







































Query id <sup>a</sup>	Subject id <sup>b</sup>	% Identity <sup>c</sup>	Alignment length <sup>d</sup>	Mismatches <sup>e</sup>	Gap opens <sup>f</sup>	Evalue <sup>g</sup>	Bit score <sup>h</sup>	Fungi vesicle <sup>i</sup>	Reference <sup>j</sup>
ath-miR5021	Supercontig_2.2	100	16	0	0	0.036	32.2	<i>S. cerevisiae</i>	
ath-miR5021	Supercontig_2.2	100	16	0	0	0.036	32.2	<i>S. cerevisiae</i>	
ath-miR5021	Supercontig_2.2	100	16	0	0	0.036	32.2	<i>S. cerevisiae</i>	
ath-miR5021	Supercontig_2.2	100	16	0	0	0.036	32.2	<i>S. cerevisiae</i>	
ath-miR5021	Supercontig_2.2	100	16	0	0	0.036	32.2	<i>S. cerevisiae</i>	
ath-miR5021	Supercontig_2.2	100	17	0	0	0.009	34.2	<i>S. cerevisiae</i>	
ath-miR5021	Supercontig_2.2	100	17	0	0	0.009	34.2	<i>S. cerevisiae</i>	
ath-miR5021	Supercontig_2.2	100	17	0	0	0.009	34.2	<i>S. cerevisiae</i>	
ath-miR5021	Supercontig_2.2	100	17	0	0	0.009	34.2	<i>S. cerevisiae</i>	
ath-miR5021	Supercontig_2.2	100	17	0	0	0.009	34.2	<i>S. cerevisiae</i>	
ath-miR5021	Supercontig_2.2	100	17	0	0	0.009	34.2	<i>S. cerevisiae</i>	
ath-miR5021	Supercontig_2.2	100	17	0	0	0.009	34.2	<i>S. cerevisiae</i>	
ath-miR5021	Supercontig_2.2	100	17	0	0	0.009	34.2	<i>S. cerevisiae</i>	
ath-miR5021	Supercontig_2.2	100	18	0	0	0.002	36.2	<i>S. cerevisiae</i>	
ath-miR5021	Supercontig_2.2	100	18	0	0	0.002	36.2	<i>S. cerevisiae</i>	
ath-miR5021	Supercontig_2.2	100	18	0	0	0.002	36.2	<i>S. cerevisiae</i>	
ath-miR5021	Supercontig_2.2	100	18	0	0	0.002	36.2	<i>S. cerevisiae</i>	
ath-miR5021	Supercontig_2.2	100	18	0	0	0.002	36.2	<i>S. cerevisiae</i>	
ath-miR5021	Supercontig_2.2	100	18	0	0	0.002	36.2	<i>S. cerevisiae</i>	
ath-miR5021	Supercontig_2.2	100	18	0	0	0.002	36.2	<i>S. cerevisiae</i>	
ath-miR5021	Supercontig_2.2	100	18	0	0	0.002	36.2	<i>S. cerevisiae</i>	
ath-miR5021	Supercontig_2.2	100	18	0	0	0.002	36.2	<i>S. cerevisiae</i>	
ath-miR5021	Supercontig_2.2	100	19	0	0	6.00E-04	38.2	<i>S. cerevisiae</i>	
ath-miR5021	Supercontig_2.21	100	16	0	0	0.036	32.2	<i>S. cerevisiae</i>	
ath-miR5021	Supercontig_2.21	100	16	0	0	0.036	32.2	<i>S. cerevisiae</i>	
ath-miR5021	Supercontig_2.21	100	16	0	0	0.036	32.2	<i>S. cerevisiae</i>	
ath-miR5021	Supercontig_2.23	100	16	0	0	0.036	32.2	<i>S. cerevisiae</i>	
ath-miR5021	Supercontig_2.23	100	16	0	0	0.036	32.2	<i>S. cerevisiae</i>	
ath-miR5021	Supercontig_2.23	100	16	0	0	0.036	32.2	<i>S. cerevisiae</i>	
ath-miR5021	Supercontig_2.23	100	16	0	0	0.036	32.2	<i>S. cerevisiae</i>	
ath-miR5021	Supercontig_2.23	100	16	0	0	0.036	32.2	<i>S. cerevisiae</i>	
ath-miR5021	Supercontig_2.23	100	16	0	0	0.036	32.2	<i>S. cerevisiae</i>	
ath-miR5021	Supercontig_2.23	100	18	0	0	0.002	36.2	<i>S. cerevisiae</i>	
ath-miR5021	Supercontig_2.24	100	16	0	0	0.036	32.2	<i>S. cerevisiae</i>	
ath-miR5021	Supercontig_2.24	100	16	0	0	0.036	32.2	<i>S. cerevisiae</i>	
ath-miR5021	Supercontig_2.24	100	16	0	0	0.036	32.2	<i>S. cerevisiae</i>	
ath-miR5021	Supercontig_2.25	100	16	0	0	0.036	32.2	<i>S. cerevisiae</i>	
ath-miR5021	Supercontig_2.25	100	16	0	0	0.036	32.2	<i>S. cerevisiae</i>	
ath-miR5021	Supercontig_2.25	100	16	0	0	0.036	32.2	<i>S. cerevisiae</i>	
ath-miR5021	Supercontig_2.25	100	16	0	0	0.036	32.2	<i>S. cerevisiae</i>	
ath-miR5021	Supercontig_2.25	100	17	0	0	0.009	34.2	<i>S. cerevisiae</i>	
ath-miR5021	Supercontig_2.3	100	16	0	0	0.036	32.2	<i>S. cerevisiae</i>	
ath-miR5021	Supercontig_2.3	100	16	0	0	0.036	32.2	<i>S. cerevisiae</i>	
ath-miR5021	Supercontig_2.3	100	16	0	0	0.036	32.2	<i>S. cerevisiae</i>	
ath-miR5021	Supercontig_2.3	100	16	0	0	0.036	32.2	<i>S. cerevisiae</i>	
ath-miR5021	Supercontig_2.3	100	16	0	0	0.036	32.2	<i>S. cerevisiae</i>	





































Query id <sup>a</sup>	Subject id <sup>b</sup>	% Identity <sup>c</sup>	Alignment length <sup>d</sup>	Mismatches <sup>e</sup>	Gap opens <sup>f</sup>	Evalue <sup>g</sup>	Bit score <sup>h</sup>	Fungi vesicle <sup>i</sup>	Reference <sup>j</sup>
bta-miR-2304	Supercontig_2.10	100	16	0	0	0.036	32.2	<i>C.neoformans</i>	
bta-miR-2304	Supercontig_2.4	100	16	0	0	0.036	32.2	<i>C.neoformans</i>	
bta-miR-2437	Supercontig_2.8	100	16	0	0	0.042	32.2	<i>C. albicans</i>	
cfa-miR-214	Supercontig_2.6	100	17	0	0	0.012	34.2	<i>C.neoformans</i>	
cin-miR-367-5p	Supercontig_2.2	100	17	0	0	0.009	34.2	<i>C.neoformans/C. albicans</i>	
cin-miR-4171-5p	Supercontig_2.11	100	16	0	0	0.036	32.2	<i>C.neoformans/C. albicans/S. cerevisiae</i>	
cin-miR-4171-5p	Supercontig_2.32	95	20	1	0	0.036	32.2	<i>C.neoformans/C. albicans/S. cerevisiae</i>	
cin-miR-4171-5p	Supercontig_2.32	95	20	1	0	0.036	32.2	<i>C.neoformans/C. albicans/S. cerevisiae</i>	
cin-miR-4171-5p	Supercontig_2.32	95	20	1	0	0.036	32.2	<i>C.neoformans/C. albicans/S. cerevisiae</i>	
cin-miR-4171-5p	Supercontig_2.32	95	20	1	0	0.036	32.2	<i>C.neoformans/C. albicans/S. cerevisiae</i>	
cin-miR-4171-5p	Supercontig_2.32	95	20	1	0	0.036	32.2	<i>C.neoformans/C. albicans/S. cerevisiae</i>	
cin-miR-4171-5p	Supercontig_2.32	95	20	1	0	0.036	32.2	<i>C.neoformans/C. albicans/S. cerevisiae</i>	
cin-miR-4171-5p	Supercontig_2.32	95	20	1	0	0.036	32.2	<i>C.neoformans/C. albicans/S. cerevisiae</i>	
cin-miR-4171-5p	Supercontig_2.8	95	20	1	0	0.036	32.2	<i>C.neoformans/C. albicans/S. cerevisiae</i>	
cin-miR-4171-5p	Supercontig_2.8	95	20	1	0	0.036	32.2	<i>C.neoformans/C. albicans/S. cerevisiae</i>	
cin-miR-4171-5p	Supercontig_2.8	95	20	1	0	0.036	32.2	<i>C.neoformans/C. albicans/S. cerevisiae</i>	
csi-miR3946	Supercontig_2.13	100	16	0	0	0.06	32.2	<i>C.neoformans/S. cerevisiae</i>	
csi-miR3946	Supercontig_2.2	100	16	0	0	0.06	32.2	<i>C.neoformans/S. cerevisiae</i>	
csi-miR3946	Supercontig_2.3	100	16	0	0	0.06	32.2	<i>C.neoformans/S. cerevisiae</i>	
csi-miR3946	Supercontig_2.6	100	16	0	0	0.06	32.2	<i>C.neoformans/S. cerevisiae</i>	
csi-miR3946	Supercontig_2.6	100	16	0	0	0.06	32.2	<i>C.neoformans/S. cerevisiae</i>	
csi-miR3946	Supercontig_2.8	100	16	0	0	0.06	32.2	<i>C.neoformans/S. cerevisiae</i>	
csi-miR3946	Supercontig_2.8	100	17	0	0	0.015	34.2	<i>C.neoformans/S. cerevisiae</i>	
der-miR-13b	Supercontig_2.11	100	16	0	0	0.048	32.2	<i>P.brasiliensis/C.neoformans/S. cerevisiae</i>	
dme-miR-2491-3p*	Supercontig_2.10	100	17	0	0	0.008	34.2	<i>S. cerevisiae</i>	
dme-miR-2491-3p*	Supercontig_2.10	100	17	0	0	0.008	34.2	<i>S. cerevisiae</i>	
dme-miR-2491-3p*	Supercontig_2.10	100	18	0	0	0.002	36.2	<i>S. cerevisiae</i>	
dme-miR-2491-3p*	Supercontig_2.1	100	16	0	0	0.03	32.2	<i>S. cerevisiae</i>	
dme-miR-2491-3p*	Supercontig_2.1	100	17	0	0	0.008	34.2	<i>S. cerevisiae</i>	
dme-miR-2491-3p*	Supercontig_2.1	100	17	0	0	0.008	34.2	<i>S. cerevisiae</i>	
dme-miR-2491-3p*	Supercontig_2.1	100	18	0	0	0.002	36.2	<i>S. cerevisiae</i>	
dme-miR-2491-3p*	Supercontig_2.1	100	18	0	0	0.002	36.2	<i>S. cerevisiae</i>	
dme-miR-2491-3p*	Supercontig_2.11	100	17	0	0	0.008	34.2	<i>S. cerevisiae</i>	
dme-miR-2491-3p*	Supercontig_2.12	100	17	0	0	0.008	34.2	<i>S. cerevisiae</i>	
dme-miR-4968-3p*	Supercontig_2.10	100	16	0	0	0.048	32.2	<i>C.neoformans/S. cerevisiae</i>	
dme-miR-4968-3p*	Supercontig_2.10	100	16	0	0	0.048	32.2	<i>C.neoformans/S. cerevisiae</i>	
dme-miR-4968-3p*	Supercontig_2.10	100	17	0	0	0.012	34.2	<i>C.neoformans/S. cerevisiae</i>	
dme-miR-4968-3p*	Supercontig_2.10	100	17	0	0	0.012	34.2	<i>C.neoformans/S. cerevisiae</i>	
dme-miR-4968-3p*	Supercontig_2.10	100	17	0	0	0.012	34.2	<i>C.neoformans/S. cerevisiae</i>	
dme-miR-4968-3p*	Supercontig_2.10	100	18	0	0	0.003	36.2	<i>C.neoformans/S. cerevisiae</i>	
dme-miR-4968-3p*	Supercontig_2.10	100	21	0	0	5.00E-05	42.1	<i>C.neoformans/S. cerevisiae</i>	
dme-miR-4968-3p*	Supercontig_2.10	100	21	0	0	5.00E-05	42.1	<i>C.neoformans/S. cerevisiae</i>	
dme-miR-4968-3p*	Supercontig_2.10	95	20	1	0	0.048	32.2	<i>C.neoformans/S. cerevisiae</i>	
dme-miR-4968-3p*	Supercontig_2.10	95	20	1	0	0.048	32.2	<i>C.neoformans/S. cerevisiae</i>	
dme-miR-4968-3p*	Supercontig_2.10	95	20	1	0	0.048	32.2	<i>C.neoformans/S. cerevisiae</i>	
dme-miR-4968-3p*	Supercontig_2.10	95	20	1	0	0.048	32.2	<i>C.neoformans/S. cerevisiae</i>	







Query id <sup>a</sup>	Subject id <sup>b</sup>	% Identity <sup>c</sup>	Alignment length <sup>d</sup>	Mismatches <sup>e</sup>	Gap opens <sup>f</sup>	Evalue <sup>g</sup>	Bit score <sup>h</sup>	Fungi vesicle <sup>i</sup>	Reference <sup>j</sup>
dme-miR-4968-3p*	Supercontig_2.2	100	16	0	0	4.80E-02	32.2	<i>C.neoformans/S. cerevisiae</i>	
dme-miR-4968-3p*	Supercontig_2.2	100	16	0	0	4.80E-02	32.2	<i>C.neoformans/S. cerevisiae</i>	
dme-miR-4968-3p*	Supercontig_2.2	100	16	0	0	0.048	32.2	<i>C.neoformans/S. cerevisiae</i>	
dme-miR-4968-3p*	Supercontig_2.2	100	16	0	0	0.048	32.2	<i>C.neoformans/S. cerevisiae</i>	
dme-miR-4968-3p*	Supercontig_2.2	100	16	0	0	0.048	32.2	<i>C.neoformans/S. cerevisiae</i>	
dme-miR-4968-3p*	Supercontig_2.2	100	16	0	0	0.048	32.2	<i>C.neoformans/S. cerevisiae</i>	
dme-miR-4968-3p*	Supercontig_2.2	100	16	0	0	0.048	32.2	<i>C.neoformans/S. cerevisiae</i>	
dme-miR-4968-3p*	Supercontig_2.2	100	16	0	0	0.048	32.2	<i>C.neoformans/S. cerevisiae</i>	
dme-miR-4968-3p*	Supercontig_2.2	100	16	0	0	0.048	32.2	<i>C.neoformans/S. cerevisiae</i>	
dme-miR-4968-3p*	Supercontig_2.2	100	16	0	0	0.048	32.2	<i>C.neoformans/S. cerevisiae</i>	
dme-miR-4968-3p*	Supercontig_2.2	100	17	0	0	0.012	34.2	<i>C.neoformans/S. cerevisiae</i>	
dme-miR-4968-3p*	Supercontig_2.2	100	18	0	0	0.003	36.2	<i>C.neoformans/S. cerevisiae</i>	
dme-miR-4968-3p*	Supercontig_2.2	100	18	0	0	0.003	36.2	<i>C.neoformans/S. cerevisiae</i>	
dme-miR-4968-3p*	Supercontig_2.2	100	18	0	0	0.003	36.2	<i>C.neoformans/S. cerevisiae</i>	
dme-miR-4968-3p*	Supercontig_2.2	100	18	0	0	0.003	36.2	<i>C.neoformans/S. cerevisiae</i>	
dme-miR-4968-3p*	Supercontig_2.2	100	18	0	0	0.003	36.2	<i>C.neoformans/S. cerevisiae</i>	
dpe-miR-13a	Supercontig_2.11	100	16	0	0	0.048	32.2	<i>C.neoformans</i>	
dps-miR-2565-5p	Supercontig_2.3	100	16	0	0	0.048	32.2	<i>S. cerevisiae</i>	
dps-miR-968-3p*	Supercontig_2.3	100	16	0	0	0.06	32.2	<i>C. albicans</i>	
dre-miR-216a	Supercontig_2.18	100	17	0	0	0.012	34.2	<i>C. albicans</i>	
dwi-miR-13a	Supercontig_2.11	100	16	0	0	0.048	32.2	<i>C. albicans</i>	
gga-miR-1457	Supercontig_2.2	100	16	0	0	0.048	32.2	<i>C. albicans</i>	
gga-miR-1458	Supercontig_2.1	100	16	0	0	0.042	32.2	<i>S. cerevisiae</i>	
gga-miR-1692	Supercontig_2.1	100	17	0	0	0.009	34.2	<i>C. albicans/S. cerevisiae/C.neoformans</i>	
gga-miR-1692	Supercontig_2.2	100	17	0	0	0.009	34.2	<i>C. albicans/S. cerevisiae/C.neoformans</i>	
gga-miR-1814	Supercontig_2.12	100	16	0	0	0.036	32.2	<i>C.neoformans</i>	
gga-miR-29a-5p	Supercontig_2.4	100	17	0	0	0.012	34.2	<i>C. albicans</i>	
gga-miR-3540	Supercontig_2.5	100	16	0	0	0.048	32.2	<i>S. cerevisiae</i>	
gga-miR-466	Supercontig_2.1	100	17	0	0	0.014	34.2	<i>C.neoformans</i>	
gga-miR-466	Supercontig_2.11	100	16	0	0	0.054	32.2	<i>C.neoformans</i>	
gga-miR-466	Supercontig_2.17	100	16	0	0	0.054	32.2	<i>C.neoformans</i>	
gga-miR-466	Supercontig_2.3	100	16	0	0	0.054	32.2	<i>C.neoformans</i>	
gga-miR-466	Supercontig_2.8	100	16	0	0	0.054	32.2	<i>C.neoformans</i>	
gra-miR482	Supercontig_2.6	95	20	1	0	0.048	32.2	<i>C.neoformans</i>	
hsa-miR-320a	Supercontig_2.9	100	16	0	0	0.048	32.2	<i>C. albicans</i>	
hsa-miR-3620-5p	Supercontig_2.10	100	18	0	0	0.003	36.2	<i>C.neoformans/S. cerevisiae</i>	
hsa-miR-3620-5p	Supercontig_2.10	100	19	0	0	8.00E-04	38.2	<i>C.neoformans/S. cerevisiae</i>	
hsa-miR-3620-5p	Supercontig_2.10	100	20	0	0	2.00E-04	40.1	<i>C.neoformans/S. cerevisiae</i>	
hsa-miR-3620-5p	Supercontig_2.1	100	17	0	0	0.012	34.2	<i>C.neoformans/S. cerevisiae</i>	
hsa-miR-3620-5p	Supercontig_2.3	100	16	0	0	0.048	32.2	<i>C.neoformans/S. cerevisiae</i>	
hsa-miR-3620-5p	Supercontig_2.4	100	17	0	0	0.012	34.2	<i>C.neoformans/S. cerevisiae</i>	
hsa-miR-3620-5p	Supercontig_2.4	95.24	21	1	0	0.012	34.2	<i>C.neoformans/S. cerevisiae</i>	
hsa-miR-3620-5p	Supercontig_2.6	100	18	0	0	0.003	36.2	<i>C.neoformans/S. cerevisiae</i>	
hsa-miR-3620-5p	Supercontig_2.6	100	19	0	0	8.00E-04	38.2	<i>C.neoformans/S. cerevisiae</i>	
hsa-miR-3925-5p	Supercontig_2.2	100	16	0	0	0.048	32.2	<i>C. albicans</i>	

Query id <sup>a</sup>	Subject id <sup>b</sup>	% Identity <sup>c</sup>	Alignment length <sup>d</sup>	Mismatches <sup>e</sup>	Gap opens <sup>f</sup>	Evalue <sup>g</sup>	Bit score <sup>h</sup>	Fungi vesicle <sup>i</sup>	Reference <sup>j</sup>
hsa-miR-3976	Supercontig_2.31	100	16	0	0	0.06	32.2	<i>C.neoformans</i>	
hsa-miR-4507	Supercontig_2.10	95	20	1	0	0.036	32.2	<i>C.neoformans/S. cerevisiae</i>	
hsa-miR-4507	Supercontig_2.10	95	20	1	0	0.036	32.2	<i>C.neoformans/S. cerevisiae</i>	
hsa-miR-4507	Supercontig_2.3	100	16	0	0	0.036	32.2	<i>C.neoformans/S. cerevisiae</i>	
hsa-miR-4507	Supercontig_2.4	100	17	0	0	0.009	34.2	<i>C.neoformans/S. cerevisiae</i>	
hsa-miR-4507	Supercontig_2.6	95	20	1	0	0.036	32.2	<i>C.neoformans/S. cerevisiae</i>	
hsa-miR-4539	Supercontig_2.6	100	16	0	0	0.048	32.2	<i>C. albicans</i>	
hsa-miR-5194	Supercontig_2.11	100	16	0	0	0.048	32.2	<i>S. cerevisiae</i>	
hsa-miR-5195-3p*	Supercontig_2.4	100	17	0	0	0.011	34.2	<i>S. cerevisiae</i>	
hsv2-miR-H13	Supercontig_2.12	100	16	0	0	0.048	32.2	<i>S. cerevisiae</i>	
mml-miR-938	Supercontig_2.31	100	16	0	0	0.048	32.2	<i>C.neoformans</i>	
mml-miR-938	Supercontig_2.31	100	16	0	0	0.048	32.2	<i>C.neoformans</i>	
mmu-let-7e-3p*	Supercontig_2.2	100	16	0	0	0.048	32.2	<i>C. albicans/C.neoformans</i>	
mmu-miR-1895	Supercontig_2.10	95.24	21	1	0	0.012	34.2	<i>S. cerevisiae</i>	
mmu-miR-1903	Supercontig_2.12	100	16	0	0	0.048	32.2	<i>S. cerevisiae</i>	
mmu-miR-1903	Supercontig_2.2	100	16	0	0	0.048	32.2	<i>S. cerevisiae</i>	
mmu-miR-1903	Supercontig_2.3	100	16	0	0	0.048	32.2	<i>S. cerevisiae</i>	
mmu-miR-1903	Supercontig_2.3	100	16	0	0	0.048	32.2	<i>S. cerevisiae</i>	
mmu-miR-1903	Supercontig_2.4	100	17	0	0	0.012	34.2	<i>S. cerevisiae</i>	
mmu-miR-1903	Supercontig_2.7	100	16	0	0	0.048	32.2	<i>S. cerevisiae</i>	
mmu-miR-297a-5p	Supercontig_2.2	95.24	21	1	0	0.012	34.2	<i>C. albicans</i>	
mmu-miR-297a-5p	Supercontig_2.3	100	16	0	0	4.80E-02	32.2	<i>C. albicans</i>	
mmu-miR-297a-5p	Supercontig_2.3	100	17	0	0	1.20E-02	34.2	<i>C. albicans</i>	
mmu-miR-339-5p	Supercontig_2.3	100	16	0	0	5.40E-02	32.2	<i>C. albicans</i>	
mmu-miR-383-3p*	Supercontig_2.32	100	16	0	0	4.20E-02	32.2	<i>S. cerevisiae</i>	
mmu-miR-383-3p*	Supercontig_2.32	100	16	0	0	4.20E-02	32.2	<i>S. cerevisiae</i>	
mmu-miR-383-3p*	Supercontig_2.32	100	16	0	0	4.20E-02	32.2	<i>S. cerevisiae</i>	
mmu-miR-383-3p*	Supercontig_2.32	100	16	0	0	4.20E-02	32.2	<i>S. cerevisiae</i>	
mmu-miR-383-3p*	Supercontig_2.32	100	16	0	0	4.20E-02	32.2	<i>S. cerevisiae</i>	
mmu-miR-383-3p*	Supercontig_2.32	100	16	0	0	0.042	32.2	<i>S. cerevisiae</i>	
mmu-miR-383-3p*	Supercontig_2.8	100	16	0	0	0.042	32.2	<i>S. cerevisiae</i>	
mmu-miR-383-3p*	Supercontig_2.8	100	16	0	0	0.042	32.2	<i>S. cerevisiae</i>	
mmu-miR-383-3p*	Supercontig_2.8	100	16	0	0	0.042	32.2	<i>S. cerevisiae</i>	
mmu-miR-466f-5p	Supercontig_2.3	100	18	0	0	0.003	36.2	<i>C. albicans</i>	
mmu-miR-466h-3p*	Supercontig_2.1	100	17	0	0	0.008	34.2	<i>C.neoformans</i>	
mmu-miR-466h-3p*	Supercontig_2.11	100	18	0	0	0.002	36.2	<i>C.neoformans</i>	
mmu-miR-466h-3p*	Supercontig_2.2	100	16	0	0	0.03	32.2	<i>C.neoformans</i>	
mmu-miR-466h-3p*	Supercontig_2.3	100	16	0	0	0.03	32.2	<i>C.neoformans</i>	
mmu-miR-466h-3p*	Supercontig_2.3	100	18	0	0	0.002	36.2	<i>C.neoformans</i>	
mmu-miR-466h-3p*	Supercontig_2.6	100	17	0	0	0.008	34.2	<i>C.neoformans</i>	
mmu-miR-466h-5p	Supercontig_2.3	95	20	1	0	0.048	32.2	<i>C.neoformans</i>	
mmu-miR-466h-5p	Supercontig_2.6	100	16	0	0	0.048	32.2	<i>C.neoformans</i>	
mmu-miR-466j	Supercontig_2.1	100	19	0	0	9.00E-04	38.2	<i>S. cerevisiae</i>	
mmu-miR-466j	Supercontig_2.11	100	16	0	0	0.054	32.2	<i>S. cerevisiae</i>	
mmu-miR-466j	Supercontig_2.11	100	16	0	0	0.054	32.2	<i>S. cerevisiae</i>	
mmu-miR-466j	Supercontig_2.2	100	17	0	0	0.014	34.2	<i>S. cerevisiae</i>	



Query id <sup>a</sup>	Subject id <sup>b</sup>	% Identity <sup>c</sup>	Alignment length <sup>d</sup>	Mismatches <sup>e</sup>	Gap opens <sup>f</sup>	Evalue <sup>g</sup>	Bit score <sup>h</sup>	Fungi vesicle <sup>i</sup>	Reference <sup>j</sup>
mmu-miR-466j	Supercontig_2.3	100	16	0	0	0.054	32.2	<i>S. cerevisiae</i>	
mmu-miR-466j	Supercontig_2.3	100	16	0	0	0.054	32.2	<i>S. cerevisiae</i>	
mmu-miR-466j	Supercontig_2.3	100	16	0	0	0.054	32.2	<i>S. cerevisiae</i>	
mmu-miR-466j	Supercontig_2.3	100	16	0	0	0.054	32.2	<i>S. cerevisiae</i>	
mmu-miR-466j	Supercontig_2.3	100	17	0	0	0.014	34.2	<i>S. cerevisiae</i>	
mmu-miR-466j	Supercontig_2.3	100	18	0	0	0.003	36.2	<i>S. cerevisiae</i>	
mmu-miR-466j	Supercontig_2.3	100	20	0	0	2.00E-04	40.1	<i>S. cerevisiae</i>	
mmu-miR-466j	Supercontig_2.3	95.24	21	1	0	0.014	34.2	<i>S. cerevisiae</i>	
mmu-miR-466k	Supercontig_2.6	100	16	0	0	0.054	32.2	<i>C.neoformans/S. cerevisiae</i>	
mmu-miR-466k	Supercontig_2.8	100	16	0	0	0.054	32.2	<i>C.neoformans/S. cerevisiae</i>	
mmu-miR-466k	Supercontig_2.18	100	16	0	0	0.054	32.2	<i>C.neoformans/S. cerevisiae</i>	
mmu-miR-466k	Supercontig_2.3	100	16	0	0	0.054	32.2	<i>C.neoformans/S. cerevisiae</i>	
mmu-miR-466k	Supercontig_2.3	100	16	0	0	0.054	32.2	<i>C.neoformans/S. cerevisiae</i>	
mmu-miR-466k	Supercontig_2.3	100	16	0	0	0.054	32.2	<i>C.neoformans/S. cerevisiae</i>	
mmu-miR-466k	Supercontig_2.3	100	16	0	0	0.054	32.2	<i>C.neoformans/S. cerevisiae</i>	
mmu-miR-466k	Supercontig_2.4	100	16	0	0	0.054	32.2	<i>C.neoformans/S. cerevisiae</i>	
mmu-miR-466k	Supercontig_2.4	100	16	0	0	0.054	32.2	<i>C.neoformans/S. cerevisiae</i>	
mmu-miR-466k	Supercontig_2.5	100	16	0	0	0.054	32.2	<i>C.neoformans/S. cerevisiae</i>	
mmu-miR-467a-3p*	Supercontig_2.22	100	16	0	0	0.048	32.2	<i>S. cerevisiae</i>	
mmu-miR-467a-3p*	Supercontig_2.4	100	16	0	0	0.048	32.2	<i>S. cerevisiae</i>	
mmu-miR-467a-3p*	Supercontig_2.9	100	16	0	0	0.048	32.2	<i>S. cerevisiae</i>	
mmu-miR-467g	Supercontig_2.10	100	18	0	0	0.003	36.2	<i>C. albicans/ P. brasiliensis</i>	
mmu-miR-467g	Supercontig_2.12	100	17	0	0	1.10E-02	34.2	<i>C. albicans/ P. brasiliensis</i>	
mmu-miR-467g	Supercontig_2.16	100	16	0	0	4.20E-02	32.2	<i>C. albicans/ P. brasiliensis</i>	
mmu-miR-467g	Supercontig_2.27	100	16	0	0	0.042	32.2	<i>C. albicans/ P. brasiliensis</i>	
mmu-miR-467g	Supercontig_2.3	95	20	1	0	0.042	32.2	<i>C. albicans/ P. brasiliensis</i>	
mmu-miR-467g	Supercontig_2.4	100	16	0	0	0.042	32.2	<i>C. albicans/ P. brasiliensis</i>	
mmu-miR-467g	Supercontig_2.5	100	18	0	0	0.003	36.2	<i>C. albicans/ P. brasiliensis</i>	
mmu-miR-467g	Supercontig_2.7	100	17	0	0	0.011	34.2	<i>C. albicans/ P. brasiliensis</i>	
mmu-miR-669f-3p*	Supercontig_2.10	100	16	0	0	0.054	32.2	<i>S. cerevisiae</i>	
mmu-miR-669f-3p*	Supercontig_2.13	100	16	0	0	0.054	32.2	<i>S. cerevisiae</i>	
mmu-miR-669f-3p*	Supercontig_2.16	100	17	0	0	0.014	34.2	<i>S. cerevisiae</i>	
mmu-miR-669f-3p*	Supercontig_2.2	100	16	0	0	0.054	32.2	<i>S. cerevisiae</i>	
mmu-miR-669f-3p*	Supercontig_2.22	100	16	0	0	0.054	32.2	<i>S. cerevisiae</i>	
mmu-miR-669f-3p*	Supercontig_2.3	95	20	1	0	0.054	32.2	<i>S. cerevisiae</i>	
mmu-miR-669f-3p*	Supercontig_2.4	100	16	0	0	0.054	32.2	<i>S. cerevisiae</i>	
mmu-miR-669f-3p*	Supercontig_2.4	100	18	0	0	0.003	36.2	<i>S. cerevisiae</i>	
mmu-miR-669f-3p*	Supercontig_2.7	100	16	0	0	0.054	32.2	<i>S. cerevisiae</i>	
mmu-miR-669f-3p*	Supercontig_2.9	100	16	0	0	0.054	32.2	<i>S. cerevisiae</i>	
mmu-miR-669f-3p*	Supercontig_2.9	100	16	0	0	0.054	32.2	<i>S. cerevisiae</i>	
mmu-miR-669f-5p	Supercontig_2.11	100	16	0	0	0.06	32.2	<i>S. cerevisiae</i>	
mmu-miR-669f-5p	Supercontig_2.2	100	17	0	0	0.015	34.2	<i>S. cerevisiae</i>	
mmu-miR-669f-5p	Supercontig_2.3	100	16	0	0	0.06	32.2	<i>S. cerevisiae</i>	
mmu-miR-669f-5p	Supercontig_2.3	100	16	0	0	0.06	32.2	<i>S. cerevisiae</i>	
mmu-miR-669f-5p	Supercontig_2.3	100	16	0	0	0.06	32.2	<i>S. cerevisiae</i>	
mmu-miR-669f-5p	Supercontig_2.3	100	16	0	0	0.06	32.2	<i>S. cerevisiae</i>	
mmu-miR-669f-5p	Supercontig_2.3	100	16	0	0	0.06	32.2	<i>S. cerevisiae</i>	
mmu-miR-669f-5p	Supercontig_2.3	100	17	0	0	0.015	34.2	<i>S. cerevisiae</i>	

Query id <sup>a</sup>	Subject id <sup>b</sup>	% Identity <sup>c</sup>	Alignment length <sup>d</sup>	Mismatches <sup>e</sup>	Gap opens <sup>f</sup>	Evalue <sup>g</sup>	Bit score <sup>h</sup>	Fungi vesicle <sup>i</sup>	Reference <sup>j</sup>
mmu-miR-669f-5p	Supercontig_2.3	100	17	0	0	0.015	34.2	<i>S. cerevisiae</i>	
mmu-miR-669f-5p	Supercontig_2.3	100	20	0	0	2.00E-04	40.1	<i>S. cerevisiae</i>	
mmu-miR-669f-5p	Supercontig_2.6	100	16	0	0	6.00E-02	32.2	<i>S. cerevisiae</i>	
mtr-miR5227	Supercontig_2.1	100	16	0	0	0.048	32.2	<i>C. albicans</i>	
oan-miR-1346	Supercontig_2.10	100	16	0	0	0.03	32.2	<i>C. neoformans</i>	
oan-miR-1351-3p*	Supercontig_2.1	100	16	0	0	0.042	32.2	<i>S. cerevisiae/C. albicans/C. neoformans</i>	
oan-miR-1418-5p	Supercontig_2.3	100	16	0	0	0.042	32.2	<i>C. neoformans</i>	
oan-miR-1420e-5p	Supercontig_2.3	100	17	0	0	0.014	34.2	<i>P. brasiliensis</i>	
oan-miR-1421n-2-5p	Supercontig_2.1	100	17	0	0	0.012	34.2	<i>P. brasiliensis</i>	
oan-miR-1422q-5p	Supercontig_2.7	100	16	0	0	0.048	32.2	<i>S. cerevisiae</i>	
osa-miR1438	Supercontig_2.1	100	16	0	0	4.80E-02	32.2	<i>C. albicans</i>	
osa-miR1438	Supercontig_2.1	100	16	0	0	4.80E-02	32.2	<i>C. albicans</i>	
osa-miR1438	Supercontig_2.5	100	16	0	0	4.80E-02	32.2	<i>C. albicans</i>	
osa-miR1438	Supercontig_2.9	100	16	0	0	4.80E-02	32.2	<i>C. albicans</i>	
osa-miR1438	Supercontig_2.9	100	17	0	0	0.012	34.2	<i>C. albicans</i>	
osa-miR156k	Supercontig_2.1	100	16	0	0	0.042	32.2	<i>S. cerevisiae</i>	
osa-miR156k	Supercontig_2.8	100	16	0	0	0.042	32.2	<i>S. cerevisiae</i>	
osa-miR2921	Supercontig_2.14	100	16	0	0	0.06	32.2	<i>C. neoformans</i>	
osa-miR2921	Supercontig_2.46	100	16	0	0	0.06	32.2	<i>C. neoformans</i>	
osa-miR399c	Supercontig_2.3	100	16	0	0	0.042	32.2	<i>C. neoformans</i>	
osa-miR5144-5p	Supercontig_2.17	100	16	0	0	0.042	32.2	<i>C. neoformans/S. cerevisiae</i>	
osa-miR821c	Supercontig_2.12	95	20	1	0	0.06	32.2	<i>P. brasiliensis</i>	
osa-miR821c	Supercontig_2.4	100	16	0	0	0.06	32.2	<i>P. brasiliensis</i>	
pab-miR482d	Supercontig_2.1	100	16	0	0	0.042	32.2	<i>S. cerevisiae</i>	
pma-miR-130e	Supercontig_2.3	100	16	0	0	0.054	32.2	<i>P. brasiliensis</i>	
pma-miR-20a-5p	Supercontig_2.3	100	17	0	0	0.014	34.2	<i>C. albicans/C. neoformans</i>	
ppt-miR1047-5p	Supercontig_2.10	100	16	0	0	0.042	32.2	<i>P. brasiliensis</i>	
ppy-miR-1228	Supercontig_2.7	100	16	0	0	0.036	32.2	<i>S. cerevisiae</i>	
rno-let-7e-3p*	Supercontig_2.2	100	16	0	0	0.048	32.2	<i>C. albicans/C. neoformans</i>	
rno-miR-483-5p	Supercontig_2.13	100	16	0	0	0.048	32.2	<i>C. neoformans</i>	
rno-miR-483-5p	Supercontig_2.2	100	16	0	0	0.048	32.2	<i>C. neoformans</i>	
rno-miR-483-5p	Supercontig_2.6	95.24	21	1	0	0.012	34.2	<i>C. neoformans</i>	
rno-miR-487b-5p	Supercontig_2.3	100	16	0	0	0.054	32.2	<i>S. cerevisiae</i>	
sbi-miR821e	Supercontig_2.4	100	18	0	0	0.003	36.2	<i>C. neoformans</i>	
sha-miR-23b	Supercontig_2.11	100	16	0	0	0.03	32.2	<i>C. albicans</i>	
sme-miR-2149-5p	Supercontig_2.2	100	16	0	0	0.042	32.2	<i>C. neoformans</i>	
smo-miR1097	Supercontig_2.2	100	16	0	0	0.042	32.2	<i>C. albicans</i>	
ssc-miR-664-5p	Supercontig_2.2	100	16	0	0	0.054	32.2	<i>P. brasiliensis</i>	
tgu-miR-200a-5p	Supercontig_2.26	95	20	1	0	0.042	32.2	<i>C. albicans/S. cerevisiae</i>	
tgu-miR-2976	Supercontig_2.11	100	16	0	0	0.042	32.2	<i>C. albicans/C. neoformans/ P. brasiliensis</i>	
vvi-miR3631c	Supercontig_2.7	100	17	0	0	0.012	34.2	<i>C. neoformans/S. cerevisiae</i>	
vvi-miR3631d	Supercontig_2.7	100	17	0	0	0.012	34.2	<i>S. cerevisiae/ P. brasiliensis</i>	

a) Identifier of the microRNAs;

b) Sequence;

c) Percent of the identity between the sequences;

d) Size of alignment between the sequences of microRNAs and the genome region of *P. brasiliensis* (Pb18);

e) Number of different bases between the aligned sequences;

f) Absence of complementary bases between the sequences;

g) Likelihood sequence analyzed to align randomly to other sequences in the database. false positive rate;

- h) Normalized score obtained using the following formula:  $S' = (I S - \ln K) / \ln 2$ ;
- i) Microorganism which microRNAs have been described;
- j) Article describing microRNAs in fungi vesicles; (\*) microRNA star.