Supplemental Table S2.

(Chip ID)	SF	RawQ	Bg Avg	Noise Avg	**#P**	**%P**	Signal (All)	Gapdh Ratio	β-Actin Ratio
MHV #A	7,56	1,10	34,31	1,31	**19191**	**42,55**	791,98	0,62	1,82
MHV #B	7,10	1,10	33,45	1,30	**19772**	**43,84**	790,72	0,59	1,65
MHV #C	9,97	0,88	28,83	1,04	**18512**	**41,05**	800,34	0,65	1,59
mock #A	5,25	0,92	29,65	1,14	20432	45,30	801,53	0,67	1,11
mock #B	3,50	1,10	33,61	1,47	21362	47,36	779,64	0,68	1,08
mock #C	3,66	1,11	34,76	1,44	21311	47,25	774,95	0,69	1,14
MHV (vRNA depleted) #A	4,68	1,00	32,44	1,20	**21265***	**47,15***	734,54	0,85	1,81
MHV (vRNA depleted) #B	5,28	0,96	30,42	1,21	**20888***	**46,31***	750,52	0,72	1,59
MHV (vRNA depleted) #C	6,44	1,01	32,21	1,21	**20168***	**44,72***	757,22	0,85	1,92
mock (vRNA depleted) #A	4,77	0,96	31,21	1,20	20722	45,95	797,83	0,79	1,26
mock (vRNA depleted) #B	4,99	1,05	34,41	1,26	20611	45,70	789,74	0,77	1,29
mock (vRNA depleted) #C	3,73	1,06	33,42	1,36	21239	47,09	779,72	0,73	1,19

*Note that the number/percentage of detected probe sets (#P and %P) is increased in the arrays hybridized with cRNA from MHV-infected cells after vRNA depletion. The other QC parameters indicate that the generated data are of high quality.