	Sense Seq.		P_3			$G_3/(G_3+C_3)$			$A_3/(A_3+T_3)$			Midpoint		Difference in PR2-bias		
Chromosome	#lead	#lagg	Lead	Lagg	Sig.	x_1	x_2	Sig.	y_1	y_2	Sig.	x_c	y_c	B_I	B_{II}	B_I %
B. hal	2689	869	0.404	0.402	ns	0.530	0.438	***	0.478	0.477	ns	0.484	0.477	0.092	0.028	76.9
B. sub	2705	924	0.422	0.429	*	0.504	0.428	***	0.473	0.480	**	0.466	0.476	0.076	0.041	**64.9**
B. bur	505	267	0.192	0.205	***	0.626	0.280	***	0.362	0.555	***	0.453	0.459	0.397	0.063	**86.3**
Buch	298	225	0.122	0.124	ns	0.473	0.380	***	0.442	0.485	***	0.426	0.464	0.102	0.082	**55.5**
C.cre	1861	1596	0.860	0.853	**	0.435	0.405	***	0.303	0.361	***	0.420	0.332	0.065	0.186	**26.0**
C. jej	914	583	0.172	0.181	***	0.542	0.309	***	0.415	0.453	***	0.425	0.434	0.236	0.100	**70.3**
C. mur	403	340	0.313	0.321	**	0.598	0.346	***	0.409	0.449	***	0.472	0.429	0.255	0.076	**77.0**
C. pne	532	436	0.323	0.342	***	0.505	0.360	***	0.421	0.454	***	0.433	0.437	0.149	0.092	**61.8**
C. pneAR39	468	385	0.323	0.341	***	0.506	0.364	***	0.423	0.454	***	0.435	0.439	0.145	0.089	**61.9**
C. pneJ138	541	441	0.323	0.342	***	0.503	0.360	***	0.420	0.454	***	0.431	0.437	0.147	0.093	**61.2**
C. tra	453	381	0.324	0.336	***	0.585	0.356	***	0.419	0.448	***	0.471	0.434	0.231	0.073	**76.1**

D. rad1	1261	1162	0.804	0.798	ns	0.444	0.449	ns	0.428	0.463	***	0.447	0.446	0.035	0.076	31.6
D. rad2	207	139	0.818	0.832	ns	0.440	0.448	ns	0.435	0.440	ns	0.444	0.438	0.009	0.084	10.1
E. col	2146	1768	0.533	0.535	ns	0.503	0.453	***	0.397	0.410	***	0.478	0.403	0.052	0.099	**34.3**
E.colEDL	2707	1927	0.526	0.527	ns	0.512	0.454	***	0.398	0.415	***	0.483	0.406	0.060	0.095	**38.9**
E.colRIMD	2733	1890	0.527	0.528	ns	0.512	0.453	***	0.399	0.415	***	.483	.407	.061	.095	**39.2**
H. inf	809	696	0.257	0.275	***	0.484	0.403	***	0.451	0.473	***	0.444	0.462	0.084	0.068	**55.3**
H. pyl	805	587	0.404	0.403	ns	0.478	0.419	***	0.439	0.441	ns	0.449	0.440	0.060	0.079	42.9
H. pylJ99	782	590	0.413	0.408	ns	0.479	0.415	***	0.441	0.441	ns	0.447	0.441	0.064	0.079	44.6
L.lac	1628	391	0.226	0.242	***	0.468	0.343	***	0.452	0.425	***	0.406	0.439	0.128	0.113	**53.1**
M.lep	1473	958	0.640	0.635	ns	0.487	0.418	***	0.384	0.505	***	0.453	0.445	0.139	0.073	**65.6**
M. tub	2153	1535	0.786	0.788	ns	0.467	0.423	***	0.412	0.476	***	0.445	0.444	0.078	0.079	**49.9**
M.tubCDC	2153	1499	0.782	0.784	ns	0.470	0.424	***	0.412	0.476	***	0.447	0.444	0.079	0.077	**50.5**
M. gen	358	93	0.225	0.205	**	0.429	0.419	ns	0.430	0.439	ns	0.424	0.435	0.014	0.100	11.9
M. pne	520	139	0.404	0.401	ns	0.427	0.410	**	0.435	0.442	ns	0.419	0.438	0.019	0.102	15.6
M.pul	459	242	0.138	0.143	*	0.339	0.330	ns	0.475	0.468	*	0.335	0.472	0.011	0.168	6.4

N. menA	880	873	0.596	0.601	ns	0.423	0.348	***	0.466	0.522	***	0.385	0.494	0.094	0.115	**44.9**
N. menB	910	716	0.578	0.610	***	0.434	0.327	***	0.454	0.536	***	0.381	0.495	0.135	0.120	**53.0**
P.mul	1111	795	0.318	0.330	***	0.515	0.395	***	0.456	0.470	***	0.455	0.463	0.121	0.058	**67.5**
P. aer	2920	2335	0.861	0.881	***	0.433	0.376	***	0.408	0.539	***	0.404	0.474	0.143	0.099	**59.0**
P. aby	965	798	0.512	0.511	ns	0.535	0.507	***	0.451	0.515	***	0.521	0.483	0.070	0.027	**72.4**
P. hor	1098	875	0.429	0.428	ns	0.525	0.469	***	0.444	0.490	***	0.497	0.467	0.073	0.033	**68.7**
R. pro	476	297	0.165	0.171	**	0.572	0.407	***	0.425	0.455	***	0.490	0.440	0.168	0.061	**73.4**
S.aur	1760	568	0.201	0.220	***	0.494	0.341	***	0.486	0.469	***	0.417	0.477	0.154	0.086	**64.3**
S.aurN315	1744	553	0.200	0.217	***	0.496	0.335	***	0.485	0.470	***	0.415	0.477	0.162	0.087	**64.9**
S.pyo	1196	314	0.294	0.308	***	0.461	0.329	***	0.430	0.424	ns	0.395	0.427	0.132	0.128	50.8
T. aci	763	625	0.557	0.560	ns	0.476	0.453	***	0.446	0.455	**	0.465	0.451	0.025	0.061	**28.8**
T. mar	905	781	0.524	0.523	ns	0.480	0.443	***	0.499	0.531	***	0.461	0.515	0.049	0.041	**54.4**
T. pal	596	321	0.527	0.558	***	0.610	0.435	***	0.343	0.439	***	0.522	0.391	0.200	0.112	**64.2**
U. ure	384	176	0.109	0.119	***	0.426	0.362	***	0.450	0.450	ns	0.394	0.450	0.064	0.117	35.3
V. cho1	1418	947	0.464	0.481	***	0.505	0.414	***	0.413	0.439	***	0.460	0.426	0.095	0.084	**52.9**

V. cho2	516	354	0.443	0.478	***	0.513	0.419	***	0.415	0.441	***	0.466	0.428	0.098	0.080	**55.1**
X. fas	1190	851	0.541	0.568	***	0.549	0.351	***	0.332	0.528	***	0.450	0.430	0.279	0.086	**76.4**

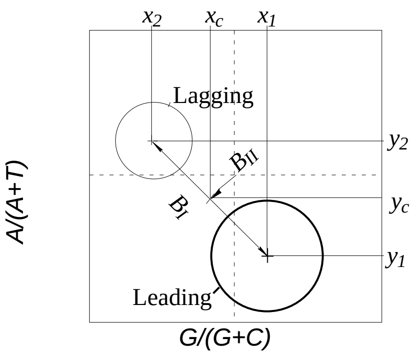
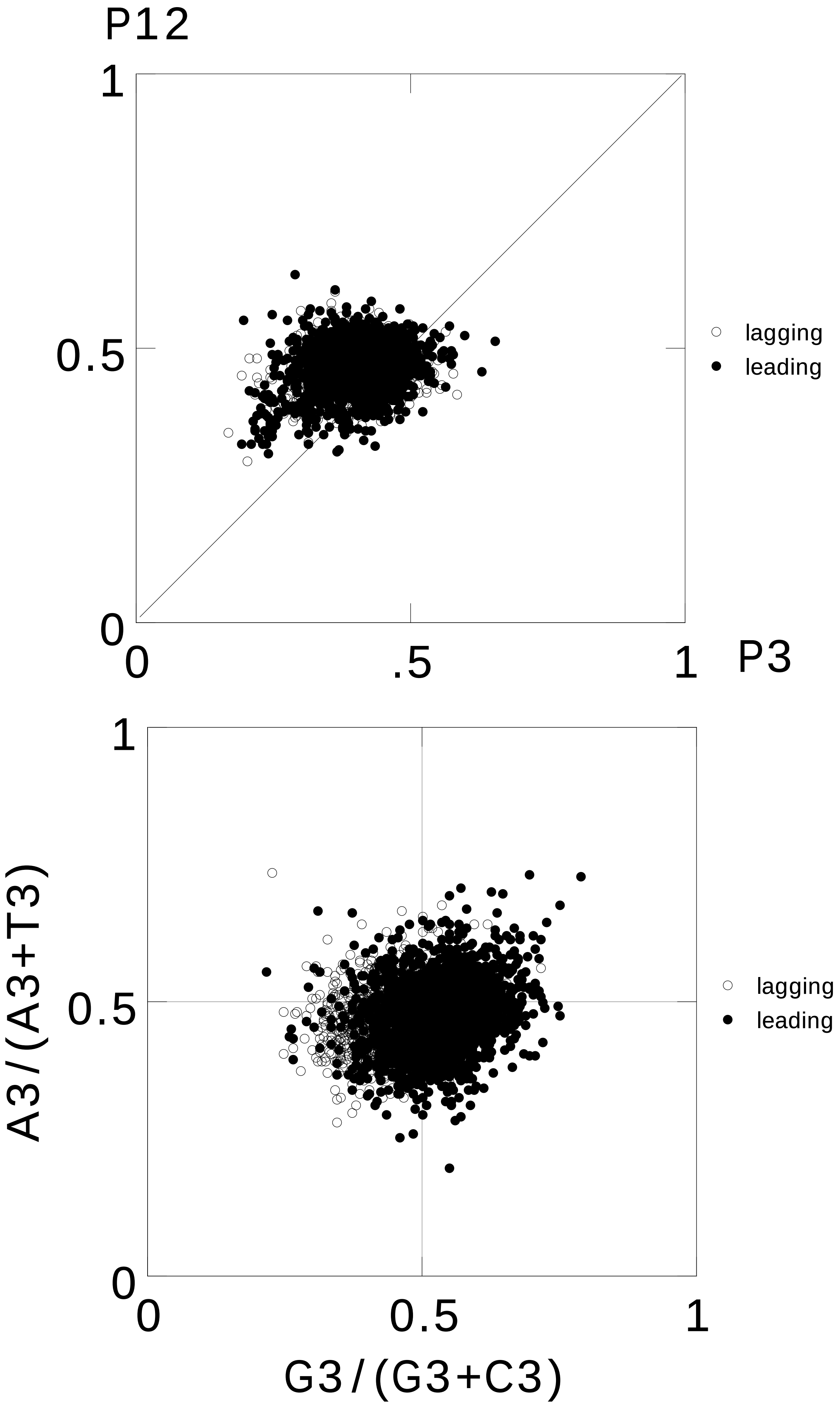
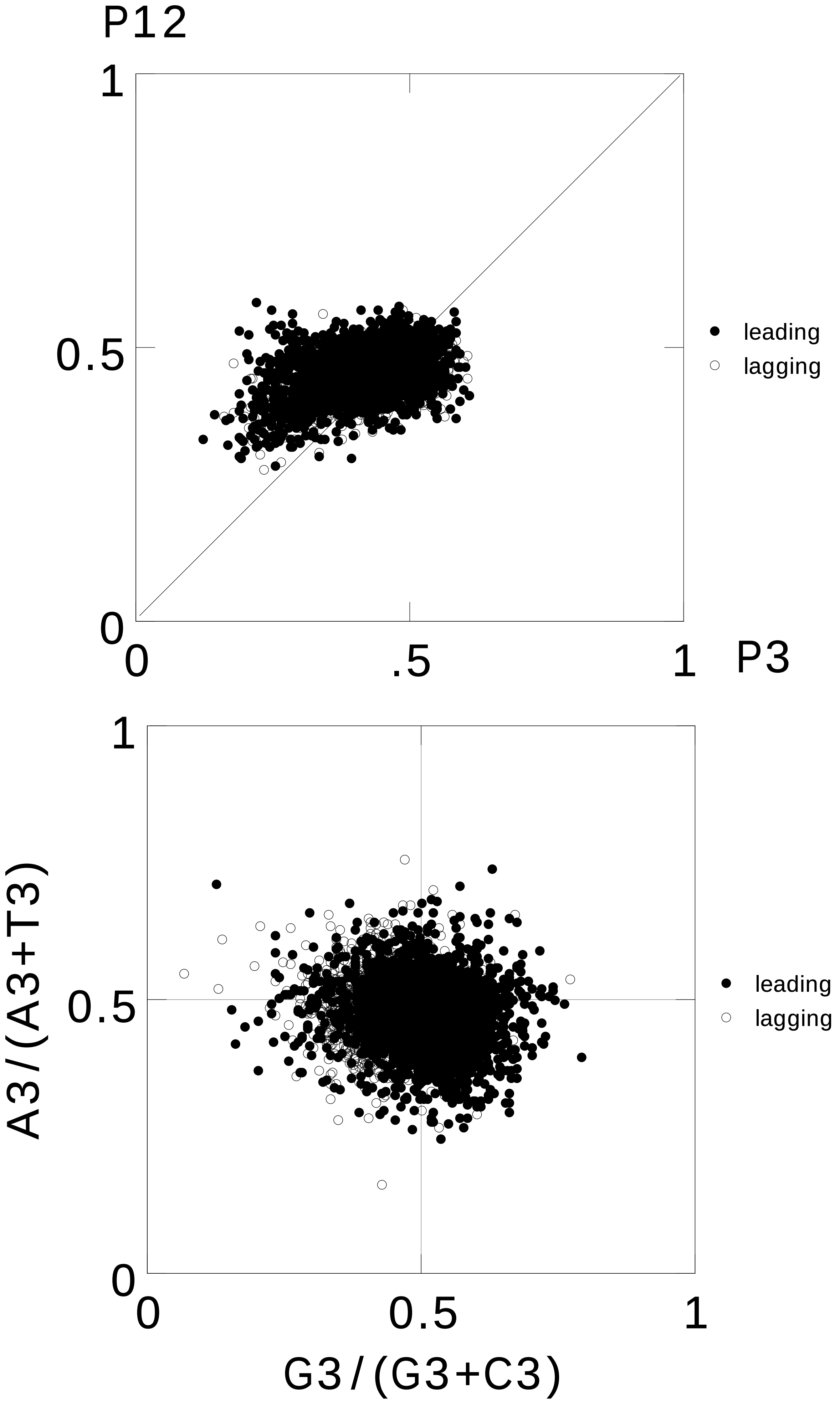


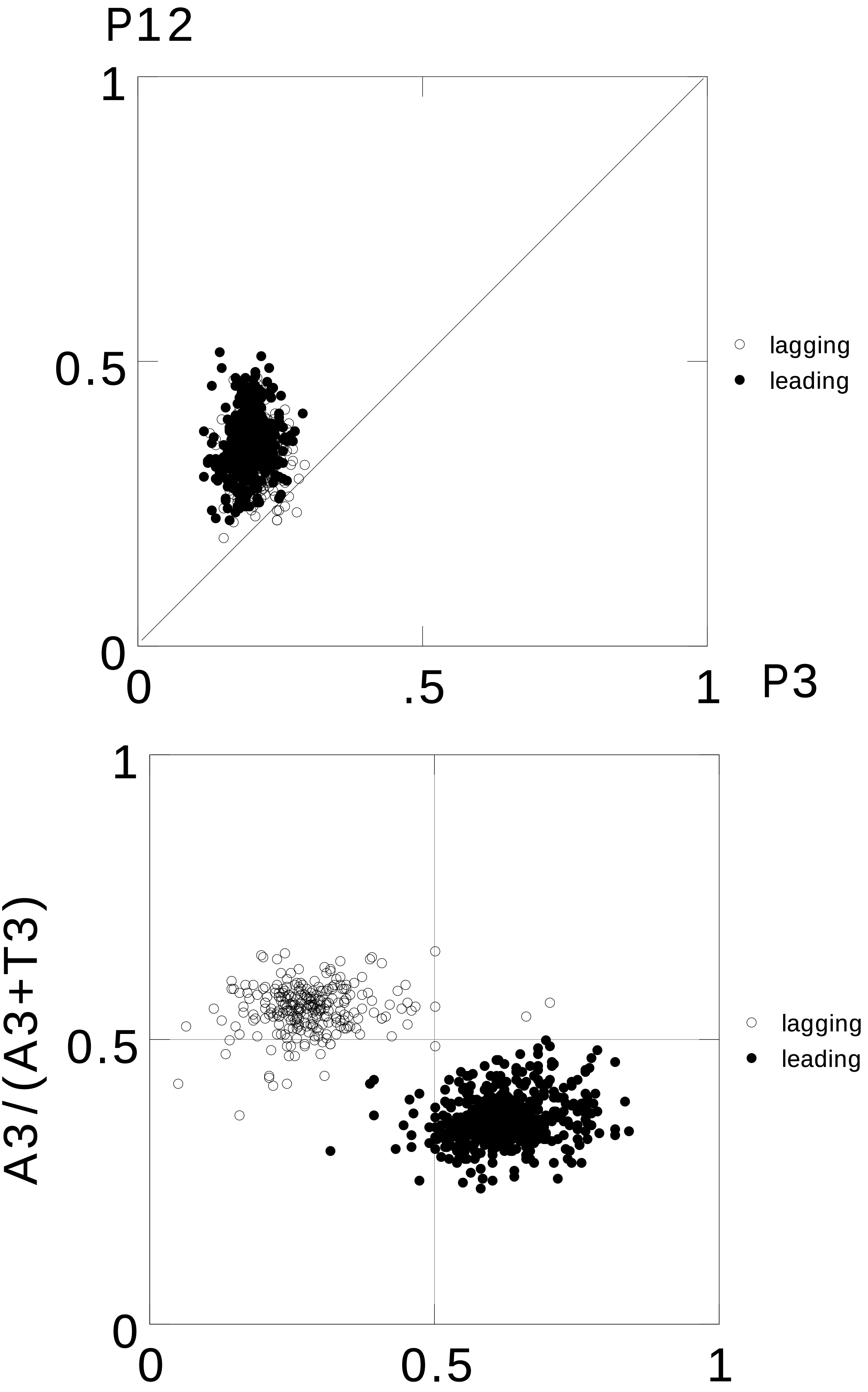
Table 2. Base composition in third codon positions between the leading and the lagging strands. Indices are defined in the material and method section. #lead and #lag are the number of genes in the leading and the lagging strand. The significance level (Sig.) for a difference between the two groups are: ns (not significant, $p \geq 0.05$); * ($0.01 \leq p < 0.05$); ** ($0.001 \leq p < 0.01$); *** ($p < 0.001$). The contribution in percent of replication-associated effects to PR2 deviations (B_I %) is given in **bold** when both differences $x_1 - x_2$ and $y_1 - y_2$ are highly significant ($p < 0.01$). When a difference is significant between the two groups a red color outlines the highest value and a blue color the lowest value.



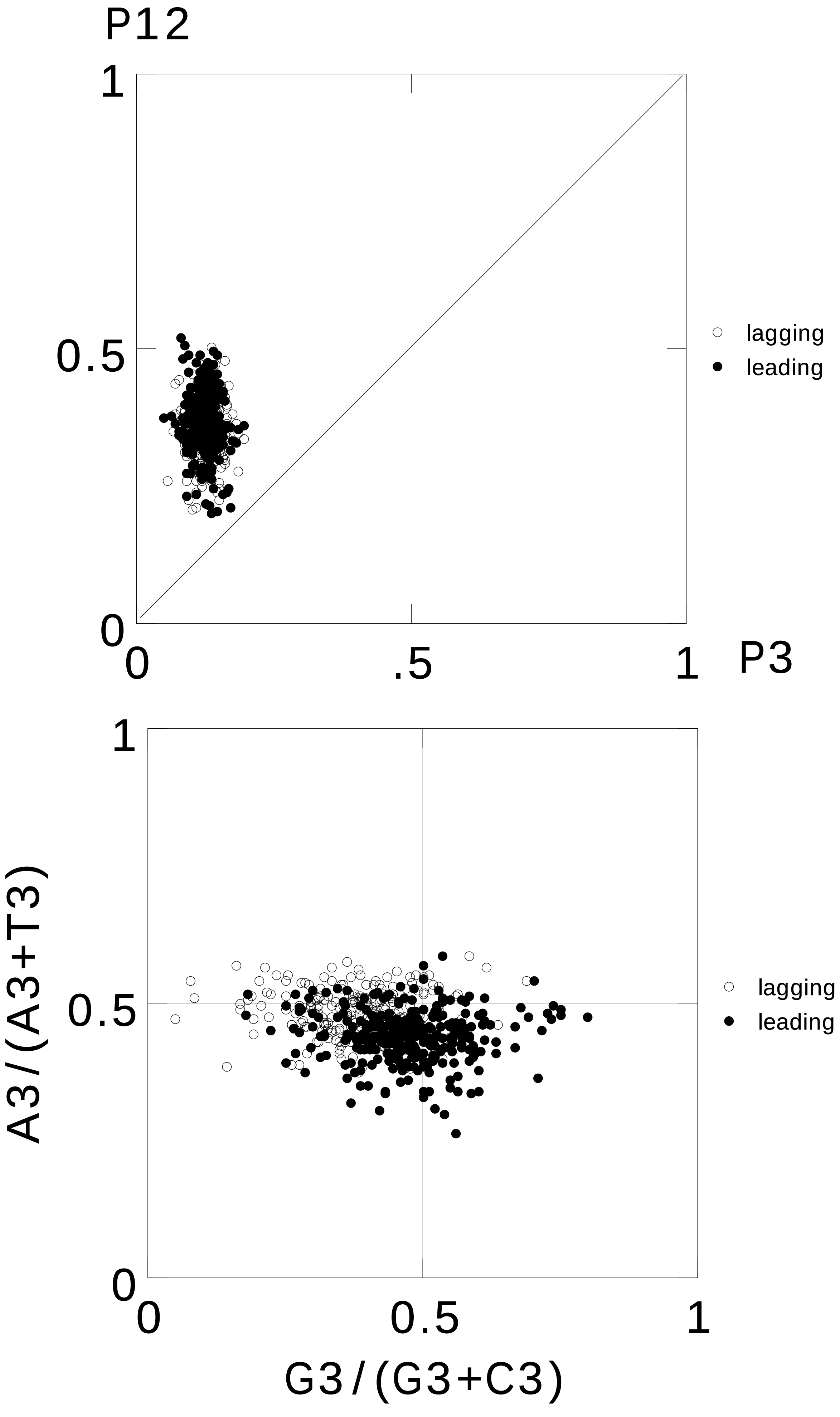
Bacillus halodurans



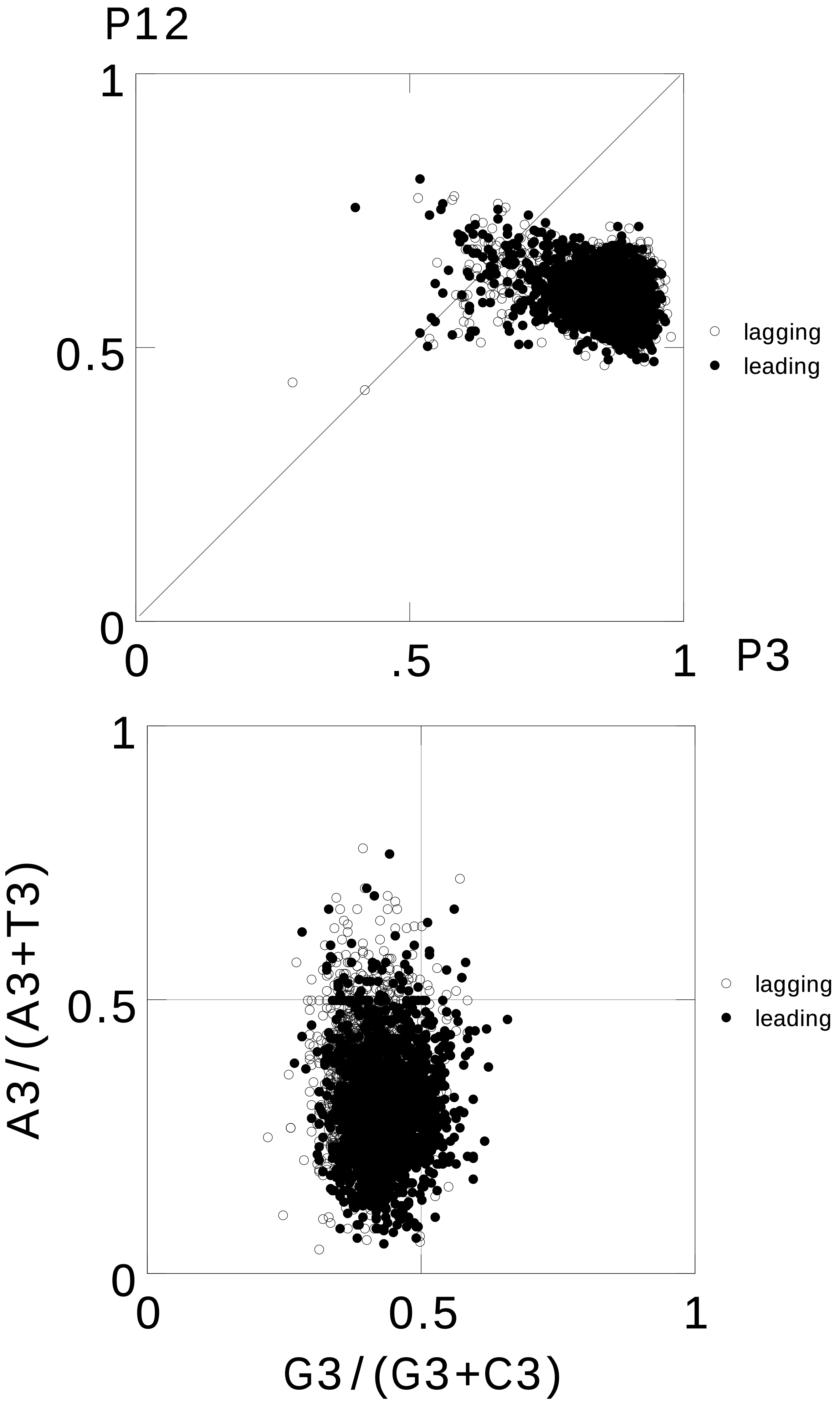
Bacillus subtilis



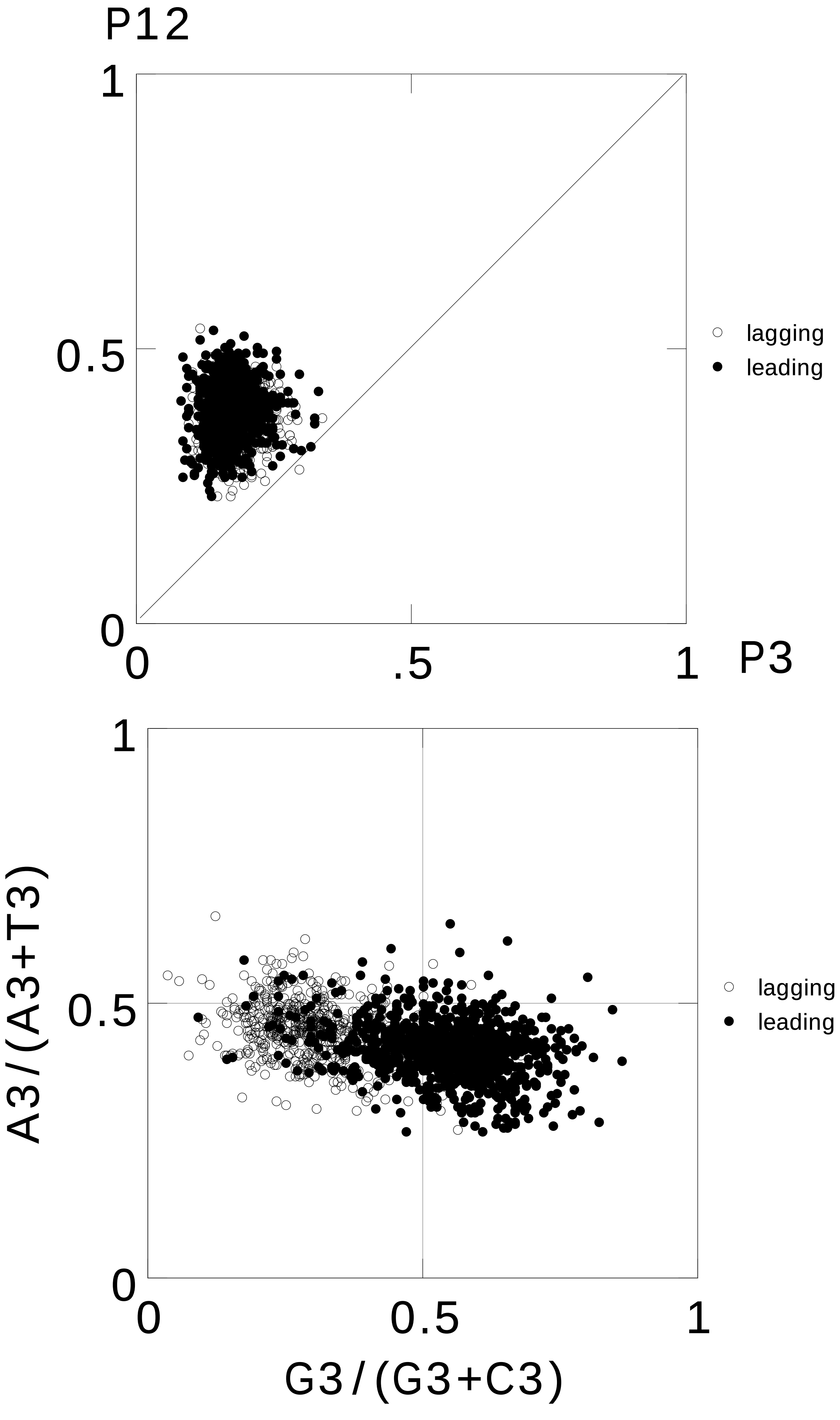
Borrelia burgdorferi


P12
1
0.5
0
0
.5
1
P3
○ lagging
● leading
1
0.5
0
0
0.5
1
A3/(A3+T3)
G3/(G3+C3)
○ lagging
● leading

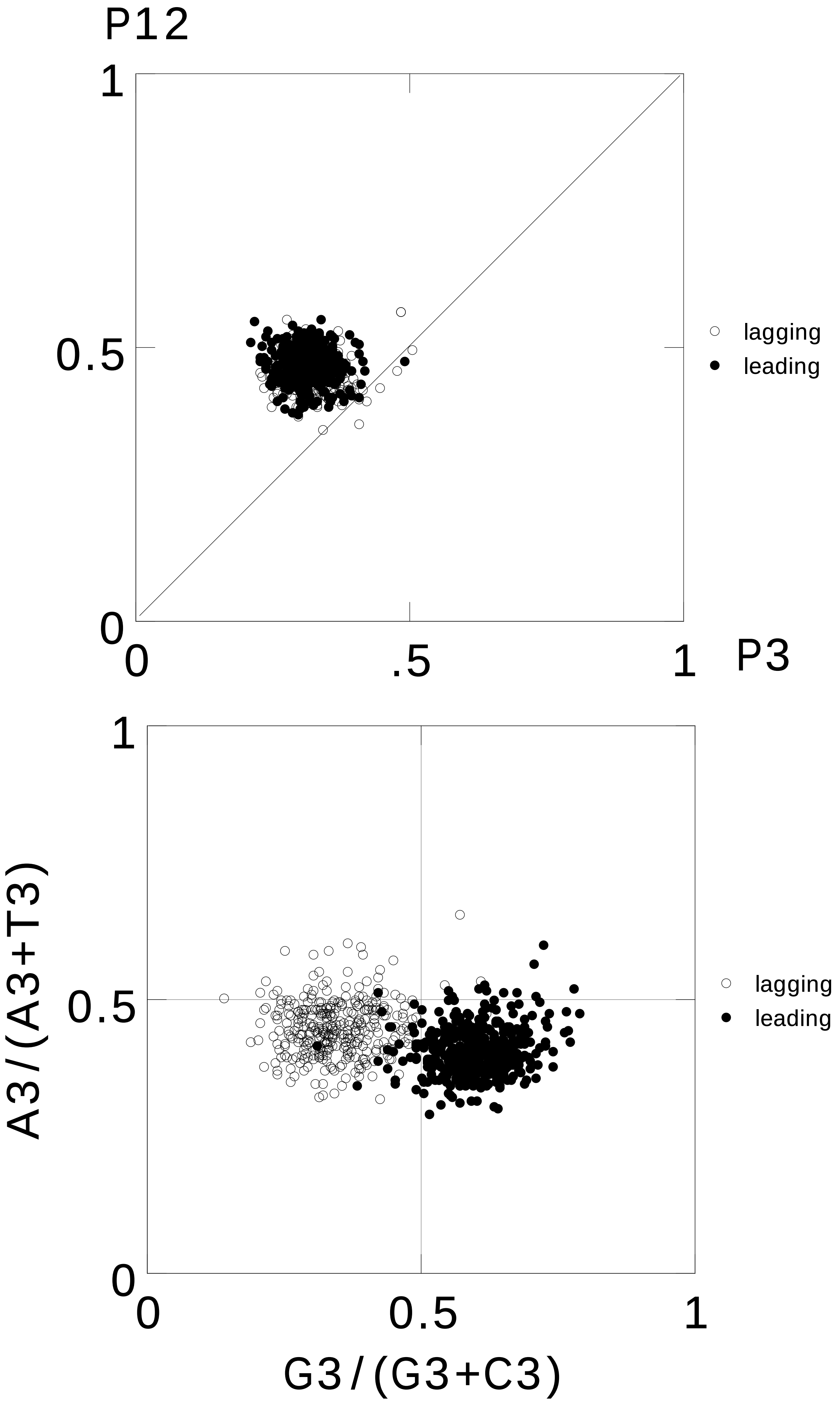
Buchnera sp.



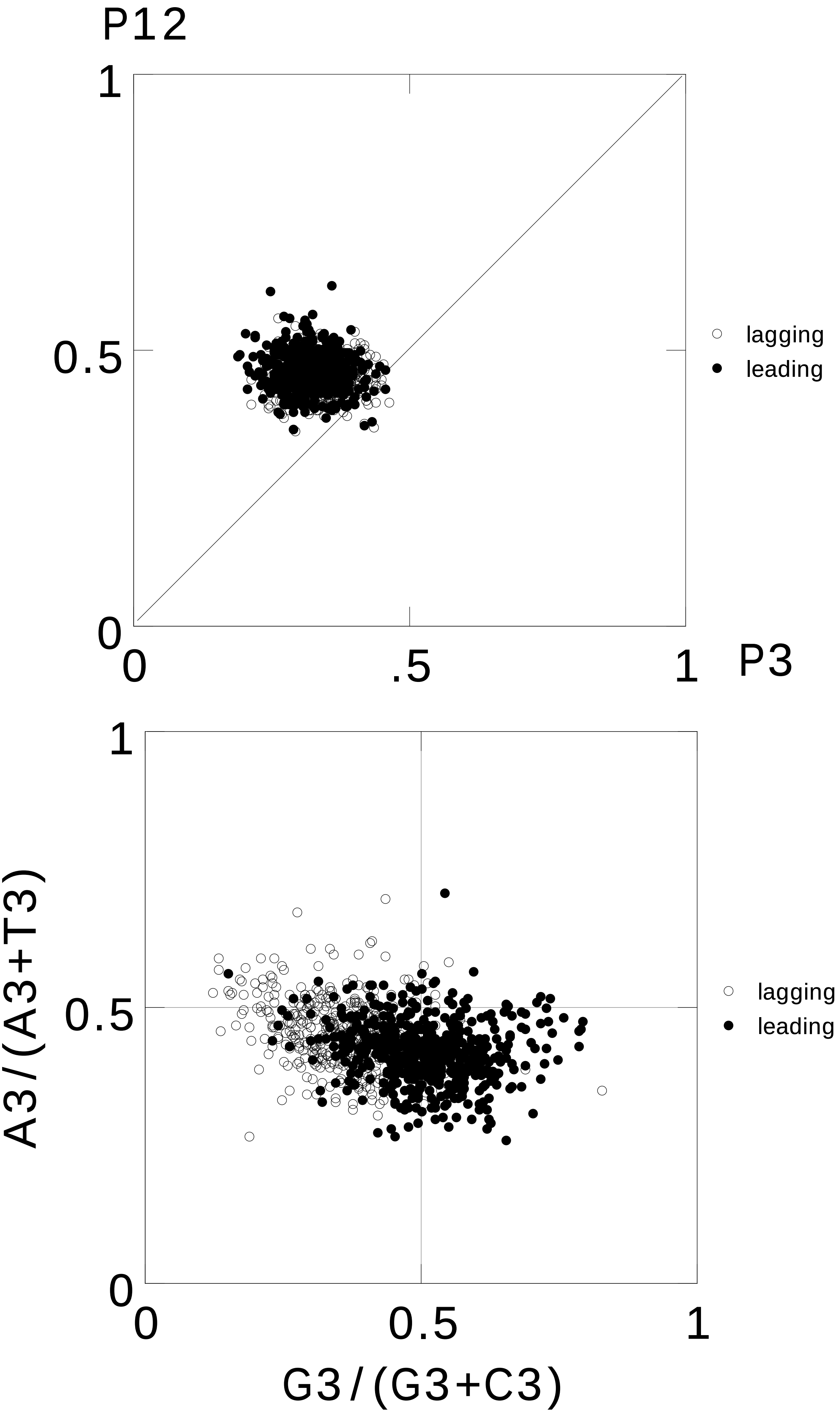
Caulobacter crescentus



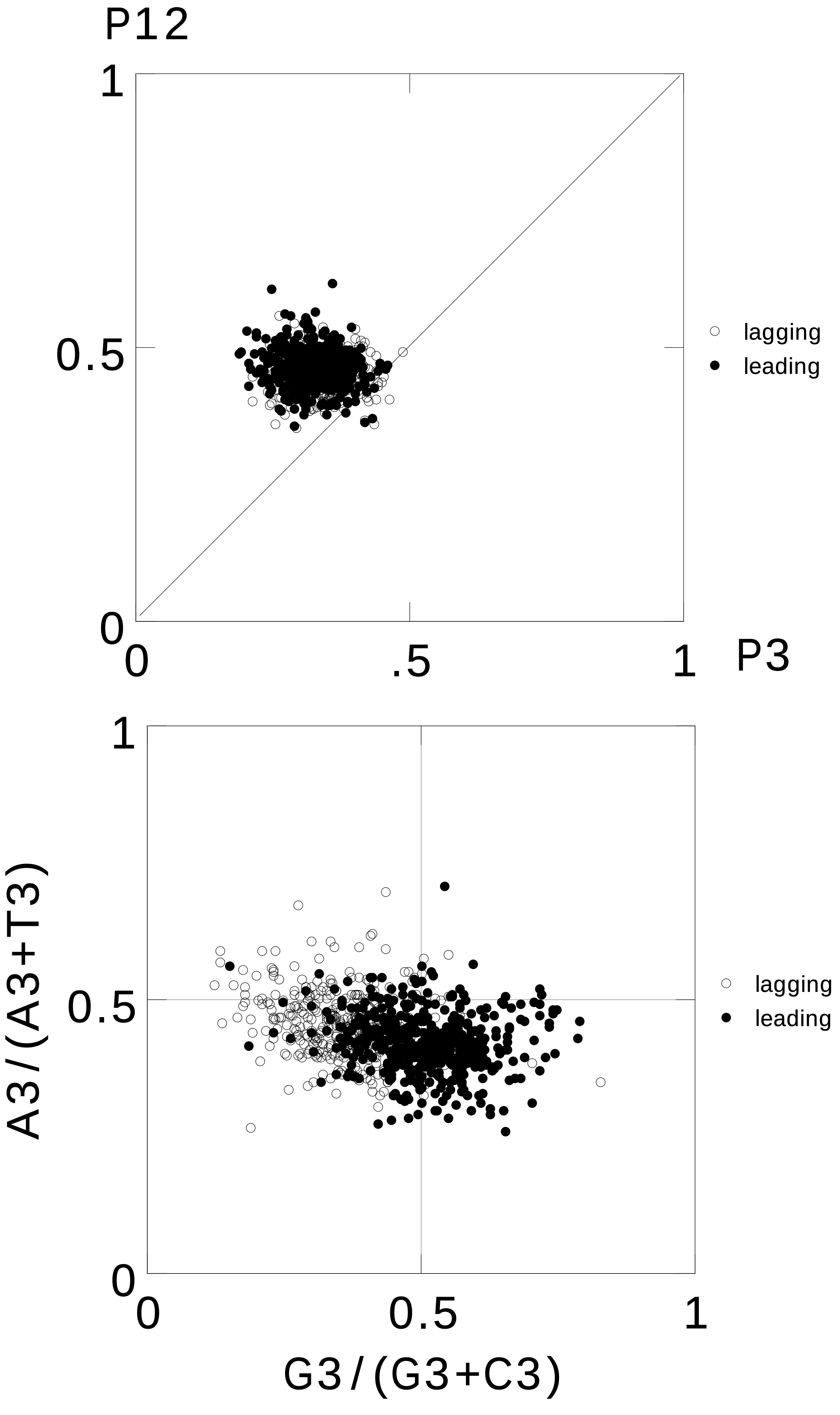
Campylobacter jejuni



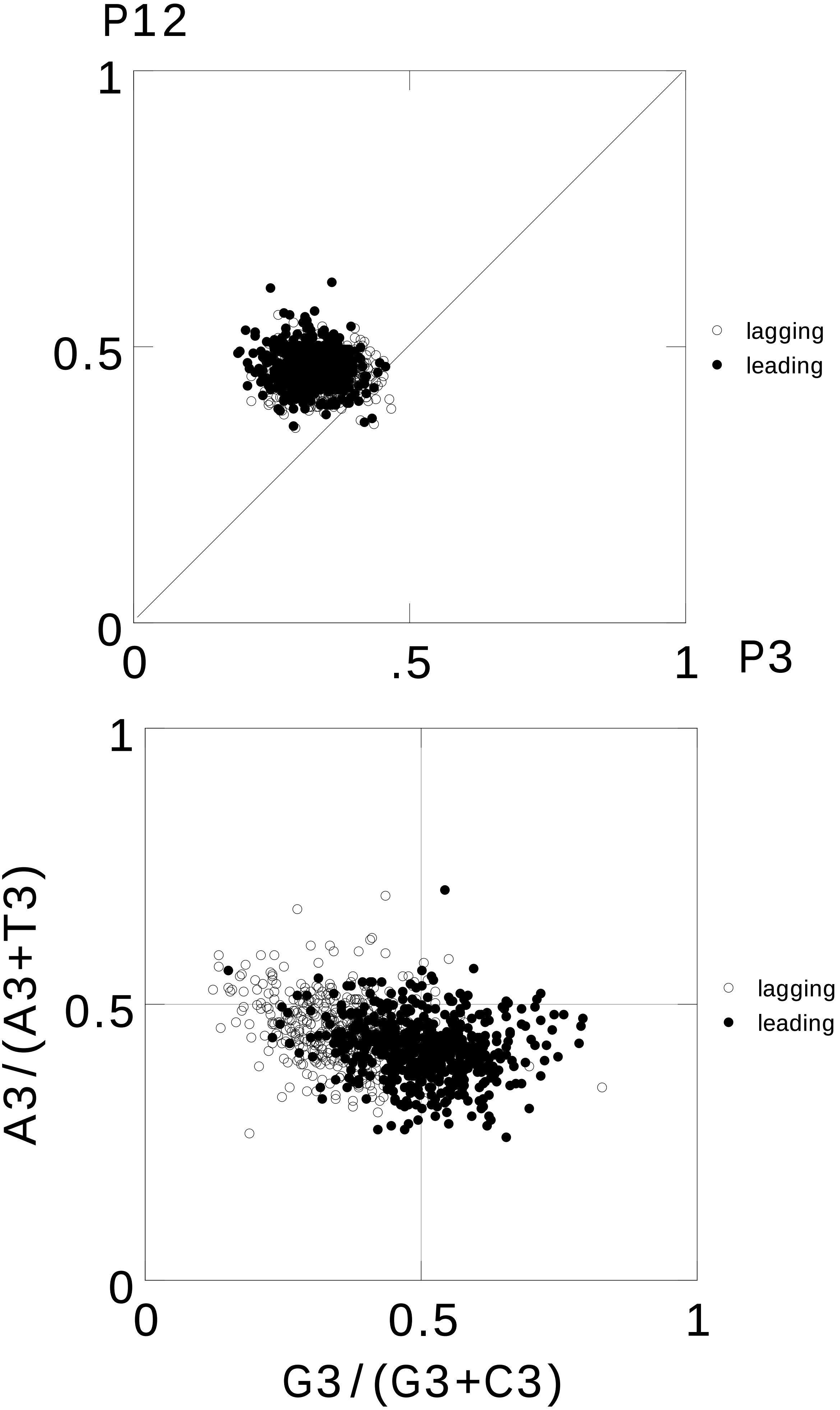
Chlamydia muridarum



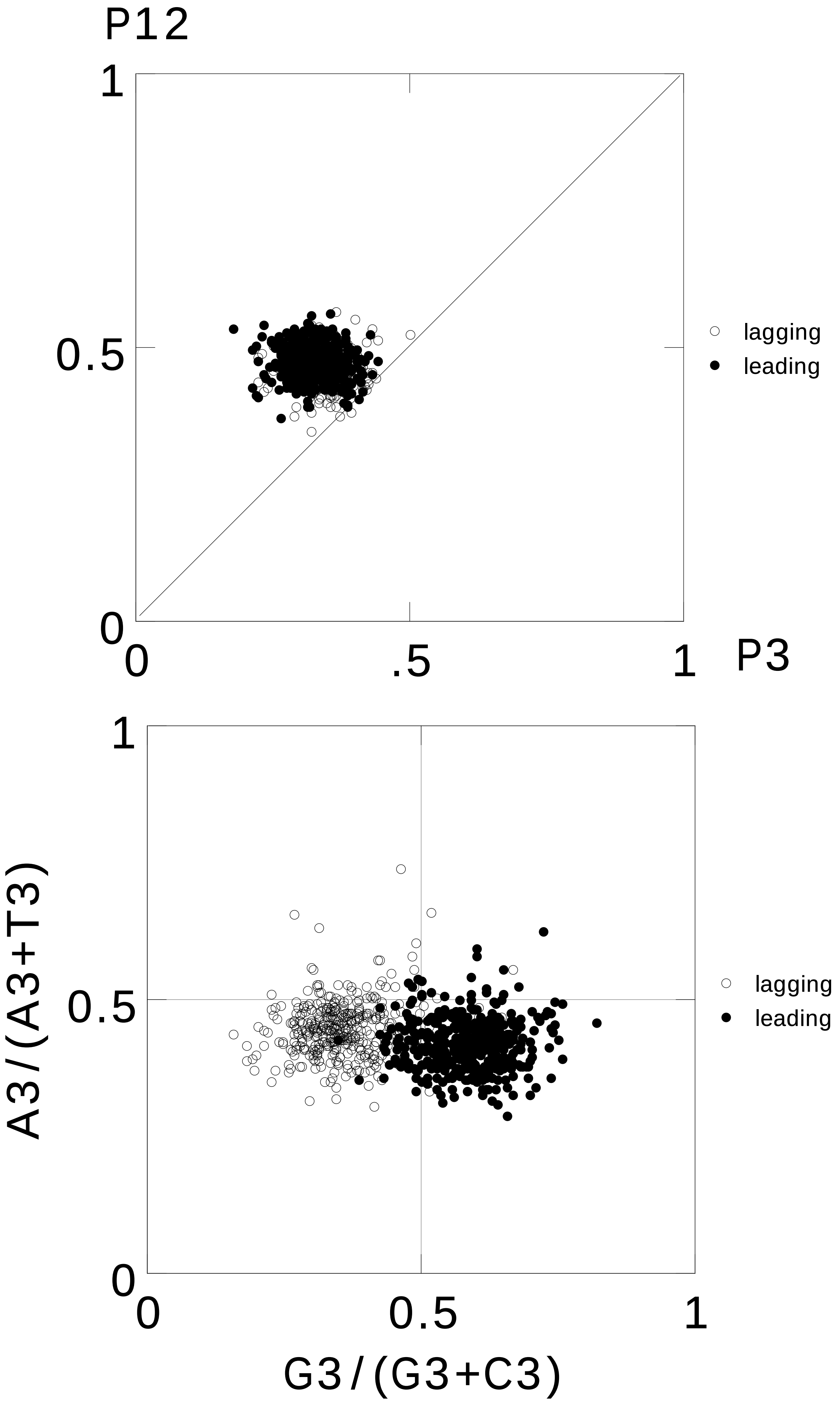
Chlamydophila pneumoniae CWL029



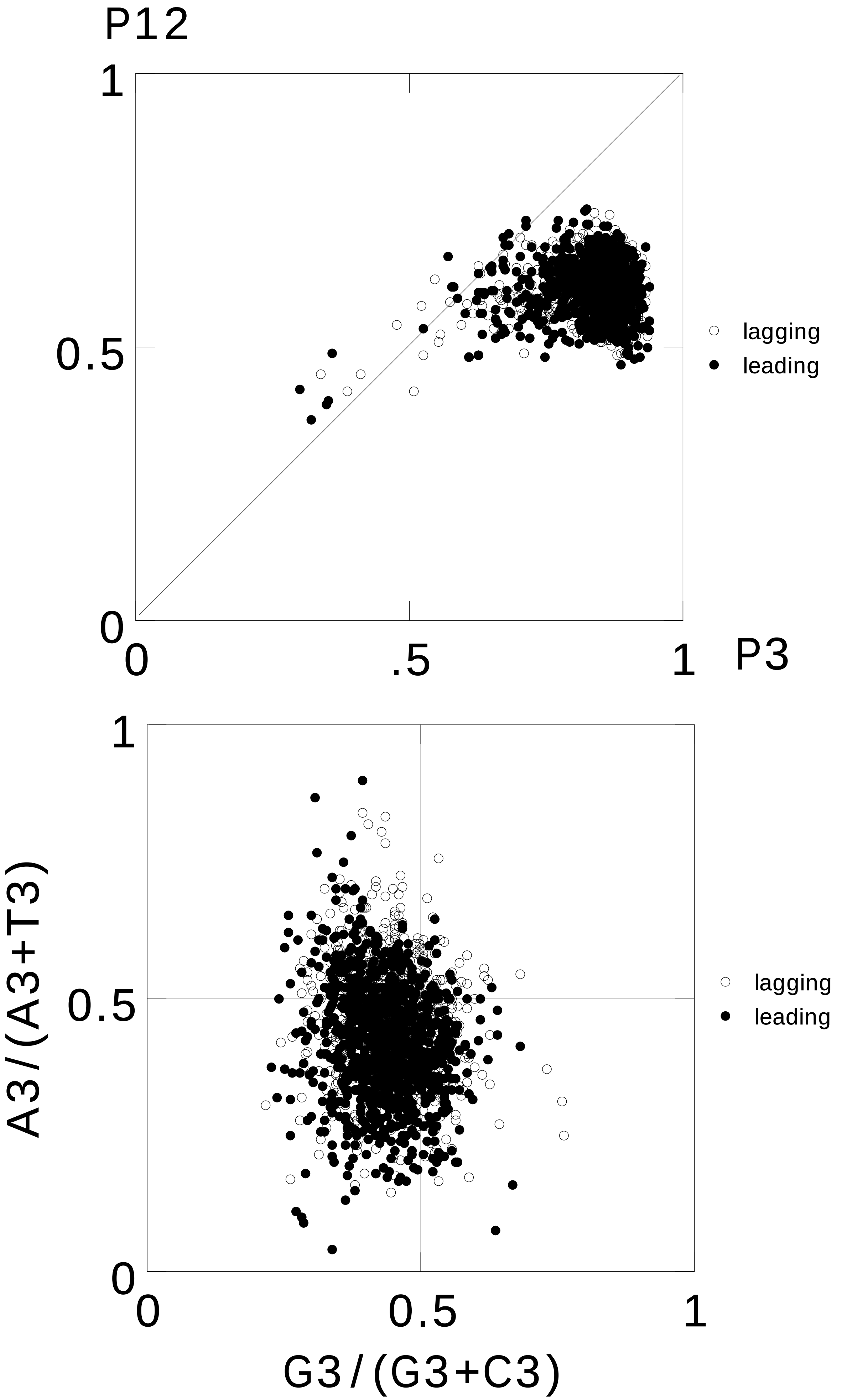
Chlamydophila pneumoniae AR39



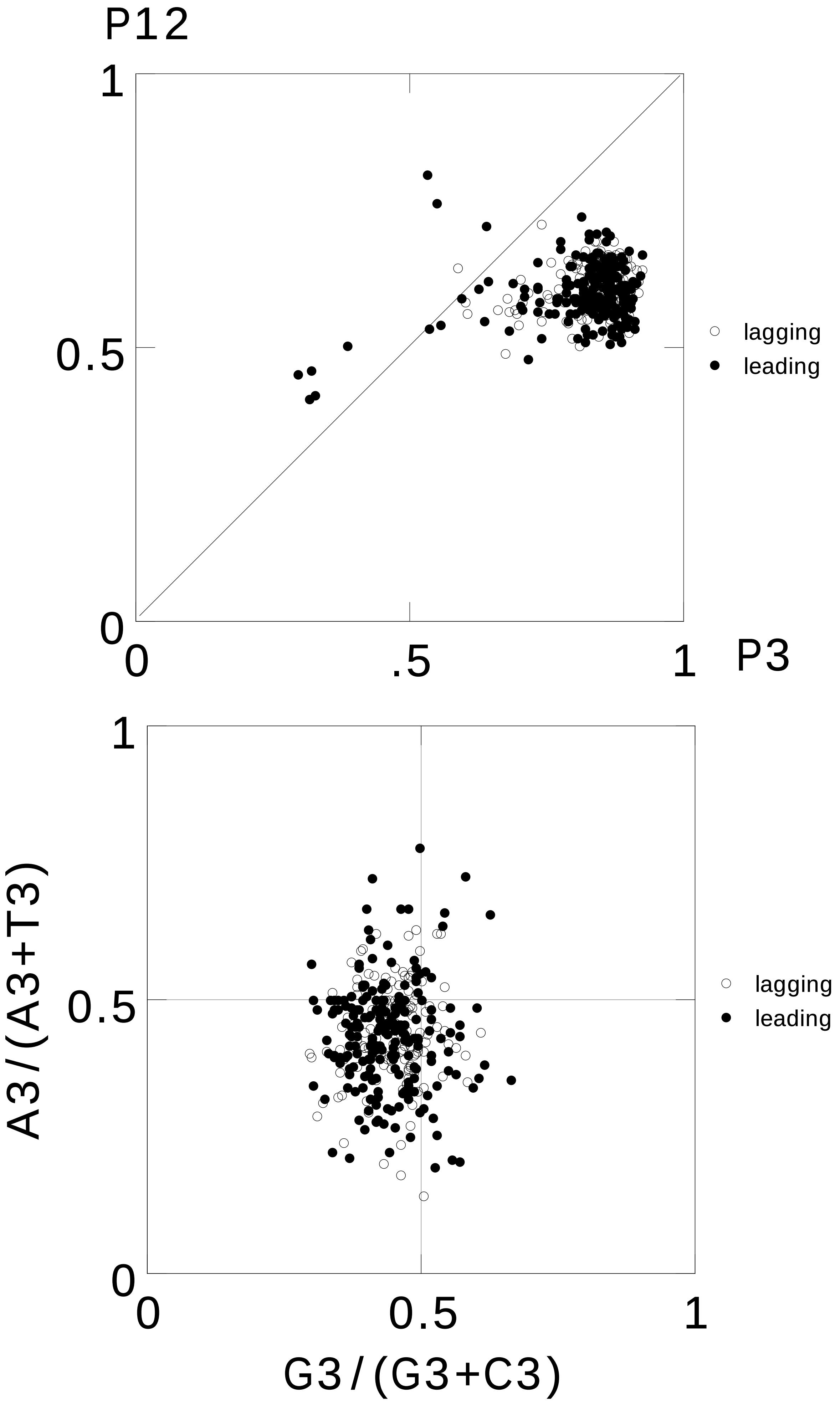
Chlamydophila pneumoniae J138



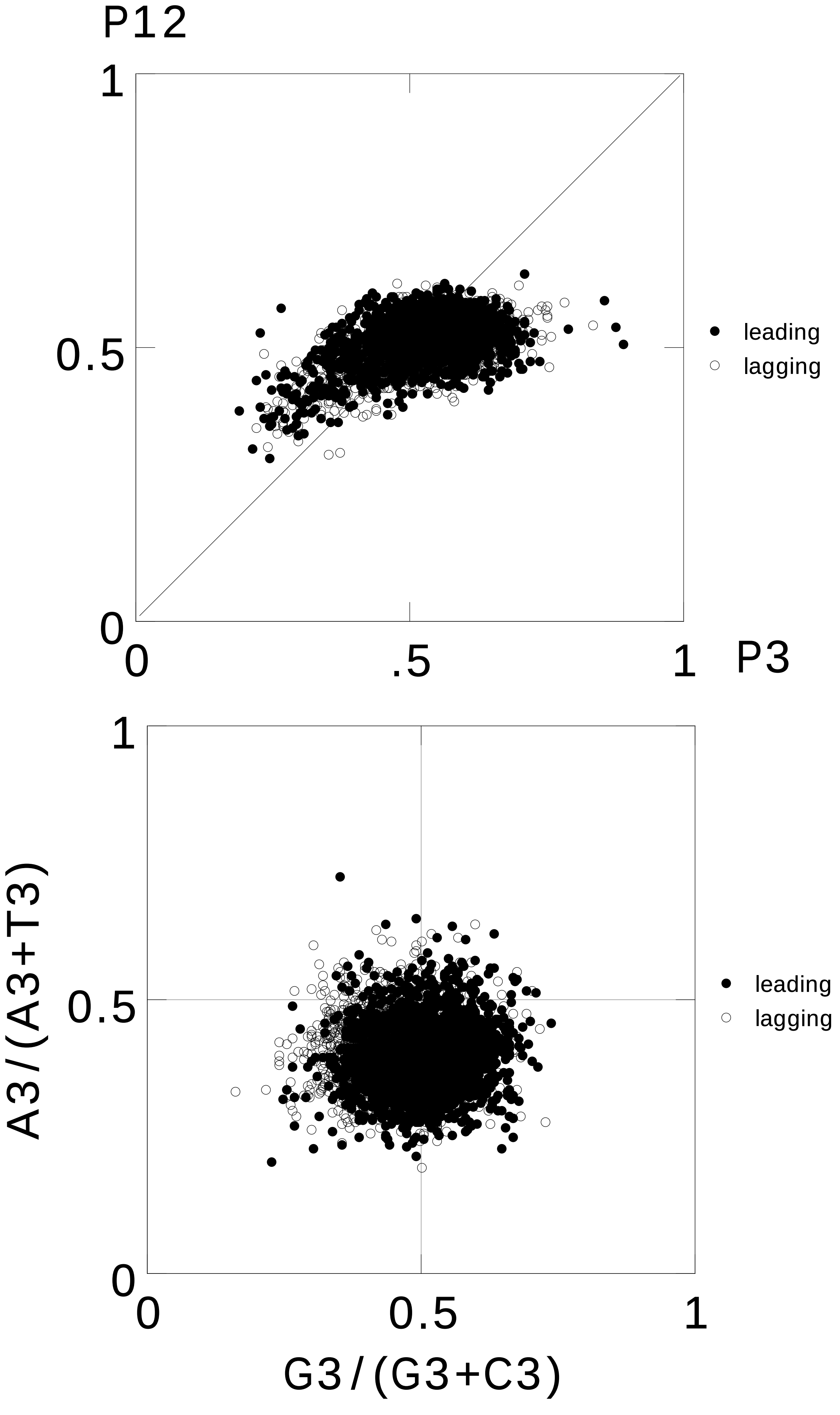
Chlamydia trachomatis



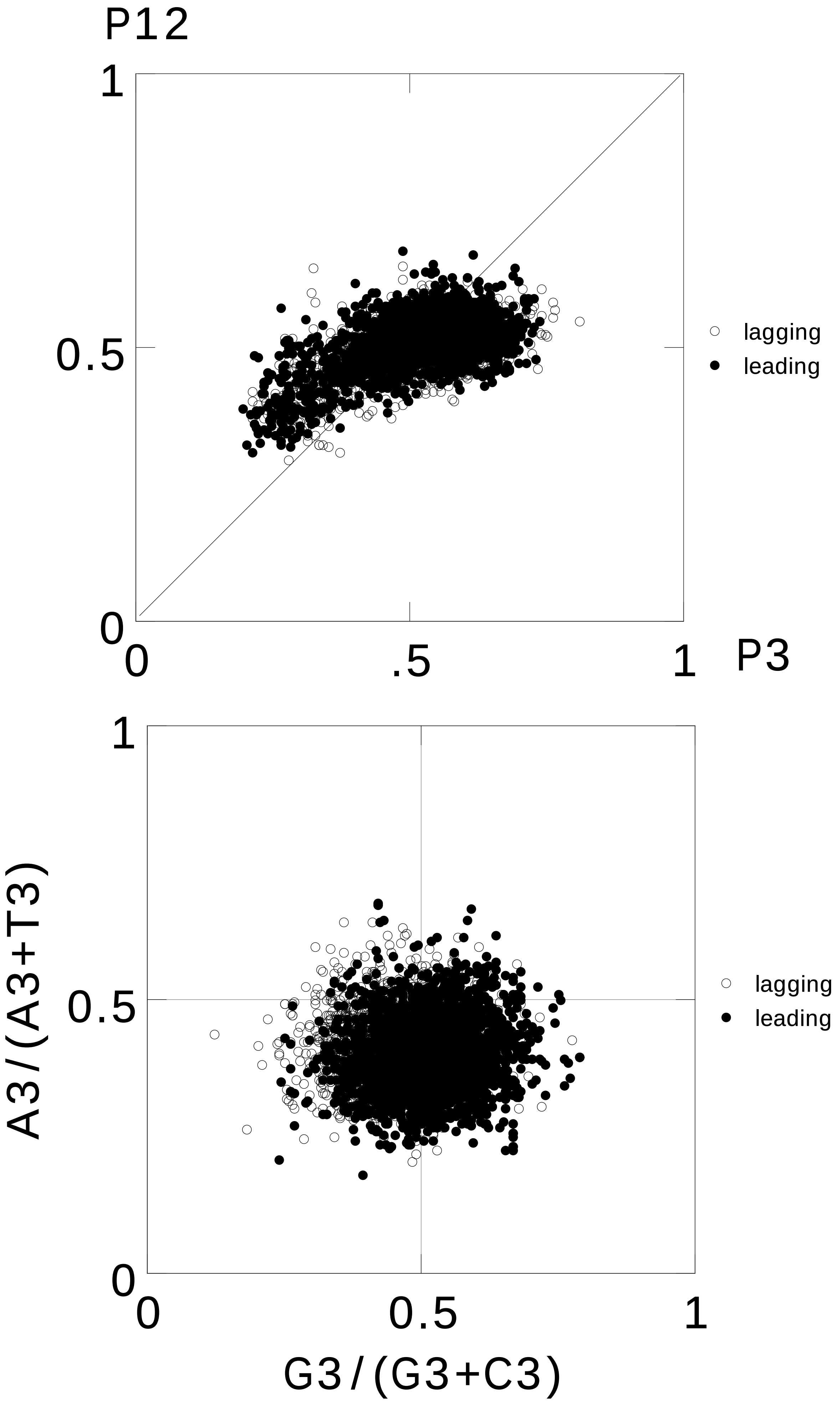
Deinococcus radiodurans chromosome 1



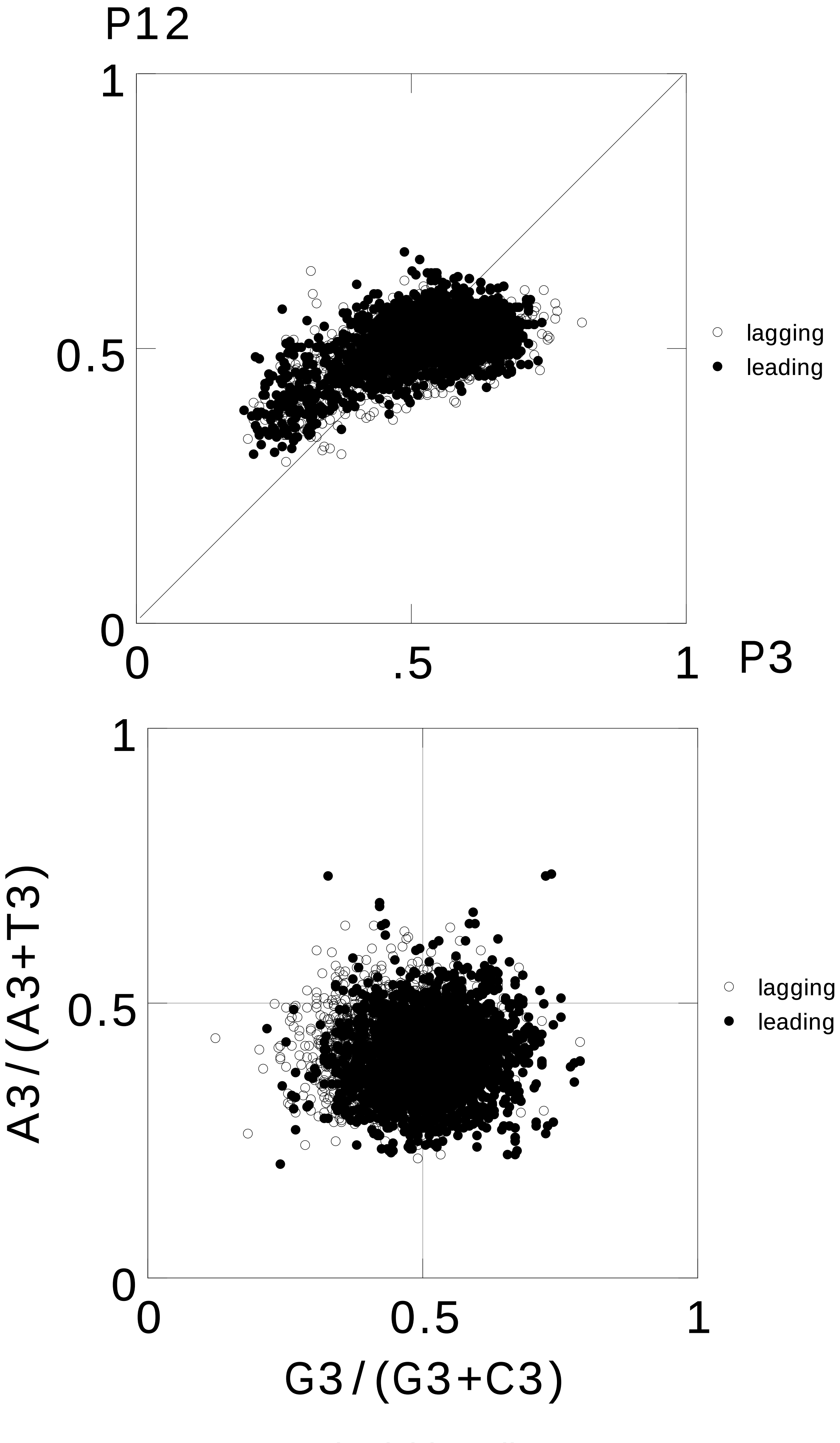
Deinococcus radiodurans chromosome 2



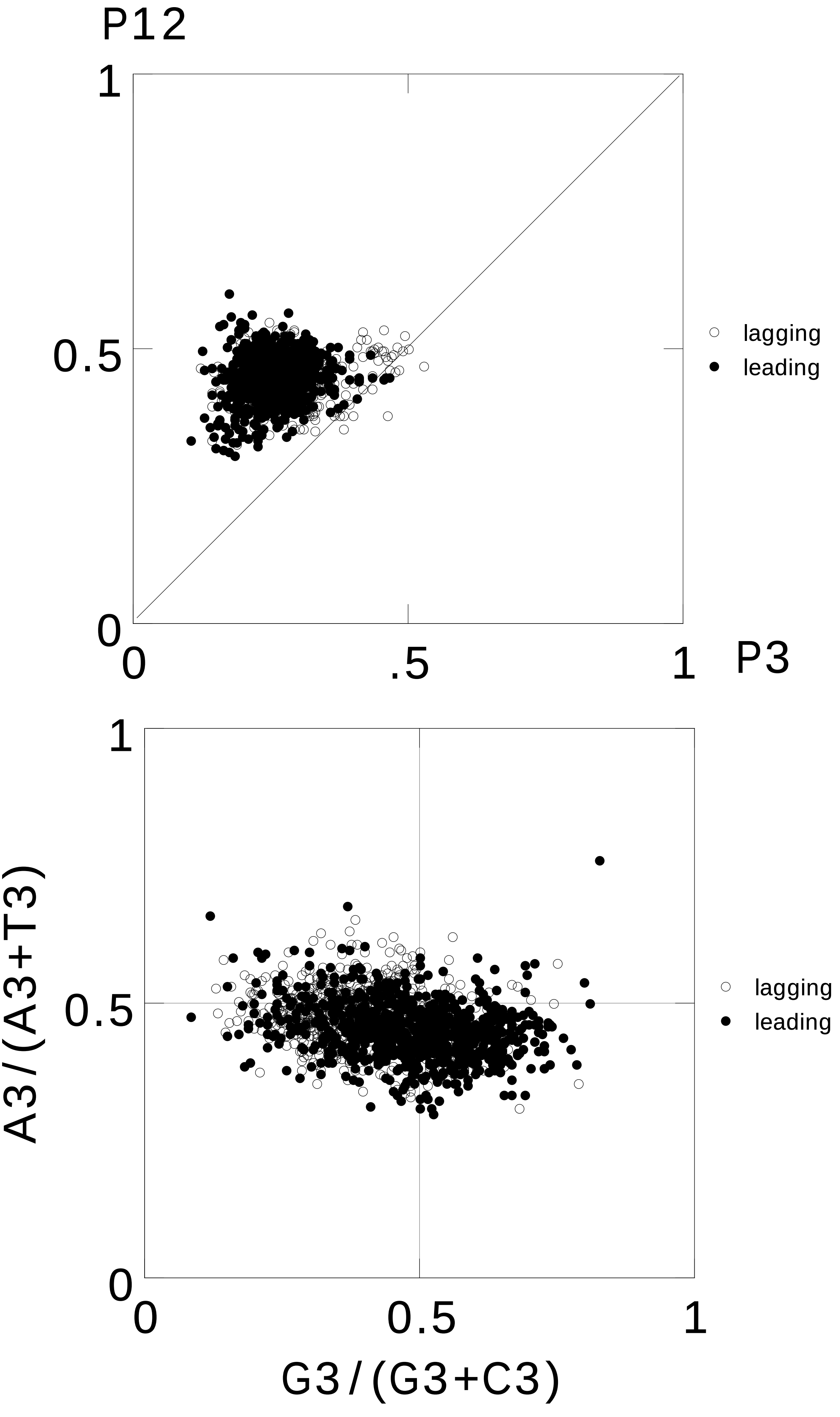
Escherichia coli K-12



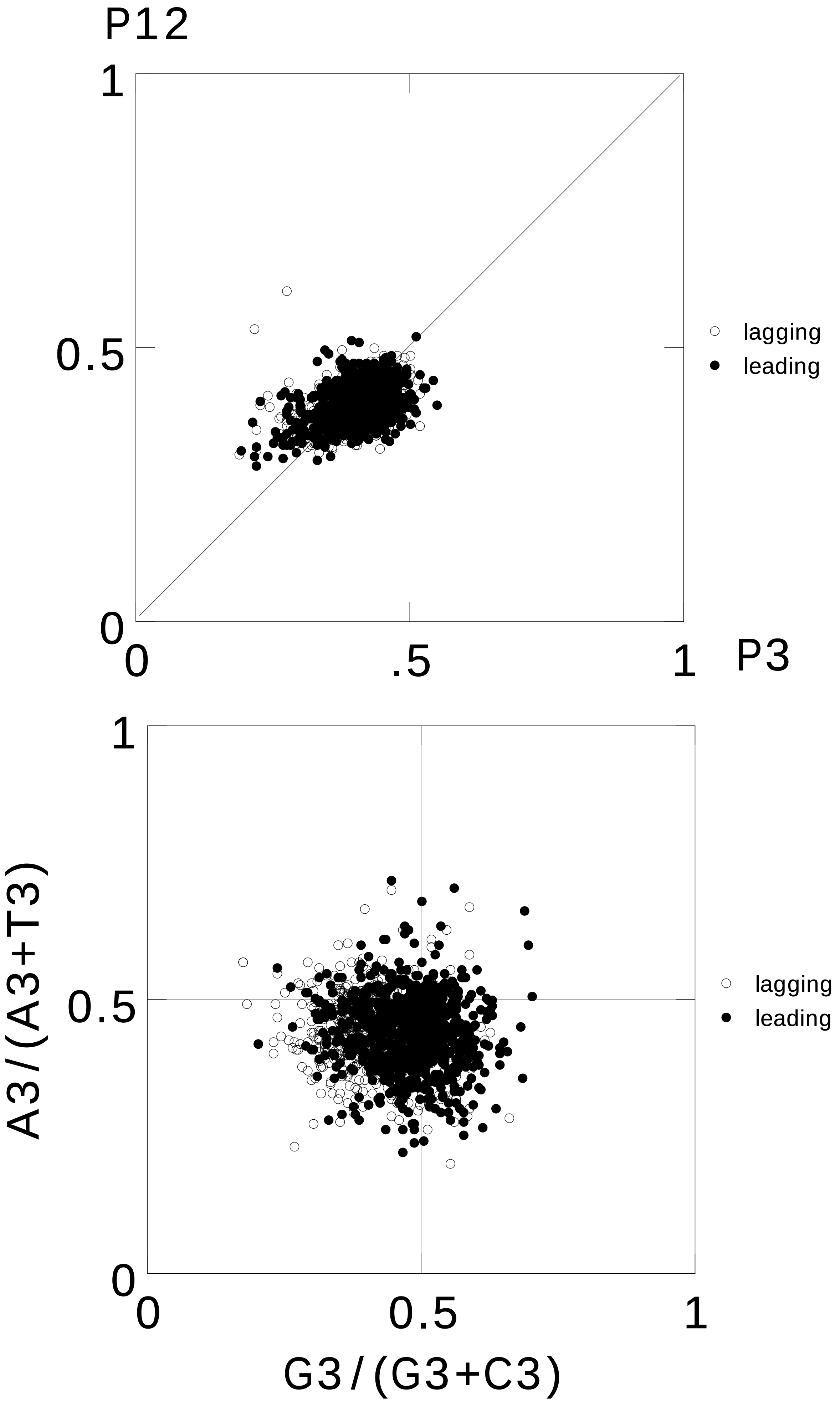
Escherichia coli EDL933



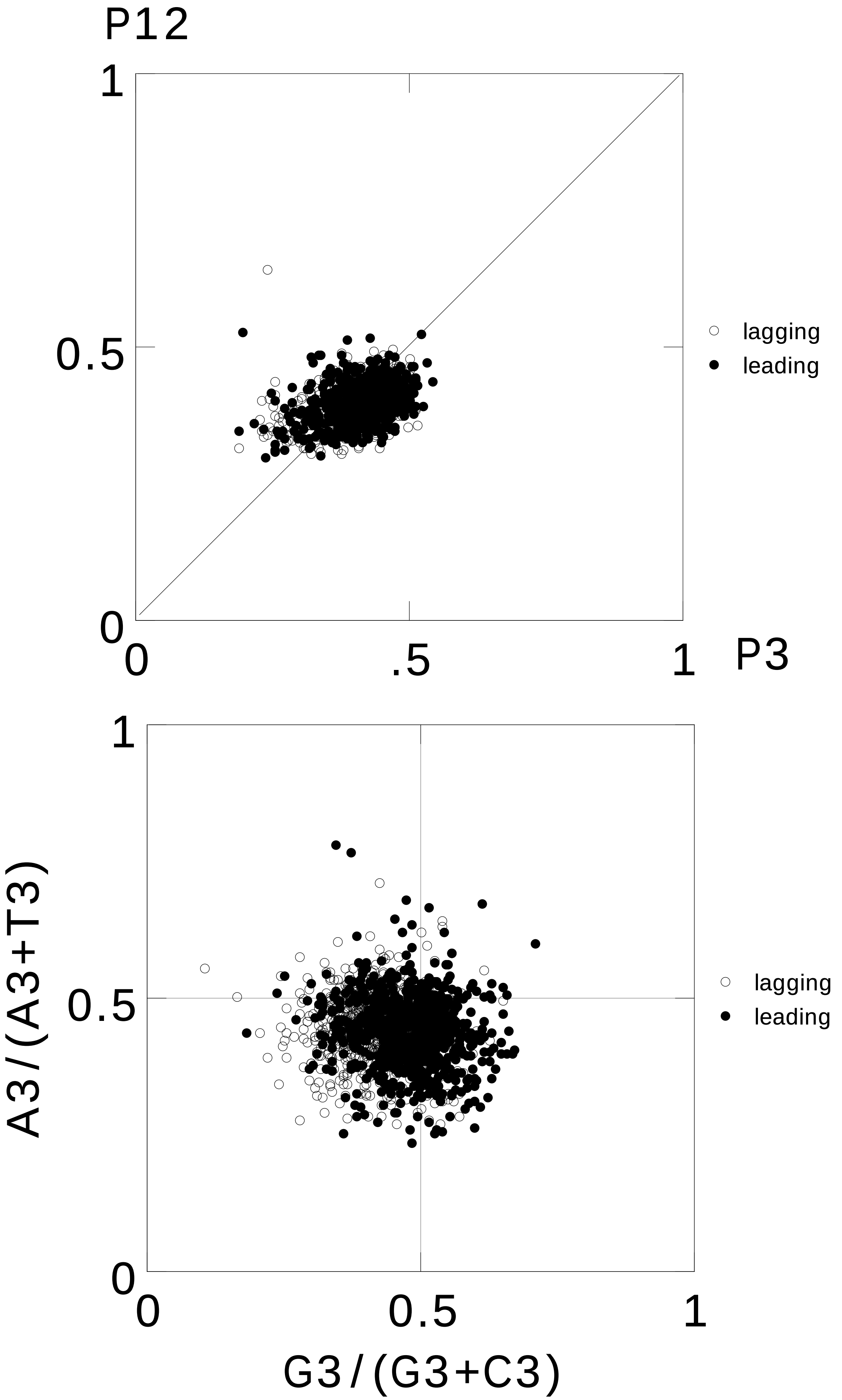
Escherichia coli RIMD 0509952



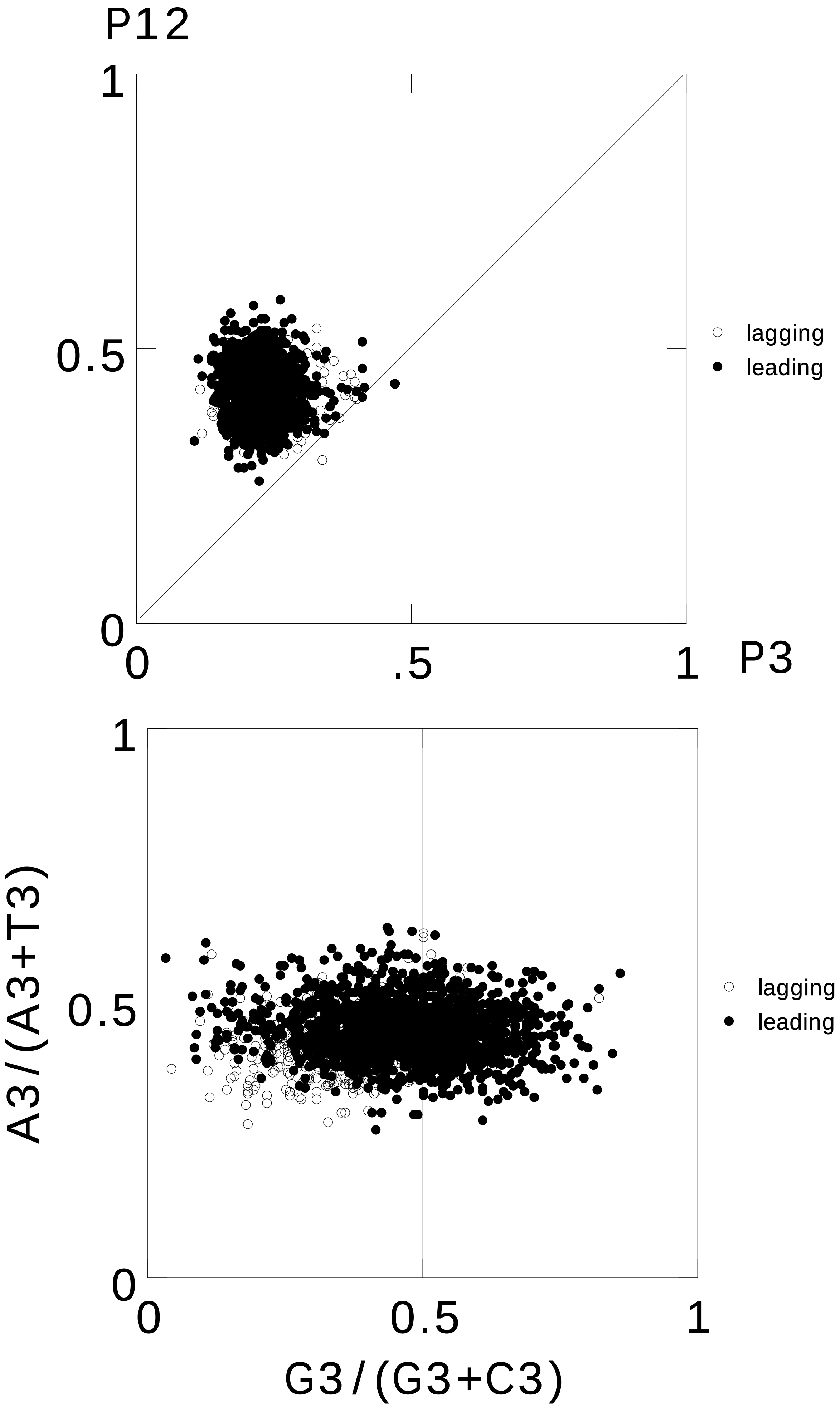
Haemophilus influenzae



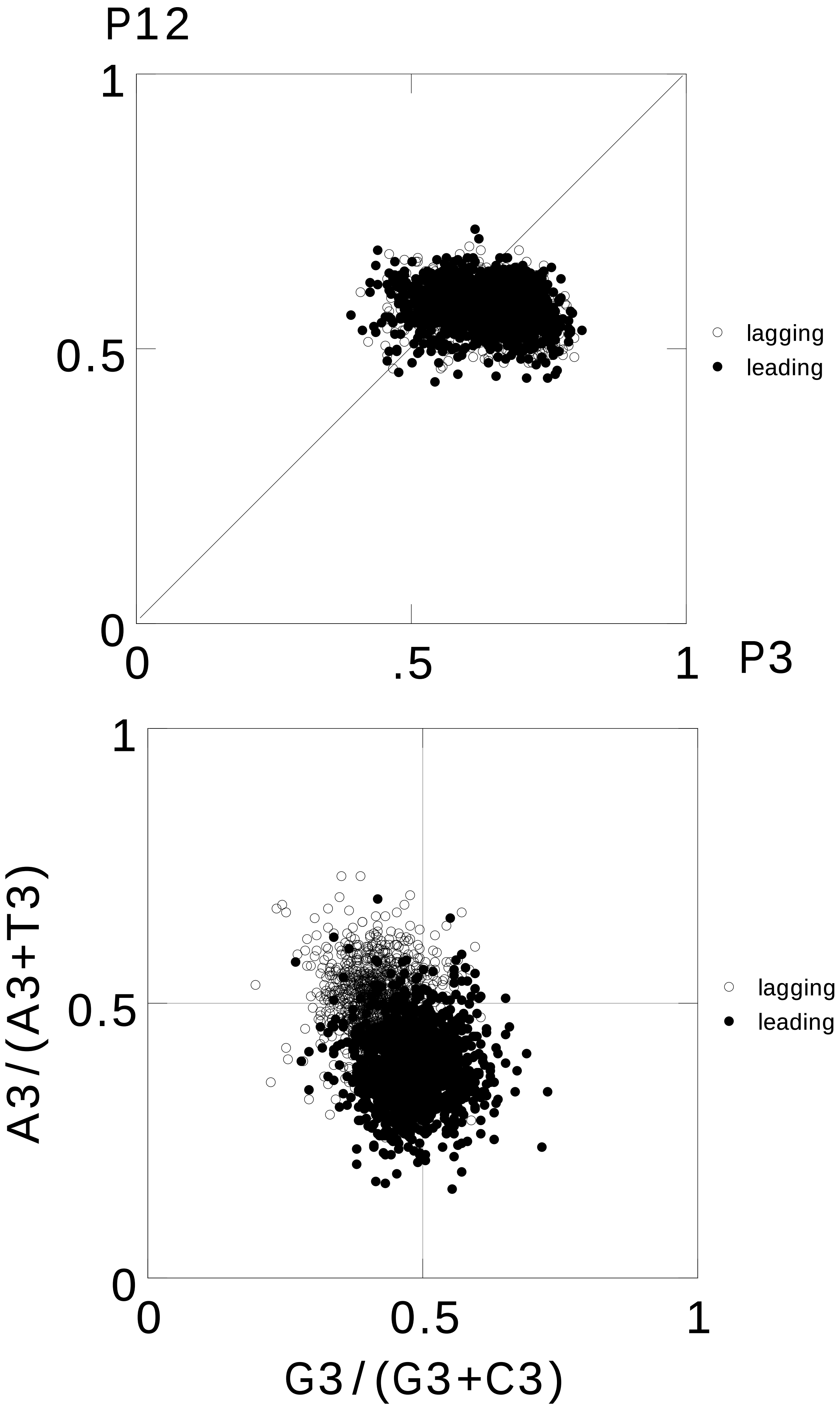
Helicobacter pylori 26695



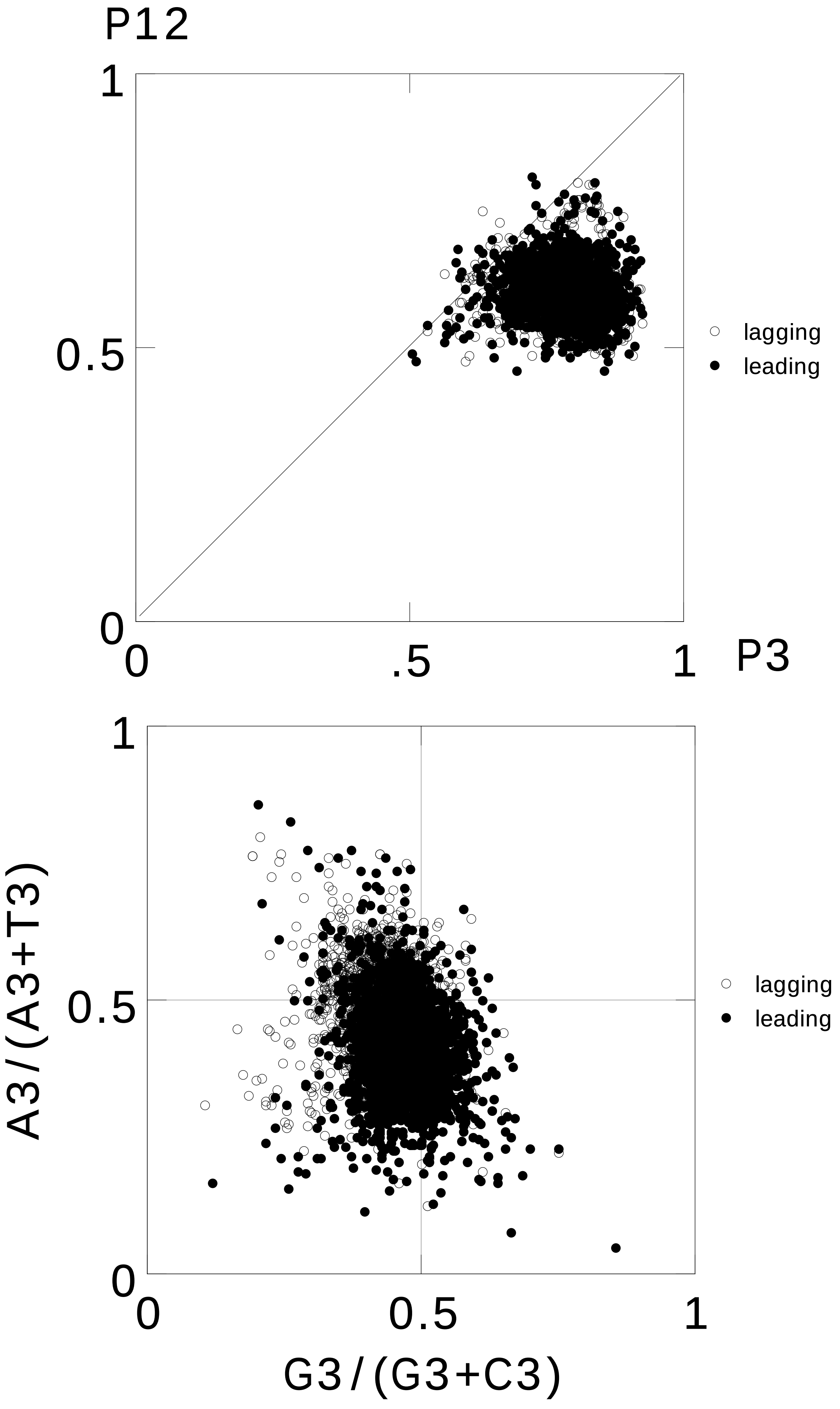
Helicobacter pylori J99



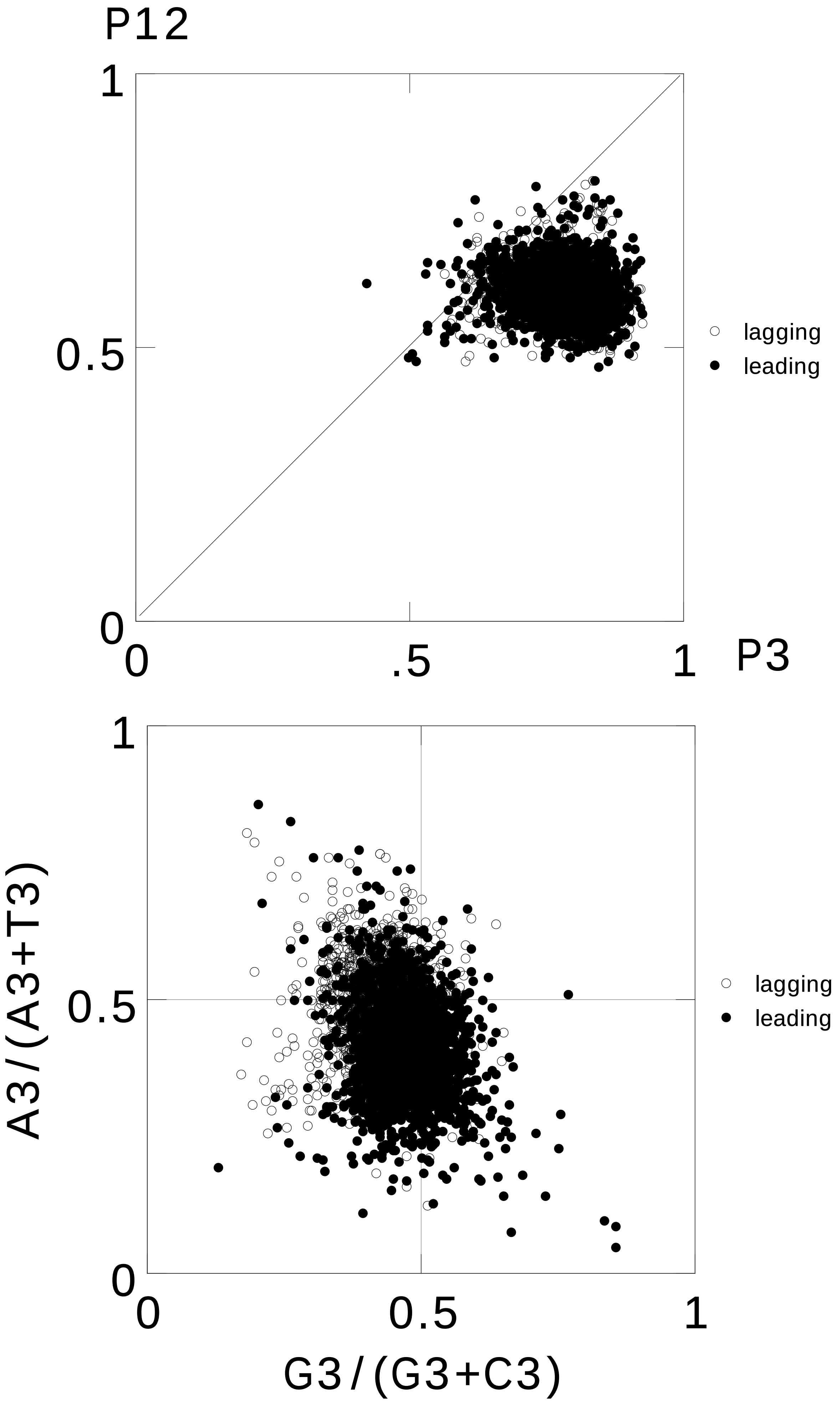
Lactococcus lactis



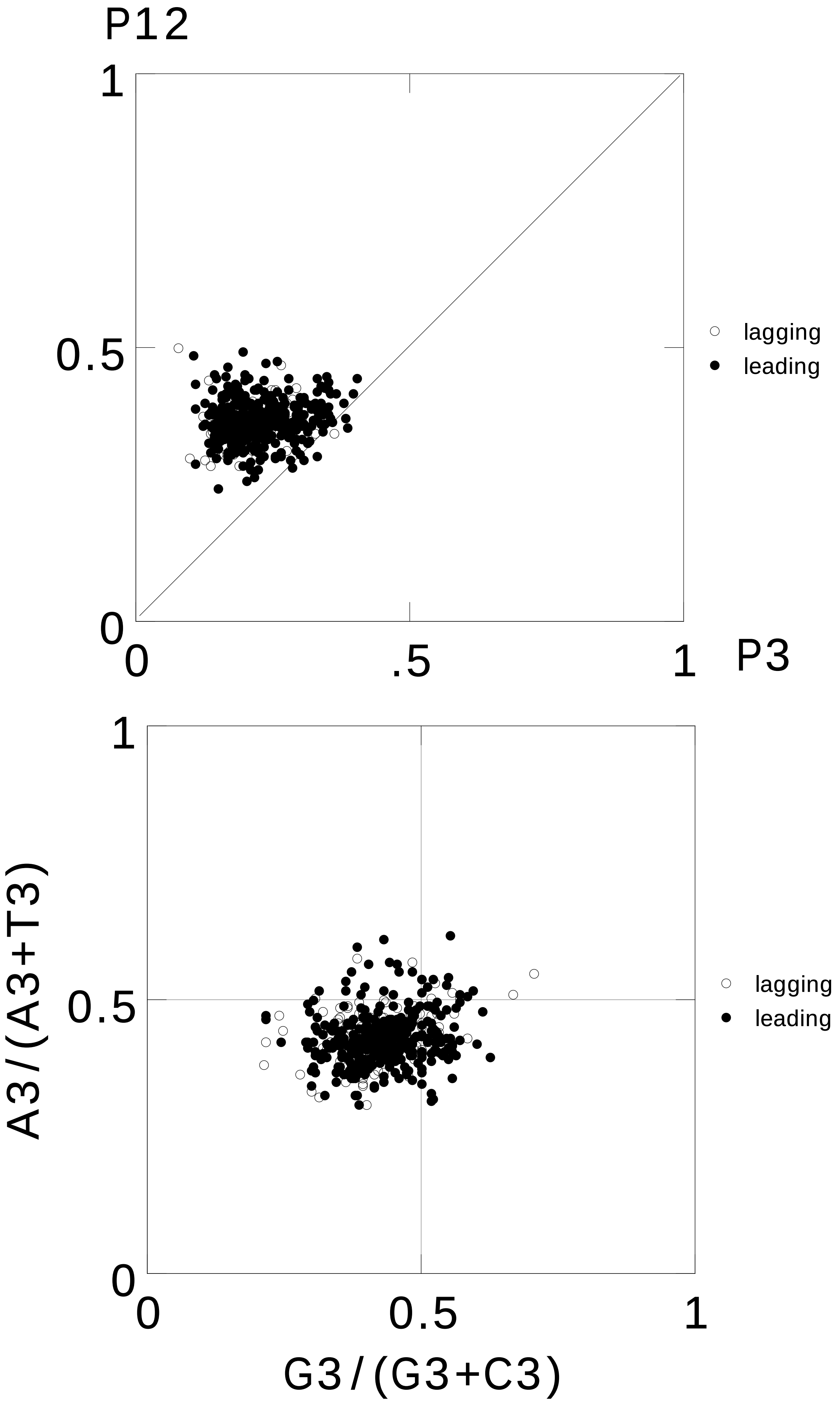
Mycobacterium leprae



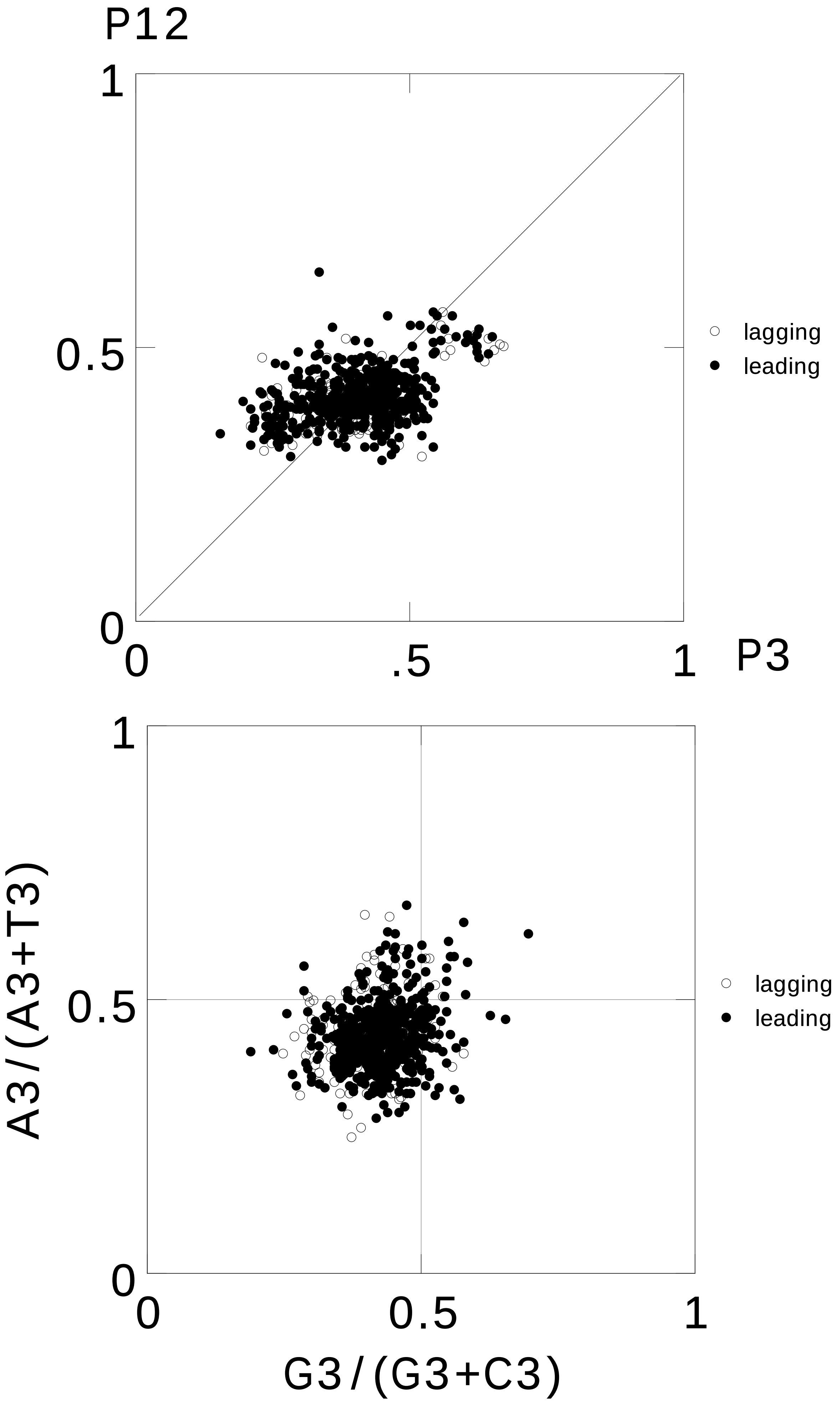
Mycobacterium tuberculosis H37Rv



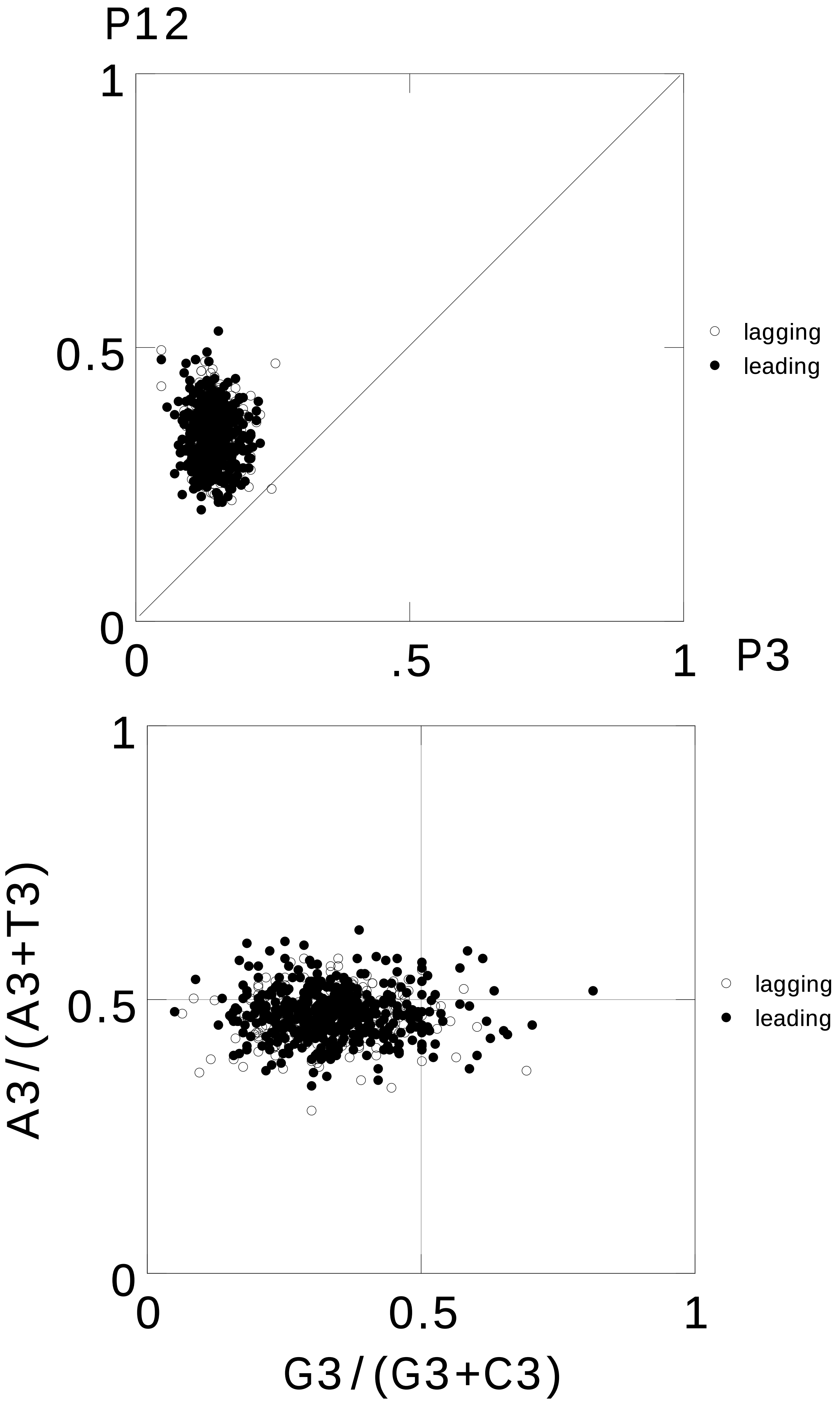
Mycobacterium tuberculosis CDC1551



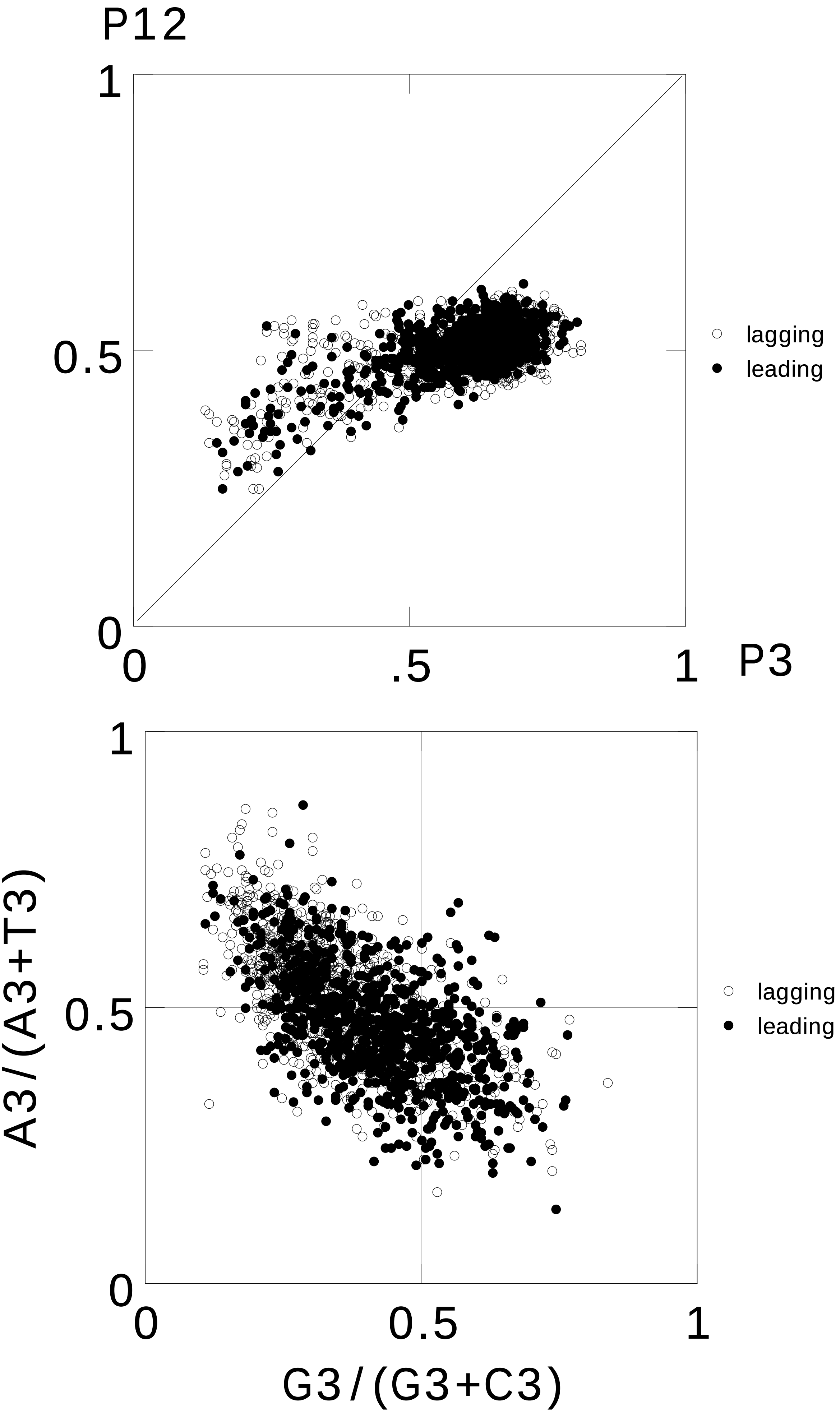
Mycoplasma genitalium



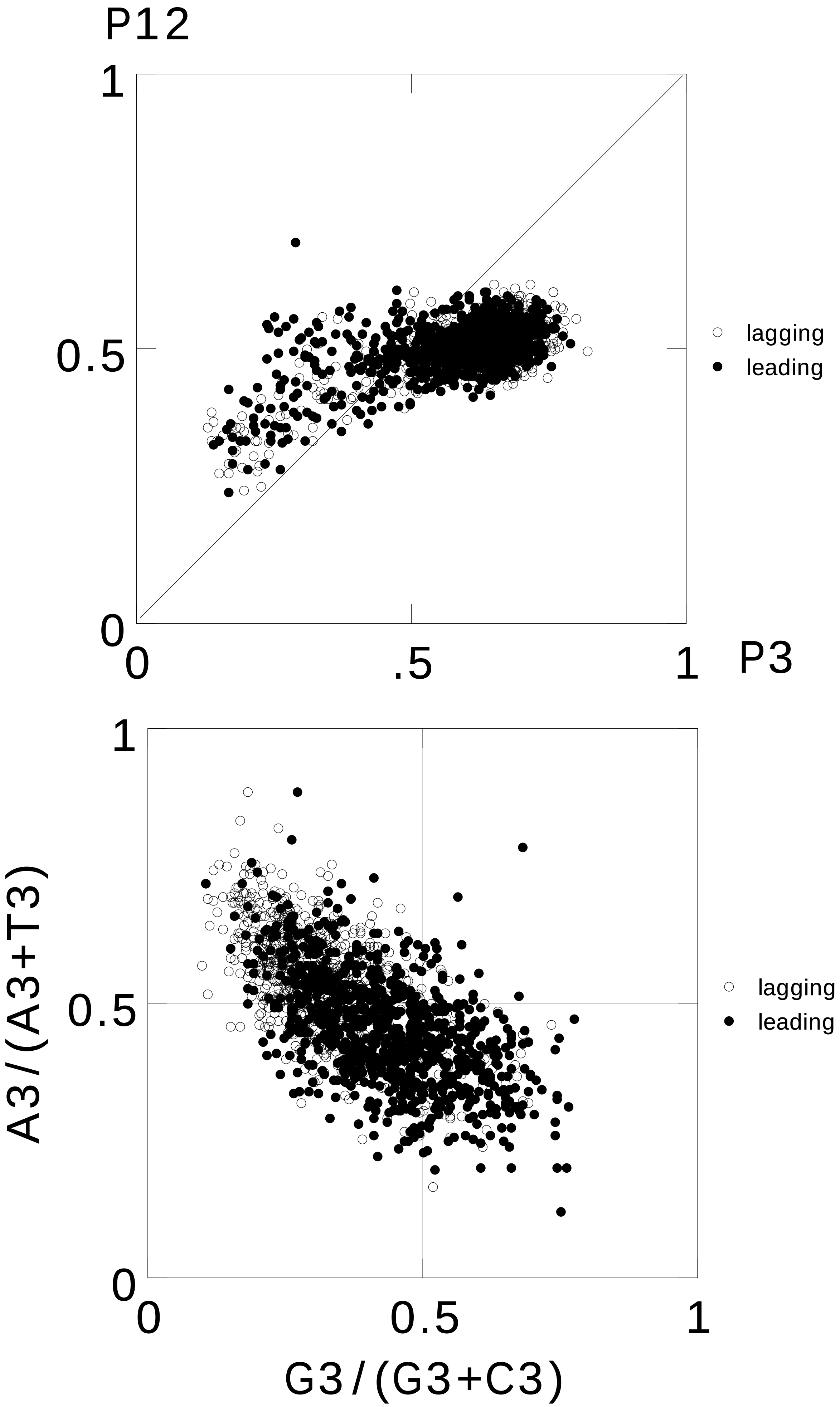
Mycoplasma pneumoniae



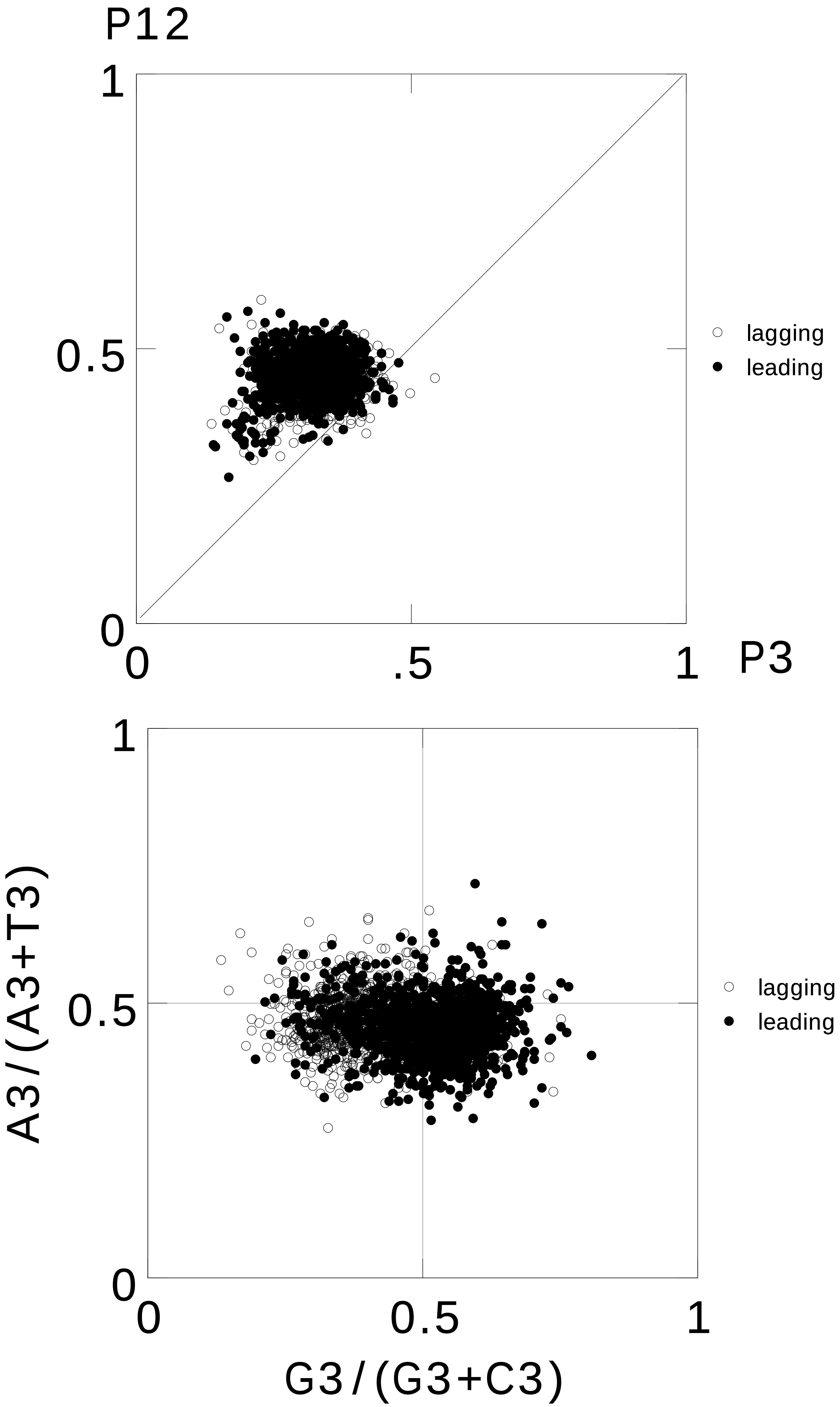
Mycoplasma pulmonis



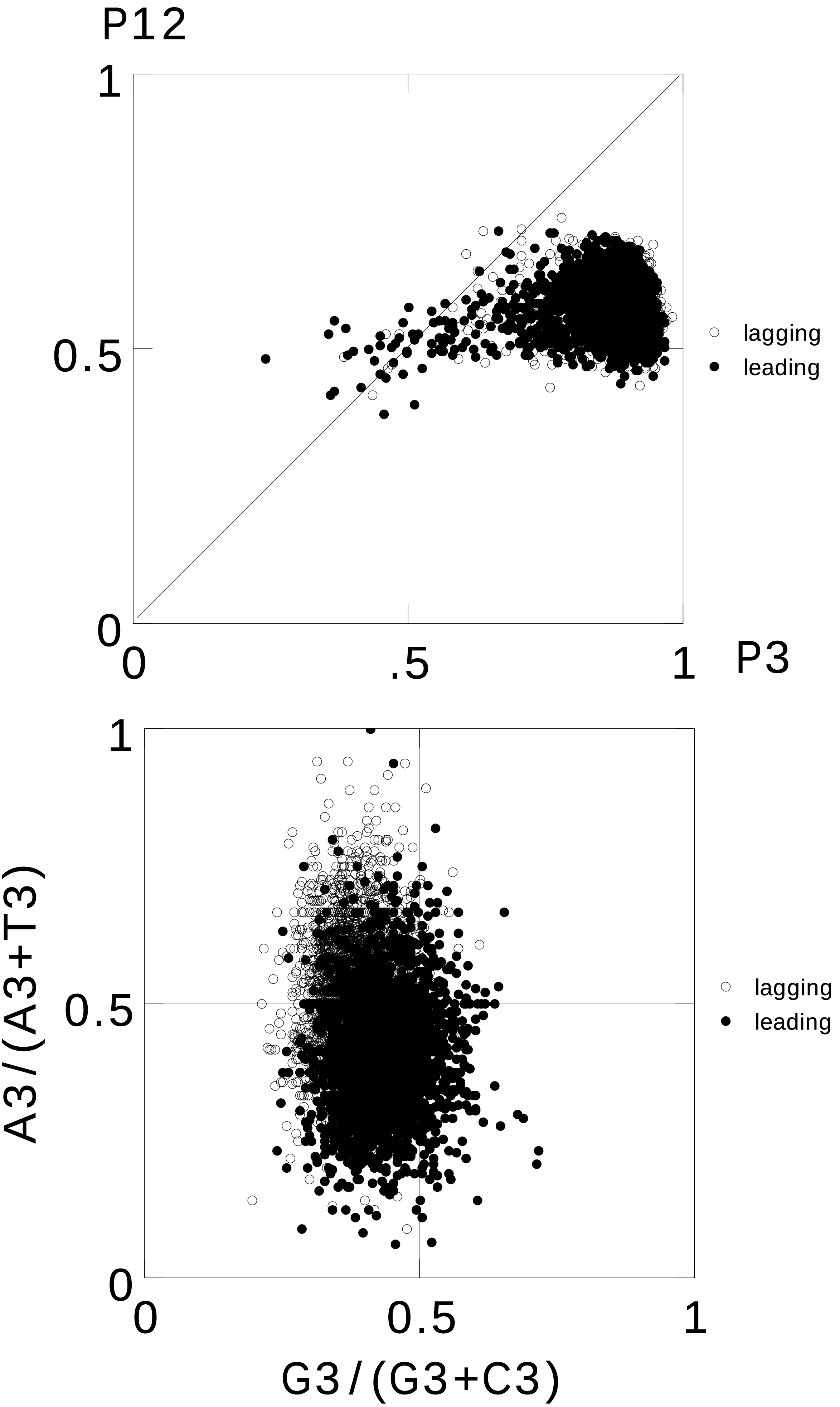
Neisseria meningitidis Z2491 (A)



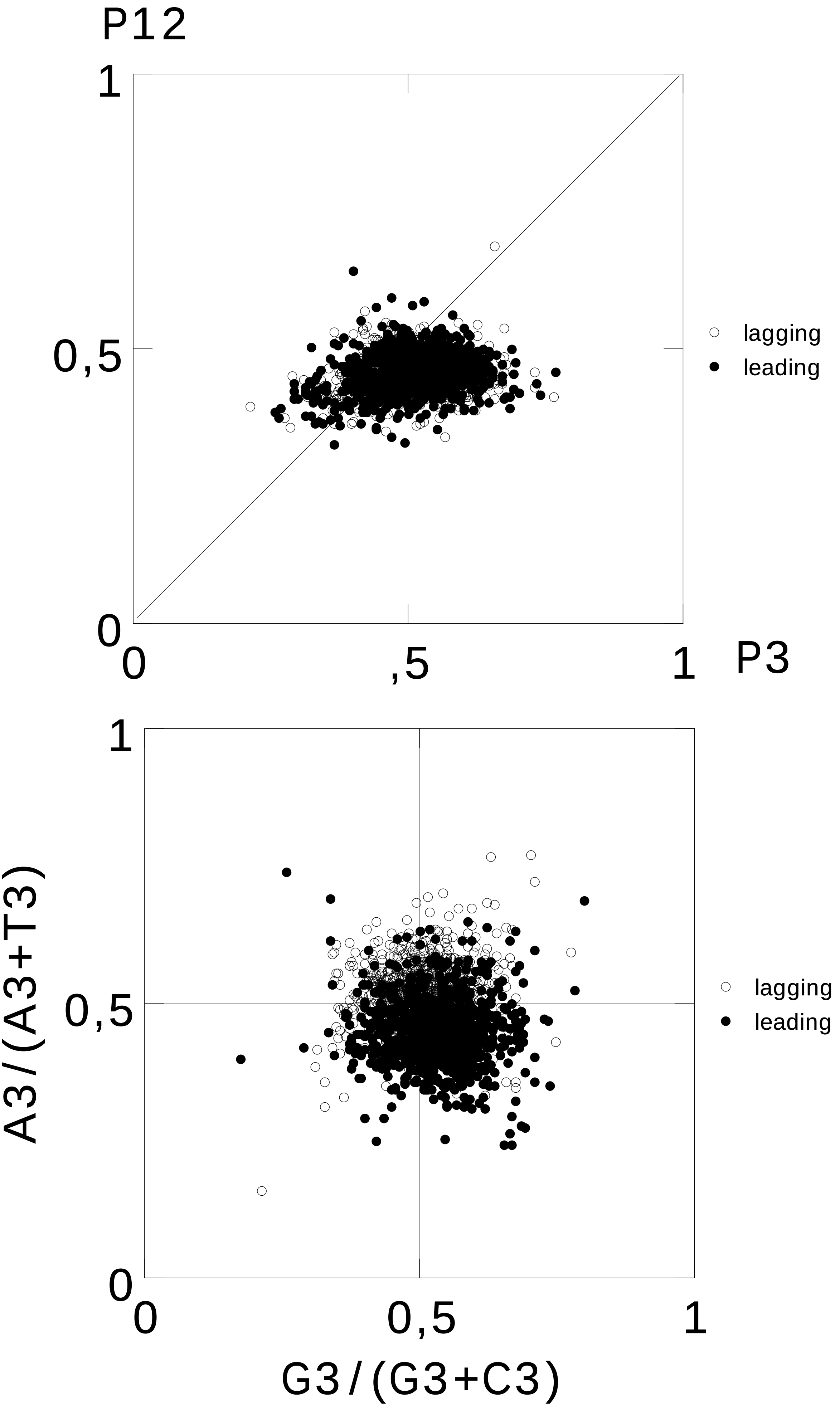
Neisseria meningitidis MC58 (B)



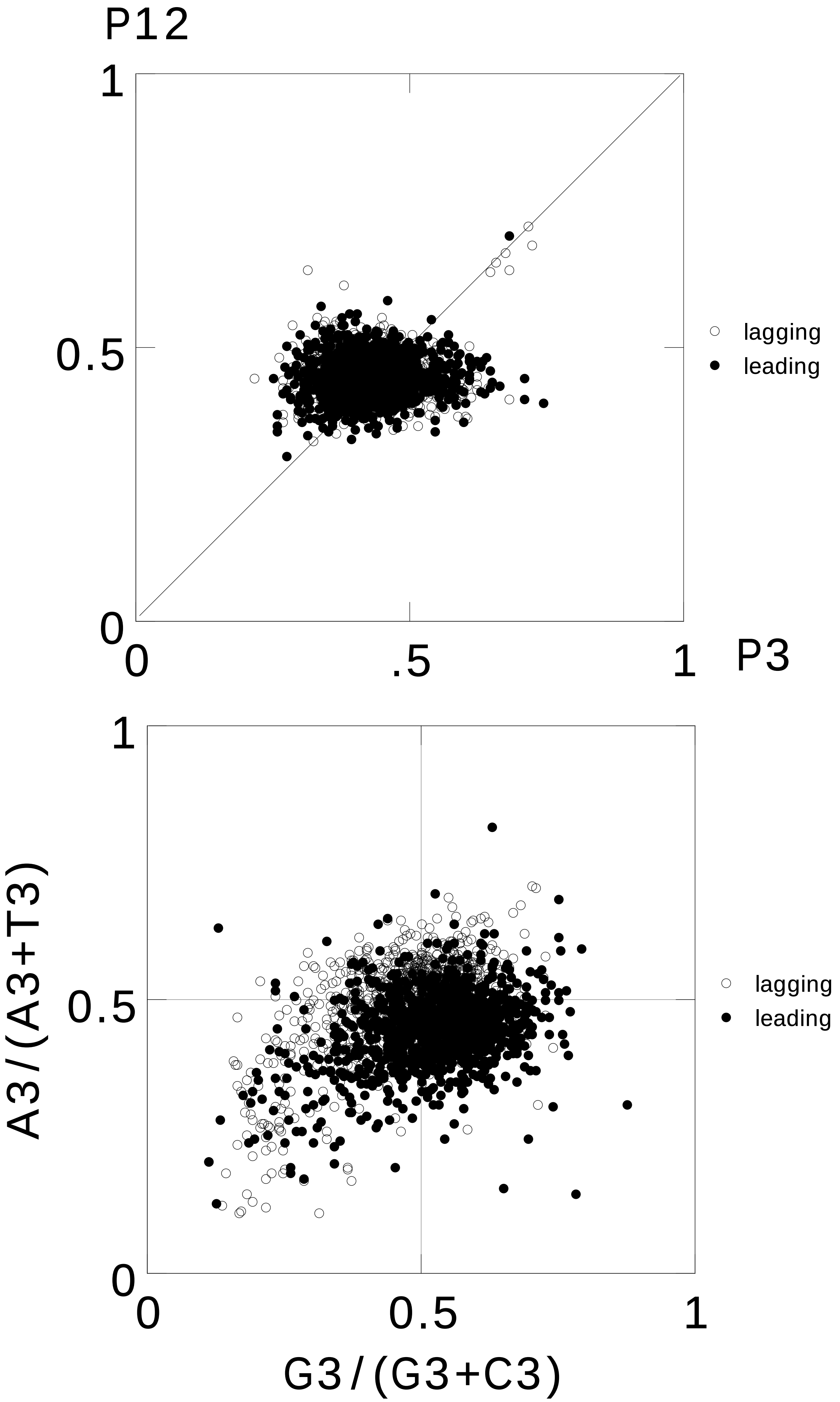
Pasteurella multocida



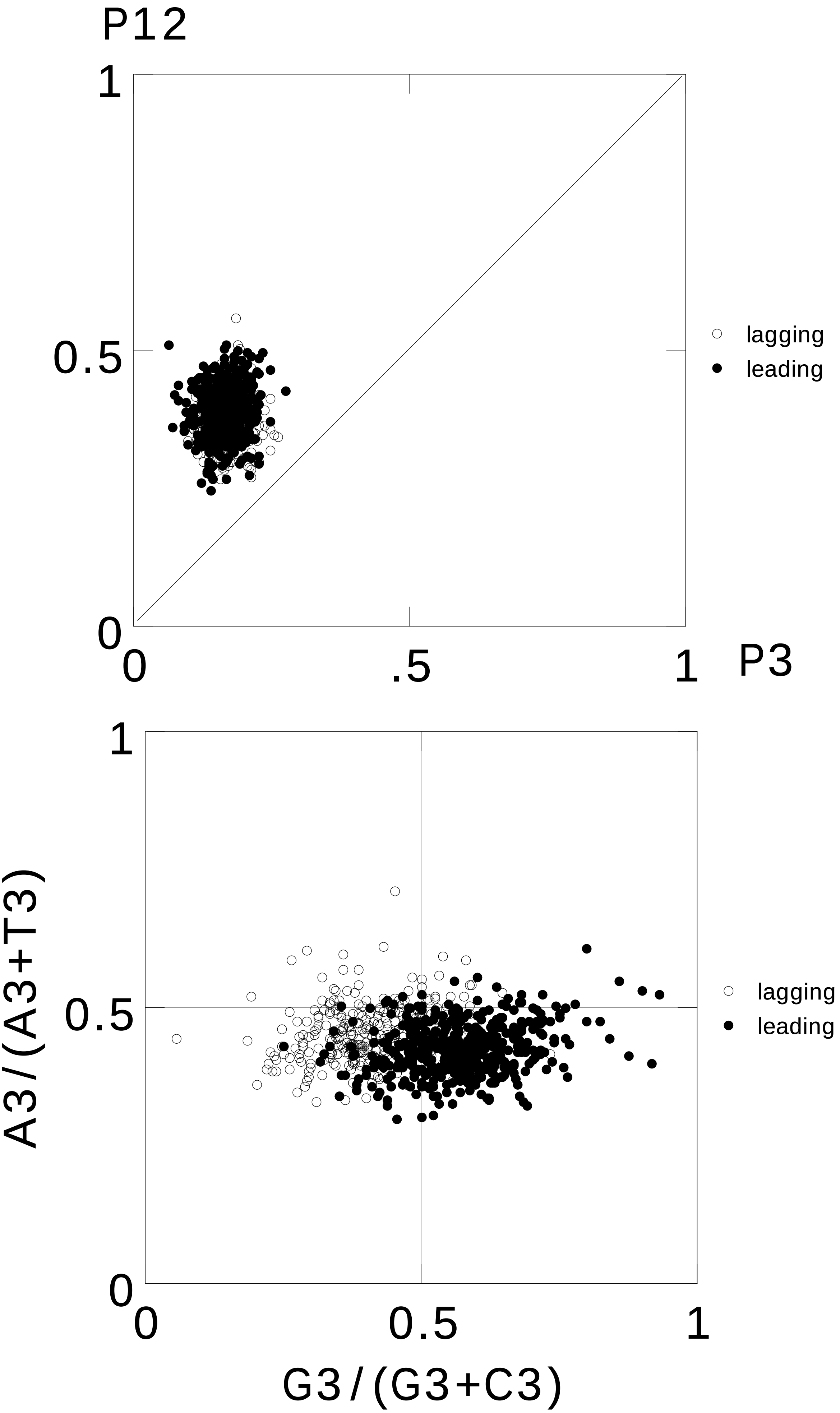
Pseudomonas aeruginosa



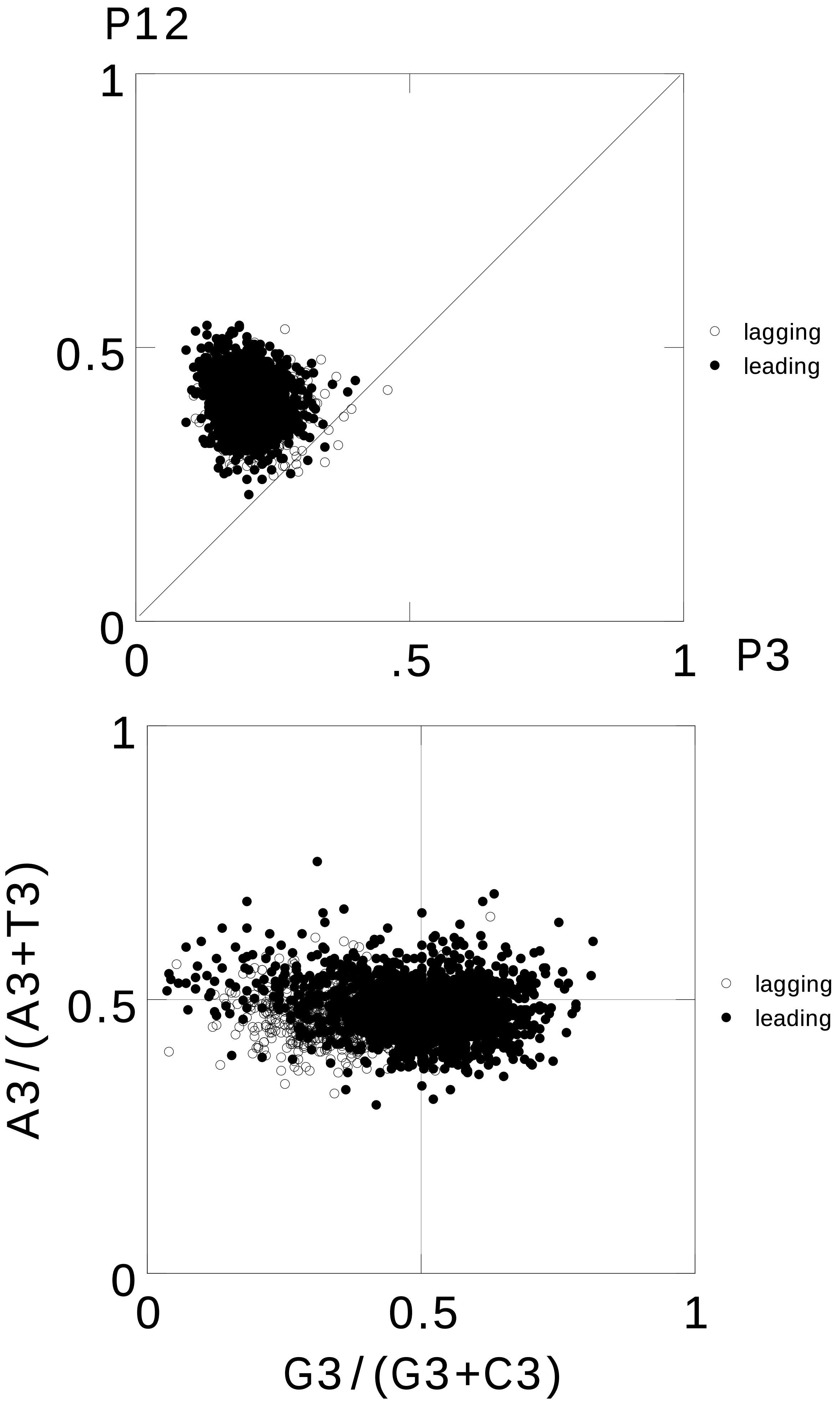
Pyrococcus abyssi



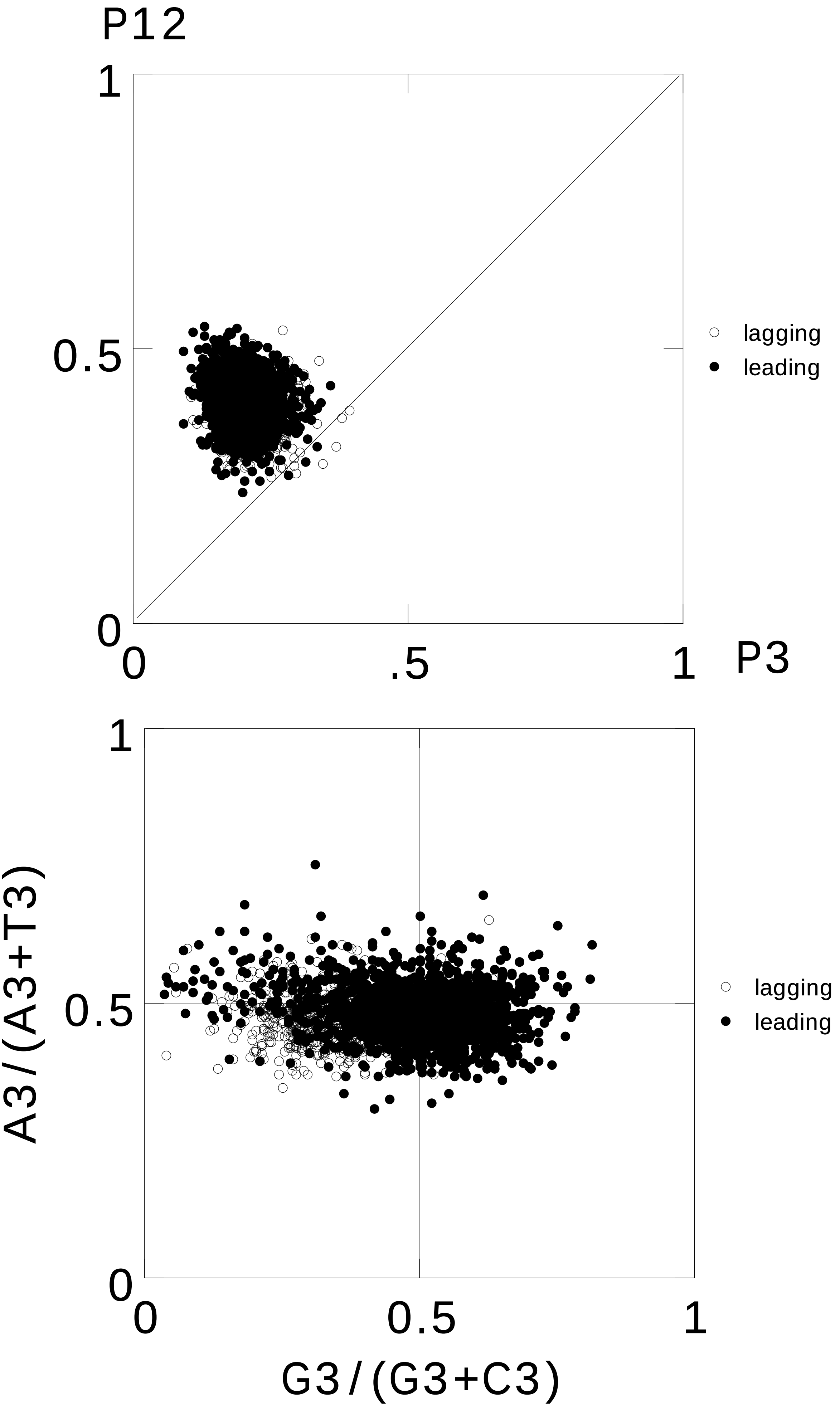
Pyrococcus horikoshii



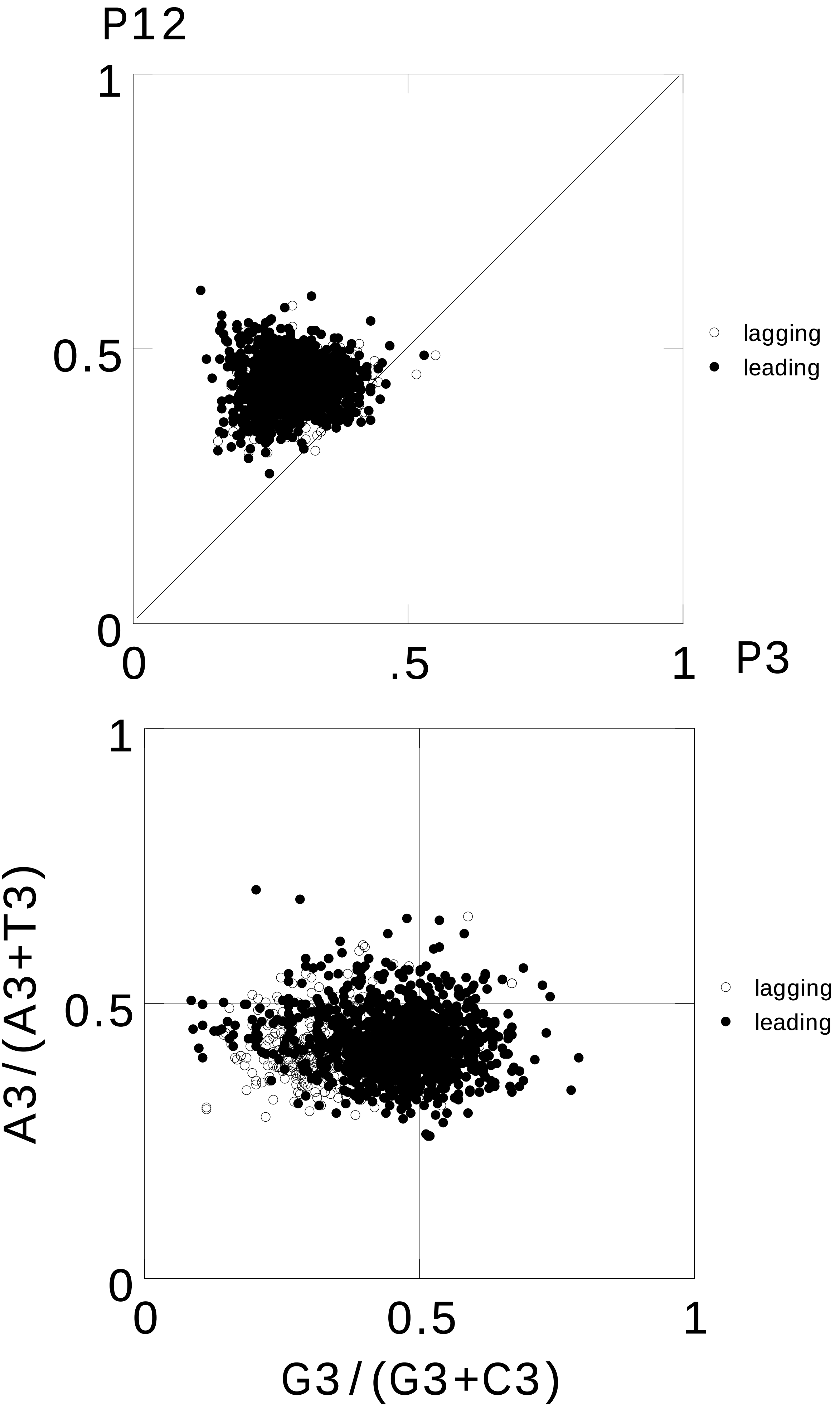
Rickettsia prowazekii



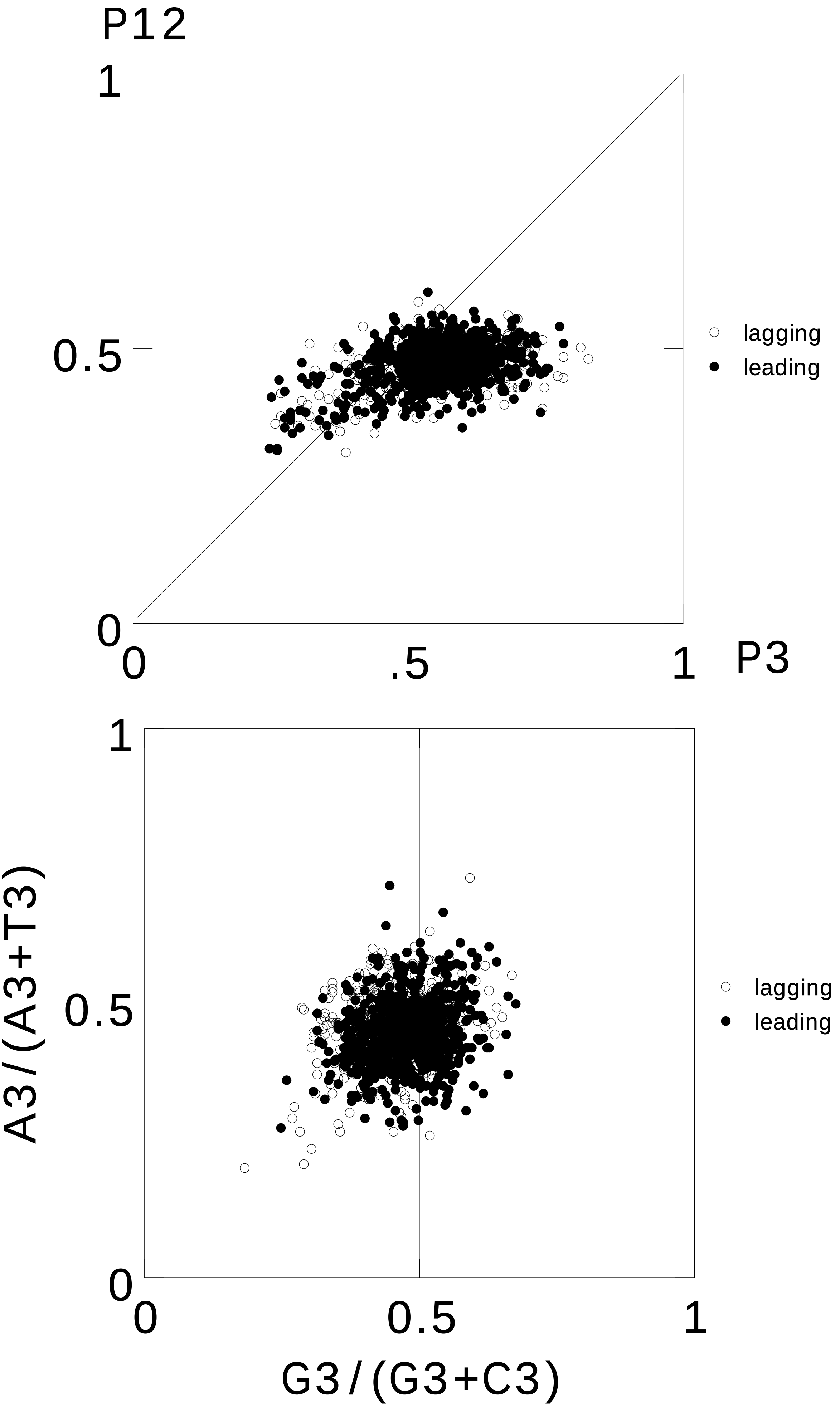
Staphylococcus aureus Mu50



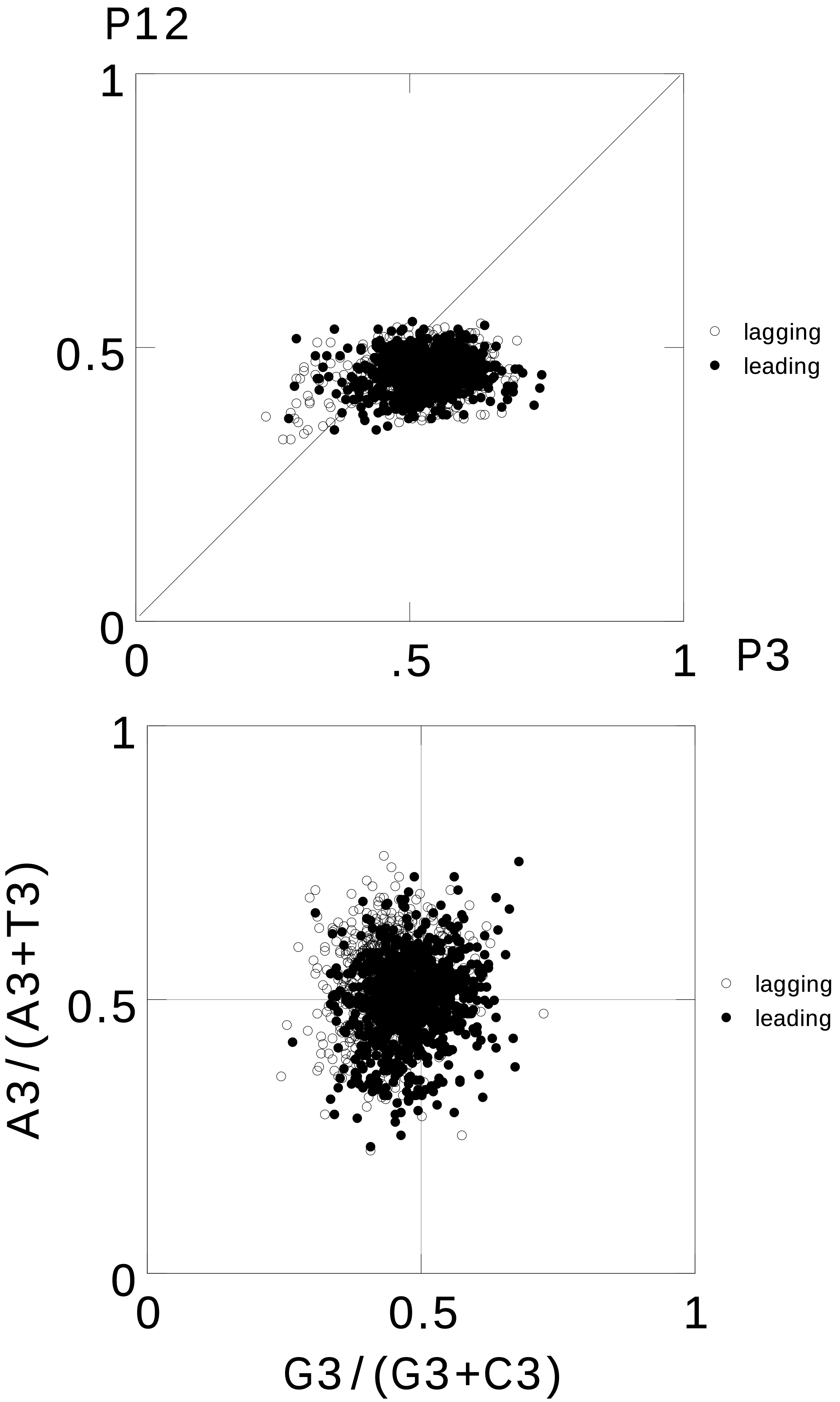
Staphylococcus aureus N315



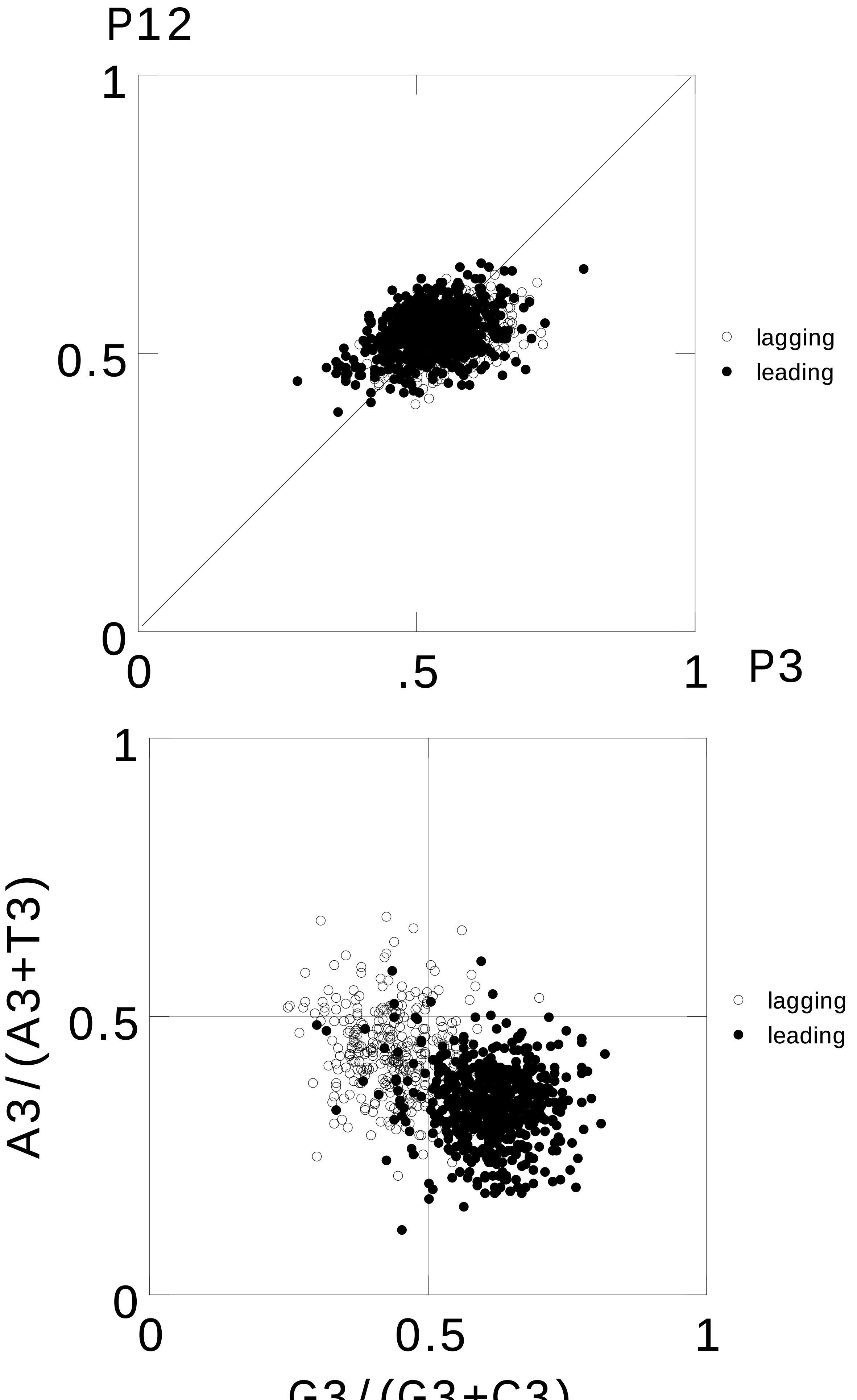
Streptococcus pyogenes



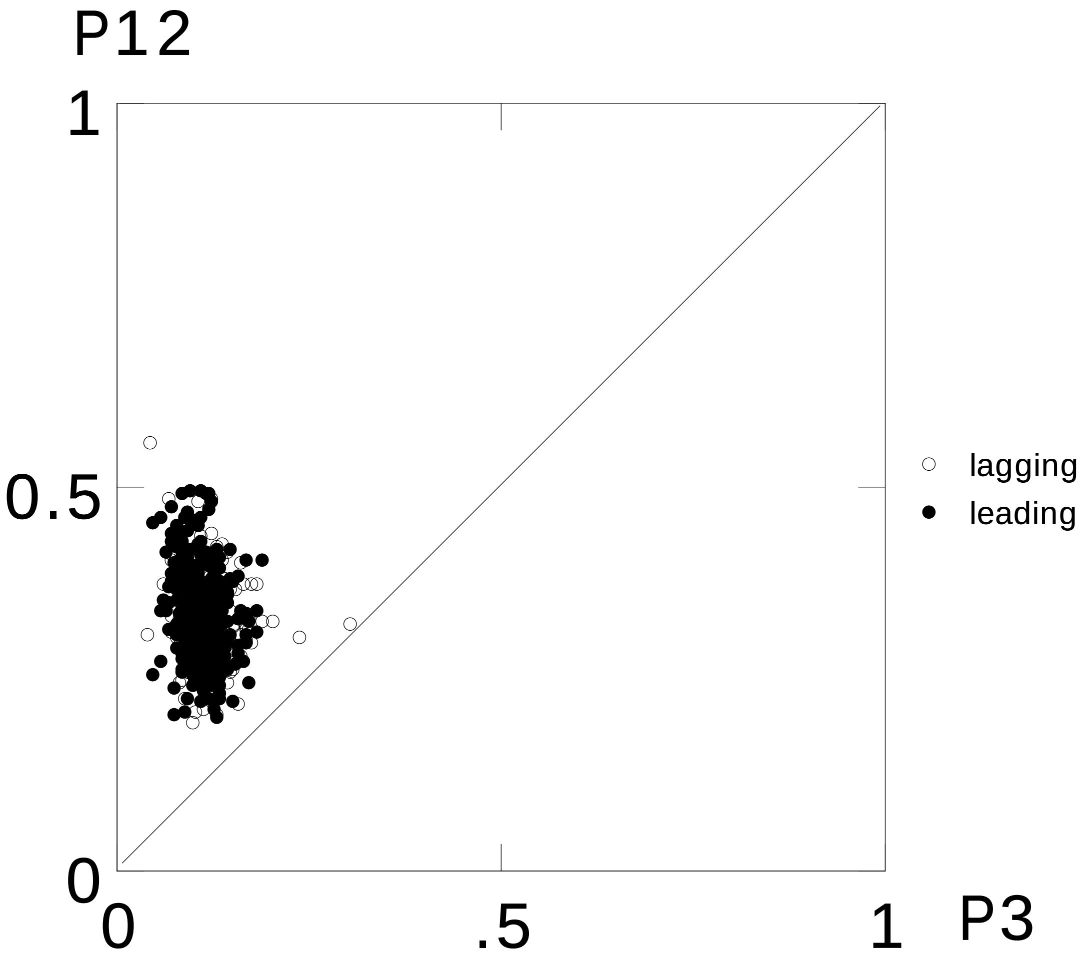
Thermoplasma acidophilum

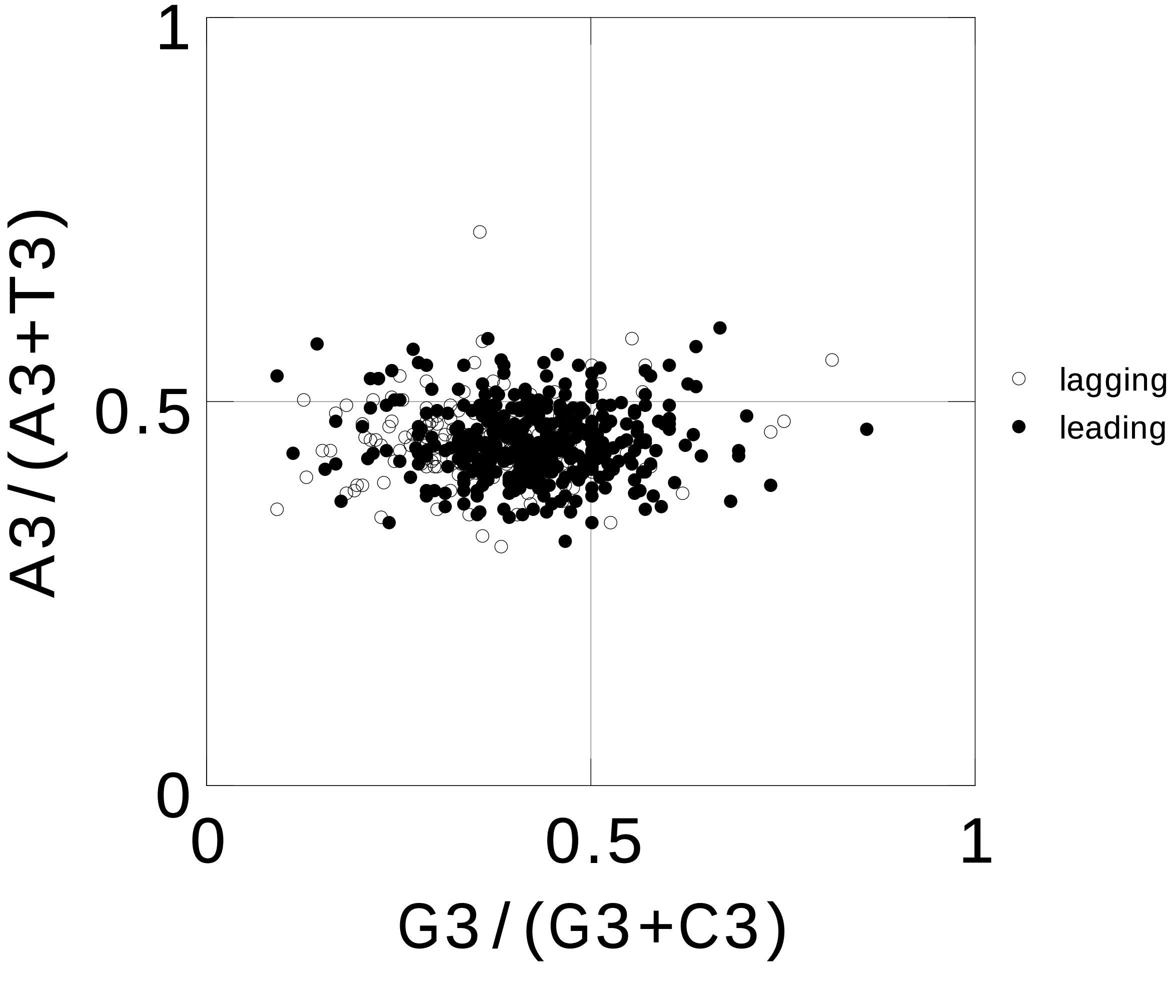


Thermotoga maritima

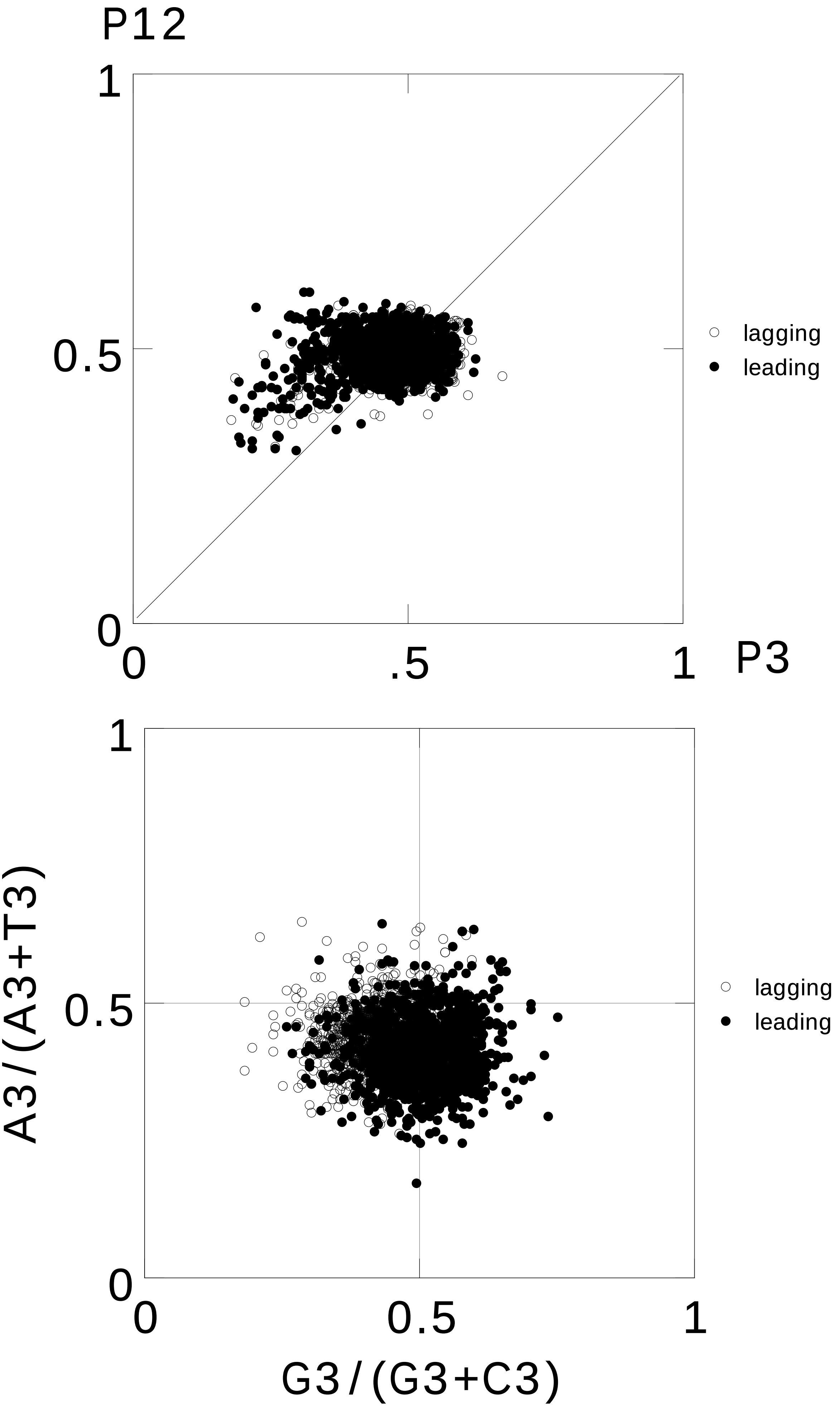


Treponema pallidum

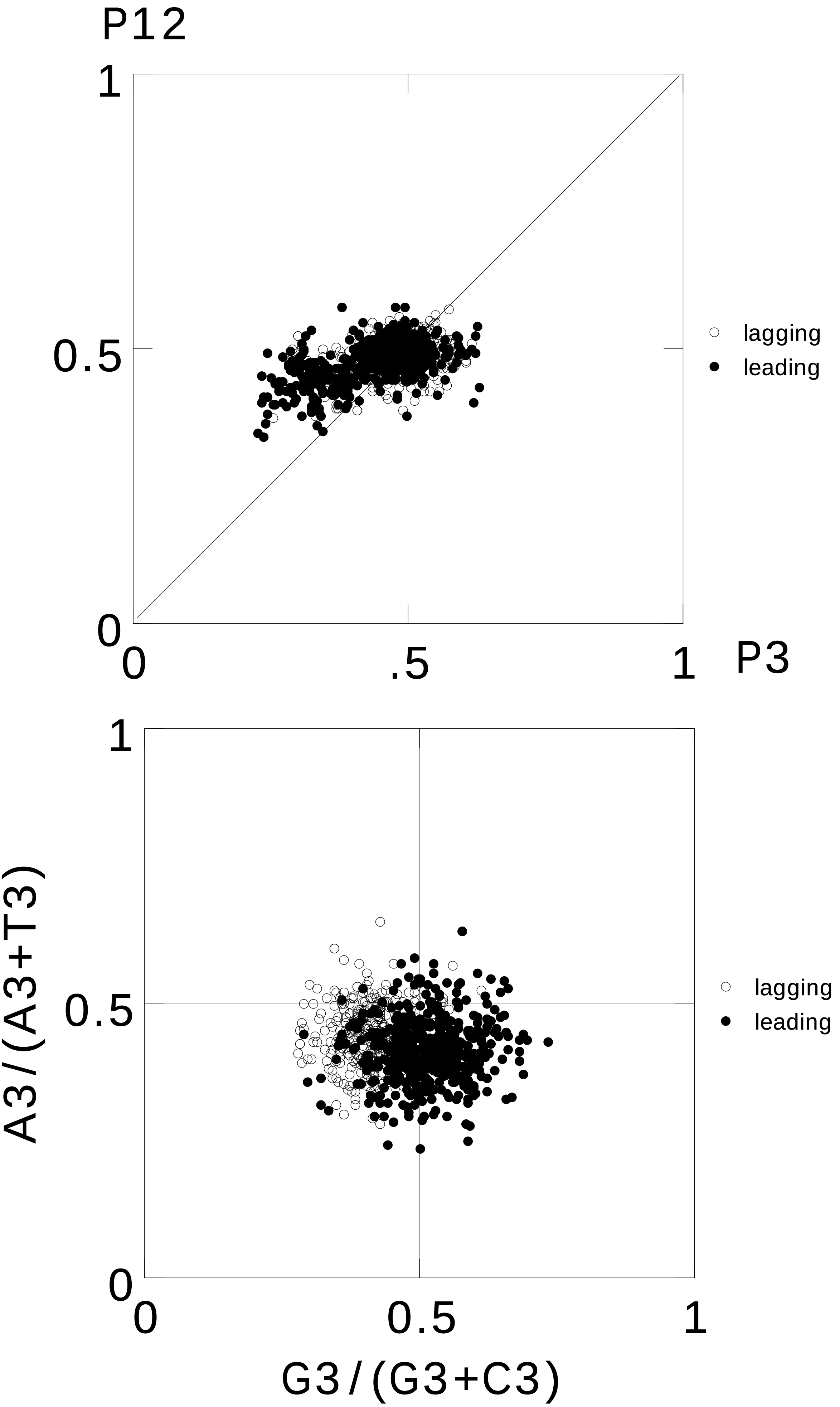




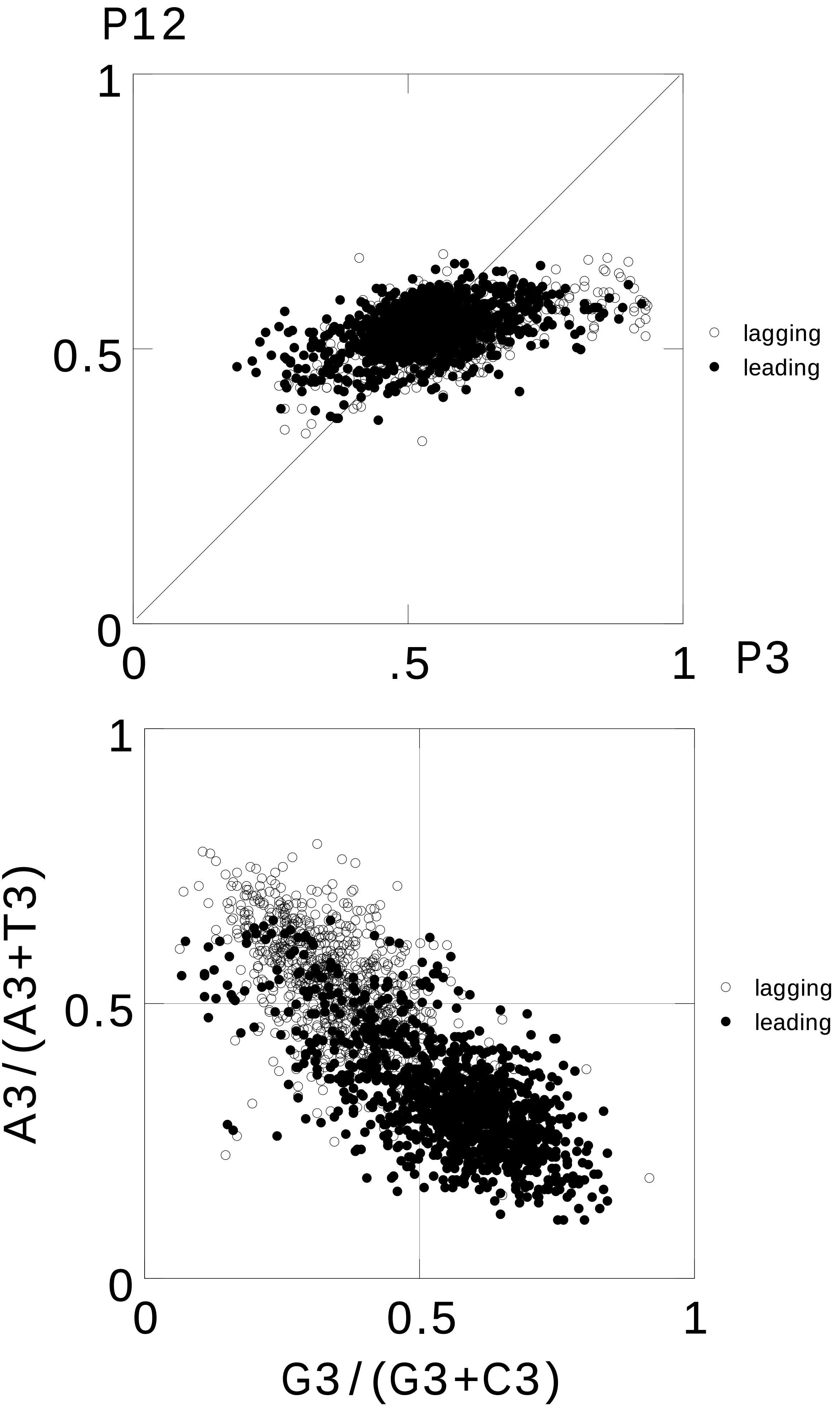
Ureaplasma urealyticum



Vibrio cholerae chromosome 1



Vibrio cholerae chromosome 2



Xylella fastidiosa

	Published Seq		GC_{IGR}			$G/(G+C)$			$A\ (A+T)$			Midpoint		Difference in PR2-bias		
Chromosome.	#lead	#lagg	lead	lagg	Sig.	x_1	x_2	Sig.	y_1	y_2	Sig.	x_c	y_c	B_I	B_{II}	B_I%
B. hal	912	1013	0.385	0.382	ns	0.559	0.450	***	0.516	0.491	***	0.505	0.504	0.112	0.006	**95.1**
B. sub	829	934	0.365	0.362	ns	0.545	0.454	***	0.511	0.489	***	0.500	0.500	0.094	0.000	**99.6**
B. bur	85	76	0.213	0.210	ns	0.616	0.400	***	0.425	0.573	***	0.508	0.499	0.261	0.008	**97.0**
Buch	118	123	0.159	0.152	ns	0.541	0.488	***	0.482	0.530	***	0.514	0.506	0.072	0.016	**82.0**
C.cre	630	753	0.623	0.626	ns	0.514	0.491	***	0.484	0.513	***	0.502	0.498	0.037	0.003	**92.7**
C. jej	150	118	0.200	0.211	ns	0.535	0.477	***	0.488	0.514	***	0.506	0.501	0.064	0.006	**91.3**
C. mur	166	190	0.359	0.362	ns	0.579	0.435	***	0.490	0.513	***	0.507	0.502	0.146	0.007	**95.3**
C. pne	191	236	0.326	0.320	ns	0.541	0.451	***	0.477	0.521	***	0.496	0.499	0.101	0.004	**96.0**
C. pneAR39	256	198	0.337	0.344	ns	0.548	0.459	***	0.474	0.523	***	0.504	0.498	0.102	0.004	**96.4**
C. pneJ138	190	240	0.329	0.318	*	0.540	0.451	***	0.476	0.522	***	0.496	0.499	0.100	0.005	**95.6**
C. tra	170	176	0.359	0.361	ns	0.578	0.430	***	0.497	0.519	**	0.504	0.508	0.150	0.009	**94.6**

D. rad1	417	439	0.609	0.636	***	0.505	0.496	*	0.495	0.512	**	0.500	0.504	0.019	0.004	84.5
D. rad2	47	50	0.579	0.606	ns	0.491	0.483	ns	0.490	0.538	**	0.487	0.514	0.049	0.019	71.8
E. col	912	863	0.428	0.423	ns	0.522	0.479	***	0.497	0.506	**	0.501	0.502	0.044	0.002	**96.4**
E.colEDL	1153	1077	0.429	0.421	**	0.523	0.478	***	0.495	0.507	***	0.500	0.501	0.047	0.001	**97.7**
E.colRIMD	1088	1000	.425	.422	ns	0.523	0.479	***	0.494	0.507	***	0.501	0.500	0.046	0.001	**97.6**
H. inf	351	347	0.313	0.310	ns	0.525	0.475	***	0.494	0.510	***	0.500	0.502	0.052	0.002	**96.6**
H. pyl	221	250	0.303	0.301	ns	0.516	0.474	***	0.500	0.494	ns	0.495	0.497	0.042	0.006	87.6
H. pylJ99	204	240	0.304	0.311	ns	0.524	0.475	***	0.497	0.502	ns	0.500	0.500	0.049	0.000	99.1
L.lac	606	507	0.277	0.274	ns	0.566	0.426	***	0.526	0.465	***	0.496	0.496	0.153	0.006	**96.2**
M.lep	703	717	0.546	0.546	ns	0.536	0.470	***	0.459	0.536	***	0.503	0.498	0.101	0.004	**96.3**
M. tub	656	649	0.623	0.627	ns	0.515	0.482	***	0.489	0.516	***	0.498	0.503	0.043	0.003	**93.4**
M.tubCDC	593	628	0.628	0.626	ns	0.516	0.484	***	0.486	0.515	***	0.500	0.500	0.043	0.000	**98.9**
M. gen	33	48	0.305	0.249	***	0.490	0.490	ns	0.523	0.507	ns	0.490	0.515	0.016	0.018	45.9
M. pne	104	131	0.342	0.336	ns	0.495	0.494	ns	0.501	0.502	ns	0.494	0.501	0.002	0.006	23.7
M.pul	161	110	0.184	0.178	ns	0.504	0.482	*	0.506	0.498	ns	0.493	0.502	0.023	0.007	76.3

N. menA	605	385	0.447	0.439	ns	0.524	0.462	***	0.488	0.506	***	0.493	0.497	0.065	0.008	**89.4**
N. menB	552	459	0.448	0.459	ns	0.538	0.468	***	0.491	0.515	***	0.503	0.503	0.074	0.004	**94.6**
P.mul	415	304	0.332	0.323	*	0.541	0.465	***	0.492	0.513	***	0.503	0.502	0.079	0.004	**95.3**
P. aer	871	1344	0.620	0.614	ns	0.526	0.476	***	0.476	0.529	***	0.501	0.502	0.073	0.003	**96.4**
P. aby	175	202	0.386	0.373	ns	0.508	0.495	ns	0.489	0.504	*	0.501	0.496	0.020	0.004	83.4
P. hor	141	308	0.381	0.373	ns	0.526	0.482	***	0.496	0.507	ns	0.504	0.501	0.046	0.004	91.7
R. pro	267	213	0.237	0.248	**	0.535	0.465	***	0.485	0.518	***	0.500	0.501	0.077	0.001	**98.1**
S.aur	655	735	0.278	0.276	ns	0.570	0.435	***	0.514	0.487	***	0.502	0.500	0.138	0.003	**98.2**
S.aurN315	683	702	0.273	0.275	ns	0.573	0.426	***	0.515	0.485	***	0.499	0.500	0.150	0.001	**99.7**
S.pyo	408	381	0.328	0.322	ns	0.567	0.440	***	0.517	0.486	***	.503	.502	.131	.004	**97.2**
T. aci	301	297	0.360	0.363	ns	0.512	0.491	***	0.498	0.506	**	0.502	0.502	0.022	0.003	**90.0**
T. mar	122	127	0.400	0.394	ns	0.518	0.500	ns	0.494	0.507	ns	0.509	0.500	0.023	0.009	71.0
T. pal	135	117	0.538	0.546	ns	0.583	0.432	***	0.452	0.525	***	0.508	0.489	0.167	0.014	**92.4**
U. ure	122	62	0.178	0.178	ns	0.515	0.469	**	0.497	0.504	ns	0.492	0.500	0.047	0.008	85.3
V. cho1	553	460	0.408	0.416	*	0.529	0.476	***	0.483	0.511	***	0.502	0.497	0.060	0.004	**93.9**

V. cho2	301	228	0.444	0.414	***	0.545	0.466	***	0.459	0.519	***	0.506	0.489	0.099	0.012	**89.0**
X. fas	842	404	0.467	0.470	ns	0.582	0.441	***	0.428	0.557	***	0.511	0.493	0.191	0.014	**93.3**

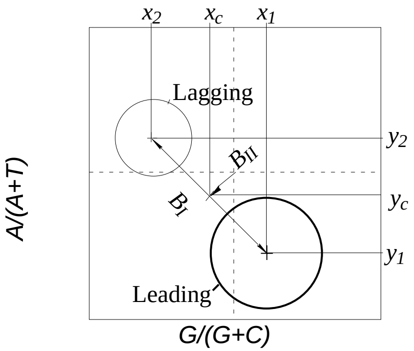
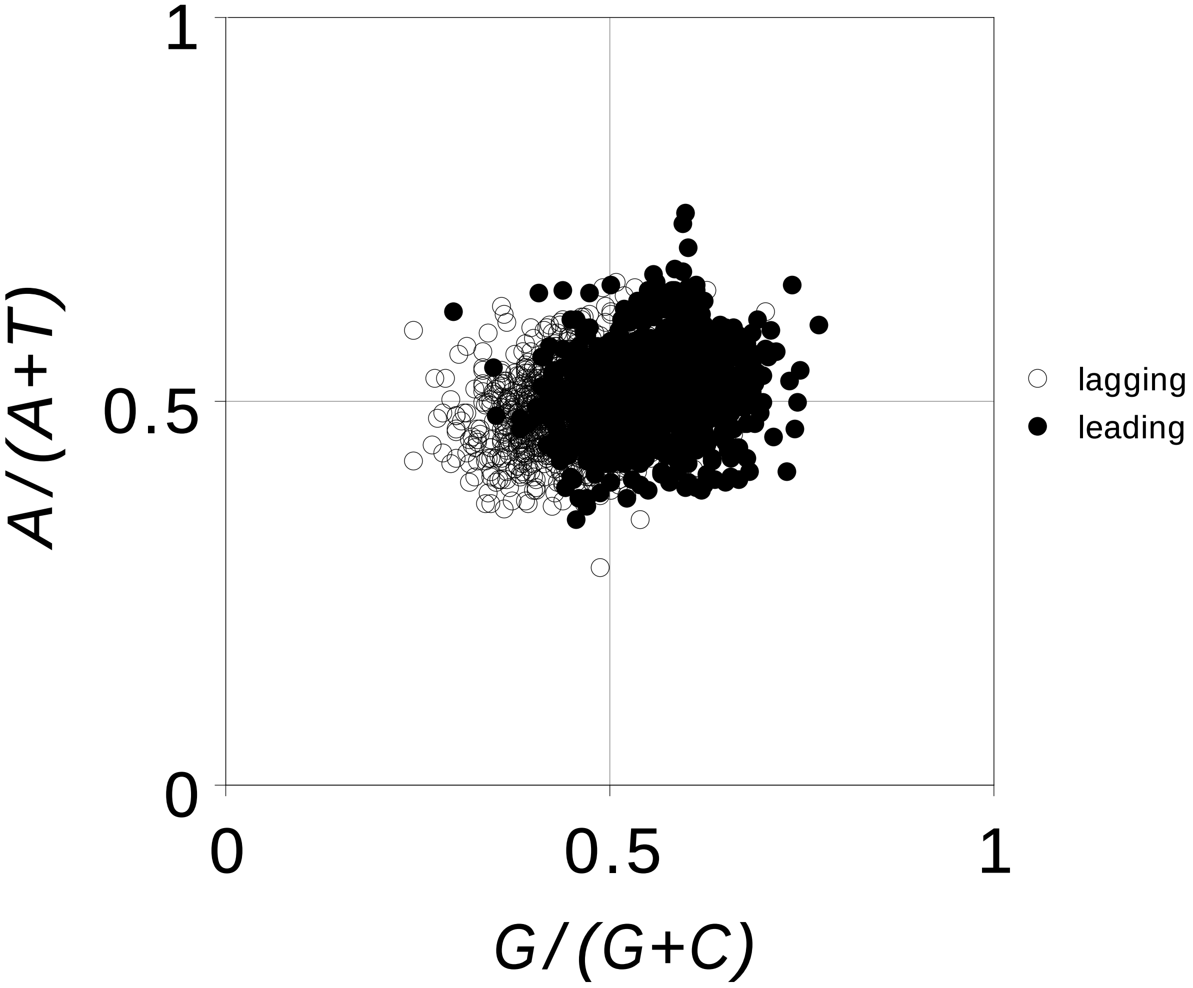
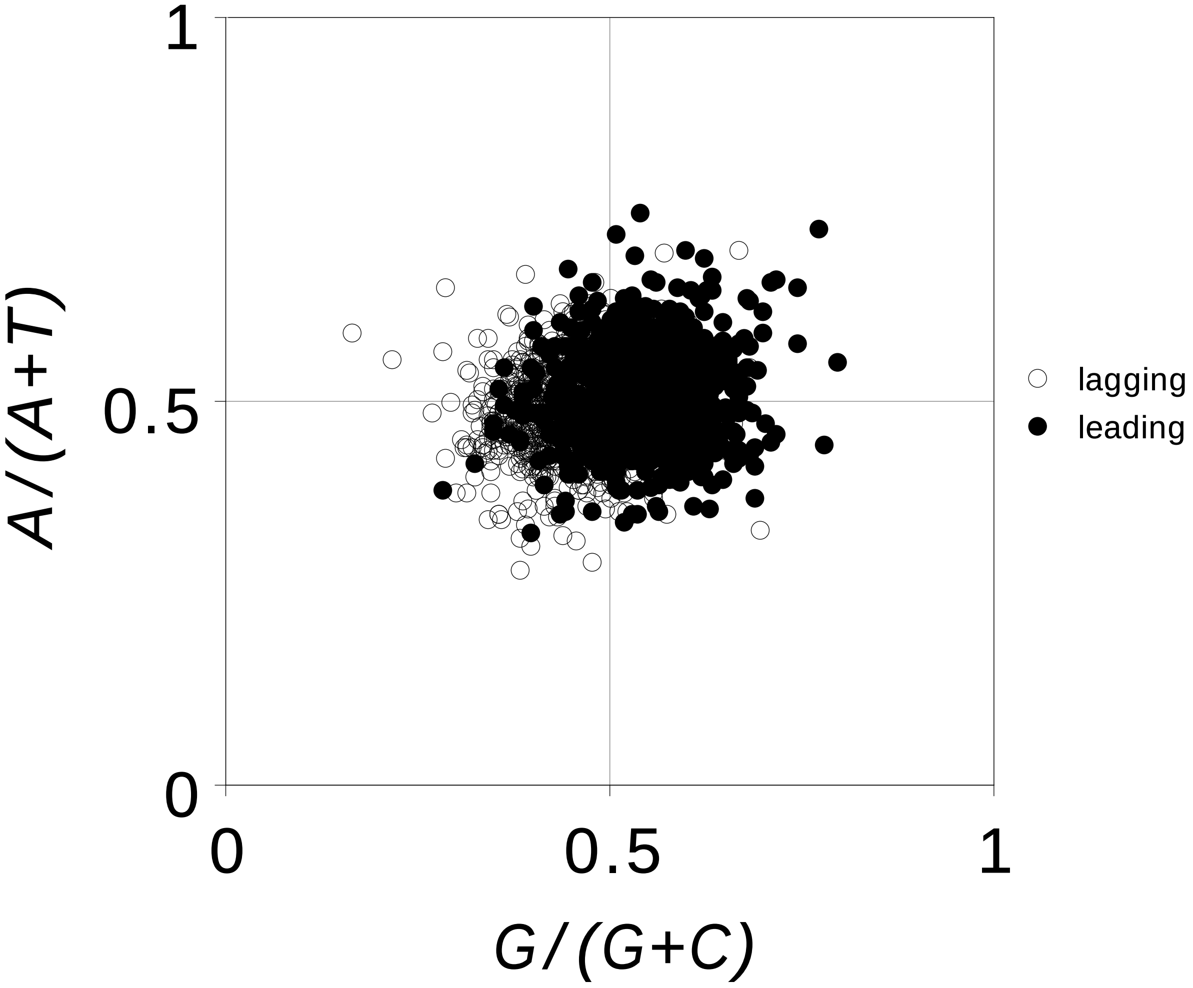


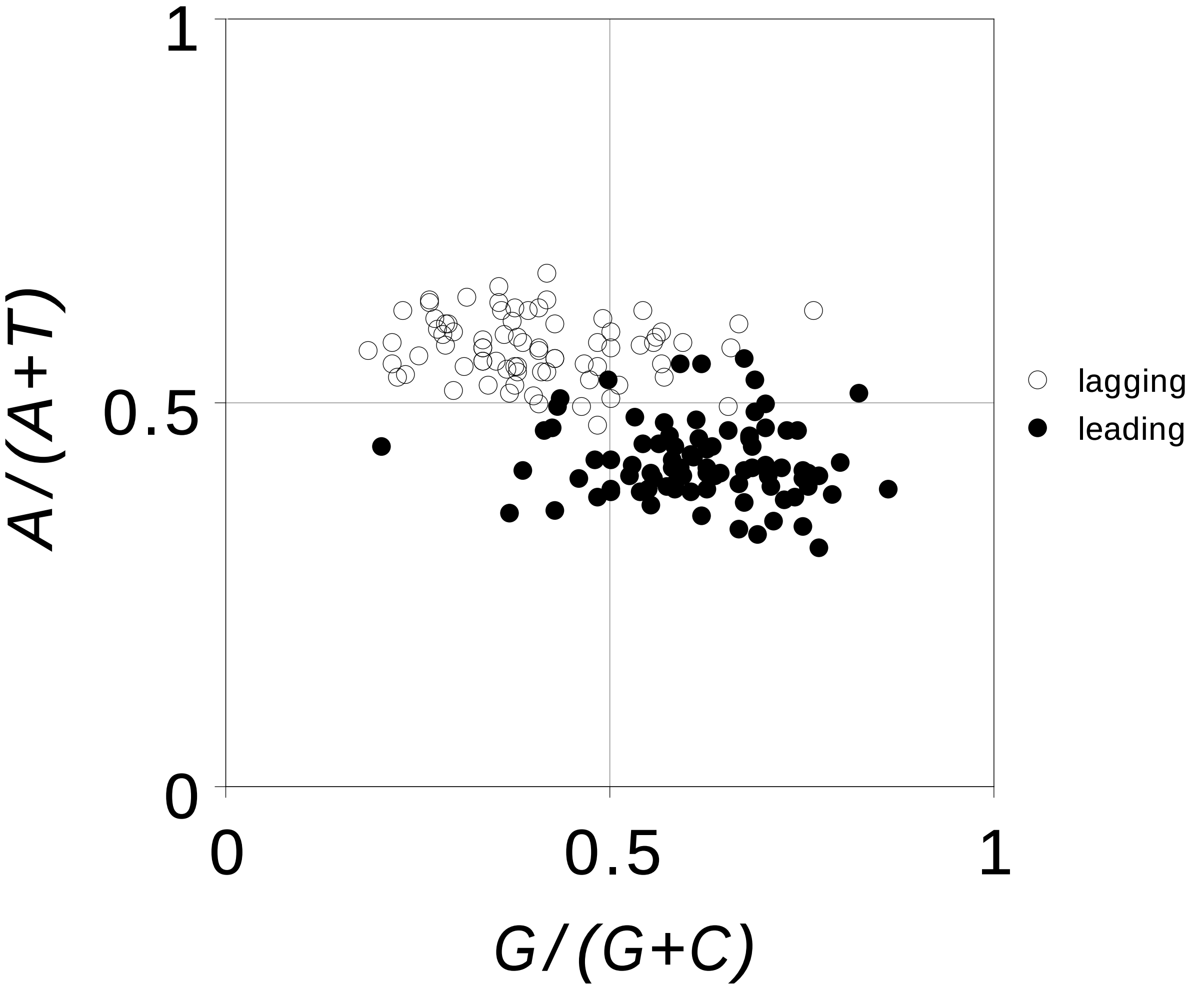
Table 3. Base composition in intergenic spaces (>100 bp) between the leading and the lagging groups. Indices are defined in the material and method section. #lead and #lag are the number of intergenic spaces in the leading and the lagging strand. The significance level (Sig.) for a difference between the two groups are: ns (not significant, $p \geq 0.05$); * ($0.01 \leq p < 0.05$); ** ($0.001 \leq p < 0.01$); *** ($p < 0.001$). The contribution in percent of replication-associated effects to PR2 deviations (B_I %) is given in **bold** when both differences x_1 - x_2 and y_1 - y_2 are highly significant ($p < 0.01$). When a difference is significant between the two groups a red color outlines the highest value and a blue color the lowest value.



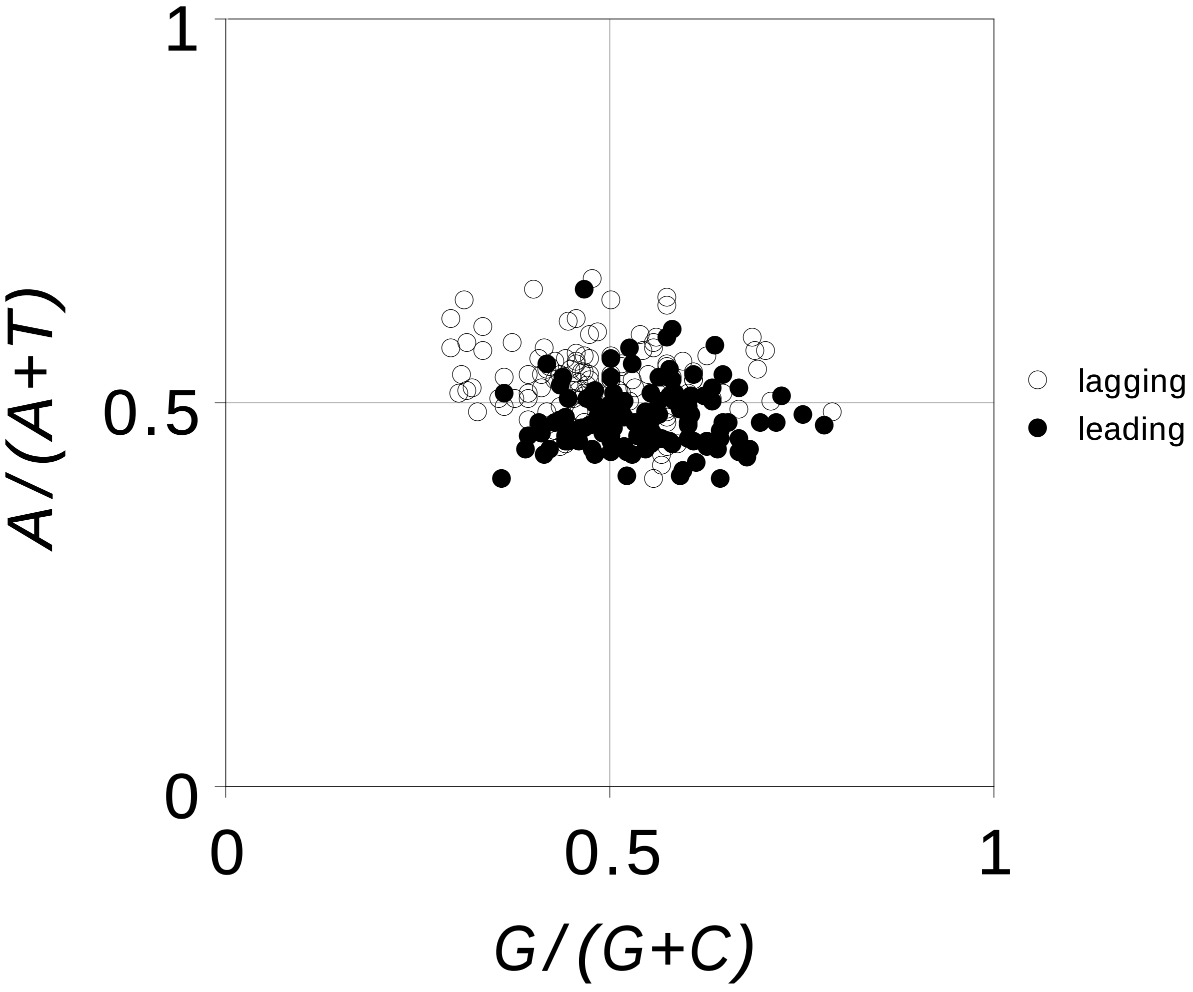
Bacillus halodurans



Bacillus subtilis



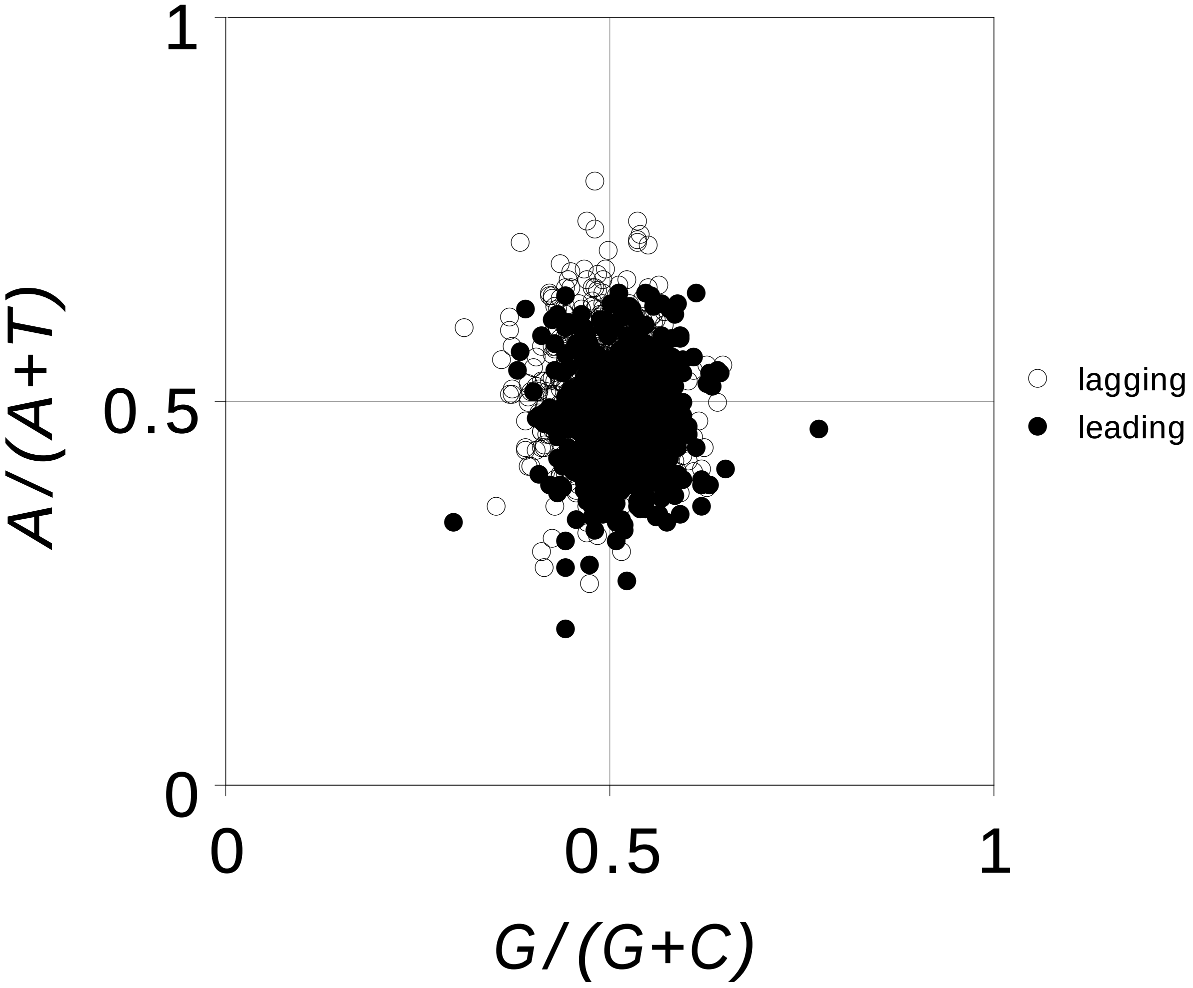
Borrelia burgdorferi



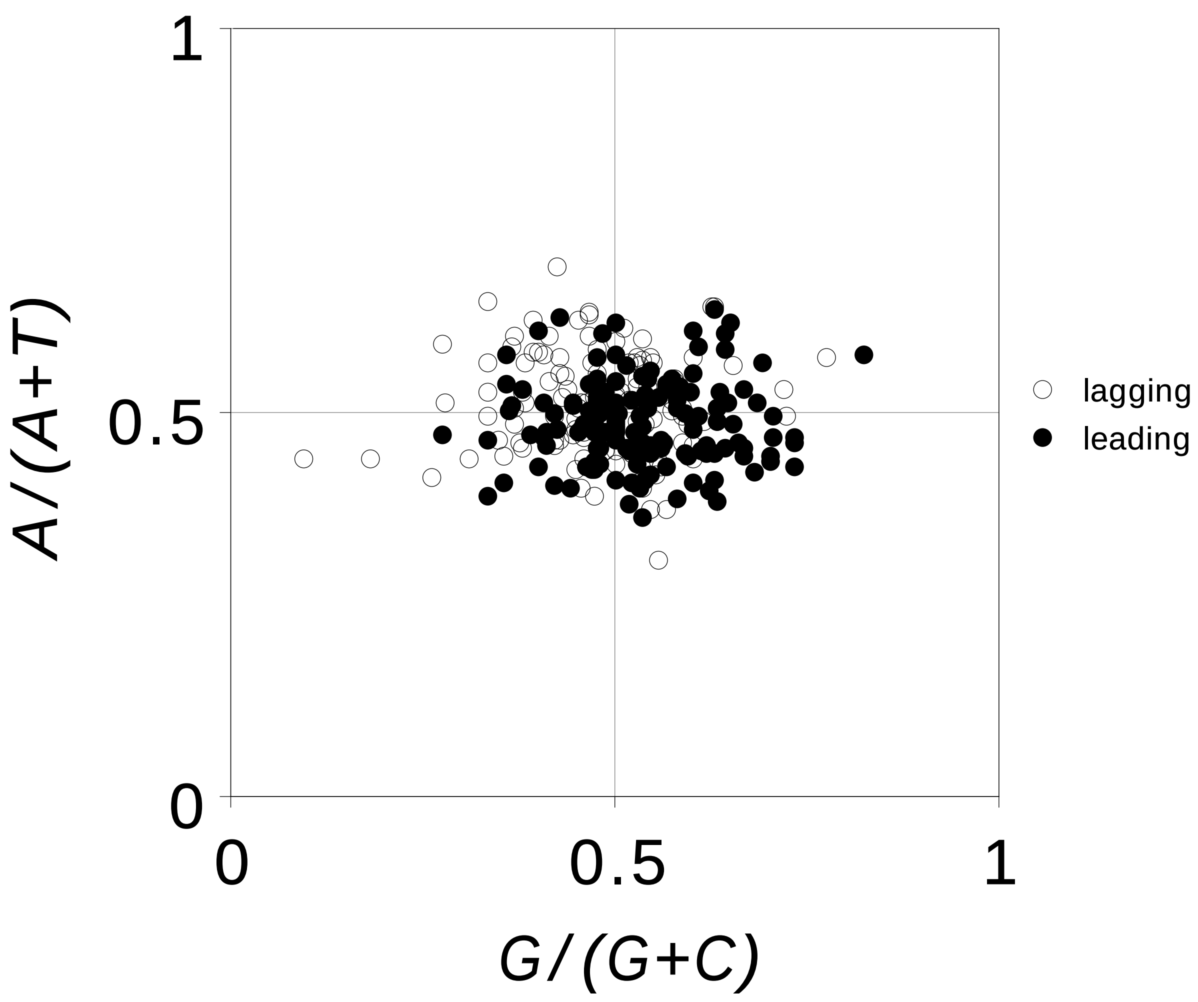
Buchnera sp.

To coding sequences in Buch

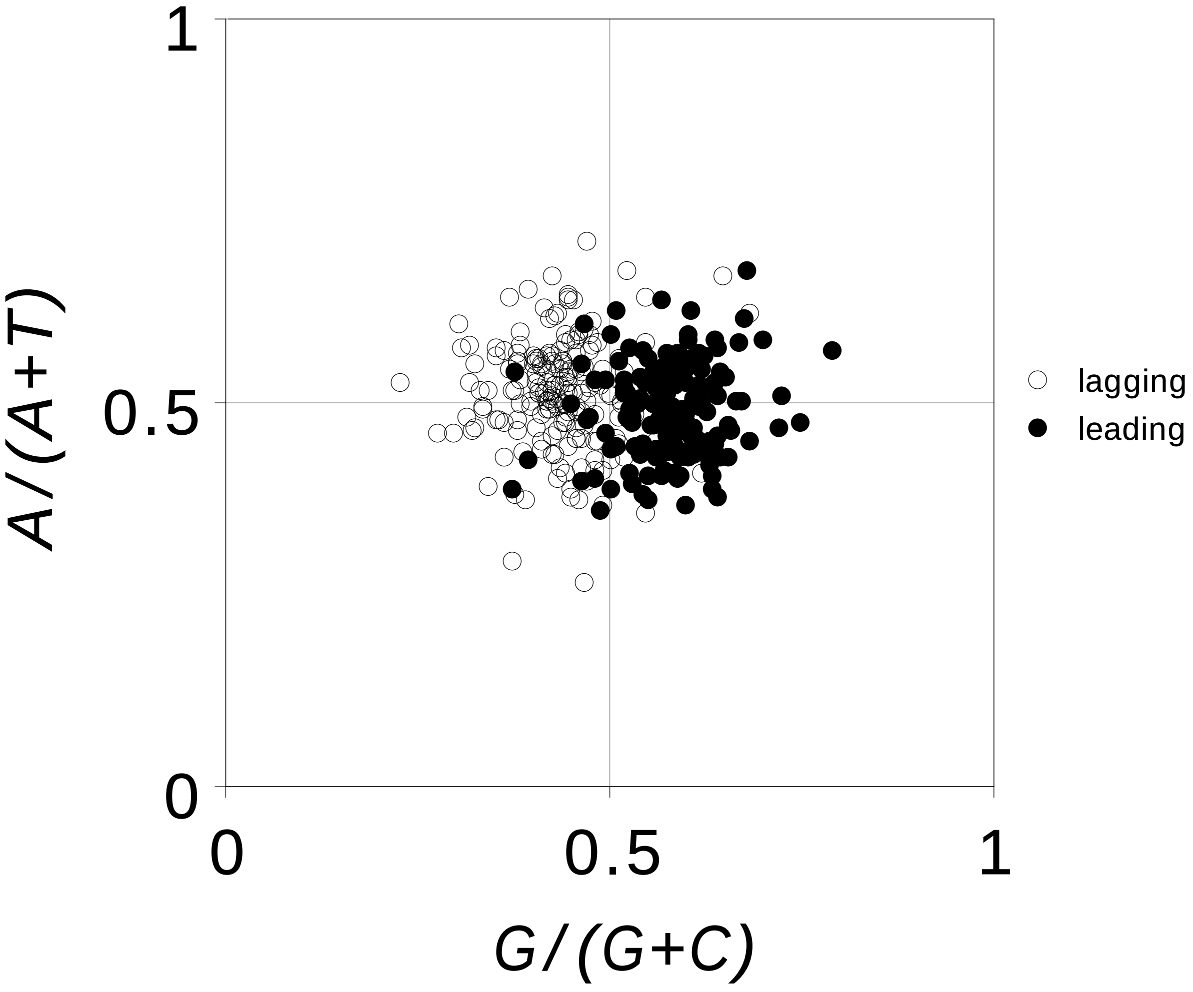
To small intergenic spaces in Buch



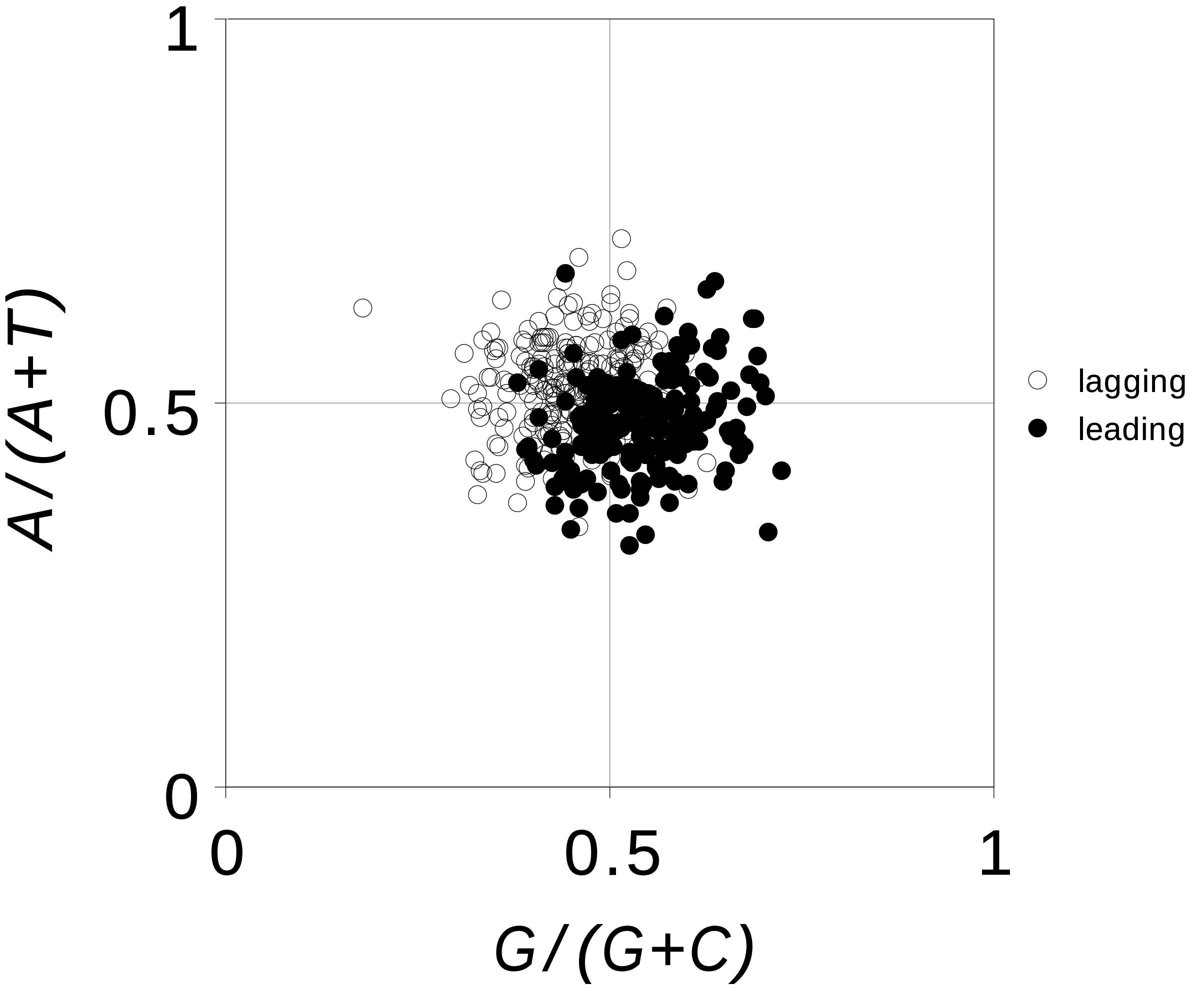
Caulobacter crescentus



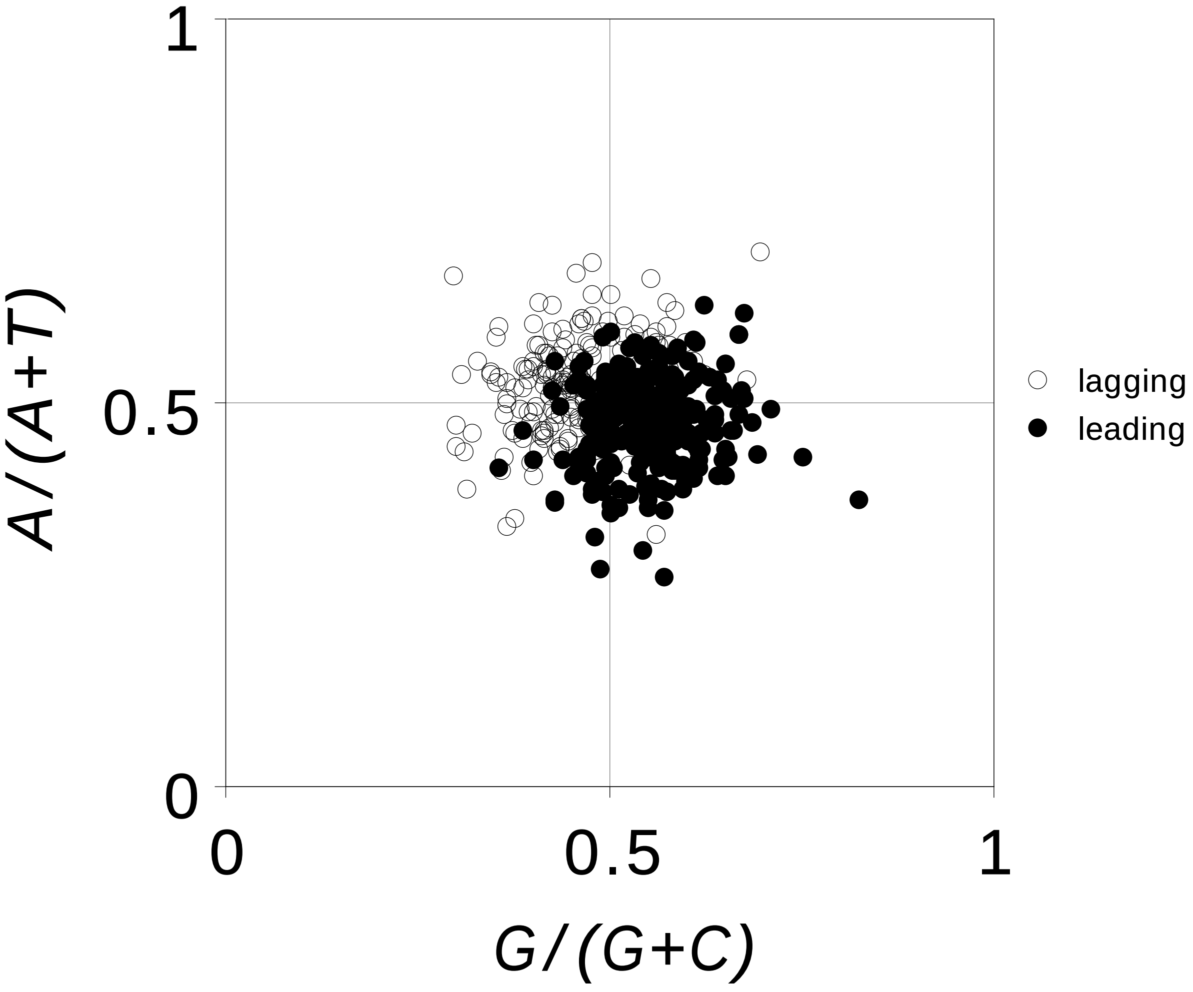
Campylobacter jejuni



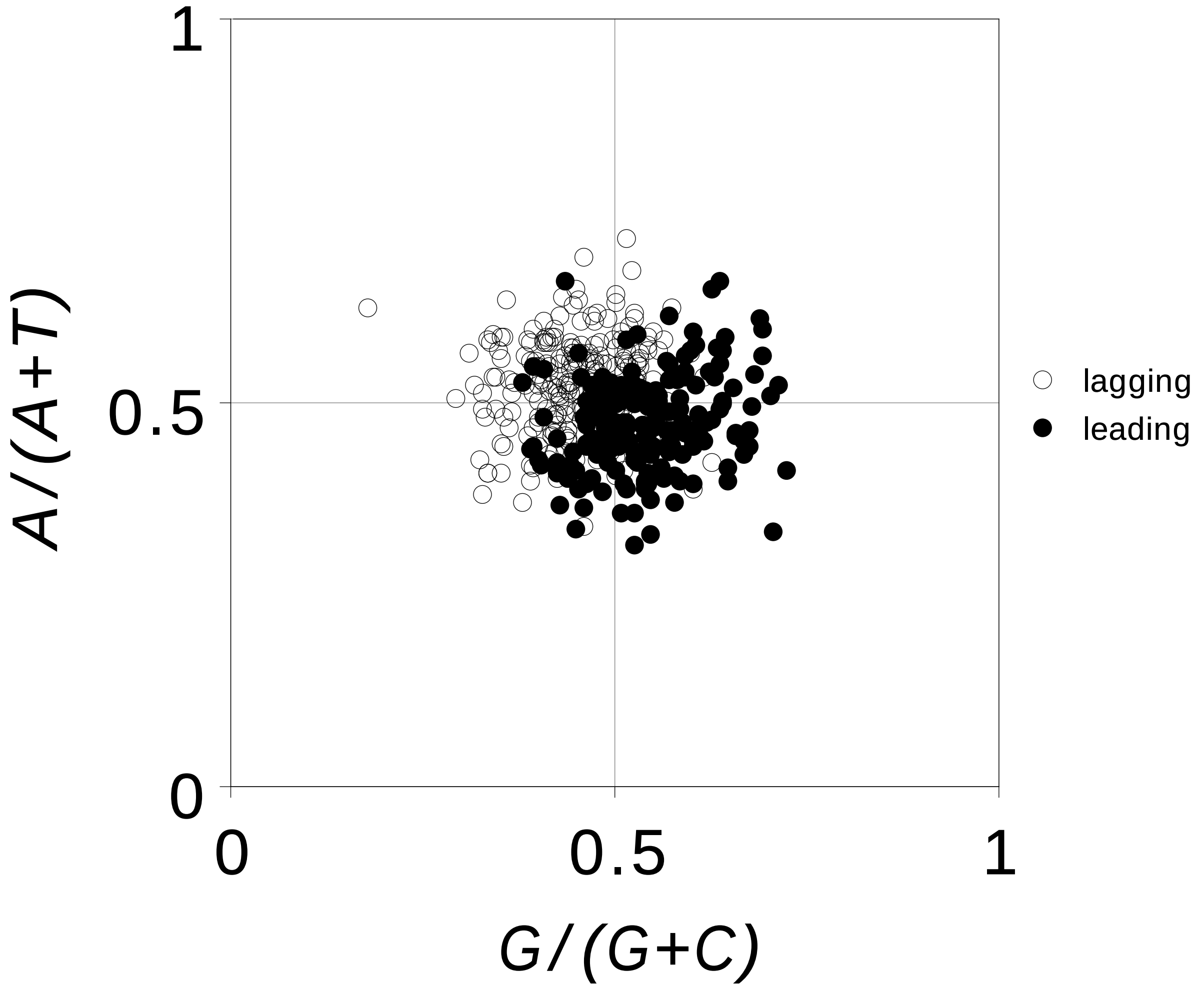
Chlamydia muridarum



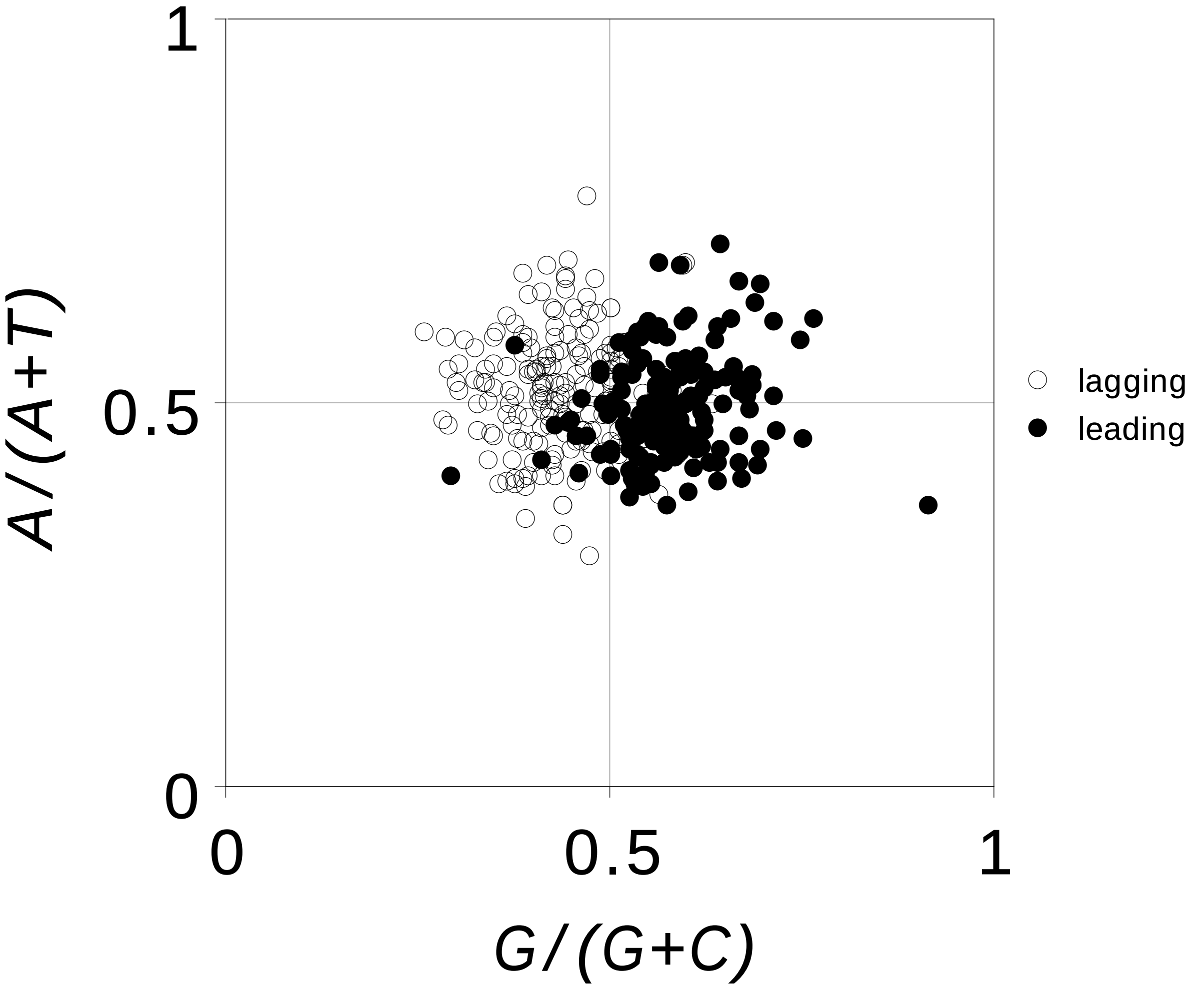
Chlamydophila pneumoniae CWL029



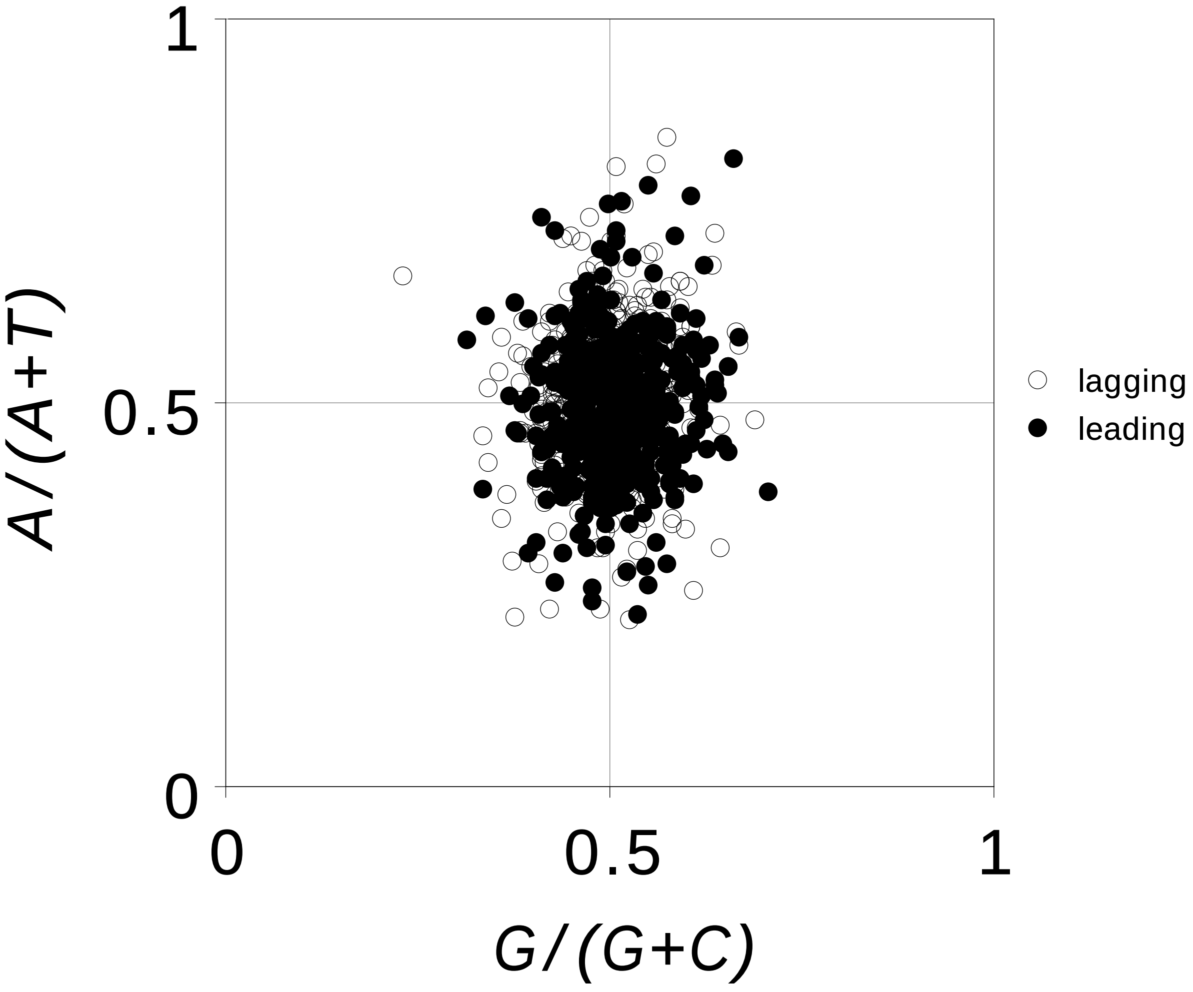
Chlamydophila pneumoniae AR39



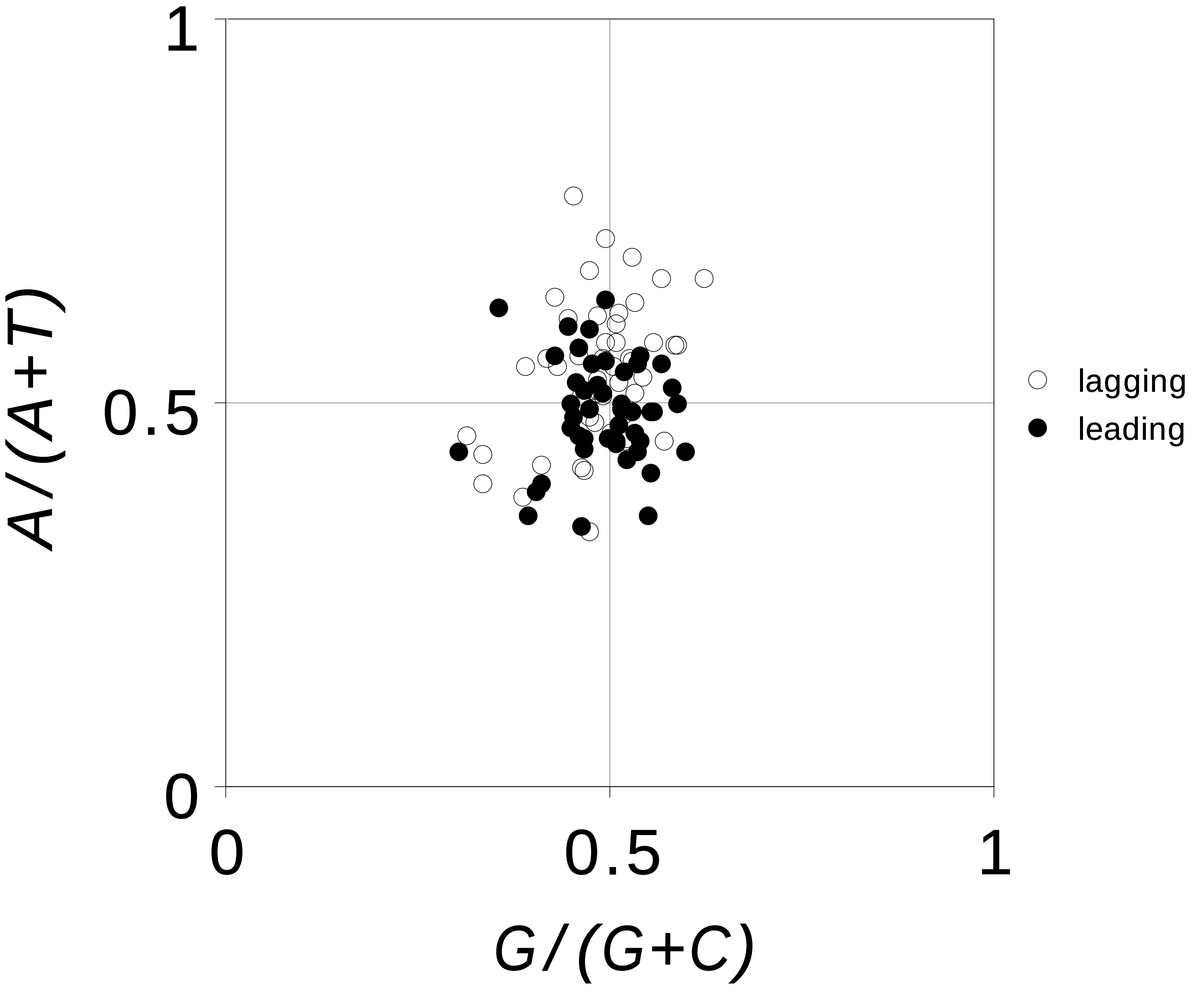
Chlamydophila pneumoniae J138



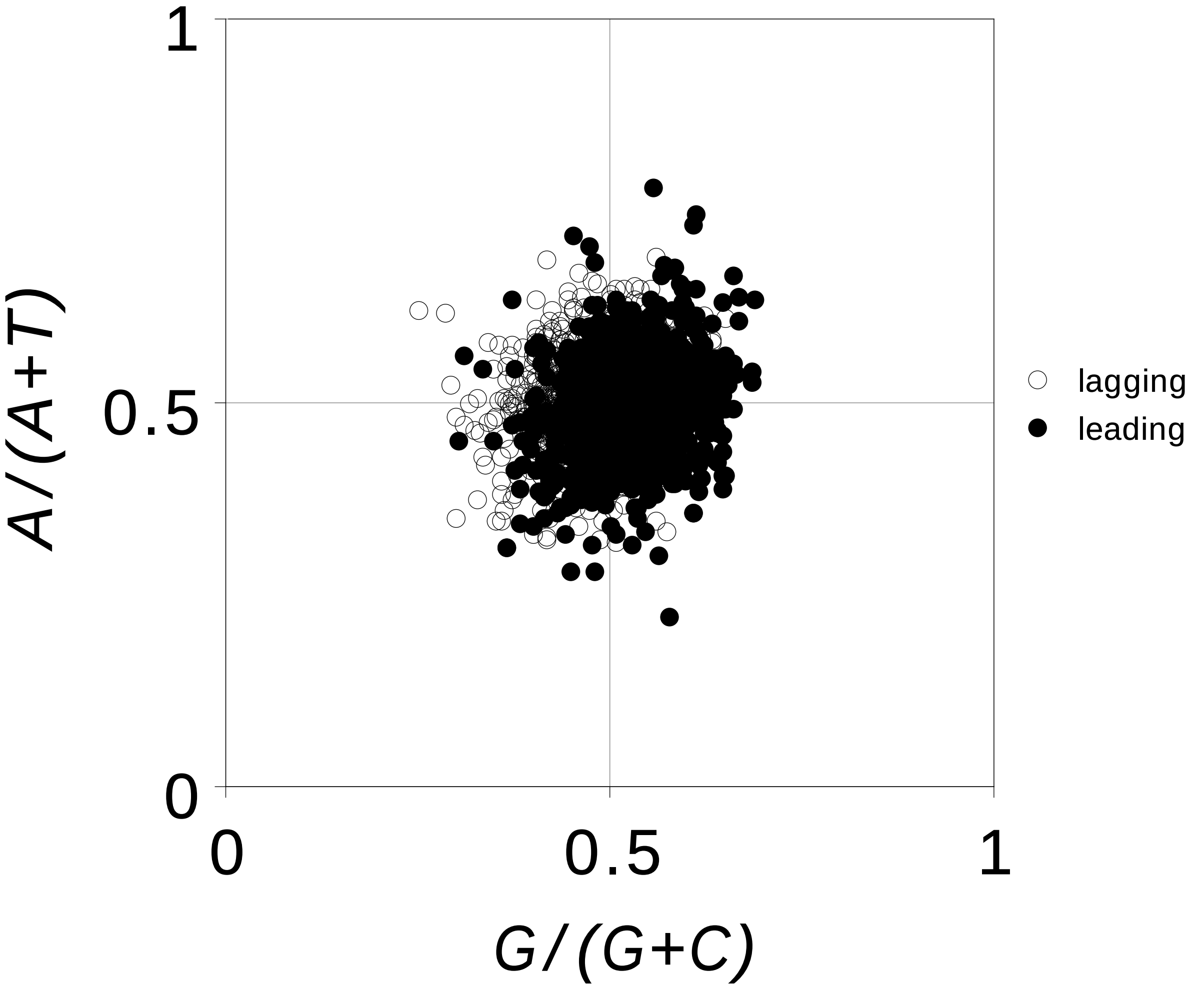
Chlamydia trachomatis



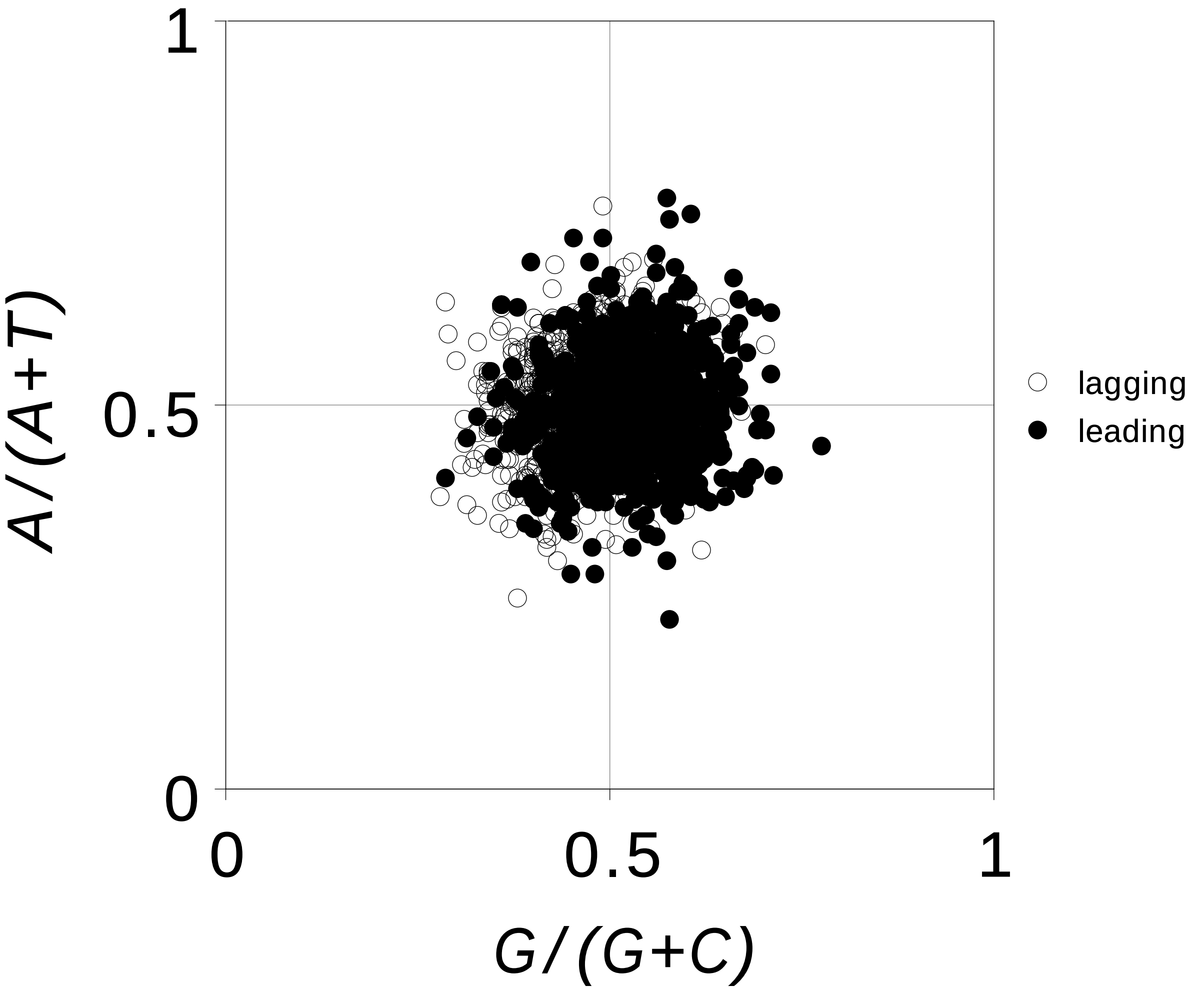
Deinococcus radiodurans chromosome 1



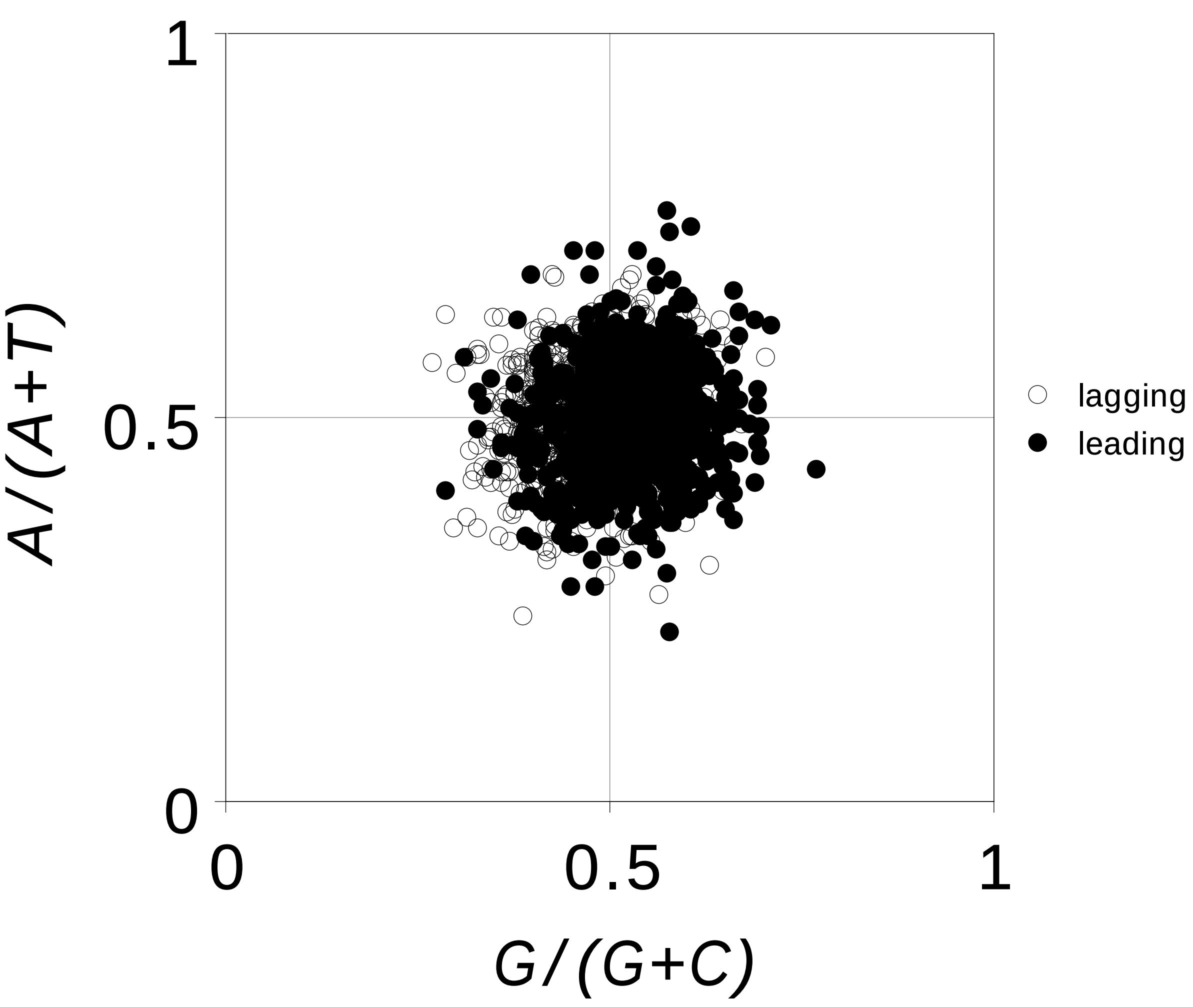
Deinococcus radiodurans chromosome 2



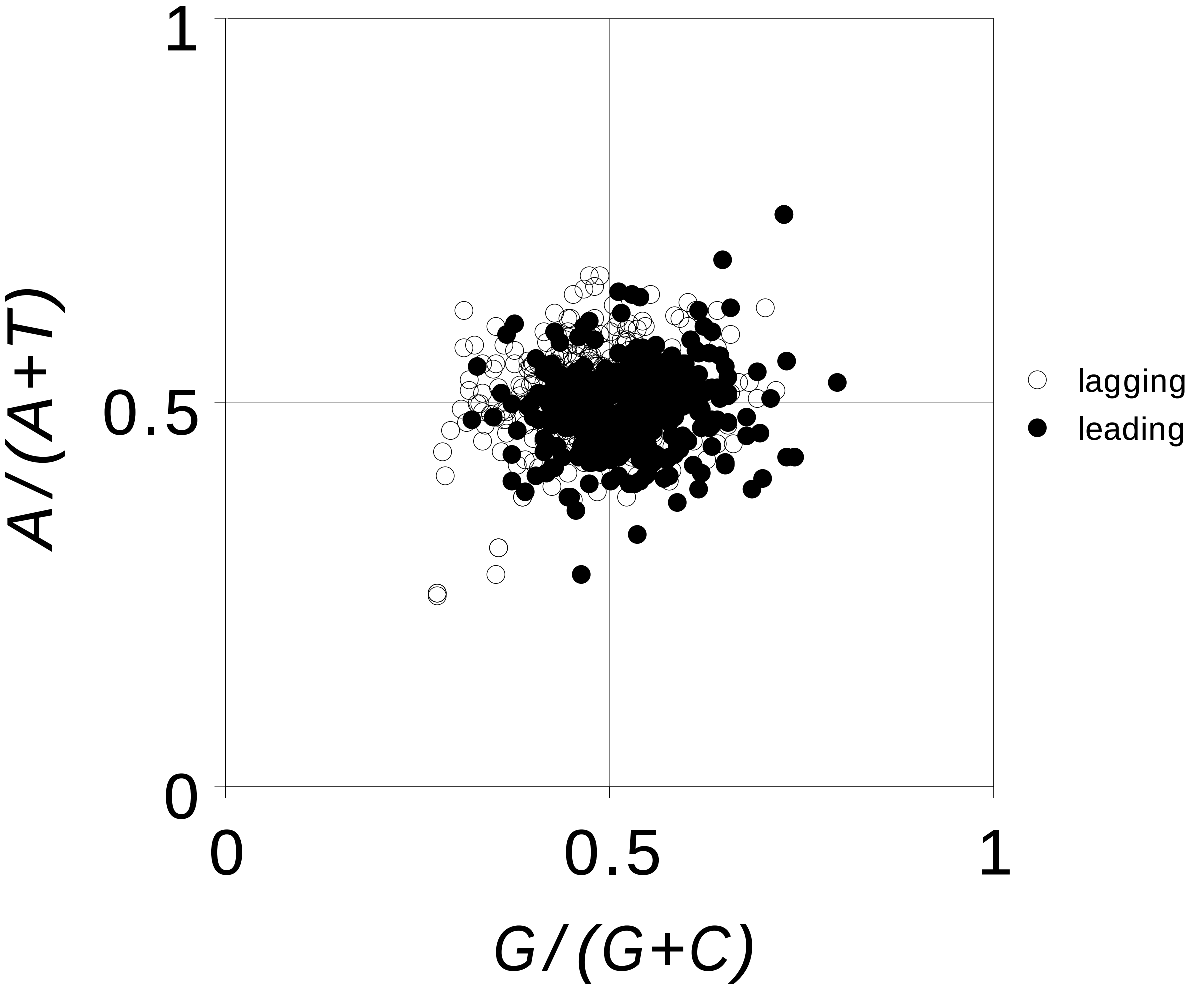
Escherichia coli K-12



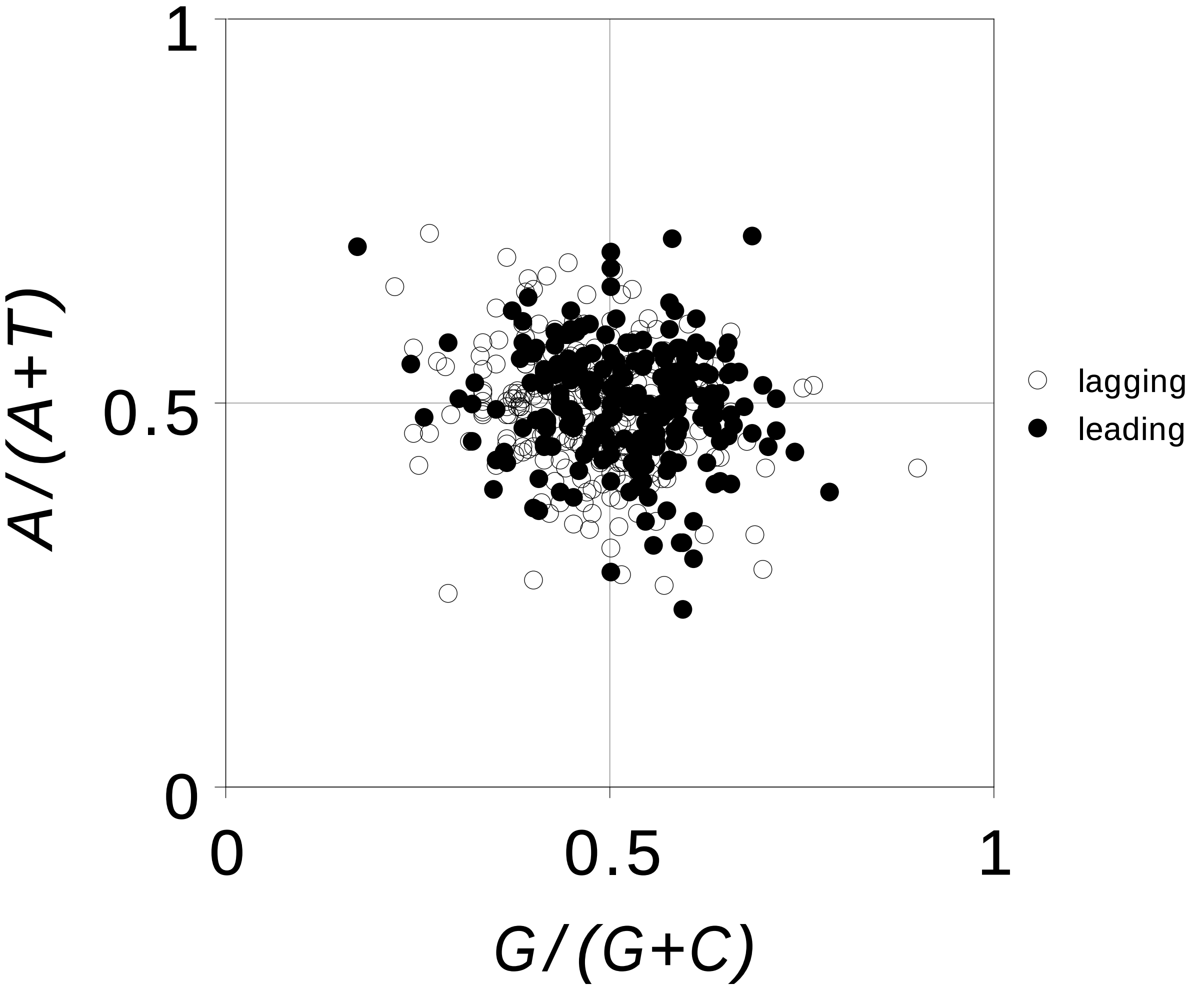
Escherichia coli EDL933



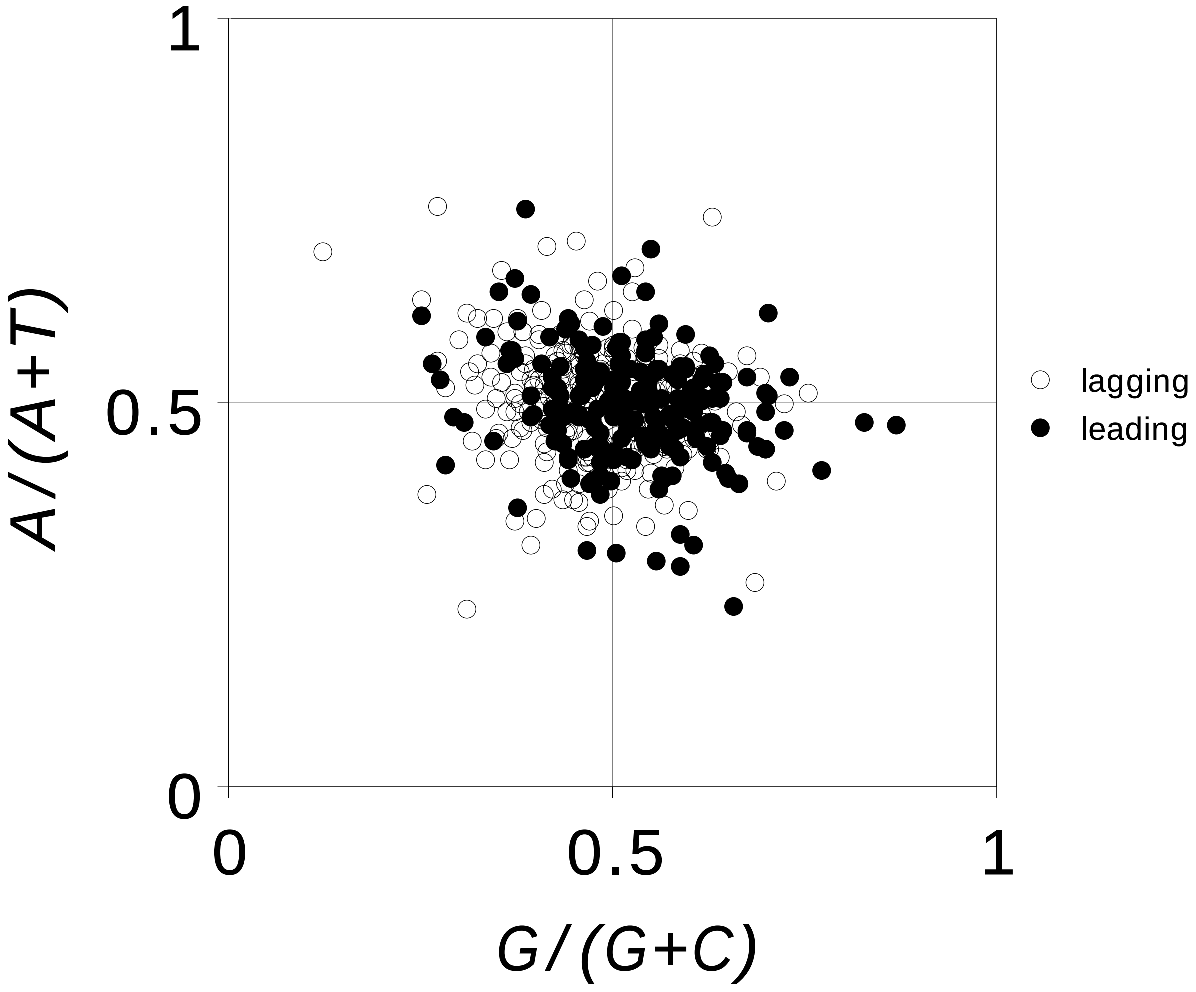
Escherichia coli RIMD 0509952



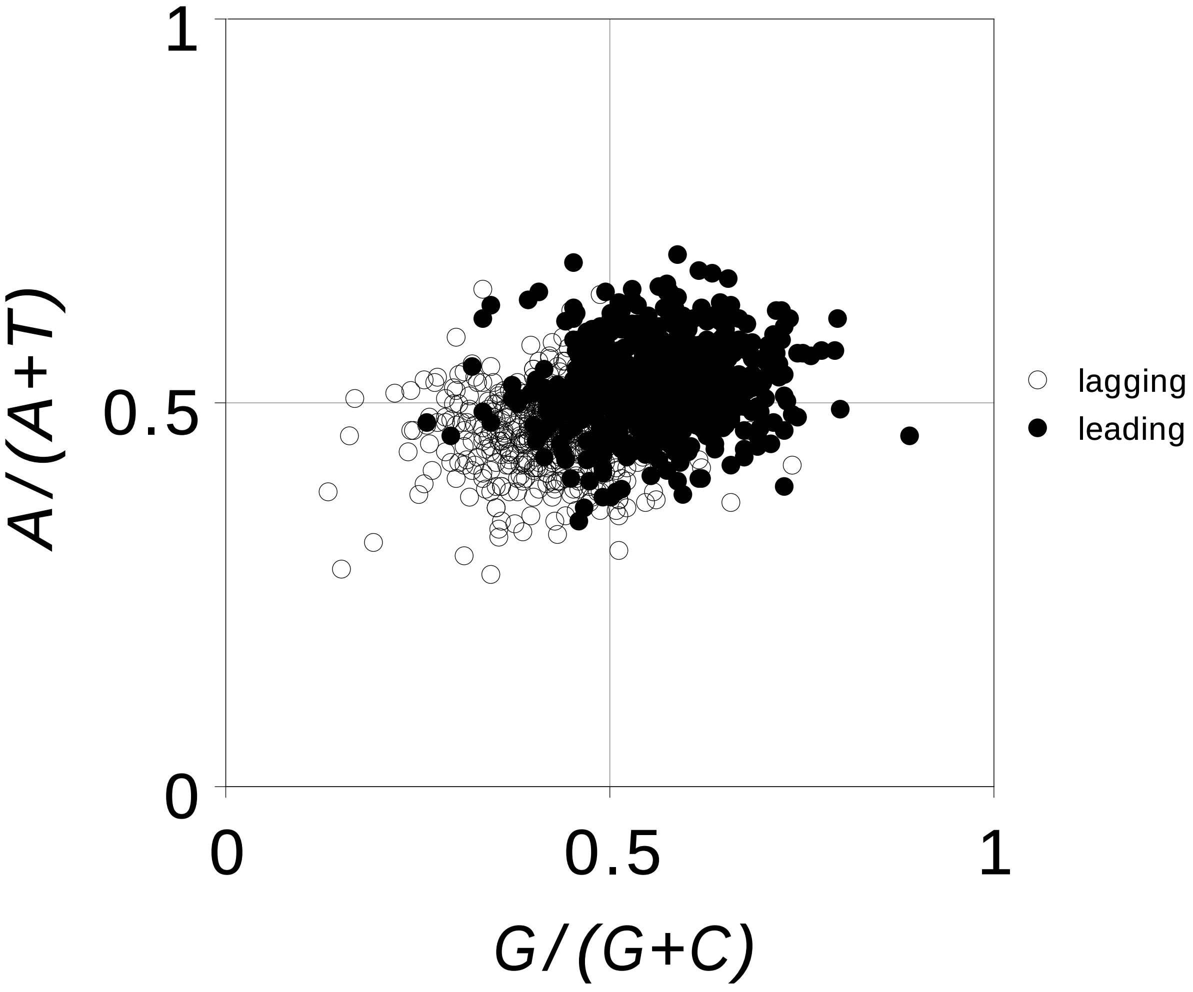
Haemophilus influenzae



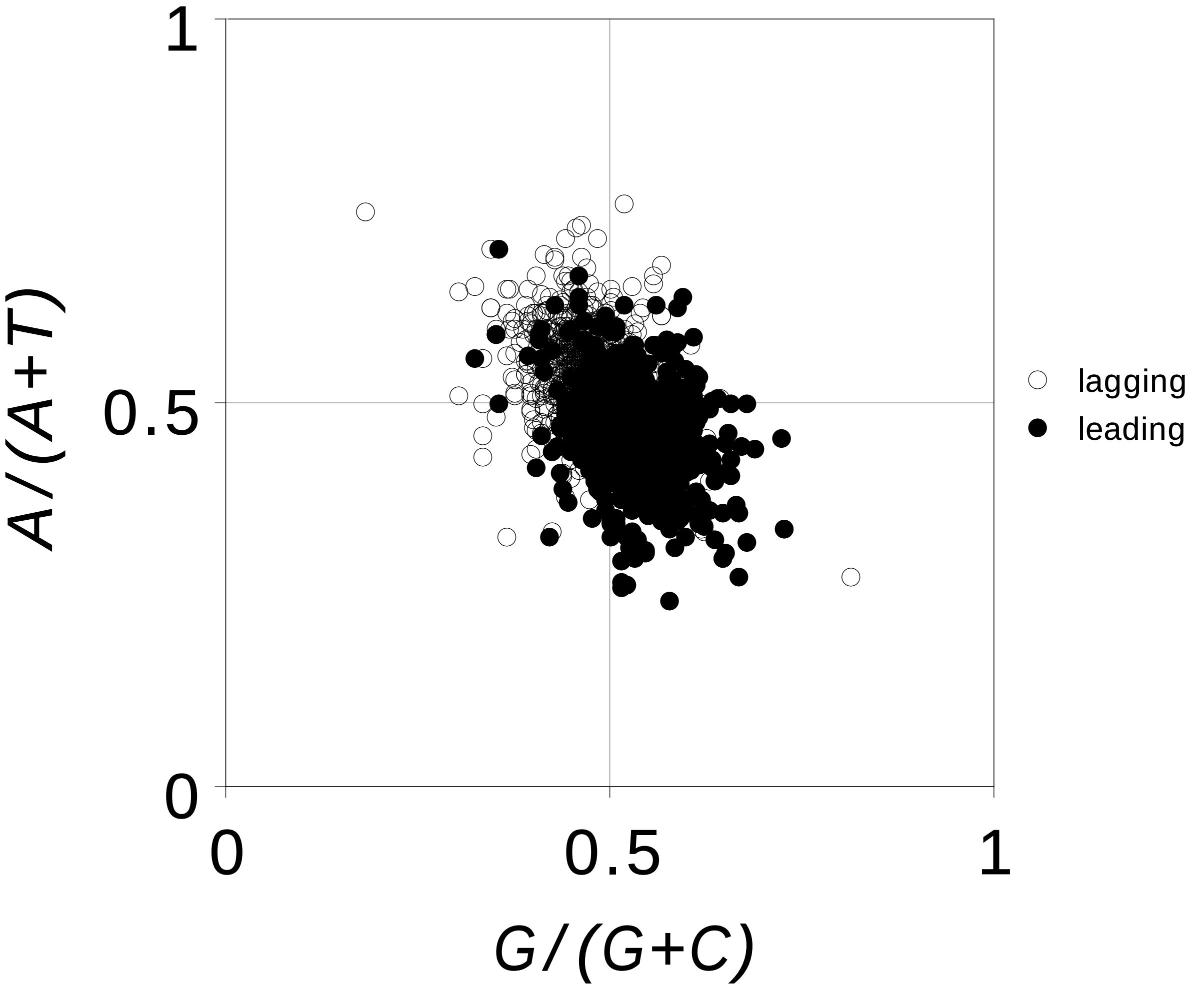
Helicobacter pylori 26695



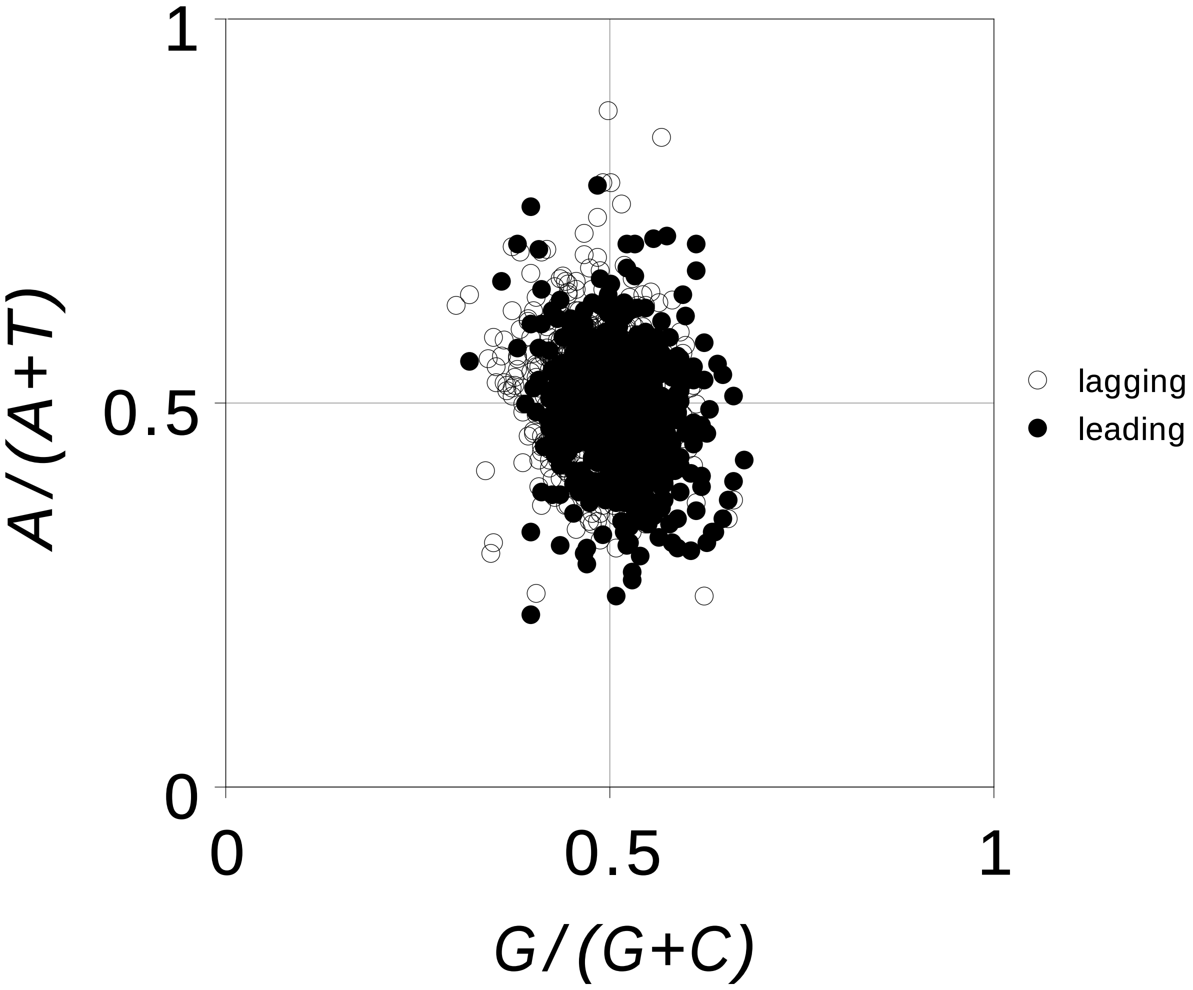
Helicobacter pylori J99



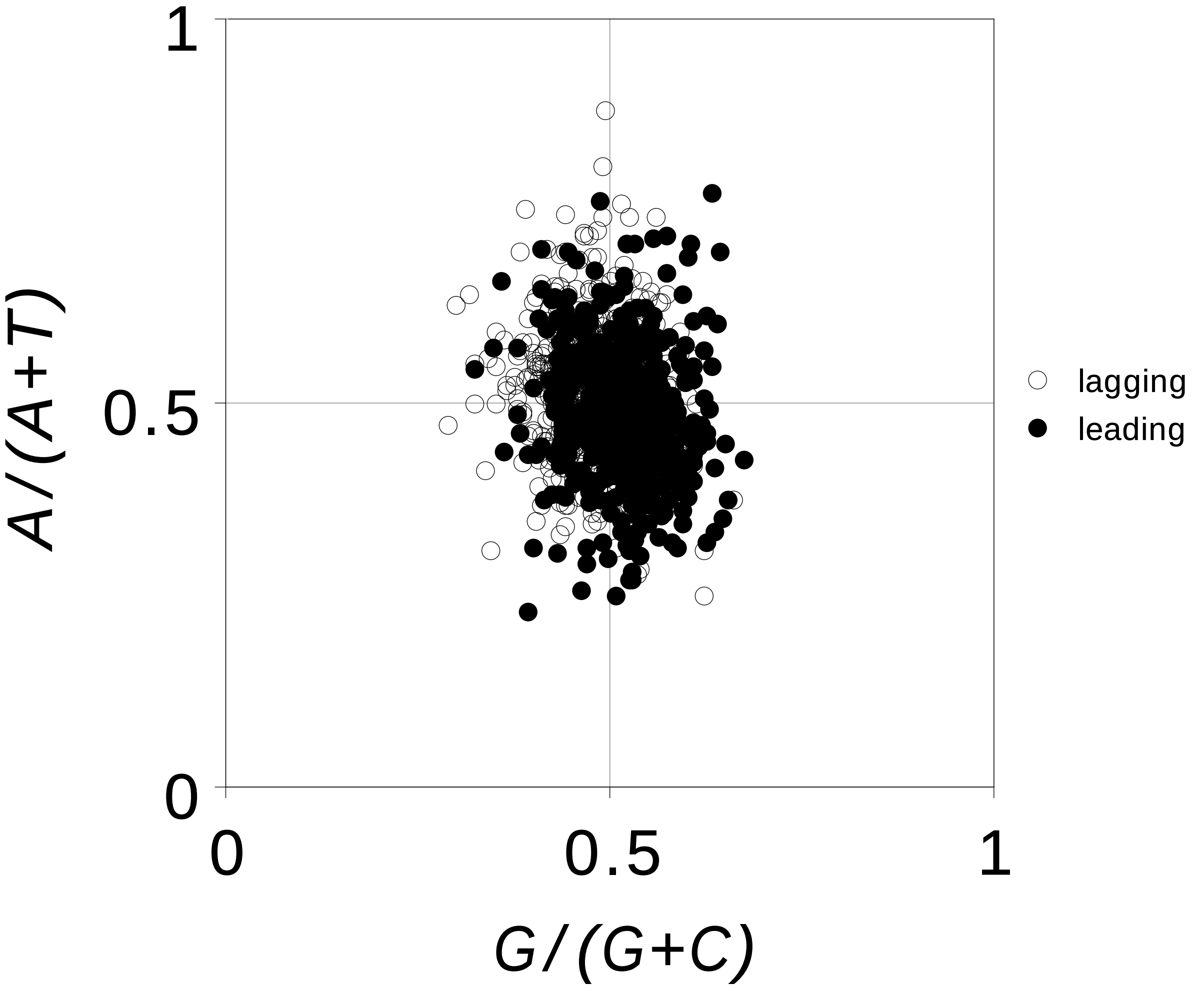
Lactococcus lactis



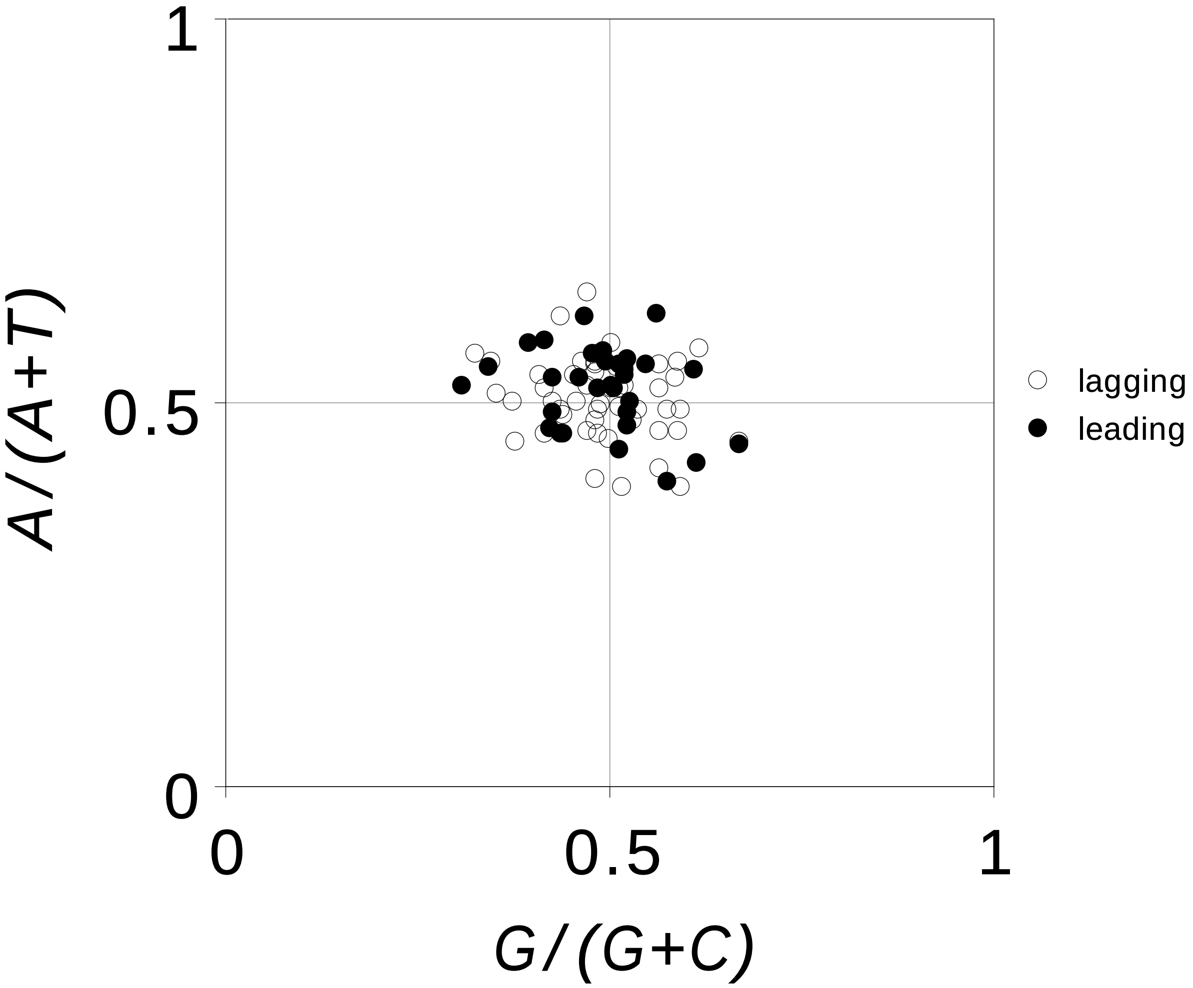
Mycobacterium leprae



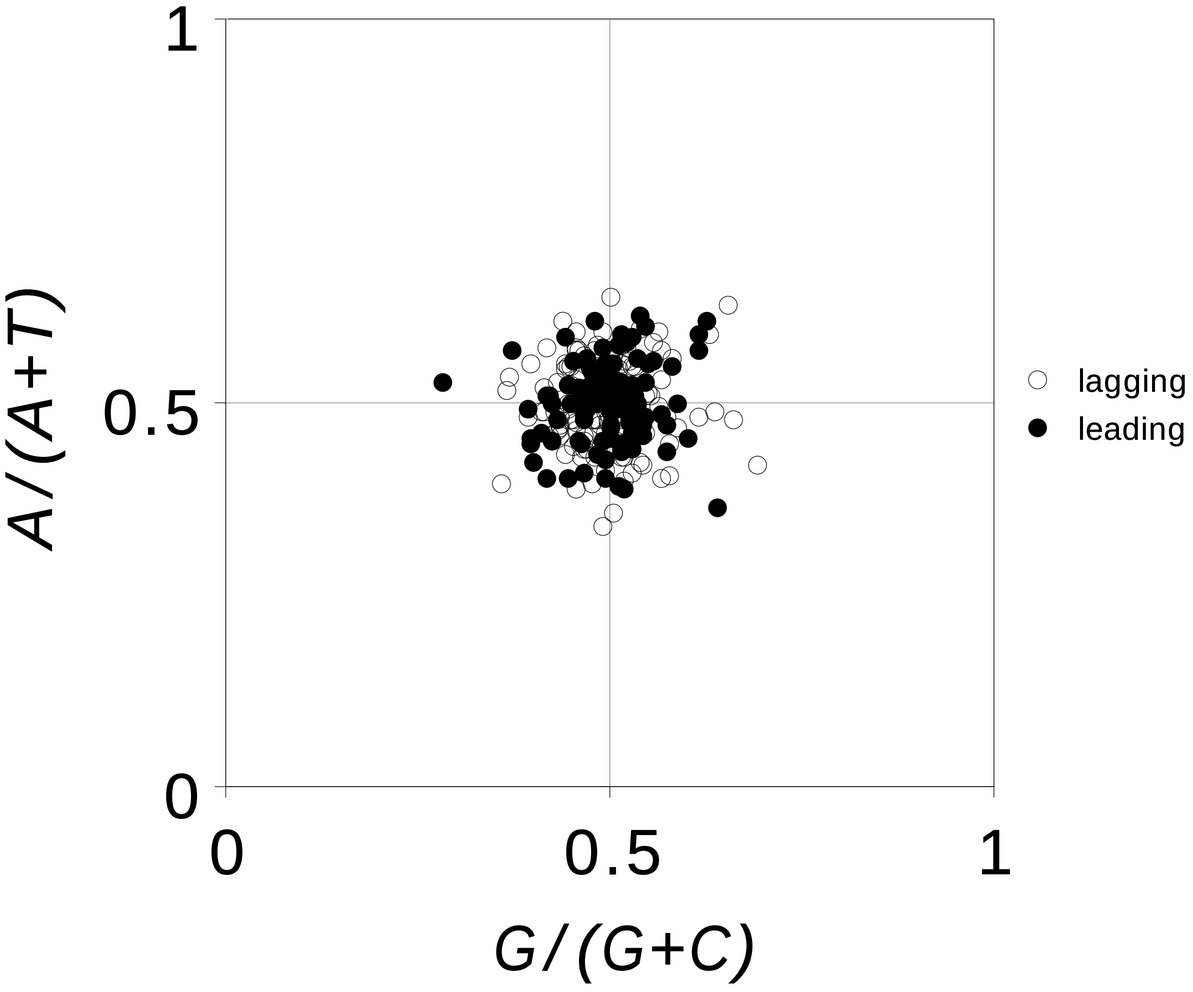
Mycobacterium tuberculosis H37Rv



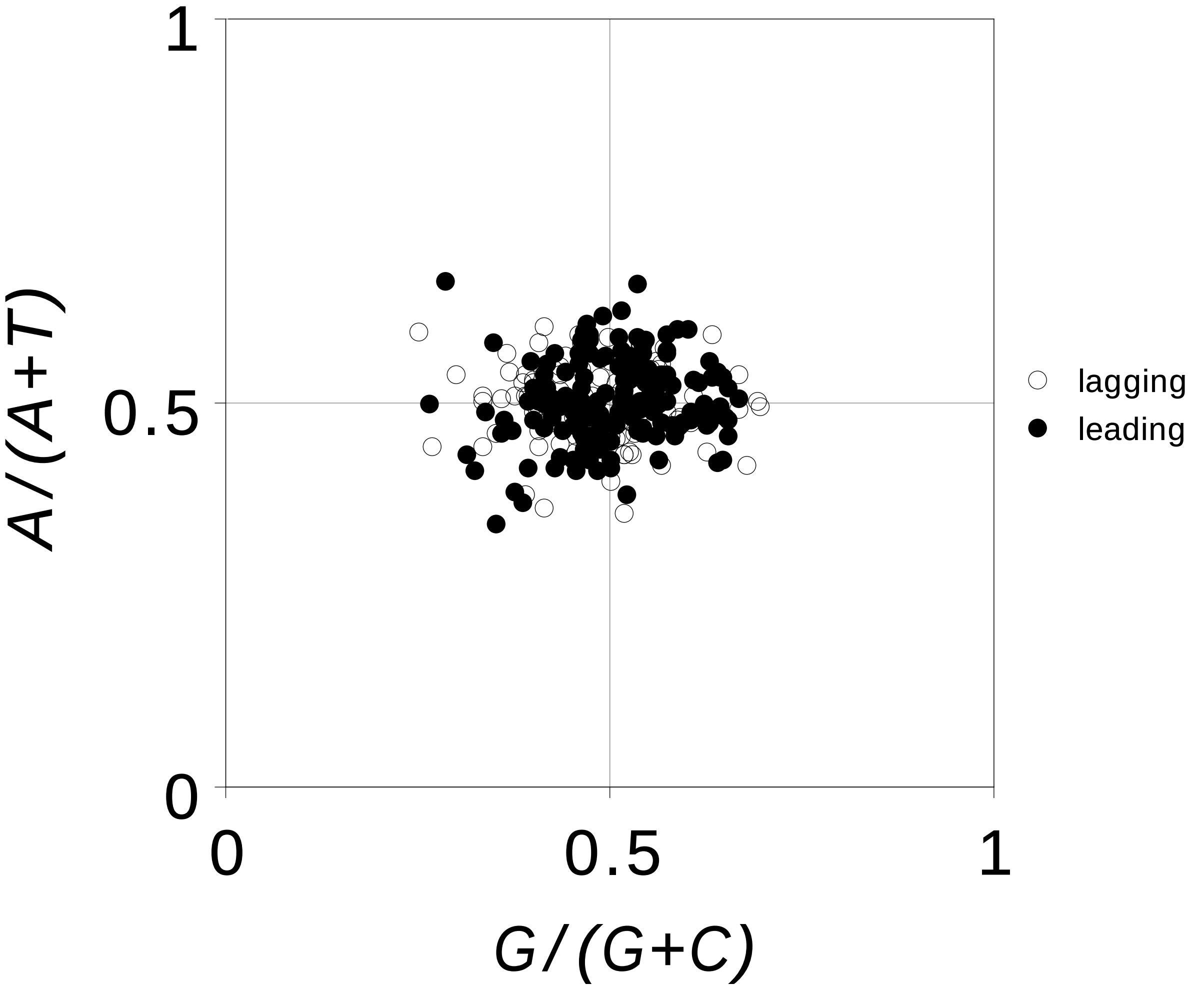
Mycobacterium tuberculosis CDC1551



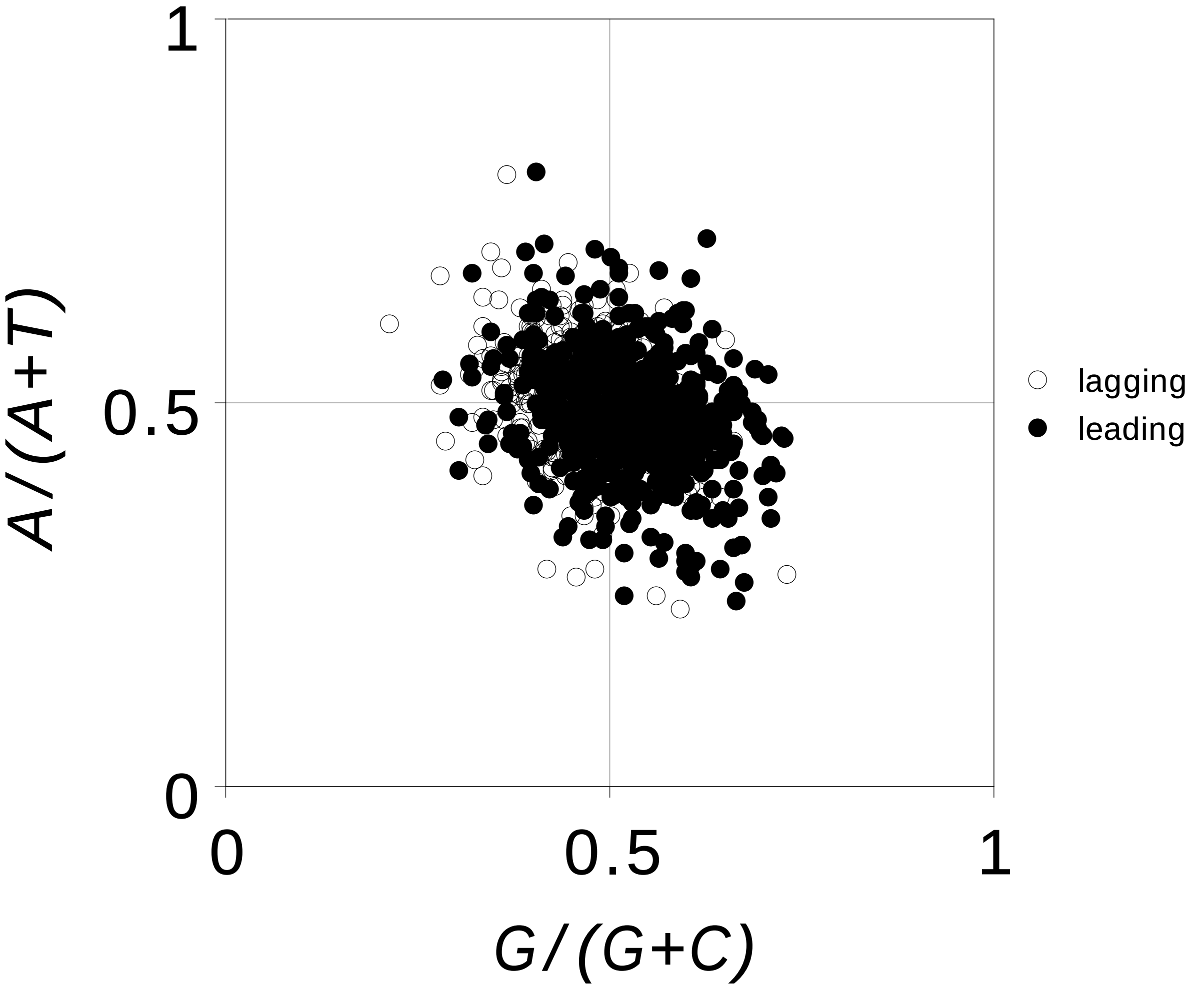
Mycoplasma genitalium



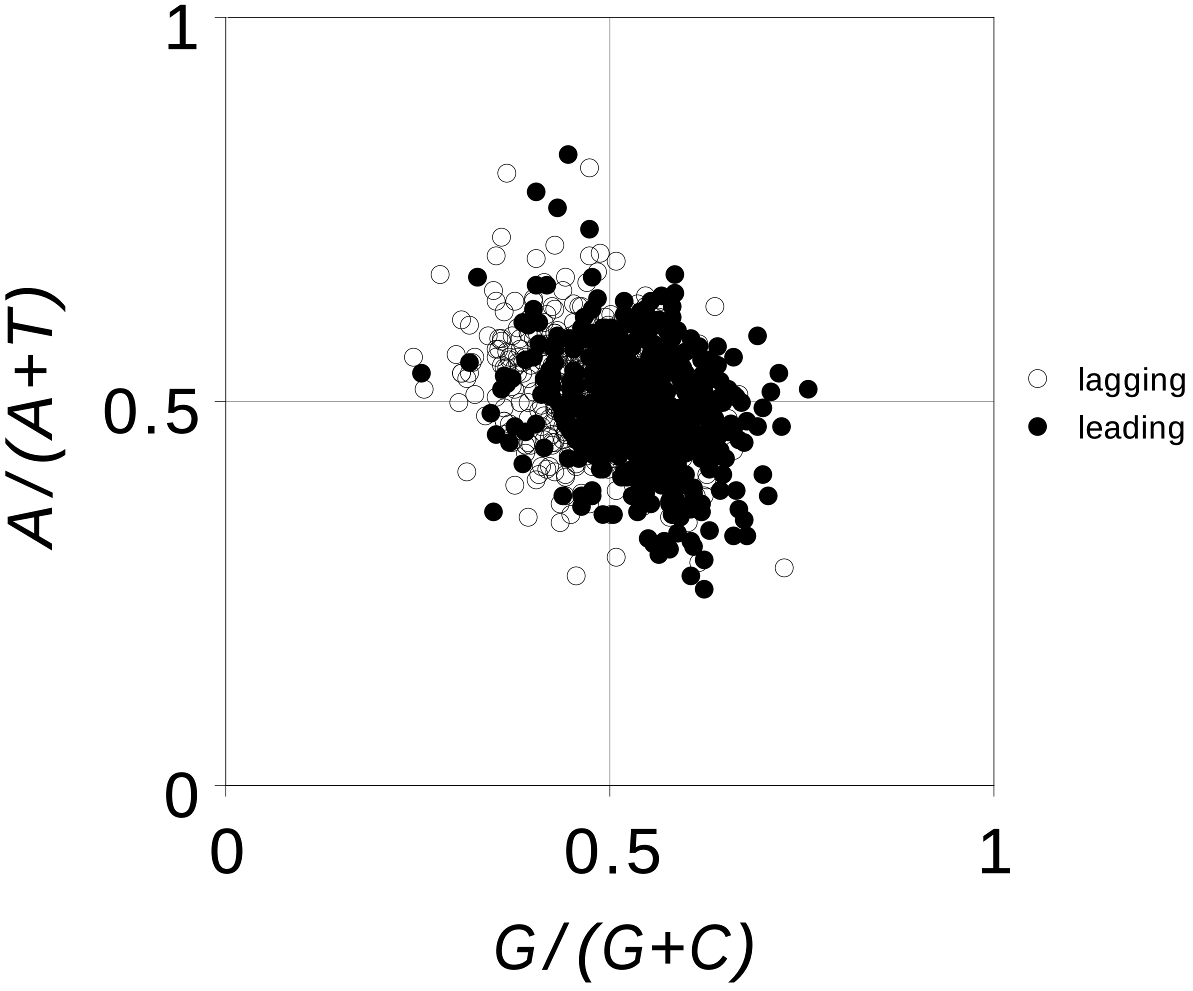
Mycoplasma pneumoniae



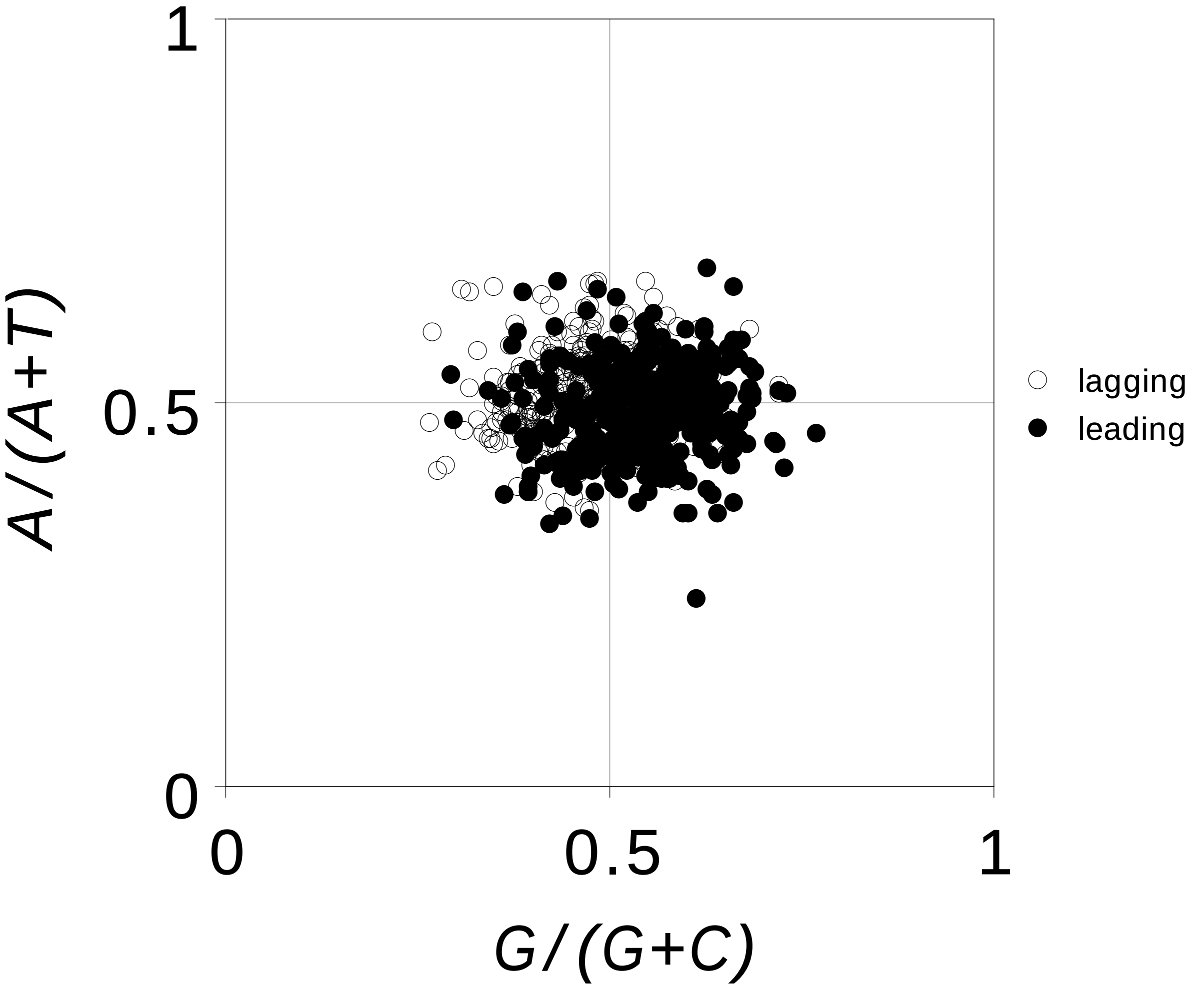
Mycoplasma pulmonis



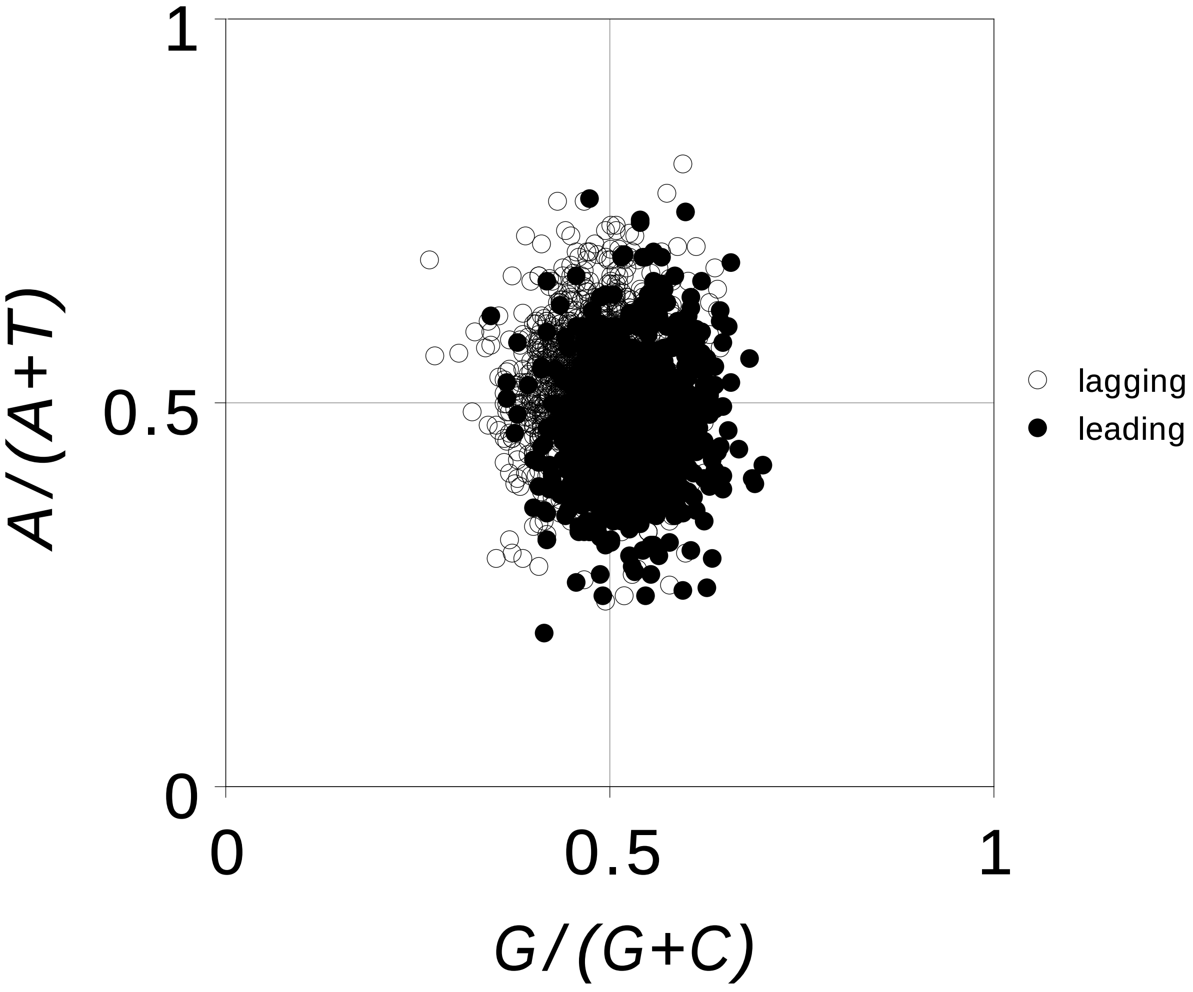
Neisseria meningitidis Z2491 (A)



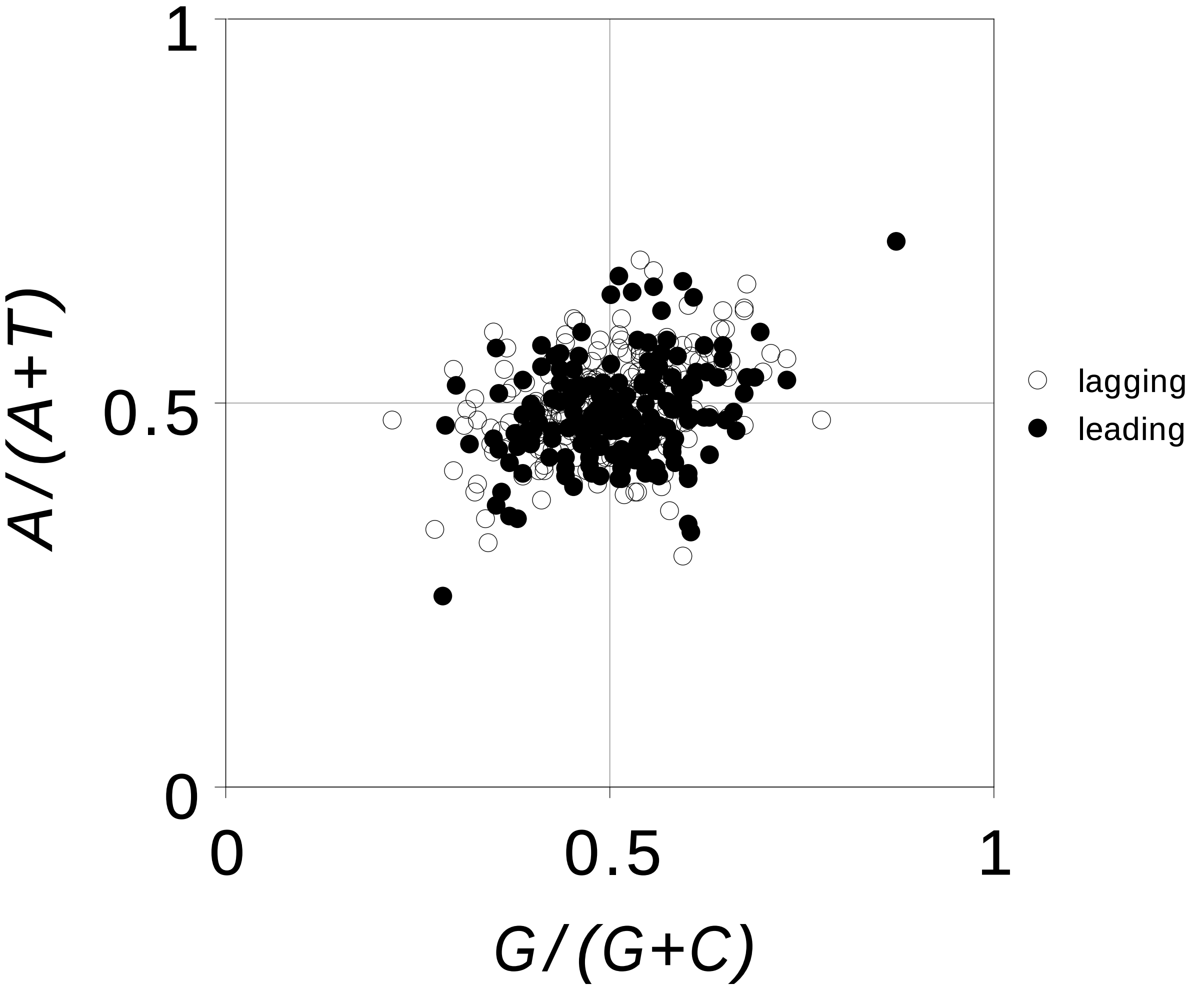
Neisseria meningitidis MC58 (B)



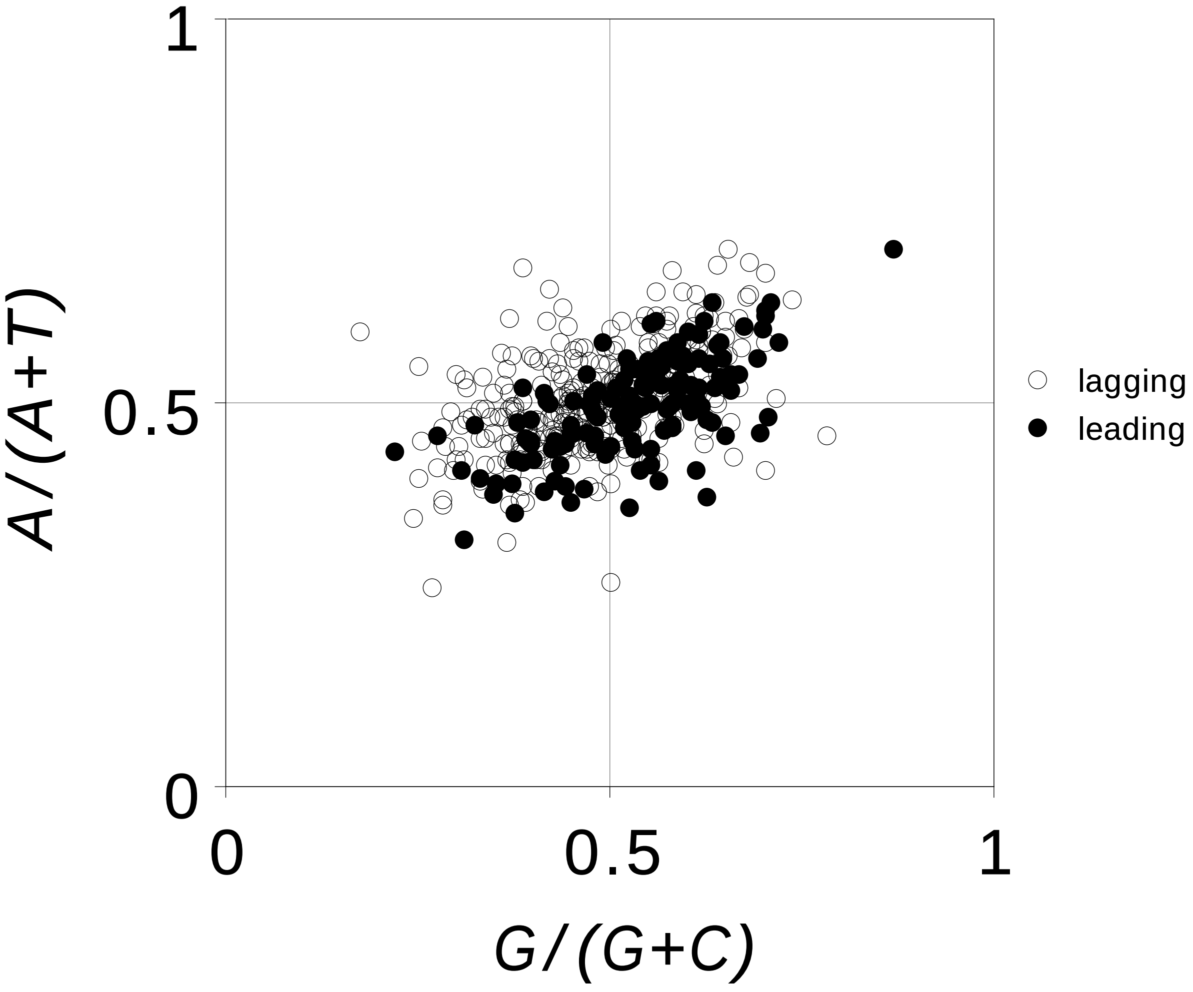
Pasteurella multocida



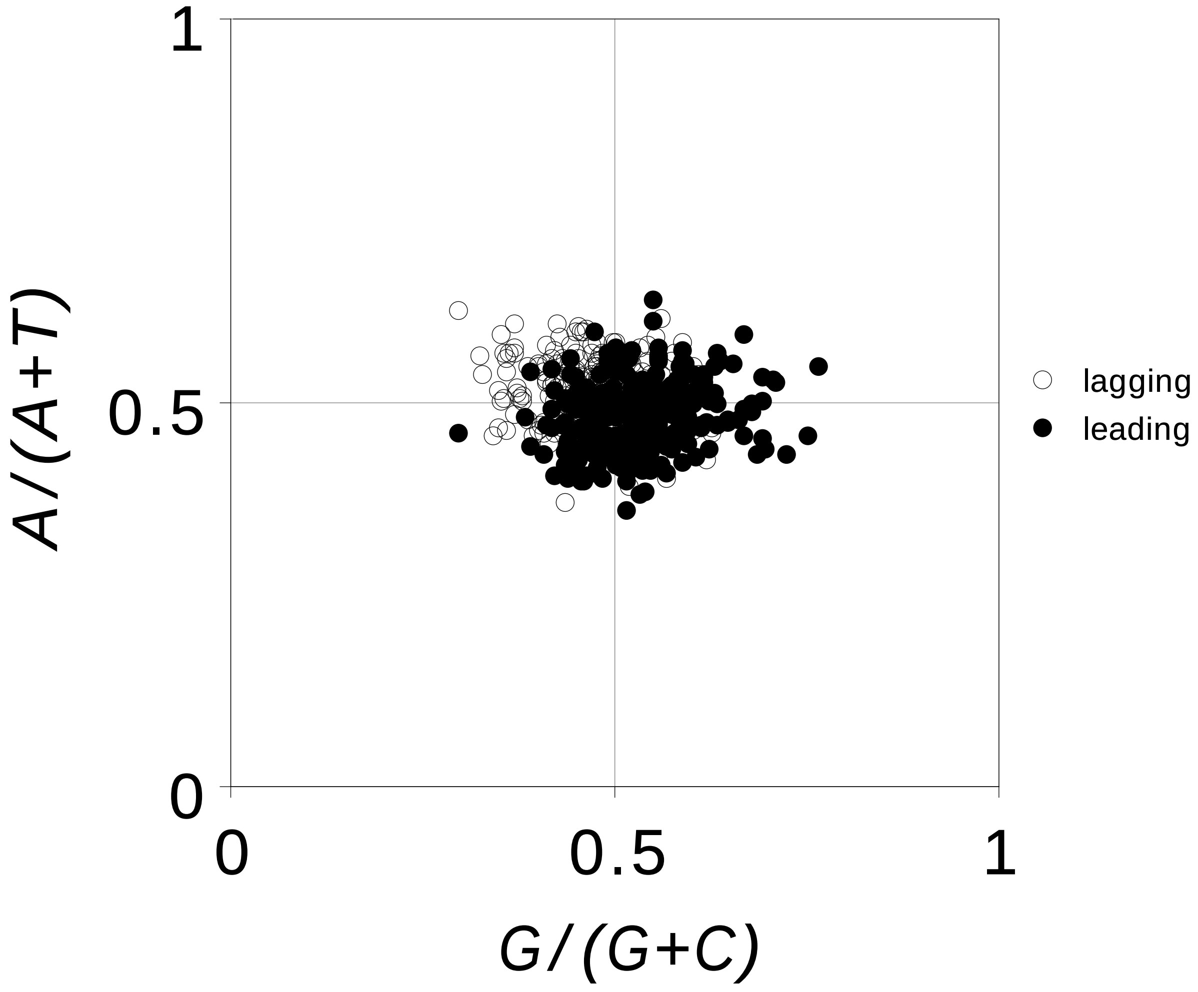
Pseudomonas aeruginosa



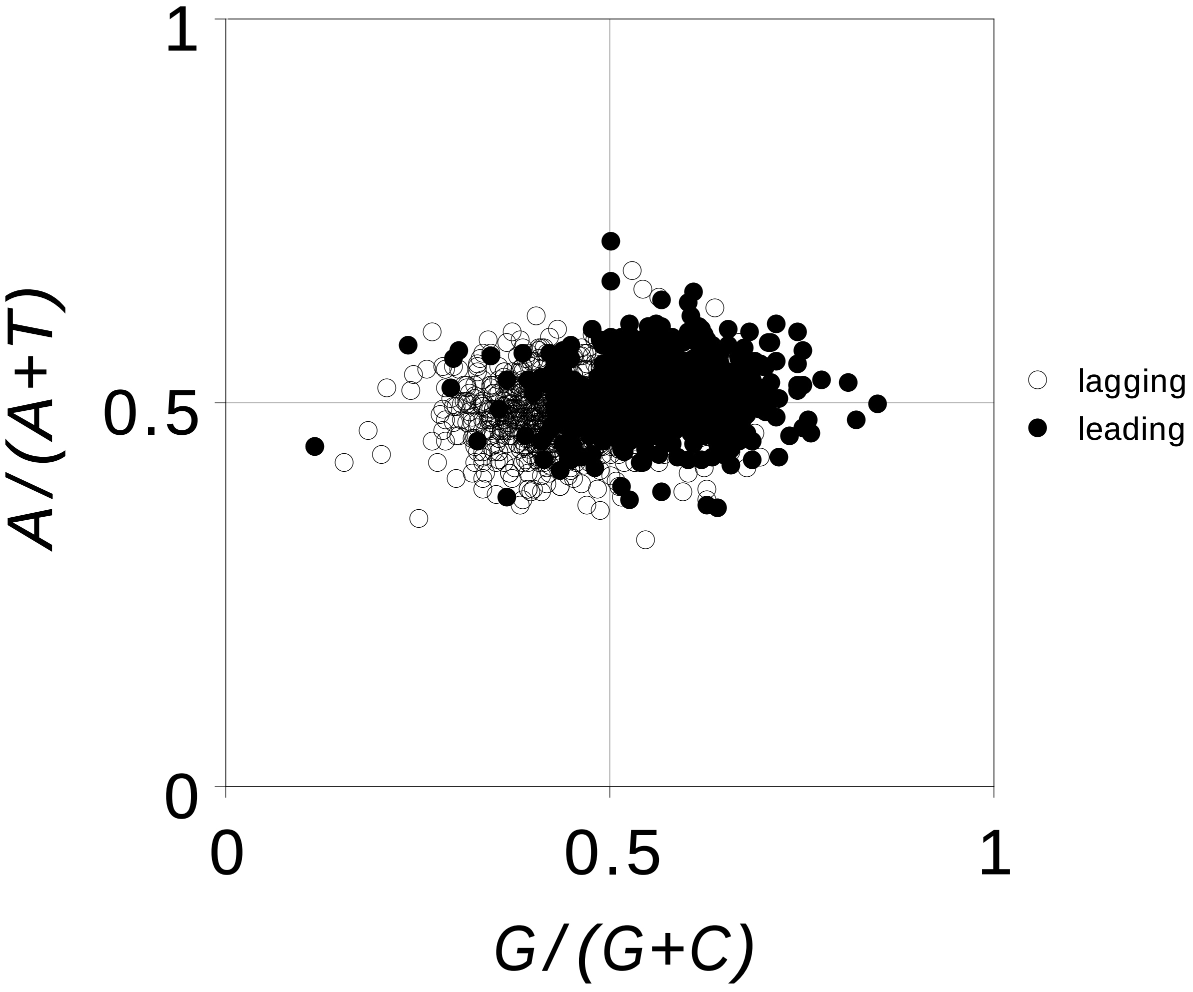
Pyrococcus abyssi



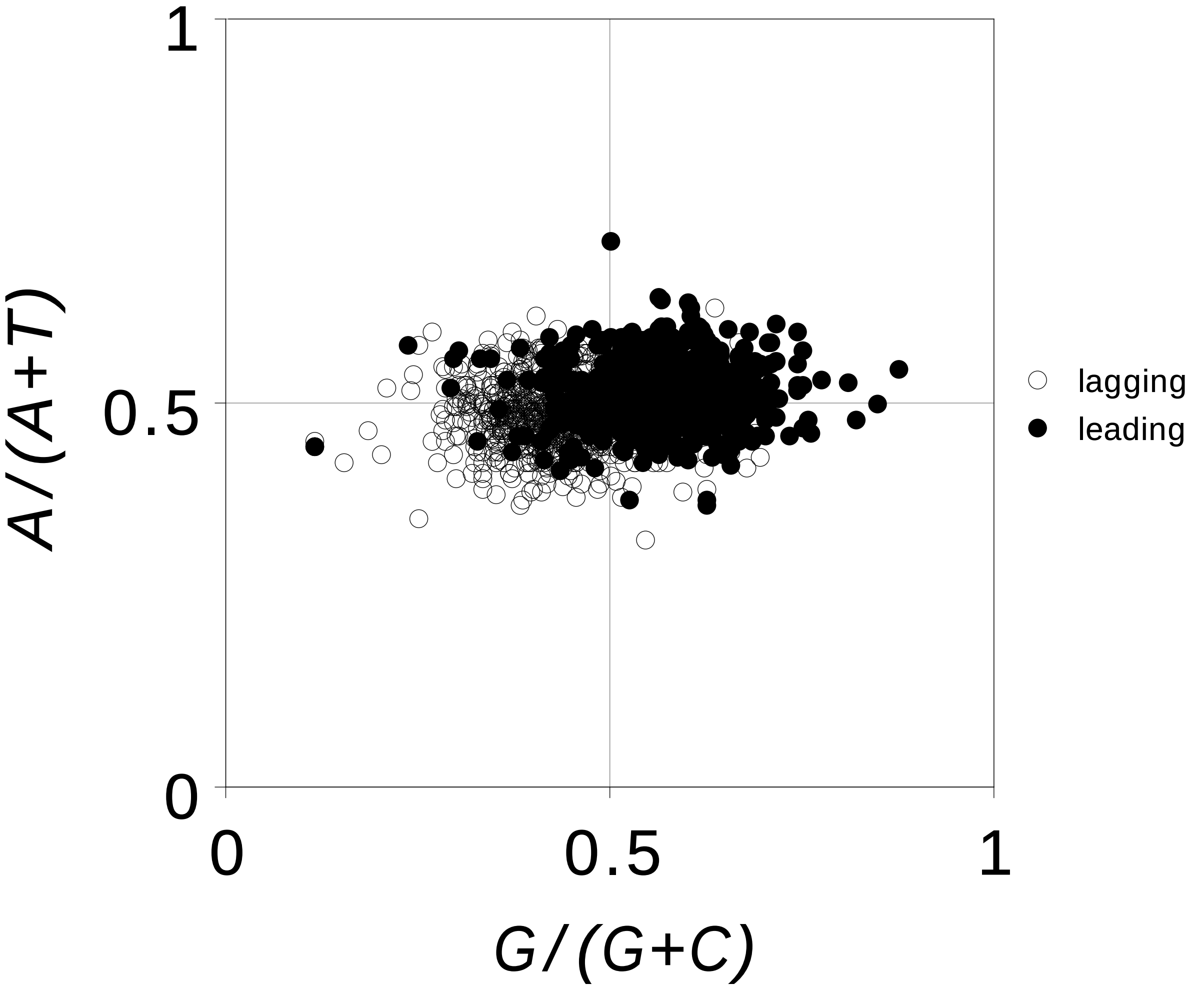
Pyrococcus horikoshii



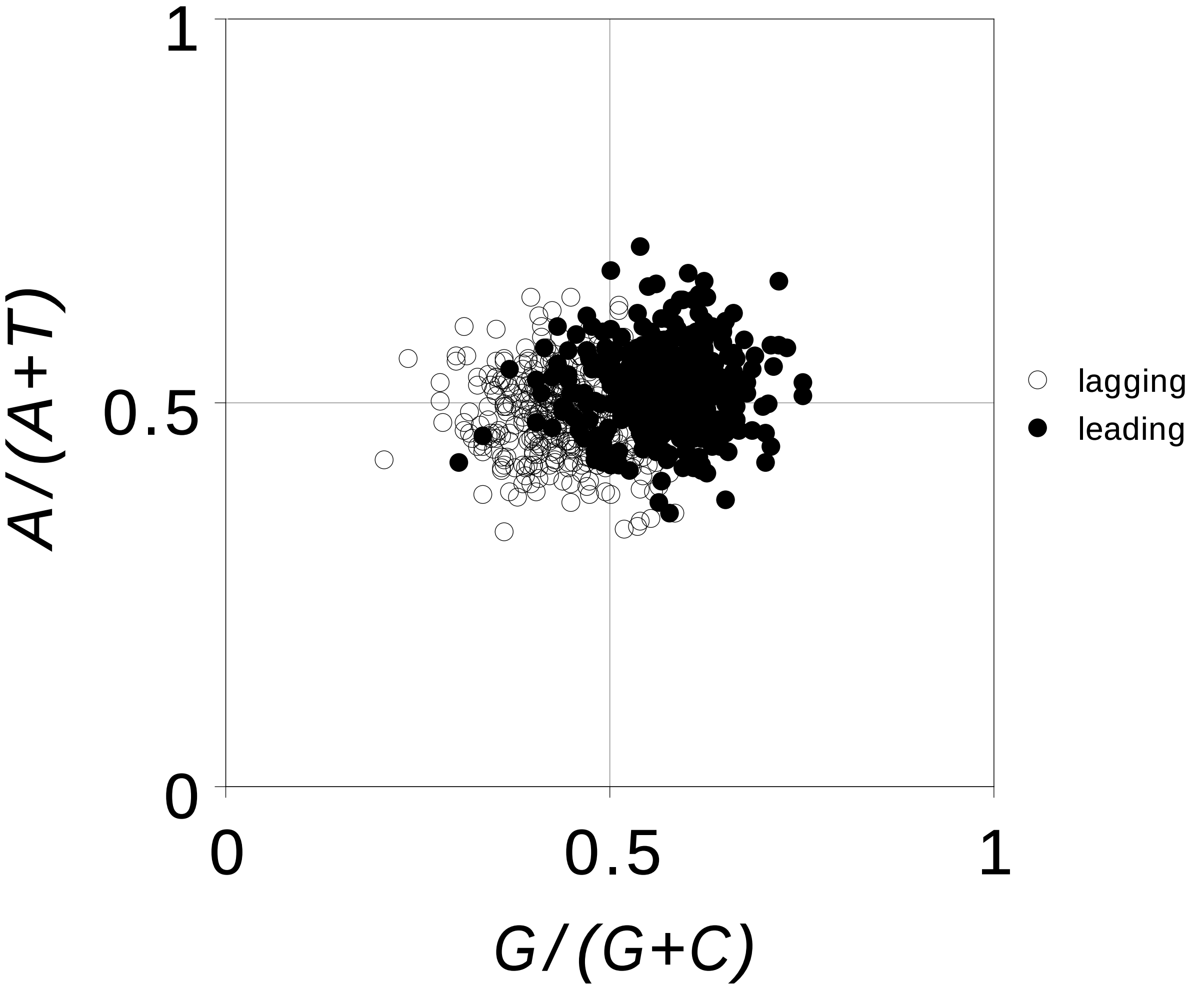
Rickettsia prowazekii



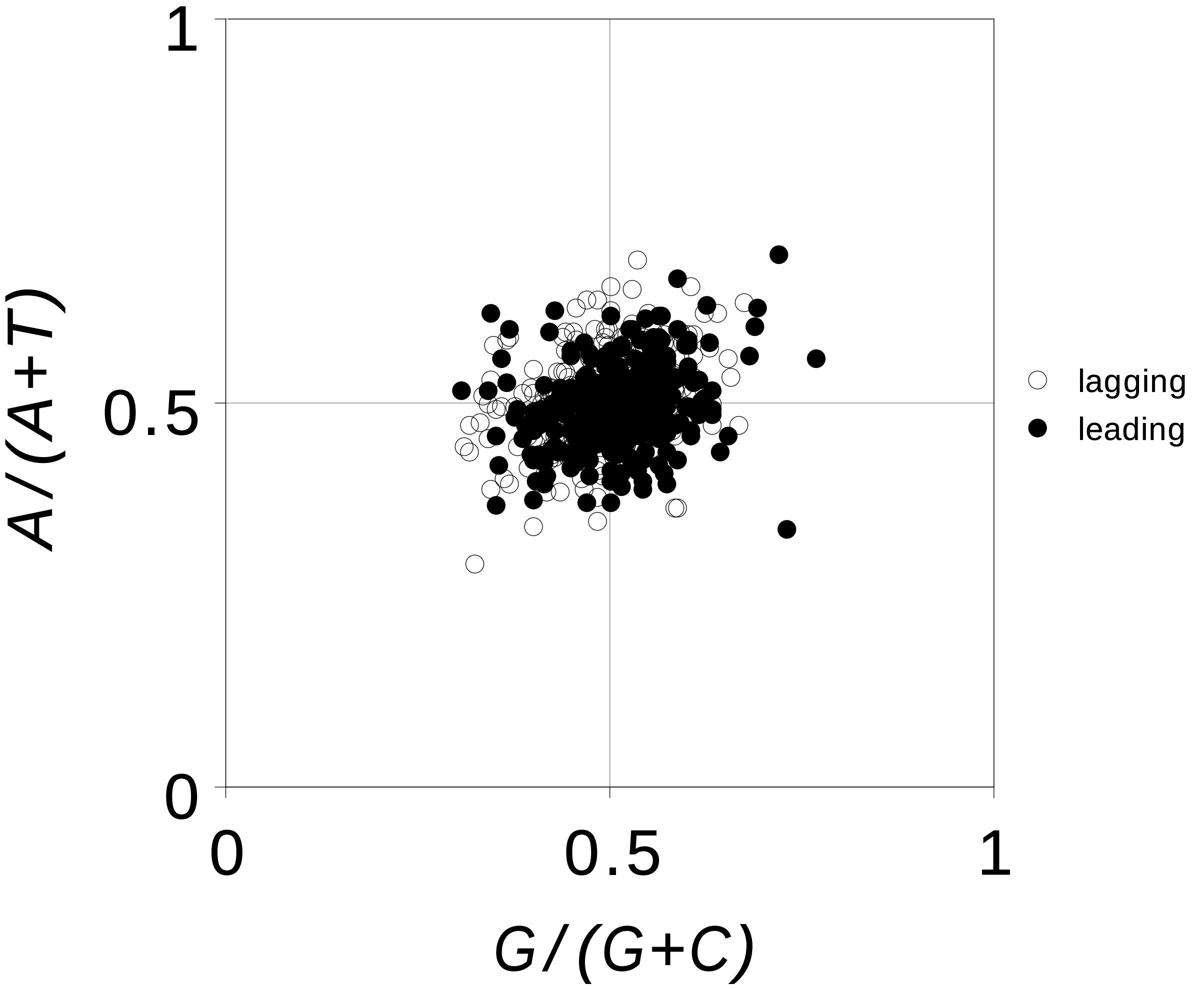
Staphylococcus aureus Mu50



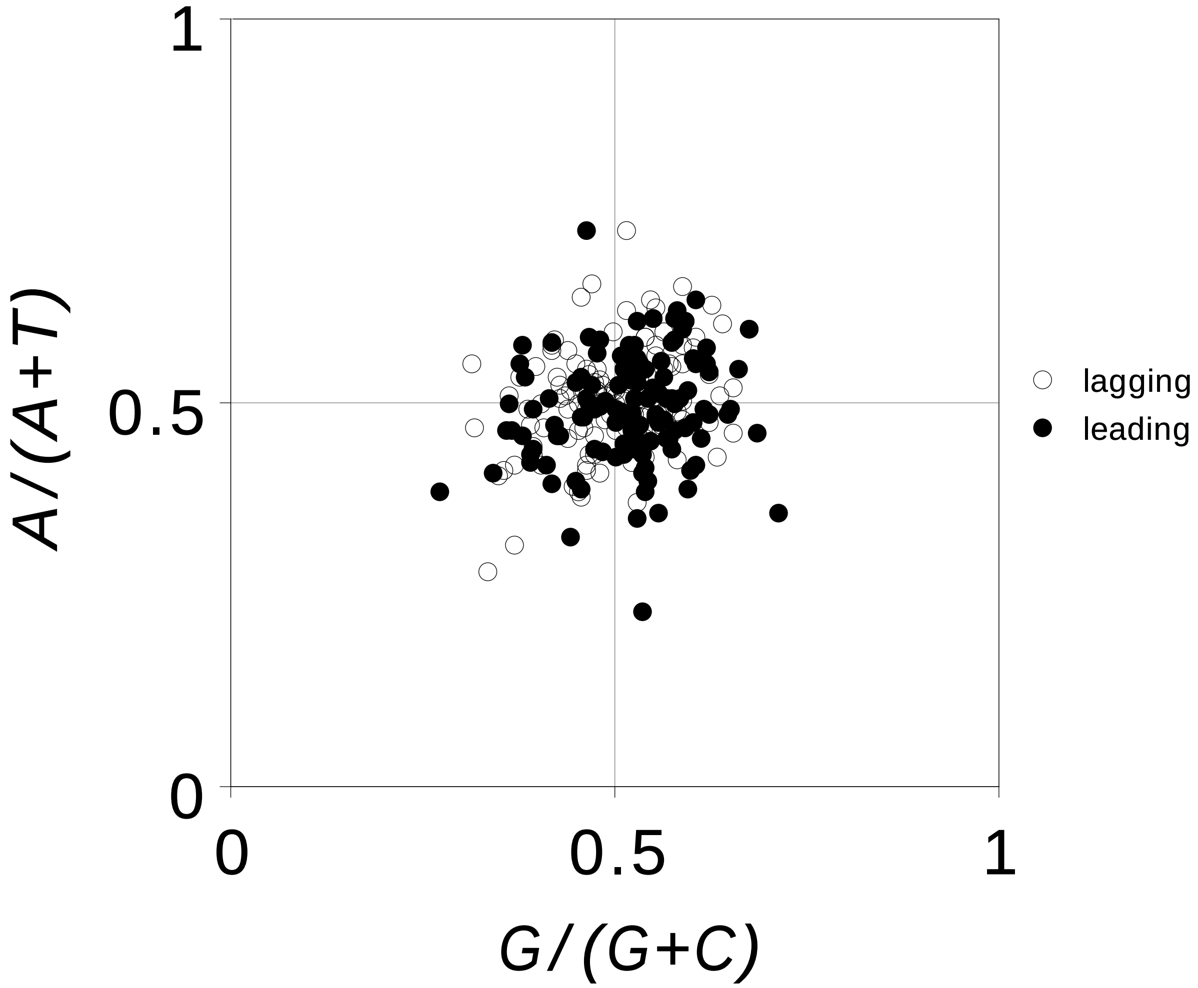
Staphylococcus aureus N315



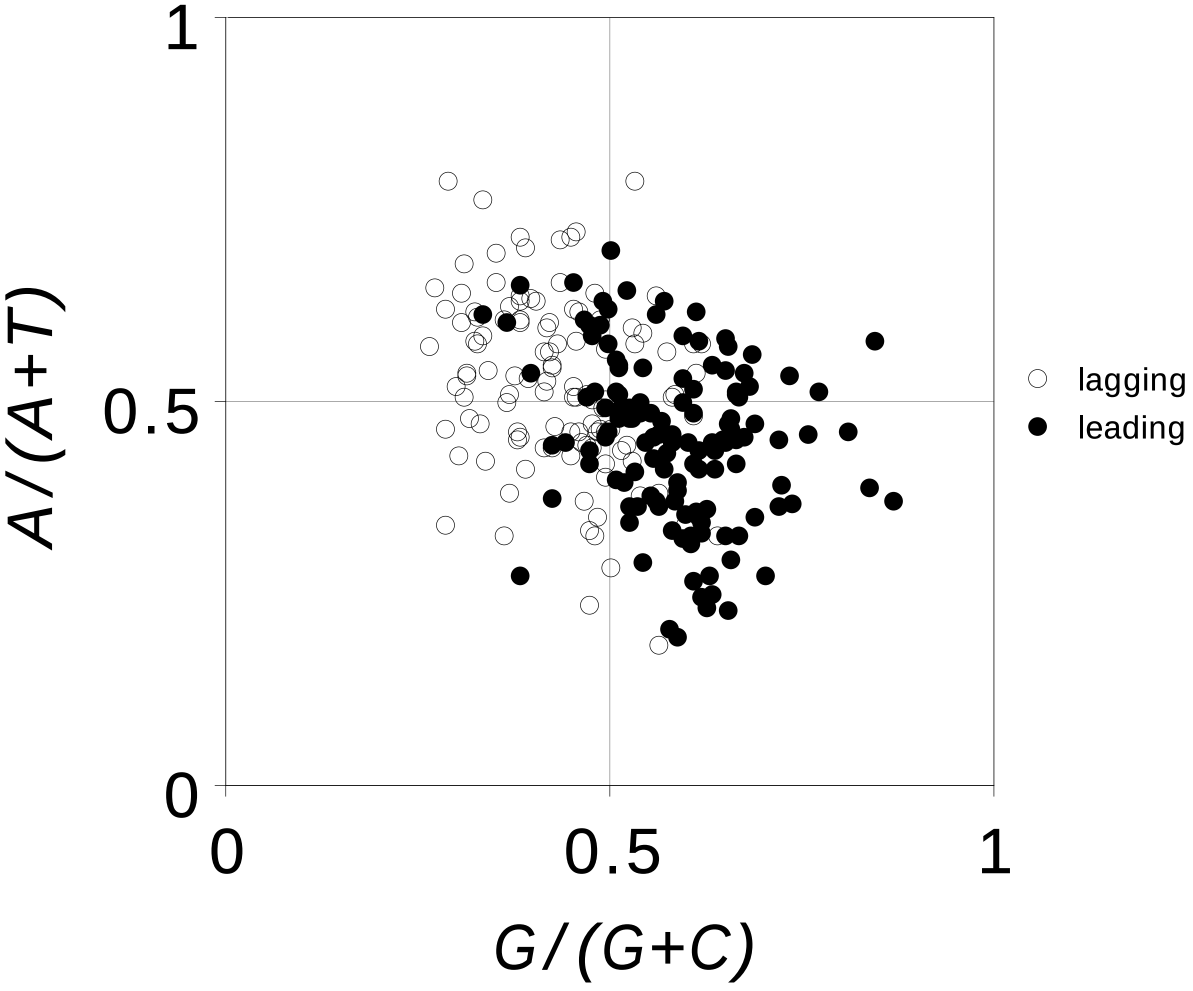
Streptococcus pyogenes



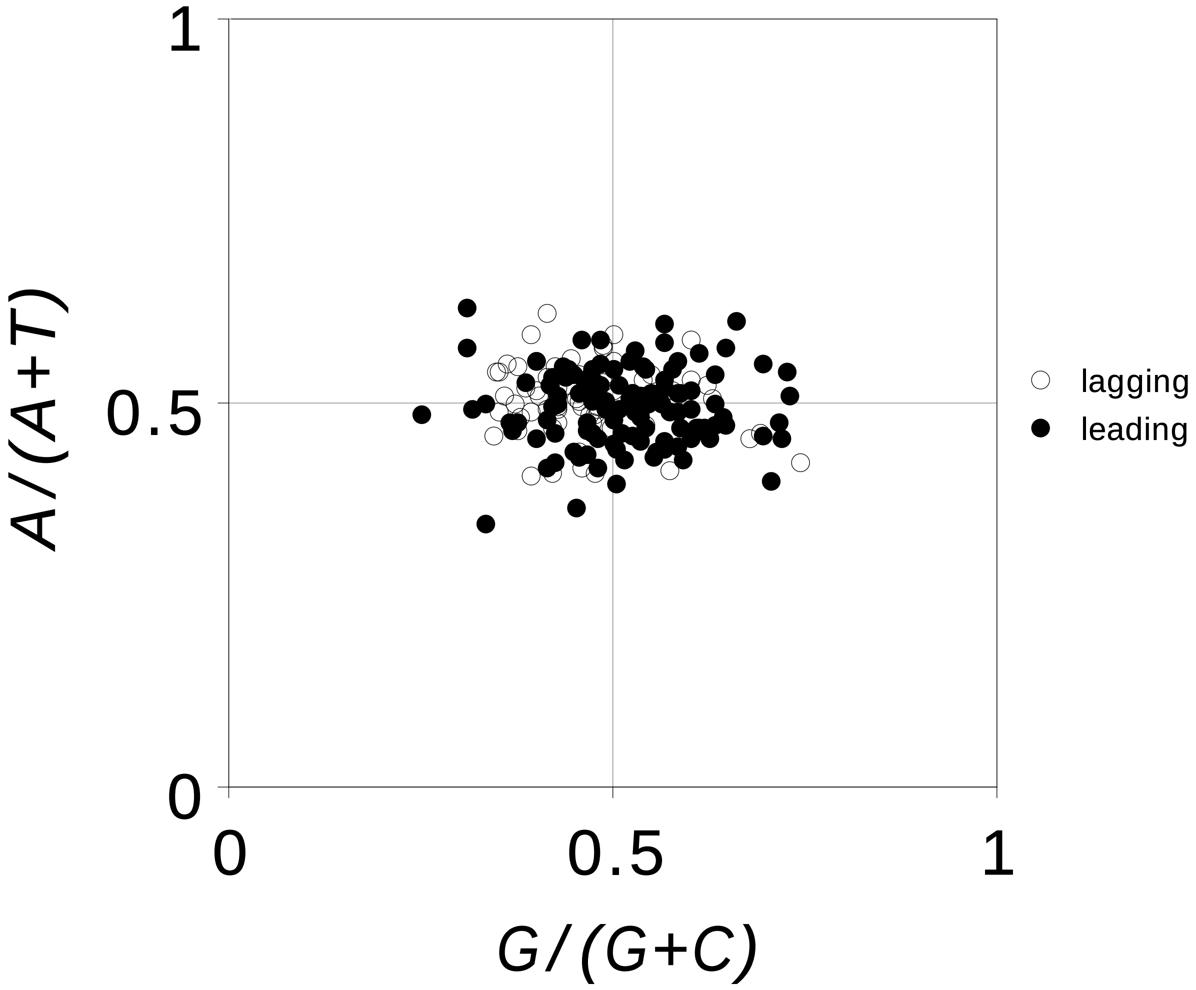
Thermoplasma acidophilum



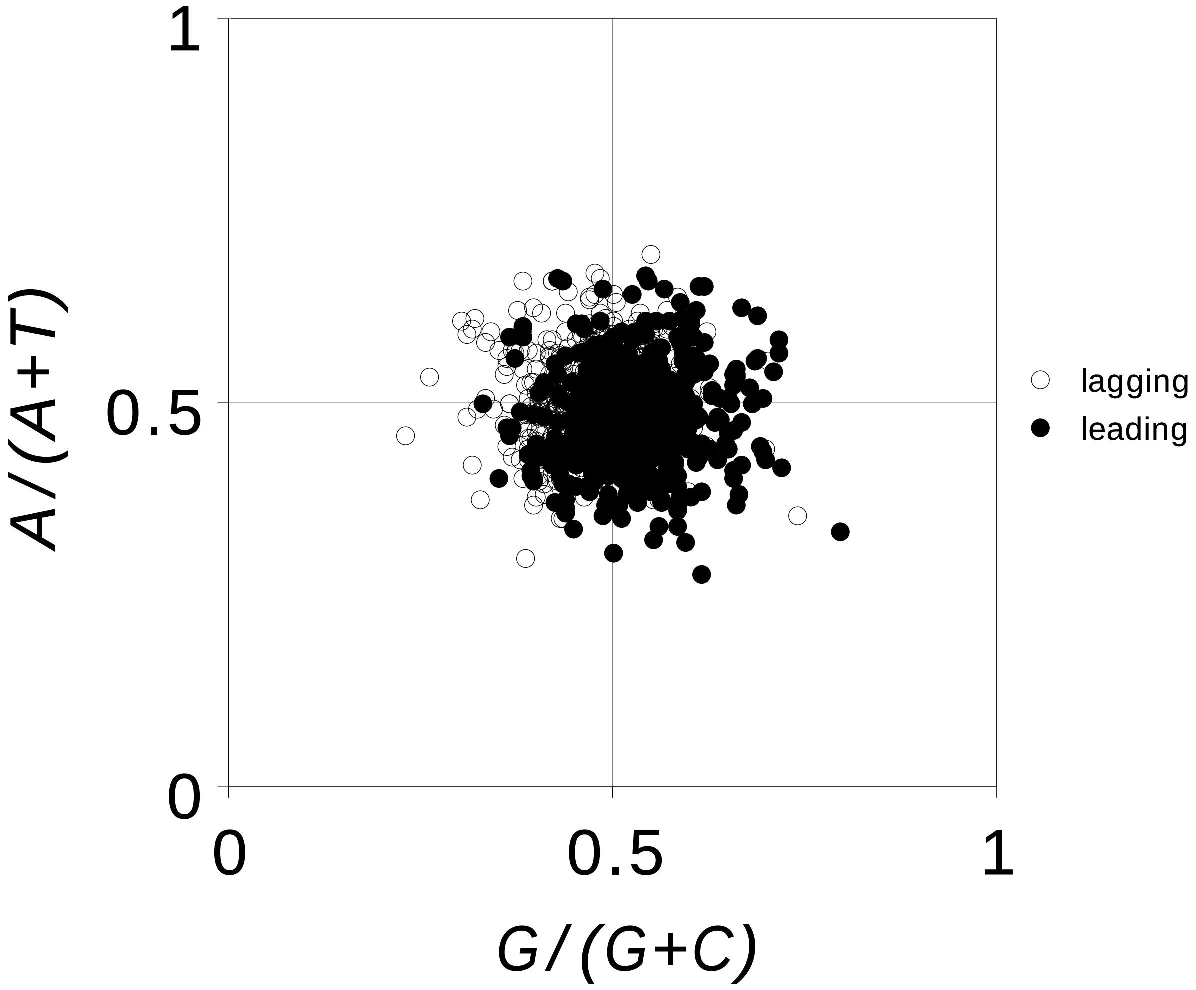
Thermotoga maritima



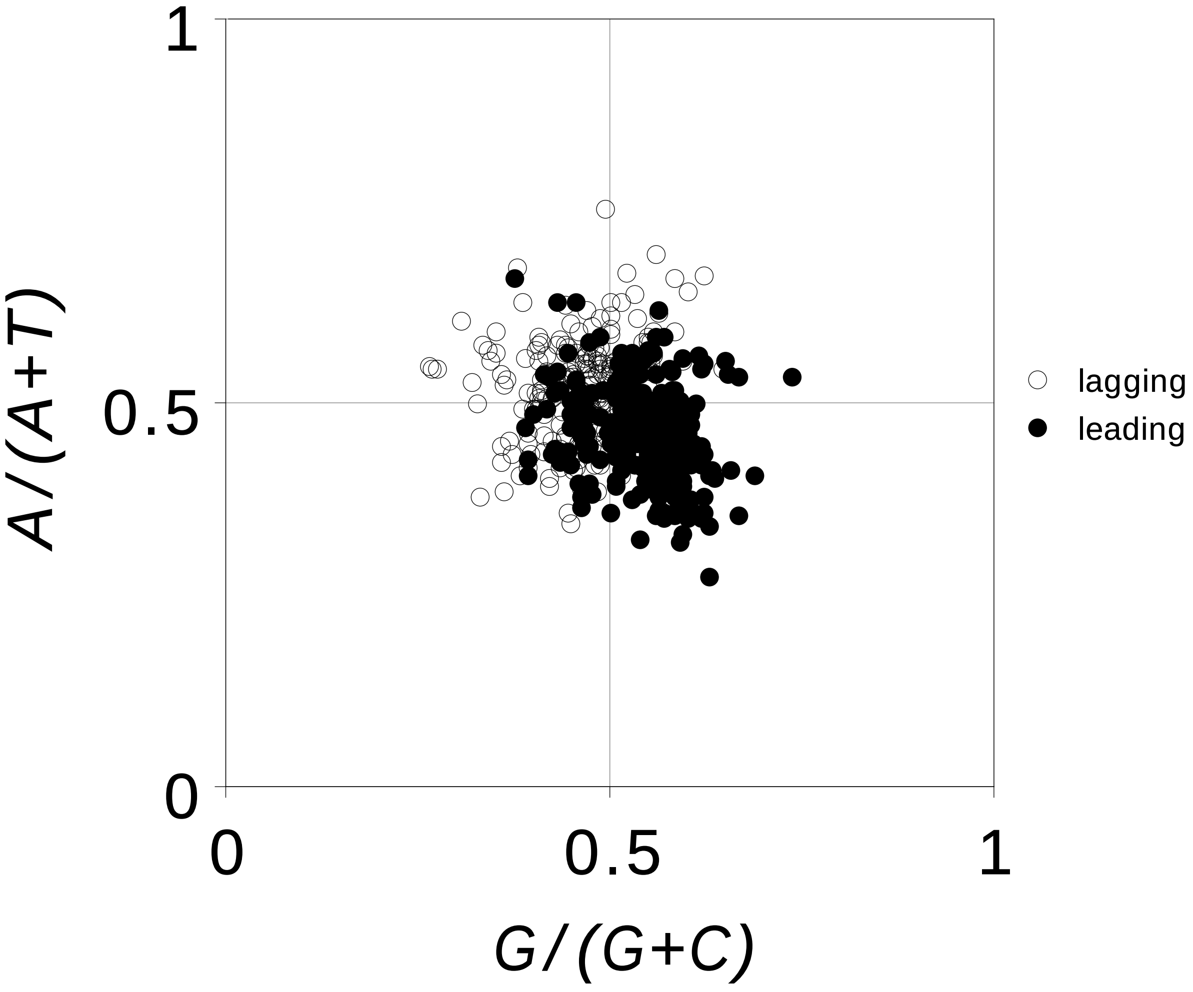
Treponema pallidum



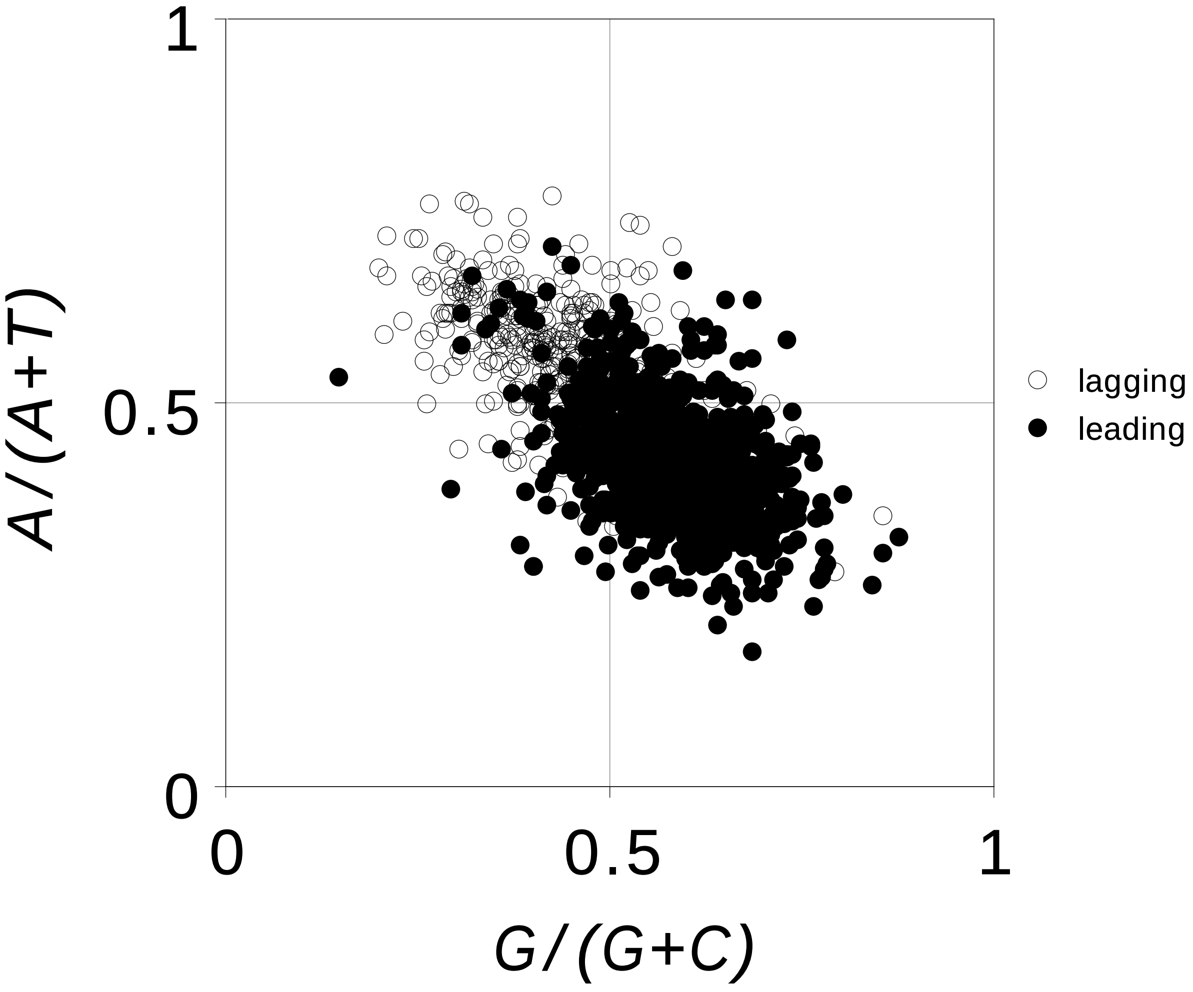
Ureaplasma urealyticum



Vibrio cholerae chromosome 1



Vibrio cholerae chromosome 2



Xylella fastidiosa

	Template Seq.		GC_{IGR}			$G/(G+C)$			$A\ (A+T)$			x,y Midpoint		Difference in PR2-bias		
Chromosome	#lead	#lagg	lead	lagg	Sig.	x_1	x_2	Sig.	y_1	y_2	Sig.	x_c	y_c	B_I	B_{II}	$B_I\%$
B. hal	348	70	0.407	0.397	ns	0.619	0.553	***	0.536	0.537	ns	0.586	0.536	0.066	0.093	41.4
B. sub	416	89	0.385	0.388	ns	0.604	0.558	***	0.536	0.507	**	0.581	0.522	0.054	0.084	**39.4**
B. bur	47	18	0.206	0.203	ns	0.697	0.492	***	0.445	0.589	***	0.595	0.517	0.251	0.096	**72.3**
Buch	47	36	0.145	0.154	ns	0.547	0.552	ns	0.502	0.542	*	0.550	0.522	0.040	0.054	42.7
C.cre	234	191	0.624	0.625	ns	0.495	0.478	*	0.485	0.504	ns	0.486	0.494	0.025	0.015	63.6
C. jej	91	51	0.198	0.193	ns	0.620	0.555	*	0.526	0.512	ns	0.588	0.519	0.066	0.090	42.6
C. mur	34	30	0.329	0.324	ns	0.626	0.428	***	0.445	0.464	ns	0.527	0.455	0.199	0.053	79.0
C. pne	44	38	0.327	0.312	ns	0.552	0.491	*	0.469	0.519	*	0.522	0.494	0.079	0.022	77.9
C. pneAR39	43	41	0.317	0.312	ns	0.544	0.464	**	0.466	0.501	ns	0.504	0.484	0.087	0.017	83.7
C. pneJ138	138	93	0.373	0.378	ns	0.654	0.506	***	0.510	0.471	ns	0.580	0.490	0.153	0.081	65.5
C. tra	46	36	0.344	0.363	ns	0.604	0.452	***	0.489	0.467	ns	0.528	0.478	0.154	0.036	81.2

D. rad1	172	165	0.630	0.645	ns	0.473	0.455	ns	0.458	0.469	ns	0.464	0.464	0.021	0.051	29.2
D. rad2	25	14	0.610	0.633	ns	0.452	0.403	ns	0.498	0.387	ns	0.427	0.443	0.121	0.093	56.7
E. col	260	167	0.446	0.444	ns	0.520	0.472	***	0.502	0.482	ns	0.496	0.492	0.052	0.009	85.3
E.colEDL	357	214	0.448	0.442	ns	0.525	0.482	***	0.492	0.491	ns	0.504	0.491	0.043	0.009	82.4
E.colRIMD	377	211	0.446	0.448	ns	0.531	0.480	***	0.492	0.491	ns	0.506	0.491	0.051	0.010	83.4
H. inf	120	80	0.305	0.316	ns	0.548	0.457	***	0.500	0.522	ns	0.503	0.511	0.094	0.011	89.2
H. pyl	86	57	0.307	0.284	ns	0.582	0.574	ns	0.508	0.511	ns	0.578	0.510	0.009	0.079	9.8
H. pylJ99	70	52	0.294	0.284	ns	0.609	0.580	ns	0.526	0.505	ns	0.595	0.516	0.036	0.096	27.2
L.lac	217	41	0.276	0.279	ns	0.621	0.554	***	0.545	0.543	ns	0.588	0.544	0.067	0.098	40.6
M.lep	185	94	0.553	0.546	ns	0.545	0.481	***	0.501	0.576	***	0.513	0.538	0.099	0.041	**70.8**
M. tub	218	169	0.630	0.631	ns	0.508	0.505	ns	0.520	0.522	ns	0.506	0.521	0.004	0.022	14.1
M.tubCDC	261	161	0.630	0.632	ns	0.520	0.492	***	0.511	0.531	ns	0.506	0.521	0.034	0.022	61.2
M. gen	14	4	0.265	0.258	ns	0.534	0.472	ns	0.463	0.516	ns	0.503	0.490	0.082	0.011	88.2
M. pne	35	6	0.331	0.415	*	0.438	0.445	ns	0.493	0.453	ns	0.442	0.473	0.041	0.064	38.7
M.pul	52	21	0.191	0.160	*	0.533	0.594	ns	0.539	0.500	ns	0.564	0.520	0.072	0.066	52.2

N. menA	157	145	0.443	0.465	*	0.498	0.447	***	0.531	0.542	ns	0.473	0.536	0.052	0.046	53.3
N. menB	174	120	0.443	0.465	*	0.523	0.428	***	0.518	0.555	**	0.476	0.536	0.102	0.044	**69.9**
P.mul	152	89	0.331	0.341	ns	0.573	0.480	***	0.486	0.512	*	.526	.499	.097	.027	78.5
P. aer	402	313	0.635	0.665	***	0.495	0.447	***	0.494	0.544	***	0.471	0.519	0.069	0.035	**66.7**
P. aby	81	78	0.347	0.363	ns	0.496	0.512	ns	0.451	0.485	*	0.504	0.468	0.038	0.032	53.8
P. hor	73	53	0.318	0.358	**	0.494	0.512	ns	0.452	0.478	ns	0.503	0.465	0.032	0.035	47.4
R. pro	50	27	0.232	0.235	ns	0.547	0.503	ns	0.493	0.533	*	0.525	0.513	0.059	0.028	67.8
S.aur	140	34	0.278	0.282	ns	0.653	0.543	***	0.548	0.519	ns	0.598	0.534	0.114	0.104	52.3
S.aurN315	128	30	0.279	0.287	ns	0.658	0.562	***	0.549	0.542	ns	0.610	0.546	0.096	0.119	44.7
S.pyo	137	30	0.327	0.331	ns	0.612	0.540	**	0.555	0.494	***	0.576	0.524	0.094	0.080	**54.2**
T. aci	85	72	0.331	0.345	ns	0.523	0.468	**	0.515	0.483	*	0.496	0.499	0.064	0.005	93.2
T. mar	61	53	0.437	0.419	ns	0.593	0.585	ns	0.511	0.519	ns	0.589	0.515	0.011	0.090	11.1
T. pal	75	64	0.541	0.557	ns	0.634	0.574	**	0.416	0.447	ns	0.604	0.431	0.068	0.125	35.2
U. ure	70	18	0.174	0.172	ns	0.610	0.631	ns	0.503	0.523	ns	0.621	0.513	0.029	0.121	19.3
V. cho1	174	102	0.420	0.420	ns	0.529	0.468	***	0.485	0.501	ns	0.499	0.493	0.063	0.007	89.8

V. cho2	51	31	0.459	0.431	ns	0.509	0.455	**	0.526	0.506	ns	0.482	0.516	0.058	0.024	70.5
X. fas	148	111	0.483	0.515	**	0.511	0.406	***	0.437	0.548	***	0.459	0.493	0.153	0.042	**78.4**

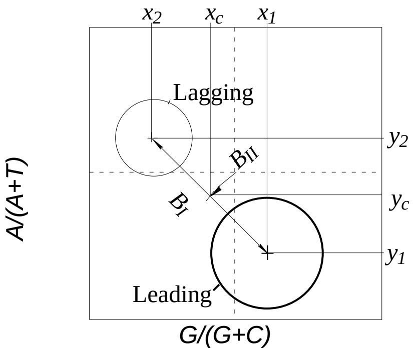
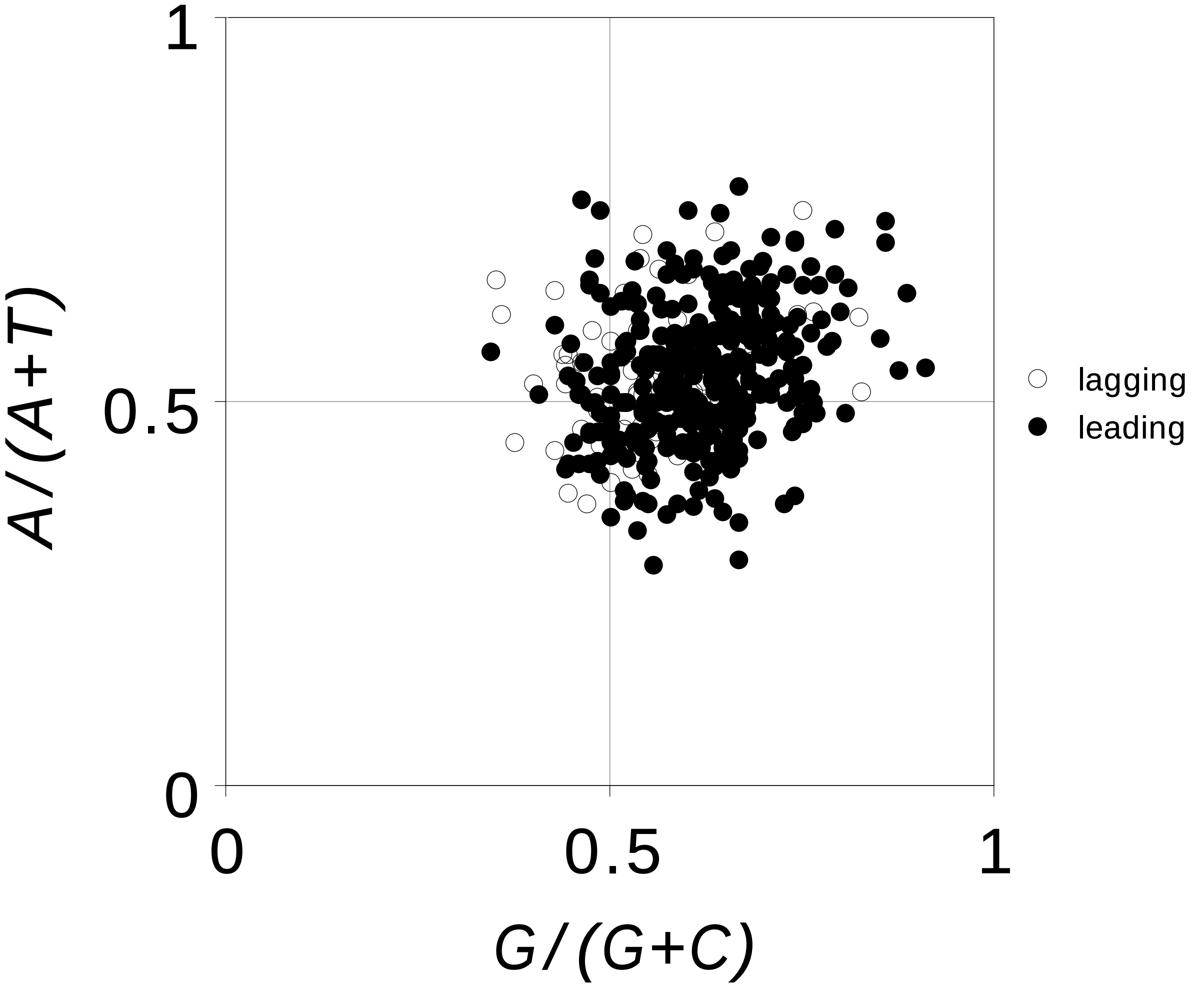
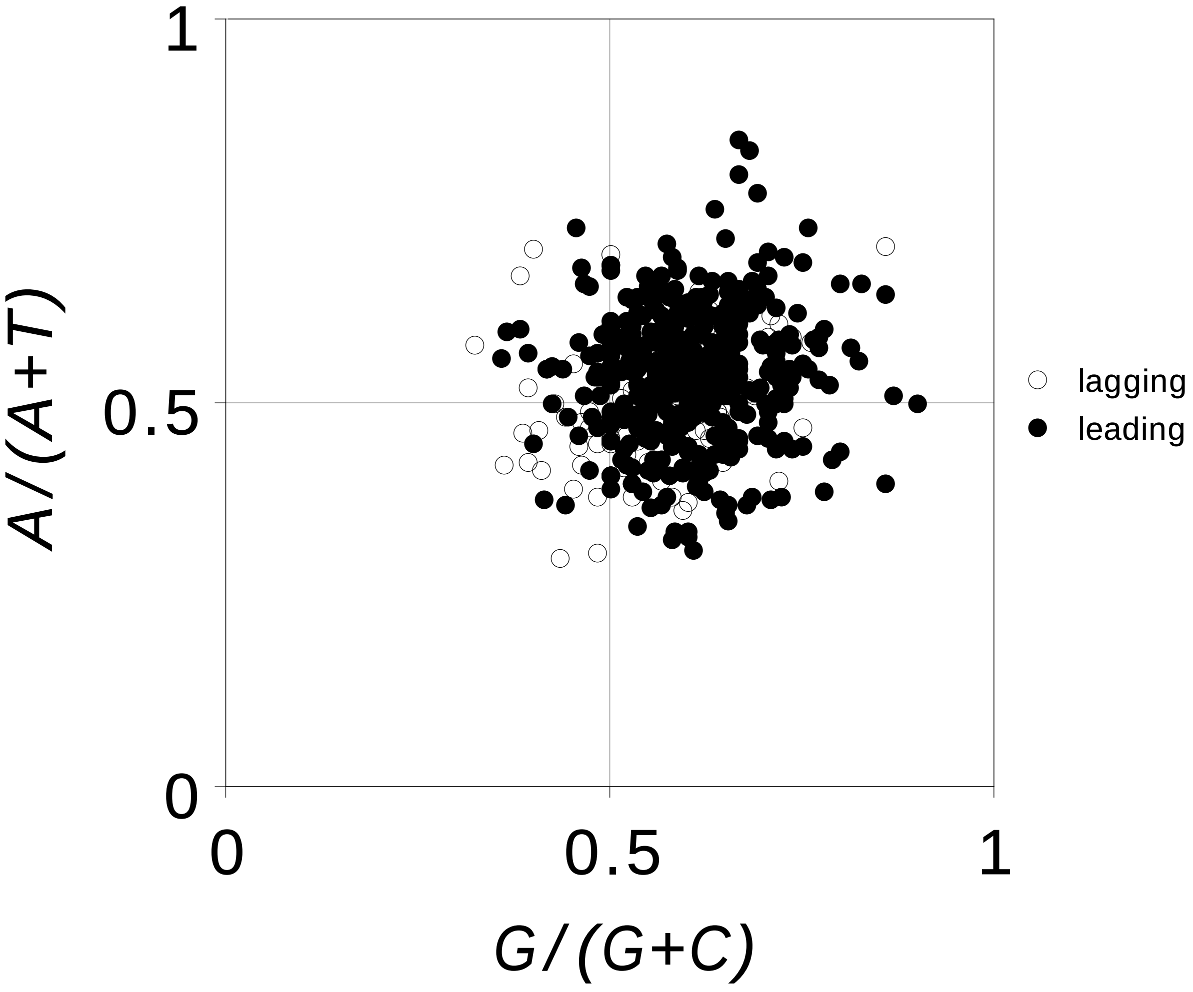


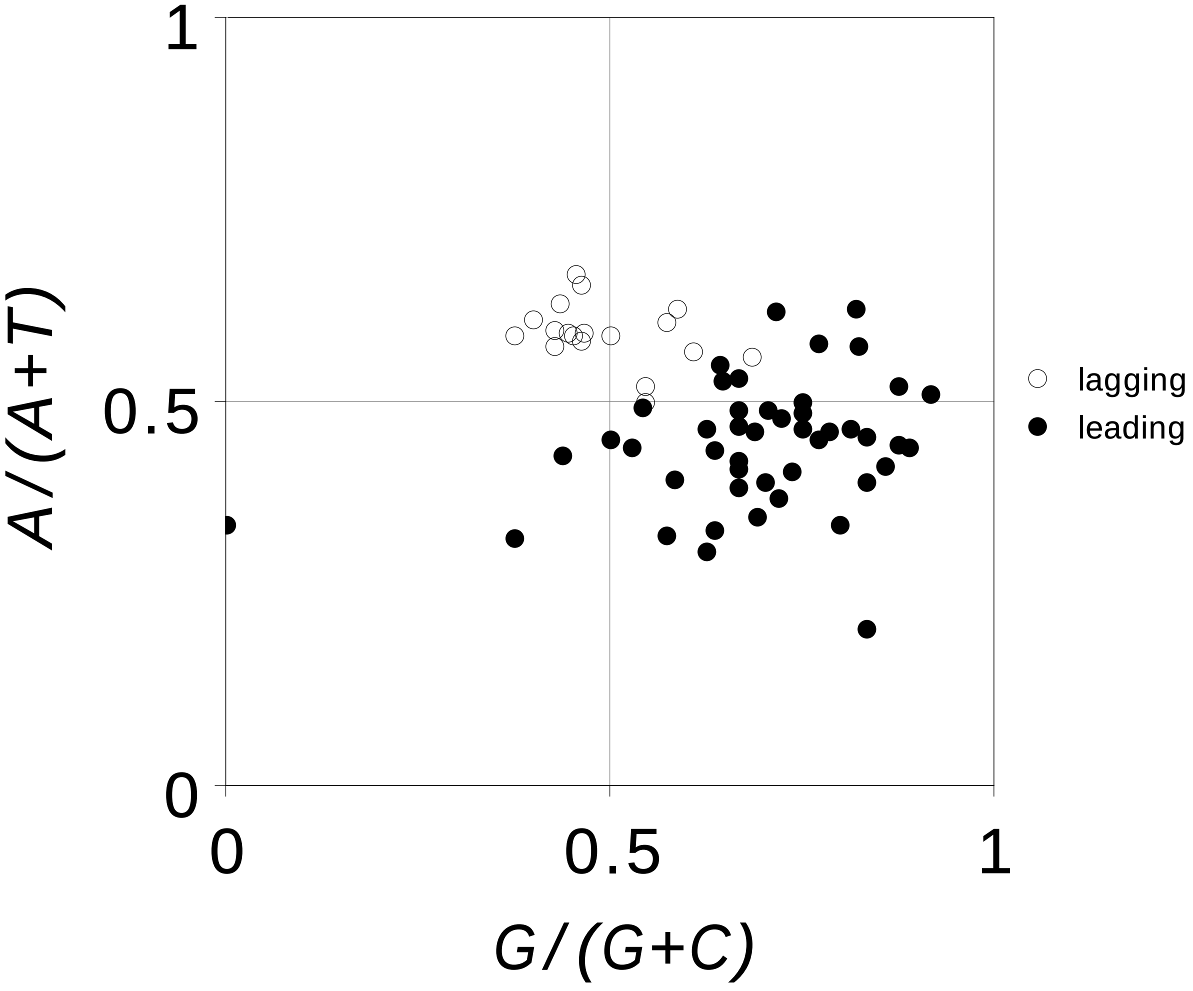
Table 4. Base composition in small intergenic regions (from 50 to100 bp) among co-oriented genes.. Indices are defined in the material and method section. #lead and #lag are the number of regions in the leading and the lagging strand. The significance level (Sig.) for a difference between the two groups are: ns (not significant, $p \geq 0.05$); * ($0.01 \leq p < 0.05$); ** ($0.001 \leq p < 0.01$); *** ($p < 0.001$). The contribution in percent of replication-associated effects to PR2 deviations (B_I %) is given in **bold** when both differences $x_1 - x_2$ and $y_1 - y_2$ are highly significant ($p < 0.01$). When a difference is significant between the two groups a red color outlines the highest value and a blue color the lowest value.



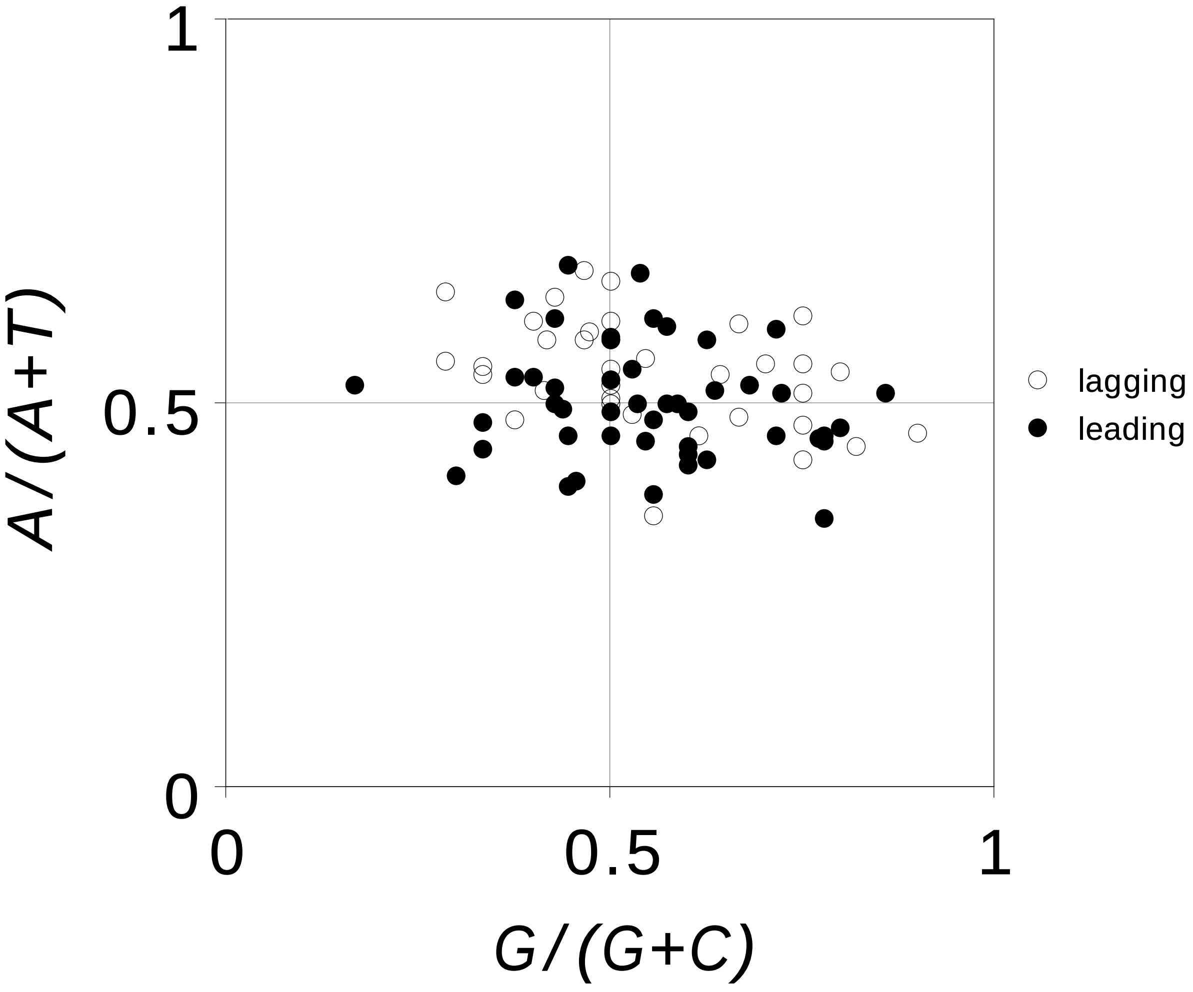
Bacillus halodurans



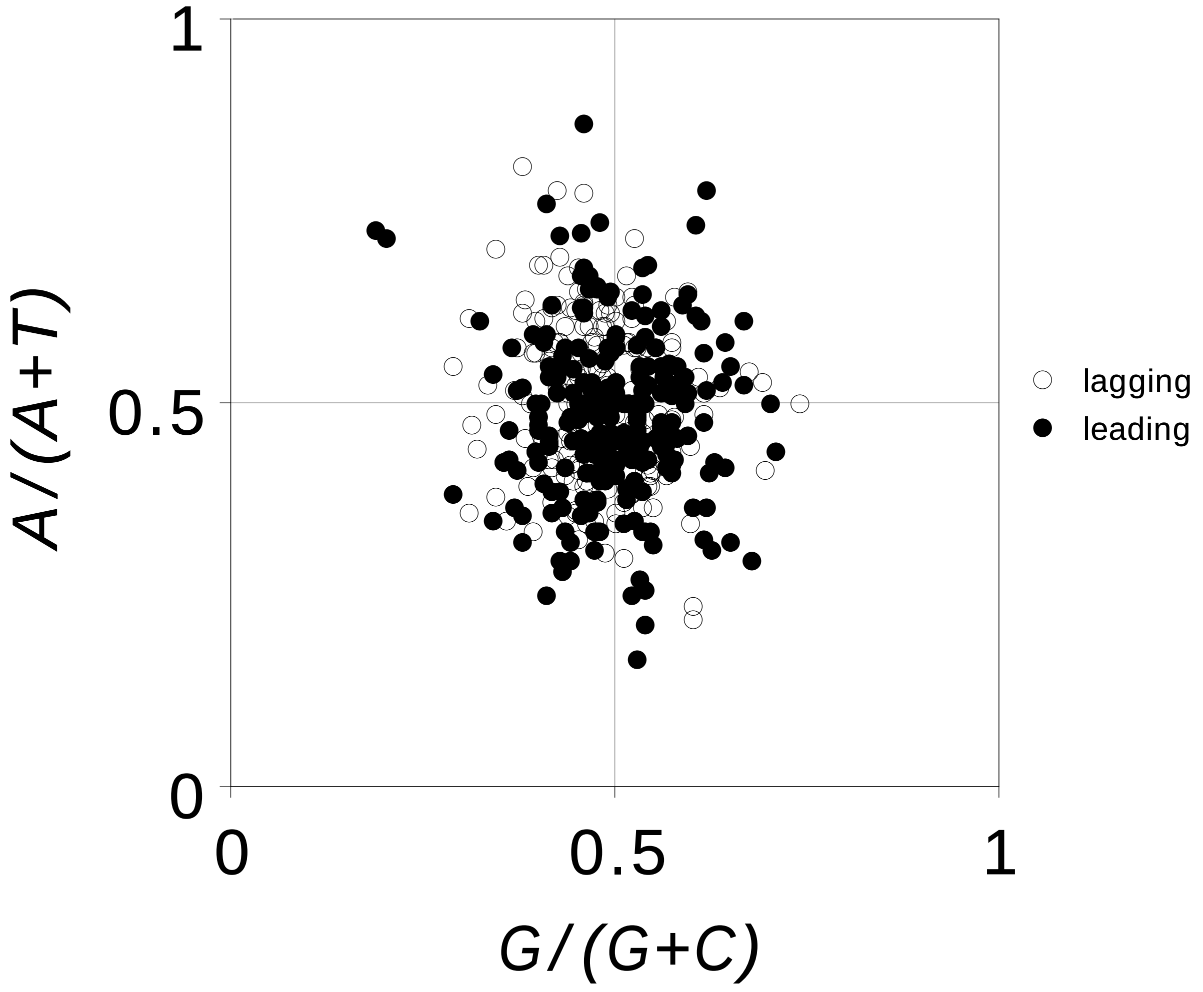
Bacillus subtilis



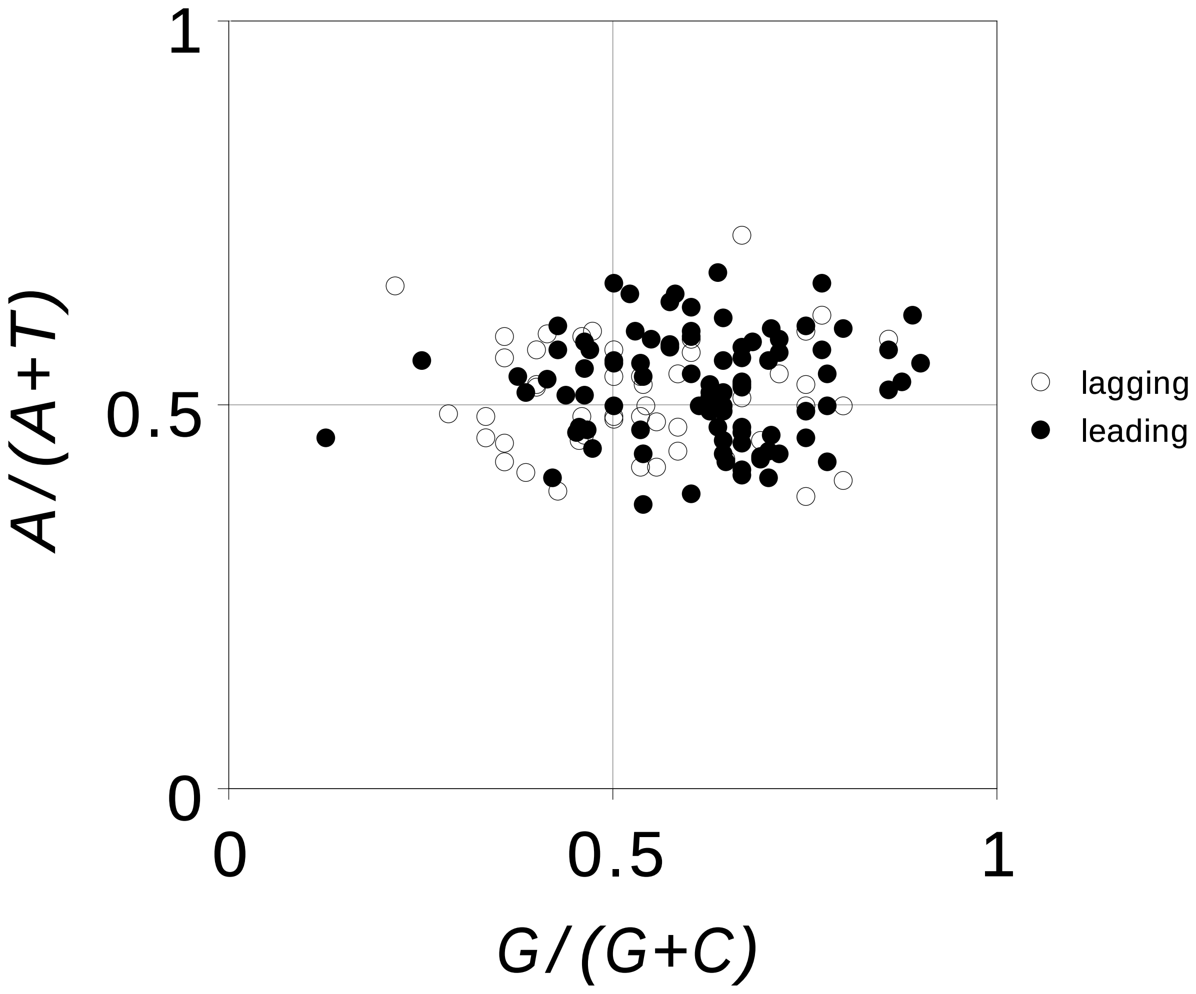
Borrelia burgdorferi



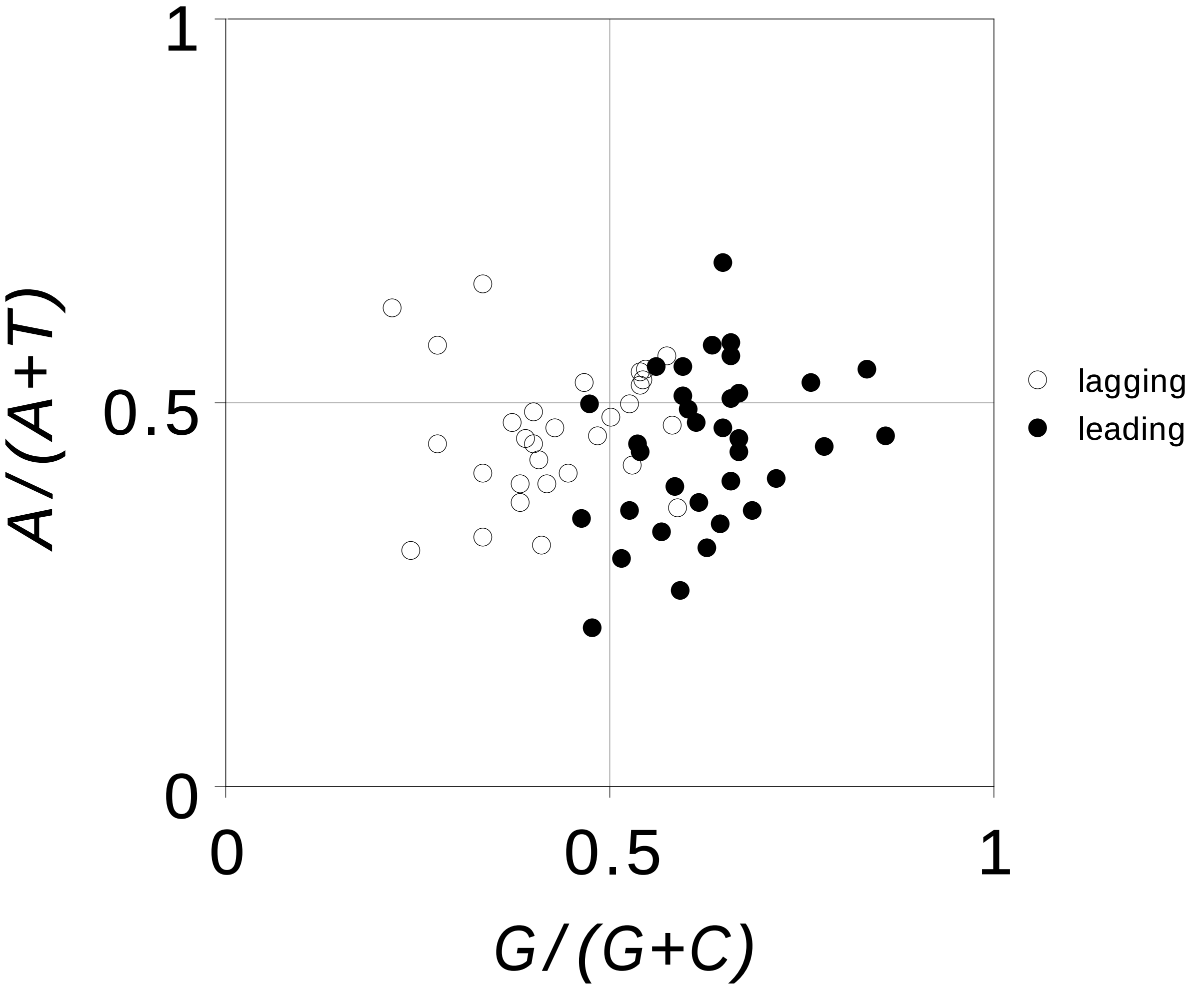
Buchnera sp.



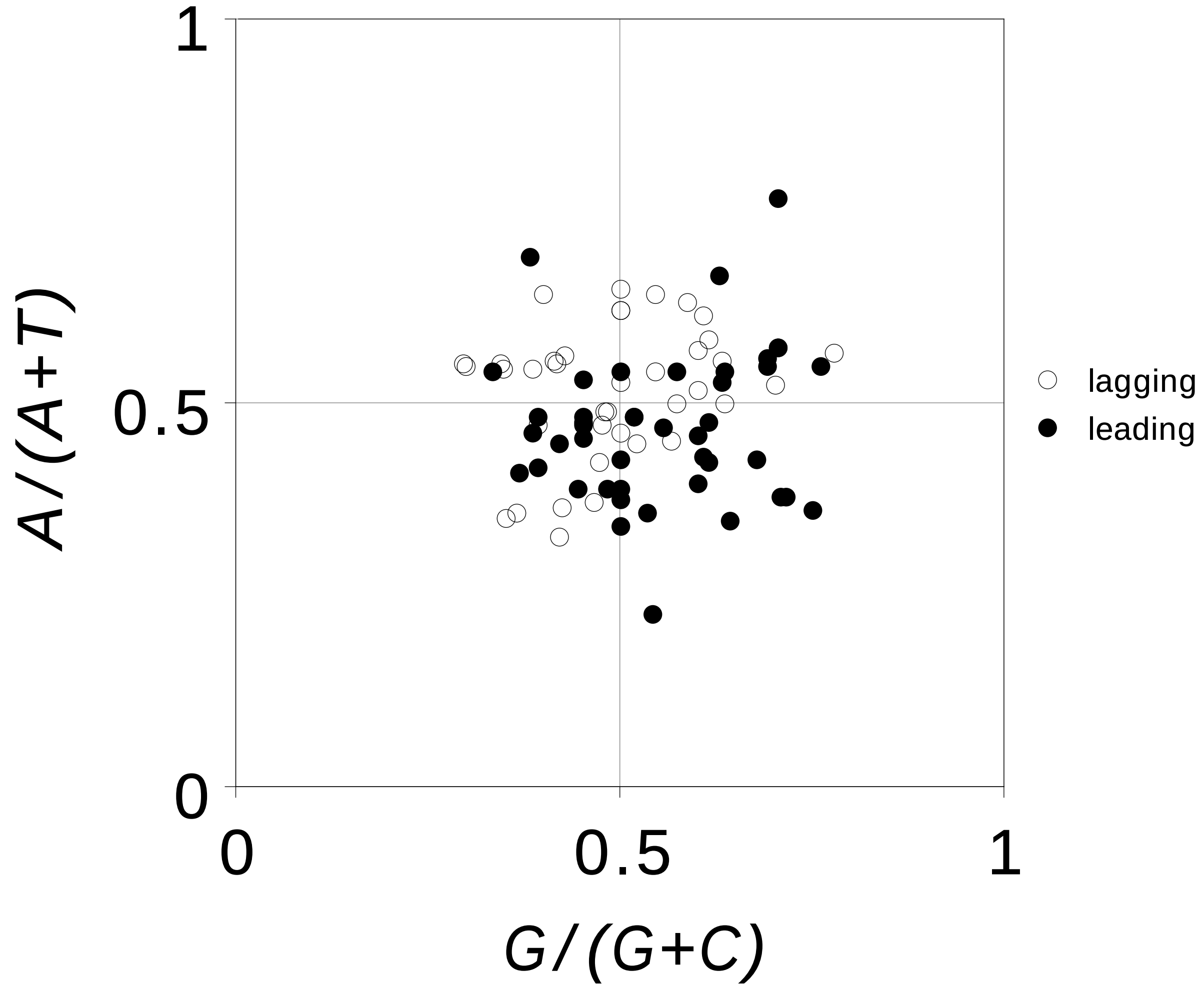
Caulobacter crescentus



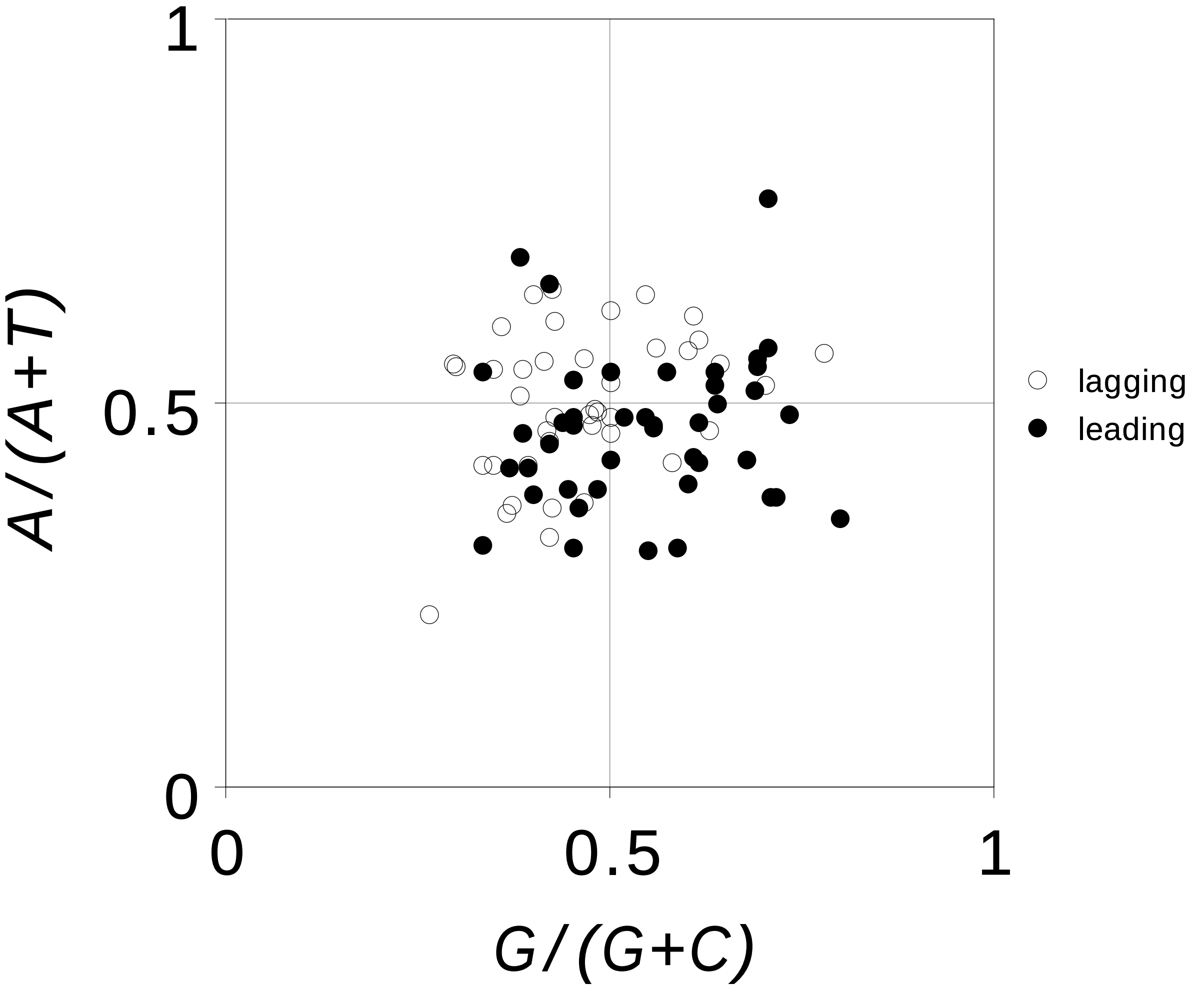
Campylobacter jejuni



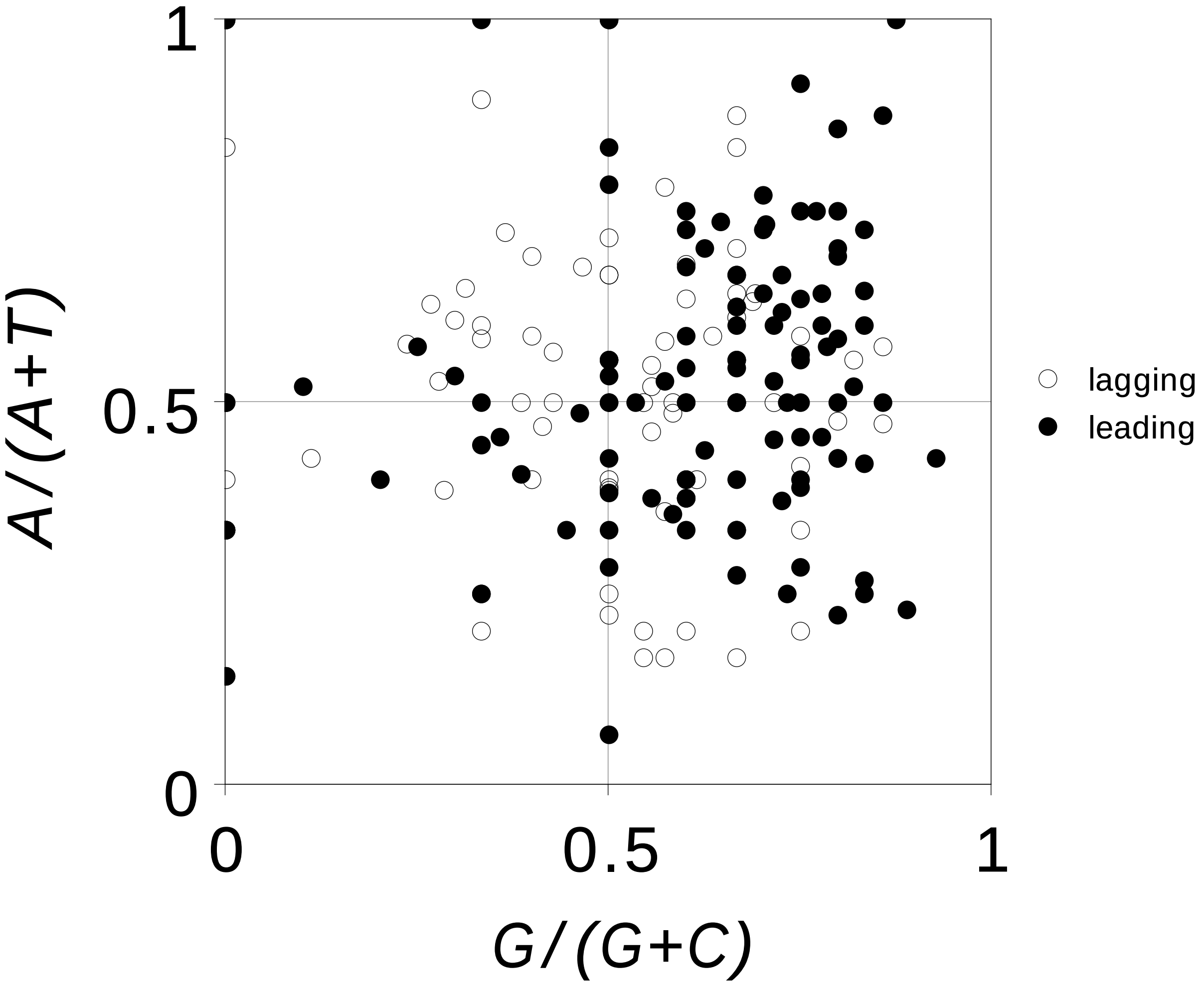
Chlamydia muridarum



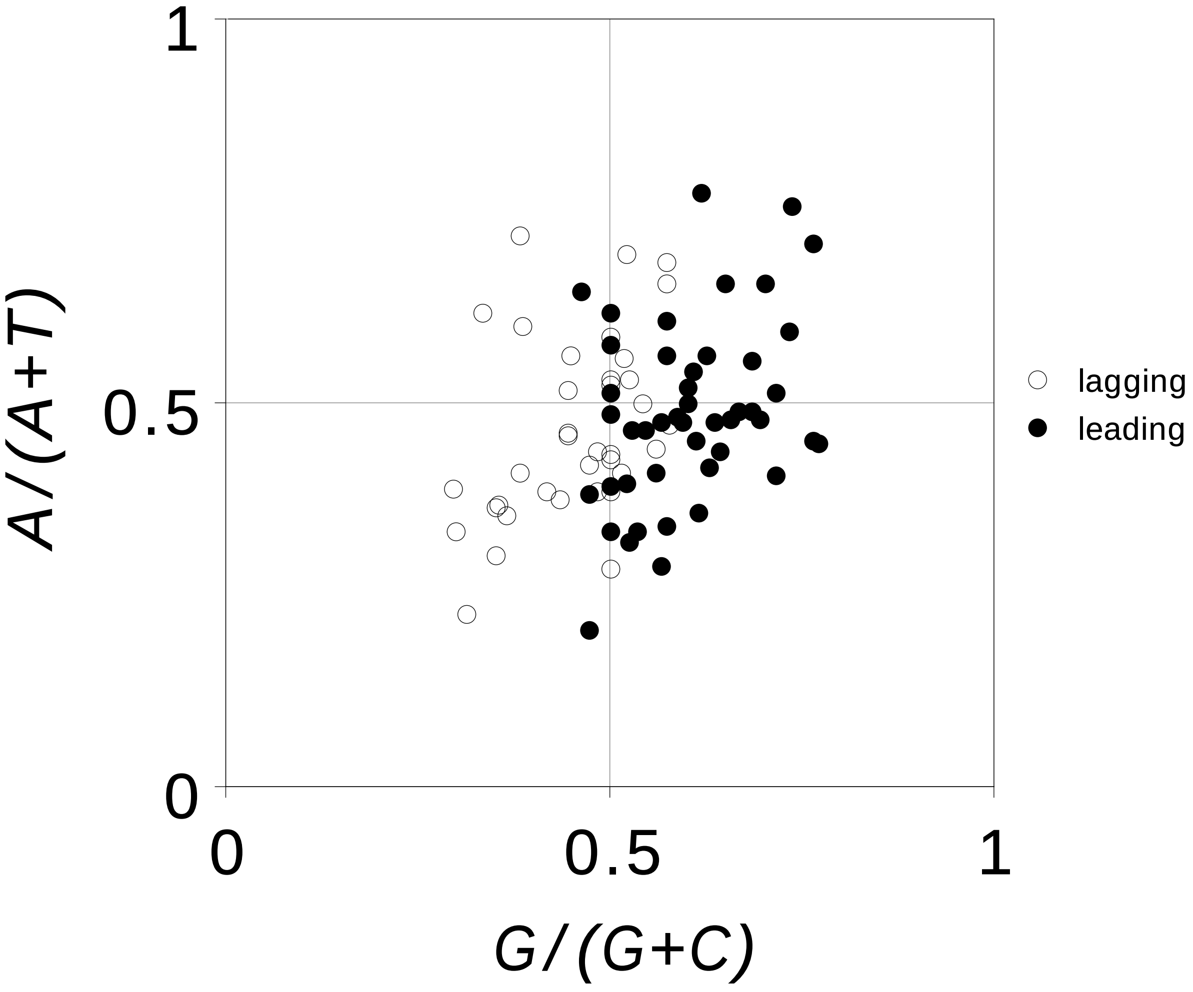
Chlamydophila pneumoniae CWL029



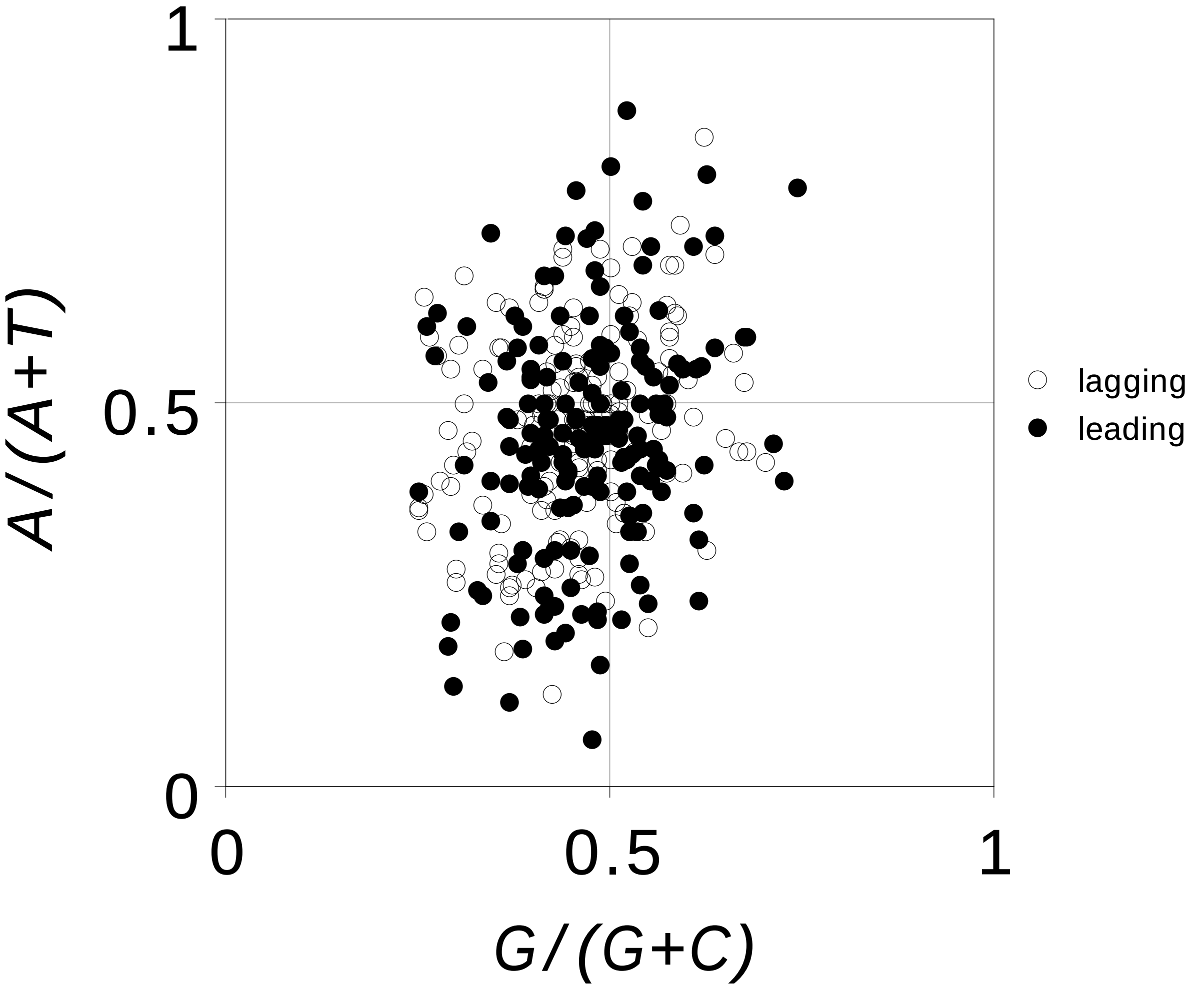
Chlamydophila pneumoniae AR39



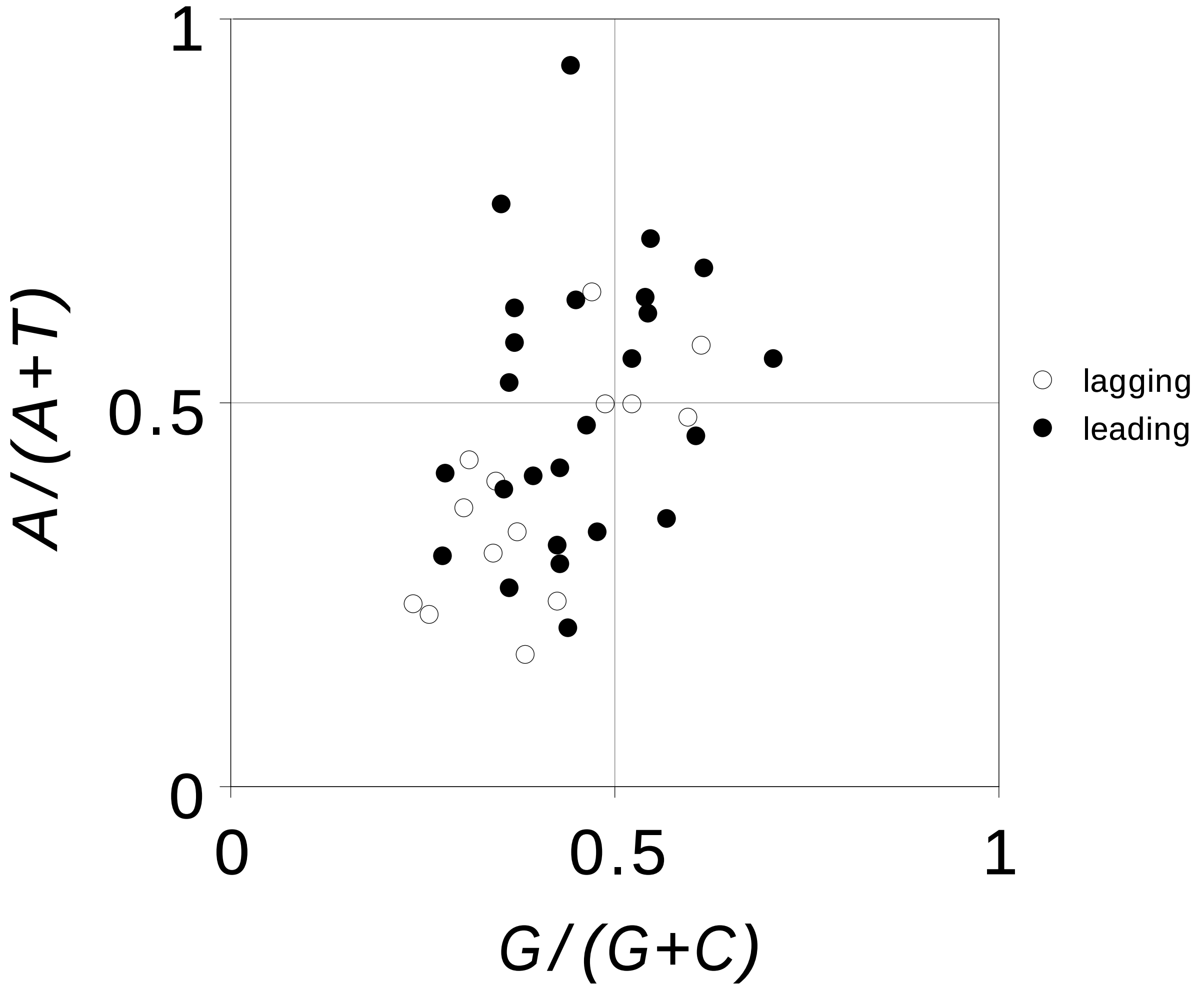
Chlamydophila pneumoniae J138



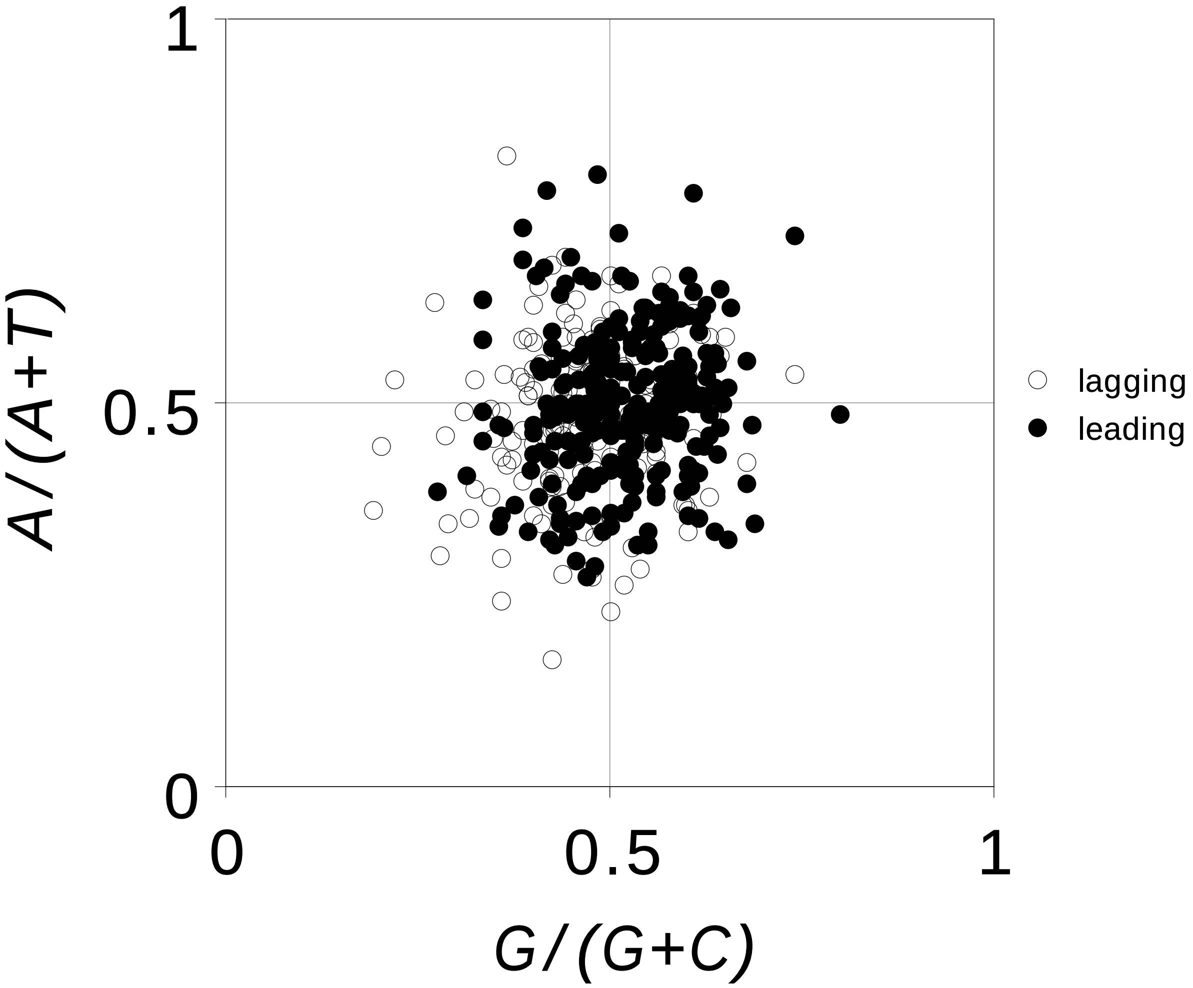
Chlamydia trachomatis



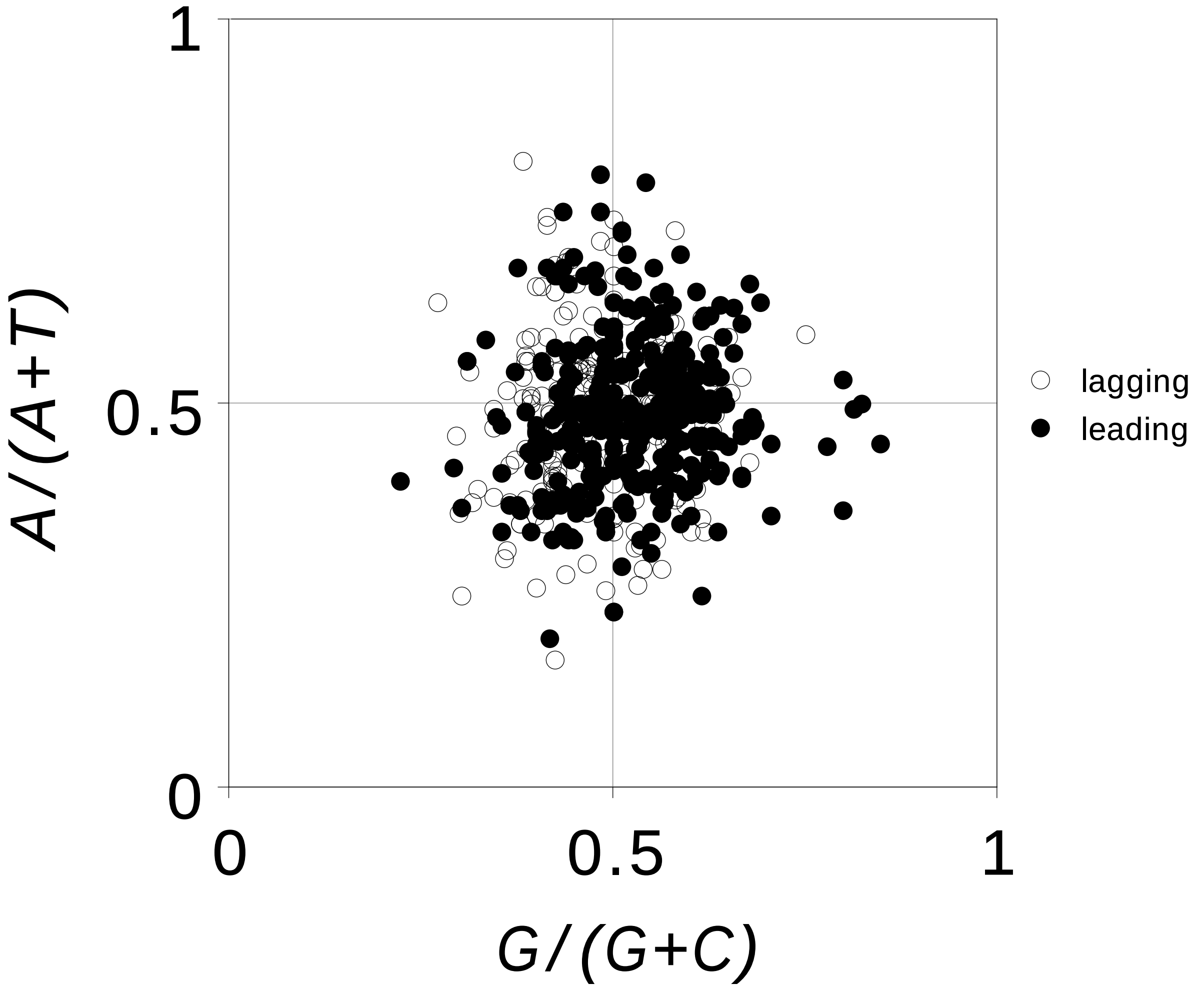
Deinococcus radiodurans chromosome 1



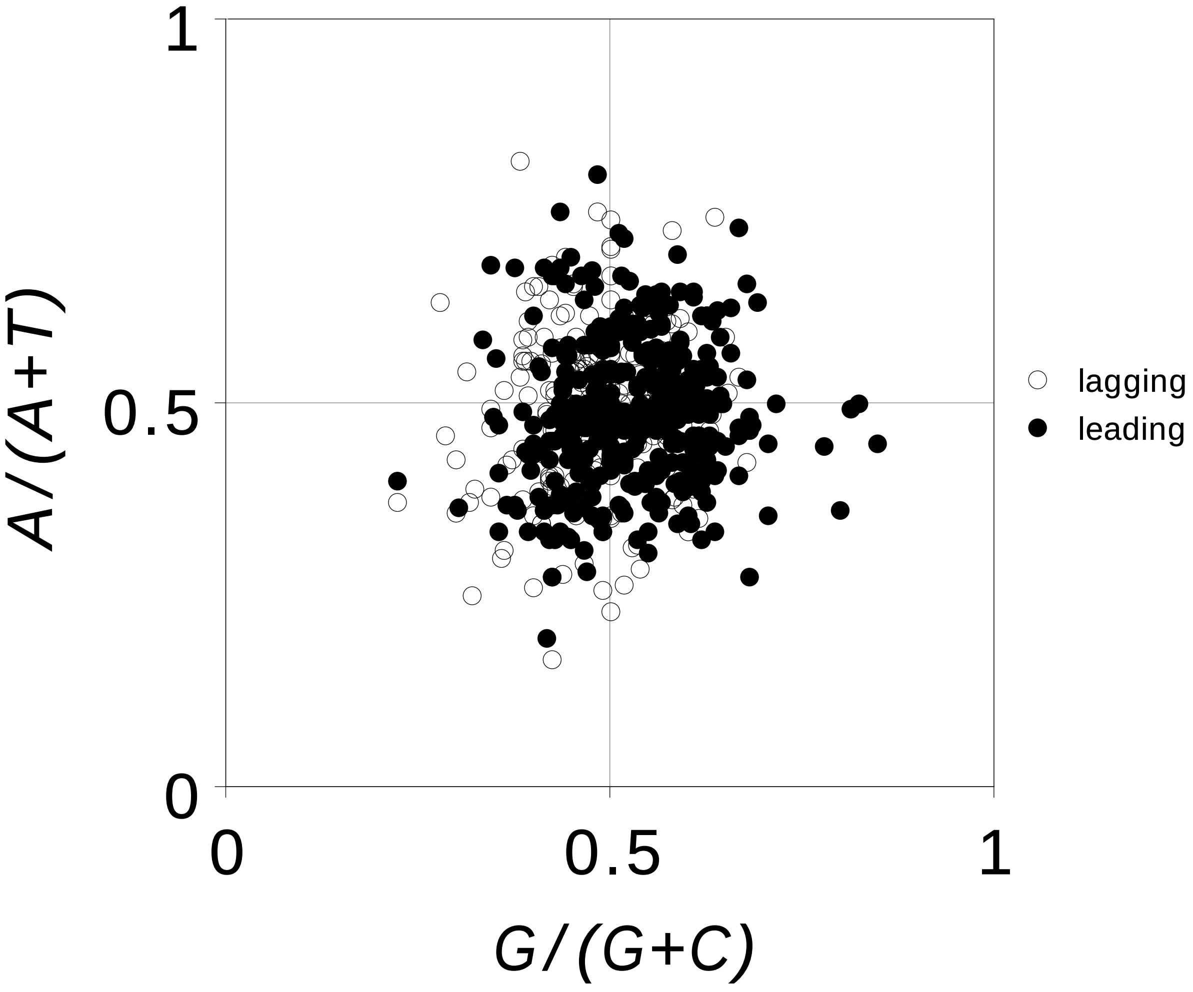
Deinococcus radiodurans chromosome 2



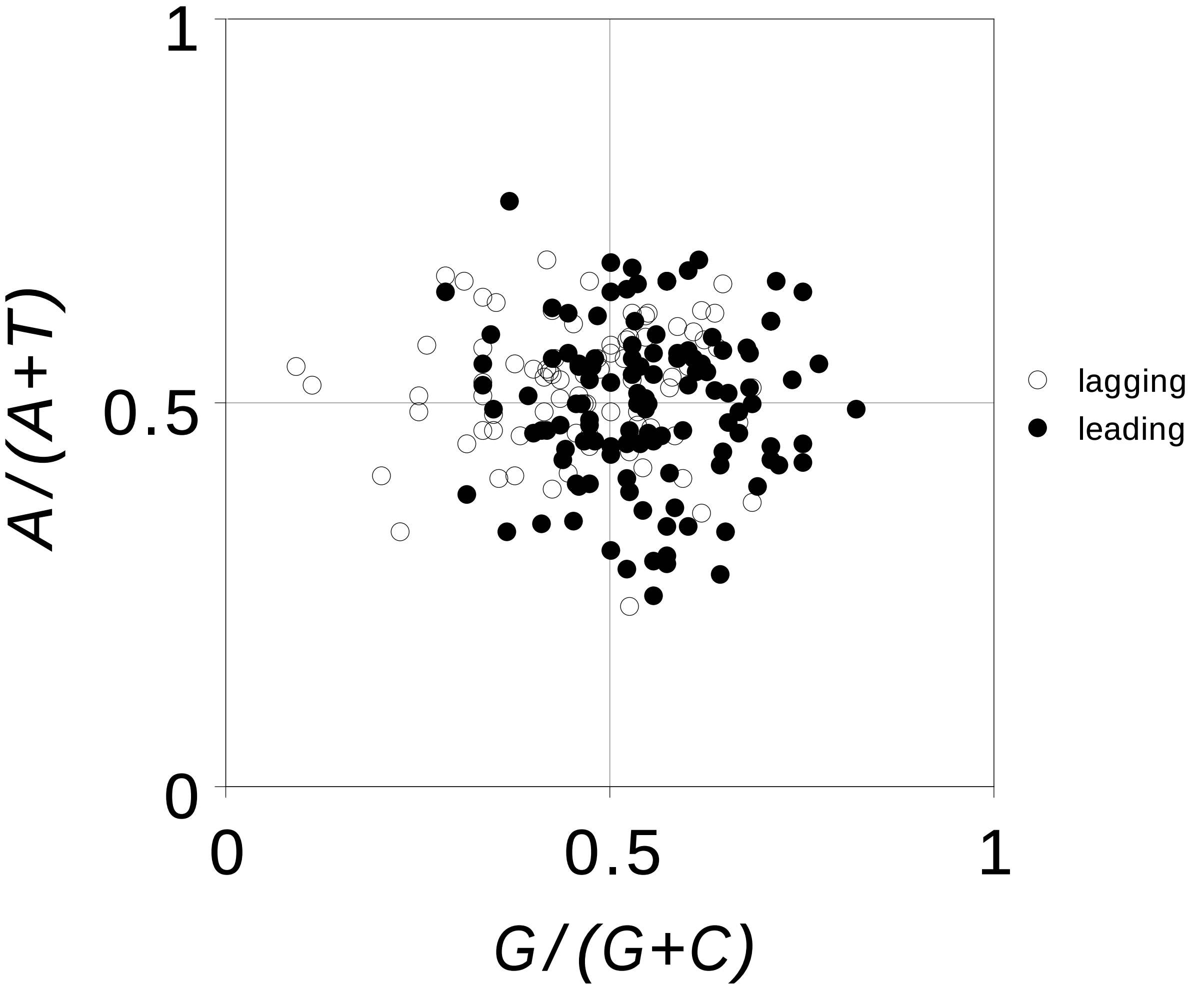
Escherichia coli K-12



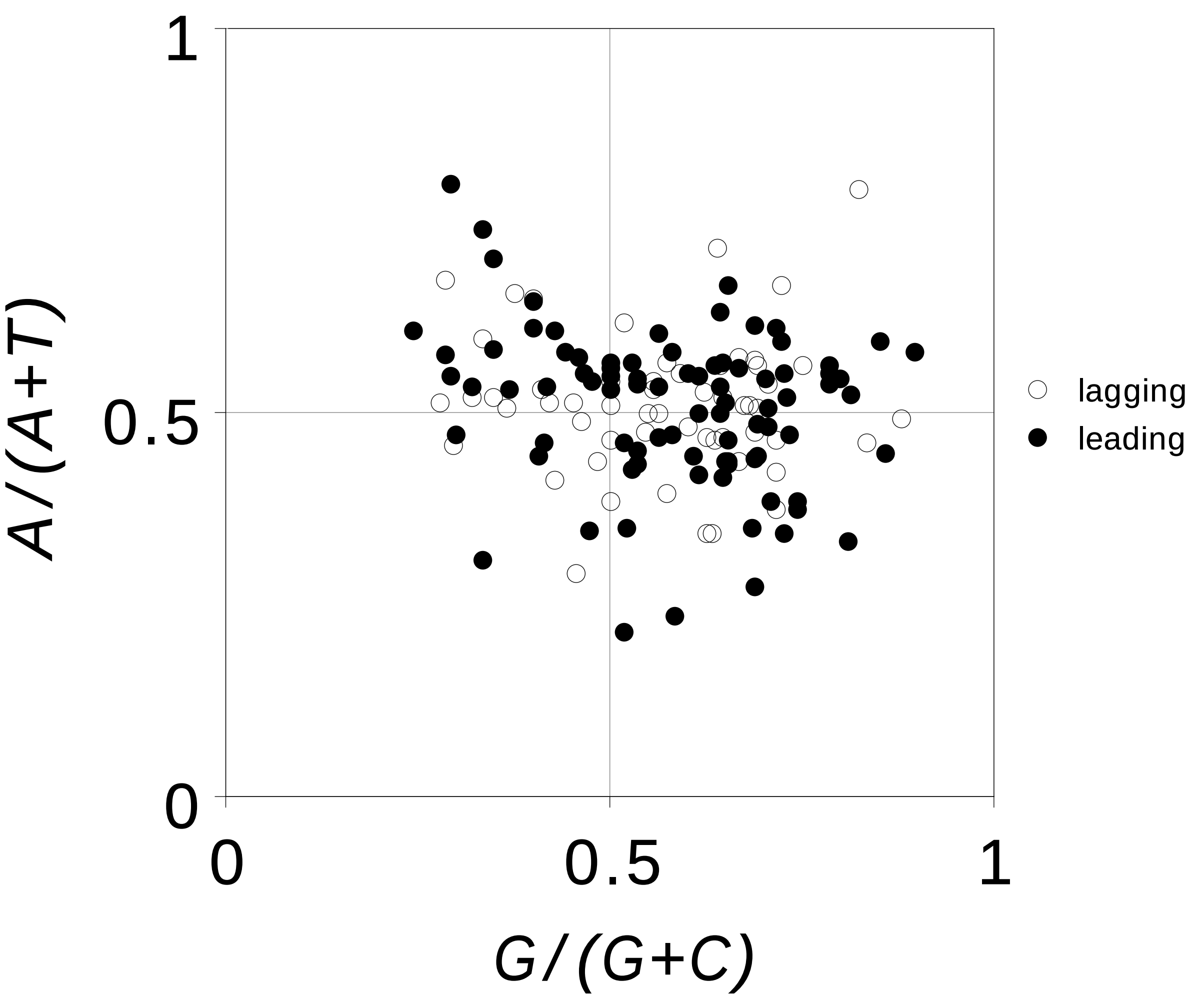
Escherichia coli EDL933



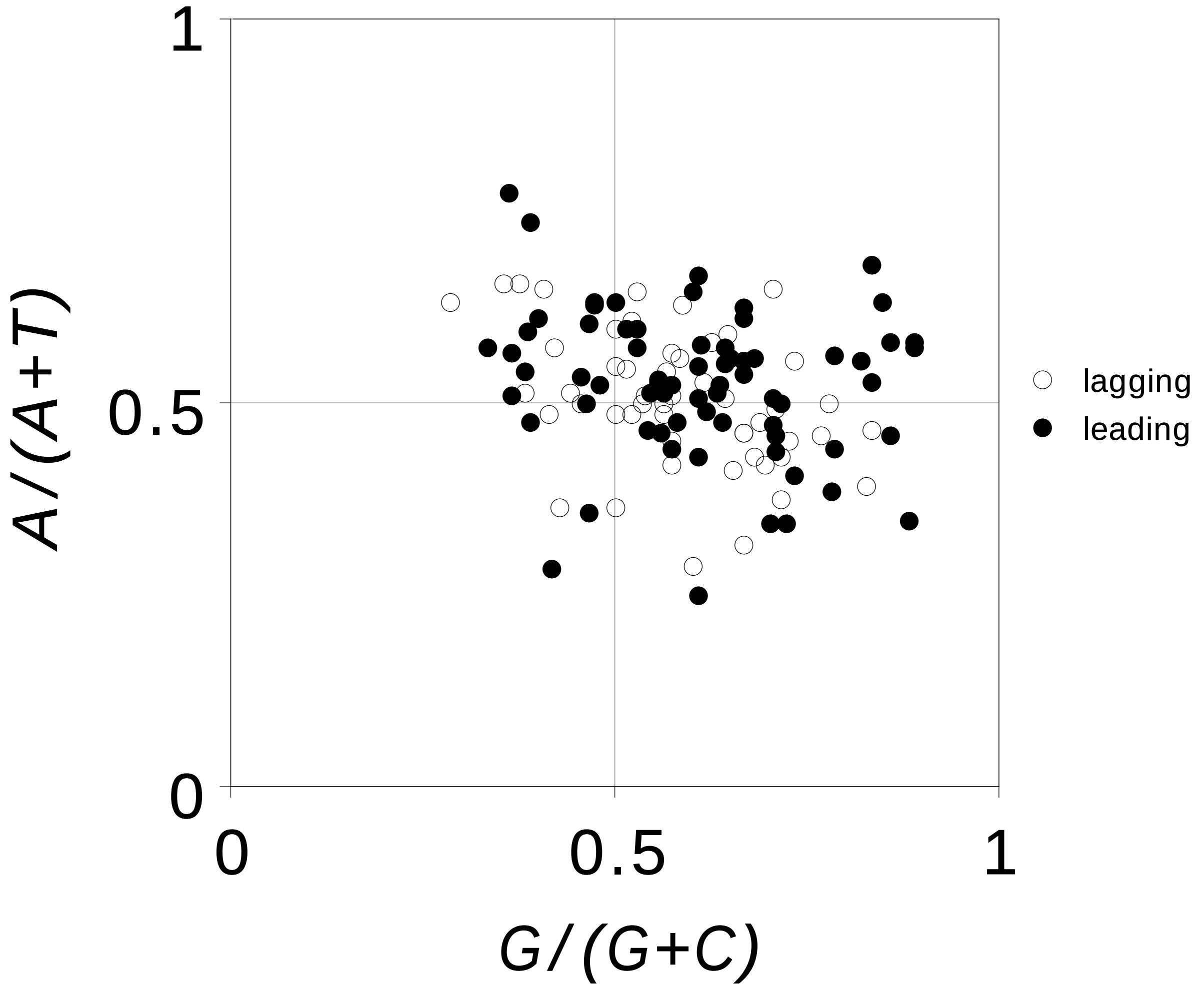
Escherichia coli RIMD 0509952



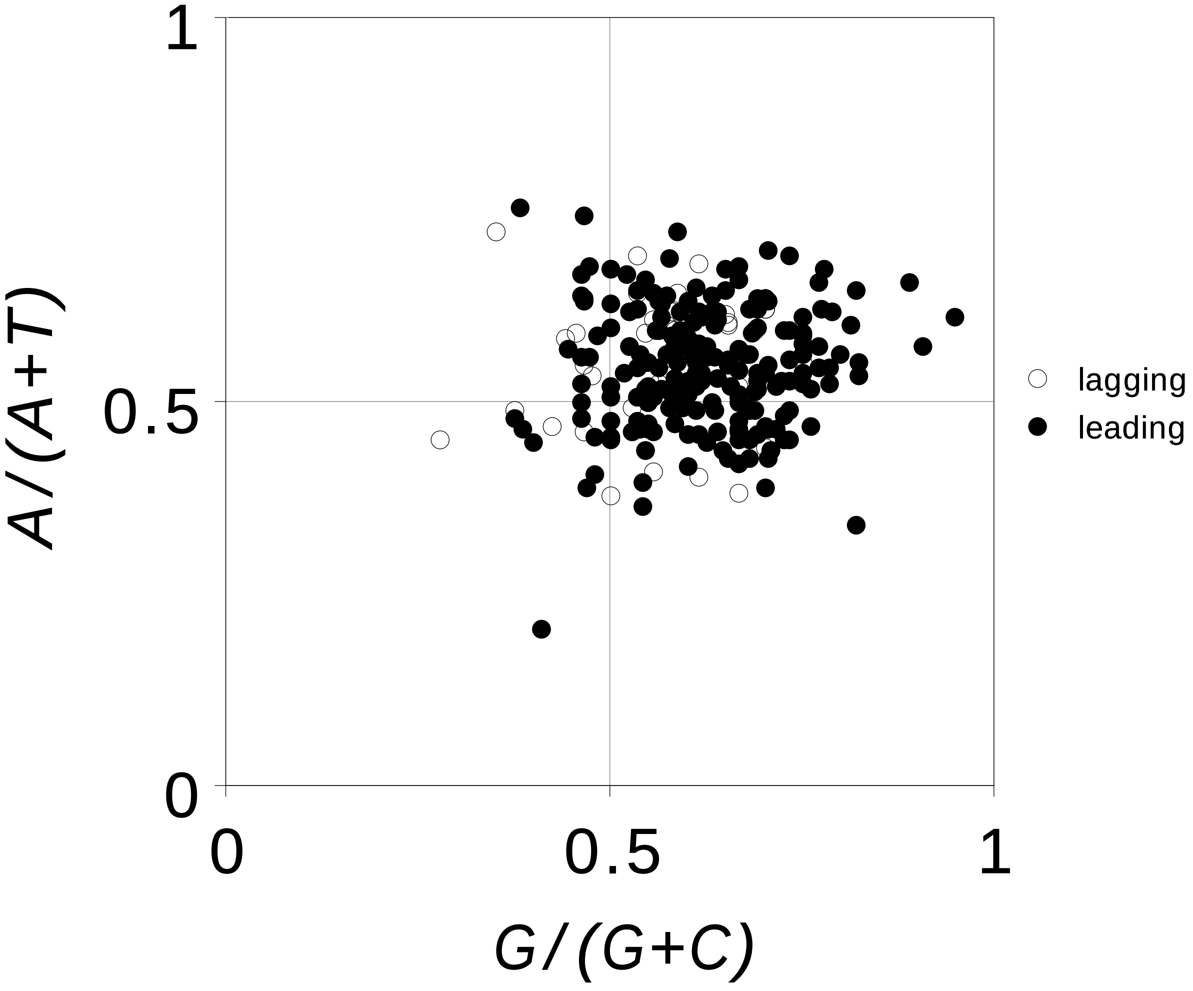
Haemophilus influenzae



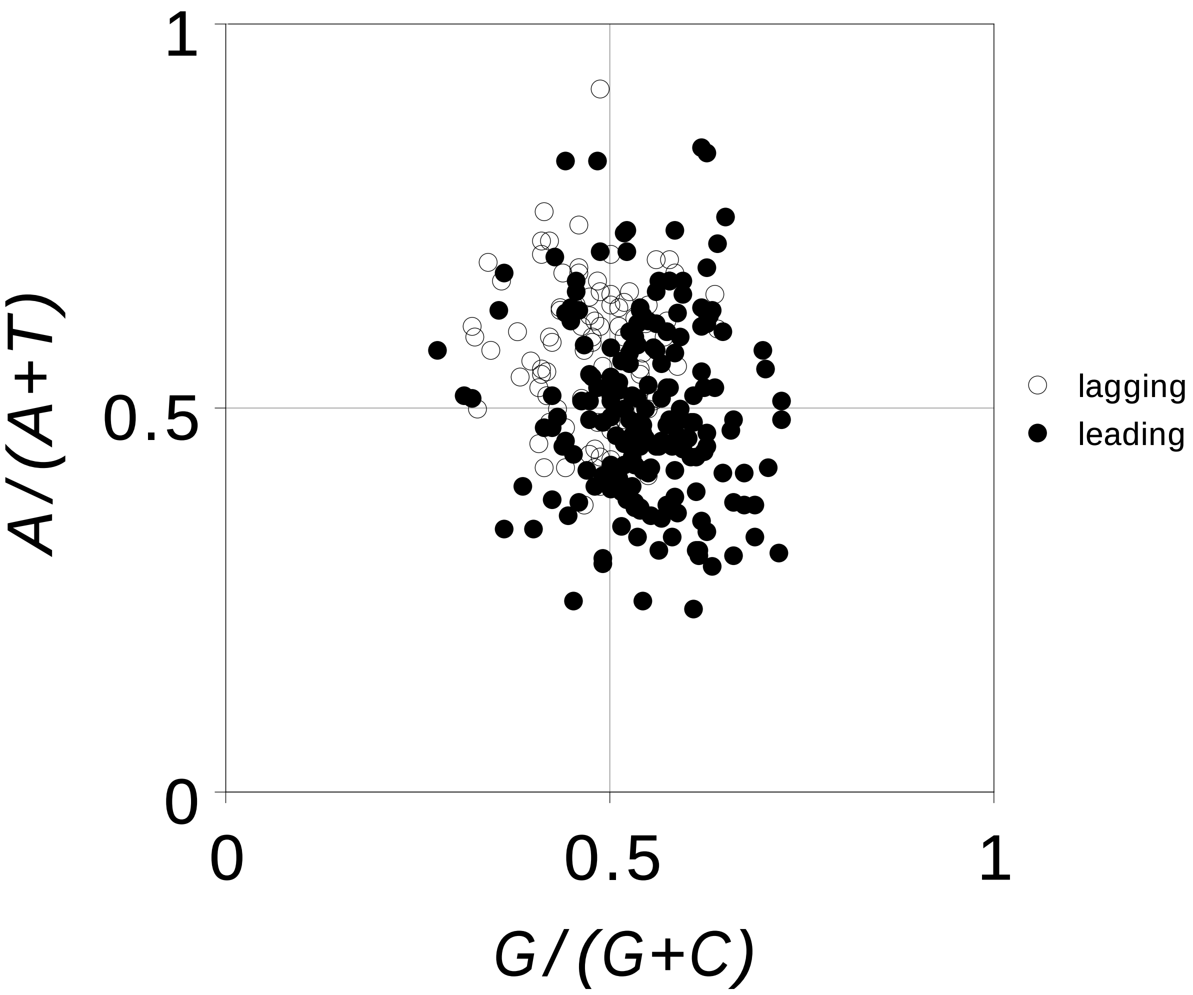
Helicobacter pylori 26695



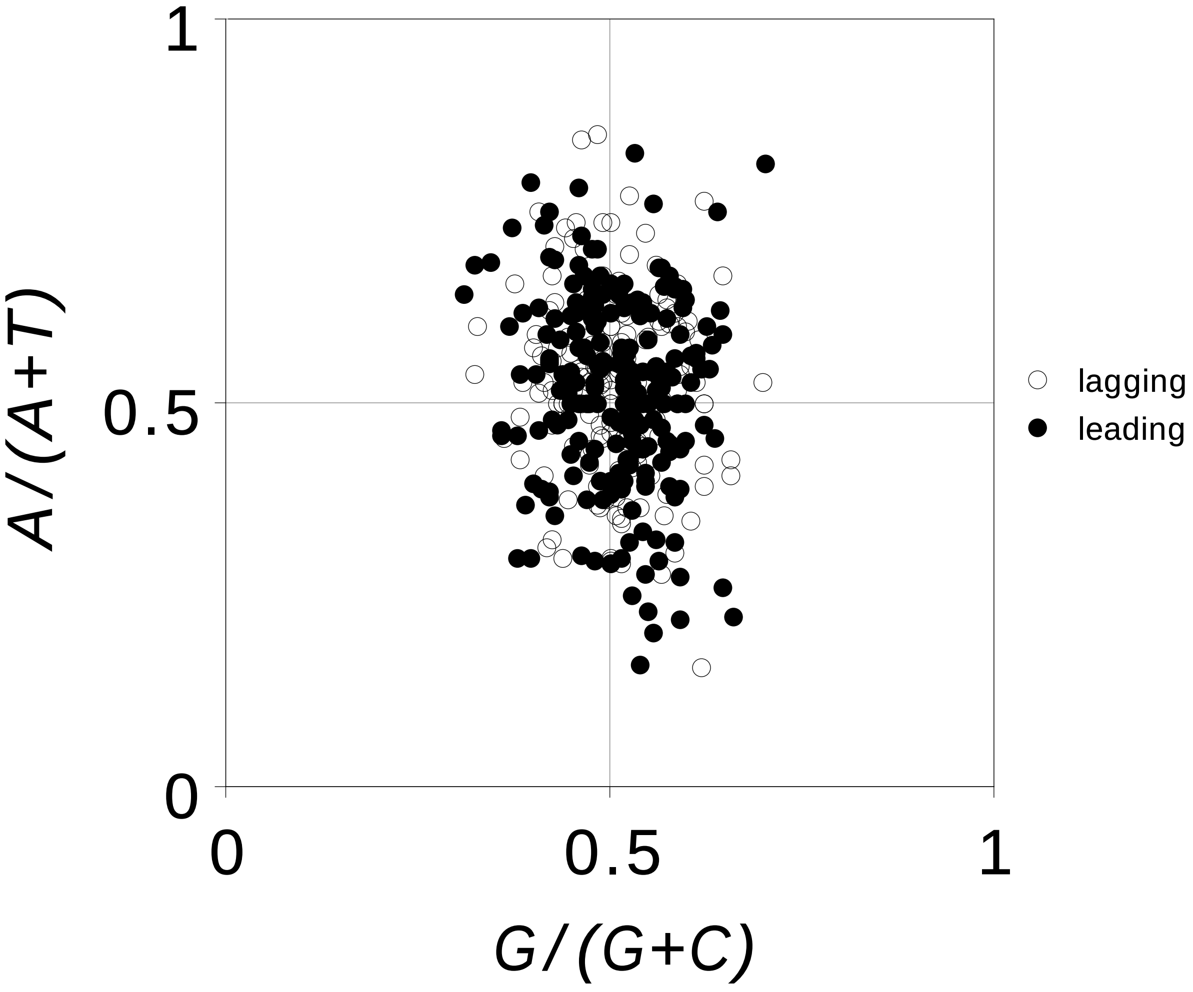
Helicobacter pylori J99



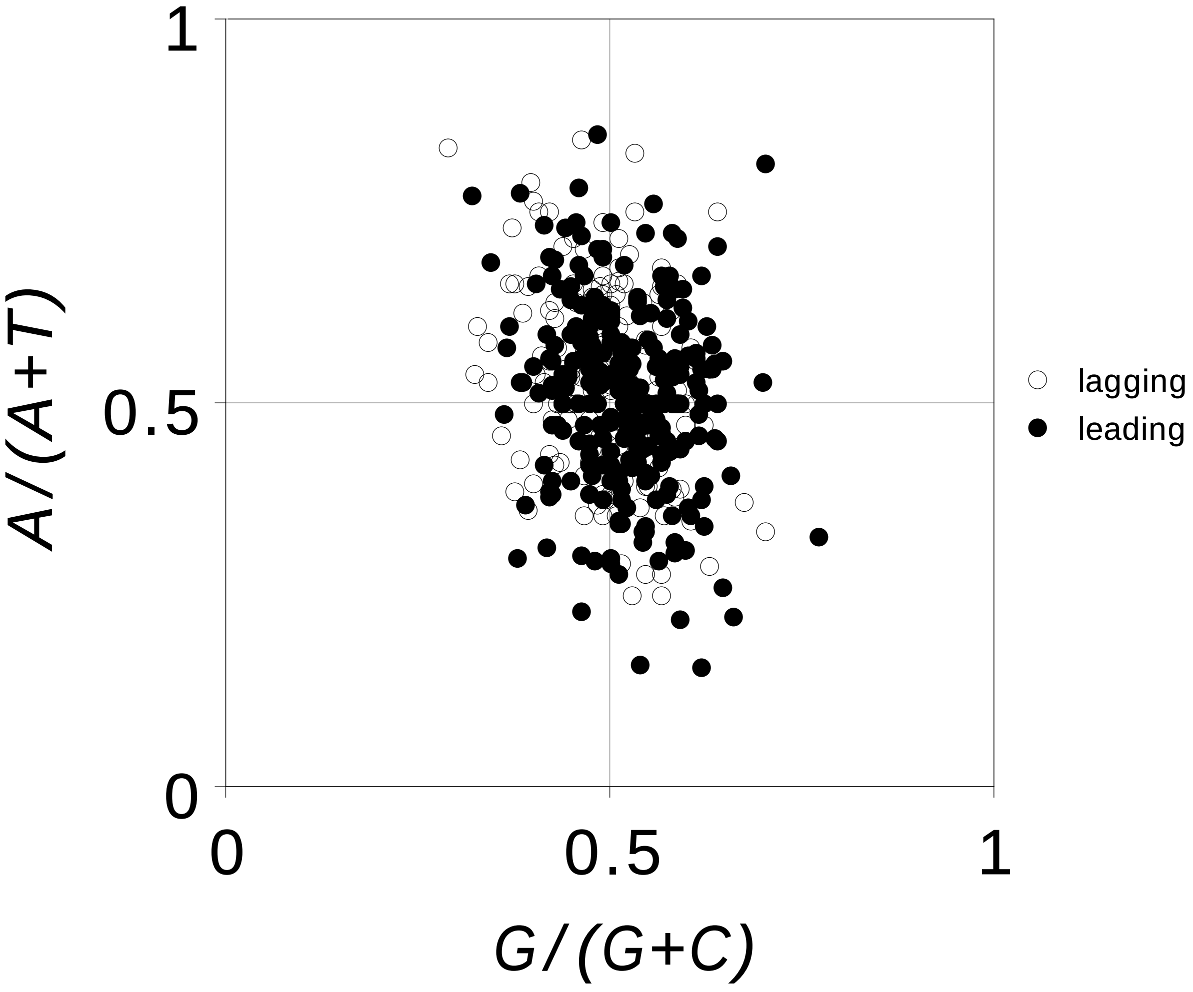
Lactococcus lactis



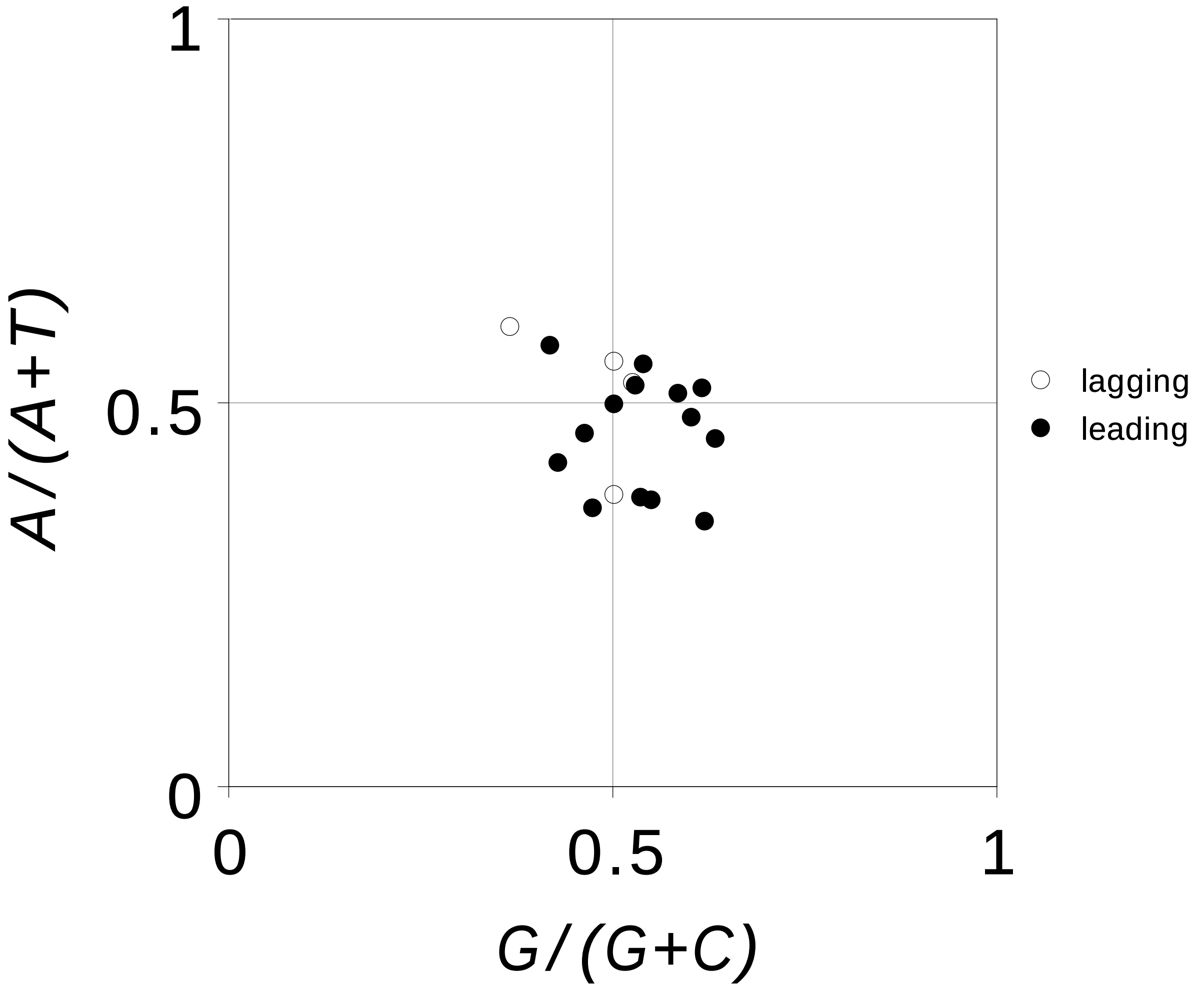
Mycobacterium leprae



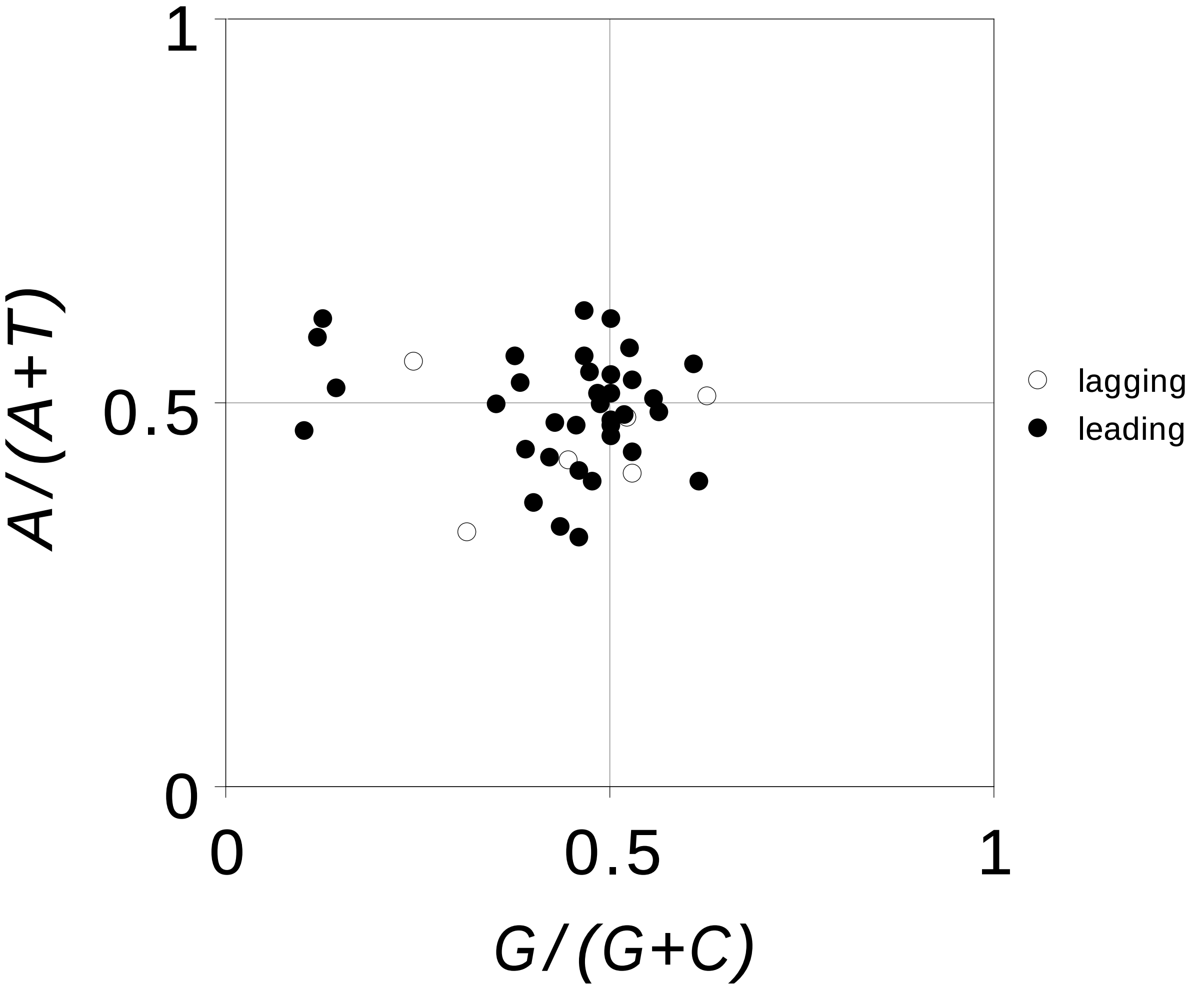
Mycobacterium tuberculosis H37Rv



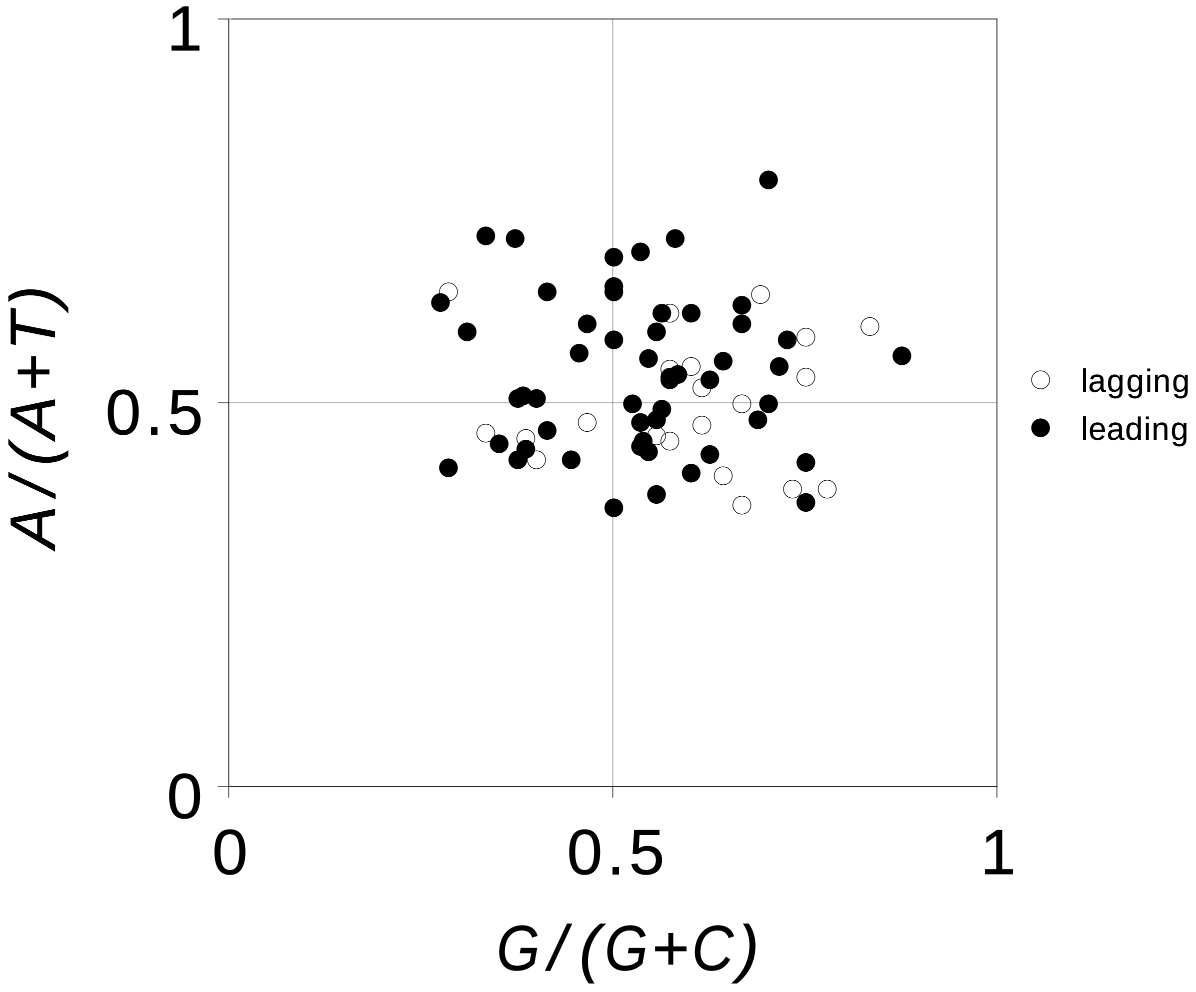
Mycobacterium tuberculosis CDC1551



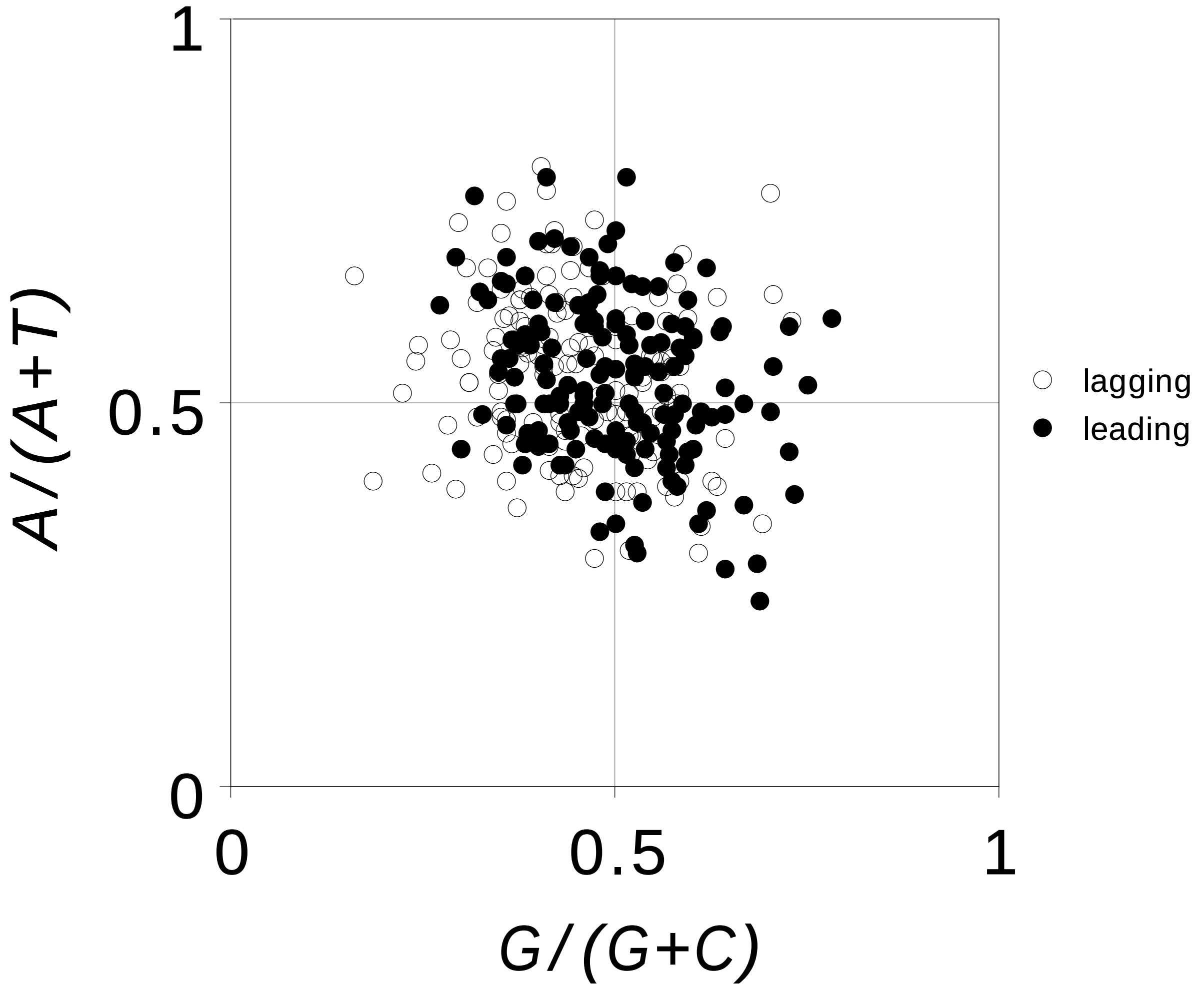
Mycoplasma genitalium



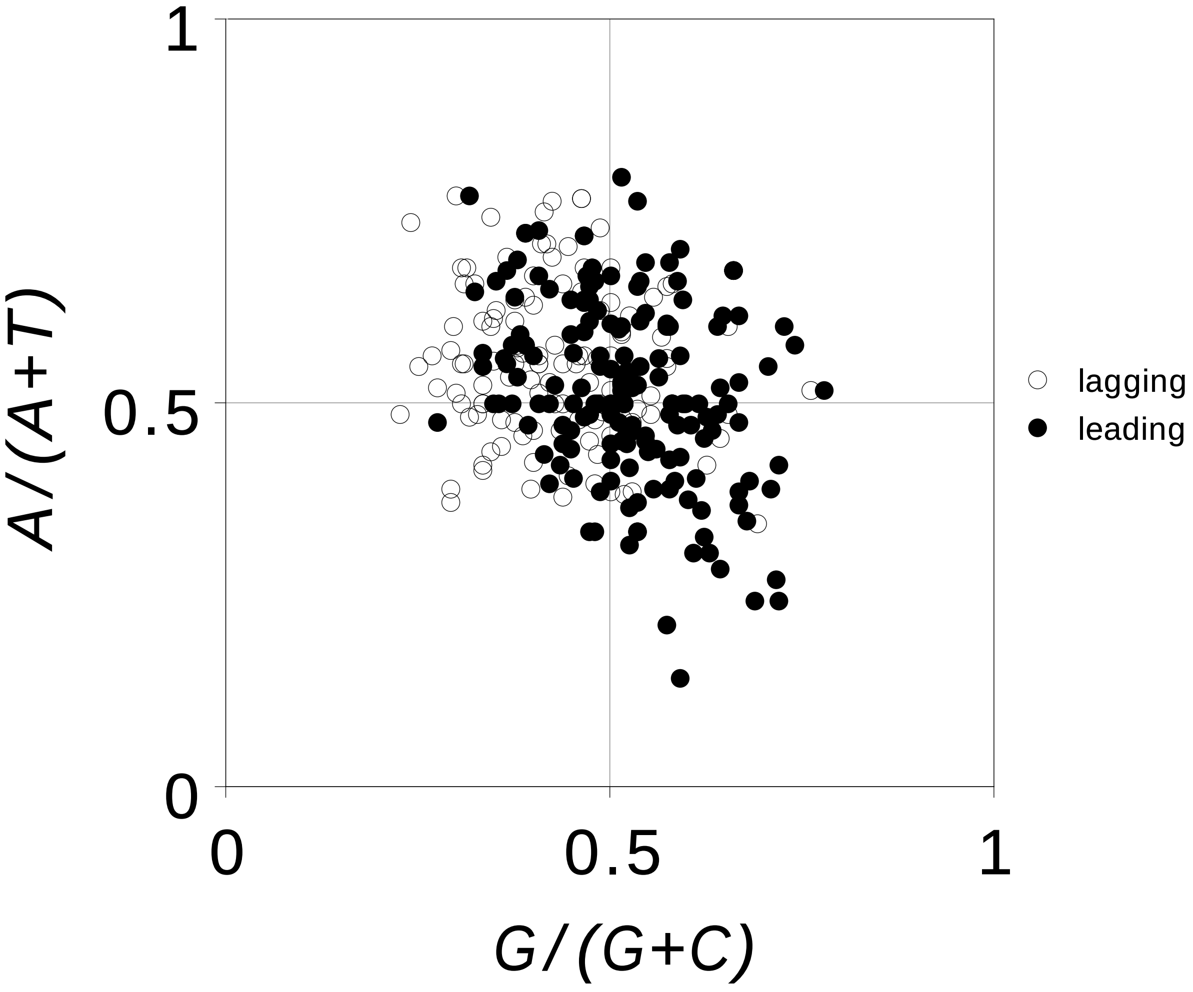
Mycoplasma pneumoniae



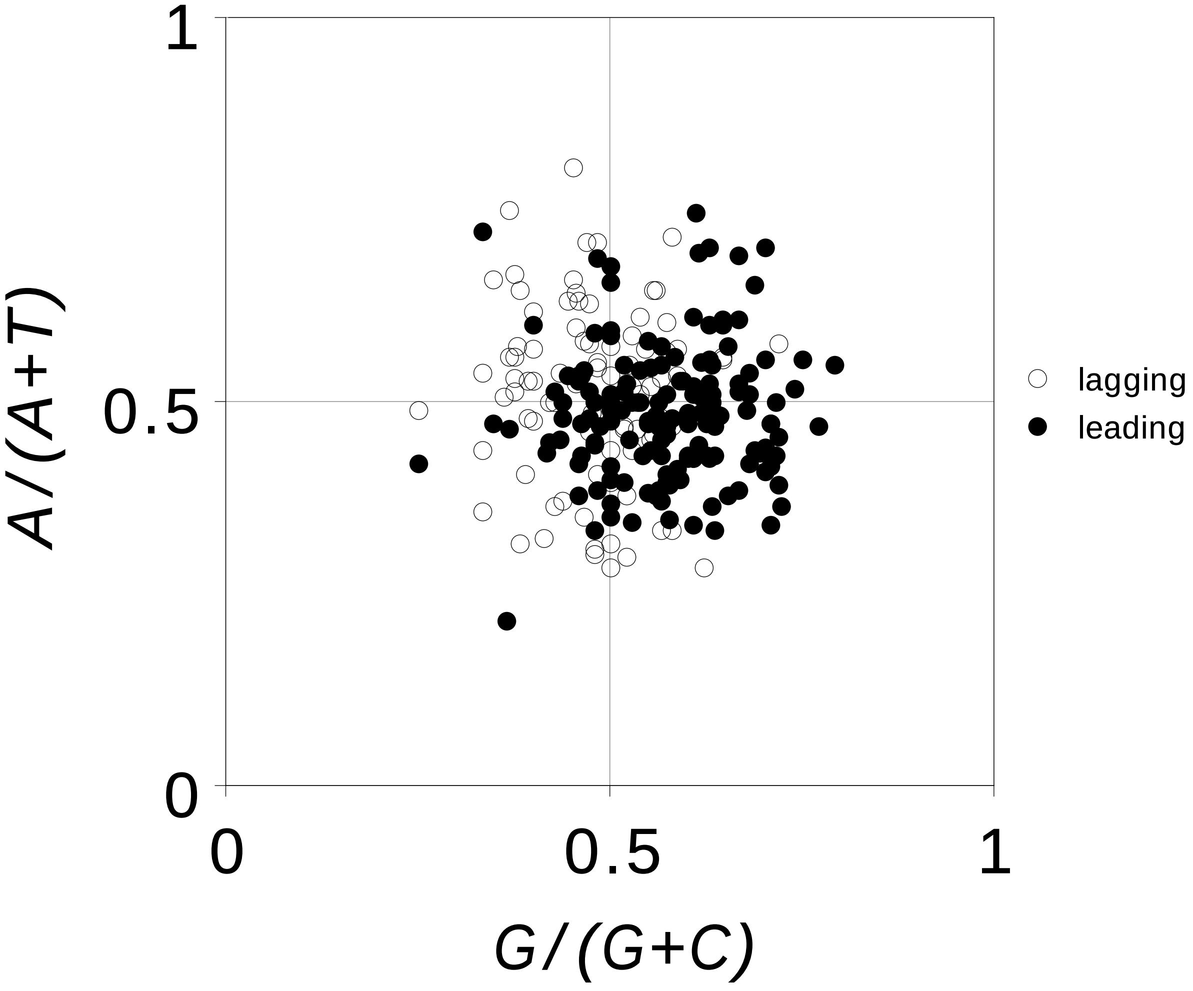
Mycoplasma pulmonis



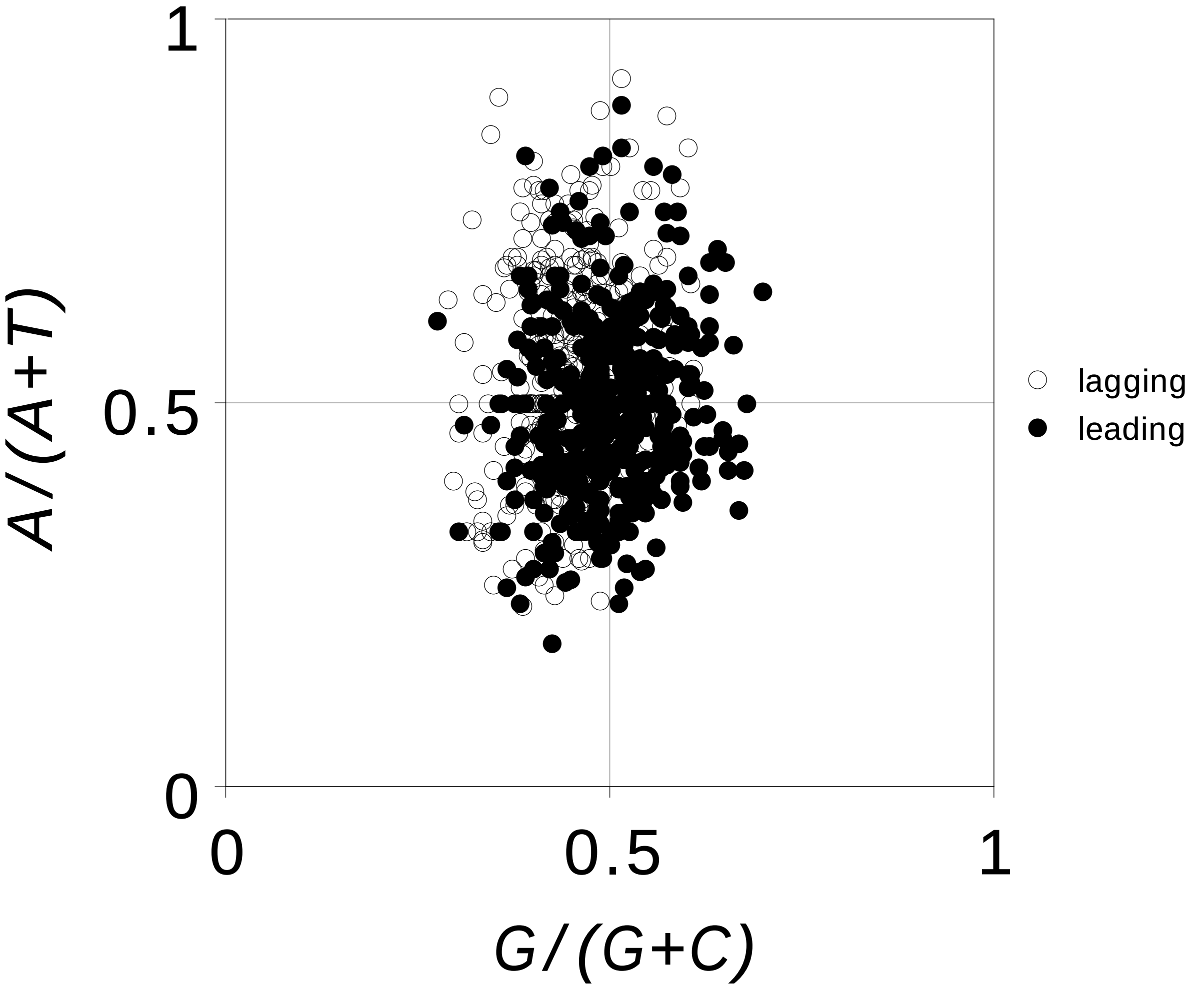
Neisseria meningitidis Z2491 (A)



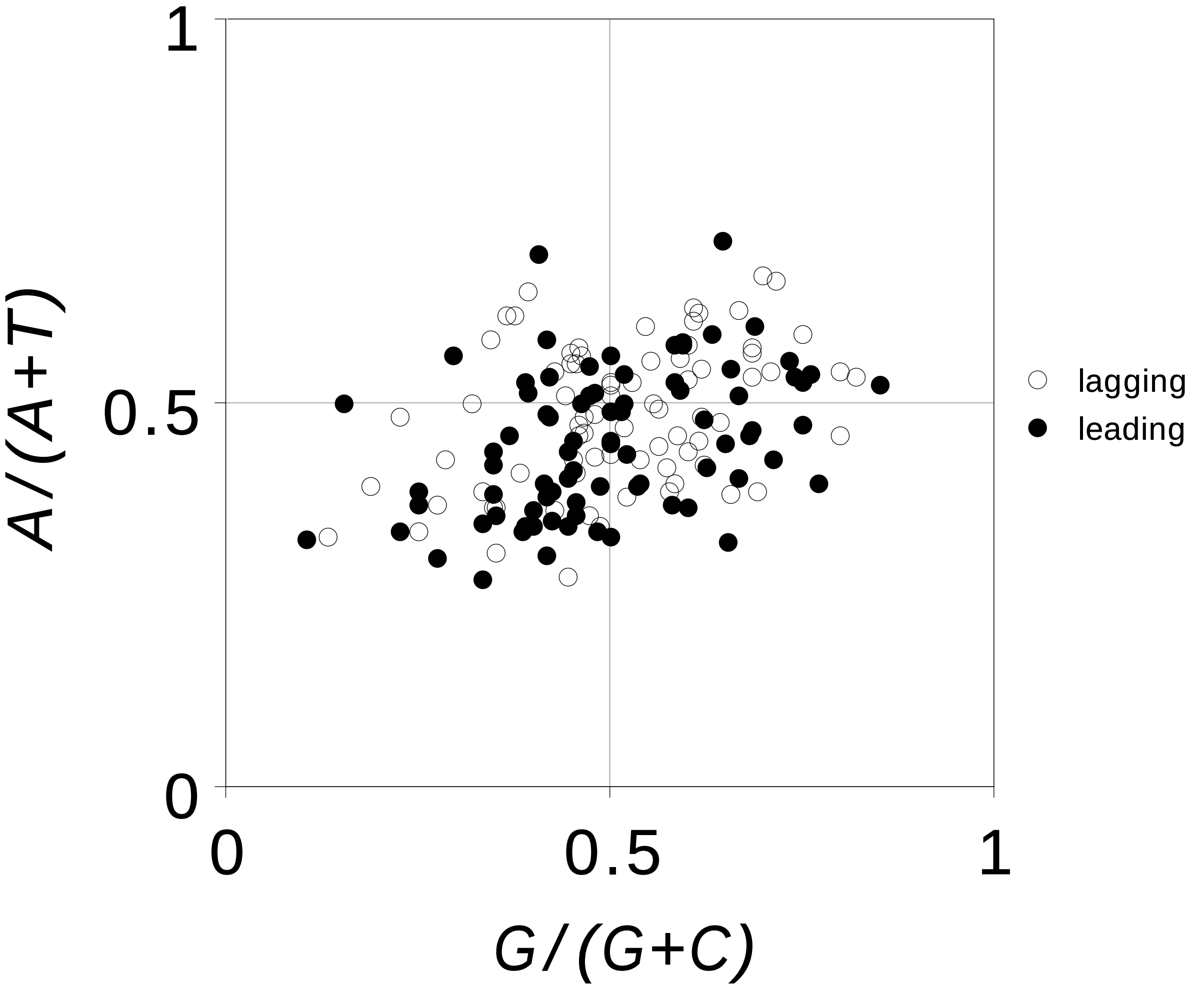
Neisseria meningitidis MC58 (B)



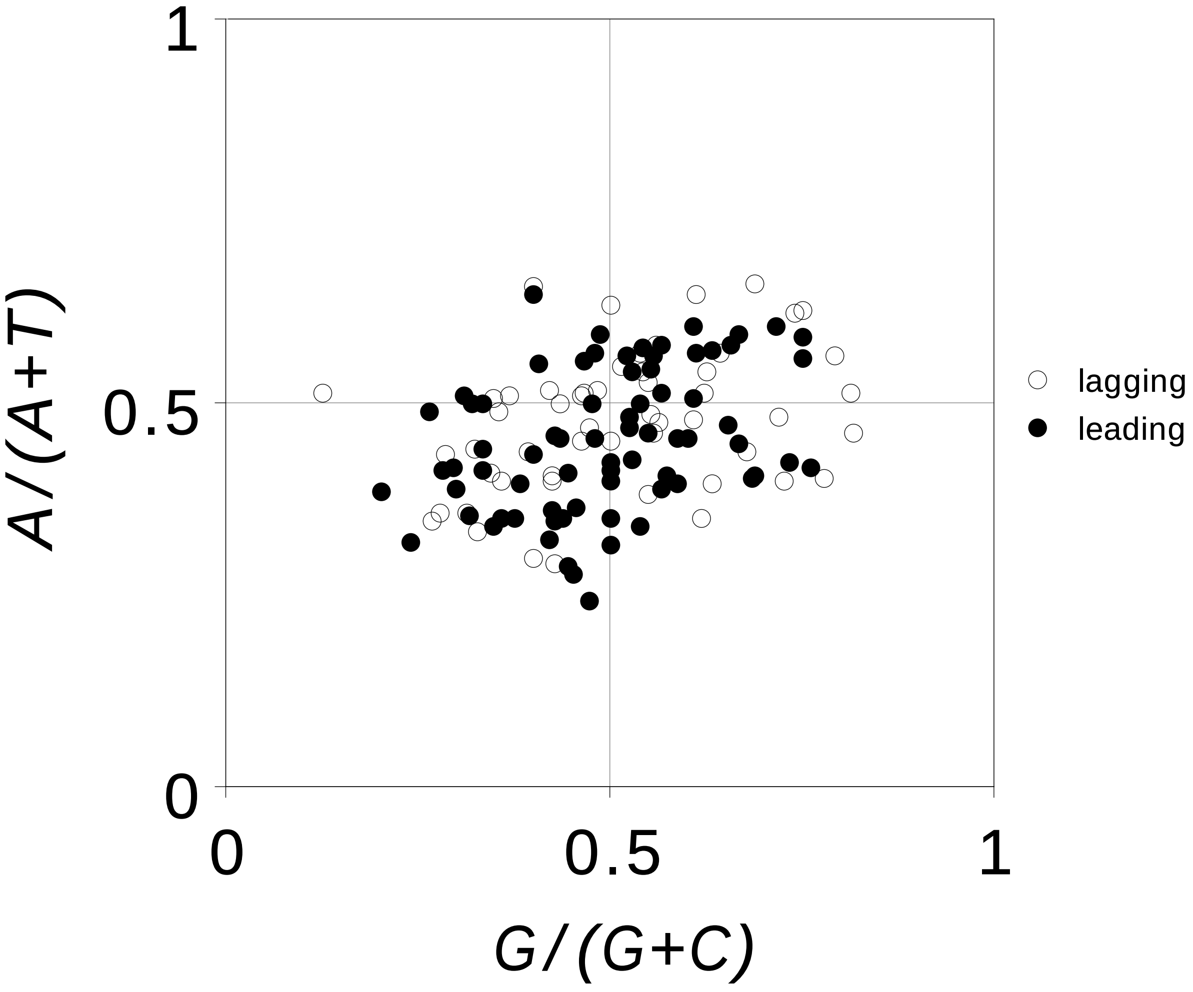
Pasteurella multocida



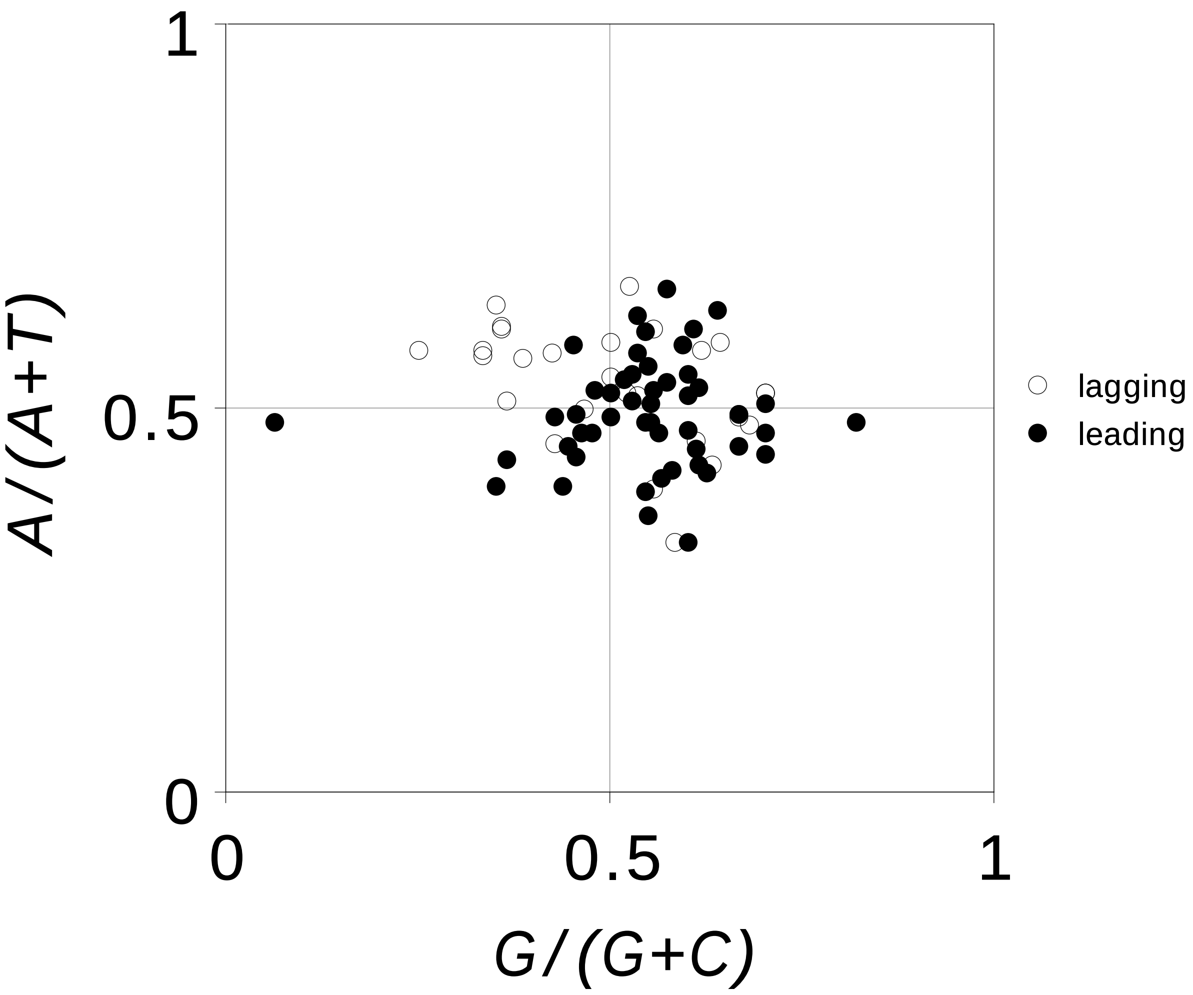
Pseudomonas aeruginosa



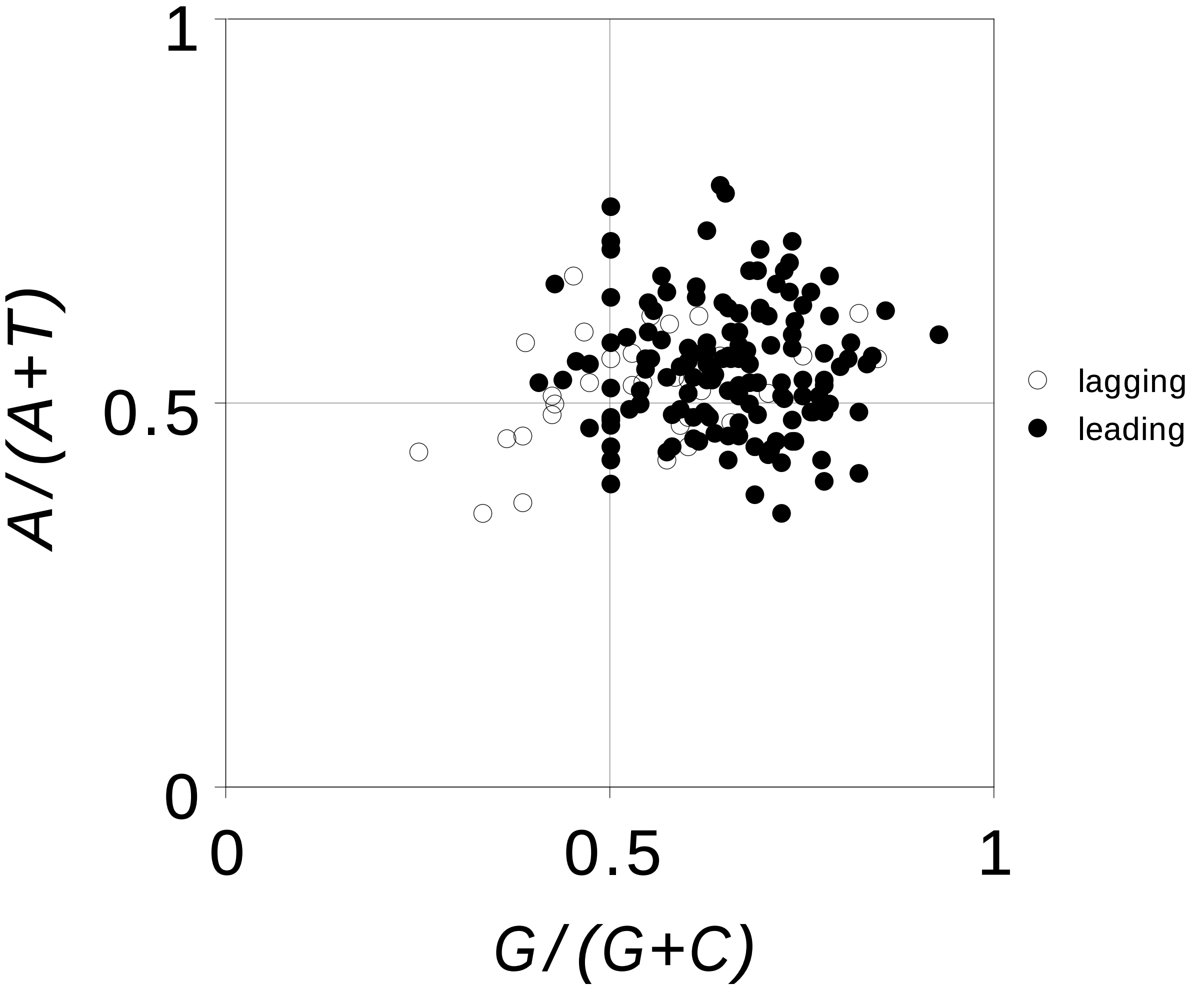
Pyrococcus abyssi



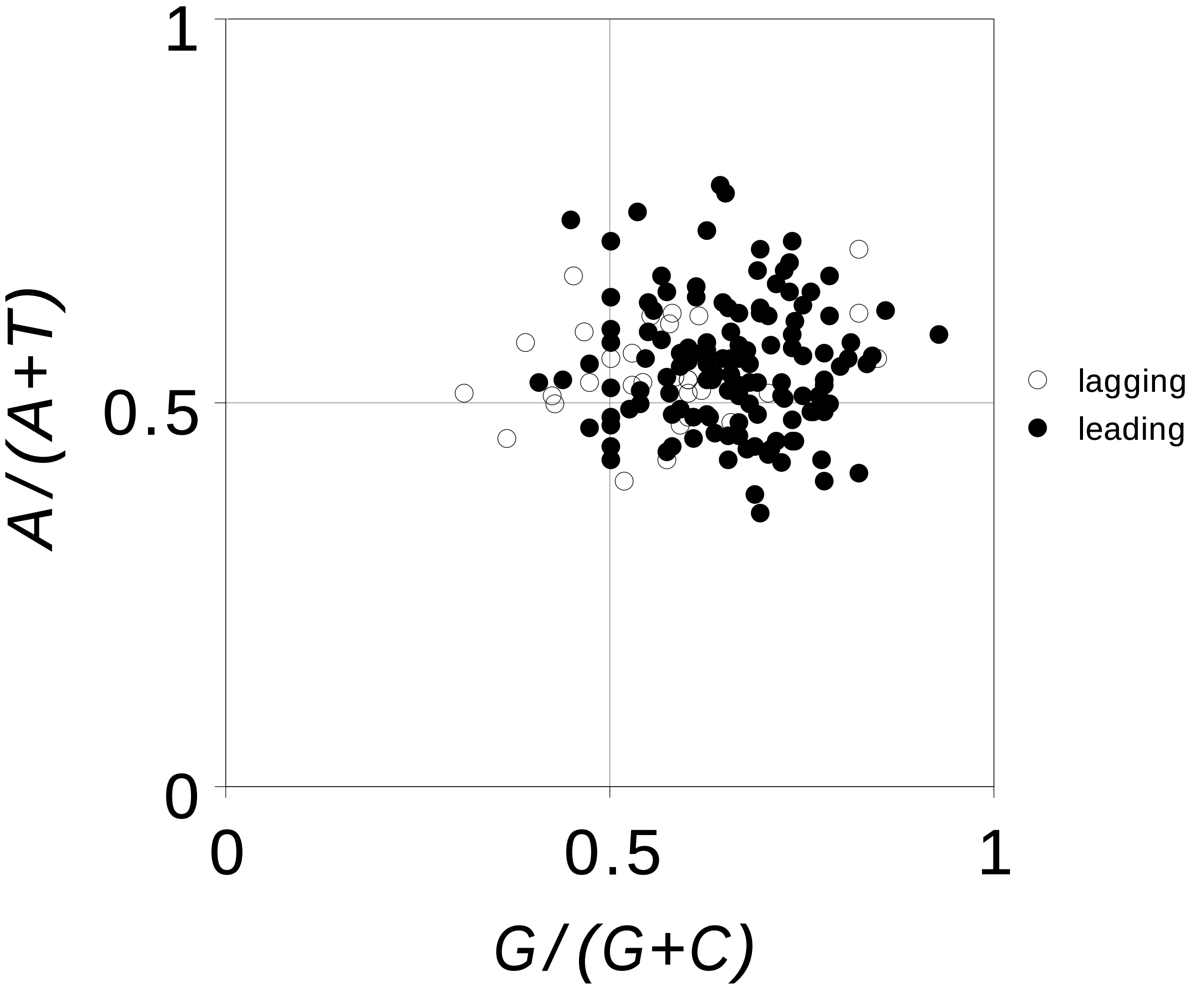
Pyrococcus horikoshii



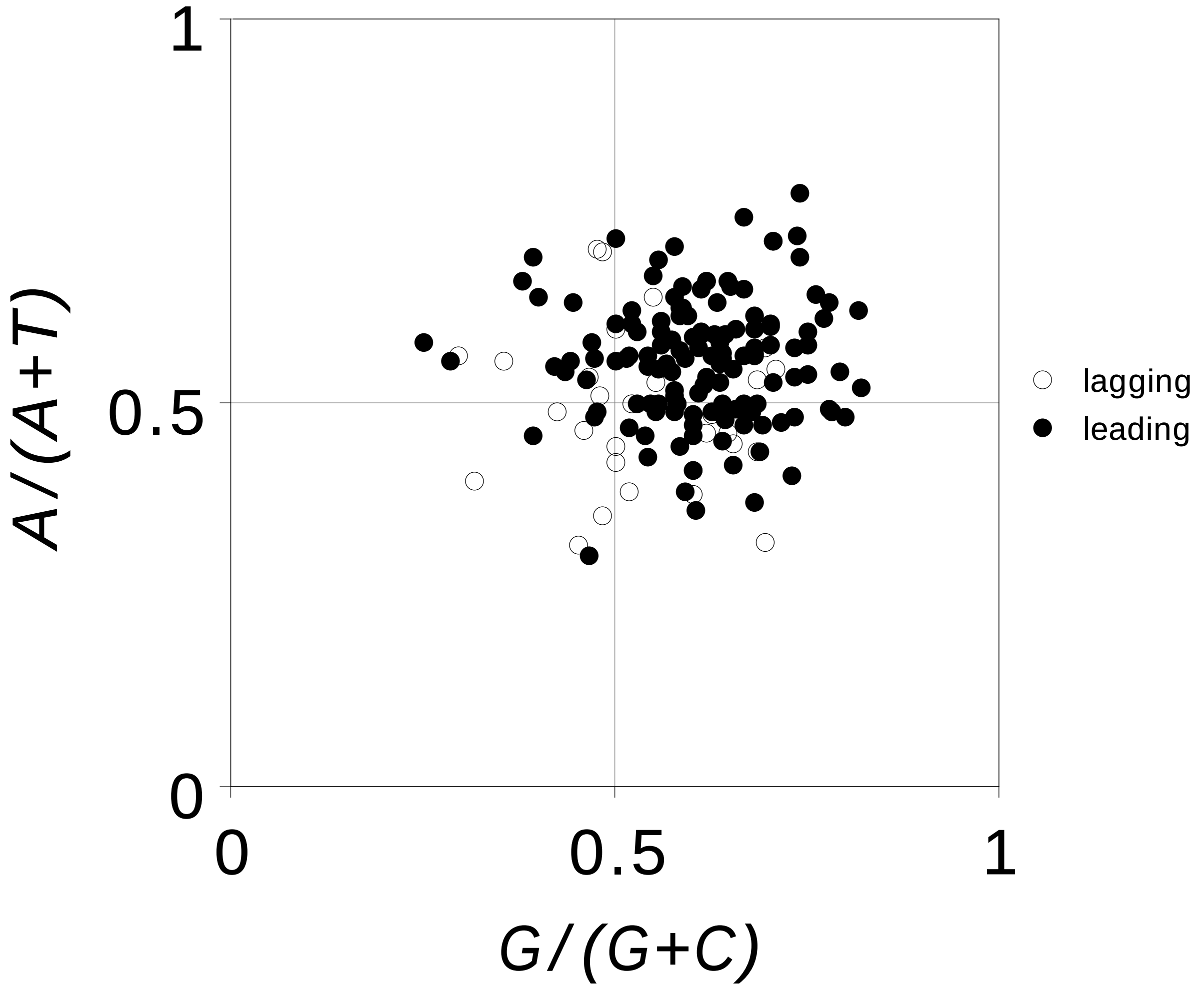
Rickettsia prowazekii



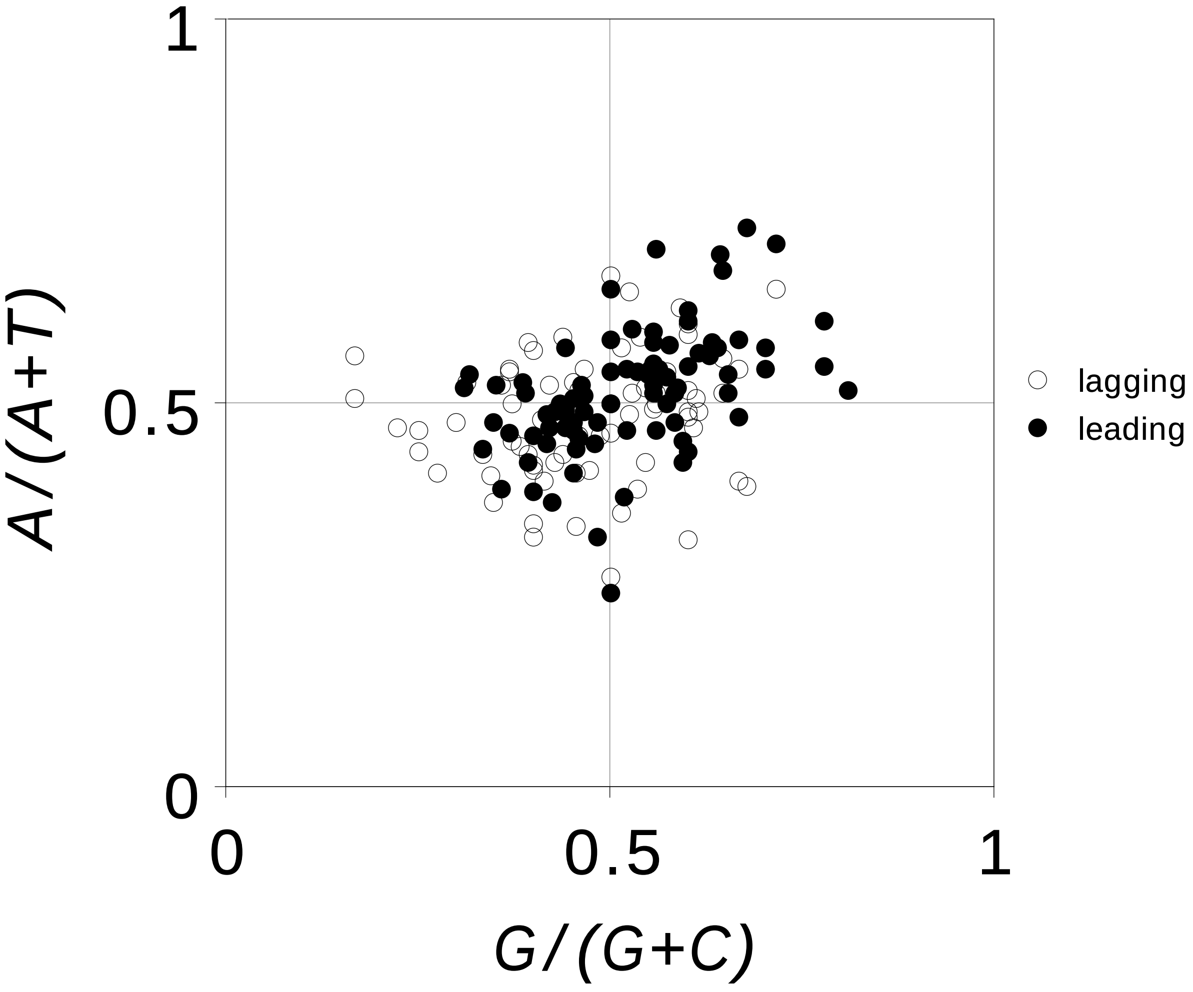
Staphylococcus aureus Mu50



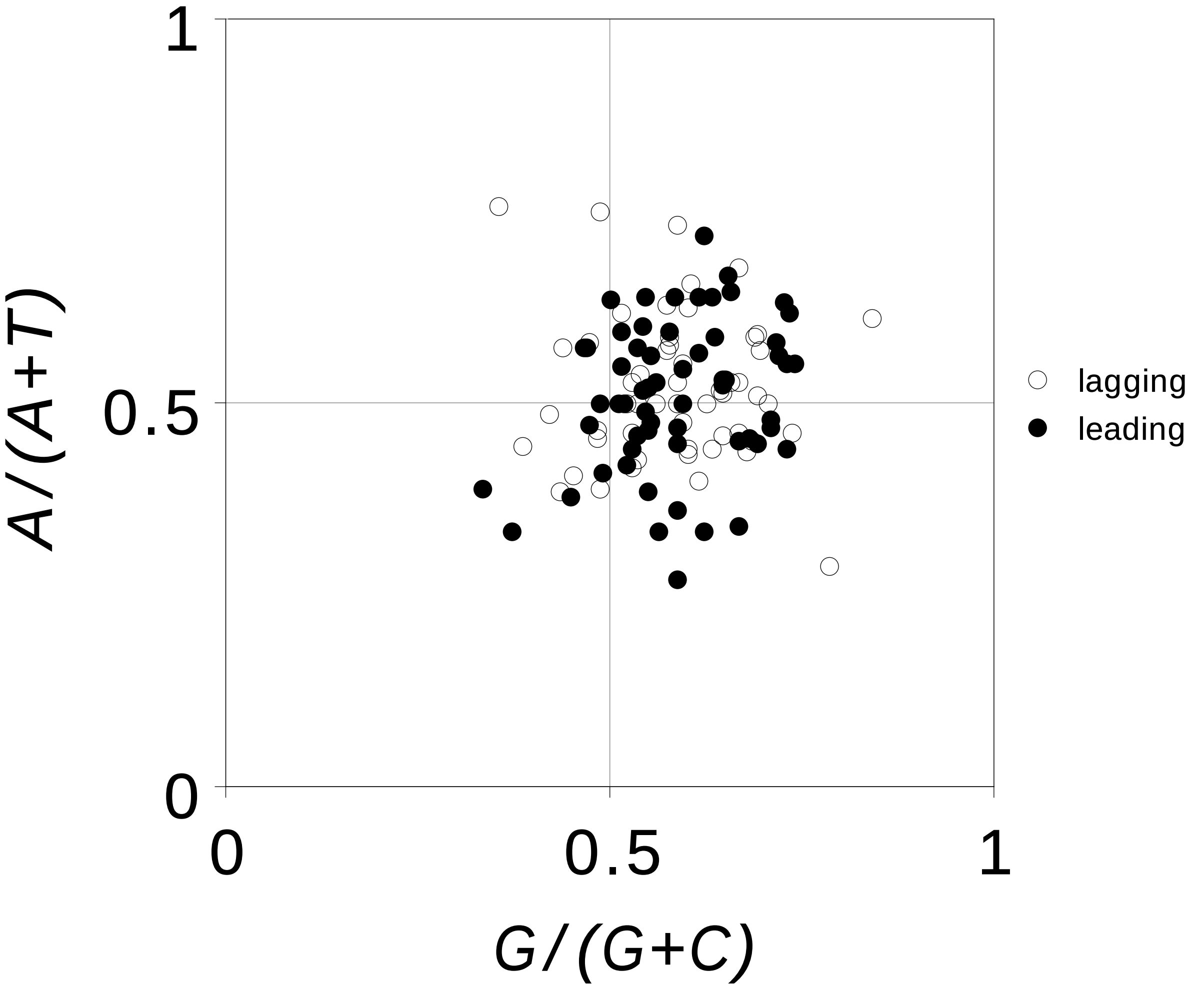
Staphylococcus aureus N315



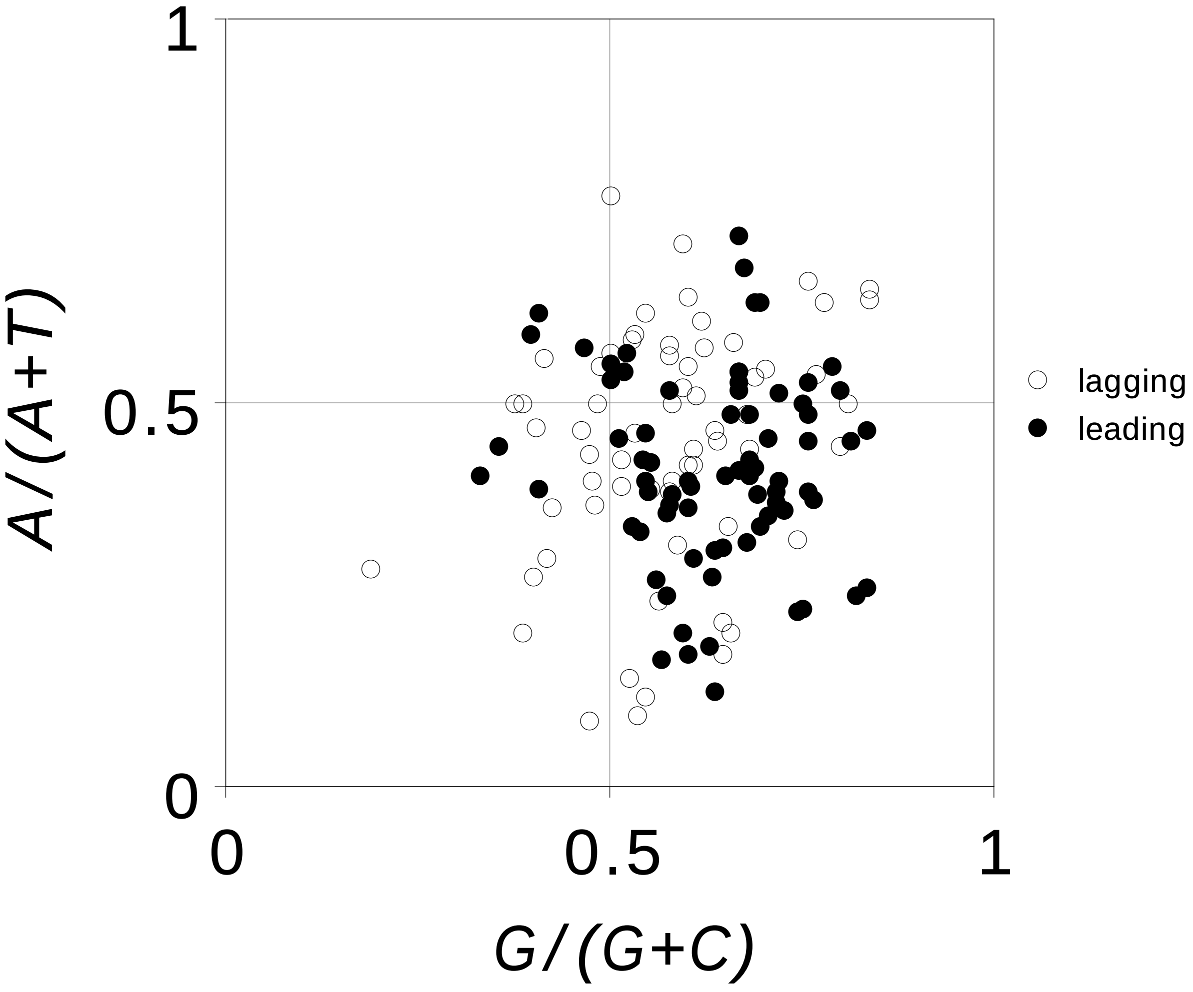
Streptococcus pyogenes



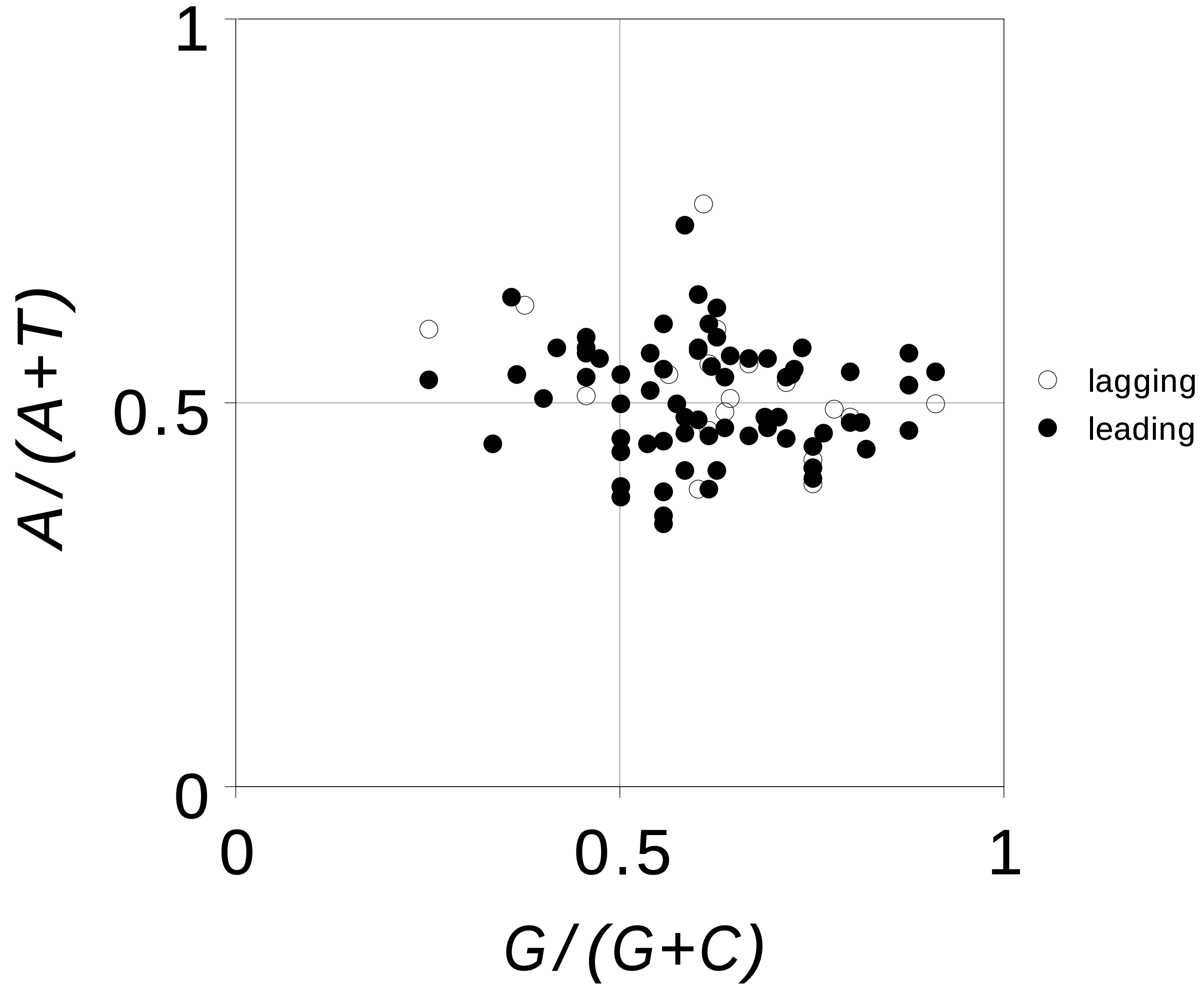
Thermoplasma acidophilum



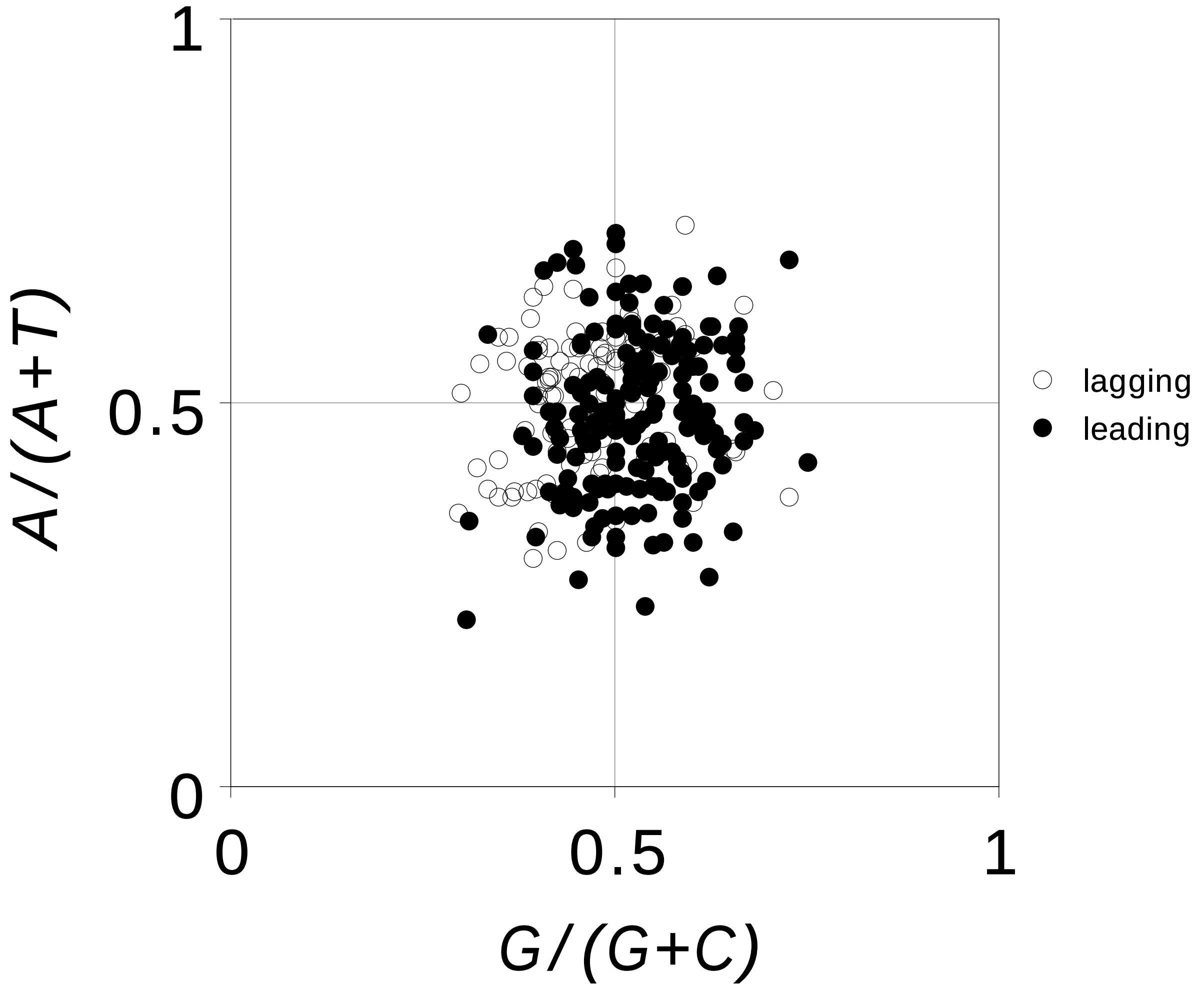
Thermotoga maritima



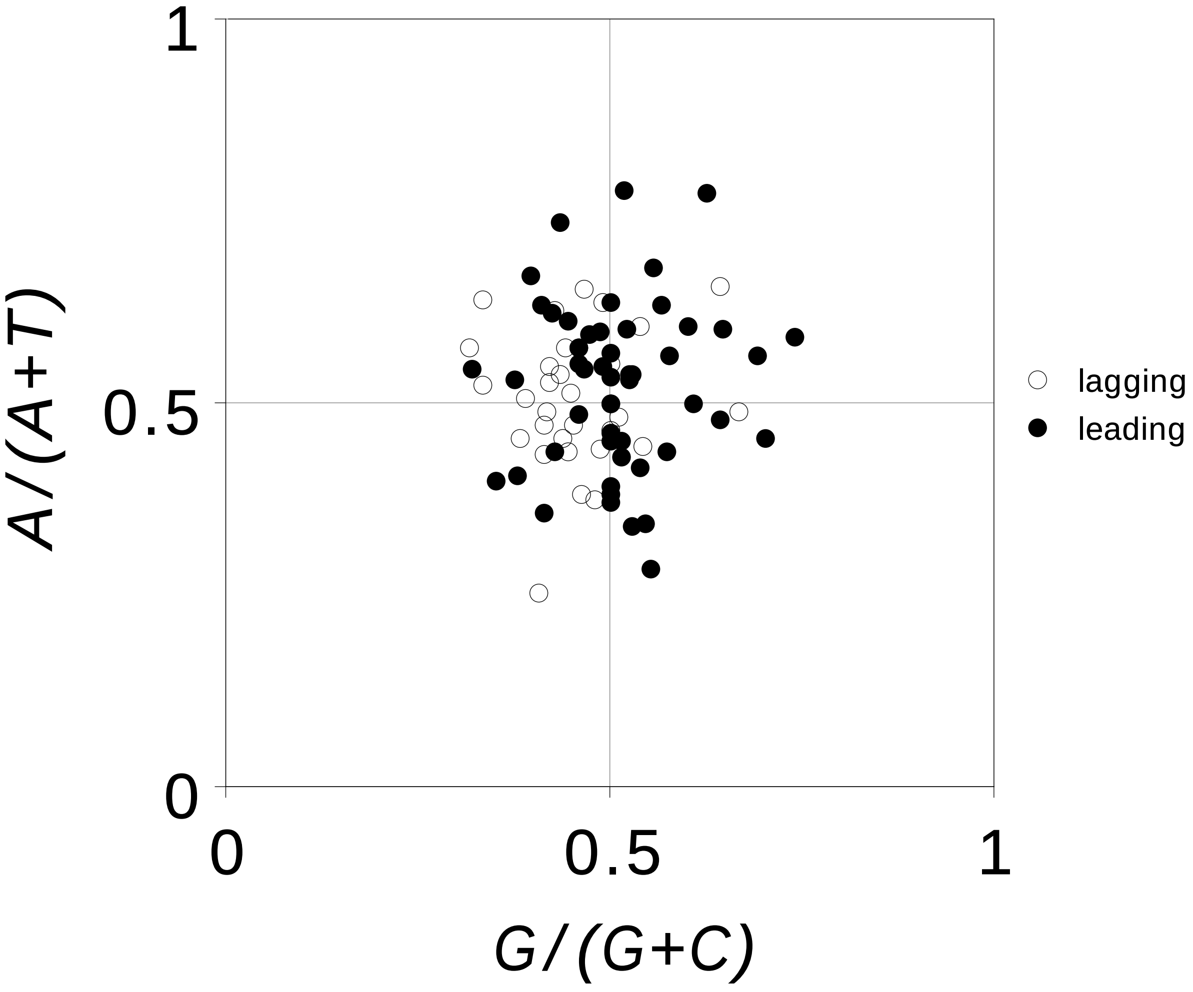
Treponema pallidum



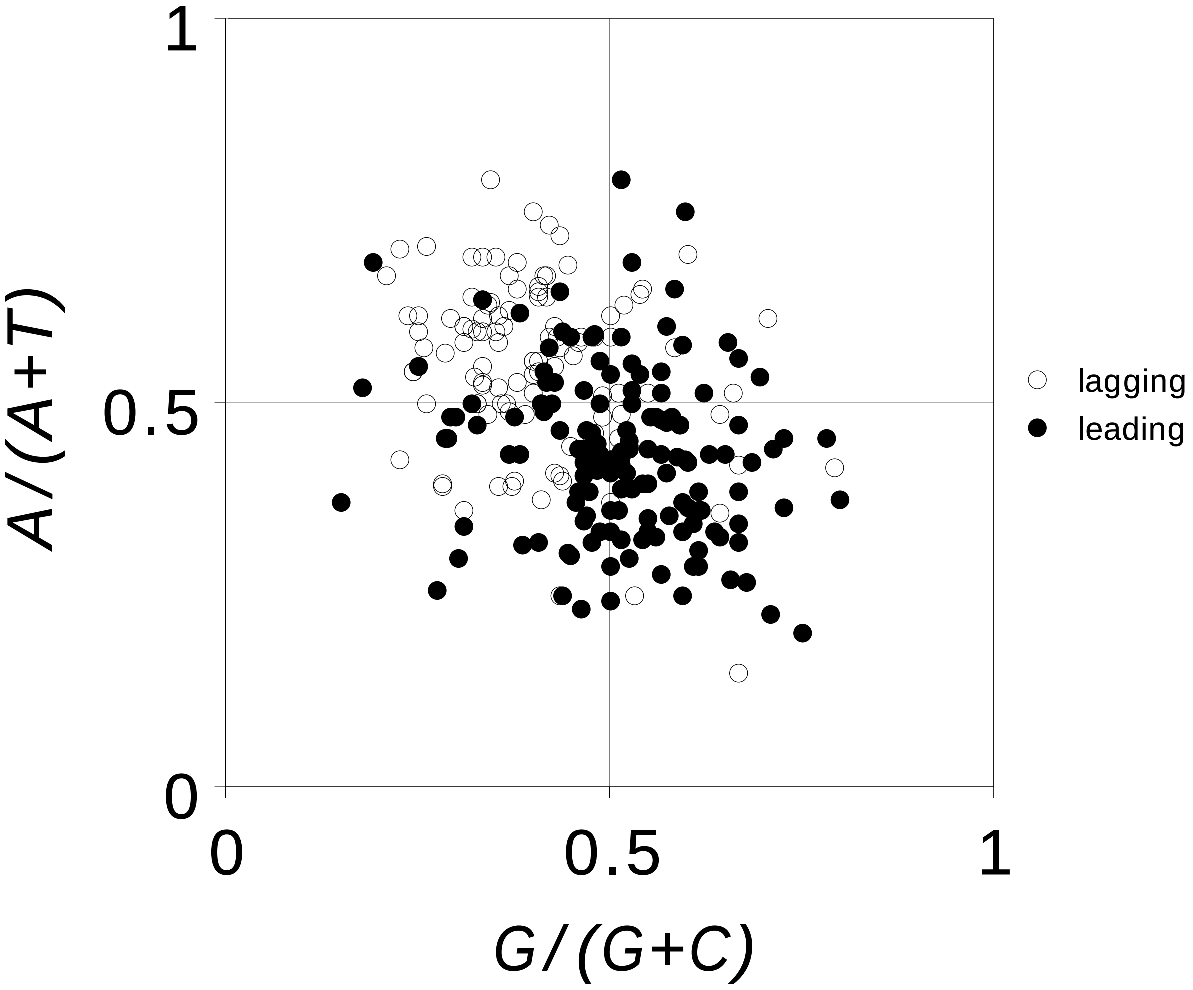
Ureaplasma urealyticum



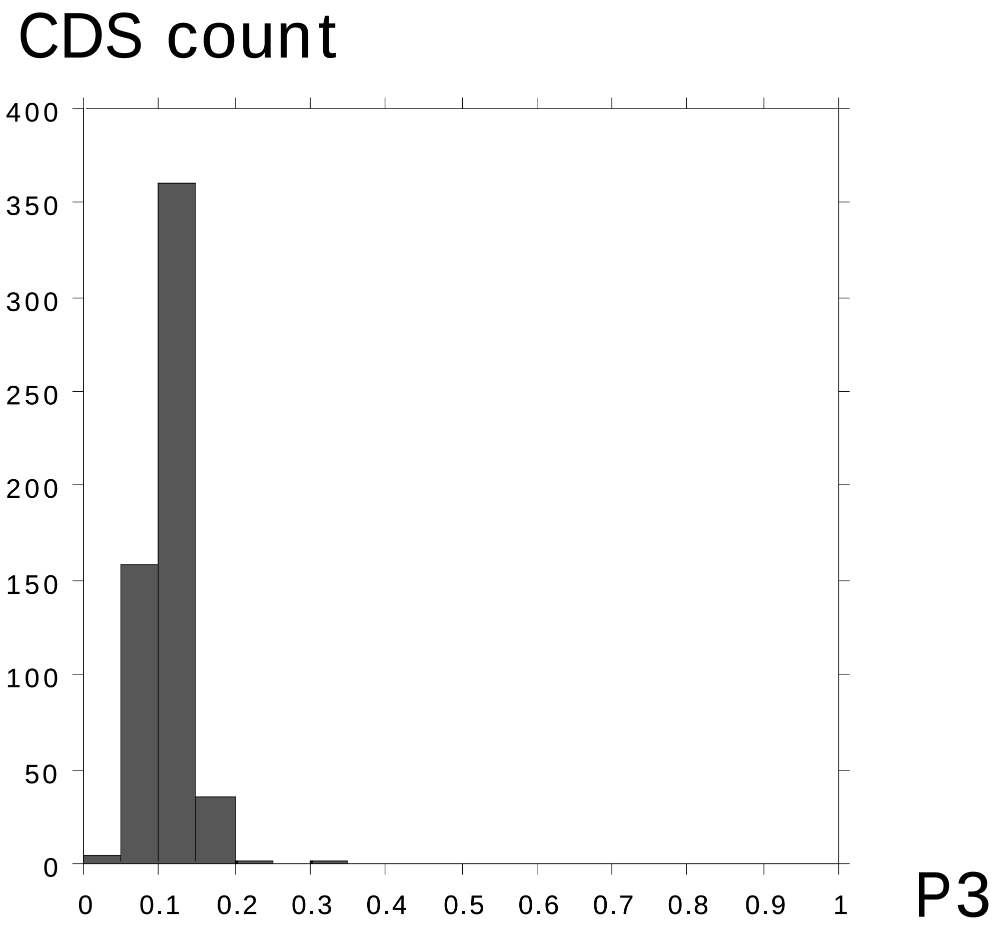
Vibrio cholerae chromosome 1



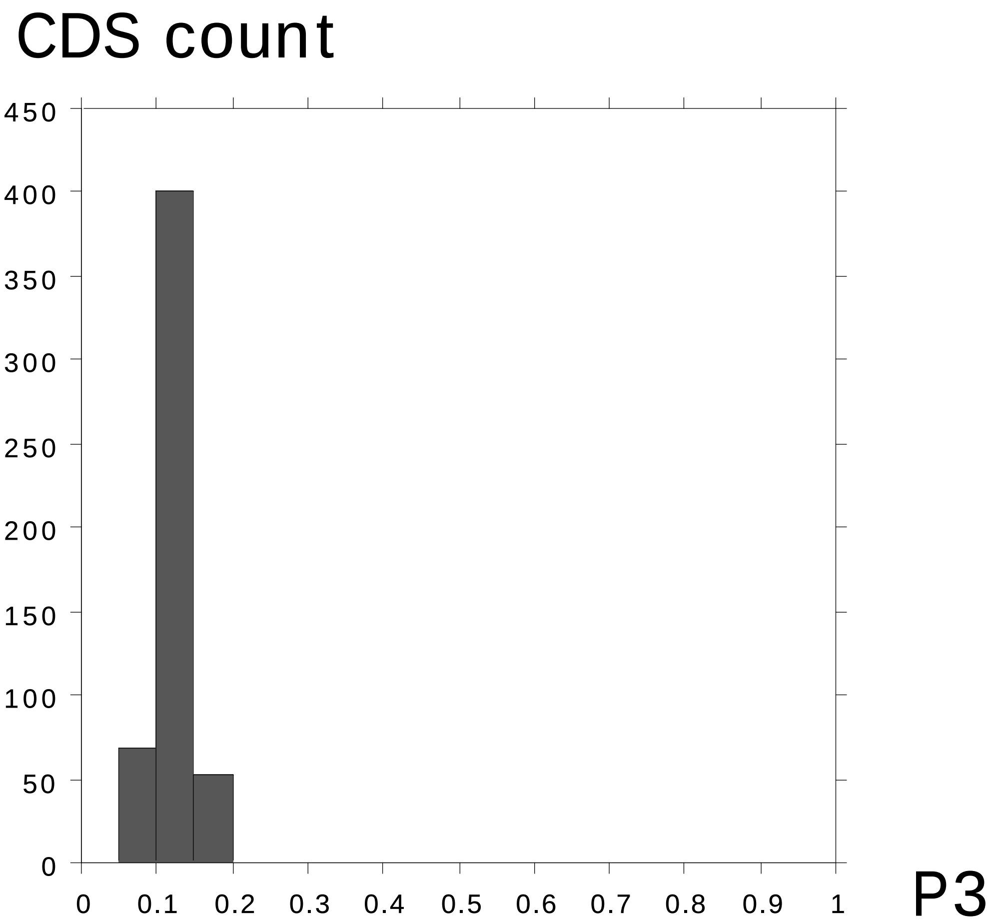
Vibrio cholerae chromosome 2



Xylella fastidiosa



Ureaplasma urealyticum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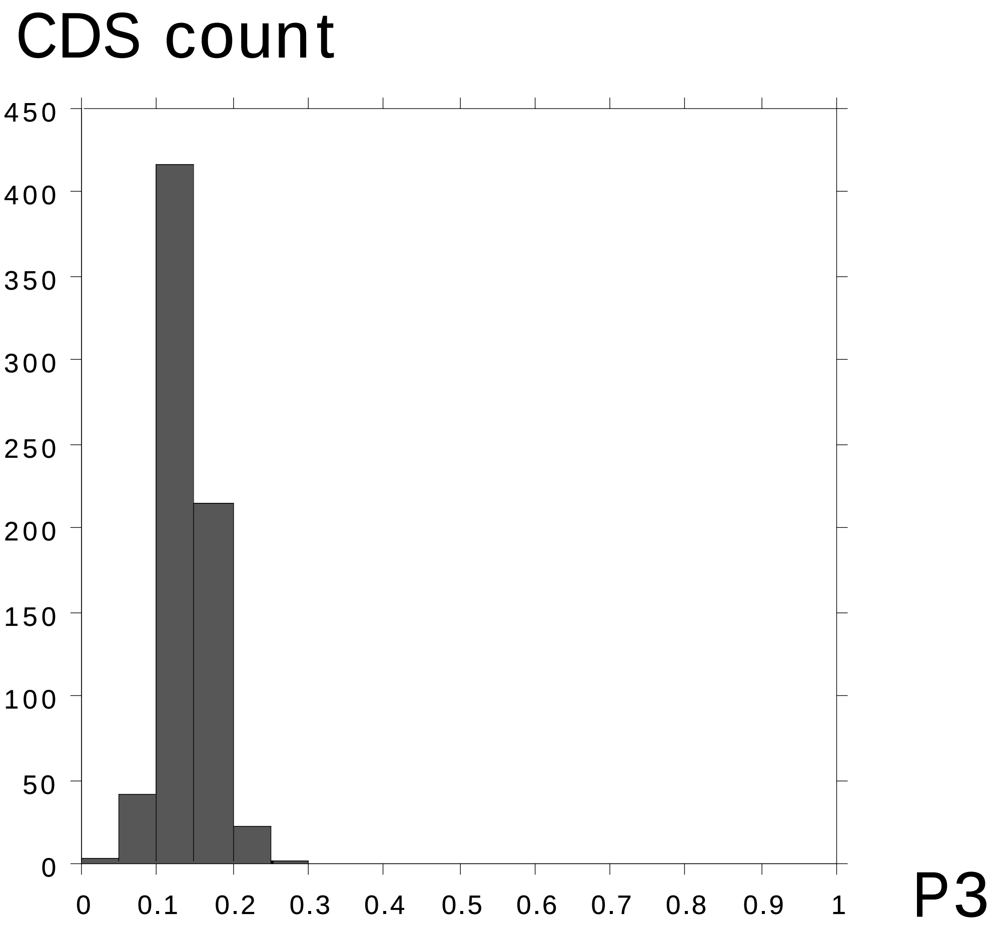
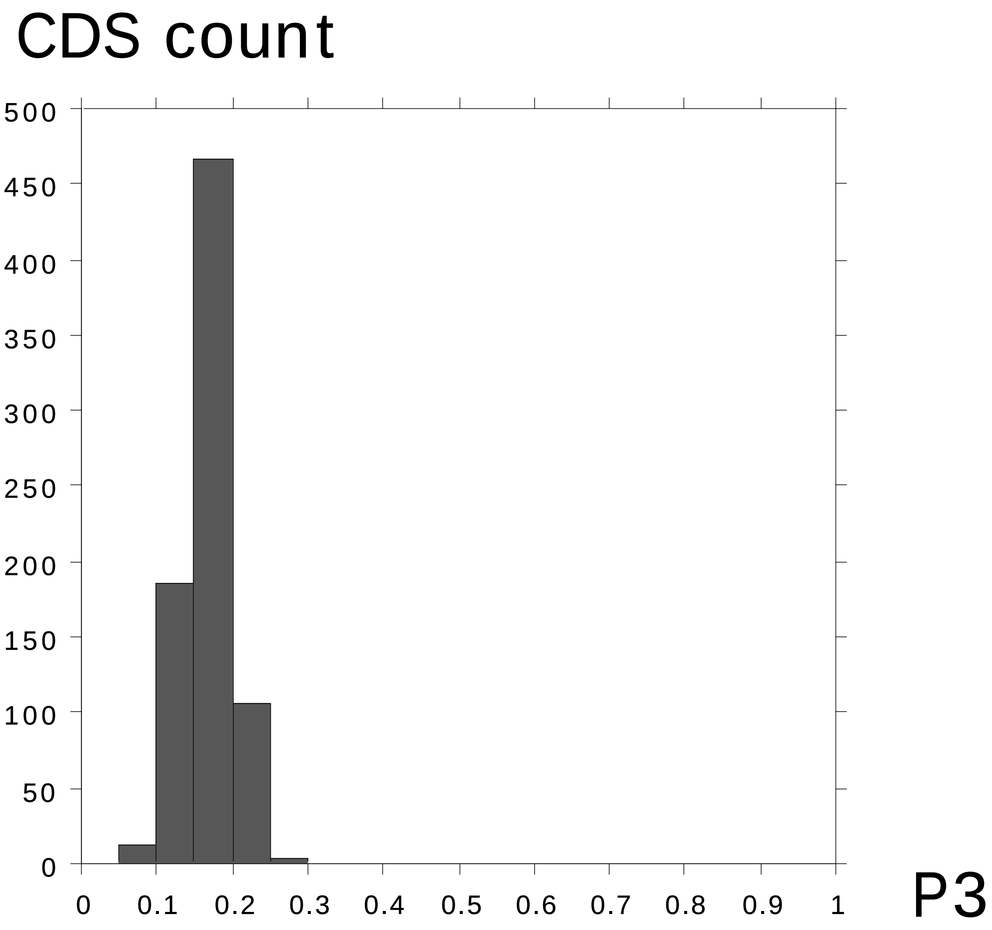
P3

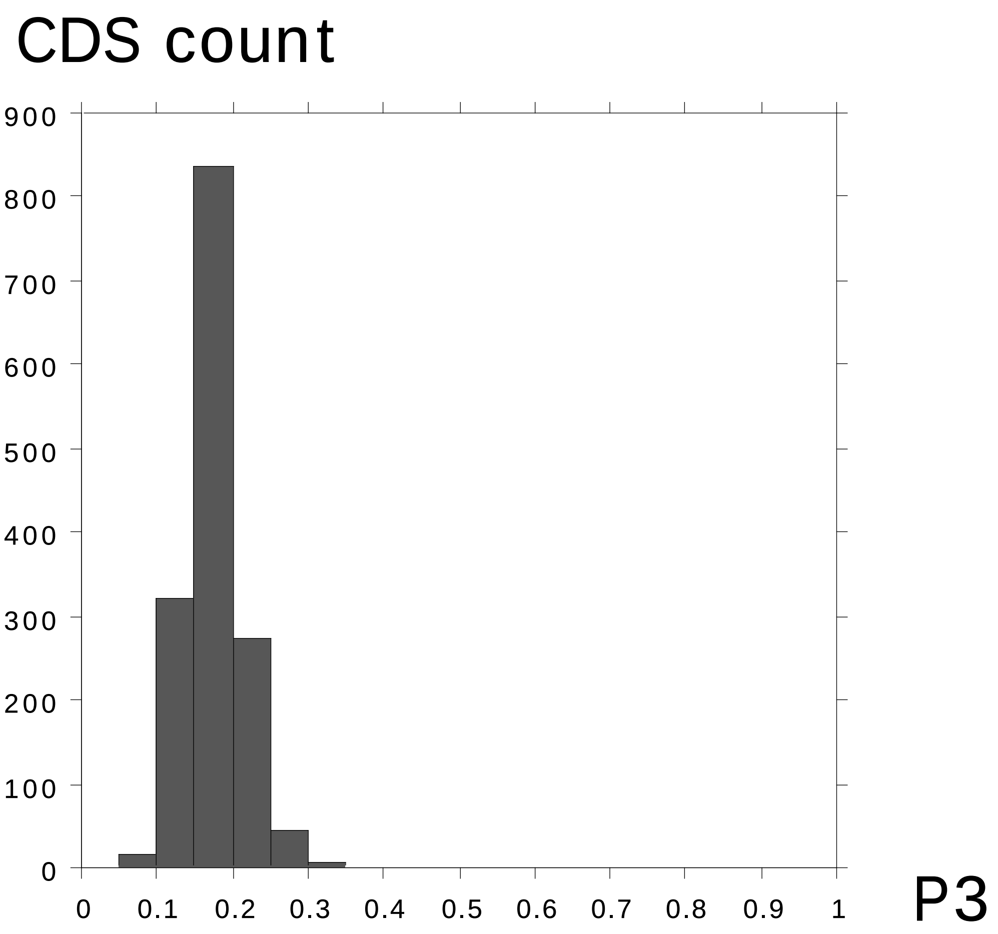
Buchnera sp.



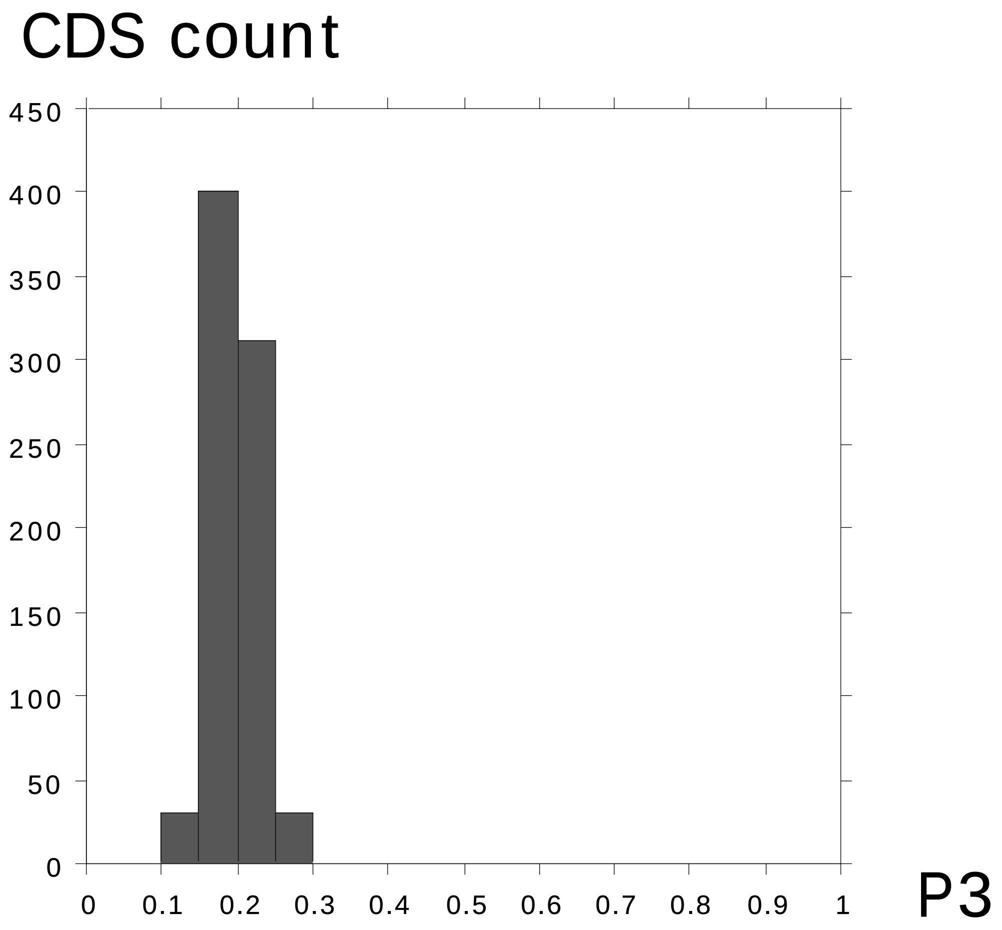
Mycoplasma pulmonis



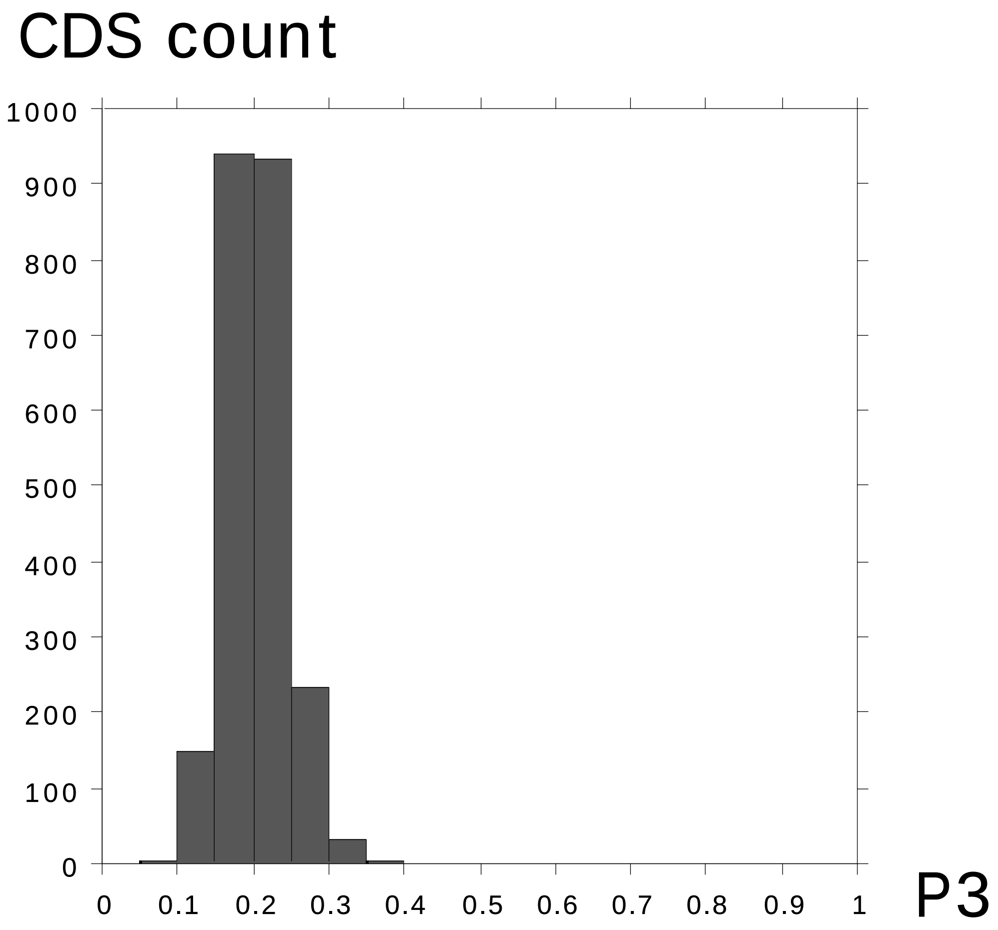
Rickettsia prowazekii



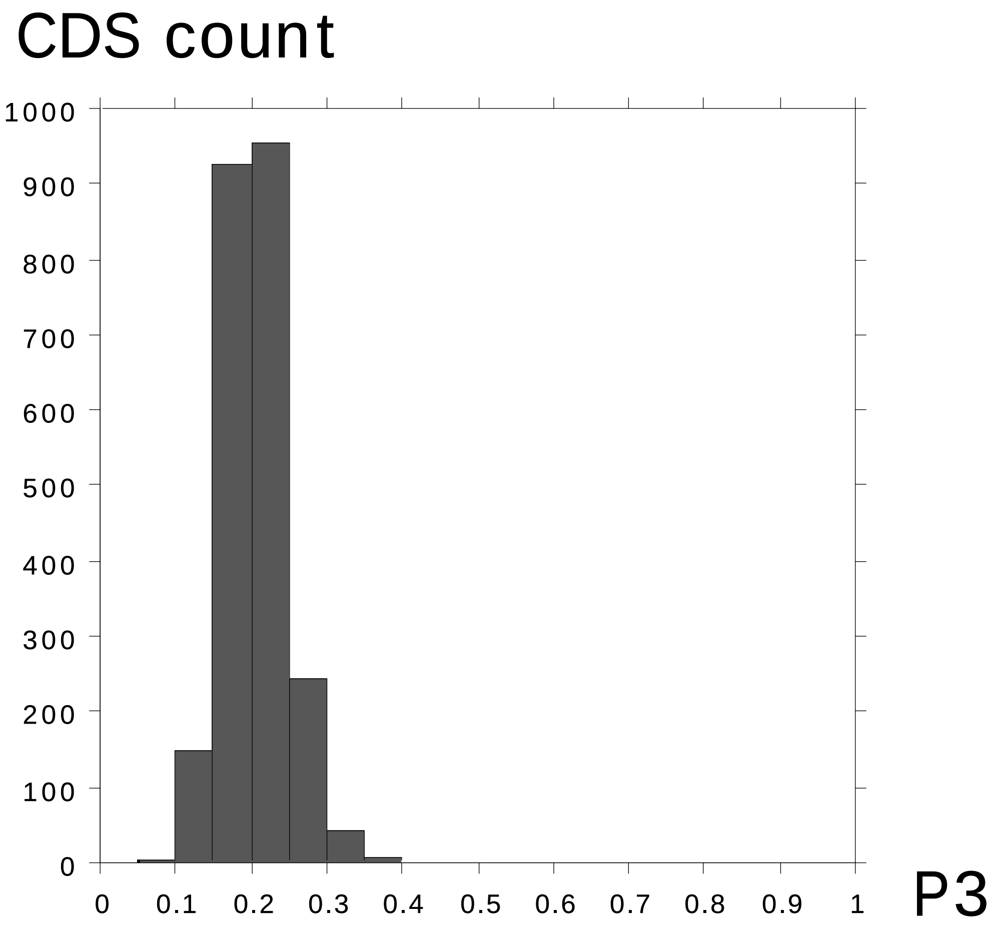
Campylobacter jejuni



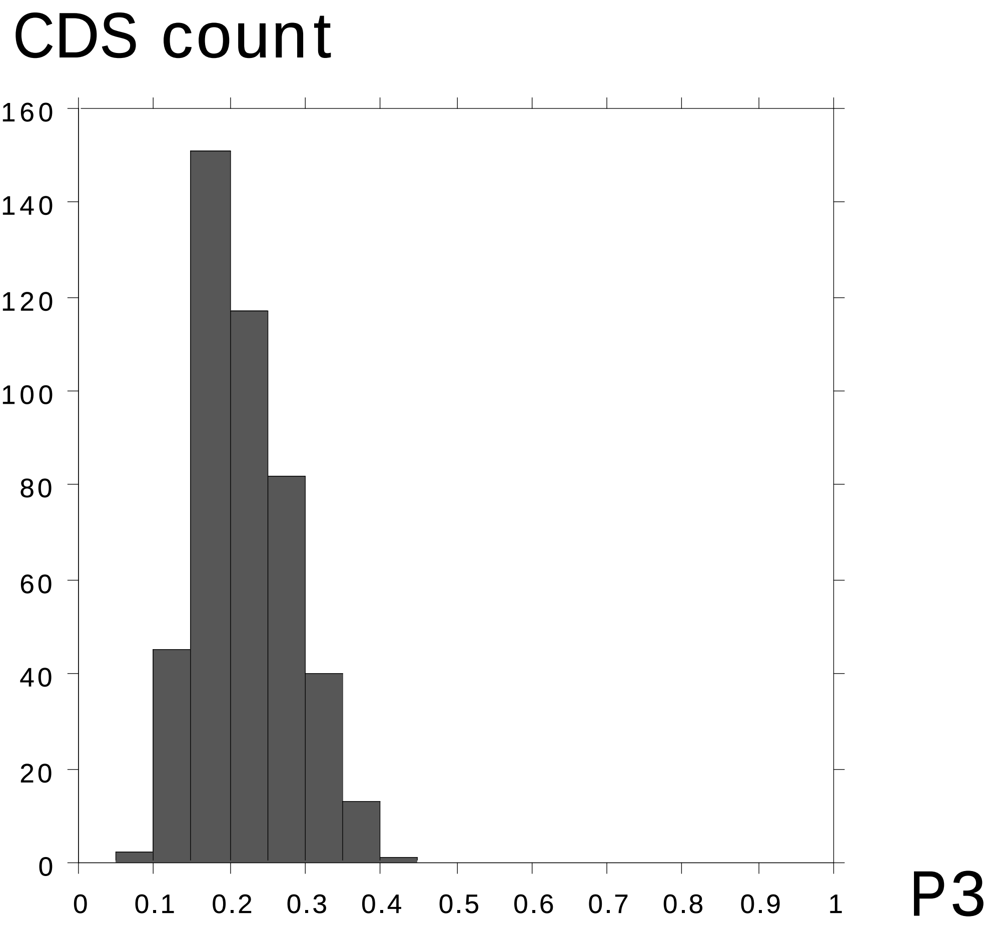
Borrelia burgdorferi



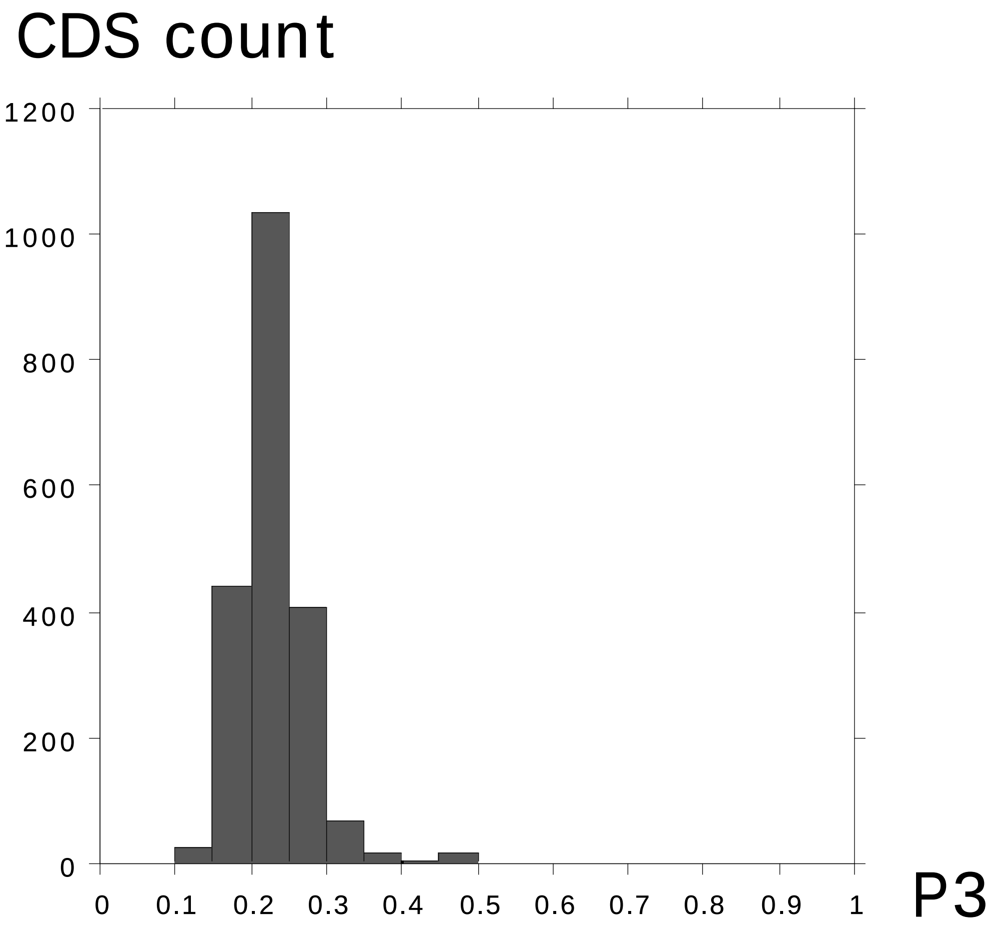
Staphylococcus aureus N315



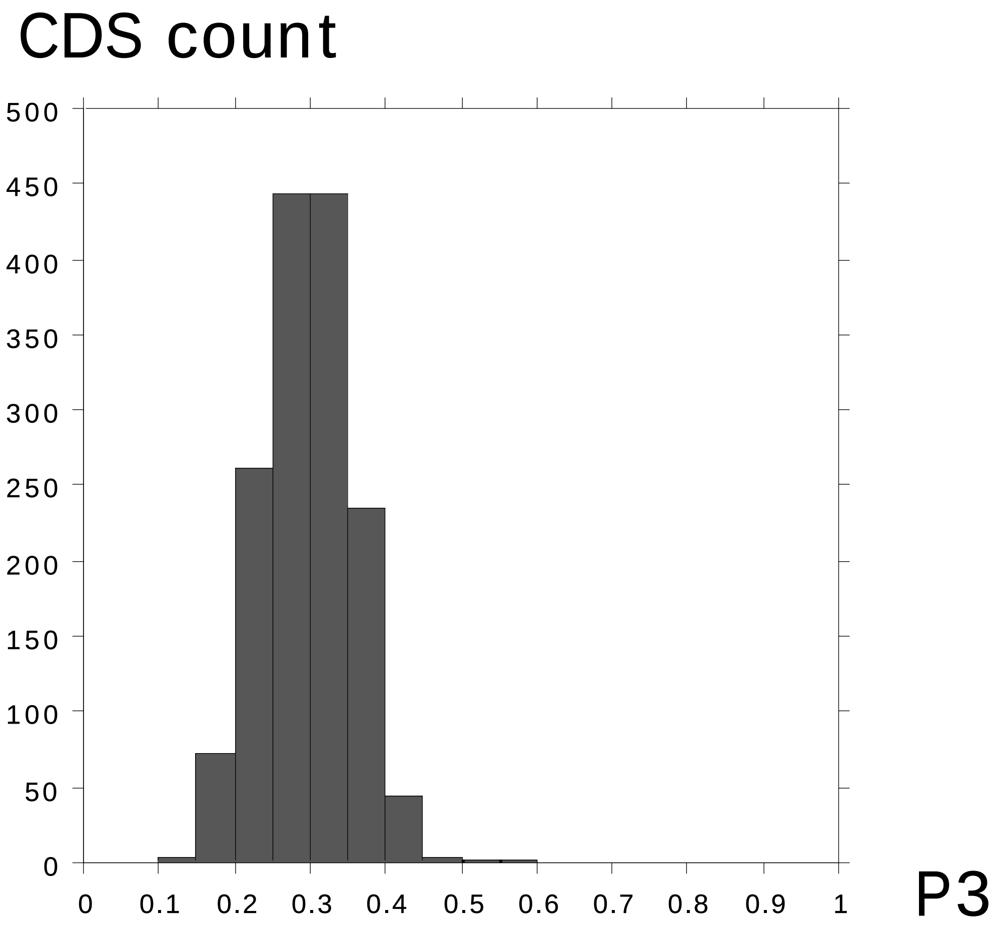
Staphylococcus aureus Mu50



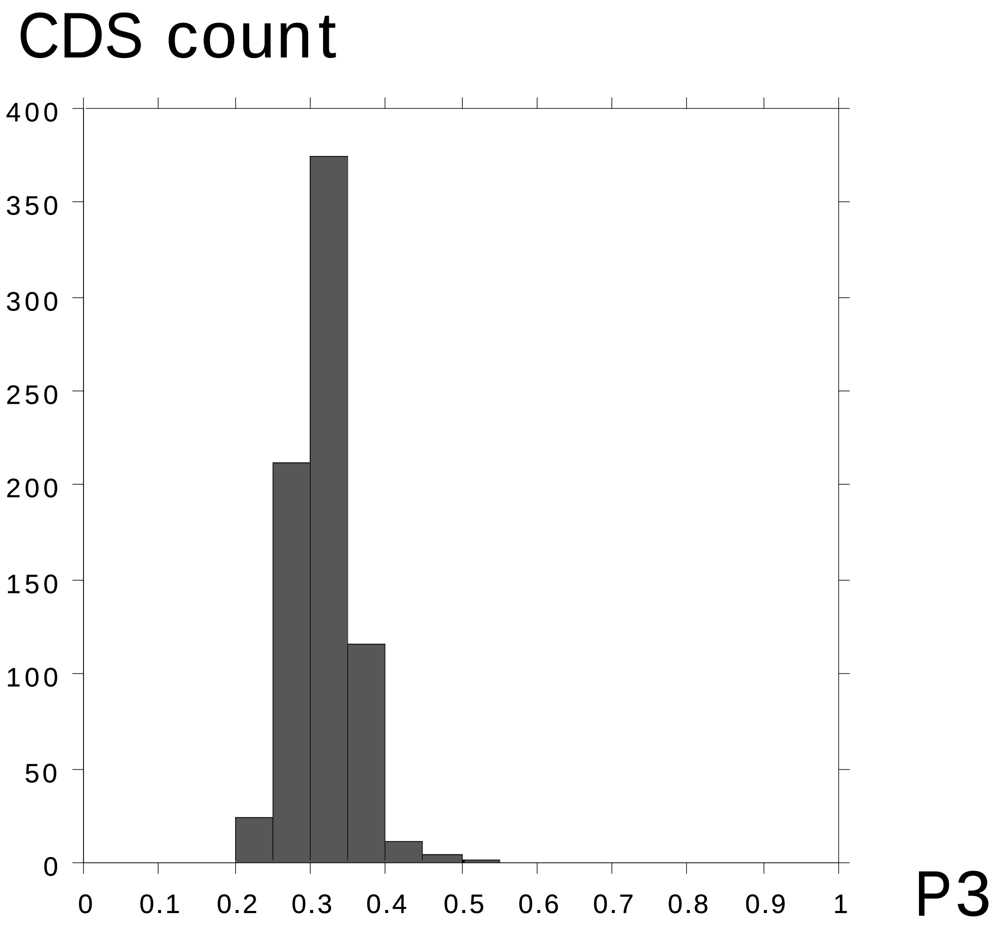
Mycoplasma genitalium



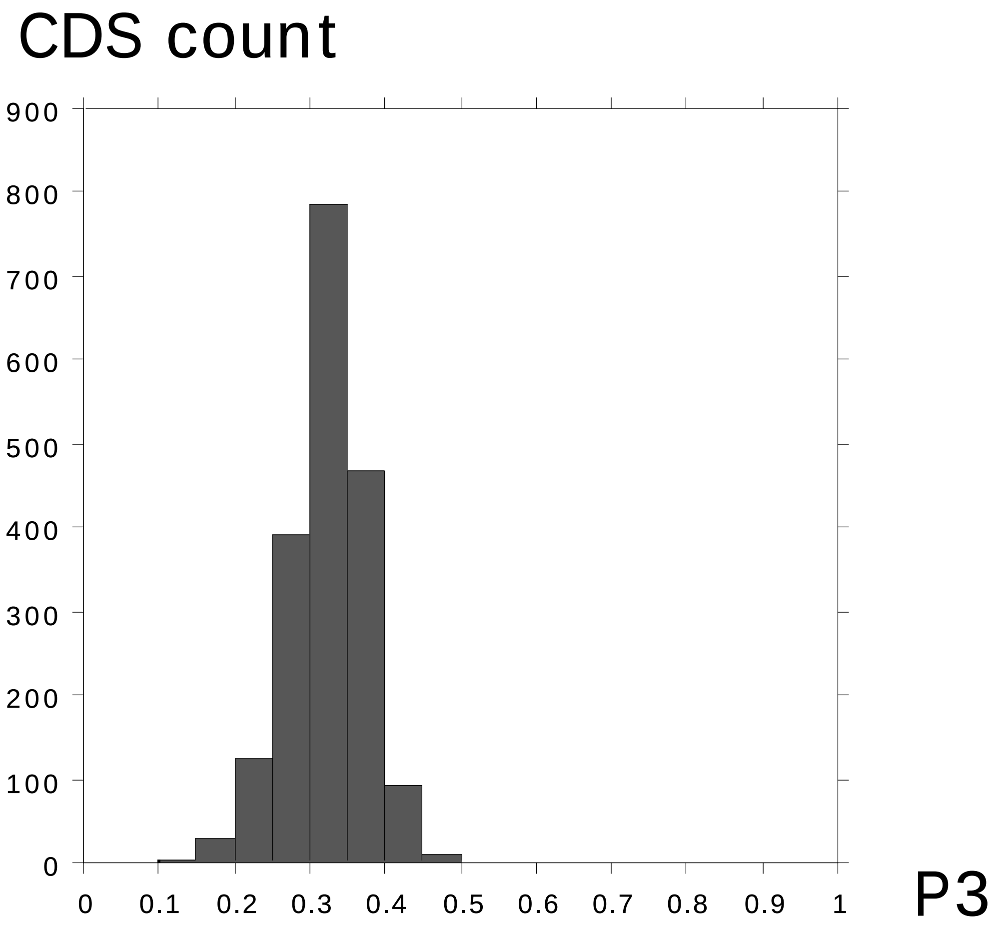
Lactococcus lactis



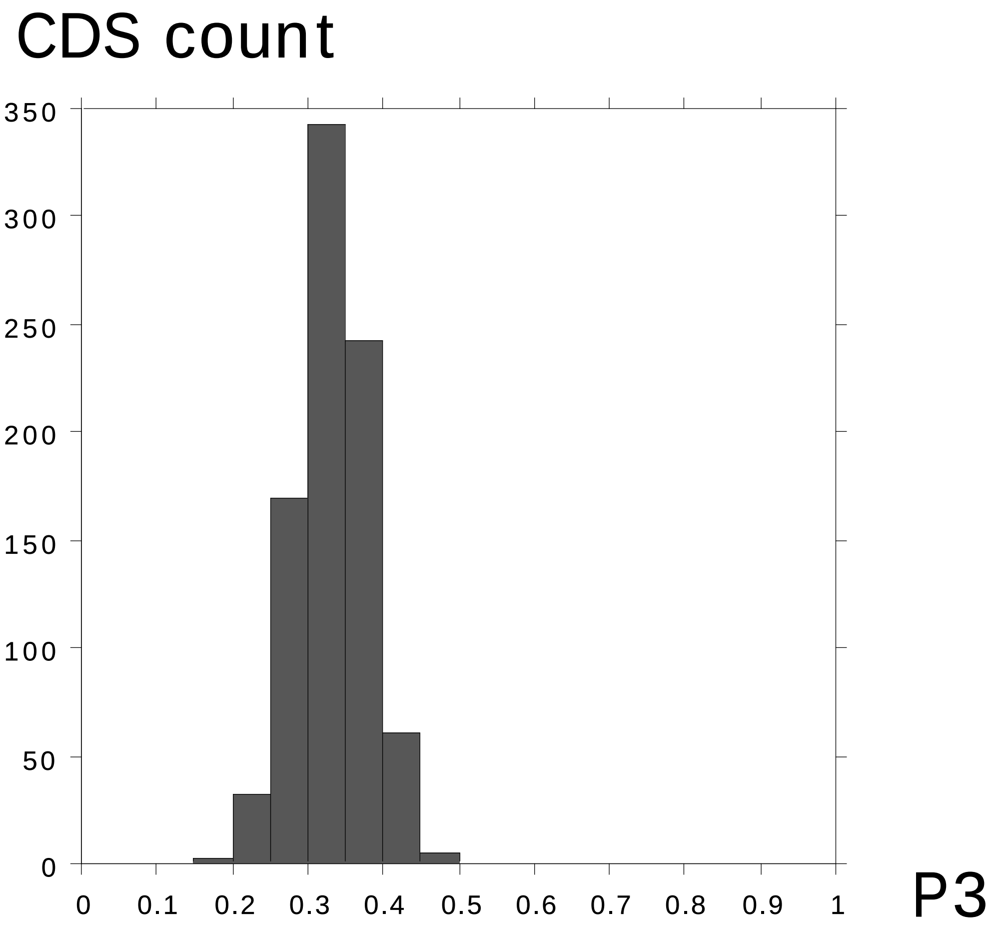
Streptococcus pyogenes



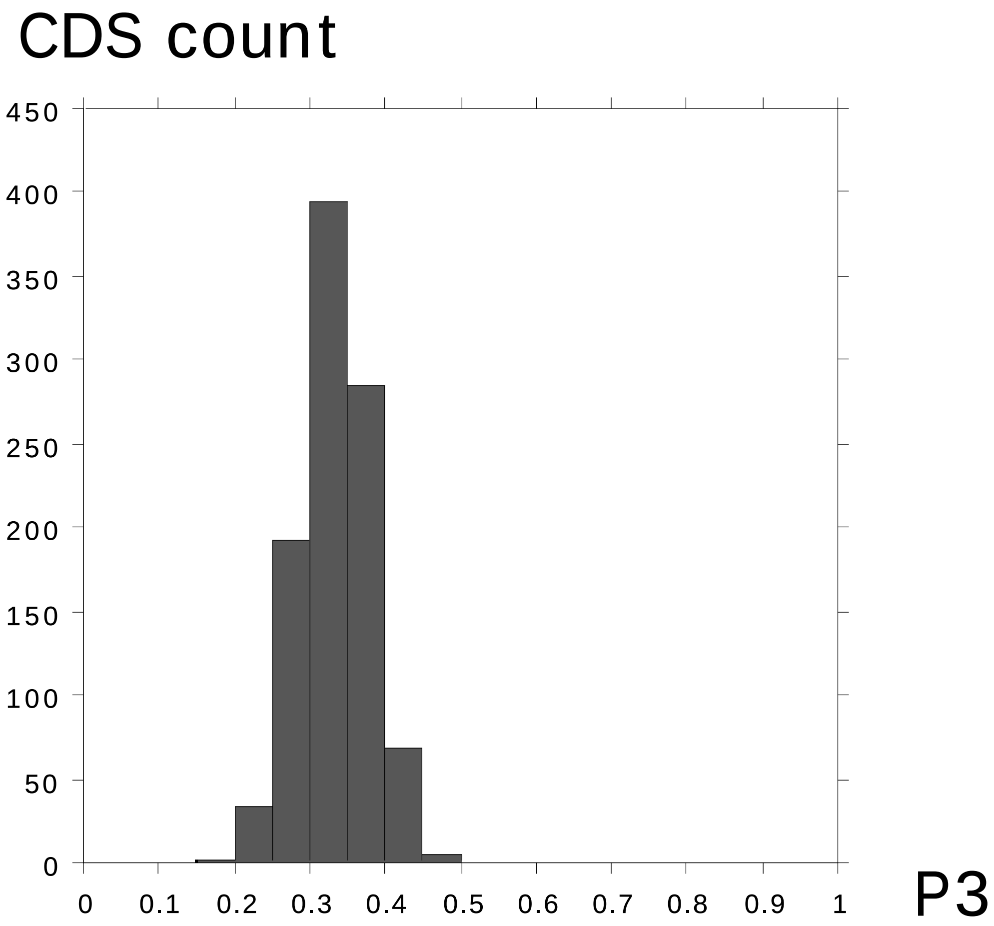
Chlamydia muridarum



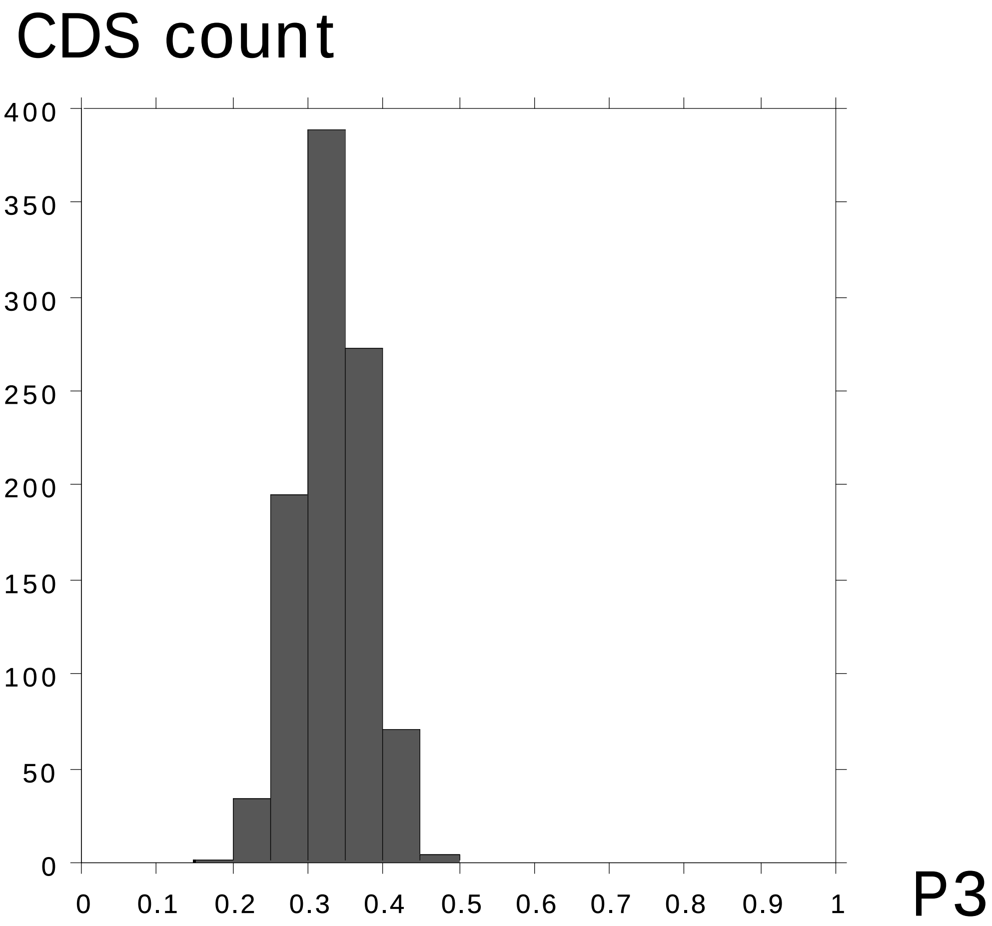
Pasteurella multocida



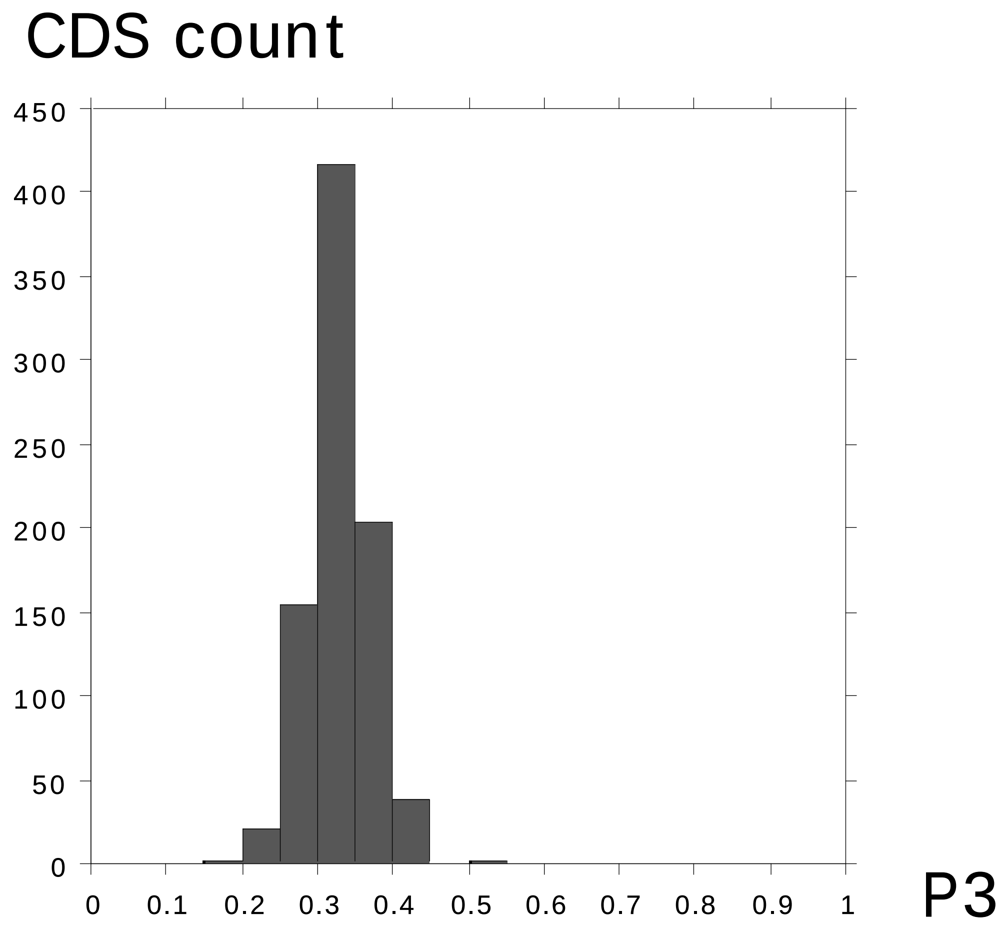
Chlamydophila pneumoniae AR39



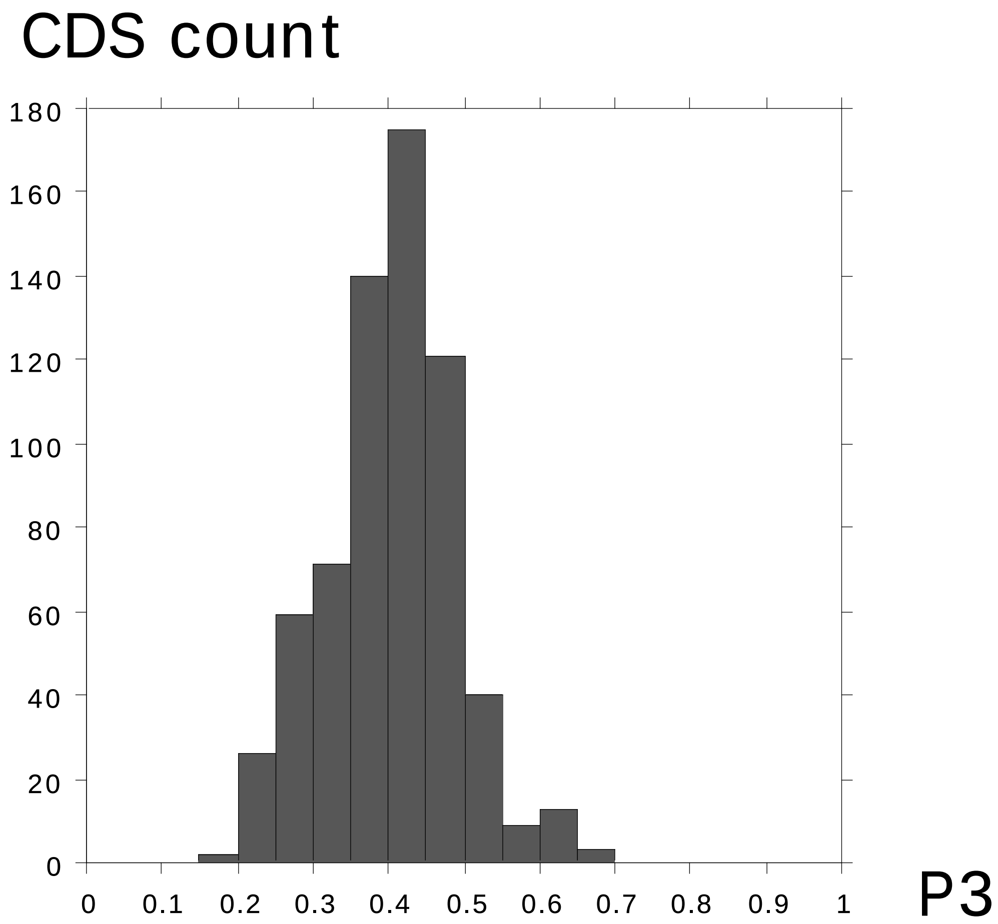
Chlamydophila pneumoniae J138



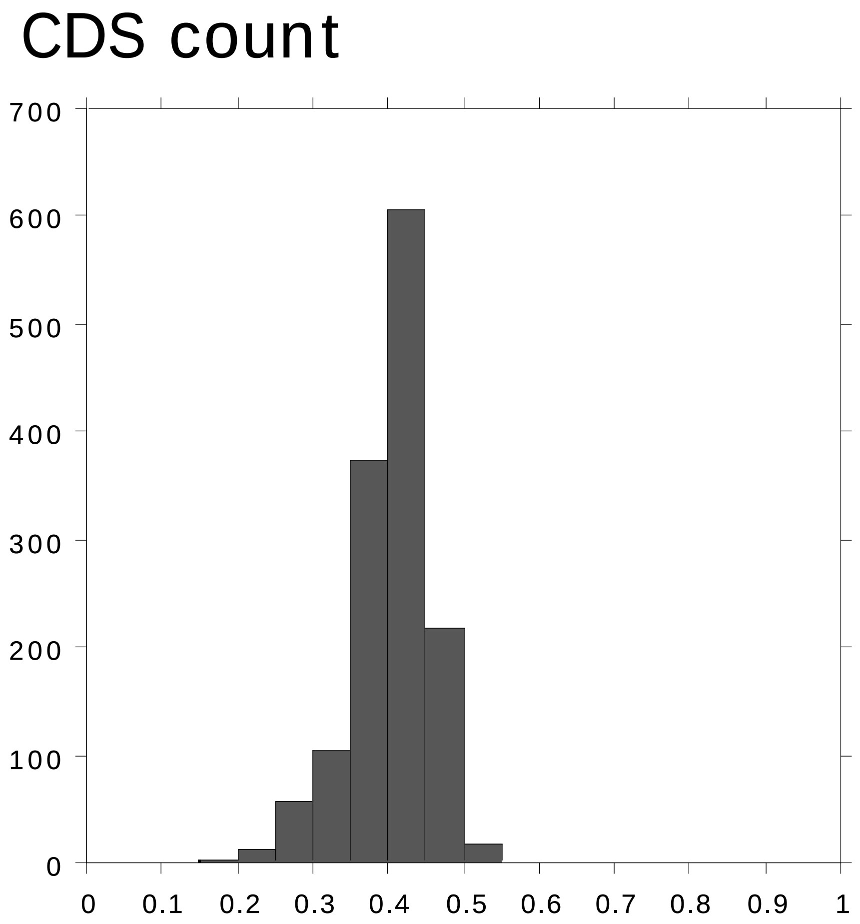
Chlamydophila pneumoniae CWL029



Chlamydia trachomatis



Mycoplasma pneumoniae



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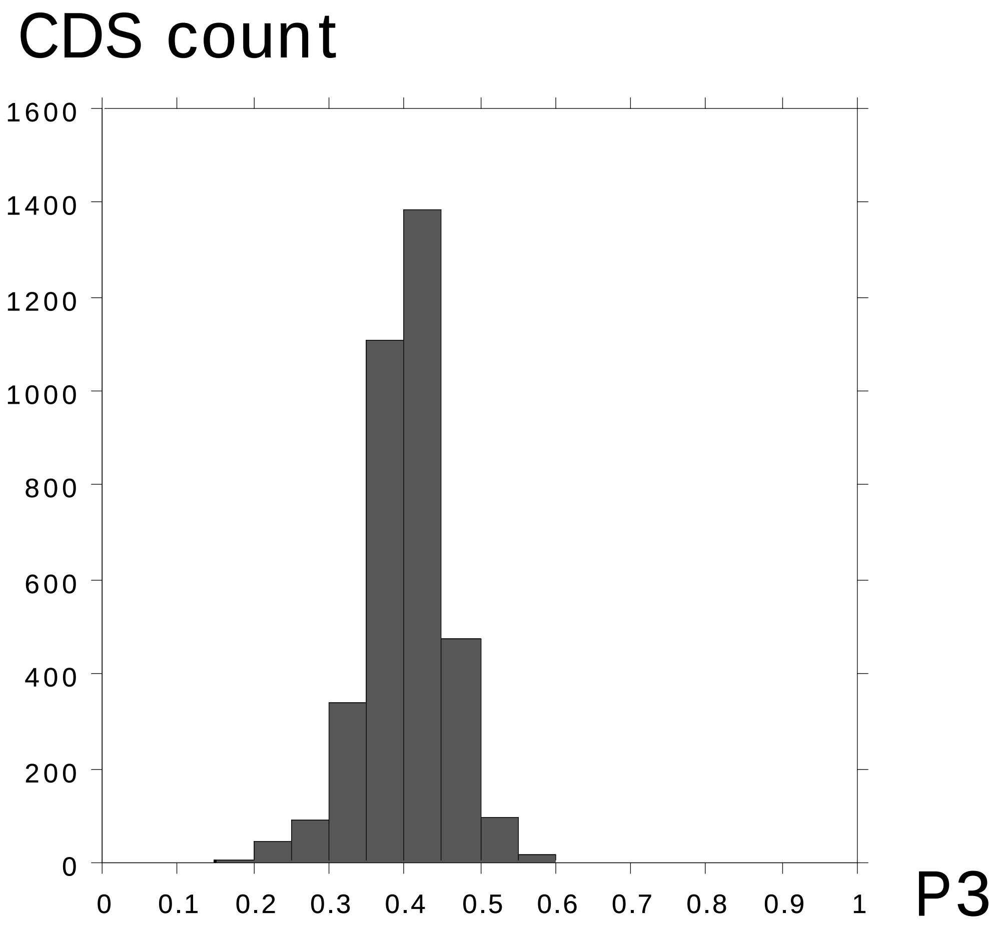
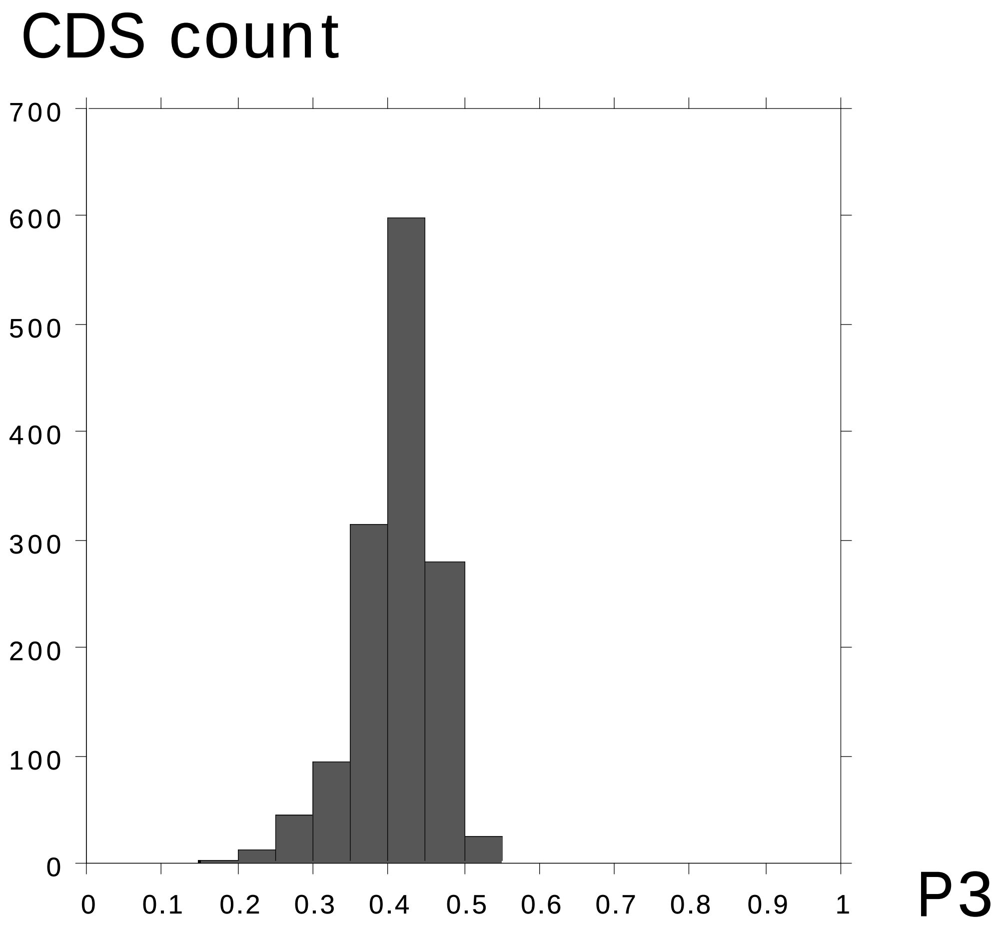
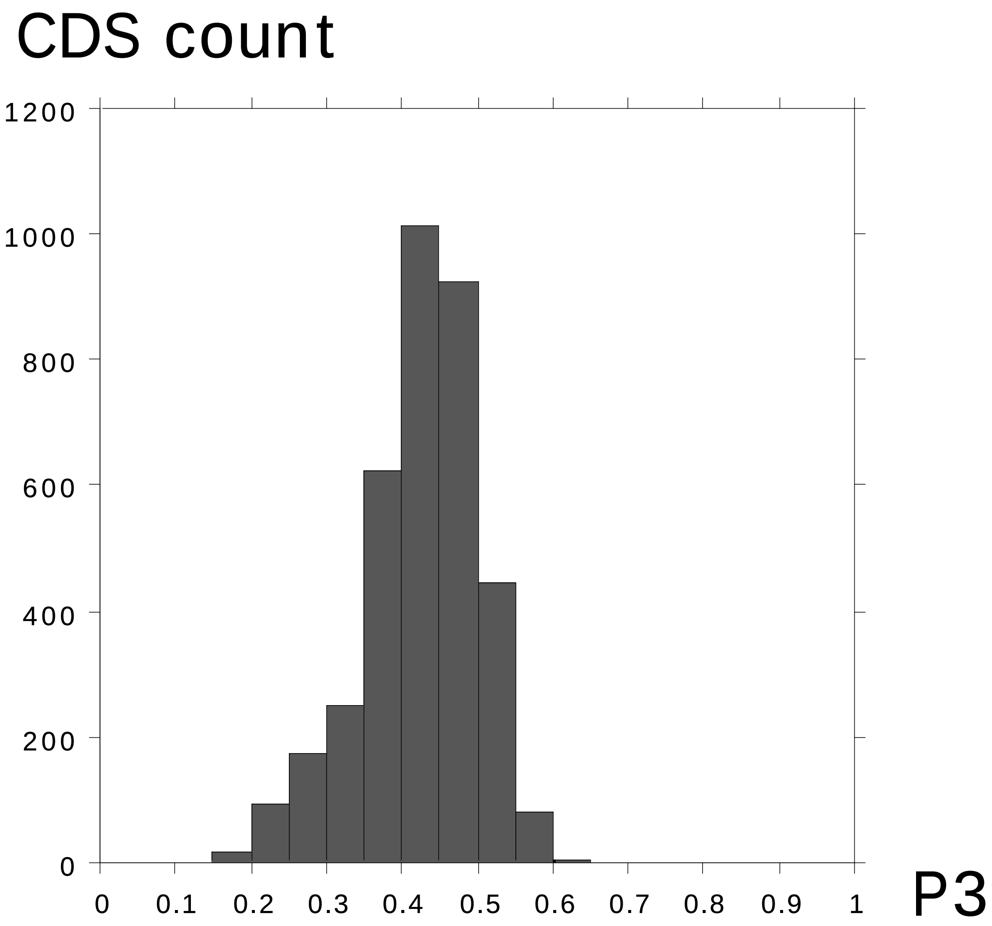
Helicobacter pylori 26695



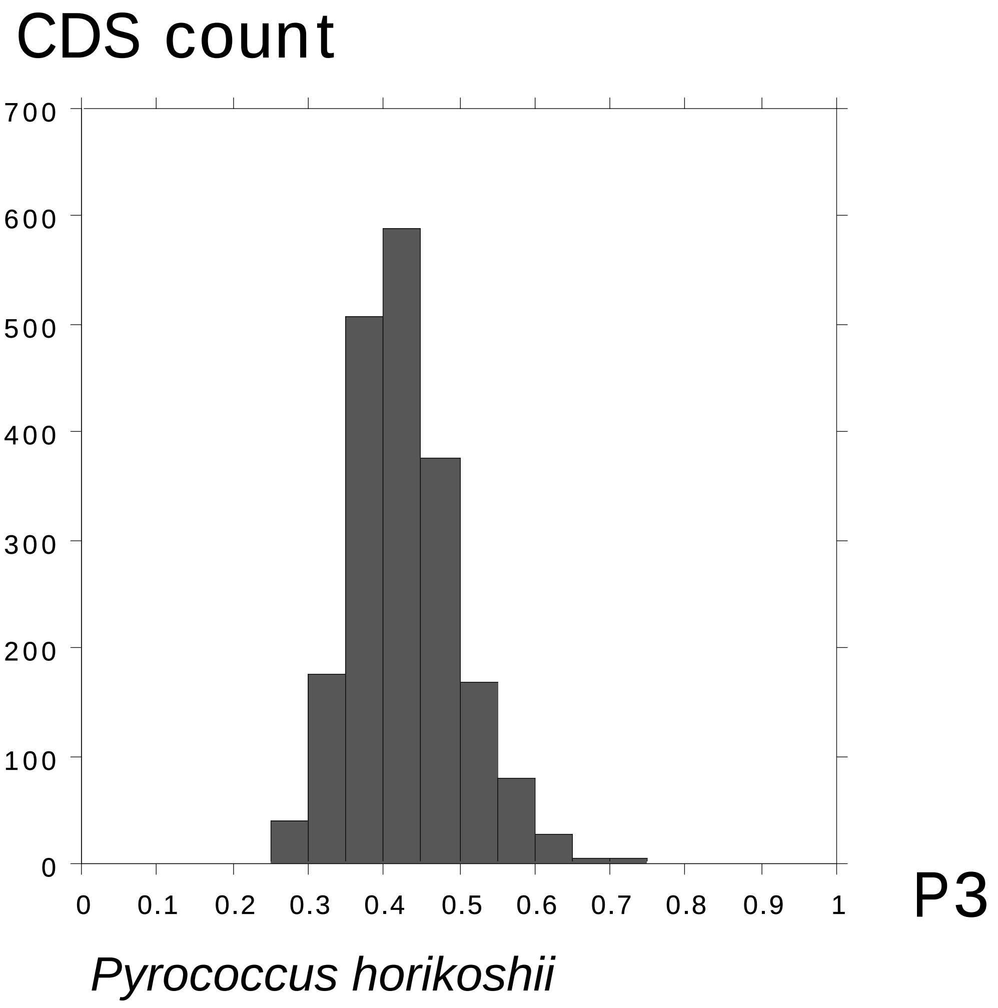
Bacillus halodurans



Helicobacter pylori J99



Bacillus subtilis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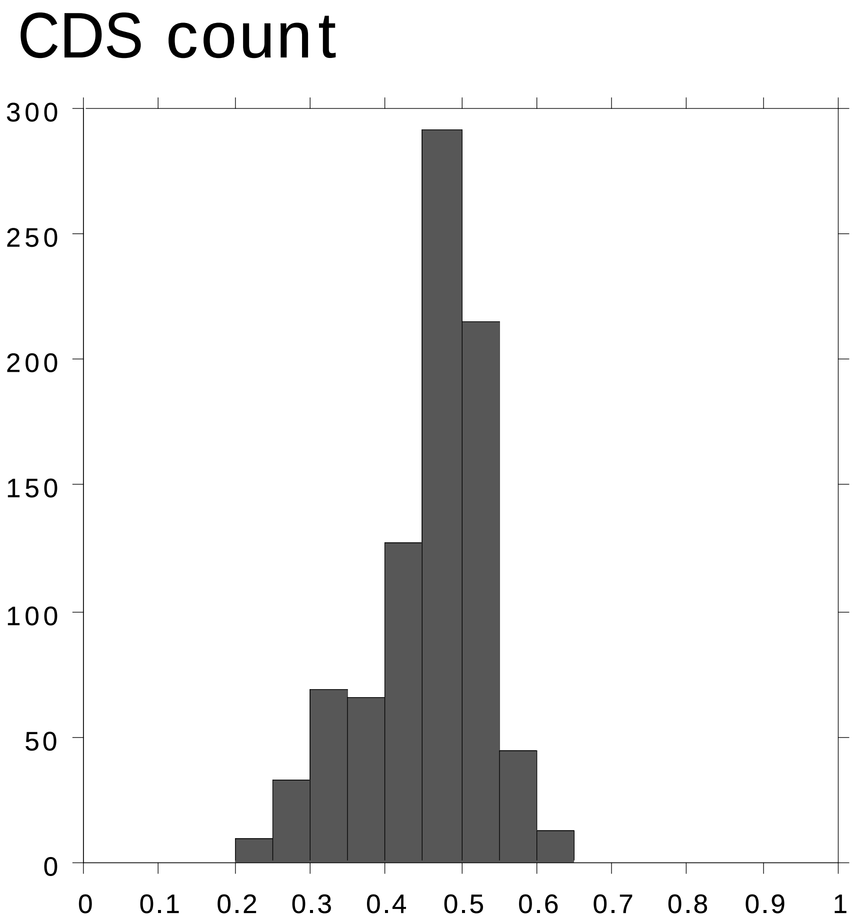
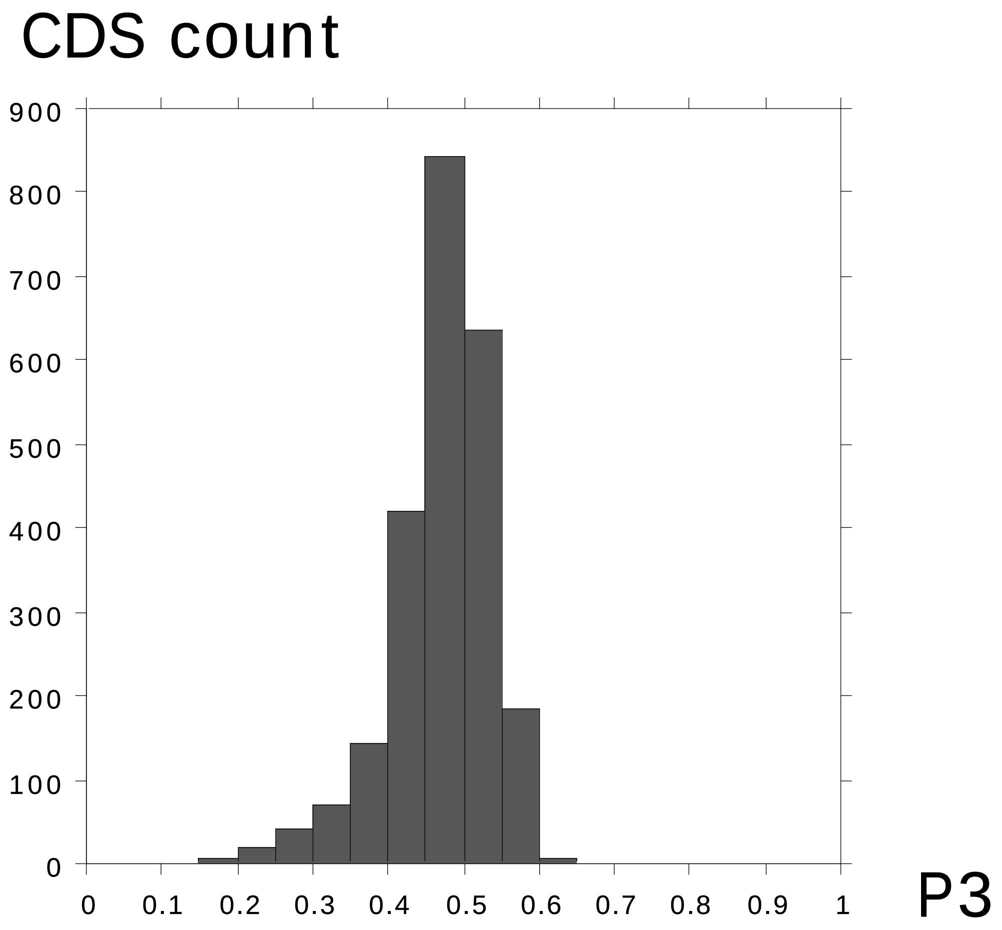
Pyrococcus horikoshii

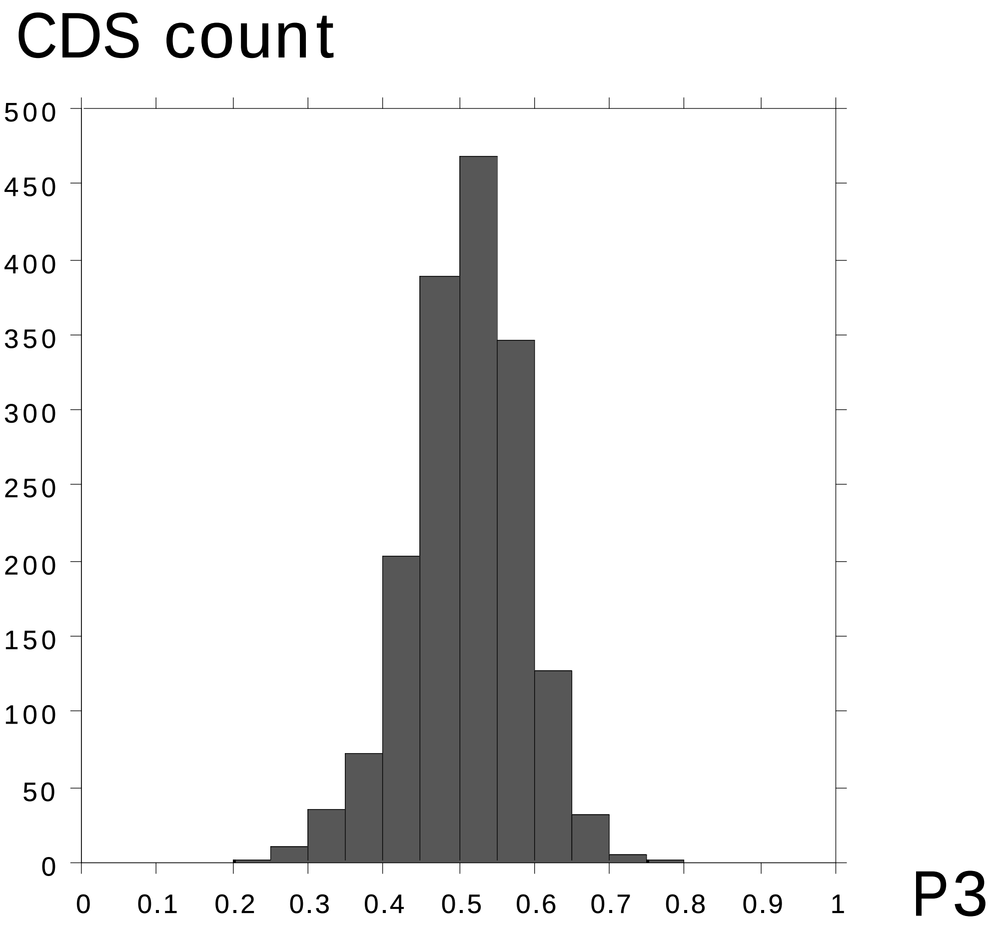


P3

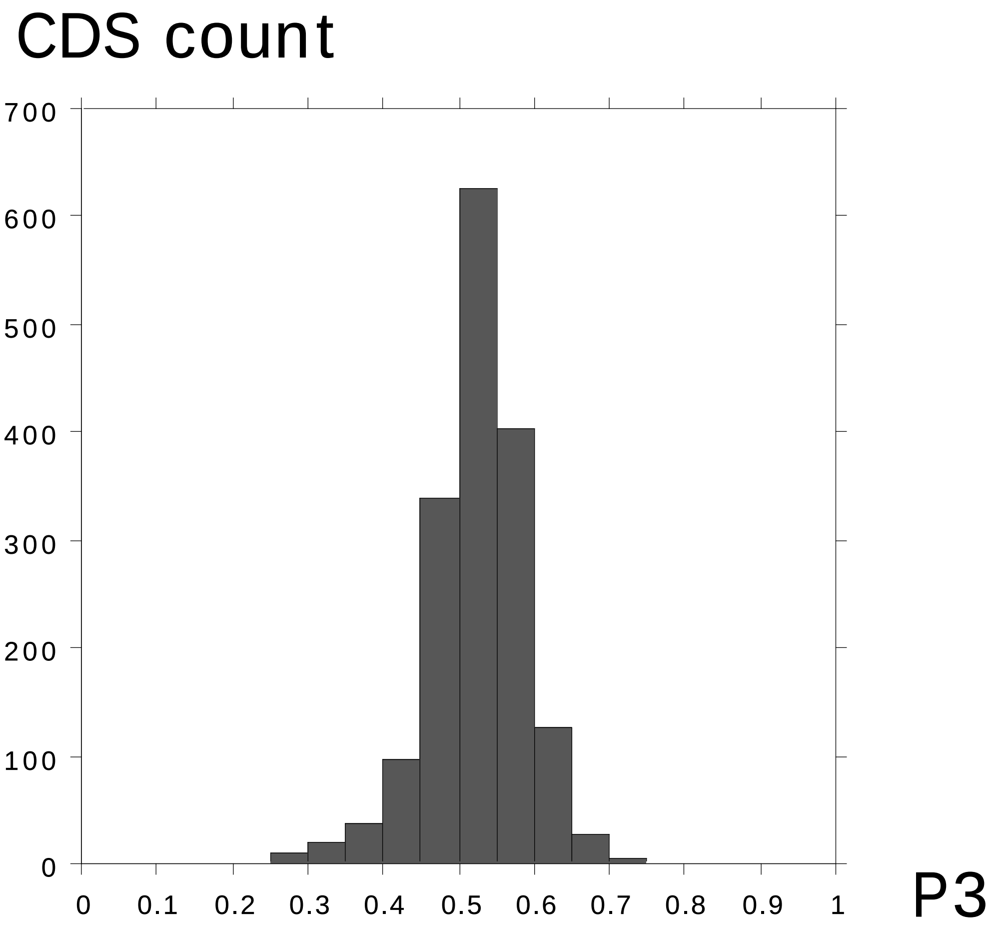
Vibrio cholerae chromosome 2



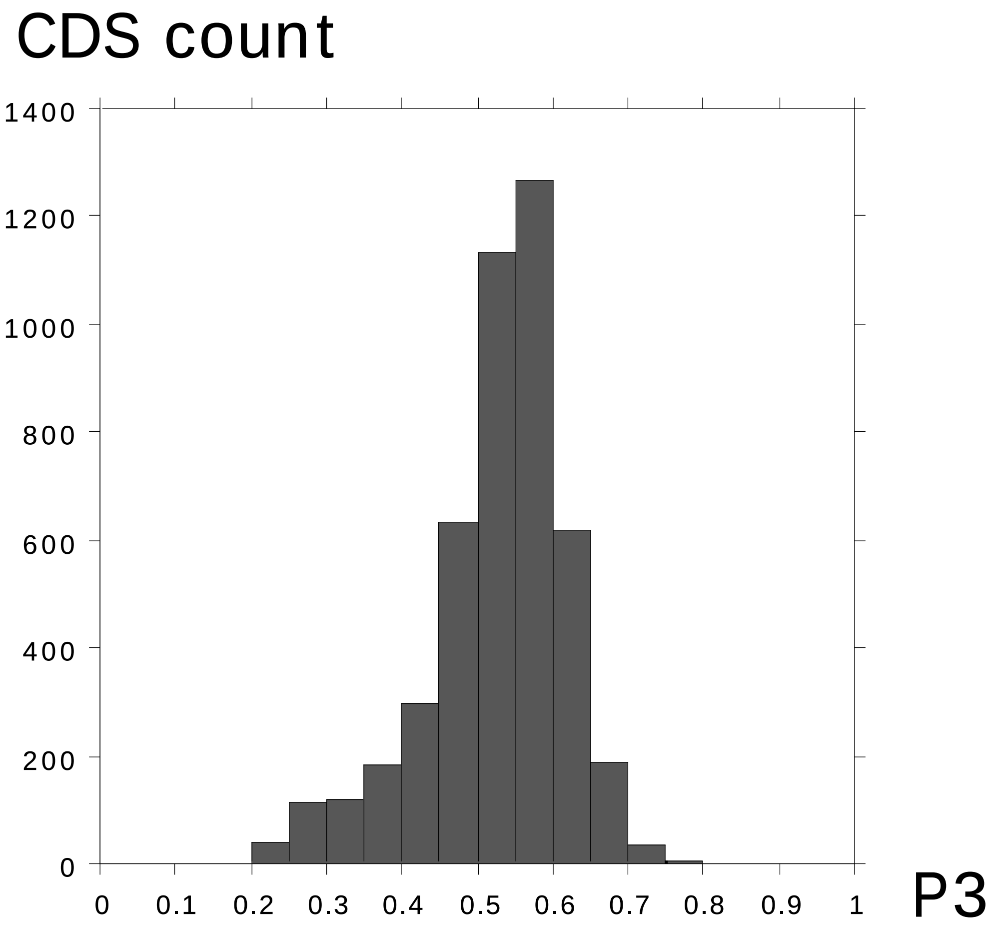
Vibrio cholerae chromosome 1



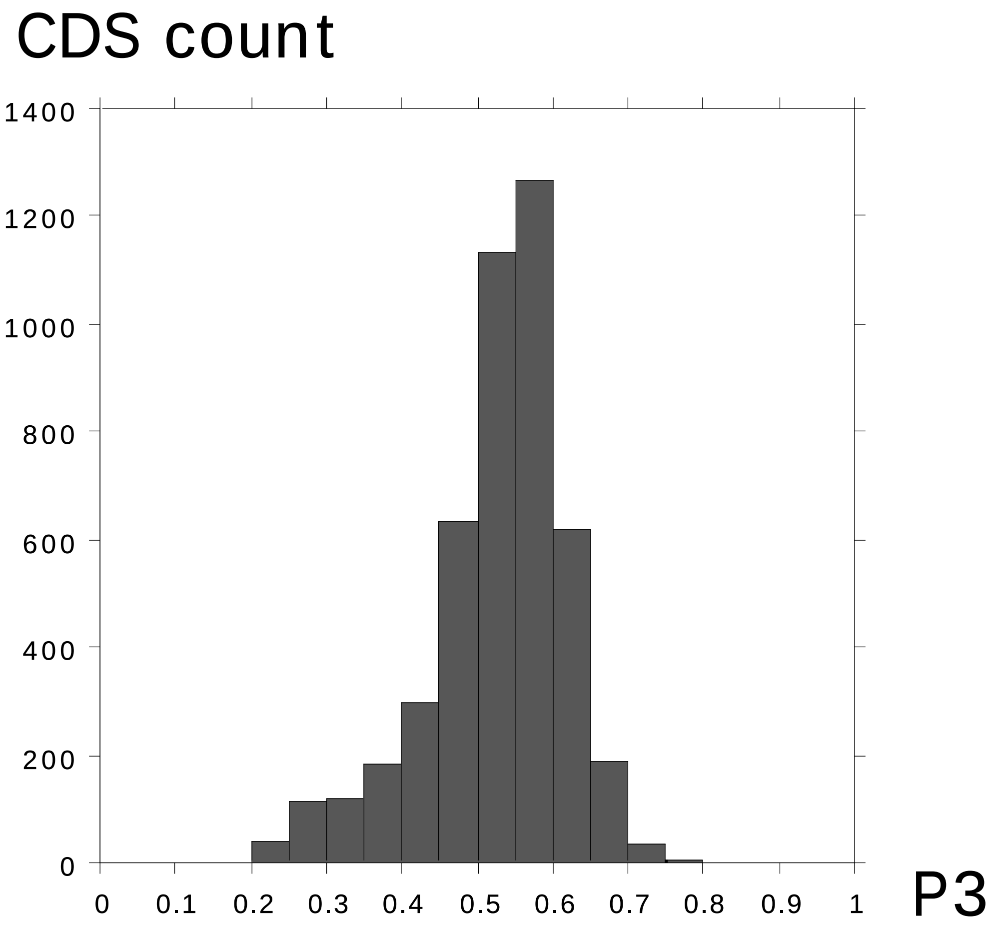
Pyrococcus abyssi



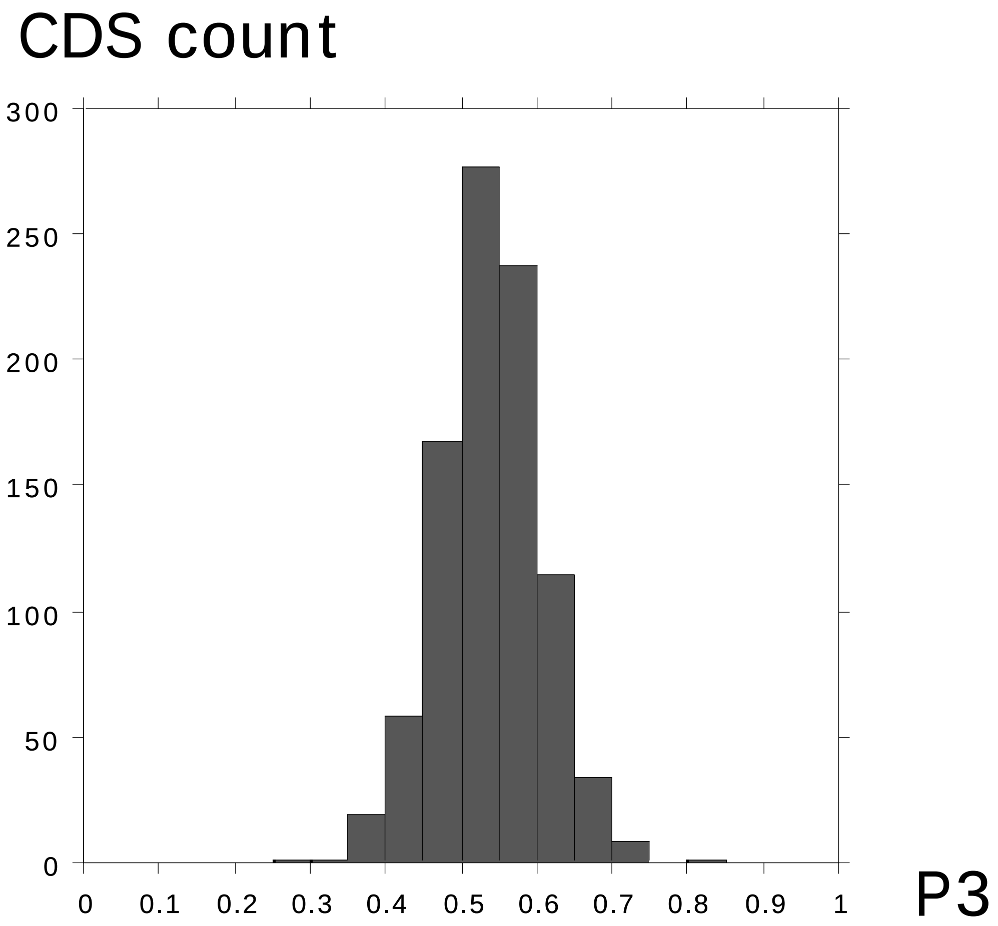
Thermotoga maritima



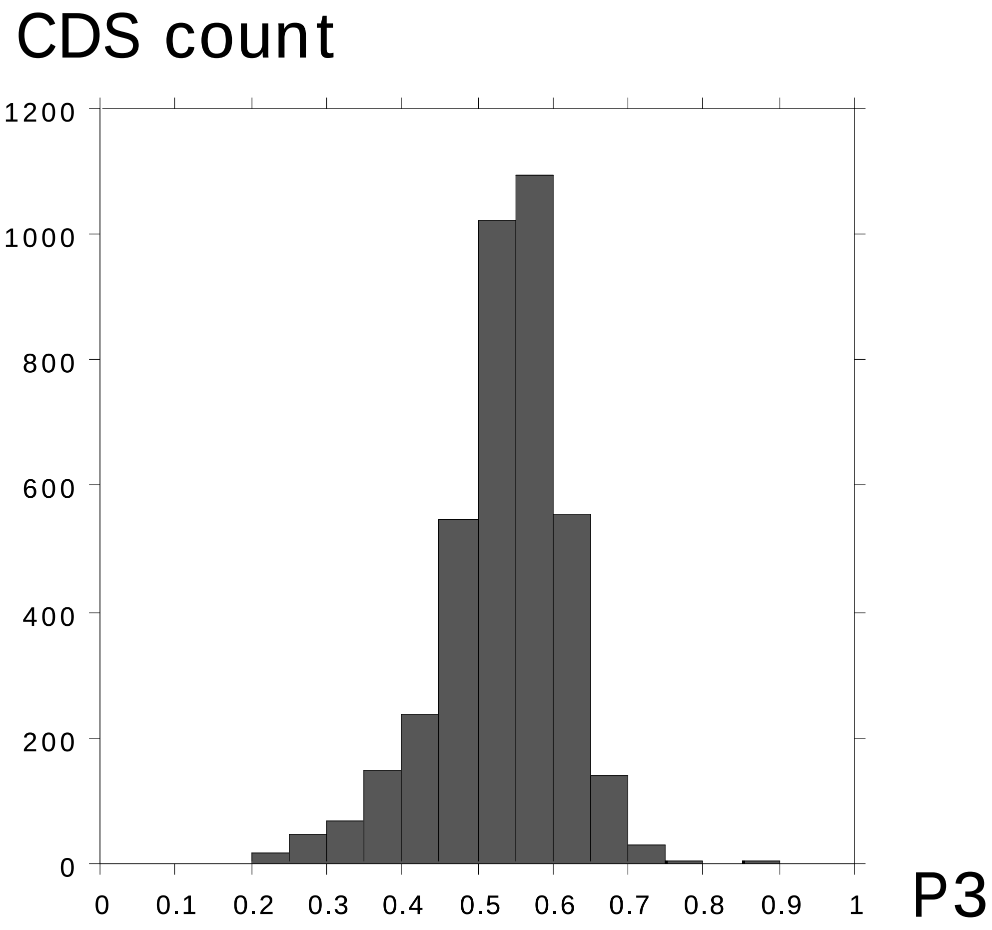
Escherichia coli EDL933



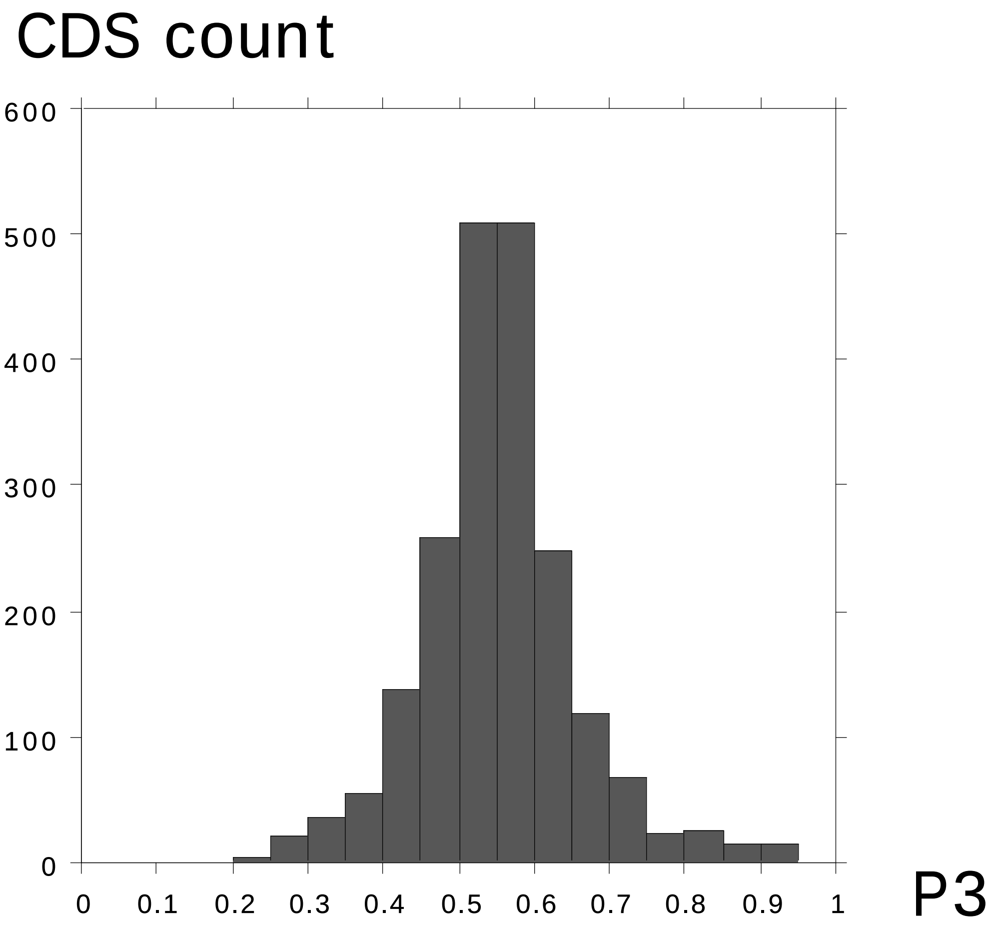
Escherichia coli RIMD 0509952



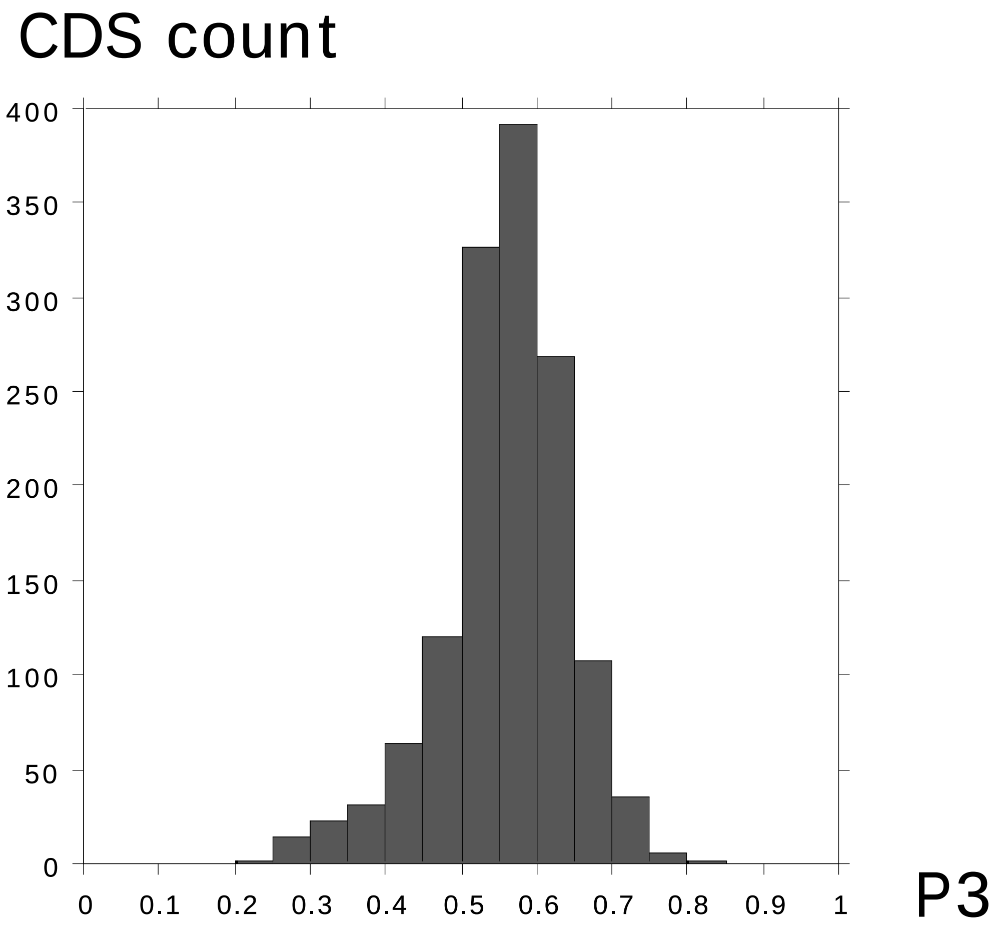
Treponema pallidum



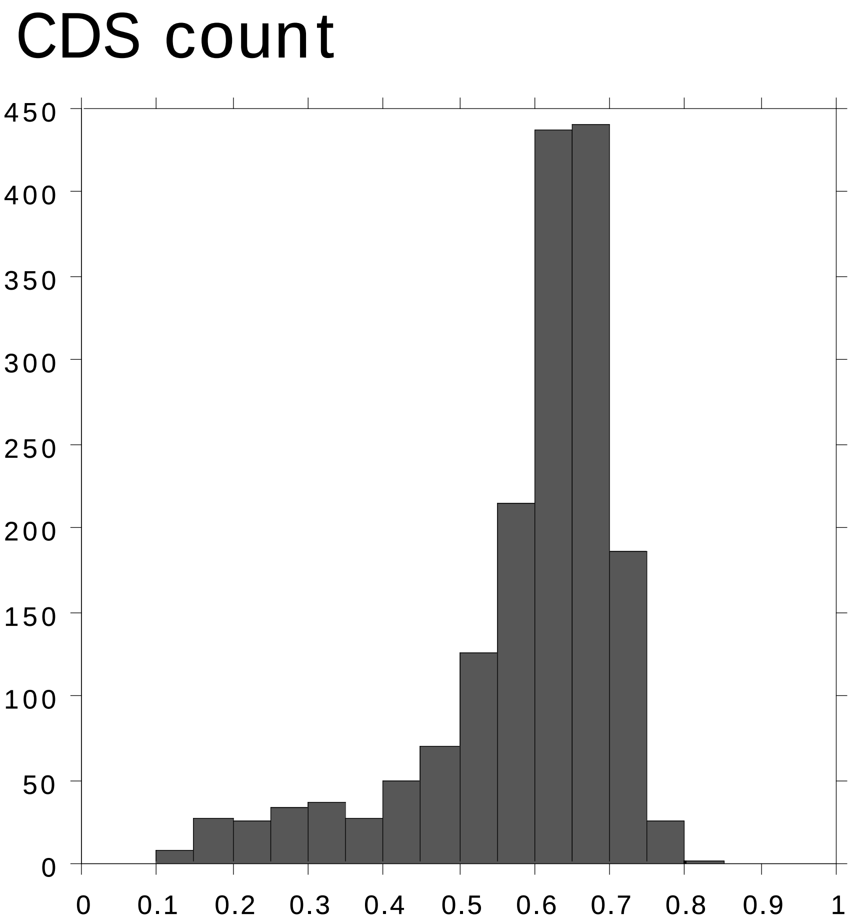
Escherichia coli K-12



Xylella fastidiosa

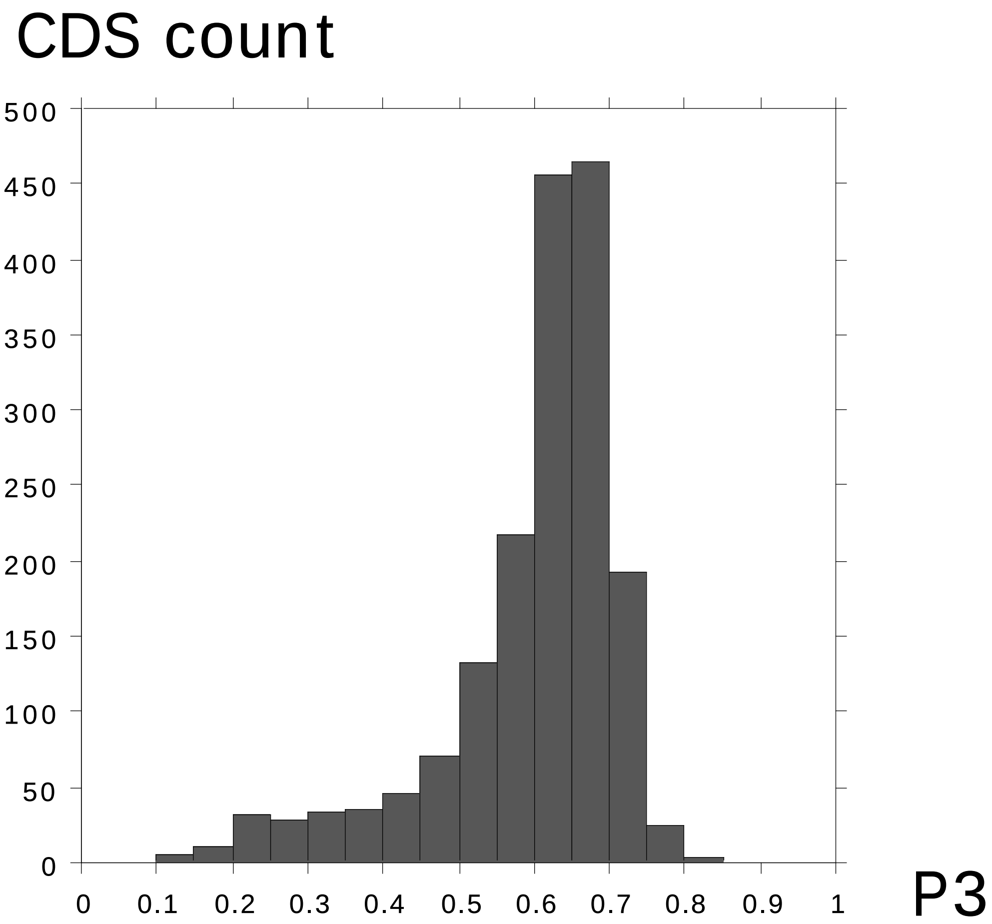


Thermoplasma acidophilum

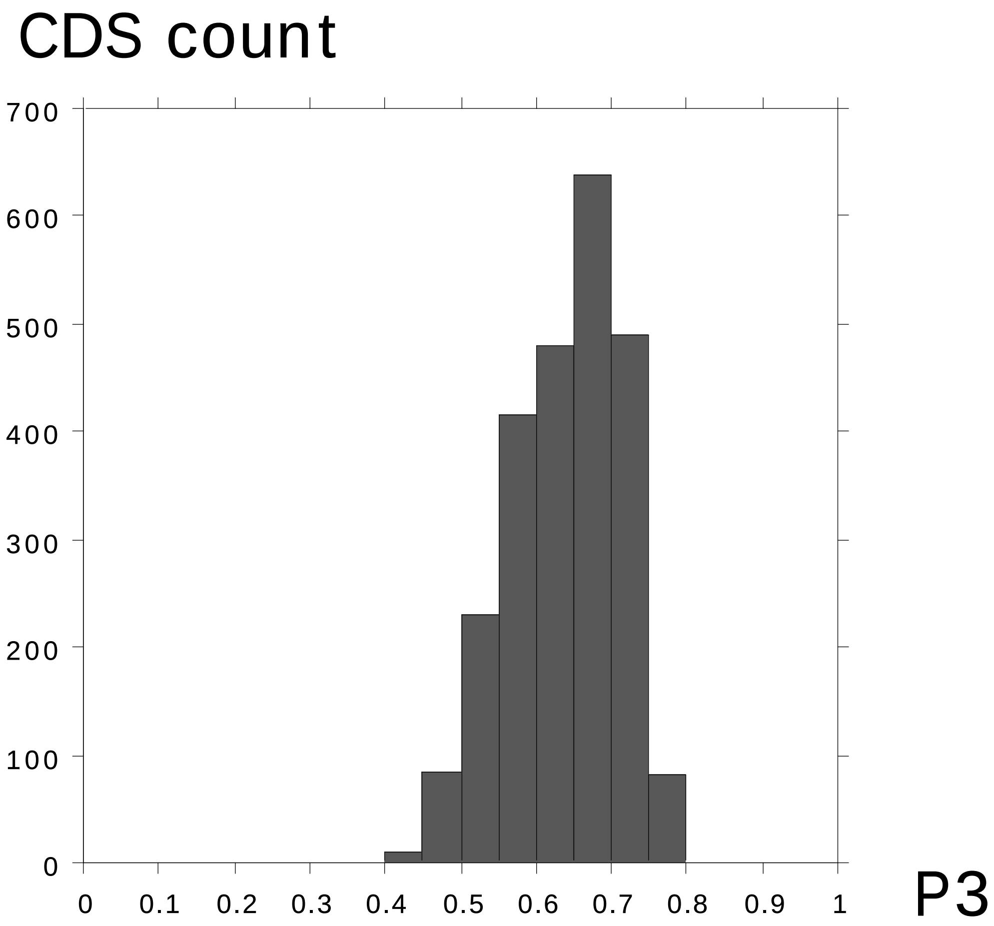


P3

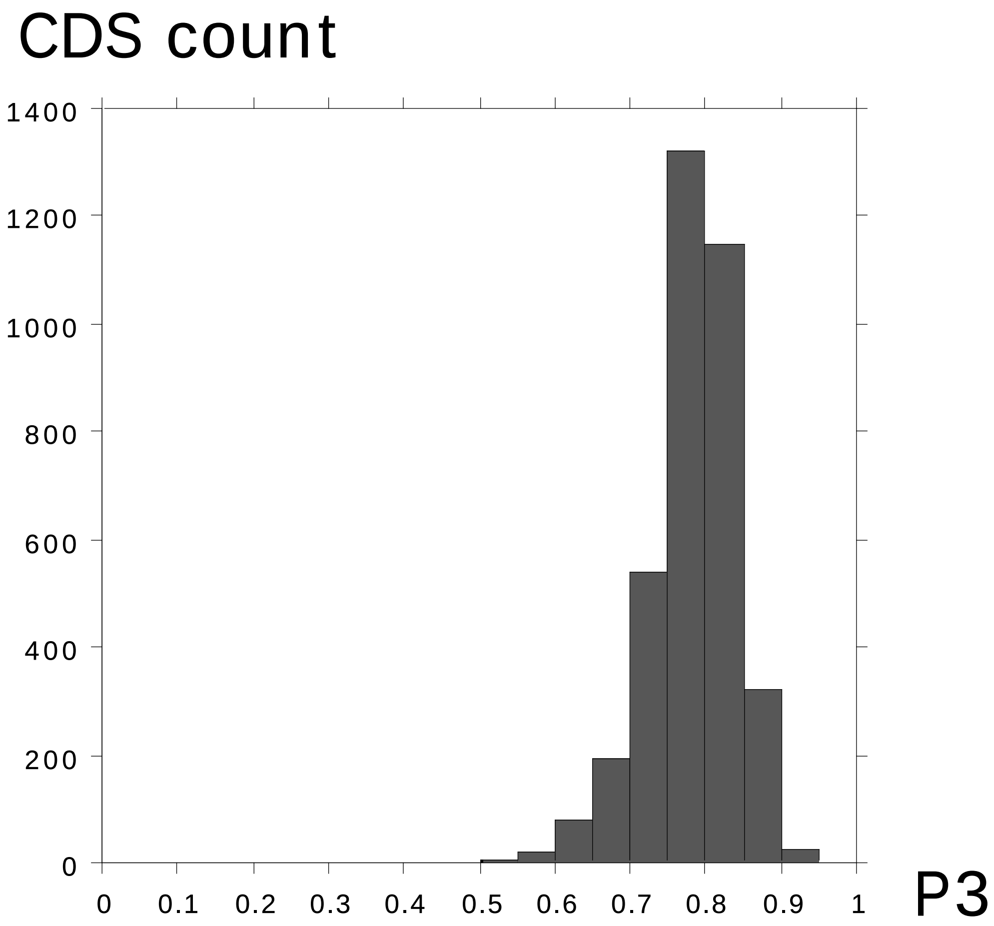
Neisseria meningitidis MC58 (B)



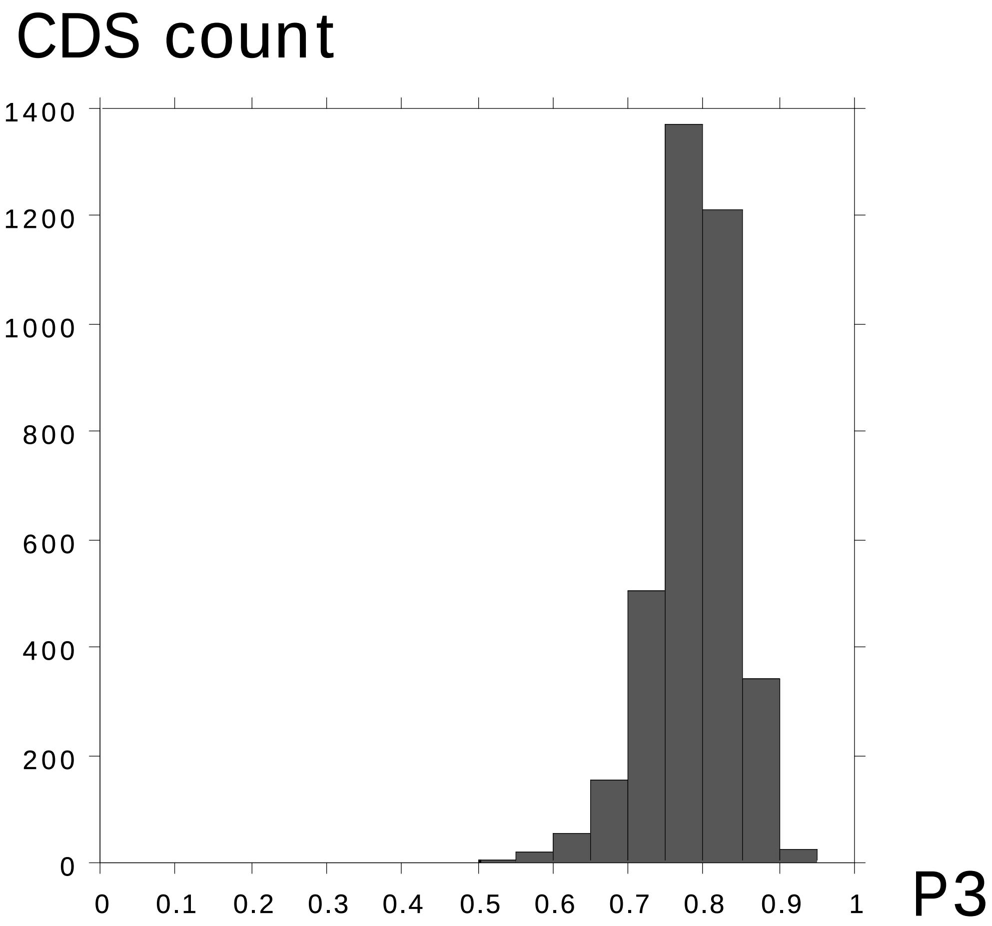
Neisseria meningitidis Z2491 (A)



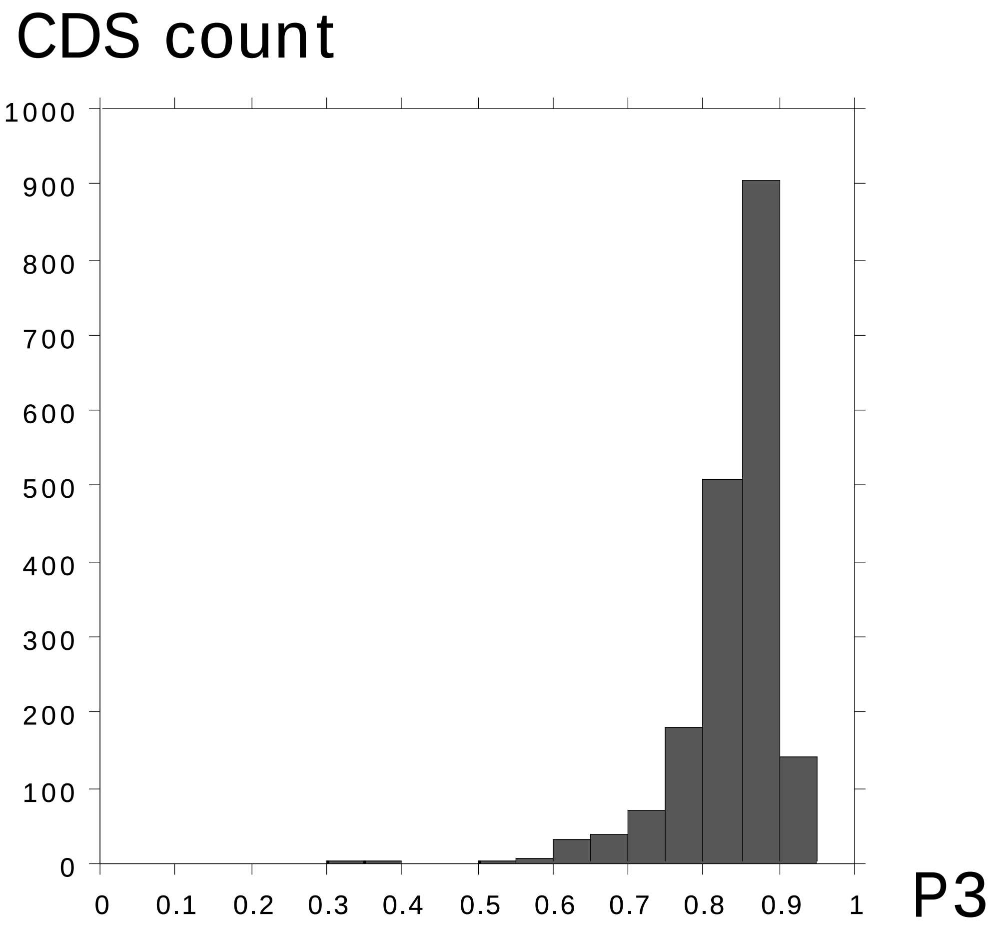
Mycobacterium leprae



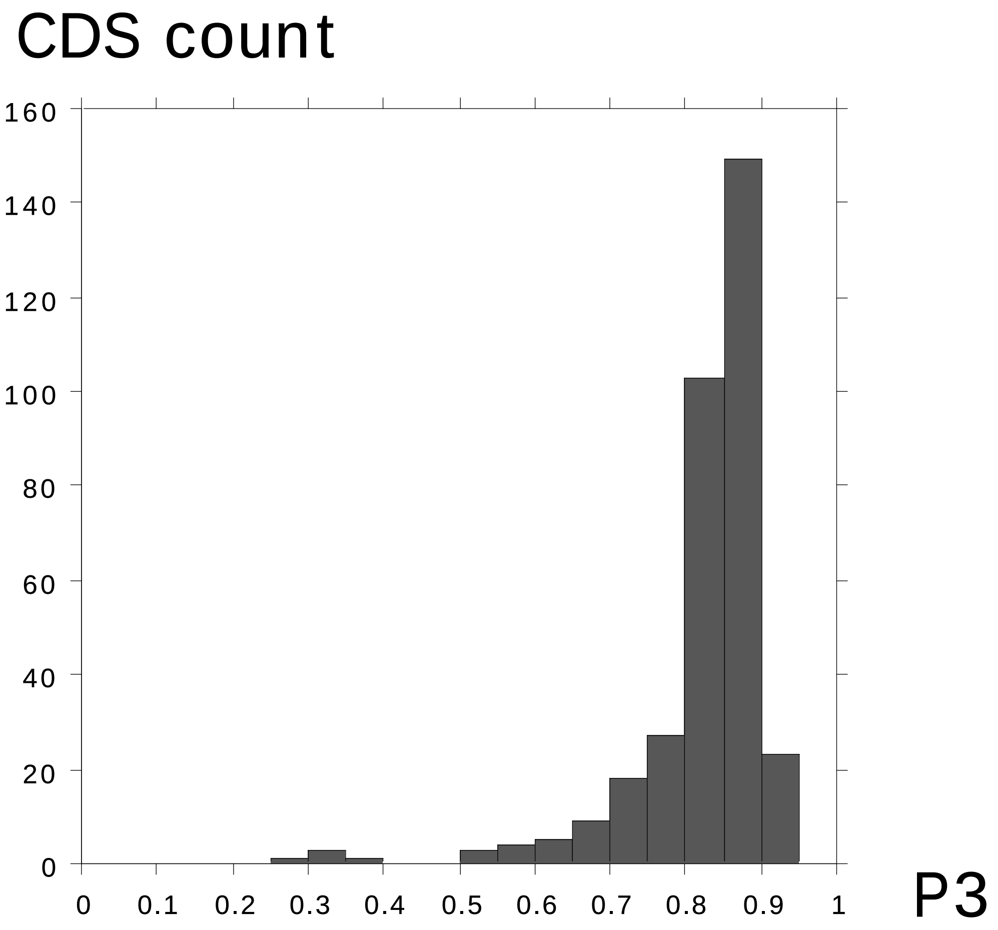
Mycobacterium tuberculosis CDC1551



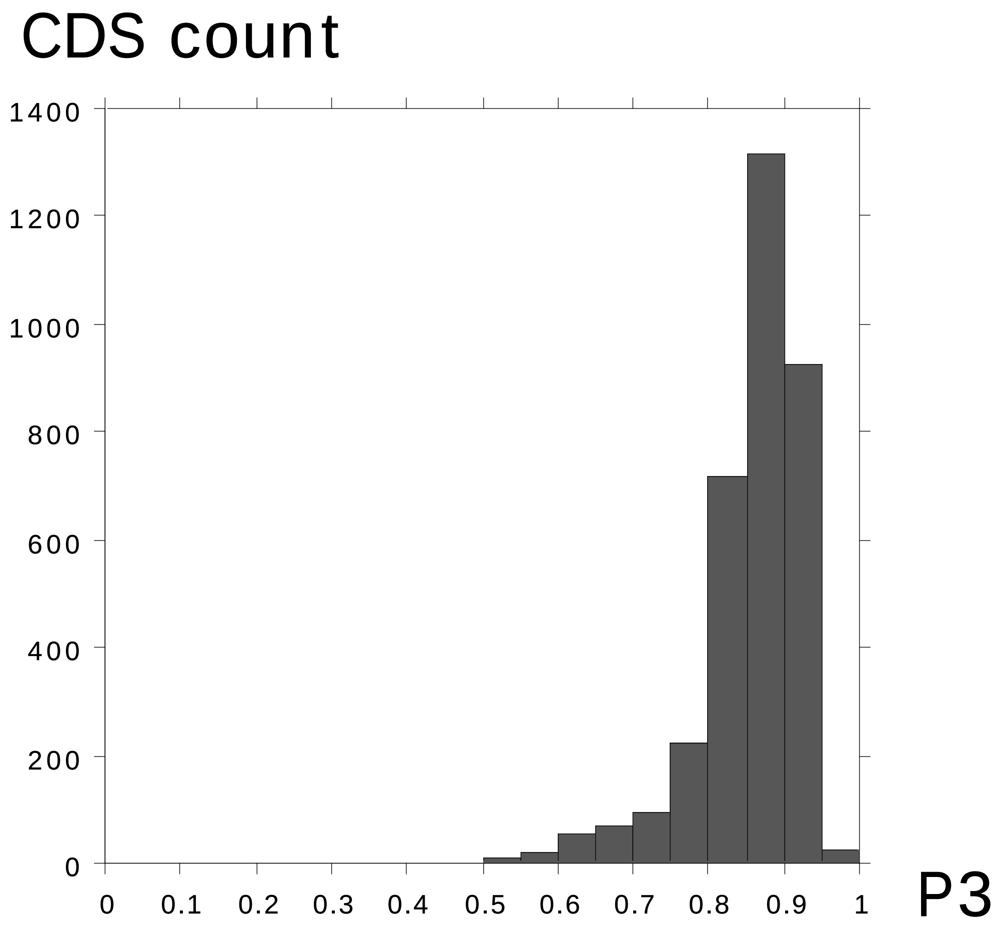
Mycobacterium tuberculosis H37Rv



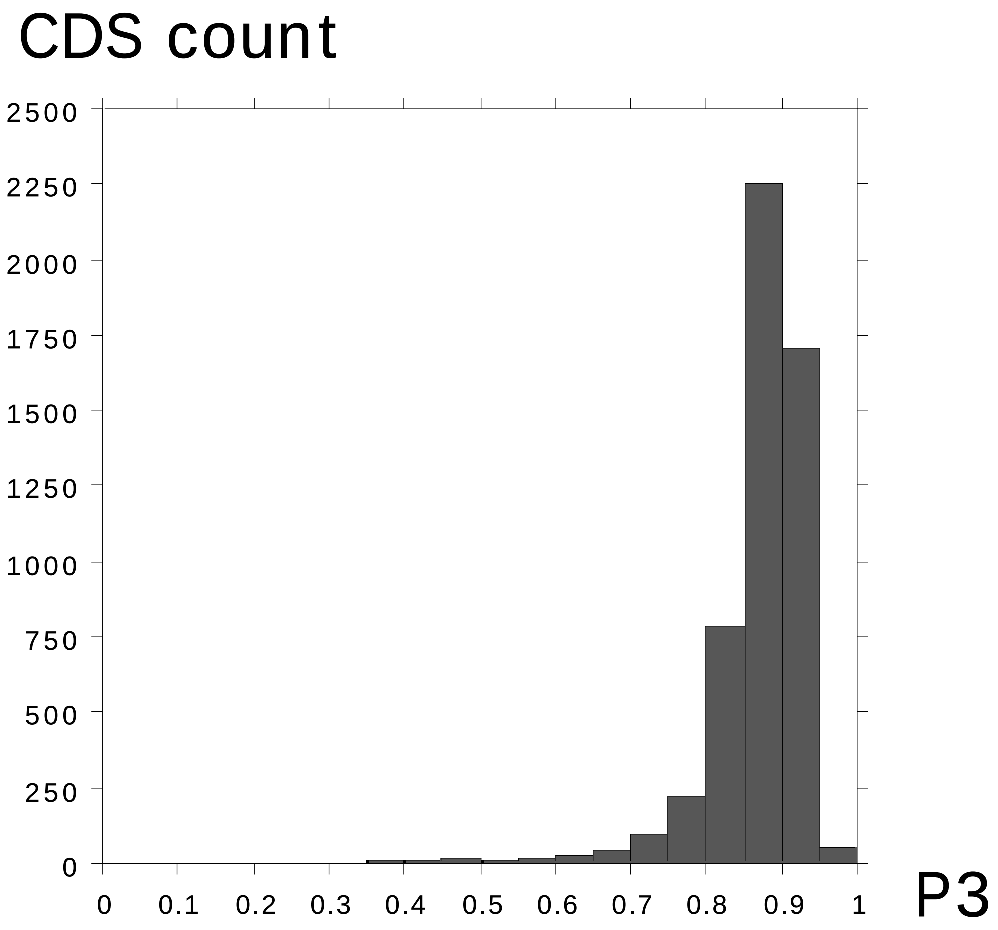
Deinococcus radiodurans chromosome 1



Deinococcus radiodurans chromosome 2



Caulobacter crescentus



Pseudomonas aeruginosa