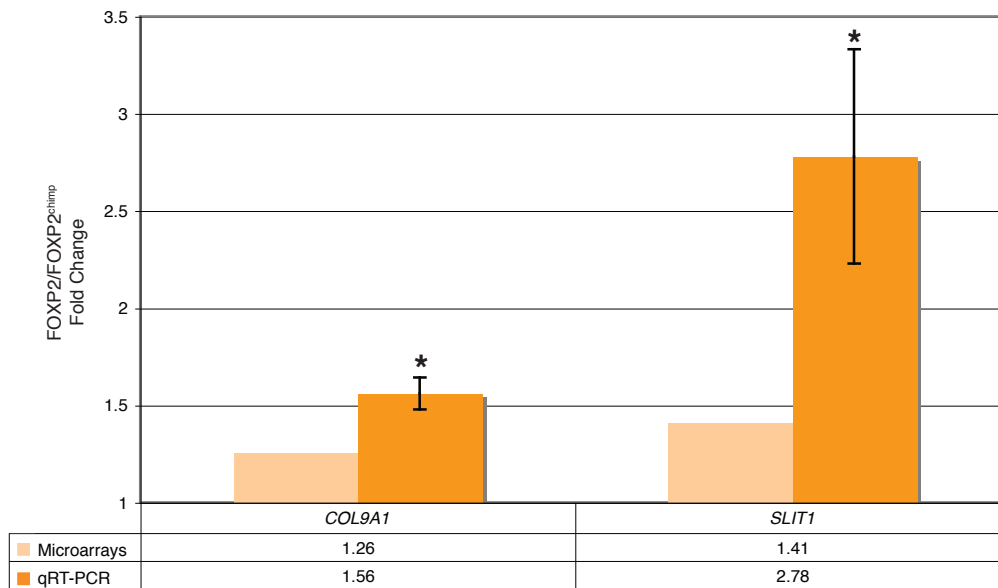
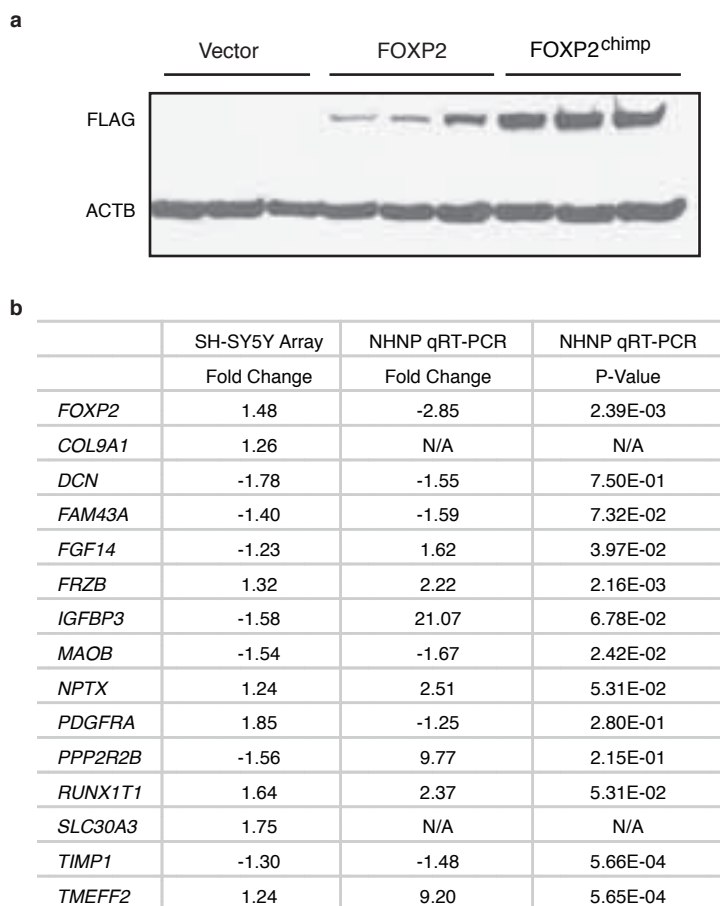


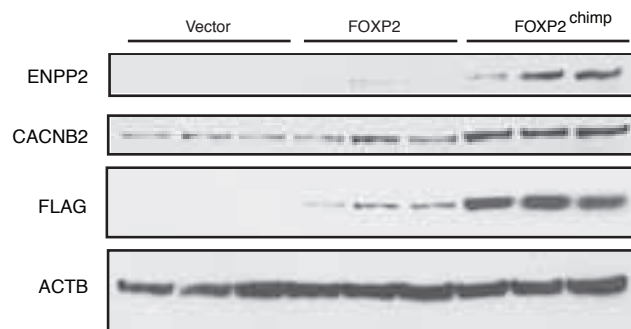
SUPPLEMENTARY INFORMATION



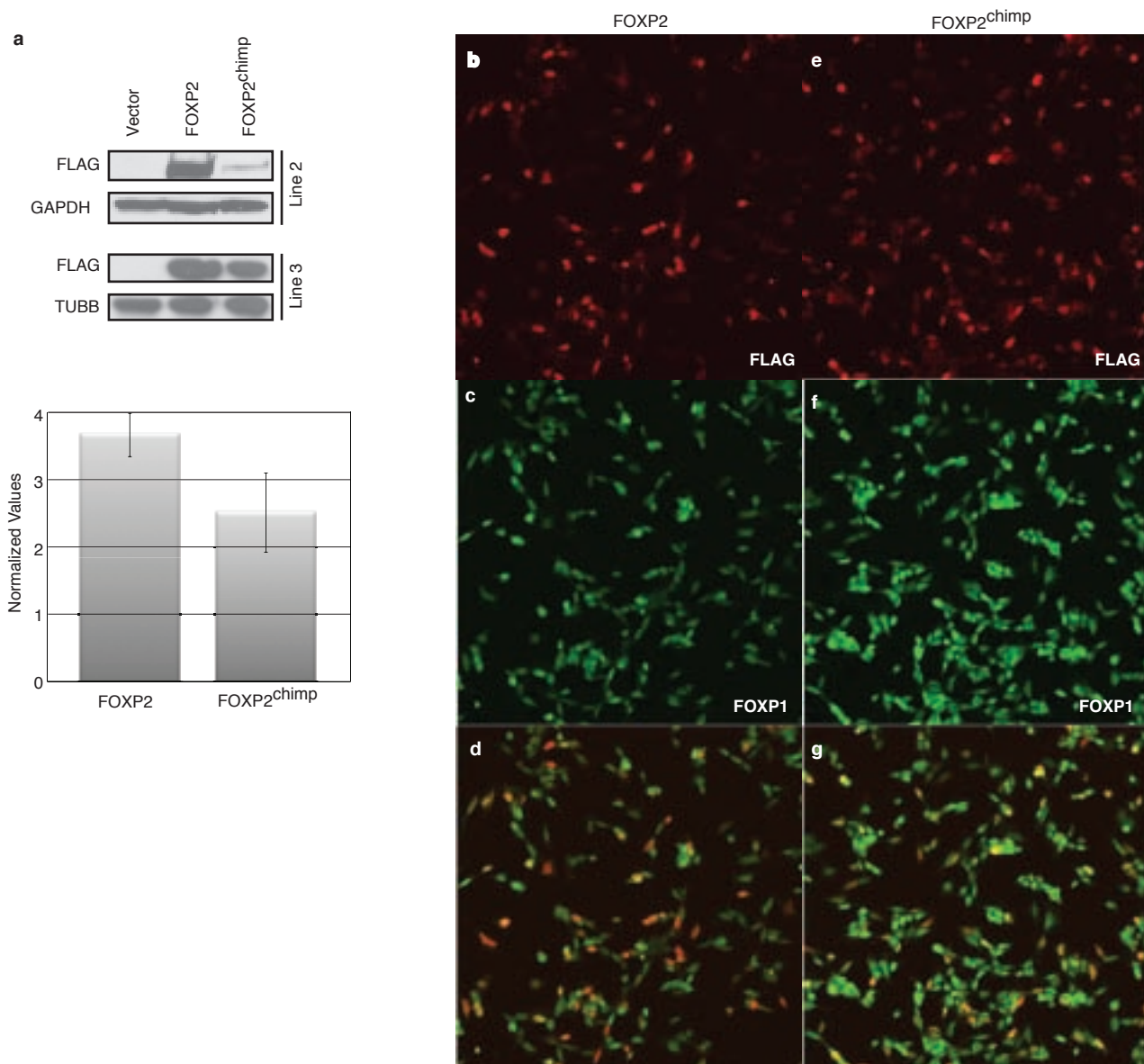
Supplementary Figure 1. Confirmation of additional differentially expressed genes that overlap with previously identified FOXP2 ChIP-chip targets. Quantitative RT-PCR of *COL9A1* and *SLIT1*. Independent RNA was used, and both showed fold changes in the same direction as the microarrays. Asterisks indicate $P < 0.05$ and error bars are \pm s.e.m. (two-tailed Student's t-test, $n=3$).



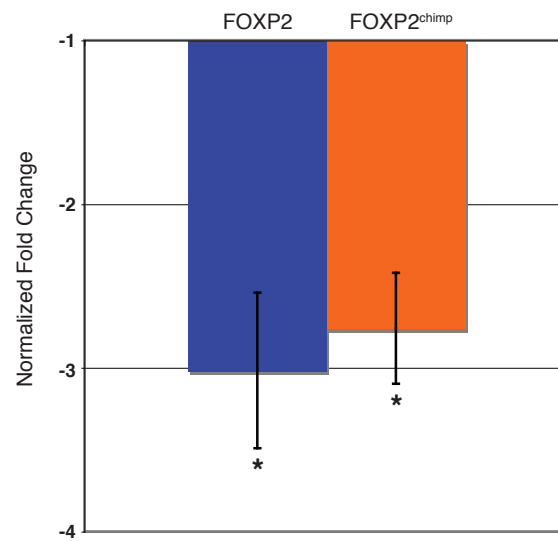
Supplementary Figure 2. Confirmation of targets in another human neuronal system. **a**, Immunoblotting of undifferentiated normal human neuronal progenitors (NHNP) transduced with lentivirus to overexpress either the human or chimpanzee form of FLAG-tagged FOXP2. In these cells the chimpanzee version of FOXP2 was more highly expressed than the human version. ACTB indicates equal loading using an antibody to beta-actin. **b**, Real-time RT-PCR was conducted on a subset of differential targets in NHNPs. Most of these genes had already been confirmed in SH-SY5Y cells by qRT-PCR, and many of these genes were also differentially expressed in tissue. 8/12 of the genes showed the same change in direction in both cell lines, and four of these were significant. 4/10 of the genes had changes in the opposite direction in the two cell lines, but only one of these values in the NHNPs was significant. (Two-tailed Student's test, n=3) N/A indicates that these genes were not expressed at detectable levels in the undifferentiated NHNPs.



Supplementary Figure 3. Confirmation of targets by immunoblotting in an independent cell line. Immunoblotting of SH-SY5Y transduced with lentivirus to overexpress either the human or chimpanzee form of FLAG-tagged FOXP2. In these cells, the chimpanzee version of FOXP2 was more highly expressed than the human version. ENPP2 indicates an antibody to ectonucleotide pyrophosphatase/phosphodiesterase 2. CACNB2 indicates an antibody to the voltage-dependent calcium channel beta 2 subunit. The mRNAs of ENPP2 and CACNB2 were reduced with forced human FOXP2 expression compared to chimpanzee FOXP2 in other SH-SY5Y cells, and were also lower in human brain compared to chimpanzee brain in certain tissues examined. ACTB indicates equal loading using an antibody to beta-actin.

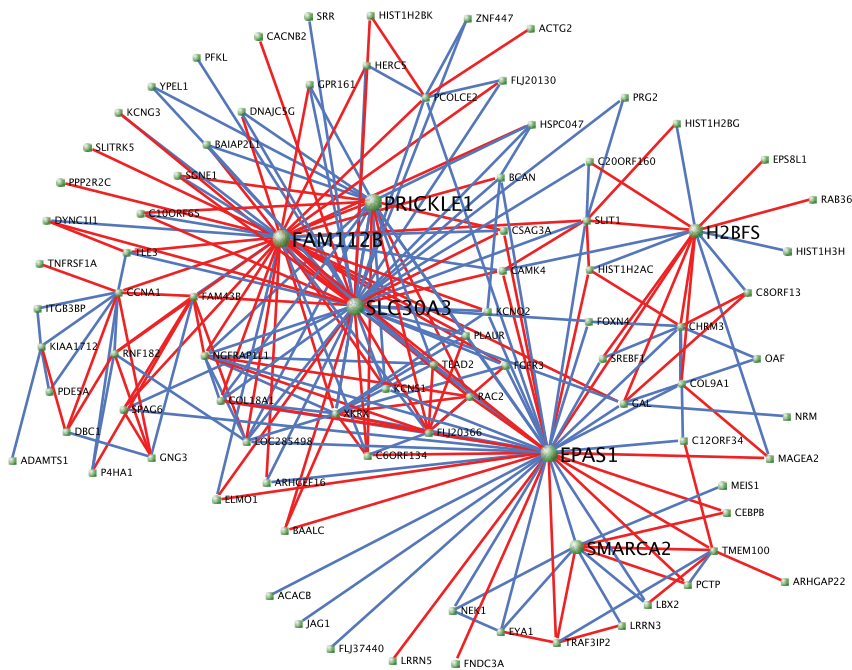


Supplementary Figure 4. FOXP2 expression in multiple independent cell lines. **a**, Upper panel: immunoblotting for FLAG-tagged FOXP2 in the two other SH-SY5Y cell lines run on the microarrays. GAPDH or beta-tubulin (TUBB) indicates equal loading. Lower panel: densitometric analysis of FLAG immunoblotting to loading control for all cell lines. FOXP2 and FOXP2chimp levels as measured by FLAG immunoblotting is not significantly different (two-tailed Student's t-test, $n=3$, $P<0.05$), error bars are \pm s.e.m. **b-g**, Immunofluorescent staining of antibodies against FLAG epitope (red) and FOXP1 (green) in additional independent stable SH-SY5Y cell lines not run on microarrays. Both FOXP2 (**b**) and FOXP2chimp (**e**) expressing cells have FLAG-tagged FOXP2 in the cell nucleus. **d**, and **g**, are overlaps of the FLAG and FOXP1 staining indicating the majority of FLAG immunoreactivity co-localizes with FOXP1.

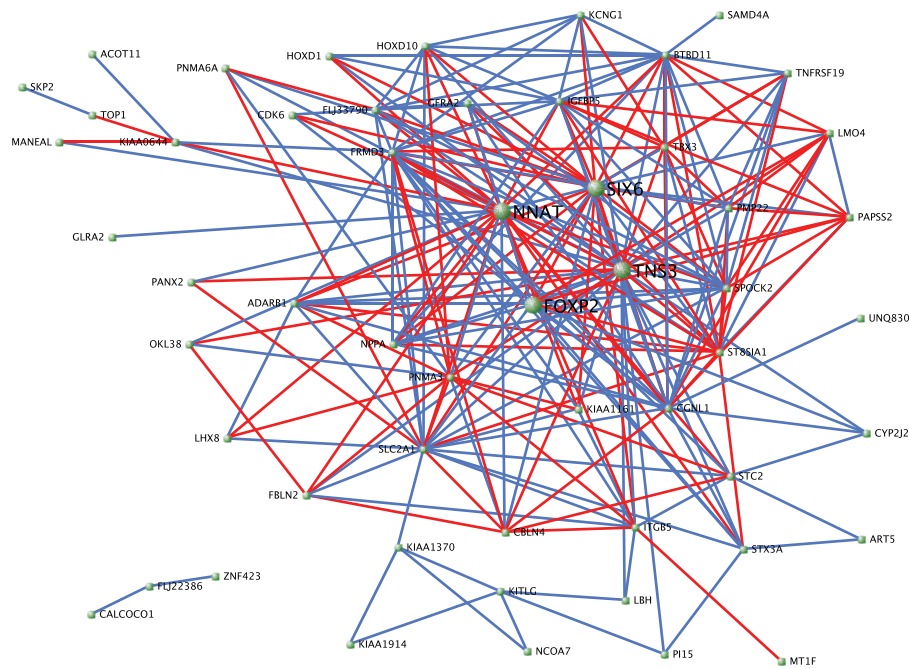


Supplementary Figure 5. Transactivation of a canonical FOXP2 binding site. Both FOXP2 and FOXP2^{chimp} significantly repress activity of a canonical FOXP2 binding site in triplicate driving expression of a luciferase reporter. Asterisks indicate $P < 0.01$ and error bars are \pm s.e.m. (two-tailed Student's *t*-test, $n=4$).

a



b



Supplementary Figure 6. Visualization of two other modules from WGCNA analysis. Five hundred pairs of genes with the greatest topological overlap are shown for each network plot. **a**, A module containing differentially regulated genes and **b**, a module containing FOXP2 and genes similarly regulated by FOXP2 and FOXP2chimp. Positive correlations are depicted in red and negative correlations are depicted in blue. The gene symbol for “hub” genes (i.e. genes with the greatest number of correlations) are accentuated in large bold text.

Konopka_Supplementary_Table_1						
Annotation information and raw intensity values for all differentially expressed genes.						
Upregulated						
ProbeName	GeneName	Accession	FOXP2	FOXP2chimp	Fold Change	pValue
ILMN_11549	GRM8	NM_000845.1	12.2	11.3	1.87	1.30E-03
ILMN_13757	PDGFRA	NM_006206.3	11.09	10.21	1.85	2.72E-02
ILMN_14646	CDCA7L	NM_018719.2	12.73	11.91	1.77	1.68E-03
ILMN_6028	SLC30A3	NM_003459.4	11.46	10.65	1.75	3.08E-04
ILMN_11177	PRNP	NM_183079.1	11.33	10.54	1.74	2.89E-02
ILMN_26360	EPAS1	NM_001430.3	13.06	12.29	1.7	6.61E-04
ILMN_21130	HEBP2	NM_014320.2	9.43	8.68	1.68	3.89E-02
ILMN_22834	ROR2	NM_004560.2	11.18	10.47	1.64	8.28E-04
ILMN_1412	RUNX1T1	NM_175636.1	9.22	8.51	1.64	3.38E-03
ILMN_22533	ZNF521	NM_015461.1	10.88	10.21	1.6	3.02E-03
ILMN_9887	EYA1	NM_172059.1	11.78	11.14	1.55	3.00E-02
ILMN_13272	AGTR1	NM_032049.1	11.67	11.04	1.55	2.24E-02
ILMN_9515	SNCAIP	NM_005460.2	9.05	8.47	1.49	9.12E-03
ILMN_424	FOXP2	NM_148898.1	11.17	10.61	1.48	2.13E-03
ILMN_14978	RSRC1	NM_016625.2	11.27	10.72	1.46	7.63E-03
ILMN_3096	ARHGEF16	NM_014448.2	8.68	8.14	1.45	4.51E-06
ILMN_15149	PRICKLE1	NM_153026.1	13.18	12.65	1.45	2.40E-02
ILMN_21875	SYT4	NM_020783.2	14.52	13.98	1.45	1.36E-03
ILMN_2941	TGIF	NM_170695.2	9.79	9.27	1.43	2.02E-02
ILMN_23270	SMARCA2	NM_139045.2	10.3	9.81	1.41	2.77E-04
ILMN_17043	SLIT1	NM_003061.1	8.76	8.27	1.41	1.03E-04
ILMN_25618	FOXP2	NM_148898.1	11.17	10.61	1.48	2.13E-03
ILMN_14250	ADAMTS9	NM_182920.1	12.88	12.43	1.37	9.95E-03
ILMN_28172	LRRN6A	NM_032808.5	9.69	9.24	1.36	2.40E-06
ILMN_29514	ADM	NM_001124.1	12.19	11.77	1.34	1.98E-02
ILMN_7344	ZCCHC12	NM_173798.2	10.94	10.52	1.33	3.36E-06
ILMN_27829	HIST1H2BH	NM_003524.2	9.14	8.73	1.33	1.85E-04
ILMN_29091	FRZB	NM_001463.2	10.42	10.02	1.32	1.05E-02
ILMN_24422	ZNF702	NM_024924.3	8.61	8.21	1.32	2.45E-02
ILMN_19002	DPYD	NM_000110.2	9.05	8.65	1.31	5.56E-05
ILMN_21827	PROM1	NM_006017.1	8.69	8.3	1.31	4.24E-02
ILMN_19345	ISLR2	NM_020851.1	12.18	11.8	1.31	2.77E-04
ILMN_28633	RDX	NM_002906.3	11.29	10.92	1.3	7.26E-04
ILMN_9683	BCAN	NM_021948.3	9.13	8.76	1.29	1.27E-03
ILMN_3827	EFNB2	NM_004093.2	12.53	12.16	1.29	4.87E-05
ILMN_1023	LRRRC8C	NM_032270.2	10.45	10.08	1.29	8.34E-05
ILMN_19382	MEIS1	NM_002398.2	10.68	10.32	1.28	3.68E-02
ILMN_2509	FSTL5	NM_020116.2	11.41	11.05	1.28	9.06E-03
ILMN_9513	TFAP2D	NM_172238.1	8.22	7.86	1.28	7.93E-03
ILMN_527	ABCB4	NM_000443.2	8.46	8.11	1.28	8.83E-03
ILMN_10482	MFHAS1	NM_004225.1	8.61	8.27	1.27	3.96E-03
ILMN_9309	IGFBP4	NM_001552.2	10.77	10.43	1.27	1.69E-02
ILMN_22596	PCAF	NM_003884.3	10.58	10.24	1.27	2.78E-02
ILMN_15063	C7	NM_000587.2	10.07	9.73	1.26	3.23E-04
ILMN_11325	CCNA1	NM_003914.2	9.48	9.15	1.26	2.87E-02
ILMN_30102	EXPH5	NM_015065.1	8.42	8.08	1.26	2.42E-02
ILMN_6526	RNF182	NM_152737.1	10.23	9.9	1.26	3.94E-03
ILMN_1591	TMTC2	NM_152588.1	8.75	8.42	1.26	9.50E-03
ILMN_988	MGST1	NM_020300.3	7.77	7.44	1.26	1.34E-07
ILMN_19900	ZNF608	NM_020747.1	8.14	7.8	1.26	6.26E-04
ILMN_15997	COL9A1	NM_001851.3	8.68	8.35	1.26	1.03E-03
ILMN_5233	MORC4	NM_024657.2	11.08	10.76	1.25	4.21E-03
ILMN_17743	POPDC2	NM_022135.2	10.14	9.83	1.25	3.10E-02
ILMN_8126	SYK	NM_003177.3	8.06	7.75	1.25	8.37E-05
ILMN_26338	HDAC9	NM_014707.1	9.04	8.72	1.25	8.00E-03
ILMN_4553	LRRRC4C	NM_020929.1	7.86	7.55	1.24	7.22E-05
ILMN_28348	SH3PXD2B	NM_001017995.1	10.14	9.84	1.24	2.72E-05
ILMN_22638	NPTX2	NM_002523.1	12.99	12.68	1.24	5.64E-05
ILMN_17013	TMEFF2	NM_016192.2	9.78	9.47	1.24	3.73E-02
ILMN_6340	FLJ35409	NM_001001688.1	9.63	9.33	1.23	8.28E-06
ILMN_24970	L3MBTL3	NM_001007102.1	8.39	8.09	1.23	9.22E-03

Konopka_Supplementary_Table_1 (continued)						
Downregulated						
ProbeName	GeneName	Accession	FOXP2	FOXP2chimp	Fold Change	pValue
ILMN_6395	PRPH	NM_006262.3	8	9.02	-2.04	1.31E-02
ILMN_1179	DCN	NM_133504.2	7.72	8.55	-1.78	3.43E-03
ILMN_9088	MAGEA10	NM_001011543.1	8.92	9.71	-1.73	4.88E-02
ILMN_6588	ACTA2	NM_001613.1	9.3	10.05	-1.69	1.39E-02
ILMN_8606	EDNRA	NM_001957.1	8.31	9	-1.62	1.12E-02
ILMN_4881	TMEM100	NM_018286.1	11.11	11.78	-1.58	1.00E-05
ILMN_5341	PCDH17	NM_014459.2	10.07	10.73	-1.58	1.02E-02
ILMN_25529	IGFBP3	NM_001013398.1	8.39	9.05	-1.58	1.03E-06
ILMN_1007	PPP2R2B	NM_181676.1	10.9	11.54	-1.56	7.45E-04
ILMN_9884	MAOB	NM_000898.3	8.18	8.8	-1.54	2.75E-03
ILMN_5889	IRF6	NM_006147.2	9	9.63	-1.54	1.14E-03
ILMN_2335	TAGLN	NM_003186.3	8.18	8.8	-1.53	2.90E-02
ILMN_28729	TUBA6	NM_032704.2	8.06	8.63	-1.48	1.02E-02
ILMN_25383	FLJ46082	NM_207417.1	8.54	9.06	-1.44	1.31E-02
ILMN_5518	H2BFS	NM_017445.1	12.15	12.65	-1.41	1.41E-02
ILMN_13579	FAM43B	NM_207334.1	8.19	8.68	-1.41	6.71E-03
ILMN_21212	FAM43A	NM_153690.4	9.88	10.37	-1.4	3.67E-06
ILMN_26722	ENPP2	NM_006209.2	7.69	8.17	-1.39	6.79E-03
ILMN_24238	LRRN6C	NM_152570.1	9.95	10.43	-1.39	8.87E-03
ILMN_21387	LRRN5	NM_006338.2	9.24	9.69	-1.36	7.12E-04
ILMN_13759	GPR30	NM_001031682.1	10.39	10.82	-1.34	3.07E-02
ILMN_5895	CDKN1A	NM_078467.1	10.64	11.05	-1.33	3.63E-02
ILMN_506	BTBD11	NM_152322.2	9.15	9.56	-1.32	4.47E-03
ILMN_13950	FLJ20366	NM_017786.2	9.75	10.14	-1.31	2.98E-02
ILMN_28293	HIST2H2BE	NM_003528.2	10.83	11.21	-1.3	3.93E-05
ILMN_3162	TIMP1	NM_003254.2	11.45	11.82	-1.3	3.85E-03
ILMN_15041	ENC1	NM_003633.1	10.36	10.73	-1.3	7.66E-05
ILMN_22606	GLRX	NM_002064.1	10.19	10.56	-1.29	6.48E-05
ILMN_11202	AMT	NM_000481.2	11.75	12.11	-1.28	4.04E-02
ILMN_138534	ELMO1	NM_130442.1	8.94	9.3	-1.28	9.38E-03
ILMN_8275	MGC33846	NM_175885.3	10.3	10.65	-1.28	4.01E-02
ILMN_23792	C6orf117	NM_138409.1	10.93	11.28	-1.28	2.94E-05
ILMN_13364	ACTG2	NM_001615.3	7.2	7.55	-1.28	1.96E-02
ILMN_26493	HIST1H2AC	NM_003512.3	9.7	10.05	-1.27	4.50E-02
ILMN_27702	C8orf13	NM_053279.1	13.48	13.83	-1.27	1.43E-03
ILMN_22375	DSCR8	NM_032589.2	7.54	7.88	-1.27	2.34E-02
ILMN_11170	PHACTR2	NM_014721.1	9.92	10.26	-1.27	2.53E-04
ILMN_4152	MAB21L2	NM_006439.3	7.43	7.77	-1.27	9.13E-04
ILMN_3534	ACCN2	NM_020039.2	9.75	10.1	-1.27	9.91E-07
ILMN_20169	FLJ11286	NM_018381.1	8.22	8.56	-1.27	3.70E-02
ILMN_22301	PTRF	NM_012232.2	7.59	7.93	-1.27	1.24E-02
ILMN_23268	CHRNA3	NM_000743.2	12.07	12.4	-1.26	1.93E-02
ILMN_9913	ZNF556	NM_024967.1	9.05	9.38	-1.26	1.60E-05
ILMN_29202	HTR2B	NM_000867.2	7.48	7.81	-1.25	2.87E-05
ILMN_1394	MAN1A1	NM_005907.2	7.55	7.87	-1.25	5.88E-04
ILMN_6786	GJA12	NM_020435.2	9.63	9.95	-1.25	9.39E-06
ILMN_22069	HIST2H4	NM_003548.2	11	11.32	-1.24	1.52E-02
ILMN_138549	B3GNT1	NM_006577.3	9	9.31	-1.24	2.42E-02
ILMN_28123	IFIT2	NM_001547.3	7.73	8.03	-1.24	1.62E-04
ILMN_16651	ENO3	NM_001976.2	11.61	11.91	-1.24	3.87E-02
ILMN_26733	HIST2H2AA	NM_003516.2	10.04	10.35	-1.24	8.15E-03
ILMN_23954	MSRB3	NM_198080.2	7.38	7.69	-1.24	4.11E-02
ILMN_16171	FGF14	NM_175929.1	9.64	9.94	-1.23	2.82E-03
ILMN_14234	C6orf48	NM_016947.1	10.55	10.86	-1.23	7.51E-05
ILMN_2192	CACNB2	NM_201572.1	7.08	7.38	-1.23	8.35E-04

Konopka_Supplementary_Table_2				
Genes regulated by both FOXP2 and FOXP2chimp				
Upregulated				
GeneName	Human vs Cntl Fold Change	Pvalue	Chimp vs Cntl Fold Change	Pvalue
ALDH1A3	1.34	2.56E-03	1.27	1.09E-02
BOC	1.23	3.28E-03	1.37	6.12E-05
C20orf102	1.27	2.30E-04	1.25	7.70E-04
C20orf103	1.27	1.55E-05	1.51	9.93E-10
CD3Z	1.25	7.11E-06	1.26	4.72E-06
CGNL1	1.85	3.59E-15	1.75	6.74E-14
CRABP2	1.72	1.90E-04	2.1	2.85E-06
DPYSL3	1.51	2.23E-06	1.24	4.39E-03
FRAS1	1.32	8.20E-04	1.51	7.46E-06
FRMD3	1.37	5.60E-05	1.49	1.23E-06
GNG8	1.47	8.70E-04	1.69	2.30E-05
IGSF21	1.33	3.95E-05	1.47	7.65E-07
ITGB5	1.53	7.40E-04	1.73	3.37E-05
JSRP1	1.25	9.30E-04	1.45	8.53E-07
KIAA1161	1.33	2.20E-04	1.4	2.82E-05
LBH	1.27	1.14E-03	1.32	1.90E-04
NEUROG2	1.65	2.85E-03	2.01	9.88E-05
NPPA	1.39	1.77E-06	1.44	4.31E-07
PI15	1.25	5.85E-05	1.43	3.58E-08
PTPRM	1.24	9.76E-05	1.28	1.27E-05
RAFTLIN	1.39	1.25E-10	1.64	1.31E-14
RAMP1	1.28	2.09E-05	1.51	6.26E-09
RET	1.35	8.05E-05	1.57	2.21E-07
RUNX3	1.28	9.53E-03	1.26	1.50E-02
SERPINE2	1.35	2.56E-03	1.35	3.38E-03
SIX5	1.32	3.73E-08	1.34	2.39E-08
SLC6A2	1.23	2.00E-04	1.24	1.60E-04
SPOCK	1.64	4.73E-08	1.4	1.81E-05
STC2	1.34	4.65E-11	1.64	3.25E-16
STX3A	1.27	4.93E-08	1.35	1.07E-09
TNS3	1.58	3.40E-05	1.61	1.76E-05
VIM	1.44	8.27E-06	1.75	1.03E-08
Downregulated				
GeneName	Human vs Cntl Fold Change	Pvalue	Chimp vs Cntl Fold Change	Pvalue
CBLN4	-1.77	1.61E-12	-1.95	4.30E-14
CDH11	-1.38	7.76E-05	-1.62	1.38E-07
CDH12	-1.27	1.42E-03	-1.27	1.32E-03
CHD5	-1.37	4.51E-08	-1.43	5.27E-09
DACH1	-1.39	1.48E-07	-1.35	5.71E-07
DYNLT3	-1.41	4.19E-06	-1.54	1.95E-07
EGR1	-1.27	1.43E-06	-1.35	2.24E-08
IL7	-1.25	8.44E-05	-1.32	6.35E-06
KCNT1	-1.45	1.80E-04	-1.62	6.87E-06
KIAA0125	-1.64	4.21E-12	-1.93	4.49E-15
LMO4	-1.38	1.39E-10	-1.31	1.07E-08
MYD88	-1.26	3.20E-04	-1.3	4.77E-05
MYOZ3	-1.57	1.44E-03	-1.55	1.89E-03
NNAT	-3.76	1.60E-04	-3.78	1.40E-04
OKL38	-1.27	1.98E-03	-1.28	1.70E-03
PMCH	-1.47	6.48E-03	-1.32	4.53E-02
PNMA3	-1.43	2.01E-03	-1.51	6.40E-04
PPP2R2C	-1.25	1.72E-02	-1.51	7.76E-05
PRKCA	-1.33	8.14E-03	-1.32	9.84E-03
SCGN	-1.24	4.33E-03	-1.27	1.38E-03
SIX6	-1.48	4.43E-07	-1.36	3.37E-05
ST8SIA1	-1.39	2.22E-06	-1.44	5.08E-07
TMEM54	-1.3	2.01E-06	-1.32	1.38E-06
VIP	-3.12	8.92E-09	-2.93	4.60E-08
VSNL1	-1.36	1.10E-05	-1.42	9.53E-07
Table of genes significantly changed with human FOXP2 compared to control cells (Cntl) and FOXP2chimp (Chimp) compared to control cells, but not more than log 0.3 fold change between FOXP2 and FOXP2chimp. Genes had to be changed in any combination of two out of three independent cell lines.				

Konopka_Supplementary_Table_3					
Directional changes of differentially expressed genes					
Human more upregulated			Opposite Directions		
	Human vs Cntl	Chimp vs Cntl		Human vs Cntl	Chimp vs Cntl
FOXP2	13.83	9.38	ABCB4	1.21	-1.06
PROM1	1.5	1.15	TFAP2D	1.17	-1.09
			EXPH5	1.16	-1.09
			POPODC2	1.16	-1.08
Chimp more upregulated			RUNX1T1	1.16	-1.41
	Human vs Cntl	Chimp vs Cntl	ADAMTS9	1.15	-1.19
PRPH	1.08	2.20	FRZB	1.15	-1.15
EDNRA	1.19	1.93	LRR8C8	1.15	-1.13
IGFBP3	1.17	1.85	HEBP2	1.14	-1.47
C6orf117	1.33	1.71	IGFBP4	1.14	-1.11
PPP2R2B	1.06	1.65	ZNF608	1.14	-1.10
BTBD11	1.16	1.55	EPAS1	1.14	-1.49
FLJ46082	1.04	1.49	FSTL5	1.13	-1.13
CDKN1A	1.12	1.48	LRRN6A	1.13	-1.20
FAM43A	1.02	1.43	PDGFRA	1.13	-1.64
FAM43B	1.01	1.42	SYK	1.13	-1.10
ENPP2	1.01	1.41	TMEFF2	1.12	-1.11
PHACTR2	1.08	1.38	EYA1	1.11	-1.40
GLRX	1.02	1.31	ZNF521	1.11	-1.43
AMT	1.01	1.28	MORC4	1.09	-1.15
CHRNA3	1.01	1.27	SLIT1	1.09	-1.28
FLJ11286	1.01	1.27	SH3PXD2B	1.08	-1.15
HTR2B	1.01	1.27	TGIF	1.07	-1.34
ZNF556	1.01	1.27	SYT4	1.07	-1.36
ENO3	1.02	1.27	COL9A1	1.06	-1.18
TIMP1	1.02	1.27	L3MBTL3	1.06	-1.16
			MFHAS1	1.06	-1.20
			NPTX2	1.06	-1.17
Human more downregulated			RDX	1.06	-1.22
	Human vs Cntl	Chimp vs Cntl	TMTC2	1.06	-1.19
MAGEA10	-1.88	-1.09	SMARCA2	1.06	-1.33
			C7	1.05	-1.20
			MEIS1	1.05	-1.22
			ROR2	1.05	-1.57
Chimp more downregulated			FLJ20366	1.04	1.27
	Human vs Cntl	Chimp vs Cntl	PRNP	1.04	-1.67
GRM8	-1.12	-2.08	RSRC1	1.04	-1.41
CDCA7L	-1.06	-1.89	ZCCHC12	1.04	-1.29
ARHGGEF16	-1.05	-1.53	HDAC9	1.02	-1.21
DPYD	-1.09	-1.43	LRR4C4	1.02	-1.22
FOXP4	-1.01	-1.41	AGTR1	1.02	-1.52
HIST1H2BH	-1.06	-1.40	CCNA1	1.02	-1.28
ISLR2	-1.04	-1.35	MGST1	1.01	-1.24
ADM	-1.01	-1.35	PRICKLE1	1.01	-1.44
PCAF	-1.06	-1.34	SLC30A3	1.01	-1.73
RNF182	-1.06	-1.34	SNCAIP	1.01	-1.48
BCAN	0	-1.29	ZNF702	1.01	-1.30
EFNB2	0	-1.29	B3GNT1	-1.02	1.22
FLJ35409	-1.03	-1.27	ACCN2	-1.03	1.23
			ELMO1	-1.03	1.25
			FGF14	-1.04	1.20
			MGC33846	-1.04	1.23
			C6orf48	-1.05	1.17
			GJA12	-1.05	1.20
			LRRN5	-1.05	1.30
			MAN1A1	-1.06	1.17
			CACNB2	-1.07	1.15
			IFIT2	-1.07	1.16
			MAB21L2	-1.07	1.19
			MSRB3	-1.08	1.14
			LRRN6C	-1.08	1.29
			TUBA6	-1.08	1.37
			GPR30	-1.11	1.21
			HIST2H2BE	-1.11	1.17
			ACTA2	-1.11	1.52
			DCN	-1.12	1.59
			HIST2H4	-1.13	1.10
			PCDH17	-1.13	1.39
			C8orf13	-1.14	1.10
			ENC1	-1.16	1.12
			HIST1H2AC	-1.16	1.10
			PTRF	-1.16	1.09
			TMEM100	-1.16	1.37
			HIST2H2AA	-1.17	1.06
			H2BFS	-1.20	1.18
			ACTG2	-1.21	1.21
			DSCR8	-1.21	1.04
			MAOB	-1.21	1.27
			TAGLN	-1.29	1.18
			IRF6	-1.34	1.16

Fold changes in gene expression in cells expressing human FOXP2 compared to control cells (Cntl) versus in cells expressing FOXP2chimp (Chimp) compared to control cells.

Konopka_Supplementary_Table_4
Potential FOXP2 binding sites in promoters of differentially expressed genes.

GeneName	AATTTG	CAAATT	[G/A][T/C][A/C]AA[C/T]A	T[A/G]TT[T/G][A/G][T/C]	A[C/T]AAATA	TATTT[A/G]T	ACAAAT	ATTTGT	AATTTGT	ACAAATT	ATTT	AAAT
ABCB4	1	0	3	4	1	2	2	2	0	0	16	14
ACCN2	0	1	0	1	0	0	0	0	0	0	2	1
ACTA2	0	2	4	2	0	1	1	1	0	1	8	10
ACTG2	0	0	3	1	0	0	1	0	0	0	7	5
ADAMTS9	0	0	0	0	0	0	0	0	0	0	1	3
ADM	0	0	0	0	0	0	0	0	0	0	5	9
AGTR1	1	0	3	3	0	2	1	1	0	0	12	10
AMT	0	0	2	2	1	1	0	1	0	0	3	2
ARHGEF16	0	0	1	1	0	0	0	0	0	0	1	2
B3GNT1	2	1	3	2	1	1	0	2	0	0	11	14
BCAN	0	0	1	1	1	0	1	1	0	0	7	3
BTBD11	0	1	0	0	0	0	1	0	0	0	5	8
C6orf117	0	0	0	3	0	1	0	1	0	0	7	5
C6orf48	0	1	2	4	1	0	0	2	0	0	14	10
C7	0	0	0	1	0	0	0	0	0	0	9	14
C8orf13	0	0	0	1	0	0	0	0	0	0	5	2
CACNB2	1	2	1	5	0	1	1	1	0	1	22	9
CCNA1	0	0	0	1	0	0	0	0	0	0	6	5
CDCA7L	0	2	4	4	1	2	0	2	0	0	13	12
CDKN1A	0	0	2	1	0	1	0	1	0	0	14	8
CHRNA3	1	0	2	1	1	0	0	1	1	0	5	11
COL9A1	1	0	3	2	1	0	1	0	0	0	13	9
DCN	1	1	4	3	1	0	2	2	0	1	18	19
DPYD	2	2	1	3	0	2	1	1	0	1	18	14
DSCR8	0	0	4	2	0	1	0	1	0	0	4	8
EDNRA	1	0	0	0	0	0	0	2	1	0	5	4
EFNB2	0	0	0	0	0	0	0	0	0	0	0	0
ELMO1	2	1	5	6	1	1	3	2	1	0	16	12
ENC1	0	0	1	1	0	0	0	0	0	0	5	8
ENO3	0	0	0	1	0	0	0	0	0	0	1	1
ENPP2	0	1	1	0	1	0	1	1	0	0	13	12
EPAS1	0	1	1	3	0	2	1	0	0	1	13	10
EXPH5	0	0	5	5	0	0	0	1	0	0	7	15
EYA1	1	1	4	3	1	0	1	1	0	0	16	15
FAM43A	1	0	0	2	0	1	0	1	0	0	7	8
FAM43B	0	0	1	1	1	0	1	0	0	0	3	5
FGF14	1	0	1	2	1	0	1	1	0	0	15	8
FLJ11286	1	0	3	2	0	2	0	0	0	0	8	6
FLJ20366	2	1	3	4	1	0	3	1	1	1	13	12
FLJ35409	0	0	0	0	0	0	0	0	0	0	6	3
FLJ46082	1	0	0	1	0	0	1	0	0	0	6	4
FOXP4	0	0	1	1	1	0	1	0	0	0	4	3
FOXP2	2	1	5	5	0	2	1	3	2	1	20	19
FRZB	0	0	1	0	1	0	0	0	0	0	2	3
FSTL5	0	0	2	1	2	0	1	1	0	0	8	10
GJA12	0	0	0	0	0	0	0	0	0	0	0	3
GLRX	2	0	3	2	0	0	0	1	0	0	10	8
GPR30	1	1	2	0	1	0	2	1	1	1	9	13
GRM8	1	0	2	3	1	1	1	2	0	0	13	15
H2BFS	0	2	1	1	0	0	0	0	0	0	8	7
HDAC9	1	2	3	2	1	2	1	2	1	0	16	17
HEBP2	2	0	2	11	0	11	0	0	0	0	16	10
HIST1H2AC	1	0	0	3	0	0	0	0	0	0	9	8
HIST1H2BH	1	0	2	3	1	1	0	0	0	0	18	11
HIST2H2AA	1	1	0	1	0	0	0	0	0	0	3	3
HIST2H2BE	1	0	0	3	0	0	0	0	0	0	3	5
HIST2H4	0	0	1	0	0	0	1	0	0	0	7	8
HTR2B	1	2	1	0	0	0	2	0	0	1	13	21
IFIT2	0	0	1	1	0	0	0	0	0	0	10	9
IGFBP3	0	0	1	4	0	3	0	1	0	0	11	7

Konopka_Supplementary_Table_4 (continued)												
Potential FOXP2 binding sites in promoters of differentially expressed genes.												
IGFBP4	0	0	2	0	1	0	1	0	0	0	2	5
IRF6	0	0	3	2	1	2	1	2	0	0	6	3
ISLR2	0	1	0	1	0	0	0	0	0	0	3	5
L3MBTL3	1	0	2	4	0	1	0	2	0	0	7	6
LRRC4C	0	0	0	3	0	3	0	0	0	0	14	0
LRRC8C	0	0	3	0	1	0	0	0	0	0	9	11
LRRN5	0	1	1	2	0	0	1	1	0	1	4	6
LRRN6A	0	0	1	0	0	0	0	0	0	0	0	1
LRRN6C	1	1	0	2	0	1	1	2	0	1	24	10
MAB21L2	0	0	0	1	0	0	1	0	0	0	14	10
MAGEA10	0	0	1	0	0	0	0	0	0	0	3	5
MAN1A1	1	0	0	1	0	1	0	1	0	0	5	4
MAOB	1	0	0	2	0	0	0	1	0	0	6	4
MEIS1	2	2	2	3	0	2	1	1	1	1	15	16
MFHAS1	0	0	1	1	0	0	0	0	0	0	6	9
MGC33846	0	0	1	0	0	0	0	0	0	0	2	6
MGST1	1	2	1	0	1	0	0	0	0	0	10	12
MORC4	0	0	3	2	0	2	0	1	0	0	10	6
MSRB3	0	0	0	1	0	0	0	0	0	0	8	2
NPTX2	1	1	0	0	0	0	1	0	0	1	1	1
PCAF	0	0	1	1	0	1	1	0	0	0	6	7
PCDH17	0	0	0	2	0	0	0	0	0	0	5	6
PDGFRA	0	0	1	1	0	0	0	0	0	0	6	6
PHACTR2	1	2	2	4	1	3	1	3	0	1	23	16
POPOC2	2	1	1	3	1	1	1	1	0	0	7	8
PPP2R2B	2	1	1	3	0	1	1	1	1	1	13	13
PRICKLE1	1	1	1	4	1	1	2	2	1	1	11	9
PRNP	2	0	4	2	1	1	0	1	0	0	19	15
PROM1	0	1	2	0	0	0	0	1	0	0	5	6
PRPH	0	0	1	0	0	0	0	0	0	0	1	2
PTRF	0	0	2	0	0	0	0	0	0	0	4	11
RDX	1	0	1	1	0	0	0	0	0	0	6	8
RNF182	1	0	2	4	1	0	0	2	1	0	11	8
ROR2	1	1	1	1	1	0	1	2	0	0	7	4
RSRC1	2	0	4	4	0	1	0	1	0	0	15	16
RUNX1T1	2	1	4	5	2	2	1	2	0	1	19	17
SH3PXD2B	0	0	1	0	0	0	0	2	0	0	2	4
SLC30A3	1	0	1	1	0	0	0	1	0	0	6	3
SLIT1	0	0	1	0	1	0	1	0	0	0	3	4
SMARCA2	3	1	2	5	1	1	1	2	2	0	21	20
SNCAIP	0	1	1	3	0	1	1	1	0	1	13	11
SYK	1	0	1	1	0	0	0	0	0	0	7	6
SYT4	2	0	0	2	0	0	0	2	1	0	14	10
TAGLN	0	0	0	1	0	0	0	0	0	0	0	3
TFAP2D	0	1	2	3	0	2	0	0	0	0	11	10
TGIF	1	1	3	2	1	0	1	1	1	0	9	9
TIMP1	2	0	1	3	0	1	2	2	1	0	9	6
TMEFF2	0	0	1	0	0	0	1	0	0	0	1	2
TMEM100	2	1	4	1	1	0	1	1	0	0	6	13
TMTC2	0	0	1	0	0	0	0	0	0	0	1	2
TUBA6	0	0	0	0	0	0	0	0	0	0	1	1
ZCCHC12	0	1	0	2	0	0	0	0	0	0	5	6
ZNF521	1	1	3	5	1	0	1	0	0	1	11	7
ZNF556	0	0	0	1	0	0	0	0	0	0	3	1
ZNF608	1	0	0	2	0	0	0	1	1	0	11	10
ZNF702	0	1	4	6	4	2	2	1	0	0	17	9

Promoters were defined as 1000bp upstream of the transcriptional start site of all isoforms of a given gene in Ensemble. Binding sites were derived from the following sources:
AATTTG or CAAATT, complete FOXP2 binding site based on crystal structure of DNA binding domain (Stroud et al., Structure, 2006)
[G/A]T[C]/[A/C]A[A/C]T]A or T[A/G]T[T]/G][A/G][T/C], forkhead binding domain (Pierrou et al., EMBO, 1994; Overdier et al., MCB, 1994)
A[C/T]AAATA or TATTT[A/G]T, FOXP1 or FOXP2 consensus sequence (Wang et al., 2003)
ACAAAT, ATTTGT, AATTTGT, ACAAAT, ATTT, AAAT, variations on the FOXP2 binding sequence from (Stroud et al., Structure, 2006),
with the shortest sequences denoted as "core" sequences

Konopka_Supplementary_Table_5				
Gene ontology of differentially expressed genes				
Category	Term	Count	%	PValue
Upregulated				
GOTERM_BP_ALL	GO:0032501-multicellular organismal process	25	42.37%	5.07E-05
GOTERM_BP_ALL	GO:0050789-regulation of biological process	26	44.07%	4.87E-04
INTERPRO	IPR003591:Leucine-rich repeat, typical subtype	5	8.47%	7.57E-04
GOTERM_BP_ALL	GO:0065007-biological regulation	27	45.76%	8.84E-04
INTERPRO	IPR013098:Immunoglobulin I-set	5	8.47%	8.91E-04
GOTERM_BP_ALL	GO:0007275-multicellular organismal development	17	28.81%	1.30E-03
GOTERM_BP_ALL	GO:0048856-anatomical structure development	16	27.12%	1.70E-03
GOTERM_BP_ALL	GO:0048513-organ development	12	20.34%	1.80E-03
SMART	SM00369:LRR_TYP	5	8.47%	1.84E-03
GOTERM_BP_ALL	GO:0009653-anatomical structure morphogenesis	11	18.64%	2.25E-03
GOTERM_BP_ALL	GO:0048731-system development	14	23.73%	2.41E-03
GOTERM_BP_ALL	GO:0032502-developmental process	20	33.90%	2.47E-03
GOTERM_BP_ALL	GO:0050794-regulation of cellular process	23	38.98%	3.09E-03
UP_SEQ_FEATURE	disulfide bond	16	27.12%	5.06E-03
GOTERM_BP_ALL	GO:0009887-organ morphogenesis	6	10.17%	9.95E-03
INTERPRO	IPR001611:Leucine-rich repeat	5	8.47%	1.01E-02
SP_PIR_KEYWORDS	leucine-rich repeat	5	8.47%	1.03E-02
UP_SEQ_FEATURE	signal peptide	16	27.12%	1.04E-02
SP_PIR_KEYWORDS	chromosomal rearrangement	5	8.47%	1.05E-02
INTERPRO	IPR007110:Immunoglobulin-like	6	10.17%	1.23E-02
GOTERM_BP_ALL	GO:0045055-regulated secretory pathway	3	5.08%	1.25E-02
COG_ONTOLOGY	Function unknown	4	6.78%	1.31E-02
GOTERM_BP_ALL	GO:0019222-regulation of metabolic process	16	27.12%	1.56E-02
SP_PIR_KEYWORDS	tyrosine-specific protein kinase	3	5.08%	1.59E-02
INTERPRO	IPR013783:Immunoglobulin-like fold	6	10.17%	1.74E-02
SP_PIR_KEYWORDS	activator	6	10.17%	1.79E-02
GOTERM_BP_ALL	GO:0007267-cell-cell signaling	7	11.86%	1.82E-02
SP_PIR_KEYWORDS	Transcription	13	22.03%	1.84E-02
UP_SEQ_FEATURE	domain:EGF-like	3	5.08%	1.86E-02
SP_PIR_KEYWORDS	Developmental protein	7	11.86%	2.25E-02
SP_PIR_KEYWORDS	Secreted	11	18.64%	2.37E-02
GOTERM_BP_ALL	GO:0031323-regulation of cellular metabolic process	15	25.42%	2.60E-02
GOTERM_BP_ALL	GO:0003001-generation of a signal involved in cell-cell signaling	3	5.08%	2.62E-02
SP_PIR_KEYWORDS	disease mutation	11	18.64%	2.63E-02
INTERPRO	IPR003598:Immunoglobulin subtype 2	4	6.78%	2.85E-02
GOTERM_BP_ALL	GO:0046903-secretion	5	8.47%	2.87E-02
GOTERM_CC_ALL	GO:0005667-transcription factor complex	4	6.78%	2.91E-02
SP_PIR_KEYWORDS	signal	17	28.81%	3.04E-02
GOTERM_BP_ALL	GO:0019219-regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	14	23.73%	3.04E-02
GOTERM_MF_ALL	GO:0005488-binding	45	76.27%	3.14E-02
INTERPRO	IPR000483:Cysteine-rich flanking region, C-terminal	3	5.08%	3.18E-02
INTERPRO	IPR000372:Leucine-rich repeat, cysteine-rich flanking region, N-terminal	3	5.08%	3.66E-02
SP_PIR_KEYWORDS	Transcription regulation	12	20.34%	3.69E-02
SP_PIR_KEYWORDS	egf-like domain	4	6.78%	3.74E-02
GOTERM_BP_ALL	GO:0010468-regulation of gene expression	14	23.73%	4.06E-02
GOTERM_BP_ALL	GO:0006139-nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	18	30.51%	4.27E-02
SP_PIR_KEYWORDS	ubl conjugation	5	8.47%	4.29E-02
UP_SEQ_FEATURE	glycosylation site:N-linked (GlcNAc...)	17	28.81%	4.32E-02
INTERPRO	IPR008266:Tyrosine protein kinase, active site	3	5.08%	4.33E-02
Dowregulated				
Category	Term	Count	%	PValue
SP_PIR_KEYWORDS	acetylation	8	17.78%	3.61E-04
GOTERM_MF_ALL	GO:0019888-protein phosphatase regulator activity	3	6.67%	4.51E-03
GOTERM_MF_ALL	GO:0019208-phosphatase regulator activity	3	6.67%	4.91E-03
GOTERM_BP_ALL	GO:0048856-anatomical structure development	11	24.44%	1.28E-02
GOTERM_BP_ALL	GO:0048731-system development	9	20.00%	3.20E-02
GOTERM_BP_ALL	GO:0032502-developmental process	13	28.89%	3.23E-02
GOTERM_BP_ALL	GO:0001558-regulation of cell growth	3	6.67%	4.33E-02
GOTERM_BP_ALL	GO:0048468-cell development	7	15.56%	4.98E-02

Konopka_Supplementary_Table_6						
Luciferase promoter information.						
Gene Symbol	Chromosome	Strand	Start	End	Number of canonical FOXP2 sites (AATTG or CAAAT)	Number of Forkhead Sites ([A/G][C/T][A/C]AA[C/T]A or T[G/A]T[T/G][G/A][T/C])
ACTA2	10	-	90702408	90703345	2	2
CDCA7L	7	-	21758652	21759743	2	4
GRM8	7	-	126486678	126487590	0	2
IGFBP3	7	-	45733923	45734957	0	2
PPP2R2B	5	-	146067396	146068457	1	1
ROR2	9	-	91791863	91792803	2	2
SLC30A3	2	-	27397409	27398508	0	1
TAGLN	11	+	116574429	116575369	0	1

Coordinates are from UCSC May 2004 assembly.

Konopka Supplementary Table 7
Connectivity values for all genes in WGCNA modules.

Fig 3 Network		Fig 3 Network	
	Kme		Kme
SYT4	0.9116	DOC2B	0.5457
GRM7	0.8918	BC37295_3	0.5316
ZCCHC12	0.8862	IER3IP1	0.5281
C7	0.8854	WNT3	0.5261
RBPM52	0.8791	FLJ90231	0.5203
ADAMTS9	0.8783	GYPE	0.5058
ROR2	0.8774	CRYBB1	0.4869
ADM	0.8746	RUNX1T1	0.3812
TRIM36	0.8713	UBE2H	-0.5045
ELF4	0.8582	AHNAK	-0.5421
ISLR2	0.8562	CDH18	-0.5479
C3orf32	0.8528	CAPS	-0.5486
PDGFRA	0.8526	KIAA1862	-0.5565
RDX	0.8330	TNFRSF14	-0.5586
AMOT	0.8302	NRTN	-0.5631
EFNB2	0.8276	EMB	-0.5643
MGST1	0.8249	NTS	-0.5707
RUNX1T1	0.8231	IFITM2	-0.5715
ZNF702	0.8223	ISG20	-0.5950
FRZB	0.8135	BID	-0.6051
CXCR4	0.8124	GLS	-0.6200
ZNF521	0.8112	PCDH44	-0.6215
SMAD3	0.8095	TACC2	-0.6258
PIWIL1	0.8090	HOXD13	-0.6292
FLJ35409	0.8067	C9orf103	-0.6308
NDN	0.8041	ARHGEP7	-0.6354
ASB9	0.8008	FLJ45909	-0.6400
CWF19L2	0.8005	HCST	-0.6471
METRNL	0.8001	C6orf117	-0.6478
C9orf58	0.7937	CSEN	-0.6489
LRRTM4	0.7918	OVCA2	-0.6575
RAB32	0.7879	C9orf4	-0.6580
ZNF537	0.7832	SDSL	-0.6584
CPNE2	0.7830	MATR3	-0.6612
TCEAL2	0.7817	NME3	-0.6614
SLC25A24	0.7812	GLRX2	-0.6652
ALKBH8	0.7789	GBG1	-0.6688
SPSB4	0.7727	SYT1	-0.6716
LOX	0.7710	SALL4	-0.6773
PCAF	0.7702	PNCK	-0.6790
SNCAIP	0.7585	MAGEA3	-0.6793
IGFBP4	0.7554	PLAGL1	-0.6814
RFC3	0.7527	FNDC5	-0.6840
RASL11B	0.7457	SGK	-0.6868
NELL1	0.7439	C1orf85	-0.6893
ACSL3	0.7404	GCH1	-0.6898
RAI2	0.7401	DDIT4	-0.6899
S100A6	0.7361	C9orf111	-0.6932
LIG1	0.7326	ABCC3	-0.6955
FLJ36748	0.7308	HTR2B	-0.7112
MTA3	0.7205	FLRT3	-0.7191
LRRC8C	0.7177	STEAP3	-0.7219
CDC47L	0.7160	GRIA3	-0.7264
HEBP2	0.7156	HIST2H2AA	-0.7268
TMPO	0.7042	GYG2	-0.7298
NCAM1	0.7035	BSCL2	-0.7329
POPCD2	0.6994	LOC352909	-0.7343
XK	0.6936	RAB31	-0.7411
TFAP2D	0.6919	HIST1H4H	-0.7479
FSTL1	0.6881	PQBP1	-0.7490
ICK	0.6849	BCE	-0.7499
FLJ14001	0.6830	CPB1	-0.7567
PITPNM1	0.6816	MAGEA6	-0.7606
SYK	0.6803	ATP6V1G2	-0.7637
LRRK1	0.6779	AXUD1	-0.7654
MRC2	0.6745	ENO3	-0.7689
L3MBTL3	0.6715	FLJ11286	-0.7855
STMN4	0.6615	MGC33846	-0.7867
RTN4R	0.6596	HIST1H2AE	-0.7911
KCNQ2	0.6586	EGFR	-0.7913
PFTK1	0.6556	ACTA2	-0.7979
PTPRR	0.6535	GARNL3	-0.7998
CNTNAP5	0.6489	RGS16	-0.8000
GYPE	0.6423	SYNPR	-0.8012
TMEFF2	0.6370	GABRA3	-0.8025
PPIL6	0.6340	PVRL2	-0.8092
HDAC9	0.6333	MAOB	-0.8160
FBXO27	0.6333	GPR30	-0.8165
DECR1	0.6304	PPP2R2B	-0.8169
HSD17B1	0.6274	TIMP1	-0.8172
WDR62	0.6270	ZNF488	-0.8203
MSN	0.6162	FLJ46082	-0.8265
BCL6B	0.6160	C1orf53	-0.8307
NGB	0.6148	WDR22	-0.8379
PRTFDC1	0.6108	HIST2H2BE	-0.8435
HR	0.6105	GLRX	-0.8467
CCDC71	0.6041	LRRN6C	-0.8573
SCRG1	0.6037	CHRNA3	-0.8612
RBL1	0.6017	DLX5	-0.8793
EMID1	0.5963	AMT	-0.8857
SH3PXD2B	0.5842	ZNF556	-0.9025
C10orf39	0.5730	PRPH	-0.9152
ECT2	0.5716	FAM43A	-0.9410
TMTC2	0.5683	EBF3	-0.9436
KIAA1522	0.5560		

Supp Fig 6a Network		Supp Fig 6b Network	
	Kme		Kme
SLC30A3	0.9373	TNS3	0.9266
EPAS1	0.9293	FRMD3	0.8635
ARHGEP16	0.8778	SLC2A1	0.8525
XKRX	0.8770	BTBD11	0.8487
BCAN	0.8703	SPOCK2	0.8399
PCOLCE2	0.8670	CGNL1	0.8329
PRICKLE1	0.8549	IGFBP5	0.8196
EYA1	0.8529	STX3A	0.7941
GAL	0.8523	ITGB5	0.7778
SLIT1	0.8458	KIAA0644	0.7771
SMARCA2	0.8429	HOXD10	0.7734
KIAA1712	0.8348	ADARB1	0.7693
NGFRAP1L1	0.8280	FOXP2	0.7605
TLE3	0.8254	KIAA1161	0.7523
TEAD2	0.8246	FLJ33790	0.7491
FBXL7	0.8239	PMP22	0.7481
SPAG6	0.8144	FBLN2	0.7442
CHRM3	0.8118	NPPA	0.7364
CCNA1	0.8071	PI15	0.7282
BAIAP2L1	0.8017	HOXD1	0.7274
KCN51	0.8014	STC2	0.7224
RNF182	0.8008	LBH	0.7191
FGFR3	0.7980	TNFRSF19	0.6831
FLJ37440	0.7930	CDK6	0.6493
HERC5	0.7883	KCNG1	0.6483
FLJ20130	0.7834	ABHD1	0.6435
COL18A1	0.7720	GFRA2	0.6319
PDE5A	0.7718	LHX8	0.6251
PPP2R2C	0.7713	KIAA1370	0.6234
LBX2	0.7694	UNQ830	0.6066
LOC285498	0.7672	CYP2J2	0.6053
NEK1	0.7607	SAMD4A	0.5926
C12orf34	0.7557	KITLG	0.5811
SULF2	0.7541	ART5	0.5746
SREBF1	0.7536	ACOT11	0.5710
ACACB	0.7438	ZNF423	0.5702
FOXN4	0.7427	BHMT2	0.5577
PFKL	0.7424	FLJ22386	0.5564
SLITRK5	0.7399	NCOA7	0.5501
KCNQ2	0.7318	DLL1	0.4844
ZNF447	0.7258	KIAA1914	0.3594
GPR161	0.7227	CALCOCCO1	0.3169
C20orf160	0.7192	RKHD2	-0.3335
EPS8L1	0.7047	PRRG1	-0.5086
SRR	0.7012	SKP2	-0.5095
MEIS1	0.7003	MT1F	-0.5165
COL9A1	0.6981	TOP1	-0.5477
ADAMTS19	0.6977	OKL38	-0.5990
DOCK6	0.6960	MANEAL	-0.6491
RAB36	0.6918	PNMA6A	-0.6575
JAG1	0.6913	GLRA2	-0.6642
NRM	0.6869	LMO4	-0.6986
KCNH8	0.6849	PAPSS2	-0.7154
ARHGAP22	0.6789	PANX2	-0.7284
SCARA3	0.6730	TBX3	-0.7451
OAF	0.6723	CBLN4	-0.7578
HSPCO47	0.6684	ST8SIA1	-0.8041
PRG2	0.6670	PNMA3	-0.8276
YPEL1	0.6648	SIX6	-0.8667
ITGB3BP	0.6475	NNAT	-0.9038
DNAJC5G	0.6457		
PLAUR	0.6402		
P4HA1	0.6401		
ZNF704	0.6345		
CCDC64	0.6343		
CBR3	0.6311		
ADAMTS1	0.6278		
GCGR	0.6272		
BRUNOL5	0.6221		
KIAA0961	0.6171		
CCDC33	0.6001		
LRRN3	0.5402		
IFIT2	-0.5533		
GPC3	-0.6149		
NGG3	-0.6266		
HIST1H2AG	-0.6344		
PIGZ	-0.6636		
MXRA8	-0.6696		
MGC14376	-0.6725		
CEBPB	-0.6778		
C8orf13	-0.6856		
FNDC3A	-0.6864		
CACNB2	-0.6912		
TPST2	-0.6929		
HIST1H3H	-0.6987		
PCTP	-0.7005		
ACTG2	-0.7072		
C10orf65	-0.7082		
BAALC	-0.7131		
TNFRSF1A	-0.7243		
HIST1H2BG	-0.7365		
LRRN5	-0.7370		
DBC1	-0.7403		
HIST1H2BK	-0.7452		
FAM43B	-0.7469		
KCNQ3	-0.7514		
TRAF3IP2	-0.7552		
HIST1H2AC	-0.7661		
SLC31A2	-0.7817		
CSAG3A	-0.7976		
CAMK4	-0.8063		
C6orf134	-0.8066		
RAC2	-0.8092		
MAGEA2	-0.8192		
TMEM100	-0.8302		
DYNC111	-0.8391		
SGNE1	-0.8404		
FLJ20366	-0.8532		
H2BFS	-0.8569		
ELMO1	-0.8679		
FAM112B	-0.9385		

Konopka_Supplementary_Table_8		
Differentially expressed genes enriched in specific human fetal brain regions or containing a human accelerated highly conserved noncoding sequence (haCNS).		
Gene Symbol	Fetal Brain Region Enrichment	
<i>AGTR1</i>	Cerebellum	
<i>CHRNA3</i>	Cerebellum	
<i>ENC1</i>	Perisylvian Cortex	
<i>EXPH5</i>	Cerebellum	
<i>FOXP2</i>	Perisylvian Cortex	
<i>GOLSYN (FLJ20366)</i>	Perisylvian Cortex	
<i>HDAC9</i>	Neocortex + Hippocampus	
<i>HIST1H2AC</i>	Cerebellum	
<i>LINGO1 (LRRN6A)</i>	Perisylvian Cortex	
<i>MAOB</i>	Hippocampus	
<i>PRICKLE1</i>	Thalamus	
<i>PROM1</i>	Neocortex	
<i>RSRC1</i>	Thalamus	
<i>SMARCA2</i>	Neocortex	
Gene Symbol	haCNS	caCNS
<i>DPYD</i>	Yes	No
<i>EFNB2</i>	Yes	Yes
<i>FOXP2</i>	Yes	Yes
<i>GRM8</i>	Yes	Yes
<i>LINGO1 (LRRN6A)</i>	Yes	No
<i>LRRN2 (LRRN5)</i>	Yes	No
<i>MAN1A1</i>	Yes	Yes
<i>MEIS1</i>	Yes	Yes
<i>PPP2R2B</i>	Yes	No
<i>RUNX1T1</i>	Yes	Yes
<i>SMARCA2</i>	Yes	Yes
<i>TFAP2D</i>	Yes	No
<i>ZNF608</i>	Yes	Yes
<p>The perisylvian cortex and cerebellum, two brain regions with elevated <i>FOXP2</i> expression, have a significant enrichment of differentially expressed genes ($P=1.1e-04$ and $P=1.3e-04$). Fourteen differentially expressed genes have a haCNS ($P=1.2e-06$), and five of these are specific to the human lineage, as they do not have a chimpanzee accelerated CNS (caCNS) ($P=0.04$). Data for comparison is from Johnson et al., <i>Neuron</i>, 2009.</p>		

Konopka_Supplementary_Table_9										
Positive selection of differentially expressed genes.										
Upregulated GeneName	Human vs. Chimpanzee			Human vs. Chimpanzee Chimpanzee Sequencing Consortium			Chimpanzee vs. Rhesus Macaque			
	Ensemble	dN	dS	dN/dS	Ka	Ks	Ka/Ks	Ensemble	dN	dS
ADM		0.0000	0.0000	N/A	0.0000	0.0000	N/A	0.0191	0.0848	0.2252
FLJ35409		N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
ZNF702 (FLJ12985)		N/A	N/A	N/A	0.0038	0.0000	N/A	N/A	N/A	N/A
ZCCHC12		0.0025	0.0026	0.9615	N/A	N/A	N/A	0.0163	0.0617	0.2642
COL9A1		0.0045	0.0053	0.8491	N/A	N/A	N/A	0.0151	0.0603	0.2504
EXPH5		0.0065	0.0088	0.7386	N/A	N/A	N/A	0.0316	0.0642	0.4922
C7		0.0044	0.0103	0.4272	N/A	N/A	N/A	0.0193	0.0707	0.2730
ZNF608		0.0019	0.0080	0.2375	N/A	N/A	N/A	0.0029	0.0427	0.0679
PCAF		0.0091	0.0426	0.2136	N/A	N/A	N/A	0.0008	0.0441	0.0181
SNCAIP		0.0019	0.0123	0.1545	N/A	N/A	N/A	0.0107	0.05	0.2140
ISLR2		0.0012	0.0084	0.1429	N/A	N/A	N/A	0.0146	0.0992	0.1472
FOXN4		0.0017	0.0137	0.1241	N/A	N/A	N/A	0.0044	0.1067	0.0412
SMARCA2		0.0028	0.0358	0.0782	N/A	N/A	N/A	0.0004	0.0695	0.0058
L3MBTL3		0.0006	0.0092	0.0652	N/A	N/A	N/A	0.0201	0.1026	0.1959
DPYD		0.0009	0.0213	0.0423	N/A	N/A	N/A	0.0082	0.0395	0.2076
LRRC4C		0.0000	0.0104	0.0000	N/A	N/A	N/A	0.0000	0.0318	0.0000
RSRC1		0.0000	0.0069	0.0000	N/A	N/A	N/A	0.0040	0.0405	0.0988
SH3PXD2B (KIAA1295)		0.0116	0.0305	0.3803	0.0145	0.0074	1.9595	0.0163	0.0912	0.1787
HEBP2		0.0047	0.0058	0.8103	0.0047	0.0058	0.8103	0.0150	0.071	0.2113
MORC4 (FLJ11565)		0.0073	0.0215	0.3395	0.0018	0.0031	0.5806	0.0183	0.055	0.3327
FSTL5 (DKFZp566D234)		0.0041	0.0102	0.4020	0.0041	0.0089	0.4607	0.0150	0.0541	0.2773
CCNA1		0.0042	0.0093	0.4516	0.0042	0.0093	0.4516	0.0205	0.0671	0.3055
EYA1		0.0025	0.0075	0.3333	0.0025	0.0075	0.3333	0.0055	0.0496	0.1109
CDCATL (RAM2)		0.0131	0.0289	0.4533	0.0043	0.0134	0.3209	0.0195	0.0745	0.2617
LRRC8C (AD158)		0.0007	0.0033	0.2121	0.0007	0.0022	0.3182	0.0006	0.0372	0.0161
MGST1		0.0029	0.0093	0.3118	0.0029	0.0093	0.3118	0.0363	0.0261	1.3908
TGIF		0.0060	0.0197	0.3046	0.0060	0.0197	0.3046	0.0541	0.1187	0.4558
PROM1		0.0038	0.0146	0.2603	0.0040	0.0145	0.2759	0.0236	0.0703	0.3357
ABCB4		0.0022	0.0082	0.2683	0.0019	0.0084	0.2262	0.0244	0.0728	0.3352
HDAC9		0.0019	0.0085	0.2235	0.0018	0.0083	0.2169	0.0019	0.044	0.0432
SLIT1 (SLIT3)		0.0006	0.0212	0.0283	0.0034	0.0179	0.1899	0.0190	0.171	0.1111
AGTR1		0.0013	0.0069	0.1884	0.0013	0.0069	0.1884	0.0042	0.0369	0.1138
GRM8		0.0011	0.0061	0.1803	0.0011	0.0063	0.1746	0.0026	0.0411	0.0633
PRNP		0.0036	0.0211	0.1706	0.0036	0.0211	0.1706	0.0168	0.1304	0.1288
MFHAS1		0.0038	0.0250	0.1520	0.0030	0.0237	0.1266	0.0108	0.0887	0.1218
FOXP2		0.0013	0.0205	0.0634	0.0013	0.0110	0.1182	0.0000	0.0329	0.0000
PDGFRA		0.0014	0.0124	0.1129	0.0014	0.0125	0.1120	0.0043	0.0481	0.0894
ADAMTS9		0.0017	0.0166	0.1024	0.0015	0.0162	0.0926	0.0058	0.0763	0.0760
ROR2		0.0055	0.0276	0.1993	0.0024	0.0271	0.0886	0.0079	0.1502	0.0526
BCAN		0.0015	0.0138	0.1087	0.0010	0.0131	0.0763	0.0172	0.0908	0.1894
TMT2C (DKFZp762A217)		0.0030	0.0203	0.1478	0.0015	0.0203	0.0739	N/A	N/A	N/A
SYK		0.0008	0.0130	0.0615	0.0009	0.0141	0.0638	0.0043	0.0817	0.0526
ARHGAP16		0.0137	0.0454	0.3018	0.0033	0.0518	0.0637	0.0231	0.1922	0.1202
PRICKLE1		0.0006	0.0129	0.0465	0.0006	0.0130	0.0462	0.0017	0.0708	0.0240
IGFBP4		0.0015	0.0342	0.0439	0.0015	0.0342	0.0439	0.0015	0.126	0.0119
EPAS1		0.0557	0.1092	0.5101	0.0005	0.0115	0.0435	0.0217	0.133	0.1632
ZNF521 (EHZF)		0.0115	0.0288	0.3993	0.0004	0.0108	0.0370	0.0026	0.0389	0.0668
HIST1H2BH		0.0000	0.0533	0.0000	0.0001	0.0636	0.0016	N/A	N/A	N/A
MEIS1		0.0034	0.0099	0.3434	0.0000	0.0051	0.0000	0.0011	0.0228	0.0482
POPDC2		0.0013	0.0244	0.0533	0.0000	0.0408	0.0000	0.0200	0.0785	0.2548
NPTX2		0.0019	0.0390	0.0487	0.0000	0.0332	0.0000	0.0076	0.1798	0.0423
EFNB2		0.0000	0.0197	0.0000	0.0000	0.0197	0.0000	0.0061	0.0288	0.2118
FRZB		0.0000	0.0137	0.0000	0.0000	0.0138	0.0000	0.0028	0.0799	0.0350
LRRN6A (FLJ14594)		0.0000	0.0228	0.0000	0.0000	0.0220	0.0000	0.0007	0.1591	0.0044
RDX		0.0000	0.0119	0.0000	0.0000	0.0124	0.0000	0.0008	0.0425	0.0188
RNF182 (MGC33993)		0.0000	0.0118	0.0000	0.0000	0.0118	0.0000	0.0018	0.0595	0.0303
RUNX1T1 (CBFA2T1)		0.0000	0.0093	0.0000	0.0000	0.0095	0.0000	0.0448	0.0857	0.5228
SLC30A3		0.0000	0.0255	0.0000	0.0000	0.0255	0.0000	0.0046	0.0902	0.0510
SYT4		0.0000	0.0078	0.0000	0.0000	0.0080	0.0000	0.0058	0.0341	0.1701
TFAP2D (TFAP2BL1)		0.0000	0.0065	0.0000	0.0000	0.0088	0.0000	0.0010	0.0411	0.0243
TMEFF2		0.0000	0.0060	0.0000	0.0000	0.0060	0.0000	0.0013	0.0303	0.0429

Konopka_Supplementary_Table_9 (continued)									
Positive selection of differentially expressed genes.									
Downregulated GeneNames	Human vs. Chimpanzee			Human vs. Chimpazee			Chimpanzee vs. Rhesus Macaque		
	Ensemble dN	dS	dN/dS	Chimpanzee Sequencing Consortium Ka	Ks	Ka/Ks	Ensemble dN	dS	dN/dS
AMT	0.0034	0.0033	1.0303	N/A	N/A	N/A	0.0118	0.0568	0.2077
C6orf117	0.0021	0.0286	0.0734	N/A	N/A	N/A	0.0050	0.0415	0.1205
C6orf48	0.0210	0.0161	1.3043	N/A	N/A	N/A	N/A	N/A	N/A
CDKN1A	0.0000	0.0064	0.0000	0.0000	0.0000	N/A	0.0174	0.0601	0.2895
DSCR8	0.0000	0.0000	N/A	0.0000	0.0000	N/A	0.0141	0.0875	0.1611
ENO3	0.0022	0.0000	N/A	0.0022	0.0000	N/A	0.0066	0.0805	0.0820
FAM43B	0.0012	0.0086	0.1395	N/A	N/A	N/A	0.0104	0.13	0.0800
FLJ46082	0.0000	0.0223	0.0000	N/A	N/A	N/A	0.0296	0.0969	0.3055
H2BFS	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
HIST2H2AA	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
HIST2H4	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
IFIT2	0.0040	0.0073	0.5479	N/A	N/A	N/A	0.0086	0.0557	0.1544
MGC33846	0.0062	0.0107	0.5794	N/A	N/A	N/A	0.0167	0.109	0.1532
MSRB3	0.0000	0.0052	0.0000	N/A	N/A	N/A	0.1036	0.2236	0.4633
PCDH17	0.0004	0.0137	0.0292	N/A	N/A	N/A	0.0019	0.0858	0.0221
TIMP1	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
MAGEA10	0.0110	0.0209	0.5263	0.0084	0.0058	1.4483	0.0235	0.067	0.3507
PHACTR2 (C6orf56)	0.0092	0.0070	1.3143	0.0093	0.0070	1.3286	0.0179	0.0517	0.3462
ZNF556 (FLJ11637)	0.0075	0.0091	0.8242	0.0075	0.0091	0.8242	N/A	N/A	N/A
MAN1A1	0.0027	0.0039	0.6923	0.0029	0.0041	0.7073	0.0713	0.1353	0.5270
FLJ20366	0.0029	0.0050	0.5800	0.0033	0.0056	0.5893	N/A	N/A	N/A
ENPP2	0.0031	0.0116	0.2672	0.0027	0.0124	0.2177	0.0035	0.076	0.0461
CHRNA3	0.0019	0.0125	0.1520	0.0019	0.0125	0.1520	N/A	N/A	N/A
C8orf13	0.0040	0.0297	0.1347	0.0040	0.0297	0.1347	0.0824	0.2142	0.3847
LRRN5 (GAC1)	0.0039	0.0183	0.2131	0.0015	0.0116	0.1293	0.0196	0.0904	0.2168
HTR2B	0.0021	0.0171	0.1228	0.0021	0.0171	0.1228	0.0115	0.0495	0.2323
GJA12	0.0373	0.1020	0.3657	0.0019	0.0174	0.1092	0.0093	0.1915	0.0486
FAM43A (FLJ90022)	0.0019	0.0205	0.0927	0.0019	0.0206	0.0922	0.0038	0.1683	0.0226
LRRN6C (FLJ31810)	0.0008	0.0141	0.0567	0.0008	0.0141	0.0567	0.0008	0.0711	0.0113
MAOB	0.0017	0.0232	0.0733	0.0010	0.0184	0.0543	0.0078	0.0537	0.1453
PTRF	0.0061	0.0758	0.0805	0.0013	0.0288	0.0451	0.0130	0.2274	0.0572
ENC1	0.0009	0.0209	0.0431	0.0009	0.0209	0.0431	0.0000	0.0354	0.0000
ACCN2	0.0000	0.0225	0.0000	0.0000	0.0239	0.0000	0.0023	0.0629	0.0366
ACTA2	0.0000	0.0180	0.0000	0.0000	0.0180	0.0000	0.0000	0.079	0.0000
ACTG2	0.0000	0.0163	0.0000	0.0000	0.0162	0.0000	0.0000	0.0632	0.0000
B3GNT1	0.0000	0.0139	0.0000	0.0000	0.0116	0.0000	0.0069	0.0967	0.0714
BTBD11 (FLJ33957)	0.0004	0.0205	0.0195	0.0000	0.0267	0.0000	0.0104	0.1661	0.0626
CACNB2	0.0030	0.0131	0.2290	0.0000	0.0104	0.0000	0.0058	0.0582	0.0997
DCN	0.0000	0.0087	0.0000	0.0000	0.0027	0.0000	0.0111	0.0338	0.3284
EDNRA	0.0000	0.0105	0.0000	0.0000	0.0110	0.0000	0.0054	0.0403	0.1340
ELMO1	0.0000	0.0083	0.0000	0.0000	0.0083	0.0000	0.0025	0.0543	0.0460
FGF14	0.0000	0.0039	0.0000	0.0000	0.0040	0.0000	0.0000	0.0212	0.0000
FLJ11286	0.0031	0.0155	0.2000	0.0000	0.0059	0.0000	0.0068	0.0687	0.0990
GLRX	0.0000	0.0174	0.0000	0.0000	0.0175	0.0000	0.0083	0.0424	0.1958
GPR30	0.0020	0.0413	0.0484	0.0000	0.0483	0.0000	0.1033	0.6325	0.1633
HIST1H2AC	0.0000	0.0210	0.0000	0.0000	0.0210	0.0000	0.0000	0.2104	0.0000
HIST2H2BE	N/A	N/A	N/A	0.0000	0.0410	0.0000	N/A	N/A	N/A
IGFBP3	0.0278	0.0581	0.4785	0.0000	0.0335	0.0000	0.0057	0.1089	0.0523
IRF6	0.0000	0.0161	0.0000	0.0000	0.0161	0.0000	0.0000	0.0598	0.0000
MAB21L2	0.0000	0.0051	0.0000	0.0000	0.0051	0.0000	0.0000	0.0979	0.0000
PPP2R2B	0.0000	0.0080	0.0000	0.0000	0.0094	0.0000	0.0009	0.0337	0.0267
PRPH	0.0000	0.0050	0.0000	0.0000	0.0060	0.0000	0.0008	0.132	0.0061
TAGLN	0.0000	0.0204	0.0000	0.0000	0.0205	0.0000	0.0021	0.0974	0.0216
TMEM100 (FLJ10970)	0.0000	0.0249	0.0000	0.0000	0.0250	0.0000	0.0072	0.0747	0.0964
TUBA6	0.0000	0.0241	0.0000	0.0000	0.0244	0.0000	N/A	N/A	N/A

Estimation of proteins undergoing positive selection in humans compared to chimpanzees using a ratio of non-synonymous substitutions (Ka or dN) to synonymous substitutions (Ks or dS). Values were obtained from either the Ensembl database (www.ensembl.org), or from the published draft of the chimpanzee genome (Chimpanzee sequencing and analysis consortium, Nature, 2005, 437(7055): 69-87). Ratios greater than 1.0 indicate positive selection. Comparisons between chimpanzee and rhesus macaque proteins are also provided from Ensembl to determine whether positive selection occurred along the human lineage.

Konopka_Supplementary_Table_10		
Real-time PCR primers.		
Gene Symbol	Forward Primer (5'-3')	Reverse Primer (5'-3')
<i>ACTA2</i>	GACCGAATGCAGAAGGAGAT	CGGCTTCATCGTATTCTCTGT
<i>CDCA7L</i>	GGAGGATATCACCGAAGAGGA	CACTGTCTTGGTGTGCGATGG
<i>COL9A1</i>	AACGGTTTGCCTGGAGCTAT	TTGTAAATGCTCGCTGACC
<i>DCN</i>	TGCTGTTGACAATGGCTCTC	GCCTTTTTGGTGTGTTGTCC
<i>EDNRA</i>	ATCACCGTCCTCAACCTCTG	GGTACCATGACGAAGCCAAT
<i>EPAS1</i>	GTCTGAACGTCTCAAAGGGC	ACACCTCCGTCTCCTTGCTC
<i>EYA1</i>	CCAATGCCACTTACCAGCTT	TTTCCCATCTGAACCTCGAC
<i>FAM43A</i>	AAGGGCTAAAGGGTTGCATT	GAGGAGGAGGGGTTCACTTC
<i>GRM8</i>	GTGGACATCGTGACAGCACT	TTCACGTGGGATTTTCTGTG
<i>HEBP2</i>	CACCCAGGCCTTTAGAGTCA	GGGCACTAGAAAATCCATCG
<i>IGFBP3</i>	GTCAACGCTAGTGCCGTCAG	CTTGGGATCAGACACCCG
<i>IRF6</i>	CAGATTCCTGGAACATGC	TTCCATTTAGCTGGGTCAAG
<i>MAGEA10</i>	AAGCGAGTTCTCGTTCTGA	GAAAAGAGGGGTTCCCTGTG
<i>MAOB</i>	CATGAGCAACAAATGCGAC	GGCTTCCAGAACAACCACAT
<i>NPTX</i>	TCTGGTGACTTAAAGGCGCT	GAGGACGAGAAGTCCCTGCT
<i>PCDH17</i>	AGGGACTAATGCAAGCGAGA	CTGTCTCTCAGGCTGGCTCT
<i>PDGFRA</i>	ATTGCGGAATAACATCGGAG	GGGTAATGAAAGCTGGCAGA
<i>PPP2R2B</i>	GTGTGTGTGGAATGGGTCAG	ACTTTTCGGGGTTTGAGGAT
<i>PRNP</i>	CGAGCTTCTCCTCTCCTCAC	GTTCCATCCTCCAGGCTTC
<i>PRPH</i>	CCTGGAAGTAGAGCGCAAGA	CTGGCTCTCCCACTCACCT
<i>ROR2</i>	GCTTCTGCTCTCAGTGTCCT	CTGGCTCCAGAAAATTCAGA
<i>RUNX1T1</i>	GACGCACTGGCAGTTATCAA	GCTTCTCCAGTCTTTGTGC
<i>SLC30A3</i>	CTTGGAGACCACTCGCCTG	TCCACAGGTTTGGACTCCTC
<i>SLIT1</i>	TGATGACATGAAGGAGCTGG	GAAAAGCTTTCCTGGGGATG
<i>SYK</i>	CAGGCCATCATCAGTCAGAA	CGTAGGAGCCGTTGTTGTCT
<i>TAGLN</i>	GACCAAGAATGATGGGCACT	AAGGCCAATGACATGCTTTC
<i>TIMP1</i>	TTGACTTCTGGTGTCCCCAC	GCTTCTGGCATCCTGTTGTT
<i>TMEFF2</i>	CGTCACATTCTGCACCAAAC	GGATCAGGATCTGGAGATGG
<i>TMEM100</i>	CTTCCCAGAAGTTGGACGA	CCTTGATGGGCTCTTCAGTC
<i>ZNF521</i>	TGGGATATTCAGGTTTCATGTTG	TTGGCAGGAGAGTCAAAGGT