g2785	probable copper-transporting ATPase HMA5[Durio zibethinus] (93%) PREDICTED: probable copper-transporting ATPase HMA5 [Theobroma cacao](95%)
g609	nucleoside diphosphate kinase B-like[Durio zibethinus] (99%) nucleoside diphosphate kinase B [Juglans regia] (99%)
g2461	uncharacterized protein LOC111289413 isoform X1 [Durio zibethinus](97%)
G2792	PHD finger protein MALE STERILITY 1 [Durio zibethinus] (99%)
g2915	oleosin 1-like [Durio zibethinus] (97%)
G338	uncharacterized protein LOC111290630 [Durio zibethinus] (100%)
G560	protein RESPONSE TO LOW SULFUR 3-like [Durio zibethinus]
G2626	bifunctional UDP-glucose 4-epimerase and UDP-xylose 4-epimerase 1-like isoform X1[Durio zibethinus] (100%)
G3008	uncharacterized protein LOC111289749 [Durio zibethinus]
G1500	hypothetical protein POUND7_018145, partial [Theobroma cacao]
g2586	protein STAY-GREEN, chloroplastic-like [Durio zibethinus] LOW QUALITY PROTEIN: protein STAY-GREEN 1, chloroplastic-like [Durio zibethinus]
G1373	LOW QUALITY PROTEIN: serine/threonine-protein kinase SAPK3-like [Herrania umbratica] hypothetical protein SCA6_005032 [Theobroma cacao] hypothetical protein POUND7_004779 [Theobroma cacao]
G2109	hypothetical protein CXB51_009482 [Gossypium anomalum] hypothetical protein HRI_004635400 [Hibiscus trionum]
G977	uncharacterized protein LOC111289873 [Durio zibethinus] uncharacterized protein LOC105765307 [Gossypium raimondii]
G2628	NO SIGNIFICANT RESULT FOUND

G2457	Uncharacterized protein TCM_012439 [Theobroma cacao] (83%similarity) hypothetical protein QQP08_011397, partial [Theobroma cacao] hypothetical protein L484_013263 [Morus notabilis]
g2961	Carotenoid oxygenase - like 5 [Theobroma cacao] probable carotenoid cleavage dioxygenase 4, chloroplastic [Herrania umbratica]
g1341	putative invertase inhibitor [Durio zibethinus]
g514	uncharacterized protein LOC111290118 [Durio zibethinus] (only one blast output)
G2465	PREDICTED: non-specific lipid-transfer protein 2 [Theobroma cacao] hypothetical protein SCA6_003700 [Theobroma cacao] non-specific lipid-transfer protein 2-like [Herrania umbratica]
G2603	uncharacterized protein LOC111318268 isoform X1 [Durio zibethinus]
G449	Uncharacterized protein TCM_012229 [Theobroma cacao] putative Mediator of RNA polymerase II transcription subunit 13 (99% similarity)
G2914	ethylene-responsive transcription factor ERF105-like [Durio zibethinus]
G2081	U-box domain-containing protein 19-like [Durio zibethinus] (100%similarity)
G2082	aldehyde dehydrogenase family 2 member B4, mitochondrial-like [Durio zibethinus] (98%)
G2843	uncharacterized protein LOC111289861 [Durio zibethinus] (100%)
G2770	putative UPF0481 protein At3g02645 [Durio zibethinus] (47%)
G995	Guanine nucleotide-binding protein subunit beta-like protein [Hibiscus syriacus] (84%)
G2427	lysine-specific demethylase JMJ706-like isoform X2 [Durio zibethinus] (97%)

Percentage means “Per. Ident” stands for percent identity, which is the percentage of the nucleotides that are the same between the two sequences. 100% indicates that at each position of the alignment, the nucleotide in the subject sequence is identical to the reference sequence.