

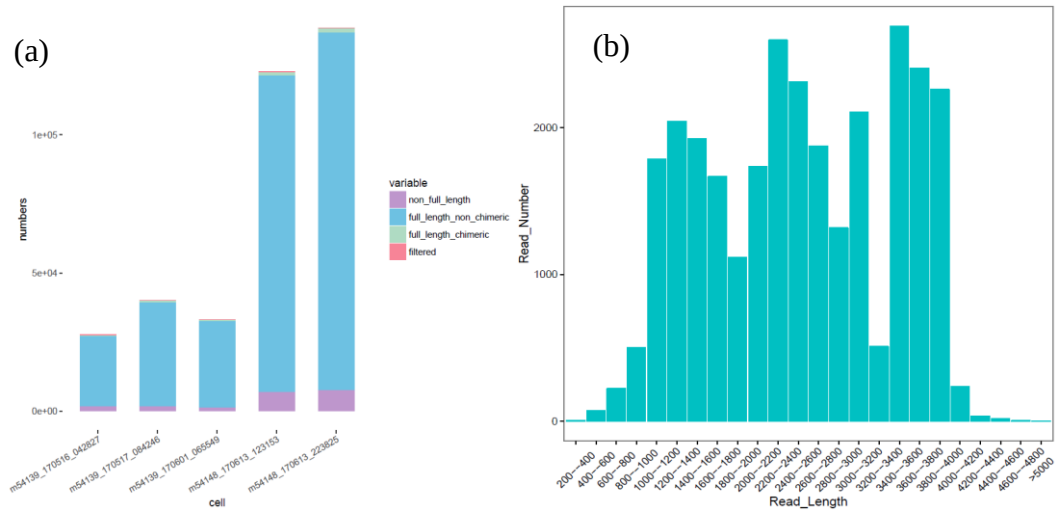


Figure S1 (a) Number of each type of reads (b) Length distribution of full-length non-chimeric reads

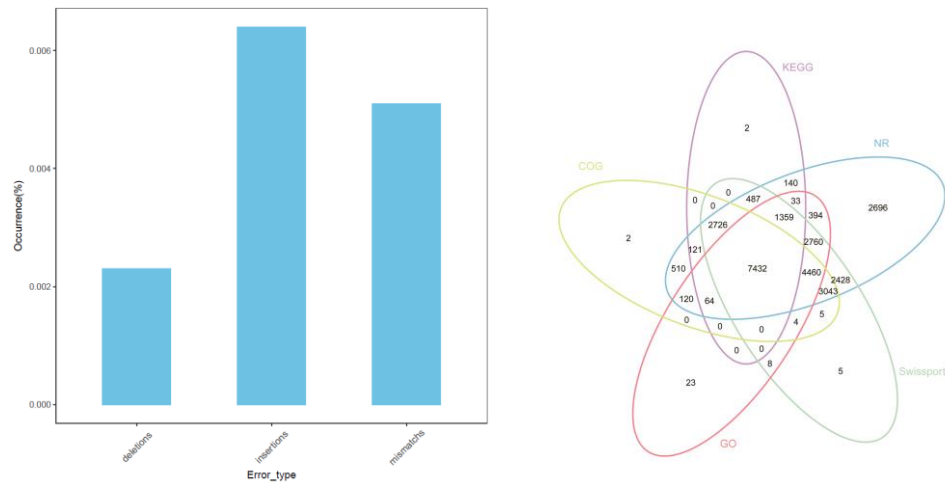


Figure S2 Error type distribution.

Figure S3 Venn diagrams of transcripts annotations.

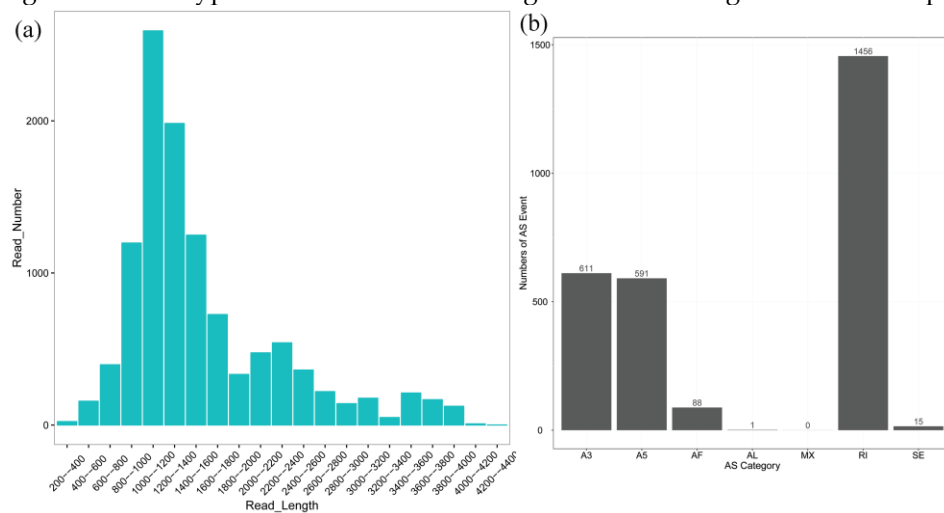


Figure S4 Analysis of lncRNAs (a) Length distribution of lncRNAs (b) Distribution of types of isoforms of lncRNAs

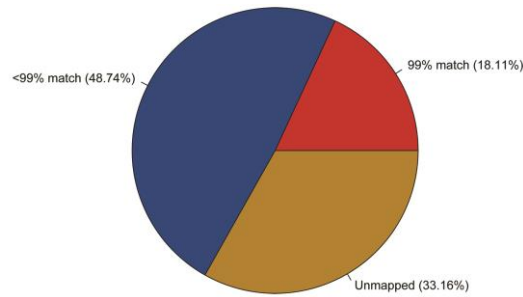
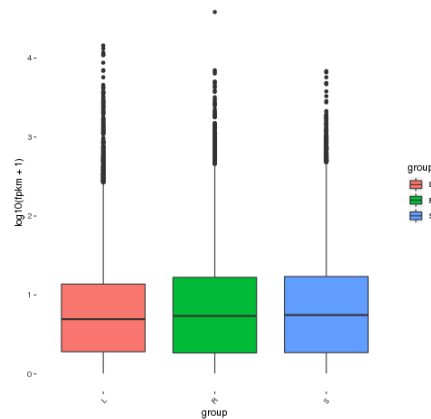


Figure S5 Pie chart of mapped vs. unmapped contigs assembled from Illumina sequencing with a 99% mapping level threshold. The unmapped value represents the proportion of Illumina sequencing contigs not aligned to PacBio corrected long reads.



FigureS6 FPKM box plots

Note: X-axis: L, R, S group; Y-axis: $\log_{10}(\text{FPKM} + 1)$ was used to measure the expression of the genes in different tissue samples. The box plots of each region correspond to five statistic values. The top-down five statistic values are the maximum, the top quartile, the middle quartile, the bottom quartile and the minimum, respectively.

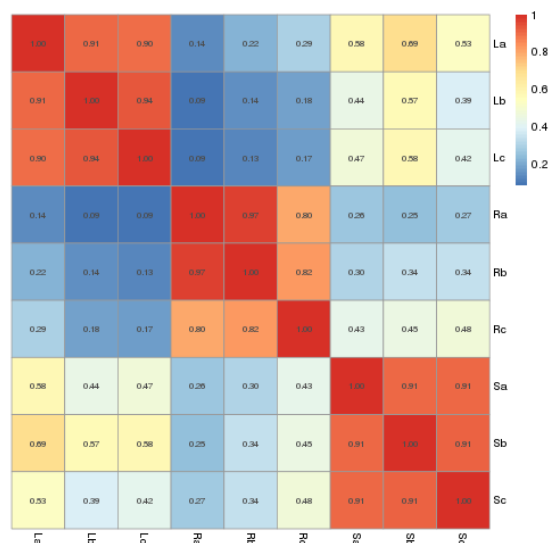


Figure S7 Correlation heatmap of all samples

Note: The gradient from blue to red indicates the correlation between the two samples from low to high

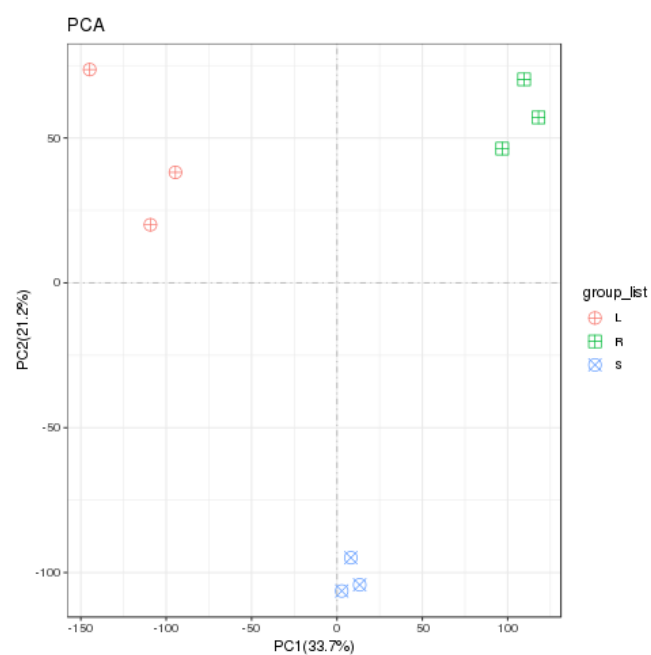


Figure S8 Principal Component Analysis of all samples

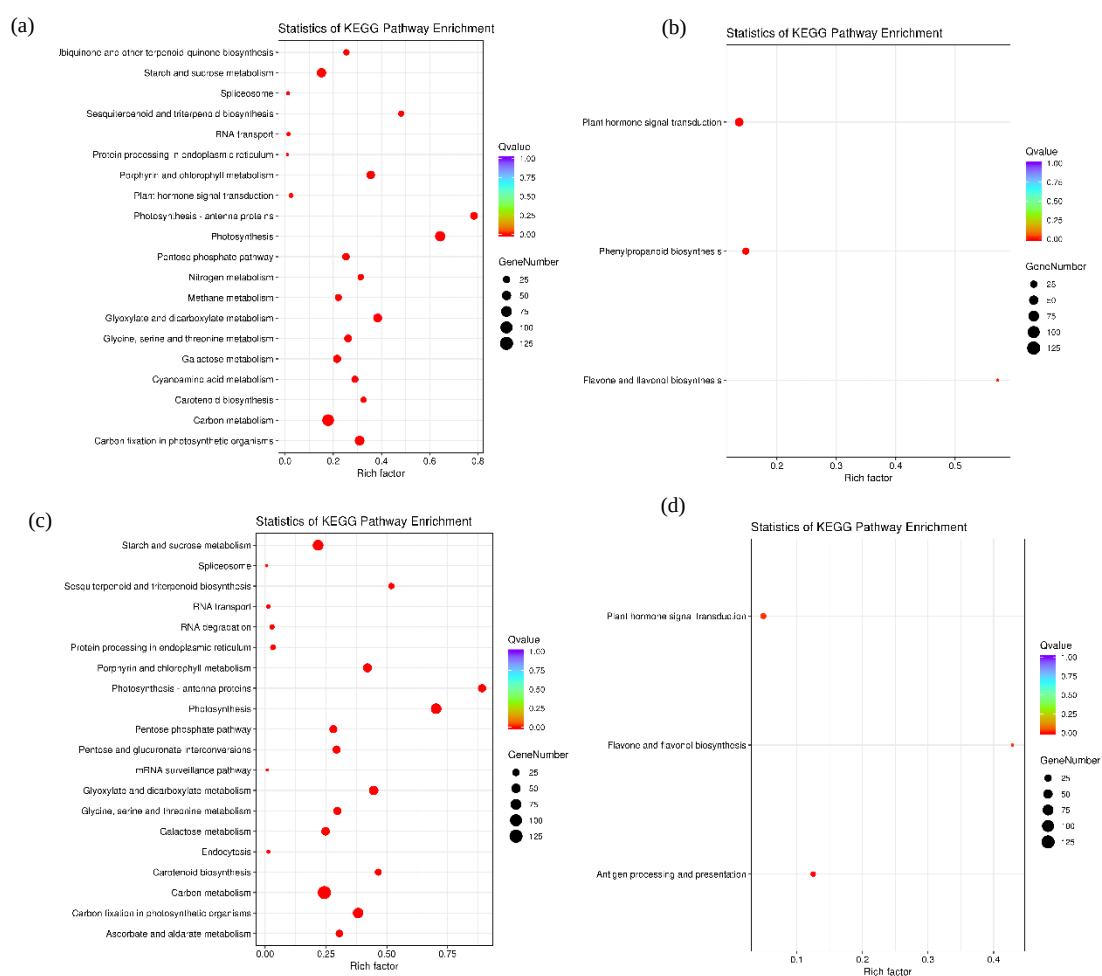


Figure S9 KEGG enrichment analysis of DEGs among different tissues of *Scutellaria baicalensis*. (a) Leaf vs. stem down (b) Leaf vs. root up (c) Leaf vs. root down (d) Root vs. stem down

14211. 2	MENANSLCDDPLNWKMAAESLSGSHLDEVKRMVAEYRKAVVRLGGETLTIGQVAAVATRE	60
5982. 6	MENANSLCDDPLNWKMAAESLSGSHLDEVKRMVAEYRKAVVRLGGETLTIGQVAAVATRE	60
5440	MENANSLCDDPLNWKMAAESLSGSHLNEVKRMVAEYRKAVVRLGGETLTIGQVAAVATRE	60
5982. 14	MENANSLCDDPLNWKMAAESLSGSHLDEVKRMVAEYRRAVVRLGGETLTIGQVAAVATRE	60
5982. 8	-----	0
5982. 9	-----	0
5982. 10	-----	0
5982. 2	-----	0
5982. 3	-----	0
5982. 5	-----	0
5982. 4	-----	0
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5982. 6	AAVKVELAESAREGVKASSDWVMESMDKGTDSYGVTTFGATSHRRTKQGGALQKELIRF	120
5440	AAVKVELAESAREGVKASSDWVMESMDKGTDSYGVTTFGATSHRRTKQGGALQKELIRF	120
5982. 14	AAVKVELAESAREGVKASSDWVMESMDKGTDSYGVTTFGATSHRRTKQGGALQKELIRF	120
5982. 8	-----	0
5982. 9	-----	0
5982. 10	-----	0
5982. 2	-----	0
5982. 3	-----	0
5982. 5	-----	0
5982. 4	-----	0
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5440	LNAGIFGKGSADHTLPHTATRASMFVRINTLLQGYSGIRFEVLEAITKFLNHNITPCLP	180
5982. 14	LNAGIFGKGSADHTLPHTATRASMLVRINTLLQGYSGIRFEVLEAITKFLNHNITPCLP	180
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5982. 10	-----	0
5982. 2	-----	0
5982. 3	-----	0
5982. 5	-----	0
5982. 4	-----	0
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5982. 8	LRGTITASGDLVPLSYIAGLLLGRPNKATGPNGEALGPAQAFALAGIDS---GFFELQP	93
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5982. 10	-----	0
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5982. 3	-----	0
5982. 5	-----	0
5982. 4	-----	0
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5440	KEGLALVNGTAVGSGLASMVLFEANILAVLSEVMSAVFAEVMQKGPEFTDHLTHKLKHHP	300
5982. 14	KEGLALVNGTAVGSGPASMVLFEANILAVLSEVMSAVFAEVMQKGPEFTDHLTHKLKHHP	297
5982. 8	KEGLALVNGTAVGSGPASMVLFEANILAVLSEVMSAVFAEVMQKGPEFTDHLTHKLKHHP	153
5982. 9	-----MVLFEANILAVLSEVMSAVFAEVMQKGPEFTDHLTHKLKHHP	42
5982. 10	-----MVLFEANILAVLSEVMSAVFAEVMQKGPEFTDHLTHKLKHHP	42
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5982. 3	-----	0
5982. 5	-----	0
5982. 4	-----	0
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5440	GQIEAAAIMEHILDGSSIVKEAEKVHELDPLQKPKQDRYALRTSPQWLGPQIEVIRAATK	360

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5982. 9	GQIEAAAIMEHILDGSSIVKEAEKVHELDPLQKPKQDRYALRTSPQWLGPQIEVIRAATK	102
5982. 10	GQIEAAAIMEHILDGSSIVKEAEKVHELDPLQKPKQDRYALRTSPQWLGPQIEVIRAATK	102
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5982. 3	-----	0
5982. 5	-----	0
5982. 4	-----	0
14211. 2	SIEREINSVNDNPLIDVSRNKALHGGNFQGTPIGVSMNTRLAIASIGKLMFAQFSELVN	417
5982. 6	SIEREINSVNDNPLIDVSRNKALHGGNFQGTPIGVSMNTRLAIASIGKLMFAQFSELVN	417
5440	SIEREINSVNDNPLIDVSRNKALHGGNFQGTPIGVSMNTRLAIASIGKLMFAQFSELVN	420
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5982. 9	SIEREINSVNDNPLIDVSRNKALHGGNFQGTPIGVSMNTRLAIASIGKLMFAQFSELVN	162
5982. 10	SIEREINSVNDNPLIDVSRNKALHGGNFQGTPIGVSMNTRLAIASIGKLMFAQFSELVN	162
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5982. 3	-----MDNTRLAIASIGKLMFAQFSELVN	24
5982. 5	-----MDNTRLAIASIGKLMFAQFSELVN	24
5982. 4	-----	0
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5440	DFYNNGLPSNLSGGRNPSLDYGFKGAEIAMAAYCSELQFLANPVTNHVQSAEQHNQDVNS	480
5982. 14	DFYNNGLPSNLSGGRNPSLDYGFKGAEIAMAAYCSELQFLANPVTNHVQSAEQHNQDVNS	477
5982. 8	DFYNNGLPSNLSGGRNPSLDYGFKGAEIAMAAYCSELQFLANPVTNHVQSAEQHNQDVNS	333
5982. 9	DFYNNGLPSNLSGGRNPSLDYGFKGAEIAMAAYCSELQFLANPVTNHVQSAEQHNQDVNS	222
5982. 10	DFYNNGLPSNLSGGRNPSLDYGFKGAEIAMAAYCSELQFLANPVTNHVQSAEQHNQDVNS	222
5982. 2	DFYNNGLPSNLSGGRNPSLDYGFKGAEIAMAAYCSELQFLANPVTNHVQSAEQHNQDVNS	84
5982. 3	DFYNNGLPSNLSGGRNPSLDYGFKGAEIAMAAYCSELQFLANPVTNHVQSAEQHNQDVNS	84
5982. 5	DFYNNGLPSNLSGGRNPSLDYGFKGAEIAMAAYCSELQFLANPVTNHVQSAEQHNQDVNS	84
5982. 4	-----MAAYCSELQFLANPVTNHVQSAEQHNQDVNS	31

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5982. 4	LGLISSRKTGEAVEILKMSSTFLVGLCQAIDLRHLEENLKASVKNTVSLVAKKVLTMGQ	91
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5982. 4	NFGSSIFHKIGAFEEELKALLPKEVESARLEVETGKAAIGNRIKNCRSLPLYKFVREEAG	211
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5982. 14	TGFLTGEKDRSPGEEFDKVFTAICEGKLIDPILLECLKEWNGAPIPIC	704
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5982. 10	TGFLTGEKDRSPGEEFDKVFTAICEGKLIDPILLECLKEWNGAPIPIC	449
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5982. 5	TGFLTGEKDRSPGEEFDKVFTAICEGKLIDPILLECLKEWNGAPIPIC	311
5982. 4	TGFLTGEKDRSPGEEFDKVFTAICEGKLIDPILLECLKEWNGAPIPIC	258
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16858. 22	MAARNESDRIKGPWSPEEDELLQRLVEKHGPRNWSLISKSIPGRSGKSCRLRWCNQLSPQ	60
16858. 10	MAARNESDRIKGPWSPEEDLLQRLVEKHGPRNWSLISKSIPGRSGKSCRLRWCNQLSPQ	60
8950	MAARNESDRIKGPWSPEEDELLQRLVEKHGPRNWSLISKSISGRSGKSCRLRWCNQLSPQ	60
16858. 14	-----	0
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16858. 20	MAARNESDRIKGPWSPEEDELLQRLVEKHGPRNWSLISKSIPGRSGKSCRLRWCNQLSPQ	60
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16858. 10	VEHRAFTPEEDETIIIRAHAKFGNKWAT IARLLSGRTDNAIKNHWNSTLKRKCVSMSEEFN	120
8950	VEHRAFTPEEDETIIIRAHAKFGNKWAT IARLLSGRTDNAIKNHWNSTLKRKCVSMSEEFN	120
16858. 14	-----MSEEFN	6
16858. 17	VEHRAFTPEEDETIIIRAHAKFGNKWAT IARLLSGRTDNAIKNHWNSTLKRKCVSMSEEFN	120
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16858. 10	NFDPRRSAAAQAVR-----	134
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16858. 17	NFDPDAPPLKRSASVGPGSNISTSGFCFNPGSPTESDVSDSSHGHVYRPIPRTGGIS	180
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16858. 22	PPDHQDPDITSLSLPGCDTNPTSPNDPITVLDALIPGPVLP IYPIQMIPSHPPPP	240
16858. 10	-----	134
8950	PPDHQDPDITSLSLPGCDTNPTSPNDPITVLDALIPGPVLP IYPIQMIPSHPPPP	240
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16858. 17	PPDHQDPDITSLSLPGCDTNPTSPNDPITVLDALIPGPVLP IYPIQMIPSHPPPP	240
16858. 20	PPDHQDPDITSLSLPGCDTNPTSPNDPITVLDALIPGPVLP IYPIQMIPSHPPPP	240
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16858. 22	PPAPTTRYGHGGGETVLQH-----	262
16858. 10	-----	134
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16858. 17	PPPPQPADMGTAAEKQFFSTEFLSVMQEMVKKEVRNYMAGIEQNGLCMQSEAIRNAV	300
16858. 20	PPPPQPADMGTAAEKQFFSTEFLSVMQEMVKKEVRNYMAGIEQNGLCMQSEAIRNAV	300
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16858. 22	-----	262

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12545. 12	-----MVVEEFRNPVVKIGGENLTI	19	
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12545. 18	-----	0	
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12545. 8	-----	0	
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12545. 18	-----	0	
12545. 9	-----	0	
12545. 10	-----	0	
12545. 7	-----	0	
12545. 1	-----	0	
12545. 8	-----	0	
12545. 15	GALQKELIRFLNAGIFGKGTEGCHTLPHATRAAMLVRINTLLQGYSGIRFEILELTKF	180	
12545. 16	-----MLVRINTLLQGYSGIRFEILELTKF	26	
4655	GALQKELIRFLNAGIFGKGTEGCHTLPHATRAAMLVRIITLLQGYSGIRFEILELTKF	180	
12545. 17	GALQKELIRFLNAGIFGKGTEGCHTLPHATRAAMLVRIITLLQGYSGIRFEILELTKF	180	
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12545. 6	GALQKELIRFLNAGIFGKGTEGCHTLPHATRAAMLVRINTLLQGYSGIRFEILELTKF	180	
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12545. 8	-----	0	
12545. 15	LNHNITPCLPLRGTITASGDLVPLSYIAGLLTGRPNKAVGPKGEELNAEEAFKLAGVSG	240	
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12545. 4	LNHNITPCLPLRGTITASGDLVPLSYIAGLLTGRPNKAVGPKGEELNAEEAFKLAGVSG	148	
12545. 5	LNHNITPCLPLRGTITASGDLVPLSYIAGLLTGRPNKAVGPKGEELNAEEAFKLAGVSG	240	
12545. 6	LNHNITPCLPLRGTITASGDLVPLSYIAGLLTGRPNKAVGPKGEELNAEEAFKLAGVSG	240	

14470. 1	LNHNITPCLPLRGTITASGDLVPLSYIAGLLTGRPNKAVGPKGEELNAEEAFKLAGVSG	240
12545. 12	LNHNITPCLPLRGTITASGDLVPLSYIAGLLTGRPNKAVGPKGEELNAEEAFKLAGVSG	199
12545. 11	LNHNITPCLPLRGTITASGDLVPLSYIAGLLTGRPNKAVGPKGEELNAEEAFKLAGVSG	86
12545. 18	LNHNITPCLPLRGTITASGDLVPLSYIAGLLTGRPNKAVGPKGEELNAEEAFKLAGVSG	86
12545. 9	-----	0
12545. 10	-----	0
12545. 7	-----	0
12545. 1	-----	0
12545. 8	-----	0
12545. 15	GFFELQPK EGLALVNGTAVGSGLASIALYEANV LALLAEVMSAIFAEVMNGKPEFTDHLT	300
12545. 16	GFFELQPK EGLALVNGTAVGSGLASIALYEANV LALLAEVMSAIFAEVMNGKPEFTDHLT	146
4655	GFFELQPK EGLALVNGTAVGSGLASIALYEANV LALLAEVMSAIFAEVMNGKPEFTDHLT	300
12545. 17	GFFELQPK EGLALVNGTAVGSGLASIALYEANV LALLAEVMSAIFAEVMNGKPEFTDHLT	300
12545. 4	GFFELQPK EGLALVNGTAVGSGLASIALYEANV LALLAEVMSAIFAEVMNGKPEFTDHLT	208
12545. 5	GFFELQPK EGLALVNGTAVGSGLASIALYEANV LALLAEVMSAIFAEVMNGKPEFTDHLT	300
12545. 6	GFFELQPK EGLALVNGTAVGSGLASIALYEANV LALLAEVMSAIFAEVMNGKPEFTDHLT	300
14470. 1	GFFELQPK EGLALVNGTAVGSGLASIALYEANV LALLAEVMSAIFAEVMNGKPEFTDHLT	300
12545. 12	GFFELQPK EGLALVNGTAVGSGLASIALYEANV LALLAEVMSAIFAEVMNGKPEFTDHLT	259
12545. 11	GFFELQPK EGLALVNGTAVGSGLASIALYEANV LALLAEVMSAIFAEVMNGKPEFTDHLT	146
12545. 18	GFFELQPK EGLALVNGTAVGSGLASIALYEANV LALLAEVMSAIFAEVMNGKPEFTDHLT	146
12545. 9	-----MSAIFAEVMNGKPEFTDHLT	20
12545. 10	-----MSAIFAEVMNGKPEFTDHLT	20
12545. 7	-----MNGKPEFTDHLT	12
12545. 1	-----	0
12545. 8	-----	0
12545. 15	HKLKHHPGQIEAAAAIMEHILDGSAYVKAQAQKMHMDPLQKPKQDRYALRTSPQWLG PQIE	360
12545. 16	HKLKHHPGQIEAAAAIMEHILDGSAYVKAQAQKMHMDPLQKPKQDRYALRTSPQWLG PQIE	206
4655	HKLKHHPGQIEAAAAIMEHILDGSAYVKAQAQKMHMDPLQKPKQDRYALRTSPQWLG PQIE	360
12545. 17	HKLKHHPGQIEAAAAIMEHILDGSAYVKAQAQKMHMDPLQKPKQDRYALRTSPQWLG PQIE	360
12545. 4	HKLKHHPGQIEAAAAIMEHILDGSAYVKAQAQKMHMDPLQKPKQDRYALRTSPQWLG PQIE	268
12545. 5	HKLKHHPGQIEAAAAIMEHILDGSAYVKAQAQKMHMDPLQKPKQDRYALRTSPQWLG PQIE	360
12545. 6	HKLKHHPGQIEAAAAIMEHILDGSAYVKAQAQKMHMDPLQKPKQDRYALRTSPQWLG PQIE	360
14470. 1	HKLKHHPGQIEAAAAIMEHILDGSAYVKAQAQKMHMDPLQKPKQDRYALRTSPQWLG PQIE	360
12545. 12	HKLKHHPGQIEAAAAIMEHILDGSAYVKAQAQKMHMDPLQKPKQDRYALRTSPQWLG PQIE	319
12545. 11	HKLKHHPGQIEAAAAIMEHILDGSAYVKAQAQKMHMDPLQKPKQDRYALRTSPQWLG PQIE	206
12545. 18	HKLKHHPGQIEAAAAIMEHILDGSAYVKAQAQKMHMDPLQKPKQDRYALRTSPQWLG PQIE	206
12545. 9	HKLKHHPGQIEAAAAIMEHILDGSAYVKAQAQKMHMDPLQKPKQDRYALRTSPQWLG PQIE	80
12545. 10	HKLKHHPGQIEAAAAIMEHILDGSAYVKAQAQKMHMDPLQKPKQDRYALRTSPQWLG PQIE	80
12545. 7	HKLKHHPGQIEAAAAIMEHILDGSAYVKAQAQKMHMDPLQKPKQDRYALRTSPQWLG PQIE	72
12545. 1	-----	0
12545. 8	-----	0
12545. 15	VIRTATKMIEREINSVNDNPLIDVSRNKA IHGGNFQGTPIGVSM DNTRLAIAAIGKLMFA	420
12545. 16	VIRTATKMIEREINSVNDNPLIDVSRNKA IHGGNFQGTPIGVSM YNTRLAIAAIGKLMFA	266
4655	VIRTATKMIEREIHSVNDNPLIDVSRNKA IHGGNFQGTPIGVSM DNTRLAIAAIGKLMFA	420
12545. 17	VIRTATKMIEREIHSVNDNPLIDVSRNKA IHGGNFQGTPIGVSM DNTRLAIAAIGKLMFA	420
12545. 4	VIRTATKMIEREINSVNDNPLIDVSRNKA IHGGNFQGTPIGVSM DNTRLAIAAIGKLMFA	328
12545. 5	VIRTATKMIEREINSVNDNPLIDVSRNKA IHGGNFQGTPIGVSM DNTRLAIAAIGKLMFA	420
12545. 6	VIRTATKMIEREINSVNDNPLIDVSRNKA IHGGNFQGTPIGVSM DNTRLAIAAIGKLMFA	420
14470. 1	VIRTATKMIEREINSVNDNPLIDVSRNKA IHGGNFQGTPIGVSM DNTRLAIAAIGKLMFA	420
12545. 12	VIRTATKMIEREINSVNDNPLIDVSRNKA IHGGNFQGTPIGVSM DNTRLAIAAIGKLMFA	379
12545. 11	VIRTATKMIEREINSVNDNPLIDVSRNKA IHGGNFQGTPIGVSM DNTRLAIAAIGKLMFA	266
12545. 18	VIRTATKMIEREINSVNDNPLIDVSRNKA IHGGNFQGTPIGVSM DNTRLAIAAIGKLMFA	266
12545. 9	VIRTATKMIEREINSVNDNPLIDVSRNKA IHGGNFQGTPIGVSM DNTRLAIAAIGKLMFA	140
12545. 10	VIRTATKMIEREINSVNDNPLIDVSRNKA IHGGNFQGTPIGVSM DNTRLAIAAIGKLMFA	140
12545. 7	VIRTATKMIEREINSVNDNPLIDVSRNKA IHGGNFQGTPIGVSM DNTRLAIAAIGKLMFA	132
12545. 1	-----MIEREINSVNDNPLIDVSRNKA IHGGNFQGTPIGVSM DNTRLAIAAIGKLMFA	53
12545. 8	-----MDNTRLAIAAIGKLMFA	17
* *****		
12545. 15	QFSELVNDFYNNGLPSNLSGGRNPSLDYGFKGSEIAMASYCSELQFLANPVTNHVQSAEQ	480
12545. 16	QFSELVNDFYNNGLPSNLSGGRNPSLDYGFKGSEIAMASYCSELQFLANPVTNHVQSAEQ	326
4655	QFSELVNDFYNNGLPSNLSGGRNPSLDYGFKGSEIAMASYCSELQFLANPVTNHVQSAEQ	480
12545. 17	QFSELVNDFYNNGLPSNLSGGRNPSLDYGFKGSEIAMASYCSELQFLANPVTNHVQSAEQ	480

12545. 4	QFSELVNDFYNNGLPSNLSGGRNPSLDYGFKGSEIAMASYCSELQFLANPVTNHVQSAEQ	388
12545. 5	QFSELVNDFYNNGLPSNLSGGRNPSLDYGFKGSEIAMASYCSELQFLANPVTNHVQSAEQ	480
12545. 6	QFSELVNDFYNNGLPSNLSGGRNPSLDYGFKGSEIAMASYCSELQFLANPVTNHVQSAEQ	480
14470. 1	QFSELVNDFYNNGLPSNLSGGRNPSLDYGFKGSEIAMASYCSELQFLANPVTNHVQSAEQ	480
12545. 12	QFSELVNDFYNNGLPSNLSGGRNPSLDYGFKGSEIAMASYCSELQFLANPVTNHVQSAEQ	439
12545. 11	QFSELVNDFYNNGLPSNLSGGRNPSLDYGFKGSEIAMASYCSELQFLANPVTNHVQSAEQ	326
12545. 18	QFSELVNDFYNNGLPSNLSGGRNPSLDYGFKGSEIAMASYCSELQFLANPVTNHVQSAEQ	326
12545. 9	QFSELVNDFYNNGLPSNLSGGRNPSLDYGFKGSEIAMASYCSELQFLANPVTNHVQSAEQ	200
12545. 10	QFSELVNDFYNNGLPSNLSGGRNPSLDYGFKGSEIAMASYCSELQFLANPVTNHVQSAEQ	200
12545. 7	QFSELVNDFYNNGLPSNLSGGRNPSLDYGFKGSEIAMASYCSELQFLANPVTNHVQSAEQ	192
12545. 1	QFSELVNDFYNNGLPSNLSGGRNPSLDYGFKGSEIAMASYCSELQFLANPVTNHVQSAEQ	113
12545. 8	QFSELVNDFYNNGLPSNLSGGRNPSLDYGFKGSEIAMASYCSELQFLANPVTNHVQSAEQ	77

12545. 15	HNQDVNSLGLISSRKTVEALDILKMSSTYLVALCQAVDLRHLEENLRLAVKNTVSQLAK	540
12545. 16	HNQDVNSLGLISSRKTVAALDILKMSSTYLVALCQAVDLRHLEENLRLAVKNTVSQLAK	386
4655	HNQDVNSLGLISSRKTVEALDILKMSSTYLVALCQAVDLRHLEENLRLAVKNTVSQLAK	540
12545. 17	HNQDVNSLGLISSRKTVEALDILKMSSTYLVALCQAVDLRHLEENLRLAVKNTVSQLAK	540
12545. 4	HNQDVNSLGLISSRKTVEALDILKMSSTYLVALCQAVDLRHLEENLRLAVKNTVSQLAK	448
12545. 5	HNQDVNSLGLISSRKTVEALDILKMSSTYLVALCQAVDLRHLEENLRLAVKNTVSQLAK	540
12545. 6	HNQDVNSLGLISSRKTVEALDILKMSSTYLVALCQAVDLRHLEENLRLAVKNTVSQLAK	540
14470. 1	HNQDVNSLGLISSRKTVEALDILKMSSTYLVALCQAVDLRHLEENLRLAVKNTVSQLAK	540
12545. 12	HNQDVNSLGLISSRKTVEALDILKMSSTYLVALCQAVDLRHLEENLRLAVKNTVSQLAK	499
12545. 11	HNQDVNSLGLISSRKTVEALDILKMSSTYLVALCQAVDLRHLEENLRLAVKNTVSQLAK	386
12545. 18	HNQDVNSLGLISSRKTVEALDILKMSSTYLVALCQAVDLRHLEENLRLAVKNTVSQLAK	386
12545. 9	HNQDVNSLGLISSRKTVEALDILKMSSTYLVALCQAVDLRHLEENLRLAVKNTVSQLAK	260
12545. 10	HNQDVNSLGLISSRKTVEALDILKMSSTYLVALCQAVDLRHLEENLRLAVKNTVSQLAK	260
12545. 7	HNQDVNSLGLISSRKTVEALDILKMSSTYLVALCQAVDLRHLEENLRLAVKNTVSQLAK	252
12545. 1	HNQDVNSLGLISSRKTVEALDILKMSSTYLVALCQAVDLRHLEENLRLAVKNTVSQLAK	173
12545. 8	HNQDVNSLGLISSRKTVEALDILKMSSTYLVALCQAVDLRHLEENLRLAVKNTVSQLAK	137

12545. 15	RTLTMGANGELHPSRFCEKDLLRVVDREYVFAYIDDPCSANYPLMQKLRQVLVDHALKNG	600
12545. 16	RTLTMGANGELHPSRFCEKDLLRVVDREYVFAYIDDPCSANYPLMQKLRQVLVDHALKNG	446
4655	RTLTMGANGELHPSRFCEKDLLRVVDREYVFAYIDDPCSANYPLMQKLRQVLVDHALKNG	600
12545. 17	RTLTMGANGELHPSRFCEKDLLRVVDREYVFAYIDDPCSANYPLMQKLRQVLVDHALKNG	600
12545. 4	RTLTMGANGELHPSRFCEKDLLRVVDREYVFAYIDDPCSANYPLMQKLRQVLVDHALKNG	508
12545. 5	RTLTMGANGELHPSRFCEKDLLRVVDREYVFAYIDDPCSANYPLMQKLRQVLVDHALKNG	600
12545. 6	RTLTMGANGELHPSRFCEKDLLRVVDREYVFAYIDDPCSANYPLMQKLRQVLVDHALKNG	600
14470. 1	RTLTMGANGELHPSRFCEKDLLRVVDREYVFAYIDDPCSANYPLMQKLRQVLVDHALKNG	600
12545. 12	RTLTMGANGELHPSRFCEKDLLRVVDREYVFAYIDDPCSANYPLMQKLRQVLVDHALKNG	559
12545. 11	RTLTMGANGELHPSRFCEKDLLRVVDREYVFAYIDDPCSANYPLMQKLRQVLVDHALKNG	446
12545. 18	RTLTMGANGELHPSRFCEKDLLRVVDREYVFAYIDDPCSANYPLMQKLRQVLVDHALKNG	446
12545. 9	RTLTMGANGELHPSRFCEKDLLRVVDREYVFAYIDDPCSANYPLMQKLRQVLVDHALKNG	320
12545. 10	RTLTMGANGELHPSRFCEKDLLRVVDREYVFAYIDDPCSANYPLMQKLRQVLVDHALKNG	320
12545. 7	RTLTMGANGELHPSRFCEKDLLRVVDREYVFAYIDDPCSANYPLMQKLRQVLVDHALKNG	312
12545. 1	RTLTMGANGELHPSRFCEKDLLRVVDREYVFAYIDDPCSANYPLMQKLRQVLVDHALKNG	233
12545. 8	RTLTMGANGELHPSRFCEKDLLRVVDREYVFAYIDDPCSANYPLMQKLRQVLVDHALKNG	197

12545. 15	ENEKNASTSIFQKIEAFEELKALLPKEVESARMALEAGNPAVPNRITECRSYPLYKFIR	660
12545. 16	ENEKNASTSIFQKIEAFEELKALLPKEVESARMALEAGNPAVPNRITECRSYPLYKFIR	506
4655	ENEKNASTSIFQKIEAFEELKALLPKEVESARMALEAGNPAVPNRITECRSYPLYKFIR	660
12545. 17	ENEKNASTSIFQKIEAFEELKALLPKEVESARMALEAGNPAVPNRITECRSYPLYKFIR	660
12545. 4	ENEKNASTSIFQKIEAFEELKALLPKEVESARMALEAGNPAVPNRITECRSYPLYKFIR	568
12545. 5	ENEKNASTSIFQKIEAFEELKALLPKEVESARMALEAGNPAVPNRITECRSYPLYKFIR	660
12545. 6	ENEKNASTSIFQKIEAFEELKALLPKEVESARMALEAGNPAVPNRITECRSYPLYKFIR	660
14470. 1	ENEKNASTSIFQKIEAFEELKALLPKEVESARMALEAGNPAVPNRITECRSYPLYKFIR	660
12545. 12	ENEKNASTSIFQKIEAFEELKALLPKEVESARMALEAGNPAVPNRITECRSYPLYKFIR	619
12545. 11	ENEKNASTSIFQKIEAFEELKALLPKEVESARMALEAGNPAVPNRITECRSYPLYKFIR	506
12545. 18	ENEKNASTSIFQKIEAFEELKALLPKEVESARMALEAGNPAVPNRITECRSYPLYKFIR	506
12545. 9	ENEKNASTSIFQKIEAFEELKALLPKEVESARMALEAGNPAVPNRITECRSYPLYKFIR	380
12545. 10	ENEKNASTSIFQKIEAFEELKALLPKEVESARMALEAGNPAVPNRITECRSYPLYKFIR	380
12545. 7	ENEKNASTSIFQKIEAFEELKALLPKEVESARMALEAGNPAVPNRITECRSYPLYKFIR	372
12545. 1	ENEKNASTSIFQKIEAFEELKALLPKEVESARMALEAGNPAVPNRITECRSYPLYKFIR	293
12545. 8	ENEKNASTSIFQKIEAFEELKALLPKEVESARMALEAGNPAVPNRITECRSYPLYKFIR	257

12545. 15	EEAGTEFLTGR-----	672
12545. 16	EEAGTEFLTGEKGTSPGEEDKVFTALTNGFIIDPLLTCLAWNGAPLPIC	557
4655	EEAGTEFLTGEKVTSPPGEEDKVFTALTNGFIIDPLLTCLGAWNGAPLPIC	711
12545. 17	EEAGTEFLTGEKVTSPPGEEDKVFTALTNGFIIDPLLTCLGAWNGAPLPIC	711
12545. 4	EEAGTEFLTGEKVTSPPGEEDKVFTALTNGFIIDPLLTCLAWNGAPLPIC	619
12545. 5	EEAGTEFLTGEKVTSPPGEEDKVFTALTNGFIIDPLLTCLAWNGAPLPIC	711
12545. 6	EEAGTEFLTGEKVTSPPGEEDKVFTALTNGFIIDPLLTCLAWNGAPLPIC	711
14470. 1	EEAGTEFLTGEKVTSPPGEEDKVFTALTNGFIIDPLLTCLAWNGAPLPIC	711
12545. 12	EEAGTEFLTGEKVTSPPGEEDKVFTALTNGFIIDPLLTCLAWNGAPLPIC	670
12545. 11	EEAGTEFLTGEKVTSPPGEEDKVFTALTNGFIIDPLLTCLAWNGAPLPIC	557
12545. 18	EEAGTEFLTGEKVTSPPGEEDKVFTALTNGFIIDPLLTCLAWNGAPLPIC	557
12545. 9	EEAGTEFLTGEKVTSPPGEEDKVFTALTNGFIIDPLLTCLAWNGAPLPIC	431
12545. 10	EEAGTEFLTGEKVTSPPGEEDKVFTALTNGFIIDPLLTCLAWNGAPLPIC	431
12545. 7	EEAGTEFLTGEKVTSPPGEEDKVFTALTNGFIIDPLLTCLAWNGAPLPIC	423
12545. 1	EEAGTEFLTGEKVTSPPGEEDKVFTALTNGFIIDPLLTCLAWNGAPLPIC	344
12545. 8	EEAGTEFLTGEKVTSPPGEEDKVFTALTNGFIIDPLLTCLAWNGAPLPIC	308
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20665. 1	----MKELAKRFDKIFESIIDQRLKMKVQVGTESKDFLQVLLSLKD-NGDSKTPFTMTHL	55
20304. 1	VQRKMKELAKRFDKIFESIIDQRLKMKGVQVGTESKDFLQVLLQLKD-NGDSKTPFTMTHL	108
20665. 2	VQRKMKELAKRFDKIFESIIDQRLKMKGVQVGTESKDFLQVLLQLKD-NGDSKTPFTMTHL	157
7939	VQRKMKVLAKRFDKIFESIIDQRLKMKGVQVGTESKDFLQVLLQLKD-NGDSKTPFTMTHL	299
20304. 3	VQRKMKVLAKRFDKIFESIIDQRLKMKGVQVGTESKDFLQVLLQLKD-NGDSKTPFTMTHL	299
20304. 2	VQRKMKVLAKRFDKIFESIIDQRLKMKGVQVGTESKDFLQVLLQLKD-NGDSKTPFTMTHL	299
20665. 3	VQRKMKELAKRFDKIFESIIDQRLKMKGVQVGTESKDFLQVLLQLKD-NGDSKTPFTMTHL	299
** *****. *****		
20665. 1	KALLMDMVGGTDTTSTNTVEFALAEIMKKPQILKKVQQELEIVVGEDKIVEESHITKLPY	115
20304. 1	KALLMDMVGGTDTTSTNTVEFALAEIMKKPQILKKVQQELEIVVGKDKIVEESHITKLPY	168
20665. 2	KALLMDMVGGTDTTSTNTVEFALAEIMKKPQILKKVQQELEIVVGKDKIVEESHITKLPY	217
7939	KALLMDMVGGTDTTSTNTVEFALAEIMKKPQILKKVQQELEIVVGEDKIVEESHITKLPY	359
20304. 3	KALLMDMVGGTDTTSTNTVEFALAEIMKK-----	328
20304. 2	KALLMVSSLSLSLS-----LSLSHLND-----	321
20665. 3	KALLM-----	304

20665. 1	LHTVMKEVLRHLHPALPLLPHCPMSTSNVAGYTI PKGSRVF INVWAIHRDPSIWENPLEF	175
20304. 1	LHTVMKEVLRHLHPALPLLPHCPMSTSNVAGYTI PKGSRVF INVWAIHRDPSIWENPLEF	228
20665. 2	LHTVMKEVLRHLHPALPLLPHCPMSTSNVAGYTI PKGSRVF INVWAIHRDPSIWENPLEF	277
7939	LHTVMKEVLRHLHPALPLLPHCPMSTSNVAGYTI PKGSRVF INVWAIHRDPSIWENPLEF	419
20304. 3	-----	328
20304. 2	-----	321
20665. 3	-----	304
20665. 1	NPERFSDGKWDYSGNDFSYPFGSGRMICAGIAMGERMF7939SLASLVHSLSGVCLQARSW	235
20304. 1	NPERFSDGKWDYSGNDFSYPFGSGRRICAGIAMGERMF7939SLASLVHSFEWSLPAGEKL	288
20665. 2	NPERFSDGKWDYSGNDFSYPFGSGRRICAGIAMGERMF7939SLASLVHSFEWSLPAGEKL	337
7939	NPERFSDGKWDYSGNDFSYPFGSGRMICAGIAMGERMF7939SLASLVHSLSWSLPAGEKL	479
20304. 3	-----	328
20304. 2	-----	321
20665. 3	-----	304
20665. 1	TCLRSLGFE-----	244
20304. 1	DLSEKFGIVLKKNAPLVAIPTPRLSDPTLYE	319
20665. 2	DLSEKFGIVLKKNAPLVAIPTPRLSDPTLYE	368
7939	DLSEKFGIVLKKNAPLVAIPTPRLSDPTLYE	510
20304. 3	-----	328
20304. 2	-----	321
20665. 3	-----	304

Figure S10 Multiple alignment of protein sequences of isoforms corresponded to key genes related to flavonoid biosynthesis in *Scutellaria baicalensis*

Table S1 Statistics of errors of two types of correction

Correction Type	Ratio of mapping base/ total base (%)	Mismatch		Deletion		Insertion	
		No. of bases	Ratio (%)	No. of bases	Ratio (%)	No. of bases	Ratio (%)
Self-corrected	59.97	91,726	0.0415	10,949	0.0050	20,128	0.0050
Illumina -corrected	62.14	80,529	0.0351	5,758	0.0025	6,075	0.0025

Table S2 Statistics of number of reads from each replicate in Illumina RNA-seq

Sample	Read Length(bp)	No. of Clean reads	No. of Clean Bases	Q30 Rate (%)
La	150	43,330,053	6,300,058,391	86.36
Lb	150	48,326,188	6,996,365,095	86.26
Lc	150	44,637,776	6,561,085,654	90.74
Ra	150	42,784,651	6,253,629,269	85.81
Rb	150	39,274,282	5,720,351,097	86.55
Rc	150	34,810,082	5,087,411,044	88.43
Sa	150	39,873,764	5,783,768,897	87.67
Sb	150	39,743,026	5,756,046,456	86.68
Sc	150	38,784,804	5,631,379,767	89.76

Table S3 AS statistics of transcripts corresponded to the key genes related to flavonoid biosynthesis in *Scutellaria baicalensis*

Transcript	Key gene	UniTransModel	AS_type
PB.11197.1	flavones 3-hydroxylase	4055_0 path0	RI
PB.11197.2	flavones 3-hydroxylase	4055_0 path1	RI
PB.11197.3	flavone 3-hydroxylase	4055_0 path0	RI
PB.12545.1	phenylalanine ammonia-lyase	4655_0 path1	RI
PB.12545.10	phenylalanine ammonia-lyase	4655_0 path0	RI
PB.12545.11	phenylalanine ammonia-lyase	4655_0 path2	RI
PB.12545.12	phenylalanine ammonia-lyase	4655_0 path6	RI,A5
PB.12545.14	phenylalanine ammonia-lyase	4655_0 path6	RI
PB.12545.15	phenylalanine ammonia-lyase	4655_0 path2	RI,A5
PB.12545.16	phenylalanine ammonia-lyase	4655_0 path1	RI,A3,A5
PB.12545.17	phenylalanine ammonia-lyase	4655_0 path6	RI,A5
PB.16858.19	R2R3MYB	8950_0 path7	RI
PB.16858.2	R2R3MYB	8950_0 path11	RI
PB.16858.20	R2R3MYB	8950_0 path9	RI

PB.16858.21	R2R3MYB	8950_0 path11	RI
PB.16858.22	R2R3MYB	8950_0 path6	RI,A3,A5
PB.16858.23	R2R3MYB	8950_0 path11	RI
PB.16858.3	R2R3MYB	8950_0 path11	RI
PB.16858.4	R2R3MYB	8950_0 path9	RI,A3,A5
PB.16858.6	R2R3MYB	8950_0 path11	RI
PB.16858.7	R2R3MYB	8950_0 path11	RI
PB.16858.8	R2R3MYB	8950_0 path11	RI
PB.17903.2	4-CoumarateCoA ligases(4CL)	8071_0 path0	RI
PB.17903.3	4-CoumarateCoA ligases(4CL)	8071_0 path0	RI
PB.17907.1	4-CoumarateCoA ligases(4CL)	6946_0 path3	RI
PB.18647.1	4-CoumarateCoA ligases(4CL)	6946_0 path3	RI
PB.18647.3	4-CoumarateCoA ligases(4CL)	6946_0 path3	RI
PB.18647.4	4-CoumarateCoA ligases(4CL)	6946_0 path3	RI
PB.18647.5	4-CoumarateCoA ligases(4CL)	6946_0 path2	RI
PB.19775.1	4-CoumarateCoA ligases(4CL)	8071_0 path0	RI
PB.19775.2	4-CoumarateCoA ligases(4CL)	8071_0 path0	RI
PB.20062.1	4-CoumarateCoA ligases(4CL)	7837_0 path0	RI
PB.20062.2	4-CoumarateCoA ligases(4CL)	7837_0 path0	RI
PB.20062.3	4-CoumarateCoA ligases(4CL)	7837_0 path0	RI
PB.20062.4	4-CoumarateCoA ligases(4CL)	7837_0 path0	RI
PB.20304.1	flavone 8-hydroxylase	7939_0 path0	RI,A3
PB.20304.2	flavone 8-hydroxylase	7939_0 path0	RI
PB.20304.3	flavone 8-hydroxylase	7939_0 path0	RI,A3,A5
PB.4908.1	4-CoumarateCoA ligases(4CL)	2491_0 path1	RI
PB.4908.2	4-CoumarateCoA ligases(4CL)	2491_0 path1	RI
PB.4991.1	R2R3MYB	12012_0 path0	RI
PB.4991.2	R2R3MYB	12012_0 path0	RI
PB.5982.10	phenylalanine ammonia-lyase	5440_0 path7	RI
PB.5982.12	phenylalanine ammonia-lyase	5440_0 path1	RI
PB.5982.13	phenylalanine ammonia-lyase	5440_0 path3	RI
PB.5982.14	phenylalanine ammonia-lyase	5440_0 path2	RI
PB.5982.16	phenylalanine ammonia-lyase	5440_0 path8	RI
PB.5982.17	phenylalanine ammonia-lyase	5440_0 path1	RI
PB.5982.2	phenylalanine ammonia-lyase	5440_0 path2	RI
PB.5982.3	phenylalanine ammonia-lyase	5440_0 path7	RI
PB.5982.4	phenylalanine ammonia-lyase	5440_0 path2	RI
PB.5982.5	phenylalanine ammonia-lyase	5440_0 path2	RI
PB.5982.6	phenylalanine ammonia-lyase	5440_0 path2	RI
PB.5982.7	phenylalanine ammonia-lyase	5440_0 path7	RI
PB.5982.8	phenylalanine ammonia-lyase	5440_0 path7	RI
PB.5982.9	phenylalanine ammonia-lyase	5440_0 path1	RI
PB.976.1	4-CoumarateCoA ligases(4CL)	716_0 path0	RI

Table S4 Specific primers flanking the AS site for PCR amplification

Primer	Sequence	Isoforms	Amplification length (bp)
7939-F	CAGAGGAAGATGAAGGAGTTGG	PB.20304.1	467
7939-R	GAGCCCTTTGGAATGGTGTA	PB.20304.2	530
		PB.20304.3	0
		PB.20665.1	466
		PB.20665.2	467
		PB.20665.3	457
8950-F	TATAATCATGGCGGCGAGAAA	PB.16858.12	526
8950-R	GGATTAGGGCAGAGTCCAATAC	PB.16858.8	472
		others	668
		others	668
4655-F	GTGCTCTCCAGAAGGAGCTC	others	142
4655-R	CCTGAGTATCCTTGAAGAAGAGTG	PB.12545.18	426
5440-F	CCACAAGATTGGTGCGTTTG	PB.14211.2	86
5440-R	CCTGTTAGGAAACCAGTCCCAGC	others	177