Table SI. List of antibodies.

Antibody	Supplier	Cat. no.	Dilution
DAZAP1	Santa Cruz Biotechnology, Inc.	sc-373987	WB: 1:100 IHC: 1:200
NOTCH1	Proteintech Group, Inc.	10062-2-AP	WB: 1:4,000 IHC: 1:200
JAG1	Wuhan Boster Biological Technology, Ltd.	MA00640	WB: 1:2,000 IHC: 1:150
HES1	ABclonal Biotech Co., Ltd.	A0925	WB: 1:2,000
E-cadherin	Proteintech Group, Inc.	20874-1-AP	WB: 1:20,000 IHC: 1:5,000
N-cadherin	Proteintech Group, Inc.	22018-1-AP	WB: 1:2,000
Vimentin	Cell Signaling Technology, Inc.	D21H3	WB: 1:1,000 IHC: 1:400
β-tubulin	Proteintech Group,	10094-1-AP	WB: 1:5,000

	Inc.		
Flag	Proteintech Group, Inc.	66008-4-Ig	WB: 1:2,000

DAZAP, deleted in azoospermia-associated protein; JAG, jagged; HES, hairy and enhancer of split; WB, western blotting; IHC, immunohistochemistry.

Table SII. siRNAs and shRNAs for transient transfection

Name		Sequence, 5’→3’
DAZAP1	siRNA1	Forward: GAUAUUUGUCGGUGGAAUUTT Reverse: AAUUCCACCGACAAAUAUC
	siRNA2	Forward: GGAGGUAGUCAUGAUCUAUTT Reverse: AUAGAUC AUGACUACCUCC
NOTCH1	siRNA1	Forward: AUUGAUCUUGUCCAGGCAGCG Reverse: CGCUGCCUGGACAAGAUCAUU
	siRNA2	Forward: UAGCCACUGGUCAUGUCUUUG Reverse: CAAAGACAUGACCAGUGGCUA
JAG1	siRNA1	Forward: UUCAUUUGCAUCUAACUGG Reverse: UAGCCACUGGUCAUGUCUUUG
	siRNA2	Forward: UUGUCCUGUUUGUUUGUCC Reverse: GGACAAACAAACAGGACAA
Scramble siRNA		Forward: UUCUCCGAACGUGUCACGUTT Reverse: ACGUGACACGUUCGGAGAA
DAZAP1 shRNA		Forward: GGAGGTAGTCATGATCTAT

	Reverse: AUAGAUCAUGACUACCUCC
NOTCH1 shRNA	Forward: CGCTGCCTGGACAAGATCAAT Reverse: ATTGATCTTGTCCAGGCAGCG
Scramble shRNA	Forward: TTCTCCGAACGTGTCACGT Reverse: CGTGACACGTTCGGAGAA

si, small interfering; sh, short hairpin; DAZAP, deleted in azoospermia-associated protein; JAG, jagged.

Table SIII. Primers used for quantitative PCR.

Name	Direction	Sequence, 5'→3'
DAZAP1	F	AGAAGTTCGGAGTGGTCACG
	R	ACTGATTGTTCGTCCTCGAAAG
NOTCH1	F	GAGGCGTGGCAGACTATGC
	R	CTTGTACTCCGTCAGCGTGA
JAG1	F	GTCCATGCAGAACGTGAACG
	R	GCGGGACTGATACTCCTTGA
GAPDH	F	AAATCCCATCACCATCTTCC
	R	TCACACCCATGACGAACA

DAZAP, deleted in azoospermia-associated protein; JAG, jagged 1; F, forward; R, reverse.

Table SIV. List of probe sequences for *in situ* hybridization.

Gene	Probe no.	Sequence, 5'→3'
NOTCH1	1	Forward: CCCGTGGCACCCAGAACTGC Reverse: GTGCAGCGCGTCAATGACTT
	2	Forward: TCAACGGGCTCTTGTGCCACA Reverse: TCCTGGACTACAGCTTCGG
	3	Forward: ACCCCTGGAAGAACTGCACG Reverse: CAGTCTCTGCAGTGCTGGAA
Jagged 1	1	Forward: ACTTTGAGTATCAGATCCGC Reverse: GTGACCTGTG ATGACTACTA
	2	Forward: TCCCCATCCTGGACGACCAG Reverse: TGCTTCGTCCACCCCTGCAC
	3	Forward: ACTCCTATTACCAGGATAACTG Reverse: TGCGAACATCACATTTAC

Table SV. Clinicopathological features of patients with gastric cancer.

Characteristic	Cases (n=90)	DAZAP1 expression (%)		P-value
		Low (n=19)	High (n=71)	
Age, years				0.69
<60	27	5 (18.52)	22 (81.58)	
≥60	63	14 (22.22)	49 (77.88)	
Sex				0.29
Male	70	17 (24.28)	53 (75.71)	
Female	20	2 (10.00)	18 (90.00)	
Differentiation				0.26
Well	26	3 (11.53)	23 (88.57)	
Moderate	16	3 (18.75)	13 (81.35)	
Poor	48	13 (27.08)	35 (72.90)	
Local invasion (pT status)				<0.01
T1/T2	11	6 (54.54)	5 (45.55)	
T3/T4	79	13 (16.45)	66 (83.55)	

AJCC stage				
I/II	37	13 (35.14)	24 (64.86)	<0.01
III/IV	53	6 (11.32)	47 (88.68)	
Lymph node (pN status)				
N0	22	9 (40.90)	13 (59.10)	0.02
N1	68	10 (14.70)	58 (85.30)	
Tumor size, cm				<0.01
<5	32	14 (43.75)	18 (56.25)	
≥5	58	5 (8.62)	53 (91.38)	

AJCC, American Joint Committee on Cancer; DAZAP, deleted in azoospermia-associated protein.

Table SVI. Transcripts potentially bound to DAZAP1.

Transcript	Gene	P-value	Gene ID	Description	Type
XM_011542241.3	ATAD3B	0.00116938	83858	ATPase family AAA domain-containing 3B, transcript variant X4	mRNA
NM_182752.4	TPRG1L	0.0026633	127262	Tumor protein p63-regulated 1-like	mRNA
NM_020710.3	LRRC47	0.00240192	57470	Leucine-rich repeat-containing 47	mRNA
NM_001302883.1	CLSTN1	0.0081583	22883	Calsyntenin 1, transcript variant 3	mRNA
NM_001302883.1	CLSTN1	1.43E-05	22883	Calsyntenin 1, transcript variant 3	mRNA
NM_001105562.3	UBE4B	0.0433858	10277	Ubiquitination factor E4B, transcript variant 1	mRNA
XR_001736907.2	UBE4B	0.000822568	10277	Ubiquitination factor E4B, transcript variant X7	misc_RNA
XR_0017369	UBE4B	0.000777	10277	Ubiquitination factor E4B, transcript variant X7	misc_R

07.2		792			NA
NM_183416.4	KIF1B	0.000118363	23095	Kinesin family member 1B, transcript variant 2	mRNA
NM_001365952.1	KIF1B	0.0364492	23095	Kinesin family member 1B, transcript variant 4	mRNA
NM_001365952.1	KIF1B	0.00425539	23095	Kinesin family member 1B, transcript variant 4	mRNA
NM_001304451.2	PGD	0.0236925	5226	Phosphogluconate dehydrogenase, transcript variant 2	mRNA
NM_001304451.2	PGD	0.000452538	5226	Phosphogluconate dehydrogenase, transcript variant 2	mRNA
XM_017001495.2	EXOSC10	0.00240192	5394	Exosome component 10, transcript variant X7	mRNA
NM_001386501.1	MTOR	0.00728668	2475	Mechanistic target of rapamycin kinase, transcript variant 3	mRNA
NM_001386500.1	MTOR	0.0110174	2475	Mechanistic target of rapamycin kinase, transcript variant 2	mRNA
NM_001386	MTOR	0.001316	2475	Mechanistic target of rapamycin kinase, transcript variant 2	mRNA

500.1		87			
NM_001386500.1	MTOR	0.0148488	2475	Mechanistic target of rapamycin kinase, transcript variant 2	mRNA
NM_001386500.1	MTOR	0.000199653	2475	Mechanistic target of rapamycin kinase, transcript variant 2	mRNA
NM_001386500.1	MTOR	0.0139253	2475	Mechanistic target of rapamycin kinase, transcript variant 2	mRNA
XM_017000902.1	MTOR	2.78E-09	2475	Mechanistic target of rapamycin kinase, transcript variant X7	mRNA
NM_000302.4	PLOD1	0.0268866	5351	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1, transcript variant 2	mRNA
XM_005263547.3	MFN2	3.40E-13	9927	Mitofusin 2, transcript variant X1	mRNA
XM_017002211.1	TNFRSF1B	0.048575	7133	TNF receptor superfamily member 1B, transcript variant X1	mRNA
XM_011542060.2	TNFRSF1B	1.69E-05	7133	TNF receptor superfamily member 1B, transcript variant X2	mRNA
NM_018156.	VPS13D	0.000740	55187	Vacuolar protein sorting 13 homolog D, transcript variant 2	mRNA

4		067			
XM_005245790.4	PLEKHM2	0.00190081	23207	Pleckstrin homology and RUN domain containing M2, transcript variant X3	mRNA
NM_017940.6	NBPF1	0.012354	55672	NBPF member 1	mRNA
XM_017000847.1	ATP13A2	0.000561997	23400	ATPase cation-transporting 13A2, transcript variant X10	mRNA
XM_017000847.1	ATP13A2	3.05E-07	23400	ATPase cation-transporting 13A2, transcript variant X10	mRNA
NM_018715.4	RCC2	1.90E-07	55920	Regulator of chromosome condensation 2, transcript variant 1	mRNA
XM_011540630.2	IFFO2	0.00728668	126917	Intermediate filament family orphan 2, transcript variant X1	mRNA
XM_011541113.3	UBR4	0.000657308	23352	Ubiquitin protein ligase E3 component n-recognin 4, transcript variant X6	mRNA
XM_017000824.2	UBR4	0.00607462	23352	Ubiquitin protein ligase E3 component n-recognin 4, transcript variant X14	mRNA
XM_017000	UBR4	0.009268	23352	Ubiquitin protein ligase E3 component n-recognin 4, transcript variant X14	mRNA

824.2		78			
XM_017000824.2	UBR4	0.000257885	23352	Ubiquitin protein ligase E3 component n-recognin 4, transcript variant X14	mRNA
XM_017000824.2	UBR4	3.69E-06	23352	Ubiquitin protein ligase E3 component n-recognin 4, transcript variant X14	mRNA
XM_011541113.3	UBR4	3.99E-07	23352	Ubiquitin protein ligase E3 component n-recognin 4, transcript variant X6	mRNA
XM_017000824.2	UBR4	0.000358192	23352	Ubiquitin protein ligase E3 component n-recognin 4, transcript variant X14	mRNA
XM_017002675.2	EIF4G3	0.012354	8672	Eukaryotic translation initiation factor 4 γ3, transcript variant X6	mRNA
NM_001013693.3	LDLRAD2	3.40E-13	401944	Low-density lipoprotein receptor class A domain-containing 2	mRNA
XM_011541318.2	HSPG2	9.25E-08	3339	Heparan sulfate proteoglycan 2, transcript variant X1	mRNA
XM_011541318.2	HSPG2	3.40E-13	3339	Heparan sulfate proteoglycan 2, transcript variant X1	mRNA
XM_017000	KDM1A	0.001786	23028	Lysine demethylase 1A, transcript variant X6	mRNA

717.1		4			
NM_003198.3	ELOA	0.00358226	6924	Elongin A	mRNA
NM_006015.6	ARID1A	2.13E-06	8289	AT-rich interaction domain 1A, transcript variant 1	mRNA
NM_139135.4	ARID1A	0.000338213	8289	AT-rich interaction domain 1A, transcript variant 2	mRNA
NM_015023.5	WDTC1	0.00543382	23038	WD and tetratricopeptide repeats 1, transcript variant 2	mRNA
NM_001201404.3	WASF2	0.00476676	10163	WASP family member 2, transcript variant 2	mRNA
NM_001350161.2	PHACTR4	0.0166276	65979	Phosphatase and actin regulator 4, transcript variant 6	mRNA
NM_005704.5	PTPRU	0.000125229	10076	Protein tyrosine phosphatase receptor type U, transcript variant 3	mRNA
NM_014676.3	PUM1	0.000425096	9698	Pumilio RNA-binding family member 1, transcript variant 2	mRNA
NM_001321	THRAP3	8.52E-09	9967	Thyroid hormone receptor-associated protein 3, transcript variant 3	mRNA

473.2					
NM_012090.5	MACF1	0.0300443	23499	Microtubule actin crosslinking factor 1, transcript variant 1	mRNA
NM_001394062.1	MACF1	2.54E-06	23499	Microtubule actin crosslinking factor 1, transcript variant 2	mRNA
NM_001394062.1	MACF1	4.80E-10	23499	Microtubule actin crosslinking factor 1, transcript variant 2	mRNA
NM_001394062.1	MACF1	0.000510829	23499	Microtubule actin crosslinking factor 1, transcript variant 2	mRNA
NM_001394062.1	MACF1	0.0040224	23499	Microtubule actin crosslinking factor 1, transcript variant 2	mRNA
NM_001394062.1	MACF1	0.00644537	23499	Microtubule actin crosslinking factor 1, transcript variant 2	mRNA
NM_001394062.1	MACF1	3.40E-13	23499	Microtubule actin crosslinking factor 1, transcript variant 2	mRNA
NM_001135653.2	PABPC4	6.31E-06	8761	poly(A) binding protein cytoplasmic 4, transcript variant 1	mRNA
NM_014663.	KDM4A	0.026886	9682	Lysine demethylase 4A	mRNA

3		6			
XM_005271355.3	KDM4A	0.0148488	9682	Lysine demethylase 4A, transcript variant X1	mRNA
NM_001297655.2	KIF2C	0.0156332	11004	Kinesin family member 2C, transcript variant 2	mRNA
XR_001737358.2	GPBP1L1	0.000273438	60313	GC-rich promoter binding protein 1 like 1, transcript variant X6	misc_RNA
NM_001242361.2	NRDC	6.76E-05	4898	Nardilysin convertase, transcript variant 3	mRNA
XM_011542437.2	ZFYVE9	0.0104319	9372	Zinc finger FYVE-type-containing 9, transcript variant X1	mRNA
XM_005270590.2	CC2D1B	7.11E-05	200014	Coiled-coil and C2 domain-containing 1B, transcript variant X1	mRNA
XM_017000559.1	CC2D1B	0.0253262	200014	Coiled-coil and C2 domain-containing 1B, transcript variant X8	mRNA
NM_001305066.2	TMEM59	0.000187923	9528	Transmembrane protein 59, transcript variant 5	mRNA
XM_017000	USP24	0.045986	23358	Ubiquitin-specific peptidase 24, transcript variant X2	mRNA

832.1					
XM_017000832.1	USP24	4.01E-08	23358	Ubiquitin-specific peptidase 24, transcript variant X2	mRNA
XM_017000832.1	USP24	2.87E-07	23358	Ubiquitin-specific peptidase 24, transcript variant X2	mRNA
XM_017000832.1	USP24	0.0139253	23358	Ubiquitin-specific peptidase 24, transcript variant X2	mRNA
XM_017002740.2	FUBP1	3.52E-09	8880	Far upstream element-binding protein 1, transcript variant X5	mRNA
XM_006710802.2	ABCD3	0.00131687	5825	ATP-binding cassette subfamily D member 3, transcript variant X1	mRNA
XM_017000245.2	CNN3	7.11E-05	1266	Calponin 3, transcript variant X1	mRNA
NM_033055.3	MFSD14A	0.00358226	64645	Major facilitator superfamily domain-containing 14A	mRNA
NM_003729.4	RTCA	0.00303624	8634	RNA 3’-terminal phosphate cyclase, transcript variant 2	mRNA
XM_017000	SLC30A7	0.013087	148867	Solute carrier family 30 member 7, transcript variant X4	mRNA

401.2		7			
NM_001010883.3	FAM102B	0.00868541	284611	Family with sequence similarity 102 member B	mRNA
NM_013296.5	GPSM2	0.00054628	29899	G protein signaling modulator 2, transcript variant 3	mRNA
XM_006710589.3	GPSM2	0.0176209	29899	G protein signaling modulator 2, transcript variant X5	mRNA
XM_005271100.2	SORT1	0.0211033	6272	Sortilin 1, transcript variant X1	mRNA
XM_011540535.2	AHCYL1	1.72E-08	10768	Adenosylhomocysteinase-like 1, transcript variant X1	mRNA
XM_011540535.2	AHCYL1	0.000169724	10768	Aenosylhomocysteinase-like 1, transcript variant X1	mRNA
XR_002957854.1	STRIP1	0.0040224	85369	Striatin-interacting protein 1, transcript variant X3	misc_RNA
NR_073071.2	STRIP1	0.00644537	85369	Striatin-interacting protein 1, transcript variant 3	misc_RNA
NM_002884.	RAP1A	0.040914	5906	RAP1A, member of RAS oncogene family, transcript variant 2	mRNA

4					
XR_001737185.2	MOV10	0.00686488	4343	Mov10 RISC complex RNA helicase, transcript variant X6	misc_RNA
NM_002524.5	NRAS	0.0221864	4893	NRAS proto-oncogene, GTPase	mRNA
NM_001242893.2	CSDE1	4.60E-10	7812	Cold shock domain-containing E1, transcript variant 6	mRNA
XM_017001361.1	ATP1A1	0.00926878	476	ATPase Na^+/K^+ transporting subunit α1, transcript variant X2	mRNA
NM_024408.4	NOTCH2	5.39E-10	4853	Notch receptor 2, transcript variant 1	mRNA
NM_024408.4	NOTCH2	2.09E-07	4853	Notch receptor 2, transcript variant 1	mRNA
NM_001200001.2	NOTCH2	0.00339383	4853	Notch receptor 2, transcript variant 2	mRNA
XM_005272971.4	BCL9	0.0185913	607	BCL9 transcription coactivator, transcript variant X1	mRNA
NM_020205.	OTUD7B	0.034207	56957	OTU deubiquitinase 7B	mRNA

4		6			
XM_017001294.1	ARNT	0.045986	405	Aryl hydrocarbon receptor nuclear translocator, transcript variant X13	mRNA
NM_001350226.2	ARNT	0.00476676	405	Aryl hydrocarbon receptor nuclear translocator, transcript variant 9	mRNA
NM_001369624.1	PI4KB	0.000178792	5298	Phosphatidylinositol 4-kinase beta, transcript variant 7	mRNA
XM_005245365.5	CGN	5.78E-08	57530	Cingulin, transcript variant X1	mRNA
XM_005245365.5	CGN	0.000101311	57530	Cingulin, transcript variant X1	mRNA
NM_001367466.1	DENND4B	0.00358226	9909	DENN domain-containing 4B, transcript variant 2	mRNA
XM_011510219.1	DENND4B	3.98E-05	9909	DENN domain-containing 4B, transcript variant X1	mRNA
XM_011510219.1	DENND4B	0.0116648	9909	DENN domain-containing 4B, transcript variant X1	mRNA
XM_024451	UBAP2L	6.74E-06	9898	Ubiquitin-associated protein 2-like, transcript variant X29	mRNA

291.1					
NM_001365045.1	ADAR	0.00103918	103	Adenosine deaminase RNA specific, transcript variant 6	mRNA
NM_001171811.2	GBA	0.0282828	2629	Glucosylceramidase β, transcript variant 4	mRNA
XM_017002797.2	ARHGEF2	0.0282828	9181	Rho/Rac guanine nucleotide exchange factor 2, transcript variant X13	mRNA
NM_001257374.3	LMNA	3.40E-13	4000	Lamin A/C, transcript variant 4	mRNA
XM_024453274.1	IQGAP3	0.040914	128239	IQ motif-containing GTPase-activating protein 3, transcript variant X2	mRNA
XM_011509198.3	IQGAP3	0.048575	128239	IQ motif-containing GTPase-activating protein 3, transcript variant X4	mRNA
NM_006617.2	NES	0.0148488	10763	Nestin	mRNA
NM_001377419.1	ARHGEF11	0.0282828	9826	ρ guanine nucleotide exchange factor 11, transcript variant 4	mRNA
NM_001377	ARHGEF11	0.006074	9826	ρ guanine nucleotide exchange factor 11, transcript variant 4	mRNA

419.1		62			
XM_006711661.3	ARHGEF11	0.012354	9826	ρ guanine nucleotide exchange factor 11, transcript variant X4	mRNA
XM_006711661.3	ARHGEF11	0.0156332	9826	ρ guanine nucleotide exchange factor 11, transcript variant X4	mRNA
NM_001135050.2	IGSF9	0.00110625	57549	Immunoglobulin superfamily member 9, transcript variant 1	mRNA
NR_028103.2	DCAF8	0.0116648	50717	DDB1 and CUL4-associated factor 8, transcript variant 2	misc_RNA
NM_001098398.2	COPA	0.00358226	1314	COPI coat complex subunit α, transcript variant 1	mRNA
NM_004371.4	COPA	1.47E-07	1314	COPI coat complex subunit α, transcript variant 2	mRNA
NM_004550.5	NDUFS2	0.00574795	4720	NADH:ubiquinone oxidoreductase core subunit S2, transcript variant 1	mRNA
XM_011509308.1	ATF6	0.000273438	22926	Activating transcription factor 6, transcript variant X1	mRNA
NM_000696.	ALDH9A1	0.013087	223	Aldehyde dehydrogenase 9 family member A1, transcript variant 1	mRNA

4		7			
NM_000696.4	ALDH9A1	0.000273438	223	Aldehyde dehydrogenase 9 family member A1, transcript variant 1	mRNA
NM_003953.6	MPZL1	4.76E-05	9019	Myelin protein zero like 1, transcript variant 1	mRNA
XM_005245023.2	PRRC2C	4.23E-05	23215	Proline-rich coiled-coil 2C, transcript variant X10	mRNA
NM_014283.5	SUCO	1.92E-05	51430	SUN domain containing ossification factor, transcript variant 1	mRNA
NM_014283.5	SUCO	9.53E-05	51430	SUN domain containing ossification factor, transcript variant 1	mRNA
NM_016227.4	SUCO	0.0116648	51430	SUN domain containing ossification factor, transcript variant 2	mRNA
NM_001365213.2	DARS2	0.0282828	55157	Aspartyl-tRNA synthetase 2, mitochondrial, transcript variant 3	mRNA
NM_172071.4	RC3H1	0.00985934	149041	Ring finger and CCCH-type domains 1, transcript variant 2	mRNA
XM_017001	RALGPS2	0.000338	55103	Ral GEF with PH domain and SH3 binding motif 2, transcript variant X4	mRNA

591.2		213			
XM_017002930.1	CEP350	9.29E-06	9857	Centrosomal protein 350, transcript variant X3	mRNA
NM_001033044.4	GLUL	8.06E-06	2752	Glutamate-ammonia ligase, transcript variant 2	mRNA
NM_001357.5	DHX9	7.43E-08	1660	DExH-box helicase 9, transcript variant 1	mRNA
NM_001357.5	DHX9	3.87E-06	1660	DExH-box helicase 9, transcript variant 1	mRNA
NM_001357.5	DHX9	9.29E-06	1660	DExH-box helicase 9, transcript variant 1	mRNA
NM_002293.4	LAMC1	3.40E-13	3915	Laminin subunit gamma 1	mRNA
XM_017001273.2	LAMC2	0.0040224	3918	Laminin subunit γ2, transcript variant X1	mRNA
NM_018891.3	LAMC2	0.00574795	3918	Laminin subunit γ2, transcript variant 2	mRNA
XM_011510	SMG7	4.60E-10	9887	SMG7 nonsense-mediated mRNA decay factor, transcript variant X1	mRNA

205.3					
NM_003292.3	TPR	0.00148402	7175	Translocated promoter region, nuclear basket protein	mRNA
NM_003292.3	TPR	0.0342076	7175	Translocated promoter region, nuclear basket protein	mRNA
NM_003292.3	TPR	0.00770001	7175	Translocated promoter region, nuclear basket protein	mRNA
XM_017000731.1	KIF21B	0.00103918	23046	Kinesin family member 21B, transcript variant X1	mRNA
XM_011509092.2	KDM5B	6.38E-05	10765	Lysine demethylase 5B, transcript variant X3	mRNA
NM_001365783.2	ATP2B4	0.00985934	493	ATPase plasma membrane Ca2+ transporting 4, transcript variant 3	mRNA
XM_017001474.1	PIK3C2B	0.00770001	5287	Phosphatidylinositol-4-phosphate 3-kinase catalytic subunit type 2β, transcript variant X5	mRNA
XM_005273164.3	PLXNA2	0.0156332	5362	Plexin A2, transcript variant X1	mRNA
XM_005273	PLXNA2	0.012354	5362	Plexin A2, transcript variant X1	mRNA

164.3					
NM_001017402.2	LAMB3	3.69E-06	3914	Laminin subunit β3, transcript variant 2	mRNA
NM_016343.4	CENPF	0.00253827	1063	Centromere protein F	mRNA
XM_017000086.2	CENPF	1.43E-05	1063	Centromere protein F, transcript variant X1	mRNA
NM_004446.3	EPRS1	0.000178792	2058	Glutamyl-prolyl-tRNA synthetase 1	mRNA
NM_018060.4	IARS2	3.40E-13	55699	Isoleucyl-tRNA synthetase 2, mitochondrial	mRNA
NM_018060.4	IARS2	2.16E-07	55699	Isoleucyl-tRNA synthetase 2, mitochondrial	mRNA
XM_011544185.3	LBR	6.38E-05	3930	Lamin B receptor, transcript variant X1	mRNA
NM_001618.4	PARP1	4.80E-10	142	Poly(ADP-ribose) polymerase 1	mRNA
NM_001618.	PARP1	1.42E-06	142	Poly(ADP-ribose) polymerase 1	mRNA

4					
NM_001618.4	PARP1	0.00449729	142	Poly(ADP-ribose) polymerase 1	mRNA
XM_011544238.1	COQ8A	0.0016763	56997	Coenzyme Q8A, transcript variant X3	mRNA
XM_017002580.2	CDC42BPA	3.37E-07	8476	CDC42-binding protein kinase α, transcript variant X14	mRNA
XR_001737299.2	NUP133	0.0081583	55746	Nucleoporin 133, transcript variant X1	misc_RNA
NM_007357.3	COG2	0.0139253	22796	Component of oligomeric golgi complex 2, transcript variant 1	mRNA
NM_001145036.2	COG2	0.0221864	22796	Component of oligomeric golgi complex 2, transcript variant 2	mRNA
NM_001145036.2	COG2	0.00926878	22796	Component of oligomeric golgi complex 2, transcript variant 2	mRNA
NM_018072.6	HEATR1	3.69E-06	55127	HEAT repeat-containing 1	mRNA
NM_018072.	HEATR1	0.018591	55127	HEAT repeat-containing 1	mRNA

6		3			
NM_018072.6	HEATR1	0.00190081	55127	HEAT repeat-containing 1	mRNA
NM_018072.6	HEATR1	0.0156332	55127	HEAT repeat-containing 1	mRNA
NM_001291939.1	MTR	0.00574795	4548	5-Methyltetrahydrofolate-homocysteine methyltransferase, transcript variant 2	mRNA
XM_011544325.2	EXO1	0.0236925	9156	Exonuclease 1, transcript variant X7	mRNA
XM_017002951.2	CEP170	1.35E-06	9859	Centrosomal protein 170, transcript variant X32	mRNA
NM_001322463.1	SH3BP5L	0.0110174	80851	SH3-binding domain protein 5 like, transcript variant 3	mRNA
XM_017015990.1	LARP4B	8.86E-07	23185	La ribonucleoprotein 4B, transcript variant X4	mRNA
NM_001242339.2	PFKP	0.0148488	5214	Phosphofructokinase, platelet, transcript variant 2	mRNA
NM_001323	PFKP	0.000380	5214	Phosphofructokinase, platelet, transcript variant 8	mRNA

072.2		287			
NM_001242339.2	PFKP	6.31E-06	5214	Phosphofructokinase, platelet, transcript variant 2	mRNA
NM_014889.4	PITRM1	0.0319763	10531	Pitrilysin metallopeptidase 1, transcript variant 2	mRNA
NM_001391960.1	USP6NL	0.0211033	9712	USP6 N-terminal-like, transcript variant 5	mRNA
NM_018706.7	DHTKD1	0.000141056	55526	Dehydrogenase E1 and transketolase domain containing 1	mRNA
NM_018706.7	DHTKD1	0.048575	55526	Dehydrogenase E1 and transketolase domain-containing 1	mRNA
NM_001324287.2	STAM	0.0221864	8027	Signal transducing adaptor molecule, transcript variant 2	mRNA
XM_017016536.2	DNAJC1	0.0433858	64215	DnaJ heat shock protein family 40 member C1, transcript variant X2	mRNA
NM_005180.9	BMI1	0.00253827	648	BMI1 proto-oncogene, polycomb ring finger	mRNA
NM_001282	KIAA1217	0.000425	56243	KIAA1217, transcript variant 4	mRNA

767.2		096			
NM_001253866.2	YME1L1	0.0037981	10730	YME1-like 1 ATPase, transcript variant 4	mRNA
NM_001253866.2	YME1L1	1.52E-05	10730	YME1-like 1 ATPase, transcript variant 4	mRNA
XM_024448146.1	SVIL	0.00770001	6840	Supervillin, transcript variant X14	mRNA
NM_004521.3	KIF5B	0.0148488	3799	Kinesin family member 5B	mRNA
NM_002211.4	ITGB1	3.40E-13	3688	Integrin subunit β1, transcript variant 1A	mRNA
NM_020987.5	ANK3	4.23E-05	288	Ankyrin 3, transcript variant 1	mRNA
NM_001322366.1	HK1	0.0433858	3098	Hexokinase 1, transcript variant 8	mRNA
NM_004096.5	EIF4EBP2	0.00644537	1979	Eukaryotic translation initiation factor 4E-binding protein 2	mRNA
NM_001320	ANXA7	0.003216	310	Annexin A7, transcript variant 3	mRNA

880.2		51			
NM_014000.3	VCL	0.000338213	7414	Vinculin, transcript variant 1	mRNA
XM_011540346.2	DLG5	7.51E-05	9231	Discs large MAGUK scaffold protein 5, transcript variant X8	mRNA
XM_017016913.1	DLG5	5.04E-05	9231	Discs large MAGUK scaffold protein 5, transcript variant X4	mRNA
NM_007055.4	POLR3A	0.00686488	11128	RNA polymerase III subunit A	mRNA
NM_001377163.1	SHLD2	0.0282828	54537	Shieldin complex subunit 2, transcript variant 8	mRNA
NM_004523.4	KIF11	0.000242029	3832	Kinesin family member 11	mRNA
XM_017016069.1	MYOF	3.40E-13	26509	Myoferlin, transcript variant X5	mRNA
XM_017016069.1	MYOF	0.00131687	26509	Myoferlin, transcript variant X5	mRNA
XM_017016	MYOF	3.40E-13	26509	Myoferlin, transcript variant X5	mRNA

069.1					
XM_011539632.2	MYOF	0.0081583	26509	Myoferlin, transcript variant X3	mRNA
NM_001289069.2	HELLS	0.000358192	3070	Helicase, lymphoid-specific, transcript variant 4	mRNA
NM_020992.4	PDLIM1	0.0221864	9124	PDZ and LIM domain 1	mRNA
NM_015631.6	TCTN3	0.00098721	26123	Tectonic family member 3, transcript variant 1	mRNA
NM_002079.3	GOT1	1.94E-08	2805	Glutamic-oxaloacetic transaminase 1	mRNA
NM_001347858.2	ERLIN1	0.0156332	10613	ER lipid raft associated 1, transcript variant 8	mRNA
NM_001320928.2	CHUK	0.048575	1147	Component of inhibitor of nuclear factor κB kinase complex, transcript variant 2	mRNA
NM_001391927.1	GBF1	0.00686488	8729	Golgi brefeldin A resistant guanine nucleotide exchange factor 1, transcript variant 19	mRNA
NM_014720.	SLK	0.040914	9748	STE20-like kinase, transcript variant 1	mRNA

4					
NM_014720.4	SLK	0.00201629	9748	STE20-like kinase, transcript variant 1	mRNA
XM_024447797.1	ADD3	3.40E-13	120	Adducin 3, transcript variant X4	mRNA
NM_005445.4	SMC3	0.000777792	9126	Structural maintenance of chromosomes 3	mRNA
NM_001351086.2	ZDHHC6	0.000822568	64429	Zinc finger DHHC-type palmitoyltransferase 6, transcript variant 7	mRNA
XM_017016763.1	CASP7	0.0385333	840	Caspase 7, transcript variant X1	mRNA
NM_001135051.2	FHIP2A	1.28E-06	57700	FHF complex subunit HOOK interacting protein 2A, transcript variant 2	mRNA
NM_003750.4	EIF3A	2.43E-07	8661	Eukaryotic translation initiation factor 3 subunit A	mRNA
NM_001256378.2	MCMBP	9.53E-05	79892	Minichromosome maintenance complex binding protein, transcript variant 2	mRNA
XM_017016	MCMBP	1.43E-05	79892	Minichromosome maintenance complex binding protein, transcript variant X2	mRNA

663.1					
XM_017016663.1	MCMBP	3.05E-06	79892	Minichromosome maintenance complex binding protein, transcript variant X2	mRNA
XM_011539410.3	DMBT1	0.0198244	1755	Deleted in malignant brain tumors 1, transcript variant X22	mRNA
NM_001322974.2	OAT	3.40E-13	4942	Ornithine aminotransferase, transcript variant 10	mRNA
NM_001377546.1	DOCK1	0.00607462	1793	Dedicator of cytokinesis 1, transcript variant 5	mRNA
NM_001290223.2	DOCK1	0.00321651	1793	Dedicator of cytokinesis 1, transcript variant 1	mRNA
NM_002417.5	MKI67	3.00E-08	4288	Marker of proliferation Ki-67, transcript variant 1	mRNA
XR_002957107.1	LOC112268067	0.0110174	112268067	Uncharacterized LOC112268067	lnc_RNA
NM_006659.4	TUBGCP2	0.048575	10844	Tubulin γ complex-associated protein 2, transcript variant 2	mRNA
NM_001286	PHRF1	0.000822	57661	PHD and ring finger domains 1, transcript variant 4	mRNA

583.2		568			
XM_011519930.3	AP2A2	3.40E-13	161	Adaptor-related protein complex 2 subunit α2, transcript variant X2	mRNA
NM_004420.3	DUSP8	0.0104319	1850	Dual specificity phosphatase 8	mRNA
XM_024448705.1	CARS1	8.96E-06	833	Cysteinyl-tRNA synthetase 1, transcript variant X11	mRNA
NM_001318065.1	RRM1	0.012354	6240	Ribonucleotide reductase catalytic subunit M1, transcript variant 3	mRNA
NM_001033.5	RRM1	0.0385333	6240	Ribonucleotide reductase catalytic subunit M1, transcript variant 1	mRNA
NM_001286094.2	TMEM9B	0.0221864	56674	TMEM9 domain family member B, transcript variant 2	mRNA
XM_017018375.2	SBF2	0.00110625	81846	SET binding factor 2, transcript variant X7	mRNA
NM_001418.4	EIF4G2	0.00339383	1982	Eukaryotic translation initiation factor 4 γ2, transcript variant 1	mRNA
NM_016451.	COPB1	2.16E-07	1315	COPI coat complex subunit β1, transcript variant 1	mRNA

5					
NM_001144061.2	COPB1	0.00253827	1315	COPI coat complex subunit β1, transcript variant 2	mRNA
NM_016451.5	COPB1	0.0198244	1315	COPI coat complex subunit β1, transcript variant 1	mRNA
NM_001321380.2	PIK3C2A	0.00868541	5286	Phosphatidylinositol-4-phosphate 3-kinase catalytic subunit type 2 α, transcript variant 3	mRNA
XM_017018520.2	NAV2	0.000323968	89797	Neuron navigator 2, transcript variant X9	mRNA
NM_006360.6	EIF3M	0.00040024	10480	Eukaryotic translation initiation factor 3 subunit M, transcript variant 1	mRNA
XR_002957197.1	QSER1	0.0037981	79832	Glutamine and serine-rich 1, transcript variant X5	misc_RNA
NM_001278162.2	HIPK3	0.0433858	10114	Homeodomain interacting protein kinase 3, transcript variant 2	mRNA
NM_145804.3	ABTB2	0.00574795	25841	Ankyrin repeat and BTB domain containing 2	mRNA
NM_001389	EXT2	0.000618	2132	Exostosin glycosyltransferase 2, transcript variant 4	mRNA

628.1		347			
NM_052854.4	CREB3L1	0.0166276	90993	cAMP responsive element binding protein 3 like 1	mRNA
NM_001008938.4	CKAP5	1.94E-06	9793	Cytoskeleton associated protein 5, transcript variant 1	mRNA
NM_014756.4	CKAP5	0.00283312	9793	Cytoskeleton associated protein 5, transcript variant 2	mRNA
NM_014756.4	CKAP5	0.000358192	9793	Cytoskeleton associated protein 5, transcript variant 2	mRNA
XM_011520103.2	LRP4	0.00770001	4038	LDL receptor related protein 4, transcript variant X2	mRNA
XR_001747908.2	ACP2	0.0433858	53	Acid phosphatase 2, lysosomal, transcript variant X1	misc_RNA
NM_001376648.1	MADD	0.00213581	8567	MAP kinase activating death domain, transcript variant 82	mRNA
XM_017017105.2	CELF1	7.59E-06	10658	CUGBP Elav-like family member 1, transcript variant X5	mRNA
XM_017017	CELF1	0.000118	10658	CUGBP Elav-like family member 1, transcript variant X5	mRNA

105.2		363			
NM_015231.2	NUP160	0.048575	23279	Nucleoporin 160, transcript variant 1	mRNA
NR_134636.3	NUP160	0.00131687	23279	Nucleoporin 160, transcript variant 3	misc_RNA
XM_017018085.1	PTPRJ	0.00321651	5795	Protein tyrosine phosphatase receptor type J, transcript variant X3	mRNA
XM_006718725.3	TNKS1BP1	0.0185913	85456	Tankyrase 1 binding protein 1, transcript variant X1	mRNA
NR_037646.1	TMX2-CTNND1	3.40E-13	100528016	TMX2-CTNND1 readthrough (NMD candidate)	lnc_RNA
NM_001206885.2	CTNND1	0.00770001	1500	Catenin Δ1, transcript variant 16	mRNA
NM_001331.3	CTNND1	0.0319763	1500	Catenin Δ1, transcript variant 3	mRNA
NM_002556.3	OSBP	0.00116938	5007	Oxysterol-binding protein	mRNA
NM_152716.	PATL1	0.031976	219988	PAT1 homolog 1, processing body mRNA decay factor	mRNA

3		3			
NM_001923.5	DDB1	6.01E-05	1642	Damage-specific DNA-binding protein 1	mRNA
NM_001923.5	DDB1	3.40E-13	1642	Damage-specific DNA-binding protein 1	mRNA
NM_001923.5	DDB1	2.02E-05	1642	Damage-specific DNA-binding protein 1	mRNA
NM_001923.5	DDB1	2.40E-06	1642	Damage-specific DNA-binding protein 1	mRNA
NM_153611.6	CYB561A3	0.048575	220002	Cytochrome b561 family member A3, transcript variant 2	mRNA
NM_020238.3	INCENP	0.0176209	3619	Inner centromere protein, transcript variant 2	mRNA
NR_037946.1	HNRNPUL2-BSCL2	0.0110174	100534595	HNRNPUL2-BSCL2 readthrough (NMD candidate)	lnc_RNA
XR_001747724.2	NXF1	0.0221864	10482	Nuclear RNA export factor 1, transcript variant X1	misc_RNA
XM_011545	PLCB3	4.47E-05	5331	Phospholipase C beta 3, transcript variant X1	mRNA

101.2					
XM_011545101.2	PLCB3	0.048575	5331	Phospholipase C beta 3, transcript variant X1	mRNA
XM_011544866.2	ATG2A	0.0110174	23130	Autophagy-related 2A, transcript variant X6	mRNA
XM_011544867.3	ATG2A	1.21E-05	23130	Autophagy-related 2A, transcript variant X8	mRNA
XM_011545345.2	SART1	0.00253827	9092	Spliceosome-associated factor 1, recruiter of U4/U6.U5 tri-snRNP, transcript variant X2	mRNA
XM_011544740.3	SF3B2	5.01E-06	10992	Splicing factor 3b subunit 2, transcript variant X2	mRNA
NM_001256670.2	DPP3	2.43E-05	10072	Dipeptidyl peptidase 3, transcript variant 3	mRNA
NM_001256670.2	DPP3	3.15E-08	10072	Dipeptidyl peptidase 3, transcript variant 3	mRNA
XR_002957210.1	PITPNM1	0.00253827	9600	Phosphatidylinositol transfer protein membrane associated 1, transcript variant X4	misc_RNA
XR_0029572	PITPNM1	0.000125	9600	Phosphatidylinositol transfer protein membrane-associated 1, transcript variant X4	misc_R

10.1		229			NA
XM_005273994.2	LRP5	4.80E-10	4041	LDL receptor related protein 5, transcript variant X2	mRNA
NM_001876.4	CPT1A	0.0116648	1374	Carnitine palmitoyltransferase 1A, transcript variant 1	mRNA
XM_011545306.3	PPFIA1	0.00926878	8500	PTPRF interacting protein alpha 1, transcript variant X2	mRNA
XM_011545065.2	NUMA1	0.000338213	4926	Nuclear mitotic apparatus protein 1, transcript variant X13	mRNA
NR_161388.1	ARAP1	0.00425539	116985	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 1, transcript variant 6	misc_RNA
NR_161388.1	ARAP1	0.0221864	116985	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 1, transcript variant 6	misc_RNA
NM_014786.4	ARHGEF17	0.0037981	9828	ρ guanine nucleotide exchange factor 17	mRNA
NM_014752.3	SPCS2	0.045986	9789	Signal peptidase complex subunit 2	mRNA
XM_006718	AMOTL1	0.022186	154810	Angiomotin like-1, transcript variant X4	mRNA

772.3		4			
XM_024448598.1	PPP2R1B	0.0319763	5519	Protein phosphatase 2 scaffold subunit Aβ, transcript variant X1	mRNA
NM_001372041.1	DLAT	0.0236925	1737	Dihydrolipoamide S-acetyltransferase, transcript variant 12	mRNA
XR_428984.4	PCSK7	0.040914	9159	Proprotein convertase subtilisin/kexin type 7, transcript variant X3	misc_RNA
NM_001244995.2	TMPRSS13	0.0176209	84000	Transmembrane serine protease 13, transcript variant 4	mRNA
NM_004788.4	UBE4A	0.0116648	9354	Ubiquitination factor E4A, transcript variant 1	mRNA
XM_011542831.2	KMT2A	3.87E-06	4297	Lysine methyltransferase 2A, transcript variant X3	mRNA
XM_011542831.2	KMT2A	0.000695991	4297	Lysine methyltransferase 2A, transcript variant X3	mRNA
NM_001164280.2	SLC37A4	0.0268866	2542	Solute carrier family 37 member 4, transcript variant 5	mRNA
NM_005188.	CBL	0.013087	867	Cbl proto-oncogene	mRNA

4		7			
XM_011542720.2	ARHGEF12	0.00985934	23365	ρ guanine nucleotide exchange factor 12, transcript variant X1	mRNA
NM_003105.6	SORL1	0.0385333	6653	Sortilin related receptor 1	mRNA
NM_003105.6	SORL1	1.52E-05	6653	Sortilin related receptor 1	mRNA
NM_003105.6	SORL1	4.80E-10	6653	Sortilin related receptor 1	mRNA
NM_003105.6	SORL1	0.0130877	6653	Sortilin related receptor 1	mRNA
NR_033839.1	GSEC	0.0300443	399972	G-quadruplex forming sequence containing lncRNA	lnc_RNA
XM_011543075.2	ARHGAP32	0.000307575	9743	ρ GTPase activating protein 32, transcript variant X6	mRNA
XM_011543075.2	ARHGAP32	0.048575	9743	ρ GTPase activating protein 32, transcript variant X6	mRNA
XM_017017	NFRKB	0.004766	4798	Nuclear factor related to κB binding protein, transcript variant X1	mRNA

793.2		76			
NR_168393.1	APLP2	0.0300443	334	Amyloid β precursor-like protein 2, transcript variant 38	misc_RNA
NM_021978.4	ST14	0.00644537	6768	ST14 transmembrane serine protease matriptase	mRNA
NM_021978.4	ST14	1.80E-05	6768	ST14 transmembrane serine protease matriptase	mRNA
NM_001372065.1	NCAPD3	0.00358226	23310	Non-SMC condensin II complex subunit D3, transcript variant 3	mRNA
NM_015261.3	NCAPD3	0.00686488	23310	Non-SMC condensin II complex subunit D3, transcript variant 1	mRNA
NM_173593.4	B4GALNT3	0.0081583	283358	β-1,4-N-acetyl-galactosaminyltransferase 3	mRNA
XM_011521008.2	WNK1	5.95E-06	65125	WNK lysine deficient protein kinase 1, transcript variant X18	mRNA
XM_011520912.3	TSPAN9	0.048575	10867	Tetraspanin 9, transcript variant X1	mRNA
XM_006718	PLEKHG6	0.000987	55200	Pleckstrin homology and RhoGEF domain containing G6, transcript variant X3	mRNA

985.3		21			
NM_002342.3	LTBR	2.16E-07	4055	Lymphotoxin β receptor, transcript variant 1	mRNA
NM_014865.4	NCAPD2	3.56E-06	9918	Non-SMC condensin I complex subunit D2	mRNA
NM_014865.4	NCAPD2	0.0185913	9918	Non-SMC condensin I complex subunit D2	mRNA
NM_014718.4	CLSTN3	0.012354	9746	Calsyntenin 3	mRNA
XM_011520600.2	PHC1	8.56E-06	1911	Polyhomeotic homolog 1, transcript variant X4	mRNA
XM_011520603.2	PHC1	0.0385333	1911	Polyhomeotic homolog 1, transcript variant X8	mRNA
NM_001025356.3	ANO6	1.72E-07	196527	Anoctamin 6, transcript variant 1	mRNA
NM_001278390.1	SLC38A1	0.0110174	81539	Solute carrier family 38 member 1, transcript variant 6	mRNA
XM_024448	ARF3	0.001786	377	ADP ribosylation factor 3, transcript variant X1	mRNA

972.1		4			
XM_011538773.2	KMT2D	1.64E-06	8085	Lysine methyltransferase 2D, transcript variant X4	mRNA
XM_011538773.2	KMT2D	5.12E-08	8085	Lysine methyltransferase 2D, transcript variant X4	mRNA
XM_011538773.2	KMT2D	0.00985934	8085	Lysine methyltransferase 2D, transcript variant X4	mRNA
XM_011538773.2	KMT2D	0.0116648	8085	Lysine methyltransferase 2D, transcript variant X4	mRNA
XM_017019225.2	RACGAP1	0.00926878	29127	Rac GTPase activating protein 1, transcript variant X8	mRNA
NM_173602.3	DIP2B	0.000822568	57609	Disco interacting protein 2 homolog B	mRNA
NM_173602.3	DIP2B	0.0211033	57609	Disco interacting protein 2 homolog B	mRNA
XM_006719214.2	GALNT6	0.00116938	11226	polypeptide N-acetylgalactosaminyltransferase 6, transcript variant X10	mRNA
XM_011539	ESPL1	0.007286	9700	extra spindle pole bodies like 1, separase, transcript variant X2	mRNA

024.2		68			
NM_002205.5	ITGA5	2.30E-05	3678	integrin subunit alpha 5	mRNA
NM_001982.4	ERBB3	0.00157844	2065	erb-b2 receptor tyrosine kinase 3, transcript variant 1	mRNA
XM_011537803.2	BAZ2A	3.87E-06	11176	bromodomain adjacent to zinc finger domain 2A, transcript variant X4	mRNA
XM_017019303.1	LRP1	0.0116648	4035	LDL receptor related protein 1, transcript variant X1	mRNA
XM_017019303.1	LRP1	6.76E-05	4035	LDL receptor related protein 1, transcript variant X1	mRNA
XM_017019303.1	LRP1	0.000581772	4035	LDL receptor related protein 1, transcript variant X1	mRNA
XM_017019303.1	LRP1	0.00131687	4035	LDL receptor related protein 1, transcript variant X1	mRNA
XM_017019303.1	LRP1	1.01E-08	4035	LDL receptor related protein 1, transcript variant X1	mRNA
NM_002332.	LRP1	0.005747	4035	LDL receptor related protein 1	mRNA

3		95			
XM_017019303.1	LRP1	0.000931169	4035	LDL receptor related protein 1, transcript variant X1	mRNA
NM_001351212.2	R3HDM2	0.00283312	22864	R3H domain containing 2, transcript variant 12	mRNA
XR_002957327.1	MARS1	7.63E-09	4141	methionyl-tRNA synthetase 1, transcript variant X2	misc_RNA
XR_944484.3	XPOT	0.00157844	11260	exportin for tRNA, transcript variant X2	misc_RNA
NM_002076.4	GNS	9.29E-06	2799	glucosamine (N-acetyl)-6-sulfatase	mRNA
NM_001282610.2	TMBIM4	5.31E-06	51643	transmembrane BAX inhibitor motif containing 4, transcript variant 4	mRNA
NM_001278354.2	FRS2	0.0385333	10818	fibroblast growth factor receptor substrate 2, transcript variant 5	mRNA
XR_001748703.2	LTA4H	0.0040224	4048	leukotriene A4 hydrolase, transcript variant X3	misc_RNA
NM_001317	SCYL2	3.23E-06	55681	SCY1 like pseudokinase 2, transcript variant 2	mRNA

784.2					
XM_005269004.2	DRAM1	0.0236925	55332	DNA damage regulated autophagy modulator 1, transcript variant X1	mRNA
NM_001363612.2	TDG	0.000482835	6996	thymine DNA glycosylase, transcript variant 2	mRNA
XM_005268593.1	PRDM4	0.0166276	11108	PR/SET domain 4, transcript variant X1	mRNA
NM_014706.4	SART3	6.76E-05	9733	spliceosome associated factor 3, U4/U6 recycling protein	mRNA
XM_006719682.2	UBE3B	0.048575	89910	ubiquitin protein ligase E3B, transcript variant X4	mRNA
XM_005253980.3	ANKRD13A	0.0026633	88455	ankyrin repeat domain 13A, transcript variant X1	mRNA
XM_017019394.1	GPN3	0.00770001	51184	GPN-loop GTPase 3, transcript variant X1	mRNA
XM_024448869.1	PPTC7	0.0198244	160760	protein phosphatase targeting COQ7, transcript variant X1	mRNA
XM_017019	NAA25	0.000125	80018	N-alpha-acetyltransferase 25, NatB auxiliary subunit, transcript variant X3	mRNA

977.1		229			
NM_001388303.1	HECTD4	0.00425539	283450	HECT domain E3 ubiquitin protein ligase 4, transcript variant 2	mRNA
NM_001388303.1	HECTD4	2.03E-06	283450	HECT domain E3 ubiquitin protein ligase 4, transcript variant 2	mRNA
NM_001388303.1	HECTD4	0.0114449	283450	HECT domain E3 ubiquitin protein ligase 4, transcript variant 2	mRNA
NM_001388303.1	HECTD4	0.0211033	283450	HECT domain E3 ubiquitin protein ligase 4, transcript variant 2	mRNA
NM_001388303.1	HECTD4	0.00574795	283450	HECT domain E3 ubiquitin protein ligase 4, transcript variant 2	mRNA
NM_080601.3	PTPN11	3.40E-13	5781	protein tyrosine phosphatase non-receptor type 11, transcript variant 2	mRNA
NM_006187.4	OAS3	2.60E-05	4940	2'-5'-oligoadenylate synthetase 3	mRNA
NM_173542.4	PLBD2	0.00240192	196463	phospholipase B domain containing 2, transcript variant 1	mRNA
XM_011538	MED13L	0.008685	23389	mediator complex subunit 13L, transcript variant X3	mRNA

082.2		41			
XM_017018736.1	CIT	0.0268866	11113	citron rho-interacting serine/threonine kinase, transcript variant X5	mRNA
NM_006836.2	GCN1	0.048575	10985	GCN1 activator of EIF2AK4	mRNA
NM_001002.4	RPLP0	3.40E-13	6175	ribosomal protein lateral stalk subunit P0, transcript variant 1	mRNA
XM_011537925.2	SPPL3	4.78E-09	121665	signal peptide peptidase like 3, transcript variant X1	mRNA
XM_011538875.3	KDM2B	0.000452538	84678	lysine demethylase 2B, transcript variant X6	mRNA
NM_018183.5	SBNO1	0.00227362	55206	strawberry notch homolog 1, transcript variant 2	mRNA
NM_001167856.3	SBNO1	2.09E-07	55206	strawberry notch homolog 1, transcript variant 1	mRNA
NM_001167856.3	SBNO1	0.000118363	55206	strawberry notch homolog 1, transcript variant 1	mRNA
NM_006312.	NCOR2	0.000118	9612	nuclear receptor corepressor 2, transcript variant 1	mRNA

6		363			
NR_160422.1	SCARB1	4.47E-05	949	scavenger receptor class B member 1, transcript variant 18	misc_RNA
XR_001748820.1	DHX37	0.00339383	57647	DEAH-box helicase 37, transcript variant X4	misc_RNA
XM_017020737.1	ZMYM2	0.00201629	7750	zinc finger MYM-type containing 2, transcript variant X12	mRNA
XM_017020737.1	ZMYM2	0.00190081	7750	zinc finger MYM-type containing 2, transcript variant X12	mRNA
NM_022459.5	XPO4	0.0342076	64328	exportin 4, transcript variant 1	mRNA
NM_006437.4	PARP4	4.47E-05	143	poly(ADP-ribose) polymerase family member 4	mRNA
XM_011534931.1	PARP4	0.000257885	143	poly(ADP-ribose) polymerase family member 4, transcript variant X1	mRNA
NM_006644.4	HSPH1	0.000105814	10808	heat shock protein family H (Hsp110) member 1, transcript variant 1	mRNA
NM_001012	NHLRC3	0.013925	387921	NHL repeat containing 3, transcript variant 1	mRNA

754.4		3			
XM_011535171.2	RB1	2.02E-05	5925	RB transcriptional corepressor 1, transcript variant X1	mRNA
XM_011535135.2	RCBTB1	0.0282828	55213	RCC1 and BTB domain containing protein 1, transcript variant X2	mRNA
XM_011535135.2	RCBTB1	0.0156332	55213	RCC1 and BTB domain containing protein 1, transcript variant X2	mRNA
NM_001322349.2	DIS3	0.000169724	22894	DIS3 homolog, exosome endoribonuclease and 3'-5' exoribonuclease, transcript variant 4	mRNA
XM_006719785.3	MYCBP2	0.000777792	23077	MYC binding protein 2, transcript variant X10	mRNA
XM_017020464.2	MYCBP2	0.000290692	23077	MYC binding protein 2, transcript variant X23	mRNA
XM_011535185.3	RBM26	0.00425539	64062	RNA binding motif protein 26, transcript variant X13	mRNA
XM_005254053.3	IPO5	0.00148402	3843	importin 5, transcript variant X7	mRNA
NM_001366	DOCK9	0.000380	23348	dedicator of cytokinesis 9, transcript variant 14	mRNA

684.2		287			
NM_001366684.2	DOCK9	0.040914	23348	dedicator of cytokinesis 9, transcript variant 14	mRNA
XM_005254070.2	TPP2	0.0385333	7174	tripeptidyl peptidase 2, transcript variant X1	mRNA
NM_001354940.2	CUL4A	0.0026633	8451	cullin 4A, transcript variant 7	mRNA
NM_138376.3	TTC5	0.0282828	91875	tetratricopeptide repeat domain 5	mRNA
XR_001750531.1	TEP1	0.00728668	7011	telomerase associated protein 1, transcript variant X2	misc_RNA
NM_007110.5	TEP1	0.0037981	7011	telomerase associated protein 1, transcript variant 1	mRNA
NM_001170629.2	CHD8	0.0130877	57680	chromodomain helicase DNA binding protein 8, transcript variant 1	mRNA
NM_020920.4	CHD8	6.01E-05	57680	chromodomain helicase DNA binding protein 8, transcript variant 2	mRNA
NM_004995.	MMP14	0.002135	4323	matrix metallopeptidase 14	mRNA

4		81			
XM_011536526.2	NOP9	0.0433858	161424	NOP9 nucleolar protein, transcript variant X2	mRNA
XM_024449526.1	HECTD1	0.0364492	25831	HECT domain E3 ubiquitin protein ligase 1, transcript variant X2	mRNA
NM_015473.4	HEATR5A	0.0040224	25938	HEAT repeat containing 5A	mRNA
XM_006720099.3	RALGAPA1	0.040914	253959	Ral GTPase activating protein catalytic subunit alpha 1, transcript variant X2	mRNA
XM_005267262.2	SEC23A	0.000105814	10484	SEC23 homolog A, COPII coat complex component, transcript variant X1	mRNA
NM_001354139.2	MIA2	0.00574795	4253	MIA SH3 domain ER export factor 2, transcript variant 12	mRNA
NM_001008396.3	WDHD1	0.0319763	11169	WD repeat and HMG-box DNA binding protein 1, transcript variant 2	mRNA
XM_017021840.2	DLGAP5	0.0026633	9787	DLG associated protein 5, transcript variant X1	mRNA
NR_073128.	KTN1	0.000740	3895	kinectin 1, transcript variant 6	misc_R

1		067			NA
XM_006720138.2	KTN1	0.0104319	3895	kinectin 1, transcript variant X1	mRNA
XR_943916.3	PCNX4-DT	0.00607462	105370524	PCNX4 divergent transcript, transcript variant X1	lnc_RNA
XM_005267458.1	SYNE2	0.00116938	23224	spectrin repeat containing nuclear envelope protein 2, transcript variant X14	mRNA
XM_005267458.1	SYNE2	0.045986	23224	spectrin repeat containing nuclear envelope protein 2, transcript variant X14	mRNA
XM_005267458.1	SYNE2	0.00476676	23224	spectrin repeat containing nuclear envelope protein 2, transcript variant X14	mRNA
NM_005956.4	MTHFD1	8.06E-06	4522	methylenetetrahydrofolate dehydrogenase, cyclohydrolase and formyltetrahydrofolate synthetase 1, transcript variant 1	mRNA
XM_017021156.2	PLEKHG3	7.11E-06	26030	pleckstrin homology and RhoGEF domain containing G3, transcript variant X7	mRNA
XM_011537265.2	ACTN1	1.90E-07	87	actinin alpha 1, transcript variant X7	mRNA
XM_017021	ACTN1	0.001484	87	actinin alpha 1, transcript variant X2	mRNA

721.2		02			
NM_014734.4	SUSD6	0.00213581	9766	sushi domain containing 6	mRNA
XM_017021097.1	PCNX1	0.000118363	22990	pecanex 1, transcript variant X13	mRNA
NM_001367710.1	MIDEAS	0.0104319	91748	mitotic deacetylase associated SANT domain protein, transcript variant 3	mRNA
NM_001043318.3	MIDEAS	0.000105814	91748	mitotic deacetylase associated SANT domain protein, transcript variant 2	mRNA
XM_006720344.3	AREL1	0.00644537	9870	apoptosis resistant E3 ubiquitin protein ligase 1, transcript variant X2	mRNA
NM_001329238.2	NEK9	0.0116648	91754	NIMA related kinase 9, transcript variant 3	mRNA
NM_005065.6	SEL1L	0.00868541	6400	SEL1L adaptor subunit of ERAD E3 ubiquitin ligase, transcript variant 1	mRNA
XM_005267988.3	SEL1L	0.0385333	6400	SEL1L adaptor subunit of ERAD E3 ubiquitin ligase, transcript variant X1	mRNA
XM_005267	SEL1L	0.011017	6400	SEL1L adaptor subunit of ERAD E3 ubiquitin ligase, transcript variant X1	mRNA

988.3		4			
XM_005267989.4	SEL1L	0.00728668	6400	SEL1L adaptor subunit of ERAD E3 ubiquitin ligase, transcript variant X2	mRNA
NM_001326296.2	ZC3H14	0.000931169	79882	zinc finger CCCH-type containing 14, transcript variant 8	mRNA
NM_001128595.3	TC2N	0.000618347	123036	tandem C2 domains, nuclear, transcript variant 2	mRNA
XM_011536939.2	BTBD7	8.48E-05	55727	BTB domain containing 7, transcript variant X1	mRNA
NM_001195573.1	DICER1	0.0385333	23405	dicer 1, ribonuclease III, transcript variant 3	mRNA
XM_017021122.2	DICER1	0.00449729	23405	dicer 1, ribonuclease III, transcript variant X7	mRNA
NM_018036.7	ATG2B	0.0364492	55102	autophagy related 2B	mRNA
NM_001376.5	DYNC1H1	3.23E-06	1778	dynein cytoplasmic 1 heavy chain 1	mRNA
NM_001376.	DYNC1H1	5.31E-06	1778	dynein cytoplasmic 1 heavy chain 1	mRNA

5					
NM_001376.5	DYNC1H1	0.0253262	1778	dynein cytoplasmic 1 heavy chain 1	mRNA
NM_001376.5	DYNC1H1	3.40E-13	1778	dynein cytoplasmic 1 heavy chain 1	mRNA
NM_001394840.1	KLC1	0.00425539	3831	kinesin light chain 1, transcript variant 12	mRNA
NM_001382433.1	AKT1	0.0198244	207	AKT serine/threonine kinase 1, transcript variant 7	mRNA
NM_001350929.2	AHNAK2	7.51E-05	113146	AHNAK nucleoprotein 2, transcript variant 2	mRNA
NM_001324122.3	CYFIP1	0.000133274	23191	cytoplasmic FMR1 interacting protein 1, transcript variant 9	mRNA
NM_001324122.3	CYFIP1	3.40E-13	23191	cytoplasmic FMR1 interacting protein 1, transcript variant 9	mRNA
NM_001324122.3	CYFIP1	1.49E-09	23191	cytoplasmic FMR1 interacting protein 1, transcript variant 9	mRNA
NM_001324	CYFIP1	1.64E-07	23191	cytoplasmic FMR1 interacting protein 1, transcript variant 9	mRNA

122.3					
NM_001324119.2	CYFIP1	0.0185913	23191	cytoplasmic FMR1 interacting protein 1, transcript variant 5	mRNA
NM_004667.6	HERC2	1.90E-07	8924	HECT and RLD domain containing E3 ubiquitin protein ligase 2	mRNA
XM_005268276.5	HERC2	0.0026633	8924	HECT and RLD domain containing E3 ubiquitin protein ligase 2, transcript variant X3	mRNA
XM_005268276.5	HERC2	0.0166276	8924	HECT and RLD domain containing E3 ubiquitin protein ligase 2, transcript variant X3	mRNA
NM_004667.6	HERC2	0.00110625	8924	HECT and RLD domain containing E3 ubiquitin protein ligase 2	mRNA
NM_004667.6	HERC2	0.000212686	8924	HECT and RLD domain containing E3 ubiquitin protein ligase 2	mRNA
NM_199357.3	ARHGAP11A	0.00157844	9824	Rho GTPase activating protein 11A, transcript variant 2	mRNA
NM_020154.3	EMC7	0.000118363	56851	ER membrane protein complex subunit 7	mRNA
NM_014691.	AQR	0.008685	9716	aquarius intron-binding spliceosomal factor	mRNA

3		41			
NM_001013703.4	EIF2AK4	3.69E-06	440275	eukaryotic translation initiation factor 2 alpha kinase 4	mRNA
NM_001013703.4	EIF2AK4	0.00201629	440275	eukaryotic translation initiation factor 2 alpha kinase 4	mRNA
NR_152822.1	OIP5-AS1	0.000777792	729082	OIP5 antisense RNA 1, transcript variant 4	lnc_RNA
NM_153260.3	LRRC57	0.0148488	255252	leucine rich repeat containing 57	mRNA
XM_011521986.3	TP53BP1	0.00644537	7158	tumor protein p53 binding protein 1, transcript variant X3	mRNA
XM_005254722.3	SPPL2A	1.64E-06	84888	signal peptide peptidase like 2A, transcript variant X1	mRNA
NM_014547.5	TMOD3	0.00971563	29766	tropomodulin 3	mRNA
XM_005254537.3	MAPK6	0.0364492	5597	mitogen-activated protein kinase 6, transcript variant X1	mRNA
NM_001018	ICE2	0.021103	79664	interactor of little elongation complex ELL subunit 2, transcript variant 2	mRNA

089.3		3			
NM_018080.4	VPS13C	0.000178792	54832	vacuolar protein sorting 13 homolog C, transcript variant 1B	mRNA
NM_018080.4	VPS13C	0.0433858	54832	vacuolar protein sorting 13 homolog C, transcript variant 1B	mRNA
NM_018080.4	VPS13C	0.00103918	54832	vacuolar protein sorting 13 homolog C, transcript variant 1B	mRNA
XR_001751332.1	VPS13C	0.0166276	54832	vacuolar protein sorting 13 homolog C, transcript variant X1	misc_RNA
NM_018080.4	VPS13C	0.00770001	54832	vacuolar protein sorting 13 homolog C, transcript variant 1B	mRNA
NM_018080.4	VPS13C	0.0253262	54832	vacuolar protein sorting 13 homolog C, transcript variant 1B	mRNA
XM_017022666.1	TLN2	0.00131687	83660	talin 2, transcript variant X7	mRNA
XM_017022701.2	HERC1	0.000581772	8925	HECT and RLD domain containing E3 ubiquitin protein ligase family member 1, transcript variant X3	mRNA
XM_017022	HERC1	0.026886	8925	HECT and RLD domain containing E3 ubiquitin protein ligase family member 1, transcript	mRNA

701.2		6		variant X3	
XM_011521164.3	CLPX	0.0185913	10845	caseinolytic mitochondrial matrix peptidase chaperone subunit X, transcript variant X1	mRNA
NM_001287823.2	ZWILCH	0.00607462	55055	zwilch kinetochore protein, transcript variant 4	mRNA
XM_024450053.1	AAGAB	0.048575	79719	alpha and gamma adaptin binding protein, transcript variant X3	mRNA
NM_004856.7	KIF23	0.0300443	9493	kinesin family member 23, transcript variant 2	mRNA
NM_001282980.2	TLE3	4.80E-10	7090	TLE family member 3, transcriptional corepressor, transcript variant 4	mRNA
NM_001320941.2	IREB2	0.0037981	3658	iron responsive element binding protein 2, transcript variant 2	mRNA
NM_004136.4	IREB2	0.0104319	3658	iron responsive element binding protein 2, transcript variant 1	mRNA
XM_011521764.2	FANCI	0.0110174	55215	FA complementation group I, transcript variant X3	mRNA
NM_001113	FANCI	0.003582	55215	FA complementation group I, transcript variant 1	mRNA

378.2		26			
NM_001113378.2	FANCI	0.0198244	55215	FA complementation group I, transcript variant 1	mRNA
NM_020210.5	SEMA4B	0.00283312	10509	semaphorin 4B, transcript variant 1	mRNA
NM_001324030.3	SEMA4B	0.00476676	10509	semaphorin 4B, transcript variant 4	mRNA
NM_003870.4	IQGAP1	0.000150569	8826	IQ motif containing GTPase activating protein 1	mRNA
NM_003870.4	IQGAP1	0.000581772	8826	IQ motif containing GTPase activating protein 1	mRNA
NR_168464.1	FURIN	1.94E-06	5045	furin, paired basic amino acid cleaving enzyme, transcript variant 8	misc_RNA
NM_001271.4	CHD2	0.0037981	1106	chromodomain helicase DNA binding protein 2, transcript variant 1	mRNA
NM_001271.4	CHD2	0.00449729	1106	chromodomain helicase DNA binding protein 2, transcript variant 1	mRNA
NM_021259.	PGAP6	1.59E-05	58986	post-glycosylphosphatidylinositol attachment to proteins 6	mRNA

3					
XM_024450299.1	PKD1	0.0385333	5310	polycystin 1, transient receptor potential channel interacting, transcript variant X4	mRNA
NM_001761.3	CCNF	0.0385333	899	cyclin F, transcript variant 1	mRNA
XR_002957796.1	SRRM2	0.0268866	23524	serine/arginine repetitive matrix 2, transcript variant X13	misc_RNA
NM_001318918.2	GLIS2	0.000323968	84662	GLIS family zinc finger 2, transcript variant 2	mRNA
NM_001351729.2	CORO7	0.0130877	79585	coronin 7, transcript variant 4	mRNA
NM_001201479.2	CORO7-PAM16	0.0185913	100529144	CORO7-PAM16 readthrough	mRNA
NM_002705.5	PPL	6.76E-05	5493	periplakin	mRNA
NM_002705.5	PPL	0.00240192	5493	periplakin	mRNA
XM_017023	PPL	3.40E-13	5493	periplakin, transcript variant X2	mRNA

375.2					
NM_002705.5	PPL	0.000105814	5493	periplakin	mRNA
NM_002705.5	PPL	0.00425539	5493	periplakin	mRNA
XR_932882.3	ALG1	0.0319763	56052	ALG1 chitobiosyldiphosphodolichol beta-mannosyltransferase, transcript variant X3	misc_RNA
NM_003470.3	USP7	2.87E-07	7874	ubiquitin specific peptidase 7, transcript variant 1	mRNA
XM_017023705.2	ATF7IP2	0.0050794	80063	activating transcription factor 7 interacting protein 2, transcript variant X1	mRNA
NM_014287.4	NOMO1	0.00190081	23420	NODAL modulator 1	mRNA
NM_014287.4	NOMO1	0.0342076	23420	NODAL modulator 1	mRNA
NM_014287.4	NOMO1	0.000178792	23420	NODAL modulator 1	mRNA
NM_001324	PDXDC1	0.000105	23042	pyridoxal dependent decarboxylase domain containing 1, transcript variant 8	mRNA

019.2		814			
XM_005255706.2	MARF1	0.00321651	9665	meiosis regulator and mRNA stability factor 1, transcript variant X4	mRNA
XM_005255706.2	MARF1	0.0016763	9665	meiosis regulator and mRNA stability factor 1, transcript variant X4	mRNA
NM_004996.4	ABCC1	0.0130877	4363	ATP binding cassette subfamily C member 1	mRNA
NM_004996.4	ABCC1	0.00686488	4363	ATP binding cassette subfamily C member 1	mRNA
NR_036447.1	PKD1P1	0.0156332	339044	polycystin 1, transient receptor potential channel interacting pseudogene 1	misc_RNA
XM_017023156.2	NOMO2	1.16E-08	283820	NODAL modulator 2, transcript variant X1	mRNA
XM_017023156.2	NOMO2	0.000695991	283820	NODAL modulator 2, transcript variant X1	mRNA
XM_017023066.2	SMG1	0.00283312	23049	SMG1 nonsense mediated mRNA decay associated PI3K related kinase, transcript variant X4	mRNA
XM_024450	SMG1	0.045986	23049	SMG1 nonsense mediated mRNA decay associated PI3K related kinase, transcript variant X6	mRNA

198.1					
NM_001258034.2	POLR3E	0.00116938	55718	RNA polymerase III subunit E, transcript variant 4	mRNA
XM_024450200.1	GGA2	0.0319763	23062	golgi associated, gamma adaptin ear containing, ARF binding protein 2, transcript variant X1	mRNA
XM_017023144.2	TNRC6A	5.95E-06	27327	trinucleotide repeat containing adaptor 6A, transcript variant X2	mRNA
XM_017023188.2	GTF3C1	0.000931169	2975	general transcription factor IIIC subunit 1, transcript variant X1	mRNA
XM_005255198.2	XPO6	0.00574795	23214	exportin 6, transcript variant X3	mRNA
NM_005115.5	MVP	2.54E-06	9961	major vault protein, transcript variant 2	mRNA
NM_005115.5	MVP	0.0026633	9961	major vault protein, transcript variant 2	mRNA
NM_001243332.2	SEZ6L2	0.000510829	26470	seizure related 6 homolog like 2, transcript variant 5	mRNA
NM_006662.	SRCAP	0.000118	10847	Snf2 related CREBBP activator protein	mRNA

3		363			
NM_001031835.3	PHKB	0.0104319	5257	phosphorylase kinase regulatory subunit beta, transcript variant 2	mRNA
NM_001363837.1	PHKB	0.00425539	5257	phosphorylase kinase regulatory subunit beta, transcript variant 3	mRNA
NM_001323511.2	AMFR	0.00040024	267	autocrine motility factor receptor, transcript variant 5	mRNA
NM_001323512.2	AMFR	0.0221864	267	autocrine motility factor receptor, transcript variant 4	mRNA
NM_001377456.1	BBS2	0.00770001	583	Bardet-Biedl syndrome 2, transcript variant 2	mRNA
NM_002428.4	MMP15	7.63E-09	4324	matrix metallopeptidase 15	mRNA
NM_002428.4	MMP15	1.35E-05	4324	matrix metallopeptidase 15	mRNA
XM_017022945.2	CSNK2A2	1.14E-07	1459	casein kinase 2 alpha 2, transcript variant X2	mRNA
NM_016284.	CNOT1	0.000338	23019	CCR4-NOT transcription complex subunit 1, transcript variant 1	mRNA

5		213			
NR_049763.2	CNOT1	4.80E-10	23019	CCR4-NOT transcription complex subunit 1, transcript variant 4	misc_RNA
NM_002080.4	GOT2	0.00098721	2806	glutamic-oxaloacetic transaminase 2, transcript variant 1	mRNA
NM_006141.3	DYNC1LI2	0.000338213	1783	dynein cytoplasmic 1 light intermediate chain 2, transcript variant 1	mRNA
NM_001191022.2	CTCF	7.11E-05	10664	CCCTC-binding factor, transcript variant 2	mRNA
NM_001145961.2	SLC12A4	0.000338213	6560	solute carrier family 12 member 4, transcript variant 2	mRNA
XM_017023387.1	PDPR	0.0130877	55066	pyruvate dehydrogenase phosphatase regulatory subunit, transcript variant X3	mRNA
NM_058219.3	EXOSC6	0.000133274	118460	exosome component 6	mRNA
XR_933220.3	AARS1	0.0185913	16	alanyl-tRNA synthetase 1, transcript variant X1	misc_RNA
NM_001605.	AARS1	1.85E-06	16	alanyl-tRNA synthetase 1	mRNA

3					
NM_012426.5	SF3B3	0.0110174	23450	splicing factor 3b subunit 3	mRNA
NM_012426.5	SF3B3	0.045986	23450	splicing factor 3b subunit 3	mRNA
NM_012426.5	SF3B3	0.048575	23450	splicing factor 3b subunit 3	mRNA
NM_012426.5	SF3B3	0.000141056	23450	splicing factor 3b subunit 3	mRNA
XM_017023880.2	MTSS2	0.0185913	92154	MTSS I-BAR domain containing 2, transcript variant X4	mRNA
NM_001137675.4	ATXN1L	0.0364492	342371	ataxin 1 like	mRNA
XM_011523484.2	DHX38	0.0282828	9785	DEAH-box helicase 38, transcript variant X2	mRNA
XM_011523484.2	DHX38	0.0166276	9785	DEAH-box helicase 38, transcript variant X2	mRNA
NR_027265.	GLG1	0.000400	2734	golgi glycoprotein 1, transcript variant 5	misc_R

2		24			NA
NM_012201.6	GLG1	0.000187923	2734	golgi glycoprotein 1, transcript variant 1	mRNA
XM_011523352.1	CMIP	2.71E-06	80790	c-Maf inducing protein, transcript variant X1	mRNA
NM_030629.3	CMIP	0.000740067	80790	c-Maf inducing protein, transcript variant 2	mRNA
XM_017023735.1	SLC7A5	0.0282828	8140	solute carrier family 7 member 5, transcript variant X1	mRNA
NM_006086.4	TUBB3	0.000323968	10381	tubulin beta 3 class III, transcript variant 1	mRNA
XM_024450769.1	MYO1C	0.00476676	4641	myosin IC, transcript variant X3	mRNA
NM_033375.5	MYO1C	1.47E-07	4641	myosin IC, transcript variant 3	mRNA
XM_024450769.1	MYO1C	0.00148402	4641	myosin IC, transcript variant X3	mRNA
XM_024450	PRPF8	3.40E-13	10594	pre-mRNA processing factor 8, transcript variant X1	mRNA

537.1					
NM_006445.4	PRPF8	3.40E-13	10594	pre-mRNA processing factor 8	mRNA
XM_005256561.2	ZZEF1	0.0156332	23140	zinc finger ZZ-type and EF-hand domain containing 1, transcript variant X3	mRNA
XM_005256561.2	ZZEF1	2.02E-05	23140	zinc finger ZZ-type and EF-hand domain containing 1, transcript variant X3	mRNA
XM_005256561.2	ZZEF1	0.000273438	23140	zinc finger ZZ-type and EF-hand domain containing 1, transcript variant X3	mRNA
XM_017024733.1	ANKFY1	0.0253262	51479	ankyrin repeat and FYVE domain containing 1, transcript variant X1	mRNA
XM_011523928.2	ANKFY1	4.60E-10	51479	ankyrin repeat and FYVE domain containing 1, transcript variant X3	mRNA
XM_011523616.2	MYBBP1A	0.0026633	10514	MYB binding protein 1a, transcript variant X2	mRNA
NM_001100812.2	CXCL16	3.40E-13	58191	C-X-C motif chemokine ligand 16, transcript variant 2	mRNA
XM_005256	KIF1C	9.29E-06	10749	kinesin family member 1C, transcript variant X1	mRNA

424.2					
XR_001752570.2	DHX33	0.000141056	56919	DEAH-box helicase 33, transcript variant X2	misc_RNA
XR_934069.2	DHX33	0.00644537	56919	DEAH-box helicase 33, transcript variant X1	misc_RNA
XM_017025404.2	NCOR1	0.0081583	9611	nuclear receptor corepressor 1, transcript variant X17	mRNA
XM_017025411.2	NCOR1	1.21E-06	9611	nuclear receptor corepressor 1, transcript variant X27	mRNA
XM_005256563.4	MPRIP	3.40E-13	23164	myosin phosphatase Rho interacting protein, transcript variant X6	mRNA
XM_005256556.4	FLII	0.0385333	2314	FLII actin remodeling protein, transcript variant X2	mRNA
NM_001316919.1	TVP23B	0.040914	51030	trans-golgi network vesicle protein 23 homolog B, transcript variant 2	mRNA
NM_015276.2	USP22	3.37E-07	23326	ubiquitin specific peptidase 22	mRNA
NM_001363	KIAA0100	0.021103	9703	KIAA0100, transcript variant 5	mRNA

827.1		3			
NM_001363829.1	KIAA0100	9.92E-06	9703	KIAA0100, transcript variant 7	mRNA
XR_001752595.1	SUPT6H	0.000169724	6830	SPT6 homolog, histone chaperone and transcription elongation factor, transcript variant X4	misc_RNA
XR_001752595.1	SUPT6H	0.000657308	6830	SPT6 homolog, histone chaperone and transcription elongation factor, transcript variant X4	misc_RNA
NM_001303542.3	RAB11FIP4	0.0185913	84440	RAB11 family interacting protein 4, transcript variant 2	mRNA
NM_015355.4	SUZ12	1.35E-05	23512	SUZ12 polycomb repressive complex 2 subunit, transcript variant 1	mRNA
XM_024450957.1	MYO19	0.0221864	80179	myosin XIX, transcript variant X12	mRNA
XM_024450957.1	MYO19	1.64E-06	80179	myosin XIX, transcript variant X12	mRNA
NM_198839.3	ACACA	3.57E-05	31	acetyl-CoA carboxylase alpha, transcript variant 2	mRNA
NM_198839.	ACACA	0.022186	31	acetyl-CoA carboxylase alpha, transcript variant 2	mRNA

3		4			
NM_198839.3	ACACA	1.69E-05	31	acetyl-CoA carboxylase alpha, transcript variant 2	mRNA
NM_198839.3	ACACA	0.040914	31	acetyl-CoA carboxylase alpha, transcript variant 2	mRNA
XR_001752504.1	ACACA	0.0176209	31	acetyl-CoA carboxylase alpha, transcript variant X9	misc_RNA
XM_017024078.1	SYNRG	0.048575	11276	synergin gamma, transcript variant X3	mRNA
NM_014598.4	SOCS7	0.0221864	30837	suppressor of cytokine signaling 7	mRNA
XM_011525076.2	ARHGAP23	0.012354	57636	Rho GTPase activating protein 23, transcript variant X7	mRNA
NM_001005862.3	ERBB2	3.40E-13	2064	erb-b2 receptor tyrosine kinase 2, transcript variant 2	mRNA
NM_001005862.3	ERBB2	0.000593431	2064	erb-b2 receptor tyrosine kinase 2, transcript variant 2	mRNA
NM_001145	RARA	0.002401	5914	retinoic acid receptor alpha, transcript variant 3	mRNA

301.3		92			
XM_011525165.2	TOP2A	5.37E-05	7153	DNA topoisomerase II alpha, transcript variant X2	mRNA
NM_198830.2	ACLY	0.00607462	47	ATP citrate lyase, transcript variant 2	mRNA
NM_198830.2	ACLY	5.67E-06	47	ATP citrate lyase, transcript variant 2	mRNA
NM_198830.2	ACLY	0.000187923	47	ATP citrate lyase, transcript variant 2	mRNA
XM_024450898.1	STAT5B	0.0300443	6777	signal transducer and activator of transcription 5B, transcript variant X2	mRNA
XM_017024977.1	STAT5B	0.0026633	6777	signal transducer and activator of transcription 5B, transcript variant X3	mRNA
NM_001384988.1	STAT3	0.00985934	6774	signal transducer and activator of transcription 3, transcript variant 16	mRNA
XM_011524440.2	RETREG3	0.0385333	162427	reticulophagy regulator family member 3, transcript variant X1	mRNA
NM_002087.	GRN	0.002538	2896	granulin precursor	mRNA

4		27			
NM_004247.4	EFTUD2	0.000822568	9343	elongation factor Tu GTP binding domain containing 2, transcript variant 1	mRNA
XM_017025372.2	NPEPPS	3.40E-13	9520	aminopeptidase puromycin sensitive, transcript variant X1	mRNA
XM_005257308.2	ITGA3	3.40E-13	3675	integrin subunit alpha 3, transcript variant X1	mRNA
XM_005257572.4	XYLT2	0.0176209	64132	xylosyltransferase 2, transcript variant X1	mRNA
XM_017025283.2	SPAG9	0.00148402	9043	sperm associated antigen 9, transcript variant X3	mRNA
NM_021626.3	SCPEP1	0.00339383	59342	serine carboxypeptidase 1	mRNA
NM_004859.4	CLTC	0.0104319	1213	clathrin heavy chain, transcript variant 1	mRNA
NM_001288653.2	CLTC	3.40E-13	1213	clathrin heavy chain, transcript variant 2	mRNA
XM_011525	USP32	4.60E-10	84669	ubiquitin specific peptidase 32, transcript variant X7	mRNA

378.1					
XM_011525374.1	USP32	0.0176209	84669	ubiquitin specific peptidase 32, transcript variant X4	mRNA
XM_011525378.1	USP32	0.000323968	84669	ubiquitin specific peptidase 32, transcript variant X7	mRNA
NM_025185.4	TANC2	0.0253262	26115	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 2	mRNA
NM_005828.5	DCAF7	0.0176209	10238	DDB1 and CUL4 associated factor 7, transcript variant 1	mRNA
NR_073585.2	DCAF7	2.01E-07	10238	DDB1 and CUL4 associated factor 7, transcript variant 2	misc_RNA
NR_073585.2	DCAF7	6.09E-08	10238	DDB1 and CUL4 associated factor 7, transcript variant 2	misc_RNA
XM_006721657.1	DDX42	0.00213581	11325	DEAD-box helicase 42, transcript variant X1	mRNA
NM_001330439.1	SMARCD2	0.0300443	6603	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 2, transcript variant 2	mRNA
XM_005257	SMURF2	0.001484	64750	SMAD specific E3 ubiquitin protein ligase 2, transcript variant X1	mRNA

585.3		02			
NM_002266.4	KPNA2	2.30E-05	3838	karyopherin subunit alpha 2, transcript variant 2	mRNA
XM_017024389.1	GGA3	0.040914	23163	golgi associated, gamma adaptin ear containing, ARF binding protein 3, transcript variant X6	mRNA
XM_017024628.1	LLGL2	0.00358226	3993	LLGL scribble cell polarity complex component 2, transcript variant X10	mRNA
NM_001320747.2	EVPL	0.0176209	2125	envoplakin, transcript variant 1	mRNA
NM_001260503.2	SRP68	1.07E-06	6730	signal recognition particle 68, transcript variant 3	mRNA
XM_011525065.2	USP36	0.045986	57602	ubiquitin specific peptidase 36, transcript variant X5	mRNA
XM_024450582.1	TBC1D16	0.00201629	125058	TBC1 domain family member 16, transcript variant X13	mRNA
NM_014740.4	EIF4A3	0.00227362	9775	eukaryotic translation initiation factor 4A3	mRNA
NM_014740.	EIF4A3	2.77E-05	9775	eukaryotic translation initiation factor 4A3	mRNA

4					
NM_001256071.3	RNF213	0.00728668	57674	ring finger protein 213, transcript variant 3	mRNA
XM_006721995.3	RNF213	0.0433858	57674	ring finger protein 213, transcript variant X2	mRNA
NR_026857.1	BAIAP2-DT	0.00103918	440465	BAIAP2 divergent transcript	lnc_RNA
XR_934502.1	NPLOC4	1.94E-06	55666	NPL4 homolog, ubiquitin recognition factor, transcript variant X7	misc_RNA
XR_001753173.1	SMCHD1	0.0026633	23347	structural maintenance of chromosomes flexible hinge domain containing 1, transcript variant X3	misc_RNA
NM_001375809.1	LPIN2	0.00985934	9663	lipin 2, transcript variant 3	mRNA
NM_005406.3	ROCK1	0.0110174	6093	Rho associated coiled-coil containing protein kinase 1	mRNA
NM_020774.4	MIB1	0.00728668	57534	MIB E3 ubiquitin protein ligase 1	mRNA
XM_017025	MIB1	0.000987	57534	MIB E3 ubiquitin protein ligase 1, transcript variant X1	mRNA

873.1		21			
XM_011525980.2	LAMA3	0.0268866	3909	laminin subunit alpha 3, transcript variant X3	mRNA
XM_011525980.2	LAMA3	0.0050794	3909	laminin subunit alpha 3, transcript variant X3	mRNA
XM_011525980.2	LAMA3	0.0385333	3909	laminin subunit alpha 3, transcript variant X3	mRNA
XM_011525982.2	LAMA3	1.35E-06	3909	laminin subunit alpha 3, transcript variant X6	mRNA
XM_011525980.2	LAMA3	3.56E-06	3909	laminin subunit alpha 3, transcript variant X3	mRNA
XM_011526145.1	SS18	0.00131687	6760	SS18 subunit of BAF chromatin remodeling complex, transcript variant X1	mRNA
NM_004949.5	DSC2	1.59E-06	1824	desmocollin 2, transcript variant Dsc2b	mRNA
NM_024422.6	DSC2	0.000740067	1824	desmocollin 2, transcript variant Dsc2a	mRNA
NM_004949.	DSC2	0.000400	1824	desmocollin 2, transcript variant Dsc2b	mRNA

5		24			
XM_024451095.1	DSG2	3.40E-13	1829	desmoglein 2, transcript variant X1	mRNA
NM_001384443.1	GALNT1	0.0300443	2589	polypeptide N-acetylgalactosaminyltransferase 1, transcript variant 7	mRNA
XM_017025789.1	ATP5F1A	0.00868541	498	ATP synthase F1 subunit alpha, transcript variant X1	mRNA
XM_024451137.1	NEDD4L	2.96E-05	23327	NEDD4 like E3 ubiquitin protein ligase, transcript variant X23	mRNA
XM_005266663.4	NEDD4L	0.0040224	23327	NEDD4 like E3 ubiquitin protein ligase, transcript variant X4	mRNA
NM_001375912.1	ZNF532	0.0319763	55205	zinc finger protein 532, transcript variant 19	mRNA
NM_005570.4	LMAN1	0.00253827	3998	lectin, mannose binding 1	mRNA
NM_194449.4	PHLPP1	0.00770001	23239	PH domain and leucine rich repeat protein phosphatase 1	mRNA
NM_001370	CNDP2	0.038533	55748	carnosine dipeptidase 2, transcript variant 6	mRNA

254.1		3			
XR_001753706.2	POLRMT	0.0185913	5442	RNA polymerase mitochondrial, transcript variant X1	misc_RNA
XR_002958339.1	REXO1	0.0037981	57455	RNA exonuclease 1 homolog, transcript variant X9	misc_RNA
XM_011528360.1	DOT1L	9.05E-05	84444	DOT1 like histone lysine methyltransferase, transcript variant X4	mRNA
NM_001300846.2	TLE2	0.00040024	7089	TLE family member 2, transcriptional corepressor, transcript variant 4	mRNA
NM_001300846.2	TLE2	0.0050794	7089	TLE family member 2, transcriptional corepressor, transcript variant 4	mRNA
NM_002067.5	GNA11	0.000323968	2767	G protein subunit alpha 11	mRNA
XM_017026834.2	NFIC	0.000105814	4782	nuclear factor I C, transcript variant X1	mRNA
XM_005259573.5	FZR1	3.56E-06	51343	fizzy and cell division cycle 20 related 1, transcript variant X3	mRNA
NM_006339.	HMG20B	0.010431	10362	high mobility group 20B	mRNA

3		9			
XM_011527846.1	PIP5K1C	2.03E-06	23396	phosphatidylinositol-4-phosphate 5-kinase type 1 gamma, transcript variant X2	mRNA
NM_001267560.2	TJP3	0.00157844	27134	tight junction protein 3, transcript variant 1	mRNA
NM_001271996.2	CREB3L3	0.000338213	84699	cAMP responsive element binding protein 3 like 3, transcript variant 3	mRNA
NM_001271996.2	CREB3L3	0.0300443	84699	cAMP responsive element binding protein 3 like 3, transcript variant 3	mRNA
NM_001384611.1	DPP9	0.0016763	91039	dipeptidyl peptidase 9, transcript variant 4	mRNA
XM_011528394.1	RANBP3	0.0433858	8498	RAN binding protein 3, transcript variant X6	mRNA
XM_011528394.1	RANBP3	1.01E-08	8498	RAN binding protein 3, transcript variant X6	mRNA
NM_000208.4	INSR	0.000380287	3643	insulin receptor, transcript variant 1	mRNA
NM_000208.	INSR	0.008685	3643	insulin receptor, transcript variant 1	mRNA

4		41			
NM_000208.4	INSR	0.040914	3643	insulin receptor, transcript variant 1	mRNA
NM_001166112.2	PNPLA6	0.000290692	10908	patatin like phospholipase domain containing 6, transcript variant 4	mRNA
XR_001753728.1	CAMSAP3	0.0300443	57662	calmodulin regulated spectrin associated protein family member 3, transcript variant X4	misc_RNA
NM_001318730.2	DNMT1	7.04E-08	1786	DNA methyltransferase 1, transcript variant 3	mRNA
NM_133452.3	RAVER1	0.000112562	125950	ribonucleoprotein, PTB binding 1, transcript variant 1	mRNA
XM_024451661.1	SMARCA4	8.56E-06	6597	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4, transcript variant X7	mRNA
XM_011528151.1	DOCK6	6.01E-05	57572	dedicator of cytokinesis 6, transcript variant X2	mRNA
XM_011528151.1	DOCK6	3.36E-05	57572	dedicator of cytokinesis 6, transcript variant X2	mRNA
XM_011528	DOCK6	7.63E-09	57572	dedicator of cytokinesis 6, transcript variant X2	mRNA

151.1					
XM_005260000.2	DOCK6	0.00125407	57572	dedicator of cytokinesis 6, transcript variant X6	mRNA
NM_001379609.1	PRKCSH	3.40E-13	5589	protein kinase C substrate 80K-H, transcript variant 7	mRNA
NM_001173498.2	MAN2B1	9.94E-09	4125	mannosidase alpha class 2B member 1, transcript variant 2	mRNA
XM_024451562.1	CC2D1A	0.000307575	54862	coiled-coil and C2 domain containing 1A, transcript variant X1	mRNA
NM_002741.5	PKN1	0.0221864	5585	protein kinase N1, transcript variant 2	mRNA
NM_014299.3	BRD4	0.0236925	23476	bromodomain containing 4, transcript variant short	mRNA
NM_001130065.2	MYO9B	6.38E-05	4650	myosin IXB, transcript variant 2	mRNA
NM_004145.4	MYO9B	0.000112562	4650	myosin IXB, transcript variant 1	mRNA
XM_011528	COLGALT1	2.58E-08	79709	collagen beta(1-O)galactosyltransferase 1, transcript variant X4	mRNA

299.3					
XM_017026516.1	MAST3	0.0166276	23031	microtubule associated serine/threonine kinase 3, transcript variant X20	mRNA
NR_162071.1	PIK3R2	0.000290692	5296	phosphoinositide-3-kinase regulatory subunit 2, transcript variant 3	misc_RNA
XM_006722666.2	SSBP4	8.48E-05	170463	single stranded DNA binding protein 4, transcript variant X8	mRNA
XM_017027106.2	UPF1	0.0385333	5976	UPF1 RNA helicase and ATPase, transcript variant X2	mRNA
XR_935753.2	DPY19L3	0.048575	147991	dpy-19 like C-mannosyltransferase 3, transcript variant X6	misc_RNA
XM_017027349.1	ANKRD27	0.0385333	84079	ankyrin repeat domain 27, transcript variant X2	mRNA
NM_014686.5	GARRE1	8.76E-08	9710	granule associated Rac and RHOG effector 1	mRNA
XR_001753641.1	HAUS5	0.00574795	23354	HAUS augmin like complex subunit 5, transcript variant X1	misc_RNA
NM_001319	RBM42	0.000160	79171	RNA binding motif protein 42, transcript variant 2	mRNA

113.2		289			
NM_024321.5	RBM42	0.00201629	79171	RNA binding motif protein 42, transcript variant 1	mRNA
XM_011526838.1	WDR62	0.0253262	284403	WD repeat domain 62, transcript variant X4	mRNA
NR_169274.1	SAMD4B	2.13E-06	55095	sterile alpha motif domain containing 4B, transcript variant 34	misc_RNA
NM_001384571.1	SAMD4B	0.012354	55095	sterile alpha motif domain containing 4B, transcript variant 8	mRNA
NM_022835.3	PLEKHG2	2.78E-09	64857	pleckstrin homology and RhoGEF domain containing G2, transcript variant 1	mRNA
NM_001130825.2	SUPT5H	0.000338213	6829	SPT5 homolog, DSIF elongation factor subunit, transcript variant 4	mRNA
NM_001130825.2	SUPT5H	0.0040224	6829	SPT5 homolog, DSIF elongation factor subunit, transcript variant 4	mRNA
NM_001130825.2	SUPT5H	5.68E-05	6829	SPT5 homolog, DSIF elongation factor subunit, transcript variant 4	mRNA
NM_001130	SUPT5H	0.002016	6829	SPT5 homolog, DSIF elongation factor subunit, transcript variant 4	mRNA

825.2		29			
NM_004706.4	ARHGEF1	0.00339383	9138	Rho guanine nucleotide exchange factor 1, transcript variant 2	mRNA
NM_001329922.1	CALM3	0.00321651	808	calmodulin 3, transcript variant 3	mRNA
XM_011526878.1	STRN4	3.56E-08	29888	striatin 4, transcript variant X8	mRNA
XM_005258677.4	ZC3H4	0.0081583	23211	zinc finger CCCH-type containing 4, transcript variant X4	mRNA
XM_005258677.4	ZC3H4	0.000695991	23211	zinc finger CCCH-type containing 4, transcript variant X4	mRNA
XM_005258677.4	ZC3H4	5.80E-10	23211	zinc finger CCCH-type containing 4, transcript variant X4	mRNA
NM_001161354.2	PLEKHA4	0.0221864	57664	pleckstrin homology domain containing A4, transcript variant 2	mRNA
NM_006184.6	NUCB1	0.000199653	4924	nucleobindin 1	mRNA
XM_024451	TRPM4	0.004022	54795	transient receptor potential cation channel subfamily M member 4, transcript variant X2	mRNA

557.1		4			
NM_001195227.2	TRPM4	0.000777792	54795	transient receptor potential cation channel subfamily M member 4, transcript variant 2	mRNA
XM_024451721.1	MYH14	3.98E-05	79784	myosin heavy chain 14, transcript variant X5	mRNA
XM_011526993.3	CNOT3	0.0433858	4849	CCR4-NOT transcription complex subunit 3, transcript variant X9	mRNA
XM_005259013.4	PPP1R12C	0.0156332	54776	protein phosphatase 1 regulatory subunit 12C, transcript variant X1	mRNA
NM_001321263.2	EPN1	0.0017864	29924	epsin 1, transcript variant 4	mRNA
NM_015677.4	SH3YL1	0.00240192	26751	SH3 and SYLF domain containing 1, transcript variant 1	mRNA
XM_017003900.1	GRHL1	0.0221864	29841	grainyhead like transcription factor 1, transcript variant X5	mRNA
XM_017005378.2	ROCK2	1.28E-05	9475	Rho associated coiled-coil containing protein kinase 2, transcript variant X2	mRNA
XM_017005	ROCK2	0.038533	9475	Rho associated coiled-coil containing protein kinase 2, transcript variant X2	mRNA

378.2		3			
XM_005246190.3	ROCK2	3.05E-06	9475	Rho associated coiled-coil containing protein kinase 2, transcript variant X1	mRNA
NM_004939.3	DDX1	0.0110174	1653	DEAD-box helicase 1	mRNA
NM_002997.5	SDC1	0.0166276	6382	syndecan 1, transcript variant 2	mRNA
NM_016131.5	RAB10	0.000150569	10890	RAB10, member RAS oncogene family	mRNA
NM_000182.5	HADHA	8.48E-05	3030	hydroxyacyl-CoA dehydrogenase trifunctional multienzyme complex subunit alpha	mRNA
NR_137633.2	SELENOI	0.00040024	85465	selenoprotein I, transcript variant 2	misc_RNA
NM_017877.4	SLC35F6	0.00425539	54978	solute carrier family 35 member F6	mRNA
XR_001738791.2	TMEM214	0.0081583	54867	transmembrane protein 214, transcript variant X4	misc_RNA
XM_017004	BIRC6	0.011017	57448	baculoviral IAP repeat containing 6, transcript variant X19	mRNA

560.1		4			
XM_005264454.5	BIRC6	0.0037981	57448	baculoviral IAP repeat containing 6, transcript variant X11	mRNA
XM_005264357.5	CRIM1	2.27E-06	51232	cysteine rich transmembrane BMP regulator 1, transcript variant X4	mRNA
XM_005264357.5	CRIM1	3.54E-07	51232	cysteine rich transmembrane BMP regulator 1, transcript variant X4	mRNA
NM_001382394.1	SOS1	0.045986	6654	SOS Ras/Rac guanine nucleotide exchange factor 1, transcript variant 2	mRNA
XM_006711991.1	EML4	0.000358192	27436	EMAP like 4, transcript variant X2	mRNA
XR_002958896.1	LRPPRC	0.0364492	10128	leucine rich pentatricopeptide repeat containing, transcript variant X4	misc_RNA
NM_001374325.1	FBXO11	0.048575	80204	F-box protein 11, transcript variant 5	mRNA
NM_014614.3	PSME4	4.47E-05	23198	proteasome activator subunit 4	mRNA
NM_014614.	PSME4	0.023692	23198	proteasome activator subunit 4	mRNA

3		5			
XM_017004779.1	SPTBN1	2.03E-06	6711	spectrin beta, non-erythrocytic 1, transcript variant X3	mRNA
XM_017004779.1	SPTBN1	1.28E-05	6711	spectrin beta, non-erythrocytic 1, transcript variant X3	mRNA
XM_017005172.1	PNPT1	0.0342076	87178	polyribonucleotide nucleotidyltransferase 1, transcript variant X2	mRNA
NM_014709.4	USP34	0.048575	9736	ubiquitin specific peptidase 34	mRNA
NM_014709.4	USP34	0.0116648	9736	ubiquitin specific peptidase 34	mRNA
NM_014709.4	USP34	0.00543382	9736	ubiquitin specific peptidase 34	mRNA
NM_001256721.1	CCT4	9.29E-06	10575	chaperonin containing TCP1 subunit 4, transcript variant 2	mRNA
NM_001199111.2	MDH1	6.01E-05	4190	malate dehydrogenase 1, transcript variant 2	mRNA
XM_017004	PELI1	0.006074	57162	pellino E3 ubiquitin protein ligase 1, transcript variant X1	mRNA

520.1		62			
XM_017003801.1	GFPT1	0.00425539	2673	glutamine--fructose-6-phosphate transaminase 1, transcript variant X1	mRNA
XM_017003801.1	GFPT1	0.00040024	2673	glutamine--fructose-6-phosphate transaminase 1, transcript variant X1	mRNA
XM_017003802.2	GFPT1	0.00103918	2673	glutamine--fructose-6-phosphate transaminase 1, transcript variant X2	mRNA
XM_017003802.2	GFPT1	2.43E-05	2673	glutamine--fructose-6-phosphate transaminase 1, transcript variant X2	mRNA
NM_015120.4	ALMS1	0.0185913	7840	ALMS1 centrosome and basal body associated protein, transcript variant 1	mRNA
NR_033935.2	DCTN1	1.49E-06	1639	dynactin subunit 1, transcript variant 7	misc_RNA
NM_001371525.1	HK2	0.040914	3099	hexokinase 2, transcript variant 2	mRNA
NM_001371525.1	HK2	1.59E-05	3099	hexokinase 2, transcript variant 2	mRNA
NM_015425.	POLR1A	0.038533	25885	RNA polymerase I subunit A	mRNA

6		3			
NM_014014.5	SNRNP200	4.60E-10	23020	small nuclear ribonucleoprotein U5 subunit 200	mRNA
NM_014014.5	SNRNP200	8.96E-06	23020	small nuclear ribonucleoprotein U5 subunit 200	mRNA
NM_014014.5	SNRNP200	0.0156332	23020	small nuclear ribonucleoprotein U5 subunit 200	mRNA
NM_014014.5	SNRNP200	7.63E-09	23020	small nuclear ribonucleoprotein U5 subunit 200	mRNA
NM_014014.5	SNRNP200	0.00131687	23020	small nuclear ribonucleoprotein U5 subunit 200	mRNA
NM_001349256.2	KANSL3	0.048575	55683	KAT8 regulatory NSL complex subunit 3, transcript variant 8	mRNA
NM_001349262.2	KANSL3	0.0185913	55683	KAT8 regulatory NSL complex subunit 3, transcript variant 14	mRNA
NM_001349262.2	KANSL3	0.000101311	55683	KAT8 regulatory NSL complex subunit 3, transcript variant 14	mRNA
NM_015348.	TMEM131	0.004497	23505	transmembrane protein 131	mRNA

2		29			
XM_005264068.3	MAP4K4	0.000307575	9448	mitogen-activated protein kinase kinase kinase kinase 4, transcript variant X33	mRNA
NM_001384508.1	MAP4K4	7.51E-05	9448	mitogen-activated protein kinase kinase kinase kinase 4, transcript variant 29	mRNA
XM_005264048.2	MAP4K4	2.58E-08	9448	mitogen-activated protein kinase kinase kinase kinase 4, transcript variant X1	mRNA
XR_001739079.1	GCC2	0.0176209	9648	GRIP and coiled-coil domain containing 2, transcript variant X6	misc_RNA
NM_001371494.1	LIMS1	3.40E-13	3987	LIM zinc finger domain containing 1, transcript variant 7	mRNA
XM_005264003.3	RANBP2	0.00040024	5903	RAN binding protein 2, transcript variant X3	mRNA
XM_011511634.2	ANAPC1	3.77E-05	64682	anaphase promoting complex subunit 1, transcript variant X4	mRNA
NM_001282779.2	POLR1B	0.0319763	84172	RNA polymerase I subunit B, transcript variant 7	mRNA
NM_001282	POLR1B	0.002273	84172	RNA polymerase I subunit B, transcript variant 5	mRNA

776.2		62			
NR_102318.1	ACTR3	1.42E-06	10096	actin related protein 3, transcript variant 3	misc_RNA
NM_002830.4	PTPN4	0.0026633	5775	protein tyrosine phosphatase non-receptor type 4	mRNA
XM_006712382.1	CLASP1	0.000338213	23332	cytoplasmic linker associated protein 1, transcript variant X24	mRNA
NM_004622.3	TSN	0.0300443	7247	translin, transcript variant 1	mRNA
NM_001320642.1	BIN1	0.00148402	274	bridging integrator 1, transcript variant 15	mRNA
NM_006609.5	MAP3K2	0.0342076	10746	mitogen-activated protein kinase kinase kinase 2, transcript variant 1	mRNA
XM_017004508.1	UGGT1	0.00607462	56886	UDP-glucose glycoprotein glucosyltransferase 1, transcript variant X6	mRNA
XM_017004508.1	UGGT1	0.000931169	56886	UDP-glucose glycoprotein glucosyltransferase 1, transcript variant X6	mRNA
XM_017004	UGGT1	0.030044	56886	UDP-glucose glycoprotein glucosyltransferase 1, transcript variant X7	mRNA

509.1		3			
NM_005915.6	MCM6	0.000307575	4175	minichromosome maintenance complex component 6	mRNA
NM_005915.6	MCM6	0.0123624	4175	minichromosome maintenance complex component 6	mRNA
XM_011511395.3	RIF1	0.0385333	55183	replication timing regulatory factor 1, transcript variant X14	mRNA
XM_011511395.3	RIF1	0.00283312	55183	replication timing regulatory factor 1, transcript variant X14	mRNA
XM_011510530.1	FMNL2	0.012354	114793	formin like 2, transcript variant X1	mRNA
XM_011510530.1	FMNL2	0.0268866	114793	formin like 2, transcript variant X1	mRNA
XM_006712814.3	TANC1	9.05E-05	85461	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 1, transcript variant X25	mRNA
XM_017003357.1	UBR3	0.0211033	130507	ubiquitin protein ligase E3 component n-recognin 3, transcript variant X9	mRNA
XM_024453	TLK1	0.008158	9874	tousled like kinase 1, transcript variant X4	mRNA

262.1		3			
NM_001271789.2	DYNC1I2	0.000242029	1781	dynein cytoplasmic 1 intermediate chain 2, transcript variant 6	mRNA
NR_073366.2	DNAJC10	0.000112562	54431	DnaJ heat shock protein family (Hsp40) member C10, transcript variant 4	misc_RNA
NM_002210.5	ITGAV	0.00321651	3685	integrin subunit alpha V, transcript variant 1	mRNA
NM_014585.6	SLC40A1	0.0221864	30061	solute carrier family 40 member 1	mRNA
NM_001321315.1	NAB1	0.0253262	4664	NGFI-A binding protein 1, transcript variant 5	mRNA
XR_001738915.2	STAT1	0.045986	6772	signal transducer and activator of transcription 1, transcript variant X4	misc_RNA
NM_001384887.1	STAT1	0.000169724	6772	signal transducer and activator of transcription 1, transcript variant 8	mRNA
NM_001384887.1	STAT1	3.40E-13	6772	signal transducer and activator of transcription 1, transcript variant 8	mRNA
XM_024452	MYO1B	0.013925	4430	myosin IB, transcript variant X2	mRNA

914.1		3			
XM_024452914.1	MYO1B	0.0016763	4430	myosin IB, transcript variant X2	mRNA
XR_001738680.2	SF3B1	4.23E-05	23451	splicing factor 3b subunit 1, transcript variant X1	misc_RNA
NM_001321690.1	BZW1	0.0185913	9689	basic leucine zipper and W2 domains 1, transcript variant 6	mRNA
NM_001321693.2	BZW1	7.85E-08	9689	basic leucine zipper and W2 domains 1, transcript variant 8	mRNA
NM_020919.4	ALS2	0.0236925	57679	alsin Rho guanine nucleotide exchange factor ALS2, transcript variant 1	mRNA
NM_001114132.2	NBEAL1	0.0139253	65065	neurobeachin like 1, transcript variant 1	mRNA
NM_213589.3	RAPH1	0.00140507	65059	Ras association (RalGDS/AF-6) and pleckstrin homology domains 1, transcript variant 1	mRNA
XM_017003568.1	PIKFYVE	0.045986	200576	phosphoinositide kinase, FYVE-type zinc finger containing, transcript variant X5	mRNA
XM_017003	PIKFYVE	0.013925	200576	phosphoinositide kinase, FYVE-type zinc finger containing, transcript variant X20	mRNA

574.1		3			
XM_017003568.1	PIKFYVE	0.000931169	200576	phosphoinositide kinase, FYVE-type zinc finger containing, transcript variant X5	mRNA
NM_021141.4	XRCC5	0.00449729	7520	X-ray repair cross complementing 5	mRNA
NM_021141.4	XRCC5	0.0156332	7520	X-ray repair cross complementing 5	mRNA
NM_007127.3	VIL1	0.045986	7429	villin 1	mRNA
NM_007127.3	VIL1	2.33E-08	7429	villin 1	mRNA
NM_007127.3	VIL1	0.0364492	7429	villin 1	mRNA
XM_011511787.2	ZNF142	0.045986	7701	zinc finger protein 142, transcript variant X6	mRNA
NR_130154.2	FARSB	0.045986	10056	phenylalanyl-tRNA synthetase subunit beta, transcript variant 2	misc_RNA
NM_001354	ACSL3	3.40E-13	2181	acyl-CoA synthetase long chain family member 3, transcript variant 3	mRNA

158.2					
NM_001354158.2	ACSL3	0.0185913	2181	acyl-CoA synthetase long chain family member 3, transcript variant 3	mRNA
NM_020830.5	WDFY1	0.00140507	57590	WD repeat and FYVE domain containing 1	mRNA
NM_001135187.2	AGFG1	7.11E-05	3267	ArfGAP with FG repeats 1, transcript variant 1	mRNA
NM_001130849.2	CAB39	3.40E-13	51719	calcium binding protein 39, transcript variant 2	mRNA
NM_001191037.2	PSMD1	1.35E-05	5707	proteasome 26S subunit, non-ATPase 1, transcript variant 2	mRNA
XM_011512035.1	DGKD	3.40E-06	8527	diacylglycerol kinase delta, transcript variant X12	mRNA
XM_017003789.1	TRAF3IP1	0.0185913	26146	TRAF3 interacting protein 1, transcript variant X2	mRNA
NM_023083.4	CAPN10	0.00227362	11132	calpain 10, transcript variant 1	mRNA
XM_011511	HDLBP	7.63E-09	3069	high density lipoprotein binding protein, transcript variant X4	mRNA

058.3					
NM_001282308.2	STK25	2.03E-06	10494	serine/threonine kinase 25, transcript variant 7	mRNA
NM_016143.5	NSFL1C	0.0176209	55968	NSFL1 cofactor, transcript variant 1	mRNA
NM_001323332.2	ATRN	0.000510829	8455	attractin, transcript variant 5	mRNA
NR_136336.2	CDC25B	0.048575	994	cell division cycle 25B, transcript variant 12	misc_RNA
XM_024452016.1	CDS2	0.00140507	8760	CDP-diacylglycerol synthase 2, transcript variant X3	mRNA
XM_024452016.1	CDS2	0.0198244	8760	CDP-diacylglycerol synthase 2, transcript variant X3	mRNA
NM_017671.5	FERMT1	9.53E-05	55612	FERM domain containing kindlin 1	mRNA
XM_024451935.1	FERMT1	0.00425539	55612	FERM domain containing kindlin 1, transcript variant X1	mRNA
NM_000214.	JAG1	8.96E-06	182	jagged canonical Notch ligand 1	mRNA

3					
NM_000214.3	JAG1	0.0139253	182	jagged canonical Notch ligand 1	mRNA
NM_001365613.2	RRBP1	0.0166276	6238	ribosome binding protein 1, transcript variant 3	mRNA
NM_001172745.3	SEC23B	1.13E-05	10483	SEC23 homolog B, COPII coat complex component, transcript variant 4	mRNA
NM_001242581.2	RIN2	0.0268866	54453	Ras and Rab interactor 2, transcript variant 1	mRNA
NM_012255.5	XRN2	0.0268866	22803	5'-3' exoribonuclease 2, transcript variant 2	mRNA
XM_011528700.3	TPX2	7.04E-08	22974	TPX2 microtubule nucleation factor, transcript variant X3	mRNA
XM_006723691.1	CEP250	0.000323968	11190	centrosomal protein 250, transcript variant X3	mRNA
NM_012156.2	EPB41L1	0.000482835	2036	erythrocyte membrane protein band 4.1 like 1, transcript variant 1	mRNA
NM_001258	EPB41L1	0.003393	2036	erythrocyte membrane protein band 4.1 like 1, transcript variant 5	mRNA

331.2		83			
XM_017028025.1	SRC	4.76E-05	6714	SRC proto-oncogene, non-receptor tyrosine kinase, transcript variant X2	mRNA
XM_005260465.3	RALGAPB	9.78E-08	57148	Ral GTPase activating protein non-catalytic subunit beta, transcript variant X5	mRNA
NM_182811.2	PLCG1	0.000105814	5335	phospholipase C gamma 1, transcript variant 2	mRNA
NM_175914.5	HNF4A	0.000695991	3172	hepatocyte nuclear factor 4 alpha, transcript variant 5	mRNA
NM_052951.3	DNTTIP1	0.00240192	116092	deoxynucleotidyltransferase terminal interacting protein 1	mRNA
XM_005260504.4	ZNF335	0.045986	63925	zinc finger protein 335, transcript variant X1	mRNA
NM_006534.4	NCOA3	1.64E-06	8202	nuclear receptor coactivator 3, transcript variant 2	mRNA
XM_005260252.3	ARFGEF2	0.000199653	10564	ADP ribosylation factor guanine nucleotide exchange factor 2, transcript variant X1	mRNA
NM_006420.	ARFGEF2	0.003393	10564	ADP ribosylation factor guanine nucleotide exchange factor 2	mRNA

3		83			
XM_005260252.3	ARFGEF2	0.00476676	10564	ADP ribosylation factor guanine nucleotide exchange factor 2, transcript variant X1	mRNA
NM_001316.4	CSE1L	0.000227166	1434	chromosome segregation 1 like, transcript variant 1	mRNA
NM_018683.4	RNF114	0.00358226	55905	ring finger protein 114	mRNA
NM_018683.4	RNF114	0.040914	55905	ring finger protein 114	mRNA
NM_001001433.3	STX16	0.0282828	8675	syntaxin 16, transcript variant 1	mRNA
XM_024451840.1	LSM14B	0.040914	149986	LSM family member 14B, transcript variant X13	mRNA
XR_936532.2	LAMA5	0.0026633	3911	laminin subunit alpha 5, transcript variant X4	misc_RNA
XR_936532.2	LAMA5	4.80E-10	3911	laminin subunit alpha 5, transcript variant X4	misc_RNA
XR_0017543	ARFGAP1	0.026886	55738	ADP ribosylation factor GTPase activating protein 1, transcript variant X7	misc_R

30.2		6			NA
NM_014825.3	URB1	0.000452538	9875	URB1 ribosome biogenesis homolog	mRNA
NM_014825.3	URB1	3.40E-06	9875	URB1 ribosome biogenesis homolog	mRNA
NM_014825.3	URB1	0.0364492	9875	URB1 ribosome biogenesis homolog	mRNA
NM_001350335.2	CFAP298	0.0130877	56683	cilia and flagella associated protein 298, transcript variant 3	mRNA
NM_005441.3	CHAF1B	0.00926878	8208	chromatin assembly factor 1 subunit B	mRNA
XM_005261052.1	TTC3	0.0110174	7267	tetratricopeptide repeat domain 3, transcript variant X8	mRNA
XR_002958632.1	TTC3	0.000307575	7267	tetratricopeptide repeat domain 3, transcript variant X17	misc_RNA
XM_005261052.1	TTC3	0.0211033	7267	tetratricopeptide repeat domain 3, transcript variant X8	mRNA
XM_005261	TTC3	0.018591	7267	tetratricopeptide repeat domain 3, transcript variant X8	mRNA

052.1		3			
NM_001848.3	COL6A1	2.09E-07	1291	collagen type VI alpha 1 chain	mRNA
NM_001145436.2	LSS	7.11E-06	4047	lanosterol synthase, transcript variant 3	mRNA
NR_110566.1	MCM3AP-AS1	0.0282828	114044	MCM3AP antisense RNA 1, transcript variant 3	lnc_RNA
XM_005261205.4	MCM3AP	0.000452538	8888	minichromosome maintenance complex component 3 associated protein, transcript variant X3	mRNA
XM_005261205.4	MCM3AP	0.00253827	8888	minichromosome maintenance complex component 3 associated protein, transcript variant X3	mRNA
XM_024452082.1	PCNT	0.0433858	5116	pericentrin, transcript variant X5	mRNA
NM_014339.7	IL17RA	0.0156332	23765	interleukin 17 receptor A, transcript variant 1	mRNA
NM_014339.7	IL17RA	0.00728668	23765	interleukin 17 receptor A, transcript variant 1	mRNA
XM_024452	HDHD5	8.48E-05	27440	haloacid dehalogenase like hydrolase domain containing 5, transcript variant X3	mRNA

232.1					
NM_015241.3	MICAL3	0.00358226	57553	microtubule associated monooxygenase, calponin and LIM domain containing 3, transcript variant 1	mRNA
NM_001122731.2	MICAL3	0.00321651	57553	microtubule associated monooxygenase, calponin and LIM domain containing 3, transcript variant 3	mRNA
NM_003325.4	HIRA	3.69E-06	7290	histone cell cycle regulator	mRNA
XR_937868.1	PI4KA	0.0364492	5297	phosphatidylinositol 4-kinase alpha, transcript variant X3	misc_RNA
XR_937868.1	PI4KA	6.15E-07	5297	phosphatidylinositol 4-kinase alpha, transcript variant X3	misc_RNA
NM_021574.3	BCR	0.0282828	613	BCR activator of RhoGEF and GTPase, transcript variant 2	mRNA
XM_024452185.1	CABIN1	0.00240192	23523	calcineurin binding protein 1, transcript variant X3	mRNA
NM_001386930.1	KIAA1671	1.06E-05	85379	KIAA1671, transcript variant 1	mRNA
NM_001386	KIAA1671	0.000212	85379	KIAA1671, transcript variant 1	mRNA

930.1		686			
XR_001755346.1	THOC5	0.00116938	8563	THO complex 5, transcript variant X7	misc_RNA
NM_153051.3	MTMR3	0.0110174	8897	myotubularin related protein 3, transcript variant 2	mRNA
NM_005877.6	SF3A1	7.51E-05	10291	splicing factor 3a subunit 1	mRNA
NM_014941.3	MORC2	0.0104319	22880	MORC family CW-type zinc finger 2, transcript variant 3	mRNA
NM_001257990.2	FBXO7	0.0211033	25793	F-box protein 7, transcript variant 3	mRNA
NM_002133.3	HMOX1	0.0026633	3162	heme oxygenase 1	mRNA
NM_002473.6	MYH9	7.00E-07	4627	myosin heavy chain 9	mRNA
NR_156418.2	EIF3D	0.00116938	8664	eukaryotic translation initiation factor 3 subunit D, transcript variant 2	misc_RNA
NM_014550.	CARD10	0.004766	29775	caspase recruitment domain family member 10	mRNA

4		76			
XM_005261791.3	MICALL1	0.000618347	85377	MICAL like 1, transcript variant X4	mRNA
NM_015140.4	TTLL12	1.14E-07	23170	tubulin tyrosine ligase like 12	mRNA
NM_016426.7	GTSE1	0.000212686	51512	G2 and S-phase expressed 1	mRNA
NM_001378328.1	CELSR1	0.000618347	9620	cadherin EGF LAG seven-pass G-type receptor 1, transcript variant 1	mRNA
XM_011530553.1	CELSR1	0.00770001	9620	cadherin EGF LAG seven-pass G-type receptor 1, transcript variant X2	mRNA
NM_001376881.1	PLXNB2	0.00190081	23654	plexin B2, transcript variant 19	mRNA
XM_024453798.1	BHLHE40	0.0026633	8553	basic helix-loop-helix family member e40, transcript variant X1	mRNA
XR_001740383.1	EDEM1	0.000822568	9695	ER degradation enhancing alpha-mannosidase like protein 1, transcript variant X1	misc_RNA
XR_0017403	EDEM1	0.005747	9695	ER degradation enhancing alpha-mannosidase like protein 1, transcript variant X1	misc_R

83.1		95			NA
XM_017006774.1	SETD5	0.000777792	55209	SET domain containing 5, transcript variant X14	mRNA
XM_017007176.2	TMEM43	0.00770001	79188	transmembrane protein 43, transcript variant X1	mRNA
NM_001354730.2	XPC	0.00476676	7508	XPC complex subunit, DNA damage recognition and repair factor, transcript variant 6	mRNA
NR_164763.1	CAPN7	0.00358226	23473	calpain 7, transcript variant 10	misc_RNA
NM_001349078.2	TBC1D5	0.0156332	9779	TBC1 domain family member 5, transcript variant 8	mRNA
NM_001354715.2	THRB	0.0198244	7068	thyroid hormone receptor beta, transcript variant 12	mRNA
XM_011534057.3	TOP2B	0.000880173	7155	DNA topoisomerase II beta, transcript variant X1	mRNA
NM_001330700.2	TOP2B	4.60E-10	7155	DNA topoisomerase II beta, transcript variant 1	mRNA
XM_017005	CLASP2	0.002273	23122	cytoplasmic linker associated protein 2, transcript variant X5	mRNA

948.1		62			
NM_001162429.3	PDCD6IP	0.0156332	10015	programmed cell death 6 interacting protein, transcript variant 2	mRNA
XM_017005911.1	TRAK1	0.0268866	22906	trafficking kinesin protein 1, transcript variant X9	mRNA
XR_940392.3	SACM1L	2.43E-05	22908	SAC1 like phosphatidylinositide phosphatase, transcript variant X2	misc_RNA
NM_001365116.2	NBEAL2	0.00728668	23218	neurobeachin like 2, transcript variant 2	mRNA
NM_001384776.1	MAP4	3.40E-13	4134	microtubule associated protein 4, transcript variant 37	mRNA
NM_001384806.1	MAP4	0.0185913	4134	microtubule associated protein 4, transcript variant 65	mRNA
NM_001320583.2	QRICH1	0.00449729	54870	glutamine rich 1, transcript variant 6	mRNA
NM_001389602.1	USP19	0.000125229	10869	ubiquitin specific peptidase 19, transcript variant 24	mRNA
NM_001304	ALAS1	8.48E-07	211	5'-aminolevulinate synthase 1, transcript variant 4	mRNA

444.1					
NM_001304444.1	ALAS1	0.00213581	211	5'-aminolevulinate synthase 1, transcript variant 4	mRNA
XM_011534136.2	WDR82	0.000338213	80335	WD repeat domain 82, transcript variant X1	mRNA
NM_025222.4	WDR82	5.37E-05	80335	WD repeat domain 82	mRNA
XM_011534151.3	BAP1	1.59E-05	8314	BRCA1 associated protein 1, transcript variant X3	mRNA
XM_006713384.3	RFT1	0.00213581	91869	RFT1 homolog, transcript variant X4	mRNA
NM_212539.2	PRKCD	3.00E-08	5580	protein kinase C delta, transcript variant 2	mRNA
NM_212539.2	PRKCD	0.0268866	5580	protein kinase C delta, transcript variant 2	mRNA
XM_011534054.1	TKT	2.13E-06	7086	transketolase, transcript variant X1	mRNA
NM_012096.	APPL1	0.022186	26060	adaptor protein, phosphotyrosine interacting with PH domain and leucine zipper 1	mRNA

3		4			
NM_007114.3	TMF1	0.0116648	7110	TATA element modulatory factor 1, transcript variant 1	mRNA
XR_924220.2	CD47	0.000323968	961	CD47 molecule, transcript variant X10	misc_RNA
NM_001690.4	ATP6V1A	0.0016763	523	ATPase H+ transporting V1 subunit A	mRNA
NM_002093.4	GSK3B	0.0342076	2932	glycogen synthase kinase 3 beta, transcript variant 1	mRNA
XM_006713588.2	GOLGB1	0.000133274	2804	golgin B1, transcript variant X4	mRNA
XM_011512699.3	GOLGB1	0.000160289	2804	golgin B1, transcript variant X2	mRNA
XR_427359.1	PDIA5	0.0040224	10954	protein disulfide isomerase family A member 5, transcript variant X1	misc_RNA
XM_017007431.1	KALRN	0.000178792	8997	kalirin RhoGEF kinase, transcript variant X12	mRNA
XM_006713	ITGB5	0.000657	3693	integrin subunit beta 5, transcript variant X2	mRNA

630.3		308			
NM_020733.2	HEG1	0.0319763	57493	heart development protein with EGF like domains 1	mRNA
NM_032242.4	PLXNA1	0.0130877	5361	plexin A1	mRNA
NM_032242.4	PLXNA1	0.0040224	5361	plexin A1	mRNA
NM_032242.4	PLXNA1	1.42E-06	5361	plexin A1	mRNA
NM_001003794.3	MGLL	0.000822568	11343	monoglyceride lipase, transcript variant 2	mRNA
XM_011512549.2	COPG1	0.0211033	22820	COPI coat complex subunit gamma 1, transcript variant X1	mRNA
NM_001370344.1	HMCES	0.040914	56941	5-hydroxymethylcytosine binding, ES cell specific, transcript variant 5	mRNA
NM_014602.3	PIK3R4	0.00644537	30849	phosphoinositide-3-kinase regulatory subunit 4	mRNA
NM_014602.	PIK3R4	0.015633	30849	phosphoinositide-3-kinase regulatory subunit 4	mRNA

3		2			
NM_001199181.3	ATP2C1	1.64E-07	27032	ATPase secretory pathway Ca2+ transporting 1, transcript variant 7	mRNA
NM_001199182.2	ATP2C1	0.0104319	27032	ATPase secretory pathway Ca2+ transporting 1, transcript variant 8	mRNA
NM_001178014.2	PCCB	0.0211033	5096	propionyl-CoA carboxylase subunit beta, transcript variant 2	mRNA
XM_017006627.1	PLS1	0.00339383	5357	plastin 1, transcript variant X6	mRNA
NM_001320222.2	U2SURP	0.00131687	23350	U2 snRNP associated SURP domain containing, transcript variant 4	mRNA
NM_001002800.3	SMC4	0.0282828	10051	structural maintenance of chromosomes 4, transcript variant 2	mRNA
NM_015028.4	TNIK	0.00103918	23043	TRAF2 and NCK interacting kinase, transcript variant 1	mRNA
NM_001349099.2	ECT2	0.00607462	1894	epithelial cell transforming 2, transcript variant 9	mRNA
XM_006713	ECT2	6.15E-07	1894	epithelial cell transforming 2, transcript variant X6	mRNA

524.4					
XM_011512593.2	ATP11B	0.000227166	23200	ATPase phospholipid transporting 11B (putative), transcript variant X3	mRNA
XM_017005562.1	IGF2BP2	0.00686488	10644	insulin like growth factor 2 mRNA binding protein 2, transcript variant X7	mRNA
NM_130832.3	OPA1	0.0282828	4976	OPA1 mitochondrial dynamin like GTPase, transcript variant 3	mRNA
NM_001354663.2	OPA1	0.000105814	4976	OPA1 mitochondrial dynamin like GTPase, transcript variant 9	mRNA
XM_011513124.3	ATP13A3	5.95E-06	79572	ATPase 13A3, transcript variant X6	mRNA
NM_001367549.1	ATP13A3	7.04E-08	79572	ATPase 13A3, transcript variant 2	mRNA
XM_017006796.1	LSG1	0.000380287	55341	large 60S subunit nuclear export GTPase 1, transcript variant X1	mRNA
XM_011512605.2	ACAP2	0.0282828	23527	ArfGAP with coiled-coil, ankyrin repeat and PH domains 2, transcript variant X8	mRNA
XM_006713	MELTF	0.000101	4241	melanotransferrin, transcript variant X2	mRNA

643.3		311			
XM_017007544.1	RUBCN	0.040914	9711	rubicon autophagy regulator, transcript variant X9	mRNA
XM_011513425.2	GAK	0.00213581	2580	cyclin G associated kinase, transcript variant X1	mRNA
XM_011513425.2	GAK	0.00868541	2580	cyclin G associated kinase, transcript variant X1	mRNA
NM_012318.3	LETM1	1.11E-08	3954	leucine zipper and EF-hand containing transmembrane protein 1	mRNA
NM_001256666.2	FAM193A	0.048575	8603	family with sequence similarity 193 member A, transcript variant 2	mRNA
NM_002111.8	HTT	0.000273438	3064	huntingtin, transcript variant 2	mRNA
NM_002111.8	HTT	0.00148402	3064	huntingtin, transcript variant 2	mRNA
NM_002111.8	HTT	2.43E-07	3064	huntingtin, transcript variant 2	mRNA
NM_001388	HTT	3.40E-13	3064	huntingtin, transcript variant 1	mRNA

492.1					
NM_001388492.1	HTT	0.0282828	3064	huntingtin, transcript variant 1	mRNA
NM_001388492.1	HTT	8.96E-06	3064	huntingtin, transcript variant 1	mRNA
NM_002111.8	HTT	5.89E-07	3064	huntingtin, transcript variant 2	mRNA
NR_110005.2	LRPAP1	0.000187923	4043	LDL receptor related protein associated protein 1, transcript variant 2	misc_RNA
XM_011513711.2	PGM2	0.0185913	55276	phosphoglucomutase 2, transcript variant X1	mRNA
NM_001204747.2	RFC1	3.57E-05	5981	replication factor C subunit 1, transcript variant 2	mRNA
NM_003359.4	UGDH	0.000358192	7358	UDP-glucose 6-dehydrogenase, transcript variant 1	mRNA
NM_001347827.2	PDGFRA	3.77E-05	5156	platelet derived growth factor receptor alpha, transcript variant 2	mRNA
NM_001347	PDGFRA	0.000257	5156	platelet derived growth factor receptor alpha, transcript variant 2	mRNA

827.2		885			
XM_024454284.1	CLOCK	0.0282828	9575	clock circadian regulator, transcript variant X3	mRNA
NM_001392011.1	PAICS	0.00686488	10606	phosphoribosylaminoimidazole carboxylase and phosphoribosylaminoimidazolesuccinocarboxamide synthase, transcript variant 5	mRNA
NM_000938.3	POLR2B	0.0268866	5431	RNA polymerase II subunit B, transcript variant 1	mRNA
NM_000938.3	POLR2B	3.40E-13	5431	RNA polymerase II subunit B, transcript variant 1	mRNA
NM_000938.3	POLR2B	8.89E-09	5431	RNA polymerase II subunit B, transcript variant 1	mRNA
NM_001031732.4	YTHDC1	0.0016763	91746	YTH domain containing 1, transcript variant 1	mRNA
NM_015574.2	ANKRD17	0.000482835	26057	ankyrin repeat domain 17, transcript variant 4	mRNA
NM_003715.4	USO1	0.0130877	8615	USO1 vesicle transport factor, transcript variant 2	mRNA
XM_017008	SEPTIN11	0.000425	55752	septin 11, transcript variant X3	mRNA

402.1		096			
XR_244659.4	LOC101928864	0.00303624	101928864	uncharacterized LOC101928864	lnc_RNA
XM_011532399.2	CCNG2	0.00449729	901	cyclin G2, transcript variant X2	mRNA
NM_001318119.2	SEC31A	0.0221864	22872	SEC31 homolog A, COPII coat complex component, transcript variant 9	mRNA
NM_001077207.4	SEC31A	0.012354	22872	SEC31 homolog A, COPII coat complex component, transcript variant 5	mRNA
XM_017007906.2	WDFY3	7.51E-05	23001	WD repeat and FYVE domain containing 3, transcript variant X2	mRNA
XM_017007906.2	WDFY3	0.00770001	23001	WD repeat and FYVE domain containing 3, transcript variant X2	mRNA
NM_001256426.2	PDLIM5	0.00157844	10611	PDZ and LIM domain 5, transcript variant 6	mRNA
NM_000671.4	ADH5	0.0300443	128	alcohol dehydrogenase 5 (class III), chi polypeptide	mRNA
NM_000944.	PPP3CA	0.001578	5530	protein phosphatase 3 catalytic subunit alpha, transcript variant 1	mRNA

5		44			
NM_001382627.1	NFKB1	0.045986	4790	nuclear factor kappa B subunit 1, transcript variant 6	mRNA
NM_001382627.1	NFKB1	0.048575	4790	nuclear factor kappa B subunit 1, transcript variant 6	mRNA
NM_001221.4	CAMK2D	0.00543382	817	calcium/calmodulin dependent protein kinase II delta, transcript variant 3	mRNA
NM_014822.4	SEC24D	0.00728668	9871	SEC24 homolog D, COPII coat complex component, transcript variant 1	mRNA
NM_014822.4	SEC24D	0.00425539	9871	SEC24 homolog D, COPII coat complex component, transcript variant 1	mRNA
XM_011532324.1	KIAA1109	0.0364492	84162	KIAA1109, transcript variant X6	mRNA
NM_032557.6	USP38	0.000242029	84640	ubiquitin specific peptidase 38, transcript variant 1	mRNA
XR_001741338.1	SMARCA5	0.000141056	8467	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5, transcript variant X1	misc_RNA
NM_002940.	ABCE1	3.37E-07	6059	ATP binding cassette subfamily E member 1, transcript variant 1	mRNA

3					
NM_001378126.1	SH3D19	0.000105814	152503	SH3 domain containing 19, transcript variant 9	mRNA
NM_021871.4	FGA	0.0116648	2243	fibrinogen alpha chain, transcript variant alpha	mRNA
NM_000508.5	FGA	0.0185913	2243	fibrinogen alpha chain, transcript variant alpha-E	mRNA
NM_001243372.2	CLCN3	0.0268866	1182	chloride voltage-gated channel 3, transcript variant a	mRNA
NM_021942.6	TRAPPC11	0.00116938	60684	trafficking protein particle complex subunit 11, transcript variant 1	mRNA
NM_021942.6	TRAPPC11	0.00131687	60684	trafficking protein particle complex subunit 11, transcript variant 1	mRNA
NM_020827.3	CFAP97	0.048575	57587	cilia and flagella associated protein 97, transcript variant 1	mRNA
XM_017009685.2	SDHA	0.040914	6389	succinate dehydrogenase complex flavoprotein subunit A, transcript variant X1	mRNA
XM_005248	TPPP	0.045986	11076	tubulin polymerization promoting protein, transcript variant X3	mRNA

237.3					
XM_024446221.1	CLPTM1L	0.0176209	81037	CLPTM1 like, transcript variant X3	mRNA
NM_001270660.2	MARCHF6	0.000695991	10299	membrane associated ring-CH-type finger 6, transcript variant 2	mRNA
NR_134469.2	TRIO	0.0300443	7204	trio Rho guanine nucleotide exchange factor, transcript variant 2	misc_RNA
XM_005248307.2	MYO10	1.85E-06	4651	myosin X, transcript variant X4	mRNA
XM_011514046.2	MYO10	2.02E-05	4651	myosin X, transcript variant X3	mRNA
XM_006714475.3	MYO10	0.00110625	4651	myosin X, transcript variant X1	mRNA
NM_016107.5	ZFR	1.14E-07	51663	zinc finger RNA binding protein	mRNA
NR_144318.2	ZFR	0.000510829	51663	zinc finger RNA binding protein	misc_RNA
NM_001258	TARS1	0.002663	6897	threonyl-tRNA synthetase 1, transcript variant 2	mRNA

437.1		3			
NR_169875.1	TTC23L	0.0319763	153657	tetratricopeptide repeat domain 23 like, transcript variant 8	misc_RNA
NM_001243120.2	SKP2	0.0040224	6502	S-phase kinase associated protein 2, transcript variant 3	mRNA
XM_017009330.2	NIPBL	0.00425539	25836	NIPBL cohesin loading factor, transcript variant X7	mRNA
NM_003999.3	OSMR	0.00728668	9180	oncostatin M receptor, transcript variant 1	mRNA
NR_073104.2	ITGA2	3.40E-13	3673	integrin subunit alpha 2, transcript variant 3	misc_RNA
NR_073104.2	ITGA2	8.11E-10	3673	integrin subunit alpha 2, transcript variant 3	misc_RNA
NR_073104.2	ITGA2	3.40E-13	3673	integrin subunit alpha 2, transcript variant 3	misc_RNA
NR_073105.2	ITGA2	3.40E-13	3673	integrin subunit alpha 2, transcript variant 4	misc_RNA
NM_001345	DHX29	0.028282	54505	DExH-box helicase 29, transcript variant 3	mRNA

965.2		8			
NM_175767.3	IL6ST	9.53E-05	3572	interleukin 6 cytokine family signal transducer, transcript variant 2	mRNA
NM_175767.3	IL6ST	1.59E-05	3572	interleukin 6 cytokine family signal transducer, transcript variant 2	mRNA
NM_001203246.2	GPBP1	0.0433858	65056	GC-rich promoter binding protein 1, transcript variant 4	mRNA
NM_001006600.3	ERBIN	0.0176209	55914	erbb2 interacting protein, transcript variant 7	mRNA
NM_001297651.2	MAST4	0.00240192	375449	microtubule associated serine/threonine kinase family member 4, transcript variant 7	mRNA
XM_017008913.2	OCLN	3.40E-13	100506658	occludin, transcript variant X1	mRNA
NM_018429.3	BDP1	0.000581772	55814	B double prime 1, subunit of RNA polymerase III transcription initiation factor IIIB	mRNA
NM_022132.5	MCCC2	9.53E-05	64087	methylcrotonyl-CoA carboxylase subunit 2, transcript variant 1	mRNA
NM_001364	TNPO1	0.001316	3842	transportin 1, transcript variant 3	mRNA

292.3		87			
NM_001130996.2	HMGCR	0.00985934	3156	3-hydroxy-3-methylglutaryl-CoA reductase, transcript variant 2	mRNA
XM_011543358.1	HMGCR	0.00321651	3156	3-hydroxy-3-methylglutaryl-CoA reductase, transcript variant X2	mRNA
XM_024454336.1	IQGAP2	3.77E-05	10788	IQ motif containing GTPase activating protein 2, transcript variant X1	mRNA
NR_104285.2	CAST	0.048575	831	calpastatin, transcript variant 15	misc_RNA
NM_000414.4	HSD17B4	0.00644537	3295	hydroxysteroid 17-beta dehydrogenase 4, transcript variant 2	mRNA
NM_001374500.1	HSD17B4	8.86E-07	3295	hydroxysteroid 17-beta dehydrogenase 4, transcript variant 9	mRNA
NM_001349541.2	GRAMD2B	0.0385333	65983	GRAM domain containing 2B, transcript variant 6	mRNA
NM_001182.5	ALDH7A1	0.00985934	501	aldehyde dehydrogenase 7 family member A1, transcript variant 1	mRNA
NM_001286	PRRC1	0.000425	133619	proline rich coiled-coil 1, transcript variant 1	mRNA

808.2		096			
NM_001033503.3	SAR1B	0.000323968	51128	secretion associated Ras related GTPase 1B, transcript variant 1	mRNA
NM_004661.4	CDC23	0.00985934	8697	cell division cycle 23	mRNA
XM_011543489.2	KDM3B	0.00449729	51780	lysine demethylase 3B, transcript variant X2	mRNA
NM_001323999.1	CTNNA1	5.95E-06	1495	catenin alpha 1, transcript variant 23	mRNA
NM_001194956.2	MATR3	8.03E-05	9782	matrin 3, transcript variant 5	mRNA
NM_001194956.2	MATR3	3.24E-07	9782	matrin 3, transcript variant 5	mRNA
XM_024454387.1	DIAPH1	3.69E-06	1729	diaphanous related formin 1, transcript variant X4	mRNA
XM_024454387.1	DIAPH1	0.000178792	1729	diaphanous related formin 1, transcript variant X4	mRNA
XM_024454	DIAPH1	0.000695	1729	diaphanous related formin 1, transcript variant X4	mRNA

387.1		991			
NM_020117.11	LARS1	8.76E-08	51520	leucyl-tRNA synthetase 1, transcript variant 1	mRNA
NM_020117.11	LARS1	3.40E-06	51520	leucyl-tRNA synthetase 1, transcript variant 1	mRNA
XM_011537662.1	RBM27	0.00770001	54439	RNA binding motif protein 27, transcript variant X7	mRNA
XM_011537577.2	STK32A	0.0148488	202374	serine/threonine kinase 32A, transcript variant X2	mRNA
XM_024446223.1	FBXO38	0.0016763	81545	F-box protein 38, transcript variant X2	mRNA
NM_014983.3	HMGXB3	1.14E-07	22993	HMG-box containing 3, transcript variant 1	mRNA
NM_005754.3	G3BP1	1.70E-09	10146	G3BP stress granule assembly factor 1, transcript variant 1	mRNA
NM_198321.4	GALNT10	0.0156332	55568	polypeptide N-acetylgalactosaminyltransferase 10	mRNA
NM_001252	GEMIN5	0.010431	25929	gem nuclear organelle associated protein 5, transcript variant 2	mRNA

156.2		9			
NM_001364018.1	CCNG1	1.87E-09	900	cyclin G1, transcript variant 4	mRNA
NM_033645.3	FBXW11	0.0156332	23291	F-box and WD repeat domain containing 11, transcript variant 1	mRNA
NM_001308191.2	CPEB4	0.040914	80315	cytoplasmic polyadenylation element binding protein 4, transcript variant 3	mRNA
XM_017009985.1	THOC3	3.87E-06	84321	THO complex 3, transcript variant X1	mRNA
NM_001291980.2	FGFR4	0.000657308	2264	fibroblast growth factor receptor 4, transcript variant 4	mRNA
NM_001291980.2	FGFR4	0.00449729	2264	fibroblast growth factor receptor 4, transcript variant 4	mRNA
XM_024446153.1	NSD1	0.0116648	64324	nuclear receptor binding SET domain protein 1, transcript variant X4	mRNA
XR_001742164.1	CNOT6	0.0148488	57472	CCR4-NOT transcription complex subunit 6, transcript variant X10	misc_RNA
XR_0017421	CNOT6	0.014848	57472	CCR4-NOT transcription complex subunit 6, transcript variant X10	misc_R

64.1		8			NA
XM_017011415.2	PRPF4B	0.00868541	8899	pre-mRNA processing factor 4B, transcript variant X5	mRNA
XM_011514546.2	HIVEP1	0.000822568	3096	HIVEP zinc finger 1, transcript variant X1	mRNA
XM_005249507.3	NUP153	1.66E-09	9972	nucleoporin 153, transcript variant X2	mRNA
XM_017011013.1	CARMIL1	9.53E-05	55604	capping protein regulator and myosin 1 linker 1, transcript variant X8	mRNA
NM_001387911.1	DDR1	1.51E-09	780	discoidin domain receptor tyrosine kinase 1, transcript variant 29	mRNA
XM_017011283.2	BAG6	0.000510829	7917	BAG cochaperone 6, transcript variant X11	mRNA
NM_001387946.1	BAG6	0.000777792	7917	BAG cochaperone 6, transcript variant 11	mRNA
NM_001136153.2	ATF6B	0.0130877	1388	activating transcription factor 6 beta, transcript variant 2	mRNA
NM_002224.	ITPR3	0.001039	3710	inositol 1,4,5-trisphosphate receptor type 3	mRNA

4		18			
XM_017010832.1	ITPR3	1.64E-08	3710	inositol 1,4,5-trisphosphate receptor type 3, transcript variant X2	mRNA
XM_011514577.3	ITPR3	0.00543382	3710	inositol 1,4,5-trisphosphate receptor type 3, transcript variant X1	mRNA
NM_021705.4	NFYA	6.15E-07	4800	nuclear transcription factor Y subunit alpha, transcript variant 2	mRNA
NM_021705.4	NFYA	7.11E-05	4800	nuclear transcription factor Y subunit alpha, transcript variant 2	mRNA
XM_017010999.1	TMEM63B	0.00358226	55362	transmembrane protein 63B, transcript variant X2	mRNA
NM_002388.6	MCM3	2.43E-05	4172	minichromosome maintenance complex component 3, transcript variant 1	mRNA
XM_017010749.1	GCLC	2.02E-05	2729	glutamate-cysteine ligase catalytic subunit, transcript variant X1	mRNA
NM_001197115.2	GCLC	3.57E-05	2729	glutamate-cysteine ligase catalytic subunit, transcript variant 2	mRNA
XM_017011	DST	0.004497	667	dystonin, transcript variant X26	mRNA

219.1		29			
XM_017011216.2	DST	0.000187923	667	dystonin, transcript variant X17	mRNA
XM_017011209.1	DST	0.0050794	667	dystonin, transcript variant X6	mRNA
XM_017011209.1	DST	3.56E-06	667	dystonin, transcript variant X6	mRNA
XM_017011216.2	DST	0.0116648	667	dystonin, transcript variant X17	mRNA
XM_005248994.2	ZNF451	0.0221864	26036	zinc finger protein 451, transcript variant X4	mRNA
XM_017010989.2	PHIP	0.00213581	55023	pleckstrin homology domain interacting protein, transcript variant X3	mRNA
NM_017934.7	PHIP	0.000125229	55023	pleckstrin homology domain interacting protein	mRNA
XM_011536099.3	TTK	0.0081583	7272	TTK protein kinase, transcript variant X1	mRNA
XM_006715	IBTK	0.001316	25998	inhibitor of Bruton tyrosine kinase, transcript variant X1	mRNA

453.3		87			
NM_001010853.3	PM20D2	0.000510829	135293	peptidase M20 domain containing 2	mRNA
NM_014611.3	MDN1	0.0282828	23195	midasin AAA ATPase 1	mRNA
NM_014611.3	MDN1	0.0156332	23195	midasin AAA ATPase 1	mRNA
NM_015323.5	UFL1	7.44E-07	23376	UFM1 specific ligase 1	mRNA
XM_011535395.3	ASCC3	1.75E-06	10973	activating signal cointegrator 1 complex subunit 3, transcript variant X2	mRNA
NM_138459.5	NUS1	3.54E-07	116150	NUS1 dehydrodolichyl diphosphate synthase subunit	mRNA
NM_001291984.2	PTPRK	0.000777792	5796	protein tyrosine phosphatase receptor type K, transcript variant 6	mRNA
NM_001350301.2	EPB41L2	0.0156332	2037	erythrocyte membrane protein band 4.1 like 2, transcript variant 8	mRNA
NM_001350	EPB41L2	0.022186	2037	erythrocyte membrane protein band 4.1 like 2, transcript variant 8	mRNA

301.2		4			
NM_006620.4	HBS1L	0.0185913	10767	HBS1 like translational GTPase, transcript variant 1	mRNA
NM_006620.4	HBS1L	0.000695991	10767	HBS1 like translational GTPase, transcript variant 1	mRNA
XR_001743524.1	ARFGEF3	0.00339383	57221	ARFGEF family member 3, transcript variant X1	misc_RNA
XR_001743524.1	ARFGEF3	0.000510829	57221	ARFGEF family member 3, transcript variant X1	misc_RNA
XR_001743524.1	ARFGEF3	0.00283312	57221	ARFGEF family member 3, transcript variant X1	misc_RNA
XM_024446536.1	UTRN	0.0081583	7402	utrophin, transcript variant X9	mRNA
XM_006715560.4	UTRN	0.0253262	7402	utrophin, transcript variant X12	mRNA
XR_001743393.2	NUP43	0.000358192	348995	nucleoporin 43, transcript variant X7	misc_RNA
XM_006715	SYNE1	0.036449	23345	spectrin repeat containing nuclear envelope protein 1, transcript variant X20	mRNA

420.2		2			
NM_001286199.2	SCAF8	0.0176209	22828	SR-related CTD associated factor 8, transcript variant 5	mRNA
XM_005267200.1	SYNJ2	0.0385333	8871	synaptojanin 2, transcript variant X10	mRNA
NM_000876.4	IGF2R	0.0050794	3482	insulin like growth factor 2 receptor	mRNA
NM_000876.4	IGF2R	5.04E-05	3482	insulin like growth factor 2 receptor	mRNA
NM_000876.4	IGF2R	7.63E-09	3482	insulin like growth factor 2 receptor	mRNA
NM_000876.4	IGF2R	0.00040024	3482	insulin like growth factor 2 receptor	mRNA
XM_017011960.1	INTS1	3.40E-13	26173	integrator complex subunit 1, transcript variant X2	mRNA
NM_001080453.3	INTS1	4.85E-08	26173	integrator complex subunit 1	mRNA
NM_001033	WIPI2	3.40E-13	26100	WD repeat domain, phosphoinositide interacting 2, transcript variant 4	mRNA

519.2					
XM_017012733.1	TNRC18	4.40E-06	84629	trinucleotide repeat containing 18, transcript variant X5	mRNA
XM_024446619.1	ZNF316	0.00103918	100131017	zinc finger protein 316, transcript variant X3	mRNA
XM_024446619.1	ZNF316	0.0433858	100131017	zinc finger protein 316, transcript variant X3	mRNA
NM_138426.4	GLCCI1	0.00213581	113263	glucocorticoid induced 1	mRNA
NM_001362794.2	TAX1BP1	3.98E-05	8887	Tax1 binding protein 1, transcript variant 5	mRNA
NM_001166118.3	NT5C3A	0.0319763	51251	5'-nucleotidase, cytosolic IIIA, transcript variant 4	mRNA
NM_015283.2	DPY19L1	0.00574795	23333	dpy-19 like C-mannosyltransferase 1, transcript variant 2	mRNA
NM_001122956.2	DBNL	0.0433858	28988	drebrin like, transcript variant 3	mRNA
NM_001363	YKT6	0.016627	10652	YKT6 v-SNARE homolog, transcript variant 2	mRNA

678.2		6			
XM_024446783.1	OGDH	0.048575	4967	oxoglutarate dehydrogenase, transcript variant X4	mRNA
XM_011515480.3	TNS3	9.29E-06	64759	tensin 3, transcript variant X7	mRNA
XM_017012538.1	TNS3	0.000777792	64759	tensin 3, transcript variant X3	mRNA
XM_011515239.1	COBL	0.000338213	23242	cordon-bleu WH2 repeat protein, transcript variant X9	mRNA
NM_201282.2	EGFR	0.0110174	1956	epidermal growth factor receptor, transcript variant 2	mRNA
XM_024446747.1	ZNF680	0.0176209	340252	zinc finger protein 680, transcript variant X12	mRNA
NM_001387691.1	POM121	2.88E-06	9883	POM121 transmembrane nucleoporin, transcript variant 10	mRNA
NM_032408.4	BAZ1B	0.0156332	9031	bromodomain adjacent to zinc finger domain 1B, transcript variant 2	mRNA
XM_017012	CASTOR2	0.022186	729438	cytosolic arginine sensor for mTORC1 subunit 2, transcript variant X1	mRNA

574.1		4			
NM_001350120.2	SEMA3C	0.0110174	10512	semaphorin 3C, transcript variant 1	mRNA
NM_001379277.1	AKAP9	0.0236925	10142	A-kinase anchoring protein 9, transcript variant 6	mRNA
XR_927503.3	GATAD1	0.045986	57798	GATA zinc finger domain containing 1, transcript variant X8	misc_RNA
XM_005250453.1	PON2	1.35E-05	5445	paraoxonase 2, transcript variant X1	mRNA
NR_147989.1	CZ1P-ASNS	0.00098721	107986827	CZ1P-ASNS readthrough	lnc_RNA
NM_003496.4	TRRAP	0.0110174	8295	transformation/transcription domain associated protein, transcript variant 2	mRNA
NM_003496.4	TRRAP	0.000187923	8295	transformation/transcription domain associated protein, transcript variant 2	mRNA
NM_001244580.2	TRRAP	0.0198244	8295	transformation/transcription domain associated protein, transcript variant 1	mRNA
XM_006715	ARPC1B	0.017620	10095	actin related protein 2/3 complex subunit 1B, transcript variant X2	mRNA

826.2		9			
XM_005250348.3	MCM7	1.39E-08	4176	minichromosome maintenance complex component 7, transcript variant X2	mRNA
NM_001364999.1	TAF6	0.0342076	6878	TATA-box binding protein associated factor 6, transcript variant 8	mRNA
NM_001363493.2	SLC12A9	0.00449729	56996	solute carrier family 12 member 9, transcript variant 4	mRNA
NM_001128853.2	SRRT	0.045986	51593	serrate, RNA effector molecule, transcript variant 4	mRNA
XM_011516589.3	TRIM56	0.0130877	81844	tripartite motif containing 56, transcript variant X1	mRNA
NM_001084.5	PLOD3	1.64E-06	8985	procollagen-lysine,2-oxoglutarate 5-dioxygenase 3	mRNA
NM_005746.3	NAMPT	0.0050794	10135	nicotinamide phosphoribosyltransferase	mRNA
NM_005746.3	NAMPT	3.77E-05	10135	nicotinamide phosphoribosyltransferase	mRNA
XM_011516	MET	1.59E-05	4233	MET proto-oncogene, receptor tyrosine kinase, transcript variant X1	mRNA

223.1					
NM_001127500.3	MET	2.87E-07	4233	MET proto-oncogene, receptor tyrosine kinase, transcript variant 1	mRNA
XM_011515736.2	FAM3C	2.77E-05	10447	FAM3 metabolism regulating signaling molecule C, transcript variant X1	mRNA
NM_001382221.1	TNPO3	0.000187923	23534	transportin 3, transcript variant 9	mRNA
XM_011516289.2	ZC3HC1	0.0319763	51530	zinc finger C3HC-type containing 1, transcript variant X3	mRNA
XM_005250233.5	KLHDC10	0.000425096	23008	kelch domain containing 10, transcript variant X1	mRNA
NM_005397.4	PODXL	5.68E-05	5420	podocalyxin like, transcript variant 2	mRNA
NM_015135.3	NUP205	0.012354	23165	nucleoporin 205, transcript variant 1	mRNA
NM_001318246.2	CREB3L2	0.00339383	64764	cAMP responsive element binding protein 3 like 2, transcript variant 3	mRNA
NM_016019.	LUC7L2	0.001484	51631	LUC7 like 2, pre-mRNA splicing factor, transcript variant 1	mRNA

5		02			
NR_156491.1	SLC37A3	0.0026633	84255	solute carrier family 37 member 3, transcript variant 12	misc_RNA
NM_005232.5	EPHA1	0.0081583	2041	EPH receptor A1	mRNA
XM_005250075.3	TCAF1	0.00054628	9747	TRPM8 channel associated factor 1, transcript variant X3	mRNA
NM_001371245.1	PDIA4	1.11E-08	9601	protein disulfide isomerase family A member 4, transcript variant 3	mRNA
NM_152411.4	ZNF786	0.0364492	136051	zinc finger protein 786	mRNA
NR_171548.1	CHPF2	0.00607462	54480	chondroitin polymerizing factor 2, transcript variant 7	misc_RNA
XM_005250027.4	KMT2C	8.96E-06	58508	lysine methyltransferase 2C, transcript variant X5	mRNA
XM_017012482.1	KMT2C	0.00926878	58508	lysine methyltransferase 2C, transcript variant X9	mRNA
XM_005250	KMT2C	0.022186	58508	lysine methyltransferase 2C, transcript variant X5	mRNA

027.4		4			
XR_927552.3	UBE3C	0.00476676	9690	ubiquitin protein ligase E3C, transcript variant X3	misc_RNA
NM_001348081.2	DLC1	0.012354	10395	DLC1 Rho GTPase activating protein, transcript variant 6	mRNA
NM_006094.5	DLC1	0.012354	10395	DLC1 Rho GTPase activating protein, transcript variant 2	mRNA
NM_006094.5	DLC1	0.00574795	10395	DLC1 Rho GTPase activating protein, transcript variant 2	mRNA
NM_021630.6	PDLIM2	0.00103918	64236	PDZ and LIM domain 2, transcript variant 2	mRNA
NM_001393997.1	CCAR2	1.64E-08	57805	cell cycle and apoptosis regulator 2, transcript variant 1	mRNA
NM_001128930.3	ENTPD4	0.045986	9583	ectonucleoside triphosphate diphosphohydrolase 4, transcript variant 2	mRNA
NM_024940.8	DOCK5	9.29E-06	80005	dedicator of cytokinesis 5, transcript variant 1	mRNA
NM_024940.	DOCK5	0.015633	80005	dedicator of cytokinesis 5, transcript variant 1	mRNA

8		2			
NM_024940.8	DOCK5	0.00321651	80005	dedicator of cytokinesis 5, transcript variant 1	mRNA
NM_001197293.3	DPYSL2	0.00358226	1808	dihydropyrimidinase like 2, transcript variant 1	mRNA
NM_001195102.3	GSR	2.71E-08	2936	glutathione-disulfide reductase, transcript variant 2	mRNA
NM_001362912.2	DDHD2	1.80E-05	23259	DDHD domain containing 2, transcript variant 5	mRNA
NM_001362912.2	DDHD2	3.98E-05	23259	DDHD domain containing 2, transcript variant 5	mRNA
NM_023034.2	NSD3	0.00339383	54904	nuclear receptor binding SET domain protein 3, transcript variant long	mRNA
NM_001352779.2	TACC1	0.00253827	6867	transforming acidic coiled-coil containing protein 1, transcript variant 6	mRNA
NM_032237.5	POMK	0.0236925	84197	protein O-mannose kinase, transcript variant 1	mRNA
NM_001081	PRKDC	2.40E-06	5591	protein kinase, DNA-activated, catalytic subunit, transcript variant 2	mRNA

640.2					
NM_001081640.2	PRKDC	0.000777792	5591	protein kinase, DNA-activated, catalytic subunit, transcript variant 2	mRNA
NM_001081640.2	PRKDC	5.78E-10	5591	protein kinase, DNA-activated, catalytic subunit, transcript variant 2	mRNA
NM_001081640.2	PRKDC	6.42E-08	5591	protein kinase, DNA-activated, catalytic subunit, transcript variant 2	mRNA
NM_001081640.2	PRKDC	5.67E-09	5591	protein kinase, DNA-activated, catalytic subunit, transcript variant 2	mRNA
NM_006904.7	PRKDC	5.68E-05	5591	protein kinase, DNA-activated, catalytic subunit, transcript variant 1	mRNA
XM_017014108.2	RB1CC1	0.045986	9821	RB1 inducible coiled-coil 1, transcript variant X7	mRNA
XM_011517529.3	LYN	0.000141056	4067	LYN proto-oncogene, Src family tyrosine kinase, transcript variant X1	mRNA
NM_017813.5	BPNT2	4.80E-10	54928	3'(2'), 5'-bisphosphate nucleotidase 2	mRNA
NM_001144	NSMAF	0.000987	8439	neutral sphingomyelinase activation associated factor, transcript variant 2	mRNA

772.1		21			
NM_003580.4	NSMAF	0.00607462	8439	neutral sphingomyelinase activation associated factor, transcript variant 1	mRNA
XM_017013612.1	CHD7	0.00321651	55636	chromodomain helicase DNA binding protein 7, transcript variant X3	mRNA
XM_017013612.1	CHD7	0.0130877	55636	chromodomain helicase DNA binding protein 7, transcript variant X3	mRNA
XM_017013266.1	TRAM1	0.00607462	23471	translocation associated membrane protein 1, transcript variant X1	mRNA
NR_170693.1	TPD52	0.00449729	7163	tumor protein D52, transcript variant 16	misc_RNA
NM_152284.4	CHMP4C	0.0026633	92421	charged multivesicular body protein 4C	mRNA
NM_002568.4	PABPC1	1.59E-05	26986	poly(A) binding protein cytoplasmic 1	mRNA
XM_005250962.5	UBR5	0.000618347	51366	ubiquitin protein ligase E3 component n-recognin 5, transcript variant X11	mRNA
XM_005250	UBR5	0.038533	51366	ubiquitin protein ligase E3 component n-recognin 5, transcript variant X11	mRNA

962.5		3			
XM_011517104.3	UBR5	0.0282828	51366	ubiquitin protein ligase E3 component n-recognin 5, transcript variant X1	mRNA
NM_006265.3	RAD21	0.0364492	5885	RAD21 cohesin complex component	mRNA
NM_006265.3	RAD21	4.87E-07	5885	RAD21 cohesin complex component	mRNA
NM_014078.6	MRPL13	0.0282828	28998	mitochondrial ribosomal protein L13	mRNA
NM_001317918.1	FAM91A1	4.13E-06	157769	family with sequence similarity 91 member A1, transcript variant 3	mRNA
NM_001317918.1	FAM91A1	0.000178792	157769	family with sequence similarity 91 member A1, transcript variant 3	mRNA
XM_017014113.2	WASHC5	0.000740067	9897	WASH complex subunit 5, transcript variant X1	mRNA
XM_017014113.2	WASHC5	5.04E-05	9897	WASH complex subunit 5, transcript variant X1	mRNA
NM_001330	WASHC5	0.010431	9897	WASH complex subunit 5, transcript variant 2	mRNA

609.2		9			
NM_001323553.2	EFR3A	0.0300443	23167	EFR3 homolog A, transcript variant 2	mRNA
XM_011516968.2	AGO2	0.00148402	27161	argonaute RISC catalytic component 2, transcript variant X1	mRNA
NM_001352744.2	PTK2	5.01E-06	5747	protein tyrosine kinase 2, transcript variant 55	mRNA
NM_198488.5	FAM83H	0.045986	286077	family with sequence similarity 83 member H	mRNA
NM_015356.5	SCRIB	3.40E-13	23513	scribble planar cell polarity protein, transcript variant 2	mRNA
NM_023080.3	C8orf33	0.00644537	65265	chromosome 8 open reading frame 33	mRNA
XR_929340.2	ERMP1	3.36E-05	79956	endoplasmic reticulum metallopeptidase 1, transcript variant X6	misc_RNA
XR_001746180.2	UHRF2	0.040914	115426	ubiquitin like with PHD and ring finger domains 2, transcript variant X7	misc_RNA
NM_001128	PSIP1	0.008158	11168	PC4 and SFRS1 interacting protein 1, transcript variant 3	mRNA

217.3		3			
NM_001386037.1	DENND4C	0.00358226	55667	DENN domain containing 4C	mRNA
NM_004529.4	MLLT3	0.0282828	4300	MLLT3 super elongation complex subunit, transcript variant 1	mRNA
NM_001370062.2	UBAP2	0.012354	55833	ubiquitin associated protein 2, transcript variant 9	mRNA
NM_007126.5	VCP	7.11E-06	7415	valosin containing protein, transcript variant 1	mRNA
NM_006377.6	UNC13B	0.0282828	10497	unc-13 homolog B, transcript variant 1	mRNA
NM_006377.6	UNC13B	0.0166276	10497	unc-13 homolog B, transcript variant 1	mRNA
NM_006289.4	TLN1	0.0104319	7094	talin 1	mRNA
NM_006289.4	TLN1	4.80E-10	7094	talin 1	mRNA
NM_006289.	TLN1	0.000290	7094	talin 1	mRNA

4		692			
NM_001376037.1	PIP5K1B	0.00190081	8395	phosphatidylinositol-4-phosphate 5-kinase type 1 beta, transcript variant 5	mRNA
XM_011519204.1	TJP2	0.00110625	9414	tight junction protein 2, transcript variant X2	mRNA
NM_001170415.1	TJP2	8.86E-07	9414	tight junction protein 2, transcript variant 4	mRNA
XR_929807.2	PCSK5	1.21E-06	5125	proprotein convertase subtilisin/kexin type 5, transcript variant X6	misc_RNA
XM_006717258.1	TLE1	1.72E-07	7088	TLE family member 1, transcriptional corepressor, transcript variant X3	mRNA
XM_017014195.1	SEMA4D	0.0166276	10507	semaphorin 4D, transcript variant X9	mRNA
NM_001378571.1	IARS1	0.000931169	3376	isoleucyl-tRNA synthetase 1, transcript variant 8	mRNA
NM_001378571.1	IARS1	1.28E-06	3376	isoleucyl-tRNA synthetase 1, transcript variant 8	mRNA
NR_149061.	PTCH1	0.048575	5727	patched 1, transcript variant 10	misc_R

2					NA
NM_001201575.2	CTSV	0.000777792	1515	cathepsin V, transcript variant 2	mRNA
XM_017015354.1	TRIM14	0.00283312	9830	tripartite motif containing 14, transcript variant X6	mRNA
XM_017015063.1	TGFBR1	0.0221864	7046	transforming growth factor beta receptor 1, transcript variant X2	mRNA
XM_017015063.1	TGFBR1	0.00644537	7046	transforming growth factor beta receptor 1, transcript variant X2	mRNA
XM_017015063.1	TGFBR1	0.012354	7046	transforming growth factor beta receptor 1, transcript variant X2	mRNA
XM_017014211.2	SMC2	0.000931169	10592	structural maintenance of chromosomes 2, transcript variant X11	mRNA
NM_001318360.2	ELP1	0.00770001	8518	elongator acetyltransferase complex subunit 1, transcript variant 2	mRNA
XM_017014572.1	TMEM245	4.60E-10	23731	transmembrane protein 245, transcript variant X7	mRNA
XM_017014	TMEM245	3.76E-07	23731	transmembrane protein 245, transcript variant X7	mRNA

572.1					
NM_001136562.3	PALM2AKAP2	0.0433858	445815	PALM2 and AKAP2 fusion, transcript variant 7	mRNA
NM_001363756.2	ECPAS	0.0385333	23392	Ecm29 proteasome adaptor and scaffold, transcript variant 2	mRNA
NM_001363756.2	ECPAS	0.0050794	23392	Ecm29 proteasome adaptor and scaffold, transcript variant 2	mRNA
XM_011518395.3	PTGR1	0.0139253	22949	prostaglandin reductase 1, transcript variant X5	mRNA
XM_005252186.5	UGCG	2.87E-07	7357	UDP-glucose ceramide glucosyltransferase, transcript variant X1	mRNA
XM_011519265.1	PTBP3	0.00253827	9991	polypyrimidine tract binding protein 3, transcript variant X1	mRNA
NM_001353059.2	GSN	0.00201629	2934	gelsolin, transcript variant 17	mRNA
XM_011518264.3	DAB2IP	3.40E-13	153090	DAB2 interacting protein, transcript variant X1	mRNA
XM_011518	GAPVD1	0.043385	26130	GTPase activating protein and VPS9 domains 1, transcript variant X5	mRNA

506.2		8			
NM_001131017.2	CIZ1	0.0433858	25792	CDKN1A interacting zinc finger protein 1, transcript variant 3	mRNA
XM_006717246.1	SPTAN1	0.0282828	6709	spectrin alpha, non-erythrocytic 1, transcript variant X2	mRNA
NM_001375958.1	ZER1	0.00227362	10444	zyg-11 related cell cycle regulator, transcript variant 6	mRNA
NM_015354.3	NUP188	0.0037981	23511	nucleoporin 188	mRNA
XM_011518837.2	PTPA	0.000169724	5524	protein phosphatase 2 phosphatase activator, transcript variant X4	mRNA
NM_017873.4	ASB6	0.0130877	140459	ankyrin repeat and SOCS box containing 6, transcript variant 1	mRNA
XM_005251822.3	FNBP1	0.000187923	23048	formin binding protein 1, transcript variant X11	mRNA
XM_011519173.2	FUBP3	0.000657308	8939	far upstream element binding protein 3, transcript variant X3	mRNA
NM_007313.	ABL1	0.022186	25	ABL proto-oncogene 1, non-receptor tyrosine kinase, transcript variant b	mRNA

3		4			
NM_001384823.1	PRRC2B	0.00240192	84726	proline rich coiled-coil 2B, transcript variant 5	mRNA
XM_017015318.1	GTF3C4	0.0300443	9329	general transcription factor IIIC subunit 4, transcript variant X1	mRNA
NM_001362177.2	TSC1	0.0104319	7248	TSC complex subunit 1, transcript variant 5	mRNA
XM_017015109.1	VAV2	0.000880173	7410	vav guanine nucleotide exchange factor 2, transcript variant X2	mRNA
XM_011518272.1	CAMSAP1	0.00201629	157922	calmodulin regulated spectrin associated protein 1, transcript variant X4	mRNA
XM_017014302.1	CAMSAP1	1.07E-06	157922	calmodulin regulated spectrin associated protein 1, transcript variant X3	mRNA
XR_929881.2	SEC16A	3.40E-13	9919	SEC16 homolog A, endoplasmic reticulum export factor, transcript variant X21	misc_RNA
XM_011518717.2	NOTCH1	0.00116938	4851	notch receptor 1, transcript variant X1	mRNA
XM_011518	NOTCH1	0.019824	4851	notch receptor 1, transcript variant X1	mRNA

717.2		4			
NM_024718.5	RABL6	0.00607462	55684	RAB, member RAS oncogene family like 6, transcript variant 1	mRNA
NM_015456.5	NELFB	0.0433858	25920	negative elongation factor complex member B	mRNA
XM_017015138.1	EHMT1	0.0433858	79813	euchromatic histone lysine methyltransferase 1, transcript variant X11	mRNA
NM_005647.4	TBL1X	0.00985934	6907	transducin beta like 1 X-linked, transcript variant 1	mRNA
NM_005647.4	TBL1X	0.0282828	6907	transducin beta like 1 X-linked, transcript variant 1	mRNA
NM_015691.4	WWC3	0.00339383	55841	WWC family member 3	mRNA
NM_001198719.2	RBBP7	0.0198244	5931	RB binding protein 7, chromatin remodeling factor, transcript variant 1	mRNA
NM_001173455.2	PDHA1	0.00131687	5160	pyruvate dehydrogenase E1 subunit alpha 1, transcript variant 3	mRNA
NM_001173	PDHA1	0.011664	5160	pyruvate dehydrogenase E1 subunit alpha 1, transcript variant 3	mRNA

455.2		8			
XM_011544000.3	MED14	0.0319763	9282	mediator complex subunit 14, transcript variant X3	mRNA
XM_005272675.4	USP9X	0.0268866	8239	ubiquitin specific peptidase 9 X-linked, transcript variant X1	mRNA
XM_005272656.5	KDM6A	0.0300443	7403	lysine demethylase 6A, transcript variant X5	mRNA
NM_001257291.2	SLC9A7	0.00339383	84679	solute carrier family 9 member A7, transcript variant 1	mRNA
XM_011543924.2	CDK16	0.0176209	5127	cyclin dependent kinase 16, transcript variant X6	mRNA
XM_017029569.1	CDK16	0.000160289	5127	cyclin dependent kinase 16, transcript variant X3	mRNA
NM_001371072.1	USP11	0.0104319	8237	ubiquitin specific peptidase 11	mRNA
NM_001654.5	ARAF	0.0221864	369	A-Raf proto-oncogene, serine/threonine kinase, transcript variant 1	mRNA
NM_001353	KDM5C	0.004497	8242	lysine demethylase 5C, transcript variant 5	mRNA

979.2		29			
NM_001353979.2	KDM5C	0.00240192	8242	lysine demethylase 5C, transcript variant 5	mRNA
NM_001281463.1	SMC1A	0.0139253	8243	structural maintenance of chromosomes 1A, transcript variant 2	mRNA
NM_031407.7	HUWE1	0.000380287	10075	HECT, UBA and WWE domain containing E3 ubiquitin protein ligase 1	mRNA
XM_011530747.1	HUWE1	0.0081583	10075	HECT, UBA and WWE domain containing E3 ubiquitin protein ligase 1, transcript variant X14	mRNA
XM_011530747.1	HUWE1	5.04E-05	10075	HECT, UBA and WWE domain containing E3 ubiquitin protein ligase 1, transcript variant X14	mRNA
NM_019067.6	GNL3L	0.00574795	54552	G protein nucleolar 3 like, transcript variant 2	mRNA
NM_002444.3	MSN	3.40E-13	4478	moesin	mRNA
XM_017029322.2	DLG3	0.00607462	1741	discs large MAGUK scaffold protein 3, transcript variant X4	mRNA
XM_024452	OGT	0.011664	8473	O-linked N-acetylglucosamine (GlcNAc) transferase, transcript variant X1	mRNA

467.1		8			
NM_181673.3	OGT	0.0282828	8473	O-linked N-acetylglucosamine (GlcNAc) transferase, transcript variant 2	mRNA
XM_017029605.1	ATRX	0.0433858	546	ATRX chromatin remodeler, transcript variant X10	mRNA
NM_000291.4	PGK1	3.40E-13	5230	phosphoglycerate kinase 1	mRNA
NM_001204402.2	PRPS1	0.00103918	5631	phosphoribosyl pyrophosphate synthetase 1, transcript variant 2	mRNA
XM_005262109.2	ACSL4	1.49E-06	2182	acyl-CoA synthetase long chain family member 4, transcript variant X2	mRNA
NM_001282338.2	PLS3	0.00476676	5358	plastin 3, transcript variant 5	mRNA
NM_001560.3	IL13RA1	0.000307575	3597	interleukin 13 receptor subunit alpha 1	mRNA
NM_001375377.1	STAG2	0.0017864	10735	stromal antigen 2, transcript variant 17	mRNA
NM_001375	STAG2	0.028282	10735	stromal antigen 2, transcript variant 17	mRNA

377.1		8			
NM_001130847.4	AIFM1	0.00686488	9131	apoptosis inducing factor mitochondria associated 1, transcript variant 5	mRNA
NM_001042452.2	STK26	0.0139253	51765	serine/threonine kinase 26, transcript variant 3	mRNA
NM_001448.3	GPC4	3.36E-05	2239	glypican 4	mRNA
NR_033699.2	FMR1	5.68E-05	2332	FMRP translational regulator 1, transcript variant ISO4	misc_RNA
NM_001301228.2	HMGB3	0.00140507	3149	high mobility group box 3, transcript variant 1	mRNA
NM_000425.5	L1CAM	0.000931169	3897	L1 cell adhesion molecule, transcript variant 1	mRNA
XM_017029471.2	HCFC1	0.00770001	3054	host cell factor C1, transcript variant X5	mRNA
XM_005274668.4	IRAK1	5.89E-07	3654	interleukin 1 receptor associated kinase 1, transcript variant X1	mRNA
NM_001363.	DKC1	7.11E-05	1736	dyskerin pseudouridine synthase 1, transcript variant 1	mRNA

5					

Table SVII. EMT-related genes from the EMT database.

VIM	CTNND1	HS3ST3A1	IFITM3	COLGALT2	PRC1	CCN5	MIR30C1
CDH1	CXADR	IFI44	IGF1	COMP	PRKCA	TRIM62	SNHG6
FN1	DAB2	IFIT1	IGF1R	CORO1A	PRKCH	SASH1	MIR616
ZEB1	DPYSL3	IGFBP2	IL18	CPA4	PRKD1	PFN2	CCAT2
CDH2	DST	IL4R	INPP4B	CSF1	PROCR	DAB2IP	MIR187
MMP2	ELF3	IRF7	ISG15	CTHRC1	PRR15	TRPS1	HOXA11-AS
SNAI2	EPB41L4B	ITGAV	ITGA2	CXCL6	PRR5-ARHGAP8	MET	MIR153-1
ZEB2	EPN3	ITGB3	ITGA3	CXCL8	PRRG4	BTRC	MIR491
SPARC	F3	JUN	ITGB4	CXCR4	PRSS22	EPB41L3	GHET1
SNAI1	GADD45B	KDF1	ITGB5	CYP27B1	PTAFR	WASF3	MIR148A
CCN2	GRHL1	KLK5	JAM3	CYP2F1	PTGER2	OSM	MIR106B
TWIST1	IL1RN	KLK8	KCNK1	CYP4F11	PTGS1	SEMA4C	MIR655
CDH11	JAG1	KRT16	KIAA1191	DAPP1	RAB26	TIAM1	MIR9-1
CLDN4	KRT14	KRT8	KIT	DBN1	RAPGEF5	EPAS1	CPS1-IT1
EPCAM	KRT15	LHFPL6	KRT17	DEPTOR	RBMS1	PDPN	MIR26B

SERPINE1	LAD1	LRRC1	KRT7	DHRS2	RBMS3	SNAI3	MIR124-1
TGFB1	LAMA3	LUM	KRTCAP3	DIO2	RGL1	SATB1	MIR9-3
COL3A1	LLGL2	MAPKAP1	LAMA2	DIXDC1	RGS2	WNT1	MIR96
ESRP1	LTBP2	MCAM	LAMA5	DMKN	RHOB	SOX9	MIR489
INHBA	MAPK13	MRAS	LAMB1	DNAJB4	RLN2	HTATIP2	MIR379
PMP22	MARVELD2	MSRB3	LARP6	DOCK10	RNF128	ASCL2	HOTTIP
WNT5A	MARVELD3	NECTIN4	LAS1L	DOCK9	RNF14	FOXF2	MIR15A
ST14	MISP	NEXN	LIX1L	DPP8	ROR1	PARD6A	MIR194-1
TNC	MMP14	NID1	LMCD1	DPT	RUNX2	SOX5	NKILA
CLDN7	MRC2	NID2	LOXL1	ECM2	S100A9	TRIM44	MIR630
EMP3	MUC1	OVOL2	LRATD2	EFCAB14	SBNO1	TRIM16	CCAT1
FSTL1	MYL9	P3H1	LRP1	EFHD2	SCRIB	FOXD3	MIR143
ITGA5	MYO5B	P3H2	LRRC15	EFNA1	SEC23A	DLX2	MIR132
LAMC2	NT5C2	PDGFC	LTBP4	EGF	SELENBP1	PDCD4	MIR644A
VCAN	PMEPA1	PERP	LY6E	EGR2	SEMA3C	NTRK2	MIR361
CDH3	PRRX1	PLOD2	MACF1	EIF4A2	SEMA5A	RASAL2	MIR490
COL5A2	RGS4	PVR	MAF	EPDR1	SEPTIN6	FZD2	UCA1
DCN	SCNN1A	RBM47	MAP4K4	ERMP1	SERPINH1	CIP2A	MIR382

DSP	SFRP1	RFTN1	MARK3	ESR1	SFRP2	ID1	PVT1
ERBB3	SH2D3A	RHOD	MBNL1	ETS2	SHROOM3	BMP4	MIR23A
POSTN	SH3YL1	S100A4	MGP	FAAH2	SKIL	FOXA1	MIR485
RAB25	SRPX	SAA1	MMP10	FAM110C	SLC16A5	GKN1	MIR31
SPINT2	TGFB1I1	SDC1	MMP7	FAM83A	SLC22A4	HCFC1R1	MIR125B2
TGM2	TGFB2	SERPINB5	MPP7	FAT4	SLC37A2	USP22	AFAP1-AS1
CDS1	THY1	SFRP4	MYLK	FBN2	SLC3A2	EFEMP1	MIR598
COL1A1	TMPRSS4	SHC1	MYO6	FGF5	SLC7A5	DYRK2	MIR876
ESRP2	ABLIM1	SLC2A3	MYO9A	FILIP1L	SMC5	PITPNM3	MIR181B1
GRHL2	ACTA2	SLC6A8	NAP1L3	FLNB	SNCA	ONECUT2	MIR30C2
HTRA1	ADAM12	SLIT2	NDRG1	FUCA1	SNTB1	TRIM66	MIR1236
MAP7	AGR2	SLIT3	NNMT	FUT1	SOX10	SUZ12	MIR612
MMP9	AKT3	SMAD3	NPHP3	FUT3	SOX2	SATB2	MIR139
OCLN	ANGPTL2	SMPDL3B	NRG1	FYN	SPINK5	CCL21	MIR22
PDGFRB	ANK3	SPRR1B	NRP2	GALE	ST3GAL2	JARID2	MIR520C
PRSS8	ARHGAP8	STAT1	OSBPL3	GALNT2	STAT5A	TP53INP1	MIR495
AP1M2	BSPRY	SULF1	PAK6	GGCT	STEAP1	BCL9	MIR29B1

AP1S2	CA2	SYDE1	PARD6B	GLDC	STEAP4	GFER	SNHG15
AXL	CAVIN1	SYK	PATJ	GLI3	STRA6	RHOC	HOXA-AS2
CD44	CCN1	TACSTD2	PEA15	GLIPR2	STX19	NODAL	ZEB1-AS1
COL1A2	CHN1	TFPI	PIK3CD	GLS2	STX3	FHOD1	CBR3-AS1
COL5A1	CKMT1B	TGFB3	PLAU	GLYR1	STXBP5	GOLM1	MIR195
FBN1	CLDN1	THBS2	PROM2	GNAL	SUSD5	NANOGP8	MIR27B
FGFBP1	CLDN11	TIMP2	PRR16	GPC1	SYNE1	HIPK2	NORAD
FGFR1	COL7A1	TIMP3	PTGIS	GSDME	SYT11	TFAP4	BCAR4
FOXC2	CXCL12	TJP3	PTK2	GSE1	SYTL1	SENP1	CYTOR
IRF6	DDR1	TMEM125	PTPN3	GSK3B	TBC1D23	RCOR1	MIR214
KRT5	DLC1	TMEM158	PXDC1	HACL1	TC2N	CD274	MIR340
PCOLCE	ELMO3	TMPRSS11E	RAB31	HBEGF	TGFBR1	FLOT2	MIR661
S100A14	EML1	TPD52	RAB6A	HEY1	THBD	CCN6	MIR9-2
CLDN3	EPB41L5	TPM2	RASEF	HMBS	TMEM126	CUX1	MIR26A1

					B		
COL6A1	EPHA1	TRIM29	RFLNB	HPS5	TMEM167A	TBX1	MIR16-2
COL6A2	FA2H	VEGFA	SACS	HS3ST1	TMEM37	NES	MIR100
FXYD3	FHL1	WIPF1	SAT1	HS3ST3B1	TMEM47	MIR23B	LINC00261
GNG11	ID2	WWC1	SCEL	HSPG2	TMPRSS13	MIR29C	LINC01186
GREM1	IFIT3	ZCCHC24	SCG2	IER3	TNFAIP3	MIR203A	LINC02231
IGFBP7	IGFBP5	ZFPM2	SDC4	IFIT2	TNFRSF11B	MIR155	LINC02599
ITGB1	ITGA6	ABCA12	SERPINB2	IGF2	TOB1	MIR370	BX111
KRT19	ITGB6	ABI1	SHMT1	IKBIP	TSPAN13	LINC00312	TBILA
LOX	JAG2	ACAA1	SMAD2	IL11	TSPAN4	ASAP1-IT1	SLC25A25-AS1
LOXL2	KLK10	ACTN1	SMAD7	IL13RA2	TUBA4A	DUBR	LOC111162621

PDGFRA	LAMB3	ADAM23	SPHK1	IL1B	TUFT1	MSC-AS1	TP73-AS1
PTX3	LCN2	ADAMTS1	SPP1	IL1R1	TUT7	MIR193BHG	MIR93
SERPINE2	LEF1	ADORA2B	SPRR1A	IL32	ULBP2	FAM225B	MIR153-2
SLPI	MLPH	ALDH1A3	SPRY1	ILDR1	VAV3	LINC00313	MIR448
SPOCK1	MME	ALDH3A2	STEAP3	ILK	VPS13A	FAM225A	MIR338
TCF4	MYH14	ALOX5AP	SYNE2	INAVA	VSNL1	SNHG18	HULC
TMEM30B	NOTCH1	ANGPTL4	TCF3	INHBB	WFDC2	LINC02085	MIR1290
TPM1	NREP	ANKRD22	TGFBR2	IQCB1	WNK1	MIR31HG	PANDAR
TSPAN1	NT5E	ANTXR1	TGFBR3	ITGA11	WNT11	AGAP2-AS1	MIR135B
BMP1	PALLD	ANXA9	TIA1	KCNMA1	XDH	SNHG12	MIR10A
C1ORF116	PKP2	APLP2	TJP2	KDELR3	XYLT1	MIR9-3HG	LET-7A-5P
CALD1	PLEK2	AQP3	TMEM45B	KIAA0040	YAP1	LINC00239	MIR1

CMTM3	PLPP3	AREG	TNFRSF12A	KLC3	ZBTB38	FAM201A	MIR103A-3P
COL4A1	PLS1	ATP2C2	TOX3	KLF10	ZNF207	UNC5B-AS1	MIR122-5P
CXCL1	PPL	ATP8B1	TP53I3	KLK6	ZNF788P	PXN-AS1	MIR124-3P
CYP1B1	PRR15L	B3GNT3	TP63	KLK7	CTNNB1	IGF2-AS	MIR128A
DDR2	PTHLH	BDNF	TPD52L1	KRT6B	BMI1	MIR141	MIR128-2
DSC2	PXN	BGN	TPM4	LAMA4	STAT3	MIR200A	MIR129
EHF	QSOX1	BIN1	TTC28	LBH	GLI1	MIR200B	MIR133A
GLIPR1	RECK	BPGM	TTC39A	LCP1	HIF1A	MIR200C	MIR140-3P
HOOK1	SDC2	C1ORF210	TWIST2	LIPG	FOXQ1	MIR429	MIR142-3P
IGFBP4	SERPINB1	CALB2	UAP1	LRATD1	FOXM1	MIR542	MIR16-5P
JUP	STAP2	CAP2	UPP1	MAFB	MTDH	MIR30B	MIR181A
KRT18	STC1	CASK	VCAM1	MANSC1	TBXT	MIR30D	MIR181C
LGALS1	TBX3	CBLC	ZNF165	MAP3K7	SOX4	MIR30E	MIR181D

MAL2	TFPI2	CCND2	ABCA1	MATN2	SIX1	MIR130B	MIR18A
MPZL2	TIMP1	CD46	ABCB8	MATN3	NANOG	MIR192	MIR18B
MST1R	TJP1	CD68	ABCC4	MCM7	FAM3C	MIR193B	MIR197
NR2F1	TMC4	CDH12	ACTA1	MEST	KLF17	MIR215	MIR199A
NRP1	TMC5	CDH13	ADIRF	METTL7A	DCLK1	MIR17	MIR19B-3P
PKP3	UCHL1	CDKN2C	AHNAK	MFAP5	TM4SF5	LINC02693	MIR210
S100A8	VEGFC	CEACAM6	AK5	MITF	KLF8	C5ORF66	MIR222
SEC31A	WNT5B	CHST11	AKT1	MMP12	WWTR1	MIR22HG	MIR223
SPINT1	ADAM15	COA1	ALDH1A1	MMP13	PDGFD	MEG3	MIR224
TAGLN	ADAM19	COL12A1	ANKHD1	MPRIP	TDGF1	SCAMP1-AS1	MIR24-1
THBS1	ADGRF1	COL13A1	ANKLE2	MSN	EZH2	ASH1L-AS1	MIR27A
CCL2	ADGRG1	COL16A1	ANKRD1	MUC20	CCR7	LOC730101	MIR296-5P
CD24	AKAP12	COL17A1	ANO1	MXRA5	SMAD4	MIR600H	MIR301

						G	
COL6A3	AKAP13	COL8A1	ANPEP	NAV1	KDM1A	NEAT1	MIR30C-5P
CYBRD1	ALPK2	CRLF1	ANXA3	NDN	KLF4	PAXIP1-AS1	MIR324-3P
ECM1	AOX1	DENND2D	ANXA6	NECTIN3	SLC39A6	MALAT1	MIR328-3P
EGFR	ARHGAP17	DSE	ANXA8	NEGR1	PTEN	MIR205	MIR335-5P
F11R	BICC1	EDIL3	ARFGAP1	NFATC1	CTNNBIP1	MIR30A	MIR33A
FAP	BIK	EDN1	ARHGEF40	NQO1	EIF5A2	MIR145	MIR34B
FBLN1	BMP7	EFEMP2	ARMCX1	NRIP3	BTBD7	SPRY4-IT1	MIR34C
FBLN5	BNC2	ELF5	ARTN	NUAK1	YBX1	MIR21	MIR374A-5P
FERMT2	C1S	ELK3	B2M	OGDH	CCL18	MIR300	MIR486-3P
FGF2	CD59	ENAH	B4GALT4	OLFML3	CTBP2	LINC-ROR	MIR488

GALNT3	CELSR2	ENPP2	BCL2A1	OVOL1	CTBP1	HOTAIR	MIR513
GAS1	CFH	EPHB2	BCL3	P4HA2	MACC1	MIR34A	MIR518F
GFPT2	CGN	EPS8L1	BICDL2	P4HA3	L1CAM	TUG1	MIR628-5P
HAS2	CKMT1A	EPS8L2	BIRC3	PAFAH1B1	PROM1	MIR204	MIR636
HMGA2 X	CTSZ	ERBB2	BLNK	PAG1	CUL4A	MIR221	MIR769-5P
IGFBP3	DACT1	EVPL	BMERB1	PAM	PARD3	MIR101-1	MIR92A-3P
LSR	DKK1	FBLN2	BMP2	PAPSS2	NEDD9	MIR182	MIR95
LTBP1	DKK3	FGFR3	CALU	PDGFA	SALL4	MIR186	MIR98
MAP1B	DSG2	FMNL2	CAPG	PDLIM7	SIRT1	MIR137	MIR99A
MFF	EPPK1	FOXA2	CAV1	PHGDH	HDGF	ZEB2-AS1	MIR291A-5P
MMP1	EVI2A	FOXC1	CAVIN2	PI3	PAQR3	MIR373	MIR3092-3P
MMP3	EXPH5	GADD45A	CBR3	PKP1	TET1	H19	MIR3104-3P

MYO5C	FGFR2	GALNT10	CCDC50	PLA2G7	SHH	ZFAS1	MIR422B
PLAT	FLNA	GJA1	CCND1	PLAAT4	PEBP1	MIR506	MIR5046
PLAUR	FLRT2	GNB4	CD9	PLAGL1	POU5F1	MIR1271	MIR669H-3P
S100P	FST	GOLGA2	CD99L2	PLEKHO1	SCUBE3	MIR15B	MIR674-5P
SRGN	FSTL3	GPC6	CDH6	PLPP2	FOSL1	MIR375	
TGFBI	FZD7	GRTP1	CDK14	PNMA2	PCBP1	MIR150	
TNFAIP6	GEM	HEG1	CDKN1A	POPDC3	MRTFA	MIR211	
TUBA1A	GJB3	HMOX1	CEACAM1	PPARG	TNFAIP8L2	MIR10B	
ACKR3	GOLT1A	HRH1	CEACAM5	PPFIBP2	MAPK7	MIR134	
COL4A2	GRB7	ID4	CNKSR1	PPIB	FBXW7	MIR138-1	
CRB3	GSC	IFI30	COBL	PPP1R14C	MTA1	,IR183	

EMT, epithelial-mesenchymal transition.

Table SVIII. Epithelial-mesenchymal transition-associated genes potentially bound to DAZAP1.

ITGA5	MACF1	TC2N	MET	OGDH	BCL9	DSG2	JAG1
DSC2	LAMB3	KDM1A	ITGB1	ITGAV	STAT3	ITGA2	LAMA3
ITGA2	LAMA3	STAT1	GALNT10	EPHA1	SEC23A	TPD52	L1CAM
FAM3C	HMOX1	SLC7A5	EGFR	DAB2IP	ERBB3	ERBB2	SDC1
SUZ12	LAMC2	CTNND1	CUL4A	AKT1	PDGFRA	SCRIB	DDR1
MAP4K4	WNK1	FMNL2	NOTCH1	ITGB5	SEMA3C	SYNE2	MSN
ITGA3	PTK2	LLGL2	ERMP1	TJP3	PPL	GRHL1	PLS1
TMPRSS13	TGFBR1	LAMA5	GSK3B	HEG1	SEC31A	BIN1	DOCK9
MYH14	LRP1	OCLN	SH3YL1	MMP14	MCM7	APLP2	SYNE1
ST14	COBL	BTBD7	USP22	DLC1	TJP2	NES	BMI1
CGN	COL6A1	MPRIP	ACTN1	SBNO1	HSPG2	EVPL	ARFGAP1

Table SIX. Kyoto Encyclopedia of Genes and Genomes enrichment analysis from Web-based Gene Set Analysis Toolkit database.

Gene set	Pathway	Genes	Enrichment ratio	P-value
hsa04510	Focal adhesion	ITGA5, MET, LAMB3, ITGB1, ITGAV, ITGA2, LAMA3, EGFR, ERBB2, LAMC2, AKT1, PDGFRA, ITGB5	13.57114142	$2.85x10^{-12}$
hsa05205	Proteoglycans in cancer	ITGA5, MET, ITGB1, ITGAV, STAT3, ITGA2, EGFR, ERBB3, ERBB2, SDC1, AKT1, ITGB5	12.59047619	$5.75x10^{-11}$
hsa04512	ECM-receptor interaction	ITGA5, LAMB3, ITGB1, ITGAV, ITGA2, LAMA3, SDC1, LAMC2, ITGB5	22.8010453	$1.05x10^{-10}$
hsa05165	Human papillomavirus infection	ITGA5, JAG1, LAMB3, ITGB1, ITGAV, ITGA2, LAMA3, STAT1, EGFR, LAMC2, AKT1, SCRIB, NOTCH1, ITGB5	8.579351032	$1.68x10^{-10}$

hsa04151	PI3K-Akt signaling pathway	ITGA5, MET, LAMB3, ITGB1, ITGAV, ITGA2, LAMA3, EGFR, ERBB3, ERBB2, LAMC2, AKT1, PDGFRA, ITGB5	8.215819209	2.98×10^{-10}
hsa05200	Pathways in cancer	MET, JAG1, NOTCH1, LAMB3, ITGB1, ITGAV, STAT3, ITGA2, LAMA3, STAT1, HMOX1, EGFR, ERBB2, LAMC2, AKT1, PDGFRA	6.343293348	4.76×10^{-10}
hsa05206	MicroRNAs in cancer	ITGA5, MET, STAT3, HMOX1, EGFR, ERBB3, ERBB2, PDGFRA, NOTCH1	12.46457143	$2.38 x 10^{-8}$
hsa05412	Arrhythmogenic right ventricular cardiomyopathy (ARVC)	ITGA5, DSG2, DSC2, ITGB1, ITGAV, ITGA2, ITGB5	20.19722222	$3.74 x 10^{-8}$
hsa01521	EGFR tyrosine kinase inhibitor resistance	MET, STAT3, EGFR, ERBB3, ERBB2, AKT1, PDGFRA	18.40759494	$7.19 x 10^{-8}$

hsa05222	Small cell lung cancer	LAMB3, ITGB1, ITGAV, ITGA2, LAMA3, LAMC2, AKT1	15.80652174	2.08×10^{-7}

Table SX. Transcription factors that may regulate the abnormal expression of deleted in azoospermia-associated protein 1.

Transcription factor	Database source	Binding start site	Binding termination site	P-value	Matched sequence, 5’→3’
AHCTF1	CISBP	948	955	3.23×10^{-5}	AAATAAAT
AHR	HOCOMOCO	1,713	1,721	3.54×10^{-5}	CTTGCGTGC
AR	hTFtarget	313	330	9.95×10^{-6}	TGTTTTGTACTATTTGTC
ARID3A	CISBP	1,416	1,424	4.47×10^{-5}	AAATCAAAA
ARNT	TRANSFAC	1,532	1,551	1.53×10^{-6}	GGACGCTCACGTGCCGTTCC
ARNT2	hTFtarget	1,537	1,546	1.43×10^{-5}	GGCACGTGAG
ARNTL	hTFtarget	1,741	1,751	2.74×10^{-6}	GCCACGTGCGT
ASCL1	hTFtarget	485	497	5.92×10^{-5}	AGGCGCCTGCCAC
ASCL2	hTFtarget	1,147	1,156	3.36×10^{-5}	ACACGACGAC
ATF3	HOCOMOCO	1,463	1,471	3.31×10^{-6}	CTGAGTCAC
ATF4	hTFtarget	244	257	6.92×10^{-5}	CAATGATGCAGTCA

ATF6	hTFtarget	920	931	3.50x10-^{6}	GGTGAGGTGGCG
ATF6B	CISBP	920	931	2.68x10-^{7}	GGTGAGGTGGCG
ATOH1	HOCOMOCO	1,318	1,326	7.46x10-^{5}	AACAGATGC
BACH1	hTFtarget	1,462	1,474	2.59x10-^{6}	AGTGACTCAGCCT
BACH2	HOCOMOCO	1,463	1,473	1.49x10-^{6}	GGCTGAGTCAC
BARHL1	TRANSFAC	1,408	1,417	7.12x10-^{5}	GTTAATTGTT
BARHL2	CISBP	1,311	1,320	3.18 x 10-^{5}	GTTAATTGCA
BARX1	HOCOMOCO	1,408	1,419	2.25 x 10-^{7}	GTTAATTGTTTT
BARX2	hTFtarget	1,409	1,420	1.22 x 10-^{5}	CAAAACAATTAA
BATF	hTFtarget	287	304	2.33 x 10-^{5}	TCTTTTATTTTGAGACAG
BATF3	CISBP	921	931	1.07 x 10-^{5}	GGTGAGGTGGC
BBX	TRANSFAC	1,392	1,406	3.05 x 10-^{5}	AAATTCAATGACTAT
BCL11A	hTFtarget	1,640	1,656	1.37 x 10-^{6}	TAAAGAGGAAGCGGCAG

BCL11B	CISBP	142	150	3.82 x 10-^{5}	ATCCGGCCA
BCL6	CISBP	187	216	9.77 x 10-^{6}	ACTCCAGCTATCCTCCCTCCTCAGCCTCCC
BCL6B	CISBP	646	657	7.87 x 10-^{5}	TTTTTTCTAAGA
BHLHE40	hTFtarget	1,537	1,546	1.23 x 10-^{6}	GGCACGTGAG
BHLHE41	hTFtarget	1,537	1,546	3.46 x 10-^{6}	CTCACGTGCC
BLIMP-1	TRANSFAC	1,507	1,522	4.32 x 10-^{5}	CGGACAGGGGAAGGAG
BNC2	JASPAR	1,462	1,473	2.57 x 10-^{5}	GGCTGAGTCACT
BSX	TRANSFAC	1,404	1,419	3.50 x 10-^{5}	AAAACAATTAACTAAA
CEBPA	HOCOMOCO	265	275	3.53 x 10-^{5}	GCTTGGGCAAC
CEBPB	hTFtarget	536	546	4.31 x 10-^{5}	GGTTTCACCAT
CEBPD	hTFtarget	265	275	4.69 x 10-^{5}	GTTGCCCAAGC
CEBPE	hTFtarget	265	276	9.81 x 10-^{5}	GCTTGGGCAACA
CEBPG	hTFtarget	243	257	2.65 x 10-^{5}	CAATGATGCAGTCAT
CIC	CISBP	1,107	1,116	2.16 x 10-^{5}	TCTGCTGACA

CLOCK	hTFtarget	1,742	1,751	1.62 x 10-^{6}	GCCACGTGCG
CPEB1	CISBP	296	303	5.88 x 10-^{5}	AATAAAAG
CREB3	CISBP	920	931	1.33 x 10-^{6}	CGCCACCTCACC
CREB3L1	CISBP	920	931	1.87 x 10-^{6}	CGCCACCTCACC
CREB3L2	TRANSFAC	920	932	2.64 x 10-^{5}	CGCCACCTCACCC
CREB3L4	CISBP	920	931	5.22 x 10-^{7}	CGCCACCTCACC
CRX	hTFtarget	905	912	8.30 x 10-^{5}	ATAATCCC
CTCF	hTFtarget	2,324	2,343	4.23 x 10-^{7}	CGAGTCCGCCCCCGGCCGGC
CTCFL	HOCOMOCO	2,324	2,341	5.72 x 10-^{7}	GCCGGCCGGGGGCGGACT
CUX1	hTFtarget	980	997	4.45 x 10-^{5}	AACGATCAGGCTGTCAAT
CUX2	CISBP	968	985	3.90 x 10-^{5}	ATGAATAAACCAAACGAT
DBX2	CISBP	1,312	1,318	7.93 x 10-^{5}	TAATTGC
DLX2	JASPAR	1,310	1,321	1.75 x 10-^{5}	ATGCAATTAACA
DLX3	hTFtarget	1,312	1,319	6.53 x 10-^{5}	TTAATTGC
DLX4	CISBP	1,312	1,319	6.14 x 10-^{5}	TTAATTGC
DLX5	JASPAR	1,310	1,321	1.62 x 10-^{5}	ATGCAATTAACA

DMBX1	CISBP	118	1,25	5.87 x 10-^{5}	GTAATCCC
DMRTC2	CISBP	1,127	1,136	1.54 x 10-^{5}	GGTATCATTC
E2F1	hTFtarget	1,950	1,964	8.63 x 10-^{8}	CGGGAGCGCGCCCGG
E2F2	hTFtarget	1,729	1,739	4.92 x 10-^{7}	CGTGCGCGCGC
E2F3	HOCOMOCO	2,134	2,143	9.24 x 10-^{6}	AGGCGGGAGC
E2F4	HOCOMOCO	1,777	1,790	1.51 x 10-^{6}	CAGGGGCGGGGCCA
E2F5	HOCOMOCO	1,880	1,889	9.03 x 10-^{6}	GGCGCGAAAT
E2F6	hTFtarget	2,132	2,144	3.65 x 10-^{6}	GGAGGCGGGAGCG
E2F7	HOCOMOCO	1,545	1,557	2.59 x 10-^{6}	GGAGCGGGAACGG
EBF1	HOCOMOCO	2,295	2,307	7.18 x 10-^{6}	GGCCCCGGGGGGC
EBF2	JASPAR	1,267	1,279	5.82 x 10-^{5}	TCCCCTAGGGGGC
EBF3	JASPAR	1,267	1,279	3.99 x 10-^{5}	TCCCCTAGGGGGC
EBF4	TRANSFA	1,233	1,252	7.89 x 10-^{6}	AACCAAAACCGTGTTTTCAG

	C				
EGR1	hTFtarget	1,921	1,940	2.41 x 10^{-7}	CCCCTGGACCCGCCCCCGGA
EGR2	hTFtarget	2,413	2,421	1.50 x 10^{-6}	CGCCCCCGC
EGR3	hTFtarget	2,413	2,421	1.50 x 10^{-6}	CGCCCCCGC
EGR4	hTFtarget	1,708	1,720	8.17 x 10^{-6}	CACGCGCACGCAA
EHF	HOCOMOCO	1,640	1,654	9.41 x 10^{-6}	TAAAGAGGAAGCGGC
ELF1	hTFtarget	719	732	4.09 x 10^{-6}	AGGCAGGAAGTAGA
ELF2	hTFtarget	1,641	1,653	1.26 x 10^{-5}	AAAGAGGAAGCGG
ELF3	hTFtarget	718	731	2.21 x 10^{-6}	CTCTACTTCCTGCC
ELF4	hTFtarget	1,641	1,652	2.49 x 10^{-5}	AAAGAGGAAGCG
ELF5	HOCOMOCO	718	734	6.07 x 10^{-6}	GAAGGCAGGAAGTAGAG
ELK1	hTFtarget	721	731	1.39 x 10^{-5}	GGCAGGAAGTA
ELK3	hTFtarget	139	149	4.47 x 10^{-5}	GGCCGGATGCA
ELK4	HOCOMOCO	720	732	8.26 x 10^{-6}	AGGCAGGAAGTAG
EMX1	CISBP	1,402	1,415	2.46 x 10^{-5}	AATTTAGTTAATTG

EMX2	hTFtarget	1,402	1,415	3.26×10^{-5}	CAATTAACTAAATT
EN2	CISBP	1,311	1,320	3.16×10^{-5}	GTTAATTGCA
EPAS1	hTFtarget	1,031	1,040	6.13×10^{-7}	GCACGTACCC
ERF	hTFtarget	721	730	7.95×10^{-5}	GCAGGAAGTA
ERG	hTFtarget	720	732	5.10×10^{-7}	AGGCAGGAAGTAG
ESR1	hTFtarget	1,448	1,461	4.50×10^{-8}	TGGCCAAGGTCACC
ESR2	HOCOMOCO	2,317	2,331	4.38×10^{-6}	CGGCCGGCGTGACCT
ESRRA	hTFtarget	1,445	1,459	5.39×10^{-8}	GCCAAGGTCACCCAG
ESRRB	CISBP	1,447	1,461	4.49×10^{-8}	TGGCCAAGGTCACCC
ESRRG	hTFtarget	2,313	2,323	2.05×10^{-7}	GTCAAGGTCAC
ETS1	hTFtarget	1,797	1,817	8.12×10^{-10}	GCACGCTGGGAAATGGAGTCC
ETS2	HOCOMOCO	719	731	4.80×10^{-6}	GGCAGGAAGTAGA
ETV1	hTFtarget	721	731	3.98×10^{-6}	GGCAGGAAGTA
ETV2	HOCOMOCO	719	734	2.92×10^{-7}	GAAGGCAGGAAGTAGA
ETV3	hTFtarget	710	730	7.24×10^{-5}	ACTGCAACCTCTACTTCCTGC

ETV4	hTFtarget	721	731	3.52 x 10-^{6}	GGCAGGAAGTA
ETV5	hTFtarget	721	734	1.26 x 10-^{6}	GAAGGCAGGAAGTA
ETV6	CISBP	2,130	2,144	3.12 x 10-^{6}	CCGGAGGCGGGAGCG
ETV7	hTFtarget	721	731	3.61 x 10-^{5}	GGCAGGAAGTA
EVX2	TRANSFAC	794	810	9.24 x 10-^{5}	CCCGGCTAATTTTCTTT
FEV	HOCOMOCO	2,425	2,434	6.65 x 10-^{6}	CCGGGAAGCG
FEZF1	TRANSFAC	1,799	1,813	4.28 x 10-^{5}	GCTGGGAAATGGAGT
FLI1	hTFtarget	717	734	2.38 x 10-^{8}	GAAGGCAGGAAGTAGAGG
FOS	hTFtarget	1,461	1,475	9.08 x 10-^{6}	AAGTGACTCAGCCTC
FOSB	HOCOMOCO	1,463	1,471	1.96 x 10-^{5}	CTGAGTCAC
FOSL1	hTFtarget	1,462	1,473	1.42 x 10-^{6}	GGCTGAGTCACT
FOSL2	hTFtarget	1,462	1,475	1.86 x 10-^{6}	AGTGACTCAGCCTC
FOXA1	hTFtarget	1,064	1,075	3.38 x 10-^{5}	TAGTAAACAGGT
FOXA2	hTFtarget	1,065	1,075	4.43 x 10-^{5}	TAGTAAACAGG

FOXA3	hTFtarget	1,065	1,075	4.51 x 10^{-5}	TAGTAAACAGG
FOXB1	CISBP	1,066	1,074	5.92 x 10^{-5}	CTGTTTACT
FOXC1	hTFtarget	947	959	4.69 x 10^{-6}	AATTAAATAAATA
FOXC2	hTFtarget	947	957	1.92 x 10^{-5}	TTAAATAAATA
FOXD1	hTFtarget	1,066	1,073	6.14 x 10^{-5}	GTAAACAG
FOXD2	JASPAR	947	958	1.02 x 10^{-5}	ATTAAATAAATA
FOXD3	hTFtarget	1,374	1,387	7.74 x 10^{-5}	GGTCAATAATATCT
FOXE1	JASPAR	809	822	4.68 x 10^{-5}	ACTAAAAATACAAA
FOXF1	JASPAR	1,065	1,075	4.70 x 10^{-5}	TAGTAAACAGG
FOXG1	TRANSFAC	1,188	1,199	1.46 x 10^{-5}	CTGGACCCACTC
FOXI1	hTFtarget	944	955	2.57 x 10^{-5}	TTGTATTTATTT
FOXJ2	HOCOMOCO	947	956	1.47 x 10^{-5}	TATTTATTTA
FOXJ3	HOCOMOCO	347	359	2.55 x 10^{-5}	GTATTTTTTTTTT
FOXK1	hTFtarget	1,063	1,076	2.70 x 10^{-5}	GTAGTAAACAGGTG
FOXK2	JASPAR	1,065	1,075	2.01 x 10^{-5}	TAGTAAACAGG

FOXL1	hTFtarget	946	958	1.91 x 10-^{5}	ATTAAATAAATAC
FOXM1	CISBP	1,762	1,769	1.21 x 10-^{5}	CGCATCCT
FOXN1	CISBP	2,289	2,298	1.74 x 10-^{5}	GACGCCGCCC
FOXN2	CISBP	1,986	2,004	1.77 x 10-^{6}	GCGCGTCCCCGCGCCGCCG
FOXN4	CISBP	1,995	2,004	1.59 x 10-^{5}	GGGGACGCGC
FOXO1	JASPAR	1,064	1,074	4.94 x 10-^{6}	ACCTGTTTACT
FOXP1	hTFtarget	1,064	1,075	3.41 x 10-^{6}	TAGTAAACAGGT
FOXP2	HOCOMOCO	1,066	1,074	4.91 x 10-^{6}	CTGTTTACT
FOXP3	hTFtarget	1,067	1,073	7.93 x 10-^{5}	GTAAACA
GABPA	hTFtarget	719	732	5.79x10-^{6}	TCTACTTCCTGCCT
GATA3	hTFtarget	300	310	8.29x10-^{5}	AAAGAAAAAAA
GBX2	CISBP	1,312	1,319	5.75x10-^{5}	TTAATTGC
GCM1	hTFtarget	1,572	1,580	1.17x10-^{5}	GGTGCGGGC
GCM2	CISBP	1,573	1,581	2.38x10-^{5}	GTGCGGGCG
GFI1	hTFtarget	1,405	1,425	1.47x10-^{5}	CAAATCAAAACAATTAACTAA
GFI1B	hTFtarget	1,405	1,425	7.06x10-^{6}	CAAATCAAAACAATTAACTAA
GLI1	hTFtarget	1,139	1,149	2.80x10-^{5}	GACCCCCCAAA

GLI2	hTFtarget	1,136	1,149	6.21x10-^{6}	GACCCCCCAAAAAG
GLI3	hTFtarget	1,135	1,150	3.48x10-^{6}	CGACCCCCCAAAAAGA
GLI4	CISBP	1,679	1,699	3.57x10-^{5}	CGAGACCGGCGCTCCGGGCTA
GLIS1	CISBP	2,294	2,307	5.55x10-^{7}	GGCCCCGGGGGGCG
GLIS2	TRANSFAC	1,138	1,153	1.06x10-^{6}	CGACGACCCCCCAAAA
GLIS3	hTFtarget	1,136	1,149	6.21x10-^{7}	CTTTTTGGGGGGTC
GMEB1	hTFtarget	1,899	1,907	3.02x10-^{5}	GGACGCACG
GRHL1	JASPAR	1,085	1,096	4.02x10-^{6}	AAAACCGGTCTA
GRHL2	HOCOMOCO	1,087	1,098	3.54x10-^{6}	GACCGGTTTTTC
GSC	CISBP	905	912	4.72x10-^{5}	ATAATCCC
GSC2	CISBP	905	912	8.30x10-^{5}	ATAATCCC
HAND2	hTFtarget	1,318	1,327	8.92x10-^{5}	AACAGATGCA
HES1	hTFtarget	1,537	1,546	1.26x10-^{5}	CTCACGTGCC
HES2	CISBP	1,538	1,550	2.98x10-^{6}	TCACGTGCCGTTC
HES5	CISBP	1,742	1,751	1.50x10-^{5}	CGCACGTGGC
HES7	CISBP	1,742	1,751	7.01x10-^{6}	CGCACGTGGC

HESX1	hTFtarget	838	846	5.98x10-^{6}	CATATATAG
HEY1	hTFtarget	1,724	1,733	1.34x10-^{5}	CGCACGCGCG
HEY2	CISBP	1,743	1,751	7.18x10-^{6}	GCACGTGGC
HIC1	HOCOMOCO	2,384	2,392	2.52x10-^{5}	CGGGTGCCC
HIF1A	hTFtarget	1,029	1,038	1.31x10-^{5}	GTACGTGCTG
HINFP	hTFtarget	1,741	1,760	5.46x10-^{6}	GCGGGCCGAGCCACGTGCGT
HKR1	CISBP	2,016	2,036	1.72x10-^{6}	GCTGCCTCCTCCCCTCGGCGC
HMG20B	CISBP	19	29	1.62x10-^{5}	TTATTATTTTT
HMX1	hTFtarget	1,312	1,320	1.30x10-^{5}	GTTAATTGC
HMX2	JASPAR	1,308	1,324	1.05x10-^{5}	GTATGCAATTAACAGAT
HMX3	JASPAR	1,308	1,324	1.80x10-^{5}	GTATGCAATTAACAGAT
HNF4A	hTFtarget	2,335	2,349	2.38x10-^{5}	GCGGACTCGGGACCC
HNF4G	hTFtarget	1,273	1,287	7.37x10-^{5}	AGGGGGCAAAGTCAC
HOXA13	hTFtarget	1,376	1,386	6.89x10-^{5}	GATATTATTGA
HOXA6	hTFtarget	1,311	1,320	1.73x10-^{5}	GTTAATTGCA
HOXA7	hTFtarget	1,312	1,319	3.96x10-^{5}	GCAATTAA
HOXA9	hTFtarget	1,312	1,321	8.61x10-^{5}	TGTTAATTGC

HOXB6	hTFtarget	1,312	1,319	2.18x10-^{5}	TTAATTGC
HOXB7	CISBP	1,312	1,319	3.96x10-^{5}	TTAATTGC
HOXB8	hTFtarget	1,312	1,319	5.43x10-^{5}	TTAATTGC
HOXC12	CISBP	1,068	1,077	4.45x10-^{5}	GTTTACTACC
HOXC4	hTFtarget	1,409	1,416	8.53x10-^{5}	TTAATTGT
HOXC6	CISBP	1,312	1,319	8.06x10-^{5}	TTAATTGC
HOXC8	CISBP	1,311	1,319	6.24x10-^{5}	TTAATTGCA
HOXD13	hTFtarget	1,043	1,050	4.83x10-^{5}	TTGTAAAA
HOXD8	hTFtarget	798	807	2.44x10-^{5}	GAAAATTAGC
HOXD9	CISBP	1,312	1,321	8.12x10-^{5}	TGTTAATTGC
HSF1	hTFtarget	558	575	5.06x10-^{5}	GTCAGGAGATCGAGACCA
IKZF1	hTFtarget	185	192	1.21x10-^{5}	TTGGGAGG
IKZF3	JASPAR	718	732	3.07x10-^{6}	AGGCAGGAAGTAGAG
INSM2	TRANSFAC	1,229	1,244	6.46x10-^{5}	TGACAACCAAAACCGT
IRF1	hTFtarget	293	312	2.40x10-^{5}	CAAAATAAAAGAAAAAAAAG
IRF2	HOCOMOCO	1,634	1,653	4.69x10-^{5}	AAGAGTTAAAGAGGAAGCGG

IRF3	HOCOMOCO	1,841	1,860	2.47x10-^{5}	CGAGGAGAAAGGAAAACGCG
IRF4	hTFtarget	1,640	1,657	2.51x10-^{5}	TAAAGAGGAAGCGGCAGC
IRF5	CISBP	559	568	7.73x10-^{5}	GATCGAGACC
IRF7	HOCOMOCO	1,847	1,856	4.52x10-^{5}	GAAAGGAAAA
IRX3	TRANSFAC	44	55	2.68x10-^{7}	CAACATGACAAA
IRX5	CISBP	44	55	1.79x10-^{5}	CAACATGACAAA
ISL2	JASPAR	1,312	1,319	7.22x10-^{5}	GCAATTAA
JDP2	CISBP	1,462	1,472	5.96x10-^{5}	AGTGACTCAGC
JUN	HOCOMOCO	1,463	1,472	3.31x10-^{6}	GCTGAGTCAC
JUNB	hTFtarget	1,461	1,475	4.58x10-^{6}	AAGTGACTCAGCCTC
JUND	HOCOMOCO	1,463	1,473	1.82x10-^{6}	GGCTGAGTCAC
KLF1	hTFtarget	1,779	1,793	1.07x10-^{7}	CGCTGGCCCCGCCCC
KLF10	JASPAR	1,779	1,787	1.50x10-^{6}	GGGGCGGGG

KLF11	hTFtarget	1,927	1,937	6.59x10-^{6}	GACCCGCCCCC
KLF12	CISBP	1,778	1,792	3.95x10-^{8}	GCTGGCCCCGCCCCT
KLF13	hTFtarget	1,777	1,789	5.12x10-^{6}	GGCCCCGCCCCTG
KLF14	CISBP	1,776	1,789	5.76x10-^{7}	GGCCCCGCCCCTGC
KLF15	hTFtarget	1,779	1,793	7.03x10-^{8}	CGCTGGCCCCGCCCC
KLF16	JASPAR	1,927	1,937	8.10x10-^{7}	GACCCGCCCCC
KLF17	CISBP	1,778	1,789	1.13x10-^{5}	GGCCCCGCCCCT
KLF2	CISBP	1,779	1,789	6.59x10-^{7}	GGCCCCGCCCC
KLF3	HOCOMOCO	1,774	1,792	1.40x10-^{6}	TTGCAGGGGCGGGGCCAGC
KLF4	CISBP	1,779	1,789	1.59x10-^{6}	GGCCCCGCCCC
KLF5	hTFtarget	1,779	1,788	3.39x10-^{7}	GCCCCGCCCC
KLF6	hTFtarget	1,776	1,794	1.95x10-^{7}	GCAGGGGCGGGGCCAGCGC
KLF7	CISBP	1,779	1,789	7.65x10-^{8}	GGCCCCGCCCC
KLF8	CISBP	1,779	1,788	1.67x10-^{6}	GCCCCGCCCC
KLF9	hTFtarget	1,775	1,789	1.05x10-^{6}	TGCAGGGGCGGGGCC
LBX2	CISBP	1,405	1,416	8.81x10-^{5}	ACAATTAACTAA
LCORL	CISBP	874	881	6.14x10-^{5}	CCTAAATT

LEF1	HOCOMOCO	806	819	6.56x10-^{5}	TCTTTTGTATTTTT
LHX2	hTFtarget	1,401	1,415	6.84x10-^{5}	GAATTTAGTTAATTG
LHX3	JASPAR	948	960	4.23x10-^{5}	GAATTAAATAAAT
LIN28B	CISBP	2,355	2,369	1.98x10-^{6}	CGCGAAGCCGCGGCG
MAFA	hTFtarget	1,104	1,116	3.76x10-^{5}	TGTCAGCAGAAGG
MAFB	CISBP	1,299	1,316	1.74x10-^{5}	ATTGCATACATCAGTGGT
MAFF	HOCOMOCO	448	469	2.26x10-^{5}	CAGGAGGCTGAGGCAGTAGAAT
MAFG	hTFtarget	1,109	1,118	1.13x10-^{5}	AATGTCAGCA
MAFK	hTFtarget	1,461	1,475	3.27x10-^{6}	AAGTGACTCAGCCTC
MAX	hTFtarget	1,742	1,751	5.03x10-^{7}	CGCACGTGGC
MAZ	hTFtarget	2,132	2,153	1.53x10-^{7}	GGAGGCGGGAGCGAGCGAGGAG
MBD2	HOCOMOCO	2,325	2,335	6.77x10-^{6}	CCGGCCGGGGG
MECOM	hTFtarget	1,378	1,393	2.58x10-^{5}	ATGAAAAGATATTATT
MECP2	HOCOMOCO	1,682	1,688	3.60x10-^{5}	CCCGGAG

MEF2A	hTFtarget	809	823	3.50x10-^{6}	TACTAAAAATACAAA
MEF2B	JASPAR	1,344	1,355	1.50x10-^{6}	ACTATTAATAGC
MEF2C	hTFtarget	1,345	1,356	1.42x10-^{6}	TACTATTAATAG
MEF2D	hTFtarget	1,344	1,355	2.44x10-^{6}	ACTATTAATAGC
MEIS1	JASPAR	988	1,002	1.38x10-^{5}	GGCTGTCAATGTGCT
MEIS2	hTFtarget	989	996	1.47x10-^{5}	TTGACAGC
MEIS3	hTFtarget	989	996	2.94x10-^{5}	TTGACAGC
MEOX2	CISBP	962	975	6.82x10-^{5}	GTGATGATGAATAA
MITF	CISBP	575	584	1.47x10-^{5}	CCTCGTGATC
MLX	CISBP	1,538	1,545	2.20x10-^{5}	GCACGTGA
MLXIP	JASPAR	1,743	1,750	3.40x10-^{5}	GCACGTGG
MLXIPL	hTFtarget	1,537	1,546	7.23x10-^{5}	CTCACGTGCC
MNT	CISBP	1,742	1,750	1.71x10-^{5}	CCACGTGCG
MSX1	JASPAR	1,312	1,319	6.14x10-^{5}	GCAATTAA
MSX2	hTFtarget	1,312	1,319	3.96x10-^{5}	TTAATTGC
MTF1	CISBP	1,152	1,160	7.67x10-^{6}	CGTGTGCAC
MTF-1	TRANSFAC	1,148	1,161	3.25x10-^{5}	AGTGCACACGACGA

MXI1	TRANSFAC	1,743	1,757	8.30x10-^{7}	GCACGTGGCTCGGCC
MYB	HOCOMOCO	2,005	2,016	1.73x10-^{6}	GGTGACCGTTGG
MYBL1	HOCOMOCO	2,005	2,019	2.50x10-^{6}	GGTGACCGTTGGCGC
MYBL2	CISBP	2,007	2,015	4.57x10-^{5}	CAACGGTCA
MYC	TRANSFAC	1,742	1,751	5.03x10-^{7}	CGCACGTGGC
MYCN	TRANSFAC	1,742	1,751	5.03x10-^{7}	CGCACGTGGC
MYF6	hTFtarget	1,060	1,071	2.94x10-^{5}	AAACAGGTGACC
MYNN	CISBP	294	305	8.01x10-^{5}	TTCTTTTATTTT
MYOD1	hTFtarget	1,060	1,071	8.42x10-^{5}	AAACAGGTGACC
MZF1	CISBP	2,445	2,454	2.13x10-^{5}	GGATCCCCCA
NANOG	hTFtarget	1,312	1,319	2.18x10-^{5}	TTAATTGC
NEUROD2	HOCOMOCO	1,318	1,326	4.98x10-^{5}	AACAGATGC

NFAT5	JASPAR	1,092	1,103	4.10x10-^{5}	AGGTGGAAAAAC
NFATC1	hTFtarget	1,093	1,102	1.74x10-^{5}	TTTTTCCACC
NFATC2	HOCOMOCO	1,092	1,100	3.27x10-^{5}	TGGAAAAAC
NFATC3	hTFtarget	1,092	1,100	1.98x10-^{5}	TGGAAAAAC
NFATC4	hTFtarget	1,092	1,101	5.77x10-^{5}	GTTTTTCCAC
NFE2	hTFtarget	1,461	1,473	4.66x10-^{6}	AAGTGACTCAGCC
NFE2L1	hTFtarget	1,463	1,471	9.53x10-^{5}	GTGACTCAG
NFE2L2	hTFtarget	1,463	1,473	3.83x10-^{6}	GTGACTCAGCC
NFIA	CISBP	1,255	1,264	3.74x10-^{5}	ATTGCCAAGT
NFIB	JASPAR	2,376	2,396	4.70x10-^{6}	GCCCTGGACGGGTGCCCGGGG
NFIC	hTFtarget	2,378	2,394	3.44x10-^{7}	CCGGGCACCCGTCCAGG
NFIX	CISBP	2,378	2,394	1.28x10-^{5}	CCTGGACGGGTGCCCGG
NFKB1	hTFtarget	2,302	2,312	2.11x10-^{5}	GGGGCGGCCCC
NFKB2	hTFtarget	533	545	2.94x10-^{5}	TGGTGAAACCCCG
NHLH1	hTFtarget	1,654	1,671	8.53x10-^{6}	CAGCCGCGCCTGCGCCCA
NHLH2	CISBP	1,654	1,671	1.98x10-^{5}	CAGCCGCGCCTGCGCCCA
NKX1-2	CISBP	1,312	1,320	5.46x10-^{5}	GTTAATTGC

NKX2-1	hTFtarget	1,216	1,225	1.90x10-^{5}	CTTGAGTGCG
NKX2-2	hTFtarget	1,214	1,227	4.47x10-^{5}	CCCGCACTCAAGTT
NKX2-4	CISBP	1,192	1,201	5.77x10-^{5}	TCGAGTGGGT
NKX2-5	HOCOMOCO	257	266	1.37x10-^{5}	GCTGGAGTGC
NKX2-8	hTFtarget	1,194	1,201	2.41x10-^{5}	TCGAGTGG
NKX2-9	CISBP	1,216	1,225	4.03x10-^{5}	CTTGAGTGCG
NKX6-1	HOCOMOCO	1,336	1,354	3.61x10-^{5}	AGTATTTGGCTATTAATAG
NKX6-2	CISBP	1,312	1,319	4.83x10-^{5}	TTAATTGC
NKX6-3	CISBP	1,312	1,320	7.37x10-^{5}	GTTAATTGC
NPAS2	CISBP	1,742	1,751	1.08x10-^{5}	CGCACGTGGC
NPAS4	JASPAR	400	410	9.22x10-^{5}	GATCGTGCCAC
NR1D1	hTFtarget	862	881	8.50x10-^{6}	AATTTAGGTCAGGAGATCGA
NR1D2	CISBP	862	881	1.28x10-^{5}	AATTTAGGTCAGGAGATCGA
NR1H2	CISBP	871	886	2.34x10-^{5}	GGATCAATTTAGGTCA
NR1H3	HOCOMOCO	1,449	1,463	2.08x10-^{5}	CTTGGCCAAGGTCAC

NR1H4	HOCOMOCO	1,973	1,991	1.86x10-^{5}	AGGGGCGGCGGCGCGGCGG
NR1I2	hTFtarget	1,441	1,455	7.13x10-^{7}	AGGTCACCCAGTTCG
NR1I3	hTFtarget	1,572	1,587	3.81x10-^{5}	GGTGCGGGCGGGTACA
NR2C1	CISBP	2,315	2,324	2.81x10-^{5}	CAAGGTCACG
NR2C2	hTFtarget	1,620	1,634	5.14x10-^{6}	ACCGCTTCCGAGTGA
NR2E1	CISBP	570	579	1.79x10-^{5}	CGAGGTCAGG
NR2E3	hTFtarget	331	340	3.38x10-^{5}	CAAGATCACA
NR2F1	hTFtarget	571	586	6.95x10-^{6}	CGGATCACGAGGTCAG
NR2F2	HOCOMOCO	569	581	7.70x10-^{6}	CACGAGGTCAGGA
NR2F6	CISBP	572	586	6.75x10-^{6}	CGGATCACGAGGTCA
NR3C2	hTFtarget	1,580	1,588	2.82x10-^{5}	CGGGTACAC
NR4A1	hTFtarget	2,122	2,131	2.04x10-^{5}	GGAAGGTCAC
NR4A2	HOCOMOCO	2,122	2,130	1.14x10-^{5}	GAAGGTCAC
NR5A1	hTFtarget	2,313	2,323	2.05x10-^{7}	GTCAAGGTCAC
NR5A2	hTFtarget	2,313	2,323	2.05x10-^{7}	GTCAAGGTCAC

NR6A1	hTFtarget	63	75	1.90x10-^{5}	GAGTTCAAGACCA
NRF1	JASPAR	1,704	1,718	2.64x10-^{8}	GCGTGCGCGTGCGCG
NRL	CISBP	1,105	1,115	2.30x10-^{5}	GTCAGCAGAAG
OBOX1	CISBP	903	912	6.60x10-^{5}	ATAATCCCAA
OBOX5	CISBP	905	912	5.04x10-^{5}	ATAATCCC
OBOX6	CISBP	904	912	7.49x10-^{5}	ATAATCCCA
ONECUT2	hTFtarget	1,415	1,425	7.35x10-^{5}	GTTTTGATTTG
OSR1	TRANSFAC	1,068	1,083	8.10x10-^{5}	GCTGACGGTAGTAAAC
OSR2	HOCOMOCO	466	481	6.64x10-^{6}	GTCCCAGCTACTCAGG
OTX1	hTFtarget	118	125	6.19x10-^{5}	GTAATCCC
OTX2	hTFtarget	903	914	4.02x10-^{5}	TTGGGATTATAG
P53	TRANSFAC	1,175	1,194	4.14x10-^{6}	CGGCATGTCTGGTCTGGACC
PATZ1	hTFtarget	2,412	2,433	1.37x10-^{7}	CGGGAAGCGGCGGCGGGGGCGC
PAX1	JASPAR	2,375	2,391	7.13x10-^{5}	GGCCCTGGACGGGTGCC
PAX2	hTFtarget	2,375	2,392	5.74x10-^{5}	GGCCCTGGACGGGTGCCC

PAX3	hTFtarget	1,313	1,320	2.18x10-^{5}	GTTAATTG
PAX4	JASPAR	1,368	1,397	5.84x10-^{6}	GACTATGAAAAGATATTATTGACCCCCCCC
PAX5	hTFtarget	662	682	1.06x10-^{9}	ACCTGGGCAACAGAGCAAGAC
PAX6	hTFtarget	1,954	1,970	2.22x10-^{6}	GCACGCCCGGGCGCGCT
PAX7	CISBP	2,318	2,327	3.42x10-^{5}	GGTCACGCCG
PAX8	hTFtarget	786	805	9.98x10-^{5}	AAATTAGCCGGGCGTGGTGG
PAX9	JASPAR	2,375	2,391	8.76x10-^{5}	GGCCCTGGACGGGTGCC
PBX1	CISBP	2,310	2,318	2.34x10-^{5}	CTTGACGGG
PBX2	hTFtarget	989	1000	3.85x10-^{5}	CACATTGACAGC
PBX3	hTFtarget	273	289	9.60x10-^{5}	AACAGAGTGAGAGCCTG
PBX4	CISBP	2,309	2,318	8.87x10-^{5}	CTTGACGGGG
PEG3	TRANSFAC	1,587	1,594	8.01x10-^{5}	GTGGGAGT
PHOX2B	hTFtarget	794	803	1.07x10-^{5}	CCCGGCTAAT
PITX1	JASPAR	905	912	9.40x10-^{5}	ATAATCCC
PITX2	TRANSFAC	116	126	5.53x10-^{7}	TGTAATCCCAG

PITX3	CISBP	118	125	4.72x10-^{5}	GTAATCCC
PKNOX1	CISBP	988	995	5.35x10-^{5}	TGACAGCC
PKNOX2	CISBP	988	997	2.86x10-^{5}	ATTGACAGCC
PLAG1	TRANSFAC	2,251	2,269	3.16x10-^{7}	GCGGCGGGCCGGGCTCGGG
PLAGL1	CISBP	2,477	2,486	3.39x10-^{7}	GGGGCCCCCC
PLAGL2	JASPAR	2,477	2,486	4.02x10-^{6}	GGGGCCCCCC
POU1F1	hTFtarget	1,303	1,315	4.25x10-^{5}	TTGCATACATCAG
POU2F2	hTFtarget	1,303	1,314	3.52x10-^{6}	CTGATGTATGCA
POU2F3	hTFtarget	1,532	1,542	8.21x10-^{5}	GGACGCTCACG
POU3F1	hTFtarget	1,303	1,315	1.49x10-^{5}	CTGATGTATGCAA
POU3F2	hTFtarget	955	971	2.33x10-^{5}	TAATTCTGTGATGATGA
POU3F3	hTFtarget	1,304	1,315	7.74x10-^{5}	TTGCATACATCA
POU3F4	CISBP	1,303	1,315	1.83x10-^{5}	TTGCATACATCAG
POU4F3	CISBP	968	975	5.88x10-^{5}	TTATTCAT
POU5F1	CISBP	351	365	5.77x10-^{5}	TTTTTTTTTTTGAGA
POU5F1B	CISBP	1,312	1,318	7.93x10-^{5}	TAATTGC
POU6F1	hTFtarget	1,009	1,018	9.75x10-^{5}	TTAAGGAGAA

PPARD	hTFtarget	2,315	2,330	5.71x10^{-5}	CAAGGTCACGCCGGCC
PPARG	hTFtarget	1,272	1,291	1.42x10^{-6}	CTGGGTGACTTTGCCCCCTA
PRDM1	hTFtarget	1,843	1,853	7.11x10^{-6}	TCCTTTCTCCT
PRDM16	HOCOMOCO	1,893	1,902	4.39x10^{-5}	CCTCAGGGAC
PRDM4	CISBP	2,421	2,440	2.92x10^{-5}	CCGCCGCTTCCCGGCTTCCC
PRDM5	HOCOMOCO	217	231	1.04x10^{-5}	CCAGGAGTTCAAGGC
PRDM6	CISBP	340	360	2.33x10^{-6}	GTTCCTTGTATTTTTTTTTTT
PRDM9	CISBP	2,405	2,428	1.38x10^{-7}	GGTCCTGGCGCCCCCGCCGCCGCT
PROX1	CISBP	656	667	7.20x10^{-5}	GAGGGAGTCTTG
PTF1A	HOCOMOCO	2,022	2,039	2.37x10^{-5}	GCGGCTGCCTCCTCCCCT
RARA	hTFtarget	211	230	2.12x10^{-7}	TGGAGTCCAGGAGTTCAAGG
RARB	CISBP	1,448	1,457	4.37x10^{-6}	CAAGGTCACC
RARG	HOCOMOCO	2,317	2,334	7.27x10^{-7}	AGGTCACGCCGGCCGGGG
RBAK	CISBP	2,019	2,033	5.25x10^{-6}	GCCTCCTCCCCTCGG

RBPJ	HOCOMOCO	1,804	1,814	2.99x10-^{5}	CGCTGGGAAAT
RBPJL	CISBP	1,804	1,813	7.62x10-^{5}	ATTTCCCAGC
REL	hTFtarget	1,090	1,099	7.53x10-^{5}	CGGTTTTTCC
RELA	CISBP	188	217	7.42x10-^{5}	GACTCCAGCTATCCTCCCTCCTCAGCCTCC
REST	hTFtarget	107	120	1.46x10-^{6}	TCCAAGGTGCTGGG
RFX1	HOCOMOCO	1,813	1,834	3.11x10-^{6}	CCTGGCGTTGCCGCGGGGCACG
RFX2	HOCOMOCO	2,097	2,118	2.59x10-^{5}	GGCTGTGGGGAGGGCGACGGAG
RFX3	TRANSFAC	1,813	1,835	8.21x10-^{5}	CGTGCCCCGCGGCAACGCCAGGA
RFX4	CISBP	672	681	7.19x10-^{5}	GTTGCCCAGG
RFX5	hTFtarget	2,003	2,019	6.64x10-^{6}	GCGCCAACGGTCACCGC
RFX6	HOCOMOCO	670	680	6.93x10-^{6}	CTGTTGCCCAG
RFX7	JASPAR	1,821	1,829	1.83x10-^{5}	CGTTGCCGC

RHOXF1	CISBP	905	912	7.40x10-^{5}	ATAATCCC
RORA	hTFtarget	863	881	2.31x10-^{6}	AATTTAGGTCAGGAGATCG
RORB	CISBP	862	881	1.62x10-^{6}	AATTTAGGTCAGGAGATCGA
RORC	hTFtarget	862	881	2.91x10-^{6}	AATTTAGGTCAGGAGATCGA
RUNX1	hTFtarget	1,643	1,654	5.02x10-^{5}	GCCGCTTCCTCT
RUNX3	hTFtarget	1,228	1,248	1.41x10-^{5}	GTGACAACCAAAACCGTGTTT
RXRA	HOCOMOCO	63	83	1.70x10-^{7}	GAGCCCAGGAGTTCAAGACCA
RXRB	HOCOMOCO	570	579	3.91x10-^{5}	CGAGGTCAGG
RXRG	HOCOMOCO	212	233	2.70x10-^{7}	GGAGTCCAGGAGTTCAAGGCTG
SALL1	TRANSFAC	2,404	2,415	6.04x10-^{5}	GGGTCCTGGCGC
SALL2	TRANSFAC	138	151	5.31x10-^{6}	CTGCATCCGGCCAG
SALL4	HOCOMOCO	2,101	2,110	2.38x10-^{5}	GTGGGGAGGG

SCRT1	CISBP	1,063	1,074	3.43x10-^{5}	AGTAAACAGGTG
SCRT2	TRANSFAC	389	406	2.29x10-^{5}	GCTGGAGTGTAGTGGCAC
SIX1	CISBP	1,125	1,134	6.98x10-^{6}	ATGATACCCG
SIX2	CISBP	376	385	8.18x10-^{6}	CCGTGTCGCC
SIX3	JASPAR	1,122	1,138	2.02x10-^{5}	GGACGGGTATCATTCTT
SIX4	CISBP	1,126	1,134	4.03x10-^{6}	ATGATACCC
SIX5	hTFtarget	1,799	1,808	3.39x10-^{5}	GAAATGGAGT
SIX6	CISBP	1,126	1,136	3.21x10-^{6}	GAATGATACCC
SMAD2	hTFtarget	619	630	3.31x10-^{5}	TGGCTCACTCCT
SMAD3	HOCOMOCO	426	437	1.60x10-^{7}	CTCTGCCTCCTG
SMAD4	hTFtarget	1,177	1,186	3.71x10-^{5}	GCATGTCTGG
SMAD5	TRANSFAC	968	979	7.28x10-^{5}	ATGAATAAACCA
SMAD7	TRANSFAC	1,042	1,053	3.73x10-^{5}	GTTTTGTAAAAC
SNAI1	CISBP	988	997	2.71x10-^{5}	GGCTGTCAAT

SNAI2	hTFtarget	1,063	1,072	4.87×10^{-5}	CACCTGTTTA
SNAI3	CISBP	1,061	1,070	8.93×10^{-5}	GTCACCTGTT
SOHLH2	CISBP	1,537	1,546	1.53×10^{-5}	CTCACGTGCC
SOX1	CISBP	964	973	2.14×10^{-5}	GATGATGAAT
SOX10	hTFtarget	993	1006	4.66×10^{-5}	TCAATGTGCTGTGA
SOX11	CISBP	1,412	1,420	7.82×10^{-5}	ATTGTTTTG
SOX14	CISBP	1,412	1,419	4.83×10^{-5}	AAAACAAT
SOX15	CISBP	1,412	1,420	4.37×10^{-5}	ATTGTTTTG
SOX17	CISBP	879	887	2.19×10^{-5}	AGGATCAAT
SOX18	CISBP	1,412	1,419	4.83×10^{-5}	AAAACAAT
SOX2	hTFtarget	1,842	1,854	1.52×10^{-5}	TTCCTTTCTCCTC
SOX21	CISBP	1,412	1,420	3.96×10^{-5}	ATTGTTTTG
SOX3	CISBP	1,412	1,419	2.65×10^{-5}	ATTGTTTT
SOX4	HOCOMOCO	1,842	1,853	2.44×10^{-5}	TCCTTTCTCCTC
SOX6	CISBP	1,412	1,420	5.98×10^{-6}	ATTGTTTTG
SOX7	CISBP	1,412	1,419	8.79×10^{-5}	AAAACAAT
SOX8	CISBP	1,407	1,423	4.99×10^{-5}	AGTTAATTGTTTTGATT

SOX9	hTFtarget	992	1,007	1.23x10-^{5}	GTCAATGTGCTGTGAG
SP1	hTFtarget	1,777	1,798	1.06x10-^{9}	CAGGGGCGGGGCCAGCGCAGGG
SP110	CISBP	1,792	1,800	2.65x10-^{5}	CGCAGGGAC
SP2	HOCOMOCO	2,476	2,497	4.25x10-^{8}	GAGGCGGCGGCGGGGCCCCCCG
SP3	HOCOMOCO	1,774	1,793	1.05x10-^{7}	TTGCAGGGGCGGGGCCAGCG
SP4	CISBP	1,777	1,789	3.05x10-^{7}	GGCCCCGCCCCTG
SP5	TRANSFAC	2,270	2,282	1.42x10-^{7}	TCCCCGCCGCCCG
SP8	CISBP	1,927	1,938	8.83x10-^{6}	GACCCGCCCCCG
SP9	JASPAR	1,777	1,788	1.02x10-^{5}	GCCCCGCCCCTG
SPDEF	CISBP	2,084	2,093	3.04x10-^{5}	GCCCGGATCT
SPI1	JASPAR	1,639	1,655	1.41x10-^{6}	TTAAAGAGGAAGCGGCA
SPIB	hTFtarget	1,641	1,652	8.78x10-^{7}	AAAGAGGAAGCG
SPIC	CISBP	1,642	1,650	1.34x10-^{5}	AAGAGGAAG
SPZ1	JASPAR	534	544	6.38x10-^{5}	GGGGTTTCACC
SREBF1	hTFtarget	2,212	2,222	5.05x10-^{6}	GATCGGGTGAG

SREBF2	hTFtarget	692	701	1.93×10^{-5}	ATCGCGCCAC
SRY	hTFtarget	1,390	1,402	7.56×10^{-5}	TCAATGACTATGA
STAT2	hTFtarget	1,844	1,862	5.91×10^{-5}	GGAGAAAGGAAAACGCGCG
STAT3	HOCOMOCO	2,425	2,436	4.33×10^{-5}	CGCTTCCCGGCT
STAT5A	HOCOMOCO	1,494	1,503	8.90×10^{-5}	TTCACAGAAG
STAT5B	HOCOMOCO	1,494	1,505	2.41×10^{-5}	CTTCTGTGAAAT
T	hTFtarget	318	342	1.48×10^{-5}	TGTACTATTTGTCTGTGATCTTGTT
TAL1	hTFtarget	93	111	9.98×10^{-5}	TTGGAAGGCTGAGATGAGA
TBX1	CISBP	98	120	3.75×10^{-5}	TCTCAGCCTTCCAAGGTGCTGGG
TBX18	CISBP	1,094	1,105	7.47×10^{-5}	GGAGGTGGAAAA
TBX2	CISBP	1,797	1,817	1.60×10^{-7}	GCACGCTGGGAAATGGAGTCC
TBX20	TRANSFAC	1,502	1,514	7.90×10^{-5}	AAATGCGGACAGG
TBX21	HOCOMOCO	1,587	1,598	8.93×10^{-5}	GGGAGTGGGAGT

TBX3	hTFtarget	1,095	1,105	1.11x10-^{5}	GGAGGTGGAAA
TBX4	CISBP	913	932	7.65x10-^{5}	GGGTGAGGTGGCGCACGCCT
TBX5	TRANSFAC	1,569	1,583	2.27x10-^{6}	TGGGGTGCGGGCGGG
TCF12	hTFtarget	1,658	1,668	4.33x10-^{5}	CGCGCCTGCGC
TCF3	hTFtarget	1,658	1,668	4.76x10-^{5}	CGCGCCTGCGC
TCF4	hTFtarget	1,657	1,669	4.53x10-^{5}	CCGCGCCTGCGCC
TCF7	hTFtarget	327	342	1.42x10-^{5}	AACAAGATCACAGACA
TCF7L1	CISBP	2,244	2,258	7.79x10-^{5}	GGCTCGGGGCGGAGA
TCF7L2	HOCOMOCO	328	340	8.97x10-^{5}	GTCTGTGATCTTG
TCFCP2L1	CISBP	138	158	4.17x10-^{5}	CTGCATCCGGCCAGTTTTATT
TCFL5	CISBP	1,707	1,716	5.03x10-^{7}	GCACGCGCAC
TEAD1	hTFtarget	388	400	6.34x10-^{5}	CTACACTCCAGCC
TEAD2	CISBP	612	621	5.40x10-^{5}	CCTGGAATCC
TEAD4	CISBP	612	621	2.22x10-^{5}	CCTGGAATCC
TFAP2A	CISBP	1,891	1,900	1.83x10-^{6}	CGCCTCAGGG
TFAP2B	hTFtarget	1,891	1,901	1.25x10-^{6}	TCCCTGAGGCG

TFAP2C	hTFtarget	1,889	1,902	1.22x10^{-6}	GTCCCTGAGGCGGA
TFAP2E	CISBP	1,815	1,826	1.06x10^{-6}	TGCCGCGGGGCA
TFAP4	hTFtarget	1,061	1,070	9.38x10^{-5}	AACAGGTGAC
TFCP2	hTFtarget	1,086	1,095	2.18x10^{-5}	AAACCGGTCT
TFCP2L1	HOCOMOCO	2,322	2,340	6.27x10^{-5}	GTCCGCCCCCGGCCGGCGT
TFDP1	hTFtarget	2,131	2,144	7.95x10^{-6}	CGGAGGCGGGAGCG
TFE3	CISBP	575	584	1.21x10^{-5}	CCTCGTGATC
TFEB	hTFtarget	1,537	1,546	2.25x10^{-5}	CTCACGTGCC
TFEC	CISBP	575	584	1.56x10^{-5}	CCTCGTGATC
TGIF1	CISBP	988	997	7.35x10^{-6}	ATTGACAGCC
TGIF2	CISBP	988	997	2.79x10^{-5}	ATTGACAGCC
THAP1	hTFtarget	2,037	2,058	1.56x10^{-7}	CGCCGCCGCCGCCGCCGCCGCC
THAP11	HOCOMOCO	1,797	1,818	4.19x10^{-10}	GGCACGCTGGGAAATGGAGTCC
THRA	hTFtarget	870	886	5.27x10^{-6}	GGATCAATTTAGGTCAG
THRB	hTFtarget	2,305	2,323	2.65x10^{-6}	GTGACCTTGACGGGGCGGC
TLX2	CISBP	951	958	6.46x10^{-5}	ATTAAATA

TP53	hTFtarget	1,175	1,194	2.82x10^{-6}	GGTCCAGACCAGACATGCCG
TP63	hTFtarget	1,175	1,194	1.77x10^{-6}	GGTCCAGACCAGACATGCCG
TP73	hTFtarget	1,176	1,194	4.50x10^{-7}	GGTCCAGACCAGACATGCC
TRP53	CISBP	1,954	1,971	8.28x10^{-5}	AGCGCGCCCGGGCGTGCG
TRP73	TRANSFAC	1,176	1,193	6.33x10^{-5}	GGCATGTCTGGTCTGGAC
TWIST1	hTFtarget	1,302	1,318	8.76x10^{-5}	ACTGATGTATGCAATTA
UBP1	hTFtarget	2,323	2,340	6.54x10^{-5}	CGCCGGCCGGGGGCGGAC
USF1	hTFtarget	1,538	1,547	1.74x10^{-5}	TCACGTGCCG
USF2	HOCOMOCO	1,530	1,548	7.61x10^{-6}	ACGGCACGTGAGCGTCCCG
VDR	JASPAR	1,441	1,456	2.10x10^{-6}	AAGGTCACCCAGTTCG
VENTX	CISBP	1,311	1,320	5.84x10^{-5}	GTTAATTGCA
VEZF1	hTFtarget	2,130	2,151	1.23x10^{-6}	CCGGAGGCGGGAGCGAGCGAGG
VSX2	hTFtarget	506	514	6.89x10^{-5}	GCTAATTTT
WT1	hTFtarget	1,969	1,988	8.81x10^{-7}	GCGCAGGGGCGGCGGCGCGG
XBP1	hTFtarget	920	931	6.21x10^{-7}	CGCCACCTCACC
XPA	CISBP	922	932	4.75x10^{-7}	GGGTGAGGTGG

YY1	hTFtarget	2,183	2,193	1.84x10-^{5}	GCCGCCATGAA
YY2	hTFtarget	2,182	2,192	1.93x10-^{6}	TCATGGCGGCG
ZBTB1	CISBP	1,946	1,955	2.43x10-^{5}	CTCCCGCACG
ZBTB12	CISBP	2,086	2,099	4.77x10-^{5}	ATCCGGGCCGCGGC
ZBTB14	hTFtarget	1727	1742	1.11x10-^{7}	ACGCGCGCGCACGCAC
ZBTB17	HOCOMOCO	2,480	2,498	3.58x10-^{7}	GGAGGCGGCGGCGGGGCCC
ZBTB18	hTFtarget	1,657	1,668	9.43x10-^{5}	GCGCAGGCGCGG
ZBTB20	TRANSFAC	2,317	2,328	7.64x10-^{5}	AGGTCACGCCGG
ZBTB22	CISBP	1,216	1,232	8.18x10-^{5}	GTCACAACTTGAGTGCG
ZBTB24	TRANSFAC	669	680	1.61x10-^{5}	CTGGGCAACAGA
ZBTB26	CISBP	1,726	1,746	6.57x10-^{12}	CACGCGCGCGCACGCACGCAC
ZBTB3	TRANSFAC	1,153	1,169	5.10x10-^{6}	GTGTGCACTGCAGGGTG
ZBTB33	hTFtarget	1,523	1,537	1.06x10-^{5}	GCGTCCCGCGCGAGG
ZBTB37	CISBP	2,172	2,188	3.45x10-^{6}	TCGCCGCCGCCGCCGCC

ZBTB41	TRANSFAC	2,370	2,380	4.51x10-^{6}	AGGGCCCCCGG
ZBTB43	CISBP	1,673	1,692	2.18x10-^{5}	AGTGCCTAGCCCGGAGCGCC
ZBTB44	CISBP	136	146	7.86x10-^{5}	CGGATGCAGTG
ZBTB5	TRANSFAC	1,101	1,110	1.20x10-^{5}	CAGAAGGAGG
ZBTB6	hTFtarget	2,108	2,122	1.22x10-^{6}	CCCGCTCCGTCGCCC
ZBTB7A	hTFtarget	2,367	2,381	2.67x10-^{6}	CAGGGCCCCCGGCGC
ZBTB7B	TRANSFAC	1,136	1,150	1.80x10-^{6}	CGACCCCCCAAAAAG
ZBTB7C	CISBP	779	790	9.65x10-^{6}	GCGCCCACCACC
ZEB1	CISBP	1,062	1,069	1.47x10-^{5}	TCACCTGT
ZFP1	TRANSFAC	298	316	5.45x10-^{5}	TAAAAGAAAAAAAAGTGTT
ZFP105	TRANSFAC	19	33	1.51x10-^{5}	TACAAAAAATAATAA
ZFP14	CISBP	2,150	2,164	1.78x10-^{8}	CGCTCCCGGGCCTCC
ZFP182	TRANSFA	806	817	3.28x10-^{5}	AAATACAAAAGA

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ZFP184	TRANSFAC	2,028	2,039	4.53x10-^{6}	GGAGGCAGCCGC
ZFP202	CISBP	1,365	1,374	2.83x10-^{5}	CCCCCCCCCA
ZFP260	TRANSFAC	1,373	1,384	3.66x10-^{5}	GGGTCAATAATA
ZFP28	HOCOMOCO	288	307	1.06x10-^{5}	TTTTCTTTTATTTTGAGACA
ZFP281	TRANSFAC	1,364	1,378	1.05x10-^{6}	TGACCCCCCCCCCAA
ZFP287	TRANSFAC	1,373	1,384	3.97x10-^{5}	GGGTCAATAATA
ZFP3	TRANSFAC	645	656	1.89x10-^{5}	CTTAGAAAAAAA
ZFP30	TRANSFAC	1,040	1,051	3.70x10-^{7}	CGGTTTTACAAA
ZFP316	TRANSFAC	1,506	1,517	7.06x10-^{5}	GCGGACAGGGGA
ZFP319	TRANSFA	534	545	1.46x10-^{5}	TGGTGAAACCCC

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ZFP329	TRANSFAC	440	458	2.79x10-^{5}	GGCAGTAGAATTGCTTGAA
ZFP37	TRANSFAC	990	1001	3.18x10-^{5}	CTGTCAATGTGC
ZFP39	TRANSFAC	596	607	1.43x10-^{5}	AGTTTGGGAGGC
ZFP414	TRANSFAC	998	1010	7.13x10-^{5}	AATCTCACAGCAC
ZFP42	HOCOMOCO	1,797	1,808	3.07x10-^{5}	GGACTCCATTTC
ZFP445	TRANSFAC	768	785	2.16x10-^{6}	TGGGATTACAGGCGCCCA
ZFP46	TRANSFAC	583	594	3.36x10-^{6}	AAGGTGGGCGGA
ZFP513	TRANSFAC	187	204	2.57x10-^{6}	GGGAGGCTGAGGAGGGAG
ZFP516	TRANSFAC	141	147	8.00x10-^{5}	CCGGATG

ZFP526	TRANSFAC	679	690	2.44x10-^{5}	AGGTTGGTGTGC
ZFP532	TRANSFAC	2,445	2,452	7.28x10-^{5}	TGGGGGAT
ZFP536	TRANSFAC	2,130	2,136	3.60x10-^{5}	CCGGAGG
ZFP553	TRANSFAC	2,333	2,342	1.39x10-^{5}	GGGCGGACTC
ZFP57	HOCOMOCO	1,819	1,828	1.37x10-^{5}	CCGCGGCAAC
ZFP574	TRANSFAC	1,585	1,605	5.15x10-^{5}	CGCTGCGGGGAGTGGGAGTGT
ZFP579	TRANSFAC	2,396	2,406	3.65x10-^{7}	CCCCCCCAGAC
ZFP583	TRANSFAC	1,087	1,106	9.16x10-^{6}	AGGAGGTGGAAAAACCGGTC
ZFP629	TRANSFAC	76	87	7.33x10-^{5}	CTGGGCTCAAGC
ZFP637	CISBP	839	847	2.34x10-^{5}	TATATATGT

ZFP64	CISBP	2,295	2,309	1.55x10-^{6}	GCCCCCCGGGGCCGC
ZFP641	TRANSFAC	1,364	1,375	1.06x10-^{6}	TTGGGGGGGGGG
ZFP652	TRANSFAC	1,631	1,643	1.52x10-^{5}	GTGAAGAGTTAAA
ZFP653	TRANSFAC	1,363	1,372	2.81x10-^{5}	CTTGGGGGGG
ZFP654	TRANSFAC	26	41	2.50x10-^{5}	TTTTTGTAGAGATGGG
ZFP664	TRANSFAC	534	545	8.96x10-^{5}	TGGTGAAACCCC
ZFP668	TRANSFAC	2,473	2,486	6.95x10-^{5}	GTCCGGGGGGCCCC
ZFP672	TRANSFAC	111	122	6.19x10-^{6}	AGGTGCTGGGAT
ZFP689	TRANSFAC	2,119	2,130	8.12x10-^{5}	CGGGTGACCTTC
ZFP697	TRANSFAC	2,471	2,482	1.12x10-^{5}	GGGTCCGGGGGG

ZFP711	CISBP	2,478	2,487	1.84x10-^{6}	GGGGGCCCCG
ZFP74	TRANSFAC	346	364	8.49x10-^{5}	CTCAAAAAAAAAAAATACA
ZFP740	TRANSFAC	1,361	1,376	1.98x10-^{7}	ACCCCCCCCCCAAGTG
ZFP768	TRANSFAC	2,071	2,082	8.13x10-^{5}	CGCAACGGCGGC
ZFP770	TRANSFAC	1,367	1,376	1.03x10-^{5}	GGGGGGGGGT
ZFP786	TRANSFAC	2,007	2,024	7.39x10-^{5}	CCTCGGCGCCAACGGTCA
ZFP787	TRANSFAC	1,488	1,499	1.05x10-^{5}	CAGAAGAGGATC
ZFP800	TRANSFAC	160	167	9.01x10-^{5}	TAAATGGG
ZFP90	TRANSFAC	2,205	2,223	7.74x10-^{5}	CCGACGAGATCGGGTGAGG
ZFP92	TRANSFAC	2,331	2,342	2.52x10-^{6}	GGGGGCGGACTC

ZFX	HOCOMOCO	2,277	2,295	2.00x10-^{6}	CGCCCGGCCTCAGACGCCG
ZIC1	TRANSFAC	2,294	2,307	2.41x10-^{6}	GGCCCCGGGGGGCG
ZIC2	TRANSFAC	2,295	2,309	6.21x10-^{6}	GCCCCCCGGGGCCGC
ZIC3	hTFtarget	1,592	1,606	2.56x10-^{6}	CACTCCCCGCAGCGC
ZIC4	CISBP	1,592	1,606	1.62x10-^{6}	CACTCCCCGCAGCGC
ZIC5	CISBP	2,475	2,484	1.17x10-^{6}	GGCCCCCCGG
ZIK1	CISBP	1,275	1,295	1.10x10-^{5}	TCTTCTGGGTGACTTTGCCCC
ZIM2	CISBP	1,546	1,575	1.38x10-^{8}	CGTTCCCGCTCCGTCCGCCCGCCTGGGGTG
ZKSCAN1	CISBP	1,709	1,718	3.82x10-^{5}	ACGCGCACGC
ZKSCAN3	JASPAR	844	863	2.38x10-^{5}	GAGACCAGCCTAGCCAACAT
ZKSCAN5	JASPAR	1,095	1,108	6.69x10-^{5}	GAAGGAGGTGGAAA
ZNF100	CISBP	2,036	2,050	7.42x10-^{9}	CCGCCGCCGCCGCCG
ZNF101	CISBP	1,967	1,981	3.92x10-^{5}	GTGCGCAGGGGCGGC
ZNF12	CISBP	2,093	2,110	5.84x10-^{7}	CCCTCCCCACAGCCGCGG

ZNF121	HOCOMOCO	661	680	1.85x10-^{11}	CTGGGCAACAGAGCAAGACT
ZNF124	CISBP	1,847	1,858	6.33x10-^{5}	CGTTTTCCTTTC
ZNF132	CISBP	2,425	2,439	6.69x10-^{6}	CGCTTCCCGGCTTCC
ZNF135	JASPAR	885	898	2.30x10-^{7}	CCTCGGCCTCCCAA
ZNF136	CISBP	354	374	2.34x10-^{5}	TTTTTTTTGAGACAGAGTCTT
ZNF140	JASPAR	439	459	1.42x10-^{6}	AGGCAGTAGAATTGCTTGAAC
ZNF141	CISBP	2,301	2,324	2.32x10-^{6}	CGTGACCTTGACGGGGCGGCCCCG
ZNF143	HOCOMOCO	1,797	1,818	1.16x10-^{10}	GGCACGCTGGGAAATGGAGTCC
ZNF146	HOCOMOCO	1,330	1,353	2.52x10-^{5}	TATTAATAGCCAAATACTGTTTTA
ZNF148	hTFtarget	2,264	2,275	9.78x10-^{6}	CGCCGCTCCCCG
ZNF154	CISBP	214	228	8.98x10-^{5}	AGTCCAGGAGTTCAA
ZNF16	CISBP	2,372	2,386	5.29x10-^{5}	CCGTCCAGGGCCCCC
ZNF174	CISBP	1,532	1,547	2.33x10-^{5}	GGACGCTCACGTGCCG
ZNF175	CISBP	14	34	2.30x10-^{5}	TATTATTATTATTTTTGTAG
ZNF18	CISBP	684	698	3.43x10-^{5}	GGTGTGCAGTGGCGC

ZNF180	CISBP	2,036	2,056	1.12×10^{-7}	CCGCCGCCGCCGCCGCCGCCG
ZNF181	CISBP	174	197	2.11×10^{-9}	GTCCCAGCTACTTGGGAGGCTGAG
ZNF182	CISBP	350	361	5.90×10^{-6}	TTTTTTTTTTTT
ZNF189	CISBP	1,536	1,553	3.18×10^{-6}	CGGGAACGGCACGTGAGC
ZNF19	CISBP	2,373	2,390	1.56×10^{-5}	GCACCCGTCCAGGGCCCC
ZNF2	CISBP	2,411	2,419	1.11×10^{-5}	GGCGCCCCC
ZNF200	CISBP	2,126	2,137	7.30×10^{-5}	CCTTCCGGAGGC
ZNF202	CISBP	2,132	2,139	1.63×10^{-5}	CCGCCTCC
ZNF212	CISBP	275	304	5.12×10^{-5}	TCTTTTATTTTGAGACAGGCTCTCACTCTG
ZNF213	CISBP	2,274	2,288	1.00×10^{-5}	CGCCGCCCGGCCTCA
ZNF214	JASPAR	987	1,001	7.95×10^{-5}	GCACATTGACAGCCT
ZNF22	CISBP	350	358	8.86×10^{-6}	TTTTTTTTT
ZNF222	CISBP	1,110	1,118	1.06×10^{-5}	GCTGACATT
ZNF223	CISBP	1,102	1,115	9.27×10^{-6}	CTCCTTCTGCTGAC
ZNF224	CISBP	52	87	1.64×10^{-6}	GTTGGCCAGGCTGGTCTTGAACTCCTGGGCTCAAGC
ZNF225	CISBP	333	360	7.35×10^{-5}	TGATCTTGTTCCTTGTATTTTTTTTT

					TT
ZNF23	CISBP	1,779	1,797	6.40x10-^{6}	CCTGCGCTGGCCCCGCCCC
ZNF235	CISBP	1	30	1.05x10-^{7}	TTTGTATTATTATTATTATTATTATTTTTT
ZNF248	CISBP	1,386	1,406	8.74x10-^{5}	CTTTTCATAGTCATTGAATTT
ZNF25	CISBP	1,388	1,416	8.99x10-^{5}	TTTCATAGTCATTGAATTTAGTTAATTGT
ZNF250	hTFtarget	1,772	1,780	8.74x10-^{6}	CCTTGCAGG
ZNF254	CISBP	184	195	4.82x10-^{5}	CTTGGGAGGCTG
ZNF257	JASPAR	2,131	2,142	7.18x10-^{6}	CGGAGGCGGGAG
ZNF260	CISBP	2,105	2,119	8.50x10-^{7}	GCTCCGTCGCCCTCC
ZNF263	hTFtarget	2,021	2,032	2.47x10-^{7}	GAGGGGAGGAGG
ZNF264	CISBP	2,281	2,310	6.83x10-^{5}	GGCGGCCCCGGGGGGCGGCGTCTGAGGCCG
ZNF267	CISBP	1,957	1,977	2.17x10-^{7}	CCCCTGCGCACGCCCGGGCGC
ZNF273	CISBP	1,649	1,665	8.95x10-^{5}	AGCGGCAGCCGCGCCTG
ZNF274	hTFtarget	1,285	1,304	9.34x10-^{5}	CACCCAGAAGAAGAACCACT
ZNF28	CISBP	2,410	2,427	9.83x10-^{7}	TGGCGCCCCCGCCGCCGC

ZNF281	hTFtarget	1,927	1,938	5.39×10^{-6}	GACCCGCCCCCG
ZNF282	CISBP	1,587	1,600	1.12×10^{-5}	ACTCCCACTCCCCG
ZNF283	CISBP	2,249	2,272	9.02×10^{-7}	GCCCCGAGCCCGGCCCGCCGCTCC
ZNF284	CISBP	696	704	1.74×10^{-5}	CGCGATCTC
ZNF287	CISBP	327	359	5.97×10^{-8}	TGTCTGTGATCTTGTTCCTTGTATTTTTTTTTT
ZNF30	CISBP	2,033	2,047	2.70×10^{-8}	CAGCCGCCGCCGCCG
ZNF300	CISBP	2,254	2,282	1.18×10^{-5}	GAGCCCGGCCCGCCGCTCCCCGCCGCCCG
ZNF304	CISBP	1,861	1,884	4.69×10^{-7}	GCGCCGCCGCAGTCGGGGCCGTCG
ZNF311	CISBP	2,032	2,052	2.25×10^{-10}	GCAGCCGCCGCCGCCGCCGCC
ZNF317	JASPAR	1,105	1,116	3.61×10^{-5}	TGTCAGCAGAAG
ZNF320	CISBP	2,471	2,491	9.31×10^{-7}	GCGGCGGGGCCCCCCGGACCC
ZNF322	CISBP	2,235	2,255	3.73×10^{-6}	GGGCCTGCGTCTCCGCCCCGA
ZNF324	HOCOMOCO	80	102	3.03×10^{-6}	GCTCAAGCGATCCTCTCATCTCA
ZNF329	CISBP	2,436	2,456	2.43×10^{-5}	CAGGATCCCCCAGGACGGGAA
ZNF331	JASPAR	1,154	1,167	2.72×10^{-5}	CCCTGCAGTGCACA

ZNF333	hTFtarget	1,614	1,622	7.18x10-^{6}	GGCTCCACC
ZNF343	CISBP	2,425	2,433	6.69x10-^{6}	CGCTTCCCG
ZNF345	CISBP	666	687	2.41x10-^{5}	TGCTCTGTTGCCCAGGTTGGTG
ZNF35	CISBP	24	53	2.42x10-^{5}	ATTTTTTGTAGAGATGGGGTTTTGTCATGT
ZNF350	hTFtarget	638	655	1.71x10-^{6}	CGGCCCTTTTTTTTCTAA
ZNF354A	JASPAR	291	311	6.91x10-^{5}	CTCAAAATAAAAGAAAAAAAA
ZNF354B	CISBP	948	959	2.08x10-^{5}	ATTTATTTAATT
ZNF37A	CISBP	197	205	2.23x10-^{6}	CCTCCCTCC
ZNF383	CISBP	2,418	2,444	3.85x10-^{6}	CCGCCGCCGCTTCCCGGCTTCCCGTCC
ZNF384	hTFtarget	352	363	1.85x10-^{6}	TCAAAAAAAAAA
ZNF394	CISBP	2,232	2,251	1.68x10-^{5}	CGCGGGCCTGCGTCTCCGCC
ZNF398	CISBP	2,022	2,035	2.14x10-^{5}	CTGCCTCCTCCCCT
ZNF41	CISBP	619	633	1.19x10-^{6}	TGGTGGCTCACTCCT
ZNF415	CISBP	2,108	2,122	2.27x10-^{6}	CCCGCTCCGTCGCCC
ZNF416	JASPAR	673	683	4.74x10-^{5}	AACCTGGGCAA
ZNF417	CISBP	2,013	2,033	4.83x10-^{6}	TTGGCGCCGAGGGGAGGAGGC

ZNF418	CISBP	3	32	4.34x10-^{6}	ACAAAAAATAATAATAATAATAATAATACA
ZNF419	CISBP	1,915	1,935	7.77x10-^{5}	GGAGTACCCCTGGACCCGCCC
ZNF425	CISBP	2,106	2,112	7.21x10-^{5}	CGCCCTC
ZNF430	CISBP	488	505	2.81x10-^{5}	TCGGCATGGTGGCAGGCG
ZNF432	CISBP	1,537	1,566	2.53x10-^{5}	CTCACGTGCCGTTCCCGCTCCGTCCGCCCG
ZNF436	HOCOMOCO	1,890	1,913	6.11x10-^{6}	TCTGTGCGTGCGTCCCTGAGGCGG
ZNF44	CISBP	2,080	2,109	1.18x10-^{7}	CCTCCCCACAGCCGCGGCCCGGATCTGCGC
ZNF440	CISBP	1,290	1,304	5.60x10-^{6}	AGTGGTTCTTCTTCT
ZNF441	CISBP	1,778	1,789	2.34x10-^{6}	GGCCCCGCCCCT
ZNF443	CISBP	103	123	4.75x10-^{9}	GCCTTCCAAGGTGCTGGGATT
ZNF444	CISBP	2,101	2,116	2.06x10-^{6}	CCGTCGCCCTCCCCAC
ZNF445	CISBP	533	561	8.66x10-^{5}	ACCATCCTGGCTAACATGGTGAAACCCCG
ZNF449	CISBP	1,728	1,742	7.63x10-^{6}	GTGCGTGCGCGCGCG

ZNF454	JASPAR	1,470	1,487	8.99x10-^{7}	AGCCTCTCGGACCCTCGG
ZNF460	JASPAR	456	471	1.54x10-^{8}	GCCTCAGCCTCCTGAG
ZNF467	HOCOMOCO	2,103	2,124	4.49x10-^{7}	GGGGAGGGCGACGGAGCGGGTG
ZNF480	CISBP	1,588	1,599	8.32x10-^{5}	CTCCCACTCCCC
ZNF484	CISBP	2,021	2,041	2.96x10-^{5}	CGGCGGCTGCCTCCTCCCCTC
ZNF486	CISBP	1,960	1,972	5.46x10-^{6}	GCGCACGCCCGGG
ZNF487	CISBP	333	361	6.88x10-^{6}	AAAAAAAAAAAATACAAGGAACAAGATCA
ZNF490	CISBP	1,201	1,215	3.45x10-^{6}	GGGTGCTGCTGGCAT
ZNF492	CISBP	296	313	5.36x10-^{6}	ACTTTTTTTTCTTTTATT
ZNF496	CISBP	672	701	4.18x10-^{15}	ATCGCGCCACTGCACACCAACCTGGGCAAC
ZNF501	CISBP	1,704	1,718	2.58x10-^{5}	CGCGCACGCGCACGC
ZNF502	CISBP	124	150	1.12x10-^{5}	ACAGGCATGAGCCACTGCATCCGGCCA
ZNF506	CISBP	1,137	1,154	2.52x10-^{5}	TTTTTGGGGGGTCGTCGT
ZNF513	CISBP	189	203	6.79x10-^{6}	TCCCTCCTCAGCCTC

ZNF519	CISBP	2,036	2,050	7.37x10-^{9}	CCGCCGCCGCCGCCG
ZNF524	CISBP	1,475	1,488	2.82x10-^{6}	CTCGGACCCTCGGG
ZNF527	CISBP	2,036	2,056	2.26x10-^{5}	CCGCCGCCGCCGCCGCCGCCG
ZNF528	HOCOMOCO	1,792	1,811	1.92x10-^{6}	CGCAGGGACTCCATTTCCCA
ZNF529	CISBP	2,252	2,278	1.19x10-^{6}	CCGAGCCCGGCCCGCCGCTCCCCGCCG
ZNF530	CISBP	1,776	1,793	1.08x10-^{6}	CGCTGGCCCCGCCCCTGC
ZNF534	CISBP	1,511	1,525	7.10x10-^{6}	AGGCTCCTTCCCCTG
ZNF543	CISBP	2,480	2,491	1.07x10-^{6}	GGGCCCCGCCGC
ZNF547	HOCOMOCO	737	756	4.82x10-^{5}	AGCTAAGGCCGGAGAAATGC
ZNF548	CISBP	2,315	2,335	7.31x10-^{7}	CCCCCGGCCGGCGTGACCTTG
ZNF549	CISBP	1,019	1,033	2.44x10-^{5}	TGCTGCCTACTGCTT
ZNF554	HOCOMOCO	1,602	1,621	1.37x10-^{6}	GTGGAGCCGCGTGGGGCGCT
ZNF555	CISBP	2,053	2,082	6.79x10-^{7}	CGCAACGGCGGCGGCGGCGGCGGCGGCGGC

ZNF563	CISBP	1,671	1,688	3.34x10^{-6}	CTCCGGGCTAGGCACTGT
ZNF566	CISBP	2,407	2,427	1.38x10^{-6}	TCCTGGCGCCCCCGCCGCCGC
ZNF567	CISBP	1,279	1,308	9.75x10^{-7}	CATCAGTGGTTCTTCTTCTGGGTGACTTTG
ZNF570	CISBP	800	820	3.43x10^{-6}	TAATTTTCTTTTGTATTTTTA
ZNF571	CISBP	2,036	2,050	4.38x10^{-10}	CCGCCGCCGCCGCCG
ZNF574	CISBP	1,688	1,707	9.18x10^{-5}	GCGCCGGTCTCGCAAGCGCG
ZNF580	CISBP	587	604	1.72x10^{-5}	CCCACCTTGGCCTCCCAA
ZNF582	CISBP	1,012	1,038	2.83x10^{-6}	GTACGTGCTGCCTACTGCTTTTCTCCT
ZNF586	HOCOMOCO	190	209	1.93x10^{-5}	AGGCTGAGGAGGGAGGATAG
ZNF587	CISBP	1,597	1,620	5.23x10^{-6}	CCCGCAGCGCCCCACGCGGCTCCA
ZNF594	CISBP	276	290	7.35x10^{-6}	ACAGGCTCTCACTCT
ZNF596	CISBP	425	439	2.23x10^{-6}	GCTCTGCCTCCTGGG
ZNF605	CISBP	1,274	1,294	3.78x10^{-6}	CTTCTGGGTGACTTTGCCCCC
ZNF610	JASPAR	2,262	2,275	5.34x10^{-9}	CCCGCCGCTCCCCG
ZNF611	CISBP	2,295	2,312	7.22x10^{-7}	GGGGCGGCCCCGGGGGGC

ZNF613	CISBP	304	312	7.28x10-^{6}	CTTTTTTTT
ZNF614	CISBP	222	242	2.77x10-^{5}	AGCTCACTGCAGCCTTGAACT
ZNF616	CISBP	2,213	2,227	1.52x10-^{5}	TCGTCCTCACCCGAT
ZNF619	CISBP	2,124	2,146	1.84x10-^{6}	CTCGCTCCCGCCTCCGGAAGGTC
ZNF620	CISBP	939	967	3.68x10-^{5}	GTTCCTTGTATTTATTTAATTCTGTGATG
ZNF626	CISBP	1,161	1,187	4.72x10-^{5}	ACCAGACATGCCGCTCAGCACCCTGCA
ZNF641	CISBP	2,399	2,407	2.23x10-^{6}	ACCCCCCCA
ZNF652	JASPAR	1,632	1,643	3.02x10-^{6}	TGAAGAGTTAAA
ZNF662	CISBP	2,131	2,148	1.76x10-^{5}	CGCTCGCTCCCGCCTCCG
ZNF669	CISBP	867	893	3.87x10-^{5}	AGGCCGAGGATCAATTTAGGTCAGGAG
ZNF674	CISBP	2,407	2,418	2.16x10-^{6}	TCCTGGCGCCCC
ZNF675	CISBP	572	591	7.11x10-^{6}	TGACCTCGTGATCCGCCCAC
ZNF680	JASPAR	1,131	1,145	2.73x10-^{5}	CCCCAAAAAGAATGA
ZNF681	CISBP	1,097	1,108	5.11x10-^{5}	TCCACCTCCTTC
ZNF682	CISBP	2,292	2,312	2.11x10-^{6}	GCCGCCCCCCGGGGCCGCCCC

ZNF684	CISBP	1,768	1,776	1.21x10^{-5}	CTCCCCTTG
ZNF692	CISBP	2,477	2,489	4.96x10^{-6}	GGGGGGCCCCGCC
ZNF701	JASPAR	1,358	1,378	3.31x10^{-5}	TAGCACTTGGGGGGGGGGTCA
ZNF704	CISBP	2,323	2,334	1.52x10^{-6}	CCCCGGCCGGCG
ZNF707	JASPAR	614	628	2.80x10^{-5}	GCTCACTCCTGGAAT
ZNF708	JASPAR	422	436	1.06x10^{-5}	CAAGCTCTGCCTCCT
ZNF71	CISBP	1,542	1,565	2.25x10^{-5}	GTGCCGTTCCCGCTCCGTCCGCCC
ZNF711	hTFtarget	2,152	2,159	9.80x10^{-5}	CCGGGCCT
ZNF713	CISBP	340	358	4.72x10^{-6}	GTTCCTTGTATTTTTTTTT
ZNF714	CISBP	1,205	1,216	7.71x10^{-6}	GGGGTGCTGCTG
ZNF730	CISBP	752	760	3.31x10^{-6}	GGGAAGCTA
ZNF740	JASPAR	1,364	1,376	1.36x10^{-6}	ACCCCCCCCCCAA
ZNF749	CISBP	36	44	7.55x10^{-5}	AACCCCATC
ZNF75A	CISBP	1,090	1,103	1.74x10^{-5}	CGGTTTTTCCACCT
ZNF75D	CISBP	1,090	1,101	3.06x10^{-5}	GTGGAAAAACCG
ZNF76	hTFtarget	1,799	1,820	5.15x10^{-11}	GGGGCACGCTGGGAAATGGAGT
ZNF764	CISBP	215	235	4.65x10^{-5}	GTCCAGGAGTTCAAGGCTGCA
ZNF765	CISBP	1,670	1,687	2.02x10^{-6}	TCCGGGCTAGGCACTGTG

ZNF768	HOCOMOCO	1,466	1,485	1.10x10-^{6}	GAGGGTCCGAGAGGCTGAGT
ZNF770	HOCOMOCO	187	208	1.38x10-^{11}	GGGAGGCTGAGGAGGGAGGATA
ZNF771	CISBP	778	792	4.26x10-^{5}	GGCGCCCACCACCAC
ZNF774	CISBP	2,455	2,472	1.12x10-^{7}	CCCTCAGGCTCTCCTTCA
ZNF776	CISBP	2,252	2,272	3.51x10-^{6}	CCGAGCCCGGCCCGCCGCTCC
ZNF778	CISBP	2,284	2,298	9.96x10-^{6}	GGGCGGCGTCTGAGG
ZNF780A	CISBP	718	741	5.01x10-^{5}	CTCTACTTCCTGCCTTCAAGCATT
ZNF783	CISBP	2,091	2,098	6.67x10-^{6}	CCGCGGCC
ZNF784	CISBP	2,124	2,132	4.28x10-^{5}	GACCTTCCG
ZNF785	CISBP	1,154	1,182	3.09x10-^{5}	TGTGCACTGCAGGGTGCTGAGCGGCATGT
ZNF786	CISBP	174	180	8.00x10-^{5}	CTGGGAC
ZNF787	CISBP	1,878	1,897	9.65x10-^{6}	GCGGCGCGAAATCCGCCTCA
ZNF789	CISBP	488	499	9.66x10-^{6}	CGCCTGCCACCA
ZNF791	CISBP	1,638	1,661	3.08x10-^{5}	CGCGGCTGCCGCTTCCTCTTTAAC
ZNF792	CISBP	1,959	1,988	4.39x10-^{8}	CCGCGCCGCCGCCCCTGCGCACGC

					CCGGGC
ZNF793	CISBP	2,160	2,171	8.68x10^{-6}	GAGCGCCGAGCG
ZNF8	CISBP	1,033	1,044	9.31x10^{-5}	ACGTACCCGGTT
ZNF805	CISBP	1,706	1,723	6.62x10^{-5}	GGCTTGCGTGCGCGTGCG
ZNF816	CISBP	1,989	2,009	1.97x10^{-5}	TCACCGCGCGTCCCCGCGCCG
ZNF821	CISBP	1,898	1,912	2.51x10^{-5}	CTGTGCGTGCGTCCC
ZNF823	CISBP	188	202	3.09x10^{-5}	CCCTCCTCAGCCTCC
ZNF84	CISBP	334	354	4.12x10^{-5}	GATCTTGTTCCTTGTATTTTT
ZNF85	CISBP	603	620	2.61x10^{-6}	AAACTGCTGGGATTCCAG
ZNF860	CISBP	2,263	2,277	6.04x10^{-6}	CCGCCGCTCCCCGCC
ZNF879	CISBP	320	358	3.28x10^{-5}	TACTATTTGTCTGTGATCTTGTTCCTTGTATTTTTTTTT
ZNF880	CISBP	186	212	9.71x10^{-6}	CAGCTATCCTCCCTCCTCAGCCTCCCA
ZNF891	CISBP	2,265	2,285	1.17x10^{-5}	GCCGCTCCCCGCCGCCCGGCC
ZNF90	CISBP	576	590	5.00x10^{-6}	CTCGTGATCCGCCCA
ZNF93	CISBP	2,035	2,073	2.30x10^{-10}	GCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCC

ZNF98	CISBP	799	819	1.89x10-^{5}	CTAATTTTCTTTTGTATTTTT
ZSCAN10	CISBP	1,583	1,593	8.06x10-^{5}	GTACACTCCCA
ZSCAN22	CISBP	2,140	2,157	1.20x10-^{6}	GGGCCTCCTCGCTCGCTC
ZSCAN23	CISBP	1,309	1,327	1.84x10-^{5}	TGCATCTGTTAATTGCATA
ZSCAN29	CISBP	1,031	1,050	4.47x10-^{5}	GCACGTACCCGGTTTTACAA
ZSCAN30	CISBP	1,829	1,843	3.19x10-^{6}	GCCAGGAGCCTCCGA
ZSCAN31	CISBP	1,406	1,421	2.35x10-^{6}	TAGTTAATTGTTTTGA
ZSCAN4C	CISBP	684	692	2.54x10-^{5}	GGTGTGCAG
ZSCAN5	CISBP	1,134	1,151	3.99x10-^{5}	ACGACCCCCCAAAAAGAA
ZSCAN5C	CISBP	1,892	1,906	8.05x10-^{5}	GCCTCAGGGACGCAC