

Table S4 Sequence identity between *P. farinosa* CBS 2001 and *P. sorbitophila* subgenomes

region	feature	chr_1*	position_1 \$	locus_1	Identity_1 to P. farinosa CBS2001 &	subgenome attribution for locus_1 £	chr_2*	position_2 \$	locus_2	Identity_2 to P. farinosa CBS2001 &	subgenome attribution for locus_2 £	accession number
heterozygous	gene	B	176663..177097	PIS00B02069g	93	Pe	A	168748..169182	PIS00A01892g	100	Py	FN994818
homozygous	gene	B	796873..797371	PIS00B09835g	94	Pe	A	789096..789594	PIS00A09768g	94	Pe	FN994814
homozygous	NUMT p1	B	992082..991685	PIS00B12453g- PIS00B12475g	73 (no NUMT)	Pe	A	983908..984305	PIS00A12386g- PIS00A12408g	73 (no NUMT)	Pe	JQ267632
heterozygous	gene	C	151119..151546	PIS00C01806g	92	Pe	D	158180..158610	PIS00D01895g	100	Py	FN994825
heterozygous	gene : Py-Pe exchange	C	383527..384113	PIS00C04512g	98-99	Py	D	391163..391749	PIS00D04623g	99-97	Py	JQ267644
homozygous	gene	C	868158..868568	PIS00C10474g	100	Py	D	875207..875617	PIS00D10541g	100	Py	FN994821
heterozygous	gene	E	99549..100005	PIS00E01214g	92	Pe	I	84142..84602	PIS00I01042g	100	Py	FN994836
heterozygous	gene	E	254393..254869	PIS00E02930g	93	Pe	F	361850..362326	PIS00F04339g	99	Py	FN994833
heterozygous	gene	E	1185601..1186066	PIS00E13534g	95	Pe	F	1289721..1290186	PIS00F14921g	100	Py	FN994829
heterozygous	gene	J	208409..208838	PIS00J02473g	93	Pe	F	211321..211750	PIS00F02513g	100	Py	FN994840
heterozygous	last gene in F/J syeny	J	283861..284508	PIS00J03419g	90	Pe	F	287111..287770	PIS00F03459g	100	Py	JQ267642
heterozygous	end of F/J syeny	J	285133..285342	PIS00J03419g	85	Pe	F	288395..288881		100	Py	JQ267639
heterozygous	begining of F/E syeny	E	181320..181550	PIS00E02050g- PIS00E02072g	91	Pe			PIS00F03459g- PIS00F03481g		Py	
heterozygous	last gene in I/E syeny	E	177149..177618	PIS00E02006g	91	Pe	I	161728..162198	PIS00I01856g	100	Py	JQ267640
heterozygous	end of I/E syeny	E	177685..177840	PIS00E02006g- PIS00E02028g	93	Pe	I	162265..162748		99	Py	JQ267643
heterozygous	begining of I/J syeny	J	305395..305708	PIS00J03661g	94	Pe			PIS00I01856g- PIS00I01878g		Py	
heterozygous	gene	J	516929..517387	PIS00J06081g	91	Pe	I	375063..375521	PIS00I04276g	100	Py	FN994853
heterozygous	gene	J	1521249..11521709	PIS00J18269g	93	Pe	I	1384553..1385013	PIS00I16508g	100	Py	FN994849
homozygous	gene	G	172080..172490	PIS00G02294g	100	Py	H	172080..172490	PIS00H02295g	100	Py	FN994846
homozygous	gene	G	301055..301682	PIS00G03856g	100	Py	H	301055..301682	PIS00H03857g	100	Py	JQ267635

homozygous	gene	G	301813..302440	PISOOG03856g	100	Py	H	301813..302440	PISOOH03857g	100	Py	JQ267641
homozygous	NUMTs p14-15	G	480960..481261	PISOOG06122g- PISOOG06144g	100	Py	H	480960..481261	PISOOH06123g- PISOOH06145g	100	Py	JQ267633
homozygous	Intergene	G	1083262..1084635	PISOOG13734g- PISOOG13712g	99	Py	H	1083262..1084635	PISOOH13735g- PISOOH13713g	99	Py	JQ267636
homozygous	gene	G	1236388..1236848	PISOOG15538g	100	Py	H	1236388..1236848	PISOOH15539g	100	Py	FN994843
homozygous	intergene	K	100922..101449	PISOOK01286g- PISOOK01264g	99	Py	L	100922..101449	PISOOLO1287g- PISOOLO1265g	99	Py	JQ267637
homozygous	gene	K	234563..234998	PISOOK02738g	100	Py	L	234563..234998	PISOOLO2739g	100	Py	FN994860
homozygous	intergene	K	1063363..1063459	PISOOK12528g- PISOOK12506g	100	Py	L	1063363..1063459	PISOOLO12529g- PISOOLO12507g	100	Py	**
homozygous	intergene	K	1063482..1063698	PISOOK12528g- PISOOK12550g	100	Py	L	1063482..1063698	PISOOLO12529g- PISOOLO12551g	100	Py	JQ267645
homozygous	gene	K	1749204..1749606	PISOOK21350g	100	Py	L	1749204..1749606	PISOOLO21351g	100	Py	FN556130
homozygous	intergene	K	1462003..1462275	PISOOK17830g- PISOOK17808g	100	Py	L	1462003..1462275	PISOOLO17831g- PISOOLO17809g	100	Py	JQ267638
heterozygous	gene	M	169354..169782	PISOOM02058g	96	Pe	N	188531..188959	PISOON02191g	99	Py	FN994867
heterozygous	NUMT p24	M	158164..158608	PISOOM01926g- PISOOM01924g	75	Pe	N	177405..177814	PISOON02059g- PISOON02037g	100	Py	JQ267634
heterozygous	gene	M	1827135..1827615	PISOOM21550g	95	Pe	N	1837559..1838039	PISOON21793g	100	Py	FN994863

The table indicates the position of selected markers in *P. sorbitophila* genome used in Mallet *et al.* (in preparation) for a taxonomical study of *P. farinosa* species (in blue) and used in these study (in black). These markers are present in two allelic versions (_1 and _2) either at a heterozygous or at a homozygous state (column "region"). They correspond to part of genes, intergenes or NUMTs (column "feature"). Position of each allele is indicated(*). These markers were used for PCR amplifications and sequencing in *P. farinosa* CBS 2001 using oligonucleotides that hybridized on both alleles. Identity between the obtained *P. farinosa* sequences and each allele of *P. sorbitophila* are indicated (\$). According to the sequence identities shared between *P. farinosa* and *P. sorbitophila* alleles, the belonging of each allele into one parental subgenome Py or Pe is proposed (E). These markers are plotted on Figure 1

**corresponding sequence : GATAATTATGATGTGTAATCGAACTGGAAATTCACAAATACTGCAATTTTTTCTACTCTTTTTTCCAAGACTTCTGGGCACAATG