

SI Guide

Supplementary Table 1. List of differentially expressed genes from bulk RNA-seq between control and androgen-treated organoids

Up- and downregulated differentially expressed genes (DEGs) between control and androgen (DHT and T) -treated XX 35d organoids. SZ – schizophrenia, SZDB – A Database for Schizophrenia Genetic research (szdb.org).

Supplementary Table 2. List of cluster markers from scRNA-seq

Upregulated genes in individual RG clusters obtained by comparing within the RG subset using Seurat FindAllMarkers on RG subclusters with arguments `only.pos = TRUE`, `min.pct = 0.25`, `logfc.threshold = 0.25`.

Supplementary Table 3. List of differentially expressed genes from scRNA-seq. Upregulated genes in DHT treatment within RG clusters (sheet 2) using Seurat FindMarkers comparing DHT to control with arguments `only.pos = TRUE`, `logfc.threshold = 0.2`.

Supplementary Table 4. Chi-square contingency table

Count matrix of cell numbers in each RG cluster and in each treatment condition. Values reported are: observed counts (expected counts) [chi-square statistic] P-value. Asterisks demarcate values that significantly diverge from expected.

Supplementary Table 5. Numbers of analysed batches and ventricles

Exact numbers of analysed organoid batches and ventricles, organised by the individual quantification and the location in the manuscript.

Supplementary Figure 1. Full scans of western blots for AR and GAPDH.

Full scanned areas. The membrane was physically cut into an upper section where AR was expected, and into a lower section where GAPDH was expected, and the two pieces were blotted separately for AR and GAPDH. Most of the cut membrane was scanned for AR on the Li-COR system while for GAPDH only the region of the expected band was scanned. A longer exposure reveals the ladder.

Supplementary Video 1.

Live imaging of XX organoids, electroporated at 31d, and imaged at 33d for >48 hours. Cells labelled with pCAG-mCherry are in magenta. Cells electroporated with EGFP-C1-AR-V7 are in green. Still images from this movie are shown in **Extended Data Fig. 5a**. Time scale: hours:minutes.

Supplementary Video 2.

Live imaging of XX organoids, electroporated at 54d, and imaged at 56d for >48 hours. Cells labelled with pCAG-mCherry are in magenta. Cells electroporated with EGFP-C1-AR-V7 are in green. Still images from this movie are shown in **Extended Data Fig. 5b**. Time scale: hours:minutes.

Supplementary Video 3.

Green channel (EGFP-C1-AR-V7) from **Supplementary Video 2** for easier tracking of electroporated, GFP+ cells. Time scale: hours:minutes.

Supplementary Table 1

UPREGULATED DEGs				
ESEMBL ID	Gene name	Full name	SFARI gene (Gene score ≥ 3)	DE in SZ (SZDB)
ENSG00000065978	YBX1	Y-Box Binding Protein 1		
ENSG00000066629	EML1	EMAP Like 1		
ENSG00000070785	EIF2B3	Eukaryotic Translation Initiation Factor 2B Subunit Gamma		
ENSG00000082068	WDR70	WD Repeat Domain 70		
ENSG00000089009	RPL6	Ribosomal Protein L6		
ENSG00000100029	PES1	Pescadillo Ribosomal Biogenesis Factor 1		Yes
ENSG00000100281	HMGXB4	HMG-Box Containing 4		Yes
ENSG00000104738	MCM4	Minichromosome Maintenance Complex Component 4	Yes	
ENSG00000106628	POLD2	DNA Polymerase Delta 2, Accessory Subunit		
ENSG00000108179	PPIF	Peptidylprolyl Isomerase F (Cyclophilin D)		
ENSG00000109919	MTCH2	Mitochondrial Carrier 2		Yes
ENSG00000110080	ST3GAL4	ST3 Beta-Galactoside Alpha-2,3-Sialyltransferase 4		
ENSG00000116161	CACYBP	Calcyclin Binding Protein		
ENSG00000116514	RNF19B	Ring Finger Protein 19B		Yes
ENSG00000121152	NCAPH	Non-SMC Condensin I Complex Subunit H		
ENSG00000121390	PSPC1	Paraspeckle Component 1		
ENSG00000121680	PEX16	Peroxisomal Biogenesis Factor 16		Yes
ENSG00000123395	ATG101	Autophagy Related 101		
ENSG00000123416	TUBA1B	Tubulin Alpha 1b		
ENSG00000124688	MAD2L1BP	MAD2L1 Binding Protein		
ENSG00000129680	MAP7D3	MAP7 Domain Containing 3		
ENSG00000130021	PUDP	Pseudouridine 5'-Phosphatase		
ENSG00000132341	RAN	RAN, Member RAS Oncogene Family		
ENSG00000134057	CCNB1	Cyclin B1		
ENSG00000137691	C11orf70 (CFAP300)	Cilia And Flagella Associated Protein 300		
ENSG00000137876	RSL24D1	Ribosomal L24 Domain Containing 1		
ENSG00000138231	DBR1	Debranching RNA Lariats 1		
ENSG00000138764	CCNG2	Cyclin G2		
ENSG00000139921	TMX1	Thioredoxin Related Transmembrane Protein 1		
ENSG00000143575	HAX1	HCLS1 Associated Protein X-1		
ENSG00000145545	SRD5A1	Steroid 5 Alpha-Reductase 1		Yes
ENSG00000148229	POLE3	DNA Polymerase Epsilon 3, Accessory Subunit		Yes
ENSG00000152465	NMT2	N-Myristoyltransferase 2		
ENSG00000156508	EEF1A1	Eukaryotic Translation Elongation Factor 1 Alpha 1		
ENSG00000162704	ARPC5	Actin Related Protein 2/3 Complex Subunit 5		
ENSG00000164087	POC1A	POC1 Centriolar Protein A		
ENSG00000164109	MAD2L1	Mitotic Arrest Deficient 2 Like 1		
ENSG00000164758	MED30	Mediator Complex Subunit 30		
ENSG00000165526	RPUSD4	RNA Pseudouridine Synthase D4		
ENSG00000165775	FUNDC2	FUN14 Domain Containing 2		
ENSG00000166347	CYB5A	Cytochrome B5 Type A		
ENSG00000166557	TMED3	Transmembrane P24 Trafficking Protein 1		
ENSG00000166851	PLK1	Polo Like Kinase 1		
ENSG00000167085	PHB	Prohibitin	Yes	
ENSG00000167112	TRUB2	TruB Pseudouridine Synthase Family Member 2		
ENSG00000168282	MGAT2	Alpha-1,6-Mannosyl-Glycoprotein 2-Beta-N-Acetylglucosaminyltransferase		
ENSG00000169714	CNBP	CCHC-Type Zinc Finger Nucleic Acid Binding Protein		
ENSG00000170364	SETMAR	SET Domain And Mariner Transposase Fusion Gene		
ENSG00000171720	HDAC3	Histone Deacetylase 3		
ENSG00000172053	QARS	Glutamyl-tRNA Synthetase		Yes
ENSG00000176903	PNMA1	PNMA Family Member 1		
ENSG00000180581	SRP9P1	Signal Recognition Particle 9 Pseudogene 1		
ENSG00000182054	IDH2	Isocitrate Dehydrogenase (NADP(+)) 2		Yes
ENSG00000183431	SF3A3	Splicing Factor 3a Subunit 3		
ENSG00000183684	ALYREF	Aly/REF Export Factor		
ENSG00000186665	C17orf58	Chromosome 17 Open Reading Frame 58		
ENSG00000196262	PPIA	Peptidylprolyl Isomerase A		
ENSG00000196591	HDAC2	Histone Deacetylase 2		Yes
ENSG00000198039	ZNF273	Zinc Finger Protein 273		
ENSG00000229119	AC026403.1	60S acidic ribosomal protein (RPLP0) pseudogene		
ENSG00000244563	RPS26P19	Ribosomal protein S26 pseudogene 19		
ENSG00000251668	AC113404.2	pseudogene similar to part of microtubule associated serine/threonine kinase 2 MAST2		
ENSG00000255302	EID1	EP300 Interacting Inhibitor Of Differentiation 1		
ENSG00000270800	RPS10-NUDT3	RPS10-NUDT3 readthrough		
ENSG00000280071	GATD3B	Glutamine amidotransferase like class 1 domain containing 3B		

DOWNREGULATED DEGs				
ESEMBL ID	Gene name	Full name	SFARI gene (Gene score ≥ 3)	DE in SZ (SZDB)
ENSG0000015568	RGPD5	RANBP2 Like And GRIP Domain Containing 5		Yes
ENSG00000092929	UNC13D	Unc-13 Homolog D		
ENSG00000099840	IZUMO4	IZUMO Family Member 4		
ENSG00000100596	SPTLC2	Serine Palmitoyltransferase Long Chain Base Subunit 2		
ENSG00000101104	PABPC1L	Poly(A) Binding Protein Cytoplasmic 1 Like		
ENSG00000107317	PTGDS	Prostaglandin D2 Synthase		Yes
ENSG00000108515	ENO3	Enolase 3		
ENSG00000112855	HARS2	Histidyl-TRNA Synthetase 2, Mitochondrial		
ENSG00000116266	STXB3	Syntaxin Binding Protein 3		
ENSG00000123473	STIL	STIL Centriolar Assembly Protein		
ENSG00000129003	VPS13C (PARK23)	Vacuolar Protein Sorting 13 Homolog C		
ENSG00000132485	ZRANB2	Zinc Finger RANBP2-Type Containing 2		Yes
ENSG00000136100	VPS36	Vacuolar Protein Sorting 36 Homolog		
ENSG00000137831	UACA	Uveal Autoantigen With Coiled-Coil Domains And Ankyrin Repeats		
ENSG00000139219	COL2A1	Collagen Type II Alpha 1 Chain		
ENSG00000143416	SELENBP1	Selenium Binding Protein 1		Yes
ENSG00000147654	EBAG9	Estrogen Receptor Binding Site Associated Antigen 9		
ENSG00000148600	CDHR1	Cadherin Related Family Member 1		
ENSG00000154222	CC2D1B	Coiled-Coil And C2 Domain Containing 1B		
ENSG00000157036	EXOG	Exo/Endonuclease G		
ENSG00000157379	DHRS1	Dehydrogenase/Reductase 1		
ENSG00000160194	NDUFV3	NADH:Ubiquinone Oxidoreductase Subunit V3		Yes
ENSG00000161298	ZNF382	Zinc Finger Protein 382		
ENSG00000167264	DUS2	Dihydrouridine Synthase 2		
ENSG00000168300	PCMTD1	Protein-L-Isoaspartate (D-Aspartate) O-Methyltransferase Domain Containing 1		
ENSG00000176809	LRRC37A3	Leucine Rich Repeat Containing 37 Member A3		
ENSG00000179889	PDXDC1	Pyridoxal Dependent Decarboxylase Domain Containing 1		
ENSG00000181085	MAPK15	Mitogen-Activated Protein Kinase 15		
ENSG00000181666	HKR1 (ZNF875)	Zinc Finger Protein 875		
ENSG00000188234	AGAP4	ArfGAP With GTPase Domain, Ankyrin Repeat And PH Domain 4		
ENSG00000196275	GTF2IRD2	GTF2I Repeat Domain Containing 2		
ENSG00000196739	COL27A1	Collagen Type XXVII Alpha 1 Chain		
ENSG00000198804	MT-CO1	Mitochondrially Encoded Cytochrome C Oxidase I		
ENSG00000198840	MT-ND3	Mitochondrially Encoded NADH:Ubiquinone Oxidoreductase Core Subunit 3		
ENSG00000198888	MT-ND1	Mitochondrially Encoded NADH:Ubiquinone Oxidoreductase Core Subunit 1		Yes
ENSG00000204681	GABBR1	Gamma-Aminobutyric Acid Type B Receptor Subunit 1		
ENSG00000205583	STAG3L1	Stromal Antigen 3-Like 1 (Pseudogene)		
ENSG00000225630	MTND2P28	MT-ND2 Pseudogene 28		
ENSG00000226232	NPIP14P	Nuclear pore complex interacting protein family member B14, pseudogene		
ENSG00000228253	MT-ATP8	Mitochondrially encoded ATP synthase membrane subunit 8		
ENSG00000232196	MTRNR2L4	MT-RNR2 Like 4		
ENSG00000234441	AC105272.1			
ENSG00000237732	CT75	Cancer/testis associated transcript 75		
ENSG00000237973	MTCO1P12	MT-CO1 pseudogene 12		
ENSG00000239912	RPL39P36	Ribosomal protein L39 pseudogene 36		
ENSG00000243716	NPIP5	Nuclear pore complex interacting protein family member B5		
ENSG00000248527	MTATP6P1	MT-ATP6 pseudogene 1		
ENSG00000256618	MTRNR2L1	MT-RNR2 Like 1		
ENSG00000258366	RTEL1	Regulator Of Telomere Elongation Helicase 1		
ENSG00000258890	CEP95	Centrosomal Protein 95		
ENSG00000274615	AC233968.1	Aminopeptidase puromycin sensitive (NPEPPS) pseudogene		

Supplementary Table 2

	p_val	avg_logFC	pct.1	pct.2	p_val_adj	cluster	gene
EEF1A1	7.20E-206	0.58128601	1	0.987	1.18E-201	RG1	EEF1A1
RPS24	5.38E-204	0.66466052	1	0.974	8.81E-200	RG1	RPS24
RPS23	1.00E-203	0.64479529	0.999	0.96	1.65E-199	RG1	RPS23
RPS27	6.63E-197	0.71319427	0.999	0.959	1.09E-192	RG1	RPS27
RPL36	3.26E-193	0.64219367	0.994	0.917	5.34E-189	RG1	RPL36
RPL34	1.19E-191	0.66496163	1	0.958	1.96E-187	RG1	RPL34
RPS18	4.85E-189	0.61982496	1	0.965	7.95E-185	RG1	RPS18
RPL32	7.70E-189	0.65503914	0.999	0.955	1.26E-184	RG1	RPL32
RPS28	2.03E-183	0.65487349	0.996	0.944	3.33E-179	RG1	RPS28
RPS12	4.08E-182	0.64736472	0.998	0.937	6.69E-178	RG1	RPS12
RPS3	1.95E-181	0.56117174	0.999	0.947	3.20E-177	RG1	RPS3
RPL13	8.10E-180	0.57384817	1	0.977	1.33E-175	RG1	RPL13
RPS3A	1.11E-179	0.60468795	0.999	0.967	1.82E-175	RG1	RPS3A
RPS19	1.91E-179	0.62128767	1	0.977	3.13E-175	RG1	RPS19
RPL26	5.07E-179	0.62761508	0.996	0.901	8.32E-175	RG1	RPL26
RPL30	5.30E-179	0.62322156	0.999	0.941	8.69E-175	RG1	RPL30
RPL39	1.26E-177	0.69105919	1	0.961	2.06E-173	RG1	RPL39
RPS15A	2.09E-176	0.64631755	0.999	0.947	3.43E-172	RG1	RPS15A
RPL9	3.15E-175	0.58890939	0.999	0.924	5.17E-171	RG1	RPL9
RPL5	8.30E-175	0.54099879	0.996	0.95	1.36E-170	RG1	RPL5
RPS27A	5.48E-173	0.58195713	0.999	0.948	8.99E-169	RG1	RPS27A
RPL18A	7.46E-173	0.60476261	1	0.95	1.22E-168	RG1	RPL18A
RPL11	1.43E-171	0.53136684	0.999	0.972	2.34E-167	RG1	RPL11
RPS4X	1.73E-171	0.55815363	1	0.969	2.84E-167	RG1	RPS4X
RPL3	1.78E-171	0.53501235	0.999	0.96	2.91E-167	RG1	RPL3
RPLP1	1.98E-171	0.62557027	1	0.969	3.25E-167	RG1	RPLP1
RPS7	2.06E-169	0.5564908	0.999	0.95	3.37E-165	RG1	RPS7
RPL35	4.66E-168	0.56908442	0.994	0.92	7.64E-164	RG1	RPL35
RPL24	5.05E-166	0.55542376	0.996	0.916	8.29E-162	RG1	RPL24
RPS2	1.60E-163	0.52151964	0.999	0.961	2.62E-159	RG1	RPS2
RPS15	8.55E-163	0.55618186	0.999	0.964	1.40E-158	RG1	RPS15
RPL41	3.73E-162	0.5835083	0.994	0.922	6.12E-158	RG1	RPL41
RPL10	6.39E-162	0.54301843	0.999	0.975	1.05E-157	RG1	RPL10
RPS13	6.67E-160	0.62104587	0.996	0.912	1.09E-155	RG1	RPS13
RPL37	1.91E-159	0.6041748	0.999	0.942	3.14E-155	RG1	RPL37
RPL28	2.30E-158	0.57010667	0.997	0.926	3.77E-154	RG1	RPL28
RPS25	4.90E-158	0.54132374	0.994	0.905	8.04E-154	RG1	RPS25
RPL8	2.50E-155	0.50174632	0.996	0.934	4.10E-151	RG1	RPL8
RPS14	1.08E-154	0.53097549	0.999	0.949	1.78E-150	RG1	RPS14
NACA	1.35E-154	0.50098499	0.995	0.933	2.22E-150	RG1	NACA
RPL29	3.92E-152	0.52263147	0.999	0.932	6.43E-148	RG1	RPL29
RPL7A	6.98E-151	0.46284744	0.998	0.958	1.14E-146	RG1	RPL7A
RPS8	1.97E-149	0.53516873	0.999	0.974	3.23E-145	RG1	RPS8
RPL15	4.59E-149	0.48020038	0.995	0.923	7.53E-145	RG1	RPL15
RPL35A	7.08E-149	0.53719424	0.998	0.93	1.16E-144	RG1	RPL35A
RPS29	1.87E-147	0.59114142	0.996	0.914	3.07E-143	RG1	RPS29
RPL14	1.09E-146	0.48760525	0.994	0.924	1.78E-142	RG1	RPL14
RPL22	6.45E-146	0.54966138	0.983	0.866	1.06E-141	RG1	RPL22
RPL18	1.01E-144	0.49584098	0.997	0.94	1.65E-140	RG1	RPL18
RPS6	2.66E-144	0.56389044	0.999	0.944	4.36E-140	RG1	RPS6
RPL19	3.81E-143	0.50117452	0.999	0.938	6.26E-139	RG1	RPL19
GNB2L1	7.21E-142	0.4831145	0.996	0.939	1.18E-137	RG1	GNB2L1
RPL6	2.36E-140	0.48192617	0.999	0.96	3.87E-136	RG1	RPL6
RPS9	1.82E-134	0.50774049	0.992	0.897	2.98E-130	RG1	RPS9
RPL38	1.15E-130	0.51113513	0.97	0.843	1.89E-126	RG1	RPL38
RPL12	2.54E-130	0.55042653	0.979	0.857	4.17E-126	RG1	RPL12
TPT1	1.93E-128	0.53294537	0.992	0.901	3.16E-124	RG1	TPT1
RPL27	1.31E-127	0.51257885	0.976	0.842	2.15E-123	RG1	RPL27
FAU	2.07E-127	0.46489912	0.985	0.872	3.39E-123	RG1	FAU
RPS21	4.96E-127	0.55815894	0.958	0.819	8.14E-123	RG1	RPS21
RPS5	4.77E-117	0.49021616	0.984	0.872	7.83E-113	RG1	RPS5
RPSA	1.74E-109	0.43923903	0.988	0.899	2.85E-105	RG1	RPSA
RPL27A	1.01E-108	0.4970958	0.982	0.86	1.66E-104	RG1	RPL27A
RPS11	1.21E-106	0.48179761	0.97	0.861	1.99E-102	RG1	RPS11
COX7C	2.86E-105	0.40707387	0.929	0.751	4.68E-101	RG1	COX7C
RPL10A	1.08E-103	0.44555906	0.988	0.901	1.77E-99	RG1	RPL10A
RPLP2	4.24E-103	0.47709092	0.969	0.853	6.96E-99	RG1	RPLP2
RPL21	8.85E-102	0.47850021	0.988	0.899	1.45E-97	RG1	RPL21
YBX1	1.71E-98	0.40703275	0.985	0.889	2.80E-94	RG1	YBX1
RPL23	8.05E-98	0.45000314	0.964	0.839	1.32E-93	RG1	RPL23
RPLP0	6.50E-96	0.41565136	0.996	0.942	1.07E-91	RG1	RPLP0
RPS10	2.17E-94	0.46532489	0.796	0.608	3.57E-90	RG1	RPS10
FTH1	1.36E-91	0.42106334	0.986	0.899	2.22E-87	RG1	FTH1
UBA52	9.48E-91	0.41517517	0.9	0.745	1.55E-86	RG1	UBA52
ATP5E	2.40E-87	0.44827242	0.861	0.663	3.93E-83	RG1	ATP5E
FTL	1.29E-86	0.43920241	0.951	0.804	2.11E-82	RG1	FTL
RPS16	6.57E-83	0.40726501	0.958	0.831	1.08E-78	RG1	RPS16
RPL37A	2.93E-82	0.43404501	0.993	0.923	4.81E-78	RG1	RPL37A
HNRNPA1	5.65E-81	0.37597984	0.974	0.9	9.26E-77	RG1	HNRNPA1
GAPDH	2.02E-80	0.34802129	0.988	0.907	3.32E-76	RG1	GAPDH
RPL7	3.17E-80	0.37767542	0.977	0.86	5.20E-76	RG1	RPL7
COMMD6	5.48E-75	0.44706128	0.732	0.55	8.99E-71	RG1	COMMD6
RPL4	5.47E-71	0.37006385	0.886	0.746	8.97E-67	RG1	RPL4
RPL23A	7.13E-71	0.35787566	0.935	0.804	1.17E-66	RG1	RPL23A
MIF	3.52E-68	0.34943353	0.84	0.655	5.78E-64	RG1	MIF
RPL17	2.66E-64	0.38917253	0.599	0.384	4.36E-60	RG1	RPL17
BT3	5.04E-56	0.29013026	0.88	0.732	8.27E-52	RG1	BT3
TMSB4X	1.00E-53	0.27042864	0.999	0.975	1.64E-49	RG1	TMSB4X
ZFAS1	1.65E-53	0.3978265	0.645	0.493	2.70E-49	RG1	ZFAS1
ATP5G2	9.76E-53	0.29575762	0.869	0.725	1.60E-48	RG1	ATP5G2
EIF3E	5.30E-50	0.33684077	0.701	0.551	8.69E-46	RG1	EIF3E
AC090498.1	2.22E-44	0.29165582	0.496	0.314	3.64E-40	RG1	AC090498.1
EEF1D	8.70E-44	0.29638937	0.772	0.659	1.43E-39	RG1	EEF1D
HINT1	5.16E-43	0.26649231	0.845	0.711	8.47E-39	RG1	HINT1
EEF2	2.84E-42	0.30882998	0.725	0.619	4.65E-38	RG1	EEF2
ATP5L	1.12E-40	0.29992641	0.687	0.556	1.84E-36	RG1	ATP5L
RPL36A	1.75E-38	0.32183542	0.579	0.441	2.86E-34	RG1	RPL36A
PFND5	1.86E-38	0.30884537	0.652	0.541	3.05E-34	RG1	PFND5
TCEB2	3.26E-35	0.26626513	0.671	0.539	5.35E-31	RG1	TCEB2
TOMM7	2.70E-34	0.27329311	0.577	0.444	4.43E-30	RG1	TOMM7
Clorf61	2.15E-33	0.28381088	0.946	0.904	3.52E-29	RG1	Clorf61
SERF2	7.90E-32	0.26025762	0.731	0.629	1.29E-27	RG1	SERF2
EIF3H	1.87E-31	0.2533865	0.544	0.394	3.07E-27	RG1	EIF3H
EIF3F	4.43E-30	0.25907147	0.646	0.539	7.26E-26	RG1	EIF3F
RPS17	4.56E-29	0.26196022	0.691	0.577	7.48E-25	RG1	RPS17
RPL13A	1.00E-28	0.28527633	0.917	0.798	1.65E-24	RG1	RPL13A
EEF1B2	1.76E-28	0.28074487	0.718	0.643	2.88E-24	RG1	EEF1B2
TMA7	6.46E-28	0.25145982	0.622	0.505	1.06E-23	RG1	TMA7
UQCRCB	7.83E-27	0.2520723	0.593	0.481	1.28E-22	RG1	UQCRCB
MALAT1	0	2.42786005	1	0.674	0	RG2	MALAT1
LUC7L3	0	0.99693829	0.838	0.143	0	RG2	LUC7L3
PTPRZ1	0	0.92852762	0.797	0.144	0	RG2	PTPRZ1

ARGLU1	0	0.91859763	0.808	0.146	0	RG2	ARGLU1
WSB1	0	0.89578662	0.747	0.097	0	RG2	WSB1
VCAN	5.42E-289	0.76914889	0.755	0.168	8.89E-285	RG2	VCAN
PLCG2	1.47E-278	0.74275165	0.629	0.084	2.40E-274	RG2	PLCG2
PNISR	8.33E-259	0.66908053	0.74	0.174	1.37E-254	RG2	PNISR
NKTR	2.28E-253	0.53999545	0.538	0.055	3.74E-249	RG2	NKTR
SYNE2	1.15E-247	0.78108216	0.825	0.263	1.89E-243	RG2	SYNE2
GOLGA8A	4.21E-242	0.51303895	0.477	0.035	6.91E-238	RG2	GOLGA8A
N4BP2L2	4.37E-232	0.57846168	0.657	0.141	7.16E-228	RG2	N4BP2L2
MT-CO1	5.52E-232	0.97446923	0.984	0.809	9.05E-228	RG2	MT-CO1
COL4A5	2.17E-226	0.49136568	0.499	0.054	3.56E-222	RG2	COL4A5
CHD9	8.60E-216	0.51921899	0.59	0.106	1.41E-211	RG2	CHD9
MT-CO2	2.71E-214	0.85440113	0.979	0.771	4.44E-210	RG2	MT-CO2
GABPB1-AS1	2.12E-209	0.46688008	0.467	0.051	3.47E-205	RG2	GABPB1-AS1
PAXBP1	6.71E-200	0.46847313	0.482	0.063	1.10E-195	RG2	PAXBP1
LINC00461	1.16E-195	0.52057199	0.654	0.165	1.91E-191	RG2	LINC00461
CD46	2.21E-195	0.41286671	0.445	0.047	3.63E-191	RG2	CD46
PRPF4B	1.63E-194	0.49523146	0.554	0.105	2.67E-190	RG2	PRPF4B
MT-CO3	4.74E-193	0.79311042	0.924	0.613	7.78E-189	RG2	MT-CO3
MT-ATP6	1.28E-191	0.88760187	0.942	0.699	2.10E-187	RG2	MT-ATP6
MT-ND4	4.56E-187	0.69934447	0.926	0.573	7.48E-183	RG2	MT-ND4
MT-ND2	6.68E-185	0.58266112	0.755	0.263	1.10E-180	RG2	MT-ND2
MT-ND5	6.78E-184	0.58385153	0.72	0.235	1.11E-179	RG2	MT-ND5
INTU	5.19E-178	0.43033193	0.459	0.067	8.51E-174	RG2	INTU
SQLE	1.61E-177	0.55465985	0.664	0.198	2.63E-173	RG2	SQLE
PNN	1.09E-175	0.5709407	0.6	0.157	1.79E-171	RG2	PNN
ZCCHC11	3.33E-175	0.49462132	0.569	0.131	5.46E-171	RG2	ZCCHC11
MT-CYB	2.01E-174	0.76240049	0.838	0.417	3.29E-170	RG2	MT-CYB
COL4A6	5.78E-171	0.40864156	0.47	0.079	9.48E-167	RG2	COL4A6
HSP90B1	1.44E-170	0.52805138	0.661	0.186	2.37E-166	RG2	HSP90B1
MT-ND1	1.54E-165	0.57580537	0.724	0.256	2.53E-161	RG2	MT-ND1
MT-ND3	5.58E-164	0.67119773	0.887	0.484	9.15E-160	RG2	MT-ND3
MT-ND4L	6.43E-163	0.55825751	0.73	0.266	1.06E-158	RG2	MT-ND4L
ADAMTS6	3.43E-161	0.34917139	0.363	0.035	5.62E-157	RG2	ADAMTS6
ANKRD36C	2.55E-159	0.33403386	0.356	0.033	4.18E-155	RG2	ANKRD36C
SRGAP3	6.31E-158	0.42579217	0.514	0.113	1.04E-153	RG2	SRGAP3
MEIS2	1.42E-154	0.45695758	0.521	0.122	2.32E-150	RG2	MEIS2
CDH2	2.69E-152	0.46019934	0.589	0.169	4.41E-148	RG2	CDH2
ZRANB2	8.05E-152	0.433251	0.558	0.149	1.32E-147	RG2	ZRANB2
SRRM2	3.92E-151	0.49364203	0.682	0.236	6.42E-147	RG2	SRRM2
FGFBP3	1.17E-150	0.52933835	0.647	0.217	1.92E-146	RG2	FGFBP3
BAZ2B	9.38E-149	0.36241928	0.4	0.059	1.54E-144	RG2	BAZ2B
MARCH6	1.36E-147	0.3568305	0.406	0.064	2.24E-143	RG2	Mar-06 MARCH6
MLLT4	2.13E-147	0.42242225	0.518	0.128	3.49E-143	RG2	MLLT4
DDX17	1.18E-146	0.42263321	0.578	0.166	1.94E-142	RG2	DDX17
HMGCR	3.53E-146	0.4405875	0.508	0.122	5.79E-142	RG2	HMGCR
DDX46	3.41E-143	0.38656073	0.511	0.126	5.60E-139	RG2	DDX46
RP3-525N10.1	1.21E-140	0.3164603	0.336	0.037	1.98E-136	RG2	RP3-525N10.2
FGFR3	1.61E-139	0.3978821	0.503	0.124	2.64E-135	RG2	FGFR3
ZMYM2	2.97E-136	0.30677408	0.381	0.059	4.87E-132	RG2	ZMYM2
KNOP1	2.55E-135	0.3678449	0.534	0.143	4.19E-131	RG2	KNOP1
NCAM1	2.82E-135	0.31994429	0.38	0.059	4.63E-131	RG2	NCAM1
GPC4	2.08E-134	0.36470177	0.454	0.102	3.42E-130	RG2	GPC4
PKN2	9.62E-134	0.34153117	0.408	0.076	1.58E-129	RG2	PKN2
SYT1	4.86E-131	0.33637375	0.392	0.069	7.98E-127	RG2	SYT1
RBM25	1.67E-130	0.33750601	0.441	0.096	2.74E-126	RG2	RBM25
PHF14	3.62E-130	0.34016304	0.443	0.097	5.94E-126	RG2	PHF14
NCKAP5	8.35E-130	0.30531909	0.343	0.047	1.37E-125	RG2	NCKAP5
COL11A1	1.57E-129	0.28701219	0.322	0.038	2.57E-125	RG2	COL11A1
AHI1	2.14E-129	0.31861816	0.368	0.059	3.52E-125	RG2	AHI1
KTN1	2.31E-129	0.34956275	0.457	0.106	3.79E-125	RG2	KTN1
IL1RAPL1	4.31E-129	0.29435903	0.3	0.03	7.07E-125	RG2	IL1RAPL1
LINC00632	3.38E-128	0.28641583	0.319	0.037	5.55E-124	RG2	LINC00632
ATRX	2.00E-127	0.3612487	0.473	0.118	3.28E-123	RG2	ATRX
CANX	8.59E-126	0.35637853	0.467	0.118	1.41E-121	RG2	CANX
WHSC1L1	1.93E-125	0.35019361	0.494	0.131	3.16E-121	RG2	WHSC1L1
SON	2.38E-125	0.37880366	0.624	0.218	3.90E-121	RG2	SON
ADGRB3	2.63E-125	0.26143957	0.287	0.026	4.32E-121	RG2	ADGRB3
SLC39A10	2.45E-123	0.33259025	0.385	0.073	4.01E-119	RG2	SLC39A10
MSMO1	3.03E-123	0.42685205	0.614	0.221	4.98E-119	RG2	MSMO1
SFPQ	9.08E-123	0.41076728	0.707	0.284	1.49E-118	RG2	SFPQ
DDX18	1.08E-122	0.32593231	0.452	0.106	1.77E-118	RG2	DDX18
PABPN1	2.72E-121	0.37491348	0.485	0.135	4.46E-117	RG2	PABPN1
MTRNR2L12	2.52E-120	0.52292307	0.864	0.505	4.14E-116	RG2	MTRNR2L12
PDIA3	1.41E-119	0.3942419	0.493	0.14	2.31E-115	RG2	PDIA3
CD47	1.42E-119	0.27802119	0.32	0.044	2.32E-115	RG2	CD47
ZNF638	2.37E-119	0.31181865	0.408	0.088	3.89E-115	RG2	ZNF638
AMBN	3.27E-117	0.30212073	0.402	0.088	5.36E-113	RG2	AMBN
RNPC3	6.36E-117	0.27586921	0.286	0.032	1.04E-112	RG2	RNPC3
TMBIM6	3.78E-116	0.3667228	0.559	0.185	6.19E-112	RG2	TMBIM6
ANKRD26	5.17E-116	0.25218939	0.276	0.027	8.47E-112	RG2	ANKRD26
GPC1	1.73E-115	0.37106628	0.554	0.185	2.84E-111	RG2	GPC1
FKBP10	5.04E-115	0.27869447	0.328	0.051	8.26E-111	RG2	FKBP10
SFRP1	8.49E-115	0.46499264	0.715	0.321	1.39E-110	RG2	SFRP1
RBM39	1.93E-114	0.34087349	0.48	0.135	3.16E-110	RG2	RBM39
HSPA5	2.92E-112	0.34387161	0.443	0.115	4.78E-108	RG2	HSPA5
HES4	1.70E-111	0.5131838	0.764	0.39	2.79E-107	RG2	HES4
HELLS	2.46E-111	0.35763973	0.419	0.103	4.03E-107	RG2	HELLS
SPAG9	4.00E-111	0.32241229	0.431	0.109	6.56E-107	RG2	SPAG9
PHF3	1.98E-110	0.31167679	0.445	0.117	3.25E-106	RG2	PHF3
KMT2A	1.08E-109	0.31930636	0.415	0.103	1.77E-105	RG2	KMT2A
CPE	2.10E-108	0.29662098	0.385	0.086	3.44E-104	RG2	CPE
IFI44L	7.39E-108	0.2891894	0.396	0.092	1.21E-103	RG2	IFI44L
MDM4	1.03E-107	0.28607608	0.34	0.063	1.69E-103	RG2	MDM4
CCDC14	4.71E-107	0.27292229	0.325	0.056	7.73E-103	RG2	CCDC14
HNRNPDL	1.58E-105	0.38162755	0.79	0.393	2.59E-101	RG2	HNRNPDL
AKAP9	2.39E-105	0.27464308	0.348	0.067	3.92E-101	RG2	AKAP9
UPF2	6.25E-105	0.28434824	0.335	0.063	1.03E-100	RG2	UPF2
MAP1B	1.10E-104	0.42847187	0.902	0.619	1.80E-100	RG2	MAP1B
PDIA6	8.45E-104	0.37495798	0.571	0.217	1.39E-99	RG2	PDIA6
SRSF1	2.10E-103	0.28241256	0.396	0.096	3.45E-99	RG2	SRSF1
SLCIA3	3.46E-103	0.26402176	0.275	0.036	5.68E-99	RG2	SLCIA3
KMT2C	2.13E-102	0.27358047	0.339	0.067	3.50E-98	RG2	KMT2C
SLCA47	2.58E-102	0.27085886	0.329	0.062	4.22E-98	RG2	SLCA47
FNBP4	2.43E-100	0.25588841	0.332	0.064	3.98E-96	RG2	FNBP4
ATAD5	9.91E-100	0.28769139	0.293	0.047	1.62E-95	RG2	ATAD5
SLC25A36	1.19E-99	0.26993177	0.346	0.074	1.95E-95	RG2	SLC25A36
RNMT	2.60E-97	0.28100999	0.41	0.108	4.26E-93	RG2	RNMT
GPM6B	1.39E-95	0.27687455	0.484	0.156	2.28E-91	RG2	GPM6B
FZD3	2.30E-95	0.25648226	0.335	0.071	3.77E-91	RG2	FZD3
ZNF292	3.22E-95	0.25206218	0.357	0.082	5.27E-91	RG2	ZNF292
CADM1	4.62E-94	0.26228541	0.339	0.076	7.57E-90	RG2	CADM1
TM9SF3	4.92E-93	0.25217443	0.297	0.055	8.07E-89	RG2	TM9SF3

RCN1	1.08E-92	0.30280983	0.479	0.162	1.77E-88	RG2	RCN1
TAF1D	1.63E-92	0.26184238	0.385	0.101	2.67E-88	RG2	TAF1D
RERE	2.44E-92	0.25568918	0.348	0.081	4.00E-88	RG2	RERE
PHIP	2.77E-92	0.26714541	0.396	0.108	4.55E-88	RG2	PHIP
ARL6IP5	1.13E-91	0.27680962	0.394	0.109	1.86E-87	RG2	ARL6IP5
MPHOSPH8	1.57E-91	0.25841463	0.322	0.069	2.57E-87	RG2	MPHOSPH8
UPF3A	1.08E-90	0.25888861	0.351	0.084	1.77E-86	RG2	UPF3A
CREB5	7.99E-90	0.264456	0.355	0.088	1.31E-85	RG2	CREB5
SCD	8.93E-90	0.33387762	0.498	0.177	1.47E-85	RG2	SCD
USP34	1.14E-89	0.25636563	0.353	0.088	1.87E-85	RG2	USP34
CALD1	5.05E-89	0.27893595	0.43	0.131	8.27E-85	RG2	CALD1
EFNB1	3.80E-88	0.28963149	0.423	0.131	6.23E-84	RG2	EFNB1
SF3B1	2.04E-87	0.26341142	0.445	0.143	3.34E-83	RG2	SF3B1
SRSF10	2.21E-87	0.27902678	0.476	0.162	3.63E-83	RG2	SRSF10
SPCS2	7.41E-86	0.29928074	0.469	0.165	1.22E-81	RG2	SPCS2
SOX2	2.48E-85	0.3301057	0.66	0.308	4.07E-81	RG2	SOX2
CLU	8.35E-84	0.34901869	0.583	0.249	1.37E-79	RG2	CLU
PRRC2C	3.30E-81	0.254979	0.477	0.167	5.41E-77	RG2	PRRC2C
ARHGAP21	4.11E-81	0.25261931	0.339	0.09	6.74E-77	RG2	ARHGAP21
APP	1.55E-79	0.25440188	0.325	0.083	2.55E-75	RG2	APP
SEC62	4.09E-78	0.26316123	0.383	0.119	6.71E-74	RG2	SEC62
FOXG1	4.33E-78	0.29651256	0.533	0.218	7.11E-74	RG2	FOXG1
SRSF11	2.49E-77	0.25144271	0.415	0.136	4.09E-73	RG2	SRSF11
BSG	2.10E-76	0.32400182	0.598	0.273	3.44E-72	RG2	BSG
QKI	7.42E-76	0.29505194	0.638	0.3	1.22E-71	RG2	QKI
CALR	3.67E-75	0.32443277	0.479	0.19	6.02E-71	RG2	CALR
RTN4	7.85E-74	0.25290053	0.489	0.19	1.29E-69	RG2	RTN4
FUS	8.73E-73	0.27276368	0.562	0.248	1.43E-68	RG2	FUS
TCF4	1.11E-69	0.25793364	0.486	0.196	1.82E-65	RG2	TCF4
CD81	1.14E-69	0.30201205	0.515	0.225	1.87E-65	RG2	CD81
HMGN3	1.09E-68	0.30090093	0.778	0.44	1.79E-64	RG2	HMGN3
ITM2B	7.24E-68	0.26385927	0.491	0.204	1.19E-63	RG2	ITM2B
BTG1	8.38E-67	0.25616986	0.45	0.178	1.37E-62	RG2	BTG1
PRKDC	6.63E-66	0.25698815	0.484	0.202	1.09E-61	RG2	PRKDC
HMGCS1	8.95E-66	0.33036957	0.714	0.398	1.47E-61	RG2	HMGCS1
SRSF2	3.48E-64	0.2603752	0.536	0.245	5.70E-60	RG2	SRSF2
IGFBP2	3.89E-60	0.45197522	0.704	0.41	6.38E-56	RG2	IGFBP2
PRDX4	1.04E-58	0.26178523	0.554	0.272	1.71E-54	RG2	PRDX4
ID4	2.45E-56	0.30238202	0.856	0.562	4.02E-52	RG2	ID4
HNRNPA2B1	5.42E-51	0.25562019	0.908	0.648	8.89E-47	RG2	HNRNPA2B1
CD63	1.03E-49	0.25373197	0.511	0.257	1.70E-45	RG2	CD63
CCND2	1.99E-49	0.26682969	0.682	0.413	3.27E-45	RG2	CCND2
HES5	1.95E-43	0.27689296	0.503	0.265	3.20E-39	RG2	HES5
TTYH1	7.05E-40	0.26995794	0.831	0.619	1.16E-35	RG2	TTYH1
HNRNPH1	5.07E-28	0.27127517	0.474	0.296	8.31E-24	RG2	HNRNPH1
UBE2C	0	1.23967144	0.626	0.067	0	DivRG	UBE2C
HMGB2	4.62E-276	1.25160748	0.773	0.207	7.57E-272	DivRG	HMGB2
PTTG1	1.49E-246	1.20744775	0.655	0.142	2.44E-242	DivRG	PTTG1
BIRC5	1.85E-237	0.68671213	0.506	0.053	3.03E-233	DivRG	BIRC5
CDC20	2.10E-223	0.62975491	0.374	0.013	3.44E-219	DivRG	CDC20
TOP2A	7.91E-204	0.92529649	0.542	0.095	1.30E-199	DivRG	TOP2A
HMGN2	2.18E-203	0.9179516	0.896	0.565	3.58E-199	DivRG	HMGN2
HIST1H4C	2.23E-203	1.32395607	0.753	0.3	3.66E-199	DivRG	HIST1H4C
TUBB4B	5.04E-203	1.03587305	0.651	0.183	8.27E-199	DivRG	TUBB4B
UBE2S	1.23E-202	1.01400505	0.607	0.145	2.01E-198	DivRG	UBE2S
NUSAP1	1.63E-200	0.77396957	0.549	0.102	2.67E-196	DivRG	NUSAP1
HMGB1	1.29E-196	0.82027901	0.987	0.833	2.12E-192	DivRG	HMGB1
CCNB1	5.55E-195	0.75492666	0.386	0.03	9.10E-191	DivRG	CCNB1
CKS2	5.91E-188	0.97698563	0.634	0.185	9.68E-184	DivRG	CKS2
TUBA1B	5.38E-184	0.78950307	0.96	0.754	8.82E-180	DivRG	TUBA1B
DLGAP5	2.06E-179	0.54152617	0.365	0.029	3.37E-175	DivRG	DLGAP5
TPX2	1.39E-175	0.65495271	0.449	0.066	2.27E-171	DivRG	TPX2
KPNA2	1.08E-168	0.857041	0.489	0.097	1.77E-164	DivRG	KPNA2
CCNB2	2.78E-164	0.594507	0.38	0.044	4.56E-160	DivRG	CCNB2
AURKB	3.95E-160	0.43065403	0.345	0.031	6.48E-156	DivRG	AURKB
PLK1	3.64E-157	0.37407124	0.26	0.007	5.97E-153	DivRG	PLK1
CDKN3	3.29E-153	0.4993821	0.352	0.038	5.40E-149	DivRG	CDKN3
H2AFZ	3.03E-150	0.72423411	0.911	0.683	4.97E-146	DivRG	H2AFZ
STMN1	1.70E-146	0.70443656	0.909	0.64	2.80E-142	DivRG	STMN1
H2AFX	9.21E-145	0.64216369	0.575	0.178	1.51E-140	DivRG	H2AFX
CDK1	1.15E-139	0.51607372	0.374	0.056	1.89E-135	DivRG	CDK1
CCNA2	1.51E-137	0.36354817	0.311	0.031	2.48E-133	DivRG	CCNA2
CDCA8	2.51E-137	0.3367672	0.267	0.016	4.12E-133	DivRG	CDCA8
HIST1H1B	1.56E-135	0.47089619	0.347	0.045	2.56E-131	DivRG	HIST1H1B
TUBB	6.44E-126	0.60284882	0.951	0.766	1.06E-121	DivRG	TUBB
CKS1B	1.75E-124	0.59722961	0.562	0.19	2.87E-120	DivRG	CKS1B
PBK	4.19E-124	0.37455338	0.316	0.04	6.87E-120	DivRG	PBK
MKI67	4.37E-123	0.51791857	0.319	0.043	7.17E-119	DivRG	MKI67
FAM64A	4.63E-121	0.38659409	0.319	0.044	7.60E-117	DivRG	FAM64A
PTMS	8.95E-121	0.64988005	0.869	0.668	1.47E-116	DivRG	PTMS
PRC1	6.57E-114	0.42753573	0.339	0.057	1.08E-109	DivRG	PRC1
CENPF	1.14E-111	1.03618604	0.425	0.114	1.87E-107	DivRG	CENPF
HIST1H1C	3.14E-109	0.65812102	0.456	0.135	5.15E-105	DivRG	HIST1H1C
UBE2T	1.46E-108	0.48108996	0.444	0.119	2.40E-104	DivRG	UBE2T
MAD2L1	3.81E-102	0.42804561	0.408	0.105	6.25E-98	DivRG	MAD2L1
CALM2	4.02E-101	0.65420896	0.728	0.448	6.59E-97	DivRG	CALM2
NUF2	4.32E-100	0.37091362	0.274	0.039	7.08E-96	DivRG	NUF2
HIFX	6.87E-81	0.51720497	0.806	0.585	1.13E-76	DivRG	HIFX
NUCKS1	1.23E-77	0.57559061	0.715	0.478	2.02E-73	DivRG	NUCKS1
ARL6IP1	4.70E-76	0.4421064	0.292	0.069	7.71E-72	DivRG	ARL6IP1
HIST1H1E	1.28E-74	0.41378615	0.369	0.116	2.10E-70	DivRG	HIST1H1E
SPC25	1.28E-74	0.27346155	0.274	0.057	2.11E-70	DivRG	SPC25
ASPM	2.07E-72	0.5770457	0.282	0.068	3.39E-68	DivRG	ASPM
CKB	4.89E-67	0.41969404	0.982	0.912	8.02E-63	DivRG	CKB
HIST2H2AC	2.62E-62	0.28604521	0.252	0.059	4.30E-58	DivRG	HIST2H2AC
HMGB3	2.86E-61	0.48179111	0.541	0.296	4.68E-57	DivRG	HMGB3
SMC4	1.43E-59	0.32370942	0.288	0.083	2.34E-55	DivRG	SMC4
HN1	1.18E-57	0.51402285	0.656	0.468	1.93E-53	DivRG	HN1
ACTB	5.16E-57	0.35597891	0.985	0.899	8.46E-53	DivRG	ACTB
CALM3	1.60E-54	0.35300129	0.484	0.237	2.63E-50	DivRG	CALM3
PTMA	1.24E-53	0.33608422	0.993	0.94	2.03E-49	DivRG	PTMA
CKAP2	2.50E-51	0.32326572	0.293	0.099	4.10E-47	DivRG	CKAP2
HIST1H1D	7.38E-50	0.32979478	0.266	0.082	1.21E-45	DivRG	HIST1H1D
H2AFV	2.60E-48	0.38178377	0.574	0.36	4.26E-44	DivRG	H2AFV
H3F3A	7.71E-48	0.33171086	0.972	0.884	1.26E-43	DivRG	H3F3A
TUBA1A	5.62E-46	0.32277471	0.981	0.925	9.22E-42	DivRG	TUBA1A
DYNLL1	1.46E-44	0.42702358	0.541	0.35	2.39E-40	DivRG	DYNLL1
BUB3	2.98E-43	0.28959992	0.302	0.119	4.89E-39	DivRG	BUB3
DCTN3	1.84E-41	0.28541707	0.361	0.165	3.02E-37	DivRG	DCTN3
RAN	5.91E-40	0.34018948	0.732	0.598	9.68E-36	DivRG	RAN
HNRNPA2B1	2.23E-35	0.30800889	0.833	0.709	3.66E-31	DivRG	HNRNPA2B1
RAD21	7.47E-33	0.28513326	0.328	0.16	1.22E-28	DivRG	RAD21
TUBB2B	1.14E-32	0.25921859	0.891	0.777	1.87E-28	DivRG	TUBB2B

PTGES3	4.08E-32	0.31234164	0.654	0.516	6.69E-28	DivRG	PTGES3
ANP32E	9.90E-32	0.30807713	0.431	0.256	1.62E-27	DivRG	ANP32E
UBC	2.39E-30	0.32495579	0.699	0.575	3.91E-26	DivRG	UBC
MAZ	3.69E-30	0.28585728	0.455	0.286	6.06E-26	DivRG	MAZ
TYMS	4.46E-30	0.25174679	0.361	0.187	7.31E-26	DivRG	TYMS
RHEB	7.32E-30	0.25336287	0.405	0.23	1.20E-25	DivRG	RHEB
YWHAE	1.33E-29	0.26312193	0.834	0.711	2.18E-25	DivRG	YWHAE
H3F3B	9.05E-29	0.25159114	0.86	0.708	1.48E-24	DivRG	H3F3B
PHGDH	7.92E-28	0.26405778	0.464	0.289	1.30E-23	DivRG	PHGDH
COX8A	2.64E-27	0.30188191	0.514	0.364	4.33E-23	DivRG	COX8A
MORF4L2	2.72E-27	0.29944526	0.512	0.36	4.46E-23	DivRG	MORF4L2
BANF1	9.54E-27	0.25924079	0.488	0.327	1.56E-22	DivRG	BANF1
EIF1	2.13E-26	0.2558166	0.864	0.771	3.50E-22	DivRG	EIF1
ILF2	3.90E-26	0.26821223	0.452	0.295	6.40E-22	DivRG	ILF2
ERH	1.01E-22	0.25819664	0.641	0.529	1.66E-18	DivRG	ERH
TMSB10	1.90E-21	0.25511554	0.921	0.823	3.11E-17	DivRG	TMSB10
HSP90AA1	5.07E-18	0.25569881	0.745	0.653	8.31E-14	DivRG	HSP90AA1
NTRK2	6.42E-278	0.83801811	0.578	0.009	1.05E-273	bRG	NTRK2
IRX1	2.50E-236	0.48239594	0.398	0.003	4.10E-232	bRG	IRX1
ZIC1	1.56E-233	0.53514134	0.458	0.006	2.56E-229	bRG	ZIC1
CSorf38	4.23E-185	0.28029187	0.277	0.001	6.94E-181	bRG	CSorf38
IRX2	7.77E-161	0.4183572	0.361	0.006	1.27E-156	bRG	IRX2
WLS	2.73E-154	1.03276651	0.578	0.026	4.48E-150	bRG	WLS
SUIT1	3.93E-147	0.33929509	0.289	0.004	6.45E-143	bRG	SUIT1
ZNF503	7.17E-101	0.29995194	0.277	0.007	1.18E-96	bRG	ZNF503
ATP1A2	2.49E-100	0.38970753	0.386	0.017	4.08E-96	bRG	ATP1A2
ERBB4	1.33E-92	0.34191238	0.289	0.009	2.19E-88	bRG	ERBB4
EDNRB	1.29E-87	0.78508459	0.554	0.048	2.12E-83	bRG	EDNRB
PTN	1.77E-64	2.12015743	0.819	0.189	2.91E-60	bRG	PTN
FRZB	3.73E-62	0.37071848	0.253	0.012	6.12E-58	bRG	FRZB
EPHA3	1.80E-53	0.49163199	0.398	0.04	2.96E-49	bRG	EPHA3
ARL4A	4.76E-49	0.35497418	0.349	0.033	7.80E-45	bRG	ARL4A
MASP1	2.45E-46	0.73444562	0.639	0.125	4.02E-42	bRG	MASP1
LIFR	4.65E-45	0.53414183	0.41	0.051	7.63E-41	bRG	LIFR
MEST	3.10E-44	0.32234022	0.301	0.027	5.08E-40	bRG	MEST
PDE1A	5.84E-43	0.35274072	0.373	0.043	9.59E-39	bRG	PDE1A
GRID2	2.72E-38	0.35059409	0.265	0.024	4.46E-34	bRG	GRID2
ID1	3.43E-38	0.76079388	0.47	0.076	5.62E-34	bRG	ID1
NLRP1	1.55E-36	0.69799405	0.602	0.138	2.54E-32	bRG	NLRP1
CRNDE	2.85E-33	0.29767888	0.289	0.033	4.67E-29	bRG	CRNDE
NR2F2	6.35E-33	0.45391439	0.349	0.049	1.04E-28	bRG	NR2F2
NES	9.58E-31	0.6134739	0.566	0.14	1.57E-26	bRG	NES
PSAP	4.91E-30	0.60348387	0.542	0.131	8.05E-26	bRG	PSAP
GPM6B	3.37E-29	1.06054158	0.699	0.259	5.53E-25	bRG	GPM6B
MGST1	2.23E-28	0.28759216	0.289	0.039	3.65E-24	bRG	MGST1
RFX4	2.54E-26	0.50376966	0.506	0.125	4.17E-22	bRG	RFX4
HES4	5.19E-25	1.03216161	0.904	0.51	8.51E-21	bRG	HES4
TTYH1	6.05E-25	0.81977473	0.964	0.686	9.93E-21	bRG	TTYH1
CXCR4	2.39E-23	0.320722	0.277	0.043	3.92E-19	bRG	CXCR4
RND2	2.42E-23	0.29404629	0.253	0.036	3.97E-19	bRG	RND2
DRAXIN	5.59E-23	0.26891457	0.277	0.043	9.17E-19	bRG	DRAXIN
APLP1	2.18E-22	0.32493761	0.361	0.074	3.57E-18	bRG	APLP1
DLL1	2.32E-22	0.35711822	0.253	0.038	3.81E-18	bRG	DLL1
LFNG	5.43E-22	0.3199172	0.325	0.061	8.91E-18	bRG	LFNG
CRB2	2.69E-19	0.42692775	0.458	0.129	4.41E-15	bRG	CRB2
ID3	6.27E-19	0.58859831	0.53	0.165	1.03E-14	bRG	ID3
RP3-395M20	8.87E-19	0.33143512	0.337	0.074	1.46E-14	bRG	RP3-395M20.12
ZIC2	2.74E-18	0.39196291	0.398	0.106	4.49E-14	bRG	ZIC2
CRABP2	3.30E-18	0.44494875	0.337	0.077	5.42E-14	bRG	CRABP2
BOC	1.47E-16	0.26701192	0.313	0.072	2.41E-12	bRG	BOC
DDIT4	4.39E-16	0.38891081	0.458	0.145	7.20E-12	bRG	DDIT4
SC5D	9.03E-16	0.25603816	0.289	0.065	1.48E-11	bRG	SC5D
HSPA51	2.43E-14	0.6837136	0.53	0.221	3.99E-10	bRG	HSPA5
DDR1	3.86E-14	0.31597628	0.361	0.106	6.33E-10	bRG	DDR1
APP	6.74E-14	0.41885457	0.458	0.159	1.11E-09	bRG	APP
MDK	7.40E-14	0.51822638	0.47	0.179	1.21E-09	bRG	MDK
DKK3	1.48E-13	0.26569437	0.325	0.088	2.42E-09	bRG	DKK3
TUBB2A	1.76E-13	0.38508461	0.47	0.173	2.88E-09	bRG	TUBB2A
ADGRG1	4.95E-13	0.35382952	0.373	0.12	8.12E-09	bRG	ADGRG1
PEA15	5.78E-13	0.45937988	0.578	0.258	9.48E-09	bRG	PEA15
RCN2	9.92E-13	0.5047983	0.602	0.305	1.63E-08	bRG	RCN2
CALR	3.17E-12	0.6412205	0.578	0.283	5.21E-08	bRG	CALR
CD24	6.33E-12	0.32839599	0.41	0.143	1.04E-07	bRG	CD24
ITGB8	6.55E-12	0.28027862	0.313	0.094	1.07E-07	bRG	ITGB8
ATPGAP2	6.84E-12	0.29336741	0.361	0.118	1.12E-07	bRG	ATPGAP2
TUBA1A1	2.33E-10	0.52464261	0.964	0.937	3.82E-06	bRG	TUBA1A
FZD31	5.99E-10	0.33048329	0.398	0.156	9.83E-06	bRG	FZD3
CD99	1.54E-09	0.40036401	0.578	0.31	2.52E-05	bRG	CD99
TM9SF2	1.96E-09	0.27525171	0.253	0.078	3.21E-05	bRG	TM9SF2
RCN1	2.09E-09	0.43557128	0.53	0.265	3.44E-05	bRG	RCN1
NCKAP5	4.50E-09	0.37353191	0.361	0.144	7.39E-05	bRG	NCKAP5
ACSL3	4.52E-09	0.26892721	0.301	0.105	7.41E-05	bRG	ACSL3
SLC1A3	5.28E-09	0.40560843	0.313	0.113	8.65E-05	bRG	SLC1A3
TMBIM6	6.77E-09	0.41722406	0.578	0.307	0.00011094	bRG	TMBIM6
MARCKS	1.26E-08	0.45585113	0.867	0.699	0.00020604	bRG	MARCKS
PIIB	2.07E-08	0.3859435	0.542	0.3	0.00033898	bRG	PIIB
HESS1	5.89E-08	0.35185211	0.614	0.341	0.00096636	bRG	HESS
VIM	6.17E-08	0.46733165	0.964	0.911	0.00101165	bRG	VIM
CDH2	1.31E-07	0.47331835	0.53	0.308	0.00214518	bRG	CDH2
SARAF	3.06E-07	0.29866715	0.446	0.222	0.00502549	bRG	SARAF
CCND1	4.12E-07	0.35191439	0.313	0.135	0.00674922	bRG	CCND1
RTN3	6.75E-07	0.29698699	0.578	0.327	0.01106394	bRG	RTN3
ITM2B	9.27E-07	0.35721018	0.518	0.298	0.01520461	bRG	ITM2B
NFIA	9.34E-07	0.31779563	0.434	0.223	0.01530933	bRG	NFIA
FGFBP3	9.89E-07	0.61373901	0.554	0.36	0.01622084	bRG	FGFBP3
MSMO1	1.10E-06	0.39240003	0.554	0.351	0.01809738	bRG	MSMO1
PPDPF	6.37E-06	0.29121221	0.614	0.416	0.10452549	bRG	PPDPF
GNG5	1.26E-05	0.26783037	0.578	0.357	0.20620563	bRG	GNG5
PDIA6	1.34E-05	0.35107061	0.542	0.334	0.21988307	bRG	PDIA6
HSP90B1	2.20E-05	0.52271882	0.542	0.344	0.36028257	bRG	HSP90B1
CANX	2.35E-05	0.35016807	0.41	0.233	0.3857807	bRG	CANX
CD63	3.57E-05	0.2525385	0.542	0.339	0.58563198	bRG	CD63
IGFBP2	5.43E-05	0.29877414	0.699	0.506	0.89088991	bRG	IGFBP2
PDIA3	9.75E-05	0.38141091	0.41	0.258	1	bRG	PDIA3
HMGCR	0.00019432	0.30889965	0.41	0.251	1	bRG	HMGCR
SCD	0.00033362	0.2666529	0.446	0.283	1	bRG	SCD
PRPF4B	0.00146226	0.25001186	0.398	0.256	1	bRG	PRPF4B
PTPRZ1	0.00590606	0.30600272	0.47	0.366	1	bRG	PTPRZ1
HMGCS1	0.00681632	0.34441833	0.578	0.505	1	bRG	HMGCS1

Supplementary Table 3

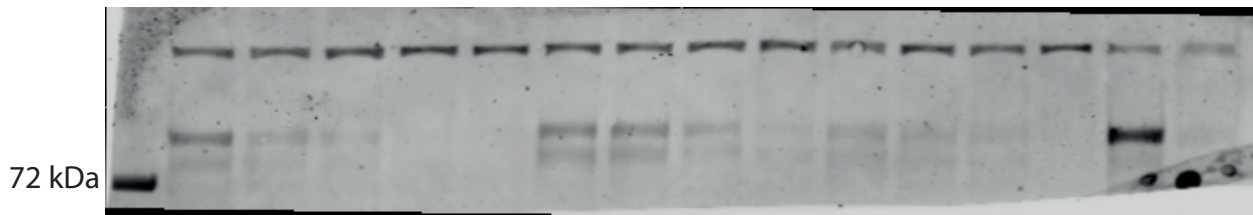
gene	p_val	avg_logFC	pct.1	pct.2	p_val_adj
RPL41	3.99E-85	0.51409253	0.978	0.937	6.55E-81
RPS21	2.06E-69	0.48678277	0.93	0.845	3.39E-65
RPS27	6.79E-56	0.447453	0.985	0.981	1.11E-51
RPL39	2.80E-48	0.4300905	0.991	0.973	4.59E-44
RPS28	7.35E-47	0.40059002	0.982	0.968	1.21E-42
RPL36	6.15E-39	0.34061242	0.963	0.951	1.01E-34
RPS10	5.78E-38	0.34991991	0.765	0.637	9.48E-34
RPS15A	9.38E-38	0.35856147	0.979	0.974	1.54E-33
RPL35	6.58E-34	0.3067754	0.971	0.953	1.08E-29
RPL26	4.90E-31	0.31149741	0.957	0.942	8.03E-27
RPL38	2.29E-30	0.30824787	0.923	0.891	3.76E-26
ATP5E	9.28E-30	0.34720459	0.8	0.721	1.52E-25
RPS24	1.31E-29	0.29493143	0.995	0.988	2.15E-25
MIF	3.69E-25	0.25107147	0.798	0.7	6.05E-21
RPS29	6.70E-25	0.32404832	0.954	0.951	1.10E-20
TMSB10	7.76E-25	0.27575047	0.889	0.822	1.27E-20
RPL36A	1.19E-24	0.30403931	0.564	0.423	1.95E-20
RPL30	3.02E-24	0.2728332	0.981	0.973	4.96E-20
RPL32	6.44E-23	0.26985304	0.982	0.977	1.06E-18
RPL34	6.79E-23	0.28196928	0.983	0.981	1.11E-18
TMA7	1.24E-22	0.25285737	0.634	0.494	2.03E-18
HNRNPH1	7.31E-22	0.3279653	0.425	0.276	1.20E-17
C4orf48	2.43E-21	0.25188982	0.542	0.39	3.99E-17
RPL27	4.52E-21	0.23652493	0.921	0.896	7.42E-17
ATP5I	1.73E-19	0.24054092	0.542	0.399	2.84E-15
SEC61G	1.92E-19	0.21854699	0.457	0.3	3.15E-15
RPL17	7.88E-19	0.26037869	0.542	0.423	1.29E-14
RPLP1	1.04E-18	0.23904048	0.988	0.991	1.71E-14
COX7C	1.64E-18	0.20357435	0.862	0.814	2.69E-14
USMG5	6.82E-18	0.22188319	0.402	0.26	1.12E-13
NDUFA3	2.16E-16	0.21711404	0.384	0.25	3.54E-12
RPS12	2.65E-16	0.23040563	0.969	0.975	4.35E-12
RPS15	1.28E-15	0.20547186	0.988	0.98	2.10E-11
RPS13	2.91E-15	0.23623071	0.963	0.95	4.77E-11
RPL37	2.02E-14	0.22608855	0.973	0.966	3.32E-10
RPS23	4.52E-14	0.20128877	0.985	0.982	7.41E-10
COMMD6	2.37E-11	0.20253543	0.692	0.642	3.89E-07
PTN	1.68E-05	0.28994092	0.223	0.162	0.27501291

Supplementary Table 4

	Control	DHT	E
RG1	580 (655.17) [8.62] P=0.196104	524 (443.54) [14.59] *P=0.023697	466 (471.29) [0.06] P=0.999996
RG2	673 (538.74) [33.46] **P=0.000008551	261 (364.72) [29.50] **P=0.00004891	357 (387.54) [2.41] P=0.8784
DivRG	309 (352.62) [5.40] P=0.4936	235 (238.72) [0.06] P=0.999996	301 (253.66) [8.84] P=0.1828
bRG	20 (35.47) [6.75] P=0.3446	51 (24.01) [30.33] **P=0.00003402	14 (25.52) [5.20] P=0.5184

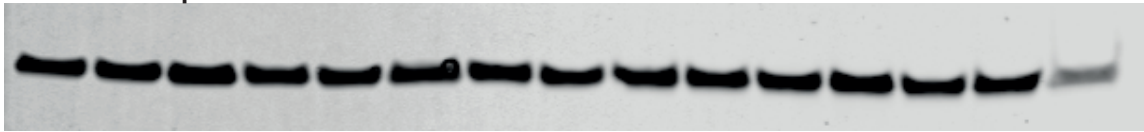
Supplementary Figure 1

AR blot:



GAPDH blot:

Shorter exposure:



Longer exposure:



Supplementary Figure 1. Full scans of western blots for AR and GAPDH.

Full scanned areas. The membrane was physically cut into an upper section where AR was expected, and into a lower section where GAPDH was expected, and the two pieces were blotted separately for AR and GAPDH. Most of the cut membrane was scanned for AR on the Li-COR system while for GAPDH only the region of the expected band was scanned. A longer exposure reveals the ladder.