Table S1. Results for the site-model approach (PAML package) for each POG localized in non-mating-type chromosomes (non-MATs) (A), mating-type chromosome non-recombining regions (NRRs) (B) or mating-type chromosome recombining regions (MATRRs) (C). Statistics (likelihood ratio test) testing the selective model against the neutral model at the scale of a POG. When a selective scenario was found more likely than a neutral one, positive selection has been tested per site using BEB statistics. The total number of site inferred under positive selection in the full POG is given. Details on these sites (i.e., position and nature) are indicated in the next three columns which indicate the sites under significant positive selection, at the 5% , 1% column and 0.1% levels , respectively. In red are highlighted the POGs significantly supporting a selective scenario and displaying at least one site inferred to evolve under positive selection. D: summary , where the proportions of POGs displaying signatures of positive selection are compared between genomic compartments.

A

Locus	lnL_Model_1a	lnL_Model_2a	Delta 2*(lnL2 - lnL1)	p_value	Significance	BEB nb	[BEB 3*]	[BEB 2*]	[BEB 1*]	Annotation_Broad	Annotation_ID	Annotation_Name
Supercontig_1.50_MVLG_04468_9sp	-503,86002	-483,07384	41,5724	1	***	28	[]	['5M', '7A', '9F', '15T', '20S', '29L', '31P', '36I', '39I', '41N', '42L', '43P', '44I', '45P', '48N', '49L', '54Y', '55P']	['10E', '16P', '23P', '24N', '28P', '30P', '34P', '35P', '52F', '53L']	hypothetical protein	NA	NA
Supercontig_1.33_MVLG_03478_11sp	-1237,3816	-1223,05	28,6632	1	***	6	[]	['22G', '97G']	['50D', '52A', '125D', '127A']	hypothetical protein	PF00168.23	C2(C2 domain)
Supercontig_1.296_MVLG_07235_9sp	-972,99166	-957,22363	31,5361	1	***	6	[]	['31R', '131P', '139L']	['41K', '104A', '138S']	hypothetical protein	NA	NA
Supercontig_1.6_MVLG_01067_12sp	-464,18671	-458,78645	10,8005	0,99548	***	6	[]	['38T']	['2K', '5N', '16G', '52A', '54S']	hypothetical protein	PF04882.5	Peroxin-3(Peroxin-3)
Supercontig_1.713_MVLG_07301_10sp	-567,94536	-552,20972	31,4713	1	***	6	[]	['7N', '31W', '36V', '37P', '39N']	['47L']	hypothetical protein	NA	NA
Supercontig_1.28_MVLG_03199_10sp	-502,93295	-493,35526	19,1554	0,99993	***	5	[]	['11L', '35A', '38P']	['21V', '23R']	hypothetical protein	NA	NA
Supercontig_1.24_MVLG_02872_6sp	-521,31485	-512,4641	17,7015	0,99986	***	5	[]	['19N', '39T']	['3A', '10Y', '11I']	hypothetical protein	PF00026.16	Asp(Eukaryotic aspartyl protease)
Supercontig_1.116_MVLG_06380_12sp	-1331,5645	-1309,1119	44,9053	1	***	5	[]	['19R', '38R', '105E', '107P', '118L']	[]	hypothetical protein	NA	NA
Supercontig_1.24_MVLG_02865_10sp	-787,04885	-774,92944	24,2388	0,99999	***	4	[]	['35S', '46Y']	['60K', '61L']	hypothetical protein	NA	NA
Supercontig_1.21_MVLG_02646_8sp	-718,78491	-707,40486	22,7601	0,99999	***	4	[]	['44L', '45D']	['48V', '81R']	hypothetical protein	NA	NA
Supercontig_1.154_MVLG_06808_7sp	-2182,7735	-2175,2254	15,0962	0,99947	***	4	[]	[]	['25H', '139A', '176H', '290A']	hypothetical protein	PF07250.4	Glyoxal_oxid_N(Glyoxal oxidase N-terminus)
Supercontig_1.80_MVLG_05664_7sp	-667,63315	-661,31397	12,6384	0,9982	***	4	[]	[]	['28T', '31S', '40Q', '45N']	hypothetical protein	PF00026.16	Asp(Eukaryotic aspartyl protease)
Supercontig_1.12_MVLG_01848_10sp	-609,86527	-600,13188	19,4668	0,99994	***	3	[]	['18P']	['34H', '35S']	hypothetical protein	NA	NA
Supercontig_1.3_MVLG_00566_6sp	-428,08467	-417,14054	21,8883	0,99998	***	3	[]	['37G', '45K', '57E']	[]	hypothetical protein	NA	NA
Supercontig_1.31_MVLG_03333_7sp	-567,28082	-554,3271	25,9074	1	***	3	[]	['3L', '9L', '36A']	[]	hypothetical protein	PF00538.12	Linker_histone(linker histone H1 and H5 family)
Supercontig_1.10_MVLG_01635_7sp	-1289,4255	-1277,9	23,0509	0,99999	***	3	[]	['43D']	['81A', '83T']	hypothetical protein	NA	NA

Supercontig_1.126_MVLG_06525_10sp	-556,6503	-544,92947	23,4417	0,99999	*******	**3**	**[]**	**['4S', '15H']**	**['26R']**	hypothetical protein	NA	NA
Supercontig_1.113_MVLG_06337_10sp	-1419,7298	-1408,6681	22,1233	0,99998	*******	**3**	**[]**	**[]**	**['45L', '88G', '166L']**	hypothetical protein	NA	NA
Supercontig_1.222_MVLG_07164_6sp	-455,10806	-447,83449	14,5471	0,99931	*******	**3**	**[]**	**[]**	**['8D', '41S', '45N']**	hypothetical protein	NA	NA
Supercontig_1.1_MVLG_00256_9sp	-1036,0069	-1028,7522	14,5093	0,99929	*******	**2**	**[]**	**['121I']**	**['76G']**	hypothetical protein	PF01470.10	Peptidase_C15(Pyroglutamyl peptidase)
Supercontig_1.63_MVLG_05046_9sp	-1108,8088	-1101,8946	13,8284	0,99901	*******	**2**	**[]**	**['127A']**	**['54S']**	hypothetical protein	NA	NA
Supercontig_1.86_MVLG_05819_9sp	-1237,8036	-1228,0393	19,5287	0,99994	*******	**2**	**[]**	**['128R']**	**['13A']**	hypothetical protein	NA	NA
Supercontig_1.23_MVLG_02763_7sp	-1781,11	-1770,9045	20,4108	0,99996	*******	**2**	**[]**	**['156H']**	**['93Q']**	hypothetical protein	PF00082.15	Peptidase_S8(Subtilase family)
Supercontig_1.27_MVLG_03067_10sp	-471,29701	-459,90025	22,7935	0,99999	*******	**2**	**[]**	**['19R', '24Q']**	**[]**	hypothetical protein	PF01697.20	DUF23(Domain of unknown function)
Supercontig_1.8_MVLG_01421_12sp	-543,984	-536,57678	14,8144	0,99939	*******	**2**	**[]**	**['23G', '64G']**	**[]**	hypothetical protein	NA	NA
Supercontig_1.11_MVLG_01720_10sp	-567,63938	-561,5962	12,0864	0,99763	*******	**2**	**[]**	**['23Q']**	**['62S']**	hypothetical protein	PF05303.5	DUF727(Protein of unknown function (DUF727))
Supercontig_1.31_MVLG_03375_9sp	-712,23177	-706,80046	10,8626	0,99562	*******	**2**	**[]**	**['24P']**	**['53A']**	hypothetical protein	NA	NA
Supercontig_1.16_MVLG_02224_6sp	-422,64083	-416,37793	12,5258	0,99809	*******	**2**	**[]**	**['24T']**	**['3G']**	hypothetical protein	NA	NA
Supercontig_1.16_MVLG_02165_11sp	-476,39008	-469,38551	14,0091	0,99909	*******	**2**	**[]**	**['26S']**	**['24D']**	hypothetical protein	NA	NA
Supercontig_1.45_MVLG_04219_8sp	-500,70726	-490,01178	21,391	0,99998	*******	**2**	**[]**	**['27L']**	**['7R']**	hypothetical protein	PF00645.11	zf-PARP(Poly(ADP-ribose) polymerase and DNA-Ligase Zn-finger region)
Supercontig_1.48_MVLG_04359_8sp	-838,51942	-831,68815	13,6625	0,99892	*******	**2**	**[]**	**['27N']**	**['49Q']**	hypothetical protein	NA	NA
Supercontig_1.1_MVLG_00121_10sp	-1608,3178	-1601,317	14,0016	0,99909	*******	**2**	**[]**	**['28N', '136N']**	**[]**	hypothetical protein	NA	NA
Supercontig_1.6_MVLG_01163_10sp	-697,19766	-689,58769	15,2199	0,9995	*******	**2**	**[]**	**['29M', '37K']**	**[]**	hypothetical protein	PF01062.14	Bestrophin(Bestrophin)
Supercontig_1.48_MVLG_04353_8sp	-759,43871	-750,47602	17,9254	0,99987	*******	**2**	**[]**	**['38A']**	**['35Q']**	hypothetical protein	PF07519.4	Tannase(Tannase and feruloyl esterase)
Supercontig_1.2_MVLG_00321_10sp	-911,3591	-897,1227	28,4728	1	*******	**2**	**[]**	**['40Q', '98Q']**	**[]**	hypothetical protein	NA	NA
Supercontig_1.2_MVLG_00414_10sp	-362,11244	-356,5583	11,1083	0,99613	*******	**2**	**[]**	**['48P']**	**['49G']**	hypothetical protein	PF00150.11	Cellulase(Cellulase (glycosyl hydrolase family 5))
Supercontig_1.91_MVLG_05932_10sp	-533,37286	-523,15492	20,4359	0,99996	*******	**2**	**[]**	**['52K', '58A']**	**[]**	hypothetical protein	PF01184.12	Grp1_Fun34_YaaH(GPR1/FUN34/yaaH family)
Supercontig_1.13_MVLG_01896_10sp	-1144,3283	-1136,4869	15,6829	0,99961	*******	**2**	**[]**	**['55D', '61A']**	**[]**	hypothetical protein	TIGR00756	TIGR00756(PPR: pentatricopeptide repeat domain)
Supercontig_1.88_MVLG_05893_7sp	-1001,0235	-992,91269	16,2216	0,9997	*******	**2**	**[]**	**['64D', '66G']**	**[]**	hypothetical protein	PF04046.9	PSP(PSP)
Supercontig_1.24_MVLG_02869_7sp	-563,38873	-554,44728	17,8829	0,99987	*******	**2**	**[]**	**['7S', '56L']**	**[]**	hypothetical protein	NA	NA
Supercontig_1.47_MVLG_04349_10sp	-739,62609	-733,1459	12,9604	0,99847	*******	**2**	**[]**	**['80T']**	**['73L']**	hypothetical protein	NA	NA

Supercontig_1.86_MVLG_05837_8sp	-1543,0008	-1536,3584	13,2848	0,9987	***	**2**	[]	**['87E']**	**['69G']**	hypothetical protein	PF00097.18	zf-C3HC4(Zinc finger, C3HC4 type (RING finger))
Supercontig_1.203_MVLG_07099_7sp	-795,42931	-790,1982	10,4622	0,99465	***	**2**	[]	**['89S']**	**['54I']**	hypothetical protein	NA	NA
Supercontig_1.11_MVLG_01694_11sp	-569,48294	-563,60609	11,7537	0,9972	***	**2**	[]	**['8S', '44S']**	**[]**	hypothetical protein	PF03215.8	Rad17(Rad17 cell cycle checkpoint protein)
Supercontig_1.122_MVLG_06457_7sp	-815,60259	-807,98372	15,2377	0,99951	***	**2**	[]	**['8T']**	**['39K']**	hypothetical protein	PF01585.16	G-patch(G-patch domain)
Supercontig_1.16_MVLG_02208_6sp	-441,70311	-435,49625	12,4137	0,99798	***	**2**	[]	[]	**['12K', '35N']**	hypothetical protein	NA	NA
Supercontig_1.113_MVLG_06351_8sp	-479,6288	-472,72927	13,7991	0,99899	***	**2**	[]	[]	**['15R', '52R']**	hypothetical protein	PF09649.3	CHZ(Histone chaperone domain CHZ)
Supercontig_1.81_MVLG_05673_10sp	-1033,2766	-1027,9189	10,7154	0,99529	***	**2**	[]	[]	**['15T', '78T']**	hypothetical protein	PF07818.6	HCNGP(HCNGP-like protein)
Supercontig_1.7_MVLG_01314_8sp	-2247,7552	-2242,1514	11,2076	0,99632	***	**2**	[]	[]	**['164R', '329R']**	hypothetical protein	PF00097.18	zf-C3HC4(Zinc finger, C3HC4 type (RING finger))
Supercontig_1.1_MVLG_00012_10sp	-623,41063	-616,60196	13,6173	0,9989	***	**2**	[]	[]	**['17E', '52E']**	hypothetical protein	PF01067.15	Calpain_III(Calpain large subunit, domain III)
Supercontig_1.1_MVLG_00096_10sp	-875,1454	-868,82971	12,6314	0,99819	***	**2**	[]	[]	**['20P', '50P']**	hypothetical protein	PF00076.15	RRM_1(RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain))
Supercontig_1.4_MVLG_00718_11sp	-1086,2726	-1080,7421	11,0609	0,99604	***	**2**	[]	[]	**['31A', '106A']**	hypothetical protein	PF01553.14	Acyltransferase(Acyltransferase)
Supercontig_1.80_MVLG_05641_9sp	-840,86729	-834,69986	12,3349	0,9979	***	**2**	[]	[]	**['32P', '111S']**	hypothetical protein	PF03492.8	Methyltransf_7(SAM dependent carboxyl methyltransferase)
Supercontig_1.44_MVLG_04150_6sp	-882,46362	-873,60817	17,7109	0,99986	***	**2**	[]	[]	**['3Q', '38T']**	hypothetical protein	NA	NA
Supercontig_1.31_MVLG_03368_6sp	-490,41947	-485,24056	10,3578	0,99437	***	**2**	[]	[]	**['45A', '51L']**	hypothetical protein	NA	NA
Supercontig_1.110_MVLG_06292_11sp	-797,45318	-792,28741	10,3315	0,99429	***	**2**	[]	[]	**['45F', '104F']**	hypothetical protein	PF00083.17	Sugar_tr(Sugar (and other) transporter)
Supercontig_1.85_MVLG_05804_10sp	-553,78109	-548,19844	11,1653	0,99624	***	**2**	[]	[]	**['47A', '50K']**	hypothetical protein	NA	NA
Supercontig_1.66_MVLG_05181_10sp	-1404,5814	-1398,4932	12,1763	0,99773	***	**2**	[]	[]	**['57R', '148R']**	hypothetical protein	PF01068.14	DNA_ligase_A_M(ATP dependent DNA ligase domain)
Supercontig_1.54_MVLG_04666_6sp	-904,01692	-897,47464	13,0846	0,99856	***	**2**	[]	[]	**['61T', '79E']**	hypothetical protein	NA	NA
Supercontig_1.22_MVLG_02726_10sp	-1521,8744	-1516,4297	10,8895	0,99568	***	**2**	[]	[]	**['69A', '160A']**	hypothetical protein	PF03330.11	DPBB_1(Rare lipoprotein A (RlpA)-like double-psi beta-barrel)
Supercontig_1.15_MVLG_02117_10sp	-557,87212	-550,85371	14,0368	0,9991	***	**2**	[]	[]	**['6S', '13S']**	60S ribosomal protein L27-B	PF01777.11	Ribosomal_L27e(Ribosomal L27e protein family)
Supercontig_1.18_MVLG_02415_9sp	-983,30943	-977,71337	11,1921	0,99629	***	**1**	[]	**['111Q']**	[]	hypothetical protein	PF12621.1	DUF3779(Phosphate metabolism protein)
Supercontig_1.21_MVLG_02680_7sp	-803,1166	-798,37008	9,49304	0,99132	***	**1**	[]	**['115V']**	[]	hypothetical protein	NA	NA
Supercontig_1.30_MVLG_03285_12sp	-548,64727	-543,8411	9,61234	0,99182	***	**1**	[]	**['11I']**	[]	hypothetical protein	PF00632.18	HECT(HECT-domain (ubiquitin-transferase))

Supercontig_1.28_MVLG_03161_11sp	-616,57859	-608,34343	16,4703	0,99973	***	1	[]	['11L']	[]	hypothetical protein	TIGR00727	TIGR00727(ISP4_OPT: small oligopeptide transporter, OPT family)
Supercontig_1.100_MVLG_06138_10sp	-1273,9688	-1267,2683	13,4011	0,99877	***	1	[]	['129R']	[]	hypothetical protein	NA	NA
Supercontig_1.78_MVLG_05599_7sp	-933,88771	-928,5134	10,7486	0,99537	***	1	[]	['131N']	[]	hypothetical protein	PF00560.26	LRR_1(Leucine Rich Repeat)
Supercontig_1.48_MVLG_04396_8sp	-842,35101	-836,43316	11,8357	0,99731	***	1	[]	['13R']	[]	hypothetical protein	PF03571.8	Peptidase_M49(Peptidase family M49)
Supercontig_1.9_MVLG_01501_11sp	-434,32209	-428,97769	10,6888	0,99523	***	1	[]	['15A']	[]	hypothetical protein	PF00916.13	Sulfate_transp(Sulfate transporter family)
Supercontig_1.13_MVLG_01931_8sp	-918,54231	-913,17342	10,7378	0,99534	***	1	[]	['15G']	[]	hypothetical protein	TIGR00229	TIGR00229(sensory_box: PAS domain S-box protein)
Supercontig_1.78_MVLG_05592_11sp	-660,68565	-655,58787	10,1956	0,99389	***	1	[]	['17S']	[]	hypothetical protein	PF03151.9	TPT(Triose-phosphate Transporter family)
Supercontig_1.20_MVLG_02576_6sp	-1165,4458	-1156,5994	17,6928	0,99986	***	1	[]	['185C']	[]	hypothetical protein	PF00096.19	zf-C2H2(Zinc finger, C2H2 type)
Supercontig_1.9_MVLG_01499_8sp	-786,31682	-777,97072	16,6922	0,99976	***	1	[]	['21T']	[]	hypothetical protein	PF00294.17	PfkB(pfkB family carbohydrate kinase)
Supercontig_1.16_MVLG_02246_10sp	-678,52408	-672,42242	12,2033	0,99776	***	1	[]	['22N']	[]	hypothetical protein	PF00797.10	Acetyltransf_2(N-acetyltransferase)
Supercontig_1.19_MVLG_02508_10sp	-581,88374	-576,90843	9,95062	0,99309	***	1	[]	['24A']	[]	hypothetical protein	TIGR00907	TIGR00907(2A0304: amino acid permease)
Supercontig_1.80_MVLG_05662_10sp	-752,62949	-744,2871	16,6848	0,99976	***	1	[]	['27Q']	[]	hypothetical protein	PF00172.11	Zn_clus(Fungal Zn(2)-Cys(6) binuclear cluster domain)
Supercontig_1.48_MVLG_04366_12sp	-559,7212	-554,18963	11,0631	0,99604	***	1	[]	['30P']	[]	hypothetical protein	PF05577.5	Peptidase_S28(Serine carboxypeptidase S28)
Supercontig_1.48_MVLG_04368_12sp	-495,63218	-488,7388	13,7868	0,99899	***	1	[]	['32K']	[]	hypothetical protein	PF01161.13	PBP(Phosphatidylethanolamine-binding protein)
Supercontig_1.22_MVLG_02685_9sp	-692,19596	-686,34144	11,709	0,99713	***	1	[]	['37N']	[]	hypothetical protein	PF00172.11	Zn_clus(Fungal Zn(2)-Cys(6) binuclear cluster domain)
Supercontig_1.150_MVLG_06779_9sp	-439,08155	-431,66156	14,84	0,9994	***	1	[]	['3T']	[]	hypothetical protein	PF09597.3	IGR(IGR protein motif)
Supercontig_1.82_MVLG_05724_8sp	-488,08031	-483,41493	9,33076	0,99058	***	1	[]	['40V']	[]	hypothetical protein	PF08240.5	ADH_N(Alcohol dehydrogenase GroES-like domain)
Supercontig_1.1_MVLG_00044_9sp	-397,71628	-392,98845	9,45566	0,99115	***	1	[]	['43E']	[]	methylenetetrahydrofolate dehydrogenase (NAD+)	PF02882.12	THF_DHG_CYH_C(Tetrahydrofolate dehydrogenase/cyclohydrolase, NAD(P)-binding domain)
Supercontig_1.6_MVLG_01214_6sp	-506,0491	-500,8738	10,3506	0,99435	***	1	[]	['44I']	[]	hypothetical protein	PF10263.2	SprT-like(SprT-like family)
Supercontig_1.95_MVLG_06022_12sp	-497,05429	-491,8084	10,4918	0,99473	***	1	[]	['46L']	[]	hypothetical protein	PF00225.16	Kinesin(Kinesin motor domain)
Supercontig_1.33_MVLG_03452_8sp	-424,52833	-419,10506	10,8465	0,99559	***	1	[]	['46T']	[]	hypothetical protein	PF01494.12	FAD_binding_3(FAD binding domain)
Supercontig_1.20_MVLG_02572_11sp	-745,25338	-740,22731	10,0521	0,99344	***	1	[]	['47V']	[]	hypothetical protein	PF01266.17	DAO(FAD dependent oxidoreductase)
Supercontig_1.33_MVLG_03470_6sp	-523,44274	-515,20442	16,4766	0,99974	***	1	[]	['4K']	[]	hypothetical protein	NA	NA
Supercontig_1.27_MVLG_03084_7sp	-628,3948	-623,64656	9,49648	0,99133	***	1	[]	['51K']	[]	histone H2B	PF00125.17	Histone(Core histone H2A/H2B/H3/H4)

Supercontig_1.40_MVLG_03952_9sp	-398,42057	-392,3833	12,0745	0,99761	***	1	[]	['52S']	[]	hypothetical protein	NA	NA
Supercontig_1.7_MVLG_01234_9sp	-444,04324	-438,86222	10,362	0,99438	***	1	[]	['53R']	[]	hypothetical protein	PF10294.2	Methyltransf_16(Putative methyltransferase)
Supercontig_1.1_MVLG_00170_9sp	-558,21584	-550,4912	15,4493	0,99956	***	1	[]	['56G']	[]	ATP-dependent RNA helicase DED1	PF00270.22	DEAD(DEAD/DEAH box helicase)
Supercontig_1.61_MVLG_04964_8sp	-506,06201	-500,51712	11,0898	0,99609	***	1	[]	['64T']	[]	hypothetical protein	NA	NA
Supercontig_1.112_MVLG_06325_9sp	-516,26636	-511,08398	10,3648	0,99439	***	1	[]	['65E']	[]	hypothetical protein	PF05208.6	ALG3(ALG3 protein)
Supercontig_1.35_MVLG_03593_8sp	-527,22735	-521,90364	10,6474	0,99513	***	1	[]	['66H']	[]	hypothetical protein	NA	NA
Supercontig_1.13_MVLG_01973_10sp	-781,70768	-776,47518	10,465	0,99466	***	1	[]	['6G']	[]	hypothetical protein	PF04652.9	DUF605(Vta1 like)
Supercontig_1.2_MVLG_00459_12sp	-737,58052	-732,95547	9,2501	0,9902	***	1	[]	['72H']	[]	hypothetical protein	PF04762.5	IKI3(IKI3 family)
Supercontig_1.181_MVLG_07009_9sp	-773,37618	-766,17371	14,4049	0,99926	***	1	[]	['89K']	[]	hypothetical protein	NA	NA
Supercontig_1.40_MVLG_03903_6sp	-527,42086	-522,44716	9,9474	0,99308	***	1	[]	['8K']	[]	hypothetical protein	PF00026.16	Asp(Eukaryotic aspartyl protease)
Supercontig_1.83_MVLG_05748_10sp	-1020,863	-1015,6383	10,4494	0,99462	***	1	[]	['93L']	[]	hypothetical protein	PF00149.21	Metallophos(Calcineurin-like phosphoesterase)
Supercontig_1.3_MVLG_00579_9sp	-775,18843	-768,41442	13,548	0,99886	***	1	[]	['97I']	[]	hypothetical protein	NA	NA
Supercontig_1.5_MVLG_00961_6sp	-1314,6109	-1306,69	15,8418	0,99964	***	1	[]	[]	['108T']	hypothetical protein	TIGR00820	TIGR00820(zip: ZIP zinc/iron transport family)
Supercontig_1.21_MVLG_02628_6sp	-810,54287	-802,32723	16,4313	0,99973	***	1	[]	[]	['123S']	hypothetical protein	PF00172.11	Zn_clus(Fungal Zn(2)-Cys(6) binuclear cluster domain)
Supercontig_1.11_MVLG_01793_6sp	-618,26385	-613,59175	9,3442	0,99065	***	1	[]	[]	['17A']	hypothetical protein	PF00111.20	Fer2(2Fe-2S iron-sulfur cluster binding domain)
Supercontig_1.4_MVLG_00783_7sp	-624,68466	-619,1216	11,1261	0,99616	***	1	[]	[]	['18S']	hypothetical protein	NA	NA
Supercontig_1.49_MVLG_04418_7sp	-758,73657	-753,90948	9,65418	0,99199	***	1	[]	[]	['1S']	hypothetical protein	PF00026.16	Asp(Eukaryotic aspartyl protease)
Supercontig_1.53_MVLG_04615_10sp	-373,15781	-368,53384	9,24794	0,99019	***	1	[]	[]	['34A']	40S ribosomal protein	PF07650.10	KH_2(KH domain)
Supercontig_1.26_MVLG_03024_10sp	-589,03878	-583,20715	11,6633	0,99707	***	1	[]	[]	['35R']	hypothetical protein	NA	NA
Supercontig_1.39_MVLG_03871_6sp	-427,78077	-422,93001	9,70152	0,99218	***	1	[]	[]	['36L']	hypothetical protein	NA	NA
Supercontig_1.10_MVLG_01647_8sp	-397,92464	-393,2659	9,31748	0,99052	***	1	[]	[]	['37S']	hypothetical protein	NA	NA
Supercontig_1.26_MVLG_03033_10sp	-834,66265	-829,76454	9,79622	0,99254	***	1	[]	[]	['43L']	hypothetical protein	PF04193.7	PQ-loop(PQ loop repeat)
Supercontig_1.25_MVLG_02949_8sp	-598,86009	-593,31845	11,0833	0,99608	***	1	[]	[]	['45G']	hypothetical protein	NA	NA
Supercontig_1.39_MVLG_03874_10sp	-1098,177	-1093,1405	10,0729	0,9935	***	1	[]	[]	['56I']	hypothetical protein	PF07724.7	AAA_2(AAA domain (Cdc48 subfamily))
Supercontig_1.88_MVLG_05881_7sp	-769,52989	-764,4284	10,203	0,99391	***	1	[]	[]	['74G']	hypothetical protein	PF02112.8	PDEase_II(cAMP phosphodiesterases class-II)
Supercontig_1.23_MVLG_02781_8sp	-694,2602	-689,07237	10,3757	0,99442	***	1	[]	[]	['74R']	hypothetical protein	PF00069.18	Pkinase(Protein kinase domain)

Supercontig_1.60_MVLG_04931_10sp	-684,61677	-678,42709	12,3794	0,99795	***	1	[]	[]	['7A']	hypothetical protein	NA	NA
Supercontig_1.31_MVLG_03367_9sp	-1011,4964	-1005,7905	11,4117	0,99667	***	1	[]	[]	['85V']	hypothetical protein	NA	NA
Supercontig_1.17_MVLG_02280_7sp	-856,35086	-851,56405	9,57362	0,99166	***	1	[]	[]	['87K']	hypothetical protein	NA	NA
Supercontig_1.45_MVLG_04200_6sp	-567,404	-562,13919	10,5296	0,99483	***	1	[]	[]	['9K']	hypothetical protein	PF05093.6	CIAPIN1(Cytokine-induced anti-apoptosis inhibitor 1, Fe-S biogenesis)
Supercontig_1.65_MVLG_05141_6sp	-454,41614	-449,9036	9,02508	0,98903	**	5	[]	['30S']	['8L', '20E', '26D', '42V']	hypothetical protein	NA	NA
Supercontig_1.3_MVLG_00513_9sp	-417,02003	-412,51809	9,00388	0,98891	**	2	[]	['1E']	['5E']	hypothetical protein	NA	NA
Supercontig_1.24_MVLG_02883_12sp	-424,21689	-420,05785	8,31808	0,98438	**	2	[]	['9G']	['20V']	hypothetical protein	NA	NA
Supercontig_1.13_MVLG_01961_7sp	-1537,6998	-1534,1412	7,11726	0,97152	**	2	[]	[]	['102I', '130Y']	hypothetical protein	TIGR00229	TIGR00229(sensory_box: PAS domain S-box protein)
Supercontig_1.3_MVLG_00607_10sp	-1622,6712	-1618,1432	9,05602	0,9892	**	2	[]	[]	['146N', '191S']	hypothetical protein	PF07500.7	TFIIS_M(Transcription factor S-II (TFIIS), central domain)
Supercontig_1.46_MVLG_04271_8sp	-1275,6482	-1272,019	7,25844	0,97346	**	2	[]	[]	['16V', '132V']	hypothetical protein	PF08689.3	Med5(Mediator complex subunit Med5)
Supercontig_1.82_MVLG_05725_8sp	-747,35331	-743,02186	8,6629	0,98685	**	2	[]	[]	['31T', '53E']	hypothetical protein	PF03134.12	TB2_DP1_HVA22(TB2/DP1, HVA22 family)
Supercontig_1.34_MVLG_03543_11sp	-1221,9563	-1217,3581	9,19646	0,98993	**	2	[]	[]	['7A', '90A']	hypothetical protein	NA	NA
Supercontig_1.8_MVLG_01410_9sp	-997,75797	-993,20653	9,10288	0,98945	**	2	[]	[]	['7K', '13A']	hypothetical protein	PF03813.7	Nrap(Nrap protein)
Supercontig_1.14_MVLG_01977_9sp	-1516,3105	-1512,0596	8,50184	0,98575	**	2	[]	[]	['8R', '152R']	alpha,alpha-trehalose-phosphate synthase	TIGR02400	TIGR02400(trehalose_OtsA: alpha,alpha-trehalose-phosphate synthase (UDP-forming))
Supercontig_1.25_MVLG_02986_12sp	-431,99458	-427,6844	8,62036	0,98657	**	2	[]	[]	['8T', '33I']	hypothetical protein	PF00560.26	LRR_1(Leucine Rich Repeat)
Supercontig_1.140_MVLG_06676_7sp	-1162,682	-1159,1021	7,15974	0,97212	**	2	[]	[]	['9Q', '57Q']	hypothetical protein	PF00270.22	DEAD(DEAD/DEAH box helicase)
Supercontig_1.57_MVLG_04833_12sp	-845,139	-841,15648	7,96504	0,98136	**	1	[]	['106A']	[]	hypothetical protein	PF10345.2	Cohesin_load(Cohesin loading factor)
Supercontig_1.38_MVLG_03816_9sp	-1044,3239	-1039,7529	9,14204	0,98965	**	1	[]	['119R']	[]	hypothetical protein	NA	NA
Supercontig_1.32_MVLG_03415_7sp	-1245,2648	-1242,0162	6,49722	0,96117	**	1	[]	['146S']	[]	hypothetical protein	PF00070.20	Pyr_redox(Pyridine nucleotide-disulphide oxidoreductase)
Supercontig_1.5_MVLG_00892_10sp	-450,29847	-445,88731	8,82232	0,98786	**	1	[]	['18F']	[]	hypothetical protein	PF00795.15	CN_hydrolase(Carbon-nitrogen hydrolase)
Supercontig_1.34_MVLG_03539_10sp	-396,90858	-392,52075	8,77566	0,98757	**	1	[]	['18L']	[]	hypothetical protein	NA	NA
Supercontig_1.50_MVLG_04465_6sp	-442,35616	-438,86908	6,97416	0,96941	**	1	[]	['19P']	[]	hypothetical protein	NA	NA
Supercontig_1.86_MVLG_05820_9sp	-348,54919	-344,14812	8,80214	0,98774	**	1	[]	['1N']	[]	hypothetical protein	PF02668.9	TauD(Taurine catabolism dioxygenase TauD, TfdA family)
Supercontig_1.58_MVLG_04841_9sp	-843,38917	-839,4297	7,91894	0,98093	**	1	[]	['24D']	[]	hypothetical protein	NA	NA

Supercontig_1.5_MVLG_01006_10sp	-551,89991	-547,3082	9,18342	0,98986	**	**1**	[]	**['24P']**	[]	hypothetical protein	NA	NA
Supercontig_1.77_MVLG_05553_9sp	-664,14162	-661,01587	6,2515	0,9561	**	**1**	[]	**['27T']**	[]	hypothetical protein	PF00168.23	C2(C2 domain)
Supercontig_1.105_MVLG_06213_6sp	-1104,6929	-1100,5704	8,24488	0,9838	**	**1**	[]	**['36E']**	[]	hypothetical protein	NA	NA
Supercontig_1.48_MVLG_04374_8sp	-604,3647	-599,76233	9,20474	0,98997	**	**1**	[]	**['40D']**	[]	hypothetical protein	NA	NA
Supercontig_1.47_MVLG_04300_9sp	-400,89887	-397,65549	6,48676	0,96097	**	**1**	[]	**['40F']**	[]	hypothetical protein	NA	NA
Supercontig_1.40_MVLG_03923_10sp	-624,2154	-620,52247	7,38586	0,9751	**	**1**	[]	**['42H']**	[]	hypothetical protein	PF02221.8	E1_DerP2_DerF2(ML domain)
Supercontig_1.18_MVLG_02406_8sp	-1020,079	-1016,0185	8,1209	0,98276	**	**1**	[]	**['44R']**	[]	hypothetical protein	NA	NA
Supercontig_1.8_MVLG_01383_9sp	-339,66122	-336,02425	7,27394	0,97367	**	**1**	[]	**['4T']**	[]	histone H2B	PF00125.17	Histone(Core histone H2A/H2B/H3/H4)
Supercontig_1.27_MVLG_03106_10sp	-904,64041	-900,42623	8,42836	0,98522	**	**1**	[]	**['66S']**	[]	hypothetical protein	TIGR00727	TIGR00727(ISP4_OPT: small oligopeptide transporter, OPT family)
Supercontig_1.2_MVLG_00278_9sp	-453,34499	-448,9984	8,69318	0,98705	**	**1**	[]	**['8S']**	[]	hypothetical protein	PF10343.2	DUF2419(Protein of unknown function (DUF2419))
Supercontig_1.8_MVLG_01406_8sp	-894,07348	-890,39061	7,36574	0,97485	**	**1**	[]	[]	**['100I']**	hypothetical protein	NA	NA
Supercontig_1.30_MVLG_03259_8sp	-838,25319	-834,8769	6,75258	0,96583	**	**1**	[]	[]	**['102N']**	hypothetical protein	PF01432.13	Peptidase_M3(Peptidase family M3)
Supercontig_1.39_MVLG_03848_9sp	-608,2822	-604,42242	7,71956	0,97893	**	**1**	[]	[]	**['10G']**	hypothetical protein	PF03364.13	Polyketide_cyc(Polyketide cyclase / dehydrase and lipid transport)
Supercontig_1.86_MVLG_05838_8sp	-589,31346	-585,96355	6,69982	0,96491	**	**1**	[]	[]	**['12F']**	hypothetical protein	PF00781.17	DAGK_cat(Diacylglycerol kinase catalytic domain)
Supercontig_1.9_MVLG_01485_8sp	-928,55028	-925,26831	6,56394	0,96245	**	**1**	[]	[]	**['131G']**	hypothetical protein	PF00248.14	Aldo_ket_red(Aldo/keto reductase family)
Supercontig_1.16_MVLG_02222_6sp	-968,25692	-964,56317	7,3875	0,97512	**	**1**	[]	[]	**['141L']**	hypothetical protein	NA	NA
Supercontig_1.30_MVLG_03288_10sp	-1174,529	-1170,9655	7,12692	0,97166	**	**1**	[]	[]	**['143R']**	hypothetical protein	PF01545.14	Cation_efflux(Cation efflux family)
Supercontig_1.17_MVLG_02263_11sp	-418,84996	-414,45972	8,78048	0,9876	**	**1**	[]	[]	**['17A']**	hypothetical protein	PF04136.8	Sec34(Sec34-like family)
Supercontig_1.198_MVLG_07075_6sp	-882,04345	-878,72778	6,63134	0,96369	**	**1**	[]	[]	**['1D']**	hypothetical protein	PF04739.8	AMPKBI(5'-AMP-activated protein kinase beta subunit, interation domain)
Supercontig_1.101_MVLG_06149_6sp	-1020,198	-1017,0869	6,22214	0,95545	**	**1**	[]	[]	**['1S']**	hypothetical protein	PF02984.12	Cyclin_C(Cyclin, C-terminal domain)
Supercontig_1.64_MVLG_05110_9sp	-646,68344	-643,67342	6,02004	0,95071	**	**1**	[]	[]	**['20G']**	hypothetical protein	NA	NA
Supercontig_1.15_MVLG_02097_6sp	-395,25471	-392,21225	6,08492	0,95228	**	**1**	[]	[]	**['22S']**	hypothetical protein	PF08122.5	NDUF_B12(NADH-ubiquinone oxidoreductase B12 subunit family)
Supercontig_1.269_MVLG_07222_8sp	-515,03147	-511,82548	6,41198	0,95948	**	**1**	[]	[]	**['23K']**	hypothetical protein	NA	NA
Supercontig_1.16_MVLG_02217_8sp	-862,86774	-859,20814	7,3192	0,97426	**	**1**	[]	[]	**['24E']**	hypothetical protein	PF02574.9	S-methyl_trans(Homocysteine S-methyltransferase)

Supercontig_1.22_MVLG_02728_9sp	-371,42003	-368,24809	6,34388	0,95808	**	1	[]	[]	**['26Y']**	hypothetical protein	TIGR00727	TIGR00727(ISP4_OPT: small oligopeptide transporter, OPT family)
Supercontig_1.120_MVLG_06421_10sp	-1798,935	-1794,901	8,06798	0,9823	**	1	[]	[]	**['277C']**	hypothetical protein	NA	NA
Supercontig_1.13_MVLG_01897_8sp	-513,68486	-510,01505	7,33962	0,97452	**	1	[]	[]	**['27K']**	hypothetical protein	PF00704.21	Glyco_hydro_18(Glycosyl hydrolases family 18)
Supercontig_1.29_MVLG_03218_7sp	-557,75738	-554,35291	6,80894	0,96678	**	1	[]	[]	**['28L']**	hypothetical protein	PF00254.21	FKBP_C(FKBP-type peptidyl-prolyl cis-trans isomerase)
Supercontig_1.126_MVLG_06526_8sp	-768,20124	-764,61048	7,18152	0,97242	**	1	[]	[]	**['29S']**	hypothetical protein	NA	NA
Supercontig_1.5_MVLG_00974_10sp	-602,41036	-598,00028	8,82016	0,98785	**	1	[]	[]	**['31T']**	hypothetical protein	NA	NA
Supercontig_1.11_MVLG_01750_7sp	-374,42151	-370,54464	7,75374	0,97928	**	1	[]	[]	**['32H']**	tRNA methyl transferase	PF03054.9	tRNA_Me_trans(tRNA methyl transferase)
Supercontig_1.20_MVLG_02519_10sp	-509,00357	-505,48291	7,04132	0,97042	**	1	[]	[]	**['32L']**	hypothetical protein	PF01738.11	DLH(Dienelactone hydrolase family)
Supercontig_1.60_MVLG_04941_7sp	-1060,5769	-1056,0294	9,09498	0,98941	**	1	[]	[]	**['33N']**	hypothetical protein	PF08447.4	PAS_3(PAS fold)
Supercontig_1.25_MVLG_02959_11sp	-483,32118	-479,60783	7,4267	0,9756	**	1	[]	[]	**['33R']**	hypothetical protein	NA	NA
Supercontig_1.85_MVLG_05800_7sp	-940,92608	-936,37635	9,09946	0,98943	**	1	[]	[]	**['35E']**	6-phosphogluconate dehydrogenase, decarboxylating 1	PF03446.8	NAD_binding_2(NAD binding domain of 6-phosphogluconate dehydrogenase)
Supercontig_1.20_MVLG_02593_12sp	-595,69636	-591,38916	8,6144	0,98653	**	1	[]	[]	**['38Q']**	hypothetical protein	NA	NA
Supercontig_1.12_MVLG_01822_12sp	-617,05933	-613,18262	7,75342	0,97928	**	1	[]	[]	**['39L']**	hypothetical protein	TIGR02250	TIGR02250(FCP1_euk: FCP1-like phosphatase, phosphatase domain)
Supercontig_1.16_MVLG_02248_12sp	-806,78119	-803,72016	6,12206	0,95316	**	1	[]	[]	**['41G']**	hypothetical protein	NA	NA
Supercontig_1.2_MVLG_00454_8sp	-349,78943	-345,76677	8,04532	0,98209	**	1	[]	[]	**['43A']**	hypothetical protein	NA	NA
Supercontig_1.12_MVLG_01827_10sp	-527,51724	-523,24654	8,5414	0,98603	**	1	[]	[]	**['48E']**	hypothetical protein	NA	NA
Supercontig_1.98_MVLG_06101_8sp	-402,64942	-399,26263	6,77358	0,96618	**	1	[]	[]	**['48G']**	V-type ATPase, G subunit	PF03179.8	V-ATPase_G(Vacuolar (H+)-ATPase G subunit)
Supercontig_1.40_MVLG_03935_11sp	-682,91446	-679,24288	7,34316	0,97456	**	1	[]	[]	**['48Q']**	hypothetical protein	PF06728.6	PIG-U(GPI transamidase subunit PIG-U)
Supercontig_1.155_MVLG_06819_6sp	-640,41898	-637,17013	6,4977	0,96118	**	1	[]	[]	**['4M']**	hypothetical protein	NA	NA
Supercontig_1.22_MVLG_02732_7sp	-492,96929	-489,726	6,48658	0,96096	**	1	[]	[]	**['50I']**	hypothetical protein	NA	NA
Supercontig_1.39_MVLG_03852_8sp	-460,93182	-457,37543	7,11278	0,97146	**	1	[]	[]	**['52G']**	hypothetical protein	PF01138.14	RNase_PH(3' exoribonuclease family, domain 1)
Supercontig_1.20_MVLG_02527_12sp	-506,83232	-502,23273	9,19918	0,98994	**	1	[]	[]	**['56R']**	hypothetical protein	NA	NA
Supercontig_1.50_MVLG_04472_6sp	-584,733	-581,12215	7,2217	0,97297	**	1	[]	[]	**['56V']**	hypothetical protein	PF09793.2	AD(Anticodon-binding domain)

Supercontig_1.22_MVLG_02744_10sp	-756,77689	-753,73226	6,08926	0,95239	**	**1**	**[]**	**[]**		**['56V']**	hypothetical protein	PF03151.9	TPT(Triose-phosphate Transporter family)
Supercontig_1.10_MVLG_01623_11sp	-644,51621	-640,70544	7,62154	0,97787	**	**1**	**[]**	**[]**		**['58T']**	hypothetical protein	PF03725.8	RNase_PH_C(3' exoribonuclease family, domain 2)
Supercontig_1.6_MVLG_01140_7sp	-397,8582	-393,70622	8,30396	0,98427	**	**1**	**[]**	**[]**		**['60S']**	hypothetical protein	NA	NA
Supercontig_1.109_MVLG_06274_7sp	-621,74526	-618,50444	6,48164	0,96087	**	**1**	**[]**	**[]**		**['61V']**	hypothetical protein	PF03398.7	Ist1(Regulator of Vps4 activity in the MVB pathway)
Supercontig_1.180_MVLG_07001_10sp	-623,16552	-619,78512	6,7608	0,96597	**	**1**	**[]**	**[]**		**['65S']**	hypothetical protein	NA	NA
Supercontig_1.91_MVLG_05928_9sp	-673,12156	-669,58464	7,07384	0,9709	**	**1**	**[]**	**[]**		**['67Q']**	hypothetical protein	TIGR00431	TIGR00431(TruB: tRNA pseudouridine synthase B)
Supercontig_1.7_MVLG_01316_8sp	-449,47674	-445,99661	6,96026	0,9692	**	**1**	**[]**	**[]**		**['6L']**	hypothetical protein	NA	NA
Supercontig_1.21_MVLG_02654_10sp	-1059,2546	-1055,8482	6,81282	0,96684	**	**1**	**[]**	**[]**		**['70T']**	hypothetical protein	NA	NA
Supercontig_1.126_MVLG_06531_9sp	-842,1933	-838,32212	7,74236	0,97917	**	**1**	**[]**	**[]**		**['74S']**	hypothetical protein	NA	NA
Supercontig_1.25_MVLG_02916_8sp	-1045,1983	-1041,5015	7,39362	0,9752	**	**1**	**[]**	**[]**		**['84R']**	hypothetical protein	PF07535.5	zf-DBF(DBF zinc finger)
Supercontig_1.12_MVLG_01845_12sp	-737,27519	-733,85741	6,83556	0,96721	**	**1**	**[]**	**[]**		**['89E']**	hypothetical protein	PF00704.21	Glyco_hydro_18(Glycosyl hydrolases family 18)
Supercontig_1.1_MVLG_00072_8sp	-574,26586	-571,17573	6,18026	0,9545	**	**1**	**[]**	**[]**		**['8S']**	hypothetical protein	PF00083.17	Sugar_tr(Sugar (and other) transporter)
Supercontig_1.4_MVLG_00822_10sp	-977,16197	-973,72973	6,86448	0,96769	**	**1**	**[]**	**[]**		**['92A']**	hypothetical protein	PF00564.17	PB1(PB1 domain)
Supercontig_1.6_MVLG_01202_8sp	-554,12995	-551,30986	5,64018	0,9404	*	**2**	**[]**	**[]**		**['45E', '93Q']**	hypothetical protein	PF04851.8	ResIII(Type III restriction enzyme, res subunit)
Supercontig_1.38_MVLG_03812_11sp	-488,69338	-486,04607	5,29462	0,92916	*	**1**	**[]**	**['11K']**		**[]**	hypothetical protein	PF12146.1	Hydrolase_4(Putative lysophospholipase)
Supercontig_1.17_MVLG_02260_11sp	-1308,3931	-1305,4843	5,81758	0,94546	*	**1**	**[]**	**['126K']**		**[]**	hypothetical protein	NA	NA
Supercontig_1.41_MVLG_04004_7sp	-642,79258	-639,96595	5,65326	0,94079	*	**1**	**[]**	**[]**		**['107K']**	hypothetical protein	PF08386.3	Abhydrolase_4(TAP-like protein)
Supercontig_1.10_MVLG_01581_7sp	-1503,9206	-1501,1583	5,52448	0,93685	*	**1**	**[]**	**[]**		**['113Q']**	hypothetical protein	PF04389.10	Peptidase_M28(Peptidase family M28)
Supercontig_1.24_MVLG_02832_7sp	-1032,9314	-1030,3117	5,2394	0,92718	*	**1**	**[]**	**[]**		**['11N']**	hypothetical protein	PF02096.13	60KD_IMP(60Kd inner membrane protein)
Supercontig_1.3_MVLG_00675_6sp	-934,3397	-931,88896	4,90148	0,91377	*	**1**	**[]**	**[]**		**['128R']**	hypothetical protein	NA	NA
Supercontig_1.10_MVLG_01663_10sp	-498,0988	-495,23376	5,73008	0,94302	*	**1**	**[]**	**[]**		**['13R']**	hypothetical protein	NA	NA
Supercontig_1.66_MVLG_05158_12sp	-1204,1892	-1201,6024	5,1737	0,92474	*	**1**	**[]**	**[]**		**['148S']**	hypothetical protein	PF00566.11	TBC(TBC domain)
Supercontig_1.10_MVLG_01606_11sp	-637,07615	-634,24897	5,65436	0,94082	*	**1**	**[]**	**[]**		**['14K']**	hypothetical protein	PF10585.2	UBA_e1_thiolCys(Ubiquitin-activating enzyme active site)
Supercontig_1.3_MVLG_00543_9sp	-457,72519	-454,8961	5,65818	0,94093	*	**1**	**[]**	**[]**		**['15S']**	hypothetical protein	PF05620.4	DUF788(Protein of unknown function (DUF788))
Supercontig_1.10_MVLG_01578_9sp	-716,5291	-713,69436	5,66948	0,94127	*	**1**	**[]**	**[]**		**['16E']**	hypothetical protein	NA	NA

Supercontig_1.46_MVLG_04239_10sp	-461,51129	-459,05837	4,90584	0,91396	*****	**1**	[]	[]	**['16K']**	hypothetical protein	PF00083.17	Sugar_tr(Sugar (and other) transporter)
Supercontig_1.40_MVLG_03939_7sp	-498,72624	-496,30727	4,83794	0,91099	*****	**1**	[]	[]	**['16V']**	60S ribosomal protein L9-A	PF00347.16	Ribosomal_L6(Ribosomal protein L6)
Supercontig_1.46_MVLG_04258_10sp	-1351,8859	-1348,9142	5,9434	0,94878	*****	**1**	[]	[]	**['173I']**	hypothetical protein	PF10384.2	Scm3(Centromere protein Scm3)
Supercontig_1.55_MVLG_04749_12sp	-519,86747	-517,07219	5,59056	0,9389	*****	**1**	[]	[]	**['18T']**	hypothetical protein	NA	NA
Supercontig_1.1_MVLG_00068_9sp	-814,51434	-811,80931	5,41006	0,93313	*****	**1**	[]	[]	**['1D']**	hypothetical protein	PF09732.2	CactinC_cactus(Cactus-binding C-terminus of cactin protein)
Supercontig_1.77_MVLG_05541_10sp	-638,79311	-636,38469	4,81684	0,91004	*****	**1**	[]	[]	**['1T']**	hypothetical protein	TIGR00880	TIGR00880(2_A_01_02: Multidrug resistance protein)
Supercontig_1.10_MVLG_01611_6sp	-296,81542	-294,43721	4,75642	0,90728	*****	**1**	[]	[]	**['23G']**	hypothetical protein	PF00240.16	ubiquitin(Ubiquitin family)
Supercontig_1.31_MVLG_03337_8sp	-427,25261	-424,57017	5,36488	0,9316	*****	**1**	[]	[]	**['28E']**	hypothetical protein	NA	NA
Supercontig_1.17_MVLG_02329_9sp	-530,37463	-527,68999	5,36928	0,93175	*****	**1**	[]	[]	**['28M']**	hypothetical protein	TIGR00879	TIGR00879(SP: MFS transporter, sugar porter (SP) family)
Supercontig_1.4_MVLG_00770_10sp	-542,67771	-540,19991	4,9556	0,91607	*****	**1**	[]	[]	**['29R']**	hypothetical protein	PF00755.13	Carn_acyltransf(Choline/Carnitine o-acyltransferase)
Supercontig_1.59_MVLG_04888_7sp	-1456,3884	-1453,9399	4,897	0,91358	*****	**1**	[]	[]	**['2S']**	hypothetical protein	PF09757.2	Arb2(Arb2 domain)
Supercontig_1.12_MVLG_01798_8sp	-429,24708	-426,92744	4,63928	0,90169	*****	**1**	[]	[]	**['36L']**	hypothetical protein	PF04180.7	LTV(Low temperature viability protein)
Supercontig_1.2_MVLG_00404_9sp	-678,43795	-675,81399	5,24792	0,92748	*****	**1**	[]	[]	**['36L']**	hypothetical protein	PF02771.9	Acyl-CoA_dh_N(Acyl-CoA dehydrogenase, N-terminal domain)
Supercontig_1.112_MVLG_06329_9sp	-443,50249	-440,80642	5,39214	0,93253	*****	**1**	[]	[]	**['36R']**	hypothetical protein	PF00657.15	Lipase_GDSL(GDSL-like Lipase/Acylhydrolase)
Supercontig_1.10_MVLG_01632_8sp	-373,44225	-370,69941	5,48568	0,93561	*****	**1**	[]	[]	**['3D']**	hypothetical protein	NA	NA
Supercontig_1.15_MVLG_02078_9sp	-757,38738	-754,6065	5,56176	0,93802	*****	**1**	[]	[]	**['3D']**	Transcription coactivator	PF00249.24	Myb_DNA-binding(Myb-like DNA-binding domain)
Supercontig_1.6_MVLG_01133_9sp	-748,50393	-745,71306	5,58174	0,93863	*****	**1**	[]	[]	**['3N']**	hypothetical protein	PF00743.12	FMO-like(Flavin-binding monooxygenase-like)
Supercontig_1.16_MVLG_02243_12sp	-774,58036	-771,97806	5,2046	0,9259	*****	**1**	[]	[]	**['40R']**	histone H2A.1	PF00808.16	CBFD_NFYB_HMF(Histone-like transcription factor (CBF/NF-Y) and archaeal histone)
Supercontig_1.22_MVLG_02741_9sp	-759,72467	-757,32749	4,79436	0,90903	*****	**1**	[]	[]	**['41K']**	hypothetical protein	PF02338.12	OTU(OTU-like cysteine protease)
Supercontig_1.8_MVLG_01445_9sp	-994,84238	-991,9072	5,87036	0,94688	*****	**1**	[]	[]	**['44P']**	hypothetical protein	NA	NA
Supercontig_1.170_MVLG_06940_7sp	-456,28986	-453,8093	4,96112	0,9163	*****	**1**	[]	[]	**['45S']**	hypothetical protein	NA	NA
Supercontig_1.67_MVLG_05202_7sp	-595,11653	-592,43182	5,36942	0,93176	*****	**1**	[]	[]	**['47E']**	hypothetical protein	PF08433.3	KTI12(Chromatin associated protein KTI12)
Supercontig_1.36_MVLG_03633_7sp	-399,37083	-396,93601	4,86964	0,91239	*****	**1**	[]	[]	**['48L']**	hypothetical protein	NA	NA

Supercontig_1.14_MVLG_02015_9sp	**-755,68258**	**-753,12606**	**5,11304**	**0,92243**	*****	**1**	**[]**	**[]**	**['56N']**	**hypothetical protein**	**NA**	**NA**
Supercontig_1.63_MVLG_05062_10sp	**-751,67012**	**-749,30587**	**4,7285**	**0,90598**	*****	**1**	**[]**	**[]**	**['60I']**	**hypothetical protein**	**PF08219.4**	**TOM13(Outer membrane protein TOM13)**
Supercontig_1.3_MVLG_00631_7sp	**-546,94486**	**-544,43818**	**5,01336**	**0,91846**	*****	**1**	**[]**	**[]**	**['63R']**	**hypothetical protein**	**PF08592.4**	**DUF1772(Domain of unknown function (DUF1772))**
Supercontig_1.30_MVLG_03302_10sp	**-439,58847**	**-436,71823**	**5,74048**	**0,94331**	*****	**1**	**[]**	**[]**	**['64A']**	**hypothetical protein**	**PF00018.21**	**SH3_1(SH3 domain)**
Supercontig_1.5_MVLG_00886_11sp	**-524,24498**	**-521,528**	**5,43396**	**0,93393**	*****	**1**	**[]**	**[]**	**['6V']**	**hypothetical protein**	**NA**	**NA**
Supercontig_1.31_MVLG_03336_12sp	**-1220,8148**	**-1218,3916**	**4,8464**	**0,91136**	*****	**1**	**[]**	**[]**	**['78F']**	**hypothetical protein**	**PF00069.18**	**Pkinase(Protein kinase domain)**
Supercontig_1.6_MVLG_01084_8sp	**-583,38793**	**-581,06447**	**4,64692**	**0,90207**	*****	**1**	**[]**	**[]**	**['7Q']**	**cell division control protein 3**	**PF03193.9**	**DUF258(Protein of unknown function, DUF258)**
Supercontig_1.1_MVLG_00052_8sp	-361,32604	-359,07049	4,5111	0,89518	NS	1	[]	['39H']	[]	hypothetical protein	NA	NA
Supercontig_1.44_MVLG_04155_10sp	-1302,7502	-1300,4838	4,53282	0,89632	NS	1	[]	[]	['104K']	hypothetical protein	PF01163.15	RIO1(RIO1 family)
Supercontig_1.76_MVLG_05535_11sp	-692,88287	-691,3464	3,07294	0,78486	NS	1	[]	[]	['10K']	hypothetical protein	PF08477.6	Miro(Miro-like protein)
Supercontig_1.15_MVLG_02154_9sp	-522,09692	-519,79468	4,60448	0,89997	NS	1	[]	[]	['13N']	hypothetical protein	PF01243.13	Pyridox_oxidase(Pyridoxamine 5'-phosphate oxidase)
Supercontig_1.19_MVLG_02461_7sp	-664,97375	-662,83723	4,27304	0,88194	NS	1	[]	[]	['13S']	hypothetical protein	PF01040.11	UbiA(UbiA prenyltransferase family)
Supercontig_1.105_MVLG_06219_7sp	-470,73498	-468,51391	4,44214	0,89151	NS	1	[]	[]	['15S']	hypothetical protein	PF01008.10	IF-2B(Initiation factor 2 subunit family)
Supercontig_1.42_MVLG_04049_10sp	-1128,3598	-1126,7354	3,24878	0,80297	NS	1	[]	[]	['164K']	hypothetical protein	PF00063.14	Myosin_head(Myosin head (motor domain))
Supercontig_1.40_MVLG_03947_9sp	-465,80204	-463,58998	4,42412	0,89053	NS	1	[]	[]	['16N']	hypothetical protein	NA	NA
Supercontig_1.26_MVLG_03019_8sp	-651,6836	-649,4428	4,4816	0,89363	NS	2	[]	[]	['21E', '72E']	hypothetical protein	NA	NA
Supercontig_1.29_MVLG_03242_6sp	-1040,7807	-1038,9196	3,72228	0,8445	NS	1	[]	[]	['23H']	hypothetical protein	PF01565.16	FAD_binding_4(FAD binding domain)
Supercontig_1.88_MVLG_05886_9sp	-491,97617	-490,73341	2,48552	0,71141	NS	1	[]	[]	['25H']	hypothetical protein	TIGR00049	TIGR00049(TIGR00049: iron-sulfur cluster assembly accessory protein)
Supercontig_1.191_MVLG_07043_10sp	-485,41481	-483,15509	4,51944	0,89562	NS	1	[]	[]	['30P']	hypothetical protein	PF06991.4	MFAP1_C(Micro-fibrillar-associated protein 1 C-terminus)
Supercontig_1.11_MVLG_01786_7sp	-396,17814	-393,90123	4,55382	0,8974	NS	1	[]	[]	['34M']	hypothetical protein	NA	NA
Supercontig_1.80_MVLG_05642_11sp	-560,48214	-558,65903	3,64622	0,83848	NS	1	[]	[]	['39A']	guanine nucleotide-binding protein alpha-1 subunit	PF00025.14	Arf(ADP-ribosylation factor family)
Supercontig_1.1_MVLG_00085_11sp	-475,16047	-472,9302	4,46054	0,8925	NS	1	[]	[]	['3Q']	hypothetical protein	PF03330.11	DPBB_1(Rare lipoprotein A (RlpA)-like double-psi beta-barrel)
Supercontig_1.4_MVLG_00841_10sp	-394,10809	-391,97245	4,27128	0,88183	NS	1	[]	[]	['40S']	glucose 1-dehydrogenase	PF00106.18	adh_short(short chain dehydrogenase)
Supercontig_1.60_MVLG_04953_6sp	-807,2362	-805,24499	3,98242	0,86347	NS	1	[]	[]	['46T']	hypothetical protein	NA	NA

Supercontig_1.22_MVLG_02745_9sp	-570,98151	-568,93557	4,09188	0,87074	NS	1	[]	[]	['49N']	hypothetical protein	NA	NA
Supercontig_1.6_MVLG_01119_11sp	-520,81728	-519,21721	3,20014	0,79812	NS	1	[]	[]	['50S']	hypothetical protein	NA	NA
Supercontig_1.16_MVLG_02241_7sp	-502,85317	-501,53003	2,64628	0,7337	NS	1	[]	[]	['51A']	hypothetical protein	NA	NA
Supercontig_1.14_MVLG_02049_7sp	-1030,3519	-1028,1869	4,33014	0,88526	NS	1	[]	[]	['51S']	hypothetical protein	PF04670.5	Gtr1_RagA(Gtr1/RagA G protein conserved region)
Supercontig_1.21_MVLG_02651_9sp	-773,48915	-771,57825	3,8218	0,85205	NS	1	[]	[]	['56Q']	hypothetical protein	PF02535.15	Zip(ZIP Zinc transporter)
Supercontig_1.33_MVLG_03496_12sp	-397,88949	-396,04422	3,69054	0,84202	NS	1	[]	[]	['6T']	hypothetical protein	PF07540.4	NOC3p(Nucleolar complex-associated protein)
Supercontig_1.39_MVLG_03900_10sp	-586,3153	-584,4506	3,7294	0,84506	NS	1	[]	[]	['70I']	hypothetical protein	PF00447.10	HSF_DNA-bind(HSF-type DNA-binding)
Supercontig_1.16_MVLG_02196_12sp	-601,20465	-599,03582	4,33766	0,88569	NS	1	[]	[]	['76N']	hypothetical protein	NA	NA
Supercontig_1.1_MVLG_00242_7sp	-499,09938	-497,20367	3,79142	0,84979	NS	1	[]	[]	['77R']	hypothetical protein	PF00620.20	RhoGAP(RhoGAP domain)
Supercontig_1.185_MVLG_07019_10sp	-723,58867	-721,44466	4,28802	0,88282	NS	1	[]	[]	['86G']	hypothetical protein	PF10607.2	RanBPM_CRA(Ran binding protein in the microtubule-organising centre)
Supercontig_1.35_MVLG_03581_8sp	-693,90936	-692,32446	3,1698	0,79503	NS	1	[]	[]	['87V']	hypothetical protein	TIGR01313	TIGR01313(therm_gnt_kin: carbohydrate kinase, thermoresistant glucokinase family)
Supercontig_1.99_MVLG_06119_10sp	-945,80216	-943,64417	4,31598	0,88444	NS	1	[]	[]	['8N']	hypothetical protein	NA	NA
Supercontig_1.45_MVLG_04222_10sp	-622,13402	-620,02422	4,2196	0,87874	NS	1	[]	[]	['93T']	protein phosphatase PP2A regulatory subunit A	PF02985.15	HEAT(HEAT repeat)
Supercontig_1.96_MVLG_06049_9sp	-723,64672	-721,61214	4,06916	0,86926	NS	1	[]	[]	['99K']	hypothetical protein	NA	NA
Supercontig_1.26_MVLG_03052_6sp	-404,70375	-404,10267	1,20216	0,45178	NS	0	[]	[]	[]	hypothetical protein	PF03016.8	Exostosin(Exostosin family)
Supercontig_1.63_MVLG_05081_7sp	-643,67905	-643,67905	0	0	NS	0	[]	[]	[]	hypothetical protein	TIGR00625	TIGR00625(tfb2: Transcription factor tfb2)
Supercontig_1.19_MVLG_02439_7sp	-673,67538	-673,67478	0,0012	0,0006	NS	0	[]	[]	[]	heme-binding peroxidase	PF00141.16	peroxidase(Peroxidase)
Supercontig_1.23_MVLG_02765_9sp	-853,77291	-851,49197	4,56188	0,89781	NS	0	[]	[]	[]	hypothetical protein	PF00611.16	FCH(Fes/CIP4 homology domain)
Supercontig_1.11_MVLG_01754_9sp	-430,01612	-430,01599	0,00026	0,00013	NS	0	[]	[]	[]	Small GTPase	PF08477.6	Miro(Miro-like protein)
Supercontig_1.150_MVLG_06780_9sp	-317,91112	-317,91096	0,00032	0,00016	NS	0	[]	[]	[]	proteasome subunit alpha type-2	PF00227.19	Proteasome(Proteasome subunit)
Supercontig_1.7_MVLG_01341_11sp	-534,63855	-534,63855	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01697.20	DUF23(Domain of unknown function)
Supercontig_1.142_MVLG_06711_7sp	-505,4449	-505,4449	0	0	NS	0	[]	[]	[]	triosephosphate isomerase	TIGR00419	TIGR00419(tim: triose-phosphate isomerase)
Supercontig_1.8_MVLG_01409_7sp	-507,52366	-507,52357	0,00018	0	NS	0	[]	[]	[]	hsp70-like protein	TIGR02350	TIGR02350(prok_dnaK: chaperone protein DnaK)
Supercontig_1.87_MVLG_05859_9sp	-749,54708	-749,54708	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00400.25	WD40(WD domain, G-beta repeat)

Supercontig_1.3_MVLG_00589_11sp	-446,75614	-446,75614	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00328.15	Acid_phosphat_A(Histidine acid phosphatase)
Supercontig_1.180_MVLG_06997_8sp	-622,88709	-622,26344	1,2473	0,46402	NS	0	[]	[]	[]	hypothetical protein	PF04280.8	Tim44(Tim44-like domain)
Supercontig_1.196_MVLG_07064_6sp	-431,96213	-431,96171	0,00084	0,00042	NS	0	[]	[]	[]	dihydroxy-acid dehydratase	PF00920.14	ILVD_EDD(Dehydratase family)
Supercontig_1.96_MVLG_06030_7sp	-618,94205	-618,94205	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00098.16	zf-CCHC(Zinc knuckle)
Supercontig_1.63_MVLG_05055_7sp	-343,82866	-343,82864	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.40_MVLG_03967_10sp	-430,07216	-427,91673	4,31086	0,88415	NS	0	[]	[]	[]	phosphoacetylglucosamine mutase	PF02880.9	PGM_PMM_III(Phosphoglucomutase/phosphomannomutase, alpha/beta/alpha domain III)
Supercontig_1.113_MVLG_06338_6sp	-438,90485	-438,23289	1,34392	0,48929	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.23_MVLG_02793_6sp	-1583,8247	-1583,396	0,85752	0,34868	NS	0	[]	[]	[]	hypothetical protein	PF00271.24	Helicase_C(Helicase conserved C-terminal domain)
Supercontig_1.88_MVLG_05897_6sp	-406,21263	-406,21262	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.40_MVLG_03907_10sp	-642,03528	-642,03528	0	0	NS	0	[]	[]	[]	hypothetical protein	PF08676.4	MutL_C(MutL C terminal dimerisation domain)
Supercontig_1.5_MVLG_00988_6sp	-330,79713	-330,79713	0	0	NS	0	[]	[]	[]	60S ribosomal protein L35	PF00831.16	Ribosomal_L29(Ribosomal L29 protein)
Supercontig_1.12_MVLG_01823_7sp	-460,64731	-460,64731	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01464.13	SLT(Transglycosylase SLT domain)
Supercontig_1.30_MVLG_03323_9sp	-548,73177	-548,73177	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02466.12	Tim17(Tim17/Tim22/Tim23 family)
Supercontig_1.149_MVLG_06762_12sp	-421,06261	-421,06261	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00999.14	Na_H_Exchanger(Sodium/hydrogen exchanger family)
Supercontig_1.3_MVLG_00536_6sp	-487,07233	-486,91406	0,31654	0,14638	NS	0	[]	[]	[]	hypothetical protein	PF01852.12	START(START domain)
Supercontig_1.24_MVLG_02885_8sp	-769,1366	-769,1366	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01412.11	ArfGap(Putative GTPase activating protein for Arf)
Supercontig_1.51_MVLG_04530_10sp	-409,57085	-409,56041	0,02088	0,01039	NS	0	[]	[]	[]	hypothetical protein	PF05916.4	Sld5(GINS complex subunit Sld5)
Supercontig_1.98_MVLG_06096_12sp	-436,19432	-436,19432	0	0	NS	0	[]	[]	[]	UDP-glucose 6-dehydrogenase	TIGR03026	TIGR03026(NDP-sugDHase: nucleotide sugar dehydrogenase)
Supercontig_1.66_MVLG_05166_9sp	-404,10765	-404,10749	0,00032	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF00004.22	AAA(ATPase family associated with various cellular activities (AAA))
Supercontig_1.11_MVLG_01780_9sp	-1826,8365	-1825,941	1,79114	0,59163	NS	0	[]	[]	[]	TKL protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.9_MVLG_01542_7sp	-395,61839	-395,50241	0,23196	0,10951	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.83_MVLG_05752_9sp	-574,9529	-574,03482	1,83616	0,60072	NS	0	[]	[]	[]	hypothetical protein	PF00004.22	AAA(ATPase family associated with various cellular activities (AAA))
Supercontig_1.51_MVLG_04546_10sp	-496,30232	-496,30003	0,00458	0,00229	NS	0	[]	[]	[]	hypothetical protein	TIGR00727	TIGR00727(ISP4_OPT: small oligopeptide transporter, OPT family)

Supercontig_1.26_MVLG_03026_6sp	-1143,6677	-1143,6676	0,00016	0	NS	0	[]	[]	[]	hypothetical protein	PF08242.5	Methyltransf_12(Methyltransferase domain)
Supercontig_1.17_MVLG_02264_7sp	-885,57824	-885,57824	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00171.15	Aldedh(Aldehyde dehydrogenase family)
Supercontig_1.34_MVLG_03534_10sp	-611,16468	-611,16468	0	0	NS	0	[]	[]	[]	hypothetical protein	TIGR00040	TIGR00040(yfcE: phosphodiesterase, MJ0936 family)
Supercontig_1.17_MVLG_02270_9sp	-387,18694	-387,18684	0,0002	0	NS	0	[]	[]	[]	hypothetical protein	PF04193.7	PQ-loop(PQ loop repeat)
Supercontig_1.2_MVLG_00395_10sp	-413,73469	-413,73467	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00400.25	WD40(WD domain, G-beta repeat)
Supercontig_1.60_MVLG_04930_6sp	-1076,2152	-1076,2152	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03765.8	CRAL_TRIO_N(CRAL/TRIO, N-terminus)
Supercontig_1.48_MVLG_04367_6sp	-1124,6262	-1124,6262	0	0	NS	0	[]	[]	[]	hypothetical protein	PF05577.5	Peptidase_S28(Serine carboxypeptidase S28)
Supercontig_1.8_MVLG_01420_7sp	-457,75153	-457,75143	0,0002	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.46_MVLG_04242_8sp	-501,00187	-500,98899	0,02576	0,0128	NS	0	[]	[]	[]	hypothetical protein	PF05730.4	CFEM(CFEM domain)
Supercontig_1.1_MVLG_00227_10sp	-577,37315	-577,37315	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00583.17	Acetyltransf_1(Acetyltransferase (GNAT) family)
Supercontig_1.35_MVLG_03597_9sp	-422,42268	-422,42247	0,00042	0,00021	NS	0	[]	[]	[]	hypothetical protein	PF03810.12	IBN_N(Importin-beta N-terminal domain)
Supercontig_1.3_MVLG_00640_9sp	-709,1273	-707,24864	3,75732	0,84721	NS	0	[]	[]	[]	hypothetical protein	PF00226.24	DnaJ(DnaJ domain)
Supercontig_1.10_MVLG_01593_9sp	-822,68349	-822,68349	0	0	NS	0	[]	[]	[]	hypothetical protein	PF07728.7	AAA_5(AAA domain (dynein-related subfamily))
Supercontig_1.17_MVLG_02317_8sp	-311,16855	-311,12917	0,07876	0,03861	NS	0	[]	[]	[]	hypothetical protein	PF01408.15	GFO_IDH_MocA(Oxidoreductase family, NAD-binding Rossmann fold)
Supercontig_1.28_MVLG_03130_12sp	-508,88583	-508,88581	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04616.7	Glyco_hydro_43(Glycosyl hydrolases family 43)
Supercontig_1.156_MVLG_06829_6sp	-886,24998	-886,13579	0,22838	0,10791	NS	0	[]	[]	[]	hypothetical protein	PF00400.25	WD40(WD domain, G-beta repeat)
Supercontig_1.63_MVLG_05061_7sp	-553,35161	-553,35154	0,00014	0	NS	0	[]	[]	[]	hypothetical protein	PF00226.24	DnaJ(DnaJ domain)
Supercontig_1.94_MVLG_05987_10sp	-516,90525	-515,56115	2,6882	0,73923	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.15_MVLG_02063_8sp	-507,17426	-507,17426	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.38_MVLG_03782_10sp	-648,39708	-647,94661	0,90094	0,36267	NS	0	[]	[]	[]	hypothetical protein	PF08118.4	MDM31_MDM32(Yeast mitochondrial distribution and morphology (MDM) proteins)
Supercontig_1.15_MVLG_02122_10sp	-406,15848	-403,8681	4,58076	0,89877	NS	0	[]	[]	[]	hypothetical protein	PF09808.2	SNAPc_SNAP43(Small nuclear RNA activating complex (SNAPc), subunit SNAP43)
Supercontig_1.34_MVLG_03515_7sp	-534,90861	-534,79683	0,22356	0,10576	NS	0	[]	[]	[]	hypothetical protein	PF05216.6	UNC-50(UNC-50 family)
Supercontig_1.4_MVLG_00867_9sp	-697,08536	-697,06114	0,04844	0,02393	NS	0	[]	[]	[]	hypothetical protein	NA	NA

Supercontig_1.5_MVLG_00989_8sp	-586,78762	-586,78762	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02229.9	PC4(Transcriptional Coactivator p15 (PC4))
Supercontig_1.39_MVLG_03883_10sp	-721,51263	-721,5126	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04145.8	Ctr(Ctr copper transporter family)
Supercontig_1.12_MVLG_01828_7sp	-903,67539	-903,44772	0,45534	0,20361	NS	0	[]	[]	[]	hypothetical protein	PF09751.2	Es2(Nuclear protein Es2)
Supercontig_1.61_MVLG_04985_10sp	-378,02304	-378,02276	0,00056	0,00028	NS	0	[]	[]	[]	hypothetical protein	PF02770.12	Acyl-CoA_dh_M(Acyl-CoA dehydrogenase, middle domain)
Supercontig_1.76_MVLG_05523_10sp	-706,89971	-706,89939	0,00064	0,00032	NS	0	[]	[]	[]	hypothetical protein	PF09377.3	SBDS_C(SBDS protein C-terminal domain)
Supercontig_1.18_MVLG_02350_11sp	-323,61732	-323,6172	0,00024	0,00012	NS	0	[]	[]	[]	hypothetical protein	PF00233.12	PDEase_I(3'5'-cyclic nucleotide phosphodiesterase)
Supercontig_1.25_MVLG_02977_9sp	-434,72704	-434,72703	0	0	NS	0	[]	[]	[]	26S proteasome regulatory subunit N9	PF01399.20	PCI(PCI domain)
Supercontig_1.155_MVLG_06817_9sp	-800,58233	-800,58229	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00400.25	WD40(WD domain, G-beta repeat)
Supercontig_1.5_MVLG_00977_8sp	-518,1699	-517,96132	0,41716	0,18826	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.175_MVLG_06973_9sp	-373,4157	-373,11486	0,60168	0,2598	NS	0	[]	[]	[]	hypothetical protein	PF01735.11	PLA2_B(Lysophospholipase catalytic domain)
Supercontig_1.96_MVLG_06032_6sp	-574,15514	-573,70776	0,89476	0,3607	NS	0	[]	[]	[]	hypothetical protein	TIGR02251	TIGR02251(HIF-SF_euk: Dullard-like phosphatase domain)
Supercontig_1.1_MVLG_00220_10sp	-423,43075	-423,43075	0	0	NS	0	[]	[]	[]	hypothetical protein	PF06544.5	DUF1115(Protein of unknown function (DUF1115))
Supercontig_1.7_MVLG_01324_9sp	-1211,9315	-1210,3945	3,0739	0,78496	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.68_MVLG_05247_8sp	-1110,3992	-1109,9765	0,84544	0,34474	NS	0	[]	[]	[]	hypothetical protein	PF00566.11	TBC(TBC domain)
Supercontig_1.42_MVLG_04082_9sp	-435,04566	-435,04552	0,00028	0,00014	NS	0	[]	[]	[]	hypothetical protein	PF06609.6	TRI12(Fungal trichothecene efflux pump (TRI12))
Supercontig_1.35_MVLG_03586_7sp	-543,98385	-540,91921	6,12928	0,95333	**	0	[]	[]	[]	hypothetical protein	PF00447.10	HSF_DNA-bind(HSF-type DNA-binding)
Supercontig_1.13_MVLG_01952_9sp	-2260,8464	-2260,8459	0,00108	0,00054	NS	0	[]	[]	[]	hypothetical protein	PF00118.17	Cpn60_TCP1(TCP-1/cpn60 chaperonin family)
Supercontig_1.20_MVLG_02524_10sp	-527,9349	-527,92333	0,02314	0,0115	NS	0	[]	[]	[]	hypothetical protein	PF03151.9	TPT(Triose-phosphate Transporter family)
Supercontig_1.112_MVLG_06332_9sp	-348,37248	-348,37248	0	0	NS	0	[]	[]	[]	hypothetical protein	PF05033.9	Pre-SET(Pre-SET motif)
Supercontig_1.161_MVLG_06871_10sp	-624,57467	-623,99833	1,15268	0,43805	NS	0	[]	[]	[]	hypothetical protein	PF05686.5	DUF821(Arabidopsis thaliana protein of unknown function (DUF821))
Supercontig_1.63_MVLG_05089_9sp	-699,55452	-699,55392	0,0012	0,0006	NS	0	[]	[]	[]	hypothetical protein	PF00448.15	SRP54(SRP54-type protein, GTPase domain)
Supercontig_1.5_MVLG_00880_7sp	-901,55987	-901,55987	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.60_MVLG_04944_9sp	-697,97112	-697,97112	0	0	NS	0	[]	[]	[]	hypothetical protein	PF05794.6	Tcp11(T-complex protein 11)

Supercontig_1.21_MVLG_02656_10sp	-816,18315	-816,18315	0	0	NS	0	[]	[]	[]	hydroxymethylglutaryl-CoA synthase	PF08540.3	HMG_CoA_synt_C(Hydroxymethylglutaryl-coenzyme A synthase C terminal)
Supercontig_1.2_MVLG_00380_10sp	-418,9392	-418,86182	0,15476	0,07446	NS	0	[]	[]	[]	hypothetical protein	PF01485.14	IBR(IBR domain)
Supercontig_1.51_MVLG_04507_6sp	-649,70486	-649,70484	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.81_MVLG_05682_10sp	-471,34037	-471,34037	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01984.13	dsDNA_bind(Double-stranded DNA-binding domain)
Supercontig_1.20_MVLG_02573_12sp	-502,38517	-502,38517	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04253.8	TFR_dimer(Transferrin receptor-like dimerisation domain)
Supercontig_1.1_MVLG_00132_7sp	-477,17284	-477,17279	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00657.15	Lipase_GDSL(GDSL-like Lipase/Acylhydrolase)
Supercontig_1.194_MVLG_07058_7sp	-434,80139	-434,80129	0,0002	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.28_MVLG_03208_7sp	-449,35419	-447,18446	4,33946	0,88579	NS	0	[]	[]	[]	hypothetical protein	PF09802.2	Sec66(Preprotein translocase subunit Sec66)
Supercontig_1.4_MVLG_00769_10sp	-514,61204	-513,2743	2,67548	0,73756	NS	0	[]	[]	[]	hypothetical protein	PF02146.10	SIR2(Sir2 family)
Supercontig_1.22_MVLG_02683_11sp	-344,59926	-344,59882	0,00088	0,00044	NS	0	[]	[]	[]	hypothetical protein	PF02460.11	Patched(Patched family)
Supercontig_1.6_MVLG_01086_10sp	-846,31921	-846,28799	0,06244	0,03074	NS	0	[]	[]	[]	hypothetical protein	PF00018.21	SH3_1(SH3 domain)
Supercontig_1.1_MVLG_00153_8sp	-859,14082	-858,98551	0,31062	0,14385	NS	0	[]	[]	[]	hypothetical protein	PF01380.15	SIS(SIS domain)
Supercontig_1.91_MVLG_05925_10sp	-671,03212	-670,24235	1,57954	0,54605	NS	0	[]	[]	[]	hypothetical protein	PF00789.13	UBX(UBX domain)
Supercontig_1.53_MVLG_04598_10sp	-645,61912	-644,97782	1,2826	0,47339	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.3_MVLG_00540_8sp	-565,17021	-564,34881	1,6428	0,56018	NS	0	[]	[]	[]	hypothetical protein	PF01245.13	Ribosomal_L19(Ribosomal protein L19)
Supercontig_1.48_MVLG_04382_8sp	-504,00777	-503,55109	0,91336	0,36662	NS	0	[]	[]	[]	hypothetical protein	PF00730.18	HhH-GPD(HhH-GPD superfamily base excision DNA repair protein)
Supercontig_1.59_MVLG_04894_11sp	-489,07205	-489,04814	0,04782	0,02363	NS	0	[]	[]	[]	hypothetical protein	PF00172.11	Zn_clus(Fungal Zn(2)-Cys(6) binuclear cluster domain)
Supercontig_1.3_MVLG_00663_9sp	-562,74765	-562,74765	0	0	NS	0	[]	[]	[]	F-type H+-transporting ATPase subunit D	PF05873.5	Mt_ATP-synt_D(ATP synthase D chain, mitochondrial (ATP5H))
Supercontig_1.82_MVLG_05710_10sp	-724,1575	-724,1575	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.85_MVLG_05786_7sp	-619,9365	-619,93632	0,00036	0,00018	NS	0	[]	[]	[]	hypothetical protein	PF00472.13	RF-1(RF-1 domain)
Supercontig_1.9_MVLG_01526_11sp	-493,11854	-493,11854	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.49_MVLG_04423_8sp	-459,82287	-459,00952	1,6267	0,55663	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.1_MVLG_00031_10sp	-306,97347	-306,97339	0,00016	0	NS	0	[]	[]	[]	hypothetical protein	PF08613.4	Cyclin(Cyclin)

Supercontig_1.30_MVLG_03308_12sp	-501,7011	-501,68107	0,04006	0,01983	NS	0	[]	[]	[]	ubiquitin-40S ribosomal protein S27a-1	PF11976.1	Rad60-SLD(Ubiquitin-2 like Rad60 SUMO-like)
Supercontig_1.29_MVLG_03247_8sp	-354,30431	-354,3039	0,00082	0,00041	NS	0	[]	[]	[]	hypothetical protein	PF03676.7	UPF0183(Uncharacterised protein family (UPF0183))
Supercontig_1.26_MVLG_03030_8sp	-449,57949	-449,56423	0,03052	0,01514	NS	0	[]	[]	[]	hypothetical protein	PF00070.20	Pyr_redox(Pyridine nucleotide-disulphide oxidoreductase)
Supercontig_1.53_MVLG_04646_8sp	-556,97691	-556,97691	0	0	NS	0	[]	[]	[]	hypothetical protein	PF12597.1	DUF3767(Protein of unknown function (DUF3767))
Supercontig_1.4_MVLG_00847_8sp	-482,7986	-482,7986	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.52_MVLG_04594_7sp	-591,58733	-591,35395	0,46676	0,20815	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.17_MVLG_02301_9sp	-337,7158	-337,7158	0	0	NS	0	[]	[]	[]	hypothetical protein	PF10785.2	NADH-u_ox-rdase(NADH-ubiquinone oxidoreductase 21 kDa subunit)
Supercontig_1.5_MVLG_00987_7sp	-731,53312	-731,53312	0	0	NS	0	[]	[]	[]	NADH-ubiquinone oxidoreductase 24 kDa subunit	PF01257.12	Complex1_24kDa(Respiratory-chain NADH dehydrogenase 24 Kd subunit)
Supercontig_1.4_MVLG_00734_10sp	-681,47152	-681,18634	0,57036	0,24812	NS	0	[]	[]	[]	hypothetical protein	PF00887.12	ACBP(Acyl CoA binding protein)
Supercontig_1.44_MVLG_04143_8sp	-723,90845	-723,90843	4.0e-05	0	NS	0	[]	[]	[]	electron transfer flavoprotein subunit beta	PF01012.14	ETF(Electron transfer flavoprotein domain)
Supercontig_1.27_MVLG_03066_9sp	-430,2031	-430,20308	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.24_MVLG_02896_9sp	-476,70783	-477,58321	0	0	NS	0	[]	[]	[]	prohibitin-2	PF01145.18	Band_7(SPFH domain / Band 7 family)
Supercontig_1.19_MVLG_02510_7sp	-433,72829	-433,72828	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.19_MVLG_02483_9sp	-1323,2784	-1323,2784	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00999.14	Na_H_Exchanger(Sodium/hydrogen exchanger family)
Supercontig_1.88_MVLG_05899_9sp	-316,27952	-316,27951	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.42_MVLG_04056_10sp	-434,7468	-434,74672	0,00016	0	NS	0	[]	[]	[]	hypothetical protein	PF03169.8	OPT(OPT oligopeptide transporter protein)
Supercontig_1.62_MVLG_05015_7sp	-660,57096	-658,16666	4,8086	0,90967	*	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.36_MVLG_03661_9sp	-505,74126	-505,43139	0,61974	0,26646	NS	0	[]	[]	[]	hypothetical protein	PF00412.15	LIM(LIM domain)
Supercontig_1.121_MVLG_06438_6sp	-1501,4632	-1500,4648	1,99692	0,63155	NS	0	[]	[]	[]	hypothetical protein	PF12257.1	DUF3608(Protein of unknown function (DUF3608))
Supercontig_1.21_MVLG_02615_10sp	-793,75149	-793,75149	0	0	NS	0	[]	[]	[]	hypothetical protein	PF07690.9	MFS_1(Major Facilitator Superfamily)
Supercontig_1.62_MVLG_05033_9sp	-548,84925	-548,84921	0	0	NS	0	[]	[]	[]	AP-1 complex subunit mu-1	PF01217.13	Clat_adaptor_s(Clathrin adaptor complex small chain)
Supercontig_1.23_MVLG_02809_9sp	-990,46956	-990,46956	0	0	NS	0	[]	[]	[]	hypothetical protein	PF10513.2	EPL1(Enhancer of polycomb-like)
Supercontig_1.2_MVLG_00465_8sp	-445,24289	-445,19579	0,0942	0,04601	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.10_MVLG_01599_8sp	-395,5035	-395,50336	0,00028	0,00014	NS	0	[]	[]	[]	hypothetical protein	PF01553.14	Acyltransferase(Acyltransferase)

Supercontig_1.29_MVLG_03256_9sp	-1102,688	-1100,7151	3,94578	0,86095	NS	0	[]	[]	[]	AAT family amino acid transporter	TIGR00913	TIGR00913(2A0310: amino acid permease (yeast))
Supercontig_1.50_MVLG_04490_12sp	-579,99409	-579,13536	1,71746	0,5763	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.3_MVLG_00669_8sp	-503,10695	-503,10695	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04185.7	Phosphoesterase(Phosphoesterase family)
Supercontig_1.77_MVLG_05567_9sp	-771,30436	-771,30436	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.69_MVLG_05280_7sp	-747,97147	-747,97135	0,00024	0,00012	NS	0	[]	[]	[]	hypothetical protein	PF01061.17	ABC2_membrane(ABC-2 type transporter)
Supercontig_1.6_MVLG_01158_11sp	-1154,0883	-1153,5048	1,16696	0,44205	NS	0	[]	[]	[]	hypothetical protein	PF00621.13	RhoGEF(RhoGEF domain)
Supercontig_1.3_MVLG_00658_9sp	-671,58189	-671,58189	0	0	NS	0	[]	[]	[]	transaldolase	PF00923.12	Transaldolase(Transaldolase)
Supercontig_1.6_MVLG_01102_10sp	-901,25333	-901,25333	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04851.8	ResIII(Type III restriction enzyme, res subunit)
Supercontig_1.25_MVLG_02920_8sp	-1051,4766	-1050,7108	1,53174	0,53507	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.5_MVLG_00904_9sp	-642,54363	-642,54363	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00168.23	C2(C2 domain)
Supercontig_1.38_MVLG_03796_8sp	-550,64192	-550,64192	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00995.16	Sec1(Sec1 family)
Supercontig_1.80_MVLG_05647_9sp	-515,24623	-515,24623	0	0	NS	0	[]	[]	[]	hexokinase	PF00349.14	Hexokinase_1(Hexokinase)
Supercontig_1.79_MVLG_05609_10sp	-1037,8512	-1037,8512	0	0	NS	0	[]	[]	[]	hypothetical protein	PF05422.5	SIN1(Stress-activated map kinase interacting protein 1 (SIN1))
Supercontig_1.42_MVLG_04078_11sp	-575,53686	-575,15751	0,7587	0,31569	NS	0	[]	[]	[]	proteasome component PRE2	PF00227.19	Proteasome(Proteasome subunit)
Supercontig_1.34_MVLG_03559_8sp	-424,16115	-424,16114	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03694.6	Erg28(Erg28 like protein)
Supercontig_1.117_MVLG_06391_9sp	-327,74533	-327,74533	0	0	NS	0	[]	[]	[]	hypothetical protein	TIGR00592	TIGR00592(pol2: DNA polymerase (pol2))
Supercontig_1.229_MVLG_07183_8sp	-757,41798	-757,41795	0	0	NS	0	[]	[]	[]	hypothetical protein	PF05346.4	DUF747(Eukaryotic membrane protein family)
Supercontig_1.22_MVLG_02723_8sp	-360,62983	-360,62973	0,0002	0	NS	0	[]	[]	[]	hypothetical protein	PF03162.6	Y_phosphatase2(Tyrosine phosphatase family)
Supercontig_1.5_MVLG_00976_9sp	-322,93278	-322,93236	0,00084	0,00042	NS	0	[]	[]	[]	proteasome subunit alpha type-5	PF00227.19	Proteasome(Proteasome subunit)
Supercontig_1.25_MVLG_02932_9sp	-799,1321	-799,13197	0,00026	0,00013	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.47_MVLG_04333_7sp	-731,16259	-729,64679	3,0316	0,78037	NS	0	[]	[]	[]	hypothetical protein	PF01585.16	G-patch(G-patch domain)
Supercontig_1.36_MVLG_03643_12sp	-455,79632	-455,28662	1,0194	0,39932	NS	0	[]	[]	[]	hypothetical protein	PF00443.22	UCH(Ubiquitin carboxyl-terminal hydrolase)
Supercontig_1.122_MVLG_06453_10sp	-587,55576	-587,55576	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.57_MVLG_04813_9sp	-684,95651	-684,95651	0	0	NS	0	[]	[]	[]	glucose-regulated protein	TIGR02350	TIGR02350(prok_dnaK: chaperone protein DnaK)
Supercontig_1.1_MVLG_00217_9sp	-544,8114	-544,8114	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00107.19	ADH_zinc_N(Zinc-binding dehydrogenase)

Supercontig_1.73_MVLG_05427_10sp	-232,35703	-232,35668	0,0007	0,00035	NS	0	[]	[]	[]	proteasome subunit beta type-3	PF00227.19	Proteasome(Proteasome subunit)
Supercontig_1.63_MVLG_05091_10sp	-966,90815	-966,90815	0	0	NS	0	[]	[]	[]	hypothetical protein	PF11559.1	ADIP(Afadin- and alpha -actinin-Binding)
Supercontig_1.81_MVLG_05671_7sp	-390,00155	-389,21055	1,582	0,54661	NS	0	[]	[]	[]	hypothetical protein	PF00625.14	Guanylate_kin(Guanylate kinase)
Supercontig_1.92_MVLG_05967_6sp	-1282,1713	-1282,1594	0,02384	0,01185	NS	0	[]	[]	[]	hypothetical protein	PF04388.5	Hamartin(Hamartin protein)
Supercontig_1.17_MVLG_02328_8sp	-251,84146	-251,84127	0,00038	0,00019	NS	0	[]	[]	[]	60S ribosomal protein L33-B	PF01247.11	Ribosomal_L35Ae(Ribosomal protein L35Ae)
Supercontig_1.207_MVLG_07116_7sp	-409,04663	-409,04663	0	0	NS	0	[]	[]	[]	cytoplasmic tRNA 2-thiolation protein 1	PF01171.13	ATP_bind_3(PP-loop family)
Supercontig_1.38_MVLG_03789_11sp	-570,02838	-569,99581	0,06514	0,03205	NS	0	[]	[]	[]	hypothetical protein	PF01425.14	Amidase(Amidase)
Supercontig_1.26_MVLG_03025_9sp	-590,73306	-590,7327	0,00072	0,00036	NS	0	[]	[]	[]	C-1-tetrahydrofolate synthase, cytoplasmic	PF01268.12	FTHFS(Formate--tetrahydrofolate ligase)
Supercontig_1.18_MVLG_02347_11sp	-467,73731	-467,73731	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.56_MVLG_04759_7sp	-857,57871	-857,57871	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.1_MVLG_00252_7sp	-402,45114	-402,39804	0,1062	0,05171	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.84_MVLG_05775_10sp	-386,79987	-386,79987	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02431.8	Chalcone(Chalcone-flavanone isomerase)
Supercontig_1.35_MVLG_03603_6sp	-1209,838	-1209,7503	0,17536	0,08395	NS	0	[]	[]	[]	hypothetical protein	PF00076.15	RRM_1(RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain))
Supercontig_1.1_MVLG_00091_9sp	-683,87211	-683,59066	0,5629	0,24531	NS	0	[]	[]	[]	hypothetical protein	PF01529.13	zf-DHHC(DHHC zinc finger domain)
Supercontig_1.2_MVLG_00473_10sp	-476,66632	-476,66617	0,0003	0,00015	NS	0	[]	[]	[]	hypothetical protein	PF04851.8	ResIII(Type III restriction enzyme, res subunit)
Supercontig_1.78_MVLG_05574_11sp	-346,09934	-346,09922	0,00024	0,00012	NS	0	[]	[]	[]	hypothetical protein	PF01544.11	CorA(CorA-like Mg2+ transporter protein)
Supercontig_1.17_MVLG_02277_6sp	-923,30693	-923,30693	0	0	NS	0	[]	[]	[]	fimbrin	PF00307.24	CH(Calponin homology (CH) domain)
Supercontig_1.4_MVLG_00877_12sp	-441,33005	-439,90845	2,8432	0,75867	NS	0	[]	[]	[]	hypothetical protein	PF06687.5	SUR7(SUR7/PalI family)
Supercontig_1.4_MVLG_00696_6sp	-611,1	-611,1	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01557.11	FAA_hydrolase(Fumarylacetoacetate (FAA) hydrolase family)
Supercontig_1.82_MVLG_05701_8sp	-1031,1274	-1031,1274	0	0	NS	0	[]	[]	[]	omega-6 fatty acid desaturase (delta-12 desaturase)	PF11960.1	DUF3474(Domain of unknown function (DUF3474))
Supercontig_1.111_MVLG_06304_7sp	-245,12497	-245,12497	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00070.20	Pyr_redox(Pyridine nucleotide-disulphide oxidoreductase)
Supercontig_1.99_MVLG_06110_10sp	-1145,7251	-1143,841	3,76818	0,84803	NS	0	[]	[]	[]	hypothetical protein	PF07716.8	bZIP_2(Basic region leucine zipper)
Supercontig_1.94_MVLG_05990_8sp	-1188,1545	-1187,1948	1,91924	0,61696	NS	0	[]	[]	[]	hypothetical protein	PF05188.10	MutS_II(MutS domain II)
Supercontig_1.143_MVLG_06720_10sp	-573,61212	-573,61197	0,0003	0,00015	NS	0	[]	[]	[]	hypothetical protein	PF04116.6	FA_hydroxylase(Fatty acid hydroxylase superfamily)

Supercontig_1.68_MVLG_05263_9sp	-589,0294	-589,0294	0	0	NS	0	[]	[]	[]	hypothetical protein	PF11635.1	Med16(Mediator complex subunit 16)
Supercontig_1.78_MVLG_05600_8sp	-1168,8307	-1168,8306	0,00016	0	NS	0	[]	[]	[]	hypothetical protein	PF00481.14	PP2C(Protein phosphatase 2C)
Supercontig_1.80_MVLG_05645_9sp	-318,54934	-318,54897	0,00074	0,00037	NS	0	[]	[]	[]	26S protease regulatory subunit 8	PF07724.7	AAA_2(AAA domain (Cdc48 subfamily))
Supercontig_1.75_MVLG_05489_6sp	-738,63645	-736,8317	3,6095	0,83548	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.123_MVLG_06480_6sp	-524,60842	-524,13245	0,95194	0,37872	NS	0	[]	[]	[]	hypothetical protein	PF00459.18	Inositol_P(Inositol monophosphatase family)
Supercontig_1.27_MVLG_03059_9sp	-1175,7122	-1174,1154	3,19362	0,79746	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.6_MVLG_01129_10sp	-439,11291	-439,11255	0,00072	0,00036	NS	0	[]	[]	[]	hypothetical protein	PF00270.22	DEAD(DEAD/DEAH box helicase)
Supercontig_1.64_MVLG_05093_9sp	-1145,836	-1145,836	0	0	NS	0	[]	[]	[]	hypothetical protein	TIGR00879	TIGR00879(SP: MFS transporter, sugar porter (SP) family)
Supercontig_1.66_MVLG_05186_9sp	-315,5359	-315,53578	0,00024	0,00012	NS	0	[]	[]	[]	hypothetical protein	PF00956.11	NAP(Nucleosome assembly protein (NAP))
Supercontig_1.14_MVLG_02010_12sp	-697,97955	-696,59057	2,77796	0,75067	NS	0	[]	[]	[]	hypothetical protein	PF00616.12	RasGAP(GTPase-activator protein for Ras-like GTPase)
Supercontig_1.62_MVLG_05006_9sp	-966,62339	-966,62303	0,00072	0,00036	NS	0	[]	[]	[]	26S proteasome regulatory subunit N1	PF01851.15	PC_rep(Proteasome/cyclosome repeat)
Supercontig_1.51_MVLG_04529_7sp	-1108,4217	-1108,4217	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04515.5	Choline_transpo(Plasma-membrane choline transporter)
Supercontig_1.62_MVLG_05043_7sp	-477,30982	-477,30982	0	0	NS	0	[]	[]	[]	large subunit ribosomal protein LP1	PF00428.12	Ribosomal_60s(60s Acidic ribosomal protein)
Supercontig_1.192_MVLG_07050_7sp	-581,50097	-580,73963	1,52268	0,53296	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.14_MVLG_02027_11sp	-1833,9681	-1833,4951	0,94606	0,37689	NS	0	[]	[]	[]	hypothetical protein	PF00560.26	LRR_1(Leucine Rich Repeat)
Supercontig_1.5_MVLG_01003_6sp	-741,35133	-740,89746	0,90774	0,36483	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.13_MVLG_01948_10sp	-690,98393	-690,45479	1,05828	0,41089	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.88_MVLG_05892_9sp	-861,59143	-861,29851	0,58584	0,25392	NS	0	[]	[]	[]	hypothetical protein	PF07779.5	Cas1p(Cas1p-like protein)
Supercontig_1.22_MVLG_02759_9sp	-576,60953	-576,54444	0,13018	0,06302	NS	0	[]	[]	[]	hypothetical protein	PF07766.6	LETM1(LETM1-like protein)
Supercontig_1.50_MVLG_04464_7sp	-857,6945	-857,61761	0,15378	0,07401	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.12_MVLG_01832_6sp	-387,69998	-387,43158	0,5368	0,2354	NS	0	[]	[]	[]	hypothetical protein	PF01545.14	Cation_efflux(Cation efflux family)
Supercontig_1.15_MVLG_02100_6sp	-716,93562	-716,93562	0	0	NS	0	[]	[]	[]	hypothetical protein	PF10354.2	DUF2431(Domain of unknown function (DUF2431))
Supercontig_1.36_MVLG_03694_8sp	-961,70729	-961,51968	0,37522	0,17106	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.38_MVLG_03776_7sp	-824,7213	-824,7213	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA

Supercontig_1.41_MVLG_04018_7sp	-900,05868	-899,10982	1,89772	0,61282	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.139_MVLG_06667_9sp	-427,10705	-427,10705	0	0	NS	0	[]	[]	[]	20S proteasome subunit beta 1	PF00227.19	Proteasome(Proteasome subunit)
Supercontig_1.79_MVLG_05621_9sp	-351,5342	-350,94141	1,18558	0,44722	NS	0	[]	[]	[]	hypothetical protein	PF11779.1	DUF3317(Protein of unknown function (DUF3317))
Supercontig_1.23_MVLG_02822_7sp	-593,48663	-593,46302	0,04722	0,02333	NS	0	[]	[]	[]	hypothetical protein	PF01435.11	Peptidase_M48(Peptidase family M48)
Supercontig_1.82_MVLG_05707_7sp	-987,4729	-987,47282	0,00016	0	NS	0	[]	[]	[]	hydroxyacid-oxoacid transhydrogenase	PF00465.12	Fe-ADH(Iron-containing alcohol dehydrogenase)
Supercontig_1.53_MVLG_04639_12sp	-368,66632	-368,66609	0,00046	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.55_MVLG_04718_9sp	-412,98421	-412,98412	0,00018	0	NS	0	[]	[]	[]	hypothetical protein	PF00400.25	WD40(WD domain, G-beta repeat)
Supercontig_1.1_MVLG_00253_7sp	-805,82942	-805,82865	0,00154	0	NS	0	[]	[]	[]	hypothetical protein	PF00909.14	Ammonium_transp(Ammonium Transporter Family)
Supercontig_1.122_MVLG_06458_7sp	-783,79665	-783,79665	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03060.8	NPD(2-nitropropane dioxygenase)
Supercontig_1.20_MVLG_02533_10sp	-794,10752	-794,10752	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.42_MVLG_04059_8sp	-693,16615	-692,43985	1,4526	0,5163	NS	0	[]	[]	[]	hypothetical protein	PF00333.13	Ribosomal_S5(Ribosomal protein S5, N-terminal domain)
Supercontig_1.86_MVLG_05826_7sp	-548,10115	-547,9972	0,2079	0,09873	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.38_MVLG_03813_9sp	-1142,3983	-1142,398	0,00062	0,00031	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.4_MVLG_00832_9sp	-954,60036	-954,60036	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04083.9	Abhydro_lipase(ab-hydrolase associated lipase region)
Supercontig_1.185_MVLG_07018_8sp	-1156,6685	-1156,6684	0,00022	0,00011	NS	0	[]	[]	[]	hypothetical protein	PF08623.3	TIP120(TATA-binding protein interacting (TIP20))
Supercontig_1.24_MVLG_02856_7sp	-1116,9147	-1116,2928	1,2438	0,46308	NS	0	[]	[]	[]	hypothetical protein	PF02515.10	CoA_transf_3(CoA-transferase family III)
Supercontig_1.1_MVLG_00183_8sp	-576,23187	-576,23187	0	0	NS	0	[]	[]	[]	L-lactate dehydrogenase (cytochrome)	PF01070.11	FMN_dh(FMN-dependent dehydrogenase)
Supercontig_1.39_MVLG_03835_8sp	-777,9512	-777,9512	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01997.9	Translin(Translin family)
Supercontig_1.156_MVLG_06828_7sp	-404,61559	-404,36719	0,4968	0,21995	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.107_MVLG_06251_7sp	-672,93346	-672,93346	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.63_MVLG_05059_9sp	-355,19087	-355,19087	0	0	NS	0	[]	[]	[]	hypothetical protein	PF06110.4	DUF953(Eukaryotic protein of unknown function (DUF953))
Supercontig_1.39_MVLG_03845_8sp	-464,27191	-464,1378	0,26822	0,12551	NS	0	[]	[]	[]	hypothetical protein	PF09668.3	Asp_protease(Aspartyl protease)
Supercontig_1.15_MVLG_02106_9sp	-1201,5165	-1199,2723	4,48844	0,89399	NS	0	[]	[]	[]	hypothetical protein	PF01501.13	Glyco_transf_8(Glycosyl transferase family 8)
Supercontig_1.15_MVLG_02109_8sp	-961,43016	-961,43016	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00248.14	Aldo_ket_red(Aldo/keto reductase family)
Supercontig_1.33_MVLG_03451_10sp	-436,05588	-436,0558	0,00016	0	NS	0	[]	[]	[]	argininosuccinate synthase	PF00764.12	Arginosuc_synth(Arginosuccinate synthase)

Supercontig_1.30_MVLG_03267_6sp	-504,05392	-504,05312	0,0016	0	NS	0	[]	[]	[]	hypothetical protein	PF04366.5	DUF500(Family of unknown function (DUF500))
Supercontig_1.122_MVLG_06466_10sp	-851,2868	-851,28676	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.15_MVLG_02131_7sp	-658,0385	-658,0385	0	0	NS	0	[]	[]	[]	hypothetical protein	PF08638.4	Med14(Mediator complex subunit MED14)
Supercontig_1.68_MVLG_05271_9sp	-526,41782	-526,41782	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.15_MVLG_02099_9sp	-396,34067	-396,24878	0,18378	0,08779	NS	0	[]	[]	[]	40S ribosomal protein S23	PF00164.18	Ribosomal_S12(Ribosomal protein S12)
Supercontig_1.226_MVLG_07178_6sp	-461,89737	-459,89742	3,9999	0,86466	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.42_MVLG_04083_10sp	-416,46295	-416,46296	0	0	NS	0	[]	[]	[]	hypothetical protein	PF06427.4	UDP-g_GGTase(UDP-glucose:Glycoprotein Glucosyltransferase)
Supercontig_1.31_MVLG_03348_8sp	-544,89517	-542,83331	4,12372	0,87278	NS	0	[]	[]	[]	hypothetical protein	PF00069.18	Pkinase(Protein kinase domain)
Supercontig_1.55_MVLG_04741_11sp	-822,25685	-821,14837	2,21696	0,66994	NS	0	[]	[]	[]	hypothetical protein	PF00850.12	Hist_deacetyl(Histone deacetylase domain)
Supercontig_1.2_MVLG_00338_9sp	-564,5394	-563,46745	2,1439	0,65766	NS	0	[]	[]	[]	hypothetical protein	PF00581.13	Rhodanese(Rhodanese-like domain)
Supercontig_1.87_MVLG_05868_8sp	-341,61718	-341,61718	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00515.21	TPR_1(Tetratricopeptide repeat)
Supercontig_1.11_MVLG_01717_8sp	-470,56315	-470,43435	0,2576	0,12085	NS	0	[]	[]	[]	hypothetical protein	PF01556.11	DnaJ_C(DnaJ C terminal region)
Supercontig_1.57_MVLG_04832_10sp	-665,26749	-664,32423	1,88652	0,61064	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.76_MVLG_05530_8sp	-325,57175	-325,57175	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.4_MVLG_00748_10sp	-512,48039	-512,45539	0,05	0,02469	NS	0	[]	[]	[]	protein geranylgeranyltransferase type II	PF00432.14	Prenyltrans(Prenyltransferase and squalene oxidase repeat)
Supercontig_1.18_MVLG_02373_10sp	-560,85823	-560,8582	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00176.16	SNF2_N(SNF2 family N-terminal domain)
Supercontig_1.17_MVLG_02341_8sp	-311,76069	-311,76069	0	0	NS	0	[]	[]	[]	hypothetical protein	PF10075.2	PCI_Csn8(COP9 signalosome, subunit CSN8)
Supercontig_1.23_MVLG_02801_10sp	-674,43088	-674,43075	0,00026	0,00013	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.56_MVLG_04765_9sp	-526,45685	-526,45685	0	0	NS	0	[]	[]	[]	hypothetical protein	PF12569.1	NARP1(NMDA receptor-regulated protein 1)
Supercontig_1.44_MVLG_04146_6sp	-649,64328	-649,64319	0,00018	0	NS	0	[]	[]	[]	ATP phosphoribosyltransferase	PF08029.4	HisG_C(HisG, C-terminal domain)
Supercontig_1.39_MVLG_03879_6sp	-438,23441	-438,23441	0	0	NS	0	[]	[]	[]	PTH2 family peptidyl-tRNA hydrolase	TIGR00283	TIGR00283(arch_pth2: peptidyl-tRNA hydrolase)
Supercontig_1.6_MVLG_01172_9sp	-474,34894	-472,89601	2,90586	0,76612	NS	0	[]	[]	[]	hypothetical protein	PF04749.10	PLAC8(PLAC8 family)
Supercontig_1.95_MVLG_06009_10sp	-760,46522	-759,92093	1,08858	0,41975	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.82_MVLG_05703_9sp	-501,16549	-501,16549	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01786.10	AOX(Alternative oxidase)

Supercontig_1.88_MVLG_05901_10sp	-774,77262	-773,78439	1,97646	0,62777	NS	0	[]	[]	[]	hypothetical protein	PF02518.19	HATPase_c(Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase)
Supercontig_1.92_MVLG_05953_10sp	-373,22122	-373,2165	0,00944	0,00471	NS	0	[]	[]	[]	hypothetical protein	PF08232.5	Striatin(Striatin family)
Supercontig_1.5_MVLG_00923_10sp	-1139,7993	-1138,6724	2,25378	0,67596	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.78_MVLG_05596_8sp	-286,4879	-286,48784	0,00012	0	NS	0	[]	[]	[]	hypothetical protein	PF03992.9	ABM(Antibiotic biosynthesis monooxygenase)
Supercontig_1.16_MVLG_02219_9sp	-1022,831	-1022,831	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00580.14	UvrD-helicase(UvrD/REP helicase)
Supercontig_1.95_MVLG_06021_7sp	-765,08406	-765,08406	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03876.10	RNA_pol_Rpb7_N(RNA polymerase Rpb7-like, N-terminal domain)
Supercontig_1.104_MVLG_06201_7sp	-596,65166	-596,65166	0	0	NS	0	[]	[]	[]	hypothetical protein	PF05719.4	GPP34(Golgi phosphoprotein 3 (GPP34))
Supercontig_1.4_MVLG_00698_9sp	-1195,3831	-1194,6218	1,52264	0,53295	NS	0	[]	[]	[]	hypothetical protein	PF07819.6	PGAP1(PGAP1-like protein)
Supercontig_1.50_MVLG_04477_7sp	-756,74531	-756,74531	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.2_MVLG_00460_6sp	-279,44902	-279,44896	0,00012	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.67_MVLG_05237_8sp	-688,0637	-686,32711	3,47318	0,82388	NS	0	[]	[]	[]	hypothetical protein	PF00795.15	CN_hydrolase(Carbon-nitrogen hydrolase)
Supercontig_1.100_MVLG_06130_9sp	-658,59405	-658,5938	0,0005	0,00025	NS	0	[]	[]	[]	hypothetical protein	PF00324.14	AA_permease(Amino acid permease)
Supercontig_1.84_MVLG_05781_9sp	-878,6087	-878,6087	0	0	NS	0	[]	[]	[]	hypothetical protein	PF12271.1	Chs3p(Chitin synthase III catalytic subunit)
Supercontig_1.14_MVLG_02017_10sp	-1241,1506	-1241,1506	0	0	NS	0	[]	[]	[]	hypothetical protein	TIGR00800	TIGR00800(ncs1: NCS1 nucleoside transporter family)
Supercontig_1.2_MVLG_00369_11sp	-474,74626	-474,74626	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.39_MVLG_03864_9sp	-352,44538	-352,4453	0,00016	0	NS	0	[]	[]	[]	protein hob3	PF03114.11	BAR(BAR domain)
Supercontig_1.143_MVLG_06716_12sp	-561,33893	-558,96368	4,7505	0,90701	*	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.7_MVLG_01292_8sp	-739,04592	-738,70363	0,68458	0,28986	NS	0	[]	[]	[]	hypothetical protein	PF01205.12	UPF0029(Uncharacterized protein family UPF0029)
Supercontig_1.51_MVLG_04505_10sp	-495,68668	-495,57424	0,22488	0,10635	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.7_MVLG_01272_7sp	-862,18486	-862,18149	0,00674	0,00336	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.40_MVLG_03929_11sp	-757,27725	-756,80101	0,95248	0,37889	NS	0	[]	[]	[]	hypothetical protein	PF04757.7	Pex2_Pex12(Pex2 / Pex12 amino terminal region)
Supercontig_1.10_MVLG_01625_10sp	-346,82263	-346,82263	0	0	NS	0	[]	[]	[]	calcium-binding protein 39	PF08569.4	Mo25(Mo25-like)
Supercontig_1.47_MVLG_04348_9sp	-534,98008	-534,98007	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02257.8	RFX_DNA_binding(RFX DNA-binding domain)
Supercontig_1.41_MVLG_03994_9sp	-408,34848	-408,34848	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.46_MVLG_04267_10sp	-1020,6245	-1020,6245	0	0	NS	0	[]	[]	[]	hypothetical protein	PF06738.5	DUF1212(Protein of unknown function (DUF1212))

Supercontig_1.1_MVLG_00230_8sp	-426,00922	-423,71272	4,593	0,89939	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.55_MVLG_04732_6sp	-731,17785	-731,17779	0,00012	0	NS	0	[]	[]	[]	ornithine aminotransferase	PF00202.14	Aminotran_3(Aminotransferase class-III)
Supercontig_1.27_MVLG_03075_11sp	-487,83477	-487,83455	0,00044	0,00022	NS	0	[]	[]	[]	hypothetical protein	PF10510.2	PIG-S(Phosphatidylinositol-glycan biosynthesis class S protein)
Supercontig_1.46_MVLG_04289_8sp	-482,17654	-482,17654	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.15_MVLG_02076_8sp	-1056,9694	-1056,9694	0	0	NS	0	[]	[]	[]	hypothetical protein	PF08313.5	SCA7(SCA7)
Supercontig_1.36_MVLG_03688_10sp	-366,99075	-366,30796	1,36558	0,49479	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.123_MVLG_06481_9sp	-1153,4696	-1150,0313	6,87666	0,96788	**	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.56_MVLG_04754_10sp	-467,97701	-467,97701	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00730.18	HhH-GPD(HhH-GPD superfamily base excision DNA repair protein)
Supercontig_1.22_MVLG_02734_7sp	-480,82103	-480,82103	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.6_MVLG_01115_10sp	-548,88034	-548,88003	0,00062	0,00031	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.1_MVLG_00259_10sp	-854,22955	-854,22955	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.41_MVLG_04021_7sp	-422,15913	-422,15913	0	0	NS	0	[]	[]	[]	isopentenyl-diphosphate Delta-isomerase	TIGR02150	TIGR02150(IPP_isom_1: isopentenyl-diphosphate delta-isomerase)
Supercontig_1.74_MVLG_05470_9sp	-618,70881	-618,49655	0,42452	0,19125	NS	0	[]	[]	[]	imidazole glycerol phosphate synthase hisHF	TIGR00735	TIGR00735(hisF: imidazoleglycerol phosphate synthase, cyclase subunit)
Supercontig_1.10_MVLG_01669_7sp	-1129,4736	-1128,7055	1,5362	0,53611	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.12_MVLG_01803_9sp	-578,18914	-578,18914	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02148.12	zf-UBP(Zn-finger in ubiquitin-hydrolases and other protein)
Supercontig_1.14_MVLG_01976_10sp	-554,73738	-554,7368	0,00116	0,00058	NS	0	[]	[]	[]	hypothetical protein	PF07970.5	COPIIcoated_ERV(Endoplasmic reticulum vesicle transporter)
Supercontig_1.149_MVLG_06761_10sp	-766,46735	-766,36636	0,20198	0,09606	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.36_MVLG_03683_9sp	-489,17276	-488,92737	0,49078	0,2176	NS	0	[]	[]	[]	Ras-like protein	PF08477.6	Miro(Miro-like protein)
Supercontig_1.2_MVLG_00450_10sp	-432,13341	-431,19437	1,87808	0,609	NS	0	[]	[]	[]	hypothetical protein	PF04059.5	RRM_2(RNA recognition motif 2)
Supercontig_1.1_MVLG_00272_10sp	-516,52252	-516,52252	0	0	NS	0	[]	[]	[]	potassium/sodium efflux P-type ATPase, fungal-type	TIGR01494	TIGR01494(ATPase_P-type: HAD ATPase, P-type, family IC)
Supercontig_1.30_MVLG_03320_10sp	-395,77011	-395,77011	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04908.8	SH3BGR(SH3-binding, glutamic acid-rich protein)
Supercontig_1.99_MVLG_06124_7sp	-759,43039	-759,43039	0	0	NS	0	[]	[]	[]	kynureninase	TIGR01814	TIGR01814(kynureninase: kynureninase)
Supercontig_1.585_MVLG_07284_9sp	-395,88427	-394,91813	1,93228	0,61945	NS	0	[]	[]	[]	hypothetical protein	PF03583.7	LIP(Secretory lipase)

Supercontig_1.44_MVLG_04162_9sp	-517,71409	-517,71409	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.40_MVLG_03937_6sp	-1083,9992	-1083,999	0,00036	0,00018	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.62_MVLG_05003_9sp	-827,72302	-825,95484	3,53636	0,82936	NS	0	[]	[]	[]	hypothetical protein	PF00172.11	Zn_clus(Fungal Zn(2)-Cys(6) binuclear cluster domain)
Supercontig_1.20_MVLG_02544_10sp	-408,39878	-407,70553	1,3865	0,50005	NS	0	[]	[]	[]	hypothetical protein	PF00076.15	RRM_1(RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain))
Supercontig_1.5_MVLG_00972_9sp	-608,99115	-608,87857	0,22516	0,10647	NS	0	[]	[]	[]	hypothetical protein	PF08241.5	Methyltransf_11(Methyltransferase domain)
Supercontig_1.14_MVLG_01997_11sp	-585,18535	-585,18535	0	0	NS	0	[]	[]	[]	alcohol dehydrogenase (NADP+)	PF00248.14	Aldo_ket_red(Aldo/keto reductase family)
Supercontig_1.91_MVLG_05924_9sp	-409,06169	-408,1101	1,90318	0,61387	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.164_MVLG_06895_8sp	-589,18606	-589,18606	0	0	NS	0	[]	[]	[]	vacuolar protein 8	PF05804.5	KAP(Kinesin-associated protein (KAP))
Supercontig_1.19_MVLG_02433_8sp	-334,92664	-334,45103	0,95122	0,37849	NS	0	[]	[]	[]	hypothetical protein	PF06978.4	POP1(Ribonucleases P/MRP protein subunit POP1)
Supercontig_1.20_MVLG_02549_11sp	-335,44383	-335,44383	0	0	NS	0	[]	[]	[]	hypothetical protein	TIGR00535	TIGR00535(SAM_DCase: S-adenosylmethionine decarboxylase proenzyme)
Supercontig_1.14_MVLG_01994_10sp	-715,33406	-715,33406	0	0	NS	0	[]	[]	[]	histone deacetylase phd1	PF00850.12	Hist_deacetyl(Histone deacetylase domain)
Supercontig_1.1_MVLG_00035_6sp	-324,86189	-324,86184	0,0001	0	NS	0	[]	[]	[]	hypothetical protein	PF08991.3	DUF1903(Domain of unknown function (DUF1903))
Supercontig_1.18_MVLG_02378_6sp	-834,48384	-834,4838	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04410.7	Gar1(Gar1/Naf1 RNA binding region)
Supercontig_1.10_MVLG_01602_7sp	-677,88675	-677,88626	0,00098	0,00049	NS	0	[]	[]	[]	CK1/CK1/CK1-G protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.123_MVLG_06476_9sp	-636,82357	-636,82357	0	0	NS	0	[]	[]	[]	hypothetical protein	PF11968.1	DUF3321(Protein of unknown function (DUF3321))
Supercontig_1.9_MVLG_01560_8sp	-1606,0703	-1606,0703	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02383.11	Syja_N(SacI homology domain)
Supercontig_1.39_MVLG_03844_9sp	-1143,6695	-1143,5984	0,14224	0,06865	NS	0	[]	[]	[]	hypothetical protein	PF08553.3	VID27(VID27 cytoplasmic protein)
Supercontig_1.4_MVLG_00775_6sp	-766,79447	-766,79447	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02421.11	FeoB_N(Ferrous iron transport protein B)
Supercontig_1.92_MVLG_05956_6sp	-672,41457	-671,29768	2,23378	0,6727	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.75_MVLG_05491_8sp	-610,16764	-610,10317	0,12894	0,06244	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.59_MVLG_04903_10sp	-571,36971	-571,17168	0,39606	0,17965	NS	0	[]	[]	[]	hypothetical protein	PF01000.19	RNA_pol_A_bac(RNA polymerase Rpb3/RpoA insert domain)
Supercontig_1.27_MVLG_03098_9sp	-393,60405	-393,06163	1,08484	0,41866	NS	0	[]	[]	[]	hypothetical protein	PF07690.9	MFS_1(Major Facilitator Superfamily)
Supercontig_1.47_MVLG_04330_10sp	-576,54083	-576,54083	0	0	NS	0	[]	[]	[]	hypothetical protein	PF07716.8	bZIP_2(Basic region leucine zipper)
Supercontig_1.48_MVLG_04356_11sp	-542,7231	-542,45752	0,53116	0,23324	NS	0	[]	[]	[]	hypothetical protein	PF05739.12	SNARE(SNARE domain)

Supercontig_1.3_MVLG_00515_9sp	-688,32918	-688,32918	0	0	NS	0	[]	[]	[]	hypothetical protein	PF11735.1	CAP59_mtransfer(Cryptococcal mannosyltransferase 1)
Supercontig_1.84_MVLG_05782_6sp	-1397,0633	-1397,0633	0	0	NS	0	[]	[]	[]	hypothetical protein	PF06159.6	DUF974(Protein of unknown function (DUF974))
Supercontig_1.6_MVLG_01107_10sp	-463,70897	-463,70897	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00857.13	Isochorismatase(Isochorismatase family)
Supercontig_1.51_MVLG_04497_10sp	-1270,2542	-1270,1972	0,1139	0,05536	NS	0	[]	[]	[]	hypothetical protein	PF00150.11	Cellulase(Cellulase (glycosyl hydrolase family 5))
Supercontig_1.94_MVLG_06001_10sp	-1028,9622	-1028,9622	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01852.12	START(START domain)
Supercontig_1.202_MVLG_07089_9sp	-258,22644	-258,22613	0,00062	0,00031	NS	0	[]	[]	[]	40S ribosomal protein S27	PF01667.10	Ribosomal_S27e(Ribosomal protein S27)
Supercontig_1.18_MVLG_02374_9sp	-626,80626	-626,80626	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.6_MVLG_01215_10sp	-419,8589	-419,00803	1,70174	0,57296	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.14_MVLG_02023_8sp	-1022,2693	-1019,4018	5,73502	0,94316	*	0	[]	[]	[]	hypothetical protein	PF08528.4	Whi5(Whi5 like)
Supercontig_1.97_MVLG_06072_10sp	-675,18475	-675,18471	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.3_MVLG_00645_10sp	-909,72636	-909,38128	0,69016	0,29184	NS	0	[]	[]	[]	hypothetical protein	PF00293.21	NUDIX(NUDIX domain)
Supercontig_1.24_MVLG_02863_10sp	-474,912	-474,912	0	0	NS	0	[]	[]	[]	hypothetical protein	PF07724.7	AAA_2(AAA domain (Cdc48 subfamily))
Supercontig_1.9_MVLG_01532_8sp	-640,04782	-640,04757	0,0005	0,00025	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.9_MVLG_01576_9sp	-612,55808	-612,55808	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.99_MVLG_06113_11sp	-692,22126	-692,22126	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00400.25	WD40(WD domain, G-beta repeat)
Supercontig_1.132_MVLG_06604_8sp	-416,5127	-416,5127	0	0	NS	0	[]	[]	[]	hypothetical protein	TIGR00149	TIGR00149(TIGR00149_YbjQ: secondary thiamine-phosphate synthase enzyme)
Supercontig_1.105_MVLG_06221_8sp	-484,19149	-483,17142	2,04014	0,63943	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.53_MVLG_04621_8sp	-724,09353	-724,09333	0,0004	0,0002	NS	0	[]	[]	[]	hypothetical protein	PF00615.12	RGS(Regulator of G protein signaling domain)
Supercontig_1.20_MVLG_02577_8sp	-346,31403	-346,31403	0	0	NS	0	[]	[]	[]	beta-lactamase	PF00144.17	Beta-lactamase(Beta-lactamase)
Supercontig_1.55_MVLG_04725_10sp	-829,62141	-829,62141	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03259.10	Robl_LC7(Roadblock/LC7 domain)
Supercontig_1.49_MVLG_04412_8sp	-596,4975	-596,4975	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.74_MVLG_05455_9sp	-330,68854	-330,67043	0,03622	0,01795	NS	0	[]	[]	[]	hypothetical protein	PF01920.13	Prefoldin_2(Prefoldin subunit)
Supercontig_1.30_MVLG_03303_7sp	-521,42976	-521,37538	0,10876	0,05293	NS	0	[]	[]	[]	beta-lactamase	PF00144.17	Beta-lactamase(Beta-lactamase)
Supercontig_1.45_MVLG_04230_9sp	-1377,4634	-1376,4121	2,1025	0,6505	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.3_MVLG_00578_9sp	-569,69798	-569,69798	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA

Supercontig_1.96_MVLG_06040_11sp	-616,32723	-614,80991	3,03464	0,7807	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.23_MVLG_02766_9sp	-540,74708	-540,74708	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01425.14	Amidase(Amidase)
Supercontig_1.4_MVLG_00852_11sp	-424,83144	-424,83128	0,00032	0,00016	NS	0	[]	[]	[]	ABC1-C atypical protein kinase	PF03109.9	ABC1(ABC1 family)
Supercontig_1.62_MVLG_05027_9sp	-1018,4908	-1018,4907	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.186_MVLG_07031_10sp	-364,91635	-364,91601	0,00068	0,00034	NS	0	[]	[]	[]	serine/threonine-protein phosphatase PP1	PF00149.21	Metallophos(Calcineurin-like phosphoesterase)
Supercontig_1.2_MVLG_00316_8sp	-383,36509	-383,36509	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.7_MVLG_01225_9sp	-606,48593	-606,48593	0	0	NS	0	[]	[]	[]	hypothetical protein	PF09335.4	SNARE_assoc(SNARE associated Golgi protein)
Supercontig_1.54_MVLG_04662_8sp	-339,02846	-339,02846	0	0	NS	0	[]	[]	[]	hypothetical protein	TIGR02970	TIGR02970(succ_dehyd_cytB: succinate dehydrogenase, cytochrome b556 subunit)
Supercontig_1.8_MVLG_01402_11sp	-417,95321	-417,95321	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00240.16	ubiquitin(Ubiquitin family)
Supercontig_1.5_MVLG_00928_8sp	-373,94475	-373,94473	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00170.14	bZIP_1(bZIP transcription factor)
Supercontig_1.48_MVLG_04377_10sp	-292,68907	-292,68891	0,00032	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF00205.15	TPP_enzyme_M(Thiamine pyrophosphate enzyme, central domain)
Supercontig_1.16_MVLG_02204_8sp	-1086,5592	-1084,9092	3,30002	0,80795	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.26_MVLG_02988_11sp	-394,1142	-394,11424	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01769.9	MgtE(Divalent cation transporter)
Supercontig_1.20_MVLG_02530_9sp	-448,97601	-446,62147	4,70908	0,90506	*	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.4_MVLG_00806_7sp	-314,12603	-314,12593	0,0002	0	NS	0	[]	[]	[]	hypothetical protein	PF08583.3	Cmc1(Cytochrome c oxidase biogenesis protein Cmc1 like)
Supercontig_1.1164_MVLG_07354_6sp	-632,78882	-632,78849	0,00066	0,00033	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.2_MVLG_00382_10sp	-577,38585	-577,37535	0,021	0,01045	NS	0	[]	[]	[]	hypothetical protein	PF08022.5	FAD_binding_8(FAD-binding domain)
Supercontig_1.61_MVLG_04977_10sp	-786,6151	-786,61439	0,00142	0,00071	NS	0	[]	[]	[]	hypothetical protein	PF01490.11	Aa_trans(Transmembrane amino acid transporter protein)
Supercontig_1.11_MVLG_01714_10sp	-668,28628	-668,28628	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.78_MVLG_05583_12sp	-463,50139	-462,71281	1,57716	0,54551	NS	0	[]	[]	[]	hypothetical protein	PF00494.12	SQS_PSY(Squalene/phytoene synthase)
Supercontig_1.14_MVLG_01987_7sp	-650,70957	-650,70957	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02862.10	DDHD(DDHD domain)
Supercontig_1.46_MVLG_04257_11sp	-485,66025	-485,66025	0	0	NS	0	[]	[]	[]	hypothetical protein	PF08508.3	DUF1746(Fungal domain of unknown function (DUF1746))
Supercontig_1.57_MVLG_04825_10sp	-497,65623	-497,65623	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00443.22	UCH(Ubiquitin carboxyl-terminal hydrolase)

Supercontig_1.5_MVLG_00908_9sp	-943,66925	-943,66925	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00022.12	Actin(Actin)
Supercontig_1.30_MVLG_03262_10sp	-434,19532	-434,19532	0	0	NS	0	[]	[]	[]	AP-2 complex subunit sigma	PF01217.13	Clat_adaptor_s(Clathrin adaptor complex small chain)
Supercontig_1.9_MVLG_01521_10sp	-778,83607	-778,83607	0	0	NS	0	[]	[]	[]	CAMK/CAMKL/AMPK protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.73_MVLG_05423_10sp	-501,97815	-501,97815	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00013.22	KH_1(KH domain)
Supercontig_1.4_MVLG_00782_7sp	-295,06521	-295,06521	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03587.7	EMG1(EMG1/NEP1 methyltransferase)
Supercontig_1.65_MVLG_05139_7sp	-1212,5682	-1212,4703	0,19578	0,09325	NS	0	[]	[]	[]	hypothetical protein	PF07722.6	Peptidase_C26(Peptidase C26)
Supercontig_1.19_MVLG_02482_11sp	-1272,3414	-1270,9053	2,87226	0,76215	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.3_MVLG_00629_6sp	-955,22573	-953,91144	2,62858	0,73133	NS	0	[]	[]	[]	hypothetical protein	PF02628.8	COX15-CtaA(Cytochrome oxidase assembly protein)
Supercontig_1.51_MVLG_04516_8sp	-1039,9416	-1039,9416	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01490.11	Aa_trans(Transmembrane amino acid transporter protein)
Supercontig_1.36_MVLG_03692_10sp	-720,5623	-720,5623	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00732.12	GMC_oxred_N(GMC oxidoreductase)
Supercontig_1.101_MVLG_06159_7sp	-861,35103	-861,35096	0,00014	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.26_MVLG_02990_8sp	-437,66024	-437,66024	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00076.15	RRM_1(RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain))
Supercontig_1.31_MVLG_03363_10sp	-766,98996	-766,87775	0,22442	0,10614	NS	0	[]	[]	[]	hypothetical protein	PF09810.2	Morph_protein1(Defects in morphology protein 1, mitochondrial precursor)
Supercontig_1.34_MVLG_03550_8sp	-1067,0594	-1067,0594	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00439.18	Bromodomain(Bromodomain)
Supercontig_1.74_MVLG_05444_10sp	-618,64998	-618,64997	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00076.15	RRM_1(RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain))
Supercontig_1.15_MVLG_02061_8sp	-745,53219	-744,79744	1,4695	0,52037	NS	0	[]	[]	[]	hypothetical protein	PF00069.18	Pkinase(Protein kinase domain)
Supercontig_1.66_MVLG_05168_10sp	-616,00818	-616,00789	0,00058	0,00029	NS	0	[]	[]	[]	hypothetical protein	PF05721.6	PhyH(Phytanoyl-CoA dioxygenase (PhyH))
Supercontig_1.7_MVLG_01315_8sp	-564,38061	-562,94731	2,8666	0,76148	NS	0	[]	[]	[]	hypothetical protein	PF06911.5	Senescence(Senescence-associated protein)
Supercontig_1.16_MVLG_02169_12sp	-1025,8317	-1025,8317	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.27_MVLG_03103_8sp	-720,4413	-720,44094	0,00072	0,00036	NS	0	[]	[]	[]	hypothetical protein	PF00642.17	zf-CCCH(Zinc finger C-x8-C-x5-C-x3-H type (and similar))
Supercontig_1.84_MVLG_05768_11sp	-454,90196	-454,70222	0,39948	0,18106	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.9_MVLG_01547_8sp	-831,52807	-831,52791	0,00032	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF00501.21	AMP-binding(AMP-binding enzyme)
Supercontig_1.94_MVLG_06004_9sp	-352,04079	-352,04079	0	0	NS	0	[]	[]	[]	Ras-like protein Rab-7a	PF04670.5	Gtr1_RagA(Gtr1/RagA G protein conserved region)
Supercontig_1.70_MVLG_05325_8sp	-1803,8355	-1803,8355	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA

Supercontig_1.61_MVLG_04960_9sp	-337,58332	-337,58332	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.18_MVLG_02377_10sp	-1708,2123	-1707,2809	1,8627	0,60598	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.66_MVLG_05189_11sp	-584,84877	-582,66036	4,37682	0,88791	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.49_MVLG_04411_8sp	-824,97086	-824,81259	0,31654	0,14638	NS	0	[]	[]	[]	hypothetical protein	TIGR00560	TIGR00560(pgsA: CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase)
Supercontig_1.16_MVLG_02211_7sp	-758,39729	-758,39729	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.7_MVLG_01349_8sp	-954,87292	-954,87292	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00635.19	Motile_Sperm(MSP (Major sperm protein) domain)
Supercontig_1.67_MVLG_05222_9sp	-406,49237	-406,49237	0	0	NS	0	[]	[]	[]	ubiquitin-conjugating enzyme E2 G1	PF00179.19	UQ_con(Ubiquitin-conjugating enzyme)
Supercontig_1.47_MVLG_04342_10sp	-1102,302	-1102,302	0	0	NS	0	[]	[]	[]	Peroxisomal targeting signal (PTS1) receptor protein peroxin 5	PF00515.21	TPR_1(Tetratricopeptide repeat)
Supercontig_1.39_MVLG_03839_8sp	-686,83102	-686,83064	0,00076	0,00038	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.19_MVLG_02432_7sp	-406,03177	-405,24433	1,57488	0,54499	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.63_MVLG_05090_8sp	-456,47729	-456,47729	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.35_MVLG_03598_9sp	-330,66831	-330,64963	0,03736	0,01851	NS	0	[]	[]	[]	hypothetical protein	TIGR00506	TIGR00506(ribB: 3,4-dihydroxy-2-butanone-4-phosphate synthase)
Supercontig_1.1_MVLG_00043_10sp	-361,47477	-360,94138	1,06678	0,41339	NS	0	[]	[]	[]	hypothetical protein	PF00857.13	Isochorismatase(Isochorismatase family)
Supercontig_1.8_MVLG_01381_7sp	-380,68715	-380,53331	0,30768	0,14259	NS	0	[]	[]	[]	glycerol dehydrogenase	PF00248.14	Aldo_ket_red(Aldo/keto reductase family)
Supercontig_1.7_MVLG_01328_10sp	-420,50142	-420,28861	0,42562	0,19169	NS	0	[]	[]	[]	hypothetical protein	PF07491.4	PPI_Ypi1(Protein phosphatase inhibitor)
Supercontig_1.15_MVLG_02079_7sp	-556,68116	-556,63068	0,10096	0,04923	NS	0	[]	[]	[]	prefoldin	PF01920.13	Prefoldin_2(Prefoldin subunit)
Supercontig_1.5_MVLG_00909_8sp	-662,86427	-661,91144	1,90566	0,61435	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.8_MVLG_01404_10sp	-686,08042	-686,08042	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.39_MVLG_03831_9sp	-507,80806	-507,80762	0,00088	0,00044	NS	0	[]	[]	[]	hypothetical protein	TIGR01509	TIGR01509(HAD-SF-IA-v3: HAD hydrolase, family IA, variant 3)
Supercontig_1.6_MVLG_01189_7sp	-562,48496	-560,75867	3,45258	0,82206	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.10_MVLG_01616_10sp	-580,77618	-580,77618	0	0	NS	0	[]	[]	[]	hypothetical protein	PF12223.1	DUF3602(Protein of unknown function (DUF3602))
Supercontig_1.52_MVLG_04566_7sp	-675,69215	-675,62256	0,13918	0,06722	NS	0	[]	[]	[]	hypothetical protein	PF00775.14	Dioxygenase_C(Dioxygenase)
Supercontig_1.20_MVLG_02538_10sp	-896,67053	-895,91327	1,51452	0,53105	NS	0	[]	[]	[]	hypothetical protein	PF10419.2	TFIIIC_subunit(TFIIIC subunit)

Supercontig_1.20_MVLG_02606_6sp	-633,60899	-633,60889	0,0002	0	NS	0	[]	[]	[]	hypothetical protein	PF03348.8	Serinc(Serine incorporator (Serinc))
Supercontig_1.6_MVLG_01184_11sp	-735,36678	-735,36678	0	0	NS	0	[]	[]	[]	hypothetical protein	TIGR00434	TIGR00434(cysH: phosophoadenylyl-sulfate reductase)
Supercontig_1.5_MVLG_00963_7sp	-567,81888	-567,04108	1,5556	0,54058	NS	0	[]	[]	[]	hypothetical protein	PF02423.8	OCD_Mu_crystall(Ornithine cyclodeaminase/mu-crystallin family)
Supercontig_1.73_MVLG_05412_9sp	-1307,3681	-1306,8053	1,1256	0,43039	NS	0	[]	[]	[]	hypothetical protein	PF00855.10	PWWP(PWWP domain)
Supercontig_1.3_MVLG_00648_12sp	-1034,0382	-1030,0699	7,93672	0,9811	**	0	[]	[]	[]	hypothetical protein	PF02225.15	PA(PA domain)
Supercontig_1.54_MVLG_04652_7sp	-779,96025	-779,96025	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00172.11	Zn_clus(Fungal Zn(2)-Cys(6) binuclear cluster domain)
Supercontig_1.24_MVLG_02871_10sp	-417,0197	-417,00975	0,0199	0,0099	NS	0	[]	[]	[]	hypothetical protein	PF10193.2	Telomere_reg-2(Telomere length regulation protein)
Supercontig_1.6_MVLG_01211_9sp	-410,14677	-409,53963	1,21428	0,45509	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.161_MVLG_06870_8sp	-484,36092	-484,36073	0,00038	0,00019	NS	0	[]	[]	[]	malate dehydrogenase	PF02866.11	Ldh_1_C(lactate/malate dehydrogenase, alpha/beta C-terminal domain)
Supercontig_1.52_MVLG_04587_9sp	-486,73822	-485,91455	1,64734	0,56118	NS	0	[]	[]	[]	hypothetical protein	PF08636.3	Pkr1(ER protein Pkr1)
Supercontig_1.9_MVLG_01561_8sp	-494,05892	-494,0589	0	0	NS	0	[]	[]	[]	hypothetical protein	PF08227.4	DASH_Hsk3(DASH complex subunit Hsk3 like)
Supercontig_1.59_MVLG_04904_12sp	-493,75054	-493,7505	0	0	NS	0	[]	[]	[]	hypothetical protein	PF08939.3	DUF1917(Domain of unknown function (DUF1917))
Supercontig_1.1_MVLG_00143_9sp	-517,11901	-516,54807	1,14188	0,43501	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.4_MVLG_00864_11sp	-337,31264	-337,31264	0	0	NS	0	[]	[]	[]	glutamine synthetase	PF03951.12	Gln-synt_N(Glutamine synthetase, beta-Grasp domain)
Supercontig_1.13_MVLG_01968_8sp	-530,85164	-530,85164	0	0	NS	0	[]	[]	[]	rho-like protein rac1B	PF08477.6	Miro(Miro-like protein)
Supercontig_1.76_MVLG_05538_10sp	-427,91512	-427,30142	1,2274	0,45866	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.128_MVLG_06553_11sp	-613,55024	-613,55024	0	0	NS	0	[]	[]	[]	hypothetical protein	PF11911.1	DUF3429(Protein of unknown function (DUF3429))
Supercontig_1.42_MVLG_04052_11sp	-470,91262	-470,91262	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00350.16	Dynamin_N(Dynamin family)
Supercontig_1.2_MVLG_00319_11sp	-484,21905	-484,21905	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04072.7	LCM(Leucine carboxyl methyltransferase)
Supercontig_1.170_MVLG_06938_8sp	-394,03299	-394,03289	0,0002	0	NS	0	[]	[]	[]	hypothetical protein	PF00282.12	Pyridoxal_deC(Pyridoxal-dependent decarboxylase conserved domain)
Supercontig_1.67_MVLG_05234_6sp	-1546,4261	-1546,4261	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00664.16	ABC_membrane(ABC transporter transmembrane region)
Supercontig_1.7_MVLG_01267_11sp	-606,99832	-606,99826	0,00012	0	NS	0	[]	[]	[]	hypothetical protein	PF01428.9	zf-AN1(AN1-like Zinc finger)

Supercontig_1.12_MVLG_01841_12sp	-735,28397	-734,64532	1,2773	0,472	NS	0	[]	[]	[]	hypothetical protein	PF11701.1	UNC45-central(Myosin-binding striated muscle assembly central)
Supercontig_1.34_MVLG_03547_8sp	-317,81651	-317,81644	0,00014	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.165_MVLG_06907_7sp	-461,28256	-461,28248	0,00016	0	NS	0	[]	[]	[]	hypothetical protein	PF00012.13	HSP70(Hsp70 protein)
Supercontig_1.11_MVLG_01690_10sp	-389,84965	-389,84965	0	0	NS	0	[]	[]	[]	hypothetical protein	PF05730.4	CFEM(CFEM domain)
Supercontig_1.121_MVLG_06429_7sp	-653,95118	-653,95118	0	0	NS	0	[]	[]	[]	hypothetical protein	PF12090.1	Spt20(Spt20 family)
Supercontig_1.25_MVLG_02944_9sp	-1285,3496	-1285,3496	0	0	NS	0	[]	[]	[]	histidinol-phosphate aminotransferase	TIGR01141	TIGR01141(hisC: histidinol-phosphate transaminase)
Supercontig_1.5_MVLG_00991_7sp	-557,54242	-557,54242	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01266.17	DAO(FAD dependent oxidoreductase)
Supercontig_1.3_MVLG_00623_11sp	-403,95104	-403,86908	0,16392	0,07869	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.67_MVLG_05229_6sp	-824,99158	-824,99158	0	0	NS	0	[]	[]	[]	inositol-3-phosphate synthase 1-B	PF07994.5	NAD_binding_5(Myo-inositol-1-phosphate synthase)
Supercontig_1.80_MVLG_05639_11sp	-382,30595	-382,3058	0,0003	0,00015	NS	0	[]	[]	[]	hypothetical protein	PF02100.10	ODC_AZ(Ornithine decarboxylase antizyme)
Supercontig_1.55_MVLG_04745_11sp	-754,25771	-754,25744	0,00054	0,00027	NS	0	[]	[]	[]	hypothetical protein	PF00565.10	SNase(Staphylococcal nuclease homologue)
Supercontig_1.3_MVLG_00662_8sp	-862,16949	-862,16949	0	0	NS	0	[]	[]	[]	40S ribosomal protein S1	PF01015.11	Ribosomal_S3Ae(Ribosomal S3Ae family)
Supercontig_1.135_MVLG_06635_10sp	-641,1359	-641,13577	0,00026	0,00013	NS	0	[]	[]	[]	hypothetical protein	TIGR00081	TIGR00081(purC: phosphoribosylaminoimidazolesuccinocarboxamide synthase)
Supercontig_1.47_MVLG_04313_6sp	-559,53477	-559,36992	0,3297	0,15198	NS	0	[]	[]	[]	hit family protein 1	PF11969.1	DcpS_C(Scavenger mRNA decapping enzyme C-term binding)
Supercontig_1.56_MVLG_04797_9sp	-1087,4598	-1087,4598	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.21_MVLG_02620_10sp	-494,05841	-493,13506	1,8467	0,60281	NS	0	[]	[]	[]	hypothetical protein	PF00319.11	SRF-TF(SRF-type transcription factor (DNA-binding and dimerisation domain))
Supercontig_1.77_MVLG_05546_10sp	-805,81556	-805,81537	0,00038	0,00019	NS	0	[]	[]	[]	hypothetical protein	PF10296.2	DUF2404(Putative integral membrane protein conserved region (DUF2404))
Supercontig_1.220_MVLG_07159_7sp	-419,07503	-419,07466	0,00074	0,00037	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.7_MVLG_01288_12sp	-513,45286	-512,48708	1,93156	0,61931	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.6_MVLG_01169_12sp	-315,80031	-315,80028	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00743.12	FMO-like(Flavin-binding monooxygenase-like)
Supercontig_1.5_MVLG_00964_10sp	-635,89965	-635,89964	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00320.20	GATA(GATA zinc finger)
Supercontig_1.74_MVLG_05460_10sp	-292,61518	-292,61514	0	0	NS	0	[]	[]	[]	hypothetical protein	PF08700.4	Vps51(Vps51/Vps67)

Supercontig_1.35_MVLG_03600_9sp	-516,63698	-516,54567	0,18262	0,08727	NS	0	[]	[]	[]	hypothetical protein	PF00276.13	Ribosomal_L23(Ribosomal protein L23)
Supercontig_1.150_MVLG_06769_10sp	-296,13136	-296,13105	0,00062	0,00031	NS	0	[]	[]	[]	20S proteasome subunit alpha 6	PF00227.19	Proteasome(Proteasome subunit)
Supercontig_1.53_MVLG_04612_8sp	-374,54259	-374,54259	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00583.17	Acetyltransf_1(Acetyltransferase (GNAT) family)
Supercontig_1.54_MVLG_04650_11sp	-397,2852	-397,2852	0	0	NS	0	[]	[]	[]	glycerol-3-phosphate dehydrogenase [NAD+] 1	TIGR03376	TIGR03376(glycerol3P_DH: glycerol-3-phosphate dehydrogenase (NAD(+)))
Supercontig_1.30_MVLG_03287_8sp	-462,91784	-461,57022	2,69524	0,74014	NS	0	[]	[]	[]	hypothetical protein	PF05572.6	Peptidase_M43(Pregnancy-associated plasma protein-A)
Supercontig_1.8_MVLG_01426_10sp	-1019,0864	-1019,0859	0,00088	0,00044	NS	0	[]	[]	[]	prolyl-tRNA synthetase	PF00587.18	tRNA-synt_2b(tRNA synthetase class II core domain (G, H, P, S and T))
Supercontig_1.63_MVLG_05071_9sp	-638,22335	-637,04383	2,35904	0,69257	NS	0	[]	[]	[]	hypothetical protein	PF01105.17	EMP24_GP25L(emp24/gp25L/p24 family/GOLD)
Supercontig_1.31_MVLG_03335_7sp	-281,26781	-281,26749	0,00064	0,00032	NS	0	[]	[]	[]	hypothetical protein	PF09495.3	DUF2462(Protein of unknown function (DUF2462))
Supercontig_1.7_MVLG_01354_12sp	-532,21279	-532,21276	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03178.8	CPSF_A(CPSF A subunit region)
Supercontig_1.38_MVLG_03817_12sp	-350,15214	-350,15214	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.23_MVLG_02779_8sp	-895,4829	-895,48267	0,00046	0,00023	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.8_MVLG_01472_7sp	-1141,3415	-1141,3415	0	0	NS	0	[]	[]	[]	hypothetical protein	PF10277.2	Frag1(Frag1/DRAM/Sfk1 family)
Supercontig_1.67_MVLG_05210_11sp	-866,50941	-865,30923	2,40036	0,69886	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.104_MVLG_06205_10sp	-960,52918	-960,52918	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00018.21	SH3_1(SH3 domain)
Supercontig_1.10_MVLG_01594_6sp	-801,58219	-801,58219	0	0	NS	0	[]	[]	[]	ATP synthase (E/31 kDa) subunit	PF01991.11	vATP-synt_E(ATP synthase (E/31 kDa) subunit)
Supercontig_1.76_MVLG_05532_7sp	-333,87286	-333,87286	0	0	NS	0	[]	[]	[]	hypothetical protein	PF08982.4	DUF1857(Domain of unknown function (DUF1857))
Supercontig_1.38_MVLG_03781_11sp	-604,43531	-604,43531	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.66_MVLG_05174_7sp	-905,374	-905,08395	0,5801	0,25177	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.32_MVLG_03390_10sp	-439,75849	-439,75849	0	0	NS	0	[]	[]	[]	hypothetical protein	PF09542.3	FFD_TFG(FFD and TFG box motifs)
Supercontig_1.48_MVLG_04373_9sp	-470,48668	-470,26864	0,43608	0,19591	NS	0	[]	[]	[]	aldehyde dehydrogenase (NAD+)	PF00171.15	Aldedh(Aldehyde dehydrogenase family)
Supercontig_1.110_MVLG_06293_8sp	-483,98314	-483,69854	0,5692	0,24768	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.79_MVLG_05628_11sp	-429,13567	-429,13567	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.17_MVLG_02346_8sp	-319,95002	-319,94998	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA

Supercontig_1.66_MVLG_05179_7sp	-561,06974	-561,06973	0	0	NS	0	[]	[]	[]	hypothetical protein	TIGR00879	TIGR00879(SP: MFS transporter, sugar porter (SP) family)
Supercontig_1.12_MVLG_01860_10sp	-733,71199	-733,71199	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04880.6	NUDE_C(NUDE protein, C-terminal conserved region)
Supercontig_1.11_MVLG_01702_10sp	-547,59004	-547,59004	0	0	NS	0	[]	[]	[]	DNA replication licensing factor mcm7	PF00493.16	MCM(MCM2/3/5 family)
Supercontig_1.5_MVLG_00883_11sp	-424,38221	-422,90991	2,9446	0,7706	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.53_MVLG_04607_7sp	-620,71292	-620,71292	0	0	NS	0	[]	[]	[]	BUD32 protein kinase	PF00069.18	Pkinase(Protein kinase domain)
Supercontig_1.7_MVLG_01342_8sp	-442,84102	-442,841	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01126.13	Heme_oxygenase(Heme oxygenase)
Supercontig_1.1_MVLG_00113_10sp	-591,03701	-590,85094	0,37214	0,16978	NS	0	[]	[]	[]	hypothetical protein	PF00046.22	Homeobox(Homeobox domain)
Supercontig_1.53_MVLG_04638_11sp	-412,7453	-411,94485	1,6009	0,55087	NS	0	[]	[]	[]	hypothetical protein	PF04248.5	DUF427(Domain of unknown function (DUF427))
Supercontig_1.60_MVLG_04949_10sp	-1157,1645	-1156,9381	0,45274	0,20258	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.5_MVLG_00948_10sp	-323,94333	-323,9432	0,00026	0,00013	NS	0	[]	[]	[]	hypothetical protein	PF07728.7	AAA_5(AAA domain (dynein-related subfamily))
Supercontig_1.19_MVLG_02438_9sp	-887,01394	-886,53207	0,96374	0,38237	NS	0	[]	[]	[]	hypothetical protein	PF01762.14	Galactosyl_T(Galactosyltransferase)
Supercontig_1.27_MVLG_03079_10sp	-375,57267	-375,55742	0,0305	0,01513	NS	0	[]	[]	[]	CMGC/MAPK protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.59_MVLG_04920_10sp	-320,62595	-320,62588	0,00014	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.68_MVLG_05252_10sp	-538,60903	-538,60232	0,01342	0	NS	0	[]	[]	[]	hypothetical protein	PF07859.6	Abhydrolase_3(alpha/beta hydrolase fold)
Supercontig_1.36_MVLG_03673_9sp	-556,4229	-556,4222	0,0014	0	NS	0	[]	[]	[]	hypothetical protein	PF01433.13	Peptidase_M1(Peptidase family M1)
Supercontig_1.7_MVLG_01320_8sp	-481,28696	-481,28688	0,00016	0	NS	0	[]	[]	[]	hypothetical protein	PF04667.10	Endosulfine(cAMP-regulated phosphoprotein/endosulfine conserved region)
Supercontig_1.3_MVLG_00548_7sp	-354,35331	-354,35306	0,0005	0,00025	NS	0	[]	[]	[]	small COPII coat GTPase	PF04670.5	Gtr1_RagA(Gtr1/RagA G protein conserved region)
Supercontig_1.75_MVLG_05485_12sp	-555,28555	-555,10635	0,3584	0,16406	NS	0	[]	[]	[]	hypothetical protein	PF09350.3	DUF1992(Domain of unknown function (DUF1992))
Supercontig_1.1_MVLG_00237_10sp	-742,9016	-742,9016	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.62_MVLG_05028_8sp	-464,99342	-464,81686	0,35312	0,16185	NS	0	[]	[]	[]	hypothetical protein	PF04795.5	PAPA-1(PAPA-1-like conserved region)
Supercontig_1.38_MVLG_03772_12sp	-457,17707	-457,17707	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04147.5	Nop14(Nop14-like family)
Supercontig_1.65_MVLG_05134_10sp	-816,62513	-816,60437	0,04152	0,02055	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.9_MVLG_01494_11sp	-1074,3595	-1074,3595	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.3_MVLG_00517_7sp	-767,96141	-767,10635	1,71012	0,57474	NS	0	[]	[]	[]	hypothetical protein	PF00400.25	WD40(WD domain, G-beta repeat)

Supercontig_1.26_MVLG_03041_9sp	-1265,6281	-1265,6281	0	0	NS	0	[]	[]	[]	hypothetical protein	PF07690.9	MFS_1(Major Facilitator Superfamily)
Supercontig_1.101_MVLG_06153_10sp	-456,13184	-456,13184	0	0	NS	0	[]	[]	[]	hypothetical protein	PF08696.4	Dna2(DNA replication factor Dna2)
Supercontig_1.42_MVLG_04053_9sp	-605,90351	-605,69543	0,41616	0,18786	NS	0	[]	[]	[]	hypothetical protein	PF05008.8	V-SNARE(Vesicle transport v-SNARE protein N-terminus)
Supercontig_1.53_MVLG_04604_7sp	-1123,0655	-1123,0655	0	0	NS	0	[]	[]	[]	hypothetical protein	TIGR01241	TIGR01241(FtsH_fam: ATP-dependent metallopeptidase HflB)
Supercontig_1.10_MVLG_01597_7sp	-1151,0602	-1151,0602	0	0	NS	0	[]	[]	[]	hypothetical protein	PF06772.4	LtrA(Bacterial low temperature requirement A protein (LtrA))
Supercontig_1.5_MVLG_01036_10sp	-507,46443	-507,46443	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00092.21	VWA(von Willebrand factor type A domain)
Supercontig_1.6_MVLG_01112_8sp	-846,10489	-845,79475	0,62028	0,26666	NS	0	[]	[]	[]	hypothetical protein	PF00106.18	adh_short(short chain dehydrogenase)
Supercontig_1.808_MVLG_07315_10sp	-377,96137	-378,58416	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01636.16	APH(Phosphotransferase enzyme family)
Supercontig_1.77_MVLG_05560_6sp	-1664,4679	-1664,4679	0	0	NS	0	[]	[]	[]	E3 ubiquitin-protein ligase NEDD4	PF00632.18	HECT(HECT-domain (ubiquitin-transferase))
Supercontig_1.10_MVLG_01670_7sp	-818,61033	-818,61033	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.36_MVLG_03696_8sp	-651,69697	-651,69693	0	0	NS	0	[]	[]	[]	hypothetical protein	TIGR01685	TIGR01685(MDP-1: magnesium-dependent phosphatase-1)
Supercontig_1.6_MVLG_01090_10sp	-1344,417	-1344,4167	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02985.15	HEAT(HEAT repeat)
Supercontig_1.3_MVLG_00535_6sp	-730,32421	-730,32412	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00378.13	ECH(Enoyl-CoA hydratase/isomerase family)
Supercontig_1.7_MVLG_01282_10sp	-886,84722	-885,67847	2,3375	0,68924	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.54_MVLG_04682_9sp	-787,6204	-787,47665	0,2875	0,1339	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.135_MVLG_06632_7sp	-498,65958	-498,10019	1,11878	0,42844	NS	0	[]	[]	[]	CDF-like metal transporter	PF01545.14	Cation_efflux(Cation efflux family)
Supercontig_1.24_MVLG_02841_9sp	-1504,3786	-1504,2118	0,33366	0,15366	NS	0	[]	[]	[]	hypothetical protein	PF03815.12	LCCL(LCCL domain)
Supercontig_1.39_MVLG_03859_10sp	-748,62642	-748,62642	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01490.11	Aa_trans(Transmembrane amino acid transporter protein)
Supercontig_1.4_MVLG_00863_11sp	-508,27483	-508,04178	0,4661	0,20789	NS	0	[]	[]	[]	hypothetical protein	PF00515.21	TPR_1(Tetratricopeptide repeat)
Supercontig_1.52_MVLG_04564_10sp	-501,78123	-501,7803	0,00186	0,00093	NS	0	[]	[]	[]	hypothetical protein	PF08662.4	eIF2A(Eukaryotic translation initiation factor eIF2A)
Supercontig_1.110_MVLG_06302_8sp	-315,54559	-315,54559	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01423.15	LSM(LSM domain)
Supercontig_1.109_MVLG_06284_12sp	-397,47307	-397,4232	0,09974	0,04865	NS	0	[]	[]	[]	hypothetical protein	TIGR00030	TIGR00030(S21p: ribosomal protein S21)
Supercontig_1.64_MVLG_05095_9sp	-460,22079	-460,22079	0	0	NS	0	[]	[]	[]	hypothetical protein	PF08578.3	DUF1765(Protein of unknown function (DUF1765))

Supercontig_1.2_MVLG_00350_10sp	-622,27902	-622,27834	0,00136	0,00068	NS	0	[]	[]	[]	TATA-box-binding protein	PF00352.14	TBP(Transcription factor TFIID (or TATA-binding protein, TBP))
Supercontig_1.5_MVLG_00888_9sp	-556,19919	-555,26801	1,86236	0,60591	NS	0	[]	[]	[]	hsp10-like protein	PF00166.14	Cpn10(Chaperonin 10 Kd subunit)
Supercontig_1.21_MVLG_02614_8sp	-885,15413	-885,1538	0,00066	0,00033	NS	0	[]	[]	[]	hypothetical protein	PF00400.25	WD40(WD domain, G-beta repeat)
Supercontig_1.21_MVLG_02632_12sp	-378,84489	-378,5996	0,49058	0,21752	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.4_MVLG_00720_10sp	-374,80699	-374,18928	1,23542	0,46082	NS	0	[]	[]	[]	uracil phosphoribosyltransferase	TIGR01091	TIGR01091(upp: uracil phosphoribosyltransferase)
Supercontig_1.15_MVLG_02153_9sp	-378,86383	-378,86383	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.11_MVLG_01762_8sp	-368,0302	-366,50967	3,04106	0,7814	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.2_MVLG_00440_11sp	-349,80317	-349,80305	0,00024	0,00012	NS	0	[]	[]	[]	hypothetical protein	PF03547.11	Mem_trans(Membrane transport protein)
Supercontig_1.35_MVLG_03592_9sp	-518,02786	-517,58866	0,8784	0,35545	NS	0	[]	[]	[]	DNA-directed RNA polymerase II subunit H	PF03870.8	RNA_pol_Rpb8(RNA polymerase Rpb8)
Supercontig_1.14_MVLG_02033_6sp	-1180,8213	-1180,8107	0,02138	0,01063	NS	0	[]	[]	[]	hypothetical protein	TIGR01494	TIGR01494(ATPase_P-type: HAD ATPase, P-type, family IC)
Supercontig_1.36_MVLG_03660_10sp	-589,72577	-589,67867	0,0942	0,04601	NS	0	[]	[]	[]	CAMKK/ELM protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.54_MVLG_04653_9sp	-542,81259	-542,81205	0,00108	0,00054	NS	0	[]	[]	[]	hypothetical protein	PF04189.6	Gcd10p(Gcd10p family)
Supercontig_1.77_MVLG_05544_9sp	-655,11902	-655,11857	0,0009	0,00045	NS	0	[]	[]	[]	hypothetical protein	PF11799.1	IMS_C(impB/mucB/samB family C-terminal)
Supercontig_1.32_MVLG_03440_7sp	-854,6293	-854,32068	0,61724	0,26554	NS	0	[]	[]	[]	imidazoleglycerol-phosphate dehydratase	PF00475.11	IGPD(Imidazoleglycerol-phosphate dehydratase)
Supercontig_1.38_MVLG_03797_6sp	-600,08081	-600,08063	0,00036	0,00018	NS	0	[]	[]	[]	hypothetical protein	TIGR00177	TIGR00177(molyb_syn: molybdenum cofactor synthesis domain)
Supercontig_1.102_MVLG_06182_7sp	-357,58371	-356,82802	1,51138	0,53031	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.41_MVLG_03984_11sp	-622,90448	-622,90448	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02893.13	GRAM(GRAM domain)
Supercontig_1.56_MVLG_04785_6sp	-625,39487	-625,24728	0,29518	0,13722	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.99_MVLG_06117_6sp	-618,48777	-618,48777	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.24_MVLG_02847_9sp	-456,87945	-456,56542	0,62806	0,2695	NS	0	[]	[]	[]	hypothetical protein	PF00237.12	Ribosomal_L22(Ribosomal protein L22p/L17e)
Supercontig_1.17_MVLG_02291_6sp	-726,52411	-725,46641	2,1154	0,65275	NS	0	[]	[]	[]	hypothetical protein	PF06966.5	DUF1295(Protein of unknown function (DUF1295))
Supercontig_1.122_MVLG_06467_8sp	-509,47046	-509,47037	0,00018	0	NS	0	[]	[]	[]	hypothetical protein	PF00400.25	WD40(WD domain, G-beta repeat)

Supercontig_1.49_MVLG_04434_6sp	-317,22267	-317,22257	0,0002	0	NS	0	[]	[]	[]	small nuclear ribonucleoprotein Sm D1	PF01423.15	LSM(LSM domain)
Supercontig_1.17_MVLG_02339_6sp	-439,36564	-439,36564	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.6_MVLG_01070_6sp	-825,56769	-825,50571	0,12396	0,0601	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.124_MVLG_06492_8sp	-543,8538	-542,97574	1,75612	0,58441	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.8_MVLG_01391_10sp	-493,83058	-493,83058	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04438.9	zf-HIT(HIT zinc finger)
Supercontig_1.56_MVLG_04780_7sp	-360,08873	-359,4443	1,28886	0,47504	NS	0	[]	[]	[]	hypothetical protein	PF00117.21	GATase(Glutamine amidotransferase class-I)
Supercontig_1.156_MVLG_06834_6sp	-828,98196	-828,86847	0,22698	0,10729	NS	0	[]	[]	[]	hypothetical protein	PF00026.16	Asp(Eukaryotic aspartyl protease)
Supercontig_1.2_MVLG_00283_10sp	-601,59285	-599,74299	3,69972	0,84274	NS	0	[]	[]	[]	hypothetical protein	PF00400.25	WD40(WD domain, G-beta repeat)
Supercontig_1.6_MVLG_01074_6sp	-379,48229	-379,48216	0,00026	0,00013	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.1_MVLG_00262_10sp	-511,79435	-511,27778	1,03314	0,40344	NS	0	[]	[]	[]	hypothetical protein	PF08652.4	RAI1(RAI1 like)
Supercontig_1.22_MVLG_02687_9sp	-467,21374	-467,17087	0,08574	0,04196	NS	0	[]	[]	[]	regulator-nonsense transcripts 1	PF04851.8	ResIII(Type III restriction enzyme, res subunit)
Supercontig_1.303_MVLG_07236_6sp	-407,5158	-407,51578	0	0	NS	0	[]	[]	[]	hypothetical protein	PF09369.3	DUF1998(Domain of unknown function (DUF1998))
Supercontig_1.53_MVLG_04643_8sp	-1214,3504	-1214,3499	0,00102	0,00051	NS	0	[]	[]	[]	4-aminobutyrate aminotransferase	PF00202.14	Aminotran_3(Aminotransferase class-III)
Supercontig_1.74_MVLG_05463_10sp	-585,50574	-586,70894	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.20_MVLG_02557_9sp	-470,61073	-470,02736	1,16674	0,44199	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.57_MVLG_04820_8sp	-457,50342	-457,50342	0	0	NS	0	[]	[]	[]	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino] imidazole-4-carboxamide isomerase	TIGR02129	TIGR02129(hisA_euk: phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase)
Supercontig_1.9_MVLG_01488_8sp	-701,99365	-701,97896	0,02938	0,01458	NS	0	[]	[]	[]	hypothetical protein	PF03403.6	PAF-AH_p_II(isoform II)
Supercontig_1.202_MVLG_07093_9sp	-569,99672	-569,99672	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02837.11	Glyco_hydro_2_N(Glycosyl hydrolases family 2, sugar binding domain)
Supercontig_1.8_MVLG_01453_10sp	-534,03229	-534,03229	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.13_MVLG_01951_11sp	-755,92214	-754,28007	3,28414	0,80642	NS	0	[]	[]	[]	hypothetical protein	PF10282.2	Muc_lac_enz(3-carboxy-cis,cis-muconate lactonizing enzyme)
Supercontig_1.57_MVLG_04822_10sp	-580,71182	-580,04473	1,33418	0,4868	NS	0	[]	[]	[]	hypothetical protein	NA	NA

Supercontig_1.123_MVLG_06471_9sp	-1818,341	-1818,031	0,6201	0,26659	NS	0	[]	[]	[]	hypothetical protein	PF03099.12	BPL_LplA_LipB(Biotin/lipoate A/B protein ligase family)
Supercontig_1.22_MVLG_02695_12sp	-407,34514	-407,34514	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04851.8	ResIII(Type III restriction enzyme, res subunit)
Supercontig_1.2_MVLG_00411_9sp	-907,14959	-906,16966	1,95986	0,62466	NS	0	[]	[]	[]	hypothetical protein	PF01239.15	PPTA(Protein prenyltransferase alpha subunit repeat)
Supercontig_1.20_MVLG_02531_8sp	-770,88233	-770,88233	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.11_MVLG_01787_10sp	-606,71811	-606,34083	0,75456	0,31428	NS	0	[]	[]	[]	hypothetical protein	PF01544.11	CorA(CorA-like Mg2+ transporter protein)
Supercontig_1.19_MVLG_02505_9sp	-437,18386	-436,88246	0,6028	0,26022	NS	0	[]	[]	[]	40S ribosomal protein S6-B	PF01092.12	Ribosomal_S6e(Ribosomal protein S6e)
Supercontig_1.3_MVLG_00547_11sp	-526,12482	-526,12446	0,00072	0,00036	NS	0	[]	[]	[]	V-type proton ATPase subunit D	PF01813.10	ATP-synt_D(ATP synthase subunit D)
Supercontig_1.17_MVLG_02304_7sp	-449,21587	-448,26984	1,89206	0,61172	NS	0	[]	[]	[]	CMGC/CDK/CDK7 protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.19_MVLG_02481_11sp	-561,69223	-559,17278	5,0389	0,9195	*	0	[]	[]	[]	hypothetical protein	PF12239.1	DUF3605(Protein of unknown function (DUF3605))
Supercontig_1.77_MVLG_05555_9sp	-763,36996	-762,68811	1,3637	0,49432	NS	0	[]	[]	[]	hypothetical protein	PF00454.20	PI3_PI4_kinase(Phosphatidylinositol 3- and 4-kinase)
Supercontig_1.70_MVLG_05341_10sp	-580,10958	-580,10958	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.40_MVLG_03926_9sp	-1106,2856	-1106,2856	0	0	NS	0	[]	[]	[]	acetyl-CoA acetyltransferase	TIGR01930	TIGR01930(AcCoA-C-Actrans: acetyl-CoA C-acetyltransferase)
Supercontig_1.128_MVLG_06552_8sp	-483,5704	-483,53507	0,07066	0,03471	NS	0	[]	[]	[]	hypothetical protein	PF01753.11	zf-MYND(MYND finger)
Supercontig_1.1_MVLG_00184_9sp	-899,22926	-897,81206	2,8344	0,75761	NS	0	[]	[]	[]	hypothetical protein	PF07859.6	Abhydrolase_3(alpha/beta hydrolase fold)
Supercontig_1.7_MVLG_01351_9sp	-659,16047	-659,03907	0,2428	0,11432	NS	0	[]	[]	[]	hypothetical protein	PF09749.2	HVSL(Uncharacterised conserved protein)
Supercontig_1.14_MVLG_02035_12sp	-570,98708	-569,80928	2,3556	0,69204	NS	0	[]	[]	[]	hypothetical protein	PF05277.5	DUF726(Protein of unknown function (DUF726))
Supercontig_1.27_MVLG_03118_6sp	-927,58947	-926,65264	1,87366	0,60813	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.24_MVLG_02834_6sp	-676,212	-676,212	0	0	NS	0	[]	[]	[]	hypothetical protein	PF11815.1	DUF3336(Domain of unknown function (DUF3336))
Supercontig_1.8_MVLG_01418_10sp	-778,6045	-778,6045	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03343.6	SART-1(SART-1 family)
Supercontig_1.27_MVLG_03072_10sp	-487,28615	-487,20849	0,15532	0,07472	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.154_MVLG_06807_9sp	-493,50849	-493,50698	0,00302	0,00151	NS	0	[]	[]	[]	hypothetical protein	PF07250.4	Glyoxal_oxid_N(Glyoxal oxidase N-terminus)
Supercontig_1.143_MVLG_06722_9sp	-741,61568	-741,54658	0,1382	0,06677	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.25_MVLG_02936_8sp	-605,66173	-605,66157	0,00032	0,00016	NS	0	[]	[]	[]	gamma-glutamyltransferase	PF01019.14	G_glu_transpept(Gamma-glutamyltranspeptidase)
Supercontig_1.64_MVLG_05115_11sp	-808,28296	-808,28296	0	0	NS	0	[]	[]	[]	aldehyde dehydrogenase (NAD+)	PF00171.15	Aldedh(Aldehyde dehydrogenase family)

Supercontig_1.62_MVLG_05000_7sp	-513,47765	-513,47765	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00005.20	ABC_tran(ABC transporter)
Supercontig_1.17_MVLG_02258_10sp	-843,16454	-841,91481	2,49946	0,71342	NS	0	[]	[]	[]	hypothetical protein	PF00226.24	DnaJ(DnaJ domain)
Supercontig_1.5_MVLG_01008_8sp	-438,39967	-438,39953	0,00028	0,00014	NS	0	[]	[]	[]	seryl-tRNA synthetase, cytoplasmic	PF00587.18	tRNA-synt_2b(tRNA synthetase class II core domain (G, H, P, S and T))
Supercontig_1.15_MVLG_02140_7sp	-1050,1691	-1049,8044	0,7294	0,3056	NS	0	[]	[]	[]	diphosphomevalonate decarboxylase	PF00288.19	GHMP_kinases_N(GHMP kinases N terminal domain)
Supercontig_1.94_MVLG_05999_9sp	-386,89664	-386,88185	0,02958	0,01468	NS	0	[]	[]	[]	hypothetical protein	PF03381.8	CDC50(LEM3 (ligand-effect modulator 3) family / CDC50 family)
Supercontig_1.52_MVLG_04561_9sp	-960,47572	-960,42017	0,1111	0,05404	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.8_MVLG_01416_9sp	-1012,6235	-1012,6235	0	0	NS	0	[]	[]	[]	protein SEY1	PF00350.16	Dynamin_N(Dynamin family)
Supercontig_1.6_MVLG_01111_9sp	-388,29845	-386,65212	3,29266	0,80724	NS	0	[]	[]	[]	hypothetical protein	PF01633.13	Choline_kinase(Choline/ethanolamine kinase)
Supercontig_1.41_MVLG_03993_12sp	-926,09344	-926,09294	0,001	0,0005	NS	0	[]	[]	[]	hypothetical protein	TIGR00378	TIGR00378(cax: calcium/proton exchanger)
Supercontig_1.87_MVLG_05847_12sp	-661,95747	-661,31875	1,27744	0,47203	NS	0	[]	[]	[]	hypothetical protein	TIGR00879	TIGR00879(SP: MFS transporter, sugar porter (SP) family)
Supercontig_1.5_MVLG_01016_9sp	-477,20141	-477,04809	0,30664	0,14214	NS	0	[]	[]	[]	hypothetical protein	PF00096.19	zf-C2H2(Zinc finger, C2H2 type)
Supercontig_1.24_MVLG_02892_12sp	-683,01789	-683,01789	0	0	NS	0	[]	[]	[]	U5 small nuclear ribonucleoprotein component	PF03144.18	GTP_EFTU_D2(Elongation factor Tu domain 2)
Supercontig_1.4_MVLG_00722_8sp	-789,43178	-789,43158	0,0004	0,0002	NS	0	[]	[]	[]	hypothetical protein	PF00153.20	Mito_carr(Mitochondrial carrier protein)
Supercontig_1.28_MVLG_03183_7sp	-1036,3612	-1036,3063	0,10988	0,05346	NS	0	[]	[]	[]	hypothetical protein	PF07264.4	EI24(Etoposide-induced protein 2.4 (EI24))
Supercontig_1.62_MVLG_05030_10sp	-400,3515	-400,35138	0,00024	0,00012	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.141_MVLG_06701_6sp	-1012,7675	-1012,7675	0	0	NS	0	[]	[]	[]	hypothetical protein	PF09402.3	MSC(Man1-Src1p-C-terminal domain)
Supercontig_1.7_MVLG_01346_10sp	-1755,9768	-1755,9768	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.213_MVLG_07134_10sp	-518,42358	-518,42358	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.111_MVLG_06308_11sp	-657,26752	-657,26751	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02475.9	Met_10(Met-10+ like-protein)
Supercontig_1.83_MVLG_05742_11sp	-511,27945	-511,27902	0,00086	0,00043	NS	0	[]	[]	[]	hypothetical protein	PF03663.7	Glyco_hydro_76(Glycosyl hydrolase family 76)
Supercontig_1.61_MVLG_04970_10sp	-401,16658	-401,16658	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04116.6	FA_hydroxylase(Fatty acid hydroxylase superfamily)
Supercontig_1.101_MVLG_06158_11sp	-430,67368	-430,67368	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01637.11	Arch_ATPase(Archaeal ATPase)
Supercontig_1.6_MVLG_01161_7sp	-289,89175	-289,79551	0,19248	0,09175	NS	0	[]	[]	[]	hypothetical protein	PF03765.8	CRAL_TRIO_N(CRAL/TRIO, N-terminus)
Supercontig_1.46_MVLG_04262_10sp	-352,5893	-352,5893	0	0	NS	0	[]	[]	[]	hypothetical protein	PF07719.10	TPR_2(Tetratricopeptide repeat)

Supercontig_1.58_MVLG_04863_11sp	-526,16893	-525,17057	1,99672	0,63152	NS	0	[]	[]	[]	hypothetical protein	PF08615.4	RNase_H2_suC(Ribonuclease H2 non-catalytic subunit (Ylr154p-like))
Supercontig_1.45_MVLG_04187_10sp	-743,78526	-743,78487	0,00078	0,00039	NS	0	[]	[]	[]	carbamoyl-phosphate synthase arginine-specific large chain	PF02222.15	ATP-grasp(ATP-grasp domain)
Supercontig_1.49_MVLG_04419_7sp	-504,98355	-504,97803	0,01104	0,0055	NS	0	[]	[]	[]	hypothetical protein	PF08287.4	DASH_Spc19(Spc19)
Supercontig_1.4_MVLG_00697_10sp	-943,10423	-943,10423	0	0	NS	0	[]	[]	[]	hypothetical protein	PF06333.5	Med13_C(Mediator complex subunit 13 C-terminal)
Supercontig_1.56_MVLG_04775_8sp	-550,51118	-550,51118	0	0	NS	0	[]	[]	[]	hypothetical protein	PF06912.4	DUF1275(Protein of unknown function (DUF1275))
Supercontig_1.203_MVLG_07098_9sp	-890,31915	-890,31915	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04499.8	SAPS(SIT4 phosphatase-associated protein)
Supercontig_1.5_MVLG_00967_11sp	-434,07552	-434,0755	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00226.24	DnaJ(DnaJ domain)
Supercontig_1.156_MVLG_06830_8sp	-783,32727	-783,32727	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00909.14	Ammonium_transp(Ammonium Transporter Family)
Supercontig_1.44_MVLG_04181_9sp	-560,91539	-560,91539	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00106.18	adh_short(short chain dehydrogenase)
Supercontig_1.180_MVLG_07002_9sp	-970,8806	-970,72563	0,30994	0,14356	NS	0	[]	[]	[]	AGC/AKT protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.27_MVLG_03126_9sp	-688,81907	-688,81907	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00995.16	Sec1(Sec1 family)
Supercontig_1.29_MVLG_03212_8sp	-1148,2445	-1148,2444	0,00014	0	NS	0	[]	[]	[]	hypothetical protein	PF00400.25	WD40(WD domain, G-beta repeat)
Supercontig_1.24_MVLG_02891_6sp	-361,26105	-361,26093	0,00024	0,00012	NS	0	[]	[]	[]	endoribonuclease L-PSP	PF01042.14	Ribonuc_L-PSP(Endoribonuclease L-PSP)
Supercontig_1.30_MVLG_03270_8sp	-520,65305	-520,65288	0,00034	0,00017	NS	0	[]	[]	[]	tryptophan synthase	TIGR00262	TIGR00262(trpA: tryptophan synthase, alpha subunit)
Supercontig_1.20_MVLG_02561_12sp	-538,849	-538,8397	0,0186	0,00926	NS	0	[]	[]	[]	hypothetical protein	PF05721.6	PhyH(Phytanoyl-CoA dioxygenase (PhyH))
Supercontig_1.7_MVLG_01232_11sp	-521,87066	-521,87065	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.1_MVLG_00181_7sp	-620,6297	-619,24085	2,7777	0,75064	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.40_MVLG_03927_8sp	-396,50533	-396,16062	0,68942	0,29157	NS	0	[]	[]	[]	NADH-ubiquinone oxidoreductase 78 kDa subunit	PF00384.15	Molybdopterin(Molybdopterin oxidoreductase)
Supercontig_1.63_MVLG_05073_10sp	-444,47821	-444,47821	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03126.11	Plus-3(Plus-3 domain)
Supercontig_1.34_MVLG_03573_10sp	-457,85764	-457,85765	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.15_MVLG_02156_7sp	-620,27785	-619,07064	2,41442	0,70097	NS	0	[]	[]	[]	hypothetical protein	PF10165.2	Ric8(Guanine nucleotide exchange factor synembryn)
Supercontig_1.41_MVLG_04003_10sp	-442,47188	-442,28535	0,37306	0,17017	NS	0	[]	[]	[]	hypothetical protein	PF04194.6	PDCD2_C(Programmed cell death protein 2, C-terminal putative domain)
Supercontig_1.20_MVLG_02562_6sp	-1287,5319	-1287,446	0,17168	0,08226	NS	0	[]	[]	[]	hypothetical protein	PF00106.18	adh_short(short chain dehydrogenase)

Supercontig_1.11_MVLG_01691_8sp	-850,71199	-848,848	3,72798	0,84495	NS	0	[]	[]	[]	hypothetical protein	PF04177.5	TAP42(TAP42-like family)
Supercontig_1.112_MVLG_06322_9sp	-570,39765	-570,39765	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03171.13	2OG-FeII_Oxy(2OG-Fe(II) oxygenase superfamily)
Supercontig_1.45_MVLG_04220_8sp	-1296,8861	-1296,8615	0,0492	0,0243	NS	0	[]	[]	[]	hypothetical protein	PF00378.13	ECH(Enoyl-CoA hydratase/isomerase family)
Supercontig_1.14_MVLG_02020_10sp	-1071,2261	-1070,2334	1,98536	0,62942	NS	0	[]	[]	[]	hypothetical protein	PF00664.16	ABC_membrane(ABC transporter transmembrane region)
Supercontig_1.16_MVLG_02240_9sp	-633,25867	-633,16879	0,17976	0,08596	NS	0	[]	[]	[]	hypothetical protein	PF05071.9	NDUFA12(NADH ubiquinone oxidoreductase subunit NDUFA12)
Supercontig_1.52_MVLG_04571_8sp	-656,84232	-656,72075	0,24314	0,11447	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.18_MVLG_02419_10sp	-527,97605	-527,90857	0,13496	0,06525	NS	0	[]	[]	[]	hypothetical protein	TIGR00614	TIGR00614(recQ_fam: ATP-dependent DNA helicase, RecQ family)
Supercontig_1.3_MVLG_00625_11sp	-380,22075	-380,22023	0,00104	0,00052	NS	0	[]	[]	[]	homocitrate synthase	PF00682.12	HMGL-like(HMGL-like)
Supercontig_1.23_MVLG_02811_9sp	-404,89642	-404,89642	0	0	NS	0	[]	[]	[]	hypothetical protein	PF05870.4	PA_decarbox(Phenolic acid decarboxylase (PAD))
Supercontig_1.9_MVLG_01575_9sp	-561,28075	-561,28075	0	0	NS	0	[]	[]	[]	tRNA uridine 5-carboxymethylaminomethyl modification enzyme GidA	PF01134.15	GIDA(Glucose inhibited division protein A)
Supercontig_1.83_MVLG_05736_10sp	-784,31175	-784,31155	0,0004	0,0002	NS	0	[]	[]	[]	hypothetical protein	PF09333.4	ATG_C(ATG C terminal domain)
Supercontig_1.79_MVLG_05611_6sp	-1174,3301	-1174,3301	0	0	NS	0	[]	[]	[]	hypothetical protein	PF10607.2	RanBPM_CRA(Ran binding protein in the microtubule-organising centre)
Supercontig_1.59_MVLG_04891_6sp	-469,9114	-468,47523	2,87234	0,76216	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.9_MVLG_01502_8sp	-626,52355	-626,52247	0,00216	0,00108	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.196_MVLG_07060_8sp	-680,77999	-680,16575	1,22848	0,45895	NS	0	[]	[]	[]	hypothetical protein	PF00450.15	Peptidase_S10(Serine carboxypeptidase)
Supercontig_1.3_MVLG_00666_7sp	-499,12901	-499,1287	0,00062	0,00031	NS	0	[]	[]	[]	Cys-Gly metallodipeptidase dug1	PF01546.21	Peptidase_M20(Peptidase family M20/M25/M40)
Supercontig_1.26_MVLG_03040_12sp	-1055,6998	-1055,6997	0,00016	0	NS	0	[]	[]	[]	hypothetical protein	PF02383.11	Syja_N(SacI homology domain)
Supercontig_1.131_MVLG_06581_7sp	-518,91668	-518,75195	0,32946	0,15188	NS	0	[]	[]	[]	hypothetical protein	PF00153.20	Mito_carr(Mitochondrial carrier protein)
Supercontig_1.15_MVLG_02138_8sp	-471,38546	-470,99424	0,78244	0,32377	NS	0	[]	[]	[]	hypothetical protein	PF01479.18	S4(S4 domain)
Supercontig_1.15_MVLG_02130_10sp	-598,23617	-598,23617	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04111.5	APG6(Autophagy protein Apg6)
Supercontig_1.22_MVLG_02713_6sp	-664,30068	-663,35825	1,88486	0,61032	NS	0	[]	[]	[]	hypothetical protein	PF09271.4	LAG1-DNAbind(LAG1, DNA binding)
Supercontig_1.69_MVLG_05281_8sp	-1174,7425	-1174,742	0,00084	0,00042	NS	0	[]	[]	[]	hypothetical protein	NA	NA

Supercontig_1.32_MVLG_03394_7sp	-620,3348	-618,88992	2,88976	0,76423	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.113_MVLG_06336_11sp	-453,19869	-452,13362	2,13014	0,6553	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.96_MVLG_06050_7sp	-517,26108	-517,26097	0,00022	0,00011	NS	0	[]	[]	[]	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 8	PF06747.6	CHCH(CHCH domain)
Supercontig_1.20_MVLG_02564_7sp	-1216,3112	-1216,2496	0,12326	0,05977	NS	0	[]	[]	[]	hypothetical protein	PF03781.9	FGE-sulfatase(Formylglycine-generating sulfatase enzyme)
Supercontig_1.25_MVLG_02952_10sp	-1210,2763	-1210,2763	0	0	NS	0	[]	[]	[]	hypothetical protein	PF09421.3	FRQ(Frequency clock protein)
Supercontig_1.47_MVLG_04345_8sp	-608,28789	-608,28789	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.31_MVLG_03359_11sp	-2439,2361	-2437,4468	3,57856	0,83292	NS	0	[]	[]	[]	CAMK protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.1_MVLG_00248_8sp	-615,40745	-614,05891	2,69708	0,74038	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.132_MVLG_06592_8sp	-778,80074	-778,80073	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.7_MVLG_01338_8sp	-412,29513	-412,00184	0,58658	0,25419	NS	0	[]	[]	[]	hypothetical protein	PF04142.8	Nuc_sug_transp(Nucleotide-sugar transporter)
Supercontig_1.42_MVLG_04061_6sp	-505,77255	-505,67823	0,18864	0,09001	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.26_MVLG_03009_10sp	-679,55221	-676,98636	5,1317	0,92315	*	0	[]	[]	[]	hypothetical protein	PF01285.11	TEA(TEA/ATTS domain family)
Supercontig_1.12_MVLG_01883_8sp	-394,6998	-394,69979	0	0	NS	0	[]	[]	[]	actin	PF00022.12	Actin(Actin)
Supercontig_1.59_MVLG_04912_8sp	-606,24385	-606,24385	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.88_MVLG_05877_10sp	-413,58363	-413,58347	0,00032	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF02225.15	PA(PA domain)
Supercontig_1.10_MVLG_01659_6sp	-266,06125	-266,06096	0,00058	0,00029	NS	0	[]	[]	[]	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 2	PF05047.9	L51_S25_CI-B8(Mitochondrial ribosomal protein L51 / S25 / CI-B8 domain)
Supercontig_1.27_MVLG_03085_7sp	-400,97587	-400,75162	0,4485	0,20088	NS	0	[]	[]	[]	histone H2A	PF00808.16	CBFD_NFYB_HMF(Histone-like transcription factor (CBF/NF-Y) and archaeal histone)
Supercontig_1.27_MVLG_03064_7sp	-686,89858	-686,89858	0	0	NS	0	[]	[]	[]	hypothetical protein	TIGR02967	TIGR02967(guan_deamin: guanine deaminase)
Supercontig_1.117_MVLG_06399_7sp	-296,98741	-296,94067	0,09348	0,04566	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.15_MVLG_02080_9sp	-653,38295	-653,38295	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04664.6	OGFr_N(Opioid growth factor receptor (OGFr) conserved region)
Supercontig_1.74_MVLG_05450_6sp	-812,26122	-812,26103	0,00038	0,00019	NS	0	[]	[]	[]	hypothetical protein	PF07978.6	NIPSNAP(NIPSNAP)
Supercontig_1.54_MVLG_04693_9sp	-871,03462	-871,03462	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00534.13	Glycos_transf_1(Glycosyl transferases group 1)

Supercontig_1.18_MVLG_02408_10sp	-453,49006	-453,49006	0	0	NS	0	[]	[]	[]	hypothetical protein	PF09768.2	Peptidase_M76(Peptidase M76 family)
Supercontig_1.59_MVLG_04900_9sp	-367,03958	-367,03951	0,00014	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.2_MVLG_00392_10sp	-583,53328	-583,53328	0	0	NS	0	[]	[]	[]	hypothetical protein	PF05729.5	NACHT(NACHT domain)
Supercontig_1.4_MVLG_00764_6sp	-1111,3435	-1110,9165	0,854	0,34754	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.26_MVLG_03003_9sp	-488,95306	-488,95297	0,00018	0	NS	0	[]	[]	[]	hypothetical protein	PF00400.25	WD40(WD domain, G-beta repeat)
Supercontig_1.50_MVLG_04460_12sp	-982,32984	-982,32984	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00515.21	TPR_1(Tetratricopeptide repeat)
Supercontig_1.50_MVLG_04459_9sp	-736,06432	-736,06432	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.4_MVLG_00862_8sp	-702,08014	-701,70348	0,75332	0,31385	NS	0	[]	[]	[]	hypothetical protein	PF00102.20	Y_phosphatase(Protein-tyrosine phosphatase)
Supercontig_1.41_MVLG_03974_6sp	-405,6353	-405,63527	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00485.11	PRK(Phosphoribulokinase / Uridine kinase family)
Supercontig_1.30_MVLG_03295_7sp	-609,6218	-609,62111	0,00138	0,00069	NS	0	[]	[]	[]	40S ribosomal protein S14	PF00411.12	Ribosomal_S11(Ribosomal protein S11)
Supercontig_1.3_MVLG_00527_12sp	-658,08352	-657,86071	0,44562	0,19973	NS	0	[]	[]	[]	hypothetical protein	PF01369.13	Sec7(Sec7 domain)
Supercontig_1.2_MVLG_00307_10sp	-729,54805	-729,54805	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.6_MVLG_01142_7sp	-530,24137	-528,76614	2,95046	0,77127	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.4_MVLG_00876_8sp	-554,72114	-554,72114	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01399.20	PCI(PCI domain)
Supercontig_1.33_MVLG_03455_10sp	-279,71613	-278,47267	2,48692	0,71162	NS	0	[]	[]	[]	hypothetical protein	PF01053.13	Cys_Met_Meta_PP(Cys/Met metabolism PLP-dependent enzyme)
Supercontig_1.36_MVLG_03684_10sp	-495,42823	-494,8882	1,08006	0,41727	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.18_MVLG_02398_9sp	-584,63282	-583,76865	1,72834	0,5786	NS	0	[]	[]	[]	hypothetical protein	PF06745.6	KaiC(KaiC)
Supercontig_1.70_MVLG_05317_8sp	-824,77113	-824,6204	0,30146	0,13992	NS	0	[]	[]	[]	hypothetical protein	PF00135.21	COesterase(Carboxylesterase)
Supercontig_1.2_MVLG_00357_8sp	-495,1591	-495,1591	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01025.12	GrpE(GrpE)
Supercontig_1.28_MVLG_03158_10sp	-570,60263	-570,60238	0,0005	0,00025	NS	0	[]	[]	[]	protein ARG5,6	PF01118.17	Semialdhyde_dh(Semialdehyde dehydrogenase, NAD binding domain)
Supercontig_1.3_MVLG_00667_9sp	-1407,3772	-1406,6803	1,39386	0,50189	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.1_MVLG_00004_7sp	-392,10661	-392,1065	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00153.20	Mito_carr(Mitochondrial carrier protein)
Supercontig_1.9_MVLG_01558_10sp	-333,74053	-333,74049	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.17_MVLG_02333_8sp	-1067,3619	-1066,775	1,17374	0,44393	NS	0	[]	[]	[]	hypothetical protein	PF02985.15	HEAT(HEAT repeat)
Supercontig_1.11_MVLG_01703_7sp	-848,07056	-848,15724	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04658.6	TAFII55_N(TAFII55 protein conserved region)

Supercontig_1.141_MVLG_06691_11sp	-486,11854	-484,92106	2,39496	0,69805	NS	0	[]	[]	[]	hypothetical protein	PF00107.19	ADH_zinc_N(Zinc-binding dehydrogenase)
Supercontig_1.74_MVLG_05448_6sp	-490,3117	-490,3117	0	0	NS	0	[]	[]	[]	CAMK/CAMK1 protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.189_MVLG_07039_8sp	-361,93435	-361,56088	0,74694	0,31166	NS	0	[]	[]	[]	hypothetical protein	PF04112.6	Mak10(Mak10 subunit, NatC N(alpha)-terminal acetyltransferase)
Supercontig_1.16_MVLG_02253_9sp	-577,30856	-576,62811	1,3609	0,49361	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.4_MVLG_00834_10sp	-277,34554	-277,34526	0,00056	0,00028	NS	0	[]	[]	[]	40S ribosomal protein S28	PF01200.11	Ribosomal_S28e(Ribosomal protein S28e)
Supercontig_1.15_MVLG_02134_7sp	-725,57361	-725,57361	0	0	NS	0	[]	[]	[]	hypothetical protein	TIGR02411	TIGR02411(leuko_A4_hydro: leukotriene A-4 hydrolase/aminopeptidase)
Supercontig_1.63_MVLG_05079_11sp	-695,89614	-695,89582	0,00064	0,00032	NS	0	[]	[]	[]	hypothetical protein	PF03151.9	TPT(Triose-phosphate Transporter family)
Supercontig_1.2_MVLG_00412_10sp	-1393,9752	-1393,9752	0	0	NS	0	[]	[]	[]	hypothetical protein	PF07823.4	CPDase(Cyclic phosphodiesterase-like protein)
Supercontig_1.42_MVLG_04067_6sp	-348,78714	-348,78711	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00018.21	SH3_1(SH3 domain)
Supercontig_1.59_MVLG_04917_10sp	-586,89325	-586,89325	0	0	NS	0	[]	[]	[]	NADPH2:quinone reductase	PF00107.19	ADH_zinc_N(Zinc-binding dehydrogenase)
Supercontig_1.30_MVLG_03321_10sp	-384,97582	-384,97582	0	0	NS	0	[]	[]	[]	hypothetical protein	PF08610.3	Pex16(Peroxisomal membrane protein (Pex16))
Supercontig_1.26_MVLG_03001_9sp	-600,4656	-600,46331	0,00458	0,00229	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.19_MVLG_02448_10sp	-486,70949	-486,64451	0,12996	0,06291	NS	0	[]	[]	[]	hypothetical protein	PF01529.13	zf-DHHC(DHHC zinc finger domain)
Supercontig_1.56_MVLG_04763_11sp	-581,19976	-581,08942	0,22068	0,10447	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.55_MVLG_04744_8sp	-589,79655	-589,79646	0,00018	0	NS	0	[]	[]	[]	hypothetical protein	PF03810.12	IBN_N(Importin-beta N-terminal domain)
Supercontig_1.141_MVLG_06692_6sp	-620,00248	-620,00242	0,00012	0	NS	0	[]	[]	[]	importin subunit alpha-1	PF02985.15	HEAT(HEAT repeat)
Supercontig_1.42_MVLG_04066_7sp	-896,99412	-896,67134	0,64556	0,27587	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.6_MVLG_01154_7sp	-602,53563	-602,53563	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00378.13	ECH(Enoyl-CoA hydratase/isomerase family)
Supercontig_1.47_MVLG_04329_9sp	-567,96911	-567,93301	0,0722	0,03546	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.12_MVLG_01850_6sp	-580,62999	-580,62999	0	0	NS	0	[]	[]	[]	hypothetical protein	PF05648.7	PEX11(Peroxisomal biogenesis factor 11 (PEX11))
Supercontig_1.34_MVLG_03529_9sp	-506,5868	-506,5868	0	0	NS	0	[]	[]	[]	NADH-cytochrome b5 reductase 1	PF00175.14	NAD_binding_1(Oxidoreductase NAD-binding domain)
Supercontig_1.11_MVLG_01749_10sp	-398,69902	-396,74588	3,90628	0,85817	NS	0	[]	[]	[]	hypothetical protein	PF11711.1	Tim54(Inner membrane protein import complex subunit Tim54)
Supercontig_1.25_MVLG_02953_6sp	-418,33242	-418,33214	0,00056	0,00028	NS	0	[]	[]	[]	ADP-ribosylation factor 6	PF04670.5	Gtr1_RagA(Gtr1/RagA G protein conserved region)
Supercontig_1.5_MVLG_00914_7sp	-828,38993	-827,48016	1,81954	0,59738	NS	0	[]	[]	[]	hypothetical protein	PF03583.7	LIP(Secretory lipase)

Supercontig_1.14_MVLG_02041_8sp	-618,38604	-618,0951	0,58188	0,25244	NS	0	[]	[]	[]	hypothetical protein	PF07690.9	MFS_1(Major Facilitator Superfamily)
Supercontig_1.69_MVLG_05295_9sp	-350,95171	-350,95161	0,0002	0	NS	0	[]	[]	[]	60S ribosomal protein L15-B	PF00827.10	Ribosomal_L15e(Ribosomal L15)
Supercontig_1.27_MVLG_03062_9sp	-517,99245	-517,99245	0	0	NS	0	[]	[]	[]	hypothetical protein	TIGR01429	TIGR01429(AMP_deaminase: AMP deaminase)
Supercontig_1.1_MVLG_00018_6sp	-676,83458	-676,83288	0,0034	0,0017	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.56_MVLG_04794_8sp	-357,21431	-356,44254	1,54354	0,53781	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.56_MVLG_04760_11sp	-423,66811	-423,66811	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.2_MVLG_00406_8sp	-919,07656	-918,13373	1,88566	0,61048	NS	0	[]	[]	[]	alkanesulfonate monooxygenase	TIGR04021	TIGR04021(LLM_DMSO2_sfnG: dimethyl sulfone monooxygenase SfnG)
Supercontig_1.3_MVLG_00525_9sp	-452,94605	-452,94605	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02225.15	PA(PA domain)
Supercontig_1.7_MVLG_01274_10sp	-693,71558	-693,30669	0,81778	0,33561	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.98_MVLG_06103_9sp	-1852,4402	-1852,4402	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00226.24	DnaJ(DnaJ domain)
Supercontig_1.5_MVLG_00882_11sp	-459,43527	-459,13825	0,59404	0,25697	NS	0	[]	[]	[]	hypothetical protein	PF00400.25	WD40(WD domain, G-beta repeat)
Supercontig_1.165_MVLG_06900_10sp	-467,65751	-467,45316	0,4087	0,18482	NS	0	[]	[]	[]	hypothetical protein	PF00107.19	ADH_zinc_N(Zinc-binding dehydrogenase)
Supercontig_1.67_MVLG_05209_9sp	-1002,0458	-1002,0458	0,00014	0	NS	0	[]	[]	[]	hypothetical protein	PF01933.11	UPF0052(Uncharacterised protein family UPF0052)
Supercontig_1.69_MVLG_05308_11sp	-344,75732	-344,69314	0,12836	0,06216	NS	0	[]	[]	[]	hypothetical protein	PF05188.10	MutS_II(MutS domain II)
Supercontig_1.28_MVLG_03174_11sp	-1176,7031	-1174,4415	4,52312	0,89581	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.16_MVLG_02226_10sp	-971,73713	-971,73699	0,00028	0,00014	NS	0	[]	[]	[]	hypothetical protein	PF00501.21	AMP-binding(AMP-binding enzyme)
Supercontig_1.75_MVLG_05490_10sp	-646,71423	-646,71422	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.6_MVLG_01108_7sp	-763,80684	-762,66454	2,2846	0,68092	NS	0	[]	[]	[]	hypothetical protein	PF02826.12	2-Hacid_dh_C(D-isomer specific 2-hydroxyacid dehydrogenase, NAD binding domain)
Supercontig_1.79_MVLG_05603_7sp	-747,18337	-746,22918	1,90838	0,61488	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.21_MVLG_02624_10sp	-539,53813	-539,53768	0,0009	0,00045	NS	0	[]	[]	[]	hypothetical protein	PF00106.18	adh_short(short chain dehydrogenase)
Supercontig_1.9_MVLG_01552_9sp	-728,04217	-728,04217	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02260.13	FATC(FATC domain)
Supercontig_1.59_MVLG_04885_7sp	-645,44529	-645,32304	0,2445	0,11507	NS	0	[]	[]	[]	hypothetical protein	PF00025.14	Arf(ADP-ribosylation factor family)
Supercontig_1.25_MVLG_02926_10sp	-348,12786	-348,12786	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00806.12	PUF(Pumilio-family RNA binding repeat)
Supercontig_1.18_MVLG_02372_7sp	-316,80056	-316,80054	0	0	NS	0	[]	[]	[]	hypothetical protein	PF07650.10	KH_2(KH domain)

Supercontig_1.13_MVLG_01909_10sp	-612,43522	-612,43522	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04479.6	RTA1(RTA1 like protein)
Supercontig_1.52_MVLG_04589_9sp	-425,07862	-425,07854	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.40_MVLG_03965_9sp	-524,60606	-523,26962	2,67288	0,73722	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.6_MVLG_01159_7sp	-585,16941	-585,16941	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.127_MVLG_06543_12sp	-1357,4274	-1357,4266	0,0017	0,00085	NS	0	[]	[]	[]	hypothetical protein	PF00018.21	SH3_1(SH3 domain)
Supercontig_1.13_MVLG_01919_9sp	-448,12219	-447,65915	0,92608	0,37063	NS	0	[]	[]	[]	hypothetical protein	PF02141.14	DENN(DENN (AEX-3) domain)
Supercontig_1.39_MVLG_03856_7sp	-480,10999	-480,10977	0,00044	0,00022	NS	0	[]	[]	[]	vacuolar transporter chaperone 1	PF02656.8	DUF202(Domain of unknown function DUF)
Supercontig_1.85_MVLG_05790_6sp	-623,55705	-623,41417	0,28576	0,13314	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.17_MVLG_02271_8sp	-450,22603	-450,22595	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04193.7	PQ-loop(PQ loop repeat)
Supercontig_1.30_MVLG_03263_10sp	-766,37549	-766,37549	0	0	NS	0	[]	[]	[]	5'-methylthioadenosine phosphorylase	TIGR01694	TIGR01694(MTAP: methylthioadenosine phosphorylase)
Supercontig_1.11_MVLG_01692_8sp	-903,55136	-903,55135	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04670.5	Gtr1_RagA(Gtr1/RagA G protein conserved region)
Supercontig_1.81_MVLG_05669_10sp	-501,1239	-501,12343	0	0	NS	0	[]	[]	[]	sterol 24-C-methyltransferase	PF08242.5	Methyltransf_12(Methyltransferase domain)
Supercontig_1.6_MVLG_01052_10sp	-543,08765	-543,0876	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04000.8	Sas10_Utp3(Sas10/Utp3/C1D family)
Supercontig_1.59_MVLG_04895_10sp	-765,81227	-765,81227	0	0	NS	0	[]	[]	[]	Poly(A)+ RNA export protein	PF00400.25	WD40(WD domain, G-beta repeat)
Supercontig_1.21_MVLG_02612_9sp	-719,53645	-719,53609	0,00072	0,00036	NS	0	[]	[]	[]	hypothetical protein	PF10358.2	Eeig1(Oestrogen-responsive protein Fam102A-B)
Supercontig_1.18_MVLG_02362_8sp	-374,29296	-374,21561	0,1547	0,07443	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.1_MVLG_00084_9sp	-311,46831	-311,46807	0,00048	0,00024	NS	0	[]	[]	[]	50S ribosomal protein L19e	PF01280.13	Ribosomal_L19e(Ribosomal protein L19e)
Supercontig_1.15_MVLG_02095_8sp	-429,71155	-429,71142	0,00026	0,00013	NS	0	[]	[]	[]	ATP synthase F1, gamma subunit	PF00231.12	ATP-synt(ATP synthase)
Supercontig_1.9_MVLG_01503_8sp	-509,03025	-509,03025	0	0	NS	0	[]	[]	[]	hypothetical protein	PF05875.5	aPHC(Alkaline phytoceramidase (aPHC))
Supercontig_1.17_MVLG_02302_8sp	-280,45163	-280,45162	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02544.9	Steroid_dh(3-oxo-5-alpha-steroid 4-dehydrogenase)
Supercontig_1.2_MVLG_00394_8sp	-376,13537	-376,13505	0,00064	0,00032	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.1_MVLG_00212_8sp	-1752,355	-1752,0964	0,51708	0,22782	NS	0	[]	[]	[]	hypothetical protein	PF12350.1	CTK3_C(CTD kinase subunit gamma CTK3 C-terminus)
Supercontig_1.56_MVLG_04768_10sp	-454,02321	-452,76691	2,5126	0,71529	NS	0	[]	[]	[]	hypothetical protein	PF02230.9	Abhydrolase_2(Phospholipase/Carboxylesterase)
Supercontig_1.5_MVLG_00959_11sp	-689,514	-689,514	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.68_MVLG_05262_10sp	-558,11254	-558,11254	0	0	NS	0	[]	[]	[]	methionine aminopeptidase 1	PF00557.17	Peptidase_M24(Metallopeptidase family M24)

Supercontig_1.47_MVLG_04307_7sp	-1217,7104	-1217,7104	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00498.19	FHA(FHA domain)
Supercontig_1.23_MVLG_02813_11sp	-716,7097	-715,19555	3,0283	0,78	NS	0	[]	[]	[]	CAMK/CAMKL/PASK protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.94_MVLG_06005_8sp	-322,68422	-322,68415	0	0	NS	0	[]	[]	[]	GTP-binding protein ypt2	PF04670.5	Gtr1_RagA(Gtr1/RagA G protein conserved region)
Supercontig_1.12_MVLG_01805_10sp	-691,35197	-691,35197	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00400.25	WD40(WD domain, G-beta repeat)
Supercontig_1.34_MVLG_03528_9sp	-388,23582	-388,23573	0	0	NS	0	[]	[]	[]	ribosome biogenesis protein N	PF01201.15	Ribosomal_S8e(Ribosomal protein S8e)
Supercontig_1.9_MVLG_01528_8sp	-221,80022	-221,80017	0	0	NS	0	[]	[]	[]	hypothetical protein	TIGR01160	TIGR01160(SUI1_MOF2: translation initiation factor SUI1)
Supercontig_1.28_MVLG_03175_7sp	-525,07287	-525,07287	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.8_MVLG_01440_7sp	-559,07813	-558,66487	0,82652	0,33851	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.48_MVLG_04354_7sp	-712,33317	-712,33317	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00642.17	zf-CCCH(Zinc finger C-x8-C-x5-C-x3-H type (and similar))
Supercontig_1.51_MVLG_04499_8sp	-418,52858	-418,43889	0,17938	0,08579	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.7_MVLG_01293_10sp	-562,2908	-562,23669	0,10822	0,05267	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.87_MVLG_05872_6sp	-1190,8807	-1190,8806	0,00038	0,00019	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.94_MVLG_06006_7sp	-336,10226	-335,84173	0,52106	0,22936	NS	0	[]	[]	[]	hypothetical protein	PF03134.12	TB2_DP1_HVA22(TB2/DP1, HVA22 family)
Supercontig_1.7_MVLG_01269_10sp	-394,25101	-394,24345	0,01512	0,00753	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.7_MVLG_01226_9sp	-1003,7306	-1003,6778	0,10558	0,05142	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.91_MVLG_05942_6sp	-752,12518	-752,125	0,00036	0,00018	NS	0	[]	[]	[]	replication factor C subunit 3	PF08542.4	Rep_fac_C(Replication factor C)
Supercontig_1.32_MVLG_03403_6sp	-994,32683	-994,32646	0,00074	0,00037	NS	0	[]	[]	[]	hypothetical protein	PF03328.7	HpcH_HpaI(HpcH/HpaI aldolase/citrate lyase family)
Supercontig_1.50_MVLG_04483_10sp	-751,66893	-751,66893	0	0	NS	0	[]	[]	[]	spermidine synthase	PF03435.11	Saccharop_dh(Saccharopine dehydrogenase)
Supercontig_1.40_MVLG_03921_10sp	-645,54384	-645,54384	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01053.13	Cys_Met_Meta_PP(Cys/Met metabolism PLP-dependent enzyme)
Supercontig_1.30_MVLG_03297_11sp	-592,29837	-592,29837	0	0	NS	0	[]	[]	[]	hypothetical protein	PF09724.2	DUF2036(Uncharacterized conserved protein (DUF2036))
Supercontig_1.32_MVLG_03400_11sp	-709,40674	-709,39076	0,03196	0,01585	NS	0	[]	[]	[]	hypothetical protein	PF00150.11	Cellulase(Cellulase (glycosyl hydrolase family 5))
Supercontig_1.155_MVLG_06824_8sp	-406,39937	-406,39924	0,00026	0,00013	NS	0	[]	[]	[]	hypothetical protein	PF00070.20	Pyr_redox(Pyridine nucleotide-disulphide oxidoreductase)
Supercontig_1.38_MVLG_03810_7sp	-847,37426	-847,30009	0,14834	0,07149	NS	0	[]	[]	[]	dihydroxy-acid dehydratase	PF00920.14	ILVD_EDD(Dehydratase family)
Supercontig_1.57_MVLG_04826_10sp	-1172,4376	-1170,9016	3,07198	0,78476	NS	0	[]	[]	[]	hypothetical protein	PF00320.20	GATA(GATA zinc finger)

Supercontig_1.31_MVLG_03346_9sp	-1234,8768	-1234,8764	0,00092	0,00046	NS	0	[]	[]	[]	hypothetical protein	PF00564.17	PB1(PB1 domain)
Supercontig_1.17_MVLG_02314_9sp	-1133,3791	-1133,2277	0,30278	0,14049	NS	0	[]	[]	[]	hypothetical protein	PF08580.3	KAR9(Yeast cortical protein KAR9)
Supercontig_1.13_MVLG_01892_12sp	-391,76153	-391,76153	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00172.11	Zn_clus(Fungal Zn(2)-Cys(6) binuclear cluster domain)
Supercontig_1.739_MVLG_07306_8sp	-370,33113	-370,33113	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.38_MVLG_03822_10sp	-776,30765	-775,79508	1,02514	0,40105	NS	0	[]	[]	[]	hypothetical protein	PF00076.15	RRM_1(RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain))
Supercontig_1.5_MVLG_01005_8sp	-483,65162	-483,65162	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.183_MVLG_07015_7sp	-386,3057	-385,81813	0,97514	0,38588	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.23_MVLG_02819_11sp	-560,13321	-560,13321	0	0	NS	0	[]	[]	[]	hypothetical protein	PF12269.1	zf-CpG_bind_C(CpG binding protein zinc finger C terminal domain)
Supercontig_1.25_MVLG_02958_8sp	-813,113	-813,113	0	0	NS	0	[]	[]	[]	hypothetical protein	PF05859.5	Mis12(Mis12 protein)
Supercontig_1.2_MVLG_00304_10sp	-473,32342	-473,15101	0,34482	0,15837	NS	0	[]	[]	[]	hypothetical protein	PF00339.22	Arrestin_N(Arrestin (or S-antigen), N-terminal domain)
Supercontig_1.61_MVLG_04976_6sp	-430,12298	-428,25241	3,74114	0,84596	NS	0	[]	[]	[]	ubiquitin-conjugating enzyme E2 8	PF00179.19	UQ_con(Ubiquitin-conjugating enzyme)
Supercontig_1.4_MVLG_00861_8sp	-605,86534	-605,86534	0	0	NS	0	[]	[]	[]	iron sulfur cluster assembly protein 1	PF01592.9	NifU_N(NifU-like N terminal domain)
Supercontig_1.52_MVLG_04591_6sp	-1008,0795	-1008,0788	0,00138	0,00069	NS	0	[]	[]	[]	phenylalanine ammonia-lyase	PF00221.12	PAL(Phenylalanine and histidine ammonia-lyase)
Supercontig_1.1_MVLG_00115_7sp	-756,00728	-754,68623	2,6421	0,73315	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.3_MVLG_00639_9sp	-1044,7574	-1044,7571	0,00076	0,00038	NS	0	[]	[]	[]	hypothetical protein	PF04082.11	Fungal_trans(Fungal specific transcription factor domain)
Supercontig_1.59_MVLG_04887_8sp	-425,53732	-425,53711	0,00042	0,00021	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.12_MVLG_01868_10sp	-757,16108	-757,16108	0	0	NS	0	[]	[]	[]	hypothetical protein	PF07732.8	Cu-oxidase_3(Multicopper oxidase)
Supercontig_1.166_MVLG_06918_7sp	-500,8374	-499,9925	1,6898	0,5704	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.220_MVLG_07158_7sp	-275,70648	-275,70644	0	0	NS	0	[]	[]	[]	50S ribosomal protein L36e	PF01158.11	Ribosomal_L36e(Ribosomal protein L36e)
Supercontig_1.197_MVLG_07072_9sp	-430,27261	-430,27261	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00995.16	Sec1(Sec1 family)
Supercontig_1.5_MVLG_01027_7sp	-650,46767	-650,46767	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.25_MVLG_02931_9sp	-420,93468	-420,93456	0	0	NS	0	[]	[]	[]	40S ribosomal protein S17	PF00833.11	Ribosomal_S17e(Ribosomal S17)
Supercontig_1.61_MVLG_04972_6sp	-1100,803	-1100,803	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00400.25	WD40(WD domain, G-beta repeat)
Supercontig_1.112_MVLG_06330_9sp	-846,43429	-846,43422	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04488.8	Gly_transf_sug(Glycosyltransferase sugar-binding region containing DXD motif)

Supercontig_1.41_MVLG_04030_10sp	-484,45438	-484,45438	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.32_MVLG_03393_6sp	-988,99051	-988,99046	0	0	NS	0	[]	[]	[]	hypothetical protein	PF07716.8	bZIP_2(Basic region leucine zipper)
Supercontig_1.9_MVLG_01553_8sp	-887,68584	-887,12894	1,1138	0,42702	NS	0	[]	[]	[]	hypothetical protein	PF00505.12	HMG_box(HMG (high mobility group) box)
Supercontig_1.32_MVLG_03399_6sp	-695,14933	-695,14933	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.100_MVLG_06145_12sp	-1113,7188	-1113,7188	0	0	NS	0	[]	[]	[]	hypothetical protein	PF08572.3	PRP3(pre-mRNA processing factor 3 (PRP3))
Supercontig_1.61_MVLG_04995_10sp	-589,11401	-588,94587	0,33628	0,15476	NS	0	[]	[]	[]	hypothetical protein	PF03062.12	MBOAT(MBOAT family)
Supercontig_1.9_MVLG_01565_6sp	-1278,9296	-1276,6806	4,498	0,8945	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.20_MVLG_02567_9sp	-630,03062	-629,86284	0,33556	0,15446	NS	0	[]	[]	[]	hypothetical protein	PF04564.8	U-box(U-box domain)
Supercontig_1.34_MVLG_03524_9sp	-602,04372	-602,04341	0,00062	0,00031	NS	0	[]	[]	[]	SCY1 protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.3_MVLG_00510_10sp	-558,84639	-558,84639	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.11_MVLG_01778_8sp	-362,91783	-362,91783	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00179.19	UQ_con(Ubiquitin-conjugating enzyme)
Supercontig_1.87_MVLG_05858_10sp	-366,76535	-366,76498	0,00074	0,00037	NS	0	[]	[]	[]	tubulin beta chain	PF00091.18	Tubulin(Tubulin/FtsZ family, GTPase domain)
Supercontig_1.7_MVLG_01353_12sp	-497,07618	-497,07615	0,00028	0,00028	NS	0	[]	[]	[]	hypothetical protein	PF00018.21	SH3_1(SH3 domain)
Supercontig_1.19_MVLG_02463_11sp	-605,56505	-604,94518	1,23974	0,46199	NS	0	[]	[]	[]	urease	PF00547.11	Urease_gamma(Urease, gamma subunit)
Supercontig_1.91_MVLG_05929_10sp	-316,65453	-316,34768	0,6137	0,26424	NS	0	[]	[]	[]	serine/threonine protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.60_MVLG_04927_9sp	-525,94573	-525,94573	0	0	NS	0	[]	[]	[]	hypothetical protein	PF08653.3	DASH_Dam1(DASH complex subunit Dam1)
Supercontig_1.34_MVLG_03530_9sp	-667,08068	-666,92461	0,31214	0,1445	NS	0	[]	[]	[]	hypothetical protein	TIGR00614	TIGR00614(recQ_fam: ATP-dependent DNA helicase, RecQ family)
Supercontig_1.7_MVLG_01290_11sp	-357,16073	-356,469	1,38346	0,49929	NS	0	[]	[]	[]	hypothetical protein	PF00300.15	PGAM(Phosphoglycerate mutase family)
Supercontig_1.92_MVLG_05955_11sp	-546,82064	-546,82036	0,00056	0,00028	NS	0	[]	[]	[]	CAMK/CAMK1 protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.6_MVLG_01065_8sp	-299,69763	-299,69763	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.3_MVLG_00524_9sp	-475,90271	-475,90189	0,00164	0,00082	NS	0	[]	[]	[]	hypothetical protein	PF00400.25	WD40(WD domain, G-beta repeat)
Supercontig_1.13_MVLG_01954_12sp	-658,73085	-658,48731	0,48708	0,21615	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.83_MVLG_05741_12sp	-562,79902	-561,7595	2,07904	0,64638	NS	0	[]	[]	[]	hypothetical protein	PF09770.2	PAT1(Topoisomerase II-associated protein PAT1)
Supercontig_1.2_MVLG_00313_10sp	-460,62802	-460,62796	0,00012	0,00028	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.38_MVLG_03795_8sp	-1680,8178	-1680,8143	0,0071	0,00354	NS	0	[]	[]	[]	hypothetical protein	PF01764.18	Lipase_3(Lipase (class 3))

Supercontig_1.15_MVLG_02075_8sp	-464,15182	-464,15171	0,00022	0,00011	NS	0	[]	[]	[]	CMGC/CDK protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.113_MVLG_06353_10sp	-449,6571	-449,26452	0,78516	0,32469	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.1_MVLG_00008_12sp	-455,96496	-455,96496	0	0	NS	0	[]	[]	[]	hypothetical protein	PF12537.1	DUF3735(Protein of unknown function (DUF3735))
Supercontig_1.77_MVLG_05563_8sp	-359,67084	-359,5604	0,22088	0,10456	NS	0	[]	[]	[]	pre-mRNA branch site protein p14	PF00076.15	RRM_1(RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain))
Supercontig_1.30_MVLG_03275_9sp	-525,41234	-521,26245	8,29978	0,98423	**	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.9_MVLG_01509_10sp	-654,11285	-653,01583	2,19404	0,66614	NS	0	[]	[]	[]	hypothetical protein	PF01412.11	ArfGap(Putative GTPase activating protein for Arf)
Supercontig_1.6_MVLG_01207_8sp	-480,66727	-480,66727	0	0	NS	0	[]	[]	[]	actin-like protein 2/3 complex subunit 3	PF04062.7	P21-Arc(ARP2/3 complex ARPC3 (21 kDa) subunit)
Supercontig_1.29_MVLG_03231_9sp	-324,75	-324,74975	0,0005	0,00025	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.111_MVLG_06306_10sp	-654,3831	-652,66175	3,4427	0,82118	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.20_MVLG_02520_8sp	-544,44923	-544,44923	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.39_MVLG_03866_10sp	-396,71843	-396,6336	0,16966	0,08133	NS	0	[]	[]	[]	hypothetical protein	PF07896.5	DUF1674(Protein of unknown function (DUF1674))
Supercontig_1.98_MVLG_06083_9sp	-412,82965	-412,82965	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00293.21	NUDIX(NUDIX domain)
Supercontig_1.191_MVLG_07046_6sp	-714,77422	-714,77411	0,00022	0,00011	NS	0	[]	[]	[]	V-type H+-transporting ATPase 54 kDa subunit	PF03224.7	V-ATPase_H_N(V-ATPase subunit H)
Supercontig_1.59_MVLG_04918_6sp	-1206,8834	-1206,8834	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01424.15	R3H(R3H domain)
Supercontig_1.13_MVLG_01924_8sp	-544,38755	-542,61831	3,53848	0,82954	NS	0	[]	[]	[]	hypothetical protein	PF00097.18	zf-C3HC4(Zinc finger, C3HC4 type (RING finger))
Supercontig_1.46_MVLG_04294_8sp	-751,86254	-751,86254	0	0	NS	0	[]	[]	[]	lanosterol synthase	PF00432.14	Prenyltrans(Prenyltransferase and squalene oxidase repeat)
Supercontig_1.67_MVLG_05226_7sp	-438,6659	-437,09823	3,13534	0,79147	NS	0	[]	[]	[]	hypothetical protein	PF00153.20	Mito_carr(Mitochondrial carrier protein)
Supercontig_1.19_MVLG_02516_8sp	-663,10618	-663,10618	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00160.14	Pro_isomerase(Cyclophilin type peptidyl-prolyl cis-trans isomerase/CLD)
Supercontig_1.112_MVLG_06324_10sp	-688,16215	-688,16215	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.38_MVLG_03807_8sp	-1240,9628	-1240,0958	1,73398	0,57979	NS	0	[]	[]	[]	hypothetical protein	PF00176.16	SNF2_N(SNF2 family N-terminal domain)
Supercontig_1.12_MVLG_01871_6sp	-313,99955	-313,99955	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.75_MVLG_05499_10sp	-834,34342	-834,34342	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00400.25	WD40(WD domain, G-beta repeat)
Supercontig_1.57_MVLG_04830_8sp	-1358,0354	-1358,0354	0	0	NS	0	[]	[]	[]	VPS15 protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.5_MVLG_01039_11sp	-487,28069	-486,24762	2,06614	0,64409	NS	0	[]	[]	[]	hypothetical protein	NA	NA

Supercontig_1.117_MVLG_06387_10sp	-564,99222	-564,81893	0,34658	0,15911	NS	0	[]	[]	[]	hypothetical protein	PF00383.15	dCMP_cyt_deam_1(Cytidine and deoxycytidylate deaminase zinc-binding region)
Supercontig_1.123_MVLG_06472_6sp	-545,96258	-545,96258	0	0	NS	0	[]	[]	[]	dolichol-phosphate mannosyltransferase	PF00535.19	Glycos_transf_2(Glycosyl transferase family 2)
Supercontig_1.26_MVLG_03032_9sp	-376,02406	-376,02406	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.14_MVLG_01984_9sp	-280,77987	-280,77981	0,00012	0,00028	NS	0	[]	[]	[]	hypothetical protein	PF00887.12	ACBP(Acyl CoA binding protein)
Supercontig_1.64_MVLG_05118_12sp	-700,51378	-700,36222	0,30312	0,14063	NS	0	[]	[]	[]	hypothetical protein	PF00018.21	SH3_1(SH3 domain)
Supercontig_1.143_MVLG_06723_11sp	-646,21891	-643,12085	6,19612	0,95486	**	0	[]	[]	[]	hypothetical protein	PF00884.16	Sulfatase(Sulfatase)
Supercontig_1.53_MVLG_04595_11sp	-537,39367	-534,13003	6,52728	0,96175	**	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.66_MVLG_05180_10sp	-380,39179	-380,05643	0,67072	0,28492	NS	0	[]	[]	[]	hypothetical protein	PF04824.9	Rad21_Rec8(Conserved region of Rad21 / Rec8 like protein)
Supercontig_1.164_MVLG_06896_8sp	-866,67233	-866,67233	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00400.25	WD40(WD domain, G-beta repeat)
Supercontig_1.120_MVLG_06427_8sp	-312,69608	-311,92798	1,5362	0,53611	NS	0	[]	[]	[]	hypothetical protein	PF05773.15	RWD(RWD domain)
Supercontig_1.8_MVLG_01367_6sp	-287,2976	-286,93252	0,73016	0,30586	NS	0	[]	[]	[]	hypothetical protein	PF00501.21	AMP-binding(AMP-binding enzyme)
Supercontig_1.5_MVLG_00947_10sp	-785,50246	-784,47271	2,0595	0,6429	NS	0	[]	[]	[]	hypothetical protein	PF00856.21	SET(SET domain)
Supercontig_1.62_MVLG_05004_10sp	-539,36928	-539,36928	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01590.19	GAF(GAF domain)
Supercontig_1.12_MVLG_01831_10sp	-375,46659	-374,98004	0,9731	0,38526	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.10_MVLG_01664_8sp	-552,84884	-552,50807	0,68154	0,28878	NS	0	[]	[]	[]	hypothetical protein	PF00385.17	Chromo('chromo' (CHRromatin Organisation MOdifier) domain)
Supercontig_1.16_MVLG_02177_9sp	-700,43783	-700,1899	0,49586	0,21959	NS	0	[]	[]	[]	hypothetical protein	PF03981.5	Ubiq_cyt_C_chap(Ubiquinol-cytochrome C chaperone)
Supercontig_1.49_MVLG_04440_10sp	-679,57363	-679,15169	0,84388	0,34423	NS	0	[]	[]	[]	hypothetical protein	PF00083.17	Sugar_tr(Sugar (and other) transporter)
Supercontig_1.6_MVLG_01083_6sp	-891,81873	-891,81871	0,00028	0,00028	NS	0	[]	[]	[]	hypothetical protein	PF00560.26	LRR_1(Leucine Rich Repeat)
Supercontig_1.2_MVLG_00343_7sp	-477,12434	-476,25497	1,73874	0,58078	NS	0	[]	[]	[]	hypothetical protein	PF00505.12	HMG_box(HMG (high mobility group) box)
Supercontig_1.1_MVLG_00147_7sp	-749,75569	-749,77928	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02902.12	Peptidase_C48(Ulp1 protease family, C-terminal catalytic domain)
Supercontig_1.9_MVLG_01564_8sp	-1090,5003	-1090,5003	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.94_MVLG_05993_10sp	-786,47422	-784,65312	3,6422	0,83815	NS	0	[]	[]	[]	hypothetical protein	NA	NA

Supercontig_1.3_MVLG_00596_11sp	-374,63179	-374,63179	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00076.15	RRM_1(RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain))
Supercontig_1.36_MVLG_03671_7sp	-598,61374	-598,61355	0,00038	0,00019	NS	0	[]	[]	[]	UDP-glucose 4-epimerase	PF07993.5	NAD_binding_4(Male sterility protein)
Supercontig_1.11_MVLG_01698_9sp	-371,41242	-371,41242	0	0	NS	0	[]	[]	[]	hypothetical protein	PF09334.4	tRNA-synt_1g(tRNA synthetases class I (M))
Supercontig_1.1_MVLG_00030_8sp	-422,29821	-422,29821	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00248.14	Aldo_ket_red(Aldo/keto reductase family)
Supercontig_1.11_MVLG_01779_9sp	-424,77208	-424,7716	0,00096	0,00048	NS	0	[]	[]	[]	26S protease subunit rpt4	PF07724.7	AAA_2(AAA domain (Cdc48 subfamily))
Supercontig_1.32_MVLG_03408_6sp	-1011,3785	-1011,3785	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04042.9	DNA_pol_E_B(DNA polymerase alpha/epsilon subunit B)
Supercontig_1.22_MVLG_02742_10sp	-1015,0575	-1013,6984	2,71808	0,74309	NS	0	[]	[]	[]	hypothetical protein	PF09409.3	PUB(PUB domain)
Supercontig_1.25_MVLG_02935_10sp	-429,38532	-429,38505	0,00054	0,00027	NS	0	[]	[]	[]	hypothetical protein	PF01569.14	PAP2(PAP2 superfamily)
Supercontig_1.160_MVLG_06859_11sp	-739,87622	-739,87622	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02854.12	MIF4G(MIF4G domain)
Supercontig_1.3_MVLG_00624_9sp	-280,49636	-280,4962	0,00032	0,00016	NS	0	[]	[]	[]	large subunit ribosomal protein L26e	TIGR01080	TIGR01080(rplX_A_E: ribosomal protein L24)
Supercontig_1.85_MVLG_05787_10sp	-868,72825	-868,72825	0	0	NS	0	[]	[]	[]	amidophosphoribosyltransferase	PF00156.20	Pribosyltran(Phosphoribosyl transferase domain)
Supercontig_1.2_MVLG_00300_6sp	-785,5281	-785,52806	0,00028	0,00028	NS	0	[]	[]	[]	hypothetical protein	PF02598.10	DUF171(Uncharacterized ACR, COG2106)
Supercontig_1.8_MVLG_01371_10sp	-875,36004	-875,35974	0,0006	0,0003	NS	0	[]	[]	[]	hypothetical protein	PF08581.3	Tup_N(Tup N-terminal)
Supercontig_1.60_MVLG_04938_9sp	-1020,9801	-1018,9128	4,13464	0,87348	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.45_MVLG_04231_10sp	-735,46687	-735,46687	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.1_MVLG_00014_9sp	-594,82147	-594,7524	0,13814	0,06674	NS	0	[]	[]	[]	hypothetical protein	PF01532.13	Glyco_hydro_47(Glycosyl hydrolase family 47)
Supercontig_1.38_MVLG_03766_8sp	-442,23406	-442,23405	0,00028	0,00028	NS	0	[]	[]	[]	hypothetical protein	PF10315.2	DUF2416(Protein of unknown function (DUF2416))
Supercontig_1.21_MVLG_02653_8sp	-1626,8601	-1625,6121	2,49604	0,71293	NS	0	[]	[]	[]	hypothetical protein	PF00566.11	TBC(TBC domain)
Supercontig_1.9_MVLG_01513_10sp	-577,13178	-577,13178	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00520.24	Ion_trans(Ion transport protein)
Supercontig_1.44_MVLG_04165_10sp	-706,10444	-706,10444	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00620.20	RhoGAP(RhoGAP domain)
Supercontig_1.107_MVLG_06242_9sp	-601,84703	-601,84703	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00439.18	Bromodomain(Bromodomain)
Supercontig_1.4_MVLG_00865_11sp	-455,7187	-455,7186	0,0002	0,00028	NS	0	[]	[]	[]	hypothetical protein	PF00083.17	Sugar_tr(Sugar (and other) transporter)
Supercontig_1.19_MVLG_02457_10sp	-438,58977	-438,58977	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00083.17	Sugar_tr(Sugar (and other) transporter)
Supercontig_1.97_MVLG_06067_11sp	-410,72411	-410,7239	0,00042	0,00021	NS	0	[]	[]	[]	protein phosphatase	PF00481.14	PP2C(Protein phosphatase 2C)

Supercontig_1.66_MVLG_05184_9sp	-305,83429	-305,68536	0,29786	0,13837	NS	0	[]	[]	[]	hypothetical protein	PF03992.9	ABM(Antibiotic biosynthesis monooxygenase)
Supercontig_1.1_MVLG_00036_11sp	-468,44243	-468,44238	0,00028	0,00028	NS	0	[]	[]	[]	hypothetical protein	PF03151.9	TPT(Triose-phosphate Transporter family)
Supercontig_1.4_MVLG_00821_10sp	-433,41802	-433,41802	0	0	NS	0	[]	[]	[]	galactokinase	PF00288.19	GHMP_kinases_N(GHMP kinases N terminal domain)
Supercontig_1.24_MVLG_02861_8sp	-672,20824	-672,20792	0,00064	0,00032	NS	0	[]	[]	[]	hypothetical protein	PF03810.12	IBN_N(Importin-beta N-terminal domain)
Supercontig_1.62_MVLG_05040_6sp	-557,18196	-557,18196	0	0	NS	0	[]	[]	[]	Skp1 family tetramerisation domain-containing protein	PF03931.8	Skp1_POZ(Skp1 family, tetramerisation domain)
Supercontig_1.181_MVLG_07007_9sp	-864,62874	-864,62874	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.117_MVLG_06390_9sp	-594,38918	-594,38912	0,00012	0,00028	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.17_MVLG_02273_10sp	-598,32816	-597,7671	1,12212	0,4294	NS	0	[]	[]	[]	hypothetical protein	PF00385.17	Chromo('chromo' (CHRromatin Organisation MOdifier) domain)
Supercontig_1.1_MVLG_00139_9sp	-911,80026	-910,53341	2,5337	0,71828	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.6_MVLG_01051_11sp	-385,026	-385,01323	0,02554	0,01269	NS	0	[]	[]	[]	hypothetical protein	PF00416.15	Ribosomal_S13(Ribosomal protein S13/S18)
Supercontig_1.41_MVLG_03995_6sp	-437,64422	-437,64411	0,00022	0,00011	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.8_MVLG_01422_10sp	-332,46062	-332,35772	0,2058	0,09778	NS	0	[]	[]	[]	hypothetical protein	PF00339.22	Arrestin_N(Arrestin (or S-antigen), N-terminal domain)
Supercontig_1.140_MVLG_06687_8sp	-1403,6894	-1402,3846	2,60976	0,72879	NS	0	[]	[]	[]	hypothetical protein	PF00501.21	AMP-binding(AMP-binding enzyme)
Supercontig_1.13_MVLG_01959_12sp	-503,82935	-503,05367	1,55136	0,53961	NS	0	[]	[]	[]	hypothetical protein	PF01490.11	Aa_trans(Transmembrane amino acid transporter protein)
Supercontig_1.15_MVLG_02107_10sp	-624,36688	-624,36688	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00535.19	Glycos_transf_2(Glycosyl transferase family 2)
Supercontig_1.68_MVLG_05249_6sp	-359,74608	-358,06214	3,36788	0,81436	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.5_MVLG_00983_10sp	-1196,2849	-1193,4783	5,6132	0,93959	*	0	[]	[]	[]	STE/STE11 protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.77_MVLG_05547_12sp	-311,04163	-311,04134	0,00058	0,00029	NS	0	[]	[]	[]	hypothetical protein	PF00675.13	Peptidase_M16(Insulinase (Peptidase family M16))
Supercontig_1.5_MVLG_00953_10sp	-500,04311	-500,04311	0	0	NS	0	[]	[]	[]	hypothetical protein	PF06550.4	DUF1119(Protein of unknown function (DUF1119))
Supercontig_1.51_MVLG_04531_7sp	-470,98796	-470,98789	0,00014	0,00028	NS	0	[]	[]	[]	hypothetical protein	PF00106.18	adh_short(short chain dehydrogenase)
Supercontig_1.58_MVLG_04858_7sp	-477,2728	-476,20594	2,13372	0,65591	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.82_MVLG_05714_12sp	-604,55934	-604,55908	0,00052	0,00026	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.4_MVLG_00790_7sp	-716,04617	-716,04617	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.45_MVLG_04228_8sp	-719,84631	-718,72193	2,24876	0,67515	NS	0	[]	[]	[]	hypothetical protein	TIGR00165	TIGR00165(S18: ribosomal protein S18)

Supercontig_1.14_MVLG_02053_6sp	-504,07566	-504,07566	0	0	NS	0	[]	[]	[]	hypothetical protein	PF08544.6	GHMP_kinases_C(GHMP kinases C terminal)
Supercontig_1.8_MVLG_01461_9sp	-2365,8629	-2362,2364	7,25282	0,97339	**	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.47_MVLG_04321_10sp	-408,37786	-407,47651	1,8027	0,59398	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.16_MVLG_02163_8sp	-585,65256	-584,46107	2,38298	0,69623	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.2_MVLG_00445_6sp	-693,88977	-693,88976	0,00028	0,00028	NS	0	[]	[]	[]	hypothetical protein	PF00102.20	Y_phosphatase(Protein-tyrosine phosphatase)
Supercontig_1.76_MVLG_05509_8sp	-511,84345	-510,91279	1,86132	0,60571	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.227_MVLG_07181_9sp	-541,54782	-540,48158	2,13248	0,6557	NS	0	[]	[]	[]	hypothetical protein	PF03501.8	S10_plectin(Plectin/S10 domain)
Supercontig_1.1_MVLG_00194_8sp	-331,59859	-331,59859	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04716.7	ETC_C1_NDUFA5(ETC complex I subunit conserved region)
Supercontig_1.69_MVLG_05297_10sp	-493,06021	-492,67269	0,77504	0,32126	NS	0	[]	[]	[]	hypothetical protein	TIGR00706	TIGR00706(SppA_dom: signal peptide peptidase SppA, 36K type)
Supercontig_1.2_MVLG_00324_6sp	-481,15583	-479,3077	3,69626	0,84247	NS	0	[]	[]	[]	hypothetical protein	TIGR00233	TIGR00233(trpS: tryptophan--tRNA ligase)
Supercontig_1.24_MVLG_02894_7sp	-561,12268	-561,12268	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.55_MVLG_04721_9sp	-526,23198	-526,23176	0,00044	0,00022	NS	0	[]	[]	[]	hypothetical protein	PF01217.13	Clat_adaptor_s(Clathrin adaptor complex small chain)
Supercontig_1.7_MVLG_01301_6sp	-802,39262	-801,67104	1,44316	0,51402	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.17_MVLG_02281_10sp	-555,03823	-555,03029	0,01588	0,00791	NS	0	[]	[]	[]	hypothetical protein	PF00083.17	Sugar_tr(Sugar (and other) transporter)
Supercontig_1.25_MVLG_02942_6sp	-1216,2918	-1216,2478	0,08794	0,04302	NS	0	[]	[]	[]	hypothetical protein	PF03452.7	Anp1(Anp1)
Supercontig_1.140_MVLG_06677_6sp	-352,21362	-352,21362	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.49_MVLG_04416_8sp	-687,10488	-684,41654	5,37668	0,93201	*	0	[]	[]	[]	hypothetical protein	PF00026.16	Asp(Eukaryotic aspartyl protease)
Supercontig_1.6_MVLG_01204_9sp	-1019,0667	-1019,0667	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.17_MVLG_02282_8sp	-968,26168	-968,25073	0,0219	0,01089	NS	0	[]	[]	[]	hypothetical protein	PF02668.9	TauD(Taurine catabolism dioxygenase TauD, TfdA family)
Supercontig_1.22_MVLG_02691_6sp	-885,46428	-885,46428	0	0	NS	0	[]	[]	[]	hypothetical protein	TIGR00577	TIGR00577(fpg: formamidopyrimidine-DNA glycosylase)
Supercontig_1.1_MVLG_00145_8sp	-620,51537	-620,51537	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01151.11	ELO(GNS1/SUR4 family)
Supercontig_1.39_MVLG_03840_7sp	-699,6123	-698,06697	3,09066	0,78676	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.12_MVLG_01842_6sp	-1064,09	-1064,09	0	0	NS	0	[]	[]	[]	RuvB-like helicase 1	PF05496.5	RuvB_N(Holliday junction DNA helicase ruvB N-terminus)
Supercontig_1.29_MVLG_03221_10sp	-1402,7618	-1400,6022	4,31916	0,88463	NS	0	[]	[]	[]	hypothetical protein	NA	NA

Supercontig_1.1_MVLG_00070_9sp	-766,04116	-765,65067	0,78098	0,32327	NS	0	[]	[]	[]	hypothetical protein	TIGR00094	TIGR00094(tRNA_TruD_broad: tRNA pseudouridine synthase, TruD family)
Supercontig_1.8_MVLG_01468_9sp	-1497,2001	-1497,2001	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.98_MVLG_06097_10sp	-841,71862	-841,70026	0,03672	0,01819	NS	0	[]	[]	[]	pre-mRNA-splicing factor CLF1	PF05843.7	Suf(Suppressor of forked protein (Suf))
Supercontig_1.5_MVLG_00941_9sp	-1129,8976	-1129,8976	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04615.6	Utp14(Utp14 protein)
Supercontig_1.53_MVLG_04597_7sp	-375,03805	-374,26554	1,54502	0,53815	NS	0	[]	[]	[]	hypothetical protein	PF04117.5	Mpv17_PMP22(Mpv17 / PMP22 family)
Supercontig_1.140_MVLG_06688_7sp	-700,5476	-700,5476	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.24_MVLG_02837_8sp	-651,26307	-651,26307	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.26_MVLG_02992_11sp	-436,27377	-436,10998	0,32758	0,15108	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.46_MVLG_04241_11sp	-520,26761	-520,26761	0	0	NS	0	[]	[]	[]	hypothetical protein	PF05730.4	CFEM(CFEM domain)
Supercontig_1.1_MVLG_00221_10sp	-805,93479	-805,85434	0,1609	0,0773	NS	0	[]	[]	[]	hypothetical protein	PF00083.17	Sugar_tr(Sugar (and other) transporter)
Supercontig_1.58_MVLG_04869_10sp	-501,76107	-501,29854	0,92506	0,37031	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.42_MVLG_04091_11sp	-452,08431	-452,08431	0	0	NS	0	[]	[]	[]	hypothetical protein	PF08241.5	Methyltransf_11(Methyltransferase domain)
Supercontig_1.38_MVLG_03804_8sp	-526,82123	-526,82119	0,00028	0,00028	NS	0	[]	[]	[]	citrate synthase	PF00285.14	Citrate_synt(Citrate synthase)
Supercontig_1.10_MVLG_01629_9sp	-328,40711	-328,82828	0	0	NS	0	[]	[]	[]	histone	PF00125.17	Histone(Core histone H2A/H2B/H3/H4)
Supercontig_1.24_MVLG_02846_9sp	-1502,4425	-1501,7892	1,30674	0,47971	NS	0	[]	[]	[]	hypothetical protein	PF00454.20	PI3_PI4_kinase(Phosphatidylinositol 3- and 4-kinase)
Supercontig_1.26_MVLG_03056_11sp	-596,04052	-596,04052	0	0	NS	0	[]	[]	[]	CMGC/DYRK/PRP4 protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.31_MVLG_03342_7sp	-859,0676	-859,0676	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01267.10	F-actin_cap_A(F-actin capping protein alpha subunit)
Supercontig_1.81_MVLG_05674_6sp	-677,80448	-677,56508	0,4788	0,2129	NS	0	[]	[]	[]	hypothetical protein	PF01650.11	Peptidase_C13(Peptidase C13 family)
Supercontig_1.65_MVLG_05154_8sp	-350,25907	-350,2589	0,00034	0,00017	NS	0	[]	[]	[]	T-complex protein 1 subunit alpha	TIGR02340	TIGR02340(chap_CCT_alpha: T-complex protein 1, alpha subunit)
Supercontig_1.1_MVLG_00126_8sp	-711,32831	-711,32823	0,00016	0,00028	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.17_MVLG_02344_7sp	-290,28077	-289,8706	0,82034	0,33646	NS	0	[]	[]	[]	hypothetical protein	PF03901.10	Glyco_transf_22(Alg9-like mannosyltransferase family)
Supercontig_1.2_MVLG_00376_10sp	-457,33433	-457,33433	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04051.9	TRAPP(Transport protein particle (TRAPP) component)
Supercontig_1.36_MVLG_03636_7sp	-527,55663	-527,5565	0,00026	0,00013	NS	0	[]	[]	[]	hypothetical protein	PF11578.1	DUF3237(Protein of unknown function (DUF3237))
Supercontig_1.6_MVLG_01139_10sp	-1467,7116	-1467,7116	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.44_MVLG_04134_10sp	-530,68805	-530,68789	0,00032	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF02913.12	FAD-oxidase_C(FAD linked oxidases, C-terminal domain)

Supercontig_1.125_MVLG_06504_10sp	-1302,6271	-1301,7942	1,66584	0,56522	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.83_MVLG_05732_11sp	-498,17464	-498,17452	0,00024	0,00012	NS	0	[]	[]	[]	hypothetical protein	PF00618.13	RasGEF_N(motif)
Supercontig_1.6_MVLG_01104_10sp	-603,81024	-603,52014	0,5802	0,25181	NS	0	[]	[]	[]	hypothetical protein	PF01988.12	VIT1(VIT family)
Supercontig_1.39_MVLG_03878_8sp	-1002,3214	-1001,2772	2,0885	0,64804	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.12_MVLG_01882_6sp	-1069,5183	-1069,4968	0,04312	0,02133	NS	0	[]	[]	[]	hypothetical protein	PF12066.1	DUF3546(Domain of unknown function (DUF3546))
Supercontig_1.14_MVLG_01995_7sp	-603,93839	-603,85159	0,1736	0,08314	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.88_MVLG_05876_8sp	-482,42049	-482,11388	0,61322	0,26406	NS	0	[]	[]	[]	hypothetical protein	PF02225.15	PA(PA domain)
Supercontig_1.4_MVLG_00858_8sp	-437,57766	-437,57766	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00153.20	Mito_carr(Mitochondrial carrier protein)
Supercontig_1.20_MVLG_02547_8sp	-1017,6198	-1017,6197	0,00028	0,00014	NS	0	[]	[]	[]	hypothetical protein	PF00168.23	C2(C2 domain)
Supercontig_1.35_MVLG_03623_10sp	-643,78413	-641,59027	4,38772	0,88851	NS	0	[]	[]	[]	hypothetical protein	PF08424.3	DUF1740(Protein of unknown function (DUF1740))
Supercontig_1.154_MVLG_06806_9sp	-476,17884	-476,11793	0,12182	0,05909	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.1_MVLG_00129_9sp	-394,7557	-394,75563	0,00014	0,00028	NS	0	[]	[]	[]	hypothetical protein	PF03982.6	DAGAT(Diacylglycerol acyltransferase)
Supercontig_1.35_MVLG_03580_9sp	-346,39073	-346,39073	0	0	NS	0	[]	[]	[]	hypothetical protein	PF09349.3	OHCU_decarbox(OHCU decarboxylase)
Supercontig_1.46_MVLG_04237_7sp	-822,85671	-822,85658	0,00026	0,00013	NS	0	[]	[]	[]	hypothetical protein	PF11754.1	Velvet(Velvet factor)
Supercontig_1.3_MVLG_00487_7sp	-1011,0971	-1011,0055	0,1832	0,08753	NS	0	[]	[]	[]	hypothetical protein	PF11799.1	IMS_C(impB/mucB/samB family C-terminal)
Supercontig_1.19_MVLG_02436_10sp	-560,60905	-560,60905	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.5_MVLG_00884_11sp	-463,9463	-463,91206	0,06848	0,03366	NS	0	[]	[]	[]	hypothetical protein	PF01209.11	Ubie_methyltran(ubiE/COQ5 methyltransferase family)
Supercontig_1.109_MVLG_06281_12sp	-391,14198	-390,04221	2,19954	0,66705	NS	0	[]	[]	[]	hypothetical protein	PF00096.19	zf-C2H2(Zinc finger, C2H2 type)
Supercontig_1.25_MVLG_02963_7sp	-416,99509	-416,99509	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00046.22	Homeobox(Homeobox domain)
Supercontig_1.46_MVLG_04264_8sp	-809,49725	-809,49124	0,01202	0,00599	NS	0	[]	[]	[]	glutamate-5-semialdehyde dehydrogenase	PF00171.15	Aldedh(Aldehyde dehydrogenase family)
Supercontig_1.6_MVLG_01085_9sp	-418,65711	-418,6571	0,00028	0,00028	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.69_MVLG_05293_7sp	-1265,8135	-1265,7675	0,09206	0,04499	NS	0	[]	[]	[]	hypothetical protein	PF00005.20	ABC_tran(ABC transporter)
Supercontig_1.41_MVLG_04015_6sp	-1437,4781	-1437,4286	0,099	0,04829	NS	0	[]	[]	[]	hypothetical protein	PF03439.6	Spt5-NGN(Early transcription elongation factor of RNA pol II, NGN section)
Supercontig_1.6_MVLG_01073_10sp	-446,09522	-446,0951	0,00024	0,00012	NS	0	[]	[]	[]	pyridoxine biosynthesis protein PDX1	PF05690.7	ThiG(Thiazole biosynthesis protein ThiG)

Supercontig_1.25_MVLG_02946_7sp	-1005,2117	-1005,2117	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.18_MVLG_02370_9sp	-438,57263	-438,33616	0,47294	0,21059	NS	0	[]	[]	[]	hypothetical protein	PF00578.14	AhpC-TSA(AhpC/TSA family)
Supercontig_1.74_MVLG_05475_6sp	-685,55574	-684,49257	2,12634	0,65464	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.54_MVLG_04696_12sp	-421,25021	-421,25013	0,00016	0,00028	NS	0	[]	[]	[]	hypothetical protein	PF02985.15	HEAT(HEAT repeat)
Supercontig_1.79_MVLG_05630_8sp	-646,84399	-646,84399	0	0	NS	0	[]	[]	[]	transketolase	PF02780.13	Transketolase_C(Transketolase, C-terminal domain)
Supercontig_1.149_MVLG_06758_10sp	-603,9397	-603,9397	0	0	NS	0	[]	[]	[]	hypothetical protein	PF08643.3	DUF1776(Fungal family of unknown function (DUF1776))
Supercontig_1.76_MVLG_05508_9sp	-510,5476	-510,53267	0,02986	0,01482	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.73_MVLG_05403_10sp	-718,30782	-718,02724	0,56116	0,24465	NS	0	[]	[]	[]	hypothetical protein	PF01564.10	Spermine_synth(Spermine/spermidine synthase)
Supercontig_1.20_MVLG_02574_12sp	-939,25603	-939,25603	0	0	NS	0	[]	[]	[]	hypothetical protein	PF08214.4	KAT11(Histone acetylation protein)
Supercontig_1.27_MVLG_03073_11sp	-530,98073	-528,97329	4,01488	0,86567	NS	0	[]	[]	[]	hypothetical protein	PF04034.6	DUF367(Domain of unknown function (DUF367))
Supercontig_1.139_MVLG_06669_10sp	-554,65143	-554,65143	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00753.20	Lactamase_B(Metallo-beta-lactamase superfamily)
Supercontig_1.60_MVLG_04951_8sp	-1116,8295	-1116,3232	1,01244	0,39723	NS	0	[]	[]	[]	hypothetical protein	PF00176.16	SNF2_N(SNF2 family N-terminal domain)
Supercontig_1.18_MVLG_02371_8sp	-741,53899	-741,46754	0,1429	0,06896	NS	0	[]	[]	[]	histone acetyltransferase type B subunit 2	PF00400.25	WD40(WD domain, G-beta repeat)
Supercontig_1.18_MVLG_02388_7sp	-520,46484	-520,46381	0,00206	0,00103	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.122_MVLG_06463_6sp	-388,77984	-388,77981	0,00028	0,00028	NS	0	[]	[]	[]	nuclear distribution protein PAC1	PF00400.25	WD40(WD domain, G-beta repeat)
Supercontig_1.60_MVLG_04940_10sp	-552,39612	-552,39587	0,0005	0,00025	NS	0	[]	[]	[]	hypothetical protein	PF00664.16	ABC_membrane(ABC transporter transmembrane region)
Supercontig_1.132_MVLG_06595_9sp	-470,65806	-470,56453	0,18706	0,08929	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.25_MVLG_02917_12sp	-685,73909	-685,50114	0,4759	0,21176	NS	0	[]	[]	[]	hypothetical protein	PF01476.13	LysM(LysM domain)
Supercontig_1.10_MVLG_01637_11sp	-872,88347	-871,59869	2,56956	0,72329	NS	0	[]	[]	[]	hypothetical protein	PF02225.15	PA(PA domain)
Supercontig_1.58_MVLG_04842_10sp	-381,84781	-381,84781	0	0	NS	0	[]	[]	[]	hypothetical protein	PF05127.7	DUF699(Putative ATPase (DUF699))
Supercontig_1.96_MVLG_06034_7sp	-543,65812	-543,65812	0	0	NS	0	[]	[]	[]	60S ribosomal protein L1-B	PF00687.14	Ribosomal_L1(Ribosomal protein L1p/L10e family)
Supercontig_1.36_MVLG_03686_10sp	-349,93832	-349,93793	0,00078	0,00039	NS	0	[]	[]	[]	hypothetical protein	PF02020.11	W2(eIF4-gamma/eIF5/eIF2-epsilon)
Supercontig_1.131_MVLG_06582_12sp	-768,94614	-768,58908	0,71412	0,30027	NS	0	[]	[]	[]	hypothetical protein	PF07742.5	BTG(BTG family)
Supercontig_1.66_MVLG_05183_11sp	-799,92947	-799,92947	0	0	NS	0	[]	[]	[]	hypothetical protein	TIGR02251	TIGR02251(HIF-SF_euk: Dullard-like phosphatase domain)

Supercontig_1.21_MVLG_02674_12sp	-451,35463	-450,16244	2,38438	0,69644	NS	0	[]	[]	[]	hypothetical protein	PF04163.5	Tht1(Tht1-like nuclear fusion protein)
Supercontig_1.124_MVLG_06494_12sp	-787,87938	-787,87898	0,0008	0,0004	NS	0	[]	[]	[]	hypothetical protein	PF04851.8	ResIII(Type III restriction enzyme, res subunit)
Supercontig_1.3_MVLG_00642_9sp	-753,55965	-753,4317	0,2559	0,1201	NS	0	[]	[]	[]	hypothetical protein	TIGR00886	TIGR00886(2A0108: nitrite transporter)
Supercontig_1.41_MVLG_04036_9sp	-399,69039	-399,69019	0,0004	0,0002	NS	0	[]	[]	[]	hypothetical protein	PF02383.11	Syja_N(SacI homology domain)
Supercontig_1.4_MVLG_00774_8sp	-648,10737	-647,23238	1,74998	0,58313	NS	0	[]	[]	[]	vesicle transporter SEC22	PF00957.14	Synaptobrevin(Synaptobrevin)
Supercontig_1.4_MVLG_00784_7sp	-624,22613	-624,22613	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.91_MVLG_05927_12sp	-637,99871	-637,99871	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.44_MVLG_04175_7sp	-628,6161	-628,6161	0	0	NS	0	[]	[]	[]	cysteinyl-tRNA synthetase	TIGR00435	TIGR00435(cysS: cysteine--tRNA ligase)
Supercontig_1.1_MVLG_00011_6sp	-407,33706	-407,14778	0,37856	0,17245	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.2_MVLG_00470_11sp	-494,63996	-494,63996	0	0	NS	0	[]	[]	[]	hypothetical protein	PF12271.1	Chs3p(Chitin synthase III catalytic subunit)
Supercontig_1.5_MVLG_00968_10sp	-391,95245	-391,95242	0,00028	0,00028	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.58_MVLG_04876_8sp	-786,08902	-786,08232	0,0134	0,00668	NS	0	[]	[]	[]	hypothetical protein	PF00026.16	Asp(Eukaryotic aspartyl protease)
Supercontig_1.86_MVLG_05842_12sp	-453,57862	-453,57862	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00653.14	BIR(Inhibitor of Apoptosis domain)
Supercontig_1.30_MVLG_03293_11sp	-409,18312	-409,16931	0,02762	0,01372	NS	0	[]	[]	[]	hypothetical protein	PF05572.6	Peptidase_M43(Pregnancy-associated plasma protein-A)
Supercontig_1.3_MVLG_00652_6sp	-883,5578	-883,55721	0,00118	0,00059	NS	0	[]	[]	[]	hypothetical protein	PF00328.15	Acid_phosphat_A(Histidine acid phosphatase)
Supercontig_1.32_MVLG_03419_11sp	-563,89815	-563,89814	0,00028	0,00028	NS	0	[]	[]	[]	hypothetical protein	PF00400.25	WD40(WD domain, G-beta repeat)
Supercontig_1.38_MVLG_03821_7sp	-635,42705	-635,4269	0,00028	0,00028	NS	0	[]	[]	[]	hypothetical protein	TIGR00598	TIGR00598(rad14: DNA repair protein)
Supercontig_1.40_MVLG_03911_6sp	-313,46891	-313,46882	0,00028	0,00028	NS	0	[]	[]	[]	hypothetical protein	PF03357.14	Snf7(Snf7)
Supercontig_1.19_MVLG_02455_6sp	-356,23012	-356,23012	0	0	NS	0	[]	[]	[]	hypothetical protein	TIGR01126	TIGR01126(pdi_dom: protein disulfide-isomerase domain)
Supercontig_1.10_MVLG_01677_6sp	-680,75406	-680,55223	0,40366	0,18277	NS	0	[]	[]	[]	hypothetical protein	PF07690.9	MFS_1(Major Facilitator Superfamily)
Supercontig_1.8_MVLG_01407_10sp	-517,99726	-517,58875	0,81702	0,33536	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.5_MVLG_00896_10sp	-668,98572	-668,98572	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.11_MVLG_01755_9sp	-533,73202	-533,73174	0,00056	0,00028	NS	0	[]	[]	[]	hypothetical protein	TIGR00677	TIGR00677(fadh2_euk: methylenetetrahydrofolate reductase)
Supercontig_1.11_MVLG_01774_8sp	-733,40423	-729,99396	6,82054	0,96697	**	0	[]	[]	[]	hypothetical protein	PF04632.5	FUSC(Fusaric acid resistance protein family)
Supercontig_1.76_MVLG_05512_9sp	-1674,2423	-1673,72	1,04468	0,40687	NS	0	[]	[]	[]	hypothetical protein	PF00566.11	TBC(TBC domain)

Supercontig_1.1_MVLG_00095_7sp	-1070,748	-1070,748	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00004.22	AAA(ATPase family associated with various cellular activities (AAA))
Supercontig_1.9_MVLG_01530_9sp	-498,96889	-497,44687	3,04404	0,78173	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.78_MVLG_05575_10sp	-562,1756	-562,1756	0	0	NS	0	[]	[]	[]	S-adenosylmethionine transporter	PF00153.20	Mito_carr(Mitochondrial carrier protein)
Supercontig_1.23_MVLG_02828_10sp	-948,07898	-948,07862	0,00072	0,00036	NS	0	[]	[]	[]	hypothetical protein	PF01637.11	Arch_ATPase(Archaeal ATPase)
Supercontig_1.141_MVLG_06697_10sp	-493,1669	-492,94282	0,44816	0,20075	NS	0	[]	[]	[]	hypothetical protein	PF05011.6	DBR1(Lariat debranching enzyme, C-terminal domain)
Supercontig_1.122_MVLG_06461_9sp	-470,17132	-470,17132	0	0	NS	0	[]	[]	[]	acetyl-CoA acyltransferase	TIGR01930	TIGR01930(AcCoA-C-Actrans: acetyl-CoA C-acetyltransferase)
Supercontig_1.3_MVLG_00533_9sp	-408,63589	-408,63569	0,0004	0,0002	NS	0	[]	[]	[]	hypothetical protein	PF04389.10	Peptidase_M28(Peptidase family M28)
Supercontig_1.80_MVLG_05656_10sp	-354,80493	-354,80448	0,0009	0,00045	NS	0	[]	[]	[]	serine/threonine-protein phosphatase	PF00149.21	Metallophos(Calcineurin-like phosphoesterase)
Supercontig_1.51_MVLG_04540_10sp	-374,05683	-373,53312	1,04742	0,40768	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.213_MVLG_07133_10sp	-860,46418	-859,91936	1,08964	0,42005	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.155_MVLG_06826_8sp	-522,59936	-522,59927	0,00018	0,00028	NS	0	[]	[]	[]	hypothetical protein	PF08743.3	Nse4(Nse4)
Supercontig_1.141_MVLG_06698_9sp	-465,24875	-465,20641	0,08468	0,04146	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.47_MVLG_04306_11sp	-372,29854	-372,29849	0,00028	0,00028	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.1_MVLG_00265_11sp	-343,66992	-343,66992	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01222.10	ERG4_ERG24(Ergosterol biosynthesis ERG4/ERG24 family)
Supercontig_1.68_MVLG_05266_11sp	-499,58094	-499,58094	0	0	NS	0	[]	[]	[]	26S protease regulatory subunit 7	PF07728.7	AAA_5(AAA domain (dynein-related subfamily))
Supercontig_1.1_MVLG_00032_9sp	-628,45569	-627,37832	2,15474	0,65951	NS	0	[]	[]	[]	hypothetical protein	PF01656.16	CbiA(CobQ/CobB/MinD/ParA nucleotide binding domain)
Supercontig_1.191_MVLG_07047_10sp	-898,48669	-898,48667	0,00028	0,00028	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.84_MVLG_05769_12sp	-499,83292	-499,83292	0	0	NS	0	[]	[]	[]	hypothetical protein	PF08447.4	PAS_3(PAS fold)
Supercontig_1.8_MVLG_01434_9sp	-1014,834	-1014,8334	0,00116	0,00058	NS	0	[]	[]	[]	hypothetical protein	PF04841.6	Vps16_N(Vps16, N-terminal region)
Supercontig_1.4_MVLG_00760_10sp	-1319,2549	-1318,7845	0,94074	0,37523	NS	0	[]	[]	[]	hypothetical protein	PF02469.15	Fasciclin(Fasciclin domain)
Supercontig_1.135_MVLG_06637_10sp	-869,89601	-869,88785	0,01632	0,00813	NS	0	[]	[]	[]	hypothetical protein	PF00176.16	SNF2_N(SNF2 family N-terminal domain)
Supercontig_1.16_MVLG_02252_8sp	-755,8358	-755,81886	0,03388	0,0168	NS	0	[]	[]	[]	hypothetical protein	PF03151.9	TPT(Triose-phosphate Transporter family)
Supercontig_1.81_MVLG_05693_8sp	-331,00669	-331,00669	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.62_MVLG_05005_10sp	-416,97118	-416,35615	1,23006	0,45938	NS	0	[]	[]	[]	hypothetical protein	PF11022.1	DUF2611(Protein of unknown function (DUF2611))

Supercontig_1.7_MVLG_01310_10sp	-452,56099	-452,56099	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.11_MVLG_01765_9sp	-1107,2132	-1106,6034	1,21972	0,45657	NS	0	[]	[]	[]	hypothetical protein	PF00581.13	Rhodanese(Rhodanese-like domain)
Supercontig_1.10_MVLG_01584_10sp	-389,63836	-389,63836	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.73_MVLG_05409_9sp	-463,62232	-461,94791	3,34882	0,81258	NS	0	[]	[]	[]	hypothetical protein	PF01412.11	ArfGap(Putative GTPase activating protein for Arf)
Supercontig_1.2_MVLG_00469_8sp	-1208,1051	-1208,1051	0	0	NS	0	[]	[]	[]	glutamyl-tRNA synthetase	TIGR00464	TIGR00464(gltX_bact: glutamate--tRNA ligase)
Supercontig_1.33_MVLG_03454_6sp	-306,34666	-305,41641	1,8605	0,60554	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.35_MVLG_03620_10sp	-557,32373	-557,32353	0,0004	0,0002	NS	0	[]	[]	[]	hypothetical protein	PF02913.12	FAD-oxidase_C(FAD linked oxidases, C-terminal domain)
Supercontig_1.28_MVLG_03145_6sp	-592,6345	-591,40368	2,46164	0,70795	NS	0	[]	[]	[]	S-formylglutathione hydrolase	PF00756.13	Esterase(Putative esterase)
Supercontig_1.125_MVLG_06513_10sp	-425,89814	-425,89809	0,00028	0,00028	NS	0	[]	[]	[]	hypothetical protein	PF00172.11	Zn_clus(Fungal Zn(2)-Cys(6) binuclear cluster domain)
Supercontig_1.49_MVLG_04449_8sp	-593,58062	-593,58062	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04821.7	TIMELESS(Timeless protein)
Supercontig_1.83_MVLG_05733_6sp	-500,9293	-500,89891	0,06078	0,02993	NS	0	[]	[]	[]	hypothetical protein	PF10276.2	zf-CHCC(Zinc-finger domain)
Supercontig_1.113_MVLG_06344_6sp	-477,39508	-477,39504	0,00028	0,00028	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.140_MVLG_06689_6sp	-671,78644	-671,78644	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00150.11	Cellulase(Cellulase (glycosyl hydrolase family 5))
Supercontig_1.6_MVLG_01050_10sp	-841,98279	-841,98279	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.132_MVLG_06603_10sp	-590,0326	-590,0326	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00782.13	DSPc(Dual specificity phosphatase, catalytic domain)
Supercontig_1.1_MVLG_00069_6sp	-572,09246	-571,56169	1,06154	0,41185	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.22_MVLG_02757_7sp	-497,76225	-497,00113	1,52224	0,53286	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.69_MVLG_05276_8sp	-436,34053	-436,34053	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.32_MVLG_03391_10sp	-955,64837	-955,57846	0,13982	0,06752	NS	0	[]	[]	[]	hypothetical protein	PF12455.1	Dynactin(Dynein associated protein)
Supercontig_1.46_MVLG_04270_9sp	-437,88822	-437,88822	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00097.18	zf-C3HC4(Zinc finger, C3HC4 type (RING finger))
Supercontig_1.17_MVLG_02323_9sp	-536,71718	-536,71718	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.150_MVLG_06783_10sp	-792,59664	-790,95727	3,27874	0,8059	NS	0	[]	[]	[]	hypothetical protein	PF00412.15	LIM(LIM domain)
Supercontig_1.4_MVLG_00793_9sp	-945,14323	-945,14323	0	0	NS	0	[]	[]	[]	hypothetical protein	PF05827.5	ATP-synt_S1(Vacuolar ATP synthase subunit S1 (ATP6S1))
Supercontig_1.20_MVLG_02532_10sp	-725,99906	-725,95241	0,0933	0,04558	NS	0	[]	[]	[]	hypothetical protein	PF07690.9	MFS_1(Major Facilitator Superfamily)
Supercontig_1.3_MVLG_00621_9sp	-618,10955	-617,80964	0,59982	0,25912	NS	0	[]	[]	[]	hypothetical protein	TIGR00951	TIGR00951(2A43: Lysosomal Cystine Transporter)

Supercontig_1.34_MVLG_03557_6sp	-364,12487	-364,12487	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.36_MVLG_03678_6sp	-435,8638	-435,86365	0,0003	0,00015	NS	0	[]	[]	[]	60S ribosomal protein L34-B	PF01199.11	Ribosomal_L34e(Ribosomal protein L34e)
Supercontig_1.11_MVLG_01733_8sp	-349,04192	-349,04192	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00411.12	Ribosomal_S11(Ribosomal protein S11)
Supercontig_1.5_MVLG_00912_9sp	-477,60308	-477,10613	0,9939	0,39162	NS	0	[]	[]	[]	hypothetical protein	PF01849.11	NAC(NAC domain)
Supercontig_1.41_MVLG_03985_10sp	-323,76112	-323,76094	0,00036	0,00018	NS	0	[]	[]	[]	hypothetical protein	PF04116.6	FA_hydroxylase(Fatty acid hydroxylase superfamily)
Supercontig_1.49_MVLG_04405_9sp	-446,31969	-446,31968	0,00028	0,00028	NS	0	[]	[]	[]	hypothetical protein	PF08511.4	COQ9(COQ9)
Supercontig_1.26_MVLG_02995_8sp	-1613,7109	-1612,2412	2,9393	0,76999	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.66_MVLG_05194_10sp	-439,69	-439,69	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00561.13	Abhydrolase_1(alpha/beta hydrolase fold)
Supercontig_1.15_MVLG_02157_9sp	-715,13985	-715,11236	0,05498	0,02712	NS	0	[]	[]	[]	hypothetical protein	PF01237.11	Oxysterol_BP(Oxysterol-binding protein)
Supercontig_1.83_MVLG_05747_7sp	-1839,6526	-1839,5044	0,29644	0,13776	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.142_MVLG_06702_7sp	-945,88922	-945,76051	0,25742	0,12077	NS	0	[]	[]	[]	hypothetical protein	PF03619.9	DUF300(Domain of unknown function)
Supercontig_1.23_MVLG_02790_7sp	-1220,2669	-1220,2669	0	0	NS	0	[]	[]	[]	hypothetical protein	PF07304.4	SRA1(Steroid receptor RNA activator (SRA1))
Supercontig_1.91_MVLG_05933_12sp	-375,20243	-375,20243	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03193.9	DUF258(Protein of unknown function, DUF258)
Supercontig_1.38_MVLG_03778_11sp	-449,40078	-449,40076	0,00028	0,00028	NS	0	[]	[]	[]	hypothetical protein	PF00172.11	Zn_clus(Fungal Zn(2)-Cys(6) binuclear cluster domain)
Supercontig_1.61_MVLG_04996_8sp	-565,56648	-565,56629	0,00038	0,00019	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.15_MVLG_02060_6sp	-591,68868	-591,68836	0,00064	0,00032	NS	0	[]	[]	[]	hypothetical protein	PF06644.4	ATP11(ATP11 protein)
Supercontig_1.8_MVLG_01398_7sp	-501,64979	-501,64979	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.205_MVLG_07107_9sp	-366,99228	-366,99227	0,00028	0,00028	NS	0	[]	[]	[]	hypothetical protein	PF04418.5	DUF543(Domain of unknown function (DUF543))
Supercontig_1.8_MVLG_01457_7sp	-786,58943	-781,32395	10,531	0,99483	***	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.26_MVLG_03044_9sp	-417,7628	-417,7628	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.18_MVLG_02365_9sp	-507,33867	-507,31287	0,0516	0,02547	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.1_MVLG_00002_9sp	-416,27833	-416,27833	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00728.15	Glyco_hydro_20(Glycosyl hydrolase family 20, catalytic domain)
Supercontig_1.3_MVLG_00643_6sp	-378,53692	-378,53684	0,00016	0,00028	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.49_MVLG_04420_11sp	-894,18859	-892,94731	2,48256	0,71099	NS	0	[]	[]	[]	hypothetical protein	PF09258.3	Glyco_transf_64(Glycosyl transferase family 64 domain)
Supercontig_1.13_MVLG_01937_10sp	-887,53893	-886,56933	1,9392	0,62077	NS	0	[]	[]	[]	hypothetical protein	PF00320.20	GATA(GATA zinc finger)

Supercontig_1.27_MVLG_03112_9sp	-786,85153	-786,18026	1,34254	0,48894	NS	0	[]	[]	[]	hypothetical protein	PF00724.13	Oxidored_FMN(NADH:flavin oxidoreductase / NADH oxidase family)
Supercontig_1.78_MVLG_05590_10sp	-809,73829	-809,73829	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03178.8	CPSF_A(CPSF A subunit region)
Supercontig_1.14_MVLG_01979_6sp	-539,45269	-539,45265	0,00028	0,00028	NS	0	[]	[]	[]	hypothetical protein	PF00169.22	PH(PH domain)
Supercontig_1.30_MVLG_03292_9sp	-429,56279	-429,56279	0	0	NS	0	[]	[]	[]	hypothetical protein	PF05572.6	Peptidase_M43(Pregnancy-associated plasma protein-A)
Supercontig_1.65_MVLG_05153_10sp	-656,09335	-656,09335	0	0	NS	0	[]	[]	[]	hypothetical protein	PF07890.5	Rrp15p(Rrp15p)
Supercontig_1.135_MVLG_06627_8sp	-1198,2574	-1198,2574	0	0	NS	0	[]	[]	[]	hypothetical protein	PF08164.5	TRAUB(TRAUB (NUC102) domain)
Supercontig_1.88_MVLG_05875_9sp	-384,51543	-384,51543	0	0	NS	0	[]	[]	[]	hypothetical protein	PF06280.5	DUF1034(Fn3-like domain (DUF1034))
Supercontig_1.9_MVLG_01549_8sp	-494,48527	-494,38459	0,20136	0,09578	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.46_MVLG_04272_11sp	-447,65051	-447,65028	0,00046	0,00023	NS	0	[]	[]	[]	hypothetical protein	PF00278.15	Orn_DAP_Arg_deC(Pyridoxal-dependent decarboxylase, C-terminal sheet domain)
Supercontig_1.53_MVLG_04623_8sp	-351,46852	-351,46846	0,00012	0,00028	NS	0	[]	[]	[]	hypothetical protein	PF10526.2	NADH_ub_rd_NUML(NADH-ubiquinone reductase complex 1 MLRQ subunit)
Supercontig_1.26_MVLG_03021_10sp	-456,01731	-455,98758	0,05946	0,02929	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.68_MVLG_05251_8sp	-606,54215	-606,42838	0,22754	0,10754	NS	0	[]	[]	[]	hypothetical protein	PF01124.11	MAPEG(MAPEG family)
Supercontig_1.56_MVLG_04761_9sp	-501,79269	-501,79269	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.42_MVLG_04068_8sp	-518,83878	-518,83872	0,00012	0,00028	NS	0	[]	[]	[]	hypothetical protein	PF00173.21	Cyt-b5(Cytochrome b5-like Heme/Steroid binding domain)
Supercontig_1.15_MVLG_02118_11sp	-1062,5966	-1062,2253	0,74254	0,31014	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.58_MVLG_04856_8sp	-1048,0327	-1045,7623	4,54086	0,89673	NS	0	[]	[]	[]	hypothetical protein	PF00149.21	Metallophos(Calcineurin-like phosphoesterase)
Supercontig_1.16_MVLG_02237_7sp	-757,17081	-757,08312	0,17538	0,08396	NS	0	[]	[]	[]	hypothetical protein	PF03937.9	Sdh5(Protein of unknown function (DUF339))
Supercontig_1.34_MVLG_03532_10sp	-789,38359	-788,89725	0,97268	0,38513	NS	0	[]	[]	[]	hypothetical protein	PF04137.8	ERO1(Endoplasmic Reticulum Oxidoreductin 1 (ERO1))
Supercontig_1.63_MVLG_05083_9sp	-310,34447	-310,34445	0,00028	0,00028	NS	0	[]	[]	[]	hypothetical protein	PF08033.5	Sec23_BS(Sec23/Sec24 beta-sandwich domain)
Supercontig_1.4_MVLG_00763_9sp	-887,22291	-887,22275	0,00032	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF07690.9	MFS_1(Major Facilitator Superfamily)
Supercontig_1.48_MVLG_04379_6sp	-591,1886	-591,1886	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.7_MVLG_01227_8sp	-669,377	-669,3766	0,0008	0,0004	NS	0	[]	[]	[]	30S ribosomal protein S9	PF00380.12	Ribosomal_S9(Ribosomal protein S9/S16)
Supercontig_1.4_MVLG_00725_6sp	-1165,4328	-1165,4328	0	0	NS	0	[]	[]	[]	hypothetical protein	PF06414.5	Zeta_toxin(Zeta toxin)
Supercontig_1.23_MVLG_02774_7sp	-509,38387	-509,38387	0	0	NS	0	[]	[]	[]	2-methylcitrate dehydratase	PF03972.7	MmgE_PrpD(MmgE/PrpD family)

Supercontig_1.79_MVLG_05614_8sp	-302,85629	-302,8562	0,00018	8.99959501216428e-05	NS	0	[]	[]	[]	hypothetical protein	PF08718.4	GLTP(Glycolipid transfer protein (GLTP))
Supercontig_1.12_MVLG_01811_12sp	-399,10106	-397,78427	2,63358	0,73201	NS	0	[]	[]	[]	hypothetical protein	TIGR00491	TIGR00491(aIF-2: translation initiation factor aIF-2)
Supercontig_1.1_MVLG_00141_10sp	-623,06585	-621,98897	2,15376	0,65934	NS	0	[]	[]	[]	3-oxoacyl-[acyl-carrier protein] reductase	PF00106.18	adh_short(short chain dehydrogenase)
Supercontig_1.26_MVLG_03039_7sp	-509,73843	-509,73839	0,00028	0,00028	NS	0	[]	[]	[]	hypothetical protein	PF00326.14	Peptidase_S9(Prolyl oligopeptidase family)
Supercontig_1.1_MVLG_00219_9sp	-740,7296	-740,72879	0,00162	0,00081	NS	0	[]	[]	[]	hypothetical protein	PF04675.7	DNA_ligase_A_N(DNA ligase N terminus)
Supercontig_1.46_MVLG_04261_8sp	-412,61863	-412,49427	0,24872	0,11694	NS	0	[]	[]	[]	hypothetical protein	PF00076.15	RRM_1(RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain))
Supercontig_1.34_MVLG_03542_7sp	-1581,9379	-1581,7021	0,4716	0,21006	NS	0	[]	[]	[]	hypothetical protein	PF09346.3	SMI1_KNR4(SMI1 / KNR4 family)
Supercontig_1.52_MVLG_04552_8sp	-415,90605	-415,72119	0,36972	0,16878	NS	0	[]	[]	[]	hypothetical protein	PF08316.4	Pal1(Pal1 cell morphology protein)
Supercontig_1.34_MVLG_03544_11sp	-426,89273	-426,89239	0,00068	0,00034	NS	0	[]	[]	[]	hypothetical protein	PF00400.25	WD40(WD domain, G-beta repeat)
Supercontig_1.64_MVLG_05104_12sp	-662,64276	-662,64276	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00533.19	BRCT(BRCA1 C Terminus (BRCT) domain)
Supercontig_1.14_MVLG_02043_10sp	-1716,7591	-1714,1092	5,29986	0,92934	*	0	[]	[]	[]	gamma-glutamyltransferase	PF01019.14	G_glu_transpept(Gamma-glutamyltranspeptidase)
Supercontig_1.1_MVLG_00057_11sp	-394,12263	-393,50502	1,23522	0,46077	NS	0	[]	[]	[]	hypothetical protein	PF00654.13	Voltage_CLC(Voltage gated chloride channel)
Supercontig_1.51_MVLG_04512_7sp	-1145,0213	-1145,0213	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00462.17	Glutaredoxin(Glutaredoxin)
Supercontig_1.10_MVLG_01634_8sp	-674,46516	-674,46516	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.155_MVLG_06816_9sp	-710,11051	-709,025	2,17102	0,66227	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.56_MVLG_04786_9sp	-534,07721	-533,50416	1,1461	0,4362	NS	0	[]	[]	[]	hypothetical protein	PF03462.11	PCRF(PCRF domain)
Supercontig_1.6_MVLG_01167_11sp	-839,63679	-839,63678	0,00028	0,00028	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.55_MVLG_04710_8sp	-625,38864	-625,34104	0,0952	0,04648	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.3_MVLG_00545_11sp	-562,72619	-562,72619	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.5_MVLG_01034_11sp	-937,32011	-937,32011	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00385.17	Chromo('chromo' (CHRromatin Organisation MOdifier) domain)
Supercontig_1.6_MVLG_01054_9sp	-782,27059	-782,27059	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00076.15	RRM_1(RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain))
Supercontig_1.207_MVLG_07115_6sp	-1147,411	-1147,411	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.9_MVLG_01533_11sp	-558,13905	-557,18001	1,91808	0,61674	NS	0	[]	[]	[]	hypothetical protein	PF07690.9	MFS_1(Major Facilitator Superfamily)

Supercontig_1.17_MVLG_02278_9sp	-1190,1365	-1189,4611	1,35088	0,49107	NS	0	[]	[]	[]	hypothetical protein	PF07716.8	bZIP_2(Basic region leucine zipper)
Supercontig_1.5_MVLG_00997_8sp	-1231,9011	-1231,9011	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00400.25	WD40(WD domain, G-beta repeat)
Supercontig_1.3_MVLG_00571_9sp	-1055,1784	-1055,1784	0	0	NS	0	[]	[]	[]	hypothetical protein	PF05686.5	DUF821(Arabidopsis thaliana protein of unknown function (DUF821))
Supercontig_1.51_MVLG_04496_12sp	-396,49588	-396,0898	0,81216	0,33374	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.2_MVLG_00355_7sp	-327,75109	-327,74657	0,00904	0,00451	NS	0	[]	[]	[]	hypothetical protein	PF06110.4	DUF953(Eukaryotic protein of unknown function (DUF953))
Supercontig_1.16_MVLG_02231_11sp	-495,02871	-495,02844	0,00054	0,00027	NS	0	[]	[]	[]	hypothetical protein	PF01504.11	PIP5K(Phosphatidylinositol-4-phosphate 5-Kinase)
Supercontig_1.163_MVLG_06886_8sp	-612,27641	-612,27566	0,0015	0,00075	NS	0	[]	[]	[]	60S acidic ribosomal protein P0	PF00428.12	Ribosomal_60s(60s Acidic ribosomal protein)
Supercontig_1.10_MVLG_01630_8sp	-920,48408	-920,484	0,00016	0,00028	NS	0	[]	[]	[]	hypothetical protein	PF00368.11	HMG-CoA_red(Hydroxymethylglutaryl-coenzyme A reductase)
Supercontig_1.46_MVLG_04259_8sp	-566,06038	-566,06036	0,00028	0,00028	NS	0	[]	[]	[]	hypothetical protein	PF01212.14	Beta_elim_lyase(Beta-eliminating lyase)
Supercontig_1.38_MVLG_03828_9sp	-784,10683	-782,81556	2,58254	0,72508	NS	0	[]	[]	[]	hypothetical protein	PF07823.4	CPDase(Cyclic phosphodiesterase-like protein)
Supercontig_1.20_MVLG_02601_12sp	-646,93657	-646,93657	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03517.6	ICln_channel(Nucleotide-sensitive chloride conductance regulator (ICln))
Supercontig_1.82_MVLG_05722_12sp	-494,62595	-494,02714	1,19762	0,45053	NS	0	[]	[]	[]	hypothetical protein	PF04003.5	Utp12(Dip2/Utp12 Family)
Supercontig_1.15_MVLG_02137_9sp	-1063,304	-1063,0216	0,56484	0,24604	NS	0	[]	[]	[]	hypothetical protein	PF05183.5	RdRP(RNA dependent RNA polymerase)
Supercontig_1.60_MVLG_04933_8sp	-1388,6339	-1388,0052	1,25742	0,46672	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.33_MVLG_03499_10sp	-981,11842	-981,05498	0,12688	0,06147	NS	0	[]	[]	[]	hypothetical protein	PF01613.11	Flavin_Reduct(Flavin reductase like domain)
Supercontig_1.8_MVLG_01417_6sp	-524,69206	-524,6786	0,02692	0,01337	NS	0	[]	[]	[]	hypothetical protein	PF00107.19	ADH_zinc_N(Zinc-binding dehydrogenase)
Supercontig_1.41_MVLG_04010_6sp	-394,0377	-394,03768	0,00028	0,00028	NS	0	[]	[]	[]	hypothetical protein	PF01868.9	UPF0086(Domain of unknown function UPF0086)
Supercontig_1.1_MVLG_00180_6sp	-1209,9144	-1208,4197	2,98934	0,77568	NS	0	[]	[]	[]	tubulin beta chain	PF10644.2	Misat_Myo_SegII(Misato Segment II myosin-like domain)
Supercontig_1.38_MVLG_03761_9sp	-771,63725	-771,63697	0,00056	0,00028	NS	0	[]	[]	[]	succinate-semialdehyde dehydrogenase [NADP+]	PF00171.15	Aldedh(Aldehyde dehydrogenase family)
Supercontig_1.38_MVLG_03762_12sp	-533,92891	-533,92891	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02985.15	HEAT(HEAT repeat)
Supercontig_1.4_MVLG_00747_9sp	-391,44671	-391,44648	0,00046	0,00023	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.36_MVLG_03652_6sp	-646,99301	-646,99246	0,0011	0,00055	NS	0	[]	[]	[]	hypothetical protein	TIGR00589	TIGR00589(ogt: methylated-DNA-[protein]-cysteine S-methyltransferase)

Supercontig_1.23_MVLG_02824_9sp	-1267,8003	-1267,8003	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.6_MVLG_01145_8sp	-654,93604	-654,00777	1,85654	0,60476	NS	0	[]	[]	[]	hypothetical protein	PF00067.15	p450(Cytochrome P450)
Supercontig_1.45_MVLG_04208_6sp	-1053,1505	-1052,4173	1,46632	0,51961	NS	0	[]	[]	[]	DNA repair helicase ercc3	PF04851.8	ResIII(Type III restriction enzyme, res subunit)
Supercontig_1.19_MVLG_02475_7sp	-614,98577	-614,98577	0	0	NS	0	[]	[]	[]	hypothetical protein	PF05179.7	CDC73(RNA pol II accessory factor, Cdc73 family)
Supercontig_1.98_MVLG_06080_8sp	-1312,8498	-1311,9467	1,80618	0,59468	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.26_MVLG_03002_10sp	-966,99192	-966,99192	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.14_MVLG_02028_7sp	-564,7568	-564,7568	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.8_MVLG_01397_6sp	-1431,5978	-1430,2737	2,6482	0,73396	NS	0	[]	[]	[]	hypothetical protein	PF00476.13	DNA_pol_A(DNA polymerase family A)
Supercontig_1.2_MVLG_00358_7sp	-490,13505	-490,12619	0,01772	0,00882	NS	0	[]	[]	[]	hypothetical protein	PF03061.15	4HBT(Thioesterase superfamily)
Supercontig_1.2_MVLG_00379_7sp	-687,90062	-687,73303	0,33518	0,1543	NS	0	[]	[]	[]	hypothetical protein	PF01522.14	Polysacc_deac_1(Polysaccharide deacetylase)
Supercontig_1.21_MVLG_02610_11sp	-457,62354	-457,62354	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.18_MVLG_02357_7sp	-673,99541	-673,7115	0,56782	0,24717	NS	0	[]	[]	[]	hypothetical protein	PF00153.20	Mito_carr(Mitochondrial carrier protein)
Supercontig_1.123_MVLG_06473_7sp	-888,03257	-888,03257	0	0	NS	0	[]	[]	[]	hypothetical protein	PF05291.4	Bystin(Bystin)
Supercontig_1.56_MVLG_04762_12sp	-437,20878	-437,55661	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00282.12	Pyridoxal_deC(Pyridoxal-dependent decarboxylase conserved domain)
Supercontig_1.69_MVLG_05305_9sp	-389,38913	-389,38913	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.1_MVLG_00150_7sp	-743,61908	-743,61873	0,0007	0,00035	NS	0	[]	[]	[]	hypothetical protein	PF03169.8	OPT(OPT oligopeptide transporter protein)
Supercontig_1.22_MVLG_02698_8sp	-660,20756	-658,67785	3,05942	0,7834	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.4_MVLG_00868_6sp	-1088,4838	-1088,1054	0,7567	0,31501	NS	0	[]	[]	[]	hypothetical protein	PF09812.2	MRP-L28(Mitochondrial ribosomal protein L28)
Supercontig_1.205_MVLG_07113_10sp	-837,80677	-837,80677	0	0	NS	0	[]	[]	[]	hypothetical protein	TIGR01494	TIGR01494(ATPase_P-type: HAD ATPase, P-type, family IC)
Supercontig_1.3_MVLG_00538_7sp	-441,93782	-440,95253	1,97058	0,62667	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.4_MVLG_00715_9sp	-306,7128	-306,71265	0,0003	0,00015	NS	0	[]	[]	[]	hypothetical protein	PF02953.8	zf-Tim10_DDP(Tim10/DDP family zinc finger)
Supercontig_1.31_MVLG_03380_8sp	-311,64033	-311,63983	0,001	0,0005	NS	0	[]	[]	[]	hypothetical protein	PF04893.10	Yip1(Yip1 domain)
Supercontig_1.46_MVLG_04240_9sp	-595,94799	-595,94799	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01073.12	3Beta_HSD(3-beta hydroxysteroid dehydrogenase/isomerase family)
Supercontig_1.41_MVLG_03988_10sp	-471,62991	-471,62991	0	0	NS	0	[]	[]	[]	hypothetical protein	PF06221.6	zf-C2HC5(Putative zinc finger motif, C2HC5-type)

Supercontig_1.59_MVLG_04902_8sp	-572,2158	-572,20383	0,02394	0,0119	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.124_MVLG_06493_6sp	-580,4523	-580,45212	0,00036	0,00018	NS	0	[]	[]	[]	hypothetical protein	PF00787.17	PX(PX domain)
Supercontig_1.17_MVLG_02275_6sp	-736,38477	-736,38477	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02518.19	HATPase_c(Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase)
Supercontig_1.85_MVLG_05797_9sp	-641,18019	-640,50719	1,346	0,48982	NS	0	[]	[]	[]	hypothetical protein	PF00076.15	RRM_1(RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain))
Supercontig_1.7_MVLG_01336_6sp	-607,53503	-607,53498	0,00016	0,00016	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.21_MVLG_02647_10sp	-805,3527	-805,3527	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.32_MVLG_03385_8sp	-654,04814	-653,95494	0,1864	0,08899	NS	0	[]	[]	[]	hypothetical protein	PF03798.9	TRAM_LAG1_CLN8(TLC domain)
Supercontig_1.7_MVLG_01295_10sp	-334,22546	-334,20828	0,03436	0,01703	NS	0	[]	[]	[]	hypothetical protein	TIGR00152	TIGR00152(TIGR00152: dephospho-CoA kinase)
Supercontig_1.3_MVLG_00582_8sp	-805,86682	-805,86667	0,0003	0,00015	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.45_MVLG_04195_6sp	-382,91348	-382,47764	0,87168	0,35328	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.6_MVLG_01201_11sp	-316,45851	-315,13102	2,65498	0,73486	NS	0	[]	[]	[]	C-22 sterol desaturase	PF00067.15	p450(Cytochrome P450)
Supercontig_1.198_MVLG_07077_8sp	-983,21761	-983,16934	0,09654	0,04712	NS	0	[]	[]	[]	hypothetical protein	PF01602.13	Adaptin_N(Adaptin N terminal region)
Supercontig_1.2_MVLG_00372_10sp	-323,04604	-323,04603	0,00016	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF00806.12	PUF(Pumilio-family RNA binding repeat)
Supercontig_1.13_MVLG_01908_10sp	-298,57586	-298,55796	0,0358	0,01774	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.36_MVLG_03655_11sp	-313,08705	-313,40809	0	0	NS	0	[]	[]	[]	acyl-CoA dehydrogenase	PF02770.12	Acyl-CoA_dh_M(Acyl-CoA dehydrogenase, middle domain)
Supercontig_1.91_MVLG_05921_9sp	-350,23954	-350,23948	0,00012	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF00787.17	PX(PX domain)
Supercontig_1.39_MVLG_03855_6sp	-385,67934	-385,58934	0,18	0,08607	NS	0	[]	[]	[]	hypothetical protein	PF00041.14	fn3(Fibronectin type III domain)
Supercontig_1.28_MVLG_03138_8sp	-676,6656	-676,66551	0,00018	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF08659.3	KR(KR domain)
Supercontig_1.6_MVLG_01135_10sp	-583,98858	-583,91508	0,147	0,07086	NS	0	[]	[]	[]	hypothetical protein	PF05700.4	BCAS2(Breast carcinoma amplified sequence 2 (BCAS2))
Supercontig_1.67_MVLG_05243_7sp	-458,32393	-458,32208	0,0037	0,00185	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.88_MVLG_05887_8sp	-683,04745	-683,04718	0,00054	0,00027	NS	0	[]	[]	[]	hypothetical protein	PF01398.14	Mov34(Mov34/MPN/PAD-1 family)
Supercontig_1.44_MVLG_04137_10sp	-390,81067	-390,81036	0,00062	0,00031	NS	0	[]	[]	[]	tubulin alpha-1A chain	PF00091.18	Tubulin(Tubulin/FtsZ family, GTPase domain)
Supercontig_1.1_MVLG_00178_10sp	-540,58168	-540,58168	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03144.18	GTP_EFTU_D2(Elongation factor Tu domain 2)
Supercontig_1.6_MVLG_01068_9sp	-568,96912	-568,96912	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA

Supercontig_1.111_MVLG_06312_8sp	-1033,7937	-1033,7937	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00168.23	C2(C2 domain)
Supercontig_1.32_MVLG_03416_7sp	-465,85979	-464,458	2,80358	0,75384	NS	0	[]	[]	[]	hypothetical protein	PF00106.18	adh_short(short chain dehydrogenase)
Supercontig_1.31_MVLG_03332_12sp	-785,73714	-784,53412	2,40604	0,69971	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.102_MVLG_06176_7sp	-790,27084	-790,27071	0,00026	0,00013	NS	0	[]	[]	[]	hypothetical protein	PF00106.18	adh_short(short chain dehydrogenase)
Supercontig_1.88_MVLG_05900_10sp	-887,20587	-885,81189	2,78796	0,75191	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.3_MVLG_00620_11sp	-329,9272	-329,927	0,0004	0,0002	NS	0	[]	[]	[]	hypothetical protein	PF08159.5	NUC153(NUC153 domain)
Supercontig_1.7_MVLG_01311_7sp	-955,59211	-953,56799	4,04824	0,86789	NS	0	[]	[]	[]	hypothetical protein	PF00581.13	Rhodanese(Rhodanese-like domain)
Supercontig_1.95_MVLG_06024_7sp	-751,63626	-751,45918	0,35416	0,16229	NS	0	[]	[]	[]	hypothetical protein	PF07690.9	MFS_1(Major Facilitator Superfamily)
Supercontig_1.56_MVLG_04792_10sp	-551,60485	-551,60483	0,00016	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF03473.10	MOSC(MOSC domain)
Supercontig_1.63_MVLG_05088_10sp	-845,81744	-845,69876	0,23736	0,11191	NS	0	[]	[]	[]	hypothetical protein	PF05739.12	SNARE(SNARE domain)
Supercontig_1.107_MVLG_06249_12sp	-664,09146	-664,09146	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.112_MVLG_06327_9sp	-548,98036	-548,98036	0	0	NS	0	[]	[]	[]	AGC/PKA protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.3_MVLG_00568_7sp	-437,49459	-437,49459	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00781.17	DAGK_cat(Diacylglycerol kinase catalytic domain)
Supercontig_1.12_MVLG_01867_9sp	-456,37425	-456,37389	0,00072	0,00036	NS	0	[]	[]	[]	hypothetical protein	PF01417.13	ENTH(ENTH domain)
Supercontig_1.176_MVLG_06979_11sp	-920,39607	-920,39607	0	0	NS	0	[]	[]	[]	IRE protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.16_MVLG_02239_10sp	-364,58288	-364,58278	0,00016	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF01193.17	RNA_pol_L(RNA polymerase Rpb3/Rpb11 dimerisation domain)
Supercontig_1.1_MVLG_00088_8sp	-228,23419	-228,23418	0,00016	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF08598.4	Sds3(Sds3-like)
Supercontig_1.94_MVLG_05988_8sp	-420,07546	-420,07546	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.42_MVLG_04077_10sp	-788,53968	-788,3019	0,47556	0,21162	NS	0	[]	[]	[]	hypothetical protein	PF00628.22	PHD(PHD-finger)
Supercontig_1.42_MVLG_04064_10sp	-491,33262	-491,2457	0,17384	0,08325	NS	0	[]	[]	[]	hypothetical protein	PF03914.10	CBF(CBF/Mak21 family)
Supercontig_1.5_MVLG_01019_9sp	-441,94579	-441,59461	0,70236	0,29614	NS	0	[]	[]	[]	hypothetical protein	PF08613.4	Cyclin(Cyclin)
Supercontig_1.11_MVLG_01772_8sp	-280,12339	-280,12326	0,00026	0,00013	NS	0	[]	[]	[]	hypothetical protein	PF00400.25	WD40(WD domain, G-beta repeat)
Supercontig_1.5_MVLG_00966_10sp	-658,8747	-658,41671	0,91598	0,36745	NS	0	[]	[]	[]	hypothetical protein	PF00400.25	WD40(WD domain, G-beta repeat)
Supercontig_1.40_MVLG_03960_8sp	-335,30543	-335,30543	0	0	NS	0	[]	[]	[]	RIO2 atypical protein kinase	PF09202.4	Rio2_N(Rio2, N-terminal)
Supercontig_1.45_MVLG_04196_7sp	-344,78207	-344,782	0,00014	0,00016	NS	0	[]	[]	[]	dihydroorotase	TIGR00856	TIGR00856(pyrC_dimer: dihydroorotase, homodimeric type)

Supercontig_1.31_MVLG_03364_9sp	-492,78809	-492,78809	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02984.12	Cyclin_C(Cyclin, C-terminal domain)
Supercontig_1.6_MVLG_01122_8sp	-1271,0129	-1271,0129	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.17_MVLG_02268_10sp	-345,60425	-345,60425	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.31_MVLG_03352_12sp	-1044,7836	-1044,7836	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00270.22	DEAD(DEAD/DEAH box helicase)
Supercontig_1.9_MVLG_01480_10sp	-1037,5849	-1037,4782	0,21346	0,10123	NS	0	[]	[]	[]	hypothetical protein	PF02373.15	JmjC(JmjC domain)
Supercontig_1.9_MVLG_01540_10sp	-652,90132	-652,90132	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.15_MVLG_02151_8sp	-798,5249	-798,5249	0	0	NS	0	[]	[]	[]	hypothetical protein	TIGR00512	TIGR00512(salvage_mtnA: S-methyl-5-thioribose-1-phosphate isomerase)
Supercontig_1.22_MVLG_02694_6sp	-836,05198	-836,05198	0	0	NS	0	[]	[]	[]	hypothetical protein	PF10294.2	Methyltransf_16(Putative methyltransferase)
Supercontig_1.33_MVLG_03453_8sp	-371,23378	-371,23322	0,00112	0,00056	NS	0	[]	[]	[]	hypothetical protein	PF03660.7	PHF5(PHF5-like protein)
Supercontig_1.36_MVLG_03675_9sp	-376,62936	-376,62936	0	0	NS	0	[]	[]	[]	high-affinity iron transporter	PF03239.7	FTR1(Iron permease FTR1 family)
Supercontig_1.7_MVLG_01309_6sp	-1154,1938	-1154,1938	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00067.15	p450(Cytochrome P450)
Supercontig_1.11_MVLG_01726_9sp	-1300,8615	-1300,7857	0,15162	0,07301	NS	0	[]	[]	[]	hypothetical protein	PF09739.2	DUF2044(Conserved membrane protein (DUF2044))
Supercontig_1.21_MVLG_02658_12sp	-861,49008	-855,57399	11,8322	0,9973	***	0	[]	[]	[]	hypothetical protein	PF00324.14	AA_permease(Amino acid permease)
Supercontig_1.35_MVLG_03615_9sp	-381,19103	-381,19108	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01172.11	SBDS(Shwachman-Bodian-Diamond syndrome (SBDS) protein)
Supercontig_1.24_MVLG_02851_7sp	-543,16434	-543,01036	0,30796	0,14271	NS	0	[]	[]	[]	hypothetical protein	PF09816.2	EAF(RNA polymerase II transcription elongation factor)
Supercontig_1.4_MVLG_00746_8sp	-1141,9002	-1141,9002	0	0	NS	0	[]	[]	[]	hypothetical protein	PF06745.6	KaiC(KaiC)
Supercontig_1.7_MVLG_01252_9sp	-460,80566	-459,15994	3,29144	0,80713	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.28_MVLG_03207_8sp	-951,237	-950,38821	1,69758	0,57207	NS	0	[]	[]	[]	hypothetical protein	PF00657.15	Lipase_GDSL(GDSL-like Lipase/Acylhydrolase)
Supercontig_1.20_MVLG_02563_10sp	-545,00475	-544,43213	1,14524	0,43595	NS	0	[]	[]	[]	hypothetical protein	PF08704.3	GCD14(tRNA methyltransferase complex GCD14 subunit)
Supercontig_1.68_MVLG_05261_7sp	-1150,9608	-1150,9608	0,00016	0,00016	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.7_MVLG_01343_9sp	-706,64386	-706,26372	0,76028	0,31623	NS	0	[]	[]	[]	hypothetical protein	PF00535.19	Glycos_transf_2(Glycosyl transferase family 2)
Supercontig_1.58_MVLG_04870_6sp	-1081,7575	-1081,7575	0	0	NS	0	[]	[]	[]	STE/STE20/YSK protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.81_MVLG_05688_9sp	-602,43368	-602,36109	0,14518	0,07002	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.7_MVLG_01322_8sp	-282,64494	-282,24242	0,80504	0,33137	NS	0	[]	[]	[]	hypothetical protein	NA	NA

Supercontig_1.25_MVLG_02951_8sp	-1313,0315	-1313,0315	0	0	NS	0	[]	[]	[]	hypothetical protein	PF11708.1	Slu7(Pre-mRNA splicing Prp18-interacting factor)
Supercontig_1.64_MVLG_05112_6sp	-1030,4229	-1030,1869	0,472	0,21022	NS	0	[]	[]	[]	hypothetical protein	PF00185.17	OTCace(Aspartate/ornithine carbamoyltransferase, Asp/Orn binding domain)
Supercontig_1.1_MVLG_00076_10sp	-726,60467	-725,7783	1,65274	0,56236	NS	0	[]	[]	[]	hypothetical protein	PF00628.22	PHD(PHD-finger)
Supercontig_1.30_MVLG_03294_8sp	-448,94199	-448,94199	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.96_MVLG_06051_8sp	-425,09824	-421,52362	7,14924	0,97197	**	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.2_MVLG_00418_6sp	-346,64672	-346,64671	0,00016	0,00016	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.32_MVLG_03401_6sp	-489,06865	-485,25079	7,63572	0,97803	**	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.3_MVLG_00555_8sp	-357,12063	-357,12063	0	0	NS	0	[]	[]	[]	metal homeostasis factor ATX1	PF00403.19	HMA(Heavy-metal-associated domain)
Supercontig_1.6_MVLG_01105_9sp	-778,10264	-778,10264	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01398.14	Mov34(Mov34/MPN/PAD-1 family)
Supercontig_1.60_MVLG_04946_8sp	-680,27271	-679,03142	2,48258	0,71099	NS	0	[]	[]	[]	GTP-binding protein rhoA	PF08477.6	Miro(Miro-like protein)
Supercontig_1.9_MVLG_01527_8sp	-875,75661	-875,75661	0	0	NS	0	[]	[]	[]	CMGC/RCK/MAK protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.36_MVLG_03682_10sp	-708,20516	-708,02796	0,3544	0,16239	NS	0	[]	[]	[]	6-phosphofructokinase	PF00365.13	PFK(Phosphofructokinase)
Supercontig_1.11_MVLG_01743_8sp	-278,62544	-278,62539	0,0001	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF08603.4	CAP_C(Adenylate cyclase associated (CAP) C terminal)
Supercontig_1.80_MVLG_05636_9sp	-580,67276	-580,67242	0,00068	0,00034	NS	0	[]	[]	[]	mitochondrial chaperone BCS1	PF08740.4	BCS1_N(BCS1 N terminal)
Supercontig_1.68_MVLG_05270_12sp	-428,0651	-427,32216	1,48588	0,52429	NS	0	[]	[]	[]	hypothetical protein	PF07934.5	OGG_N(8-oxoguanine DNA glycosylase, N-terminal domain)
Supercontig_1.16_MVLG_02181_6sp	-815,71127	-815,71127	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.97_MVLG_06056_6sp	-884,58664	-884,58664	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03171.13	2OG-FeII_Oxy(2OG-Fe(II) oxygenase superfamily)
Supercontig_1.35_MVLG_03621_6sp	-774,39077	-774,39077	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00501.21	AMP-binding(AMP-binding enzyme)
Supercontig_1.11_MVLG_01722_9sp	-655,58258	-655,58241	0,00034	0,00017	NS	0	[]	[]	[]	V-type H+-transporting ATPase subunit I	PF01496.12	V_ATPase_I(V-type ATPase 116kDa subunit family)
Supercontig_1.68_MVLG_05267_6sp	-1458,6476	-1458,6476	0	0	NS	0	[]	[]	[]	SCY1 protein kinase	NA	NA
Supercontig_1.91_MVLG_05936_11sp	-1192,9565	-1192,9374	0,03834	0,01899	NS	0	[]	[]	[]	hypothetical protein	PF00621.13	RhoGEF(RhoGEF domain)
Supercontig_1.14_MVLG_01996_8sp	-537,54733	-537,54733	0	0	NS	0	[]	[]	[]	hypothetical protein	PF12621.1	DUF3779(Phosphate metabolism protein)
Supercontig_1.16_MVLG_02245_8sp	-631,10874	-631,10872	0,00016	0,00016	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.8_MVLG_01413_8sp	-858,82136	-858,68354	0,27564	0,12874	NS	0	[]	[]	[]	hypothetical protein	NA	NA

Supercontig_1.38_MVLG_03777_6sp	-693,54267	-693,54263	0,00016	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF00615.12	RGS(Regulator of G protein signaling domain)
Supercontig_1.2_MVLG_00405_6sp	-621,55655	-621,55655	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00107.19	ADH_zinc_N(Zinc-binding dehydrogenase)
Supercontig_1.33_MVLG_03466_10sp	-475,98212	-475,53119	0,90186	0,36296	NS	0	[]	[]	[]	hypothetical protein	PF04117.5	Mpv17_PMP22(Mpv17 / PMP22 family)
Supercontig_1.1_MVLG_00020_9sp	-386,32107	-386,32085	0,00044	0,00022	NS	0	[]	[]	[]	hypothetical protein	PF01417.13	ENTH(ENTH domain)
Supercontig_1.183_MVLG_07014_9sp	-350,86077	-350,49113	0,73928	0,30902	NS	0	[]	[]	[]	hypothetical protein	TIGR00336	TIGR00336(pyrE: orotate phosphoribosyltransferase)
Supercontig_1.1_MVLG_00080_10sp	-682,65831	-682,65831	0	0	NS	0	[]	[]	[]	bifunctional purine biosynthesis protein ADE17	TIGR00355	TIGR00355(purH: phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase)
Supercontig_1.11_MVLG_01741_10sp	-621,87015	-621,77727	0,18576	0,0887	NS	0	[]	[]	[]	hypothetical protein	PF07557.4	Shugoshin_C(Shugoshin C terminus)
Supercontig_1.9_MVLG_01562_11sp	-354,06203	-354,06185	0,00036	0,00018	NS	0	[]	[]	[]	hypothetical protein	PF04774.8	HABP4_PAI-RBP1(Hyaluronan / mRNA binding family)
Supercontig_1.30_MVLG_03260_12sp	-483,41923	-483,41923	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.96_MVLG_06039_11sp	-443,23823	-443,23822	0,00016	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF01086.10	Clathrin_lg_ch(Clathrin light chain)
Supercontig_1.97_MVLG_06055_7sp	-604,27307	-604,27307	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04140.7	ICMT(Isoprenylcysteine carboxyl methyltransferase (ICMT) family)
Supercontig_1.35_MVLG_03578_9sp	-732,11766	-732,11716	0,001	0,0005	NS	0	[]	[]	[]	carboxymethylenebutenolidase	PF01738.11	DLH(Dienelactone hydrolase family)
Supercontig_1.46_MVLG_04253_8sp	-1013,9041	-1013,9041	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04438.9	zf-HIT(HIT zinc finger)
Supercontig_1.131_MVLG_06578_7sp	-603,04887	-603,04887	0	0	NS	0	[]	[]	[]	methyltransferase BUD23	PF12589.1	WBS_methylT(Methyltransferase involved in Williams-Beuren syndrome)
Supercontig_1.2_MVLG_00402_8sp	-708,28311	-708,28311	0	0	NS	0	[]	[]	[]	hypothetical protein	PF07690.9	MFS_1(Major Facilitator Superfamily)
Supercontig_1.4_MVLG_00735_10sp	-650,46903	-650,46903	0	0	NS	0	[]	[]	[]	hypothetical protein	TIGR03804	TIGR03804(para_beta_helix: parallel beta-helix repeat)
Supercontig_1.7_MVLG_01265_8sp	-529,23828	-529,23828	0	0	NS	0	[]	[]	[]	histone	PF00125.17	Histone(Core histone H2A/H2B/H3/H4)
Supercontig_1.18_MVLG_02418_6sp	-634,70417	-634,66403	0,08028	0,03935	NS	0	[]	[]	[]	hypothetical protein	PF02290.8	SRP14(Signal recognition particle 14kD protein)
Supercontig_1.151_MVLG_06784_7sp	-1122,1041	-1122,099	0,01026	0,00512	NS	0	[]	[]	[]	hypothetical protein	PF00270.22	DEAD(DEAD/DEAH box helicase)
Supercontig_1.64_MVLG_05116_6sp	-1267,7781	-1267,7781	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01399.20	PCI(PCI domain)
Supercontig_1.33_MVLG_03487_9sp	-303,40669	-303,40669	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03223.8	V-ATPase_C(V-ATPase subunit C)
Supercontig_1.35_MVLG_03617_6sp	-1019,3573	-1019,3126	0,08946	0,04374	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.11_MVLG_01737_9sp	-269,59463	-269,59451	0,00024	0,00012	NS	0	[]	[]	[]	hypothetical protein	PF02375.10	JmjN(jmjN domain)

Supercontig_1.62_MVLG_05041_9sp	-439,06409	-439,06409	0	0	NS	0	[]	[]	[]	Histone acetyltransferase subunit NuA4	PF09340.3	NuA4(Histone acetyltransferase subunit NuA4)
Supercontig_1.81_MVLG_05678_6sp	-797,29758	-797,29758	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04446.5	Thg1(tRNAHis guanylyltransferase)
Supercontig_1.5_MVLG_00894_7sp	-599,91086	-599,34956	1,1226	0,42953	NS	0	[]	[]	[]	nicotinate (nicotinamide) nucleotide adenylyltransferase	PF01467.19	CTP_transf_2(Cytidylyltransferase)
Supercontig_1.7_MVLG_01337_9sp	-1576,5307	-1576,5045	0,0524	0,02586	NS	0	[]	[]	[]	hypothetical protein	PF00083.17	Sugar_tr(Sugar (and other) transporter)
Supercontig_1.96_MVLG_06031_10sp	-428,78765	-428,78719	0,00092	0,00046	NS	0	[]	[]	[]	hypothetical protein	PF03357.14	Snf7(Snf7)
Supercontig_1.13_MVLG_01885_10sp	-475,01761	-475,0176	0,00016	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF00172.11	Zn_clus(Fungal Zn(2)-Cys(6) binuclear cluster domain)
Supercontig_1.139_MVLG_06657_9sp	-1187,275	-1187,275	0	0	NS	0	[]	[]	[]	hypothetical protein	PF08389.5	Xpo1(Exportin 1-like protein)
Supercontig_1.36_MVLG_03666_9sp	-848,73566	-848,59394	0,28344	0,13214	NS	0	[]	[]	[]	hypothetical protein	PF00172.11	Zn_clus(Fungal Zn(2)-Cys(6) binuclear cluster domain)
Supercontig_1.4_MVLG_00744_11sp	-465,39983	-465,39952	0,00062	0,00031	NS	0	[]	[]	[]	hypothetical protein	PF00152.13	tRNA-synt_2(tRNA synthetases class II (D, K and N))
Supercontig_1.78_MVLG_05589_9sp	-431,69695	-429,44848	4,49694	0,89444	NS	0	[]	[]	[]	hypothetical protein	TIGR00049	TIGR00049(TIGR00049: iron-sulfur cluster assembly accessory protein)
Supercontig_1.88_MVLG_05896_7sp	-434,39891	-434,39888	0,00016	0,00016	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.140_MVLG_06684_10sp	-411,29913	-411,29911	0,00016	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF00172.11	Zn_clus(Fungal Zn(2)-Cys(6) binuclear cluster domain)
Supercontig_1.36_MVLG_03662_10sp	-393,39364	-393,39364	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01150.10	GDA1_CD39(GDA1/CD39 (nucleoside phosphatase) family)
Supercontig_1.100_MVLG_06142_10sp	-537,75123	-537,41436	0,67374	0,286	NS	0	[]	[]	[]	Dolichyl-diphosphooligosaccharide-protein glycotransferase	PF04756.6	OST3_OST6(OST3 / OST6 family)
Supercontig_1.40_MVLG_03958_8sp	-759,90578	-759,90567	0,00022	0,00011	NS	0	[]	[]	[]	3-oxoacyl-[acyl-carrier protein] reductase	PF00106.18	adh_short(short chain dehydrogenase)
Supercontig_1.38_MVLG_03764_10sp	-438,60794	-437,95237	1,31114	0,48085	NS	0	[]	[]	[]	3-isopropylmalate dehydrogenase	TIGR00169	TIGR00169(leuB: 3-isopropylmalate dehydrogenase)
Supercontig_1.81_MVLG_05680_9sp	-939,51552	-939,50555	0,01994	0,00992	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.55_MVLG_04726_7sp	-986,18251	-986,14279	0,07944	0,03894	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.95_MVLG_06007_6sp	-930,0085	-930,0085	0	0	NS	0	[]	[]	[]	ADP,ATP carrier protein	PF00153.20	Mito_carr(Mitochondrial carrier protein)
Supercontig_1.5_MVLG_01030_9sp	-482,8708	-482,78241	0,17678	0,0846	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.4_MVLG_00866_7sp	-953,47073	-953,47058	0,0003	0,00015	NS	0	[]	[]	[]	hypothetical protein	PF06814.6	Lung_7-TM_R(Lung seven transmembrane receptor)

Supercontig_1.4_MVLG_00777_8sp	-1005,5849	-1005,0127	1,14452	0,43575	NS	0	[]	[]	[]	hypothetical protein	PF10282.2	Muc_lac_enz(3-carboxy-cis,cis-muconate lactonizing enzyme)
Supercontig_1.10_MVLG_01683_10sp	-607,66974	-607,66974	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.66_MVLG_05192_9sp	-1250,5381	-1250,4143	0,24752	0,11641	NS	0	[]	[]	[]	hypothetical protein	PF04547.5	Anoctamin(Calcium-activated chloride channel)
Supercontig_1.121_MVLG_06433_11sp	-475,44498	-475,44498	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04488.8	Gly_transf_sug(Glycosyltransferase sugar-binding region containing DXD motif)
Supercontig_1.11_MVLG_01771_7sp	-717,66683	-717,66683	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03134.12	TB2_DP1_HVA22(TB2/DP1, HVA22 family)
Supercontig_1.63_MVLG_05074_8sp	-480,55422	-480,53779	0,03286	0,0163	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.52_MVLG_04556_9sp	-1888,5593	-1886,3882	4,34236	0,88596	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.69_MVLG_05314_7sp	-866,48903	-865,26301	2,45204	0,70654	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.35_MVLG_03608_11sp	-1032,738	-1032,5941	0,28788	0,13406	NS	0	[]	[]	[]	heat shock protein 104	PF07724.7	AAA_2(AAA domain (Cdc48 subfamily))
Supercontig_1.50_MVLG_04466_9sp	-925,96219	-925,96145	0,00148	0,00074	NS	0	[]	[]	[]	hypothetical protein	PF01656.16	CbiA(CobQ/CobB/MinD/ParA nucleotide binding domain)
Supercontig_1.6_MVLG_01200_9sp	-379,90208	-379,90201	0,00014	0,00016	NS	0	[]	[]	[]	vacuolar protein sorting-associated protein 4	PF01695.10	IstB(IstB-like ATP binding protein)
Supercontig_1.83_MVLG_05730_9sp	-536,95441	-537,43762	0	0	NS	0	[]	[]	[]	diphthine synthase	TIGR00522	TIGR00522(dph5: diphthine synthase)
Supercontig_1.58_MVLG_04847_6sp	-1832,1411	-1830,7423	2,79754	0,7531	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.41_MVLG_04032_7sp	-850,82146	-850,82069	0,00154	0,00077	NS	0	[]	[]	[]	hypothetical protein	PF08790.4	zf-LYAR(LYAR-type C2HC zinc finger)
Supercontig_1.29_MVLG_03219_9sp	-644,64772	-644,64762	0,0002	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF00018.21	SH3_1(SH3 domain)
Supercontig_1.91_MVLG_05938_6sp	-478,64644	-477,23126	2,83036	0,75712	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.131_MVLG_06587_8sp	-1185,8612	-1185,7359	0,25058	0,11776	NS	0	[]	[]	[]	hypothetical protein	PF08559.3	Cut8(Cut8)
Supercontig_1.127_MVLG_06540_6sp	-313,18847	-313,18845	0,00016	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF01722.11	BolA(BolA-like protein)
Supercontig_1.2_MVLG_00348_12sp	-666,64284	-666,64284	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01363.14	FYVE(FYVE zinc finger)
Supercontig_1.97_MVLG_06064_9sp	-725,61978	-725,32463	0,5903	0,25558	NS	0	[]	[]	[]	hypothetical protein	PF00636.19	Ribonuclease_3(RNase3 domain)
Supercontig_1.21_MVLG_02665_8sp	-849,77741	-849,77686	0,0011	0,00055	NS	0	[]	[]	[]	GTP-binding protein LepA	TIGR01393	TIGR01393(lepA: GTP-binding protein LepA)
Supercontig_1.65_MVLG_05148_11sp	-643,0815	-643,0815	0	0	NS	0	[]	[]	[]	STE/STE11 protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.75_MVLG_05480_12sp	-368,26109	-368,26109	0	0	NS	0	[]	[]	[]	Ca2+-transporting ATPase	TIGR01494	TIGR01494(ATPase_P-type: HAD ATPase, P-type, family IC)
Supercontig_1.50_MVLG_04492_9sp	-645,9158	-645,91565	0,0003	0,00015	NS	0	[]	[]	[]	hypothetical protein	PF11715.1	Nup160(Nucleoporin Nup120/160)

Supercontig_1.21_MVLG_02635_7sp	-414,12628	-413,93698	0,3786	0,17246	NS	0	[]	[]	[]	hypothetical protein	PF03171.13	2OG-FeII_Oxy(2OG-Fe(II) oxygenase superfamily)
Supercontig_1.17_MVLG_02276_8sp	-461,02703	-461,02718	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03330.11	DPBB_1(Rare lipoprotein A (RlpA)-like double-psi beta-barrel)
Supercontig_1.39_MVLG_03858_6sp	-870,62755	-870,62755	0	0	NS	0	[]	[]	[]	hypothetical protein	PF07393.4	Sec10(Exocyst complex component Sec10)
Supercontig_1.25_MVLG_02918_8sp	-344,60875	-344,31461	0,58828	0,25483	NS	0	[]	[]	[]	hypothetical protein	PF00956.11	NAP(Nucleosome assembly protein (NAP))
Supercontig_1.109_MVLG_06278_6sp	-1552,6411	-1552,6411	0,00016	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF00319.11	SRF-TF(SRF-type transcription factor (DNA-binding and dimerisation domain))
Supercontig_1.69_MVLG_05304_9sp	-781,94492	-781,94456	0,00072	0,00036	NS	0	[]	[]	[]	AP-1 complex subunit gamma-1	PF01602.13	Adaptin_N(Adaptin N terminal region)
Supercontig_1.13_MVLG_01913_10sp	-408,42979	-407,09813	2,66332	0,73596	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.49_MVLG_04421_9sp	-331,54852	-331,35401	0,38902	0,17676	NS	0	[]	[]	[]	hypothetical protein	PF08657.3	DASH_Spc34(DASH complex subunit Spc34)
Supercontig_1.166_MVLG_06914_10sp	-765,8449	-765,83551	0,01878	0,00935	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.39_MVLG_03851_9sp	-939,1055	-939,1055	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02463.12	SMC_N(RecF/RecN/SMC N terminal domain)
Supercontig_1.64_MVLG_05107_11sp	-398,52719	-398,45958	0,13522	0,06538	NS	0	[]	[]	[]	hypothetical protein	PF01522.14	Polysacc_deac_1(Polysaccharide deacetylase)
Supercontig_1.7_MVLG_01250_10sp	-529,57664	-528,82389	1,5055	0,52893	NS	0	[]	[]	[]	hypothetical protein	PF00172.11	Zn_clus(Fungal Zn(2)-Cys(6) binuclear cluster domain)
Supercontig_1.81_MVLG_05666_7sp	-431,77902	-431,77902	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01569.14	PAP2(PAP2 superfamily)
Supercontig_1.61_MVLG_04959_10sp	-1030,0007	-1029,9855	0,03036	0,01507	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.81_MVLG_05675_9sp	-1117,0733	-1117,0733	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01494.12	FAD_binding_3(FAD binding domain)
Supercontig_1.81_MVLG_05692_10sp	-340,25635	-340,25635	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00172.11	Zn_clus(Fungal Zn(2)-Cys(6) binuclear cluster domain)
Supercontig_1.123_MVLG_06477_8sp	-484,05406	-483,46291	1,1823	0,44631	NS	0	[]	[]	[]	hypothetical protein	PF02330.9	MAM33(Mitochondrial glycoprotein)
Supercontig_1.60_MVLG_04945_7sp	-433,89676	-433,89676	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.70_MVLG_05336_8sp	-721,78224	-721,78221	0,00016	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF00849.15	PseudoU_synth_2(RNA pseudouridylate synthase)
Supercontig_1.165_MVLG_06901_9sp	-1222,7707	-1222,7707	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.28_MVLG_03181_6sp	-710,42962	-709,80894	1,24136	0,46242	NS	0	[]	[]	[]	hypothetical protein	PF00270.22	DEAD(DEAD/DEAH box helicase)
Supercontig_1.26_MVLG_02989_9sp	-805,11337	-804,24278	1,74118	0,5813	NS	0	[]	[]	[]	hypothetical protein	PF10198.2	Ada3(Histone acetyltransferases subunit 3)
Supercontig_1.20_MVLG_02560_10sp	-1403,0506	-1402,6928	0,71552	0,30076	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.54_MVLG_04695_8sp	-571,77621	-571,77621	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01008.10	IF-2B(Initiation factor 2 subunit family)

Supercontig_1.2_MVLG_00298_6sp	-263,62031	-263,62026	0,0001	0,00016	NS	0	[]	[]	[]	ATPase GET3	PF01656.16	CbiA(CobQ/CobB/MinD/ParA nucleotide binding domain)
Supercontig_1.139_MVLG_06660_8sp	-619,02505	-618,68213	0,68584	0,29031	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.76_MVLG_05524_8sp	-1219,2179	-1219,2179	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.47_MVLG_04344_10sp	-509,48243	-509,48242	0,00016	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF08640.4	U3_assoc_6(U3 small nucleolar RNA-associated protein 6)
Supercontig_1.17_MVLG_02296_11sp	-741,38562	-741,38555	0,00016	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF01485.14	IBR(IBR domain)
Supercontig_1.40_MVLG_03941_6sp	-899,25898	-899,06386	0,39024	0,17726	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.7_MVLG_01258_9sp	-507,33871	-507,33871	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.1_MVLG_00173_8sp	-742,01582	-742,01582	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00026.16	Asp(Eukaryotic aspartyl protease)
Supercontig_1.73_MVLG_05425_8sp	-1234,4548	-1234,4548	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00172.11	Zn_clus(Fungal Zn(2)-Cys(6) binuclear cluster domain)
Supercontig_1.15_MVLG_02104_8sp	-520,94511	-520,9451	0,00016	0,00016	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.4_MVLG_00693_11sp	-553,39017	-552,73611	1,30812	0,48007	NS	0	[]	[]	[]	CAMK/RAD53 protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.74_MVLG_05465_8sp	-615,95199	-615,95171	0,00056	0,00028	NS	0	[]	[]	[]	T-complex protein 1 subunit gamma	TIGR02344	TIGR02344(chap_CCT_gamma: T-complex protein 1, gamma subunit)
Supercontig_1.11_MVLG_01687_8sp	-708,64329	-708,64299	0,0006	0,0003	NS	0	[]	[]	[]	hypothetical protein	PF03151.9	TPT(Triose-phosphate Transporter family)
Supercontig_1.202_MVLG_07091_6sp	-820,91335	-819,29639	3,23392	0,8015	NS	0	[]	[]	[]	hypothetical protein	PF01073.12	3Beta_HSD(3-beta hydroxysteroid dehydrogenase/isomerase family)
Supercontig_1.38_MVLG_03774_9sp	-1547,6102	-1547,605	0,01048	0,00523	NS	0	[]	[]	[]	hypothetical protein	PF07250.4	Glyoxal_oxid_N(Glyoxal oxidase N-terminus)
Supercontig_1.7_MVLG_01270_9sp	-441,23791	-441,23791	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00505.12	HMG_box(HMG (high mobility group) box)
Supercontig_1.18_MVLG_02396_8sp	-575,47767	-575,47765	0,00016	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF09429.3	Wbp11(WW domain binding protein 11)
Supercontig_1.17_MVLG_02332_6sp	-299,64977	-299,64975	0,00016	0,00016	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.202_MVLG_07094_8sp	-283,10141	-283,10141	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00248.14	Aldo_ket_red(Aldo/keto reductase family)
Supercontig_1.63_MVLG_05069_6sp	-417,45839	-417,45839	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.1_MVLG_00211_6sp	-733,96471	-733,96471	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03061.15	4HBT(Thioesterase superfamily)
Supercontig_1.191_MVLG_07048_9sp	-380,51935	-380,11108	0,81654	0,3352	NS	0	[]	[]	[]	hypothetical protein	TIGR00800	TIGR00800(ncs1: NCS1 nucleoside transporter family)
Supercontig_1.2_MVLG_00364_11sp	-710,64252	-710,64252	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA

Supercontig_1.76_MVLG_05521_7sp	-851,15132	-851,15093	0,00078	0,00039	NS	0	[]	[]	[]	hypothetical protein	TIGR02251	TIGR02251(HIF-SF_euk: Dullard-like phosphatase domain)
Supercontig_1.88_MVLG_05898_8sp	-642,48351	-642,48351	0	0	NS	0	[]	[]	[]	translation initiation factor eIF-5	PF02020.11	W2(eIF4-gamma/eIF5/eIF2-epsilon)
Supercontig_1.45_MVLG_04189_11sp	-448,54715	-448,54715	0	0	NS	0	[]	[]	[]	DNAJ chaparonin	PF00226.24	DnaJ(DnaJ domain)
Supercontig_1.74_MVLG_05452_12sp	-298,49154	-298,06102	0,86104	0,34983	NS	0	[]	[]	[]	hypothetical protein	TIGR00378	TIGR00378(cax: calcium/proton exchanger)
Supercontig_1.23_MVLG_02799_9sp	-706,72941	-706,72941	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00400.25	WD40(WD domain, G-beta repeat)
Supercontig_1.55_MVLG_04703_8sp	-1543,7933	-1543,7933	0	0	NS	0	[]	[]	[]	phosphoribosylformylglycinamidine synthase	TIGR01735	TIGR01735(FGAM_synt: phosphoribosylformylglycinamidine synthase)
Supercontig_1.4_MVLG_00745_12sp	-403,95028	-403,58361	0,73334	0,30696	NS	0	[]	[]	[]	hypothetical protein	PF00561.13	Abhydrolase_1(alpha/beta hydrolase fold)
Supercontig_1.25_MVLG_02919_10sp	-861,93354	-861,14724	1,5726	0,54447	NS	0	[]	[]	[]	hypothetical protein	PF00010.19	HLH(Helix-loop-helix DNA-binding domain)
Supercontig_1.66_MVLG_05160_8sp	-413,99877	-413,99736	0,00282	0,00141	NS	0	[]	[]	[]	hypothetical protein	PF01494.12	FAD_binding_3(FAD binding domain)
Supercontig_1.22_MVLG_02703_12sp	-375,74677	-375,74677	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.1_MVLG_00251_9sp	-447,95404	-447,95379	0,0005	0,00025	NS	0	[]	[]	[]	hypothetical protein	TIGR00798	TIGR00798(mtc: tricarboxylate carrier)
Supercontig_1.63_MVLG_05047_9sp	-690,22817	-690,22802	0,0003	0,00015	NS	0	[]	[]	[]	adenylosuccinate synthetase	TIGR00184	TIGR00184(purA: adenylosuccinate synthase)
Supercontig_1.16_MVLG_02213_9sp	-512,20936	-512,20936	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.78_MVLG_05577_9sp	-403,81964	-403,81964	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03153.6	TFIIA(Transcription factor IIA, alpha/beta subunit)
Supercontig_1.16_MVLG_02249_9sp	-677,32812	-677,32812	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.80_MVLG_05660_6sp	-705,82429	-705,82429	0	0	NS	0	[]	[]	[]	hypothetical protein	PF09996.2	DUF2237(Uncharacterized protein conserved in bacteria (DUF2237))
Supercontig_1.12_MVLG_01847_8sp	-402,33429	-402,33413	0,00032	0,00016	NS	0	[]	[]	[]	transcription elongation factor SPT4	PF06093.6	Spt4(Spt4/RpoE2 zinc finger)
Supercontig_1.85_MVLG_05811_9sp	-1176,267	-1176,2668	0,00036	0,00018	NS	0	[]	[]	[]	pre-mRNA-processing-splicing factor 8	PF12134.1	PRP8_domainIV(PRP8 domain IV core)
Supercontig_1.1_MVLG_00112_8sp	-507,21188	-507,19654	0,03068	0,01522	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.142_MVLG_06703_7sp	-571,14253	-570,10855	2,06796	0,64441	NS	0	[]	[]	[]	hypothetical protein	PF00755.13	Carn_acyltransf(Choline/Carnitine o-acyltransferase)
Supercontig_1.1_MVLG_00090_7sp	-1023,9207	-1023,9207	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03372.16	Exo_endo_phos(Endonuclease/Exonuclease/phosphatase family)
Supercontig_1.79_MVLG_05626_8sp	-627,43389	-626,82047	1,22684	0,4585	NS	0	[]	[]	[]	hypothetical protein	PF09531.3	Ndc1_Nup(Nucleoporin protein Ndc1-Nup)
Supercontig_1.4_MVLG_00755_10sp	-1100,6995	-1100,2524	0,89408	0,36048	NS	0	[]	[]	[]	hypothetical protein	PF05021.8	NPL4(NPL4 family)

Supercontig_1.11_MVLG_01740_6sp	-1160,0823	-1159,7174	0,72988	0,30576	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.7_MVLG_01303_12sp	-700,92026	-700,92026	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02940.8	mRNA_triPase(mRNA capping enzyme, beta chain)
Supercontig_1.13_MVLG_01929_10sp	-478,7134	-478,6991	0,0286	0,0142	NS	0	[]	[]	[]	hypothetical protein	PF07225.5	NDUF_B4(NADH-ubiquinone oxidoreductase B15 subunit (NDUFB4))
Supercontig_1.23_MVLG_02802_9sp	-1098,9112	-1098,9112	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00107.19	ADH_zinc_N(Zinc-binding dehydrogenase)
Supercontig_1.22_MVLG_02708_8sp	-487,82849	-487,82336	0,01026	0,00512	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.2_MVLG_00368_9sp	-492,66278	-492,61941	0,08674	0,04244	NS	0	[]	[]	[]	hypothetical protein	PF10313.2	DUF2415(Uncharacterised protein domain (DUF2415))
Supercontig_1.32_MVLG_03429_9sp	-837,47357	-837,47357	0	0	NS	0	[]	[]	[]	ATP-dependent RNA helicase eIF4A	PF00270.22	DEAD(DEAD/DEAH box helicase)
Supercontig_1.3_MVLG_00518_8sp	-411,75738	-411,75733	0,00016	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF00856.21	SET(SET domain)
Supercontig_1.58_MVLG_04867_7sp	-459,70304	-459,70304	0	0	NS	0	[]	[]	[]	hypothetical protein	PF06687.5	SUR7(SUR7/PalI family)
Supercontig_1.124_MVLG_06497_9sp	-775,3468	-775,3468	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02732.8	ERCC4(ERCC4 domain)
Supercontig_1.165_MVLG_06904_9sp	-517,62924	-517,62924	0	0	NS	0	[]	[]	[]	hypothetical protein	PF08375.4	Rpn3_C(Proteasome regulatory subunit C-terminal)
Supercontig_1.5_MVLG_00960_10sp	-681,39834	-681,39834	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01435.11	Peptidase_M48(Peptidase family M48)
Supercontig_1.96_MVLG_06054_7sp	-398,97627	-397,41341	3,12572	0,79046	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.113_MVLG_06352_9sp	-393,89465	-393,8945	0,0003	0,00015	NS	0	[]	[]	[]	hypothetical protein	PF03810.12	IBN_N(Importin-beta N-terminal domain)
Supercontig_1.1_MVLG_00119_10sp	-720,04172	-720,04164	0,00016	0,00016	NS	0	[]	[]	[]	CAMK/CAMKL/KIN1 protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.3_MVLG_00649_11sp	-381,34563	-381,34563	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.8_MVLG_01369_12sp	-651,81466	-651,69184	0,24564	0,11558	NS	0	[]	[]	[]	hypothetical protein	PF02845.9	CUE(CUE domain)
Supercontig_1.3_MVLG_00493_9sp	-481,91546	-480,53714	2,75664	0,748	NS	0	[]	[]	[]	hypothetical protein	PF07572.5	BCNT(Bucentaur or craniofacial development)
Supercontig_1.40_MVLG_03924_12sp	-676,42854	-676,42854	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04152.7	Mre11_DNA_bind(Mre11 DNA-binding presumed domain)
Supercontig_1.96_MVLG_06035_9sp	-365,24544	-365,24544	0	0	NS	0	[]	[]	[]	hypothetical protein	PF10156.2	Med17(Subunit 17 of Mediator complex)
Supercontig_1.19_MVLG_02441_7sp	-977,39592	-977,39592	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00400.25	WD40(WD domain, G-beta repeat)
Supercontig_1.39_MVLG_03868_12sp	-852,68467	-852,68468	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00201.11	UDPGT(UDP-glucoronosyl and UDP-glucosyl transferase)
Supercontig_1.34_MVLG_03504_12sp	-683,81102	-683,80162	0,0188	0,00936	NS	0	[]	[]	[]	WEE protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.5_MVLG_00946_7sp	-875,27321	-875,20655	0,13332	0,06449	NS	0	[]	[]	[]	hypothetical protein	PF03144.18	GTP_EFTU_D2(Elongation factor Tu domain 2)
Supercontig_1.44_MVLG_04147_6sp	-471,89483	-471,89476	0,00014	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF04081.6	DNA_pol_delta_4(DNA polymerase delta, subunit 4)

Supercontig_1.8_MVLG_01361_9sp	-483,08065	-482,82784	0,50562	0,22338	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.24_MVLG_02849_11sp	-418,80716	-416,4259	4,76252	0,90757	*	0	[]	[]	[]	hypothetical protein	PF00172.11	Zn_clus(Fungal Zn(2)-Cys(6) binuclear cluster domain)
Supercontig_1.33_MVLG_03462_7sp	-473,41757	-473,32821	0,17872	0,08548	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.15_MVLG_02093_8sp	-531,69106	-531,39131	0,5995	0,259	NS	0	[]	[]	[]	hypothetical protein	PF01169.12	UPF0016(Uncharacterized protein family UPF0016)
Supercontig_1.33_MVLG_03488_10sp	-287,96979	-287,92412	0,09134	0,04464	NS	0	[]	[]	[]	hypothetical protein	TIGR00728	TIGR00728(OPT_sfam: oligopeptide transporters, OPT superfamily)
Supercontig_1.24_MVLG_02887_9sp	-633,05338	-633,05338	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00735.11	Septin(Septin)
Supercontig_1.87_MVLG_05862_7sp	-645,81122	-645,42266	0,77712	0,32197	NS	0	[]	[]	[]	hypothetical protein	PF03909.10	BSD(BSD domain)
Supercontig_1.29_MVLG_03245_9sp	-582,09501	-582,09501	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.8_MVLG_01462_7sp	-1194,495	-1194,495	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02463.12	SMC_N(RecF/RecN/SMC N terminal domain)
Supercontig_1.47_MVLG_04317_9sp	-480,36757	-480,36757	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.204_MVLG_07104_11sp	-456,81185	-456,81169	0,00032	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF10273.2	WGG(Pre-rRNA-processing protein TSR2)
Supercontig_1.91_MVLG_05943_9sp	-605,40449	-604,91351	0,98196	0,38797	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.33_MVLG_03446_12sp	-461,67058	-461,67026	0,00064	0,00032	NS	0	[]	[]	[]	hypothetical protein	PF04515.5	Choline_transpo(Plasma-membrane choline transporter)
Supercontig_1.12_MVLG_01856_8sp	-838,86793	-838,52003	0,6958	0,29383	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.42_MVLG_04084_9sp	-1106,0812	-1106,0812	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02735.9	Ku(Ku70/Ku80 beta-barrel domain)
Supercontig_1.21_MVLG_02627_10sp	-587,22915	-586,47347	1,51136	0,53031	NS	0	[]	[]	[]	hypothetical protein	PF10513.2	EPL1(Enhancer of polycomb-like)
Supercontig_1.44_MVLG_04140_12sp	-905,22268	-905,22264	0,00016	0,00016	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.102_MVLG_06177_10sp	-406,7843	-406,7843	0	0	NS	0	[]	[]	[]	hypothetical protein	PF08242.5	Methyltransf_12(Methyltransferase domain)
Supercontig_1.54_MVLG_04680_9sp	-523,2359	-523,16992	0,13196	0,06385	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.1_MVLG_00247_10sp	-360,2484	-360,16761	0,16158	0,07761	NS	0	[]	[]	[]	hypothetical protein	PF09273.4	Rubis-subs-bind(Rubisco LSMT substrate-binding)
Supercontig_1.6_MVLG_01222_8sp	-598,45169	-598,45169	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00248.14	Aldo_ket_red(Aldo/keto reductase family)
Supercontig_1.81_MVLG_05672_8sp	-1156,3369	-1156,3369	0	0	NS	0	[]	[]	[]	hypothetical protein	PF07690.9	MFS_1(Major Facilitator Superfamily)
Supercontig_1.9_MVLG_01491_10sp	-411,88448	-411,65101	0,46694	0,20822	NS	0	[]	[]	[]	hypothetical protein	PF07992.7	Pyr_redox_2(Pyridine nucleotide-disulphide oxidoreductase)
Supercontig_1.78_MVLG_05585_9sp	-859,03183	-857,81569	2,43228	0,70363	NS	0	[]	[]	[]	hypothetical protein	TIGR02734	TIGR02734(crtI_fam: phytoene desaturase)

Supercontig_1.9_MVLG_01534_9sp	-824,99498	-824,99494	0,00016	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF03372.16	Exo_endo_phos(Endonuclease/ Exonuclease/phosphatase family)
Supercontig_1.3_MVLG_00616_10sp	-425,30354	-425,30341	0,00026	0,00013	NS	0	[]	[]	[]	hypothetical protein	PF04851.8	ResIII(Type III restriction enzyme, res subunit)
Supercontig_1.19_MVLG_02495_8sp	-707,68424	-707,68424	0	0	NS	0	[]	[]	[]	hypothetical protein	PF07690.9	MFS_1(Major Facilitator Superfamily)
Supercontig_1.1_MVLG_00239_8sp	-400,19306	-400,19306	0	0	NS	0	[]	[]	[]	hypothetical protein	PF12348.1	CLASP_N(CLASP N terminal)
Supercontig_1.11_MVLG_01696_7sp	-559,35979	-559,17616	0,36726	0,16776	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.38_MVLG_03769_8sp	-385,50268	-385,50135	0,00266	0,00133	NS	0	[]	[]	[]	translationally-controlled tumor protein	PF00838.10	TCTP(Translationally controlled tumour protein)
Supercontig_1.12_MVLG_01870_11sp	-576,59361	-576,59325	0,00072	0,00036	NS	0	[]	[]	[]	hypothetical protein	PF09440.3	eIF3_N(eIF3 subunit 6 N terminal domain)
Supercontig_1.6_MVLG_01116_7sp	-591,31171	-591,31171	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00018.21	SH3_1(SH3 domain)
Supercontig_1.3_MVLG_00664_11sp	-449,61052	-449,71549	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01602.13	Adaptin_N(Adaptin N terminal region)
Supercontig_1.24_MVLG_02860_8sp	-312,25706	-312,25702	0,00016	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF10791.2	F1F0-ATPsyn_F(Mitochondrial F1-F0 ATP synthase subunit F of fungi)
Supercontig_1.67_MVLG_05238_8sp	-859,29822	-859,29822	0	0	NS	0	[]	[]	[]	hypothetical protein	PF07724.7	AAA_2(AAA domain (Cdc48 subfamily))
Supercontig_1.149_MVLG_06768_9sp	-1168,5388	-1168,5388	0	0	NS	0	[]	[]	[]	hypothetical protein	PF08327.4	AHSA1(Activator of Hsp90 ATPase homolog 1-like protein)
Supercontig_1.27_MVLG_03125_10sp	-412,36974	-412,36963	0,00022	0,00011	NS	0	[]	[]	[]	histidyl-tRNA synthetase	PF00587.18	tRNA-synt_2b(tRNA synthetase class II core domain (G, H, P, S and T))
Supercontig_1.11_MVLG_01728_10sp	-503,51463	-503,48496	0,05934	0,02923	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.63_MVLG_05054_6sp	-1239,533	-1239,4474	0,1712	0,08204	NS	0	[]	[]	[]	hypothetical protein	PF00172.11	Zn_clus(Fungal Zn(2)-Cys(6) binuclear cluster domain)
Supercontig_1.191_MVLG_07044_11sp	-382,10582	-382,10575	0,00014	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF00450.15	Peptidase_S10(Serine carboxypeptidase)
Supercontig_1.30_MVLG_03264_12sp	-344,20257	-344,20257	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00171.15	Aldedh(Aldehyde dehydrogenase family)
Supercontig_1.45_MVLG_04204_6sp	-549,12091	-549,12091	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.27_MVLG_03123_8sp	-457,62077	-457,6206	0,00034	0,00017	NS	0	[]	[]	[]	hypothetical protein	PF01529.13	zf-DHHC(DHHC zinc finger domain)
Supercontig_1.23_MVLG_02777_12sp	-583,80229	-583,80229	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00621.13	RhoGEF(RhoGEF domain)
Supercontig_1.87_MVLG_05851_7sp	-709,50866	-709,21955	0,57822	0,25107	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.39_MVLG_03849_11sp	-657,05009	-657,05009	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00076.15	RRM_1(RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain))

Supercontig_1.36_MVLG_03640_9sp	-566,90511	-566,78713	0,23596	0,11129	NS	0	[]	[]	[]	hypothetical protein	PF04828.7	GFA(Glutathione-dependent formaldehyde-activating enzyme)
Supercontig_1.13_MVLG_01915_10sp	-570,48205	-570,48205	0	0	NS	0	[]	[]	[]	hypothetical protein	PF05964.7	FYRN(F/Y-rich N-terminus)
Supercontig_1.9_MVLG_01522_9sp	-483,84728	-483,84693	0,0007	0,00035	NS	0	[]	[]	[]	hypothetical protein	PF04133.7	Vps55(Vacuolar protein sorting 55)
Supercontig_1.24_MVLG_02858_9sp	-332,05733	-332,05693	0,0008	0,0004	NS	0	[]	[]	[]	ADP-ribosylation factor 1	PF04670.5	Gtr1_RagA(Gtr1/RagA G protein conserved region)
Supercontig_1.9_MVLG_01568_9sp	-1214,9444	-1214,8822	0,12446	0,06033	NS	0	[]	[]	[]	hypothetical protein	PF06011.5	TRP(Transient receptor potential (TRP) ion channel)
Supercontig_1.57_MVLG_04817_8sp	-1508,4863	-1507,6353	1,70202	0,57302	NS	0	[]	[]	[]	hypothetical protein	PF04130.6	Spc97_Spc98(Spc97 / Spc98 family)
Supercontig_1.67_MVLG_05224_9sp	-525,67096	-525,67067	0,00058	0,00029	NS	0	[]	[]	[]	hypothetical protein	PF08953.4	DUF1899(Domain of unknown function (DUF1899))
Supercontig_1.45_MVLG_04236_10sp	-1476,3206	-1476,3206	0	0	NS	0	[]	[]	[]	guanine nucleotide-binding protein subunit alpha	PF00025.14	Arf(ADP-ribosylation factor family)
Supercontig_1.12_MVLG_01844_9sp	-565,3086	-565,20235	0,2125	0,1008	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.19_MVLG_02440_9sp	-876,60297	-874,34552	4,5149	0,89538	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.1_MVLG_00142_12sp	-620,18963	-620,18963	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04488.8	Gly_transf_sug(Glycosyltransferase sugar-binding region containing DXD motif)
Supercontig_1.25_MVLG_02976_9sp	-903,5847	-903,18242	0,80456	0,33121	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.73_MVLG_05431_6sp	-1267,1549	-1267,1549	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.22_MVLG_02731_8sp	-727,7287	-727,7287	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00106.18	adh_short(short chain dehydrogenase)
Supercontig_1.79_MVLG_05622_6sp	-482,42232	-482,38839	0,06786	0,03336	NS	0	[]	[]	[]	hypothetical protein	PF01161.13	PBP(Phosphatidylethanolamine-binding protein)
Supercontig_1.46_MVLG_04296_11sp	-533,92828	-533,86791	0,12074	0,05858	NS	0	[]	[]	[]	hypothetical protein	PF07576.5	BRAP2(BRCA1-associated protein 2)
Supercontig_1.22_MVLG_02697_9sp	-686,67098	-686,63464	0,07268	0,03569	NS	0	[]	[]	[]	hypothetical protein	PF00173.21	Cyt-b5(Cytochrome b5-like Heme/Steroid binding domain)
Supercontig_1.2_MVLG_00451_11sp	-440,31413	-440,31413	0	0	NS	0	[]	[]	[]	hypothetical protein	PF08801.4	Nucleoporin_N(Nup133 N terminal like)
Supercontig_1.76_MVLG_05518_11sp	-343,70344	-343,70327	0,00034	0,00017	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.2_MVLG_00463_8sp	-541,53111	-541,53102	0,00018	0,00016	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.87_MVLG_05844_7sp	-538,38023	-538,38014	0,00018	0,00016	NS	0	[]	[]	[]	formate dehydrogenase	PF02826.12	2-Hacid_dh_C(D-isomer specific 2-hydroxyacid dehydrogenase, NAD binding domain)
Supercontig_1.124_MVLG_06486_9sp	-669,73682	-668,77418	1,92528	0,61812	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.175_MVLG_06972_8sp	-561,02688	-561,02688	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01738.11	DLH(Dienelactone hydrolase family)

Supercontig_1.1_MVLG_00188_10sp	-558,87618	-557,80208	2,1482	0,65839	NS	0	[]	[]	[]	hypothetical protein	PF05686.5	DUF821(Arabidopsis thaliana protein of unknown function (DUF821))
Supercontig_1.3_MVLG_00529_9sp	-727,87675	-727,32473	1,10404	0,42421	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.57_MVLG_04834_10sp	-589,55344	-588,3585	2,38988	0,69728	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.8_MVLG_01437_10sp	-597,20482	-597,20482	0	0	NS	0	[]	[]	[]	hypothetical protein	TIGR00720	TIGR00720(sda_mono: L-serine ammonia-lyase)
Supercontig_1.56_MVLG_04764_7sp	-810,31435	-810,17289	0,28292	0,13191	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.154_MVLG_06812_8sp	-847,77072	-847,77026	0,00092	0,00046	NS	0	[]	[]	[]	tubulin gamma chain	PF10644.2	Misat_Myo_SegII(Misato Segment II myosin-like domain)
Supercontig_1.6_MVLG_01205_11sp	-427,08131	-427,08119	0,00024	0,00012	NS	0	[]	[]	[]	hypothetical protein	PF00620.20	RhoGAP(RhoGAP domain)
Supercontig_1.40_MVLG_03953_10sp	-648,49472	-648,49472	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.98_MVLG_06077_11sp	-536,94813	-536,94813	0	0	NS	0	[]	[]	[]	hypothetical protein	PF07690.9	MFS_1(Major Facilitator Superfamily)
Supercontig_1.11_MVLG_01752_11sp	-361,17451	-360,9385	0,47202	0,21023	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.30_MVLG_03277_9sp	-482,74398	-481,97938	1,5292	0,53448	NS	0	[]	[]	[]	hypothetical protein	PF02037.20	SAP(SAP domain)
Supercontig_1.99_MVLG_06118_12sp	-659,51476	-659,51476	0	0	NS	0	[]	[]	[]	protein pyrABCN	PF02222.15	ATP-grasp(ATP-grasp domain)
Supercontig_1.85_MVLG_05816_8sp	-886,77774	-886,77774	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02373.15	JmjC(JmjC domain)
Supercontig_1.5_MVLG_00980_6sp	-605,62813	-602,69916	5,85794	0,94655	*	0	[]	[]	[]	mitochondrial peroxiredoxin PRX1	PF10417.2	1-cysPrx_C(C-terminal domain of 1-Cys peroxiredoxin)
Supercontig_1.142_MVLG_06705_10sp	-1810,3361	-1810,3361	0	0	NS	0	[]	[]	[]	hypothetical protein	PF08161.5	NUC173(NUC173 domain)
Supercontig_1.78_MVLG_05598_10sp	-1137,5156	-1137,515	0,00134	0,00067	NS	0	[]	[]	[]	hypothetical protein	PF00128.17	Alpha-amylase(Alpha amylase, catalytic domain)
Supercontig_1.11_MVLG_01735_6sp	-446,57239	-446,21283	0,71912	0,30202	NS	0	[]	[]	[]	hypothetical protein	PF00578.14	AhpC-TSA(AhpC/TSA family)
Supercontig_1.36_MVLG_03657_8sp	-1261,5291	-1260,4915	2,07526	0,64571	NS	0	[]	[]	[]	hypothetical protein	PF01061.17	ABC2_membrane(ABC-2 type transporter)
Supercontig_1.55_MVLG_04747_10sp	-998,43527	-995,30395	6,26264	0,95634	**	0	[]	[]	[]	hypothetical protein	PF01388.14	ARID(ARID/BRIGHT DNA binding domain)
Supercontig_1.5_MVLG_01000_10sp	-1707,6743	-1707,4241	0,50038	0,22135	NS	0	[]	[]	[]	hypothetical protein	PF00498.19	FHA(FHA domain)
Supercontig_1.77_MVLG_05554_9sp	-1079,7937	-1079,7937	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01697.20	DUF23(Domain of unknown function)
Supercontig_1.7_MVLG_01231_11sp	-651,37497	-651,37482	0,0003	0,00015	NS	0	[]	[]	[]	valyl-tRNA synthetase	TIGR00422	TIGR00422(valS: valine--tRNA ligase)
Supercontig_1.5_MVLG_00938_7sp	-324,95907	-324,95898	0,00018	0,00016	NS	0	[]	[]	[]	homoisocitrate dehydrogenase	PF00180.13	Iso_dh(Isocitrate/isopropylmalate dehydrogenase)
Supercontig_1.6_MVLG_01089_8sp	-715,74728	-715,74702	0,00052	0,00026	NS	0	[]	[]	[]	hypothetical protein	NA	NA

Supercontig_1.39_MVLG_03895_9sp	-479,7815	-479,7815	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.42_MVLG_04074_6sp	-510,92029	-510,62189	0,5968	0,258	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.20_MVLG_02565_9sp	-469,7215	-469,7213	0,0004	0,0002	NS	0	[]	[]	[]	hypothetical protein	PF10331.2	AlcB(Siderophore biosynthesis protein domain)
Supercontig_1.131_MVLG_06577_9sp	-578,90253	-578,90253	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.141_MVLG_06694_10sp	-812,08421	-810,54375	3,08092	0,78572	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.69_MVLG_05285_9sp	-468,94238	-468,63918	0,6064	0,26155	NS	0	[]	[]	[]	thioredoxin reductase	PF00070.20	Pyr_redox(Pyridine nucleotide-disulphide oxidoreductase)
Supercontig_1.2_MVLG_00286_10sp	-1525,3521	-1525,3521	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00439.18	Bromodomain(Bromodomain)
Supercontig_1.63_MVLG_05068_7sp	-348,31537	-348,31533	0,00016	0,00016	NS	0	[]	[]	[]	pyruvate dehydrogenase [lipoamide] kinase	PF02518.19	HATPase_c(Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase)
Supercontig_1.85_MVLG_05792_10sp	-416,78735	-416,78721	0,00028	0,00014	NS	0	[]	[]	[]	30S ribosomal protein S6	PF01250.10	Ribosomal_S6(Ribosomal protein S6)
Supercontig_1.6_MVLG_01171_8sp	-839,23423	-839,16872	0,13102	0,06341	NS	0	[]	[]	[]	hypothetical protein	PF06423.5	GWT1(GWT1)
Supercontig_1.74_MVLG_05459_8sp	-400,10479	-398,74512	2,71934	0,74325	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.73_MVLG_05405_10sp	-503,63983	-503,08925	1,10116	0,42338	NS	0	[]	[]	[]	sulfate adenylyltransferase	TIGR00455	TIGR00455(apsK: adenylylsulfate kinase)
Supercontig_1.74_MVLG_05454_10sp	-404,50781	-403,78053	1,45456	0,51678	NS	0	[]	[]	[]	hypothetical protein	PF03807.10	F420_oxidored(NADP oxidoreductase coenzyme F420-dependent)
Supercontig_1.34_MVLG_03502_9sp	-378,80212	-378,80199	0,00026	0,00013	NS	0	[]	[]	[]	delta-aminolevulinic acid dehydratase	PF00490.14	ALAD(Delta-aminolevulinic acid dehydratase)
Supercontig_1.8_MVLG_01380_8sp	-1088,0819	-1088,0819	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02179.9	BAG(BAG domain)
Supercontig_1.9_MVLG_01572_10sp	-389,15037	-389,14921	0,00232	0,00116	NS	0	[]	[]	[]	2-nitropropane dioxygenase	PF03060.8	NPD(2-nitropropane dioxygenase)
Supercontig_1.3_MVLG_00546_10sp	-758,42524	-758,42524	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03142.8	Chitin_synth_2(Chitin synthase)
Supercontig_1.31_MVLG_03366_9sp	-754,14901	-753,68402	0,92998	0,37186	NS	0	[]	[]	[]	hypothetical protein	PF00856.21	SET(SET domain)
Supercontig_1.107_MVLG_06255_11sp	-860,35051	-859,25998	2,18106	0,66396	NS	0	[]	[]	[]	hypothetical protein	PF09174.3	Maf1(Maf1 regulator)
Supercontig_1.6_MVLG_01185_11sp	-455,81104	-455,81104	0	0	NS	0	[]	[]	[]	glutaryl-CoA dehydrogenase	PF02770.12	Acyl-CoA_dh_M(Acyl-CoA dehydrogenase, middle domain)
Supercontig_1.10_MVLG_01586_9sp	-583,08678	-583,08665	0,00026	0,00013	NS	0	[]	[]	[]	hypothetical protein	PF00400.25	WD40(WD domain, G-beta repeat)
Supercontig_1.6_MVLG_01213_8sp	-821,17078	-821,17078	0	0	NS	0	[]	[]	[]	UTP-glucose-1-phosphate uridylyltransferase	PF01704.11	UDPGP(UTP--glucose-1-phosphate uridylyltransferase)
Supercontig_1.5_MVLG_01043_9sp	-1045,8179	-1045,8179	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00667.13	FAD_binding_1(FAD binding domain)
Supercontig_1.57_MVLG_04808_10sp	-591,82559	-591,82558	0,00016	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF03647.6	Tmemb_14(Transmembrane proteins 14C)

Supercontig_1.7_MVLG_01289_9sp	-1459,4498	-1456,3667	6,16632	0,95419	**	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.105_MVLG_06220_8sp	-714,53362	-712,63214	3,80296	0,85065	NS	0	[]	[]	[]	hypothetical protein	PF08613.4	Cyclin(Cyclin)
Supercontig_1.10_MVLG_01643_8sp	-391,16663	-391,30393	0	0	NS	0	[]	[]	[]	hypothetical protein	PF10237.2	N6-adenineMlase(Probable N6-adenine methyltransferase)
Supercontig_1.30_MVLG_03300_9sp	-360,91144	-360,91128	0,00032	0,00016	NS	0	[]	[]	[]	pyruvate kinase	TIGR01064	TIGR01064(pyruv_kin: pyruvate kinase)
Supercontig_1.99_MVLG_06111_9sp	-401,18111	-400,40695	1,54832	0,53891	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.18_MVLG_02359_12sp	-512,39019	-512,13509	0,5102	0,22516	NS	0	[]	[]	[]	hypothetical protein	PF03542.9	Tuberin(Tuberin)
Supercontig_1.33_MVLG_03493_10sp	-363,8672	-363,86707	0,00026	0,00013	NS	0	[]	[]	[]	hypothetical protein	TIGR00177	TIGR00177(molyb_syn: molybdenum cofactor synthesis domain)
Supercontig_1.3_MVLG_00637_10sp	-479,84399	-479,84399	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00175.14	NAD_binding_1(Oxidoreductase NAD-binding domain)
Supercontig_1.11_MVLG_01709_10sp	-417,17609	-417,12871	0,09476	0,04628	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.15_MVLG_02081_11sp	-1534,3415	-1534,2575	0,16792	0,08053	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.41_MVLG_03991_10sp	-914,24153	-914,24123	0,0006	0,0003	NS	0	[]	[]	[]	methylenetetrahydrofolate reductase (NADPH)	TIGR00677	TIGR00677(fadh2_euk: methylenetetrahydrofolate reductase)
Supercontig_1.233_MVLG_07194_7sp	-896,4386	-896,32495	0,2273	0,10743	NS	0	[]	[]	[]	hypothetical protein	PF01344.18	Kelch_1(Kelch motif)
Supercontig_1.66_MVLG_05170_9sp	-754,15306	-752,40376	3,4986	0,8261	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.44_MVLG_04156_12sp	-453,36401	-453,00734	0,71334	0,3	NS	0	[]	[]	[]	hypothetical protein	PF05007.6	Mannosyl_trans(Mannosyltransferase (PIG-M))
Supercontig_1.62_MVLG_05042_10sp	-278,91076	-278,91072	0,00016	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF00155.14	Aminotran_1_2(Aminotransferase class I and II)
Supercontig_1.20_MVLG_02540_7sp	-363,87861	-362,87149	2,01424	0,63473	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.76_MVLG_05534_8sp	-539,75973	-539,75969	0,00016	0,00016	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.17_MVLG_02261_9sp	-357,56464	-357,39004	0,3492	0,16021	NS	0	[]	[]	[]	hypothetical protein	PF09759.2	Atx10homo_assoc(Spinocerebellar ataxia type 10 protein domain)
Supercontig_1.25_MVLG_02967_6sp	-810,56744	-810,56744	0	0	NS	0	[]	[]	[]	hypothetical protein	PF08624.3	CRC_subunit(Chromatin remodelling complex subunit)
Supercontig_1.161_MVLG_06868_10sp	-518,82485	-517,23891	3,17188	0,79524	NS	0	[]	[]	[]	hypothetical protein	PF05686.5	DUF821(Arabidopsis thaliana protein of unknown function (DUF821))
Supercontig_1.4_MVLG_00856_8sp	-586,29496	-586,27178	0,04636	0,02291	NS	0	[]	[]	[]	hypothetical protein	TIGR00222	TIGR00222(panB: 3-methyl-2-oxobutanoate hydroxymethyltransferase)
Supercontig_1.33_MVLG_03474_9sp	-424,45826	-424,45826	0	0	NS	0	[]	[]	[]	hypothetical protein	PF07690.9	MFS_1(Major Facilitator Superfamily)
Supercontig_1.68_MVLG_05254_8sp	-473,02754	-473,02704	0,001	0,0005	NS	0	[]	[]	[]	acetolactate synthase	PF00205.15	TPP_enzyme_M(Thiamine pyrophosphate enzyme, central domain)

Supercontig_1.53_MVLG_04605_6sp	-438,00069	-438,00069	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.59_MVLG_04909_11sp	-1189,0113	-1189,0113	0	0	NS	0	[]	[]	[]	pre-mRNA-splicing factor PRP46	PF00400.25	WD40(WD domain, G-beta repeat)
Supercontig_1.122_MVLG_06451_9sp	-318,58854	-318,58847	0,00014	0,00016	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.30_MVLG_03272_9sp	-1682,9342	-1682,9342	0	0	NS	0	[]	[]	[]	hypothetical protein	PF08632.3	Zds_C(Activator of mitotic machinery Cdc14 phosphatase activation C-term)
Supercontig_1.126_MVLG_06520_9sp	-522,7951	-522,77121	0,04778	0,02361	NS	0	[]	[]	[]	hypothetical protein	PF11709.1	Mit_ribos_Mrp51(Mitochondrial ribosomal protein subunit)
Supercontig_1.62_MVLG_05023_8sp	-843,42817	-843,42808	0,00018	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF10334.2	DUF2421(Protein of unknown function (DUF2421))
Supercontig_1.181_MVLG_07005_9sp	-316,91324	-316,91324	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.17_MVLG_02306_9sp	-896,55215	-895,56366	1,97698	0,62786	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.78_MVLG_05573_9sp	-646,66179	-644,51976	4,28406	0,88258	NS	0	[]	[]	[]	hypothetical protein	TIGR00685	TIGR00685(T6PP: trehalose-phosphatase)
Supercontig_1.3_MVLG_00550_7sp	-419,52751	-419,52745	0,00016	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF04935.5	SURF6(Surfeit locus protein 6)
Supercontig_1.12_MVLG_01843_8sp	-577,31827	-577,31826	0,00016	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF00628.22	PHD(PHD-finger)
Supercontig_1.1_MVLG_00201_7sp	-578,65361	-578,65361	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.57_MVLG_04823_10sp	-675,68339	-675,68339	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00889.12	EF_TS(Elongation factor TS)
Supercontig_1.36_MVLG_03654_9sp	-416,53396	-416,53395	0,00016	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF12054.1	DUF3535(Domain of unknown function (DUF3535))
Supercontig_1.11_MVLG_01697_9sp	-487,78589	-487,7858	0,00018	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF01753.11	zf-MYND(MYND finger)
Supercontig_1.58_MVLG_04866_10sp	-783,39453	-781,37416	4,04074	0,86739	NS	0	[]	[]	[]	hypothetical protein	PF00501.21	AMP-binding(AMP-binding enzyme)
Supercontig_1.13_MVLG_01960_12sp	-428,52282	-428,5224	0,00084	0,00042	NS	0	[]	[]	[]	hypothetical protein	PF02463.12	SMC_N(RecF/RecN/SMC N terminal domain)
Supercontig_1.38_MVLG_03765_9sp	-613,77544	-613,77537	0,00014	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF08772.4	NOB1_Zn_bind(Nin one binding (NOB1) Zn-ribbon like)
Supercontig_1.111_MVLG_06310_6sp	-1021,4093	-1021,3503	0,11802	0,0573	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.28_MVLG_03131_8sp	-451,19273	-451,19264	0,00018	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF01115.10	F_actin_cap_B(F-actin capping protein, beta subunit)
Supercontig_1.85_MVLG_05799_10sp	-333,53466	-333,03658	0,99616	0,3923	NS	0	[]	[]	[]	hypothetical protein	PF03798.9	TRAM_LAG1_CLN8(TLC domain)
Supercontig_1.6_MVLG_01198_11sp	-1128,8827	-1128,8827	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.132_MVLG_06591_12sp	-737,11103	-737,11103	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01585.16	G-patch(G-patch domain)
Supercontig_1.26_MVLG_03049_9sp	-717,96652	-717,96651	0,00016	0,00016	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.70_MVLG_05329_6sp	-495,21755	-495,21749	0,00016	0,00016	NS	0	[]	[]	[]	hypothetical protein	NA	NA

Supercontig_1.100_MVLG_06132_9sp	-942,68666	-942,61914	0,13504	0,06529	NS	0	[]	[]	[]	hypothetical protein	PF02373.15	JmjC(JmjC domain)
Supercontig_1.247_MVLG_07211_7sp	-352,9288	-352,79456	0,26848	0,12562	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.28_MVLG_03149_10sp	-663,68459	-663,68459	0	0	NS	0	[]	[]	[]	hypothetical protein	PF07885.9	Ion_trans_2(Ion channel)
Supercontig_1.13_MVLG_01938_7sp	-1361,0783	-1358,827	4,50256	0,89474	NS	0	[]	[]	[]	hypothetical protein	PF09779.2	DUF2349(Uncharacterized conserved protein (DUF2349))
Supercontig_1.4_MVLG_00750_9sp	-881,65432	-880,48758	2,33348	0,68862	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.94_MVLG_05992_10sp	-809,07831	-808,54583	1,06496	0,41285	NS	0	[]	[]	[]	hypothetical protein	PF00172.11	Zn_clus(Fungal Zn(2)-Cys(6) binuclear cluster domain)
Supercontig_1.126_MVLG_06518_11sp	-331,30616	-331,30571	0,0009	0,00045	NS	0	[]	[]	[]	septin like spn2	PF04548.9	AIG1(AIG1 family)
Supercontig_1.2_MVLG_00423_10sp	-439,24998	-438,83876	0,82244	0,33716	NS	0	[]	[]	[]	hypothetical protein	PF12572.1	DUF3752(Protein of unknown function (DUF3752))
Supercontig_1.32_MVLG_03410_6sp	-824,13036	-824,13036	0	0	NS	0	[]	[]	[]	hypothetical protein	PF07690.9	MFS_1(Major Facilitator Superfamily)
Supercontig_1.52_MVLG_04563_7sp	-659,63714	-659,63714	0	0	NS	0	[]	[]	[]	hypothetical protein	PF07722.6	Peptidase_C26(Peptidase C26)
Supercontig_1.58_MVLG_04849_10sp	-1227,0887	-1227,0601	0,0572	0,02819	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.3_MVLG_00541_10sp	-992,88159	-992,88159	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00270.22	DEAD(DEAD/DEAH box helicase)
Supercontig_1.12_MVLG_01855_6sp	-1034,9439	-1034,9439	0,0001	0,00016	NS	0	[]	[]	[]	hypothetical protein	TIGR00555	TIGR00555(panK_eukar: pantothenate kinase)
Supercontig_1.45_MVLG_04214_9sp	-895,66401	-895,17272	0,98258	0,38816	NS	0	[]	[]	[]	hypothetical protein	PF01735.11	PLA2_B(Lysophospholipase catalytic domain)
Supercontig_1.69_MVLG_05275_6sp	-953,72976	-953,72778	0,00396	0,00198	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.76_MVLG_05516_10sp	-413,90189	-413,90188	0,00016	0,00016	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.6_MVLG_01098_10sp	-338,83445	-338,83426	0,00038	0,00019	NS	0	[]	[]	[]	isocitrate dehydrogenase [NAD] subunit 2	TIGR00175	TIGR00175(mito_nad_idh: isocitrate dehydrogenase, NAD-dependent)
Supercontig_1.67_MVLG_05225_8sp	-1035,0962	-1035,0962	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00364.15	Biotin_lipoyl(Biotin-requiring enzyme)
Supercontig_1.5_MVLG_00969_9sp	-1008,6251	-1008,6251	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.8_MVLG_01430_9sp	-909,49209	-909,47959	0,025	0,01242	NS	0	[]	[]	[]	hypothetical protein	PF06248.6	Zw10(Centromere/kinetochore Zw10)
Supercontig_1.140_MVLG_06678_6sp	-400,68461	-400,68442	0,00038	0,00019	NS	0	[]	[]	[]	synaptobrevin like 1	PF00957.14	Synaptobrevin(Synaptobrevin)
Supercontig_1.69_MVLG_05288_6sp	-821,6998	-821,6998	0	0	NS	0	[]	[]	[]	glucose-6-phosphate isomerase	PF00342.12	PGI(Phosphoglucose isomerase)
Supercontig_1.3_MVLG_00611_11sp	-627,4673	-627,4673	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00447.10	HSF_DNA-bind(HSF-type DNA-binding)

Supercontig_1.240_MVLG_07203_7sp	-471,83727	-471,83727	0	0	NS	0	[]	[]	[]	5-methyltetrahydropteroyltriglutamate-homocysteine methyltransferase	PF01717.11	Meth_synt_2(Cobalamin-independent synthase, Catalytic domain)
Supercontig_1.49_MVLG_04422_8sp	-743,829	-743,20928	1,23944	0,4619	NS	0	[]	[]	[]	hypothetical protein	PF07690.9	MFS_1(Major Facilitator Superfamily)
Supercontig_1.30_MVLG_03290_10sp	-560,80077	-560,80044	0,00066	0,00033	NS	0	[]	[]	[]	hypothetical protein	PF02540.10	NAD_synthase(NAD synthase)
Supercontig_1.26_MVLG_03028_10sp	-441,74596	-441,74596	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02301.11	HORMA(HORMA domain)
Supercontig_1.9_MVLG_01543_11sp	-707,02845	-707,02845	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04801.6	Sin_N(Sin-like protein conserved region)
Supercontig_1.67_MVLG_05207_9sp	-1144,2833	-1144,2833	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01048.13	PNP_UDP_1(Phosphorylase superfamily)
Supercontig_1.9_MVLG_01571_12sp	-377,51031	-377,50985	0,00092	0,00046	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.32_MVLG_03425_10sp	-655,24398	-655,24398	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.12_MVLG_01819_11sp	-686,43183	-686,43183	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.11_MVLG_01724_12sp	-634,64986	-634,64986	0	0	NS	0	[]	[]	[]	hypothetical protein	TIGR01241	TIGR01241(FtsH_fam: ATP-dependent metallopeptidase HflB)
Supercontig_1.85_MVLG_05805_8sp	-329,76624	-329,76619	0,00016	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF04622.5	ERG2_Sigma1R(ERG2 and Sigma1 receptor like protein)
Supercontig_1.1_MVLG_00228_9sp	-483,69409	-481,69903	3,99012	0,86399	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.13_MVLG_01894_9sp	-687,91985	-687,91985	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00888.15	Cullin(Cullin family)
Supercontig_1.38_MVLG_03805_8sp	-499,2897	-499,2897	0	0	NS	0	[]	[]	[]	serine/threonine-protein phosphatase PP-X isozyme 1	PF00149.21	Metallophos(Calcineurin-like phosphoesterase)
Supercontig_1.22_MVLG_02709_10sp	-452,83885	-451,52408	2,62954	0,73146	NS	0	[]	[]	[]	hypothetical protein	PF00076.15	RRM_1(RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain))
Supercontig_1.55_MVLG_04743_8sp	-396,7162	-396,4018	0,6288	0,26977	NS	0	[]	[]	[]	hypothetical protein	PF02146.10	SIR2(Sir2 family)
Supercontig_1.59_MVLG_04890_8sp	-435,1159	-435,11584	0,00012	0,00016	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.4_MVLG_00812_10sp	-799,46101	-799,46101	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00160.14	Pro_isomerase(Cyclophilin type peptidyl-prolyl cis-trans isomerase/CLD)
Supercontig_1.15_MVLG_02085_10sp	-487,4528	-486,85047	1,20466	0,45247	NS	0	[]	[]	[]	hypothetical protein	PF03770.9	IPK(Inositol polyphosphate kinase)
Supercontig_1.61_MVLG_04971_10sp	-461,55111	-461,55108	0,00016	0,00016	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.14_MVLG_02019_9sp	-595,5095	-595,50944	0,00016	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF00324.14	AA_permease(Amino acid permease)
Supercontig_1.36_MVLG_03645_6sp	-315,49059	-315,49059	0	0	NS	0	[]	[]	[]	UcrQ family protein	PF02939.9	UcrQ(UcrQ family)

Supercontig_1.92_MVLG_05968_9sp	-368,58061	-368,79674	0	0	NS	0	[]	[]	[]	3-ketoacyl-CoA thiolase, peroxisomal	TIGR01930	TIGR01930(AcCoA-C-Actrans: acetyl-CoA C-acetyltransferase)
Supercontig_1.58_MVLG_04872_7sp	-840,38268	-840,38257	0,00022	0,00011	NS	0	[]	[]	[]	hypothetical protein	TIGR00879	TIGR00879(SP: MFS transporter, sugar porter (SP) family)
Supercontig_1.84_MVLG_05777_8sp	-606,10926	-606,1088	0,00092	0,00046	NS	0	[]	[]	[]	GTP-binding protein ypt1	PF04670.5	Gtr1_RagA(Gtr1/RagA G protein conserved region)
Supercontig_1.63_MVLG_05056_12sp	-378,43986	-378,09191	0,6959	0,29387	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.36_MVLG_03689_6sp	-690,04652	-690,04652	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.113_MVLG_06342_12sp	-503,47079	-503,47079	0	0	NS	0	[]	[]	[]	hypothetical protein	PF08596.3	Lgl_C(Lethal giant larvae(Lgl) like, C-terminal)
Supercontig_1.69_MVLG_05294_7sp	-572,96722	-572,96722	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.63_MVLG_05060_8sp	-557,0644	-557,0644	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00450.15	Peptidase_S10(Serine carboxypeptidase)
Supercontig_1.46_MVLG_04288_10sp	-596,09641	-596,09641	0	0	NS	0	[]	[]	[]	hypothetical protein	PF11712.1	Vma12(Endoplasmic reticulum-based factor for assembly of V-ATPase)
Supercontig_1.49_MVLG_04410_8sp	-1130,3436	-1130,3436	0	0	NS	0	[]	[]	[]	hypothetical protein	PF10236.2	DAP3(Mitochondrial ribosomal death-associated protein 3)
Supercontig_1.56_MVLG_04774_12sp	-942,47109	-942,35799	0,2262	0,10694	NS	0	[]	[]	[]	hypothetical protein	PF03205.7	MobB(Molybdopterin guanine dinucleotide synthesis protein B)
Supercontig_1.6_MVLG_01072_7sp	-441,22846	-440,54912	1,35868	0,49305	NS	0	[]	[]	[]	hypothetical protein	PF07685.7	GATase_3(CobB/CobQ-like glutamine amidotransferase domain)
Supercontig_1.211_MVLG_07124_9sp	-509,63181	-509,46147	0,34068	0,15662	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.26_MVLG_03011_12sp	-1187,2084	-1187,2084	0	0	NS	0	[]	[]	[]	hypothetical protein	PF12253.1	CAF1A(Chromatin assembly factor 1 subunit A)
Supercontig_1.54_MVLG_04651_9sp	-1079,1449	-1079,1449	0	0	NS	0	[]	[]	[]	hypothetical protein	TIGR00010	TIGR00010(TIGR00010: hydrolase, TatD family)
Supercontig_1.27_MVLG_03076_8sp	-749,39319	-747,96399	2,8584	0,7605	NS	0	[]	[]	[]	hypothetical protein	TIGR00604	TIGR00604(rad3: DNA repair helicase (rad3))
Supercontig_1.28_MVLG_03140_10sp	-698,0286	-698,01221	0,03278	0,01626	NS	0	[]	[]	[]	hypothetical protein	PF04421.6	Mss4(Mss4 protein)
Supercontig_1.14_MVLG_02000_10sp	-387,41735	-387,07375	0,6872	0,29079	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.53_MVLG_04620_6sp	-680,7667	-680,58197	0,36946	0,16867	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.170_MVLG_06941_9sp	-420,37607	-420,37607	0	0	NS	0	[]	[]	[]	hypothetical protein	TIGR00879	TIGR00879(SP: MFS transporter, sugar porter (SP) family)
Supercontig_1.97_MVLG_06060_11sp	-455,53575	-455,53575	0	0	NS	0	[]	[]	[]	hypothetical protein	PF05691.5	Raffinose_syn(Raffinose synthase or seed inhibition protein Sip1)
Supercontig_1.69_MVLG_05312_8sp	-499,51928	-499,51928	0	0	NS	0	[]	[]	[]	hypothetical protein	PF07542.4	ATP12(ATP12 chaperone protein)

Supercontig_1.93_MVLG_05977_10sp	-508,818	-508,81801	0	0	NS	0	[]	[]	[]	AGC/PDK1 protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.154_MVLG_06810_7sp	-908,40498	-907,18049	2,44898	0,70609	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.2_MVLG_00342_12sp	-378,8601	-378,85957	0,00106	0,00053	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.1_MVLG_00023_9sp	-1292,7791	-1292,7791	0	0	NS	0	[]	[]	[]	AGC/PKA protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.165_MVLG_06909_9sp	-563,64803	-563,64803	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.5_MVLG_01033_11sp	-534,58278	-534,58275	0,00016	0,00016	NS	0	[]	[]	[]	hypothetical protein	TIGR00855	TIGR00855(L12: ribosomal protein L7/L12)
Supercontig_1.52_MVLG_04565_8sp	-895,79255	-895,79255	0,00016	0,00016	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.9_MVLG_01490_7sp	-424,87223	-424,87223	0	0	NS	0	[]	[]	[]	hypothetical protein	PF10163.2	EnY2(Transcription factor e(y)2)
Supercontig_1.22_MVLG_02715_9sp	-1307,2479	-1307,2479	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00443.22	UCH(Ubiquitin carboxyl-terminal hydrolase)
Supercontig_1.26_MVLG_03058_6sp	-873,35618	-871,67287	3,36662	0,81424	NS	0	[]	[]	[]	hypothetical protein	PF00884.16	Sulfatase(Sulfatase)
Supercontig_1.26_MVLG_03022_12sp	-537,85129	-537,85129	0	0	NS	0	[]	[]	[]	2-isopropylmalate synthase	PF00682.12	HMGL-like(HMGL-like)
Supercontig_1.39_MVLG_03836_9sp	-747,85881	-747,85881	0	0	NS	0	[]	[]	[]	pyruvate dehydrogenase E1 component subunit beta	PF02780.13	Transketolase_C(Transketolase, C-terminal domain)
Supercontig_1.45_MVLG_04199_10sp	-719,82393	-719,82393	0	0	NS	0	[]	[]	[]	AGC protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.4_MVLG_00809_9sp	-389,48984	-389,48962	0,00044	0,00022	NS	0	[]	[]	[]	hypothetical protein	PF00150.11	Cellulase(Cellulase (glycosyl hydrolase family 5))
Supercontig_1.87_MVLG_05854_7sp	-357,21583	-357,21583	0	0	NS	0	[]	[]	[]	hypothetical protein	TIGR01164	TIGR01164(rplP_bact: ribosomal protein L16)
Supercontig_1.4_MVLG_00830_11sp	-644,50847	-644,50847	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.24_MVLG_02855_7sp	-812,69791	-812,25795	0,87992	0,35594	NS	0	[]	[]	[]	hypothetical protein	PF10996.1	Beta-Casp(Beta-Casp domain)
Supercontig_1.231_MVLG_07192_8sp	-419,64919	-419,64905	0,00028	0,00014	NS	0	[]	[]	[]	hypothetical protein	PF00412.15	LIM(LIM domain)
Supercontig_1.19_MVLG_02503_7sp	-580,4135	-580,13644	0,55412	0,24199	NS	0	[]	[]	[]	hypothetical protein	PF06703.4	SPC25(Microsomal signal peptidase 25 kDa subunit (SPC25))
Supercontig_1.7_MVLG_01244_8sp	-780,97881	-780,65551	0,6466	0,27624	NS	0	[]	[]	[]	AGC/PKC protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.27_MVLG_03097_10sp	-970,20093	-969,89277	0,61632	0,2652	NS	0	[]	[]	[]	hypothetical protein	PF01055.19	Glyco_hydro_31(Glycosyl hydrolases family 31)
Supercontig_1.34_MVLG_03517_8sp	-808,4443	-808,43999	0,00862	0,0043	NS	0	[]	[]	[]	hypothetical protein	PF00557.17	Peptidase_M24(Metallopeptidase family M24)
Supercontig_1.122_MVLG_06452_7sp	-1358,3404	-1358,2748	0,13112	0,06346	NS	0	[]	[]	[]	hypothetical protein	PF11957.1	efThoc1(THO complex subunit 1 transcription elongation factor)
Supercontig_1.4_MVLG_00729_8sp	-1004,5129	-1003,8866	1,25262	0,46544	NS	0	[]	[]	[]	hypothetical protein	NA	NA

Supercontig_1.101_MVLG_06155_11sp	-329,65721	-329,38639	0,54164	0,23725	NS	0	[]	[]	[]	hypothetical protein	PF01119.12	DNA_mis_repair(DNA mismatch repair protein, C-terminal domain)
Supercontig_1.54_MVLG_04687_10sp	-369,47483	-369,399	0,15166	0,07303	NS	0	[]	[]	[]	methylthioribulose-1-phosphate dehydratase	PF00596.14	Aldolase_II(Class II Aldolase and Adducin N-terminal domain)
Supercontig_1.97_MVLG_06065_8sp	-735,43121	-734,66883	1,52476	0,53345	NS	0	[]	[]	[]	hypothetical protein	PF03227.9	GILT(Gamma interferon inducible lysosomal thiol reductase (GILT))
Supercontig_1.16_MVLG_02203_10sp	-1032,6861	-1032,6861	0	0	NS	0	[]	[]	[]	hypothetical protein	PF08295.5	HDAC_interact(Histone deacetylase (HDAC) interacting)
Supercontig_1.51_MVLG_04542_9sp	-637,3693	-637,3693	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00172.11	Zn_clus(Fungal Zn(2)-Cys(6) binuclear cluster domain)
Supercontig_1.55_MVLG_04704_9sp	-1207,8043	-1207,7815	0,04546	0,02247	NS	0	[]	[]	[]	hypothetical protein	PF00076.15	RRM_1(RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain))
Supercontig_1.4_MVLG_00824_10sp	-537,29893	-537,29893	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00557.17	Peptidase_M24(Metallopeptidase family M24)
Supercontig_1.81_MVLG_05670_7sp	-513,22807	-513,22807	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.24_MVLG_02898_10sp	-500,31822	-500,31822	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.16_MVLG_02174_9sp	-597,18543	-597,08051	0,20984	0,0996	NS	0	[]	[]	[]	hypothetical protein	PF08213.4	DUF1713(Mitochondrial domain of unknown function (DUF1713))
Supercontig_1.19_MVLG_02484_11sp	-288,97833	-288,90708	0,1425	0,06877	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.107_MVLG_06250_10sp	-514,24804	-514,24786	0,00036	0,00018	NS	0	[]	[]	[]	hypothetical protein	PF04118.7	Dopey_N(Dopey, N-terminal)
Supercontig_1.18_MVLG_02416_11sp	-499,19496	-499,19487	0,00018	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF00270.22	DEAD(DEAD/DEAH box helicase)
Supercontig_1.17_MVLG_02343_8sp	-852,18561	-852,18561	0	0	NS	0	[]	[]	[]	methylase	TIGR00537	TIGR00537(hemK_rel_arch: putative methylase)
Supercontig_1.14_MVLG_02002_8sp	-395,06036	-395,05987	0,00098	0,00049	NS	0	[]	[]	[]	NADH dehydrogenase (ubiquinone) Fe-S protein 7	PF01058.15	Oxidored_q6(NADH ubiquinone oxidoreductase, 20 Kd subunit)
Supercontig_1.2_MVLG_00448_12sp	-904,63113	-903,66735	1,92756	0,61855	NS	0	[]	[]	[]	hypothetical protein	TIGR01494	TIGR01494(ATPase_P-type: HAD ATPase, P-type, family IC)
Supercontig_1.8_MVLG_01385_8sp	-949,86203	-949,8618	0,00046	0,00023	NS	0	[]	[]	[]	acyl-CoA dehydrogenase	PF02770.12	Acyl-CoA_dh_M(Acyl-CoA dehydrogenase, middle domain)
Supercontig_1.25_MVLG_02934_7sp	-501,3534	-501,33454	0,03772	0,01868	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.1_MVLG_00065_9sp	-1238,075	-1238,075	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.52_MVLG_04560_7sp	-928,73904	-928,73904	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00097.18	zf-C3HC4(Zinc finger, C3HC4 type (RING finger))
Supercontig_1.4_MVLG_00781_9sp	-584,81802	-584,81802	0	0	NS	0	[]	[]	[]	hypothetical protein	PF09811.2	Yae1_N(Essential protein Yae1, N terminal)

Supercontig_1.60_MVLG_04954_9sp	-572,82826	-572,82826	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.22_MVLG_02707_7sp	-579,14313	-579,14304	0,00018	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF04142.8	Nuc_sug_transp(Nucleotide-sugar transporter)
Supercontig_1.1_MVLG_00155_9sp	-314,41962	-313,95628	0,92668	0,37082	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.6_MVLG_01123_12sp	-443,21276	-443,17821	0,0691	0,03396	NS	0	[]	[]	[]	hypothetical protein	PF00400.25	WD40(WD domain, G-beta repeat)
Supercontig_1.48_MVLG_04357_12sp	-779,98479	-779,73883	0,49192	0,21805	NS	0	[]	[]	[]	hypothetical protein	PF01735.11	PLA2_B(Lysophospholipase catalytic domain)
Supercontig_1.81_MVLG_05676_6sp	-1184,119	-1184,119	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03097.11	BRO1(BRO1-like domain)
Supercontig_1.53_MVLG_04622_8sp	-634,26135	-634,26117	0,00036	0,00018	NS	0	[]	[]	[]	hypothetical protein	PF10300.2	IML2(Putative mitochondrial outer membrane protein)
Supercontig_1.18_MVLG_02394_8sp	-397,52518	-397,5251	0,00016	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF08295.5	HDAC_interact(Histone deacetylase (HDAC) interacting)
Supercontig_1.49_MVLG_04447_7sp	-552,8605	-552,8605	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00366.13	Ribosomal_S17(Ribosomal protein S17)
Supercontig_1.6_MVLG_01220_6sp	-452,2375	-452,2375	0	0	NS	0	[]	[]	[]	V-type proton ATPase subunit F	PF01990.10	ATP-synt_F(ATP synthase (F/14-kDa) subunit)
Supercontig_1.33_MVLG_03448_7sp	-678,36807	-677,65783	1,42048	0,50847	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.2_MVLG_00401_8sp	-1220,0754	-1220,0754	0	0	NS	0	[]	[]	[]	AGC/NDR protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.69_MVLG_05287_7sp	-874,27856	-874,26715	0,02282	0,01135	NS	0	[]	[]	[]	hypothetical protein	PF10213.2	MRP-S28(Mitochondrial ribosomal subunit protein)
Supercontig_1.163_MVLG_06883_10sp	-608,98414	-608,98411	0,00016	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF00651.24	BTB(BTB/POZ domain)
Supercontig_1.12_MVLG_01853_7sp	-750,70065	-750,70065	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04502.6	DUF572(Family of unknown function (DUF572))
Supercontig_1.2_MVLG_00434_10sp	-920,54517	-920,54517	0	0	NS	0	[]	[]	[]	CAMK/CAMKL protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.55_MVLG_04702_9sp	-333,33366	-333,23056	0,2062	0,09796	NS	0	[]	[]	[]	hypothetical protein	PF00578.14	AhpC-TSA(AhpC/TSA family)
Supercontig_1.2_MVLG_00384_9sp	-573,9265	-573,92584	0,00132	0,00066	NS	0	[]	[]	[]	40S ribosomal protein S0	PF00318.13	Ribosomal_S2(Ribosomal protein S2)
Supercontig_1.107_MVLG_06248_6sp	-441,19695	-441,11827	0,15736	0,07566	NS	0	[]	[]	[]	hypothetical protein	PF09184.4	PPP4R2(PPP4R2)
Supercontig_1.12_MVLG_01817_12sp	-470,9987	-470,99858	0,00024	0,00012	NS	0	[]	[]	[]	hypothetical protein	PF00172.11	Zn_clus(Fungal Zn(2)-Cys(6) binuclear cluster domain)
Supercontig_1.1_MVLG_00003_9sp	-1080,8941	-1080,887	0,01432	0,00713	NS	0	[]	[]	[]	T-complex protein 1 subunit theta	PF00118.17	Cpn60_TCP1(TCP-1/cpn60 chaperonin family)
Supercontig_1.18_MVLG_02364_9sp	-755,31309	-755,31303	0,00012	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF07859.6	Abhydrolase_3(alpha/beta hydrolase fold)
Supercontig_1.8_MVLG_01379_9sp	-646,29723	-645,98087	0,63272	0,2712	NS	0	[]	[]	[]	hypothetical protein	PF08954.4	DUF1900(Domain of unknown function (DUF1900))
Supercontig_1.22_MVLG_02705_12sp	-607,03831	-607,0351	0,00642	0,0032	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.78_MVLG_05579_9sp	-594,84941	-592,60826	4,4823	0,89366	NS	0	[]	[]	[]	hypothetical protein	NA	NA

Supercontig_1.82_MVLG_05708_9sp	-779,98743	-779,98743	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01535.13	PPR(PPR repeat)
Supercontig_1.150_MVLG_06771_7sp	-459,10219	-458,82809	0,5482	0,23974	NS	0	[]	[]	[]	GTP-binding protein rhb1	PF08477.6	Miro(Miro-like protein)
Supercontig_1.68_MVLG_05259_10sp	-984,34554	-984,34534	0,0004	0,0002	NS	0	[]	[]	[]	Ca2+:H+ antiporter	TIGR00378	TIGR00378(cax: calcium/proton exchanger)
Supercontig_1.34_MVLG_03510_11sp	-438,50181	-438,50181	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01138.14	RNase_PH(3' exoribonuclease family, domain 1)
Supercontig_1.67_MVLG_05216_8sp	-791,69882	-791,69882	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00723.14	Glyco_hydro_15(Glycosyl hydrolases family 15)
Supercontig_1.10_MVLG_01603_10sp	-414,32033	-414,32033	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03016.8	Exostosin(Exostosin family)
Supercontig_1.21_MVLG_02623_10sp	-956,13953	-954,43582	3,40742	0,81799	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.13_MVLG_01923_10sp	-663,02492	-663,02492	0	0	NS	0	[]	[]	[]	short/branched chain specific acyl-CoA dehydrogenase	PF02770.12	Acyl-CoA_dh_M(Acyl-CoA dehydrogenase, middle domain)
Supercontig_1.46_MVLG_04273_9sp	-348,82195	-348,82195	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.40_MVLG_03938_10sp	-544,68249	-544,68218	0,00062	0,00031	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.1_MVLG_00038_12sp	-406,39497	-403,70286	5,38422	0,93226	*	0	[]	[]	[]	hypothetical protein	PF04670.5	Gtr1_RagA(Gtr1/RagA G protein conserved region)
Supercontig_1.51_MVLG_04513_8sp	-517,98655	-517,98646	0,00018	0,00016	NS	0	[]	[]	[]	STE/STE20/YSK protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.16_MVLG_02199_12sp	-395,2588	-395,25863	0,00034	0,00017	NS	0	[]	[]	[]	hypothetical protein	PF00205.15	TPP_enzyme_M(Thiamine pyrophosphate enzyme, central domain)
Supercontig_1.11_MVLG_01777_11sp	-435,39753	-434,89183	1,0114	0,39692	NS	0	[]	[]	[]	hypothetical protein	PF03372.16	Exo_endo_phos(Endonuclease/ Exonuclease/phosphatase family)
Supercontig_1.16_MVLG_02210_8sp	-421,96176	-421,96176	0	0	NS	0	[]	[]	[]	hypothetical protein	PF10615.2	DUF2470(Protein of unknown function (DUF2470))
Supercontig_1.124_MVLG_06488_6sp	-671,25181	-670,8478	0,80802	0,33236	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.1_MVLG_00028_12sp	-831,86718	-831,86718	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01119.12	DNA_mis_repair(DNA mismatch repair protein, C-terminal domain)
Supercontig_1.26_MVLG_03037_12sp	-358,71	-358,71	0	0	NS	0	[]	[]	[]	hypothetical protein	PF07719.10	TPR_2(Tetratricopeptide repeat)
Supercontig_1.58_MVLG_04852_9sp	-1329,1504	-1328,1015	2,0977	0,64966	NS	0	[]	[]	[]	hypothetical protein	PF00293.21	NUDIX(NUDIX domain)
Supercontig_1.67_MVLG_05215_10sp	-373,47753	-373,38769	0,17968	0,08592	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.41_MVLG_03979_9sp	-460,4299	-460,42949	0,00082	0,00041	NS	0	[]	[]	[]	ubiquitin-conjugating enzyme E2-18 kDa	PF00179.19	UQ_con(Ubiquitin-conjugating enzyme)
Supercontig_1.62_MVLG_05001_8sp	-502,95445	-502,95445	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.81_MVLG_05687_10sp	-1027,6669	-1027,6669	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00097.18	zf-C3HC4(Zinc finger, C3HC4 type (RING finger))

Supercontig_1.4_MVLG_00706_8sp	-413,72134	-413,72127	0,00014	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF08555.3	DUF1754(Eukaryotic family of unknown function (DUF1754))
Supercontig_1.3_MVLG_00638_10sp	-501,03976	-500,0336	2,01232	0,63438	NS	0	[]	[]	[]	nitrite reductase (NAD(P)H) large subunit	PF00070.20	Pyr_redox(Pyridine nucleotide-disulphide oxidoreductase)
Supercontig_1.3_MVLG_00530_11sp	-629,89392	-629,89392	0	0	NS	0	[]	[]	[]	hypothetical protein	PF06325.6	PrmA(Ribosomal protein L11 methyltransferase (PrmA))
Supercontig_1.27_MVLG_03091_9sp	-498,26812	-498,22913	0,07798	0,03824	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.9_MVLG_01486_12sp	-330,61555	-330,54365	0,1438	0,06938	NS	0	[]	[]	[]	hypothetical protein	PF08101.4	DUF1708(Domain of unknown function (DUF1708))
Supercontig_1.33_MVLG_03483_6sp	-820,77806	-820,7781	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04280.8	Tim44(Tim44-like domain)
Supercontig_1.4_MVLG_00870_7sp	-386,8773	-386,87688	0,00084	0,00042	NS	0	[]	[]	[]	CK1/CK1/CK1-D protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.180_MVLG_07000_10sp	-700,08431	-700,0843	0,00016	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF05188.10	MutS_II(MutS domain II)
Supercontig_1.126_MVLG_06529_10sp	-500,60254	-500,60254	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01336.18	tRNA_anti(OB-fold nucleic acid binding domain)
Supercontig_1.5_MVLG_00917_9sp	-463,52371	-463,5235	0,00042	0,00021	NS	0	[]	[]	[]	hypothetical protein	PF00176.16	SNF2_N(SNF2 family N-terminal domain)
Supercontig_1.28_MVLG_03129_7sp	-883,95027	-883,95026	0,00016	0,00016	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.12_MVLG_01880_7sp	-402,59939	-401,20728	2,78422	0,75145	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.34_MVLG_03520_8sp	-629,8361	-629,83605	0,00016	0,00016	NS	0	[]	[]	[]	succinate dehydrogenase [ubiquinone] iron-sulfur subunit	TIGR00384	TIGR00384(dhsB: succinate dehydrogenase and fumarate reductase iron-sulfur protein)
Supercontig_1.81_MVLG_05667_12sp	-422,59641	-422,59607	0,00068	0,00034	NS	0	[]	[]	[]	hypothetical protein	TIGR00399	TIGR00399(metG_C_term: methionine--tRNA ligase, beta subunit)
Supercontig_1.104_MVLG_06208_9sp	-913,13251	-913,13251	0	0	NS	0	[]	[]	[]	hypothetical protein	PF08621.3	RPAP1_N(RPAP1-like, N-terminal)
Supercontig_1.4_MVLG_00743_9sp	-296,2846	-296,28442	0,00036	0,00018	NS	0	[]	[]	[]	NADH dehydrogenase (ubiquinone) 1 alpha/beta subcomplex 1	PF00550.18	PP-binding(Phosphopantetheine attachment site)
Supercontig_1.65_MVLG_05147_9sp	-717,2051	-715,42117	3,56786	0,83202	NS	0	[]	[]	[]	hypothetical protein	PF00929.17	Exonuc_X-T(Exonuclease)
Supercontig_1.25_MVLG_02971_6sp	-955,9194	-955,91939	0,00016	0,00016	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.6_MVLG_01053_9sp	-527,09622	-527,09622	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00026.16	Asp(Eukaryotic aspartyl protease)
Supercontig_1.87_MVLG_05855_8sp	-807,40211	-807,05608	0,69206	0,29251	NS	0	[]	[]	[]	hypothetical protein	PF00153.20	Mito_carr(Mitochondrial carrier protein)
Supercontig_1.47_MVLG_04304_7sp	-446,76605	-446,56136	0,40938	0,1851	NS	0	[]	[]	[]	hypothetical protein	PF07724.7	AAA_2(AAA domain (Cdc48 subfamily))

Supercontig_1.41_MVLG_03980_7sp	-1081,9789	-1081,9789	0	0	NS	0	[]	[]	[]	hypothetical protein	PF12460.1	MMS19_N(NER and RNAPII transcription protein n terminal)
Supercontig_1.1_MVLG_00099_8sp	-863,98752	-863,98748	0,00016	0,00016	NS	0	[]	[]	[]	squalene synthase	PF00494.12	SQS_PSY(Squalene/phytoene synthase)
Supercontig_1.24_MVLG_02836_8sp	-430,26137	-430,26137	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.28_MVLG_03189_10sp	-1035,6732	-1035,6732	0	0	NS	0	[]	[]	[]	hypothetical protein	PF09454.3	Vps23_core(Vps23 core domain)
Supercontig_1.128_MVLG_06555_10sp	-1653,3954	-1652,928	0,9349	0,3734	NS	0	[]	[]	[]	hypothetical protein	PF08514.4	STAG(STAG domain)
Supercontig_1.247_MVLG_07212_7sp	-477,47738	-477,47738	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.26_MVLG_03046_10sp	-296,52936	-296,52936	0	0	NS	0	[]	[]	[]	ubiquitin thiolesterase	PF12436.1	USP7(Ubiquitin-specific protease 7)
Supercontig_1.3_MVLG_00574_10sp	-393,29609	-393,29601	0,00016	0,00016	NS	0	[]	[]	[]	CMGC/GSK protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.3_MVLG_00490_7sp	-880,67446	-880,67467	0	0	NS	0	[]	[]	[]	hypothetical protein	PF11735.1	CAP59_mtransfer(Cryptococcal mannosyltransferase 1)
Supercontig_1.56_MVLG_04755_9sp	-699,32975	-698,62986	1,39978	0,50336	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.127_MVLG_06535_6sp	-476,6966	-476,68432	0,02456	0,0122	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.77_MVLG_05542_10sp	-858,82897	-857,36206	2,93382	0,76936	NS	0	[]	[]	[]	hypothetical protein	PF00642.17	zf-CCCH(Zinc finger C-x8-C-x5-C-x3-H type (and similar))
Supercontig_1.85_MVLG_05814_6sp	-304,19164	-304,19149	0,0003	0,00015	NS	0	[]	[]	[]	3-hydroxybutyryl-CoA dehydrogenase	PF00725.15	3HCDH(3-hydroxyacyl-CoA dehydrogenase, C-terminal domain)
Supercontig_1.117_MVLG_06401_7sp	-726,52513	-726,52425	0,00176	0,00088	NS	0	[]	[]	[]	hypothetical protein	PF04777.6	Evr1_Alr(Erv1 / Alr family)
Supercontig_1.9_MVLG_01545_8sp	-624,68794	-624,68794	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02182.10	YDG_SRA(YDG/SRA domain)
Supercontig_1.132_MVLG_06601_11sp	-294,21899	-294,21878	0,00042	0,00021	NS	0	[]	[]	[]	glutamine synthetase	PF00120.17	Gln-synt_C(Glutamine synthetase, catalytic domain)
Supercontig_1.180_MVLG_06998_9sp	-1989,775	-1986,6371	6,27586	0,95663	**	0	[]	[]	[]	hypothetical protein	PF03061.15	4HBT(Thioesterase superfamily)
Supercontig_1.7_MVLG_01223_12sp	-620,94383	-618,41504	5,05758	0,92024	*	0	[]	[]	[]	hypothetical protein	PF00780.15	CNH(CNH domain)
Supercontig_1.27_MVLG_03077_8sp	-1250,8972	-1250,0859	1,62256	0,55571	NS	0	[]	[]	[]	hypothetical protein	PF00172.11	Zn_clus(Fungal Zn(2)-Cys(6) binuclear cluster domain)
Supercontig_1.41_MVLG_04022_8sp	-569,77959	-569,75671	0,04576	0,02262	NS	0	[]	[]	[]	hypothetical protein	PF00177.14	Ribosomal_S7(Ribosomal protein S7p/S5e)
Supercontig_1.160_MVLG_06854_7sp	-1078,9866	-1078,8156	0,34214	0,15724	NS	0	[]	[]	[]	hypothetical protein	PF00067.15	p450(Cytochrome P450)
Supercontig_1.11_MVLG_01688_11sp	-514,04639	-512,88579	2,3212	0,6867	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.4_MVLG_00733_7sp	-453,2099	-453,20978	0,00024	0,00012	NS	0	[]	[]	[]	hypothetical protein	PF12333.1	Ipi1_N(Rix1 complex component involved in 60S ribosome maturation)
Supercontig_1.1_MVLG_00165_10sp	-382,93986	-382,93986	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA

Supercontig_1.33_MVLG_03473_12sp	-512,13973	-512,13911	0,00124	0,00062	NS	0	[]	[]	[]	STE/STE20/PAKA protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.124_MVLG_06495_9sp	-462,67269	-462,67262	0,00014	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF07798.4	DUF1640(Protein of unknown function (DUF1640))
Supercontig_1.74_MVLG_05473_7sp	-724,93228	-724,49157	0,88142	0,35642	NS	0	[]	[]	[]	biotin synthase	PF06968.6	BATS(Biotin and Thiamin Synthesis associated domain)
Supercontig_1.9_MVLG_01555_8sp	-918,42253	-918,42253	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00617.12	RasGEF(RasGEF domain)
Supercontig_1.28_MVLG_03205_7sp	-1177,1585	-1177,1585	0	0	NS	0	[]	[]	[]	hypothetical protein	PF08477.6	Miro(Miro-like protein)
Supercontig_1.11_MVLG_01708_10sp	-1076,6066	-1076,2645	0,6841	0,28969	NS	0	[]	[]	[]	hypothetical protein	PF01968.11	Hydantoinase_A(Hydantoinase/oxoprolinase)
Supercontig_1.12_MVLG_01876_12sp	-379,95848	-379,95846	0,00016	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF00072.17	Response_reg(Response regulator receiver domain)
Supercontig_1.6_MVLG_01103_7sp	-833,20852	-833,20852	0	0	NS	0	[]	[]	[]	aminotransferase	PF01053.13	Cys_Met_Meta_PP(Cys/Met metabolism PLP-dependent enzyme)
Supercontig_1.87_MVLG_05850_10sp	-508,53028	-508,53028	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00013.22	KH_1(KH domain)
Supercontig_1.41_MVLG_04011_10sp	-765,248	-765,248	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02515.10	CoA_transf_3(CoA-transferase family III)
Supercontig_1.3_MVLG_00514_8sp	-619,74882	-619,74853	0,00058	0,00029	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.7_MVLG_01257_10sp	-331,315	-331,3022	0,0256	0,01272	NS	0	[]	[]	[]	V-type proton ATPase proteolipid subunit 2	TIGR01100	TIGR01100(V_ATP_synt_C: V-type ATPase, C subunit)
Supercontig_1.46_MVLG_04252_11sp	-496,91006	-496,8159	0,18832	0,08986	NS	0	[]	[]	[]	hypothetical protein	PF02167.8	Cytochrom_C1(Cytochrome C1 family)
Supercontig_1.86_MVLG_05829_11sp	-451,37142	-451,37142	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04082.11	Fungal_trans(Fungal specific transcription factor domain)
Supercontig_1.33_MVLG_03459_11sp	-366,40474	-365,74288	1,32372	0,48411	NS	0	[]	[]	[]	hypothetical protein	PF00787.17	PX(PX domain)
Supercontig_1.25_MVLG_02969_11sp	-345,78901	-345,78901	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00128.17	Alpha-amylase(Alpha amylase, catalytic domain)
Supercontig_1.16_MVLG_02234_8sp	-845,41156	-845,41147	0,00018	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF10375.2	GRAB(GRIP-related Arf-binding domain)
Supercontig_1.41_MVLG_04034_9sp	-443,22921	-443,22921	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00153.20	Mito_carr(Mitochondrial carrier protein)
Supercontig_1.47_MVLG_04322_6sp	-579,58398	-579,58398	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.96_MVLG_06052_8sp	-501,58346	-500,08539	2,99614	0,77644	NS	0	[]	[]	[]	hypothetical protein	PF00564.17	PB1(PB1 domain)
Supercontig_1.46_MVLG_04297_11sp	-441,48916	-441,48913	0,00016	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF00319.11	SRF-TF(SRF-type transcription factor (DNA-binding and dimerisation domain))
Supercontig_1.4_MVLG_00817_9sp	-627,67207	-627,67207	0	0	NS	0	[]	[]	[]	hypothetical protein	PF05255.4	UPF0220(Uncharacterised protein family (UPF0220))
Supercontig_1.84_MVLG_05778_12sp	-777,60407	-776,43111	2,34592	0,69055	NS	0	[]	[]	[]	60S ribosomal protein L5-B	PF00861.15	Ribosomal_L18p(Ribosomal L18p/L5e family)
Supercontig_1.8_MVLG_01363_10sp	-813,40227	-813,39747	0,0096	0,00479	NS	0	[]	[]	[]	hypothetical protein	PF08242.5	Methyltransf_12(Methyltransferase domain)

Supercontig_1.29_MVLG_03253_7sp	-388,46036	-388,46017	0,00038	0,00019	NS	0	[]	[]	[]	40S ribosomal protein S20	TIGR01046	TIGR01046(S10_Arc_S20_Euk: ribosomal protein S10)
Supercontig_1.47_MVLG_04302_7sp	-499,04818	-498,70132	0,69372	0,2931	NS	0	[]	[]	[]	hypothetical protein	PF00083.17	Sugar_tr(Sugar (and other) transporter)
Supercontig_1.16_MVLG_02225_8sp	-338,57461	-338,57441	0,0004	0,0002	NS	0	[]	[]	[]	hypothetical protein	PF04003.5	Utp12(Dip2/Utp12 Family)
Supercontig_1.54_MVLG_04669_6sp	-621,59507	-621,59491	0,00032	0,00016	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.8_MVLG_01365_12sp	-349,66459	-349,66455	0,00016	0,00016	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.110_MVLG_06300_12sp	-1185,6342	-1185,5617	0,14516	0,07001	NS	0	[]	[]	[]	hypothetical protein	PF00415.11	RCC1(Regulator of chromosome condensation (RCC1) repeat)
Supercontig_1.49_MVLG_04401_10sp	-1009,4285	-1008,57	1,71694	0,57619	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.55_MVLG_04715_7sp	-908,26352	-908,26352	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00294.17	PfkB(pfkB family carbohydrate kinase)
Supercontig_1.28_MVLG_03155_7sp	-368,98345	-368,98321	0,00048	0,00024	NS	0	[]	[]	[]	hypothetical protein	PF01679.10	UPF0057(Uncharacterized protein family UPF0057)
Supercontig_1.29_MVLG_03248_11sp	-518,00186	-517,75059	0,50254	0,22219	NS	0	[]	[]	[]	hypothetical protein	PF00172.11	Zn_clus(Fungal Zn(2)-Cys(6) binuclear cluster domain)
Supercontig_1.87_MVLG_05846_7sp	-837,187	-837,18534	0,00332	0,00166	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.66_MVLG_05169_9sp	-890,22036	-888,80648	2,82776	0,7568	NS	0	[]	[]	[]	dihydroxy-acid dehydratase	PF00920.14	ILVD_EDD(Dehydratase family)
Supercontig_1.104_MVLG_06207_7sp	-475,19827	-473,62369	3,14916	0,79291	NS	0	[]	[]	[]	hypothetical protein	PF03073.8	TspO_MBR(TspO/MBR family)
Supercontig_1.15_MVLG_02055_7sp	-603,90644	-603,90644	0	0	NS	0	[]	[]	[]	hypothetical protein	TIGR00322	TIGR00322(diphth2_R: diphthamide biosynthesis enzyme Dph1/Dph2 domain)
Supercontig_1.14_MVLG_02029_7sp	-1989,6989	-1989,5571	0,28346	0,13214	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.5_MVLG_00929_6sp	-836,61236	-835,63758	1,94956	0,62272	NS	0	[]	[]	[]	hypothetical protein	PF05769.4	DUF837(Protein of unknown function (DUF837))
Supercontig_1.1_MVLG_00083_6sp	-655,54037	-655,54037	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00967.10	Barwin(Barwin family)
Supercontig_1.38_MVLG_03819_8sp	-1028,4647	-1028,4647	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00153.20	Mito_carr(Mitochondrial carrier protein)
Supercontig_1.83_MVLG_05735_7sp	-537,9125	-537,82136	0,18228	0,08711	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.24_MVLG_02864_11sp	-759,11728	-757,12006	3,99444	0,86429	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.135_MVLG_06631_8sp	-769,59221	-769,59221	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.74_MVLG_05458_7sp	-641,24255	-641,24255	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.60_MVLG_04942_9sp	-1057,227	-1057,227	0	0	NS	0	[]	[]	[]	hypothetical protein	PF06609.6	TRI12(Fungal trichothecene efflux pump (TRI12))
Supercontig_1.19_MVLG_02447_10sp	-713,73299	-713,51474	0,4365	0,19608	NS	0	[]	[]	[]	hypothetical protein	PF00580.14	UvrD-helicase(UvrD/REP helicase)
Supercontig_1.22_MVLG_02753_12sp	-572,84272	-571,63474	2,41596	0,7012	NS	0	[]	[]	[]	hypothetical protein	PF02985.15	HEAT(HEAT repeat)

Supercontig_1.18_MVLG_02425_10sp	-1013,6907	-1012,9782	1,4249	0,50956	NS	0	[]	[]	[]	hypothetical protein	PF00083.17	Sugar_tr(Sugar (and other) transporter)
Supercontig_1.8_MVLG_01375_8sp	-723,90296	-723,56178	0,68236	0,28907	NS	0	[]	[]	[]	hypothetical protein	PF08510.5	PIG-P(PIG-P)
Supercontig_1.15_MVLG_02150_8sp	-487,33048	-487,3304	0,00016	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF04401.7	DUF540(Protein of unknown function (DUF540))
Supercontig_1.10_MVLG_01661_8sp	-653,74248	-653,38859	0,70778	0,29805	NS	0	[]	[]	[]	hypothetical protein	PF07690.9	MFS_1(Major Facilitator Superfamily)
Supercontig_1.46_MVLG_04260_6sp	-481,80193	-481,80178	0,0003	0,00015	NS	0	[]	[]	[]	arginase	PF00491.14	Arginase(Arginase family)
Supercontig_1.84_MVLG_05759_11sp	-570,70204	-570,52761	0,34886	0,16006	NS	0	[]	[]	[]	hypothetical protein	PF00035.18	dsrm(Double-stranded RNA binding motif)
Supercontig_1.5_MVLG_00935_10sp	-326,90395	-326,90354	0,00082	0,00041	NS	0	[]	[]	[]	ubiquitin-conjugating enzyme E2 2	PF00179.19	UQ_con(Ubiquitin-conjugating enzyme)
Supercontig_1.4_MVLG_00780_7sp	-1410,0593	-1407,7901	4,53828	0,8966	NS	0	[]	[]	[]	hypothetical protein	PF00023.23	Ank(Ankyrin repeat)
Supercontig_1.113_MVLG_06340_6sp	-402,95532	-402,95532	0	0	NS	0	[]	[]	[]	hypothetical protein	PF09138.4	Urm1(Urm1 (Ubiquitin related modifier))
Supercontig_1.98_MVLG_06102_6sp	-354,83244	-354,60727	0,45034	0,20162	NS	0	[]	[]	[]	hypothetical protein	PF00076.15	RRM_1(RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain))
Supercontig_1.23_MVLG_02797_7sp	-2114,5641	-2114,5641	0	0	NS	0	[]	[]	[]	hypothetical protein	PF07713.6	DUF1604(Protein of unknown function (DUF1604))
Supercontig_1.22_MVLG_02706_7sp	-637,59571	-637,59539	0,00064	0,00032	NS	0	[]	[]	[]	hypothetical protein	PF00106.18	adh_short(short chain dehydrogenase)
Supercontig_1.83_MVLG_05751_8sp	-300,24267	-300,24246	0,00042	0,00021	NS	0	[]	[]	[]	hypothetical protein	PF04091.5	Sec15(Exocyst complex subunit Sec15-like)
Supercontig_1.121_MVLG_06445_10sp	-747,29903	-746,56057	1,47692	0,52215	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.27_MVLG_03094_11sp	-478,73991	-478,73991	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00172.11	Zn_clus(Fungal Zn(2)-Cys(6) binuclear cluster domain)
Supercontig_1.77_MVLG_05559_11sp	-662,74032	-662,74027	0,00016	0,00016	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.156_MVLG_06835_7sp	-1844,6575	-1843,9561	1,40268	0,50408	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.68_MVLG_05245_10sp	-669,67463	-669,61935	0,11056	0,05378	NS	0	[]	[]	[]	hypothetical protein	PF04641.5	Rtf2(Replication termination factor 2)
Supercontig_1.14_MVLG_01998_6sp	-1706,4994	-1706,4994	0	0	NS	0	[]	[]	[]	phosphatidylinositol 3-kinase	PF00454.20	PI3_PI4_kinase(Phosphatidylinositol 3- and 4-kinase)
Supercontig_1.56_MVLG_04750_10sp	-539,45338	-539,4533	0,00016	0,00016	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.5_MVLG_00934_7sp	-1114,7954	-1113,163	3,26472	0,80453	NS	0	[]	[]	[]	hypothetical protein	PF03583.7	LIP(Secretory lipase)
Supercontig_1.13_MVLG_01904_9sp	-697,43045	-696,864	1,1329	0,43246	NS	0	[]	[]	[]	hypothetical protein	PF10282.2	Muc_lac_enz(3-carboxy-cis,cis-muconate lactonizing enzyme)
Supercontig_1.18_MVLG_02361_7sp	-1064,0008	-1064,0008	0	0	NS	0	[]	[]	[]	hypothetical protein	TIGR01930	TIGR01930(AcCoA-C-Actrans: acetyl-CoA C-acetyltransferase)
Supercontig_1.8_MVLG_01390_8sp	-286,08251	-286,08238	0,00026	0,00013	NS	0	[]	[]	[]	hypothetical protein	PF00701.15	DHDPS(Dihydrodipicolinate synthetase family)

Supercontig_1.7_MVLG_01235_9sp	-373,43592	-373,43554	0,00076	0,00038	NS	0	[]	[]	[]	60S ribosomal protein L23	PF00238.12	Ribosomal_L14(Ribosomal protein L14p/L23e)
Supercontig_1.120_MVLG_06422_9sp	-1009,1263	-1009,1263	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.2_MVLG_00340_6sp	-734,87859	-734,85995	0,03728	0,01847	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.96_MVLG_06043_9sp	-973,91756	-973,91756	0	0	NS	0	[]	[]	[]	cytoplasmic dynein 1 heavy chain 1	PF07728.7	AAA_5(AAA domain (dynein-related subfamily))
Supercontig_1.61_MVLG_04986_9sp	-1725,1922	-1724,9121	0,56008	0,24425	NS	0	[]	[]	[]	hypothetical protein	PF07792.5	DUF1630(Protein of unknown function (DUF1630))
Supercontig_1.41_MVLG_04037_10sp	-465,93842	-465,93822	0,0004	0,0002	NS	0	[]	[]	[]	serine/threonine-protein phosphatase PP-Z	PF00149.21	Metallophos(Calcineurin-like phosphoesterase)
Supercontig_1.7_MVLG_01296_7sp	-990,09302	-989,41084	1,36436	0,49449	NS	0	[]	[]	[]	hypothetical protein	PF07690.9	MFS_1(Major Facilitator Superfamily)
Supercontig_1.6_MVLG_01132_9sp	-540,9165	-540,91641	0,00018	0,00016	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.121_MVLG_06442_9sp	-533,64401	-533,644	0,00016	0,00016	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.24_MVLG_02840_10sp	-391,33696	-391,33693	0,00016	0,00016	NS	0	[]	[]	[]	hypothetical protein	TIGR02967	TIGR02967(guan_deamin: guanine deaminase)
Supercontig_1.141_MVLG_06690_7sp	-678,89459	-678,89455	0,00016	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF01027.13	UPF0005(Uncharacterised protein family UPF0005)
Supercontig_1.63_MVLG_05085_9sp	-344,81848	-344,8181	0,00016	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF00400.25	WD40(WD domain, G-beta repeat)
Supercontig_1.28_MVLG_03182_11sp	-415,00846	-415,00837	0,00016	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF05024.8	Gpi1(N-acetylglucosaminyl transferase component (Gpi1))
Supercontig_1.24_MVLG_02850_8sp	-731,23027	-730,97005	0,52044	0,22912	NS	0	[]	[]	[]	hypothetical protein	PF01425.14	Amidase(Amidase)
Supercontig_1.73_MVLG_05432_8sp	-673,05872	-673,05841	0,00062	0,00031	NS	0	[]	[]	[]	hypothetical protein	PF02020.11	W2(eIF4-gamma/eIF5/eIF2-epsilon)
Supercontig_1.56_MVLG_04766_10sp	-518,47234	-516,5574	3,82988	0,85265	NS	0	[]	[]	[]	hypothetical protein	PF00790.12	VHS(VHS domain)
Supercontig_1.67_MVLG_05231_7sp	-808,16344	-808,16344	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00664.16	ABC_membrane(ABC transporter transmembrane region)
Supercontig_1.3_MVLG_00635_10sp	-847,2768	-847,2768	0	0	NS	0	[]	[]	[]	hypothetical protein	TIGR01494	TIGR01494(ATPase_P-type: HAD ATPase, P-type, family IC)
Supercontig_1.24_MVLG_02903_6sp	-751,28758	-751,26444	0,04628	0,02287	NS	0	[]	[]	[]	hypothetical protein	PF08613.4	Cyclin(Cyclin)
Supercontig_1.40_MVLG_03944_12sp	-557,03775	-556,55289	0,96972	0,38422	NS	0	[]	[]	[]	PEK/GCN2 protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.18_MVLG_02355_12sp	-366,5115	-366,51146	0,00016	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF07717.9	DUF1605(Domain of unknown function (DUF1605))
Supercontig_1.2_MVLG_00295_9sp	-1648,0739	-1648,0739	0	0	NS	0	[]	[]	[]	hypothetical protein	PF06920.6	Ded_cyto(Dedicator of cytokinesis)
Supercontig_1.9_MVLG_01546_9sp	-614,65107	-614,65107	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.58_MVLG_04851_12sp	-402,97294	-402,97267	0,00054	0,00027	NS	0	[]	[]	[]	hypothetical protein	PF04109.9	APG9(Autophagy protein Apg9)

Supercontig_1.65_MVLG_05127_10sp	-451,02256	-450,89383	0,25746	0,12079	NS	0	[]	[]	[]	hypothetical protein	PF03232.6	COQ7(Ubiquinone biosynthesis protein COQ7)
Supercontig_1.64_MVLG_05098_9sp	-781,00512	-781,06534	0	0	NS	0	[]	[]	[]	hypothetical protein	PF07039.4	DUF1325(SGF29 tudor-like domain)
Supercontig_1.12_MVLG_01825_10sp	-343,22551	-343,22543	0,00016	0,00016	NS	0	[]	[]	[]	aspartate aminotransferase	PF00155.14	Aminotran_1_2(Aminotransferase class I and II)
Supercontig_1.57_MVLG_04838_8sp	-339,74506	-339,74487	0,00038	0,00019	NS	0	[]	[]	[]	hypothetical protein	PF07716.8	bZIP_2(Basic region leucine zipper)
Supercontig_1.61_MVLG_04961_8sp	-562,47791	-562,43981	0,0762	0,03738	NS	0	[]	[]	[]	methylene-fatty-acyl-phospholipid synthase	PF04191.6	PEMT(Phospholipid methyltransferase)
Supercontig_1.32_MVLG_03409_8sp	-463,02017	-463,02017	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00501.21	AMP-binding(AMP-binding enzyme)
Supercontig_1.52_MVLG_04574_8sp	-610,83212	-610,83203	0,00018	0,00016	NS	0	[]	[]	[]	actin-2	PF00022.12	Actin(Actin)
Supercontig_1.6_MVLG_01058_9sp	-1078,3633	-1078,3633	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.34_MVLG_03535_6sp	-712,09609	-712,09595	0,00028	0,00014	NS	0	[]	[]	[]	hypothetical protein	PF03357.14	Snf7(Snf7)
Supercontig_1.58_MVLG_04854_9sp	-618,99179	-618,93594	0,1117	0,05432	NS	0	[]	[]	[]	hypothetical protein	PF00135.21	COesterase(Carboxylesterase)
Supercontig_1.7_MVLG_01344_11sp	-467,312	-467,312	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03151.9	TPT(Triose-phosphate Transporter family)
Supercontig_1.5_MVLG_01026_7sp	-427,01394	-426,88945	0,24898	0,11705	NS	0	[]	[]	[]	hypothetical protein	PF03144.18	GTP_EFTU_D2(Elongation factor Tu domain 2)
Supercontig_1.54_MVLG_04688_9sp	-1066,9911	-1066,9911	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.34_MVLG_03536_10sp	-750,83454	-750,83454	0	0	NS	0	[]	[]	[]	hypothetical protein	PF05970.7	DUF889(PIF1 helicase)
Supercontig_1.3_MVLG_00681_7sp	-626,6225	-626,61355	0,0179	0,00891	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.83_MVLG_05734_8sp	-234,65885	-234,65881	0,00016	0,00016	NS	0	[]	[]	[]	ribosomal protein L37ae	PF01780.12	Ribosomal_L37ae(Ribosomal L37ae protein family)
Supercontig_1.121_MVLG_06435_7sp	-1075,3307	-1075,3307	0	0	NS	0	[]	[]	[]	hypothetical protein	TIGR00879	TIGR00879(SP: MFS transporter, sugar porter (SP) family)
Supercontig_1.8_MVLG_01393_6sp	-728,75634	-728,75634	0	0	NS	0	[]	[]	[]	hypothetical protein	PF06201.6	PITH(C-terminal proteasome-interacting domain of thioredoxin-like)
Supercontig_1.70_MVLG_05318_7sp	-588,86904	-588,86898	0,00012	0,00016	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.101_MVLG_06160_9sp	-1035,5005	-1035,4646	0,0718	0,03526	NS	0	[]	[]	[]	hypothetical protein	PF12223.1	DUF3602(Protein of unknown function (DUF3602))
Supercontig_1.9_MVLG_01496_8sp	-1023,0079	-1023,0079	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00171.15	Aldedh(Aldehyde dehydrogenase family)
Supercontig_1.42_MVLG_04080_6sp	-1068,0636	-1067,7702	0,58684	0,25429	NS	0	[]	[]	[]	hypothetical protein	TIGR00446	TIGR00446(nop2p: NOL1/NOP2/sun family putative RNA methylase)
Supercontig_1.1_MVLG_00040_8sp	-285,38083	-285,38054	0,00058	0,00029	NS	0	[]	[]	[]	transitional endoplasmic reticulum ATPase	PF07724.7	AAA_2(AAA domain (Cdc48 subfamily))

Supercontig_1.29_MVLG_03217_10sp	-565,75079	-565,75059	0,0004	0,0002	NS	0	[]	[]	[]	ATP-citrate synthase	PF02629.12	CoA_binding(CoA binding domain)
Supercontig_1.6_MVLG_01173_10sp	-826,43064	-826,43058	0,00012	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF03016.8	Exostosin(Exostosin family)
Supercontig_1.16_MVLG_02227_6sp	-822,20384	-822,20384	0	0	NS	0	[]	[]	[]	coatomer subunit alpha	PF06957.4	COPI_C(Coatomer (COPI) alpha subunit C-terminus)
Supercontig_1.5_MVLG_00982_6sp	-1343,3426	-1343,0493	0,5866	0,2542	NS	0	[]	[]	[]	hypothetical protein	PF00097.18	zf-C3HC4(Zinc finger, C3HC4 type (RING finger))
Supercontig_1.8_MVLG_01455_8sp	-445,87741	-445,4689	0,81702	0,33536	NS	0	[]	[]	[]	hypothetical protein	PF02045.8	CBFB_NFYA(CCAAT-binding transcription factor (CBF-B/NF-YA) subunit B)
Supercontig_1.34_MVLG_03571_7sp	-475,06367	-475,06358	0,00018	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF01329.12	Pterin_4a(Pterin 4 alpha carbinolamine dehydratase)
Supercontig_1.8_MVLG_01388_7sp	-361,92673	-360,04031	3,77284	0,84839	NS	0	[]	[]	[]	hypothetical protein	PF10521.2	DUF2454(Protein of unknown function (DUF2454))
Supercontig_1.1_MVLG_00086_12sp	-359,76842	-359,76824	0,00036	0,00018	NS	0	[]	[]	[]	hypothetical protein	PF00226.24	DnaJ(DnaJ domain)
Supercontig_1.96_MVLG_06033_11sp	-348,42065	-348,42048	0,00034	0,00017	NS	0	[]	[]	[]	hypothetical protein	PF00400.25	WD40(WD domain, G-beta repeat)
Supercontig_1.18_MVLG_02429_10sp	-852,56544	-852,52424	0,0824	0,04036	NS	0	[]	[]	[]	hypothetical protein	PF04851.8	ResIII(Type III restriction enzyme, res subunit)
Supercontig_1.16_MVLG_02186_9sp	-630,10923	-629,74695	0,72456	0,30391	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.24_MVLG_02859_12sp	-946,61808	-946,61808	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00560.26	LRR_1(Leucine Rich Repeat)
Supercontig_1.5_MVLG_00955_10sp	-636,52796	-636,52796	0	0	NS	0	[]	[]	[]	hypothetical protein	PF07719.10	TPR_2(Tetratricopeptide repeat)
Supercontig_1.5_MVLG_00893_7sp	-986,88665	-986,88661	0,00016	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF01585.16	G-patch(G-patch domain)
Supercontig_1.56_MVLG_04796_9sp	-465,83441	-465,39943	0,86996	0,35272	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.19_MVLG_02512_10sp	-508,74012	-508,74012	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.46_MVLG_04247_10sp	-637,14585	-637,14564	0,00042	0,00021	NS	0	[]	[]	[]	hypothetical protein	PF00571.21	CBS(CBS domain)
Supercontig_1.8_MVLG_01395_7sp	-750,30779	-748,97782	2,65994	0,73551	NS	0	[]	[]	[]	hypothetical protein	PF06413.4	Neugrin(Neugrin)
Supercontig_1.12_MVLG_01800_9sp	-1533,5117	-1530,4167	6,18996	0,95472	**	0	[]	[]	[]	hypothetical protein	PF12234.1	Rav1p_C(RAVE protein 1 C terminal)
Supercontig_1.41_MVLG_04023_10sp	-621,19275	-620,9109	0,5637	0,24561	NS	0	[]	[]	[]	hypothetical protein	PF01652.11	IF4E(Eukaryotic initiation factor 4E)
Supercontig_1.128_MVLG_06556_11sp	-520,83758	-520,03345	1,60826	0,55252	NS	0	[]	[]	[]	hypothetical protein	PF01661.14	Macro(Macro domain)
Supercontig_1.92_MVLG_05954_9sp	-332,84427	-332,69992	0,2887	0,13442	NS	0	[]	[]	[]	hypothetical protein	PF04749.10	PLAC8(PLAC8 family)
Supercontig_1.99_MVLG_06105_12sp	-468,75205	-468,75189	0,00032	0,00016	NS	0	[]	[]	[]	hypothetical protein	TIGR00133	TIGR00133(gatB: aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase, B subunit)
Supercontig_1.15_MVLG_02102_11sp	-421,34966	-421,34966	0	0	NS	0	[]	[]	[]	hypothetical protein	TIGR00578	TIGR00578(ku70: ATP-dependent DNA helicase ii, 70 kDa subunit (ku70))

Supercontig_1.117_MVLG_06395_10sp	-660,06894	-660,02931	0,07926	0,03886	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.1_MVLG_00027_6sp	-656,52873	-655,63249	1,79248	0,5919	NS	0	[]	[]	[]	hypothetical protein	PF00098.16	zf-CCHC(Zinc knuckle)
Supercontig_1.85_MVLG_05803_6sp	-283,83152	-283,78868	0,08568	0,04194	NS	0	[]	[]	[]	hypothetical protein	PF08315.5	cwf18(cwf18 pre-mRNA splicing factor)
Supercontig_1.2_MVLG_00356_10sp	-765,74261	-765,66099	0,16324	0,07838	NS	0	[]	[]	[]	hypothetical protein	PF03908.6	Sec20(Sec20)
Supercontig_1.116_MVLG_06377_6sp	-736,87308	-736,87308	0	0	NS	0	[]	[]	[]	mitochondrial-processing peptidase subunit beta	PF00675.13	Peptidase_M16(Insulinase (Peptidase family M16))
Supercontig_1.1_MVLG_00156_9sp	-800,31575	-800,31142	0,00866	0,00432	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.1_MVLG_00092_11sp	-388,97288	-388,91184	0,12208	0,05921	NS	0	[]	[]	[]	hypothetical protein	PF00226.24	DnaJ(DnaJ domain)
Supercontig_1.104_MVLG_06209_10sp	-785,33155	-785,33136	0,00038	0,00019	NS	0	[]	[]	[]	hypothetical protein	PF00454.20	PI3_PI4_kinase(Phosphatidylinositol 3- and 4-kinase)
Supercontig_1.9_MVLG_01567_7sp	-888,55537	-888,55508	0,00058	0,00029	NS	0	[]	[]	[]	hypothetical protein	PF00107.19	ADH_zinc_N(Zinc-binding dehydrogenase)
Supercontig_1.3_MVLG_00588_10sp	-441,25192	-440,45383	1,59618	0,54981	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.15_MVLG_02064_7sp	-624,86167	-624,50061	0,72212	0,30306	NS	0	[]	[]	[]	hypothetical protein	PF01435.11	Peptidase_M48(Peptidase family M48)
Supercontig_1.69_MVLG_05291_11sp	-759,09744	-759,09735	0,00018	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF11875.1	DUF3395(Domain of unknown function (DUF3395))
Supercontig_1.54_MVLG_04692_8sp	-1112,9691	-1112,7335	0,47108	0,20986	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.98_MVLG_06081_10sp	-894,29249	-893,96743	0,65012	0,27752	NS	0	[]	[]	[]	hypothetical protein	PF01433.13	Peptidase_M1(Peptidase family M1)
Supercontig_1.63_MVLG_05070_8sp	-1137,1932	-1137,1932	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02012.13	BNR(BNR/Asp-box repeat)
Supercontig_1.107_MVLG_06245_8sp	-559,55282	-559,30774	0,49016	0,21736	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.26_MVLG_03050_11sp	-369,06639	-368,99914	0,1345	0,06504	NS	0	[]	[]	[]	hypothetical protein	PF00172.11	Zn_clus(Fungal Zn(2)-Cys(6) binuclear cluster domain)
Supercontig_1.1_MVLG_00190_7sp	-481,85921	-481,85841	0,0016	0,0008	NS	0	[]	[]	[]	small subunit ribosomal protein S7e	PF01251.11	Ribosomal_S7e(Ribosomal protein S7e)
Supercontig_1.1_MVLG_00049_10sp	-511,11182	-511,08119	0,06126	0,03017	NS	0	[]	[]	[]	hypothetical protein	PF00293.21	NUDIX(NUDIX domain)
Supercontig_1.75_MVLG_05498_8sp	-2053,9796	-2053,9796	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.23_MVLG_02806_12sp	-681,40269	-677,22899	8,3474	0,9846	**	0	[]	[]	[]	hypothetical protein	PF00447.10	HSF_DNA-bind(HSF-type DNA-binding)
Supercontig_1.93_MVLG_05974_10sp	-769,93345	-769,93345	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01590.19	GAF(GAF domain)
Supercontig_1.41_MVLG_03975_6sp	-365,45988	-365,45942	0,00092	0,00046	NS	0	[]	[]	[]	histone	PF00125.17	Histone(Core histone H2A/H2B/H3/H4)
Supercontig_1.34_MVLG_03567_11sp	-360,48642	-360,27727	0,4183	0,18873	NS	0	[]	[]	[]	hypothetical protein	PF00241.13	Cofilin_ADF(Cofilin/tropomyosin-type actin-binding protein)

Supercontig_1.77_MVLG_05548_11sp	-445,07277	-443,28734	3,57086	0,83228	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.28_MVLG_03187_10sp	-544,24022	-544,24022	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.50_MVLG_04458_8sp	-370,10197	-370,09128	0,02138	0,01063	NS	0	[]	[]	[]	proteasome subunit beta type-7	PF12465.1	Pr_beta_C(Proteasome beta subunits C terminal)
Supercontig_1.101_MVLG_06152_10sp	-315,4448	-315,44465	0,0003	0,00015	NS	0	[]	[]	[]	hypothetical protein	PF08566.3	Pam17(Mitochondrial import protein Pam17)
Supercontig_1.1_MVLG_00079_11sp	-502,74169	-502,68195	0,11948	0,05799	NS	0	[]	[]	[]	hypothetical protein	PF08618.3	Opi1(Transcription factor Opi1)
Supercontig_1.20_MVLG_02602_6sp	-1007,1052	-1006,7488	0,71272	0,29978	NS	0	[]	[]	[]	hypothetical protein	PF01151.11	ELO(GNS1/SUR4 family)
Supercontig_1.15_MVLG_02054_7sp	-1049,0554	-1048,9485	0,2138	0,10138	NS	0	[]	[]	[]	hypothetical protein	PF05653.7	DUF803(Protein of unknown function (DUF803))
Supercontig_1.80_MVLG_05637_8sp	-1712,3932	-1712,3932	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03208.12	PRA1(PRA1 family protein)
Supercontig_1.28_MVLG_03154_11sp	-704,29625	-704,29625	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01189.10	Nol1_Nop2_Fmu(NOL1/NOP2/sun family)
Supercontig_1.14_MVLG_02042_9sp	-683,20347	-683,20347	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00012.13	HSP70(Hsp70 protein)
Supercontig_1.69_MVLG_05302_9sp	-523,06232	-523,06232	0	0	NS	0	[]	[]	[]	hypothetical protein	PF07716.8	bZIP_2(Basic region leucine zipper)
Supercontig_1.69_MVLG_05298_10sp	-2202,2269	-2202,2269	0	0	NS	0	[]	[]	[]	hypothetical protein	PF08302.4	tRNA_lig_CPD(Fungal tRNA ligase phosphodiesterase domain)
Supercontig_1.25_MVLG_02956_11sp	-674,05462	-674,05462	0	0	NS	0	[]	[]	[]	hypothetical protein	PF05158.5	RNA_pol_Rpc34(RNA polymerase Rpc34 subunit)
Supercontig_1.25_MVLG_02938_12sp	-401,94558	-401,92133	0,0485	0,02396	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.67_MVLG_05200_6sp	-1132,3958	-1132,3958	0	0	NS	0	[]	[]	[]	hypothetical protein	TIGR00727	TIGR00727(ISP4_OPT: small oligopeptide transporter, OPT family)
Supercontig_1.2_MVLG_00422_6sp	-1121,8058	-1121,8018	0,00794	0,00396	NS	0	[]	[]	[]	hypothetical protein	PF04468.5	PSP1(PSP1 C-terminal conserved region)
Supercontig_1.100_MVLG_06135_12sp	-392,4438	-392,4438	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01302.18	CAP_GLY(CAP-Gly domain)
Supercontig_1.6_MVLG_01081_6sp	-937,37442	-937,37442	0	0	NS	0	[]	[]	[]	hypothetical protein	PF06283.4	ThuA(Trehalose utilisation)
Supercontig_1.116_MVLG_06379_11sp	-777,71365	-777,71365	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03328.7	HpcH_HpaI(HpcH/HpaI aldolase/citrate lyase family)
Supercontig_1.3_MVLG_00492_9sp	-576,07467	-575,36115	1,42704	0,51008	NS	0	[]	[]	[]	hypothetical protein	PF08242.5	Methyltransf_12(Methyltransferase domain)
Supercontig_1.30_MVLG_03307_12sp	-627,29596	-627,29595	0,00016	0,00016	NS	0	[]	[]	[]	hypothetical protein	TIGR00756	TIGR00756(PPR: pentatricopeptide repeat domain)
Supercontig_1.47_MVLG_04327_10sp	-481,23231	-480,38278	1,69906	0,57238	NS	0	[]	[]	[]	hypothetical protein	PF01545.14	Cation_efflux(Cation efflux family)
Supercontig_1.24_MVLG_02830_11sp	-569,37876	-566,36087	6,03578	0,9511	**	0	[]	[]	[]	hypothetical protein	PF03770.9	IPK(Inositol polyphosphate kinase)
Supercontig_1.7_MVLG_01334_9sp	-452,27369	-451,79279	0,9618	0,38177	NS	0	[]	[]	[]	hypothetical protein	PF05057.7	DUF676(Putative serine esterase (DUF676))

Supercontig_1.57_MVLG_04835_10sp	-473,30024	-473,29981	0,00086	0,00043	NS	0	[]	[]	[]	ubiquitin-activating enzyme E1 C	PF10585.2	UBA_e1_thiolCys(Ubiquitin-activating enzyme active site)
Supercontig_1.47_MVLG_04340_8sp	-657,61757	-657,61757	0	0	NS	0	[]	[]	[]	guanine nucleotide-binding protein subunit beta-like protein	PF00400.25	WD40(WD domain, G-beta repeat)
Supercontig_1.30_MVLG_03316_12sp	-597,60283	-597,60283	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.12_MVLG_01826_11sp	-494,33817	-493,64085	1,39464	0,50208	NS	0	[]	[]	[]	hypothetical protein	PF00664.16	ABC_membrane(ABC transporter transmembrane region)
Supercontig_1.15_MVLG_02065_7sp	-370,69047	-370,69037	0,0002	0,00016	NS	0	[]	[]	[]	hypothetical protein	TIGR00311	TIGR00311(aIF-2beta: putative translation initiation factor aIF-2, beta subunit)
Supercontig_1.17_MVLG_02267_7sp	-1029,1285	-1028,873	0,511	0,22547	NS	0	[]	[]	[]	hypothetical protein	PF10516.2	SHNi-TPR(SHNi-TPR)
Supercontig_1.116_MVLG_06383_6sp	-386,02639	-384,35413	3,34452	0,81218	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.3_MVLG_00565_11sp	-834,83509	-834,83509	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00400.25	WD40(WD domain, G-beta repeat)
Supercontig_1.24_MVLG_02890_9sp	-732,46988	-731,36849	2,20278	0,66759	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.140_MVLG_06673_10sp	-501,98056	-501,43884	1,08344	0,41825	NS	0	[]	[]	[]	hypothetical protein	PF08561.3	Ribosomal_L37(Mitochondrial ribosomal protein L37)
Supercontig_1.7_MVLG_01323_7sp	-559,13637	-559,00324	0,26626	0,12465	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.24_MVLG_02839_10sp	-520,94159	-520,94149	0,0002	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF00787.17	PX(PX domain)
Supercontig_1.44_MVLG_04139_8sp	-1329,5478	-1329,4655	0,16478	0,07909	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.140_MVLG_06686_9sp	-463,55447	-463,55447	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00400.25	WD40(WD domain, G-beta repeat)
Supercontig_1.41_MVLG_04009_8sp	-473,75272	-473,75272	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.65_MVLG_05138_9sp	-1189,7114	-1189,7114	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.54_MVLG_04691_10sp	-570,87079	-570,15379	1,434	0,51179	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.22_MVLG_02743_8sp	-472,32878	-472,32873	0,00016	0,00016	NS	0	[]	[]	[]	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 9	PF07993.5	NAD_binding_4(Male sterility protein)
Supercontig_1.8_MVLG_01467_7sp	-472,51515	-472,51515	0	0	NS	0	[]	[]	[]	hypothetical protein	PF11969.1	DcpS_C(Scavenger mRNA decapping enzyme C-term binding)
Supercontig_1.4_MVLG_00759_6sp	-744,92639	-744,60166	0,64946	0,27728	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.100_MVLG_06141_9sp	-467,51571	-467,51571	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.9_MVLG_01566_6sp	-738,73269	-738,15259	1,1602	0,44016	NS	0	[]	[]	[]	adenosine deaminase	PF00962.15	A_deaminase(Adenosine/AMP deaminase)

Supercontig_1.4_MVLG_00789_9sp	-1353,4301	-1351,6072	3,64576	0,83844	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.100_MVLG_06136_9sp	-775,72877	-775,59782	0,2619	0,12274	NS	0	[]	[]	[]	glutamate-cysteine ligase catalytic subunit	PF03074.9	GCS(Glutamate-cysteine ligase)
Supercontig_1.18_MVLG_02422_10sp	-626,95539	-626,92215	0,06648	0,03269	NS	0	[]	[]	[]	hypothetical protein	PF00171.15	Aldedh(Aldehyde dehydrogenase family)
Supercontig_1.63_MVLG_05051_8sp	-841,3863	-840,81582	1,14096	0,43475	NS	0	[]	[]	[]	GMP synthase	PF03054.9	tRNA_Me_trans(tRNA methyl transferase)
Supercontig_1.33_MVLG_03479_8sp	-1595,918	-1592,8225	6,19104	0,95475	**	0	[]	[]	[]	hypothetical protein	PF00067.15	p450(Cytochrome P450)
Supercontig_1.52_MVLG_04588_7sp	-1034,1803	-1034,1803	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.31_MVLG_03356_7sp	-606,65658	-605,44618	2,4208	0,70192	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.70_MVLG_05332_9sp	-970,2785	-968,65695	3,2431	0,80241	NS	0	[]	[]	[]	hypothetical protein	PF12612.1	TFCD_C(Tubulin folding cofactor D C terminal)
Supercontig_1.8_MVLG_01392_7sp	-352,99418	-352,9941	0,00016	0,00016	NS	0	[]	[]	[]	mandelate racemase	PF01188.14	MR_MLE(Mandelate racemase / muconate lactonizing enzyme, C-terminal domain)
Supercontig_1.40_MVLG_03966_9sp	-377,82339	-377,82339	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.41_MVLG_03978_8sp	-608,29709	-608,29709	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03985.6	Paf1(Paf1)
Supercontig_1.2_MVLG_00409_7sp	-567,60217	-567,22735	0,74964	0,31259	NS	0	[]	[]	[]	hypothetical protein	PF07876.5	Dabb(Stress responsive A/B Barrel Domain)
Supercontig_1.19_MVLG_02467_6sp	-937,25627	-937,25627	0	0	NS	0	[]	[]	[]	hypothetical protein	PF05786.7	Barren(Barren protein)
Supercontig_1.1_MVLG_00196_6sp	-480,01781	-480,01764	0,00034	0,00017	NS	0	[]	[]	[]	hypothetical protein	PF11176.1	DUF2962(Protein of unknown function (DUF2962))
Supercontig_1.8_MVLG_01370_11sp	-450,78925	-450,78924	0,00016	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF02517.9	Abi(CAAX amino terminal protease family)
Supercontig_1.2_MVLG_00328_9sp	-613,58817	-613,58817	0	0	NS	0	[]	[]	[]	hypothetical protein	PF08616.3	SPB_interacting(Spindle pole body interacting protein)
Supercontig_1.38_MVLG_03771_9sp	-436,20398	-436,20398	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.15_MVLG_02092_8sp	-730,3955	-730,3955	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00702.19	Hydrolase(haloacid dehalogenase-like hydrolase)
Supercontig_1.123_MVLG_06470_9sp	-1134,2565	-1133,9376	0,63774	0,27303	NS	0	[]	[]	[]	hypothetical protein	PF00172.11	Zn_clus(Fungal Zn(2)-Cys(6) binuclear cluster domain)
Supercontig_1.83_MVLG_05729_10sp	-570,50342	-570,50328	0,00028	0,00014	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.9_MVLG_01570_6sp	-310,79887	-309,63037	2,337	0,68917	NS	0	[]	[]	[]	ATP-dependent RNA helicase DBP5	PF00270.22	DEAD(DEAD/DEAH box helicase)
Supercontig_1.154_MVLG_06805_9sp	-372,81792	-372,47721	0,68142	0,28873	NS	0	[]	[]	[]	hypothetical protein	PF00179.19	UQ_con(Ubiquitin-conjugating enzyme)
Supercontig_1.110_MVLG_06297_7sp	-620,6568	-620,6568	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01590.19	GAF(GAF domain)
Supercontig_1.13_MVLG_01972_7sp	-1708,4391	-1708,4148	0,04854	0,02398	NS	0	[]	[]	[]	hypothetical protein	PF00179.19	UQ_con(Ubiquitin-conjugating enzyme)
Supercontig_1.47_MVLG_04343_9sp	-638,90291	-637,76191	2,282	0,6805	NS	0	[]	[]	[]	non-B type DNA binding protein	PF00505.12	HMG_box(HMG (high mobility group) box)

Supercontig_1.96_MVLG_06038_9sp	-760,70628	-760,70582	0,00092	0,00046	NS	0	[]	[]	[]	hypothetical protein	PF01315.15	Ald_Xan_dh_C(Aldehyde oxidase and xanthine dehydrogenase, a/b hammerhead domain)
Supercontig_1.3_MVLG_00587_10sp	-411,14949	-410,53281	1,23336	0,46027	NS	0	[]	[]	[]	hypothetical protein	PF04153.11	NOT2_3_5(NOT2 / NOT3 / NOT5 family)
Supercontig_1.18_MVLG_02348_10sp	-516,60252	-516,30306	0,59892	0,25878	NS	0	[]	[]	[]	hypothetical protein	PF01062.14	Bestrophin(Bestrophin)
Supercontig_1.97_MVLG_06070_6sp	-570,96796	-570,96779	0,00034	0,00017	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.10_MVLG_01612_10sp	-725,34699	-725,34699	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02714.8	DUF221(Domain of unknown function DUF221)
Supercontig_1.74_MVLG_05471_10sp	-580,26231	-580,26231	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.6_MVLG_01109_10sp	-329,94919	-329,95086	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02201.11	SWIB(SWIB/MDM2 domain)
Supercontig_1.45_MVLG_04234_9sp	-808,8999	-808,8999	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00005.20	ABC_tran(ABC transporter)
Supercontig_1.12_MVLG_01834_7sp	-487,16073	-487,16058	0,0003	0,00015	NS	0	[]	[]	[]	hypothetical protein	PF00248.14	Aldo_ket_red(Aldo/keto reductase family)
Supercontig_1.35_MVLG_03591_7sp	-471,53874	-471,5387	0,00016	0,00016	NS	0	[]	[]	[]	mitochondrial DNA replication protein YHM2	PF00153.20	Mito_carr(Mitochondrial carrier protein)
Supercontig_1.5_MVLG_00998_10sp	-349,28594	-349,28553	0,00082	0,00041	NS	0	[]	[]	[]	hypothetical protein	PF08154.5	NLE(NLE (NUC135) domain)
Supercontig_1.34_MVLG_03521_10sp	-990,87851	-990,61067	0,53568	0,23497	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.31_MVLG_03379_8sp	-611,46532	-611,46532	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.36_MVLG_03665_8sp	-648,21522	-647,22847	1,9735	0,62721	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.5_MVLG_00986_11sp	-394,90005	-394,90005	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.107_MVLG_06246_7sp	-793,76349	-793,37574	0,7755	0,32142	NS	0	[]	[]	[]	hypothetical protein	PF00091.18	Tubulin(Tubulin/FtsZ family, GTPase domain)
Supercontig_1.11_MVLG_01718_9sp	-532,32265	-532,32265	0	0	NS	0	[]	[]	[]	hypothetical protein	PF10394.2	Hat1_N(Histone acetyl transferase HAT1 N-terminus)
Supercontig_1.5_MVLG_00994_10sp	-410,23788	-409,14445	2,18686	0,66493	NS	0	[]	[]	[]	hypothetical protein	PF11969.1	DcpS_C(Scavenger mRNA decapping enzyme C-term binding)
Supercontig_1.59_MVLG_04919_11sp	-1304,7227	-1304,0226	1,4001	0,50344	NS	0	[]	[]	[]	hypothetical protein	PF06371.6	Drf_GBD(Diaphanous GTPase-binding Domain)
Supercontig_1.27_MVLG_03092_9sp	-540,85451	-539,67348	2,36206	0,69304	NS	0	[]	[]	[]	hypothetical protein	PF07732.8	Cu-oxidase_3(Multicopper oxidase)
Supercontig_1.28_MVLG_03206_6sp	-1208,3777	-1208,3002	0,15504	0,07459	NS	0	[]	[]	[]	hypothetical protein	PF08320.5	PIG-X(PIG-X / PBN1)
Supercontig_1.97_MVLG_06073_7sp	-373,38114	-373,38111	0,00016	0,00016	NS	0	[]	[]	[]	U6 snRNA-associated Sm-like protein LSm3	PF01423.15	LSM(LSM domain)
Supercontig_1.47_MVLG_04314_10sp	-750,32337	-750,32337	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01265.10	Cyto_heme_lyase(Cytochrome c/c1 heme lyase)

Supercontig_1.175_MVLG_06975_7sp	-369,79502	-367,43569	4,71866	0,90552	*	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.46_MVLG_04287_10sp	-654,12321	-654,12321	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.24_MVLG_02857_7sp	-1224,2745	-1224,1641	0,22092	0,10458	NS	0	[]	[]	[]	HAL protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.61_MVLG_04979_9sp	-1135,1171	-1135,1171	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.1_MVLG_00236_6sp	-647,55381	-647,55381	0	0	NS	0	[]	[]	[]	hypothetical protein	PF07690.9	MFS_1(Major Facilitator Superfamily)
Supercontig_1.6_MVLG_01080_6sp	-667,61708	-667,61708	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.109_MVLG_06282_10sp	-486,70323	-486,25374	0,89898	0,36205	NS	0	[]	[]	[]	hypothetical protein	PF00097.18	zf-C3HC4(Zinc finger, C3HC4 type (RING finger))
Supercontig_1.4_MVLG_00860_8sp	-1128,9969	-1128,8754	0,24294	0,11438	NS	0	[]	[]	[]	hypothetical protein	PF07019.5	Rab5ip(Rab5-interacting protein (Rab5ip))
Supercontig_1.23_MVLG_02803_10sp	-1260,8758	-1260,5796	0,59238	0,25635	NS	0	[]	[]	[]	hypothetical protein	PF01412.11	ArfGap(Putative GTPase activating protein for Arf)
Supercontig_1.6_MVLG_01174_11sp	-488,55918	-488,55914	0,00016	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF09612.3	HtrL_YibB(Bacterial protein of unknown function (HtrL_YibB))
Supercontig_1.10_MVLG_01641_7sp	-748,5231	-748,37987	0,28646	0,13345	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.25_MVLG_02961_7sp	-1309,6828	-1306,7504	5,86466	0,94673	*	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.41_MVLG_04007_7sp	-449,18862	-449,1885	0,00024	0,00012	NS	0	[]	[]	[]	hypothetical protein	PF04851.8	ResIII(Type III restriction enzyme, res subunit)
Supercontig_1.19_MVLG_02504_8sp	-503,08648	-503,08618	0,0006	0,0003	NS	0	[]	[]	[]	40S ribosomal protein S13	PF08069.5	Ribosomal_S13_N(Ribosomal S13/S15 N-terminal domain)
Supercontig_1.42_MVLG_04062_9sp	-345,66614	-345,66582	0,00064	0,00032	NS	0	[]	[]	[]	PLK/PLK1 protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.13_MVLG_01933_9sp	-420,01809	-420,01795	0,00028	0,00014	NS	0	[]	[]	[]	hypothetical protein	PF00557.17	Peptidase_M24(Metallopeptidase family M24)
Supercontig_1.1_MVLG_00097_7sp	-426,77021	-426,68554	0,16934	0,08118	NS	0	[]	[]	[]	hypothetical protein	PF01757.15	Acyl_transf_3(Acyltransferase family)
Supercontig_1.95_MVLG_06026_8sp	-363,70831	-363,70831	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02391.10	MoaE(MoaE protein)
Supercontig_1.61_MVLG_04993_10sp	-741,29179	-741,29179	0	0	NS	0	[]	[]	[]	hypothetical protein	PF10637.2	Ofd1_CTDD(Oxoglutarate and iron-dependent oxygenase degradation C-term)
Supercontig_1.55_MVLG_04730_6sp	-1819,0801	-1817,6272	2,90564	0,76609	NS	0	[]	[]	[]	hypothetical protein	PF10033.2	ATG13(Autophagy-related protein 13)
Supercontig_1.10_MVLG_01681_6sp	-312,89717	-312,86766	0,05902	0,02908	NS	0	[]	[]	[]	mitochondrial import inner membrane translocase subunit Tim9	PF02953.8	zf-Tim10_DDP(Tim10/DDP family zinc finger)
Supercontig_1.107_MVLG_06254_7sp	-626,9354	-626,9354	0	0	NS	0	[]	[]	[]	peptidyl-prolyl cis-trans isomerase	PF00160.14	Pro_isomerase(Cyclophilin type peptidyl-prolyl cis-trans isomerase/CLD)
Supercontig_1.6_MVLG_01110_8sp	-1353,1946	-1352,377	1,6352	0,55851	NS	0	[]	[]	[]	hypothetical protein	NA	NA

Supercontig_1.176_MVLG_06980_8sp	-424,2431	-424,2431	0	0	NS	0	[]	[]	[]	hypothetical protein	PF10270.2	MMgT(Membrane magnesium transporter)
Supercontig_1.150_MVLG_06781_11sp	-396,04728	-396,04724	0,00016	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF01636.16	APH(Phosphotransferase enzyme family)
Supercontig_1.14_MVLG_02005_7sp	-1010,9574	-1010,9572	0,00032	0,00016	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.154_MVLG_06811_8sp	-837,01034	-837,01034	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01494.12	FAD_binding_3(FAD binding domain)
Supercontig_1.104_MVLG_06211_10sp	-343,42799	-343,42799	0	0	NS	0	[]	[]	[]	histone H2A.Z	PF00125.17	Histone(Core histone H2A/H2B/H3/H4)
Supercontig_1.22_MVLG_02736_8sp	-483,1877	-483,1877	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00043.18	GST_C(Glutathione S-transferase, C-terminal domain)
Supercontig_1.24_MVLG_02879_12sp	-1193,7099	-1192,9545	1,51078	0,53017	NS	0	[]	[]	[]	CMGC/CDK/CRK7 protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.1_MVLG_00125_11sp	-381,87527	-381,87521	0,00012	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF11754.1	Velvet(Velvet factor)
Supercontig_1.19_MVLG_02462_8sp	-697,27095	-697,27076	0,00038	0,00019	NS	0	[]	[]	[]	hypothetical protein	TIGR00879	TIGR00879(SP: MFS transporter, sugar porter (SP) family)
Supercontig_1.11_MVLG_01730_9sp	-516,98547	-516,98547	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.67_MVLG_05242_10sp	-394,34854	-394,28711	0,12286	0,05958	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.14_MVLG_02013_7sp	-596,43213	-596,24917	0,36592	0,1672	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.22_MVLG_02748_7sp	-414,21488	-414,14829	0,13318	0,06442	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.45_MVLG_04190_11sp	-472,74093	-471,01653	3,4488	0,82172	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.59_MVLG_04898_9sp	-602,84033	-602,76581	0,14904	0,07181	NS	0	[]	[]	[]	fatty acid synthase	TIGR00556	TIGR00556(pantethn_trn: phosphopantethiene--protein transferase domain)
Supercontig_1.25_MVLG_02972_9sp	-674,54736	-674,54736	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04100.5	Vps53_N(Vps53-like, N-terminal)
Supercontig_1.54_MVLG_04697_8sp	-836,10463	-835,90453	0,4002	0,18135	NS	0	[]	[]	[]	hypothetical protein	PF05008.8	V-SNARE(Vesicle transport v-SNARE protein N-terminus)
Supercontig_1.98_MVLG_06098_11sp	-1090,4019	-1090,4019	0	0	NS	0	[]	[]	[]	AGC/YANK protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.24_MVLG_02876_10sp	-631,65686	-631,65686	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00534.13	Glycos_transf_1(Glycosyl transferases group 1)
Supercontig_1.16_MVLG_02179_11sp	-406,29207	-405,69847	1,1872	0,44766	NS	0	[]	[]	[]	hypothetical protein	PF00723.14	Glyco_hydro_15(Glycosyl hydrolases family 15)
Supercontig_1.10_MVLG_01665_7sp	-350,99654	-350,99646	0,00016	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF03144.18	GTP_EFTU_D2(Elongation factor Tu domain 2)
Supercontig_1.10_MVLG_01580_12sp	-456,73597	-456,73597	0	0	NS	0	[]	[]	[]	glycogen [starch] synthase	PF00534.13	Glycos_transf_1(Glycosyl transferases group 1)
Supercontig_1.107_MVLG_06240_7sp	-743,66831	-743,66831	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00560.26	LRR_1(Leucine Rich Repeat)
Supercontig_1.22_MVLG_02693_9sp	-397,81433	-397,81415	0,00036	0,00018	NS	0	[]	[]	[]	hypothetical protein	NA	NA

Supercontig_1.10_MVLG_01676_10sp	-315,83783	-315,44465	0,78636	0,32509	NS	0	[]	[]	[]	hypothetical protein	PF05721.6	PhyH(Phytanoyl-CoA dioxygenase (PhyH))
Supercontig_1.19_MVLG_02494_8sp	-723,22831	-720,96678	4,52306	0,89581	NS	0	[]	[]	[]	hypothetical protein	PF09419.3	DUF2010(Protein of unknown function)
Supercontig_1.77_MVLG_05565_10sp	-392,56786	-392,56768	0,00036	0,00018	NS	0	[]	[]	[]	hypothetical protein	PF03666.6	NPR3(Nitrogen Permease regulator of amino acid transport activity 3)
Supercontig_1.80_MVLG_05655_9sp	-403,78519	-401,46111	4,64816	0,90213	*	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.62_MVLG_05019_7sp	-605,51045	-605,5086	0,0037	0,00185	NS	0	[]	[]	[]	hypothetical protein	PF02567.9	PhzC-PhzF(Phenazine biosynthesis-like protein)
Supercontig_1.2_MVLG_00288_11sp	-360,34796	-360,34796	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00412.15	LIM(LIM domain)
Supercontig_1.99_MVLG_06107_9sp	-571,83998	-571,83983	0,0003	0,00015	NS	0	[]	[]	[]	hypothetical protein	PF04420.7	CHD5(CHD5-like protein)
Supercontig_1.49_MVLG_04407_8sp	-1725,2946	-1724,9678	0,65358	0,27876	NS	0	[]	[]	[]	hypothetical protein	PF11935.1	DUF3453(Domain of unknown function (DUF3453))
Supercontig_1.14_MVLG_02039_6sp	-421,2987	-421,29868	0,00016	0,00016	NS	0	[]	[]	[]	prefoldin, alpha subunit	TIGR00293	TIGR00293(TIGR00293: prefoldin, alpha subunit)
Supercontig_1.6_MVLG_01187_8sp	-510,53874	-510,13551	0,80646	0,33184	NS	0	[]	[]	[]	hypothetical protein	PF01566.11	Nramp(Natural resistance-associated macrophage protein)
Supercontig_1.22_MVLG_02754_7sp	-1055,8701	-1055,8701	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00096.19	zf-C2H2(Zinc finger, C2H2 type)
Supercontig_1.19_MVLG_02466_10sp	-475,32684	-475,32671	0,00026	0,00013	NS	0	[]	[]	[]	hypothetical protein	PF04161.6	Arv1(Arv1-like family)
Supercontig_1.1_MVLG_00268_10sp	-541,472	-541,472	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00191.13	Annexin(Annexin)
Supercontig_1.67_MVLG_05211_9sp	-583,07117	-582,86711	0,40812	0,18459	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.36_MVLG_03651_10sp	-370,82048	-370,29857	1,04382	0,40661	NS	0	[]	[]	[]	indoleamine 2,3-dioxygenase	PF01231.11	IDO(Indoleamine 2,3-dioxygenase)
Supercontig_1.64_MVLG_05123_9sp	-444,51564	-444,50961	0,01206	0,00601	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.140_MVLG_06685_6sp	-477,51124	-477,48576	0,05096	0,02516	NS	0	[]	[]	[]	hypothetical protein	PF07228.5	SpoIIE(Stage II sporulation protein E (SpoIIE))
Supercontig_1.19_MVLG_02513_9sp	-780,99583	-780,7513	0,48906	0,21693	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.44_MVLG_04138_8sp	-687,85784	-687,85784	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03330.11	DPBB_1(Rare lipoprotein A (RlpA)-like double-psi beta-barrel)
Supercontig_1.49_MVLG_04448_12sp	-344,04322	-344,04287	0,0007	0,00035	NS	0	[]	[]	[]	hypothetical protein	PF00036.25	efhand(EF hand)
Supercontig_1.88_MVLG_05890_7sp	-274,45646	-274,45622	0,00048	0,00024	NS	0	[]	[]	[]	26S proteasome regulatory subunit	PF00004.22	AAA(ATPase family associated with various cellular activities (AAA))
Supercontig_1.7_MVLG_01285_6sp	-386,26906	-386,26267	0,01278	0,00637	NS	0	[]	[]	[]	hypothetical protein	PF02156.8	Glyco_hydro_26(Glycosyl hydrolase family 26)
Supercontig_1.69_MVLG_05301_10sp	-858,84901	-858,84899	0,00016	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF01179.13	Cu_amine_oxid(Copper amine oxidase, enzyme domain)
Supercontig_1.30_MVLG_03291_10sp	-557,20693	-556,91471	0,58444	0,2534	NS	0	[]	[]	[]	hypothetical protein	PF04005.5	Hus1(Hus1-like protein)

Supercontig_1.65_MVLG_05146_10sp	-1576,0574	-1576,0574	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01231.11	IDO(Indoleamine 2,3-dioxygenase)
Supercontig_1.17_MVLG_02338_8sp	-705,92606	-705,92602	0,00016	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF00664.16	ABC_membrane(ABC transporter transmembrane region)
Supercontig_1.8_MVLG_01435_11sp	-538,57744	-538,57744	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.20_MVLG_02551_10sp	-463,76476	-462,61887	2,29178	0,68206	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.6_MVLG_01217_9sp	-910,00249	-909,72159	0,5618	0,2449	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.1_MVLG_00208_7sp	-568,62973	-568,62766	0,00414	0,00207	NS	0	[]	[]	[]	histone H1	PF00538.12	Linker_histone(linker histone H1 and H5 family)
Supercontig_1.22_MVLG_02735_9sp	-394,50212	-394,49735	0,00954	0,00476	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.68_MVLG_05246_10sp	-527,67601	-527,676	0,00016	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF01805.13	Surp(Surp module)
Supercontig_1.45_MVLG_04221_8sp	-919,93675	-919,93675	0,00016	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF09783.2	Vac_ImportDeg(Vacuolar import and degradation protein)
Supercontig_1.75_MVLG_05504_9sp	-737,90572	-737,90572	0,00016	0,00016	NS	0	[]	[]	[]	CDC7 protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.4_MVLG_00838_6sp	-639,60089	-639,60085	0,00016	0,00016	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.66_MVLG_05175_11sp	-503,64852	-502,81818	1,66068	0,5641	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.95_MVLG_06017_11sp	-582,56874	-581,54029	2,0569	0,64244	NS	0	[]	[]	[]	hypothetical protein	PF04851.8	ResIII(Type III restriction enzyme, res subunit)
Supercontig_1.27_MVLG_03109_9sp	-548,47663	-548,4607	0,03186	0,0158	NS	0	[]	[]	[]	hypothetical protein	PF04303.6	PrpF(PrpF protein)
Supercontig_1.61_MVLG_04984_11sp	-398,95837	-398,95837	0	0	NS	0	[]	[]	[]	hypothetical protein	PF07690.9	MFS_1(Major Facilitator Superfamily)
Supercontig_1.4_MVLG_00738_9sp	-450,09814	-450,0806	0,03508	0,01739	NS	0	[]	[]	[]	hypothetical protein	TIGR00756	TIGR00756(PPR: pentatricopeptide repeat domain)
Supercontig_1.21_MVLG_02633_10sp	-636,22434	-636,01855	0,41158	0,186	NS	0	[]	[]	[]	hypothetical protein	PF00787.17	PX(PX domain)
Supercontig_1.8_MVLG_01425_8sp	-803,95998	-803,95966	0,00064	0,00032	NS	0	[]	[]	[]	hypothetical protein	PF00664.16	ABC_membrane(ABC transporter transmembrane region)
Supercontig_1.80_MVLG_05633_11sp	-563,58764	-563,58764	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.125_MVLG_06507_6sp	-369,06902	-369,06871	0,00062	0,00031	NS	0	[]	[]	[]	60S ribosomal protein L10	PF00252.11	Ribosomal_L16(Ribosomal protein L16p/L10e)
Supercontig_1.70_MVLG_05334_9sp	-289,55568	-289,55535	0,00066	0,00033	NS	0	[]	[]	[]	glycerol-3-phosphate dehydrogenase	PF00890.17	FAD_binding_2(FAD binding domain)
Supercontig_1.48_MVLG_04398_10sp	-753,95953	-753,95895	0,00116	0,00058	NS	0	[]	[]	[]	hypothetical protein	PF00536.23	SAM_1(SAM domain (Sterile alpha motif))
Supercontig_1.20_MVLG_02604_9sp	-511,89598	-511,89583	0,0003	0,00015	NS	0	[]	[]	[]	citrate synthase	TIGR01793	TIGR01793(cit_synth_euk: citrate (Si)-synthase, eukaryotic)

Supercontig_1.2_MVLG_00477_6sp	-1106,67	-1106,5102	0,31974	0,14775	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.105_MVLG_06222_9sp	-608,77118	-607,07359	3,39518	0,81688	NS	0	[]	[]	[]	hypothetical protein	PF00561.13	Abhydrolase_1(alpha/beta hydrolase fold)
Supercontig_1.4_MVLG_00778_10sp	-382,26328	-382,26328	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.35_MVLG_03605_10sp	-876,09842	-874,93521	2,32642	0,68752	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.55_MVLG_04746_9sp	-550,64836	-550,64836	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.176_MVLG_06978_10sp	-754,72487	-754,72487	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01266.17	DAO(FAD dependent oxidoreductase)
Supercontig_1.48_MVLG_04360_6sp	-370,02528	-370,02517	0,00022	0,00011	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.50_MVLG_04485_8sp	-877,0158	-877,0158	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03124.7	EXS(EXS family)
Supercontig_1.155_MVLG_06823_12sp	-319,58665	-319,58635	0,0006	0,0003	NS	0	[]	[]	[]	hypothetical protein	PF02170.15	PAZ(PAZ domain)
Supercontig_1.5_MVLG_00897_9sp	-867,21329	-867,16968	0,08722	0,04267	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.40_MVLG_03964_6sp	-551,33393	-551,33393	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03367.6	zf-ZPR1(ZPR1 zinc-finger domain)
Supercontig_1.82_MVLG_05702_7sp	-874,33178	-874,06464	0,53428	0,23443	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.40_MVLG_03906_6sp	-804,06878	-802,23785	3,66186	0,83974	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.11_MVLG_01699_12sp	-578,96016	-578,96002	0,00028	0,00014	NS	0	[]	[]	[]	hypothetical protein	PF03357.14	Snf7(Snf7)
Supercontig_1.30_MVLG_03289_8sp	-1472,394	-1469,654	5,47998	0,93543	*	0	[]	[]	[]	hypothetical protein	PF06046.6	Sec6(Exocyst complex component Sec6)
Supercontig_1.22_MVLG_02751_7sp	-720,36181	-720,36181	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.31_MVLG_03355_9sp	-788,99959	-788,88509	0,229	0,10819	NS	0	[]	[]	[]	hypothetical protein	PF00953.14	Glycos_transf_4(Glycosyl transferase family 4)
Supercontig_1.40_MVLG_03957_10sp	-665,45153	-665,45153	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00076.15	RRM_1(RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain))
Supercontig_1.24_MVLG_02908_7sp	-673,98248	-673,89042	0,18412	0,08795	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.5_MVLG_00933_9sp	-872,68761	-871,61843	2,13836	0,65671	NS	0	[]	[]	[]	hypothetical protein	PF03583.7	LIP(Secretory lipase)
Supercontig_1.10_MVLG_01642_8sp	-906,1324	-905,81513	0,63454	0,27187	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.27_MVLG_03093_7sp	-804,33598	-804,33598	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02207.13	zf-UBR(Putative zinc finger in N-recognin (UBR box))
Supercontig_1.47_MVLG_04299_10sp	-534,85065	-534,85065	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01214.11	CK_II_beta(Casein kinase II regulatory subunit)
Supercontig_1.40_MVLG_03919_6sp	-359,49564	-359,49564	0	0	NS	0	[]	[]	[]	peptidyl-prolyl cis-trans isomerase B	PF00160.14	Pro_isomerase(Cyclophilin type peptidyl-prolyl cis-trans isomerase/CLD)
Supercontig_1.87_MVLG_05845_8sp	-466,3994	-466,3992	0,0004	0,0002	NS	0	[]	[]	[]	hypothetical protein	PF00642.17	zf-CCCH(Zinc finger C-x8-C-x5-C-x3-H type (and similar))

Supercontig_1.205_MVLG_07112_11sp	-407,70954	-405,66671	4,08566	0,87034	NS	0	[]	[]	[]	hypothetical protein	PF08321.5	PPP5(PPP5)
Supercontig_1.66_MVLG_05176_12sp	-1708,2709	-1708,0745	0,3928	0,17832	NS	0	[]	[]	[]	hypothetical protein	PF00097.18	zf-C3HC4(Zinc finger, C3HC4 type (RING finger))
Supercontig_1.62_MVLG_05008_11sp	-611,41742	-611,41378	0,00728	0,00363	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.85_MVLG_05789_8sp	-678,00538	-677,8121	0,38656	0,17575	NS	0	[]	[]	[]	hypothetical protein	PF01735.11	PLA2_B(Lysophospholipase catalytic domain)
Supercontig_1.16_MVLG_02254_12sp	-607,19173	-607,19173	0	0	NS	0	[]	[]	[]	hypothetical protein	PF11521.1	TFIIE-A_C-term(C-terminal general transcription factor TFIIE alpha)
Supercontig_1.88_MVLG_05878_8sp	-753,46271	-753,46265	0,00012	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF07250.4	Glyoxal_oxid_N(Glyoxal oxidase N-terminus)
Supercontig_1.160_MVLG_06856_9sp	-873,82975	-873,61047	0,43856	0,1969	NS	0	[]	[]	[]	hypothetical protein	PF00773.12	RNB(RNB domain)
Supercontig_1.172_MVLG_06948_7sp	-697,95045	-697,94553	0,00984	0,00491	NS	0	[]	[]	[]	hypothetical protein	PF02268.9	TFIIA_gamma_N(Transcription initiation factor IIA, gamma subunit, helical domain)
Supercontig_1.107_MVLG_06260_6sp	-992,6748	-992,6748	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.13_MVLG_01918_9sp	-386,05168	-386,0514	0,00056	0,00028	NS	0	[]	[]	[]	hypothetical protein	PF02714.8	DUF221(Domain of unknown function DUF221)
Supercontig_1.3_MVLG_00671_6sp	-779,78707	-778,83671	1,90072	0,6134	NS	0	[]	[]	[]	hypothetical protein	PF04193.7	PQ-loop(PQ loop repeat)
Supercontig_1.78_MVLG_05597_10sp	-1010,2375	-1008,8347	2,80566	0,7541	NS	0	[]	[]	[]	hypothetical protein	PF07690.9	MFS_1(Major Facilitator Superfamily)
Supercontig_1.213_MVLG_07135_9sp	-606,38597	-605,85799	1,05596	0,4102	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.4_MVLG_00786_7sp	-575,61978	-575,61978	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.14_MVLG_01990_11sp	-374,64138	-374,64128	0,0002	0,00016	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.9_MVLG_01487_7sp	-671,0869	-669,79938	2,57504	0,72405	NS	0	[]	[]	[]	hypothetical protein	PF03403.6	PAF-AH_p_II(isoform II)
Supercontig_1.202_MVLG_07090_7sp	-620,26512	-620,26512	0	0	NS	0	[]	[]	[]	fructose-bisphosphate aldolase	PF01116.13	F_bP_aldolase(Fructose-bisphosphate aldolase class-II)
Supercontig_1.45_MVLG_04233_10sp	-567,61727	-566,88293	1,46868	0,52018	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.28_MVLG_03169_9sp	-412,75306	-412,753	0,00012	0,00016	NS	0	[]	[]	[]	40S ribosomal protein S19-A	PF01090.12	Ribosomal_S19e(Ribosomal protein S19e)
Supercontig_1.50_MVLG_04478_6sp	-971,66324	-970,99805	1,33038	0,48582	NS	0	[]	[]	[]	haspin protein kinase	PF12330.1	DUF3635(Domain of unknown function (DUF3635))
Supercontig_1.45_MVLG_04229_9sp	-517,0253	-517,02511	0,00038	0,00019	NS	0	[]	[]	[]	hypothetical protein	PF10176.2	DUF2370(Protein of unknown function (DUF2370))
Supercontig_1.4_MVLG_00857_8sp	-1276,4924	-1276,4924	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.47_MVLG_04350_7sp	-825,46023	-825,46023	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.125_MVLG_06514_12sp	-373,12006	-373,12006	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00439.18	Bromodomain(Bromodomain)

Supercontig_1.48_MVLG_04364_9sp	-662,60163	-662,58931	0,02464	0,01224	NS	0	[]	[]	[]	hypothetical protein	TIGR00365	TIGR00365(TIGR00365: monothiol glutaredoxin, Grx4 family)
Supercontig_1.1_MVLG_00164_10sp	-851,29557	-849,65473	3,28168	0,80618	NS	0	[]	[]	[]	hypothetical protein	PF04851.8	ResIII(Type III restriction enzyme, res subunit)
Supercontig_1.22_MVLG_02686_9sp	-757,53337	-757,53337	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.111_MVLG_06313_6sp	-661,02586	-661,02586	0	0	NS	0	[]	[]	[]	CAMK/CAMK1 protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.6_MVLG_01165_10sp	-989,08803	-989,08794	0,00016	0,00016	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.64_MVLG_05105_9sp	-909,68237	-909,68235	0,00016	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF04130.6	Spc97_Spc98(Spc97 / Spc98 family)
Supercontig_1.1_MVLG_00046_10sp	-337,6356	-337,6356	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00036.25	efhand(EF hand)
Supercontig_1.50_MVLG_04474_10sp	-454,82262	-454,82262	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.125_MVLG_06509_11sp	-430,26921	-430,20809	0,12224	0,05929	NS	0	[]	[]	[]	hypothetical protein	PF10602.2	RPN7(26S proteasome subunit RPN7)
Supercontig_1.51_MVLG_04525_10sp	-369,54741	-369,40677	0,28128	0,1312	NS	0	[]	[]	[]	hypothetical protein	PF00107.19	ADH_zinc_N(Zinc-binding dehydrogenase)
Supercontig_1.5_MVLG_00962_7sp	-274,13036	-274,06751	0,1257	0,06092	NS	0	[]	[]	[]	hypothetical protein	PF03637.10	Mob1_phocein(Mob1/phocein family)
Supercontig_1.44_MVLG_04163_11sp	-1215,0243	-1211,2495	7,54968	0,97706	**	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.173_MVLG_06960_6sp	-1222,2714	-1222,1171	0,30856	0,14297	NS	0	[]	[]	[]	hypothetical protein	PF01053.13	Cys_Met_Meta_PP(Cys/Met metabolism PLP-dependent enzyme)
Supercontig_1.1_MVLG_00144_9sp	-827,45303	-826,17934	2,54738	0,7202	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.54_MVLG_04686_9sp	-709,48154	-709,48154	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00443.22	UCH(Ubiquitin carboxyl-terminal hydrolase)
Supercontig_1.47_MVLG_04334_11sp	-952,07273	-952,07273	0	0	NS	0	[]	[]	[]	acyl-CoA oxidase	PF02770.12	Acyl-CoA_dh_M(Acyl-CoA dehydrogenase, middle domain)
Supercontig_1.15_MVLG_02129_7sp	-925,91648	-925,72995	0,37306	0,17017	NS	0	[]	[]	[]	hypothetical protein	PF00291.18	PALP(Pyridoxal-phosphate dependent enzyme)
Supercontig_1.65_MVLG_05125_10sp	-395,0231	-395,0231	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.5_MVLG_00940_8sp	-1348,5623	-1347,5698	1,98518	0,62938	NS	0	[]	[]	[]	hypothetical protein	PF01571.14	GCV_T(Aminomethyltransferase folate-binding domain)
Supercontig_1.88_MVLG_05879_8sp	-601,11145	-600,91773	0,38744	0,17611	NS	0	[]	[]	[]	hypothetical protein	PF01266.17	DAO(FAD dependent oxidoreductase)
Supercontig_1.35_MVLG_03609_10sp	-434,14351	-434,14351	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00743.12	FMO-like(Flavin-binding monooxygenase-like)
Supercontig_1.33_MVLG_03475_7sp	-323,16496	-323,09	0,14992	0,07222	NS	0	[]	[]	[]	hypothetical protein	PF01679.10	UPF0057(Uncharacterized protein family UPF0057)
Supercontig_1.30_MVLG_03282_9sp	-1048,6889	-1048,6889	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.143_MVLG_06719_8sp	-1222,7791	-1222,7791	0	0	NS	0	[]	[]	[]	hypothetical protein	PF10288.2	DUF2392(Protein of unknown function (DUF2392))

Supercontig_1.14_MVLG_02004_10sp	-1402,6131	-1402,292	0,6422	0,27465	NS	0	[]	[]	[]	hypothetical protein	PF10294.2	Methyltransf_16(Putative methyltransferase)
Supercontig_1.36_MVLG_03637_9sp	-845,08611	-845,08611	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01529.13	zf-DHHC(DHHC zinc finger domain)
Supercontig_1.56_MVLG_04793_8sp	-490,57779	-490,57764	0,0003	0,00015	NS	0	[]	[]	[]	hypothetical protein	TIGR00879	TIGR00879(SP: MFS transporter, sugar porter (SP) family)
Supercontig_1.44_MVLG_04179_9sp	-1526,7773	-1526,7491	0,05646	0,02784	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.165_MVLG_06911_9sp	-516,66363	-516,66363	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.85_MVLG_05809_10sp	-488,13622	-488,13622	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01765.12	RRF(Ribosome recycling factor)
Supercontig_1.21_MVLG_02648_8sp	-1123,2985	-1123,2192	0,15866	0,07626	NS	0	[]	[]	[]	hypothetical protein	PF00076.15	RRM_1(RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain))
Supercontig_1.25_MVLG_02923_8sp	-524,01112	-523,95708	0,10808	0,05261	NS	0	[]	[]	[]	hypothetical protein	PF02913.12	FAD-oxidase_C(FAD linked oxidases, C-terminal domain)
Supercontig_1.24_MVLG_02843_10sp	-2150,9527	-2150,533	0,83932	0,34273	NS	0	[]	[]	[]	hypothetical protein	PF00153.20	Mito_carr(Mitochondrial carrier protein)
Supercontig_1.1_MVLG_00275_9sp	-826,89641	-822,64472	8,50338	0,98576	**	0	[]	[]	[]	hypothetical protein	PF00505.12	HMG_box(HMG (high mobility group) box)
Supercontig_1.4_MVLG_00810_10sp	-379,86597	-379,0133	1,70534	0,57372	NS	0	[]	[]	[]	hypothetical protein	PF09423.3	PhoD(PhoD-like phosphatase)
Supercontig_1.173_MVLG_06956_6sp	-388,57858	-388,57858	0	0	NS	0	[]	[]	[]	histone H2B	PF00125.17	Histone(Core histone H2A/H2B/H3/H4)
Supercontig_1.26_MVLG_03035_7sp	-791,56087	-791,56087	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00096.19	zf-C2H2(Zinc finger, C2H2 type)
Supercontig_1.5_MVLG_01047_7sp	-879,002	-879,002	0	0	NS	0	[]	[]	[]	electron-transferring-flavoprotein dehydrogenase	PF01494.12	FAD_binding_3(FAD binding domain)
Supercontig_1.73_MVLG_05415_10sp	-470,87074	-469,0852	3,57108	0,83229	NS	0	[]	[]	[]	hypothetical protein	PF09497.3	Med12(Transcription mediator complex subunit Med12)
Supercontig_1.15_MVLG_02155_11sp	-628,9092	-628,9092	0	0	NS	0	[]	[]	[]	hypothetical protein	TIGR00861	TIGR00861(MIP: MIP family channel proteins)
Supercontig_1.57_MVLG_04810_10sp	-628,20247	-628,19698	0,01098	0,00547	NS	0	[]	[]	[]	AGC protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.34_MVLG_03507_8sp	-634,48062	-634,48062	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01323.13	DSBA(DSBA-like thioredoxin domain)
Supercontig_1.42_MVLG_04086_8sp	-341,63377	-341,63335	0,00084	0,00042	NS	0	[]	[]	[]	SUMO-conjugating enzyme ubc9	PF00179.19	UQ_con(Ubiquitin-conjugating enzyme)
Supercontig_1.36_MVLG_03687_8sp	-444,3657	-444,3657	0	0	NS	0	[]	[]	[]	hypothetical protein	PF12352.1	V-SNARE_C(Snare region anchored in the vesicle membrane C-terminus)
Supercontig_1.30_MVLG_03312_12sp	-466,69924	-466,56273	0,27302	0,1276	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.49_MVLG_04450_10sp	-318,17351	-318,17341	0,0002	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF03142.8	Chitin_synth_2(Chitin synthase)
Supercontig_1.7_MVLG_01339_10sp	-451,22647	-450,92051	0,61192	0,26358	NS	0	[]	[]	[]	hypothetical protein	PF08574.3	DUF1762(Protein of unknown function (DUF1762))
Supercontig_1.161_MVLG_06865_8sp	-323,60582	-323,6057	0,00024	0,00012	NS	0	[]	[]	[]	hypothetical protein	PF00650.13	CRAL_TRIO(CRAL/TRIO domain)

Supercontig_1.48_MVLG_04358_6sp	-960,48554	-960,48554	0	0	NS	0	[]	[]	[]	hypothetical protein	PF06417.5	DUF1077(Protein of unknown function (DUF1077))
Supercontig_1.39_MVLG_03890_9sp	-528,29293	-528,29278	0,0003	0,00015	NS	0	[]	[]	[]	tRNA modification GTPase TrmE	TIGR00450	TIGR00450(mnmE_trmE_thdF: tRNA modification GTPase TrmE)
Supercontig_1.158_MVLG_06849_6sp	-520,16415	-520,16415	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.28_MVLG_03197_12sp	-578,71664	-578,71654	0,0002	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF03370.6	CBM_21(Putative phosphatase regulatory subunit)
Supercontig_1.3_MVLG_00641_8sp	-438,50381	-438,50381	0	0	NS	0	[]	[]	[]	CMGC/MAPK protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.74_MVLG_05441_11sp	-406,77085	-406,77085	0	0	NS	0	[]	[]	[]	NEDD8-conjugating enzyme UBC12	PF00179.19	UQ_con(Ubiquitin-conjugating enzyme)
Supercontig_1.34_MVLG_03540_6sp	-489,75158	-489,75153	0,00016	0,00016	NS	0	[]	[]	[]	hypothetical protein	TIGR01359	TIGR01359(UMP_CMP_kin_fam: UMP-CMP kinase family)
Supercontig_1.80_MVLG_05649_10sp	-618,87712	-618,66472	0,4248	0,19136	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.44_MVLG_04167_6sp	-470,91387	-470,91387	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.16_MVLG_02192_10sp	-810,2354	-810,23529	0,00022	0,00011	NS	0	[]	[]	[]	2-deoxy-D-gluconate 3-dehydrogenase	PF00106.18	adh_short(short chain dehydrogenase)
Supercontig_1.17_MVLG_02305_10sp	-1054,5703	-1051,272	6,59664	0,96305	**	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.57_MVLG_04806_7sp	-740,32465	-736,36072	7,92786	0,98101	**	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.16_MVLG_02215_7sp	-652,15746	-650,38516	3,5446	0,83006	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.41_MVLG_03971_11sp	-546,00798	-546,00797	0,00016	0,00016	NS	0	[]	[]	[]	acetyl-CoA carboxylase	PF00364.15	Biotin_lipoyl(Biotin-requiring enzyme)
Supercontig_1.28_MVLG_03160_8sp	-446,6084	-446,60824	0,00032	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF02265.9	S1-P1_nuclease(S1/P1 Nuclease)
Supercontig_1.56_MVLG_04791_6sp	-709,02025	-709,02025	0	0	NS	0	[]	[]	[]	hypothetical protein	PF05739.12	SNARE(SNARE domain)
Supercontig_1.23_MVLG_02783_8sp	-502,52588	-502,52588	0	0	NS	0	[]	[]	[]	hypothetical protein	TIGR00505	TIGR00505(ribA: GTP cyclohydrolase II)
Supercontig_1.139_MVLG_06665_10sp	-551,17894	-551,17894	0	0	NS	0	[]	[]	[]	deoxyhypusine hydroxylase	PF03130.9	HEAT_PBS(PBS lyase HEAT-like repeat)
Supercontig_1.57_MVLG_04802_10sp	-1177,135	-1177,135	0,00016	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF00867.11	XPG_I(XPG I-region)
Supercontig_1.181_MVLG_07004_11sp	-415,23919	-415,23901	0,00036	0,00018	NS	0	[]	[]	[]	FK506-binding protein 1	PF00254.21	FKBP_C(FKBP-type peptidyl-prolyl cis-trans isomerase)
Supercontig_1.100_MVLG_06131_12sp	-908,69152	-908,44714	0,48876	0,21681	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.75_MVLG_05486_11sp	-413,263	-413,26196	0,00208	0,00104	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.3_MVLG_00576_9sp	-864,41708	-864,39516	0,04384	0,02168	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.65_MVLG_05136_8sp	-982,42829	-982,40901	0,03856	0,0191	NS	0	[]	[]	[]	hypothetical protein	NA	NA

Supercontig_1.54_MVLG_04661_8sp	-574,08941	-573,10879	1,96124	0,62492	NS	0	[]	[]	[]	hypothetical protein	TIGR00568	TIGR00568(alkb: alkylated DNA repair protein AlkB)
Supercontig_1.16_MVLG_02221_6sp	-695,04882	-694,64917	0,7993	0,32945	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.127_MVLG_06545_10sp	-548,91059	-548,1028	1,61558	0,55416	NS	0	[]	[]	[]	hypothetical protein	PF09731.2	Mitofilin(Mitochondrial inner membrane protein)
Supercontig_1.17_MVLG_02297_10sp	-494,71416	-494,7871	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01388.14	ARID(ARID/BRIGHT DNA binding domain)
Supercontig_1.15_MVLG_02058_10sp	-227,48583	-227,48559	0,00048	0,00024	NS	0	[]	[]	[]	hypothetical protein	PF00832.13	Ribosomal_L39(Ribosomal L39 protein)
Supercontig_1.18_MVLG_02423_8sp	-354,31181	-354,31181	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.4_MVLG_00692_10sp	-942,6396	-942,55848	0,16224	0,07792	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.65_MVLG_05149_10sp	-495,96743	-495,96743	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.61_MVLG_04965_7sp	-536,91441	-536,91441	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.11_MVLG_01710_7sp	-1650,7606	-1650,6988	0,12362	0,05994	NS	0	[]	[]	[]	hypothetical protein	TIGR01494	TIGR01494(ATPase_P-type: HAD ATPase, P-type, family IC)
Supercontig_1.24_MVLG_02835_8sp	-753,61209	-753,6116	0,00098	0,00049	NS	0	[]	[]	[]	AGC/NDR/NDR protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.54_MVLG_04668_11sp	-360,72404	-360,72389	0,0003	0,00015	NS	0	[]	[]	[]	hypothetical protein	PF03798.9	TRAM_LAG1_CLN8(TLC domain)
Supercontig_1.8_MVLG_01386_8sp	-1012,326	-1012,3115	0,02886	0,01433	NS	0	[]	[]	[]	hypothetical protein	PF00867.11	XPG_I(XPG I-region)
Supercontig_1.38_MVLG_03820_8sp	-560,41293	-560,41261	0,00064	0,00032	NS	0	[]	[]	[]	hypothetical protein	PF00400.25	WD40(WD domain, G-beta repeat)
Supercontig_1.161_MVLG_06872_8sp	-1138,1958	-1138,0162	0,35926	0,16442	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.41_MVLG_04029_8sp	-297,07055	-297,07053	0,00016	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF03997.5	VPS28(VPS28 protein)
Supercontig_1.67_MVLG_05233_9sp	-326,05681	-326,05655	0,00052	0,00026	NS	0	[]	[]	[]	hypothetical protein	PF00005.20	ABC_tran(ABC transporter)
Supercontig_1.203_MVLG_07100_8sp	-416,63164	-416,63163	0,00016	0,00016	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.57_MVLG_04807_11sp	-698,62583	-698,14503	0,9616	0,38171	NS	0	[]	[]	[]	CAMKK protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.25_MVLG_02974_8sp	-404,07737	-404,07733	0,00016	0,00016	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.54_MVLG_04658_7sp	-675,93489	-675,93489	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03371.8	PRP38(PRP38 family)
Supercontig_1.77_MVLG_05564_7sp	-1000,1827	-999,3007	1,76392	0,58603	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.6_MVLG_01147_6sp	-531,09449	-529,80312	2,58274	0,72511	NS	0	[]	[]	[]	hypothetical protein	PF06212.5	GRIM-19(GRIM-19 protein)
Supercontig_1.14_MVLG_02034_9sp	-704,63352	-704,63352	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04050.7	Upf2(Up-frameshift suppressor 2)
Supercontig_1.5_MVLG_01018_9sp	-860,73006	-860,73006	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA

Supercontig_1.46_MVLG_04245_10sp	-1361,5642	-1361,4952	0,13798	0,06666	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.28_MVLG_03164_6sp	-540,5394	-540,5394	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.100_MVLG_06129_7sp	-504,60184	-504,26315	0,67738	0,2873	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.19_MVLG_02442_9sp	-746,78879	-745,30139	2,9748	0,77404	NS	0	[]	[]	[]	hypothetical protein	PF00378.13	ECH(Enoyl-CoA hydratase/isomerase family)
Supercontig_1.1_MVLG_00098_10sp	-469,35739	-469,35708	0,00062	0,00031	NS	0	[]	[]	[]	ribose-phosphate pyrophosphokinase	TIGR01251	TIGR01251(ribP_PPkin: ribose-phosphate diphosphokinase)
Supercontig_1.5_MVLG_01002_10sp	-506,81411	-506,81411	0	0	NS	0	[]	[]	[]	nicotinate phosphoribosyltransferase	TIGR01514	TIGR01514(NAPRTase: nicotinate phosphoribosyltransferase)
Supercontig_1.63_MVLG_05048_7sp	-303,12321	-303,12314	0,00014	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF08991.3	DUF1903(Domain of unknown function (DUF1903))
Supercontig_1.85_MVLG_05796_11sp	-609,89642	-609,89642	0	0	NS	0	[]	[]	[]	pre-mRNA-splicing factor RSE1	PF03178.8	CPSF_A(CPSF A subunit region)
Supercontig_1.76_MVLG_05510_10sp	-556,18059	-556,18029	0,0006	0,0003	NS	0	[]	[]	[]	hypothetical protein	PF00571.21	CBS(CBS domain)
Supercontig_1.5_MVLG_00921_7sp	-783,26822	-781,78981	2,95682	0,772	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.83_MVLG_05745_8sp	-763,30112	-761,90244	2,79736	0,75308	NS	0	[]	[]	[]	hypothetical protein	PF06966.5	DUF1295(Protein of unknown function (DUF1295))
Supercontig_1.11_MVLG_01693_9sp	-1180,3907	-1180,3192	0,14304	0,06902	NS	0	[]	[]	[]	DNA polymerase epsilon catalytic subunit A	PF10108.2	Exon_PolB(Predicted 3'-5' exonuclease related to the exonuclease domain of PolB)
Supercontig_1.10_MVLG_01685_9sp	-413,35302	-413,14818	0,40968	0,18522	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.4_MVLG_00837_8sp	-1171,3186	-1170,533	1,57104	0,54412	NS	0	[]	[]	[]	hypothetical protein	PF00649.11	Copper-fist(Copper fist DNA binding domain)
Supercontig_1.34_MVLG_03555_8sp	-752,01559	-752,01544	0,0003	0,00015	NS	0	[]	[]	[]	pre-mRNA-splicing factor CEF1	PF00249.24	Myb_DNA-binding(Myb-like DNA-binding domain)
Supercontig_1.48_MVLG_04362_7sp	-798,69458	-798,69458	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.19_MVLG_02453_8sp	-627,78275	-627,78275	0	0	NS	0	[]	[]	[]	hypothetical protein	PF09848.2	DUF2075(Uncharacterized conserved protein (DUF2075))
Supercontig_1.110_MVLG_06301_9sp	-393,75225	-393,75212	0,00026	0,00013	NS	0	[]	[]	[]	carnitine O-acetyltransferase	PF00755.13	Carn_acyltransf(Choline/Carnitine o-acyltransferase)
Supercontig_1.76_MVLG_05536_11sp	-415,2823	-415,27251	0,01958	0,00974	NS	0	[]	[]	[]	hypothetical protein	PF07103.4	DUF1365(Protein of unknown function (DUF1365))
Supercontig_1.34_MVLG_03527_8sp	-252,73724	-252,73719	0,0001	0,00016	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.34_MVLG_03512_11sp	-470,65897	-469,76065	1,79664	0,59275	NS	0	[]	[]	[]	hypothetical protein	PF09320.4	DUF1977(Domain of unknown function (DUF1977))
Supercontig_1.30_MVLG_03311_9sp	-637,43686	-635,75285	3,36802	0,81437	NS	0	[]	[]	[]	hypothetical protein	PF03399.9	SAC3_GANP(SAC3/GANP/Nin1/mts3/eIF-3 p25 family)
Supercontig_1.15_MVLG_02062_8sp	-404,74301	-404,73575	0,01452	0,00723	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.18_MVLG_02420_10sp	-439,37804	-439,39325	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01494.12	FAD_binding_3(FAD binding domain)

Supercontig_1.2_MVLG_00310_6sp	-592,09152	-591,38046	1,42212	0,50888	NS	0	[]	[]	[]	hypothetical protein	PF04083.9	Abhydro_lipase(ab-hydrolase associated lipase region)
Supercontig_1.10_MVLG_01682_11sp	-568,49665	-568,49639	0,00052	0,00026	NS	0	[]	[]	[]	eukaryotic translation initiation factor 6	TIGR00323	TIGR00323(eIF-6: putative translation initiation factor eIF-6)
Supercontig_1.50_MVLG_04473_11sp	-1259,8327	-1259,8321	0,00118	0,00059	NS	0	[]	[]	[]	hypothetical protein	PF02127.8	Peptidase_M18(Aminopeptidase I zinc metalloprotease (M18))
Supercontig_1.17_MVLG_02288_6sp	-872,22186	-870,31026	3,8232	0,85216	NS	0	[]	[]	[]	hypothetical protein	PF00188.19	CAP(Cysteine-rich secretory protein family)
Supercontig_1.34_MVLG_03568_9sp	-405,73164	-405,73164	0	0	NS	0	[]	[]	[]	cytochrome c peroxidase	PF00141.16	peroxidase(Peroxidase)
Supercontig_1.24_MVLG_02889_10sp	-818,30576	-818,30564	0,00024	0,00012	NS	0	[]	[]	[]	CAMK protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.113_MVLG_06347_7sp	-1427,5289	-1427,5288	0,00014	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF00557.17	Peptidase_M24(Metallopeptidase family M24)
Supercontig_1.16_MVLG_02228_6sp	-676,18569	-676,18518	0,00102	0,00051	NS	0	[]	[]	[]	hypothetical protein	PF02421.11	FeoB_N(Ferrous iron transport protein B)
Supercontig_1.16_MVLG_02250_8sp	-345,29522	-345,29519	0,00016	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF09809.2	MRP-L27(Mitochondrial ribosomal protein L27)
Supercontig_1.2_MVLG_00387_11sp	-472,25603	-472,25598	0,00016	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF00571.21	CBS(CBS domain)
Supercontig_1.13_MVLG_01967_7sp	-476,65855	-476,65855	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.79_MVLG_05616_9sp	-463,2325	-463,23237	0,00026	0,00013	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.155_MVLG_06818_10sp	-862,86148	-860,67632	4,37032	0,88754	NS	0	[]	[]	[]	hypothetical protein	PF03828.12	PAP_assoc(Poly(A) polymerase)
Supercontig_1.18_MVLG_02381_8sp	-1040,505	-1040,4354	0,1392	0,06723	NS	0	[]	[]	[]	proline iminopeptidase	TIGR01249	TIGR01249(pro_imino_pep_1: prolyl aminopeptidase)
Supercontig_1.25_MVLG_02982_9sp	-601,1115	-601,1115	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02114.9	Phosducin(Phosducin)
Supercontig_1.16_MVLG_02214_8sp	-538,81754	-538,81754	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.35_MVLG_03614_9sp	-779,46859	-779,46859	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.5_MVLG_00931_7sp	-998,33743	-992,04201	12,5908	0,99816	***	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.41_MVLG_03973_6sp	-431,25353	-431,22854	0,04998	0,02468	NS	0	[]	[]	[]	hypothetical protein	PF00076.15	RRM_1(RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain))
Supercontig_1.7_MVLG_01266_6sp	-1435,1542	-1432,1119	6,08456	0,95227	**	0	[]	[]	[]	hypothetical protein	PF10250.2	O-FucT(GDP-fucose protein O-fucosyltransferase)
Supercontig_1.29_MVLG_03240_9sp	-665,67085	-665,6706	0,0005	0,00025	NS	0	[]	[]	[]	tubulin alpha chain	PF00091.18	Tubulin(Tubulin/FtsZ family, GTPase domain)
Supercontig_1.56_MVLG_04790_7sp	-528,74703	-528,55123	0,3916	0,17782	NS	0	[]	[]	[]	hypothetical protein	PF02798.13	GST_N(Glutathione S-transferase, N-terminal domain)
Supercontig_1.170_MVLG_06939_8sp	-510,69659	-510,52906	0,33506	0,15425	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.29_MVLG_03244_7sp	-1775,6351	-1775,6351	0	0	NS	0	[]	[]	[]	hypothetical protein	PF09335.4	SNARE_assoc(SNARE associated Golgi protein)

Supercontig_1.67_MVLG_05236_12sp	-558,02241	-558,02241	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02900.11	LigB(Catalytic LigB subunit of aromatic ring-opening dioxygenase)
Supercontig_1.32_MVLG_03424_10sp	-488,75005	-488,75005	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.16_MVLG_02178_9sp	-568,23684	-568,23671	0,00026	0,00013	NS	0	[]	[]	[]	glutathione S-transferase omega-like 2	PF00043.18	GST_C(Glutathione S-transferase, C-terminal domain)
Supercontig_1.131_MVLG_06585_9sp	-616,06884	-615,97954	0,1786	0,08543	NS	0	[]	[]	[]	hypothetical protein	PF03061.15	4HBT(Thioesterase superfamily)
Supercontig_1.25_MVLG_02984_10sp	-1744,8945	-1744,8341	0,12072	0,05857	NS	0	[]	[]	[]	hypothetical protein	PF00018.21	SH3_1(SH3 domain)
Supercontig_1.6_MVLG_01128_10sp	-433,71	-431,58406	4,25188	0,88068	NS	0	[]	[]	[]	hypothetical protein	PF01602.13	Adaptin_N(Adaptin N terminal region)
Supercontig_1.120_MVLG_06425_11sp	-849,41604	-849,38921	0,05366	0,02647	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.13_MVLG_01922_6sp	-590,07197	-590,07197	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00324.14	AA_permease(Amino acid permease)
Supercontig_1.70_MVLG_05322_9sp	-1264,4695	-1264,4345	0,07012	0,03445	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.10_MVLG_01674_9sp	-705,52924	-704,96646	1,12556	0,43038	NS	0	[]	[]	[]	hypothetical protein	PF01424.15	R3H(R3H domain)
Supercontig_1.47_MVLG_04310_10sp	-642,73262	-642,73262	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02678.9	Pirin(Pirin)
Supercontig_1.26_MVLG_03023_8sp	-600,02695	-599,11591	1,82208	0,59789	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.2_MVLG_00431_9sp	-367,70353	-367,68133	0,0444	0,02196	NS	0	[]	[]	[]	hypothetical protein	PF04051.9	TRAPP(Transport protein particle (TRAPP) component)
Supercontig_1.12_MVLG_01812_10sp	-566,3886	-565,96604	0,84512	0,34463	NS	0	[]	[]	[]	hypothetical protein	PF00856.21	SET(SET domain)
Supercontig_1.97_MVLG_06061_9sp	-990,8519	-990,56138	0,58104	0,25213	NS	0	[]	[]	[]	hypothetical protein	PF00388.12	PI-PLC-X(Phosphatidylinositol-specific phospholipase C, X domain)
Supercontig_1.33_MVLG_03476_10sp	-658,23899	-658,23899	0	0	NS	0	[]	[]	[]	hypothetical protein	PF08217.4	DUF1712(Fungal domain of unknown function (DUF1712))
Supercontig_1.5_MVLG_00945_11sp	-611,57758	-611,57758	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00249.24	Myb_DNA-binding(Myb-like DNA-binding domain)
Supercontig_1.15_MVLG_02071_10sp	-671,61531	-671,61127	0,00808	0,00403	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.7_MVLG_01247_6sp	-266,33793	-266,30445	0,06696	0,03293	NS	0	[]	[]	[]	histone H4	PF00125.17	Histone(Core histone H2A/H2B/H3/H4)
Supercontig_1.42_MVLG_04060_8sp	-792,23874	-792,23874	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00400.25	WD40(WD domain, G-beta repeat)
Supercontig_1.26_MVLG_03029_10sp	-1093,5487	-1093,5487	0	0	NS	0	[]	[]	[]	hypothetical protein	PF08637.3	NCA2(ATP synthase regulation protein NCA2)
Supercontig_1.52_MVLG_04581_8sp	-663,98906	-663,98899	0,00014	0,00016	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.10_MVLG_01649_11sp	-914,18155	-914,18155	0	0	NS	0	[]	[]	[]	IKS protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.55_MVLG_04731_8sp	-484,61971	-484,61961	0,0002	0,00016	NS	0	[]	[]	[]	STE/STE7 protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)

Supercontig_1.21_MVLG_02640_10sp	-731,29143	-731,29143	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00732.12	GMC_oxred_N(GMC oxidoreductase)
Supercontig_1.40_MVLG_03912_9sp	-573,48607	-573,486	0,00014	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF00567.17	TUDOR(Tudor domain)
Supercontig_1.1_MVLG_00166_12sp	-438,30395	-436,92064	2,76662	0,74925	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.100_MVLG_06127_7sp	-981,181	-981,181	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00270.22	DEAD(DEAD/DEAH box helicase)
Supercontig_1.143_MVLG_06718_6sp	-494,96496	-494,96486	0,0002	0,00016	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.2_MVLG_00312_10sp	-611,10554	-609,51968	3,17172	0,79523	NS	0	[]	[]	[]	hypothetical protein	PF06108.5	DUF952(Protein of unknown function (DUF952))
Supercontig_1.82_MVLG_05704_7sp	-619,3765	-619,3765	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.33_MVLG_03484_11sp	-390,1943	-389,21357	1,96146	0,62496	NS	0	[]	[]	[]	hypothetical protein	PF01161.13	PBP(Phosphatidylethanolamine-binding protein)
Supercontig_1.56_MVLG_04782_6sp	-480,56305	-480,55821	0,00968	0,00483	NS	0	[]	[]	[]	hypothetical protein	PF04389.10	Peptidase_M28(Peptidase family M28)
Supercontig_1.73_MVLG_05414_7sp	-709,34307	-708,22096	2,24422	0,67441	NS	0	[]	[]	[]	cysteine synthase	PF00291.18	PALP(Pyridoxal-phosphate dependent enzyme)
Supercontig_1.5_MVLG_00993_9sp	-376,60119	-376,60119	0	0	NS	0	[]	[]	[]	hypothetical protein	PF10209.2	DUF2340(Uncharacterized conserved protein (DUF2340))
Supercontig_1.11_MVLG_01713_8sp	-384,54309	-383,95922	1,16774	0,44226	NS	0	[]	[]	[]	hypothetical protein	PF01464.13	SLT(Transglycosylase SLT domain)
Supercontig_1.2_MVLG_00419_8sp	-1974,572	-1972,657	3,82996	0,85266	NS	0	[]	[]	[]	hypothetical protein	PF08737.3	Rgp1(Rgp1)
Supercontig_1.3_MVLG_00668_9sp	-500,09724	-500,09724	0	0	NS	0	[]	[]	[]	short-chain dehydrogenase	PF00106.18	adh_short(short chain dehydrogenase)
Supercontig_1.85_MVLG_05806_10sp	-601,68413	-601,68412	0,00016	0,00016	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.116_MVLG_06371_9sp	-553,44363	-552,25606	2,37514	0,69504	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.31_MVLG_03338_6sp	-533,51496	-532,93745	1,15502	0,43871	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.9_MVLG_01541_6sp	-787,09629	-784,83029	4,532	0,89627	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.9_MVLG_01531_10sp	-400,35269	-400,32704	0,0513	0,02532	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.2_MVLG_00475_6sp	-642,06206	-641,43495	1,25422	0,46587	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.16_MVLG_02188_10sp	-481,81696	-481,81696	0	0	NS	0	[]	[]	[]	glucose-repressible alcohol dehydrogenase transcriptional effector	PF03372.16	Exo_endo_phos(Endonuclease/Exonuclease/phosphatase family)
Supercontig_1.39_MVLG_03865_7sp	-336,56423	-336,31704	0,49438	0,21901	NS	0	[]	[]	[]	hypothetical protein	PF09421.3	FRQ(Frequency clock protein)
Supercontig_1.3_MVLG_00673_8sp	-644,96555	-644,96555	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03162.6	Y_phosphatase2(Tyrosine phosphatase family)
Supercontig_1.59_MVLG_04905_6sp	-522,32639	-522,32639	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA

Supercontig_1.5_MVLG_00999_7sp	-645,59309	-644,75142	1,68334	0,56901	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.5_MVLG_00913_8sp	-974,47954	-974,37884	0,2014	0,0958	NS	0	[]	[]	[]	hypothetical protein	PF02833.7	DHHA2(DHHA2 domain)
Supercontig_1.135_MVLG_06625_8sp	-503,70447	-503,60197	0,205	0,09742	NS	0	[]	[]	[]	hypothetical protein	PF09435.3	DUF2015(Fungal protein of unknown function (DUF2015))
Supercontig_1.96_MVLG_06037_10sp	-619,11982	-619,11982	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03473.10	MOSC(MOSC domain)
Supercontig_1.80_MVLG_05644_11sp	-677,62068	-677,57427	0,09282	0,04535	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.4_MVLG_00768_12sp	-436,48881	-436,48873	0,00016	0,00016	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.26_MVLG_02994_9sp	-734,1904	-734,1904	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04603.5	Mog1(Ran-interacting Mog1 protein)
Supercontig_1.14_MVLG_01978_8sp	-441,89539	-441,89539	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02148.12	zf-UBP(Zn-finger in ubiquitin-hydrolases and other protein)
Supercontig_1.205_MVLG_07109_8sp	-376,55799	-376,55799	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.3_MVLG_00665_11sp	-504,93766	-504,93766	0	0	NS	0	[]	[]	[]	hypothetical protein	PF09729.2	Gti1_Pac2(Gti1/Pac2 family)
Supercontig_1.156_MVLG_06836_12sp	-341,84495	-341,84482	0,00026	0,00013	NS	0	[]	[]	[]	minichromosome maintenance protein 4 (cell division control protein 54)	PF00493.16	MCM(MCM2/3/5 family)
Supercontig_1.6_MVLG_01180_10sp	-482,752	-482,11703	1,26994	0,47005	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.86_MVLG_05827_10sp	-785,14972	-784,14713	2,00518	0,63307	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.99_MVLG_06106_10sp	-795,90922	-795,90922	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.28_MVLG_03159_9sp	-288,94284	-287,99726	1,89116	0,61155	NS	0	[]	[]	[]	acetyl-CoA acetyltransferase	TIGR01930	TIGR01930(AcCoA-C-Actrans: acetyl-CoA C-acetyltransferase)
Supercontig_1.61_MVLG_04962_8sp	-595,90476	-595,90476	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.41_MVLG_04019_8sp	-595,86434	-595,86434	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02582.7	DUF155(Uncharacterised ACR, YagE family COG1723)
Supercontig_1.12_MVLG_01859_7sp	-821,11657	-821,11657	0	0	NS	0	[]	[]	[]	hypothetical protein	TIGR00879	TIGR00879(SP: MFS transporter, sugar porter (SP) family)
Supercontig_1.34_MVLG_03516_6sp	-961,16097	-960,59859	1,12476	0,43015	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.2_MVLG_00483_7sp	-1553,6344	-1552,4775	2,31372	0,68553	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.39_MVLG_03867_8sp	-1845,5171	-1845,5171	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.111_MVLG_06305_9sp	-898,8714	-897,07877	3,58526	0,83348	NS	0	[]	[]	[]	hypothetical protein	TIGR00322	TIGR00322(diphth2_R: diphthamide biosynthesis enzyme Dph1/Dph2 domain)
Supercontig_1.51_MVLG_04517_8sp	-717,43241	-717,43241	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01764.18	Lipase_3(Lipase (class 3))

Supercontig_1.48_MVLG_04376_9sp	-552,58806	-552,58785	0,00042	0,00021	NS	0	[]	[]	[]	hypothetical protein	PF02906.7	Fe_hyd_lg_C(Iron only hydrogenase large subunit, C-terminal domain)
Supercontig_1.12_MVLG_01807_7sp	-942,19652	-940,96682	2,4594	0,70762	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.78_MVLG_05580_8sp	-383,82608	-383,82571	0,00074	0,00037	NS	0	[]	[]	[]	protein transporter SEC61 subunit alpha	TIGR00967	TIGR00967(3a0501s007: preprotein translocase, SecY subunit)
Supercontig_1.2_MVLG_00311_8sp	-1199,1921	-1199,1921	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.1_MVLG_00104_7sp	-616,49436	-616,49423	0,00026	0,00013	NS	0	[]	[]	[]	hypothetical protein	PF00107.19	ADH_zinc_N(Zinc-binding dehydrogenase)
Supercontig_1.27_MVLG_03110_9sp	-892,80677	-892,52321	0,56712	0,2469	NS	0	[]	[]	[]	hypothetical protein	PF03941.8	INCENP_ARK-bind(Inner centromere protein, ARK binding region)
Supercontig_1.23_MVLG_02791_9sp	-770,02355	-769,66614	0,71482	0,30051	NS	0	[]	[]	[]	hypothetical protein	PF03372.16	Exo_endo_phos(Endonuclease/ Exonuclease/phosphatase family)
Supercontig_1.45_MVLG_04217_9sp	-694,31407	-694,31407	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04869.7	Uso1_p115_head(Uso1 / p115 like vesicle tethering protein, head region)
Supercontig_1.109_MVLG_06288_12sp	-362,33118	-362,33095	0,00046	0,00023	NS	0	[]	[]	[]	hypothetical protein	PF00262.11	Calreticulin(Calreticulin family)
Supercontig_1.3_MVLG_00647_9sp	-779,6316	-778,84791	1,56738	0,54328	NS	0	[]	[]	[]	hypothetical protein	PF02225.15	PA(PA domain)
Supercontig_1.105_MVLG_06212_6sp	-622,45617	-622,2037	0,50494	0,22312	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.12_MVLG_01849_9sp	-513,86306	-513,4585	0,80912	0,33273	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.88_MVLG_05882_11sp	-374,8828	-374,88269	0,00022	0,00011	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.1_MVLG_00207_6sp	-873,24365	-873,24346	0,00038	0,00019	NS	0	[]	[]	[]	poly(A) polymerase	PF04926.8	PAP_RNA-bind(Poly(A) polymerase predicted RNA binding domain)
Supercontig_1.39_MVLG_03833_12sp	-677,64698	-677,64666	0,00064	0,00032	NS	0	[]	[]	[]	hypothetical protein	PF05091.5	eIF-3_zeta(Eukaryotic translation initiation factor 3 subunit 7 (eIF-3))
Supercontig_1.61_MVLG_04988_11sp	-485,45831	-485,45831	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00176.16	SNF2_N(SNF2 family N-terminal domain)
Supercontig_1.12_MVLG_01884_8sp	-1109,5229	-1106,9355	5,17482	0,92479	*	0	[]	[]	[]	hypothetical protein	PF02902.12	Peptidase_C48(Ulp1 protease family, C-terminal catalytic domain)
Supercontig_1.36_MVLG_03690_6sp	-561,88787	-561,726	0,32374	0,14945	NS	0	[]	[]	[]	hypothetical protein	PF00076.15	RRM_1(RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain))
Supercontig_1.69_MVLG_05279_9sp	-604,92758	-604,92736	0,00044	0,00022	NS	0	[]	[]	[]	hypothetical protein	PF00324.14	AA_permease(Amino acid permease)
Supercontig_1.57_MVLG_04803_8sp	-1163,5585	-1163,5585	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00383.15	dCMP_cyt_deam_1(Cytidine and deoxycytidylate deaminase zinc-binding region)

Supercontig_1.99_MVLG_06123_7sp	-1154,2896	-1153,839	0,90112	0,36273	NS	0	[]	[]	[]	hypothetical protein	PF00270.22	DEAD(DEAD/DEAH box helicase)
Supercontig_1.154_MVLG_06802_10sp	-489,17057	-488,96944	0,40226	0,18219	NS	0	[]	[]	[]	hypothetical protein	PF07479.7	NAD_Gly3P_dh_C(NAD-dependent glycerol-3-phosphate dehydrogenase C-terminus)
Supercontig_1.16_MVLG_02166_6sp	-475,82133	-475,82076	0,00114	0,00057	NS	0	[]	[]	[]	DNA repair protein RAD51	PF06745.6	KaiC(KaiC)
Supercontig_1.109_MVLG_06279_7sp	-445,34036	-445,34036	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04127.8	DFP(DNA / pantothenate metabolism flavoprotein)
Supercontig_1.1_MVLG_00243_11sp	-910,57211	-909,60744	1,92934	0,61889	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.32_MVLG_03443_9sp	-1158,6225	-1158,5123	0,22048	0,10438	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.10_MVLG_01639_8sp	-998,80825	-997,71367	2,18916	0,66532	NS	0	[]	[]	[]	hypothetical protein	PF00270.22	DEAD(DEAD/DEAH box helicase)
Supercontig_1.1_MVLG_00177_10sp	-448,13069	-448,13042	0,00054	0,00027	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.38_MVLG_03786_10sp	-396,05531	-395,96109	0,18844	0,08992	NS	0	[]	[]	[]	hypothetical protein	PF04032.9	Rpr2(RNAse P Rpr2/Rpp21/SNM1 subunit domain)
Supercontig_1.1_MVLG_00257_10sp	-312,51897	-312,51897	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.28_MVLG_03167_11sp	-1401,2269	-1401,2267	0,00044	0,00022	NS	0	[]	[]	[]	hypothetical protein	PF07817.6	GLE1(GLE1-like protein)
Supercontig_1.27_MVLG_03105_7sp	-489,19754	-488,65723	1,08062	0,41743	NS	0	[]	[]	[]	hypothetical protein	PF00651.24	BTB(BTB/POZ domain)
Supercontig_1.35_MVLG_03596_8sp	-730,5295	-730,52936	0,00028	0,00014	NS	0	[]	[]	[]	hypothetical protein	TIGR00111	TIGR00111(pelota: putative translation factor pelota)
Supercontig_1.41_MVLG_04013_10sp	-580,97204	-580,97202	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.19_MVLG_02488_10sp	-443,76042	-442,10538	3,31008	0,80892	NS	0	[]	[]	[]	hypothetical protein	PF04031.6	Las1(Las1-like)
Supercontig_1.36_MVLG_03695_10sp	-296,30547	-296,30521	0,00052	0,00026	NS	0	[]	[]	[]	pre-mRNA splicing factor	PF04851.8	ResIII(Type III restriction enzyme, res subunit)
Supercontig_1.7_MVLG_01327_10sp	-385,66117	-385,66117	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02826.12	2-Hacid_dh_C(D-isomer specific 2-hydroxyacid dehydrogenase, NAD binding domain)
Supercontig_1.8_MVLG_01368_11sp	-866,88558	-865,94088	1,8894	0,6112	NS	0	[]	[]	[]	hypothetical protein	PF08598.4	Sds3(Sds3-like)
Supercontig_1.39_MVLG_03841_8sp	-542,00685	-541,77167	0,47036	0,20957	NS	0	[]	[]	[]	synaptobrevin like YKT6	PF00957.14	Synaptobrevin(Synaptobrevin)
Supercontig_1.76_MVLG_05515_7sp	-489,61573	-489,61573	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.29_MVLG_03228_8sp	-1006,9495	-1006,8327	0,23342	0,11016	NS	0	[]	[]	[]	60S ribosomal protein L4-A	PF00573.15	Ribosomal_L4(Ribosomal protein L4/L1 family)
Supercontig_1.117_MVLG_06396_10sp	-484,29243	-484,29219	0,00048	0,00024	NS	0	[]	[]	[]	hypothetical protein	PF00155.14	Aminotran_1_2(Aminotransferase class I and II)
Supercontig_1.22_MVLG_02699_11sp	-413,17834	-413,17829	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00179.19	UQ_con(Ubiquitin-conjugating enzyme)

Supercontig_1.53_MVLG_04644_7sp	-1115,2522	-1114,7082	1,08798	0,41957	NS	0	[]	[]	[]	hypothetical protein	PF06984.6	MRP-L47(Mitochondrial 39-S ribosomal protein L47 (MRP-L47))
Supercontig_1.24_MVLG_02907_9sp	-549,33442	-548,49116	1,68652	0,56969	NS	0	[]	[]	[]	hypothetical protein	PF00860.13	Xan_ur_permease(Permease family)
Supercontig_1.17_MVLG_02269_11sp	-705,46632	-705,46632	0	0	NS	0	[]	[]	[]	hypothetical protein	PF09949.2	DUF2183(Uncharacterized conserved protein (DUF2183))
Supercontig_1.96_MVLG_06048_9sp	-1855,0633	-1855,0633	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01734.15	Patatin(Patatin-like phospholipase)
Supercontig_1.3_MVLG_00656_10sp	-828,61079	-828,61079	0	0	NS	0	[]	[]	[]	hypothetical protein	PF06432.4	GPI2(Phosphatidylinositol N-acetylglucosaminyltransferase)
Supercontig_1.17_MVLG_02310_12sp	-544,7378	-544,73771	0,00018	0	NS	0	[]	[]	[]	hypothetical protein	TIGR00907	TIGR00907(2A0304: amino acid permease)
Supercontig_1.1_MVLG_00082_8sp	-306,16351	-306,15327	0,02048	0,01019	NS	0	[]	[]	[]	hypothetical protein	PF00795.15	CN_hydrolase(Carbon-nitrogen hydrolase)
Supercontig_1.18_MVLG_02401_8sp	-482,52469	-482,52469	0	0	NS	0	[]	[]	[]	hypothetical protein	PF05821.4	NDUF_B8(NADH-ubiquinone oxidoreductase ASHI subunit (CI-ASHI or NDUFB8))
Supercontig_1.24_MVLG_02881_12sp	-769,52692	-769,52692	0	0	NS	0	[]	[]	[]	glutamate dehydrogenase	PF00208.14	ELFV_dehydrog(Glutamate/Leucine/Phenylalanine/Valine dehydrogenase)
Supercontig_1.13_MVLG_01900_10sp	-520,75777	-520,75754	0,00046	0,00023	NS	0	[]	[]	[]	hypothetical protein	PF09725.2	Fra10Ac1(Folate-sensitive fragile site protein Fra10Ac1)
Supercontig_1.40_MVLG_03909_7sp	-550,41137	-550,02148	0,77978	0,32287	NS	0	[]	[]	[]	hypothetical protein	PF04438.9	zf-HIT(HIT zinc finger)
Supercontig_1.13_MVLG_01912_10sp	-1236,147	-1235,0623	2,16944	0,662	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.17_MVLG_02315_6sp	-402,84636	-402,84636	0	0	NS	0	[]	[]	[]	hypothetical protein	PF05546.4	She9_MDM33(She9 / Mdm33 family)
Supercontig_1.67_MVLG_05227_8sp	-854,9729	-854,9729	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00175.14	NAD_binding_1(Oxidoreductase NAD-binding domain)
Supercontig_1.75_MVLG_05494_9sp	-972,2382	-972,2382	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04857.13	CAF1(CAF1 family ribonuclease)
Supercontig_1.52_MVLG_04579_10sp	-593,76755	-593,76754	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01852.12	START(START domain)
Supercontig_1.4_MVLG_00869_11sp	-674,95502	-674,25963	1,39078	0,50112	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.12_MVLG_01852_10sp	-354,25799	-354,25799	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00076.15	RRM_1(RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain))
Supercontig_1.77_MVLG_05562_10sp	-1192,0828	-1192,0828	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01483.13	P_proprotein(Proprotein convertase P-domain)
Supercontig_1.58_MVLG_04878_8sp	-1113,5625	-1113,5481	0,02874	0,01427	NS	0	[]	[]	[]	hypothetical protein	PF02586.7	DUF159(Uncharacterised ACR, COG2135)
Supercontig_1.140_MVLG_06679_10sp	-792,30288	-792,30288	0	0	NS	0	[]	[]	[]	adenosinetriphosphatase	PF00270.22	DEAD(DEAD/DEAH box helicase)
Supercontig_1.4_MVLG_00726_9sp	-396,41761	-396,31392	0,20738	0,0985	NS	0	[]	[]	[]	hypothetical protein	PF04048.7	Sec8_exocyst(Sec8 exocyst complex component specific domain)

Supercontig_1.15_MVLG_02135_10sp	-499,30447	-497,52283	3,56328	0,83164	NS	0	[]	[]	[]	methionyl-tRNA synthetase	PF09334.4	tRNA-synt_1g(tRNA synthetases class I (M))
Supercontig_1.111_MVLG_06311_10sp	-1220,4098	-1219,6523	1,51492	0,53114	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.3_MVLG_00628_10sp	-684,76627	-684,7203	0,09194	0,04493	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.112_MVLG_06333_9sp	-689,47565	-689,42653	0,09824	0,04793	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.19_MVLG_02437_6sp	-1429,7247	-1429,7247	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.33_MVLG_03480_10sp	-1086,8969	-1085,0207	3,75242	0,84683	NS	0	[]	[]	[]	hypothetical protein	PF08317.4	Spc7(Spc7 kinetochore protein)
Supercontig_1.20_MVLG_02545_10sp	-709,37509	-708,48046	1,78926	0,59124	NS	0	[]	[]	[]	hypothetical protein	PF12110.1	Nup96(Nuclear protein 96)
Supercontig_1.2_MVLG_00303_6sp	-699,97985	-699,50937	0,94096	0,3753	NS	0	[]	[]	[]	DNA-directed RNA polymerase I, II, and III subunit RPABC1	PF01191.12	RNA_pol_Rpb5_C(RNA polymerase Rpb5, C-terminal domain)
Supercontig_1.48_MVLG_04383_10sp	-435,01478	-433,45133	3,1269	0,79059	NS	0	[]	[]	[]	NAK protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.62_MVLG_05038_7sp	-887,81563	-887,81563	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02077.8	SURF4(SURF4 family)
Supercontig_1.7_MVLG_01254_10sp	-385,07355	-385,07355	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.33_MVLG_03494_11sp	-487,84847	-486,00107	3,6948	0,84235	NS	0	[]	[]	[]	hypothetical protein	PF02770.12	Acyl-CoA_dh_M(Acyl-CoA dehydrogenase, middle domain)
Supercontig_1.64_MVLG_05094_8sp	-1324,8355	-1324,8355	0	0	NS	0	[]	[]	[]	glutaminyl-tRNA synthetase	TIGR00440	TIGR00440(glnS: glutamine--tRNA ligase)
Supercontig_1.35_MVLG_03575_6sp	-598,81298	-596,55208	4,5218	0,89574	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.34_MVLG_03549_8sp	-364,22965	-364,22965	0	0	NS	0	[]	[]	[]	hypothetical protein	PF06658.5	DUF1168(Protein of unknown function (DUF1168))
Supercontig_1.8_MVLG_01473_8sp	-415,33533	-415,33513	0,0004	0,0002	NS	0	[]	[]	[]	hypothetical protein	PF00106.18	adh_short(short chain dehydrogenase)
Supercontig_1.2_MVLG_00291_6sp	-904,88795	-904,88795	0	0	NS	0	[]	[]	[]	hypothetical protein	PF07173.5	DUF1399(Protein of unknown function (DUF1399))
Supercontig_1.42_MVLG_04050_7sp	-755,44432	-755,30797	0,2727	0,12746	NS	0	[]	[]	[]	hypothetical protein	PF00675.13	Peptidase_M16(Insulinase (Peptidase family M16))
Supercontig_1.9_MVLG_01554_9sp	-478,91599	-478,27669	1,2786	0,47234	NS	0	[]	[]	[]	hypothetical protein	PF00227.19	Proteasome(Proteasome subunit)
Supercontig_1.2_MVLG_00294_6sp	-577,10722	-577,10722	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03656.6	Pam16(Pam16)
Supercontig_1.6_MVLG_01203_11sp	-327,21222	-327,21219	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00023.23	Ank(Ankyrin repeat)
Supercontig_1.113_MVLG_06348_10sp	-710,68091	-710,68091	0	0	NS	0	[]	[]	[]	hypothetical protein	TIGR02962	TIGR02962(hdxy_isourate: hydroxyisourate hydrolase)
Supercontig_1.91_MVLG_05922_8sp	-607,28582	-607,11999	0,33166	0,15281	NS	0	[]	[]	[]	hypothetical protein	PF07933.7	DUF1681(Protein of unknown function (DUF1681))
Supercontig_1.55_MVLG_04724_9sp	-1057,9597	-1057,9213	0,07686	0,0377	NS	0	[]	[]	[]	hypothetical protein	PF00856.21	SET(SET domain)

Supercontig_1.27_MVLG_03080_7sp	-636,91352	-636,81201	0,20302	0,09653	NS	0	[]	[]	[]	hypothetical protein	PF00432.14	Prenyltrans(Prenyltransferase and squalene oxidase repeat)
Supercontig_1.110_MVLG_06296_9sp	-891,45559	-890,71461	1,48196	0,52335	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.20_MVLG_02586_6sp	-1016,2149	-1016,2149	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00581.13	Rhodanese(Rhodanese-like domain)
Supercontig_1.3_MVLG_00632_10sp	-465,34299	-465,34299	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03155.8	Alg6_Alg8(ALG6, ALG8 glycosyltransferase family)
Supercontig_1.32_MVLG_03431_12sp	-636,25182	-636,25182	0	0	NS	0	[]	[]	[]	pre-mRNA-splicing factor SYF1	NA	NA
Supercontig_1.2_MVLG_00396_10sp	-608,25519	-608,23993	0,03052	0,01514	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.2_MVLG_00317_10sp	-294,16375	-293,58232	1,16286	0,4409	NS	0	[]	[]	[]	hypothetical protein	PF12022.1	DUF3510(Domain of unknown function (DUF3510))
Supercontig_1.9_MVLG_01544_8sp	-634,57523	-634,57523	0	0	NS	0	[]	[]	[]	hypothetical protein	TIGR00227	TIGR00227(ribD_Cterm: riboflavin-specific deaminase C-terminal domain)
Supercontig_1.14_MVLG_02024_11sp	-797,8933	-797,8931	0,0004	0,0002	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.63_MVLG_05063_8sp	-753,45252	-753,45252	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01480.10	PWI(PWI domain)
Supercontig_1.20_MVLG_02605_9sp	-356,18511	-355,87239	0,62544	0,26855	NS	0	[]	[]	[]	actin-like protein 2/3 complex subunit 2	PF04045.7	P34-Arc(Arp2/3 complex, 34 kD subunit p34-Arc)
Supercontig_1.3_MVLG_00519_12sp	-426,1447	-426,14469	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01798.11	Nop(Putative snoRNA binding domain)
Supercontig_1.38_MVLG_03790_10sp	-742,21611	-742,20649	0,01924	0,00957	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.39_MVLG_03896_7sp	-449,44318	-448,58179	1,72278	0,57743	NS	0	[]	[]	[]	hypothetical protein	PF11221.1	Med21(Subunit 21 of Mediator complex)
Supercontig_1.81_MVLG_05694_12sp	-1154,8183	-1152,8977	3,84116	0,85348	NS	0	[]	[]	[]	hypothetical protein	PF01778.10	Ribosomal_L28e(Ribosomal L28e protein family)
Supercontig_1.4_MVLG_00707_6sp	-495,56939	-495,56909	0,0006	0,0003	NS	0	[]	[]	[]	secretory pathway GDP dissociation inhibitor 1	PF00996.11	GDI(GDP dissociation inhibitor)
Supercontig_1.57_MVLG_04818_12sp	-695,77431	-695,77431	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.2_MVLG_00480_9sp	-350,93444	-350,93015	0,00858	0,00428	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.2_MVLG_00457_8sp	-544,77332	-544,77332	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.40_MVLG_03963_8sp	-703,17494	-703,17486	0,00016	0	NS	0	[]	[]	[]	hypothetical protein	PF00268.14	Ribonuc_red_sm(Ribonucleotide reductase, small chain)
Supercontig_1.55_MVLG_04717_7sp	-232,01078	-232,01078	0	0	NS	0	[]	[]	[]	small nuclear ribonucleoprotein F	PF01423.15	LSM(LSM domain)
Supercontig_1.109_MVLG_06280_8sp	-628,47031	-628,47031	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.76_MVLG_05528_7sp	-550,74922	-548,74927	3,9999	0,86466	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.3_MVLG_00556_10sp	-539,77133	-539,77133	0	0	NS	0	[]	[]	[]	hypothetical protein	TIGR00879	TIGR00879(SP: MFS transporter, sugar porter (SP) family)

Supercontig_1.62_MVLG_05031_7sp	-388,27753	-388,27734	0,00038	0,00019	NS	0	[]	[]	[]	hypothetical protein	PF11705.1	RNA_pol_3_Rpc31(DNA-directed RNA polymerase III subunit Rpc31)
Supercontig_1.3_MVLG_00610_10sp	-1639,162	-1639,162	0	0	NS	0	[]	[]	[]	hypothetical protein	PF09444.3	MRC1(MRC1-like domain)
Supercontig_1.93_MVLG_05973_11sp	-795,56409	-793,48928	4,14962	0,87442	NS	0	[]	[]	[]	hypothetical protein	PF00328.15	Acid_phosphat_A(Histidine acid phosphatase)
Supercontig_1.19_MVLG_02476_10sp	-819,9366	-819,26757	1,33806	0,48779	NS	0	[]	[]	[]	hypothetical protein	PF01853.11	MOZ_SAS(MOZ/SAS family)
Supercontig_1.197_MVLG_07070_6sp	-483,80992	-483,78717	0,0455	0,02249	NS	0	[]	[]	[]	hypothetical protein	PF00929.17	Exonuc_X-T(Exonuclease)
Supercontig_1.91_MVLG_05934_8sp	-700,89122	-700,89122	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00326.14	Peptidase_S9(Prolyl oligopeptidase family)
Supercontig_1.53_MVLG_04640_10sp	-281,82469	-281,82466	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00132.17	Hexapep(Bacterial transferase hexapeptide (three repeats))
Supercontig_1.4_MVLG_00849_10sp	-614,05663	-614,05663	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01501.13	Glyco_transf_8(Glycosyl transferase family 8)
Supercontig_1.12_MVLG_01804_9sp	-405,95442	-405,75218	0,40448	0,1831	NS	0	[]	[]	[]	STE/STE11/CDC15 protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.15_MVLG_02119_8sp	-1052,8553	-1052,8553	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00083.17	Sugar_tr(Sugar (and other) transporter)
Supercontig_1.38_MVLG_03815_6sp	-288,22495	-288,22478	0,00034	0,00017	NS	0	[]	[]	[]	Ras-like protein Rab-11B	PF08477.6	Miro(Miro-like protein)
Supercontig_1.22_MVLG_02727_7sp	-767,00069	-767,00069	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.4_MVLG_00724_6sp	-1150,9307	-1150,9307	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00809.15	Pterin_bind(Pterin binding enzyme)
Supercontig_1.122_MVLG_06455_11sp	-845,50767	-845,50767	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.18_MVLG_02382_10sp	-360,14538	-359,71045	0,86986	0,35269	NS	0	[]	[]	[]	hypothetical protein	PF00828.12	Ribosomal_L18e(Ribosomal protein L18e/L15)
Supercontig_1.4_MVLG_00827_9sp	-633,87284	-633,87218	0,00132	0,00066	NS	0	[]	[]	[]	splicing factor 3B subunit 1	PF02985.15	HEAT(HEAT repeat)
Supercontig_1.45_MVLG_04207_10sp	-863,75402	-862,9835	1,54104	0,53723	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.40_MVLG_03962_10sp	-1686,2906	-1686,2906	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00481.14	PP2C(Protein phosphatase 2C)
Supercontig_1.163_MVLG_06884_8sp	-498,22517	-498,21401	0,02232	0,0111	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.28_MVLG_03185_8sp	-419,51678	-419,50501	0,02354	0,0117	NS	0	[]	[]	[]	hypothetical protein	PF03467.8	Smg4_UPF3(Smg-4/UPF3 family)
Supercontig_1.11_MVLG_01783_6sp	-766,07232	-764,28298	3,57868	0,83293	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.63_MVLG_05086_9sp	-605,10789	-605,10789	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.5_MVLG_01029_8sp	-520,41486	-520,41486	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02338.12	OTU(OTU-like cysteine protease)
Supercontig_1.8_MVLG_01433_11sp	-275,25417	-275,25385	0,00064	0,00032	NS	0	[]	[]	[]	hypothetical protein	PF04098.8	Rad52_Rad22(Rad52/22 family double-strand break repair protein)

Supercontig_1.98_MVLG_06087_8sp	-573,8633	-573,85758	0,01144	0,0057	NS	0	[]	[]	[]	hypothetical protein	PF02656.8	DUF202(Domain of unknown function DUF)
Supercontig_1.278_MVLG_07229_6sp	-638,93686	-638,01708	1,83956	0,60139	NS	0	[]	[]	[]	hypothetical protein	PF03583.7	LIP(Secretory lipase)
Supercontig_1.3_MVLG_00506_10sp	-935,54888	-935,54888	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01055.19	Glyco_hydro_31(Glycosyl hydrolases family 31)
Supercontig_1.22_MVLG_02720_11sp	-519,4332	-519,4332	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00226.24	DnaJ(DnaJ domain)
Supercontig_1.15_MVLG_02101_7sp	-984,14195	-983,81118	0,66154	0,28163	NS	0	[]	[]	[]	CAMK/CAMKL protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.11_MVLG_01721_7sp	-598,58583	-598,58583	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01472.13	PUA(PUA domain)
Supercontig_1.20_MVLG_02580_6sp	-1181,6166	-1181,6098	0,01358	0,00677	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.41_MVLG_04000_10sp	-405,35559	-405,35538	0,00042	0,00021	NS	0	[]	[]	[]	STE/STE20/FRAY protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.82_MVLG_05715_7sp	-812,78488	-812,75954	0,05068	0,02502	NS	0	[]	[]	[]	hypothetical protein	PF08045.4	CDC14(Cell division control protein 14, SIN component)
Supercontig_1.42_MVLG_04041_8sp	-1358,3676	-1357,821	1,0932	0,42109	NS	0	[]	[]	[]	hypothetical protein	PF05172.6	MPPN(MPPN (rrm-like) domain)
Supercontig_1.59_MVLG_04893_11sp	-439,88582	-439,64049	0,49066	0,21755	NS	0	[]	[]	[]	hypothetical protein	PF04597.7	Ribophorin_I(Ribophorin I)
Supercontig_1.13_MVLG_01966_10sp	-947,83984	-946,93935	1,80098	0,59363	NS	0	[]	[]	[]	hypothetical protein	PF00293.21	NUDIX(NUDIX domain)
Supercontig_1.203_MVLG_07101_6sp	-576,89568	-576,89537	0,00062	0,00031	NS	0	[]	[]	[]	ribonucleoprotein-associated protein	PF01248.19	Ribosomal_L7Ae(Ribosomal protein L7Ae/L30e/S12e/Gadd45 family)
Supercontig_1.15_MVLG_02121_8sp	-356,42304	-356,42298	0,00012	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.17_MVLG_02324_7sp	-595,25914	-594,90546	0,70736	0,2979	NS	0	[]	[]	[]	hypothetical protein	PF01180.14	DHO_dh(Dihydroorotate dehydrogenase)
Supercontig_1.4_MVLG_00814_9sp	-537,15744	-537,15744	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.22_MVLG_02716_7sp	-845,64003	-845,64003	0	0	NS	0	[]	[]	[]	glycine cleavage system H protein	TIGR00527	TIGR00527(gcvH: glycine cleavage system H protein)
Supercontig_1.24_MVLG_02854_10sp	-665,65872	-665,63138	0,05468	0,02697	NS	0	[]	[]	[]	hypothetical protein	PF00076.15	RRM_1(RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain))
Supercontig_1.202_MVLG_07088_9sp	-726,42337	-724,61684	3,61306	0,83578	NS	0	[]	[]	[]	hypothetical protein	PF08597.3	eIF3_subunit(Translation initiation factor eIF3 subunit)
Supercontig_1.65_MVLG_05145_10sp	-489,92617	-489,92617	0	0	NS	0	[]	[]	[]	hypothetical protein	PF10294.2	Methyltransf_16(Putative methyltransferase)
Supercontig_1.7_MVLG_01308_9sp	-349,66215	-349,66215	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00067.15	p450(Cytochrome P450)
Supercontig_1.155_MVLG_06821_7sp	-839,53378	-839,20069	0,66618	0,28329	NS	0	[]	[]	[]	hypothetical protein	PF01793.9	Glyco_transf_15(Glycolipid 2-alpha-mannosyltransferase)
Supercontig_1.56_MVLG_04788_8sp	-614,46062	-614,46031	0,00062	0,00031	NS	0	[]	[]	[]	adenosylhomocysteinase	TIGR00936	TIGR00936(ahcY: adenosylhomocysteinase)
Supercontig_1.109_MVLG_06283_8sp	-621,96647	-621,10495	1,72304	0,57748	NS	0	[]	[]	[]	hypothetical protein	PF10000.2	DUF2241(Uncharacterized protein conserved in bacteria (DUF2241))

Supercontig_1.109_MVLG_06287_11sp	-382,34031	-382,34031	0	0	NS	0	[]	[]	[]	YjeF	TIGR00197	TIGR00197(yjeF_nterm: YjeF homolog, N-terminus)
Supercontig_1.121_MVLG_06444_10sp	-731,42994	-731,19367	0,47254	0,21043	NS	0	[]	[]	[]	hypothetical protein	PF05739.12	SNARE(SNARE domain)
Supercontig_1.8_MVLG_01451_10sp	-575,54166	-575,54161	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03547.11	Mem_trans(Membrane transport protein)
Supercontig_1.97_MVLG_06057_6sp	-331,54832	-331,54806	0,00052	0,00026	NS	0	[]	[]	[]	peptidyl-prolyl cis-trans isomerase-like 3	PF00160.14	Pro_isomerase(Cyclophilin type peptidyl-prolyl cis-trans isomerase/CLD)
Supercontig_1.107_MVLG_06258_10sp	-606,44103	-606,26354	0,35498	0,16263	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.1_MVLG_00171_9sp	-483,85178	-483,85161	0,00034	0,00017	NS	0	[]	[]	[]	hypothetical protein	PF01613.11	Flavin_Reduct(Flavin reductase like domain)
Supercontig_1.6_MVLG_01137_8sp	-1263,6181	-1262,9573	1,3217	0,48359	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.58_MVLG_04843_10sp	-570,14296	-570,14296	0	0	NS	0	[]	[]	[]	hypothetical protein	PF06419.4	COG6(Conserved oligomeric complex COG6)
Supercontig_1.38_MVLG_03823_8sp	-420,49787	-420,49787	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00106.18	adh_short(short chain dehydrogenase)
Supercontig_1.77_MVLG_05552_10sp	-672,23723	-672,23723	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.35_MVLG_03610_10sp	-316,40438	-316,40438	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00614.15	PLDc(Phospholipase D Active site motif)
Supercontig_1.26_MVLG_03020_12sp	-298,17865	-298,11754	0,12222	0,05928	NS	0	[]	[]	[]	hypothetical protein	PF00400.25	WD40(WD domain, G-beta repeat)
Supercontig_1.40_MVLG_03946_6sp	-804,71836	-804,61016	0,2164	0,10255	NS	0	[]	[]	[]	hypothetical protein	PF03987.8	Autophagy_act_C(Autophagocytosis associated protein, active-site domain)
Supercontig_1.113_MVLG_06343_10sp	-846,38539	-845,97959	0,8116	0,33356	NS	0	[]	[]	[]	hypothetical protein	PF00173.21	Cyt-b5(Cytochrome b5-like Heme/Steroid binding domain)
Supercontig_1.5_MVLG_00943_12sp	-373,97984	-373,9797	0,00028	0,00014	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.22_MVLG_02710_6sp	-505,30962	-505,12564	0,36796	0,16805	NS	0	[]	[]	[]	hypothetical protein	PF04144.6	SCAMP(SCAMP family)
Supercontig_1.28_MVLG_03171_6sp	-1236,098	-1236,0951	0,0058	0,0029	NS	0	[]	[]	[]	hypothetical protein	PF02148.12	zf-UBP(Zn-finger in ubiquitin-hydrolases and other protein)
Supercontig_1.87_MVLG_05866_11sp	-296,86329	-296,8632	0,00018	0	NS	0	[]	[]	[]	hypothetical protein	PF01553.14	Acyltransferase(Acyltransferase)
Supercontig_1.98_MVLG_06085_10sp	-347,92932	-347,92897	0,0007	0,00035	NS	0	[]	[]	[]	hypothetical protein	PF00063.14	Myosin_head(Myosin head (motor domain))
Supercontig_1.47_MVLG_04324_8sp	-733,70826	-733,50191	0,4127	0,18645	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.21_MVLG_02639_9sp	-338,55587	-338,55587	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01852.12	START(START domain)
Supercontig_1.42_MVLG_04085_8sp	-575,20926	-575,20922	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.25_MVLG_02973_7sp	-322,46628	-322,4662	0,00016	0	NS	0	[]	[]	[]	hypothetical protein	PF03095.8	PTPA(Phosphotyrosyl phosphate activator (PTPA) protein)
Supercontig_1.46_MVLG_04265_6sp	-436,1308	-434,90071	2,46018	0,70773	NS	0	[]	[]	[]	hypothetical protein	NA	NA

Supercontig_1.1_MVLG_00015_6sp	-709,17312	-708,03599	2,27426	0,67926	NS	0	[]	[]	[]	hypothetical protein	PF00505.12	HMG_box(HMG (high mobility group) box)
Supercontig_1.13_MVLG_01895_7sp	-1073,7163	-1073,7163	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.55_MVLG_04727_9sp	-454,76855	-454,76838	0,00034	0,00017	NS	0	[]	[]	[]	hypothetical protein	PF07859.6	Abhydrolase_3(alpha/beta hydrolase fold)
Supercontig_1.70_MVLG_05328_10sp	-503,96806	-503,95594	0,02424	0,01205	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.79_MVLG_05605_12sp	-418,25076	-417,35423	1,79306	0,59202	NS	0	[]	[]	[]	hypothetical protein	PF00753.20	Lactamase_B(Metallo-beta-lactamase superfamily)
Supercontig_1.56_MVLG_04756_8sp	-620,83104	-620,83104	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00009.20	GTP_EFTU(Elongation factor Tu GTP binding domain)
Supercontig_1.62_MVLG_05039_9sp	-696,75896	-696,75857	0,00078	0,00039	NS	0	[]	[]	[]	hypothetical protein	PF04934.7	Med6(MED6 mediator sub complex component)
Supercontig_1.5_MVLG_01021_7sp	-623,73331	-623,7107	0,04522	0,02236	NS	0	[]	[]	[]	hypothetical protein	TIGR00449	TIGR00449(tgt_general: tRNA-guanine transglycosylases, various specificities)
Supercontig_1.69_MVLG_05284_10sp	-781,10238	-781,10238	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01575.12	MaoC_dehydratas(MaoC like domain)
Supercontig_1.7_MVLG_01236_9sp	-365,51805	-365,51781	0,00048	0,00024	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.61_MVLG_04958_12sp	-653,35402	-653,35402	0	0	NS	0	[]	[]	[]	hypothetical protein	TIGR00097	TIGR00097(HMP-P_kinase: phosphomethylpyrimidine kinase)
Supercontig_1.64_MVLG_05117_7sp	-625,49113	-625,49088	0,0005	0,00025	NS	0	[]	[]	[]	hypothetical protein	TIGR01145	TIGR01145(ATP_synt_delta: ATP synthase F1, delta subunit)
Supercontig_1.1_MVLG_00021_8sp	-384,86739	-384,86734	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02733.10	Dak1(Dak1 domain)
Supercontig_1.35_MVLG_03616_8sp	-834,19586	-834,19586	0	0	NS	0	[]	[]	[]	hypothetical protein	PF09445.3	Methyltransf_15(RNA cap guanine-N2 methyltransferase)
Supercontig_1.38_MVLG_03792_11sp	-423,78069	-423,78056	0,00026	0,00013	NS	0	[]	[]	[]	hypothetical protein	PF04707.7	PRELI(PRELI-like family)
Supercontig_1.24_MVLG_02902_8sp	-335,32424	-335,32417	0,00014	0	NS	0	[]	[]	[]	signal peptidase I	TIGR02228	TIGR02228(sigpep_I_arch: signal peptidase I)
Supercontig_1.42_MVLG_04047_7sp	-712,06171	-710,10898	3,90546	0,85811	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.14_MVLG_01993_8sp	-1084,9171	-1084,9171	0	0	NS	0	[]	[]	[]	CAMK protein kinase	TIGR00456	TIGR00456(argS: arginine--tRNA ligase)
Supercontig_1.92_MVLG_05965_11sp	-1637,0256	-1636,5261	0,9991	0,3932	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.6_MVLG_01117_7sp	-409,07741	-409,07729	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00400.25	WD40(WD domain, G-beta repeat)
Supercontig_1.19_MVLG_02443_9sp	-491,39474	-491,39471	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00400.25	WD40(WD domain, G-beta repeat)
Supercontig_1.33_MVLG_03501_10sp	-921,95224	-921,53125	0,84198	0,3436	NS	0	[]	[]	[]	Ca2+-transporting ATPase	TIGR01494	TIGR01494(ATPase_P-type: HAD ATPase, P-type, family IC)
Supercontig_1.18_MVLG_02404_8sp	-491,58967	-491,29578	0,58778	0,25464	NS	0	[]	[]	[]	hypothetical protein	PF03803.8	Scramblase(Scramblase)

Supercontig_1.32_MVLG_03402_9sp	-1091,0217	-1090,9269	0,1896	0,09045	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.98_MVLG_06094_8sp	-470,47701	-470,20498	0,54406	0,23817	NS	0	[]	[]	[]	hypothetical protein	PF08616.3	SPB_interacting(Spindle pole body interacting protein)
Supercontig_1.30_MVLG_03313_10sp	-1101,3136	-1100,9249	0,77732	0,32204	NS	0	[]	[]	[]	hypothetical protein	PF08552.4	Kei1(Inositolphosphorylceramide synthase subunit Kei1)
Supercontig_1.53_MVLG_04608_11sp	-444,47294	-444,47252	0,00084	0,00042	NS	0	[]	[]	[]	small nuclear ribonucleoprotein Sm D2	PF01423.15	LSM(LSM domain)
Supercontig_1.33_MVLG_03460_9sp	-373,89763	-373,89761	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00022.12	Actin(Actin)
Supercontig_1.60_MVLG_04928_8sp	-973,864	-973,864	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.51_MVLG_04535_9sp	-423,48449	-423,48449	0	0	NS	0	[]	[]	[]	hypothetical protein	PF05046.7	Img2(Mitochondrial large subunit ribosomal protein (Img2))
Supercontig_1.31_MVLG_03343_9sp	-957,18399	-957,18399	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02885.10	Glycos_trans_3N(Glycosyl transferase family, helical bundle domain)
Supercontig_1.64_MVLG_05096_7sp	-773,97934	-773,97934	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00173.21	Cyt-b5(Cytochrome b5-like Heme/Steroid binding domain)
Supercontig_1.38_MVLG_03825_7sp	-1103,0435	-1103,0435	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00400.25	WD40(WD domain, G-beta repeat)
Supercontig_1.220_MVLG_07160_9sp	-589,62649	-589,62649	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02731.8	SKIP_SNW(SKIP/SNW domain)
Supercontig_1.102_MVLG_06181_7sp	-805,57569	-805,57569	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.22_MVLG_02701_8sp	-311,55661	-310,8787	1,35582	0,49232	NS	0	[]	[]	[]	hypothetical protein	PF01066.14	CDP-OH_P_transf(CDP-alcohol phosphatidyltransferase)
Supercontig_1.21_MVLG_02660_10sp	-522,71578	-522,71851	0	0	NS	0	[]	[]	[]	glucosamine-fructose-6-phosphate aminotransferase	PF01380.15	SIS(SIS domain)
Supercontig_1.4_MVLG_00761_8sp	-862,63306	-862,63306	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01553.14	Acyltransferase(Acyltransferase)
Supercontig_1.2_MVLG_00374_10sp	-401,8253	-401,82525	0,0001	0	NS	0	[]	[]	[]	hypothetical protein	PF00097.18	zf-C3HC4(Zinc finger, C3HC4 type (RING finger))
Supercontig_1.11_MVLG_01723_10sp	-344,46128	-344,46114	0,00028	0,00014	NS	0	[]	[]	[]	hypothetical protein	PF10255.2	Paf67(RNA polymerase I-associated factor PAF67)
Supercontig_1.79_MVLG_05606_6sp	-767,66209	-767,12642	1,07134	0,41472	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.34_MVLG_03508_9sp	-467,92145	-467,92145	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00400.25	WD40(WD domain, G-beta repeat)
Supercontig_1.4_MVLG_00690_6sp	-512,49736	-511,59626	1,8022	0,59388	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.211_MVLG_07126_8sp	-437,9729	-437,97277	0,00026	0,00013	NS	0	[]	[]	[]	AP-1 complex subunit sigma-1	PF01217.13	Clat_adaptor_s(Clathrin adaptor complex small chain)
Supercontig_1.18_MVLG_02391_11sp	-544,4672	-544,46712	0,00016	0	NS	0	[]	[]	[]	adenylosuccinate lyase	PF10397.2	ADSL_C(Adenylosuccinate lyase C-terminus)
Supercontig_1.67_MVLG_05199_7sp	-862,58271	-862,58271	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA

Supercontig_1.7_MVLG_01281_8sp	-854,63368	-854,63349	0,00038	0,00019	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.11_MVLG_01716_7sp	-707,37777	-707,18405	0,38744	0,17611	NS	0	[]	[]	[]	hypothetical protein	PF11699.1	Mif2(Mif2/CENP-C like)
Supercontig_1.78_MVLG_05594_7sp	-456,39996	-456,06878	0,66236	0,28192	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.1_MVLG_00109_9sp	-299,64149	-298,11487	3,05324	0,78273	NS	0	[]	[]	[]	hypothetical protein	PF05730.4	CFEM(CFEM domain)
Supercontig_1.44_MVLG_04178_9sp	-811,63934	-811,29633	0,68602	0,29037	NS	0	[]	[]	[]	hypothetical protein	PF01490.11	Aa_trans(Transmembrane amino acid transporter protein)
Supercontig_1.40_MVLG_03910_11sp	-335,63809	-335,63809	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04670.5	Gtr1_RagA(Gtr1/RagA G protein conserved region)
Supercontig_1.5_MVLG_01045_10sp	-641,99135	-641,92084	0,14102	0,06808	NS	0	[]	[]	[]	hypothetical protein	PF04406.7	TP6A_N(Type IIB DNA topoisomerase)
Supercontig_1.28_MVLG_03151_7sp	-520,86885	-520,86871	0,00028	0,00014	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.14_MVLG_02046_10sp	-828,91942	-828,91893	0,00098	0,00049	NS	0	[]	[]	[]	hypothetical protein	PF10296.2	DUF2404(Putative integral membrane protein conserved region (DUF2404))
Supercontig_1.16_MVLG_02247_8sp	-846,23801	-846,23801	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02789.10	Peptidase_M17_N(Cytosol aminopeptidase family, N-terminal domain)
Supercontig_1.101_MVLG_06166_10sp	-727,97779	-727,97779	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.28_MVLG_03170_7sp	-379,50326	-379,45514	0,09624	0,04698	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.57_MVLG_04809_10sp	-643,45141	-643,45118	0,00046	0,00023	NS	0	[]	[]	[]	hypothetical protein	PF05185.9	PRMT5(PRMT5 arginine-N-methyltransferase)
Supercontig_1.15_MVLG_02105_8sp	-416,8169	-416,8169	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00724.13	Oxidored_FMN(NADH:flavin oxidoreductase / NADH oxidase family)
Supercontig_1.3_MVLG_00561_11sp	-747,05491	-747,05491	0	0	NS	0	[]	[]	[]	hypothetical protein	TIGR00707	TIGR00707(argD: acetylornithine and succinylornithine aminotransferases)
Supercontig_1.3_MVLG_00599_10sp	-546,84947	-545,24188	3,21518	0,79963	NS	0	[]	[]	[]	hypothetical protein	PF05686.5	DUF821(Arabidopsis thaliana protein of unknown function (DUF821))
Supercontig_1.9_MVLG_01493_6sp	-1060,1828	-1060,1828	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04987.7	PigN(Phosphatidylinositolglycan class N (PIG-N))
Supercontig_1.9_MVLG_01506_7sp	-1311,2721	-1311,1524	0,23946	0,11284	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.2_MVLG_00354_8sp	-1041,1962	-1039,8141	2,76424	0,74895	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.3_MVLG_00657_8sp	-360,08606	-358,37242	3,42728	0,81979	NS	0	[]	[]	[]	hypothetical protein	PF00106.18	adh_short(short chain dehydrogenase)
Supercontig_1.194_MVLG_07057_10sp	-549,75807	-549,75803	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04157.9	EAP30(EAP30/Vps36 family)
Supercontig_1.20_MVLG_02599_8sp	-1159,0528	-1158,6664	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA

Supercontig_1.23_MVLG_02800_8sp	-1157,993	-1155,4365	5,11314	0,92243	*	0	[]	[]	[]	hypothetical protein	PF00892.13	EamA(EamA-like transporter family)
Supercontig_1.65_MVLG_05131_9sp	-382,59451	-382,59439	0,00024	0,00012	NS	0	[]	[]	[]	hypothetical protein	PF01148.13	CTP_transf_1(Cytidylyltransferase family)
Supercontig_1.1_MVLG_00120_10sp	-469,45594	-469,45594	0	0	NS	0	[]	[]	[]	hypothetical protein	PF07719.10	TPR_2(Tetratricopeptide repeat)
Supercontig_1.13_MVLG_01969_9sp	-503,2682	-503,2682	0	0	NS	0	[]	[]	[]	saccharopine dehydrogenase (NAD+, L-lysine forming)	PF05222.8	AlaDh_PNT_N(Alanine dehydrogenase/PNT, N-terminal domain)
Supercontig_1.1_MVLG_00078_6sp	-767,88646	-767,88536	0,0022	0,0011	NS	0	[]	[]	[]	hypothetical protein	PF07690.9	MFS_1(Major Facilitator Superfamily)
Supercontig_1.6_MVLG_01094_12sp	-547,76255	-547,76255	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03661.6	UPF0121(Uncharacterised protein family (UPF0121))
Supercontig_1.73_MVLG_05434_8sp	-978,73965	-978,73965	0	0	NS	0	[]	[]	[]	carbamoyl-phosphate synthase, small subunit	PF07722.6	Peptidase_C26(Peptidase C26)
Supercontig_1.73_MVLG_05404_7sp	-1115,9466	-1115,9167	0,05978	0,02945	NS	0	[]	[]	[]	hypothetical protein	PF10253.2	PRCC_Cterm(Mitotic checkpoint protein PRCC_Cterm)
Supercontig_1.7_MVLG_01273_8sp	-318,59978	-318,59964	0,00028	0,00014	NS	0	[]	[]	[]	peptidylprolyl isomerase	PF00400.25	WD40(WD domain, G-beta repeat)
Supercontig_1.40_MVLG_03915_9sp	-512,58479	-512,58479	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00076.15	RRM_1(RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain))
Supercontig_1.34_MVLG_03552_10sp	-840,64741	-840,64741	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.42_MVLG_04069_8sp	-947,2845	-947,17972	0,20956	0,09948	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.67_MVLG_05239_8sp	-393,28652	-393,28041	0,01222	0,00609	NS	0	[]	[]	[]	hypothetical protein	PF03162.6	Y_phosphatase2(Tyrosine phosphatase family)
Supercontig_1.161_MVLG_06869_10sp	-544,61385	-544,6137	0,0003	0,00015	NS	0	[]	[]	[]	hypothetical protein	PF01593.17	Amino_oxidase(Flavin containing amine oxidoreductase)
Supercontig_1.3_MVLG_00504_8sp	-951,27266	-951,2169	0,11152	0,05423	NS	0	[]	[]	[]	hypothetical protein	PF11700.1	ATG22(Vacuole effluxer Atg22 like)
Supercontig_1.5_MVLG_00984_8sp	-697,11282	-696,21543	1,79478	0,59237	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.5_MVLG_00937_9sp	-728,56682	-728,19489	0,74386	0,3106	NS	0	[]	[]	[]	hypothetical protein	PF07798.4	DUF1640(Protein of unknown function (DUF1640))
Supercontig_1.21_MVLG_02644_10sp	-431,17903	-431,17903	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.21_MVLG_02649_7sp	-872,31344	-872,07633	0,47422	0,2111	NS	0	[]	[]	[]	hypothetical protein	PF03446.8	NAD_binding_2(NAD binding domain of 6-phosphogluconate dehydrogenase)
Supercontig_1.81_MVLG_05690_11sp	-796,20185	-796,1967	0,0103	0,00514	NS	0	[]	[]	[]	hypothetical protein	PF08799.4	PRP4(pre-mRNA processing factor 4 (PRP4) like)
Supercontig_1.5_MVLG_00905_11sp	-466,47904	-466,36514	0,2278	0,10765	NS	0	[]	[]	[]	hypothetical protein	PF00179.19	UQ_con(Ubiquitin-conjugating enzyme)

Supercontig_1.16_MVLG_02189_9sp	-409,65653	-409,65653	0	0	NS	0	[]	[]	[]	hypothetical protein	PF05176.7	ATP-synt_10(ATP10 protein)
Supercontig_1.16_MVLG_02205_10sp	-474,91726	-474,9172	0,00012	0	NS	0	[]	[]	[]	inorganic pyrophosphatase	PF00719.12	Pyrophosphatase(Inorganic pyrophosphatase)
Supercontig_1.1_MVLG_00149_7sp	-550,30944	-549,66059	1,2977	0,47735	NS	0	[]	[]	[]	hypothetical protein	PF03169.8	OPT(OPT oligopeptide transporter protein)
Supercontig_1.10_MVLG_01610_10sp	-803,03178	-803,03178	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01138.14	RNase_PH(3' exoribonuclease family, domain 1)
Supercontig_1.31_MVLG_03350_7sp	-767,09602	-767,09573	0,00058	0,00029	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.126_MVLG_06523_7sp	-400,813	-400,813	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.3_MVLG_00521_8sp	-527,01056	-527,01056	0	0	NS	0	[]	[]	[]	hypothetical protein	PF10338.2	DUF2423(Protein of unknown function (DUF2423))
Supercontig_1.78_MVLG_05576_6sp	-425,42419	-424,27051	2,30736	0,68453	NS	0	[]	[]	[]	ATP synthase subunit delta	TIGR01216	TIGR01216(ATP_synt_epsi: ATP synthase F1, epsilon subunit)
Supercontig_1.11_MVLG_01789_8sp	-408,9702	-408,9702	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04968.5	CHORD(CHORD)
Supercontig_1.30_MVLG_03309_7sp	-279,07186	-279,07166	0,0004	0,0002	NS	0	[]	[]	[]	60S ribosomal protein L37-A	PF01907.12	Ribosomal_L37e(Ribosomal protein L37e)
Supercontig_1.84_MVLG_05764_7sp	-319,04437	-319,04432	0	0	NS	0	[]	[]	[]	hypothetical protein	PF08523.3	MBF1(Multiprotein bridging factor 1)
Supercontig_1.8_MVLG_01419_9sp	-1002,7397	-1000,3184	4,8426	0,91119	*	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.9_MVLG_01573_11sp	-492,9405	-492,45672	0,96756	0,38355	NS	0	[]	[]	[]	hypothetical protein	PF02893.13	GRAM(GRAM domain)
Supercontig_1.41_MVLG_04008_12sp	-718,89675	-718,89671	0	0	NS	0	[]	[]	[]	hypothetical protein	PF10441.2	Urb2(Urb2/Npa2 family)
Supercontig_1.16_MVLG_02195_9sp	-799,32565	-797,54389	3,56352	0,83166	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.117_MVLG_06393_7sp	-822,06989	-822,06987	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.6_MVLG_01127_9sp	-372,73654	-372,73636	0,00036	0,00018	NS	0	[]	[]	[]	eukaryotic translation initiation factor 2 subunit alpha	PF00575.16	S1(S1 RNA binding domain)
Supercontig_1.31_MVLG_03329_7sp	-1287,577	-1287,577	0	0	NS	0	[]	[]	[]	hypothetical protein	PF07926.5	TPR_MLP1_2(TPR/MLP1/MLP2-like protein)
Supercontig_1.84_MVLG_05756_7sp	-710,56033	-710,5602	0,00026	0,00013	NS	0	[]	[]	[]	hypothetical protein	PF04427.11	Brix(Brix domain)
Supercontig_1.9_MVLG_01551_7sp	-581,10065	-579,86067	2,47996	0,71061	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.41_MVLG_03996_8sp	-1273,117	-1272,974	0,286	0,13325	NS	0	[]	[]	[]	hypothetical protein	PF04727.6	ELMO_CED12(ELMO/CED-12 family)
Supercontig_1.33_MVLG_03469_9sp	-548,81473	-548,81473	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.39_MVLG_03830_9sp	-356,25484	-356,25484	0	0	NS	0	[]	[]	[]	hypothetical protein	PF05327.4	RRN3(RNA polymerase I specific transcription initiation factor RRN3)

Supercontig_1.141_MVLG_06696_6sp	-929,37286	-927,815	3,11572	0,78941	NS	0	[]	[]	[]	hypothetical protein	PF04757.7	Pex2_Pex12(Pex2 / Pex12 amino terminal region)
Supercontig_1.6_MVLG_01191_6sp	-1589,1329	-1589,0154	0,23498	0,11085	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.34_MVLG_03525_9sp	-692,8351	-692,12871	1,41278	0,50658	NS	0	[]	[]	[]	hypothetical protein	PF03874.9	RNA_pol_Rpb4(RNA polymerase Rpb4)
Supercontig_1.3_MVLG_00557_11sp	-594,47039	-594,43283	0,07512	0,03686	NS	0	[]	[]	[]	hypothetical protein	PF08613.4	Cyclin(Cyclin)
Supercontig_1.101_MVLG_06150_7sp	-416,63635	-416,44229	0,38812	0,17639	NS	0	[]	[]	[]	hypothetical protein	PF01764.18	Lipase_3(Lipase (class 3))
Supercontig_1.11_MVLG_01758_9sp	-2852,463	-2852,33	0,266	0,12453	NS	0	[]	[]	[]	hypothetical protein	PF02752.15	Arrestin_C(Arrestin (or S-antigen), C-terminal domain)
Supercontig_1.24_MVLG_02862_9sp	-1069,2443	-1065,1147	8,25914	0,98391	**	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.29_MVLG_03233_6sp	-337,55676	-337,55656	0,0004	0,0002	NS	0	[]	[]	[]	gluconate 5-dehydrogenase	PF00106.18	adh_short(short chain dehydrogenase)
Supercontig_1.7_MVLG_01246_12sp	-703,19276	-703,15406	0,0774	0,03796	NS	0	[]	[]	[]	hypothetical protein	PF00171.15	Aldedh(Aldehyde dehydrogenase family)
Supercontig_1.3_MVLG_00597_7sp	-463,27218	-463,27205	0,00026	0,00013	NS	0	[]	[]	[]	hypothetical protein	PF03907.6	Spo7(Spo7-like protein)
Supercontig_1.132_MVLG_06594_11sp	-985,1293	-984,8063	0,646	0,27603	NS	0	[]	[]	[]	hypothetical protein	PF00102.20	Y_phosphatase(Protein-tyrosine phosphatase)
Supercontig_1.33_MVLG_03458_11sp	-470,86155	-470,86155	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.26_MVLG_03007_7sp	-921,72087	-920,45042	2,5409	0,71929	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.42_MVLG_04044_8sp	-699,78406	-699,54352	0,48108	0,2138	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.5_MVLG_01048_9sp	-379,22279	-379,21627	0,01304	0,0065	NS	0	[]	[]	[]	hypothetical protein	PF07942.5	N2227(N2227-like protein)
Supercontig_1.3_MVLG_00672_6sp	-809,87672	-809,39826	0,95692	0,38026	NS	0	[]	[]	[]	hypothetical protein	PF01694.15	Rhomboid(Rhomboid family)
Supercontig_1.150_MVLG_06776_8sp	-1077,1719	-1077,1719	0	0	NS	0	[]	[]	[]	hypothetical protein	PF06428.4	Sec2p(GDP/GTP exchange factor Sec2p)
Supercontig_1.2_MVLG_00308_11sp	-448,34249	-448,3064	0,07218	0,03545	NS	0	[]	[]	[]	hypothetical protein	TIGR00880	TIGR00880(2_A_01_02: Multidrug resistance protein)
Supercontig_1.7_MVLG_01304_9sp	-1055,7508	-1054,9504	1,60092	0,55088	NS	0	[]	[]	[]	hypothetical protein	PF04488.8	Gly_transf_sug(Glycosyltransferase sugar-binding region containing DXD motif)
Supercontig_1.2_MVLG_00362_6sp	-780,6035	-780,60348	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.2_MVLG_00335_7sp	-1114,8955	-1114,8955	0	0	NS	0	[]	[]	[]	hypothetical protein	PF11312.1	DUF3115(Protein of unknown function (DUF3115))
Supercontig_1.12_MVLG_01833_8sp	-665,91593	-665,01932	1,79322	0,59205	NS	0	[]	[]	[]	hypothetical protein	PF00018.21	SH3_1(SH3 domain)
Supercontig_1.66_MVLG_05159_6sp	-968,80514	-968,14528	1,31972	0,48308	NS	0	[]	[]	[]	hypothetical protein	PF00226.24	DnaJ(DnaJ domain)
Supercontig_1.28_MVLG_03179_6sp	-886,1775	-885,54917	1,25666	0,46652	NS	0	[]	[]	[]	sarcoplasmic/endoplasmic reticulum calcium ATPase 3	TIGR01494	TIGR01494(ATPase_P-type: HAD ATPase, P-type, family IC)
Supercontig_1.99_MVLG_06114_10sp	-572,51068	-570,79428	3,4328	0,82029	NS	0	[]	[]	[]	hypothetical protein	PF04188.6	Mannosyl_trans2(Mannosyltransferase (PIG-V)))

Supercontig_1.3_MVLG_00507_8sp	-932,94954	-932,94954	0	0	NS	0	[]	[]	[]	hypothetical protein	TIGR00887	TIGR00887(2A0109: phosphate:H+ symporter)
Supercontig_1.17_MVLG_02284_9sp	-1073,3958	-1073,3958	0	0	NS	0	[]	[]	[]	peroxisomal hydratase-dehydrogenase-epimerase	PF00106.18	adh_short(short chain dehydrogenase)
Supercontig_1.82_MVLG_05718_8sp	-381,28003	-381,28003	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00782.13	DSPc(Dual specificity phosphatase, catalytic domain)
Supercontig_1.55_MVLG_04742_11sp	-473,23231	-473,23172	0,00118	0,00059	NS	0	[]	[]	[]	iron-sulfur clusters transporter ATM1	PF00664.16	ABC_membrane(ABC transporter transmembrane region)
Supercontig_1.29_MVLG_03216_9sp	-875,31173	-875,25918	0,1051	0,05119	NS	0	[]	[]	[]	stearoyl-CoA desaturase (delta-9 desaturase)	PF00173.21	Cyt-b5(Cytochrome b5-like Heme/Steroid binding domain)
Supercontig_1.64_MVLG_05109_8sp	-584,27688	-583,26127	2,03122	0,63782	NS	0	[]	[]	[]	hypothetical protein	PF05207.6	zf-CSL(CSL zinc finger)
Supercontig_1.3_MVLG_00604_9sp	-384,76518	-384,76504	0,00028	0,00014	NS	0	[]	[]	[]	hypothetical protein	PF02845.9	CUE(CUE domain)
Supercontig_1.44_MVLG_04182_12sp	-554,95274	-554,90366	0,09816	0,0479	NS	0	[]	[]	[]	hypothetical protein	TIGR00913	TIGR00913(2A0310: amino acid permease (yeast))
Supercontig_1.102_MVLG_06174_7sp	-344,53596	-344,27528	0,52136	0,22947	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.10_MVLG_01638_8sp	-831,53983	-831,53957	0,00052	0,00026	NS	0	[]	[]	[]	clathrin heavy chain	PF01394.13	Clathrin_propel(Clathrin propeller repeat)
Supercontig_1.80_MVLG_05650_8sp	-644,39428	-643,89204	1,00448	0,39483	NS	0	[]	[]	[]	hypothetical protein	PF09295.3	ChAPs(ChAPs (Chs5p-Arf1p-binding proteins))
Supercontig_1.6_MVLG_01218_8sp	-1455,7501	-1455,6576	0,18488	0,0883	NS	0	[]	[]	[]	1,3-beta-glucan synthase component FKS1	PF02364.8	Glucan_synthase(1,3-beta-glucan synthase component)
Supercontig_1.34_MVLG_03509_6sp	-615,11568	-615,11568	0	0	NS	0	[]	[]	[]	hypothetical protein	PF06244.5	DUF1014(Protein of unknown function (DUF1014))
Supercontig_1.6_MVLG_01192_8sp	-925,47479	-925,47479	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.13_MVLG_01886_10sp	-673,83343	-672,48465	2,69756	0,74044	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.58_MVLG_04850_8sp	-1187,6213	-1187,6138	0,0149	0,00742	NS	0	[]	[]	[]	hypothetical protein	PF01940.9	DUF92(Integral membrane protein DUF92)
Supercontig_1.1_MVLG_00117_8sp	-303,79336	-303,72573	0,13526	0,06539	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.170_MVLG_06937_10sp	-879,80848	-879,02659	1,56378	0,54246	NS	0	[]	[]	[]	hypothetical protein	PF00400.25	WD40(WD domain, G-beta repeat)
Supercontig_1.98_MVLG_06079_6sp	-799,67952	-799,63383	0,09138	0,04466	NS	0	[]	[]	[]	hypothetical protein	PF00083.17	Sugar_tr(Sugar (and other) transporter)
Supercontig_1.6_MVLG_01150_8sp	-535,16047	-535,16009	0,00076	0,00038	NS	0	[]	[]	[]	hypothetical protein	PF02551.8	Acyl_CoA_thio(Acyl-CoA thioesterase)
Supercontig_1.1_MVLG_00100_10sp	-715,88286	-715,87512	0,01548	0,00771	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.8_MVLG_01366_10sp	-468,916	-468,916	0	0	NS	0	[]	[]	[]	DNA primase small subunit	PF01896.12	DNA_primase_S(Eukaryotic and archaeal DNA primase small subunit)

Supercontig_1.73_MVLG_05407_8sp	-733,065	-732,69437	0,74126	0,3097	NS	0	[]	[]	[]	hypothetical protein	PF02176.11	zf-TRAF(TRAF-type zinc finger)
Supercontig_1.6_MVLG_01175_7sp	-527,01161	-525,91699	2,18924	0,66533	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.87_MVLG_05865_10sp	-812,78175	-811,33129	2,90092	0,76554	NS	0	[]	[]	[]	hypothetical protein	PF04479.6	RTA1(RTA1 like protein)
Supercontig_1.18_MVLG_02399_9sp	-659,36991	-659,36978	0,00026	0,00013	NS	0	[]	[]	[]	hypothetical protein	PF11702.1	DUF3295(Protein of unknown function (DUF3295))
Supercontig_1.198_MVLG_07079_9sp	-407,8607	-407,8607	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.57_MVLG_04824_11sp	-517,02219	-517,02219	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04410.7	Gar1(Gar1/Naf1 RNA binding region)
Supercontig_1.4_MVLG_00842_10sp	-661,27874	-661,27874	0	0	NS	0	[]	[]	[]	prephenate dehydratase	PF00800.11	PDT(Prephenate dehydratase)
Supercontig_1.58_MVLG_04882_7sp	-1149,5845	-1149,5845	0	0	NS	0	[]	[]	[]	hypothetical protein	PF08698.4	Fcf2(Fcf2 pre-rRNA processing)
Supercontig_1.3_MVLG_00549_9sp	-825,55324	-825,55324	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02109.9	DAD(DAD family)
Supercontig_1.13_MVLG_01939_8sp	-1126,4655	-1126,4655	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.25_MVLG_02911_7sp	-391,30646	-391,2238	0,16532	0,07934	NS	0	[]	[]	[]	hypothetical protein	PF00436.18	SSB(Single-strand binding protein family)
Supercontig_1.21_MVLG_02609_9sp	-440,65518	-440,65518	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00153.20	Mito_carr(Mitochondrial carrier protein)
Supercontig_1.69_MVLG_05292_7sp	-433,56203	-433,55	0,02406	0,01196	NS	0	[]	[]	[]	hypothetical protein	PF03105.12	SPX(SPX domain)
Supercontig_1.139_MVLG_06664_9sp	-397,16321	-397,16302	0,00038	0,00019	NS	0	[]	[]	[]	hypothetical protein	PF00466.13	Ribosomal_L10(Ribosomal protein L10)
Supercontig_1.33_MVLG_03463_12sp	-393,64588	-392,52267	2,24642	0,67477	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.185_MVLG_07021_8sp	-477,39551	-477,14231	0,5064	0,22369	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.75_MVLG_05484_7sp	-656,85757	-656,85663	0,00188	0,00094	NS	0	[]	[]	[]	GTP-binding nuclear protein spi1	PF04670.5	Gtr1_RagA(Gtr1/RagA G protein conserved region)
Supercontig_1.113_MVLG_06339_9sp	-367,38052	-367,38052	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00627.24	UBA(UBA/TS-N domain)
Supercontig_1.65_MVLG_05144_9sp	-520,89005	-520,54451	0,69108	0,29216	NS	0	[]	[]	[]	hypothetical protein	PF05907.6	DUF866(Eukaryotic protein of unknown function (DUF866))
Supercontig_1.24_MVLG_02884_9sp	-998,04681	-998,04681	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00149.21	Metallophos(Calcineurin-like phosphoesterase)
Supercontig_1.8_MVLG_01438_8sp	-1493,4539	-1492,9101	1,08756	0,41945	NS	0	[]	[]	[]	hypothetical protein	PF01501.13	Glyco_transf_8(Glycosyl transferase family 8)
Supercontig_1.11_MVLG_01764_10sp	-527,03428	-527,03397	0,00062	0,00031	NS	0	[]	[]	[]	hypothetical protein	PF00248.14	Aldo_ket_red(Aldo/keto reductase family)
Supercontig_1.149_MVLG_06766_6sp	-460,5796	-460,57948	0,00024	0,00012	NS	0	[]	[]	[]	hypothetical protein	PF09803.2	DUF2346(Uncharacterized conserved protein (DUF2346))
Supercontig_1.2_MVLG_00370_10sp	-490,69518	-490,661	0,06836	0,0336	NS	0	[]	[]	[]	hypothetical protein	PF00400.25	WD40(WD domain, G-beta repeat)
Supercontig_1.2_MVLG_00386_11sp	-940,97082	-940,42502	1,0916	0,42062	NS	0	[]	[]	[]	hypothetical protein	NA	NA

Supercontig_1.111_MVLG_06315_8sp	-652,67048	-652,47307	0,39482	0,17915	NS	0	[]	[]	[]	hypothetical protein	PF01263.13	Aldose_epim(Aldose 1-epimerase)
Supercontig_1.9_MVLG_01563_7sp	-773,18078	-773,18078	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.52_MVLG_04585_6sp	-531,24233	-531,22495	0,03476	0,01723	NS	0	[]	[]	[]	hypothetical protein	PF00172.11	Zn_clus(Fungal Zn(2)-Cys(6) binuclear cluster domain)
Supercontig_1.77_MVLG_05557_8sp	-454,74715	-454,74703	0,00024	0,00012	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.42_MVLG_04088_10sp	-528,65965	-527,55404	2,21122	0,66899	NS	0	[]	[]	[]	hypothetical protein	PF08325.3	WLM(WLM domain)
Supercontig_1.38_MVLG_03802_8sp	-473,33148	-473,33148	0	0	NS	0	[]	[]	[]	hypothetical protein	PF10247.2	Romo1(Reactive mitochondrial oxygen species modulator 1)
Supercontig_1.6_MVLG_01077_9sp	-833,85675	-833,85675	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04408.16	HA2(Helicase associated domain (HA2))
Supercontig_1.63_MVLG_05045_9sp	-594,94036	-594,94035	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.13_MVLG_01953_7sp	-780,87932	-780,85657	0,0455	0,02249	NS	0	[]	[]	[]	hypothetical protein	PF00582.19	Usp(Universal stress protein family)
Supercontig_1.45_MVLG_04197_11sp	-269,43286	-269,4327	0,00032	0,00016	NS	0	[]	[]	[]	small nuclear ribonucleoprotein G	PF01423.15	LSM(LSM domain)
Supercontig_1.58_MVLG_04846_6sp	-1884,201	-1884,201	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00225.16	Kinesin(Kinesin motor domain)
Supercontig_1.41_MVLG_04017_7sp	-594,55283	-592,73376	3,63814	0,83782	NS	0	[]	[]	[]	elongation factor Tu	PF03144.18	GTP_EFTU_D2(Elongation factor Tu domain 2)
Supercontig_1.3_MVLG_00522_6sp	-1099,9594	-1099,867	0,1849	0,08831	NS	0	[]	[]	[]	hypothetical protein	PF05890.5	Ebp2(Eukaryotic rRNA processing protein EBP2)
Supercontig_1.11_MVLG_01739_7sp	-399,35518	-399,3551	0,00016	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.16_MVLG_02218_6sp	-640,19005	-640,19005	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.14_MVLG_02044_9sp	-971,35762	-971,16614	0,38296	0,17426	NS	0	[]	[]	[]	hypothetical protein	PF00083.17	Sugar_tr(Sugar (and other) transporter)
Supercontig_1.59_MVLG_04896_11sp	-469,86855	-466,79274	6,15162	0,95385	**	0	[]	[]	[]	hypothetical protein	TIGR00163	TIGR00163(PS_decarb: phosphatidylserine decarboxylase)
Supercontig_1.8_MVLG_01432_7sp	-484,20968	-483,11207	2,19522	0,66633	NS	0	[]	[]	[]	DNA repair and recombination protein RAD54 and RAD54-like protein	PF04851.8	ResIII(Type III restriction enzyme, res subunit)
Supercontig_1.59_MVLG_04886_10sp	-504,95783	-504,95783	0	0	NS	0	[]	[]	[]	guanine nucleotide-binding protein alpha-1 subunit	PF00025.14	Arf(ADP-ribosylation factor family)
Supercontig_1.14_MVLG_02012_11sp	-492,51777	-491,78859	1,45836	0,5177	NS	0	[]	[]	[]	hypothetical protein	PF00172.11	Zn_clus(Fungal Zn(2)-Cys(6) binuclear cluster domain)
Supercontig_1.42_MVLG_04045_9sp	-444,16818	-443,83215	0,67206	0,2854	NS	0	[]	[]	[]	hypothetical protein	PF09736.2	Bud13(Pre-mRNA-splicing factor of RES complex)
Supercontig_1.79_MVLG_05629_9sp	-401,44114	-401,333	0,21628	0,1025	NS	0	[]	[]	[]	hypothetical protein	TIGR00879	TIGR00879(SP: MFS transporter, sugar porter (SP) family)
Supercontig_1.67_MVLG_05240_9sp	-343,03153	-343,03149	0	0	NS	0	[]	[]	[]	hypothetical protein	PF05405.7	Mt_ATP-synt_B(Mitochondrial ATP synthase B chain precursor (ATP-synt_B))

Supercontig_1.131_MVLG_06588_7sp	-1043,6488	-1043,6488	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00172.11	Zn_clus(Fungal Zn(2)-Cys(6) binuclear cluster domain)
Supercontig_1.76_MVLG_05531_10sp	-632,07594	-632,07594	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00432.14	Prenyltrans(Prenyltransferase and squalene oxidase repeat)
Supercontig_1.51_MVLG_04533_11sp	-651,8615	-651,8615	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.12_MVLG_01838_8sp	-1035,3885	-1035,3431	0,09076	0,04437	NS	0	[]	[]	[]	hypothetical protein	PF00515.21	TPR_1(Tetratricopeptide repeat)
Supercontig_1.34_MVLG_03506_6sp	-1040,1428	-1040,1428	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01207.10	Dus(Dihydrouridine synthase (Dus))
Supercontig_1.1_MVLG_00229_9sp	-646,3386	-646,3386	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00225.16	Kinesin(Kinesin motor domain)
Supercontig_1.75_MVLG_05493_7sp	-1012,861	-1012,861	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00443.22	UCH(Ubiquitin carboxyl-terminal hydrolase)
Supercontig_1.6_MVLG_01148_9sp	-338,63897	-338,63897	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.10_MVLG_01622_11sp	-478,16698	-478,16675	0,00046	0,00023	NS	0	[]	[]	[]	hypothetical protein	PF04042.9	DNA_pol_E_B(DNA polymerase alpha/epsilon subunit B)
Supercontig_1.21_MVLG_02661_9sp	-996,70461	-996,67326	0,0627	0,03086	NS	0	[]	[]	[]	heat shock protein 90-1	PF02518.19	HATPase_c(Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase)
Supercontig_1.16_MVLG_02244_9sp	-370,04795	-366,79252	6,51086	0,96144	**	0	[]	[]	[]	hypothetical protein	PF01042.14	Ribonuc_L-PSP(Endoribonuclease L-PSP)
Supercontig_1.1_MVLG_00197_8sp	-1037,8459	-1037,8459	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03915.6	AIP3(Actin interacting protein 3)
Supercontig_1.92_MVLG_05966_9sp	-495,95367	-495,95367	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00557.17	Peptidase_M24(Metallopeptidase family M24)
Supercontig_1.1_MVLG_00222_9sp	-555,06653	-555,0663	0,00046	0,00023	NS	0	[]	[]	[]	phospholipid-translocating ATPase	TIGR01494	TIGR01494(ATPase_P-type: HAD ATPase, P-type, family IC)
Supercontig_1.186_MVLG_07029_8sp	-559,20032	-559,19957	0,0015	0,00075	NS	0	[]	[]	[]	ubiquitin-conjugating enzyme E2-16 kDa	PF00179.19	UQ_con(Ubiquitin-conjugating enzyme)
Supercontig_1.35_MVLG_03583_8sp	-541,63293	-539,01097	5,24392	0,92734	*	0	[]	[]	[]	hypothetical protein	PF00320.20	GATA(GATA zinc finger)
Supercontig_1.31_MVLG_03330_10sp	-511,66729	-511,66729	0	0	NS	0	[]	[]	[]	mitochondrial Rho GTPase 1	PF08477.6	Miro(Miro-like protein)
Supercontig_1.7_MVLG_01275_9sp	-463,54511	-463,54511	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00076.15	RRM_1(RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain))
Supercontig_1.26_MVLG_03008_11sp	-599,70737	-599,70687	0,001	0,0005	NS	0	[]	[]	[]	hypothetical protein	PF00743.12	FMO-like(Flavin-binding monooxygenase-like)
Supercontig_1.25_MVLG_02978_6sp	-524,1691	-524,1691	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01728.12	FtsJ(FtsJ-like methyltransferase)
Supercontig_1.3_MVLG_00614_9sp	-1996,0139	-1994,3978	3,23222	0,80133	NS	0	[]	[]	[]	AGC/RSK protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.2_MVLG_00462_8sp	-236,50632	-234,14015	4,73234	0,90616	*	0	[]	[]	[]	60S ribosomal protein L8	PF00181.16	Ribosomal_L2(Ribosomal Proteins L2, RNA binding domain)

Supercontig_1.62_MVLG_05014_9sp	-349,66609	-348,46566	2,40086	0,69894	NS	0	[]	[]	[]	nascent polypeptide-associated complex subunit beta	PF01849.11	NAC(NAC domain)
Supercontig_1.19_MVLG_02491_9sp	-520,33595	-520,33595	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.35_MVLG_03631_6sp	-521,01321	-521,01321	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.1_MVLG_00224_12sp	-645,30562	-645,30562	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00916.13	Sulfate_transp(Sulfate transporter family)
Supercontig_1.38_MVLG_03787_7sp	-1985,2958	-1982,5625	5,46664	0,935	*	0	[]	[]	[]	hypothetical protein	PF10168.2	Nup88(Nuclear pore component)
Supercontig_1.32_MVLG_03432_7sp	-1286,3093	-1283,8474	4,9239	0,91473	*	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.46_MVLG_04254_9sp	-538,9115	-538,9115	0	0	NS	0	[]	[]	[]	OPT family small oligopeptide transporter	TIGR00727	TIGR00727(ISP4_OPT: small oligopeptide transporter, OPT family)
Supercontig_1.1_MVLG_00176_11sp	-455,46542	-455,46542	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02450.8	LACT(Lecithin:cholesterol acyltransferase)
Supercontig_1.61_MVLG_04957_9sp	-892,63774	-892,09698	1,08152	0,41769	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.2_MVLG_00337_7sp	-383,15658	-383,14423	0,0247	0,01227	NS	0	[]	[]	[]	hypothetical protein	PF00581.13	Rhodanese(Rhodanese-like domain)
Supercontig_1.29_MVLG_03235_9sp	-495,34861	-495,3486	0	0	NS	0	[]	[]	[]	hypothetical protein	PF08241.5	Methyltransf_11(Methyltransferase domain)
Supercontig_1.11_MVLG_01695_8sp	-852,33438	-850,96447	2,73982	0,74587	NS	0	[]	[]	[]	hypothetical protein	PF04193.7	PQ-loop(PQ loop repeat)
Supercontig_1.12_MVLG_01861_7sp	-336,49754	-336,49754	0	0	NS	0	[]	[]	[]	hypothetical protein	PF08660.4	Alg14(Oligosaccharide biosynthesis protein Alg14 like)
Supercontig_1.10_MVLG_01646_7sp	-803,41953	-803,41953	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.64_MVLG_05106_8sp	-370,95983	-370,72913	0,4614	0,20602	NS	0	[]	[]	[]	voltage-gated potassium channel subunit beta	TIGR01293	TIGR01293(Kv_beta: voltage-dependent potassium channel beta subunit)
Supercontig_1.10_MVLG_01579_7sp	-781,29077	-781,29077	0	0	NS	0	[]	[]	[]	hypothetical protein	PF08585.5	DUF1767(Domain of unknown function (DUF1767))
Supercontig_1.11_MVLG_01736_8sp	-1001,0873	-999,97033	2,23402	0,67274	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.30_MVLG_03279_12sp	-432,41749	-432,41749	0	0	NS	0	[]	[]	[]	hypothetical protein	TIGR00879	TIGR00879(SP: MFS transporter, sugar porter (SP) family)
Supercontig_1.10_MVLG_01662_6sp	-294,58347	-294,58332	0,0003	0,00015	NS	0	[]	[]	[]	hypothetical protein	PF00076.15	RRM_1(RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain))
Supercontig_1.1_MVLG_00087_11sp	-347,93788	-347,93783	0	0	NS	0	[]	[]	[]	YggS family pyridoxal phosphate enzyme	PF01168.13	Ala_racemase_N(Alanine racemase, N-terminal domain)
Supercontig_1.38_MVLG_03780_6sp	-461,6646	-461,65454	0,02012	0,01001	NS	0	[]	[]	[]	hypothetical protein	PF00173.21	Cyt-b5(Cytochrome b5-like Heme/Steroid binding domain)
Supercontig_1.5_MVLG_00879_8sp	-643,97795	-643,97765	0,0006	0,0003	NS	0	[]	[]	[]	hypothetical protein	PF08265.4	YL1_C(YL1 nuclear protein C-terminal domain)

Supercontig_1.116_MVLG_06378_10sp	-520,07647	-520,07647	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.63_MVLG_05058_10sp	-282,29871	-282,29852	0,00038	0,00019	NS	0	[]	[]	[]	succinate dehydrogenase [ubiquinone] flavoprotein subunit	TIGR01812	TIGR01812(sdhA_frdA_Gneg: succinate dehydrogenase or fumarate reductase, flavoprotein subunit)
Supercontig_1.26_MVLG_02993_11sp	-993,64965	-991,73991	3,81948	0,85188	NS	0	[]	[]	[]	hypothetical protein	PF00046.22	Homeobox(Homeobox domain)
Supercontig_1.2_MVLG_00416_7sp	-1097,3369	-1096,1932	2,28736	0,68136	NS	0	[]	[]	[]	hypothetical protein	PF00076.15	RRM_1(RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain))
Supercontig_1.17_MVLG_02285_9sp	-635,72171	-635,72171	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.53_MVLG_04630_7sp	-874,25249	-874,25249	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04427.11	Brix(Brix domain)
Supercontig_1.86_MVLG_05840_7sp	-765,07456	-764,44135	1,26642	0,46912	NS	0	[]	[]	[]	hypothetical protein	PF00328.15	Acid_phosphat_A(Histidine acid phosphatase)
Supercontig_1.107_MVLG_06241_7sp	-1259,4965	-1259,4113	0,1703	0,08163	NS	0	[]	[]	[]	hypothetical protein	PF02845.9	CUE(CUE domain)
Supercontig_1.6_MVLG_01160_9sp	-831,06694	-830,05928	2,01532	0,63493	NS	0	[]	[]	[]	hypothetical protein	PF00018.21	SH3_1(SH3 domain)
Supercontig_1.38_MVLG_03767_7sp	-895,35205	-895,35205	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03099.12	BPL_LplA_LipB(Biotin/lipoate A/B protein ligase family)
Supercontig_1.99_MVLG_06104_9sp	-588,17526	-588,17495	0,00062	0,00031	NS	0	[]	[]	[]	hypothetical protein	PF08426.3	ICE2(ICE2)
Supercontig_1.13_MVLG_01975_12sp	-724,824	-724,45853	0,73094	0,30613	NS	0	[]	[]	[]	hypothetical protein	PF01636.16	APH(Phosphotransferase enzyme family)
Supercontig_1.36_MVLG_03667_8sp	-357,79963	-357,79962	0	0	NS	0	[]	[]	[]	hypothetical protein	PF10306.2	FLILHELTA(Hypothetical protein FLILHELTA)
Supercontig_1.12_MVLG_01824_10sp	-540,85276	-540,394	0,91752	0,36793	NS	0	[]	[]	[]	hypothetical protein	PF07250.4	Glyoxal_oxid_N(Glyoxal oxidase N-terminus)
Supercontig_1.39_MVLG_03873_11sp	-539,95842	-539,95784	0,00116	0,00058	NS	0	[]	[]	[]	hypothetical protein	PF00892.13	EamA(EamA-like transporter family)
Supercontig_1.88_MVLG_05885_10sp	-901,7098	-901,20619	1,00722	0,39565	NS	0	[]	[]	[]	hypothetical protein	PF09420.3	Nop16(Ribosome biogenesis protein Nop16)
Supercontig_1.101_MVLG_06163_11sp	-579,04685	-579,04685	0	0	NS	0	[]	[]	[]	hypothetical protein	PF08801.4	Nucleoporin_N(Nup133 N terminal like)
Supercontig_1.1_MVLG_00140_11sp	-362,78641	-362,78758	0	0	NS	0	[]	[]	[]	hypothetical protein	PF08477.6	Miro(Miro-like protein)
Supercontig_1.154_MVLG_06813_9sp	-586,42796	-586,42796	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.125_MVLG_06500_6sp	-337,65567	-337,65564	0	0	NS	0	[]	[]	[]	cyclin-dependent kinase regulatory subunit	PF01111.12	CKS(Cyclin-dependent kinase regulatory subunit)
Supercontig_1.142_MVLG_06707_10sp	-1120,6882	-1120,6882	0	0	NS	0	[]	[]	[]	elongator complex protein 3	PF00583.17	Acetyltransf_1(Acetyltransferase (GNAT) family)
Supercontig_1.121_MVLG_06430_11sp	-708,04374	-707,92997	0,22754	0,10754	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.36_MVLG_03664_12sp	-463,24767	-461,2295	4,03634	0,8671	NS	0	[]	[]	[]	hypothetical protein	NA	NA

Supercontig_1.1_MVLG_00193_11sp	-887,67935	-886,85468	1,64934	0,56162	NS	0	[]	[]	[]	2-dehydropantoate 2-reductase	TIGR00745	TIGR00745(apbA_panE: 2-dehydropantoate 2-reductase)
Supercontig_1.13_MVLG_01916_8sp	-337,24998	-336,97181	0,55634	0,24283	NS	0	[]	[]	[]	isocitrate lyase	TIGR01346	TIGR01346(isocit_lyase: isocitrate lyase)
Supercontig_1.36_MVLG_03676_9sp	-702,91488	-702,77472	0,28032	0,13078	NS	0	[]	[]	[]	hypothetical protein	PF00501.21	AMP-binding(AMP-binding enzyme)
Supercontig_1.60_MVLG_04939_12sp	-691,37874	-691,37874	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03200.9	Glyco_hydro_63(Mannosyl oligosaccharide glucosidase)
Supercontig_1.127_MVLG_06534_7sp	-706,95909	-706,65152	0,61514	0,26477	NS	0	[]	[]	[]	hypothetical protein	PF02469.15	Fasciclin(Fasciclin domain)
Supercontig_1.128_MVLG_06554_10sp	-361,71336	-361,71336	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.9_MVLG_01539_9sp	-412,7435	-412,70516	0,07668	0,03761	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.2_MVLG_00289_12sp	-496,13913	-496,13913	0	0	NS	0	[]	[]	[]	hypothetical protein	PF08123.6	DOT1(Histone methylation protein DOT1)
Supercontig_1.45_MVLG_04227_8sp	-1380,382	-1379,4775	1,80906	0,59527	NS	0	[]	[]	[]	hypothetical protein	PF10257.2	RAI16-like(Retinoic acid induced 16-like protein)
Supercontig_1.186_MVLG_07027_7sp	-936,98034	-936,92607	0,10854	0,05282	NS	0	[]	[]	[]	protein-L-isoaspartate(D-aspartate) O-methyltransferase	PF06325.6	PrmA(Ribosomal protein L11 methyltransferase (PrmA))
Supercontig_1.6_MVLG_01212_8sp	-794,63947	-794,50149	0,27596	0,12888	NS	0	[]	[]	[]	hypothetical protein	PF04752.5	ChaC(ChaC-like protein)
Supercontig_1.30_MVLG_03266_10sp	-1556,2826	-1555,2533	2,05864	0,64275	NS	0	[]	[]	[]	hypothetical protein	PF00566.11	TBC(TBC domain)
Supercontig_1.15_MVLG_02088_12sp	-417,14186	-417,1417	0,00032	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF00328.15	Acid_phosphat_A(Histidine acid phosphatase)
Supercontig_1.4_MVLG_00704_11sp	-418,44027	-417,55638	1,76778	0,58683	NS	0	[]	[]	[]	hypothetical protein	PF00172.11	Zn_clus(Fungal Zn(2)-Cys(6) binuclear cluster domain)
Supercontig_1.74_MVLG_05451_7sp	-882,20386	-882,20386	0	0	NS	0	[]	[]	[]	hypothetical protein	TIGR01137	TIGR01137(cysta_beta: cystathionine beta-synthase)
Supercontig_1.62_MVLG_05021_8sp	-290,31942	-290,21063	0,21758	0,10308	NS	0	[]	[]	[]	calmodulin	PF00036.25	efhand(EF hand)
Supercontig_1.18_MVLG_02356_9sp	-448,33808	-448,32864	0,01888	0,0094	NS	0	[]	[]	[]	hypothetical protein	TIGR00861	TIGR00861(MIP: MIP family channel proteins)
Supercontig_1.34_MVLG_03503_8sp	-553,10649	-552,76238	0,68822	0,29115	NS	0	[]	[]	[]	hypothetical protein	PF01027.13	UPF0005(Uncharacterised protein family UPF0005)
Supercontig_1.23_MVLG_02786_12sp	-603,66326	-603,66326	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.2_MVLG_00472_7sp	-792,11679	-790,09234	4,0489	0,86793	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.56_MVLG_04767_7sp	-840,8041	-840,8038	0,0006	0,0003	NS	0	[]	[]	[]	hypothetical protein	PF03061.15	4HBT(Thioesterase superfamily)
Supercontig_1.12_MVLG_01814_8sp	-1078,5526	-1078,396	0,31308	0,1449	NS	0	[]	[]	[]	glutamate decarboxylase	PF00282.12	Pyridoxal_deC(Pyridoxal-dependent decarboxylase conserved domain)
Supercontig_1.2_MVLG_00292_8sp	-413,57934	-413,57933	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01467.19	CTP_transf_2(Cytidylyltransferase)
Supercontig_1.25_MVLG_02921_7sp	-889,67707	-889,67697	0	0	NS	0	[]	[]	[]	actin-like protein 3	PF00022.12	Actin(Actin)

Supercontig_1.1_MVLG_00172_9sp	-409,23035	-409,22989	0,00092	0,00046	NS	0	[]	[]	[]	40S ribosomal protein S18	PF00416.15	Ribosomal_S13(Ribosomal protein S13/S18)
Supercontig_1.25_MVLG_02962_9sp	-858,0837	-858,06837	0,03066	0,01521	NS	0	[]	[]	[]	hypothetical protein	PF00380.12	Ribosomal_S9(Ribosomal protein S9/S16)
Supercontig_1.44_MVLG_04157_9sp	-870,0981	-869,96644	0,26332	0,12336	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.2_MVLG_00428_6sp	-417,49593	-417,41942	0,15302	0,07366	NS	0	[]	[]	[]	hypothetical protein	PF06726.5	BC10(Bladder cancer-related protein BC10)
Supercontig_1.186_MVLG_07024_6sp	-1566,3242	-1564,0856	4,4773	0,8934	NS	0	[]	[]	[]	hypothetical protein	PF09814.2	DUF2351(Uncharacterized conserved protein (DUF2351))
Supercontig_1.49_MVLG_04415_6sp	-348,71812	-348,71812	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.17_MVLG_02345_10sp	-1108,6242	-1108,6242	0	0	NS	0	[]	[]	[]	hypothetical protein	PF10537.2	WAC_Acf1_DNA_bd(ATP-utilising chromatin assembly and remodelling N-terminal)
Supercontig_1.1_MVLG_00266_7sp	-1416,2427	-1416,2427	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.19_MVLG_02487_9sp	-1051,3531	-1051,3531	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.1_MVLG_00182_10sp	-798,05244	-796,76762	2,56964	0,7233	NS	0	[]	[]	[]	hypothetical protein	PF03959.6	FSH1(Serine hydrolase (FSH1))
Supercontig_1.58_MVLG_04877_11sp	-440,95057	-440,91576	0,06962	0,03421	NS	0	[]	[]	[]	hypothetical protein	PF00026.16	Asp(Eukaryotic aspartyl protease)
Supercontig_1.34_MVLG_03505_9sp	-519,07854	-519,06858	0,01992	0,00991	NS	0	[]	[]	[]	hypothetical protein	PF01853.11	MOZ_SAS(MOZ/SAS family)
Supercontig_1.18_MVLG_02385_9sp	-866,52258	-866,52258	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00324.14	AA_permease(Amino acid permease)
Supercontig_1.78_MVLG_05584_7sp	-752,53326	-752,53326	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01036.11	Bac_rhodopsin(Bacteriorhodopsin-like protein)
Supercontig_1.22_MVLG_02758_8sp	-782,02298	-781,31184	1,42228	0,50892	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.84_MVLG_05754_12sp	-470,15687	-470,15687	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00150.11	Cellulase(Cellulase (glycosyl hydrolase family 5))
Supercontig_1.10_MVLG_01648_7sp	-803,64573	-803,64573	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01399.20	PCI(PCI domain)
Supercontig_1.46_MVLG_04284_8sp	-886,48759	-885,03913	2,89692	0,76507	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.62_MVLG_05044_9sp	-670,58522	-670,58522	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01603.13	B56(Protein phosphatase 2A regulatory B subunit (B56 family))
Supercontig_1.51_MVLG_04501_10sp	-627,70763	-627,60574	0,20378	0,09687	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.131_MVLG_06589_9sp	-851,42707	-851,42707	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01694.15	Rhomboid(Rhomboid family)
Supercontig_1.148_MVLG_06755_8sp	-604,93574	-604,54255	0,78638	0,3251	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.20_MVLG_02525_10sp	-644,38603	-644,38579	0,00048	0,00024	NS	0	[]	[]	[]	hypothetical protein	PF08241.5	Methyltransf_11(Methyltransferase domain)
Supercontig_1.91_MVLG_05926_7sp	-742,46082	-740,81112	3,2994	0,80789	NS	0	[]	[]	[]	hypothetical protein	PF00076.15	RRM_1(RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain))

Supercontig_1.10_MVLG_01607_7sp	-977,73246	-977,73246	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04082.11	Fungal_trans(Fungal specific transcription factor domain)
Supercontig_1.56_MVLG_04779_9sp	-431,42264	-431,42264	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.2_MVLG_00433_11sp	-788,67314	-788,67314	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00533.19	BRCT(BRCA1 C Terminus (BRCT) domain)
Supercontig_1.44_MVLG_04170_9sp	-452,29427	-451,9781	0,63234	0,27106	NS	0	[]	[]	[]	hypothetical protein	PF00730.18	HhH-GPD(HhH-GPD superfamily base excision DNA repair protein)
Supercontig_1.10_MVLG_01626_11sp	-588,64119	-587,22932	2,82374	0,75631	NS	0	[]	[]	[]	hypothetical protein	PF08238.5	Sel1(Sel1 repeat)
Supercontig_1.19_MVLG_02464_10sp	-576,76084	-576,76069	0,0003	0,00015	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.6_MVLG_01208_9sp	-1064,7414	-1064,7413	0,00016	0	NS	0	[]	[]	[]	MFS transporter, SIT family, siderophore-iron:H+ symporter	NA	NA
Supercontig_1.42_MVLG_04093_8sp	-624,93336	-624,88666	0,0934	0,04563	NS	0	[]	[]	[]	3-deoxy-7-phosphoheptulonate synthase	TIGR00034	TIGR00034(aroFGH: 3-deoxy-7-phosphoheptulonate synthase)
Supercontig_1.14_MVLG_01986_6sp	-650,21711	-649,03989	2,35444	0,69187	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.16_MVLG_02191_8sp	-480,96837	-480,96817	0,0004	0,0002	NS	0	[]	[]	[]	dolichyl-diphosphooligosaccharide-protein glycosyltransferase subunit stt3	PF02516.7	STT3(Oligosaccharyl transferase STT3 subunit)
Supercontig_1.4_MVLG_00699_8sp	-578,92609	-578,92609	0	0	NS	0	[]	[]	[]	non-specific lipid-transfer protein	PF00108.16	Thiolase_N(Thiolase, N-terminal domain)
Supercontig_1.11_MVLG_01700_8sp	-350,86122	-350,86122	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.69_MVLG_05286_8sp	-404,17329	-404,11793	0,11072	0,05386	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.97_MVLG_06058_7sp	-406,09723	-405,72357	0,74732	0,31179	NS	0	[]	[]	[]	hypothetical protein	PF01451.14	LMWPc(Low molecular weight phosphotyrosine protein phosphatase)
Supercontig_1.56_MVLG_04787_9sp	-408,54751	-408,5475	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.74_MVLG_05449_7sp	-565,93454	-564,41897	3,03114	0,78032	NS	0	[]	[]	[]	methylcrotonoyl-CoA carboxylase beta chain	PF01039.15	Carboxyl_trans(Carboxyl transferase domain)
Supercontig_1.29_MVLG_03223_10sp	-721,13681	-719,09859	4,07644	0,86974	NS	0	[]	[]	[]	hypothetical protein	PF03847.6	TFIID_20kDa(Transcription initiation factor TFIID subunit A)
Supercontig_1.75_MVLG_05488_9sp	-399,68836	-399,68827	0,00018	0	NS	0	[]	[]	[]	hypothetical protein	PF07728.7	AAA_5(AAA domain (dynein-related subfamily))
Supercontig_1.175_MVLG_06970_9sp	-689,86479	-689,86479	0	0	NS	0	[]	[]	[]	enoyl-CoA hydratase	PF00378.13	ECH(Enoyl-CoA hydratase/isomerase family)
Supercontig_1.200_MVLG_07083_9sp	-714,6586	-714,57285	0,1715	0,08218	NS	0	[]	[]	[]	hypothetical protein	PF02678.9	Pirin(Pirin)
Supercontig_1.76_MVLG_05533_8sp	-511,48381	-511,48381	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA

Supercontig_1.31_MVLG_03378_10sp	-673,82687	-673,82687	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.46_MVLG_04246_10sp	-419,44453	-419,44453	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03901.10	Glyco_transf_22(Alg9-like mannosyltransferase family)
Supercontig_1.24_MVLG_02833_10sp	-674,43537	-674,43537	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00400.25	WD40(WD domain, G-beta repeat)
Supercontig_1.4_MVLG_00815_7sp	-341,22688	-339,62274	3,20828	0,79894	NS	0	[]	[]	[]	hypothetical protein	PF05730.4	CFEM(CFEM domain)
Supercontig_1.17_MVLG_02337_9sp	-513,3031	-513,14901	0,30818	0,14281	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.1_MVLG_00039_7sp	-469,50313	-469,32322	0,35982	0,16465	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.19_MVLG_02499_11sp	-672,19663	-670,01287	4,36752	0,88738	NS	0	[]	[]	[]	hypothetical protein	PF07967.6	zf-C3HC(C3HC zinc finger-like)
Supercontig_1.6_MVLG_01087_10sp	-583,5796	-582,89801	1,36318	0,49419	NS	0	[]	[]	[]	hypothetical protein	PF08294.4	TIM21(TIM21)
Supercontig_1.15_MVLG_02114_6sp	-576,9833	-576,98293	0,00074	0,00037	NS	0	[]	[]	[]	dynactin 5	PF00132.17	Hexapep(Bacterial transferase hexapeptide (three repeats))
Supercontig_1.6_MVLG_01076_12sp	-968,39393	-968,39393	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00270.22	DEAD(DEAD/DEAH box helicase)
Supercontig_1.34_MVLG_03558_8sp	-932,29812	-932,07009	0,45606	0,2039	NS	0	[]	[]	[]	hypothetical protein	PF02845.9	CUE(CUE domain)
Supercontig_1.29_MVLG_03239_10sp	-416,42273	-416,42257	0,00032	0,00016	NS	0	[]	[]	[]	eukaryotic translation initiation factor 2 subunit gamma	PF09173.4	eIF2_C(Initiation factor eIF2 gamma, C terminal)
Supercontig_1.86_MVLG_05834_8sp	-764,68729	-764,68729	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04479.6	RTA1(RTA1 like protein)
Supercontig_1.46_MVLG_04291_7sp	-557,27441	-556,36932	1,81018	0,59549	NS	0	[]	[]	[]	hypothetical protein	PF03540.6	TFIID_30kDa(Transcription initiation factor TFIID 23-30kDa subunit)
Supercontig_1.112_MVLG_06326_6sp	-634,58406	-634,58387	0,00038	0,00019	NS	0	[]	[]	[]	hypothetical protein	PF05495.5	zf-CHY(CHY zinc finger)
Supercontig_1.85_MVLG_05808_10sp	-589,76459	-589,76459	0	0	NS	0	[]	[]	[]	hypothetical protein	PF08774.4	VRR_NUC(VRR-NUC domain)
Supercontig_1.28_MVLG_03141_6sp	-990,68999	-990,50957	0,36084	0,16508	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.61_MVLG_04981_8sp	-804,16114	-803,39765	1,52698	0,53396	NS	0	[]	[]	[]	hypothetical protein	PF00326.14	Peptidase_S9(Prolyl oligopeptidase family)
Supercontig_1.2_MVLG_00421_10sp	-350,61481	-350,61474	0,00014	0	NS	0	[]	[]	[]	hypothetical protein	PF08539.4	HbrB(HbrB-like)
Supercontig_1.31_MVLG_03357_12sp	-588,80774	-588,80198	0,01152	0,00574	NS	0	[]	[]	[]	hypothetical protein	PF00995.16	Sec1(Sec1 family)
Supercontig_1.17_MVLG_02293_9sp	-615,08067	-615,08067	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03330.11	DPBB_1(Rare lipoprotein A (RlpA)-like double-psi beta-barrel)
Supercontig_1.19_MVLG_02486_6sp	-711,75855	-711,43781	0,64148	0,27439	NS	0	[]	[]	[]	hypothetical protein	PF05742.5	DUF833(Protein of unknown function (DUF833))
Supercontig_1.4_MVLG_00819_10sp	-637,3668	-637,3668	0	0	NS	0	[]	[]	[]	hypothetical protein	PF07958.4	DUF1688(Protein of unknown function (DUF1688))

Supercontig_1.18_MVLG_02407_10sp	-836,10501	-836,10501	0	0	NS	0	[]	[]	[]	hypothetical protein	PF05182.6	Fip1(Fip1 motif)
Supercontig_1.1_MVLG_00267_8sp	-511,05531	-511,05521	0,0002	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.35_MVLG_03630_12sp	-1394,7291	-1394,7291	0	0	NS	0	[]	[]	[]	STE/STE11/CDC15 protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.32_MVLG_03439_8sp	-408,2181	-407,82334	0,78952	0,32616	NS	0	[]	[]	[]	hypothetical protein	PF00475.11	IGPD(Imidazoleglycerol-phosphate dehydratase)
Supercontig_1.5_MVLG_00995_10sp	-401,60937	-401,60937	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00929.17	Exonuc_X-T(Exonuclease)
Supercontig_1.48_MVLG_04391_9sp	-571,15402	-571,15374	0,00056	0,00028	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.12_MVLG_01846_8sp	-500,69436	-500,67825	0,03222	0,01598	NS	0	[]	[]	[]	hypothetical protein	PF00153.20	Mito_carr(Mitochondrial carrier protein)
Supercontig_1.20_MVLG_02575_6sp	-822,44455	-822,44455	0	0	NS	0	[]	[]	[]	galactose-1-phosphate uridylyltransferase	PF02744.10	GalP_UDP_tr_C(Galactose-1-phosphate uridyl transferase, C-terminal domain)
Supercontig_1.1_MVLG_00056_7sp	-597,95409	-596,25711	3,39396	0,81676	NS	0	[]	[]	[]	hypothetical protein	PF07524.6	Bromo_TP(Bromodomain associated)
Supercontig_1.11_MVLG_01776_6sp	-1062,9863	-1062,5329	0,90676	0,36452	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.17_MVLG_02283_10sp	-973,94025	-972,09707	3,68636	0,84169	NS	0	[]	[]	[]	hypothetical protein	PF00188.19	CAP(Cysteine-rich secretory protein family)
Supercontig_1.9_MVLG_01479_9sp	-609,49536	-609,49536	0	0	NS	0	[]	[]	[]	60S ribosomal protein L11-B	PF00281.12	Ribosomal_L5(Ribosomal protein L5)
Supercontig_1.7_MVLG_01279_10sp	-376,28793	-376,28793	0	0	NS	0	[]	[]	[]	hypothetical protein	TIGR00880	TIGR00880(2_A_01_02: Multidrug resistance protein)
Supercontig_1.1_MVLG_00019_11sp	-354,41897	-354,41889	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01244.14	Peptidase_M19(Membrane dipeptidase (Peptidase family M19))
Supercontig_1.23_MVLG_02773_8sp	-425,15678	-425,15678	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00484.12	Pro_CA(Carbonic anhydrase)
Supercontig_1.21_MVLG_02613_11sp	-393,7189	-393,71864	0	0	NS	0	[]	[]	[]	hypothetical protein	PF07534.9	TLD(TLD)
Supercontig_1.17_MVLG_02336_6sp	-487,48643	-487,48639	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00664.16	ABC_membrane(ABC transporter transmembrane region)
Supercontig_1.49_MVLG_04425_9sp	-417,14314	-417,14312	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04181.6	RPAP2_Rtr1(Rtr1/RPAP2 family)
Supercontig_1.2_MVLG_00361_9sp	-750,50369	-750,44965	0,10808	0,05261	NS	0	[]	[]	[]	hypothetical protein	PF02194.8	PXA(PXA domain)
Supercontig_1.5_MVLG_00996_12sp	-467,6903	-467,69008	0,00044	0,00022	NS	0	[]	[]	[]	hypothetical protein	PF01479.18	S4(S4 domain)
Supercontig_1.28_MVLG_03184_12sp	-382,37101	-382,37101	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03009.10	GDPD(Glycerophosphoryl diester phosphodiesterase family)
Supercontig_1.11_MVLG_01763_6sp	-901,48208	-901,48208	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00753.20	Lactamase_B(Metallo-beta-lactamase superfamily)
Supercontig_1.307_MVLG_07237_10sp	-328,38759	-328,38759	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00107.19	ADH_zinc_N(Zinc-binding dehydrogenase)
Supercontig_1.21_MVLG_02611_7sp	-525,72738	-525,72738	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02311.12	AraC_binding(AraC-like ligand binding domain)

Supercontig_1.236_MVLG_07197_11sp	-630,21115	-629,36731	1,68768	0,56994	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.212_MVLG_07129_9sp	-1095,4388	-1094,9323	1,01308	0,39742	NS	0	[]	[]	[]	hypothetical protein	PF00400.25	WD40(WD domain, G-beta repeat)
Supercontig_1.161_MVLG_06867_10sp	-816,5649	-814,56499	3,99982	0,86465	NS	0	[]	[]	[]	hypothetical protein	PF10374.2	EST1(Telomerase activating protein Est1)
Supercontig_1.45_MVLG_04210_7sp	-1367,67	-1365,2944	4,7511	0,90704	*	0	[]	[]	[]	hypothetical protein	PF04129.5	Vps52(Vps52 / Sac2 family)
Supercontig_1.4_MVLG_00836_6sp	-987,47628	-986,37482	2,20292	0,66761	NS	0	[]	[]	[]	hypothetical protein	PF00076.15	RRM_1(RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain))
Supercontig_1.61_MVLG_04968_11sp	-586,87532	-586,87532	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.1_MVLG_00122_10sp	-386,9094	-386,9094	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.1_MVLG_00134_9sp	-1030,9149	-1030,8487	0,13256	0,06413	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.67_MVLG_05244_8sp	-913,25856	-913,21483	0,08746	0,04279	NS	0	[]	[]	[]	hypothetical protein	PF00501.21	AMP-binding(AMP-binding enzyme)
Supercontig_1.36_MVLG_03663_8sp	-568,6958	-568,08732	1,21696	0,45582	NS	0	[]	[]	[]	hypothetical protein	PF01008.10	IF-2B(Initiation factor 2 subunit family)
Supercontig_1.1_MVLG_00047_11sp	-569,97718	-569,97714	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.18_MVLG_02363_8sp	-252,07763	-251,71772	0,71982	0,30226	NS	0	[]	[]	[]	hypothetical protein	PF08609.3	Fes1(Nucleotide exchange factor Fes1)
Supercontig_1.24_MVLG_02906_6sp	-586,88435	-586,53182	0,70506	0,29709	NS	0	[]	[]	[]	hypothetical protein	PF00860.13	Xan_ur_permease(Permease family)
Supercontig_1.60_MVLG_04932_7sp	-350,47986	-350,47986	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04800.5	ETC_C1_NDUFA4(ETC complex I subunit conserved region)
Supercontig_1.39_MVLG_03897_9sp	-625,79462	-625,79458	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00439.18	Bromodomain(Bromodomain)
Supercontig_1.197_MVLG_07073_6sp	-458,02792	-458,0279	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01105.17	EMP24_GP25L(emp24/gp25L/p24 family/GOLD)
Supercontig_1.31_MVLG_03362_7sp	-350,13972	-349,21998	1,83948	0,60138	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.1_MVLG_00218_7sp	-640,32295	-639,03435	2,5772	0,72434	NS	0	[]	[]	[]	hypothetical protein	PF10262.2	Rdx(Rdx family)
Supercontig_1.1_MVLG_00050_7sp	-537,11035	-536,70816	0,80438	0,33115	NS	0	[]	[]	[]	hypothetical protein	PF04979.7	IPP-2(Protein phosphatase inhibitor 2 (IPP-2))
Supercontig_1.4_MVLG_00820_8sp	-861,32738	-857,13883	8,3771	0,98483	**	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.26_MVLG_03042_9sp	-471,23347	-471,23347	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03291.9	Pox_MCEL(mRNA capping enzyme)
Supercontig_1.28_MVLG_03186_10sp	-1107,4484	-1107,4484	0	0	NS	0	[]	[]	[]	hypothetical protein	PF07034.4	ORC3_N(Origin recognition complex (ORC) subunit 3 N-terminus)
Supercontig_1.22_MVLG_02733_9sp	-573,47792	-573,47788	0	0	NS	0	[]	[]	[]	hypothetical protein	TIGR01358	TIGR01358(DAHP_synth_II: 3-deoxy-7-phosphoheptulonate synthase)

Supercontig_1.24_MVLG_02905_7sp	-767,90294	-767,08779	1,6303	0,55743	NS	0	[]	[]	[]	electron transfer flavoprotein alpha subunit	PF00766.12	ETF_alpha(Electron transfer flavoprotein FAD-binding domain)
Supercontig_1.6_MVLG_01182_7sp	-495,33384	-495,33384	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01730.9	UreF(UreF)
Supercontig_1.25_MVLG_02939_9sp	-585,90639	-585,90588	0,00102	0,00051	NS	0	[]	[]	[]	kinesin heavy chain	PF00225.16	Kinesin(Kinesin motor domain)
Supercontig_1.87_MVLG_05856_7sp	-344,81238	-344,81234	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03171.13	2OG-FeII_Oxy(2OG-Fe(II) oxygenase superfamily)
Supercontig_1.94_MVLG_05995_9sp	-512,48382	-512,00536	0,95692	0,38026	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.15_MVLG_02136_9sp	-691,88507	-691,88507	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00339.22	Arrestin_N(Arrestin (or S-antigen), N-terminal domain)
Supercontig_1.5_MVLG_00979_6sp	-458,90851	-458,9085	0	0	NS	0	[]	[]	[]	hypothetical protein	TIGR00556	TIGR00556(pantethn_trn: phosphopantethiene--protein transferase domain)
Supercontig_1.74_MVLG_05461_7sp	-622,62248	-622,62248	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01066.14	CDP-OH_P_transf(CDP-alcohol phosphatidyltransferase)
Supercontig_1.140_MVLG_06680_7sp	-345,10869	-344,28222	1,65294	0,56241	NS	0	[]	[]	[]	ubiquitin-conjugating enzyme E2 35	PF00179.19	UQ_con(Ubiquitin-conjugating enzyme)
Supercontig_1.42_MVLG_04089_6sp	-496,70653	-496,53251	0,34804	0,15972	NS	0	[]	[]	[]	hypothetical protein	PF06201.6	PITH(C-terminal proteasome-interacting domain of thioredoxin-like)
Supercontig_1.53_MVLG_04642_6sp	-476,7959	-476,7959	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.7_MVLG_01357_8sp	-541,09212	-541,09212	0	0	NS	0	[]	[]	[]	hypothetical protein	PF10250.2	O-FucT(GDP-fucose protein O-fucosyltransferase)
Supercontig_1.79_MVLG_05625_9sp	-489,43284	-489,43276	0,00016	0	NS	0	[]	[]	[]	acetoacetate-CoA ligase	TIGR01217	TIGR01217(ac_ac_CoA_syn: acetoacetate-CoA ligase)
Supercontig_1.28_MVLG_03135_7sp	-404,75002	-404,11473	1,27058	0,47022	NS	0	[]	[]	[]	hypothetical protein	TIGR03421	TIGR03421(FeS_CyaY: iron donor protein CyaY)
Supercontig_1.12_MVLG_01806_11sp	-551,6594	-551,6593	0,0002	0	NS	0	[]	[]	[]	hypothetical protein	PF10230.2	DUF2305(Uncharacterised conserved protein (DUF2305))
Supercontig_1.48_MVLG_04397_9sp	-401,84555	-401,84555	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02297.10	COX6B(Cytochrome oxidase c subunit VIb)
Supercontig_1.128_MVLG_06551_6sp	-786,42956	-786,02087	0,81738	0,33548	NS	0	[]	[]	[]	hypothetical protein	PF07950.4	DUF1691(Protein of unknown function (DUF1691))
Supercontig_1.16_MVLG_02200_8sp	-910,6133	-910,6133	0	0	NS	0	[]	[]	[]	T-complex protein 1 subunit epsilon	TIGR02343	TIGR02343(chap_CCT_epsi: T-complex protein 1, epsilon subunit)
Supercontig_1.4_MVLG_00799_7sp	-642,911	-642,43571	0,95058	0,3783	NS	0	[]	[]	[]	hypothetical protein	PF02800.13	Gp_dh_C(Glyceraldehyde 3-phosphate dehydrogenase, C-terminal domain)
Supercontig_1.34_MVLG_03511_11sp	-370,81579	-369,2641	3,10338	0,78811	NS	0	[]	[]	[]	hypothetical protein	PF05615.6	THOC7(Tho complex subunit 7)
Supercontig_1.54_MVLG_04671_11sp	-760,68556	-759,81076	1,7496	0,58305	NS	0	[]	[]	[]	hypothetical protein	PF01068.14	DNA_ligase_A_M(ATP dependent DNA ligase domain)
Supercontig_1.16_MVLG_02223_9sp	-773,333	-771,81213	3,04174	0,78148	NS	0	[]	[]	[]	hypothetical protein	PF06745.6	KaiC(KaiC)

Supercontig_1.2_MVLG_00377_12sp	-528,2446	-528,24439	0,00042	0,00021	NS	0	[]	[]	[]	hypothetical protein	PF01546.21	Peptidase_M20(Peptidase family M20/M25/M40)
Supercontig_1.22_MVLG_02725_6sp	-767,09454	-766,82945	0,53018	0,23286	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.2_MVLG_00385_8sp	-617,66465	-617,37232	0,58466	0,25348	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.3_MVLG_00613_10sp	-517,54259	-517,41049	0,2642	0,12375	NS	0	[]	[]	[]	aminotransferase, classes I and II	PF00155.14	Aminotran_1_2(Aminotransferase class I and II)
Supercontig_1.161_MVLG_06873_10sp	-434,81076	-434,77746	0,0666	0,03275	NS	0	[]	[]	[]	hypothetical protein	PF05686.5	DUF821(Arabidopsis thaliana protein of unknown function (DUF821))
Supercontig_1.20_MVLG_02590_8sp	-592,25306	-592,14586	0,2144	0,10165	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.38_MVLG_03759_11sp	-491,39991	-491,39985	0,00012	0	NS	0	[]	[]	[]	hypothetical protein	PF00481.14	PP2C(Protein phosphatase 2C)
Supercontig_1.1_MVLG_00089_10sp	-412,87219	-411,30059	3,1432	0,79229	NS	0	[]	[]	[]	hypothetical protein	PF00155.14	Aminotran_1_2(Aminotransferase class I and II)
Supercontig_1.40_MVLG_03904_10sp	-428,29315	-426,39896	3,78838	0,84956	NS	0	[]	[]	[]	hypothetical protein	PF08648.5	DUF1777(Protein of unknown function (DUF1777))
Supercontig_1.365_MVLG_07249_7sp	-871,65711	-870,99836	1,3175	0,4825	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.49_MVLG_04444_11sp	-1171,1144	-1171,1144	0	0	NS	0	[]	[]	[]	aspartate aminotransferase	PF00155.14	Aminotran_1_2(Aminotransferase class I and II)
Supercontig_1.51_MVLG_04508_10sp	-679,26982	-679,26982	0	0	NS	0	[]	[]	[]	pyruvate dehydrogenase E1 component subunit alpha	TIGR03182	TIGR03182(PDH_E1_alph_y: pyruvate dehydrogenase (acetyl-transferring) E1 component, alpha subunit)
Supercontig_1.101_MVLG_06165_11sp	-532,86319	-532,71167	0,30304	0,1406	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.2_MVLG_00331_6sp	-601,59762	-601,59725	0,00074	0,00037	NS	0	[]	[]	[]	hypothetical protein	PF00735.11	Septin(Septin)
Supercontig_1.173_MVLG_06957_9sp	-693,89212	-693,89212	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03124.7	EXS(EXS family)
Supercontig_1.9_MVLG_01519_12sp	-800,22529	-800,11127	0,22804	0,10776	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.36_MVLG_03635_9sp	-854,31951	-854,31951	0	0	NS	0	[]	[]	[]	hypothetical protein	PF08645.4	PNK3P(Polynucleotide kinase 3 phosphatase)
Supercontig_1.1_MVLG_00041_9sp	-707,67784	-707,67763	0,00042	0,00021	NS	0	[]	[]	[]	NADP-specific glutamate dehydrogenase	PF02812.11	ELFV_dehydrog_N(Glu/Leu/Phe/Val dehydrogenase, dimerisation domain)
Supercontig_1.27_MVLG_03099_9sp	-470,28791	-470,16178	0,25226	0,1185	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.51_MVLG_04504_10sp	-707,02967	-707,02916	0,00102	0,00051	NS	0	[]	[]	[]	exportin-1	PF03810.12	IBN_N(Importin-beta N-terminal domain)
Supercontig_1.1_MVLG_00060_6sp	-392,25676	-392,25671	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.87_MVLG_05843_7sp	-886,71994	-886,71994	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00125.17	Histone(Core histone H2A/H2B/H3/H4)
Supercontig_1.29_MVLG_03237_7sp	-1420,206	-1420,1391	0,13374	0,06468	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.15_MVLG_02059_9sp	-325,00994	-323,5939	2,83208	0,75733	NS	0	[]	[]	[]	hypothetical protein	NA	NA

Supercontig_1.19_MVLG_02473_10sp	-459,38517	-459,37439	0,02156	0,01072	NS	0	[]	[]	[]	hypothetical protein	PF08799.4	PRP4(pre-mRNA processing factor 4 (PRP4) like)
Supercontig_1.15_MVLG_02146_8sp	-730,37825	-730,37825	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01062.14	Bestrophin(Bestrophin)
Supercontig_1.15_MVLG_02152_9sp	-1262,2926	-1262,2222	0,14086	0,06801	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.59_MVLG_04913_7sp	-768,14691	-768,14691	0	0	NS	0	[]	[]	[]	CAMK/CAMKL/PASK protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.13_MVLG_01925_9sp	-529,37714	-527,59956	3,55516	0,83095	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.51_MVLG_04538_7sp	-689,48443	-689,48443	0	0	NS	0	[]	[]	[]	hypothetical protein	PF08711.4	Med26(TFIIS helical bundle-like domain)
Supercontig_1.8_MVLG_01429_6sp	-341,64983	-341,64983	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00581.13	Rhodanese(Rhodanese-like domain)
Supercontig_1.46_MVLG_04255_11sp	-1047,5739	-1047,5497	0,04836	0,02389	NS	0	[]	[]	[]	hypothetical protein	PF00149.21	Metallophos(Calcineurin-like phosphoesterase)
Supercontig_1.60_MVLG_04935_11sp	-461,09256	-461,09256	0	0	NS	0	[]	[]	[]	dihydrolipoyl dehydrogenase	PF00070.20	Pyr_redox(Pyridine nucleotide-disulphide oxidoreductase)
Supercontig_1.4_MVLG_00795_7sp	-1214,2462	-1214,2462	0	0	NS	0	[]	[]	[]	hypothetical protein	TIGR00756	TIGR00756(PPR: pentatricopeptide repeat domain)
Supercontig_1.66_MVLG_05190_6sp	-665,06175	-664,90603	0,31144	0,1442	NS	0	[]	[]	[]	hypothetical protein	PF08547.5	CIA30(Complex I intermediate-associated protein 30 (CIA30))
Supercontig_1.29_MVLG_03255_11sp	-603,46452	-603,43559	0,05786	0,02852	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.49_MVLG_04438_10sp	-1212,6236	-1212,6236	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00076.15	RRM_1(RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain))
Supercontig_1.82_MVLG_05713_9sp	-589,90709	-589,88548	0,04322	0,02138	NS	0	[]	[]	[]	hypothetical protein	PF05691.5	Raffinose_syn(Raffinose synthase or seed inhibition protein Sip1)
Supercontig_1.13_MVLG_01935_12sp	-700,35218	-699,41468	1,875	0,60839	NS	0	[]	[]	[]	hypothetical protein	PF00916.13	Sulfate_transp(Sulfate transporter family)
Supercontig_1.66_MVLG_05167_7sp	-869,66151	-869,66151	0	0	NS	0	[]	[]	[]	hypothetical protein	PF08530.3	PepX_C(X-Pro dipeptidyl-peptidase C-terminal non-catalytic domain)
Supercontig_1.98_MVLG_06082_7sp	-623,06254	-623,06254	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00400.25	WD40(WD domain, G-beta repeat)
Supercontig_1.19_MVLG_02517_9sp	-792,41323	-792,41323	0	0	NS	0	[]	[]	[]	hypothetical protein	PF12171.1	zf-C2H2_jaz(Zinc-finger double-stranded RNA-binding)
Supercontig_1.95_MVLG_06015_9sp	-597,95557	-597,13592	1,6393	0,55941	NS	0	[]	[]	[]	hypothetical protein	PF00313.15	CSD('Cold-shock' DNA-binding domain)
Supercontig_1.13_MVLG_01920_10sp	-647,12298	-645,85373	2,5385	0,71896	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.12_MVLG_01795_8sp	-2083,6402	-2083,6402	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00172.11	Zn_clus(Fungal Zn(2)-Cys(6) binuclear cluster domain)
Supercontig_1.2_MVLG_00439_10sp	-311,75062	-311,75048	0,00028	0,00014	NS	0	[]	[]	[]	acetyl-coenzyme A synthetase	TIGR02188	TIGR02188(Ac_CoA_lig_AcsA: acetate--CoA ligase)
Supercontig_1.150_MVLG_06772_7sp	-671,20489	-671,20489	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA

Supercontig_1.34_MVLG_03563_9sp	-644,36681	-644,3663	0,00102	0,00051	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.1_MVLG_00037_10sp	-693,3151	-693,3151	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.30_MVLG_03268_9sp	-724,89481	-723,98416	1,8213	0,59774	NS	0	[]	[]	[]	hypothetical protein	PF01494.12	FAD_binding_3(FAD binding domain)
Supercontig_1.14_MVLG_01985_7sp	-1102,0603	-1102,0603	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.20_MVLG_02589_12sp	-454,11524	-454,11524	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04495.7	GRASP55_65(GRASP55/65 family)
Supercontig_1.25_MVLG_02914_10sp	-731,67607	-730,95029	1,45156	0,51605	NS	0	[]	[]	[]	hypothetical protein	PF00172.11	Zn_clus(Fungal Zn(2)-Cys(6) binuclear cluster domain)
Supercontig_1.7_MVLG_01224_9sp	-308,25836	-308,15001	0,2167	0,10269	NS	0	[]	[]	[]	hypothetical protein	PF01779.10	Ribosomal_L29e(Ribosomal L29e protein family)
Supercontig_1.18_MVLG_02383_8sp	-475,2865	-475,28621	0,00058	0,00029	NS	0	[]	[]	[]	hypothetical protein	PF07956.4	DUF1690(Protein of Unknown function (DUF1690))
Supercontig_1.132_MVLG_06598_8sp	-336,54179	-336,54173	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01715.10	IPPT(IPP transferase)
Supercontig_1.62_MVLG_05025_11sp	-536,51794	-536,51792	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.3_MVLG_00682_9sp	-1062,0433	-1061,9087	0,26934	0,126	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.42_MVLG_04054_11sp	-735,89154	-735,89154	0	0	NS	0	[]	[]	[]	hypothetical protein	PF08243.4	SPT2(SPT2 chromatin protein)
Supercontig_1.69_MVLG_05310_8sp	-266,92473	-266,92458	0,0003	0,00015	NS	0	[]	[]	[]	fructose-1,6-bisphosphatase, cytosolic	PF00316.13	FBPase(Fructose-1-6-bisphosphatase)
Supercontig_1.16_MVLG_02232_7sp	-468,13766	-468,05451	0,1663	0,07979	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.22_MVLG_02729_9sp	-951,06382	-950,99702	0,1336	0,06462	NS	0	[]	[]	[]	hypothetical protein	TIGR00727	TIGR00727(ISP4_OPT: small oligopeptide transporter, OPT family)
Supercontig_1.174_MVLG_06965_8sp	-540,69641	-540,69641	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.3_MVLG_00551_8sp	-698,87952	-698,87927	0,0005	0,00025	NS	0	[]	[]	[]	hypothetical protein	PF08520.3	DUF1748(Fungal protein of unknown function (DUF1748))
Supercontig_1.62_MVLG_05011_7sp	-644,16758	-643,75037	0,83442	0,34112	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.8_MVLG_01436_10sp	-544,10426	-544,10426	0	0	NS	0	[]	[]	[]	hypothetical protein	PF07690.9	MFS_1(Major Facilitator Superfamily)
Supercontig_1.27_MVLG_03104_8sp	-846,68453	-845,37491	2,61924	0,73008	NS	0	[]	[]	[]	hypothetical protein	PF07748.6	Glyco_hydro_38C(Glycosyl hydrolases family 38 C-terminal domain)
Supercontig_1.42_MVLG_04065_8sp	-719,23013	-718,3564	1,74746	0,58261	NS	0	[]	[]	[]	hypothetical protein	PF00270.22	DEAD(DEAD/DEAH box helicase)
Supercontig_1.99_MVLG_06115_8sp	-483,2394	-482,5023	1,4742	0,5215	NS	0	[]	[]	[]	hypothetical protein	PF07808.6	RED_N(RED-like protein N-terminal region)
Supercontig_1.6_MVLG_01100_10sp	-943,3592	-943,33167	0,05506	0,02715	NS	0	[]	[]	[]	hypothetical protein	NA	NA

Supercontig_1.2_MVLG_00277_7sp	-419,22972	-419,22962	0,0002	0	NS	0	[]	[]	[]	U6 snRNA-associated Sm-like protein LSm2	PF01423.15	LSM(LSM domain)
Supercontig_1.175_MVLG_06968_9sp	-293,87462	-293,87451	0,00022	0,00011	NS	0	[]	[]	[]	40S ribosomal protein S26E	PF01283.12	Ribosomal_S26e(Ribosomal protein S26e)
Supercontig_1.191_MVLG_07045_8sp	-930,18432	-930,18432	0	0	NS	0	[]	[]	[]	hypothetical protein	PF06813.6	Nodulin-like(Nodulin-like)
Supercontig_1.40_MVLG_03922_9sp	-668,19191	-668,19191	0	0	NS	0	[]	[]	[]	adenine phosphoribosyltransferase	TIGR01090	TIGR01090(apt: adenine phosphoribosyltransferase)
Supercontig_1.12_MVLG_01820_10sp	-507,27836	-505,01524	4,52624	0,89597	NS	0	[]	[]	[]	hypothetical protein	PF00743.12	FMO-like(Flavin-binding monooxygenase-like)
Supercontig_1.91_MVLG_05930_10sp	-479,8514	-478,93266	1,83748	0,60098	NS	0	[]	[]	[]	hypothetical protein	PF07156.7	Prenylcys_lyase(Prenylcysteine lyase)
Supercontig_1.66_MVLG_05196_10sp	-473,03298	-473,03298	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00083.17	Sugar_tr(Sugar (and other) transporter)
Supercontig_1.47_MVLG_04315_10sp	-406,69735	-406,69735	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02515.10	CoA_transf_3(CoA-transferase family III)
Supercontig_1.1_MVLG_00138_9sp	-660,55569	-660,55569	0	0	NS	0	[]	[]	[]	hypothetical protein	PF12519.1	DUF3722(Protein of unknown function (DUF3722))
Supercontig_1.46_MVLG_04266_10sp	-1119,2098	-1119,2093	0,0009	0,00045	NS	0	[]	[]	[]	hypothetical protein	PF01851.15	PC_rep(Proteasome/cyclosome repeat)
Supercontig_1.1_MVLG_00009_7sp	-1058,048	-1058,048	0	0	NS	0	[]	[]	[]	hypothetical protein	PF08238.5	Sel1(Sel1 repeat)
Supercontig_1.41_MVLG_04033_7sp	-750,26961	-750,00913	0,52096	0,22932	NS	0	[]	[]	[]	hypothetical protein	PF01652.11	IF4E(Eukaryotic initiation factor 4E)
Supercontig_1.34_MVLG_03554_9sp	-429,54735	-429,54735	0	0	NS	0	[]	[]	[]	hypothetical protein	TIGR00601	TIGR00601(rad23: UV excision repair protein Rad23)
Supercontig_1.116_MVLG_06375_8sp	-500,4222	-500,38434	0,07572	0,03715	NS	0	[]	[]	[]	hypothetical protein	PF11976.1	Rad60-SLD(Ubiquitin-2 like Rad60 SUMO-like)
Supercontig_1.49_MVLG_04402_12sp	-1175,6624	-1175,6624	0	0	NS	0	[]	[]	[]	hypothetical protein	PF11196.1	DUF2834(Protein of unknown function (DUF2834))
Supercontig_1.12_MVLG_01815_12sp	-501,52291	-501,52148	0,00286	0,00143	NS	0	[]	[]	[]	hypothetical protein	PF00027.22	cNMP_binding(Cyclic nucleotide-binding domain)
Supercontig_1.81_MVLG_05679_11sp	-800,6948	-800,6948	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.155_MVLG_06827_9sp	-923,73901	-923,73901	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02434.9	Fringe(Fringe-like)
Supercontig_1.26_MVLG_03048_9sp	-480,66198	-480,15519	1,01358	0,39757	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.15_MVLG_02148_12sp	-362,5569	-362,08349	0,94682	0,37713	NS	0	[]	[]	[]	hypothetical protein	PF09363.3	XFP_C(XFP C-terminal domain)
Supercontig_1.140_MVLG_06683_8sp	-538,92984	-538,92984	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.52_MVLG_04553_8sp	-1501,4577	-1500,7479	1,41958	0,50825	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.58_MVLG_04845_10sp	-556,0417	-555,92809	0,22722	0,10739	NS	0	[]	[]	[]	hypothetical protein	PF05347.8	Complex1_LYR(Complex 1 protein (LYR family))
Supercontig_1.29_MVLG_03229_7sp	-422,26245	-422,26245	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.5_MVLG_01037_8sp	-556,42535	-556,42525	0,0002	0	NS	0	[]	[]	[]	hypothetical protein	PF07716.8	bZIP_2(Basic region leucine zipper)

Supercontig_1.13_MVLG_01936_12sp	-652,88135	-652,88092	0,00086	0,00043	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.40_MVLG_03954_8sp	-480,26962	-480,26962	0	0	NS	0	[]	[]	[]	3-isopropylmalate dehydratase	PF00694.12	Aconitase_C(Aconitase C-terminal domain)
Supercontig_1.192_MVLG_07049_11sp	-1004,2038	-1004,1986	0,01046	0,00522	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.226_MVLG_07176_6sp	-865,72534	-864,39774	2,6552	0,73489	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.15_MVLG_02094_10sp	-385,07268	-384,65709	0,83118	0,34005	NS	0	[]	[]	[]	queuine tRNA-ribosyltransferase	TIGR00449	TIGR00449(tgt_general: tRNA-guanine transglycosylases, various specificities)
Supercontig_1.121_MVLG_06448_11sp	-433,4279	-433,42784	0,00012	0	NS	0	[]	[]	[]	hypothetical protein	PF00566.11	TBC(TBC domain)
Supercontig_1.140_MVLG_06675_12sp	-507,52883	-507,52874	0,00018	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.78_MVLG_05582_8sp	-1097,6275	-1097,5247	0,20556	0,09767	NS	0	[]	[]	[]	hypothetical protein	PF03055.8	RPE65(Retinal pigment epithelial membrane protein)
Supercontig_1.149_MVLG_06759_8sp	-1146,8371	-1146,6814	0,31134	0,14416	NS	0	[]	[]	[]	homoserine O-acetyltransferase	TIGR01392	TIGR01392(homoserO_Ac_trn: homoserine O-acetyltransferase)
Supercontig_1.67_MVLG_05219_6sp	-407,56089	-407,56089	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.203_MVLG_07096_6sp	-1326,5224	-1325,7706	1,50358	0,52848	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.74_MVLG_05442_10sp	-386,93868	-386,93868	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.47_MVLG_04305_9sp	-983,92442	-983,92438	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00664.16	ABC_membrane(ABC transporter transmembrane region)
Supercontig_1.10_MVLG_01650_10sp	-497,29053	-497,29053	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00083.17	Sugar_tr(Sugar (and other) transporter)
Supercontig_1.23_MVLG_02794_8sp	-657,21705	-657,21705	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00620.20	RhoGAP(RhoGAP domain)
Supercontig_1.33_MVLG_03485_10sp	-791,23589	-791,23589	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00534.13	Glycos_transf_1(Glycosyl transferases group 1)
Supercontig_1.60_MVLG_04950_10sp	-710,10693	-710,10693	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.57_MVLG_04837_8sp	-406,60437	-406,60419	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00153.20	Mito_carr(Mitochondrial carrier protein)
Supercontig_1.15_MVLG_02147_9sp	-484,44377	-484,44375	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03029.10	ATP_bind_1(Conserved hypothetical ATP binding protein)
Supercontig_1.28_MVLG_03162_10sp	-530,79477	-530,79477	0	0	NS	0	[]	[]	[]	hypothetical protein	TIGR00727	TIGR00727(ISP4_OPT: small oligopeptide transporter, OPT family)
Supercontig_1.6_MVLG_01176_10sp	-794,64948	-794,64948	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02585.10	PIG-L(GlcNAc-PI de-N-acetylase)
Supercontig_1.1_MVLG_00255_9sp	-446,74294	-446,74294	0	0	NS	0	[]	[]	[]	hypothetical protein	PF05160.6	DSS1_SEM1(DSS1/SEM1 family)
Supercontig_1.2_MVLG_00449_8sp	-961,98091	-961,98091	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03142.8	Chitin_synth_2(Chitin synthase)

Supercontig_1.8_MVLG_01373_7sp	-1094,4886	-1094,4886	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03839.9	Sec62(Translocation protein Sec62)
Supercontig_1.5_MVLG_01011_10sp	-800,68198	-800,68198	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.34_MVLG_03513_6sp	-811,93491	-809,77426	4,3213	0,88475	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.142_MVLG_06704_8sp	-567,59106	-567,59106	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01687.10	Flavokinase(Riboflavin kinase)
Supercontig_1.135_MVLG_06629_11sp	-450,78772	-449,63299	2,30946	0,68486	NS	0	[]	[]	[]	hypothetical protein	PF00515.21	TPR_1(Tetratricopeptide repeat)
Supercontig_1.12_MVLG_01799_8sp	-289,46984	-289,46482	0,01004	0,00501	NS	0	[]	[]	[]	hypothetical protein	PF04893.10	Yip1(Yip1 domain)
Supercontig_1.1_MVLG_00235_9sp	-662,0698	-661,26197	1,61566	0,55418	NS	0	[]	[]	[]	hypothetical protein	PF04116.6	FA_hydroxylase(Fatty acid hydroxylase superfamily)
Supercontig_1.197_MVLG_07068_9sp	-804,2021	-804,2021	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.1_MVLG_00175_9sp	-525,51196	-525,51196	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.53_MVLG_04635_8sp	-414,58208	-414,46335	0,23746	0,11195	NS	0	[]	[]	[]	hypothetical protein	PF01070.11	FMN_dh(FMN-dependent dehydrogenase)
Supercontig_1.4_MVLG_00695_8sp	-344,44052	-344,42135	0,03834	0,01899	NS	0	[]	[]	[]	hypothetical protein	PF01284.16	MARVEL(Membrane-associating domain)
Supercontig_1.36_MVLG_03659_11sp	-680,2415	-679,80556	0,87188	0,35334	NS	0	[]	[]	[]	hypothetical protein	PF06220.5	zf-U1(U1 zinc finger)
Supercontig_1.18_MVLG_02387_10sp	-736,27518	-736,27518	0	0	NS	0	[]	[]	[]	coatomer subunit beta	PF01602.13	Adaptin_N(Adaptin N terminal region)
Supercontig_1.161_MVLG_06864_9sp	-451,26828	-451,26828	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00732.12	GMC_oxred_N(GMC oxidoreductase)
Supercontig_1.32_MVLG_03426_10sp	-903,39638	-903,31073	0,1713	0,08208	NS	0	[]	[]	[]	hypothetical protein	PF02375.10	JmjN(jmjN domain)
Supercontig_1.49_MVLG_04427_11sp	-612,08718	-612,08718	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.58_MVLG_04880_9sp	-526,19262	-526,19245	0,00034	0,00017	NS	0	[]	[]	[]	60S ribosomal protein L3-A	PF00297.15	Ribosomal_L3(Ribosomal protein L3)
Supercontig_1.30_MVLG_03296_8sp	-687,17296	-687,17296	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.3_MVLG_00595_11sp	-502,39356	-502,32079	0,14554	0,07019	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.4_MVLG_00831_10sp	-554,21812	-554,21812	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02104.8	SURF1(SURF1 family)
Supercontig_1.39_MVLG_03869_8sp	-945,9825	-945,78614	0,39272	0,17828	NS	0	[]	[]	[]	hypothetical protein	PF00018.21	SH3_1(SH3 domain)
Supercontig_1.27_MVLG_03074_9sp	-535,21177	-535,21177	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03357.14	Snf7(Snf7)
Supercontig_1.15_MVLG_02127_9sp	-1009,713	-1009,2338	0,95852	0,38076	NS	0	[]	[]	[]	hypothetical protein	PF03151.9	TPT(Triose-phosphate Transporter family)
Supercontig_1.5_MVLG_01038_11sp	-316,1271	-316,12706	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00400.25	WD40(WD domain, G-beta repeat)
Supercontig_1.19_MVLG_02451_9sp	-303,29591	-303,29562	0,00058	0,00029	NS	0	[]	[]	[]	flap endonuclease 1-A	PF00867.11	XPG_I(XPG I-region)
Supercontig_1.139_MVLG_06663_6sp	-308,09608	-308,0954	0,00136	0,00068	NS	0	[]	[]	[]	hypothetical protein	PF03226.7	Yippee(Yippee putative zinc-binding protein)

Supercontig_1.16_MVLG_02209_11sp	-441,84845	-441,8482	0,0005	0,00025	NS	0	[]	[]	[]	ER membrane protein SH3	PF08229.4	SHR3_chaperone(ER membrane protein SH3)
Supercontig_1.7_MVLG_01321_8sp	-311,37107	-311,17203	0,39808	0,18048	NS	0	[]	[]	[]	cofilin	PF00241.13	Cofilin_ADF(Cofilin/tropomyosin-type actin-binding protein)
Supercontig_1.26_MVLG_03013_11sp	-717,42493	-717,42493	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.98_MVLG_06095_8sp	-567,5749	-567,46933	0,21114	0,10019	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.11_MVLG_01715_10sp	-403,2899	-403,08583	0,40814	0,18459	NS	0	[]	[]	[]	V-type proton ATPase catalytic subunit A isoform 2	PF00306.20	ATP-synt_ab_C(ATP synthase alpha/beta chain, C terminal domain)
Supercontig_1.24_MVLG_02874_9sp	-542,28267	-542,24034	0,08466	0,04145	NS	0	[]	[]	[]	hypothetical protein	PF00512.18	HisKA(His Kinase A (phosphoacceptor) domain)
Supercontig_1.21_MVLG_02631_12sp	-493,4742	-493,47402	0,00036	0,00018	NS	0	[]	[]	[]	hypothetical protein	PF01426.11	BAH(BAH domain)
Supercontig_1.15_MVLG_02120_8sp	-500,09774	-500,0974	0,00068	0,00034	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.3_MVLG_00661_9sp	-378,30327	-378,30287	0,0008	0,0004	NS	0	[]	[]	[]	26S protease regulatory subunit 6B	PF07724.7	AAA_2(AAA domain (Cdc48 subfamily))
Supercontig_1.6_MVLG_01216_10sp	-804,27764	-804,27729	0,0007	0,00035	NS	0	[]	[]	[]	hypothetical protein	PF00176.16	SNF2_N(SNF2 family N-terminal domain)
Supercontig_1.125_MVLG_06510_8sp	-257,64218	-257,64291	0	0	NS	0	[]	[]	[]	60S acidic ribosomal protein P2	PF00428.12	Ribosomal_60s(60s Acidic ribosomal protein)
Supercontig_1.85_MVLG_05791_7sp	-470,59951	-470,59951	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00534.13	Glycos_transf_1(Glycosyl transferases group 1)
Supercontig_1.38_MVLG_03788_11sp	-513,04093	-513,04084	0,00018	0	NS	0	[]	[]	[]	hypothetical protein	TIGR01159	TIGR01159(DRP1: density-regulated protein DRP1)
Supercontig_1.110_MVLG_06298_6sp	-549,40638	-549,40398	0,0048	0,0024	NS	0	[]	[]	[]	hypothetical protein	PF05622.5	HOOK(HOOK protein)
Supercontig_1.21_MVLG_02655_10sp	-985,48329	-984,4182	2,13018	0,6553	NS	0	[]	[]	[]	hypothetical protein	PF02815.12	MIR(MIR domain)
Supercontig_1.67_MVLG_05232_10sp	-533,41796	-533,41796	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00664.16	ABC_membrane(ABC transporter transmembrane region)
Supercontig_1.34_MVLG_03574_10sp	-951,60241	-951,60241	0	0	NS	0	[]	[]	[]	hypothetical protein	TIGR00861	TIGR00861(MIP: MIP family channel proteins)
Supercontig_1.7_MVLG_01305_10sp	-348,58867	-348,17146	0,83442	0,34112	NS	0	[]	[]	[]	hypothetical protein	PF10502.2	Peptidase_S26(Peptidase S26)
Supercontig_1.101_MVLG_06161_7sp	-639,56348	-639,56348	0	0	NS	0	[]	[]	[]	hypothetical protein	TIGR00106	TIGR00106(TIGR00106: uncharacterized protein, MTH1187 family)
Supercontig_1.150_MVLG_06774_7sp	-394,18995	-394,18979	0,00032	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF05669.5	Med31(SOH1)
Supercontig_1.17_MVLG_02274_10sp	-287,64396	-287,64395	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.2_MVLG_00455_11sp	-574,13799	-573,23294	1,8101	0,59548	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.41_MVLG_03999_10sp	-818,79843	-818,79838	0,0001	0	NS	0	[]	[]	[]	hypothetical protein	PF05794.6	Tcp11(T-complex protein 11)
Supercontig_1.77_MVLG_05570_10sp	-547,02998	-547,02998	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA

Supercontig_1.51_MVLG_04539_9sp	-735,31042	-735,10628	0,40828	0,18465	NS	0	[]	[]	[]	hypothetical protein	PF00326.14	Peptidase_S9(Prolyl oligopeptidase family)
Supercontig_1.40_MVLG_03913_7sp	-375,05977	-375,05977	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00226.24	DnaJ(DnaJ domain)
Supercontig_1.165_MVLG_06908_8sp	-629,27499	-629,27499	0	0	NS	0	[]	[]	[]	CMGC/CDK protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.33_MVLG_03465_10sp	-854,54249	-854,54249	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.86_MVLG_05823_11sp	-982,09067	-982,0901	0,00114	0,00057	NS	0	[]	[]	[]	autophagy-like protein 18	PF00400.25	WD40(WD domain, G-beta repeat)
Supercontig_1.25_MVLG_02933_7sp	-688,937	-688,937	0	0	NS	0	[]	[]	[]	hypothetical protein	PF05254.5	UPF0203(Uncharacterised protein family (UPF0203))
Supercontig_1.55_MVLG_04711_11sp	-578,38674	-578,38611	0,00126	0,00063	NS	0	[]	[]	[]	hypothetical protein	PF00672.18	HAMP(HAMP domain)
Supercontig_1.161_MVLG_06866_12sp	-771,2118	-769,21341	3,99678	0,86445	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.86_MVLG_05841_10sp	-1292,3237	-1292,3237	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00454.20	PI3_PI4_kinase(Phosphatidylinositol 3- and 4-kinase)
Supercontig_1.93_MVLG_05983_8sp	-858,32078	-858,32078	0	0	NS	0	[]	[]	[]	hypothetical protein	TIGR00745	TIGR00745(apbA_panE: 2-dehydropantoate 2-reductase)
Supercontig_1.17_MVLG_02325_11sp	-1270,3845	-1270,3845	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00521.13	DNA_topoisoIV(DNA gyrase/topoisomerase IV, subunit A)
Supercontig_1.1_MVLG_00254_10sp	-523,24429	-523,24414	0,0003	0,00015	NS	0	[]	[]	[]	hypothetical protein	PF00909.14	Ammonium_transp(Ammonium Transporter Family)
Supercontig_1.21_MVLG_02678_9sp	-1194,5089	-1194,5045	0,00884	0,00441	NS	0	[]	[]	[]	hypothetical protein	PF10544.2	T5orf172(T5orf172 domain)
Supercontig_1.124_MVLG_06491_7sp	-981,99195	-981,99195	0	0	NS	0	[]	[]	[]	hypothetical protein	PF08447.4	PAS_3(PAS fold)
Supercontig_1.16_MVLG_02207_8sp	-697,37167	-697,37162	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.22_MVLG_02690_7sp	-274,10619	-274,10614	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.41_MVLG_04035_10sp	-440,06901	-440,06901	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01878.11	DUF55(Protein of unknown function DUF55)
Supercontig_1.78_MVLG_05602_8sp	-932,60018	-932,27866	0,64304	0,27495	NS	0	[]	[]	[]	hypothetical protein	PF04082.11	Fungal_trans(Fungal specific transcription factor domain)
Supercontig_1.3_MVLG_00564_7sp	-320,33429	-320,33395	0,00068	0,00034	NS	0	[]	[]	[]	40S ribosomal protein S21	PF01249.11	Ribosomal_S21e(Ribosomal protein S21e)
Supercontig_1.52_MVLG_04575_9sp	-527,80857	-527,80857	0	0	NS	0	[]	[]	[]	hypothetical protein	PF09685.3	Tic20(Chloroplast import component protein (Tic20))
Supercontig_1.27_MVLG_03124_7sp	-841,41797	-841,41797	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00150.11	Cellulase(Cellulase (glycosyl hydrolase family 5))
Supercontig_1.23_MVLG_02784_9sp	-1022,7068	-1022,7068	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03969.9	AFG1_ATPase(AFG1-like ATPase)
Supercontig_1.81_MVLG_05696_8sp	-487,7696	-486,56244	2,41432	0,70095	NS	0	[]	[]	[]	hypothetical protein	PF01485.14	IBR(IBR domain)
Supercontig_1.74_MVLG_05440_9sp	-322,7828	-322,78271	0,00018	0	NS	0	[]	[]	[]	hypothetical protein	PF01967.14	MoaC(MoaC family)
Supercontig_1.4_MVLG_00826_8sp	-357,79207	-357,79199	0,00016	0	NS	0	[]	[]	[]	hypothetical protein	PF00704.21	Glyco_hydro_18(Glycosyl hydrolases family 18)

Supercontig_1.54_MVLG_04689_10sp	-337,08527	-337,08505	0,00044	0,00022	NS	0	[]	[]	[]	NADH-ubiquinone oxidoreductase 49 kDa subunit	TIGR01962	TIGR01962(NuoD: NADH dehydrogenase (quinone), D subunit)
Supercontig_1.4_MVLG_00700_9sp	-373,33443	-373,24556	0,17774	0,08504	NS	0	[]	[]	[]	hypothetical protein	PF00808.16	CBFD_NFYB_HMF(Histone-like transcription factor (CBF/NF-Y) and archaeal histone)
Supercontig_1.31_MVLG_03354_10sp	-628,00947	-628,00947	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.95_MVLG_06028_10sp	-410,86204	-410,47523	0,77362	0,32078	NS	0	[]	[]	[]	large subunit ribosomal protein L13e	PF01294.11	Ribosomal_L13e(Ribosomal protein L13e)
Supercontig_1.75_MVLG_05500_9sp	-607,79356	-607,76964	0,04784	0,02364	NS	0	[]	[]	[]	hypothetical protein	PF10334.2	DUF2421(Protein of unknown function (DUF2421))
Supercontig_1.29_MVLG_03227_10sp	-557,4774	-557,47721	0,00038	0,00019	NS	0	[]	[]	[]	isovaleryl-CoA dehydrogenase	PF02770.12	Acyl-CoA_dh_M(Acyl-CoA dehydrogenase, middle domain)
Supercontig_1.9_MVLG_01510_10sp	-412,43038	-412,01335	0,83406	0,341	NS	0	[]	[]	[]	hypothetical protein	PF00067.15	p450(Cytochrome P450)
Supercontig_1.7_MVLG_01331_7sp	-486,35686	-486,33608	0,04156	0,02057	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.28_MVLG_03194_11sp	-751,40931	-746,48682	9,84498	0,99272	***	0	[]	[]	[]	hypothetical protein	PF10342.2	Drmip_Hesp(Developmentally Regulated MAPK Interacting Protein)
Supercontig_1.54_MVLG_04663_12sp	-636,15195	-636,15195	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00787.17	PX(PX domain)
Supercontig_1.73_MVLG_05426_6sp	-934,91057	-934,91054	0	0	NS	0	[]	[]	[]	hypothetical protein	PF09451.3	ATG27(Autophagy-related protein 27)
Supercontig_1.39_MVLG_03847_11sp	-566,00018	-565,99998	0,0004	0,0002	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.2_MVLG_00453_11sp	-433,78892	-433,78892	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00023.23	Ank(Ankyrin repeat)
Supercontig_1.135_MVLG_06624_8sp	-351,91917	-351,91901	0,00032	0,00016	NS	0	[]	[]	[]	myosin regulatory light chain cdc4	NA	NA
Supercontig_1.2_MVLG_00344_6sp	-905,62734	-905,58389	0,0869	0,04252	NS	0	[]	[]	[]	inosine-5'-monophosphate dehydrogenase IMD4	TIGR01302	TIGR01302(IMP_dehydrog: inosine-5'-monophosphate dehydrogenase)
Supercontig_1.2_MVLG_00391_12sp	-517,30076	-517,30075	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.92_MVLG_05962_9sp	-603,49926	-603,49926	0	0	NS	0	[]	[]	[]	ATP-dependent rRNA helicase RRP3	PF00270.22	DEAD(DEAD/DEAH box helicase)
Supercontig_1.160_MVLG_06855_11sp	-348,27866	-348,27859	0	0	NS	0	[]	[]	[]	glycine cleavage system T protein	TIGR00528	TIGR00528(gcvT: glycine cleavage system T protein)
Supercontig_1.1_MVLG_00042_11sp	-392,33818	-391,81182	1,05272	0,40925	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.34_MVLG_03522_9sp	-554,55292	-554,55281	0,00022	0,00011	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.25_MVLG_02955_6sp	-1364,7928	-1364,63	0,32562	0,15025	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.11_MVLG_01704_10sp	-657,74035	-657,61008	0,26054	0,12214	NS	0	[]	[]	[]	hypothetical protein	NA	NA

Supercontig_1.11_MVLG_01761_10sp	-355,00931	-355,00931	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04727.6	ELMO_CED12(ELMO/CED-12 family)
Supercontig_1.5_MVLG_01001_9sp	-335,00948	-335,00939	0,00018	0	NS	0	[]	[]	[]	hypothetical protein	PF00096.19	zf-C2H2(Zinc finger, C2H2 type)
Supercontig_1.4_MVLG_00687_10sp	-572,6703	-571,88671	1,56718	0,54324	NS	0	[]	[]	[]	hypothetical protein	PF05625.4	PAXNEB(PAXNEB protein)
Supercontig_1.3_MVLG_00544_6sp	-326,63834	-326,63834	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04099.5	Sybindin(Sybindin-like family)
Supercontig_1.2_MVLG_00332_9sp	-677,26064	-677,26064	0	0	NS	0	[]	[]	[]	hypothetical protein	PF07690.9	MFS_1(Major Facilitator Superfamily)
Supercontig_1.29_MVLG_03246_7sp	-569,97353	-568,08199	3,78308	0,84916	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.46_MVLG_04256_11sp	-763,88788	-763,88753	0,0007	0,00035	NS	0	[]	[]	[]	hypothetical protein	PF00787.17	PX(PX domain)
Supercontig_1.35_MVLG_03585_11sp	-499,88843	-499,87925	0,01836	0,00914	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.17_MVLG_02262_7sp	-809,84328	-809,84328	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04004.6	Leo1(Leo1-like protein)
Supercontig_1.28_MVLG_03176_8sp	-621,04422	-621,04422	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00378.13	ECH(Enoyl-CoA hydratase/isomerase family)
Supercontig_1.44_MVLG_04154_10sp	-540,54675	-538,43869	4,21612	0,87853	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.49_MVLG_04414_7sp	-367,85385	-367,85383	0	0	NS	0	[]	[]	[]	hypothetical protein	PF10499.2	Pmp24(Peroxisomal membrane protein 24)
Supercontig_1.2_MVLG_00442_11sp	-472,45634	-472,45634	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.112_MVLG_06331_8sp	-898,19971	-898,19971	0	0	NS	0	[]	[]	[]	hypothetical protein	PF09333.4	ATG_C(ATG C terminal domain)
Supercontig_1.38_MVLG_03785_6sp	-469,78115	-469,7811	0,0001	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.41_MVLG_03983_10sp	-914,92043	-914,92003	0,0008	0,0004	NS	0	[]	[]	[]	hypothetical protein	PF02463.12	SMC_N(RecF/RecN/SMC N terminal domain)
Supercontig_1.75_MVLG_05482_12sp	-1191,1059	-1188,1416	5,9286	0,9484	*	0	[]	[]	[]	hypothetical protein	PF07064.6	RIC1(RIC1)
Supercontig_1.91_MVLG_05920_9sp	-600,32005	-599,76513	1,10984	0,42588	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.15_MVLG_02125_10sp	-351,82385	-351,82379	0,00012	0	NS	0	[]	[]	[]	hypothetical protein	PF00856.21	SET(SET domain)
Supercontig_1.69_MVLG_05303_8sp	-424,93433	-424,93433	0	0	NS	0	[]	[]	[]	hypothetical protein	PF11034.1	DUF2823(Protein of unknown function (DUF2823))
Supercontig_1.11_MVLG_01760_9sp	-800,50535	-800,44101	0,12868	0,06231	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.5_MVLG_01022_9sp	-831,2069	-831,2069	0	0	NS	0	[]	[]	[]	hypothetical protein	PF07690.9	MFS_1(Major Facilitator Superfamily)
Supercontig_1.1_MVLG_00234_6sp	-569,1541	-569,15408	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01423.15	LSM(LSM domain)
Supercontig_1.4_MVLG_00728_8sp	-594,14542	-594,14533	0,00018	0	NS	0	[]	[]	[]	hypothetical protein	PF08551.3	DUF1751(Eukaryotic integral membrane protein (DUF1751))
Supercontig_1.67_MVLG_05204_8sp	-751,86542	-751,86502	0,0008	0,0004	NS	0	[]	[]	[]	hypothetical protein	PF08590.3	DUF1771(Domain of unknown function (DUF1771))

Supercontig_1.28_MVLG_03201_6sp	-1112,8193	-1112,7755	0,08772	0,04291	NS	0	[]	[]	[]	hypothetical protein	PF12171.1	zf-C2H2_jaz(Zinc-finger double-stranded RNA-binding)
Supercontig_1.51_MVLG_04503_10sp	-1875,4389	-1875,4389	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.67_MVLG_05218_8sp	-676,57164	-676,57152	0,00024	0,00012	NS	0	[]	[]	[]	hypothetical protein	PF10235.2	Cript(Microtubule-associated protein CRIPT)
Supercontig_1.74_MVLG_05462_12sp	-550,55448	-550,55448	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.6_MVLG_01168_8sp	-389,3148	-389,31466	0,00028	0,00014	NS	0	[]	[]	[]	hypothetical protein	PF05047.9	L51_S25_CI-B8(Mitochondrial ribosomal protein L51 / S25 / CI-B8 domain)
Supercontig_1.9_MVLG_01574_11sp	-405,76499	-405,76499	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.3_MVLG_00660_8sp	-350,41129	-350,41103	0,00052	0,00026	NS	0	[]	[]	[]	ADP-ribosylation factor-like protein 1	PF04670.5	Gtr1_RagA(Gtr1/RagA G protein conserved region)
Supercontig_1.186_MVLG_07028_7sp	-618,00821	-618,00803	0,00036	0,00018	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.111_MVLG_06303_10sp	-512,36283	-512,36281	0	0	NS	0	[]	[]	[]	hypothetical protein	PF08314.4	Sec39(Secretory pathway protein Sec39)
Supercontig_1.92_MVLG_05957_6sp	-355,79685	-355,68464	0,22442	0,10614	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.57_MVLG_04815_8sp	-343,17172	-343,17172	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.5_MVLG_00900_11sp	-334,0404	-334,0404	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01553.14	Acyltransferase(Acyltransferase)
Supercontig_1.95_MVLG_06010_7sp	-1258,2877	-1258,2871	0,00122	0,00061	NS	0	[]	[]	[]	hypothetical protein	PF00013.22	KH_1(KH domain)
Supercontig_1.4_MVLG_00776_7sp	-576,41496	-576,38755	0,05482	0,02704	NS	0	[]	[]	[]	hypothetical protein	PF00641.11	zf-RanBP(Zn-finger in Ran binding protein and others)
Supercontig_1.17_MVLG_02290_9sp	-605,56329	-605,56322	0,00014	0	NS	0	[]	[]	[]	hypothetical protein	PF08447.4	PAS_3(PAS fold)
Supercontig_1.8_MVLG_01405_11sp	-548,00732	-548,00721	0,00022	0,00011	NS	0	[]	[]	[]	hypothetical protein	PF00383.15	dCMP_cyt_deam_1(Cytidine and deoxycytidylate deaminase zinc-binding region)
Supercontig_1.31_MVLG_03377_11sp	-801,57017	-801,48124	0,17786	0,08509	NS	0	[]	[]	[]	hypothetical protein	PF04683.6	Proteasom_Rpn13(Proteasome complex subunit Rpn13 ubiquitin receptor)
Supercontig_1.25_MVLG_02950_7sp	-1127,2652	-1127,0808	0,36878	0,16839	NS	0	[]	[]	[]	hypothetical protein	PF04494.8	TFIID_90kDa(WD40 associated region in TFIID subunit)
Supercontig_1.25_MVLG_02981_9sp	-390,96017	-390,96017	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04479.6	RTA1(RTA1 like protein)
Supercontig_1.205_MVLG_07111_9sp	-504,43262	-504,29455	0,27614	0,12896	NS	0	[]	[]	[]	hypothetical protein	PF00107.19	ADH_zinc_N(Zinc-binding dehydrogenase)
Supercontig_1.24_MVLG_02831_10sp	-639,25008	-638,74643	1,0073	0,39568	NS	0	[]	[]	[]	hypothetical protein	PF07690.9	MFS_1(Major Facilitator Superfamily)
Supercontig_1.47_MVLG_04301_10sp	-946,38594	-946,27721	0,21746	0,10303	NS	0	[]	[]	[]	hypothetical protein	NA	NA

Supercontig_1.65_MVLG_05130_9sp	-436,20372	-436,20362	0	0	NS	0	[]	[]	[]	40S ribosomal protein S12	PF01248.19	Ribosomal_L7Ae(Ribosomal protein L7Ae/L30e/S12e/Gadd45 family)
Supercontig_1.39_MVLG_03885_7sp	-451,88449	-451,88445	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04430.7	DUF498(Protein of unknown function (DUF498/DUF598))
Supercontig_1.6_MVLG_01082_9sp	-501,16935	-501,16935	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03330.11	DPBB_1(Rare lipoprotein A (RlpA)-like double-psi beta-barrel)
Supercontig_1.3_MVLG_00609_8sp	-392,64762	-391,76601	1,76322	0,58588	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.75_MVLG_05487_12sp	-1191,0756	-1189,657	2,8373	0,75796	NS	0	[]	[]	[]	hypothetical protein	PF10310.2	DUF2413(Protein of unknown function (DUF2413))
Supercontig_1.165_MVLG_06903_9sp	-352,2457	-352,2457	0	0	NS	0	[]	[]	[]	hypothetical protein	PF05817.7	Ribophorin_II(Oligosaccharyltransferase subunit Ribophorin II)
Supercontig_1.20_MVLG_02535_8sp	-445,72906	-445,72906	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.9_MVLG_01517_10sp	-1520,6983	-1518,9659	3,46482	0,82314	NS	0	[]	[]	[]	hypothetical protein	PF07529.6	HSA(HSA)
Supercontig_1.15_MVLG_02133_8sp	-542,19594	-541,74552	0,90084	0,36264	NS	0	[]	[]	[]	hypothetical protein	PF10382.2	DUF2439(Protein of unknown function (DUF2439))
Supercontig_1.202_MVLG_07092_8sp	-377,80621	-377,80621	0	0	NS	0	[]	[]	[]	beta-glucosidase 1B	PF00232.11	Glyco_hydro_1(Glycosyl hydrolase family 1)
Supercontig_1.38_MVLG_03798_6sp	-1131,5021	-1131,5021	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.135_MVLG_06634_10sp	-423,4394	-423,33829	0,20222	0,09617	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.6_MVLG_01066_9sp	-539,89117	-539,89117	0	0	NS	0	[]	[]	[]	hypothetical protein	PF06687.5	SUR7(SUR7/PalI family)
Supercontig_1.35_MVLG_03582_11sp	-1274,1195	-1274,1194	0	0	NS	0	[]	[]	[]	DNA polymerase delta catalytic subunit	TIGR00592	TIGR00592(pol2: DNA polymerase (pol2))
Supercontig_1.28_MVLG_03202_7sp	-1129,2105	-1128,9981	0,42484	0,19137	NS	0	[]	[]	[]	hypothetical protein	PF06268.6	Fascin(Fascin domain)
Supercontig_1.6_MVLG_01197_10sp	-636,09374	-636,09028	0,00692	0,00345	NS	0	[]	[]	[]	protein Ras-2	PF08477.6	Miro(Miro-like protein)
Supercontig_1.23_MVLG_02807_9sp	-606,01652	-606,01652	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00400.25	WD40(WD domain, G-beta repeat)
Supercontig_1.42_MVLG_04072_7sp	-671,77356	-671,77342	0,00028	0,00014	NS	0	[]	[]	[]	hypothetical protein	PF01095.12	Pectinesterase(Pectinesterase)
Supercontig_1.51_MVLG_04495_8sp	-621,56262	-621,56262	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02668.9	TauD(Taurine catabolism dioxygenase TauD, TfdA family)
Supercontig_1.46_MVLG_04280_9sp	-380,65171	-380,65171	0	0	NS	0	[]	[]	[]	homoserine kinase	PF00288.19	GHMP_kinases_N(GHMP kinases N terminal domain)
Supercontig_1.62_MVLG_05036_9sp	-580,80608	-580,80608	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01063.12	Aminotran_4(Aminotransferase class IV)
Supercontig_1.21_MVLG_02675_10sp	-410,00987	-409,8782	0,26334	0,12337	NS	0	[]	[]	[]	hypothetical protein	NA	NA

Supercontig_1.2_MVLG_00373_10sp	-458,40661	-458,40661	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00596.14	Aldolase_II(Class II Aldolase and Adducin N-terminal domain)
Supercontig_1.73_MVLG_05430_11sp	-515,5349	-515,52873	0,01234	0,00615	NS	0	[]	[]	[]	hypothetical protein	PF07716.8	bZIP_2(Basic region leucine zipper)
Supercontig_1.74_MVLG_05467_7sp	-615,492	-615,492	0	0	NS	0	[]	[]	[]	aldehyde dehydrogenase family 7 member A1	PF00171.15	Aldedh(Aldehyde dehydrogenase family)
Supercontig_1.20_MVLG_02596_10sp	-325,83912	-325,74397	0,1903	0,09076	NS	0	[]	[]	[]	hypothetical protein	PF00076.15	RRM_1(RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain))
Supercontig_1.28_MVLG_03128_8sp	-499,47275	-498,91894	1,10762	0,42524	NS	0	[]	[]	[]	hypothetical protein	PF05175.7	MTS(Methyltransferase small domain)
Supercontig_1.54_MVLG_04679_6sp	-651,43401	-651,43379	0,00044	0,00022	NS	0	[]	[]	[]	enolase	PF00113.15	Enolase_C(Enolase, C-terminal TIM barrel domain)
Supercontig_1.47_MVLG_04325_10sp	-500,98545	-499,47643	3,01804	0,77887	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.59_MVLG_04889_6sp	-429,07168	-429,07103	0,0013	0,00065	NS	0	[]	[]	[]	hypothetical protein	PF00227.19	Proteasome(Proteasome subunit)
Supercontig_1.47_MVLG_04323_6sp	-301,72816	-301,47805	0,50022	0,22128	NS	0	[]	[]	[]	hypothetical protein	PF12585.1	DUF3759(Protein of unknown function (DUF3759))
Supercontig_1.27_MVLG_03070_9sp	-1199,2336	-1194,1303	10,2066	0,99392	***	0	[]	[]	[]	hypothetical protein	PF07646.8	Kelch_2(Kelch motif)
Supercontig_1.52_MVLG_04572_8sp	-1118,3389	-1115,8082	5,0614	0,9204	*	0	[]	[]	[]	hypothetical protein	PF00955.14	HCO3_cotransp(HCO3- transporter family)
Supercontig_1.18_MVLG_02366_7sp	-336,39164	-336,39164	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.7_MVLG_01233_8sp	-455,96336	-455,96336	0	0	NS	0	[]	[]	[]	hypothetical protein	TIGR02245	TIGR02245(HAD_IIID1: HAD hydrolase, family IIID)
Supercontig_1.36_MVLG_03670_10sp	-250,83674	-250,83646	0,00056	0,00028	NS	0	[]	[]	[]	casein kinase 2, beta polypeptide	PF01214.11	CK_II_beta(Casein kinase II regulatory subunit)
Supercontig_1.172_MVLG_06955_8sp	-311,57917	-311,57917	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04178.5	Got1(Got1/Sft2-like family)
Supercontig_1.41_MVLG_03987_12sp	-440,24404	-440,24404	0	0	NS	0	[]	[]	[]	hypothetical protein	PF10350.2	DUF2428(Putative death-receptor fusion protein (DUF2428))
Supercontig_1.53_MVLG_04633_10sp	-1200,821	-1200,821	0	0	NS	0	[]	[]	[]	hypothetical protein	PF09296.4	NUDIX-like(NADH pyrophosphatase-like rudimentary NUDIX domain)
Supercontig_1.30_MVLG_03304_9sp	-373,28191	-373,2819	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00106.18	adh_short(short chain dehydrogenase)
Supercontig_1.67_MVLG_05201_9sp	-425,63343	-425,63343	0	0	NS	0	[]	[]	[]	hypothetical protein	TIGR00727	TIGR00727(ISP4_OPT: small oligopeptide transporter, OPT family)
Supercontig_1.9_MVLG_01523_11sp	-603,04753	-602,67669	0,74168	0,30985	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.94_MVLG_05998_8sp	-585,23251	-585,23251	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01663.15	Phosphodiest(Type I phosphodiesterase / nucleotide pyrophosphatase)
Supercontig_1.38_MVLG_03773_9sp	-1330,6083	-1330,6083	0	0	NS	0	[]	[]	[]	hypothetical protein	PF07093.4	SGT1(SGT1 protein)

Supercontig_1.174_MVLG_06963_6sp	-888,09471	-888,09471	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04488.8	Gly_transf_sug(Glycosyltransferase sugar-binding region containing DXD motif)
Supercontig_1.4_MVLG_00828_11sp	-1072,4159	-1072,4159	0	0	NS	0	[]	[]	[]	hypothetical protein	PF08241.5	Methyltransf_11(Methyltransferase domain)
Supercontig_1.19_MVLG_02450_12sp	-870,26664	-869,01337	2,50654	0,71443	NS	0	[]	[]	[]	hypothetical protein	PF03221.9	Transposase_Tc5(Tc5 transposase DNA-binding domain)
Supercontig_1.14_MVLG_02011_10sp	-477,87953	-477,87953	0	0	NS	0	[]	[]	[]	hypothetical protein	TIGR01697	TIGR01697(PNPH-PUNA-XAPA: inosine guanosine and xanthosine phosphorylase family)
Supercontig_1.7_MVLG_01263_6sp	-1077,6308	-1077,2496	0,7624	0,31696	NS	0	[]	[]	[]	hypothetical protein	PF03097.11	BRO1(BRO1-like domain)
Supercontig_1.35_MVLG_03606_8sp	-749,41258	-748,90556	1,01404	0,39771	NS	0	[]	[]	[]	hypothetical protein	PF00153.20	Mito_carr(Mitochondrial carrier protein)
Supercontig_1.44_MVLG_04158_7sp	-400,45827	-400,45821	0,00012	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.20_MVLG_02581_8sp	-460,34171	-459,71495	1,25352	0,46568	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.33_MVLG_03481_7sp	-533,57872	-533,57864	0,00016	0	NS	0	[]	[]	[]	methionine-R-sulfoxide reductase	PF01641.11	SelR(SelR domain)
Supercontig_1.26_MVLG_03014_9sp	-373,63356	-373,63348	0,00016	0	NS	0	[]	[]	[]	pre-mRNA-splicing factor SLT11	PF00076.15	RRM_1(RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain))
Supercontig_1.55_MVLG_04735_6sp	-948,66524	-948,19929	0,9319	0,37246	NS	0	[]	[]	[]	hypothetical protein	PF00076.15	RRM_1(RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain))
Supercontig_1.66_MVLG_05185_8sp	-307,68534	-307,25768	0,85532	0,34797	NS	0	[]	[]	[]	hypothetical protein	PF00107.19	ADH_zinc_N(Zinc-binding dehydrogenase)
Supercontig_1.18_MVLG_02389_11sp	-364,30995	-364,3099	0	0	NS	0	[]	[]	[]	hypothetical protein	PF05739.12	SNARE(SNARE domain)
Supercontig_1.1_MVLG_00270_7sp	-270,6111	-270,61105	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.45_MVLG_04191_10sp	-649,7221	-649,7221	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00503.13	G-alpha(G-protein alpha subunit)
Supercontig_1.33_MVLG_03444_11sp	-1017,5656	-1017,5656	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.25_MVLG_02957_7sp	-491,89224	-490,77762	2,22924	0,67196	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.52_MVLG_04573_12sp	-586,13388	-586,12235	0,02306	0,01146	NS	0	[]	[]	[]	hypothetical protein	PF05193.14	Peptidase_M16_C(Peptidase M16 inactive domain)
Supercontig_1.33_MVLG_03468_12sp	-818,57052	-818,57052	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02260.13	FATC(FATC domain)
Supercontig_1.65_MVLG_05150_10sp	-286,80738	-286,80738	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00153.20	Mito_carr(Mitochondrial carrier protein)
Supercontig_1.11_MVLG_01731_7sp	-384,4227	-384,42261	0,00018	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.45_MVLG_04188_11sp	-443,36799	-443,36799	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.21_MVLG_02643_7sp	-1179,9221	-1179,9221	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00172.11	Zn_clus(Fungal Zn(2)-Cys(6) binuclear cluster domain)

Supercontig_1.14_MVLG_02014_9sp	-490,5925	-490,59239	0,00022	0,00011	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.8_MVLG_01387_9sp	-263,8735	-263,8735	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00808.16	CBFD_NFYB_HMF(Histone-like transcription factor (CBF/NF-Y) and archaeal histone)
Supercontig_1.7_MVLG_01283_7sp	-514,53346	-514,53331	0,0003	0,00015	NS	0	[]	[]	[]	V-type proton ATPase subunit D	PF01992.9	vATP-synt_AC39(ATP synthase (C/AC39) subunit)
Supercontig_1.42_MVLG_04055_11sp	-1390,264	-1389,481	1,56588	0,54294	NS	0	[]	[]	[]	STE/STE20/YSK protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.4_MVLG_00757_6sp	-393,95473	-393,95473	0	0	NS	0	[]	[]	[]	hypothetical protein	PF05978.9	UNC-93(Ion channel regulatory protein UNC-93)
Supercontig_1.74_MVLG_05466_8sp	-946,67118	-946,21531	0,91174	0,3661	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.6_MVLG_01101_8sp	-1026,3769	-1023,5122	5,7293	0,943	*	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.49_MVLG_04445_10sp	-1026,5447	-1026,5447	0	0	NS	0	[]	[]	[]	hypothetical protein	PF07915.6	PRKCSH(Glucosidase II beta subunit-like protein)
Supercontig_1.28_MVLG_03200_8sp	-322,78661	-322,78622	0,00078	0,00039	NS	0	[]	[]	[]	ATP-dependent RNA helicase FAL1	PF00270.22	DEAD(DEAD/DEAH box helicase)
Supercontig_1.96_MVLG_06036_10sp	-700,11175	-700,11175	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00732.12	GMC_oxred_N(GMC oxidoreductase)
Supercontig_1.18_MVLG_02390_7sp	-1224,9442	-1224,9442	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.1_MVLG_00016_10sp	-795,61407	-795,61366	0,00082	0,00041	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.9_MVLG_01492_8sp	-981,62216	-981,13035	0,98362	0,38848	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.6_MVLG_01177_9sp	-1288,8838	-1288,8838	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.28_MVLG_03190_6sp	-389,16016	-389,16013	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.19_MVLG_02445_9sp	-535,65031	-535,64721	0,0062	0,0031	NS	0	[]	[]	[]	hypothetical protein	PF01553.14	Acyltransferase(Acyltransferase)
Supercontig_1.47_MVLG_04336_7sp	-484,00976	-484,00941	0,0007	0,00035	NS	0	[]	[]	[]	phosphoglycerate mutase	PF00300.15	PGAM(Phosphoglycerate mutase family)
Supercontig_1.29_MVLG_03211_8sp	-503,00667	-502,54026	0,93282	0,37275	NS	0	[]	[]	[]	hypothetical protein	PF02537.8	CRCB(CrcB-like protein)
Supercontig_1.33_MVLG_03491_8sp	-1253,7582	-1253,7582	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.19_MVLG_02460_8sp	-1086,6419	-1085,4883	2,30722	0,6845	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.127_MVLG_06538_10sp	-342,97478	-342,97471	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00106.18	adh_short(short chain dehydrogenase)
Supercontig_1.38_MVLG_03829_10sp	-538,07487	-538,07486	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.44_MVLG_04159_7sp	-701,20817	-701,20788	0,00058	0,00029	NS	0	[]	[]	[]	cysteine desulfurase	TIGR02006	TIGR02006(IscS: cysteine desulfurase IscS)
Supercontig_1.46_MVLG_04281_8sp	-659,98007	-659,98001	0,00012	0	NS	0	[]	[]	[]	hypothetical protein	PF02984.12	Cyclin_C(Cyclin, C-terminal domain)
Supercontig_1.135_MVLG_06638_10sp	-1480,4118	-1480,4118	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00018.21	SH3_1(SH3 domain)

Supercontig_1.16_MVLG_02235_8sp	-614,52279	-614,52279	0	0	NS	0	[]	[]	[]	aldehyde dehydrogenase	PF00171.15	Aldedh(Aldehyde dehydrogenase family)
Supercontig_1.121_MVLG_06446_10sp	-875,04164	-873,80487	2,47354	0,70968	NS	0	[]	[]	[]	hypothetical protein	PF03372.16	Exo_endo_phos(Endonuclease/Exonuclease/phosphatase family)
Supercontig_1.30_MVLG_03314_12sp	-628,51959	-627,70326	1,63266	0,55795	NS	0	[]	[]	[]	hypothetical protein	PF01974.10	tRNA_int_endo(tRNA intron endonuclease, catalytic C-terminal domain)
Supercontig_1.3_MVLG_00489_6sp	-547,28611	-547,28606	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02230.9	Abhydrolase_2(Phospholipase/Carboxylesterase)
Supercontig_1.110_MVLG_06299_11sp	-440,12631	-440,12631	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00098.16	zf-CCHC(Zinc knuckle)
Supercontig_1.13_MVLG_01899_8sp	-330,8856	-330,69523	0,38074	0,17335	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.65_MVLG_05129_11sp	-476,62986	-476,62986	0	0	NS	0	[]	[]	[]	hypothetical protein	PF12400.1	DUF3661(Vaculolar membrane protein)
Supercontig_1.19_MVLG_02459_9sp	-325,51271	-325,51249	0,00044	0,00022	NS	0	[]	[]	[]	hypothetical protein	PF01545.14	Cation_efflux(Cation efflux family)
Supercontig_1.196_MVLG_07063_10sp	-762,43657	-762,43657	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.7_MVLG_01276_7sp	-633,12382	-633,1238	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.1_MVLG_00077_11sp	-734,74831	-734,74831	0	0	NS	0	[]	[]	[]	hypothetical protein	PF05131.7	Pep3_Vps18(Pep3/Vps18/deep orange family)
Supercontig_1.77_MVLG_05549_9sp	-453,12219	-453,12219	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03583.7	LIP(Secretory lipase)
Supercontig_1.26_MVLG_02996_11sp	-487,67872	-487,67872	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04427.11	Brix(Brix domain)
Supercontig_1.28_MVLG_03168_6sp	-824,80388	-822,98807	3,63162	0,83729	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.13_MVLG_01907_8sp	-630,64373	-630,64373	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.196_MVLG_07061_9sp	-527,86486	-527,18148	1,36676	0,49509	NS	0	[]	[]	[]	hypothetical protein	PF10294.2	Methyltransf_16(Putative methyltransferase)
Supercontig_1.35_MVLG_03627_10sp	-463,21943	-463,17765	0,08356	0,04092	NS	0	[]	[]	[]	hypothetical protein	PF00076.15	RRM_1(RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain))
Supercontig_1.2_MVLG_00301_7sp	-494,619	-494,61881	0,00038	0,00019	NS	0	[]	[]	[]	CMGC/CK2 protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.4_MVLG_00694_10sp	-607,34582	-606,58799	1,51566	0,53132	NS	0	[]	[]	[]	hypothetical protein	PF00076.15	RRM_1(RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain))
Supercontig_1.186_MVLG_07030_8sp	-458,8435	-457,51821	2,65058	0,73427	NS	0	[]	[]	[]	asparaginyl-tRNA synthetase	PF01336.18	tRNA_anti(OB-fold nucleic acid binding domain)
Supercontig_1.47_MVLG_04316_10sp	-332,50838	-332,39483	0,2271	0,10734	NS	0	[]	[]	[]	AUR protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.33_MVLG_03492_6sp	-680,80742	-680,80732	0,0002	0	NS	0	[]	[]	[]	ketol-acid reductoisomerase	TIGR00465	TIGR00465(ilvC: ketol-acid reductoisomerase)
Supercontig_1.6_MVLG_01153_9sp	-290,055	-290,055	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03226.7	Yippee(Yippee putative zinc-binding protein)
Supercontig_1.57_MVLG_04827_9sp	-321,75	-321,75	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00128.17	Alpha-amylase(Alpha amylase, catalytic domain)

Supercontig_1.3_MVLG_00619_11sp	-961,14415	-961,14415	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00349.14	Hexokinase_1(Hexokinase)
Supercontig_1.4_MVLG_00702_7sp	-449,06359	-449,06358	0	0	NS	0	[]	[]	[]	hypothetical protein	PF05721.6	PhyH(Phytanoyl-CoA dioxygenase (PhyH))
Supercontig_1.85_MVLG_05794_12sp	-623,11284	-623,11249	0,0007	0,00035	NS	0	[]	[]	[]	rRNA 2'-O-methyltransferase fibrillarin	PF08704.3	GCD14(tRNA methyltransferase complex GCD14 subunit)
Supercontig_1.18_MVLG_02417_9sp	-712,91418	-712,91418	0	0	NS	0	[]	[]	[]	hypothetical protein	PF07842.5	GCFC(GC-rich sequence DNA-binding factor-like protein)
Supercontig_1.87_MVLG_05852_12sp	-595,73233	-595,7323	0	0	NS	0	[]	[]	[]	hypothetical protein	PF11969.1	DcpS_C(Scavenger mRNA decapping enzyme C-term binding)
Supercontig_1.116_MVLG_06369_10sp	-1174,9639	-1174,7076	0,51254	0,22607	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.45_MVLG_04203_6sp	-373,27754	-373,27752	0	0	NS	0	[]	[]	[]	hypothetical protein	PF10294.2	Methyltransf_16(Putative methyltransferase)
Supercontig_1.47_MVLG_04311_7sp	-657,9048	-656,93004	1,94952	0,62272	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.20_MVLG_02600_8sp	-408,01186	-407,97383	0,07606	0,03732	NS	0	[]	[]	[]	hypothetical protein	TIGR00308	TIGR00308(TRM1: N2,N2-dimethylguanosine tRNA methyltransferase)
Supercontig_1.2_MVLG_00446_10sp	-441,4306	-441,42678	0,00764	0,00381	NS	0	[]	[]	[]	hypothetical protein	PF10018.2	Med4(Vitamin-D-receptor interacting Mediator subunit 17t)
Supercontig_1.12_MVLG_01873_8sp	-518,27539	-518,26436	0,02206	0,01097	NS	0	[]	[]	[]	hypothetical protein	PF10256.2	Erf4(Golgin subfamily A member 7/ERF4 family)
Supercontig_1.128_MVLG_06557_8sp	-342,3364	-342,33629	0,00022	0,00011	NS	0	[]	[]	[]	hypothetical protein	PF08654.3	DASH_Dad2(DASH complex subunit Dad2)
Supercontig_1.21_MVLG_02666_10sp	-564,94021	-564,94021	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01485.14	IBR(IBR domain)
Supercontig_1.4_MVLG_00848_11sp	-971,58454	-970,36789	2,4333	0,70378	NS	0	[]	[]	[]	O-sialoglycoprotein endopeptidase	TIGR00329	TIGR00329(gcp_kae1: metallohydrolase, glycoprotease/Kae1 family)
Supercontig_1.2_MVLG_00284_10sp	-501,29279	-499,25287	4,07984	0,86996	NS	0	[]	[]	[]	CMGC/SRPK protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.98_MVLG_06093_9sp	-799,61482	-799,61482	0	0	NS	0	[]	[]	[]	hypothetical protein	PF07690.9	MFS_1(Major Facilitator Superfamily)
Supercontig_1.58_MVLG_04879_12sp	-845,23727	-845,2213	0,03194	0,01584	NS	0	[]	[]	[]	hypothetical protein	PF10305.2	Fmp27_SW(RNA pol II promoter Fmp27 protein domain)
Supercontig_1.14_MVLG_02052_8sp	-1129,1991	-1129,1991	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.54_MVLG_04654_6sp	-631,04505	-631,045	0	0	NS	0	[]	[]	[]	RuvB-like helicase 2	PF03796.8	DnaB_C(DnaB-like helicase C terminal domain)
Supercontig_1.20_MVLG_02598_8sp	-1103,5376	-1103,5376	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00270.22	DEAD(DEAD/DEAH box helicase)
Supercontig_1.94_MVLG_05994_9sp	-420,75376	-420,75376	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.30_MVLG_03301_7sp	-810,7662	-810,72702	0,07836	0,03842	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.92_MVLG_05964_8sp	-585,07884	-584,437	1,28368	0,47368	NS	0	[]	[]	[]	hypothetical protein	NA	NA

Supercontig_1.4_MVLG_00855_9sp	-1019,1824	-1019,1824	0	0	NS	0	[]	[]	[]	gamma-glutamyltranspeptidase	PF01019.14	G_glu_transpept(Gamma-glutamyltranspeptidase)
Supercontig_1.80_MVLG_05654_8sp	-433,71196	-433,69501	0,0339	0,01681	NS	0	[]	[]	[]	hypothetical protein	PF02566.12	OsmC(OsmC-like protein)
Supercontig_1.32_MVLG_03434_8sp	-1060,3192	-1060,3192	0	0	NS	0	[]	[]	[]	hypothetical protein	PF07910.6	Peptidase_C78(Peptidase family C78)
Supercontig_1.1_MVLG_00238_9sp	-473,32842	-473,07977	0,4973	0,22015	NS	0	[]	[]	[]	hypothetical protein	PF05648.7	PEX11(Peroxisomal biogenesis factor 11 (PEX11))
Supercontig_1.52_MVLG_04567_10sp	-313,11258	-313,07664	0,07188	0,0353	NS	0	[]	[]	[]	hypothetical protein	PF10282.2	Muc_lac_enz(3-carboxy-cis,cis-muconate lactonizing enzyme)
Supercontig_1.1_MVLG_00161_9sp	-395,58551	-395,5626	0,04582	0,02265	NS	0	[]	[]	[]	hypothetical protein	PF00085.13	Thioredoxin(Thioredoxin)
Supercontig_1.6_MVLG_01164_9sp	-952,89815	-952,71158	0,37314	0,1702	NS	0	[]	[]	[]	hypothetical protein	PF00076.15	RRM_1(RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain))
Supercontig_1.15_MVLG_02068_7sp	-379,16266	-379,16266	0	0	NS	0	[]	[]	[]	hypothetical protein	PF07690.9	MFS_1(Major Facilitator Superfamily)
Supercontig_1.14_MVLG_01980_8sp	-912,62472	-912,58479	0,07986	0,03914	NS	0	[]	[]	[]	hypothetical protein	PF01545.14	Cation_efflux(Cation efflux family)
Supercontig_1.9_MVLG_01569_6sp	-766,8659	-766,21186	1,30808	0,48006	NS	0	[]	[]	[]	hypothetical protein	PF04140.7	ICMT(Isoprenylcysteine carboxyl methyltransferase (ICMT) family)
Supercontig_1.6_MVLG_01126_11sp	-385,10074	-384,85445	0,49258	0,2183	NS	0	[]	[]	[]	hypothetical protein	PF08614.4	ATG16(Autophagy protein 16 (ATG16))
Supercontig_1.5_MVLG_01028_7sp	-395,53474	-395,45649	0,1565	0,07527	NS	0	[]	[]	[]	hypothetical protein	PF04434.10	SWIM(SWIM zinc finger)
Supercontig_1.69_MVLG_05289_11sp	-390,94668	-390,94668	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01212.14	Beta_elim_lyase(Beta-eliminating lyase)
Supercontig_1.95_MVLG_06018_11sp	-406,68666	-406,68654	0,00024	0,00012	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.49_MVLG_04439_11sp	-436,57003	-436,32332	0,49342	0,21863	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.39_MVLG_03843_10sp	-714,51991	-714,28586	0,4681	0,20868	NS	0	[]	[]	[]	hypothetical protein	TIGR00952	TIGR00952(S15_bact: ribosomal protein S15)
Supercontig_1.3_MVLG_00502_9sp	-579,88064	-578,42497	2,91134	0,76676	NS	0	[]	[]	[]	hypothetical protein	PF04912.7	Dynamitin(Dynamitin)
Supercontig_1.42_MVLG_04071_6sp	-823,77636	-823,69107	0,17058	0,08175	NS	0	[]	[]	[]	hypothetical protein	PF05502.6	Dynactin_p62(Dynactin p62 family)
Supercontig_1.36_MVLG_03679_8sp	-484,75305	-483,5563	2,3935	0,69783	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.24_MVLG_02909_8sp	-1353,0325	-1353,0325	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.10_MVLG_01592_8sp	-877,51937	-877,51854	0,00166	0,00083	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.13_MVLG_01942_9sp	-606,48701	-606,48691	0,0002	0	NS	0	[]	[]	[]	hypothetical protein	PF00096.19	zf-C2H2(Zinc finger, C2H2 type)
Supercontig_1.6_MVLG_01194_8sp	-658,69801	-657,04071	3,3146	0,80935	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.53_MVLG_04626_10sp	-494,52364	-494,52364	0	0	NS	0	[]	[]	[]	hypothetical protein	TIGR02765	TIGR02765(crypto_DASH: cryptochrome, DASH family)

Supercontig_1.69_MVLG_05283_9sp	-908,54651	-905,79736	5,4983	0,93602	*	0	[]	[]	[]	hypothetical protein	PF01408.15	GFO_IDH_MocA(Oxidoreductase family, NAD-binding Rossmann fold)
Supercontig_1.10_MVLG_01589_7sp	-1173,9866	-1173,8903	0,1927	0,09185	NS	0	[]	[]	[]	hypothetical protein	PF04130.6	Spc97_Spc98(Spc97 / Spc98 family)
Supercontig_1.54_MVLG_04674_6sp	-1267,29	-1266,0565	2,46682	0,7087	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.6_MVLG_01190_7sp	-784,78543	-784,78543	0	0	NS	0	[]	[]	[]	hypothetical protein	PF08216.4	DUF1716(Eukaryotic domain of unknown function (DUF1716))
Supercontig_1.3_MVLG_00563_10sp	-317,03122	-316,48462	1,0932	0,42109	NS	0	[]	[]	[]	hypothetical protein	PF01459.15	Porin_3(Eukaryotic porin)
Supercontig_1.3_MVLG_00659_7sp	-360,68697	-360,68697	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02777.11	Sod_Fe_C(Iron/manganese superoxide dismutases, C-terminal domain)
Supercontig_1.53_MVLG_04602_9sp	-468,34053	-468,21485	0,25136	0,1181	NS	0	[]	[]	[]	hypothetical protein	PF00642.17	zf-CCCH(Zinc finger C-x8-C-x5-C-x3-H type (and similar))
Supercontig_1.125_MVLG_06501_10sp	-767,72495	-767,45178	0,54634	0,23904	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.60_MVLG_04952_7sp	-399,21214	-398,78709	0,8501	0,34626	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.47_MVLG_04328_9sp	-346,76023	-346,08188	1,3567	0,49255	NS	0	[]	[]	[]	hypothetical protein	PF00397.19	WW(WW domain)
Supercontig_1.1_MVLG_00075_10sp	-449,74682	-449,74682	0	0	NS	0	[]	[]	[]	DNA-directed RNA polymerase I subunit RPA2	PF06883.5	RNA_pol_Rpa2_4(RNA polymerase I, Rpa2 specific domain)
Supercontig_1.5_MVLG_01013_7sp	-620,67781	-620,67781	0	0	NS	0	[]	[]	[]	acyl-CoA dehydrogenase	PF02770.12	Acyl-CoA_dh_M(Acyl-CoA dehydrogenase, middle domain)
Supercontig_1.27_MVLG_03086_10sp	-380,13466	-380,13438	0,00056	0,00028	NS	0	[]	[]	[]	26S protease regulatory subunit 4	PF07724.7	AAA_2(AAA domain (Cdc48 subfamily))
Supercontig_1.9_MVLG_01538_10sp	-596,37624	-596,37624	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.54_MVLG_04667_10sp	-333,18018	-333,18	0,00036	0,00018	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.8_MVLG_01359_9sp	-505,09554	-504,59547	1,00014	0,39351	NS	0	[]	[]	[]	hypothetical protein	PF00551.12	Formyl_trans_N(Formyl transferase)
Supercontig_1.20_MVLG_02603_8sp	-444,94063	-444,94058	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.204_MVLG_07103_10sp	-358,76654	-358,76618	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02466.12	Tim17(Tim17/Tim22/Tim23 family)
Supercontig_1.95_MVLG_06008_8sp	-2416,8722	-2416,8722	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02891.13	zf-MIZ(MIZ/SP-RING zinc finger)
Supercontig_1.9_MVLG_01484_9sp	-854,76752	-854,7675	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00009.20	GTP_EFTU(Elongation factor Tu GTP binding domain)
Supercontig_1.83_MVLG_05728_7sp	-329,98929	-329,98929	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00704.21	Glyco_hydro_18(Glycosyl hydrolases family 18)
Supercontig_1.20_MVLG_02579_12sp	-482,48425	-482,4842	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.7_MVLG_01248_6sp	-544,36202	-544,36202	0	0	NS	0	[]	[]	[]	histone	PF00125.17	Histone(Core histone H2A/H2B/H3/H4)

Supercontig_1.41_MVLG_04006_10sp	-340,03564	-340,03561	0	0	NS	0	[]	[]	[]	maf-like protein	PF02545.7	Maf(Maf-like protein)
Supercontig_1.15_MVLG_02096_8sp	-627,95677	-627,85974	0,19406	0,09247	NS	0	[]	[]	[]	hypothetical protein	PF02919.8	Topoisom_I_N(Eukaryotic DNA topoisomerase I, DNA binding fragment)
Supercontig_1.10_MVLG_01675_9sp	-679,87636	-678,34407	3,06458	0,78396	NS	0	[]	[]	[]	acetolactate synthase I/III small subunit	PF10369.2	ALS_ss_C(Small subunit of acetolactate synthase)
Supercontig_1.1_MVLG_00001_10sp	-1093,0945	-1093,0941	0,00078	0,00039	NS	0	[]	[]	[]	pyruvate carboxylase	PF02222.15	ATP-grasp(ATP-grasp domain)
Supercontig_1.1_MVLG_00225_9sp	-630,94484	-630,94484	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00698.14	Acyl_transf_1(Acyl transferase domain)
Supercontig_1.1_MVLG_00240_11sp	-269,85143	-269,85129	0,00028	0,00014	NS	0	[]	[]	[]	hypothetical protein	PF04049.6	APC8(Anaphase promoting complex subunit 8 / Cdc23)
Supercontig_1.39_MVLG_03901_9sp	-732,88111	-732,88107	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02421.11	FeoB_N(Ferrous iron transport protein B)
Supercontig_1.85_MVLG_05798_9sp	-649,99037	-649,99037	0	0	NS	0	[]	[]	[]	hypothetical protein	PF06741.6	LsmAD(LsmAD domain)
Supercontig_1.33_MVLG_03477_9sp	-449,09573	-449,09561	0,00024	0,00012	NS	0	[]	[]	[]	hypothetical protein	PF00728.15	Glyco_hydro_20(Glycosyl hydrolase family 20, catalytic domain)
Supercontig_1.33_MVLG_03445_7sp	-577,19297	-575,88825	2,60944	0,72875	NS	0	[]	[]	[]	hypothetical protein	PF00023.23	Ank(Ankyrin repeat)
Supercontig_1.58_MVLG_04859_11sp	-393,10096	-393,10096	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01344.18	Kelch_1(Kelch motif)
Supercontig_1.70_MVLG_05321_6sp	-649,98697	-649,90336	0,16722	0,08021	NS	0	[]	[]	[]	hypothetical protein	TIGR00001	TIGR00001(rpmI_bact: ribosomal protein L35)
Supercontig_1.61_MVLG_04969_6sp	-493,42865	-493,42865	0	0	NS	0	[]	[]	[]	hypothetical protein	PF09696.3	Ctf8(Ctf8)
Supercontig_1.1_MVLG_00250_10sp	-471,78484	-471,78484	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.98_MVLG_06100_7sp	-608,71175	-608,71156	0,00038	0,00019	NS	0	[]	[]	[]	hypothetical protein	PF00076.15	RRM_1(RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain))
Supercontig_1.112_MVLG_06318_7sp	-645,26224	-645,17445	0,17558	0,08405	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.82_MVLG_05705_10sp	-383,56777	-383,56777	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01398.14	Mov34(Mov34/MPN/PAD-1 family)
Supercontig_1.23_MVLG_02815_8sp	-675,60276	-675,60253	0,00046	0,00023	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.3_MVLG_00655_8sp	-373,91487	-373,79376	0,24222	0,11406	NS	0	[]	[]	[]	hypothetical protein	PF05603.5	DUF775(Protein of unknown function (DUF775))
Supercontig_1.13_MVLG_01910_9sp	-365,40251	-365,40244	0	0	NS	0	[]	[]	[]	chorismate synthase	TIGR00033	TIGR00033(aroC: chorismate synthase)
Supercontig_1.5_MVLG_00958_9sp	-386,54838	-386,54837	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.79_MVLG_05627_11sp	-640,31606	-640,29145	0,04922	0,02431	NS	0	[]	[]	[]	hypothetical protein	PF00096.19	zf-C2H2(Zinc finger, C2H2 type)
Supercontig_1.3_MVLG_00626_7sp	-917,77553	-917,76934	0,01238	0,00617	NS	0	[]	[]	[]	branched-chain amino acid aminotransferase	PF01063.12	Aminotran_4(Aminotransferase class IV)

Supercontig_1.4_MVLG_00874_9sp	-1175,5836	-1175,5431	0,0809	0,03964	NS	0	[]	[]	[]	hypothetical protein	PF08158.5	NUC130_3NT(NUC130/3NT domain)
Supercontig_1.9_MVLG_01548_7sp	-742,04445	-742,04445	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.40_MVLG_03918_6sp	-379,60571	-379,60561	0,0002	0	NS	0	[]	[]	[]	hypothetical protein	PF09430.3	DUF2012(Protein of unknown function (DUF2012))
Supercontig_1.6_MVLG_01183_9sp	-443,98668	-443,98655	0,00026	0,00013	NS	0	[]	[]	[]	hypothetical protein	PF00083.17	Sugar_tr(Sugar (and other) transporter)
Supercontig_1.1_MVLG_00187_11sp	-839,75464	-839,75464	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.9_MVLG_01482_6sp	-1902,4718	-1902,3846	0,17428	0,08345	NS	0	[]	[]	[]	hypothetical protein	PF02460.11	Patched(Patched family)
Supercontig_1.109_MVLG_06275_11sp	-327,28339	-327,28339	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04939.5	RRS1(Ribosome biogenesis regulatory protein (RRS1))
Supercontig_1.1_MVLG_00174_9sp	-850,48969	-850,46271	0,05396	0,02662	NS	0	[]	[]	[]	hypothetical protein	PF00082.15	Peptidase_S8(Subtilase family)
Supercontig_1.45_MVLG_04211_10sp	-513,10259	-512,8708	0,46358	0,20689	NS	0	[]	[]	[]	hypothetical protein	PF03810.12	IBN_N(Importin-beta N-terminal domain)
Supercontig_1.83_MVLG_05731_8sp	-902,10581	-901,77295	0,66572	0,28313	NS	0	[]	[]	[]	hypothetical protein	PF00929.17	Exonuc_X-T(Exonuclease)
Supercontig_1.52_MVLG_04559_11sp	-348,3395	-348,3395	0	0	NS	0	[]	[]	[]	hypothetical protein	PF08518.4	GIT_SHD(Spa2 homology domain (SHD) of GIT)
Supercontig_1.164_MVLG_06899_6sp	-558,12224	-558,12222	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02170.15	PAZ(PAZ domain)
Supercontig_1.10_MVLG_01618_9sp	-642,649	-642,03044	1,23712	0,46128	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.17_MVLG_02308_8sp	-771,37004	-771,37004	0	0	NS	0	[]	[]	[]	hypothetical protein	PF10303.2	DUF2408(Protein of unknown function (DUF2408))
Supercontig_1.30_MVLG_03258_11sp	-725,64289	-725,64289	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03600.9	CitMHS(Citrate transporter)
Supercontig_1.49_MVLG_04431_9sp	-524,0815	-523,8664	0,4302	0,19354	NS	0	[]	[]	[]	hypothetical protein	PF10914.1	DUF2781(Protein of unknown function (DUF2781))
Supercontig_1.31_MVLG_03373_7sp	-311,22257	-311,22634	0	0	NS	0	[]	[]	[]	NEDD8	PF11976.1	Rad60-SLD(Ubiquitin-2 like Rad60 SUMO-like)
Supercontig_1.80_MVLG_05631_9sp	-661,87534	-661,87534	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02037.20	SAP(SAP domain)
Supercontig_1.5_MVLG_01007_10sp	-595,19349	-594,9691	0,44878	0,201	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.1_MVLG_00106_7sp	-506,93265	-506,93265	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03943.6	TAP_C(TAP C-terminal domain)
Supercontig_1.35_MVLG_03626_9sp	-1812,7938	-1806,3132	12,9611	0,99847	***	0	[]	[]	[]	hypothetical protein	PF00250.11	Fork_head(Fork head domain)
Supercontig_1.100_MVLG_06134_9sp	-524,94886	-522,90228	4,09316	0,87082	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.68_MVLG_05260_8sp	-449,31191	-448,63952	1,34478	0,48951	NS	0	[]	[]	[]	hypothetical protein	PF00253.14	Ribosomal_S14(Ribosomal protein S14p/S29e)
Supercontig_1.1_MVLG_00261_11sp	-905,93637	-905,8507	0,17134	0,0821	NS	0	[]	[]	[]	hypothetical protein	PF00924.11	MS_channel(Mechanosensitive ion channel)
Supercontig_1.1_MVLG_00186_9sp	-496,50655	-496,5064	0,0003	0,00015	NS	0	[]	[]	[]	hypothetical protein	NA	NA

Supercontig_1.6_MVLG_01221_9sp	-639,26413	-639,26413	0	0	NS	0	[]	[]	[]	succinyl-CoA ligase [GDP-forming] subunit beta, hydrogenosomal	PF00549.12	Ligase_CoA(CoA-ligase)
Supercontig_1.47_MVLG_04341_9sp	-607,93916	-607,93916	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03097.11	BRO1(BRO1-like domain)
Supercontig_1.5_MVLG_00978_10sp	-373,5159	-373,51582	0,00016	0	NS	0	[]	[]	[]	hypothetical protein	PF00172.11	Zn_clus(Fungal Zn(2)-Cys(6) binuclear cluster domain)
Supercontig_1.10_MVLG_01605_12sp	-544,418	-544,34033	0,15534	0,07473	NS	0	[]	[]	[]	hypothetical protein	PF00899.14	ThiF(ThiF family)
Supercontig_1.30_MVLG_03318_6sp	-785,62985	-784,91683	1,42604	0,50984	NS	0	[]	[]	[]	hypothetical protein	PF00892.13	EamA(EamA-like transporter family)
Supercontig_1.12_MVLG_01809_11sp	-607,84938	-606,52536	2,64804	0,73394	NS	0	[]	[]	[]	hypothetical protein	TIGR00071	TIGR00071(hisT_truA: tRNA pseudouridine synthase A)
Supercontig_1.2_MVLG_00363_10sp	-493,94086	-492,91275	2,05622	0,64232	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.6_MVLG_01188_11sp	-444,07471	-444,07456	0,0003	0,00015	NS	0	[]	[]	[]	hypothetical protein	PF00867.11	XPG_I(XPG I-region)
Supercontig_1.239_MVLG_07202_8sp	-434,77117	-434,48554	0,57126	0,24846	NS	0	[]	[]	[]	hypothetical protein	PF02798.13	GST_N(Glutathione S-transferase, N-terminal domain)
Supercontig_1.9_MVLG_01512_7sp	-577,27806	-577,25942	0,03728	0,01847	NS	0	[]	[]	[]	MC family mitochondrial carrier protein	PF00153.20	Mito_carr(Mitochondrial carrier protein)
Supercontig_1.7_MVLG_01355_7sp	-528,47493	-528,02732	0,89522	0,36085	NS	0	[]	[]	[]	hypothetical protein	PF01459.15	Porin_3(Eukaryotic porin)
Supercontig_1.26_MVLG_03055_7sp	-697,12312	-697,12312	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.13_MVLG_01921_7sp	-975,84849	-972,46294	6,7711	0,96614	**	0	[]	[]	[]	hypothetical protein	PF00010.19	HLH(Helix-loop-helix DNA-binding domain)
Supercontig_1.44_MVLG_04164_9sp	-483,01493	-483,01493	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01150.10	GDA1_CD39(GDA1/CD39 (nucleoside phosphatase) family)
Supercontig_1.2_MVLG_00482_8sp	-700,71528	-700,69393	0,0427	0,02112	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.6_MVLG_01049_12sp	-594,52162	-594,52162	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.45_MVLG_04186_8sp	-465,04818	-465,04761	0,00114	0,00057	NS	0	[]	[]	[]	hypothetical protein	PF04777.6	Evr1_Alr(Erv1 / Alr family)
Supercontig_1.24_MVLG_02838_8sp	-465,49648	-465,49648	0	0	NS	0	[]	[]	[]	3-oxoacyl-[acyl-carrier protein] reductase	PF00106.18	adh_short(short chain dehydrogenase)
Supercontig_1.117_MVLG_06388_11sp	-601,13269	-601,13269	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.6_MVLG_01092_7sp	-770,09994	-770,09969	0,0005	0,00025	NS	0	[]	[]	[]	vesicle-fusing ATPase	PF07724.7	AAA_2(AAA domain (Cdc48 subfamily))
Supercontig_1.55_MVLG_04707_9sp	-463,05233	-463,05233	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01070.11	FMN_dh(FMN-dependent dehydrogenase)
Supercontig_1.67_MVLG_05223_6sp	-466,9119	-466,91137	0,00106	0,00053	NS	0	[]	[]	[]	CMGC/CK2 protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.126_MVLG_06522_10sp	-1135,8191	-1135,2766	1,085	0,41871	NS	0	[]	[]	[]	hypothetical protein	PF00675.13	Peptidase_M16(Insulinase (Peptidase family M16))

Supercontig_1.53_MVLG_04624_11sp	-701,11649	-701,11649	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04006.5	Mpp10(Mpp10 protein)
Supercontig_1.2_MVLG_00476_11sp	-478,05669	-478,05669	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03051.8	Peptidase_C1_2(Peptidase C1-like family)
Supercontig_1.99_MVLG_06108_9sp	-328,93038	-328,68583	0,4891	0,21694	NS	0	[]	[]	[]	hypothetical protein	PF08271.5	TF_Zn_Ribbon(TFIIB zinc-binding)
Supercontig_1.1_MVLG_00274_10sp	-835,53849	-835,53792	0,00114	0,00057	NS	0	[]	[]	[]	hypothetical protein	PF01569.14	PAP2(PAP2 superfamily)
Supercontig_1.39_MVLG_03902_6sp	-289,2749	-289,27484	0,00012	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.150_MVLG_06777_8sp	-730,86932	-730,86921	0,00022	0,00011	NS	0	[]	[]	[]	hypothetical protein	PF00782.13	DSPc(Dual specificity phosphatase, catalytic domain)
Supercontig_1.13_MVLG_01901_7sp	-613,58824	-613,58823	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02636.10	DUF185(Uncharacterized ACR, COG1565)
Supercontig_1.34_MVLG_03518_7sp	-372,16097	-371,91055	0,50084	0,22153	NS	0	[]	[]	[]	hypothetical protein	PF00293.21	NUDIX(NUDIX domain)
Supercontig_1.24_MVLG_02895_7sp	-1292,6807	-1292,6807	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.26_MVLG_03036_10sp	-604,02854	-604,02852	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02269.9	TFIID-18kDa(Transcription initiation factor IID, 18kD subunit)
Supercontig_1.3_MVLG_00594_10sp	-581,283	-581,283	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04938.5	SIP1(Survival motor neuron (SMN) interacting protein 1 (SIP1))
Supercontig_1.62_MVLG_05020_6sp	-1035,8654	-1035,8187	0,09334	0,0456	NS	0	[]	[]	[]	hypothetical protein	PF00786.21	PBD(P21-Rho-binding domain)
Supercontig_1.70_MVLG_05339_10sp	-419,51533	-419,51533	0	0	NS	0	[]	[]	[]	hypothetical protein	PF07767.4	Nop53(Nop53 (60S ribosomal biogenesis))
Supercontig_1.5_MVLG_01044_10sp	-595,81138	-595,81138	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.32_MVLG_03435_8sp	-406,76166	-406,76151	0,0003	0,00015	NS	0	[]	[]	[]	hypothetical protein	PF02144.9	Rad1(Repair protein Rad1/Rec1/Rad17)
Supercontig_1.52_MVLG_04592_12sp	-797,67519	-797,67502	0,00034	0,00017	NS	0	[]	[]	[]	hypothetical protein	PF03104.12	DNA_pol_B_exo(DNA polymerase family B, exonuclease domain)
Supercontig_1.91_MVLG_05937_10sp	-1600,7993	-1600,7904	0,01778	0,00885	NS	0	[]	[]	[]	hypothetical protein	PF00650.13	CRAL_TRIO(CRAL/TRIO domain)
Supercontig_1.197_MVLG_07071_10sp	-843,01611	-842,49964	1,03294	0,40338	NS	0	[]	[]	[]	hypothetical protein	PF12152.1	eIF_4G1(Eukaryotic translation initiation factor 4G1)
Supercontig_1.39_MVLG_03892_10sp	-589,21868	-588,79792	0,84152	0,34345	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.121_MVLG_06440_11sp	-464,68768	-464,4874	0,40056	0,1815	NS	0	[]	[]	[]	hypothetical protein	PF07738.6	Sad1_UNC(Sad1 / UNC-like C-terminal)
Supercontig_1.36_MVLG_03653_8sp	-465,03818	-464,01496	2,04644	0,64056	NS	0	[]	[]	[]	phosphoglycerate kinase	PF00162.12	PGK(Phosphoglycerate kinase)
Supercontig_1.107_MVLG_06243_12sp	-453,45885	-453,45885	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00515.21	TPR_1(Tetratricopeptide repeat)
Supercontig_1.125_MVLG_06508_8sp	-724,04749	-724,04728	0,00042	0,00021	NS	0	[]	[]	[]	19S proteasome regulatory subunit Rpn6	PF01399.20	PCI(PCI domain)

Supercontig_1.19_MVLG_02458_10sp	-708,39714	-708,39714	0	0	NS	0	[]	[]	[]	hypothetical protein	PF06687.5	SUR7(SUR7/PalI family)
Supercontig_1.46_MVLG_04276_8sp	-709,56383	-709,56383	0	0	NS	0	[]	[]	[]	hypothetical protein	PF07859.6	Abhydrolase_3(alpha/beta hydrolase fold)
Supercontig_1.22_MVLG_02718_10sp	-702,70577	-702,42069	0,57016	0,24805	NS	0	[]	[]	[]	hypothetical protein	PF07717.9	DUF1605(Domain of unknown function (DUF1605))
Supercontig_1.53_MVLG_04617_10sp	-373,2413	-373,24116	0,00028	0,00014	NS	0	[]	[]	[]	hypothetical protein	PF08242.5	Methyltransf_12(Methyltransferase domain)
Supercontig_1.113_MVLG_06341_6sp	-760,81583	-760,81583	0	0	NS	0	[]	[]	[]	GDP-mannose 4,6 dehydratase	TIGR01472	TIGR01472(gmd: GDP-mannose 4,6-dehydratase)
Supercontig_1.66_MVLG_05195_7sp	-942,38092	-941,90688	0,94808	0,37752	NS	0	[]	[]	[]	hypothetical protein	PF04502.6	DUF572(Family of unknown function (DUF572))
Supercontig_1.58_MVLG_04868_9sp	-457,53539	-457,16791	0,73496	0,30752	NS	0	[]	[]	[]	hypothetical protein	PF06687.5	SUR7(SUR7/PalI family)
Supercontig_1.2_MVLG_00408_11sp	-441,88904	-440,21356	3,35096	0,81278	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.80_MVLG_05651_8sp	-561,87582	-561,87573	0,00018	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.42_MVLG_04087_11sp	-657,32095	-656,56991	1,50208	0,52812	NS	0	[]	[]	[]	hypothetical protein	PF00443.22	UCH(Ubiquitin carboxyl-terminal hydrolase)
Supercontig_1.3_MVLG_00670_10sp	-707,97836	-707,84974	0,25724	0,12069	NS	0	[]	[]	[]	hypothetical protein	PF07732.8	Cu-oxidase_3(Multicopper oxidase)
Supercontig_1.85_MVLG_05815_9sp	-494,98402	-494,98402	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00010.19	HLH(Helix-loop-helix DNA-binding domain)
Supercontig_1.24_MVLG_02897_8sp	-609,74408	-609,7002	0,08776	0,04293	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.54_MVLG_04664_10sp	-682,31149	-682,31128	0,00042	0,00021	NS	0	[]	[]	[]	hypothetical protein	PF07728.7	AAA_5(AAA domain (dynein-related subfamily))
Supercontig_1.4_MVLG_00762_9sp	-427,41143	-427,41109	0,00068	0,00034	NS	0	[]	[]	[]	HAL protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.40_MVLG_03948_10sp	-527,95879	-527,95879	0	0	NS	0	[]	[]	[]	hypothetical protein	PF06398.4	Pex24p(Integral peroxisomal membrane peroxin)
Supercontig_1.96_MVLG_06042_6sp	-888,54998	-888,54998	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.2_MVLG_00481_9sp	-737,35705	-737,35469	0,00472	0,00236	NS	0	[]	[]	[]	hypothetical protein	PF10557.2	Cullin_Nedd8(Cullin protein neddylation domain)
Supercontig_1.52_MVLG_04562_11sp	-417,49866	-417,49866	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.69_MVLG_05290_10sp	-634,88379	-634,88379	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01103.16	Bac_surface_Ag(Surface antigen)
Supercontig_1.35_MVLG_03602_6sp	-526,47673	-525,68621	1,58104	0,54639	NS	0	[]	[]	[]	asparaginyl-tRNA synthetase	PF01336.18	tRNA_anti(OB-fold nucleic acid binding domain)
Supercontig_1.49_MVLG_04433_9sp	-503,97688	-503,97688	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00097.18	zf-C3HC4(Zinc finger, C3HC4 type (RING finger))
Supercontig_1.10_MVLG_01613_6sp	-318,75911	-318,75903	0,00016	0	NS	0	[]	[]	[]	hypothetical protein	PF00076.15	RRM_1(RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain))
Supercontig_1.55_MVLG_04728_6sp	-746,96106	-746,7435	0,43512	0,19552	NS	0	[]	[]	[]	hypothetical protein	PF00583.17	Acetyltransf_1(Acetyltransferase (GNAT) family)
Supercontig_1.124_MVLG_06487_11sp	-462,14901	-461,93891	0,4202	0,1895	NS	0	[]	[]	[]	hypothetical protein	TIGR01740	TIGR01740(pyrF: orotidine 5'-phosphate decarboxylase)

Supercontig_1.6_MVLG_01061_10sp	-945,21429	-945,21429	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.12_MVLG_01839_8sp	-687,17534	-687,03204	0,2866	0,13351	NS	0	[]	[]	[]	hypothetical protein	PF00018.21	SH3_1(SH3 domain)
Supercontig_1.53_MVLG_04603_7sp	-452,65921	-452,65916	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00307.24	CH(Calponin homology (CH) domain)
Supercontig_1.53_MVLG_04636_8sp	-298,9228	-298,92245	0,0007	0,00035	NS	0	[]	[]	[]	mannose-1-phosphate guanyltransferase	PF00132.17	Hexapep(Bacterial transferase hexapeptide (three repeats))
Supercontig_1.3_MVLG_00537_7sp	-435,80358	-435,80358	0	0	NS	0	[]	[]	[]	rRNA-processing protein FCF1	PF04900.5	Fcf1(Fcf1)
Supercontig_1.66_MVLG_05178_9sp	-428,4767	-428,47661	0,00018	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.39_MVLG_03853_6sp	-947,08346	-947,00782	0,15128	0,07285	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.6_MVLG_01125_8sp	-528,80203	-528,80171	0,00064	0,00032	NS	0	[]	[]	[]	homoaconitase	PF00694.12	Aconitase_C(Aconitase C-terminal domain)
Supercontig_1.4_MVLG_00751_11sp	-632,19866	-632,06821	0,2609	0,1223	NS	0	[]	[]	[]	glycogen phosphorylase 1	PF00343.13	Phosphorylase(Carbohydrate phosphorylase)
Supercontig_1.47_MVLG_04318_12sp	-797,7738	-797,25502	1,03756	0,40475	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.24_MVLG_02893_10sp	-535,25451	-535,25388	0,00126	0,00063	NS	0	[]	[]	[]	actin-like protein 2	PF00022.12	Actin(Actin)
Supercontig_1.20_MVLG_02554_10sp	-1284,9622	-1284,9622	0	0	NS	0	[]	[]	[]	hypothetical protein	TIGR00606	TIGR00606(rad50: rad50)
Supercontig_1.1_MVLG_00215_9sp	-379,21346	-378,2822	1,86252	0,60594	NS	0	[]	[]	[]	hypothetical protein	PF00153.20	Mito_carr(Mitochondrial carrier protein)
Supercontig_1.46_MVLG_04290_8sp	-816,37858	-815,76588	1,2254	0,45811	NS	0	[]	[]	[]	hypothetical protein	PF05132.7	RNA_pol_Rpc4(RNA polymerase III RPC4)
Supercontig_1.8_MVLG_01358_8sp	-1535,2735	-1534,5806	1,38588	0,4999	NS	0	[]	[]	[]	protoporphyrinogen oxidase	TIGR00562	TIGR00562(proto_IX_ox: protoporphyrinogen oxidase)
Supercontig_1.7_MVLG_01345_10sp	-641,74687	-641,74447	0,0048	0,0024	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.164_MVLG_06893_8sp	-472,46237	-472,46033	0,00408	0,00204	NS	0	[]	[]	[]	hypothetical protein	PF06047.4	SynMuv_product(Ras-induced vulval development antagonist)
Supercontig_1.1_MVLG_00269_8sp	-846,62343	-846,62343	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00172.11	Zn_clus(Fungal Zn(2)-Cys(6) binuclear cluster domain)
Supercontig_1.20_MVLG_02529_9sp	-450,18756	-450,17954	0,01604	0,00799	NS	0	[]	[]	[]	hypothetical protein	PF10173.2	DUF2343(Uncharacterised conserved protein (DUF2343))
Supercontig_1.13_MVLG_01932_8sp	-413,48762	-413,48754	0,00016	0	NS	0	[]	[]	[]	hypothetical protein	PF08210.4	APOBEC_N(APOBEC-like N-terminal domain)
Supercontig_1.57_MVLG_04828_12sp	-1221,7697	-1221,7697	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00623.13	RNA_pol_Rpb1_2(RNA polymerase Rpb1, domain 2)
Supercontig_1.126_MVLG_06519_10sp	-928,1325	-928,06543	0,13414	0,06487	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.23_MVLG_02826_7sp	-538,58669	-538,58669	0	0	NS	0	[]	[]	[]	hypothetical protein	PF07819.6	PGAP1(PGAP1-like protein)
Supercontig_1.19_MVLG_02507_8sp	-917,64791	-917,59413	0,10756	0,05236	NS	0	[]	[]	[]	hypothetical protein	PF10405.2	BHD_3(Rad4 beta-hairpin domain 3)

Supercontig_1.127_MVLG_06537_6sp	-1174,8424	-1174,8424	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00181.16	Ribosomal_L2(Ribosomal Proteins L2, RNA binding domain)
Supercontig_1.111_MVLG_06307_8sp	-477,80606	-477,80606	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03435.11	Saccharop_dh(Saccharopine dehydrogenase)
Supercontig_1.29_MVLG_03254_8sp	-837,37326	-837,37316	0,0002	0	NS	0	[]	[]	[]	hypothetical protein	PF03031.11	NIF(NLI interacting factor-like phosphatase)
Supercontig_1.107_MVLG_06259_6sp	-949,54712	-948,71791	1,65842	0,56361	NS	0	[]	[]	[]	hypothetical protein	PF03810.12	IBN_N(Importin-beta N-terminal domain)
Supercontig_1.35_MVLG_03589_9sp	-644,37248	-644,37248	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03388.6	Lectin_leg-like(Legume-like lectin family)
Supercontig_1.6_MVLG_01093_10sp	-806,2749	-806,2749	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00787.17	PX(PX domain)
Supercontig_1.41_MVLG_04028_7sp	-1090,6933	-1090,6933	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.1_MVLG_00051_8sp	-1577,9656	-1577,3902	1,1508	0,43752	NS	0	[]	[]	[]	hypothetical protein	PF04802.8	SMK-1(Component of IIS longevity pathway SMK-1)
Supercontig_1.39_MVLG_03888_7sp	-627,76604	-627,15331	1,22546	0,45813	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.14_MVLG_02003_7sp	-614,60582	-614,60582	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02581.10	TMP-TENI(Thiamine monophosphate synthase/TENI)
Supercontig_1.151_MVLG_06785_9sp	-427,05547	-426,90206	0,30682	0,14222	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.57_MVLG_04819_8sp	-790,25297	-790,25297	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00535.19	Glycos_transf_2(Glycosyl transferase family 2)
Supercontig_1.11_MVLG_01705_10sp	-829,46736	-829,46736	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02854.12	MIF4G(MIF4G domain)
Supercontig_1.18_MVLG_02428_11sp	-391,99074	-391,99072	0	0	NS	0	[]	[]	[]	hypothetical protein	TIGR01266	TIGR01266(fum_ac_acetase: fumarylacetoacetase)
Supercontig_1.3_MVLG_00591_9sp	-466,88957	-466,39713	0,98488	0,38887	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.44_MVLG_04144_9sp	-485,86206	-485,86197	0,00018	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.2_MVLG_00293_6sp	-395,10957	-395,10957	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01472.13	PUA(PUA domain)
Supercontig_1.17_MVLG_02320_9sp	-756,11665	-756,11647	0,00036	0,00018	NS	0	[]	[]	[]	alanine-glyoxylate transaminase	PF00266.12	Aminotran_5(Aminotransferase class-V)
Supercontig_1.58_MVLG_04848_12sp	-544,02905	-544,02905	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04675.7	DNA_ligase_A_N(DNA ligase N terminus)
Supercontig_1.85_MVLG_05802_8sp	-616,78652	-616,78652	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00999.14	Na_H_Exchanger(Sodium/hydrogen exchanger family)
Supercontig_1.50_MVLG_04457_7sp	-610,67132	-610,67097	0,0007	0,00035	NS	0	[]	[]	[]	hypothetical protein	PF03114.11	BAR(BAR domain)
Supercontig_1.39_MVLG_03882_11sp	-463,88196	-463,88171	0,0005	0,00025	NS	0	[]	[]	[]	hypothetical protein	PF04921.7	XAP5(XAP5 protein)
Supercontig_1.70_MVLG_05320_11sp	-867,1451	-867,1247	0,0408	0,02019	NS	0	[]	[]	[]	hypothetical protein	TIGR00378	TIGR00378(cax: calcium/proton exchanger)
Supercontig_1.36_MVLG_03672_10sp	-312,05253	-312,05248	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03800.7	Nuf2(Nuf2 family)
Supercontig_1.18_MVLG_02380_8sp	-1272,0973	-1272,0973	0	0	NS	0	[]	[]	[]	AAT family amino acid transporter	TIGR00913	TIGR00913(2A0310: amino acid permease (yeast))

Supercontig_1.99_MVLG_06112_12sp	-879,63826	-879,63826	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00225.16	Kinesin(Kinesin motor domain)
Supercontig_1.4_MVLG_00765_10sp	-905,87215	-905,67054	0,40322	0,18259	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.30_MVLG_03310_8sp	-907,15621	-906,39304	1,52634	0,53381	NS	0	[]	[]	[]	hypothetical protein	PF02204.11	VPS9(Vacuolar sorting protein 9 (VPS9) domain)
Supercontig_1.49_MVLG_04406_9sp	-1233,2132	-1232,0992	2,22796	0,67175	NS	0	[]	[]	[]	hypothetical protein	PF03568.10	Peptidase_C50(Peptidase family C50)
Supercontig_1.40_MVLG_03932_9sp	-921,85252	-921,40989	0,88526	0,35766	NS	0	[]	[]	[]	hypothetical protein	TIGR00813	TIGR00813(sss: transporter, solute:sodium symporter (SSS) family)
Supercontig_1.49_MVLG_04443_7sp	-580,96543	-580,71164	0,50758	0,22415	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.57_MVLG_04821_10sp	-442,49673	-442,49662	0,00022	0,00011	NS	0	[]	[]	[]	hypothetical protein	PF07859.6	Abhydrolase_3(alpha/beta hydrolase fold)
Supercontig_1.50_MVLG_04493_7sp	-357,2461	-357,24603	0,00014	0	NS	0	[]	[]	[]	hypothetical protein	PF00023.23	Ank(Ankyrin repeat)
Supercontig_1.34_MVLG_03569_8sp	-729,65446	-729,65432	0,00028	0,00014	NS	0	[]	[]	[]	hypothetical protein	PF00628.22	PHD(PHD-finger)
Supercontig_1.2_MVLG_00400_7sp	-667,08096	-667,08082	0,00028	0,00014	NS	0	[]	[]	[]	hypothetical protein	PF08234.5	Spindle_Spc25(Chromosome segregation protein Spc25)
Supercontig_1.53_MVLG_04601_9sp	-1157,39	-1157,3317	0,11674	0,0567	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.23_MVLG_02795_10sp	-568,23238	-566,24898	3,9668	0,8624	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.32_MVLG_03414_10sp	-670,89615	-670,89615	0	0	NS	0	[]	[]	[]	ATP-binding cassette, sub-family F, member 3	PF00005.20	ABC_tran(ABC transporter)
Supercontig_1.32_MVLG_03396_8sp	-462,68034	-462,51045	0,33978	0,15624	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.14_MVLG_02037_6sp	-743,65993	-743,65961	0,00064	0,00032	NS	0	[]	[]	[]	hypothetical protein	PF05653.7	DUF803(Protein of unknown function (DUF803))
Supercontig_1.20_MVLG_02594_8sp	-951,1949	-951,19488	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.34_MVLG_03523_9sp	-337,69597	-337,69577	0,0004	0,0002	NS	0	[]	[]	[]	hypothetical protein	PF00134.16	Cyclin_N(Cyclin, N-terminal domain)
Supercontig_1.21_MVLG_02669_10sp	-602,15076	-602,15067	0,00018	0	NS	0	[]	[]	[]	hypothetical protein	PF00566.11	TBC(TBC domain)
Supercontig_1.62_MVLG_05007_9sp	-750,23601	-750,23046	0,0111	0,00553	NS	0	[]	[]	[]	hypothetical protein	PF00782.13	DSPc(Dual specificity phosphatase, catalytic domain)
Supercontig_1.23_MVLG_02821_10sp	-394,16498	-392,71553	2,8989	0,7653	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.124_MVLG_06483_8sp	-572,48353	-571,00329	2,96048	0,77242	NS	0	[]	[]	[]	hypothetical protein	PF00364.15	Biotin_lipoyl(Biotin-requiring enzyme)
Supercontig_1.10_MVLG_01628_7sp	-763,17471	-762,90448	0,54046	0,2368	NS	0	[]	[]	[]	hypothetical protein	PF00928.14	Adap_comp_sub(Adaptor complexes medium subunit family)
Supercontig_1.1_MVLG_00160_10sp	-400,16336	-400,1633	0,00012	0	NS	0	[]	[]	[]	hypothetical protein	PF04719.7	TAFII28(hTAFII28-like protein conserved region)

Supercontig_1.10_MVLG_01679_7sp	-889,72634	-889,72634	0	0	NS	0	[]	[]	[]	phosphoglucomutase	PF02880.9	PGM_PMM_III(Phosphoglucomutase/phosphomannomutase, alpha/beta/alpha domain III)
Supercontig_1.19_MVLG_02435_8sp	-546,78548	-546,78548	0	0	NS	0	[]	[]	[]	ribose-phosphate pyrophosphokinase	TIGR01251	TIGR01251(ribP_PPkin: ribose-phosphate diphosphokinase)
Supercontig_1.38_MVLG_03770_7sp	-776,38163	-776,38063	0,002	0,001	NS	0	[]	[]	[]	ATP-binding cassette, sub-family F, member 2	PF00005.20	ABC_tran(ABC transporter)
Supercontig_1.24_MVLG_02866_7sp	-543,52093	-543,52087	0,00012	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.38_MVLG_03801_10sp	-434,48831	-434,48831	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01743.13	PolyA_pol(Poly A polymerase head domain)
Supercontig_1.18_MVLG_02402_11sp	-703,61375	-703,61375	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01699.17	Na_Ca_ex(Sodium/calcium exchanger protein)
Supercontig_1.3_MVLG_00501_8sp	-642,13525	-641,89513	0,48024	0,21347	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.104_MVLG_06210_10sp	-379,50862	-379,15042	0,7164	0,30107	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.28_MVLG_03152_10sp	-390,64379	-388,91408	3,45942	0,82266	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.1_MVLG_00034_12sp	-673,88855	-673,88835	0,0004	0,0002	NS	0	[]	[]	[]	hypothetical protein	PF04389.10	Peptidase_M28(Peptidase family M28)
Supercontig_1.23_MVLG_02812_7sp	-1873,017	-1873,017	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01369.13	Sec7(Sec7 domain)
Supercontig_1.39_MVLG_03889_8sp	-599,55543	-598,2282	2,65446	0,73479	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.1_MVLG_00136_10sp	-796,35563	-796,35194	0,00738	0,00368	NS	0	[]	[]	[]	hypothetical protein	PF02518.19	HATPase_c(Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase)
Supercontig_1.28_MVLG_03157_8sp	-1179,5181	-1179,0179	1,0003	0,39356	NS	0	[]	[]	[]	hypothetical protein	PF00293.21	NUDIX(NUDIX domain)
Supercontig_1.51_MVLG_04518_10sp	-545,76022	-545,66001	0,20042	0,09535	NS	0	[]	[]	[]	hypothetical protein	PF07993.5	NAD_binding_4(Male sterility protein)
Supercontig_1.117_MVLG_06400_11sp	-415,71951	-415,48074	0,47754	0,2124	NS	0	[]	[]	[]	prephenate dehydrogenase (NADP+)	PF03446.8	NAD_binding_2(NAD binding domain of 6-phosphogluconate dehydrogenase)
Supercontig_1.5_MVLG_00915_11sp	-535,20285	-535,20285	0	0	NS	0	[]	[]	[]	AGC/AKT protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.74_MVLG_05453_7sp	-578,34976	-578,34967	0,00018	0	NS	0	[]	[]	[]	hypothetical protein	PF07855.5	DUF1649(Protein of unknown function (DUF1649))
Supercontig_1.14_MVLG_02047_10sp	-1236,1895	-1236,1837	0,01162	0,00579	NS	0	[]	[]	[]	hypothetical protein	PF00899.14	ThiF(ThiF family)
Supercontig_1.23_MVLG_02804_10sp	-1144,0885	-1143,8813	0,41436	0,18713	NS	0	[]	[]	[]	hypothetical protein	PF04376.6	ATE_N(Arginine-tRNA-protein transferase, N terminus)
Supercontig_1.7_MVLG_01240_10sp	-657,6287	-657,58025	0,0969	0,0473	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.8_MVLG_01414_9sp	-444,57907	-443,07878	3,00058	0,77693	NS	0	[]	[]	[]	hypothetical protein	PF00752.10	XPG_N(XPG N-terminal domain)
Supercontig_1.39_MVLG_03850_9sp	-482,27211	-482,27211	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00097.18	zf-C3HC4(Zinc finger, C3HC4 type (RING finger))

Supercontig_1.7_MVLG_01326_9sp	-911,85856	-911,60235	0,51242	0,22602	NS	0	[]	[]	[]	CAMK/CAMKL protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.26_MVLG_03051_10sp	-924,24898	-924,21697	0,06402	0,0315	NS	0	[]	[]	[]	hypothetical protein	PF00282.12	Pyridoxal_deC(Pyridoxal-dependent decarboxylase conserved domain)
Supercontig_1.104_MVLG_06203_6sp	-496,10768	-496,10756	0,00024	0,00012	NS	0	[]	[]	[]	hypothetical protein	PF02222.15	ATP-grasp(ATP-grasp domain)
Supercontig_1.1_MVLG_00213_12sp	-864,71012	-864,71008	0	0	NS	0	[]	[]	[]	hypothetical protein	PF07539.5	DRIM(Down-regulated in metastasis)
Supercontig_1.3_MVLG_00581_11sp	-1967,8864	-1967,8748	0,02318	0,01152	NS	0	[]	[]	[]	hypothetical protein	PF11732.1	Thoc2(Transcription- and export-related complex subunit)
Supercontig_1.76_MVLG_05519_9sp	-597,50084	-597,5007	0,00028	0,00014	NS	0	[]	[]	[]	syntaxin 5	PF05739.12	SNARE(SNARE domain)
Supercontig_1.62_MVLG_05029_10sp	-427,60677	-427,60663	0,00028	0,00014	NS	0	[]	[]	[]	hypothetical protein	PF02780.13	Transketolase_C(Transketolase, C-terminal domain)
Supercontig_1.70_MVLG_05337_8sp	-330,09899	-330,09889	0,0002	0	NS	0	[]	[]	[]	hypothetical protein	PF05832.5	DUF846(Eukaryotic protein of unknown function (DUF846))
Supercontig_1.1_MVLG_00045_6sp	-867,47319	-867,47312	0,00014	0	NS	0	[]	[]	[]	hypothetical protein	PF01956.9	DUF106(Integral membrane protein DUF106)
Supercontig_1.5_MVLG_00881_8sp	-590,8822	-590,84852	0,06736	0,03312	NS	0	[]	[]	[]	hypothetical protein	PF06602.7	Myotub-related(Myotubularin-related)
Supercontig_1.9_MVLG_01536_10sp	-476,97292	-477,29562	0	0	NS	0	[]	[]	[]	hypothetical protein	PF12247.1	MKT1_N(Temperature dependent protein affecting M2 dsRNA replication)
Supercontig_1.19_MVLG_02471_9sp	-530,78476	-530,78471	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00328.15	Acid_phosphat_A(Histidine acid phosphatase)
Supercontig_1.69_MVLG_05300_8sp	-1356,8387	-1356,2262	1,22508	0,45803	NS	0	[]	[]	[]	hypothetical protein	PF08568.3	Kinetochor_Ybp2(Central kinetochore-associated)
Supercontig_1.180_MVLG_06995_8sp	-1031,4611	-1031,4233	0,07552	0,03706	NS	0	[]	[]	[]	hypothetical protein	PF01846.12	FF(FF domain)
Supercontig_1.3_MVLG_00511_11sp	-633,01518	-632,92831	0,17374	0,0832	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.69_MVLG_05282_10sp	-697,67529	-697,67529	0	0	NS	0	[]	[]	[]	hypothetical protein	PF06859.5	Bin3(Bicoid-interacting protein 3 (Bin3))
Supercontig_1.21_MVLG_02645_8sp	-1687,0545	-1687,0514	0,00622	0,00311	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.125_MVLG_06505_7sp	-415,35548	-415,35548	0	0	NS	0	[]	[]	[]	ATP synthase subunit alpha	PF00306.20	ATP-synt_ab_C(ATP synthase alpha/beta chain, C terminal domain)
Supercontig_1.200_MVLG_07082_7sp	-1506,1195	-1506,1195	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00400.25	WD40(WD domain, G-beta repeat)
Supercontig_1.1_MVLG_00216_7sp	-396,24869	-396,24866	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00664.16	ABC_membrane(ABC transporter transmembrane region)
Supercontig_1.1_MVLG_00128_10sp	-498,36596	-498,36588	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00415.11	RCC1(Regulator of chromosome condensation (RCC1) repeat)
Supercontig_1.16_MVLG_02202_8sp	-638,76981	-638,76981	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00010.19	HLH(Helix-loop-helix DNA-binding domain)

Supercontig_1.23_MVLG_02771_10sp	-531,43369	-531,43339	0,0006	0,0003	NS	0	[]	[]	[]	hypothetical protein	PF01490.11	Aa_trans(Transmembrane amino acid transporter protein)
Supercontig_1.28_MVLG_03147_9sp	-292,9554	-292,95524	0,00032	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF01246.13	Ribosomal_L24e(Ribosomal protein L24e)
Supercontig_1.3_MVLG_00494_7sp	-1243,2995	-1240,9664	4,66608	0,903	*	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.7_MVLG_01243_9sp	-1059,6676	-1059,4136	0,50782	0,22424	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.276_MVLG_07227_11sp	-402,33466	-402,33454	0,00024	0,00012	NS	0	[]	[]	[]	hypothetical protein	PF01926.16	MMR_HSR1(GTPase of unknown function)
Supercontig_1.99_MVLG_06126_12sp	-1717,9197	-1717,9197	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.1_MVLG_00066_7sp	-708,19755	-708,19755	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00638.11	Ran_BP1(RanBP1 domain)
Supercontig_1.13_MVLG_01963_8sp	-459,64183	-459,64165	0,00036	0,00018	NS	0	[]	[]	[]	hypothetical protein	PF10447.2	EXOSC1(Exosome component EXOSC1/CSL4)
Supercontig_1.30_MVLG_03299_9sp	-365,48162	-365,43071	0,10182	0,04964	NS	0	[]	[]	[]	CMGC/CDK/CDK8 protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.18_MVLG_02426_8sp	-401,48125	-401,48112	0,00026	0,00013	NS	0	[]	[]	[]	hypothetical protein	PF08530.3	PepX_C(X-Pro dipeptidyl-peptidase C-terminal non-catalytic domain)
Supercontig_1.10_MVLG_01655_7sp	-444,74365	-444,74361	0	0	NS	0	[]	[]	[]	hypothetical protein	PF07297.5	DPM2(Dolichol phosphate-mannose biosynthesis regulatory protein (DPM2))
Supercontig_1.21_MVLG_02642_10sp	-363,83713	-363,83713	0	0	NS	0	[]	[]	[]	hypothetical protein	PF05199.6	GMC_oxred_C(GMC oxidoreductase)
Supercontig_1.172_MVLG_06952_10sp	-400,49852	-400,49849	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00149.21	Metallophos(Calcineurin-like phosphoesterase)
Supercontig_1.10_MVLG_01619_10sp	-984,43309	-984,43309	0	0	NS	0	[]	[]	[]	hypothetical protein	PF06058.6	DCP1(Dcp1-like decapping family)
Supercontig_1.60_MVLG_04922_8sp	-2318,6028	-2318,6028	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04676.7	CwfJ_C_2(Protein similar to CwfJ C-terminus 2)
Supercontig_1.28_MVLG_03188_7sp	-1942,5572	-1942,5572	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.3_MVLG_00677_6sp	-446,8376	-446,79255	0,0901	0,04405	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.6_MVLG_01152_9sp	-577,63902	-577,63896	0,00012	0	NS	0	[]	[]	[]	hypothetical protein	PF01694.15	Rhomboid(Rhomboid family)
Supercontig_1.55_MVLG_04722_7sp	-785,52547	-785,52547	0	0	NS	0	[]	[]	[]	hypothetical protein	PF07690.9	MFS_1(Major Facilitator Superfamily)
Supercontig_1.21_MVLG_02662_10sp	-518,84819	-518,84819	0	0	NS	0	[]	[]	[]	hypothetical protein	PF05383.10	La(La domain)
Supercontig_1.150_MVLG_06773_8sp	-940,94673	-940,94673	0	0	NS	0	[]	[]	[]	ferrochelatase	PF00762.12	Ferrochelatase(Ferrochelatase)
Supercontig_1.1_MVLG_00189_10sp	-899,61794	-898,81168	1,61252	0,55348	NS	0	[]	[]	[]	hypothetical protein	PF05686.5	DUF821(Arabidopsis thaliana protein of unknown function (DUF821))
Supercontig_1.58_MVLG_04871_8sp	-1234,9049	-1234,9049	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00899.14	ThiF(ThiF family)
Supercontig_1.48_MVLG_04389_8sp	-503,61718	-503,61718	0	0	NS	0	[]	[]	[]	hypothetical protein	PF10294.2	Methyltransf_16(Putative methyltransferase)

Supercontig_1.32_MVLG_03406_10sp	-542,91387	-542,91387	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04488.8	Gly_transf_sug(Glycosyltransferase sugar-binding region containing DXD motif)
Supercontig_1.19_MVLG_02454_12sp	-513,9185	-513,9185	0	0	NS	0	[]	[]	[]	hypothetical protein	PF06094.5	AIG2(AIG2-like family)
Supercontig_1.20_MVLG_02534_7sp	-657,61849	-657,58061	0,07576	0,03717	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.45_MVLG_04205_10sp	-657,82636	-657,82636	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.50_MVLG_04484_8sp	-575,77598	-575,77598	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.15_MVLG_02086_10sp	-438,05135	-438,05132	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.17_MVLG_02265_7sp	-1218,6601	-1218,023	1,27424	0,47119	NS	0	[]	[]	[]	hypothetical protein	TIGR00879	TIGR00879(SP: MFS transporter, sugar porter (SP) family)
Supercontig_1.28_MVLG_03191_7sp	-382,53344	-382,53344	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.9_MVLG_01504_9sp	-531,98661	-531,98661	0	0	NS	0	[]	[]	[]	hypothetical protein	PF05875.5	aPHC(Alkaline phytoceramidase (aPHC))
Supercontig_1.123_MVLG_06478_9sp	-365,14741	-365,1474	0	0	NS	0	[]	[]	[]	CAMK/CAMKL protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.36_MVLG_03674_8sp	-336,55498	-336,55498	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.112_MVLG_06320_6sp	-729,61773	-729,61773	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00651.24	BTB(BTB/POZ domain)
Supercontig_1.8_MVLG_01411_10sp	-301,84182	-301,84176	0,00012	0	NS	0	[]	[]	[]	hypothetical protein	PF09365.3	DUF2461(Conserved hypothetical protein (DUF2461))
Supercontig_1.125_MVLG_06502_6sp	-1080,0403	-1080,0403	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01846.12	FF(FF domain)
Supercontig_1.6_MVLG_01186_10sp	-364,09657	-363,84345	0,50624	0,22363	NS	0	[]	[]	[]	hypothetical protein	PF00107.19	ADH_zinc_N(Zinc-binding dehydrogenase)
Supercontig_1.18_MVLG_02393_11sp	-362,71657	-362,26475	0,90364	0,36353	NS	0	[]	[]	[]	hypothetical protein	PF01764.18	Lipase_3(Lipase (class 3))
Supercontig_1.20_MVLG_02539_8sp	-613,36414	-613,36414	0	0	NS	0	[]	[]	[]	thymidylate synthase	TIGR03284	TIGR03284(thym_sym: thymidylate synthase)
Supercontig_1.61_MVLG_04994_8sp	-684,68802	-684,68802	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00226.24	DnaJ(DnaJ domain)
Supercontig_1.28_MVLG_03193_6sp	-537,44891	-537,4452	0,00742	0,0037	NS	0	[]	[]	[]	hypothetical protein	PF10302.2	DUF2407(Putative membrane protein (DUF2407))
Supercontig_1.92_MVLG_05951_10sp	-808,59553	-808,59553	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00150.11	Cellulase(Cellulase (glycosyl hydrolase family 5))
Supercontig_1.3_MVLG_00539_8sp	-997,74377	-996,94536	1,59682	0,54996	NS	0	[]	[]	[]	hypothetical protein	PF02181.16	FH2(Formin Homology 2 Domain)
Supercontig_1.36_MVLG_03698_6sp	-645,85991	-645,70478	0,31026	0,1437	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.49_MVLG_04435_12sp	-557,87107	-556,77649	2,18916	0,66532	NS	0	[]	[]	[]	hypothetical protein	PF00018.21	SH3_1(SH3 domain)
Supercontig_1.4_MVLG_00741_8sp	-997,88721	-997,49395	0,78652	0,32515	NS	0	[]	[]	[]	hypothetical protein	NA	NA

Supercontig_1.112_MVLG_06321_10sp	-312,58126	-312,58122	0	0	NS	0	[]	[]	[]	hypothetical protein	PF09796.2	QCR10(Ubiquinol-cytochrome-c reductase complex subunit (QCR10))
Supercontig_1.40_MVLG_03955_8sp	-551,69312	-551,69312	0	0	NS	0	[]	[]	[]	hypothetical protein	PF12464.1	Mac(Maltose acetyltransferase)
Supercontig_1.13_MVLG_01934_8sp	-436,76868	-436,76037	0,01662	0,00828	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.76_MVLG_05517_7sp	-704,0091	-702,27144	3,47532	0,82407	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.57_MVLG_04814_8sp	-688,65674	-688,65674	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01170.11	UPF0020(Putative RNA methylase family UPF0020)
Supercontig_1.12_MVLG_01840_11sp	-542,20407	-542,18395	0,04024	0,01992	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.49_MVLG_04403_9sp	-614,74182	-614,74159	0,00046	0,00023	NS	0	[]	[]	[]	hypothetical protein	PF02518.19	HATPase_c(Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase)
Supercontig_1.79_MVLG_05608_6sp	-779,87007	-779,58369	0,57276	0,24902	NS	0	[]	[]	[]	eukaryotic translation initiation factor 3 subunit I	PF00400.25	WD40(WD domain, G-beta repeat)
Supercontig_1.276_MVLG_07226_7sp	-796,31636	-795,64165	1,34942	0,4907	NS	0	[]	[]	[]	hypothetical protein	PF06246.5	Isy1(Isy1-like splicing family)
Supercontig_1.59_MVLG_04906_9sp	-294,50483	-294,50436	0,00094	0,00047	NS	0	[]	[]	[]	hypothetical protein	PF00327.13	Ribosomal_L30(Ribosomal protein L30p/L7e)
Supercontig_1.5_MVLG_00975_8sp	-411,69177	-411,52601	0,33152	0,15275	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.8_MVLG_01396_10sp	-411,70039	-411,69621	0,00836	0,00417	NS	0	[]	[]	[]	hypothetical protein	PF01105.17	EMP24_GP25L(emp24/gp25L/p24 family/GOLD)
Supercontig_1.47_MVLG_04338_8sp	-617,12226	-617,1196	0,00532	0,00266	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.21_MVLG_02634_10sp	-399,9596	-398,9721	1,975	0,62749	NS	0	[]	[]	[]	hypothetical protein	PF09446.3	VMA21(VMA21-like domain)
Supercontig_1.39_MVLG_03854_8sp	-310,21183	-310,21183	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.86_MVLG_05821_12sp	-641,75158	-641,75158	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00621.13	RhoGEF(RhoGEF domain)
Supercontig_1.21_MVLG_02641_7sp	-632,34978	-632,34008	0,0194	0,00965	NS	0	[]	[]	[]	hypothetical protein	PF00732.12	GMC_oxred_N(GMC oxidoreductase)
Supercontig_1.1_MVLG_00108_9sp	-505,56572	-505,56122	0,009	0,00449	NS	0	[]	[]	[]	hypothetical protein	PF01061.17	ABC2_membrane(ABC-2 type transporter)
Supercontig_1.68_MVLG_05265_11sp	-486,42286	-486,42271	0,0003	0,00015	NS	0	[]	[]	[]	hypothetical protein	PF00134.16	Cyclin_N(Cyclin, N-terminal domain)
Supercontig_1.93_MVLG_05978_6sp	-596,36949	-596,36949	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01423.15	LSM(LSM domain)
Supercontig_1.59_MVLG_04916_7sp	-824,66875	-823,37707	2,58336	0,72519	NS	0	[]	[]	[]	hypothetical protein	PF08588.3	DUF1769(Protein of unknown function (DUF1769))
Supercontig_1.62_MVLG_05010_7sp	-1049,5524	-1049,5524	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00106.18	adh_short(short chain dehydrogenase)
Supercontig_1.101_MVLG_06162_10sp	-688,66013	-688,60967	0,10092	0,04921	NS	0	[]	[]	[]	hypothetical protein	PF03152.7	UFD1(Ubiquitin fusion degradation protein UFD1)
Supercontig_1.30_MVLG_03280_8sp	-1172,1735	-1172,1656	0,01584	0,00789	NS	0	[]	[]	[]	hypothetical protein	PF00611.16	FCH(Fes/CIP4 homology domain)

Supercontig_1.86_MVLG_05832_10sp	-642,88757	-642,88757	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.26_MVLG_03047_11sp	-543,28269	-543,28268	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.116_MVLG_06373_9sp	-375,87835	-375,38752	0,98166	0,38788	NS	0	[]	[]	[]	chorismate mutase	PF01817.14	CM_2(Chorismate mutase type II)
Supercontig_1.1_MVLG_00067_8sp	-459,67217	-459,58663	0,17108	0,08198	NS	0	[]	[]	[]	urease accessory protein UreD	PF01774.10	UreD(UreD urease accessory protein)
Supercontig_1.5_MVLG_01004_8sp	-906,18682	-906,18682	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.25_MVLG_02928_9sp	-397,8391	-397,83891	0,00038	0,00019	NS	0	[]	[]	[]	2,4-dienoyl-CoA reductase (NADPH2)	PF00106.18	adh_short(short chain dehydrogenase)
Supercontig_1.2_MVLG_00458_8sp	-440,97404	-440,97404	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00070.20	Pyr_redox(Pyridine nucleotide-disulphide oxidoreductase)
Supercontig_1.18_MVLG_02349_8sp	-500,61084	-500,61084	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04096.7	Nucleoporin2(Nucleoporin autopeptidase)
Supercontig_1.32_MVLG_03395_8sp	-1607,1878	-1607,1878	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.39_MVLG_03877_10sp	-569,4343	-569,4343	0	0	NS	0	[]	[]	[]	hypothetical protein	PF10391.2	DNA_pol_lambd_f(Fingers domain of DNA polymerase lambda)
Supercontig_1.31_MVLG_03353_8sp	-643,93657	-643,93657	0	0	NS	0	[]	[]	[]	GTP-binding protein rho2	PF08477.6	Miro(Miro-like protein)
Supercontig_1.249_MVLG_07214_7sp	-567,19132	-567,1913	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03556.8	DUF298(Domain of unknown function (DUF298))
Supercontig_1.6_MVLG_01196_12sp	-499,43012	-499,43011	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01300.11	Sua5_yciO_yrdC(yrdC domain)
Supercontig_1.22_MVLG_02752_8sp	-1360,1455	-1360,1455	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00169.22	PH(PH domain)
Supercontig_1.109_MVLG_06277_7sp	-615,69933	-615,6984	0,00186	0,00093	NS	0	[]	[]	[]	hypothetical protein	PF00076.15	RRM_1(RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain))
Supercontig_1.32_MVLG_03397_10sp	-461,37968	-461,36155	0,03626	0,01797	NS	0	[]	[]	[]	hypothetical protein	TIGR00880	TIGR00880(2_A_01_02: Multidrug resistance protein)
Supercontig_1.4_MVLG_00846_8sp	-536,28222	-536,28221	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.53_MVLG_04648_10sp	-434,41659	-434,41655	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00348.10	polyprenyl_synt(Polyprenyl synthetase)
Supercontig_1.97_MVLG_06069_11sp	-788,21316	-787,97599	0,47434	0,21114	NS	0	[]	[]	[]	hypothetical protein	PF00149.21	Metallophos(Calcineurin-like phosphoesterase)
Supercontig_1.26_MVLG_02997_12sp	-459,034	-457,30291	3,46218	0,82291	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.70_MVLG_05338_12sp	-357,60588	-357,60575	0,00026	0,00013	NS	0	[]	[]	[]	hypothetical protein	PF12074.1	DUF3554(Domain of unknown function (DUF3554))
Supercontig_1.64_MVLG_05097_8sp	-874,81348	-874,81348	0	0	NS	0	[]	[]	[]	threonine dehydratase	PF00291.18	PALP(Pyridoxal-phosphate dependent enzyme)
Supercontig_1.1_MVLG_00006_10sp	-516,63964	-516,63964	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00850.12	Hist_deacetyl(Histone deacetylase domain)
Supercontig_1.10_MVLG_01601_10sp	-418,68565	-418,6855	0,0003	0,00015	NS	0	[]	[]	[]	hypothetical protein	PF03168.6	LEA_2(Late embryogenesis abundant protein)
Supercontig_1.66_MVLG_05198_9sp	-616,09952	-616,09952	0	0	NS	0	[]	[]	[]	acetoacetate-CoA ligase	TIGR01217	TIGR01217(ac_ac_CoA_syn: acetoacetate-CoA ligase)

Supercontig_1.56_MVLG_04769_9sp	-1073,4094	-1071,7606	3,29778	0,80774	NS	0	[]	[]	[]	hypothetical protein	PF02778.7	tRNA_int_endo_N(tRNA intron endonuclease, N-terminal domain)
Supercontig_1.94_MVLG_05996_11sp	-370,24363	-368,89123	2,7048	0,74138	NS	0	[]	[]	[]	hypothetical protein	TIGR00163	TIGR00163(PS_decarb: phosphatidylserine decarboxylase)
Supercontig_1.13_MVLG_01906_10sp	-790,71589	-790,71589	0	0	NS	0	[]	[]	[]	hypothetical protein	PF10360.2	DUF2433(Protein of unknown function (DUF2433))
Supercontig_1.94_MVLG_05997_8sp	-949,33698	-949,33679	0,00038	0,00019	NS	0	[]	[]	[]	branched-chain amino acid aminotransferase	PF01063.12	Aminotran_4(Aminotransferase class IV)
Supercontig_1.27_MVLG_03081_7sp	-708,82478	-708,40306	0,84344	0,34408	NS	0	[]	[]	[]	hypothetical protein	PF04117.5	Mpv17_PMP22(Mpv17 / PMP22 family)
Supercontig_1.48_MVLG_04385_8sp	-1198,3014	-1198,3014	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00155.14	Aminotran_1_2(Aminotransferase class I and II)
Supercontig_1.87_MVLG_05870_7sp	-446,59953	-446,36871	0,46164	0,20612	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.117_MVLG_06394_7sp	-313,92032	-313,92022	0,0002	0	NS	0	[]	[]	[]	3-hydroxyanthranilate 3,4-dioxygenase 2	TIGR03037	TIGR03037(anthran_nbaC: 3-hydroxyanthranilate 3,4-dioxygenase)
Supercontig_1.57_MVLG_04839_7sp	-578,03764	-578,03764	0	0	NS	0	[]	[]	[]	4-aminobutyrate aminotransferase	PF00202.14	Aminotran_3(Aminotransferase class-III)
Supercontig_1.52_MVLG_04583_10sp	-773,21736	-773,21619	0,00234	0,00117	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.5_MVLG_00985_7sp	-390,81265	-390,81265	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.55_MVLG_04716_9sp	-433,73949	-433,73928	0,00042	0,00021	NS	0	[]	[]	[]	hypothetical protein	PF00808.16	CBFD_NFYB_HMF(Histone-like transcription factor (CBF/NF-Y) and archaeal histone)
Supercontig_1.105_MVLG_06216_8sp	-1486,7469	-1486,7469	0	0	NS	0	[]	[]	[]	hypothetical protein	PF09763.2	Sec3(Exocyst complex component Sec3)
Supercontig_1.1_MVLG_00163_10sp	-776,57551	-776,57532	0,00038	0,00019	NS	0	[]	[]	[]	hypothetical protein	PF07724.7	AAA_2(AAA domain (Cdc48 subfamily))
Supercontig_1.91_MVLG_05931_7sp	-1368,6944	-1368,6826	0,02378	0,01182	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.1_MVLG_00026_10sp	-657,77926	-657,44747	0,66358	0,28236	NS	0	[]	[]	[]	hypothetical protein	PF01565.16	FAD_binding_4(FAD binding domain)
Supercontig_1.88_MVLG_05883_11sp	-450,6027	-450,6027	0	0	NS	0	[]	[]	[]	18S rRNA biogenesis protein RCL1	PF05189.6	RTC_insert(RNA 3'-terminal phosphate cyclase (RTC), insert domain)
Supercontig_1.12_MVLG_01797_8sp	-1644,5159	-1644,5159	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00575.16	S1(S1 RNA binding domain)
Supercontig_1.8_MVLG_01464_8sp	-472,09169	-472,09169	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.5_MVLG_00911_7sp	-370,03775	-368,40202	3,27146	0,80519	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.34_MVLG_03526_6sp	-649,57527	-649,57527	0	0	NS	0	[]	[]	[]	hypothetical protein	PF05856.5	ARPC4(ARP2/3 complex 20 kDa subunit (ARPC4))
Supercontig_1.24_MVLG_02904_6sp	-653,65589	-653,65581	0,00016	0	NS	0	[]	[]	[]	hypothetical protein	PF00326.14	Peptidase_S9(Prolyl oligopeptidase family)

Supercontig_1.11_MVLG_01770_7sp	-564,1819	-564,18069	0,00242	0,00121	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.2_MVLG_00375_12sp	-468,41375	-468,39936	0,02878	0,01429	NS	0	[]	[]	[]	hypothetical protein	PF00022.12	Actin(Actin)
Supercontig_1.5_MVLG_00910_10sp	-677,11229	-676,56249	1,0996	0,42293	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.66_MVLG_05191_8sp	-685,1982	-684,69854	0,99932	0,39326	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.11_MVLG_01689_8sp	-416,58408	-416,58408	0	0	NS	0	[]	[]	[]	hypothetical protein	PF07985.5	SRR1(SRR1)
Supercontig_1.31_MVLG_03383_6sp	-543,8599	-543,8599	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00875.11	DNA_photolyase(DNA photolyase)
Supercontig_1.52_MVLG_04576_7sp	-951,13446	-951,13427	0,00038	0,00019	NS	0	[]	[]	[]	hypothetical protein	PF11051.1	Mannosyl_trans3(Mannosyltransferase putative)
Supercontig_1.109_MVLG_06286_7sp	-476,92185	-476,92185	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00348.10	polyprenyl_synt(Polyprenyl synthetase)
Supercontig_1.6_MVLG_01181_7sp	-359,363	-359,28248	0,16104	0,07736	NS	0	[]	[]	[]	hypothetical protein	TIGR01068	TIGR01068(thioredoxin: thioredoxin)
Supercontig_1.94_MVLG_06000_7sp	-453,37778	-453,37778	0	0	NS	0	[]	[]	[]	hypothetical protein	PF06080.5	DUF938(Protein of unknown function (DUF938))
Supercontig_1.33_MVLG_03490_7sp	-357,52588	-354,84159	5,36858	0,93173	*	0	[]	[]	[]	hypothetical protein	PF07993.5	NAD_binding_4(Male sterility protein)
Supercontig_1.33_MVLG_03450_7sp	-1376,8153	-1376,7568	0,11708	0,05686	NS	0	[]	[]	[]	hypothetical protein	PF11735.1	CAP59_mtransfer(Cryptococcal mannosyltransferase 1)
Supercontig_1.1_MVLG_00137_11sp	-521,12621	-521,12497	0,00248	0,00124	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.5_MVLG_00944_7sp	-733,60389	-732,6826	1,84258	0,60199	NS	0	[]	[]	[]	AGC/NDR protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.18_MVLG_02424_11sp	-326,53107	-326,53106	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04082.11	Fungal_trans(Fungal specific transcription factor domain)
Supercontig_1.123_MVLG_06474_9sp	-917,09436	-917,09436	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00135.21	COesterase(Carboxylesterase)
Supercontig_1.28_MVLG_03172_6sp	-675,03521	-675,0352	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02845.9	CUE(CUE domain)
Supercontig_1.39_MVLG_03857_9sp	-429,81063	-429,81045	0,00036	0,00018	NS	0	[]	[]	[]	hypothetical protein	PF00583.17	Acetyltransf_1(Acetyltransferase (GNAT) family)
Supercontig_1.87_MVLG_05869_7sp	-648,67989	-648,67988	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01758.9	SBF(Sodium Bile acid symporter family)
Supercontig_1.87_MVLG_05849_12sp	-441,01181	-441,01181	0	0	NS	0	[]	[]	[]	acetate kinase	TIGR00016	TIGR00016(ackA: acetate kinase)
Supercontig_1.4_MVLG_00808_10sp	-768,49266	-767,35094	2,28344	0,68073	NS	0	[]	[]	[]	hypothetical protein	PF00884.16	Sulfatase(Sulfatase)
Supercontig_1.11_MVLG_01790_10sp	-653,94579	-651,841	4,20958	0,87813	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.11_MVLG_01712_11sp	-375,14735	-375,14735	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03765.8	CRAL_TRIO_N(CRAL/TRIO, N-terminus)
Supercontig_1.17_MVLG_02287_9sp	-677,67186	-677,64328	0,05716	0,02818	NS	0	[]	[]	[]	hypothetical protein	PF09335.4	SNARE_assoc(SNARE associated Golgi protein)
Supercontig_1.25_MVLG_02915_10sp	-535,95016	-535,95016	0	0	NS	0	[]	[]	[]	hypothetical protein	PF05557.6	MAD(Mitotic checkpoint protein)

Supercontig_1.75_MVLG_05481_7sp	-894,94186	-894,94136	0,001	0,0005	NS	0	[]	[]	[]	developmentally-regulated GTP-binding protein 2	PF02421.11	FeoB_N(Ferrous iron transport protein B)
Supercontig_1.5_MVLG_01024_11sp	-392,71714	-392,71714	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00172.11	Zn_clus(Fungal Zn(2)-Cys(6) binuclear cluster domain)
Supercontig_1.35_MVLG_03577_9sp	-897,77159	-897,24248	1,05822	0,41087	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.5_MVLG_00901_8sp	-671,04026	-670,62026	0,84	0,34295	NS	0	[]	[]	[]	hypothetical protein	PF08477.6	Miro(Miro-like protein)
Supercontig_1.6_MVLG_01178_7sp	-289,12472	-289,12455	0,00034	0,00017	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.66_MVLG_05187_7sp	-797,45636	-797,45623	0,00026	0,00013	NS	0	[]	[]	[]	CAMK/CAMKL/CHK1 protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.63_MVLG_05057_6sp	-730,2798	-730,2798	0	0	NS	0	[]	[]	[]	serine/threonine-protein phosphatase PP2A catalytic subunit	PF00149.21	Metallophos(Calcineurin-like phosphoesterase)
Supercontig_1.19_MVLG_02509_9sp	-660,68339	-660,68318	0,00042	0,00021	NS	0	[]	[]	[]	hypothetical protein	PF01556.11	DnaJ_C(DnaJ C terminal region)
Supercontig_1.3_MVLG_00542_10sp	-826,90481	-826,77224	0,26514	0,12416	NS	0	[]	[]	[]	hypothetical protein	TIGR01494	TIGR01494(ATPase_P-type: HAD ATPase, P-type, family IC)
Supercontig_1.2_MVLG_00336_9sp	-401,71744	-401,71744	0	0	NS	0	[]	[]	[]	hypothetical protein	PF06687.5	SUR7(SUR7/PalI family)
Supercontig_1.121_MVLG_06437_10sp	-486,6109	-486,36324	0,49532	0,21937	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.4_MVLG_00785_11sp	-603,56778	-600,70608	5,7234	0,94283	*	0	[]	[]	[]	hypothetical protein	PF11861.1	DUF3381(Domain of unknown function (DUF3381))
Supercontig_1.5_MVLG_00954_6sp	-805,01183	-805,01165	0,00036	0,00018	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.52_MVLG_04568_11sp	-889,86782	-888,73403	2,26758	0,67819	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.62_MVLG_05002_11sp	-2182,8572	-2179,8899	5,93454	0,94856	*	0	[]	[]	[]	hypothetical protein	PF11001.1	DUF2841(Protein of unknown function (DUF2841))
Supercontig_1.84_MVLG_05753_12sp	-450,42668	-450,42668	0	0	NS	0	[]	[]	[]	hypothetical protein	PF09830.2	ATP_transf(ATP adenylyltransferase)
Supercontig_1.141_MVLG_06700_8sp	-929,09108	-927,49701	3,18814	0,7969	NS	0	[]	[]	[]	hypothetical protein	PF10231.2	DUF2315(Uncharacterised conserved protein (DUF2315))
Supercontig_1.40_MVLG_03917_11sp	-375,21919	-375,21919	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00160.14	Pro_isomerase(Cyclophilin type peptidyl-prolyl cis-trans isomerase/CLD)
Supercontig_1.2_MVLG_00371_9sp	-797,73166	-797,73157	0,00018	0	NS	0	[]	[]	[]	hypothetical protein	PF00004.22	AAA(ATPase family associated with various cellular activities (AAA))
Supercontig_1.3_MVLG_00512_6sp	-484,11997	-483,51603	1,20788	0,45335	NS	0	[]	[]	[]	60S ribosomal protein L19	PF00298.12	Ribosomal_L11(Ribosomal protein L11, RNA binding domain)
Supercontig_1.22_MVLG_02696_9sp	-938,45765	-938,4304	0,0545	0,02688	NS	0	[]	[]	[]	hypothetical protein	PF06881.4	Elongin_A(RNA polymerase II transcription factor SIII (Elongin) subunit A)

Supercontig_1.22_MVLG_02738_9sp	-494,22832	-494,22831	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02417.8	Chromate_transp(Chromate transporter)
Supercontig_1.23_MVLG_02825_10sp	-799,74427	-799,74427	0	0	NS	0	[]	[]	[]	hypothetical protein	PF06422.5	PDR_CDR(CDR ABC transporter)
Supercontig_1.2_MVLG_00285_9sp	-479,47057	-479,47057	0	0	NS	0	[]	[]	[]	6-phosphogluconolactonase	PF01182.13	Glucosamine_iso(Glucosamine-6-phosphate isomerases/6-phosphogluconolactonase)
Supercontig_1.94_MVLG_06003_8sp	-893,71957	-892,66857	2,102	0,65041	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.22_MVLG_02702_8sp	-882,79074	-881,21571	3,15006	0,793	NS	0	[]	[]	[]	hypothetical protein	PF00400.25	WD40(WD domain, G-beta repeat)
Supercontig_1.93_MVLG_05980_9sp	-413,17849	-413,17847	0	0	NS	0	[]	[]	[]	medium-chain specific acyl-CoA dehydrogenase	PF02770.12	Acyl-CoA_dh_M(Acyl-CoA dehydrogenase, middle domain)
Supercontig_1.120_MVLG_06424_10sp	-1018,4281	-1018,4281	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00722.14	Glyco_hydro_16(Glycosyl hydrolases family 16)
Supercontig_1.6_MVLG_01136_6sp	-1649,557	-1649,557	0	0	NS	0	[]	[]	[]	hypothetical protein	PF05843.7	Suf(Suppressor of forked protein (Suf))
Supercontig_1.6_MVLG_01162_10sp	-340,19136	-340,19126	0	0	NS	0	[]	[]	[]	hypothetical protein	PF05793.5	TFIIF_alpha(Transcription initiation factor IIF, alpha subunit (TFIIF-alpha))
Supercontig_1.19_MVLG_02515_8sp	-479,18531	-479,18531	0	0	NS	0	[]	[]	[]	hypothetical protein	PF09139.4	Mmp37(Mitochondrial matrix Mmp37)
Supercontig_1.8_MVLG_01376_6sp	-468,50691	-468,50683	0	0	NS	0	[]	[]	[]	CMGC/CDK protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.5_MVLG_00895_10sp	-700,22791	-698,87138	2,71306	0,74245	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.50_MVLG_04469_9sp	-1015,7298	-1015,4274	0,60478	0,26095	NS	0	[]	[]	[]	hypothetical protein	PF11882.1	DUF3402(Domain of unknown function (DUF3402))
Supercontig_1.4_MVLG_00792_9sp	-1115,0356	-1115,0356	0	0	NS	0	[]	[]	[]	hypothetical protein	PF07522.7	DRMBL(DNA repair metallo-beta-lactamase)
Supercontig_1.79_MVLG_05617_8sp	-475,7212	-475,7208	0,0008	0,0004	NS	0	[]	[]	[]	vacuolar protein sorting-associated protein 1	PF00350.16	Dynamin_N(Dynamin family)
Supercontig_1.18_MVLG_02379_10sp	-642,5675	-642,5675	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.7_MVLG_01307_12sp	-606,39984	-606,39591	0,00786	0,00392	NS	0	[]	[]	[]	hypothetical protein	PF08613.4	Cyclin(Cyclin)
Supercontig_1.54_MVLG_04698_10sp	-427,85709	-427,65146	0,41126	0,18587	NS	0	[]	[]	[]	hypothetical protein	PF08628.5	Nexin_C(Sorting nexin C terminal)
Supercontig_1.88_MVLG_05895_7sp	-788,01689	-788,01689	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.1_MVLG_00169_9sp	-486,17858	-486,17858	0	0	NS	0	[]	[]	[]	initiator tRNA phosphoribosyl transferase	PF04179.5	Init_tRNA_PT(Initiator tRNA phosphoribosyl transferase)
Supercontig_1.12_MVLG_01881_10sp	-497,89676	-496,15166	3,4902	0,82537	NS	0	[]	[]	[]	hypothetical protein	PF09748.2	Med10(Transcription factor subunit Med10 of Mediator complex)
Supercontig_1.104_MVLG_06197_10sp	-802,87206	-802,2386	1,26692	0,46925	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.3_MVLG_00558_10sp	-386,40859	-386,36769	0,0818	0,04007	NS	0	[]	[]	[]	hypothetical protein	PF03151.9	TPT(Triose-phosphate Transporter family)

Supercontig_1.10_MVLG_01633_10sp	-350,39544	-350,39536	0,00016	0	NS	0	[]	[]	[]	gluconate 5-dehydrogenase	PF00106.18	adh_short(short chain dehydrogenase)
Supercontig_1.73_MVLG_05419_8sp	-759,66339	-759,66304	0,0007	0,00035	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.63_MVLG_05082_7sp	-1099,814	-1099,814	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00150.11	Cellulase(Cellulase (glycosyl hydrolase family 5))
Supercontig_1.58_MVLG_04857_10sp	-415,95671	-415,31275	1,28792	0,47479	NS	0	[]	[]	[]	hypothetical protein	PF04892.5	VanZ(VanZ like family)
Supercontig_1.142_MVLG_06709_10sp	-391,6603	-391,65989	0,00082	0,00041	NS	0	[]	[]	[]	CAMK protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.41_MVLG_04016_7sp	-327,65652	-327,65605	0,00094	0,00047	NS	0	[]	[]	[]	large subunit ribosomal protein L31e	PF01198.12	Ribosomal_L31e(Ribosomal protein L31e)
Supercontig_1.7_MVLG_01306_7sp	-784,09145	-784,09118	0,00054	0,00027	NS	0	[]	[]	[]	hypothetical protein	PF07690.9	MFS_1(Major Facilitator Superfamily)
Supercontig_1.14_MVLG_02021_8sp	-949,562	-949,48101	0,16198	0,0778	NS	0	[]	[]	[]	hypothetical protein	PF00172.11	Zn_clus(Fungal Zn(2)-Cys(6) binuclear cluster domain)
Supercontig_1.49_MVLG_04426_8sp	-418,34621	-418,34621	0	0	NS	0	[]	[]	[]	hypothetical protein	PF05328.5	CybS(CybS)
Supercontig_1.33_MVLG_03447_7sp	-741,29449	-741,29449	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.50_MVLG_04480_8sp	-688,40932	-686,27975	4,25914	0,88111	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.94_MVLG_05991_11sp	-285,83638	-285,83626	0,00024	0,00012	NS	0	[]	[]	[]	hypothetical protein	PF00076.15	RRM_1(RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain))
Supercontig_1.14_MVLG_02045_8sp	-384,25639	-384,25639	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.63_MVLG_05076_7sp	-595,78929	-595,61522	0,34814	0,15976	NS	0	[]	[]	[]	hypothetical protein	PF04193.7	PQ-loop(PQ loop repeat)
Supercontig_1.203_MVLG_07097_6sp	-476,79096	-476,79096	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01557.11	FAA_hydrolase(Fumarylacetoacetate (FAA) hydrolase family)
Supercontig_1.6_MVLG_01209_10sp	-582,93888	-582,5039	0,86996	0,35272	NS	0	[]	[]	[]	hypothetical protein	PF04828.7	GFA(Glutathione-dependent formaldehyde-activating enzyme)
Supercontig_1.14_MVLG_02009_8sp	-1050,9468	-1049,7001	2,49338	0,71255	NS	0	[]	[]	[]	hypothetical protein	PF00320.20	GATA(GATA zinc finger)
Supercontig_1.83_MVLG_05737_10sp	-506,73873	-505,242	2,99346	0,77614	NS	0	[]	[]	[]	hypothetical protein	PF00704.21	Glyco_hydro_18(Glycosyl hydrolases family 18)
Supercontig_1.18_MVLG_02376_10sp	-608,13279	-608,13279	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00755.13	Carn_acyltransf(Choline/Carnitine o-acyltransferase)
Supercontig_1.56_MVLG_04758_7sp	-580,25388	-580,25388	0	0	NS	0	[]	[]	[]	hypothetical protein	PF09783.2	Vac_ImportDeg(Vacuolar import and degradation protein)
Supercontig_1.121_MVLG_06432_9sp	-786,52203	-786,50887	0,02632	0,01307	NS	0	[]	[]	[]	hypothetical protein	PF07690.9	MFS_1(Major Facilitator Superfamily)
Supercontig_1.3_MVLG_00650_11sp	-910,96049	-910,96044	0,0001	0	NS	0	[]	[]	[]	hypothetical protein	TIGR00800	TIGR00800(ncs1: NCS1 nucleoside transporter family)
Supercontig_1.42_MVLG_04081_10sp	-354,17278	-354,17278	0	0	NS	0	[]	[]	[]	hypothetical protein	TIGR03188	TIGR03188(histidine_hisI: phosphoribosyl-ATP diphosphatase)

Supercontig_1.22_MVLG_02711_9sp	-797,65428	-797,65428	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00400.25	WD40(WD domain, G-beta repeat)
Supercontig_1.29_MVLG_03214_8sp	-1109,2488	-1108,3215	1,8547	0,6044	NS	0	[]	[]	[]	hypothetical protein	PF09431.3	DUF2013(Protein of unknown function (DUF2013))
Supercontig_1.73_MVLG_05429_12sp	-549,12479	-548,90106	0,44746	0,20047	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.22_MVLG_02740_11sp	-508,28667	-508,28667	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00797.10	Acetyltransf_2(N-acetyltransferase)
Supercontig_1.10_MVLG_01680_11sp	-794,64771	-794,46766	0,3601	0,16477	NS	0	[]	[]	[]	hypothetical protein	PF04153.11	NOT2_3_5(NOT2 / NOT3 / NOT5 family)
Supercontig_1.261_MVLG_07219_7sp	-386,36857	-385,23541	2,26632	0,67799	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.56_MVLG_04789_7sp	-677,99041	-677,98999	0,00084	0,00042	NS	0	[]	[]	[]	hypothetical protein	PF00657.15	Lipase_GDSL(GDSL-like Lipase/Acylhydrolase)
Supercontig_1.6_MVLG_01195_7sp	-841,22053	-839,6202	3,20066	0,79817	NS	0	[]	[]	[]	hypothetical protein	PF07986.5	TBCC(Tubulin binding cofactor C)
Supercontig_1.32_MVLG_03422_9sp	-1096,817	-1096,817	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00566.11	TBC(TBC domain)
Supercontig_1.69_MVLG_05299_8sp	-348,91197	-348,91188	0,00018	0	NS	0	[]	[]	[]	vesicle-associated membrane protein 7	PF00957.14	Synaptobrevin(Synaptobrevin)
Supercontig_1.56_MVLG_04783_7sp	-513,38923	-513,38923	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.4_MVLG_00797_6sp	-349,7907	-349,79035	0,0007	0,00035	NS	0	[]	[]	[]	proteasome subunit alpha type-6	PF00227.19	Proteasome(Proteasome subunit)
Supercontig_1.30_MVLG_03261_7sp	-944,59007	-944,59007	0	0	NS	0	[]	[]	[]	hypothetical protein	PF07575.6	Nucleopor_Nup85(Nup85 Nucleoporin)
Supercontig_1.6_MVLG_01062_7sp	-903,84243	-903,84243	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03062.12	MBOAT(MBOAT family)
Supercontig_1.154_MVLG_06804_11sp	-545,84598	-545,84598	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02225.15	PA(PA domain)
Supercontig_1.58_MVLG_04844_8sp	-581,27344	-581,08648	0,37392	0,17052	NS	0	[]	[]	[]	hypothetical protein	PF06179.5	Med22(Surfeit locus protein 5 subunit 22 of Mediator complex)
Supercontig_1.16_MVLG_02251_10sp	-351,14486	-351,1445	0,00072	0,00036	NS	0	[]	[]	[]	protein transporter SEC23	PF08033.5	Sec23_BS(Sec23/Sec24 beta-sandwich domain)
Supercontig_1.211_MVLG_07125_8sp	-765,16052	-764,4923	1,33644	0,48738	NS	0	[]	[]	[]	hypothetical protein	PF03798.9	TRAM_LAG1_CLN8(TLC domain)
Supercontig_1.8_MVLG_01423_8sp	-918,88514	-918,88514	0	0	NS	0	[]	[]	[]	leucyl-tRNA synthetase, cytoplasmic	PF01406.12	tRNA-synt_1e(tRNA synthetases class I (C) catalytic domain)
Supercontig_1.47_MVLG_04319_9sp	-1276,2478	-1276,1298	0,23604	0,11132	NS	0	[]	[]	[]	hypothetical protein	PF00400.25	WD40(WD domain, G-beta repeat)
Supercontig_1.9_MVLG_01515_10sp	-387,58677	-387,58677	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01399.20	PCI(PCI domain)
Supercontig_1.52_MVLG_04580_8sp	-498,82903	-498,82903	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00293.21	NUDIX(NUDIX domain)
Supercontig_1.4_MVLG_00872_6sp	-572,5108	-572,13181	0,75798	0,31545	NS	0	[]	[]	[]	pyruvate dehydrogenase E2 component (dihydrolipoamide acetyltransferase)	PF00364.15	Biotin_lipoyl(Biotin-requiring enzyme)

Supercontig_1.77_MVLG_05568_12sp	-335,88267	-335,52892	0,7075	0,29795	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.53_MVLG_04618_7sp	-1440,1036	-1439,5207	1,1658	0,44172	NS	0	[]	[]	[]	hypothetical protein	PF01746.14	tRNA_m1G_MT(tRNA (Guanine-1)-methyltransferase)
Supercontig_1.8_MVLG_01442_6sp	-387,09066	-387,09066	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.63_MVLG_05072_11sp	-523,5545	-523,5545	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00498.19	FHA(FHA domain)
Supercontig_1.25_MVLG_02980_9sp	-688,3133	-688,31307	0,00046	0,00023	NS	0	[]	[]	[]	hypothetical protein	TIGR00800	TIGR00800(ncs1: NCS1 nucleoside transporter family)
Supercontig_1.15_MVLG_02084_9sp	-333,3519	-333,35181	0,00018	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.74_MVLG_05469_10sp	-1198,5224	-1198,1494	0,74614	0,31138	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.1_MVLG_00233_9sp	-631,28873	-631,28873	0	0	NS	0	[]	[]	[]	hypothetical protein	PF05653.7	DUF803(Protein of unknown function (DUF803))
Supercontig_1.11_MVLG_01753_11sp	-490,88316	-490,8831	0,00012	0	NS	0	[]	[]	[]	hypothetical protein	PF08231.5	SYF2(SYF2 splicing factor)
Supercontig_1.102_MVLG_06178_10sp	-521,40747	-520,42591	1,96312	0,62527	NS	0	[]	[]	[]	hypothetical protein	PF00790.12	VHS(VHS domain)
Supercontig_1.30_MVLG_03286_9sp	-594,00004	-594,00004	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00128.17	Alpha-amylase(Alpha amylase, catalytic domain)
Supercontig_1.5_MVLG_00992_8sp	-1030,9669	-1030,9645	0,0049	0,00245	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.17_MVLG_02279_8sp	-444,19818	-443,8927	0,61096	0,26323	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.68_MVLG_05269_7sp	-503,60496	-503,60483	0,00026	0,00013	NS	0	[]	[]	[]	peptidyl-prolyl cis-trans isomerase-like 1	PF00160.14	Pro_isomerase(Cyclophilin type peptidyl-prolyl cis-trans isomerase/CLD)
Supercontig_1.5_MVLG_00907_10sp	-790,84605	-790,8459	0,0003	0,00015	NS	0	[]	[]	[]	hypothetical protein	PF08145.5	BOP1NT(BOP1NT (NUC169) domain)
Supercontig_1.27_MVLG_03096_10sp	-638,20704	-638,20704	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.101_MVLG_06156_10sp	-475,38006	-475,38004	0	0	NS	0	[]	[]	[]	hypothetical protein	PF10277.2	Frag1(Frag1/DRAM/Sfk1 family)
Supercontig_1.62_MVLG_05017_6sp	-1457,5575	-1457,5575	0	0	NS	0	[]	[]	[]	hypothetical protein	PF08760.4	DUF1793(Domain of unknown function (DUF1793))
Supercontig_1.10_MVLG_01627_7sp	-314,40284	-314,40281	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03911.9	Sec61_beta(Sec61beta family)
Supercontig_1.4_MVLG_00731_9sp	-432,94288	-431,22397	3,43782	0,82074	NS	0	[]	[]	[]	hypothetical protein	PF00581.13	Rhodanese(Rhodanese-like domain)
Supercontig_1.4_MVLG_00840_9sp	-896,49243	-896,49194	0,00098	0,00049	NS	0	[]	[]	[]	hypothetical protein	PF03171.13	2OG-FeII_Oxy(2OG-Fe(II) oxygenase superfamily)
Supercontig_1.26_MVLG_03005_8sp	-835,54958	-835,53814	0,02288	0,01137	NS	0	[]	[]	[]	hypothetical protein	PF08700.4	Vps51(Vps51/Vps67)
Supercontig_1.27_MVLG_03119_12sp	-424,81739	-424,81739	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.20_MVLG_02522_7sp	-751,30792	-750,84468	0,92648	0,37076	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.51_MVLG_04534_8sp	-1288,8379	-1287,4043	2,8672	0,76155	NS	0	[]	[]	[]	hypothetical protein	PF10513.2	EPL1(Enhancer of polycomb-like)

Supercontig_1.61_MVLG_04966_10sp	-774,37564	-774,37564	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04116.6	FA_hydroxylase(Fatty acid hydroxylase superfamily)
Supercontig_1.41_MVLG_04020_6sp	-1176,385	-1176,385	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00581.13	Rhodanese(Rhodanese-like domain)
Supercontig_1.3_MVLG_00608_6sp	-296,71375	-296,71369	0,00012	0	NS	0	[]	[]	[]	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 9	PF05347.8	Complex1_LYR(Complex 1 protein (LYR family))
Supercontig_1.11_MVLG_01751_8sp	-462,23673	-462,23666	0,00014	0,00316	NS	0	[]	[]	[]	hypothetical protein	PF00153.20	Mito_carr(Mitochondrial carrier protein)
Supercontig_1.20_MVLG_02556_10sp	-622,8224	-622,78661	0,07158	0,03516	NS	0	[]	[]	[]	hypothetical protein	PF01593.17	Amino_oxidase(Flavin containing amine oxidoreductase)
Supercontig_1.3_MVLG_00526_12sp	-793,4603	-793,4603	0	0	NS	0	[]	[]	[]	nucleolar protein 56	PF08156.6	NOP5NT(NOP5NT (NUC127) domain)
Supercontig_1.12_MVLG_01810_7sp	-1480,283	-1480,2069	0,15214	0,07325	NS	0	[]	[]	[]	hypothetical protein	PF00176.16	SNF2_N(SNF2 family N-terminal domain)
Supercontig_1.1_MVLG_00148_8sp	-464,24593	-464,24593	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.10_MVLG_01645_7sp	-425,44235	-425,30416	0,27638	0,12907	NS	0	[]	[]	[]	hypothetical protein	PF05383.10	La(La domain)
Supercontig_1.6_MVLG_01088_7sp	-469,55646	-469,31737	0,47818	0,21266	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.44_MVLG_04148_8sp	-486,52324	-486,52313	0,00022	0,00011	NS	0	[]	[]	[]	mps one binder kinase activator-like 1B	PF03637.10	Mob1_phocein(Mob1/phocein family)
Supercontig_1.5_MVLG_00957_10sp	-562,66334	-562,66334	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00096.19	zf-C2H2(Zinc finger, C2H2 type)
Supercontig_1.51_MVLG_04509_11sp	-304,50468	-304,50466	0,00316	0,00316	NS	0	[]	[]	[]	hypothetical protein	PF02936.7	COX4(Cytochrome c oxidase subunit IV)
Supercontig_1.12_MVLG_01874_9sp	-716,71184	-716,71184	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.6_MVLG_01155_11sp	-1868,2224	-1867,3729	1,69912	0,5724	NS	0	[]	[]	[]	hypothetical protein	PF00501.21	AMP-binding(AMP-binding enzyme)
Supercontig_1.53_MVLG_04609_12sp	-540,47592	-540,15899	0,63386	0,27162	NS	0	[]	[]	[]	hypothetical protein	PF03914.10	CBF(CBF/Mak21 family)
Supercontig_1.52_MVLG_04593_6sp	-378,59355	-378,59354	0,00316	0,00316	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.21_MVLG_02677_11sp	-534,46234	-534,4623	0,00316	0,00316	NS	0	[]	[]	[]	haloacid dehalogenase, type II	TIGR01428	TIGR01428(HAD_type_II: haloacid dehalogenase, type II)
Supercontig_1.27_MVLG_03063_10sp	-955,68064	-955,64825	0,06478	0,03187	NS	0	[]	[]	[]	hypothetical protein	PF00270.22	DEAD(DEAD/DEAH box helicase)
Supercontig_1.10_MVLG_01588_6sp	-703,93096	-703,93096	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.7_MVLG_01259_9sp	-490,35552	-490,35552	0	0	NS	0	[]	[]	[]	hypothetical protein	TIGR00101	TIGR00101(ureG: urease accessory protein UreG)
Supercontig_1.4_MVLG_00825_9sp	-905,52091	-905,52091	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00134.16	Cyclin_N(Cyclin, N-terminal domain)
Supercontig_1.13_MVLG_01940_6sp	-968,71392	-968,43426	0,55932	0,24396	NS	0	[]	[]	[]	hypothetical protein	NA	NA

Supercontig_1.39_MVLG_03876_7sp	-735,34632	-735,34632	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03144.18	GTP_EFTU_D2(Elongation factor Tu domain 2)
Supercontig_1.139_MVLG_06668_7sp	-1009,6956	-1009,6956	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03399.9	SAC3_GANP(SAC3/GANP/Nin1/mts3/eIF-3 p25 family)
Supercontig_1.32_MVLG_03423_9sp	-746,42587	-746,42579	0,00316	0,00316	NS	0	[]	[]	[]	hypothetical protein	PF00501.21	AMP-binding(AMP-binding enzyme)
Supercontig_1.25_MVLG_02924_10sp	-388,12057	-388,12052	0,00316	0,00316	NS	0	[]	[]	[]	hypothetical protein	PF00246.17	Peptidase_M14(Zinc carboxypeptidase)
Supercontig_1.7_MVLG_01287_10sp	-503,99443	-503,99443	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03254.6	XG_FTase(Xyloglucan fucosyltransferase)
Supercontig_1.39_MVLG_03893_9sp	-265,5329	-264,97927	1,10726	0,42514	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.17_MVLG_02342_9sp	-779,00456	-779,00456	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00098.16	zf-CCHC(Zinc knuckle)
Supercontig_1.20_MVLG_02559_10sp	-401,78422	-401,77512	0,0182	0,00906	NS	0	[]	[]	[]	hypothetical protein	PF00076.15	RRM_1(RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain))
Supercontig_1.51_MVLG_04526_9sp	-393,39707	-393,39692	0,0003	0,00015	NS	0	[]	[]	[]	hypothetical protein	PF03901.10	Glyco_transf_22(Alg9-like mannosyltransferase family)
Supercontig_1.149_MVLG_06767_9sp	-382,38996	-382,38996	0	0	NS	0	[]	[]	[]	hypothetical protein	PF05022.5	SRP40_C(SRP40, C-terminal domain)
Supercontig_1.28_MVLG_03204_7sp	-1377,3377	-1377,3377	0	0	NS	0	[]	[]	[]	hypothetical protein	PF08573.3	SAE2(DNA repair protein endonuclease SAE2/CtIP C-terminus)
Supercontig_1.5_MVLG_00981_9sp	-645,71163	-645,71159	0,00316	0,00316	NS	0	[]	[]	[]	hypothetical protein	TIGR00296	TIGR00296(TIGR00296: uncharacterized protein, PH0010 family)
Supercontig_1.36_MVLG_03699_7sp	-785,4525	-785,45072	0,00356	0,00178	NS	0	[]	[]	[]	hypothetical protein	PF00172.11	Zn_clus(Fungal Zn(2)-Cys(6) binuclear cluster domain)
Supercontig_1.121_MVLG_06431_6sp	-1383,4459	-1382,8303	1,2312	0,45968	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.76_MVLG_05539_8sp	-654,33779	-653,87637	0,92284	0,36961	NS	0	[]	[]	[]	hypothetical protein	PF03151.9	TPT(Triose-phosphate Transporter family)
Supercontig_1.39_MVLG_03891_6sp	-816,61426	-815,35573	2,51706	0,71593	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.53_MVLG_04645_6sp	-1210,0856	-1210,0856	0	0	NS	0	[]	[]	[]	STE/STE7/MEK1 protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.18_MVLG_02411_12sp	-689,11181	-689,11181	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00153.20	Mito_carr(Mitochondrial carrier protein)
Supercontig_1.220_MVLG_07156_7sp	-789,99326	-789,99269	0,00114	0,00057	NS	0	[]	[]	[]	AGC/AKT protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.161_MVLG_06863_7sp	-421,97012	-421,97012	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04855.5	SNF5(SNF5 / SMARCB1 / INI1)
Supercontig_1.23_MVLG_02770_9sp	-696,36586	-695,67661	1,3785	0,49805	NS	0	[]	[]	[]	hypothetical protein	PF00107.19	ADH_zinc_N(Zinc-binding dehydrogenase)
Supercontig_1.20_MVLG_02526_7sp	-503,67212	-503,67211	0,00316	0,00316	NS	0	[]	[]	[]	hypothetical protein	PF07970.5	COPIIcoated_ERV(Endoplasmic reticulum vesicle transporter)
Supercontig_1.36_MVLG_03693_10sp	-495,98788	-495,9877	0,00036	0,00018	NS	0	[]	[]	[]	methylmalonate-semialdehyde dehydrogenase [acylating]	PF00171.15	Aldedh(Aldehyde dehydrogenase family)

Supercontig_1.38_MVLG_03784_11sp	-284,74887	-285,53449	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01556.11	DnaJ_C(DnaJ C terminal region)
Supercontig_1.7_MVLG_01253_8sp	-414,99471	-414,66799	0,65344	0,27871	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.95_MVLG_06020_8sp	-376,33541	-376,33514	0,00054	0,00027	NS	0	[]	[]	[]	60S ribosomal protein L32	PF01655.11	Ribosomal_L32e(Ribosomal protein L32)
Supercontig_1.27_MVLG_03078_10sp	-750,12977	-750,12977	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00132.17	Hexapep(Bacterial transferase hexapeptide (three repeats))
Supercontig_1.20_MVLG_02585_6sp	-1076,6292	-1076,6292	0	0	NS	0	[]	[]	[]	ribonucleoside-diphosphate reductase small chain	PF00268.14	Ribonuc_red_sm(Ribonucleotide reductase, small chain)
Supercontig_1.18_MVLG_02412_8sp	-832,53565	-832,53558	0,00014	0,00316	NS	0	[]	[]	[]	hypothetical protein	PF00153.20	Mito_carr(Mitochondrial carrier protein)
Supercontig_1.62_MVLG_05022_7sp	-475,69607	-475,69607	0	0,00316	NS	0	[]	[]	[]	hypothetical protein	PF00378.13	ECH(Enoyl-CoA hydratase/isomerase family)
Supercontig_1.83_MVLG_05750_10sp	-327,5835	-327,58344	0,00012	0,00316	NS	0	[]	[]	[]	hypothetical protein	PF00787.17	PX(PX domain)
Supercontig_1.31_MVLG_03358_8sp	-1041,0757	-1041,0757	0	0	NS	0	[]	[]	[]	phosphoenolpyruvate carboxykinase [ATP]	PF01293.13	PEPCK_ATP(Phosphoenolpyruvate carboxykinase)
Supercontig_1.18_MVLG_02409_10sp	-427,64162	-427,64145	0,00034	0,00017	NS	0	[]	[]	[]	hypothetical protein	PF03159.11	XRN_N(XRN 5'-3' exonuclease N-terminus)
Supercontig_1.63_MVLG_05053_7sp	-372,80821	-372,80821	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00173.21	Cyt-b5(Cytochrome b5-like Heme/Steroid binding domain)
Supercontig_1.6_MVLG_01118_7sp	-671,92831	-670,92939	1,99784	0,63172	NS	0	[]	[]	[]	hypothetical protein	PF00226.24	DnaJ(DnaJ domain)
Supercontig_1.4_MVLG_00845_9sp	-553,05232	-552,6035	0,89764	0,36162	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.26_MVLG_03012_8sp	-1088,3395	-1087,5115	1,65594	0,56306	NS	0	[]	[]	[]	hypothetical protein	PF08542.4	Rep_fac_C(Replication factor C)
Supercontig_1.18_MVLG_02397_11sp	-431,68071	-431,63893	0,08356	0,04092	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.2_MVLG_00464_9sp	-1049,9842	-1049,9842	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04130.6	Spc97_Spc98(Spc97 / Spc98 family)
Supercontig_1.36_MVLG_03680_8sp	-1596,3148	-1595,3665	1,89652	0,61259	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.60_MVLG_04947_9sp	-684,48268	-684,39508	0,1752	0,08387	NS	0	[]	[]	[]	hypothetical protein	PF07973.7	tRNA_SAD(Threonyl and Alanyl tRNA synthetase second additional domain)
Supercontig_1.58_MVLG_04840_10sp	-411,70735	-411,62365	0,1674	0,08029	NS	0	[]	[]	[]	hypothetical protein	PF01189.10	Nol1_Nop2_Fmu(NOL1/NOP2/sun family)
Supercontig_1.132_MVLG_06605_8sp	-330,14788	-330,14788	0	0	NS	0	[]	[]	[]	H/ACA ribonucleoprotein complex subunit 3	PF04135.5	Nop10p(Nucleolar RNA-binding protein, Nop10p family)
Supercontig_1.101_MVLG_06164_8sp	-847,78115	-847,78115	0	0	NS	0	[]	[]	[]	hypothetical protein	PF08286.4	Spc24(Spc24 subunit of Ndc80)
Supercontig_1.92_MVLG_05959_9sp	-263,18397	-263,18388	0,00018	0,00316	NS	0	[]	[]	[]	hypothetical protein	PF00501.21	AMP-binding(AMP-binding enzyme)
Supercontig_1.156_MVLG_06833_10sp	-683,95667	-683,95641	0,00052	0,00026	NS	0	[]	[]	[]	hypothetical protein	PF03188.9	Cytochrom_B561(Eukaryotic cytochrome b561)

Supercontig_1.6_MVLG_01069_9sp	-400,19135	-399,93168	0,51934	0,22869	NS	0	[]	[]	[]	hypothetical protein	PF00153.20	Mito_carr(Mitochondrial carrier protein)
Supercontig_1.12_MVLG_01835_11sp	-398,8301	-398,5145	0,6312	0,27065	NS	0	[]	[]	[]	3-phosphoshikimate 1-carboxyvinyltransferase	PF08501.4	Shikimate_dh_N(Shikimate dehydrogenase substrate binding domain)
Supercontig_1.12_MVLG_01829_12sp	-911,89428	-910,87463	2,0393	0,63928	NS	0	[]	[]	[]	hypothetical protein	PF00249.24	Myb_DNA-binding(Myb-like DNA-binding domain)
Supercontig_1.35_MVLG_03599_6sp	-1138,4813	-1138,4813	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.98_MVLG_06091_10sp	-845,25741	-845,25741	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.150_MVLG_06770_7sp	-381,2279	-381,22785	0,00316	0,00316	NS	0	[]	[]	[]	60S ribosome subunit biogenesis protein nip7	PF03657.6	UPF0113(Uncharacterised protein family (UPF0113))
Supercontig_1.32_MVLG_03421_6sp	-412,92123	-412,91658	0,0093	0,00464	NS	0	[]	[]	[]	hypothetical protein	PF10181.2	PIG-H(GPI-GlcNAc transferase complex, PIG-H component)
Supercontig_1.49_MVLG_04437_9sp	-1235,9162	-1235,9162	0	0	NS	0	[]	[]	[]	hypothetical protein	PF08588.3	DUF1769(Protein of unknown function (DUF1769))
Supercontig_1.8_MVLG_01394_12sp	-376,71094	-376,54907	0,32374	0,14945	NS	0	[]	[]	[]	hypothetical protein	PF12539.1	Csm1(Chromosome segregation protein Csm1/Pcs1)
Supercontig_1.44_MVLG_04173_9sp	-1095,489	-1095,489	0	0	NS	0	[]	[]	[]	glutathione synthetase	TIGR01986	TIGR01986(glut_syn_euk: glutathione synthetase)
Supercontig_1.31_MVLG_03381_11sp	-1005,3397	-1005,3397	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.3_MVLG_00586_9sp	-1099,8868	-1099,8868	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02197.10	RIIa(Regulatory subunit of type II PKA R-subunit)
Supercontig_1.12_MVLG_01877_6sp	-573,51704	-573,46418	0,10572	0,05149	NS	0	[]	[]	[]	hypothetical protein	PF00097.18	zf-C3HC4(Zinc finger, C3HC4 type (RING finger))
Supercontig_1.10_MVLG_01656_8sp	-760,86516	-759,64494	2,44044	0,70483	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.68_MVLG_05257_10sp	-1137,0215	-1137,0215	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01722.11	BolA(BolA-like protein)
Supercontig_1.77_MVLG_05558_8sp	-362,06165	-359,60214	4,91902	0,91452	*	0	[]	[]	[]	hypothetical protein	PF01363.14	FYVE(FYVE zinc finger)
Supercontig_1.125_MVLG_06503_8sp	-808,8821	-808,8821	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00400.25	WD40(WD domain, G-beta repeat)
Supercontig_1.64_MVLG_05111_11sp	-365,88496	-365,88472	0,00048	0,00024	NS	0	[]	[]	[]	hypothetical protein	PF02146.10	SIR2(Sir2 family)
Supercontig_1.13_MVLG_01943_12sp	-760,13905	-760,13904	0,00316	0,00316	NS	0	[]	[]	[]	hypothetical protein	PF02463.12	SMC_N(RecF/RecN/SMC N terminal domain)
Supercontig_1.5_MVLG_01009_8sp	-404,62727	-404,62727	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00155.14	Aminotran_1_2(Aminotransferase class I and II)
Supercontig_1.54_MVLG_04670_9sp	-1594,3672	-1593,5553	1,62396	0,55602	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.4_MVLG_00742_8sp	-1282,3921	-1282,3918	0,00054	0,00027	NS	0	[]	[]	[]	bifunctional purine biosynthetic protein ADE1	PF01071.12	GARS_A(Phosphoribosylglycinamide synthetase, ATP-grasp (A) domain)
Supercontig_1.6_MVLG_01060_11sp	-335,12698	-335,12698	0	0	NS	0	[]	[]	[]	hypothetical protein	PF06859.5	Bin3(Bicoid-interacting protein 3 (Bin3))

Supercontig_1.1_MVLG_00110_11sp	-343,97245	-343,86507	0,21476	0,10182	NS	0	[]	[]	[]	hypothetical protein	PF04855.5	SNF5(SNF5 / SMARCB1 / INI1)
Supercontig_1.27_MVLG_03121_10sp	-579,26095	-578,75072	1,02046	0,39964	NS	0	[]	[]	[]	hypothetical protein	PF00830.12	Ribosomal_L28(Ribosomal L28 family)
Supercontig_1.41_MVLG_04039_6sp	-841,08579	-841,08565	0,00028	0,00014	NS	0	[]	[]	[]	calcium/proton exchanger	TIGR00378	TIGR00378(cax: calcium/proton exchanger)
Supercontig_1.75_MVLG_05483_10sp	-783,79416	-783,6519	0,28452	0,1326	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.18_MVLG_02413_6sp	-614,61909	-614,38671	0,46476	0,20736	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.132_MVLG_06596_11sp	-527,14195	-526,41723	1,44944	0,51554	NS	0	[]	[]	[]	hypothetical protein	PF00650.13	CRAL_TRIO(CRAL/TRIO domain)
Supercontig_1.21_MVLG_02630_10sp	-344,79878	-344,6138	0,36996	0,16888	NS	0	[]	[]	[]	hypothetical protein	PF00892.13	EamA(EamA-like transporter family)
Supercontig_1.95_MVLG_06023_8sp	-830,37173	-830,21628	0,3109	0,14397	NS	0	[]	[]	[]	hypothetical protein	PF00313.15	CSD('Cold-shock' DNA-binding domain)
Supercontig_1.186_MVLG_07026_7sp	-778,61744	-776,81966	3,59556	0,83433	NS	0	[]	[]	[]	hypothetical protein	PF04366.5	DUF500(Family of unknown function (DUF500))
Supercontig_1.74_MVLG_05468_7sp	-382,89532	-382,84629	0,09806	0,04785	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.99_MVLG_06109_6sp	-606,45392	-606,07728	0,75328	0,31384	NS	0	[]	[]	[]	hypothetical protein	PF01544.11	CorA(CorA-like Mg2+ transporter protein)
Supercontig_1.8_MVLG_01454_12sp	-1007,401	-1003,5368	7,7285	0,97902	**	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.164_MVLG_06892_7sp	-416,02487	-416,02428	0,00118	0,00059	NS	0	[]	[]	[]	prohibitin-1	PF01145.18	Band_7(SPFH domain / Band 7 family)
Supercontig_1.86_MVLG_05836_6sp	-611,12134	-611,12134	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.30_MVLG_03269_10sp	-472,84719	-472,84703	0,00032	0,00016	NS	0	[]	[]	[]	6,7-dimethyl-8-ribityllumazine synthase	PF00885.12	DMRL_synthase(6,7-dimethyl-8-ribityllumazine synthase)
Supercontig_1.51_MVLG_04500_8sp	-574,94539	-574,5931	0,70458	0,29692	NS	0	[]	[]	[]	hypothetical protein	PF03171.13	2OG-FeII_Oxy(2OG-Fe(II) oxygenase superfamily)
Supercontig_1.139_MVLG_06662_6sp	-1268,1867	-1267,6676	1,0382	0,40494	NS	0	[]	[]	[]	hypothetical protein	PF02902.12	Peptidase_C48(Ulp1 protease family, C-terminal catalytic domain)
Supercontig_1.56_MVLG_04753_10sp	-1115,6147	-1114,5312	2,16698	0,66159	NS	0	[]	[]	[]	hypothetical protein	PF04130.6	Spc97_Spc98(Spc97 / Spc98 family)
Supercontig_1.98_MVLG_06078_10sp	-719,72828	-718,68466	2,08724	0,64782	NS	0	[]	[]	[]	hypothetical protein	PF07690.9	MFS_1(Major Facilitator Superfamily)
Supercontig_1.41_MVLG_04027_11sp	-451,05133	-451,05131	0,00316	0,00316	NS	0	[]	[]	[]	hypothetical protein	PF07716.8	bZIP_2(Basic region leucine zipper)
Supercontig_1.22_MVLG_02730_6sp	-807,91729	-807,91729	0	0	NS	0	[]	[]	[]	hypothetical protein	PF10332.2	DUF2418(Protein of unknown function (DUF2418))
Supercontig_1.5_MVLG_00899_9sp	-362,77776	-360,94298	3,66956	0,84035	NS	0	[]	[]	[]	hypothetical protein	PF03388.6	Lectin_leg-like(Legume-like lectin family)
Supercontig_1.1_MVLG_00061_11sp	-449,88505	-448,45128	2,86754	0,76159	NS	0	[]	[]	[]	hypothetical protein	PF00318.13	Ribosomal_S2(Ribosomal protein S2)
Supercontig_1.86_MVLG_05839_12sp	-660,918	-658,09766	5,64068	0,94041	*	0	[]	[]	[]	hypothetical protein	PF00400.25	WD40(WD domain, G-beta repeat)
Supercontig_1.2_MVLG_00296_11sp	-583,773	-583,6458	0,2544	0,11944	NS	0	[]	[]	[]	hypothetical protein	NA	NA

Supercontig_1.49_MVLG_04429_12sp	-814,21118	-814,21118	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00018.21	SH3_1(SH3 domain)
Supercontig_1.30_MVLG_03265_8sp	-539,99966	-540,27479	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00107.19	ADH_zinc_N(Zinc-binding dehydrogenase)
Supercontig_1.121_MVLG_06441_12sp	-608,17062	-607,66841	1,00442	0,39481	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.49_MVLG_04424_10sp	-669,69738	-669,69722	0,00032	0,00016	NS	0	[]	[]	[]	phosphatidylinositol 3-kinase tor2	PF02260.13	FATC(FATC domain)
Supercontig_1.27_MVLG_03083_9sp	-623,61929	-622,37694	2,4847	0,7113	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.123_MVLG_06475_10sp	-891,16525	-890,99561	0,33928	0,15603	NS	0	[]	[]	[]	hypothetical protein	PF00135.21	COesterase(Carboxylesterase)
Supercontig_1.5_MVLG_00930_8sp	-1156,3829	-1155,287	2,19172	0,66575	NS	0	[]	[]	[]	hypothetical protein	PF00172.11	Zn_clus(Fungal Zn(2)-Cys(6) binuclear cluster domain)
Supercontig_1.3_MVLG_00634_8sp	-259,83882	-259,83871	0,00022	0,00011	NS	0	[]	[]	[]	proteasome subunit beta type-2	PF00227.19	Proteasome(Proteasome subunit)
Supercontig_1.46_MVLG_04274_7sp	-532,63517	-529,41337	6,4436	0,96012	**	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.101_MVLG_06154_9sp	-567,6321	-567,5788	0,1066	0,0519	NS	0	[]	[]	[]	hypothetical protein	PF03452.7	Anp1(Anp1)
Supercontig_1.35_MVLG_03604_10sp	-642,29438	-642,29436	0,00316	0,00316	NS	0	[]	[]	[]	hypothetical protein	PF07919.5	DUF1683(Protein of unknown function (DUF1683))
Supercontig_1.55_MVLG_04738_8sp	-566,26743	-565,33013	1,8746	0,60832	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.10_MVLG_01595_12sp	-1121,9965	-1121,9965	0	0	NS	0	[]	[]	[]	hypothetical protein	TIGR00596	TIGR00596(rad1: DNA repair protein (rad1))
Supercontig_1.86_MVLG_05818_6sp	-1057,1314	-1057,1313	0,00024	0,00012	NS	0	[]	[]	[]	hypothetical protein	PF00023.23	Ank(Ankyrin repeat)
Supercontig_1.20_MVLG_02543_7sp	-326,9407	-326,94056	0,00028	0,00014	NS	0	[]	[]	[]	hypothetical protein	PF08477.6	Miro(Miro-like protein)
Supercontig_1.172_MVLG_06947_8sp	-477,4978	-477,4978	0	0	NS	0	[]	[]	[]	hypothetical protein	PF06807.7	Clp1(Pre-mRNA cleavage complex II protein Clp1)
Supercontig_1.190_MVLG_07041_7sp	-660,82909	-658,44237	4,77344	0,90807	*	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.11_MVLG_01794_7sp	-858,3078	-856,393	3,8296	0,85263	NS	0	[]	[]	[]	hypothetical protein	TIGR00329	TIGR00329(gcp_kae1: metallohydrolase, glycoprotease/Kae1 family)
Supercontig_1.15_MVLG_02066_10sp	-300,93782	-300,93773	0,00018	0,00316	NS	0	[]	[]	[]	hypothetical protein	PF00153.20	Mito_carr(Mitochondrial carrier protein)
Supercontig_1.47_MVLG_04332_12sp	-1608,9945	-1608,9945	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.7_MVLG_01347_7sp	-552,93644	-552,88081	0,11126	0,05411	NS	0	[]	[]	[]	hypothetical protein	PF08059.6	SEP(SEP domain)
Supercontig_1.74_MVLG_05446_11sp	-420,93562	-420,93556	0,00012	0,00316	NS	0	[]	[]	[]	hypothetical protein	PF01207.10	Dus(Dihydrouridine synthase (Dus))
Supercontig_1.87_MVLG_05860_8sp	-561,30288	-561,30259	0,00058	0,00029	NS	0	[]	[]	[]	hypothetical protein	PF08649.3	DASH_Dad1(DASH complex subunit Dad1)
Supercontig_1.127_MVLG_06532_6sp	-766,23808	-765,74287	0,99042	0,39056	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.10_MVLG_01671_9sp	-721,90455	-721,90455	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01833.17	TIG(IPT/TIG domain)

Supercontig_1.88_MVLG_05880_10sp	-1283,3342	-1282,4563	1,75572	0,58433	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.21_MVLG_02681_8sp	-497,11272	-493,24667	7,7321	0,97906	**	0	[]	[]	[]	hypothetical protein	PF01095.12	Pectinesterase(Pectinesterase)
Supercontig_1.15_MVLG_02091_9sp	-555,04203	-554,62333	0,8374	0,3421	NS	0	[]	[]	[]	hypothetical protein	PF00107.19	ADH_zinc_N(Zinc-binding dehydrogenase)
Supercontig_1.116_MVLG_06384_9sp	-481,84237	-480,20162	3,2815	0,80617	NS	0	[]	[]	[]	hypothetical protein	PF00069.18	Pkinase(Protein kinase domain)
Supercontig_1.4_MVLG_00788_6sp	-753,95319	-753,77586	0,35466	0,1625	NS	0	[]	[]	[]	hypothetical protein	PF00400.25	WD40(WD domain, G-beta repeat)
Supercontig_1.1_MVLG_00123_10sp	-1260,2926	-1259,9013	0,78254	0,3238	NS	0	[]	[]	[]	hypothetical protein	PF00097.18	zf-C3HC4(Zinc finger, C3HC4 type (RING finger))
Supercontig_1.1_MVLG_00093_6sp	-625,74143	-624,06112	3,36062	0,81368	NS	0	[]	[]	[]	hypothetical protein	PF00300.15	PGAM(Phosphoglycerate mutase family)
Supercontig_1.156_MVLG_06831_9sp	-492,10054	-489,68161	4,83786	0,91098	*	0	[]	[]	[]	hypothetical protein	PF00551.12	Formyl_trans_N(Formyl transferase)
Supercontig_1.3_MVLG_00585_10sp	-415,54384	-415,5394	0,00888	0,00443	NS	0	[]	[]	[]	hypothetical protein	PF02115.10	Rho_GDI(RHO protein GDP dissociation inhibitor)
Supercontig_1.69_MVLG_05307_7sp	-733,18543	-733,13777	0,09532	0,04654	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.52_MVLG_04549_9sp	-993,84567	-993,8456	0,00014	0,00316	NS	0	[]	[]	[]	hypothetical protein	PF00782.13	DSPc(Dual specificity phosphatase, catalytic domain)
Supercontig_1.88_MVLG_05891_9sp	-829,32631	-829,32631	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04054.8	Not1(CCR4-Not complex component, Not1)
Supercontig_1.30_MVLG_03271_6sp	-392,96339	-392,96312	0,00054	0,00027	NS	0	[]	[]	[]	ubiquitin-conjugating enzyme spm2	PF00179.19	UQ_con(Ubiquitin-conjugating enzyme)
Supercontig_1.77_MVLG_05556_11sp	-372,29919	-372,299	0,00038	0,00019	NS	0	[]	[]	[]	hypothetical protein	PF08142.5	AARP2CN(AARP2CN (NUC121) domain)
Supercontig_1.5_MVLG_01014_8sp	-348,05994	-348,05992	0,00316	0,00316	NS	0	[]	[]	[]	hypothetical protein	PF03987.8	Autophagy_act_C(Autophagocytosis associated protein, active-site domain)
Supercontig_1.27_MVLG_03101_8sp	-922,07212	-922,07212	0	0	NS	0	[]	[]	[]	hypothetical protein	PF10602.2	RPN7(26S proteasome subunit RPN7)
Supercontig_1.17_MVLG_02259_11sp	-355,50011	-355,49991	0,0004	0,0002	NS	0	[]	[]	[]	hypothetical protein	PF08022.5	FAD_binding_8(FAD-binding domain)
Supercontig_1.20_MVLG_02597_8sp	-658,43137	-658,24138	0,37998	0,17303	NS	0	[]	[]	[]	hypothetical protein	PF07859.6	Abhydrolase_3(alpha/beta hydrolase fold)
Supercontig_1.44_MVLG_04152_6sp	-461,1626	-459,89327	2,53866	0,71898	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.25_MVLG_02941_8sp	-535,92276	-535,46325	0,91902	0,36841	NS	0	[]	[]	[]	CAMK/CAMK1 protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.10_MVLG_01614_9sp	-1668,8816	-1667,9585	1,84622	0,60272	NS	0	[]	[]	[]	hypothetical protein	PF07738.6	Sad1_UNC(Sad1 / UNC-like C-terminal)
Supercontig_1.33_MVLG_03467_9sp	-465,51346	-465,51346	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00023.23	Ank(Ankyrin repeat)
Supercontig_1.22_MVLG_02746_8sp	-764,16508	-763,46164	1,40688	0,50512	NS	0	[]	[]	[]	hypothetical protein	PF08445.3	FR47(FR47-like protein)
Supercontig_1.30_MVLG_03322_9sp	-750,41725	-750,41725	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA

Supercontig_1.181_MVLG_07006_10sp	-520,04742	-520,04722	0,0004	0,0002	NS	0	[]	[]	[]	hypothetical protein	TIGR00879	TIGR00879(SP: MFS transporter, sugar porter (SP) family)
Supercontig_1.9_MVLG_01478_8sp	-478,91668	-478,91665	0,00316	0,00316	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.6_MVLG_01095_6sp	-551,97988	-551,97988	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.1_MVLG_00151_10sp	-560,4104	-560,27522	0,27036	0,12644	NS	0	[]	[]	[]	hypothetical protein	PF00481.14	PP2C(Protein phosphatase 2C)
Supercontig_1.92_MVLG_05948_11sp	-380,01881	-379,51572	1,00618	0,39534	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.21_MVLG_02668_8sp	-581,41891	-580,32483	2,18816	0,66515	NS	0	[]	[]	[]	hypothetical protein	PF04139.6	Rad9(Rad9)
Supercontig_1.110_MVLG_06291_8sp	-708,14793	-707,85776	0,58034	0,25186	NS	0	[]	[]	[]	hypothetical protein	PF00106.18	adh_short(short chain dehydrogenase)
Supercontig_1.12_MVLG_01869_10sp	-544,97824	-544,97819	0,00316	0,00316	NS	0	[]	[]	[]	hypothetical protein	PF10297.2	Hap4_Hap_bind(Minimal binding domain of Hap4 for binding to Hap2/3/5)
Supercontig_1.29_MVLG_03250_10sp	-958,16695	-958,16695	0	0	NS	0	[]	[]	[]	hypothetical protein	PF10392.2	COG5(Golgi transport complex subunit 5)
Supercontig_1.60_MVLG_04921_9sp	-718,53563	-718,53563	0	0	NS	0	[]	[]	[]	elongation factor EF-1 beta subunit	PF10587.2	EF-1_beta_acid(Eukaryotic elongation factor 1 beta central acidic region)
Supercontig_1.15_MVLG_02113_7sp	-566,3497	-566,3497	0	0	NS	0	[]	[]	[]	hypothetical protein	PF07859.6	Abhydrolase_3(alpha/beta hydrolase fold)
Supercontig_1.16_MVLG_02185_12sp	-519,9894	-519,92752	0,12376	0,06	NS	0	[]	[]	[]	hypothetical protein	PF00010.19	HLH(Helix-loop-helix DNA-binding domain)
Supercontig_1.12_MVLG_01818_9sp	-331,65092	-331,65089	0,00316	0,00316	NS	0	[]	[]	[]	hypothetical protein	PF07940.6	Hepar_II_III(Heparinase II/III-like protein)
Supercontig_1.44_MVLG_04172_7sp	-1082,2956	-1082,2956	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00566.11	TBC(TBC domain)
Supercontig_1.28_MVLG_03143_7sp	-671,78324	-671,78324	0	0	NS	0	[]	[]	[]	GDP-L-fucose synthase	PF01370.14	Epimerase(NAD dependent epimerase/dehydratase family)
Supercontig_1.113_MVLG_06349_9sp	-539,22863	-538,9753	0,50666	0,22379	NS	0	[]	[]	[]	hypothetical protein	PF00296.13	Bac_luciferase(Luciferase-like monooxygenase)
Supercontig_1.20_MVLG_02570_9sp	-1012,0852	-1012,0852	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.38_MVLG_03763_11sp	-544,39349	-544,39349	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03162.6	Y_phosphatase2(Tyrosine phosphatase family)
Supercontig_1.9_MVLG_01483_6sp	-684,35439	-684,35408	0,00062	0,00031	NS	0	[]	[]	[]	ribosomal protein L4	PF01248.19	Ribosomal_L7Ae(Ribosomal protein L7Ae/L30e/S12e/Gadd45 family)
Supercontig_1.101_MVLG_06157_12sp	-386,30582	-386,30567	0,0003	0,00015	NS	0	[]	[]	[]	hypothetical protein	TIGR00797	TIGR00797(matE: MATE efflux family protein)
Supercontig_1.33_MVLG_03500_10sp	-612,55522	-612,55522	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.48_MVLG_04371_12sp	-368,50296	-368,50273	0,00046	0,00023	NS	0	[]	[]	[]	hypothetical protein	PF01494.12	FAD_binding_3(FAD binding domain)
Supercontig_1.45_MVLG_04213_8sp	-2189,2423	-2186,8238	4,83698	0,91094	*	0	[]	[]	[]	hypothetical protein	PF02181.16	FH2(Formin Homology 2 Domain)

Supercontig_1.5_MVLG_00898_6sp	-613,25921	-612,93883	0,64076	0,27413	NS	0	[]	[]	[]	hypothetical protein	PF05032.5	Spo12(Spo12 family)
Supercontig_1.4_MVLG_00712_6sp	-573,35805	-573,02477	0,66656	0,28343	NS	0	[]	[]	[]	hypothetical protein	PF00106.18	adh_short(short chain dehydrogenase)
Supercontig_1.4_MVLG_00772_7sp	-814,98324	-814,98304	0,0004	0,0002	NS	0	[]	[]	[]	hypothetical protein	PF01926.16	MMR_HSR1(GTPase of unknown function)
Supercontig_1.166_MVLG_06915_9sp	-823,70101	-823,52765	0,34672	0,15917	NS	0	[]	[]	[]	hypothetical protein	PF04696.6	Pinin_SDK_memA(pinin/SDK/memA/ protein conserved region)
Supercontig_1.1_MVLG_00053_7sp	-1031,2794	-1031,2794	0,00316	0,00316	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.33_MVLG_03461_11sp	-336,45751	-336,45739	0,00024	0,00012	NS	0	[]	[]	[]	arginine biosynthesis ArgJ	PF01960.11	ArgJ(ArgJ family)
Supercontig_1.25_MVLG_02979_7sp	-313,84659	-313,84659	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03081.8	Exo70(Exo70 exocyst complex subunit)
Supercontig_1.2_MVLG_00327_10sp	-581,67368	-581,67352	0,00032	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF04003.5	Utp12(Dip2/Utp12 Family)
Supercontig_1.47_MVLG_04309_8sp	-577,30314	-577,30314	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03824.9	NicO(High-affinity nickel-transport protein)
Supercontig_1.6_MVLG_01193_7sp	-485,00167	-485,00167	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.28_MVLG_03134_10sp	-746,31511	-746,31484	0,00054	0,00027	NS	0	[]	[]	[]	hypothetical protein	PF00400.25	WD40(WD domain, G-beta repeat)
Supercontig_1.86_MVLG_05822_10sp	-1135,1032	-1135,1032	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.33_MVLG_03497_11sp	-889,73764	-889,71767	0,03994	0,01977	NS	0	[]	[]	[]	hypothetical protein	PF08576.3	DUF1764(Eukaryotic protein of unknown function (DUF1764))
Supercontig_1.1_MVLG_00059_6sp	-297,10881	-297,10879	0,00316	0,00316	NS	0	[]	[]	[]	ubiquitin-like protein 5	PF00240.16	ubiquitin(Ubiquitin family)
Supercontig_1.3_MVLG_00508_10sp	-769,41986	-769,41986	0,00316	0,00316	NS	0	[]	[]	[]	ribosomal RNA methyltransferase 1	TIGR00438	TIGR00438(rrmJ: 23S rRNA (uridine(2552)-2'-O-)-methyltransferase)
Supercontig_1.32_MVLG_03413_9sp	-562,3008	-562,29923	0,00316	0,00316	NS	0	[]	[]	[]	proteasome subunit alpha type-7 like-protein	PF00227.19	Proteasome(Proteasome subunit)
Supercontig_1.80_MVLG_05635_10sp	-796,70404	-796,70399	0,00316	0,00316	NS	0	[]	[]	[]	hypothetical protein	PF08524.4	rRNA_processing(rRNA processing)
Supercontig_1.61_MVLG_04987_8sp	-456,07188	-456,07181	0,00316	0,00316	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.12_MVLG_01796_6sp	-822,1748	-822,1747	0,00316	0,00316	NS	0	[]	[]	[]	DNA-directed RNA polymerase II subunit RPB2	PF04565.9	RNA_pol_Rpb2_3(RNA polymerase Rpb2, domain 3)
Supercontig_1.2_MVLG_00417_10sp	-690,74204	-690,74204	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.48_MVLG_04355_9sp	-563,34656	-563,34627	0,00058	0,00029	NS	0	[]	[]	[]	hypothetical protein	PF03836.8	RasGAP_C(RasGAP C-terminus)
Supercontig_1.64_MVLG_05099_10sp	-653,14603	-652,41366	1,46474	0,51923	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.23_MVLG_02772_12sp	-898,45348	-898,45348	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA

Supercontig_1.66_MVLG_05197_10sp	-840,51937	-840,51937	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00250.11	Fork_head(Fork head domain)
Supercontig_1.19_MVLG_02501_9sp	-455,29387	-455,29387	0	0	NS	0	[]	[]	[]	hypothetical protein	PF08022.5	FAD_binding_8(FAD-binding domain)
Supercontig_1.60_MVLG_04937_9sp	-508,38507	-508,37413	0,02188	0,01088	NS	0	[]	[]	[]	threonine synthase	PF00291.18	PALP(Pyridoxal-phosphate dependent enzyme)
Supercontig_1.36_MVLG_03644_10sp	-511,64473	-511,64473	0	0	NS	0	[]	[]	[]	hypothetical protein	PF08318.5	COG4(COG4 transport protein)
Supercontig_1.243_MVLG_07207_6sp	-465,5659	-465,56589	0,00316	0,00316	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.5_MVLG_00990_9sp	-740,58835	-740,58835	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01556.11	DnaJ_C(DnaJ C terminal region)
Supercontig_1.25_MVLG_02912_10sp	-395,40656	-395,40647	0,00018	0,00316	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.1_MVLG_00260_6sp	-374,65249	-373,21175	2,88148	0,76325	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.47_MVLG_04331_7sp	-757,5592	-756,41762	2,28316	0,68069	NS	0	[]	[]	[]	hypothetical protein	PF03399.9	SAC3_GANP(SAC3/GANP/Nin1/mts3/eIF-3 p25 family)
Supercontig_1.31_MVLG_03347_11sp	-678,52865	-678,52865	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.59_MVLG_04911_10sp	-632,28634	-632,28634	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04145.8	Ctr(Ctr copper transporter family)
Supercontig_1.8_MVLG_01450_11sp	-610,58435	-610,58415	0,0004	0,0002	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.17_MVLG_02340_10sp	-519,59591	-519,59573	0,00036	0,00018	NS	0	[]	[]	[]	hypothetical protein	PF02815.12	MIR(MIR domain)
Supercontig_1.12_MVLG_01872_8sp	-575,15834	-575,15831	0,00316	0,00316	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.121_MVLG_06443_8sp	-531,16243	-531,1624	0,00316	0,00316	NS	0	[]	[]	[]	hypothetical protein	PF00172.11	Zn_clus(Fungal Zn(2)-Cys(6) binuclear cluster domain)
Supercontig_1.42_MVLG_04046_10sp	-529,75158	-529,14067	1,22182	0,45714	NS	0	[]	[]	[]	hypothetical protein	PF02204.11	VPS9(Vacuolar sorting protein 9 (VPS9) domain)
Supercontig_1.5_MVLG_00878_11sp	-601,53829	-601,53829	0	0	NS	0	[]	[]	[]	hypothetical protein	PF08241.5	Methyltransf_11(Methyltransferase domain)
Supercontig_1.18_MVLG_02354_10sp	-514,94312	-514,94306	0,00012	0,00316	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.117_MVLG_06386_12sp	-770,77579	-770,77579	0	0	NS	0	[]	[]	[]	hypothetical protein	TIGR02041	TIGR02041(CysI: sulfite reductase (NADPH) hemoprotein, beta-component)
Supercontig_1.84_MVLG_05765_7sp	-505,56215	-502,22402	6,67626	0,9645	**	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.2_MVLG_00320_10sp	-396,38664	-396,38664	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00733.14	Asn_synthase(Asparagine synthase)
Supercontig_1.44_MVLG_04177_11sp	-734,85841	-734,85808	0,00066	0,00033	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.8_MVLG_01400_7sp	-452,20781	-450,07971	4,2562	0,88094	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.7_MVLG_01271_7sp	-813,10129	-811,67182	2,85894	0,76056	NS	0	[]	[]	[]	hypothetical protein	PF06441.5	EHN(Epoxide hydrolase N terminus)
Supercontig_1.30_MVLG_03276_10sp	-658,25602	-658,25602	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01713.14	Smr(Smr domain)

Supercontig_1.54_MVLG_04656_11sp	-558,3432	-558,34238	0,00164	0,00082	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.50_MVLG_04494_6sp	-378,60873	-378,27436	0,66874	0,28421	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.58_MVLG_04855_8sp	-1000,2795	-1000,2795	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.113_MVLG_06345_9sp	-557,974	-556,82993	2,28814	0,68148	NS	0	[]	[]	[]	hypothetical protein	PF00923.12	Transaldolase(Transaldolase)
Supercontig_1.48_MVLG_04386_7sp	-1184,3127	-1184,3127	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.40_MVLG_03920_9sp	-1422,4292	-1422,4292	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00168.23	C2(C2 domain)
Supercontig_1.76_MVLG_05525_9sp	-508,46859	-508,28088	0,37542	0,17114	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.97_MVLG_06059_10sp	-792,40103	-792,10363	0,5948	0,25725	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.19_MVLG_02492_6sp	-1102,3186	-1102,3186	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00533.19	BRCT(BRCA1 C Terminus (BRCT) domain)
Supercontig_1.7_MVLG_01313_10sp	-518,10973	-517,85226	0,51494	0,227	NS	0	[]	[]	[]	hypothetical protein	PF00620.20	RhoGAP(RhoGAP domain)
Supercontig_1.28_MVLG_03178_8sp	-1525,4424	-1524,3873	2,1103	0,65186	NS	0	[]	[]	[]	hypothetical protein	PF00225.16	Kinesin(Kinesin motor domain)
Supercontig_1.46_MVLG_04293_8sp	-506,59393	-506,59393	0	0	NS	0	[]	[]	[]	phosphomannomutase	PF03332.6	PMM(Eukaryotic phosphomannomutase)
Supercontig_1.3_MVLG_00580_9sp	-564,29979	-564,23237	0,13484	0,0652	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.14_MVLG_02048_11sp	-669,99683	-668,60852	2,77662	0,7505	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.38_MVLG_03803_7sp	-585,79853	-585,58215	0,43276	0,19457	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.38_MVLG_03826_6sp	-1647,1125	-1646,7486	0,7279	0,30507	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.1_MVLG_00101_7sp	-457,43724	-457,28891	0,29666	0,13785	NS	0	[]	[]	[]	hypothetical protein	PF09830.2	ATP_transf(ATP adenylyltransferase)
Supercontig_1.10_MVLG_01644_6sp	-440,65259	-440,65251	0,00016	0,00316	NS	0	[]	[]	[]	COP9 signalosome complex subunit 5	PF01398.14	Mov34(Mov34/MPN/PAD-1 family)
Supercontig_1.48_MVLG_04394_6sp	-403,6294	-402,16263	2,93354	0,76933	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.55_MVLG_04713_10sp	-699,63027	-698,87794	1,50466	0,52873	NS	0	[]	[]	[]	hypothetical protein	PF01243.13	Pyridox_oxidase(Pyridoxamine 5'-phosphate oxidase)
Supercontig_1.55_MVLG_04714_6sp	-735,14675	-732,33836	5,61678	0,9397	*	0	[]	[]	[]	hypothetical protein	PF00875.11	DNA_photolyase(DNA photolyase)
Supercontig_1.1_MVLG_00271_12sp	-502,42672	-502,42672	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01602.13	Adaptin_N(Adaptin N terminal region)
Supercontig_1.24_MVLG_02867_9sp	-1068,3464	-1068,3464	0	0	NS	0	[]	[]	[]	hypothetical protein	PF07842.5	GCFC(GC-rich sequence DNA-binding factor-like protein)
Supercontig_1.53_MVLG_04599_12sp	-391,11179	-389,33031	3,56296	0,83161	NS	0	[]	[]	[]	ubiquitin-activating enzyme E1 1	PF10585.2	UBA_e1_thiolCys(Ubiquitin-activating enzyme active site)
Supercontig_1.2_MVLG_00407_8sp	-778,50268	-778,50268	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03099.12	BPL_LplA_LipB(Biotin/lipoate A/B protein ligase family)
Supercontig_1.75_MVLG_05495_10sp	-831,02807	-831,02011	0,01592	0,00793	NS	0	[]	[]	[]	hypothetical protein	NA	NA

Supercontig_1.28_MVLG_03163_7sp	-491,58267	-491,58267	0	0	NS	0	[]	[]	[]	hypothetical protein	PF06544.5	DUF1115(Protein of unknown function (DUF1115))
Supercontig_1.10_MVLG_01640_7sp	-319,15923	-319,15923	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.7_MVLG_01325_7sp	-822,20143	-822,20142	0,00316	0,00316	NS	0	[]	[]	[]	hypothetical protein	PF03155.8	Alg6_Alg8(ALG6, ALG8 glycosyltransferase family)
Supercontig_1.140_MVLG_06682_6sp	-413,40174	-413,40174	0	0	NS	0	[]	[]	[]	U6 snRNA-associated Sm-like protein LSm6	PF01423.15	LSM(LSM domain)
Supercontig_1.24_MVLG_02886_8sp	-535,43569	-535,43558	0,00022	0,00011	NS	0	[]	[]	[]	ubiquitin-conjugating enzyme (huntingtin interacting protein 2)	PF00179.19	UQ_con(Ubiquitin-conjugating enzyme)
Supercontig_1.54_MVLG_04675_8sp	-1377,1973	-1376,6862	1,0223	0,40019	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.28_MVLG_03139_7sp	-670,66386	-670,6633	0,00112	0,00056	NS	0	[]	[]	[]	septum-promoting GTP-binding protein 1	PF04670.5	Gtr1_RagA(Gtr1/RagA G protein conserved region)
Supercontig_1.14_MVLG_02016_9sp	-415,72919	-415,20869	1,041	0,40578	NS	0	[]	[]	[]	hypothetical protein	PF06747.6	CHCH(CHCH domain)
Supercontig_1.142_MVLG_06708_7sp	-901,09078	-899,87661	2,42834	0,70304	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.239_MVLG_07201_9sp	-793,91303	-793,69285	0,44036	0,19763	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.42_MVLG_04090_7sp	-809,13751	-809,13751	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00704.21	Glyco_hydro_18(Glycosyl hydrolases family 18)
Supercontig_1.14_MVLG_01981_7sp	-801,77095	-801,65674	0,22842	0,10793	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.2_MVLG_00441_8sp	-507,54964	-507,54964	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.48_MVLG_04390_10sp	-544,4261	-544,41009	0,03202	0,01588	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.2_MVLG_00353_9sp	-815,45589	-813,89749	3,1168	0,78953	NS	0	[]	[]	[]	hypothetical protein	PF08159.5	NUC153(NUC153 domain)
Supercontig_1.11_MVLG_01782_9sp	-1245,7878	-1245,7878	0	0	NS	0	[]	[]	[]	heat shock protein HSS1	TIGR02350	TIGR02350(prok_dnaK: chaperone protein DnaK)
Supercontig_1.51_MVLG_04537_10sp	-415,86337	-415,86337	0	0	NS	0	[]	[]	[]	hypothetical protein	TIGR01509	TIGR01509(HAD-SF-IA-v3: HAD hydrolase, family IA, variant 3)
Supercontig_1.69_MVLG_05306_9sp	-854,60741	-853,85001	1,5148	0,53112	NS	0	[]	[]	[]	hypothetical protein	PF04931.6	DNA_pol_phi(DNA polymerase phi)
Supercontig_1.21_MVLG_02622_8sp	-412,96588	-412,96574	0,00028	0,00014	NS	0	[]	[]	[]	hypothetical protein	PF00106.18	adh_short(short chain dehydrogenase)
Supercontig_1.25_MVLG_02964_9sp	-486,93194	-486,93038	0,00312	0,00156	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.14_MVLG_02038_9sp	-873,94433	-873,8706	0,14746	0,07108	NS	0	[]	[]	[]	hypothetical protein	PF09801.2	SYS1(Integral membrane protein S linking to the trans Golgi network)
Supercontig_1.33_MVLG_03482_9sp	-865,88967	-865,88967	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.142_MVLG_06710_12sp	-709,66435	-709,66435	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA

Supercontig_1.15_MVLG_02115_11sp	-286,14248	-286,14231	0,00034	0,00017	NS	0	[]	[]	[]	DNA replication licensing factor mcm5	PF00493.16	MCM(MCM2/3/5 family)
Supercontig_1.29_MVLG_03238_12sp	-645,11795	-644,97654	0,28282	0,13187	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.165_MVLG_06905_9sp	-541,17367	-540,44886	1,44962	0,51558	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.73_MVLG_05435_9sp	-427,31669	-427,30199	0,0294	0,01459	NS	0	[]	[]	[]	hypothetical protein	PF06011.5	TRP(Transient receptor potential (TRP) ion channel)
Supercontig_1.3_MVLG_00622_9sp	-640,13495	-640,13495	0	0	NS	0	[]	[]	[]	mannose-1-phosphate guanyltransferase	PF00483.16	NTP_transferase(Nucleotidyl transferase)
Supercontig_1.154_MVLG_06803_8sp	-555,76146	-555,76127	0,00038	0,00019	NS	0	[]	[]	[]	NAD(P)H-dependent D-xylose reductase xyl1	PF00248.14	Aldo_ket_red(Aldo/keto reductase family)
Supercontig_1.3_MVLG_00633_10sp	-737,71739	-737,66467	0,10544	0,05135	NS	0	[]	[]	[]	hypothetical protein	PF00651.24	BTB(BTB/POZ domain)
Supercontig_1.56_MVLG_04757_10sp	-599,32368	-599,17703	0,2933	0,1364	NS	0	[]	[]	[]	hypothetical protein	PF00096.19	zf-C2H2(Zinc finger, C2H2 type)
Supercontig_1.6_MVLG_01149_10sp	-485,98452	-482,61837	6,7323	0,96548	**	0	[]	[]	[]	STE/STE11 protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.45_MVLG_04194_10sp	-1062,7232	-1058,9762	7,49398	0,97641	**	0	[]	[]	[]	hypothetical protein	PF00169.22	PH(PH domain)
Supercontig_1.55_MVLG_04701_8sp	-863,40255	-863,40234	0,00042	0,00021	NS	0	[]	[]	[]	hypothetical protein	PF00324.14	AA_permease(Amino acid permease)
Supercontig_1.54_MVLG_04659_7sp	-403,93483	-403,88092	0,10782	0,05248	NS	0	[]	[]	[]	hypothetical protein	PF01016.12	Ribosomal_L27(Ribosomal L27 protein)
Supercontig_1.5_MVLG_01015_8sp	-746,86098	-746,86098	0	0	NS	0	[]	[]	[]	hypothetical protein	PF05192.11	MutS_III(MutS domain III)
Supercontig_1.12_MVLG_01813_8sp	-1452,3471	-1452,3471	0	0	NS	0	[]	[]	[]	hypothetical protein	PF09073.3	BUD22(BUD22)
Supercontig_1.77_MVLG_05545_8sp	-1176,0963	-1176,0963	0	0	NS	0	[]	[]	[]	centromere/microtubule-binding protein cbf5	TIGR00431	TIGR00431(TruB: tRNA pseudouridine synthase B)
Supercontig_1.3_MVLG_00528_9sp	-477,65843	-474,71928	5,8783	0,94709	*	0	[]	[]	[]	hypothetical protein	PF04722.6	Ssu72(Ssu72-like protein)
Supercontig_1.19_MVLG_02496_8sp	-278,17674	-278,1767	0,00316	0,00316	NS	0	[]	[]	[]	cyanate hydratase	TIGR00673	TIGR00673(cynS: cyanate hydratase)
Supercontig_1.1_MVLG_00167_8sp	-373,95523	-373,88362	0,14322	0,06911	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.18_MVLG_02368_7sp	-2315,0884	-2314,8293	0,51832	0,2283	NS	0	[]	[]	[]	hypothetical protein	PF01965.17	DJ-1_PfpI(DJ-1/PfpI family)
Supercontig_1.7_MVLG_01242_7sp	-461,0779	-461,0779	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.28_MVLG_03137_8sp	-1288,1638	-1288,1638	0	0	NS	0	[]	[]	[]	hypothetical protein	PF07690.9	MFS_1(Major Facilitator Superfamily)
Supercontig_1.97_MVLG_06075_10sp	-543,68224	-543,68153	0,00142	0,00071	NS	0	[]	[]	[]	nucleolar GTP-binding protein 1	PF02421.11	FeoB_N(Ferrous iron transport protein B)
Supercontig_1.1_MVLG_00127_6sp	-1077,2787	-1077,2713	0,01478	0,00736	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.48_MVLG_04395_7sp	-738,32515	-738,30039	0,04952	0,02446	NS	0	[]	[]	[]	hypothetical protein	PF05739.12	SNARE(SNARE domain)

Supercontig_1.143_MVLG_06721_6sp	-1072,4081	-1072,4081	0	0	NS	0	[]	[]	[]	CAMK/CAMKL/MARK protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.30_MVLG_03317_8sp	-552,58308	-552,61022	0	0	NS	0	[]	[]	[]	NAD binding Rossmann fold oxidoreductase	PF01408.15	GFO_IDH_MocA(Oxidoreductase family, NAD-binding Rossmann fold)
Supercontig_1.4_MVLG_00773_9sp	-1038,8516	-1038,8515	0,00018	0,00316	NS	0	[]	[]	[]	hypothetical protein	TIGR01346	TIGR01346(isocit_lyase: isocitrate lyase)
Supercontig_1.4_MVLG_00708_10sp	-545,6971	-545,07643	1,24134	0,46242	NS	0	[]	[]	[]	hypothetical protein	TIGR00745	TIGR00745(apbA_panE: 2-dehydropantoate 2-reductase)
Supercontig_1.4_MVLG_00688_9sp	-339,66411	-339,66404	0,00014	0,00316	NS	0	[]	[]	[]	U3 small nucleolar ribonucleoprotein IMP4	PF04427.11	Brix(Brix domain)
Supercontig_1.53_MVLG_04628_9sp	-542,8031	-542,8031	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04889.5	Cwf_Cwc_15(Cwf15/Cwc15 cell cycle control protein)
Supercontig_1.60_MVLG_04934_7sp	-931,8306	-931,8306	0	0	NS	0	[]	[]	[]	hypothetical protein	PF07859.6	Abhydrolase_3(alpha/beta hydrolase fold)
Supercontig_1.3_MVLG_00598_12sp	-748,71515	-747,75329	1,92372	0,61782	NS	0	[]	[]	[]	hypothetical protein	PF07393.4	Sec10(Exocyst complex component Sec10)
Supercontig_1.198_MVLG_07078_8sp	-1302,3721	-1300,9942	2,75572	0,74788	NS	0	[]	[]	[]	hypothetical protein	PF12146.1	Hydrolase_4(Putative lysophospholipase)
Supercontig_1.54_MVLG_04690_10sp	-623,39735	-623,39735	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00878.11	CIMR(Cation-independent mannose-6-phosphate receptor repeat)
Supercontig_1.54_MVLG_04681_7sp	-400,39833	-400,3035	0,18966	0,09047	NS	0	[]	[]	[]	hypothetical protein	PF01428.9	zf-AN1(AN1-like Zinc finger)
Supercontig_1.39_MVLG_03899_8sp	-656,34301	-656,31819	0,04964	0,02451	NS	0	[]	[]	[]	hypothetical protein	PF00249.24	Myb_DNA-binding(Myb-like DNA-binding domain)
Supercontig_1.12_MVLG_01821_7sp	-322,80395	-322,80395	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.88_MVLG_05884_12sp	-357,88046	-357,88036	0,0002	0,00316	NS	0	[]	[]	[]	hypothetical protein	PF08613.4	Cyclin(Cyclin)
Supercontig_1.5_MVLG_00956_8sp	-430,99761	-430,99444	0,00634	0,00316	NS	0	[]	[]	[]	hypothetical protein	PF00106.18	adh_short(short chain dehydrogenase)
Supercontig_1.14_MVLG_02007_9sp	-323,29373	-322,29687	1,99372	0,63096	NS	0	[]	[]	[]	farnesyl pyrophosphate synthase	PF00348.10	polyprenyl_synt(Polyprenyl synthetase)
Supercontig_1.6_MVLG_01151_11sp	-434,25774	-433,10115	2,31318	0,68544	NS	0	[]	[]	[]	hypothetical protein	PF08783.4	DWNN(DWNN domain)
Supercontig_1.56_MVLG_04776_10sp	-422,35707	-422,35701	0,00012	0	NS	0	[]	[]	[]	MC family mitochondrial carrier protein	PF00153.20	Mito_carr(Mitochondrial carrier protein)
Supercontig_1.4_MVLG_00813_8sp	-526,94906	-526,9489	0,00032	0,00016	NS	0	[]	[]	[]	hypothetical protein	PF01733.11	Nucleoside_tran(Nucleoside transporter)
Supercontig_1.57_MVLG_04804_8sp	-585,39922	-585,39922	0	0	NS	0	[]	[]	[]	hypothetical protein	PF11274.1	DUF3074(Protein of unknown function (DUF3074))
Supercontig_1.48_MVLG_04384_12sp	-479,87745	-479,87535	0,0042	0,0021	NS	0	[]	[]	[]	hypothetical protein	PF00202.14	Aminotran_3(Aminotransferase class-III)
Supercontig_1.102_MVLG_06170_9sp	-787,22863	-785,91908	2,6191	0,73006	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.10_MVLG_01653_9sp	-1063,2559	-1062,4281	1,65556	0,56298	NS	0	[]	[]	[]	hypothetical protein	NA	NA

Supercontig_1.19_MVLG_02500_7sp	-549,48675	-549,48675	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01532.13	Glyco_hydro_47(Glycosyl hydrolase family 47)
Supercontig_1.30_MVLG_03324_10sp	-659,78731	-659,78731	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.7_MVLG_01340_6sp	-912,20098	-912,20098	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04564.8	U-box(U-box domain)
Supercontig_1.98_MVLG_06089_9sp	-404,39238	-404,39238	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00026.16	Asp(Eukaryotic aspartyl protease)
Supercontig_1.27_MVLG_03088_8sp	-488,88644	-488,74092	0,29104	0,13543	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.7_MVLG_01335_8sp	-398,3108	-396,70787	3,20586	0,79869	NS	0	[]	[]	[]	hypothetical protein	PF08613.4	Cyclin(Cyclin)
Supercontig_1.4_MVLG_00839_10sp	-676,77779	-675,529	2,49758	0,71315	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.80_MVLG_05638_11sp	-612,92719	-612,92719	0	0	NS	0	[]	[]	[]	phenylalanyl-tRNA synthetase	PF03147.7	FDX-ACB(Ferredoxin-fold anticodon binding domain)
Supercontig_1.21_MVLG_02625_9sp	-906,65982	-905,33464	2,65036	0,73424	NS	0	[]	[]	[]	hypothetical protein	PF00018.21	SH3_1(SH3 domain)
Supercontig_1.1_MVLG_00048_8sp	-875,45714	-875,34618	0,22192	0,10503	NS	0	[]	[]	[]	hypothetical protein	PF01399.20	PCI(PCI domain)
Supercontig_1.27_MVLG_03090_8sp	-947,0247	-947,02193	0,00554	0,00277	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.59_MVLG_04899_10sp	-688,49571	-688,49543	0,00056	0,00028	NS	0	[]	[]	[]	hypothetical protein	PF08354.3	DUF1729(Domain of unknown function (DUF1729))
Supercontig_1.73_MVLG_05410_7sp	-395,09745	-395,09745	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00254.21	FKBP_C(FKBP-type peptidyl-prolyl cis-trans isomerase)
Supercontig_1.23_MVLG_02827_10sp	-680,07196	-680,07196	0	0	NS	0	[]	[]	[]	calcium-transporting P-type ATPase, PMR1-type	TIGR01494	TIGR01494(ATPase_P-type: HAD ATPase, P-type, family IC)
Supercontig_1.39_MVLG_03832_12sp	-560,56902	-560,56902	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01697.20	DUF23(Domain of unknown function)
Supercontig_1.8_MVLG_01389_9sp	-529,04422	-529,04413	0,00018	0	NS	0	[]	[]	[]	CMGC/MAPK protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.21_MVLG_02670_7sp	-889,12335	-889,12335	0	0	NS	0	[]	[]	[]	dynamin GTPase	PF00350.16	Dynamin_N(Dynamin family)
Supercontig_1.46_MVLG_04251_9sp	-648,26426	-648,22097	0,08658	0,04237	NS	0	[]	[]	[]	hypothetical protein	PF00005.20	ABC_tran(ABC transporter)
Supercontig_1.34_MVLG_03561_7sp	-953,03014	-952,25848	1,54332	0,53775	NS	0	[]	[]	[]	hypothetical protein	PF12328.1	Rpp20(Rpp20 subunit of nuclear RNase MRP and P)
Supercontig_1.63_MVLG_05087_6sp	-1130,9665	-1130,9665	0	0	NS	0	[]	[]	[]	hypothetical protein	TIGR00071	TIGR00071(hisT_truA: tRNA pseudouridine synthase A)
Supercontig_1.22_MVLG_02684_9sp	-631,54516	-631,54514	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00383.15	dCMP_cyt_deam_1(Cytidine and deoxycytidylate deaminase zinc-binding region)
Supercontig_1.239_MVLG_07200_8sp	-1068,4365	-1068,4365	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.97_MVLG_06066_8sp	-550,2599	-550,2599	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03909.10	BSD(BSD domain)
Supercontig_1.39_MVLG_03872_10sp	-738,64609	-737,61284	2,0665	0,64415	NS	0	[]	[]	[]	hypothetical protein	PF04148.6	Erv26(Transmembrane adaptor Erv26)

Supercontig_1.46_MVLG_04275_11sp	-661,98305	-661,98305	0	0	NS	0	[]	[]	[]	hypothetical protein	PF07859.6	Abhydrolase_3(alpha/beta hydrolase fold)
Supercontig_1.32_MVLG_03436_8sp	-768,06466	-768,06466	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00400.25	WD40(WD domain, G-beta repeat)
Supercontig_1.7_MVLG_01228_6sp	-693,915	-693,86324	0,10352	0,05044	NS	0	[]	[]	[]	hypothetical protein	PF00443.22	UCH(Ubiquitin carboxyl-terminal hydrolase)
Supercontig_1.18_MVLG_02375_9sp	-1022,3794	-1020,9704	2,81784	0,75559	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.82_MVLG_05721_6sp	-1840,9917	-1840,9917	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02213.9	GYF(GYF domain)
Supercontig_1.7_MVLG_01262_7sp	-636,94725	-635,14994	3,59462	0,83426	NS	0	[]	[]	[]	hypothetical protein	PF01997.9	Translin(Translin family)
Supercontig_1.66_MVLG_05172_7sp	-594,00676	-593,81339	0,38674	0,17582	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.12_MVLG_01879_7sp	-526,16969	-526,08141	0,17656	0,0845	NS	0	[]	[]	[]	hypothetical protein	PF01170.11	UPF0020(Putative RNA methylase family UPF0020)
Supercontig_1.85_MVLG_05812_11sp	-390,25644	-390,22247	0,06794	0,0334	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.40_MVLG_03930_10sp	-462,54708	-462,54707	0	0	NS	0	[]	[]	[]	hypothetical protein	PF07933.7	DUF1681(Protein of unknown function (DUF1681))
Supercontig_1.34_MVLG_03545_6sp	-974,14722	-974,14722	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00125.17	Histone(Core histone H2A/H2B/H3/H4)
Supercontig_1.88_MVLG_05889_9sp	-477,00963	-477,00957	0	0	NS	0	[]	[]	[]	mitochondrial GTP/GDP carrier protein 1	PF00153.20	Mito_carr(Mitochondrial carrier protein)
Supercontig_1.82_MVLG_05723_9sp	-683,72865	-682,68844	2,08042	0,64662	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.12_MVLG_01837_7sp	-463,93779	-463,93779	0	0	NS	0	[]	[]	[]	T-complex protein 1 subunit eta	PF00118.17	Cpn60_TCP1(TCP-1/cpn60 chaperonin family)
Supercontig_1.70_MVLG_05333_8sp	-679,7153	-679,14949	1,13162	0,4321	NS	0	[]	[]	[]	hypothetical protein	PF06775.7	Seipin(Putative adipose-regulatory protein (Seipin))
Supercontig_1.6_MVLG_01113_10sp	-1360,0872	-1360,0872	0	0	NS	0	[]	[]	[]	elongation factor EF-3	PF00005.20	ABC_tran(ABC transporter)
Supercontig_1.41_MVLG_04038_8sp	-522,7198	-522,71976	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01351.11	RNase_HII(Ribonuclease HII)
Supercontig_1.3_MVLG_00509_6sp	-1004,8176	-1004,8176	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00753.20	Lactamase_B(Metallo-beta-lactamase superfamily)
Supercontig_1.5_MVLG_00924_7sp	-524,49533	-524,49533	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00636.19	Ribonuclease_3(RNase3 domain)
Supercontig_1.80_MVLG_05657_9sp	-625,21706	-625,21706	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04434.10	SWIM(SWIM zinc finger)
Supercontig_1.2_MVLG_00429_9sp	-796,465	-796,44097	0,04806	0,02374	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.4_MVLG_00716_7sp	-615,22814	-615,22733	0,00162	0,00081	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.8_MVLG_01459_10sp	-1254,6636	-1254,6636	0	0	NS	0	[]	[]	[]	hypothetical protein	PF06818.8	Fez1(Fez1)
Supercontig_1.78_MVLG_05595_10sp	-388,84673	-388,84673	0	0	NS	0	[]	[]	[]	hypothetical protein	PF11790.1	Glyco_hydro_cc(Glycosyl hydrolase catalytic core)
Supercontig_1.7_MVLG_01317_9sp	-380,65878	-379,03498	3,2476	0,80285	NS	0	[]	[]	[]	hypothetical protein	PF12449.1	DUF3684(Protein of unknown function (DUF3684))

Supercontig_1.33_MVLG_03464_10sp	-805,73715	-805,73689	0,00052	0,00026	NS	0	[]	[]	[]	hypothetical protein	PF00400.25	WD40(WD domain, G-beta repeat)
Supercontig_1.26_MVLG_03004_10sp	-375,2079	-375,20786	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00628.22	PHD(PHD-finger)
Supercontig_1.15_MVLG_02072_7sp	-505,68827	-505,68827	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03171.13	2OG-FeII_Oxy(2OG-Fe(II) oxygenase superfamily)
Supercontig_1.52_MVLG_04558_9sp	-803,77412	-803,77391	0,00042	0,00021	NS	0	[]	[]	[]	hypothetical protein	TIGR00614	TIGR00614(recQ_fam: ATP-dependent DNA helicase, RecQ family)
Supercontig_1.1_MVLG_00168_9sp	-656,64399	-656,62199	0,044	0,02176	NS	0	[]	[]	[]	hypothetical protein	PF02891.13	zf-MIZ(MIZ/SP-RING zinc finger)
Supercontig_1.87_MVLG_05863_12sp	-708,90763	-708,90763	0	0	NS	0	[]	[]	[]	CMGC/DYRK/YAK protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.99_MVLG_06121_8sp	-340,07869	-339,6234	0,91058	0,36574	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.15_MVLG_02087_8sp	-662,49107	-662,49087	0,0004	0,0002	NS	0	[]	[]	[]	succinyl-CoA:3-ketoacid-coenzyme A transferase 1	TIGR02429	TIGR02429(pcaI_scoA_fam: 3-oxoacid CoA-transferase, A subunit)
Supercontig_1.2_MVLG_00452_9sp	-445,51138	-445,51138	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04097.7	Nic96(Nup93/Nic96)
Supercontig_1.64_MVLG_05100_11sp	-1176,7853	-1176,7853	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00176.16	SNF2_N(SNF2 family N-terminal domain)
Supercontig_1.2_MVLG_00410_11sp	-379,54626	-379,54525	0,00202	0,00101	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.36_MVLG_03691_10sp	-302,61474	-302,61473	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.2_MVLG_00341_10sp	-1132,9984	-1131,8044	2,3879	0,69698	NS	0	[]	[]	[]	hypothetical protein	PF01412.11	ArfGap(Putative GTPase activating protein for Arf)
Supercontig_1.2_MVLG_00486_7sp	-459,40421	-459,40421	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.15_MVLG_02111_10sp	-640,33617	-640,33617	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00642.17	zf-CCCH(Zinc finger C-x8-C-x5-C-x3-H type (and similar))
Supercontig_1.46_MVLG_04269_10sp	-557,38024	-557,38024	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01965.17	DJ-1_PfpI(DJ-1/PfpI family)
Supercontig_1.27_MVLG_03113_6sp	-707,55376	-707,26419	0,57914	0,25141	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.65_MVLG_05143_10sp	-508,41323	-508,41314	0,00018	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.27_MVLG_03115_9sp	-652,556	-652,556	0	0	NS	0	[]	[]	[]	hypothetical protein	PF08238.5	Sel1(Sel1 repeat)
Supercontig_1.63_MVLG_05066_9sp	-1240,3133	-1240,3133	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.1_MVLG_00162_7sp	-1261,3503	-1258,9166	4,86748	0,91229	*	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.13_MVLG_01947_7sp	-2420,7516	-2420,7516	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00664.16	ABC_membrane(ABC transporter transmembrane region)
Supercontig_1.65_MVLG_05128_10sp	-471,18665	-471,18646	0,00038	0,00019	NS	0	[]	[]	[]	hypothetical protein	PF00933.14	Glyco_hydro_3(Glycosyl hydrolase family 3 N terminal domain)
Supercontig_1.198_MVLG_07076_11sp	-565,33995	-565,33968	0,00054	0,00027	NS	0	[]	[]	[]	hypothetical protein	NA	NA

Supercontig_1.1_MVLG_00081_9sp	-453,04708	-453,04706	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04064.6	DUF384(Domain of unknown function (DUF384))
Supercontig_1.32_MVLG_03405_11sp	-834,26206	-834,26206	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01408.15	GFO_IDH_MocA(Oxidoreductase family, NAD-binding Rossmann fold)
Supercontig_1.1_MVLG_00064_12sp	-555,89805	-555,21792	1,36026	0,49345	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.36_MVLG_03681_7sp	-364,05683	-364,05676	0,00014	0	NS	0	[]	[]	[]	threonyl-tRNA synthetase, cytoplasmic	TIGR00418	TIGR00418(thrS: threonine--tRNA ligase)
Supercontig_1.38_MVLG_03811_10sp	-575,38653	-575,38653	0	0	NS	0	[]	[]	[]	hypothetical protein	PF07690.9	MFS_1(Major Facilitator Superfamily)
Supercontig_1.11_MVLG_01734_9sp	-447,45372	-447,45355	0,00034	0,00017	NS	0	[]	[]	[]	hypothetical protein	PF02383.11	Syja_N(SacI homology domain)
Supercontig_1.48_MVLG_04399_10sp	-412,03368	-412,03368	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03452.7	Anp1(Anp1)
Supercontig_1.6_MVLG_01057_10sp	-624,60801	-624,60145	0,01312	0,00654	NS	0	[]	[]	[]	hypothetical protein	TIGR00711	TIGR00711(efflux_EmrB: drug resistance MFS transporter, drug:H+ antiporter-2 (14 Spanner) (DHA2) family)
Supercontig_1.80_MVLG_05661_11sp	-460,04952	-460,04906	0,00092	0,00046	NS	0	[]	[]	[]	hypothetical protein	PF00240.16	ubiquitin(Ubiquitin family)
Supercontig_1.34_MVLG_03553_10sp	-553,00949	-553,0088	0,00138	0,00069	NS	0	[]	[]	[]	serine/threonine-protein phosphatase 2B catalytic subunit A1	PF00149.21	Metallophos(Calcineurin-like phosphoesterase)
Supercontig_1.3_MVLG_00570_9sp	-428,27701	-428,27699	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.73_MVLG_05411_6sp	-459,87387	-459,70035	0,34704	0,1593	NS	0	[]	[]	[]	hypothetical protein	TIGR01489	TIGR01489(DKMTPPase-SF: 2,3-diketo-5-methylthio-1-phosphopentane phosphatase)
Supercontig_1.3_MVLG_00590_6sp	-843,9019	-843,9019	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00067.15	p450(Cytochrome P450)
Supercontig_1.33_MVLG_03489_12sp	-390,89919	-389,77559	2,2472	0,67489	NS	0	[]	[]	[]	hypothetical protein	PF01764.18	Lipase_3(Lipase (class 3))
Supercontig_1.46_MVLG_04295_9sp	-645,01814	-645,01808	0,00012	0	NS	0	[]	[]	[]	hypothetical protein	PF00022.12	Actin(Actin)
Supercontig_1.170_MVLG_06942_7sp	-507,41541	-506,58651	1,6578	0,56347	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.16_MVLG_02187_11sp	-596,59227	-596,59227	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03062.12	MBOAT(MBOAT family)
Supercontig_1.25_MVLG_02960_11sp	-342,64265	-342,64265	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04099.5	Sybindin(Sybindin-like family)
Supercontig_1.57_MVLG_04811_12sp	-711,33675	-711,28842	0,09666	0,04718	NS	0	[]	[]	[]	hypothetical protein	PF08729.3	HPC2(Histone promoter control 2 (HPC2))
Supercontig_1.29_MVLG_03249_9sp	-1127,0526	-1127,0526	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.11_MVLG_01784_9sp	-320,21416	-320,21414	0	0	NS	0	[]	[]	[]	hypothetical protein	PF07571.6	DUF1546(Protein of unknown function (DUF1546))
Supercontig_1.74_MVLG_05445_10sp	-403,36235	-401,04686	4,63098	0,90128	*	0	[]	[]	[]	hypothetical protein	PF04401.7	DUF540(Protein of unknown function (DUF540))

Supercontig_1.66_MVLG_05193_10sp	-353,72087	-353,72074	0,00026	0,00013	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.140_MVLG_06681_9sp	-595,18137	-595,18114	0,00046	0,00023	NS	0	[]	[]	[]	hypothetical protein	PF01423.15	LSM(LSM domain)
Supercontig_1.18_MVLG_02421_10sp	-437,22448	-436,88136	0,68624	0,29045	NS	0	[]	[]	[]	hypothetical protein	PF02900.11	LigB(Catalytic LigB subunit of aromatic ring-opening dioxygenase)
Supercontig_1.14_MVLG_02050_7sp	-739,93285	-739,93285	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.40_MVLG_03956_10sp	-648,69204	-648,43228	0,51952	0,22876	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.47_MVLG_04308_10sp	-667,14469	-666,86856	0,55226	0,24129	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.12_MVLG_01866_7sp	-660,59081	-660,5904	0,00082	0,00041	NS	0	[]	[]	[]	hypothetical protein	PF02889.9	Sec63(Sec63 Brl domain)
Supercontig_1.66_MVLG_05163_9sp	-357,09842	-356,95599	0,28486	0,13275	NS	0	[]	[]	[]	hypothetical protein	PF08530.3	PepX_C(X-Pro dipeptidyl-peptidase C-terminal non-catalytic domain)
Supercontig_1.64_MVLG_05114_8sp	-531,54983	-530,26909	2,56148	0,72217	NS	0	[]	[]	[]	hypothetical protein	TIGR00907	TIGR00907(2A0304: amino acid permease)
Supercontig_1.24_MVLG_02899_8sp	-708,41566	-708,41558	0,00016	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.50_MVLG_04452_9sp	-700,3931	-700,3931	0	0	NS	0	[]	[]	[]	hypothetical protein	PF05871.5	ESCRT-II(ESCRT-II complex subunit)
Supercontig_1.32_MVLG_03392_7sp	-878,81466	-878,81466	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00856.21	SET(SET domain)
Supercontig_1.32_MVLG_03407_8sp	-386,35406	-383,21294	6,28224	0,95677	**	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.102_MVLG_06179_9sp	-400,11999	-400,11997	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.41_MVLG_03981_7sp	-538,72053	-538,72029	0	0	NS	0	[]	[]	[]	nucleolar protein 58	PF08156.6	NOP5NT(NOP5NT (NUC127) domain)
Supercontig_1.16_MVLG_02175_6sp	-278,68518	-278,6851	0	0	NS	0	[]	[]	[]	hypothetical protein	TIGR01126	TIGR01126(pdi_dom: protein disulfide-isomerase domain)
Supercontig_1.51_MVLG_04502_10sp	-600,63552	-600,63552	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03407.9	Nucleotid_trans(Nucleotide-diphospho-sugar transferase)
Supercontig_1.53_MVLG_04613_9sp	-667,21088	-667,21088	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.1_MVLG_00010_10sp	-590,73061	-590,73061	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03248.6	Rer1(Rer1 family)
Supercontig_1.58_MVLG_04853_10sp	-660,12612	-660,12098	0,01028	0,00513	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.3_MVLG_00603_8sp	-439,73891	-439,7388	0,00022	0,00011	NS	0	[]	[]	[]	rab family, other	PF08477.6	Miro(Miro-like protein)
Supercontig_1.121_MVLG_06439_12sp	-414,76567	-412,82911	3,87312	0,8558	NS	0	[]	[]	[]	hypothetical protein	PF05739.12	SNARE(SNARE domain)
Supercontig_1.20_MVLG_02587_9sp	-968,1843	-968,1843	0	0	NS	0	[]	[]	[]	hypothetical protein	PF07716.8	bZIP_2(Basic region leucine zipper)
Supercontig_1.7_MVLG_01294_8sp	-1107,4385	-1107,4385	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02585.10	PIG-L(GlcNAc-PI de-N-acetylase)

Supercontig_1.104_MVLG_06204_8sp	-373,349	-372,35174	1,99452	0,63111	NS	0	[]	[]	[]	hypothetical protein	PF00582.19	Usp(Universal stress protein family)
Supercontig_1.10_MVLG_01654_8sp	-468,16102	-468,16103	0	0	NS	0	[]	[]	[]	tubulin binding cofactor A	PF02970.9	TBCA(Tubulin binding cofactor A)
Supercontig_1.15_MVLG_02082_10sp	-254,32878	-254,32878	0	0	NS	0	[]	[]	[]	lactoylglutathione lyase	PF00903.18	Glyoxalase(Glyoxalase/Bleomycin resistance protein/Dioxygenase superfamily)
Supercontig_1.40_MVLG_03940_10sp	-700,88955	-699,31606	3,14698	0,79268	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.21_MVLG_02636_9sp	-988,25689	-988,25689	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.19_MVLG_02434_6sp	-951,41418	-951,3295	0,16936	0,08119	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.4_MVLG_00873_8sp	-457,04858	-457,04858	0	0	NS	0	[]	[]	[]	replication factor C subunit 4	PF08542.4	Rep_fac_C(Replication factor C)
Supercontig_1.10_MVLG_01617_6sp	-373,34541	-373,34502	0,00078	0,00039	NS	0	[]	[]	[]	histone	PF00125.17	Histone(Core histone H2A/H2B/H3/H4)
Supercontig_1.124_MVLG_06490_8sp	-350,78662	-350,74444	0,08436	0,0413	NS	0	[]	[]	[]	hypothetical protein	PF00076.15	RRM_1(RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain))
Supercontig_1.4_MVLG_00689_7sp	-1225,2061	-1223,7254	2,96142	0,77252	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.22_MVLG_02692_8sp	-457,1914	-457,1914	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.62_MVLG_05035_9sp	-584,01012	-584,00998	0,00028	0,00014	NS	0	[]	[]	[]	DNA mismatch repair protein MSH2	PF05188.10	MutS_II(MutS domain II)
Supercontig_1.19_MVLG_02452_8sp	-488,78308	-488,06758	1,431	0,51105	NS	0	[]	[]	[]	hypothetical protein	TIGR00628	TIGR00628(ung: uracil-DNA glycosylase)
Supercontig_1.3_MVLG_00516_7sp	-677,12062	-677,12062	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02269.9	TFIID-18kDa(Transcription initiation factor IID, 18kD subunit)
Supercontig_1.67_MVLG_05230_7sp	-1412,8872	-1412,8872	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02900.11	LigB(Catalytic LigB subunit of aromatic ring-opening dioxygenase)
Supercontig_1.58_MVLG_04874_10sp	-1169,87	-1168,5755	2,58904	0,72597	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.24_MVLG_02845_7sp	-479,78934	-479,78934	0	0	NS	0	[]	[]	[]	aldehyde reductase 1	PF00248.14	Aldo_ket_red(Aldo/keto reductase family)
Supercontig_1.63_MVLG_05067_7sp	-364,58524	-364,58524	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.36_MVLG_03685_6sp	-1226,0104	-1223,9746	4,07156	0,86942	NS	0	[]	[]	[]	hypothetical protein	PF03619.9	DUF300(Domain of unknown function)
Supercontig_1.16_MVLG_02162_8sp	-291,65496	-291,65489	0,00014	0	NS	0	[]	[]	[]	3-ketoacyl-CoA thiolase	TIGR01930	TIGR01930(AcCoA-C-Actrans: acetyl-CoA C-acetyltransferase)
Supercontig_1.8_MVLG_01443_12sp	-496,71584	-495,23482	2,96204	0,77259	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.22_MVLG_02749_9sp	-1521,9731	-1521,9731	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00245.13	Alk_phosphatase(Alkaline phosphatase)
Supercontig_1.18_MVLG_02386_12sp	-437,35198	-437,35198	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00364.15	Biotin_lipoyl(Biotin-requiring enzyme)

Supercontig_1.16_MVLG_02168_6sp	-565,41725	-565,4172	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00179.19	UQ_con(Ubiquitin-conjugating enzyme)
Supercontig_1.19_MVLG_02479_7sp	-371,63964	-371,53553	0,20822	0,09887	NS	0	[]	[]	[]	cytoplasm protein	PF02421.11	FeoB_N(Ferrous iron transport protein B)
Supercontig_1.32_MVLG_03411_7sp	-791,37204	-790,17637	2,39134	0,6975	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.22_MVLG_02722_11sp	-300,66342	-300,66337	0	0	NS	0	[]	[]	[]	60S ribosomal protein L16	TIGR01077	TIGR01077(L13_A_E: ribosomal protein L13)
Supercontig_1.20_MVLG_02528_10sp	-693,18427	-691,69948	2,96958	0,77345	NS	0	[]	[]	[]	hypothetical protein	PF02902.12	Peptidase_C48(Ulp1 protease family, C-terminal catalytic domain)
Supercontig_1.4_MVLG_00732_8sp	-545,90539	-545,90533	0,00012	0	NS	0	[]	[]	[]	hypothetical protein	PF00270.22	DEAD(DEAD/DEAH box helicase)
Supercontig_1.104_MVLG_06200_10sp	-1464,2826	-1464,2823	0,00064	0,00032	NS	0	[]	[]	[]	2-oxoglutarate dehydrogenase	PF00676.13	E1_dh(Dehydrogenase E1 component)
Supercontig_1.35_MVLG_03625_7sp	-1693,6242	-1693,4138	0,4208	0,18974	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.30_MVLG_03257_10sp	-1188,1769	-1186,5636	3,2267	0,80078	NS	0	[]	[]	[]	hypothetical protein	PF00018.21	SH3_1(SH3 domain)
Supercontig_1.9_MVLG_01505_10sp	-1179,3828	-1179,3828	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.12_MVLG_01854_10sp	-553,24713	-553,15889	0,17648	0,08446	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.25_MVLG_02948_10sp	-669,12403	-669,12402	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.5_MVLG_00925_9sp	-427,54318	-427,54318	0	0	NS	0	[]	[]	[]	hypothetical protein	PF10199.2	Adaptin_binding(Alpha and gamma adaptin binding protein p34)
Supercontig_1.17_MVLG_02295_9sp	-378,36859	-378,36736	0,00246	0,00123	NS	0	[]	[]	[]	hypothetical protein	PF01494.12	FAD_binding_3(FAD binding domain)
Supercontig_1.5_MVLG_00952_8sp	-780,83293	-780,83293	0	0	NS	0	[]	[]	[]	hypothetical protein	PF09424.3	YqeY(Yqey-like protein)
Supercontig_1.41_MVLG_03982_9sp	-594,18731	-594,18719	0,00024	0,00012	NS	0	[]	[]	[]	hypothetical protein	PF00400.25	WD40(WD domain, G-beta repeat)
Supercontig_1.6_MVLG_01097_7sp	-340,13288	-338,30811	3,64954	0,83875	NS	0	[]	[]	[]	hypothetical protein	PF03311.7	Cornichon(Cornichon protein)
Supercontig_1.11_MVLG_01747_10sp	-461,95429	-461,9542	0,00018	0	NS	0	[]	[]	[]	tryptophanyl-tRNA synthetase	TIGR00233	TIGR00233(trpS: tryptophan--tRNA ligase)
Supercontig_1.2_MVLG_00437_7sp	-464,67549	-464,67549	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01106.10	NifU(NifU-like domain)
Supercontig_1.88_MVLG_05888_8sp	-333,8771	-333,87707	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00179.19	UQ_con(Ubiquitin-conjugating enzyme)
Supercontig_1.7_MVLG_01330_8sp	-889,10816	-889,08802	0,04028	0,01994	NS	0	[]	[]	[]	L-aminoadipate-semialdehyde dehydrogenase	PF01073.12	3Beta_HSD(3-beta hydroxysteroid dehydrogenase/isomerase family)
Supercontig_1.32_MVLG_03427_8sp	-460,09276	-459,06649	2,05254	0,64166	NS	0	[]	[]	[]	hypothetical protein	PF08477.6	Miro(Miro-like protein)
Supercontig_1.9_MVLG_01529_8sp	-1443,1236	-1443,1236	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.117_MVLG_06392_8sp	-1219,2279	-1219,2279	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00225.16	Kinesin(Kinesin motor domain)

Supercontig_1.3_MVLG_00600_8sp	-1140,5945	-1140,5945	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.100_MVLG_06146_7sp	-1293,9375	-1291,9098	4,05536	0,86836	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.35_MVLG_03629_7sp	-1340,5968	-1340,2495	0,6946	0,29341	NS	0	[]	[]	[]	hypothetical protein	PF08642.3	Rxt3(Histone deacetylation protein Rxt3)
Supercontig_1.75_MVLG_05496_10sp	-780,01772	-779,81295	0,40954	0,18517	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.65_MVLG_05126_8sp	-1116,1121	-1116,1121	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02487.10	CLN3(CLN3 protein)
Supercontig_1.123_MVLG_06479_7sp	-760,49611	-760,49611	0	0	NS	0	[]	[]	[]	hypothetical protein	PF10558.2	MTP18(Mitochondrial 18 KDa protein (MTP18))
Supercontig_1.9_MVLG_01477_8sp	-418,38331	-418,38317	0,00028	0,00014	NS	0	[]	[]	[]	hypothetical protein	PF10153.2	DUF2361(Uncharacterised conserved protein (DUF2361))
Supercontig_1.180_MVLG_06996_10sp	-453,81903	-453,81882	0,00042	0,00021	NS	0	[]	[]	[]	large subunit ribosomal protein L14e	PF00467.22	KOW(KOW motif)
Supercontig_1.10_MVLG_01678_7sp	-734,0621	-734,0621	0	0	NS	0	[]	[]	[]	hypothetical protein	PF07690.9	MFS_1(Major Facilitator Superfamily)
Supercontig_1.6_MVLG_01063_9sp	-515,44561	-515,44101	0,0092	0,00459	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.2_MVLG_00479_10sp	-269,66206	-269,66205	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00249.24	Myb_DNA-binding(Myb-like DNA-binding domain)
Supercontig_1.14_MVLG_01988_9sp	-756,18947	-756,18933	0,00028	0,00014	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.65_MVLG_05124_10sp	-844,42299	-844,42299	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01467.19	CTP_transf_2(Cytidylyltransferase)
Supercontig_1.35_MVLG_03618_9sp	-457,71454	-457,50577	0,41754	0,18842	NS	0	[]	[]	[]	hypothetical protein	PF00107.19	ADH_zinc_N(Zinc-binding dehydrogenase)
Supercontig_1.40_MVLG_03942_8sp	-717,31326	-717,31325	0	0	NS	0	[]	[]	[]	hypothetical protein	TIGR02777	TIGR02777(LigD_PE_dom: DNA ligase D, 3'-phosphoesterase domain)
Supercontig_1.79_MVLG_05618_10sp	-415,5285	-415,5285	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01656.16	CbiA(CobQ/CobB/MinD/ParA nucleotide binding domain)
Supercontig_1.3_MVLG_00602_6sp	-1517,1145	-1517,1009	0,02728	0,01355	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.18_MVLG_02392_7sp	-310,41971	-310,41971	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.24_MVLG_02870_8sp	-687,61942	-687,61907	0,0007	0,00035	NS	0	[]	[]	[]	hypothetical protein	PF02798.13	GST_N(Glutathione S-transferase, N-terminal domain)
Supercontig_1.1_MVLG_00258_7sp	-673,12206	-670,82414	4,59584	0,89953	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.2_MVLG_00325_10sp	-419,53298	-419,53283	0,0003	0,00015	NS	0	[]	[]	[]	hypothetical protein	PF04115.5	Ureidogly_hydro(Ureidoglycolate hydrolase)
Supercontig_1.3_MVLG_00569_8sp	-1095,5312	-1095,5312	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00621.13	RhoGEF(RhoGEF domain)
Supercontig_1.156_MVLG_06838_6sp	-866,33434	-866,33434	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00447.10	HSF_DNA-bind(HSF-type DNA-binding)
Supercontig_1.7_MVLG_01329_11sp	-470,38214	-470,38211	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00153.20	Mito_carr(Mitochondrial carrier protein)

Supercontig_1.27_MVLG_03117_8sp	-406,03078	-406,03078	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01480.10	PWI(PWI domain)
Supercontig_1.24_MVLG_02852_12sp	-599,15112	-597,87836	2,54552	0,71994	NS	0	[]	[]	[]	hypothetical protein	PF00400.25	WD40(WD domain, G-beta repeat)
Supercontig_1.55_MVLG_04736_10sp	-545,70228	-545,70228	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.91_MVLG_05935_10sp	-700,35471	-699,81646	1,0765	0,41623	NS	0	[]	[]	[]	hypothetical protein	PF00326.14	Peptidase_S9(Prolyl oligopeptidase family)
Supercontig_1.35_MVLG_03628_7sp	-451,55467	-451,55459	0,00016	0	NS	0	[]	[]	[]	hypothetical protein	PF01553.14	Acyltransferase(Acyltransferase)
Supercontig_1.28_MVLG_03192_8sp	-1120,2954	-1120,2954	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.163_MVLG_06882_8sp	-1353,9163	-1353,8334	0,16572	0,07952	NS	0	[]	[]	[]	hypothetical protein	PF11707.1	Npa1(Ribosome 60S biogenesis N-terminal)
Supercontig_1.1_MVLG_00135_10sp	-304,64725	-304,64723	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.16_MVLG_02158_10sp	-1036,5237	-1036,5237	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.2_MVLG_00430_6sp	-477,36523	-476,93875	0,85296	0,3472	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.16_MVLG_02238_9sp	-371,09103	-371,09103	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00828.12	Ribosomal_L18e(Ribosomal protein L18e/L15)
Supercontig_1.4_MVLG_00798_10sp	-1140,0987	-1139,9446	0,30812	0,14278	NS	0	[]	[]	[]	hypothetical protein	PF01208.10	URO-D(Uroporphyrinogen decarboxylase (URO-D))
Supercontig_1.164_MVLG_06894_8sp	-933,44093	-933,44093	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03853.8	YjeF_N(YjeF-related protein N-terminus)
Supercontig_1.22_MVLG_02762_7sp	-685,03795	-683,21013	3,65564	0,83924	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.67_MVLG_05221_10sp	-1988,8737	-1988,8737	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.1_MVLG_00263_10sp	-777,74843	-777,7105	0,07586	0,03722	NS	0	[]	[]	[]	hypothetical protein	PF00773.12	RNB(RNB domain)
Supercontig_1.15_MVLG_02143_6sp	-1452,2565	-1452,2565	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02990.9	EMP70(Endomembrane protein 70)
Supercontig_1.12_MVLG_01862_9sp	-1071,8021	-1070,1901	3,22396	0,80051	NS	0	[]	[]	[]	hypothetical protein	PF00010.19	HLH(Helix-loop-helix DNA-binding domain)
Supercontig_1.8_MVLG_01415_9sp	-640,13287	-640,13287	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02179.9	BAG(BAG domain)
Supercontig_1.39_MVLG_03886_6sp	-340,63815	-340,63815	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01266.17	DAO(FAD dependent oxidoreductase)
Supercontig_1.75_MVLG_05492_8sp	-614,91236	-614,9123	0,00012	0	NS	0	[]	[]	[]	hypothetical protein	PF00172.11	Zn_clus(Fungal Zn(2)-Cys(6) binuclear cluster domain)
Supercontig_1.38_MVLG_03791_6sp	-1045,6437	-1045,6437	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.172_MVLG_06953_7sp	-459,51078	-459,51078	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00096.19	zf-C2H2(Zinc finger, C2H2 type)
Supercontig_1.15_MVLG_02149_9sp	-388,61136	-388,61107	0,00058	0,00029	NS	0	[]	[]	[]	hypothetical protein	PF00578.14	AhpC-TSA(AhpC/TSA family)
Supercontig_1.22_MVLG_02714_8sp	-1283,4354	-1283,196	0,47872	0,21287	NS	0	[]	[]	[]	hypothetical protein	PF07928.5	Vps54(Vps54-like protein)
Supercontig_1.131_MVLG_06574_9sp	-275,62774	-275,25197	0,75154	0,31324	NS	0	[]	[]	[]	hypothetical protein	PF03357.14	Snf7(Snf7)

Supercontig_1.122_MVLG_06468_8sp	-536,34447	-533,71449	5,25996	0,92792	*	0	[]	[]	[]	hypothetical protein	PF00657.15	Lipase_GDSL(GDSL-like Lipase/Acylhydrolase)
Supercontig_1.52_MVLG_04569_8sp	-342,10158	-342,10145	0,00026	0,00013	NS	0	[]	[]	[]	hypothetical protein	PF02627.13	CMD(Carboxymuconolactone decarboxylase family)
Supercontig_1.57_MVLG_04829_12sp	-717,42882	-716,63056	1,59652	0,54989	NS	0	[]	[]	[]	hypothetical protein	PF04157.9	EAP30(EAP30/Vps36 family)
Supercontig_1.18_MVLG_02395_9sp	-1155,9579	-1155,9578	0,00026	0,00013	NS	0	[]	[]	[]	hypothetical protein	PF00018.21	SH3_1(SH3 domain)
Supercontig_1.21_MVLG_02663_8sp	-468,4639	-468,4639	0	0	NS	0	[]	[]	[]	hypothetical protein	PF06201.6	PITH(C-terminal proteasome-interacting domain of thioredoxin-like)
Supercontig_1.52_MVLG_04577_11sp	-498,25936	-498,25932	0	0	NS	0	[]	[]	[]	hypothetical protein	PF08700.4	Vps51(Vps51/Vps67)
Supercontig_1.79_MVLG_05623_9sp	-880,07155	-880,07155	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02163.15	Peptidase_M50(Peptidase family M50)
Supercontig_1.50_MVLG_04482_12sp	-1032,4365	-1032,4365	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.2_MVLG_00443_12sp	-713,79636	-713,79636	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.13_MVLG_01956_9sp	-511,88182	-511,90603	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.34_MVLG_03570_8sp	-367,06827	-366,49508	1,14638	0,43628	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.35_MVLG_03622_7sp	-767,97306	-767,97305	0	0	NS	0	[]	[]	[]	tubulin-tyrosine ligase	PF03133.8	TTL(Tubulin-tyrosine ligase family)
Supercontig_1.50_MVLG_04467_7sp	-554,61443	-554,61443	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03366.9	YEATS(YEATS family)
Supercontig_1.196_MVLG_07062_9sp	-443,75397	-443,75393	0	0	NS	0	[]	[]	[]	40S ribosomal protein S24	PF01282.12	Ribosomal_S24e(Ribosomal protein S24e)
Supercontig_1.116_MVLG_06370_9sp	-489,2565	-489,2565	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00155.14	Aminotran_1_2(Aminotransferase class I and II)
Supercontig_1.11_MVLG_01701_9sp	-644,55543	-644,55543	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04724.6	Glyco_transf_17(Glycosyltransferase family 17)
Supercontig_1.10_MVLG_01672_9sp	-550,68967	-550,65133	0,07668	0,03761	NS	0	[]	[]	[]	hypothetical protein	PF01753.11	zf-MYND(MYND finger)
Supercontig_1.6_MVLG_01199_9sp	-1255,8076	-1255,4818	0,6516	0,27805	NS	0	[]	[]	[]	hypothetical protein	PF04707.7	PRELI(PRELI-like family)
Supercontig_1.20_MVLG_02582_7sp	-1369,3871	-1369,3389	0,09652	0,04711	NS	0	[]	[]	[]	hypothetical protein	PF00611.16	FCH(Fes/CIP4 homology domain)
Supercontig_1.388_MVLG_07257_7sp	-322,15437	-322,15432	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.6_MVLG_01131_8sp	-413,69729	-413,67348	0,04762	0,02353	NS	0	[]	[]	[]	cytochrome b-c1 complex subunit Rieske	PF02921.7	UCR_TM(Ubiquinol cytochrome reductase transmembrane region)
Supercontig_1.78_MVLG_05578_8sp	-892,62696	-892,6269	0,00012	5.99982001118831e-05	NS	0	[]	[]	[]	CMGC/CDK protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.58_MVLG_04865_8sp	-627,47552	-627,47551	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA

Supercontig_1.10_MVLG_01631_7sp	-510,90319	-510,90319	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02270.8	TFIIF_beta(Transcription initiation factor IIF, beta subunit)
Supercontig_1.92_MVLG_05946_10sp	-405,92942	-405,92941	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.17_MVLG_02319_10sp	-587,15186	-587,15186	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.46_MVLG_04263_7sp	-1075,5885	-1075,5885	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02724.7	CDC45(CDC45-like protein)
Supercontig_1.86_MVLG_05835_9sp	-422,13171	-421,2668	1,72982	0,57891	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.82_MVLG_05720_7sp	-483,70528	-482,00267	3,40522	0,81779	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.116_MVLG_06372_8sp	-1911,785	-1910,8871	1,79584	0,59258	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.1_MVLG_00159_11sp	-1585,3265	-1584,9134	0,82618	0,3384	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.213_MVLG_07132_10sp	-725,45444	-725,45444	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.7_MVLG_01286_6sp	-614,177	-614,177	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.15_MVLG_02057_8sp	-1062,329	-1061,6809	1,2962	0,47696	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.112_MVLG_06334_6sp	-414,68595	-414,68594	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00646.26	F-box(F-box domain)
Supercontig_1.173_MVLG_06961_6sp	-535,56663	-535,56655	0,00016	0	NS	0	[]	[]	[]	hypothetical protein	PF01302.18	CAP_GLY(CAP-Gly domain)
Supercontig_1.9_MVLG_01476_9sp	-886,25533	-886,25533	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01435.11	Peptidase_M48(Peptidase family M48)
Supercontig_1.51_MVLG_04498_9sp	-786,32705	-786,10716	0,43978	0,19739	NS	0	[]	[]	[]	hypothetical protein	PF00560.26	LRR_1(Leucine Rich Repeat)
Supercontig_1.79_MVLG_05613_7sp	-618,34288	-618,22077	0,24422	0,11495	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.8_MVLG_01452_10sp	-508,71351	-508,71351	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00107.19	ADH_zinc_N(Zinc-binding dehydrogenase)
Supercontig_1.1_MVLG_00157_8sp	-340,75381	-340,75381	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.23_MVLG_02764_10sp	-692,86562	-692,85542	0,0204	0,01015	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.29_MVLG_03252_10sp	-714,24399	-714,24375	0,00048	0,00024	NS	0	[]	[]	[]	glucose-6-phosphate 1-dehydrogenase	PF00479.15	G6PD_N(Glucose-6-phosphate dehydrogenase, NAD binding domain)
Supercontig_1.19_MVLG_02456_7sp	-699,39953	-699,39943	0,0002	0	NS	0	[]	[]	[]	hypothetical protein	PF00076.15	RRM_1(RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain))
Supercontig_1.4_MVLG_00691_9sp	-992,79828	-992,79828	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00621.13	RhoGEF(RhoGEF domain)
Supercontig_1.3_MVLG_00505_10sp	-509,37575	-508,88101	0,98948	0,39027	NS	0	[]	[]	[]	histidinol-phosphatase (PHP family)	PF02811.12	PHP(PHP domain)
Supercontig_1.212_MVLG_07128_8sp	-522,42067	-522,42067	0	0	NS	0	[]	[]	[]	hypothetical protein	PF06441.5	EHN(Epoxide hydrolase N terminus)

Supercontig_1.17_MVLG_02292_8sp	-559,39221	-559,39217	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.85_MVLG_05788_9sp	-465,11503	-465,11503	0	0	NS	0	[]	[]	[]	hypothetical protein	PF08293.4	MRP-S33(Mitochondrial ribosomal subunit S27)
Supercontig_1.1_MVLG_00199_10sp	-339,29761	-339,29761	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00645.11	zf-PARP(Poly(ADP-ribose) polymerase and DNA-Ligase Zn-finger region)
Supercontig_1.25_MVLG_02983_8sp	-853,31561	-853,31561	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04427.11	Brix(Brix domain)
Supercontig_1.24_MVLG_02900_7sp	-738,32274	-738,24103	0,16342	0,07846	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.22_MVLG_02761_7sp	-1227,7208	-1227,6664	0,1088	0,05295	NS	0	[]	[]	[]	hypothetical protein	PF04146.8	YTH(YT521-B-like family)
Supercontig_1.44_MVLG_04136_9sp	-630,88574	-630,88568	0,00012	0	NS	0	[]	[]	[]	hypothetical protein	PF03142.8	Chitin_synth_2(Chitin synthase)
Supercontig_1.8_MVLG_01444_8sp	-385,89747	-385,89747	0	0	NS	0	[]	[]	[]	hypothetical protein	PF11654.1	DUF2665(Protein of unknown function (DUF2665))
Supercontig_1.80_MVLG_05640_9sp	-356,25356	-356,14568	0,21576	0,10226	NS	0	[]	[]	[]	hypothetical protein	PF02466.12	Tim17(Tim17/Tim22/Tim23 family)
Supercontig_1.29_MVLG_03251_11sp	-841,4397	-841,08664	0,70612	0,29746	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.31_MVLG_03365_12sp	-796,99014	-796,70853	0,56322	0,24543	NS	0	[]	[]	[]	BUB protein kinase	PF00069.18	Pkinase(Protein kinase domain)
Supercontig_1.3_MVLG_00630_6sp	-404,53584	-404,30697	0,45774	0,20457	NS	0	[]	[]	[]	ABC1 atypical protein kinase	PF03109.9	ABC1(ABC1 family)
Supercontig_1.69_MVLG_05311_9sp	-424,14512	-424,1451	0	0	NS	0	[]	[]	[]	hypothetical protein	PF09813.2	Coiled-coil_56(Coiled-coil domain-containing protein 56)
Supercontig_1.48_MVLG_04392_8sp	-481,56955	-481,25426	0,63058	0,27042	NS	0	[]	[]	[]	hypothetical protein	PF00472.13	RF-1(RF-1 domain)
Supercontig_1.77_MVLG_05543_10sp	-569,75013	-568,87903	1,7422	0,58151	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.67_MVLG_05217_9sp	-683,73561	-683,73542	0,00038	0,00019	NS	0	[]	[]	[]	hypothetical protein	PF00270.22	DEAD(DEAD/DEAH box helicase)
Supercontig_1.74_MVLG_05474_11sp	-867,33805	-866,77356	1,12898	0,43135	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.55_MVLG_04737_8sp	-382,80156	-382,80156	0	0	NS	0	[]	[]	[]	hypothetical protein	PF10497.2	zf-4CXXC_R1(Zinc-finger domain of monoamine-oxidase A repressor R1)
Supercontig_1.95_MVLG_06012_10sp	-634,36377	-634,36377	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.38_MVLG_03806_8sp	-517,17191	-517,17191	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00572.11	Ribosomal_L13(Ribosomal protein L13)
Supercontig_1.54_MVLG_04655_7sp	-1762,9506	-1762,9506	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.5_MVLG_00918_9sp	-332,73105	-332,73085	0,0004	0,0002	NS	0	[]	[]	[]	hypothetical protein	PF01148.13	CTP_transf_1(Cytidylyltransferase family)
Supercontig_1.4_MVLG_00767_9sp	-470,14047	-470,14047	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00164.18	Ribosomal_S12(Ribosomal protein S12)
Supercontig_1.60_MVLG_04923_7sp	-1153,0181	-1152,4324	1,17154	0,44332	NS	0	[]	[]	[]	hypothetical protein	PF07217.4	Het-C(Heterokaryon incompatibility protein Het-C)
Supercontig_1.60_MVLG_04929_7sp	-671,29424	-671,29411	0,00026	0,00013	NS	0	[]	[]	[]	hypothetical protein	PF03765.8	CRAL_TRIO_N(CRAL/TRIO, N-terminus)

Supercontig_1.6_MVLG_01064_8sp	-802,17422	-802,17365	0,00114	0,00057	NS	0	[]	[]	[]	minichromosome maintenance protein 6	PF00493.16	MCM(MCM2/3/5 family)
Supercontig_1.58_MVLG_04873_11sp	-369,42918	-369,42899	0,00038	0,00019	NS	0	[]	[]	[]	3-hydroxyacyl-CoA dehydrogenase	PF00725.15	3HCDH(3-hydroxyacyl-CoA dehydrogenase, C-terminal domain)
Supercontig_1.88_MVLG_05894_7sp	-476,48878	-476,20907	0,55942	0,244	NS	0	[]	[]	[]	hypothetical protein	PF08547.5	CIA30(Complex I intermediate-associated protein 30 (CIA30))
Supercontig_1.4_MVLG_00717_10sp	-323,51502	-323,51501	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.142_MVLG_06706_8sp	-490,17531	-490,17516	0,0003	0,00015	NS	0	[]	[]	[]	hypothetical protein	PF04099.5	Sybindin(Sybindin-like family)
Supercontig_1.42_MVLG_04042_9sp	-392,80093	-392,80093	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00707.15	IF3_C(Translation initiation factor IF-3, C-terminal domain)
Supercontig_1.35_MVLG_03584_10sp	-429,06314	-429,02828	0,06972	0,03426	NS	0	[]	[]	[]	hypothetical protein	PF00106.18	adh_short(short chain dehydrogenase)
Supercontig_1.70_MVLG_05315_9sp	-582,25419	-582,25412	0,00014	0	NS	0	[]	[]	[]	hypothetical protein	PF00067.15	p450(Cytochrome P450)
Supercontig_1.5_MVLG_01046_9sp	-609,69682	-609,6966	0,00044	0,00022	NS	0	[]	[]	[]	hypothetical protein	PF03935.8	SKN1(Beta-glucan synthesis-associated protein (SKN1))
Supercontig_1.125_MVLG_06511_7sp	-1177,7356	-1177,7356	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.6_MVLG_01056_12sp	-715,10801	-715,10801	0	0	NS	0	[]	[]	[]	hypothetical protein	PF06087.5	Tyr-DNA_phospho(Tyrosyl-DNA phosphodiesterase)
Supercontig_1.65_MVLG_05137_9sp	-348,10609	-348,10608	0	0	NS	0	[]	[]	[]	hypothetical protein	PF08209.4	Sgf11(Sgf11 (transcriptional regulation protein))
Supercontig_1.67_MVLG_05208_8sp	-458,91796	-458,91787	0,00018	0	NS	0	[]	[]	[]	hypothetical protein	PF01237.11	Oxysterol_BP(Oxysterol-binding protein)
Supercontig_1.3_MVLG_00612_10sp	-934,38084	-934,38084	0	0	NS	0	[]	[]	[]	hypothetical protein	PF08022.5	FAD_binding_8(FAD-binding domain)
Supercontig_1.49_MVLG_04446_8sp	-458,07945	-457,29967	1,55956	0,54149	NS	0	[]	[]	[]	hypothetical protein	PF00675.13	Peptidase_M16(Insulinase (Peptidase family M16))
Supercontig_1.141_MVLG_06699_8sp	-320,75578	-320,44574	0,62008	0,26658	NS	0	[]	[]	[]	hypothetical protein	PF01883.12	DUF59(Domain of unknown function DUF59)
Supercontig_1.96_MVLG_06041_7sp	-348,20536	-346,71697	2,97678	0,77426	NS	0	[]	[]	[]	hypothetical protein	PF00825.11	Ribonuclease_P(Ribonuclease P)
Supercontig_1.14_MVLG_01989_7sp	-657,0143	-657,01429	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04113.7	Gpi16(Gpi16 subunit, GPI transamidase component)
Supercontig_1.59_MVLG_04908_8sp	-354,36996	-354,36986	0,0002	0	NS	0	[]	[]	[]	hypothetical protein	PF02656.8	DUF202(Domain of unknown function DUF)
Supercontig_1.46_MVLG_04283_6sp	-820,91942	-819,16617	3,5065	0,82679	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.2_MVLG_00349_10sp	-760,5142	-760,5142	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00439.18	Bromodomain(Bromodomain)
Supercontig_1.79_MVLG_05612_8sp	-449,8086	-449,19564	1,22592	0,45826	NS	0	[]	[]	[]	hypothetical protein	PF00929.17	Exonuc_X-T(Exonuclease)
Supercontig_1.135_MVLG_06636_12sp	-529,47896	-528,88071	1,1965	0,45023	NS	0	[]	[]	[]	hypothetical protein	PF04851.8	ResIII(Type III restriction enzyme, res subunit)
Supercontig_1.2_MVLG_00305_9sp	-580,69015	-580,69013	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA

Supercontig_1.3_MVLG_00646_10sp	-858,59879	-857,68857	1,82044	0,59756	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.78_MVLG_05591_7sp	-629,04794	-628,31299	1,4699	0,52047	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.7_MVLG_01299_8sp	-326,19441	-326,1943	0,00022	0,00011	NS	0	[]	[]	[]	DNA-directed RNA polymerase III subunit RPC10	PF02150.9	RNA_POL_M_15KD(RNA polymerases M/15 Kd subunit)
Supercontig_1.73_MVLG_05421_10sp	-449,90961	-449,90949	0,00024	0,00012	NS	0	[]	[]	[]	hypothetical protein	TIGR01425	TIGR01425(SRP54_euk: signal recognition particle protein SRP54)
Supercontig_1.112_MVLG_06335_7sp	-842,57622	-841,69904	1,75436	0,58405	NS	0	[]	[]	[]	hypothetical protein	PF00673.14	Ribosomal_L5_C(ribosomal L5P family C-terminus)
Supercontig_1.1_MVLG_00013_9sp	-844,26652	-843,65598	1,22108	0,45694	NS	0	[]	[]	[]	hypothetical protein	PF01532.13	Glyco_hydro_47(Glycosyl hydrolase family 47)
Supercontig_1.44_MVLG_04161_9sp	-906,8841	-905,9546	1,859	0,60525	NS	0	[]	[]	[]	hypothetical protein	PF08911.4	NUP50(NUP50 (Nucleoporin 50 kDa))
Supercontig_1.17_MVLG_02266_11sp	-356,74471	-356,74464	0,00014	0	NS	0	[]	[]	[]	hypothetical protein	PF00564.17	PB1(PB1 domain)
Supercontig_1.1_MVLG_00214_11sp	-1213,2819	-1213,2819	0	0	NS	0	[]	[]	[]	hypothetical protein	PF05178.5	Kri1(KRI1-like family)
Supercontig_1.131_MVLG_06575_10sp	-599,35493	-599,35463	0,0006	0,0003	NS	0	[]	[]	[]	hypothetical protein	PF00063.14	Myosin_head(Myosin head (motor domain))
Supercontig_1.80_MVLG_05663_6sp	-559,96434	-559,96434	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00106.18	adh_short(short chain dehydrogenase)
Supercontig_1.29_MVLG_03243_10sp	-558,68618	-558,68618	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01565.16	FAD_binding_4(FAD binding domain)
Supercontig_1.54_MVLG_04665_8sp	-347,71318	-347,69255	0,04126	0,02042	NS	0	[]	[]	[]	hypothetical protein	PF03798.9	TRAM_LAG1_CLN8(TLC domain)
Supercontig_1.84_MVLG_05755_9sp	-1297,1493	-1296,9823	0,33394	0,15378	NS	0	[]	[]	[]	hypothetical protein	PF08221.4	HTH_9(RNA polymerase III subunit RPC82 helix-turn-helix domain)
Supercontig_1.22_MVLG_02755_7sp	-905,43464	-905,36792	0,13344	0,06454	NS	0	[]	[]	[]	hypothetical protein	PF06090.5	Ins_P5_2-kin(Inositol-pentakisphosphate 2-kinase)
Supercontig_1.44_MVLG_04169_10sp	-703,26333	-703,22611	0,07444	0,03654	NS	0	[]	[]	[]	hypothetical protein	PF04424.6	DUF544(Protein of unknown function (DUF544))
Supercontig_1.5_MVLG_00902_12sp	-381,73228	-376,7106	10,0434	0,99341	***	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.55_MVLG_04719_9sp	-655,75202	-653,93744	3,62916	0,83709	NS	0	[]	[]	[]	hypothetical protein	PF00400.25	WD40(WD domain, G-beta repeat)
Supercontig_1.2_MVLG_00474_11sp	-309,68361	-309,68354	0,00014	0	NS	0	[]	[]	[]	hypothetical protein	PF00172.11	Zn_clus(Fungal Zn(2)-Cys(6) binuclear cluster domain)
Supercontig_1.164_MVLG_06897_8sp	-754,38698	-754,38698	0	0	NS	0	[]	[]	[]	hypothetical protein	PF09468.3	RNase_H2-Ydr279(Ydr279p protein family (RNase H2 complex component))
Supercontig_1.1_MVLG_00073_7sp	-866,05486	-866,05227	0,00518	0,00259	NS	0	[]	[]	[]	hypothetical protein	PF06609.6	TRI12(Fungal trichothecene efflux pump (TRI12))
Supercontig_1.16_MVLG_02206_7sp	-1236,2897	-1234,8594	2,86066	0,76077	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.20_MVLG_02566_9sp	-628,22315	-626,68335	3,0796	0,78558	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.79_MVLG_05607_10sp	-520,71449	-520,71449	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02137.11	A_deamin(Adenosine-deaminase (editase) domain)

Supercontig_1.92_MVLG_05963_8sp	-1106,3531	-1104,6657	3,37492	0,81501	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.74_MVLG_05477_12sp	-402,30357	-402,30341	0,00032	0,00016	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.233_MVLG_07193_9sp	-522,2672	-521,83058	0,87324	0,35378	NS	0	[]	[]	[]	hypothetical protein	PF00535.19	Glycos_transf_2(Glycosyl transferase family 2)
Supercontig_1.83_MVLG_05727_7sp	-1216,2919	-1215,4413	1,70116	0,57283	NS	0	[]	[]	[]	transcription elongation factor S-II	PF08711.4	Med26(TFIIS helical bundle-like domain)
Supercontig_1.31_MVLG_03376_11sp	-400,37379	-399,91272	0,92214	0,36939	NS	0	[]	[]	[]	hypothetical protein	PF12471.1	GTP_CH_N(GTP cyclohydrolase N terminal)
Supercontig_1.31_MVLG_03361_9sp	-1263,1781	-1262,898	0,56014	0,24427	NS	0	[]	[]	[]	hypothetical protein	PF00664.16	ABC_membrane(ABC transporter transmembrane region)
Supercontig_1.36_MVLG_03656_8sp	-1753,6684	-1753,6572	0,02232	0,0111	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.64_MVLG_05102_8sp	-404,87515	-404,87515	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03966.9	Trm112p(Trm112p-like protein)
Supercontig_1.83_MVLG_05744_9sp	-734,88929	-734,88926	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00169.22	PH(PH domain)
Supercontig_1.3_MVLG_00559_10sp	-636,12291	-636,01203	0,22176	0,10495	NS	0	[]	[]	[]	hypothetical protein	PF00326.14	Peptidase_S9(Prolyl oligopeptidase family)
Supercontig_1.53_MVLG_04611_10sp	-355,91746	-355,91746	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00412.15	LIM(LIM domain)
Supercontig_1.6_MVLG_01114_10sp	-426,9897	-426,95507	0,06926	0,03404	NS	0	[]	[]	[]	hypothetical protein	PF01522.14	Polysacc_deac_1(Polysaccharide deacetylase)
Supercontig_1.4_MVLG_00739_9sp	-468,4375	-468,4375	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.5_MVLG_00903_8sp	-1372,2349	-1372,1529	0,16402	0,07874	NS	0	[]	[]	[]	hypothetical protein	PF01513.14	NAD_kinase(ATP-NAD kinase)
Supercontig_1.1_MVLG_00192_9sp	-1238,2856	-1238,2856	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00621.13	RhoGEF(RhoGEF domain)
Supercontig_1.128_MVLG_06549_7sp	-672,31286	-672,15829	0,30914	0,14322	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.20_MVLG_02591_9sp	-773,69651	-773,69651	0	0	NS	0	[]	[]	[]	hypothetical protein	PF08389.5	Xpo1(Exportin 1-like protein)
Supercontig_1.23_MVLG_02768_10sp	-423,33315	-423,33298	0,00034	0,00017	NS	0	[]	[]	[]	hypothetical protein	PF00676.13	E1_dh(Dehydrogenase E1 component)
Supercontig_1.1_MVLG_00024_7sp	-865,48536	-865,48536	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.34_MVLG_03572_10sp	-740,88571	-740,88571	0	0	NS	0	[]	[]	[]	ATP-binding cassette, subfamily D (ALD), member 2	PF00005.20	ABC_tran(ABC transporter)
Supercontig_1.1_MVLG_00007_6sp	-718,41466	-718,41457	0,00018	0	NS	0	[]	[]	[]	hypothetical protein	PF00447.10	HSF_DNA-bind(HSF-type DNA-binding)
Supercontig_1.5_MVLG_00971_6sp	-405,58121	-405,58121	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.132_MVLG_06602_8sp	-816,70953	-814,49247	4,43412	0,89107	NS	0	[]	[]	[]	hypothetical protein	PF01068.14	DNA_ligase_A_M(ATP dependent DNA ligase domain)
Supercontig_1.77_MVLG_05561_9sp	-1023,3081	-1023,3081	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00400.25	WD40(WD domain, G-beta repeat)

Supercontig_1.11_MVLG_01746_8sp	-936,81029	-936,78946	0,04166	0,02061	NS	0	[]	[]	[]	hypothetical protein	PF00270.22	DEAD(DEAD/DEAH box helicase)
Supercontig_1.3_MVLG_00618_9sp	-331,65866	-331,65866	0	0	NS	0	[]	[]	[]	hypothetical protein	PF07690.9	MFS_1(Major Facilitator Superfamily)
Supercontig_1.70_MVLG_05323_11sp	-1484,7163	-1484,7163	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.11_MVLG_01727_11sp	-915,61638	-915,3483	0,53616	0,23515	NS	0	[]	[]	[]	hypothetical protein	PF00400.25	WD40(WD domain, G-beta repeat)
Supercontig_1.132_MVLG_06590_12sp	-653,683	-653,64556	0,07488	0,03675	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.3_MVLG_00560_11sp	-724,2224	-724,2224	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02985.15	HEAT(HEAT repeat)
Supercontig_1.53_MVLG_04631_11sp	-784,44638	-784,43322	0,02632	0,01307	NS	0	[]	[]	[]	hypothetical protein	PF06420.5	Mgm101p(Mitochondrial genome maintenance MGM101)
Supercontig_1.28_MVLG_03148_8sp	-610,32025	-610,00436	0,63178	0,27086	NS	0	[]	[]	[]	hypothetical protein	PF03999.5	MAP65_ASE1(Microtubule associated protein (MAP65/ASE1 family))
Supercontig_1.62_MVLG_05024_8sp	-490,86061	-490,86057	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.109_MVLG_06285_10sp	-321,02217	-321,02217	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01920.13	Prefoldin_2(Prefoldin subunit)
Supercontig_1.54_MVLG_04672_7sp	-332,75954	-332,75931	0,00046	0,00023	NS	0	[]	[]	[]	E3 ubiquitin ligase complex SCF subunit sconC	PF01466.12	Skp1(Skp1 family, dimerisation domain)
Supercontig_1.6_MVLG_01121_8sp	-419,5836	-419,5836	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.2_MVLG_00397_7sp	-836,11644	-836,11644	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02798.13	GST_N(Glutathione S-transferase, N-terminal domain)
Supercontig_1.26_MVLG_03057_7sp	-872,34114	-872,34114	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00248.14	Aldo_ket_red(Aldo/keto reductase family)
Supercontig_1.81_MVLG_05685_8sp	-968,60607	-964,04269	9,12676	0,98957	**	0	[]	[]	[]	hypothetical protein	PF00069.18	Pkinase(Protein kinase domain)
Supercontig_1.58_MVLG_04881_10sp	-598,22041	-598,22041	0	0	NS	0	[]	[]	[]	hypothetical protein	PF09368.3	Sas10_Utp3_C(Sas10 C-terminal domain)
Supercontig_1.51_MVLG_04527_9sp	-554,07874	-554,07872	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.19_MVLG_02468_7sp	-379,13545	-379,13545	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.175_MVLG_06969_9sp	-1043,4434	-1043,4434	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.6_MVLG_01157_7sp	-615,73008	-615,72994	0,00028	0,00014	NS	0	[]	[]	[]	transporter particle subunit bet3	PF04051.9	TRAPP(Transport protein particle (TRAPP) component)
Supercontig_1.73_MVLG_05424_7sp	-1400,6726	-1400,6726	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00128.17	Alpha-amylase(Alpha amylase, catalytic domain)
Supercontig_1.84_MVLG_05779_9sp	-819,24802	-819,24802	0	0	NS	0	[]	[]	[]	hypothetical protein	PF12451.1	VPS11_C(Vacuolar protein sorting protein 11 C terminal)
Supercontig_1.54_MVLG_04684_6sp	-594,95053	-593,62914	2,64278	0,73324	NS	0	[]	[]	[]	glutathione peroxidase 2	PF00578.14	AhpC-TSA(AhpC/TSA family)
Supercontig_1.8_MVLG_01448_7sp	-287,78253	-287,72469	0,11568	0,0562	NS	0	[]	[]	[]	histone H2B	PF00125.17	Histone(Core histone H2A/H2B/H3/H4)

Supercontig_1.13_MVLG_01890_8sp	-865,05095	-865,05052	0,00086	0,00043	NS	0	[]	[]	[]	guanine nucleotide-binding protein subunit beta	PF00400.25	WD40(WD domain, G-beta repeat)
Supercontig_1.127_MVLG_06533_10sp	-294,90027	-293,5811	2,63834	0,73264	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.63_MVLG_05064_9sp	-983,58284	-983,58284	0	0	NS	0	[]	[]	[]	hypothetical protein	PF09423.3	PhoD(PhoD-like phosphatase)
Supercontig_1.207_MVLG_07118_9sp	-516,86524	-516,84911	0,03226	0,016	NS	0	[]	[]	[]	hypothetical protein	PF00390.12	malic(Malic enzyme, N-terminal domain)
Supercontig_1.1_MVLG_00131_9sp	-295,69257	-295,69257	0	0	NS	0	[]	[]	[]	ER membrane protein SH3	PF08229.4	SHR3_chaperone(ER membrane protein SH3)
Supercontig_1.113_MVLG_06354_7sp	-524,03216	-523,2816	1,50112	0,5279	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.2_MVLG_00329_6sp	-1621,7054	-1621,6682	0,07436	0,0365	NS	0	[]	[]	[]	hypothetical protein	PF01619.11	Pro_dh(Proline dehydrogenase)
Supercontig_1.122_MVLG_06456_10sp	-498,70297	-498,63265	0,14064	0,0679	NS	0	[]	[]	[]	hypothetical protein	PF10304.2	DUF2411(Domain of unknown function (DUF2411))
Supercontig_1.65_MVLG_05152_11sp	-558,5787	-557,06038	3,03664	0,78092	NS	0	[]	[]	[]	hypothetical protein	PF07683.7	CobW_C(Cobalamin synthesis protein cobW C-terminal domain)
Supercontig_1.83_MVLG_05738_10sp	-782,1773	-782,17695	0,0007	0,00035	NS	0	[]	[]	[]	hypothetical protein	PF03151.9	TPT(Triose-phosphate Transporter family)
Supercontig_1.19_MVLG_02480_7sp	-459,73827	-459,73818	0,00018	0	NS	0	[]	[]	[]	ADP-ribosylation factor-like protein 8A	PF04670.5	Gtr1_RagA(Gtr1/RagA G protein conserved region)
Supercontig_1.27_MVLG_03111_10sp	-520,31049	-520,3025	0,01598	0,00796	NS	0	[]	[]	[]	hypothetical protein	PF05205.5	COMPASS-Shg1(COMPASS (Complex proteins associated with Set1p) component shg1)
Supercontig_1.31_MVLG_03344_7sp	-595,86935	-595,5693	0,6001	0,25922	NS	0	[]	[]	[]	hypothetical protein	PF00300.15	PGAM(Phosphoglycerate mutase family)
Supercontig_1.100_MVLG_06144_10sp	-1610,9265	-1610,9253	0,00236	0,00118	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.28_MVLG_03136_6sp	-711,51559	-711,51555	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00628.22	PHD(PHD-finger)
Supercontig_1.60_MVLG_04943_9sp	-1429,9918	-1428,053	3,8775	0,85612	NS	0	[]	[]	[]	hypothetical protein	PF06424.5	PRP1_N(PRP1 splicing factor, N-terminal)
Supercontig_1.125_MVLG_06512_8sp	-848,25538	-847,50265	1,50546	0,52892	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.60_MVLG_04936_7sp	-500,11508	-500,11508	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00107.19	ADH_zinc_N(Zinc-binding dehydrogenase)
Supercontig_1.26_MVLG_03027_8sp	-617,19768	-617,1976	0,00016	0	NS	0	[]	[]	[]	hypothetical protein	PF07250.4	Glyoxal_oxid_N(Glyoxal oxidase N-terminus)
Supercontig_1.52_MVLG_04590_11sp	-358,79366	-358,79366	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00106.18	adh_short(short chain dehydrogenase)
Supercontig_1.48_MVLG_04352_6sp	-617,53319	-616,0017	3,06298	0,78379	NS	0	[]	[]	[]	hypothetical protein	PF07519.4	Tannase(Tannase and feruloyl esterase)
Supercontig_1.122_MVLG_06454_8sp	-558,66265	-558,50105	0,3232	0,14922	NS	0	[]	[]	[]	hypothetical protein	PF01053.13	Cys_Met_Meta_PP(Cys/Met metabolism PLP-dependent enzyme)
Supercontig_1.67_MVLG_05205_11sp	-480,67759	-480,65572	0,04374	0,02163	NS	0	[]	[]	[]	hypothetical protein	PF10445.2	DUF2456(Protein of unknown function (DUF2456))
Supercontig_1.9_MVLG_01535_9sp	-634,54982	-634,37783	0,34398	0,15801	NS	0	[]	[]	[]	hypothetical protein	NA	NA

Supercontig_1.41_MVLG_03977_8sp	-929,26124	-929,26124	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04444.7	Dioxygenase_N(Catechol dioxygenase N terminus)
Supercontig_1.23_MVLG_02805_10sp	-564,85762	-564,01389	1,68746	0,5699	NS	0	[]	[]	[]	hypothetical protein	PF00667.13	FAD_binding_1(FAD binding domain)
Supercontig_1.64_MVLG_05103_9sp	-1257,9293	-1257,9293	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03801.6	Ndc80_HEC(HEC/Ndc80p family)
Supercontig_1.34_MVLG_03556_8sp	-935,55255	-935,55253	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00026.16	Asp(Eukaryotic aspartyl protease)
Supercontig_1.3_MVLG_00583_10sp	-714,24315	-714,24315	0	0	NS	0	[]	[]	[]	glycine dehydrogenase subunit 2	TIGR00461	TIGR00461(gcvP: glycine dehydrogenase)
Supercontig_1.3_MVLG_00593_8sp	-724,36909	-724,36909	0	0	NS	0	[]	[]	[]	hypothetical protein	PF06609.6	TRI12(Fungal trichothecene efflux pump (TRI12))
Supercontig_1.10_MVLG_01582_7sp	-798,79763	-797,964	1,66726	0,56553	NS	0	[]	[]	[]	hypothetical protein	PF00010.19	HLH(Helix-loop-helix DNA-binding domain)
Supercontig_1.54_MVLG_04678_7sp	-1050,4428	-1050,4428	0	0	NS	0	[]	[]	[]	hypothetical protein	PF10557.2	Cullin_Nedd8(Cullin protein neddylation domain)
Supercontig_1.149_MVLG_06765_6sp	-842,2023	-842,2023	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00072.17	Response_reg(Response regulator receiver domain)
Supercontig_1.68_MVLG_05248_7sp	-447,68428	-447,68404	0,00048	0,00024	NS	0	[]	[]	[]	protein mago nashi	PF02792.7	Mago_nashi(Mago nashi protein)
Supercontig_1.12_MVLG_01801_10sp	-1151,217	-1151,1991	0,03578	0,01773	NS	0	[]	[]	[]	hypothetical protein	PF02421.11	FeoB_N(Ferrous iron transport protein B)
Supercontig_1.2_MVLG_00323_7sp	-904,92839	-903,35874	3,1393	0,79188	NS	0	[]	[]	[]	hypothetical protein	PF08613.4	Cyclin(Cyclin)
Supercontig_1.25_MVLG_02970_12sp	-402,99988	-399,28527	7,42922	0,97564	**	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.69_MVLG_05273_6sp	-587,15023	-587,01726	0,26594	0,12451	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.23_MVLG_02789_6sp	-775,51354	-774,59963	1,82782	0,59905	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.15_MVLG_02126_9sp	-417,98295	-417,98295	0	0	NS	0	[]	[]	[]	translation initiation factor RLI1	PF00005.20	ABC_tran(ABC transporter)
Supercontig_1.60_MVLG_04926_10sp	-510,79834	-510,79823	0,00022	0,00011	NS	0	[]	[]	[]	hypothetical protein	PF03142.8	Chitin_synth_2(Chitin synthase)
Supercontig_1.98_MVLG_06092_6sp	-550,80617	-550,80611	0,00012	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.2_MVLG_00280_8sp	-1292,4735	-1292,4735	0	0	NS	0	[]	[]	[]	hypothetical protein	PF08238.5	Sel1(Sel1 repeat)
Supercontig_1.13_MVLG_01955_9sp	-1237,53	-1237,53	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.36_MVLG_03641_6sp	-746,15805	-745,98891	0,33828	0,15561	NS	0	[]	[]	[]	hypothetical protein	PF00566.11	TBC(TBC domain)
Supercontig_1.51_MVLG_04536_9sp	-397,87778	-397,87778	0	0	NS	0	[]	[]	[]	CDK-activating kinase assembly factor MAT1	PF00097.18	zf-C3HC4(Zinc finger, C3HC4 type (RING finger))
Supercontig_1.139_MVLG_06670_12sp	-522,14624	-520,44763	3,39722	0,81706	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.42_MVLG_04043_8sp	-1449,6274	-1449,2632	0,72836	0,30523	NS	0	[]	[]	[]	TTK protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.74_MVLG_05439_10sp	-425,75891	-423,87852	3,76078	0,84747	NS	0	[]	[]	[]	hypothetical protein	PF00106.18	adh_short(short chain dehydrogenase)

Supercontig_1.176_MVLG_06977_11sp	-560,09062	-558,26888	3,64348	0,83826	NS	0	[]	[]	[]	hypothetical protein	PF01421.12	Reprolysin(Reprolysin (M12B) family zinc metalloprotease)
Supercontig_1.19_MVLG_02449_10sp	-1145,7675	-1145,7675	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00632.18	HECT(HECT-domain (ubiquitin-transferase))
Supercontig_1.58_MVLG_04860_11sp	-489,474	-489,31501	0,31798	0,147	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.5_MVLG_00922_9sp	-612,83065	-612,70417	0,25296	0,11881	NS	0	[]	[]	[]	hypothetical protein	TIGR00879	TIGR00879(SP: MFS transporter, sugar porter (SP) family)
Supercontig_1.91_MVLG_05941_11sp	-946,48487	-946,48487	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.8_MVLG_01384_7sp	-956,59803	-956,59786	0,00034	0,00017	NS	0	[]	[]	[]	hypothetical protein	PF04078.6	Rcd1(Cell differentiation family, Rcd1-like)
Supercontig_1.86_MVLG_05831_8sp	-369,85433	-369,04209	1,62448	0,55614	NS	0	[]	[]	[]	hypothetical protein	PF04479.6	RTA1(RTA1 like protein)
Supercontig_1.15_MVLG_02083_7sp	-1676,3995	-1673,0118	6,77534	0,96621	**	0	[]	[]	[]	hypothetical protein	PF00082.15	Peptidase_S8(Subtilase family)
Supercontig_1.8_MVLG_01449_8sp	-458,98799	-458,98741	0,00116	0,00058	NS	0	[]	[]	[]	histone H2A	PF00808.16	CBFD_NFYB_HMF(Histone-like transcription factor (CBF/NF-Y) and archaeal histone)
Supercontig_1.7_MVLG_01249_11sp	-1132,6738	-1131,8147	1,71816	0,57645	NS	0	[]	[]	[]	hypothetical protein	PF07904.6	CT20(CT20 family)
Supercontig_1.7_MVLG_01260_11sp	-443,26216	-443,26211	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.6_MVLG_01091_7sp	-808,10622	-808,10622	0	0	NS	0	[]	[]	[]	hypothetical protein	PF08645.4	PNK3P(Polynucleotide kinase 3 phosphatase)
Supercontig_1.26_MVLG_03054_8sp	-633,10416	-633,10416	0	0	NS	0	[]	[]	[]	hypothetical protein	PF08635.3	ox_reductase_C(Putative oxidoreductase C terminal)
Supercontig_1.41_MVLG_04031_8sp	-616,42122	-615,13576	2,57092	0,72348	NS	0	[]	[]	[]	hypothetical protein	PF00400.25	WD40(WD domain, G-beta repeat)
Supercontig_1.24_MVLG_02853_9sp	-470,3858	-469,7517	1,2682	0,46959	NS	0	[]	[]	[]	V-type proton ATPase proteolipid subunit	TIGR01100	TIGR01100(V_ATP_synt_C: V-type ATPase, C subunit)
Supercontig_1.73_MVLG_05408_7sp	-875,21383	-875,21383	0	0	NS	0	[]	[]	[]	hypothetical protein	PF08647.4	BRE1(BRE1 E3 ubiquitin ligase)
Supercontig_1.16_MVLG_02193_7sp	-1655,0777	-1655,0315	0,0925	0,0452	NS	0	[]	[]	[]	CMGC/DYRK/DYRK2 protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.132_MVLG_06600_10sp	-519,4652	-519,4652	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00107.19	ADH_zinc_N(Zinc-binding dehydrogenase)
Supercontig_1.3_MVLG_00605_10sp	-615,63228	-615,63145	0,00166	0,00083	NS	0	[]	[]	[]	aspartate-semialdehyde dehydrogenase	PF01118.17	Semialdhyde_dh(Semialdehyde dehydrogenase, NAD binding domain)
Supercontig_1.16_MVLG_02171_8sp	-312,3393	-312,3392	0,0002	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.44_MVLG_04160_10sp	-1381,9195	-1381,6497	0,53964	0,23648	NS	0	[]	[]	[]	hypothetical protein	PF00145.10	DNA_methylase(C-5 cytosine-specific DNA methylase)
Supercontig_1.17_MVLG_02289_10sp	-306,7421	-306,7421	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00512.18	HisKA(His Kinase A (phosphoacceptor) domain)
Supercontig_1.200_MVLG_07081_9sp	-373,27559	-373,27546	0,00026	0,00013	NS	0	[]	[]	[]	delta-1-pyrroline-5-carboxylate dehydrogenase	PF00171.15	Aldedh(Aldehyde dehydrogenase family)

Supercontig_1.92_MVLG_05960_11sp	-910,36337	-910,34865	0,02944	0,01461	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.127_MVLG_06536_7sp	-322,41213	-322,41213	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.104_MVLG_06206_10sp	-1450,9565	-1450,9565	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00097.18	zf-C3HC4(Zinc finger, C3HC4 type (RING finger))
Supercontig_1.135_MVLG_06630_9sp	-319,36936	-319,14923	0,44026	0,19759	NS	0	[]	[]	[]	monothiol glutaredoxin	TIGR00365	TIGR00365(TIGR00365: monothiol glutaredoxin, Grx4 family)
Supercontig_1.8_MVLG_01458_7sp	-1023,4706	-1023,4706	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.110_MVLG_06295_7sp	-575,31731	-575,31724	0,00014	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.48_MVLG_04363_8sp	-1323,2991	-1321,8018	2,99446	0,77625	NS	0	[]	[]	[]	CMGC/CDK protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.31_MVLG_03371_10sp	-787,52257	-787,52257	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.9_MVLG_01520_8sp	-871,20641	-871,20641	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02225.15	PA(PA domain)
Supercontig_1.83_MVLG_05740_6sp	-652,00248	-652,00006	0,00484	0,00242	NS	0	[]	[]	[]	hypothetical protein	PF04669.6	DUF579(Protein of unknown function (DUF579))
Supercontig_1.97_MVLG_06074_6sp	-1141,8506	-1141,6682	0,3647	0,16669	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.38_MVLG_03799_9sp	-577,68268	-576,53751	2,29034	0,68183	NS	0	[]	[]	[]	hypothetical protein	PF04248.5	DUF427(Domain of unknown function (DUF427))
Supercontig_1.10_MVLG_01587_7sp	-430,01026	-427,88544	4,24964	0,88055	NS	0	[]	[]	[]	hypothetical protein	PF00571.21	CBS(CBS domain)
Supercontig_1.29_MVLG_03209_7sp	-396,769	-396,30189	0,93422	0,37319	NS	0	[]	[]	[]	hypothetical protein	PF01399.20	PCI(PCI domain)
Supercontig_1.50_MVLG_04491_9sp	-449,35082	-449,35082	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00106.18	adh_short(short chain dehydrogenase)
Supercontig_1.18_MVLG_02414_10sp	-659,85958	-659,81227	0,09462	0,04621	NS	0	[]	[]	[]	NAK protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.13_MVLG_01914_9sp	-308,17528	-307,9316	0,48736	0,21626	NS	0	[]	[]	[]	hypothetical protein	PF02301.11	HORMA(HORMA domain)
Supercontig_1.51_MVLG_04519_6sp	-383,94074	-383,94067	0,00014	0	NS	0	[]	[]	[]	hypothetical protein	PF04110.6	APG12(Ubiquitin-like autophagy protein Apg12)
Supercontig_1.6_MVLG_01078_10sp	-833,42056	-830,92686	4,9874	0,9174	*	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.35_MVLG_03594_11sp	-1131,3268	-1131,3268	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04084.7	ORC2(Origin recognition complex subunit 2)
Supercontig_1.11_MVLG_01707_10sp	-694,90603	-694,90603	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00270.22	DEAD(DEAD/DEAH box helicase)
Supercontig_1.19_MVLG_02446_8sp	-485,04529	-485,04492	0,00074	0,00037	NS	0	[]	[]	[]	Isocitrate dehydrogenase	TIGR00127	TIGR00127(nadp_idh_euk: isocitrate dehydrogenase, NADP-dependent)
Supercontig_1.84_MVLG_05770_6sp	-560,09527	-560,09527	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.122_MVLG_06459_10sp	-369,36814	-369,36769	0,0009	0,00045	NS	0	[]	[]	[]	ATP synthase subunit beta	PF00306.20	ATP-synt_ab_C(ATP synthase alpha/beta chain, C terminal domain)

Supercontig_1.22_MVLG_02724_11sp	-442,26008	-442,08568	0,3488	0,16004	NS	0	[]	[]	[]	nucleoside diphosphate kinase	PF00334.12	NDK(Nucleoside diphosphate kinase)
Supercontig_1.45_MVLG_04202_9sp	-1029,3372	-1029,3372	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00498.19	FHA(FHA domain)
Supercontig_1.10_MVLG_01615_9sp	-319,08477	-319,0847	0,00014	0	NS	0	[]	[]	[]	hypothetical protein	PF06609.6	TRI12(Fungal trichothecene efflux pump (TRI12))
Supercontig_1.17_MVLG_02294_10sp	-567,92484	-567,83956	0,17056	0,08174	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.7_MVLG_01245_8sp	-878,12706	-878,12706	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03151.9	TPT(Triose-phosphate Transporter family)
Supercontig_1.99_MVLG_06122_11sp	-482,78602	-481,98746	1,59712	0,55002	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.150_MVLG_06775_6sp	-493,59303	-493,59303	0	0	NS	0	[]	[]	[]	hypothetical protein	PF05071.9	NDUFA12(NADH ubiquinone oxidoreductase subunit NDUFA12)
Supercontig_1.56_MVLG_04773_10sp	-293,01223	-293,01201	0,00044	0,00022	NS	0	[]	[]	[]	serine hydroxymethyltransferase 1	PF00464.12	SHMT(Serine hydroxymethyltransferase)
Supercontig_1.94_MVLG_05989_9sp	-378,97057	-378,97055	0	0	NS	0	[]	[]	[]	hypothetical protein	PF07719.10	TPR_2(Tetratricopeptide repeat)
Supercontig_1.4_MVLG_00835_7sp	-467,5378	-467,53771	0,00018	0	NS	0	[]	[]	[]	hypothetical protein	PF04241.8	DUF423(Protein of unknown function (DUF423))
Supercontig_1.127_MVLG_06539_6sp	-353,73153	-353,73148	0,0001	0	NS	0	[]	[]	[]	hypothetical protein	PF01625.14	PMSR(Peptide methionine sulfoxide reductase)
Supercontig_1.102_MVLG_06172_9sp	-472,18063	-470,85286	2,65554	0,73493	NS	0	[]	[]	[]	hypothetical protein	PF04900.5	Fcf1(Fcf1)
Supercontig_1.84_MVLG_05767_11sp	-520,30601	-520,30601	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00107.19	ADH_zinc_N(Zinc-binding dehydrogenase)
Supercontig_1.87_MVLG_05867_10sp	-492,31309	-492,31266	0,00086	0,00043	NS	0	[]	[]	[]	hypothetical protein	PF01595.13	DUF21(Domain of unknown function DUF21)
Supercontig_1.93_MVLG_05969_12sp	-446,50586	-446,48283	0,04606	0,02277	NS	0	[]	[]	[]	hypothetical protein	PF08726.3	efhand_Ca_insen(Ca2+ insensitive EF hand)
Supercontig_1.7_MVLG_01332_11sp	-604,33533	-604,33506	0,00054	0,00027	NS	0	[]	[]	[]	hypothetical protein	PF01663.15	Phosphodiest(Type I phosphodiesterase / nucleotide pyrophosphatase)
Supercontig_1.13_MVLG_01887_10sp	-499,83078	-499,83057	0,00042	0,00021	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.1_MVLG_00102_10sp	-467,53786	-467,26832	0,53908	0,23627	NS	0	[]	[]	[]	hypothetical protein	TIGR02180	TIGR02180(GRX_euk: Glutaredoxin)
Supercontig_1.21_MVLG_02679_8sp	-941,99824	-941,99824	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01239.15	PPTA(Protein prenyltransferase alpha subunit repeat)
Supercontig_1.3_MVLG_00523_10sp	-1138,5043	-1138,0676	0,87332	0,35381	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.102_MVLG_06171_7sp	-1377,2007	-1377,2007	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04106.5	APG5(Autophagy protein Apg5)
Supercontig_1.84_MVLG_05762_11sp	-361,15157	-359,9309	2,44134	0,70497	NS	0	[]	[]	[]	hypothetical protein	PF00153.20	Mito_carr(Mitochondrial carrier protein)
Supercontig_1.5_MVLG_00906_8sp	-501,40232	-501,29857	0,2075	0,09855	NS	0	[]	[]	[]	hypothetical protein	PF06202.7	GDE_C(Amylo-alpha-1,6-glucosidase)
Supercontig_1.2_MVLG_00467_7sp	-1033,4182	-1033,4178	0,00096	0,00048	NS	0	[]	[]	[]	hypothetical protein	PF04990.5	RNA_pol_Rpb1_7(RNA polymerase Rpb1, domain 7)

Supercontig_1.100_MVLG_06133_7sp	-1044,4529	-1043,0265	2,85278	0,75983	NS	0	[]	[]	[]	hypothetical protein	PF00753.20	Lactamase_B(Metallo-beta-lactamase superfamily)
Supercontig_1.117_MVLG_06389_10sp	-1280,5857	-1280,3556	0,46018	0,20554	NS	0	[]	[]	[]	hypothetical protein	PF02696.7	UPF0061(Uncharacterized ACR, YdiU/UPF0061 family)
Supercontig_1.35_MVLG_03624_7sp	-1103,5662	-1103,5662	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01388.14	ARID(ARID/BRIGHT DNA binding domain)
Supercontig_1.25_MVLG_02925_8sp	-651,37328	-651,36834	0,00988	0,00493	NS	0	[]	[]	[]	hypothetical protein	PF06916.6	DUF1279(Protein of unknown function (DUF1279))
Supercontig_1.51_MVLG_04528_8sp	-1458,9171	-1458,6217	0,59084	0,25578	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.5_MVLG_00965_10sp	-741,12413	-740,92851	0,39124	0,17768	NS	0	[]	[]	[]	hypothetical protein	PF03029.10	ATP_bind_1(Conserved hypothetical ATP binding protein)
Supercontig_1.1_MVLG_00223_10sp	-1005,419	-1004,6363	1,56522	0,54279	NS	0	[]	[]	[]	hypothetical protein	PF09734.2	Tau95(RNA polymerase III transcription factor (TF)IIIC subunit)
Supercontig_1.68_MVLG_05264_11sp	-532,44554	-532,44544	0,0002	0	NS	0	[]	[]	[]	hypothetical protein	PF01853.11	MOZ_SAS(MOZ/SAS family)
Supercontig_1.20_MVLG_02571_6sp	-645,15783	-645,15723	0,0012	0,0006	NS	0	[]	[]	[]	hypothetical protein	PF00254.21	FKBP_C(FKBP-type peptidyl-prolyl cis-trans isomerase)
Supercontig_1.21_MVLG_02664_10sp	-450,37155	-450,3712	0,0007	0,00035	NS	0	[]	[]	[]	hypothetical protein	PF02301.11	HORMA(HORMA domain)
Supercontig_1.207_MVLG_07117_9sp	-353,35258	-353,35223	0,0007	0,00035	NS	0	[]	[]	[]	replication factor C subunit 5	PF06144.6	DNA_pol3_delta(DNA polymerase III, delta subunit)
Supercontig_1.10_MVLG_01673_10sp	-452,59458	-452,54453	0,1001	0,04882	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.2_MVLG_00322_10sp	-1034,6399	-1031,6152	6,04948	0,95143	**	0	[]	[]	[]	hypothetical protein	PF00447.10	HSF_DNA-bind(HSF-type DNA-binding)
Supercontig_1.10_MVLG_01621_6sp	-1238,4792	-1238,4237	0,11098	0,05398	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.22_MVLG_02719_12sp	-509,62828	-509,62828	0	0	NS	0	[]	[]	[]	hypothetical protein	TIGR00879	TIGR00879(SP: MFS transporter, sugar porter (SP) family)
Supercontig_1.84_MVLG_05763_8sp	-589,77577	-589,77546	0,00062	0,00031	NS	0	[]	[]	[]	hypothetical protein	PF00515.21	TPR_1(Tetratricopeptide repeat)
Supercontig_1.8_MVLG_01408_6sp	-752,15711	-752,10681	0,1006	0,04906	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.3_MVLG_00584_9sp	-619,45455	-619,42986	0,04938	0,02439	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.58_MVLG_04864_7sp	-857,99228	-857,99227	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.19_MVLG_02489_8sp	-282,92196	-282,92185	0,00022	0,00011	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.101_MVLG_06151_10sp	-1542,911	-1540,5533	4,71544	0,90536	*	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.26_MVLG_03038_8sp	-860,8792	-860,87891	0,00058	0,00029	NS	0	[]	[]	[]	asparagine synthetase	PF00733.14	Asn_synthase(Asparagine synthase)
Supercontig_1.42_MVLG_04051_9sp	-1528,8211	-1528,8159	0,01048	0,00523	NS	0	[]	[]	[]	hypothetical protein	PF08700.4	Vps51(Vps51/Vps67)
Supercontig_1.28_MVLG_03165_8sp	-745,67616	-745,67616	0	0	NS	0	[]	[]	[]	hypothetical protein	PF10356.2	DUF2034(Protein of unknown function (DUF2034))

Supercontig_1.13_MVLG_01903_9sp	-491,16125	-491,16111	0,00028	0,00014	NS	0	[]	[]	[]	hypothetical protein	PF00083.17	Sugar_tr(Sugar (and other) transporter)
Supercontig_1.13_MVLG_01893_6sp	-1021,7602	-1021,7602	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00176.16	SNF2_N(SNF2 family N-terminal domain)
Supercontig_1.24_MVLG_02882_6sp	-831,54007	-831,54007	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02833.7	DHHA2(DHHA2 domain)
Supercontig_1.1_MVLG_00185_9sp	-354,89804	-354,89785	0,00038	0,00019	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.49_MVLG_04417_7sp	-574,25243	-570,48117	7,54252	0,97698	**	0	[]	[]	[]	hypothetical protein	PF08287.4	DASH_Spc19(Spc19)
Supercontig_1.41_MVLG_03997_8sp	-695,66026	-695,66017	0,00018	0	NS	0	[]	[]	[]	hypothetical protein	PF08622.3	Svf1(Svf1-like)
Supercontig_1.6_MVLG_01079_7sp	-890,35778	-889,96445	0,78666	0,32519	NS	0	[]	[]	[]	hypothetical protein	PF00505.12	HMG_box(HMG (high mobility group) box)
Supercontig_1.24_MVLG_02888_9sp	-1172,2055	-1172,2055	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.98_MVLG_06084_8sp	-709,04566	-709,04566	0	0	NS	0	[]	[]	[]	hypothetical protein	PF10607.2	RanBPM_CRA(Ran binding protein in the microtubule-organising centre)
Supercontig_1.605_MVLG_07288_9sp	-521,8362	-520,4885	2,6954	0,74016	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.5_MVLG_00951_10sp	-676,72228	-675,85912	1,72632	0,57817	NS	0	[]	[]	[]	hypothetical protein	PF01369.13	Sec7(Sec7 domain)
Supercontig_1.9_MVLG_01525_9sp	-519,57633	-519,57633	0	0	NS	0	[]	[]	[]	hypothetical protein	PF11894.1	DUF3414(Protein of unknown function (DUF3414))
Supercontig_1.28_MVLG_03180_7sp	-386,25392	-386,25392	0	0	NS	0	[]	[]	[]	hypothetical protein	PF09784.2	L31(Mitochondrial ribosomal protein L31)
Supercontig_1.25_MVLG_02965_6sp	-670,93094	-670,93088	0,00012	0	NS	0	[]	[]	[]	NEK protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.70_MVLG_05340_10sp	-997,14417	-997,14389	0,00056	0,00028	NS	0	[]	[]	[]	hypothetical protein	PF00153.20	Mito_carr(Mitochondrial carrier protein)
Supercontig_1.87_MVLG_05873_10sp	-290,49629	-289,71959	1,5534	0,54008	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.83_MVLG_05726_8sp	-309,09236	-309,09196	0,0008	0,0004	NS	0	[]	[]	[]	hypothetical protein	PF00808.16	CBFD_NFYB_HMF(Histone-like transcription factor (CBF/NF-Y) and archaeal histone)
Supercontig_1.2_MVLG_00318_7sp	-1105,5601	-1103,6774	3,76532	0,84782	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.2_MVLG_00435_7sp	-703,40657	-703,40644	0,00026	0,00013	NS	0	[]	[]	[]	aconitate hydratase 2	PF00694.12	Aconitase_C(Aconitase C-terminal domain)
Supercontig_1.100_MVLG_06137_9sp	-481,05001	-480,6963	0,70742	0,29792	NS	0	[]	[]	[]	hypothetical protein	PF06588.4	Muskelin_N(Muskelin N-terminus)
Supercontig_1.41_MVLG_03972_6sp	-496,47621	-496,47621	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00561.13	Abhydrolase_1(alpha/beta hydrolase fold)
Supercontig_1.13_MVLG_01917_7sp	-1503,9535	-1503,9535	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00787.17	PX(PX domain)
Supercontig_1.109_MVLG_06273_11sp	-649,76891	-649,69923	0,13936	0,06731	NS	0	[]	[]	[]	hypothetical protein	PF09103.3	BRCA-2_OB1(BRCA2, oligonucleotide/oligosaccharide-binding, domain 1)

Supercontig_1.15_MVLG_02098_9sp	-1131,8395	-1131,8395	0	0	NS	0	[]	[]	[]	hypothetical protein	PF09745.2	DUF2040(Coiled-coil domain-containing protein 55 (DUF2040))
Supercontig_1.14_MVLG_02051_12sp	-721,3475	-721,18493	0,32514	0,15004	NS	0	[]	[]	[]	hypothetical protein	PF10366.2	Vps39_1(Vacuolar sorting protein 39 domain 1)
Supercontig_1.83_MVLG_05739_9sp	-360,44835	-360,35531	0,18608	0,08884	NS	0	[]	[]	[]	hypothetical protein	TIGR00055	TIGR00055(uppS: di-trans,poly-cis-decaprenylcistransferase)
Supercontig_1.160_MVLG_06857_10sp	-428,51249	-426,176	4,67298	0,90333	*	0	[]	[]	[]	hypothetical protein	PF04442.7	CtaG_Cox11(Cytochrome c oxidase assembly protein CtaG/Cox11)
Supercontig_1.165_MVLG_06910_9sp	-662,88673	-662,88673	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01177.15	Asp_Glu_race(Asp/Glu/Hydantoin racemase)
Supercontig_1.205_MVLG_07108_11sp	-1175,889	-1175,889	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00387.12	PI-PLC-Y(Phosphatidylinositol-specific phospholipase C, Y domain)
Supercontig_1.25_MVLG_02945_11sp	-1038,6708	-1038,6708	0,00012	0	NS	0	[]	[]	[]	phenylalanyl-tRNA synthetase, beta subunit	PF03483.10	B3_4(B3/4 domain)
Supercontig_1.4_MVLG_00851_8sp	-731,48798	-731,48798	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00400.25	WD40(WD domain, G-beta repeat)
Supercontig_1.10_MVLG_01600_10sp	-631,82987	-631,82987	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03878.8	YIF1(YIF1)
Supercontig_1.81_MVLG_05681_12sp	-556,10477	-556,10477	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01656.16	CbiA(CobQ/CobB/MinD/ParA nucleotide binding domain)
Supercontig_1.73_MVLG_05416_9sp	-611,48531	-611,48274	0,00514	0,00257	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.3_MVLG_00627_10sp	-704,97355	-704,7031	0,5409	0,23696	NS	0	[]	[]	[]	hypothetical protein	PF05686.5	DUF821(Arabidopsis thaliana protein of unknown function (DUF821))
Supercontig_1.131_MVLG_06586_6sp	-525,94678	-525,94678	0	0	NS	0	[]	[]	[]	Ham1 family protein	TIGR00042	TIGR00042(TIGR00042: non-canonical purine NTP pyrophosphatase, rdgB/HAM1 family)
Supercontig_1.29_MVLG_03220_10sp	-603,25934	-603,25934	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00595.17	PDZ(PDZ domain (Also known as DHR or GLGF))
Supercontig_1.5_MVLG_01017_9sp	-792,09979	-790,91552	2,36854	0,69403	NS	0	[]	[]	[]	hypothetical protein	TIGR00756	TIGR00756(PPR: pentatricopeptide repeat domain)
Supercontig_1.140_MVLG_06674_8sp	-1244,4539	-1244,4539	0	0	NS	0	[]	[]	[]	hypothetical protein	PF05019.6	Coq4(Coenzyme Q (ubiquinone) biosynthesis protein Coq4)
Supercontig_1.21_MVLG_02629_8sp	-455,0862	-453,71365	2,7451	0,74654	NS	0	[]	[]	[]	hypothetical protein	PF08022.5	FAD_binding_8(FAD-binding domain)
Supercontig_1.38_MVLG_03827_8sp	-391,08137	-391,08135	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04046.9	PSP(PSP)
Supercontig_1.2_MVLG_00276_8sp	-471,57301	-471,57301	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00153.20	Mito_carr(Mitochondrial carrier protein)
Supercontig_1.40_MVLG_03928_10sp	-980,11027	-979,7506	0,71934	0,30209	NS	0	[]	[]	[]	hypothetical protein	PF00175.14	NAD_binding_1(Oxidoreductase NAD-binding domain)
Supercontig_1.76_MVLG_05507_8sp	-530,43665	-530,43651	0,00028	0,00014	NS	0	[]	[]	[]	hypothetical protein	PF00018.21	SH3_1(SH3 domain)

Supercontig_1.36_MVLG_03677_7sp	-906,79507	-906,79507	0	0	NS	0	[]	[]	[]	methionine aminopeptidase 2	PF00557.17	Peptidase_M24(Metallopeptidase family M24)
Supercontig_1.17_MVLG_02307_9sp	-742,29302	-742,28093	0,02418	0,01202	NS	0	[]	[]	[]	hypothetical protein	PF00326.14	Peptidase_S9(Prolyl oligopeptidase family)
Supercontig_1.27_MVLG_03114_11sp	-899,93263	-899,77958	0,3061	0,14191	NS	0	[]	[]	[]	hypothetical protein	PF10058.2	DUF2296(Predicted integral membrane metal-binding protein (DUF2296))
Supercontig_1.92_MVLG_05947_9sp	-870,89416	-870,83567	0,11698	0,05681	NS	0	[]	[]	[]	hypothetical protein	PF00063.14	Myosin_head(Myosin head (motor domain))
Supercontig_1.10_MVLG_01657_9sp	-563,49868	-562,79526	1,40684	0,50511	NS	0	[]	[]	[]	hypothetical protein	PF00076.15	RRM_1(RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain))
Supercontig_1.7_MVLG_01280_12sp	-517,96619	-517,48883	0,95472	0,37958	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.16_MVLG_02197_10sp	-516,04657	-515,90606	0,28102	0,13109	NS	0	[]	[]	[]	hypothetical protein	PF00023.23	Ank(Ankyrin repeat)
Supercontig_1.79_MVLG_05615_9sp	-502,09315	-502,01411	0,15808	0,076	NS	0	[]	[]	[]	hypothetical protein	PF08202.4	Mis12_component(Mis12-Mtw1 protein family)
Supercontig_1.81_MVLG_05668_11sp	-561,61661	-561,37251	0,4882	0,21659	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.93_MVLG_05976_11sp	-664,57111	-664,57089	0,00044	0,00022	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.16_MVLG_02242_10sp	-478,21778	-476,49094	3,45368	0,82215	NS	0	[]	[]	[]	histone H2B	PF00125.17	Histone(Core histone H2A/H2B/H3/H4)
Supercontig_1.38_MVLG_03793_8sp	-982,21802	-982,21802	0	0	NS	0	[]	[]	[]	hypothetical protein	PF05064.6	Nsp1_C(Nsp1-like C-terminal region)
Supercontig_1.150_MVLG_06778_8sp	-366,86351	-366,77371	0,1796	0,08589	NS	0	[]	[]	[]	hypothetical protein	PF00179.19	UQ_con(Ubiquitin-conjugating enzyme)
Supercontig_1.13_MVLG_01926_10sp	-1747,3395	-1747,3395	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03142.8	Chitin_synth_2(Chitin synthase)
Supercontig_1.29_MVLG_03236_7sp	-399,20128	-399,20128	0	0	NS	0	[]	[]	[]	hypothetical protein	PF08520.3	DUF1748(Fungal protein of unknown function (DUF1748))
Supercontig_1.87_MVLG_05874_8sp	-518,42708	-518,42707	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00566.11	TBC(TBC domain)
Supercontig_1.41_MVLG_03989_6sp	-500,57908	-500,57908	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.233_MVLG_07195_7sp	-274,36097	-274,36086	0,00022	0,00011	NS	0	[]	[]	[]	hypothetical protein	PF04525.5	DUF567(Protein of unknown function (DUF567))
Supercontig_1.56_MVLG_04752_6sp	-932,83677	-931,92882	1,8159	0,59665	NS	0	[]	[]	[]	hypothetical protein	PF01233.12	NMT(Myristoyl-CoA:protein N-myristoyltransferase, N-terminal domain)
Supercontig_1.35_MVLG_03579_9sp	-620,34461	-620,34461	0	0	NS	0	[]	[]	[]	hypothetical protein	TIGR01065	TIGR01065(hlyIII: channel protein, hemolysin III family)
Supercontig_1.5_MVLG_01032_8sp	-795,07208	-795,07208	0	0	NS	0	[]	[]	[]	hypothetical protein	PF08477.6	Miro(Miro-like protein)
Supercontig_1.98_MVLG_06086_11sp	-386,97662	-385,53376	2,88572	0,76375	NS	0	[]	[]	[]	argininosuccinate lyase	TIGR00838	TIGR00838(argH: argininosuccinate lyase)
Supercontig_1.14_MVLG_02032_9sp	-677,78552	-677,78513	0,00078	0,00039	NS	0	[]	[]	[]	hypothetical protein	PF00270.22	DEAD(DEAD/DEAH box helicase)
Supercontig_1.22_MVLG_02756_12sp	-453,81264	-453,03955	1,54618	0,53842	NS	0	[]	[]	[]	hypothetical protein	NA	NA

Supercontig_1.6_MVLG_01143_9sp	-424,48078	-424,48028	0,001	0,0005	NS	0	[]	[]	[]	CMGC/CDK/CDK5 protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.51_MVLG_04545_12sp	-532,48632	-532,48629	0	0	NS	0	[]	[]	[]	hypothetical protein	TIGR00727	TIGR00727(ISP4_OPT: small oligopeptide transporter, OPT family)
Supercontig_1.17_MVLG_02331_8sp	-380,68897	-380,68887	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00082.15	Peptidase_S8(Subtilase family)
Supercontig_1.55_MVLG_04720_6sp	-1105,9324	-1105,9324	0	0	NS	0	[]	[]	[]	hypothetical protein	PF07065.7	D123(D123)
Supercontig_1.9_MVLG_01497_7sp	-624,87063	-624,51657	0,70812	0,29817	NS	0	[]	[]	[]	hypothetical protein	PF00153.20	Mito_carr(Mitochondrial carrier protein)
Supercontig_1.81_MVLG_05665_8sp	-724,44835	-723,16492	2,56686	0,72291	NS	0	[]	[]	[]	hypothetical protein	PF04818.6	DUF618(Protein of unknown function, DUF618)
Supercontig_1.2_MVLG_00346_8sp	-694,08886	-694,08883	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00498.19	FHA(FHA domain)
Supercontig_1.16_MVLG_02184_8sp	-698,73066	-698,16181	1,1377	0,43382	NS	0	[]	[]	[]	hypothetical protein	PF07732.8	Cu-oxidase_3(Multicopper oxidase)
Supercontig_1.7_MVLG_01298_10sp	-626,06218	-626,06219	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.7_MVLG_01291_9sp	-365,64786	-365,63275	0,03022	0,015	NS	0	[]	[]	[]	hypothetical protein	PF08512.5	Rtt106(Histone chaperone Rttp106-like)
Supercontig_1.57_MVLG_04831_11sp	-433,57948	-433,11353	0,9319	0,37246	NS	0	[]	[]	[]	hypothetical protein	PF05680.5	ATP-synt_E(ATP synthase E chain)
Supercontig_1.74_MVLG_05472_11sp	-440,73753	-440,73753	0	0	NS	0	[]	[]	[]	D-3-phosphoglycerate dehydrogenase 2	PF02826.12	2-Hacid_dh_C(D-isomer specific 2-hydroxyacid dehydrogenase, NAD binding domain)
Supercontig_1.117_MVLG_06403_10sp	-505,5945	-505,59441	0,00018	0	NS	0	[]	[]	[]	ribulose-phosphate 3-epimerase	PF00834.12	Ribul_P_3_epim(Ribulose-phosphate 3 epimerase family)
Supercontig_1.112_MVLG_06323_9sp	-304,9551	-304,46093	0,98834	0,38992	NS	0	[]	[]	[]	Plasma membrane (H+) ATPase	TIGR01494	TIGR01494(ATPase_P-type: HAD ATPase, P-type, family IC)
Supercontig_1.25_MVLG_02940_6sp	-691,09562	-691,09562	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00106.18	adh_short(short chain dehydrogenase)
Supercontig_1.87_MVLG_05864_11sp	-517,29455	-517,29455	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00667.13	FAD_binding_1(FAD binding domain)
Supercontig_1.63_MVLG_05075_9sp	-437,14778	-437,14771	0,00014	0	NS	0	[]	[]	[]	cytidine deaminase	TIGR01354	TIGR01354(cyt_deam_tetra: cytidine deaminase)
Supercontig_1.52_MVLG_04557_8sp	-377,39663	-377,39663	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00505.12	HMG_box(HMG (high mobility group) box)
Supercontig_1.65_MVLG_05133_11sp	-317,92856	-317,92829	0,00054	0,00027	NS	0	[]	[]	[]	hypothetical protein	PF01145.18	Band_7(SPFH domain / Band 7 family)
Supercontig_1.38_MVLG_03824_8sp	-1046,1722	-1046,1721	0,00026	0,00013	NS	0	[]	[]	[]	hypothetical protein	PF00443.22	UCH(Ubiquitin carboxyl-terminal hydrolase)
Supercontig_1.9_MVLG_01524_8sp	-431,86666	-431,86666	0	0	NS	0	[]	[]	[]	hypothetical protein	PF03879.7	Cgr1(Cgr1 family)
Supercontig_1.62_MVLG_05009_11sp	-430,15875	-430,15862	0,00026	0,00013	NS	0	[]	[]	[]	hypothetical protein	PF00179.19	UQ_con(Ubiquitin-conjugating enzyme)
Supercontig_1.16_MVLG_02201_7sp	-1071,6074	-1070,1145	2,98584	0,77528	NS	0	[]	[]	[]	hypothetical protein	PF01507.12	PAPS_reduct(Phosphoadenosine phosphosulfate reductase family)

Supercontig_1.44_MVLG_04180_6sp	-1106,6517	-1106,2072	0,88904	0,35887	NS	0	[]	[]	[]	hypothetical protein	PF04193.7	PQ-loop(PQ loop repeat)
Supercontig_1.55_MVLG_04723_7sp	-911,78701	-911,78701	0	0	NS	0	[]	[]	[]	cyclopropane-fatty-acyl-phospholipid synthase	PF08123.6	DOT1(Histone methylation protein DOT1)
Supercontig_1.96_MVLG_06047_9sp	-560,84177	-560,84177	0	0	NS	0	[]	[]	[]	hypothetical protein	PF08513.4	LisH(LisH)
Supercontig_1.47_MVLG_04337_8sp	-501,8884	-499,55597	4,66486	0,90294	*	0	[]	[]	[]	hypothetical protein	PF07819.6	PGAP1(PGAP1-like protein)
Supercontig_1.65_MVLG_05132_7sp	-556,13308	-556,13308	0	0	NS	0	[]	[]	[]	hypothetical protein	PF07690.9	MFS_1(Major Facilitator Superfamily)
Supercontig_1.21_MVLG_02673_10sp	-748,16001	-748,16001	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00493.16	MCM(MCM2/3/5 family)
Supercontig_1.86_MVLG_05825_6sp	-1129,2048	-1129,2048	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.18_MVLG_02351_7sp	-1127,6158	-1127,5324	0,1668	0,08002	NS	0	[]	[]	[]	hypothetical protein	PF01602.13	Adaptin_N(Adaptin N terminal region)
Supercontig_1.39_MVLG_03842_7sp	-425,04327	-425,04303	0,00048	0,00024	NS	0	[]	[]	[]	protein BUD31	PF01125.10	G10(G10 protein)
Supercontig_1.87_MVLG_05853_10sp	-578,68916	-578,68916	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.5_MVLG_01020_9sp	-839,69564	-839,59182	0,20764	0,09861	NS	0	[]	[]	[]	hypothetical protein	PF01652.11	IF4E(Eukaryotic initiation factor 4E)
Supercontig_1.78_MVLG_05601_10sp	-564,38577	-564,38156	0,00842	0,0042	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.45_MVLG_04192_12sp	-365,28025	-365,28025	0	0	NS	0	[]	[]	[]	hypothetical protein	TIGR00832	TIGR00832(acr3: arsenical-resistance protein)
Supercontig_1.15_MVLG_02141_12sp	-846,11614	-846,10072	0,03084	0,0153	NS	0	[]	[]	[]	hypothetical protein	PF01454.12	MAGE(MAGE family)
Supercontig_1.55_MVLG_04705_11sp	-350,95018	-350,95003	0,0003	0,00015	NS	0	[]	[]	[]	hypothetical protein	PF03151.9	TPT(Triose-phosphate Transporter family)
Supercontig_1.66_MVLG_05173_9sp	-320,37975	-320,37961	0,00028	0,00014	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.1_MVLG_00054_8sp	-769,63008	-769,53205	0,19606	0,09338	NS	0	[]	[]	[]	hypothetical protein	PF10496.2	Syntaxin-18_N(SNARE-complex protein Syntaxin-18 N-terminus)
Supercontig_1.14_MVLG_02040_8sp	-312,69435	-312,69392	0,00086	0,00043	NS	0	[]	[]	[]	hypothetical protein	PF02036.10	SCP2(SCP-2 sterol transfer family)
Supercontig_1.4_MVLG_00816_10sp	-529,55247	-529,55238	0,00018	0	NS	0	[]	[]	[]	hypothetical protein	PF04042.9	DNA_pol_E_B(DNA polymerase alpha/epsilon subunit B)
Supercontig_1.7_MVLG_01277_8sp	-544,65636	-544,18828	0,93616	0,3738	NS	0	[]	[]	[]	hypothetical protein	PF01042.14	Ribonuc_L-PSP(Endoribonuclease L-PSP)
Supercontig_1.93_MVLG_05984_7sp	-886,74817	-886,74817	0	0	NS	0	[]	[]	[]	1,4-alpha-glucan-branching enzyme	PF00128.17	Alpha-amylase(Alpha amylase, catalytic domain)
Supercontig_1.45_MVLG_04226_7sp	-815,578	-815,57405	0,0079	0,00394	NS	0	[]	[]	[]	methylsterol monooxygenase	PF04116.6	FA_hydroxylase(Fatty acid hydroxylase superfamily)
Supercontig_1.6_MVLG_01130_10sp	-652,23183	-652,23183	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00176.16	SNF2_N(SNF2 family N-terminal domain)
Supercontig_1.7_MVLG_01312_8sp	-355,59825	-355,54975	0,097	0,04734	NS	0	[]	[]	[]	hypothetical protein	PF01900.12	RNase_P_Rpp14(Rpp14/Pop5 family)

Supercontig_1.86_MVLG_05833_7sp	-428,06099	-428,0479	0,02618	0,013	NS	0	[]	[]	[]	hypothetical protein	PF00106.18	adh_short(short chain dehydrogenase)
Supercontig_1.69_MVLG_05309_9sp	-448,86543	-447,34359	3,04368	0,78169	NS	0	[]	[]	[]	hypothetical protein	PF01040.11	UbiA(UbiA prenyltransferase family)
Supercontig_1.34_MVLG_03551_10sp	-762,73576	-762,73561	0,0003	0,00015	NS	0	[]	[]	[]	ribose-5-phosphate isomerase	PF06026.7	Rib_5-P_isom_A(Ribose 5-phosphate isomerase A (phosphoriboisomerase A))
Supercontig_1.10_MVLG_01583_12sp	-967,21918	-967,21918	0	0	NS	0	[]	[]	[]	X-Pro aminopeptidase	PF00557.17	Peptidase_M24(Metallopeptidase family M24)
Supercontig_1.98_MVLG_06090_10sp	-524,80057	-524,02993	1,54128	0,53728	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.34_MVLG_03566_8sp	-1587,883	-1587,883	0	0	NS	0	[]	[]	[]	hypothetical protein	PF11987.1	IF-2(Translation-initiation factor 2)
Supercontig_1.2_MVLG_00399_12sp	-665,31198	-665,31198	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04930.8	FUN14(FUN14 family)
Supercontig_1.55_MVLG_04700_6sp	-703,12508	-703,11782	0,01452	0,00723	NS	0	[]	[]	[]	hypothetical protein	PF01612.13	3_5_exonuc(3'-5' exonuclease)
Supercontig_1.1_MVLG_00202_6sp	-305,69825	-305,69824	0	0	NS	0	[]	[]	[]	hypothetical protein	TIGR00730	TIGR00730(TIGR00730: TIGR00730 family protein)
Supercontig_1.10_MVLG_01686_12sp	-530,78842	-530,78837	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00773.12	RNB(RNB domain)
Supercontig_1.60_MVLG_04955_12sp	-879,84197	-879,84197	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00415.11	RCC1(Regulator of chromosome condensation (RCC1) repeat)
Supercontig_1.86_MVLG_05830_11sp	-1013,6131	-1013,6131	0	0	NS	0	[]	[]	[]	hypothetical protein	PF10261.2	Scs3p(Inositol phospholipid synthesis protein Scs3p)
Supercontig_1.44_MVLG_04135_10sp	-602,85065	-602,85065	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.91_MVLG_05940_9sp	-746,5657	-745,31894	2,49352	0,71257	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.26_MVLG_03010_9sp	-1412,8689	-1412,8689	0	0	NS	0	[]	[]	[]	hypothetical protein	PF04389.10	Peptidase_M28(Peptidase family M28)
Supercontig_1.82_MVLG_05719_11sp	-454,83724	-452,74466	4,18516	0,87663	NS	0	[]	[]	[]	NADH dehydrogenase (ubiquinone) Fe-S protein 8	TIGR01971	TIGR01971(NuoI: NADH-quinone oxidoreductase, chain I)
Supercontig_1.121_MVLG_06436_10sp	-659,0299	-659,0299	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01222.10	ERG4_ERG24(Ergosterol biosynthesis ERG4/ERG24 family)
Supercontig_1.22_MVLG_02689_7sp	-732,71412	-732,71412	0	0	NS	0	[]	[]	[]	T-complex protein 1 subunit delta	PF00118.17	Cpn60_TCP1(TCP-1/cpn60 chaperonin family)
Supercontig_1.81_MVLG_05695_7sp	-1729,1217	-1729,1217	0	0	NS	0	[]	[]	[]	hypothetical protein	PF08550.3	DUF1752(Fungal protein of unknown function (DUF1752))
Supercontig_1.18_MVLG_02358_7sp	-1461,0535	-1459,8259	2,45524	0,70701	NS	0	[]	[]	[]	hypothetical protein	PF00083.17	Sugar_tr(Sugar (and other) transporter)
Supercontig_1.25_MVLG_02966_9sp	-1871,3991	-1867,568	7,66222	0,97831	**	0	[]	[]	[]	hypothetical protein	PF02187.10	GAS2(Growth-Arrest-Specific Protein 2 Domain)
Supercontig_1.4_MVLG_00850_8sp	-1089,2299	-1087,7008	3,05818	0,78327	NS	0	[]	[]	[]	hypothetical protein	PF08427.3	DUF1741(Domain of unknown function (DUF1741))
Supercontig_1.5_MVLG_00889_12sp	-465,32336	-465,3231	0,00052	0,00026	NS	0	[]	[]	[]	heat shock protein 60	PF00118.17	Cpn60_TCP1(TCP-1/cpn60 chaperonin family)

Supercontig_1.155_MVLG_06825_6sp	-1291,9194	-1291,9195	0	0	NS	0	[]	[]	[]	ABC1-B atypical protein kinase	PF03109.9	ABC1(ABC1 family)
Supercontig_1.13_MVLG_01889_9sp	-466,73281	-466,53244	0,40074	0,18157	NS	0	[]	[]	[]	hypothetical protein	PF03256.9	APC10(Anaphase-promoting complex, subunit 10 (APC10))
Supercontig_1.165_MVLG_06906_9sp	-500,53204	-499,68444	1,6952	0,57156	NS	0	[]	[]	[]	hypothetical protein	PF04588.6	HIG_1_N(Hypoxia induced protein conserved region)
Supercontig_1.12_MVLG_01802_9sp	-822,66322	-822,66322	0	0	NS	0	[]	[]	[]	hypothetical protein	PF06862.5	DUF1253(Protein of unknown function (DUF1253))
Supercontig_1.101_MVLG_06168_10sp	-1288,2774	-1286,9058	2,74326	0,74631	NS	0	[]	[]	[]	hypothetical protein	PF03556.8	DUF298(Domain of unknown function (DUF298))
Supercontig_1.52_MVLG_04554_9sp	-399,19019	-399,18974	0,0009	0,00045	NS	0	[]	[]	[]	septin like spn4	PF03193.9	DUF258(Protein of unknown function, DUF258)
Supercontig_1.99_MVLG_06116_9sp	-295,14516	-295,14507	0,00018	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.2_MVLG_00461_8sp	-711,32033	-711,31996	0,00074	0,00037	NS	0	[]	[]	[]	hypothetical protein	PF03900.8	Porphobil_deamC(Porphobilinogen deaminase, C-terminal domain)
Supercontig_1.65_MVLG_05140_7sp	-474,07924	-474,07894	0,0006	0,0003	NS	0	[]	[]	[]	metacaspase-1	PF00656.15	Peptidase_C14(Caspase domain)
Supercontig_1.70_MVLG_05330_9sp	-597,91928	-597,91918	0,0002	0	NS	0	[]	[]	[]	hypothetical protein	PF03005.8	DUF231(Arabidopsis proteins of unknown function)
Supercontig_1.28_MVLG_03166_6sp	-936,98056	-936,98056	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00856.21	SET(SET domain)
Supercontig_1.49_MVLG_04430_8sp	-732,39006	-730,88832	3,00348	0,77726	NS	0	[]	[]	[]	hypothetical protein	PF04851.8	ResIII(Type III restriction enzyme, res subunit)
Supercontig_1.10_MVLG_01658_8sp	-603,2885	-603,10789	0,36122	0,16524	NS	0	[]	[]	[]	hypothetical protein	PF10357.2	Kin17_mid(Domain of Kin17 curved DNA-binding protein)
Supercontig_1.93_MVLG_05979_10sp	-425,18373	-425,18339	0,00068	0,00034	NS	0	[]	[]	[]	hypothetical protein	PF00300.15	PGAM(Phosphoglycerate mutase family)
Supercontig_1.47_MVLG_04346_7sp	-871,55274	-871,55248	0,00052	0,00026	NS	0	[]	[]	[]	hypothetical protein	PF00501.21	AMP-binding(AMP-binding enzyme)
Supercontig_1.68_MVLG_05268_11sp	-386,99216	-386,99216	0	0	NS	0	[]	[]	[]	AP-2 complex subunit mu	PF01217.13	Clat_adaptor_s(Clathrin adaptor complex small chain)
Supercontig_1.94_MVLG_05986_6sp	-517,52808	-517,52808	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01263.13	Aldose_epim(Aldose 1-epimerase)
Supercontig_1.61_MVLG_04967_9sp	-884,45795	-883,39619	2,12352	0,65415	NS	0	[]	[]	[]	hypothetical protein	PF05063.7	MT-A70(MT-A70)
Supercontig_1.1_MVLG_00005_7sp	-1373,162	-1373,162	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00160.14	Pro_isomerase(Cyclophilin type peptidyl-prolyl cis-trans isomerase/CLD)
Supercontig_1.6_MVLG_01134_6sp	-550,17344	-550,16986	0,00716	0,00357	NS	0	[]	[]	[]	hypothetical protein	PF00583.17	Acetyltransf_1(Acetyltransferase (GNAT) family)
Supercontig_1.33_MVLG_03449_10sp	-593,42872	-592,5077	1,84204	0,60189	NS	0	[]	[]	[]	hypothetical protein	PF00172.11	Zn_clus(Fungal Zn(2)-Cys(6) binuclear cluster domain)
Supercontig_1.31_MVLG_03369_10sp	-531,85942	-530,98745	1,74394	0,58187	NS	0	[]	[]	[]	hypothetical protein	PF06682.5	DUF1183(Protein of unknown function (DUF1183))
Supercontig_1.98_MVLG_06099_7sp	-681,38081	-681,37353	0,01456	0,00725	NS	0	[]	[]	[]	hypothetical protein	PF07574.6	SMC_Nse1(Nse1 non-SMC component of SMC5-6 complex)
Supercontig_1.38_MVLG_03768_8sp	-562,80183	-562,15521	1,29324	0,47619	NS	0	[]	[]	[]	40S ribosomal protein S11	TIGR03630	TIGR03630(arch_S17P: archaeal ribosomal protein S17P)

Supercontig_1.53_MVLG_04616_10sp	-268,4509	-268,45047	0,00086	0,00043	NS	0	[]	[]	[]	hypothetical protein	PF00450.15	Peptidase_S10(Serine carboxypeptidase)
Supercontig_1.23_MVLG_02776_7sp	-724,18884	-724,18884	0	0	NS	0	[]	[]	[]	hypothetical protein	PF06999.5	Suc_Fer-like(Sucrase/ferredoxin-like)
Supercontig_1.42_MVLG_04076_9sp	-432,40292	-430,80407	3,1977	0,79787	NS	0	[]	[]	[]	hypothetical protein	PF01535.13	PPR(PPR repeat)
Supercontig_1.93_MVLG_05985_6sp	-1457,1181	-1456,8113	0,61362	0,26421	NS	0	[]	[]	[]	hypothetical protein	PF01323.13	DSBA(DSBA-like thioredoxin domain)
Supercontig_1.32_MVLG_03412_10sp	-574,60778	-574,60775	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00097.18	zf-C3HC4(Zinc finger, C3HC4 type (RING finger))
Supercontig_1.8_MVLG_01362_7sp	-598,7077	-598,7077	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02146.10	SIR2(Sir2 family)
Supercontig_1.11_MVLG_01759_8sp	-916,35888	-916,17426	0,36924	0,16858	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.3_MVLG_00577_8sp	-368,66634	-368,66627	0,00014	0	NS	0	[]	[]	[]	hypothetical protein	PF04252.6	RNA_Me_trans(Predicted SAM-dependent RNA methyltransferase)
Supercontig_1.8_MVLG_01372_9sp	-353,43258	-353,43253	0	0	NS	0	[]	[]	[]	hypothetical protein	PF08033.5	Sec23_BS(Sec23/Sec24 beta-sandwich domain)
Supercontig_1.60_MVLG_04924_10sp	-675,38917	-675,3864	0,00554	0,00277	NS	0	[]	[]	[]	homoserine dehydrogenase	PF00742.12	Homoserine_dh(Homoserine dehydrogenase)
Supercontig_1.38_MVLG_03814_9sp	-637,42107	-637,42107	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01753.11	zf-MYND(MYND finger)
Supercontig_1.2_MVLG_00415_9sp	-435,82626	-435,82625	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.33_MVLG_03471_9sp	-531,45309	-530,14653	2,61312	0,72925	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.40_MVLG_03908_10sp	-711,45286	-711,35242	0,20088	0,09556	NS	0	[]	[]	[]	hypothetical protein	PF05970.7	DUF889(PIF1 helicase)
Supercontig_1.46_MVLG_04279_9sp	-681,14578	-681,14576	0	0	NS	0	[]	[]	[]	hypothetical protein	PF10336.2	DUF2420(Protein of unknown function (DUF2420))
Supercontig_1.156_MVLG_06832_12sp	-507,80312	-507,7778	0,05064	0,025	NS	0	[]	[]	[]	hypothetical protein	PF00627.24	UBA(UBA/TS-N domain)
Supercontig_1.5_MVLG_00936_8sp	-995,65519	-995,65519	0	0	NS	0	[]	[]	[]	nicotinate-nucleotide pyrophosphorylase	TIGR00078	TIGR00078(nadC: nicotinate-nucleotide diphosphorylase (carboxylating))
Supercontig_1.51_MVLG_04510_10sp	-484,22353	-484,22351	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.23_MVLG_02788_7sp	-835,93582	-835,93564	0,00036	0,00018	NS	0	[]	[]	[]	tubulin beta chain	PF00091.18	Tubulin(Tubulin/FtsZ family, GTPase domain)
Supercontig_1.2_MVLG_00315_6sp	-963,96475	-963,96474	0	0	NS	0	[]	[]	[]	hypothetical protein	PF10348.2	DUF2427(Domain of unknown function (DUF2427))
Supercontig_1.54_MVLG_04673_12sp	-487,59722	-487,59722	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.4_MVLG_00710_10sp	-1429,3934	-1428,5359	1,7149	0,57576	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.10_MVLG_01651_9sp	-594,30474	-594,30474	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.17_MVLG_02316_9sp	-1313,3609	-1312,9643	0,79308	0,32736	NS	0	[]	[]	[]	hypothetical protein	PF00443.22	UCH(Ubiquitin carboxyl-terminal hydrolase)
Supercontig_1.55_MVLG_04729_10sp	-632,58955	-630,89565	3,3878	0,8162	NS	0	[]	[]	[]	hypothetical protein	TIGR02180	TIGR02180(GRX_euk: Glutaredoxin)

Supercontig_1.122_MV LG_06460_8sp	-785,66755	-785,66755	0	0	NS	0	[]	[]	[]	hypothetical protein	PF09797.2	NatB_MDM20(N-acetyltransferase B complex (NatB) non catalytic subunit)
Supercontig_1.45_MV LG_04218_6sp	-895,81411	-895,81411	0	0	NS	0	[]	[]	[]	hypothetical protein	PF00439.18	Bromodomain(Bromodomain)
Supercontig_1.18_MV LG_02400_11sp	-858,59013	-858,42527	0,32972	0,15199	NS	0	[]	[]	[]	hypothetical protein	PF00076.15	RRM_1(RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain))
Supercontig_1.116_MV LG_06376_6sp	-473,91025	-473,88184	0,05682	0,02801	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.11_MV LG_01791_6sp	-709,91022	-709,8972	0,02604	0,01294	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.30_MV LG_03284_10sp	-832,55178	-832,55174	0	0	NS	0	[]	[]	[]	hypothetical protein	PF01369.13	Sec7(Sec7 domain)
Supercontig_1.17_MV LG_02299_9sp	-967,07306	-967,07305	0	0	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.45_MV LG_04212_9sp	-1159,2345	-1159,0419	0,3853	0,17523	NS	0	[]	[]	[]	hypothetical protein	PF06422.5	PDR_CDR(CDR ABC transporter)
Supercontig_1.32_MV LG_03386_10sp	-627,59948	-627,55566	0,08764	0,04287	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.36_MV LG_03668_10sp	-411,21641	-408,877	4,67882	0,90362	*	0	[]	[]	[]	hypothetical protein	PF00270.22	DEAD(DEAD/DEAH box helicase)
Supercontig_1.32_MV LG_03404_10sp	-521,8892	-521,8892	0	0	NS	0	[]	[]	[]	hypothetical protein	PF02815.12	MIR(MIR domain)
Supercontig_1.18_MV LG_02410_10sp	-774,5774	-773,30578	2,54324	0,71962	NS	0	[]	[]	[]	AGC/DMPK protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
B												
Supercontig_1.167_MV LG_06924_9sp	-776,16	-773,25	5,83	0,95	*	**1**	[]	[]	**['48S']**	hypothetical protein	NA	NA
Supercontig_1.103_MV LG_06196_11sp	-511,82	-507,56	8,51	0,99	**	**1**	[]	**['10W']**	[]	mannosyl transferase	PF11051.1	Mannosyl_trans3(Mannosyltransferase putative)
Supercontig_1.230_MV LG_07186_10sp	-412,73	-408,52	8,42	0,99	**	**1**	[]	**['2V']**	[]	hypothetical protein	NA	NA
Supercontig_1.119_MV LG_06419_12sp	-856,65	-852,51	8,29	0,98	**	**2**	[]	[]	**['20T', '69T']**	hypothetical protein	PF08601.3	PAP1(Transcription factor PAP1)
Supercontig_1.71_MV LG_05356_9sp	-644,12	-640,57	7,10	0,97	**	**1**	[]	[]	**['43T']**	hypothetical protein	NA	NA
Supercontig_1.72_MV LG_05394_7sp	-572,06	-568,71	6,70	0,96	**	**1**	[]	[]	**['4S']**	uroporphyrinogen-III synthase	PF02602.8	HEM4(Uroporphyrinogen-III synthase HemD)
Supercontig_1.90_MV LG_05914_8sp	-576,20	-572,93	6,55	0,96	**	**1**	[]	[]	**['84Y']**	hypothetical protein	PF06325.6	PrmA(Ribosomal protein L11 methyltransferase (PrmA))
Supercontig_1.133_MV LG_06610_9sp	-532,16	-522,64	19,04	1,00	***	**1**	[]	**['49Q']**	[]	hypothetical protein	NA	NA
Supercontig_1.108_MV LG_06269_8sp	-2589,51	-2583,08	12,87	1,00	***	**4**	[]	[]	**['23I', '113E', '205I', '295E']**	hypothetical protein	NA	NA
Supercontig_1.108_MV LG_06272_7sp	-1334,55	-1329,66	9,77	0,99	***	**1**	[]	[]	**['37F']**	hypothetical protein	NA	NA
Supercontig_1.133_MV LG_06611_12sp	-1408,84	-1403,57	10,55	0,99	***	**1**	[]	[]	**['97A']**	Proteophosphoglycan	NA	NA
Supercontig_1.153_MV LG_06801_7sp	-455,20	-450,08	10,25	0,99	***	**2**	[]	[]	**['9V', '35E']**	hypothetical protein	NA	NA

Supercontig_1.169_MVLG_06936_9sp	-629,56	-627,38	4,36	0,89	NS	1	[]	[]	['49A']	hypothetical protein	TIGR00037	TIGR00037(eIF_5A: translation initiation factor eIF-5A)
Supercontig_1.136_MVLG_06643_10sp	-461,82	-465,98	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF07774.6	DUF1620(Protein of unknown function (DUF1620))
Supercontig_1.106_MVLG_06232_10sp	-348,38	-348,25	0,27	0,13	NS	0	[]	[]	[]	hypothetical protein	PF01184.12	Grp1_Fun34_YaaH(GPR1/FUN34/yaaH family)
Supercontig_1.218_MVLG_07152_10sp	-810,35	-810,35	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF03159.11	XRN_N(XRN 5'-3' exonuclease N-terminus)
Supercontig_1.144_MVLG_06728_10sp	-640,32	-639,57	1,49	0,53	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.420_MVLG_07266_10sp	-310,48	-310,48	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.145_MVLG_06734_10sp	-960,13	-960,13	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	TIGR00840	TIGR00840(b_cpa1: sodium/hydrogen exchanger 3)
Supercontig_1.106_MVLG_06237_8sp	-735,87	-735,87	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.178_MVLG_06987_7sp	-1244,47	-1244,47	0,00	5.99982001118831e-05	NS	0	[]	[]	[]	hypothetical protein	PF00085.13	Thioredoxin(Thioredoxin)
Supercontig_1.157_MVLG_06842_8sp	-616,51	-616,51	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.137_MVLG_06648_11sp	-490,15	-490,15	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.169_MVLG_06933_9sp	-681,40	-681,40	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF00782.13	DSPc(Dual specificity phosphatase, catalytic domain)
Supercontig_1.169_MVLG_06934_9sp	-482,72	-482,72	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.217_MVLG_07148_9sp	-677,92	-677,66	0,51	0,22	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.153_MVLG_06797_7sp	-736,05	-736,05	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF08617.3	CGI-121(Kinase binding protein CGI-121)
Supercontig_1.136_MVLG_06639_7sp	-467,87	-467,87	0,00	0,00	NS	0	[]	[]	[]	protein KES1	PF01237.11	Oxysterol_BP(Oxysterol-binding protein)
Supercontig_1.137_MVLG_06647_8sp	-1503,68	-1501,87	3,61	0,84	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.71_MVLG_05370_11sp	-618,83	-618,83	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF00400.25	WD40(WD domain, G-beta repeat)
Supercontig_1.201_MVLG_07087_9sp	-500,21	-500,06	0,29	0,13	NS	0	[]	[]	[]	STE/STE20/PAKA protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.145_MVLG_06731_9sp	-877,04	-876,91	0,25	0,12	NS	0	[]	[]	[]	hypothetical protein	PF01195.12	Pept_tRNA_hydro(Peptidyl-tRNA hydrolase)
Supercontig_1.273_MVLG_07224_6sp	-443,50	-443,50	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.71_MVLG_05343_11sp	-399,76	-398,03	3,46	0,82	NS	0	[]	[]	[]	hypothetical protein	PF07690.9	MFS_1(Major Facilitator Superfamily)
Supercontig_1.230_MVLG_07187_6sp	-1177,10	-1177,10	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	NA	NA

Supercontig_1.188_MVLG_07036_9sp	-458,04	-458,04	0,00	0,00	NS	0	[]	[]	[]	phospho-2-dehydro-3-deoxyheptonate aldolase, tyrosine-inhibited	TIGR00034	TIGR00034(aroFGH: 3-deoxy-7-phosphoheptulonate synthase)
Supercontig_1.108_MVLG_06268_7sp	-579,33	-579,33	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	TIGR01126	TIGR01126(pdi_dom: protein disulfide-isomerase domain)
Supercontig_1.167_MVLG_06926_8sp	-654,80	-654,77	0,05	0,03	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.146_MVLG_06743_8sp	-445,18	-443,46	3,45	0,82	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.167_MVLG_06919_10sp	-544,42	-544,35	0,15	0,07	NS	0	[]	[]	[]	hypothetical protein	PF07646.8	Kelch_2(Kelch motif)
Supercontig_1.103_MVLG_06186_6sp	-1822,95	-1822,95	1.99999999495049e-05	9.99994997491935e-06	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.217_MVLG_07147_9sp	-655,93	-655,62	0,63	0,27	NS	0	[]	[]	[]	hypothetical protein	PF01569.14	PAP2(PAP2 superfamily)
Supercontig_1.179_MVLG_06989_10sp	-336,69	-336,69	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF02714.8	DUF221(Domain of unknown function DUF221)
Supercontig_1.157_MVLG_06845_9sp	-637,35	-637,35	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.108_MVLG_06270_10sp	-434,20	-434,20	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF00169.22	PH(PH domain)
Supercontig_1.146_MVLG_06740_7sp	-319,47	-319,47	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.137_MVLG_06645_6sp	-543,37	-543,37	4.00000001263834e-05	1.99998000645238e-05	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.72_MVLG_05389_12sp	-637,17	-637,16	0,02	0,01	NS	0	[]	[]	[]	hypothetical protein	PF04851.8	ResIII(Type III restriction enzyme, res subunit)
Supercontig_1.90_MVLG_05913_6sp	-1030,02	-1030,02	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	TIGR00627	TIGR00627(tfb4: transcription factor tfb4)
Supercontig_1.72_MVLG_05386_9sp	-920,42	-920,42	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF00097.18	zf-C3HC4(Zinc finger, C3HC4 type (RING finger))
Supercontig_1.169_MVLG_06935_10sp	-1023,11	-1022,18	1,86	0,61	NS	0	[]	[]	[]	hypothetical protein	PF12397.1	U3snoRNP10(U3 small nucleolar RNA-associated protein 10)
Supercontig_1.153_MVLG_06799_7sp	-388,20	-388,20	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.182_MVLG_07011_6sp	-658,20	-658,20	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.71_MVLG_05349_9sp	-1007,55	-1007,55	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF01138.14	RNase_PH(3' exoribonuclease family, domain 1)
Supercontig_1.114_MVLG_06355_9sp	-444,33	-444,33	0,00	0,00	NS	0	[]	[]	[]	60S ribosomal protein L20	PF01775.10	Ribosomal_L18ae(Ribosomal L18ae/LX protein domain)
Supercontig_1.218_MVLG_07153_6sp	-543,94	-543,92	0,04	0,02	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.193_MVLG_07053_7sp	-681,74	-681,74	0,00	0,00	NS	0	[]	[]	[]	uricase	TIGR03383	TIGR03383(urate_oxi: urate oxidase)

Supercontig_1.106_MVLG_06235_11sp	-426,89	-426,89	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.72_MVLG_05401_8sp	-874,06	-874,06	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF00790.12	VHS(VHS domain)
Supercontig_1.71_MVLG_05347_10sp	-610,09	-610,09	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF00172.11	Zn_clus(Fungal Zn(2)-Cys(6) binuclear cluster domain)
Supercontig_1.145_MVLG_06732_8sp	-983,34	-981,78	3,11	0,79	NS	0	[]	[]	[]	hypothetical protein	TIGR01499	TIGR01499(folC: bifunctional protein FolC)
Supercontig_1.187_MVLG_07035_9sp	-814,05	-814,05	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.71_MVLG_05348_10sp	-334,79	-334,79	0,00	5.99982000550431e-05	NS	0	[]	[]	[]	hypothetical protein	TIGR00440	TIGR00440(glnS: glutamine--tRNA ligase)
Supercontig_1.71_MVLG_05365_10sp	-357,28	-357,28	0,00	0,00	NS	0	[]	[]	[]	TKL/LISK/LISK-DD1 protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.138_MVLG_06653_10sp	-1102,07	-1101,81	0,53	0,23	NS	0	[]	[]	[]	hypothetical protein	PF04030.7	ALO(D-arabinono-1,4-lactone oxidase)
Supercontig_1.138_MVLG_06654_6sp	-477,08	-477,08	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF02985.15	HEAT(HEAT repeat)
Supercontig_1.188_MVLG_07037_8sp	-1432,41	-1432,41	0,00	6.9997549880445e-05	NS	0	[]	[]	[]	hypothetical protein	PF07724.7	AAA_2(AAA domain (Cdc48 subfamily))
Supercontig_1.146_MVLG_06744_10sp	-728,92	-728,92	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF00618.13	RasGEF_N(motif)
Supercontig_1.71_MVLG_05359_6sp	-371,30	-371,30	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF02953.8	zf-Tim10_DDP(Tim10/DDP family zinc finger)
Supercontig_1.271_MVLG_07223_8sp	-494,04	-493,66	0,76	0,32	NS	0	[]	[]	[]	RNA polymerase Rpb3/Rpb11 dimerization domain-containing protein	PF01000.19	RNA_pol_A_bac(RNA polymerase Rpb3/RpoA insert domain)
Supercontig_1.72_MVLG_05380_7sp	-507,07	-506,90	0,35	0,16	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.115_MVLG_06365_11sp	-462,44	-462,44	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.115_MVLG_06366_7sp	-664,75	-664,73	0,03	0,01	NS	0	[]	[]	[]	hypothetical protein	PF00790.12	VHS(VHS domain)
Supercontig_1.108_MVLG_06261_10sp	-441,53	-440,03	2,99	0,78	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.217_MVLG_07145_8sp	-413,99	-413,98	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF01088.14	Peptidase_C12(Ubiquitin carboxyl-terminal hydrolase, family 1)
Supercontig_1.137_MVLG_06646_9sp	-1503,42	-1503,42	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.115_MVLG_06364_12sp	-592,24	-591,72	1,03	0,40	NS	0	[]	[]	[]	hypothetical protein	PF07989.4	Microtub_assoc(Microtubule associated)
Supercontig_1.71_MVLG_05360_8sp	-796,97	-796,97	0,00	0,00	NS	0	[]	[]	[]	phospholipid-translocating ATPase	TIGR01494	TIGR01494(ATPase_P-type: HAD ATPase, P-type, family IC)
Supercontig_1.169_MVLG_06932_8sp	-700,62	-700,62	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	NA	NA

Supercontig_1.71_MVLG_05367_12sp	-960,88	-958,71	4,34	0,89	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.146_MVLG_06739_6sp	-861,46	-861,46	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.115_MVLG_06367_7sp	-772,04	-771,98	0,12	0,06	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.162_MVLG_06880_8sp	-793,64	-793,64	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF04729.6	ASF1_hist_chap(ASF1 like histone chaperone)
Supercontig_1.133_MVLG_06607_10sp	-965,26	-965,26	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.167_MVLG_06923_6sp	-972,05	-971,22	1,66	0,56	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.114_MVLG_06360_9sp	-588,08	-588,08	2.00000001768785e-05	9.99995008860505e-06	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.72_MVLG_05377_9sp	-462,18	-462,18	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.72_MVLG_05397_11sp	-1077,03	-1077,03	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF08558.3	TRF(Telomere repeat binding factor (TRF))
Supercontig_1.118_MVLG_06408_10sp	-480,84	-480,84	0,00	9.999500014156 3e-05	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.182_MVLG_07012_6sp	-685,15	-685,15	0,00	0,00	NS	0	[]	[]	[]	deoxyuridine 5'-triphosphate nucleotidohydrolase	TIGR00576	TIGR00576(dut: dUTP diphosphatase)
Supercontig_1.146_MVLG_06738_9sp	-443,29	-441,28	4,02	0,87	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.72_MVLG_05398_6sp	-604,10	-602,45	3,30	0,81	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.72_MVLG_05390_10sp	-1190,80	-1190,80	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF08101.4	DUF1708(Domain of unknown function (DUF1708))
Supercontig_1.405_MVLG_07262_10sp	-615,91	-614,37	3,08	0,79	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.146_MVLG_06737_7sp	-613,08	-610,52	5,12	0,92	*	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.71_MVLG_05344_6sp	-315,64	-315,64	6.00000000758882e-05	2.99995500424429e-05	NS	0	[]	[]	[]	hypothetical protein	TIGR00091	TIGR00091(TIGR00091: tRNA (guanine-N(7)-)-methyltransferase)
Supercontig_1.71_MVLG_05369_7sp	-692,18	-692,18	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF08241.5	Methyltransf_11(Methyltransferase domain)
Supercontig_1.72_MVLG_05382_6sp	-619,27	-619,27	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.137_MVLG_06644_6sp	-432,62	-432,62	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.72_MVLG_05402_10sp	-445,17	-445,08	0,19	0,09	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.214_MVLG_07139_7sp	-832,56	-832,56	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF10540.2	Membr_traf_MHD(Munc13 (mammalian uncoordinated) homology domain)

Supercontig_1.146_MVLG_06742_9sp	-1107,77	-1107,76	0,01	0,01	NS	0	[]	[]	[]	hypothetical protein	PF00494.12	SQS_PSY(Squalene/phytoene synthase)
Supercontig_1.118_MVLG_06407_9sp	-563,09	-563,09	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF00106.18	adh_short(short chain dehydrogenase)
Supercontig_1.108_MVLG_06264_10sp	-640,76	-640,76	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF07524.6	Bromo_TP(Bromodomain associated)
Supercontig_1.162_MVLG_06878_7sp	-896,78	-894,67	4,21	0,88	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.133_MVLG_06609_6sp	-724,10	-721,13	5,94	0,95	*	0	[]	[]	[]	hypothetical protein	PF10275.2	Peptidase_C65(Peptidase C65 Otubain)
Supercontig_1.103_MVLG_06194_7sp	-548,91	-548,91	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF04450.5	BSP(Plant Basic Secretory Protein)
Supercontig_1.201_MVLG_07086_10sp	-646,71	-646,71	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF03810.12	IBN_N(Importin-beta N-terminal domain)
Supercontig_1.106_MVLG_06231_6sp	-826,54	-826,54	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.153_MVLG_06798_9sp	-454,26	-454,23	0,06	0,03	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.144_MVLG_06726_7sp	-412,57	-412,57	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF03715.6	Noc2(Noc2p family)
Supercontig_1.72_MVLG_05391_7sp	-674,35	-673,32	2,05	0,64	NS	0	[]	[]	[]	hypothetical protein	PF05653.7	DUF803(Protein of unknown function (DUF803))
Supercontig_1.71_MVLG_05355_11sp	-394,12	-394,12	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF01784.11	NIF3(NIF3 (NGG1p interacting factor 3))
Supercontig_1.106_MVLG_06236_10sp	-977,67	-977,67	0,00	6.999755010780 28e-05	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.134_MVLG_06618_11sp	-459,95	-459,44	1,02	0,40	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.90_MVLG_05907_9sp	-386,29	-385,10	2,39	0,70	NS	0	[]	[]	[]	hypothetical protein	PF00076.15	RRM_1(RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain))
Supercontig_1.145_MVLG_06730_10sp	-477,78	-475,73	4,10	0,87	NS	0	[]	[]	[]	adenosinetriphosphatase	PF00270.22	DEAD(DEAD/DEAH box helicase)
Supercontig_1.103_MVLG_06184_7sp	-498,57	-498,55	0,04	0,02	NS	0	[]	[]	[]	hypothetical protein	PF00565.10	SNase(Staphylococcal nuclease homologue)
Supercontig_1.187_MVLG_07034_6sp	-344,26	-344,26	0,00	5.999819999820 31e-05	NS	0	[]	[]	[]	U3 small nucleolar ribonucleoprotein IMP3	PF01479.18	S4(S4 domain)
Supercontig_1.153_MVLG_06795_11sp	-844,91	-844,91	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF03357.14	Snf7(Snf7)
Supercontig_1.195_MVLG_07059_7sp	-764,88	-763,65	2,46	0,71	NS	0	[]	[]	[]	hypothetical protein	PF04699.7	P16-Arc(ARP2/3 complex 16 kDa subunit (p16-Arc))
Supercontig_1.72_MVLG_05378_6sp	-765,28	-765,24	0,07	0,04	NS	0	[]	[]	[]	hypothetical protein	PF00856.21	SET(SET domain)
Supercontig_1.90_MVLG_05916_7sp	-767,43	-767,43	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF11899.1	DUF3419(Protein of unknown function (DUF3419))
Supercontig_1.134_MVLG_06615_10sp	-586,25	-585,49	1,52	0,53	NS	0	[]	[]	[]	hypothetical protein	PF05529.5	Bap31(B-cell receptor-associated protein 31-like)

Supercontig_1.71_MVLG_05368_8sp	-744,89	-744,89	0,00	0,00	NS	0	[]	[]	[]	DNA-directed RNA polymerase III subunit RPC2	PF04565.9	RNA_pol_Rpb2_3(RNA polymerase Rpb2, domain 3)
Supercontig_1.136_MVLG_06642_9sp	-593,89	-593,65	0,48	0,21	NS	0	[]	[]	[]	hypothetical protein	PF03345.7	DDOST_48kD(Oligosaccharyltransferase 48 kDa subunit beta)
Supercontig_1.179_MVLG_06990_8sp	-322,15	-322,15	0,00	4.99987500651233e-05	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.157_MVLG_06844_7sp	-414,76	-414,40	0,73	0,31	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.162_MVLG_06877_8sp	-415,65	-414,78	1,72	0,58	NS	0	[]	[]	[]	hypothetical protein	PF04573.5	SPC22(Signal peptidase subunit)
Supercontig_1.71_MVLG_05350_9sp	-611,47	-611,47	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF02770.12	Acyl-CoA_dh_M(Acyl-CoA dehydrogenase, middle domain)
Supercontig_1.71_MVLG_05363_6sp	-285,90	-285,84	0,13	0,06	NS	0	[]	[]	[]	hypothetical protein	PF10775.2	ATP_sub_h(ATP synthase complex subunit h)
Supercontig_1.119_MVLG_06420_8sp	-385,07	-382,96	4,22	0,88	NS	0	[]	[]	[]	hypothetical protein	PF02466.12	Tim17(Tim17/Tim22/Tim23 family)
Supercontig_1.103_MVLG_06191_8sp	-536,06	-536,06	1.99999999495049e-05	9.99994997491935e-06	NS	0	[]	[]	[]	hypothetical protein	PF00642.17	zf-CCCH(Zinc finger C-x8-C-x5-C-x3-H type (and similar))
Supercontig_1.90_MVLG_05905_9sp	-355,48	-355,44	0,08	0,04	NS	0	[]	[]	[]	mitochondrial 2-oxodicarboxylate carrier 2	PF00153.20	Mito_carr(Mitochondrial carrier protein)
Supercontig_1.118_MVLG_06409_9sp	-387,67	-387,67	0,00	0,00	NS	0	[]	[]	[]	CMGC/MAPK/P38 protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.72_MVLG_05376_9sp	-1117,64	-1117,64	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.71_MVLG_05357_9sp	-991,58	-991,54	0,07	0,03	NS	0	[]	[]	[]	hypothetical protein	PF00928.14	Adap_comp_sub(Adaptor complexes medium subunit family)
Supercontig_1.179_MVLG_06993_7sp	-523,61	-522,19	2,85	0,76	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.71_MVLG_05361_7sp	-280,33	-280,33	0,01	0,01	NS	0	[]	[]	[]	hypothetical protein	PF04387.7	PTPLA(Protein tyrosine phosphatase-like protein, PTPLA)
Supercontig_1.72_MVLG_05384_12sp	-735,86	-735,86	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF00012.13	HSP70(Hsp70 protein)
Supercontig_1.133_MVLG_06612_8sp	-2103,41	-2100,92	4,98	0,92	*	0	[]	[]	[]	hypothetical protein	PF04969.9	CS(CS domain)
Supercontig_1.208_MVLG_07121_8sp	-1114,96	-1114,86	0,19	0,09	NS	0	[]	[]	[]	hypothetical protein	PF03828.12	PAP_assoc(Poly(A) polymerase)
Supercontig_1.144_MVLG_06727_6sp	-261,22	-261,22	7.99999999117063e-05	3.99991999665215e-05	NS	0	[]	[]	[]	hypothetical protein	NA	NA

Supercontig_1.144_MVLG_06724_7sp	-1218,48	-1218,48	1.99999999495049e-05	9.99994997491935e-06	NS	0	[]	[]	[]	hypothetical protein	PF00611.16	FCH(Fes/CIP4 homology domain)
Supercontig_1.118_MVLG_06405_7sp	-319,21	-318,35	1,72	0,58	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.193_MVLG_07052_10sp	-549,65	-548,53	2,24	0,67	NS	0	[]	[]	[]	hypothetical protein	PF00319.11	SRF-TF(SRF-type transcription factor (DNA-binding and dimerisation domain))
Supercontig_1.71_MVLG_05364_9sp	-701,50	-701,36	0,28	0,13	NS	0	[]	[]	[]	60S ribosomal protein L21-A	PF01157.11	Ribosomal_L21e(Ribosomal protein L21e)
Supercontig_1.177_MVLG_06982_7sp	-987,06	-986,54	1,04	0,41	NS	0	[]	[]	[]	hypothetical protein	PF03635.10	Vps35(Vacuolar protein sorting-associated protein 35)
Supercontig_1.72_MVLG_05393_6sp	-506,05	-506,05	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF00153.20	Mito_carr(Mitochondrial carrier protein)
Supercontig_1.119_MVLG_06418_9sp	-377,06	-375,68	2,76	0,75	NS	0	[]	[]	[]	hypothetical protein	PF10075.2	PCI_Csn8(COP9 signalosome, subunit CSN8)
Supercontig_1.218_MVLG_07151_7sp	-500,11	-499,13	1,96	0,62	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.106_MVLG_06230_9sp	-420,51	-420,51	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.119_MVLG_06416_10sp	-655,61	-655,42	0,38	0,17	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.90_MVLG_05912_9sp	-331,97	-331,49	0,95	0,38	NS	0	[]	[]	[]	hypothetical protein	PF00564.17	PB1(PB1 domain)
Supercontig_1.71_MVLG_05345_9sp	-537,16	-537,16	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF00171.15	Aldedh(Aldehyde dehydrogenase family)
Supercontig_1.115_MVLG_06368_8sp	-498,74	-497,56	2,35	0,69	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.144_MVLG_06725_8sp	-1038,14	-1038,13	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF06870.5	RNA_pol_I_A49(A49-like RNA polymerase I associated factor)
Supercontig_1.72_MVLG_05387_10sp	-379,46	-379,46	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF00400.25	WD40(WD domain, G-beta repeat)
Supercontig_1.217_MVLG_07146_10sp	-479,61	-479,61	0,00	0,00	NS	0	[]	[]	[]	T-complex protein 1 subunit beta	TIGR02341	TIGR02341(chap_CCT_beta: T-complex protein 1, beta subunit)
Supercontig_1.72_MVLG_05399_10sp	-605,25	-605,25	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF01937.12	DUF89(Protein of unknown function DUF89)
Supercontig_1.103_MVLG_06195_8sp	-467,28	-467,28	2.00000000631917e-05	9.9999500317622e-06	NS	0	[]	[]	[]	hypothetical protein	PF12542.1	CWC25(Pre-mRNA splicing factor)
Supercontig_1.219_MVLG_07155_8sp	-794,84	-794,84	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF02450.8	LACT(Lecithin:cholesterol acyltransferase)
Supercontig_1.138_MVLG_06656_10sp	-756,41	-755,13	2,55	0,72	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.72_MVLG_05379_7sp	-554,65	-554,27	0,75	0,31	NS	0	[]	[]	[]	hypothetical protein	NA	NA

Supercontig_1.214_MVLG_07138_8sp	-834,17	-833,89	0,58	0,25	NS	0	[]	[]	[]	hypothetical protein	PF00004.22	AAA(ATPase family associated with various cellular activities (AAA))
Supercontig_1.134_MVLG_06623_8sp	-625,78	-625,78	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF04182.5	B-block_TFIIIC(B-block binding subunit of TFIIIC)
Supercontig_1.119_MVLG_06413_8sp	-647,42	-647,42	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF00076.15	RRM_1(RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain))
Supercontig_1.179_MVLG_06991_8sp	-793,70	-793,44	0,51	0,23	NS	0	[]	[]	[]	hypothetical protein	PF00443.22	UCH(Ubiquitin carboxyl-terminal hydrolase)
Supercontig_1.153_MVLG_06800_10sp	-971,49	-971,49	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.252_MVLG_07215_11sp	-1252,66	-1252,01	1,29	0,48	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.133_MVLG_06608_10sp	-1487,11	-1487,11	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.72_MVLG_05374_7sp	-745,83	-745,83	0,00	0,00	NS	0	[]	[]	[]	malate dehydrogenase, NAD-dependent	PF02866.11	Ldh_1_C(lactate/malate dehydrogenase, alpha/beta C-terminal domain)
Supercontig_1.218_MVLG_07149_6sp	-699,45	-698,71	1,47	0,52	NS	0	[]	[]	[]	hypothetical protein	PF05920.4	Coprinus_mating(Coprinus cinereus mating-type protein)
Supercontig_1.72_MVLG_05385_10sp	-631,46	-630,41	2,09	0,65	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.90_MVLG_05918_8sp	-429,06	-428,41	1,30	0,48	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.108_MVLG_06267_12sp	-507,18	-507,18	1.99999999495049e-05	9.99994997491935e-06	NS	0	[]	[]	[]	hypothetical protein	PF09462.3	Mus7(Mus7/MMS22 family)
Supercontig_1.237_MVLG_07198_10sp	-1060,53	-1060,53	0,00	0,00	NS	0	[]	[]	[]	DNA replication licensing factor mcm2	PF12619.1	MCM2_N(Minichromosone maintenance protein 2)
Supercontig_1.221_MVLG_07163_8sp	-339,94	-337,72	4,43	0,89	NS	0	[]	[]	[]	hypothetical protein	PF12251.1	zf-SNAP50_C(snRNA-activating protein of 50kDa MW C terminal)
Supercontig_1.136_MVLG_06640_6sp	-348,56	-348,19	0,75	0,31	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.201_MVLG_07085_10sp	-348,01	-348,00	0,01	0,00	NS	0	[]	[]	[]	hypothetical protein	PF01423.15	LSM(LSM domain)
Supercontig_1.72_MVLG_05375_7sp	-639,02	-639,02	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF01557.11	FAA_hydrolase(Fumarylacetoacetate (FAA) hydrolase family)
Supercontig_1.119_MVLG_06417_9sp	-723,04	-722,63	0,82	0,34	NS	0	[]	[]	[]	hypothetical protein	PF00153.20	Mito_carr(Mitochondrial carrier protein)
Supercontig_1.115_MVLG_06363_8sp	-477,84	-477,84	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF02630.7	SCO1-SenC(SCO1/SenC)
Supercontig_1.187_MVLG_07032_8sp	-412,58	-412,58	0,00	0,00	NS	0	[]	[]	[]	Beta glucosidase	PF00933.14	Glyco_hydro_3(Glycosyl hydrolase family 3 N terminal domain)
Supercontig_1.162_MVLG_06876_9sp	-409,08	-409,04	0,08	0,04	NS	0	[]	[]	[]	hypothetical protein	NA	NA

Supercontig_1.103_MVLG_06193_10sp	-819,53	-819,02	1,02	0,40	NS	0	[]	[]	[]	hypothetical protein	PF07819.6	PGAP1(PGAP1-like protein)
Supercontig_1.182_MVLG_07013_10sp	-311,96	-311,85	0,23	0,11	NS	0	[]	[]	[]	hypothetical protein	PF00225.16	Kinesin(Kinesin motor domain)
Supercontig_1.72_MVLG_05400_12sp	-672,31	-672,31	3.999999989900097e-05	1.999979995083092e-05	NS	0	[]	[]	[]	hypothetical protein	PF03435.11	Saccharop_dh(Saccharopine dehydrogenase)
Supercontig_1.118_MVLG_06404_6sp	-453,07	-453,07	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.72_MVLG_05392_8sp	-544,76	-544,59	0,35	0,16	NS	0	[]	[]	[]	hypothetical protein	PF04178.5	Got1(Got1/Sft2-like family)
Supercontig_1.177_MVLG_06985_11sp	-516,93	-516,93	1.999999994950049e-05	9.999949974919035e-06	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.146_MVLG_06741_10sp	-439,40	-439,40	1.999999994950049e-05	9.999949974919035e-06	NS	0	[]	[]	[]	hypothetical protein	PF00135.21	COesterase(Carboxylesterase)
Supercontig_1.106_MVLG_06233_9sp	-1993,61	-1993,54	0,14	0,07	NS	0	[]	[]	[]	hypothetical protein	PF00443.22	UCH(Ubiquitin carboxyl-terminal hydrolase)

C

Supercontig_1.37_MVLG_03701_7sp	-460,61	-455,26	10,69	1,00	*******	**1**	[]	**['22W']**	[]	hypothetical protein	NA	NA
Supercontig_1.37_MVLG_03730_7sp	-537,71	-532,46	10,50	0,99	*******	**1**	[]	**['24T']**	[]	hypothetical protein	NA	NA
Supercontig_1.43_MVLG_04125_11sp	-779,90	-774,48	10,84	1,00	*******	**1**	[]	**['72N']**	[]	DNA-directed RNA polymerase III subunit rpc1	PF00623.13	RNA_pol_Rpb1_2(RNA polymerase Rpb1, domain 2)
Supercontig_1.37_MVLG_03732_9sp	-685,39	-684,54	1,69	0,57	NS	1	[]	[]	['79Q']	hypothetical protein	PF01522.14	Polysacc_deac_1(Polysaccharide deacetylase)
Supercontig_1.37_MVLG_03719_7sp	-806,85	-805,98	1,73	0,58	NS	0	[]	[]	[]	hypothetical protein	PF00076.15	RRM_1(RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain))
Supercontig_1.37_MVLG_03717_10sp	-451,75	-451,73	0,04	0,02	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.37_MVLG_03706_8sp	-882,39	-882,39	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.37_MVLG_03757_11sp	-406,71	-406,71	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF02201.11	SWIB(SWIB/MDM2 domain)
Supercontig_1.43_MVLG_04101_11sp	-392,98	-392,98	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF00520.24	Ion_trans(Ion transport protein)
Supercontig_1.37_MVLG_03756_6sp	-375,60	-375,60	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.37_MVLG_03713_12sp	-555,36	-554,85	1,01	0,40	NS	0	[]	[]	[]	CAMK/CAMKL/KIN4 protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.37_MVLG_03752_7sp	-540,34	-540,34	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF04695.6	Pex14_N(Peroxisomal membrane anchor protein (Pex14p) conserved region)
Supercontig_1.37_MVLG_03716_6sp	-1167,28	-1167,28	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF07969.4	Amidohydro_3(Amidohydrolase family)

Supercontig_1.37_MVLG_03718_6sp	-375,08	-375,07	0,02	0,01	NS	0	[]	[]	[]	hypothetical protein	PF05983.4	Med7(MED7 protein)
Supercontig_1.43_MVLG_04130_9sp	-665,50	-665,32	0,36	0,17	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.37_MVLG_03739_9sp	-658,05	-657,86	0,38	0,17	NS	0	[]	[]	[]	hypothetical protein	PF07524.6	Bromo_TP(Bromodomain associated)
Supercontig_1.37_MVLG_03724_8sp	-971,20	-971,20	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF08651.3	DASH_Duo1(DASH complex subunit Duo1)
Supercontig_1.43_MVLG_04094_12sp	-780,33	-780,33	0,00	0,00	NS	0	[]	[]	[]	ribonucleoside-diphosphate reductase large chain	PF02867.8	Ribonuc_red_lgC(Ribonucleotide reductase, barrel domain)
Supercontig_1.43_MVLG_04095_10sp	-546,61	-546,61	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF06398.4	Pex24p(Integral peroxisomal membrane peroxin)
Supercontig_1.37_MVLG_03727_9sp	-469,65	-469,65	0,00	0,00	NS	0	[]	[]	[]	3'(2'),5'-bisphosphate nucleotidase	TIGR01330	TIGR01330(bisphos_HAL2: 3'(2'),5'-bisphosphate nucleotidase)
Supercontig_1.43_MVLG_04112_9sp	-888,71	-888,71	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF00226.24	DnaJ(DnaJ domain)
Supercontig_1.37_MVLG_03747_6sp	-709,13	-707,43	3,39	0,82	NS	0	[]	[]	[]	hypothetical protein	PF00295.10	Glyco_hydro_28(Glycosyl hydrolases family 28)
Supercontig_1.37_MVLG_03705_7sp	-410,64	-410,64	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF00013.22	KH_1(KH domain)
Supercontig_1.43_MVLG_04127_6sp	-746,68	-746,68	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF08450.5	SGL(SMP-30/Gluconolaconase/LRE-like region)
Supercontig_1.37_MVLG_03738_9sp	-508,87	-508,87	2.00000000631917e-05	9.9999500317622e-06	NS	0	[]	[]	[]	hypothetical protein	PF01432.13	Peptidase_M3(Peptidase family M3)
Supercontig_1.43_MVLG_04099_10sp	-542,03	-542,03	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF09088.4	MIF4G_like(MIF4G like)
Supercontig_1.37_MVLG_03715_6sp	-568,34	-567,87	0,93	0,37	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.37_MVLG_03729_10sp	-715,87	-715,87	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	TIGR00290	TIGR00290(MJ0570_dom: MJ0570-related uncharacterized domain)
Supercontig_1.37_MVLG_03734_8sp	-372,42	-372,42	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF01522.14	Polysacc_deac_1(Polysaccharide deacetylase)
Supercontig_1.43_MVLG_04097_9sp	-464,25	-464,25	4.0000000126965e-05	1.99998000076815e-05	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.37_MVLG_03728_12sp	-333,82	-333,82	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF00940.12	RNA_pol(DNA-dependent RNA polymerase)
Supercontig_1.37_MVLG_03742_6sp	-595,00	-595,00	0,00	5.99981999982031e-05	NS	0	[]	[]	[]	hypothetical protein	NA	NA

Supercontig_1.43_MVLG_04115_6sp	-310,64	-310,64	5.99999999622014e-05	2.99995499856012e-05	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.43_MVLG_04109_12sp	-732,68	-732,68	9.99999999748979e-05	4.99987500082827e-05	NS	0	[]	[]	[]	hypothetical protein	PF12157.1	DUF3591(Protein of unknown function (DUF3591))
Supercontig_1.37_MVLG_03725_10sp	-569,10	-569,10	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF01207.10	Dus(Dihydrouridine synthase (Dus))
Supercontig_1.37_MVLG_03731_10sp	-400,45	-400,45	9.99999999748979e-05	4.99987500082827e-05	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.43_MVLG_04132_8sp	-550,39	-550,25	0,29	0,13	NS	0	[]	[]	[]	hypothetical protein	PF00097.18	zf-C3HC4(Zinc finger, C3HC4 type (RING finger))
Supercontig_1.37_MVLG_03708_9sp	-622,12	-619,98	4,28	0,88	NS	0	[]	[]	[]	hypothetical protein	PF01937.12	DUF89(Protein of unknown function DUF89)
Supercontig_1.37_MVLG_03711_9sp	-812,55	-812,55	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF01565.16	FAD_binding_4(FAD binding domain)
Supercontig_1.43_MVLG_04110_11sp	-666,03	-666,03	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF11696.1	DUF3292(Protein of unknown function (DUF3292))
Supercontig_1.43_MVLG_04114_7sp	-666,49	-666,49	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.43_MVLG_04131_7sp	-896,15	-896,15	0,00	0,00	NS	0	[]	[]	[]	catalase	PF00199.12	Catalase(Catalase)
Supercontig_1.43_MVLG_04129_7sp	-1252,36	-1252,35	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF08711.4	Med26(TFIIS helical bundle-like domain)
Supercontig_1.37_MVLG_03720_7sp	-468,29	-468,26	0,07	0,03	NS	0	[]	[]	[]	GTP-binding protein ypt5	PF04670.5	Gtr1_RagA(Gtr1/RagA G protein conserved region)
Supercontig_1.43_MVLG_04108_6sp	-361,27	-361,20	0,14	0,07	NS	0	[]	[]	[]	DNA-directed RNA polymerase I, II, and III subunit RPABC2	PF01192.15	RNA_pol_Rpb6(RNA polymerase Rpb6)
Supercontig_1.37_MVLG_03736_8sp	-910,05	-909,82	0,46	0,21	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.37_MVLG_03743_7sp	-606,48	-606,29	0,39	0,18	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.37_MVLG_03714_10sp	-490,20	-490,13	0,15	0,07	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.43_MVLG_04102_9sp	-625,28	-625,28	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.37_MVLG_03753_8sp	-957,48	-957,41	0,13	0,06	NS	0	[]	[]	[]	hypothetical protein	PF00096.19	zf-C2H2(Zinc finger, C2H2 type)
Supercontig_1.43_MVLG_04119_8sp	-557,36	-556,56	1,61	0,55	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.37_MVLG_03709_9sp	-517,96	-517,96	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF08613.4	Cyclin(Cyclin)
Supercontig_1.43_MVLG_04120_7sp	-362,37	-362,37	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.37_MVLG_03754_9sp	-406,87	-406,87	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF00498.19	FHA(FHA domain)

Supercontig_1.43_MVLG_04123_6sp	-595,86	-595,08	1,55	0,54	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.43_MVLG_04111_8sp	-633,08	-633,08	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF08487.3	VIT(Vault protein inter-alpha-trypsin)
Supercontig_1.37_MVLG_03722_8sp	-391,43	-391,43	2.00000000631917e-05	9.9999500317622e-06	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.43_MVLG_04113_11sp	-945,05	-945,05	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF04910.7	DUF654(Protein of unknown function, DUF654)
Supercontig_1.37_MVLG_03712_12sp	-461,72	-461,72	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF06428.4	Sec2p(GDP/GTP exchange factor Sec2p)
Supercontig_1.43_MVLG_04124_10sp	-613,62	-613,62	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	TIGR00059	TIGR00059(L17: ribosomal protein L17)
Supercontig_1.37_MVLG_03710_7sp	-479,79	-479,79	7.99999999117063e-05	3.99991999665215e-05	NS	0	[]	[]	[]	hypothetical protein	PF01553.14	Acyltransferase(Acyltransferase)
Supercontig_1.37_MVLG_03737_7sp	-464,23	-464,07	0,32	0,15	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.43_MVLG_04117_10sp	-602,16	-602,16	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF05236.7	TAF4(Transcription initiation factor TFIID component TAF4 family)
Supercontig_1.37_MVLG_03723_12sp	-394,98	-394,98	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	TIGR00879	TIGR00879(SP: MFS transporter, sugar porter (SP) family)
Supercontig_1.43_MVLG_04121_6sp	-658,72	-658,72	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.37_MVLG_03755_8sp	-427,92	-427,92	0,00	0,00	NS	0	[]	[]	[]	cytochrome c oxidase subunit Va	PF02284.9	COX5A(Cytochrome c oxidase subunit Va)
Supercontig_1.37_MVLG_03758_7sp	-2081,50	-2081,12	0,76	0,32	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.37_MVLG_03701_7sp	-460,61	-455,26	10,69	1,00	*******	**1**	[]	**['22W']**	[]	hypothetical protein	NA	NA
Supercontig_1.37_MVLG_03730_7sp	-537,71	-532,46	10,50	0,99	*******	**1**	[]	**['24T']**	[]	hypothetical protein	NA	NA
Supercontig_1.43_MVLG_04125_11sp	-779,90	-774,48	10,84	1,00	*******	**1**	[]	**['72N']**	[]	DNA-directed RNA polymerase III subunit rpc1	PF00623.13	RNA_pol_Rpb1_2(RNA polymerase Rpb1, domain 2)
Supercontig_1.37_MVLG_03732_9sp	-685,39	-684,54	1,69	0,57	NS	1	[]	[]	['79Q']	hypothetical protein	PF01522.14	Polysacc_deac_1(Polysaccharide deacetylase)
Supercontig_1.37_MVLG_03719_7sp	-806,85	-805,98	1,73	0,58	NS	0	[]	[]	[]	hypothetical protein	PF00076.15	RRM_1(RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain))
Supercontig_1.37_MVLG_03717_10sp	-451,75	-451,73	0,04	0,02	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.37_MVLG_03706_8sp	-882,39	-882,39	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.37_MVLG_03757_11sp	-406,71	-406,71	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF02201.11	SWIB(SWIB/MDM2 domain)
Supercontig_1.43_MVLG_04101_11sp	-392,98	-392,98	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF00520.24	Ion_trans(Ion transport protein)

Supercontig_1.37_MVLG_03756_6sp	-375,60	-375,60	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.37_MVLG_03713_12sp	-555,36	-554,85	1,01	0,40	NS	0	[]	[]	[]	CAMK/CAMKL/KIN4 protein kinase	PF07714.10	Pkinase_Tyr(Protein tyrosine kinase)
Supercontig_1.37_MVLG_03752_7sp	-540,34	-540,34	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF04695.6	Pex14_N(Peroxisomal membrane anchor protein (Pex14p) conserved region)
Supercontig_1.37_MVLG_03716_6sp	-1167,28	-1167,28	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF07969.4	Amidohydro_3(Amidohydrolase family)
Supercontig_1.37_MVLG_03718_6sp	-375,08	-375,07	0,02	0,01	NS	0	[]	[]	[]	hypothetical protein	PF05983.4	Med7(MED7 protein)
Supercontig_1.43_MVLG_04130_9sp	-665,50	-665,32	0,36	0,17	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.37_MVLG_03739_9sp	-658,05	-657,86	0,38	0,17	NS	0	[]	[]	[]	hypothetical protein	PF07524.6	Bromo_TP(Bromodomain associated)
Supercontig_1.37_MVLG_03724_8sp	-971,20	-971,20	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF08651.3	DASH_Duo1(DASH complex subunit Duo1)
Supercontig_1.43_MVLG_04094_12sp	-780,33	-780,33	0,00	0,00	NS	0	[]	[]	[]	ribonucleoside-diphosphate reductase large chain	PF02867.8	Ribonuc_red_lgC(Ribonucleotide reductase, barrel domain)
Supercontig_1.43_MVLG_04095_10sp	-546,61	-546,61	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF06398.4	Pex24p(Integral peroxisomal membrane peroxin)
Supercontig_1.37_MVLG_03727_9sp	-469,65	-469,65	0,00	0,00	NS	0	[]	[]	[]	3'(2'),5'-bisphosphate nucleotidase	TIGR01330	TIGR01330(bisphos_HAL2: 3'(2'),5'-bisphosphate nucleotidase)
Supercontig_1.43_MVLG_04112_9sp	-888,71	-888,71	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF00226.24	DnaJ(DnaJ domain)
Supercontig_1.37_MVLG_03747_6sp	-709,13	-707,43	3,39	0,82	NS	0	[]	[]	[]	hypothetical protein	PF00295.10	Glyco_hydro_28(Glycosyl hydrolases family 28)
Supercontig_1.37_MVLG_03705_7sp	-410,64	-410,64	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF00013.22	KH_1(KH domain)
Supercontig_1.43_MVLG_04127_6sp	-746,68	-746,68	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF08450.5	SGL(SMP-30/Gluconolaconase/LRE-like region)
Supercontig_1.37_MVLG_03738_9sp	-508,87	-508,87	2.00000000631917e-05	9.999950031762 2e-06	NS	0	[]	[]	[]	hypothetical protein	PF01432.13	Peptidase_M3(Peptidase family M3)
Supercontig_1.43_MVLG_04099_10sp	-542,03	-542,03	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF09088.4	MIF4G_like(MIF4G like)
Supercontig_1.37_MVLG_03715_6sp	-568,34	-567,87	0,93	0,37	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.37_MVLG_03729_10sp	-715,87	-715,87	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	TIGR00290	TIGR00290(MJ0570_dom: MJ0570-related uncharacterized domain)
Supercontig_1.37_MVLG_03734_8sp	-372,42	-372,42	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF01522.14	Polysacc_deac_1(Polysaccharide deacetylase)
Supercontig_1.43_MVLG_04097_9sp	-464,25	-464,25	4.00000000126965e-05	1.99998000076815e-05	NS	0	[]	[]	[]	hypothetical protein	NA	NA

Supercontig_1.37_MVLG_03728_12sp	-333,82	-333,82	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF00940.12	RNA_pol(DNA-dependent RNA polymerase)
Supercontig_1.37_MVLG_03742_6sp	-595,00	-595,00	0,00	5.99981999982031e-05	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.43_MVLG_04115_6sp	-310,64	-310,64	5.99999999622014e-05	2.99995499856012e-05	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.43_MVLG_04109_12sp	-732,68	-732,68	9.99999999748979e-05	4.99987500082827e-05	NS	0	[]	[]	[]	hypothetical protein	PF12157.1	DUF3591(Protein of unknown function (DUF3591))
Supercontig_1.37_MVLG_03725_10sp	-569,10	-569,10	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF01207.10	Dus(Dihydrouridine synthase (Dus))
Supercontig_1.37_MVLG_03731_10sp	-400,45	-400,45	9.99999999748979e-05	4.99987500082827e-05	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.43_MVLG_04132_8sp	-550,39	-550,25	0,29	0,13	NS	0	[]	[]	[]	hypothetical protein	PF00097.18	zf-C3HC4(Zinc finger, C3HC4 type (RING finger))
Supercontig_1.37_MVLG_03708_9sp	-622,12	-619,98	4,28	0,88	NS	0	[]	[]	[]	hypothetical protein	PF01937.12	DUF89(Protein of unknown function DUF89)
Supercontig_1.37_MVLG_03711_9sp	-812,55	-812,55	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF01565.16	FAD_binding_4(FAD binding domain)
Supercontig_1.43_MVLG_04110_11sp	-666,03	-666,03	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF11696.1	DUF3292(Protein of unknown function (DUF3292))
Supercontig_1.43_MVLG_04114_7sp	-666,49	-666,49	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.43_MVLG_04131_7sp	-896,15	-896,15	0,00	0,00	NS	0	[]	[]	[]	catalase	PF00199.12	Catalase(Catalase)
Supercontig_1.43_MVLG_04129_7sp	-1252,36	-1252,35	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF08711.4	Med26(TFIIS helical bundle-like domain)
Supercontig_1.37_MVLG_03720_7sp	-468,29	-468,26	0,07	0,03	NS	0	[]	[]	[]	GTP-binding protein ypt5	PF04670.5	Gtr1_RagA(Gtr1/RagA G protein conserved region)
Supercontig_1.43_MVLG_04108_6sp	-361,27	-361,20	0,14	0,07	NS	0	[]	[]	[]	DNA-directed RNA polymerase I, II, and III subunit RPABC2	PF01192.15	RNA_pol_Rpb6(RNA polymerase Rpb6)
Supercontig_1.37_MVLG_03736_8sp	-910,05	-909,82	0,46	0,21	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.37_MVLG_03743_7sp	-606,48	-606,29	0,39	0,18	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.37_MVLG_03714_10sp	-490,20	-490,13	0,15	0,07	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.43_MVLG_04102_9sp	-625,28	-625,28	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.37_MVLG_03753_8sp	-957,48	-957,41	0,13	0,06	NS	0	[]	[]	[]	hypothetical protein	PF00096.19	zf-C2H2(Zinc finger, C2H2 type)
Supercontig_1.43_MVLG_04119_8sp	-557,36	-556,56	1,61	0,55	NS	0	[]	[]	[]	hypothetical protein	NA	NA

Supercontig_1.37_MVLG_03709_9sp	-517,96	-517,96	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF08613.4	Cyclin(Cyclin)
Supercontig_1.43_MVLG_04120_7sp	-362,37	-362,37	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.37_MVLG_03754_9sp	-406,87	-406,87	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF00498.19	FHA(FHA domain)
Supercontig_1.43_MVLG_04123_6sp	-595,86	-595,08	1,55	0,54	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.43_MVLG_04111_8sp	-633,08	-633,08	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF08487.3	VIT(Vault protein inter-alpha-trypsin)
Supercontig_1.37_MVLG_03722_8sp	-391,43	-391,43	2.00000000631917e-05	9.9999500317622e-06	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.43_MVLG_04113_11sp	-945,05	-945,05	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF04910.7	DUF654(Protein of unknown function, DUF654)
Supercontig_1.37_MVLG_03712_12sp	-461,72	-461,72	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF06428.4	Sec2p(GDP/GTP exchange factor Sec2p)
Supercontig_1.43_MVLG_04124_10sp	-613,62	-613,62	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	TIGR00059	TIGR00059(L17: ribosomal protein L17)
Supercontig_1.37_MVLG_03710_7sp	-479,79	-479,79	7.99999999117063e-05	3.99991999665215e-05	NS	0	[]	[]	[]	hypothetical protein	PF01553.14	Acyltransferase(Acyltransferase)
Supercontig_1.37_MVLG_03737_7sp	-464,23	-464,07	0,32	0,15	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.43_MVLG_04117_10sp	-602,16	-602,16	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	PF05236.7	TAF4(Transcription initiation factor TFIID component TAF4 family)
Supercontig_1.37_MVLG_03723_12sp	-394,98	-394,98	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	TIGR00879	TIGR00879(SP: MFS transporter, sugar porter (SP) family)
Supercontig_1.43_MVLG_04121_6sp	-658,72	-658,72	0,00	0,00	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.37_MVLG_03755_8sp	-427,92	-427,92	0,00	0,00	NS	0	[]	[]	[]	cytochrome c oxidase subunit Va	PF02284.9	COX5A(Cytochrome c oxidase subunit Va)
Supercontig_1.37_MVLG_03758_7sp	-2081,50	-2081,12	0,76	0,32	NS	0	[]	[]	[]	hypothetical protein	NA	NA
Supercontig_1.37_MVLG_03726_6sp	-502,69	-502,06	1,26	0,47	NS	0	[]	[]	[]	hypothetical protein	PF00578.14	AhpC-TSA(AhpC/TSA family)

D

	Autosomal	**NRR**	**PARs**
Number of POGs with at least one significant site under positive selection	240	12	3
Total number of POGs analyzed	5453	196	69

Ratio (%)	4,4	6,1	4,3