

Table S1: RNA integrity number of samples used for sequencing

Name	Total quantity (µg)	OD260/280	OD260/230	RIN value
CK BI04-1	4.285	1.978	1.824	7.5
CK BI04-2	4.108	2.055	1.852	6.9
CK BI04-3	4.990	2.072	1.891	7.7
CK BI28-1	5.471	2.066	2.157	7.2
CK BI28-2	5.911	2.071	1.926	7.2
CK BI28-3	5.018	2.074	1.853	6.9
CK DH45-1	13.553	2.100	1.815	6.8
CK DH45-2	7.114	2.078	2.205	7.2
CK DH45-3	4.787	2.025	1.838	7.4
LN BI04-1	5.182	2.089	1.891	7.5
LN BI04-2	3.958	2.048	1.826	7.1
LN BI04-3	6.409	2.073	1.876	6.9
LN BI28-1	9.298	2.086	2.196	8.4
LN BI28-2	5.209	2.064	2.114	7.4
LN BI28-3	3.217	2.031	1.879	7.6
LN DH45-1	1.560	2.062	1.899	7.1
LN DH45-2	3.513	2.019	1.871	7.4
LN DH45-3	5.685	2.076	1.979	7.3

Table S2: Summary of quality control for RNA-Seq data

Sample	Total raw reads No.	Total clean reads No.	N(%)	Q20 (%)	Q30(%)	Clean Reads %
CK BI-04	136,345,154	135,624,126	0.001613	97.02	92.74	99.47
CK BI-28	127,995,806	127,447,370	0.000959	97.35	93.46	99.57
CK DH45	132,055,610	131,105,758	0.002032	96.45	91.50	99.29
LN BI-04	130,560,670	129,487,894	0.002811	96.04	90.63	99.18
LN BI-28	121,972,182	121,122,070	0.00304	96.34	91.22	99.30
LN DH45	137,467,718	136,336,736	0.002581	96.07	90.66	99.17

CK means the N level with 7.5mmol·L⁻¹; LN means the N level with 0.75mmol·L⁻¹; Total Raw Reads: The number of reads before filtering; Total Clean Reads: Filtered reads; N (%): The percentage of ambiguous bases; Q20 (%): The percentage of bases whose recognition accuracy is above 99%; Q30 (%): The percentage of bases whose recognition accuracy is above 99.9%; Clean Reads Ratio (%): The proportion of filtered reads.

Table S3: Summary of mapped events for clean reads

Sample	Map_Events	Mapped_to_Gene	Mapped_to_InterGene	Mapped to Exon
CK BI04-1	33,888,898	32,260,807(95.20%)	1,628,091(4.80%)	31,989,644(99.16%)
CK BI04-2	35,867,807	34,236,826(95.45%)	1,630,981(4.55%)	33,980,017(99.25%)
CK BI04-3	35,526,589	33,814,162(95.18%)	1,712,427(4.82%)	33,551,714(99.22%)
CK BI28-1	34,065,923	32,335,504(94.92%)	1,730,419(5.08%)	32,069,746(99.18%)
CK BI28-2	32,189,874	30,539,458(94.87%)	1,650,416(5.13%)	30,277,962(99.14%)
CK BI28-3	32,613,411	30,829,754(94.53%)	1,783,657(5.47%)	30,536,466(99.05%)
CK DH45-1	31,369,781	30,002,095(95.64%)	1,367,686(4.36%)	29,781,854(99.27%)
CK DH45-2	33,545,207	31,994,554(95.38%)	1,550,653(4.62%)	31,758,179(99.26%)
CK DH45-3	34,537,693	32,724,680(94.75%)	1,813,013(5.25%)	32,454,572(99.17%)
LN BI04-1	30,439,496	28,962,068(95.15%)	1,477,428(4.85%)	28,707,006(99.12%)
LN BI04-2	34,571,444	32,766,357(94.78%)	1,805,087(5.22%)	32,431,898(98.98%)
LN BI04-3	32,330,526	30,505,288(94.35%)	1,825,238(5.65%)	30,172,115(98.91%)
LN BI28-1	30,767,263	29,221,279(94.98%)	1,545,984(5.02%)	28,978,494(99.17%)
LN BI28-2	30,768,681	29,250,460(95.07%)	1,518,221(4.93%)	28,972,412(99.05%)
LN BI28-3	29,072,572	27,583,938(94.88%)	1,488,634(5.12%)	27,356,699(99.18%)
LN DH45-1	33,556,455	31,915,988(95.11%)	1,640,467(4.89%)	31,698,210(99.32%)
LN DH45-2	34,878,170	33,173,687(95.11%)	1,704,483(4.89%)	32,917,244(99.23%)
LN DH45-3	33,580,138	32,051,766(95.45%)	1,528,372(4.55%)	31,854,734(99.39%)

Table S4: Primer information for qRT-PCR assay

Gene ID	Forward primer (5'-3')	Reverse primer (3'-5')
<i>HvActin</i>	GCTGACCGTATGAGCAAGGA	GGAAAGTGCTGAGTGAGGCT
<i>HvGAPDH</i>	AGATGCCCCTATGTTTGTGG	GGTCTTCTGTGTGGCAGTGA
<i>HORVU3Hr1G066090</i>	GGAGATGCACAAGGACAGCT	GTAGAAGTACTGCGCGACGA
<i>HORVU4Hr1G061100</i>	CACCAACGCATAGACAATGG	CAAACAAAACCTCCCCTTCCA
<i>HORVU3Hr1G073220</i>	CTGCAACTCGTGGACTGGAT	AGTAGGGTTGTGGGCACATG
<i>HORVU0Hr1G017370</i>	GCGGATCAAGAATGTTTCGGC	TCAAGCCCGTGAAGGAGAAC
<i>HORVU6Hr1G003470</i>	TCCCACTGAGGAACAATGGC	TGGCATCCCTCTCTGGATCA
<i>HORVU4Hr1G054060</i>	CATTGGCGAAGAGTGGGTCT	TTCCACGGACAAGCTCCATC
<i>HORVU4Hr1G066860</i>	AACCTCAACCTCAGCGACTG	GTCGTAGTTCCACTTGGGCA
<i>HORVU4Hr1G007610</i>	GGATGGACGTCAGGAGCAAA	AGGATGACTTCGCTGTCGTC

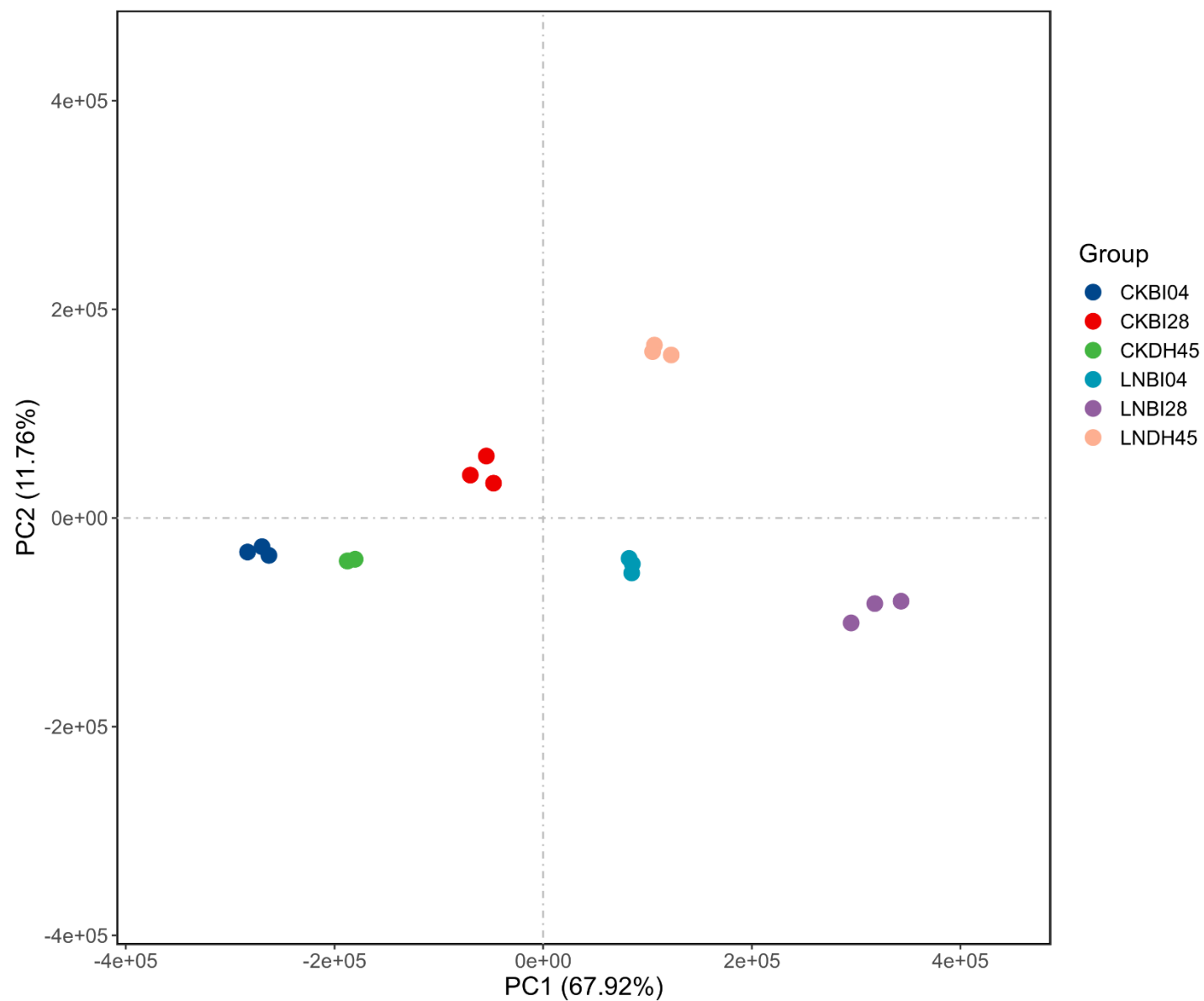


Figure S1: Principal component analysis (PCA) analysis of the samples based on gene counts

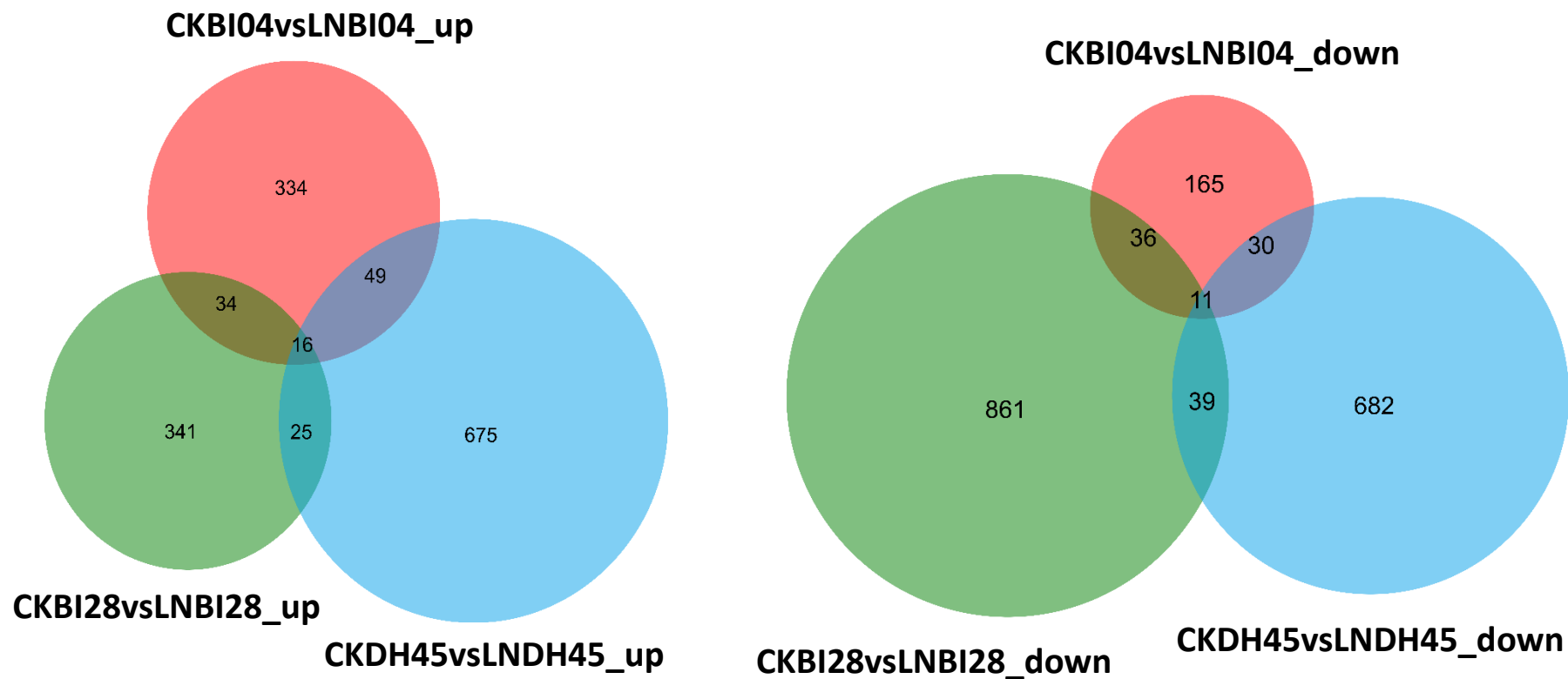


Figure S2: Up-and down-regulated differentially expression genes betweenDH45 and parents