| $a^{(t)}$	$\sigma^{(t)}$	$p^{(t)}$	n	t_1			t_2			p		
				25%	med	75%	25%	med	75%	25%	med	75%
0.5	0.1	0	100	1.20	2.14	2.80	0.72	1.32	1.74	-	-	-
			1000	1.67	2.00	2.18	0.31	0.42	0.52	-	-	-
			10000	1.99	2.03	2.07	0.43	0.46	0.51	-	-	-
0.5	0.5	0	100	1.17	1.87	2.32	0.91	1.30	1.75	-	-	-
			1000	1.87	2.02	2.25	0.50	0.80	0.94	-	-	-
			10000	1.99	2.08	2.13	0.37	0.51	0.64	-	-	-
0.1	0.1	0	100	0.29	0.62	1.15	0.29	0.76	0.97	-	-	-
			1000	1.01	1.24	1.89	0.62	0.88	1.26	-	-	-
			10000	1.40	1.80	2.23	0.48	0.62	0.75	-	-	-
0.1	0.5	0	100	1.88	2.25	3.03	1.94	2.33	3.20	-	-	-
			1000	1.38	1.66	2.00	1.34	1.52	1.67	-	-	-
			10000	1.33	1.53	1.61	0.99	1.17	1.27	-	-	-
0.5	0.1	1%	100	1.11	1.55	2.06	0.55	0.77	1.16	0.02	0.03	0.04
			1000	1.72	1.91	2.08	0.27	0.36	0.50	0.00	0.00	0.01
			10000	1.72	1.76	1.88	0.47	0.50	0.52	0.00	0.00	0.00
0.5	0.5	1%	100	1.34	2.21	3.18	1.47	2.30	2.69	0.03	0.04	0.06
			1000	1.66	2.03	2.35	0.64	0.92	1.04	0.01	0.02	0.03
			10000	1.92	1.98	2.04	0.39	0.47	0.61	0.02	0.02	0.02
0.1	0.1	1%	100	0.19	0.45	0.88	0.21	0.39	0.83	0.01	0.01	0.02
			1000	0.78	1.07	2.03	0.40	0.82	0.99	0.01	0.01	0.01
			10000	1.46	2.00	2.43	0.37	0.47	0.62	0.01	0.01	0.01
0.1	0.5	1%	100	1.59	2.22	3.24	1.46	2.67	3.62	0.02	0.03	0.04
			1000	1.39	1.63	2.22	1.15	1.50	2.15	0.02	0.02	0.02
			10000	1.14	1.33	1.52	1.11	1.31	1.42	0.02	0.02	0.02

Suppl table 1 : medians (med) and quartiles for estimates of t_1, t_2 and p over 20 simulated data sets (simulations without outgroup species). Simulated datasets of sample size n were generated with different values of 'true' parameters: $a^{(t)}$, $\sigma^{(t)}$ and $p^{(t)}$. The true values for t_1 and t_2 were 2 and 0.5 respectively.

| $a^{(t)}$	$\sigma^{(t)}$	$p^{(t)}$	n	t_1			t_2			p		
				25%	med	75%	25%	med	75%	25%	med	75%
0.5	0.1	0	600	1.22	1.50	2.66	1.16	1.53	2.37	-	-	-
			6000	0.98	1.40	1.89	0.30	0.56	0.72	-	-	-
			60000	1.40	1.55	1.65	0.16	0.33	0.45	-	-	-
0.5	0.1	1%	600	0.95	1.58	2.27	1.26	1.51	2.34	0.01	0.01	0.01
			6000	1.39	2.01	2.40	0.37	0.50	0.64	0.00	0.00	0.00
			60000	1.38	1.42	1.64	0.20	0.25	0.36	0.00	0.00	0.00

Suppl table 2: medians (med) and quartiles for estimates of $\log_2(t_1/t_2)$, a, and σ over 20 simulated data sets of interdependent expression profiles, without outgroup species. Expression levels were generated for 100, 1,000 and 10,000 transcript and then we assumed that each transcript was represented x times in the data set (where x followed a geometric distribution of mean 6) and that the within transcript measurement error followed a gaussian distribution of mean 0 and standard deviation 1.8. The true values for t_1 and t_2 were 2 and 0.5 respectively.

| $a^{(t)}$	$\sigma^{(t)}$	$p^{(t)}$	n	t1			t2			t3			t4			p		
				25%	med	75%	25%	med	75%	25%	med	75%	25%	med	75%	25%	med	75%
0.5	0.1	0	100	1.54	1.84	2.28	0.28	0.36	0.53	0.57	0.72	0.94	0.36	0.62	0.80	-	-	-
			1000	1.73	1.92	2.24	0.43	0.48	0.54	0.89	1.01	1.09	0.44	0.48	0.55	-	-	-
			10000	1.96	2.03	2.07	0.49	0.50	0.52	0.97	1.01	1.03	0.48	0.50	0.52	-	-	-
0.5	0.5	0	100	2.13	2.72	5.04	0.39	0.57	0.77	0.72	1.22	1.78	0.70	1.23	1.71	-	-	-
			1000	1.95	2.04	2.22	0.50	0.54	0.60	0.75	0.95	1.30	0.35	0.51	0.69	-	-	-
			10000	1.92	1.97	2.07	0.46	0.49	0.53	0.94	1.02	1.10	0.44	0.47	0.55	-	-	-
0.1	0.1	0	100	0.33	1.16	1.66	0.11	0.17	0.32	0.34	0.52	0.77	0.33	0.53	0.79	-	-	-
			1000	1.27	1.92	2.70	0.25	0.44	0.56	0.48	0.78	0.97	0.44	0.61	0.78	-	-	-
			10000	1.60	1.83	2.33	0.41	0.52	0.59	0.86	0.92	1.11	0.38	0.46	0.58	-	-	-
0.1	0.5	0	100	1.89	3.00	4.37	0.36	0.65	1.05	0.85	1.11	1.51	0.68	0.96	1.51	-	-	-
			1000	1.92	2.15	2.43	0.47	0.56	0.62	0.77	0.87	0.99	0.69	0.80	0.84	-	-	-
			10000	1.96	1.99	2.02	0.50	0.51	0.54	0.68	0.78	0.81	0.67	0.72	0.77	-	-	-
0.5	0.1	1%	100	1.87	2.39	3.18	0.41	0.60	0.79	0.57	0.83	0.94	0.74	0.92	1.43	0.02	0.02	0.04
			1000	1.86	2.02	2.16	0.43	0.49	0.56	0.82	0.97	1.03	0.46	0.54	0.59	0.01	0.01	0.01
			10000	1.83	1.86	1.91	0.46	0.49	0.50	0.90	0.93	0.95	0.45	0.48	0.49	0.01	0.01	0.01
0.5	0.5	1%	100	2.17	2.55	3.88	0.42	0.69	0.94	0.79	1.28	1.49	0.85	1.16	1.35	0.03	0.04	0.05
			1000	1.88	2.13	2.21	0.42	0.46	0.58	0.81	0.95	1.08	0.48	0.57	0.65	0.02	0.02	0.03
			10000	1.99	2.00	2.06	0.46	0.48	0.50	0.94	0.98	1.02	0.47	0.52	0.55	0.02	0.02	0.02
0.1	0.1	1%	100	0.39	0.76	2.64	0.13	0.36	0.51	0.24	0.57	0.90	0.26	0.63	0.92	0.01	0.02	0.02
			1000	1.34	1.84	3.09	0.26	0.38	0.50	0.54	0.72	1.24	0.47	0.68	0.96	0.01	0.01	0.01
			10000	1.96	2.35	2.56	0.44	0.55	0.68	0.72	1.09	1.31	0.46	0.68	0.82	0.01	0.01	0.01
0.1	0.5	1%	100	2.25	2.80	4.61	0.49	0.62	0.96	0.95	1.13	1.63	0.83	1.17	1.56	0.03	0.03	0.04
			1000	2.04	2.24	2.49	0.46	0.50	0.58	0.82	0.90	0.96	0.76	0.86	0.90	0.02	0.02	0.02
			10000	2.01	2.07	2.15	0.47	0.50	0.52	0.69	0.79	0.84	0.74	0.80	0.85	0.02	0.02	0.02

Suppl table 3: medians (med) and quartiles for estimates of t_1, t_2, t_3, t_4 and p over 20 simulated data sets, (including data for an outgroup species). Simulated datasets of sample size n were generated with different values of 'true' parameters: $a^{(t)}$, $\sigma^{(t)}$ and $p^{(t)}$. The true values for were t_1, t_2, t_3, t_4 were 2, 0.5, 1 and 0.5 respectively.
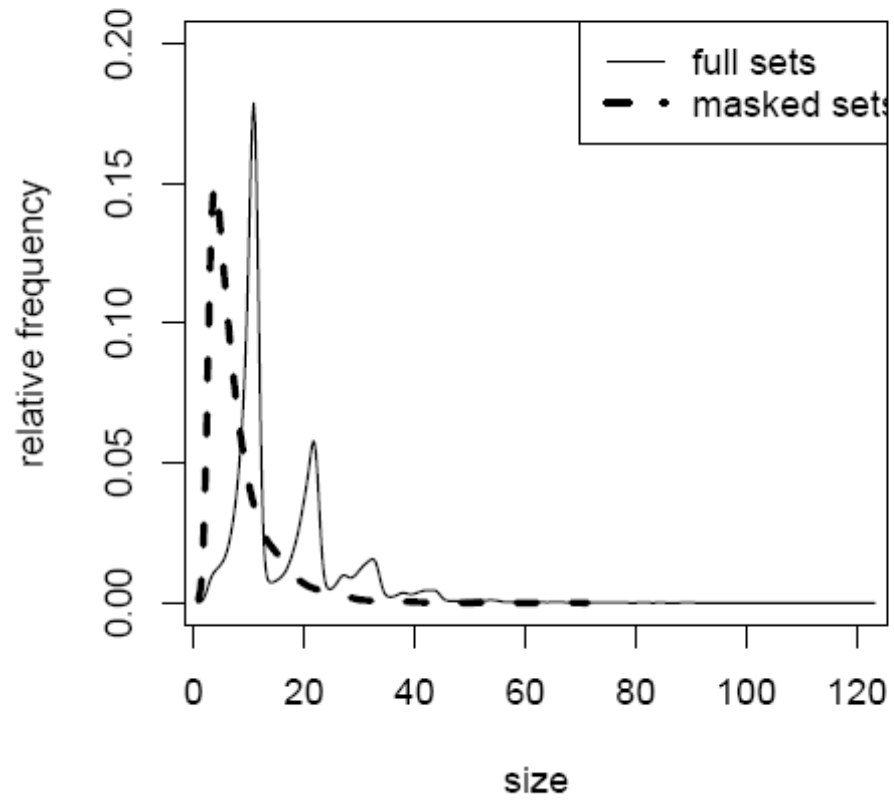
Suppl figure 1: distributions of the number of probes per probeset before and after masking mismatch probes
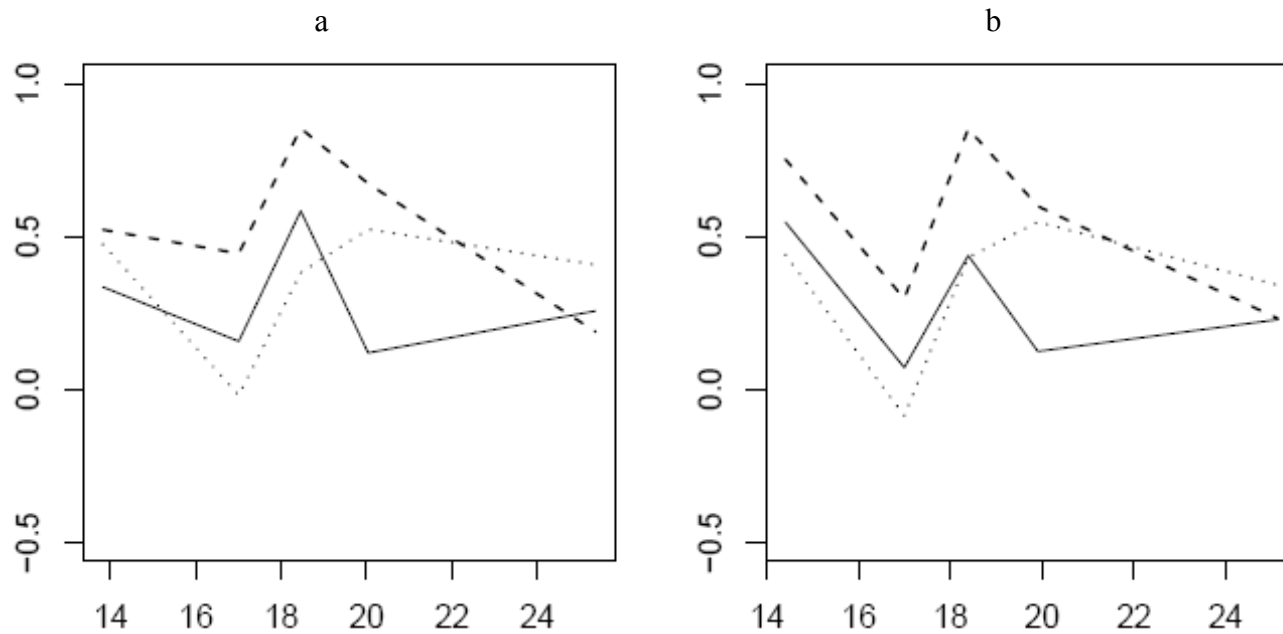
Suppl figure 2: relationship between the skewness coefficient of the expression differences distributions between two species (yaxis) and the mean expression level after variance-stabilising selection (xaxis) in data sets nn-HCR (a) and QQ-HCR (b). Solid line: human-chimpanzee distribution of differences, dashed line: human-rhesus distribution of differences, dotted line: chimpanzee-rhesus distribution of differences.
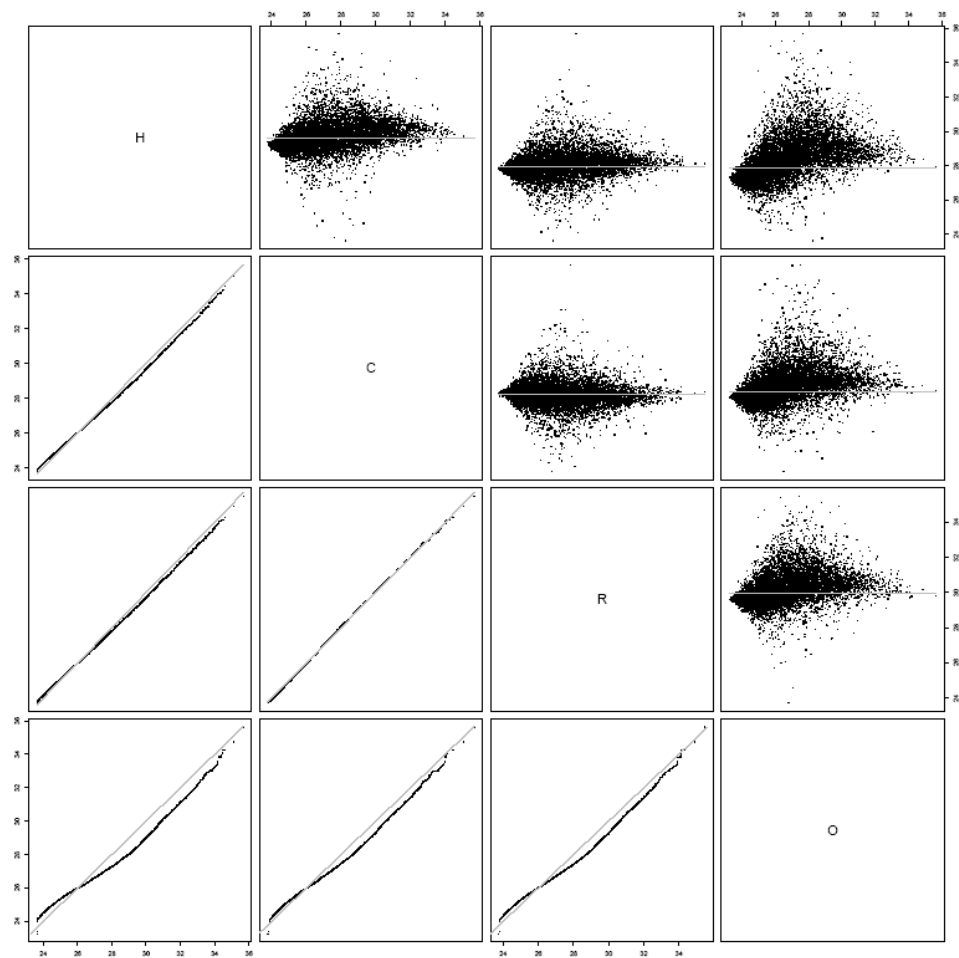
Suppl figure 3: QQ plots for the nn-HCRO data set comparing averages by species are shown in the panels below the diagonal and M(A) plots are shown in the panels above the diagonal. human (H), chimpanzee (C), rhesus macaques (R) and , orang-utan (O).
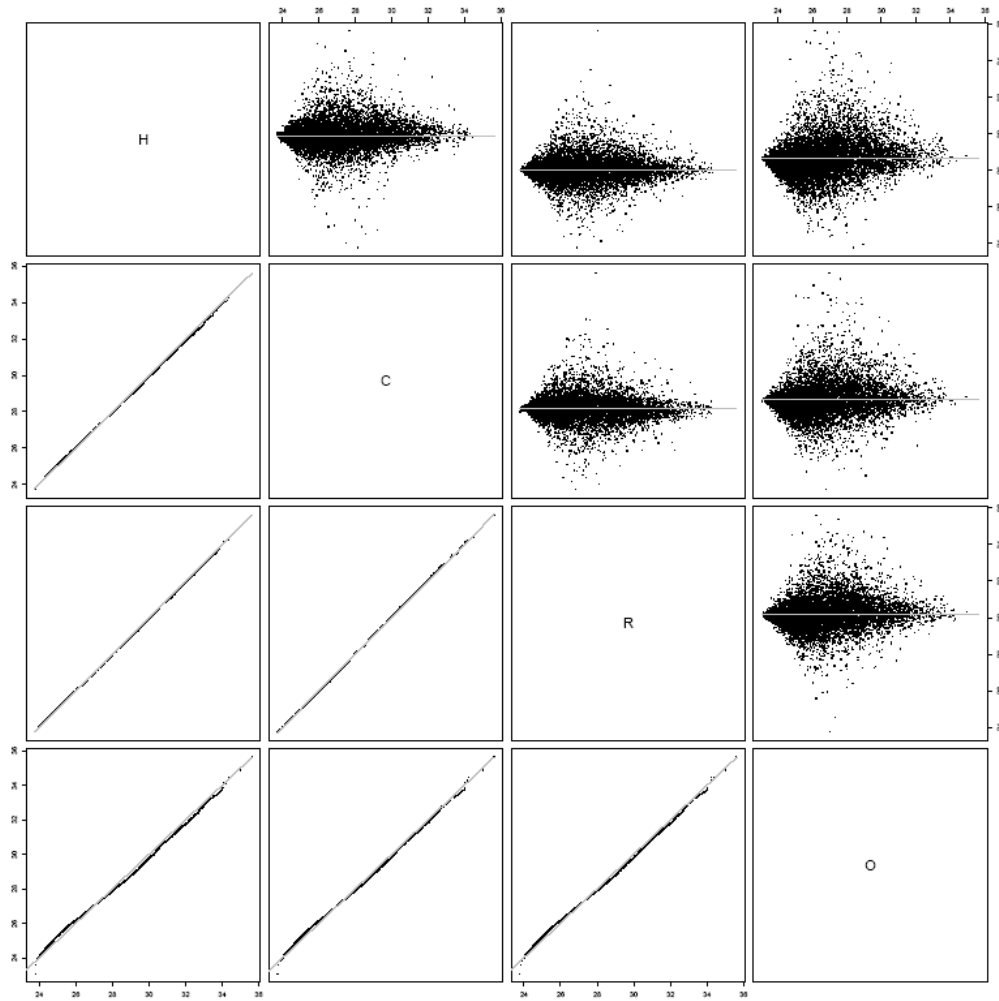
Suppl figure 4: QQ plots for the QQ-HCRO data set comparing averages by species are shown in the panels below the diagonal and M(A) plots are shown in the panels above the diagonal. human (H), chimpanzee (C), rhesus macaques (R) and , orang-utan (O).