Supplemental Table 5. Most significant GO terms enriched among genes regulated by TRα

No	GO ID	Term	Count	P value	Benjamini	FDR
1	GO:6614	SRP-dependent cotranslational protein targeting to membrane	45	<0.001	<0.001	<0.001
2	GO:19083	viral transcription	47	<0.001	<0.001	<0.001
3	GO:6413	translational initiation	51	<0.001	<0.001	<0.001
4	GO:184	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	45	<0.001	<0.001	<0.001
5	GO:6412	translation	60	<0.001	<0.001	<0.001
6	GO:6364	rRNA processing	53	<0.001	<0.001	<0.001
7	GO:51301	cell division	71	<0.001	<0.001	<0.001
8	GO:9813	flavonoid biosynthetic process	14	<0.001	<0.001	<0.001
9	GO:7067	mitotic nuclear division	54	<0.001	<0.001	<0.001
10	GO:30574	collagen catabolic process	24	<0.001	<0.001	<0.001
11	GO:7155	cell adhesion	81	<0.001	<0.001	<0.001
12	GO:52696	flavonoid glucuronidation	14	<0.001	<0.001	<0.001
13	GO:7062	sister chromatid cohesion	30	<0.001	<0.001	<0.001
14	GO:2227	innate immune response in mucosa	14	<0.001	<0.001	<0.001
15	GO:30198	extracellular matrix organization	41	<0.001	<0.001	<0.001
16	GO:30199	collagen fibril organization	16	<0.001	<0.001	<0.001
17	GO:52695	cellular glucuronidation	10	<0.001	<0.001	0.004
18	GO:2181	cytoplasmic translation	12	<0.001	<0.001	0.006
19	GO:19731	antibacterial humoral response	15	<0.001	0.003	0.028
20	GO:19433	triglyceride catabolic process	11	<0.001	0.006	0.050
21	GO:6805	xenobiotic metabolic process	20	<0.001	0.007	0.067
22	GO:50830	defense response to Gram-positive bacterium	21	<0.001	0.007	0.072
23	GO:35987	endodermal cell differentiation	11	<0.001	0.011	0.109
24	GO:7018	microtubule-based movement	20	<0.001	0.011	0.116
25	GO:22617	extracellular matrix disassembly	19	<0.001	0.014	0.158
26	GO:42493	response to drug	48	<0.001	0.018	0.208
27	GO:9235	cobalamin metabolic process	9	<0.001	0.040	0.483
28	GO:7411	axon guidance	29	<0.001	0.047	0.584
29	GO:8283	cell proliferation	53	<0.001	0.061	0.791
30	GO:55114	oxidation-reduction process	77	<0.001	0.080	1.085
31	GO:86	G2/M transition of mitotic cell cycle	25	<0.001	0.114	1.630
32	GO:7019	microtubule depolymerization	6	<0.001	0.116	1.709
33	GO:42355	L-fucose catabolic process	6	<0.001	0.116	1.709
34	GO:7080	mitotic metaphase plate congression	11	0.001	0.128	1.964
35	GO:36065	fucosylation	6	0.002	0.179	2.890
36	GO:46777	protein autophosphorylation	28	0.002	0.250	4.319
37	GO:51310	metaphase plate congression	6	0.002	0.256	4.558
38	GO:6534	cysteine metabolic process	4	0.003	0.257	4.699
39	GO:910	cytokinesis	12	0.003	0.254	4.757
40	GO:281	mitotic cytokinesis	9	0.003	0.271	5.264
41	GO:97421	liver regeneration	9	0.003	0.271	5.264
42	GO:6024	glycosaminoglycan biosynthetic process	11	0.003	0.273	5.438
43	GO:7586	digestion	14	0.003	0.269	5.477
44	GO:1822	kidney development	17	0.003	0.281	5.887
45	GO:82	G1/S transition of mitotic cell cycle	19	0.003	0.286	6.150
46	GO:8202	steroid metabolic process	11	0.004	0.294	6.501
47	GO:6334	nucleosome assembly	21	0.004	0.299	6.764
48	GO:1558	regulation of cell growth	16	0.004	0.309	7.174
49	GO:6508	proteolysis	63	0.004	0.310	7.350
50	GO:1501	skeletal system development	23	0.004	0.319	7.768
51	GO:28	ribosomal small subunit assembly	7	0.005	0.334	8.359
52	GO:9116	nucleoside metabolic process	7	0.005	0.334	8.359
53	GO:70	mitotic sister chromatid segregation	8	0.005	0.336	8.592
54	GO:42273	ribosomal large subunit biogenesis	8	0.005	0.336	8.592
55	GO:31110	regulation of microtubule polymerization or depolymerization	5	0.005	0.360	9.486
56	GO:31638	zymogen activation	5	0.005	0.360	9.486
57	GO:71243	cellular response to arsenic-containing substance	5	0.005	0.360	9.486
58	GO:32355	response to estradiol	17	0.006	0.377	10.228
59	GO:7059	chromosome segregation	14	0.006	0.382	10.596
60	GO:8152	metabolic process	26	0.007	0.414	11.892
61	GO:7076	mitotic chromosome condensation	6	0.008	0.444	13.215
62	GO:9165	nucleotide biosynthetic process	6	0.008	0.444	13.215
63	GO:42026	protein refolding	6	0.008	0.444	13.215
64	GO:31069	hair follicle morphogenesis	8	0.008	0.440	13.258
65	GO:55015	ventricular cardiac muscle cell development	5	0.008	0.462	14.343
66	GO:34501	protein localization to kinetochore	5	0.008	0.462	14.343
67	GO:32526	response to retinoic acid	10	0.008	0.461	14.537
68	GO:31397	negative regulation of protein ubiquitination	10	0.008	0.461	14.537
69	GO:6749	glutathione metabolic process	12	0.009	0.478	15.481
70	GO:16477	cell migration	26	0.009	0.476	15.648
71	GO:70301	cellular response to hydrogen peroxide	12	0.010	0.513	17.498
72	GO:5975	carbohydrate metabolic process	26	0.010	0.514	17.815
73	GO:19800	peptide cross-linking via chondroitin 4-sulfate glycosaminoglycan	4	0.011	0.534	19.021
74	GO:38063	collagen-activated tyrosine kinase receptor signaling pathway	4	0.011	0.534	19.021
75	GO:32873	negative regulation of stress-activated MAPK cascade	4	0.011	0.534	19.021
76	GO:187	activation of MAPK activity	18	0.012	0.565	20.858
77	GO:51726	regulation of cell cycle	20	0.012	0.561	20.895
78	GO:21915	neural tube development	8	0.014	0.592	22.837
79	GO:45786	negative regulation of cell cycle	9	0.014	0.588	22.915
80	GO:90102	cochlea development	7	0.016	0.631	25.736
81	GO:6695	cholesterol biosynthetic process	9	0.016	0.635	26.302
82	GO:16042	lipid catabolic process	15	0.016	0.635	26.620
83	GO:48846	axon extension involved in axon guidance	5	0.017	0.640	27.218
84	GO:43616	keratinocyte proliferation	5	0.017	0.640	27.218
85	GO:30705	cytoskeleton-dependent intracellular transport	6	0.017	0.643	27.774
86	GO:60831	smoothened signaling pathway involved in dorsal/ventral neural tube patterning	4	0.018	0.661	29.277
87	GO:51782	negative regulation of cell division	4	0.018	0.661	29.277
88	GO:60428	lung epithelium development	4	0.018	0.661	29.277
89	GO:48146	positive regulation of fibroblast proliferation	11	0.018	0.659	29.490
90	GO:7093	mitotic cell cycle checkpoint	8	0.019	0.674	30.819
91	GO:9611	response to wounding	12	0.021	0.697	32.835
92	GO:7346	regulation of mitotic cell cycle	9	0.022	0.705	33.748
93	GO:70295	renal water absorption	3	0.022	0.704	34.063
94	GO:15732	prostaglandin transport	3	0.022	0.704	34.063
95	GO:6568	tryptophan metabolic process	3	0.022	0.704	34.063
96	GO:21513	spinal cord dorsal/ventral patterning	3	0.022	0.704	34.063
97	GO:1503	ossification	14	0.022	0.707	34.660
98	GO:42060	wound healing	14	0.022	0.707	34.660
99	GO:19372	lipoxygenase pathway	5	0.023	0.705	34.863
100	GO:6312	mitotic recombination	5	0.023	0.705	34.863
101	GO:50872	white fat cell differentiation	5	0.023	0.705	34.863
102	GO:6810	transport	43	0.024	0.724	36.735
103	GO:6468	protein phosphorylation	54	0.024	0.723	36.956
104	GO:7605	sensory perception of sound	20	0.025	0.723	37.342
105	GO:51384	response to glucocorticoid	12	0.026	0.738	38.985
106	GO:43588	skin development	8	0.027	0.743	39.763
107	GO:19370	leukotriene biosynthetic process	6	0.027	0.742	39.993
108	GO:6801	superoxide metabolic process	6	0.027	0.742	39.993
109	GO:7094	mitotic spindle assembly checkpoint	6	0.027	0.742	39.993
110	GO:15889	cobalamin transport	4	0.027	0.745	40.590
111	GO:51256	mitotic spindle midzone assembly	4	0.027	0.745	40.590
112	GO:45740	positive regulation of DNA replication	9	0.029	0.755	41.879
113	GO:70208	protein heterotrimerization	5	0.030	0.762	42.941
114	GO:6641	triglyceride metabolic process	8	0.031	0.775	44.465
115	GO:1890	placenta development	8	0.031	0.775	44.465
116	GO:6865	amino acid transport	8	0.031	0.775	44.465
117	GO:9612	response to mechanical stimulus	11	0.033	0.789	46.253
118	GO:1569	patterning of blood vessels	7	0.033	0.786	46.278
119	GO:27	ribosomal large subunit assembly	6	0.033	0.784	46.465
120	GO:9636	response to toxic substance	14	0.035	0.803	48.804
121	GO:30177	positive regulation of Wnt signaling pathway	8	0.036	0.804	49.238
122	GO:6879	cellular iron ion homeostasis	9	0.037	0.811	50.375
123	GO:1843	neural tube closure	13	0.037	0.809	50.534
124	GO:15671	oxygen transport	5	0.038	0.811	51.126
125	GO:30214	hyaluronan catabolic process	5	0.038	0.811	51.126
126	GO:48008	platelet-derived growth factor receptor signaling pathway	7	0.038	0.813	51.759
127	GO:45922	negative regulation of fatty acid metabolic process	4	0.039	0.813	52.042
128	GO:52697	xenobiotic glucuronidation	4	0.039	0.813	52.042
129	GO:7614	short-term memory	4	0.039	0.813	52.042
130	GO:463	maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	4	0.039	0.813	52.042
131	GO:1502	cartilage condensation	6	0.040	0.818	52.963
132	GO:43687	post-translational protein modification	6	0.040	0.818	52.963
133	GO:31577	spindle checkpoint	3	0.041	0.830	54.715
134	GO:51409	response to nitrosative stress	3	0.041	0.830	54.715
135	GO:70370	cellular heat acclimation	3	0.041	0.830	54.715
136	GO:97490	sympathetic neuron projection extension	3	0.041	0.830	54.715
137	GO:7000	nucleolus organization	3	0.041	0.830	54.715
138	GO:90521	glomerular visceral epithelial cell migration	3	0.041	0.830	54.715
139	GO:97491	sympathetic neuron projection guidance	3	0.041	0.830	54.715
140	GO:1902285	semaphorin-plexin signaling pathway involved in neuron projection guidance	3	0.041	0.830	54.715
141	GO:45607	regulation of auditory receptor cell differentiation	3	0.041	0.830	54.715
142	GO:320	re-entry into mitotic cell cycle	3	0.041	0.830	54.715
143	GO:2001205	negative regulation of osteoclast development	3	0.041	0.830	54.715
144	GO:44331	cell-cell adhesion mediated by cadherin	3	0.041	0.830	54.715
145	GO:36486	ventral trunk neural crest cell migration	3	0.041	0.830	54.715
146	GO:9582	detection of abiotic stimulus	3	0.041	0.830	54.715
147	GO:44752	response to human chorionic gonadotropin	3	0.041	0.830	54.715
148	GO:60395	SMAD protein signal transduction	11	0.044	0.845	56.961
149	GO:7052	mitotic spindle organization	7	0.044	0.844	57.184
150	GO:6730	one-carbon metabolic process	7	0.044	0.844	57.184
151	GO:42384	cilium assembly	18	0.045	0.848	58.052
152	GO:42157	lipoprotein metabolic process	8	0.046	0.851	58.729
153	GO:7051	spindle organization	5	0.047	0.851	59.098
154	GO:8209	androgen metabolic process	5	0.047	0.851	59.098
155	GO:42274	ribosomal small subunit biogenesis	5	0.047	0.851	59.098
156	GO:48566	embryonic digestive tract development	5	0.047	0.851	59.098
157	GO:48754	branching morphogenesis of an epithelial tube	6	0.047	0.850	59.324
158	GO:83	regulation of transcription involved in G1/S transition of mitotic cell cycle	6	0.047	0.850	59.324
159	GO:51439	regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle	6	0.047	0.850	59.324
160	GO:43252	sodium-independent organic anion transport	6	0.047	0.850	59.324
161	GO:7399	nervous system development	35	0.048	0.854	60.113