

**Table S4. GO enrichment between different samples (p-value  $\leq$  0.05).****GO enrichment LM1/HM-UP and LM1/HM-DOWN**

<b>ID</b>	<b>Description</b>	<b>ONTOLOGY</b>	<b>GeneRatio</b>	<b>p-value</b>	<b>FDR</b>
GO:0016705	oxidoreductase activity	MF	35/220	9.92291E-15	1.19564E-12
GO:0020037	heme binding	MF	35/220	2.64153E-14	1.19564E-12
GO:0046906	tetrapyrrole binding	MF	35/220	2.64153E-14	1.19564E-12
GO:0004497	monooxygenase activity	MF	30/220	1.28384E-13	3.97316E-12
GO:0005506	iron ion binding	MF	33/220	1.46298E-13	3.97316E-12
GO:0048037	cofactor binding	MF	53/220	1.14396E-10	2.58897E-09
GO:0046914	transition metal ion binding	MF	43/220	3.02542E-07	5.86887E-06
GO:0004601	peroxidase activity	MF	8/220	1.25308E-05	0.000212694
GO:0016684	oxidoreductase activity, acting on peroxide as acceptor	MF	8/220	3.17983E-05	0.000479764
GO:0016831	carboxy-lyase activity	MF	10/230	1.3104E-07	2.31734E-05
GO:0016830	carbon-carbon lyase activity	MF	11/230	1.34758E-06	0.000119154
GO:0005975	carbohydrate metabolic process	BP	33/126	3.61855E-08	1.00558E-05
GO:0016051	carbohydrate biosynthetic process	BP	9/126	1.93344E-07	2.68646E-05

**GO enrichment in LM2/HHK-UP and LM2/HHK-DOWN**

GO:0017062	respiratory chain complex III assembly	BP	6/109	6.07505E-07	9.27244E-05
GO:0034551	mitochondrial respiratory chain complex III assembly	BP	6/109	6.07505E-07	9.27244E-05
GO:0006259	DNA metabolic process	BP	25/108	2.97058E-08	8.41142E-06
GO:0006260	DNA replication	BP	12/108	4.79964E-07	6.79528E-05
GO:0045786	negative regulation of cell cycle	BP	9/108	1.49856E-06	0.000141443
GO:0000075	cell cycle checkpoint	BP	7/108	2.56234E-06	0.000181387
GO:0000819	sister chromatid segregation	BP	9/108	3.53282E-06	0.000200069
GO:0007059	chromosome segregation	BP	10/108	5.5524E-06	0.000259299
GO:0005975	carbohydrate metabolic process	BP	26/108	6.41019E-06	0.000259299
GO:0007049	cell cycle	BP	16/108	8.25582E-06	0.000292212
GO:0022402	cell cycle process	BP	14/108	9.36165E-06	0.000294536
GO:0098813	nuclear chromosome segregation	BP	9/108	1.87495E-05	0.000530907
GO:0051726	regulation of cell cycle	BP	10/108	2.18667E-05	0.000562885
GO:0005618	cell wall	CC	12/215	7.45878E-07	2.39466E-05

GO:0030312	external encapsulating structure	CC	12/215	7.45878E-07	2.39466E-05
GO:0009277	fungal-type cell wall	CC	11/215	1.25152E-06	2.67869E-05
GO:0048037	cofactor binding	MF	61/257	7.48978E-12	1.15106E-09
GO:0005506	iron ion binding	MF	28/257	2.55923E-08	1.0046E-06
GO:0020037	heme binding	MF	29/257	2.61471E-08	1.0046E-06
GO:0046906	tetrapyrrole binding	MF	29/257	2.61471E-08	1.0046E-06
GO:0016705	oxidoreductase activity	MF	28/257	5.1743E-08	1.59042E-06
GO:0004497	monooxygenase activity	MF	24/257	1.21543E-07	3.11321E-06
GO:0050660	flavin adenine dinucleotide binding	MF	22/257	1.8604E-07	4.08449E-06
GO:0050662	coenzyme binding	MF	32/257	1.3018E-06	2.50083E-05
GO:0016614	oxidoreductase activity, acting on CH-OH group of donors	MF	19/257	3.65237E-06	6.2368E-05
GO:0005199	structural constituent of cell wall	MF	11/235	4.75879E-07	7.31351E-05

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