

Supplemental Material

Figure S1. Histograms of raw scores of 308 JASPAR TFBS matrices.

Histograms of raw scores of 308 JASPAR TFBS matrices were derived from upstream 1 kb promoter regions of all available RefSeq genes for hg18 (build 36) (20369 human-mouse-rat alignments, 20.4 Mb of human, 13.7 Mb of mouse and 13.4 Mb of rat sequences). The occurrences of raw scores within each 0.001 bin was recorded and plotted (red). The normal distribution was fitted to the observed values and superimposed on the histogram plots (black).

Table S2. Properties of raw score histograms for JASPAR TFBS matrices.

Properties of raw score histograms were determined using SAS Proc Univariate, including mean, standard deviation, Kolmogorov-Smirnov distance (KS distance), skewness and kurtosis. Based on whether $MEAN + STDEV < 0.5$, $KS \text{ distance} > 0.1$ and $Skewness > 0.2$, All 308 JASPAR TFBS matrices were assigned into one of eight types of histograms. For PF collections, the TF names were not available and their distributions in Types 6 and 8 histograms were associated with their degenerate bases and short length.

Table S3. Thresholds of JASPAR TFBS matrices at various cutoffs.

For each species, a series of cutoffs (from the top 0.01% to 10% of all predictions) were calculated using all predicted sites from all available RefSeq genes. Since TFLOC only reports a conserved binding site meeting the threshold in all 3 species, the lowest raw score among 3 species was chosen for the final threshold at each cutoff.

Table S4. Custom tracks in the UCSC genome browser.

Known and predicted sites were displayed as custom annotation tracks using the “pack” mode in the UCSC genome browser. The datasets in the BED format were organized as known, newly predicted tracks and the prediction tracks were organized according to the sources and the JASPAR collection.

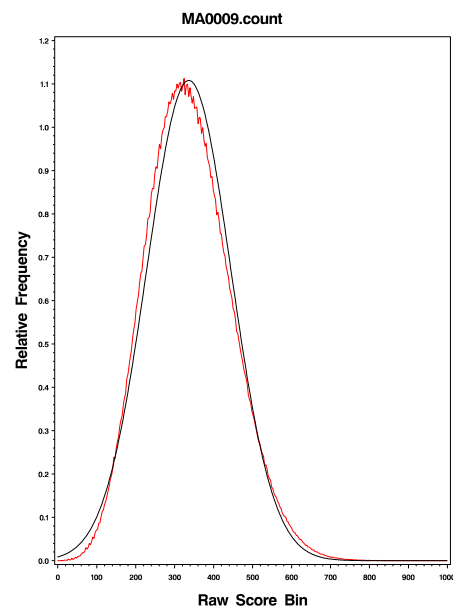
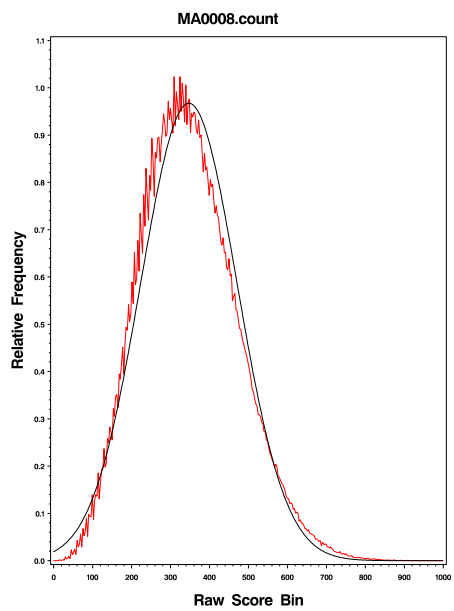
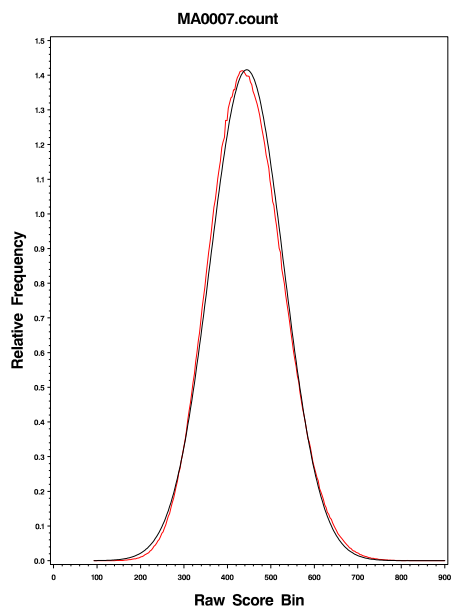
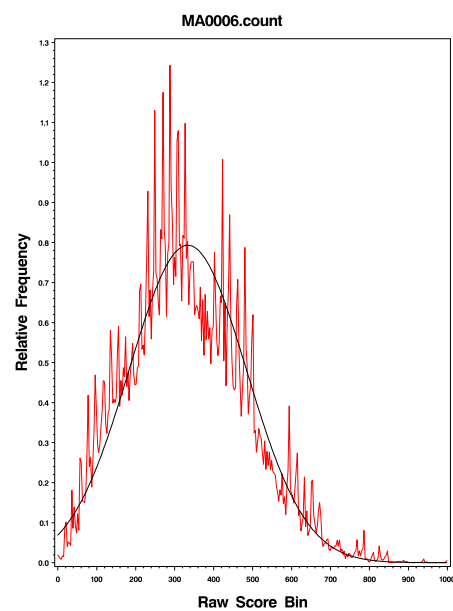
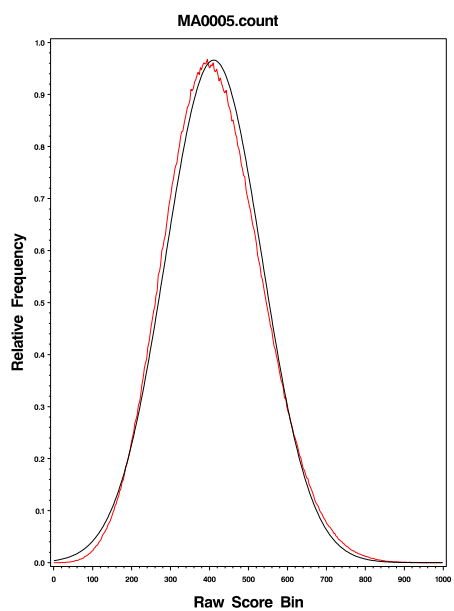
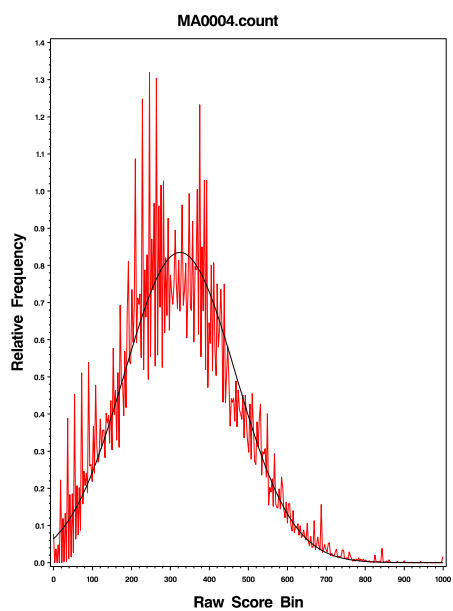
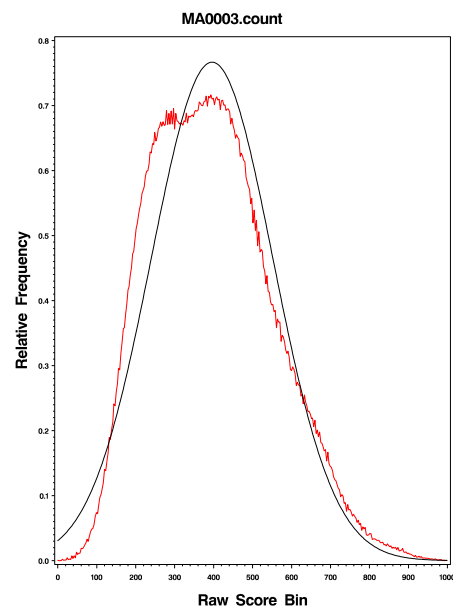
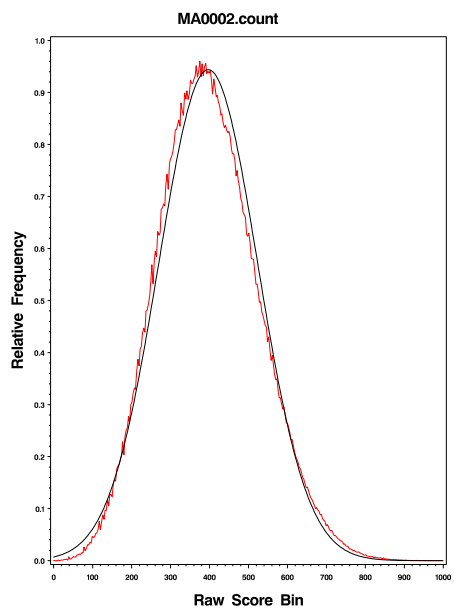
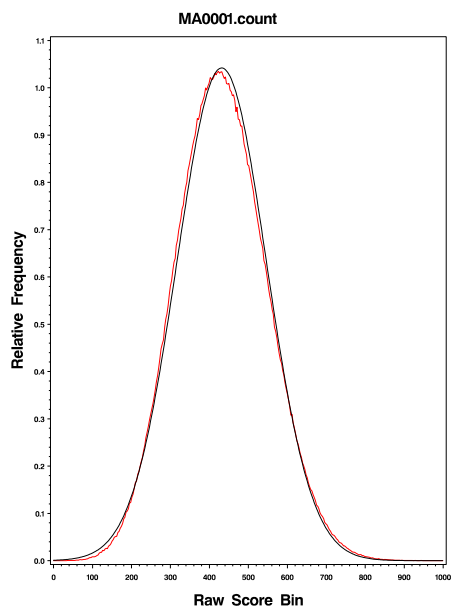
Table S5. Overlap relations between known and predicted sites.

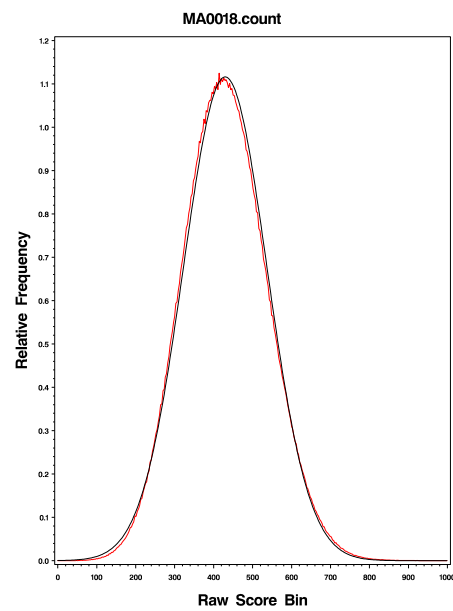
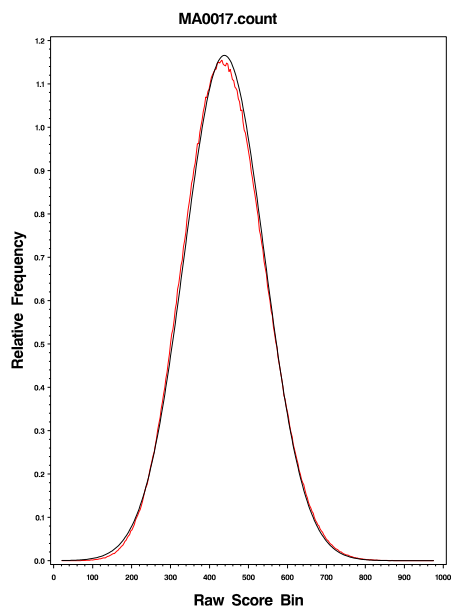
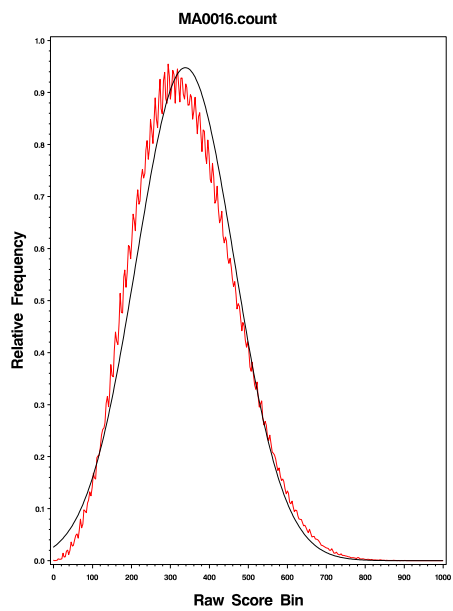
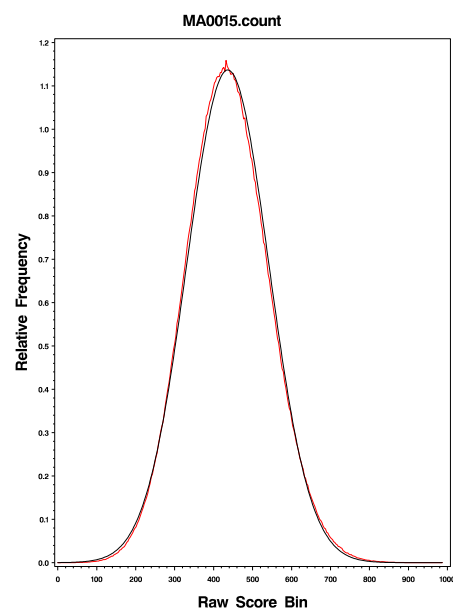
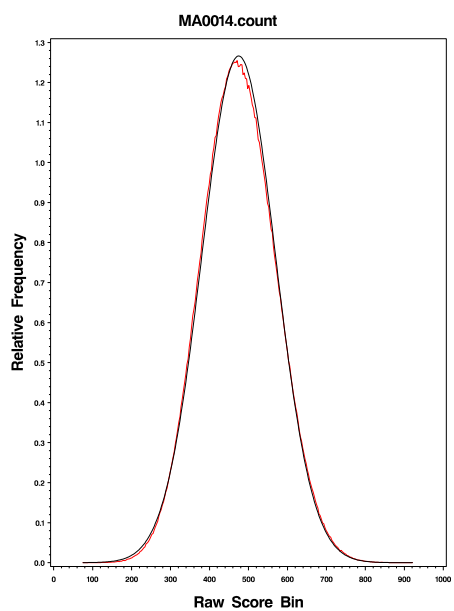
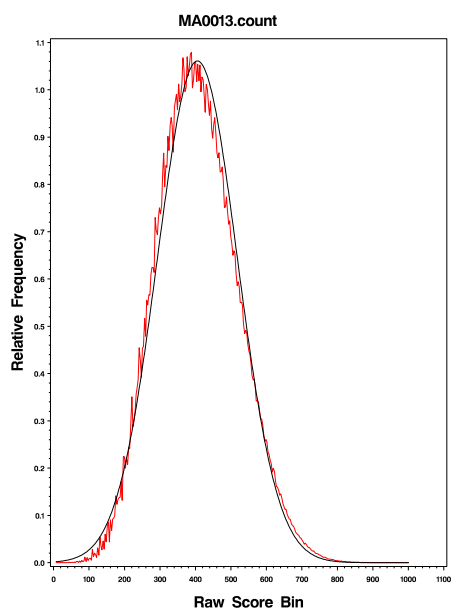
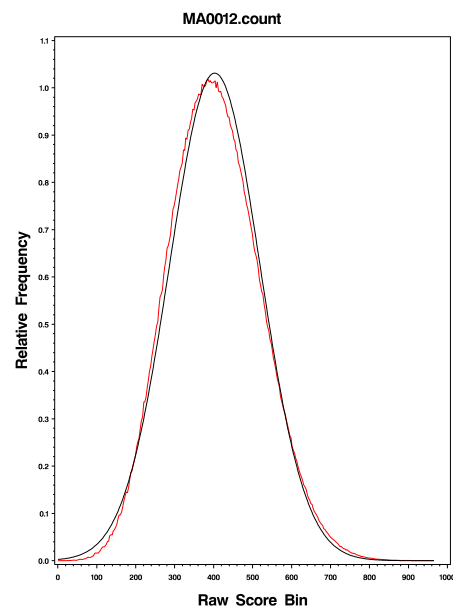
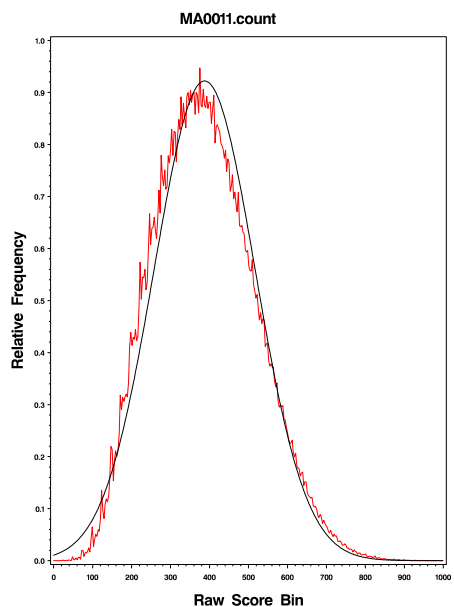
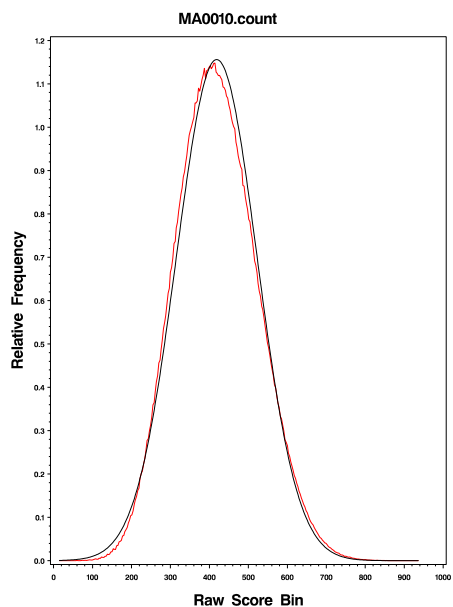
Based on the positions within alignments, the overlap relation was determined between the known and predicted sites. A. When considering mutual overlaps with coverage greater than 50%, only 4 sites were missed as described in Results (GRE, SREBP, NF1/CTF1, and CRE-2). B. When considering any overlap, CRE-2 was the only one missed, which turned out to be rodent-specific. All other known TFBS overlapped the predictions.

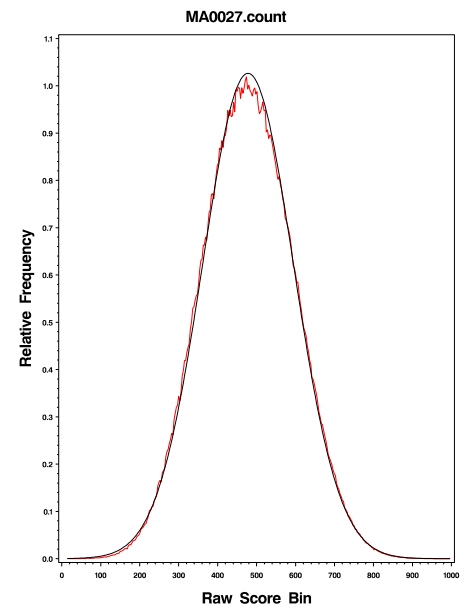
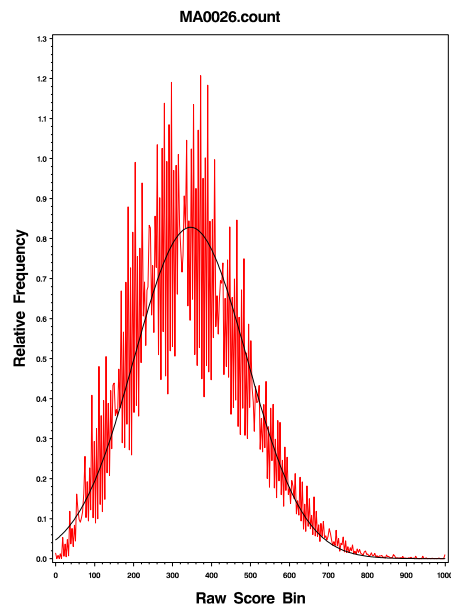
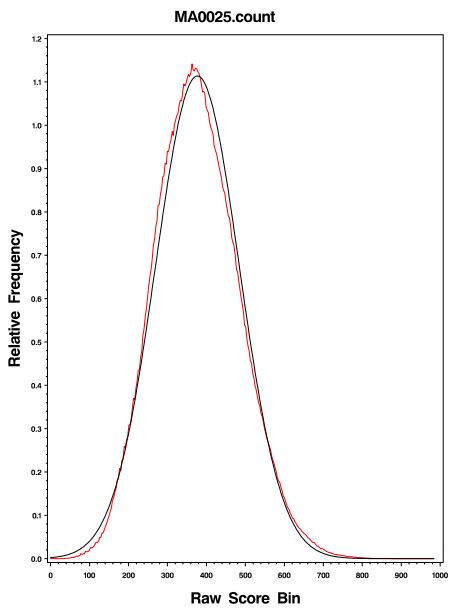
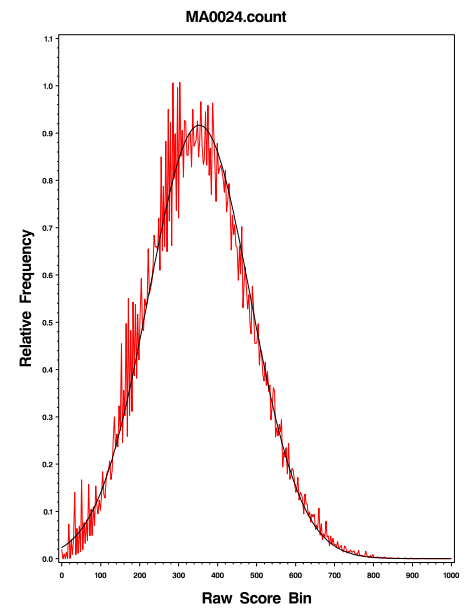
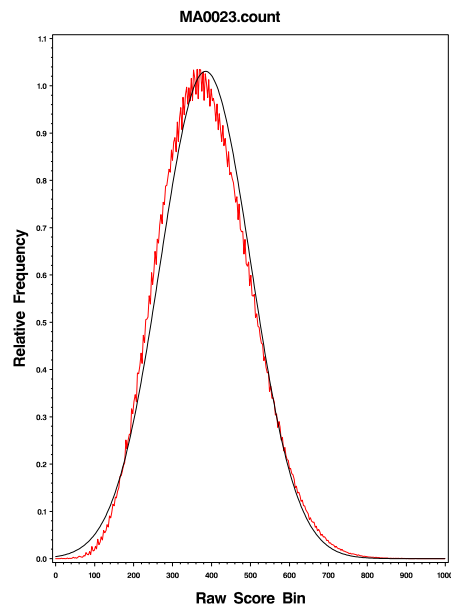
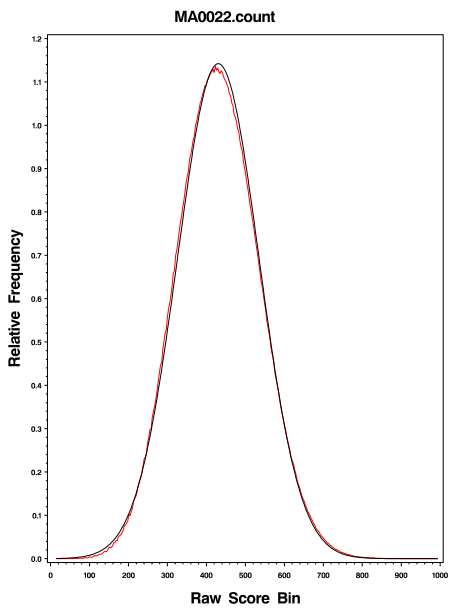
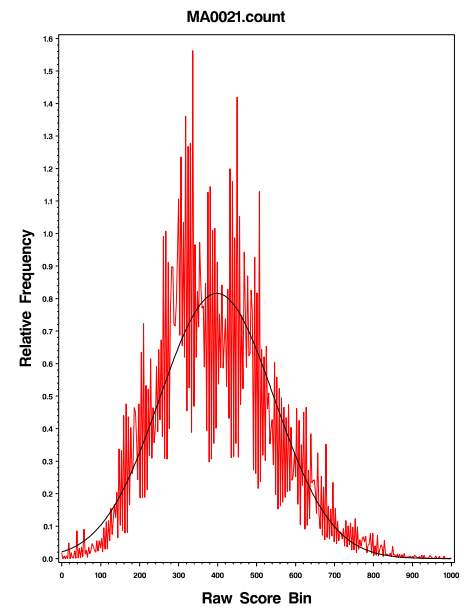
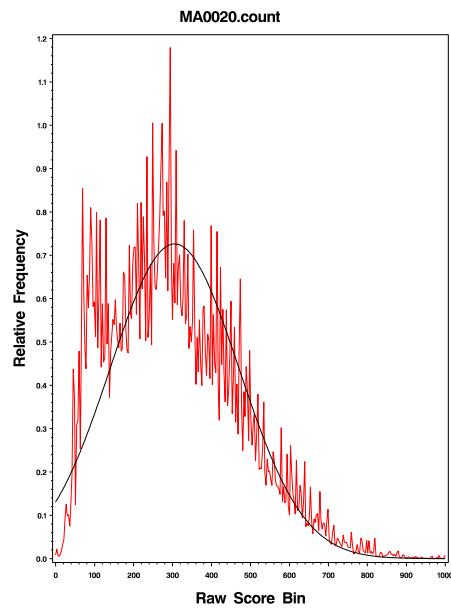
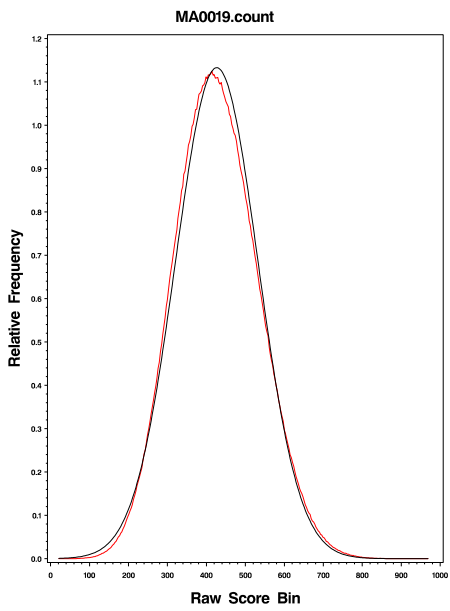
Table S6. Overlap relations between newly discovered and predicted sites.

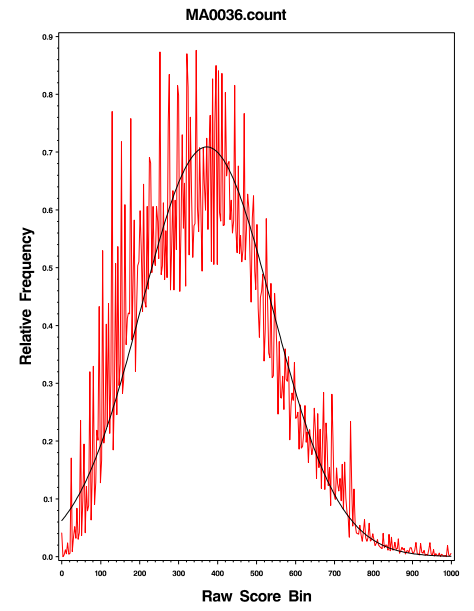
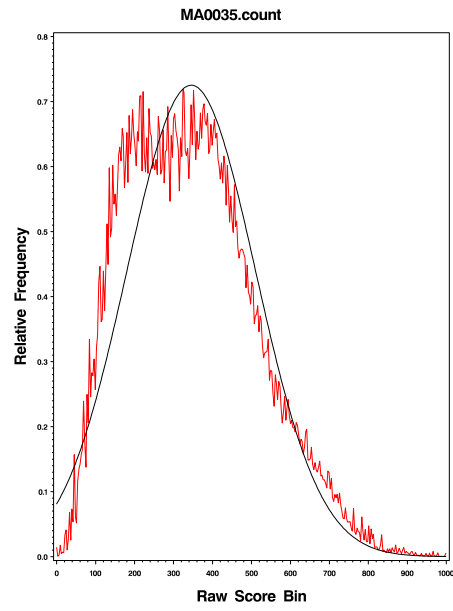
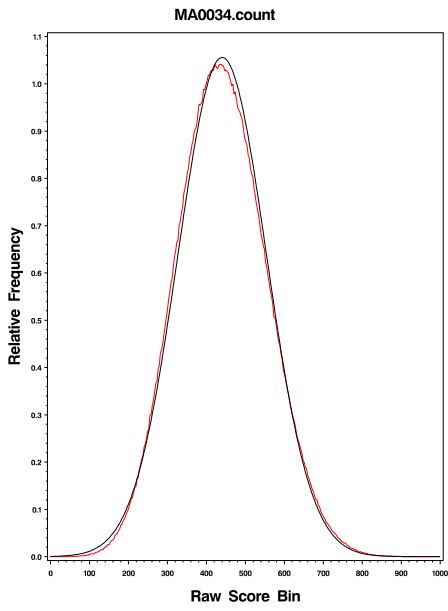
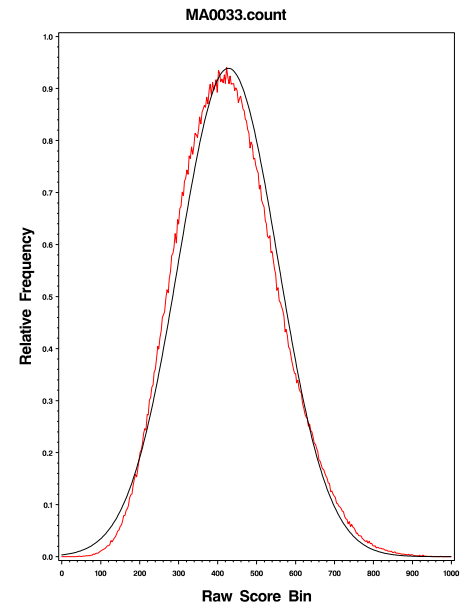
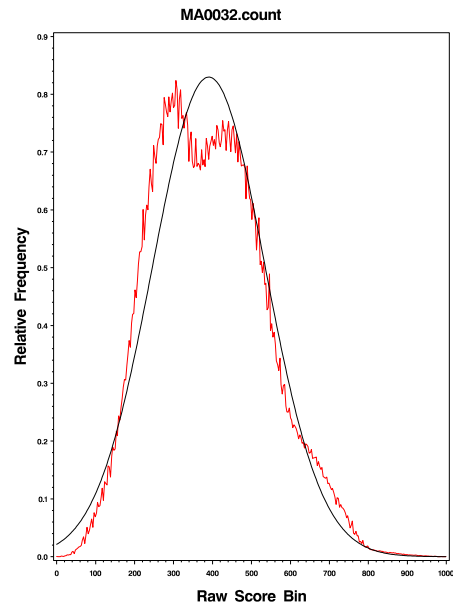
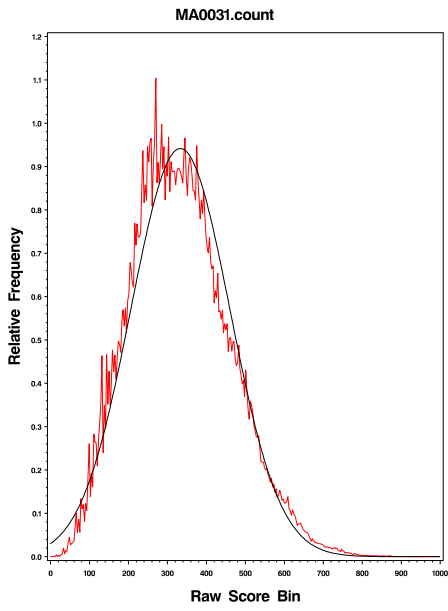
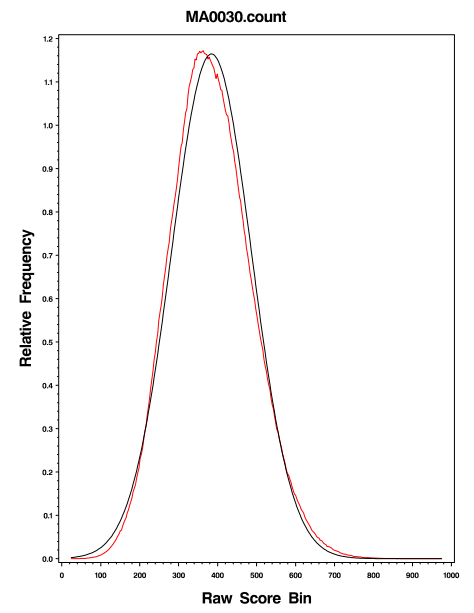
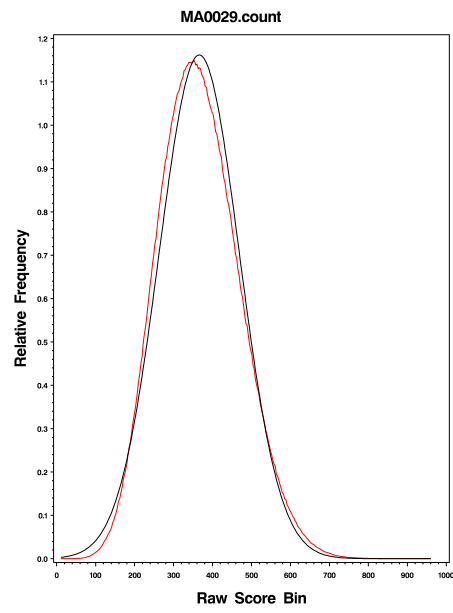
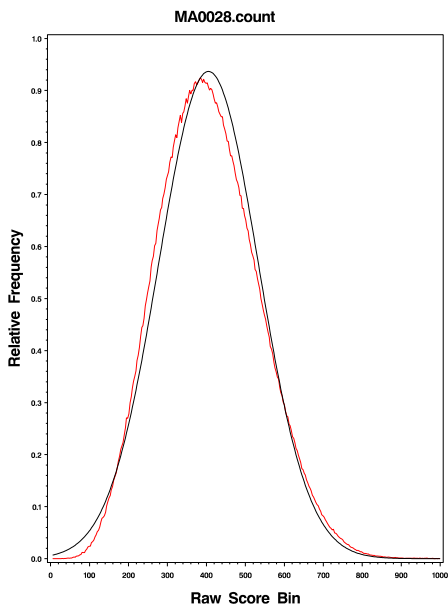
There were 7 potential novel sites with strong sequence conservation across species. They were listed in Supplemental Table S4 and displayed as a separated track (blue) in Fig. 2. For the 5 newly discovered proximal TFBS, their overlap relations with predictions were listed: A. Mutual overlaps with coverage greater than 50%. B. All overlaps.

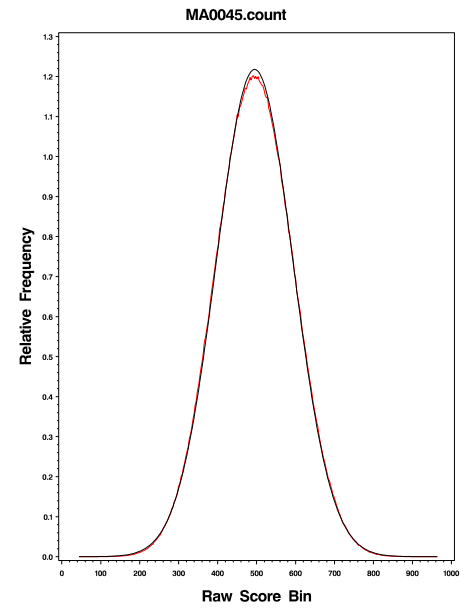
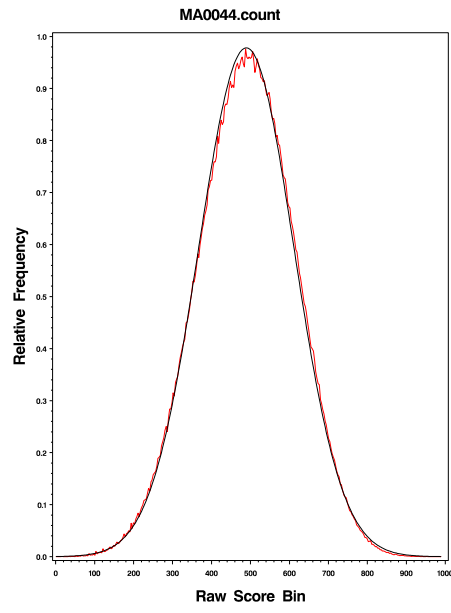
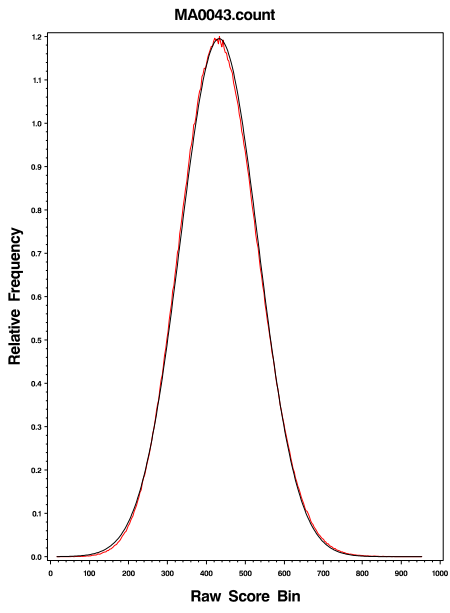
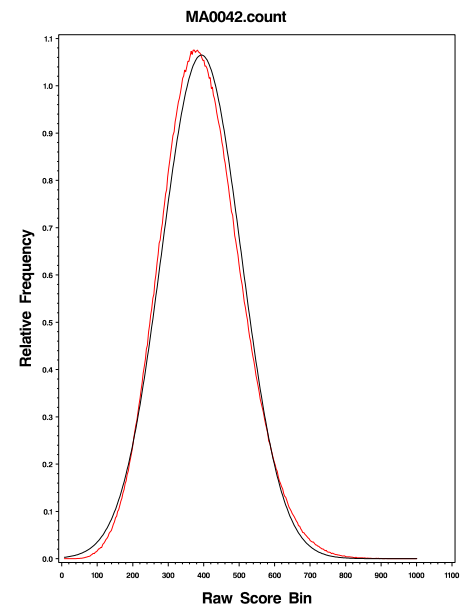
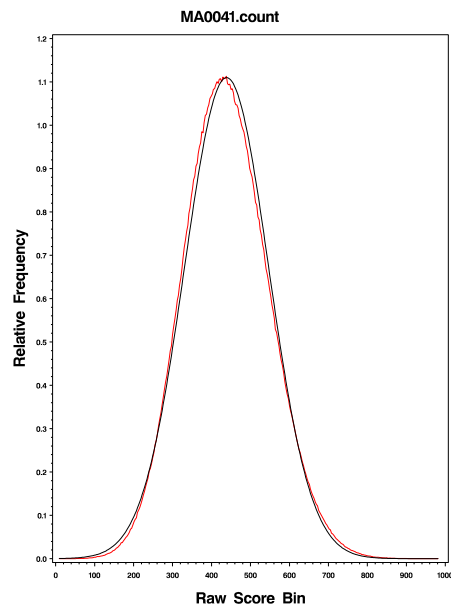
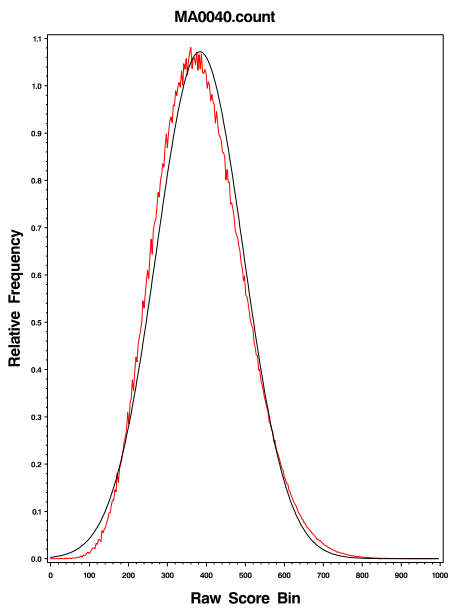
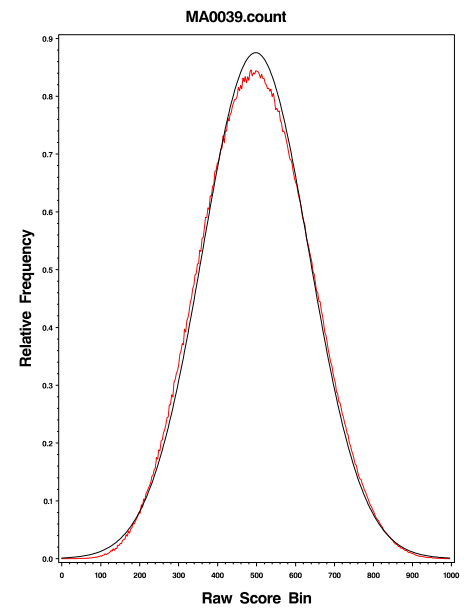
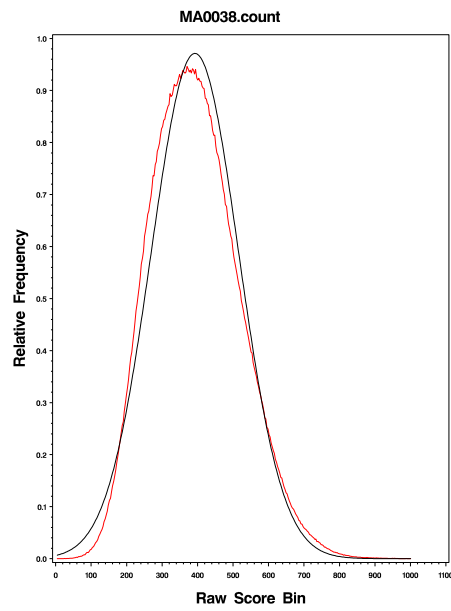
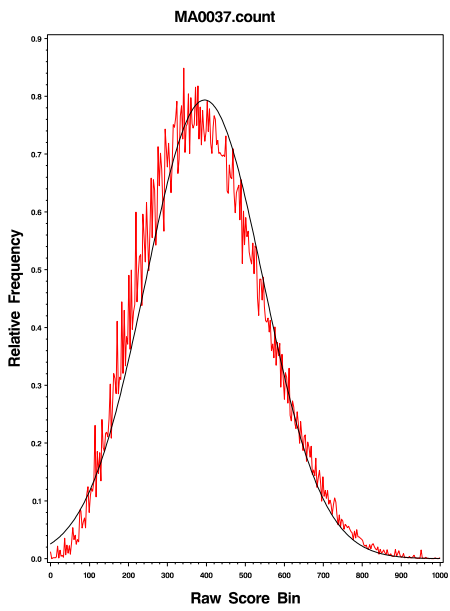
Figure S1. Histograms of raw scores of 308 JASPAR TFBS matrices.

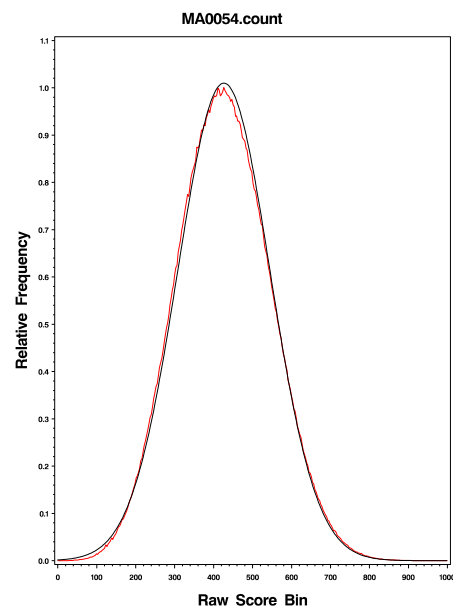
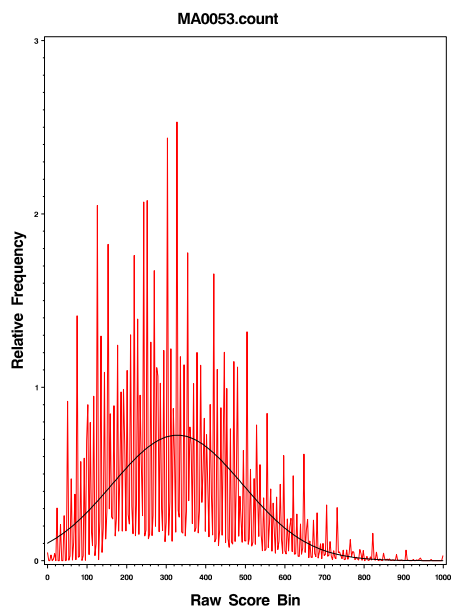
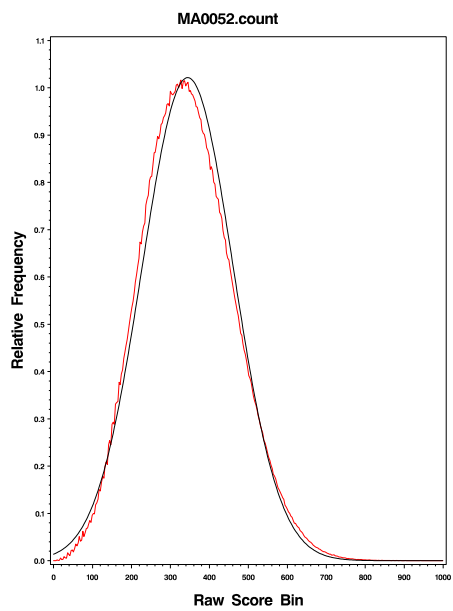
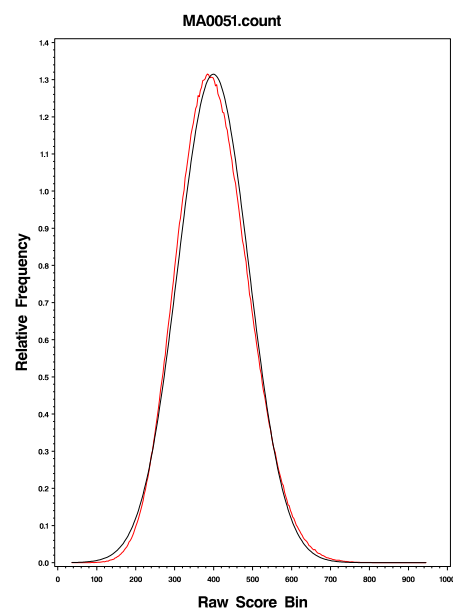
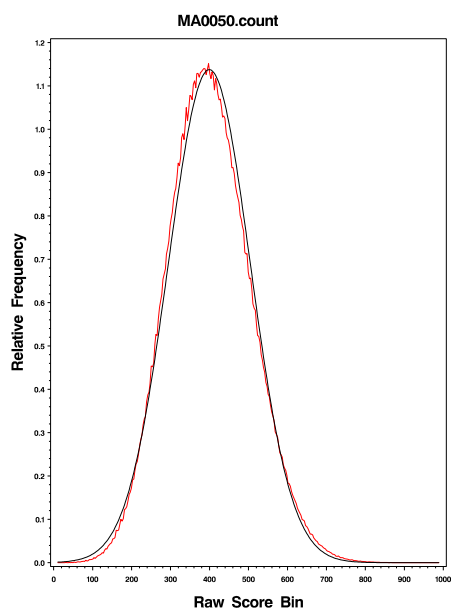
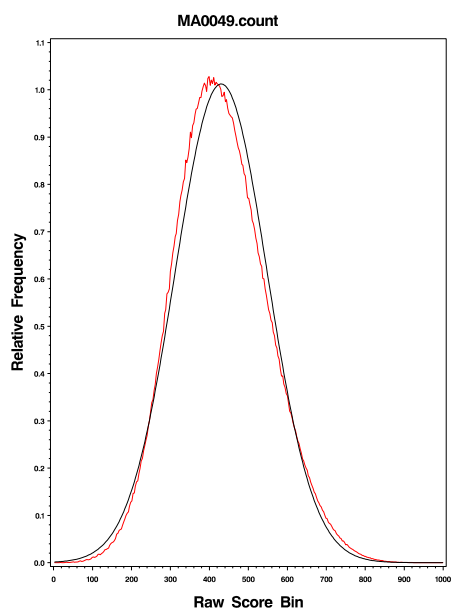
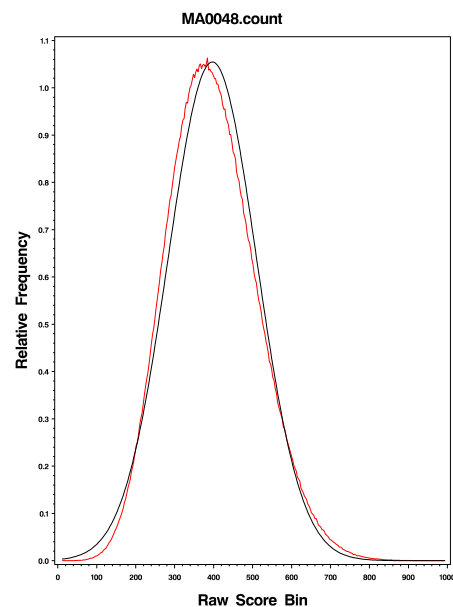
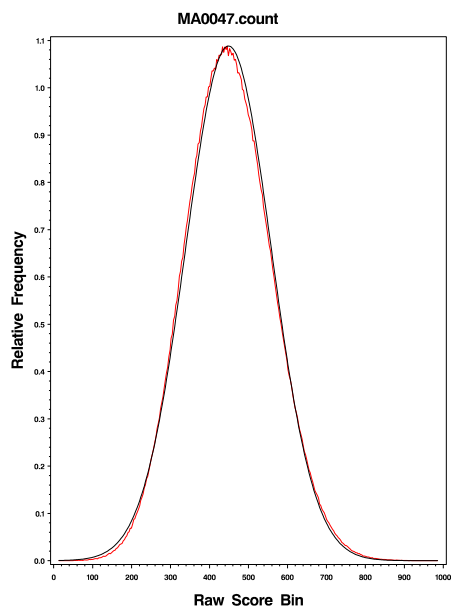
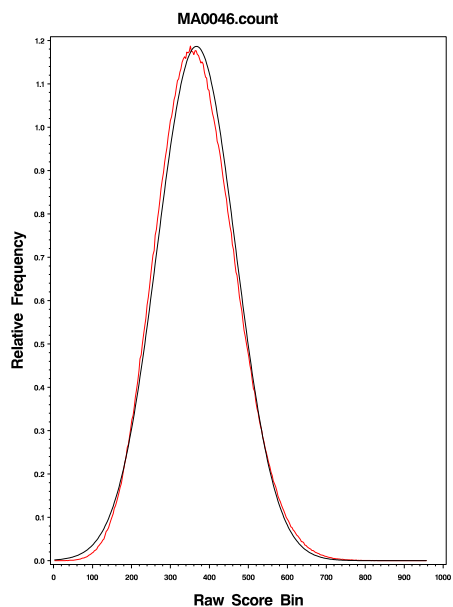


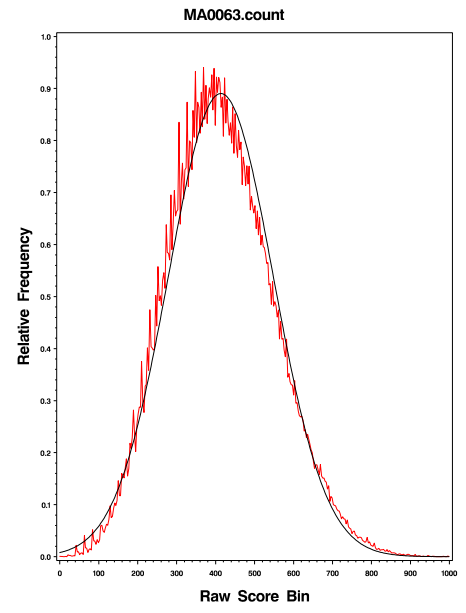
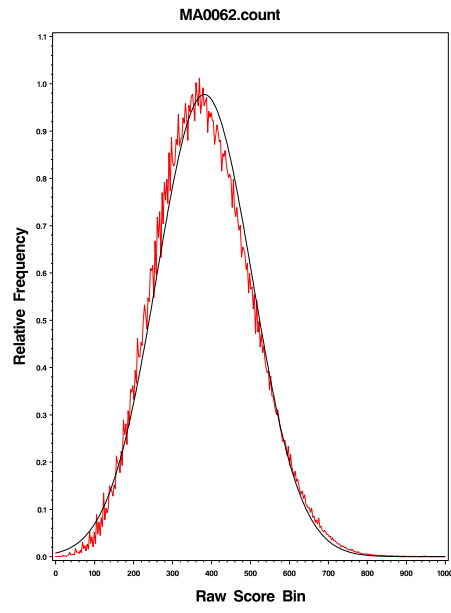
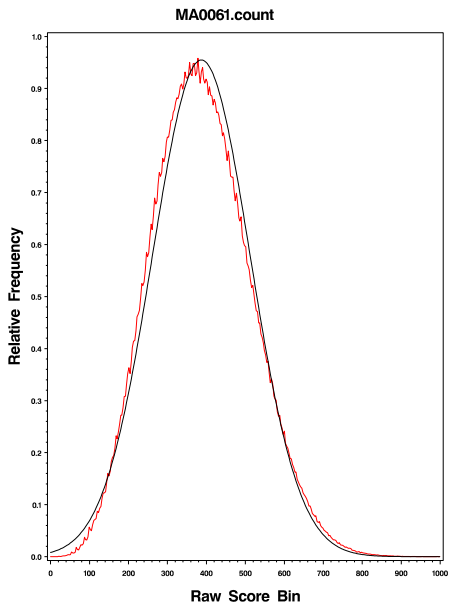
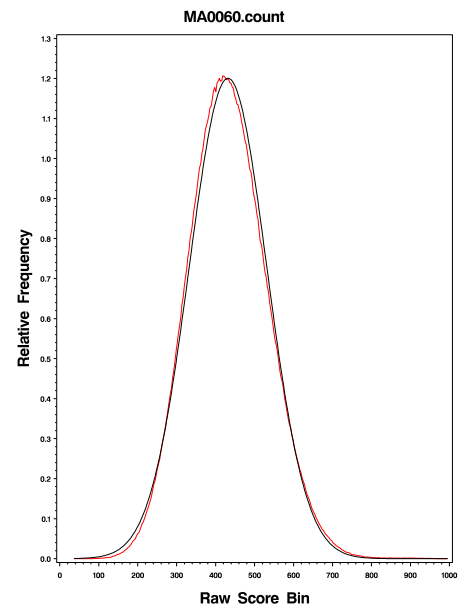
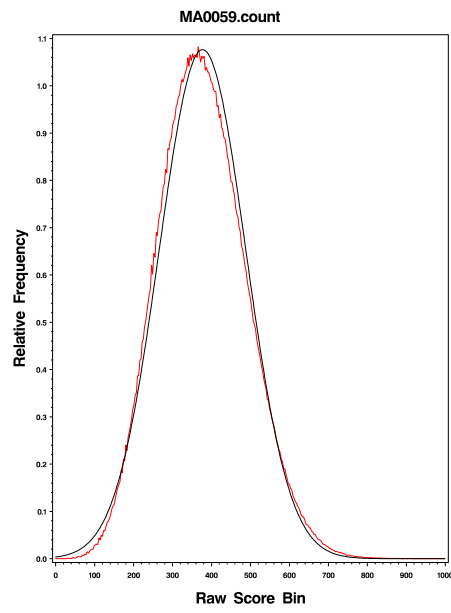
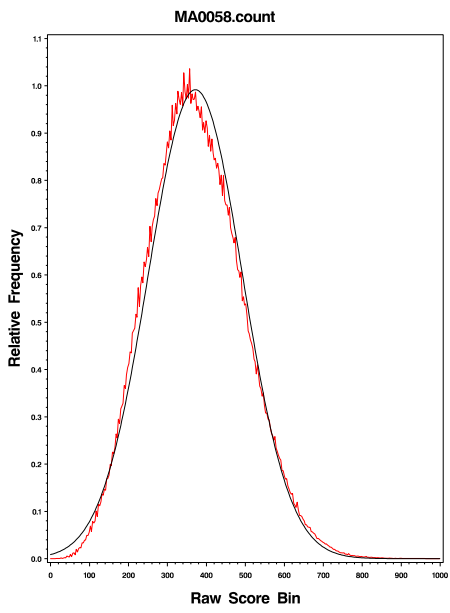
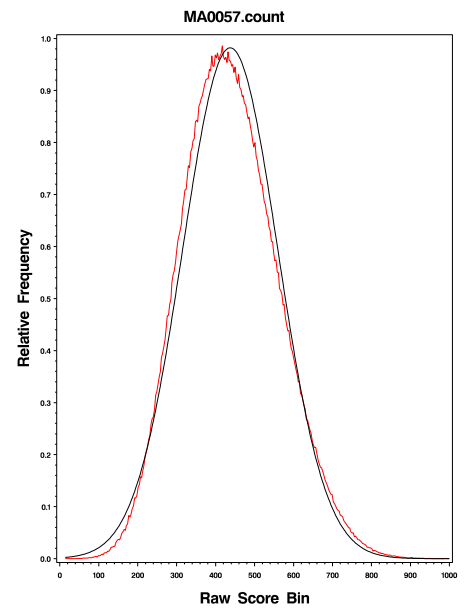
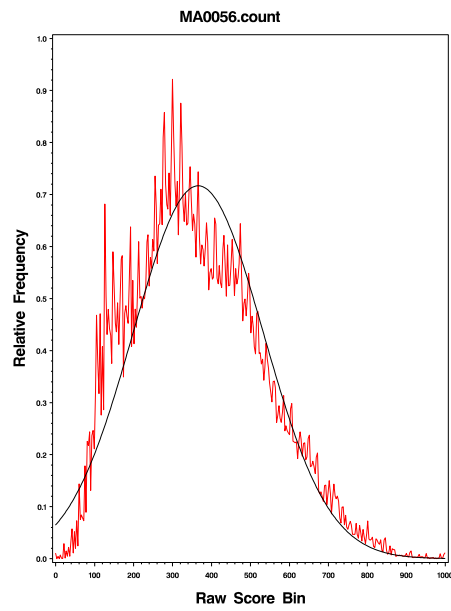
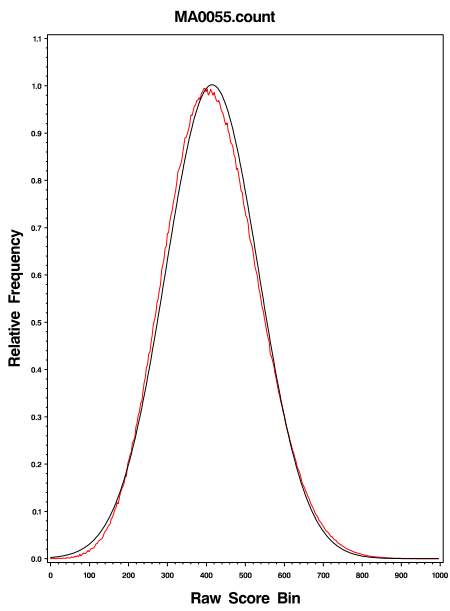


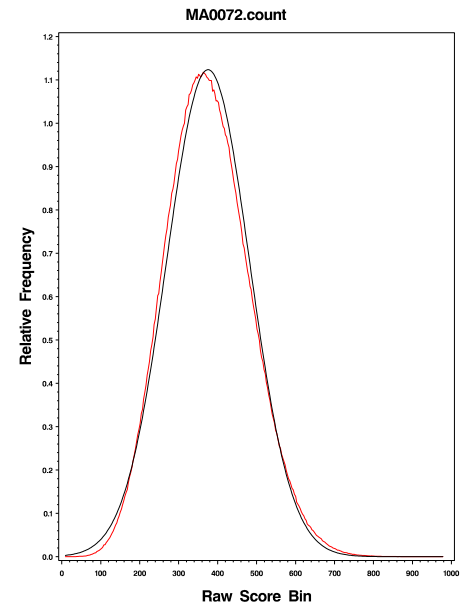
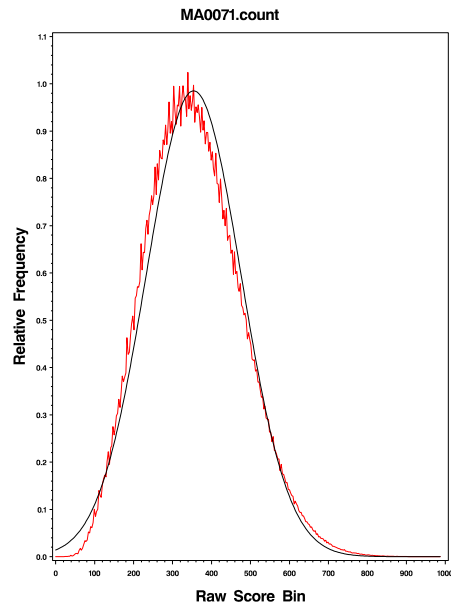
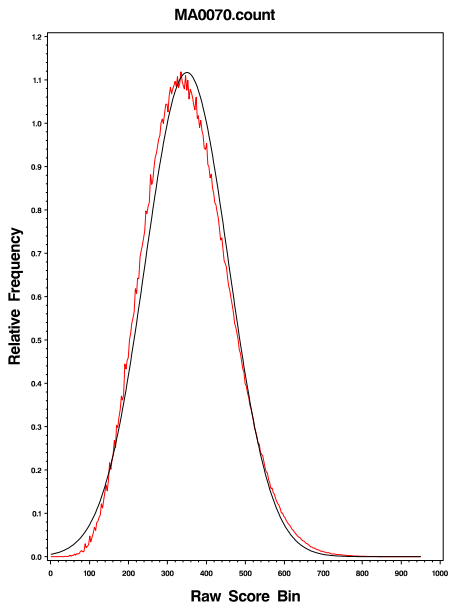
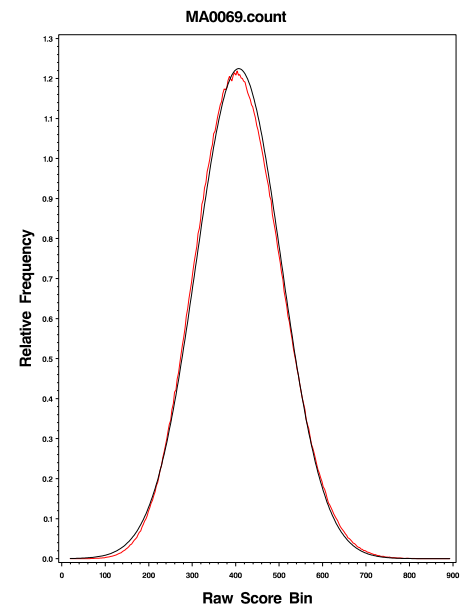
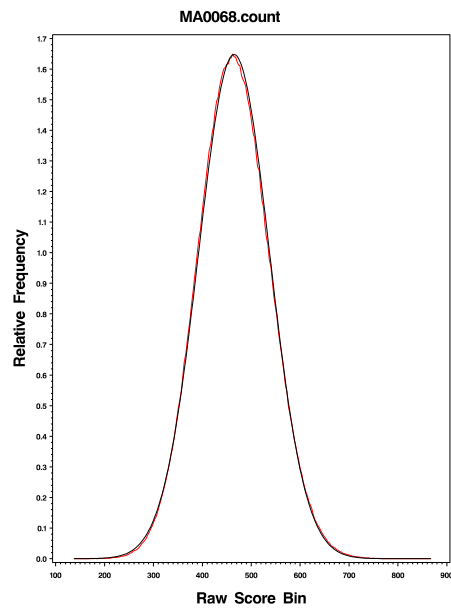
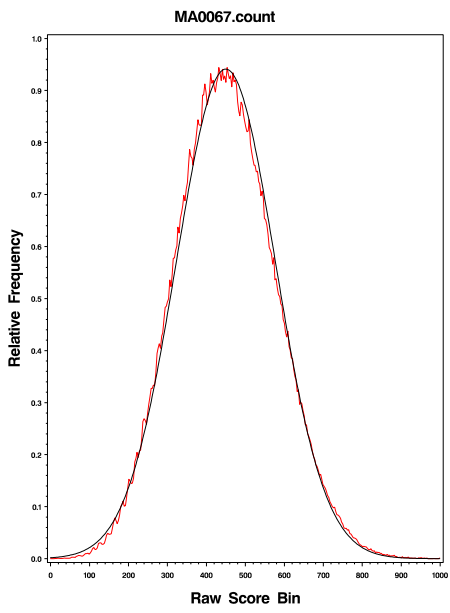
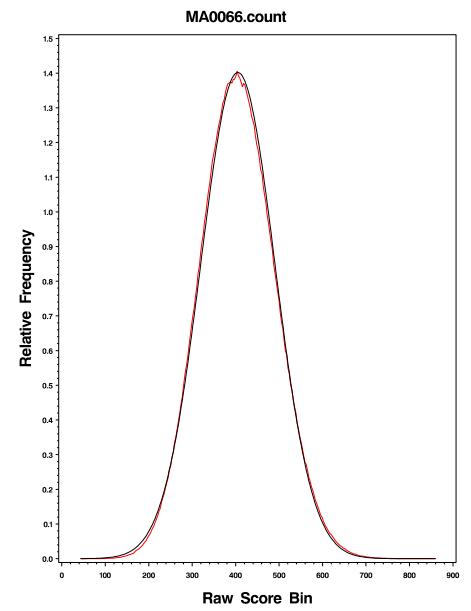
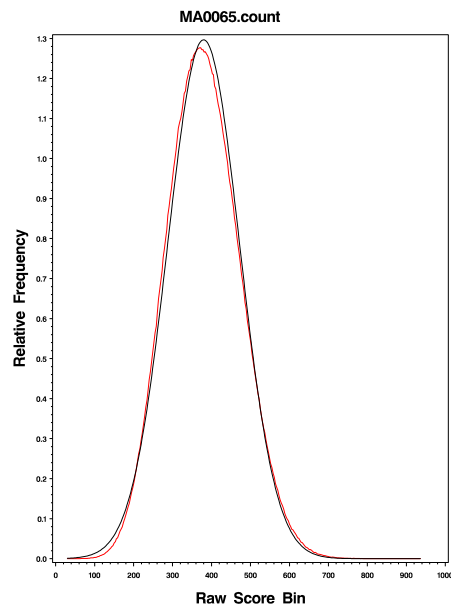
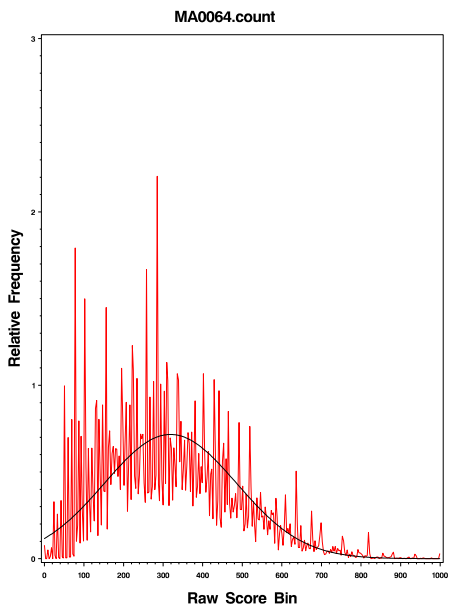


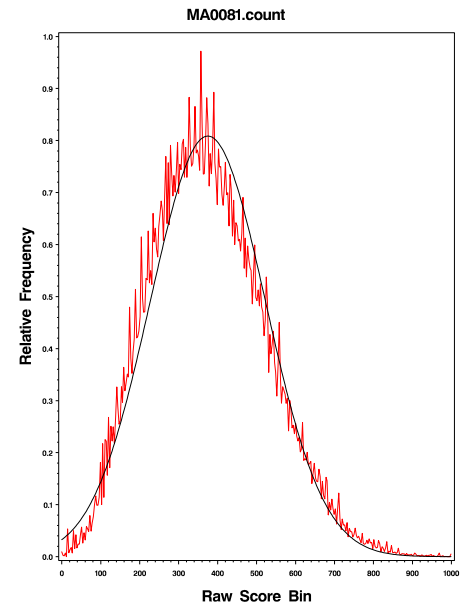
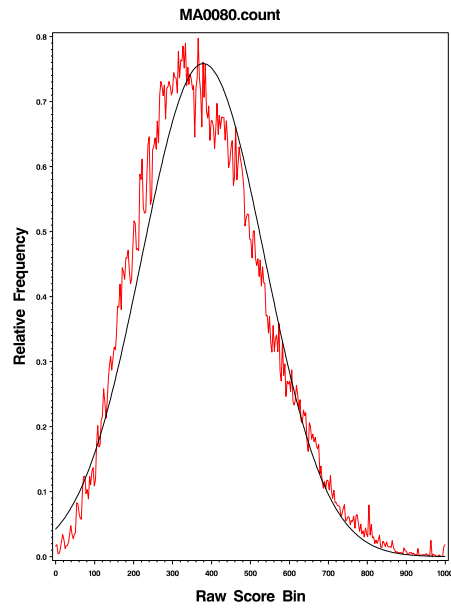
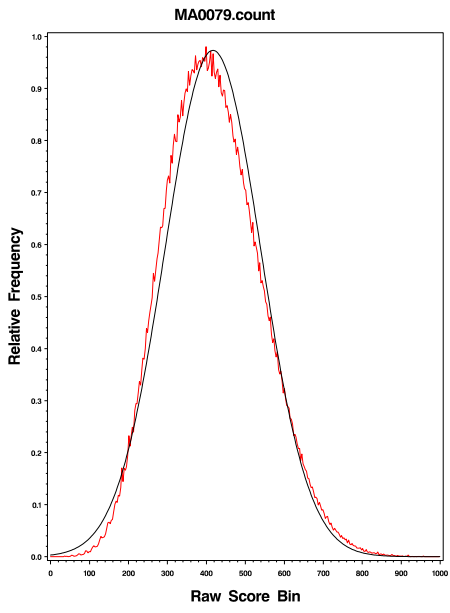
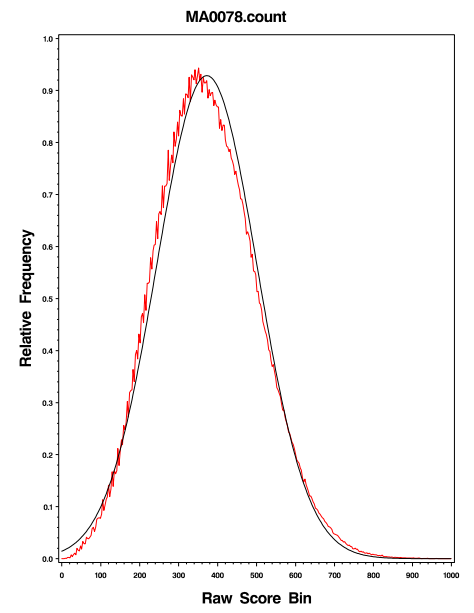
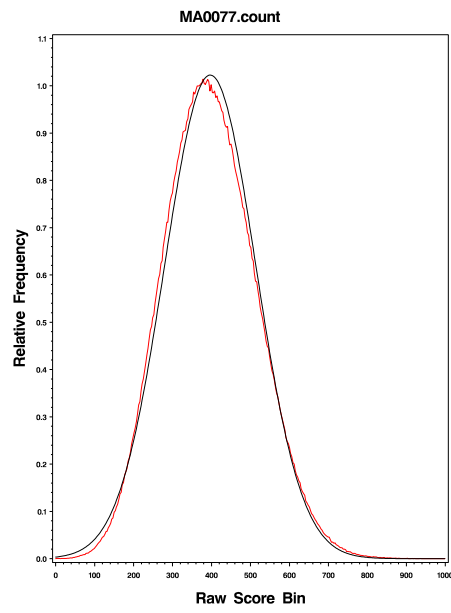
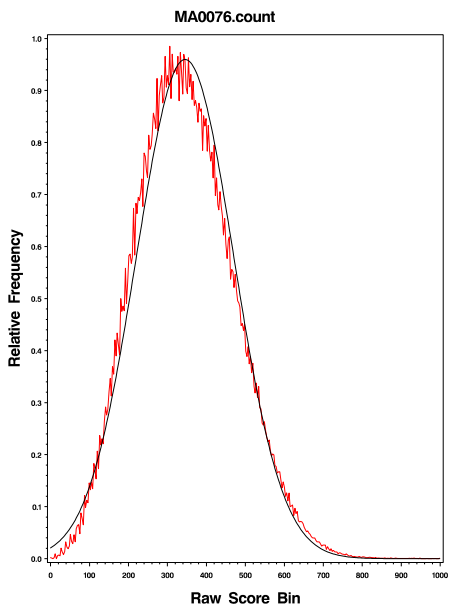
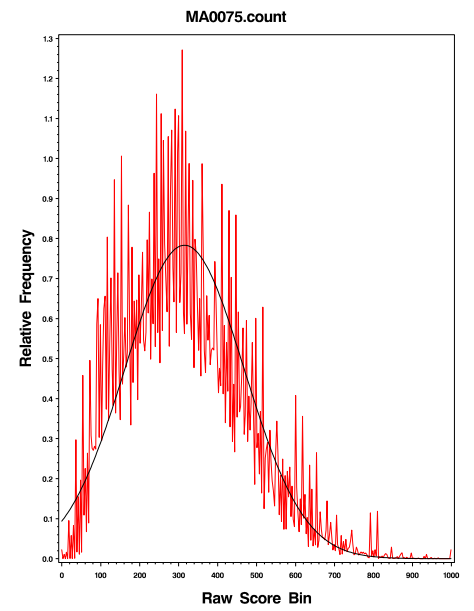
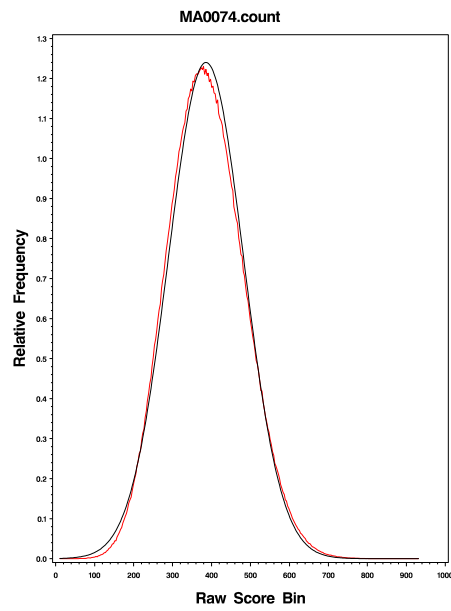
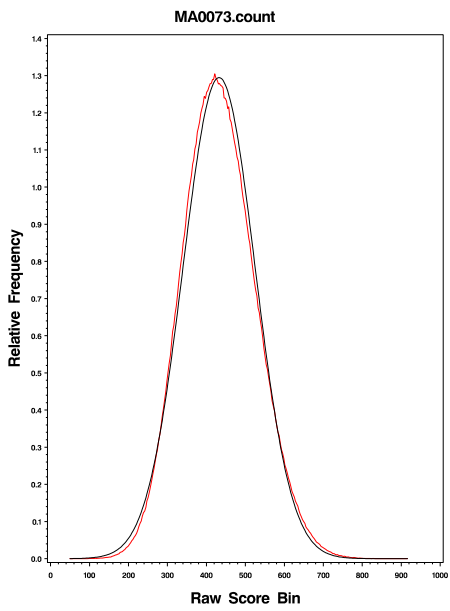


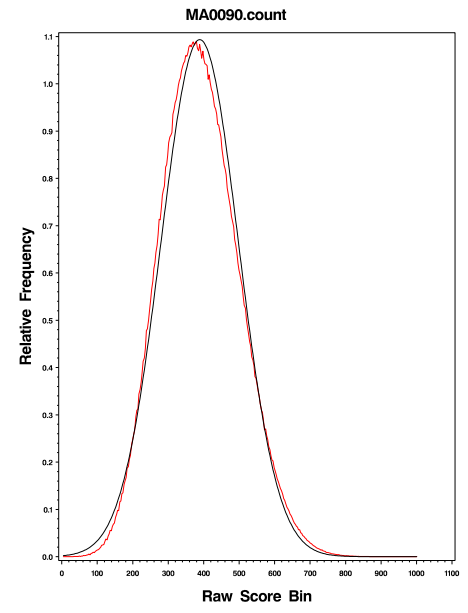
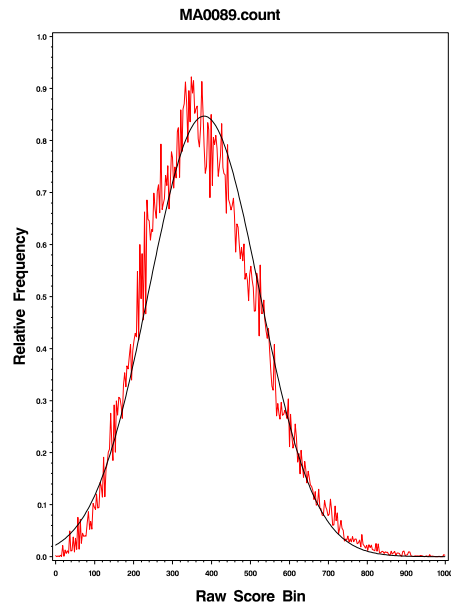
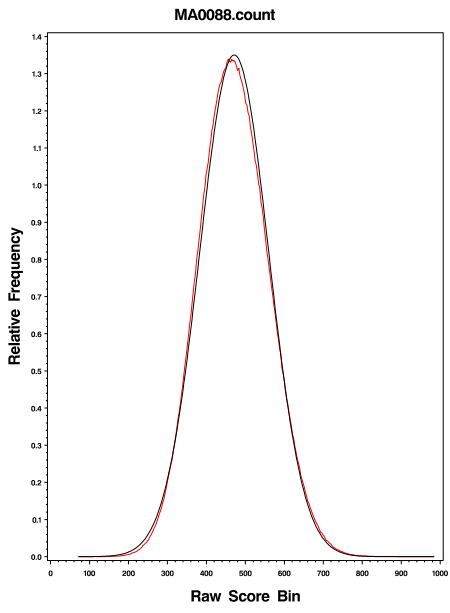
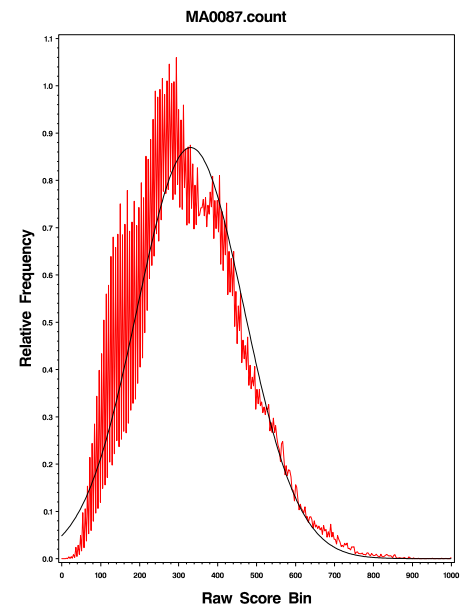
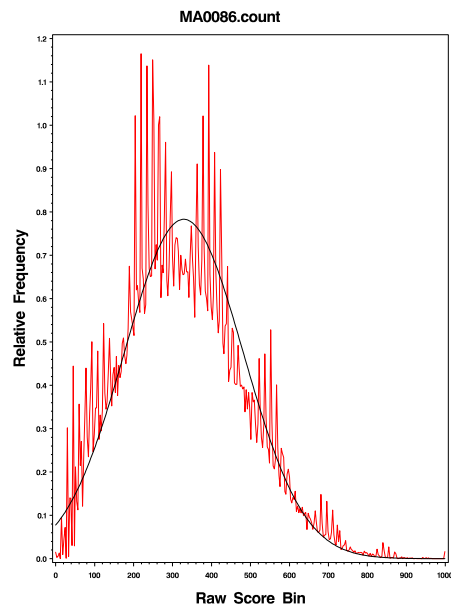
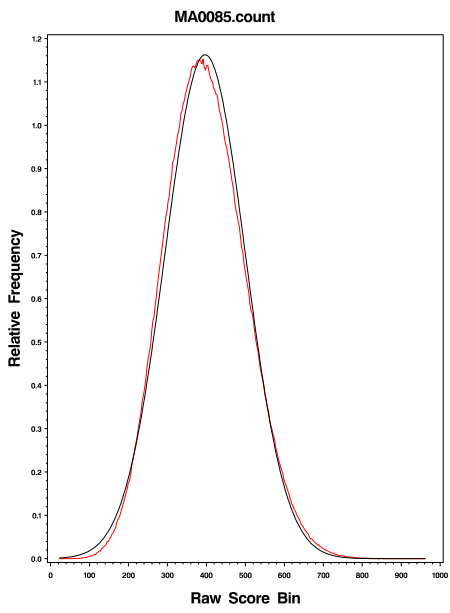
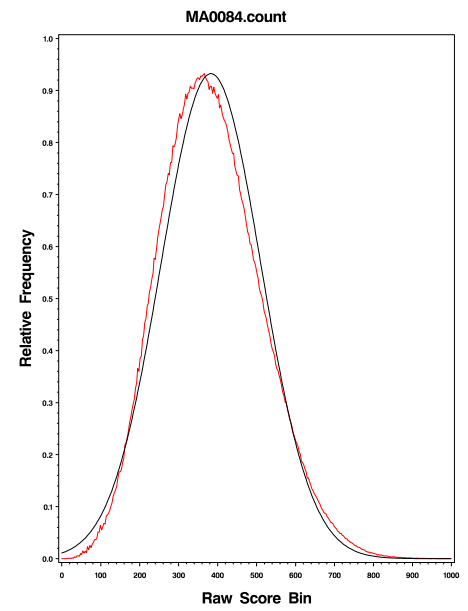
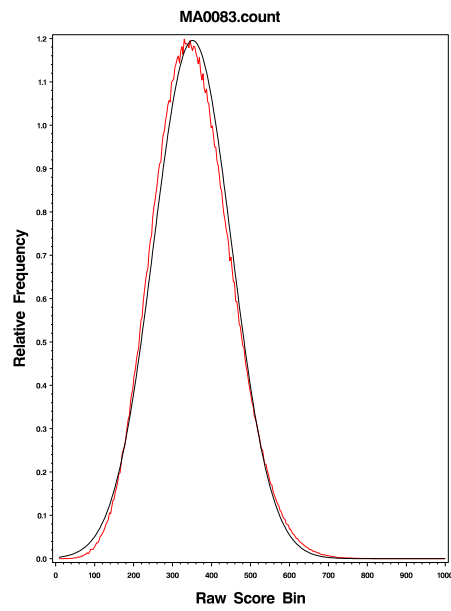
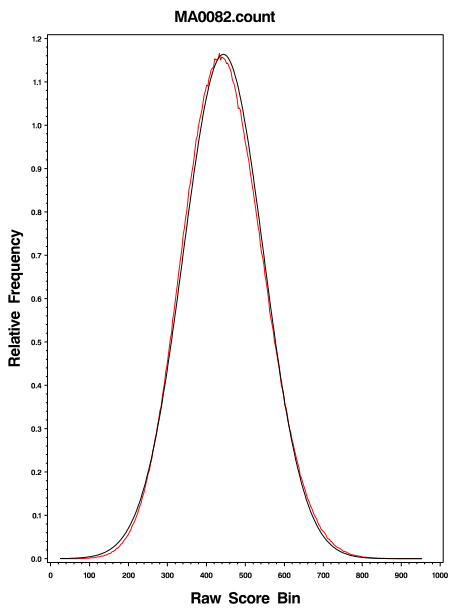


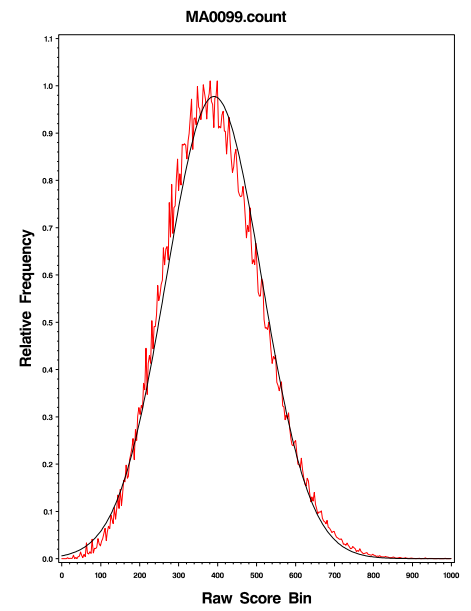
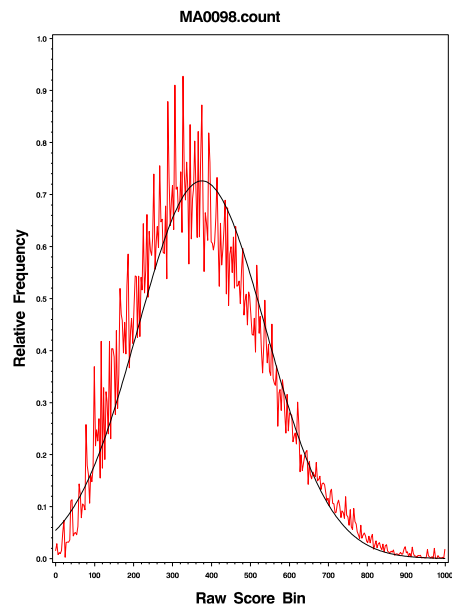
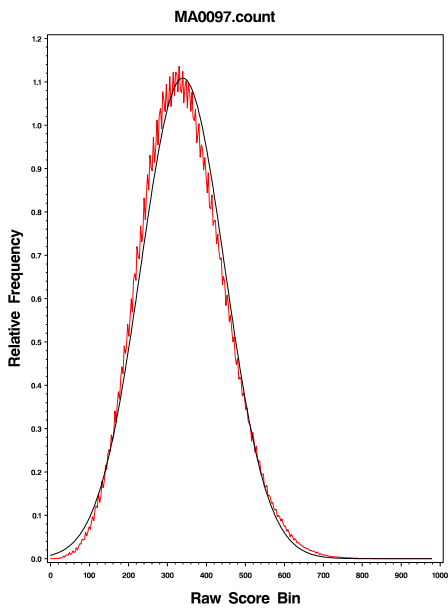
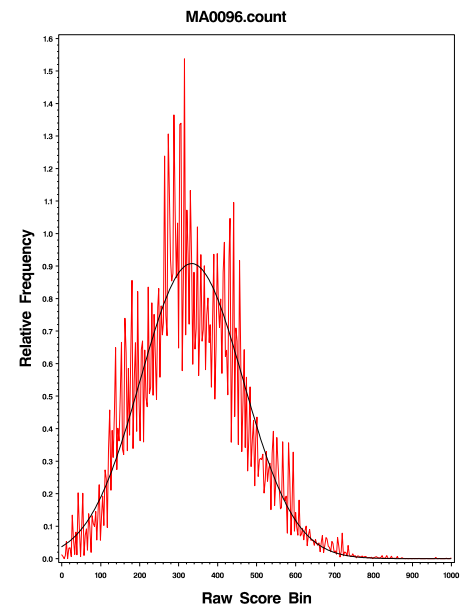
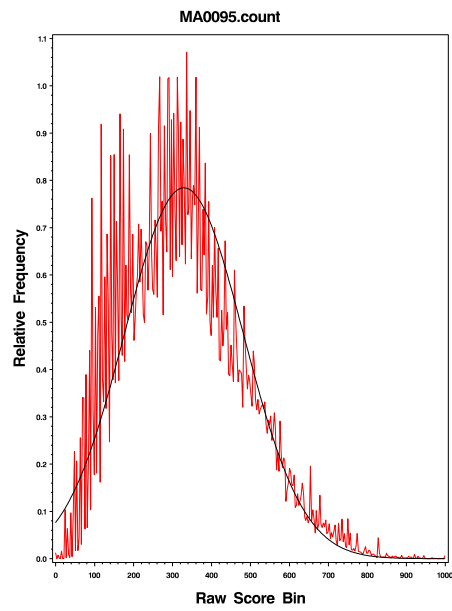
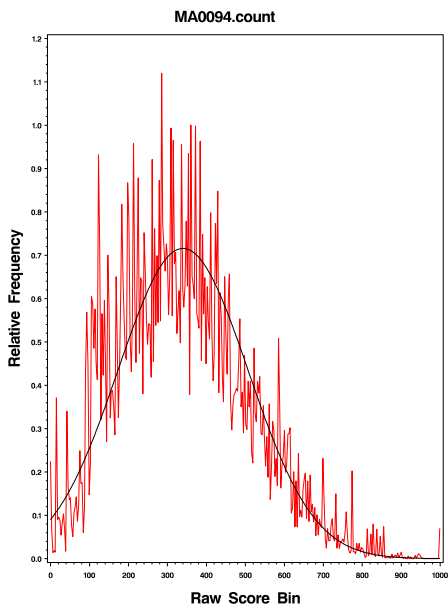
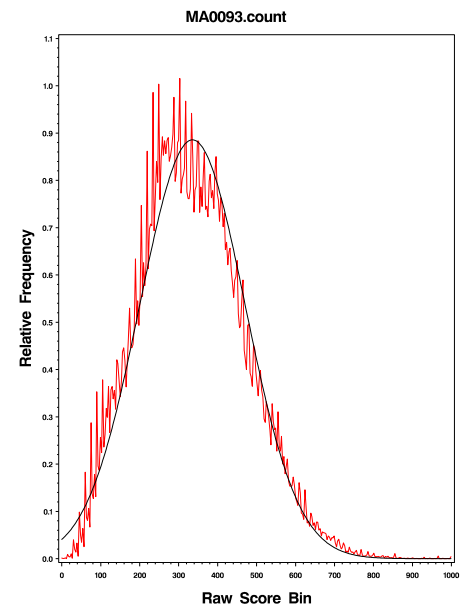
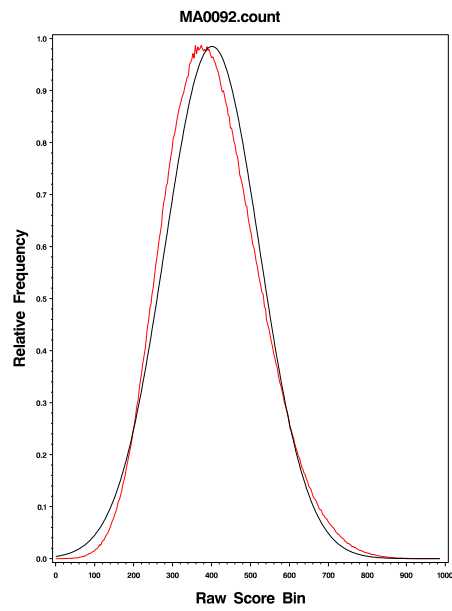
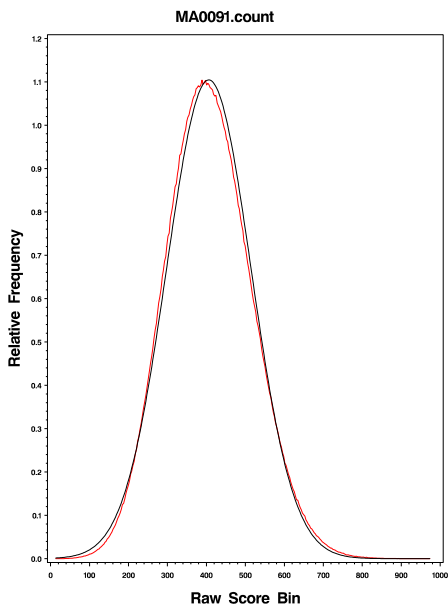


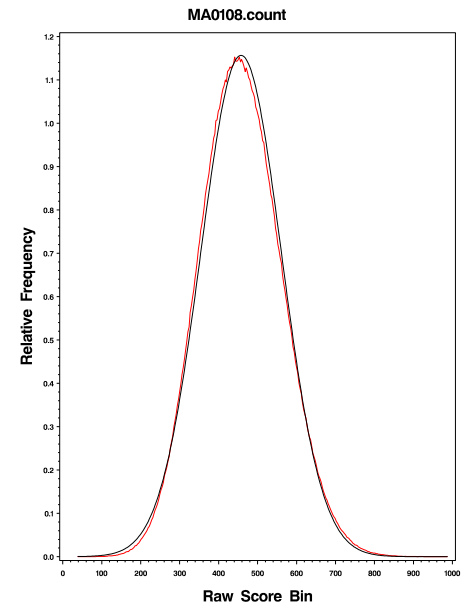
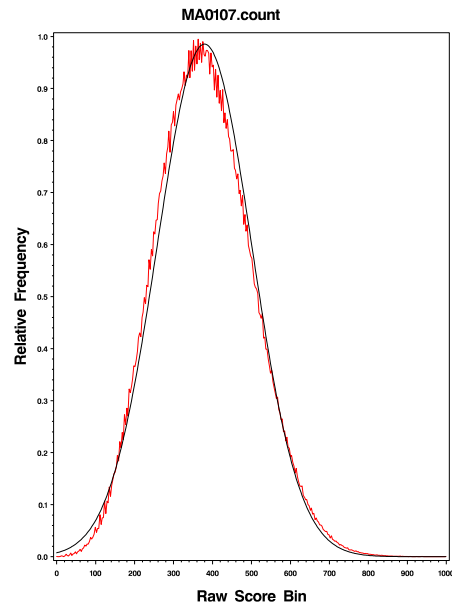
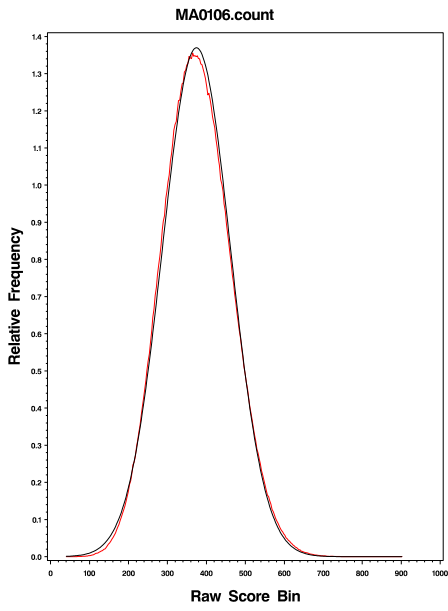
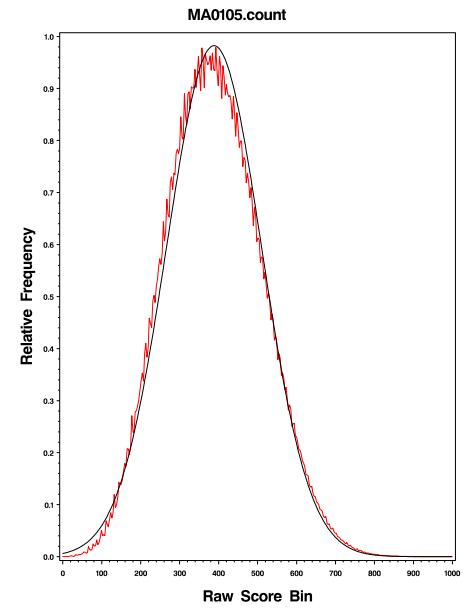
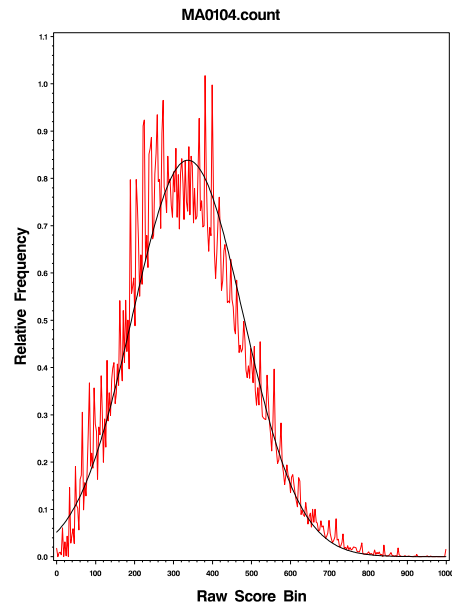
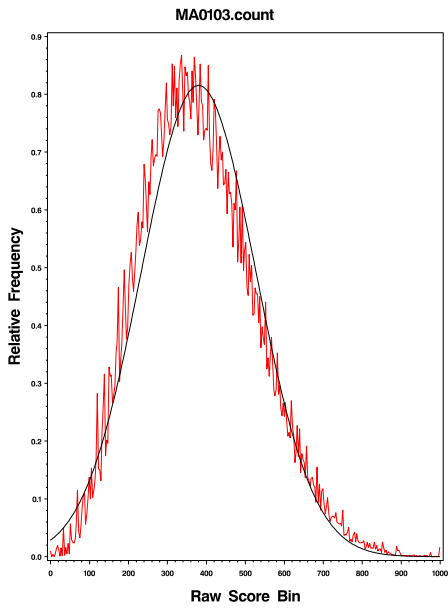
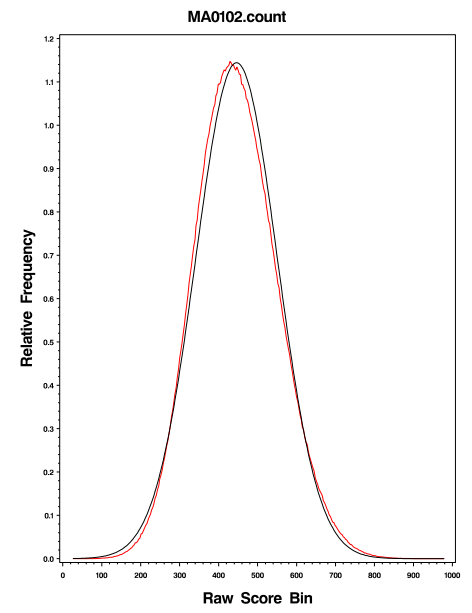
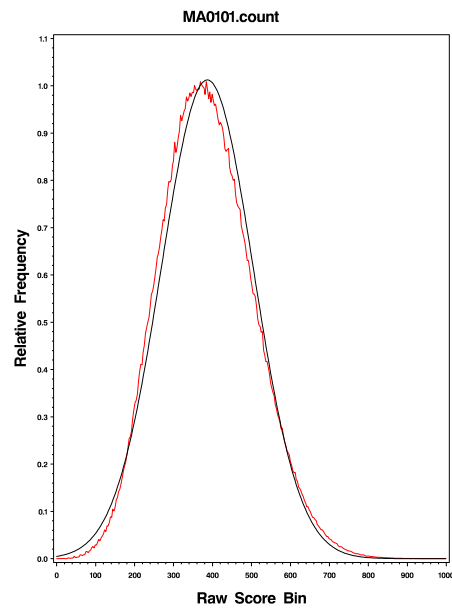
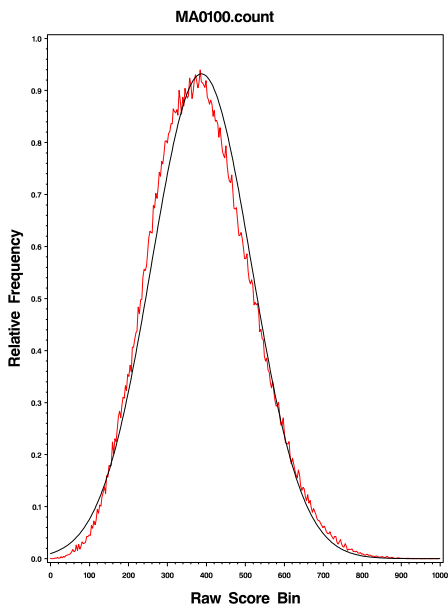


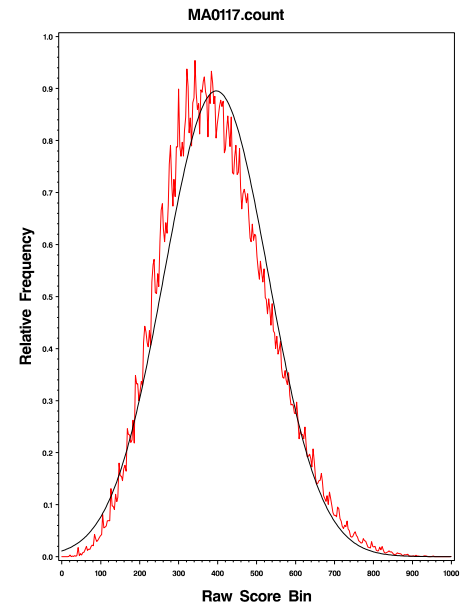
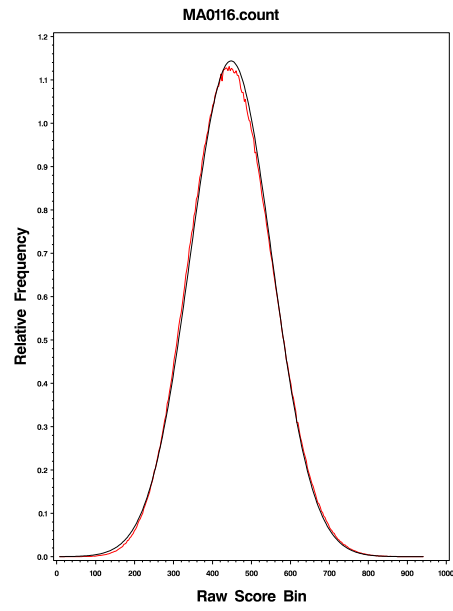
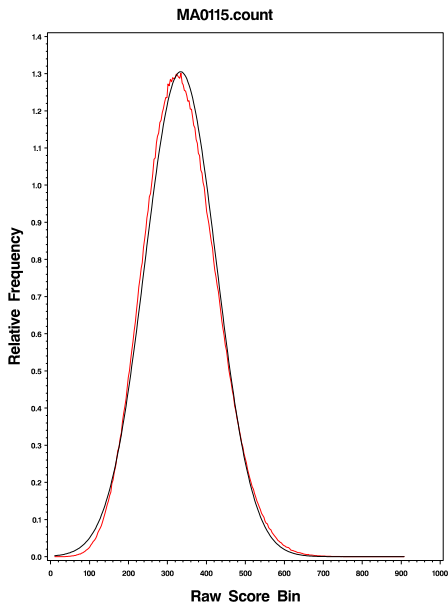
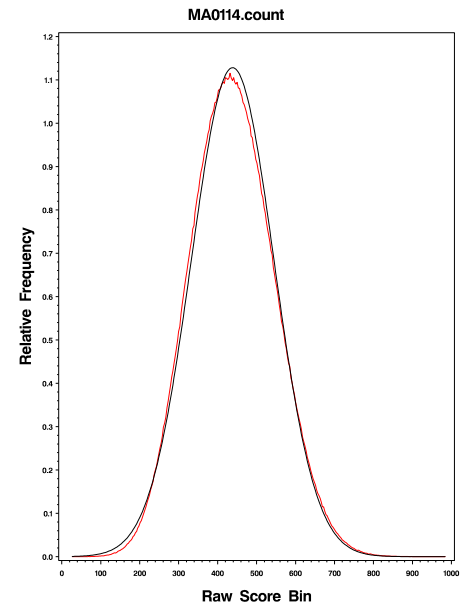
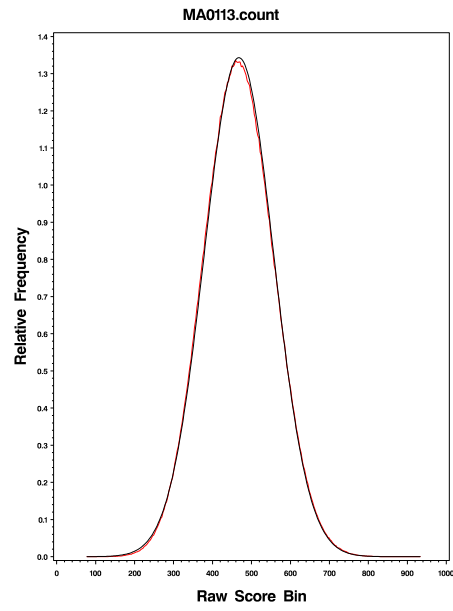
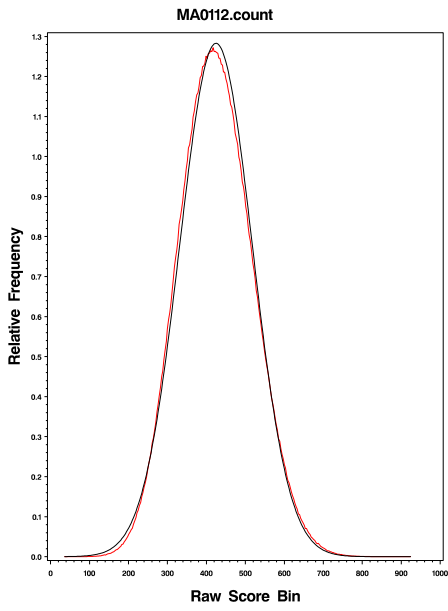
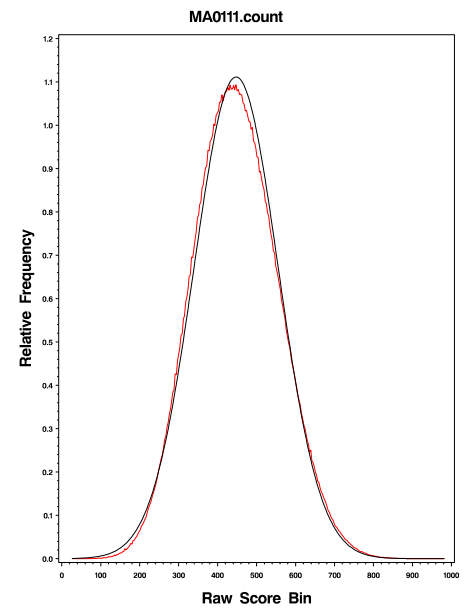
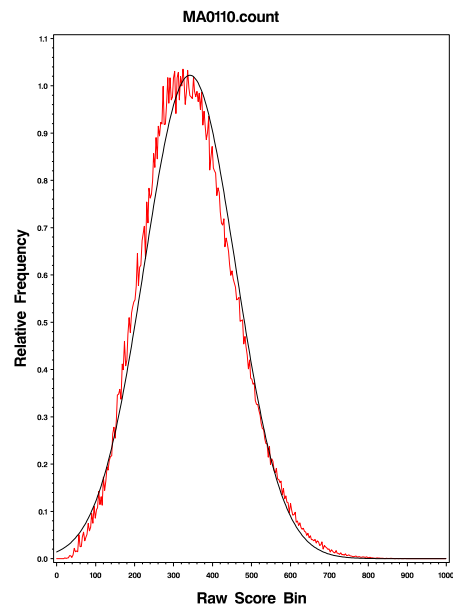
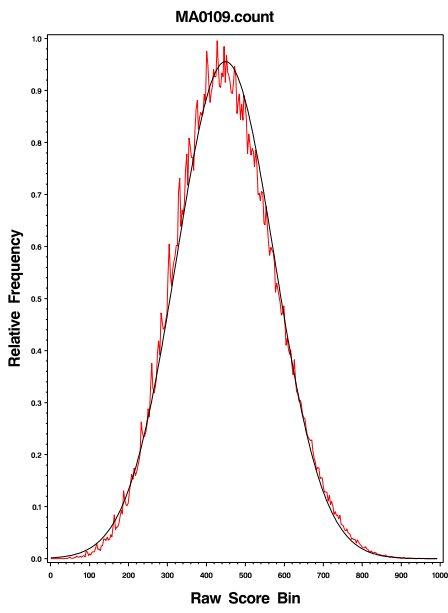


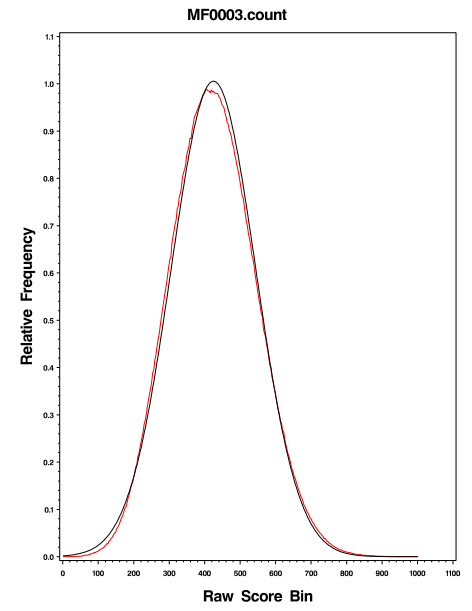
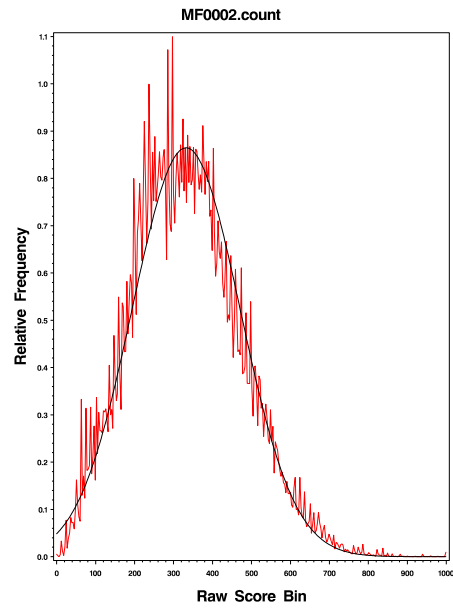
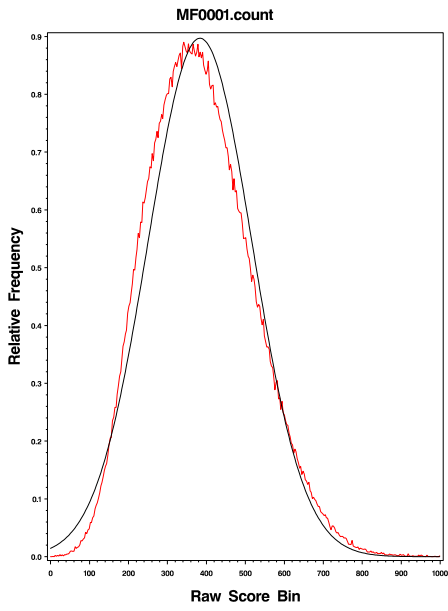
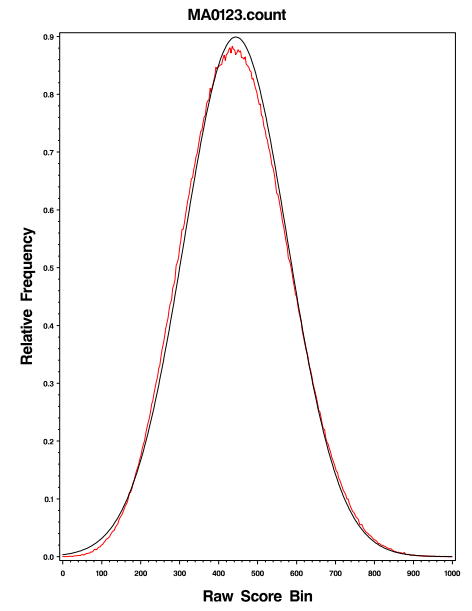
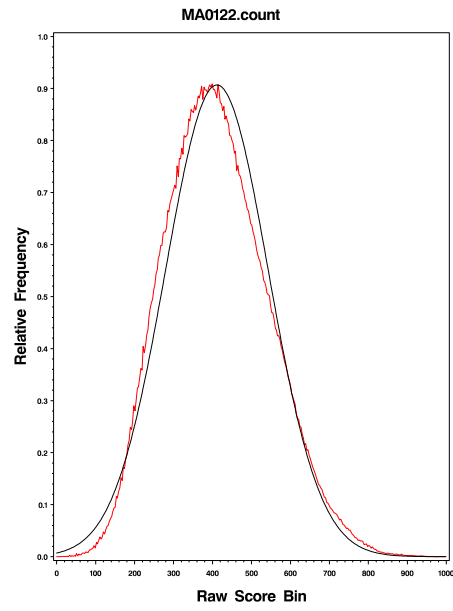
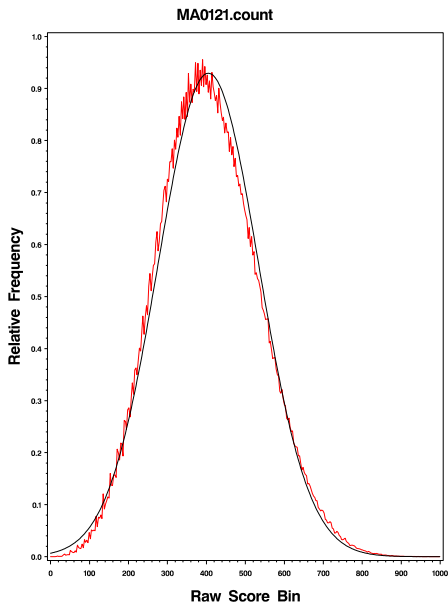
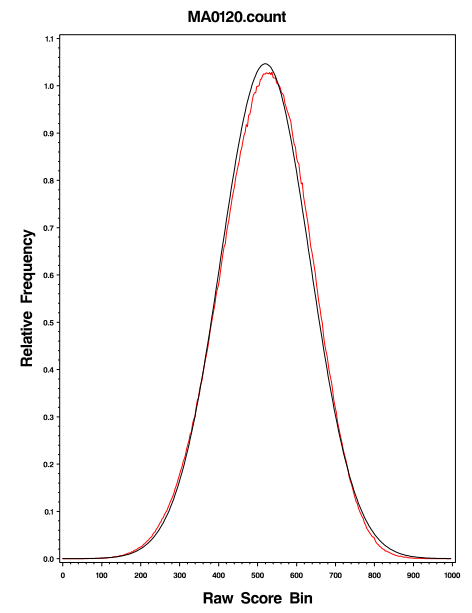
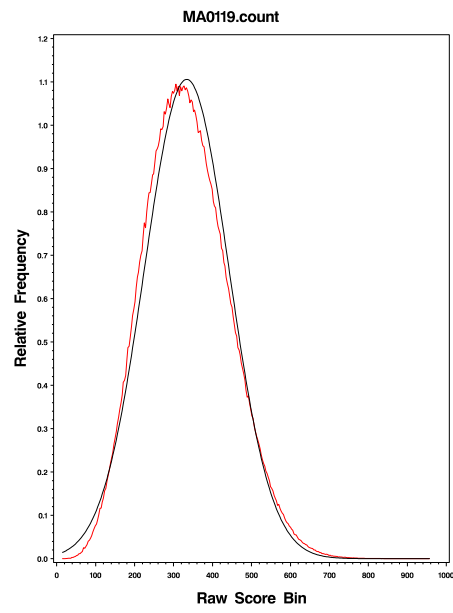
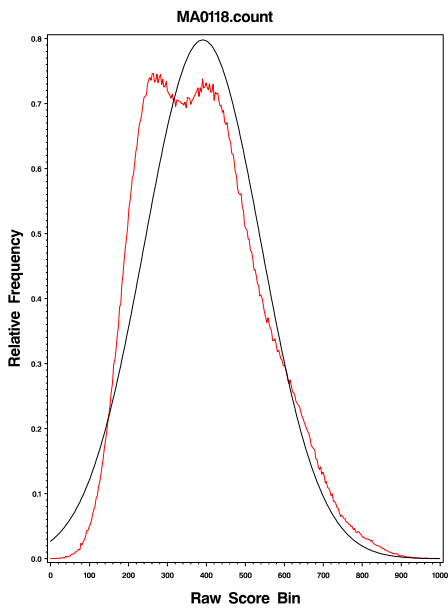


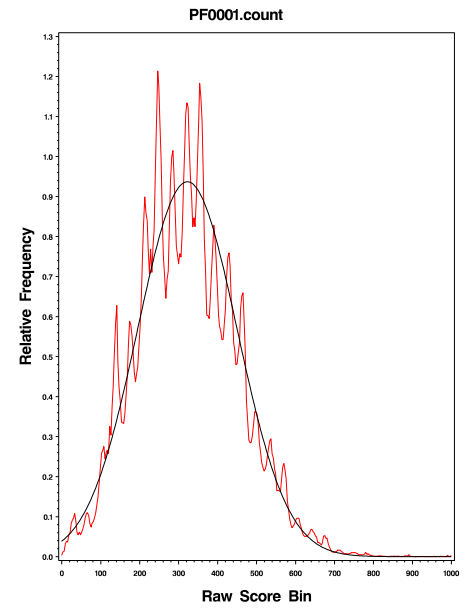
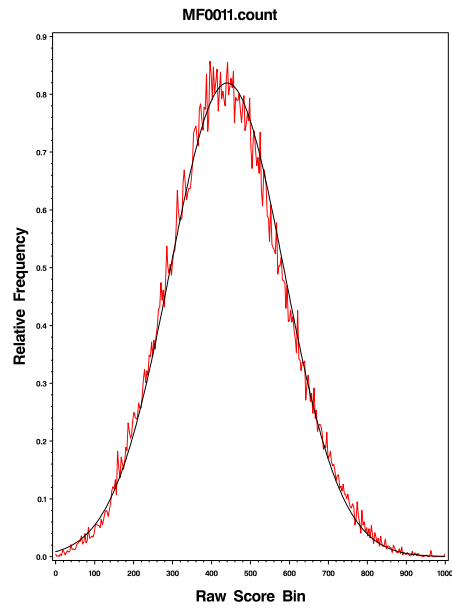
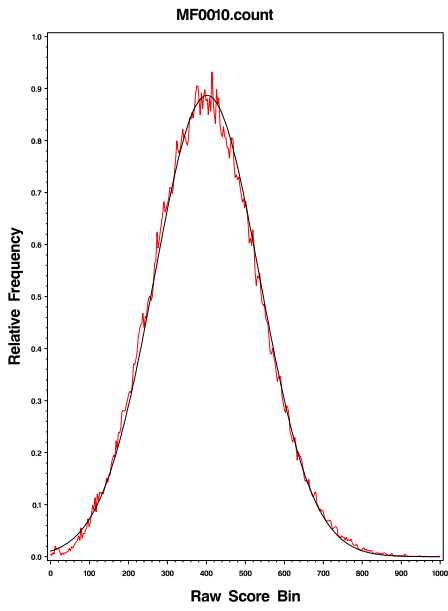
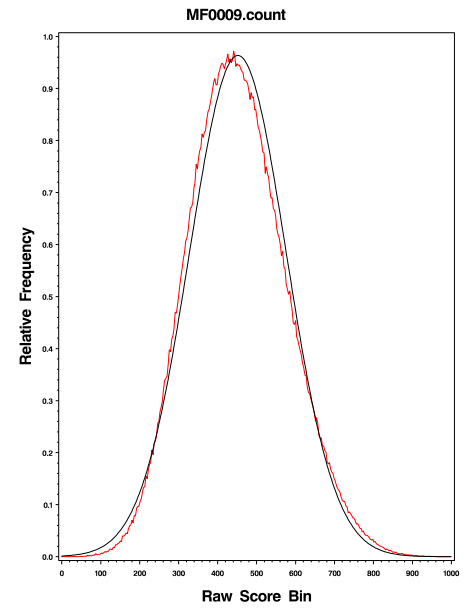
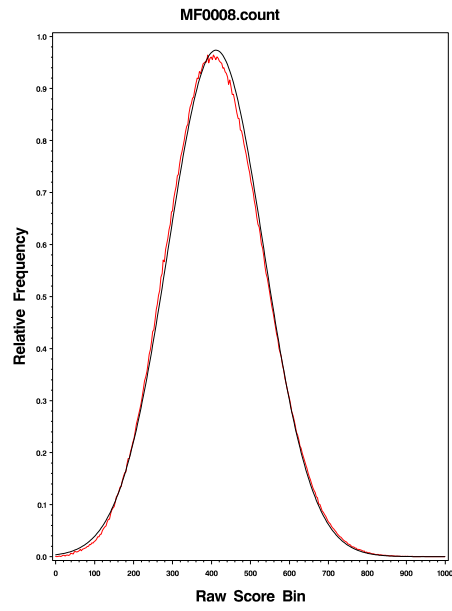
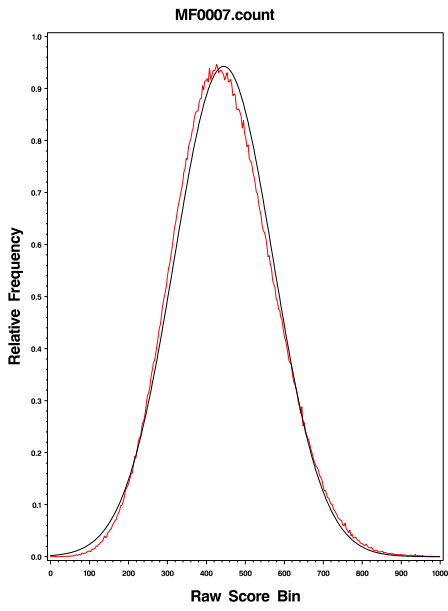
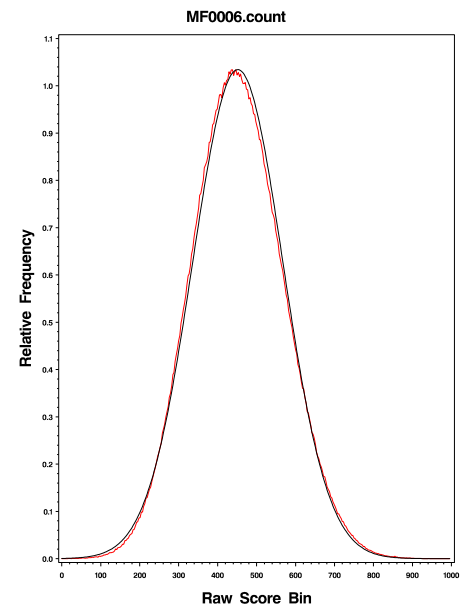
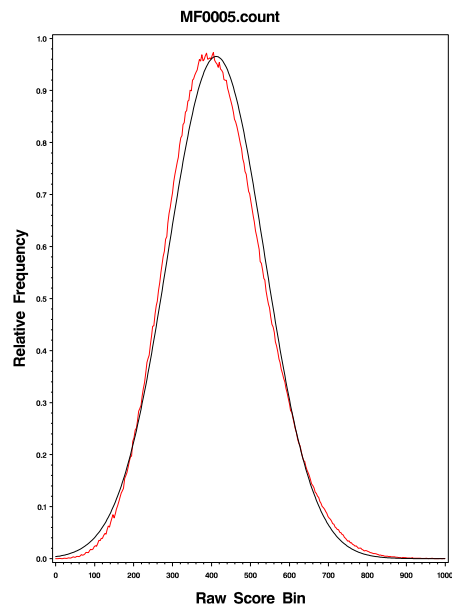
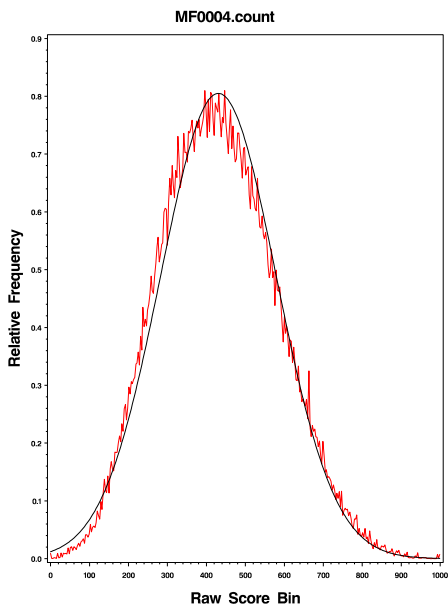




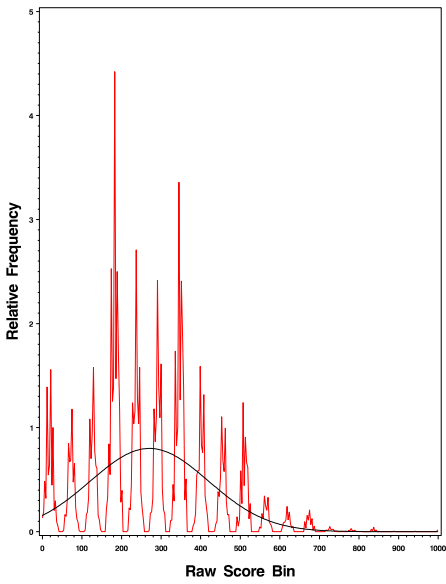




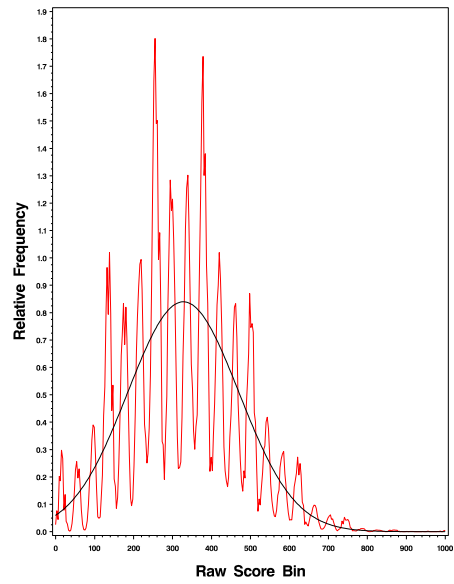




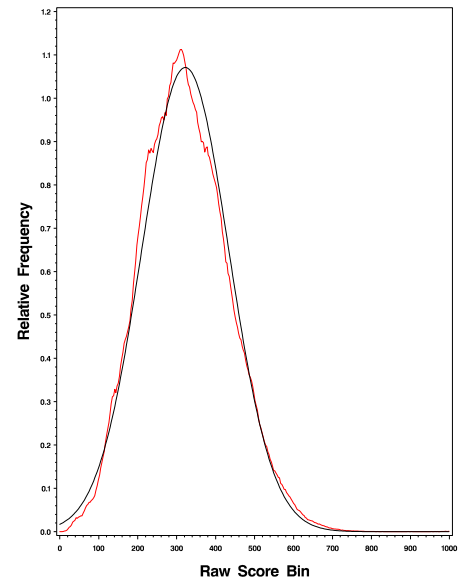
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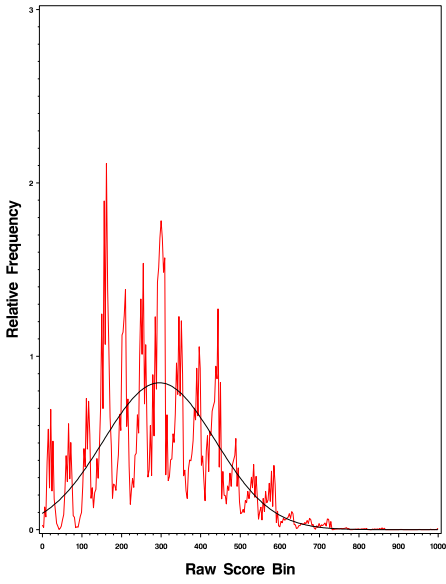
PF0003.count



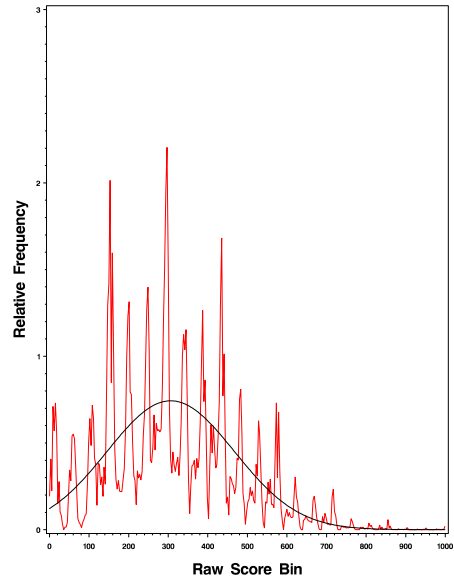
PF0004.count



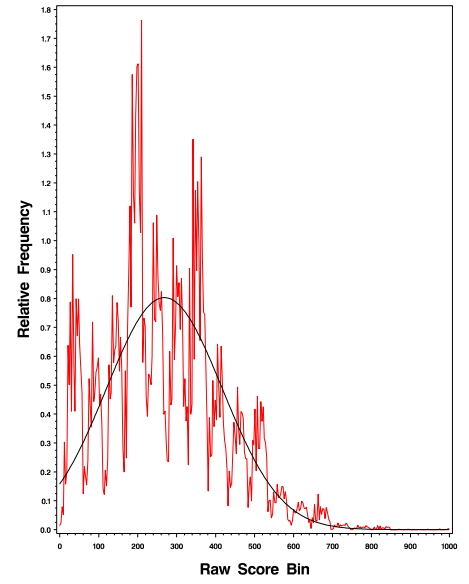
PF0005.count



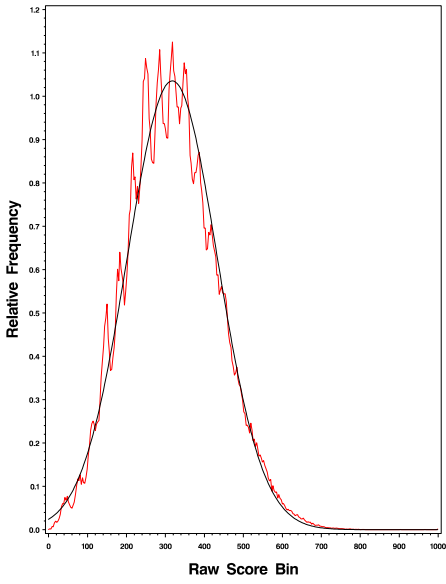
PF0006.count



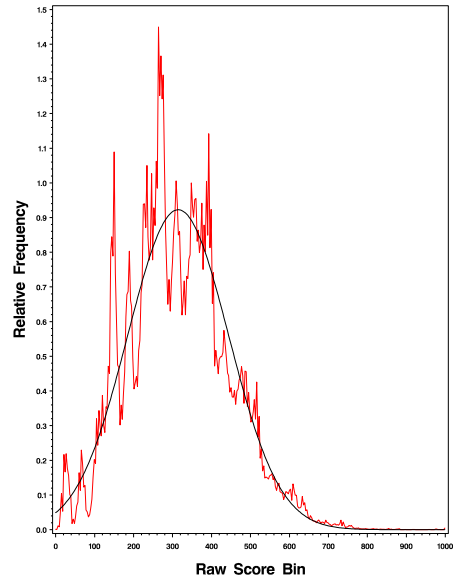
PF0007.count



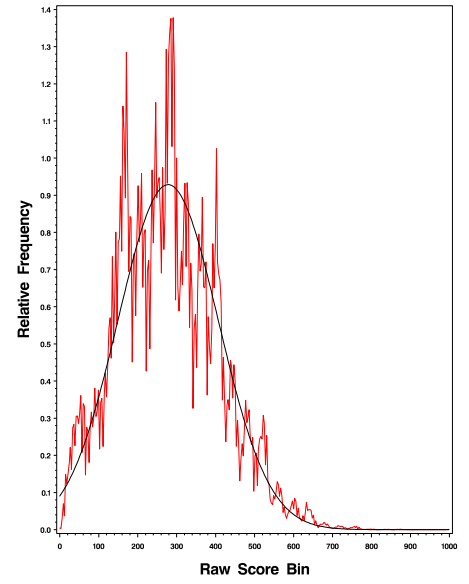
PF0008.count

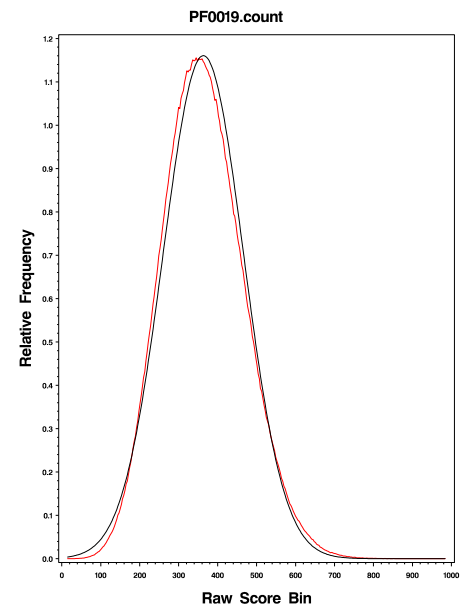
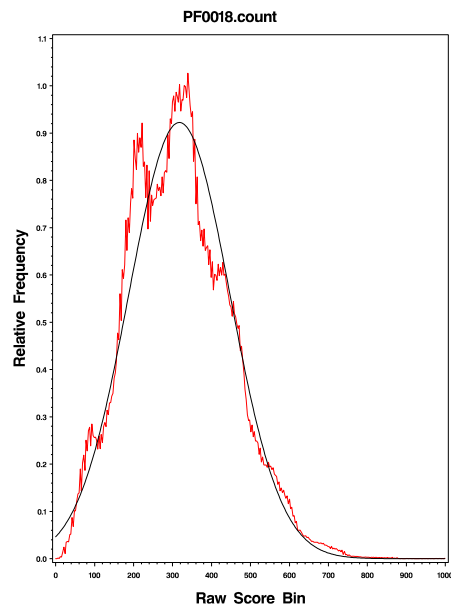
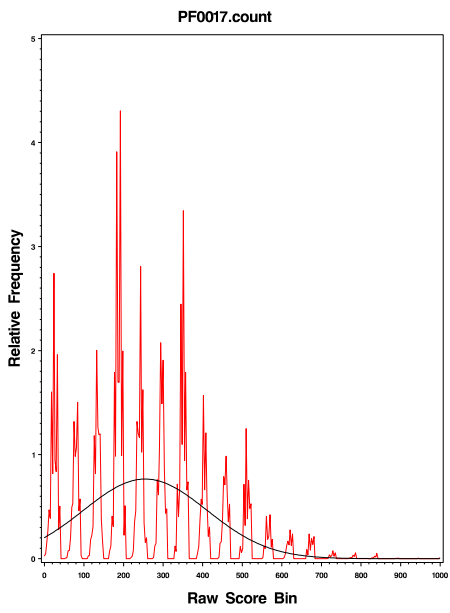
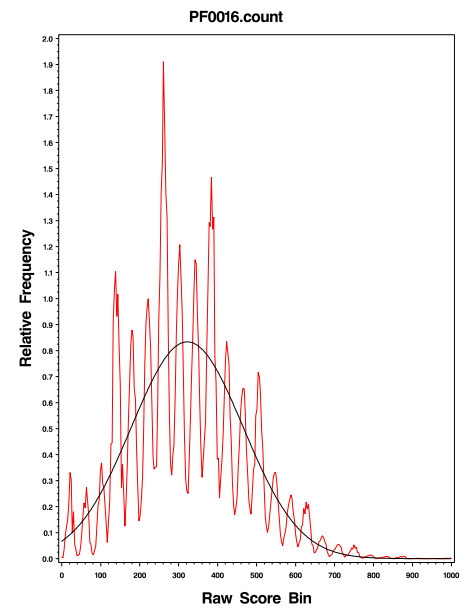
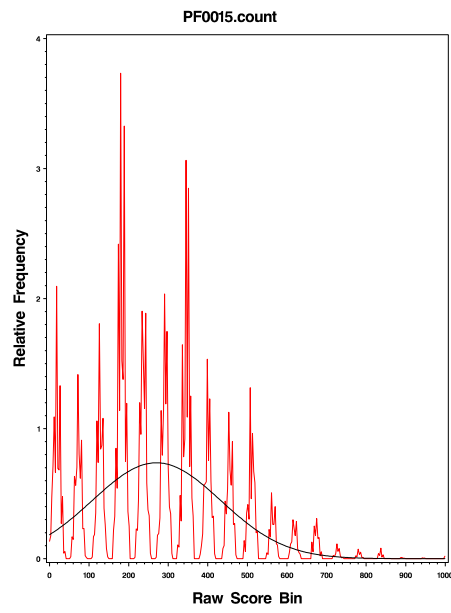
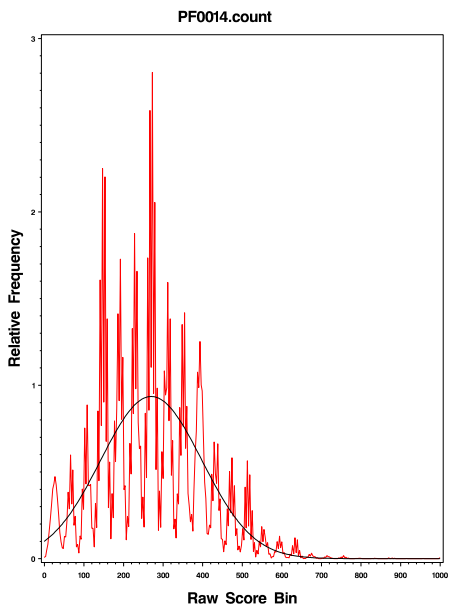
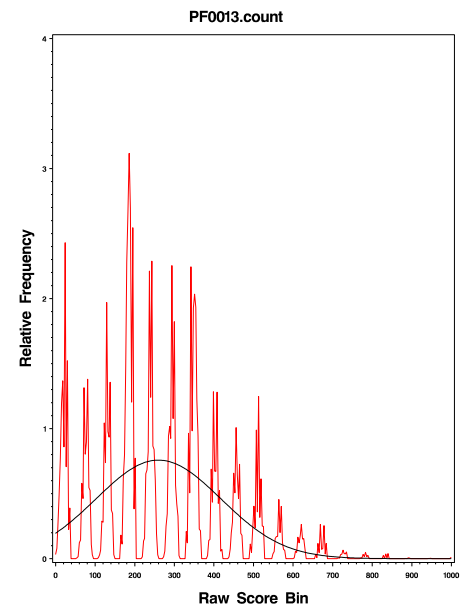
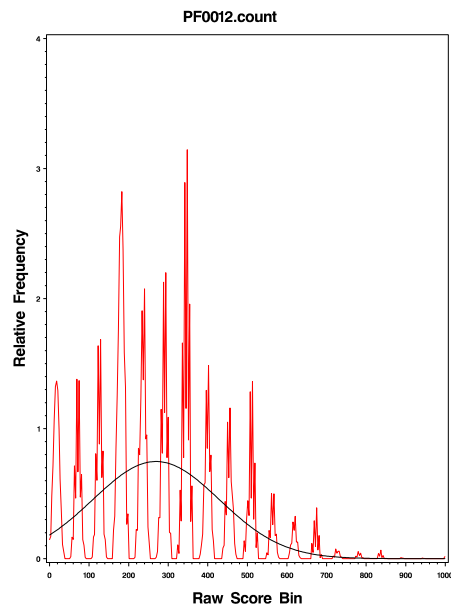
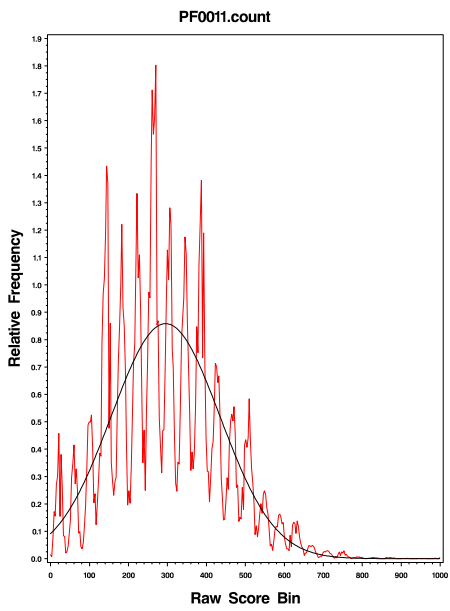


PF0009.count

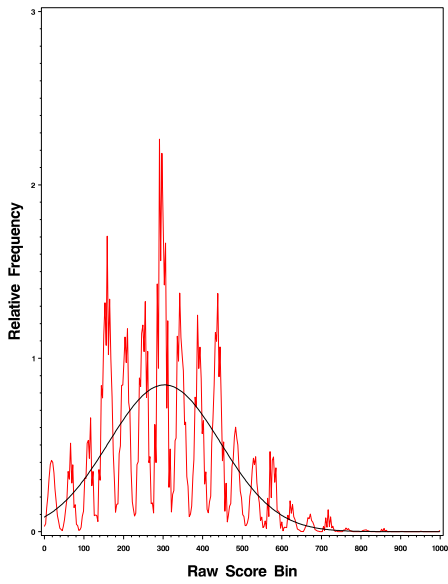


PF0010.count

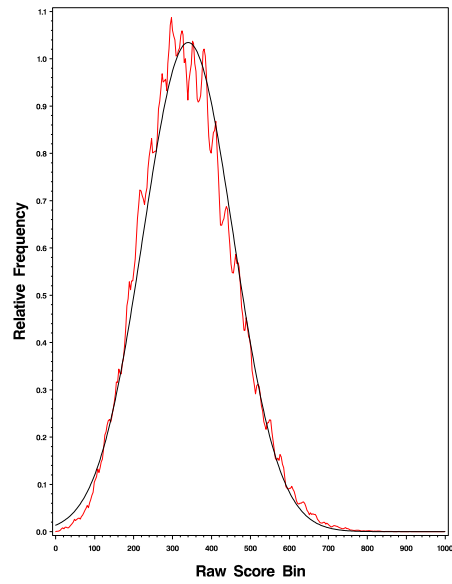




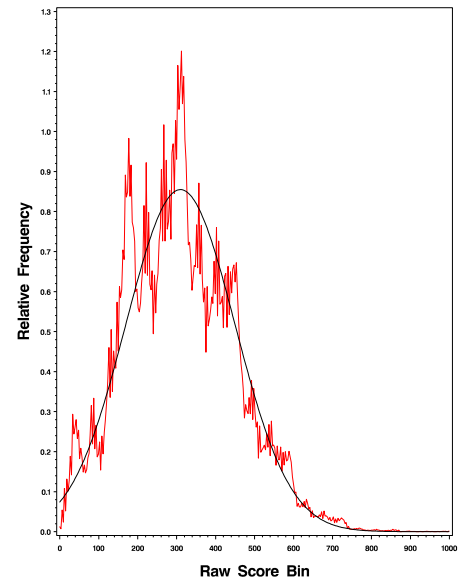
PF0020.count



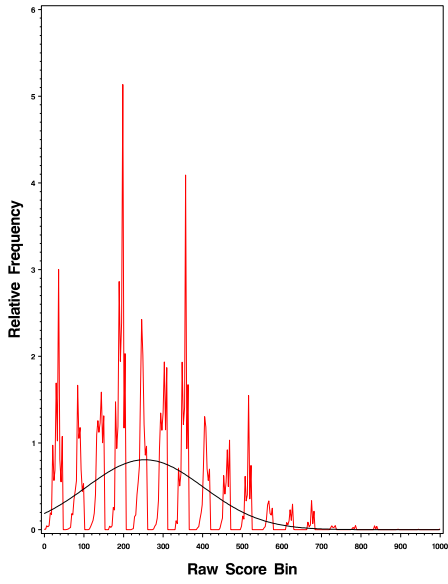
PF0021.count



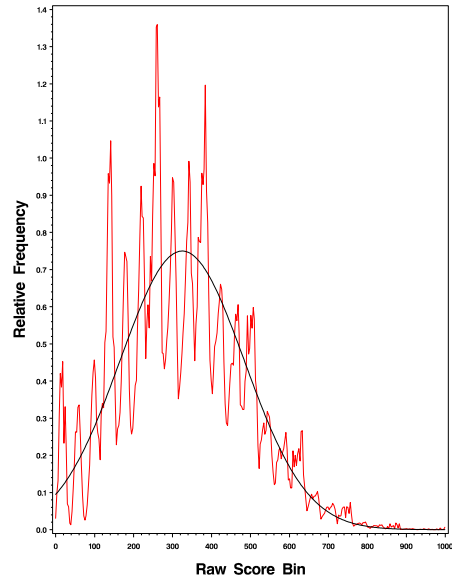
PF0022.count



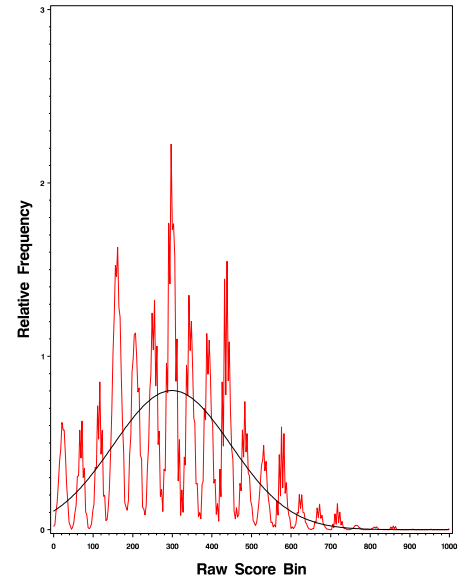
PF0023.count



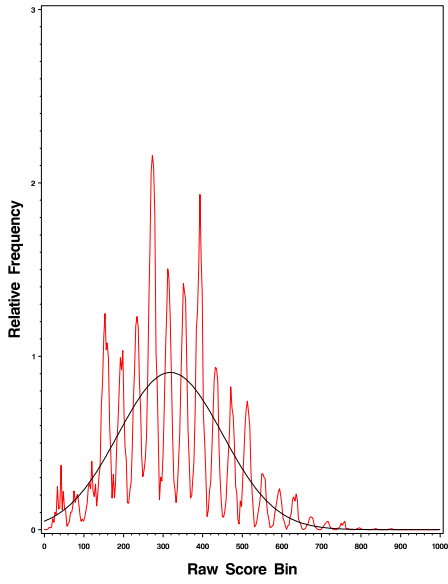
PF0024.count



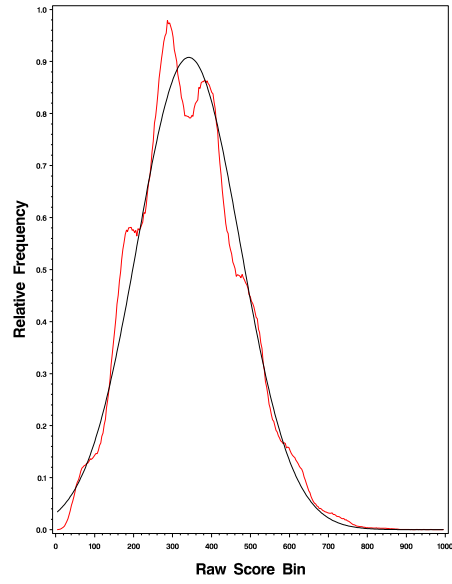
PF0025.count



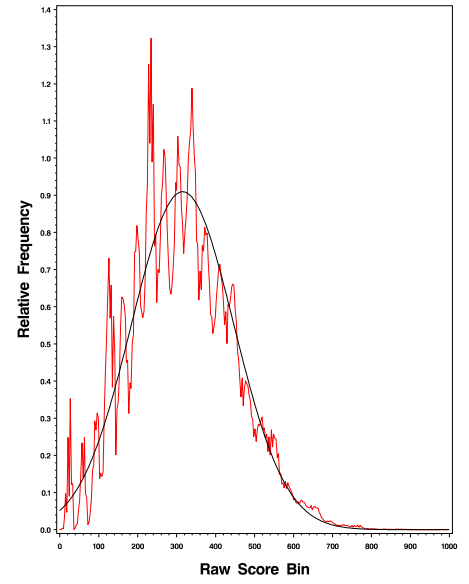
PF0026.count

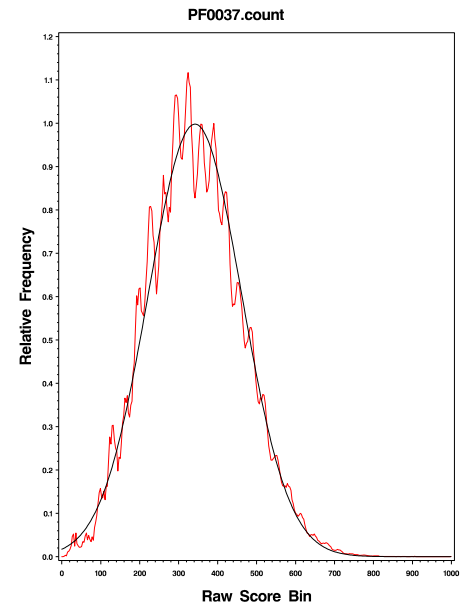
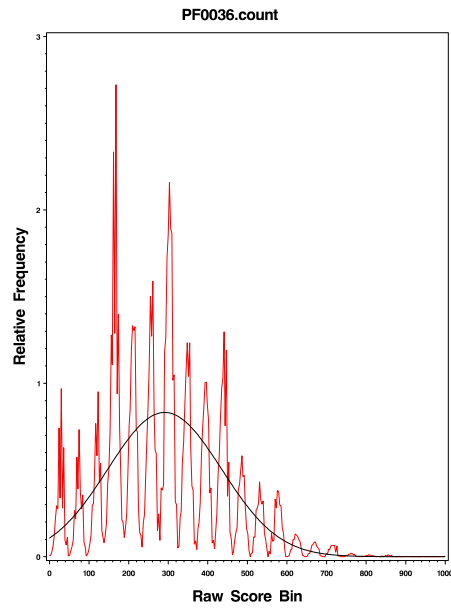
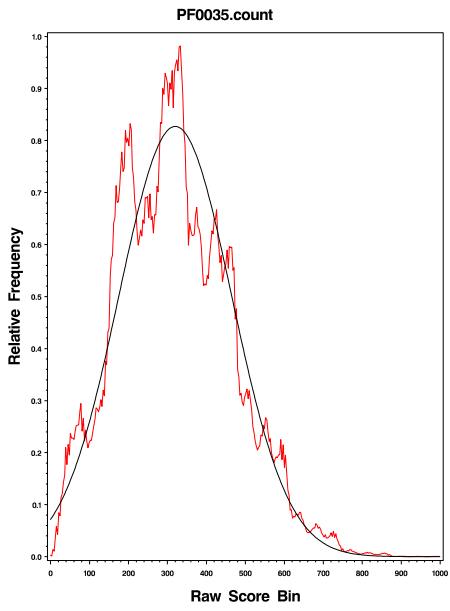
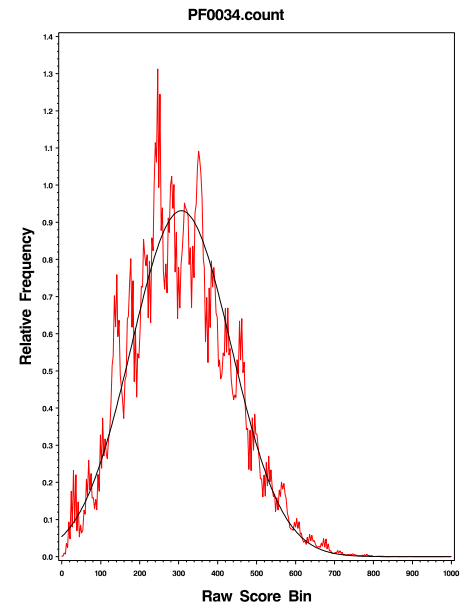
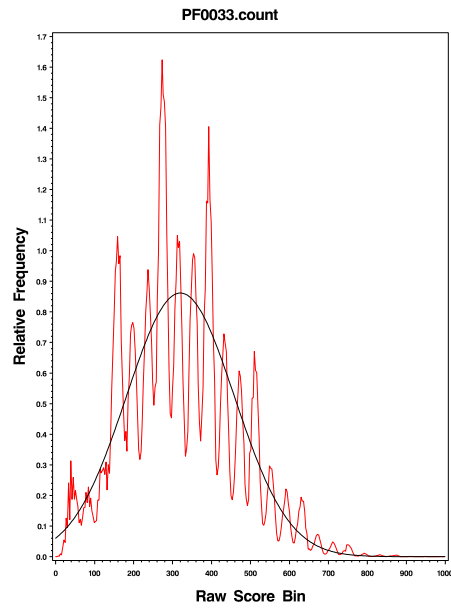
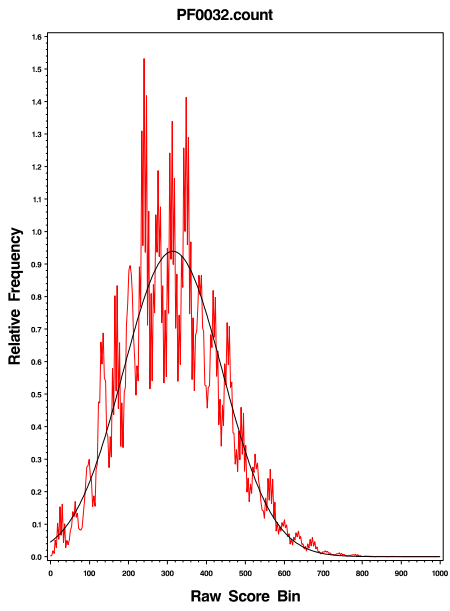
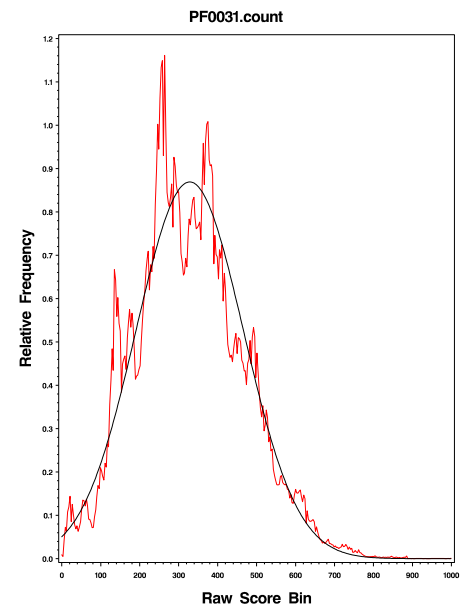
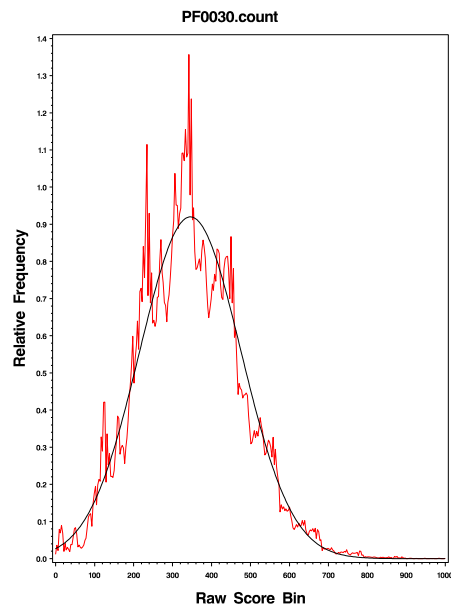
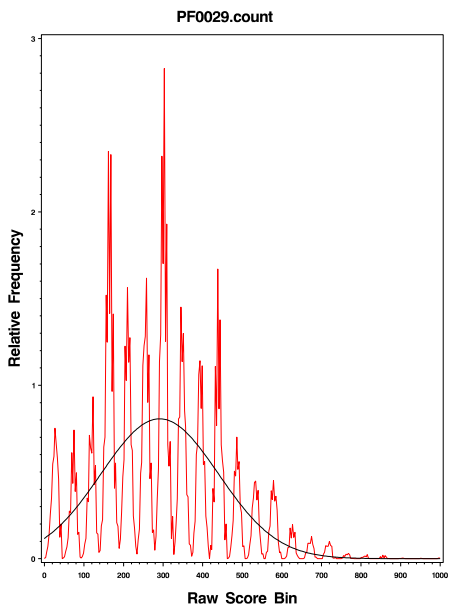


PF0027.count

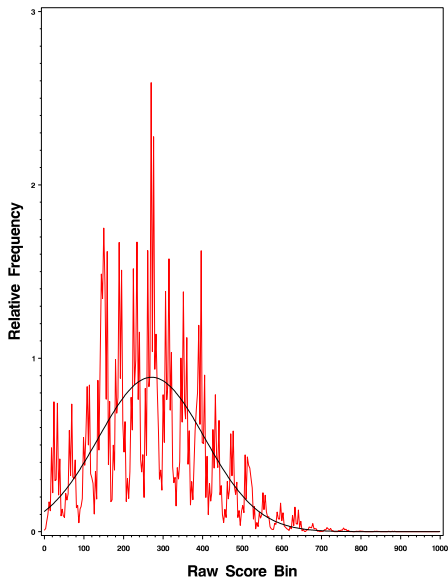


PF0028.count

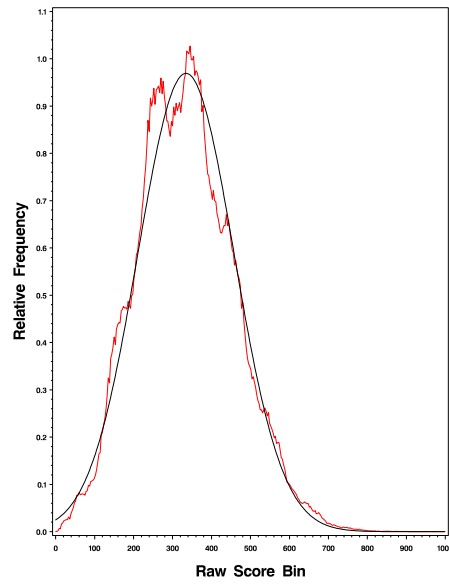




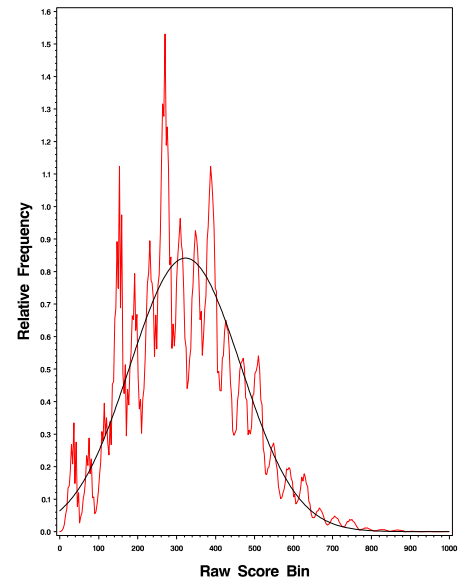
PF0038.count



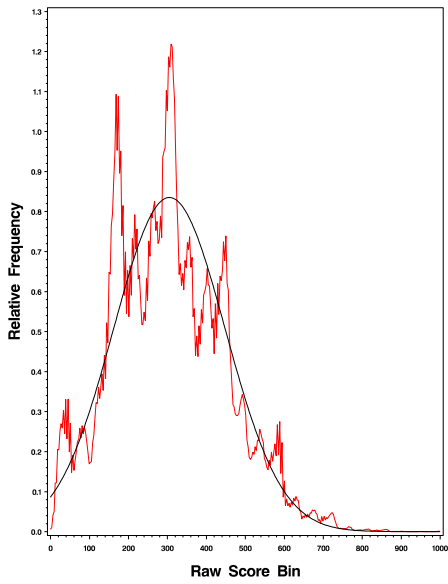
PF0039.count



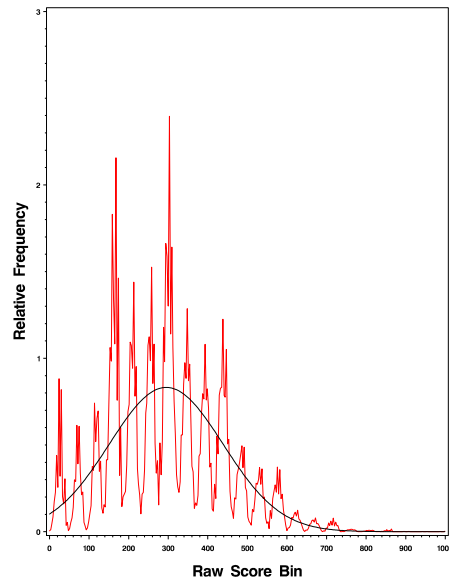
PF0040.count



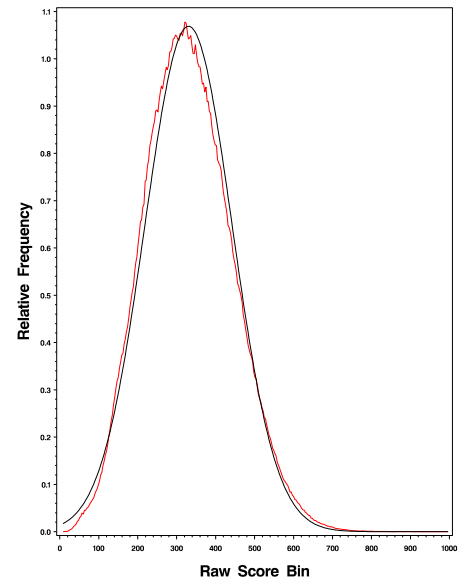
PF0041.count



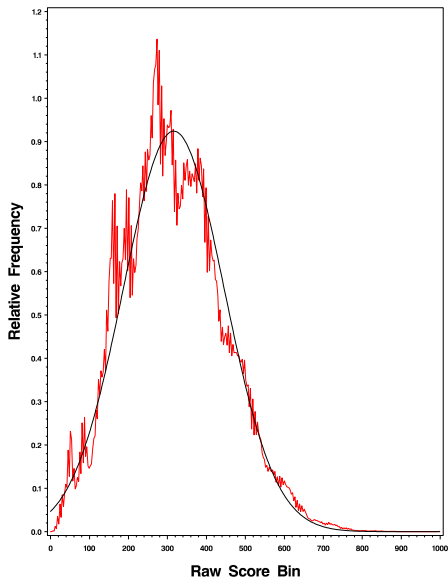
PF0042.count



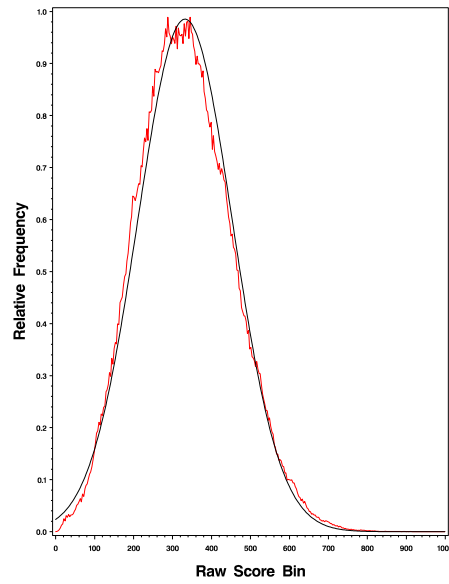
PF0043.count



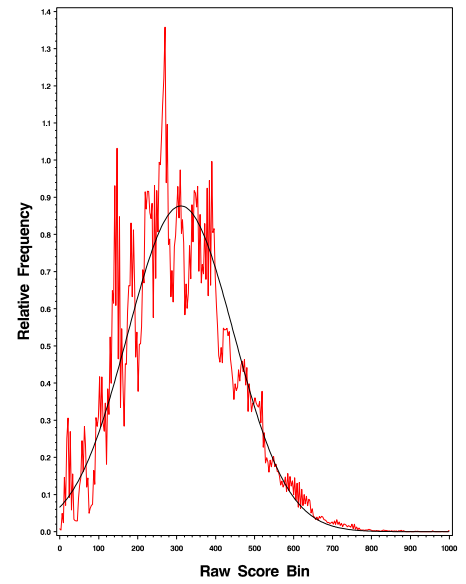
PF0044.count



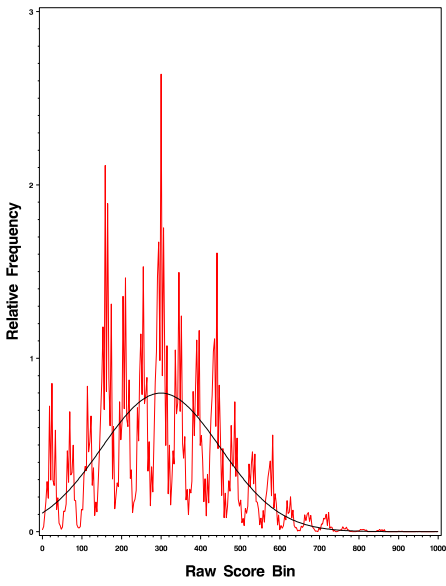
PF0045.count



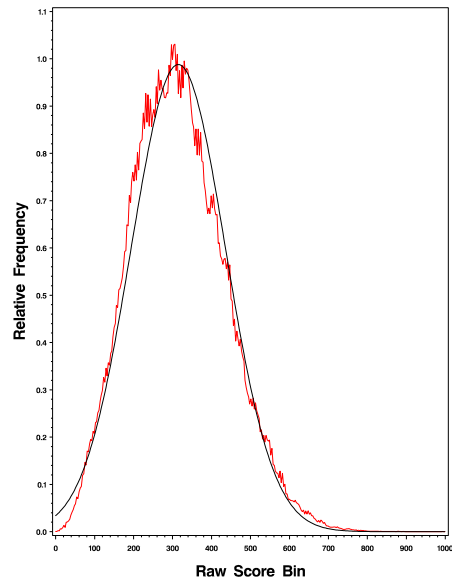
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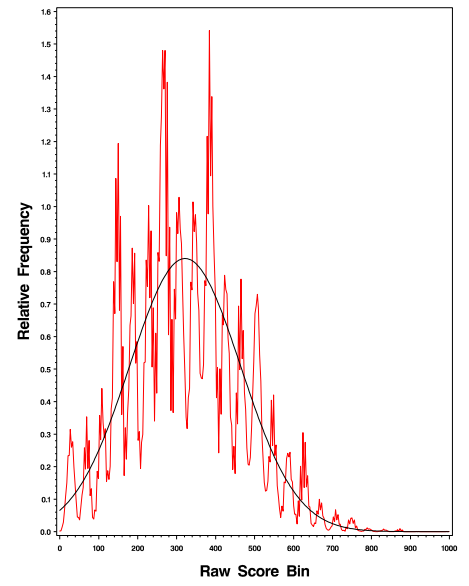
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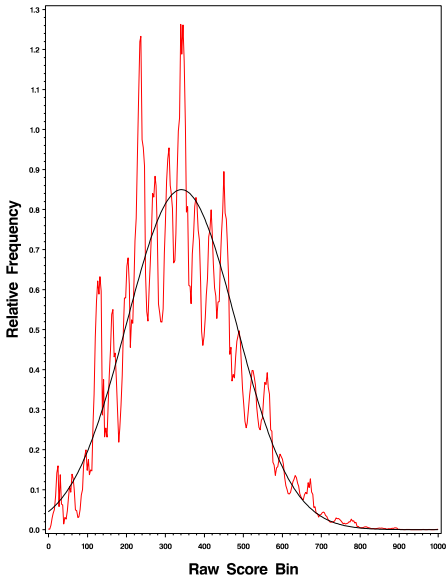
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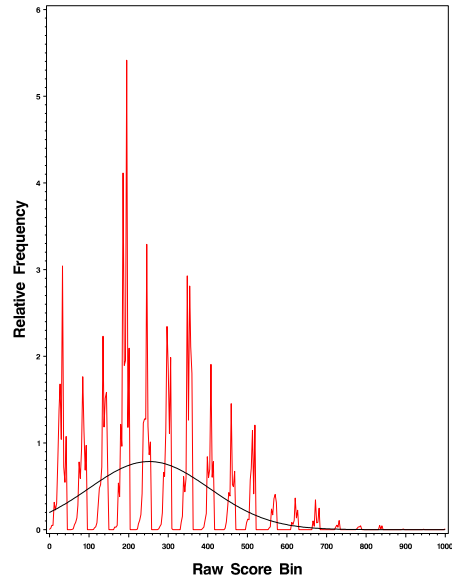
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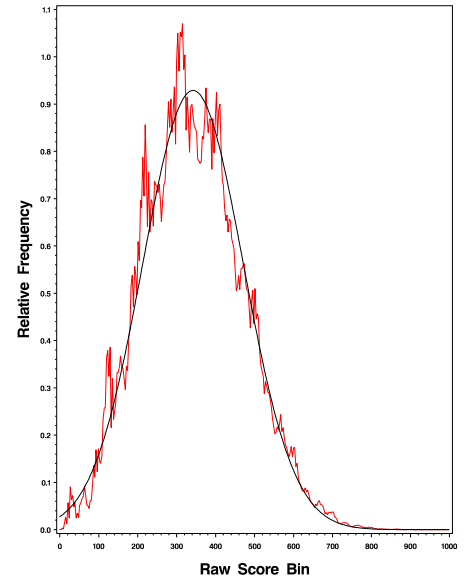
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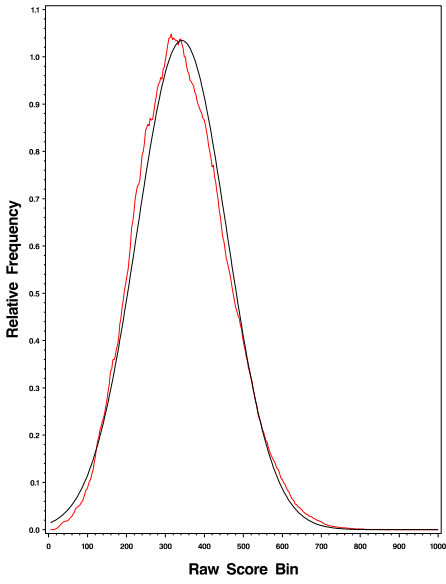
PF0051.count



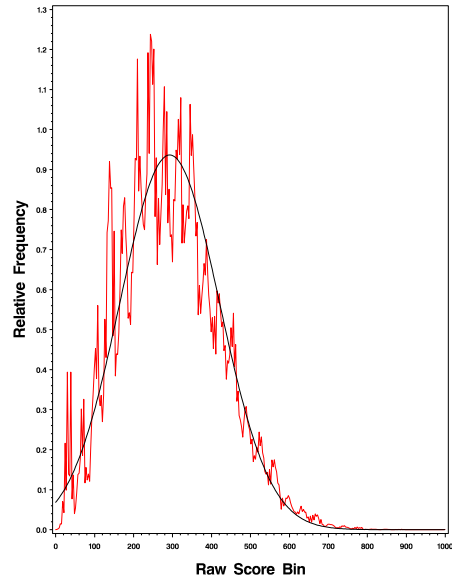
PF0052.count



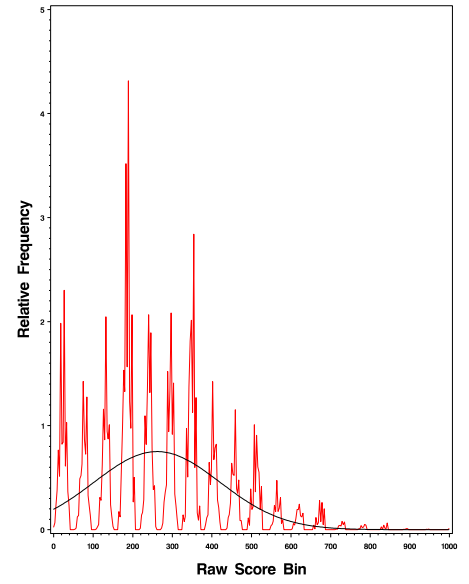
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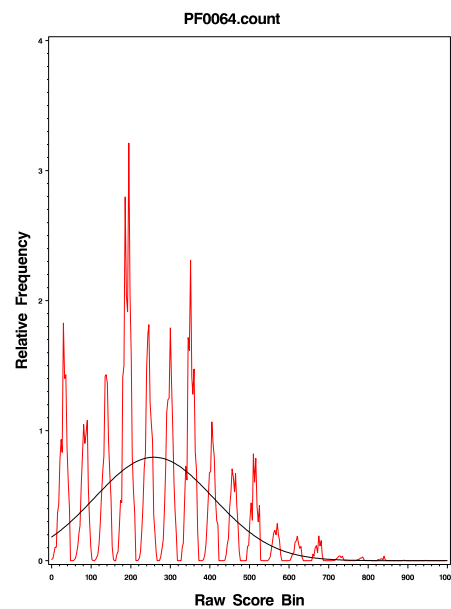
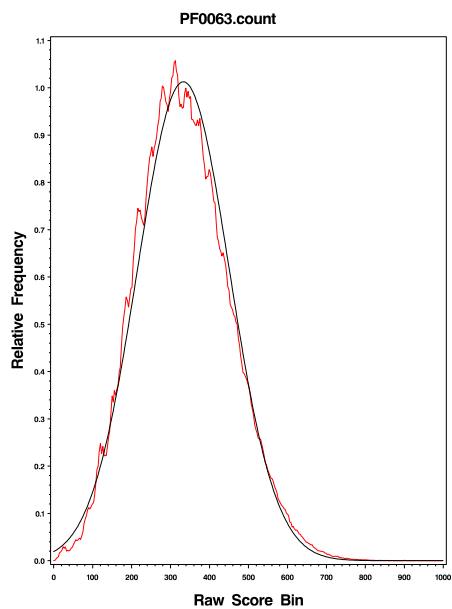
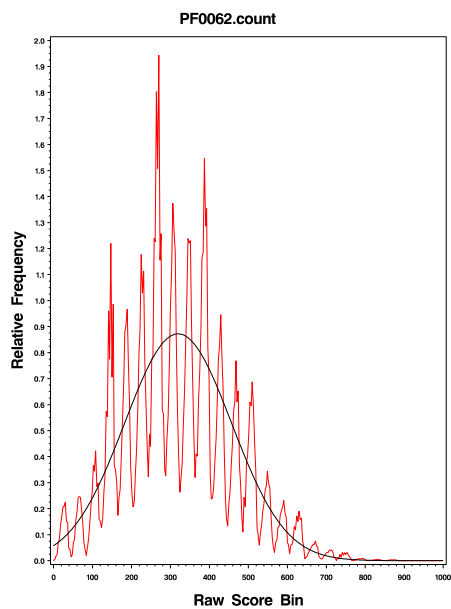
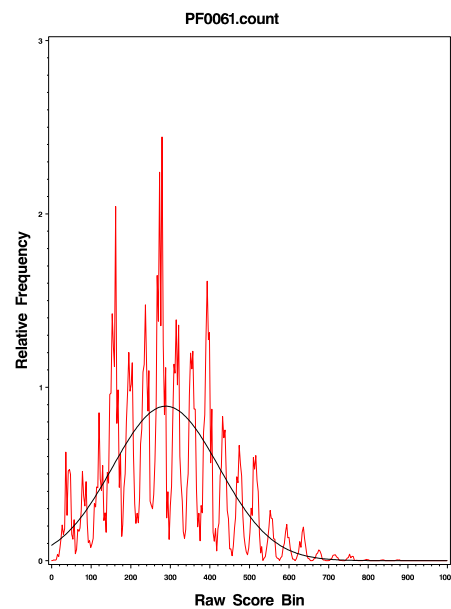
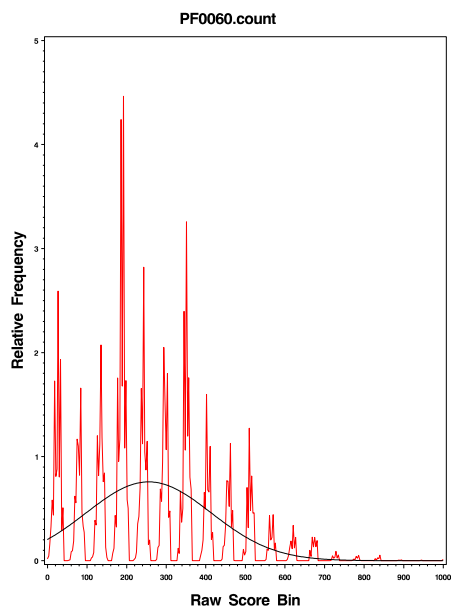
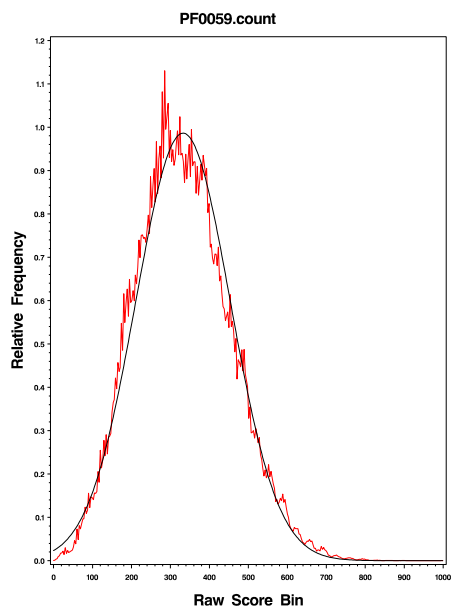
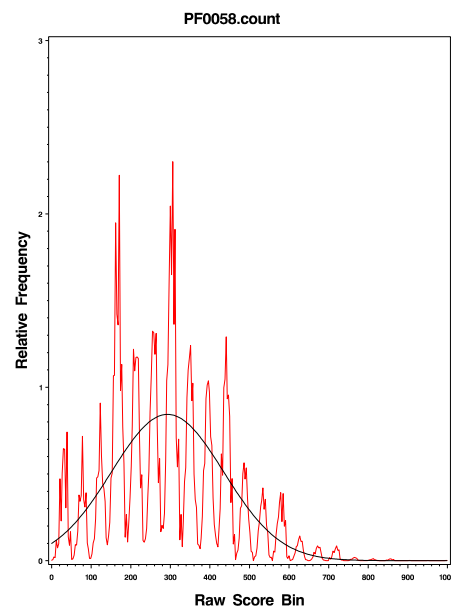
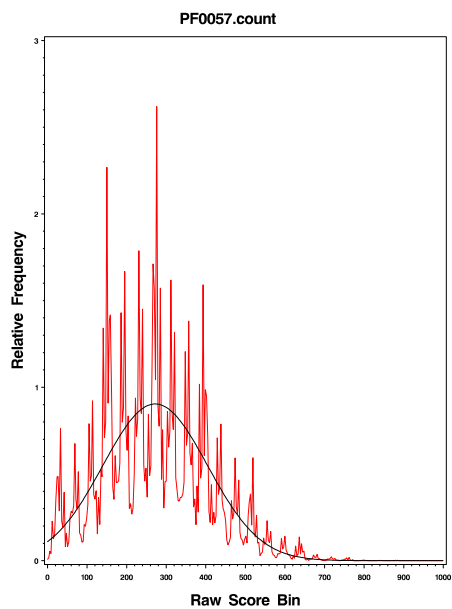
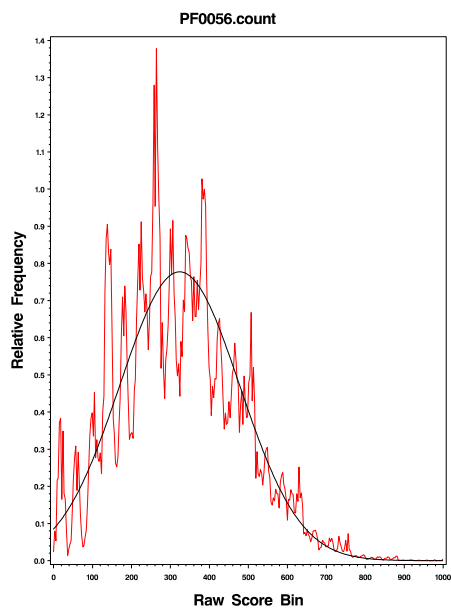


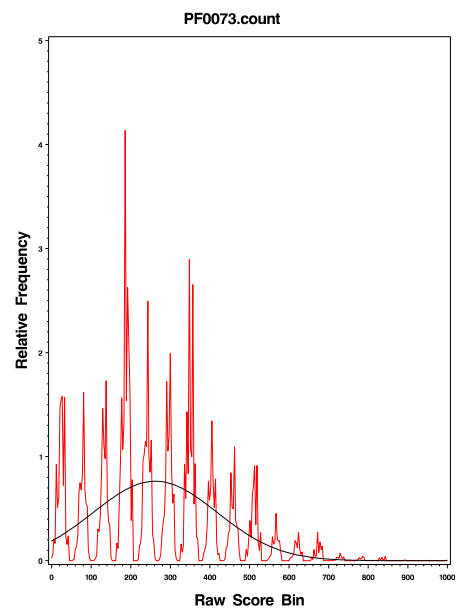
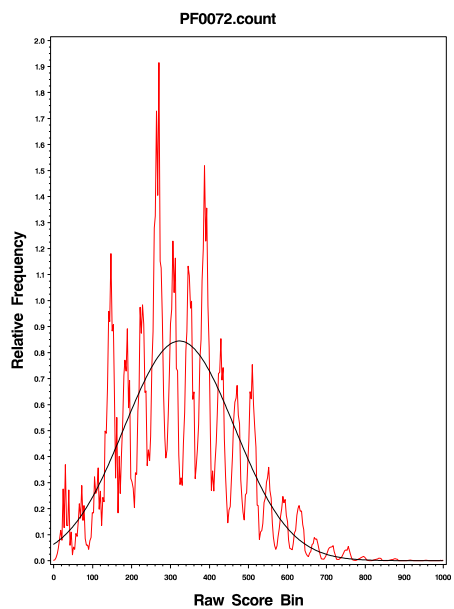
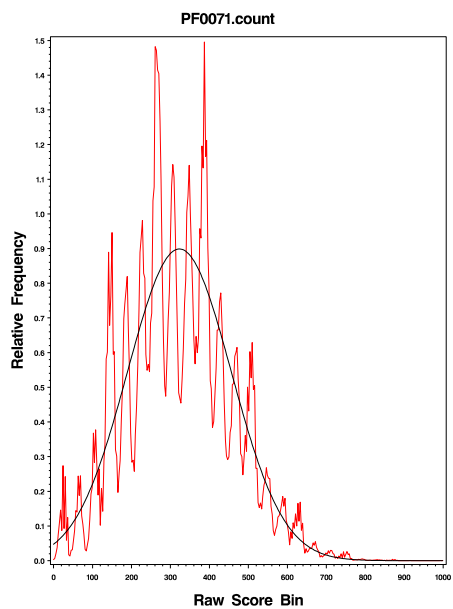
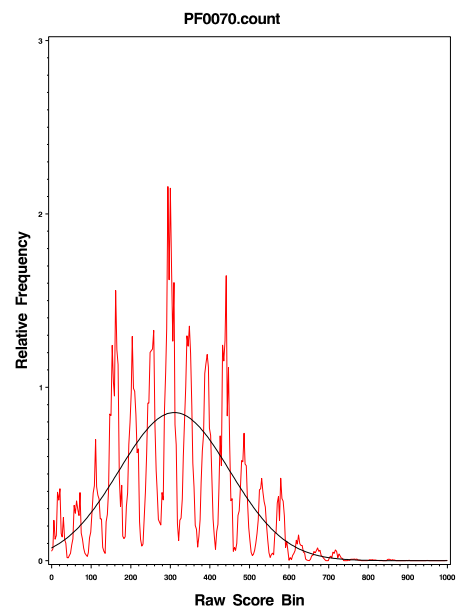
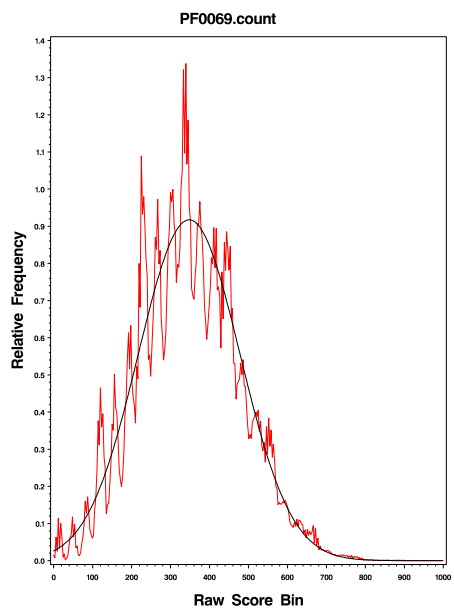
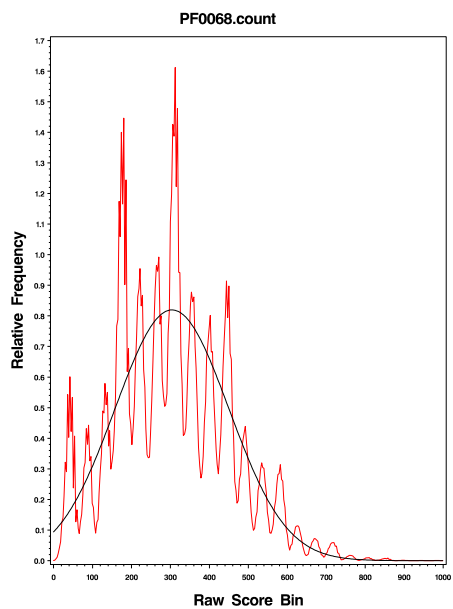
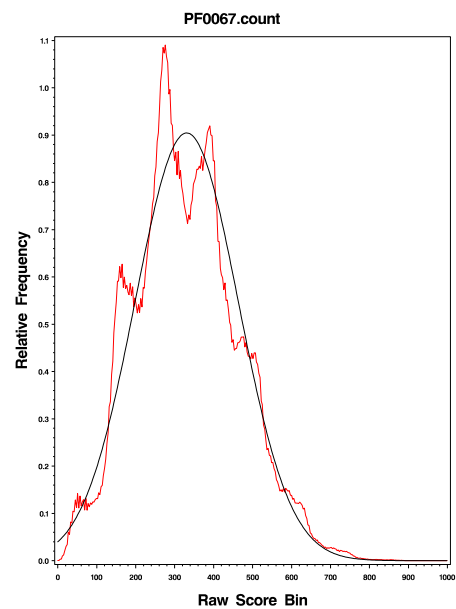
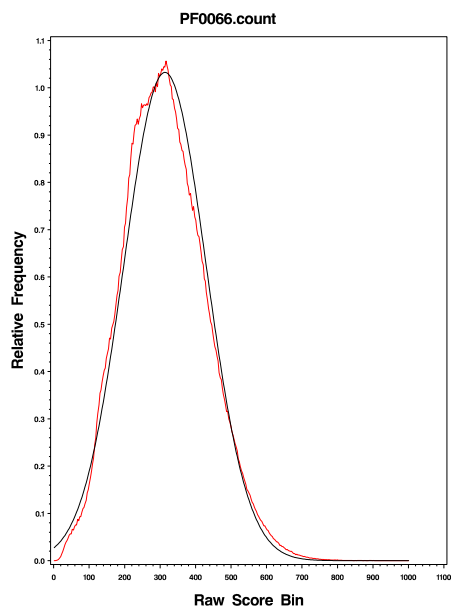
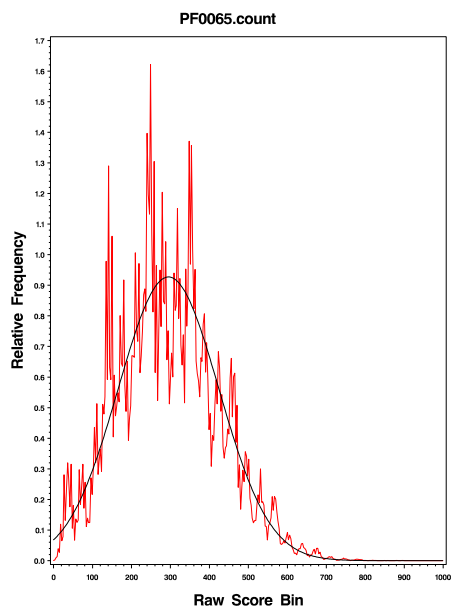
PF0054.count

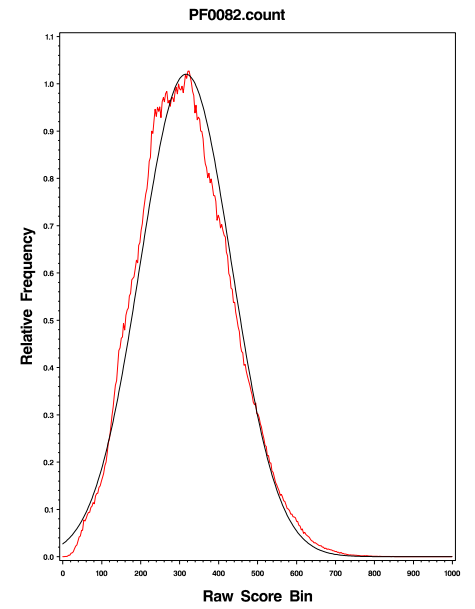
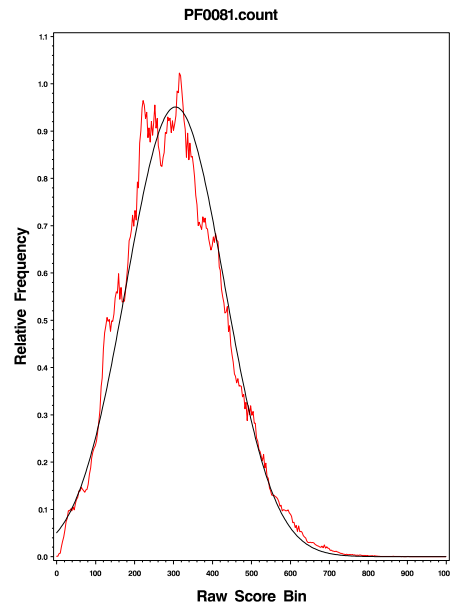
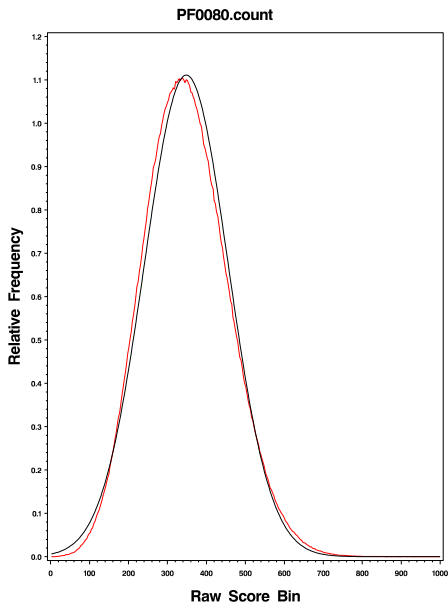
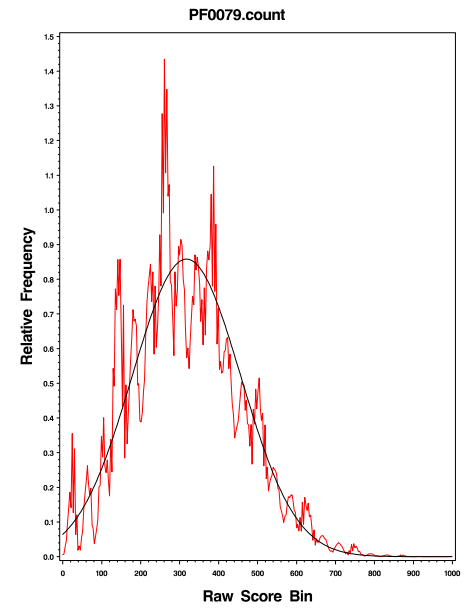
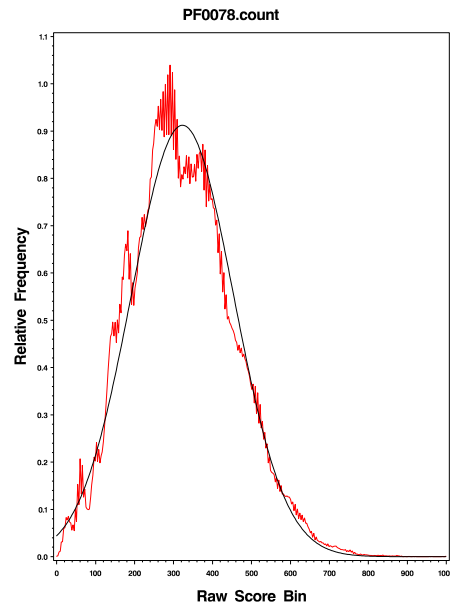
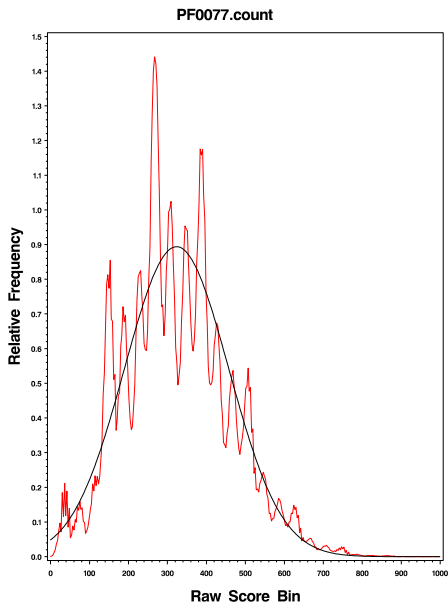
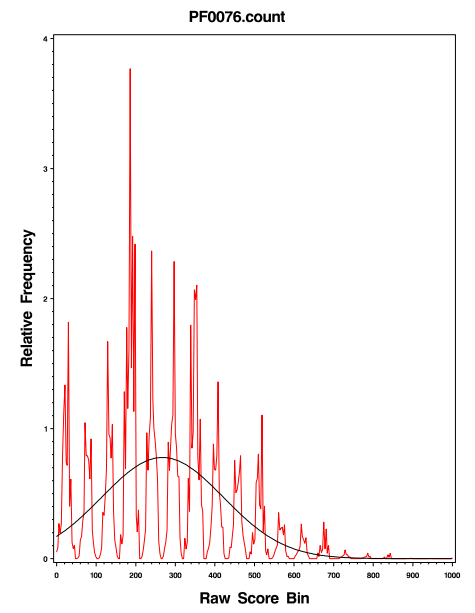
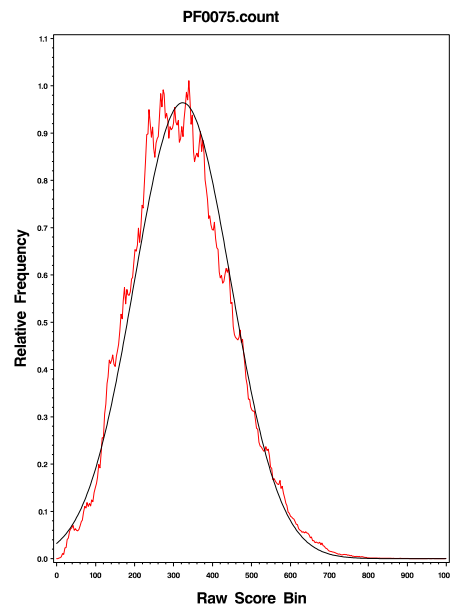
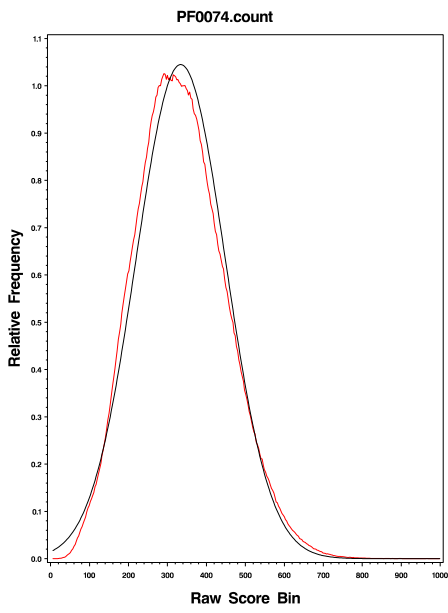


PF0055.count

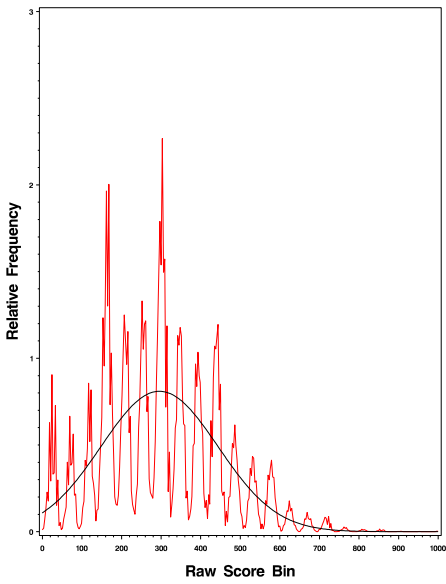




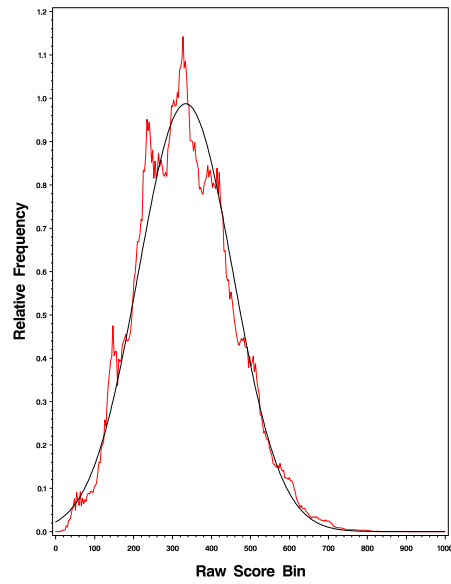




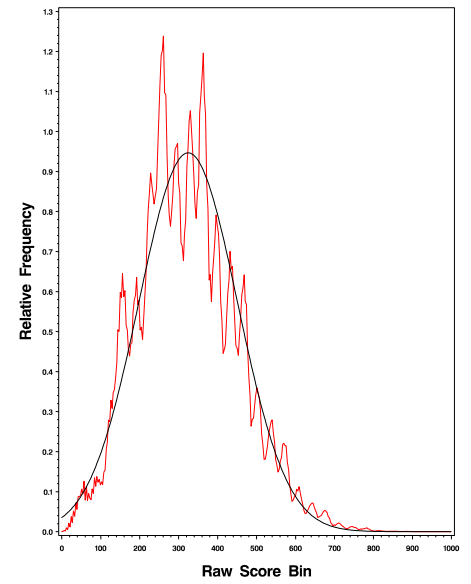
PF0083.count



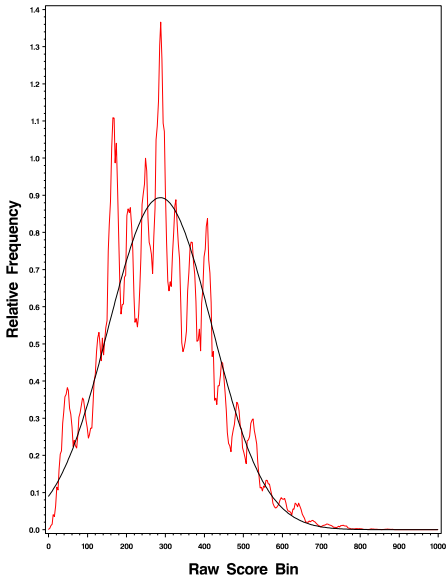
PF0084.count



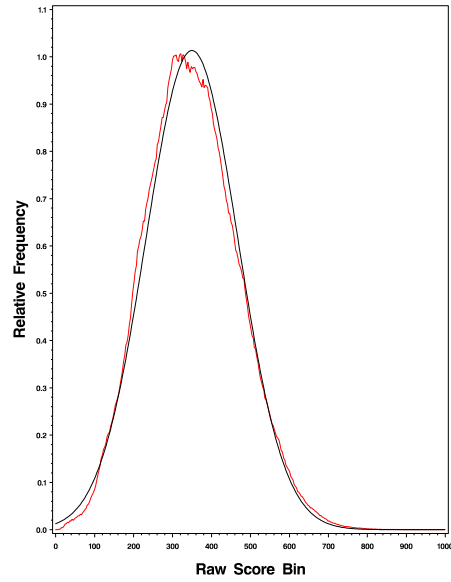
PF0085.count



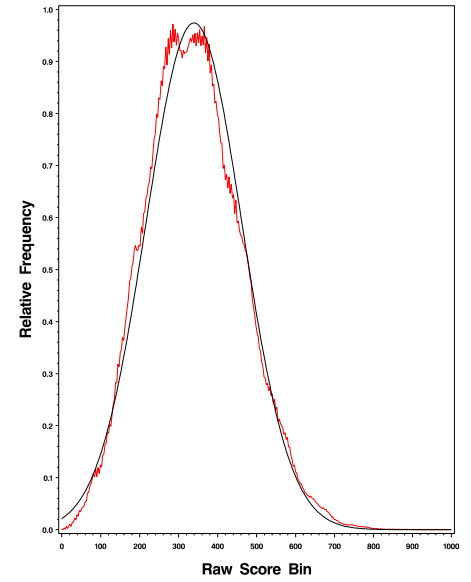
PF0086.count



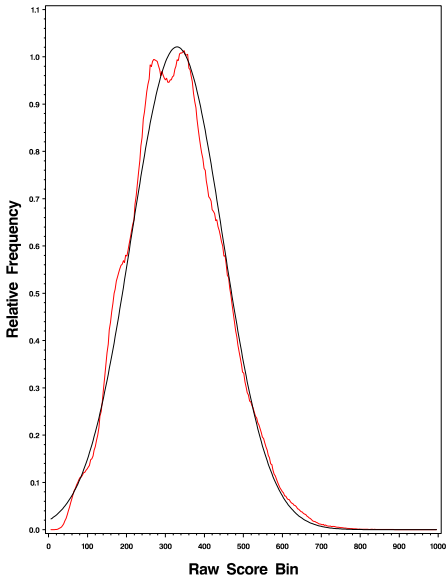
PF0087.count



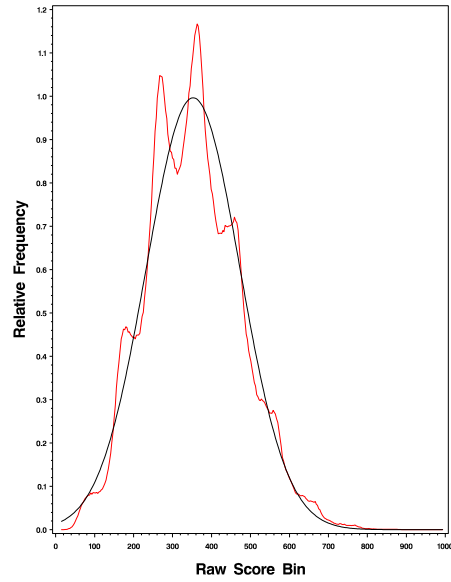
PF0088.count



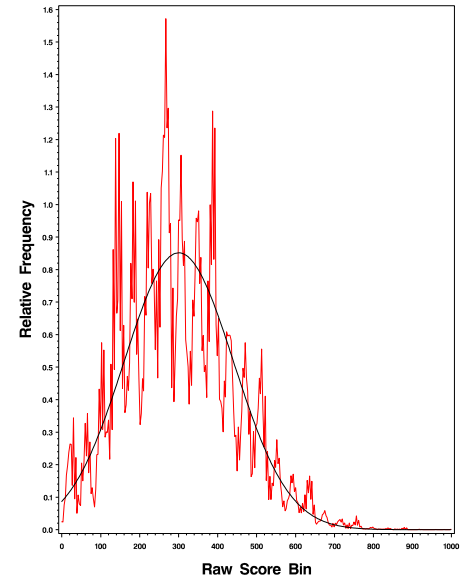
PF0089.count

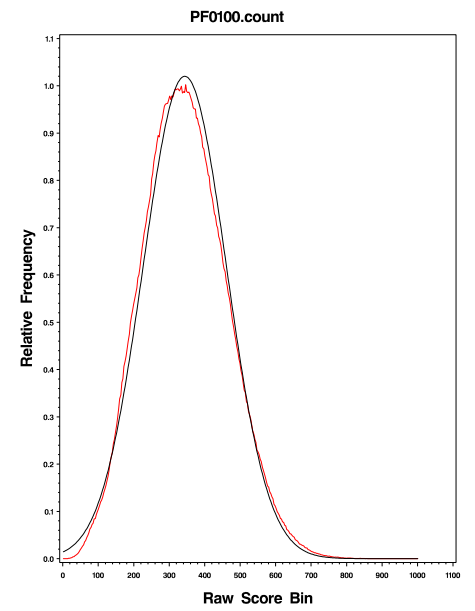
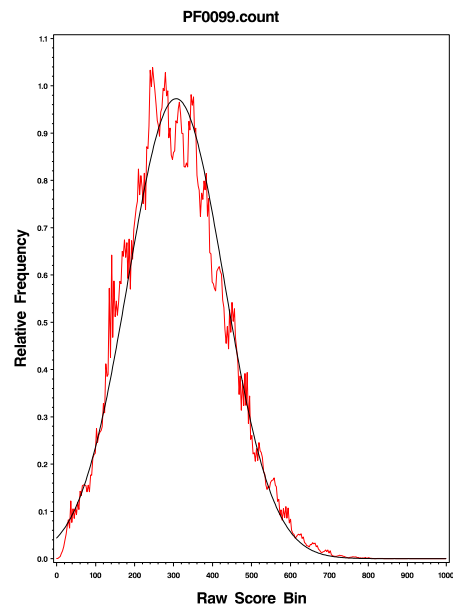
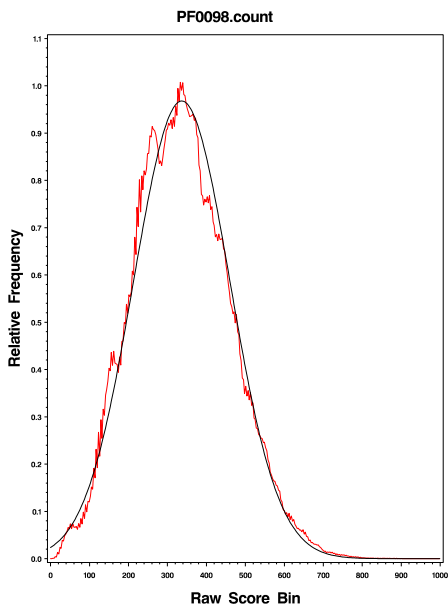
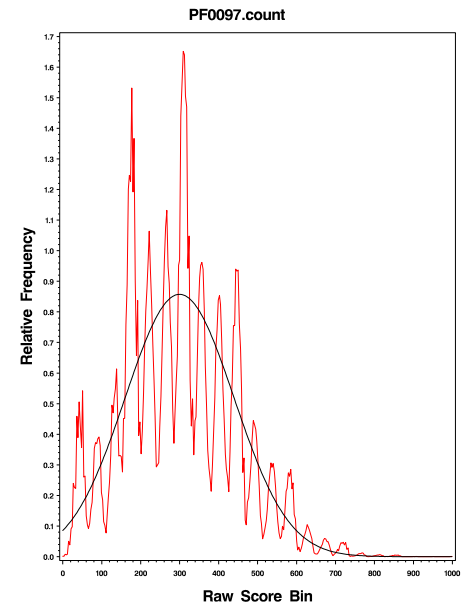
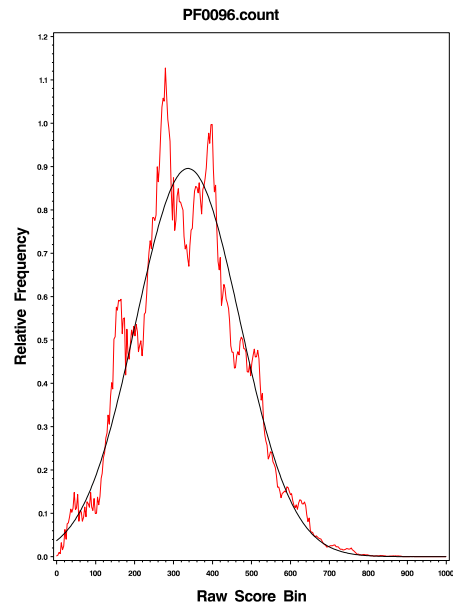
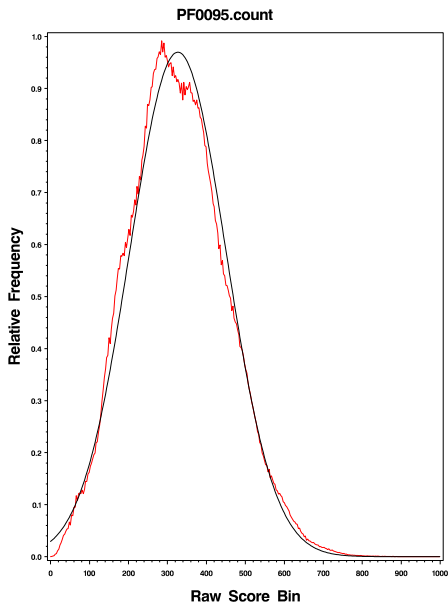
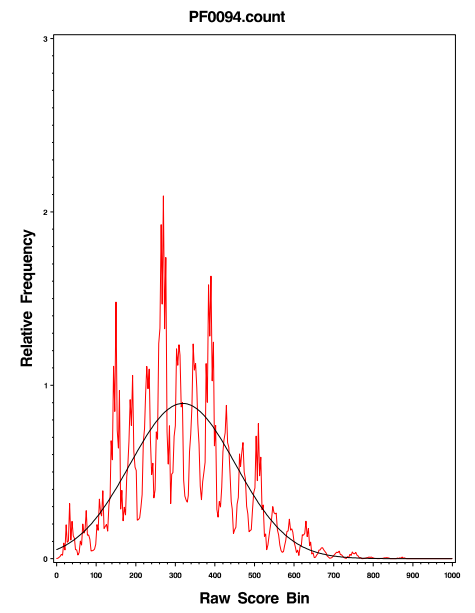
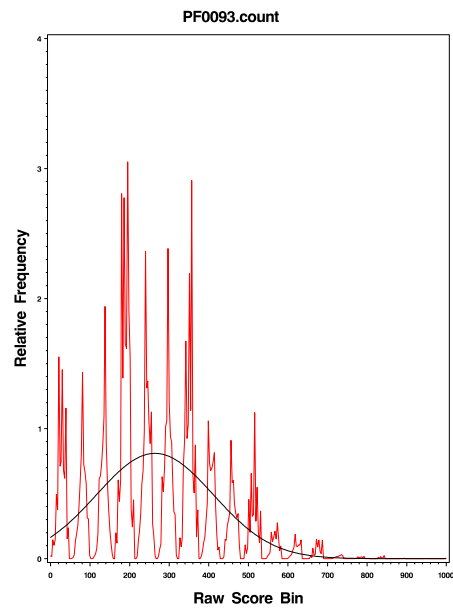
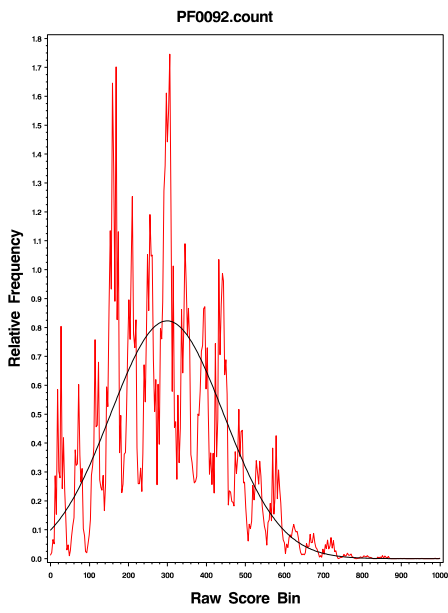


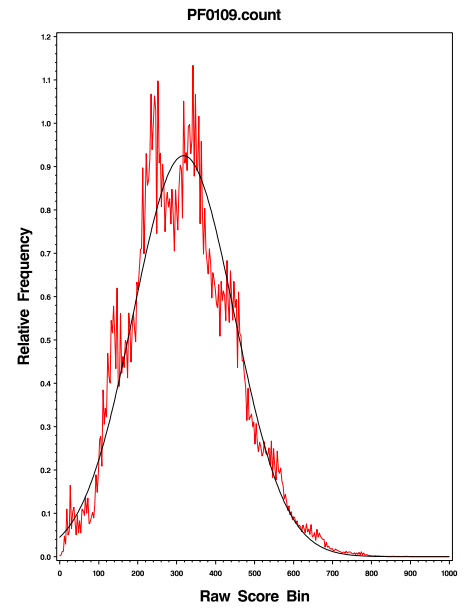
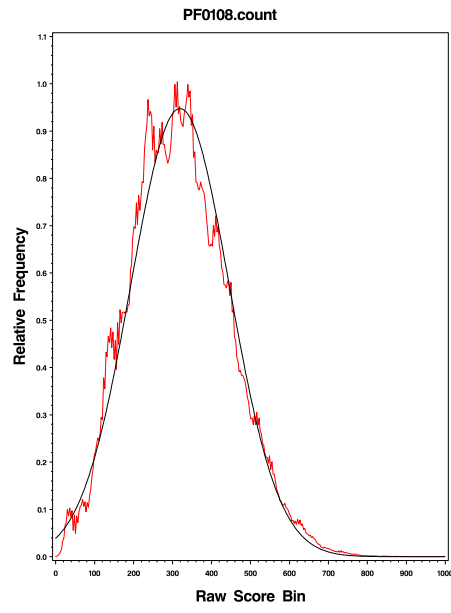
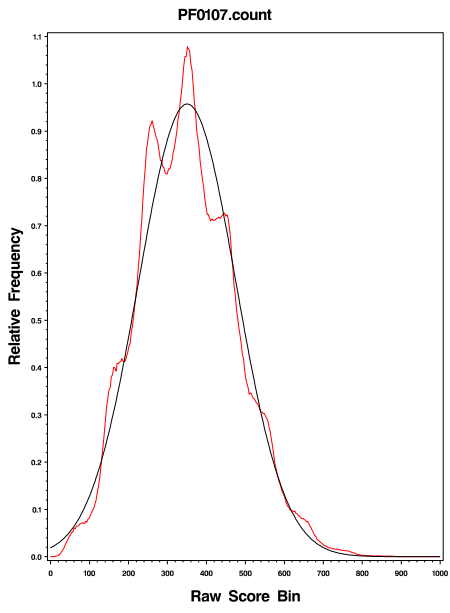
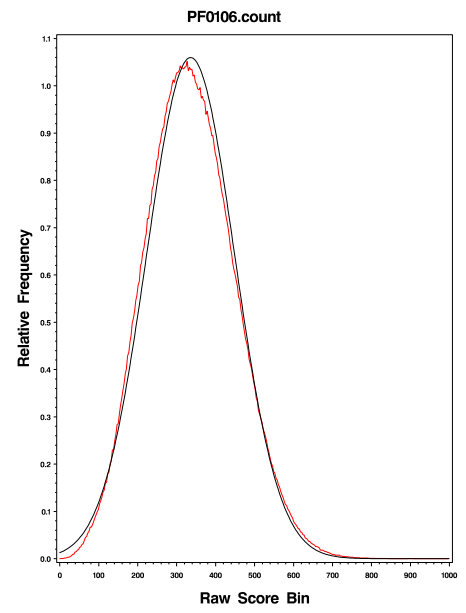
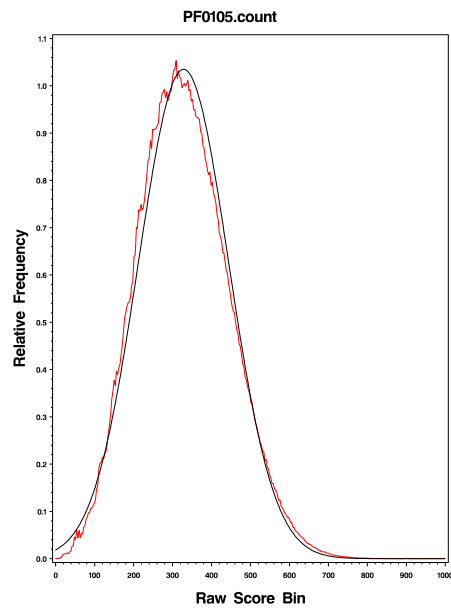
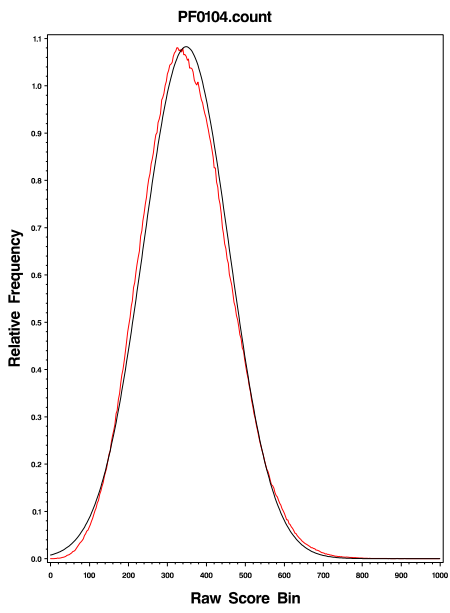
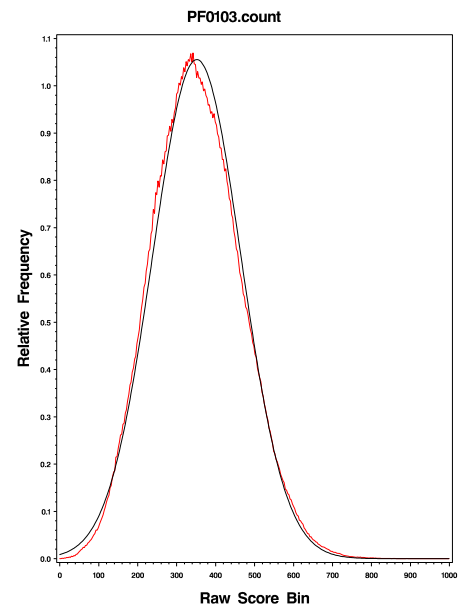
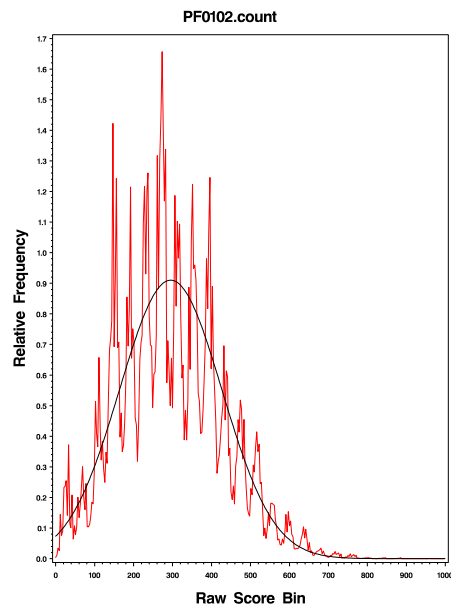
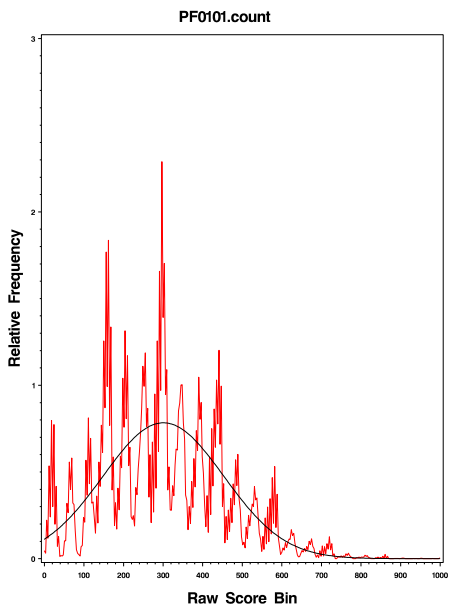
PF0090.count

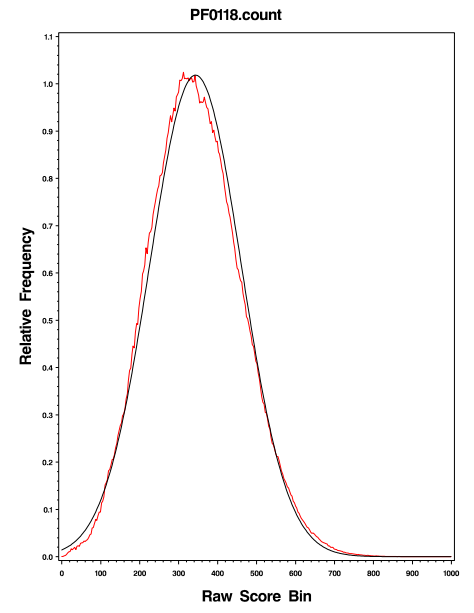
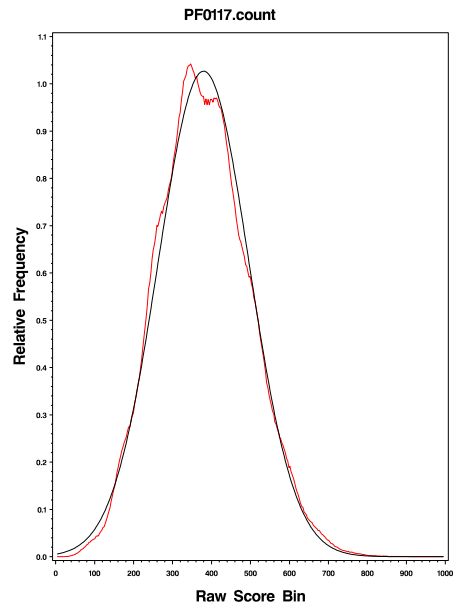
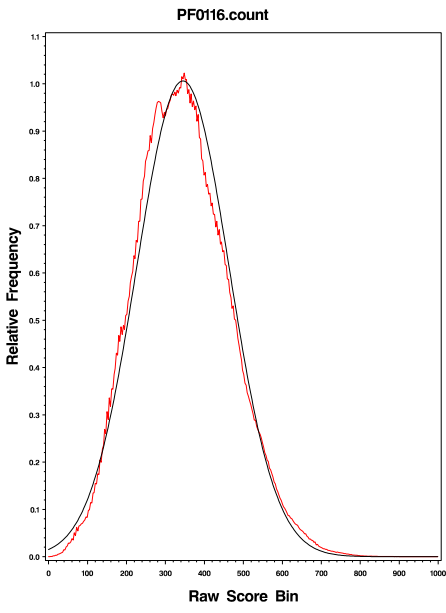
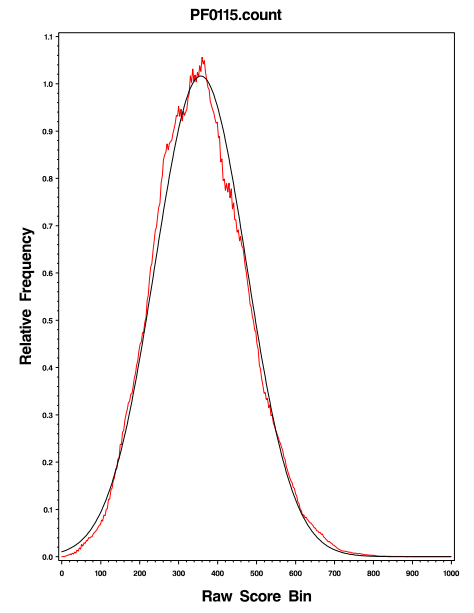
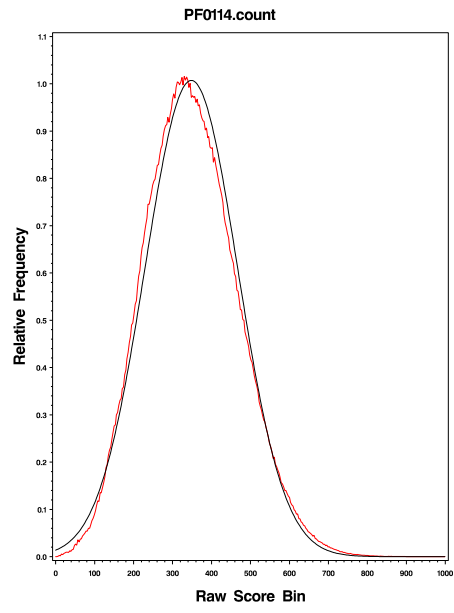
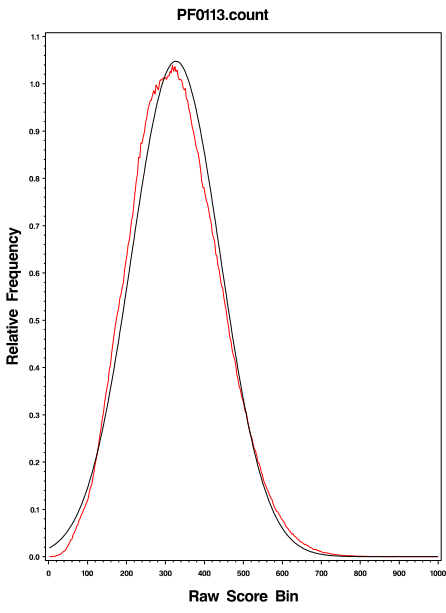
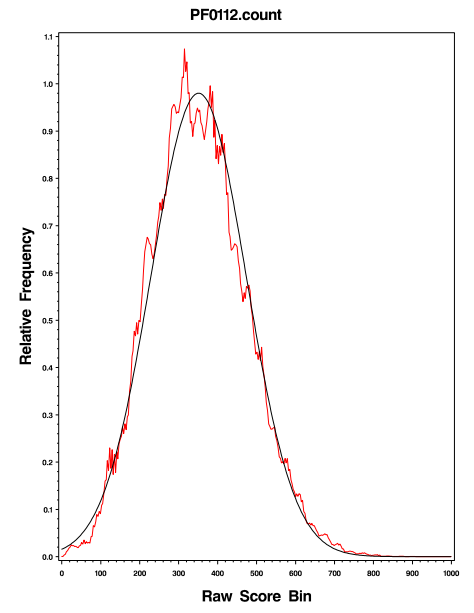
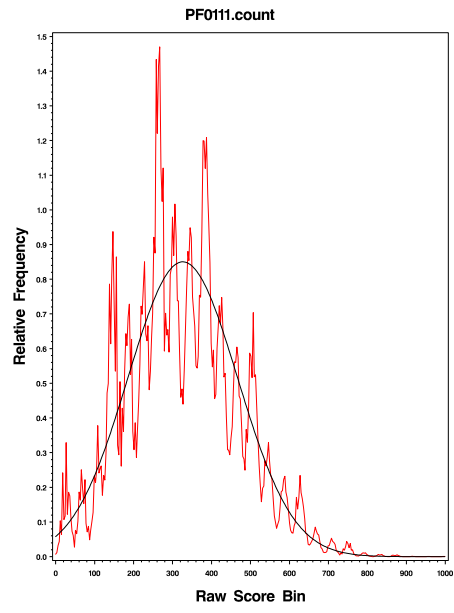
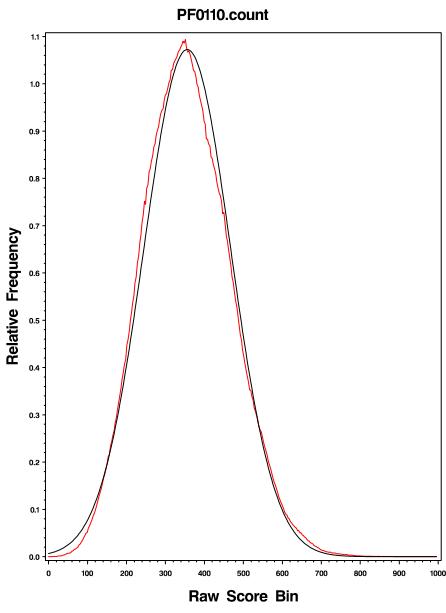


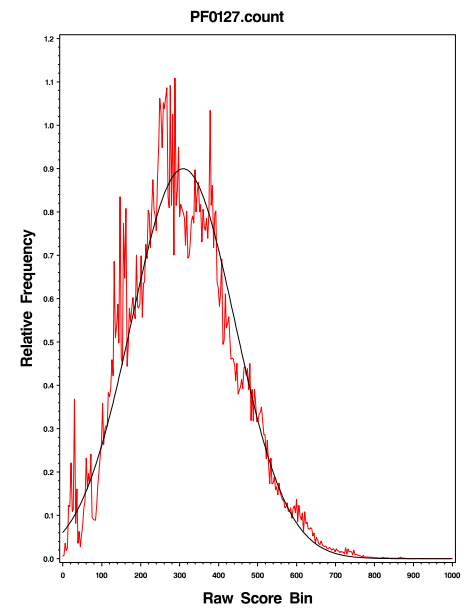
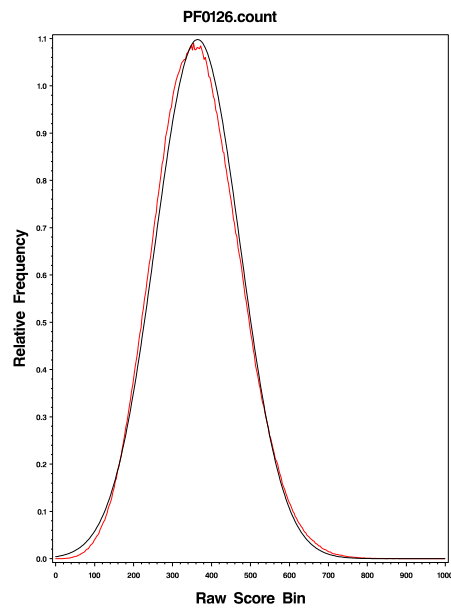
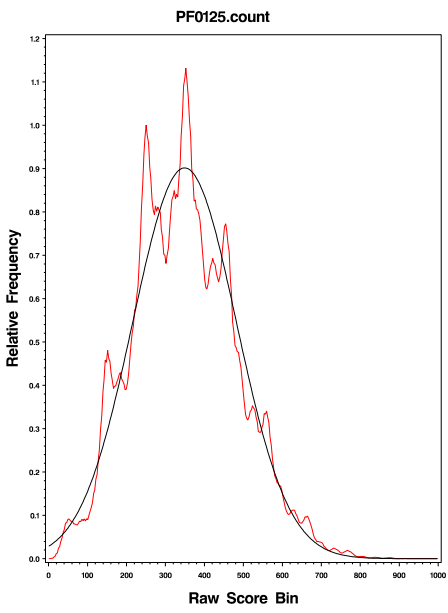
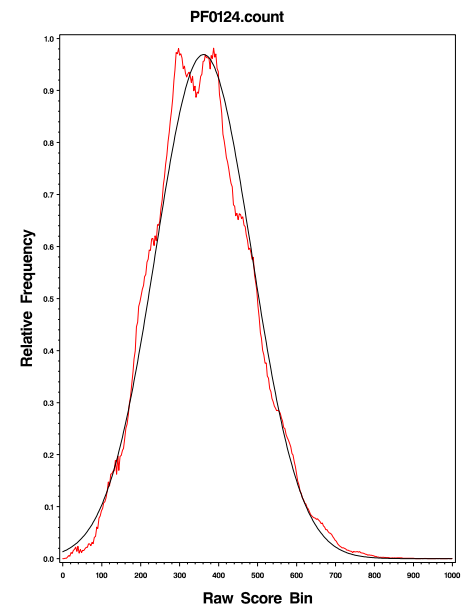
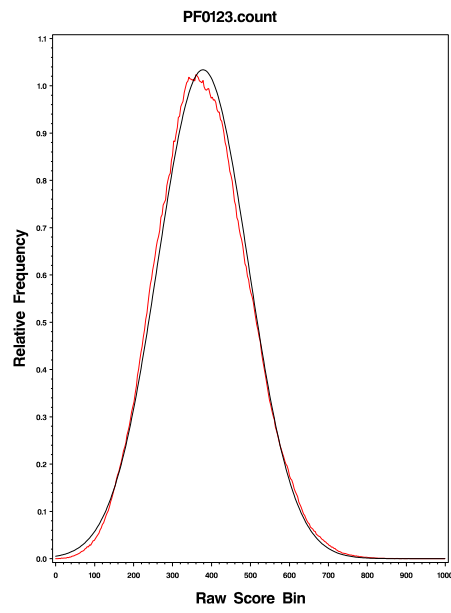
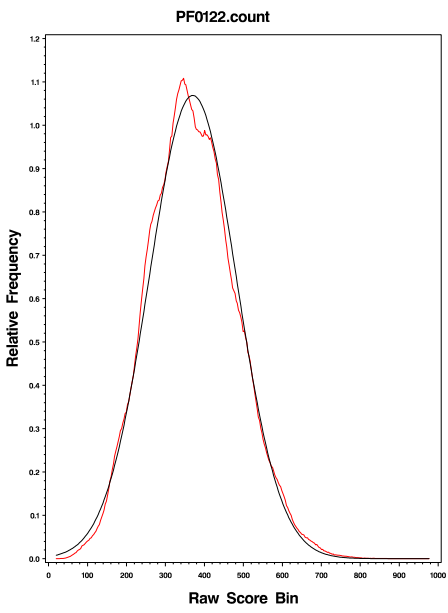
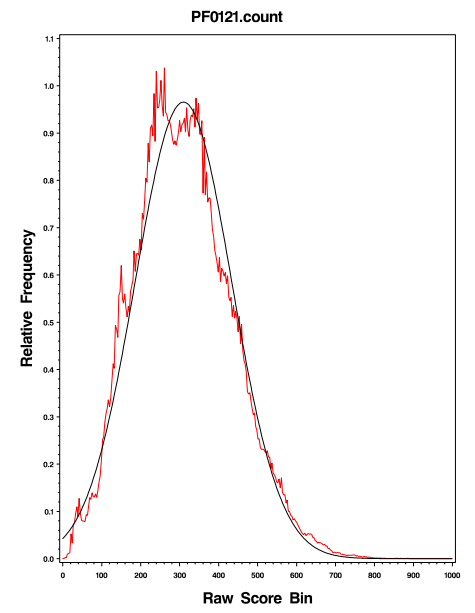
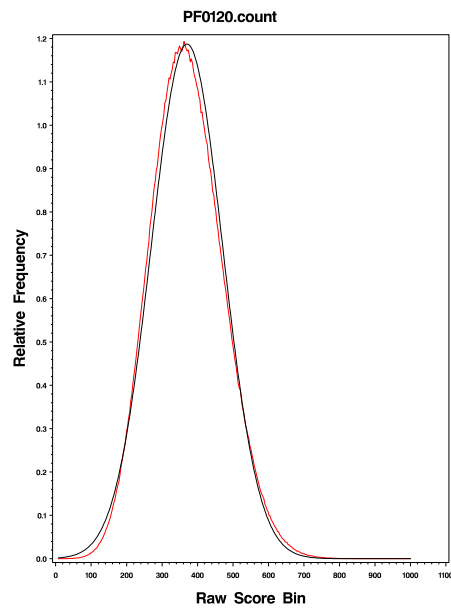
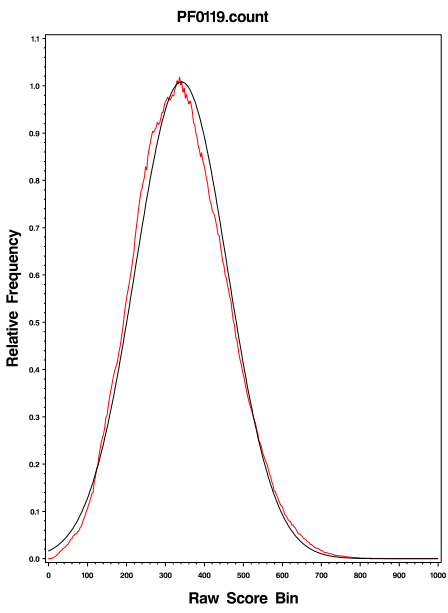
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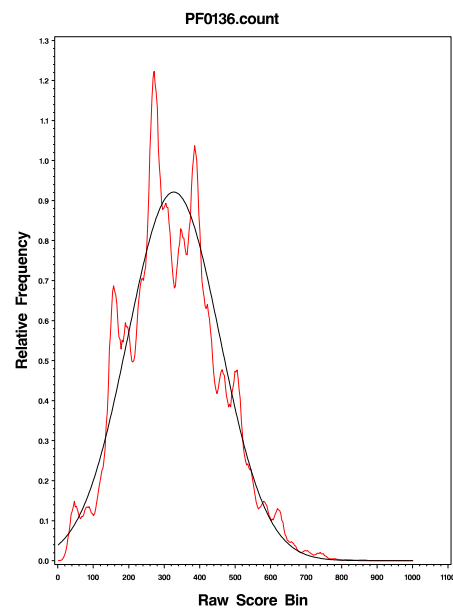
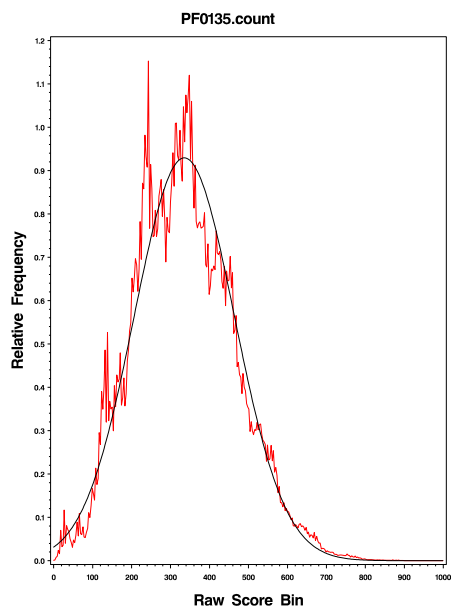
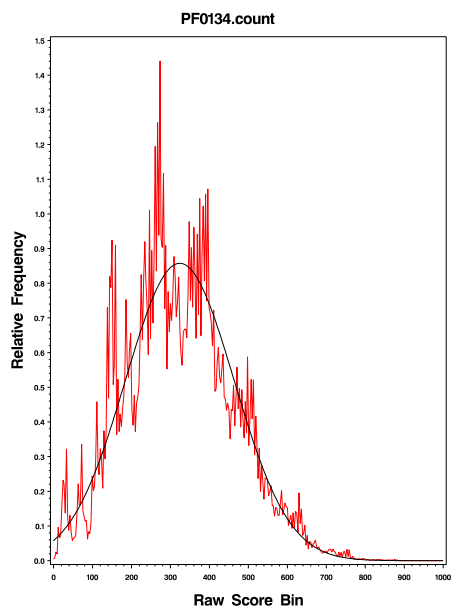
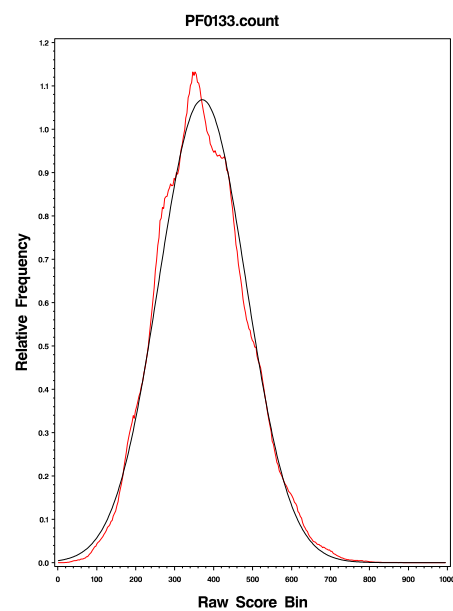
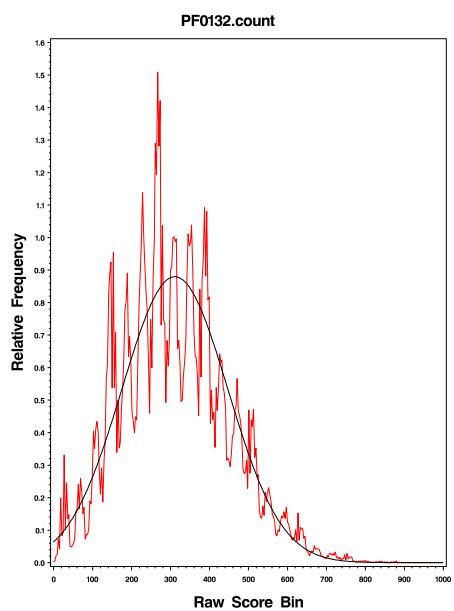
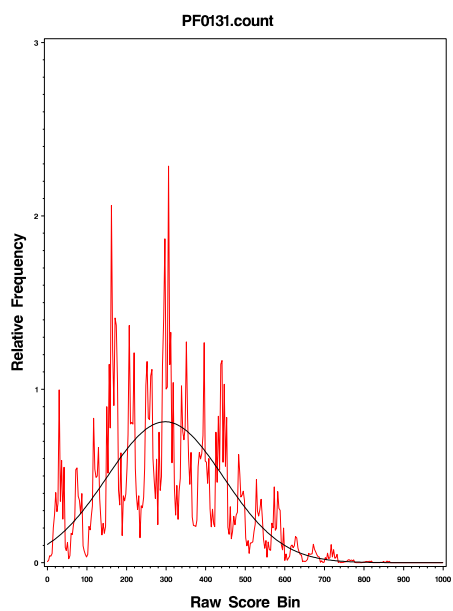
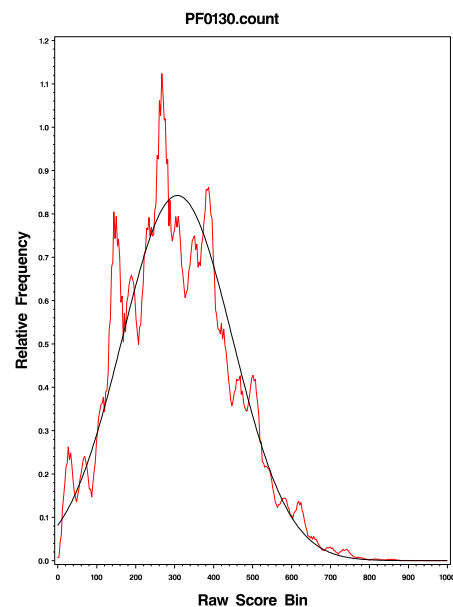
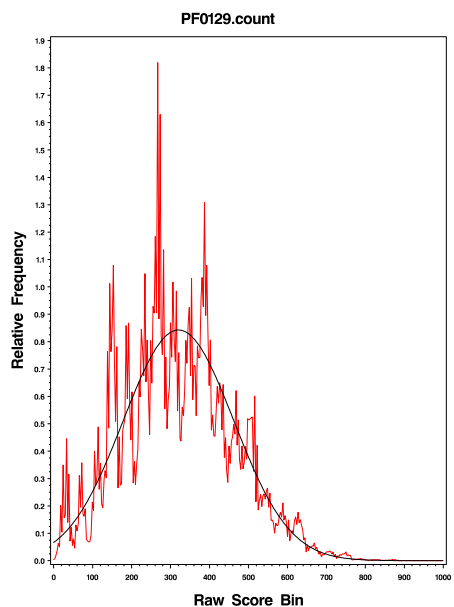
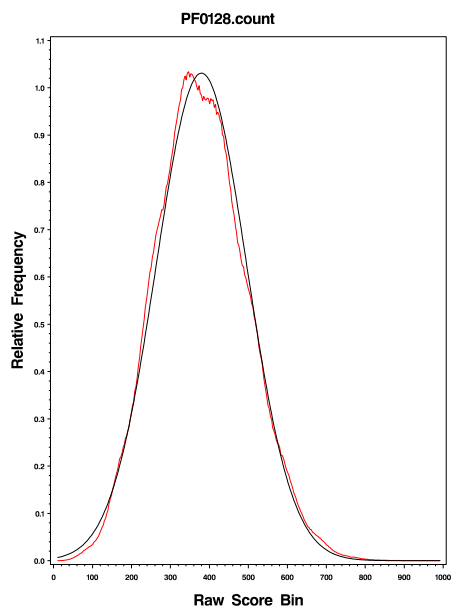


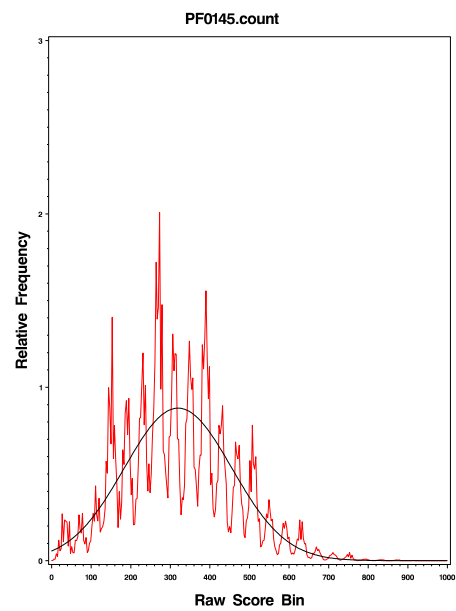
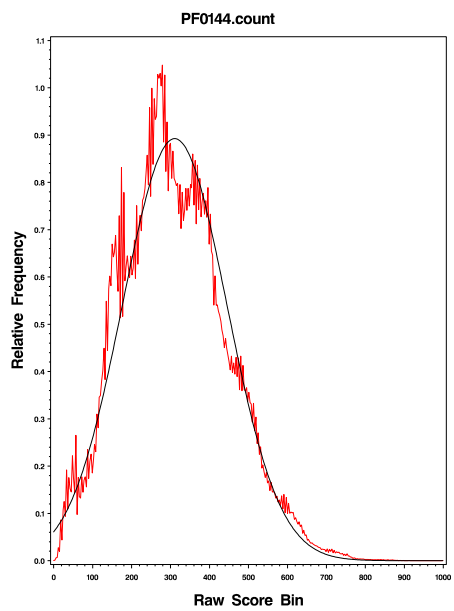
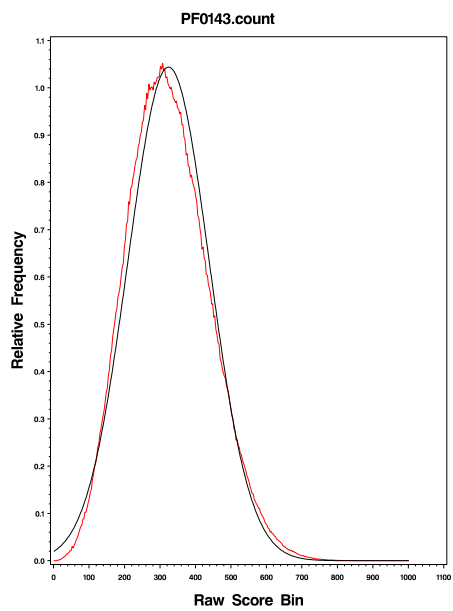
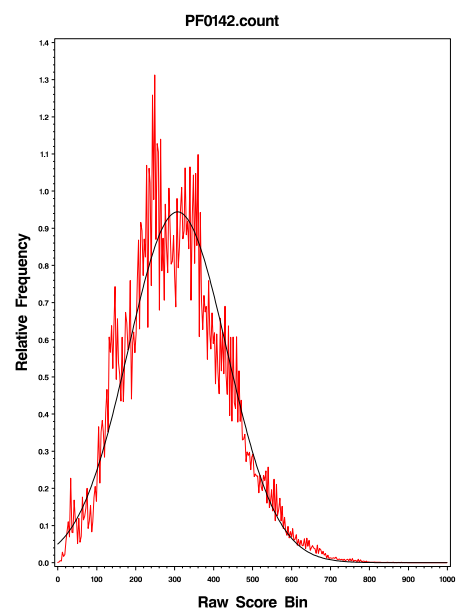
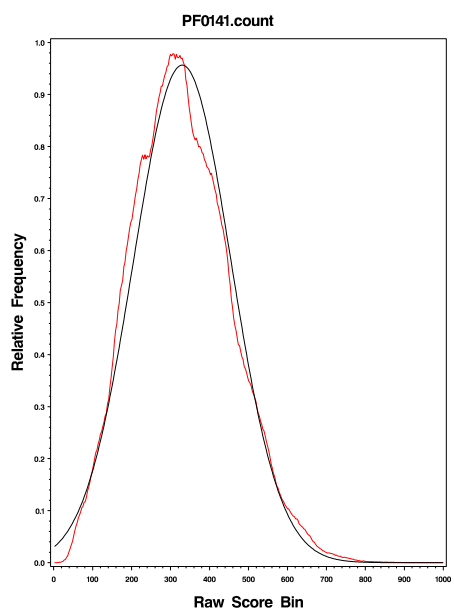
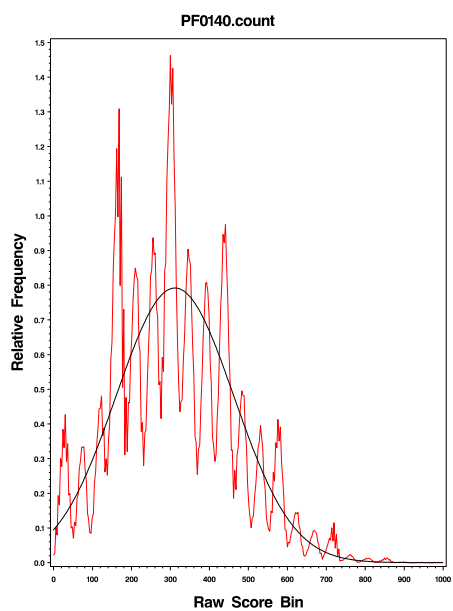
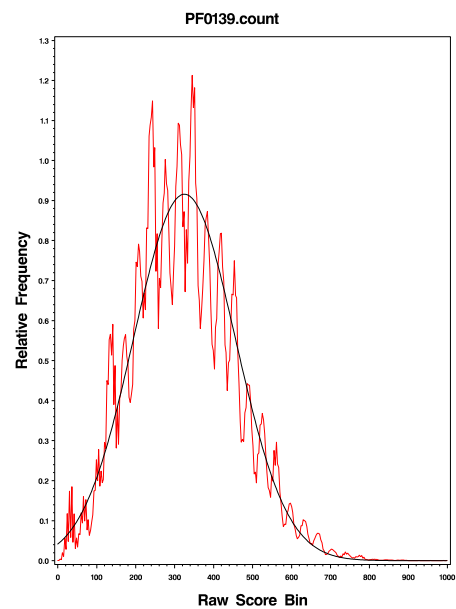
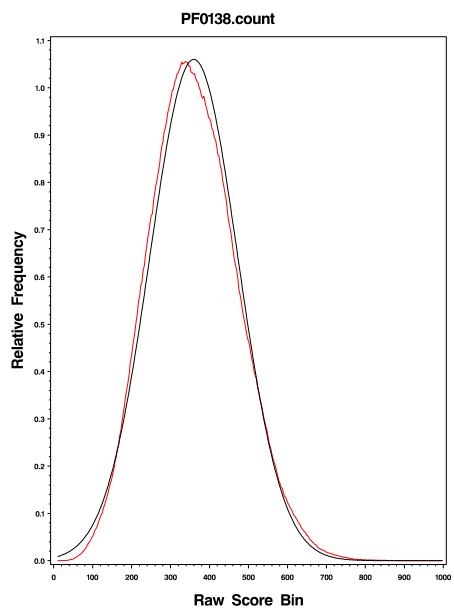
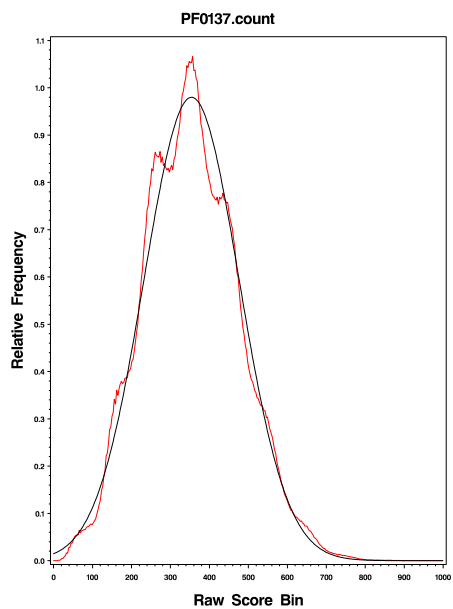


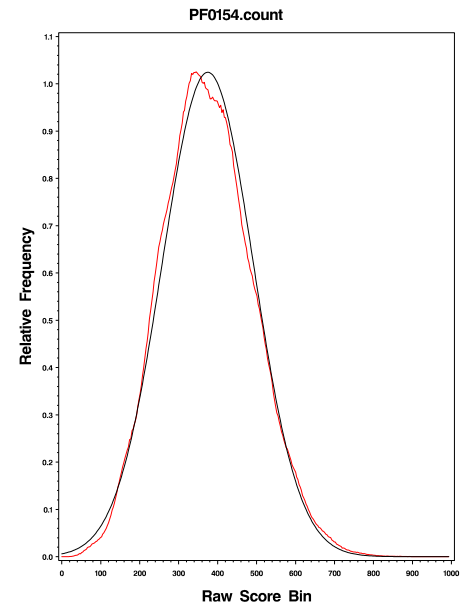
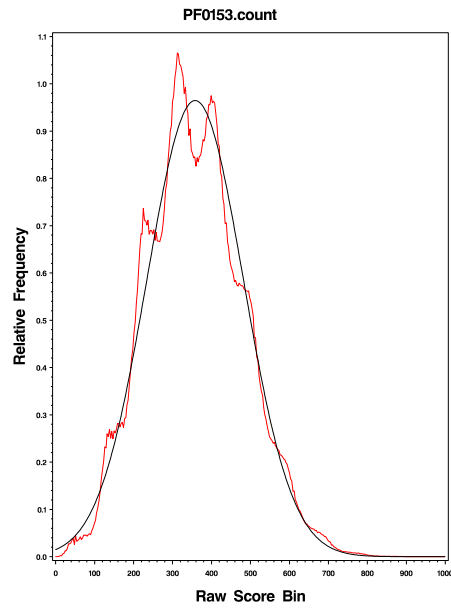
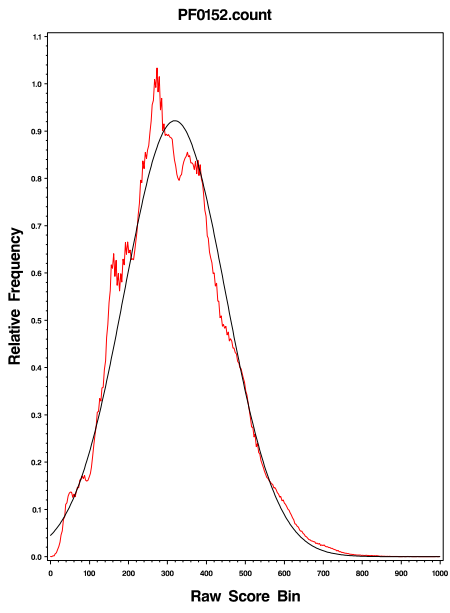
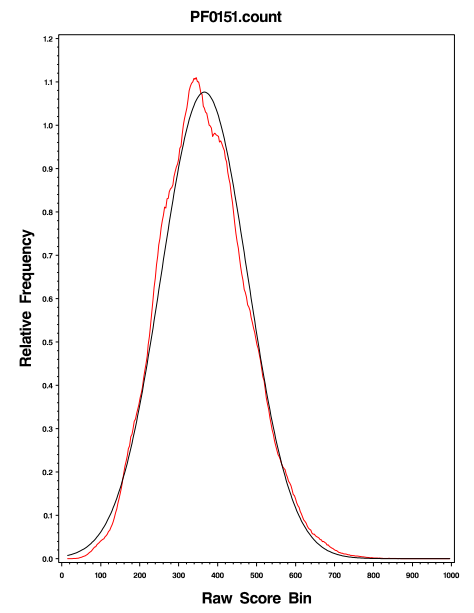
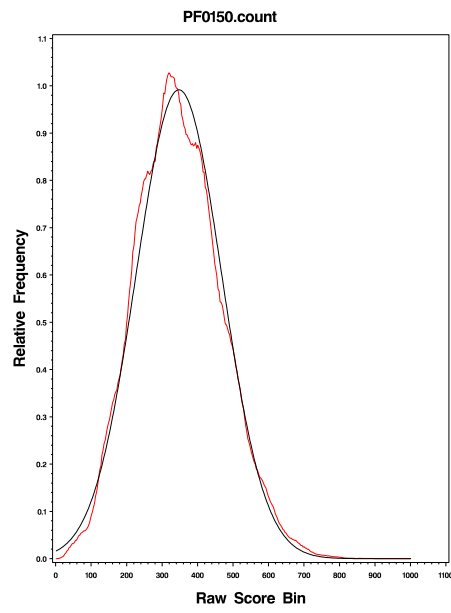
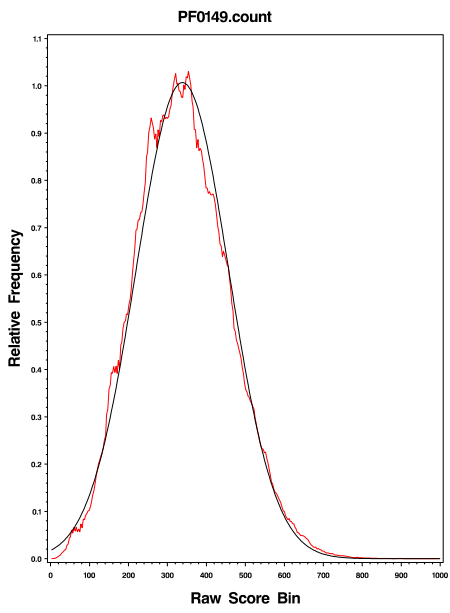
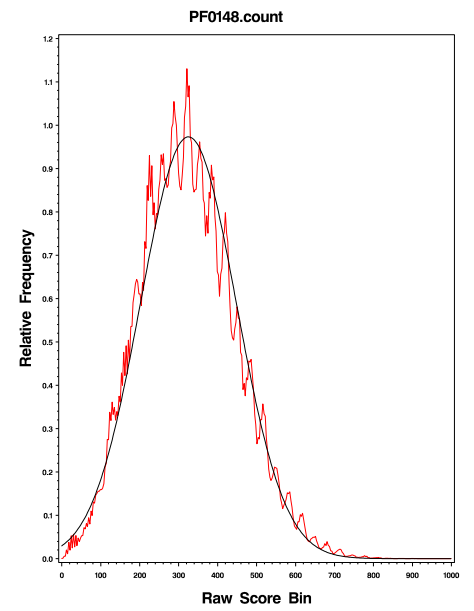
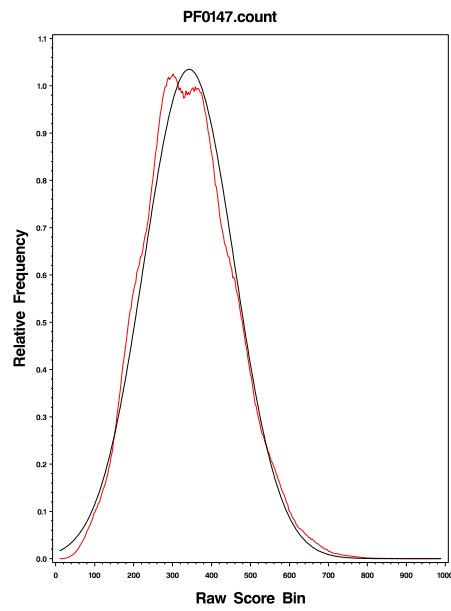
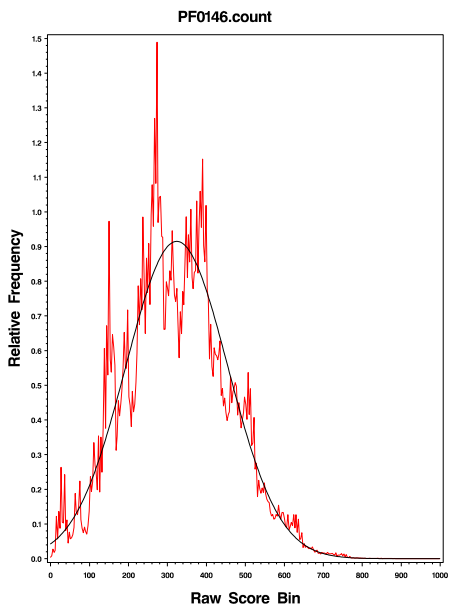


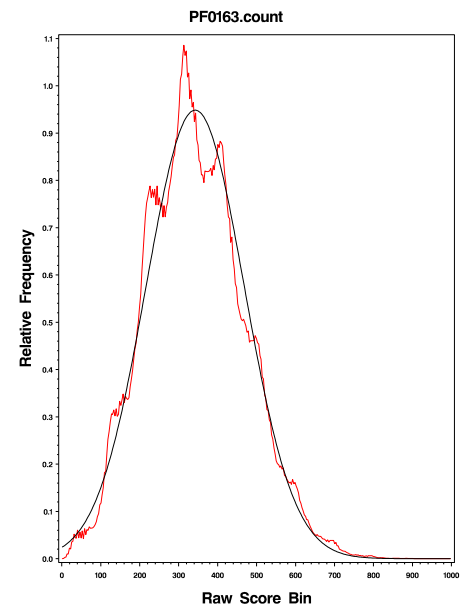
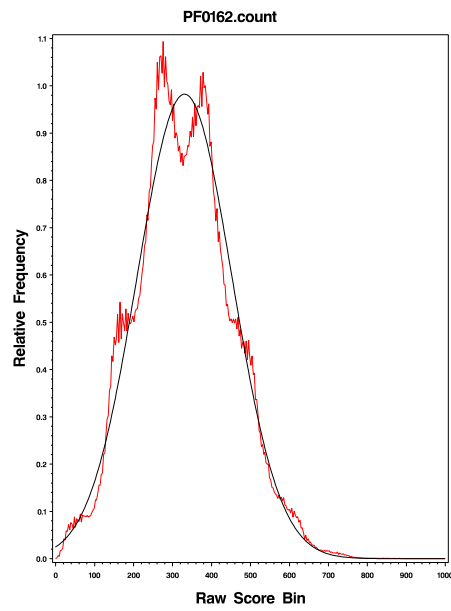
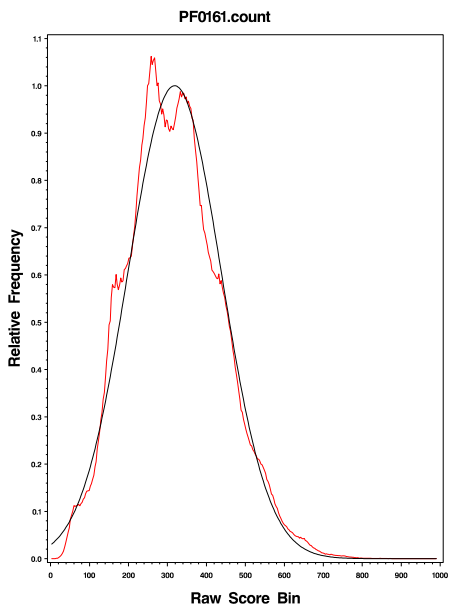
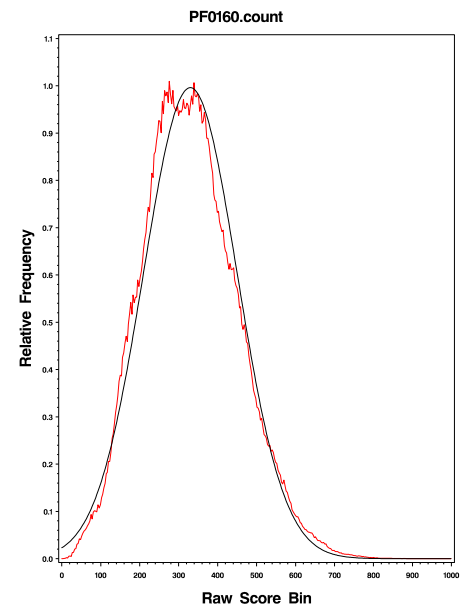
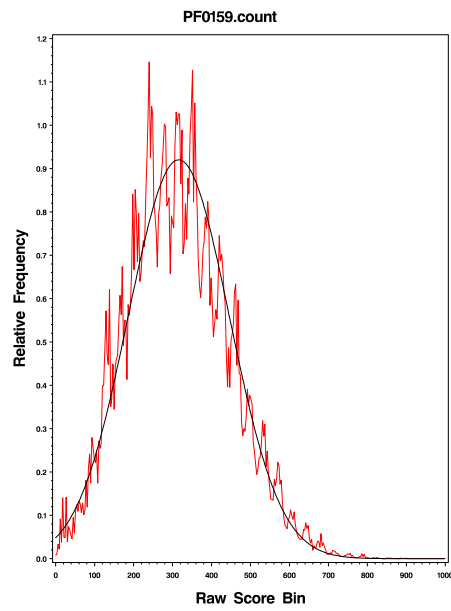
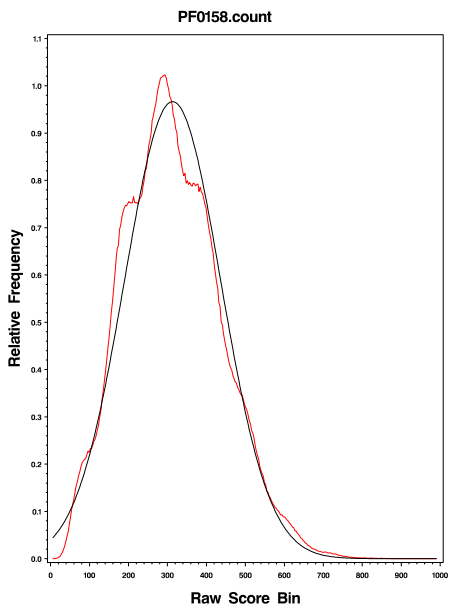
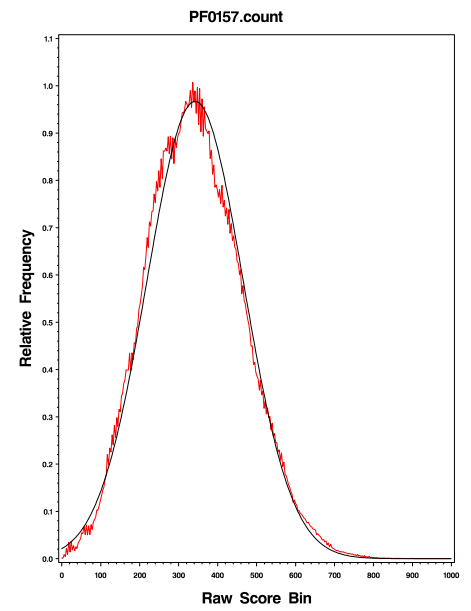
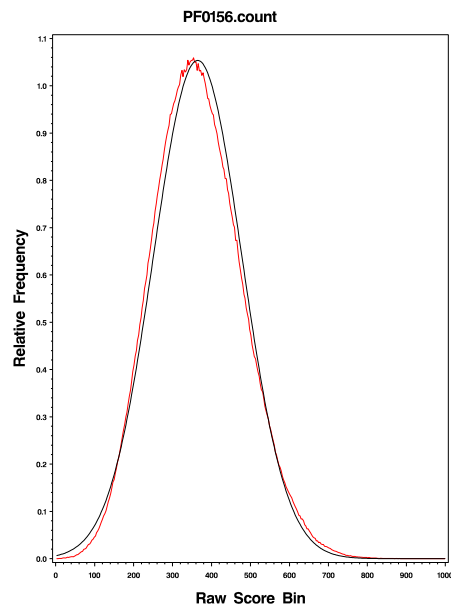
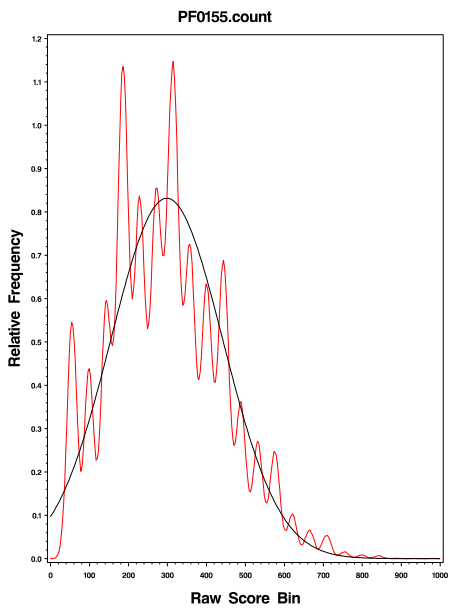


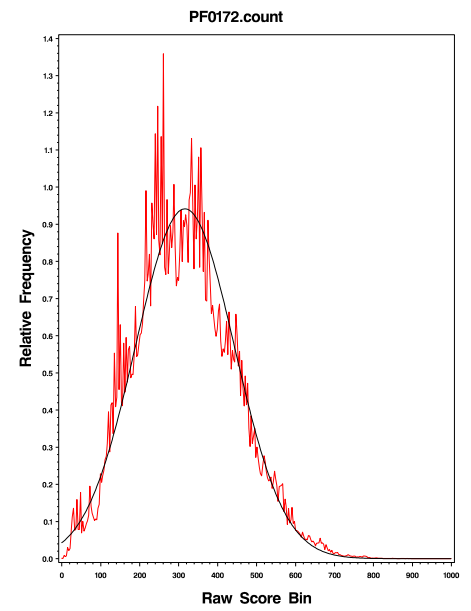
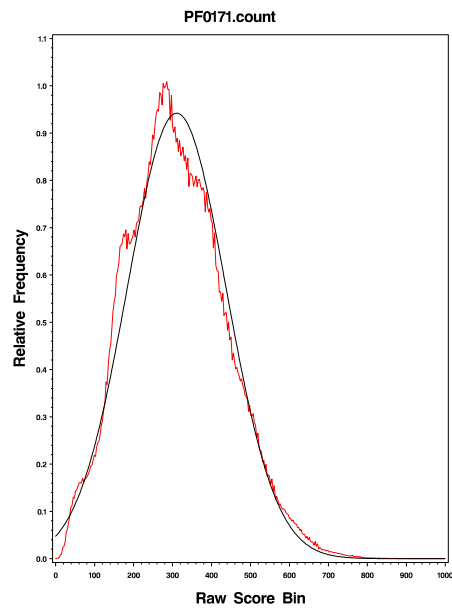
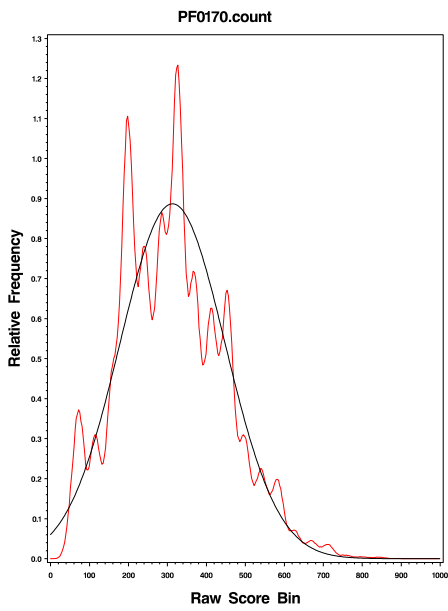
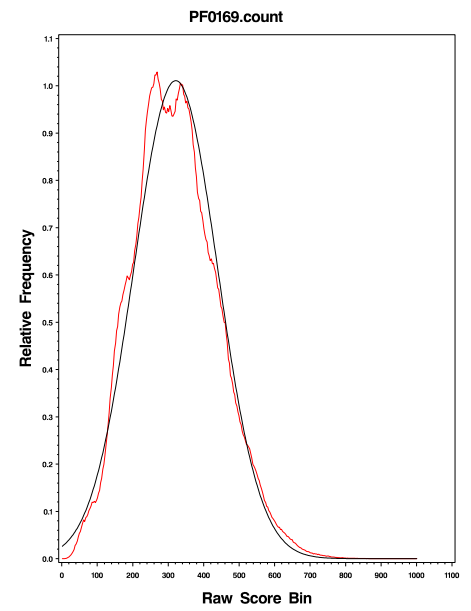
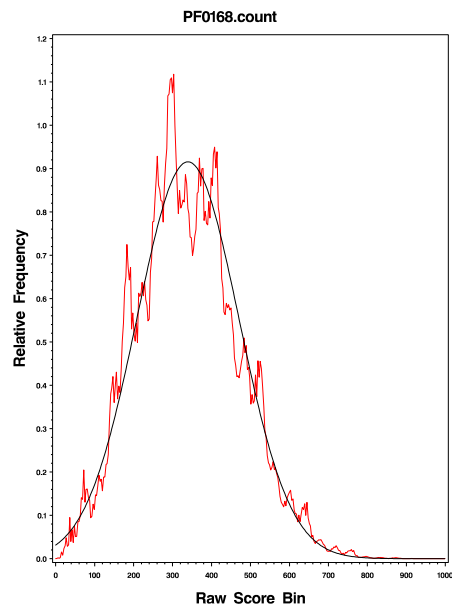
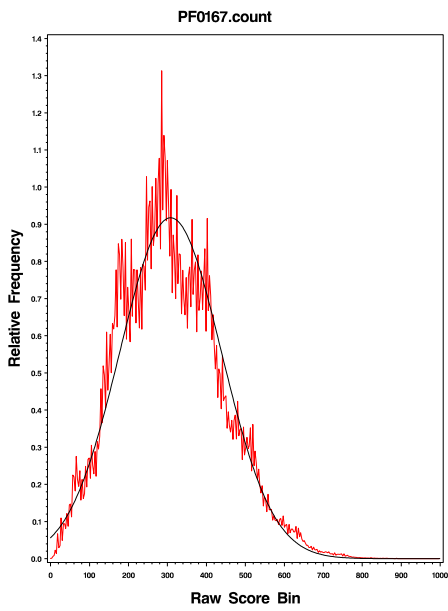
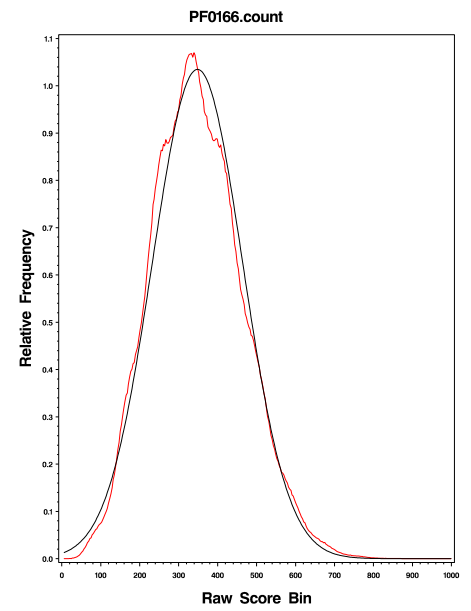
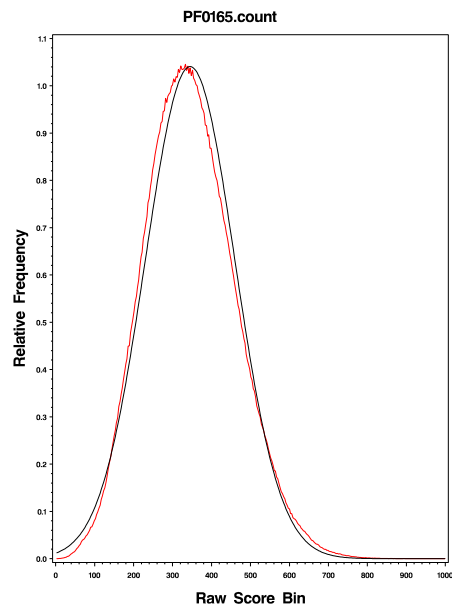
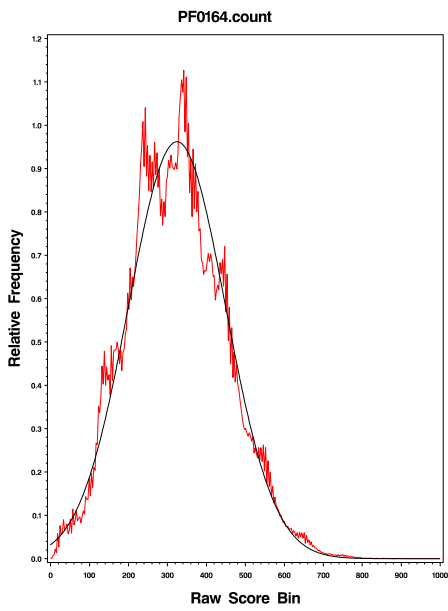




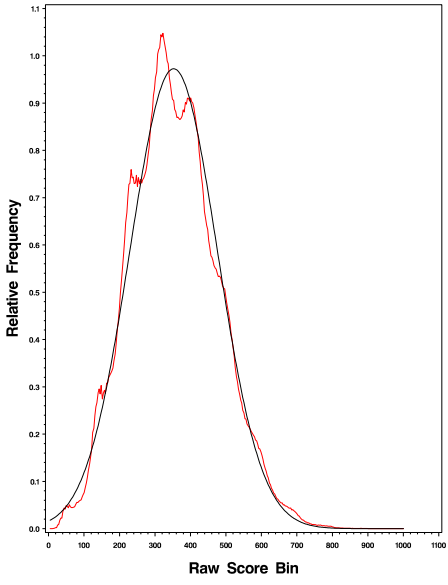








PF0173.count



PF0174.count

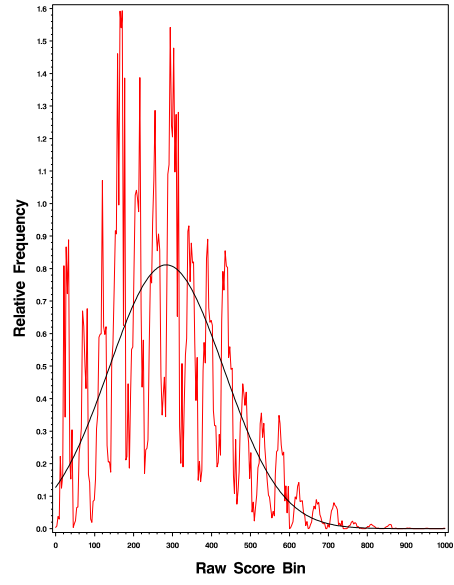


Table S2. Properties of raw score histograms for JASPAR TFBS matrices.

PWM	TF Name	Type	KS Distance	Mean	St Dev	Skewness	Kurtosis	Consensus
MA0001	AGL3	1	0.0950	431.99	115.77	0.1489	-0.0586	CCAWWWATRG
MA0002	RUNX1	1	0.0958	397.16	127.61	0.2481	-0.0461	WTTGYGGTY
MA0003	TFAP2A	2	0.0934	396.48	156.79	0.4299	-0.1862	GCCCBRRGS
MA0004	Arnt	6	0.0898	325.05	143.79	0.3214	-0.0256	CACGTG
MA0005	Agamous	1	0.0943	411.31	124.72	0.2218	-0.0657	CCWAAWWKGGH
MA0006	Arnt-Ahr	6	0.0983	334.14	151.46	0.3798	-0.0519	YGCGTG
MA0007	Ar	3	0.1279	445.09	85.74	0.1672	-0.0303	HWWRGMACRYVVTGTWCCHRMS
MA0008	Athb-1	8	0.1056	347.43	124.52	0.3725	0.0649	CAATTATT
MA0009	Brachyury	7	0.1107	336.76	108.98	0.2935	-0.0114	CTAGGTGTGAA
MA0010	Broad-complex_1	3	0.1053	419.25	104.53	0.1897	-0.1025	RTAAWWRACAARWC
MA0011	Broad-complex_2	1	0.0949	387.87	130.58	0.2996	-0.1649	WWCTATTT
MA0012	Broad-complex_3	1	0.0991	403.35	116.97	0.2161	-0.0768	WAAACWARWHS
MA0013	Broad-complex_4	3	0.1037	405.94	113.78	0.2284	-0.0958	TWRATAACWAW
MA0014	Pax5	3	0.1085	475.30	95.61	0.0809	-0.0941	DRVKCASYGRWGCRKRRCR
MA0015	CF2-II	3	0.1027	436.91	106.29	0.1270	0.0242	RTATATRTRY
MA0016	CFI-USP	6	0.0996	338.74	127.11	0.3192	-0.1257	GGGGTCACGS
MA0017	NR2F1	3	0.1027	438.69	103.69	0.1038	-0.0786	TGAMCTTTGMMCYT
MA0018	CREB1	3	0.1004	430.18	108.21	0.1415	-0.0072	BBKRTGACGYM
MA0019	Chop-cEBP	3	0.1039	427.00	106.64	0.1666	-0.0928	RRRTGCAATMCC
MA0020	Dof2	8	0.1081	305.60	165.79	0.5639	-0.0333	AAAGCM
MA0021	Dof3	4	0.1040	399.06	147.45	0.3854	-0.0111	AAAGYV
MA0022	Dorsal_1	3	0.1001	430.91	105.79	0.1082	-0.0653	SGGGTTTTTCCS
MA0023	Dorsal_2	3	0.1020	385.17	117.03	0.2661	-0.0721	GGGGWTTTCC
MA0024	E2F1	5	0.0862	353.58	131.22	0.1720	-0.1218	TTTSGCGC
MA0025	NFIL3	7	0.1084	377.33	108.42	0.2534	0.0450	TTAYGTAAYRT
MA0026	E74A	6	0.0914	346.54	145.62	0.3542	-0.0472	CMGGAAR
MA0027	En1	1	0.0859	478.54	117.49	0.0410	-0.1706	WARTDRWKBYC
MA0028	ELK1	1	0.0964	405.88	128.59	0.2706	-0.1186	VARCCGGAAR
MA0029	Evi1	7	0.1130	366.38	104.01	0.2841	-0.0475	AAGAYAAGATAABA
MA0030	FOXF2	7	0.1143	384.67	103.80	0.2705	0.0506	BMAASRTAAACAAW
MA0031	FOXD1	8	0.1017	333.60	128.00	0.3860	0.0190	GTAAACAW

MA0032	FOXC1	4	0.1010	390.90	144.93	0.3505	-0.2257	VSHVWGTA
MA0033	FOXL1	1	0.0945	428.15	128.27	0.2919	-0.0658	WWDAYATA
MA0034	GAMYB	1	0.0962	441.04	114.28	0.1366	-0.0957	GRYAACCGMC
MA0035	Gata1	2	0.0936	345.87	165.71	0.4768	-0.1881	SGATGS
MA0036	GATA2	2	0.0786	372.43	169.03	0.3435	-0.2356	GGATR
MA0037	GATA3	1	0.0846	395.81	151.42	0.2860	-0.2064	WGATWG
MA0038	Gfi	4	0.1028	393.01	124.06	0.3580	-0.0214	YMAATCACWG
MA0039	Klf4	1	0.0751	498.21	137.46	0.0482	-0.2905	WRRRRRARRG
MA0040	Foxq1	7	0.1068	383.68	112.59	0.2979	-0.0136	TAWTGTTTATW
MA0041	Foxd3	3	0.1037	439.16	108.81	0.1672	-0.0204	GWWTRTTTDTTY
MA0042	FOXI1	3	0.1058	394.04	113.30	0.2692	0.0697	KSDTRTTTTRTWT
MA0043	HLF	3	0.1049	433.20	101.19	0.1015	-0.0204	KRTTACRYAATH
MA0044	HMG-1	1	0.0841	489.78	123.20	-0.0531	-0.1525	STYGTAYTY
MA0045	HMG-IY	3	0.1007	495.49	99.34	0.0143	-0.1061	SWASAAATRSMSRAMAY
MA0046	TCF1	7	0.1082	367.16	101.90	0.2155	-0.0117	GGTTAATWWTTAMC
MA0047	Foxa2	1	0.0980	449.10	110.90	0.1278	-0.0473	MAWTRTTKRYTY
MA0048	NHLH1	4	0.1092	397.16	114.41	0.3130	0.0105	GCGCAGCTGCKY
MA0049	Hunchback	3	0.1035	430.70	119.09	0.2435	-0.0211	SMRWAAAAAA
MA0050	IRF1	3	0.1077	399.94	106.20	0.2060	0.0174	RAAARYGAAASY
MA0051	IRF2	7	0.1226	399.84	92.16	0.2189	-0.0002	SGAAAGYGAAASYRWVWM
MA0052	MEF2A	7	0.1017	344.75	118.02	0.2593	-0.0351	CTATTTWTAG
MA0053	MNB1A	6	0.0968	330.08	164.58	0.5422	-0.0222	AAAGC
MA0054	MYB.ph3	1	0.0883	426.78	119.37	0.1029	-0.1348	WAACCGTTW
MA0055	Myf	1	0.0934	415.19	120.30	0.1836	-0.0652	MRRCARCWGSWG
MA0056	ZNF42_1-4	2	0.0996	366.37	167.71	0.4327	-0.2536	YGGGGA
MA0057	ZNF42_5-13	3	0.1003	437.91	122.73	0.2603	-0.0879	BKAKGGGKRR
MA0058	MAX	5	0.0960	372.13	121.55	0.2576	-0.0382	RRMCACGTGR
MA0059	MYC-MAX	7	0.1033	377.36	112.12	0.2467	-0.0153	RASCACGTGGT
MA0060	NF-Y	3	0.1120	432.26	100.72	0.2171	0.1510	MYYRCCAATSRGMRS
MA0061	NF-kappaB	1	0.0945	387.37	126.17	0.2475	-0.0958	GGGRMTTYCC
MA0062	GABPA	1	0.0960	382.17	123.32	0.2461	-0.0538	ACCGGAAGWS
MA0063	Nkx2-5	1	0.0907	413.88	135.19	0.2450	-0.0662	WTAAKTG
MA0064	PBF	8	0.1025	319.53	167.23	0.5718	0.0030	AAAGY
MA0065	PPARG-RXRA	7	0.1167	380.27	93.42	0.1753	-0.0771	YYWRRGGTCAAAGGTCAVMK
MA0066	PPARG	7	0.1194	405.59	86.58	0.1104	-0.0411	STRGGTCACSGTGACCYACW
MA0067	Pax2	1	0.0869	450.39	127.98	0.1447	-0.0719	WGTCAYKB

MA0068	Pax4	3	0.1346	465.36	74.05	0.0777	-0.0173	RAAWAWWWKMMMWACYMCMCYMMCMCYMC
MA0069	Pax6	3	0.1074	407.78	98.79	0.1291	-0.0743	TTYACGCWTSVTK
MA0070	Pbx	8	0.1114	350.46	108.11	0.3016	-0.0276	HCATCAATCAWW
MA0071	RORA	8	0.1024	354.59	122.36	0.3268	-0.0377	WWCWAGGTCA
MA0072	RORA1	7	0.1064	375.87	107.49	0.2421	-0.0182	WWWAWBTAGGTCAR
MA0073	RREB1	3	0.1203	433.00	93.54	0.1927	-0.0155	MCMCMAMMCAMCMMCMMSM
MA0074	RXR-VDR	7	0.1140	386.25	97.56	0.1856	-0.0783	RGGTCAWCGRGTTCA
MA0075	Prrx2	8	0.1007	315.56	153.54	0.5371	0.0978	AATTA
MA0076	ELK4	5	0.0979	345.76	125.52	0.2840	-0.0386	ACCGGAAGY
MA0077	SOX9	1	0.0979	397.16	117.92	0.2030	-0.0622	RAACAATRG
MA0078	Sox17	1	0.0916	372.75	129.69	0.2578	-0.0269	YHYATTGTS
MA0079	SP1	3	0.1007	417.12	123.80	0.2914	-0.0686	KRGGSDKKGW
MA0080	SPI1	2	0.0932	379.43	158.50	0.4065	-0.0428	SGGAAS
MA0081	SPIB	2	0.0890	375.48	148.68	0.3439	-0.0620	WSMGGA
MA0082	SQUA	3	0.1054	444.11	103.88	0.1346	-0.0436	MYAWAWAWRGWAAK
MA0083	SRF	7	0.1137	351.97	101.14	0.2418	0.0041	GCCCWTATAWGG
MA0084	SRY	2	0.0991	383.25	129.18	0.3198	-0.0290	KWWAACAAW
MA0085	SU_h	3	0.1104	397.24	103.98	0.2120	-0.0632	BYGTGRGAAMCKARMT
MA0086	Snail	6	0.0957	329.31	153.60	0.3838	-0.0824	CAGGTG
MA0087	Sox5	8	0.1022	331.34	138.25	0.4313	-0.0062	WAACAAT
MA0088	Staf	3	0.1176	471.86	89.79	0.1330	-0.0372	BAYYTCCCAKMATKCMWYGM
MA0089	TCF11-MafG	2	0.0923	381.41	141.98	0.3476	0.0160	SATGAC
MA0090	TEAD	7	0.1071	389.32	110.39	0.2387	-0.0558	YRCATTCCWSBG
MA0091	TAL1-TCF3	3	0.1028	406.62	109.31	0.1896	-0.0030	MGAMCAKMTGKT
MA0092	HAND1-TCF3	4	0.1066	402.17	122.38	0.3369	-0.0169	SRTCTGGMWT
MA0093	USF1	6	0.0958	335.81	135.93	0.3509	-0.0053	CACGTGR
MA0094	Ubx	2	0.0870	340.27	167.71	0.4644	-0.0290	TAAT
MA0095	YY1	6	0.0972	329.53	153.54	0.4763	-0.0543	RCCATC
MA0096	bZIP910	7	0.1006	333.95	132.76	0.2946	-0.0026	MTGACGT
MA0097	bZIP911	7	0.1078	339.74	108.95	0.2537	-0.0007	GRTGACGTGKMC
MA0098	c-ETS	2	0.0890	375.58	165.44	0.3894	-0.1034	YWTCK
MA0099	Fos	1	0.0978	391.13	123.25	0.2456	-0.0092	RTGASTMA
MA0100	Myb	1	0.0949	387.80	129.22	0.2655	-0.0847	GRCVGTG
MA0101	REL	3	0.1016	387.04	119.11	0.2760	-0.0139	SGGRMWTTC
MA0102	cEBP	3	0.1100	446.47	105.60	0.2081	-0.0127	TTYKYGCAAYVYB
MA0103	deltaEF1	2	0.0936	380.50	147.42	0.3847	-0.0093	CACCTK

MA0104	Mycn	6	0.0911	337.34	143.65	0.3528	-0.0024	CACGTG
MA0105	NFKB1	1	0.0922	388.69	122.67	0.1797	-0.1684	GGGGRWYYCCC
MA0106	TP53	7	0.1191	374.92	88.56	0.1353	-0.0740	MSGRACATGYCCGGGCATGT
MA0107	RELA	1	0.0949	379.86	122.32	0.2273	-0.0641	GGGRATTTCC
MA0108	TBP	3	0.1043	458.10	104.48	0.1600	-0.0271	STATAWAWRSSSSSS
MA0109	RUSH1-alfa	1	0.0900	449.68	125.96	0.1441	-0.1254	MDTWTCTC
MA0110	ATHB5	8	0.1038	342.46	117.94	0.3125	0.0271	CAATKATTG
MA0111	Spz1	3	0.1021	447.91	108.66	0.1444	-0.1329	RGGGTWWCAGC
MA0112	ESR1	3	0.1135	425.08	94.38	0.1466	-0.0822	CCAGGTCACCRTGRCCYM
MA0113	NR3C1	3	0.1115	468.27	90.26	0.0584	-0.0695	RRRAACATWMYGTYCTRW
MA0114	HNF4	3	0.1023	439.04	107.08	0.1456	-0.1134	RGGBCAAAGKYCA
MA0115	NR1H2-RXR	7	0.1217	334.35	92.81	0.2277	-0.0128	AAAGGTCAAAGGTCAAC
MA0116	Roaz	1	0.0997	448.10	105.63	0.0879	-0.1043	GSMCCYWRGGKKKM
MA0117	MafB	4	0.1002	396.91	134.39	0.3403	-0.0474	GCTGACKS
MA0118	Macho-1	4	0.1024	391.33	150.73	0.4592	-0.2313	YGGGKGYM
MA0119	Hox11-CTF1	7	0.1100	334.26	109.19	0.2958	-0.0509	TGGCASSRWGCCAA
MA0120	ID1	1	0.0944	520.17	115.25	-0.1230	-0.1286	TTKYYYYTWBYG
MA0121	ARR10	1	0.0919	405.48	129.57	0.2120	-0.1074	AGATHYKS
MA0122	Bapx1	2	0.0977	411.70	132.78	0.3148	-0.1101	YTRAGTRSM
MA0123	ABI4	1	0.0816	444.77	133.89	0.1237	-0.1758	CGSYGCCCCC
MF0001	ETS-class	2	0.0981	383.98	134.23	0.3682	-0.0309	ACCGGAAG
MF0002	bZIP-CREB-G-box-like-subclass	6	0.0919	332.59	139.16	0.3393	-0.0010	TGACGT
MF0003	REL-class	1	0.0910	425.29	119.90	0.1565	-0.0927	GGGRWTTYCC
MF0004	Nuclear-Receptor-class	1	0.0802	431.24	149.36	0.1997	-0.2221	RGGTCA
MF0005	Forkhead-class	1	0.0967	412.45	124.81	0.2622	0.0313	TGTTTAYTT
MF0006	bZIP-cEBP-like-subclass	1	0.0936	452.20	116.62	0.1207	-0.0505	RTTRCRTAA
MF0007	bHLH-zip-class	1	0.0930	444.85	127.79	0.2111	-0.0459	ASCACSTG
MF0008	MADS-class	1	0.0866	411.90	123.76	0.1096	-0.0884	CYATWTWTRG
MF0009	TRP-MYB-class	1	0.0974	452.38	125.03	0.2381	-0.0706	WDWCRGTT
MF0010	Homeobox-class	1	0.0799	402.08	135.73	0.1431	-0.0805	AATAATT
MF0011	HMG-class	1	0.0760	440.49	146.70	0.1211	-0.1424	WTTGTT
PF0001	---	6	0.0928	322.85	128.71	0.3032	0.0968	RCGCANGCGY
PF0002	---	8	0.1211	269.06	152.68	0.5055	-0.1083	CACGTG
PF0003	---	5	0.0962	328.11	143.16	0.2834	-0.0537	SCGGAAGY
PF0004	---	7	0.1048	322.55	112.67	0.2807	0.0543	ACTAYRNNNCCCR

PF0005	---	8	0.1009	296.97	138.44	0.3919	0.1862	GATTGGY
PF0006	---	8	0.1103	306.04	159.36	0.4885	0.0571	GGGCGGR
PF0007	---	8	0.1093	268.95	151.74	0.4574	-0.0719	TGANTCA
PF0008	---	5	0.0967	317.90	116.59	0.2239	-0.0200	TMTCGCGANR
PF0009	---	6	0.1000	314.76	130.53	0.3209	0.0999	TGAYRTCA
PF0010	---	8	0.1120	278.51	129.60	0.3740	0.0220	GCCATNTTG
PF0011	---	6	0.0967	295.61	140.09	0.3877	0.0154	MGGAAGTG
PF0012	---	8	0.1247	266.91	161.59	0.6041	-0.0219	CAGGTG
PF0013	---	8	0.1337	257.86	161.64	0.5847	-0.1332	CTTTGT
PF0014	---	6	0.0995	270.61	128.65	0.3838	0.0904	TGACGTCA
PF0015	---	8	0.1262	269.24	164.86	0.5959	-0.0645	CAGCTG
PF0016	---	6	0.0985	322.69	144.16	0.3731	0.0334	RYTTCCTG
PF0017	---	8	0.1405	252.46	161.48	0.6036	-0.1328	AACTTT
PF0018	---	8	0.1019	318.00	130.57	0.3564	0.0497	TCANNTGAY
PF0019	---	7	0.1102	363.80	104.14	0.2639	0.0225	GKCGCNNNNNNNTGAYG
PF0020	---	6	0.0995	303.14	138.60	0.3800	0.1643	GTGACGY
PF0021	---	7	0.1027	340.71	116.62	0.2807	0.0102	GGAANCGGAANY
PF0022	---	6	0.0922	310.28	140.86	0.3110	-0.0298	TGCGCANK
PF0023	---	8	0.1309	252.21	156.31	0.5069	-0.2055	TAATTA
PF0024	---	6	0.0890	324.95	160.16	0.3520	-0.1332	GGGAGGRR
PF0025	---	6	0.0948	299.98	145.96	0.3985	0.1321	TGACCTY
PF0026	---	8	0.1013	318.85	132.77	0.3535	0.0964	TTAYRTAA
PF0027	---	6	0.0942	342.18	132.61	0.3022	-0.0634	TGGNNNNNNKCCAR
PF0028	---	6	0.0982	315.53	132.33	0.3105	-0.0446	CTAWWWATA
PF0029	---	6	0.0950	293.30	145.39	0.4176	0.2359	CTTTAAR
PF0030	---	7	0.1005	346.07	130.83	0.2678	0.1599	YGCGYRCGC
PF0031	---	6	0.0993	328.84	138.49	0.3194	0.0022	GGGYGTGNY
PF0032	---	5	0.0947	314.31	128.61	0.2976	-0.0760	TGASTMAGC
PF0033	---	8	0.1052	320.55	139.60	0.3610	0.0133	YTATTTTNR
PF0034	---	5	0.0964	307.17	129.70	0.2849	-0.1202	CYTAGCAAY
PF0035	---	6	0.0998	320.55	145.45	0.3660	-0.0497	GCANCTGNY
PF0036	---	6	0.0950	292.88	141.44	0.3996	0.1904	RTAAACA
PF0037	---	5	0.0938	342.30	120.86	0.2026	-0.0488	GTTRYCATRR
PF0038	---	6	0.1000	271.19	135.06	0.4016	-0.0352	TGACCTTG
PF0039	---	5	0.0964	334.95	124.31	0.2781	-0.0011	TCCCRNNRTGC
PF0040	---	6	0.0986	322.94	143.07	0.3506	0.0177	TTCYNRGAA

PF0041	---	6	0.0942	305.74	143.73	0.3381	-0.0218	TGACAGNY
PF0042	---	6	0.0952	296.51	141.62	0.3723	0.1462	TGACATY
PF0043	---	7	0.1042	330.88	112.91	0.2642	-0.0143	GTTGNYNNRGNAAC
PF0044	---	8	0.1014	316.76	130.29	0.3216	-0.0059	YATGNWAAT
PF0045	---	5	0.0973	332.43	122.31	0.2624	-0.0514	CCANNAGRKGGC
PF0046	---	6	0.0985	311.17	137.26	0.3612	0.0235	WTTGKCTG
PF0047	---	6	0.0917	300.56	147.45	0.3849	0.0704	TGCCAAR
PF0048	---	8	0.1012	315.23	122.07	0.3426	0.0077	GCGNNANTTCC
PF0049	---	5	0.0914	321.99	143.46	0.2562	-0.1753	CATTGTYT
PF0050	---	8	0.1001	341.35	141.70	0.3207	-0.0794	RGAGGAARY
PF0051	---	8	0.1379	249.28	159.18	0.5906	-0.1309	TATAAA
PF0052	---	5	0.0930	342.59	129.61	0.2245	-0.1068	YCATTCAWW
PF0053	---	7	0.1041	342.84	116.60	0.2610	-0.0345	RYTGCNNRGNAAC
PF0054	---	8	0.1005	292.98	128.97	0.3642	-0.0114	TAAWWATAG
PF0055	---	8	0.1368	258.92	163.11	0.6240	-0.0247	TGGAAA
PF0056	---	6	0.0885	324.26	154.56	0.3409	-0.1231	GGGTGRR
PF0057	---	8	0.1011	272.09	133.02	0.3813	-0.0366	ACCTGTTG
PF0058	---	6	0.0936	294.36	140.02	0.3490	0.1714	YCATTAA
PF0059	---	5	0.0976	332.71	122.17	0.2861	-0.0290	WTCNATGGY
PF0060	---	8	0.1400	253.43	163.21	0.6162	-0.1126	TTGTTT
PF0061	---	8	0.1060	288.78	135.37	0.3969	0.0929	YTAATTAA
PF0062	---	6	0.0910	320.14	138.05	0.3132	-0.0244	SMTTTTGT
PF0063	---	7	0.1011	333.48	119.01	0.2641	-0.0049	AAGWWRNYGGC
PF0064	---	8	0.1206	256.21	156.82	0.5191	-0.1862	TTANTCA
PF0065	---	5	0.0931	295.33	130.62	0.2740	-0.1549	ARGGGTTAA
PF0066	---	8	0.1031	314.18	116.86	0.3193	0.0594	RACTNNRTTNC
PF0067	---	7	0.1021	331.37	133.13	0.2962	-0.0697	TGANNYRGCA
PF0068	---	6	0.0902	304.48	147.18	0.3237	-0.0394	RGAANNTTC
PF0069	---	5	0.0959	348.10	131.13	0.1862	-0.0844	SGCGSSAAA
PF0070	---	5	0.0903	310.04	136.78	0.2677	0.0278	CGTSACG
PF0071	---	5	0.0898	323.31	133.93	0.2446	-0.0626	SYATTGTG
PF0072	---	6	0.0955	323.30	142.46	0.3531	0.0283	TTCYRGAA
PF0073	---	8	0.1316	259.01	160.76	0.5699	-0.1310	CTTTGA
PF0074	---	8	0.1048	334.43	115.46	0.3120	-0.0023	GGAMTNNNNNTCCY
PF0075	---	6	0.0989	323.66	124.98	0.3250	0.0086	TNCATNTCCYR
PF0076	---	8	0.1290	265.31	157.83	0.5190	-0.1859	CAGGTA

PF0077	---	8	0.1018	323.85	134.87	0.3379	0.0604	AAAYRNCTG
PF0078	---	6	0.0990	323.33	131.98	0.3216	0.0072	GCTNWTGK
PF0079	---	6	0.0986	317.98	140.08	0.3268	-0.0631	WGGAATGY
PF0080	---	7	0.1080	348.84	108.69	0.2585	0.0286	SNACANNYSYAGA
PF0081	---	6	0.0975	305.44	126.71	0.3320	-0.0212	CGGAARNGGCNG
PF0082	---	8	0.1026	316.53	118.23	0.3125	-0.0278	CTGYNNCTYTAA
PF0083	---	6	0.0940	297.40	145.24	0.3787	0.1216	TGTTTGY
PF0084	---	7	0.1031	334.15	122.24	0.2766	-0.0350	RGTTAMWNATT
PF0085	---	8	0.1049	325.02	127.34	0.3545	0.0598	STTTCRNTT
PF0086	---	8	0.1100	287.34	134.75	0.3763	-0.0145	GGGNNTTCC
PF0087	---	5	0.0991	350.18	118.97	0.2304	-0.0413	RYTGCNWTGGNR
PF0088	---	5	0.0963	339.65	123.69	0.2744	-0.0375	GGCNKCCATNK
PF0089	---	5	0.0986	330.20	118.11	0.2697	-0.0436	GTTNYNNGGTNA
PF0090	---	7	0.1003	353.40	120.96	0.2899	0.0218	YAATNRNNNYNATT
PF0091	---	6	0.0981	300.80	141.12	0.3812	-0.0266	GTGGGTGK
PF0092	---	6	0.0955	300.47	143.61	0.3884	0.0856	TGCTGAY
PF0093	---	8	0.1214	262.07	153.34	0.4690	-0.2533	GGATTA
PF0094	---	6	0.0987	319.20	134.55	0.3488	0.0949	TGATTRY
PF0095	---	5	0.0962	327.24	124.25	0.2683	-0.0519	GCCNNNWTAAAR
PF0096	---	5	0.0953	337.64	134.48	0.2329	-0.0941	YGCANTGCR
PF0097	---	5	0.0897	300.72	140.46	0.2859	-0.0624	YATTNATC
PF0098	---	5	0.0956	337.22	124.50	0.2397	-0.0544	GTCNYYATGR
PF0099	---	5	0.0999	306.98	124.01	0.2946	-0.0813	ATCMNTCCGY
PF0100	---	5	0.0994	344.45	118.21	0.2405	-0.0930	CRGAARNNNNCGA
PF0101	---	6	0.0994	301.35	150.36	0.4609	0.1312	CTGCAGY
PF0102	---	8	0.1011	295.73	132.33	0.3494	-0.0123	ATGGYGGA
PF0103	---	7	0.1012	352.02	114.29	0.2130	-0.0555	ACAWNRNSRCGG
PF0104	---	7	0.1039	348.57	111.49	0.2358	0.0103	CCAATNNSNNNGCG
PF0105	---	7	0.1013	328.71	116.52	0.2642	-0.0380	ACTWSNACTNY
PF0106	---	7	0.1005	336.35	113.86	0.2202	-0.0660	CCGNMNTNACG
PF0107	---	5	0.0959	351.25	125.92	0.2814	-0.0136	RTTTNNNYTGGM
PF0108	---	5	0.0971	319.57	127.23	0.2929	-0.0290	AACWWCAANK
PF0109	---	6	0.0967	318.47	130.30	0.3189	-0.0379	YGTCTTGR
PF0110	---	7	0.1036	356.45	112.53	0.2528	0.0073	MCAATNNNNNGCG
PF0111	---	5	0.0943	326.68	141.41	0.2789	-0.0781	RACCACAR
PF0112	---	5	0.0974	351.63	122.99	0.2483	-0.0014	KTGGYRSGAA

PF0113	---	8	0.1043	327.39	115.15	0.3070	-0.0050	AACYNNNNTTCCS
PF0114	---	7	0.1010	348.60	119.72	0.2653	-0.0074	YTCCCRNNAGGY
PF0115	---	5	0.0970	357.29	118.60	0.2314	-0.0114	YRTCANNRCGC
PF0116	---	7	0.1017	345.26	119.82	0.2933	0.0040	KMCATNNWGGGA
PF0117	---	5	0.0961	380.05	117.47	0.2122	-0.0573	TGTYNNNNNRGCARM
PF0118	---	5	0.0994	343.66	118.41	0.2306	-0.0245	GGCNRNWCTTYS
PF0119	---	7	0.1001	341.54	119.60	0.2504	-0.0618	GGGNRMNNYCAT
PF0120	---	7	0.1107	370.52	101.84	0.2380	-0.0110	KRCTCNNNNMANAGC
PF0121	---	8	0.1004	310.24	124.91	0.3435	0.0319	CCAWWNAAGG
PF0122	---	7	0.1011	370.62	112.92	0.2284	-0.0271	RNTCANNRNNYNATTW
PF0123	---	5	0.0956	378.60	116.67	0.1839	-0.0699	GGCNNMSMYNTTG
PF0124	---	5	0.0963	361.78	124.36	0.2799	0.0221	CCAWYNNGAAR
PF0125	---	5	0.0897	349.64	133.81	0.2665	-0.0671	RAAGNYNNCTTY
PF0126	---	7	0.1014	364.76	109.96	0.2117	-0.0306	WYAAANNRNNNGCG
PF0127	---	8	0.1024	309.68	133.62	0.3378	-0.0200	WWTAAGGC
PF0128	---	5	0.0968	380.13	116.97	0.2100	-0.0530	RYCACNNRNNRNCAG
PF0129	---	5	0.0929	320.97	142.55	0.2678	-0.1361	RRAGTTGT
PF0130	---	6	0.0987	307.46	142.82	0.3315	-0.1073	CCCNNGGGAR
PF0131	---	6	0.0860	298.80	145.96	0.3085	-0.0714	GATAAGR
PF0132	---	6	0.0981	311.57	136.85	0.3598	-0.0045	TCCATTKW
PF0133	---	7	0.1006	371.57	113.00	0.2328	0.0053	RYTAAWNNNTGAY
PF0134	---	5	0.0946	324.35	140.24	0.2682	-0.1229	CATRRAGC
PF0135	---	5	0.0999	335.68	129.69	0.2923	-0.0155	AGCYRWTTCC
PF0136	---	7	0.1038	327.71	130.69	0.2912	-0.0236	TAAYNRNNTCC
PF0137	---	5	0.0919	354.60	123.00	0.2060	-0.0577	GAANYNYGACNY
PF0138	---	7	0.1046	360.16	113.84	0.2637	-0.0281	MYAATNNNNNNNGGC
PF0139	---	6	0.0998	325.43	131.80	0.3261	0.0302	AAAYWAACM
PF0140	---	6	0.0947	312.10	150.05	0.3825	0.0391	RNGTGGGC
PF0141	---	8	0.1027	330.47	125.88	0.3476	-0.0158	TTCNRGNNNNTTC
PF0142	---	8	0.1001	307.76	127.85	0.3504	0.0188	ACAWYAAAG
PF0143	---	8	0.1050	324.65	115.51	0.3190	-0.0356	CAGNWMCNNGAC
PF0144	---	8	0.1032	311.05	135.03	0.3457	-0.0250	AAANWWTGC
PF0145	---	6	0.0941	319.93	136.85	0.3236	0.0223	YKACATTT
PF0146	---	5	0.0940	324.40	131.56	0.1877	-0.1410	RRCCGTTA
PF0147	---	8	0.1033	343.20	116.54	0.3003	0.0023	YAATNANRNNNCAG
PF0148	---	5	0.0974	325.36	123.87	0.2976	-0.0045	GATGKMRGCG

PF0149	---	5	0.0990	339.00	119.70	0.2509	-0.0304	YGACNNYACAR
PF0150	---	7	0.1013	347.82	121.56	0.2604	-0.0164	YTTCCNNNGGAMR
PF0151	---	7	0.1050	366.44	112.13	0.2630	0.0018	RYAAAKNNNNNNNTTGW
PF0152	---	8	0.1008	319.59	130.61	0.3330	0.0007	WCAANNNYCAG
PF0153	---	5	0.0969	358.55	124.92	0.2128	-0.0835	CTGRYYYYNATT
PF0154	---	5	0.0963	375.19	117.70	0.2212	-0.0405	RNCTGNYNRNCTGNY
PF0155	---	6	0.0924	298.54	144.85	0.4323	-0.0354	WGTTNNNNNAAA
PF0156	---	7	0.1018	364.86	114.51	0.2552	-0.0054	YRCCAKNNGNCGC
PF0157	---	5	0.0959	342.62	124.52	0.2361	-0.0644	KCCGNSWTTT
PF0158	---	8	0.1039	313.67	124.66	0.3416	-0.0506	CCCNNNNNNAAGWT
PF0159	---	5	0.0918	316.26	130.99	0.2927	-0.0915	GGCKCATGS
PF0160	---	8	0.1025	330.37	121.01	0.3307	0.0296	CAGNYGKNAAA
PF0161	---	8	0.1044	319.02	120.46	0.3349	0.0173	TTANWNANTGGM
PF0162	---	5	0.0963	331.12	122.70	0.2004	-0.0250	TAANNYSGCG
PF0163	---	5	0.0996	342.91	127.00	0.2541	-0.0324	GGARNTKYCCA
PF0164	---	5	0.0959	324.74	125.40	0.2472	-0.0494	GCGSCMNTTT
PF0165	---	7	0.1054	345.47	115.90	0.2894	0.0251	CCAWNWWNNNGGC
PF0166	---	7	0.1059	348.81	116.56	0.2814	-0.0204	YNTTTNNNANGCARM
PF0167	---	8	0.1072	308.37	131.36	0.3671	-0.0106	CCTNTMAGA
PF0168	---	5	0.0923	339.83	131.67	0.2627	-0.0776	YTAAYNGCT
PF0169	---	8	0.1042	321.74	119.28	0.3364	0.0159	TTTNNANAGCYR
PF0170	---	8	0.1061	313.48	135.65	0.3910	-0.0153	YNGTTNNNATT
PF0171	---	8	0.1029	311.06	127.85	0.3276	-0.0263	CTCNANGTGNY
PF0172	---	5	0.0956	316.44	128.05	0.2969	-0.0452	TTGCWCAAY
PF0173	---	5	0.0987	353.01	123.97	0.2356	-0.0484	YWATTWNNRGCT
PF0174	---	6	0.0971	285.06	146.17	0.4672	0.1707	WTGAAAT

Table S3. Thresholds of JASPAR TFBS matrices at various cutoffs.

PWM	Cutoff (%)												
	0.01	0.02	0.03	0.04	0.05	0.06	0.07	0.08	0.09	0.1	1	5	10
MA0001	885	860	847	836	828	821	816	811	807	803	708	624	580
MA0002	897	874	860	850	843	837	831	826	821	817	711	614	563
MA0003	968	955	946	938	932	927	922	917	913	909	793	674	610
MA0004	999	940	894	860	853	842	842	842	842	835	685	569	515
MA0005	892	869	856	846	839	833	828	823	819	815	715	622	573
MA0006	947	939	906	888	879	862	844	844	844	842	717	601	530
MA0007	777	761	751	743	738	733	729	725	722	719	650	587	554
MA0008	873	846	831	821	812	804	797	791	786	782	665	563	510
MA0009	784	761	748	737	729	722	717	712	708	704	607	522	478
MA0010	816	798	787	779	772	767	762	758	755	751	669	595	554
MA0011	900	877	864	851	843	835	830	825	821	816	708	612	560
MA0012	860	839	827	817	809	803	797	792	788	784	687	600	554
MA0013	843	822	811	801	794	789	784	779	776	772	682	599	554
MA0014	824	808	799	792	786	782	777	774	771	768	697	632	597
MA0015	851	832	820	811	803	797	792	787	783	780	691	613	572
MA0016	843	820	805	794	786	780	774	768	763	758	653	557	506
MA0017	831	811	799	790	784	778	773	769	765	762	681	609	571
MA0018	877	847	830	818	808	801	794	789	784	780	688	609	568
MA0019	830	810	799	791	785	780	775	771	767	764	681	605	564
MA0020	984	972	962	932	923	909	898	893	888	879	739	606	529
MA0021	979	968	959	946	942	929	923	918	911	908	778	657	599
MA0022	838	817	805	796	788	782	776	772	768	765	679	605	565
MA0023	861	835	821	810	801	794	788	783	778	774	672	583	537
MA0024	863	831	817	807	796	792	785	781	778	774	668	573	523
MA0025	828	803	790	780	772	766	760	755	751	747	646	560	517
MA0026	982	941	923	905	891	872	867	861	852	848	711	598	538
MA0027	889	872	862	854	848	843	839	835	831	828	746	670	628
MA0028	943	903	882	869	858	850	843	837	831	826	719	625	574
MA0029	783	762	750	741	734	728	723	718	714	711	623	543	501
MA0030	816	793	779	769	761	754	748	743	739	736	642	561	518
MA0031	873	851	834	818	807	796	789	783	778	773	657	556	502
MA0032	941	924	912	902	893	886	880	874	868	864	743	649	581
MA0033	926	906	896	888	880	874	868	863	858	854	745	649	596
MA0034	874	853	840	830	823	817	812	807	803	799	712	631	588
MA0035	978	966	956	945	932	920	913	909	902	898	764	646	571
MA0036	991	989	983	969	961	953	950	944	944	943	785	671	599
MA0037	950	950	933	923	910	905	895	894	891	885	765	657	596
MA0038	919	894	876	862	851	842	834	828	822	817	705	607	556
MA0039	946	932	922	915	909	904	901	897	894	891	809	724	676
MA0040	848	824	810	800	792	785	779	774	770	765	664	575	530
MA0041	860	839	827	819	812	806	801	797	793	789	701	621	579
MA0042	865	842	827	816	808	800	794	789	784	780	677	586	540
MA0043	835	812	798	788	780	773	768	763	759	755	671	599	561
MA0044	899	884	873	867	860	856	852	848	844	841	763	688	646
MA0045	844	828	818	812	807	802	799	795	792	790	721	656	621
MA0046	783	759	744	734	727	720	714	710	706	702	615	538	498
MA0047	873	853	841	832	825	819	814	809	805	801	712	633	591
MA0048	862	842	828	819	810	804	798	793	789	785	683	593	546
MA0049	875	859	848	841	834	829	824	820	816	813	723	635	586
MA0050	825	804	791	782	774	768	763	758	754	750	659	578	536

MA0051	770	751	739	730	724	719	715	711	707	703	623	554	518
MA0052	835	805	788	776	766	758	752	746	741	737	634	545	498
MA0053	999	999	968	940	940	937	922	909	906	906	764	629	554
MA0054	867	848	835	826	819	813	808	803	799	796	706	624	580
MA0055	884	861	847	838	830	823	817	812	808	804	705	617	570
MA0056	997	988	983	955	951	937	931	922	911	911	787	664	596
MA0057	910	890	878	868	861	855	849	844	840	836	738	648	598
MA0058	910	866	842	827	817	808	800	793	787	781	669	578	529
MA0059	846	819	803	790	781	774	767	762	757	752	652	566	522
MA0060	925	902	882	860	841	823	808	796	788	781	675	600	560
MA0061	891	867	851	839	830	823	816	811	806	802	694	601	551
MA0062	903	869	849	835	823	814	806	801	795	790	683	591	542
MA0063	943	912	898	891	881	874	869	862	857	853	745	645	590
MA0064	999	999	977	957	938	938	935	935	929	920	756	621	547
MA0065	749	727	715	707	700	694	690	686	683	680	603	535	500
MA0066	738	721	711	703	697	692	688	684	681	678	608	547	515
MA0067	948	919	905	894	885	879	874	869	864	859	756	663	615
MA0068	744	730	722	716	711	707	704	701	698	696	637	585	558
MA0069	781	764	753	745	739	733	729	725	721	719	641	571	534
MA0070	800	776	762	752	744	738	732	727	722	717	618	534	491
MA0071	864	837	820	809	800	792	785	780	775	771	660	564	514
MA0072	814	790	776	766	758	751	745	740	736	732	639	557	514
MA0073	794	778	768	761	755	750	745	742	738	735	659	589	553
MA0074	765	746	735	727	720	715	711	707	703	700	620	549	511
MA0075	999	999	935	930	896	896	883	871	870	867	721	594	517
MA0076	914	867	836	819	806	797	788	779	772	767	653	559	509
MA0077	872	849	834	822	815	806	800	794	789	784	681	595	549
MA0078	904	880	863	851	840	832	824	820	814	809	692	593	541
MA0079	912	886	874	862	853	847	840	836	832	827	722	629	579
MA0080	999	994	994	972	962	961	961	949	938	929	784	657	592
MA0081	968	957	942	925	913	905	896	888	881	875	749	633	571
MA0082	842	822	811	802	795	789	785	781	777	773	691	616	577
MA0083	772	747	731	720	713	707	701	697	693	689	599	522	482
MA0084	901	880	866	854	846	838	832	826	821	817	707	606	553
MA0085	805	784	772	764	757	751	746	742	738	734	648	572	531
MA0086	999	950	907	886	872	869	869	858	854	853	713	594	536
MA0087	904	881	861	854	848	842	836	834	829	823	690	572	516
MA0088	845	812	794	784	776	770	765	761	758	754	683	620	586
MA0089	964	939	919	907	904	895	892	889	879	875	736	626	566
MA0090	823	801	788	779	772	766	761	756	752	749	659	576	532
MA0091	847	825	811	801	792	785	780	775	770	766	671	589	547
MA0092	881	861	849	840	833	828	822	818	814	810	710	614	563
MA0093	966	912	868	855	851	837	831	822	816	808	676	568	514
MA0094	999	999	999	999	999	999	950	947	944	940	774	636	569
MA0095	966	941	923	915	905	887	879	871	862	854	729	600	537
MA0096	932	873	855	845	832	821	817	808	803	792	668	563	506
MA0097	788	766	752	741	733	726	720	714	710	705	608	523	480
MA0098	999	992	979	972	972	959	952	952	945	935	790	668	596
MA0099	908	876	857	844	834	825	818	813	807	802	694	600	551
MA0100	894	873	861	850	841	834	827	821	817	812	705	608	556
MA0101	877	851	836	824	815	808	802	796	791	787	681	590	541
MA0102	858	837	826	818	811	805	800	796	792	789	703	624	582
MA0103	999	975	960	932	916	898	894	890	888	887	753	638	576
MA0104	999	941	901	877	874	870	857	852	839	839	698	583	527
MA0105	855	831	818	808	800	794	788	783	779	775	680	594	548

MA0106	714	696	686	678	672	668	663	660	657	654	583	521	487
MA0107	876	847	832	821	812	805	798	793	788	784	678	586	538
MA0108	872	848	836	826	819	813	808	804	800	796	708	632	591
MA0109	904	885	875	867	860	855	851	846	842	838	748	661	613
MA0110	830	807	794	786	777	770	764	757	752	748	638	544	495
MA0111	846	829	818	810	804	799	795	791	788	785	704	629	588
MA0112	782	765	755	747	741	736	732	728	725	722	648	581	545
MA0113	800	784	774	767	762	757	754	750	747	744	676	615	582
MA0114	849	827	814	805	798	792	787	783	779	775	692	617	576
MA0115	715	693	679	670	663	658	652	648	644	641	560	490	453
MA0116	835	818	807	799	793	788	784	780	776	773	694	622	583
MA0117	916	892	884	875	866	862	858	851	846	843	733	631	575
MA0118	930	916	907	899	893	888	885	881	877	873	772	661	599
MA0119	785	761	745	735	726	719	713	708	703	699	604	520	476
MA0120	894	879	870	864	858	854	850	846	843	841	770	702	664
MA0121	896	874	860	850	844	838	832	828	823	819	719	625	574
MA0122	930	910	897	886	878	871	864	859	853	848	741	640	587
MA0123	924	906	894	885	878	873	868	864	859	856	759	668	617
MF0001	950	928	907	896	884	875	867	857	851	847	720	617	561
MF0002	978	920	881	861	847	836	835	830	823	822	680	570	515
MF0003	890	868	854	843	836	829	823	818	813	810	711	625	579
MF0004	993	958	942	936	922	914	909	905	899	894	785	684	627
MF0005	924	898	883	870	862	854	847	841	836	832	722	625	574
MF0006	893	871	860	852	845	838	833	828	824	820	728	646	602
MF0007	948	935	920	909	899	891	883	878	872	867	754	660	611
MF0008	884	859	845	834	826	819	813	808	804	800	703	617	570
MF0009	917	900	890	881	874	869	864	859	855	852	759	666	615
MF0010	921	905	884	874	866	859	855	850	844	839	728	627	576
MF0011	962	951	930	923	915	911	902	897	890	888	786	687	631
PF0001	972	898	884	857	826	807	791	785	780	778	644	542	489
PF0002	999	942	843	843	836	836	836	836	834	830	667	518	464
PF0003	984	906	873	868	862	853	833	827	822	816	675	577	507
PF0004	896	780	755	739	728	720	713	708	703	699	599	513	469
PF0005	986	905	864	858	852	844	833	815	809	801	657	542	480
PF0006	999	991	952	951	906	903	888	862	860	859	717	578	526
PF0007	974	884	845	842	838	835	828	821	819	814	663	524	471
PF0008	801	767	750	738	730	721	714	708	704	699	601	515	467
PF0009	959	879	855	836	816	800	787	777	770	763	638	533	486
PF0010	867	805	775	766	760	756	752	746	741	730	608	507	445
PF0011	917	876	868	858	831	823	799	792	787	782	643	538	480
PF0012	999	944	890	886	842	842	838	836	836	836	675	557	503
PF0013	1000	893	885	840	840	840	838	834	834	834	674	522	467
PF0014	883	870	801	785	761	757	755	753	748	742	596	501	434
PF0015	999	947	942	890	886	843	843	843	838	836	680	561	505
PF0016	948	882	878	874	871	867	861	840	836	832	692	578	508
PF0017	945	892	839	839	839	839	839	839	835	833	674	519	462
PF0018	886	858	842	828	816	805	795	786	778	771	648	545	485
PF0019	799	773	757	747	738	732	726	721	717	713	621	540	498
PF0020	949	864	858	857	852	851	815	812	809	805	667	558	484
PF0021	829	804	787	773	762	753	748	744	740	735	630	540	491
PF0022	940	879	861	854	847	836	823	815	808	801	666	554	492
PF0023	945	839	839	839	839	837	834	832	832	832	670	514	461
PF0024	985	956	919	904	882	881	876	875	872	872	731	607	534
PF0025	908	863	863	859	857	857	851	851	818	816	676	570	489
PF0026	877	871	837	831	799	796	793	788	766	761	644	549	502

PF0027	877	857	845	834	823	814	805	797	790	784	670	570	515	
PF0028	875	843	815	800	786	777	773	769	766	763	647	543	488	
PF0029	946	870	862	859	857	855	853	847	817	815	676	567	486	
PF0030	921	889	877	872	860	853	841	833	820	813	671	563	515	
PF0031	916	882	871	858	848	842	833	823	813	805	674	568	507	
PF0032	850	813	789	783	778	773	766	755	750	746	634	533	481	
PF0033	889	874	868	857	836	830	824	803	797	793	671	558	508	
PF0034	829	793	785	777	769	757	750	746	741	736	626	529	473	
PF0035	918	873	864	858	854	849	843	835	829	823	692	575	510	
PF0036	898	862	856	853	847	821	814	810	807	803	667	542	482	
PF0037	844	806	788	777	769	760	753	747	743	738	634	545	497	
PF0038	870	806	796	768	761	761	757	755	755	751	627	511	443	
PF0039	872	832	808	792	783	776	770	764	759	755	644	548	495	
PF0040	911	879	870	864	857	843	834	829	824	819	685	573	509	
PF0041	903	865	859	853	844	835	823	816	811	806	673	559	492	
PF0042	897	863	859	854	851	846	818	814	809	805	666	546	482	
PF0043	826	786	764	748	738	730	723	718	713	708	608	522	477	
PF0044	866	837	820	804	791	779	771	766	762	757	641	538	488	
PF0045	841	808	792	782	770	761	754	748	742	738	632	539	491	
PF0046	912	874	857	839	831	821	809	798	793	787	654	548	492	
PF0047	905	864	860	857	851	851	844	819	815	813	678	569	490	
PF0048	843	802	785	774	765	757	752	747	742	736	622	526	474	
PF0049	879	873	867	837	831	825	800	794	791	788	668	561	508	
PF0050	901	889	881	868	856	848	839	828	820	815	689	581	529	
PF0051	945	892	839	839	839	839	837	834	832	832	672	517	459	
PF0052	862	826	806	798	792	786	780	774	770	766	659	563	509	
PF0053	824	793	777	766	758	751	744	738	733	729	628	540	494	
PF0054	844	807	785	777	771	763	752	747	742	739	621	518	460	
PF0055	946	941	893	889	841	841	841	841	841	841	678	549	492	
PF0056	956	914	882	880	877	874	870	862	858	856	713	593	523	
PF0057	841	798	769	762	762	758	755	753	749	742	610	510	443	
PF0058	864	859	856	854	849	817	813	810	806	802	667	540	481	
PF0059	832	802	792	784	771	765	760	755	750	743	635	541	491	
PF0060	999	893	890	839	839	839	839	839	839	839	835	674	521	464
PF0061	876	840	833	799	794	789	762	760	760	758	635	517	472	
PF0062	876	866	852	833	825	814	796	793	789	785	665	553	504	
PF0063	827	798	783	770	761	754	748	741	736	732	627	535	488	
PF0064	893	841	839	839	838	838	834	832	830	824	669	516	462	
PF0065	817	787	779	772	754	748	743	738	727	718	610	519	463	
PF0066	827	792	773	758	748	740	733	727	721	716	607	514	466	
PF0067	865	846	829	816	803	793	784	778	772	767	657	558	506	
PF0068	903	864	858	854	850	846	840	822	814	810	677	568	493	
PF0069	874	845	820	807	793	787	782	780	776	774	664	564	519	
PF0070	897	859	855	852	820	812	806	779	770	766	655	548	487	
PF0071	872	849	829	810	794	788	779	766	761	757	643	548	501	
PF0072	917	880	875	872	865	839	836	833	829	822	678	570	509	
PF0073	946	893	884	841	841	841	841	836	834	834	674	522	469	
PF0074	841	800	782	767	757	749	742	736	730	726	621	531	484	
PF0075	863	827	804	789	781	774	767	761	755	751	638	539	486	
PF0076	895	843	843	843	843	840	836	836	836	833	673	524	470	
PF0077	878	864	854	836	825	817	804	794	788	784	662	553	503	
PF0078	880	863	841	829	816	804	795	787	780	774	651	548	496	
PF0079	878	867	842	833	826	806	797	793	789	786	666	557	502	
PF0080	833	784	765	752	742	734	727	722	717	713	616	532	489	
PF0081	839	809	793	782	772	763	756	749	742	736	621	522	471	

PF0082	808	782	767	753	744	736	729	723	718	714	610	519	471
PF0083	904	863	859	856	852	850	846	817	813	811	673	566	487
PF0084	831	803	793	785	776	768	762	755	748	742	635	541	494
PF0085	864	832	814	799	789	785	781	778	774	770	650	546	489
PF0086	868	833	807	793	781	770	765	761	758	756	633	522	464
PF0087	842	809	792	781	772	764	758	753	748	743	640	551	504
PF0088	856	821	802	790	783	777	771	766	761	757	646	551	499
PF0089	835	797	778	765	756	749	742	737	732	728	621	531	482
PF0090	859	829	809	796	786	780	775	771	768	765	657	561	509
PF0091	883	877	860	839	831	813	799	795	790	782	649	545	490
PF0092	895	865	858	851	849	838	820	815	811	807	673	563	488
PF0093	887	842	842	837	834	829	827	790	787	785	663	519	464
PF0094	877	873	866	839	833	826	800	795	792	789	661	548	502
PF0095	839	812	793	780	770	762	755	750	745	741	632	537	489
PF0096	874	856	836	823	806	797	790	784	776	771	661	563	512
PF0097	864	857	850	843	817	813	807	801	776	771	658	543	483
PF0098	852	817	797	786	777	771	764	759	755	751	642	548	498
PF0099	801	780	768	759	749	738	732	728	723	718	612	519	468
PF0100	813	789	775	766	758	751	746	741	736	731	632	544	497
PF0101	950	905	866	865	860	859	859	853	851	843	702	574	500
PF0102	851	831	801	788	770	767	763	761	757	756	634	521	472
PF0103	816	793	777	767	757	750	743	737	732	727	628	543	499
PF0104	836	799	781	769	759	750	742	735	729	724	620	535	492
PF0105	822	788	768	754	745	737	731	725	720	716	614	526	480
PF0106	807	776	759	748	739	731	725	720	715	711	612	527	483
PF0107	866	843	825	810	800	791	785	780	776	772	663	565	516
PF0108	855	823	802	785	775	768	762	756	752	748	636	537	485
PF0109	855	819	802	789	782	778	774	769	766	760	645	544	487
PF0110	845	808	787	775	767	760	753	748	743	738	633	547	501
PF0111	880	873	865	839	833	828	821	800	795	792	671	570	509
PF0112	852	821	808	800	790	782	777	773	769	765	655	560	510
PF0113	835	792	772	758	747	739	732	727	721	717	613	524	477
PF0114	852	819	802	790	781	774	767	761	756	751	644	551	503
PF0115	841	809	796	786	778	772	766	762	757	753	649	558	510
PF0116	842	812	795	785	776	770	764	759	755	751	644	550	500
PF0117	851	824	808	797	789	783	777	773	768	764	666	578	531
PF0118	825	798	783	772	764	757	751	746	741	737	633	543	496
PF0119	820	793	780	769	761	755	750	744	740	735	635	544	497
PF0120	779	758	747	738	730	725	720	715	711	708	619	542	501
PF0121	846	809	789	780	772	764	758	753	749	745	628	526	472
PF0122	825	799	786	777	770	764	759	754	749	745	647	561	516
PF0123	836	812	798	788	781	774	769	764	759	755	659	574	528
PF0124	886	861	839	825	813	803	797	792	788	784	671	574	522
PF0125	877	861	843	833	818	809	803	797	791	786	676	574	526
PF0126	814	786	771	761	753	746	740	735	730	727	632	549	506
PF0127	866	842	822	806	792	783	775	769	763	759	642	538	486
PF0128	845	819	804	795	787	781	776	772	767	764	665	577	530
PF0129	878	868	852	834	824	815	798	792	787	783	665	562	507
PF0130	874	860	849	837	823	814	806	794	786	780	659	550	497
PF0131	864	857	851	842	817	812	809	804	794	774	670	564	488
PF0132	879	863	840	832	813	802	796	791	784	773	654	548	494
PF0133	828	803	791	783	776	769	764	758	753	748	648	562	517
PF0134	874	854	839	829	815	802	795	789	783	777	666	563	507
PF0135	870	842	822	808	797	789	785	780	776	772	659	557	504
PF0136	861	840	821	806	790	781	775	768	762	758	648	548	500

PF0137	846	819	800	788	780	775	770	766	762	758	654	561	514
PF0138	837	810	791	779	769	761	755	750	746	742	639	552	508
PF0139	882	854	838	818	809	799	787	783	779	777	660	553	495
PF0140	938	889	862	860	856	855	852	849	847	842	706	577	517
PF0141	858	832	814	799	789	781	774	769	764	760	647	547	496
PF0142	850	813	793	784	776	770	764	761	756	751	633	531	473
PF0143	793	770	757	746	738	732	726	722	717	713	613	523	476
PF0144	868	847	832	818	804	794	785	778	771	765	648	543	489
PF0145	879	872	859	835	829	815	797	793	790	786	664	552	504
PF0146	839	801	782	768	762	759	753	752	749	745	636	542	497
PF0147	831	802	786	776	768	762	756	750	746	741	634	542	494
PF0148	835	810	795	782	776	771	762	753	748	745	633	536	486
PF0149	843	808	791	779	768	761	755	750	745	740	632	541	493
PF0150	844	812	800	791	783	776	771	765	760	756	648	554	505
PF0151	823	798	785	775	768	762	757	752	748	744	644	557	511
PF0152	869	840	824	811	801	791	782	775	769	764	646	544	490
PF0153	853	821	805	797	790	785	780	776	772	768	664	571	518
PF0154	848	822	806	796	788	782	776	772	767	763	662	574	527
PF0155	891	856	849	844	839	835	828	816	808	804	673	559	488
PF0156	833	808	793	783	774	767	760	755	750	745	646	559	513
PF0157	846	816	798	787	779	773	768	763	758	754	647	553	504
PF0158	833	806	787	774	764	757	751	745	741	737	625	527	478
PF0159	859	823	799	792	786	785	779	768	761	755	642	540	488
PF0160	836	807	792	781	773	767	762	756	751	747	636	539	487
PF0161	824	791	777	768	760	754	749	744	739	735	624	527	475
PF0162	840	804	780	767	758	752	747	743	739	736	627	534	490
PF0163	860	826	811	801	795	790	785	780	774	769	657	559	507
PF0164	835	801	787	776	770	763	759	754	750	747	635	539	485
PF0165	828	801	785	774	766	759	753	748	743	739	634	543	496
PF0166	824	797	785	776	768	763	757	752	747	743	637	547	500
PF0167	861	832	814	799	787	779	771	766	762	758	639	533	482
PF0168	872	847	831	815	801	794	788	779	772	768	658	562	513
PF0169	819	793	777	766	758	751	745	740	736	731	623	528	477
PF0170	866	851	842	834	823	814	806	799	793	786	663	552	488
PF0171	842	812	794	781	774	767	761	755	751	746	631	530	479
PF0172	839	805	788	780	775	772	765	760	753	748	636	538	482
PF0173	853	821	805	797	791	785	780	775	770	766	658	564	513
PF0174	904	861	859	858	854	851	844	817	814	812	672	547	480

Table S4. Custom tracks in the UCSC genome browser.

browser position chr20:55,569,120-55,569,542

#browser hide all

track name="KnownSites" description="Known Sites (Rat to Human)" visibility=2 itemRgb="On"

chr20	55569125	55569161	ERR	1	-	55569125	55569161	0,0,0
chr20	55569124	55569164	HNF4	1	-	55569124	55569164	0,0,0
chr20	55569131	55569143	RXR	1	-	55569131	55569143	0,0,0
chr20	55569167	55569183	C/EBPa,HNF3a&b	1	+	55569167	55569183	0,0,0
chr20	55569173	55569187	FKHR	1	+	55569173	55569187	0,0,0
chr20	55569197	55569227	GRE	1	-	55569197	55569227	0,0,0
chr20	55569245	55569253	ERRa	1	-	55569245	55569253	0,0,0
chr20	55569240	55569255	RARE2	1	-	55569240	55569255	0,0,0
chr20	55569253	55569260	SREBP	1	-	55569253	55569260	0,0,0
chr20	55569286	55569294	C/EBP	1	+	55569286	55569294	0,0,0
chr20	55569314	55569325	Fos/Jun	1	-	55569314	55569325	0,0,0
chr20	55569326	55569344	C/EBP	1	+	55569326	55569344	0,0,0
chr20	55569372	55569388	HNF1	1	-	55569372	55569388	0,0,0
chr20	55569417	55569437	CRE-2	1	-	55569417	55569437	0,0,0
chr20	55569449	55569486	NF1/CTF1	1	+	55569449	55569486	0,0,0
chr20	55569486	55569499	CRE-1	1	+	55569486	55569499	0,0,0

track name="NewSites" description="Newly Predicted" visibility=2 itemRgb="On"

chr20	55569298	55569318	PPAR	2	+	55569298	55569318	0,0,255
chr20	55569302	55569322	HNF4	2	+	55569302	55569322	0,0,255
chr20	55569394	55569410	HNF1	2	-	55569394	55569410	0,0,255
chr20	55569469	55569484	SP1	2	-	55569469	55569484	0,0,255
chr20	55569514	55569528	SP1	2	+	55569514	55569528	0,0,255

track name="JASPAR MA" description="JASPAR MA" visibility=2 itemRgb="On"

chr20	55568550	55568558	MYB.ph3	858	+	55568550	55568558	64,128,64
chr20	55569129	55569145	NR1H2-RXR	801	-	55569129	55569145	64,128,64
chr20	55569131	55569144	NR2F1	909	+	55569131	55569144	64,128,64
chr20	55569131	55569143	HNF4	917	-	55569131	55569143	64,128,64
chr20	55569182	55569195	Broad-complex_1	793	-	55569182	55569195	64,128,64
chr20	55569184	55569195	cEBP	832	+	55569184	55569195	64,128,64
chr20	55569301	55569320	PPARG-RXRA	761	+	55569301	55569320	64,128,64
chr20	55569303	55569319	NR1H2-RXR	739	+	55569303	55569319	64,128,64
chr20	55569304	55569317	NR2F1	869	-	55569304	55569317	64,128,64
chr20	55569305	55569317	HNF4	879	+	55569305	55569317	64,128,64
chr20	55569309	55569319	Foxq1	879	+	55569309	55569319	64,128,64
chr20	55569326	55569337	cEBP	874	-	55569326	55569337	64,128,64

chr20	55569367	55569386	Staf	816	+	55569367	55569386	64,128,64
chr20	55569373	55569384	Pbx	803	+	55569373	55569384	64,128,64
chr20	55569375	55569388	TCF1	770	-	55569375	55569388	64,128,64
chr20	55569377	55569390	FOXF2	782	+	55569377	55569390	64,128,64
chr20	55569377	55569385	ATHB5	796	-	55569377	55569385	64,128,64
chr20	55569381	55569391	Foxq1	823	-	55569381	55569391	64,128,64
chr20	55569382	55569385	Ubx	1000	-	55569382	55569385	64,128,64
chr20	55569397	55569410	TCF1	803	-	55569397	55569410	64,128,64
chr20	55569399	55569406	Athb-1	935	+	55569399	55569406	64,128,64
chr20	55569399	55569407	ATHB5	883	-	55569399	55569407	64,128,64
chr20	55569404	55569407	Ubx	1000	-	55569404	55569407	64,128,64
chr20	55569404	55569411	RUSH1-alfa	941	+	55569404	55569411	64,128,64
chr20	55569405	55569410	GATA3	934	-	55569405	55569410	64,128,64
chr20	55569484	55569490	bZIP910	1000	-	55569484	55569490	64,128,64
chr20	55569507	55569518	NHLH1	855	-	55569507	55569518	64,128,64
chr20	55569512	55569519	MafB	909	+	55569512	55569519	64,128,64
chr20	55569514	55569523	ZNF42_5-13	890	+	55569514	55569523	64,128,64
chr20	55569517	55569526	SP1	875	+	55569517	55569526	64,128,64
track	name="JASPAR MF" description="JASPAR MF" visibility=2 itemRgb="On"							
chr20	55569329	55569337	bZIP-cEBP-like-subclass	909	+	55569329	55569337	96,96,96
chr20	55569484	55569489	bZIP-CREB-G-box-like-subclass	1000	-	55569484	55569489	96,96,96
track	name="JASPAR PF" description="JASPAR PF" visibility=2 itemRgb="On"							
chr20	55568549	55568564	RYAAAKNNNNNNNTTGW	857	+	55568549	55568564	255,0,0
chr20	55568550	55568557	RRCCGTTA	853	-	55568550	55568557	255,0,0
chr20	55568551	55568556	AACTTT	840	-	55568551	55568556	255,0,0
chr20	55568588	55568594	TGCCAAR	955	+	55568588	55568594	255,0,0
chr20	55568589	55568595	GATTGGY	865	-	55568589	55568595	255,0,0
chr20	55568589	55568597	GGYGTTGNY	876	-	55568589	55568597	255,0,0
chr20	55569133	55569138	AACTTT	893	+	55569133	55569138	255,0,0
chr20	55569136	55569143	WTTGKCTG	861	+	55569136	55569143	255,0,0
chr20	55569162	55569168	TGACATY	909	+	55569162	55569168	255,0,0
chr20	55569168	55569176	YTAAYNGCT	875	+	55569168	55569176	255,0,0
chr20	55569175	55569182	RACCACAR	891	-	55569175	55569182	255,0,0
chr20	55569175	55569183	ACAWYAAAG	799	-	55569175	55569183	255,0,0
chr20	55569188	55569196	GCTNWTGK	884	-	55569188	55569196	255,0,0
chr20	55569209	55569216	SMTTTTGT	985	-	55569209	55569216	255,0,0
chr20	55569211	55569219	AAANWWTGC	865	+	55569211	55569219	255,0,0
chr20	55569245	55569252	TGACCTTG	880	+	55569245	55569252	255,0,0
chr20	55569245	55569253	YGTCTTGR	952	+	55569245	55569253	255,0,0
chr20	55569286	55569297	WGTTNNNNNAAA	854	-	55569286	55569297	255,0,0

chr20	55569288	55569297	TGANNYRGCA	854	+	55569288	55569297	255,0,0
chr20	55569307	55569319	RYTAAWNNNTGAY	955	-	55569307	55569319	255,0,0
chr20	55569310	55569315	AACTTT	947	-	55569310	55569315	255,0,0
chr20	55569313	55569321	TGASTMAGC	844	-	55569313	55569321	255,0,0
chr20	55569315	55569321	TTANTCA	1000	+	55569315	55569321	255,0,0
chr20	55569326	55569333	RRAGTTGT	902	+	55569326	55569333	255,0,0
chr20	55569371	55569381	TCCCRNNRTGC	874	+	55569371	55569381	255,0,0
chr20	55569375	55569384	YYCATTCAWW	809	+	55569375	55569384	255,0,0
chr20	55569375	55569387	RYTAAWNNNTGAY	841	-	55569375	55569387	255,0,0
chr20	55569376	55569383	WGAATGY	867	-	55569376	55569383	255,0,0
chr20	55569377	55569384	YATTNATC	851	+	55569377	55569384	255,0,0
chr20	55569378	55569388	RGTTAMWNATT	804	-	55569378	55569388	255,0,0
chr20	55569379	55569386	YTAATTAA	880	+	55569379	55569386	255,0,0
chr20	55569380	55569385	TAATTA	840	+	55569380	55569385	255,0,0
chr20	55569380	55569386	YCATTAA	996	+	55569380	55569386	255,0,0
chr20	55569396	55569406	RGTTAMWNATT	795	+	55569396	55569406	255,0,0
chr20	55569397	55569409	RYTAAWNNNTGAY	807	-	55569397	55569409	255,0,0
chr20	55569400	55569410	RGTTAMWNATT	894	-	55569400	55569410	255,0,0
chr20	55569402	55569407	TAATTA	840	+	55569402	55569407	255,0,0
chr20	55569402	55569412	TAAYNRNNTCC	868	+	55569402	55569412	255,0,0
chr20	55569450	55569457	TGACCTTG	880	+	55569450	55569457	255,0,0
chr20	55569456	55569469	TGGNNNNNNKCCAR	943	+	55569456	55569469	255,0,0
chr20	55569462	55569467	GGATTA	843	-	55569462	55569467	255,0,0
chr20	55569482	55569489	TGAYRTCA	914	+	55569482	55569489	255,0,0
chr20	55569482	55569489	TGACGTCA	914	+	55569482	55569489	255,0,0
chr20	55569484	55569490	GTGACGY	858	-	55569484	55569490	255,0,0
chr20	55569485	55569496	CCGNMNTNACG	796	-	55569485	55569496	255,0,0
chr20	55569510	55569515	CAGCTG	1000	+	55569510	55569515	255,0,0

Table S5. Overlap relations between known and predicted sites.

A. Mutual overlaps with coverage greater than 50%

RefGene	Rat Begin	Rat End	Rat Begin in 1kb promoter	Rat End in 1kb promoter	TF	strand	TFLOC Begin	TFLOC End	TFLOC TF or Motif	strand	TFLOC score	JASPAR ID	Known%	Predicted%
NM_002591	-456	-428	519	547	HNF4	-	524	540	NR1H2-RXR	-	802	MA0115	59	100
NM_002591	-455	-431	520	544	ERR	-	526	539	NR2F1	+	910	MA0017	56	100
NM_002591	-455	-431	520	544	ERR	-	524	540	NR1H2-RXR	-	802	MA0115	68	100
NM_002591	-455	-431	520	544	ERR	-	526	538	HNF4	-	917	MA0114	52	100
NM_002591	-449	-437	526	538	RXR	-	526	539	NR2F1	+	910	MA0017	100	93
NM_002591	-449	-437	526	538	RXR	-	524	540	NR1H2-RXR	-	802	MA0115	100	76
NM_002591	-449	-437	526	538	RXR	-	526	538	HNF4	-	917	MA0114	100	100
NM_002591	-449	-437	526	538	RXR	-	531	538	WTTGKCTG	+	861	PF0046	62	100
NM_002591	-425	-409	550	566	C/EBPa,HNF3a&b	+	551	559	YTAAYNGCT	+	876	PF0168	53	100
NM_002591	-425	-409	550	566	C/EBPa,HNF3a&b	+	558	566	ACAWYAAAG	-	799	PF0142	53	100
NM_002591	-419	-405	556	570	FKHR	+	558	565	RACCACAR	-	891	PF0111	53	100
NM_002591	-419	-405	556	570	FKHR	+	558	566	ACAWYAAAG	-	799	PF0142	60	100
NM_002591	-335	-319	640	656	RARE2	-	645	653	YGTCCTTGR	+	952	PF0109	53	100
NM_002591	-330	-322	645	653	ERRa	-	645	652	TGACCTTG	+	880	PF0038	89	100
NM_002591	-330	-322	645	653	ERRa	-	645	653	YGTCCTTGR	+	952	PF0109	100	100
NM_002591	-288	-280	687	695	C/EBP	+	689	698	TGANNYRGCA	+	854	PF0067	78	70
NM_002591	-288	-280	687	695	C/EBP	+	687	698	WGTTNNNNNAAA	-	854	PF0155	100	75
NM_002591	-260	-249	715	726	Fos/Jun	-	710	720	Foxq1	+	878	MA0040	50	55
NM_002591	-260	-249	715	726	Fos/Jun	-	716	722	TTANTCA	+	1000	PF0064	58	100
NM_002591	-260	-249	715	726	Fos/Jun	-	714	722	TGASTMAGC	-	844	PF0032	67	89
NM_002591	-248	-230	727	745	C/EBP	+	727	738	cEBP	-	874	MA0102	63	100
NM_002591	-200	-184	775	791	HNF1	-	780	793	FOXF2	+	782	MA0030	71	86
NM_002591	-200	-184	775	791	HNF1	-	778	791	TCF1	-	770	MA0046	82	100
NM_002591	-200	-184	775	791	HNF1	-	776	787	Pbx	+	910	MA0070	71	100
NM_002591	-200	-184	775	791	HNF1	-	770	789	Staf	+	816	MA0088	88	75
NM_002591	-200	-184	775	791	HNF1	-	780	788	ATHB5	-	796	MA0110	53	100

NM_002591	-200	-184	775	791	HNF1	-	774	784	TCCCRNNRTGC	+	874	PF0039	59	91
NM_002591	-200	-184	775	791	HNF1	-	778	787	YYCATTCAWW	+	809	PF0052	59	100
NM_002591	-200	-184	775	791	HNF1	-	781	791	RGTTAMWNATT	-	804	PF0084	65	100
NM_002591	-200	-184	775	791	HNF1	-	778	790	RYTAAWNNNTGAY	-	841	PF0133	76	100
NM_002591	-87	-74	888	901	CRE-1	+	887	898	CCGNMNNTNACG	-	796	PF0106	79	92

B. All overlaps

RefGene	Rat Begin	Rat End	Rat Begin in 1kb promoter	Rat End in 1kb promoter	TF	strand	TFLOC Begin	TFLOC End	TFLOC TF or Motif	strand	TFLOC score	JASPAR ID	Known%	Predicted%
NM_002591	-276	-256	699	719	PPAR	+	705	718	NR2F1	-	869	MA0017	67	100
NM_002591	-276	-256	699	719	PPAR	+	710	720	Foxq1	+	878	MA0040	48	91
NM_002591	-276	-256	699	719	PPAR	+	702	721	PPARG-RXRA	+	761	MA0065	86	90
NM_002591	-276	-256	699	719	PPAR	+	706	718	HNF4	+	879	MA0114	62	100
NM_002591	-276	-256	699	719	PPAR	+	704	720	NR1H2-RXR	+	739	MA0115	76	94
NM_002591	-276	-256	699	719	PPAR	+	711	716	AACTTT	-	910	PF0017	29	100
NM_002591	-276	-256	699	719	PPAR	+	716	722	TTANTCA	+	1000	PF0064	19	57
NM_002591	-276	-256	699	719	PPAR	+	714	722	TGASTMAGC	-	844	PF0032	29	67
NM_002591	-276	-256	699	719	PPAR	+	708	720	RYTAAWNNNTGAY	-	955	PF0133	57	92
NM_002591	-272	-252	703	723	HNF4	+	705	718	NR2F1	-	869	MA0017	67	100
NM_002591	-272	-252	703	723	HNF4	+	710	720	Foxq1	+	878	MA0040	52	100
NM_002591	-272	-252	703	723	HNF4	+	702	721	PPARG-RXRA	+	761	MA0065	90	95
NM_002591	-272	-252	703	723	HNF4	+	706	718	HNF4	+	879	MA0114	62	100
NM_002591	-272	-252	703	723	HNF4	+	704	720	NR1H2-RXR	+	739	MA0115	81	100
NM_002591	-272	-252	703	723	HNF4	+	711	716	AACTTT	-	946	PF0017	29	100
NM_002591	-272	-252	703	723	HNF4	+	716	722	TTANTCA	+	1000	PF0064	33	100
NM_002591	-272	-252	703	723	HNF4	+	714	722	TGASTMAGC	-	844	PF0032	43	100
NM_002591	-272	-252	703	723	HNF4	+	708	720	RYTAAWNNNTGAY	-	955	PF0133	62	100
NM_002591	-178	-162	797	813	HNF1	-	802	809	Athb-1	+	935	MA0008	47	100
NM_002591	-178	-162	797	813	HNF1	-	800	813	TCF1	-	803	MA0046	82	100
NM_002591	-178	-162	797	813	HNF1	-	808	813	GATA3	-	934	MA0037	35	100
NM_002591	-178	-162	797	813	HNF1	-	807	810	Ubx	-	1000	MA0094	24	100
NM_002591	-178	-162	797	813	HNF1	-	807	814	RUSH1-alfa	+	941	MA0109	41	88
NM_002591	-178	-162	797	813	HNF1	-	802	810	ATHB5	-	883	MA0110	53	100
NM_002591	-178	-162	797	813	HNF1	-	805	810	TAATTA	+	840	PF0023	35	100
NM_002591	-178	-162	797	813	HNF1	-	803	813	RGTTAMWNATT	-	894	PF0084	65	100
NM_002591	-178	-162	797	813	HNF1	-	799	809	RGTTAMWNATT	+	795	PF0084	65	100
NM_002591	-178	-162	797	813	HNF1	-	805	815	TAAYNRNNTCC	+	868	PF0136	53	82
NM_002591	-178	-162	797	813	HNF1	-	800	812	RYTAAWNNNTGAY	-	807	PF0133	76	100

NM_002591	-103	-89	872	886	SP1	-	886	892	bZIP910	-	1000	MA0096	7	14
NM_002591	-103	-89	872	886	SP1	-	886	891	bZIP-CREB-G-box-like-subclass	-	1000	MF0002	7	17
NM_002591	-103	-89	872	886	SP1	-	884	891	TGACGTCA	+	914	PF0014	20	38
NM_002591	-103	-89	872	886	SP1	-	884	891	TGAYRTCA	+	914	PF0009	20	38
NM_002591	-103	-89	872	886	SP1	-	886	892	GTGACGY	-	858	PF0020	7	14
NM_002591	-103	-89	872	886	SP1	-	859	872	TGGNNNNNNKCCAR	+	943	PF0027	7	7
NM_002591	-61	-47	914	928	SP1	+	907	918	NHLH1	-	855	MA0048	33	42
NM_002591	-61	-47	914	928	SP1	+	914	923	ZNF42_5-13	+	890	MA0057	67	100
NM_002591	-61	-47	914	928	SP1	+	917	926	SP1	+	875	MA0079	67	100
NM_002591	-61	-47	914	928	SP1	+	910	915	CAGCTG	+	1000	PF0015	13	33
NM_002591	-61	-47	914	928	SP1	+	912	919	MafB	+	909	MA0117	40	75

Table S6. Overlap relations between newly discovered and predicted sites.

A. Mutual overlaps with coverage greater than 50%.

RefGene	Rat Begin	Rat End	Rat Begin in 1kb promoter	Rat End in 1kb promoter	TF	strand	TFLOC Begin	TFLOC End	TFLOC TF or Motif	strand	TFLOC score	JASPAR ID	Known%	Predicted%
NM_002591	-276	-256	699	719	PPAR	+	705	718	NR2F1	-	869	MA0017	67	100
NM_002591	-276	-256	699	719	PPAR	+	702	721	PPARG-RXRA	+	761	MA0065	86	90
NM_002591	-276	-256	699	719	PPAR	+	706	718	HNF4	+	879	MA0114	62	100
NM_002591	-276	-256	699	719	PPAR	+	704	720	NR1H2-RXR	+	739	MA0115	76	94
NM_002591	-276	-256	699	719	PPAR	+	708	720	RYTAAWNNNTGAY	-	955	PF0133	57	92
NM_002591	-272	-252	703	723	HNF4	+	705	718	NR2F1	-	869	MA0017	67	100
NM_002591	-272	-252	703	723	HNF4	+	710	720	Foxq1	+	878	MA0040	52	100
NM_002591	-272	-252	703	723	HNF4	+	702	721	PPARG-RXRA	+	910	MA0065	90	95
NM_002591	-272	-252	703	723	HNF4	+	706	718	HNF4	+	879	MA0114	62	100
NM_002591	-272	-252	703	723	HNF4	+	704	720	NR1H2-RXR	+	739	MA0115	81	100
NM_002591	-272	-252	703	723	HNF4	+	708	720	RYTAAWNNNTGAY	-	955	PF0133	62	100
NM_002591	-178	-162	797	813	HNF1	-	800	813	TCF1	-	803	MA0046	82	100
NM_002591	-178	-162	797	813	HNF1	-	802	810	ATHB5	-	883	MA0110	53	100
NM_002591	-178	-162	797	813	HNF1	-	803	813	RGTTAMWNATT	-	894	PF0084	65	100
NM_002591	-178	-162	797	813	HNF1	-	799	809	RGTTAMWNATT	+	795	PF0084	65	100
NM_002591	-178	-162	797	813	HNF1	-	805	815	TAAYNRNNTCC	+	868	PF0136	53	82
NM_002591	-178	-162	797	813	HNF1	-	800	812	RYTAAWNNNTGAY	-	807	PF0133	76	100
NM_002591	-61	-47	914	928	SP1	+	914	923	ZNF42_5-13	+	890	MA0057	67	100
NM_002591	-61	-47	914	928	SP1	+	917	926	SP1	+	875	MA0079	67	100

B. All overlaps

RefGene	Rat Begin	Rat End	Rat Begin in 1kb promoter	Rat End in 1kb promoter	TF	strand	TFLOC Begin	TFLOC End	TFLOC TF or Motif	strand	TFLOC score	JASPAR ID	Known%	Predicted%
NM_002591	-276	-256	699	719	PPAR	+	705	718	NR2F1	-	869	MA0017	67	100
NM_002591	-276	-256	699	719	PPAR	+	710	720	Foxq1	+	878	MA0040	48	91
NM_002591	-276	-256	699	719	PPAR	+	702	721	PPARG-RXRA	+	761	MA0065	86	90
NM_002591	-276	-256	699	719	PPAR	+	706	718	HNF4	+	879	MA0114	62	100
NM_002591	-276	-256	699	719	PPAR	+	704	720	NR1H2-RXR	+	739	MA0115	76	94
NM_002591	-276	-256	699	719	PPAR	+	711	716	AACTTT	-	910	PF0017	29	100
NM_002591	-276	-256	699	719	PPAR	+	716	722	TTANTCA	+	1000	PF0064	19	57
NM_002591	-276	-256	699	719	PPAR	+	714	722	TGASTMAGC	-	844	PF0032	29	67
NM_002591	-276	-256	699	719	PPAR	+	708	720	RYTAAWNNNTGAY	-	955	PF0133	57	92
NM_002591	-272	-252	703	723	HNF4	+	705	718	NR2F1	-	869	MA0017	67	100
NM_002591	-272	-252	703	723	HNF4	+	710	720	Foxq1	+	878	MA0040	52	100
NM_002591	-272	-252	703	723	HNF4	+	702	721	PPARG-RXRA	+	761	MA0065	90	95
NM_002591	-272	-252	703	723	HNF4	+	706	718	HNF4	+	879	MA0114	62	100
NM_002591	-272	-252	703	723	HNF4	+	704	720	NR1H2-RXR	+	739	MA0115	81	100
NM_002591	-272	-252	703	723	HNF4	+	711	716	AACTTT	-	946	PF0017	29	100
NM_002591	-272	-252	703	723	HNF4	+	716	722	TTANTCA	+	1000	PF0064	33	100
NM_002591	-272	-252	703	723	HNF4	+	714	722	TGASTMAGC	-	844	PF0032	43	100
NM_002591	-272	-252	703	723	HNF4	+	708	720	RYTAAWNNNTGAY	-	955	PF0133	62	100
NM_002591	-178	-162	797	813	HNF1	-	802	809	Athb-1	+	935	MA0008	47	100
NM_002591	-178	-162	797	813	HNF1	-	800	813	TCF1	-	803	MA0046	82	100
NM_002591	-178	-162	797	813	HNF1	-	808	813	GATA3	-	934	MA0037	35	100
NM_002591	-178	-162	797	813	HNF1	-	807	810	Ubx	-	1000	MA0094	24	100
NM_002591	-178	-162	797	813	HNF1	-	807	814	RUSH1-alfa	+	941	MA0109	41	88
NM_002591	-178	-162	797	813	HNF1	-	802	810	ATHB5	-	883	MA0110	53	100
NM_002591	-178	-162	797	813	HNF1	-	805	810	TAATTA	+	840	PF0023	35	100
NM_002591	-178	-162	797	813	HNF1	-	803	813	RGTTAMWNATT	-	894	PF0084	65	100
NM_002591	-178	-162	797	813	HNF1	-	799	809	RGTTAMWNATT	+	795	PF0084	65	100
NM_002591	-178	-162	797	813	HNF1	-	805	815	TAAYNRNNTCC	+	868	PF0136	53	82
NM_002591	-178	-162	797	813	HNF1	-	800	812	RYTAAWNNNTGAY	-	807	PF0133	76	100

NM_002591	-103	-89	872	886	SP1	-	886	892	bZIP910	-	1000	MA0096	7	14
NM_002591	-103	-89	872	886	SP1	-	886	891	bZIP-CREB-G-box-like-subclass	-	1000	MF0002	7	17
NM_002591	-103	-89	872	886	SP1	-	884	891	TGACGTCA	+	914	PF0014	20	38
NM_002591	-103	-89	872	886	SP1	-	884	891	TGAYRTCA	+	914	PF0009	20	38
NM_002591	-103	-89	872	886	SP1	-	886	892	GTGACGY	-	858	PF0020	7	14
NM_002591	-103	-89	872	886	SP1	-	859	872	TGGNNNNNNKCCAR	+	943	PF0027	7	7
NM_002591	-61	-47	914	928	SP1	+	907	918	NHLH1	-	855	MA0048	33	42
NM_002591	-61	-47	914	928	SP1	+	914	923	ZNF42_5-13	+	890	MA0057	67	100
NM_002591	-61	-47	914	928	SP1	+	917	926	SP1	+	875	MA0079	67	100
NM_002591	-61	-47	914	928	SP1	+	910	915	CAGCTG	+	1000	PF0015	13	33
NM_002591	-61	-47	914	928	SP1	+	912	919	MafB	+	909	MA0117	40	75