

Lomb-Scargle Selected Probes for Small "N"

oligo	Period	N	p	pdr	GeneID	Annotation	Comments
a15774_2	41.7	41	4.6400E-06	8.8390E-06	PF07_0078	hypothetical protein, conserved	hypothetical protein FLJ10856 0.34
a1700_3	43.6	42	2.1300E-05	3.5448E-05	PFA0350c	hypothetical protein	hypothetical protein PFB0800c - malaria parasite (Plasmodium falciparum) 0.26
a26463_1	41.7	40	1.0400E-05	1.8263E-05	NULL	#N/A	(AL034560) PFC0060c (MAL3P8.10), Serine/threonine protein kinase, len0.47
a3310_19	45.7	42	1.0300E-06	2.4037E-06	PFA0485w	hypothetical protein	No NR protein Similarities
a6420_1	45.7	38	1.4200E-05	2.4297E-05	PFA0245w	hypothetical protein	asparagine-rich protein (clone 28C6) - Plasmodium falciparum (fragment) 0.34
a8010_30	45.7	42	2.0800E-06	4.3307E-06	PFA0205w	hypothetical protein	
a9766_1	41.7	37	2.2400E-05	3.7108E-05	PFA0405w	hypothetical protein	hypothetical protein PFB0850c - malaria parasite (Plasmodium falciparum) 0.24
b110	41.7	41	1.7100E-06	3.6761E-06	PFB0180w	5'-3' exonuclease, N-terminal resolvase-like domain, putative	exonuclease domain (5'-3') protein PFB0180w - malaria parasite (Plasmodium falciparum) 1
b325	40.0	42	5.0000E-06	9.4463E-06	PFB0470w	hypothetical protein	hypothetical protein PFB0470w - malaria parasite (Plasmodium falciparum) 1
b492	50.5	41	3.6800E-06	7.1753E-06	NULL	#N/A	No NR protein Similarities
b498	45.7	41	3.1100E-05	5.0487E-05	PFB0770c	hypothetical protein	
b52	48.0	41	2.2600E-06	4.6506E-06	PFB0090c	hypothetical protein, conserved	protein with DnaJ domain PFB0090c - malaria parasite (Plasmodium falciparum) 1
b598	53.3	40	7.9000E-07	1.9411E-06	PFB0946c	hypothetical protein	No NR protein Similarities
b68	32.0	36	3.6400E-06	7.1074E-06	PFB0110w	hypothetical protein	probable integral membrane protein PFB0110w - malaria parasite (Plasmodium falciparum) 0.9
b88	43.6	42	4.2400E-05	6.7368E-05	PFB0140w	hypothetical protein	metal binding protein (DHC domain) PFB0140w - malaria parasite (Plasmodium falciparum) 0.96
c18	48.0	39	3.4600E-05	5.5787E-05	PFC0025c	stevor, putative	(AL034560) PFC0025c (MAL3P8.4), stevor (3D7-stevorT3-1), len1
c228	38.4	42	1.1500E-06	2.6284E-06	PFC0335c	hypothetical protein	hypothetical protein C0335c - Plasmodium falciparum 0.43
c249	43.6	41	5.1100E-06	9.6303E-06	PFC0385c	serine/threonine protein kinase, putative	hypothetical protein C0385c - Plasmodium falciparum 1
c337	36.9	33	5.3000E-05	8.3115E-05	PFC0506w	hypothetical protein	(AL008970) hypothetical protein, PFC0506w [Plasmodium falciparum] 0.92
c343	43.6	40	3.7800E-06	7.3370E-06	PFC0510w	zinc finger protein, putative	
c344	45.7	39	3.5600E-05	5.7278E-05	PFC0515c	hypothetical protein	hypothetical protein C0515c - Plasmodium falciparum 1
c427	45.7	42	1.6900E-05	2.8568E-05	PFC0620w	hypothetical protein	(AL034556) predicted using hexExon; MAL3P5.10 (PFC0620w), Hypothetical protein, len0.65
c68	48.0	37	4.3200E-06	8.2938E-06	PFC0115c	VAR pseudogene	PfEMP1 fragment PFB0020c - malaria parasite (Plasmodium falciparum) 0.51
c689	43.6	40	3.4400E-05	5.5503E-05	PFC1040w	hypothetical protein	(AL034559) predicted using hexExon; MAL3P7.39 (PFC1040w), Hypothetical protein, len1
d10455_2	50.5	38	5.9700E-06	1.1072E-05	PFD1185w	hypothetical protein	No NR protein Similarities
d12635_31	43.6	41	1.7200E-06	3.6919E-06	PFD0940w	hypothetical protein	hypothetical protein PFB0540w - malaria parasite (Plasmodium falciparum) 0.22
d15909_4	53.3	41	6.3600E-07	1.6407E-06	PFD1135c	hypothetical protein	(U20661) unknown [Dictyostelium discoideum] 0.54
d17715_19	43.6	38	2.3000E-06	4.7258E-06	PFD0560w	hypothetical protein	(AL035475) hypothetical protein, MAL4P2.47 [Plasmodium falciparum] 1
d17715_40	45.7	40	2.2900E-05	3.7882E-05	PFD0490c	hypothetical protein	(AL035475) hypothetical protein, MAL4P2.35 [Plasmodium falciparum] 0.71
d21102_1	48.0	42	5.6000E-07	1.4899E-06	PFB0655c	hypothetical protein	
d23156_45	41.7	40	1.3000E-06	2.9122E-06	PFD0690c	hypothetical protein	(AL034559) predicted using hexExon; MAL3P7.34 (PFC1015c), Hypothetical protein, len0.22
d50936_1	29.1	42	1.6900E-05	2.8568E-05	PFB0800c	hypothetical protein	
d65980_2	48.0	39	1.1400E-05	1.9852E-05	NULL	#N/A	
e19870_1	56.5	39	3.5100E-05	5.6500E-05	PFE1440c	hypothetical protein	
e26853_1	40.0	42	4.7800E-06	9.0981E-06	MAL6P1.53	50S ribosomal subunit L24, putative	(AB025633) 50S ribosomal protein L24 [Arabidopsis thaliana] 0.33
e26964_1	43.6	40	4.8600E-06	9.2274E-06	NULL	#N/A	

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oligo	Period	N	p	pfd	GeneID	Annotation	Comments
e27461_1	43.6	41	2.7800E-05	4.5452E-05	PFE1545c	diaphanous homolog, putative	(AL034559) hypothetical protein, PFC0960c [Plasmodium falciparum] 0.22
f1153_1	25.3	42	8.2400E-06	1.4787E-05	PF08_0070	hypothetical protein	(AL034559) hypothetical protein, PFC0960c [Plasmodium falciparum] 0.22
f18577_4	43.6	41	1.2600E-06	2.8346E-06	MAL8P1.135	hypothetical protein	No NR protein Similarities
f24479_1	36.9	39	5.7400E-06	1.0694E-05	PF08_0051	hypothetical protein	hypothetical protein PFB0800c - malaria parasite (Plasmodium falciparum) 0.24
f26109_1	56.5	40	5.3000E-05	8.3115E-05	NULL	#N/A	No NR protein Similarities
f27079_1	40.0	41	6.9600E-06	1.2713E-05	MAL6P1.40	phenylalanine -- tRNA ligase, putative	(AL137081) phenylalanine-tRNA synthetase-like protein [Arabidopsis thaliana] 0.4
f27352_2	43.6	42	8.7200E-07	2.0998E-06	PFB0720c	hypothetical protein, conserved	
f29577_2	38.4	40	1.3500E-05	2.3209E-05	PFE1560c	hypothetical protein	No NR protein Similarities
f38531_2	56.5	39	1.7000E-05	2.8723E-05	PFE1070c	hypothetical protein	phosphatase (acid phosphatase family) PFB0380c - malaria parasite (Plasmodium falciparum) 0.23
f42564_1	36.9	41	2.6000E-06	5.2574E-06	PFE1295c	hypothetical protein	
f43059_2	43.6	42	1.0600E-06	2.4645E-06	MAL6P1.41	hypothetical protein	
f47255_1	50.5	39	4.5900E-05	7.2643E-05	NULL	#N/A	No NR protein Similarities
f54828_9	36.9	35	4.2300E-05	6.7240E-05	PFE1180c	hypothetical protein	DNA-directed RNA polymerase (EC 2.7.7.6) beta'-2 chain - Plasmodium falciparum plastid 0.25
f54854_2	43.6	42	4.2000E-07	1.2046E-06	PF07_0015	hypothetical protein	
f5510_1	35.6	42	1.7500E-06	3.7434E-06	PF00_0001	hypothetical protein	DNA-directed RNA polymerase (EC 2.7.7.6) beta'-2 chain - Plasmodium falciparum plastid 0.26
f58149_1	48.0	39	8.5400E-06	1.5250E-05	NULL	#N/A	rifin PFB0055c - malaria parasite (Plasmodium falciparum) 0.53
f59165_1	45.7	42	3.2500E-06	6.4169E-06	MAL8P1.134	hypothetical protein	(AF183184) brain otoferlin [Mus musculus] 0.27
f6022_1	41.7	39	1.0200E-05	1.7944E-05	PFD0330w	hypothetical protein	(AJ318337) Krueppel-like protein [Plasmodium falciparum] 0.47
f61856_1	45.7	41	6.0600E-06	1.1206E-05	PF08_0002	conserved hypothetical protein, conserved in P. falciparum	
f66997_1	45.7	36	5.9600E-05	9.2746E-05	MAL7P1.50	erythrocyte membrane protein 1 (PIEMP1)	(AL035475) var gene, MAL4P2.58 [Plasmodium falciparum] 0.38
i10218_1	35.6	34	1.8300E-05	3.0761E-05	MAL13P1.107	hypothetical protein	(AL034559) hypothetical protein, PFC0960c [Plasmodium falciparum] 0.22
i11056_2	34.3	34	2.7600E-05	4.5179E-05	NULL	#N/A	
i11211_1	43.6	41	1.3500E-05	2.3209E-05	NULL	#N/A	
i15351_1	43.6	42	3.0800E-06	6.1235E-06	MAL13P1.114	hypothetical protein	
i16671_5	45.7	42	6.8400E-07	1.7359E-06	PF07_0076	hypothetical protein	(AJ318337) Krueppel-like protein [Plasmodium falciparum] 0.55
i16689_1	45.7	42	7.8100E-07	1.9280E-06	MAL13P1.49	hypothetical protein	No NR protein Similarities
i16936_3	41.7	42	3.9400E-06	7.6131E-06	PFI0705w	hypothetical protein, conserved	No NR protein Similarities
i1808_1	41.7	35	1.0500E-05	1.8410E-05	NULL	#N/A	
i3340_2	48.0	41	4.3400E-06	8.3275E-06	NULL	#N/A	No NR protein Similarities
i4256_1	41.7	42	1.3400E-06	2.9824E-06	MAL13P1.19	hypothetical protein	
i6658_3	43.6	42	6.3300E-07	1.6367E-06	PFI0735c	NADH dehydrogenase, putative	
i6851_2	48.0	41	9.1400E-06	1.6216E-05	PFI0410c	hypothetical protein	No NR protein Similarities
i7097_2	45.7	39	1.8400E-06	3.9043E-06	PFI0385c	S1/P1nuclease, putative	endonuclease (EC 3.1.30.-) precursor - barley 0.27
i7243_1	40.0	39	3.5900E-05	5.7747E-05	MAL6P1.205	hypothetical protein	
i7884_1	43.6	42	9.2700E-07	2.2075E-06	PFI1255w	hypothetical protein, conserved	
j120_1	40.0	38	2.8400E-05	4.6334E-05	PF10_0032	hypothetical protein	
j151_3	38.4	37	1.0100E-05	1.7791E-05	PF10_0284	hypothetical protein	hypothetical protein C0705c - Plasmodium falciparum 0.21
j167_8	45.7	42	3.0600E-06	6.0855E-06	PF10_0334	flavoprotein subunit of succinate dehydrogenase	(D86573) flavoprotein subunit of succinate dehydrogenase [Plasmodium falciparum] 1
j180_11	41.7	38	4.6300E-06	8.8224E-06	PF10_0006	rifin	rifin PFB1040w - malaria parasite (Plasmodium falciparum) 0.56
j232_2	40.0	42	4.2100E-07	1.2070E-06	PF10_0260	hypothetical protein	hypothetical protein C0760c - Plasmodium falciparum 0.23
j245_5	36.9	42	2.4800E-06	5.0444E-06	PF10_0235	hypothetical protein	(AB025629) gene_id0.39
j269_9	53.3	41	2.1800E-06	4.5075E-06	PF10_0231	hypothetical protein	(AJ278826) hypothetical protein [Plasmodium berghei] 0.51
j40_15	48.0	38	1.0600E-05	1.8572E-05	PF10_0251	hypothetical protein	
j40_6	45.7	39	8.8200E-06	1.5697E-05	PF10_0248	hypothetical protein	No NR protein Similarities
j53_56	48.0	40	8.7400E-06	1.5575E-05	PF10_0160	3.8 protein	No NR protein Similarities

Lomb-Scargle Selected Probes for Small "N"

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j53_58	45.7	42	1.7900E-05	3.0118E-05	PF10_0161	hypothetical protein	trfA protein - slime mold (<i>Dictyostelium discoideum</i>) 0.23
j53_60	45.7	40	5.7800E-05	9.0169E-05	NULL	#N/A	hypothetical protein PFB0900c - malaria parasite (<i>Plasmodium falciparum</i>) 0.32
j58_3	21.8	40	2.7600E-05	4.5179E-05	PF10_0074	hypothetical protein	No NR protein Similarities
j697_3	53.3	41	8.2700E-06	1.4833E-05	PF10_0061	hypothetical protein	
km695_2	40.0	41	2.3700E-06	4.8508E-06	PFL1210w	hypothetical protein	ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE--TRNA LIGASE) (ILERS) (FRAGMENT) 0.33
kn1058_1	41.7	36	6.6800E-06	1.2276E-05	PFL1720w	Serine hydroxymethyltransferase	(AF195023) SHMT [<i>Plasmodium falciparum</i>] 1
kn12486_2	43.6	41	1.4300E-06	3.1510E-06	MAL6P1.41	hypothetical protein	No NR protein Similarities
kn2241_1	48.0	42	4.5500E-06	8.6917E-06	PFI0410c	hypothetical protein	
kn2725_1	45.7	38	2.3500E-05	3.8781E-05	PFL1025c	hypothetical protein	No NR protein Similarities
kn3081_1	48.0	39	6.0300E-06	1.1162E-05	PF13_0083	lipoate-protein ligase a, putative	(AE004218) lipoate-protein ligase A [<i>Vibrio cholerae</i>] 0.34
kn4809_2	50.5	40	1.1900E-06	2.7054E-06	NULL	#N/A	No NR protein Similarities
kn67_1	43.6	42	1.3100E-06	2.9279E-06	PF07_0021	hypothetical protein	
kn820_1	43.6	41	5.7700E-06	1.0739E-05	PF10_0059	hypothetical protein	
kn962_1	48.0	34	2.8900E-05	4.7071E-05	NULL	#N/A	
ks1032_1	41.7	35	5.6700E-05	8.8513E-05	PF11_0097	succinyl-CoA synthetase alpha subunit, putative	SUCCINYL-COA LIGASE [GDP-FORMING] ALPHA-CHAIN, MITOCHONDRIAL PRECURSOR (EC 6.2.1.4) (SUCCINYL-COA SYNTHETASE, ALPHA CHAIN) (SCS-ALPHA) 0.64
ks12_15	35.6	42	9.8200E-06	1.7355E-05	PF11_0214	hypothetical protein	(AL034559) hypothetical protein, PFC0960c [<i>Plasmodium falciparum</i>] 0.23
ks127_10	50.5	42	3.1400E-05	5.0902E-05	PF11_0462	hypothetical protein	hypothetical protein - <i>Plasmodium falciparum</i> 0.23
ks152_1	41.7	35	5.0000E-05	7.8697E-05	PF11_0154	hypothetical protein	(AL034556) predicted using hexExon; MAL3P5.2 (PFC0580c), Hypothetical protein, len0.25
ks186_6	43.6	39	1.8500E-05	3.1082E-05	PF11_0063	hypothetical protein	No NR protein Similarities
ks187_2	43.6	42	1.3600E-06	3.0152E-06	NULL	#N/A	No NR protein Similarities
ks187_5	36.9	34	3.4000E-05	5.4910E-05	PF11_0323	hypothetical protein	(AL034559) hypothetical protein, PFC1065w [<i>Plasmodium falciparum</i>] 0.26
ks210_10	43.6	37	4.2000E-05	6.6809E-05	NULL	#N/A	No NR protein Similarities
ks210_16	45.7	41	5.3600E-06	1.0055E-05	PF11_0237	hypothetical protein	No NR protein Similarities
ks210_4	41.7	37	3.6900E-05	5.9287E-05	PF11_0235	hypothetical protein	No NR protein Similarities
ks220_7	40.0	42	1.1900E-06	2.7054E-06	PF11_0021	rifin	rifin PFB0015c - malaria parasite (<i>Plasmodium falciparum</i>) 0.48
ks225_7	43.6	40	5.3200E-06	9.9904E-06	PF11_0468	hypothetical protein	(AL034559) hypothetical protein, PFC0960c [<i>Plasmodium falciparum</i>] 0.22
ks25_8	40.0	36	8.9400E-06	1.5882E-05	PF11_0077	hypothetical protein	
ks271_2	43.6	33	2.5800E-05	4.2394E-05	PF11_0458	hypothetical protein	
ks371_6	53.3	39	1.9100E-05	3.1965E-05	PF11_0291	hypothetical protein	hypothetical protein PFB0540w - malaria parasite (<i>Plasmodium falciparum</i>) 0.24
ks423_3	43.6	41	2.8100E-05	4.5920E-05	PF11_0330	hypothetical protein	hypothetical protein PFB0540w - malaria parasite (<i>Plasmodium falciparum</i>) 0.23
ks423_5	50.5	39	4.0200E-05	6.4228E-05	NULL	#N/A	
ks45_1	36.9	42	4.7600E-05	7.5178E-05	NULL	#N/A	(M14820) ORF2 bases 1807-2850; first start codon at 2032; putative [<i>Trypanosoma brucei</i>] 0.3
ks465_1	53.3	36	6.0700E-05	9.4329E-05	PF11_0203	hypothetical protein	AFG3 (ATPase family gene 3, yeast)-like 2 0.49
ks51_6	40.0	39	1.8300E-05	3.0761E-05	PF11_0219	hypothetical protein	No NR protein Similarities
ks694_7	43.6	38	4.9800E-06	9.4214E-06	PF11_0420	hypothetical protein	(AL034558) predicted using hexExon; MAL3P2.18 (PFC0245c), Hypothetical protein, len0.22
ks76_3	41.7	42	5.0100E-06	9.4600E-06	PF11_0420	hypothetical protein	
ks85_3	41.7	42	1.1500E-06	2.6284E-06	PF11_0365	hypothetical protein	No NR protein Similarities
ks85_6	40.0	36	6.3100E-05	9.7904E-05	NULL	#N/A	No NR protein Similarities
ks85_7	41.7	40	1.7500E-05	2.9510E-05	PF11_0367	hypothetical protein	No NR protein Similarities
ks85_8	41.7	42	2.9600E-05	4.8132E-05	PF11_0368	hypothetical protein	hypothetical protein PFB0555c - malaria parasite (<i>Plasmodium falciparum</i>) 0.22
ks85_9	53.3	42	7.2600E-07	1.8176E-06	NULL	#N/A	No NR protein Similarities

Lomb-Scargle Selected Probes for Small "N"

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ks97_16	50.5	42	5.3900E-07	1.4453E-06	PF11_0196	hypothetical protein	No NR protein Similarities
ks97_20	50.5	33	4.1700E-05	6.6409E-05	PF11_0198	hypothetical protein, conserved	(AB025628) contains similarity to unknown protein-gene_id0.32
ks98_1	43.6	38	8.6700E-06	1.5462E-05	PF11_0528	hypothetical protein	(AL034558) predicted using hexExon; MAL3P2.18 (PFC0245c), Hypothetical protein, len0.21
l2_109	43.6	42	2.1800E-06	4.5075E-06	PFL0420w	hypothetical protein	(AL034559) hypothetical protein, PFC0960c [Plasmodium falciparum] 0.23
l2_158	45.7	41	2.5800E-06	5.2215E-06	PFL0540w	mannosyltransferase, putative	(AB028127) mannosyltransferase [Homo sapiens] 0.39
l2_194	36.9	38	2.1500E-05	3.5721E-05	PFL0610w	hypothetical protein	(AB072791) hypothetical protein [Macaca fascicularis] 0.38
l2_195	38.4	39	1.0500E-05	1.8410E-05	PFL0610w	hypothetical protein	No NR protein Similarities
l2_196	38.4	36	4.0500E-05	6.4648E-05	PFL0610w	hypothetical protein	No NR protein Similarities
l2_20	45.7	42	3.6000E-07	1.0798E-06	PFL0260c	hypothetical protein	hypothetical protein PFB0800c - malaria parasite (Plasmodium falciparum) 0.26
l2_268	41.7	40	1.3200E-05	2.2733E-05	PFL0775w	hypothetical protein	No NR protein Similarities
l2_49	50.5	42	2.5400E-05	4.1786E-05	PFL0305c	hypothetical protein	hypothetical protein SPBC30D10.03c - fission yeast (Schizosaccharomyces pombe) 0.46
m1042_1	41.7	41	5.9800E-06	1.1082E-05	PF13_0337	hypothetical protein	(L36903) var1 gene product [Saccharomyces cerevisiae] 0.29
m12812_3	35.6	40	2.7700E-05	4.5310E-05	PF13_0144	oxidoreductase, putative	(AF322647) malate dehydrogenase [Sinorhizobium meliloti] 0.49
m16243_1	45.7	39	2.4600E-06	5.0126E-06	NULL	#N/A	No NR protein Similarities
m1886_1	50.5	41	1.8900E-06	3.9895E-06	MAL13P1.156	hypothetical protein	(AB018543) mkpA [Dictyostelium discoideum] 0.3
m20186_2	45.7	42	2.8600E-07	9.3187E-07	NULL	#N/A	(AF270648) mature parasite-infected erythrocyte surface antigen [Plasmodium falciparum] 0.27
m21368_2	53.3	42	3.2100E-06	6.3471E-06	MAL13P1.212	hypothetical protein	No NR protein Similarities
m2305_1	48.0	42	1.5200E-05	2.5879E-05	PF13_0078	hypothetical protein	
m2511_3	50.5	42	1.3200E-05	2.2733E-05	PF13_0060	hypothetical protein	hypothetical protein FLJ11222 0.26
m29456_3	41.7	37	5.4900E-05	8.5898E-05	MAL13P1.146	AMP deaminase, putative	
m33419_2	41.7	40	8.6900E-06	1.5494E-05	NULL	#N/A	No NR protein Similarities
m3590_1	35.6	40	3.2600E-06	6.4311E-06	MAL13P1.48	hypothetical protein	AMV258 [Amsacta moorei entomopoxvirus] 0.24
m36520_4	43.6	41	4.0500E-05	6.4648E-05	PF13_0149	chromatin assembly factor 1 subunit, putative	(AF073787) retinoblastoma A associated protein; RbAp48 [Xenopus laevis] 0.33
m37197_1	43.6	42	2.5300E-07	8.6364E-07	NULL	#N/A	No NR protein Similarities
m37744_1	41.7	36	8.5100E-06	1.5204E-05	PF13_0112	hypothetical protein	No NR protein Similarities
m40983_2	43.6	40	1.4500E-05	2.4779E-05	MAL13P1.78	hypothetical protein	
m42640_1	45.7	38	1.9100E-05	3.1965E-05	NULL	#N/A	
m50253_1	40.0	42	1.6600E-05	2.8110E-05	MAL13P1.205	GTP-binding protein, putative	No NR protein Similarities
m5455_6	41.7	42	1.0700E-05	1.8728E-05	MAL13P1.138	hypothetical protein	hypothetical protein PFB0800c - malaria parasite (Plasmodium falciparum) 0.26
m56512_12	50.5	42	1.3700E-05	2.3523E-05	PF13_0320	guanylyl cyclase	(AJ249165) guanylyl cyclase enzyme [Plasmodium falciparum] 1
m57062_1	53.3	42	2.4500E-07	8.4898E-07	PF13_0075	hypothetical protein, conserved in P. falciparum	(AL031746) hypothetical protein, MAL1P3.07 [Plasmodium falciparum] 0.31
m57062_3	56.5	38	2.2800E-06	4.6875E-06	PF13_0074	hypothetical protein	(AL360354) Pvstp1, putative transmembrane protein, some similarity to Q9XTP8 205 KDA PK1(B+)1+ SICAVAR ANTIGEN (1759 aa) fasta scores0.25
m6581_1	41.7	37	4.4100E-05	6.9939E-05	PF13_0022	cyclin 4	(AL034388) /prediction=(method0.45
m6741_1	41.7	39	2.3100E-05	3.8176E-05	MAL13P1.100	hypothetical protein	DNA-directed RNA polymerase (EC 2.7.7.6) beta'-2 chain - Plasmodium falciparum plastid 0.28
m7770_1	45.7	38	1.0400E-05	1.8263E-05	MAL13P1.29	hypothetical protein	(AL034559) hypothetical protein, PFC0960c [Plasmodium falciparum] 0.23
m7770_2	45.7	41	6.1100E-06	1.1289E-05	MAL13P1.29	hypothetical protein	
m7883_6	43.6	41	1.5300E-06	3.3393E-06	PF13_0127	hypothetical protein	asparagine-rich protein (clone 14C1) - Plasmodium falciparum 0.26
m7883_7	38.4	37	5.1500E-05	8.0892E-05	MAL13P1.127	hypothetical protein	hypothetical protein PFB0630c - malaria parasite (Plasmodium falciparum) 0.35
n127_14	43.6	40	4.8300E-06	9.1806E-06	PF14_0169	hypothetical protein	No NR protein Similarities
n127_44	36.9	41	2.3200E-05	3.8314E-05	PF14_0153	hypothetical protein	asparagine/aspartate rich protein - Plasmodium falciparum (fragment) 0.25

Lomb-Scargle Selected Probes for Small "N"

oligo	Period	N	p	pfd	GeneID	Annotation	Comments
n127_7	48.0	41	1.3600E-06	3.0152E-06	PF14_0171	hypothetical protein	(AL034559) hypothetical protein, PFC1065w [Plasmodium falciparum] 0.24
n129_17	53.3	36	2.8900E-05	4.7071E-05	PF14_0736	hypothetical protein	hypothetical protein F36H12.3 - Caenorhabditis elegans 0.4
n130_17	40.0	34	4.1900E-05	6.6681E-05	PF14_0568	hypothetical protein	DNA-directed RNA polymerase (EC 2.7.7.6) beta'-2 chain - Plasmodium falciparum plastid 0.25
n132_150	50.5	39	7.7600E-06	1.4006E-05	PF14_0337	hypothetical protein	(AL034559) hypothetical protein, PFC0960c [Plasmodium falciparum] 0.22
n132_162	40.0	39	5.5500E-06	1.0377E-05	PF14_0332	hypothetical protein	(AF063866) ORF MSV214 SCG gene family protein [Melanoplus sanguinipes entomopoxvirus] 0.26
n132_166	43.6	41	4.5700E-06	8.7250E-06	PF14_0331	cytochrome c oxidase assembly protein, putative	(AB011476) contains similarity to cytochrome oxidase assembly factor-gene_id0.4
n132_177	45.7	42	1.0900E-06	2.5181E-06	PF14_0325	hypothetical protein	
n132_22	45.7	39	4.4800E-05	7.0984E-05	PF14_0383	hypothetical protein	(AJ318337) Krueppel-like protein [Plasmodium falciparum] 0.69
n132_24	43.6	41	1.6100E-06	3.4939E-06	PF14_0382	metalloendopeptidase, putative	pitrilysin (EC 3.4.24.55) - garden pea 0.27
n134_131	43.6	41	3.3800E-06	6.6317E-06	PF14_0580	hypothetical protein	(AL034559) hypothetical protein, PFC0960c [Plasmodium falciparum] 0.24
n137_15	45.7	40	5.3700E-06	1.0071E-05	PF14_0663	hypothetical protein	hypothetical protein C0820w - Plasmodium falciparum 0.24
n137_20	41.7	42	2.4100E-06	4.9238E-06	NULL	#N/A	No NR protein Similarities
n137_25	48.0	42	1.3600E-06	3.0152E-06	PF14_0667	hypothetical protein	No NR protein Similarities
n138_21	48.0	38	1.8900E-05	3.1661E-05	NULL	#N/A	
n138_24	45.7	38	3.7600E-06	7.3043E-06	NULL	#N/A	
n138_31	41.7	37	7.6200E-06	1.3779E-05	PF14_0286	glutamate dehydrogenase, putative	(Y12927) glutamate dehydrogenase (NADP+) [Plasmodium falciparum] 0.64
n138_73	45.7	40	1.4200E-05	2.4297E-05	PF14_0303	hypothetical protein	hypothetical protein PFB0540w - malaria parasite (Plasmodium falciparum) 0.22
n139_23	56.5	35	7.5000E-06	1.3576E-05	PF14_0749	acyl CoA binding protein	Chain A, Acyl-Coa Binding Protein From Plasmodium Falciparum 1
n140_4	36.9	36	2.9200E-05	4.7515E-05	PF14_0497	hypothetical protein	(AF063866) ORF MSV140 hypothetical protein [Melanoplus sanguinipes entomopoxvirus] 0.24
n141_34	50.5	38	4.4300E-05	7.0224E-05	PF14_0222	hypothetical protein	(AF036170) homeobox-containing protein Wariai [Dictyostelium discoideum] 0.28
n141_45	43.6	41	1.9800E-06	4.1527E-06	PF14_0215	hypothetical protein	(AB012247) contains similarity to zinc finger proteins-gene_id0.32
n143_55	43.6	42	2.2300E-06	4.5985E-06	PF14_0181	calmodulin, putative	CALMODULIN 0.26
n148_9	41.7	38	5.0500E-06	9.5250E-06	PF14_0720	hypothetical protein	(AL034558) predicted using hexExon; MAL3P2.18 (PFC0245c), Hypothetical protein, len0.22
n149_1	43.6	42	6.7800E-07	1.7251E-06	PF14_0480	hypothetical protein	hypothetical protein C0335c - Plasmodium falciparum 0.22
n149_2	45.7	36	9.8900E-06	1.7466E-05	PF14_0480	hypothetical protein	No NR protein Similarities
n149_3	45.7	35	4.6300E-05	7.3243E-05	NULL	#N/A	No NR protein Similarities
n150_49	38.4	42	4.5900E-06	8.7583E-06	NULL	#N/A	No NR protein Similarities
n150_62	36.9	42	3.7600E-06	7.3043E-06	PF14_0095	hypothetical protein	DNA-directed RNA polymerase (EC 2.7.7.6) beta'-2 chain - Plasmodium falciparum plastid 0.24
n153_8	38.4	41	3.1200E-06	6.1887E-06	PF14_0534	hypothetical protein	(AY054254) AT4g37930/F20D10_50 [Arabidopsis thaliana] 0.25
n157_6	43.6	40	2.4200E-06	4.9399E-06	NULL	#N/A	
n161_1	53.3	41	7.4200E-06	1.3446E-05	PF14_0703	hypothetical protein	hypothetical protein C0425w - Plasmodium falciparum 0.25
n168_17	41.7	42	9.6700E-07	2.2830E-06	PF14_0526	hypothetical protein, conserved	No NR protein Similarities
n170_1	64.0	32	2.7400E-05	4.4894E-05	PF14_0761	fatty acyl CoA synthetase 1	(AF007828) acyl CoA synthetase [Plasmodium falciparum] 1
n231_1	45.7	41	8.4800E-07	2.0528E-06	NULL	#N/A	
opfb0685	40.0	42	2.0700E-06	4.3138E-06	PFB0960c	hypothetical protein	probable integral membrane protein PFB0985c - malaria parasite (Plasmodium falciparum) 0.74
opfblob0131	50.5	42	1.2400E-05	2.1484E-05	PFL1970w	VAR pseudogene	erythrocyte membrane protein 1 - Plasmodium falciparum 0.37
opfblob0137	43.6	42	1.2700E-06	2.8534E-06	NULL	#N/A	(AE006715) Glutaryl-tRNA amidotransferase, subunit A (gatA-2) [Sulfolobus solfataricus] 0.35
opfblob0156	43.6	36	2.6300E-05	4.3174E-05	MAL6P1.112	hypothetical protein, conserved	hypothetical protein D2013.10 - Caenorhabditis elegans Location=join(14118..14547,14670..14806)0.31

Lomb-Scargle Selected Probes for Small "N"

oligo	Period	N	p	pdr	GeneID	Annotation	Comments
opfc0768	38.4	35	1.0400E-05	1.8263E-05	PFC0506w	hypothetical protein	(AL008970) hypothetical protein, PFC0506w [Plasmodium falciparum] Location=509193..5094980.92
opfc0776	48.0	38	5.9900E-06	1.1097E-05	PFC0115c	VAR pseudogene	(AF334805) erythrocyte membrane protein 1 [Plasmodium falciparum] 0.49
opfc0777	48.0	36	7.6800E-06	1.3876E-05	NULL	#N/A	(BC012382) Unknown (protein for MGC0.44)
opfd67010	48.0	40	3.3400E-06	6.5663E-06	PFD0235c	hypothetical protein	probable chloroquine resistance protein CG2 (strain HB3) - Plasmodium falciparum 0.3
opfd67015	53.3	41	1.0700E-06	2.4835E-06	PFD0715c	hypothetical protein, conserved	hypothetical protein C0475c - Plasmodium falciparum 0.26
opff72484	45.7	39	1.1400E-05	1.9852E-05	MAL6P1.279	hypothetical protein	(AF272150) deliriumA [Dictyostelium discoideum] 0.32
opff72487	45.7	40	5.1600E-06	9.7218E-06	MAL6P1.292	integral membrane protein	(AK010312) putative [Mus musculus] 0.31
opff72504	40.0	37	3.6900E-05	5.9287E-05	NULL	#N/A	(AE003509) CG15040 gene product [Drosophila melanogaster] Location=36591..375620.28
opff72505	48.0	39	2.5900E-05	4.2548E-05	NULL	#N/A	(BC012382) Unknown (protein for MGC0.28)
opff72516	41.7	37	7.9200E-06	1.4273E-05	MAL6P1.99	hypothetical protein	hypothetical protein PFB0800c - malaria parasite (Plasmodium falciparum) Location=join(89326..91350,91761..91817)0.26
opfg0033	45.7	39	2.0300E-06	4.2472E-06	NULL	#N/A	variant-specific surface protein - Plasmodium falciparum Location=2592..60260.43
opfg0041	50.5	39	6.0200E-05	9.3595E-05	PF07_0098	dynactin 4, putative	(AF264759) dynactin Arp1 p25 subunit RO12 [Neurospora crassa] 0.36
opfg0047	40.0	42	6.9100E-06	1.2638E-05	PFE0800w	hypothetical protein	(AL034559) hypothetical protein, PFC1000w [Plasmodium falciparum] Location=join(1735..4915,5003..5016)0.32
opfh0026	48.0	36	1.7900E-05	3.0118E-05	MAL8P1.49	hypothetical protein	hypothetical protein DKFZp434E1723 [Homo sapiens] Location=join(16..747,948..1351,1746..1881)0.33
opfi17656	50.5	42	3.9000E-07	1.1381E-06	PFI0125c	hypothetical protein	(AL034560) PFC0060c (MAL3P8.10), Serine/threonine protein kinase, len0.46
opfi17665	43.6	37	5.0100E-06	9.4600E-06	PFI0660c	protease, putative	hypothetical protein - Synechocystis sp. (strain PCC 6803) 0.42
opfi17666	41.7	38	5.8800E-05	9.1584E-05	PFI0685w	pseudouridylate synthase, putative	(AE003628) CG7475 gene product [Drosophila melanogaster] Location=597789..6006560.41
opfi17679	41.7	42	1.2400E-06	2.8015E-06	PFI1050c	hypothetical protein	hypothetical protein F20B18.20 - Arabidopsis thaliana 0.37
opfi17690	53.3	32	5.0200E-05	7.8976E-05	PFI0335w	hypothetical protein	CYTOSKELETON-ASSOCIATED PROTEIN CKAPI (TUBULIN FOLDING COFACTOR B) Location=336079..3368670.33
opfi17703	45.7	41	2.0200E-05	3.3732E-05	PFI0005w	erythrocyte membrane protein 1 (PfEMP1)	(AF134154) variant-specific surface protein [Plasmodium falciparum] Location=20080..256980.32
opfi17711	53.3	42	1.0200E-05	1.7944E-05	PFI0815c	hypothetical protein, conserved	(AE003581) CG9643 gene product [Drosophila melanogaster] 0.31
opfk12899	43.6	42	1.1100E-05	1.9383E-05	NULL	#N/A	(AK021073) putative [Mus musculus] 0.48
opfl0006	48.0	35	1.8800E-05	3.1517E-05	PFL1550w	lipoamide dehydrogenase	(AF225982) lipoamide dehydrogenase [Plasmodium falciparum] Location=join(1332235..1332305,1332530..1333997)1
opfl0063	43.6	41	1.6200E-06	3.5101E-06	PFL1915w	dna gyrase subunit b, putative	DNA topoisomerase (ATP-hydrolyzing) (EC 5.99.1.3) B - Thermotoga maritima (strain MSB8) Location=1647814..16508340.41
opfl0071	40.0	42	4.8500E-06	9.2135E-06	PFL1555w	cytochrome b5, putative	(AF290427) cytochrome b5 [Rhizopus stolonifer] Location=join(1335374..1335527,1335707..1335951)0.39
opfl0075	48.0	33	1.5500E-05	2.6344E-05	PFL2585c	rifin	rifin PFB0060w - malaria parasite (Plasmodium falciparum) 0.37
opfl0091	43.6	42	3.8800E-07	1.1361E-06	PFL1845c	calcyclin binding protein, putative	(AC022455) unknown protein; 69948-68670 [Arabidopsis thaliana] 0.34
opfl0115	43.6	35	4.5000E-05	7.1285E-05	PFL1780w	hypothetical protein	(AE003539) CG11268 gene product [Drosophila melanogaster] Location=join(1531391..1532738,1532923..1533079,1533196..1533220)0.31
opfl0117	50.5	38	1.2600E-05	2.1798E-05	PFL2235w	hypothetical protein	(BC006350) Unknown (protein for MGC0.31)
opfl0122	50.5	42	6.3100E-07	1.6321E-06	PFL1350w	RNA pseudouridylate synthase, putative	(AL162754) putative RNA-binding protein [Neisseria meningitidis] Location=1137827..11395210.3
opfl0161	43.6	34	4.0900E-05	6.5256E-05	PFL2350c	hypothetical protein	DNA-directed RNA polymerase (EC 2.7.7.6) beta'-2 chain - Plasmodium falciparum plastid 0.26
opfm60492	41.7	41	2.2100E-06	4.5641E-06	PF13_0223	hypothetical protein, conserved	(AE003724) CG14290 gene product [alt 1] [Drosophila melanogaster] Location=43158..434030.49

Lomb-Scargle Selected Probes for Small "N"

oligo	Period	N	p	pdr	GeneID	Annotation	Comments
opfm60505	41.7	41	5.8300E-05	9.0908E-05	MAL13P1.69	septum formation protein MAF homologue, putative	(BC002508) acetylserotonin O-methyltransferase-like [Homo sapiens] 0.41
opfm60542	41.7	39	4.5700E-06	8.7250E-06	MAL13P1.67	methionyl-tRNA formyltransferase, putative	DNA-directed RNA polymerase (EC 2.7.7.6) beta'-2 chain - Plasmodium falciparum plastid Location=16848..179810.28
opfm60555	40.0	42	5.3500E-07	1.4373E-06	MAL13P1.255	hypothetical protein	(X65740) PfATPase3 [Plasmodium falciparum] 0.26
opfn0288	48.0	41	2.4100E-06	4.9238E-06	PF14_0222	hypothetical protein	(AF036170) homeobox-containing protein Wariai [Dictyostelium discoideum] Location=join(928913..928948,929644..931425)0.28
porf78	45.7	36	1.5400E-05	2.6194E-05	NULL	#N/A	
porf79	43.6	42	8.7200E-07	2.0998E-06	NULL	#N/A	
prps4	45.7	42	4.2700E-07	1.2181E-06	NULL	#N/A	
z_3_10	50.5	35	2.7300E-05	4.4741E-05	NULL	#N/A	
z_3_40	50.5	40	5.7000E-05	8.8961E-05	NULL	#N/A	
z_6_80	41.7	33	4.0300E-05	6.4358E-05	PFD0830w	bifunctional dihydrofolate reductase-thymidylate synthase	
z_6_90	41.7	42	1.4400E-06	3.1700E-06	PFD0830w	bifunctional dihydrofolate reductase-thymidylate synthase	