

gene ID (v1.1)	2G-Start	2G-End	Gene Lengt h	Human-Readable-Description	Xinong97 9 (CK)	Xinong979 (Inoculum)	Xinong82 2 (CK)	Xinong822 (Inoculum)	L92-47 (CK)	L92-47 (Inoculum)	Lanhangxua n121 (CK)	Lanhangxua n121 (Inoculum)
TraesCS5B02G022500.1	21034784	21036846	1071	Zinc finger CCCH domain-containing protein 4	0	0	0	0	0	0	0	0
TraesCS5B02G022600.1	21106951	21107205	255	Hepatocyte nuclear factor 4-alpha	0	0	0	0	0	0	0	0
TraesCS5B02G022700.1	21152159	21153982	1824	HSP20-like chaperones superfamily protein	0.015262	0.017775	0.01682	0.066103	0.111224	0.043718	0.016226	0.017139
TraesCS5B02G022800.1	21180706	21186594	3148	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	0.084156	1.29597	0.025682	0	2.873741	7.480759	0	0.194264
TraesCS5B02G022800.2	21180706	21186594	2789	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	8.107184	6.619599	9.279461	7.108857	0	0	7.002692	26.248922
TraesCS5B02G022800.3	21180706	21186594	2809	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	57.6237	53.401906	64.28359	44.757312	11.83665	41.01205	7.832906	40.958422
TraesCS5B02G022800.4	21180706	21186594	2498	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	0	0.6921	0.391722	0	0	0	9.557481	11.220871
TraesCS5B02G022800.5	21180706	21186594	2550	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	8.795721	10.618545	42.95751	0	0	0	17.809711	9.208028
TraesCS5B02G022900.1	21401120	21406122	2380	Folylpolyglutamate synthase	3.135726	2.685388	3.555505	2.577705	4.188436	4.953465	4.160956	3.610061
TraesCS5B02G023000.1	21410819	21413716	1584	2-aminoethanethiol dioxygenase	0.561411	0.930622	2.023649	1.261488	4.053919	3.424958	2.566691	2.097955
TraesCS5B02G023000.2	21410819	21413716	1578	2-aminoethanethiol dioxygenase	0.587873	0.324905	1.074741	0.999691	3.414083	4.617781	1.805034	1.8463
TraesCS5B02G023100.1	21524523	21526820	1196	2-aminoethanethiol dioxygenase	0	0	0	0	0	0	0	0
TraesCS5B02G023200.1	21531972	21534715	1350	Methyl-CpG-binding domain protein 4	0	0.07481	0.312296	0.164633	0.239039	0.093958	0.185583	0.071607
TraesCS5B02G023300.1	21535164	21538910	1905	cationic amino acid transporters (CATs) , vacuole membrane	28.92494	30.330822	8.669127	12.7581	28.0021	36.88505	47.451798	19.466662
TraesCS5B02G023400.1	21598828	21606365	873	2-aminoethanethiol dioxygenase	0	0	0	0	0	0	0	0
TraesCS5B02G023500.1	21635289	21637591	1443	Glycosyl hydrolases family 32 protein	7.617006	27.32866	14.01434	19.447248	7.117006	18.71113	0	0
TraesCS5B02G023600.1	21735366	21745414	3013	Disease resistance protein RPH8A	0	0	0	0	0	0	0	0
TraesCS5B02G023700.1	21749294	21752624	2182	Udp-glucose 4,6-dehydratase	0	0.945346	0.670278	1.591628	0	0	1.37504	3.36856
TraesCS5B02G023700.2	21749294	21752624	2447	Udp-glucose 4,6-dehydratase	1.716944	0.755175	1.024476	0.262107	0.919949	3.052086	1.557458	0.60568
TraesCS5B02G023800.1	22033405	22034614	396	Fatty acid desaturase	0	0	0	0	2.221339	5.134251	0	0.715394
TraesCS5B02G023800.2	22033405	22034614	414	Fatty acid desaturase	10.8057	12.4786	0.636019	1.012087	17.47227	11.61676	0.439128	0
TraesCS5B02G023900.1	22037133	22045539	1955	Ankyrin repeat protein-like	0.032095	0.048245	0	0	0.448441	2.633613	0.015098	0.015596
TraesCS5B02G024000.1	22105906	22109471	1813	Serine protease HtrA-like	0	0	0	0	0	0	0	0
TraesCS5B02G024100.1	22115011	22117221	855	Serine protease HtrA-like	0	0	0	0	0	0	0	0
TraesCS5B02G024200.1	22502625	22505893	1423	DYAD-like protein	0	0	0.022537	0	0.099092	0.281786	0	0.022383
TraesCS5B02G024300.1	22509009	22514229	2417	Protein downstream neighbor of Son	0.397136	0.127925	0	0	0.248042	0.282227	0	0
TraesCS5B02G024300.2	22509009	22514229	2414	Protein downstream neighbor of Son	0.267705	0.132034	0.085742	0.024123	0	0	0.047231	0.145548
TraesCS5B02G024500.1	23352259	23352937	679	Phosphoenolpyruvate carboxylase family protein	17.78849	24.064344	0	0	29.43825	27.41781	0.059231	0.245033
TraesCS5B02G024600.1	23424701	23427479	2549	Subtilisin-like protease	0	0	0	0	0.027113	0	0	0
TraesCS5B02G024700.1	23548049	23552482	1634	CC-NBS-LRR family disease resistance protein	0	0.00095	0.935732	1.021309	1.985384	1.822599	2.778694	8.731
TraesCS5B02G024800.1	23677656	23680412	2422	CC-NBS-LRR family disease resistance protein	0.302732	0	0	0.012018	0.73745	0.466394	0.776449	0.93049
TraesCS5B02G024900.1	23875860	23876485	519	peroxin 3-1	0	0	0	0.091071	0.718069	0	0	0
TraesCS5B02G025000.1	23885649	23891503	3666	Kinase, putative	0	0	0	0.010353	0	0	0	0
TraesCS5B02G025000.2	23885649	23891503	2749	Kinase, putative	0	0.01095	0	0	0	0	0.010235	0
TraesCS5B02G025100.1	24008309	24014574	1510	YABBY transcription factor	1.126776	0.587709	0.419779	0.391008	0.690221	1.070684	0.628065	0.354216
TraesCS5B02G025200.1	24097072	24100994	3594	No exine formation 1	3.27807	3.362095	3.127013	1.014011	1.837517	2.626581	3.504046	2.689025
TraesCS5B02G025300.1	24113073	24116626	2373	Receptor-like kinase	1.773925	1.672147	1.483965	0.92179	1.515924	6.429637	0.940086	14.4041
TraesCS5B02G025400.1	24143016	24144258	810	Cortactin-binding protein 2	0	0	0	0	0	0	0	0
TraesCS5B02G025500.1	24145063	24147543	1438	cDNA clone:J013058P10, full insert sequence	0	0	0.022683	0.021806	0	0	0.021485	0
TraesCS5B02G025600.1	24313738	24316825	873	Sterol-8,7-isomerase	0	0	0	0	0	0	0	0
TraesCS5B02G025700.1	24330927	24334080	939	Sterol-8,7-isomerase	0	0	0	0	0	0	0	0
TraesCS5B02G025800.1	24374282	24377017	862	Sterol-8,7-isomerase	0	0	0	0	0	0	0	0
TraesCS5B02G025900.1	24418260	24419063	804	Serine protease	0	0	0	0	0	0	0	0
TraesCS5B02G026000.1	24665573	24677245	1868	Serine protease HtrA-like	8.776322	7.311425	3.403861	3.646783	0.527608	0.453978	4.514604	14.1721
TraesCS5B02G026000.2	24665573	24677245	1170	Serine protease HtrA-like	0	0.920679	0	0.034643	0	0	0	0
TraesCS5B02G026100.1	24772860	24776247	1711	cDNA clone:J013058P10, full insert sequence	0.248319	0.121867	0.135556	0.099185	0.331714	0.620721	0.054163	0.094314

TraesCS5B02G026200.1	24917148	24924815	3338 Ubiquitin carboxyl-terminal hydrolase, putative	2.911947	2.092402	3.198122	1.923175	2.54481	2.999796	2.764356	2.677525
TraesCS5B02G026300.1	25061806	25062922	1117 VQ motif family protein	0.800376	2.595221	0.578038	0.267266	0.957432	2.1979	0.882405	0.908755
TraesCS5B02G026400.1	25267210	25272133	3138 EEIG1/EHBP1 N-terminal domain-containing protein	3.475057	2.362992	4.088793	1.356934	4.796211	14.30009	3.38703	2.880252
TraesCS5B02G026500.1	25327916	25335936	4042 Disease resistance protein RPM1	0.492307	0.325261	0.055998	0.027642	0.21267	0.446544	0.316886	0.290669
TraesCS5B02G026600.1	25662226	25667637	1830 Methyl-CpG binding domain containing protein, expressed	26.81122	30.474248	41.14651	20.021586	58.32732	39.25191	32.307926	32.606122
TraesCS5B02G026700.1	25667853	25668646	794 RING/U-box superfamily protein	0.248244	0.050477	0.096529	0.140095	0.33904	1.221817	0.046782	0.09659
TraesCS5B02G026800.1	25993146	25995851	2706 F-box protein	0.553437	0.177116	0.410275	0.287386	0.512993	0.864129	0.326967	0.475608
TraesCS5B02G026900.1	26005867	26008911	2861 F-box protein	1.249673	0.986898	0.944788	0.720825	0.6628	1.008013	1.219467	1.396177
TraesCS5B02G027000.1	26058398	26058946	471 DNA topoisomerase	0	0	0	0	0	0	0	0
TraesCS5B02G027100.1	26304334	26308052	2821 F-box protein	0.31166	0	0.407767	0.355846	0.019625	0	0.009941	0
TraesCS5B02G027200.1	26321238	26325102	3865 F-box protein	0.390398	0.228462	0.161416	0.123166	0.040425	0.109947	0.17678	0.164052
TraesCS5B02G027300.1	26445358	26447080	381 30S ribosomal protein S10	0.07013	0	9.647001	23.951216	0	0	10.602489	12.890909
TraesCS5B02G027400.1	26609551	26609994	405 RING/U-box superfamily protein	0	0	0	0	0	0	0	0
TraesCS5B02G027700.1	26872939	26879859	3486 NBS-LRR disease resistance protein-like	0	0	0	0	0	0	0	0
TraesCS5B02G027800.1	26915154	26916425	843 Assimilatory nitrate reductase catalytic subunit	0	0	0	0	0	0	0	0
TraesCS5B02G027900.1	26947959	26950509	1630 F-box family protein	0.645284	0.831339	0.210921	0.389441	0.796239	0.727863	0.191035	0.494644
TraesCS5B02G028000.1	26950814	26952377	754 Thioesterase family protein	25.43845	16.341775	19.66712	24.216352	18.90364	17.72178	30.244939	29.91466