



CHAPTER IV RESULTS

1. Mutation screening

The sequencing results showed no mutation in coding region or 5'UTR and 3'UTR of all candidate genes. However, in 3'UTR of *HOXD10*, TA repeats were found and seemed to be polymorphic among cases and controls (Fig. 8).

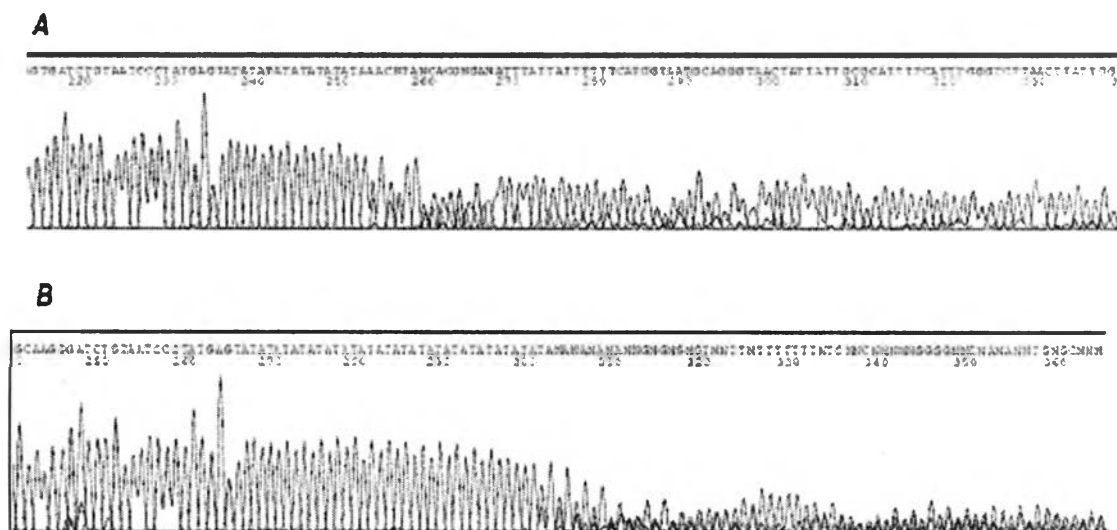


Figure 11 The TA repeat found in 3'UTR of *HOXD10* gene. (A) TA repeat in normal control and (B) in a female with MDK

2. RT-PCR

The mRNA samples were successfully transcribed without any contamination of residue genomic DNA by application of DNase-I treatment. From three genes selected; *LNP*, *EVX2* and *HOXD11*, the only one gene that expressed in both case and control lymphoblastoid cell lines in adult was *LNP* gene. Then *LNP* is selected to be a target

gene for determination of an expression level based on the assumption of GCR. A house keeping gene, *GAPDH*, was also expressed in both case and control samples as expected.

3. Real-time RT-PCR

Duplex RT-PCR were successfully done in all cDNA samples before proceed to real-time PCR. Although a control cDNA No.644 was degraded (Fig. 12), it was selected to do real-time PCR. The result from real-time PCR in controls showed no signs of probes degradation or genomic DNA contamination. The average C_t of *GAPDH* and *LNP* were about 22 and 27, respectively (Fig. 13 and 14). However, as expected, the C_t *GAPDH* and *LNP* of control sample (No. 644) seemed to be different from the other normal controls. Relative quantification showed that, in all normal controls except No.644 sample, there were no significant differences among normal controls sample. Interestingly, there were over-expression of *LNP* gene in case and control samples which was three times higher compared to calibrator (No.629) (Fig.15). However, over-expression in normal control sample was excluded based on the evidence of cDNA degradation. Therefore, the over-expression of *LNP* was only seen in the case samples.

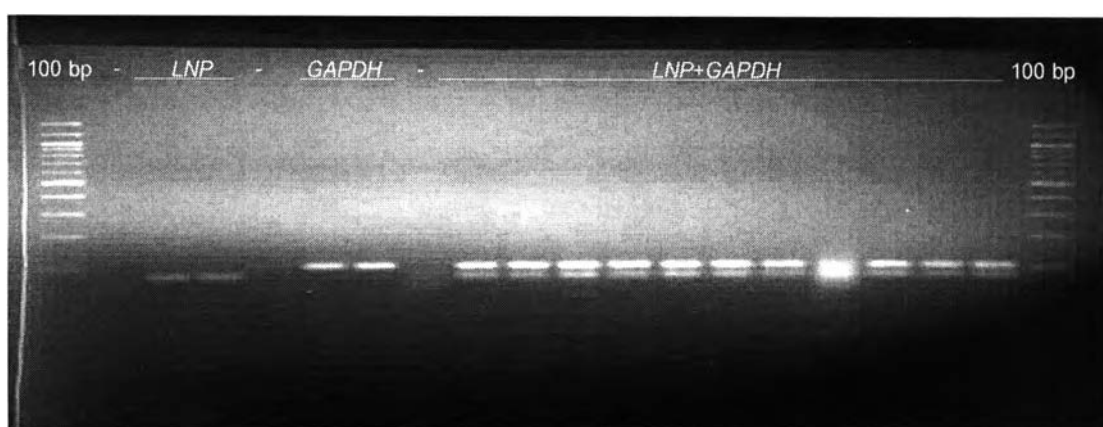
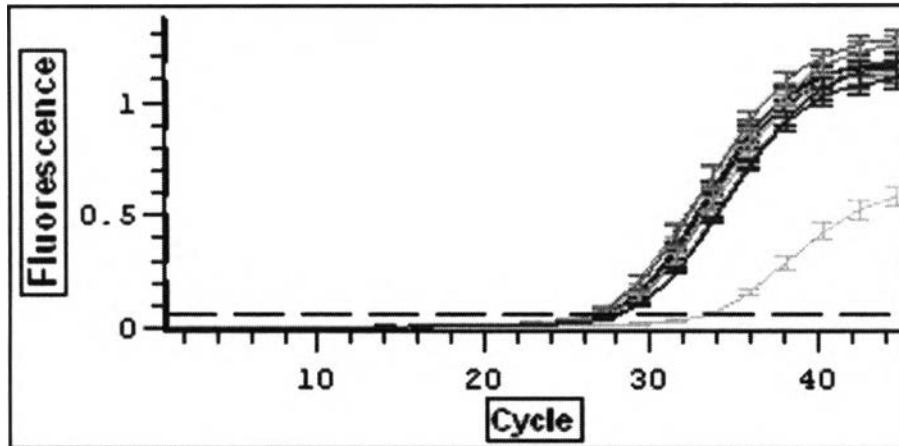


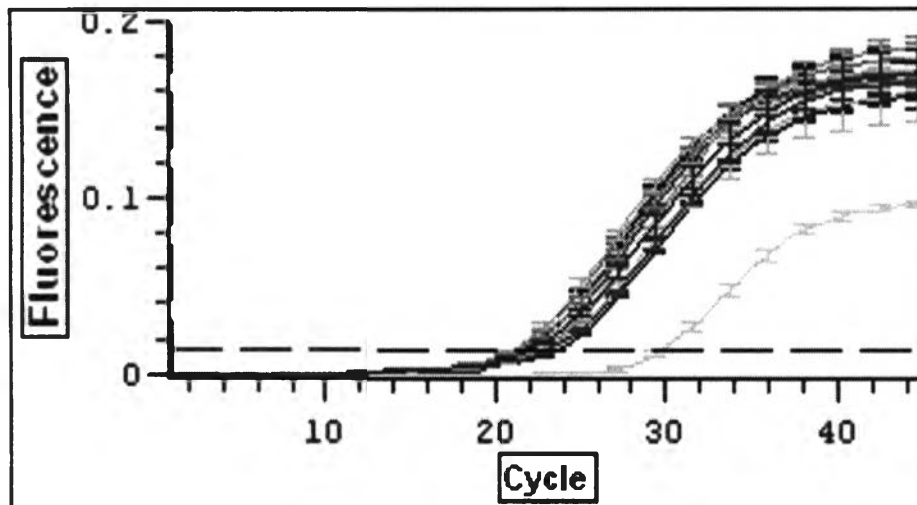
Figure 12 Conventional and duplex RT-PCR from normal and case cDNA samples. Note cDNA degradation in normal control sample (No.644.)

Quantitation Graph

Figure 13 The quantitation graph of *LNP* gene in cases and control samples.Table 13 The details of *LNP* quantitation in each samples.

Set	Dye	Type	Efficiency	C(t)	Avg C(t)	Max C(t)	Min C(t)	C(t) SD
543	FAM	Replicate	56.38	27.13	27.13	27.17	27.09	0.03
629	FAM	Calibrator	59.64	26.37	26.39	26.71	26.24	0.19
630	FAM	Replicate	58.99	27.25	27.29	27.77	27.10	0.28
631	FAM	Replicate	59.76	26.37	26.39	26.63	26.06	0.20
634	FAM	Replicate	58.89	27.12	27.13	27.23	27.06	0.07
635	FAM	Replicate	56.45	26.55	26.59	27.19	26.21	0.38
640	FAM	Replicate	55.43	27.50	27.54	27.94	27.28	0.29
643	FAM	Replicate	58.73	28.16	28.16	28.21	28.13	0.03
644	FAM	Replicate	49.21	33.26	33.29	33.65	33.07	0.26
646	FAM	Replicate	56.38	27.47	27.51	28.12	27.18	0.37
648	FAM	Replicate	54.16	28.02	28.01	28.17	27.86	0.12

Quantitation Graph

Figure 14 The quantitation graph of *GAPDH* gene in cases and control samples .Table 14 The details of *GAPDH* quantitation in each samples.

Set	Dye	Type	Efficiency	C(t)	Avg C(t)	Max C(t)	Min C(t)	C(t) SD
543	CY5	Replicate	40.67	23.50	23.49	23.60	23.40	0.08
629	CY5	Calibrator	44.71	21.10	21.09	21.20	20.96	0.09
630	CY5	Replicate	49.94	21.70	21.70	22.44	21.30	0.44
631	CY5	Replicate	58.45	20.91	20.90	21.09	20.73	0.14
634	CY5	Replicate	50.84	22.25	22.24	22.62	22.05	0.22
635	CY5	Replicate	42.62	21.38	21.36	21.56	20.83	0.31
640	CY5	Replicate	36.23	22.86	22.84	23.14	22.67	0.21
643	CY5	Replicate	40.29	22.98	22.97	23.22	22.77	0.19
644	CY5	Replicate	62.29	29.84	29.85	30.09	29.43	0.30
646	CY5	Replicate	35.80	22.52	22.52	23.08	22.10	0.35
648	CY5	Replicate	38.90	22.00	21.98	22.25	21.60	0.25

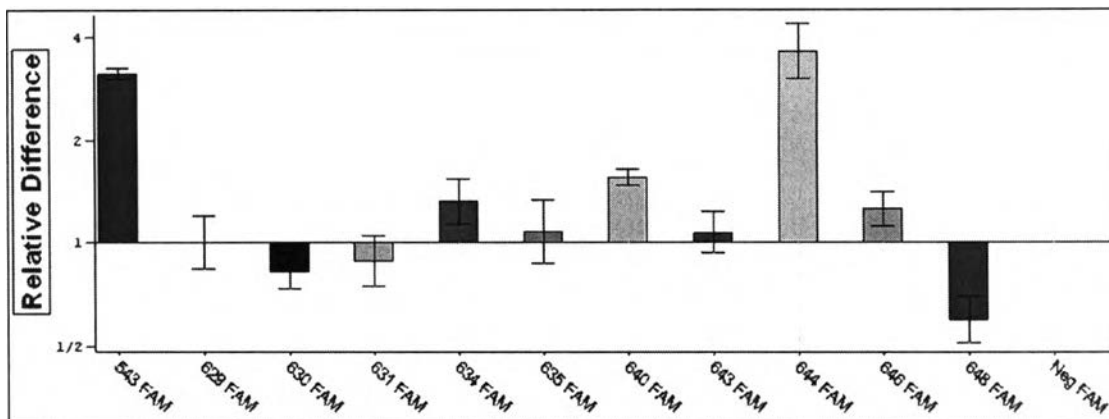


Figure 15 The relative differences in case and control samples. The first red bar represents case sample, whereas the others are control samples.

Table 13 The details of relative quantification in each samples.

Name	Dye	Type	Content	Efficiency	Rel. Dif	Avg Rel. Dif	Max Rel. Dif	Min Rel. Dif	Rel. Dif SD
543	FAM	Replicate	Sample	56.38	3.123	3.115	3.267	2.954	1.037
629	FAM	Calibrator	Sample	59.64	1	0.9854	1.114	0.7215	1.198
630	FAM	Replicate	Sample	58.99	0.8237	0.8046	0.9679	0.6992	1.128
631	FAM	Replicate	Sample	59.76	0.8822	0.8639	1.018	0.6496	1.186
634	FAM	Replicate	Sample	58.89	1.323	1.311	1.688	1.119	1.169
635	FAM	Replicate	Sample	56.45	1.075	1.034	1.342	0.7692	1.24
640	FAM	Replicate	Sample	55.43	1.561	1.488	1.587	1.392	1.055
643	FAM	Replicate	Sample	58.73	1.068	1.06	1.283	0.9292	1.148
644	FAM	Replicate	Sample	49.21	3.623	3.585	4.66	3.125	1.204
646	FAM	Replicate	Sample	56.38	1.255	1.224	1.429	1.044	1.123
648	FAM	Replicate	Sample	54.16	0.5951	0.591	0.7562	0.5071	1.163