

Table 1: Ontology for the positively correlated genes with the lowest p-values for expression correlations with COMT: Temporal Cortex

GOBPID	Pvalue	OddsRatio	ExpCount	Count	Size	Term
GO:0019752	0.00000000000000528	3.41	23.68	67	914	carboxylic acid metabolic process
GO:0006082	0.00000000000004711	3.15	26.63	70	1028	organic acid metabolic process
GO:0043436	0.00000000000007312	3.15	26.24	69	1013	oxoacid metabolic process
GO:0016054	0.00000000000143741	5.83	5.93	29	229	organic acid catabolic process
GO:0046395	0.00000000000143741	5.83	5.93	29	229	carboxylic acid catabolic process
GO:0044282	0.00000000000279114	4.67	8.78	35	339	small molecule catabolic process
GO:0055114	0.00000000001419983	3.04	22.25	58	859	oxidation-reduction process
GO:0042063	0.00000000106684051	4.92	5.88	25	227	gliogenesis
GO:0048709	0.00000000118804224	9.29	2.02	15	78	oligodendrocyte differentiation
GO:0006631	0.00000000264671170	4.09	8.08	29	312	fatty acid metabolic process
GO:0032787	0.00000000266371346	3.27	13.52	39	522	monocarboxylic acid metabolic process
GO:0044281	0.00000000344218348	2.16	49.66	91	1917	small molecule metabolic process
GO:0010001	0.00000000372380174	5.48	4.46	21	172	glial cell differentiation
GO:0009063	0.00000000744540607	7.27	2.64	16	102	cellular amino acid catabolic process
GO:1901575	0.00000004564741328	2.10	44.53	81	1719	organic substance catabolic process
GO:1901605	0.00000005977849357	4.59	5.21	21	201	alpha-amino acid metabolic process
GO:1901606	0.00000006296806240	7.25	2.31	14	89	alpha-amino acid catabolic process
GO:0009056	0.00000008253634004	1.98	54.61	93	2108	catabolic process
GO:0044255	0.00000016905629062	2.39	24.40	52	942	cellular lipid metabolic process
GO:0044248	0.00000024808585830	2.00	46.32	81	1788	cellular catabolic process

GO:0001676	0.00000030233151658	6.90	2.23	13	86	long-chain fatty acid metabolic process
GO:0006520	0.00000043360721175	3.41	8.50	26	328	cellular amino acid metabolic process
GO:0016477	0.00000065455280520	2.19	29.09	57	1123	cell migration
GO:0006629	0.00000070156197873	2.13	32.10	61	1239	lipid metabolic process
GO:0051270	0.00000134568295455	2.43	19.12	42	738	regulation of cellular component movement
GO:0048870	0.00000177328531293	2.08	32.25	60	1245	cell motility
GO:0051674	0.00000177328531293	2.08	32.25	60	1245	localization of cell
GO:2000145	0.00000184765641440	2.48	17.33	39	669	regulation of cell motility
GO:0050768	0.00000204269143609	3.76	5.91	20	228	negative regulation of neurogenesis
GO:0000038	0.00000419995998563	13.39	0.70	7	27	very long-chain fatty acid metabolic process
GO:0010721	0.00000450195285887	3.43	6.76	21	261	negative regulation of cell development
GO:0006635	0.00000525549013094	7.13	1.66	10	64	fatty acid beta-oxidation
GO:0040012	0.00000555910714895	2.33	18.83	40	727	regulation of locomotion
GO:0072329	0.00000581779815499	5.13	2.88	13	111	monocarboxylic acid catabolic process
GO:0030334	0.00000595173147121	2.44	16.16	36	624	regulation of cell migration
GO:0006081	0.00000606976203499	7.00	1.68	10	65	cellular aldehyde metabolic process
GO:0051961	0.00000650869634149	3.46	6.37	20	246	negative regulation of nervous system development
GO:0036109	0.00000774269964343	27.21	0.31	5	12	alpha-linolenic acid metabolic process
GO:0009083	0.00000827135175203	16.36	0.52	6	20	branched-chain amino acid catabolic process
GO:0030258	0.00000932545169872	3.37	6.53	20	252	lipid modification
GO:0044242	0.00000957914908668	4.01	4.43	16	171	cellular lipid catabolic process
GO:0040011	0.00001547781315349	1.88	37.69	64	1455	locomotion
GO:0009636	0.00001585247060719	3.65	5.13	17	198	response to toxic substance
GO:0050767	0.00001689829207022	2.35	16.27	35	628	regulation of neurogenesis

GO:0021529	0.00001724828776326	Inf	0.08	3	3	spinal cord oligodendrocyte cell differentiation
GO:0021530	0.00001724828776326	Inf	0.08	3	3	spinal cord oligodendrocyte cell fate specification
GO:0009081	0.00002016871955748	13.47	0.60	6	23	branched-chain amino acid metabolic process
GO:0009062	0.00002250836590462	5.30	2.36	11	91	fatty acid catabolic process
GO:0032879	0.00002360780496751	1.71	58.73	89	2267	regulation of localization
GO:0006790	0.00002382958025119	2.87	8.73	23	337	sulfur compound metabolic process
GO:0051186	0.00002556940435582	2.72	10.00	25	386	cofactor metabolic process
GO:0043651	0.00002752926561066	19.04	0.39	5	15	linoleic acid metabolic process
GO:0060284	0.00003416711937675	2.18	18.94	38	731	regulation of cell development
GO:1901565	0.00003638675209286	1.99	26.32	48	1016	organonitrogen compound catabolic process
GO:0033539	0.00003919437166453	17.31	0.41	5	16	fatty acid beta-oxidation using acyl-CoA dehydrogenase
GO:0051960	0.00004011129621459	2.19	18.37	37	709	regulation of nervous system development
GO:0008610	0.00005003513133520	2.27	15.75	33	608	lipid biosynthetic process
GO:0050793	0.00005793619094076	1.69	54.19	82	2092	regulation of developmental process
GO:0033559	0.00006051323080270	5.19	2.18	10	84	unsaturated fatty acid metabolic process
GO:1901568	0.00006094058912974	4.02	3.57	13	138	fatty acid derivative metabolic process
GO:2000177	0.00006097270163759	5.85	1.76	9	68	regulation of neural precursor cell proliferation
GO:0061351	0.00007072446668041	4.24	3.13	12	121	neural precursor cell proliferation
GO:0035338	0.00007366156004166	14.65	0.47	5	18	long-chain fatty-acyl-CoA biosynthetic process
GO:0007399	0.00007818674161043	1.69	51.29	78	1980	nervous system development
GO:0045665	0.00008474131814517	3.46	4.74	15	183	negative regulation of neuron differentiation

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