Table C.   Filter hybridization and sequencing results

Filter	Trait	Symbol	HM3		HM3/RH		HM3/S[3]	
			Im	*ESTs*	*Im*	*ESTs*	*Im*	*ESTs*
A03	54	ACTA1	0.650 ± 0.021	n.d. [a]	0.093 ± 0.004	-	0.048 ± 0.006	1
A04	804	HBA1	0.142 ± 0.013	n.d. [a]	0.014 ± 0.001	-	0.007 ± 0.000	0
A05	777	MYL2	0.419 ± 0.038	n.d. [a]	0.065 ± 0.003	-	0.013 ± 0.000	1
A06	1335	CKM	0.325 ± 0.039	24	0.076 ± 0.007	-	0.019 ± 0.002	1
A07	697	TNNT1	0.114 ± 0.015	24	0.011 ± 0.000	-	0.007 ± 0.000	0
A08	1765	RPL37A	0.165 ± 0.021	10	0.259 ± 0.040	-	0.196 ± 0.017	2
A09	1333	MB	0.182 ± 0.014	11	0.332 ± 0.017	-	0.827 ± 0.064	16
A10	1800	GAPD	0.130 ± 0.020	9	0.017 ± 0.001	-	0.014 ± 0.001	0
A11	37	MYH7	0.296 ± 0.066	13	0.059 ± 0.002	-	0.018 ± 0.001	0
A12	1673	TPM2	0.152 ± 0.025	16	0.081 ± 0.005	-	0.012 ± 0.002	1
B03	1070	TNNI1	0.207 ± 0.007	7	0.171 ± 0.002	-	0.048 ± 0.003	1
B04	1236	RPL41	0.128 ± 0.003	1	0.166 ± 0.007	-	0.451 ± 0.046	2
B05	75	MYL3	0.075 ± 0.010	3	0.249 ± 0.013	-	0.080 ± 0.006	2
B06	1284	TELE	0.113 ± 0.011	7	0.038 ± 0.001	-	0.012 ± 0.001	2
B07	1931	COX6A2	0.104 ± 0.014	5	0.085 ± 0.006	-	0.045 ± 0.002	0
B08	603	MYL2	0.101 ± 0.010	2	0.275 ± 0.028	-	0.023 ± 0.001	0
B09	1585	DES	0.245 ± 0.035	12	0.083 ± 0.008	-	0.099 ± 0.005	4
B10	1337	TNNC1	0.046 ± 0.004	0	0.031 ± 0.004	-	0.016 ± 0.001	2
B11	1495	HBB	0.038 ± 0.005	6	0.115 ± 0.002	-	0.015 ± 0.002	2
C03	1726	TNNC2	0.085 ± 0.007	3	0.040 ± 0.001	-	0.014 ± 0.000	0
C04	1057	TNNI2	0.099 ± 0.011	10	0.129 ± 0.016	-	0.065 ± 0.002	2
C05	1664	RPL37	0.088 ± 0.004	3	0.134 ± 0.012	-	0.565 ± 0.057	24
C06	1752	ALDOA	0.112 ± 0.021	6	0.109 ± 0.004	-	0.127 ± 0.020	13
C07	1646	RPLP1	0.065 ± 0.009	4	0.042 ± 0.004	-	0.012 ± 0.001	3
C08	1312	COX7A1	0.067 ± 0.008	2	0.134 ± 0.003	-	0.115 ± 0.005	7
C09	38	MYH2	0.231 ± 0.039	1	0.174 ± 0.021	-	0.037 ± 0.001	1
C10	1574	MYBPC1	0.025 ± 0.002	5	0.019 ± 0.002	-	0.029 ± 0.002	1
C11	900	TPM1	0.061 ± 0.012	3	0.110 ± 0.001	-	0.124 ± 0.008	2
C12	826	HSPB1	0.079 ± 0.006	3	0.107 ± 0.005	-	0.074 ± 0.001	2
D03	1332	ENO3	0.041 ± 0.004	4	0.067 ± 0.001	-	0.229 ± 0.007	10
D04	78	CRYAB	0.035 ± 0.002	1	0.023 ± 0.002	-	0.067 ± 0.003	0
D07	502	RPL10	0.063 ± 0.013	2	0.100 ± 0.011	-	0.165 ± 0.009	1
D08	1883	MYOZ	0.061 ± 0.009	3	0.063 ± 0.008	-	0.055 ± 0.007	0
D09	685	TNNT3	0.037 ± 0.005	8	0.048 ± 0.003	-	0.009 ± 0.001	0
D11	1944	RPLP2	0.031 ± 0.006	1	0.028 ± 0.001	-	0.008 ± 0.000	0
D12	1518	- - - - -	0.021 ± 0.004	0	0.018 ± 0.002	-	0.009 ± 0.001	0
E04	1735	RPS11	0.067 ± 0.005	0	0.040 ± 0.003	-	0.029 ± 0.002	3
E05	1085	NTRK1	0.048 ± 0.006	0	0.044 ± 0.001	-	0.012 ± 0.001	2
E06	756	- - - - -	0.101 ± 0.011	0	0.021 ± 0.001	-	0.019 ± 0.005	0
E07	1356	UBA52	0.071 ± 0.016	3	0.061 ± 0.003	-	0.022 ± 0.001	2
E08	1573	RPL32	0.035 ± 0.005	0	0.042 ± 0.001	-	0.271 ± 0.011	5
E09	1348	TPT1	0.018 ± 0.003	6	0.013 ± 0.001	-	0.023 ± 0.002	0
E10	1480	PYGM	0.068 ± 0.012	2	0.073 ± 0.002	-	0.110 ± 0.006	0
E12	168	RPS17	0.080 ± 0.013	3	0.033 ± 0.002	-	0.012 ± 0.001	0

Transcripts are identifiable by the first three columns (cfr. Table A). **Im**: mean ± standard deviation of the normalized signal intensities, calculated for each of the four replica spots on the filters. Data relative to the transcripts target of oligo-directed RNase H digestion in the HM3/RH library are boxed. **ESTs**: number of ESTs identifying each transcript in the sample of 1,000 sequences examined. [a]Not determined by sequencing; however the frequencies estimated by pre-screening tests were close to the values reported in Table A.