

A result of the survey of polymorphisms between all PM probe sequences of the Mouse Genome 430 2.0 array and MSM CDS.

### Polymorphism scores

# of probes detected in the MSM CDS \ # of SNP contain probes	11	10	9	8	7	6	5	4	3	2	1	0
11/11	67	56	46	37	29	22	16	11	7	4	2	1
10/11		68	57	47	38	30	23	17	12	8	5	3
9/11			69	58	48	39	31	24	18	13	9	6
8/11				70	59	49	40	32	25	19	14	10
7/11					71	60	50	41	33	26	20	15
6/11						72	61	51	42	34	27	21
5/11							73	62	52	43	35	28
4/11								74	63	53	44	36
3/11									75	64	54	45
2/11										76	65	55
1/11											77	66
0/11 (Not Detected)												

### Number of probe sets for each polymorphism score

# of probes detected in the MSM CDS \ # of SNP contain probes	11	10	9	8	7	6	5	4	3	2	1	0
11/11	8	19	30	63	177	387	748	1484	2508	3977	5200	9590
10/11		1	1	14	24	70	155	358	598	955	1329	2434
9/11			1	6	9	24	74	167	296	518	834	1649
8/11				3	4	13	34	65	128	235	387	842
7/11					3	2	21	23	71	119	163	458
6/11						1	3	11	24	52	104	290
5/11							4	5	16	44	53	198
4/11								9	12	22	56	151
3/11									7	16	35	142
2/11										18	29	174
1/11											38	163
0/11 (Not Detected)												7055
Total detected	8	20	32	86	217	497	1039	2122	3660	5956	8228	23146

\* Similarities of all PM probe sequences of the Mouse Genome 430 2.0 array were searched against the MSM reads (DRA000194) by Megablast <sup>1)</sup>.

1) Zhang,Z., Schwartz,S., Wagner,L. and Miller,W. (2000) A greedy algorithm for aligning DNA sequences. J. Comput. Biol., 7, 203–214.