Table S1. Identification data pertaining to the members of the DUSP gene family in cotton.

Gene ID	Gene Name	Genomic Location	Protein Length (bp)	Molecular Weight (Da)	Theoretical Isoelectric Point (pI)
Garb_01G029220. 1	*GaDUSP01*	Chr01:122,867,721-122,874,311	562	62.09	5.76
Garb_02G010450. 1	*GaDUSP02*	Chr02:63,242,590-63,246,216	862	95.66	5.77
Garb_03G003540. 1	*GaDUSP03*	Chr03:2,609,193-2,613,999	584	64.43	5.82
Garb_03G009860. 1	*GaDUSP04*	Chr03:18,095,042-18,099,638	835	91.83	5.52
Garb_04G002590. 1	*GaDUSP05*	Chr04:3,628,079-3,634,581	380	43.10	6.77
Garb_04G007170. 1	*GaDUSP06*	Chr04:14,141,801-14,147,615	850	94.08	7.71
Garb_05G027210. 1	*GaDUSP08*	Chr05:29,484,863-29,488,012	289	33.11	8.88
Garb_05G000860. 1	*GaDUSP07*	Chr05:1,027,473-1,029,943	284	31.93	9.47
Garb_06G004010. 1	*GaDUSP09*	Chr06:5,412,199-5,415,391	268	29.96	9.24
Garb_06G019920. 1	*GaDUSP10*	Chr06:125,797,240-125,799,297	283	31.89	8.74
Garb_06G019980. 1	*GaDUSP11*	Chr06:125,853,301-125,860,991	286	33.41	9.00
Garb_07G005680. 1	*GaDUSP14*	Chr07:11,699,715-11,702,014	204	23.32	5.86
Garb_07G001470. 1	*GaDUSP12*	Chr07:1,835,544-1,840,133	564	63.15	8.86
Garb_07G019800. 1	*GaDUSP17*	Chr07:91,792,909-91,795,535	213	24.45	8.47
Garb_07G009920. 1	*GaDUSP15*	Chr07:51,693,786-51,697,905	214	24.51	6.70
Garb_07G019730. 1	*GaDUSP16*	Chr07:91,465,407-91,471,745	301	33.62	8.03
Garb_07G005350. 1	*GaDUSP13*	Chr07:9,913,113-9,916,885	268	29.79	7.56
Garb_08G016040. 1	*GaDUSP18*	Chr08:32,407,767-32,423,488	1211	136.82	6.16
Garb_08G028990. 1	*GaDUSP19*	Chr08:137,528,557-137,539,928	1253	140.99	7.17
Garb_09G029940. 1	*GaDUSP21*	Chr09:89,341,873-89,347,500	935	104.10	6.00
Garb_09G024410. 1	*GaDUSP20*	Chr09:84,684,536-84,688,128	219	24.97	6.45
Garb_10G027850. 1	*GaDUSP23*	Chr10:123,774,782-123,779,809	838	93.20	6.5
Garb_10G001060. 1	*GaDUSP22*	Chr10:824,268-826,857	201	22.81	6.44
Garb_11G017040. 1	*GaDUSP29*	Chr11:19,759,668-19,763,372	271	30.23	6.50
Garb_11G005460. 1	*GaDUSP25*	Chr11:4,564,433-4,570,302	647	71.29	6.09
Garb_11G011380. 1	*GaDUSP28*	Chr11:10,679,780-10,695,664	1255	141.35	6.14
Garb_11G008400. 1	*GaDUSP27*	Chr11:7,192,982-7,196,091	314	35.31	5.93
Garb_11G007890. 1	*GaDUSP26*	Chr11:6,751,666-6,754,764	448	51.75	8.53
Garb_11G040720. 1	*GaDUSP30*	Chr11:134,410,353-134,415,804	364	40.41	6.04
Garb_11G002830. 1	*GaDUSP24*	Chr11:2,388,661-2,391,293	333	37.68	6.26
Garb_12G002410. 1	*GaDUSP31*	Chr12:3,209,340-3,215,620	618	67.18	5.79
Garb_13G021030. 1	*GaDUSP32*	Chr13:115,824,908-115,827,338	201	23.25	7.56
Gbar_A01G015500. 1	*GbDUSP01*	A01:94,311,099-94,315,503	862	95.88	5.76
Gbar_A03G014990. 1	*GbDUSP02*	A03:88,370,923-88,375,352	835	91.86	5.52
Gbar_A05G039650. 3	*GbDUSP06*	A05:99,190,595-99,197,143	380	43.16	6.53
Gbar_A05G027510. 1	*GbDUSP04*	A05:30,378,789-30,382,046	257	29.23	8.46
Gbar_A05G035700. 7	*GbDUSP05*	A05:89,681,064-89,686,978	850	93.99	7.93
Gbar_A05G002500. 2	*GbDUSP03*	A05:2,294,698-2,297,685	290	32.66	9.39
Gbar_A06G007170. 1	*GbDUSP07*	A06:15,791,657-15,793,786	283	31.89	8.74
Gbar_A07G023420. 1	*GbDUSP10*	A07:91,038,480-91,043,185	572	63.91	8.84
Gbar_A07G019960. 1	*GbDUSP09*	A07:83,658,744-83,663,102	268	29.86	7.57
Gbar_A07G009100. 1	*GbDUSP08*	A07:14,009,753-14,018,900	265	29.72	6.99
Gbar_A09G019830. 3	*GbDUSP11*	A09:71,931,759-71,938,578	932	105.62	5.79
Gbar_A09G021150. 1	*GbDUSP13*	A09:73,182,949-73,186,649	219	25.00	6.45
Gbar_A09G026570. 3	*GbDUSP14*	A09:77,812,657-77,818,804	935	104.12	6.05
Gbar_A09G021140. 14	*GbDUSP12*	A09:73,173,571-73,176,090	206	23.55	9.17
Gbar_A10G020920. 1	*GbDUSP16*	A10:100,207,985-100,210,453	138	16.15	9.78
Gbar_A10G022730. 1	*GbDUSP17*	A10:104,555,887-104,558,718	843	93.55	6.63
Gbar_A10G020810. 2	*GbDUSP15*	A10:99,928,853-99,942,122	959	107.21	5.34
Gbar_A11G007900. 1	*GbDUSP19*	A11:6,895,513-6,898,680	314	35.30	5.93
Gbar_A11G002370. 1	*GbDUSP18*	A11:1,995,428-1,998,475	333	37.67	6.26
Gbar_A11G015770. 1	*GbDUSP20*	A11:18,139,879-18,144,005	271	30.21	6.65
Gbar_A12G025220. 2	*GbDUSP21*	A12:98,915,995-98,923,036	960	107.76	5.66
Gbar_D01G016790. 2	*GbDUSP22*	D01:50,560,215-50,564,663	863	95.65	5.79
Gbar_D02G016880. 1	*GbDUSP23*	D02:55,269,200-55,273,296	835	92.07	5.62
Gbar_D04G006430. 1	*GbDUSP25*	D04:10,241,534-10,245,034	851	94.23	7.74
Gbar_D04G002260. 3	*GbDUSP24*	D04:3,019,344-3,025,906	376	42.59	6.53

Gbar_D05G028370. 1	*GbDUSP28*	D05:27,630,811-27,634,460	289	33.02	8.99
Gbar_D05G010380. 2	*GbDUSP27*	D05:8,419,712-8,423,063	284	30.88	5.43
Gbar_D05G002770. 1	*GbDUSP26*	D05:2,414,582-2,417,320	284	32.12	9.41
Gbar_D06G007410. 1	*GbDUSP29*	D06:11,706,045-11,708,179	283	31.78	8.90
Gbar_D07G024180. 1	*GbDUSP32*	D07:54,743,829-54,748,506	573	64.16	8.89
Gbar_D07G009500. 1	*GbDUSP30*	D07:11,325,590-11,331,040	265	29.68	6.65
Gbar_D07G020550. 1	*GbDUSP31*	D07:48,257,475-48,261,900	264	29.35	6.65
Gbar_D09G026140. 2	*GbDUSP36*	D09.51,393,288-51,399,490	935	104.11	6.12
Gbar_D09G020860. 2	*GbDUSP34*	D09:47,194,153-47,198,205	196	22.48	8.97
Gbar_D09G020870. 1	*GbDUSP35*	D09:47,203,407-47,206,430	176	19.97	4.59
Gbar_D09G019590. 2	*GbDUSP33*	D09:45,998,962-46,005,703	932	105.49	6.03
Gbar_D10G021090. 1	*GbDUSP37*	D10:55,834,905-55,848,216	959	107.40	5.45
Gbar_D10G023050. 1	*GbDUSP38*	D10:59,464,545-59,467,373	842	93.72	6.23
Gbar_D11G008330. 2	*GbDUSP40*	D11:6,506,996-6,510,159	314	35.39	5.58
Gbar_D11G002750. 1	*GbDUSP39*	D11:2,153,917-2,156,826	333	37.65	6.26
Gbar_D11G016570. 1	*GbDUSP41*	D11:15,806,240-15,810,374	271	30.31	8.09
Gbar_D12G025140. 2	*GbDUSP42*	D12:55,920,499-55,930,034	960	107.51	5.71
GH_A03G1540	*GhDUSP01*	A03:94,693,102-94,696,192	835	91.85	5.52
GH_A05G0273	*GhDUSP02*	A05:2,635,062-2,636,743	284	31.92	9.39
GH_A05G3715	*GhDUSP03*	A05:97,483,554-97,487,059	850	93.99	8.21
GH_A05G4143	*GhDUSP04*	A05:107,427,955-107,434,224	378	42.87	6.77
GH_A06G0743	*GhDUSP05*	A06:16,229,295-16,230,945	283	31.89	8.74
GH_A07G2141	*GhDUSP07*	A07:87,676,806-87,680,577	268	29.91	7.56
GH_A07G0942	*GhDUSP06*	A07:13,592,945-13,598,509	265	29.63	6.08
GH_A09G2171	*GhDUSP08*	A09:78,560,777-78,564,044	219	24.94	6.71
GH_A09G2699	*GhDUSP09*	A09:83,078,997-83,084,392	935	104.14	6.05
GH_A10G2332	*GhDUSP10*	A10:109,975,880-109,978,711	843	93.56	6.50
GH_A11G3500	*GhDUSP14*	A11:118,306,098-118,308,968	364	40.41	5.68
GH_A11G0784	*GhDUSP12*	A11:6,964,216-6,966,230	314	35.30	5.93
GH_A11G1592	*GhDUSP13*	A11:18,498,426-18,501,845	271	30.21	6.65
GH_A11G0262	*GhDUSP11*	A11:2,292,765-2,294,462	333	37.68	6.26
GH_D01G1827	*GhDUSP15*	D01:52,261,842-52,265,494	863	95.65	5.84
GH_D04G0235	*GhDUSP16*	D04:3,217,493-3,223,761	374	42.36	6.53
GH_D04G0631	*GhDUSP17*	D04:10,520,729-10,524,229	851	94.23	7.74
GH_D05G2823	*GhDUSP19*	D05:27,117,549-27,120,710	289	33.02	8.99
GH_D05G0277	*GhDUSP18*	D05:2,362,176-2,363,822	284	32.06	9.33
GH_D06G0719	*GhDUSP21*	D06:11,938,249-11,939,899	283	31.81	8.53
GH_D06G0537	*GhDUSP20*	D06:7,531,025-7,532,938	637	74.62	9.03
GH_D07G0943	*GhDUSP22*	D07:10,878,251-10,882,610	265	29.69	6.70
GH_D07G2079	*GhDUSP23*	D07:50,441,944-50,445,755	264	29.32	7.03
GH_D09G2619	*GhDUSP24*	D09.51,895,766-51,901,170	935	104.11	6.12
GH_D10G2426	*GhDUSP25*	D10:61,625,657-61,628,491	844	93.88	6.14
GH_D11G3506	*GhDUSP29*	D11:68,214,494-68,217,381	364	40.36	5.79
Grai_01G018320. 1	*GrDUSP01*	Chr01:40,368,261-40,371,908	863	95.72	5.85
Grai_03G019930. 1	*GrDUSP02*	Chr03:50,769,381-50,773,843	832	91.53	5.44
Grai_04G022070. 1	*GrDUSP04*	Chr04:47,528,061-47,533,544	402	45.47	8.66
Grai_04G017440. 1	*GrDUSP03*	Chr04:40,613,521-40,619,334	851	94.20	7.18
Grai_05G002900. 1	*GrDUSP05*	Chr05:2,229,317-2,231,860	284	32.12	9.41
Grai_05G029900. 1	*GrDUSP06*	Chr05.25,831,231-25,834,375	289	32.98	8.88
Grai_06G024140. 1	*GrDUSP09*	Chr06:56,591,393-56,594,756	268	30.06	9.33
Grai_06G024130. 1	*GrDUSP08*	Chr06:56,567,355-56,571,062	268	29.99	9.24
Grai_06G008210. 1	*GrDUSP07*	Chr06:11,314,637-11,316,808	283	31.78	8.9
Grai_07G005730. 1	*GrDUSP10*	Chr07:8,073,067-8,077,391	264	29.35	7.03
Grai_07G019420. 1	*GrDUSP11*	Chr07:42,623,832-42,628,755	265	29.61	6.59
Grai_09G029320. 1	*GrDUSP12*	Chr09:49,833,934-49,840,220	876	97.60	6.07
Grai_10G027350. 1	*GrDUSP13*	Chr10:56,896,256-56,901,358	842	93.70	6.23
Grai_11G002750. 1	*GrDUSP14*	Chr11:2,633,331-2,638,880	364	40.32	5.68
Grai_11G031300. 1	*GrDUSP16*	Chr11:57,022,682-57,025,519	314	35.34	5.69
Grai_11G023160. 1	*GrDUSP15*	Chr11:48,405,951-48,409,723	271	30.25	7.58
Grai_11G036870. 1	*GrDUSP17*	Chr11:61,190,843-61,192,543	333	37.65	6.26