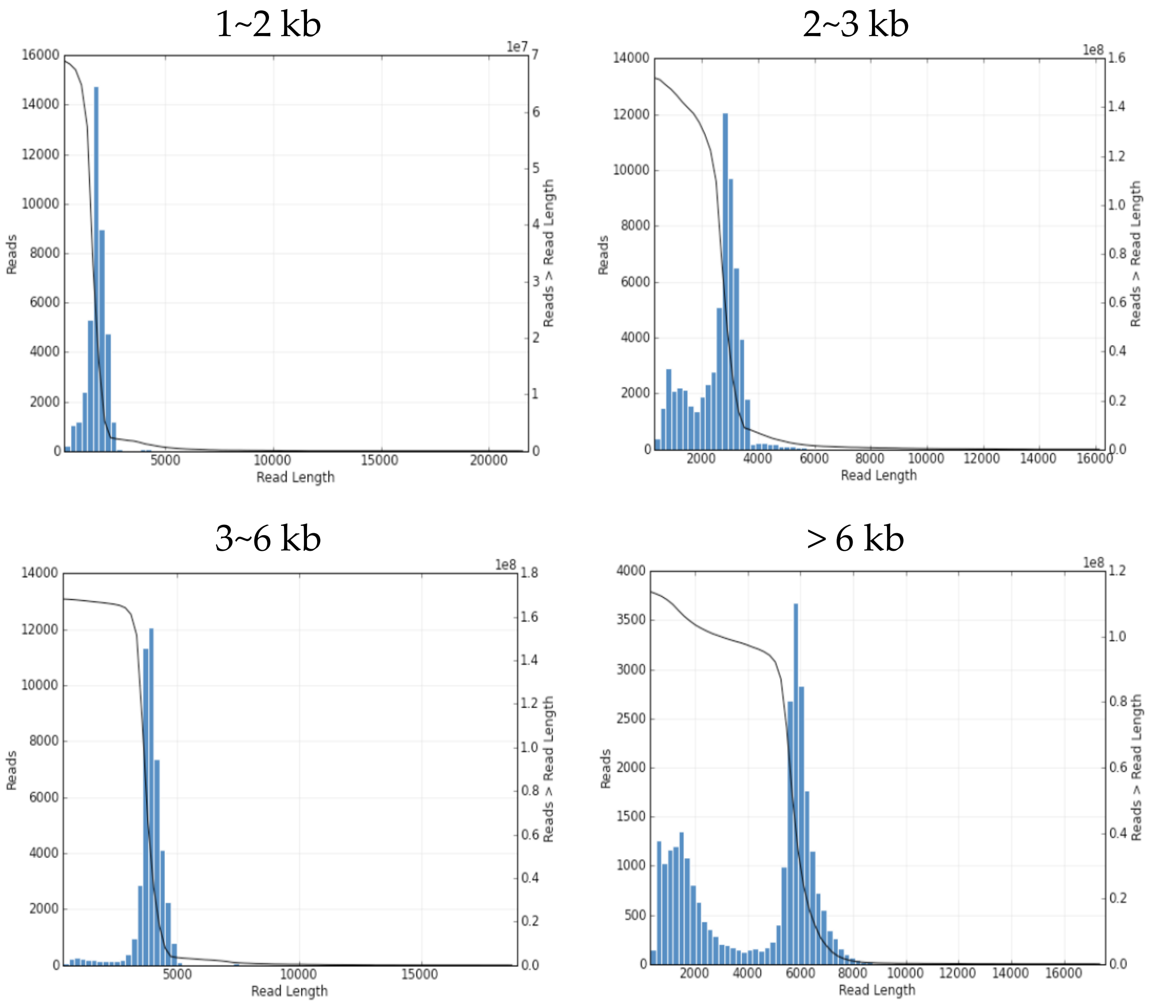

1~2 kb

2~3 kb

3~6 kb

> 6 kb

Figure S1. The distribution of read length of consensus isoforms.

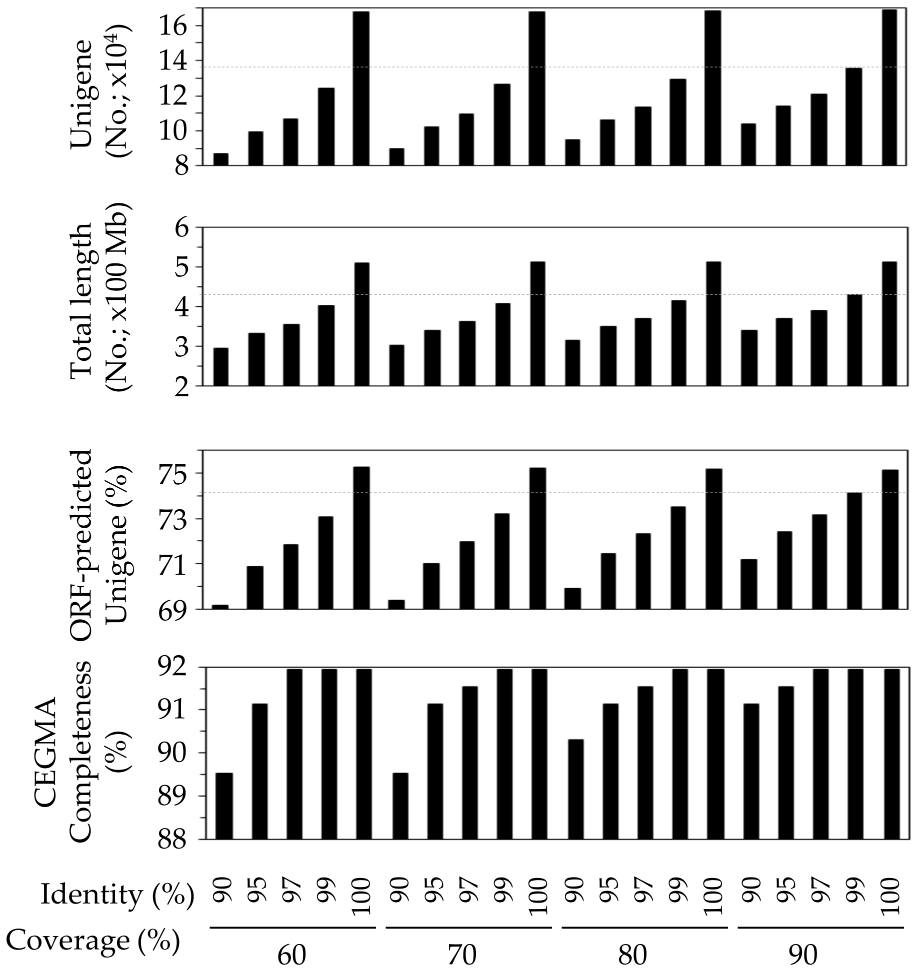

Figure S2. Summary of transcript assemblies along with sequence coverage and identity for clustering of all the libraries. The summary includes the number of unigenes (No.), total length (bases), the number of unigenes harboring ORFs predicted (No.), and CEGMA completeness (%)

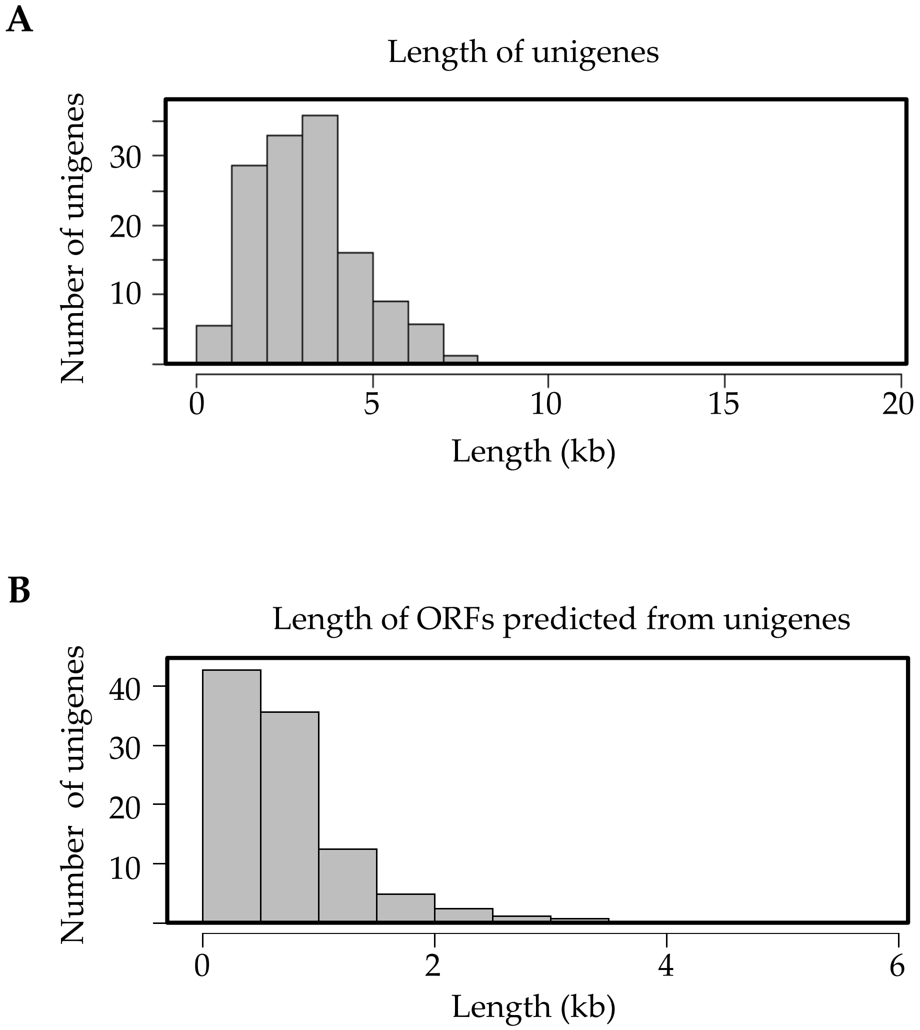

Figure S3. The length distribution of unigenes (A) and predicted ORFs (B).

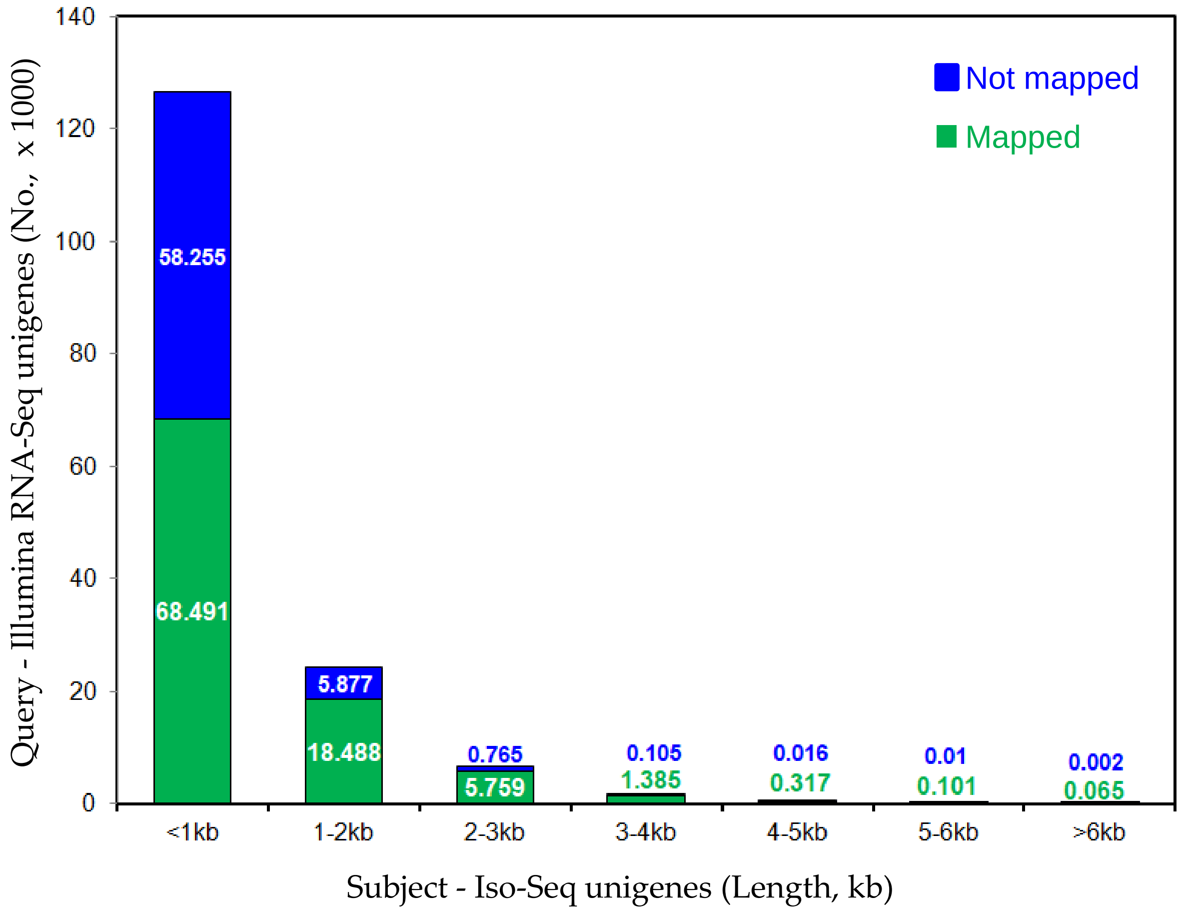

Figure S4. Mapping of unigenes (query) from Illumina RNA-Seq reported by Wang et al. (2016) to unigenes (subject) from Iso-Seq.

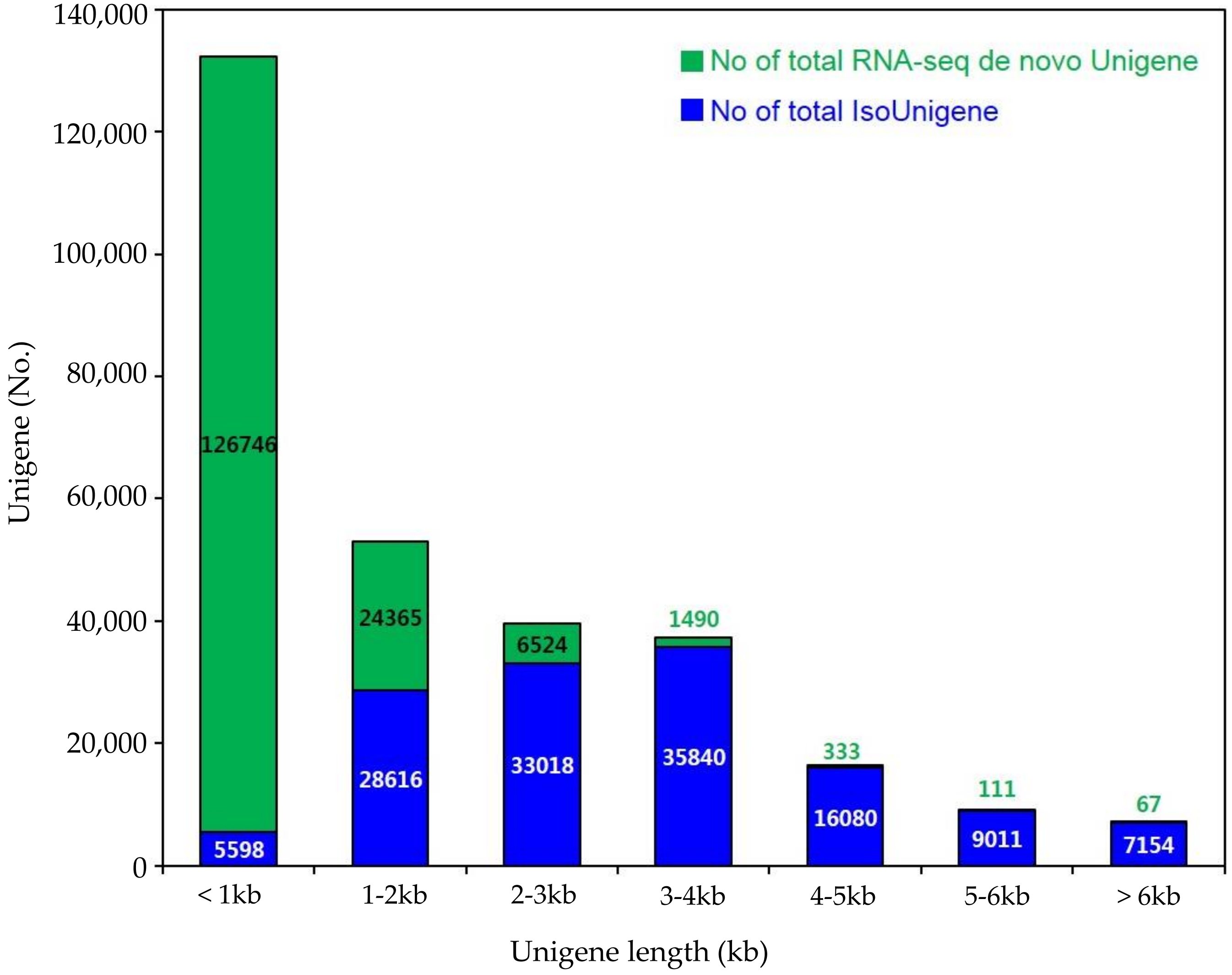

Figure S5. The length distribution of unigenes generated by Illumina RNA-Seq (green) and PacBio Iso-Seq (blue).

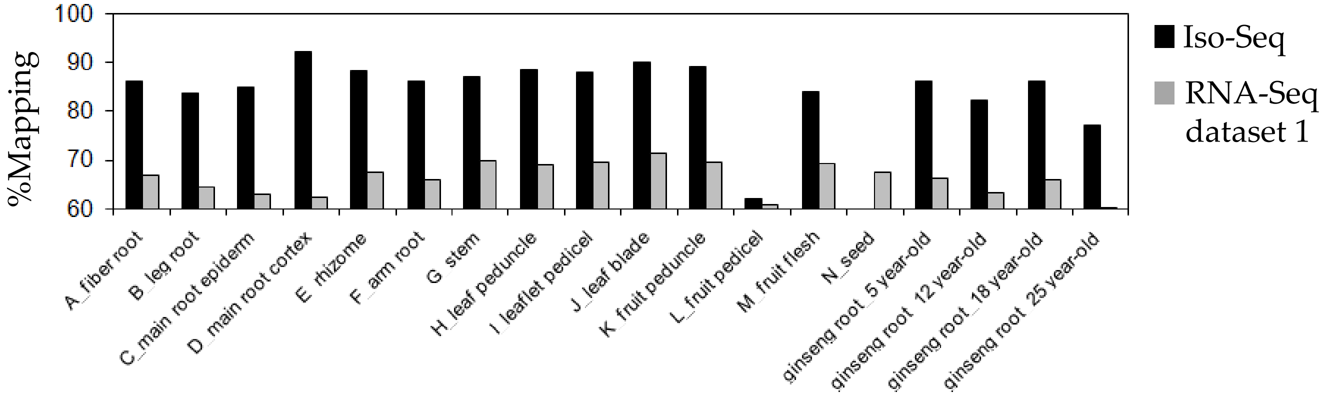

Figure S6. Mapping of Illumina RNA-seq dataset 1 to the two unigene sets from Iso-Seq and Illumina RNA-Seq dataset 1 using STAR.

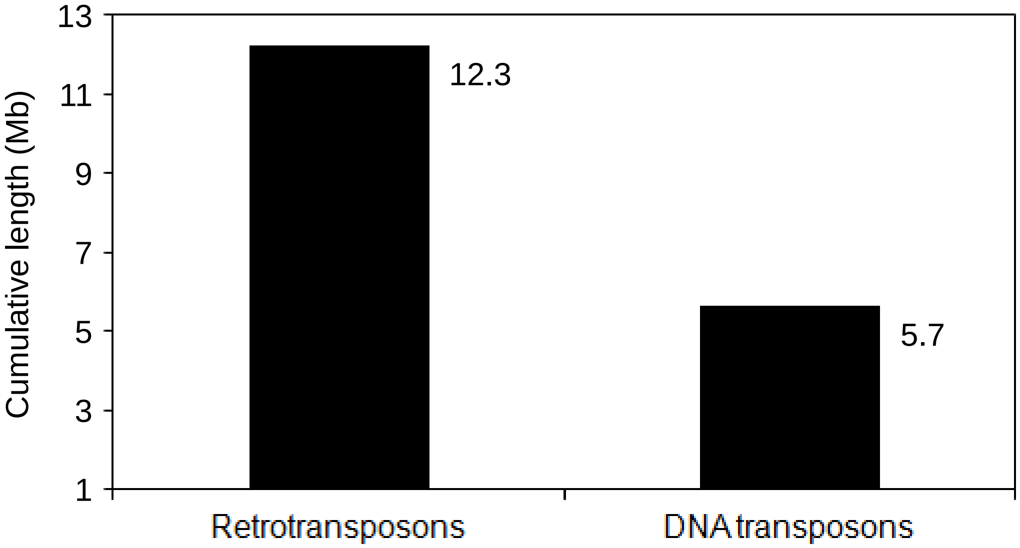

Figure S7. Abundance of TEs in *P. gineng* unigenes

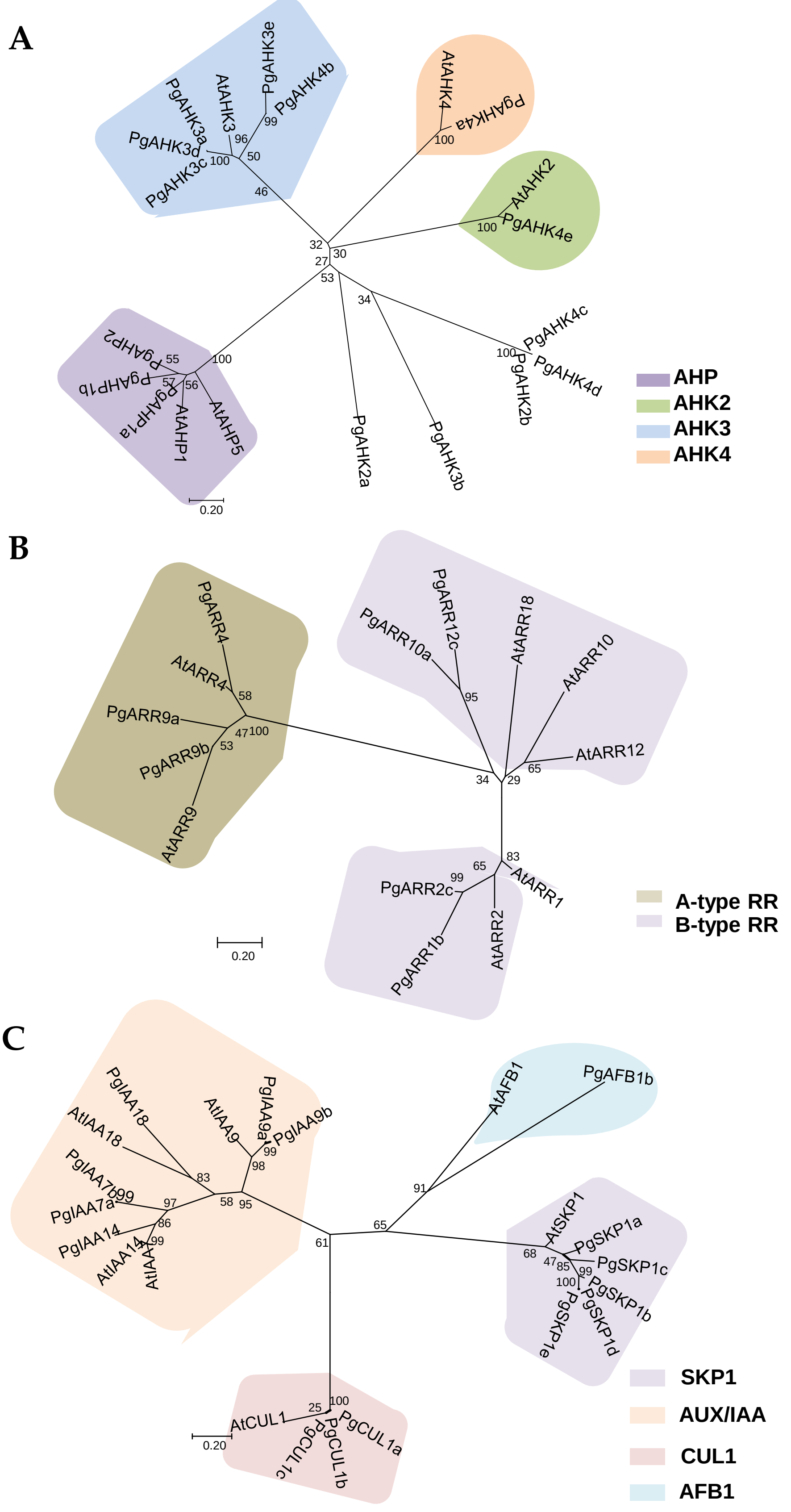

Figure S8. Identification of plant hormone signal components including cytokinin related two-component genes (histidine kinases and histidine phosphor transmitter (A) and respose regulators (B)) and auxing signaling components (C) in the *P. ginseng* transcriptome.

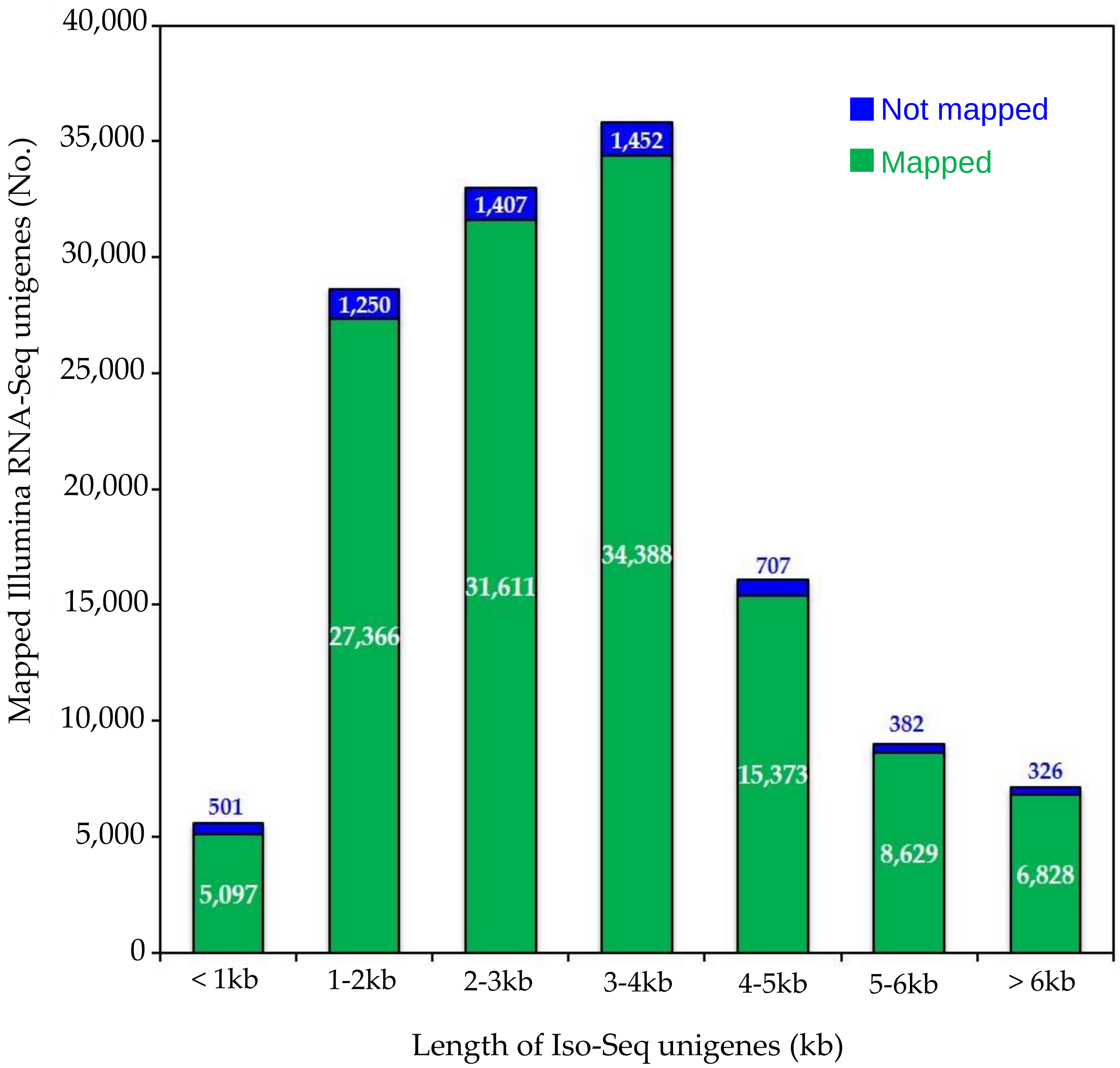

Figure S9. Mapping of Illumina RNA-Seq dataset 1 reported by Wang et al. (2016) to Iso-Seq unigene dataset as a reference.

Table S1. Summary of subreads after removal of adapters and artifacts

Library size	Replicate	Number of subreads	Total length of subreads (Gb)
1~2 kb	1	635,397	1.30
	2	555,922	1.12
	3	555,496	1.13
	4	583,622	1.22
2~3 kb	1	772,914	1.75
	2	703,751	1.63
	3	677,792	1.57
	4	720,334	1.66
3~6 kb	1	414,630	1.59
	2	442,486	1.64
	3	410,099	1.54
	4	420,446	1.62
>6 kb	1	311,013	1.43
	2	356,066	1.53
	3	319,438	1.37
	4	347,931	1.42
Total		8,227,337	23.52

Table S2. Classification of isoform clusters

	1~2 kb	2~3 kb	3~6 kb	>6 kb
Number of reads of insert	182,241	247,189	192,206	163,195
Number of 5`-reads	110,658	160,459	114,426	62,466
Number of 3`-reads	107,067	163,149	118,265	64,507
Number of poly-A reads	98,681	152,078	116,280	58,703
Number of filtered short reads	10,832	8,159	2,365	2,882
Number of non-full length reads	82,801	107,312	95,446	113,549
Number of full-length reads	88,608	131,718	97,395	446,764
Number of full-length non-chimeric reads	87,935	131,191	96,491	45,384
Average full-length non-chimeric read length	1,845	2,644	3,865	4,723

Table S3. Summary of consensus isoforms

	1~2 kb	2~3 kb	3~6 kb	>6 kb
Number of consensus isoforms	40,390	62,217	44,783	27,327
Average read length of consensus isoforms	1,843	2,543	3,871	4,271
Number of polished high-quality isoforms	28,365	43,281	20,178	11,275
Number of polished low-quality isoforms	11,914	18,426	24,603	15,868
Total number of polished isoforms	40,279	61,707	44,781	27,143

Table S4. List of protein-coding genes of *P. notoginseng* homologous to unigenes involved in triterpene saponin biosynthesis in *P. ginseng*

Gene name	No. of unigene of *P. ginseng*	No. of hit gene of *P. notoginseng*	Genes of *P. notoginseng* (ID)	Best hit *E*-value (BLASTX)
AACT, Acetyl-CoA acetyltransferase	18	2	Pjap02127 Pjap28751	0 1E-166
HMGS, Hydroxymethylglutaryl-CoA synthase	22	3	Pjap05414 Pjap33244 Pjap31618	0 1E-154 7E-121
HMGR, Hydroxymethylglutaryl-CoA reductase	35	5	Pjap29075 Pjap20004 Pjap25684 Pjap21692 Pjap10209	0 5E-145 3E-60 4E-152 2E-30
MVK, Mevalonate kinase	13	1	Pjap02763	0
PMK, Phosphomevalonate kinase	17	5	Pjap26215 Pjap05842 Pjap00173 Pjap19214 Pjap05278	7E-72 7E-41 8E-36 9E-20 1E-17
MVD, Mevalonate diphosphate decarboxylase	8	2	Pjap30796 Pjap01306	3E-117 2E-17
GGPPS, Geranylgeranyl pyrophosphate synthase	17	5	Pjap18977 Pjap18534 Pjap08347 Pjap04663 Pjap30381	4E-19 0 0 3E-157 9E-169

FPPS, Farnesyl diphosphate synthase	36	1	Pjap26546	0
IPPI, Isopentenyl diphospate isomerase	7	5	Pjap02090	1E-83
			Pjap12765	7E-36
			Pjap03732	2E-117
			Pjap31081	3E-25
			Pjap07103	2E-10
SS, Squalene synthase	15	2	Pjap06586	0
			Pjap25515	7E-111
SE, Squalene epoxidase	64	9	Pjap03499	3E-55
			Pjap08406	3E-151
			Pjap31602	1E-35
			Pjap26690	0
			Pjap12581	4E-178
			Pjap12354	2E-177
			Pjap29146	1E-19
			Pjap17933	3E-31
			Pjap29328	3E-93
DS, Dammarenediol-II synthase	33	6	Pjap27407	0
			Pjap14441	1E-143
			Pjap17978	1E-99
			Pjap16171	2E-81
			Pjap12813	2E-139
			Pjap32409	1E-105
β-AS β-amyrin synthase	5	3	Pjap27407	4E-70
			Pjap12813	0
			Pjap02808	1E-173
β-A28O β-amyrin 28-oxidase	2	1	Pjap11778	0
D12H, Dammarenediol 12-hydroxylase	13	4	Pjap05919	2E-11
			Pjap15083	8E-136
			Pjap12437	4E-131
			Pjap11778	7E-38
P6H, Protopanaxadiol 6-hydroxylase	9	3	Pjap11778	2E-172
			Pjap12437	8E-06
			Pjap05919	4E-79

* Protein-coding genes of *P. notoginseng* were searched against the candidate unigenes of *P. ginseng* by using TBLASTX with a cutoff ≤ 1*E*-10.

Table S5. Identification of alternative splicing (AS) events in unigenes of *P. ginseng*.

No	Cluster ID	Average length of ORFs analyzed (bp)	Functional description of clusters	No. of unigenes in cluster	No. of identified alternative splicing (AS) event		Length of Insertion/Deletion (InDel) in AS (bp)			
					≥ 100-bp	< 100-bp	#1	#2	#3	#4
1	KG_ISO_112454.162163_clust	1669	Protein TIME FOR COFFEE	3	1	0	1,990			
2	KG_ISO_090257.125297_clust	1857	DNA-directed RNA polymerase subunit beta	2	1	0	2,105			
3	KG_ISO_081709.109976_clust	2267	Isoleucine--tRNA ligase	2	1	0	1,905			
4	KG_ISO_016929.20726_clust	1688	Plant calmodulin-binding protein-related [TAIR10]	2	1	0	1,803			
5	KG_ISO_026079.31377_clust	1699	Putative K(+)-stimulated pyrophosphate-energized sodium pump (Fragment)	3	1	0	1,118			
6	KG_ISO_032384.38801_clust	1340	Eukaryotic translation initiation factor 3 subunit C	2	1	0	1,191			
7	KG_ISO_012760.15697_clust	1712	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	2	1	0	1,173			
8	KG_ISO_007917.9737_clust	1657	cell wall protein AWA1-like isoform X1 [NCBI NR]	5	1	0	951			
9	KG_ISO_061372.79967_clust	1076	Hybrid signal transduction histidine kinase C	3	1	0	755			
10	KG_ISO_003330.4085_clust	702	Elongation factor Tu	5	1	2	518	36	34	

11	KG_ISO_105641.150963_clust	1003	Pyrolysin	3	1	0	674			
12	KG_ISO_058574.76091_clust	947	F-box/LRR-repeat protein 15	2	1	0	843			
13	KG_ISO_076296.100249_clust	994	ATP-dependent Clp protease ATP-binding subunit clpA homolog	3	1	0	603			
14	KG_ISO_103005.146715_clust	759	Zinc finger CCCH domain-containing protein 42	2	1	0	774			
15	KG_ISO_070630.93214_clust	994	Copper-transporting P-type ATPase	2	1	0	744			
16	KG_ISO_025529.30721_clust	606	Protein MGA1	2	1	0	720			
17	KG_ISO_077542.102329_clust	986	Protein EFR3 homolog cmp44E	2	1	0	657			
18	KG_ISO_012292.15123_clust	807	Putative heat shock 70 kDa protein 7	3	1	0	431			
19	KG_ISO_052389.67114_clust	858	Translation initiation factor IF-2	2	1	0	558			
20	KG_ISO_074970.98348_clust	671	heterotrimeric G-protein GTPase; nucleoside-triphosphatase [PMD]	2	1	0	542			
21	KG_ISO_089050.123153_clust	847	WD repeat-containing protein 1-A	3	1	0	398			
22	KG_ISO_080119.107003_clust	807	Cellulose synthase catalytic subunit [UDP-forming]	4	1	0	339			
23	KG_ISO_069305.91395_clust	1058	Cyclin-dependent kinase 20	3	1	0	378			
24	KG_ISO_036247.44364_clust	1077	Interferon-induced GTP-binding protein Mx2	2	1	0	492			
25	KG_ISO_075463.99111_clust	749	Glutamate synthase large subunit-like protein	2	1	0	465			
26	KG_ISO_038748.47910_clust	1098	Protein phosphatase 1 regulatory subunit 7	3	1	1	423	84		

27	KG_ISO_032993.39683_clust	878	Probable methyltransferase PMT5	5	2	2	155	123	61	52
28	KG_ISO_098598.139226_clust	535	UDP-galactose:fucoside alpha-3-galactosyltransferase	6	1	1	215	46		
29	KG_ISO_053915.69278_clust	763	Meiotic PUF family protein 1	3	1	0	324			
30	KG_ISO_129863.193408_clust	564	Probable eukaryotic translation initiation factor 4 gamma homolog	8	1	1	235	12		
31	KG_ISO_063065.82449_clust	758	Elongation factor 4	6	2	0	282	198		
32	KG_ISO_001495.1817_clust	1142	Putative L-type lectin-domain containing receptor kinase I.1	3	1	0	304			
33	KG_ISO_035051.42611_clust	933	Myosin light chain kinase, smooth muscle (Fragment)	3	1	0	297			
34	KG_ISO_073543.96209_clust	709	26S protease regulatory subunit 7 homolog A	3	1	0	297			
35	KG_ISO_031533.37591_clust	1624	Peroxide stress-activated histidine kinase mak3	3	1	0	227			
36	KG_ISO_030210.36169_clust	654	CUGBP Elav-like family member 1	4	1	1	291	72		
37	KG_ISO_023537.28432_clust	542	Mdo Malus domestica KNOTTED1-like homeobox gene 6 [PlantTFBS]	2	1	0	376			
38	KG_ISO_007420.9117_clust	1163	Sulfate adenylyltransferase subunit 1	2	1	0	375			
39	KG_ISO_061261.79805_clust	2789	SED5-binding protein 3	3	1	0	273			
40	KG_ISO_022867.27633_clust	560	Microtubule-associated protein 70-4	2	1	0	357			
41	KG_ISO_001370.1670_clust	1293	Fasciclin-like arabinogalactan protein 18	3	1	0	261			
42	KG_ISO_020333.24691_clust	1554	Inactive peptidyl-prolyl cis-trans isomerase shutdown	2	1	0	348			

43	KG_ISO_036967.45360_clust	1710	Arachidonate 15-lipoxygenase	3	1	1	309	99		
44	KG_ISO_131111.195656_clust	375	Probable methyltransferase PMT5	6	1	0	205			
45	KG_ISO_000123.151_clust	2232	Sexual differentiation process putative subtilase-type proteinase isp6	3	1	0	252			
46	KG_ISO_080714.108119_clust	490	B3 domain-containing protein Os02g0764100	12	1	1	184	79		
47	KG_ISO_026345.31690_clust	1712	Exocyst complex component 7	2	1	0	321			
48	KG_ISO_012924.15896_clust	779	Solute carrier family 23 member 1	4	1	0	213			
49	KG_ISO_038117.47021_clust	577	Dehydrin ERD14	3	1	0	240			
50	KG_ISO_038576.47674_clust	526	Ubiquitin carboxyl-terminal hydrolase 33	3	2	0	264	207		
51	KG_ISO_048966.62197_clust	705	Growth-regulating factor 5	4	1	0	208			
52	KG_ISO_033822.40850_clust	398	ATP-dependent rRNA helicase RRP3	3	1	0	227			
53	KG_ISO_052026.66568_clust	1812	Holliday junction ATP-dependent DNA helicase RuvB	2	1	0	300			
54	KG_ISO_000634.796_clust	1553	Protein piccolo	2	1	0	297			
55	KG_ISO_109070.156713_clust	558	Beta-(1-->2)glucan export ATP-binding/permease protein NdvA	2	1	0	295			
56	KG_ISO_002789.3407_clust	1511	UBX domain-containing protein 4	3	1	0	219			
57	KG_ISO_099730.141165_clust	477	Uncharacterized protein C4G9.04c	4	1	0	184			
58	KG_ISO_030520.36532_clust	1305	RNA-binding protein Nova-1 (Fragment)	2	1	0	262			

59	KG_ISO_094048.131853_clust	814	Exocyst complex component 4	4	1	0	177			
60	KG_ISO_054969.70864_clust	718	Homeobox protein knotted-1-like 8 (Fragment)	10	1	0	147			
61	KG_ISO_102488.145900_clust	482	Auxin-responsive protein IAA26	3	1	0	191			
62	KG_ISO_091681.127724_clust	741	Nodal modulator 1	7	1	0	146			
63	KG_ISO_070431.92941_clust	488	Next to BRCA1 gene 1 protein	10	1	0	135			
64	KG_ISO_055424.71483_clust	2753	Potassium-transporting ATPase B chain	2	1	0	237			
65	KG_ISO_021336.25847_clust	498	Unknown	5	1	1	153	27		
66	KG_ISO_014023.17229_clust	1042	4-alpha-glucanotransferase	3	1	0	174			
67	KG_ISO_063709.83358_clust	1377	F-box/LRR-repeat protein 7	4	1	0	153			
68	KG_ISO_041754.52129_clust	606	AP-3 complex subunit delta	5	1	0	143			
69	KG_ISO_107936.154749_clust	400	Hsc70-interacting protein	4	1	0	151			
70	KG_ISO_112880.162869_clust	1361	Protein MPE1	3	1	0	168			
71	KG_ISO_052743.67607_clust	435	Capsular polysaccharide biosynthesis glycosyltransferase CapM	8	1	0	127			
72	KG_ISO_000655.825_clust	1187	Probable protein phosphatase 2C 60	2	1	0	219			
73	KG_ISO_064809.84926_clust	1164	Transcription factor TCP18	2	1	0	216			

74	KG_ISO_031617.37706_clust	2931	G-type lectin S-receptor-like serine/threonine-protein kinase At4g27290	2	1	0	216			
75	KG_ISO_023305.28134_clust	453	Phosphate import ATP-binding protein PstB	6	1	0	129			
76	KG_ISO_012432.15296_clust	912	Chaperone protein DnaK	3	1	0	158			
77	KG_ISO_106352.152044_clust	505	Nuclear RNAi defective-3 protein	8	1	0	120			
78	KG_ISO_001291.1575_clust	423	Eukaryotic translation initiation factor 3 subunit A	6	1	0	126			
79	KG_ISO_121073.177494_clust	657	Probable salt tolerance-like protein At1g78600	3	1	0	156			
80	KG_ISO_096467.135784_clust	453	Probable serine/threonine-protein kinase MARK-B	4	1	0	202			
81	KG_ISO_028625.34343_clust	1285	FRIGIDA-like protein 5	2	1	0	204			
82	KG_ISO_034907.42427_clust	2349	Fibroblast growth factor receptor 1	2	1	0	204			
83	KG_ISO_011306.13900_clust	1359	Uncharacterized membrane protein At1g16860	2	1	1	168	36		
84	KG_ISO_059249.77033_clust	1422	Protein unc-45 homolog A	2	1	0	204			
85	KG_ISO_028379.34049_clust	551	ABC transporter B family member 25, mitochondrial	3	1	0	152			
86	KG_ISO_032188.38532_clust	2276	Zinc finger CCCH domain-containing protein 38	3	1	1	171	39		
87	KG_ISO_015993.19649_clust	950	Probable protein kinase UbiB	3	1	1	177	51		
88	KG_ISO_038833.48020_clust	392	Poly(A) polymerase	6	1	0	121			

Table S6. Primer lists for qRT-PCR

primer name	Forward	Reverse
Aux/IAA		
PgIAA7-a	ATGAAAGGAACTGAAGCAATTGG	TCTCGTGTGCTTGTCATTGTTTG
PgIAA7-b	GATGCTCGTGGGCGATGT	GCAGGTTGCCGTTGATGTTT
PgIAA8-a	CTTGTTGGAGCAAATGGGTGTA	TCCAAGATGAAGGTCCGAGTGT
PgIAA8-b	TGGGTGCTTCAAGCCTGAAT	TGTCGTATTGAAGCCTTGATCAA
PgIAA9-a	GGCTGGATTGCGGATCAC	AATCGCACTTAACACTTCGGATTC
PgIAA9-b	CAGAAGGTTAAATGGTTTGCAGAA	GCACTTAACACTACGGATTCATATAAAGA
PgIAA9-c	CAAATGGGTGTAGGCACTGGAT	TGCTGCAGTATTCCAAGATGAAG
PgIAA14	TTGTTTGGATGCATGTGTCTCTT	TGACATAAAGGACACCAAATTAACAAC
PgIAA16	GGGAGATGTTGGTTGGTTCTTG	AGGCGACAACTAAGATCAAAGGA
PgIAA18	CGCAGTTGGAGTTGGTAGTAAGC	ACATCATTCCAAAATTCCTTTTCG
ARR		
PgARR4	GGCGCCTTAAAATGACCAACT	GGGAATGACCCACCTATATTGTAAA
PgARR6	CGCCCTCGTTGCTAACTTCT	AACAGGGAATGACCCACCTATCT
PgARR9a	GAATAGAAAGAAGACCTAAAATGAAGGAA	CATCCATATCATGGTTTAATGCAAA
PgARR9b	AACCAGTGAGATTGTCAGATGTGAA	AGCCTTCCTCTTGTTATTACTGGATT
PgARR15	GCACCAATAATGCTAACAAGAGGAA	CAGTAGGAAAGATGGTAAGCCACAT