

ProbesetID	TranscriptID	Annotation	MapMan	Tern	Consensus	E
HVSME0006K11r2_at	bab91939.1	(ap003768) putative nadp dependent malic enzyme [oryza sativa (japonica cultivar_group)]	8.2.10	35_961		
Contig6860_at	bab08888.1	gene_id:mij24.6-ref np_013897.1-similar to unknown protein [arabidopsis thaliana]		35,2	35_16191	
Contig18997_at	aam22740.1	(ac092388) putative serine/threonine protein kinase [oryza sativa (japonica cultivar_group)]	29.4.1.57	35_7561		
rbags10k08_at	bac15853.1	(ap003746) contains ests d25106(r3184) au184634(r3184)-diphosphonucleotide		35,2	35_8534	
HY06D12u_s_at	hy06d12u_s_at	no annotation		35,2	35_17271	
Contig21187_at	np_197879.1	(nm_122406) putative protein; protein id: at5g24970.1 [arabidopsis thaliana]	35.1.1	35_24327		
HVSMEA0007I03r2_at	baa95828.1	ests d47168(s1232) d46350(s10967) correspond to a region of the predicted gene.-similar to prunus armeniaca	17.5.1	35_43599		
rbah15i08_s_at	np_195066.1	dem_like protein; protein id: at4g33400.1 supported by cdna: gi_20465422 [arabidopsis thaliana]		33,99	35_18661	
HV_CEb0006P16r2_s_at	hv_ceb0006p16r2_s_at	no annotation		35,2	35_4008	
Contig8246_at	aak27799.1	(ac022457) putative amylase [oryza sativa (japonica cultivar_group)]	2.2.2.1	35_17258		
Contig21613_at	bab89059.1	(ap003290) pdi_like protein [oryza sativa (japonica cultivar_group)]		35,2	35_25874	
Contig15315_at	aag41776.1	(af212990) ent_kaurene oxidase [cucurbita maxima]	17.6.1.3	35_21965		
Contig10520_s_at	np_176898.1	integral membrane protein putative; protein id: at1g67300.1 [arabidopsis thaliana]		34,2	35_4761	
Contig7750_at	np_200309.1	putative protein; protein id: at5g54980.1 [arabidopsis thaliana] dbj bab08777.1 gb aad50013.1~gene_id:mbg8.25-similar		35,2	35_17906	
Contig9045_at	bab61860.1	p0712e02.24 [oryza sativa (japonica cultivar_group)] dbj bab89906.1 p0700a11.5 [oryza sativa (japonica cultivar_group)]		35,1	35_4008	
Contig3892_at	np_193037.1	putative protein; protein id: at4g13010.1 supported by cdna: 6276. supported by cdna: gi_15028000 supported by		26,7	35_1404	
HV05023u_at	hv05023u_at	no annotation	20.2.1	35_14861		
Contig21251_at	t10255	nitrite transport protein chloroplast _ cucumber		34,13	35_7556	
HV_CEA0014A18r2_at	aag01554.1	HvHsfB2c	heat shock transcription factor B2c	27.3.23	35_18576	
Contig2014_at	t05739	probable heat shock protein 17 _ barley emb caa45861.1 (x64560) 17 kd heat shock protein [hordeum vulgare subsp. vul	20.2.1	35_14867		
Contig9737_s_at	aal79714.1	putative senescence_associated protein [oryza sativa]	20.2.3	35_3925		
Contig3198_at	contig3198_at	no annotation		35,2	35_15390	
Contig1823_at	aag13582.1	(ac037425) unknown protein [oryza sativa]		35,2	35_8063	
HVSME0016H11r2_s_at	hvsme0016h11r2_s_at	no annotation		35,2	35_8063	
Contig16980_at	np_567058.1	auxin-regulated protein; protein id: at3g57810.1 supported by cdna: 101256. supported by cdna: 29384. [arabidopsis]	29.5.3	35_22714		
Contig3761_at	aak26822.1	(af338432) starch branching enzyme iia variant [triticum aestivum]	2.1.2.3	35_15640		
HF21J01r_at	np_174269.1	(nm_102716) hypothetical protein; protein id: at1g29760.1 [arabidopsis thaliana]		35,2	35_13219	
HS06C20u_at	np_192861.1	putative protein; protein id: at4g11220.1 supported by cdna: 23536. supported by cdna: gi_14334419 supported by		33,99	35_1261	
HS06C20u_s_at	np_192861.1	putative protein; protein id: at4g11220.1 supported by cdna: 23536. supported by cdna: gi_14334419 supported by		33,99	35_1261	
Contig6802_at	bab90152.1	calcyclin binding protein_like [oryza sativa (japonica cultivar_group)]		35,2	35_16153	
Contig1381_at	aaf68995.1	metallothionein [porterresia coarctata]		35,2	35_14134	
Contig13656_at	contig13656_at	no annotation		35,2	35_4515	
Contig15180_at	np_174785.1	atp_dependent rna helicase putative; protein id: at1g35530.1 [arabidopsis thaliana]		28,1	35_21460	
Contig20753_at	bab92552.1	putative diacylglycerol kinase [oryza sativa (japonica cultivar_group)]		11,3	35_10001	
Contig2008_s_at	caa69172.1	HvHsp16.88-Cl	17 kda class i small heat shock protein [hordeum vulgare subsp. vulgare]	20.2.1	35_14863	
HB18H23r_s_at	hb18h23r_s_at	HvHsp17.5-Cl	heat shock protein 17.5	20.2.1	35_14859	
Contig2006_s_at	s72544	HvHsp17.7-Cl	heat shock protein 17.9 _ pearl millet emb caa63903.1 heat shock protein 17.9 [pennisetum glaucum]	20.2.1	35_14861	
Contig2007_s_at	caa69172.1	HvHsp16.88-Cl	17 kda class i small heat shock protein [hordeum vulgare subsp. vulgare]	20.2.1	35_14869	
Contig2012_s_at	s72544	HvHsp17.7-Cl	heat shock protein 17.9 _ pearl millet emb caa63903.1 heat shock protein 17.9 [pennisetum glaucum]	20.2.1	35_14866	
HY03K23u_at	s72544	HvHsp17.7-Cl	heat shock protein 17.9 _ pearl millet emb caa63903.1 heat shock protein 17.9 [pennisetum glaucum]	20.2.1	35_14866	
HY10H17u_at	hy10h17u_at	no annotation		35,2	35_47455	
Contig26505_at	bac20874.1	(ap005296) putative fiber protein [oryza sativa (japonica cultivar_group)]		35,2	35_21339	
Contig10284_at	np_191190.2	glycosyl hydrolase family 27 (alpha_galactosidase/melibiose); protein id: at3g56310.1 supported by cdna: gi_18377734	3.8.2	35_18279		
Contig3811_at	t07610	wsi76 protein _ rice dbj baa05538.1 wsi76 protein induced by water stress [oryza sativa]	3.1.1.1	35_1095		
Contig9310_at	np_191720.1	(nm_116026) putative protein; protein id: at3g61610.1 [arabidopsis thaliana]		3,5	35_17271	