

Figure S1. Schematic representation of the Douro demarcated region from where the indigenous *Hanseniaspora* strains had been recovered.



Figure S2. Karyotyping of *Hanseniaspora guilliermondii* UTAD222 and CBS625, based on PFGE, rendering clear five distinct chromosomal bands, one of them (at a molecular weight of about 1.1 Mb) being considered duplicated based on the higher intensity of the signal and also on a similar trait reported in other *H. guilliermondii* strains (Cadez et al., 2002). As a ladder the chromosomes of *Hansenula wingei* were used

Chr A H. guilliermondii UTAD222

Contigs from *H. guilliermondii* UTAD222

Contigs from *H. opuntiae* AWRI3578

Contigs from *H. uvarum* DSM2768 (the contigs are ordered according with the proposed structure for chromosome I)

Contigs from *H. uvarum* AWRI3580



Figure S3 (A). Proposed structure of *H. guilliermondii* **chromosome A.** The structure of this chromosome was proposed using as a basis the one defined for *H. uvarum* DSM2768 subsequently fine-tuned using whole genome-alignment between contig sequences of *H. guilliermondii* UTAD222, *H. opuntiae* AWRI3578 and *H. uvarum* (DSM2768 and AWRI3580 strains). The back lines indicate similar regions between the different strains.

Chr A H. guilliermondii UTAD222



Figure S3 (B). Pairwise alignments were performed using all predicted H. guilliermondii, H. uvarum AWRI3580 and H. opuntiae AWRI3578 proteins. Afterwards, the homologous Hg/Ho and Hg/Hu protein pairs were mapped in the contig organization suggested for chromosome A of Hg. The results obtained shows a contiguous positioning of Ho/Hg and Hg/Hu homologous protein pairs in this genomic showing a strong co-linearity in this chromosomal region of *H. guilliermondii*, *H. uvarum* and *H. opuntiae*. The junction between contig 103 and 111 in *H. guilliermondii* UTAD222 was experimentally confirmed by PCR (results not shown).

Chr B H. guilliermondii UTAD222

Contigs from *H. guilliermondii* UTAD222

- Contigs from *H. opuntiae* AWRI3578
- Contigs from *H. uvarum* DSM2768 (the contigs are ordered according with the proposed structure for chromosome II)
- Contigs from *H. uvarum* AWRI3580

Contigs from H. uvarum DSM2768 (these are contigs allocated to chromosomes other than chromosome II)



Figure S3 (A). Proposed structure of *H. guilliermondii* chromosome **B.** The structure of this chromosome was proposed using as a basis the one defined for *H. uvarum* DSM2768 subsequently fine-tuned using whole genome-alignment between contig sequences of *H. guilliermondii* UTAD222, *H. opuntiae* AWRI3578 and *H. uvarum* (DSM2768 and AWRI3580 strains). The back lines indicate similar regions between the different strains.



Figure S3 (B). Pairwise alignments were performed using all predicted H. guilliermondii, H. uvarum AWRI3580 and H. opuntiae AWRI3578 proteins. Afterwards, the homologous Hg/Ho and Hg/Hu protein pairs were mapped in the contig organization suggested for chromosome B of Hg. The results obtained shows a contiguous positioning of Ho/Hg and Hg/Hu homologous protein pairs suggesting a strong co-linearity in this chromosomal region of *H. guilliermondii*, *H. uvarum* and *H. opuntiae* strains. The junction between contigs 89/27 and 2/67 in *H. guilliermondii* UTAD222 were experimentally confirmed by PCR (results not shown).

Chr B H. guilliermondii UTAD222

Chr C H. guilliermondii UTAD222

Contigs from *H. guilliermondii* UTAD222

Contigs from *H. opuntiae* AWRI3578

Contigs from H. uvarum DSM2768 (the contigs are ordered according with the proposed structure for chromosome III)

Contigs from H. uvarum AWRI3580



Chr III H. uvarum DSM2768

Figure S3 (A). Proposed structure of *H. guilliermondii* **chromosome C.** The structure of this chromosome was proposed using as a basis the one defined for *H. uvarum* DSM2768 subsequently fine-tuned using whole genome-alignment between contig sequences of *H. guilliermondii* UTAD222, *H. opuntiae* AWRI3578 and *H. uvarum* (DSM2768 and AWRI3580 strains). The back lines indicate similar regions between the different strains. In this case it is evident a significant genomic alteration in the second block (indicated by the black triangle) since in Hg it is not detected a genomic portion present in Hu/Ho, this absent region being found in in chromosome F, as confirmed by PCR.

Chr C H. guilliermondii UTAD222 (Block1)



Chr C H. guilliermondii UTAD222 (Block 2)

AWRI3580_g611	AWRI3580_g612 AWRI3580 g639	AWRI3580_8640	AWRI3580_g644	AWRI3580_8040	AWRI3580_g653 AWRI3580_g654	AWRI3580_8655	AWRI3580_g672 AWRI3580_g673	AWRI3580694	AWRI3580694	AWRI3580	AWRI3580_g696	AWRI3580_g705 AWRI3580_g706	TH AWRI3580_g720	AWRI3580_g721	AWRI3580_g735 AWRI3580_g736	AWRI3580_g749	AWRI3580_8750	AWRI3580_g761	AWRI3580 g770	aiti AWRI3580_g772	A WRI3580_g811	AWRI3580_8812 AWRI3580_8818	AWRI3580_8819	AWRI3580_g870 AWRI3580_g871	AWRI35808878	X	AWRI3580 8965	AWRI3580_8975	AWRI3580_g1000	AWRI3580_g1000 AWRI3580_g1019	AWRI3580_g1020	AWKI3580_g1023 AWRI3580_g1024	AWRI3580_g1025	AWRI3580_g1026	AWKI3580_B1008 AWRI3580 81070	1	AWRI3580 g4053
HGUI_03946	HGUI_03941 HGUI_03628	HGUI_03891	HGUI_03895	HGUL_03940	HGUI_03916 HGUI_03923	HGUI_03297	HGUI_03313 HGUI_03026	- HGUI_03047	HGUI_04065	HGUI_04056	HGUI_03678	HGUI_03688 HGUI_03493		HGUI_03333	HGUI_03347 HGUI_03520	- HGUI_03507	HGUI_03449	HGUI_03437	HGUI 03881	HGUI_02179	HGUI_02218	HGUI_03896 HGUI_03902	HGUI_01707	HGUI_01652 HGUI_03800	HGUI_03807	HGIII 02727	HGUI 03723	HGUI_03095		HGUI_02923 HGUI_02904	HGUI_03982	HGUI_039/9 HGUI_04042	HGUI_04043	HGUI_01934		HGUI_03983	HGUI_03989
59	46	13	3	137	177	7	79	66	199	191	10	8	91	81	L	93	8	8	130	3	6	134	24	. 1	20		112	68	8	61	153	8 1	78	30	1	54	156
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AWRI3580_g3185	4WRI3580_g3184 4WRI3580_g3155	AWRI3580_g3154	AWRI3580_g3150	AWRI3580_g3141	AWRI3580_g3140 AWRI3580_g3139	AWRI3580_83138	4WRI3580_g3121 4WRI3580_g3120	4WRI3580_g3101	4WRI3580_g3101	4WRI3580_g3101	4WRI3580_g3100	AWRI3580_g3091 AWRI3580_g3090	AWRI3580_g3076	AWRI3580_g3075	AWRI3580_g3061 AWRI3580_g3060	4WRI3580_g3046	AWRI3580_g3045	AWRI3580_g3034	WR13580 23027	AWRI3580_g3025	AWRI3580_g2986	4WRI3580_g2985 4WRI3580_g2979	4WRI3580_g2978	AWRI3580_g2922	4WRI3580_g2914	4WRI3580_g2827	AWRI3580_g2818 AWRI3580_g2817	4WRI3580_g2793	4WRI3580_g2793	4WRI3580_g2774 4WRI3580_g2773	AWRI3580_g2769	AWR13580_827681	4WRI3580_g2767	4WRI3580_g2523			

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Figure S3 (B). Pairwise alignments were performed using all predicted H. guilliermondii, H. uvarum AWRI3580 and H. opuntiae AWRI3578 proteins. Afterwards, the homologous Hg/Ho and Hg/Hu protein pairs were mapped in the contig organization suggested for chromosome C of Hg. The results obtained shows a contiguous positioning of Ho/Hg and Hg/Hu homologous protein pairs suggesting a strong co-linearity in this chromosomal region of *H. guilliermondii*, *H. uvarum* and *H. opuntiae* strains. A break in co-linearity in the region that was found to be absent in Hg (indicated in the figure with a red X). The junction between contigs 66/99; 134/24 and 120/112 in *H. guilliermondii* UTAD222 were experimentally confirmed by PCR (results not shown).

Chr D H. guilliermondii UTAD222

Contigs from *H. guilliermondii* UTAD222

Contigs from *H. opuntiae* AWRI3578

Contigs from *H. uvarum* DSM2768 (the contigs are ordered according with the proposed structure for chromosome IV)

Contigs from *H. uvarum* AWRI3580



Chr IV H. uvarum DSM2768

Figure S3 (A). Proposed structure of *H. guilliermondii* **chromosome D.** The structure of this chromosome was proposed using as a basis the one defined for *H. uvarum* DSM2768 subsequently fine-tuned using whole genome-alignment between contig sequences of *H. guilliermondii* UTAD222, *H. opuntiae* AWRI3578 and *H. uvarum* (DSM2768 and AWRI3580 strains). The back lines indicate similar regions between the different strains.

AWRI3580_g1 AWRI3580_g3 AWRI3580_g32 AWRI3580_g33 AWRI3580_g42 AWRI3580_g43	AWRI3580_g113 AWRI3580_g114 AWRI3580_g150	AWRI3580_g151 AWRI3580_g157 AWRI3580_g158 AWRI3580_g165 AWRI3580_g166 AWRI3580_g166	AWRI3580_g169 AWRI3580_g198 AWRI3580_g199 AWRI3580_g240 AWRI3580_g241	AWRI3580_g356 AWRI3580_g357	AWRI3580_g378 AWRI3580_g379 AWRI3580_g399 AWRI3580_g400 AWRI3580_g432	AWRI3580_g433 AWRI3580_g437 AWRI3580_g437 AWRI3580_g438 AWRI3580_g446 AWRI3580_g495 AWRI3580_g496 AWRI3580_g496 AWRI3580_g546 AWRI3580_g530 AWRI3580_g546 AWRI3580_g546 AWRI3580_g546 AWRI3580_g546 AWRI3580_g546 AWRI3580_g546	AWRI3580_g592
			H. uvarum A	WRI358	30 contig 1		
HGUI_02288 HGUI_02319 HGUI_03597 HGUI_03607 HGUI_00802	HGUI_00733 HGUI_02108 HGUI_02145	HGUI_03830 HGUI_03836 HGUI_03858 HGUI_03851 HGUI_03961 HGUI_03959	HGUI_02648 HGUI_02677 HGUI_02020 HGUI_01979 HGUI_00001	HGUI_00105 HGUI_03206	HGUI_03228 HGUI_03159 HGUI_03182 HGUI_02709 HGUI_02678	HGUI_04054 HGUI_03964 HGUI_03965 HGUI_03969 HGUI_03972 HGUI_03972 HGUI_03789 HGUI_03789 HGUI_03789 HGUI_03789 HGUI_03789 HGUI_04057 HGUI_04057 HGUI_01758	HGUI_01803

	H. opuntiae AWRI3578 contig 2
AWRI3578_g715 AWRI3578_g715 AWRI3578_g683 AWRI3578_g673 AWRI3578_g672 AWRI3578_g599 AWRI3578_g599 AWRI3578_g599	AWRI3578_g551 AWRI3578_g553 AWRI3578_g552 AWRI3578_g542 AWRI3578_g542 AWRI3578_g542 AWRI3578_g513 AWRI3578_g513 AWRI3578_g513 AWRI3578_g3310 AWRI3578_g3310 AWRI3578_g3310 AWRI3578_g3310 AWRI3578_g3310 AWRI3578_g277 AWRI3578_g277 AWRI3578_g212 AWRI3578_g212 AWRI3578_g212 AWRI3578_g191 AWRI3578_g189 AWRI3578_g189 AWRI3578_g163 AWRI3578_g1

127 145 51

Figure S3 (B). Pairwise alignments were performed using all predicted H. guilliermondii, H. uvarum AWRI3580 and H. opuntiae AWRI3578 proteins. Afterwards, the homologous Hg/Ho and Hg/Hu protein pairs were mapped in the contig organization suggested for chromosome D of Hg. The results obtained shows a contiguous positioning of Ho/Hg and Hg/Hu homologous protein pairs suggesting a strong co-linearity in this chromosomal region of *H. guilliermondii*, *H. uvarum* and *H. opuntiae* strains. The junction between contigs 124/127 in *H. guilliermondii* UTAD222 was experimentally confirmed by PCR (results not shown).

Chr E H. guilliermondii UTAD222

Contigs from *H. guilliermondii* UTAD222

Contigs from *H. opuntiae* AWRI3578

Contigs from *H. uvarum* DSM2768 (the contigs are ordered according with the proposed structure for chromosome V)

Contigs from *H. uvarum* AWRI3580



Figure S3 (A). Proposed structure of *H. guilliermondii* chromosome E. The structure of this chromosome was proposed using as a basis the one defined for *H. uvarum* DSM2768 subsequently fine-tuned using whole genome-alignment between contig sequences of *H. guilliermondii* UTAD222, *H. opuntiae* AWRI3578 and *H. uvarum* (DSM2768 and AWRI3580 strains). The back lines indicate similar regions between the different strains.

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AWRI3578_82523	AWRI3578 g1428	AWRI3578_g1353	AWRI3578_g1352	AWRI3578_g1351 AWRI3578_g1297		AWRI3578_g1295	AWRI3578_g1199 AWRI3578_g1193	AWRI3578_g1192 AWRI3578_g1164	AWRI3578_g1163 AWRI3578_g1155	AWRI3578_g1154 AWRI3578_g1152	AWRI3578 g1137	AWRI3578_g1136	AWRI3578_g1072 AWRI3578_g1071	AWRI3578_g1034	AWRI3578_g1030 AWRI3578_g1015	AWRI3578_g1013 AWRI3578_g1003	AWRI3578_g1002 AWRI3578_933	AWRI3578_g932 AWRI3578_g932	AWRI3578_g923	AWRI3578_g852	AWRI3578_g823 AWRI3578_g822	AWRI3578_g796 AWRI3578_g795	AWKI3578_8787 AWRI3578_8787	AWRI3578_g765 AWRI3578_g763 AWRI3578_g763	AWRI3578_g760	AWR13578_g736	AWRI3578_g734 AWRI3578_g720	AWRI3578 g717

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Figure S3 (B). Pairwise alignments were performed using all predicted H. guilliermondii, H. uvarum AWRI3580 and H. opuntiae AWRI3578 proteins. Afterwards, the homologous Hg/Ho and Hg/Hu protein pairs were mapped in the contig organization suggested for chromosome E of Hg. The results obtained shows a contiguous positioning of Ho/Hg and Hg/Hu homologous protein pairs suggesting a strong co-linearity in this chromosomal region of *H. guilliermondii*, *H. uvarum* and *H. opuntiae* strains. Despite this, it was possible to identify a lack of co-linearity in part of contig 23, this being identified as a red X. The junction between contigs 23/294, 14/33, 118/10, 101/13 in *H. guilliermondii* UTAD222 was experimentally confirmed by PCR (results not shown).

Chr F H. guilliermondii UTAD222

Contigs from *H. guilliermondii* UTAD222

Contigs from *H. opuntiae* AWRI3578

Contigs from *H. uvarum* DSM2768 (the contigs are ordered according with the proposed structure for chromosome VI)

Contigs from H. uvarum DSM2768 (these are contigs allocated to chromosomes other than chromosome VI)

Contigs from *H. uvarum* AWRI3580



Figure S3 (A). Proposed structure of *H. guilliermondii* chromosome **F.** The structure of this chromosome was proposed using as a basis the one defined for *H. uvarum* DSM2768 subsequently fine-tuned using whole genome-alignment between contig sequences of *H. guilliermondii* UTAD222, *H. opuntiae* AWRI3578 and *H. uvarum* (DSM2768 and AWRI3580 strains). The back lines indicate similar regions between the different strains. In this chromosome were observed two significant genomic alteration comparing with the H. uvarum AWRI3580 and H. opuntiae AWRI3580 counter-partners since in the Hg chromosome it is detected a genomic portion present in Hg (in contig 5) that has homology with other Hu/Ho chromosomes (2 and 7, respectively). This apparent insertion is indicated with a black triangle. There is also a portion of Hu chr. 4 and Ho chr. 4 (between Hg contigs 75 and 80) that is absent in Hg. This part absent in Hg is indicated with a red X.

HGUI_03955 HGUI_03958	HGUI_02178 HGUI_02146	HGUI_01846 HGUI_01895	HGUI_03936 HGUI_03939	HGUI_03903	HGUI_01544 HGUI_01598	HGUI_04017 HGUI_04018	HGUI_00660 HGUI_00732	HGUI_03464 HGUI_03478	HGUI_03751 HGUI_03744	HGUI_04002	HGUI_04001 HGUI_02839	HGUI_02861 HGUI_02647	HGUI_02619 HGUI_04007	HGUI_04006 HGUI_03638	HGUI_03648	HGUI_01437 HGUI_01493	HGUI_00479	HGUI_00463	HGUI_00378	HGUI_03649 HGUI_03659	HGUI_03992 HGUI_03993	HGUI_03667 HGUI_03660	HGUI_02350 HGUI_02320	HGUI_04010 HGUI_04013	
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AWRI3580_g1993	AWRI3580_g1937	AWRI3580_g1936	AWRI3580_g1925 AWRI3580_g1924	AWRI3580_g1919	AWRI3580_g1918	AWRI3580_g1917	AWRI3580_g1908	AWRI3580_g1907	AWKI3580_81876 AWRI3580_81875	AWRI3580_g1787	AWRI3580_g1786	AWRI3580_g1775 AWRI3580_g1774	AWRI3580_g1773	AWRI3580_g1772	AWRI3580_g1755	AWRI3580_g1752	AWRI3580	AWRI3580_g1750	AWRI3580_g1745	AWRI3580_g1744		AWRI3580_g1706	AWRI3580_g1689	AWRI3580_g1688	AWRI3580_g1653 AWRI3580_g1652	Not detected	AWRI3580_g1628	AWRI3580_g1626	AWRI3580_g1625 AWRI3580_g1609	AWRI3580_g1607	AWRI3580_g1602	AWRI3580_g16U1	POCTS DOCCIANA	AWRI3580_g1581	AWRI3580_g1580 AWRI3580_g1578
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HGUI_01267	HGUI_01324	HGUI_03348	HGUI_03359 HGUI_03935	HGUI_03930	HGUI_04064	HGUI_03769	HGUI_03777	HGUI_02441	HGUI_024/3 HGUI_00572	HGUI_00659	HGUI_03404	HGUI_03418 HGUI_04008	HGUI_04009	HGUI_03278	HGUI_03296	HGUI_04067	HGUI_04066	HGUI_03808	HGUI_03813	HGUI_04070	_	HGUI_03314	HGUI_03332	HGUI_02387	HGUI_02351 HGUI_02531	HGUI_02556	HGUI_03975	HGUI_03973	HGUL_03142 HGUL_03158	HGUI_03929	HGUI_03924	HGUI_03245	CD7CD DD4	HGUI_04035	HGUI_03884 HGUI_03882
 1	7	82	1	39	198	11	17	44		7	86		164	7	8	203	202	12	21	206	×	8	o	41		47	15	0	71	13	38	76	17	74	131
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AWRI3578_g1902	AWRI3578_g1959	AWRI3578_g1960	AWRI3578_g1971 AWRI3578_g1972	AWRI3578_g1978	AWRI3578_g1979	AWRI3578_g1980	AWRI3578_g1988	AWRI3578_g1989	AWRI3578_g2021 AWRI3578_g2022	AWRI3578_g2111	AWRI3578_g2112	AWRI3578_g2126 AWRI3578_g2127	AWRI3578_g2128	AWRI3578_g2129	AWRI3578_g2146	AWRI3578_g2149	AWRI3578_g2150	AWRI3578_g2151	AWRI3578_g2156	AWRI3578_g2157		AWRI3578_g2195	AWRI3578_g2213	AWRI3578_g2214	AWRI3578_g2252 AWRI3578_g2253	AWRI3578_g2277	AWRI3578_g2278	AWRI3578_g2280	AWKI35/8_g2281 AWRI3578 97798	AWRI3578_82300	AWRI3578_82305	AWRI3578_g230b	47078_0/CCINWA	AWRI3578_g2326	AWRI3578_g2327 Not detected

Figure S3 (B). Pairwise alignments were performed using all predicted H. guilliermondii, H. uvarum AWRI3580 and H. opuntiae AWRI3578 proteins. Afterwards, the homologous Hg/Ho and Hg/Hu protein pairs were mapped in the contig organization suggested for chromosome F of Hg. The results obtained shows a contiguous positioning of Ho/Hg and Hg/Hu homologous protein pairs suggesting a strong co-linearity in this chromosomal region of *H. guilliermondii*, *H. uvarum* and *H. opuntiae* strains. Despite this, it was possible to identify a lack of co-linearity in part of contig 23, this being identified as a red X. The junction between contigs 23/294, 14/33, 118/10, 101/13 in *H. guilliermondii* UTAD222 was experimentally confirmed by PCR (results not shown).

Chr G H. guilliermondii UTAD222

Contigs from *H. guilliermondii* UTAD222

Contigs from *H. opuntiae* AWRI3578

Contigs from *H. uvarum* DSM2768 (the contigs are ordered according with the proposed structure for chromosome VII)

Contigs from *H. uvarum* DSM2768 (these are contigs allocated to chromosomes other than chromosome VII)

Contigs from H. uvarum AWRI3580



Figure S3 (A). Proposed structure of *H. guilliermondii* chromosome **G.** The structure of this chromosome was proposed using as a basis the one defined for *H. uvarum* DSM2768 subsequently fine-tuned using whole genome-alignment between contig sequences of *H. guilliermondii* UTAD222, *H. opuntiae* AWRI3578 and *H. uvarum* (DSM2768 and AWRI3580 strains). The back lines indicate similar regions between the different strains. In this Hg chromosome is observed an insertion (in contig 4) showing no similarity with Hu ctg 9 or Ho ctg 6 but identical to Hu ctg 4 and Ho ctg 4. This apparent insertion in the Hg chromosome is indicated with a black triangle. Junction between contig 132 and 4 in Hg UTAD222 was experimentally validated.

<u>AWRI3580 g3135</u>	AWR13580_g735 AWR13580_g2456 AWR13580_g2457 AWR13580_g2458 AWR13580_g3824	AWRI35803772 AWRI35803771 AWRI35803770	AWRI3580	AWRI35803702	AWRI3580_g3701 AWRI3580_g3699 AWRI3580_g3698	AWR135803667 AWR135803655 AWR135803653 AWR1358033652 AWR1358033644	AWRI3580_g3642 AWRI3580_g3641 AWRI3580_g3640 AWRI3580_g3631	
H. uv	<i>arum</i> AWRI3580 cont	ig 9		×				•••
HGUI_04053	HGUI_01383 HGUI_01382 HGUI_01381 HGUI_01380 HGUI_01379	HGUI_01325 HGUI_03990 HGUI_03991	HGUI_03890 HGUI_03885 HGUI_03885 HGUI_00288	HGUI_00344 HGUI_00345 HGUI_00377	HGUI_04051 HGUI_04049 HGUI_02286	HGUI_02255 HGUI_03494 HGUI_03506 HGUI_03529 HGUI_03521	HGUI_04059 HGUI_04060 HGUI_03560 HGUI_03548	
186	18	157 19	97 132	4	183 38	92 94	193 96	
Н. ор	ountiae AWRI3578 cor	ntig 6		×				•••
AWRI3578_g2523	AWRI3578_g2524 AWRI3578_g2525 AWRI3578_g2526 AWRI3578_g2527 AWRI3578_g2528	AWRI3578_g2582 AWRI3578_g2583 AWRI3578_g2584	AWRI3578	AWRI35782653	AWRI3578_g2654 AWRI3578_g2656 AWRI3578_g2658	AWRI3578_g2688 AWRI3578_g2690 AWRI3578_g2702 AWRI3578_g2703 AWRI3578_g2711	AWRI3578_g2713 AWRI3578_g2714 AWRI3578_g2715 AWRI3578_g2726	

06362 0536101010	••	:		• •	AMB13E90 21071
WRI3578 83643	•	125		•	AWR13580_510/1
WRI3578 g3644		1	HGUI 04045		AWRI3580 g290
WRI3578_83645		79	HGUI_04044		AWRI3580_g1077
WRI3578_g3646		205	HGUI_04069		AWRI3580_g1078
WRI3578_83647		7	HGUI_03141		AWRI3580_g1079
WRI3578_g3668		0	HGUI_03120		AWRI3580_g1100
WRI3578_g3669		42	HGUI_02410		AWRI3580_g1101
WRI3578_g3691		2	HGUI_02388		AWRI3580_g1123
WRI3578_g3694		10	HGUI_03699		AWRI3580_g1126
WRI3578_g3704		9	HGUI_03689		AWRI3580_g1135
WRI3578_g3705		43	HGUI_02440		AWRI3580_g1136
WRI3578		8	HGUI_02411		AWRI3580_g1162
WRI3578_g3734		64	HGUI_03005		AWRI3580_g1163
WRI3578_g3759		ŀ	HGUI_02980		AWRI3580_g1188
WRI3578_g3760		37	HGUI_02254		AWRI3580_g1189
WRI3578_g3792		7	HGUI_02219		AWRI3580_g1222
WRI3578_g3793		73	HGUI_03183		AWRI3580_g1223
WRI3578_g3815		3	HGUI_03205		AWRI3580_g1246
WRI3578_g3816		15	HGUI_03994		AWRI3580_g1247
WRI3578_g3819	ŀ	59	HGUI_03997		AWRI3580_g1250
WRI3578_g3820	1 . o	5	HGUI_02791	Н.	AWRI3580_g1251
WRI3578_g3844	pu	6	HGUI_02815	uva	AWRI3580_g1275
WRI3578_g3845	nti	11	HGUI_03768	aru	AWRI3580_g1276
WRI3578_ <u>8</u> 3853	ae	16	HGUI_03760	m l	AWRI3580_g1284
WRI3578_g3854	AW	11	HGUI_03733	w	AWRI3580_g1285
NRI3578_g3864	/RI3	13	HGUI_03743	RI3	AWRI3580_g1295
WRI3578_ g3865	357	16	HGUI_04014	58	AWRI3580_g1296
WRI3578_g3867	<mark>8 c</mark>	56	HGUI_04016	0 c	AWRI3580_g1298
NRI3578_g3869	on	1	HGUI_01384	ont	AWRI3580_g1299
WRI3578_g3920	tig 9	9	HGUI_01436	ig 3	AWRI3580_g1348
WRI3578_g3921	9	1	HGUI_00873	3	AWRI3580_g1349
WRI3578_g4000		1	HGUI_00951		AWRI3580_g1426
WRI3578		190	HGUI_04055		AWRI3580_g1427
WRI3578_g4003		1:	HGUI_03752		AWRI3580_g1428
NRI3578_g4011		15	HGUI_03759		AWRI3580_g1435
WRI3578_g4012		2!	HGUI_01756		AWRI3580_g1437
NRI3578 g4061		5	HGUI_01708		AWRI3580_g1483
WRI3578_ 84062		3	HGUI_02021		AWRI3580_g1484
NRI3578_g4112		2	HGUI_02069		AWRI3580_g1534
WRI3578_g4113		16	HGUI_04024		AWRI3580_g1535
WRI3578_g4115		9	HGUI_04026		AWRI3580_g1537
WRI3578_g4116		13	HGUI_03915		AWRI3580_g1538
WRI3578_g4121		86	HGUI_03910		AWRI3580_g1542
WRI3578_g4122		17	HGUI_04038		AWRI3580_g1543
WRI3578_g4123		5	HGUI_04036		AWRI3580_g1544
NRI3578_g4124		87	HGUI_03436		AWRI3580_g1545
WRI3578_g4139		,	HGUI_03419		AWRI3580_g1561
WRI3578_g4141		97	HGUI_03561		AWRI3580_g1562
WRI3578_g4156		7	HGUI_03576		AWRI3580 g1069
WRI3578_g4157		14	HGUI_03962		<u>AWRI3580 g1069</u>
WRI3578_g4176		6	HGUI_03963		AWRI3580 g4053

Figure S3 (B). Pairwise alignments were performed using all predicted H. guilliermondii, H. uvarum AWRI3580 and H. opuntiae AWRI3578 proteins. Afterwards, the homologous Hg/Ho and Hg/Hu protein pairs were mapped in the contig organization suggested for chromosome G of Hg. The results obtained shows (with the exception of two regions highlighted in red) a contiguous positioning of Ho/Hg and Hg/Hu homologous protein pairs suggesting a strong co-linearity in this chromosomal region of *H. guilliermondii*, *H. uvarum* and *H. opuntiae* strains. The junction between contigs 18/157, 132/4, 92/94 in *H. guilliermondii* UTAD222 was experimentally confirmed by PCR (results not shown).



Figure S4. Metabolic reconstruction of *H. guilliermondii* focused on carbon metabolism, as unveiled by KEGG Koala metabolic reconstruction tool



Figure S5. Metabolic reconstruction of *H. guilliermondii* focused on nitrogen and sulphur metabolism, as unveiled by KEGG Koala metabolic reconstruction tool



Supplementary figure S6. (left) Growth of *H. guilliermondii* UTAD222 in rich (YP) or in mineral (MMB) medium having different sugars as the sole sources of carbon and energy; (right) Growth of *H. guilliermondii* UTAD222, at 25°C and 180 rpm, in rich YP medium having 10% glucose and 10% fructose as the sole carbon source



Supplementary figure S7. Comparison of the proteomes of *H. guilliermondii* UTAD222 with the one of *H. uvarum* AWRI3580 and *H. opuntiae* AWRI3578. The graph shows the number of proteins considered highly similar(associated e-value of the alignment lower than 1×10^{-50} and an identity above 50%), similar (e-value between 1×10^{-50} and 1×10^{-20} and/or an identity value below 50%) or dissimilar (e-value equal or above 1×10^{-20}). On top of the columns it is indicated the number of pairwise alignment (Hg vs other species) considered