

YMTHE, Volume 31

Supplemental Information

***In vivo* CRISPR gene editing**

in patients with herpetic stromal keratitis

Anji Wei, Di Yin, Zimeng Zhai, Sikai Ling, Huangying Le, Lijia Tian, Jianjiang Xu, Soren R. Paludan, Yujia Cai, and Jiaxu Hong

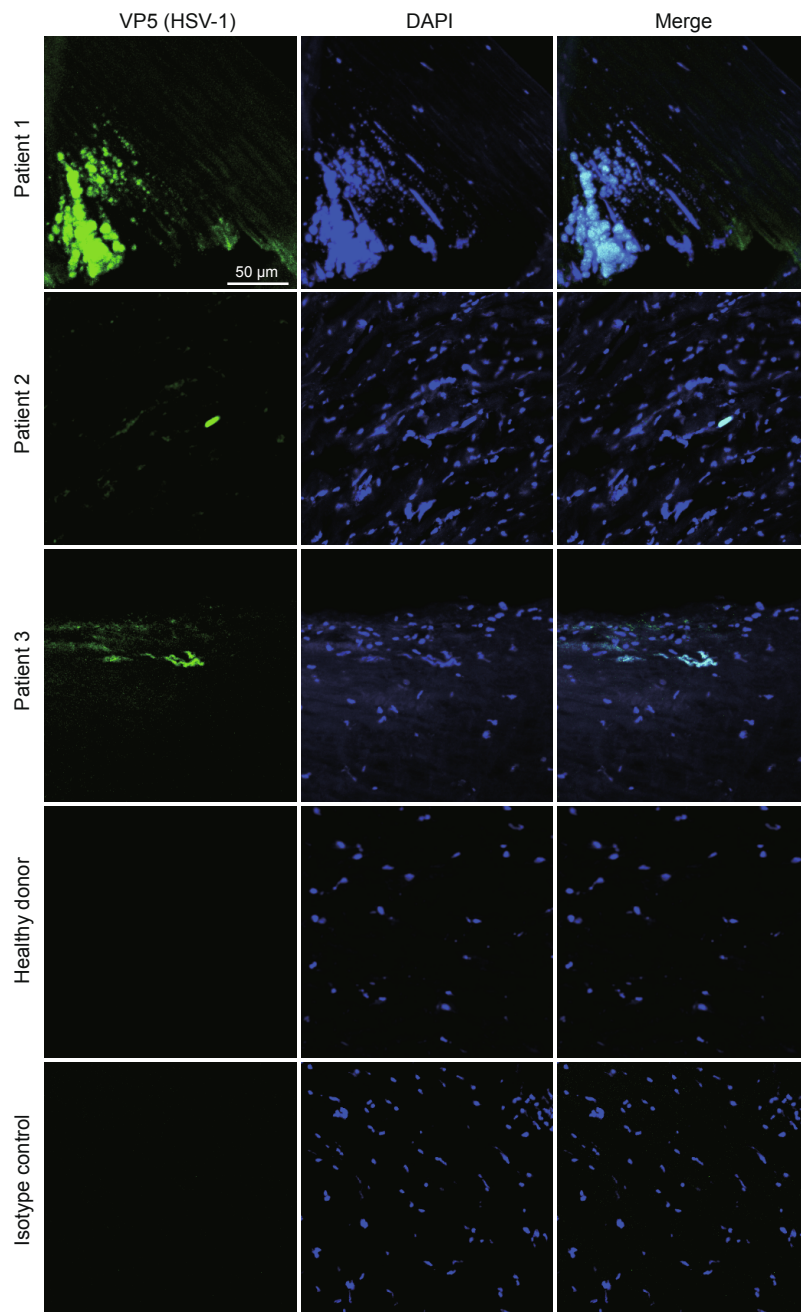


Fig. S1. Fluorescence microscopy analysis of HSV-1 in the removed corneal buttons. HSV-1 capsid protein VP5 was presented in green while DAPI was in blue. Their perfect overlap after merging suggests the presence of HSV-1 in the patient corneal tissue before CRISPR treatment.

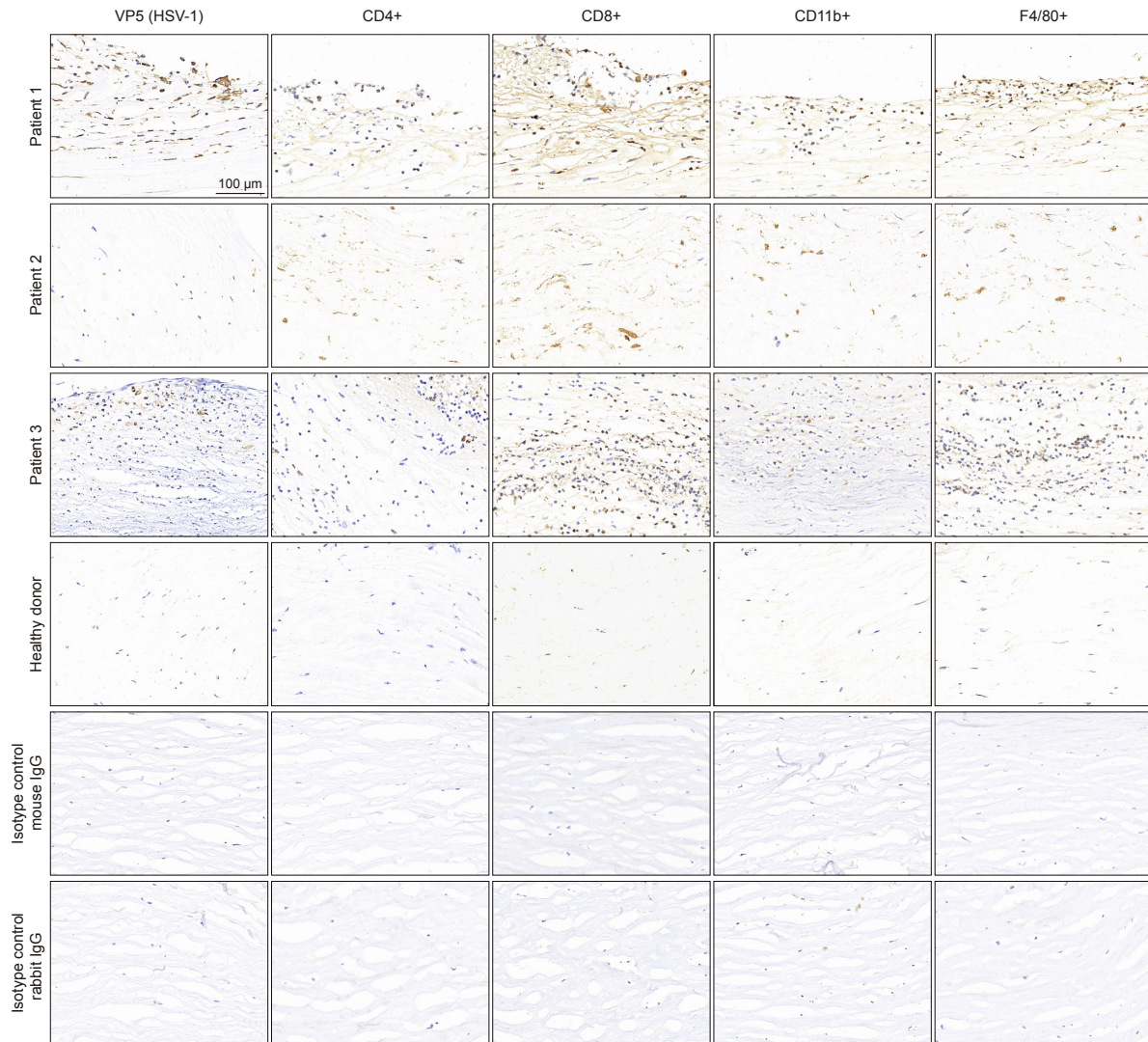


Fig. S2. Immunohistochemistry analysis of immune cells in the corneal button. The removed corneal buttons from the patients were stained for T cells (CD4+ and CD8+), myeloid-derived cells (CD11b+) and macrophages (F4/80+). Immunohistochemistry confirmed excess infiltration of inflammatory cells compared to the healthy cornea.

A

			20		40		60	
HSV-1 KOS UL23	MASYPCHQHA	SAFDQAARSR	GHSNRRTALR	PRRQQEATEV	RLEQKMP TLL	RVYIDGPHGM	60	
HSV-1 17+ UL23	MASYPCHQHA	SAFDQAARSR	GHNNRRTALR	PRRQQKATEV	RLEQKMP TLL	RVYIDGPHGM	60	
Patient 1 UL23	- - - YPCHQHA	SAFDQAARSR	GHSNRRTALR	PRRQQEATEV	RLEQKMP TLL	RVYIDGPHGM	57	
Patient 2 UL23	- - - YPCHQHA	SAFDQAARSR	GHSNRRTALR	PRRQQEATEV	RLEQKMP TLL	RVYIDGPHGM	57	
Patient 3 UL23	- - - YPCHQHA	SAFDQAARSR	GHSNRRTALR	PRRQQEATEV	RLEQKMP TLL	RVYIDGPHGM	57	
			80		100		120	
HSV-1 KOS UL23	GKTTTTQLLV	ALGSRDDIVY	VPEPMTYWQV	LGASETIANI	YTTQHRLDQG	EISAGDAAVV	120	
HSV-1 17+ UL23	GKTTTTQLLV	ALGSRDDIVY	VPEPMTYWRV	LGASETIANI	YTTQHRLDQG	EISAGDAAVV	120	
Patient 1 UL23	GKTTTTQLLV	ALGSRDDIVY	VPEPMTYWQV	LGASETIANI	YTTQHRLDQG	EISAGDAAVV	117	
Patient 2 UL23	GKTTTTQLLV	ALGSRDDIVY	VPEPMTYWQV	LGASETIANI	YTTQHRLDQG	EISAGDAAVV	117	
Patient 3 UL23	GKTTTTQLLV	ALGSRDDIVY	VPEPMTYWQV	LGASETIANI	YTTQHRLDQG	EISAGDAAVV	117	
			140		160		180	
HSV-1 KOS UL23	MTSAQITMGM	PYAVTDAVLA	PHIGGEAGSS	HAPPPALTLI	FDRHP IAALL	CYPAARYLMG	180	
HSV-1 17+ UL23	MTSAQITMGM	PYAVTDAVLA	PHIGGEAGSS	HAPPPALTLI	FDRHP IAALL	CYPAARYLMG	180	
Patient 1 UL23	MTSAQITMGM	PYAVTDAVLA	PHIGGEAGSS	HAPPPALTLI	FDRHP IAALL	CYPAARYLMG	177	
Patient 2 UL23	MTSAQITMGM	PYAVTDAVLA	PHIGGEAGSS	HAPPPALTLI	FDRHP IAALL	CYPAARYLMG	177	
Patient 3 UL23	MTSAQITMGM	PYAVTDAVLA	PHIGGEAGSS	HAPPPALTLI	FDRHP IAALL	CYPAARYLMG	177	
			200		220		240	
HSV-1 KOS UL23	SMT PQAVLAF	VALIPPTLPG	TNIVLGALPE	DRHIDRLAKR	QRPGERDLA	MLAAIRRVYV	240	
HSV-1 17+ UL23	SMT PQAVLAF	VALIPPTLPG	TNIVLGALPE	DRHIDRLAKR	QRPGERDLA	MLAAIRRVYV	240	
Patient 1 UL23	SMT PQAVLAF	VALIPPTLPG	TNIVLGALPE	DRHIDRLAKR	QRPGERDLA	MLAAIRRVYV	237	
Patient 2 UL23	SMT PQAVLAF	VALIPPTLPG	TNIVLGALPE	DRHIDRLAKR	QRPGERDLA	MLAAIRRVYV	237	
Patient 3 UL23	SMT PQAVLAF	VALIPPTLPG	TNIVLGALPE	DRHIDRLAKR	QRPGERDLA	MLAAIRRVYV	237	
			260		280		300	
HSV-1 KOS UL23	LLANTVRYLQ	GGGSWREDWG	QLSGTAVPPQ	GAEPQSNAGP	RPHIGDTLFT	LFRAPPELLAP	300	
HSV-1 17+ UL23	LLANTVRYLQ	GGGSWREDWG	QLSGAAVPPQ	GAEPQSNAGP	RPHIGDTLFT	LFRAPPELLAP	300	
Patient 1 UL23	LLANTVRYLQ	GGGSWREDWG	QLSGTAVPPQ	GAEPQSNAGP	RPHIGDTLFT	LFRAPPELLAP	297	
Patient 2 UL23	LLANTVRYLQ	GGGSWREDWG	QLSGTAVPPQ	GAEPQSNAGP	RPHIGDTLFT	LFRAPPELLAP	297	
Patient 3 UL23	LLANTVRYLQ	GGGSWREDWG	QLSGTAVPPQ	GAEPQSNAGP	RPHIGDTLFT	LFRAPPELLAP	297	
			320		340		360	
HSV-1 KOS UL23	NGDLYNVFAW	ALDVLAKRLR	PMHVFILDYD	QSPAGCRDAL	LQLTSGMVQT	HVTTPGS IPT	360	
HSV-1 17+ UL23	NGDLYNVFAW	ALDVLAKRLR	PMHVFILDYD	QSPAGCRDAL	LQLTSGMVQT	HVTTPGS IPT	360	
Patient 1 UL23	NGDLYNVFAW	ALDVLAKRLR	PMHVFILDYD	QSPAGCRDAL	LQLTSGMVQT	HVTTPGS IPT	357	
Patient 2 UL23	NGDLYNVFAW	ALDVLAKRLR	PMHVFILDYD	QSPAGCRDAL	LQLTSGMVQT	HVTTPGS IPT	357	
Patient 3 UL23	NGDLYNVFAW	ALDVLAKRLR	PMHVFILDYD	QSPAGCRDAL	LQLTSGMVQT	HVTTPGS IPT	357	
HSV-1 KOS UL23	ICDLARTFAR	EMGEAN					377	
HSV-1 17+ UL23	ICDLARTFAR	EMGEAN					377	
Patient 1 UL23	ICDLARTFAR	EMGEAN					374	
Patient 2 UL23	ICDLARTFAR	EMGEAN					374	
Patient 3 UL23	ICDLARTFAR	EMGEAN					374	

B

			20		40		60
HSV-1 KOS UL30	MFSGGGGPLS	PGGKSAARAA	SGFFAPAGPR	GAGRGGPPCL	RQNFYNPYLA	PVGTQQKPTG	60
HSV-1 17+ UL30	MFSGGGGPLS	PGGKSAARAA	SGFFAPAGPR	GASRGPPPC	RQNFYNPYLA	PVGTQQKPTG	60
Patient 1 UL30	-----	-----RAA	SGFFAPAGPR	GASRGPPPC	RQNFYNPYLA	PVGTQQKPTG	43
Patient 2 UL30	-----	-----RAA	SGFFAPAGPR	GAGRGGPPCL	RQNFYNPYLA	PVGTQQKPTG	43
Patient 3 UL30	-----	-----RAA	SGFFAPAGPR	GAGRGGPPCL	RQNFYNPYLA	PVGTQQKPTG	43
			80		100		120
HSV-1 KOS UL30	PTQRHTYYSE	CDEFRF IAPR	VLDEDAPPEK	RAGVHDGHLK	RAPKVYCGGD	ERDVLRVGSG	120
HSV-1 17+ UL30	PTQRHTYYSE	CDEFRF IAPR	VLDEDAPPEK	RAGVHDGHLK	RAPKVYCGGD	ERDVLRVGSG	120
Patient 1 UL30	PTQRHTYYSE	CDEFRF IAPR	VLDEDAPPEK	RAGVHDGHLK	RAPKVYCGGD	ERDVLRVGSG	103
Patient 2 UL30	PTQRHTYYSE	CDEFRF IAPR	VLDEDAPPEK	RAGVHDGHLK	RAPKVYCGGD	ERDVLRVGSG	103
Patient 3 UL30	PTQRHTYYSE	CDEFRF IAPR	VLDEDAPPEK	RAGVHDGHLK	RAPKVYCGGD	ERDVLRVGSG	103
			140		160		180
HSV-1 KOS UL30	GFWPRRSRLW	GGVDHAPAGF	NPTVTVFHYV	DILENVEHAY	GMRAAQFHAR	FMDAITPTGT	180
HSV-1 17+ UL30	GFWPRRSRLW	GGVDHAPAGF	NPTVTVFHYV	DILENVEHAY	GMRAAQFHAR	FMDAITPTGT	180
Patient 1 UL30	GFWPRRSRLW	GGVDHAPAGF	NPTVTVFHYV	DILENVEHAY	GMRAAQFHAR	FMDAITPTGT	163
Patient 2 UL30	GFWPRRSRLW	GGVDHAPAGF	NPTVTVFHYV	DILENVEHAY	GMRAAQFHAR	FMDAITPTGT	163
Patient 3 UL30	GFWPRRSRLW	GGVDHAPAGF	NPTVTVFHYV	DILENVEHAY	GMRAAQFHAR	FMDAITPTGT	163
			200		220		240
HSV-1 KOS UL30	VITLLGLTPE	GHRVAVHVG	TRQFYFVNKE	EVDRLQCRA	PRDLCERMAA	ALRESPGASF	240
HSV-1 17+ UL30	VITLLGLTPE	GHRVAVHVG	TRQFYFVNKE	EVDRLQCRA	PRDLCERMAA	ALRESPGASF	240
Patient 1 UL30	VITLLGLTPE	GHRVAVHVG	TRQFYFVNKE	EVDRLQCRA	PRDLCERMAA	ALRESPGASF	223
Patient 2 UL30	VITLLGLTPE	GHRVAVHVG	TRQFYFVNKE	EVDRLQCRA	PRDLCERMAA	ALRESPGASF	223
Patient 3 UL30	VITLLGLTPE	GHRVAVHVG	TRQFYFVNKE	EVDRLQCRA	PRDLCERMAA	ALRESPGASF	223
			260		280		300
HSV-1 KOS UL30	RGISADHFEA	EVVERTDVY	YETRPALFYR	VYVRSGRVLS	YLCDNFCPAI	KKYEGGV DAT	300
HSV-1 17+ UL30	RGISADHFEA	EVVERTDVY	YETRPALFYR	VYVRSGRVLS	YLCDNFCPAI	KKYEGGV DAT	300
Patient 1 UL30	RGISADHFEA	EVVERTDVY	YETRPALFYR	VYVRSGRVLS	YLCDNFCPAI	KKYEGGV DAT	283
Patient 2 UL30	RGISADHFEA	EVVERTDVY	YETRPALFYR	VYVRSGRVLS	YLCDNFCPAI	KKYEGGV DAT	283
Patient 3 UL30	RGISADHFEA	EVVERTDVY	YETRPALFYR	VYVRSGRVLS	YLCDNFCPAI	KKYEGGV DAT	283
			320		340		360
HSV-1 KOS UL30	TRFILDNPGF	VTFGWYRLKP	GRNNTLAQPR	APMAFGTSSD	VEFNCTADNL	AIEGGMSDLP	360
HSV-1 17+ UL30	TRFILDNPGF	VTFGWYRLKP	GRNNTLAQPR	APMAFGTSSD	VEFNCTADNL	AIEGGMSDLP	360
Patient 1 UL30	TRFILDNPGF	VTFGWYRLKP	GRNNTLAQPR	APMAFGTSSD	VEFNCTADNL	AIEGGMSDLP	343
Patient 2 UL30	TRFILDNPGF	VTFGWYRLKP	GRNNTLAQPR	APMAFGTSSD	VEFNCTADNL	AIEGGMSDLP	343
Patient 3 UL30	TRFILDNPGF	VTFGWYRLKP	GRNNTLAQPR	APMAFGTSSD	VEFNCTADNL	AIEGGMSDLP	343
			380		400		420
HSV-1 KOS UL30	AYKLMCFDIE	CKAGGEDELA	FPVAGHPEDL	VIQISCLLYD	LSTTALEHVL	LFSLGS CDLP	420
HSV-1 17+ UL30	AYKLMCFDIE	CKAGGEDELA	FPVAGHPEDL	VIQISCLLYD	LSTTALEHVL	LFSLGS CDLP	420
Patient 1 UL30	AYKLMCFDIE	CKAGGEDELA	FPVAGHPEDL	VIQISCLLYD	LSTTALEHVL	LFSLGS CDLP	403
Patient 2 UL30	AYKLMCFDIE	CKAGGEDELA	FPVAGHPEDL	VIQISCLLYD	LSTTALEHVL	LFSLGS CDLP	403
Patient 3 UL30	AYKLMCFDIE	CKAGGEDELA	FPVAGHPEDL	VIQISCLLYD	LSTTALEHVL	LFSLGS CDLP	403
			440		460		480
HSV-1 KOS UL30	ESHLNELAAR	GLPTPVVLEF	DSEFEMLLAF	MTLVKQYGPE	FVTGYN I INF	DWPFLAKLT	480
HSV-1 17+ UL30	ESHLNELAAR	GLPTPVVLEF	DSEFEMLLAF	MTLVKQYGPE	FVTGYN I INF	DWPFLAKLT	480
Patient 1 UL30	ESHLNELAAR	GLPTPVVLEF	DSEFEMLLAF	MTLVKQYGPE	FVTGYN I INF	DWPFLAKLT	463
Patient 2 UL30	ESHLNELAAR	GLPTPVVLEF	DSEFEMLLAF	MTLVKQYGPE	FVTGYN I INF	DWPFLAKLT	463
Patient 3 UL30	ESHLNELAAR	GLPTPVVLEF	DSEFEMLLAF	MTLVKQYGPE	FVTGYN I INF	DWPFLAKLT	463
			500		520		540
HSV-1 KOS UL30	DIYKVPLDGY	GRMNGRGVFR	VWDIGQSHFQ	KRSKIKVNGM	VNIDMYGIIT	DKIKLSSYKL	540
HSV-1 17+ UL30	DIYKVPLDGY	GRMNGRGVFR	VWDIGQSHFQ	KRSKIKVNGM	VNIDMYGIIT	DKIKLSSYKL	540
Patient 1 UL30	DIYKVPLDGY	GRMNGRGVFR	VWDIGQSHFQ	KRSKIKVNGM	VNIDMYGIIT	DKIKLSSYKL	523
Patient 2 UL30	DIYKVPLDGY	GRMNGRGVFR	VWDIGQSHFQ	KRSKIKVNGM	VNIDMYGIIT	DKIKLSSYKL	523
Patient 3 UL30	DIYKVPLDGY	GRMNGRGVFR	VWDIGQSHFQ	KRSKIKVNGM	VNIDMYGIIT	DKIKLSSYKL	523
			560		580		600
HSV-1 KOS UL30	NAVAEAVLKD	KKKDLSYRDI	PAYYATGPAQ	RGVIGEYCIQ	DSLLVGQLFF	KFLPHLELSA	600
HSV-1 17+ UL30	NAVAEAVLKD	KKKDLSYRDI	PAYYAAGPAQ	RGVIGEYCIQ	DSLLVGQLFF	KFLPHLELSA	600
Patient 1 UL30	NAVAEAVLKD	KKKDLSYRDI	PAYYAAGPAQ	RGVIGEYCIQ	DSLLVGQLFF	KFLPHLELSA	583
Patient 2 UL30	NAVAEAVLKD	KKKDLSYRDI	PAYYATGPAQ	RGVIGEYCIQ	DSLLVGQLFF	KFLPHLELSA	583
Patient 3 UL30	NAVAEAVLKD	KKKDLSYRDI	PAYYATGPAQ	RGVIGEYCIQ	DSLLVGQLFF	KFLPHLELSA	583
			620		640		660
HSV-1 KOS UL30	VARLAGINIT	RTIYDQQQIR	VFTCLLRLAD	QKGFILPDTQ	GRFRGAGGEA	PKRPA AARED	660
HSV-1 17+ UL30	VARLAGINIT	RTIYDQQQIR	VFTCLLRLAD	QKGFILPDTQ	GRFRGAGGEA	PKRPA AARED	660
Patient 1 UL30	VARLAGINIT	RTIYDQQQIR	VFTCLLRLAD	QKGFILPDTQ	GRFRGAGGEA	PKRPA AARED	643
Patient 2 UL30	VARLAGINIT	RTIYDQQQIR	VFTCLLRLAD	QKGFILPDTQ	GRFRGAGGEA	PKRPA AARED	643
Patient 3 UL30	VARLAGINIT	RTIYDQQQIR	VFTCLLRLAD	QKGFILPDTQ	GRFRGAGGEA	PKRPA AARED	643
			680		700		720
HSV-1 KOS UL30	EERPEEEGED	EDERE EGGGE	REPEGARETA	GRHVGYQGAR	VLDPTSGFHV	NPVVVDFAS	720
HSV-1 17+ UL30	EERPEEEGED	EDERE EGGGE	REPEGARETA	GRHVGYQGAR	VLDPTSGFHV	NPVVVDFAS	720
Patient 1 UL30	EERPEEEGED	EDERE EGGGE	REPEGARETA	GRHVGYQGAR	VLDPTSGFHV	NPVVVDFAS	703
Patient 2 UL30	EERPEEEGED	EDERE EGGGE	REPEGARETA	GRHVGYQGAR	VLDPTSGFHV	NPVVVDFAS	703
Patient 3 UL30	EERPEEEGED	EDERE EGGGE	REPEGARETA	GRHVGYQGAR	VLDPTSGFHV	NPVVVDFAS	703

			740			760		780	
HSV-1 KOS UL30	LYPSI IQAHN	LCFSTLSLRA	DAVAHLEAGK	DYLEIEVGGR	RLFFVKAHVR	ESLLSILLRD		780	
HSV-1 17+ UL30	LYPSI IQAHN	LCFSTLSLRA	DAVAHLEAGK	DYLEIEVGGR	RLFFVKAHVR	ESLLSILLRD		780	
Patient 1 UL30	LYPSI IQAHN	LCFSTLSLRA	DAVAHLEAGK	DYLEIEVGGR	RLFFVKAHVR	ESLLSILLRD		763	
Patient 2 UL30	LYPSI IQAHN	LCFSTLSLRA	DAVAHLEAGK	DYLEIEVGGR	RLFFVKAHVR	ESLLSILLRD		763	
Patient 3 UL30	LYPSI IQAHN	LCFSTLSLRA	DAVAHLEAGK	DYLEIEVGGR	RLFFVKAHVR	ESLLSILLRD		763	
			800			820		840	
HSV-1 KOS UL30	WLAMRKQIRS	RIPQSSPEEA	VLLDKQQAAI	KVVCNSVYGF	TGVQHGLLPC	LHVAATVTTI		840	
HSV-1 17+ UL30	WLAMRKQIRS	RIPQSSPEEA	VLLDKQQAAI	KVVCNSVYGF	TGVQHGLLPC	LHVAATVTTI		840	
Patient 1 UL30	WLAMRKQIRS	RIPQSSPEEA	VLLDKQQAAI	KVVCNSVYGF	TGVQHGLLPC	LHVAATVTTI		823	
Patient 2 UL30	WLAMRKQIRS	RIPQSSPEEA	VLLDKQQAAI	KVVCNSVYGF	TGVQHGLLPC	LHVAATVTTI		823	
Patient 3 UL30	WLAMRKQIRS	RIPQSSPEEA	VLLDKQQAAI	KVVCNSVYGF	TGVQHGLLPC	LHVAATVTTI		823	
			860			880		900	
HSV-1 KOS UL30	GREMLLATRE	YVHARWAAFE	QLLADFPEAA	DMRAPGPYSM	RIIYGDTSI	FVLCRGLTAA		900	
HSV-1 17+ UL30	GREMLLATRE	YVHARWAAFE	QLLADFPEAA	DMRAPGPYSM	RIIYGDTSI	FVLCRGLTAA		900	
Patient 1 UL30	GREMLLATRE	YVHARWAAFE	QLLADFPEAA	DMRAPGPYSM	RIIYGDTSI	FVLCRGLTAA		883	
Patient 2 UL30	GREMLLATRE	YVHARWAAFE	QLLADFPEAA	DMRAPGPYSM	RIIYGDTSI	FVLCRGLTAA		883	
Patient 3 UL30	GREMLLATRE	YVHARWAAFE	QLLADFPEAA	DMRAPGPYSM	RIIYGDTSI	FVLCRGLTAA		883	
			920			940		960	
HSV-1 KOS UL30	GLTAMGDKMA	SHISRALFLP	PIKLECEKTF	TKLLLI AKKK	YIGVIYGGKM	LIKGVDLVRK		960	
HSV-1 17+ UL30	GLTAMGDKMA	SHISRALFLP	PIKLECEKTF	TKLLLI AKKK	YIGVIYGGKM	LIKGVDLVRK		960	
Patient 1 UL30	GLTAMGDKMA	SHISRALFLP	PIKLECEKTF	TKLLLI AKKK	YIGVIYGGKM	LIKGVDLVRK		943	
Patient 2 UL30	GLTAMGDKMA	SHISRALFLP	PIKLECEKTF	TKLLLI AKKK	YIGVIYGGKM	LIKGVDLVRK		943	
Patient 3 UL30	GLTAMGDKMA	SHISRALFLP	PIKLECEKTF	TKLLLI AKKK	YIGVIYGGKM	LIKGVDLVRK		943	
			980		1,000		1,020		
HSV-1 KOS UL30	NNCAF INRTS	RALVDLLFYD	DTVSGAAAAL	AERPAEEWLA	RPLPEGLQAF	GAVLVDAHRR		1020	
HSV-1 17+ UL30	NNCAF INRTS	RALVDLLFYD	DTVSGAAAAL	AERPAEEWLA	RPLPEGLQAF	GAVLVDAHRR		1020	
Patient 1 UL30	NNCAF INRTS	RALVDLLFYD	DTVSGAAAAL	AERPAEEWLA	RPLPEGLQAF	GAVLVDAHRR		1003	
Patient 2 UL30	NNCAF INRTS	RALVDLLFYD	DTVSGAAAAL	AERPAEEWLA	RPLPEGLQAF	GAVLVDAHRR		1003	
Patient 3 UL30	NNCAF INRTS	RALVDLLFYD	DTVSGAAAAL	AERPAEEWLA	RPLPEGLQAF	GAVLVDAHRR		1003	
			1,040		1,060		1,080		
HSV-1 KOS UL30	ITDPERDIQD	FVLTAELSRH	PRAYTNKRLA	HLTVYYKLMA	RRAQVPSIKD	RIPYVIVAQT		1080	
HSV-1 17+ UL30	ITDPERDIQD	FVLTAELSRH	PRAYTNKRLA	HLTVYYKLMA	RRAQVPSIKD	RIPYVIVAQT		1080	
Patient 1 UL30	ITDPERDIQD	FVLTAELSRH	PRAYTNKRLA	HLTVYYKLMA	RRAQVPSIKD	RIPYVIVAQT		1063	
Patient 2 UL30	ITDPERDIQD	FVLTAELSRH	PRAYTNKRLA	HLTVYYKLMA	RRAQVPSIKD	RIPYVIVAQT		1063	
Patient 3 UL30	ITDPERDIQD	FVLTAELSRH	PRAYTNKRLA	HLTVYYKLMA	RRAQVPSIKD	RIPYVIVAQT		1063	
			1,100		1,120		1,140		
HSV-1 KOS UL30	REVEETVARL	AALRELDAAA	PGDEPAPPAA	LPSPAKRPRE	TPSHADPPGG	ASKPRKLLVS		1140	
HSV-1 17+ UL30	REVEETVARL	AALRELDAAA	PGDEPAPPAA	LPSPAKRPRE	TPSHADPPGG	ASKPRKLLVS		1140	
Patient 1 UL30	REVEETVARL	AALRELDAAA	PGDEPAPPAA	LPSPAKRPRE	TPSHADPPGG	ASKPRKLLVS		1123	
Patient 2 UL30	REVEETVARL	AALRELDAAA	PGDEPAPPAA	LPSPAKRPRE	TPSHADPPGG	ASKPRKLLVS		1123	
Patient 3 UL30	REVEETVARL	AALRELDAAA	PGDEPAPPAA	LPSPAKRPRE	TPSHADPPGG	ASKPRKLLVS		1123	
			1,160		1,180		1,200		
HSV-1 KOS UL30	ELAEDPAYAI	AHGVALNTDY	YFSHLLGAAC	VTFKALFGNN	AKITESLLKR	FIPEVWHPPD		1200	
HSV-1 17+ UL30	ELAEDPAYAI	AHGVALNTDY	YFSHLLGAAC	VTFKALFGNN	AKITESLLKR	FIPEVWHPPD		1200	
Patient 1 UL30	ELAEDPAYAI	AHGVALNTDY	YFSHL-----	-----	-----	-----		1152	
Patient 2 UL30	ELAEDPAYAI	AHGVALNTDY	YFSHL-----	-----	-----	-----		1152	
Patient 3 UL30	ELAEDPAYAI	AHGVALNTDY	YFSHL-----	-----	-----	-----		1152	
			1,220						
HSV-1 KOS UL30	DVAARLRAAG	FGAVGAGATA	EETRRMLHRA	FDTLA				1235	
HSV-1 17+ UL30	DVAARLRTAG	FGAVGAGATA	EETRRMLHRA	FDTLA				1235	
Patient 1 UL30	-----	-----	-----	-----				1152	
Patient 2 UL30	-----	-----	-----	-----				1152	
Patient 3 UL30	-----	-----	-----	-----				1152	

Fig. S3. Amino acids alignment for TK and DNA pol. HSV-1 strains were isolated from the three participants and sequenced for genes encoding thymidine kinase (TK, UL23) and DNA polymerase (DNA pol, UL30). Letter in red color indicated changed amino acids in TK (A) and DNA pol (B). HSV-1 KOS and 17syn+ strains were used as references. Only amino-acid changes different from both KOS and 17syn+ simultaneously are considered as ACV resistant mutations.

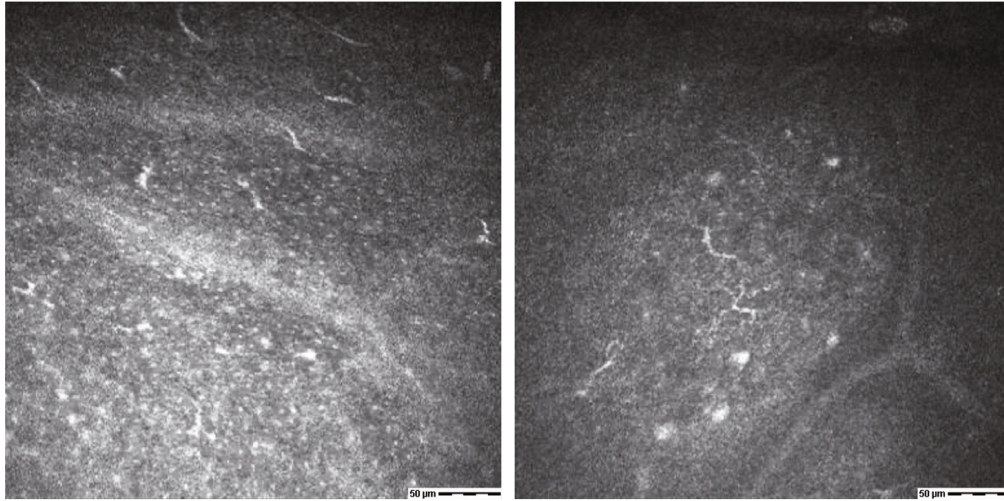


Fig. S4. Postoperative IVCM examination of patient 1. IVCM at 12-month post-injection showed very few corneal subbasal nerves in the transplanted corneal graft of patient 1.

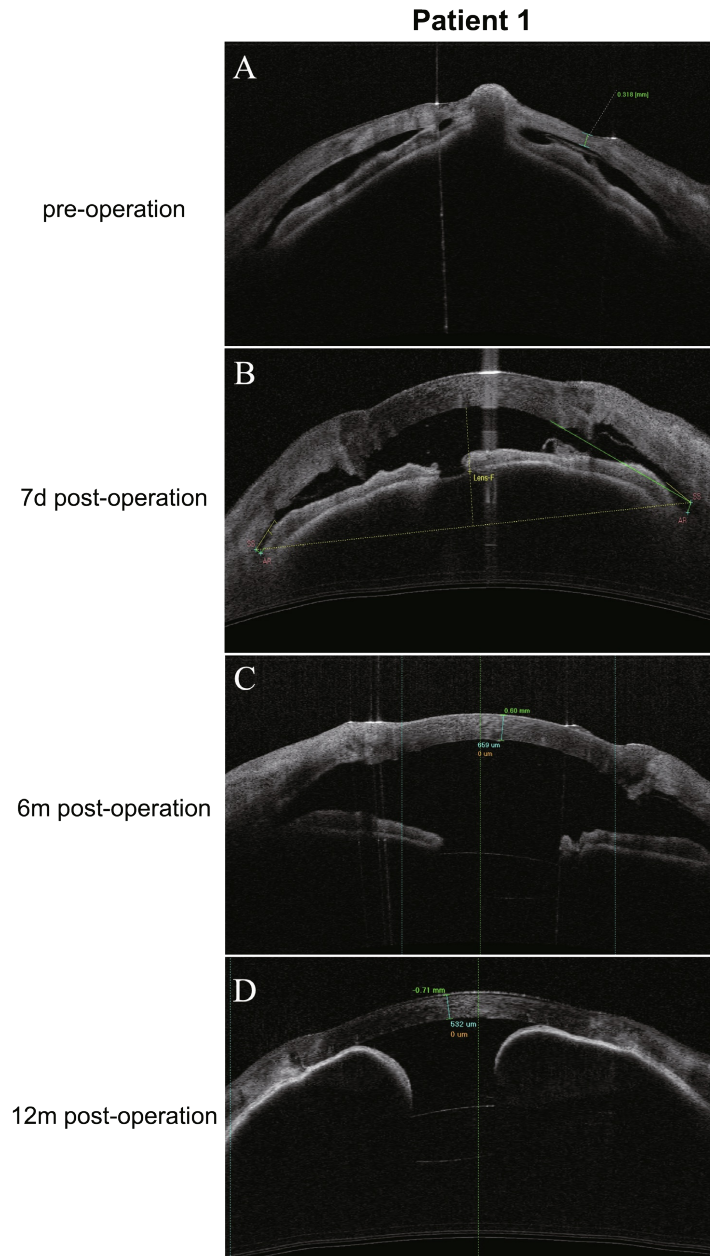


Fig. S5. Time-domain OCT of the anterior segment of patient 1. This image shows the time-domain OCT of the anterior segment of patient 1 at different time points (A-D). Before the injection, there was iris incarceration in the thinning area of the cornea. OCT showed a slightly shallow anterior chamber after 7 days post-injection and an iris adhesion at the 12-month visit, yet the intraocular pressure of patient 1 was within the normal range. Prophylactic laser therapy was conducted to prevent glaucoma.

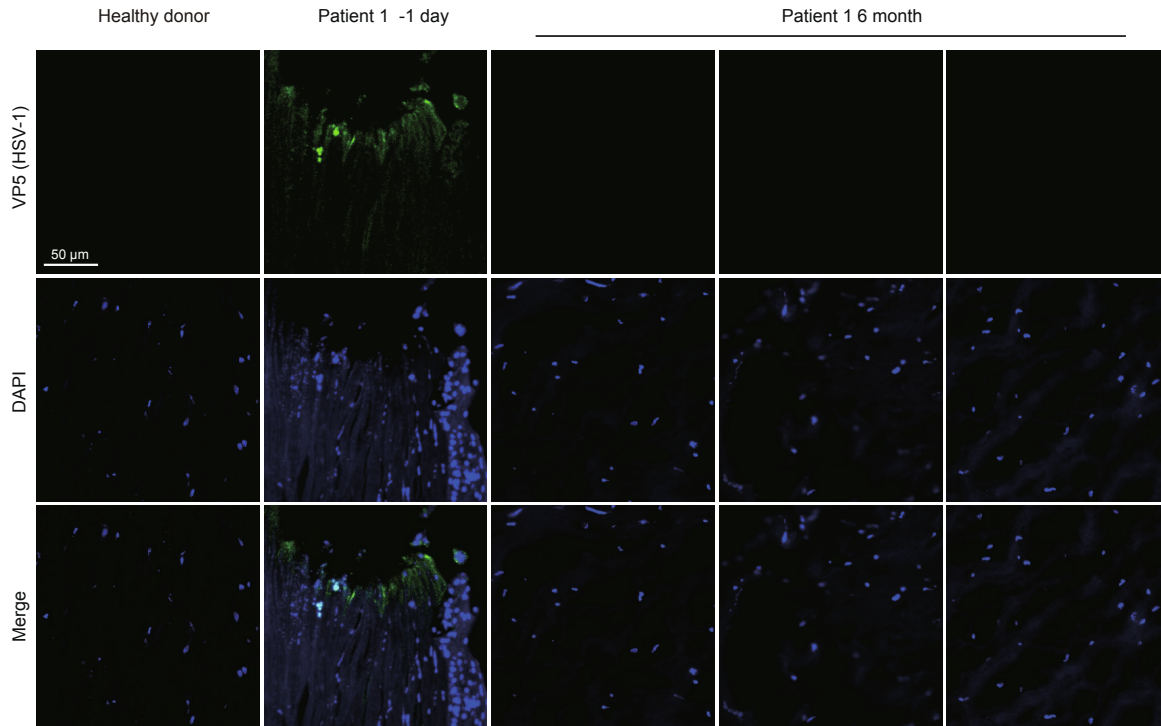


Fig. S6. Fluorescence microscopy analysis of HSV-1 in the removed corneal button. After the second corneal transplantation on the right eye of patient 1 at 6 months after PK, the removed corneal button showed no signs of HSV-1 capsid protein VP5 (green) by the fluorescence microscopy. Scale bars, 50 μm.

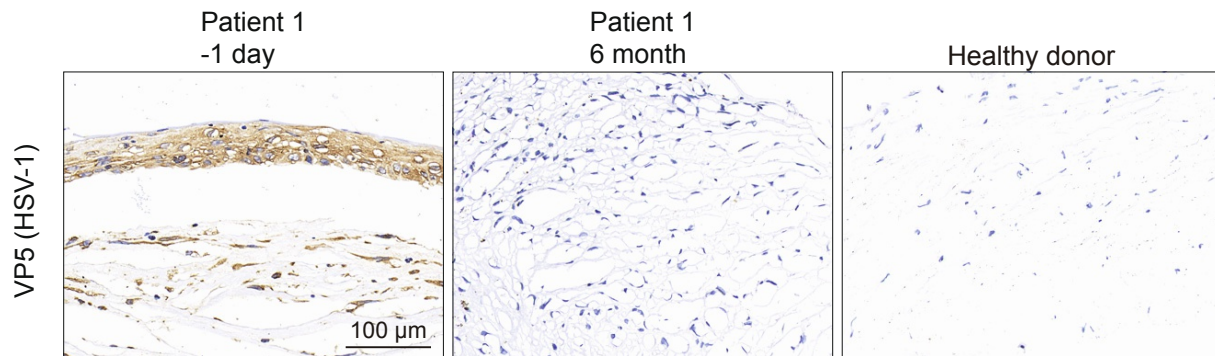


Fig. S7. Immunohistochemistry analysis of HSV-1 in the removed corneal button from patient 1. After the second corneal transplantation on his right eye 6 months after PK, the removed corneal button showed no signs of HSV-1 capsid protein VP5 (brown) by immunohistochemistry analysis.

Patient 2

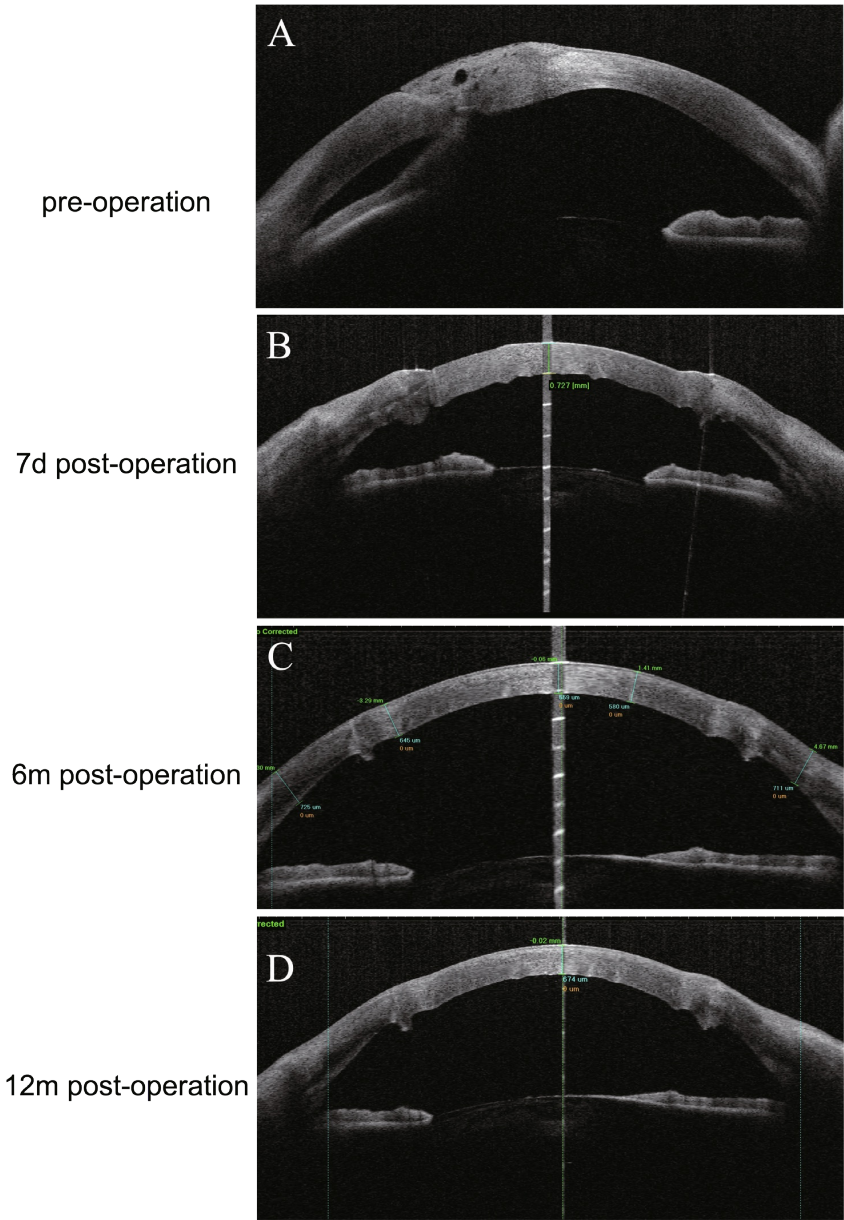


Fig. S8. Time-domain OCT of the anterior segment of patient 2. The pre-injection OCT of the anterior segment showed a possible corneal perforation site in patient 2 (A). Post-injection OCT images (B-D) indicate a deepened anterior chamber, which was maintained for over 12 months after the corneal transplantation.

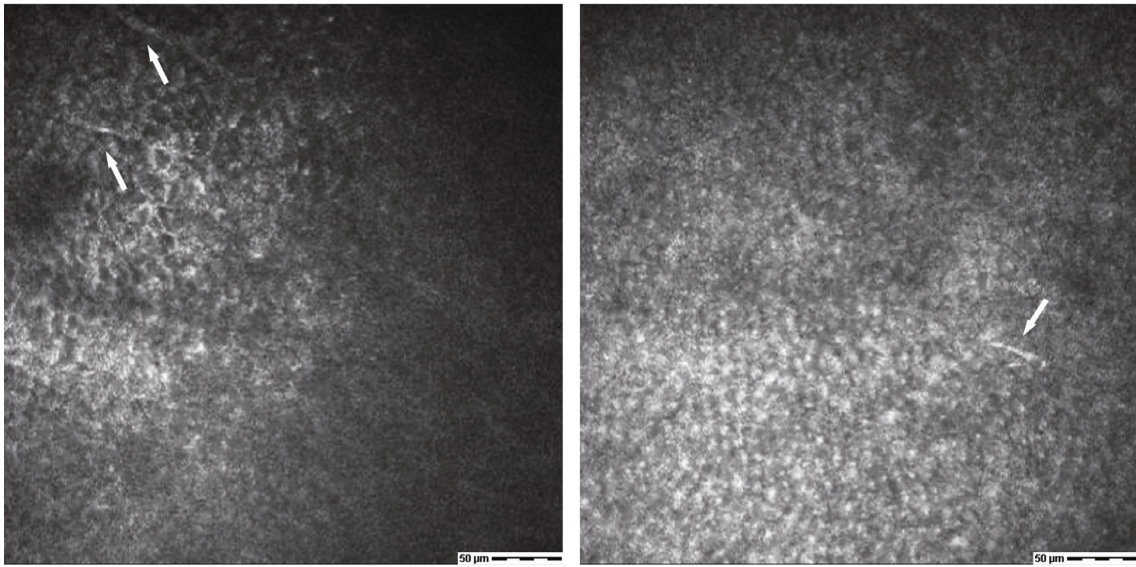


Fig. S9. Postoperative IVCM examination of patient 2. IVCM showed slight corneal nerve regeneration (white arrow) in the transplanted corneal graft at the 12 month-follow-up of patient 2.

Patient 3

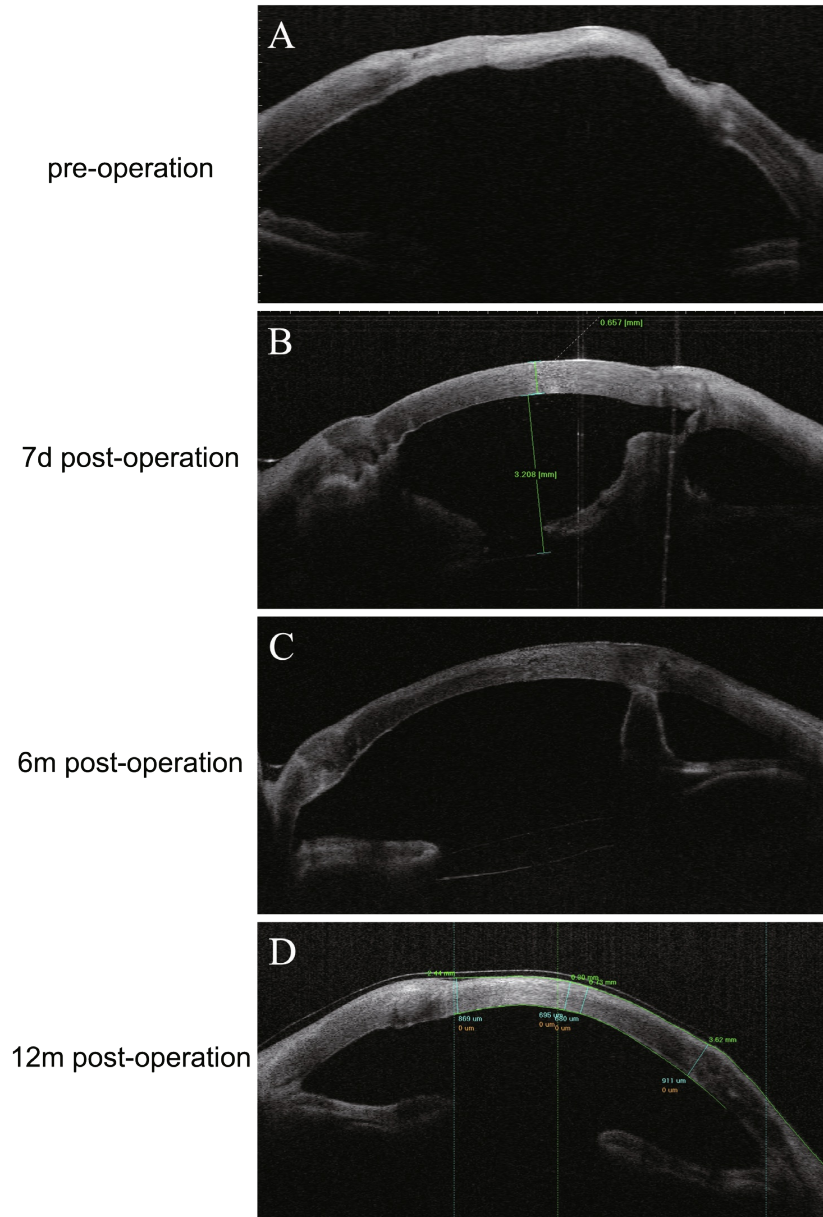


Fig. S10. Time-domain OCT of the anterior segment of patient 3. The pre-injection OCT of the anterior segment showed a corneal perforation channel in patient 3 (A). Post-injection OCT images (B-D) indicate an in-position intraocular lens and a slightly adhered iris to the posterior cornea after PK.

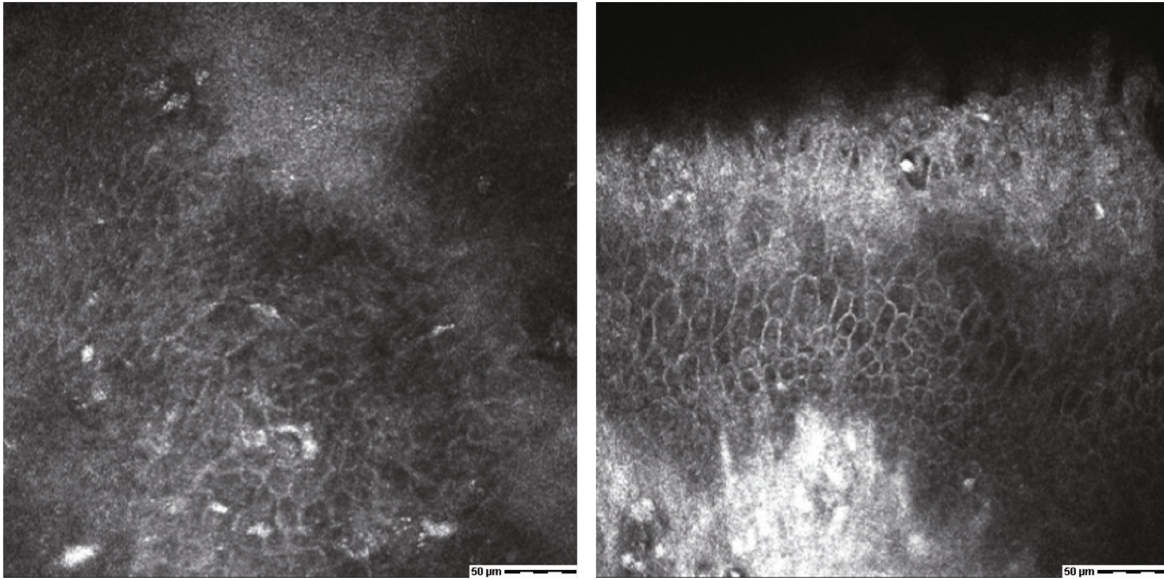


Fig.S11. Postoperative IVCM examination of patient 3. IVCM showed no signs of corneal nerve regeneration at the 12-month follow-up of patient 3. His corneal epithelium density decreased and showed irregular morphologic changes, which indicated the possibility of corneal neurological dystrophy related to HSK.

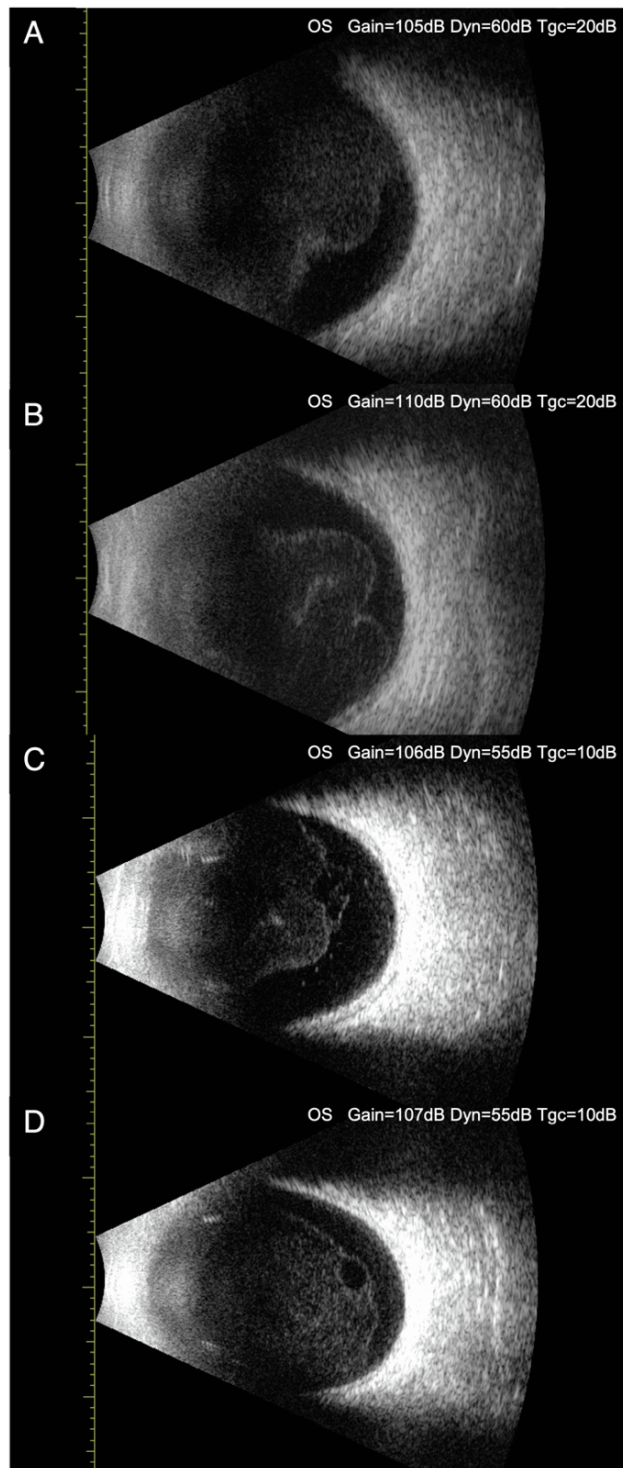


Fig. S12. Postoperative B-scan ultrasonography of patient 3. B-scan ultrasonography of the patient 3 on 7 days (A), 1 month (B), 3 months (C) and 6 months (D) post-injection. Continuous ribbon-like echo was found in the posterior vitreous body, indicating vitreous opacity with posterior detachment.

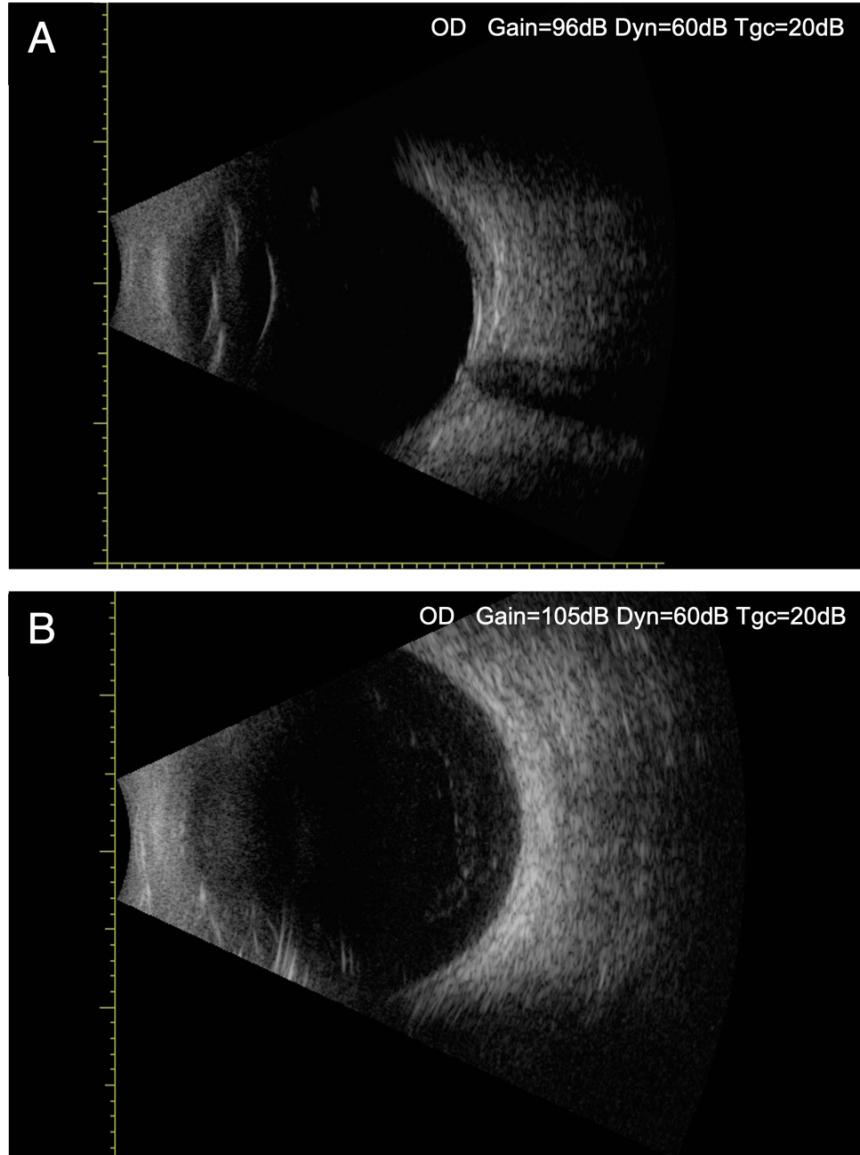


Fig. S13. Postoperative B-scan ultrasonography of patient 2. B-scan ultrasonography results of patient 2 on 6 months (A) and 9 months (B) post-injection showed no remarkable changes in the vitreous body.

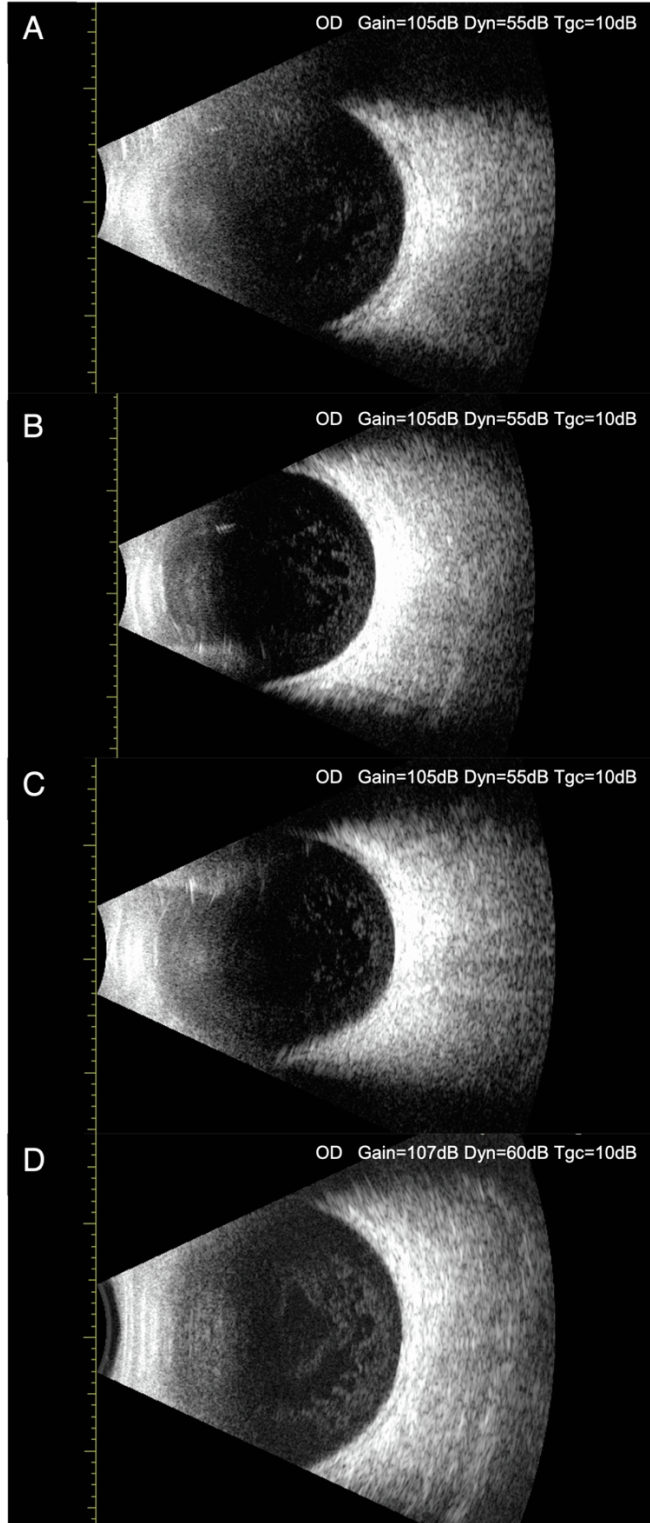


Fig. S14. Postoperative B-scan ultrasonography of patient 1. B-scan ultrasonography of patient 1 on 7 days (A), 1 month (B), 6 months (C) and 12 months (D) post-injection revealed no remarkable changes in the vitreous body.

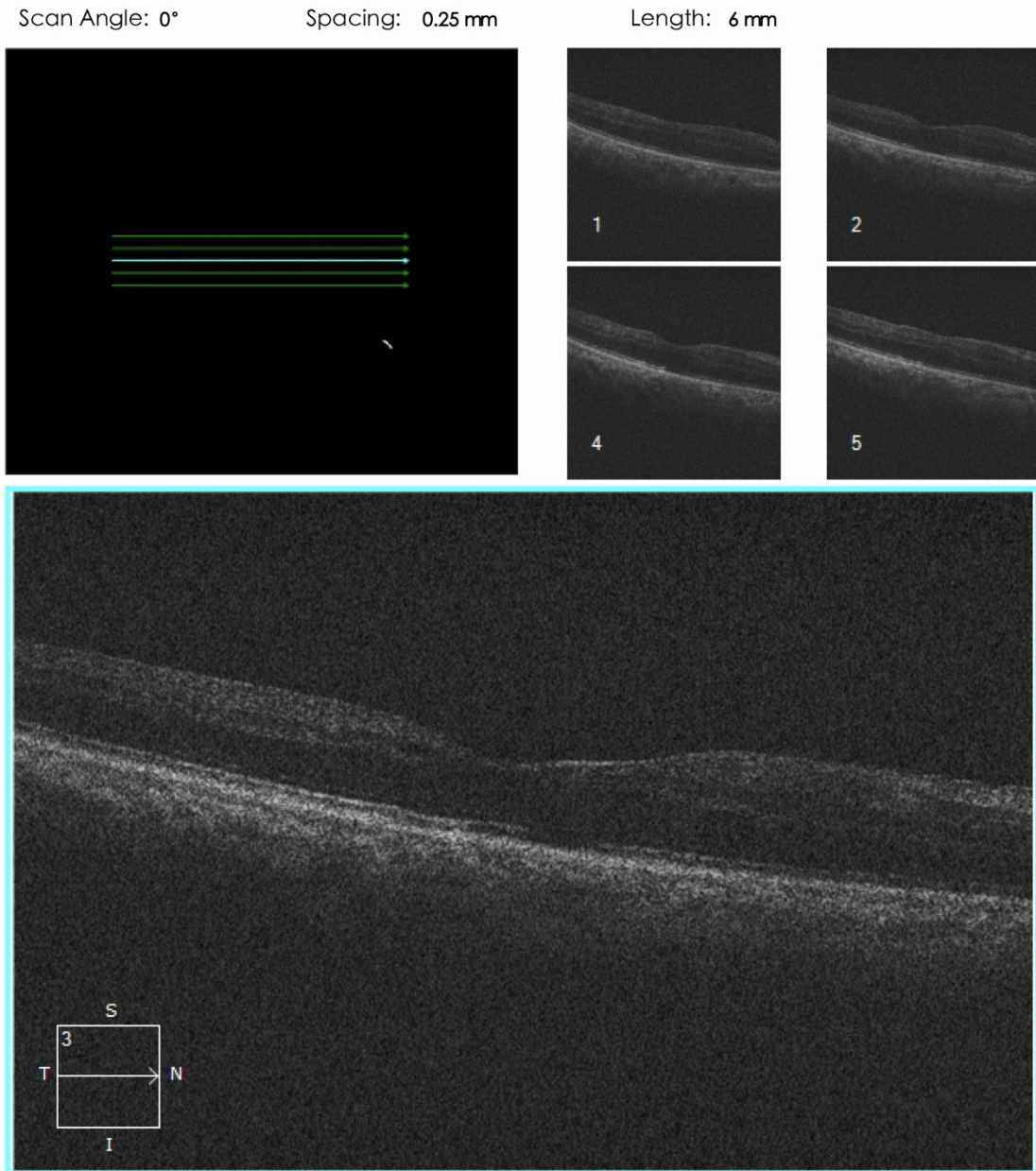


Fig. S15. Spectral-domain OCT of the retina of patient 2. The spectral-domain OCT of patient 2's retina was performed at 6 months post-injection using Cirrus OCT 5000 (Zeiss). The structure of his fundus showed no obvious exception after the administration of HELP.

Scan Angle: 0°

Spacing: 0.25 mm

Length: 6 mm

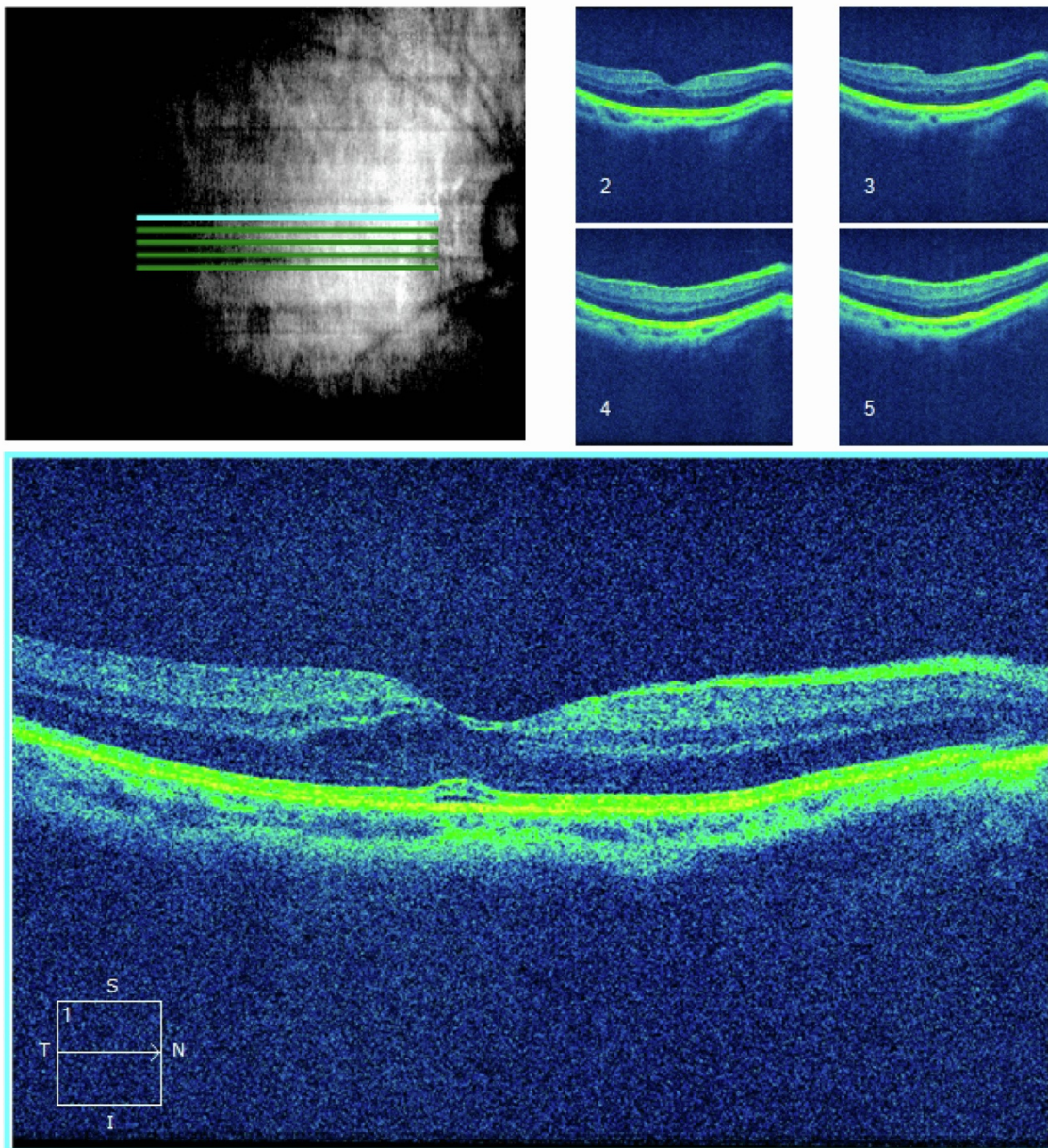
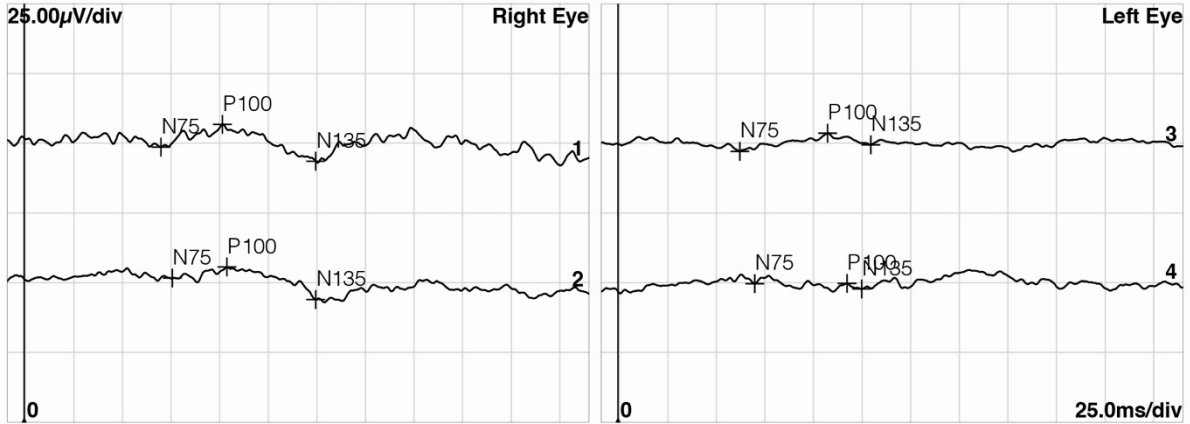


Fig. S16. Spectral-domain OCT of the retina of patient 1. The optical coherence tomography revealed mild center-involved intraretinal fluid and subfoveal fluid in the right eye of patient 1 at six months after the treatment. The ellipsoid zone was intact. We continue to follow up on this situation without any intervention.

A

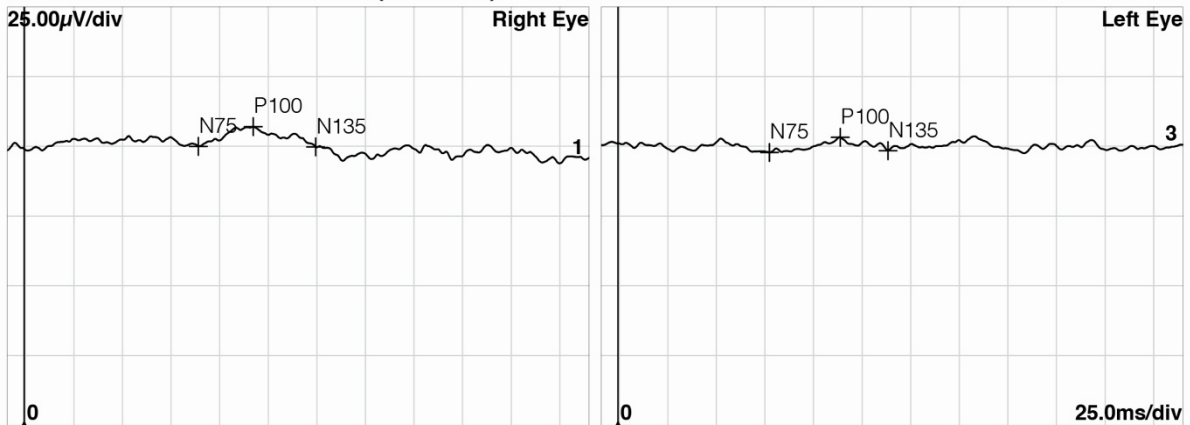
Diagnosis:

1_Pattern-VEP 2.0&1.0 deg (Monitor)



Normals	-	96-109	-	7.08µV-17.7µV	
Channel	N75 [ms]	P100 [ms]	N135 [ms]	N75-P100	P100-N135
1 R1 2,0 deg	70.5	102.2	150.3	8.13µV	13.3µV
2 R1 1,0 deg	76.3	104.5	150.3	3.94µV (!)	11.7µV
3 L1 2,0 deg	62.8	108.0	130.3	6.51µV (!)	4.14µV
4 L1 1,0 deg	70.5	118.0 (!)	125.6	83.5nV (!)	2.01µV

2_Pattern-VEP 30 min&15 min (Monitor)



Normals	-	105-126	-	7.00µV-42.5µV	
Channel	N75 [ms]	P100 [ms]	N135 [ms]	N75-P100	P100-N135
1 R1 30 min	89.8	118.0	150.3	7.13µV	7.29µV
2 R1 15 min					
3 L1 30 min	78.1	114.5	139.1	5.40µV (!)	4.80µV
4 L1 15 min					

B

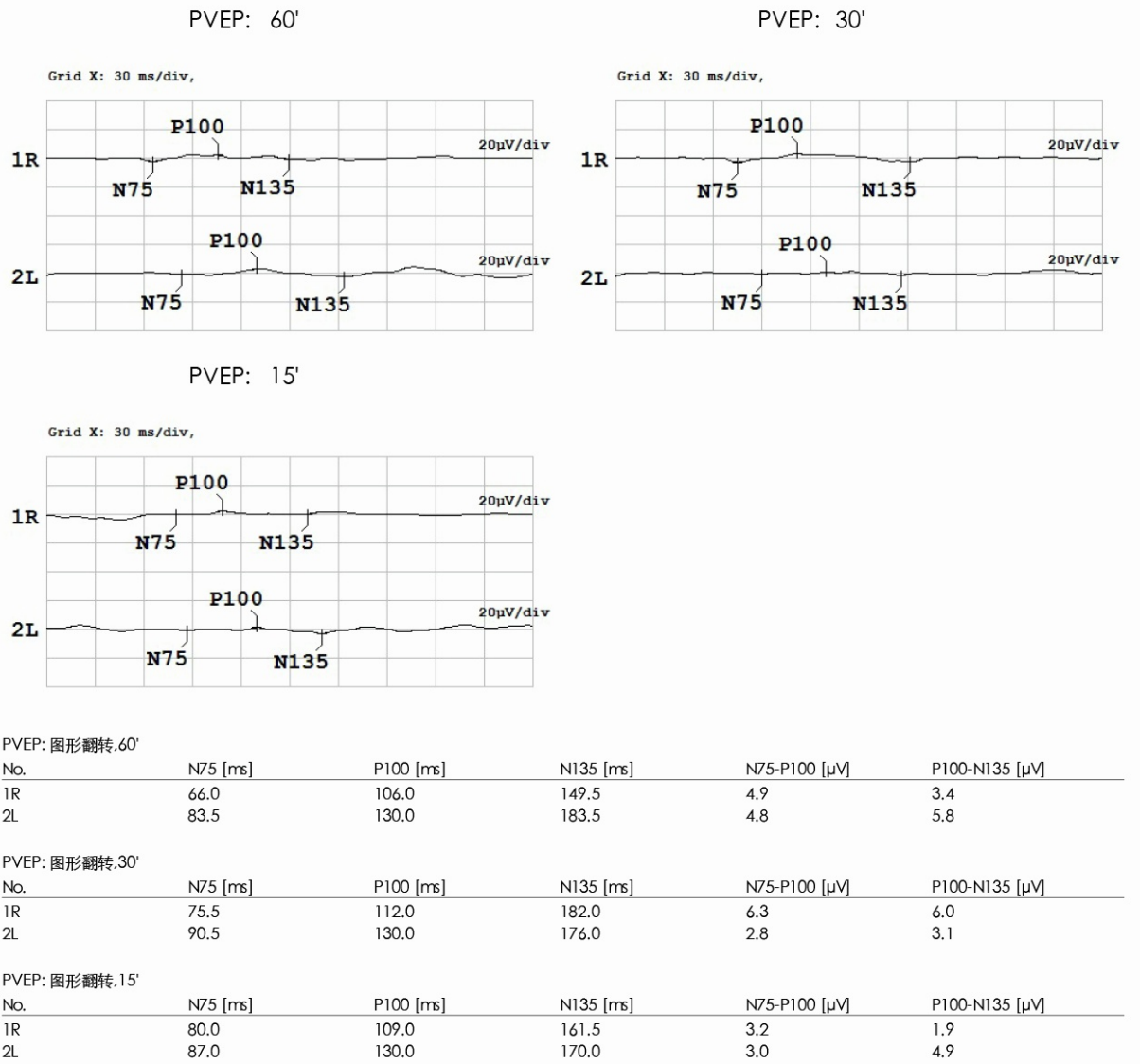
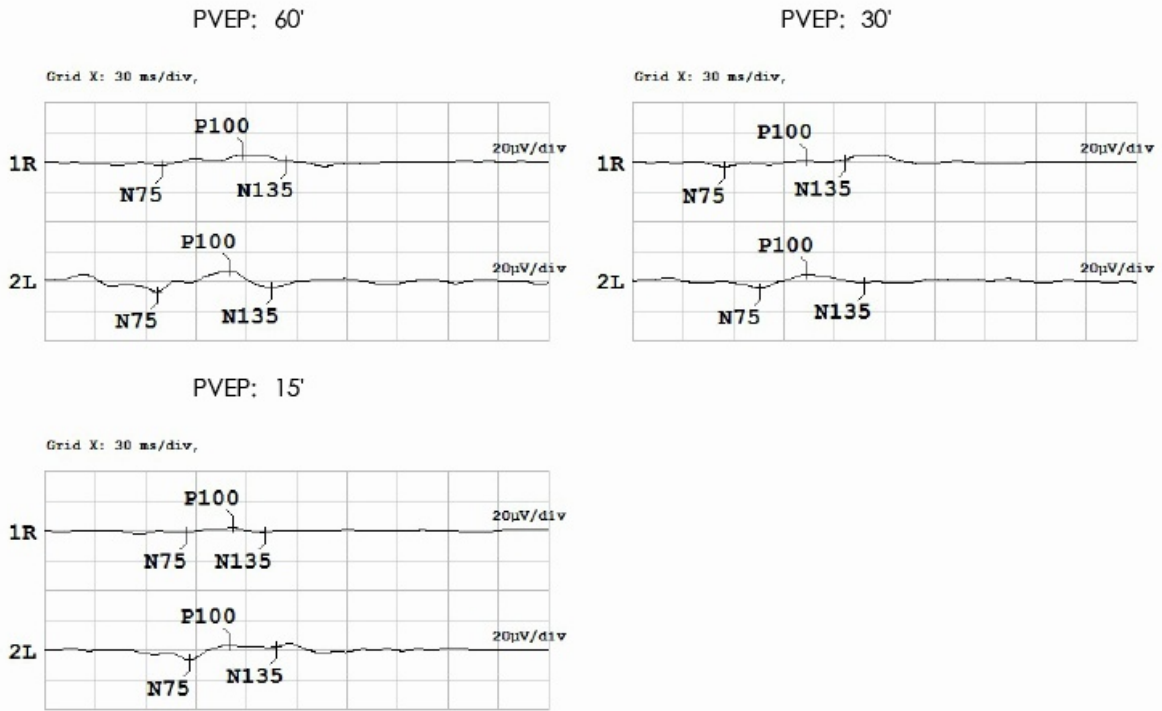


Fig. S17. Retina ERG of patient 3. The light-stimulated electrical activity of the retina indicates no remarkable change in terms of retinal function in patient 3 (A: pre-injection; B: six months post-injection).

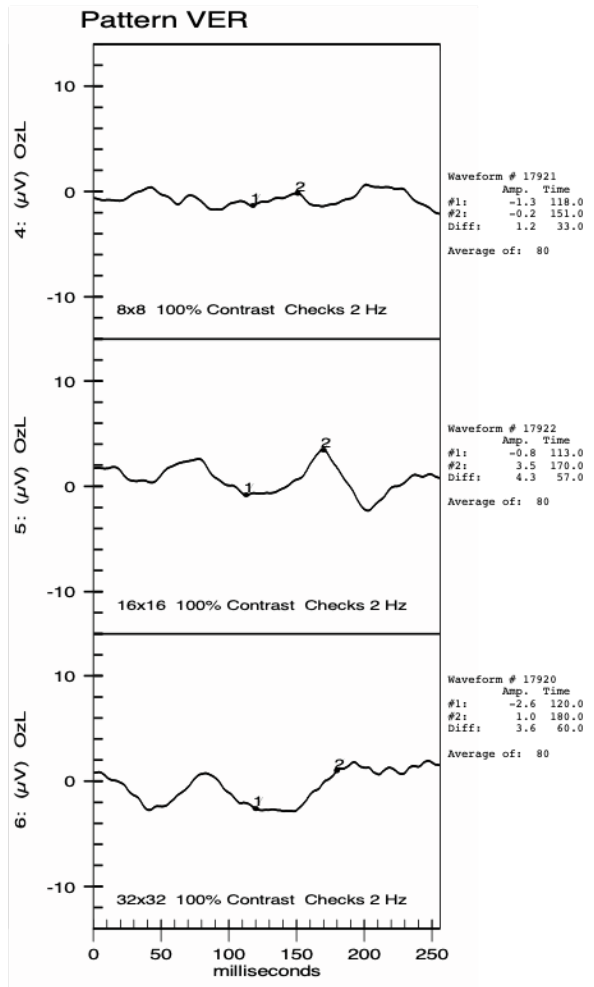
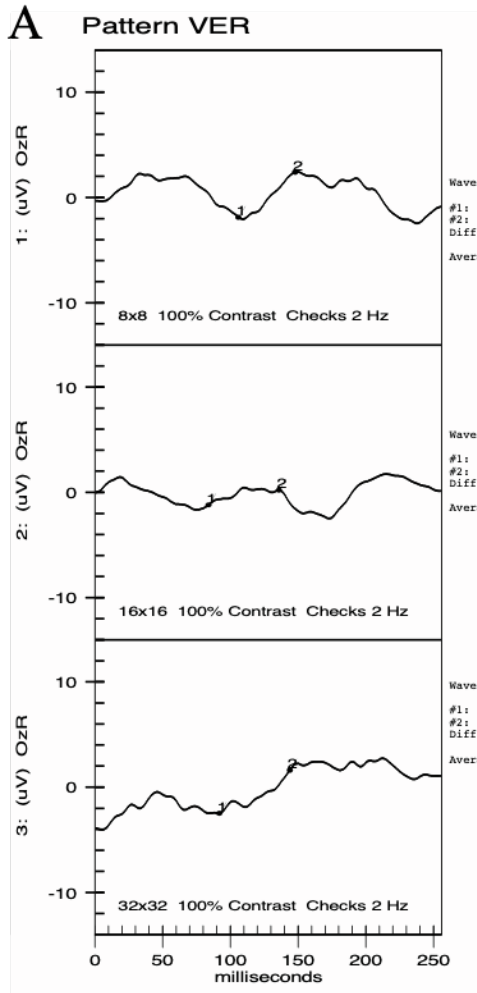


PVEP: 图形翻转.60'					
No.	N75 [ms]	P100 [ms]	N135 [ms]	N75-P100 [μV]	P100-N135 [μV]
1R	70.0	118.5	144.5	7.9	4.2
2L	67.0	110.0	135.0	14.6	11.8

PVEP: 图形翻转.30'					
No.	N75 [ms]	P100 [ms]	N135 [ms]	N75-P100 [μV]	P100-N135 [μV]
1R	55.0	103.5	126.5	4.7	-0.6
2L	76.0	104.0	138.0	9.8	6.4

PVEP: 图形翻转.15'					
No.	N75 [ms]	P100 [ms]	N135 [ms]	N75-P100 [μV]	P100-N135 [μV]
1R	84.0	112.0	131.5	3.9	4.1
2L	86.0	110.0	138.0	10.5	1.2

Fig. S18. Retina ERG of patient 2. The light-stimulated electrical activity of retina indicates no significant change in terms of retinal function in patient 2 twelve months after the treatment.



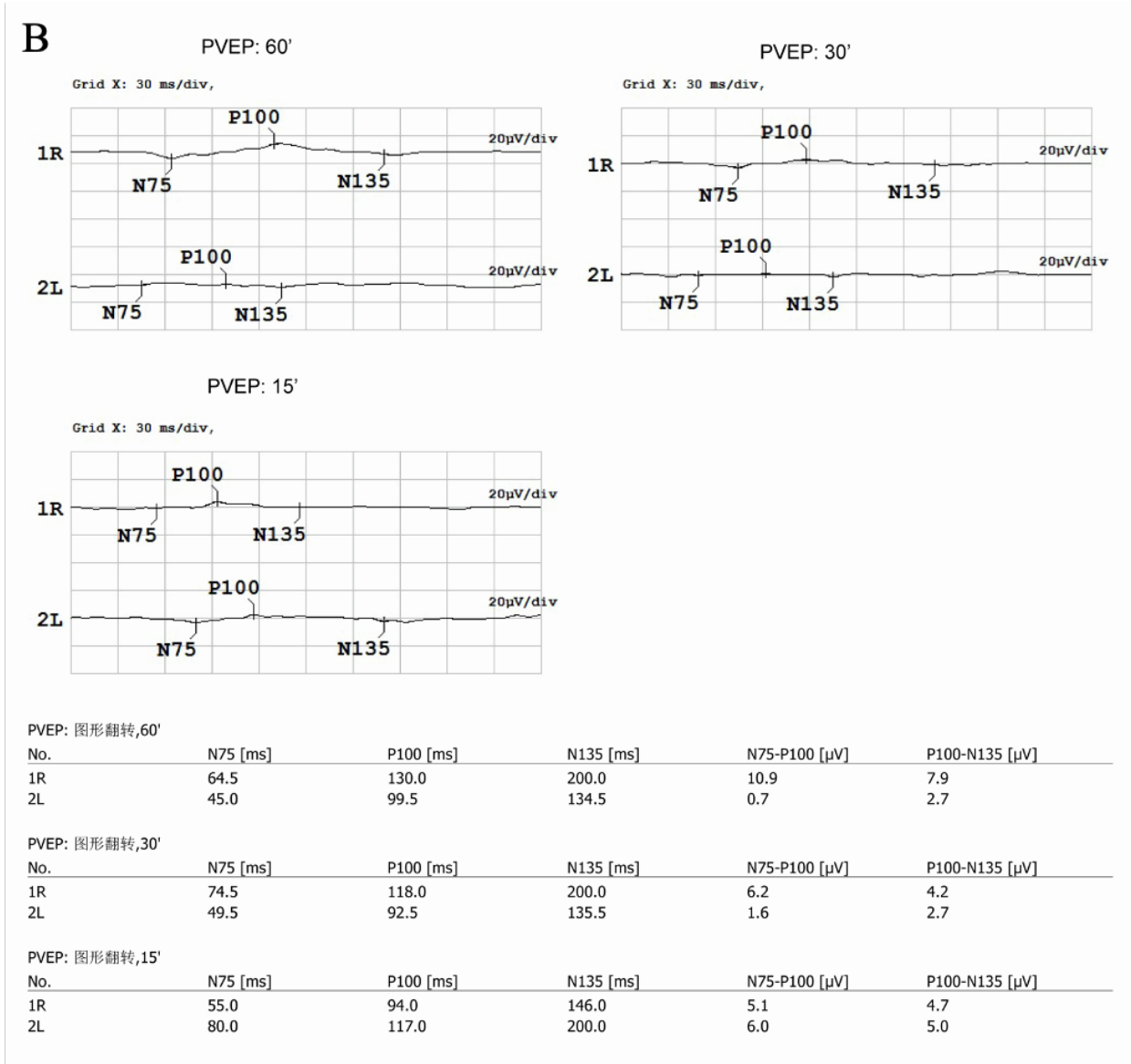


Fig. S19. Retinal ERG examination of patient 1. ERG detected no obvious changes of rod or cone responses to light stimulus in patient 1. (A: pre-injection; B: twelve months post-injection)

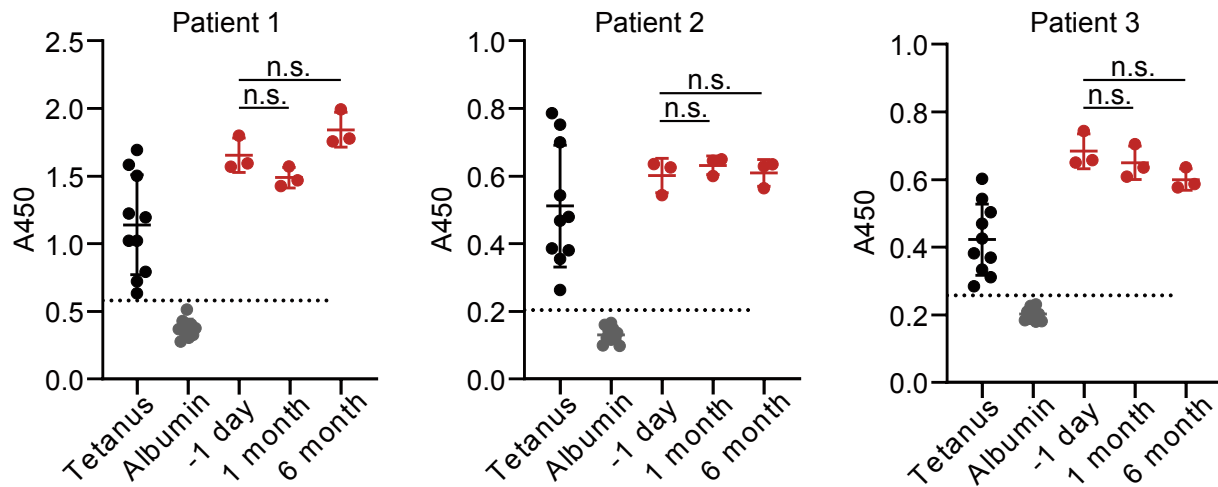


Fig. S20. ELISA results detect antibodies against SpCas9. Tetanus toxoid and human albumin in the sera from different donors served as a positive and negative control, respectively. The Cas9-specific antibodies were determined at different time points. The change in Cas9 antibody levels before and after HELP administration was insignificant. All samples above the dotted line were considered antibody-positive. The dotted line represents the mean absorbance of the negative control, human albumin, plus three s.d. from the mean. Data and error bars represent mean \pm s.e.m.; n.s., non-significant; unpaired two-tailed Student's t-tests.

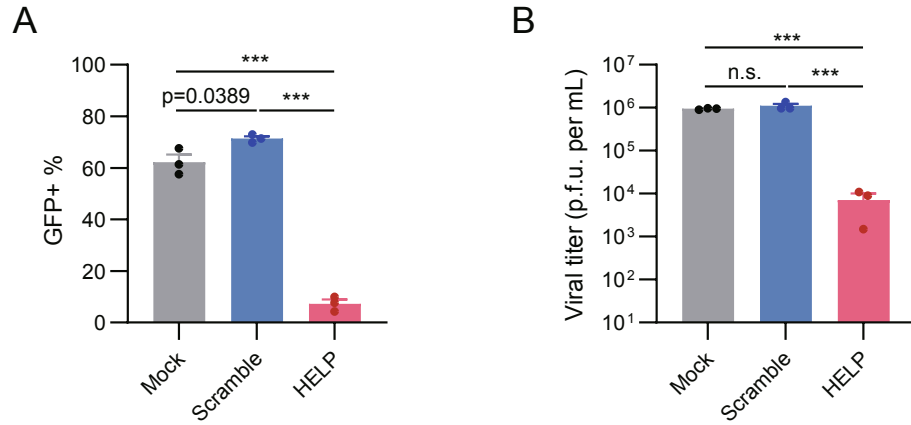


Fig. S21. In vitro antiviral activity of the clinical grade HELP. 4×10^4 293T cells were seeded in a 48-well plate and transduced with 400 ng of HELP or scramble control on the following day. The medium was refreshed 12 h post-infection (h.p.i.). 24 h after transduction, cells were infected with HSV-1-GFP at an MOI of 1. The cells and supernatants were harvested at 24 and 48 h.p.i. for flow cytometry (**A**) and plaque assay (**B**), respectively. 293T cells were transduced with HELP for 24 h and then infected with HSV-1-GFP. $n=3$ biologically independent samples. Data and error bars represent mean \pm s.e.m.; n.s., non-significant; *** $P<0.001$; unpaired two-tailed Student's t-tests.

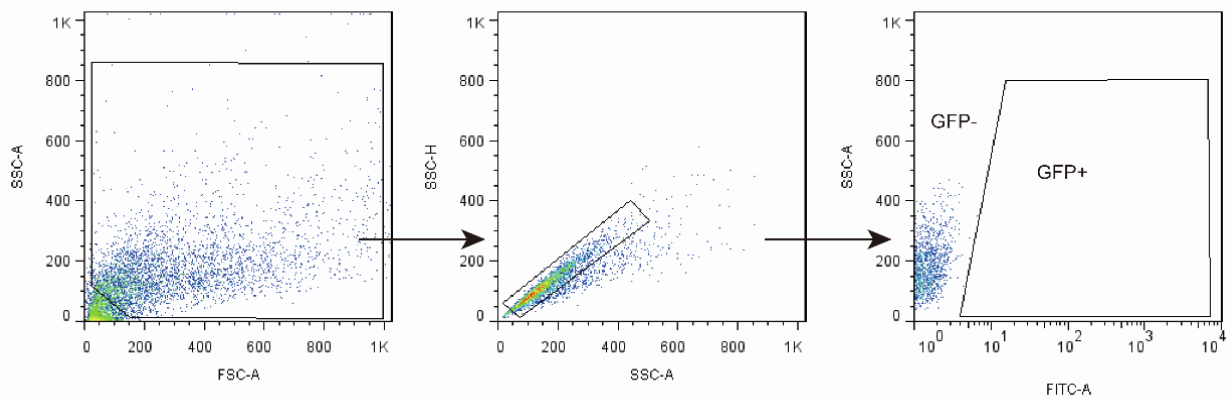


Fig. S22. Gating strategies used for cell sorting analysis. Gate strategy to sort GFP positive cells from HSV-1-GFP infected 293T cells on supplementary Fig. S21A.

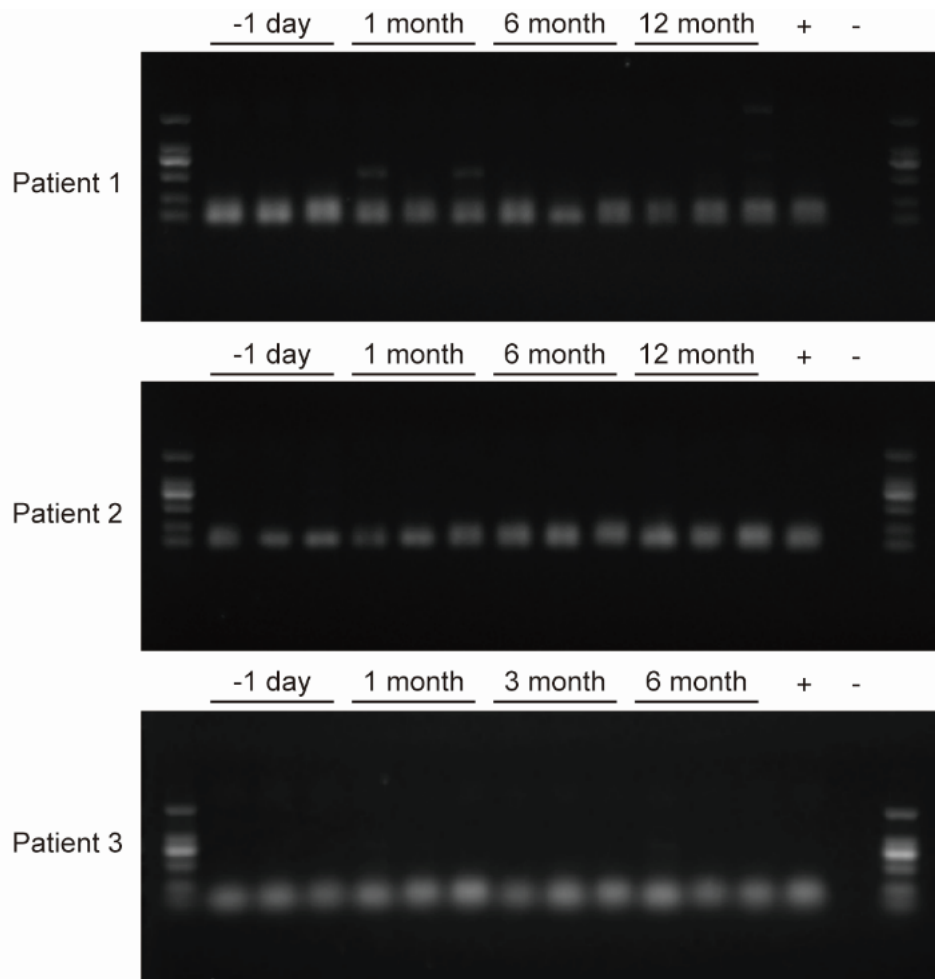


Fig. S23. Validity of patient samples. GAPDH gene in the tear swab of patients was tested by PCR to verify the validity of patient samples. Eye swab samples of 1 day pre-injection, 1 month, 6 months, 12 months post-injection of patient 1 & 2, and samples of 1 day pre-injection, 1 month, 3 months, 6 months post-injection of patient 3 were used as templates for PCR followed by nucleic acid gel electrophoresis. The results showed that GAPDH was positive in all samples, indicating that the swabs were valid.

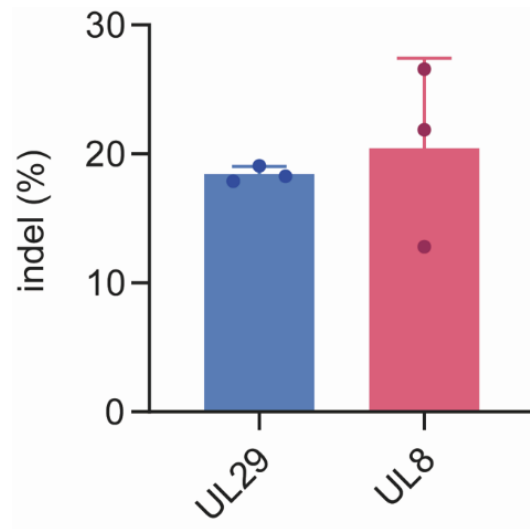
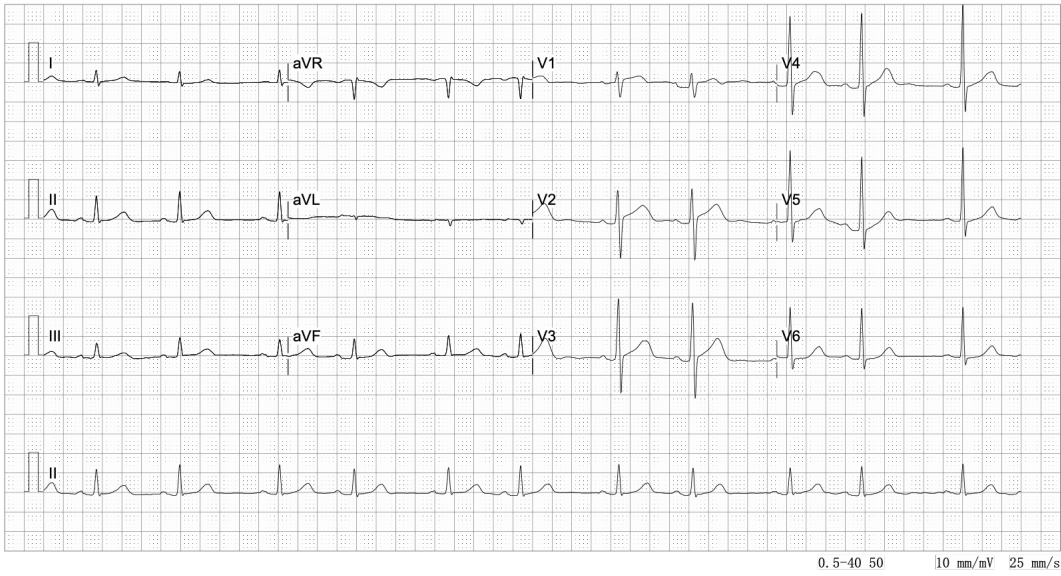


Fig. S24. Gene editing efficiency of the clinical grade HELP. TIDE analysis of indels in the HSV-1 genome. 2×10^4 293T cells were incubated with 200 ng P24 HELP, then infected with HSV-1 with MOI=1 24 h later. Virus DNA was collected at 2 days post-infection for Sanger sequencing. n=3 biologically independent samples.

A

HR: 67 bpm QRS duration: 0.09s
P-R interval: 0.16s Q-T interval: 0.42s
QTc: 0.44 Axis: 66 °
V1R+V5S: 0.71mV V5R+V1S: 2.01mV



B

HR: 63 bpm QRS duration: 0.08s
P-R interval: 0.17s Q-T interval: 0.41s
QTc: 0.42 Axis: 61 °
V1R+V5S: 0.65mV V5R+V1S: 2.51mV

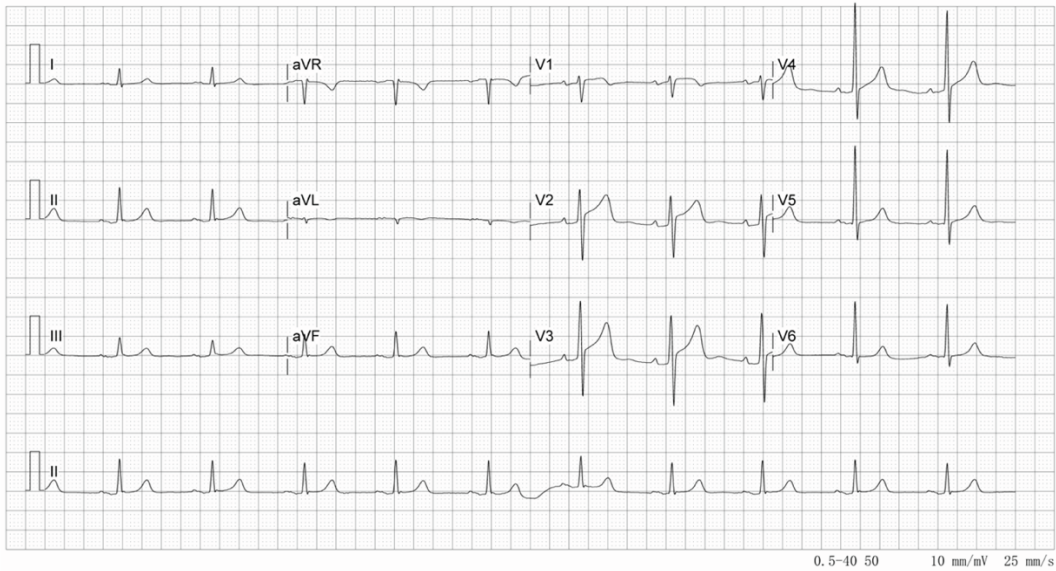
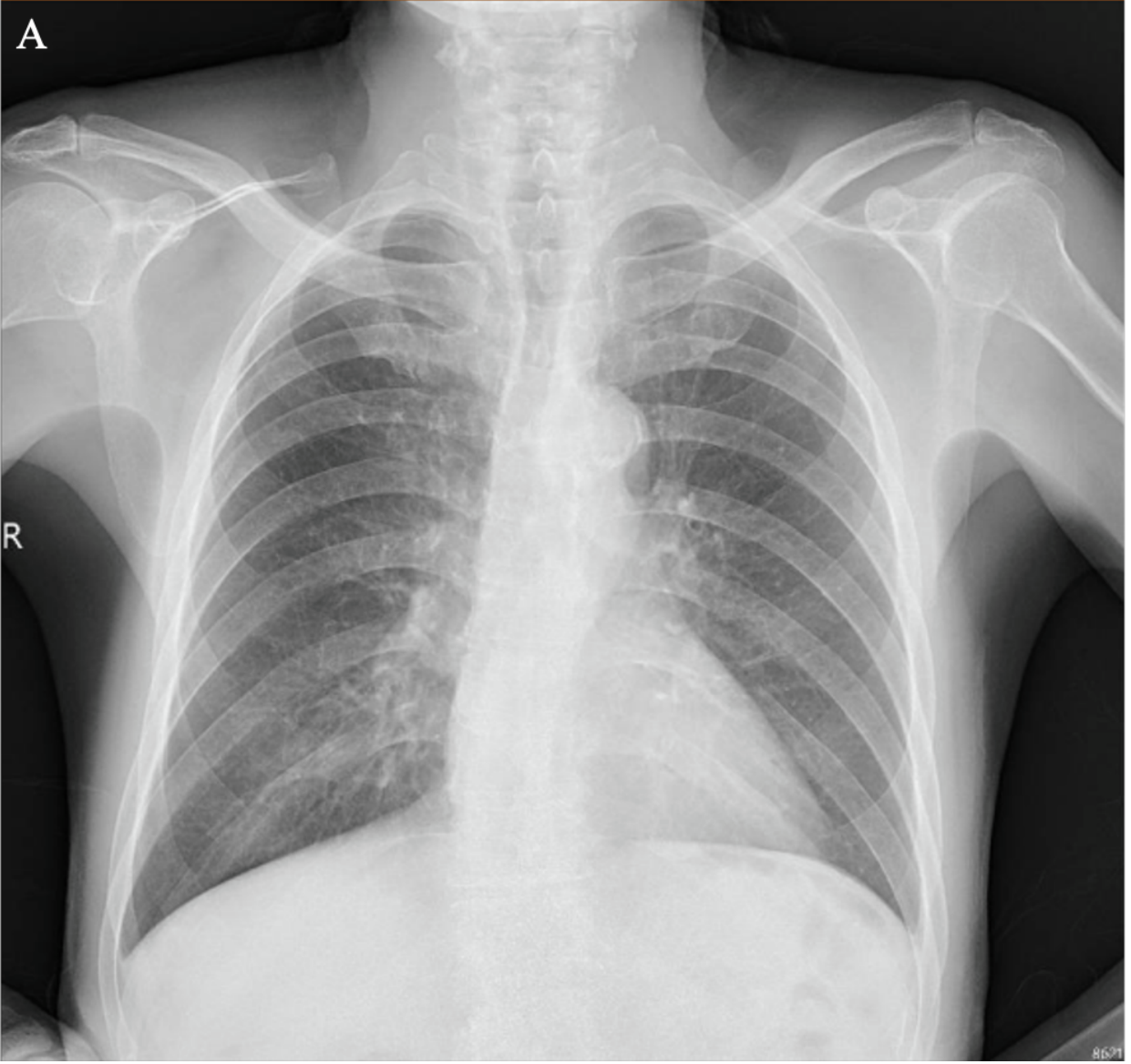


Fig. S25. The ECG examination of patient 1. The pre- and postoperative ECG of patient 1 was unremarkable. (A: pre-injection; B: twelve months post-injection)



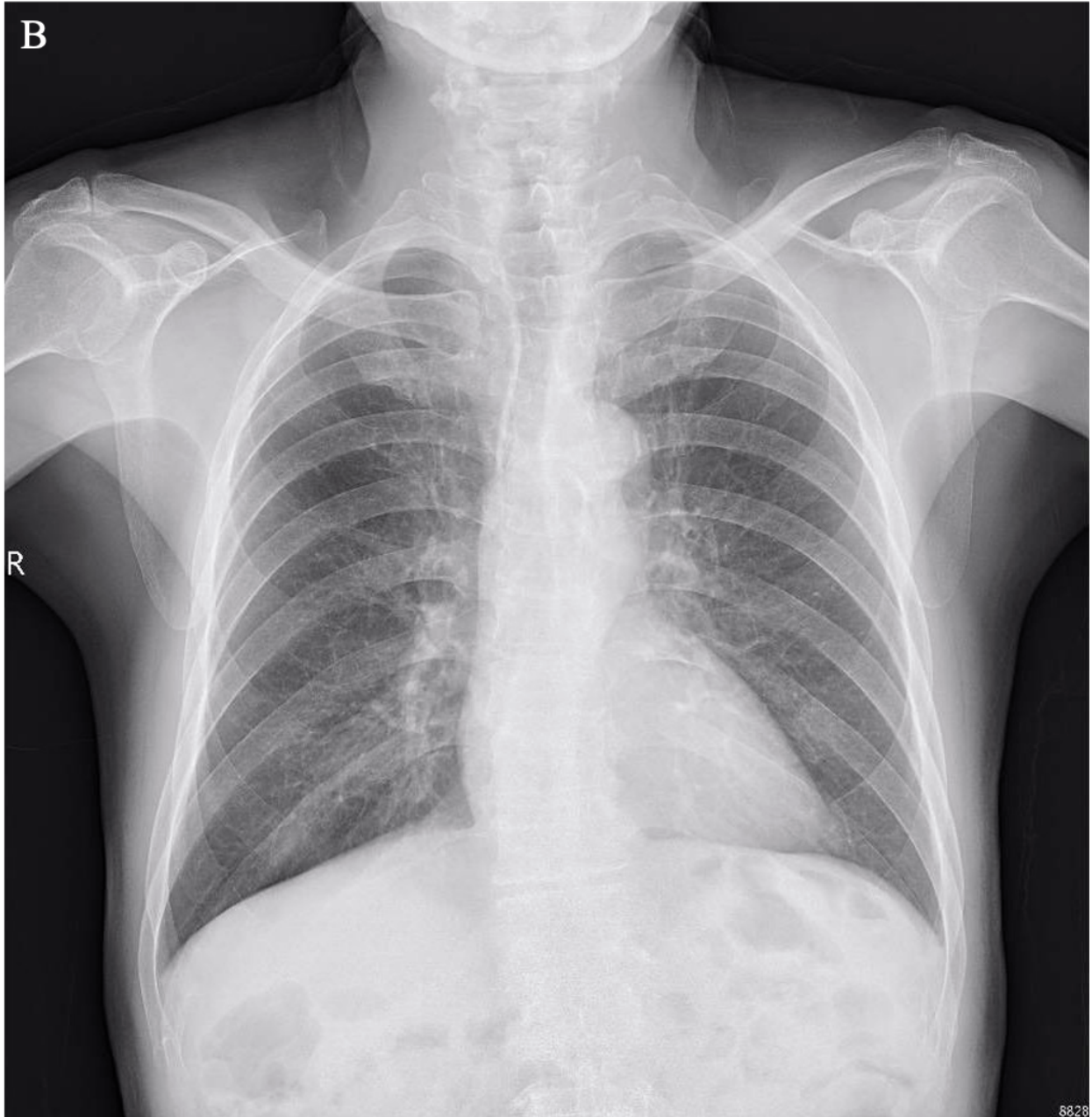


Fig. S26. Chest X-ray examination of patient 1. The Chest X-ray of patient 1 showed no remarkable changes before (A) and twelve months (B) after the injection.

HR: 70 bp QRS duration: 0.08s
P-R interval: 0.17s Q-T interval: 0.35s
QTc: 0.38 Axis: 21 °
V1R+V5S: 0.67mV V5R+V1S: 2.88mV

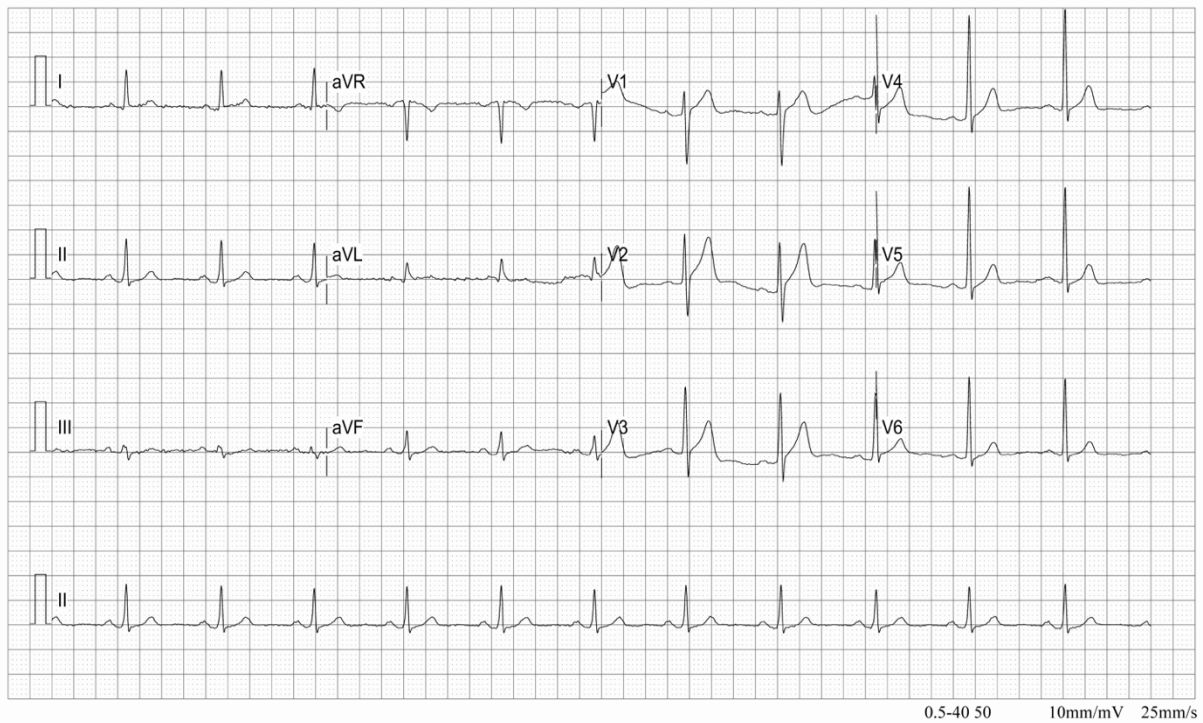


Fig. S27. The ECG of patient 2. The ECG of patient 2 showed counterclockwise transposition, indicating a possibly hypertrophic in the left ventricle. Slightly hypertrophy of the ventricle is not reckoned as a contraindication for corneal transplant surgery.

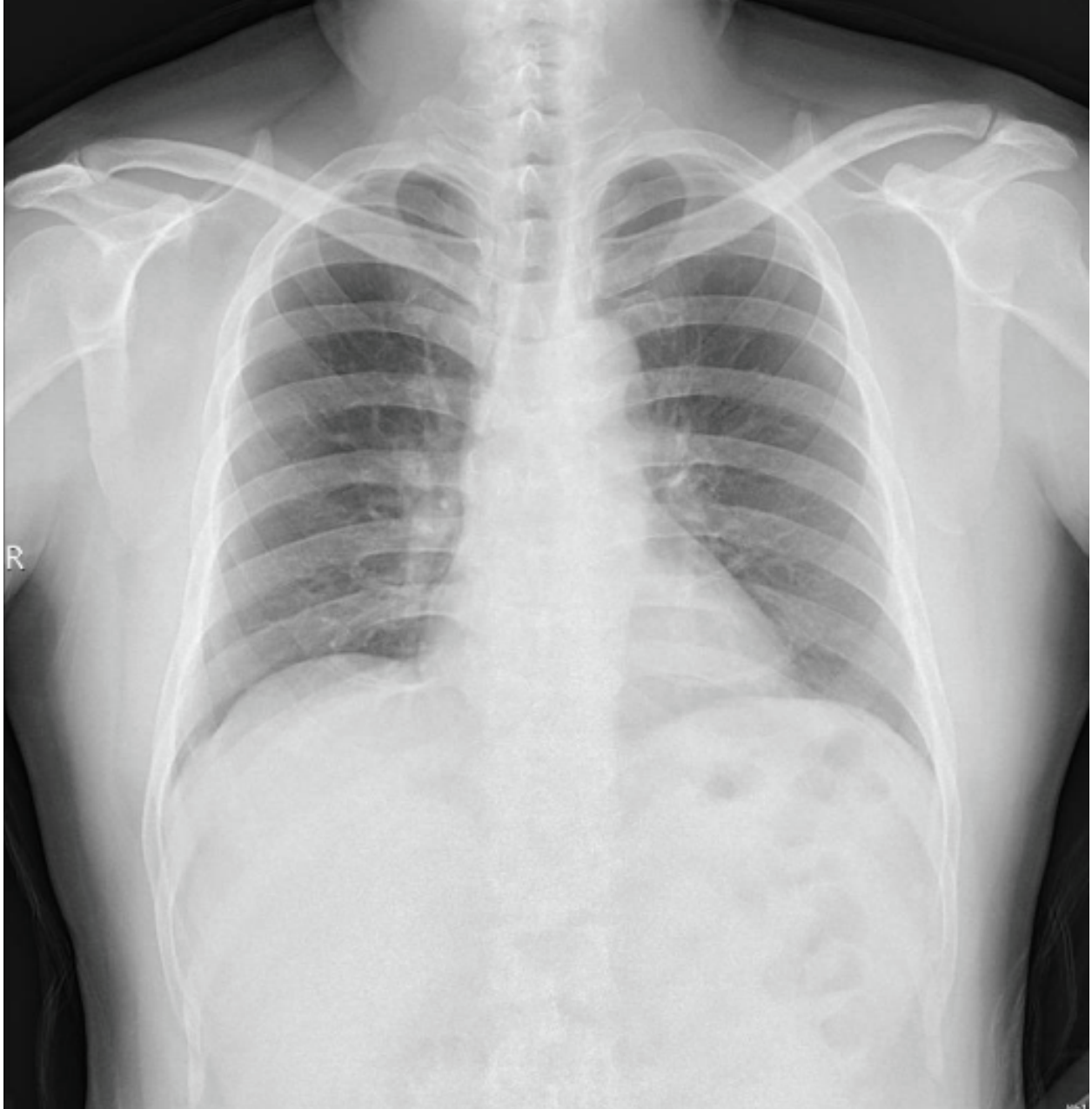


Fig. S28. Chest X-ray film of patient 2. The chest X-ray result of patient 2 was unremarkable.

HR: 69 bp QRS duration: 0.08s
P-R interval: 0.20s Q-T interval: 0.39s
QTc: 0.42 Axis: 54 °
V1R+V5S: 0.35mV V5R+V1S: 1.74mV

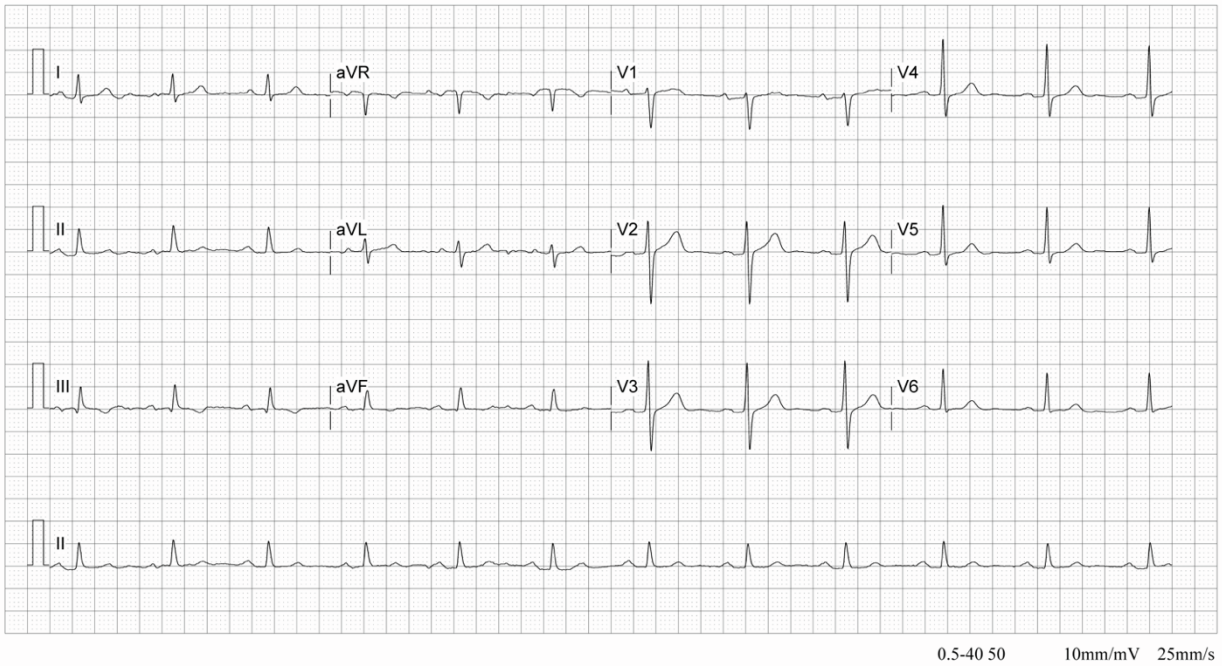


Fig. S29. The ECG examination of patient 3. The pre-operative ECG of patient 3 was unremarkable.



Fig. S30. Chest X-ray film of patient 3. The chest X-ray result of patient 3 was unremarkable.

Table S1. Visual acuity, intraocular pressure and virus tests.

		1 day	7 days	1 month	2 months	3 months	6 months	12 months
		pre-injection	post-injection	post-injection	post-injection	post-injection	post-injection	post-injection
Patient 1	Best-corrected visual acuity	Light perception	Finger count	Finger count	Finger count	Finger count	20/100	20/100
	Intraocular pressure (mmHg)	Undetectable	12.0	10.4	16	15.3	8	21.3
	HSV-1 tests (Ct value)	21.35 (Cornea) 28.37 (Aqueous) 30.55*(Tear swab)	- 24.09(Tear swab) -	28.37(Tear swab) 31.49(Tear swab) 31.08(Tear swab)	- - -	- - -	- - -	- - -
Patient 2	Best-corrected visual acuity	Hand motion	20/250	20/167	20/100	20/67	20/133	20/133
	Intraocular pressure (mmHg)	Undetectable	11.0	16.3	16.4	12.4	7.3	15.0
	HSV-1 tests (Ct value)	26.34 (Cornea) 36.50 (Aqueous) 35.01*(Tear swab)	- - -	- - -	- - -	- - -	- - -	- - -
Patient 3	Best-corrected visual acuity	Hand motion	Hand motion	Hand motion	Hand motion	Hand motion	Hand motion	Finger count
	Intraocular pressure (mmHg)	Undetectable	n.a.	15.0	24.1	18.5	18.1	19.3
	HSV-1 tests (Ct value)	34.9 (Cornea) - (Aqueous) 29.5 (Tear swab)	- - -	- - -	- - -	- - -	- - -	- - -

*Mean HSV-1 titer (Ct value) of three simultaneously sampled tear swabs; n.a., not available; -, Ct value undetectable.

Table S2. List of adverse events.

Patient	Adverse Event	Start Date	End Date	Placebo Related	Severity	Outcome	Treatment
1	corneal edema	11/2020	11/2020	possibly related	mild	resolved	concomitant medication
	conjunctival injection	11/2020	11/2020	unlikely to be related	mild	resolved	concomitant medication
	hyphema	11/2020	11/2020	unrelated	mild	resolved	none
	neurotrophic keratitis	5/2021	/	unrelated	mild	unresolved	concomitant medication
	uncontrolled corneal ulcer	9/2021	11/2021	unrelated	moderate	resolved	penetrating keratoplasty
	cataract	n.a.	11/2021	unrelated	mild	resolved	cataract surgery
	secondary glaucoma	10/2021	12/2021	unrelated	mild	resolved	concomitant medication
2	corneal edema	1/2021	1/2021	possibly related	mild	resolved	concomitant medication
	conjunctival injection	1/2021	1/2021	unlikely to be related	mild	resolved	concomitant medication
	itching	2/2021	3/2021	unrelated	mild	resolved	concomitant medication
	endophthalmitis	7/2021	7/2021	unrelated	moderate	resolved	vitrectomy and antibiotic injection
	cataract	n.a.	/	unrelated	mild	unresolved	none
3	corneal edema	5/2021	5/2021	possibly related	mild	resolved	concomitant medication
	conjunctival injection	5/2021	5/2021	unlikely to be related	mild	resolved	concomitant medication
	graft rejection	8/2021	10/2021	unrelated	mild	resolved	concomitant medication
	secondary glaucoma	7/2021	8/2021	unrelated	mild	resolved	concomitant medication
	cataract	n.a.	/	unrelated	mild	unresolved	none

Table S3. p24 antibody test.

Positive Index*	Positive control	Negative control	-1 day	1 month	3 months	6 months
Patient 1	15.3	0.49	0.45	0.45	0.45	0.45
Patient 2	13.4	0.51	0.50	0.44	0.46	0.44
Patient 3	11.62	0.49	0.46	0.49	0.5	0.47

* Calculate the mean absorbance values (OD450) for Negative Control using formula:
OD mean (negative control) = (OD (negative control 1) + OD (negative control 2)) / 2.
Calculate the cut-off value: Cut-off = OD mean (negative control) + 0.05
Calculate Positivity Index for each sample:
Positivity Index = mean OD 450 (sample) / Cut-off value.
If Positivity Index value is greater than 1.1, the result is **Positive**.
If Positivity Index value is less than 0.9, the result is **Negative**.

Table S4. Sequencing information on raw data.

Sample	Yield (Mb)	Depth (x)	Reads	Base\geqQ30 (%)	Insert size (bp)
WT	192,354	64	1,282,361,462	91.60%	420.725
HELP	185,126	62	1,234,177,196	90.93%	403.405

Note:

Depth (x): The average sequencing depth (Yield bases/Human genome size).

Yield (Mb): The number of bases in raw data.

Reads: The number of paired-end reads.

Base \geq Q30 (%): The percentage of bases with a quality score of 30 or higher. Q30 means that the sequencing error rate of a base is 0.001.

Insert size (bp): The average size of sample sequencing fragments.

Table S5. The coverage statistics of the sequence alignment.

Sample	Mapping rate	Properly mapped	Fraction of covered with $\geq 20x$	Fraction of covered with $\geq 0.2 * \text{Mean}$	Fraction of CDS regions covered with $\geq 20x$
WT	92.254%	89.592%	97.168%	98.809%	98.55%
HELP	92.537%	89.771%	97.095%	98.831%	98.50%

Note:

Mapping rate (%): The percentage of total reads mapping to the reference genome.

Properly mapped: In the paired-end sequencing mode, the percentage of total reads, with both Read1 and Read2 mapping to the genome and corresponding mapping positions consistent with the fragment size distribution of the sequencing library.

Fraction of covered with $\geq 20x$ (%): It refers to the proportion of bases with a coverage depth not less than 20x in the genome.

Fraction of covered with $\geq 0.2 * \text{Mean}$ (%): It refers to the proportion of bases with a coverage depth of no less than 0.2 fold the mean depth of coverage in the genome.

Fraction of CDS regions covered with $\geq 20x$ (%): It refers to the proportion of bases with a coverage depth not less than 20x in the CDS regions.

Table S6. The information on potential off-target site

Pos	Strand	Sequence	Variant_Classification	Variant_type	Ref	Alt	DP	DV	AF	Distance to CDS of gene	Distance
chr8:105379575	+	GCGAGaGTAAaCaacTCCCAGG	intergenic	SNP	G	T	55	3	0.0545	-10678bp to gene:DCSTAMP; +12064bp to DPYS	20

Note:

Pos: The mutation site on chromosome.

Strand: The strand where the off-target sites are located.

Sequence: Sequence of off-target sites.

Variant_Classification: The genome function regions where the mutations occurred.

Variant_type: Variant type (SNP/Indel). SNP, single nucleotide polymorphism.

Ref: The corresponding base in the reference genome (before editing) at this mutation site.

Alt: The mutated base/sequence.

DP: Sequencing depth of the locus.

DV: Sequencing depth of the mutation base.

AF: Proportion of reads carrying variant alleles.

Distance to CDS of gene: The distance between gene and the mutation.

Distance: The distance between the mutation site and the homologous region site, with negative values indicating that the mutation occurred upstream of the homologous site and positive values indicating that the mutation occurred downstream of the homologous site

Table S7. The statistics table of SV.

Group	BND	DEL	DUP	INS	INV	Total
HELP_vs_WT	7	2	0	1	0	10
WT_vs_HELP	6	1	0	0	0	7

Note:

- 1) Group: The first line is in the format case_vs_control, which is the experiment and control groups provided by the project. The second line is in the format control_vs_case. The WT of the project is the untreated HCSCs and HELP-treated HCSCs is the experimental group (case).
- 2) BND: The number of chromosomal translocation breakend variations of samples.
- 3) DEL: The number of large segment deletion variations of samples.
- 4) DUP: The number of tandem duplication variations of samples.
- 5) INS: The number of chromosome segment insertion variations of samples.
- 6) INV: The number of chromosome segment inversion variations of samples.
- 7) Total: Total number of structural variations detected of samples.

Table S8. SV annotation of sample group HELP_vs_WT.

Chrom	POS	FOR MAT	WT	HELP	Somatic Score	SV type	Cyto Band	Gene_ name	Gene count	Function_ Gene	RE_gene	ExAC _delZ	ExAC _dupZ	O MI M_ ID	Gno mAD _pLI	ExAC _pLI	ACMG_ class
chr3	6059 8188	PR:SR	46,0: 44,0	28,2:4 0,3	41	DEL	p14.2	FHIT; MIR54 8BB	2	Intron /exonic	AAGAB (HI=3/morb id/RE=mTL _miRNA);A BHD5 (morbid/RE =mTL_miR NA);.....	0.4458 9193	- 0.5564 19	.	0.005 7055	0.0013 918	3
chr8	4866 2203	PR:SR	15,0: 46,5	31,6	40	DEL	q11.21	.	0	intergenic	3
chr11	1628 828	PR	75,0	31,6	64	BND	p15.5	KRTA P5-3	1	exonic	0.164 38	0.2629 1	.
chr11	5032 5994	PR	62,0	24,0:4 3,8	60	BND	p11.12	.	0	intergenic
chr11	7123 8526	PR	75,0	74,8	48	BND	q13.4	KRTA P5-7	1	exonic	0.090 951	0.5819 6	.
chr16	2103 1742	PR:SR	2,0:1 8,0	51,7	38	INS	p12.3	DNAH 3	1	intron	.	- 2.2534 79	0.8406 6663	.	1.54 E-64	9.63E- 51	.
chr16	3515 7286	PR	62,0	74,8	49	BND	p11.1	.	0	intergenic
chr4	1875 0332 4	PR	45,0	4,0:12, 7	44	BND	q35.2	.	0	intergenic
chr4	1901 1038 8	PR	45,0	51,7	44	BND	q35.2	.	0	intergenic
chrY	9986 510	PR	231,1	199,7	33	BND	p11.2	.	0	intergenic

Note:

Chrom: Name of the chromosome.

POS: The starting site of chromosome of structural variation.

FORMAT: The FORMAT column from a VCF file. PR indicates spanning paired-read support for the ref and alt alleles in the order listed. SR indicates split reads for the ref and alt alleles in the order listed

WT: The support reads of control sample which is shown in the format indicated by column "Format"

HELP: The support reads of case sample which is shown in the format indicated by column "Format".

SomaticScore: Somatic variant quality score.

SV_type: Types of structural variation.

CytoBand: Cytogenic band annotation.

Gene_name: Gene symbol.

Gene_count: Number of overlapped genes with the copy number variation segment.

Function_Gene: The gene function regions where the variant occurred.

RE_gene: Name of the genes regulated by a regulatory element overlapped with the SV to annotate.

ExAC_delZ: Positive delZ_ExAC (Z score) from ExAC indicate gene intolerance to deletion.

ExAC_dupZ: Positive dupZ_ExAC (Z score) from ExAC indicate gene intolerance to duplication.

OMIM_ID: OMIM unique six-digit identifier.

GnomAD_pLI: Score computed by gnomAD indicating the probability that a gene is intolerant to a loss of function variation.

ExAC_pLI: Score computed by ExAC indicating the probability that a gene is intolerant to a loss of function variation. ExAC considers pLI \geq 0.9 as an extremely LoF intolerant gene.

ACMG_class: SV ranking class into 1 of 5: class 1 (benign) class 2 (likely benign) class 3 (variant of uncertain significance) class 4 (likely pathogenic) class 5 (pathogenic).

Table S9. SV annotation of sample group WT_vs_HELP.

Chrom	POS	FOR MAT	HELP	WT	Somati cScore	SV_ type	Cyto Band	Gene_ name	Gene_ count	Function_ Gene	RE_ gene	ExAC delZ	ExAC dupZ	OMI M_ID	GnomAD pLI	ExAC pLI	ACMG_ class
chr5	149029 138	PR:SR	13,0:1 0,0	16,0: 8,5	30	DEL	q32	.	0	intergenic	3
chr10	245005 27	PR:SR	29,0:1 8,1	28,0: 15,6	47	BND	p12.2	KIAA1 217	1	intron	.	1.1721 6141	0.5818 1469	.	0.0002318 5	0.0141 68	.
chr10	589393 51	PR	80,1	61,9	30	BND	q21.1	.	0	intergenic
chr15	478721 83	PR:SR	47,0:6 3,0	48,2: 54,2	34	BND	q21.1	SEMA 6D	1	intron	.	0.5020 9124	- 0.2822 914	.	0.93948	0.9994 7	3
chr3	504788 44	PR:SR	47,0:6 3,0	48,2: 54,2	34	BND	p21.31	CACN A2D2	1	intron	.	1.6857 4942	1.5114 1627	607082	0.99997	0.9996 9	3
chr5	841599 32	PR:SR	29,0:1 8,1	28,0: 15,6	47	BND	q14.3	.	0	intergenic
chr9	123131 688	PR	80,1	61,9	30	BND	q33.2	.	0	intergenic

Table S10. The primers for UL8 and UL29 amplification.

Target sites	gRNA Sequence (5'-3')	Primer names	Sequence (5'-3')
UL8	GGGGCAGCCATACCGGTAA	Y1-F	gagccgtagaatcccgcag
		Y2-R	aaacctaccaaacagaaa
UL29	GCGAGCGTACACGTATCCC	Y3-F	gggtgtagtccgaaaagccaa
		Y4-R	cacgccccaggtaaagtga

Table S11. The quality report of HELP.

Source	OBiO Technology (Shanghai) Corp., Ltd.	Specification	0.25 ml/vial
Test Category	Test	Result	
Quantification	p24 protein content	1.19E+04 ng p24/ml	
Safety	Bacteria	Negative	
	Mycoplasma	Negative	
Conclusion	Qualified		

Table S12. Intraocular bacterial and fungal culture results of patient 2. Gram+ cocci were found in the right eye of patient 2 during the vitrectomy 6 months after PK.

Culture	Presence	Species
Bacteria	+	Gram-positive cocci
Fungus	-	-

Table S13. Blood tests of patient 1. The blood tests of patient 1 showed slight anemia, hypoproteinemia, and diabetes before the injection. We observed no abnormal changes which were related to the injection in these blood tests at 12-month follow-up.

Code	Pre-Injection		Twelve Months Post-Injection		Normal Range	Unit
White blood cell count	5.24		4.39		4.0~10.0	10 ⁹ /L
Red blood cell count	2.71	↓	3.47	↓	4.3~5.8	10 ¹² /L
Hemoglobin	106	↓	122	↓	130~175	g/l
Packed red blood cell volume	30.7	↓	36.9	↓	40~50	%
Red blood cell volume distribution width-coefficient of variation	15.1	↑	15.2	↑	10.0~15.0	%
Red blood cell volume distribution width-standard deviation	62.3	↑	59.8	↑	35.0~50.0	fL
Mean corpuscular volume	113.3	↑	106.3	↑	80.0~100.0	fL
Mean corpuscular hemoglobin	39.1	↑	35.2	↑	27.0~33.0	Pg
Mean corpuscular hemoglobin concentration	345		331		320~360	g/l
Platelet count	175		213		100~400	10 ⁹ /L
Platelet distribution width	9.7		11.1		9.0~17.00	
Thrombocytocrit	0.17		0.22		0.16~0.22	%
Mean platelet volume	9.7		10.2		9.0~16.0	fL
Platelet-larger cell ratio	21.6		25.0		14.0~46.0	%
Percentage of neutrophil	61.6		56.2		50.0~70.0	%
Percentage of lymphocyte	32.1		30.8		20.0~40.0	%
Percentage of eosinophil	1.5		3.0		0.5~5.0	%
Percentage of monocyte	4.4		8.9	↑	3.0~8.0	%
Percentage of basophil	0.4		1.1	↑	0.0~1.0	%
Neutrophil count	3.23		2.47		2.0~7.0	10 ⁹ /L
Lymphocyte count	1.68		1.35		0.8~4.0	10 ⁹ /L
Monocyte count	0.23		0.39		0.10~0.80	10 ⁹ /L
Eosinophil count	0.08		0.13		0.00~0.50	10 ⁹ /L
Basophil count	0.02		0.05		0.00~0.10	10 ⁹ /L
Code	Pre-Injection		Twelve Months Post-Injection		Normal Range	Unit
Alanine aminotransferase	22		31		0~65	u/l
Aspartate aminotransferase	25		30		15~37	u/l
Total protein	67		71		64~82	g/l
Albumin	47		43		35~54	g/l
Globulin	20		28		20~40	g/l
Albumin/globulin	2.4		1.5		1.2~2.5	

γ-Glutamyltransferase	55		37		15~85	u/l
Prealbumin	150	↓	200		200~400	mg/l
Alkaline phosphatase	134		137	↑	50~136	u/l
Blood urea nitrogen	6.8	↑	9.2	↑	2.5~6.4	mmol/l
Creatinine	78		90		53~115	umol/l
Uric acid	0.42	↑	0.38	↑	0.202~0.417	mmol/l
Total bilirubin	10		6		0~17	umol/l
Connect bilirubin	5		2		1~5	umol/l
Total bile acid	14.5	↑	14.4	↑	0.0~10.0	umol/l
High density lipoprotein	1.73		1.86		0.910~2.060	mmol/l
Low density lipoprotein	1.33		2.21		0.00~3.36	mmol/l
Apoprotein A	1.53		1.28		1.100~1.700	g/l
Apoprotein B	0.56	↓	0.76	↓	0.800~1.550	g/l
Apoprotein E	35		38		27~45	mg/l
Lipoprotein small a	25		42		0~300	mg/l
Small dense low density lipoprotein	0.74		1.20		0.26~1.36	mmol/l
Calcium	2.21		2.21		2.04~2.74	mmol/l
Phosphorus	1.24		1.15		0.80~1.60	mmol/l
Potassium	4.6		4.8		3.5~5.4	mmol/l
Sodium	145		143		135~147	mmol/l
Chloride	109	↑	103		96~108	mmol/l
Carbon dioxide binding capacity	22		24		21~32	mmol/l
Lactate dehydrogenase	172		153		81~234	u/l
Creatine kinase	75		95		39~308	u/l
Complement 3c	0.73	↓	0.71	↓	0.9~1.8	g/l
Complement 4	0.20		0.16		0.1~0.4	g/l
Complement 1q	108.7	↓	117.7	↓	159~233	mg/l
Total complement	68.7	↑	62.7	↑	32.5~58.3	u/ml
Haptoglobin	56.50		92.00		32~205	mg/dl
Blood glucose	6.1		6.9	↑	3.9~6.1	mmol/l
Total cholesterol	3.04		4.54		2.80~5.20	mmol/l
Triacylglycerol	0.77		0.70		0.34~2.26	mmol/l
Code	Pre-Injection		Twelve Months Post-Injection		Normal Range	Unit
Prothrombin time	13.7		12.7		11.0~14.5	sec
International normalized ratio	1.03		0.98		0.80~1.20	INR
Activated partial thromboplastin time	35.9		32.6		28~45	s
Thrombin time	16.3		17.2		14.0~21.0	s

Fibrinogen	2.70		3.01		2.00~4.00	g/l
D-Dimer	0.67	↑	0.75	↑	0.00~0.50	ug/ml
Prothrombin time ratio	95		105		70~150	%
Code	Pre-Injection		Twelve Months Post-Injection		Normal Range	Unit
Glycated hemoglobin	6.2	↑	6.2	↑	4.0~6.0	%

*Red font denotes an elevated clinical index than the normal range; pink font denotes a decreased clinical index than the normal range. Similarly hereinafter.

Table S14. Urine tests of patient 1. The pre-injection and twelve months post-injection routine urinalysis of patient 1 was unremarkable.

Code	Pre-Injection	Twelve Months Post-Injection	Normal Range	Unit
Urine glucose	-	-	-	
Ketone body	-	-	-	
Occult blood	-	-	-	
Protein	-	-	-	
Nitrite	-	-	-	
Bilirubin	-	-	-	
Specific gravity	>=1.030 ↑	1.020	1.003~1.030	
Urine PH value	6.0	6.0	5.0~6.5	
Urobilinogen	16	16	3.0~16.0	umol/l
Leukocyte	-	-	-	
White blood cell count	2	2	0~28	/ul
Red blood cell count	1	6	0~17	/ul
Squamous epithelial cells	-	2	0~28	/ul
Non-squamous epithelial cells	-	1	0~6	/ul
Trichomonas	-	-	0~1	/ul
Kidney epithelial cells	-	-	0~6	/ul
Transparent tube	-	-	0~2	/ul
Particle tube	-	-	0~1	/LPF
Cell tube	-	-	0~1	/LPF
Triphosphate crystal	-	-		
Calcium oxalate crystal	-	-		
Leucine crystal	-	-		
Cystine crystals	-	-		

Table S15. Infectious diseases tests of patient 1. The four transfusion-associated contagion tests (hepatitis B, hepatitis C, syphilis, AIDS) of patient 1 were unremarkable.

Code	Pre-Injection	Twelve Months Post-Injection
Hepatitis B virus surface antigen	Negative	Negative
Hepatitis B virus surface antibody	Negative	Negative
Hepatitis B virus e antigen	Negative	Negative
Hepatitis B virus e antibody	Negative	Negative
Hepatitis B virus core antibody	Negative	Negative
Hepatitis B virus antibody-immunoglobulin M	Negative	Negative
Hepatitis B virus pre-S1 antigen	Negative	Negative
Hepatitis C virus antibody	Negative	Negative
Treponema pallidum particle agglutination test	Negative	Negative
Rapid plasma regain test	Negative	Negative
Human immunodeficiency virus antibody	Negative	Negative

Table S16. Blood tests of patient 2. The blood tests of patient 2 indicated mild hyperlipidemia, which had no obvious influence on the implementation of the surgery. We observed no notable changes related to the injection in these blood tests at 12-month follow-up.

Code	Pre-Injection	Twelve Months Post-Injection	Normal Range	Unit
White blood cell count	7.17	10.16 ↑	4.0~10.0	10 ⁹ /L
Red blood cell count	4.73	4.69	4.3~5.8	10 ¹² /L
Hemoglobin	148	144	130~175	g/l
Packed red blood cell volume	44.0	43.1	40~50	%
Red blood cell volume distribution width-coefficient of variation	12.1	12.9	10.0~15.0	%
Red blood cell volume distribution width-standard deviation	41.6	43.1	35.0~50.0	fL
Mean corpuscular volume	93.0	91.9	80.0~100.0	fL
Mean corpuscular hemoglobin	31.3	30.7	27.0~33.0	Pg
Mean corpuscular hemoglobin concentration	336	334	320~360	g/l
Platelet count	229	236	100~400	10 ⁹ /L
Platelet distribution width	9.3	9.8	9.0~17.00	
Thrombocytocrit	0.21	0.22	0.16~0.22	%
Mean platelet volume	9.1	9.2	9.0~16.0	fL
Platelet-larger cell ratio	17.7	18.4	14.0~46.0	%
Percentage of neutrophil	64.3	77.8 ↑	50.0~70.0	%
Percentage of lymphocyte	28.7	18.3 ↓	20.0~40.0	%
Percentage of eosinophil	1.0	0.3 ↓	0.5~5.0	%
Percentage of monocyte	5.6	3.1	3.0~8.0	%
Percentage of basophil	0.4	0.5	0.0~1.0	%
Neutrophil count	4.61	7.9 ↑	2.0~7.0	10 ⁹ /L
Lymphocyte count	2.06	1.86	0.8~4.0	10 ⁹ /L
Monocyte count	0.40	0.32	0.10~0.80	10 ⁹ /L
Eosinophil count	0.07	0.03	0.00~0.50	10 ⁹ /L
Basophil count	0.03	0.05	0.00~0.10	10 ⁹ /L
Code	Pre-Injection	Twelve Months Post-Injection	Normal Range	Unit
Alanine aminotransferase	17	19	0~65	u/l
Aspartate aminotransferase	17	15	15~37	u/l
Total protein	70	68	64~82	g/l
Albumin	46	42	35~54	g/l
Globulin	24	26	20~40	g/l
Albumin/globulin	1.9	1.6	1.2~2.5	

γ-Glutamyltransferase	33		37		15~85	u/l
Prealbumin	320		350		200~400	mg/l
Alkaline phosphatase	71		80		50~136	u/l
Blood urea nitrogen	5.5		7.5	↑	2.5~6.4	mmol/l
Creatinine	69		62		53~115	umol/l
Uric acid	0.25		0.32		0.202~0.417	mmol/l
Total bilirubin	16		10		0~17	umol/l
Connect bilirubin	5		2		1~5	umol/l
Total bile acid	2.5		11.2	↑	0.0~10.0	umol/l
High density lipoprotein	1.24		1.61		0.910~2.060	mmol/l
Low density lipoprotein	4.36	↑	4.72	↑	0.00~3.36	mmol/l
Apoprotein A	1.46		1.24		1.100~1.700	g/l
Apoprotein B	1.51		1.55		0.800~1.550	g/l
Apoprotein E	52	↑	46	↑	27~45	mg/l
Lipoprotein small a	41		47		0~75	nmol/l
Small dense low density lipoprotein	3.11	↑	2.70	↑	0.26~1.36	mmol/l
Calcium	2.34		2.25		2.04~2.74	mmol/l
Phosphorus	1.18		0.99		0.80~1.60	mmol/l
Potassium	4.2		4.0		3.5~5.4	mmol/l
Sodium	140		142		135~147	mmol/l
Chloride	104		101		96~108	mmol/l
Carbon dioxide binding capacity	23		21		21~32	mmol/l
Lactate dehydrogenase	168		182		81~234	u/l
Creatine kinase	122		128		39~308	u/l
Complement 3c	1.03		1.04		0.9~1.8	g/l
Complement 4	0.20		0.32		0.1~0.4	g/l
Complement 1q	154.5	↓	169.4		159~233	mg/l
Total complement	67.9	↑	63.5	↑	32.5~58.3	u/ml
Haptoglobin	93.30		110.50		32~205	mg/dl
Blood glucose	5.6		6.1		3.9~6.1	mmol/l
Total cholesterol	6.12	↑	7.04	↑	2.80~5.20	mmol/l
Triacylglycerol	2.33	↑	1.81		0.34~2.26	mmol/l
Code		Pre-Injection		Twelve Months Post-Injection	Normal Range	Unit
Prothrombin time	13.3		12.4		11.0~14.5	sec
International normalized ratio	0.99		0.95		0.80~1.20	INR
Activated partial thromboplastin time	35.3		33.0		28~45	s
Thrombin time	18.7		19.7		14.0~21.0	s

Fibrinogen	2.98	2.74	2.00~4.00	g/l
D-Dimer	0.24	0.23	0.00~0.50	ug/ml
Prothrombin time ratio	102	110	70~150	%
Code	Pre-Injection	Twelve Months Post-Injection	Normal Range	Unit
Glycated hemoglobin	5.9	5.9	4.0~6.0	%

Table S17. Routine urine test of patient 2. The routine urinalysis of patient 2 was unremarkable.

Code	Pre-Injection	Twelve Months Post-Injection	Normal Range	Unit
Urine glucose	-	-	-	
Ketone body	-	-	-	
Occult blood	-	-	-	
Protein	-	-	-	
Nitrite	-	-	-	
Bilirubin	-	-	-	
Specific gravity	>=1.030 ↑	1.025	1.003~1.030	
Urine PH value	5.5	6.0	5.0~6.5	
Urobilinogen	3.2	16	3.0~16.0	umol/l
Leukocyte	-	-	-	
White blood cell count	6	6	0~28	/ul
Red blood cell count	2	2	0~17	/ul
Squamous epithelial cells	2	1	0~28	/ul
Non-squamous epithelial cells	-	1	0~6	/ul
Trichomonas	-	-	0~1	/ul
Kidney epithelial cells	-	-	0~6	/ul
Transparent tube	-	-	0~2	/ul
Particle tube	-	-	0~1	/LPF
Cell tube	-	-	0~1	/LPF
Triphosphate crystal	-	-		
Calcium oxalate crystal	-	-		
Leucine crystal	-	-		
Cystine crystals	-	-		

Table S18. Transfusion-associated contagion tests of patient 2. The contagion tests of patient 2 showed specific antibodies to the hepatitis B virus. The other three transfusion-associated contagion tests (hepatitis C, syphilis, AIDS) were negative.

Code	Pre-Injection	Twelve Months Post-Injection
Hepatitis B virus surface antigen	Negative	Negative
Hepatitis B virus surface antibody	Weak Positive	Weak Positive
Hepatitis B virus e antigen	Negative	Negative
Hepatitis B virus e antibody	Negative	Negative
Hepatitis B virus core antibody	Positive	Positive
Hepatitis B virus antibody-immunoglobulin M	Negative	Negative
Hepatitis B virus pre-S1 antigen	Negative	Negative
Hepatitis C virus antibody	Negative	Negative
Treponema pallidum particle agglutination test	Negative	Negative
Rapid plasma regain test	Negative	Negative
Human immunodeficiency virus antibody	Negative	Negative

Table S19. Blood tests of patient 3. The blood tests of patient 3 indicated mild hyperlipidemia, which had no obvious influence on the implementation of the surgery.

Code	Pre-Injection	Six Months Post-Injection	Normal Range	Unit
White blood cell count	5.45	4.83	4.0~10.0	10 ⁹ /L
Red blood cell count	5.28	4.89	4.3~5.8	10 ¹² /L
Hemoglobin	159	152	130~175	g/l
Packed red blood cell volume	46.1	42.8	40~50	%
Red blood cell volume distribution width-coefficient of variation	11.9	12.4	10.0~15.0	%
Red blood cell volume distribution width-standard deviation	37.6	39.0	35.0~50.0	fL
Mean corpuscular volume	87.3	87.5	80.0~100.0	fL
Mean corpuscular hemoglobin	30.1	31.1	27.0~33.0	Pg
Mean corpuscular hemoglobin concentration	345	355	320~360	g/l
Platelet count	151	105	100~400	10 ⁹ /L
Platelet distribution width	10.8	12.2	9.0~17.00	
Thrombocytocrit	0.14 ↓	0.11 ↓	0.16~0.22	%
Mean platelet volume	9.5	10.7	9.0~16.0	fL
Platelet-larger cell ratio	21.5	30.8	14.0~46.0	%
Percentage of neutrophil	62.3	57.7	50.0~70.0	%
Percentage of lymphocyte	29.7	32.4	20.0~40.0	%
Percentage of eosinophil	1.7	2.3	0.5~5.0	%
Percentage of monocyte	5.9	7.3	3.0~8.0	%
Percentage of basophil	0.4	0.3	0.0~1.0	%
Neutrophil count	3.40	2.21	2.0~7.0	10 ⁹ /L
Lymphocyte count	1.62	1.24	0.8~4.0	10 ⁹ /L
Monocyte count	0.32	0.28	0.10~0.80	10 ⁹ /L
Eosinophil count	0.09	0.09	0.00~0.50	10 ⁹ /L
Basophil count	0.02	0.01	0.00~0.10	10 ⁹ /L
Code	Pre-Injection	Six Months Post-Injection	Normal Range	Unit
Alanine aminotransferase	29	53	0~65	u/l
Aspartate aminotransferase	18	26	15~37	u/l
Total protein	76	65	64~82	g/l
Albumin	49	40	35~54	g/l
Globulin	27	24	20~40	g/l
Albumin/globulin	1.8	1.66	1.2~2.5	
γ-Glutamyltransferase	37	49	15~85	u/l

Prealbumin	350		310		200~400	mg/l	
Alkaline phosphatase	95		103		50~136	u/l	
Blood urea nitrogen	6.6	↑	5.6		2.5~6.4	mmol/l	
Creatinine	78		77		53~115	umol/l	
Uric acid	0.32		0.37		0.202~0.417	mmol/l	
Total bilirubin	16		16		0~17	umol/l	
Connect bilirubin	7	↑	3		1~5	umol/l	
Total bile acid	6		2		0.0~10.0	umol/l	
High density lipoprotein	1.16		0.84	↓	0.910~2.060	mmol/l	
Low density lipoprotein	2.79		2.24		0.00~3.36	mmol/l	
Apoprotein A	1.29		1.00	↓	1.100~1.700	g/l	
Apoprotein B	1.000		0.800		0.800~1.550	g/l	
Apoprotein E	39		35		27~45	mg/l	
Lipoprotein small a	38		42		0~75	nmol/l	
Small dense low density lipoprotein	1.90	↑	1.87	↑	0.26~1.36	mmol/l	
Calcium	2.32		2.32		2.04~2.74	mmol/l	
Phosphorus	0.97		1.23		0.80~1.60	mmol/l	
Potassium	4.3		4.4		3.5~5.4	mmol/l	
Sodium	140		139		135~147	mmol/l	
Chloride	102		105		96~108	mmol/l	
Carbon dioxide binding capacity	26		23		21~32	mmol/l	
Lactate dehydrogenase	149		175		81~234	u/l	
Creatine kinase	75		98		39~308	u/l	
Complement 3c	1.07		1.12		0.9~1.8	g/l	
Complement 4	0.31		0.29		0.1~0.4	g/l	
Complement 1q	195.5		210.4		159~233	mg/l	
Total complement	82.5	↑	84.7	↑	32.5~58.3	u/ml	
Haptoglobin	86.50		98.20		32~205	mg/dl	
Blood glucose	5.7		4.7		3.9~6.1	mmol/l	
Total cholesterol	4.36		3.68		2.80~5.20	mmol/l	
Triacylglycerol	1.23		2.24		0.34~2.26	mmol/l	
Code			Pre-Injection		Six Months Post-Injection	Normal Range	Unit
Prothrombin time	13.3		11.1		11.0~14.5	sec	
International normalized ratio	1.00		0.94		0.80~1.20	INR	
Activated partial thromboplastin time	37.7		32.8		28~45	s	
Thrombin time	18.0		16.8		14.0~21.0	s	
Fibrinogen	3.43		2.72		2.00~4.00	g/l	

D-Dimer	0.28	0.31	0.00~0.50	ug/ml
Prothrombin time ratio	99	97	70~150	%
Code	Pre-Injection	Six Months Post-Injection	Normal Range	Unit
Glycated hemoglobin	5.3	4.89	4.0~6.0	%

Table S20. Routine urine test of patient 3. The routine urinalysis of patient 3 was unremarkable.

Code	Pre-Injection Results	Normal Range	Unit
Urine glucose	-	-	
Ketone body	-	-	
Occult blood	-	-	
Protein	-	-	
Nitrite	-	-	
Bilirubin	-	-	
Specific gravity	>=1.030 ↑	1.003~1.030	
Urine PH value	7.0 ↑	5.0~6.5	
Urobilinogen	3.2	3.0~16.0	umol/l
Leukocyte	-	-	
White blood cell count	1	0~28	/ul
Red blood cell count	1	0~17	/ul
Squamous epithelial cells	-	0~28	/ul
Non-squamous epithelial cells	-	0~6	/ul
Trichomonas	-	0~1	/ul
Kidney epithelial cells	-	0~6	/ul
Transparent tube	-	0~2	/ul
Particle tube	-	0~1	/LPF
Cell tube	-	0~1	/LPF
Triphosphate crystal	-		
Calcium oxalate crystal	-		
Leucine crystal	-		
Cystine crystals	-		

Table S21. Transfusion-associated contagion tests of patient 3. The contagion tests of patient 3 showed specific antibodies to the hepatitis B virus. The other three transfusion-associated contagion tests (hepatitis C, syphilis, AIDS) were negative.

Code	Pre-Injection Results
Hepatitis B virus surface antigen	Negative
Hepatitis B virus surface antibody	Positive
Hepatitis B virus e antigen	Negative
Hepatitis B virus e antibody	Positive
Hepatitis B virus core antibody	Positive
Hepatitis B virus antibody-immunoglobulin M	Negative
Hepatitis B virus pre-S1 antigen	Negative
Hepatitis C virus antibody	Negative
Treponema pallidum particle agglutination test	Negative
Rapid plasma regain test	Negative
Human immunodeficiency virus antibody	Negative

Video S1. HELP Administration method. Each formulation, 0.2 mL in total, was drawn into a 27g ophthalmic syringe for the intrastromal injection. Penetrating keratoplasty was performed following the routine procedures. After sewing up the donor cornea, the graft bed of the recipient was injected with the HELP formulation in 6-8 locations.

Supplemental Results of Whole Genome Sequencing (WGS)

The sequencing depth of sequencing data of the two samples (HELP-treated group and WT group) was sufficient (62x and 64x, respectively) with good sequencing quality (Q30 > 90%) (Table S4). After sequence alignment, the results showed that mapping rate to human genome (hg19) was greater than 92%, and the fraction of covered with $\geq 20x$ and $0.2 * \text{Mean}$ were greater than 97%. The fraction of CDS regions covered with $\geq 20x$ was greater than 98%. These results indicating a good quality of the sequencing data (Table S5).

The analysis of off-target sites showed that there were few potential off-target sites. In the HELP-treated cells, no potential off-target sites of UL8 sgRNA were identified, and one potential off-target site of UL29 sgRNA was identified, which was a SNP located at chr8:105,379,595 in the intergenic region and far from CDS (>10K) with low mutation frequency of 0.0545 (Table S6).

Structural variants (SVs) analysis revealed ten SVs in the HELP-treated HCSCs sample after filtering out the data of untreated HCSCs sample (WT sample), and seven SVs in the WT sample after filtering out the data of HELP-treated HCSCs sample. All the structural variants have low risk of affecting the gene function and causing pathogenicity (Table S7-9). Considering the structural variants result, it is presumed that these SVs probably occur due to the nature of the cells rather than HELP treatment.