

Table S2. DEGs analysis statistics on summary of mapping results to reference genes.

Summary	PmND3-1		PmND3-2		PmND3-3	
Map to Gene	reads number	percentage	reads number	percentage	reads number	percentage
Total Reads	23132738	100.00%	24585029	100.00%	24669635	100.00%
Total BasePairs	1133504162	100.00%	1204666421	100.00%	1208812115	100.00%
Total Mapped Reads	21490417	92.90%	22919048	93.22%	22831046	92.55%
perfect match	17044462	73.68%	18268278	74.31%	17722887	71.84%
<=2bp mismatch	4445955	19.22%	4650770	18.92%	5108159	20.71%
unique match	13286420	57.44%	13824559	56.23%	14638365	59.34%
multi-position match	8203997	35.46%	9094489	36.99%	8192681	33.21%
Total Unmapped Reads	1642321	7.10%	1665981	6.78%	1838589	7.45%
Summary	PmSD3-1		PmSD3-2		PmSD3-3	
Map to Gene	reads number	percentage	reads number	percentage	reads number	percentage
Total Reads	22948632	100.00%	23163974	100.00%	23033166	100.00%
Total BasePairs	1124482968	100.00%	1135034726	100.00%	1128625134	100.00%
Total Mapped Reads	21217663	92.46%	21507137	92.85%	21545767	93.54%
perfect match	16501517	71.91%	17045641	73.59%	16540359	71.81%
<=2bp mismatch	4716146	20.55%	4461496	19.26%	5005408	21.73%
unique match	13866649	60.42%	13814969	59.64%	14043741	60.97%
multi-position match	7351014	32.03%	7692168	33.21%	7502026	32.57%
Total Unmapped Reads	1730969	7.54%	1656837	7.15%	1487399	6.46%
Summary	PmWD3-1		PmWD3-2		PmWD3-3	
Map to Gene	reads number	percentage	reads number	percentage	reads number	percentage
Total Reads	24345082	100.00%	23040626	100.00%	24354078	100.00%
Total BasePairs	1192909018	100.00%	1128990674	100.00%	1193349822	100.00%
Total Mapped Reads	22640668	93.00%	21287803	92.39%	22589230	92.75%
perfect match	17569629	72.17%	16255149	70.55%	17501299	71.86%
<=2bp mismatch	5071039	20.83%	5032654	21.84%	5087931	20.89%
unique match	14997024	61.60%	13541731	58.77%	14810687	60.81%
multi-position match	7643644	31.40%	7746072	33.62%	7778543	31.94%
Total Unmapped Reads	1704414	7.00%	1752823	7.61%	1764848	7.25%