

Transcript ID	Gene	Similarity	Organism	UniProtKB	% Query Coverage	E-value	RW-Primer ID	Sequence of reverse primers	FW-Primer ID	Sequence of forward primers	RW-Primer concentration in RT reaction [nM]	Length of amplified fragments
Phypoly_transcript_07700	<i>anxA</i>	Annexin VII	<i>Mus musculus</i>	Q07076	39.157	1.04E-32	#1690	GTACGACTCACTATAGGGACTCTTGCCAAAGAAGGCTTG	#1689	AGGTGACACTATAGAATATGAGAAAGCCGAAGAGGATG	50.000	292
Phypoly_transcript_06541	<i>ardA</i>	Actin, plasmodial isoform	<i>Physarum polycephalum</i>	P02576	100	0	#1654	GTACGACTCACTATAGGGAAGGTGTGGTGCCAGATTTTC	#1653	AGGTGACACTATAGAATATGGTGTGATGGTTGGTATGG	0.098	183
Phypoly_transcript_11686	<i>arpA</i>	Probable basic-leucine zipper transcription factor G	<i>Dictyostelium discoideum</i>	Q54RZ9	44.068	1.15E-22	#1684	GTACGACTCACTATAGGGACCTTCAAGATCCCCAACCTT	#1683	AGGTGACACTATAGAATAATCGCACAACCCACTACTCC	50.000	272
Phypoly_transcript_05813	<i>cdcA</i>	Caltractin isoform 1	<i>Homo sapiens</i>	P41208	59.756	1.26E-32	#1652	GTACGACTCACTATAGGGACTGACGGATGAGGAGCTTTC	#1651	AGGTGACACTATAGAATAGATATGTCAACAATCGCCCC	50.000	177
Phypoly_transcript_06284	<i>cudA</i>	Putative transcriptional regulator cudA	<i>Dictyostelium discoideum</i>	O00841	43.478	3.96E-28	#1696	GTACGACTCACTATAGGGAGGGTTTGGAGATGACCTTGA	#1695	AGGTGACACTATAGAATAGACCTCAACCACATTGCCTT	12.500	309
Phypoly_transcript_01287	<i>damA</i>	DNA damage-binding protein 1	<i>Oryza sativa Japonica Group</i>	Q6L4S0	61.892	0	#1644	GTACGACTCACTATAGGGATTGTCGTGTTTCAGGTCCAA	#1643	AGGTGACACTATAGAATAGGAGGTTTTACCCACGAACA	0.390	149
Phypoly_transcript_03245	<i>dspA</i>	DNase TatD	<i>Pantoea vagans</i>	E1SKR8	28.986	9.63E-31	#1670	GTACGACTCACTATAGGGATTTTTGATCACATTTTCGGGC	#1669	AGGTGACACTATAGAATAGTGGAGAGCCTGGAGTGGTA	12.500	231
Phypoly_transcript_06735	<i>ehdA</i>	EH domain-containing protein 1	<i>Bos taurus</i>	Q5E9R3	41.315	9.57E-130	#1646	GTACGACTCACTATAGGGATTCAAGCAGGTCACAAGGTG	#1645	AGGTGACACTATAGAATAATCGAATCAGGTCTCGCTGT	3.130	159
Phypoly_transcript_16748	<i>gapA</i>	ADP-ribosylation factor GTPase-activating protein	<i>Arabidopsis thaliana</i>	O82171	35.22	2.61E-24	#1676	GTACGACTCACTATAGGGATTTATGGGCAAAGAATTTCGC	#1675	AGGTGACACTATAGAATATGAGTTGTTTTGACTGCGGA	50.000	251
Phypoly_transcript_17984	<i>hcpA</i>	Anti-silencing function protein 1 homolog A	<i>Bos taurus</i>	Q2KIG1	52.88	8.27E-64	#1706	GTACGACTCACTATAGGGATCATCTCTTCCGTCATGCTG	#1705	AGGTGACACTATAGAATATTACTGGGGGTTACTGCGAT	50.000	348
Phypoly_transcript_18509	<i>hstA</i>	Probable histone H2B 4	<i>Caenorhabditis elegans</i>	Q27876	59.559	2.41E-37	#1658	GTACGACTCACTATAGGGAAGCTCACCAGGAAGGATCA	#1657	AGGTGACACTATAGAATATCTCCAAGAAAGCGATGGTC	1.560	195
Phypoly_transcript_16372	<i>ligA</i>	Checkpoint protein hus1 homolog	<i>Dictyostelium discoideum</i>	Q54NC0	41.241	7.24E-61	#1640	GTACGACTCACTATAGGGACTGTAAAGGAACCGGGAAAA	#1639	AGGTGACACTATAGAATAAAACAACTTGGACACCCAGC	6.250	139
Phypoly_transcript_00697	<i>meiB</i>	Protein MEI2-like 5	<i>Arabidopsis thaliana</i>	Q8VWF5	73.545	6.34E-80	#1678	GTACGACTCACTATAGGGATCTGGAAGTGGGCTATGAGG	#1677	AGGTGACACTATAGAATACCACAAGGGCACCTATGACT	50.000	255
Phypoly_transcript_18969	<i>nhpA</i>	Non-histone chromosomal protein 6	<i>Debaryomyces hansenii</i>	Q6BRB4	55.224	4.57E-15	#1634	GTACGACTCACTATAGGGATTATGCGAGAGCAGCCTTTT	#1633	AGGTGACACTATAGAATACCACTGCTGCAGACAAGAAG	3.130	120
Phypoly_transcript_00387	<i>pakA</i>	Serine/threonine-protein kinase <i>pakA</i>	<i>Dictyostelium discoideum</i>	Q55D99	41.085	1.96E-87	#1650	GTACGACTCACTATAGGGATTCCAAAATCGGCTAGCAAC	#1649	AGGTGACACTATAGAATAGATTGCCTACGTTTGTGCCT	50.000	171
Phypoly_transcript_13303	<i>pcnA</i>	Proliferating cell nuclear antigen	<i>Brassica napus</i>	Q43124	55.484	1.27E-81	#1680	GTACGACTCACTATAGGGATGTGTCTCCGTTGTCTCTG	#1679	AGGTGACACTATAGAATAATCAAGCCACTTTCGACTGC	50.000	260
Phypoly_transcript_00857	<i>pikB</i>	Phosphatidylinositol 3-kinase 2	<i>Dictyostelium discoideum</i>	P54674	68.809	0	#1672	GTACGACTCACTATAGGGATGCGCAAATAGTGTGTCC	#1671	AGGTGACACTATAGAATAGCCATTTATTTTCACAGCCC	12.500	237
Phypoly_transcript_01882	<i>pikC</i>	Phosphatidylinositol 4-kinase beta	<i>Sorex araneus</i>	B3EX61	45.667	6.23E-76	#1700	GTACGACTCACTATAGGGAGAAATACGTGCGAGTGG	#1699	AGGTGACACTATAGAATAAAGCTCACGCAGGAGTTTCAT	50.000	328
Phypoly_transcript_02833	<i>pksA</i>	Serine/threonine-protein kinase phg2	<i>Dictyostelium discoideum</i>	Q54QQ1	50.68	1.34E-93	#1638	GTACGACTCACTATAGGGAGGGTGCGTAGTATCTCCCTG	#1637	AGGTGACACTATAGAATAAAGGCATGTTATTTACGCCG	12.500	135
Phypoly_transcript_02552	<i>pldA</i>	Phosphatidylinositol-glycan-specific phospholipase D	<i>Rattus norvegicus</i>	Q8R2H5	32.237	2.26E-71	#1688	GTACGACTCACTATAGGGAACAAACTGCGGCAGAGAGAT	#1687	AGGTGACACTATAGAATATGGTGAGTCAGCATACCCAA	6.250	286
Phypoly_transcript_04506	<i>pldB</i>	Phosphatidylinositol-glycan-specific phospholipase D	<i>Homo sapiens</i>	P80108	28.774	4.91E-49	#1702	GTACGACTCACTATAGGGATATCACCGCCTAAATCTGCC	#1701	AGGTGACACTATAGAATACTGTTTTTCCTGACTGGGGA	50.000	338
Phypoly_transcript_02197	<i>pldC</i>	Phosphatidylcholine-hydrolyzing phospholipase D1	<i>Schizosaccharomyces pombe</i>	Q09706	31.068	7.83E-55	#1698	GTACGACTCACTATAGGGACTTCCCCATATAAAGGCGCT	#1697	AGGTGACACTATAGAATATTGTGGGATCTGGGAACATT	50.000	317
Phypoly_transcript_23026	<i>pptA</i>	Probable inactive purple acid phosphatase 29	<i>Arabidopsis thaliana</i>	Q9FMK9	46.269	1.10E-09	#1692	GTACGACTCACTATAGGGAGGTTGACTGGTGGATGGAAC	#1691	AGGTGACACTATAGAATAAAACACAGGACTTTTTGCCG	50.000	298
Phypoly_transcript_08298	<i>pptB</i>	Probable protein phosphatase 2C 34	<i>Oryza sativa Japonica Group</i>	Q94H98	30.208	1.11E-28	#1662	GTACGACTCACTATAGGGATAGTGCTAGGGGCCAATGAG	#1661	AGGTGACACTATAGAATAGCCACCGATTAAATATCCCC	50.000	208
Phypoly_transcript_16094	<i>psgA</i>	<i>Physarum</i> -specific gene A	<i>Physarum polycephalum</i>				#1660	GTACGACTCACTATAGGGATTTACTTGCGGTGTGGAACC	#1659	AGGTGACACTATAGAATAAACACATGATTGGGTGAGCA	1.560	201
Phypoly_transcript_00670	<i>pumA</i>	Pumilio homolog 1	<i>Arabidopsis thaliana</i>	Q9ZW07	61.281	1.91E-138	#1648	GTACGACTCACTATAGGGACGATAATCTTCTCGATCCGC	#1647	AGGTGACACTATAGAATAAAAAATGCTCGATTTGGTCCG	0.390	163
Phypoly_transcript_11692	<i>pwiA</i>	Piwi-like protein Ago3	<i>Bombyx mori</i>	A9ZS22	30.672	8.11E-37	#1694	GTACGACTCACTATAGGGAAGGAAAGCCATTTTGTGTGC	#1693	AGGTGACACTATAGAATAAGGTTATGATGCCGTGAACC	50.000	303
Phypoly_transcript_17606	<i>ralA</i>	Circularly permuted Ras protein 1	<i>Dictyostelium discoideum</i>	Q75J93	39.161	7.24E-21	#1642	GTACGACTCACTATAGGGACACATTCATGTTTTGCCA	#1641	AGGTGACACTATAGAATACGAAAAACGAACACCCTTGT	0.391	146
Phypoly_transcript_09675	<i>rasA</i>	Ras-like GTP-binding protein YPT1	<i>Phytophthora infestans</i>	Q01890	43.931	3.66E-43	#1686	GTACGACTCACTATAGGGACGGAATTGCTGAGATTGGAT	#1685	AGGTGACACTATAGAATATGGGAACAAAACGGACTCTC	3.130	276
Phypoly_transcript_12613	<i>rgsA</i>	Regulator of G-protein signaling 2	<i>Mus musculus</i>	O08849	41.176	0.048	#1708	GTACGACTCACTATAGGGAGGTGCTGCAGACATCCTGTA	#1707	AGGTGACACTATAGAATAGGTGCCCTTAAGCAAATCAA	50.000	357
Phypoly_transcript_02603	<i>ribA</i>	Poly(ADP-ribose) glycohydrolase	<i>Drosophila melanogaster</i>	O46043	42.67	4.66E-95	#1632	GTACGACTCACTATAGGGAATCGCACCTTGAACCTGGTT	#1631	AGGTGACACTATAGAATAGACTGCCAGAAGAAGGACG	0.025	114
Phypoly_transcript_01309	<i>ribB</i>	Poly(ADP-ribose) glycohydrolase	<i>Oryza sativa Japonica Group</i>	Q9AV81	50.313	6.02E-146	#1682	GTACGACTCACTATAGGGATCTTGTTGTCACGACAGCTTG	#1681	AGGTGACACTATAGAATAGTGGCTGGTGTGTCTTCCTT	6.250	268
Phypoly_transcript_06597	<i>spiA</i>	Polyribonucleotide nucleotidyltransferase	<i>Staphylococcus haemolyticus</i>	Q4L5X7	23.932	0.13	#1704	GTACGACTCACTATAGGGATGTTGACCCAATAGCATCCA	#1703	AGGTGACACTATAGAATAATGCCGATTTGTTGGAGAAG	50.000	344
Phypoly_transcript_02655	<i>tspA</i>	Tumor suppressor p53-binding protein 1 homolog	<i>Caenorhabditis elegans</i>	Q7JKP6	33.803	1.16E-05	#1666	GTACGACTCACTATAGGGACCGTGAGTTCCGAGTCCTAA	#1665	AGGTGACACTATAGAATAAATCACAGCAAACGCCAATA	50.000	217
Phypoly_transcript_03260	<i>uchA</i>	Secretory immunoglobulin A-binding protein EsiB	<i>Escherichia coli</i>	A0A0H2VDN9	33.562	9.47E-14	#1674	GTACGACTCACTATAGGGATGCTCTTTTGCCTTCGAAAT	#1673	AGGTGACACTATAGAATAGATTGGACAACCTTGAGCC	12.500	245