

Supplemental Table 1: Design of oligo reconstitution experiment. We hybridized 24 oligo mixtures to two 12 well microarrays. Each mixture had a particular arrangement of ratios for each of the genes and concentrations. There were three different concentrations (L = Low, M = Medium and H = High) and the oligos corresponding to each allele of a gene were in one of seven allelic ratios (-5 = 1:32, -4 = 1:16, -1 = 1:2, 0 = 1:1, +1 = 2:1, +4 = 16:1 and +5 = 32:1). All of the arrays were hybridized with a labeled complex mixture of placental RNA except (2:02) that had oligo only. One of the mixtures had had no oligo (1:06). The experiment was run in duplicate.

Plate pos	BG only	Oligo only	Gene 1	Gene 2	Gene 3	Gene 4	Gene 5	Gene 6	Gene 7	Gene 8	Gene 9	Gene 10
1:01			L: 0	L:+4	M:-1	L: 0	L:+4	L:+1	H: 0	H:-5	L:+1	L:+4
1:02			M:+4	M: 0	L:-1	M:-4	L:+1	L:+4	H:-1	M:+4	M:+5	M:+5
1:03			M:-4	L:+1	L:+5	M: 0	H: 0	M:+1	M:+5	M: 0	H:-1	L:-4
1:04			M: 0	H: 0	H:-5	H:+5	H:+4	L:-4	L:-4	L:-1	H:+4	H:+4
1:05			L:-1	L:-4	H:+5	H:+1	M:-5	M:-5	M:+1	H:+1	M:+1	L:+1
1:06	X											
1:07			L:-5	M:-5	H:+1	M:-1	M:+1	H: 0	L:+1	L:+5	H:-4	H:-1
1:08			L:+5	M:+1	M:-4	H:-5	M:+5	M:+5	L:+4	M:-1	M: 0	H: 0
1:09			H:+5	H:-4	L: 0	L:-5	H:-1	H:-4	M: 0	M:-4	L:-4	M: 0
1:10			H:-5	H:+4	M:+4	L:+5	H:-4	H:-1	H:-4	L:-5	M:-5	M:-5
1:11			M:-1	M:+5	L:-5	L:-1	M: 0	H:+4	H:+4	H:+5	L:+4	M:+1
1:12			H:+1	H:-1	M: 0	M:+4	L:-4	M: 0	M:-5	L: 0	H: 0	H:-4
2:01			M:-5	H:-5	H: 0	M:+5	L:+5	H:-5	L:-5	M:+5	H:+5	L: 0
2:02		X										
2:03			H: 0	L:-1	M:+5	L:+1	M: 0	M:-1	M:+4	L:+4	M:-4	M: 0
2:04			M:+5	M: 0	H:+4	L:+4	M:-1	L:-1	H:+1	H:+4	L:+5	H:+1
2:05			M:+1	L:-5	M:-5	H:+4	H:-5	H:+1	M: 0	H: 0	M:-1	M:+4
2:06			H:-1	M:+4	H:-1	H:-1	L: 0	L:-5	L:+5	M:+1	L:-1	M:-1
2:07			L:+1	H:+5	L:-4	H: 0	H:+5	L: 0	M:-4	H:-1	M: 0	L:-1
2:08			L:+4	M:-1	M:+1	M:-5	L:-5	M:+4	L:-1	M: 0	M:+4	L:-5
2:09			L:-4	M:-4	L:+4	L:-4	M:-4	H:+5	H:-5	L:+1	H:-5	L:+5
2:10			M: 0	H:+1	L:+1	M:+1	H:+1	M: 0	H:+5	L:-4	L:-5	M:-4
2:11			H:+4	L: 0	H:-4	H:-4	L:-1	L:+5	L: 0	M:-5	L: 0	H:-5
2:12			H:-4	L:+5	M: 0	M: 0	M:+4	M:-4	M:-1	H:-4	H:+1	H:+5

Supplemental Table 2: Concentration (microMolar) of each allele (a, b) for each of the 10 gene (genes 1-10). Each of the genes had several oligos (on average 6) as there were 65 allelic pairs.

Mixture	1a	1b	2a	2b	3a	3b	4a	4b	5a	5b	6a	6b	7a	7b	8a	8b	9a	9b	10a	10b
1.0	4.0	4.0	3.8	0.2	6.7	3.3	1.0	1.0	0.3	4.7	3.3	1.7	50.0	50.0	6.1	193.9	2.7	1.3	7.5	0.5
2.0	4.7	75.3	20.0	20.0	0.7	0.3	1.2	18.8	1.7	3.3	4.7	0.3	33.3	66.7	18.8	1.2	38.8	1.2	77.6	2.4
3.0	75.3	4.7	2.7	1.3	0.0	1.0	10.0	10.0	125.0	125.0	33.3	16.7	9.7	0.3	10.0	10.0	100.0	200.0	0.5	7.5
4.0	40.0	40.0	150.0	150.0	97.0	3.0	193.9	6.1	14.7	235.3	0.3	4.7	0.1	0.9	0.7	1.3	282.4	17.6	141.2	8.8
5.0	5.3	2.7	0.2	3.8	3.0	97.0	133.3	66.7	48.5	1.5	1.5	48.5	6.7	3.3	133.3	66.7	26.7	13.3	5.3	2.7
6.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
7.0	7.8	0.2	1.2	38.8	33.3	66.7	6.7	13.3	16.7	33.3	125.0	125.0	0.7	0.3	1.9	0.1	17.6	282.4	50.0	100.0
8.0	0.2	7.8	26.7	13.3	9.4	0.6	6.1	193.9	1.5	48.5	48.5	1.5	0.9	0.1	6.7	13.3	20.0	20.0	75.0	75.0
9.0	4.5	145.5	17.6	282.4	0.5	0.5	0.1	1.9	166.7	83.3	14.7	235.3	5.0	5.0	1.2	18.8	0.2	3.8	40.0	40.0
10.0	145.5	4.5	282.4	17.6	0.6	9.4	1.9	0.1	235.3	14.7	83.3	166.7	5.9	94.1	0.1	1.9	1.2	38.8	2.4	77.6
11.0	53.3	26.7	38.8	1.2	1.0	0.0	0.7	1.3	25.0	25.0	235.3	14.7	94.1	5.9	193.9	6.1	3.8	0.2	53.3	26.7
12.0	50.0	100.0	100.0	200.0	5.0	5.0	18.8	1.2	4.7	0.3	25.0	25.0	0.3	9.7	1.0	1.0	150.0	150.0	8.8	141.2
13.0	77.6	2.4	9.1	290.9	50.0	50.0	19.4	0.6	0.2	4.8	7.6	242.4	0.0	1.0	19.4	0.6	290.9	9.1	4.0	4.0
14.0	40.0	40.0	20.0	20.0	5.0	5.0	10.0	10.0	25.0	25.0	25.0	25.0	5.0	5.0	10.0	10.0	20.0	20.0	40.0	40.0
15.0	75.0	75.0	1.3	2.7	0.3	9.7	1.3	0.7	25.0	25.0	16.7	33.3	9.4	0.6	1.9	0.1	2.4	37.6	40.0	40.0
16.0	2.4	77.6	20.0	20.0	5.9	94.1	1.9	0.1	33.3	16.7	1.7	3.3	66.7	33.3	188.2	11.8	3.9	0.1	100.0	50.0
17.0	26.7	53.3	0.1	3.9	9.7	0.3	188.2	11.8	242.4	7.6	166.7	83.3	5.0	5.0	100.0	100.0	13.3	26.7	75.3	4.7
18.0	100.0	50.0	37.6	2.4	66.7	33.3	66.7	133.3	2.5	2.5	0.2	4.8	1.0	0.0	13.3	6.7	1.3	2.7	26.7	53.3
19.0	2.7	5.3	290.9	9.1	0.9	0.1	100.0	100.0	7.6	242.4	2.5	2.5	0.6	9.4	66.7	133.3	20.0	20.0	2.7	5.3
20.0	0.5	7.5	13.3	26.7	3.3	6.7	0.6	19.4	4.8	0.2	47.1	2.9	0.3	0.7	10.0	10.0	37.6	2.4	0.2	7.8
21.0	7.5	0.5	2.4	37.6	0.1	0.9	0.1	1.9	47.1	2.9	242.4	7.6	3.0	97.0	1.3	0.7	9.1	290.9	7.8	0.2
22.0	40.0	40.0	200.0	100.0	0.3	0.7	13.3	6.7	83.3	166.7	25.0	25.0	97.0	3.0	0.1	1.9	0.1	3.9	4.7	75.3
23.0	8.8	141.2	2.0	2.0	94.1	5.9	11.8	188.2	3.3	1.7	4.8	0.2	0.5	0.5	0.6	19.4	2.0	2.0	4.5	145.5
24.0	141.2	8.8	3.9	0.1	5.0	5.0	10.0	10.0	2.9	47.1	2.9	47.1	3.3	6.7	11.8	188.2	200.0	100.0	145.5	4.5

Supplemental table 3: Primer information for pyrosequencing assays.

Gene name	SNP rs#	Forward primer sequence	Reverse primer sequence	Pyrosequencing primer sequence
NLRP2	rs1043673	5'-GATGAACTCAATAAGCTGCTGGAAG-3'	5'-CTTCATGGAGAATGAATGACTCGGG-3'	5'-CATGAGAAGAAGGCCTTTCT-3'
OSBPL1A	rs7226913	5'-TGTTCTCAGGGAAGCTGAGATGGA-3'	5'-AGTGTATAAAGGCCTGGCTGCTCA-3'	5'-TGTGCACGAGGGTGGGGAAG-3'
LRAP	rs2297988	5'-TGCTGGTGGTTAAACAAGACGGGT-3'	5'-GCCCTCCATTCAGGGTCTTCCT-3'	5'-ACCCCCTGGAGGAAGCGCTC-3'
PEG10	rs13073	5'-GGCAGGCTTTAATTGCCAAAGCAC-3'	5'-TGAAAGCCTAGTCACCACTTCA-3'	5'-TTCACATGTTTATTATCATC-3'
SCRN1	rs6976421	5'-TCTCAGCCAAGGAGGGAAAGAA-3'	5'-TTGCCCTCTGTCTTCCCAATGCTA-3'	5'-AGATAATGTAGTGACTGCTA-3'
TUBGCP6	rs4838865	5'-TGTTTCAGAGACGCTTATGGCGAGT-3'	5'-GTCGTGGGCAATGTGCTTCAGAAA-3'	5'-CGTAGCCATGTGTCCAGTAC-3'