

Supplementary Table 7. Mutations in 12 genes identified by targeted sequencing of 30 PCNSL specimens in the discovery cohort.

	Gene ID	Chrom	Position	Ref	Variant	RefSeq	cDNA Change	Protein Change	Frequency
TP102	B2M	chr15	45007672	C	A	NM_004048	c.C119A	p.S40*	74.9
TP105	B2M	chr15	45003745	A	T	NM_004048	c.1A>T	p.M1?	41.2
TP105	B2M	chr15	45003786.4	TCTT	-	NM_004048	c.42_45delTCTT	p.S16fs	37.5
TP49	B2M	chr15	45003781	CT	-	NM_004048	c.37_38del	p.L13fs	44.3
TP49	B2M	chr15	45007643	C	G	NM_004048	c.C90G	p.Y30X	44.8
T9	BTG2	chr1	203274739	G	A	NM_006763	c.G5A	p.S2N	30.9
T9	BTG2	chr1	203274841	A	C	NM_006763	c.A107C	p.K36T	54.1
TP31	BTG2	chr1	203274745	G	T	NM_006763	c.G11T	p.G4V	43.5
TP31	BTG2	chr1	203274761	G	A	NM_006763	c.G27A	p.M9I	43.6
TP31	BTG2	chr1	203274762	C	T	NM_006763	c.C28T	p.L10F	36.7
TP31	BTG2	chr1	203276430	G	C	NM_006763	c.G341C	p.G114A	27.7
TP31	BTG2	chr1	203276496	C	G	NM_006763	c.C407G	p.T136S	46.2
TP31	BTG2	chr1	203276551	GGCAGT	-	NM_006763	c.462_472del	p.M154fs	25.4
TP38	BTG2	chr1	203276441	T	C	NM_006763	c.T352C	p.S118P	20.7
TP43	BTG2	chr1	203274853	G	C	NM_006763	c.G119C	p.G40A	20.6
TP48	BTG2	chr1	203276241	A	G	NM_006763	c.A152G	p.K51R	48.3
TP49	BTG2	chr1	203276443	CATCTGC	-	NM_006763	c.354_376del	p.S118fs	15.6
TP5	BTG2	chr1	203274867	G	A	NM_006763	c.G133A	p.A45T	34.3
TP5	BTG2	chr1	203276251	G	C	NM_006763	c.G162C	p.W54C	33.5
TP5	BTG2	chr1	203276344	CGGACTC	-	NM_006763	c.255_264del	p.I85fs	32.3
TP5	BTG2	chr1	203276424	G	C	NM_006763	c.G335C	p.R112P	32.6
TP5	BTG2	chr1	203276427	T	-	NM_006763	c.338delT	p.L113fs	32.5
TP77	BTG2	chr1	203276344	CGGACTC	-	NM_006763	c.255_264del	p.I85fs	13.5
TP77	BTG2	chr1	203276424	G	C	NM_006763	c.G335C	p.R112P	12.4
TP77	BTG2	chr1	203276427	T	-	NM_006763	c.338delT	p.L113fs	12.6
TP82	BTG2	chr1	203276344	CGGACTC	-	NM_006763	c.255_264del	p.I85fs	12.3
TP82	BTG2	chr1	203276424	G	C	NM_006763	c.G335C	p.R112P	12.6
TP82	BTG2	chr1	203276427	T	-	NM_006763	c.338delT	p.L113fs	13.0
TP90	BTG2	chr1	203274862	A	G	NM_006763	c.A128G	p.Q43R	69.1
TP98	BTG2	chr1	203274761	G	A	NM_006763	c.G27A	p.M9I	28.0
T2	CARD11	chr7	2977652	CTT	-	NM_032415	c.1030_1032del	p.344_344del	33.6
TP102	CARD11	chr7	2979559	C	T	NM_032415	c.C687T	p.D230N	44.4
TP106	CARD11	chr7	2979559	C	T	NM_032415	c.C687T	p.D230N	68.8
TP42	CARD11	chr7	2984147	G	A	NM_032415	c.C383T	p.T128M	82.2
TP42	CARD11	chr7	2985518	T	A	NM_032415	c.A293T	p.Y98F	79.4
TP81	CARD11	chr7	2978320	C	T	NM_032415	c.G1010A	p.R337Q	44.8
TP81	CARD11	chr7	2983994	C	T	NM_032415	c.G536A	p.R179Q	39.5
T2	CD79B	chr17	62006799	A	G	NM_000626	c.T586C	p.Y196H	32.5
T8	CD79B	chr17	62006795	T	C	NM_000626	c.A590G	p.E197G	12.1
TP100	CD79B	chr17	62006798	T	C	NM_000626	c.A587G	p.Y196C	58.3
TP105	CD79B	chr17	62006798	T	G	NM_000626	c.A587C	p.Y196S	9.1
TP106	CD79B	chr17	62006798	T	G	NM_000626	c.A587C	p.Y196S	48.9
TP12	CD79B	chr17	62006798	T	G	NM_000626	c.A587C	p.Y196S	43.3
TP31	CD79B	chr17	62006798	T	G	NM_000626	c.A587C	p.Y196S	37.1
TP36	CD79B	chr17	62006798	T	G	NM_000626	c.A587C	p.Y196S	47.4
TP38	CD79B	chr17	62006798	T	A	NM_000626	c.A587T	p.Y196F	40.1
TP42	CD79B	chr17	62006798	T	C	NM_000626	c.A587G	p.Y196C	39.6
TP43	CD79B	chr17	62006799	A	C	NM_000626	c.T586G	p.Y196D	47.3
TP49	CD79B	chr17	62006663	C	G	NM_000626	c.G613C	p.A205P	46.3
TP49	CD79B	chr17	62006828	C	G	NM_000626	c.G557C	p.S186T	48.2
TP49	CD79B	chr17	62008745	G	A	NM_000626	c.C71T	p.A24V	44.2
TP5	CD79B	chr17	62006798	T	A	NM_000626	c.A587T	p.Y196F	61.7
TP53	CD79B	chr17	62006799	A	G	NM_000626	c.T586C	p.Y196H	57.0
TP82	CD79B	chr17	62006799	A	C	NM_000626	c.T586G	p.Y196D	23.9
TP94	CD79B	chr17	62006602	T	C	NM_000626	c.A677G	p.H225R	37.3
TP94	CD79B	chr17	62006825	T	A	NM_000626	c.A560T	p.K187M	31.3
TP94	CD79B	chr17	62006797.6	GT	AG	NM_000626	c.587_588delACinsCT	p.Y196S	32.4
T2	MYD88	chr3	38182641	T	C	NM_002468	c.T794C	p.L265P	31.8
T4	MYD88	chr3	38182641	T	C	NM_002468	c.T794C	p.L265P	49.2
T9	MYD88	chr3	38182641	T	C	NM_002468	c.T794C	p.L265P	34.1
TP100	MYD88	chr3	38182641	T	C	NM_002468	c.T794C	p.L265P	69.5
TP102	MYD88	chr3	38182641	T	C	NM_002468	c.T794C	p.L265P	35.7
TP104	MYD88	chr3	38182641	T	C	NM_002468	c.T794C	p.L265P	75.2
TP105	MYD88	chr3	38182337	C	T	NM_002468	c.C773T	p.P258L	28.0
TP105	MYD88	chr3	38182638	G	A	NM_002468	c.G791A	p.R272Q	36.1
TP106	MYD88	chr3	38182641	T	C	NM_002468	c.T794C	p.L265P	47.3
TP110	MYD88	chr3	38182292	G	A	NM_002468	c.G728A	p.S243N	67.4
TP12	MYD88	chr3	38182641	T	C	NM_002468	c.T794C	p.L265P	40.0

TP31	MYD88	chr3	38182641	T	C	NM_002468	c.T794C	p.L265P	38.2
TP35	MYD88	chr3	38182292	G	A	NM_002468	c.G728A	p.S243N	76.5
TP36	MYD88	chr3	38182641	T	C	NM_002468	c.T794C	p.L265P	69.2
TP38	MYD88	chr3	38182337	C	T	NM_002468	c.C773T	p.P258L	25.4
TP38	MYD88	chr3	38182641	T	C	NM_002468	c.T794C	p.L265P	21.6
TP42	MYD88	chr3	38182641	T	C	NM_002468	c.T794C	p.L265P	39.2
TP46	MYD88	chr3	38182641	T	C	NM_002468	c.T794C	p.L265P	36.5
TP48	MYD88	chr3	38182641	T	C	NM_002468	c.T794C	p.L265P	43.1
TP49	MYD88	chr3	38182337	C	T	NM_002468	c.C773T	p.P258L	44.6
TP53	MYD88	chr3	38182641	T	C	NM_002468	c.T794C	p.L265P	44.3
TP77	MYD88	chr3	38182641	T	C	NM_002468	c.T794C	p.L265P	34.3
TP80	MYD88	chr3	38182641	T	C	NM_002468	c.T794C	p.L265P	51.5
TP81	MYD88	chr3	38182641	T	C	NM_002468	c.T794C	p.L265P	44.2
TP82	MYD88	chr3	38182641	T	C	NM_002468	c.T794C	p.L265P	46.6
TP90	MYD88	chr3	38182641	T	C	NM_002468	c.T794C	p.L265P	32.2
TP94	MYD88	chr3	38182641	T	C	NM_002468	c.T794C	p.L265P	62.6
TP98	MYD88	chr3	38182641	T	C	NM_002468	c.T794C	p.L265P	77.7
T2	PIM1	chr6	37138624	A	C	NM_002648	c.A158C	p.Y53S	43.9
T2	PIM1	chr6	37138769	C	G	NM_002648	c.C202G	p.H68D	35.3
T2	PIM1	chr6	37138950	G	C	NM_002648	c.G290C	p.S97T	31.0
T2	PIM1	chr6	37138968	T	G	NM_002648	c.T308G	p.V103G	30.7
T2	PIM1	chr6	37139039	C	G	NM_002648	c.C379G	p.Q127E	30.6
T4	PIM1	chr6	37138945	G	T	NM_002648	c.G285T	p.K95N	79.5
T8	PIM1	chr6	37138769	C	A	NM_002648	c.C202A	p.H68N	9.2
TP100	PIM1	chr6	37138804	G	C	NM_002648	c.G237C	p.E79D	33.0
TP100	PIM1	chr6	37139039	C	G	NM_002648	c.C379G	p.Q127E	29.2
TP102	PIM1	chr6	37138804	G	C	NM_002648	c.G237C	p.E79D	43.2
TP105	PIM1	chr6	37138782	A	G	NM_002648	c.A215G	p.A72G	35.7
TP105	PIM1	chr6	37138805	C	G	NM_002648	c.C238G	p.L80V	43.9
TP105	PIM1	chr6	37139097	G	A	NM_002648	c.G437A	p.S146N	44.8
TP29	PIM1	chr6	37138919	C	T	NM_002648	c.C259T	p.P87S	26.1
TP29	PIM1	chr6	37138946	G	T	NM_002648	c.G286T	p.V96L	38.1
TP31	PIM1	chr6	37140805	G	A	NM_002648	c.G641A	p.R214H	83.2
TP31	PIM1	chr6	37140885	C	G	NM_002648	c.C721G	p.P241A	88.5
TP31	PIM1	chr6	37140921	G	A	NM_002648	c.G757A	p.V253I	87.1
TP35	PIM1	chr6	37139097	G	A	NM_002648	c.G437A	p.S146N	43.1
TP38	PIM1	chr6	37138769	C	T	NM_002648	c.C202T	p.H68T	65.6
TP38	PIM1	chr6	37139150	C	G	NM_002648	c.C490G	p.L164V	13.7
TP38	PIM1	chr6	37139150	C	T	NM_002648	c.C490T	p.L164F	41.7
TP43	PIM1	chr6	37139033	C	T	NM_002648	c.C373T	p.P125S	59.6
TP46	PIM1	chr6	37138630	G	A	NM_002648	c.G164A	p.G55D	29.6
TP46	PIM1	chr6	37138950	G	C	NM_002648	c.G290C	p.S97T	22.2
TP48	PIM1	chr6	37138760	G	C	NM_002648	c.G193C	p.A65P	45.4
TP48	PIM1	chr6	37138802	G	C	NM_002648	c.G235C	p.E79Q	36.7
TP48	PIM1	chr6	37139039	C	T	NM_002648	c.C379T	p.Q127X	76.4
TP49	PIM1	chr6	37138955	G	A	NM_002648	c.G295A	p.G99S	84.4
TP5	PIM1	chr6	37141811	C	T	NM_002648	c.C886T	p.P296S	31.0
TP5	PIM1	chr6	37141821	C	T	NM_002648	c.C896T	p.T299I	30.7
TP53	PIM1	chr6	37139037	TGC	-	NM_002648	c.377_379del	p.126_127del	83.6
TP77	PIM1	chr6	37138777	G	C	NM_002648	c.G210C	p.E70D	21.5
TP77	PIM1	chr6	37139111	G	A	NM_002648	c.G451A	p.V151M	46.0
TP77	PIM1	chr6	37139150	C	T	NM_002648	c.C490T	p.L164F	42.9
TP77	PIM1	chr6	37141718	C	T	NM_002648	c.C793T	p.H265Y	39.0
TP80	PIM1	chr6	37138603	G	A	NM_002648	c.G137A	p.S46N	22.4
TP82	PIM1	chr6	37139097	G	C	NM_002648	c.G437C	p.S146T	26.3
TP90	PIM1	chr6	37139061	C	T	NM_002648	c.C401T	p.T134M	82.9
TP90	PIM1	chr6	37139150	C	T	NM_002648	c.C490T	p.L164F	61.9
TP90	PIM1	chr6	37141731	G	A	NM_002648	c.G806A	p.W269*	71.1
TP94	PIM1	chr6	37138804	G	-	NM_002648	c.G237del	p.Glu79fs	26.6
TP98	PIM1	chr6	37138600	G	A	NM_002648	c.G134A	p.G45D	24.6
TP98	PIM1	chr6	37138800	G	A	NM_002648	c.G233A	p.G78G	43.4
TP98	PIM1	chr6	37138804	G	C	NM_002648	c.G237C	p.E79D	44.1
TP98	PIM1	chr6	37139039	C	T	NM_002648	c.C379T	p.Q127X	45.8
TP98	PIM1	chr6	37139073	C	T	NM_002648	c.C413T	p.A138V	61.8
TP98	PIM1	chr6	37139098	C	A	NM_002648	c.C438A	p.S146R	62.1
TP29	PRDM1	chr6	106536269	C	T	NM_001198	c.C236T	p.A79V	52.4
TP48	PRDM1	chr6	106536317	GTGAAG	-	NM_001198	c.284_291del	p.S95fs	47.7
TP77	PRDM1	chr6	106553791	C	T	NM_001198	c.C1756T	p.Q586X	43.5
T4	PRKCD	chr3	53221366	G	A	NM_006254	c.G1363A	p.A455T	88.7
T2	TBL1XR1	chr3	176756104	A	T	NM_024665	c.T1044A	p.H348Q	29.4
TP102	TBL1XR1	chr3	176750916	A	G	NM_024665	c.T1259C	p.F420S	42.7
TP36	TBL1XR1	chr3	176750794	A	G	NM_024665	c.T1381C	p.S461P	39.1

TP49	TBL1XR1	chr3	176763973	G	C	NM_024665	c.C869G	p.T290R	91.3
TP5	TBL1XR1	chr3	176765300	C	T	NM_024665	c.G740A	p.G247E	31.5
TP100	TMEM30A	chr6	75977425	T	A	NM_018247	c.A277T	p.K93*	58.4
TP105	TMEM30A	chr6	75969072	G	A	NM_018247	c.C676T	p.R226*	46.8
TP38	TNFAIP3	chr6	138200015	G	A	NM_006290	c.G1433A	p.C478Y	51.3
TP43	TNFAIP3	chr6	138202351	C	-	NM_006290	c.2268delC	p.D756fs	97.5
TP53	TNFAIP3	chr6	138195987	G	A	NM_006290	c.G301A	p.G101S	36.0
TP102	TOX	chr8	60031457	G	C	NM_014729	c.C90G	p.Y30*	74.9
TP104	TOX	chr8	60031445	C	G	NM_014729	c.G102A	p.K34N	45.6
TP5	TOX	chr8	59720716	G	T	NM_014729	c.C1505A	p.P502Q	48.6
TP77	TOX	chr8	60031465	CCAGGC	-	NM_014729	c.65_82del	p.22_28del	34.1
TP98	TOX	chr8	60031546	T	A	NM_014729	c.A1T	p.M1?	47.4