Concordance between RNA-seq data and DNA microarray data in transcriptome analysis of proliferative and quiescent fibroblasts

Supplementary figures and tables



Supplementary Figure S1: The log-transformed PRO intensity values from microarray QP1 and microarray QP2 had a strong correlation (r = 0.89).



Supplementary Figure S2: The log-transformed PRO intensity values from microarray QP1 and microarray QP3 had a strong correlation (r = 0.89).



Supplementary Figure S3: The log-transformed PRO intensity values from microarray QP1 and microarray QP4 had a strong correlation (r = 0.87).



Supplementary Figure S4: The log-transformed PRO intensity values from microarray QP2 and microarray QP3 had a moderately strong correlation (r = 0.78).



Supplementary Figure S5: The log-transformed PRO intensity values from microarray QP2 and microarray QP4 had a strong correlation (r = 0.94).



Supplementary Figure S6: The log-transformed PRO intensity values from microarray QP3 and microarray QP4 had a strong correlation (r = 0.80).



Supplementary Figure S7: The log-transformed QUI intensity values from microarray QP1 and microarray QP2 had a strong correlation (r = 0.91).



Supplementary Figure S8: The log-transformed QUI intensity values from microarray QP1 and microarray QP3 had a strong correlation (r = 0.90).



Supplementary Figure S9: The log-transformed QUI intensity values from microarray QP1 and microarray QP4 had a strong correlation (r = 0.89).



Supplementary Figure S10: The log-transformed QUI intensity values from microarray QP2 and microarray QP3 had a strong correlation (r = 0.85).



Supplementary Figure S11: The log-transformed QUI intensity values from microarray QP2 and microarray QP4 had a strong correlation (r = 0.92).



Supplementary Figure S12: The log-transformed QUI intensity values from microarray QP3 and microarray QP4 had a strong correlation (r = 0.89).



Supplementary Figure S13: The log-transformed FC values from microarray QP1 and microarray QP2 had a negative correlation (r = -0.46).



Supplementary Figure S14: The log-transformed FC values from microarray QP1 and microarray QP3 had a moderate to strong correlation (r = 0.70).



Supplementary Figure S15: The log-transformed FC values from microarray QP2 and microarray QP3 had a negative correlation (r = -0.55).



Supplementary Figure S16: The log-transformed FC values from microarray QP3 and microarray QP4 had a negative correlation (r = -0.44).



Supplementary Figure S17: RNA-seq reads from proliferative and quiescent samples. Mapped RNA-seq data were imported into SeqMonk and quantified using the RPKM method (left column). Reads for the *TNXB* (top panel), *AHD1B* (middle panel), and *PTGDS* (lower panel) genes are shown. For each gene, the gene length, mRNA (exons are shown as blocks with introns shown as arrowheads) and coding regions are indicated. Arrows and color indicate the direction of the gene on the chromosome (red, left to right; blue, right to left). Reads from proliferative (Pro) and quiescent (Qui) samples are shown (blue dash, right to left mapped read; red dash, left to right mapped read). Bars under the reads represent fold change; blue bar for proliferative reads is set to 1 as the baseline. Red bar under Qui reads represents the fold change

as compared to Pro reads; TNXB (Chromosome 6), 47-fold increase; AHD1B (Chromosome 4), 49-fold increase; PTGDS (Chromosome 9), 27-fold increase. Chromosome position is listed at the bottom of each panel. Mapped RNA-seq reads were imported into SeqMonk and the total numbers of reads at each base pair across the coding region of the gene quantified (right column). Quantification was imported as custom tracks into the UCSC genome browser and bedgraphs created for the TNXB (top panel), AHD1B (middle panel), and PTDGS (lower panel) genes. In each graph, the genomic location and scale are shown along with coding sequences (including intron and exons) for each UCSC gene. PRO and QUI indicate the bar graphs for the total reads for each sample. The scale for the number of reads is demonstrated on the left of the graph. Arrowheads indicate the direction of the genes on the chromosome. For the TNXB graph, the sequence from the ATF6B gene is shown to demonstrate near equivalent reads between the two samples. Arrowheads indicate the direction of the gene on the chromosome.



Supplementary Figure S18: The log-transformed read counts from the two RNA-seq reactions for the quiescent fibroblasts exhibited a strong linear relationship (r = 0.94).



Supplementary Figure S19: The log-transformed read counts from the two RNA-seq reactions for the proliferative fibroblasts exhibited a strong linear relationship (r = 0.94).



Supplementary Figure S20: The log-transformed RNA-seq read counts for PRO and the log-transformed PRO intensity values from microarray QP1 had a low correlation (r = 0.33).



Supplementary Figure S21: The log-transformed RNA-seq read counts for PRO and the log-transformed PRO intensity values from microarray QP2 had a low correlation (r = 0.33).



Supplementary Figure S22: The log-transformed RNA-seq read counts for PRO and the log-transformed PRO intensity values from microarray QP3 had a moderate correlation (r = 0.40).



Supplementary Figure S23: The log-transformed RNA-seq read counts for PRO and the log-transformed PRO intensity values from microarray QP4 had a low correlation (r = 0.37).



Supplementary Figure S24: The log-transformed RNA-seq read counts for QUI and the log-transformed QUI intensity values from microarray QP1 had a low correlation (r = 0.32).



Supplementary Figure S25: The log-transformed RNA-seq read counts for QUI and the log-transformed QUI intensity values from microarray QP2 had a low correlation (r = 0.32).



Supplementary Figure S26: The log-transformed RNA-seq read counts for QUI and the log-transformed QUI intensity values from microarray QP3 had a moderate correlation (r = 0.41).



Supplementary Figure S27: The log-transformed RNA-seq read counts for QUI and the log-transformed QUI intensity values from microarray QP4 had a low correlation (r = 0.35).



Supplementary Figure S28: The log-transformed RNA-seq FC values and the log-transformed FC values from microarray QP1 had a low correlation (r = 0.23).



Supplementary Figure S29: The log-transformed RNA-seq FC values and the log-transformed FC values from microarray QP2 had a low correlation (r = 0.18).



Supplementary Figure S30: The log-transformed RNA-seq FC values and the log-transformed FC values from microarray QP3 had a low correlation (r = 0.18).



Supplementary Figure S31: The log-transformed RNA-seq FC values and the log-transformed FC values from microarray QP4 had a low correlation (r = 0.17).



Supplementary Figure S32: Correspondence between the microarray data, the RNA-seq data, and the qRT-PCR data for the probes that were analyzed using qRT-PCR. Rows correspond to genes, while columns correspond to the source of the data (RNA-seq, qRT-PCR, one of the four microarrays, or the average of the four microarrays, which is denoted "Mean QP log2(FC)"). The color of each cell denotes the FC value for the corresponding gene and source. The bracketed genes were selected because they had a high FC value (QUI/PRO) in either the RNA-seq data, the microarray data, or both. Non-bracketed genes were selected arbitrarily. The raw values used to create this figure are given in Supplementary Table S6.

Supplementary Table S1: Microarray intensity values demonstrate high reproducibility. Correlations are shown for proliferative samples (PRO) or quiescent samples (QUI) for each pair of microarrays. For each cell state (PRO or QUI), the values in the upper diagonal contain the Pearson correlations, while those in the lower diagonal contain the Spearman correlations. Values not in parentheses represent correlations between intensity values after cross-channel correction and LOWESS normalization, while those in parentheses represent correlations after those values had also been log-transformed. As log transformation does not change the rank order, only one number is shown for the Spearman correlation for each pair. All correlations were ≥ 0.77 , indicating strong agreement between intensity values in all microarrays.

		Signal int	ensities for Pl	RO	Signal intensities for QUI			
	QP1	QP2	QP3	QP4	QP1	QP2	QP3	QP4
QP1	_	0.80(0.89)	0.91 (0.89)	0.80(0.87)	_	0.88(0.91)	0.92(0.90)	0.88(0.89)
QP2	0.89	_	0.78(0.78)	0.94(0.94)	0.91	_	$0.85 \ (0.85)$	0.93(0.92)
QP3	0.87	0.77	_	0.79(0.80)	0.89	0.84	_	0.89(0.89)
QP4	0.88	0.94	0.79	_	0.89	0.92	0.89	_

Supplementary Table S2: List of probes in common among the n microarray probes with the highest FC values (geometric mean; QUI/PRO) and the n RNA-seq probes with the highest FC values, where n = 10, 50, 100, 500, or 1000.

n = 10H200006183APOD-001H300018610TNXB-001 $n = 50$ H200006183APOD-001opHsV0400000146FABP3-001H30009988LRRN4CL-001H300018610TNXB-001H200004405RARRES2-001H200006911GPNMB-001H200005569PRELP-001H200005933PPL-001opHsV0400003635SBSN-001H200006005CLU-001H300014703FBLN1-001 $n = 100$ H200006183APOD-001opHsV040000146FABP3-001H300018610TNXB-001H300018610TNXB-001H300004405RARRES2-001H200006911GPNMB-001H300018610TNXB-001H300004073CFD-201opHsV0400006073CFH-001H30001096AKR1C2-001H300004073AKR1C1-001H300004073AKR1C1-001H300004073AKR1C1-001H300018014DCN-001
H200006183APOD-001H300018610TNXB-001 $n = 50$ H200006183APOD-001opHsV0400000146FABP3-001H30009988LRRN4CL-001H300018610TNXB-001H200004405RARRES2-001H200006911GPNMB-001H200014099CFD-201H300005569PRELP-001H20000605CLU-001H300014703FBLN1-001H20000605CLU-001H300014703FBLN1-001H200006183APOD-001opHsV040000146FABP3-001H300018610TNXB-001H200004405RARRES2-001H300018610TNXB-001H30001402C1R-201H200006911GPNMB-001H300004073CFH-001H300010096AKR1C2-001opHsV0400008625C5orf4-001H300004073AKR1C1-001H30000569PRELP-001H300018014DCN-001
H300018610TNXB-001 $n = 50$ H200006183APOD-001opHsV0400000146FABP3-001H300009988LRRN4CL-001H300018610TNXB-001H200004405RARRES2-001H200006911GPNMB-001H200014099CFD-201H300005569PRELP-001H20000605CLU-001H300014703FBLN1-001H20000605CLU-001H300014703FBLN1-001 $n = 100$ H200006183APOD-001opHsV040000146FABP3-001H300018610TNXB-001H300009988LRRN4CL-001H300004405RARRES2-001H200006911GPNMB-001H300004073CFH-001H30001096AKR1C2-001opHsV0400008625C5orf4-001H300004073AKR1C1-001H300004073AKR1C1-001H30000569PRELP-001H300018014DCN-001
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H200007894	PDGFRL-001
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H300021118	BBC3-201
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${\rm opHsV0400005864}$	SEPP1-001
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H200003669	PIK3IP1-001
H200006891	NR4A2-001
H200009720	GDF15-201
H200007307	GPR133-001
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<i>n</i> =	1000
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n = 1200006183 opHsV0400000146 H300009988 H300018610 H200004405	APOD-001 FABP3-001 LRRN4CL-001 TNXB-001 RARRES2-001
n = 1200006183 opHsV0400000146 H300009988 H300018610 H200004405 H200006911	APOD-001 FABP3-001 LRRN4CL-001 TNXB-001 RARRES2-001 GPNMB-001
n = 1200006183 opHsV0400000146 H300009988 H300018610 H200004405 H200006911 H300004102	APOD-001 FABP3-001 LRRN4CL-001 TNXB-001 RARRES2-001 GPNMB-001 C1R-201
n = 1200006183 opHsV0400000146 H300009988 H300018610 H200004405 H200006911 H300004102 H200014099	APOD-001 FABP3-001 LRRN4CL-001 TNXB-001 RARRES2-001 GPNMB-001 C1R-201 CFD-201
n = 1200006183 opHsV0400000146 H300009988 H300018610 H200004405 H200006911 H300004102 H200014099 H300021913	APOD-001 FABP3-001 LRRN4CL-001 TNXB-001 RARRES2-001 GPNMB-001 C1R-201 CFD-201 AKR1C3-001
n = 1200006183 opHsV0400000146 H300009988 H300018610 H200004405 H200006911 H300004102 H200014099 H300021913 opHsV0400006073	APOD-001 FABP3-001 LRRN4CL-001 TNXB-001 RARRES2-001 GPNMB-001 C1R-201 CFD-201 AKR1C3-001 CFH-001
n = 1200006183 opHsV0400000146 H300009988 H300018610 H200004405 H200006911 H300004102 H200014099 H300021913 opHsV0400006073 H300010096	APOD-001 FABP3-001 LRRN4CL-001 TNXB-001 RARRES2-001 GPNMB-001 C1R-201 CFD-201 AKR1C3-001 CFH-001 AKR1C2-001
$n = \frac{n}{1200006183}$ opHsV0400000146 H300009988 H300018610 H200004405 H200006911 H300004102 H200014099 H300021913 opHsV0400006073 H300010096 opHsV0400008625	APOD-001 FABP3-001 LRRN4CL-001 TNXB-001 RARRES2-001 GPNMB-001 C1R-201 CFD-201 AKR1C3-001 CFH-001 AKR1C2-001 C5orf4-001
$n = \frac{n}{1200006183}$ opHsV0400000146 H300009988 H300018610 H200004405 H200006911 H300004102 H200014099 H300021913 opHsV0400006073 H300010096 opHsV0400008625 H200003498	APOD-001 FABP3-001 LRRN4CL-001 TNXB-001 RARRES2-001 GPNMB-001 C1R-201 CFD-201 AKR1C3-001 CFH-001 AKR1C2-001 C5orf4-001 MAN1A1-001
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$n = \frac{n}{1200006183}$ opHsV0400000146 H300009988 H300018610 H200004405 H200006911 H300004102 H200014099 H300021913 opHsV0400006073 H300010096 opHsV0400008625 H200003498 H300004073 H300005569	APOD-001 FABP3-001 LRRN4CL-001 TNXB-001 RARRES2-001 GPNMB-001 C1R-201 CFD-201 AKR1C3-001 CFH-001 AKR1C2-001 C5orf4-001 MAN1A1-001 AKR1C1-001 PRELP-001
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$n = \frac{n}{1200006183}$ opHsV0400000146 H300009988 H300018610 H200004405 H200006911 H300004102 H200014099 H300021913 opHsV0400006073 H300010096 opHsV0400008625 H200003498 H300004073 H300005569 opHsV0400012696 H300018014	APOD-001 FABP3-001 LRRN4CL-001 TNXB-001 RARRES2-001 GPNMB-001 C1R-201 CFD-201 AKR1C3-001 CFH-001 AKR1C2-001 C5orf4-001 MAN1A1-001 AKR1C1-001 PRELP-001 HMGCS1-001 DCN-001
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$n = \frac{n}{1200006183}$ opHsV0400000146 H300009988 H300018610 H200004405 H200006911 H300004102 H200014099 H300021913 opHsV0400006073 H300010096 opHsV0400008625 H200003498 H300004073 H300005569 opHsV0400012696 H300018014 H200008754 H300001612 H200015788	APOD-001 FABP3-001 LRRN4CL-001 TNXB-001 RARRES2-001 GPNMB-001 C1R-201 CFD-201 AKR1C3-001 CFH-001 AKR1C2-001 C5orf4-001 MAN1A1-001 AKR1C1-001 PRELP-001 HMGCS1-001 DCN-001 SLC39A8-001 PCOLCE2-001 GPRC5B-001
$n = \frac{n}{1200006183}$ opHsV0400000146 H300009988 H300018610 H200004405 H200006911 H300004102 H200014099 H300021913 opHsV0400006073 H300010096 opHsV0400008625 H200003498 H300004073 H300005569 opHsV0400012696 H300018014 H200008754 H300001612 H200015788 H200005933	APOD-001 FABP3-001 LRRN4CL-001 TNXB-001 RARRES2-001 GPNMB-001 C1R-201 CFD-201 AKR1C3-001 CFH-001 AKR1C2-001 C5orf4-001 MAN1A1-001 AKR1C1-001 PRELP-001 HMGCS1-001 DCN-001 SLC39A8-001 PCOLCE2-001 GPRC5B-001 PPL-001
$n = \frac{n}{1200006183}$ opHsV0400000146 H300009988 H300018610 H200004405 H200006911 H300004102 H200014099 H300021913 opHsV0400006073 H300010096 opHsV0400008625 H200003498 H300004073 H300004073 H300005569 opHsV0400012696 H300018014 H200008754 H300001612 H200015788 H200005933 opHsV0400005905	APOD-001 FABP3-001 LRRN4CL-001 TNXB-001 RARRES2-001 GPNMB-001 C1R-201 CFD-201 AKR1C3-001 CFH-001 AKR1C2-001 C5orf4-001 MAN1A1-001 AKR1C1-001 PRELP-001 HMGCS1-001 DCN-001 SLC39A8-001 PCOLCE2-001 GPRC5B-001 PPL-001 ADH1A-001
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H200006005	CLU-001
opHsV0400004530	SCPEP1-201
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opHeV0400004408	WLS-003
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H200013978 H200000117	OSP2 002
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n500019595	CD30-000
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H200019931	CTSD-001
H300008317	SMPDL3A-001
opHsV040000678	TPP1-001
H200019102	ADD3-001
H300004858	PODN-001
H200008806	C3-001
H200011421	CDKN1C-002
H200020242	IL33-001
H200014658	DIRAS3-001
H200007894	PDGFRL-001
H300015570	FBLN2-002
H200006728	LUM-001
H300016767	PSAP-002
opHsV0400012444	FBXO32-001
H200006008	HTRA1-001
opHsV0400004093	ECM2-001
H200014829	FBLN2-002
H300019693	SVEP1-002
H200006869	GYPC-001
H200004859	F10-001
H200016555	IFI6-001
opHsV0400012949	LYNX1-001
H200004464	MYO1D-201
H300015674	SIAE-001

H300022324	ADAMTS13-001
opHsV040000297	ASAH1-001
H300018814	PMP22-002
H200006022	CHI3L1-001
opHsV0400003457	SERPING1-001
opHsV0400005637	DPP4-001
H300014091	COL14A1-001
H200018907	TRIM22-001
H300021118	BBC3-201
H200018923	SOD2-002
H300015796	LSS-002
H200010692	FAM8A1-001
H200011779	FCGRT-201
opHsV0400005894	ALDH3A2-001
opHsV0400010879	AKAP12-202
H200005403	HTRA3-001
H200007822	APOE-001
H200006553	VEGER-001
H200012068	SLC17A5-001
H300012000 H300019720	LGALS3BP-201
H200013720	DRAM1 001
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H200007999	GBP2-002
H200010211	ZNF219-001
H200000817	AGT-001
opHsV0400002899	THBS2-001
H300010511	SOD2-002
opHsV0400005864	SEPP1-001
H200013247	VIT-001
opHsV0400004072	MYO1D-201
H200006628	CCNG1-001
opHsV0400000112	CCNG1-001
H200003669	PIK3IP1-001
H200006891	NR4A2-001
H300022033	PDZRN3-001
H200005977	PRNP-002
${\rm opHsV0400005051}$	COL6A2-001
H300000866	LRRC32-001
H200009720	GDF15-201
H300019371	DDB2-201
H300011696	TGFBR2-001
H200007307	GPR133-001
H300005309	TMEM35-001
opHsV0400006111	HIST1H2AC-001
H200008267	CPXM1-001
H300018457	GRN-201

H200011392 opHsV0400010785 opHsV040000770 H300007158 H200001525 H200001162 H200015691 H300011496 opHsV0400012025 H300018970 opHsV0400007437 H200001709 H200005879 H200017694 H200007939 H300006979 opHsV0400004676 opHsV040006369 H200016323 opHsV040000698 H200013144 H300002218 H300019462 H300017367 H200011747 H300007781 H300022100 opHsV0400011450 opHsV0400003010 H300018477 H200006117 H300017119 H300011586 opHsV0400004882 H200010452 H200002015H300003822 H200007928 H300021603 H200008758 H300000904 H200003862 H200007344 H300010195 H300006654 opHsV0400012080 H300018991 opHsV040000735 H300009961 H200020465H200006772

SFRP4-001 SLC40A1-001 CST1-001 CLDN11-001 C7orf41-001 ARHGAP20-001 **MSMO1-001 FBLN2-002** AC159540.1-001 SESN1-002RP11-152F13.5-201 **QPRT-201** BMP2-001 **PCDHB6-001** PCSK6-203 NBL1-001 SLIT3-002C14orf132-001 **ZMAT3-001** COL6A2-001 CST3-001 LRIG3-001 KLF4-002 **CFHR1-001** MMP2-001 RARRES3-001 ANK1-001 ZMAT3-001 PLD3-004 PTPRU-001 **TP53INP1-001** FAM46A-003 PMP22-002 TCEAL7-001 C17orf58-201 **CTSF-001** AC135178.1-201 TFPI-201 FKBP9-001 **TSHZ1-001** AKAP12-001 HIST1H2AC-201 RENBP-004 CCDC74A-001 ZNFX1-AS1-001 **MBP-001 PGF-002 GAA-201** SPATA18-001 FAM102A-001 DPT-001

H200004653	SULF2-001
H200004209	RAMP1-001
H200005091	CD81-001
H300011592	SH3D19-201
m opHsV0400002187	KRBA2-001
H200009585	IGIP-002
H300003004	PDPN-001
H300019123	GLTSCR2-201
H200017774	PCDHB14-001
H200002317	RAB3IL1-002
H200004335	C19orf76-201
H300018539	CTSA-001
000000000000000000000000000000000000	IFITM10-001
H200006892	LAMB1-001
opHsV0400004289	APP-001
H300007451	FIBIN-001
H200006910	CHRDL1-001
H200008162	ADAM33-001
opHsV0400006844	SPRY1-002
opHsV0400003609	ADAM33-001
opHsV0400004448	PNRC1-001
H200005320	PLEKHF1-201
H200000520	TGFB3-001
H300013304	RNASET2-007
H200017630	PLTP-001
H200007742	BTN3A3-001
H300006701	C13orf16-002
H200000114	FLT3LG-201

Supplementary Table S3: Moderate overlap between the probes with the lowest FC values in the RNA-seq data and those with the lowest FC values in the DNA microarray data. k represents the size of a given list (the 10, 50, 100, 500, or 1000 probes with the lowest FC values), while n represents the number of probes in common between a list from the RNA-seq data and the corresponding list from the DNA microarray. The P-value represents the proportion of 10,000 random trials that had an equal or greater level of overlap than that actually observed. Thus, if none of the random trials had a greater level of overlap, then the P-value is 0. More overlapping probes than would be expected by chance were observed for all microarrays for k = 100, 500, and 1000. "All" represents the geometric mean of the FC values of the four microarrays; for this dataset, more overlapping probes were detected than would be expected by chance for all list sizes.

		k = 10	<i> </i>	x = 50	k	= 100	k	= 500	<i>k</i> =	= 1000
	n	P-value	n	P-value	n	P-value	n	P-value	n	P-value
QP1	0	1	1	0.08	6	0	74	0	156	0
QP2	0	1	1	0.08	8	0	91	0	214	0
QP3	0	1	2	0.002	5	0	41	0	92	0
QP4	0	1	1	0.08	6	0	78	0	183	0
All	2	0	13	0	31	0	156	0	316	0

Supplementary Table S4: List of probes in common among the n microarray probes with the lowest FC values (geometric mean; QUI/PRO) and the n RNA-seq probes with the lowest FC values, where n = 10, 50, 100, 500, or 1000.

Microarray probe ID	RNA-seq probe ID				
n = 10					
H200019509	BEX1-001				
H200006097	ID1-001				
<i>n</i> =	= 50				
H200019509	BEX1-001				
H200006097	ID1-001				
H200007186	FAM64A-201				
H200007019	MMP3-001				
H200009826	KRT34-201				
H200013276	SERPINB7-201				
H200015043	CENPM-001				
H200006195	TAGLN-006				
H300006172	CDC20-001				
H200006884	SERPINE1-001				
opHsV0400006470	KRTAP1-1-001				
H200018730	KRTAP1-5-001				
H200018729	KRTAP2-3-001				
n =	100				
H200019509	BEX1-001				
H200006097	ID1-001				
H200007186	FAM64A-201				
H200007019	MMP3-001				
H200009826	KRT34-201				
H200013276	SERPINB7-201				
H300019126	WNK4-201				
${\rm opHsV040000209}$	GINS2-001				
H20000064	FOXM1-001				
opHsV0400001096	TPM1-001				

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H200015043	CENPM-001
H300006703	LY6K-001
H200006195	TAGLN-006
H300006172	CDC20-001
H300018013	LOXL2-001
H200006884	SERPINE1-001
opHsV040006470	KRTAP1-1-001
H200018730	KRTAP1-5-001
H200014659	CCNB2-001
H300018499	TRIP13-001
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SNRPA-201
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TGM2-002
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H200005976	PSMD2-001

Supplementary Table S5: Previous studies report widely different correlations between RNA-seq data and DNA microarray data.

Description of samples used	Reported correlation(s)	Reference(s)
Human embryonic kidney cells versus B cells	0.88	[7]
Human liver cells versus kidney cells	0.67 to 0.75	[4]
Yeast cells	0.099 to 0.509	[1, 5, 8]
Human brain cells	0.51 to 0.67	[2]
Male and female Drosophila pseudoobscura	0.54 to 0.94	[3]
Human T cells	0.79 to 0.90	[9]
Rat nerves	0.84 to 0.85	[6]
Human proliferating or quiescent fibroblasts	0.02 to 0.42	This study

Supplementary Table S6: Correspondence between the microarray data, the RNA-seq data, and the qRT-PCR data for the probes that were analyzed using qRT-PCR. These are the raw values used to construct Supplementary Figure S32.

					(C)	Ð	()
	5	5	5	5	$5_2(F$	ц Ч	RI
	FO	FO	FO	FO	log	-Sec	PC
	$\mathbf{P1}$	P2	P3	P4	ĴΡ	NA	Ľ.
	Q	Q	Q	Q	n ((R)	(qI
Gene	\log_2	\log_2	\log_2	\log_2	Mea	\log_2	\log_2
MAN1A1	3.37	2.23	3.56	2.50	2.91	1.63	3.00
MME	1.64	4.00	0.35	4.49	2.62	1.98	2.33
SSFA2	0.27	1.59	0.42	3.22	1.37	0.21	0.43
SOD2	1.09	2.31	0.95	2.73	1.77	2.16	2.97
TGFBR3	3.78	1.75	2.69	1.94	2.54	1.62	2.73
WISP2	-0.24	1.60	-0.71	1.01	0.41	4.71	4.44
PCSK9	1.32	0.37	1.33	0.00	0.75	3.48	4.64
SFRP2	0.70	0.07	0.30	-0.43	0.16	3.45	2.82
BMP4	0.79	-0.59	1.63	0.93	0.69	2.61	4.01
PODN	1.77	0.90	2.63	1.48	1.69	2.69	2.63
CTSK	2.26	1.82	2.02	1.69	1.95	4.66	5.17
SPRY1	-0.15	1.15	0.04	2.63	0.92	3.36	3.38
ECM2	1.76	1.10	1.98	1.33	1.54	2.19	0.69
GPRC5B	0.87	3.63	1.03	5.19	2.68	2.40	4.86
ADH1B	2.57	1.73	2.22	0.48	1.75	5.74	3.06
TNXB	2.68	2.37	1.27	1.14	1.87	5.58	3.01
APOD	6.00	9.68	2.54	5.79	6.00	5.33	5.61
PTGDS	0.94	3.84	0.52	3.83	2.28	4.79	3.62
FABP3	3.37	2.75	6.04	4.22	4.10	4.38	5.94
PPL	3.63	2.68	3.76	0.64	2.68	4.59	8.07
Col14A1	1.26	1.26	0.47	0.39	0.85	4.00	2.43
LTBP4	1.53	0.29	1.20	-1.15	0.47	4.08	3.07
EGR2	0.04	-0.64	0.07	-0.94	-0.37	3.44	1.01
C3	2.12	1.70	2.24	0.70	1.69	3.59	4.07
RARRES2	3.91	2.06	4.72	2.98	3.42	3.52	3.88
IL34	0.14	1.22	0.92	0.56	0.71	3.22	3.03
C2	1.02	0.88	2.44	1.21	1.39	3.29	1.55
IGF2	-0.28	-0.18	-0.22	-0.04	-0.18	2.96	0.55
C1R	3.31	3.01	2.37	3.15	2.96	2.80	2.06
IDI1	1.66	1.18	2.57	2.62	2.01	2.45	0.35
CFH	2.92	1.75	2.38	0.55	1.90	2.74	2.68
C1S	2.27	1.84	2.37	1.87	2.09	2.63	1.59
IFNA1	-0.66	0.64	-3.09	0.51	-0.65	2.29	1.21
APOE	2.10	1.47	1.85	0.27	1.42	4.28	3.98
GNG4	0.98	-0.54	-0.55	-0.41	-0.13	0.12	-0.64
RARb	0.10	-0.34	0.70	-0.34	0.03	0.01	1.59
TRPC1	0.74	-0.07	0.52	0.17	0.34	0.40	-5.35
TRPC6	0.25	1.42	-0.22	1.75	0.80	0.15	0.05
Tube1	0.51	-0.62	-0.31	0.51	0.02	-0.39	0.64
Gem	2.46	2.25	1.80	1.30	1.95	2.46	0.73

ActC1	-1.75	-1.36	-0.64	-2.50	-1.56	-3.08	0.77
IGIP	1.94	-0.19	1.41	0.72	0.97	1.69	3.02
SSTR3	0.03	-0.40	0.04	-0.53	-0.21	-0.01	-2.12
EDNRB	0.52	0.98	-0.57	0.22	0.29	0.32	-4.44
Nr4a1	0.47	0.46	-0.25	0.44	0.28	-0.07	-0.01
PTGS2	-3.61	0.49	-4.41	-0.58	-2.03	-2.17	3.48
B2M	-0.16	0.27	0.01	0.30	0.10	0.90	-1.84
LIF	-0.05	-0.05	0.17	-0.21	-0.03	-0.02	0.78
ActG2	-1.05	-2.20	-0.74	-2.39	-1.60	-2.15	2.08
Il8	-1.37	2.01	-2.14	0.79	-0.18	-0.28	1.94
EREG	0.11	1.67	-0.02	1.94	0.92	0.06	2.39
CXCL1	-1.21	1.86	-1.28	0.97	0.09	-0.69	1.14
Star	0.77	-0.10	0.01	-0.50	0.05	-0.68	0.23
SFN	0.66	-0.22	0.60	0.00	0.26	-1.06	-4.18
ITGa2	-0.62	0.03	-0.14	-0.66	-0.35	0.06	2.28
CLDN4	0.09	-0.10	0.50	-0.28	0.05	1.04	-3.47
THBD	-1.30	0.74	-0.20	0.57	-0.05	-1.31	-1.38
LAMB4	0.74	-0.27	0.14	-0.29	0.08	-0.03	-0.13
Spin2a	1.50	-0.12	0.17	-3.30	-0.44	0.66	0.52
NR4a2	0.42	4.99	-0.86	0.54	1.27	1.89	0.52
Jak2	-0.07	0.47	-0.03	0.34	0.18	0.25	-1.13
SATb1	0.48	-0.67	1.84	-0.78	0.22	0.71	-1.13
Sox4	-1.11	-0.46	0.06	-0.33	-0.46	2.01	-1.03
HIVEP1	-1.77	0.99	-0.91	0.84	-0.21	0.43	-0.14
Psg8	-0.97	-2.09	0.88	0.41	-0.44	-0.89	0.93
Lacc1	0.56	-0.24	0.67	-0.38	0.15	0.77	-1.84
Neat1	1.91	0.06	0.64	1.42	1.01	0.96	-1.35
Tp53	-0.25	-0.67	0.03	-0.57	-0.36	-0.47	2.35
Rit2	0.14	-0.20	-0.62	0.34	-0.08	0.01	2.34
ELMO1	0.46	-0.64	0.51	-0.83	-0.13	0.02	-0.83
TGFA	0.22	-0.48	0.00	-0.87	-0.28	-0.28	0.96
Malat1	1.29	-0.66	0.35	0.26	0.31	0.18	-0.05
FAM180a	-0.57	2.46	-0.78	2.47	0.90	1.10	0.60
FADS3	-0.52	0.31	-0.71	0.08	-0.21	-1.33	-0.05
PRSS1	0.35	-0.41	0.69	-1.64	-0.25	0.00	4.86
PREPL	0.44	0.82	0.08	0.82	0.54	0.35	0.75

Supplementary Table S7: Parameter values used for SeqMonk.

Parameter name	Value
Importing data	
Remove duplicate reads	no
Treat as HiC data	no
Min mapping quality	0
Split spliced reads	yes
Import introns rather than exons	no
Data type	Paired end
Pair distance cutoff (bp)	1000
Generating probes	
Type Feature	probe generator
Features to design around	mRNA
Split into subfeatures (exons)	no
Remove exact duplicates	no
Ignore feature strand information	no
Make probes	Over feature
Read count quantitation	
Count reads on strand	All reads
Corect for total read count	yes
Correct to what?	Per million reads
Count total only within probes	no
Correct for probe length	yes
Log transform count	no
Count duplicated reads only once	no
Only quantitate visible stores	no

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