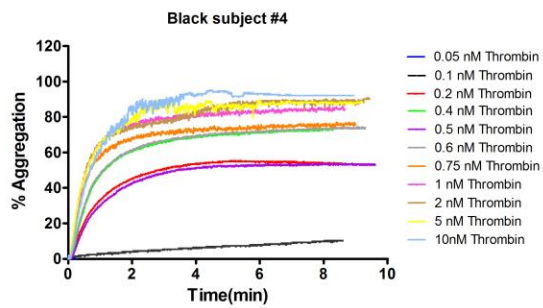
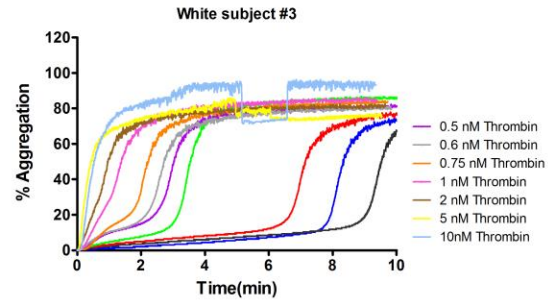
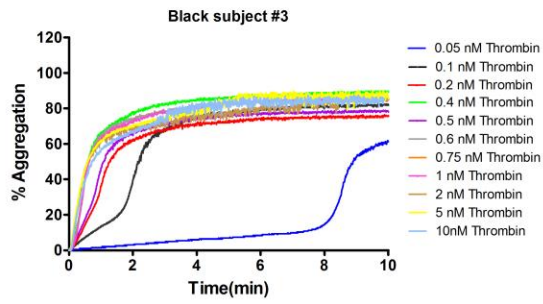
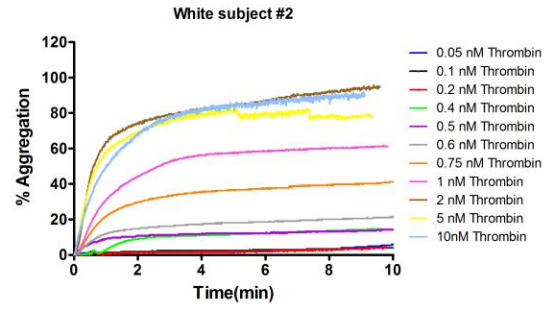
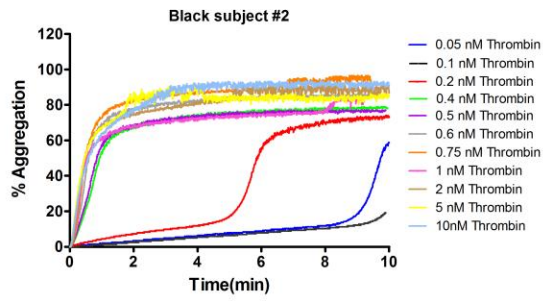
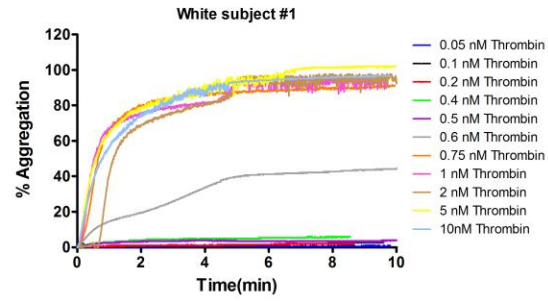
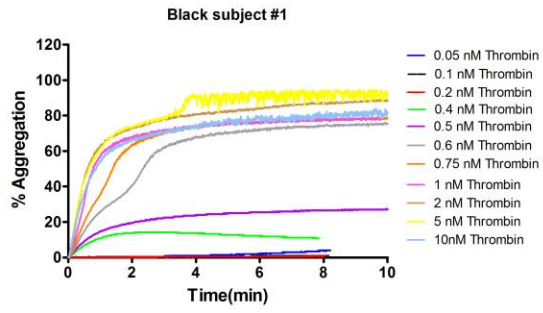


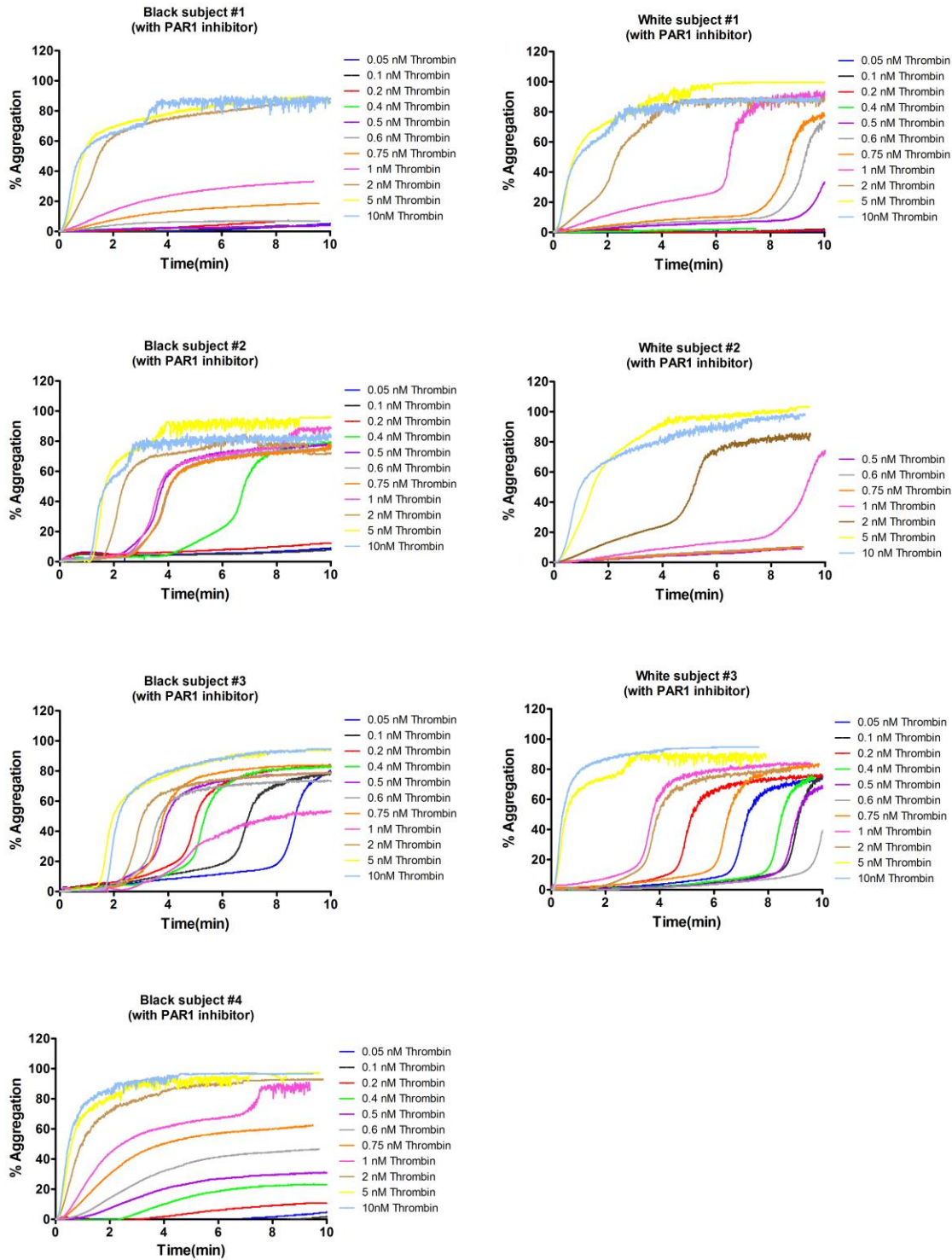
Racial Difference in Human Platelet PAR4 Reactivity Reflects Expression of *PCTP* and *miR-376c*

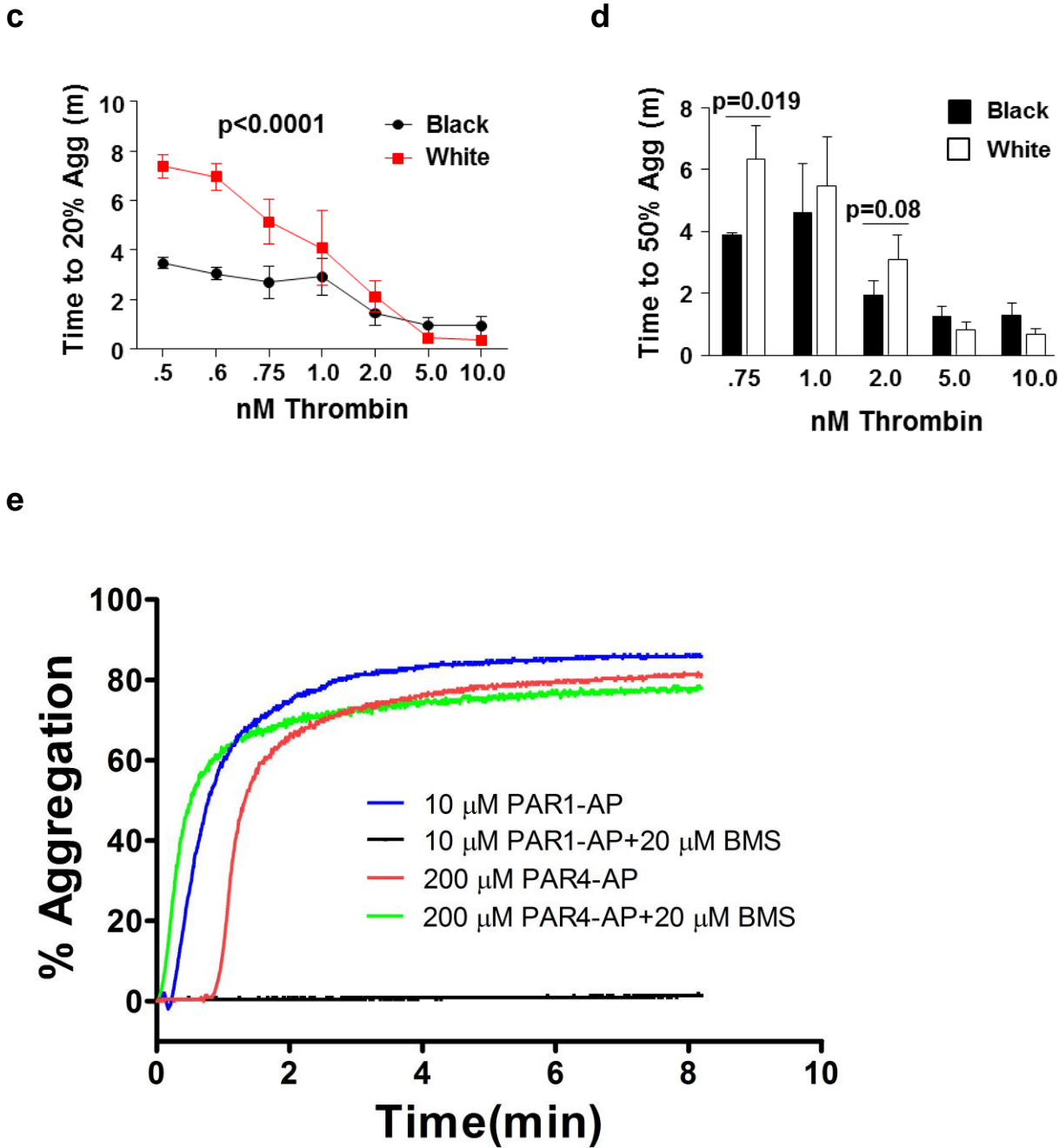
Leonard C. Edelstein¹, Lukas M. Simon², Raúl Teruel Montoya¹, Michael Holinstat¹, Edward S. Chen², Angela Bergeron³, Xianguo Kong¹, Srikanth Nagalla¹, Narla Mohandas⁴, David E. Cohen⁵, Jing-fei Dong⁶, Chad Shaw^{2,7*} and Paul F. Bray^{1*}

Supplementary Item & Number	Title or Caption
Supplementary Figure 1	Pilot study of racial differences in platelet response to thrombin.
Supplementary Figure 2	Probability density plots of all mRNAs and all miRNAs
Supplementary Figure 3	Affy Gene ST 1.0 array oligonucleotide probe level data by race.
Supplementary Figure 4	Effect of miR-376c transfection on related miRNAs.
Supplementary Figure 5	RT-PCR validation of miRNAs differentially expressed by race and identified by Nanostring technology.
Supplementary Table 1	Demographics and platelet parameters by race
Supplementary Table 2	Summary of light transmission aggregometry statistics in PRAX1.
Supplementary Table 3a	Set of mRNAs positively correlated with PAR4-mediated platelet reactivity.
Supplementary Table 3b	Set of mRNAs negatively correlated with PAR4-mediated platelet reactivity.
Supplementary Table 4	List of miRNAs differentially expressed by race.
Supplementary Table 5	List of miRNAs located in DLK1-DIO3.

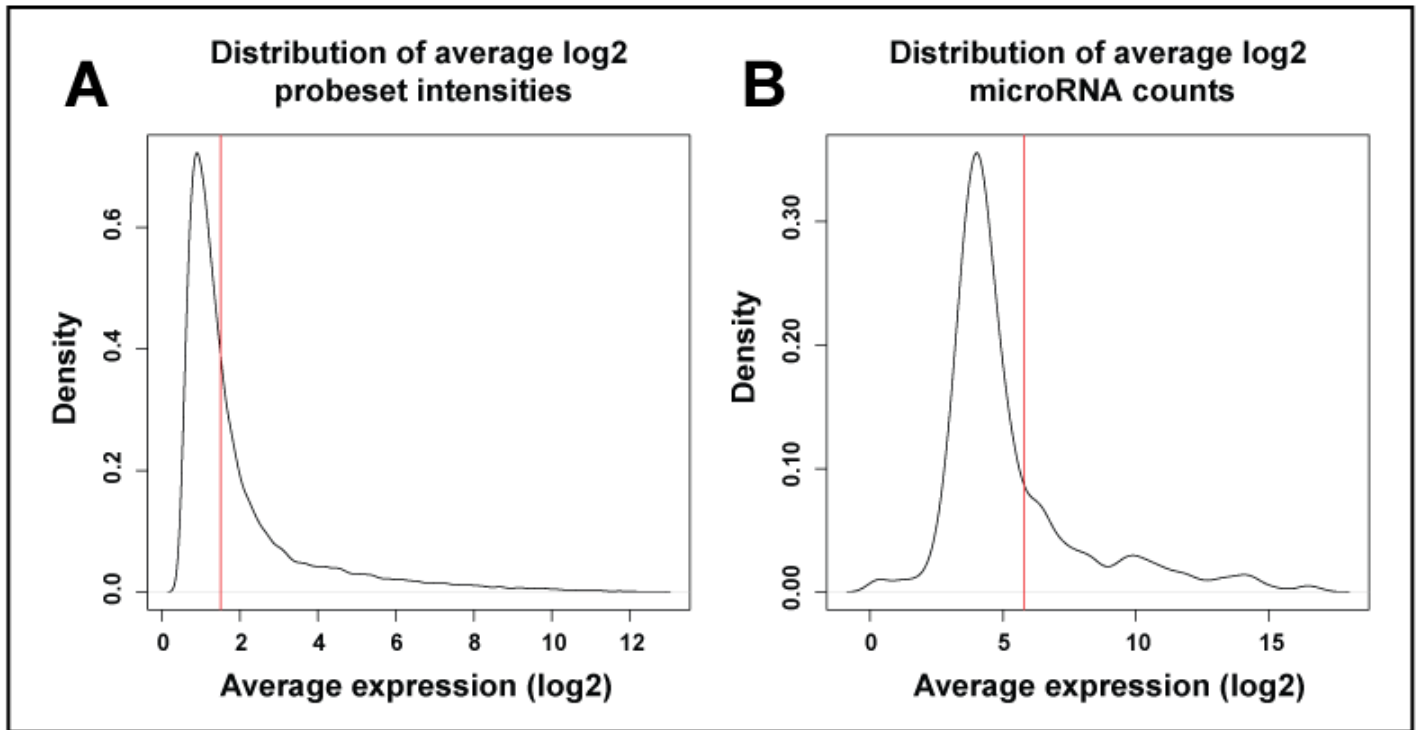
a



b



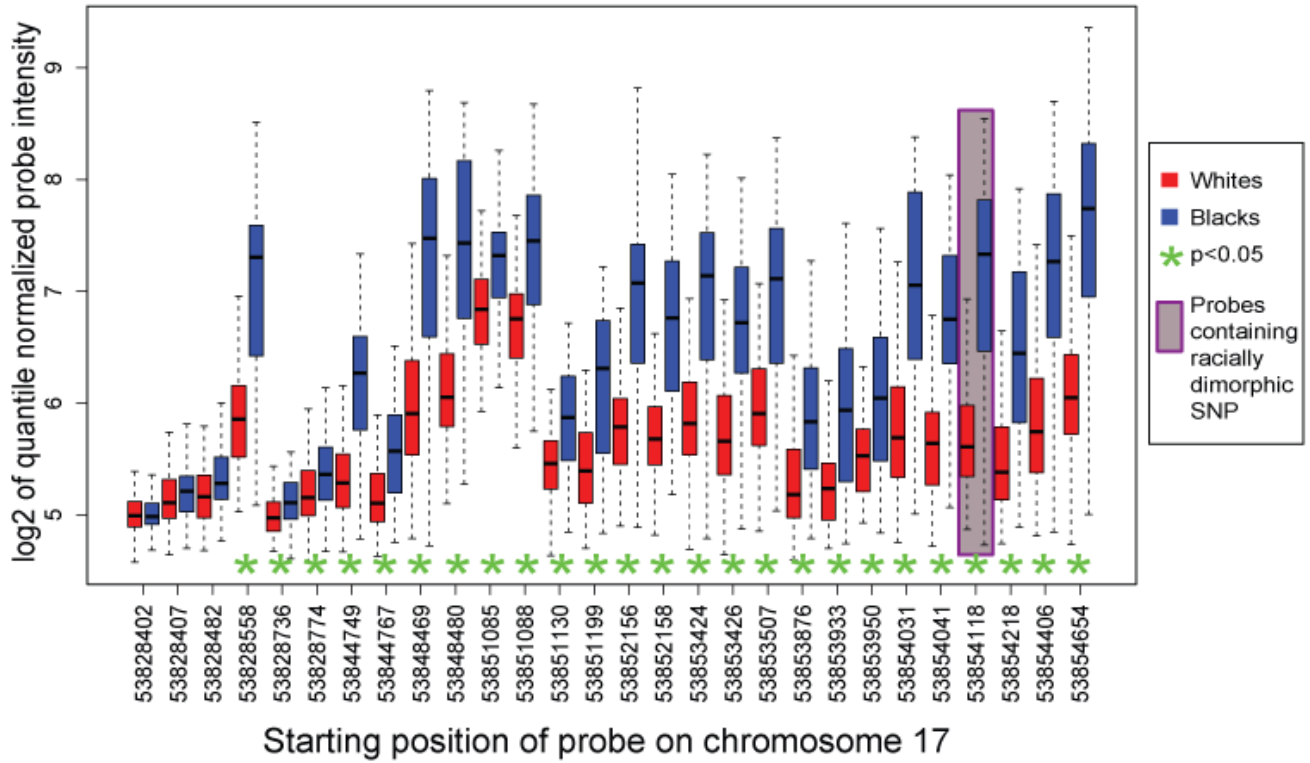
Supplementary Fig 1. Pilot study of racial differences in platelet response to thrombin. LTA was measured in washed platelets following addition of multiple concentrations of thrombin in the absence (a) or presence (b) of 20 μ M BMS-200261 (BMS, PAR1-specific antagonist) for 4 black subjects and 3 white subjects. (c,d) Cumulative quantitative results of (a) and (b) Time to both 20% (c) and 50% (d) aggregation was faster in black subjects than in white at low doses. Statistical tests: (c) 2-way ANOVA, (d) 2-sided t-test. (e) Representative LTA demonstrating BMS-200261 inhibits PAR1-AP, but not PAR4-AP mediated platelet aggregation using standard agonist concentrations to elicit maximal aggregation.



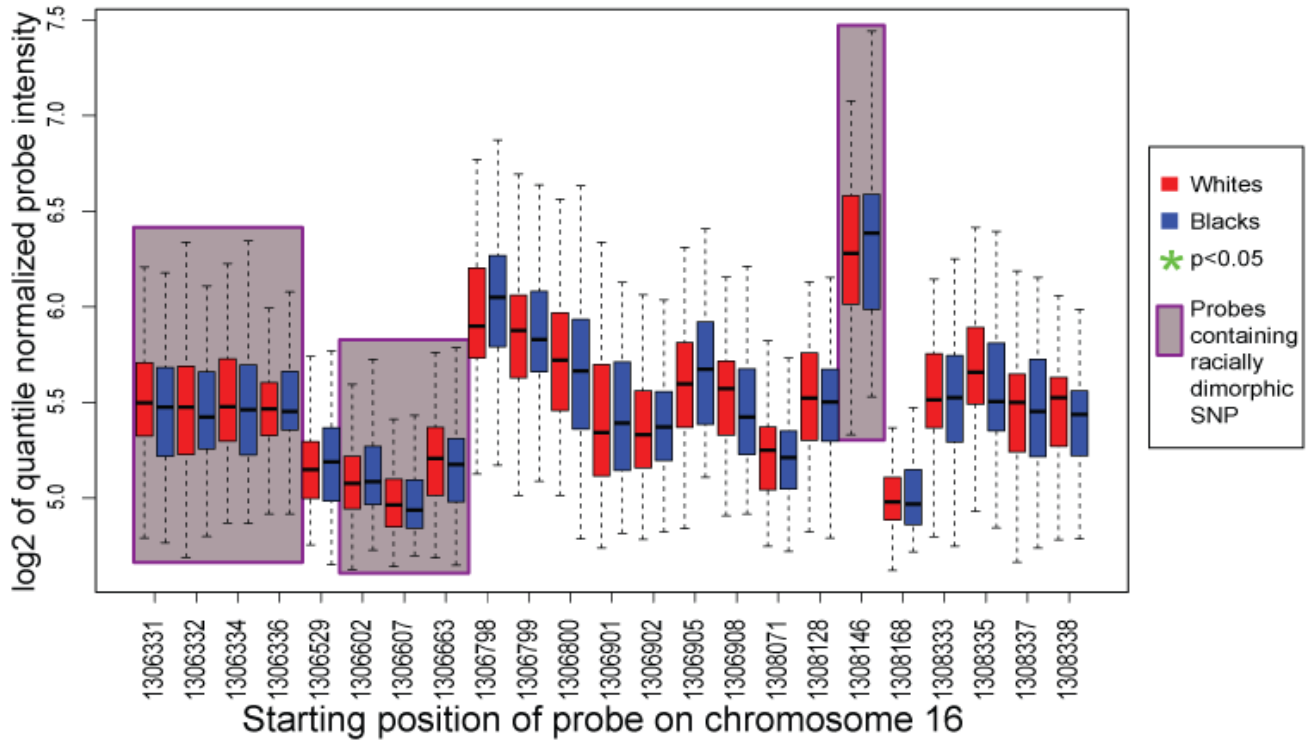
Supplementary Figure 2. Probability density plots of all mRNAs and miRNAs. Probability density plots of all mRNAs (Panel A) and all miRNAs (Panel B) plotted by the average log₂ expression. The vertical red line indicates the arbitrary threshold for the most abundantly expressed RNAs based on the shape of the curve. We defined “most commonly expressed” RNAs as those mRNAs expressed above 1.5 in at least 75% (115/154) of subjects and miRNAs expressed above 5.8 in at least 65% (100/154) of subjects.

A

PCTP probe-level intensities divided by race
Affy TranscriptID: 8008598

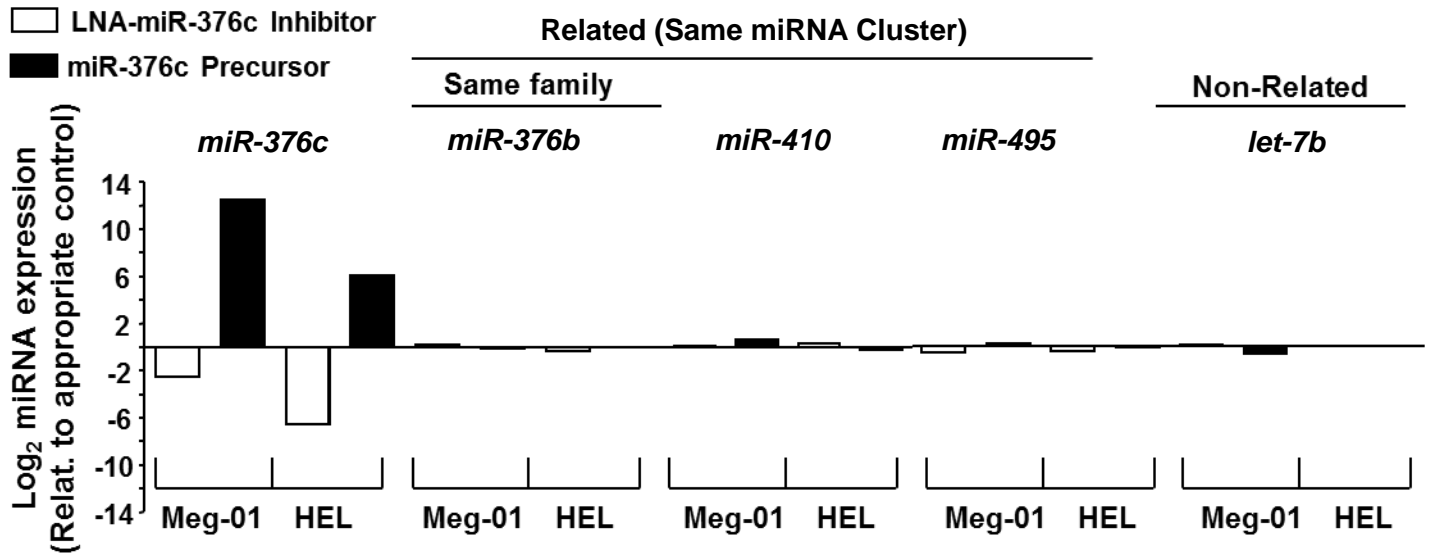
**B**

TPSD1 probe-level intensities divided by race
Affy TranscriptID: 7992191

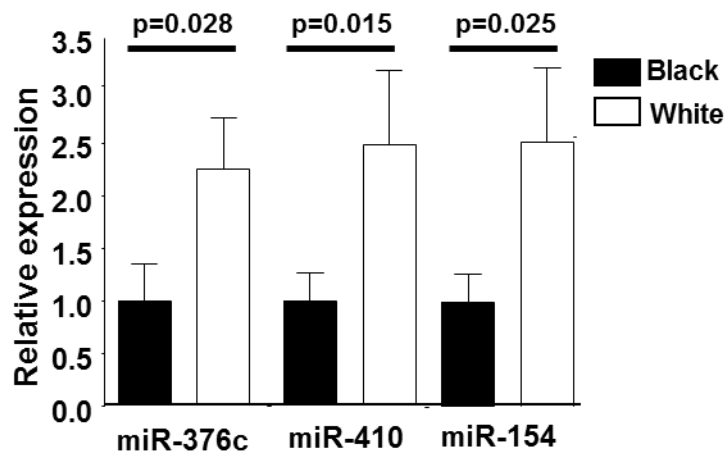


Supplementary Figure 3. Affy Gene ST 1.0 array oligonucleotide probe level data by race.

Panel **A** shows probe-level intensities for the probeset annotated to *PCTP*; panel **B** shows probe-level intensities for the probeset annotated to *TPSD1* (based on Affymetrix). Data for all black and white subjects for each individual oligo probe are shown in side-by-side boxplots, with whites denoted in red and blacks in blue. Oligo probes that harbor a racially dimorphic SNV are contained within the grey rectangles in the plot. The data in panel **A** demonstrate that probes containing racially dimorphic SNVs show a similar level of racial difference compared to what is observed for almost all of the other probes that are not racially dimorphic. Similar results were obtained for the other 160 probesets that were DE by PAR4. In addition, panel **B** shows an example probeset not differentially expressed between races but containing multiple racially dimorphic SNVs with no differential intensities between any of the probes. Thus the differences in racially dimorphic SNV variation do not drive the gene-level racial difference we observed. See **Supplementary Note 1**.



Supplementary Figure 4. Effect of *miR-376c* transfection on related miRNAs. Transfection of *miR-376c* precursor or LNA inhibitor resulted in the expected alterations in *miR-376c* levels while not affecting the level of miRNAs in the same family (*miR-376b*), genetic locus (*miR-410* and *miR-495*), or other unrelated miRNAs (*let-7b*).



Supplementary Figure 5. RT-PCR validation of miRNAs differentially expressed by race and identified by Nanostring technology. Y-axis shows expression relative to platelet RNA from black subjects. P-values calculated by t-test.

Supplementary Table 1. Demographics and platelet parameters by race

Characteristic	Black (n=70)	White (n=84)	P-Value
Age, years	29.7 ± 7.2	27.7 ± 5.8	0.060
% Female	55.7	46.4	0.262
Body mass index, kg/m ²	26.24 ± 5.9	24.53 ± 3.96	0.041
% with hypertension	4.2	1.1	0.330
% Current Smokers	4.2	5.9	0.729
Platelet count, (10 ⁴ /μl)	222 ± 74.3	198 ± 49.5	0.025
Mean platelet fL	7.27 ± 0.77	7.26 ± 0.70	0.921
Fibrinogen (mg/dL)	250 ± 52.9	251 ± 55.1	0.944
VWF activity (%)	108 ± 45.3	99 ± 35.6	0.176

Data are expressed as mean±SD or percentages.

Statistical tests were 2-sided t-test for numerical variables and Fisher's Exact for nominal parameters.

Supplementary Table 2. Summary of light transmission aggregometry statistics in PRAX1.

Agonist	Black		White		Fold difference (Black/White)	p Value (Mann Whitney)
	Mean*	SEM	Mean*	SEM		
500 µg/ml AA	86.57	1.35	87.21	1.28	0.99	0.522
4 µM ADP	40.89	3.32	45.04	3.21	0.91	0.378
10 ng/ml CRP	70.90	4.03	74.39	3.70	0.95	0.262
20 ng/ml CRP	91.94	1.91	88.50	2.68	1.04	0.733
500 ng/ml anti-CD9	36.66	4.09	40.50	4.09	0.91	0.664
750 ng/ml anti-CD9	55.16	4.79	58.12	4.48	0.95	0.833
2000 ng/ml anti-CD9	70.76	4.57	62.36	4.59	1.13	0.308
1 µM PAR1-AP	14.96	3.33	17.05	3.20	0.88	0.954
2 µM PAR1-AP	76.91	3.07	79.89	2.11	0.96	0.954
50 µM PAR4-AP	40.77	4.91	10.68	2.82	3.82	<0.0001
75 µM PAR4-AP	79.04	3.38	55.63	4.21	1.42	<0.0001

*Percent maximal aggregation

Supplementary Table 3a. Set of mRNAs positively correlated with PAR4-mediated platelet reactivity.

Using a simple linear regression at FDR $q < .25$; this FDR cutoff corresponds to a maximum p-value of 0.0028. The table shows 93 mRNAs in the same order as in the heatmap in Fig. 3a. Symbols were obtained using Affymetrix probeset annotation file. The p-value for race describes the T-test of black vs white. The coefficient and p-value for PAR4 describe the correlation between the PAR4 agonist score and mRNA expression across 154 individuals. The q-values represent the p-value accounting for multiple testing using the Benjamini & Hochberg False Discovery Rate (1995).

	Affymetrix Transcript Cluster ID	Symbol	Mean	Race p- value	Race q- value	PAR4 Coefficient	PAR4 p- value	PAR4 q- value	Significant by race
1	8008598	PCTP	4.87	1.00E-23	9.98E-20	0.31	3.49E-08	3.46E-04	yes
2	8172035	DYNLT3	6.62	2.19E-13	5.43E-10	0.35	1.13E-07	5.59E-04	yes
3	8116859	TMEM14C	2.82	1.01E-10	4.75E-08	0.57	3.78E-06	1.25E-02	yes
4	8051464	HEATR5B	2.77	1.16E-03	1.66E-02	1.01	1.41E-05	2.44E-02	yes
5	8124307	CMAHP	4.08	3.88E-09	1.13E-06	0.63	1.65E-05	2.44E-02	yes
6	8084173	ATP11B	5.08	4.86E-12	4.83E-09	0.45	1.72E-05	2.44E-02	yes
7	8045860	PKP4	3.14	3.33E-08	6.24E-06	0.58	2.75E-05	3.41E-02	yes
8	8019954	FLJ35776	3.59	1.28E-06	1.25E-04	0.59	4.05E-05	4.43E-02	yes
9	7978970	CDKL1	2.33	2.05E-02	1.11E-01	1.09	4.87E-05	4.43E-02	yes
10	7975863	C14orf118	4.21	3.35E-03	3.44E-02	1.03	4.91E-05	4.43E-02	yes
11	8068593	ETS2	3.11	1.00E-10	4.75E-08	0.51	6.46E-05	5.30E-02	yes
12	8066402	C20orf111	2.18	1.32E-04	3.72E-03	0.87	6.94E-05	5.30E-02	yes
13	8053551	REEP1	2.64	2.30E-11	1.63E-08	0.38	8.70E-05	6.17E-02	yes
14	7924526	TP53BP2	2.64	2.12E-06	1.82E-04	0.64	9.52E-05	6.30E-02	yes
15	7948656	FTH1	9.44	5.74E-06	3.70E-04	1.65	1.14E-04	7.05E-02	yes
16	8065710	E2F1	3.53	1.98E-06	1.74E-04	0.48	1.22E-04	7.12E-02	yes
17	7937378	PTDSS2	1.89	4.72E-04	8.71E-03	1.24	1.43E-04	7.86E-02	yes
18	7978538	ARHGAP5-AS1	2.57	5.15E-06	3.34E-04	0.56	1.71E-04	8.62E-02	yes
19	8139057	ELMO1	5.63	2.13E-06	1.82E-04	0.64	1.74E-04	8.62E-02	yes
20	8067011	ADNP	3.85	1.04E-03	1.54E-02	0.76	2.53E-04	1.06E-01	yes
21	8001876	NAE1	4.05	1.62E-01	3.89E-01	0.52	2.61E-04	1.06E-01	no
22	8154563	ACER2	4.36	3.28E-05	1.34E-03	0.60	2.63E-04	1.06E-01	yes
23	8026193	C19orf53	4.59	3.37E-03	3.45E-02	0.85	2.77E-04	1.06E-01	yes
24	7905519	LCE1E	3.01	1.09E-02	7.30E-02	0.88	2.77E-04	1.06E-01	yes
25	8110589	CNOT6	2.86	1.92E-02	1.06E-01	0.87	2.94E-04	1.06E-01	yes
26	7900609	ERMAP	1.74	9.12E-03	6.44E-02	1.22	3.38E-04	1.06E-01	yes
27	8171481	AP1S2	4.63	1.27E-02	8.07E-02	0.82	3.59E-04	1.06E-01	yes
28	8117608	HIST1H2AL	3.22	1.41E-07	2.11E-05	0.67	3.77E-04	1.06E-01	yes
29	7979691	---	3.17	3.28E-09	1.02E-06	0.18	3.81E-04	1.06E-01	yes
30	8123644	TUBB2A	3.30	7.64E-11	4.26E-08	0.17	3.84E-04	1.06E-01	yes
31	7975747	DLST	4.29	2.93E-04	6.35E-03	0.55	3.88E-04	1.06E-01	yes
32	8123678	PXDC1	2.72	2.76E-05	1.17E-03	0.39	3.92E-04	1.06E-01	yes
33	8117580	HIST1H2AI	4.95	2.78E-06	2.15E-04	0.44	3.95E-04	1.06E-01	yes
34	8088803	EIF4E3	4.85	7.72E-11	4.26E-08	0.27	4.08E-04	1.07E-01	yes

35	8095360	GCOM2	1.86	6.45E-05	2.22E-03	0.76	4.31E-04	1.10E-01	yes
36	8168843	RPL36A	4.38	3.22E-12	3.56E-09	0.31	5.19E-04	1.29E-01	yes
37	7920100	THEM5	2.70	2.68E-08	5.12E-06	0.73	5.64E-04	1.37E-01	yes
38	8006239	NF1	1.78	8.15E-07	8.99E-05	0.76	5.97E-04	1.40E-01	yes
39	7897561	KIF1B	3.01	3.67E-06	2.62E-04	0.47	6.32E-04	1.40E-01	yes
40	7958346	C12orf23	3.06	9.44E-03	6.59E-02	0.73	6.33E-04	1.40E-01	yes
41	8002975	CDYL2	2.20	6.90E-09	1.71E-06	0.48	6.75E-04	1.46E-01	yes
42	7983228	MAP1A	4.77	4.19E-04	8.02E-03	0.42	6.99E-04	1.47E-01	yes
43	7999478	TXNDC11	2.11	4.26E-03	4.00E-02	1.28	7.09E-04	1.47E-01	yes
44	8000791	YPEL3	5.57	9.14E-09	2.16E-06	0.66	7.62E-04	1.48E-01	yes
45	8164428	TRUB2	2.94	8.32E-10	3.44E-07	0.57	7.65E-04	1.48E-01	yes
46	8116651	---	4.52	1.98E-12	2.46E-09	0.26	8.15E-04	1.50E-01	yes
47	8106660	RASGRF2	3.09	6.34E-09	1.61E-06	0.49	8.35E-04	1.51E-01	yes
48	7946807	RPL36A	5.65	1.65E-12	2.35E-09	0.29	8.52E-04	1.51E-01	yes
49	7955441	METTL7A	2.60	1.33E-08	2.81E-06	0.37	9.34E-04	1.61E-01	yes
50	8014825	FBXL20	2.97	3.12E-04	6.58E-03	0.74	9.42E-04	1.61E-01	yes
51	8116653	TUBB2A	5.24	1.30E-12	2.16E-09	0.13	1.00E-03	1.63E-01	yes
52	8116649	TUBB2A	5.24	1.30E-12	2.16E-09	0.13	1.00E-03	1.63E-01	yes
53	7971620	KPNA3	5.22	4.36E-01	6.68E-01	0.81	1.09E-03	1.68E-01	no
54	8000706	CDIPT	3.77	1.97E-03	2.37E-02	0.57	1.12E-03	1.68E-01	yes
55	8139712	VOPP1	3.31	1.31E-03	1.80E-02	0.77	1.13E-03	1.68E-01	yes
56	7897172	---	4.71	4.11E-07	4.98E-05	0.61	1.13E-03	1.68E-01	yes
57	7924499	TLR5	2.84	4.60E-10	1.99E-07	0.65	1.22E-03	1.74E-01	yes
58	8066051	NDRG3	4.16	5.33E-03	4.58E-02	0.44	1.24E-03	1.74E-01	yes
59	8156199	DAPK1	2.03	1.19E-04	3.44E-03	0.73	1.24E-03	1.74E-01	yes
60	8088813	PROK2	5.60	9.80E-15	4.87E-11	0.20	1.24E-03	1.74E-01	yes
61	8121578	NT5DC1	2.28	2.29E-05	1.04E-03	0.59	1.28E-03	1.77E-01	yes
62	8138361	RPL36A	3.76	1.93E-11	1.49E-08	0.26	1.32E-03	1.80E-01	yes
63	7994981	ORAI3	3.52	2.76E-07	3.61E-05	0.78	1.36E-03	1.82E-01	yes
64	7925531	AKT3	7.21	2.77E-04	6.11E-03	0.74	1.41E-03	1.86E-01	yes
65	8076465	POLDIP3	2.68	1.83E-02	1.03E-01	0.78	1.46E-03	1.88E-01	yes
66	8169044	TCEAL3	2.22	3.52E-02	1.57E-01	0.49	1.66E-03	2.07E-01	yes
67	7943760	SIK2	2.30	5.36E-05	1.91E-03	0.87	1.70E-03	2.07E-01	yes
68	7905700	UBAP2L	3.22	2.75E-02	1.34E-01	0.90	1.72E-03	2.07E-01	yes
69	8141016	TFPI2	2.25	1.30E-04	3.67E-03	0.52	1.72E-03	2.07E-01	yes
70	8124388	HIST1H3B	6.52	3.43E-09	1.03E-06	0.35	1.82E-03	2.15E-01	yes
71	8117382	HIST1H2BD	7.40	2.06E-05	9.73E-04	0.39	1.92E-03	2.17E-01	yes
72	8011713	CXCL16	4.19	2.49E-06	1.96E-04	0.33	1.93E-03	2.17E-01	yes
73	8145977	PLEKHA2	2.30	2.32E-06	1.89E-04	0.45	1.97E-03	2.17E-01	yes
74	8119067	KCTD20	6.73	4.20E-02	1.74E-01	0.70	2.07E-03	2.18E-01	yes
75	7974229	KLHDC2	2.89	3.98E-03	3.85E-02	0.58	2.08E-03	2.18E-01	yes
76	7977584	TMEM55B	1.95	2.64E-01	5.09E-01	0.85	2.08E-03	2.18E-01	no
77	8063211	NCOA3	5.83	2.18E-04	5.30E-03	0.55	2.09E-03	2.18E-01	yes
78	8052149	PSME4	3.71	1.78E-02	1.01E-01	0.59	2.20E-03	2.24E-01	yes

79	7918657	PTPN22	2.96	1.55E-01	3.79E-01	0.77	2.21E-03	2.24E-01	no
80	8082350	MCM2	1.72	3.67E-03	3.66E-02	0.97	2.25E-03	2.26E-01	yes
81	7970546	EFHA1	2.19	9.48E-02	2.85E-01	0.60	2.32E-03	2.30E-01	no
82	7924773	CDC42BPA	3.19	1.16E-01	3.19E-01	0.65	2.40E-03	2.34E-01	no
83	8130474	SERAC1	2.28	3.24E-01	5.69E-01	0.70	2.41E-03	2.34E-01	no
84	8156263	SPIN1	2.93	3.96E-03	3.84E-02	0.62	2.45E-03	2.34E-01	yes
85	7919305	PRKAB2	4.23	8.49E-03	6.16E-02	0.36	2.45E-03	2.34E-01	yes
86	8117535	HIST1H2AG	8.21	1.11E-05	6.23E-04	0.51	2.48E-03	2.34E-01	yes
87	8011747	SLC25A11	1.77	1.37E-02	8.45E-02	0.70	2.55E-03	2.34E-01	yes
88	8170326	FMR1	2.90	2.67E-02	1.31E-01	0.74	2.56E-03	2.34E-01	yes
89	7939676	ATG13	2.56	5.14E-02	1.97E-01	0.62	2.56E-03	2.34E-01	yes
90	8155234	ZCCHC7	2.90	1.84E-03	2.25E-02	0.80	2.57E-03	2.34E-01	yes
91	7920912	UBQLN4	2.25	8.27E-03	6.06E-02	1.14	2.74E-03	2.44E-01	yes
92	8175393	ARHGEF6	2.68	1.65E-01	3.91E-01	0.55	2.75E-03	2.44E-01	no
93	8015946	C17orf65	3.01	3.28E-06	2.39E-04	0.54	2.82E-03	2.48E-01	yes

Supplementary Table 3b. Set of mRNAs negatively correlated with PAR4-mediated platelet reactivity.

Set of 20 mRNAs negatively correlated with PAR4-mediated platelet reactivity using a simple linear regression at FDR $q < .25$; this FDR cutoff corresponds to a maximum p-value of 0.0028. Symbols were obtained using Affymetrix probeset annotation file. The p-value for race describes the T-test of black vs white. The coefficient and p-value describe the correlation between the PAR4 agonist score and mRNA expression across 154 individuals. The q-value represents the p-value adjusted for multiple testing using the Benjamini & Hochberg False Discovery Rate (1995).

	Affymetrix Transcript Cluster ID	Symbol	Mean	Race p-value	Race q-value	PAR4 Coefficient	PAR4 p-value	PAR4 q-value	Significant by race
1	8147132	CA2	10.26	1.77E-10	7.97E-08	-0.60	6.77E-06	1.68E-02	yes
2	8042503	MXD1	6.19	3.02E-06	2.27E-04	-0.48	2.20E-04	1.04E-01	yes
3	8135319	---	1.89	2.39E-01	4.83E-01	-1.13	3.30E-04	1.06E-01	no
4	7958202	CHST11	3.08	7.40E-01	8.70E-01	-0.54	3.41E-04	1.06E-01	no
5	8000184	IGSF6	2.07	4.87E-01	7.08E-01	-0.42	6.17E-04	1.40E-01	no
6	8149137	DEFA3	4.56	3.23E-02	1.49E-01	-0.13	7.92E-04	1.48E-01	yes
7	8149126	DEFA3	4.56	3.23E-02	1.49E-01	-0.13	7.92E-04	1.48E-01	yes
8	8149116	DEFA3	4.56	3.23E-02	1.49E-01	-0.13	7.92E-04	1.48E-01	yes
9	7922219	SELL	2.91	3.08E-01	5.54E-01	-0.25	1.00E-03	1.63E-01	no
10	7912252	RN5S40	1.83	1.35E-11	1.22E-08	-0.65	1.02E-03	1.63E-01	yes
11	8127072	GSTA1	3.05	1.87E-13	5.43E-10	-0.19	1.10E-03	1.68E-01	yes
12	8018305	HN1	1.74	6.71E-01	8.31E-01	-0.90	1.45E-03	1.88E-01	no
13	7961693	LDHB	6.18	5.15E-04	9.33E-03	-0.40	1.58E-03	2.01E-01	yes
14	7992811	MMP25	1.91	1.46E-01	3.66E-01	-0.74	1.73E-03	2.07E-01	no
15	8171203	---	1.91	1.12E-03	1.62E-02	-0.57	1.91E-03	2.17E-01	yes
16	8128394	PNISR	1.77	2.76E-01	5.21E-01	-0.68	1.95E-03	2.17E-01	no
17	7973371	C14orf119	4.38	1.16E-08	2.63E-06	-0.45	1.97E-03	2.17E-01	yes
18	7961390	HEBP1	3.83	1.76E-05	8.81E-04	-0.28	2.05E-03	2.18E-01	yes
19	8070912	SLC19A1	1.83	2.04E-01	4.43E-01	-1.04	2.19E-03	2.24E-01	no
20	7934906	ACTA2	1.97	3.86E-02	1.66E-01	-0.69	2.69E-03	2.43E-01	yes
1	8147132	CA2	10.26	1.77E-10	7.97E-08	-0.60	6.77E-06	1.68E-02	yes
2	8042503	MXD1	6.19	3.02E-06	2.27E-04	-0.48	2.20E-04	1.04E-01	yes
3	8135319	---	1.89	2.39E-01	4.83E-01	-1.13	3.30E-04	1.06E-01	no
4	7958202	CHST11	3.08	7.40E-01	8.70E-01	-0.54	3.41E-04	1.06E-01	no
5	8000184	IGSF6	2.07	4.87E-01	7.08E-01	-0.42	6.17E-04	1.40E-01	no
6	8149137	DEFA3	4.56	3.23E-02	1.49E-01	-0.13	7.92E-04	1.48E-01	yes
7	8149126	DEFA3	4.56	3.23E-02	1.49E-01	-0.13	7.92E-04	1.48E-01	yes
8	8149116	DEFA3	4.56	3.23E-02	1.49E-01	-0.13	7.92E-04	1.48E-01	yes
9	7922219	SELL	2.91	3.08E-01	5.54E-01	-0.25	1.00E-03	1.63E-01	no
10	7912252	RN5S40	1.83	1.35E-11	1.22E-08	-0.65	1.02E-03	1.63E-01	yes
11	8127072	GSTA1	3.05	1.87E-13	5.43E-10	-0.19	1.10E-03	1.68E-01	yes
12	8018305	HN1	1.74	6.71E-01	8.31E-01	-0.90	1.45E-03	1.88E-01	no
13	7961693	LDHB	6.18	5.15E-04	9.33E-03	-0.40	1.58E-03	2.01E-01	yes
14	7992811	MMP25	1.91	1.46E-01	3.66E-01	-0.74	1.73E-03	2.07E-01	no

15	8171203	---	1.91	1.12E-03	1.62E-02	-0.57	1.91E-03	2.17E-01	yes
16	8128394	PNISR	1.77	2.76E-01	5.21E-01	-0.68	1.95E-03	2.17E-01	no
17	7973371	C14orf119	4.38	1.16E-08	2.63E-06	-0.45	1.97E-03	2.17E-01	yes
18	7961390	HEBP1	3.83	1.76E-05	8.81E-04	-0.28	2.05E-03	2.18E-01	yes
19	8070912	SLC19A1	1.83	2.04E-01	4.43E-01	-1.04	2.19E-03	2.24E-01	no
20	7934906	ACTA2	1.97	3.86E-02	1.66E-01	-0.69	2.69E-03	2.43E-01	yes

Supplementary Table 4. List of miRNAs differentially expressed by race.

Probe*	DLK1-DIO3 locus	White			Black			Race p-value [†]	Race q-value [‡]
		Mean	Range	StDev	Mean	Range	StDev		
hsa-miR-431	Yes	8.94	7-10.4	0.81	8.18	4.67-9.94	1.14	4.16E-06	2.94E-04
hsa-miR-410	Yes	7.71	6.12-9.3	0.76	7.08	4.23-8.82	0.93	6.72E-06	2.94E-04
hsa-miR-487a	Yes	7.15	5.26-9.1	0.84	6.49	3.93-8.4	0.92	7.32E-06	2.94E-04
hsa-miR-337-3p	Yes	8.47	6.35-10.05	0.8	7.77	4.74-9.34	1.08	7.73E-06	2.94E-04
hsa-miR-495	Yes	9.68	7.9-11.15	0.76	9.04	6.32-10.55	0.97	8.39E-06	2.94E-04
hsa-miR-377	Yes	10.41	8.19-11.95	0.79	9.75	6.69-11.38	1	9.91E-06	2.94E-04
hsa-miR-99a	No	6.3	5.49-7.41	0.41	5.96	4.4-6.71	0.54	1.65E-05	3.38E-04
hsa-miR-485-3p	Yes	6.85	0.01-11.4	2.88	4.6	0.03-8.83	3.43	1.78E-05	3.38E-04
hsa-miR-450a	No	7.12	5.3-8.08	0.52	6.69	5.22-8.46	0.69	2.00E-05	3.38E-04
hsa-miR-655	Yes	6.69	5.73-7.75	0.45	6.41	5.6-7.23	0.36	2.25E-05	3.38E-04
hsa-miR-154	Yes	8.73	6.54-10.71	0.75	8.22	6.52-9.38	0.68	2.26E-05	3.38E-04
hsa-miR-29a	No	11.48	10.72-12.39	0.36	11.21	10.21-12.13	0.4	2.28E-05	3.38E-04
hsa-miR-543	Yes	7.75	6.08-9.15	0.79	7.18	5.43-8.89	0.87	3.37E-05	4.55E-04
hsa-miR-136	Yes	10.06	7.77-12.03	1	9.31	5.97-11.43	1.17	3.68E-05	4.55E-04
hsa-miR-496	Yes	6.93	5.49-8.39	0.68	6.44	4.71-7.75	0.76	3.84E-05	4.55E-04
hsa-miR-369-3p	Yes	9.46	7.34-10.98	0.85	8.8	6.02-10.64	1.09	4.67E-05	5.20E-04
hsa-miR-150	No	6.18	5.1-7.48	0.43	6.5	5.61-8.56	0.55	9.14E-05	9.57E-04
hsa-miR-574-5p	No	6.29	5.34-7.2	0.38	6.56	5.35-7.59	0.47	1.39E-04	1.38E-03
hsa-miR-376c	Yes	10	7.69-11.67	0.87	9.37	6.19-11.11	1.12	1.47E-04	1.38E-03
hsa-miR-539	Yes	6.26	4.35-7.9	0.64	5.85	4.23-6.86	0.65	1.61E-04	1.43E-03
hsa-miR-379	Yes	7.4	5.6-8.82	0.7	6.96	5.15-8.35	0.75	1.84E-04	1.56E-03
hsa-miR-625	No	5.93	5-7.41	0.53	6.25	4.95-7.67	0.54	2.63E-04	2.13E-03
hsa-miR-656	Yes	6.34	4.58-7.68	0.75	5.86	3.9-7.33	0.83	2.84E-04	2.20E-03
hsa-miR-337-5p	Yes	6.97	3.35-8.63	0.84	6.47	4.74-7.87	0.82	3.04E-04	2.26E-03
hsa-miR-23b	No	10.04	9.38-10.55	0.28	10.24	9.05-11.03	0.39	3.26E-04	2.32E-03
hsa-miR-223	No	16.93	16.54-17.36	0.16	16.84	16.48-17.27	0.16	9.48E-04	6.49E-03

hsa-miR-382	Yes	6.56	4.42-8.71	0.92	6.04	3.93-8.29	1.02	1.06E-03	6.98E-03
hsa-miR-125b	No	8.21	6.1-9.63	0.61	7.88	6.22-8.88	0.64	1.26E-03	7.98E-03
hsa-miR-21	No	14.8	14.07-15.44	0.3	14.96	13.93-15.47	0.32	1.33E-03	8.15E-03
hsa-miR-432	Yes	6.27	4.35-7.64	0.7	5.87	4.05-7.51	0.83	1.40E-03	8.31E-03
hsa-miR-487b	Yes	8.55	6.5-10.29	0.87	8.06	5.34-9.58	1.04	2.02E-03	1.16E-02
hsa-miR-145	No	9.64	7.71-11.55	0.86	10.07	8.23-11.98	0.84	2.30E-03	1.28E-02
hsa-miR-199b-5p	No	6.29	5.6-7.04	0.3	6.14	5.44-6.75	0.3	2.71E-03	1.46E-02
hsa-miR-376b	Yes	6.62	3.97-8.8	0.9	6.19	4.3-7.53	0.85	2.88E-03	1.51E-02
hsa-miR-590-5p	No	10.55	8.58-11.55	0.47	10.24	6.1-11.59	0.82	4.24E-03	2.16E-02
hsa-miR-376a	Yes	10.19	7.75-12.47	1	9.67	6.14-11.72	1.23	4.61E-03	2.28E-02
hsa-miR-221	No	13.39	12.4-14.23	0.3	13.26	12.16-13.89	0.27	5.25E-03	2.53E-02
hsa-miR-889	Yes	6.65	5.32-8.09	0.64	6.35	4.83-7.92	0.7	5.50E-03	2.57E-02
hsa-miR-301a	No	9.94	8.92-10.38	0.22	10.03	9.53-10.48	0.19	5.79E-03	2.64E-02
hsa-miR-101	No	11.38	9.32-12.36	0.61	11.63	10.16-12.58	0.5	5.98E-03	2.65E-02
hsa-miR-143	No	8.21	6.32-10.04	0.86	8.6	6.48-10.33	0.88	6.10E-03	2.65E-02
hsa-let-7c	No	7.42	6.64-8.17	0.38	7.25	6.25-8.2	0.45	8.49E-03	3.60E-02
hsa-miR-574-3p	No	7.9	5.78-9.59	0.76	8.25	5.84-9.75	0.86	8.87E-03	3.67E-02
hsa-miR-590-3p	No	7.17	5.86-7.89	0.4	6.95	4.32-7.96	0.63	1.04E-02	4.20E-02
hsa-miR-362-5p	No	5.97	5.38-6.53	0.23	6.08	5.23-6.82	0.32	1.25E-02	4.95E-02
hsa-miR-1308	No	7.92	6.67-8.97	0.43	7.76	6.57-8.43	0.37	1.49E-02	5.77E-02
hsa-miR-1908	No	6.38	5.28-7.11	0.33	6.25	5.09-6.86	0.31	1.67E-02	6.33E-02
hsa-miR-363	No	7.46	6.68-7.96	0.26	7.36	6.81-7.92	0.27	1.78E-02	6.62E-02
hsa-miR-107	No	10.9	9.37-12.15	0.58	11.11	9.77-12.38	0.64	3.15E-02	1.14E-01
hsa-miR-486-3p	No	6.79	6.34-7.47	0.24	6.71	6.06-7.26	0.27	3.45E-02	1.23E-01
hsa-miR-660	No	6.4	5.5-7.24	0.39	6.52	5.71-7.19	0.34	3.83E-02	1.34E-01
hsa-miR-424	No	6.58	4.98-8.47	0.68	6.32	4.32-9.12	0.92	3.90E-02	1.34E-01
hsa-miR-362-3p	No	6.66	5.51-7.48	0.35	6.77	5.35-7.3	0.32	4.55E-02	1.53E-01

* Annotation provided by Nanostring Technologies

† P-value is calculated using T-test.

‡ The q-value represents the p-value adjusted for multiple testing using the Benjamini & Hochberg False Discovery Rate (1995).

Supplementary Table 5. List of miRNAs located in *DLK1-DIO3*.

Probe*	White			Black			Race p-value [†]	Race q-value [‡]
	Mean	Range	StDev	Mean	Range	StDev		
hsa-miR-431	8.94	7-10.4	0.81	8.18	4.67-9.94	1.14	4.16E-06	2.94E-04
hsa-miR-410	7.71	6.12-9.3	0.76	7.08	4.23-8.82	0.93	6.72E-06	2.94E-04
hsa-miR-487a	7.15	5.26-9.1	0.84	6.49	3.93-8.4	0.92	7.32E-06	2.94E-04
hsa-miR-337-3p	8.47	6.35-10.05	0.8	7.77	4.74-9.34	1.08	7.73E-06	2.94E-04
hsa-miR-495	9.68	7.9-11.15	0.76	9.04	6.32-10.55	0.97	8.39E-06	2.94E-04
hsa-miR-377	10.41	8.19-11.95	0.79	9.75	6.69-11.38	1	9.91E-06	2.94E-04
hsa-miR-485-3p	6.85	0.01-11.4	2.88	4.6	0.03-8.83	3.43	1.78E-05	3.38E-04
hsa-miR-655	6.69	5.73-7.75	0.45	6.41	5.6-7.23	0.36	2.25E-05	3.38E-04
hsa-miR-154	8.73	6.54-10.71	0.75	8.22	6.52-9.38	0.68	2.26E-05	3.38E-04
hsa-miR-543	7.75	6.08-9.15	0.79	7.18	5.43-8.89	0.87	3.37E-05	4.55E-04
hsa-miR-136	10.06	7.77-12.03	1	9.31	5.97-11.43	1.17	3.68E-05	4.55E-04
hsa-miR-496	6.93	5.49-8.39	0.68	6.44	4.71-7.75	0.76	3.84E-05	4.55E-04
hsa-miR-369-3p	9.46	7.34-10.98	0.85	8.8	6.02-10.64	1.09	4.67E-05	5.20E-04
hsa-miR-376c	10	7.69-11.67	0.87	9.37	6.19-11.11	1.12	1.47E-04	1.38E-03
hsa-miR-539	6.26	4.35-7.9	0.64	5.85	4.23-6.86	0.65	1.61E-04	1.43E-03
hsa-miR-379	7.4	5.6-8.82	0.7	6.96	5.15-8.35	0.75	1.84E-04	1.56E-03
hsa-miR-656	6.34	4.58-7.68	0.75	5.86	3.9-7.33	0.83	2.84E-04	2.20E-03
hsa-miR-337-5p	6.97	3.35-8.63	0.84	6.47	4.74-7.87	0.82	3.04E-04	2.26E-03
hsa-miR-382	6.56	4.42-8.71	0.92	6.04	3.93-8.29	1.02	1.06E-03	6.98E-03
hsa-miR-432	6.27	4.35-7.64	0.7	5.87	4.05-7.51	0.83	1.40E-03	8.31E-03
hsa-miR-487b	8.55	6.5-10.29	0.87	8.06	5.34-9.58	1.04	2.02E-03	1.16E-02
hsa-miR-376b	6.62	3.97-8.8	0.9	6.19	4.3-7.53	0.85	2.88E-03	1.51E-02
hsa-miR-376a	10.19	7.75-12.47	1	9.67	6.14-11.72	1.23	4.61E-03	2.28E-02
hsa-miR-889	6.65	5.32-8.09	0.64	6.35	4.83-7.92	0.7	5.50E-03	2.57E-02

* Annotation provided by Nanostring Technologies

† P-value is calculated using T-test.

‡ The q-value represents the p-value adjusted for multiple testing using the Benjamini & Hochberg False Discovery Rate (1995).