

Supplementary materials

Characterisation of genes involved in galactolipids and sulfolipids metabolism in maize and *Arabidopsis* and their differential responses to phosphate deficiency

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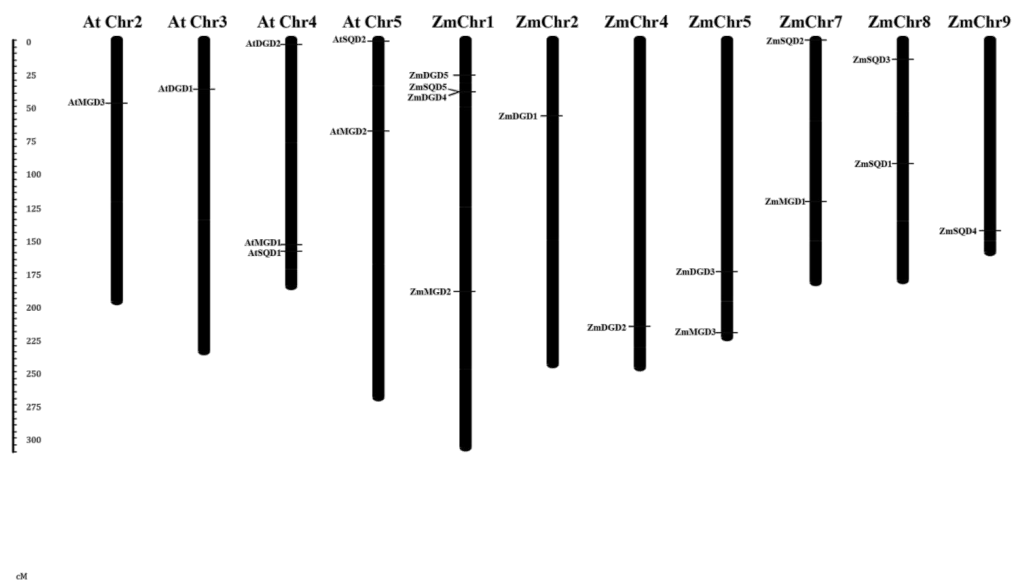


Fig.S1. Chromosomal locations of *MGD*, *DGD* and *SQD* genes on maize chromosomes. The black bar represents the chromosome, and chromosome number is displayed at the top of the bar. The scale showed a 300cM chromosomal distance.

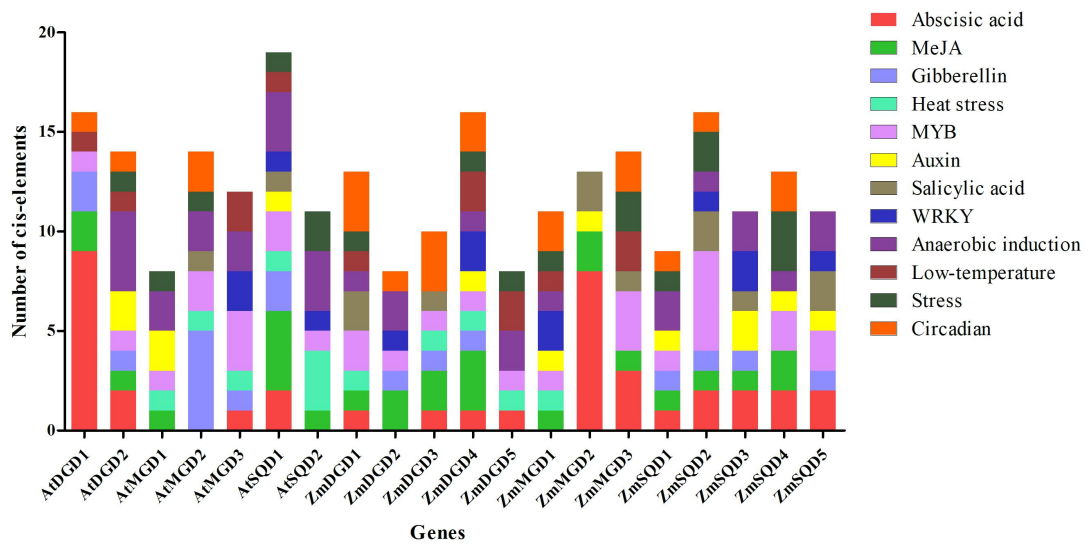


Fig.S2. The number of cis-regulatory elements in the promoter region of the maize *MGD*, *DGD* and *SQD* genes. Different colors indicate different cis-acting elements.

Table S1. The expression data of *ZmMGDs*, *ZmDGDs*, and *ZmSQDs* in maize sampled at different developing stages or various tissues.

	ZmSQD5	ZmSQD4	ZmSQD3	ZmSQD2	ZmSQD1	ZmDGD5	ZmDGD4	ZmDGD3	ZmDGD2	ZmDGD1	ZmMGD3	ZmMGD2	ZmMGD1
Germinating Seed 24h	1576.56	3390.1	538.8	1651.81	4298.95	836.53	1188.62	6504	1902.59	435.46	3346.05	70.38	3829.83
Coleoptile 6DAS GH	2650.32	4907.14	1473.49	1439.03	6911.22	1053.22	2702.07	5715.49	2152.21	807.15	6613.09	86.13	7152.44
Coleoptile 6DAS Primary Root	2866.78	4679.66	759.68	785.74	2942.17	1317.46	3836.99	5745.76	741.95	732.78	13486.6	83.06	8464.72
Stem and SAM (V1)	2931.69	4307.01	1539.8	1637.13	7800.56	2458.66	2614.34	6124.52	2208.27	939.26	11953.23	77.39	11836.43
Stem and SAM (V3)	2932.27	4793.25	1916.18	1980.41	6909.09	2035.8	3027.77	6420.97	1784.61	1517.38	11929.7	118.01	9786.44
Stem and SAM (V4)	4429.05	5155.96	1433.67	1984.05	5149.97	2520.21	3624.88	6677.3	1747.82	1805.58	6290.86	112.72	5877.74
Shoot tip (V5)	2576.12	4139.02	1913.77	1481.76	7200.42	2158.85	3214.36	6700.89	2517.27	2876	8019.98	112.33	13281.43
First Internode (V5)	2519.86	4113.83	2782.23	1850.21	6286.8	1799.59	3175.03	6699.91	2518.06	3011.39	10431.75	93.91	12574.66
First Internode (V7)	3607.56	4285.88	1413.6	1892.79	4259.73	2374.82	4638.32	6013.09	2948.63	2333.89	6674.88	92.01	9282.73
Fourth Internode (V9)	3790.92	4537.51	1521.53	1578.7	7020.47	2134.36	3612.51	4800.91	3645.51	2570.83	7122.14	120.52	11680.93
Whole Seedling (VE)	2539.16	4200.45	1733.74	4365.35	15758.5	1745.98	3169.87	10805.73	11316.4	1565.15	11071.5	104.15	17356.56
Primary Root (VE)	2698.06	4271.76	911.34	1132.39	4638.14	2064.92	2732.94	5294.51	944.29	526.83	17092	75.41	6628.79
Pooled Leaves (V1)	4428.88	6614.58	2679.54	7328.63	17636.33	1889.72	2971.24	19665.9	20891.63	3489.34	11617.18	80.69	21451.1

Primary Root (V1)	2524.89	3730.52	873.89	1604.15	2829.05	1711.81	2870.66	7448.64	1402.37	1153.17	15686.73	71.94	3755.35
Topmost Leaf (V3) visible	3913.16	5806.71	4806.62	6922.94	23161.73	2178.73	4160.12	19122.53	18449.96	3268.37	10807.83	105.31	23243.9
First Leaf (V3) visible	6142.64	8333.42	10587.04	6597.64	19509.13	1842.3	3094.5	22342.73	12400.23	5328.21	12266.83	245.61	14988.23
Tip of Stage 2 leaf (V5)	6372.67	5612.48	8450.35	9345.1	22881	1418.29	2536.72	18036.86	14095.93	4966.18	12766.03	118.32	19274.53
Base of Stage 2 leaf (V5)	3056.46	3835.43	857.79	3162.83	15385.66	2420.02	4434.83	7459.64	8420.26	1904.56	13591.86	100.46	22802.83
Tip of Stage 2 leaf (V7)	6036.42	6093.66	2879.09	7383.24	18237.7	2166	4788.57	18863.56	15074.86	2845.29	9615.31	129.81	18378.56
Base of Stage 2 leaf (V7)	4650.72	4245.34	1553.43	2590.73	9116.1	2602.17	5441.39	6142.39	4212.83	1483.35	10788.78	102.75	14296.9
Eighth Leaf (V9) visible	8253.24	8700.6	3426.43	7186.07	14605.23	2332.98	4095.18	22081.96	12947.73	4897.72	10590.6	91.12	13525.3
Eleventh Leaf (V9)	2092.89	3397.52	1612.17	3642.54	17748.33	2371.84	3692.59	10918.29	8644.01	2055.24	7806.81	118.77	14964.26
Thirteenth Leaf (V9)	2996.27	3199.56	1195.35	4016.57	15082.26	2621.52	3524.48	9501.39	8668.48	1470.72	5142.28	92.54	16859.1
Immature Leaf (V9)	3384.55	3386.62	885.77	2964.31	10103.19	3479.8	4531.03	10155.11	6628.48	2178.9	9002.14	141.8	12909.36
Thirteenth Leaf (VT)	9137.86	7900.5	1902.27	8039.89	12426.13	1362.65	4181.66	26633.73	13894.63	5336.56	13719.29	109.63	16993.6
Thirteenth Leaf (R2)	8648.6	6837.04	2644.83	8170.4	14051.66	1732.01	3161.9	25486.9	15210.46	4980.8	11662.16	106.21	14366.26
Immature Cob (V18)	3127.79	3867.23	1126.89	2469.11	6256.13	2696.63	2637.68	7712.84	2662.65	2243.28	6858.32	126.98	6123.12
Pre-pollination Cob (R1)	1938.71	3917.02	3464.76	2828.08	10366.48	1513.91	2745.51	9056.7	3429.95	2803.75	15107.4	334.01	11856.23
Silks (R1)	2139.04	4013.05	2338.06	1765.71	6075.81	1611.34	4618.46	9232.62	4063.92	2022.23	15647.66	214.85	8185
Immature Tassel (V13)	3457.93	4461.16	1135.6	2360.62	7091.6	3429.59	2431.36	7562.88	2352.62	1808.15	6229.59	124.28	8768.2

Meiotic Tassel (V18)	1760.93	2573.81	1699.88	2296.16	7714.89	2342.94	5138.7	10058.6	2608.1	901.87	9027.39	93.44	7087.07
Anthers (R1)	965.95	2147.21	1302.28	2235.58	7236.95	1116.42	7615.81	12395.03	3726.69	3176.86	35946.79	90.12	7607.35
Innermost Husk (R1)	2018.95	3771.75	1161.6	2268.93	8058.36	1646.58	4267.89	8520.79	3642.84	2002.3	16936.63	86.75	12728.03
Innermost Husk (R2)	1968.14	4638.42	1306.9	2407.84	8281.01	1451.16	2165.82	11619	3723.67	1427.89	13211.26	67.21	8981.24
Outer Husk (R2)	2645.5	4567.11	1251.28	3035.36	10171.62	1419.4	2551.75	15705.26	5635.35	1844.15	15187.36	91.99	9794.6
Embryo 16DAP	1321.17	1722.93	1200.79	2045.31	8800.67	1830.3	1913.9	8491.18	2972.22	2057.7	7646.93	119.54	9175.85
Embryo 18DAP	1575.89	1877.93	714.41	1819.48	8368.35	1749.87	1499.94	7811.38	3051.18	2088.25	8285.8	81.65	8090.9
Embryo 20DAP	1565.64	1858.27	664.53	1744.59	7674.84	1810.87	2018.61	7161.73	4387.89	1742.91	8703.55	76.69	7310.82
Embryo 22DAP	1776.29	1940.39	670.87	2353.41	7462.11	1521.19	2538.33	7443.63	5841.35	1947.49	6877.38	100.37	5965.64
Embryo 24DAP	1724.2	2011	738.22	2342.32	7485.92	1420.11	2597.57	8165.93	8564.47	1964.39	7456	84.24	5679.68
Endosperm 12DAP	879.06	1865.13	998.73	1691.95	2642.33	4312.57	3303.16	6765.35	2356.79	2760.95	7958.52	139.4	12659.83
Endosperm 14DAP	443.55	1811.81	658.01	1441.33	2692.77	3597.22	2902.61	7231.31	2546.06	3341.04	10778.28	204.5	14696.33
Endosperm 16DAP	374.66	1669.78	2471.26	2165.51	3613.74	4325.03	4150.48	8323.04	4505.49	5337.6	8931.12	761.09	13611.63
Endosperm 18DAP	487.85	1405.16	1489.25	1872.5	2874.74	3270.65	3687.6	8781.64	3373.66	4591.41	7621.69	311.29	11941.76
Endosperm 20DAP	310.8	1394.82	1290.31	1345.11	2182.43	2911.43	3877.48	7903.97	2839.72	5754.69	7017.48	239.62	10299.51
Endosperm 22DAP	507.05	1488.34	948.11	1775.69	1837.82	3168.59	4322.61	8658.26	4131.96	5404.7	6814.72	179.01	9404.94
Endosperm 24DAP	297.38	1096.42	537.3	1198.56	1776.85	2285.72	3279.37	8466.22	3764.75	5960.43	8719.81	144.22	9579.33

Seed 2DAP	1839.16	4332.03	3853.1	3263.71	10375.85	2319.36	3023.93	8518.28	2608.12	2747.64	17703.73	477.41	10569.47
Seed 4DAP	1938.51	4402.2	3415.8	3370.06	10315.25	1749	2451.36	8901.23	2912.76	2829.03	16362.13	607.12	11007.57
Seed 6DAP	2618.31	4243.47	1634.27	2348.1	5303.49	3033.75	3177.7	9937.1	2039.33	2089.08	10385.23	156.89	8811.53
Seed 8DAP	1719.24	3272.06	1922.44	2427.37	5277.94	2389.86	2853.12	10347.28	2351.21	1937.51	9846.65	190.07	10534.57
Seed 10DAP	1319.9	3281.15	1525.19	2281.25	5219.43	2173.57	2232.83	10017.81	1883.07	1999.48	11208.84	179.7	8277.77
Seed 12DAP	1203.5	2056.83	1159.07	2233.9	3637.29	2883.32	2387.4	10461.59	2928.94	2362.32	8424.05	129.43	7796.21
Seed 14DAP	693.86	1898.68	1135.9	1819.58	3994.01	3066.57	2374	11855.7	2922.49	3193.58	9337.93	205.94	11542.9
Seed 16DAP	593.07	1611.62	2763.4	2450.57	4048.57	3221.11	4045.74	9821.91	4330.76	3796.28	7929.22	486.23	11362.6
Seed 18DAP	631.27	1634.81	1345.53	1584.95	3331.99	2677.02	2720.84	10422.39	2476.13	3732.07	7990.79	208.45	9370.76
Pericarp 18DAP	1449.11	2864.42	1339.68	1604.29	4833.12	1597.25	2099.06	18661.06	2182.57	2021.39	10506.8	171.19	5868.5
Seed 20DAP	607.08	1593.12	1875.28	1812.37	3076.28	2551.2	3309.41	10066.72	2951.72	4608.39	7810.48	323.98	9202.07
Seed 22DAP	585.03	1629.97	1152.33	1831.29	3025.17	2475.37	4089.16	9169.02	3600.9	3820.94	7476.73	147.65	8155.65
Seed 24DAP	532.28	1300.04	996.25	1968.05	3500.94	2308.72	3266.23	9730.01	4449.51	4771.38	8417.82	130.74	8326.48

Table S2 . The RNA-Seq data used in the analysis.

SRASStudy	SRX2672484	SRP041183
Publication (PMID or DOI)	29250095	25569788
Publication Title	Biochemical and Transcriptional Regulation of Membrane Lipid Metabolism in Maize Leaves under Low Temperature	Transposable elements contribute to activation of maize genes in response to abiotic stress
Reference	Gu Y et al., 2017	Makarevitch et al., 2015
Sample Description	Response to cold (mRNA-Seq)	Response to heat, cold, salt, and UV (mRNA-Seq)

Table S3. The maize and *Arabidopsis* *MGD*, *DGD*, *SQD* genes primers used for quantitative real-time PCR

Genes	Primers
Actin-F	5'--CACCTTCTAVAACGAGCTCC--3'
Actin-R	5'--CAGTCAGGATCTTCATGAGG--3'
ZmGAPDH-F	5'--CCCTTCATCACCACGGACTAC--3'
ZmGAPDH-R	5'--AACCTTCTTGGCACCACCCT--3'
AtDGD1-F	5'--ACTGTTGGCATGTTTGGTTAGAC--3'
AtDGD1-R	5'--GTGCTTTGAAGAACACTGGCTAT--3'
AtDGD2-F	5'--TCCTGGAAAGTTTGCTATTGAC--3'
AtDGD2-R	5'--GATAACCTGATTACCTTGTGGC--3'
ZmDGD1-F	5'--CCATGGGCGGAGGTGGAAAAGCAAG--3'
ZmDGD1-R	5'--CCATGAACATTACAAATCACAGACC--3'
ZmDGD2-F	5'--TGGAAGAGCCCGAGCATCTAA--3'
ZmDGD2-R	5'--TGGGTGGCACCTGACAATCTG--3'
ZmDGD3-F	5'--GGAAGGAGTGGGAGGTGGTT--3'

ZmDGD3-R	5'--AGCCCTTGTTTCAGTGATTTTCAT--3'
ZmDGD4-F	5'--TAGTGCCCTGGCTTTGTAAAGT--3'
ZmDGD4-R	5'--TGGTATGAACTGTGAAGTGTCCC--3'
ZmDGD5-F	5'--AGAATGGGAGGTGCTCAGGAT--3'
ZmDGD5-R	5'--CAAGATTTGCCAGTATTTTCAGGT--3'
AtMGD1-F	5'--CCAGGTGTTTATTACGGATTT--3'
AtMGD1-R	5'--TAGGACACGAAGTGGGACAT--3'
AtMGD2-F	5'--GGAGTATAAGCCGGAGATAATCATT--3'
AtMGD2-R	5'--AGCCCATCAAACAACGCCCTTTTCG--3'
AtMGD3-F	5'--GAGGCCGGTTTAATGGAGTA--3'
AtMGD3-R	5'--AAAGATGGGCGGACAGGTAA--3'
ZmMGD1-F	5'--TGGACCCTTGTGGAAGATGA--3'
ZmMGD1-R	5'--TGAGATCCGTGATAACAGTTGC--3'
ZmMGD2-F	5'--TCTGTGGGTTCTCAAATGGC--3'
ZmMGD2-R	5'--TTCAAGTTCCTCCTCAAATC--3'
ZmMGD3-F	5'--GGCCGCTGAACGACATG--3'
ZmMGD3-R	5'--GGCTCTGCTGCCACTTGA--3'

AtSQD1-F	5'--GATTCGCACAACATTGCTTTTACTT--3'
AtSQD1-R	5'--ACATTGAACCGTGTCTCTTATATCG--3'
AtSQD2-F	5'--GATTCATGTAGGTCGCATTG--3'
AtSQD2-R	5'--AGTGTCTCCGACTCTGATGG--3'
ZmSQD1-F	5'--AAACCGCTAAAGTAGTACCAGC--3'
ZmSQD1-R	5'--CGTCTCCAACAAAGGCAATC--3'
ZmSQD2-F	5'--ATTCACGCCTCTTCACCTGG--3'
ZmSQD2-R	5'--GCTTTCTGAGTCAACACCCTTGT--3'
ZmSQD3-F	5'--GAGATGCGAGTCAGGCTAAG--3'
ZmSQD3-R	5'--CTGTGAACACTGCTGGCATTTCCTTC--3'
ZmSQD4-F	5'--GCTGTTGGGCATCCACTTAC--3'
ZmSQD4-R	5'--CCTCGACTCGTGGGTGGGTATCGA--3'
ZmSQD5-F	5'--ACATCTTCCAGCGTACATACC--3'
ZmSQD5-R	5'--TCTACACCCTTATTCCAAAGC--3'

Table S4. Detailed information of *MGD*, *DGD*, *SQD* genes identified in the *Arabidopsis* and maize genome.

Family group	Specie	Gene name	Gene locus	Chromosome location	CDS (bp)	Peptide (aa)	Molecular Weight (KD)	Isoelectric Point
MGD	<i>Arabidopsis thaliana</i>	<i>AtMGD1</i>	AT4G31780	Chr4:15373373-15377762	1602	533	58.54	9.30
		<i>AtMGD2</i>	AT5G20410	Chr5:6896133-6899224	1407	468	52.73	6.30
		<i>AtMGD3</i>	AT2G11810	Chr2:4742629-4747471	1398	465	52.99	8.47
	<i>Zea mays</i>	<i>ZmMGD1</i>	GRMZM2G142873	Chr7:121388644-121395911	1590	529	56.90	8.83
		<i>ZmMGD2</i>	GRMZM2G141320	Chr1:189808651-189811445	1434	477	53.01	9.55
		<i>ZmMGD3</i>	GRMZM2G178892	Chr5:220155283-220160847	1506	501	55.29	6.84
DGD	<i>Arabidopsis thaliana</i>	<i>AtDGD1</i>	AT3G11670	Chr3:3680159-3685290	2427	808	91.83	7.57
		<i>AtDGD2</i>	AT4G00550	Chr4:237460-241007	1422	473	53.91	7.66
	<i>Zea mays</i>	<i>ZmDGD1</i>	AC233887.1FG006	Chr2:57476582-57481295	2352	783	88.07	9.05
		<i>ZmDGD2</i>	GRMZM2G175453	Chr4:216214602-216218883	2220	739	82.61	7.34
		<i>ZmDGD3</i>	GRMZM2G092588	Chr5:174487968-174492994	2379	792	89.03	6.84
		<i>ZmDGD4</i>	GRMZM2G160452	Chr1:39418137-39423804	1395	464	53.12	6.84

		<i>ZmDGD5</i>	GRMZM2G098667	Chr1:26525264-26529804	1428	475	54.38	8.69
	<i>Arabidopsis</i>	<i>AtSQD1</i>	AT4G33030	Chr4:15934460-15938763	1434	477	53.11	8.41
	<i>thaliana</i>	<i>AtSQD2</i>	AT5G01220	Chr5:85905-90666	1533	510	56.63	8.61
		<i>ZmSQD1</i>	GRMZM2G053322	Chr8:92806123-92809601	1419	472	52.45	8.39
SQD		<i>ZmSQD2</i>	GRMZM2G100652	Chr7:180206-183058	1494	497	55.47	9.56
	<i>Zea mays</i>	<i>ZmSQD3</i>	GRMZM2G477503	Chr8:14146685-14152686	1314	437	59.26	9.51
		<i>ZmSQD4</i>	GRMZM2G117153	Chr9:143268530-143273374	1245	414	46.57	8.68
		<i>ZmSQD5</i>	GRMZM2G049190	Chr1:38638366-38643862	1290	429	48.10	8.69

Table S5. Detailed information of *MGD*, *DGD*, *SQD* genes identified in the other plants.

Family group	Specie	Gene locus	Chromosome location	Length(aa)
MGD	<i>Glycine max</i>	Glyma.14G104100	Chr14:10634347-10639492	530
		Glyma.17G108700	Chr17:8527140-8530377	456
		Glyma.17G221900	Chr17:37431137-37437980	530
	<i>Oryza sativa</i>	LOC_Os09g25580	Chr9:15349072-15355640	535
		LOC_Os08g20420	Chr8:12266091-12269671	469
		LOC_Os02g55910	Chr2:34223117-34227448	508
	<i>Sorghum bicolor</i>	Sb02g025070	Chr2:59725857-59733824	534
		Sb04g036240	Chr4:65967278-65971730	501
		Sb07g027910	Chr7:62808814-62812039	479
<i>Brachypodium distachyum</i>	BRADI3g20020	Chr3:19046558-19049231	478	
	BRADI3g54387	Chr3:54887705-54892314	504	
	BRADI4g30600	Chr4:36421768-36426528	535	

		MTR1g013650	Chr1:3322974-3329019	369
	<i>M. truncatula</i>	MTR4g115920	Chr4:47897677-47901019	467
		MTR8g027715	Chr8:10023630-10027762	418
		GRMZM2G142873 (<i>ZmMGD1</i>)	Chr7:121388644-121395911	529
	<i>Zea mays</i>	GRMZM2G141320 (<i>ZmMGD2</i>)	Chr1:189808651-189811445	477
		GRMZM2G178892 (<i>ZmMGD3</i>)	Chr5:220155283-220160847	501
		Glyma.03G202100	Chr3:41033237-41039092	783
	<i>Glycine max</i>	Glyma.18G228900	Chr18:51811174-51816178	463
		LOC_Os02g33580	Chr2:19973187-19977453	802
		LOC_Os03g11560	Chr3:5994130-5997434	476
	<i>Oryza sativa</i>	LOC_Os03g16140	Chr3:8902704-8906354	463
DGD		LOC_Os04g34000	Chr4:20587018-20593240	775
		LOC_Os11g05990	Chr11:2817601-2822373	736
		Sb01g039910	Chr01:70475265-70478917	464
	<i>Sorghum bicolor</i>	Sb01g042870	Chr01:73263114-73267752	475
		Sb04g022040	Chr04:51972203-51977473	792

	Sb05g003730	Chr5:4256070-4261872	741
	Sb06g016250	Chr6:44718330-44723317	788
<i>Brachypodium distachyum</i>	BRADI1g66940	Chr1:65694538-65697502	464
	BRADI1g69930	Chr1:68392371-68397066	477
	BRADI3g45180	Chr3:47127953-47131228	782
	BRADI4g25010	Chr4:30240529-30244464	739
	BRADI5g09680	Chr5:12992096-12996097	791
<i>M. truncatula</i>	MTR1g047640	Chr1:18001555-18006249	464
	MTR6g091670	Chr6:34522519-34526786	464
	MTR7g076400	Chr7:28764358-28767380	464
	MTR1g057700	Chr1:25356979-25362682	722
	MTR7g106250	Chr7:43192263-43198511	780
<i>Zea mays</i>	AC233887.1FG006 (<i>ZmDGD1</i>)	Chr2:57476582-57481295	783
	GRMZM2G175453 (<i>ZmDGD2</i>)	Chr4:216214602-216218883	739
	GRMZM2G092588 (<i>ZmDGD3</i>)	Chr5:174487968-174492994	792
	GRMZM2G098667 (<i>ZmDGD5</i>)	Chr1:26525264-26529804	475

		GRMZM2G160452 (<i>ZmDGD4</i>)	Chr1:39418137-39423804	464
	<i>Glycine max</i>	Glyma.03G131100	Chr3:34628886-34631900	474
		Glyma.03G078300	Chr03:19628680-19634712	517
	<i>Oryza sativa</i>	LOC_Os01g04920	Chr1:2275067-2278872	436
		LOC_Os03g15840	Chr3:8737120-8741197	415
		LOC_Os05g32140	Chr5:18738597-18741960	477
		LOC_Os07g01030	Chr7:17515-21408	479
SQD	<i>Sorghum bicolor</i>	Sb09g019100	Chr9:47591479-47595552	478
		Sb02g000240	Chr2:138220-142176	500
		Sb03g006480	Chr3:6543831-6548060	430
		Sb01g040150	Chr1:63463975-63469025	414
	<i>Brachypodium distachyum</i>	BRADI1G59860	Chr1:58789617-58792400	482
		BRADI1g67200	Chr1:65880083-65884681	420
		BRADI2G02800	Chr2:1973156-1977127	439
		BRADI2G26870	Chr2:25643425-25647136	483
	<i>M. truncatula</i>	MTR7g067340	Chr7:24544800-24551220	515

	MTR7g090510	Chr7:35621507-35625134	477
	GRMZM2G053322 (<i>ZmSQD1</i>)	Chr8:92806123-92809601	472
	GRMZM2G100652 (<i>ZmSQD2</i>)	Chr7:180206-183058	497
<i>Zea mays</i>	GRMZM2G477503 (<i>ZmSQD3</i>)	Chr8:14146685-14152686	437
	GRMZM2G117153 (<i>ZmSQD4</i>)	Chr9:143268530-143273374	414
	GRMZM2G049190 (<i>ZmSQD5</i>)	Chr1:38638366-38643862	429