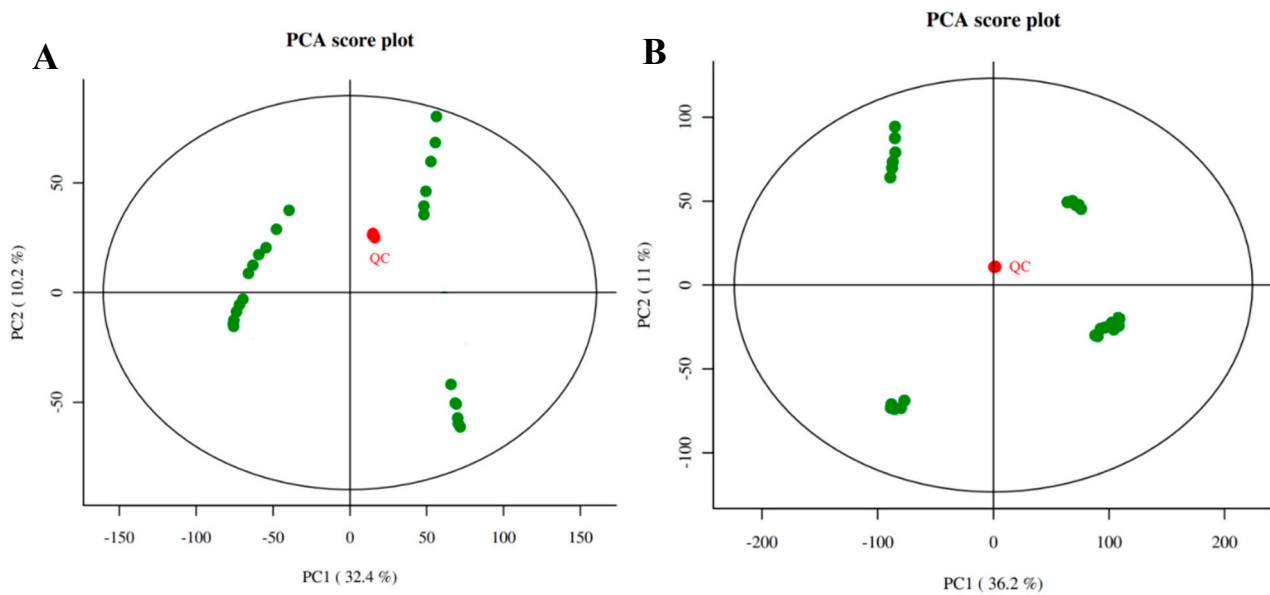


**Table S1 The primers used in this study**

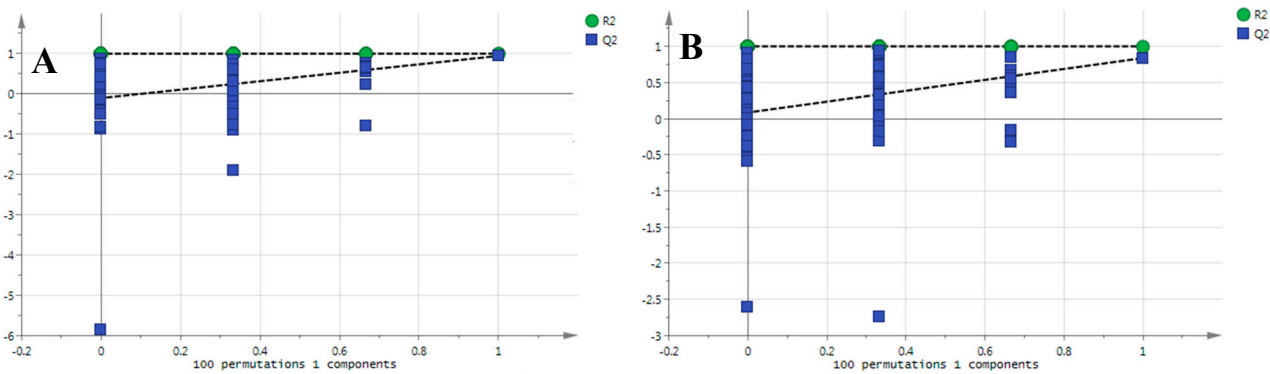
Gene ID	Forward primer (5'-3')	Reverse primer
CSS0041448(PAL)	TGCAATCTGAGGTTCTCCCG	CCGACCGACCCCAGAAATAG
CSS0007481(FLS)	CTTACGAGGGGTACGGAAGC	CATCGGCCACTTCTTCTGGT
CSS0030176(F3'H)	TCTCTCTCCCTCGAATGGCA	CTAAGCTCATCCCGGCACAT
CSS0014132(F3'5'H)	ATGCATGTGAGGTGAACGGT	TCCGGCACACATTCTTCTCC
CSS0010687(ANS)	ATTCCGGCAACAAGCGAGTA	GAGCTCTGGTTGAGGGCATT
CSS0000672(DFR)	ATTGTTCGTGCAACCGTTTCG	GGCCTCATCAAAGCTCCCTT
CSS0047425(FG3)	TTTTTGCCGCCCTAAAACCG	TCCAACCTCCAAGTCTCCGC
CSS0010486(PDT)	ACAAAACGCACAGAATGCCC	CTTTGGCACTGGAAAACCCG
CSS0007310(GLU)	ACAAAACGCACAGAATGCCC	CTTTGGCACTGGAAAACCCG
CSS0008013(ACED)	AGAGTGGCTGGAATTTGCGA	GGATTCCCTCGGCTGGAAAA

**Table S4 transcriptome quality**

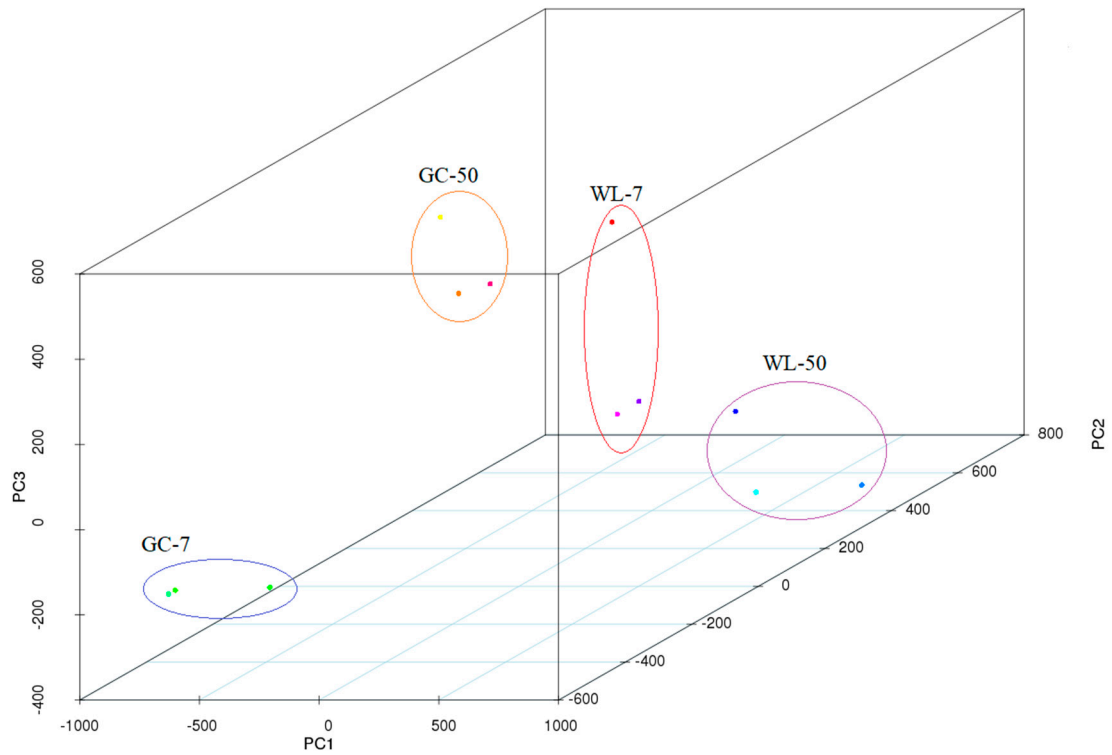
Samples	Clean reads	Clean bases	%≥Q30	Mapped Reads
WL-7a	21,375,660	6,412,698,000	93.57%	35,879,790 (83.93%)
WL-7b	23,821,013	7,146,303,900	93.51%	39,877,323 (83.70%)
WL-7c	22,251,929	6,675,578,700	93.46%	37,197,856 (83.58%)
WL-50a	21,145,793	6,343,737,900	93.58%	35,658,203 (84.32%)
WL-50b	21,308,708	6,392,612,400	93.51%	35,966,090 (84.39%)
WL-50c	21,249,726	6,374,917,800	93.48%	35,672,234 (83.94%)
GC-7a	21,948,162	6,584,448,600	93.42%	36,396,645 (82.92%)
GC-7b	21,392,207	6,417,662,100	93.31%	35,988,819 (84.12%)
GC-7c	20,320,525	6,096,157,500	93.60%	33,693,547 (82.91%)
GC-50a	21,024,858	6,307,457,400	93.49%	35,673,125 (84.84%)
GC-50b	21,286,406	6,385,921,800	93.59%	36,054,987 (84.69%)
GC-50c	21,849,876	6,554,962,800	93.08%	36,814,023 (84.24%)



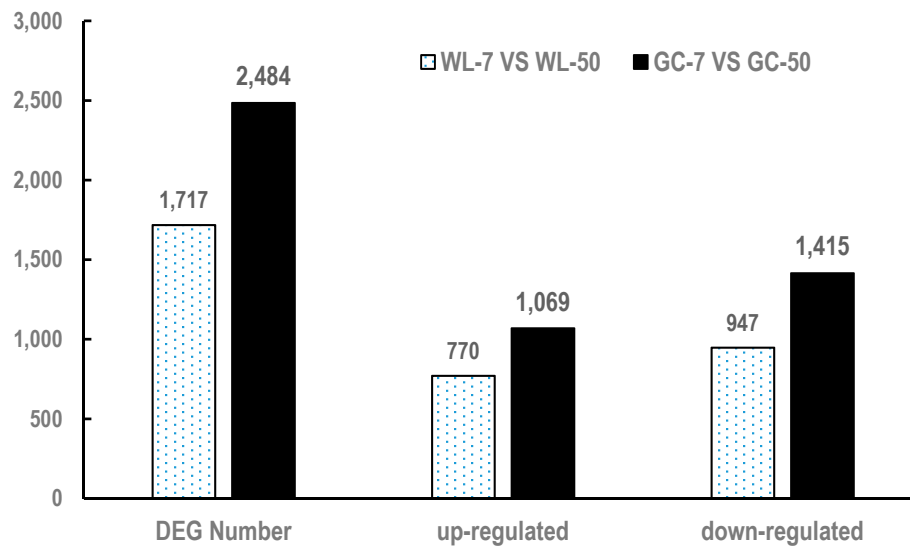
**Figure S1 Principal component analysis in positive (A) and negative (B) modes**



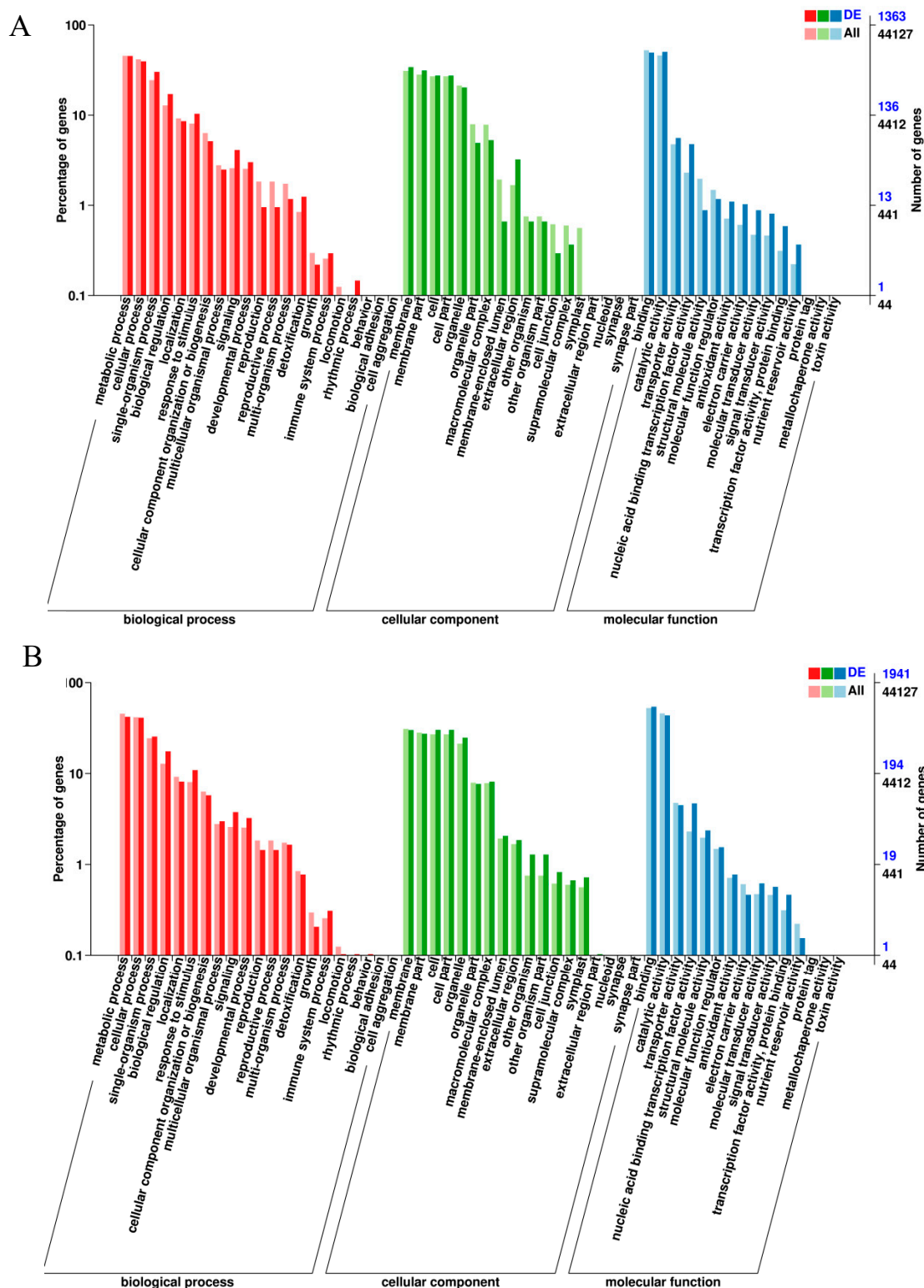
**Figure S2 Cross validation of OPLS-DA for Wulv1 (A) and Gancha 4 (B)**



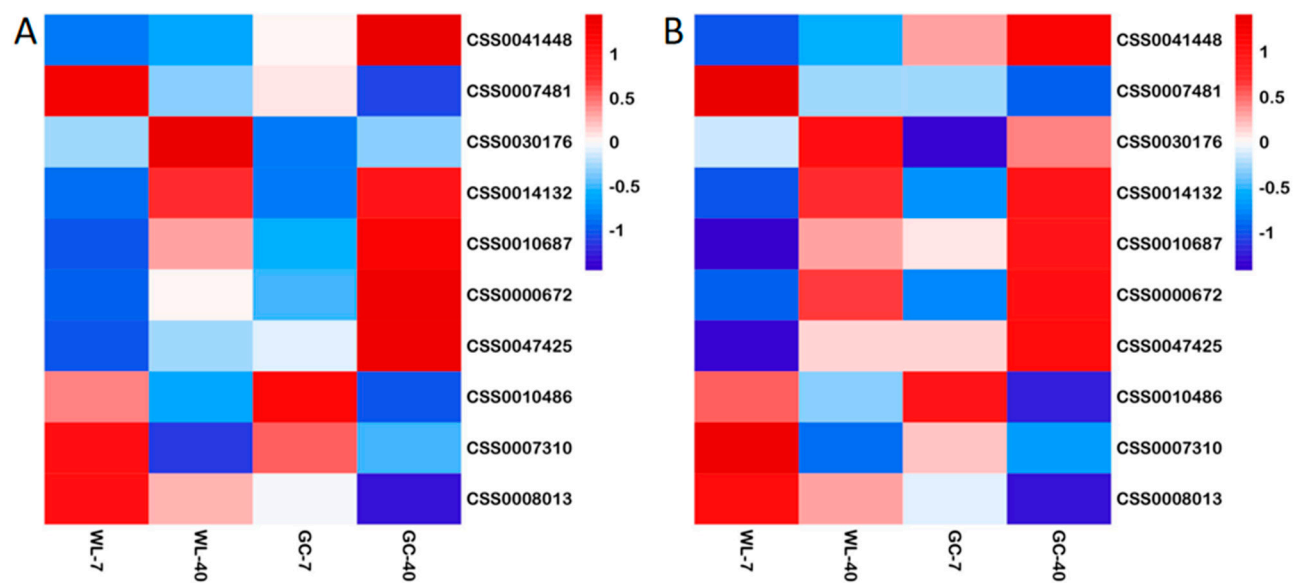
**Figure S3 PCA analysis of transcriptomics**



**Figure S4. Differentially expressed genes of two cultivars with different plant ages**



**Figure S5 GO enrichment analysis of differentially expressed genes in Wulv1 (A) and Gancha4 (B) of different plant ages**



**Figure S6 qPCR validation of transcriptome data. (A) Transcriptome gene expression. (B) qPCR gene expression.**