SUPPLEMENTAL MATERIAL

Supplemental Table 1. Correlation matrix for phenotype data.

		Absolute BP response			Percent BP response		
		Systolic	Diastolic	Mean arterial	Systolic	Diastolic	Mean arterial
Absolute BP Response	Systolic	1.00	0.53	0.80	0.99	0.49	0.78
	Diastolic	…	1.00	0.93	0.53	0.99	0.93
	Mean Arterial	…	…	1.00	0.80	0.91	0.99
Percent BP Response	Systolic	…	…	…	1.00	0.50	0.79
	Diastolic	…	…	…	…	1.00	0.93
	Mean Arterial	…	…	…	…	…	1.00

BP=Blood pressure

All Pearson correlation coefficients were highly statistically significant ($p<0.0001$).

Supplemental Table 2. SNP Characteristics.

Gene	SNP	Chromosome	Physical Location (bp)	Alleles (Major/Minor)	Minor Allele Frequency (%)	HW[*] P-Value	Genotyping Call Rate (%)	P-Value[†]	P-Value[‡]
Angiotensin II, type 1 receptor (AGTR1)	rs409742	3	149895055	T/C	14.7	0.93	100.0	0.49	0.51
	rs275651	3	149897577	T/A	14.7	0.78	98.8	0.54	0.56
	rs275652	3	149897674	A/C	14.9	0.66	96.0	0.72	0.79
	rs1492078	3	149897867	G/A	19.7	0.52	96.7	0.16	0.18
	rs2933249	3	149899210	G/A	13.1	0.61	99.9	0.73	0.74
	rs2131127	3	149906833	G/A	37.1	0.84	99.5	0.17	0.20
	rs12695877	3	149909724	T/C	36.8	0.88	99.9	0.23	0.26
	rs2638360	3	149911046	T/C	10.6	0.43	93.8	0.66	0.69
	rs931490	3	149913457	A/G	10.9	0.64	96.6	0.84	0.87
	rs4681440	3	149914722	C/T	5.0	0.81	100.0	0.05	0.05
	rs4681443	3	149915159	G/A	5.0	1.00	99.9	0.04	0.04
	rs4681444	3	149915264	T/G	5.1	1.00	99.5	0.05	0.05
	rs1492103	3	149915654	A/G	10.7	0.72	100.0	0.69	0.66
	rs718858	3	149918202	C/T	4.9	0.53	89.9	0.04	0.03
	rs1492100	3	149920117	A/T	10.0	0.44	99.9	0.03	0.04
	rs3772616	3	149920881	G/A	16.9	0.19	99.9	0.55	0.48
	rs4524238	3	149922478	C/T	9.9	0.30	99.9	0.04	0.06
	rs16860760	3	149927327	C/T	7.0	0.21	99.8	0.003	0.004
	rs389566	3	149929072	T/A	19.5	0.28	96.5	0.09	0.08
	rs3772608	3	149937364	C/T	4.8	0.16	95.9	0.05	0.06
	rs6801836	3	149938227	T/C	14.2	0.65	96.6	0.59	0.55
	rs1800766	3	149940332	T/C	20.6	0.48	99.8	0.09	0.08
	rs5186	3	149942678	A/C	5.7	0.39	97.6	0.03	0.03
	rs275646	3	149946212	C/T	9.8	0.12	100.0	0.33	0.38
	rs275645	3	149947144	A/G	20.6	0.43	97.0	0.94	0.88
	rs275642	3	149948381	A/G	10.1	0.44	99.8	0.34	0.39

Supplemental Table 2 (con't)

Gene	SNP	Chromosome	Physical Location (bp)	Alleles (Major/Minor)	Minor Allele Frequency (%)	HW[*] P-Value	Genotyping Call Rate (%)	P-Value[†]	P-Value[‡]
Purinergic receptor P2Y, G-protein coupled, 12 (P2RY12)	rs9820422	3	152546953	G/A	18.6	0.82	100.0	0.40	0.40
	rs6793061	3	152562650	A/C	16.1	0.55	99.7	0.11	0.08
	rs1388622	3	152567102	G/A	18.1	0.82	100.0	0.48	0.49
	rs17283010	3	152580081	G/A	14.6	0.40	99.5	0.03	0.02
Interleukin 18 (IL18)	rs544354	11	111517840	T/C	35.4	0.31	99.4	0.78	0.67
	rs5744280	11	111521724	G/A	49.3	0.10	99.9	0.85	0.75
	rs360729	11	111522131	A/T	12.3	0.05	100.0	0.78	0.73
	rs360722	11	111531913	T/C	35.1	0.19	100.0	0.93	0.80
	rs7106524	11	111538846	G/A	49.2	0.08	100.0	0.72	0.62
	rs360717	11	111539935	G/A	11.8	0.18	99.7	0.90	0.90
	rs360718	11	111539949	T/G	11.8	0.15	99.8	0.72	0.74
Dopamine Receptor D2 (DRD2)	rs2234689	11	112783693	G/C	3.9	0.11	99.9	0.07	0.14
	rs1554929	11	112783974	C/T	6.1	0.84	99.8	0.80	0.79
	rs1124492	11	112787485	G/T	46.8	0.93	100.0	0.53	0.58
	rs1124493	11	112787505	G/T	49.3	0.75	100.0	0.21	0.29
	rs12363125	11	112791126	C/T	6.2	0.84	100.0	0.65	0.63
	rs1107162	11	112794247	G/A	6.4	0.44	97.8	0.28	0.32
	rs1079727	11	112794392	A/G	45.1	0.85	100.0	0.12	0.19
	rs2002453	11	112794508	G/A	48.6	0.85	100.0	0.08	0.13
	rs2245805	11	112795909	C/A	48.5	1.00	99.9	0.07	0.11
	rs2734831	11	112798806	T/G	6.1	0.84	99.6	0.76	0.73
	rs2471857	11	112803549	G/A	45.5	1.00	99.9	0.11	0.17
	rs2471854	11	112804849	G/C	45.5	0.89	100.0	0.10	0.16
	rs7131440	11	112805120	G/A	6.1	1.00	99.9	0.51	0.48
	rs17115583	11	112814112	C/T	41.5	0.30	100.0	0.19	0.21
	rs7125415	11	112815891	G/A	39.8	0.21	100.0	0.17	0.21
	rs4648318	11	112818599	C/T	43.5	0.71	100.0	0.12	0.14
	rs17529477	11	112822277	C/T	3.8	0.75	100.0	0.11	0.08

Supplemental Table 2 (con't)

Gene	SNP	Chromosome	Physical Location (bp)	Alleles (Major/Minor)	Minor Allele Frequency (%)	HW[*] P-Value	Genotyping Call Rate (%)	P-Value[†]	P-Value[‡]
DRD2 (con't)	rs4245147	11	112823217	A/G	16.3	0.80	100.0	0.04	0.04
	rs4936271	11	112823915	G/A	16.2	0.61	100.0	0.05	0.06
	rs4581480	11	112829684	T/C	12.7	0.02	99.9	0.20	0.22
	rs7122454	11	112832678	G/C	38.9	0.15	99.9	0.61	0.65
	rs7131056	11	112834984	C/A	41.8	0.18	100.0	0.44	0.41
	rs11214611	11	112835429	T/C	39.5	0.33	99.8	0.45	0.49
	rs4936274	11	112835661	C/T	9.5	0.50	99.5	0.23	0.26
	rs10891551	11	112837505	G/A	39.3	0.50	100.0	0.54	0.59
	rs10891552	11	112838881	T/A	36.9	0.46	100.0	0.90	0.95
	rs4630328	11	112839419	C/T	3.5	0.28	99.9	0.06	0.05
	rs11601054	11	112841382	C/T	3.5	0.28	100.0	0.06	0.05
Nicotinamide N-methyltransferase (NNMT)	rs11600671	11	113630534	G/A	15.9	0.55	100.0	0.03	0.05
	rs683271	11	113634355	A/G	48.8	0.12	99.8	0.70	0.60
	rs560931	11	113636708	C/T	36.0	0.13	100.0	0.46	0.38
	rs611048	11	113636941	A/T	36.0	0.13	100.0	0.46	0.38
	rs10082585	11	113643284	G/A	38.4	0.30	99.4	0.31	0.26
	rs10891641	11	113644291	G/A	38.2	0.22	99.8	0.33	0.27
	rs17116793	11	113657848	C/G	38.5	0.24	100.0	0.38	0.34
	rs7115762	11	113658693	C/A	38.6	0.26	99.5	0.48	0.44
	rs4936293	11	113658715	G/C	39.3	0.33	99.9	0.26	0.25
	rs11214926	11	113659163	G/A	24.2	0.85	100.0	0.91	0.93
	rs4938087	11	113659975	C/T	7.0	0.48	100.0	0.08	0.07
	rs2244175	11	113667731	A/G	48.0	0.52	98.8	0.03	0.02
	rs2847492	11	113668981	G/A	33.8	0.57	100.0	0.78	0.73
	rs2852432	11	113669214	C/T	40.5	0.25	100.0	0.22	0.18
	rs4646335	11	113672152	A/T	43.2	0.03	100.0	0.08	0.07
	rs3819100	11	113672686	C/T	49.3	0.27	100.0	0.23	0.27
	rs2256292	11	113673149	C/G	37.8	0.20	99.9	0.80	0.87

Supplemental Table 2 (con’t)

Gene	SNP	Chromosome	Physical Location (bp)	Alleles (Major/Minor)	Minor Allele Frequency (%)	HW[*] P-Value	Genotyping Call Rate (%)	P-Value[†]	P-Value[‡]
NNMT (con’t)	rs2301128	11	113673209	G/A	9.1	0.58	99.9	0.96	0.86
	rs2155806	11	113677720	T/C	11.6	0.43	99.9	0.09	0.08
	rs11214938	11	113677870	C/T	5.5	1.00	99.9	0.41	0.45
	rs2852447	11	113684911	C/T	18.7	0.06	99.5	0.25	0.23
	rs10891647	11	113691855	T/C	12.8	0.41	100.0	0.11	0.09
Appolipoprotein A-V (APOA5)	rs651821	11	116167789	T/C	28.3	0.61	100.0	0.38	0.48
Appolipoprotein A-IV (APOA4)	rs1268354	11	116195788	T/C	42.6	0.96	100.0	0.68	0.69
	rs2071522	11	116202748	C/T	42.5	0.85	99.8	0.66	0.65
	rs2071521	11	116203058	A/G	42.7	0.92	99.9	0.67	0.66
Appolipoprotein C-III (APOC3)	rs2727789	11	116202097	T/G	42.9	0.78	99.7	0.68	0.68
	rs2849176	11	116202131	C/T	42.6	0.89	99.9	0.56	0.55
	rs2542051	11	116202948	A/C	42.8	0.81	99.8	0.63	0.63
	rs5128	11	116208850	C/G	31.8	0.24	99.7	0.87	0.77
Appolipoprotein A-I (APOA1)	rs10750098	11	116210778	T/G	32.4	0.15	99.7	0.74	0.65
	rs12718462	11	116210929	T/C	5.4	0.65	99.4	0.12	0.13
	rs632153	11	116215449	G/T	7.8	0.05	100.0	0.62	0.53
	rs480009	11	116217184	G/A	29.9	0.21	99.8	0.03	0.02
Heat shock 70kDa protein 8 (HSPA8)	rs4936770	11	122434085	T/C	44.7	0.89	99.9	0.13	0.09
Potassium inwardly-rectifying channel, subfamily J, member 1 (KCNJ1)	rs675759	11	128213185	G/C	11.6	0.02	100.0	0.24	0.20
	rs1148058	11	128217991	C/T	32.1	0.20	99.9	0.91	0.93
	rs1148059	11	128219054	C/A	32.1	0.22	99.8	0.94	0.91
	rs3758766	11	128221182	T/C	32.3	0.23	99.9	0.91	0.92
	rs17137982	11	128227400	G/C	33.3	0.09	99.7	0.90	0.73
	rs675482	11	128231804	G/A	40.9	0.60	99.9	0.68	0.44
	rs673614	11	128232211	T/C	40.9	0.92	99.7	0.53	0.35
	rs2855798	11	128238171	G/T	14.2	0.70	99.9	0.86	0.76
	rs11600347	11	128238524	C/A	4.5	0.79	100.0	0.38	0.51
	rs2855794	11	128239634	G/A	15.7	0.66	99.6	0.24	0.23
	rs3016774	11	128240876	T/C	14.9	0.31	98.8	0.68	0.84

[*] HW=Hardy-Weinberg
[†] P-value for the association between SNPs and absolute mean arterial pressure response to potassium intervention
[‡] P-value for the association between SNPs and percent mean arterial pressure response to potassium intervention