

Difference from median of controls																
Well Name	Well #	1st	2nd	3rd	Average	Standard deviation	SSMD	GeneSymbol	GeneId	GeneAccession	GINumber					
E01	49	-1.266	-1.134	-1.060	-1.153	0.104	-6.248	Dynamin-2								
F01	61	-1.246	-1.127	-1.033	-1.135	0.107	-6.012	Dynamin-2								
E12	60	-1.211	-1.111	-1.053	-1.125	0.080	-7.940	Dynamin-2								
F12	72	-1.221	-1.100	-1.040	-1.120	0.092	-6.854	Dynamin-2								
G12	84	-1.024	-0.691	-0.905	-0.873	0.169	-2.914	Clathrin heavy chain								
H12	96	-1.044	-0.586	-0.889	-0.840	0.233	-2.035	Clathrin heavy chain								
G01	73	-0.932	-0.604	-0.887	-0.807	0.178	-2.559	Clathrin heavy chain								
H01	85	-0.952	-0.553	-0.856	-0.787	0.208	-2.133	Clathrin heavy chain								
F09	69	-0.608	-0.474	-0.503	-0.528	0.070	-4.239	PPP2R2A	5520	NM_002717	32307111					
D07	43	-0.382	-0.246	-0.348	-0.325	0.070	-2.606	PTPRH	5794	NM_002842	67190343					
E08	56	-0.297	-0.334	-0.291	-0.307	0.023	-7.494	INPP4A	3631	NM_001566	4504704					
E06	54	-0.356	-0.236	-0.313	-0.302	0.061	-2.793	PR48	28227	NM_199326	41349490					
D09	45	-0.269	-0.269	-0.297	-0.278	0.016	-9.780	FLJ23751	92370	NM_152282	22748648					
H07	91	-0.309	-0.141	-0.258	-0.236	0.087	-1.538	SET	6418	NM_003011	142361523					
F05	65	-0.201	-0.195	-0.229	-0.208	0.018	-6.554	DKFZP566K0524	26095	NM_001042365	109138576					
D05	41	-0.214	-0.158	-0.247	-0.206	0.045	-2.575	PTPN2	5771	NM_002828	18104978					
F10	70	-0.196	-0.144	-0.200	-0.180	0.031	-3.253	PFKB3	5209	NM_004566	42476167					
E04	52	-0.173	-0.154	-0.194	-0.174	0.020	-5.002	EYA2	2139	NM_172110	26667229					
G02	74	-0.166	-0.176	-0.158	-0.167	0.009	-10.001	PTPN11	5781	NM_002834	33356176					
G09	81	-0.220	-0.104	-0.166	-0.163	0.058	-1.581	FLJ22405	64419	NM_022485	117938273					
F07	67	-0.171	-0.158	-0.157	-0.162	0.008	-11.419	G6PC	2538	NM_000151	119393889					
B07	19	-0.143	-0.156	-0.173	-0.157	0.015	-5.907	MTMR4	9110	NM_004687	31377795					
F04	64	-0.167	-0.155	-0.142	-0.155	0.013	-6.943	PPP1CC	5501	NM_002710	4506006					
H08	92	-0.134	-0.128	-0.175	-0.146	0.026	-3.220	NUDT3	11165	NM_006703	37622350					
B04	16	-0.109	-0.158	-0.153	-0.140	0.027	-2.950	PTPN5	84867	NM_001039970	90652860					
E02	50	-0.119	-0.151	-0.111	-0.127	0.021	-3.417	PHPT1	29085	NM_014172	142373598					
C03	27	-0.127	-0.129	-0.120	-0.125	0.005	-14.473	NUDT14	256281	NM_177533	37594466					
C11	35	-0.126	-0.065	-0.163	-0.118	0.049	-1.349	PPP2R4	5524	NM_178003	30065648					
B02	14	-0.126	-0.113	-0.086	-0.108	0.020	-3.030	SGPP1	81537	NM_030791	40254975					
F06	66	-0.108	-0.101	-0.103	-0.104	0.003	-17.617	NT5C3	51251	NM_016489	70608210					
G03	75	-0.084	-0.111	-0.105	-0.100	0.014	-3.961	PPFIA1	8500	NM_003626	29171751					
H04	88	-0.121	-0.076	-0.100	-0.099	0.022	-2.512	DUSP3	1845	NM_004090	37655179					
A08	8	-0.116	-0.106	-0.075	-0.099	0.021	-2.615	CDC25A	993	NM_201567	42490759					
F03	63	-0.097	-0.115	-0.083	-0.098	0.016	-3.451	DUSP21	63904	NM_022076	33942082					
H11	95	-0.128	-0.067	-0.096	-0.097	0.031	-1.794	CLIP	8483	NM_003613	51944961					
D03	39	-0.072	-0.144	-0.067	-0.094	0.043	-1.237	CTDP1	9150	NM_048368	67188549					
C06	30	-0.081	-0.102	-0.091	-0.092	0.010	-4.989	PTPRD	5789	NM_130393	104486447					
C09	33	-0.091	-0.076	-0.092	-0.086	0.009	-5.295	PSPH	5723	NM_004577	46249387					
G08	80	-0.116	-0.085	-0.058	-0.086	0.029	-1.674	FLJ25449	151649	NM_144714	109627669					
E10	58	-0.053	-0.117	-0.081	-0.084	0.032	-1.492	PGAM2	5224	NM_000290	50593009					
H09	93	-0.100	-0.110	-0.041	-0.083	0.037	-1.259	NT5C1A	84618	NM_032526	14210537					
G07	79	-0.092	-0.085	-0.069	-0.082	0.012	-3.804	PPP2R3A	5523	NM_002718	32967594					
F11	71	-0.084	-0.077	-0.073	-0.078	0.006	-7.842	PTPN18	26469	NM_014369	18375654					
C05	29	-0.104	-0.076	-0.053	-0.078	0.025	-1.725	DUSP5	1847	NM_004419	62865889					
F08	68	-0.144	-0.036	-0.053	-0.077	0.058	-0.750	ACP2	53	NM_001610	4557009					
H06	90	-0.068	-0.078	-0.062	-0.069	0.008	-4.764	PTPN6	5777	NM_080548	94557302					
C04	28	-0.040	-0.083	-0.076	-0.067	0.023	-1.619	EYA4	2070	NM_172103	98991762					
D06	42	-0.069	-0.082	-0.040	-0.064	0.022	-1.661	PIBSPA	27124	NM_001002837	50726959					
D08	44	-0.013	-0.091	-0.085	-0.063	0.043	-0.819	PPM1B	5495	NM_001033556	75813617					
D04	40	-0.047	-0.073	-0.069	-0.063	0.014	-2.506	NUDT15	55270	NM_018283	8922791					
A10	10	-0.126	-0.037	-0.024	-0.062	0.056	-0.630	PPFKB1	5207	NM_002625	118582285					
G06	78	-0.059	-0.034	-0.088	-0.060	0.027	-1.260	PPP3R1	5534	NM_000945	45238847					
D02	38	-0.052	-0.048	-0.071	-0.057	0.012	-2.661	PTPRT	11122	NM_007050	148539859					
A04	4	-0.072	-0.031	-0.055	-0.053	0.021	-1.428	PPP1R3C	5507	NM_005398	21314622					
F02	62	-0.120	0.004	-0.027	-0.048	0.064	-0.419	PPM1A	5494	NM_021003	29557948					
H02	86	-0.047	-0.081	-0.013	-0.047	0.034	-0.787	DUSP14	11072	NM_007026	148596940					
G04	76	-0.066	-0.052	-0.021	-0.047	0.023	-1.142	PPP1R14B	26472	XM_370630	41200335					
H05	89	-0.052	-0.075	-0.003	-0.043	0.037	-0.664	ILKAP	80895	NM_030768	29171685					
A01	1	-0.055	-0.052	-0.013	-0.040	0.023	-0.967	Non-targeted control								
E05	53	-0.067	-0.030	0.006	-0.030	0.037	-0.465	DLG1	1739	NM_001098424	148539627					
B03	15	-0.053	-0.044	0.009	-											

B06	18	0.057	0.107	0.132	0.098	0.038	1.458	PTPDC1	138639	NM_152422	30089951
A07	7	0.067	0.059	0.172	0.099	0.063	0.888	NT5M	56953	NM_020201	74229030

Difference from median of controls											
Well Name	Well #	1st	2nd	3rd	Average	Standard deviation	SSMD	GeneSymbol	Genelid	GeneAccession	GINumber
F01	61	-1.238	-1.115	-1.152	-1.168	0.063	-10.424	Dynamin-2			
E01	49	-1.233	-1.118	-1.114	-1.155	0.068	-9.633	Dynamin-2			
E12	60	-1.198	-1.076	-1.142	-1.139	0.061	-10.536	Dynamin-2			
F12	72	-1.213	-1.060	-1.124	-1.132	0.077	-8.292	Dynamin-2			
G12	84	-1.008	-0.751	-0.998	-0.919	0.146	-3.563	Clathrin heavy chain			
H12	96	-1.020	-0.714	-0.956	-0.897	0.162	-3.128	Clathrin heavy chain			
H01	85	-0.960	-0.622	-0.907	-0.830	0.181	-2.580	Clathrin heavy chain			
G01	73	-0.893	-0.652	-0.900	-0.815	0.141	-3.257	Clathrin heavy chain			
F09	69	-0.365	-0.372	-0.442	-0.393	0.042	-5.247	THTPA	79178	NM_024328	54607163
G10	82	-0.330	-0.188	-0.389	-0.302	0.103	-1.652	PPP3R2	5535	NM_147180	34303920
B05	17	-0.288	-0.184	-0.366	-0.279	0.091	-1.726	PPP1R7	5510	NM_002712	4506012
F06	66	-0.256	-0.167	-0.197	-0.207	0.045	-2.594	DKFZP761G058	152926	NM_152542	31542532
C07	31	-0.209	-0.124	-0.283	-0.205	0.079	-1.456	PPP1R2	5504	NM_006241	34147499
G04	76	-0.235	-0.154	-0.209	-0.199	0.041	-2.722	SSH3	54961	NM_017857	24586674
G02	74	-0.226	-0.148	-0.186	-0.187	0.039	-2.689	PPP2R5D	5528	NM_006245	31083266
C08	32	-0.143	-0.203	-0.195	-0.180	0.033	-3.132	WBP11	51729	NM_016312	18375679
G09	81	-0.302	-0.020	-0.190	-0.171	0.142	-0.680	PPP1R12B	4660	NM_032103	14195596
C05	29	-0.164	-0.131	-0.209	-0.168	0.039	-2.404	PPP1R1C	151242	NM_001080545	122937385
D03	39	-0.187	-0.092	-0.179	-0.153	0.052	-1.646	BPNT1	10380	NM_006085	116812594
B03	15	-0.181	-0.083	-0.178	-0.147	0.056	-1.495	PTPN14	5784	NM_005401	34328898
H06	90	-0.177	-0.067	-0.176	-0.140	0.063	-1.255	NT5E	4907	NM_002526	4505466
H08	92	-0.162	-0.108	-0.150	-0.140	0.029	-2.766	MTMR6	9107	NM_004685	134142347
A06	6	-0.188	-0.089	-0.135	-0.137	0.049	-1.573	NT5C	30833	NM_014595	7657032
D09	45	-0.136	-0.050	-0.212	-0.132	0.081	-0.922	PPP2R1B	5519	NM_181699	124269711
A09	9	-0.192	-0.064	-0.132	-0.129	0.064	-1.143	PTPN23	25930	NM_015466	110681717
B04	16	-0.123	-0.102	-0.139	-0.121	0.019	-3.632	PPP2R2B	5521	NM_181676	32307116
F04	64	-0.143	-0.099	-0.100	-0.114	0.025	-2.577	DUSP15	128853	NM_177991	29826316
C06	30	-0.098	-0.061	-0.168	-0.109	0.054	-1.133	PTP4A3	11156	NM_007079	14589853
B07	19	-0.213	-0.041	-0.068	-0.107	0.093	-0.653	KIAA0377	9677	NM_014659	7662083
D10	46	-0.102	-0.113	-0.102	-0.105	0.006	-9.176	FBP2	8789	NM_003837	22907027
G07	79	-0.035	-0.123	-0.154	-0.104	0.062	-0.948	PTPN4	5775	NM_002830	18104987
H05	89	-0.127	-0.052	-0.126	-0.102	0.043	-1.329	DUSP18	150290	NM_152511	51093844
C02	26	-0.061	-0.133	-0.107	-0.100	0.036	-1.567	PPP5C	5536	NM_006247	20127496
D04	40	-0.119	-0.073	-0.102	-0.098	0.023	-2.395	ACP5	54	NM_001611	161377449
C04	28	-0.147	-0.058	-0.084	-0.096	0.046	-1.188	PPAP2C	8612	NM_003712	29171743
E08	56	-0.230	-0.018	-0.039	-0.096	0.117	-0.463	PPP1R12A	4659	NM_002480	4505316
F05	65	-0.106	-0.087	-0.092	-0.095	0.010	-5.456	PPP1R13B	23368	NM_015316	121114286
E02	50	-0.100	-0.062	-0.120	-0.094	0.029	-1.795	PPFIA4	8497	NM_015053	55769553
F02	62	-0.117	-0.039	-0.109	-0.088	0.043	-1.161	NUDT4	11163	NM_019094	98985815
A08	8	-0.092	-0.089	-0.046	-0.075	0.026	-1.662	PPP2R1A	5518	NM_014225	32455242
C09	33	-0.071	-0.007	-0.137	-0.072	0.065	-0.625	PPP1R1A	5502	NM_006741	155030237
F07	67	-0.090	-0.060	-0.060	-0.070	0.017	-2.321	MTMR7	9108	NM_004686	142379887
E03	51	-0.093	-0.026	-0.079	-0.066	0.035	-1.061	IGBP1	3476	NM_001551	48375183
D05	41	-0.151	-0.040	-0.006	-0.065	0.076	-0.487	INPP5A	3632	NM_005539	109702905
C11	35	-0.140	0.015	-0.063	-0.063	0.078	-0.458	PTPLB	201562	NM_198402	158819030
D08	44	-0.047	-0.064	-0.067	-0.059	0.011	-3.152	PPM1F	9647	NM_014634	29826333
F03	63	-0.051	-0.038	-0.076	-0.055	0.019	-1.647	PTPN1	5770	NM_002827	18104977
H11	95	-0.059	-0.031	-0.074	-0.054	0.022	-1.407	Empty			
D06	42	-0.049	-0.017	-0.088	-0.051	0.035	-0.821	PPM1E	22843	NM_014906	30089947
E06	54	-0.050	-0.065	-0.034	-0.049	0.015	-1.816	PPP1R8	5511	NM_014110	20336237
E04	52	-0.096	-0.009	-0.030	-0.045	0.045	-0.559	DUSP13	51207	NM_016364	56237017
F08	68	-0.067	-0.039	-0.025	-0.044	0.021	-1.154	CTDSP2	10106	NM_005730	93004101
C10	34	-0.015	-0.056	-0.051	-0.041	0.022	-1.023	SGPP2	130367	NM_152386	23510288
A01	1	-0.054	-0.035	-0.031	-0.040	0.012	-1.897	Non-targeted control			
G03	75	-0.019	-0.046	-0.053	-0.039	0.018	-1.219				
A11	11	-0.058	-0.031	-0.022	-0.037	0.019	-1.107	PPAP2B	8613	NM_003713	29171739
F10	70	-0.019	-0.015	-0.077	-0.037	0.035	-0.603	DUSP22	56940	NM_020185	34147625
E05	53	-0.050	-0.007	-0.052	-0.036	0.026	-0.801	SBF1	6305	NM_002972	37574611
D11	47	-0.045	-0.025	-0.034	-0.035	0.010	-2.010	DUSP7	1849	NM_001947	85662716
D01	37	-0.027	-0.033	-0.036	-0.032	0.004	-4.233	Non-targeted control			
E09	57	-0.123	0.034	0.001	-0.030	0.083	-0.202				
H04	88	-0.040	0.008	-0.054	-0.029	0.032					

B02	14	0.078	0.113	0.088	0.093	0.018	2.907	IMPA2	3613	NM_014214	7657235
A05	5	0.106	0.081	0.174	0.120	0.048	1.407	PFKFB4	5210	NM_004567	19923257

Difference from median of controls										Genelid	GeneAccession	GINumber
Well Name	Well #	1st	2nd	3rd	Average	Standard deviation	SSMD	GeneSymbol				
E01	49	-1.174	-1.149	-1.219	-1.181	0.036	-18.749	Dynamin-2				
F01	61	-1.155	-1.105	-1.230	-1.163	0.063	-10.428	Dynamin-2				
E12	60	-1.188	-1.072	-1.213	-1.158	0.075	-8.661	Dynamin-2				
F12	72	-1.130	-1.103	-1.239	-1.157	0.072	-9.083	Dynamin-2				
H12	96	-0.998	-0.730	-1.018	-0.915	0.160	-3.217	Clathrin heavy chain				
G12	84	-0.985	-0.664	-1.068	-0.906	0.214	-2.391	Clathrin heavy chain				
G01	73	-0.874	-0.671	-0.957	-0.834	0.147	-3.198	Clathrin heavy chain				
H01	85	-0.833	-0.652	-0.976	-0.820	0.162	-2.850	Clathrin heavy chain				
G10	82	-0.302	-0.360	-0.510	-0.391	0.107	-2.059	INPP5D	3635	NM_005541	64085176	
E10	58	-0.337	-0.205	-0.271	-0.271	0.066	-2.315	PPP2CA	5515	NM_002715	57222566	
G04	76	-0.212	-0.234	-0.365	-0.270	0.082	-1.849	PTPRE	5791	NM_006504	40805849	
F03	63	-0.337	-0.143	-0.194	-0.224	0.101	-1.258	PPP1R15B	84919	NM_032833	41282220	
H06	90	-0.141	-0.172	-0.260	-0.191	0.062	-1.744	PPP2R5B	5526	NM_006244	30795206	
H07	91	-0.219	-0.101	-0.215	-0.178	0.067	-1.499	RNGTT	8732	NM_003800	134142827	
E09	57	-0.206	-0.073	-0.241	-0.174	0.089	-1.105	INPPL1	3636	NM_001567	4755141	
C11	35	-0.246	-0.008	-0.232	-0.162	0.133	-0.685	TIMM50	92609	NM_001001563	48526508	
C06	30	-0.180	-0.089	-0.202	-0.157	0.060	-1.475	PPAP2A	8611	NM_003711	29171735	
G09	81	-0.138	-0.125	-0.181	-0.148	0.030	-2.819	SACM1L	22908	NM_014016	7662337	
F06	66	-0.117	-0.115	-0.194	-0.142	0.045	-1.781	PALD	27143	NM_014431	51100971	
F11	71	-0.184	-0.043	-0.191	-0.139	0.083	-0.945	PPP3CB	5532	NM_021132	11036639	
G07	79	-0.101	-0.098	-0.217	-0.139	0.068	-1.154	PSPHL	8781	XM_926720	89024914	
H04	88	-0.100	-0.091	-0.214	-0.135	0.069	-1.110	NUDT2	318	NM_001161	22265329	
H08	92	-0.136	-0.111	-0.139	-0.129	0.015	-4.754	PPP1CA	5499	NM_206873	45827797	
F07	67	-0.076	-0.147	-0.162	-0.128	0.046	-1.563	PGAM1	5223	NM_002629	31543395	
C05	29	-0.096	-0.120	-0.144	-0.120	0.024	-2.823	DUSP9	1852	NM_001395	4503420	
E05	53	-0.153	-0.094	-0.108	-0.118	0.031	-2.154	PPP2R5A	5525	NM_006243	30795205	
G08	80	-0.089	-0.097	-0.161	-0.116	0.040	-1.646	DUSP6	1848	NM_001946	42764682	
H02	86	-0.096	-0.102	-0.144	-0.114	0.026	-2.469	PTPRK	5796	NM_002844	18860901	
E07	55	-0.126	-0.063	-0.139	-0.109	0.041	-1.514	DUSP12	11266	NM_007240	6005955	
B06	18	-0.106	-0.075	-0.139	-0.107	0.032	-1.878	DLG7	9787	NM_014750	21361644	
C08	32	-0.137	-0.017	-0.143	-0.099	0.071	-0.790	INPP4B	8821	NM_001101669	156104896	
F02	62	-0.116	-0.092	-0.082	-0.097	0.017	-3.142	PTPRB	5787	NM_002837	157952212	
H11	95	-0.081	-0.059	-0.148	-0.096	0.047	-1.165	PPP4R1	9989	NM_005134	108936951	
H05	89	-0.059	-0.076	-0.144	-0.093	0.045	-1.169	SKIP	51763	NM_016532	18765708	
D11	47	-0.137	0.015	-0.155	-0.092	0.093	-0.560	DUSP1	1843	NM_004417	7108342	
C09	33	-0.102	-0.072	-0.101	-0.092	0.017	-3.018	MTMR3	8897	NM_153051	148276975	
B09	21	-0.157	-0.021	-0.092	-0.090	0.068	-0.748	PPP1CB	5500	NM_002709	4506004	
E11	59	-0.132	-0.015	-0.114	-0.087	0.063	-0.784	TA-PP2C	160760	NM_139283	21281678	
G03	75	-0.051	-0.075	-0.128	-0.085	0.039	-1.212	PTPRN	5798	NM_002846	18860905	
G06	78	-0.055	-0.082	-0.114	-0.084	0.030	-1.604	PTPRS	5802	NM_130853	104487294	
H03	87	-0.116	-0.030	-0.097	-0.081	0.045	-1.011	PPAPDC1	196051	NM_001030059	73611919	
F04	64	-0.188	0.012	-0.066	-0.081	0.101	-0.452	INPP5B	3633	NM_005540	113722124	
H09	93	-0.036	-0.082	-0.100	-0.073	0.033	-1.240	BPGM	669	NM_001724	40353767	
G05	77	-0.052	-0.048	-0.118	-0.073	0.039	-1.050	DUSP16	80824	NM_030640	38372910	
D06	42	-0.060	-0.046	-0.110	-0.072	0.034	-1.197	PPP2R5E	5529	NM_006246	31083295	
H10	94	-0.052	-0.051	-0.103	-0.069	0.030	-1.314	PPFIA2	8499	NM_003625	29171754	
B07	19	-0.021	-0.058	-0.125	-0.068	0.053	-0.725	PTPN20A	653129	NM_001042397	109138574	
F05	65	-0.077	-0.052	-0.055	-0.061	0.014	-2.510	PTP4A1	7803	NM_003463	62865860	
G02	74	-0.029	-0.047	-0.107	-0.061	0.041	-0.837	MTMR8	55613	NM_017677	21361758	
E08	56	-0.061	0.008	-0.090	-0.048	0.050	-0.535	PPP3CC	5533	NM_005605	34147659	
E02	50	-0.069	-0.033	-0.033	-0.045	0.021	-1.224	ACPT	93650	NM_033068	18375509	
A06	6	-0.042	-0.027	-0.066	-0.045	0.020	-1.294	PTPRU	10076	NM_133178	110735403	
D01	37	-0.058	0.000	-0.076	-0.044	0.040	-0.631	Non-targeted control				
F10	70	-0.093	0.004	-0.036	-0.041	0.049	-0.482					
D05	41	-0.039	-0.031	-0.052	-0.040	0.010	-2.183	PPP2CZ	333926	NM_005167	65506327	
B08	20	-0.059	0.007	-0.059	-0.037	0.038	-0.548	SYN1	8867	NM_003895	44921605	
B03	15	-0.006	-0.053	-0.045	-0.035	0.025	-0.788	PON1	5444	NM_000446	31880793	
C01	25	-0.028	-0.017	-0.045	-0.030	0.014	-1.193	Non-targeted control				
B05	17	0.023	-0.058	-0.052	-0.029	0.045	-0.360					
F09	69	-0.089	0.033	-0.008	-0.02							

B10	22	0.098	0.083	0.051	0.077	0.024	1.811	DUSP8	1850	NM_004420	153281157
A04	4	0.106	0.062	0.102	0.090	0.024	2.087	PTPN9	5780	NM_002833	18375663
C04	28	0.045	0.087	0.140	0.091	0.048	1.074	PPAPDC2	403313	NM_203453	66773039
D03	39	0.097	0.108	0.111	0.105	0.007	7.940	NT5C2	22978	NM_012229	20149601