264 GO 0003164 reliablishment of localization in cell 1.564.07 64 10.31264 GO 0003164 reliablishment of localization in cell 1.564.07 14 7 14.1729 GO 0005124 reliablishment of localization in cell 1.564.07 14.1712 2.	Category	GO	Term	Р	Count	%
GC:000515 GO:001517product induing transition facto activity, nuclei acid binding 0.2521-049130.01303 0.015371Molecular Function GO:0001617 GO:0001617 GO:0001617existic acid binding torout acid scientify torout acid scientify 0.000268107107107GO:0001767 GO:00016173existic acid binding corout acid scientify torout acid scientify torout acid scientify torout acid scientify GO:0001782RNA splicing factor activity, transesterification mechanism 0.01029450.775194GO:0001782 GO:0001783cellular mechabic process corout acid scientify corout acid scientify corout acid scientify GO:0002184710.15221 corout acid scientify corout acid scientifyGO:0001614 GO:0001614cellular localization induct corout corout for four acid scientify macromolecule localization induct corout corout four acid scientify corout acid scientify2.951-073172.15009 corout acid scientify corout acid scientify corout acid scientify corout acid scientify corout acid scientify2.951-073172.15009 corout acid scientify corout acid scientify corout acid scientify corout acid scientify corout acid scientify2.951-073172.15009 corout acid scientify corout acid scientify <td></td> <td>GO:0003735</td> <td>structural constituent of ribosome</td> <td>2.93E-33</td> <td>52</td> <td>8.062016</td>		GO:0003735	structural constituent of ribosome	2.93E-33	52	8.062016
GO.0008135 'unsaliton factor activity, nuclei, acid hinding 2.221-04 1.4 6.21705 Molecular Function 0.300740 '9.3021-04 1.4 6.21705 GO.00016787 induciar activity transcetter/filter/in nuclein activity 0.002756 1.08 1.67411 GO.0016787 induciar activity transcetter/filter/in nuclein activity transcetter/in nuclein activity transcetter/filter/in nuclein activity transc		GO:0005515	protein binding	2.78E-18	393	60.93023
Molecular Function G321001 existing entropy 992E-04 44 6.821705 G0.0004067 medicic acid binding 0.002756 1085771 0.002756 1085771 G0.0016787 hydrolise acitivity, transesterification mechanism 0.002756 108 0.012756 108 G0.0012123 cellular metabolic process 2.08E-13 311 6.03108 0.01284 5 0.075194 G0.003106 meconolecule localization 0.974E-12 85 4.031008 G0.0051141 cellular localization 1.52E-06 64 9.922481 G0.0061141 estabilishment of localization in cell 1.55E-06 24 40.93023 G0.0061149 estabilishment of localization 1.31E-06 139 2.15049 G0.0061174 estabilishment of localization 1.31E-06 139 2.15049 G0.0006120 resize-mediated transport 2.95E-07 317 2.15049 G0.0006121 estabilishment of localization 1.0111 2.651163 G0.0006121 estabilishment of localization <	Category Molecular Function Biology Process	GO:0008135	translation factor activity, nucleic acid binding	2.22E-04	13	2.015504
MORECULAR FUNCTION Op/004-601 peroxidase activity 9.09E-04 7 1.085271 GO:0015787 byochase activity 0.002756 108 16.7419 GO:0014277 Bytochase activity 0.002756 0.075194 5 0.75194 GO:0042137 Cellular metabolic process 2.08F-13 331 51.31783 GO:0042131 anacromolecular localization 9.74E-12 70 10.85221 GO:00051649 estabilishment of protein localization 1.50E-07 66 40.31008 GO:00051649 estabilishment of localization 1.50E-07 64 9.922481 GO:00051649 estabilishment of localization 1.71E-05 137 2.12.001 GO:0005120 arasport 2.97E-05 137 2.12.001 GO:0000506 catabolic process 3.32E-05 75 1.16.2791 GO:00005114 transport 2.97E-05 137 2.12.001 GO:00005029 regulation of molecular complex subunit organization 0.001311 56 8.682171 GO:00005114		GO:0016491	oxidoreductase activity	3.92E-04	44	6.821705
GO 000376 meleic and binding 0.002098 17 22.7907 GO 0011202 RNA splicing factor activity, transesterification mechanism 0.010294 5 0.775194 GO 0004123 Cellular metabolic process 2.681-13 331 51.31783 GO 0004136 estabilishmetal of poterin localization 6.41E-11 85 13.1783 GO 00051641 estabilishmetal focalization in cell 1.50E-07 64 9.922841 GO 0005124 estabilishmetal focalization in cell 1.50E-07 64 9.922841 GO 0005124 estabilishmetal focalization 1.71E-05 137 49.14729 GO 0005124 estabilishmetal focalization 1.71E-05 137 2.120811 GO 000129 estabilishmetal focalization 1.71E-05 137 2.12081 GO 000120 transport 2.92E-05 43 6.666667 GO 0000510 transport 2.92E-05 43 6.666667 GO 0000512 cellular metabolic proces 3.31-6.666667 6.86211 GO 0000512 cellular metabolic proces <td>Molecular Function</td> <td>GO:0004601</td> <td>peroxidase activity</td> <td>9.09E-04</td> <td>7</td> <td>1.085271</td>	Molecular Function	GO:0004601	peroxidase activity	9.09E-04	7	1.085271
GO 0016787 hydrolass activity 0.002786 108 16.7419 GO 0041202 RNA ppleing factor activity, transcerification mechaniam 0.010294 5 0.75194 GO 0045184 etablishment of protein localization 9.74E-12 70 10.85271 GO 00022613 ribonucleoprotein complex biogenesis 1.52E-08 26 4.031008 GO 00051649 etablishment of localization 1.50E-07 64 9.922481 GO 00051649 etablishment of localization 1.50E-07 64 9.922481 GO 0005170 mecromolecule metabolic process 2.95E-07 317 24.91479 GO 00016192 vesicle-mediated transport 2.25E-04 137 2.158039 GO 00006810 transport 2.25E-05 137 2.124031 GO 0000690 icossyntheic process 1.23E-04 171 2.651163 GO 000010192 vesicle-mediated ramsport 0.00277 2.6 6.861271 GO 000110192 vesicle-mediated ramsport 0.002715 2.6 6.861271 GO 0000129 c		GO:0003676	nucleic acid binding	0.002698	147	22.7907
GO:0031202 RNA splicing factor activity, transsettrification mechanism 0.010294 5 0.775194 GO:004423 cellular metabolic process 2.68E-13 331 51.31783 GO:0005184 estabilishment of protein localization 6.41E-11 85 15.31783 GO:00051641 eellular localization 6.41E-11 85 15.31783 GO:00051641 eellular localization 1.50E-07 64 9.922481 GO:00051641 estabilishment of localization 1.71E-06 139 21.55039 GO:0005104 estabilishment of localization 1.71E-05 137 21.24031 GO:0005104 transport 2.92E-05 43 6.666667 GO:000509 regulation of molecular function 0.001331 56 8.682171 GO:0005129 evaluation reductinar companization 0.003318 60 83 6.666657 GO:0005129 equlation of molecular function 0.003335 43 6.666657 GO:0005120 regulation of cellular component organization 0.0013318 66 25 3.8		GO:0016787	hydrolase activity	0.002756	108	16.74419
GO.0041237 cellular metabolic process 2.48E-13 311 \$1.31783 GO.0045184 cellular motabolicul localization 9.74E-11 85 70 10.85271 GO.0033066 macromolecule localization 6.41E-11 85 13.1783 GO.0022613 ribborucleoproten complex biogenesis 1.52E-08 26 4.031008 GO.0051649 establishment of localization in cell 1.56E-07 317 49.14729 GO.0043170 macromolecule metabolic process 6.85E-46 264 40.93023 GO.006104 transport 2.37E-05 43 6.666667 GO.0009056 catabolic process 5.32E-05 75 11.62791 GO.0009124 catabolic process 5.32E-05 75 11.62791 GO.0009124 catabolic process 5.32E-05 <td></td> <td>GO:0031202</td> <td>RNA splicing factor activity, transesterification mechanism</td> <td>0.010294</td> <td>5</td> <td>0.775194</td>		GO:0031202	RNA splicing factor activity, transesterification mechanism	0.010294	5	0.775194
GO.0045184 establishment of protein localization 9.74E-12 70 10.85271 GO.003306 macromolecule localization 6.41E-11 85 13.17829 GO.002161 rebunctlocytchin complex biogenesis 1.50E-07 64 0.9.92248 GO.004238 primary metabolic process 2.95E-07 64 0.9.92248 GO.004170 macromolecule metabolic process 6.85E-06 2.64 0.9.92248 GO.0001101 maraport 2.97E-07 137 49.14729 GO.00011012 vesicle-mediated transport 2.97E-05 133 2.12.5051 GO.00001012 vesicle-mediated transport 2.92E-05 43 6.666667 GO.0000209 regulation of molecular function 0.002377 2.6 4.031008 GO.0000212 cell death 0.002377 2.6 4.031008 GO.0000219 cell death 0.002377 2.6 4.031008 GO.0000219 cell death 0.002375 3.0 6.465123 GO.0001218 regulation of cellular component asymint agymination		GO:0044237	cellular metabolic process	2.68E-13	331	51.31783
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GO:0051641cellular localizationI.50E-0768I0 54264GO:0051649establishment of localization in cell1.56E-07649922481GO:0043170macromolecule metabolic process2.95E-0731749.14729GO:0051641establishment of localization1.71E-0513921.55039GO:005102vesicle-mediated transport2.92E-054366.66667GO:0005080transport2.92E-054366.66667GO:0005080regulation of molecular function0.001314658.682171GO:00050909regulation of molecular function0.002315636.666667GO:0005114voxidation reduction0.002315436.666667GO:0005114voxidation reduction0.003355396.646512GO:0005114voxidation reduction0.003355396.646512GO:0005114ranslational initiation0.003355396.646512GO:00052114regulation of cellular component organization0.0013186610.22256GO:0005220cellular component organization0.0014148112.25814GO:0003022actin filament-based process0.009406182.2790698GO:000402521regulation of cellular process0.014346710.3876GO:0004087regulation of cellular process0.014348112.5814GO:0004087regulation of plate process0.014348112.5814GO:0004087regulation of plate process0.014034<		GO:0022613	ribonucleoprotein complex biogenesis	1.52E-08	26	4.031008
Biology ProcessGO:0051649establishment of localization in cell1.56E-076.49.922481GO:004238primary metabolic process2.95E-073174.91.4729GO:005124establishment of localization1.71E-051392.15039GO:006102transport2.57E-051356.666667GO:0009056catabolic process5.32E-057511.62791GO:0009056catabolic process5.32E-04136.666667GO:0009058biosynthetic process5.32E-04136.666667GO:0009058cotabolic process0.0020772.64.031008GO:0009124cell death0.0023753.96.066671GO:00051128regulation of cellular complex subunit organization0.0033553.96.066671GO:0016121regulation of cellular component organization0.00335871.085271GO:0016121regulation of cellular process0.009468182.2796698GO:0004333macromolecular complex subunit organization0.0112436710.3376GO:0004522positive regulation of cellular process0.018434811.255814GO:00045219cellular component sucesmbly0.01503564.26.11628GO:00045219cellular romponent signesis0.017335121.360465GO:00045219positive regulation of biological process0.018208871.348837GO:00045219cellular regross to stimulus0.035564.26.511628GO:00045		GO:0051641	cellular localization	1.50E-07	68	10.54264
G0:0044238 primary metabolic process 2.95E-07 3.17 49.1429 G0:0013170 macromolecule metabolic process 6.88E-06 2.64 40.93023 G0:001213 estabilisment of localization 1.71E-05 1.37 2.12.4031 G0:0006810 transport 2.57E-05 4.3 6.666667 G0:0009056 catabolic process 1.23E-04 7.5 1.162791 G0:0009050 regulation of molecular function 0.002077 2.6 4.031008 G0:0005210 cell duath macromolecular complex subunit organization 0.002077 2.6 4.031008 G0:0005210 cell duath cellular component organization 0.00213 5.6 8.682171 G0:0005114 oxidation reduction 0.003355 3.9 6.046512 G0:000129 cellular component organization 0.000335 3.9 6.046512 G0:000210 transfanon linitation 0.003355 3.9 6.046512 G0:000221 tregulation of cellular process 0.009468 1.8 2.790698 G0:0004221<		GO:0051649	establishment of localization in cell	1.56E-07	64	9.922481
GO:0043170macromolecule metabolic process6.85E-062.644.0.93023GO:005124establishment of localization1.71E-051.392.125039GO:0016192vesicle-mediated transport2.92E-057.511.62791GO:000506catabolic process5.32E-057.511.62791GO:0009058biosynthetic process1.23E-041.712.6511631GO:0009058cellular macromolecular complex subunit organization0.001315.68.682171GO:0005112cellular macromolecular complex subunit organization0.0020772.64.031008GO:0005112cellular macromolecular complex subunit organization0.0041883.04.651163GO:0005112regulation of cellular component organization0.0041883.04.651163GO:0005122regonose to chemical simulus0.0073186.610.23256GO:0016044membrane organization0.0014488.11.255814GO:002607ecllular process0.0094601.82.790698GO:0045219negative regulation of cellular process0.0104348.11.255814GO:0045219negative regulation of process0.012436.71.08371GO:0045219negative regulation of process0.012434.77.386822GO:0045219negative regulation of process0.012434.71.38571GO:0045219negative regulation of biological process0.0493641.82.790698GO:00052116cellular response to stimulus0.0363		GO:0044238	primary metabolic process	2.95E-07	317	49 14729
G0:0051234 establishment of localization 1.71E-05 1.39 2.153039 G0:0006810 transport 2.57E-05 1.37 2.124031 G0:0000560 establic process 5.32E-05 7.5 1.162791 G0:0000580 biosynthici process 5.32E-05 7.5 1.162791 G0:0005209 cellular macromolecular complex subunit organization 0.001331 5.6 8.682171 G0:0005219 cellular macromolecular complex subunit organization 0.004188 3.0 4.651163 G0:00051141 oxidation reduction 0.003335 3.9 6.046512 G0:00051141 translational initiation 0.007335 3.0 4.651163 G0:00042221 response to chemical simulus 0.007318 6.6 10.23256 G0:0004523 macromolecular complex subunit organization 0.001434 8.7 1.03876 G0:0004524 regulation of cellular rosponst 0.00144 8.7 1.03876 G0:0004523 macromolecular omplex subunit organization 0.011104 4.0 5.2154 G0:		GO:0043170	macromolecule metabolic process	6.85E-06	264	40.93023
G0:0006810 transport 2.57E-05 137 21.24031 G0:0016192 vesicle-mediated transport 2.92Feb5 43 6.666667 G0:000905 catababic process 5.32E-05 75 11.62791 G0:000509 regulation of molecular function 0.001331 56 8.662171 G0:0005114 coldiation reduction 0.002077 26 4.31008 G0:0005114 coldiation reduction 0.00335 38 6.666667 G0:0005112 regulation of cellular component organization 0.004188 30 4.651163 G0:0005112 regulation of cellular component organization 0.00338 7 1.085271 G0:0006112 translational initiation 0.000338 7 1.085271 G0:0016044 membrane organization 0.001434 81 1.225814 G0:0004393 negative regulation of cellular process 0.010434 81 1.25814 G0:0044823 negative regulation of cellular process 0.01143 47 7.286822 G0:0044851 negative regulation of		GO:0051234	establishment of localization	1 71E-05	139	21 55039
G0:0016192 vesicle-mediated transport 2.92E-05 43 6.666667 G0:0009056 ciatubic process 3.22E-05 75 11.62791 G0:0009056 biosynthetic process 1.23E-04 75 4.031008 G0:0005201 cellular macromolecular complex subunit organization 0.001311 56 8.682171 G0:005114 oxidation reduction 0.002315 39 6.046512 G0:005118 regulation of collular component organization 0.001318 66 10.85271 G0:005118 regulation of collular component organization 0.000338 7 1.085271 G0:0004221 transitional initiation 0.000338 7 1.085271 G0:0004231 response to chemical stimulus 0.000438 18 2.790698 G0:0004232 actin filament-based process 0.010444 81 1.225814 G0:0004232 organization 0.01143 67 1.03876 G0:00044087 regulation of collular process 0.01843 4.2 1.90698 G0:0004422 organization<		GO:0006810	transport	2.57E-05	137	21.24031
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GO:000903 biosynthetic process 1.23E-0 171 2.651163 GO:0009053 biosynthetic process 1.23E-0 171 2.651163 GO:0005009 regulation of molecular tomplex subunit organization 0.002315 56 8.682171 GO:005114 oxidation reduction 0.003355 39 6.646667 GO:005112 regulation of cellular component organization 0.004318 30 4.651163 GO:0006413 translational initiation 0.003355 7 1.085271 GO:0040221 response to chemical stimulus 0.004388 7 1.085271 GO:004042 actin filament-based process 0.009466 18 2.790698 GO:0043933 macromolecular complex subunit organization 0.011044 81 12.55814 GO:0043933 macromolecular component biogenesis 0.011243 67 10.3376 GO:0044819 regulation of cellular process 0.018020 87 1.34837 GO:0044819 regulation of cellular process 0.018202 87 1.34837 GO:0044819 <td></td> <td>GO:0009056</td> <td>catabolic process</td> <td>5 32E-05</td> <td>75</td> <td>11 62791</td>		GO:0009056	catabolic process	5 32E-05	75	11 62791
G0.000500 regulation of molecular function 0.001207 2.6 4.031008 G0.002501 cellular macromolecular complex subunit organization 0.002077 2.6 4.031008 G0.0025112 cellular macromolecular complex subunit organization 0.002375 3.9 6.666667 G0.0055112 regulation of cellular component organization 0.004188 3.0 4.651163 G0.0016413 translational initiation 0.003355 7 1.085271 G0.00160441 membrane organization 0.003022 2.5 3.875969 G0.0016044 membrane organization 0.011043 8.1 1.25514 G0.0043933 naccromolecular complex subunit organization 0.011044 81 1.25514 G0.0048523 negative regulation of cellular process 0.011043 87 7.288522 G0.0048529 positive regulation of cellular process 0.015403 47 7.288522 G0.0048529 positive regulation of biological process 0.018035 42 6.511628 G0.0048529 positive regulation of biological process 0.048516		GO:0009058	biosynthetic process	1 23E-04	171	26 51163
Biology Process GO:0003421 GO:0005114 cellular macromolecular complex subunit organization 0.00237 0.002315 4.031008 4.051008 Biology Process GO:0005114 oxidation reduction 0.00355 39 6.046512 Biology Process GO:0005114 oxidation reduction 0.00355 7 1.085271 GO:0004211 translational initiation 0.004188 30 4.651163 GO:0006413 translational initiation 0.007318 66 10.23256 GO:0016044 membrane organization 0.009302 25 3.875969 GO:0043033 macromolecular complex subunit organization 0.011104 40 6.20155 GO:0040523 negative regulation of cellular process 0.010444 81 12.55814 GO:004087 regulation of cellular process 0.011243 67 10.3876 GO:0044087 regulation of cellular process 0.018203 47 13.48837 GO:0044519 negative regulation of cellular process 0.018203 42 6.511628 GO:004519 negative regulation of cellular process		GO:0065009	regulation of molecular function	0.001331	56	8 682171
G0:00:008219 cell death 0:002315 4:3 6:6666667 Biology Process G0:0055114 oxidation reduction 0:003355 39 6:046512 Biology Process G0:0051128 regulation of cellular component organization 0:00438 7 1.085271 G0:001128 regonse to chemical stimulus 0:007318 66 10:23256 G0:00106044 membrane organization 0:009302 25 3.875969 G0:00106044 membrane organization 0:01144 81 12.25814 G0:0004523 negative regulation of cellular process 0.010434 81 12.25814 G0:0004552 nogative regulation of cellular process 0.011243 67 10:3876 G0:0002607 cellular component assembly 0.015403 47 7.286822 G0:004552 positive regulation of cellular process 0.018202 84 13.02326 G0:004419 interspecies interaction between organisms 0.038341 18 2.790698 G0:000529 negative regulation of foilogical process 0.040596 40		GO:0034621	cellular macromolecular complex subunit organization	0.002077	26	4 031008
G0.0005114 cvidation reduction 0.002355 39 6.046612 Biology Process G0.0005112 regulation of cellular component organization 0.004188 30 4.651163 G0.0004221 translational initiation 0.007318 66 10.23256 G0.0004221 tresponse to chemical stimulus 0.007318 66 10.23256 G0.0004523 membrane organization 0.009302 25 3.875969 G0.0004523 megative regulation of cellular process 0.01444 81 12.55814 G0.0004523 megative regulation of cellular process 0.01144 40 620155 G0.0004690 organelle organization 0.01144 47 7.286822 G0.0044087 regulation of cellular process 0.018202 87 13.48837 G0.0048519 negative regulation of cellular process 0.018202 87 13.48837 G0.0048519 negative regulation of metabolic process 0.018202 87 13.48837 G0.004421 interspecies interaction between organisms 0.036536 42 6.51162		GO:0008219	cell death	0.002017	13	6 666667
Biology Process GO.0031128 GO.0004112 regulation of cellular component organization GO.0004188 0.004188 30 4.651163 4.651163 Biology Process GO.0004221 response to chemical stimulus 0.007318 66 10.23256 GO.0016041 translational initiation 0.009302 25 3.875969 GO.0016042 actin filament-based process 0.0094434 81 12.55814 GO.00048523 negative regulation of cellular process 0.011104 40 6.2015 GO.0004897 cellular component biogenesis 0.011243 67 10.3876 GO.0044087 regulation of cellular process 0.01803 47 7.286822 GO.0044087 regulation of cellular process 0.01802 87 13.48837 GO.0044191 interspecies interaction between organisms 0.038534 18 2.790698 GO.004419 interspecies interaction between organisms 0.038341 18 2.790698 GO.004419 interspecies interaction between organisms 0.038341 18 2.790698 GO.00044219 intracellular organelle localiza		GO:00055114	oxidation reduction	0.002015	30	6.046512
Construction Construction<	Biology Process	GO:0051128	regulation of cellular component organization	0.003333	30	4 651163
Col:00042221 response to chemical stimulus 0.000318 66 1023256 GO:0016044 membrane organization 0.009302 25 3.875969 GO:00402921 actin filament-based process 0.009466 18 2.790698 GO:0048523 negative regulation of cellular process 0.011104 40 6.20155 GO:0048523 regulation of cellular process 0.011243 67 10.3876 GO:0040852 regulation of cellular component biogenesis 0.017935 12 1.860465 GO:0044087 regulation of cellular process 0.018202 87 13.48837 GO:00448519 negative regulation of cellular process 0.018202 87 13.48837 GO:00448519 negative regulation of metabolic process 0.028858 84 13.02326 GO:00048519 negative regulation of metabolic process 0.040596 40 6.20155 GO:00070271 protein complex biogenesis 0.040596 40 6.20155 GO:00048219 negative regulation of biological process 0.0404956 7 1.085271	Biology 1100055	GO:0006413	translational initiation	0.004188	7	1.085271
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G0:001044 Inclinitation Organization 0.009466 18 2.7 3.75703 G0:0030029 actin filament-based process 0.009466 18 2.790698 G0:0043933 macromolecular complex subunit organization 0.011104 40 6.20155 G0:00022607 cellular component assembly 0.015403 47 7.286822 G0:004852 positive regulation of cellular component biogenesis 0.018202 87 13.48837 G0:0048512 positive regulation of cellular process 0.028858 84 13.03226 G0:0048512 positive regulation of biological process 0.028858 64 13.03226 G0:00048512 negative regulation of biological process 0.038341 18 2.790698 G0:0005165 establishment of organelle localization 0.044355 7 1.085271 G0:0005165 establishment of organelle localization 0.044355 7 1.085271 G0:00048518 positive regulation of biological process 0.040773 28 4.341085 G0:0004422 intracellular organelle localization		GO:0016044	membrane organization	0.009302	25	3 875060
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Coloroda Go:0022607 regulation of cellular component assembly 0.0115403 47 7.286822 GO:0044087 regulation of cellular component assembly 0.018202 87 13.48837 GO:0048522 positive regulation of cellular process 0.018202 87 13.48837 GO:0048519 negative regulation of biological process 0.038361 42 6.511628 GO:004419 intersponse to stimulus 0.036336 42 6.511628 GO:004419 interspocies interaction between organisms 0.040596 40 6.20155 GO:0009892 negative regulation of metabolic process 0.040974 91 14.10853 GO:00048518 positive regulation of biological process 0.040274 91 14.10853 GO:00048518 positive regulation of biological process 0.040274 91 14.10853 GO:0004424 intracellular part 1.27E-35 519 80.46512 GO:00044446 intracellular organelle process 0.040274 91 14.10853 GO:0044446 intracellular organelle part 2.78E-28		GO:0006996	organelle organization	0.011243	40 67	10 3876
Colonation Colonat		GO:0022607	cellular component assembly	0.015403	17	7 286822
Coloredation Coloredation<		GO:0022007	regulation of cellular component biogenesis	0.017935	12	1 860465
Cell Component GO:0048519 negative regulation of biological process 0.028858 84 13.0337 GO:0048519 negative regulation of biological process 0.028858 84 13.02326 GO:0048519 interspecies interaction between organisms 0.038341 18 2.790698 GO:0070271 protein complex biogenesis 0.040773 28 4.341085 GO:0048518 positive regulation of biological process 0.040773 28 4.341085 GO:0048518 positive regulation of biological process 0.0404774 91 14.10853 GO:004424 intracellular part 1.27E-35 519 80.46512 GO:004424 intracellular organelle process 0.049274 91 14.10853 GO:004424 intracellular part 1.27E-35 519 80.46512 GO:004422 intracellular organelle part 2.32E-33 525 81.39535 GO:0043227 membrane-bounded organelle 1.45E-21 408 63.25581 GO:0043227 membrane-bounded organelle 1.45E-21 408 63.25581 <td></td> <td>GO:0048522</td> <td>nositive regulation of cellular process</td> <td>0.018202</td> <td>87</td> <td>13 48837</td>		GO:0048522	nositive regulation of cellular process	0.018202	87	13 48837
Cell Component GO:0051716 cellular response to stimulus 0.036536 42 6.511628 GO:0051716 cellular response to stimulus 0.036536 42 6.511628 GO:0009892 negative regulation of metabolic process 0.040596 40 6.20155 GO:0070271 protein complex biogenesis 0.040773 28 4.341085 GO:0048518 positive regulation of biological process 0.040274 91 14.10853 GO:004424 intracellular part 1.27E-35 519 80.46512 GO:004422 intracellular part 1.28E-33 88 13.64341 GO:0044424 intracellular organelle part 2.32E-33 525 81.39535 GO:0044426 intracellular organelle part 2.32E-33 525 81.39535 GO:0044420 organelle part 2.32E-33 525 81.39535 GO:0044422 organelle part 2.32E-33 525 81.39535 GO:0043227 membrane-bounded organelle 1.45E-21 408 63.25581 GO:0043227 membr		GO:0048519	negative regulation of biological process	0.028858	84	13.02326
Cell Component Constraint Constant Constraint Const		GO:0051716	cellular response to stimulus	0.036536	42	6 511628
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Cell Component GO:0007021 GO:0043228 Inclusion of inclusion process 0.040773 0.044773 28 4.341085 4.341085 GO:0051656 establishment of organelle localization 0.044774 91 14.10853 GO:0048518 positive regulation of biological process 0.049274 91 14.10853 GO:004424 intracellular part 1.27E-35 519 80.46512 GO:0005622 intracellular organelle part 2.32E-33 525 81.39535 GO:0044424 intracellular organelle part 9.42E-29 281 43.56589 GO:004422 organelle part 2.78E-28 281 43.56589 GO:0043227 membrane-bounded organelle 3.50E-27 455 70.54264 GO:0031090 organelle envelope 3.45E-14 66 10.23256 GO:0043227 membrane-bounded organelle 1.43E-03 91 14.10853 GO:0043223 organelle envelope 3.45E-14 66 10.23256 GO:0043233 organelle umenbrane 6.78E-13 91 14.10853 GO:0043234		GO:0009892	negative regulation of metabolic process	0.040596	40	6 20155
Cell Component GO:004211 protein complex biognesis 0.044385 7 1.085271 GO:0048518 positive regulation of biological process 0.049274 91 14.10853 GO:004424 intracellular part 1.27E-35 519 80.46512 GO:004529 ribonucleoprotein complex 1.08E-33 88 13.64341 GO:004424 intracellular 2.32E-33 525 81.39535 GO:004442 organelle part 9.42E-29 281 43.56589 GO:004442 organelle part 2.78E-28 281 43.56589 GO:004422 organelle part 2.78E-28 281 43.56589 GO:0043229 intracellular organelle 3.50E-27 455 70.54264 GO:0043227 membrane-bounded organelle 1.45E-21 408 63.25581 GO:0043227 membrane-bounded organelle 1.45E-21 408 63.25581 GO:0043233 organelle nembrane 6.78E-13 91 14.10853 GO:0043234 protein complex 1.16E-07 146		GO:0070271	nrotein complex higgenesis	0.040773	28	4 341085
Cell Component GO:0048518 positive regulation of biological process 0.049274 91 14.10853 GO:0048518 positive regulation of biological process 0.049274 91 14.10853 GO:0048518 intracellular part 1.27E-35 519 80.46512 GO:0030529 ribonucleoprotein complex 1.08E-33 88 13.64341 GO:0044446 intracellular organelle part 2.32E-33 525 81.39535 GO:0044422 organelle part 2.78E-28 281 43.56589 GO:0044422 organelle part 2.78E-28 281 43.56589 GO:0043229 intracellular organelle 3.50E-27 455 70.54264 GO:0043227 membrane-bounded organelle 1.45E-21 408 63.25581 GO:004323 organelle envelope 3.45E-14 66 10.23256 GO:0043233 organelle membrane 2.07E-11 124 19.22481 GO:0043234 protein complex 1.16E-07 146 22.63566 GO:0043234 protein complex <t< td=""><td></td><td>GO:0070271</td><td>establishment of organelle localization</td><td>0.040775</td><td>20</td><td>1.085271</td></t<>		GO:0070271	establishment of organelle localization	0.040775	20	1.085271
GO:001010 pointe regulation of biorgical process 0.01011 0.1 1110025 GO:004424 intracellular part 1.27E-35 519 80.46512 GO:0030529 ribonucleoprotein complex 1.08E-33 88 13.64341 GO:0005622 intracellular 2.32E-33 525 81.39535 GO:004446 intracellular organelle part 9.42E-29 281 43.56589 GO:004422 organelle part 2.78E-28 281 43.56589 GO:0043229 intracellular organelle 3.50E-27 455 70.54264 GO:0043227 membrane-bounded organelle 1.45E-21 408 63.25581 GO:0031967 organelle envelope 3.45E-14 66 10.23256 GO:0043233 organelle membrane 6.78E-13 91 14.10853 GO:0043234 protein complex 1.16E-07 146 22.63566 GO:0031982 vesicle 1.01E-04 46 7.131783 GO:0031252 cell part 0.034063 11 1.705426		GO:0051050 GO:0048518	positive regulation of biological process	0.049274	, 91	14 10853
Cell Component GO:0031967 organelle numbrane-bounded organelle 1.08E-33 88 13.64341 GO:0005622 intracellular 2.32E-33 525 81.39535 GO:0044446 intracellular organelle part 9.42E-29 281 43.56589 GO:0044422 organelle part 2.78E-28 281 43.56589 GO:0043229 intracellular organelle 3.50E-27 455 70.54264 GO:0043227 membrane-bounded organelle 1.45E-21 408 63.25581 GO:0031967 organelle envelope 3.45E-14 66 10.23256 GO:0043233 organelle membrane 6.78E-13 91 14.10853 GO:0043234 protein complex 1.16E-07 146 22.63566 GO:0043234 protein complex 1.16E-07 146 22.63566 GO:0043244 cell part 0.001136 566 87.75194 GO:0031252 cell leading edge 0.034063 11 1.705426 GO:0012505 endomembrane creterm 0.040036 10		GO:0040510	intracellular part	1 27E-35	519	80.46512
GO:0030323 intointelequiversity complex 1.001203 60 15.04341 GO:0005622 intracellular 2.32E-33 525 81.39535 GO:0044446 intracellular organelle part 9.42E-29 281 43.56589 GO:0044422 organelle part 2.78E-28 281 43.56589 GO:0043229 intracellular organelle 3.50E-27 455 70.54264 GO:0043227 membrane-bounded organelle 1.45E-21 408 63.25581 GO:0031967 organelle envelope 3.45E-14 66 10.23256 GO:0043233 organelle membrane 6.78E-13 91 14.10853 GO:0043233 organelle lumen 2.07E-11 124 19.22481 GO:0043234 protein complex 1.16E-07 146 22.63566 GO:0043234 protein complex 1.01E-04 46 7.131783 GO:0031982 vesicle 1.01E-04 46 7.131783 GO:0031252 cell part 0.034063 11 1.705426 GO:0012505 endomembrane curter 0.040236 40 620155 <		GO:0030529	ribonucleonrotein complex	1.08E-33	88	13 64341
Cell Component GO:0044446 intracellular organelle part 9.42E-29 281 43.56589 GO:0044422 organelle part 2.78E-28 281 43.56589 GO:0043229 intracellular organelle 3.50E-27 455 70.54264 GO:0043227 membrane-bounded organelle 1.45E-21 408 63.25581 GO:0031967 organelle envelope 3.45E-14 66 10.23256 GO:0043233 organelle membrane 6.78E-13 91 14.10853 GO:0043234 protein complex 1.16E-07 146 22.63566 GO:0043234 protein complex 1.01E-04 46 7.131783 GO:004324 cell part 0.001136 566 87.75194 GO:0031252 cell leading edge 0.034063 11 1.705426		GO:0005622	intracellular	2 32E-33	525	81 39535
$ \begin{array}{c} \text{GO:0044422} & \text{organelle part} & \text{D:A2D 20} & 201 & 4530303 \\ \text{GO:0044422} & \text{organelle part} & 2.78E-28 & 281 & 43.56589 \\ \text{GO:0043229} & \text{intracellular organelle} & 3.50E-27 & 455 & 70.54264 \\ \text{GO:0043227} & \text{membrane-bounded organelle} & 1.45E-21 & 408 & 63.25581 \\ \text{GO:0031967} & \text{organelle envelope} & 3.45E-14 & 66 & 10.23256 \\ \text{GO:0031090} & \text{organelle membrane} & 6.78E-13 & 91 & 14.10853 \\ \text{GO:0043233} & \text{organelle lumen} & 2.07E-11 & 124 & 19.22481 \\ \text{GO:0043228} & \text{non-membrane-bounded organelle} & 1.43E-08 & 150 & 23.25581 \\ \text{GO:0043234} & \text{protein complex} & 1.16E-07 & 146 & 22.63566 \\ \text{GO:0031982} & \text{vesicle} & 1.01E-04 & 46 & 7.131783 \\ \text{GO:0041252} & \text{cell leading edge} & 0.034063 & 11 & 1.705426 \\ \text{GO:0012505} & \text{andomembrane organel} & 0.040226 & 40 & C.20155 \\ \end{array}$		GO:00044446	intracellular organelle part	9.42E-29	281	43 56589
Cell ComponentGO:0043229intracellular organelle $3.50E-27$ 455 70.54264 GO:0043227membrane-bounded organelle $1.45E-21$ 408 63.25581 GO:0031967organelle envelope $3.45E-14$ 66 10.23256 GO:0043233organelle membrane $6.78E-13$ 91 14.10853 GO:0043228non-membrane-bounded organelle $1.43E-08$ 150 23.25581 GO:0043234protein complex $1.16E-07$ 146 22.63566 GO:0043234protein complex $1.01E-04$ 46 7.131783 GO:004464cell part 0.034063 11 1.705426 GO:0012505endomembrane organelle 0.040226 40 $C.20155$		GO:0044422	organelle part	2 78E-28	281	43 56589
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Cell Component GO:0031907 organelle unverope 5.435 14 60 10.25250 GO:0031090 organelle membrane 6.78E-13 91 14.10853 GO:0043233 organelle lumen 2.07E-11 124 19.22481 GO:0043228 non-membrane-bounded organelle 1.43E-08 150 23.25581 GO:0043234 protein complex 1.16E-07 146 22.63566 GO:0031982 vesicle 1.01E-04 46 7.131783 GO:0031252 cell part 0.001136 566 87.75194 GO:0031252 cell leading edge 0.034063 11 1.705426 GO:0012505 andomembrane custom 0.040226 40 C.20155		GO:0031967	organelle envelone	3.45E-14	66	10 23256
GO:0043233 organelle lumen 2.07E-11 124 19.22481 GO:0043228 non-membrane-bounded organelle 1.43E-08 150 23.25581 GO:0043234 protein complex 1.16E-07 146 22.63566 GO:0044264 cell part 0.001136 566 87.75194 GO:0041250 cell leading edge 0.034063 11 1.705426		GO:0031090	organelle membrane	6 78E-13	91	14 10853
GO:0043235 ron-membrane-bounded organelle 1.43E-08 150 23.25581 GO:0043234 protein complex 1.16E-07 146 22.63566 GO:0043234 vesicle 1.01E-04 46 7.131783 GO:0044464 cell part 0.001136 566 87.75194 GO:0031252 cell leading edge 0.034063 11 1.705426 GO:0012505 endomembrane custom 0.040226 40 C.20155		GO:0043233	organelle lumen	2.07E-11	124	19 22481
GO:0043226 indiminibility of the construction of galeric 1.4512-08 150 25.25381 GO:0043234 protein complex 1.16E-07 146 22.63566 GO:0031982 vesicle 1.01E-04 46 7.131783 GO:0044464 cell part 0.001136 566 87.75194 GO:0031252 cell leading edge 0.034063 11 1.705426 GO:0012505 andomembrane system 0.040226 40 C.20155		GO:0043233	non membrane bounded organelle	1.43E.08	124	23 25581
GO:0043234 protein complex 1101-07 140 22.03300 GO:0031982 vesicle 1.01E-04 46 7.131783 GO:004464 cell part 0.001136 566 87.75194 GO:0031252 cell leading edge 0.034063 11 1.705426 GO:0012505 andomembrane custom 0.040226 40 C.00155		GO:0043228	not memorane-bounded organene	1.45E-07	146	23.23361
GO:001102 reside 1.011004 40 7.131785 GO:0044464 cell part 0.001136 566 87.75194 GO:0031252 cell leading edge 0.034063 11 1.705426 GO:0012505 endomembrane system 0.040226 40 C.20155		GO:0043234	vesicle	1.01F_0/	46	7 131783
GO:001170 col part 0.001170 500 67.75174 GO:001250 cell leading edge 0.034063 11 1.705426 GO:0012505 endomembrane system 0.040226 40 (.20155)		GO:0044464	cell part	0.001136	566	87 75194
$GO_{0012505}$ and a mathematical and a mathematic		GO:0031252	cell leading edge	0.034063	11	1 705426
		GO:0012505	endomembrane system	0.020236	40	6 20155

Table S4 Gene ontology of 646 EIGs

Note: list was sorted by P-value. Only the second classification out of the five GO classes was chosen for illustration.

	Parameters in Figure 5A				Parameters in	n Figure 5B (Hig	h exp.)		Parameters in Figure 5B (Low exp.)			
mutation type	$C \rightarrow T$	A→G	C→G	G→T	C→T	A→G	C→G	$G \rightarrow T$	C→T	A→G	C→G	$G \rightarrow T$
e	10	5.5	6	5	1.2	1	0.8	0.8	1.2	0.5	0.4	0.4
h	200	175	20	170	0	160	230	10	30	10	250	160
f	176	176	233	176	176	176	233	176	176	176	233	176
B0	30.51	5.03	13.12	11.73	5.07	1.47	2.16	1.33	4.05	0.31	1.04	0.70
B1	-0.1	7.5E-4	-2.7E-3	-0.05042	-0.01135	-0.002601	-0.005453	-0.004128	-0.01564	0.0003108	-0.004825	-0.003314
B2	0.0001	-1.1E-05	1.2E-05	6.6E-05	9.4E-6	2.1E-06	5.2E-06	4.9E-06	1.9E-05	-1.3E-06	7.5E-06	4.2E-06
В3	-4E-08	6.7E-09	3.7E-09	-2.5E-08	-1.8E-09	-6.7E-10	-1.3E-09	-1.6E-09	-7.3E-09	7.9E-10	-3.3E-09	-1.5E-09
R^2	0.22	-1.112	0.06983	0.2411	0.4329	-0.5063	0.2161	-0.06369	0.731	-1.038	0.2909	-0.1742

Table S5 Parameters for nonlinear regression analysis



Figure S1 Correlations between expression levels (Log₁₀) and SNP densities of 9,732 ubiquitously-expressed genes in 10 human tissues examined. Panels A to J show data for different tissues including testis, brain, adipose, breast, colon, heart, kidney, liver, lymph-node and muscle. All *P*<0.0001.



Figure S2 Correlations between the expression intensity of EIGs and the density of each substitution type. The substitutions are categorized based on analyses of alleles in the human genome referenced to chimpanzee genome for ancestor alleles.



Figure S3 Average mutation frequencies plotted across EIGs. The mutation types $C \rightarrow T$, $A \rightarrow G$, $C \rightarrow G$ and $G \rightarrow T$ show periodicities in these TUs.



Figure S4 Power spectrum analyses of mutation frequencies. Periodicities correspond to peaks above the baseline in the plots. The major peaks for $C \rightarrow T(A)$, $A \rightarrow G(B)$, $C \rightarrow G(C)$ and $G \rightarrow T(D)$ were found at a length of either 176 nt or 233 nt.



Figure S5 Power spectrum analyses of mutation frequencies among EIGs. Periodicities are shown as peaks above the baseline and appear fluctuating when different gene sets (sense-strands and antisense-strands genes) are used for the analyses, probably caused by statistical errors. The orientation of the genes (Sense, 5' to 3' in a DNA strand; antisense, on the opposite strand) was determined based on the annotated chromosome strands.



Figure S6 The mutation gradient and periodicity extending from CDS-start to intronic regions. The blue curve indicates the boundary of the first exons and introns, which suggest that the mutation gradient and periodicity are also present in intronic regions of TUs. The insets show the length distribution of the first exons.



Figure S7 The distribution of allele frequencies in sampled populations. Most mutations are minor alleles in the populations.