

Cell wall and cell processes - 54 genes

GENE ID	GENE NAME	FUNCTION	Fragments Per Kilobase of transcript per Million mapped reads.						PPEE	PPDE	RealFC
			NORMAL Long			LSMMG Long					
			4days 35hr	4days 36hr	4days 37hr	4days 35hr	4days 36hr	4days 37hr	posterior probability that a transcript is equally expressed	posterior probability that a transcript is differentially expressed	real fold change is the ratio of the normalized mean count values for LSMMG over the normalized mean count values for normal
MMAR_0142	ltp1_1	cell wall and cell processes	61.57	57.72	49.4	125.2	112.16	96.59	6.86E-08	0.999999931	1.846561
MMAR_0218	MMAR_0218-1	cell wall and cell processes	3.08	0.85	1.99	14.86	17.99	25.46	2.21E-12	1	9.481240
MMAR_0446	mmpL3	cell wall and cell processes	740.49	804.46	641.03	469.74	442.17	495.85	8.08E-08	0.999999931	0.6755605
MMAR_0493	MMAR_0493-1	cell wall and cell processes	60.28	49.81	69.01	107.5	99.84	87.68	7.62E-07	0.999999238	1.5343403
MMAR_0495	MMAR_0495-1	cell wall and cell processes	992.25	856.25	925.39	1228.72	1236.12	1369.04	1.03E-06	0.999998972	1.2863180
MMAR_0502	MMAR_0502-1	cell wall and cell processes	318.82	242.5	238.19	404.86	397.66	407.27	3.46E-05	0.99996536	1.4165856
MMAR_0543	MMAR_0543-1	cell wall and cell processes	238.69	232.63	250.24	302.89	301.78	342.8	0.00181901	0.998180899	1.2351303
MMAR_0546	esxG	cell wall and cell processes	1782.91	1266.45	2178.41	1345.72	1153.32	1028.92	0.011496909	0.988503091	0.6233114
MMAR_0547	esxH	cell wall and cell processes	1313.97	1048.45	1390.83	869.01	866.63	675.78	0	1	0.5896789
MMAR_0548	MMAR_0548-1	cell wall and cell processes	667.37	516.46	702.43	464.92	380.42	364.4	1.11E-16	1	0.6041115
MMAR_0549	MMAR_0549-1	cell wall and cell processes	78.5	68.91	101.48	71.36	40.21	55.56	0.030723673	0.960276327	0.6324592
MMAR_0963	MMAR_0963-1	cell wall and cell processes	316.13	272.87	287.53	384.35	352.51	372.33	0.007007298	0.992992702	1.1832033
MMAR_1005	mmpL5	cell wall and cell processes	1230.29	1597.7	1059.04	214.71	325.85	380.07	0.000320702	0.999679298	0.2196233
MMAR_1006	mmpS5	cell wall and cell processes	1275.11	1301.54	1069.72	152.06	172.9	242.16	0	1	0.1428365
MMAR_1270	MMAR_1270-1	cell wall and cell processes	83.83	81.05	106.54	158.62	118.35	166.28	0.005124421	0.994875579	1.5234873
MMAR_1271	cyC	cell wall and cell processes	92.83	83.55	108.86	226.33	208.62	276.96	1.11E-16	1	2.3555137
MMAR_1345	MMAR_1345-1	cell wall and cell processes	103.76	86.56	120.85	89.04	67.1	74.69	3.07E-05	0.999969324	0.6995159
MMAR_1554	MMAR_1554-1	cell wall and cell processes	179.46	204.07	223.41	346.36	363.37	287.25	0.003278744	0.996712156	1.5385513
MMAR_1754	MMAR_1754-1	cell wall and cell processes	39.81	26.15	27.52	90.07	90.91	156.3	0.000150372	0.999849628	3.3942388
MMAR_1769	dirC	cell wall and cell processes	676.72	593.26	585.2	491.56	498.55	436.83	0.024444634	0.975555366	0.7187782
MMAR_1771	dirA	cell wall and cell processes	800.72	746.4	804.34	610.01	619.81	554.01	1.76E-11	1	0.7110274
MMAR_1840	MMAR_1840-1	cell wall and cell processes	255.24	240.67	311.85	376.54	348.11	342.85	0.010192428	0.988807572	1.2469498
MMAR_1887	efpA	cell wall and cell processes	357.22	406.34	648.38	172.99	224.02	220.09	0.020765539	0.979234461	0.4147606
MMAR_1967	ftsK	cell wall and cell processes	607.73	519.03	609.02	705.04	739.33	730.56	3.50E-07	0.999999965	1.1835313
MMAR_2004	MMAR_2004-1	cell wall and cell processes	650.2	421.27	570.24	391.52	376.33	367.78	4.09E-05	0.999959004	0.6441019
MMAR_2026	MMAR_2026-1	cell wall and cell processes	73.47	68	64.4	140.94	108.34	104.81	0.000259706	0.999740294	1.6019083
MMAR_2268	MMAR_2268-1	cell wall and cell processes	906.98	848.47	824.67	481.5	454.84	454.7	7.77E-16	1	0.5024348
MMAR_2389	MMAR_2389-1	cell wall and cell processes	366.78	607.76	562.62	208.04	234.25	235.48	0.009932428	0.990007572	0.4091572
MMAR_2424	cydD	cell wall and cell processes	30.66	19.51	27.93	59.66	52.13	42.8	1.07E-05	0.999989332	1.8802297
MMAR_2426	cydA	cell wall and cell processes	352.44	368.06	351.45	498.11	689.1	612.34	0.031809756	0.968190244	1.5739277
MMAR_2439	MMAR_2439-1	cell wall and cell processes	31.89	30.15	39.64	29.11	20.64	20.17	0.000957598	0.999042402	0.6475702
MMAR_2502	MMAR_2502-1	cell wall and cell processes	552.92	567.28	636.49	1000.2	1072.28	954.04	7.35E-14	1	1.6170171
MMAR_2716	MMAR_2716-1	cell wall and cell processes	71.39	50.75	81.83	52.34	52.29	54.84	0.049525066	0.950474934	0.7480078
MMAR_2772	MMAR_2772-1	cell wall and cell processes	502.15	491.75	788.77	1951.39	1849.68	1666.22	0	1	2.8861186
MMAR_2929	MMAR_2929-1	cell wall and cell processes	248.07	297	455.08	712.01	643.95	538.75	0.038755335	0.961244646	1.1991171
MMAR_3234	MMAR_3234-1	cell wall and cell processes	525.4	417.64	524.36	465.74	393.88	444.46	1.98E-06	0.999998023	0.8369159
MMAR_3250	MMAR_3250-1	cell wall and cell processes	334.45	337.63	435.53	255.04	266.47	284.95	3.37E-05	0.999966305	0.6821751
MMAR_3359	MMAR_3359-1	cell wall and cell processes	78.7	59.39	63.88	122.07	109.43	100.5	3.92E-07	0.999999608	1.5447549
MMAR_3364	MMAR_3364-1	cell wall and cell processes	3.46	2.84	4.42	8.48	10.48	15.34	0.001398909	0.998801091	3.0426746
MMAR_3554	MMAR_3554-1	cell wall and cell processes	367.17	447.88	240.47	34.28	50.77	35.52	2.60E-05	0.999973956	0.1059930
MMAR_3568	MMAR_3568-1	cell wall and cell processes	49.71	62.92	38.69	140.9	156.18	87.81	0.013028723	0.986971277	2.3471666
MMAR_3653	esxJ_3	cell wall and cell processes	800.02	958.65	1360.09	692.4	601.84	589.17	0.016376353	0.983623647	0.5540809
MMAR_3658	MMAR_3658-1	cell wall and cell processes	100.99	77.94	99.64	1129.35	974.27	602.57	1.23E-12	1	9.1360672
MMAR_3698	nbtA	cell wall and cell processes	25.85	19.44	21.8	50.37	49.54	55.63	2.17E-11	1	2.1859124
MMAR_3744	mmpL4_1	cell wall and cell processes	80.61	85.46	56.76	146.77	240.05	253.27	0.000487165	0.999512835	2.6774895
MMAR_4138	oppD	cell wall and cell processes	96.69	92.4	103.23	158.59	129.81	129.81	4.55E-05	0.999954475	1.4130831
MMAR_4182	MMAR_4182-1	cell wall and cell processes	11.93	7.54	9.6	21.68	17.34	28.04	0.000124517	0.999875483	2.1766399
MMAR_4576	psfS2	cell wall and cell processes	72.02	76.62	88.63	166.37	128.09	118.21	0.003817366	0.996182634	1.5807371
MMAR_4580	phoS2	cell wall and cell processes	433.4	370.59	482.39	555.17	535.61	606.18	1.28E-05	0.999987191	1.2430895
MMAR_4623	MMAR_4623-1	cell wall and cell processes	458.44	420.15	432.42	723.82	672.06	555.61	0.030735112	0.965264888	1.3975804
MMAR_5101	lsr2	cell wall and cell processes	3192.73	2662.41	3408.91	1894.27	1644.54	2197.14	1	1	0.5714249
MMAR_5368	fbpA	cell wall and cell processes	6270.93	5164.38	5902.18	3446.02	3507.05	4740.34	2.01E-05	0.999979899	0.6333741
MMAR_5369	MMAR_5369-1	cell wall and cell processes	306.85	238.27	300	237.1	194.64	207.96	3.33E-16	1	0.7148202
MMAR_5474	MMAR_5474-1	cell wall and cell processes	135.27	116.51	150.82	121.69	121.65	126.63	0.001073818	0.998926182	0.8699450

Conserved hypotheticals - 64 genes

GENE ID	GENE NAME	FUNCTION	Fragments Per Kilobase of transcript per Million mapped reads.						PPEE	PPDE	RealFC
			Fragments Per Kilobase of transcript per Million mapped reads.								
			NORMAL Long		LSMMG Long				posterior probability that a transcript is equally expressed	posterior probability that a transcript is differentially expressed	real fold change is the ratio of the normalized mean count values for LSMMG over the normalized mean count values for normal
			4days 35hr	4days 36hr	4days 37hr	4days 35hr	4days 36hr	4days 37hr			
MMAR_0022	MMAR_0022-1	conserved hypotheticals	402.44	277.06	367.6	269.55	221.33	296.11	0.003395242	0.996604758	0.710813655
MMAR_0066	MMAR_0066-1	conserved hypotheticals	162.9	116.9	187.55	59.72	73.42	85.22	2.06E-10	1	0.440140140
MMAR_0119	MMAR_0119-1	conserved hypotheticals	23.24	14.18	8.29	20.12	20.12	18.97	0.038051811	0.999999958	1.692862191
MMAR_0120	MMAR_0120-1	conserved hypotheticals	13.88	20.12	20.99	38.53	34.96	47.5	1.04E-06	0.999998958	2.047772722
MMAR_0137	MMAR_0137-1	conserved hypotheticals	365.04	384.64	368.05	229.64	313.52	220.24	0.011023625	0.988976375	0.62039191
MMAR_0232	MMAR_0232-1	conserved hypotheticals	5.51	10.03	4.29	38.68	43.18	120.39	0.021674017	0.978325983	9.20133419
MMAR_0348	MMAR_0348-1	conserved hypotheticals	86.37	113.67	116.36	165.47	162.91	215.67	0.015597188	0.984402812	1.58685485
MMAR_0398	MMAR_0398-1	conserved hypotheticals	28.72	34.3	24.23	44.14	50.8	63.15	0.03455008	0.96544992	1.668774143
MMAR_0425	MMAR_0425-1	conserved hypotheticals	42.73	30.96	34.87	50.18	45.16	24.87	0.042490501	0.975790499	1.37136216
MMAR_0447	MMAR_0447-1	conserved hypotheticals	193.81	152.14	204.83	130.64	104.62	143.58	3.07E-09	0.999999997	0.645676881
MMAR_0519	MMAR_0519-1	conserved hypotheticals	18.43	39.13	34.73	11.39	10.38	13.22	0.027084601	0.972515399	0.348392392
MMAR_0523	MMAR_0523-1	conserved hypotheticals	21.28	5.51	13.67	61.83	59.81	74.65	0	1	4.667340235
MMAR_0524	MMAR_0524-1	conserved hypotheticals	4.93	6.74	7.86	56.71	46.03	62.4	0	1	7.842456177
MMAR_0853	MMAR_0853-1	conserved hypotheticals	135.2	72.84	102.73	869.42	948.96	1150.12	0	1	8.945263929
MMAR_0905	MMAR_0905-1	conserved hypotheticals	17.8	34.92	36.35	56.27	54.57	60.85	0.002408374	0.997591626	1.788480593
MMAR_0982	MMAR_0982-1	conserved hypotheticals	260.02	256.66	355.18	130.89	173.59	168.17	3.88E-08	0.999999991	0.509518616
MMAR_1007	MMAR_1007-1	conserved hypotheticals	996.79	1050.56	1387.64	184.62	189.41	320.64	0	1	0.188325345
MMAR_1241	MMAR_1241-1	conserved hypotheticals	6.32	1.75	6.38	14.36	12.44	20.13	0.000114528	0.999885472	3.147936882
MMAR_1272	MMAR_1272-1	conserved hypotheticals	222.53	257.64	223.22	406.14	534.05	507.06	3.17E-06	0.999998323	1.66882579
MMAR_1304	MMAR_1304-1	conserved hypotheticals	434.56	466.35	532.68	671.5	716.36	694.2	8.76E-06	0.999991245	1.355024927
MMAR_1572	MMAR_1572-1	conserved hypotheticals	264.48	289.47	278.76	396.13	409.11	386.85	0.002097597	0.999702403	1.133689
MMAR_1588	MMAR_1588-1	conserved hypotheticals	48.29	40.07	43.83	73.25	68.4	57.02	0.012635489	0.967425611	1.141813523
MMAR_1915	MMAR_1915-1	conserved hypotheticals	298.97	237.24	264.1	238.42	194	214.9	0.001997949	0.998002051	0.758425525
MMAR_2009	MMAR_2009-1	conserved hypotheticals	39.46	38.99	46.31	106.42	123.4	85.88	7.00E-07	0.9999993	2.348411
MMAR_2503	MMAR_2503-1	conserved hypotheticals	255.37	289.44	350	495.22	439.53	439.56	0.000167025	0.999832975	1.437616025
MMAR_2771	MMAR_2771-1	conserved hypotheticals	142.67	135.63	135.1	124.7	333.91	308.36	1.18E-12	1	2.158940404
MMAR_2779	MMAR_2779-1	conserved hypotheticals	424.69	379.59	380.29	317.69	307.5	308.81	6.96E-06	0.999999338	0.73420424
MMAR_2935	MMAR_2935-1	conserved hypotheticals	14.98	14.05	18.91	40.47	43.56	56.22	8.66E-15	1	2.79236935
MMAR_2946	MMAR_2946-1	conserved hypotheticals	39.26	40.31	30.93	125.82	81.07	123.48	4.43E-09	0.999999996	2.735189
MMAR_3007	MMAR_3007-1	conserved hypotheticals	232.48	216.43	265.45	437.05	419.38	383.66	1	1.62859	1.62859
MMAR_3010	MMAR_3010-1	conserved hypotheticals	66.16	56.89	62.58	139.43	129.33	129	9.97E-13	1	1.9087899
MMAR_3068	MMAR_3068-1	conserved hypotheticals	87.84	66.1	85.34	140.83	143.71	101.07	0.002722745	0.999772745	1.412521
MMAR_3070	MMAR_3070-1	conserved hypotheticals	106.1	96.84	92.11	189.63	207.5	168.6	0.999999997	0.999999997	1.789703
MMAR_3088	MMAR_3088-1	conserved hypotheticals	137.77	175.01	168.99	246.04	279.89	252.77	0.000879514	0.999120486	1.507798
MMAR_3187	MMAR_3187-1	conserved hypotheticals	1884.65	1698.93	2051.86	3146.72	2432.2	2622.44	0.000534013	0.999465987	1.358888
MMAR_3207	MMAR_3207-1	conserved hypotheticals	364.08	357.36	312.85	462.93	520.8	500.96	0.037304308	0.962695692	1.337159
MMAR_3365	MMAR_3365-1	conserved hypotheticals	77.7	72.39	50.89	123.5	118.42	97.87	0.040374194	0.95962806	1.557066
MMAR_3430	MMAR_3430-1	conserved hypotheticals	77.7	45.15	68.86	87.2	68.86	87.2	0.000593686	0.999049602	1.603115
MMAR_3549	MMAR_3549-1	conserved hypotheticals	26.06	29	30.65	8.34	6.04	12.67	1.11E-16	1	0.291160
MMAR_4142	MMAR_4142-1	conserved hypotheticals	88.1	83.68	100.81	132.69	140.23	154.46	1.01E-10	1	1.47092095
MMAR_4168	MMAR_4168-1	conserved hypotheticals	109.54	120.32	142.59	252.78	245.47	213.48	8.08E-12	1	1.78330
MMAR_4248	MMAR_4248-1	conserved hypotheticals	18.95	30.01	23.94	75.09	48.25	50.98	0.018597522	0.981402788	2.172606
MMAR_4249	MMAR_4249-1	conserved hypotheticals	20.64	10.19	19.72	37.37	58.16	38.98	0.016581089	0.983418911	2.5177495
MMAR_4254	MMAR_4254-1	conserved hypotheticals	24.24	24.24	24.24	8.41	31.2	41.07	0.000978517	0.990211343	2.164413
MMAR_4275	MMAR_4275-1	conserved hypotheticals	310.05	371.21	429.09	268.13	292.45	256.77	0.016748746	0.983251254	0.683285
MMAR_4306	MMAR_4306-1	conserved hypotheticals	87668.97	50568.35	34812.06	380806.3	356581.2	247241.47	0	1	4.91127
MMAR_4356	MMAR_4356-1	conserved hypotheticals	979.94	1023.48	1332.23	681.55	887.98	834.08	0.020737167	0.970526833	0.670502
MMAR_4413	MMAR_4413-1	conserved hypotheticals	21.73	26.16	38.23	62.4	81.41	74.59	1.18E-07	0.999999882	2.396180
MMAR_4498	MMAR_4498-1	conserved hypotheticals	537.26	397.85	600.61	2432.03	2858.04	3239.66	0	1	5.047611
MMAR_4609	MMAR_4609-1	conserved hypotheticals	664.46	608.66	661.18	1070.32	1465.68	1088.99	0.000267323	0.999733623	2.446557
MMAR_4645	MMAR_4645-1	conserved hypotheticals	631.58	755.78	650.96	1037.05	1084.26	1220.16	3.36E-05	0.99996366	1.525205
MMAR_4647	MMAR_4647-1	conserved hypotheticals	296.11	312.24	367.5	519.49	597.24	483.61	0.000851696	0.999148304	1.54033
MMAR_4761	MMAR_4761-1	conserved hypotheticals	43.14	47.98	53.28	81.79	108.96	103.23	0.999982215	1.78E-06	1.91074
MMAR_4772	MMAR_4772-1	conserved hypotheticals	30.3	24.67	26.42	42.76	42.25	64.68	0.038210244	0.961789756	1.723354
MMAR_4888	MMAR_4888-1	conserved hypotheticals	131.32	85.53	116.34	91.97	70.39	87.96	0.010654538	0.989345642	0.71023
MMAR_4901	MMAR_4901-1	conserved hypotheticals	23.72	15.45	15.45	21.27	15.45	12.02	0.017038441	0.962619616	3.570639
MMAR_4959	MMAR_4959-1	conserved hypotheticals	2160.67	2472.07	3573.95	4937.68	5468.39	4739.61	0.000489384	0.999510616	1.698848
MMAR_5103	MMAR_5103-1	conserved hypotheticals	495.52	486.78	585.72	214.3	232.33	255.58	0	1	0.419771
MMAR_5106	MMAR_5106-1	conserved hypotheticals	125.98	75.75	130.13	64.13	51.87	85.3	0.01580175	0.984819825	0.575325
MMAR_5340	MMAR_5340-1	conserved hypotheticals	422.06	295.73	397.26	316.26	285.25	327.62	0.002864301	0.991573699	0.789141
MMAR_5437	MMAR_5437-1	conserved hypotheticals	239.48	164.07	327.43	509.52	506.04	397.73	0.015827519	0.984712482	1.787812
MMAR_5455	MMAR_5455-1	conserved hypotheticals	196.94	212.42	212.73	347.4	300.63	300.63	0.011651306	0.982346894	1.513147
MMAR_5457	espB	conserved hypotheticals	462.65	484.94	536.03	755.66	713.03	673.18	1.16E-06	0.99999884	1.354786
MMAR_5578	MMAR_5578-1	conserved hypotheticals	1932.04	1683.92	1603.49	1400.21	1248.93	1235.3	0.018373998	0.981626002	0.790263

Information pathways - 49 genes

GENE ID	GENE NAME	FUNCTION	Fragments Per Kilobase of transcript per Million mapped reads.						PPEE	PPDE	RealFC
			NORMAL Long			LSMMG Long					
			4days 35hr	4days 36hr	4days 37hr	4days 35hr	4days 36hr	4days 37hr	posterior probability that a transcript is equally expressed	posterior probability that a transcript is differentially expressed	real fold change is the ratio of the normalized mean count values for LSMMG over the normalized mean count values for normal
MMAR_0072	rpSf	information pathways	1171.81	958.47	873.47	680.27	587.62	695.36	0.049184346	0.950815654	0.95907251
MMAR_0073	sb	information pathways	1930.78	2393.48	2190.63	1431.88	1596.45	1327.46	0.030875475	0.969124525	0.617030489
MMAR_0074	rpJ1	information pathways	1988.72	1498.71	1574.39	1026.09	1072.76	1069.74	0.0099912161	0.999912161	0.569324291
MMAR_0972	nuS	information pathways	1549.12	1531.28	1569.76	1151.99	1255.26	1303.34	0.000893449	0.999106551	0.743862644
MMAR_0974	rpIA	information pathways	2139.34	1648.12	1997.42	1182.04	1311.14	1531.62	4.49E-08	0.999999955	0.653032306
MMAR_0975	MMAR_0975-1	information pathways	83.77	55.08	59.07	40.38	34.13	36.14	0.001717921	0.998282079	0.526538843
MMAR_0990	rpI	information pathways	1812.82	1488.46	1752.78	970.46	977.79	1156.79	0	1	0.574294408
MMAR_0996	rpOC	information pathways	2262.43	2003.14	2112.18	1545.04	1706.01	1823.03	0.008075707	0.991124293	0.74089489
MMAR_1012	rpIG	information pathways	1959.72	1755.97	2403.87	1475.98	1364.46	1806.9	0.008189108	0.991810892	0.707634337
MMAR_1031	rpIC	information pathways	4179.97	3120.82	4122.36	1971.62	2051.01	2696.71	1.54E-12	1	0.552352235
MMAR_1032	rpID	information pathways	3478.87	3285.67	3496.05	2070.38	2108.44	2315.41	0	1	0.590086874
MMAR_1034	rpIB	information pathways	3084.07	2508.48	2775.73	1790.7	1747.19	2045.37	2.08E-13	1	0.625257853
MMAR_1036	rpIV	information pathways	827.53	527.57	843.95	445.54	416.85	603.87	0.026858404	0.973141596	0.626955379
MMAR_1039	rpIC	information pathways	6878.57	5472.75	5624.71	4298.55	4163.37	4145.9	0.000845522	0.999154478	0.635502394
MMAR_1045	rpIN	information pathways	2385.59	2276.86	2547.88	1766.07	1444.76	1676.43	0	1	0.623691855
MMAR_1048	rpSN	information pathways	11883.41	11742.89	11744.89	7407.08	8901.35	8218.61	8.74E-09	0.999999991	0.6223148378
MMAR_1052	rpSE	information pathways	1276.37	1054.39	1454.81	738.48	762.45	1043.03	0.0001013	0.99989887	0.631194013
MMAR_1053	rpmD	information pathways	4702.47	4310.74	5223.47	3245.51	3205.49	4167.28	0.000454073	0.999545927	0.678193567
MMAR_1054	rpIO	information pathways	3783.43	2802.81	3677.87	2538.22	2403.73	3114.57	0.010871182	0.989128818	0.730851457
MMAR_1085	infA	information pathways	10464.68	10707.77	13649.37	7797.94	8511.49	9031.56	3.48E-06	0.999996519	0.60665658
MMAR_1086	rpmJ	information pathways	4407.08	6141.56	5360.01	2532.38	2820.83	3741.77	0.028208217	0.971791783	0.512280658
MMAR_1089	rpSD	information pathways	3894.96	3301.06	3165.25	2274.24	2365.64	2527.04	0.011908933	0.988091067	0.643333783
MMAR_1090	rpOA	information pathways	2679.13	2197.72	2698.07	1529.53	1431.79	1779.22	0	1	0.588648599
MMAR_1091	rpIQ	information pathways	1834.17	1439.17	1920.4	1032.77	896.4	1228.78	1.11E-16	1	0.568764968
MMAR_1106	rpIM	information pathways	6944.33	6779.29	6007.38	4058.25	4712.1	4132.67	0.01056793	0.98943207	0.602653796
MMAR_1107	rpS	information pathways	1794.31	1411.37	1429.78	1005.12	998.23	1031.59	0.000166834	0.999833166	0.603646388
MMAR_1134	sigH	information pathways	1048.48	1169.32	1044.65	1675.16	1809.3	1872.92	1.15E-06	0.999998846	1.524356685
MMAR_1640	nrdH	information pathways	2346.28	2386.84	1711.27	4456.24	4803.78	4654.27	3.17E-11	1	1.940080677
MMAR_1641	nrdE	information pathways	542.65	467.16	454.01	998.01	983.93	912.13	0	1	1.82815651
MMAR_1642	nrdI	information pathways	1060.68	1219.41	1011.56	2370.32	2965.18	2443.75	3.62E-09	0.999999996	2.207293017
MMAR_1647	nrdF2	information pathways	504.26	568.49	489.07	1138.09	1403.56	1256.05	1.82E-14	1	2.263339822
MMAR_1728	hupB	information pathways	3742.58	4039.4	5272.94	2901.38	3053.59	3222.13	0.010088208	0.989911792	0.657876101
MMAR_1742	recG	information pathways	96.18	78.48	97.44	133.39	111.34	114.18	0.00040964	0.999569036	1.245305358
MMAR_1789	rpSP	information pathways	1662.46	1301.98	1455.22	1090.4	904.4	1130.47	1.33E-06	0.999998668	0.656509898
MMAR_1801	rimM	information pathways	805.18	689.49	696.92	476.37	429.89	465.24	1.47E-10	1	0.580449705
MMAR_1802	trmD	information pathways	197.09	112.68	165.94	121.72	89.27	107.95	0.02972639	0.97027361	0.631968784
MMAR_1820	tsf	information pathways	1718.48	1392.49	1611.78	1051.19	1019.95	1237.36	1.08E-13	1	0.656895878
MMAR_1925	gpSI	information pathways	1490.03	1339.51	1498.18	1141.01	1122.43	1116.63	0	1	0.735608974
MMAR_2170	aiAS	information pathways	296.61	234.53	295.13	277.5	243.45	249.49	0.004479378	0.995520622	0.881804317
MMAR_2433	rpSA	information pathways	5666.52	6107.7	6100.43	4135.9	4516.8	4589.24	0.005883392	0.994116608	0.693354891
MMAR_2451	tsnR	information pathways	336.42	236	296.12	231.82	168.53	160.75	2.76E-05	0.999972442	0.607064723
MMAR_3733	rpST	information pathways	1092.9	711.87	960.83	712.55	480.33	597	0.000929874	0.999070126	0.591226474
MMAR_4105	argS	information pathways	315.28	231.06	281.12	230.22	235.05	233.58	0.003165317	0.996834683	0.79875094
MMAR_4143	sbCD	information pathways	86.09	69.59	107.13	122.64	133.58	139.75	0.006098777	0.993901223	1.42840754
MMAR_4216	sigE	information pathways	652.79	638.33	648.08	984.96	909.78	969.51	0	1	1.376251917
MMAR_4289	tyrA	information pathways	361.47	281.76	300.21	200.14	203.42	205.27	2.55E-08	0.999999975	0.608266884
MMAR_4472	rpLY	information pathways	1098.81	999.42	1155.98	684.04	700.16	839.35	0	1	0.638091609
MMAR_5240	dnazX	information pathways	96.6	84.32	99.8	68.8	73.06	84.68	5.96E-05	0.999940405	0.761004966
MMAR_5569	rnPA	information pathways	784.26	527.62	828.86	438.08	416.29	467.22	1.36E-07	0.999999864	0.574508241

Intermediary metabolism - 96 genes

GENE ID	GENE NAME	FUNCTION	Fragments Per Kilobase of transcript per Million mapped reads.							PPEE	PPDE	RealFC
			NORMAL Long			LSMMG Long						
			4days 35hr	4days 36hr	4days 37hr	4days 35hr	4days 36hr	4days 37hr	posterior probability that a transcript is equally expressed	posterior probability that a transcript is differentially expressed	real fold change is the ratio of the normalized mean count values for LSMMG over the normalized mean count values for normal	
MMAR_0065	ino1	intermediary metabolism, and respiration	793.25	874.44	1035.72	427.81	473.62	636.12	1.06E-05	0.999989427	0.533198784	
MMAR_0107	celA	intermediary metabolism, and respiration	248.81	188.13	266.7	98.96	108.51	139.65	1	1	0.466519159	
MMAR_0324	pepA	intermediary metabolism, and respiration	292.55	257.77	320.24	230.46	205.46	276.88	0.010706665	0.988293335	0.769378128	
MMAR_0346	cyp138A3	intermediary metabolism, and respiration	68.44	79.05	58.38	144.16	172.14	251.17	0.001068413	0.998931587	2.554849194	
MMAR_0379	pnfB	intermediary metabolism, and respiration	410.06	291.57	406.19	308.52	264.76	317.35	0.00025724	0.99974276	0.760828784	
MMAR_0516	nirB	intermediary metabolism, and respiration	9.81	11.25	14	4.6	6.77	6.52	1.24E-05	0.999987552	0.482279402	
MMAR_0550	mycP3	intermediary metabolism, and respiration	82.09	50.96	79.76	58.42	30.32	41.22	0.011010594	0.98889406	0.57791869	
MMAR_0728	lpqM	intermediary metabolism, and respiration	206.78	160.13	194.51	246.41	240.13	225.42	0.001564068	0.998435932	1.197565138	
MMAR_0780	putA_1	intermediary metabolism, and respiration	155.52	160.12	220.1	314.52	322.76	274.08	0.000443978	0.999556022	1.606868763	
MMAR_0792	id1	intermediary metabolism, and respiration	1292.19	2676.46	2941.96	146.37	273.67	307.4	9.95E-07	0.999999005	0.098247332	
MMAR_0829	galE2	intermediary metabolism, and respiration	366.74	264.62	325.03	248.89	197.29	228.48	6.42E-08	0.999999936	0.66437346	
MMAR_0842	hemA	intermediary metabolism, and respiration	229.37	161.69	219.19	186.4	132.9	160.04	0.014710927	0.985289073	0.741911775	
MMAR_0843	hemC	intermediary metabolism, and respiration	1805.01	1248.99	1989.72	775.71	859.8	904.76	1.10E-11	1	0.477966788	
MMAR_0844	hemD	intermediary metabolism, and respiration	472.18	368	497.66	262.76	227.58	274.51	0	1	0.540492608	
MMAR_0845	hemB	intermediary metabolism, and respiration	438.89	320.73	388.24	327.53	234.1	254.08	0.000239692	0.999760308	0.667771102	
MMAR_0913	siuP	intermediary metabolism, and respiration	155.07	114.45	115.04	260.86	190.04	209.53	0.000319559	0.999604041	1.612432869	
MMAR_0914	siuP_1	intermediary metabolism, and respiration	65.83	69.46	71.1	119.4	109.14	102.62	7.42E-10	0.999999999	1.501932721	
MMAR_1041	atsA	intermediary metabolism, and respiration	319.85	271.94	274.47	388.41	409.02	397.08	0.000260468	0.999739532	1.297958252	
MMAR_1055	MMAR_1055-1	intermediary metabolism, and respiration	166.66	104.4	137.57	94.6	72.76	107.04	0.022600238	0.977399762	0.633034448	
MMAR_1079	nmsA	intermediary metabolism, and respiration	228.82	253.17	239.94	370.89	339.62	332.42	0.000364158	0.999635842	1.348403794	
MMAR_1108	nrsA	intermediary metabolism, and respiration	248.37	202.18	280.97	155.09	151.23	169.47	0	1	0.615004602	
MMAR_1183	MMAR_1183-1	intermediary metabolism, and respiration	435.54	327.26	516.54	810.24	853.24	947.72	4.77E-15	1	1.391542395	
MMAR_1184	metA	intermediary metabolism, and respiration	495.21	261.99	392.66	925.54	854.47	1042.09	0	1	2.33257389	
MMAR_1185	metC	intermediary metabolism, and respiration	742.19	642.33	693.71	1540.69	2480.12	2601.41	3.23E-05	0.999967697	3.004138688	
MMAR_1200	sdhB	intermediary metabolism, and respiration	407.5	394.58	472.96	350.3	386.38	369.36	0.00248664	0.99755136	0.813536653	
MMAR_1202	sdhD	intermediary metabolism, and respiration	302.31	208.49	288.71	174.36	167.3	234.19	0.0159748	0.9840252	0.672900969	
MMAR_1216	MMAR_1216-1	intermediary metabolism, and respiration	152.84	147.69	151.34	206.93	220.35	198.82	0.000722519	0.999277481	1.295542056	
MMAR_1240	pcd	intermediary metabolism, and respiration	65.88	50.4	47.45	114.69	78.03	305.3	0.00019547	0.99980453	1.70348805	
MMAR_1243	lat	intermediary metabolism, and respiration	505.57	21.77	26.18	137.54	151.71	230.76	4.57E-09	0.999999995	5.01937379	
MMAR_1251	acx3	intermediary metabolism, and respiration	366.48	332.84	486	297.71	265.96	323.16	0.045915207	0.954084793	0.707657957	
MMAR_1314	MMAR_1314-1	intermediary metabolism, and respiration	43.92	36.64	36.27	51.15	64.52	74.25	0.03807203	0.96192797	1.525810033	
MMAR_1375	atsD_1	intermediary metabolism, and respiration	82.2	75.61	71.24	116.77	99.98	97.83	0.045105339	0.954894661	1.286877663	
MMAR_1644	MMAR_1644-1	intermediary metabolism, and respiration	328.41	302.83	296.61	515.76	483.78	493.42	0	1	1.507617966	
MMAR_1693	MMAR_1693-1	intermediary metabolism, and respiration	39.01	49.63	85.59	135.38	129.54	119.42	0.000596132	0.999403868	2.090705548	
MMAR_1710	ilvB1	intermediary metabolism, and respiration	401.84	402.4	419.84	285.7	309.38	360.7	0.015443336	0.984550664	0.732677734	
MMAR_1712	ilvC	intermediary metabolism, and respiration	1408.01	1148.12	1404.58	928.08	992.27	1147.89	7.78E-08	0.999999922	0.729460702	
MMAR_1749	pca	intermediary metabolism, and respiration	471.58	414.12	465.51	431.64	391.66	415.3	1.44E-07	0.999999856	0.86380057	
MMAR_1821	amiC	intermediary metabolism, and respiration	221.55	161.31	206.88	138.12	121.85	141.73	0	1	0.643449311	
MMAR_1926	pepR	intermediary metabolism, and respiration	765.21	660.46	660.41	499.46	469.16	447.93	1.59E-06	0.99999841	0.636809545	
MMAR_1988	hflX	intermediary metabolism, and respiration	84.02	71.13	92.6	153.15	124.4	155.66	1.22E-15	1	1.648181308	
MMAR_2202	glnK	intermediary metabolism, and respiration	983.53	802.32	1012.19	719.47	634.34	817.34	4.37E-08	0.999999956	0.732430021	
MMAR_2269	cds	intermediary metabolism, and respiration	379.98	404.75	375.42	207.92	216.01	197.04	9.94E-10	0.999999999	0.499793111	
MMAR_2277	trxB1	intermediary metabolism, and respiration	193.58	300.27	245.59	860.25	1155.43	1450.69	5.73E-09	0.999999994	4.267860008	
MMAR_2333	wcaA	intermediary metabolism, and respiration	359.19	339.75	421.97	367.55	309.59	303.59	0.046088902	0.953911098	0.821013897	
MMAR_2353	MMAR_2353-1	intermediary metabolism, and respiration	73.11	77.87	89.74	71.38	56.7	56.55	0.004733885	0.995266115	0.718247146	
MMAR_2403	MMAR_2403-1	intermediary metabolism, and respiration	207.6	126.36	180.33	142.64	117.04	122.58	0.042975788	0.957024212	0.703990195	
MMAR_2414	tpaB	intermediary metabolism, and respiration	1215.91	1114.09	1302.09	1192.22	1179.27	1160.65	0.02051734	0.97948266	0.914596557	
MMAR_2434	cofE	intermediary metabolism, and respiration	1131.25	878.05	940.89	619.22	561.88	639.31	4.42E-09	0.999999995	0.586881334	
MMAR_2557	MMAR_2557-1	intermediary metabolism, and respiration	38.49	41.15	36.95	85.99	83.87	68.62	2.97E-09	0.999999997	1.906886499	
MMAR_2568	MMAR_2568-1	intermediary metabolism, and respiration	74.11	68.53	70.63	94.53	99.05	88.06	0.024291682	0.975708318	1.524295235	
MMAR_2570	MMAR_2570-1	intermediary metabolism, and respiration	38.32	28.89	34.79	52.92	45.52	66.44	0.035879997	0.964120003	1.537574015	
MMAR_2775	MMAR_2775-1	intermediary metabolism, and respiration	13.64	15.52	16.12	32.67	20.66	37.29	0.022983869	0.977016131	1.859229408	
MMAR_2836	MMAR_2836-1	intermediary metabolism, and respiration	27.07	19.86	28.89	67.28	60.7	65.19	0	1	2.417137656	
MMAR_2844	MMAR_2844-1	intermediary metabolism, and respiration	269.04	263.12	308.64	427.72	369	207.84	6.87E-09	0.999999993	1.58121169	
MMAR_2902	MMAR_2902-1	intermediary metabolism, and respiration	276.58	222.24	325.24	189.1	168.52	180.36	5.21E-11	1	0.615564306	
MMAR_2992	folE_1	intermediary metabolism, and respiration	217.31	303.16	212.17	552.62	478.49	455.39	4.18E-06	0.999995822	1.861731257	
MMAR_3294	glnA2	intermediary metabolism, and respiration	713.46	742.99	730.27	403.21	501.51	535.16	0.000194932	0.999805068	0.6165771	
MMAR_3299	panB	intermediary metabolism, and respiration	277.79	406.1	349.53	144.11	173.39	203.42	0.01344654	0.98655346	0.466035311	
MMAR_3555	MMAR_3555-1	intermediary metabolism, and respiration	1190.35	1568.78	741.53	84.21	149.32	100.74	0.000476253	0.999523747	0.087952775	
MMAR_3556	MMAR_3556-1	intermediary metabolism, and respiration	241.54	232.92	117.7	11.97	13.82	14.61	4.02E-06	0.999995984	0.063121154	
MMAR_3558	MMAR_3558-1	intermediary metabolism, and respiration	1156.85	1158.12	497.43	56.58	73.18	67.86	0.000579964	0.959403036	0.064837573	
MMAR_3690	nbtF	intermediary metabolism, and respiration	42.7	34.26	37.16	67.12	52.76	51.03	0.008843736	0.991156264	1.411797101	
MMAR_3691	nbtE	intermediary metabolism, and respiration	44.91	32.78	31.78	71.2	66.95	107.29	0.005040434	0.994959566	2.111062549	
MMAR_3693	MMAR_3693-1	intermediary metabolism, and respiration	218.94	248.28	176.46	421.16	408.51	575.39	0.000161951	0.999838049	2.011405323	
MMAR_3697	nbtG	intermediary metabolism, and respiration	204.69	244.69	173.02	386.85	372.31	524.11	0.001259956	0.998740044	1.906252317	
MMAR_3701	MMAR_3701-1	intermediary metabolism, and respiration	22.49	21.82	25.86	46.72	56.37	40.53	0.000110864	0.999898136	1.924427421	
MMAR_3702	MMAR_3702-1	intermediary metabolism, and respiration	15.95	18.99	18.02	31.41	26.65	45.27	1.53E-05	0.999984722	1.997134706	
MMAR_3757	MMAR_3757-1	intermediary metabolism, and respiration	168.51	195.96	203.91	265.39	255.94	253.54	0.027080335	0.972919665	1.276646502	
MMAR_3765	obg	intermediary metabolism, and respiration	419.19	243.44	344.49	219.96	185.32	232.88	0.005956786	0.994403214	0.601291182	
MMAR_3801	nubA	intermediary metabolism, and respiration	181.58	231.91	270.96	98.65	109.84	172.12	0.014608792	0.985391208	0.516995816	
MMAR_3802	porB	intermediary metabolism, and respiration	601.22	699.14	855.59	317.04	374.12	517.96	0.002643476	0.997356524	0.525970948	
MMAR_3803	porA	intermediary metabolism, and respiration	582.12	801.23	848.31	313.24	371.46	421.84	0.000519218	0.999480782	0.46384617	
MMAR_3813	rybB											

Lipid metabolism - 36 genes			FPKM							PPEE		PPDE	RealFC
GENE_ID	GENE_NAME	FUNCTION	Fragments Per Kilobase of transcript per Million mapped reads.							posterior probability that a transcript is equally expressed		posterior probability that a transcript is differentially expressed	real fold change is the ratio of the normalized mean count values for LSMMG over the normalized mean count values for normal
			NORMAL Long			LSMMG Long							
			4days 35hr	4days 36hr	4days 37hr	4days 35hr	4days 36hr	4days 37hr					
MMAR_0336	desA3_2	lipid metabolism	536.96	427.89	199.01	1566.49	1873.72	1124.04	2.00E-06		0.999997996		3.642602765
MMAR_0452	fadD4	lipid metabolism	184.2	191.01	224.91	131.61	136.29	145.83	7.05E-10		0.999999999		0.648063347
MMAR_0466	MMAR_0466-1	lipid metabolism	30.21	23.48	21.46	45.8	44.63	34.57	0.037716856		0.962283144		1.495533171
MMAR_0505	fadE5	lipid metabolism	616.17	817.57	1107.22	289.32	364.97	389.88	0.002419515		0.997580485		0.387481623
MMAR_0706	fadD30	lipid metabolism	139.76	118.32	124.55	102.92	99.06	91.56	3.09E-05		0.999969058		0.721757377
MMAR_0793	fadB2	lipid metabolism	453.04	581.71	679.78	242.89	273.24	320.54	1.29E-05		0.999987083		0.455910375
MMAR_1154	lpqQ	lipid metabolism	162.08	210.92	241.82	368.26	379.12	295.21	0.043198966		0.956801034		1.58020147
MMAR_1250	MMAR_1250-1	lipid metabolism	10.89	6.91	11.35	5.64	5.52	7.79	0.010247034		0.989752966		0.621407258
MMAR_1315	desA3	lipid metabolism	167.47	121.67	79.31	210.33	257.76	236.06	0.013707607		0.986292393		1.786156672
MMAR_1509	fadE23	lipid metabolism	301.98	283.58	351.31	577.35	663.63	691.17	0		1		1.942642229
MMAR_1761	fadD22	lipid metabolism	868.77	844.64	928.16	784.37	701.23	702.79	5.30E-07		0.99999947		0.778317897
MMAR_1762	pkx15/1	lipid metabolism	423.34	376.72	537.39	311.02	294.39	326.72	5.33E-05		0.99996467		0.661088635
MMAR_1772	pppE	lipid metabolism	439.78	392.21	385.76	289.2	266.48	239.8	5.33E-06		0.999996473		0.614318196
MMAR_1916	pppII	lipid metabolism	295.96	255.66	264.8	214.9	209.68	177.99	8.71E-05		0.999912858		0.68881433
MMAR_2117	fadD9	lipid metabolism	104.19	97.83	112.95	142.71	157.51	187.01	0.001643775		0.998356225		1.458862323
MMAR_2759	echA8_6	lipid metabolism	69.05	45.89	61.69	103.04	92.13	79.7	0.04589198		0.95441802		1.466677763
MMAR_2936	fadD9_1	lipid metabolism	10.5	4.55	7.5	22.1	21.25	29.53	1.03E-11		1		3.09817775
MMAR_2981	fadG3_1	lipid metabolism	80.12	62.38	77.18	153.17	131.86	106.79	0.00053164		0.999446836		1.674953012
MMAR_3336	fabD	lipid metabolism	635.63	869.97	1049.36	480.73	424.55	407.45	0.002034913		0.997965087		0.479730319
MMAR_3338	kasA	lipid metabolism	1573.14	2092.64	2899.76	747.93	795.98	1026.96	0.004804236		0.995195764		0.368151227
MMAR_3339	kasB	lipid metabolism	1248.25	1486.74	2124.87	549.44	593.68	746.87	0.000178132		0.999821868		0.3664396
MMAR_3440	acCD6	lipid metabolism	540.4	799.22	1076.41	251.85	278.36	397.47	0.024221687		0.975778313		0.360483927
MMAR_3694	nbcC	lipid metabolism	101.24	79.05	59.67	165.79	124.04	217.13	0.032679826		0.967320174		1.951597776
MMAR_4030	MMAR_4030-1	lipid metabolism	108.31	132.99	110.52	224.87	227.3	249.15	2.23E-13		1		1.849925185
MMAR_4031	MMAR_4031-1	lipid metabolism	62.41	70.35	66.86	126.23	104.48	134.47	1.09E-09		0.999999999		1.702509486
MMAR_4032	MMAR_4032-1	lipid metabolism	34.45	35.61	34.69	73.72	72.31	73.66	6.13E-06		0.999993873		1.95944351
MMAR_4033	fab	lipid metabolism	72.2	70.27	68.83	103.54	148.22	132.05	0.002023377		0.997977623		1.696803576
MMAR_4476	pkx16	lipid metabolism	335.12	428.78	458.8	174.88	213.4	242.34	2.48E-05		0.999975238		0.482838688
MMAR_4334	acx12	lipid metabolism	19.44	25.35	27.5	12.36	16.13	15.79	0.005373095		0.994636915		0.574627099
MMAR_4535	fadE12	lipid metabolism	52.87	41.44	68.84	34.17	32.63	34.62	2.66E-05		0.9999734		0.581963699
MMAR_4676	fadB	lipid metabolism	375.65	387.37	531.29	227.93	261.73	317.36	0.005715207		0.994284793		0.589325262
MMAR_4691	echA8_2	lipid metabolism	288.44	265.22	260.35	204.79	212.49	227.69	0.023551829		0.976448171		0.738925902
MMAR_5236	MMAR_5236-1	lipid metabolism	270.85	308.25	319.6	451.88	411.54	399.26	0.005027144		0.994972856		1.311814126
MMAR_5275	fadD15_1	lipid metabolism	218.37	205.96	238.56	309.25	284.95	318.62	0		1		1.295070885
MMAR_5364	pkx13	lipid metabolism	375.79	409.53	410.43	232.69	230.13	266.34	1.68E-08		0.999999993		0.571739827
MMAR_5365	fadD12	lipid metabolism	637.7	754.41	715.53	409.87	410.83	427.95	1.42E-05		0.999985813		0.553160388

PE/PPE - 8 genes			FPKM							PPEE		PPDE	RealFC
GENE_ID	GENE_NAME	FUNCTION	Fragments Per Kilobase of transcript per Million mapped reads.							posterior probability that a transcript is equally expressed		posterior probability that a transcript is differentially expressed	real fold change is the ratio of the normalized mean count values for LSMMG over the normalized mean count values for normal
			NORMAL Long			LSMMG Long							
			4days 35hr	4days 36hr	4days 37hr	4days 35hr	4days 36hr	4days 37hr					
MMAR_0641	MMAR_0641-1	PE/PPE	18.49	13.01	15.19	38.71	38.86	62.54	9.84E-05		0.99990155		2.839722433
MMAR_0761	MMAR_0761-1	PE/PPE	136.24	132.34	153.69	130.03	121.22	108.89	0.004857191		0.995162809		0.801718652
MMAR_2591	MMAR_2591-1	PE/PPE	38.92	32.99	41.27	22.75	22.45	23.96	0.001398129		0.998601871		0.632025436
MMAR_3443	MMAR_3443-1	PE/PPE	79.98	101.47	107.52	40.87	60.12	58.32	0.000188664		0.999811336		0.516249998
MMAR_4561	MMAR_4561-1	PE/PPE	11.32	4.68	12.05	28.91	20.42	27.45	1.58E-08		0.999999984		2.63424715
MMAR_4562	MMAR_4562-1	PE/PPE	52.14	31.7	73.45	131.93	116.14	135.65	2.43E-10		1		2.341039958
MMAR_4899	MMAR_4899-1	PE/PPE	62.55	70.24	43.86	155.03	115.61	108.02	0.00067088		0.99931292		1.974062812
MMAR_5448	MMAR_5448-1	PE/PPE	599.5	563.85	645.48	805.73	734.17	730.84	1.74E-05		0.999982579		1.177719623

Regulatory proteins - 16 genes			FPKM							PPEE		PPDE	RealFC
GENE_ID	GENE_NAME	FUNCTION	Fragments Per Kilobase of transcript per Million mapped reads.							posterior probability that a transcript is equally expressed		posterior probability that a transcript is differentially expressed	real fold change is the ratio of the normalized mean count values for LSMMG over the normalized mean count values for normal
			NORMAL Long			LSMMG Long							
			4days 35hr	4days 36hr	4days 37hr	4days 35hr	4days 36hr	4days 37hr					
MMAR_0016	pkn8	regulatory proteins	285.3	210.87	260.69	227.14	203.84	229.66	0.007193237		0.992806763		0.824932412
MMAR_0108	MMAR_0108-1	regulatory proteins	88.52	69.91	91.18	41.01	42.52	67.17	0.000371183		0.999628817		0.565530357
MMAR_0640	hspR	regulatory proteins	143.87	132.03	164.5	632.07	579.44	858.82	1.04E-14		1		4.348963467
MMAR_0790	MMAR_0790-1	regulatory proteins	37.28	36.01	41.22	18.71	24.25	30.43	0.000219013		0.999780987		0.602912962
MMAR_1132	whiB3	regulatory proteins	346.95	402.9	407.3	117.55	115.23	242.44	4.65E-07		0.999999535		0.376107149
MMAR_1242	MMAR_1242-1	regulatory proteins	222.43	183.58	147.49	312.46	356.38	446.44	0.000928408		0.999071592		1.857277355
MMAR_1365	whiB7	regulatory proteins	111.73	70.4	65.32	186.01	180.87	336.32	0.048463671		0.951536329		2.59804091
MMAR_2281	MMAR_2281-1	regulatory proteins	156.82	156.08	234.79	121.59	100.86	125.7	0.007252402		0.992747598		0.594940856
MMAR_3454	MMAR_3454-1	regulatory proteins	218.11	166.2	235.56	118.48	156.64	181.15	0.034698044		0.965301956		0.69130916
MMAR_3703	MMAR_3703-1	regulatory proteins	109.01	96.59	107.89	190.25	289.87	408.62	0.04859521		0.95140479		2.662893181
MMAR_4325	MMAR_4325-1	regulatory proteins	75.19	70.09	65.41	115.86	104.78	107.42	7.33E-09		0.999999993		1.455162734
MMAR_4577	pknD	regulatory proteins	51.19	50.84	62.13	106.01	90.83	78.13	0.00953268		0.999046732		1.577430885
MMAR_4942	phoP	regulatory proteins	954.79	1013.72	1031.12	677.22	749.76	791.11	0.000182649		0.999817351		0.688698928
MMAR_5069	MMAR_5069-1	regulatory proteins	86.84	90.51	83.35	42.42	29.74	56.21	1.18E-05		0.999988156		0.454591254
MMAR_5170	whiB4	regulatory proteins	352.49	412.02	348.95	925.23	737.43	700.07	7.43E-09		0.999999993		1.931346496
MMAR_5405	ethR	regulatory proteins	269.76	346.71	315.26	115.41	85.47	149.99	2.72E-08		0.999999973		0.347071577

Virulence, adaptation and detoxification - 5 genes			FPKM						PPEE		PPDE	RealFC
GENE_ID	GENE_NAME	FUNCTION	Fragments Per Kilobase of transcript per Million mapped reads.						posterior probability that a transcript is equally expressed		posterior probability that a transcript is differentially expressed	real fold change is the ratio of the normalized mean count values for LSMNG over the normalized mean count values for normal
			NORMAL Long			LSMMG Long						
			4days 35hr	4days 36hr	4days 37hr	4days 35hr	4days 36hr	4days 37hr				
MMAR_0515	hsp	virulence, adaptation and detoxification	10.21	10.08	12.69	250.44	285.9	913	0.001546827		0.998453173	40.77169742
MMAR_0637	dnaK	virulence, adaptation and detoxification	620.89	802.5	920.1	2607.47	4190.37	6636.63	0.043718887		0.956281113	5.377890602
MMAR_3740	eis	virulence, adaptation and detoxification	18.46	14.1	19.5	42.16	44.17	50.55	0.000124326		0.999875674	2.487015373
MMAR_3776	rgfE	virulence, adaptation and detoxification	272.23	197.58	171.44	132.01	61.99	90.14	0.024588876		0.975411124	0.410842249
MMAR_4053	nccJ_3	virulence, adaptation and detoxification	43.81	54.1	61.29	90.7	80.11	75.55	0.013005824		0.9886699676	1.447509397