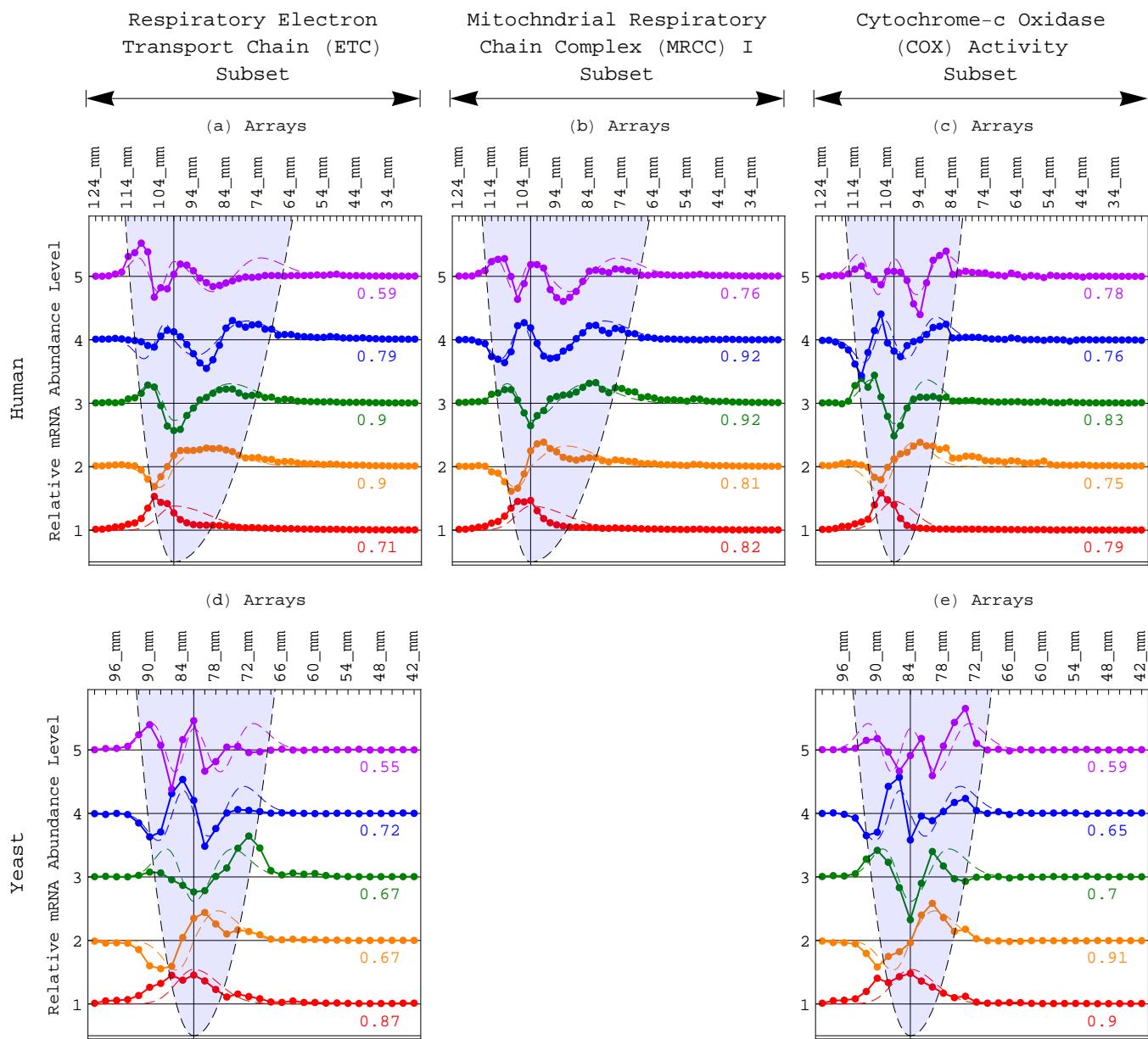
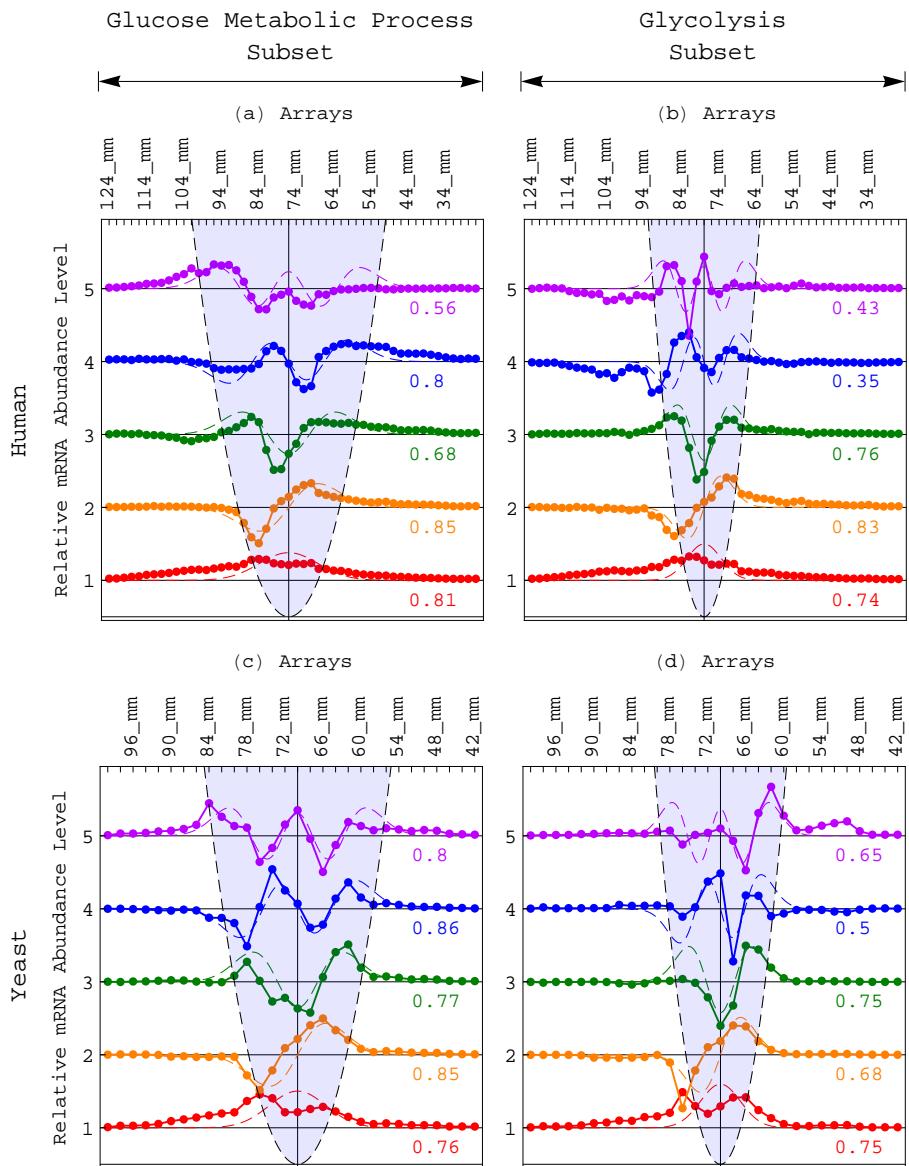


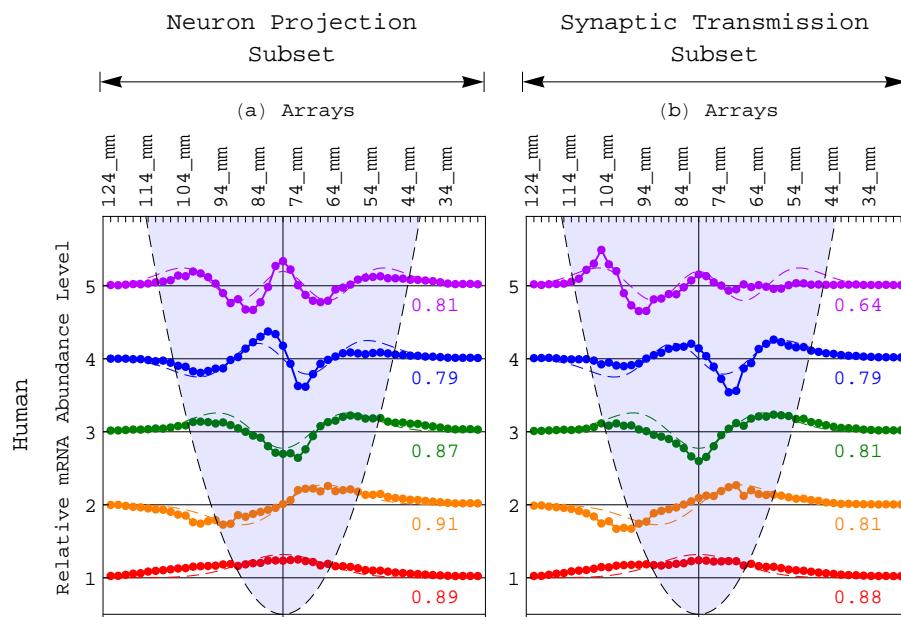
## Supporting Figures S1–S4 and Tables S1–S5



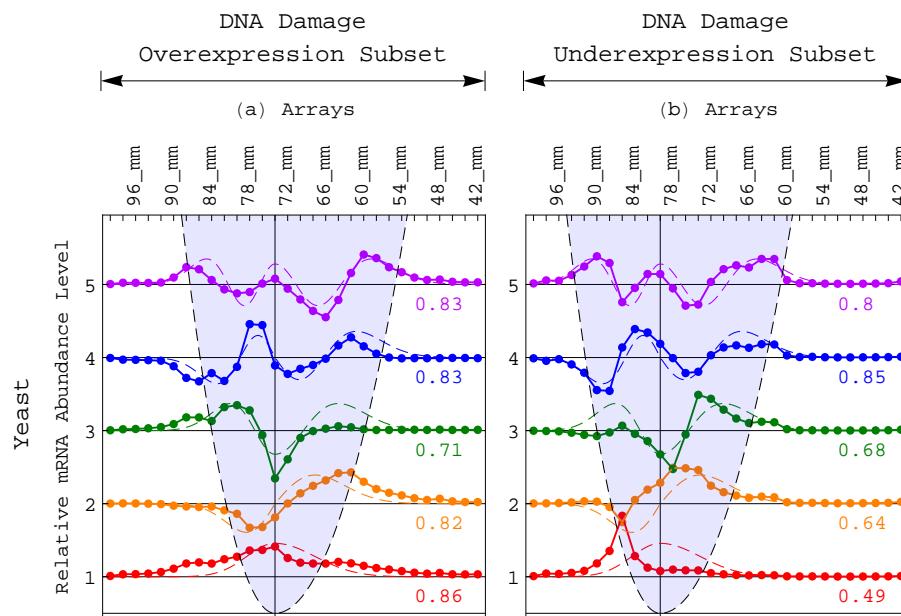
**Figure S1. Eigenvectors of the transcript length distribution data of the human and yeast mitochondrial metabolism subsets.** (a) The first (red) through fifth (violet) eigenvectors of the human respiratory electron transport chain (ETC) (GO:0022904) subset of transcripts. The equilibrium is shifted from that of the human global set to the greater migration distance of 100 mm. (b) Eigenvectors of the human mitochondrial respiratory chain complex (MRCC) I (GO:0004129) subset. (c) Eigenvectors of the human cytochrome-c oxidase (COX) activity (GO:0005747) subset. The equilibria of the human COX activity and MRCC I subsets are shifted from those of the human global set and respiratory ETC subset to the greater migration distance of 102 mm and lesser transcript length of  $\approx 925 \pm 75$  nt. (d) Eigenvectors of the yeast respiratory ETC subset. The equilibrium is shifted from that of the yeast global set to the greater migration distance of 82 mm. (e) Eigenvectors of the yeast COX activity subset. The equilibrium is shifted to the even greater migration distance of 84 mm and lesser transcript length of  $775 \pm 75$  nt.



**Figure S2. Eigenvectors of the transcript length distribution data of the human and yeast glucose metabolism subsets.** (a) Eigenvectors of the human glucose metabolic process (GO:0006006) subset of transcripts. The equilibrium is shifted from that of the human global set to the lesser migration distance of 76 mm and greater transcript length of  $\approx 2,175 \pm 125$  nt. (b) Eigenvectors of the human glycolysis (GO:0006096) subset. The equilibrium is at the migration distance of 78 mm and the transcript length of  $2,050 \pm 125$  nt. (c) Eigenvectors of the yeast glucose metabolic process subset. The equilibrium is shifted from that of the yeast global set to the lesser migration distance of 70 mm and greater transcript length of  $1,425 \pm 125$  nt. (d) Eigenvectors of the yeast glycolysis subset. The equilibrium is at the same migration distance of 70 mm as that of the yeast glucose metabolic process subset.



**Figure S3. Eigenvectors of the transcript length distribution data of the human brain activity subsets.**  
(a) Eigenvectors of the human neuron projection (GO:0043005) subset of transcripts. The equilibrium is shifted from that of the human global set to the lesser migration distance of 78 mm and greater transcript length of  $\approx 2,050 \pm 100$  nt. (b) Eigenvectors of the human synaptic transmission (GO:0007268) subset. The equilibrium is at the migration distance of 80 mm and the transcript length of  $1,875 \pm 100$  nt.



**Figure S4. Eigenvectors of the transcript length distribution data of the yeast DNA damage response subsets.**  
(a) Eigenvectors of the subset of yeast transcripts that are overexpressed in response to DNA damage. The equilibrium is shifted from that of the yeast global set to the lesser migration distance of 74 mm and greater transcript length of  $\approx 1,250 \pm 100$  nt. (b) Eigenvectors of the subset of transcripts that are underexpressed in response to DNA damage. The equilibrium is shifted to the greater migration distance of 80 mm and lesser transcript length of  $950 \pm 100$  nt.

Transcript Subset		Human			Yeast		
		$x = 0$	$k$	$s$	$x = 0$	$k$	$s$
Gene Ontology	Translation	96	2	2	84	2	2
	Ribosome	100	3	2	84	3	2
	Respiratory ETC	100	1	6	82	2	2
	MRCC I	102	1	6			
	COX Activity	102	3	2	84	2	2
	Glucose Metabolic Process	76	2	1	70	2	1
	Glycolysis	78	6	1	70	4	1
	Neuron Projection	78	1	1			
	Synaptic Transmission	80	1	1			
Overexpression	Normal $\cap$ Tumor	96	1	4			
	Tumor $\setminus$ Normal	90	1	2			
	Normal $\setminus$ Tumor	80	1	1			

**Table S1.** The generalized Hooke's constant of subsets of human and yeast transcripts. The generalized Hooke's constant  $k_x$  of Equation (3) is defined by its equilibrium  $x = 0$  gel migration distance in mm, its magnitude  $k$  relative to that of the corresponding global set, and its asymmetry  $s$ . The subsets of human transcripts that are most abundant in both the GBM tumor and normal brain, the GBM tumor only or the normal brain only are considered at the overexpression cutoff of  $c = 250$ .

**Table S2 (on p. A-5).** Typical gene ontology (GO) annotations significantly enriching the human subsets of transcripts and genes overexpressed in both the GBM tumor and normal brain, the normal brain overall or the normal brain only. The  $P$ -value of a given enrichment is calculated assuming hypergeometric probability distribution of the  $B$  annotations among the  $A$  transcripts or genes in the global set, and of the subset of  $b \subseteq B$  annotations among the subset of  $a \subseteq A$  transcripts or genes,  $P(A, a, B, b) = \binom{A}{a}^{-1} \sum_{i=b}^a \binom{B}{i} \binom{A-B}{a-i}$ . These enrichments of the subsets at the overexpression cutoffs of  $c = 300, \dots, 500$  are consistent with the enrichments of the corresponding subsets at the overexpression cutoff of  $c = 250$  (Table 3). None of the multiple GO annotations consistently enrich the human subsets of transcripts and genes that are overexpressed in the GBM tumor only. None of the multiple GO annotations consistently enrich the human subsets of transcripts and genes that are overexpressed in the GBM tumor overall beyond those that enrich the subsets that are overexpressed in both the GBM tumor and normal brain.

c	Overexpression Subset	Gene Ontology	Global Transcript Set				Global Gene Set			
			a	B	b	P-value	a	B	b	P-value
300	Normal ∩ Tumor	Translation	239	178	38	$4.9 \times 10^{-13}$	250	380	72	$7.3 \times 10^{-49}$
		Ribosome		78	28	$5.1 \times 10^{-16}$		155	58	$7.3 \times 10^{-58}$
		Respiratory ETC		55	25	$2.5 \times 10^{-17}$		89	29	$6.2 \times 10^{-27}$
		MRCC I		25	12	$3.0 \times 10^{-9}$		34	10	$1.5 \times 10^{-9}$
		COX Activity		14	9	$1.0 \times 10^{-8}$		20	9	$1.2 \times 10^{-10}$
	Normal	Glucose Metabolic Process	360	100	18	$2.3 \times 10^{-3}$	377	187	14	$3.1 \times 10^{-3}$
		Glycolysis		29	9	$5.7 \times 10^{-4}$		59	6	$1.2 \times 10^{-2}$
	Normal \ Tumor	Neuron Projection	121	259	23	$1.2 \times 10^{-6}$	127	534	26	$9.3 \times 10^{-11}$
		Synaptic Transmission		238	20	$1.5 \times 10^{-5}$		535	29	$4.3 \times 10^{-13}$
350	Normal ∩ Tumor	Translation	279	178	43	$3.1 \times 10^{-14}$	284	380	77	$3.6 \times 10^{-50}$
		Ribosome		78	28	$3.0 \times 10^{-14}$		155	58	$2.3 \times 10^{-54}$
		Respiratory ETC		55	27	$5.9 \times 10^{-18}$		89	30	$1.2 \times 10^{-26}$
		MRCC I		25	13	$1.2 \times 10^{-9}$		34	10	$5.1 \times 10^{-9}$
		COX Activity		14	10	$1.4 \times 10^{-9}$		20	9	$3.6 \times 10^{-10}$
	Normal	Glucose Metabolic Process	420	100	20	$2.3 \times 10^{-3}$	428	187	17	$5.4 \times 10^{-4}$
		Glycolysis		29	9	$1.7 \times 10^{-3}$		59	8	$1.4 \times 10^{-3}$
	Normal \ Tumor	Neuron Projection	141	259	24	$5.3 \times 10^{-6}$	144	534	27	$3.3 \times 10^{-10}$
		Synaptic Transmission		238	22	$1.4 \times 10^{-5}$		535	32	$5.7 \times 10^{-14}$
400	Normal ∩ Tumor	Translation	326	178	48	$4.3 \times 10^{-15}$	317	380	80	$1.5 \times 10^{-49}$
		Ribosome		78	30	$2.8 \times 10^{-14}$		155	59	$7.6 \times 10^{-53}$
		Respiratory ETC		55	32	$5.0 \times 10^{-22}$		89	31	$1.5 \times 10^{-26}$
		MRCC I		25	17	$7.9 \times 10^{-14}$		34	10	$1.5 \times 10^{-8}$
		COX Activity		14	11	$2.0 \times 10^{-10}$		20	9	$9.6 \times 10^{-10}$
	Normal	Glucose Metabolic Process	471	100	20	$8.4 \times 10^{-3}$	489	187	19	$3.4 \times 10^{-4}$
		Glycolysis		29	9	$3.9 \times 10^{-3}$		59	10	$1.6 \times 10^{-4}$
	Normal \ Tumor	Neuron Projection	145	259	29	$1.3 \times 10^{-8}$	172	534	27	$1.9 \times 10^{-8}$
		Synaptic Transmission		238	25	$5.3 \times 10^{-7}$		535	36	$1.1 \times 10^{-14}$
450	Normal ∩ Tumor	Translation	371	178	51	$8.6 \times 10^{-15}$	360	380	83	$4.0 \times 10^{-48}$
		Ribosome		78	31	$1.3 \times 10^{-13}$		155	62	$1.5 \times 10^{-53}$
		Respiratory ETC		55	33	$1.8 \times 10^{-21}$		89	32	$4.1 \times 10^{-26}$
		MRCC I		25	17	$6.9 \times 10^{-13}$		34	11	$3.3 \times 10^{-9}$
		COX Activity		14	11	$8.0 \times 10^{-10}$		20	9	$3.0 \times 10^{-9}$
	Normal	Glucose Metabolic Process	538	100	20	$3.2 \times 10^{-2}$	550	187	23	$2.5 \times 10^{-5}$
		Glycolysis		29	9	$9.3 \times 10^{-3}$		59	12	$1.6 \times 10^{-5}$
	Normal \ Tumor	Neuron Projection	167	259	31	$2.5 \times 10^{-8}$	190	534	32	$1.4 \times 10^{-10}$
		Synaptic Transmission		238	32	$7.2 \times 10^{-10}$		535	34	$6.7 \times 10^{-12}$
500	Normal ∩ Tumor	Translation	412	178	54	$8.7 \times 10^{-15}$	401	380	85	$3.4 \times 10^{-46}$
		Ribosome		78	33	$5.1 \times 10^{-14}$		155	63	$6.9 \times 10^{-52}$
		Respiratory ETC		55	35	$2.2 \times 10^{-22}$		89	35	$1.9 \times 10^{-28}$
		MRCC I		25	18	$1.8 \times 10^{-13}$		34	12	$6.7 \times 10^{-10}$
		COX Activity		14	11	$2.5 \times 10^{-9}$		20	10	$2.9 \times 10^{-10}$
	Normal	Glucose Metabolic Process	592	100	24	$6.7 \times 10^{-3}$	607	187	23	$1.1 \times 10^{-4}$
		Glycolysis		29	12	$3.5 \times 10^{-4}$		59	12	$4.3 \times 10^{-5}$
	Normal \ Tumor	Neuron Projection	180	259	33	$1.2 \times 10^{-8}$	206	534	32	$1.2 \times 10^{-9}$
		Synaptic Transmission		238	33	$1.3 \times 10^{-9}$		535	33	$2.9 \times 10^{-10}$

**Table S2 (caption on p. A-4).**

Gene Subset		$M$	Maximum Lengths		Minimum Lengths	
			$y(M) + x_0$	$P$ -value	$y(M) + x_0$	$P$ -value
Gene Ontology	Neuron Projection	534	147884	$4.6 \times 10^{-3}$	70714	$8.9 \times 10^{-3}$
	Synaptic Transmission	535	127673	$8.2 \times 10^{-3}$	68368	$1.0 \times 10^{-2}$
Normal $\cap$ Tumor Overexpression	$c$	250	22836	$3.9 \times 10^{-2}$	12356	$4.3 \times 10^{-2}$
		300	25155	$3.5 \times 10^{-2}$	14531	$4.2 \times 10^{-2}$
		350	27150	$3.4 \times 10^{-2}$	16009	$4.2 \times 10^{-2}$
		400	27735	$3.2 \times 10^{-2}$	16782	$4.1 \times 10^{-2}$
		450	27871	$2.8 \times 10^{-2}$	17036	$3.7 \times 10^{-2}$
		500	30961	$2.9 \times 10^{-2}$	17800	$3.6 \times 10^{-2}$

**Table S3. Human subsets of average maximum and minimum gene lengths significantly lesser than those of the global set.** The  $P$ -value of Equation (11) is calculated for the average maximum or minimum gene length  $y(M) + x_0$  in nucleotides of each subset of  $M$  genes relative to the average maximum and minimum gene lengths of  $x_0=67,448$  and 37,091 nt, respectively, of the global set. The subsets of transcripts that are most abundant in both the normal brain and GBM tumor are considered at each of the overexpression cutoffs of  $c = 250, 300, \dots, 500$ .

Gene Subset		$L$	Maximum Lengths		Minimum Lengths	
			$y(L) + x_0$	$P$ -value	$y(L) + x_0$	$P$ -value
Gene Ontology	Translation	380	39461	$9.2 \times 10^{-3}$	22790	$1.3 \times 10^{-2}$
	Ribosome	155	20949	$2.0 \times 10^{-2}$	13259	$2.6 \times 10^{-2}$
	Respiratory ETC	89	24032	$4.0 \times 10^{-2}$		
Normal $\cap$ Tumor Overexpression	$c$	250	22836	$1.4 \times 10^{-2}$	12356	$1.8 \times 10^{-2}$
		300	25155	$1.2 \times 10^{-2}$	14531	$1.5 \times 10^{-2}$
		350	27150	$1.0 \times 10^{-2}$	16009	$1.4 \times 10^{-2}$
		400	27735	$9.1 \times 10^{-3}$	16782	$1.2 \times 10^{-2}$
		450	27871	$7.9 \times 10^{-3}$	17036	$1.1 \times 10^{-2}$
		500	30961	$7.4 \times 10^{-3}$	17800	$9.8 \times 10^{-3}$
Tumor $\setminus$ Normal Overexpression		250	37059	$3.3 \times 10^{-2}$	21670	$4.5 \times 10^{-2}$
		300	37385	$2.8 \times 10^{-2}$	20104	$3.7 \times 10^{-2}$
		350	35271	$2.1 \times 10^{-2}$	18929	$2.7 \times 10^{-2}$
		400	34814	$1.8 \times 10^{-2}$	18482	$2.2 \times 10^{-2}$
		450	41723	$1.8 \times 10^{-2}$	21369	$2.2 \times 10^{-2}$
		500	38425	$1.5 \times 10^{-2}$	21348	$2.0 \times 10^{-2}$

**Table S4. Human subsets of average maximum and minimum gene lengths significantly lesser than those of the neuron projection subset.** The  $P$ -value of Equation (12) is calculated for the average maximum or minimum gene length  $y(L) + x_0$  in nucleotides of each subset of  $L$  genes relative to the average maximum and minimum gene lengths of  $y(M) + x_0=147,884$  and 70,714 nt, respectively, of the neuron projection subset of  $M=534$  genes. The subsets of transcripts that are most abundant in both the normal and tumor or the tumor only are considered at each of the overexpression cutoffs of  $c = 250, 300, \dots, 500$ .

Gene Subset		$L$	Maximum Lengths		Minimum Lengths	
			$y(L) + x_0$	$P$ -value	$y(L) + x_0$	$P$ -value
Gene Ontology	Glucose Metabolic Process	187	52201	$2.1 \times 10^{-2}$	28557	$2.9 \times 10^{-2}$
	Glycolysis	59	49394	$4.9 \times 10^{-2}$		
	Neuron Projection	534	147884	$2.0 \times 10^{-2}$	70714	$2.6 \times 10^{-2}$
	Synaptic Transmission	535	127673	$2.1 \times 10^{-2}$	68368	$2.1 \times 10^{-2}$
Normal \ Tumor Overexpression	$c$	250	105	$1.8 \times 10^{-2}$	46572	$2.2 \times 10^{-2}$
		300	127	$1.5 \times 10^{-2}$	50520	$1.7 \times 10^{-2}$
		350	144	$1.4 \times 10^{-2}$	48422	$1.7 \times 10^{-2}$
		400	172	$1.4 \times 10^{-2}$	45783	$1.8 \times 10^{-2}$
		450	190	$1.4 \times 10^{-2}$	51400	$1.8 \times 10^{-2}$
		500	206	$1.6 \times 10^{-2}$	55631	$1.6 \times 10^{-2}$

**Table S5. Human subsets of average maximum and minimum gene lengths significantly greater than those of the ribosome subset.** The  $P$ -value of Equation (12) is calculated for the average maximum or minimum gene length  $y(L) + x_0$  in nucleotides of each subset of  $L$  genes relative to the average maximum and minimum gene lengths of  $y(M) + x_0 = 20,949$  and  $13,259$  nt, respectively, of the ribosome subset of  $M=155$  genes. The subsets of transcripts that are most abundant in the normal brain only are considered at each of the overexpression cutoffs of  $c = 250, 300, \dots, 500$ .